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(54) **Single nucleotide polymorphisms associated with susceptibiliy to cardiovascular disease**

(57) The present invention provides SNPs, polymorphic variants, and haplotypes associated with cardiovascular disease. The invention also provides methods for detecting the SNPs, polymorphic variants, and haplotypes. The invention also provides methods for determining an individual's genotype with respect to one or more polymorphisms and/or haplotypes associated with cardiovascular disease. The invention further provides methods of determining whether an individual has or is susceptible to development or occurrence of a cardiovascular disease or event. The methods are useful for providing diagnostic and/or prognostic information, selecting therapeutic regimens, etc. The invention further provides reagents and kits for practicing the methods.

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Description

Description of Compact Disk

[0001] A compact disk containing Tables 1 and 2 is provided and its contents are part of this specification, incorporated herein by reference in its entirety. Tables 1 and 2 are text files saved in Unicode tab-delimited format. The contents of Tables 1 and 2 are described in detail below.

Background of the Invention

[0002] Cardiovascular diseases and conditions are a major cause of morbidity and mortality throughout the world. These diseases and conditions include, but are not limited to, the various disorders of the heart and the vascular system typically referred to as myocardial infarction (heart attack), atherosclerosis, ischemic heart disease, coronary artery disease, congestive heart failure, atrial and ventricular arrhythmias, hypertensive vascular diseases, and peripheral vascular diseases.

[0003] Atherosclerosis is a principal causative agent of heart attack and stroke. Atherosclerosis is a complex disease involving many cell types and molecular factors (for a detailed review, see Ross, Nature 362: 801-809, 1993; and Lusis, A. J., Nature 407, 233-241, 2000). The process involves the formation of fibrofatty and fibrous lesions or plaques in the vessel wall, preceded and accompanied by inflammation. Such plaques can partially or fully occlude the blood vessel concerned and thus restrict the flow of blood, resulting in ischemia. Ischemia is a general term that refers to a condition characterized by inadequate blood flow to an area of the body such as an organ or tissue, resulting in an insufficient oxygen supply. Ischemia is most frequently caused by a narrowing or complete obstruction of the arteries and may occur in any organ or tissue. The most common cause of ischemia in the heart is atherosclerotic disease of the coronary arteries, also referred to as coronary heart disease or coronary artery disease. By reducing the lumen of these vessels, atherosclerosis causes an absolute decrease in myocardial perfusion in the basal state and/or limits appropriate increases in perfusion when the demand for flow is augmented. Coronary blood flow can also be limited by arterial thrombi, spasm, and, rarely, coronary emboli, as well as by ostial narrowing due to luetic aortitis. Myocardial ischemia can also occur if myocardial oxygen demands are abnormally increased, as in severe ventricular hypertrophy due to hypertension or aortic stenosis. Severe and prolonged myocardial ischemia can lead to myocardial infarction. The triggering event for a myocardial infarction is often the rupture of an atherosclerotic plaque, leading to a blood clot that causes a sudden decrease in vessel lumen.

[0004] Approximately half of all first myocardial infarctions are fatal. Furthermore, in many instances coronary heart disease develops silently, and there may be no warning symptoms, such as chest pain, prior to onset of the heart attack. The development of effective strategies to prevent coronary artery disease and to inhibit its progression is therefore of considerable importance.

[0005] A number of approaches are currently employed for the treatment and/or prevention of cardiovascular diseases, e.g., atherosclerosis and coronary artery disease. Pharmaceutically based therapies include lipid lowering agents (e.g., statins), aspirin and other anti-platelet agents, and anti-hypertensive medications. Lifestyle modification also plays an important role since it is known that factors such as smoking, obesity, and a high fat diet increase the risk of myocardial infarction.

[0006] It is thought that genetic factors contribute to the development of atherosclerosis and coronary artery disease (Scheuner, MT, Genet Med. Jul-Aug;5(4):269-85, 2003). An individual's genetic makeup is therefore a significant determinant of the likelihood that he or she will suffer a myocardial infarction, particularly at a young age. However, while a "family history" of heart disease is a significant risk factor, many heart attack victims lack such a family history and, conversely, not all individuals with such a family history do indeed develop the disease. Thus the nature of the genetic contribution to cardiovascular disease is unclear.

[0007] There is a need in the art for methods and accompanying reagents that can be used to better assess an individual's susceptibility of developing cardiovascular disease. The need for such methods and reagents is especially acute in view of the fact that, atherosclerosis frequently remains clinically silent in its early stages and yet is often evident at post-mortem examination even among individuals in their teens and twenties (McGill, H.C. Jr & McMahan, C.A., Am. J. Cardiol., 82, 30T-36T, 1998).

Summary of the Invention

[0008] The present invention is based at least in part on the identification of single nucleotide polymorphisms (SNPs) that are informative with respect to cardiovascular disease. In particular, the invention is based in part on the discovery that particular polymorphic variants of the polymorphic sites at which these SNPs are located are associated with an increased risk of cardiovascular disease, e.g., acute coronary events such as myocardial infarction. In certain aspects,

the invention provides methods for genotyping an individual comprising steps of: providing a sample obtained from an individual in need of testing for presence of or susceptibility to a cardiovascular disease and detecting a polymorphic variant of a polymorphism listed in the column entitled "dbSNP_RS_ID" in Table 1. In certain aspects, the invention provides methods for genotyping an individual comprising steps of: providing a sample obtained from an individual in need of testing for presence of or susceptibility to a cardiovascular disease and detecting a polymorphic variant of two or more polymorphisms listed in the column entitled "dbSNP_RS_ID" in Table 1 and/or the column entitled "dbSNP_RS_ID" in Table 2.

[0009] In certain embodiments, the invention provides methods for testing the presence of a polymorphism in the sequences of a gene listed in Table 1. In certain embodiments, the invention provides methods for testing the presence of a polymorphism in the sequences of two or more genes listed in Table 1 and/or Table 2. In certain embodiments, the invention provides methods for demonstrating a link between particular allelic variants of the polymorphisms listed in Table 1 and/or Table 2 and a susceptibility to cardiovascular disease by showing that allele frequencies at the polymorphic sites differ significantly among individuals who suffered a myocardial infarction at an early age (< 50 years of age) as compared to individuals who did not suffer a myocardial infarction but had a similar pattern of classical risk factors. An individual having a particular allelic variant or combination of allelic variants, e.g., having a particular genotype with respect to one or more allelic variants is considered to have "susceptibility to cardiovascular disease" if (i) the individual is more likely to develop a cardiovascular disease or manifest a symptom or sign of cardiovascular disease than a comparable individual having a different genotype with respect to those allelic variant(s), wherein the comparable individual is otherwise similar with respect to one or more (e.g., all) of the classical CVD risk factors, and/or (ii) the individual is more likely to develop a cardiovascular disease or manifest a symptom or sign of cardiovascular disease than an individual of a similar age (e.g., up to 5 years older or younger) and the same sex but having a different genotype with respect to those allelic variant(s). It will be appreciated that various cardiovascular diseases are interrelated, and the existence of a particular cardiovascular disease or condition may contribute to the development of other(s). For example, an individual who has suffered a myocardial infarction ("MI") may have an increased risk of having a cardiac arrhythmia and may have an increased risk of heart failure.

[0010] In certain aspects, the invention provides methods of diagnosing cardiovascular disease or susceptibility to development of cardiovascular disease in an individual, said method comprising determining one, more than one, or all genotypes in said individual of the polymorphisms listed in Table 1 and/or Table 2.

[0011] In certain aspects, the invention provides a variety of reagents and kits for use in detecting a polymorphic variant of a polymorphism listed in Table 1 and/or Table 2.

[0012] The invention encompasses the recognition that the ability to classify individuals who are at increased risk of myocardial infarction on the basis of their genotype allows the establishment of a correlation between genotype and response to particular therapeutic regimens.

[0013] The invention also encompasses the recognition that an integrated assessment of an individual's risk, and/or an integrated assessment of the appropriate therapeutic regimen for a particular individual, can include an assessment of both genetic and of non-genetic factors, which can be combined in a variety of different ways. The availability of methods and reagents for evaluating the genetic factors associated with cardiovascular disease allows a more accurate assessment of whether an individual would benefit from various therapeutic interventions such as administration of particular pharmaceutical agents and/or encouragement of particular lifestyle modifications.

[0014] This application refers to various patents, patent applications, journal articles, and other publications, all of which are incorporated herein by reference. In addition, the following standard reference works are incorporated herein by reference: Ausubel, F., (ed.), Current Protocols in Molecular Biology, Current Protocols in Immunology, Current Protocols in Protein Science, and Current Protocols in Cell Biology, John Wiley & Sons, N.Y., edition as of July 2002; Sambrook, Russell, and Sambrook, Molecular Cloning: A Laboratory Manual, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 2001; Harlow, E., et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hardman, J., Limbird. E., Gilman, A. (Eds.), Braunwald, E., Zipes, D.P., and Libby, P. (eds.) Heart Disease: A Textbook of Cardiovascular Medicine. W B Saunders; 6th edition (February 15, 2001); Chien, K.R., Molecular Basis of Cardiovascular Disease: A Companion to Braunwald's Heart Disease, W B Saunders; Revised edition (2003); and Goodman and Gilman's The Pharmacological Basis of Therapeutics, 10th Ed.McGraw Hill, 2001 (referred to herein as *Goodman and Gilman*). In the event of a conflict or inconsistency between any of the incorporated references and the instant specification or the understanding of one or ordinary skill in the art, the specification shall control, it being understood that the determination of whether a conflict or inconsistency exists is within the discretion of the inventors and can be made at any time.

Brief Description of the Drawing

[0015] Figure 1 presents characteristic group statistics of individuals (study subjects) that were studied to identify SNPs and polymorphic variants associated with cardiovascular disease classified according to the number of subjects

in different PROCAM risk categories. The column labeled "PROCAM" refers to controls, and the column entitled "MI-Patients" refers to cases. Mean and standard deviation values of PROCAM and MI-patients are shown in the right two columns.

[0016] Figure 2 presents characteristics of individuals (study subjects) that were studied to identify SNPs and polymorphic variants associated with cardiovascular disease. The column labeled "PROCAM" refers to controls, and the column entitled "MI-Patients" refers to cases. The average values for various PROCAM risk factors and the overall average PROCAM score are provided. The percentage of each group exhibiting the particular risk factor is shown.

[0017] Figure 3 presents risk profiles of individuals (study subjects) that were studied to identify SNPs and polymorphic variants associated with cardiovascular disease. The column labeled "PROCAM" refers to controls, and the column entitled "MI-Patients" refers to cases.

Definitions

[0018] For purposes of convenience, definitions of a variety of terms used herein are presented below.

[0019] The term "allele" which is used interchangeably herein with the term "allelic variant" refers to alternative forms of a gene or a portion thereof. Alleles occupy the same locus or position on homologous chromosomes. When an individual has two identical alleles of a gene, the individual is said to be homozygous for the gene or allele. When an individual has two different alleles of a gene, the individual is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide or in a plurality nucleotides, and can include substitutions, deletions, and/or insertions of nucleotides with respect to each other. An allele of a gene can also be a form of a gene containing a mutation.

[0020] While the terms "allele" and "allelic variant" have traditionally been applied in the context of genes, which can include a plurality of polymorphic sites, the term is also used herein to apply to any form of a genomic DNA sequence, which can be as small as a single nucleotide and may or may not fall within a gene. Thus each polymorphic variant of a polymorphic site is considered an allele, and when referring to single nucleotide polymorphisms, the terms "polymorphic variant" and "allele" are used interchangeably herein. An "allele frequency" refers to the frequency at which a particular polymorphic variant, or allele, occurs in a population being tested, e.g., in cases or controls in an association study.

[0021] The term "allelic variant of a polymorphic region of a gene" refers to a region of a gene having one of several nucleotide sequences found in that region of the gene in different individuals in a population.

[0022] "Antibody", as used herein, refers to an immunoglobulin that binds to an antigen. An antibody may be natural or wholly or partially synthetically produced. An antibody may be derived from natural sources, e.g., purified from an animal such as a rodent, rabbit, or chicken, that has been immunized with an antigen or a construct that encodes the antigen. An antibody may be a member of any immunoglobulin class, including any of the human classes: IgG, IgM, IgA, IgD, and IgE. The antibody may be an antibody fragment such as an Fab', $F(ab')_2$, scFv (single-chain variable) or other fragment that retains an antigen binding site, or a recombinantly produced scFv fragment, including recombinantly produced fragments that comprise an immunoglobulin antigen binding domain. See, e.g., Allen, T., Nature Reviews Cancer, Vol.2, 750-765, 2002, and references therein. Antibody fragments which contain the antigen binding site of the antibody molecule can be generated by known techniques. For example, $F(ab')_2$ fragments can be produced by pepsin digestion of the antibody molecule, Fab' fragment by reducing the disulfide bridges of the $F(ab')_2$ fragment, or by treating the antibody molecule with papain and a reducing agent.

[0023] Antibodies, antibody fragments, and/or protein domains comprising an antigen binding site may be generated and/or selected *in vitro,* e.g., using techniques such as phage display (Winter, G. et al., Annu. Rev. Immunol. 12:433-455, 1994,1994), ribosome display (Hanes, J., and Pluckthun, A. Proc. Natl. Acad. Sci. USA. 94:4937-4942, 1997), etc. An antibody may be polyclonal (e.g., an affinity-purified polyclonal antibody) or monoclonal.

[0024] An antibody may be a "chimeric" antibody in which for example, a variable domain of rodent origin is fused to a constant domain of human origin, thus retaining the specificity of the rodent antibody. The domain of human origin need not originate directly from a human in the sense that it is first synthesized in a human being. Instead, "human" domains may be generated in rodents whose genome incorporates human immunoglobulin genes. Such an antibody is considered at least partially "humanized". The degree to which an antibody is "humanized" can vary. Thus part or most of the variable domain of a rodent antibody may be replaced by human sequences. For example, according to one approach murine complementarity-determining regions (CDRs) are grafted onto the variable light (VL) and variable heavy (VH) frameworks of human immunoglobulin molecules, while retaining only those murine framework residues deemed essential for the integrity of the antigen-binding site. See Gonzales NR, Tumour Biol. Jan-Feb;26(1):31-43, 2005 for a review of various methods of minimizing antigenicity of a monoclonal antibody. Such human or humanized chimeric antibodies are often advantageous for use in therapy of human diseases or disorders, since the human or humanized antibodies are much less likely than to induce an immune response.

[0025] The terms "approximately" or "about" in reference to a number are generally include numbers that fall within a range of 5% in either direction (greater than or less than) of the number unless otherwise stated or otherwise evident

from the context (except where such number would exceed 100% of a possible value).

[0026] "Classical CVD risk factors" as used herein, refer to 5 continuous variables (age, LDL cholesterol, HDL cholesterol, triglyceride (TG) level, and systolic blood pressure) and 3 discrete variables (smoking status, diabetes, and MI in family history), as described in Assmann, G., et al., Circulation, 105:310, 2002. In general, higher values for age, LDL, TG, systolic blood pressure), correlate with an increased risk of developing CVD and/or experiencing a major coronary event, while lower value for HDL correlates with a decreased risk. Smoking, diabetes, and MI in family history each correlates with an increased risk of developing CVD and/or experiencing a major coronary event. These risk factors were used to develop the PROCAM scoring system, which predicts the likelihood that an individual will experience a major coronary event within a defined period of time, e.g., within 10 years. One of ordinary skill in the art will recognize that alternative risk factors and scoring systems could be developed. One of ordinary skill in the art will also recognize that approximations and substitutions may be made to the aforesaid classical risk factors. For example, in some embodiments total cholesterol level could be used. The risk factors may also be augmented, e.g., to include measurements of diastolic blood pressure, measurements of blood level of C reactive protein, the effect of any particular therapeutic regimen the individual is following, and various cardiovascular status markers.

[0027] The term "complementary" is used herein in accordance with its art-accepted meaning to refer to the capacity for precise pairing between particular bases, nucleosides, nucleotides or nucleic acids. For example, adenine (A) and uracil (U) are complementary; adenine (A) and thymine (T) are complementary; and guanine (G) and cytosine (C), are complementary and are referred to in the art as Watson-Crick base pairings. If a nucleotide at a certain position of a first nucleic acid sequence is complementary to a nucleotide located opposite in a second nucleic acid sequence, the nucleotides form a complementary base pair, and the nucleic acids are complementary at that position. A percent complementarity of two nucleic acids within a window of evaluation may be evaluated by determining the total number of nucleotides in both strands that form complementary base pairs within the window, dividing by the total number of nucleotides within the window, and multiplying by 100. The two nucleic acids are aligned in anti-parallel orientation for maximum complementarity over the window, allowing introduction of gaps. When computing the number of complementary nucleotides needed to achieve a particular % complementarity, fractions are rounded to the nearest whole number. A position occupied by non-complementary nucleotides constitutes a mismatch. A nucleic acid that is 100% complementary to another nucleic acid is said to be its "complement". Thus a nucleic acid that is 100% complementary to its complement will base pair without a single mismatch. It is to be understood that where the invention provides a nucleic acid, the complement of the nucleic acid is also provided.

[0028] As used herein, "diagnostic information" is any information that is useful in determining whether a patient has or is susceptible to developing a disease or condition and/or in classifying the disease or condition into a phenotypic category or any category having significance with regards to the prognosis or severity of the disease or condition, or likely response to treatment (either treatment in general or any particular treatment) of the disease or condition. Diagnostic information can include, e.g., an assessment of the likelihood that an individual will develop a cardiovascular disease and/or will suffer a major coronary event within a defined time period, e.g., 10 years. "Diagnosis" refers to providing any type of diagnostic information, including, but not limited to, whether a subject has or is likely to have a condition (such as a cardiovascular disease), information related to the nature or classification of a disease, information related to prognosis and/or information useful in selecting an appropriate therapeutic regimen.

[0029] The term "gene", as used herein, has its meaning as understood in the art. In most cases, a gene as used herein comprises a nucleic acid sequence that encodes a polypeptide and can also include regulatory sequences (e.g., promoters, enhancers, etc.) and/or intron sequences. It will be appreciated that a "gene" can also refer to a nucleic acid that does not encode a protein but rather encodes a functional RNA molecule such as an rRNA, tRNA, etc.

[0030] A "gene product" or "expression product" is an RNA transcribed from the gene (e.g., either pre- or post-processing) or a polypeptide encoded by an RNA transcribed from the gene (e.g., either pre- or post-modification). RNA transcribed from a gene or polynucleotide is said to be encoded by the gene or polynucleotide.

[0031] "Genotype" refers to the identity of one or more allelic variants at one or more particular polymorphic positions in an individual. It will be appreciated that an individual's genome will contain two allelic variants for each polymorphic position (located on homologous chromosomes). The allelic variants can be the same or different. A genotype can include the identity of either or both of the allelic variants. A genotype can include the identities of allelic variants at multiple different polymorphic positions, which may or may not be located within a single gene. A genotype can also refer to the identity of an allele of a gene at a particular gene locus in an individual and can include the identity of either or both alleles. The identity of the allele of a gene may include the identity of the polymorphic variants that exist at multiple polymorphic sites within the gene. The identity of an allelic variant or an allele of a gene refers to the sequence of the allelic variant or allele of a gene, e.g., the identity of the nucleotide present at a polymorphic position or the identities of nucleotides present at each of the polymorphic positions in a gene. It will be appreciated that the identity need not be provided in terms of the sequence itself. For example, it is typical to assign identifiers such as +, -, A, a, B, b, etc., to different allelic variants or alleles for descriptive purposes. Any suitable identifier can be used. "Genotyping" an individual refers to providing the genotype of the individual with respect to one or more allelic variants or alleles.

[0032] "Haplotype" refers to the particular combinations of polymorphic variants (alleles) observed in a population at polymorphic sites on a single chromosome or within a region of a single chromosome. The polymorphic variants that constitute a haplotype are in linkage disequilibrium and thus tend to be inherited together.

[0033] A "haplotype block" is a region of the genome over which there is little evidence for historical recombination and within which only a few common haplotypes are observed. Haplotype blocks can vary in size and are separated by sites at which recombination can be inferred. Haplotype blocks are described e.g., in Gabriel, S.B., et al., Science, 296:2225-2229, 2002; Daly, M.J., et al., Nature Genetics, 29: 229-232, 2001; Reich, D.E., et al., Nature, 411: 199-204.

[0034] "Identity" refers to the extent to which the sequence of two or more nucleic acids is the same. The percent identity between first and second nucleic acids over a window of evaluation may be computed by aligning the nucleic acids, determining the number of nucleotides within the window of evaluation that are opposite an identical nucleotide allowing the introduction of gaps to maximize identity, dividing by the total number of nucleotides in the window, and multiplying by 100. When computing the number of identical nucleotides needed to achieve a particular % identity, fractions are to be rounded to the nearest whole number. When two or more sequences are compared, any of them may be considered the reference sequence.

[0035] Percent identity can be calculated using a variety of computer programs known in the art. For example, computer programs such as BLASTN, BLASTP, Gapped BLAST, etc., generate alignments and provide % identity between a sequence of interest and sequences in any of a variety of public databases. The algorithm of Karlin and Altschul (Karlin and Altschul, Proc. Natl. Acad. Sci. USA 87:22264-2268, 1990) modified as in Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873-5877,1993 is incorporated into the NBLAST and XBLAST programs of Altschul et al. (Altschul, et al., J. Mol. Biol. 215:403-410, 1990). To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Altschul, et al. Nucleic Acids Res. 25: 3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, default parameters of the respective programs may be used. Alternatively, the practitioner may use non-default parameters depending on his or her experimental and/or other requirements. See the Web site having URL www.ncbi.nlm.nih.gov. A PAM250 or BLOSUM62 matrix may be used.

[0036] "Individual" means any human being.

[0037] The term "isolated" means 1) separated from at least some of the components with which it is usually associated in nature; 2) prepared or purified by a process that involves the hand of man; and/or 3) not occurring in nature. An isolated nucleic acid, such as DNA or RNA, is typically separated from other DNAs or RNAs, respectively, that are present in the natural or original source of the macromolecule. An isolated polypeptide is typically separated from other polypeptides, respectively, that are present in the natural or original source of the macromolecule, and the term is intended to encompass purified, recombinant, and synthetically produced polypeptides.. The term isolated as used herein also refers to a nucleic acid or polypeptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. A DNA that is removed from its chromosomal location or amplified from its chromosomal location is considered "isolated". A cDNA is also considered an isolated nucleic acid in certain embodiments. In some embodiments a nucleic acid or polypeptide is considered isolated when it is expressed in a host cell system using recombinant DNA techniques. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. Any of the nucleic acids and polypeptides disclosed herein may be provided in isolated form.

[0038] As used herein, "linkage" or "linked" generally refers to genetic linkage. Two loci (e.g., two SNPs, a DNA marker locus and a disease locus such as a mutation causing disease, etc.) are said to be genetically linked when the probability of a recombination event occurring between these two loci is below 50% (which equals the probability of recombination between two unlinked loci). Two loci are closely linked genetically if the recombination frequency in the region between the loci is low, but may be essentially genetically unlinked or only weakly linked if the recombination frequency between the two loci is high even if they are in close physical proximity to one another along a chromosome.

[0039] "Linkage disequilibrium" or "LD" refers to a situation in which two or more allelic variants are linked, i.e., there is a non-random correlation between allelic variants at two or more polymorphic sites in individuals in a population. Two or more allelic variants that are linked are said to be in linkage disequilibrium. In general, allelic variants that are part of a haplotype or haplotype block are in linkage disequilibrium. A variety of metrics are known in the art to evaluate the extent to which any two polymorphic variants (alleles) are in LD. Suitable metrics include D', r^2 , and others (see, e.g., Hedrick, P.W., Genetics, 117(2):331-41, 1987). As used herein, polymorphic variants are in "strong LD" if D' >0.8.

[0040] The term "locus" refers to a position in a chromosome. For example, a locus of a gene refers to the chromosomal position of the gene.

[0041] The term "microparticle" is used herein to refer to particles having a smallest cross-sectional dimension of 50 microns or less. In certain embodiments, the smallest cross-sectional dimension of the microparticle is 10 microns or less. In certain embodiments the smallest cross-sectional dimension is approximately 3 microns or less, approximately 1 micron or less, or approximately 0.5 microns or less, e.g., approximately 0.1, 0.2, 0.3, or 0.4 microns. Microparticles may be made of a variety of inorganic or organic materials including, but not limited to, glass (e.g., controlled pore glass),

silica, zirconia, cross-linked polystyrene, polyacrylate, polymethylmethacrylate, titanium dioxide, latex, polystyrene, etc. See, e.g., U.S. Pat. No. 6,406,848, for various suitable materials and other considerations. Dyna beads, available from Dynal, Oslo, Norway, are an example of commercially available microparticles of use in the present invention. Magnetically responsive microparticles can be used. In certain embodiments, one or more populations of fluorescent microparticles are employed. The populations may have different fluorescence characteristics so that they can be distinguished from one another, e.g., using flow cytometry. In some embodiments the microparticles are modified, e.g., an oligonucleotide is attached to a microparticle to serve as a "zip code" that allows specific hybridization to a second oligonucleotide that comprises a portion that is complementary to the zip code.

[0042] The term "modulation", "modulate", and like terms, as used herein refers to both up-regulation, (e.g., activation or stimulation), for example by agonizing, and down-regulation (e.g., inhibition or suppression), for example by antagonizing of a bioactivity (e.g. expression of a gene). Thus a "modulator" may be an agent that enhances or increases the expression and/or activity of a gene, nucleic acid, or polypeptide, or an agent that reduces or inhibits the expression and/or activity of a gene, nucleic acid, or polypeptide.

[0043] The terms "nucleic acid", "polynucleotide", and "oligonucleotide" are used interchangeably herein to refer to a polymer of at least three nucleotides such as deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). An oligonucleotide is typically less than 100 nucleotides in length, although oligonucleotides of the present invention are not limited to such a length. A nucleotide comprises a nitrogenous base, a sugar molecule, and a phosphate group. A nucleoside comprises a nitrogenous base linked to a sugar molecule. In a polynucleotide phosphate groups covalently link adjacent nucleosides to form a polymer. The polymer may include natural nucleosides (e.g., adenosine, thymidine, guanosine, cytidine, uridine, deoxyadenosine, deoxythymidine, deoxyguanosine, and deoxycytidine), nucleoside analogs, chemically modified bases, biologically modified bases (e.g., methylated bases), intercalated bases, modified sugars (e.g., modified purines or pyrimidines). The phosphate groups in nucleic acid are typically considered to form the internucleoside backbone of the polymer. In naturally occurring nucleic acids (DNA or RNA), the backbone linkage is via a phosphodiester bond. However, polynucleotides containing modified backbones or non-naturally occurring internucleoside linkages can also be used in the present invention. See Kornberg and Baker, DNA Replication, 2nd Ed. (Freeman, San Francisco, 1992), Scheit, Nucleotide Analogs (John Wiley, New York, 1980), and U.S. Patent Publication No. 20040092470 and references therein for further discussion of various nucleotides, nucleosides, and backbone structures that can be used in the polynucleotides described herein, and methods for producing them. Nucleic acids can be single or double-stranded. Certain polynucleotides of the invention may be modified by chemical or biological means. In certain embodiments, these modifications lead to increased stability of the polynucleotide. Modifications include methylation, phosphorylation, end-capping, etc. The term "nucleic acid sequence" as used herein refers to the nucleic acid material itself and is not restricted to the sequence information (i.e. the succession of letters chosen among the five base letters A, G, C, T, or U) that biochemically characterizes a specific nucleic acid, e.g., a DNA or RNA molecule. A nucleic acid sequence is presented in the 5' to 3' direction unless otherwise indicated.

[0044] "Operably linked" or "operably associated" refers to a functional relationship between two nucleic acids, wherein the expression, activity, localization, etc., of one of the sequences is controlled by, directed by, regulated by, modulated by, etc., the other nucleic acid. The two nucleic acids are said to be operably linked or operably associated. "Operably linked" or "operably associated" also refers to a relationship between two polypeptides wherein the expression of one of the polypeptides is controlled by, directed by, regulated by, modulated by, etc., the other polypeptide. The two nucleic acids are said to be operably linked or operably associated. For example, transcription of a nucleic acid is directed by an operably linked promoter; post-transcriptional processing of a nucleic acid is directed by an operably linked processing sequence; translation of a nucleic acid is directed by an operably linked translational regulatory sequence such as a translation initiation sequence; transport, stability, or localization of a nucleic acid or polypeptide is directed by an operably linked transport or localization sequence such as a secretion signal sequence; and post-translational processing of a polypeptide is directed by an operably linked processing sequence. In certain embodiments, a first nucleic acid sequence that is operably linked to a second nucleic acid sequence, or a first polypeptide that is operatively linked to a second polypeptide, is covalently linked, either directly or indirectly, to such a sequence, although any effective three-dimensional association is acceptable. One of ordinary skill in the art will appreciate that multiple nucleic acids, or multiple polypeptides, may be operably linked or associated.

[0045] The term "plurality" means more than one.

[0046] The term "polymorphism" refers to the occurrence of two or more alternative genomic DNA sequences or alleles in a population. Either of the sequences themselves, or the site at which they occur, may also be referred to as a polymorphism. A "single nucleotide polymorphism" or "SNP" is a polymorphism that exists at a single nucleotide position.

[0047] A "polymorphic site" or "polymorphic position" is a location at which differences in genomic DNA sequence exist among members of a population. While in general the polymorphic sites described herein are single nucleotides, the term is not limited to sites that are only one nucleotide in length. An "ambiguity code" such as that described in U.S.S.N. 10/505,936 may be used to describe a polymorphic site. A "polymorphic region" is a region of genomic DNA that includes one or more polymorphic sites.

[0048] A "polymorphic variant" is any of the alternate sequences that may exist at a polymorphic site among members of a population. For purposes of the present invention, the term "population" may refer to the population of the world, or to a subset thereof. Typically, for the various methods described herein (e.g., diagnostic methods, methods for identifying causative mutations, etc.), it will be of interest to determine which polymorphic variant(s) is/are present in a individual, among multiple polymorphic variants that exist within a population.

[0049] "Polypeptide", as used herein, refers to a polymer of amino acids. A protein is a molecule composed of one or more polypeptides. A peptide is a relatively short polypeptide, typically between about 2 and 60 amino acids in length. The terms "protein", "polypeptide", and "peptide" are used interchangeably herein. Polypeptides as used herein may contain only amino acids that are naturally found in proteins, although non-natural amino acids (e.g., compounds that do not occur in nature but that can be incorporated into a polypeptide chain) and/or amino acid analogs as are known in the art may alternatively be employed. Non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids whether naturally occurring or non-natural can be used. One or more of the amino acids in a polypeptide may be modified, for example, by the addition of one or more chemical entities such as a carbohydrate group, a phosphate group, a lipid group, etc. Non-limiting examples include a farnesyl group, an isofarnesyl group, a fatty acid group, a glycosyl group, an acetyl group, etc. Polypeptides may contain a linker for conjugation, functionalization, or other modification, etc. In some embodiments, the modifications lead to a more stable polypeptide (e.g., greater half-life in vivo). Exemplary modifications may include cyclization of the peptide, the incorporation of D-amino acids, etc. In certain embodiments the modifications do not substantially interfere with a desired biological activity of the polypeptide.

[0050] Polypeptides may, for example, be purified from natural sources, produced *in vitro* or *in vivo* in suitable expression systems using recombinant DNA technology in suitable expression systems (e.g., by recombinant host cells or in transgenic animals or plants), synthesized through chemical means such as conventional solid phase peptide synthesis and/or methods involving chemical ligation of synthesized peptides (see, e.g., Kent, S., J Pept Sci., 9(9):574-93, 2003), or any combination of the foregoing. A polypeptide may comprise one or more chemical ligation sites as described, for example, in U.S. Pub. No. 20040115774. In certain embodiments, one or more polypeptides are modified with a polymer using one or more of the methods described or referenced therein. The term "amino acid sequence" or "polypeptide sequence" as used herein refers to the polypeptide material itself and is not restricted to the sequence information (i.e. the succession of letters or three letter codes chosen among the letters and codes used as abbreviations for amino acid names) that biochemically characterizes a polypeptide.

[0051] "Probes" or "primers", as used herein, typically refer to oligonucleotides that hybridize in a sequence-specific manner to a complementary nucleic acid molecule. The term "primer" in particular generally refers to a single-stranded oligonucleotide that can act as a point of initiation of template-directed DNA synthesis using methods including but not limited to PCR (polymerase chain reaction) or LCR (ligase chain reaction) under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase, DNA ligase, etc.) in an appropriate buffer solution containing any necessary cofactors and at a suitable temperature. A primer pair may be designed to amplify a region of DNA using PCR. Such a pair will include a "forward" and a "reverse" primer that hybridize to complementary strands of a DNA molecule at locations that delimit a region to be amplified.

[0052] Typically, a probe or primer will comprise a region of nucleotide sequence that hybridizes to at least about 8, more often at least about 10 to 15, typically about 20-25, and frequently about 40, 50 or 75, consecutive nucleotides of a target nucleic acid. In certain embodiments, a probe or primer comprises 100 or fewer nucleotides, from 6 to 50 nucleotides, or from 12 to 30 nucleotides. In certain embodiments, the probe or primer is at least 70%, 80%, 90%, 95% or more identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. In certain embodiments, a probe or primer is capable of selectively hybridizing to a target contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. In certain embodiments, a probe or primer further comprises a label. For example, a label may be a radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

[0053] Oligonucleotides that exhibit differential or selective binding to polymorphic sites may readily be designed by one of ordinary skill in the art. For example, an oligonucleotide that is perfectly complementary to a sequence that encompasses a polymorphic site (e.g., a sequence that includes the polymorphic site within it or at one or the other end) will generally hybridize preferentially to a nucleic acid comprising that sequence as opposed to a nucleic acid comprising an alternate polymorphic variant.

[0054] The term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer solution containing any necessary cofactors and at a suitable temperature. The length of a primer depends on the intended use of the primer, but typically ranges from approximately 10 to approximately 30 nucleotides. Short primer molecules generally require lower temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the template but should be sufficiently complementary to hybridize with it. One

of ordinary skill in the art will be aware of other constraints that should be considered when designing primers.

[0055] The term "regulatory element" or "regulatory sequence" in reference to a nucleic acid is generally used herein to describe a portion of nucleic acid that directs or controls one or more steps in the expression (particularly transcription, but in some cases other events such as splicing or other processing) of nucleic acid sequence(s) with which it is operatively linked. The term includes promoters and can also refer to enhancers, silencers, and other transcriptional control elements. Promoters are regions of nucleic acid that include a site to which RNA polymerase binds before initiating transcription and that are typically necessary for even basal levels of transcription to occur. Generally such elements comprise a TATA box. Enhancers are regions of nucleic acid that encompass binding sites for protein(s) that elevate transcriptional activity of a nearby or distantly located promoter, typically above some basal level of expression that would exist in the absence of the enhancer. In some embodiments, regulatory sequences may direct constitutive expression of a nucleotide sequence, e.g., expression may occur in most or all cell types and/or under most or all conditions. In some embodiments, regulatory sequences may direct cell or tissue-specific and/or inducible expression. For example, expression may be induced by the presence or addition of an inducing agent such as a hormone or other small molecule, by an increase in temperature, etc. Regulatory elements may also inhibit or decrease expression of an operatively linked nucleic acid. Regulatory elements that behave in this manner will be referred to herein as "negative regulatory elements.

[0056] In general, the level of expression may be determined using standard techniques for measuring mRNA or protein. Such methods include Northern blotting, *in situ* hybridization, RT-PCR, sequencing, immunological methods such as immunoblotting, immunodetection, or fluorescence detection following staining with fluorescently labeled antibodies, oligonucleotide or cDNA microarray or membrane array, protein array analysis, mass spectrometry, etc. A convenient way to determine expression level is to place a nucleic acid that encodes a readily detectable marker (e.g., a fluorescent or luminescent protein such as green fluorescent protein or luciferase, an enzyme such as alkaline phosphatase, etc.) in operable association with the regulatory element in an expression vector, introduce the vector into a cell type of interest or into an organism, maintain the cell or organism for a period of time, and then measure expression of the readily detectable marker, taking advantage of whatever property renders it readily detectable (e.g., fluorescence, luminescence, alteration of optical property of a substrate, etc.). Comparing expression in the absence and presence of the regulatory element indicates the degree to which the regulatory element affects expression of an operatively linked sequence.

[0057] As used herein, a "sample" obtained from a individual may include, but is not limited to, any or all of the following: a cell or cells, a portion of tissue, blood, serum, ascites, urine, saliva, amniotic fluid, cerebrospinal fluid, and other body fluids, secretions, or excretions. The sample may be a tissue sample obtained, for example, from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A sample of DNA from fetal or embryonic cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The term "sample" also includes any material derived by isolating, purifying, and/or processing a sample as previously defined. Derived samples may include nucleic acids or proteins extracted from the sample or obtained by individualing the sample to techniques such as amplification or reverse transcription of mRNA, etc.

[0058] "Specific binding" generally refers to a physical association between a target molecule and a binding molecule such as, for example, physical association between a polypeptide and an antibody or ligand. The association is typically dependent upon the presence of a particular structural feature of the target such as an antigenic determinant or epitope recognized by the binding molecule. For example, if an antibody is specific for epitope A, the presence of a polypeptide containing epitope A or the presence of free unlabeled A in a reaction containing both free labeled A and the binding molecule that binds thereto, will reduce the amount of labeled A that binds to the binding molecule. It is to be understood that specificity need not be absolute but generally refers to the context in which the binding occurs. For example, it is well known in the art that numerous antibodies cross-react with other epitopes in addition to those present in the target molecule. Such cross-reactivity may be acceptable depending upon the application for which the antibody is to be used. One of ordinary skill in the art will be able to select antibodies or ligands having a sufficient degree of specificity to perform appropriately in any given application (e.g., for detection of a target molecule, for therapeutic purposes, etc). It is also to be understood that specificity may be evaluated in the context of additional factors such as the affinity of the binding molecule for the target versus the affinity of the binding molecule for other targets, e.g., competitors. If a binding molecule exhibits a high affinity for a target molecule that it is desired to be detected and low affinity for nontarget molecules, the antibody will likely be an acceptable reagent. Once the specificity of a binding molecule is established in one or more contexts, it may be employed in other contexts without necessarily re-evaluating its specificity. Binding of two or more molecules may be considered specific if the affinity (equilibrium dissociation constant, Kd) is at least 10^{-3} M, 10^{-4} M, 10^{-5} M, e.g., 10^{-6} M, 10^{-7} M, 10^{-8} M, or 10^{-9} M or lower under the conditions tested, e.g., under physiological conditions.

[0059] The term "statin" is intended to embrace all inhibitors of the enzyme 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase. Statins specifically inhibit the enzyme HMG-CoA reductase which catalyzes the rate limiting step in cholesterol biosynthesis. Known statins include Atorvastatin, Cerivastatin, Fluvastatin, Lovastatin, Pravastatin and Simvastatin.

[0060] "Therapeutic regimen" as used herein refers to treatments aimed at the elimination or amelioration of symptoms and events associated cardiovascular disease. Such treatments include without limitation one or more of alteration in diet, lifestyle, and exercise regimen; invasive and noninvasive surgical techniques such as atherectomy, angioplasty, and coronary bypass surgery; and pharmaceutical interventions, such as administration of ACE inhibitors, angiotensin II receptor antagonists, diuretics, alpha-adrenoreceptor antagonists, cardiac glycosides, phosphodiesterase inhibitors, beta-adrenoreceptor antagonists, calcium channel blockers, HMG-CoA reductase inhibitors, imidazoline receptor blockers, endothelin receptor blockers, organic nitrites, and modulators of protein function of genes listed in Table 1 and/or Table 2. Interventions with pharmaceutical agents not yet known that are useful therapeutically in individuals with particular genotypes associated with cardiovascular disease, e.g., individuals who possess one or more of the CVDA polymorphic variants or haplotypes described herein, are also encompassed. It is contemplated, for example, that patients who are candidates for a particular therapeutic regimen will be screened for genotypes that correlate with responsivity to that particular regimen.

[0061] "Treating", as used herein, can generally include reversing, alleviating, reducing, inhibiting the progression of, or reducing the likelihood of the disease, disorder, or condition to which such term applies, or one or more symptoms or manifestations of such disease, disorder or condition. "Preventing" refers to causing a disease, disorder, condition, or symptom or manifestation of such, or worsening of the severity of such, not to occur.

Detailed Description of Certain Embodiments

[0062] Cardiovascular Disease Associated Polymorphisms and Polymorphic Variants

[0063] The present invention is based in part on results of an association study that was performed to identify genetic variations that are associated with an increased risk of cardiovascular disease, particularly acute coronary events such as MI. The association study compared the frequencies of polymorphic variants at a large number of different polymorphic sites between a group of individuals with a history of MI ("cases") and a group of individuals without a history of MI but having an otherwise similar profile of classical risk factors for cardiovascular disease ("controls", also referred to as "healthy" individuals).

[0064] The study described herein identified SNPs for which the frequencies of the polymorphic variants differed between these two groups of individuals. In general, those polymorphic variants that occur at higher frequency in individuals who are affected by a disease are said to be associated with the disease or condition, and an association is said to exist between the polymorphic variant and the disease or condition. In certain embodiments, the invention provides SNPs for which the frequencies of the polymorphic variants differ between those individuals who have or are susceptible to development or occurrence of a cardiovascular disease or major coronary event such as a myocardial infarction or sudden cardiac death and those individuals who do not have or are not susceptible (or exhibit decreased susceptibility) to development or occurrence of a cardiovascular disease or major coronary event.

[0065] Polymorphic variants that were found to be significantly associated with an acute coronary event, including MI, are referred to as "cardiovascular disease associated (CVDA) polymorphic variants", and a SNP at which such a polymorphic variant exists is referred to as a "CVDA SNP" or "CVDA polymorphism". Such SNPs are also said to be associated with cardiovascular disease although one of ordinary skill in the art will appreciate that typically only one of the polymorphic variants that can exist at the polymorphic position of the SNP is found at higher frequency among individuals who have or are susceptible to development of cardiovascular disease or major coronary event. In certain embodiments, the invention provides both polymorphic variants that are associated with cardiovascular disease and polymorphic variants that are not associated with cardiovascular disease.

[0066] Certain of the CVDA polymorphisms are located within genes. A gene that harbors one or more CVDA SNPs will be referred to herein as a "CVD associated gene" or "CVDA gene", regardless of the actual function of the gene. The CVDA genes identified in the present invention include a large number of genes that had not been previously linked to CVD. A CVDA gene will typically encode a polypeptide, although it will be understood that CVDA genes are not limited to polypeptide-encoding genes. A polypeptide encoded by a CVDA gene is referred to herein as a CVDA polypeptide. If a CVDA polymorphism occurs within a coding portion of the gene, the polymorphism may result in an alteration in the amino acid sequence of the encoded protein. A SNP at such a location that alters the coding sequence of a protein is referred to as a coding SNP (cSNP). The present invention provides cSNPs wherein the allele that is associated with cardiovascular disease alters the coding sequence of a protein encoded by a CVDA gene. Without wishing to be bound by any theory, genes that include cSNPs are particularly attractive candidates as playing a significant role in cardiovascular disease, e.g., particular alleles of these genes play a causative role in cardiovascular disease or play a protective role. Functionally relevant SNPs can also reside outside protein coding regions, e.g., in the 5' or 3' region of a gene (e.g. the promoter or the 3' untranslated region) and may influence gene expression without affecting the structure of the encoded protein. Without wishing to be bound by any theory, genes that include such functionally relevant SNPs are also attractive candidates as playing a role in CVD.

[0067] Each allelic variant of a gene may encode a different polymorphic form of the protein. Since allelic variants of

a gene can vary from one another at multiple polymorphic sites, there can be multiple different polymorphic forms of a protein, each reflecting a different combination of polymorphic variants present in the allele that encodes it. Certain aspects of the invention thus provide polymorphic forms of the proteins encoded by the genes identified herein, e.g., genes that include a SNP disclosed herein. The sequence of such proteins will differ from one another at one or more polymorphic positions in the protein, which correspond to the polymorphic positions in the gene.

[0068] It will be appreciated that SNPs may be linked to other SNPs located on the same chromosome (linkage disequilibrium) and that such SNPs may be present in haplotypes. For example, it has been shown that SNPs can be linked over significant distances, e.g., 100 kb, or in some cases over more than 150 kb (Reich D. E. et al. Nature 411, 199-204, 2001). In certain aspects, the invention therefore provides haplotypes comprising at least one CVDA polymorphic variant disclosed herein. In certain embodiments, a set of polymorphic variants that constitute a haplotype of the invention is found within a haplotype block. A haplotype block is identified as described in Gabriel, *supra*. Briefly, 95% confidence bounds on D' are generated and each comparison is called "strong LD", "inconclusive" or "strong recombination". A block is created if 95% of informative (i.e. non-inconclusive) comparisons are "strong LD".

[0069] SNPs that comprise polymorphic variants that are linked to the CVDA polymorphic variants provided herein (referred to herein as "linked SNPs") can also be used as marker SNPs for cardiovascular disease regardless of whether they are among the SNPs disclosed herein. As in the case of the CVDA SNPs, the frequencies of the polymorphic variants of a linked SNP differ between those individuals who have or are susceptible to development or occurrence of a cardiovascular disease or major coronary event and those and those individuals who do not have or are not susceptible (or exhibit decreased susceptibility) to development or occurrence of a cardiovascular disease or major coronary event. Therefore, one or more polymorphic variants of a linked SNP may be associated with cardiovascular disease and can be used in accordance with certain methods of the present invention.

[0070] A large number of SNPs and their chromosomal locations are known in the art and are publicly available in databases such as dbSNP, provided by the National Center for Biotechnology Information (NCBI) (available at the website having the URL www.ncbi.nlm.nih.gov/projects/SNP/), the International HapMap Project (available at the website having the URL www.hapmap.org/), etc. These databases provide a wide variety of information including, e.g., the identity of the nucleotide at each polymorphic position and whether it is a major or minor allele, the sequence surrounding each polymorphic position, chromosome and chromosomal location, gene names and identifiers for SNPs that lie within genes, biological annotation if available, etc. Thus one of ordinary skill in the art, provided with a SNP identifier can readily determine the exact sequence of the polymorphic variants at the polymorphic position and the surrounding sequence. Furthermore, comprehensive information about the particular SNPs that are present on the gene chips that were used to identify the SNPs of the present invention is available at the Affymetrix NetAffx™ Analysis Center (available at the web site having the URL www.affymetrix.com/analysis/index.affx).

[0071] Table 1 provides identifying information for certain CVDA SNPs of the present invention. Each row of Table 1 identifies a SNP that is encompassed within the present invention. Each row describing a SNP contains 19 columns containing data. In addition to information identifying the SNP, certain additional information related to the SNP, including the allele frequencies determined as described herein, is provided in Table 1. General information about the SNP, such as the chromosome, chromosomal location, gene name, major and minor alleles, etc., as well as additional information, can readily be found in dbSNP, HapMap, or the Affymetrix NetAffx™ Analysis Center by searching using the SNP ID. Specifically, a search box is provided at the secure website having the URL www.affymetrix.com/analysis/netaffx/quickquery.affx?mapping=true, into which the user can enter a SNP ID and perform a search to retrieve information related to the SNP. For purposes of convenience some of this information is included in Table 1.

[0072] The contents of Table 1 are now described by column, beginning on the left and moving to the right. The data set was divided based on chromosome due to the large amount of data. Thus Table 1 groups SNPs by chromosome. The first column of Table 1 (column heading "Name") is the Affymetrix ID for the SNP. The second column of Table 1 (column heading "Major_Allele_1") gives the base (nucleotide) that is present in the major allele in the cases (i.e., the more frequent allele in the cases). The third column of Table 1 (column heading "Major_Allele_2") gives the base (nucleotide) that is present in the major allele in the controls (i.e., the more frequent allele in the controls).

[0073] For example, the first row of data in Table 1 (identified by Affymetrix ID SNP_A-2084457) contains "C" under both the headings "Major_Allele_1" and "Major_Allele_2". This indicates that the major allele in both the cases and the controls contained a C at the polymorphic position. As another example, the row identified by Affymetrix ID SNP_A-2004453 contains "T' under the heading "Major_Allele_1" and "A" under the heading "Major_Allele_2". This indicates that the major allele in the cases contained a T at the polymorphic position, and the major allele in the controls contained an A at the polymorphic position.

[0074] The fourth and fifth columns of Table 1 (column headings "Case_Major" and "Case_Minor") present the actual counts for alleles A and B in cases. The sixth and seventh columns of Table 1 (column headings "Control_Major" and "Control_Minor") present the actual counts for alleles A and B in controls. For example, in the first row of data in Table 1 (SNP_A-2084457), Allele_A was detected 175 times in cases, while Allele_B was detected 75 times in cases. Similarly, Allele_A was detected 367 times in controls, while Allele_B was detected 3 times in controls. It is noted that the numbers

do not always add up to the same value because it was not possible to accurately identify the allele in some instances. The allele frequencies are readily computed from the data in this column. Consider the following example from the first row of data in Table 1 (SNP_A-2084457):

[0075]

Case ratio	Control ratio
175:75	367:3

[0076] In the cases, Allele_A has a frequency of 175/250(70%) and Allele_B has a frequency of 75/250 (30%), while in the controls Allele_A has a frequency of 367/370 (?99.2%) and Allele_B has a frequency of 3/370 (?0.8%). Thus it is evident that the allele frequencies differ between the cases and controls. The difference between the allele frequencies is statistically significant (as shown by the Chi square value of 115.58 and the P value of 5.87×10^{-27}), with Allele_B occurring more frequently in cases than in controls (i.e., Allele_B has a frequency of ?30% in cases and ?0.8% in controls) and Allele_A occurring more frequently in controls than in cases (i.e., Allele_A has a frequency of ?99.2% in controls and ?70% in cases). Therefore, Allele_B is the variant that is associated with cardiovascular disease and is a CVDA polymorphic variant of this particular CVDA polymorphism, in accordance with the terminology described above. It should be noted that both alleles of each SNP are informative with respect to CVD; thus detection of either allele, or both, of each of the SNPs identified herein, is one non-limiting aspect of this invention.

[0077] The eighth column of Table 1 (column heading "Chi_Square") presents the Pearson's Chi-square for allele frequencies.

[0078] The ninth column of Table 1 (column heading "p_value") presents the probability value (significance) for each Chi square/observation.

[0079] The tenth column (column heading "dbSNP_RS_ID") is the SNP annotation (i.e., the SNP name) as annotated in public databases (dbSNP at NCBI or HapMap), where available. Each SNP identifier begins with the letters "rs" and is followed by a string of numbers.

[0080] The eleventh column of Table 1 (column heading "Chromosome") presents the chromosome on which the SNP is located.

[0081] The twelfth column of Table 1 (column heading "Physical_Position") presents the physical position of the SNP in the human genome.

[0082] The thirteenth column of Table 1 (column heading "Cytoband") lists the chromosomal arm and band at which the SNP is located.

[0083] The fourteenth column of Table 1 (column heading "Flank") presents a portion of the genomic sequence that surrounds and includes the SNP. The polymorphic site, and the alternative nucleotides that are present in different polymorphic variants, are indicated near the center of the sequence in brackets and upper case letters.

[0084] The fifteenth and sixteenth columns of Table 1 (column headings "Allele_A" and "Allele_B" present the alternative nucleotides that are present in different polymorphic variants, with "Allele_A" representing the major Allele as assigned by Affymetrix.

[0085] The seventeenth column of Table 1 (column heading "Associated_Gene") provides information about the gene or location where the SNP resides, including relevant accession numbers for databases such as GenBank in some cases.

[0086] The eighteenth column of Table 1 (column heading "Gene_Symbol") is GENE SYMBOL (the SYMBOL that was assigned to the gene by the Human Genome Project and how it can be located in all relevant GENOME Databases).

[0087] The nineteenth column of Table 1 (column heading "Label") provides further explanation of where the SNP resides and repeats part of the information in other columns such as GENE SYMBOL, the rs-number ("dbSNP_RS_ID"); the gene name (or other identifying information, if applicable) followed by cytogenetic chromosomal location (arm and band).

[0088] Table 2 provides identifying information for additional CVDA SNPs of the present invention. Each of the columns of Table 2 corresponds to the columns described above for Table 1. The CVDA SNPs of Table 2 were previously identified from the same set of PROCAM case and control patients described in Example 1 and were disclosed in PCT/US06/029449, filed July 26, 2006, incorporated herein by reference in its entirety.

[0089] In addition to the SNPs provided in Tables 1 and 2, the present invention provides additional SNPs, e.g., SNPs located at a distance of less than about 100-150 kB of any of the CVDA SNPs of the present invention. These SNPs may readily be obtained from dbSNP, HapMap, or the Affymetrix NetAffx™ Analysis Center resources by one of ordinary skill in the art and are therefore not explicitly identified by SNP identifier herein. The SNP may be tested in a variety of ways to determine whether a polymorphic variant of the SNP is associated with cardiovascular disease. For example, the SNP may be tested as described in Example 1. In some instances, a polymorphic variant of the additional SNP may already be known to be in LD with a CVDA polymorphic variant described herein. Therefore, in certain embodiments, the invention provides a linked SNP for which the frequencies of the polymorphic variants found at the location of the

linked SNP differ between individuals who have or are susceptible to development or occurrence of a cardiovascular disease or event. In certain embodiments, a polymorphic variant of the linked SNP is in strong linkage disequilibrium with a CVDA polymorphic variant. In certain embodiments, such linked SNP is located within 1 kB of the CVDA SNP with which it is linked. In certain embodiments, a linked SNP is located up to 10 kB, up to 20 kB, up to 30 kB, up to 40 kB, up to 50 kB, up to 60 kB, up to 70 kB, up to 80 kB, up to 90 kB, or up to 100 kB away from the CVDA SNP with which it is linked. In certain embodiments, a linked SNP is located within the same gene as the CVDA SNP with which it is linked.

[0090] In general, a linked SNP comprises a polymorphic variant that is part of a haplotype that includes at least one CVDA polymorphic variant. In certain embodiments, the invention therefore provides a haplotype comprising at least one CVDA polymorphic variant and a polymorphic variant of at least one linked SNP, wherein the polymorphic variant of the linked SNP is associated with cardiovascular disease. The SNP may be any linked SNP known in the art.

[0091] An alternative approach that can be used to identify polymorphic variants that are in LD with CVDA polymorphic variants is to sequence the genomic DNA of a plurality of cases and controls in a region located in the vicinity of a CVDA SNP. For example, a region of any length located within up to approximately 150 kB of the SNP, e.g., a region approximately 1, 5, 10, 20, 50, 100, 150 kB, etc., in length can be sequenced from a plurality of individuals. In certain embodiments, such a region encompasses the CVDA SNP. Nucleotide differences among individuals, e.g., SNPs, are identified. In certain embodiments, such individuals include both cases and controls, although this is not necessary for purposes of simply identifying the SNP. A plurality of cases and controls may be genotyped with respect to the SNPs, and the allele frequencies may be determined. Alleles that are associated with cardiovascular disease, e.g., variants that occur more frequently in a statistically significant sense in individuals with cardiovascular disease may be identified. Each of such polymorphic variants is an additional CVDA polymorphic variant, and a SNP having such a variant is an additional CVDA SNP.

[0092] In certain embodiments, the invention therefore provides methods of identifying a polymorphism comprising: sequencing a region of DNA from a plurality of individuals, wherein the region of DNA lies within 150 kB of a CVDA SNP and identifying nucleotide differences in the sequence of the DNA region among individuals. Such differences occur at polymorphic positions, and the various nucleotide sequences present at those positions are polymorphic variants. The polymorphism may be a SNP. Certain methods comprise an additional step of determining whether a polymorphic variant is in LD with a CVDA polymorphic variant. The method can comprise an additional step of determining whether a polymorphic variant is associated with cardiovascular disease.

[0093] As mentioned above, and without wishing to be bound by any theory, certain of the CVDA polymorphisms may play a causative role in cardiovascular disease. For example, a particular polymorphic variant associated with cardiovascular disease may have an altered expression level, altered expression pattern, and/or altered functional activity relative to alleles that are not associated with cardiovascular disease, and such alteration may contribute to the development of cardiovascular disease. While not wishing to be bound by any theory, this is particularly likely to be the case for those polymorphisms that lie within genes, and most particularly for those that lie within coding sequences and in which the polymorphic variants result in proteins with differences in amino acid sequence. However, alterations that lie outside genes can, for example, also affect expression and can play a causative role. In certain embodiments, CVDA polymorphic variants do not play a causative role, but are in LD with polymorphic variants that do play such a role. Such non-causative CVDA polymorphic variants may not be direct targets for treatment, but they may nevertheless be of use for diagnostic purposes such as those described herein.

[0094] In certain embodiments, polymorphic variants are identified that are associated with CVD in only a subset of individuals, wherein the subset is classified based on a risk assessment based on classical risk factors and/or other markers of cardiovascular status. For example, certain variants may be associated with increased risk in individuals having a risk of <10% but not in individuals having a risk of >20%. Similarly, certain variants may be associated with increased risk in individuals having a risk of >20% but not in individuals having a risk of <10%.

[0095] Diagnostic and Prognostic Methods and Reagents

[0096] The invention encompasses a variety of methods for determining whether an individual has or is susceptible to development or occurrence of a cardiovascular disease or event, wherein the individual is in need of such determination. By "event" is meant a major coronary event such as a myocardial infarction or sudden cardiac death. In certain embodiments, methods of the present invention comprise steps of: (a) detecting a polymorphic variant of a CVDA polymorphism in the individual; (b) or detecting a polymorphic variant in strong LD with a CVDA polymorphism; or (c) detecting a haplotype comprising a polymorphic variant of the CVDA polymorphism in the individual; or (d) detecting an allele of a gene comprising the polymorphic variant of the CVDA polymorphism in the individual.

[0097] Methods described herein are typically practiced on a sample obtained from the individual and the phrase "in the individual" is to be understood in that light. The sample typically contains genetic material, e.g., DNA. Such DNA may be obtained from any cell source, including any cell source. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Cells may also be obtained from body fluids, including without limitation blood, saliva, sweat, urine, cerebrospinal fluid, feces, and tissue exudates at the site of infection or inflammation. DNA is

extracted from the cell source or body fluid using any of the numerous methods that are standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source. In some embodiments, inventive methods are practiced on cellular material other than DNA. For example, polymorphisms that lie in genes may be detected in RNA. Polymorphisms that affect expression level may be detected by measuring mRNA or protein level. Furthermore, polymorphisms that alter the coding sequence of a protein may be detected by examining the protein as described elsewhere herein.

[0098] "Detecting a polymorphic variant" is used in a broad sense and refers, e.g., to determining the identity of the polymorphic variant by any suitable means, wherein determining the identity means providing sufficient information to determine whether the variant is a variant that has been identified herein as being associated with cardiovascular disease. It will be appreciated that detecting a polymorphic variant can encompass detecting the absence of a different polymorphic variant, and thus determining that a particular variant is absent is one means of determining that a different variant is present. Thus, in certain embodiments, methods of the present invention comprise detecting, in a sample of cells from the subject, the presence or absence of a specific allelic variant, e.g., an allelic variant of one or more polymorphic regions of a gene or an allelic variant in an intergenic region. The allelic differences can be: (i) a difference in the identity of at least one nucleotide or (ii) a difference in the number of nucleotides, which difference can be a single nucleotide or several nucleotides. It will typically be of interest to detect and identify both of the individual's alleles, but this need not be the case.

[0099] In certain embodiments, suitable detection methods comprise allele specific hybridization using probes overlapping the polymorphic site and typically having about 5, 10, 20, 25, or 30 nucleotides around the polymorphic region. Examples of probes for detecting specific allelic variants of a CVDA polymorphism are probes comprising at least 10 nucleotides of a nucleotide sequence set forth in Table 1 and/or Table 2, wherein the at least 10 nucleotides include the polymorphic position. In certain embodiments, several probes capable of hybridizing specifically to allelic variants are attached to a solid support, e.g., a "chip". Oligonucleotides can be bound to a solid support by a variety of processes such as lithography. Probes can be synthesized directly on a chip. For example a chip can hold up to 250,000 oligonucleotides or more (GeneChip, Affymetrix). Hybridization, followed by scanning to determine the position(s) on the array to which a nucleic acid hybridizes, is performed according to standard methods.

[0100] Detection of polymorphic variants using chips comprising oligonucleotides, also termed "DNA probe arrays", "oligonucleotide arrays", etc., has been known in the art for some time and is described e.g., in Cronin et al., Human Mutation 7:244, 1996 and in Kozal et al., Nature Medicine 2:753, 1996. See also Matsuzaki, H., et al., Genome Research, 14:414-425, 2004, describing use of a high density oligonucleotide array for parallel genotyping of over 10,000 SNPs. The present invention utilized such arrays for the identification of the CVDA SNPs as described in more detail in Example 1.

[0101] In certain embodiments, a chip comprises all the allelic variants of at least one genomic region that comprises a polymorphic position. The solid support is then contacted with a test nucleic acid or preparation of nucleic acids (e.g., DNA or RNA extracted from a cell, a specific nucleic acid that has been amplified, etc.) and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment. For example, the identity of the allelic variant of the nucleotide polymorphism of one or more identified SNPs identified in Table 1 and/or Table 2 and that of the allelic variants of a plurality of other polymorphic regions can be determined in a single hybridization experiment.

[0102] Arrays can include multiple detection blocks (e.g., multiple groups of probes designed for detection of particular polymorphisms). Such arrays can be used to analyze multiple different polymorphisms. Detection blocks may be grouped within a single array or in multiple, separate arrays so that varying conditions (e.g., conditions optimized for particular polymorphisms) may be used during the hybridization. For example, it may be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments.

[0103] Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Pat. Nos. 5,858,659 and 5,837,832. In addition, to oligonucleotide arrays, cDNA arrays may be used similarly in certain embodiments.

[0104] In some detection methods, at least a portion of the nucleic acid is amplified prior to identifying the allelic variant. Amplification can be performed, e.g., by using the polymerase chain reaction (PCR) and/or ligase chain reaction (LCR), according to methods known in the art. In certain embodiments, genomic DNA of a cell is exposed to two PCR primers and amplification for a number of cycles sufficient to produce the required amount of amplified DNA. In certain embodiments, the primers are located between 40 and 350 base pairs apart. Primers for amplifying regions of DNA comprising the CVDA polymorphic sites may readily be designed based on the human genome sequence. Such primers will typically be complementary to portions of DNA that flank the polymorphic site. See e.g., PCR Primer: A Laboratory Manual, Dieffenbach, C.W. and Dveksler, G. S. (Eds.); PCR Basics: From Background to Bench, Springer Verlag, 2000; M. J. McPherson, *et* al; Mattila et al., Nucleic Acids Res., 19:4967 (1991); Eckert et al., PCR Methods and Applications, 1:17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. No. 4,683,202. Guidelines for selecting primers for PCR amplification are well known in the art. See, e.g., McPherson, M., et al., PCR Basics: From Background to

Bench, Springer-Verlag, 2000. A variety of computer programs for designing primers are available, e.g., 'Oligo' (National Biosciences, Inc, Plymouth MN), MacVector (Kodak/IBI), and the GCG suite of sequence analysis programs (Genetics Computer Group, Madison, Wisconsin 53711).

[0105] Alternative amplification methods include: self sustained sequence replication (Guatelli, J. C. et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:1874-1878), transcriptional amplification system (Kwoh, D. Y. et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:1173-1177), Q-Beta Replicase (Lizardi, P. M. et al., 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method. For example, other amplification methods that may be employed include the ligase chain reaction (LCR) (Wu and Wallace, Genomics, 4:560 (1989), Landegren et al., Science, 241:1077 (1988), transcription amplification (Kwoh et al., Proc. Natl. Acad. Sci. USA, 86:1173 (1989)), self-sustained sequence replication (Guatelli et al., Proc. Nat. Acad. Sci. USA, 87:1874 (1990)), and nucleic acid based sequence amplification (NASBA).

[0106] Amplification is typically followed by or occurs simultaneously with the detection of the amplified molecules using techniques well known to those of skill in the art. Detection schemes involving amplification can be especially useful for the detection of nucleic acid molecules if such molecules are present in relatively or absolutely low numbers.

[0107] The invention encompasses the use of real-time PCR, e.g., the 5' nuclease allelic discrimination or TaqMan® assay (Livak, K.J., et al., Nature Genet. 9: 341-342, 1995; Ranade, K., et al., Genome Research, Vol. 11, Issue 7, 1262-1268, 2001) for high-throughput genotyping. According to this method, the region flanking the polymorphism, typically 100 base pairs, is amplified in the presence of two probes each specific for one or the other allele. Probes have a fluor, also called a "reporter," at the 5' end but do not fluoresce when free in solution because they have a "quencher" at the 3' end that absorbs fluorescence from the reporter. During PCR, the Taq polymerase encounters a probe specifically base-paired with its target and unwinds it. The polymerase cleaves the partially unwound probe and liberates the reporter fluor from the quencher, thereby increasing net fluorescence. The presence of two probes, each labeled with a different fluor, allows one to detect both alleles in a single tube. Moreover, because probes are included in the PCR, genotypes are determined without any post-PCR processing, a feature that is unavailable with most other genotyping methods (see Landegren, U., et al., Genome Res. 8: 769-776, 1998, for a review). Other methods for performing real-time PCR, e.g., using molecular beacons or scorpions could also be used. In certain embodiments, an Invader® cleavage assay is used for detecting one or more polymorphic variants. See, e.g., Lyamichev, V., et al., Nature Biotechnol. 17: 292-296, 1999. Minisequencing on oligonucleotide arrays offers another approach (Pastinen, T., et al., Genome Res. 7: 606-614, 1997).

[0108] The invention thus provides a variety of probes and primers of use for detecting a polymorphic variant of a polymorphism listed in Table 1 and/or Table 2. In certain embodiments the probe or primer comprises a nucleotide sequence that hybridizes to at least about 8, more often at least about 10 to 15, typically about 20-25, and frequently about 40, 50 or 75, consecutive nucleotides of a target nucleic acid molecule, e.g., a nucleic acid molecule that comprises a CVDA polymorphism. In certain embodiments, a probe or primer comprises 100 or fewer nucleotides, from 6 to 50 nucleotides, or from 12 to 30 nucleotides. In certain embodiments, a probe or primer is at least 70%, 80%, 90%, 95% or more identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. In certain embodiments, a preferred probe or primer is capable of selectively hybridizing to a target contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. According to certain embodiments, a probe or primer further comprises a label, for example by incorporating a radioisotope, fluorescent compound, enzyme, enzyme co-factor, mass tag (for detection using mass spectrometry), etc.

[0109] According to certain embodiments, allele specific primers and/or probes correspond exactly with the allele to be detected (e.g., they are identical in sequence or perfectly complementary to a portion of DNA that encompasses the polymorphic site, wherein the site contains any of the possible variants), but derivatives thereof are also provided wherein, for example, about 6-8 of the nucleotides at the 3', terminus correspond to (e.g., are identical in sequence or perfectly complementary to) the allele to be detected and wherein up to 10, such as up to 8, 6, 4, 2 or 1 of the remaining nucleotides may be varied without significantly affecting the properties of the primer or probe.

[0110] The invention further provides a set of oligonucleotide primers, wherein the primers terminate adjacent to a polymorphic site of a CVDA polymorphism, or wherein the primers terminate adjacent to a polymorphic site of a CVDA polymorphism. Such primers are useful, for example, in performing fluorescence polarization template-directed dye-terminator incorporation, as described below. In certain embodiments, the invention provides oligonucleotide primers that terminate immediately adjacent to the polymorphic sites present in the CVDA SNPs identified in Table 1 and/or Table 2.

[0111] In certain embodiments, the invention provides, for each of these polymorphisms, a primer that terminates at the nucleotide position immediately adjacent to a polymorphic site on the 3' side and extends at least 8 and less than 100 nucleotides in the 5' direction from this site. It is noted that the foregoing includes two classes of primers, having sequences representing both DNA strands. According to certain embodiments, the primer extends at least 10, at least 12, at least 15, or at least 20 nucleotides in the 5' direction. According to certain embodiments, the primer extends less than 80, less than 60, less than 50, less than 40, less than 30, or less than 20 nucleotides in the 5' direction. The invention further provides primers that terminate and extend similarly for any polymorphic site of a CVDA SNP, or a polymorphic site linked to such a SNP.

[0112] In general, primers and probes of the present invention may be made using any convenient method of synthesis.

Examples of such methods may be found in standard textbooks, for example "Protocols for Oligonucleotides and Analogues; Synthesis and Properties," Methods in Molecular Biology Series; Volume 20; Ed. Sudhir Agrawal, Humana ISBN: 0-89603-247-7; 1993. According to certain embodiments, the primer(s) and/or probes are labeled to facilitate detection.

[0113] Primers and probes of the present invention may be conveniently provided in sets, e.g., sets capable of determining which polymorphic variant(s) is/are present among some or all of the possible polymorphic variants that may exist at a particular polymorphic site. The sets may include allele-specific primers or probes and/or primers that terminate immediately adjacent to a polymorphic site. Multiple sets of primers and/or probes, capable of detecting polymorphic variants at a plurality of polymorphic sites may be provided.

[0114] Oligonucleotides that exhibit differential or selective binding to polymorphic sites may readily be designed by one of ordinary skill in the art. For example, an oligonucleotide that is perfectly complementary to a sequence that encompasses a polymorphic site (e.g., a sequence that includes the polymorphic site within it or at one or the other end) will generally hybridize preferentially to a nucleic acid comprising that sequence as opposed to a nucleic acid comprising an alternate polymorphic variant

[0115] In some embodiments, any of a variety of sequencing reactions known in the art can be used to directly sequence at least a portion of genomic DNA and detect allelic variants. The sequence can be compared with the sequences of known allelic variants to determine which one(s) are present in the sample. Exemplary sequencing reactions include those based on techniques developed by Maxam and Gilbert, Proc. Natl. Acad Sci USA, 74:560, 1977 or Sanger, Proc. Nat. Acad. Sci 74:5463, 1977. It is also contemplated that any of a variety of automated sequencing procedures may be utilized when performing the subject assays (Biotechniques 19:448, 1995; Venter, et al., Science, 291:1304-1351, 2001; Lander, et al., Nature, 409:860-921, 2001), including sequencing by mass spectrometry (see, for example, U.S. Pat. No. 5,547,835 and international patent application Publication Number WO 94/16101, entitled DNA Sequencing by Mass Spectrometry by H. Koster; U.S. Pat. No. 5,547,835 and international patent application Publication Number WO 94/21822 entitled "DNA Sequencing by Mass Spectrometry Via Exonuclease Degradation" by H. Koster), and U.S. Pat. No. 5,605,798 and International Patent Application No. PCT/US96/03651 entitled DNA Diagnostics Based on Mass Spectrometry by H. Koster; Cohen et al. (1996) Adv Chromatogr 36:127-162; and Griffin et al. (1993) Appl Biochem Biotechnol 38:147-159). It will be evident to one skilled in the art that, for certain embodiments, the occurrence of only one, two or three of the nucleic acid bases need be determined in the sequencing reaction. Yet other sequencing methods are disclosed, e.g., in U.S. Pat. No. 5,580,732 entitled "Method of DNA sequencing employing a mixed DNA-polymer chain probe" and U.S. Pat. No. 5,571,676 entitled "Method for mismatch-directed in vitro DNA sequencing", and in Melamede, U.S. Pat. No. 4,863,849; Cheeseman, U.S. Pat. No. 5,302,509, Tsien et al, International application WO 91/06678; Rosenthal et al, International application WO 93/21340; Canard et al, Gene, 148: 1-6 (1994); Metzker et al, Nucleic Acids Research, 22: 4259-4267 (1994) and U.S. Pat. Nos. 5,740,341 and 6,306,597.

[0116] In some cases, the presence of a specific allele can be shown by restriction enzyme analysis. For example, a specific nucleotide polymorphism can result in a nucleotide sequence comprising a restriction site which is absent from the nucleotide sequence of another allelic variant. Additionally or alternately, a specific nucleotide polymorphism can result in the elimination of a nucleotide sequence comprising a restriction site which is present in the nucleotide sequence of another allelic variant.

[0117] In certain embodiments, alterations in electrophoretic mobility are used to identify the allelic variant. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between two similar nucleic acids (Orita et al., Proc Natl. Acad. Sci USA 86:2766, 1989, see also Cotton, Mutat Res 285:125-144, 1993; and Hayashi, Genet Anal Tech Appl 9:73-79, 1992). Single-stranded DNA fragments of sample and control nucleic acids are denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence and the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In certain embodiments, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al., Trends Genet 7:5, 1991).

[0118] In certain embodiments, the identity of an allelic variant of a polymorphic region is assayed using denaturing gradient gel electrophoresis ("DGGE"). DGGE comprises analyzing the movement of a nucleic acid comprising the polymorphic region in polyacrylamide gels containing a gradient of denaturant (DGGE) (Myers et al., Nature 313:495, 1985). When DGGE is used as the method of analysis, DNA may be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In certain embodiments, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner, Biophys Chem 265:1275, 1987).

[0119] Examples of techniques for detecting differences of at least one nucleotide between two nucleic acids include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide probes may be prepared in which the known polymorphic nucleotide is placed centrally (allele-specific probes) and then hybridized to target DNA under conditions which permit hybridization only if a perfect

match is found (Saiki et al., Nature 324:163, 1986); Saiki et al., Proc. Natl Acad. Sci USA 86:6230, 1989; and Wallace et al., Nucl. Acids Res. 6:3543, 1979). Such allele specific oligonucleotide hybridization techniques may be used for the simultaneous detection of several nucleotide changes in different polymorphic regions of DNA. For example, oligonucleotides having nucleotide sequences of specific allelic variants are attached to a hybridizing membrane and this membrane is then hybridized with labeled sample nucleic acid. Analysis of the hybridization signal will then reveal the identity of the nucleotides of the sample nucleic acid.

[0120] In certain embodiments, allele specific amplification technology which depends on selective PCR amplification may be used. Oligonucleotides used as primers for specific amplification may carry the allelic variant of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al., Nucleic Acids Res. 17:2437-2448, 1989) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner, Tibtech 11:238, 1993; Newton et al., Nucl. Acids Res. 17:2503, 1989). This technique is also termed "PROBE" for Probe Oligo Base Extension. In addition, it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al., Mol. Cell Probes 6:1, 1992).

[0121] In certain embodiments, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, e.g., in U.S. Pat. No. 4,998,617 and in Landegren, U. et al., Science 241:1077-1080, 1988. The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g., biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin, or another biotin ligand. Nickerson, D. A. et al. have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, D. A. et al., Proc. Natl. Acad. Sci. (U.S.A.) 87:8923-8927, 1990. In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

[0122] Several techniques based on this OLA method have been developed and can be used to detect specific allelic variants of a polymorphic region. For example, U.S. Pat. No. 5,593,826 discloses an OLA using an oligonucleotide having 3'-amino group and a 5'-phosphorylated oligonucleotide to form a conjugate having a phosphoramidate linkage. In another variation of OLA described in Tobe et al. (Nucleic Acids Res 24: 3728, 1996), OLA combined with PCR permits typing of two alleles in a single microtiter well. By marling each of the allele-specific primers with a unique hapten, e.g. digoxigenin or fluorescein, each LA reaction can be detected by using hapten specific antibodies that are labeled with different enzyme reporters, alkaline phosphatase or horseradish peroxidase. This system permits the detection of the two alleles using a high throughput format that leads to the production of two different colors.

[0123] Additionally or alternatively, the invention provides further methods of use for detecting single nucleotide polymorphisms. Because single nucleotide polymorphisms constitute sites of variation flanked by regions of invariant sequence, their analysis requires no more than the determination of the identity of the single nucleotide present at the site of variation. Several methods have been developed to facilitate the analysis of such single nucleotide polymorphisms.

[0124] In certain embodiments, a single nucleotide polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in Mundy, C. R. (U.S. Pat. No. 4,656,127). According to such embodiments, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was complementary to that of the nucleotide derivative used in the reaction.

[0125] In certain embodiments, a solution-based method is used for determining the identity of the nucleotide of a polymorphic site. Cohen, D. et al. (French Patent 2,650,840; PCT App. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer may be employed that is complementary to allelic sequences immediately 3' to a polymorphic site. Such a method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

[0126] An alternative method is described by Goelet, P. et al. (PCT App. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT App. No. WO91/02087) the method of Goelet, P. et al. is preferably a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

[0127] A variety of primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have

been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-0.7784, 1989; Sokolov, B. P., Nucl. Acids Res. 18:3671, 1990 ; Syvanen, A.-C., et al., Genomics 8:684-692, 1990, Kuppuswamy, M. N. et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147, 1991; Prezant, T. R. et al., Hum. Mutat. 1:159-164, 1992; Ugozzoli, L. et al., GATA 9:107-112, 1992; Nyren, P. et al., Anal. Biochem. 208:171-175, 1993). These methods rely on the incorporation of labeled deoxynucleotides to discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are proportional to the length of the run (Syvanen, A.-C., et al., Amer. J. Hum. Genet. 52:46-59 (1993)).

[0128] In certain embodiments, fluorescence polarization template-directed dye-terminator incorporation (FP-TDI) is used to determine which of multiple polymorphic variants of a polymorphism is present in a subject. This method is based on template-directed primer extension and detection by fluorescence polarization. According to this method, amplified genomic DNA containing a polymorphic site is incubated with oligonucleotide primers (designed to hybridize to the DNA template adjacent to the polymorphic site) in the presence of allele-specific dye-labeled dideoxyribonucleoside triphosphates and a commercially available modified *Taq* DNA polymerase. The primer is extended by the dye-terminator specific for the allele present on the template, increasing ?10-fold the molecular weight of the fluorophore. At the end of the reaction, the fluorescence polarization of the two dye-terminators in the reaction mixture is analyzed directly without separation or purification. Such a homogeneous DNA diagnostic method has been shown to be highly sensitive and specific and is suitable for automated genotyping of large number of samples. (Chen, X., et a/., Genome Research, Vol. 9, Issue 5, 492-498, 1999). Note that rather than involving use of allele-specific probes or primers, this method employs primers that terminate adjacent to a polymorphic site, so that extension of the primer by a single nucleotide results in incorporation of a nucleotide complementary to the polymorphic variant at the polymorphic site.

[0129] Real-time pyrophosphate DNA sequencing is yet another approach to detection of polymorphisms and polymorphic variants (Alderborn, A., et al., Genome Research, Vol. 10, Issue 8, 1249-1258, 2000). Additional methods include, for example, PCR amplification in combination with denaturing high performance liquid chromatography (dHPLC) (Underhill, P.A., et al., Genome Research, Vol. 7, No. 10, pp. 996-1005, 1997).

[0130] In general, it will be often of interest to determine the genotype of a subject with respect to both alleles of the polymorphic site present in the genome. For example, the complete genotype may be characterized as -/-, as -/+, or as +/+, where a minus sign indicates the presence of a particular sequence at the polymorphic site (e.g., the major allele, by which is meant the allele that occurs most frequently in a population), and the plus sign indicates the presence of a different polymorphic variant other than the reference sequence. Other methods simply use the identity of the base present at a polymorphic position. If multiple polymorphic variants exist at a site, this can be appropriately indicated by specifying which ones are present. Any of the detection means above may be used to determine the genotype of a subject with respect to one or both copies of the polymorphism present in the subject's genome.

[0131] According to certain embodiments, it is advantageous to employ methods that can detect the presence of multiple polymorphic variants (e.g., polymorphic variants at a plurality of polymorphic sites) in parallel or substantially simultaneously. Oligonucleotide arrays represent one suitable means for doing so. Other methods, including methods in which reactions (e.g., amplification, hybridization) are performed in individual vessels, e.g., within individual wells of a multi-well plate or other vessel may also be performed so as to detect the presence of multiple polymorphic variants (e.g., polymorphic variants at a plurality of polymorphic sites) in parallel or substantially simultaneously according to certain embodiments of the invention.

[0132] For determining the identity of the allelic variant of a polymorphic region located in the coding region of a gene, methods in addition to those described above can be used. For example, identification of an allelic variant which encodes a variant protein can be performed by using an antibody specifically recognizing the variant protein in, e.g., immunohistochemistry or immunoprecipitation. Antibodies to specific variants proteins can be prepared according to methods known in the art and as described herein. Additionally or alternatively, one can also measure a biological or biochemical activity of a protein, such as binding to a particular molecular target or cell. Suitable binding assays are known in the art.

[0133] If a polymorphic region is located in an exon, either in a coding or noncoding region of the gene, the identity of the allelic variant can be determined by determining the molecular structure of the mRNA, pre-mRNA, or cDNA. The molecular structure can be determined using any of the above described methods for determining the molecular structure of the genomic DNA, e.g., sequencing and SSCP.

[0134] Methods described herein may be performed, for example, by utilizing prepackaged diagnostic kits, such as those described herein comprising at least a reagent such as a probe or primer nucleic acid described herein, which may be conveniently used, e.g., to determine whether a subject has or is susceptible to development or occurrence of a cardiovascular disease or coronary event associated with a specific gene allelic variant.

[0135] As mentioned above, nucleic acids or proteins for use in the above-described diagnostic and prognostic methods can be obtained from any cell type or tissue of a subject. For example, a subject's bodily fluid (e.g. blood) can be obtained by known techniques (e.g. venipuncture) or from human tissues like heart (biopsies, transplanted organs). Alternatively, nucleic acid tests can be performed on dry samples (e.g. hair or skin). Fetal nucleic acid samples for prenatal diagnostics can be obtained from maternal blood as described in International Patent Application No. WO91/07660 to Bianchi.

Additionally or alternatively, amniocytes or chorionic villi may be obtained for performing prenatal testing.

[0136] Diagnostic procedures may also be performed in situ directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents may be used as probes and/or primers for such in situ procedures (see, for example, Nuovo, G. J., PCR in situ hybridization: protocols and applications, Raven Press, New York, 1992).

[0137] In certain embodiments, as mentioned above, the presence of absence of a plurality of polymorphic variants at different polymorphic sites is detected. Thus a genetic profile of an individual may be generated, wherein the genetic profile indicates which allelic variant is present at a plurality of different polymorphisms that are associated with cardiovascular disease.

[0138] In some embodiments, the genotype of a large number of individuals exhibiting particular risk factors, markers of cardiovascular status, or response to therapy for cardiovascular disease is determined with respect to one or more polymorphisms by any of the methods described above, and compared with the distribution of genotypes of individuals that have been matched for any of a plurality of characteristics such as age, ethnic origin, and/or any other statistically or medically relevant parameters, who exhibit quantitatively or qualitatively risk factors, markers of cardiovascular status, or response to therapy. "Cardiovascular status" as used herein refers to the physiological status of an individual's cardiovascular system as reflected in one or more markers or indicators. Status markers include without limitation clinical measurements such as, e.g., blood pressure, electrocardiographic profile, and differentiated blood flow analysis as well as measurements of LDL- and HDL-cholesterol levels, other lipids (e.g., TGs) and other well established clinical parameters that are standard in the art. It will be appreciated that status markers and risk factors overlap. Status markers according to the invention also include diagnoses of one or more cardiovascular symptoms or syndromes, such as, e.g., hypertension, acute myocardial infarction, silent myocardial infarction, stroke, and atherosclerosis. It will be understood that a diagnosis of a cardiovascular syndrome made by a medical practitioner encompasses clinical measurements and medical judgment. Status markers further include results of imaging analyses, e.g., magnetic resonance imaging, ultrasound imaging such as Doppler imaging, angiograms, and other means to evaluate the structure of the blood vessel wall, blood flow, and the like. Status markers according to the invention may be assessed using conventional methods well known in the art.

[0139] Also included in the evaluation of cardiovascular status are quantitative or qualitative changes in status markers with time, such as would be used, e.g., in the determination of an individual's response to a particular therapeutic regimen. Correlations are achieved using any method known in the art, including nominal logistic regression, chi square tests or standard least squares regression analysis. In this manner, it is possible to establish statistically significant correlations between particular genotypes and particular risk factors, markers of cardiovascular status, or response to therapy for cardiovascular disease (e.g., given in terms of p values). It is further possible to establish statistically significant correlations between particular genotypes and changes in markers of cardiovascular status such as, would result, e.g., from particular treatment regimens. In this manner, it is possible to correlate genotypes with responsivity to particular treatments. One of ordinary skill in the art will recognize that a variety of different statistical tests can be used to establish a correlation.

[0140] In certain embodiments, two or more polymorphic variants form a haplotype. Such polymorphic variants may be variants disclosed herein, variants known in the art, or variants yet to be described. The invention encompasses determining whether an individual has a particular haplotype comprising one or more of the polymorphic variants disclosed herein. In some embodiments, a haplotype is associated with an increased risk of development or occurrence of a cardiovascular disease or event. Without wishing to be bound by any theory, such haplotypes may provide better predictive/diagnostic information than a single SNP.

[0141] In certain embodiments, a panel of SNPs and/or haplotypes is defined that provides diagnostic and/or prognostic information when an individual is genotyped with respect to the SNPs and/or haplotypes. In certain embodiments, a panel includes at least 2 SNPs, wherein the SNPs are substantially unlinked. For example, the recombination frequency between each pair of SNPs may be approximately 0.5. In certain embodiments, a panel includes at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or more substantially unlinked SNPs. Of course a panel may also include one or more SNPs that are linked, e.g., in strong LD, with at least one other SNP. In some embodiments, at least 2 SNPs or haplotypes include a polymorphic variant that contributes a relative risk of at least 1.1 to an individual's overall risk of developing CVD and/or suffering a major coronary event within a defined period of time. In certain embodiments, at least 3, 4, 5, 6, 7, 8, 9, or 10 of the SNPs or haplotypes includes such a polymorphic variant. In certain embodiments, a panel includes at least 2 SNPs or haplotypes that are each present in at least 5% of a target population, each of which includes a polymorphic variant that contributes a relative risk of at least 1.1 to an individual's overall risk of developing CVD and/or suffering a major coronary event within a defined period of time. In certain embodiments of the invention at least 3, 4, 5, 6, 7, 8, 9, or 10 of the SNPs or haplotypes include such a polymorphic variant.

[0142] In certain embodiments, results obtained from the panel predict the risk for developing CVD and/or the risk of experiencing a major coronary event. In certain embodiments, subsequent identification and evaluation of an individual's haplotype can then help to guide specific and individualized therapy. The risk can be, e.g., absolute risk, which can be

expressed in terms of the likelihood (e.g., % likelihood) that an individual will manifest a symptom or sign of CVD and/or will experience a major coronary event within a defined time period. Additionally or alternatively, the risk can be expressed in terms of relative risk, e.g., a factor that expressed the degree to which the individual is at increased risk relative to the risk the individual would face if his or her genotype with respect to one of more of the polymorphisms or haplotypes was different. Individuals can be stratified based on their risk. Such stratification can be used, for example, to select individuals who would be likely to benefit from particular therapeutic regimens and/or can be used to identify individuals for a clinical trial. It should be emphasized that the information provided by the methods of the present invention can be qualitative or quantitative and can be expressed using any convenient means. It can be based on the evaluation of one or both alleles of a single polymorphism in an individual, or can be based on the evaluation of multiple polymorphisms and/or haplotypes.

[0143] A predictive panel can be used for genotyping of one or more individuals on a platform that can genotype multiple SNPs at the same time (multiplexing). In certain embodiments, platforms are, e.g., gene chips (Affymetrix) or the Luminex LabMAP reader. See, e.g., (Armstrong, B., et al., Cytometry 40: 102-108, 2000; Cai, H., et al., Genomics 66: 135-143, 2000; and Chen, J., et al., Genome Research 10: 549-557, 2000) for description of Luminex assays and their application for purposes of SNP genotyping. Such assays typically involve populations of fluorescent beads, which are evaluated using flow cytometery. Of course these multiplexed assays are of use for genotyping individual SNPs in either a single individual or multiple individuals.

[0144] In certain embodiments, information obtained from detecting one or more polymorphic variants is used together with information obtained by evaluating the existence of classical risk factors in a patient to provide an assessment of risk that includes the contribution of genetic factors that may or may not play a role in classical risk factors such as lipid levels. In certain embodiments, an individual's classical risk factors are evaluated according to the PROCAM method (Assmann, *supra*) and an individual is genotyped with respect to one or more of the CVDA SNPs and/or haplotypes described herein. The genotyping results in a relative risk ratio that is used to modify the PROCAM score. For example, the PROCAM score may be multiplied by a relative risk determined based on the genotype of the individual, or a value is added to or subtracted from the PROCAM score to provide a modified PROCAM score. In certain embodiments, the invention therefore provides methods for determining whether an individual has or is susceptible to development or occurrence of a cardiovascular disease or event, wherein the individual is in need of such determination, the method comprising the step of: combining information derived from an assessment of one or more classical risk factors and/or cardiovascular status markers together with genetic information obtained by (a) detecting a polymorphic variant of a CVDA polymorphism in the individual; or (b) detecting a polymorphic variant in strong LD with a CVDA polymorphism; or (c) detecting a haplotype comprising a polymorphic variant of the CVDA polymorphism in the individual; or (d) detecting an allele of a gene comprising the polymorphic variant of the CVDA polymorphism in the individual. It will be appreciated that the combining can be performed in any of a wide variety of ways.

[0145] In certain embodiments, the invention provides a database or other suitably organized and optionally searchable compendium of information comprising a list or other suitable form of presentation of CVDA polymorphisms and/or polymorphic sequences, haplotypes, and/or linked polymorphisms, stored on a computer-readable medium, wherein the contents of the database may be largely or entirely limited to polymorphisms that have been identified as useful in performing genotyping for assessing an individual's susceptibility to CVD, etc., as described herein. The database is distinguished from general compendia of information regarding polymorphisms, such as those described above, in that it specifically groups, selects, and/or identifies the polymorphisms as being related to CVD. In some embodiments the database includes information such as a relative risk, allele frequencies, or the like. It will be appreciated that the information can be stored in any of a wide variety of formats. The database may include results of genotyping one or more individuals with respect to one or more of the CVDA polymorphisms and/or haplotypes described herein. The results can be results of one or more of the tests described herein. The invention also encompasses a method comprising the step of electronically sending or receiving information such as that present in a database of the invention and/or electronically sending or receiving results of a genotyping test as described herein.

[0146] Isolated Polymorphic Nucleic Acids, Probes, and Vectors

[0147] The present invention provides isolated nucleic acids comprising the polymorphic positions and specific polymorphic variants described herein for human genes; vectors comprising the nucleic acids, and transformed host cells comprising the vectors. The invention also provides probes, primers, and other reagents that are useful for detecting the polymorphic variants of such polymorphisms.

[0148] In practicing the present invention, many conventional techniques in molecular biology, microbiology, and recombinant DNA technology may be used. Such techniques are well known and are explained fully in, for example, Sambrook et al., *supra*, Ausubel, F. (ed.), *supra*, DNA Cloning: A Practical Approach, Volumes I and II, 1985 (D. N. Glover ed.); Oligonucleotide Synthesis, 1984, (M.L. Gait ed.); Nucleic Acid Hybridization, 1985, (Hames and Higgins); Ausubel et al., Current Protocols in Molecular Biology, 1997, (John Wiley and Sons); and Methods in Enzymology Vol. 154 and Vol. 155 (Wu and Grossman, and Wu, eds., respectively).

[0149] Since the human genome has been sequenced and is publicly available, e.g., at the NCBI website, knowing

the identity of the SNPs listed in Tables 1 and 2 provides the artisan with the genomic DNA sequence located adjacent to, e.g., upstream and/or downstream of the SNP. A portion of the surrounding sequence for each SNP is provided in Tables 1 and 2. A sequence of any particular length can be selected. In certain embodiments, the portion surrounding the SNP can be used as a probe to identify a longer genomic sequence of a cDNA. Thus, in certain embodiments, the invention provides a cDNA comprising any of the polymorphic sites identified herein.

[0150] In certain embodiments, the invention provides an isolated nucleic acid comprising or immediately adjacent to the position of a SNP identified in Table 1 and/or Table 2. The isolated nucleic acid can be of any desired length. Insertion of nucleic acids (typically DNAs) comprising sequences encompassed by the present invention into a nucleic acid vector is easily accomplished when the termini of both the nucleic acids and the vector comprise compatible ends, such as those generated by cleavage with a restriction enzyme. If this is not possible, the termini of the DNAs and/or vector can be modified by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase. In certain embodiments, a specific sequence at the ends of the nucleic acids to be inserted, the vectors, or both may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki et al., Science 239:48, 1988. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing. One of ordinary skill in the art will appreciate that cloning and manipulation of nucleic acids is wholly routine in the art, and kits are commercially available for performing virtually any desired manipulation.

[0151] The nucleic acids may be isolated directly from cells or may be chemically synthesized using known methods. Alternatively, the polymerase chain reaction (PCR) method can be used to produce inventive nucleic acids, using either chemically synthesized strands or genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

[0152] Reagents and Methods for Modulating Expression and/or Activity of CVDA Polynucleotides and Polypeptides

[0153] The CVDA genes and their encoded mRNA and polypeptides are potential therapeutic targets for cardiovascular disease. Therefore, it is desirable to be able to modulate their expression and/or activity, both for therapeutic and other purposes. In certain embodiments, the invention therefore provides a variety of methods for altering expression and/or functional activity of a CVDA gene, which are further described below. The invention encompasses methods for screening compounds for preventing or treating a cardiovascular disease by assaying the ability of the compounds to modulate the expression of one or more of the CVDA genes disclosed herein or activity of the protein products of these genes. Appropriate screening methods include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the target gene or protein.

[0154] In certain embodiments, the invention provides an antisense nucleic acid that inhibits expression of a CVDA gene. In certain embodiments, such an antisense nucleic acid selectively inhibits a CVDA polymorphic variant of a CVDA gene. As is known in the art, antisense nucleic acids are generally single-stranded nucleic acids (DNA, RNA, modified DNA, modified RNA, or peptide nucleic acids) complementary to a portion of a target nucleic acid (e.g., an mRNA transcript) and therefore able to bind to the target to form a duplex. Typically they are oligonucleotides that range from 15 to 35 nucleotides in length but may range from 10 up to approximately 50 nucleotides in length. Binding typically reduces or inhibits the function of the target nucleic acid. For example, antisense oligonucleotides may block transcription when bound to genomic DNA, inhibit translation when bound to mRNA, and/or lead to degradation of the nucleic acid. Reduction in expression of a CVDA polypeptide may be achieved by the administration of an antisense nucleic acid or peptide nucleic acid (PNA) comprising sequences complementary to those of the mRNA that encodes the polypeptide. Antisense technology and its applications are well known in the art and are described in Phillips, M.I. (ed.) Antisense Technology, Methods Enzymol., Volumes 313 and 314, Academic Press, San Diego, 2000, and references mentioned therein. See also Crooke, S. (ed.) "Antisense Drug Technology: Principles, Strategies, and Applications" (1st ed), Marcel Dekker; ISBN: 0824705661; 1 st edition (2001) and references therein.

[0155] Peptide nucleic acids (PNA) are analogs of DNA in which the backbone is a pseudopeptide rather than a sugar. PNAs mimic the behavior of DNA and bind to complementary nucleic acid strands. The neutral backbone of a PNA can result in stronger binding and greater specificity than normally achieved using DNA or RNA. Binding typically reduces or inhibits the function of the target nucleic acid. Peptide nucleic acids and their use are described in Nielsen, P.E. and Egholm, M., (eds.) "Peptide Nucleic Acids: Protocols and Applications" (First Edition), Horizon Scientific Press, 1999.

[0156] According to certain embodiments, the antisense oligonucleotides have any of a variety of lengths. For example, such antisense oligonucleotides may comprise between 8 and 60 contiguous nucleotides complementary to an mRNA encoded by a CVDA gene, between 10 and 60 contiguous nucleotides complementary to an mRNA encoded by a CVDA gene, or between 12 and 60 contiguous nucleotides complementary to an mRNA encoded by a CVDA gene. According to certain embodiments, the antisense oligonucleotide need not be perfectly complementary to the mRNA to which it hybridizes but may have, for example, up to 1 or 2 mismatches per 10 nucleotides.

[0157] The invention further encompasses a method of inhibiting expression of a CVDA gene in a cell or individual comprising delivering an antisense oligonucleotide to the cell or individual or expressing such an antisense oligonucleotide within a cell or cells of the individual. Additionally or alternatively, inventive methods include treating or preventing a cardiovascular disease or condition comprising steps of (i) providing a individual in need of treatment for or prevention of a cardiovascular disease or condition; and (ii) administering a pharmaceutical composition comprising an effective amount of a an antisense oligonucleotide to the individual, wherein the antisense oligonucleotide inhibits expression of a CVDA gene.

[0158] In certain embodiments, the invention provides a ribozyme designed to cleave an mRNA encoded by a CVDA gene. Ribozymes (catalytic RNA molecules that are capable of cleaving other RNA molecules) represent another approach to reducing gene expression. Ribozymes can be designed to cleave specific mRNAs corresponding to a gene of interest. Their use is described in U.S. Patent No. 5,972,621, and references therein. Extensive discussion of ribozyme technology and its uses is found in Rossi, J.J., and Duarte, L.C., Intracellular Ribozyme Applications: Principles and Protocols, Horizon Scientific Press, 1999.

[0159] The invention further encompasses methods of inhibiting expression of a CVDA polypeptide in a cell or individual comprising delivering a ribozyme designed to cleave an mRNA encoded by a CVDA gene to the cell or individual or expressing such a ribozyme within a cell or cells of the individual. Additionally or alternatively, the invention provides methods of treating or preventing a cardiovascular disease or condition comprising steps of (i) providing a individual in need of treatment for a cardiovascular disease or condition; and (ii) administering a pharmaceutical composition comprising an effective amount of a ribozyme designed to cleave an mRNA encoded by a CVDA gene to the individual, thereby alleviating the condition.

[0160] RNA interference (RNAi) is a mechanism of post-transcriptional gene silencing mediated by double-stranded RNA (dsRNA), which is distinct from the antisense and ribozyme-based approaches described above. dsRNA molecules are believed to direct sequence-specific degradation of mRNA that contain regions complementary to one strand (the antisense strand) of the dsRNA in cells of various types after first undergoing processing by an RNase III-like enzyme called DICER (Bernstein et al., Nature 409:363, 2001) into smaller dsRNA molecules. Such molecules comprise two 21 nt strands, each of which has a 5' phosphate group and a 3' hydroxyl, and includes a 19 nt region precisely complementary with the other strand, so that there is a 19 nt duplex region flanked by 2 nt-3' overhangs and are known as short interfering RNA (siRNA). An siRNA typically comprises a double-stranded region approximately 19 nucleotides in length with 1-2 nucleotide 3' overhangs on each strand, resulting in a total length of between approximately 21 and 23 nucleotides. In mammalian cells, dsRNA longer than approximately 30 nucleotides typically induces nonspecific mRNA degradation via the interferon response. However, the presence of siRNA in mammalian cells, rather than inducing the interferon response, results in sequence-specific gene silencing.

[0161] RNAi can also be achieved using molecules referred to as short hairpin RNAs (shRNA), which are single RNA molecules comprising at least two complementary portions capable of self-hybridizing to form a duplex structure sufficiently long to mediate RNAi (typically at least 19 base pairs in length), and a loop, typically between approximately 1 and 10 nucleotides in length and more commonly between 4 and 8 nucleotides in length that connects the two nucleotides that form the last nucleotide pair at one end of the duplex structure. shRNAs are thought to be processed into siRNAs by the conserved cellular RNAi machinery. Thus shRNAs are precursors of siRNAs and are similarly capable of inhibiting expression of a target transcript.

[0162] siRNAs and shRNAs have been shown to downregulate gene expression when transferred into mammalian cells by such methods as transfection, electroporation, or microinjection, or when expressed in cells via any of a variety of plasmid-based approaches. RNA interference using siRNA and/or shRNA is reviewed in, e.g., Tuschl, T., Nat. Biotechnol., 20: 446-448, May 2002. See also Yu, J., et al., Proc. Natl. Acad. Sci., 99(9), 6047-6052, 2002; Sui, G., et al., Proc. Natl. Acad. Sci., 99(8), 5515-5520, 2002; Paddison, P., et al., Genes and Dev., 16, 948-958, 2002; Brummelkamp, T., et al., Science, 296, 550-553, 2002; Miyagashi, M. and Taira, K., Nat. Biotech., 20, 497-500, 2002; Paul, C., et al., Nat. Biotech., 20, 505-508, 2002. A number of variations in structure, length, number of mismatches, size of loop, identity of nucleotides in overhangs, etc., are consistent with effective RNAi-mediated gene silencing. For example, one or more mismatches between the target mRNA and the complementary portion of the siRNA or shRNA may still be compatible with effective silencing.

[0163] It is thought that intracellular processing (e.g., by DICER) of a variety of different precursors results in production of RNAs of various kinds that are capable of effectively mediating gene silencing. For example, in addition to the siRNA and shRNA structures described above, DICER can process ?70 nucleotide hairpin precursors with imperfect duplex structures, i.e., duplexes that are interrupted by one or more mismatches, bulges, or inner loops within the stem of the hairpin into single-stranded RNAs called microRNAs (miRNA) that are believed to hybridize within the 3' UTR of a target mRNA and repress translation. See, e.g., Lagos-Quintana, M. et al., Science, 294, 853-858, 2001; Pasquinelli, A., Trends in Genetics, 18(4), 171-173, 2002, and references in the foregoing two articles for discussion of miRNAs and their mechanisms of silencing.

[0164] Accordingly, In certain embodiments, the invention provides siRNAs and shRNAs that inhibit expression of an

mRNA encoded by any of the CVDA genes disclosed herein. An RNAi agent is considered to inhibit expression of a target transcript and thus to be targeted to the transcript if the stability or translation of the target transcript is reduced in the presence of the siRNA as compared with its absence. Typically the antisense portion of an RNAi agent shows at least about 80%, at least about 90%, at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% precise sequence complementarity with the target transcript for a stretch of at least about 17, 18 or 19 to about 21-23 or more nucleotides.

[0165] The invention encompasses methods of inhibiting expression of a CVDA gene in a cell or individual comprising delivering an siRNA or shRNA targeted to an mRNA encoded by a CVDA gene to the cell or individual. Additionally or alternatively, the invention provides methods of treating or preventing a cardiovascular disease or condition comprising steps of (i) providing a individual in need of treatment for atherosclerosis or a disease or condition associated with atherosclerosis; and (ii) administering a pharmaceutical composition comprising an effective amount of an siRNA or shRNA targeted to an mRNA encoded by a CVDA gene to the individual, thereby alleviating the condition.

[0166] As mentioned above, siRNAs and shRNAs have been shown to effectively reduce gene expression when expressed intracellularly, e.g., by delivering vectors such as plasmids, viral vectors such as adenoviral, retroviral or lentiviral vectors, or viruses to cells. Such vectors, referred to herein as RNAi-inducing vectors, are vectors whose presence within a cell results in transcription of one or more RNAs that self-hybridize or hybridize to each other to form an shRNA or siRNA. In general, the vector comprises a nucleic acid operably linked to expression signal(s) so that one or more RNA molecules that hybridize or self-hybridize to form an siRNA or shRNA are transcribed when the vector is present within a cell. Thus the vector provides a template for intracellular synthesis of the RNA or RNAs or precursors thereof. The vector will thus contain a sequence or sequences whose transcription results in synthesis of two complementary RNA strands having the properties of siRNA strands described above, or a sequence whose transcription results in synthesis of a single RNA molecule containing two complementary portions separated by an intervening portion that forms a loop when the two complementary portions hybridize to one another.

[0167] Selection of appropriate siRNA and shRNA sequences can be performed according to guidelines well known in the art, e.g., taking factors such as desirable GC content into consideration. See, e.g., (Dykxhoorn, D.M., et al., Nature Reviews Molecular Cell Biology. 4: 457-467, 2003; Elbashir, S.M., et al., Nature. 411:494-498, 2001; Elbashir, S.M., et al., Genes and Development, 15: 188-200, 2001; and WO 01/75164 and U.S. Pub. Nos. 20020086356 and 20030108923 for further information.

[0168] As is known in the art, by selecting about 5 siRNAs it will almost always be possible to identify an effective sequence. If necessary additional siRNAs can be designed and tested. It may be desirable to perform a systematic screen to identify highly effective siRNAs. A number of computer programs that aid in the selection of effective siRNA/shRNA sequences are known in the art, which yield even higher percentages of effective siRNAs. See, e.g., Cui, W., et al., "OptiRNai, a Web-based Program to Select siRNA Sequences", Proceedings of the IEEE Computer Society Conference on Bioinformatics, p. 433, 2003. Algorithms for selecting effective siRNA are also described in Reynolds, A., et al., Nat Biotechnol., 22(3):326-30, 2004. Pre-designed siRNAs targeting over 95% of the mouse or human genome are commercially available, e.g., from Ambion and/or Cenix Biosciences. As is known in the art, siRNAs and shRNAs can be delivered using a variety of delivery agents that increase their cellular uptake or potency or protect them from degradation.

[0169] Antisense nucleic acids, ribozymes, siRNAs, or shRNAs can be delivered to cells by standard techniques such as microinjection, electroporation, or transfection. Antisense nucleic acids, ribozymes, siRNAs, or shRNAs can be formulated as pharmaceutical compositions and delivered to an individual using a variety of approaches. According to certain embodiments, the delivery of antisense, ribozyme, siRNA, or shRNA molecules is accomplished via a gene therapy approach in which vectors (e.g., viral vectors such as retroviral, lentiviral, or adenoviral vectors, etc.) are delivered to a cell or individual, or cells directing expression of the molecules (e.g., cells into which a vector directing expression of the molecule has been introduced) are administered to the individual.

[0170] It may be advantageous to employ various nucleotide modifications and nucleotide analogs to confer desirable properties on the antisense nucleic acid, ribozyme, siRNA, or shRNA. Numerous nucleotide analogs, nucleotide modifications, and modifications elsewhere in a nucleic acid chain are known in the art, and their effect on properties such as hybridization and nuclease resistance has been explored. For example, various modifications to the base, sugar and internucleoside linkage have been introduced into oligonucleotides at selected positions, and the resultant effect relative to the unmodified oligonucleotide compared. A number of modifications have been shown to alter one or more aspects of the oligonucleotide such as its ability to hybridize to a complementary nucleic acid, its stability, etc. For example, useful 2'-modifications include halo, alkoxy and allyloxy groups. US patent numbers 6,403,779, 6,399,754, 6,225,460, 6,127,533, 6,031,086, 6,005,087, 5,977,089, and references therein disclose a wide variety of nucleotide analogs and modifications that may be of use in the practice of the present invention. See also Crooke, S. (ed.), referenced above, and references therein. As will be appreciated by one of ordinary skill in the art, analogs and modifications may be tested using, e.g., the assays described herein or other appropriate assays, in order to select those that effectively reduce expression of the target nucleic acid. The analog or modification advantageously results in a nucleic acid with increased

absorbability (e.g., increased absorbability across a mucus layer, increased oral absorption, etc.), increased stability in the blood stream or within cells, increased ability to cross cell membranes, etc.

[0171] Antisense RNAs, ribozymes, siRNAs or shRNAs may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include, but are not limited to, techniques for chemical synthesis such as solid phase phosphoramidite chemical synthesis. In the case of siRNAs, the structure may be stabilized, for example by including nucleotide analogs at one or more free strand ends in order to reduce digestion, e.g., by exonucleases. This may also be accomplished by the use of deoxy residues at the ends, e.g., by employing dTdT overhangs at each 3' end. Alternatively, antisense, ribozyme, siRNA or shRNA molecules may be generated by *in vitro* transcription of DNA sequences encoding the relevant molecule. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7, T3, or SP6.

[0172] Antisense, ribozyme, siRNA or shRNA molecules may be generated by intracellular synthesis of small RNA molecules, as described above, which may be followed by intracellular processing events. For example, intracellular transcription may be achieved by cloning templates into RNA polymerase III transcription units, e.g., under control of a U6 or H1 promoter. In one approach for intracellular synthesis of siRNA, sense and antisense strands are transcribed from individual promoters, which may be on the same construct. The promoters may be in opposite orientation so that they drive transcription from a single template, or they may direct synthesis from different templates. However, it may be advantageous to express a single RNA molecule that self-hybridizes to form a hairpin RNA that is then cleaved by DICER within the cell.

[0173] In some embodiments, an antisense oligonucleotide, RNAi agent, or ribozyme specifically inhibits expression of an allele of the CVDA gene that is associated with cardiovascular disease, e.g., the allele comprises one or more of the CVDA polymorphic variants disclosed herein. For example, an antisense oligonucleotide or antisense strand of an siRNA may be complementary to the disease-associated polymorphic variant at the polymorphic position. In some embodiments, an antisense oligonucleotide, ribozyme, or RNAi agent does not appreciably inhibit the polymorphic variant that is not associated with cardiovascular disease. By "does not appreciably inhibit" is meant that the expression level in the presence of the inhibitory agent is at least 90% of the expression level in the absence of the agent. In certain embodiments the expression level of the polymorphic variant that is not associated with cardiovascular disease is inhibited by less than 50% by the antisense oligonucleotide, ribozyme, or RNAi agent.

[0174] Antisense, ribozyme, siRNA, or shRNA molecules for use in accordance with the present invention may be introduced into cells by any of a variety of methods. For instance, antisense, ribozyme, siRNA, or shRNA molecules or vectors encoding them can be introduced into cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA or RNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, injection, or electroporation.

[0175] Vectors that direct *in vivo* synthesis of antisense, ribozyme, siRNA, or shRNA molecules constitutively or inducibly can be introduced into cell lines, cells, or tissues. In certain embodiments, inventive vectors are gene therapy vectors (e.g., adenoviral vectors, adeno-associated viral vectors, retroviral or lentiviral vectors, or various nonviral gene therapy vectors) appropriate for the delivery of a construct directing transcription of an siRNA to mammalian cells, including, but not limited to, human cells.

[0176] In certain embodiments, siRNA, shRNA, antisense, or ribozyme compositions reduce the level of a target transcript and/or its encoded protein by at least 2-fold. In certain embodiments, siRNA, shRNA, antisense, or ribozyme compositions reduce the level of a target transcript and/or its encoded protein by at least 4-fold. In certain embodiments, siRNA, shRNA, antisense, or ribozyme compositions reduce the level of a target transcript and/or its encoded protein by at least 10-fold or more. The ability of a candidate siRNA to reduce expression of the target transcript and/or its encoded protein may readily be tested using methods well known in the art including, but not limited to, Northern blots, RT-PCR, microarray analysis in the case of the transcript, and various immunological methods such as Western blot, ELISA, immunofluorescence, etc., in the case of the encoded protein. In addition, the potential of any siRNA, shRNA, antisense, or ribozyme composition for treatment of a particular condition or disease associated with atherosclerosis may also be tested in appropriate animal models or in human individuals, as is the case for all methods of treatment described herein. Appropriate animal models include, but are not limited to, mice, rats, rabbits, sheep, dogs, etc., with experimentally induced atherosclerosis.

[0177] Nucleic acids described herein may be delivered to an individual using any of a variety of approaches, including those applicable to non-nucleic acid agents such as IV, intranasal, oral, etc. According to certain embodiments, such nucleic acids are delivered via a gene therapy approach, in which a construct capable of directing expression of one or more of the inventive nucleic acids is delivered to cells or to the individual (ultimately to enter cells, where transcription may occur).

[0178] Additional methods for identifying compounds capable of modulating gene expression are described, for example, in U.S. Patent No. 5,976,793. These methods may be used either to identify compounds that increase gene expression or to identify compounds that decrease gene expression. Additional methods for identifying agents that

increase expression of genes are found in Ho, S., et al., Nature, 382, pp. 822-826, 1996, which describes homodimeric and heterodimeric synthetic ligands that allow ligand-dependent association and disassociation of a transcriptional activation domain with a target promoter to increase expression of an operatively linked gene.

[0179] Expression can also be increased by introducing additional copies of a coding sequence into a cell of interest, e.g., by introducing a nucleic acid comprising the coding sequence into the cell. In certain embodiments, a coding sequence is operably linked to regulatory elements such as promoters, enhancers, etc., that direct expression of the coding sequence in the cell. A nucleic acid may comprise a complete CVDA gene, or a portion thereof that contains the coding region of the gene. A nucleic acid may be introduced into cells grown in culture or cells in an individual using any suitable method, e.g., any of those described above.

[0180] Polymorphic Polypeptides and Polymorphism-Specific Binding Agents

[0181] In certain embodiments, the present invention provides isolated peptides and polypeptides encoded by genes listed in Table 1 and/or Table 2, wherein the genes comprise one or more polymorphic positions disclosed herein. In certain embodiments, such peptides and polypeptides are useful in screening targets to identify drugs for the treatment and/or prevention of cardiovascular disease. In certain embodiments, such peptides and polypeptides are capable of eliciting antibodies in a suitable host animal that react specifically with a polypeptide comprising the polymorphic position and distinguish it from other polypeptides having a different sequence at that position. In certain embodiments, a peptide or polypeptide is used to identify a specific binding reagent that binds to the peptide or polypeptide. In certain aspects, the invention thus provides antibodies and other reagents that specifically bind to a polypeptide having a specific amino acid at a polymorphic position. Certain inventive antibodies possess high affinity, e.g., a K_d of <200 nM, <100 nM, or lower for their target.

[0182] Certain inventive polypeptides are at least five or more residues in length. In certain embodiments, polypeptides of the present invention are at least fifteen residues. Certain methods for obtaining these polypeptides are described below. A variety of conventional techniques in protein biochemistry and immunology are known and my be used in accordance with the present invention. For example, certain conventional techniques are explained in Immunochemical Methods in Cell and Molecular Biology, 1987 (Mayer and Waler, eds; Academic Press, London); Scopes, 1987, Protein Purification: Principles and Practice, Second Edition (Springer-Verlag, N.Y.), Handbook of Experimental Immunology, 1986, Volumes I-IV (Weir and Blackwell eds.), Harlow, *supra*, and other references listed above.

[0183] Nucleic acids comprising protein-coding sequences can be used to direct recombinant expression of polypeptides encoded by genes disclosed herein in intact cells or in cell-free translation systems. The nucleic acids can be isolated from cells, nucleic acid libraries (e.g., cDNA libraries), synthesized chemically, etc. The genetic code can be used to design polynucleotides encoding the desired amino acid sequences. If desired, the sequence of the polynucleotides can be modified to optimize expression in a host cell or organism of choice. The polypeptides may be isolated from human cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) into which an appropriate protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

[0184] Peptides and polypeptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. In certain embodiments, polypeptides are advantageously prepared by solid phase peptide synthesis as described by Merrifield, J. Am. Chem. Soc. 85:2149, 1963.

[0185] Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it may be advantageous to produce the polypeptide in a recombinant system in which the protein contains an additional sequence tag that facilitates purification, such as, for example, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Additionally or alternatively, antibodies produced against peptides encoded by genes disclosed herein, can be used as purification reagents. Other purification methods that may be used will be known to those of ordinary skill in the art.

[0186] The present invention also encompasses derivatives and homologues of the polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, e.g., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids. In certain embodiments, a derivative or homologue of a polypeptide is at least 80% identical, at least 90% identical, at least 95%, or at least 99% identical to the polypeptide. In certain embodiments a derivative or homologue of a polypeptide has 5, 10, 20, 30, 40, or 50 or more amino acid deletions, additions, or substitutions relative to the polypeptide.

[0187] Polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly,

including, but not limited to, radioisotopes and fluorescent compounds. The polypeptides may include a tag, e.g., an epitope tag such as an HA tag, 6XHis tag, GST tag, etc., which may be useful for detection and/or purification of the polypeptide.

[0188] The present invention also encompasses antibodies that specifically recognize polypeptides differing at one or more polymorphic positions and that distinguish a peptide or polypeptide containing a particular polymorphic variant from one that contains a different sequence at that position. Such polymorphic position-specific antibodies include, for example, polyclonal and monoclonal antibodies. Such antibodies may be generated in an animal host by immunization with polypeptides encoded by genes disclosed herein or may be identified using methods such as phage display. The immunogenic components used to generate antibodies may be isolated from human cells or produced in recombinant systems. Such antibodies may also be produced in recombinant systems programmed with appropriate antibody-encoding DNA. Additionally or alternatively, antibodies may be constructed by biochemical reconstitution of purified heavy and light chains. Such antibodies include hybrid antibodies (e.g., containing two sets of heavy chain/light chain combinations, each of which recognizes a different antigen), chimeric antibodies (i.e., in which either the heavy chains, light chains, or both, are fusion proteins), and univalent antibodies (e.g., comprised of a heavy chain/light chain complex bound to the constant region of a second heavy chain). Also encompassed are Fab fragments, including Fab' and $F(ab)_2$ fragments of antibodies. Methods for the production of all of the above types of antibodies and derivatives are well-known in the art and are discussed in more detail below. For example, techniques for producing and processing polyclonal antisera are disclosed in Mayer and Walker, Immunochemical Methods in Cell and Molecular Biology, 1987 (Academic Press, London). The general methodology for making monoclonal antibodies by hybridomas is well known. See, e.g., Schreier et al., Hybridoma Techniques, 1980; U.S. Pat. Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against peptides encoded by genes disclosed herein can be screened for various properties, including, for example, isotype, epitope affinity, etc.

[0189] Antibodies of the present invention can be purified by standard methods, including but not limited to preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. Purification methods for antibodies are disclosed, e.g., in The Art of Antibody Purification, Amicon Division, W. R. Grace & Co, 1989. General protein purification methods are described in Protein Purification: Principles and Practice, R. K. Scopes, Ed., 1987, Springer-Verlag, New York, N.Y.

[0190] Methods for determining the immunogenic capability of the disclosed sequences and the characteristics of the resulting sequence-specific antibodies and immune cells are well-known in the art. For example, antibodies elicited in response to a peptide comprising a particular polymorphic sequence can be tested for their ability to specifically recognize that polymorphic sequence, e.g., to bind differentially to a peptide or polypeptide comprising the polymorphic sequence and thus distinguish it from a similar peptide or polypeptide containing a different sequence at the same position.

[0191] A variety of engineered ligand-binding proteins with antibody-like specific binding properties are known in the art. For example, anticalins offer an alternative type of ligand-binding protein, which is constructed on the basis of lipocalins as a scaffold (Skerra, J., J. Biotechnol., 74(4):257-75, 2001). Affibodies, which are binding proteins generated by phage display from combinatorial libraries constructed using the protein A-derived Z domain as a scaffold, can also be used. See, e.g., Nord K, Eur J Biochem., 268(15):4269-77, 2001. Thus the invention provides, for example, an affibody or anticalin that specifically binds to a CVDA polypeptide.

[0192] In certain embodiments, the invention also provides a variety of different additional specific binding agents which may be, for example, peptides, non-immunoglobulin polypeptides, nucleic acids, protein nucleic acids (PNAs), aptamers, small molecules, etc. Such agents will be collectively referred to herein as "ligands". Ligands that specifically bind to any of the polymorphic forms of the CVDA polypeptides described herein may be identified using any of a variety of approaches. For example, ligands may be identified by screening libraries, e.g., small molecule libraries. Naturally occurring or artificial (non-naturally occurring) ligands, particularly peptides or polypeptides, may be identified using a variety of approaches including, but not limited to, those known generically as two- or three-hybrid screens, the first version of which was described in Fields S. and Song O., Nature, 340(6230):245-6, 1989. Nucleic acid or modified nucleic acid ligands may be identified using, e.g., systematic evolution of ligands by exponential enrichment (SELEX) (Tuerk, C. and Gold., L, Science 249(4968): 505-10, 1990), or any of a variety of directed evolution techniques that are known in the art. For example, an aptamer is an oligonucleotide (e.g., DNA, RNA, which can include various modified nucleotides, e.g., 2'-O-methyl modified nucleotides) that binds to a particular protein. See, e.g., Brody EN, Gold L. J Biotechnol., 74(1):5-13, 2000. In certain embodiments, the ligand is an aptamer that binds to a CVDA polypeptide or polymorphic form thereof. Screens using nucleic acids, peptides, or polypeptides as candidate ligands may utilize nucleic acids, peptides, or polypeptides that incorporate any of a variety of nucleotide analogs, amino acid analogs, etc. Various nucleotide analogs are known in the art, and other modifications of a nucleic acid chain, e.g., in the backbone, can also be used. Peptide or polypeptide ligands may comprise amino acids that do not occur naturally (e.g., that are not used by organisms in naturally-occurring polypeptide sequences).

[0193] Antibody-Based Diagnostic Methods

[0194] In certain embodiments, the invention provides methods for detecting CVDA polymorphic variants, haplotypes,

and/or alleles in a biological sample that employ a specific binding reagent such as an antibody. In certain embodiments, inventive methods comprises steps of: (i) contacting a sample with one or more antibodies, wherein each of the antibodies is specific for a particular polymorphic form of a protein encoded by a gene disclosed herein, under conditions in which a stable antigen-antibody complex can form between the antibody and antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i) using any suitable means known in the art, wherein the detection of a complex indicates the presence of the particular polymorphic form in the sample.

[0195] Typically, immunoassays use either a labeled antibody or a labeled antigenic component (e.g., that competes with the antigen in the sample for binding to the antibody). Suitable labels include without limitation enzyme-based, fluorescent, chemiluminescent, radioactive, colorimetric, or dye molecules. Assays that amplify the signals from the probe are also known, such as, for example, those that utilize biotin and avidin, and enzyme-labeled immunoassays, such as ELISA assays.

[0196] It will be appreciated that methods described herein can be practiced using other reagents that exhibit specific binding to a polymorphic form of a polymorphic polypeptide.

[0197] Kits

[0198] In certain embodiments, inventive methods include methods for detecting the polymorphic variants, haplotypes, and alleles described herein. In certain embodiments, the invention provides methods for determining the identity of the polymorphic variants of polymorphic regions present in the genes disclosed herein, wherein specific polymorphic variants are associated with cardiovascular disease. In certain embodiments, the invention provides a variety of different kits that can be used for carrying out certain of the inventive methods. In certain embodiments, kits can be used to determine whether an individual has or is at risk of developing a cardiovascular disease. Such information can be used, optionally together with information regarding classical cardiovascular risk factors, to provide an absolute or relative risk that the individual will suffer a major coronary event. In certain embodiments, such information is used to guide the selection of a therapeutic regimen for such individuals, e.g., to optimize their treatment.

[0199] In certain embodiments, a kit comprises a probe or primer which is capable of hybridizing to a nucleic acid and that can be used to determine whether the nucleic acid contains a polymorphic variant of a polymorphic region that is associated with a risk for cardiovascular disease. Such a kit may further comprise instructions for performing the assay and/or instructions for using the results for diagnosis of an individual as having, or being susceptible to, developing a cardiovascular disease, or for prognosis. For example, a kit may comprise an informational sheet or the like that describes how to interpret the results of the test and/or how to utilize the results of the test together with information regarding the existence or value of one or more classical risk factors in the individual, or together with a comprehensive classical risk factor profile of the individual.

[0200] Probes or primers of inventive kits can be any of the probes or primers described herein, e.g., a labeled primer or labeled probe, or collection of labeled primers or labeled probes. In certain embodiments, a kit comprises probes and/or primers suitable for detection of a plurality of CVDA polymorphic variants and/or CVDA haplotypes, or CVDA alleles of a gene containing one or more such variants. In certain embodiments, a kit comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more probes or primers.

[0201] In certain embodiments, probes are covalently or noncovalently attached to a support such as a microparticle. In certain embodiments, probes are covalently or non covalently attached to a substantially planar, rigid substrate or support. In certain embodiments, such a substrate is transparent to radiation of the excitation and emission wavelengths used for excitation and detection of typical labels (e.g., fluorescent labels, quantum dots, plasmon resonant particles, nanoclusters), e.g., between approximately 400-900 nm. Materials such as glass, plastic, quartz, etc., are suitable. For example, a glass slide or the like can be used.

[0202] Kits of the present invention may further include components for detecting polymorphic forms of proteins encoded by genes that comprise the polymorphic variants described herein, wherein the polymorphic variant is in a coding region of a gene and results in a change in the amino acid sequence of the encoded polypeptide. Such kits may include one or more polymorphism-specific antibodies or other reagents exhibiting specific binding such as affibodies, aptamers, etc. Such antibodies may be pre-labeled, e.g., with an enzyme or a detectable moiety. In some embodiments, an antibody may be unlabelled and ingredients for labeling may be included in the kit in separate containers, or a secondary, labeled antibody is provided. An antibody may be covalently or noncovalently attached to a microparticle or to a support or substrate, e.g., a substantially planar, rigid support or substrate. Kits may also contain other suitably packaged reagents and materials needed for the particular immunoassay protocol, including solid-phase matrices, if applicable, and standards, e.g., molecular weight standards.

[0203] In certain embodiments, inventive kits are adaptable to high-throughput and/or automated operation. For example, kits may be suitable for performing assays in multiwell plates and may utilize automated fluid handling and/or robotic systems, plate readers, etc. In some embodiments, flow cytometry is used.

[0204] One of ordinary skill in the art will appreciate that a number of other polymorphic variants, haplotypes, and/or alleles associated with cardiovascular disease are known in the art in addition to those described herein. In certain embodiments, one or more of such known polymorphic variants, haplotypes, and/or alleles is detected in addition to

detecting one or more of the CVDA polymorphic variants, haplotypes, or alleles described herein, and the information is used in conjunction with information obtained from detecting one or more CVDA polymorphic variants, haplotypes, and/or alleles.

[0205] In certain embodiments, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or more (e.g., 100%) of the probes or primers in a kit are designed for the detection of a polymorphic variant, haplotype, or allele that is associated with cardiovascular disease. Thus, inventive kits are distinct from microarrays, also referred to as "chips" that contain probes capable of hybridizing to and detecting a wide variety of nucleic acids, e.g., a wide variety of SNPs. In particular, certain kits of the invention are distinct from the chips that were used to identify the SNPs disclosed herein, although such chips could be used to practice the inventive methods. Inventive kits of the invention that contain chips comprising one or more probes that detect a polymorphic variant of a SNP disclosed herein differ from such chips at least in the fact that they contain a high proportion of probes that are selected to detect SNPs and/or polymorphic variants that are associated with cardiovascular disease and/or are otherwise optimized for the detection of polymorphic variants of CVDA SNPs. In certain embodiments , at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or more (e.g., 100%) of the probes or primers in the kit are designed for the detection of a CVDA polymorphic variant, CVDA haplotype, or CVDA allele.

[0206] In certain embodiments, at least some of the probe(s), primer(s), and/or antibodies contained in a kit detect a polymorphic variant or allele that is associated with CVD, wherein the polymorphic variant or allele is described in U.S.S.N. 10/505,936.

[0207] Kits of the present invention can further comprise one or more additional reagents in addition to probe(s), primer(s), and/or antibodies. For example, a kit may comprise a buffer-containing solution, an enzyme such as a polymerase or ligase, nucleotides, a solution optimized for performing an enzymatic reaction using the enzyme (which may contain any necessary cofactors such as metal ions), one or more "control" nucleic acids or polypeptides, and/or a substrate (e.g., for an antibody-linked enzyme), etc. A control nucleic acid is typically a nucleic acid that has the sequence of a portion of genomic DNA or cDNA that encompasses a polymorphic region and whose sequence at the polymorphic position is known. A control polypeptide is typically a polypeptide that has the sequence of a portion of polypeptide encoded by genomic DNA or encoded by a cDNA that encompasses a polymorphic region and whose sequence at the polymorphic position is known. For example, when a kit comprises probe(s) and/or primer(s) for the detection of polymorphic variants, alleles, etc., the sequence of a positive control nucleic acid at the polymorphic position may be the same as that of a polymorphic variant that is associated with cardiovascular disease, while the sequence of a negative control nucleic acid will be the same as that of a polymorphic variant that is not associated with cardiovascular disease. In the case of a kit that contains antibodies for the detection of polymorphic proteins, a positive control polypeptide may be a polymorphic protein whose sequence at the polymorphic site is the same as that of a polymorphic variant that is associated with cardiovascular disease, while the sequence of a negative control polypeptide will be the same as that of a polymorphic variant that is not associated with cardiovascular disease.

[0208] An identifier, e.g., a bar code, radio frequency ID tag, etc., may be present in or on the kit. The identifier can be used, e.g., to uniquely identify the kit for purposes of quality control, inventory control, tracking, movement between workstations, etc.

[0209] Kits will generally include one or more vessels or containers so that certain of the individual reagents may be separately housed. The kits may also include a means for enclosing the individual containers in relatively close confinement for commercial sale, e.g., a plastic box, in which instructions, packaging materials such as styrofoam, etc., may be enclosed.

[0210] According to certain embodiments, kits are manufactured in accordance with good manufacturing practices as required for FDA-approved diagnostic kits.

[0211] Drug Targets and Screening Methods

[0212] According to certain embodiments, nucleotide sequences derived from genes disclosed herein and polypeptide sequences encoded by genes disclosed herein are useful targets to identify cardiovascular drugs, e.g., compounds that are effective in treating or preventing one or more symptoms or signs of cardiovascular disease. A "symptom" refers to a manifestation of a disease or condition that is perceived by the individual who has the condition, while a "sign" refers to a manifestation of a disease or condition that is detected by clinical diagnosis, a laboratory test, an imaging procedure, or the like. It will be appreciated that the compounds identified according to the inventive methods have a number of uses in addition to their utility for the treatment and/or prevention of cardiovascular disease. For example, such compounds can serve as lead compounds for the development of useful therapeutic agents (which term is intended to encompass agents administered for purposes of treating an existing disease or condition and agents administered prophylactically, i.e., prior to the development of a particular disease, condition, symptom, or sign). Additionally or alternatively, such compounds can also be used to gain an improved understanding of the biological functions and activities of the CVDA genes and their encoded polypeptides.

[0213] Drug targets include without limitation (i) isolated nucleic acids derived from the genes that contain the polymorphisms disclosed herein; and (ii) isolated peptides and polypeptides encoded by genes that contain the polymor-

phisms disclosed herein.

[0214] In certain embodiments, an isolated nucleic acid comprising one or more polymorphic positions is tested *in vitro* or *in vivo* (e.g., within intact cells) for its ability to bind test compounds in a sequence-specific manner. In certain embodiments, inventive methods comprise: (i) providing a first nucleic acid containing a particular sequence at a polymorphic position, e.g., a position of a CVDA polymorphism; (ii) contacting the nucleic acid with a test compound under conditions appropriate for binding; and (iii) identifying a compound that binds selectively to the first nucleic acid. In some embodiments, inventive methods comprise further providing a second nucleic acid whose sequence is identical to that of the first nucleic acid except that it has a different sequence at the same polymorphic position; and identifying a compound that binds selectively to one of the nucleic acids. For example, the first nucleic acid may contain a CVDA polymorphic variant and the second nucleic acid may contain a different polymorphic variant at the same position that is not associated with cardiovascular disease, and the method may identify a compound that binds selectively or preferentially to the nucleic acid that comprises the CVDA polymorphic variant. Any suitable method can be used to assay binding including direct methods such as isolating a complex containing the nucleic acid and the compound, detecting a label associated with a compound that has bound to the nucleic acid, etc. Functional assays can also be used. For example, an siRNA or shRNA that specifically binds to a nucleic acid can be identified by contacting a cell with the siRNA or expressing the shRNA in a cell and determining whether expression of an mRNA transcribed from a gene that includes a CVDA polymorphism and/or expression of a polypeptide encoded by the gene is inhibited.

[0215] Selective binding as used herein refers to any measurable difference in any parameter of binding, such as, e.g., binding affinity, binding capacity, etc. In some embodiments, an agent exhibits selective binding in that its binding affinity (as determined by Ka) towards a first nucleic acid or polypeptide under the particular conditions tested is, for example, at least 5-fold greater than its binding affinity towards at least 90% of the other nucleic acids or polypeptides that would be present in a typical cell or cell lysate. In other embodiments the Ka is at least 10, 20, 50, or 100-fold greater.

[0216] In certain embodiments, an isolated peptide or polypeptide comprising one or more polymorphic positions is tested *in vitro* or *in vivo* for its ability to bind a test compound in a sequence-specific manner. Certain of the screening methods involve (i) providing a first polypeptide containing a particular sequence at a polymorphic position, e.g., a position of a CVDA polymorphism; (ii) contacting the polypeptide with a test compound under conditions appropriate for binding; and (iii) identifying a compound that binds selectively to the first polypeptide. In some embodiments, inventive methods comprise also providing a second polypeptide whose sequence is identical to that of the first polypeptide except that it has a different sequence at the same polymorphic position; and identifying a compound that binds selectively to one of the polypeptide. For example, the first polypeptide may contain a CVDA polymorphic variant and the second nucleic acid may contain a polymorphic variant at the same position that is not associated with cardiovascular disease, and the method may identify a compound that binds selectively or preferentially to the polypeptide that comprises the CVDA polymorphic variant. Any suitable method can be used to assay binding including direct methods such as isolating a complex containing the polypeptide and the compound, detecting a label associated with a compound that has bound to the polypeptide, etc. A variety of immunological methods known in the art can be used for detecting specific binding agents. Functional assays can also be used in the case of polypeptides that have a known biological function or biochemical activity.

[0217] Agents such as antisense molecules, siRNAs, shRNAs, ribozymes, other nucleic acids, peptides or polypeptides, small molecules, etc., can be tested to determine whether they modulate the expression of a CVDA gene. In certain embodiments, the invention provides methods for identifying an agent that modulates expression of a CVDA polynucleotide or polypeptide comprising steps of: (i) providing a sample comprising cells that express a CVDA polynucleotide or polypeptide; (ii) contacting the cells with a test compound; (iii) determining whether the level of expression of the polynucleotide or polypeptide in the presence of the compound is increased or decreased relative to the level of expression or activity of the polynucleotide or polypeptide in the absence of the compound; and (iv) identifying the compound as a modulator of the CVDA polynucleotide or polypeptide if the level of expression or activity of the CVDA polynucleotide or polypeptide is higher or lower in the presence of the compound relative to its level of expression or activity in the absence of the compound.

[0218] Expression of a CVDA polynucleotide or polypeptide can be measured using a variety of methods well known in the art in order to determine whether any candidate agent increases or decreases expression (or for other purposes). In general, any measurement technique capable of determining RNA or protein presence or abundance may be used for these purposes. For RNA such techniques include, but are not limited to, microarray analysis. For information relating to microarrays and also RNA amplification and labeling techniques, which may also be used in conjunction with other methods for RNA detection, see, e.g., Lipshutz, R., et al., Nat Genet., 21(1 Suppl):20-4, 1999; Kricka L., Ann. Clin. Biochem., 39(2), pp. 114 -129; Schweitzer, B. and Kingsmore, S., Curr Opin Biotechnol 2001 Feb; 12(1):21-7; Vineet, G., et al., Nucleic Acids Research, 2003, Vol. 31, No. 4.; Cheung, V., et al., Nature Genetics Supplement, 21:15-19, 1999; Methods Enzymol, 303:179-205, 1999; Methods Enzymol, 306: 3-18, 1999; M. Schena (ed.), DNA Microarrays: A Practical Approach, Oxford University Press, Oxford, UK, 1999. See also U.S. Pat Nos. 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531;

5,554,501; 5,556,752; 5,561,071; 5,599,695; 5,624,711; 5,639,603; 5,658,734; 6,235,483; WO 93/17126; WO 95/11995; WO 95/35505; EP 742 287; EP 799 897; 5,514,545; 5,545,522; 5,716,785; 5,932,451; 6,132,997; 6,235,483; US Patent Application Publication 20020110827.

[0219] Other methods for detecting expression of CVDA polynucleotides include Northern blots, RNAse protection assays, reverse transcription (RT)-PCR assays, real time RT-PCR (e.g., Taqman™ assay, Applied Biosystems), SAGE (Velculescu et al. Science, vol. 270, pp. 484-487, Oct. 1995), Invader® technology (Third Wave Technologies), etc. See, e.g., Eis, P.S. et al., Nat. Biotechnol. 19:673, 2001; Berggren, W.T. et a/., Anal. Chem. 74:1745, 2002, etc. Methods for detecting DEA polypeptides include, but are not limited to, immunoblots (Western blots), immunofluorescence, flow cytometry (e.g., using appropriate antibodies), mass spectrometry, and protein microarrays (Elia, G., Trends Biotechnol, 20(12 Suppl):S19-22, 2002, and reference therein).

[0220] The invention also provides methods for identifying an agent that modulates expression or activity of a CVDA polynucleotide or polypeptide comprising steps of: (i) providing a sample comprising a CVDA polynucleotide or polypeptide; (ii) contacting the sample with a test compound; (iii) determining whether the level of expression or activity of the polynucleotide or polypeptide in the presence of the test compound is increased or decreased relative to the level of expression or activity of the polynucleotide or polypeptide in the absence of the compound; and (iv) identifying the test compound as a modulator of the expression or activity of the CVDA polynucleotide or polypeptide if the level of expression or activity of the CVDA polynucleotide or polypeptide is higher or lower in the presence of the compound relative to its level of expression or activity in the absence of the compound. In certain embodiments, a sample comprises cells that express the CVDA polypeptide. Agents to be screened may include any of those discussed above. Agents identified according to the above methods may be further tested in subjects, e.g., humans or other animals.

[0221] In certain embodiments, a multiplicity of compounds are tested either individually or in combination for their ability to bind to a nucleic acid or polypeptide comprising a CVDA polymorphism. High-throughput screening methods can advantageously be used.

[0222] Compounds suitable for screening according to the above methods include small molecules, natural products, peptides, nucleic acids, etc. In some embodiments test compounds are screened from large libraries of synthetic or natural compounds. Numerous means are currently used for random and directed synthesis of small molecules, saccharides, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from, e.g., Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, N.J.), Brandon Associates (Merrimack, N.H.), and Microsource (New Milford, Conn.). A rare chemical library is available from Aldrich (Milwaukee, Wis.). Additionally or alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g. Pan Laboratories (Bothell, Wash.) or MycoSearch (N.C.), or are readily producible. Additionally or alternatively, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

[0223] Another representative example of a library is known as DIVERSet™, available from ChemBridge Corporation, 16981 Via Tazon, Suite G, San Diego, CA 92127. DIVERSet™ contains between 10,000 and 50,000 drug-like, hand-synthesized small molecules. The compounds are pre-selected to form a "universal" library that covers the maximum pharmacophore diversity with the minimum number of compounds and is suitable for either high throughput or lower throughput screening. For descriptions of additional libraries, see, for example, Tan, et al., "Stereoselective Synthesis of Over Two Million Compounds Having Structural Features Both Reminiscent of Natural Products and Compatible with Miniaturized Cell-Based Assays", Am. Chem Soc. 120, 8565-8566, 1998; Floyd CD, Leblanc C, Whittaker M, Prog Med Chem 36:91-168, 1999. Numerous libraries are commercially available, e.g., from AnalytiCon USA Inc., P.O. Box 5926, Kingwood, TX 77325; 3-Dimensional Pharmaceuticals, Inc., 665 Stockton Drive, Suite 104, Exton, PA 19341-1151; Tripos, Inc., 1699 Hanley Rd., St. Louis, MO, 63144-2913, etc. In certain embodiments, the methods are performed in a high-throughput format using techniques that are well known in the art, e.g., in multiwell plates, using robotics for sample preparation and dispensing, etc. Representative examples of various screening methods may be found, for example, in U.S. Patent No. 5,985,829, U.S. Patent No. 5,726,025, U.S. Patent No. 5,972,621, and U.S. Patent No. 6,015,692. The skilled practitioner will readily be able to modify and adapt these methods as appropriate.

[0224] Molecular modeling can be used to identify a pharmacophore for a particular target, e.g., the minimum functionality that a molecule must have to possess activity at that target. Such modeling can be based, for example, on a predicted structure for the target (e.g., a two-dimensional or three-dimensional structure). Software programs for identifying such potential lead compounds are known in the art, and once a compound exhibiting activity is identified, standard methods may be employed to refine the structure and thereby identify more effective compounds. For example computer-based screening can be used to identify small organic compounds that bind to concave surfaces (pockets) of proteins, can identify small molecule ligands for numerous proteins of interest (Huang, Z., Pharm. & Ther. 86: 201-215, 2000). *In silico* discovery of small molecules that bind to a protein of interest will typically involve, for example pharmacophore-aided database searches, virtual protein-ligand docking, and/or structure-activity modeling. For example, the computer program DOCK and variants thereof is widely used (Lorber, D. and Shoichet, B., Protein Science, 7:938-950, 1998). Other non-limiting examples of suitable programs include Autodock and Flexx. It is noted that such programs and the hardware

used to run them have undergone significant improvement since their introduction. Databases providing compound structures suitable for virtual screening are available in the art. For example, ZINC is a database that provides a library of 727,842 molecules, each with 3D structure, which was prepared using catalogs of compounds that are commercially available (Irwin JJ and Shoichet BK. J Chem Inf Model., 45(1):177-82, 2005). Each molecule in the library contains vendor and purchasing information and is ready for docking using a number of popular docking programs. In some embodiments, the structure of a CVDA polypeptide is screened against a database using a computer-based method to identify small molecules that bind to the polypeptide. Assays to identify and/or to confirm molecules that bind to a polypeptide could include functional assays, e.g., assessing the ability of a compound to prevent blood coagulation. Radioligand binding assays, competition assays, immunologically based assays, etc., may also be used.

[0225] Intact cells or whole animals, e.g., transgenic non-human animals expressing polymorphic variants of genes disclosed herein can be used in screening methods to identify candidate cardiovascular drugs.

[0226] In certain embodiments, a cell line is established from an individual exhibiting a particular genotype with respect to one or more CVDA polymorphisms. In certain embodiments, cells (including without limitation mammalian, insect, yeast, or bacterial cells) are programmed to express a gene comprising one or more polymorphic sequences by introduction of appropriate DNA. Identification of candidate compounds can be achieved using any suitable assay, including without limitation (i) assays that measure selective binding of test compounds to particular polymorphic variants of proteins encoded by genes disclosed herein; (ii) assays that measure the ability of a test compound to modify (e.g., inhibit or enhance) a measurable activity or function of proteins encoded by genes disclosed herein; and (iii) assays that measure the ability of a compound to modify (e.g., inhibit or enhance) the transcriptional activity of sequences derived from the promoter or other regulatory regions of genes disclosed herein.

[0227] In general, a screen for a ligand that specifically binds to any particular polypeptide may comprise steps of contacting the polypeptide with a candidate ligand under conditions in which binding can take place; and determining whether binding has occurred. Any appropriate method for detecting binding, many of which are known in the art, may be used. One of ordinary skill in the art will be able to select an appropriate method taking into consideration, for example, whether the candidate ligand is a small molecule, peptide, nucleic acid, etc. For example, the candidate ligand may be tagged, e.g., with a radioactive molecule, fluorescent molecule, etc. The polypeptide can then be isolated, e.g., immunoprecipitated from the container in which the contacting has taken place (for methods performed entirely in vitro) or from a cell lysate, and assayed to determine whether radiolabel has been bound. This approach may be particularly appropriate for small molecules. Binding can be confirmed by any of a number of methods, e.g., radiolabel assays, plasmon resonance assays, etc. Phage display represents another method for the identification of ligands that specifically bind to polypeptides. In addition, determination of the partial or complete three-dimensional structure of a polypeptide (e.g., using nuclear magnetic resonance, X-ray crystallography, etc.) may facilitate the design of appropriate ligands.

[0228] Functional assays may also be used to identify ligands, particularly ligands that behave as agonists or antagonists, activators, or inhibitors of particular polypeptides. For example, a polypeptide of interest may possess a measurable or detectable functional activity and that functional activity may be increased or decreased upon binding of the ligand. Non-limiting examples of functional activities of a polypeptide include the ability to catalyze a chemical reaction either *in vitro* or in a cell, and/or the ability to induce a change of any sort in a biological system, e.g., a change in cellular phenotype, a change in gene transcription, a change in membrane current, a change in intracellular or extracellular pH, a change in the intracellular or extracellular concentration of an ion, etc. when present within a cell or when applied to a cell.

[0229] Thus, in certain embodiments, the invention provides methods for screening for a ligand for a CVDA polypeptide comprising steps of: (i) providing a sample comprising a CVDA polypeptide; (ii) contacting the sample with a candidate compound; (iii) determining whether the level of activity of the polypeptide in the presence of the compound is increased or decreased relative to the level of activity of the CVDA polypeptide in the absence of the compound; and (iv) identifying the compound as a ligand of the CVDA polypeptide if the level of activity of the CVDA polypeptide is higher or lower in the presence of the compound relative to its level of activity in the absence of the compound. In certain embodiments of the method the sample comprises cells that express the CVDA polypeptide. In some embodiments the CVDA polypeptide is encoded by a gene that comprises a polymorphic variant associated with cardiovascular disease.

[0230] In certain embodiments, transgenic non-human animals (e.g., rodents such as mice or rats) are created in which (i) one or more human genes disclosed herein, having different sequences at particular polymorphic positions are stably inserted into the genome of the transgenic animal; and/or (ii) the endogenous animal counterparts of genes disclosed herein are inactivated and replaced with human genes disclosed herein, having different sequences at particular polymorphic positions. Such transgenic non-human animals are encompassed within the scope of the invention. See, e.g., Coffman, Semin. Nephrol. 17:404, 1997; Esther et al., Lab. Invest. 74:953, 1996; Murakami et al., Blood Press. Suppl. 2:36, 1996. Such animals can be treated with candidate compounds and monitored for one or more indicators of cardiovascular disease. Any indicator can be assessed, and a wide variety of methods can be employed. For example, imaging, measurement of lipid levels, histopathologic examination, mortality rate, etc., can be used as an indicator.

[0231] In certain embodiments a candidate compound, e.g., a compound identified according to any of the methods described above, is administered to an animal model of cardiovascular disease, and the effect of the compound on the

development of cardiovascular disease in the animal, is monitored. For example, any of the screening methods can include a step of administering the compound to an animal suffering from or at risk of developing a cardiovascular disease and evaluating the response. Response can be evaluated in any of a variety of ways, e.g., by assessing clinical features, laboratory data, blood vessel images, etc. A comparison may be performed with similar animals who did not receive the compound or who received a lower or higher amount of the compound. A number of animal models (e.g., mouse, rat, rabbit, pig, etc.) for cardiovascular diseases are known in the art. Such models may involve genetic alterations, administration of drugs, etc., to induce the development of a cardiovascular disease.

[0232] Certain embodiments provide transgenic non-human animals (e.g.,. mammals such as mice or rats) in which the endogenous counterpart of a human gene disclosed herein is "knocked out" or mutated. Such animals may, without limitation, serve as useful animal models for cardiovascular disease and may be used for testing candidate compounds.

[0233] Methods of Treatment and Pharmaceutical Compositions

[0234] As mentioned above, certain of the CVDA polymorphisms may play a causative role in cardiovascular disease. Certain embodiments provide methods of treating or preventing a cardiovascular disease comprising administering an agent that modulates the expression or activity of a CVDA gene or expression product thereof to an individual in need of treatment or prevention of cardiovascular disease. The agent can be any of the CVDA nucleic acids, polypeptides, antibodies, or ligands described above. In an exemplary embodiment, if a CVDA polymorphic variant is expressed at lower levels than a polymorphic variant that is not associated with cardiovascular disease, an agent that increases its expression or functional activity, or substitutes for its functional activity, can be administered. For example, the normal form of the polypeptide can be administered. In another exemplary embodiment, if activity of the CVDA polymorphic variant contributes to cardiovascular disease, an inhibitor such as an siRNA, inhibitory ligand, antibody, etc., can be administered.

[0235] Any of the agents described herein can be formulated and administered according to methods known in the art. In certain embodiments, the invention provides compositions comprising the inventive agents, e.g., compositions comprising a pharmaceutically acceptable carrier, diluent, excipient, etc. Suitable preparations, e.g., substantially pure preparations of the compounds may be combined with pharmaceutically acceptable carriers, diluents, solvents, etc., to produce an appropriate pharmaceutical composition. In certain embodiments, the invention therefore provides a variety of pharmaceutically acceptable compositions for administration to a subject comprising (i) an agent that modulates the expression or activity of a CVDA ; and (ii) a pharmaceutically acceptable carrier, adjuvant, or vehicle. Inventive pharmaceutical compositions, when administered to a subject, may be advantageously administered for a time and in an amount sufficient to treat or prevent the disease or condition for whose treatment or prevention they are administered, e.g., a cardiovascular disease or condition, or a symptom of such.

[0236] In various embodiments, an effective amount of the pharmaceutical composition is administered to a subject by any suitable route of administration including, but not limited to, intravenous, intramuscular, by inhalation, by catheter, intraocularly, orally, rectally, intradermally, by application to the skin, etc.

[0237] Inventive compositions may be formulated for delivery by any available route including, but not limited to parenteral, oral, by inhalation to the lungs, nasal, bronchial, opthalmic, transdermal (topical), transmucosal, rectal, and vaginal routes. The term "parenteral" as used herein includes subcutaneous, intravenous, intramuscular, intra-articular, intra-synovial, intrasternal, intrathecal, intrahepatic, intralesional and intracranial injection or infusion techniques. In certain embodiments, such compositions are administered either orally or intravenously.

[0238] The term "pharmaceutically acceptable carrier, adjuvant, or vehicle" refers to a non-toxic carrier, adjuvant, or vehicle that does not destroy the pharmacological activity of the compound with which it is formulated. Pharmaceutically acceptable carriers, adjuvants or vehicles that may be used in the compositions of this invention include, but are not limited to, ion exchangers, alumina, aluminum stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts or electrolytes, such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol and wool fat. Solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration may be included. Supplementary active compounds, e.g., compounds independently active against the disease or clinical condition to be treated, or compounds that enhance activity of a compound, can also be incorporated into the compositions. Pharmaceutically acceptable salts of the compounds of this invention include those derived from pharmaceutically acceptable inorganic and organic acids and bases. Examples of suitable acid salts include acetate, adipate, alginate, aspartate, benzoate, benzenesulfonate, bisulfate, butyrate, citrate, camphorate, camphorsulfonate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, formate, fumarate, glucoheptanoate, glycerophosphate, glycolate, hemisulfate, heptanoate, hexanoate, hydrochloride, hydrobromide, hydroiodide, 2-hydroxyethanesulfonate, lactate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oxalate, palmoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, salicylate, succinate, sulfate, tartrate, thiocyanate,

tosylate and undecanoate. Other acids, such as oxalic, while not in themselves pharmaceutically acceptable, may be employed in the preparation of salts useful as intermediates in obtaining certain inventive compounds and their pharmaceutically acceptable acid addition salts.

Salts derived from appropriate bases include alkali metal (e.g., sodium and potassium), alkaline earth metal (e.g., magnesium), ammonium and N+(C1-4 alkyl)4 salts. This invention also envisions the quaternization of any basic nitrogen-containing groups of the compounds disclosed herein. Water or oil-soluble or dispersible products may be obtained by such quaternization.

[0239] A pharmaceutical composition is formulated to be compatible with its intended route of administration. Solutions or suspensions used for parenteral (e.g., intravenous), intramuscular, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[0240] Pharmaceutical compositions suitable for injectable use typically include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include, but are not limited to, physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ), phosphate buffered saline (PBS), or Ringer's solution.

[0241] Sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil may be employed including synthetic mono- or di-glycerides. Fatty acids, such as oleic acid and its glyceride derivatives are useful in the preparation of injectables, as are natural pharmaceutically-acceptable oils, such as olive oil or castor oil, especially in their polyoxyethylated versions. Such oil solutions or suspensions may also contain a long-chain alcohol diluent or dispersant, such as carboxymethyl cellulose or similar dispersing agents that are commonly used in the formulation of pharmaceutically acceptable dosage forms including emulsions and suspensions. Other commonly used surfactants, such as Tweens, Spans and other emulsifying agents or bioavailability enhancers which are commonly used in the manufacture of pharmaceutically acceptable solid, liquid, or other dosage forms may also be used for the purposes of formulation.

[0242] In all cases, the composition should be sterile, if possible, and should be fluid to the extent that easy syringability exists.

[0243] Certain pharmaceutical formulations are stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. In general, the relevant carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be advantageous to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, and/or sodium chloride in the composition. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin. Prolonged absorption of oral compositions can be achieved by various means including, but not limited to, encapsulation.

[0244] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. In certain embodiments, solutions for injection are free of endotoxin. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, certain methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0245] Oral compositions generally include an inert diluent or an edible carrier. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules, e.g., gelatin capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring. Formulations for oral delivery may advantageously incorporate

agents to improve stability within the gastrointestinal tract and/or to enhance absorption.

[0246] For administration by inhalation, the inventive compositions are advantageously delivered in the form of an aerosol spray from a pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer. Liquid or dry aerosol (e.g., dry powders, large porous particles, etc.) can be used. The present invention also contemplates delivery of compositions using a nasal spray.

[0247] For topical applications, the pharmaceutically acceptable compositions may be formulated in a suitable ointment containing the active component suspended or dissolved in one or more carriers. Carriers for topical administration of the compounds of this invention include, but are not limited to, mineral oil, liquid petrolatum, white petrolatum, propylene glycol, polyoxyethylene, polyoxypropylene compound, emulsifying wax and water. Alternatively, the pharmaceutically acceptable compositions can be formulated in a suitable lotion or cream containing the active components suspended or dissolved in one or more pharmaceutically acceptable carriers. Suitable carriers include, but are not limited to, mineral oil, sorbitan monostearate, polysorbate 60, cetyl esters wax, cetearyl alcohol, 2?octyldodecanol, benzyl alcohol and water.

[0248] For local delivery to the eye, the pharmaceutically acceptable compositions may be formulated as micronized suspensions in isotonic, pH adjusted sterile saline, or, in certain embodiments, as solutions in isotonic, pH adjusted sterile saline, either with or without a preservative such as benzylalkonium chloride. Alternatively, for ophthalmic uses, the pharmaceutically acceptable compositions may be formulated in an ointment such as petrolatum.

[0249] Pharmaceutically acceptable compositions of the present invention may also be administered by nasal aerosol or inhalation. Such compositions are prepared according to techniques well-known in the art of pharmaceutical formulation and may be prepared as solutions in saline, employing benzyl alcohol or other suitable preservatives, absorption promoters to enhance bioavailability, fluorocarbons, and/or other conventional solubilizing or dispersing agents.

[0250] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated may be in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

[0251] Compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

[0252] In certain embodiments, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polyethers, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. Certain of the materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811 and other references listed herein. Liposomes, including targeted liposomes (e.g., antibody targeted liposomes) and pegylated liposomes have been described (Hansen CB, et al., Biochim Biophys Acta. 1239(2):133-44,1995; Torchilin VP, et al., Biochim Biophys Acta, 1511(2):397-411, 2001; Ishida T, et al., FEBS Lett. 460(1):129-33, 1999). One of ordinary skill in the art will appreciate that the materials and methods selected for preparation of a controlled release formulation, implant, etc., should be such as to retain activity of the compound. For example, it may be desirable to avoid excessive heating of polypeptides, which could lead to denaturation and loss of activity.

[0253] It is typically advantageous to formulate oral or parenteral compositions in unit dosage form for ease of administration and uniformity of dosage. Unit dosage form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[0254] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ ED_{50}. Compounds that exhibit high therapeutic indices are advantageous. While compounds that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[0255] The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies advantageously within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in accordance with inventive methods disclosed herein, a therapeutically effective dose may be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the ED_{50} as determined in cell culture. Such

information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

[0256] A therapeutically effective amount of a pharmaceutical composition typically ranges from about 0.001 to 100 mg/kg body weight, about 0.01 to 25 mg/kg body weight, about 0.1 to 20 mg/kg body weight, or about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight, although it will be recognized that therapeutically effective amounts depend on the particular pharmaceutical composition. As such, these ranges are merely exemplary in nature. The pharmaceutical composition can be administered at various intervals and over different periods of time as required, e.g., multiple times per day, daily, every other day, once a week for between about 1 to 10 weeks, between 2 to 8 weeks, between about 3 to 7 weeks, about 4, 5, or 6 weeks, etc. The skilled artisan will appreciate that certain factors can influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Generally, treatment of a subject with an inventive composition can include a single treatment or, in many cases, can include a series of treatments. It will be appreciated that a range of different dosage combinations can be used.

[0257] Exemplary doses include milligram or microgram amounts of the inventive compounds per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram.) For local administration (e.g., intranasal), doses much smaller than these may be used. It will furthermore be understood that appropriate doses depend upon the potency of the agent, and may optionally be tailored to the particular recipient, for example, through administration of increasing doses until a preselected desired response is achieved. It is understood that the specific dose level for any particular subject may depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

[0258] The invention further provides pharmaceutical compositions comprising an agent and, optionally, one or more additional agents. The invention further provides pharmaceutical compositions comprising a plurality of agents and, optionally, one or more additional active agent(s). Such additional active agent(s) may include an agent that has a different mechanism of action to that of the first agent. In some embodiments, such an additional active agent is a statin. In some embodiments, such an additional active agent is an anti-inflammatory agent or an anti-platelet agent.

Examples

[0259] ***Example 1: Identification of SNPs and Haplotypes Associated with Cardiovascular Disease.***

[0260] Materials and Methods

[0261] A group of patients with a previous history of MI were recruited through the primary hospitals and care centers from the state of North Rhine Westphalia (NRW), Germany. The study sample of MI patients was compared with age- and sex-matched control individuals recruited in the Prospective Cardiovascular Münster (PROCAM) study for the identification and validation of genetic risk factors associated with coronary artery disease and to estimate additional genetic risk. The PROCAM study is a large, ongoing prospective epidemiological study in which a cohort of more than 43,000 men and women were initially examined and then followed for the occurrence of major coronary events (defined as the occurrence of sudden cardiac death or a definite fatal or nonfatal myocardial infarction) (Assmann, G., et al., Eur. Heart. J., 19:A2-A11; Cullen, P., et al., Circulation, 96:2128, 1997; Assmann, G., et al., Circulation, 105:310, 2002). This MI incidence cohort was used to establish a set of genetic markers where significant differences in allele frequency exist between individuals having previously suffered an MI (cases) and age- and sex-matched controls having a similar risk profile based on classical risk factors.

[0262] The MI study sample was selected to be 'enriched' for individuals having a genetic component to their development of CVD by including only males aged <55 years, which is a clear indication of a genetic contribution to the disease phenotype based on epidemiological studies. By selecting the study sample in this manner, we increased our statistical power to detect a statistically significant association even at a smaller sample size.

[0263] In addition, all classical risk factors were recorded and used to calculate the global risk for each study sample. Global risk was calculated by the PROCAM algorithm, taking into account 8 classical risk factors,: 5 continuous variables (age, LDL cholesterol, HDL cholesterol, triglyceride level, and systolic blood pressure) and 3 discrete variables (smoking status, diabetes, and MI in family history) (described in Assmann, G., et al., Circulation, 105:310, 2002). The global risk, as well as the distribution of the classical risk factors, was used to select our healthy control sample. The controls were selected from our PROCAM study sample, which provides us with a unique control study sample, from which we can select 'real' control individuals that are monitored for conventional risk factors and from which we can match the control population to the cases based on global risk as well as based on age and gender. Global risk for each MI patient first and then identified a pool of PROCAM individuals that matched the global risk score. From these individuals (as we had more controls than needed) we selected those who matched, based on including the individual parameters of the

PROCAM risk factors, e.g. hypertension or diabetes. The cases were scored 'retrospectively' based on the information our clinicians received at the time of MI. The blood samples for the lab parameters were collected within the first 24 hours after the first 'symptoms' so that they were reflecting the state before the MI incidence.

[0264] Without wishing to be bound by any theory, our approach to selecting cases and controls should reduce the risk of confounding factors that may bias the analysis, as cases and controls are matched according to their classical risk factors, thus allowing identification of MI-susceptibility genes and variants that are predictive of CAD and/or MI. This method of selecting cases and controls for an association study to identify polymorphisms associated with CVD is an aspect of the invention.

[0265] Figures 1-3 summarize certain characteristics of the individuals who were studied. It should be mentioned that the results described herein are based on an analysis that does not include all the individuals who participated in the study. However, it is believed that the overall characteristics of the subsets of individuals studied to date are representative of the complete groups. In Figure 3, the Risk categories of < 10%, 10-20%, and >20% refer to risk of having an acute coronary event within 10 years, as described in Assmann, *supra*. Individuals were classified as having a risk of <10%, 10-20%, or >20%. It will be appreciated that other methods of classifying could have been employed.

[0266] Genomic DNA was extracted from blood samples obtained from cases and controls after obtaining informed consent. The Affymetrix 500K Mendel array (Early Access) comprising two chips each allowing identification of 250,000 SNPs, was used according to the manufacturer's directions to identify a set of SNPs associated with MI (see information available at the web site having the URL www.affymetrix.com/products/arrays/specific/100k.affx, which provides information about the 50K chips that comprise the 100,000 SNP set). Briefly, the procedure was performed as follows, with minor modifications for the 500K array versus the 50K array:

[0267] a) Preparation of genomic DNA. The assay requires 250ng of genomic DNA extracted from any biological sample. DNA is diluted into working stocks of 50ng/uL using reduced EDTA TE buffer.

[0268] b) Restriction Enzyme Digestion. The strategy is to reduce the complexity of the genomic DNA up to 10 fold by performing a digestion with a single restriction enzyme. In order to achieve the complete coverage, two different enzymes (Xbal and HindIII) are utilized.

[0269] c) Adaptor Ligation. After digestion, the fragments are then ligated with a common set of adaptors (Adaptor Nspl and Styl). These ligation adaptors recognize the cohesive four base pair overhangs. Regardless of size, all of the digested fragments are substrates for ligation.

[0270] d) PCR Amplification and Quantification. Following ligation, the sample is diluted and the complexity of the genome is further reduced via single primer PCR amplification. This generic primer recognizes the adaptor ligated fragments and is optimized to select for product sizes ranging between 250-2000 base pairs. Each sample is set up in quadruplicate and once amplification is complete, the products are combined into a single well and purified on the QIAGEN MinElute™ 96 UF PCR Purification plate. Samples are resuspended in elution buffer. The yield of the purified product is determined spectrophotometrically.

[0271] e) Fragmentation. All samples are adjusted to the same concentration for the fragmentation step. A total of 40μg of PCR product is needed for fragmentation. PCR targets are fragmented with DNasel, which promotes a random distribution of fragments, and are cut into millions of short pieces of <200 base pairs.

[0272] f) End-Labelling. Each fragment is then labelled with biotin. The reaction is also catalyzed with Terminal Deoxynucleotidyl Tranferase (TDT) as a combination of both achieves the most efficient labelling process.

[0273] g) Hybridization. A cocktail mix is prepared with the end-labelled products. This mix contains an oligonucleotide control reagent, two blocking agents (Human Cot-1 and Herring Sperm DNA), Tetramethyl Ammonium Chloride (TMAC) for increasing the melting temperatures of T-A bonds and DMSO which decreased the melting temperatures of G-C bonds. The samples are transferred onto the array and washed over it for 16 to 18 hours.

[0274] h) Washing, Staining and Scanning. The next day the Affymetrix Fluidics Station 450 is used to rinse the array disposing of any non-bound DNA products which is followed by staining. This is a three step process consisting of a Streptavidin Phycoerythin (SAPE) stain, followed by an antibody amplification step and a final stain with SAPE. Once completed, each array is scanned using the Scanner 3000.

[0275] Data Analysis

[0276] Previously a Dynamic Model (DM)-algorithm was used for effective genotype calling of the Affymetrix GeneChip Human Mapping 500K Array sets from 210 male MI cases (<55 years old) and 210 matched controls from the PROCAM collective (e.g., see PCT application number PCT/US06/029449, filed July 26, 2006, incorporated herein by reference in its entirety). Table 2 shows 23,303 SNPs that were identified using the DM-Algorithm that are significantly associated with MI at a significance level of $p<0.05$.

[0277] Subsequently, a new, improved genotype calling algorithm was released through Affymetrix, resulting in more accurate and reliable genotype calls than the previously used DM-Algorithm. This new algorithm, called BRLMM, is based on a method published by Rabbee and Speed (Bioinformatics 2006, Vol.22:7-12). BRLMM employs a Linear Model with Mahalanobis distance classifier (RLMM), and extends the RLMM-algorithm by the addition of a Bayesian step, which provides improved estimates of cluster centers and variances, in order to improve overall performance of

500K arrays (call rates and accuracy) as well as equalization of the performance on homozygous and heterozygous genotypes. Thus, our initial data set comprising 210 male MI-cases and 210 matched controls was reanalyzed using the BRLMM-algorithm instead of the DM-algorithm.

[0278] Classical association analyses for individual polymorphisms and common haplotypes were performed after genotyping all individuals. For example, analysis described herein may be based on up to 210 cases and 210 controls. To compare allele frequencies between groups we applied the Chi-Square test (2-tailed) and to compare genotype frequencies the Armitage-Trend-Test or Fisher's-Exact-Test.

[0279] Hardy-Weinberg equilibrium and linkage disequilibrium was examined for each polymorphism. Populations that are randomly mating with respect to a polymorphism with alleles 1 and 2, whose frequencies are given by p and q, respectively (where p+q=1), are expected to have genotypic proportions given by Hardy-Weinberg expectations p^2, 2pq, and q^2, for 1/1 homozygotes, 1/2 heterozygotes, and 2/2 homozygotes, respectively. Departures from Hardy-Weinberg equilibrium (HWE) can be tested by contrasting the observed genotypic distribution with that expected under HWE. Observed departures might reflect unrecognized population admixture, non-random mating for the polymorphism being examined (or variation in linkage disequilibrium with that polymorphism), genotyping error, or simply chance. We note that since the data collected for these studies was effectively a random sample of individuals who met our criteria for "cases" and "controls", there is no expectation for departure for HWE.

[0280] We tested each polymorphism for departures from HWE and assessed the linkage disequilibrium patterns among polymorphisms. Specifically, we calculated disequilibrium coefficients (D' and r^2) for all pairs of polymorphisms and used established approaches for determining the local haplotype block structures (Gabriel et al., Science 2002, 296:2225-2229) as implemented in Haploview 3.0 (Barrett JC, et al., Bioinformatics, 21(2): 263-265, 2005). Linkage disequilibrium estimates and haplotype definitions for haplotype tagging was performed on the basis of the data obtained in the 420 individuals genotyped and cross-checked with the genotyping data and haplotype patterns available through the HapMap Consortium (available at the website having the URL www.hapmap.org). Although multilocus haplotypes can be estimated accurately in unrelated individuals of the sample sizes we have been able to ascertain (for haplotypes with frequencies greater than 0.05), it may not always be possible to assign multilocus haplotypes to individuals because of the number of possible haplotype combinations consistent with an observed genotypic configuration. Thus, we conducted our analyses considering polymorphisms individually, as well as in combination, with the combinations to be considered defined by the haplotype block structures.

[0281] The analysis described above resulted in the identification of 19,374 additional SNPs that are significantly associated with MI at a significance level of $p<0.05$. Table 1 presents the results of our analysis. The contents of Table 1 are further described above.

Equivalents and Scope of the Invention

[0282] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. The scope of the present invention is not intended to be limited to the above Description, but rather is as set forth in the appended claims. In the claims articles such as "a,", "an" and "the" may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include "or" between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. Furthermore, it is to be understood that the invention encompasses all variations, combinations, and permutations in which one or more limitations, elements, clauses, descriptive terms, etc., from one or more of the listed claims is introduced into another claim. In particular, any claim that is dependent on another claim can be modified to include one or more limitations found in any other claim that is dependent on the same base claim. In addition, it is to be understood that any particular embodiment of the present invention that falls within the prior art may be explicitly excluded from the claims. Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if not set forth explicitly herein. For example, any specific polymorphism, polymorphic variant, haplotype, gene, polynucleotide, or polypeptide can be excluded from the claims. Table 1 and Table 2 now follow containing details of the sequences of the invention. Table 1 is 1488 pages in length. Table 2 is 3628 pages in length.

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084457	C	C	175	75	367	3	115.58	5.87E-27	rs7699854	4	167029038	q32.3
SNP_A-1902305	A	A	355	15	254	88	67.492	2.12E-16	rs17169637	7	33868685	p14.3
SNP_A-1917221	A	A	407	3	287	59	66.388	3.70E-16	rs9846843	3	649171	p26.3
SNP_A-2147949	G	G	377	3	252	54	63.226	1.84E-15	rs6778321	3	134955970	q22.1
SNP_A-2120324	C	C	384	4	293	59	58.635	1.90E-14	rs17037778	3	13157096	p25.2
SNP_A-1830896	G	G	262	40	404	0	56.724	5.02E-14	rs8050381	16	82140823	q23.3
SNP_A-2118245	G	G	397	3	293	53	56.706	5.06E-14	rs16978901	20	18198368	p11.23
SNP_A-1757335	T	T	400	0	288	44	56.402	5.91E-14	rs10494062	1	107085715	p13.3
SNP_A-2211997	G	G	240	62	360	10	55.24	1.0666E-13	rs9346589	6	169097641	q27
SNP_A-2207278	A	A	418	0	345	47	53.205	3.0057E-13	rs7686272	4	39131328	p14
SNP_A-2065557	G	G	242	52	364	6	53.04	3.27E-13	---	2	177217003	q31.1
SNP_A-1804680	G	G	235	61	351	11	51.584	6.86E-13	rs8037437	15	58096734	q22.2
SNP_A-2224642	A	A	359	1	306	48	49.259	2.24E-12	rs8010814	14	62261229	q23.2
SNP_A-2024037	A	A	314	44	393	1	48.304	3.65E-12	rs1336872	1	48363454	p33
SNP_A-2134872	T	T	368	0	263	37	48.048	4.16E-12	rs16957658	18	49778840	q21.2
SNP_A-2130903	A	A	320	6	254	54	45.514	1.5151E-11	rs17030534	4	102151814	q24
SNP_A-1835766	T	T	378	2	290	42	44.925	2.05E-11	rs11024486	11	18080206	p15.1
SNP_A-2075685	C	C	317	41	391	1	44.38	2.70E-11	rs333644	17	852445	p13.3
SNP_A-1844561	T	T	387	3	311	45	43.566	4.10E-11	rs11106264	8	126262927	q24.13
SNP_A-1797803	A	A	327	11	281	67	43.549	4.13E-11	rs16830534	3	160825401	q25.33
SNP_A-2045361	T	T	393	3	310	44	43.349	4.58E-11	rs17138009	11	78684855	q14.1
SNP_A-1845418	C	C	163	123	281	67	42.206	8.21E-11	rs2197660	2	167212099	q24.3
SNP_A-2307042	A	A	339	5	275	49	41.962	9.31E-11	rs17838249	1	167652593	q24.3
SNP_A-1957729	A	A	346	2	305	45	41.917	9.52E-11	rs17135585	5	112740245	q22.2
SNP_A-2143668	C	C	370	8	284	52	41.248	1.34E-10	rs2489744	10	104497146	q24.32
SNP_A-2040804	T	T	279	51	212	126	40.832	1.66E-10	rs16867446	2	182248147	q31.3
SNP_A-2273616	A	A	344	16	260	66	40.584	1.88E-10	rs16946293	18	24988539	q12.1
SNP_A-2183057	A	A	347	5	302	50	39.938	2.621E-10	rs914798	13	72573507	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1980555	T	T	405	3	330	42	39.876	2.71E-10	rs16880162	5	8285726	p15.31
SNP_A-2246180	C	C	380	2	296	38	39.799	2.82E-10	rs6863525	5	154230370	q33.2
SNP_A-2244633	T	T	314	44	384	4	39.21	3.81E-10	rs1520246	5	127294624	q23.2
SNP_A-2264158	G	G	266	36	352	2	38.509	5.45E-10	rs4771668	13	109797868	q34
SNP_A-2123363	T	T	289	59	349	11	38.365	5.87E-10	rs11894477	2	227790559	q36.3
SNP_A-1750883	C	C	392	0	332	34	38.125	6.634E-10	rs10503537	8	15025745	p22
SNP_A-1683814	T	T	394	0	336	34	37.892	7.48E-10	rs1491442	9	72132100	q21.13
SNP_A-1916882	C	C	329	31	256	90	37.615	8.6172E-10	rs10911142	1	179519608	q25.3
SNP_A-1898521	G	G	334	32	412	0	37.567	8.83E-10	rs11869701	17	71131229	q25.1
SNP_A-2284638	G	G	297	51	349	7	37.479	9.24E-10	rs579092	2	137051341	q21.3
SNP_A-1939623	C	C	400	0	346	34	37.421	9.52E-10	rs6808472	3	65746053	p14.1
SNP_A-1855927	A	A	362	12	278	56	37.355	9.8471E-10	rs10995694	10	65357889	q21.3
SNP_A-2077946	A	A	275	137	297	49	37.014	1.17E-09	rs16961974	17	60705480	q24.1
SNP_A-1946420	A	A	326	12	287	63	36.963	1.20E-09	rs6706452	2	171075829	q31.1
SNP_A-2059153	T	T	300	50	237	121	36.785	1.32E-09	rs9431644	1	227577083	q42.2
SNP_A-1687462	G	G	345	13	297	63	36.478	1.5438E-09	rs4241	3	5575120	p26.1
SNP_A-2253987	T	T	321	55	367	9	36.138	1.84E-09	rs7024501	9	85631610	q21.33
SNP_A-1900843	G	G	414	0	339	31	36.114	1.8606E-09	rs7176832	15	40504659	q15.1
SNP_A-2163765	A	A	349	15	288	64	36.043	1.93E-09	rs2358054	6	121015082	q22.31
SNP_A-1973768	G	G	348	2	298	38	35.999	1.9739E-09	rs16850546	3	106038775	q13.11
SNP_A-2219138	A	A	341	1	341	41	35.995	1.9781E-09	rs6763185	3	83605888	p12.1
SNP_A-1977549	A	A	352	4	303	43	35.892	2.09E-09	rs4321609	4	72906542	q13.3
SNP_A-1746044	G	G	260	32	389	3	35.815	2.1695E-09	rs10491572	9	7921125	p24.1
SNP_A-2243594	G	G	282	34	393	3	35.688	2.32E-09	rs11056485	12	15481094	p12.3
SNP_A-2031537	C	C	341	9	275	51	35.664	2.34E-09	rs4491939	3	111527071	q13.13
SNP_A-1881130	A	A	392	2	322	36	35.642	2.37E-09	rs541088	18	6033257	p11.31
SNP_A-2261889	A	A	343	1	322	38	35.42	2.66E-09	rs12589634	14	86683896	q31.3
SNP_A-2205177	G	G	334	2	299	39	35.32	2.7977E-09	rs2920688	8	6268508	p23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1874404	A	A	314	46	372	6	35.255	2.89E-09	rs541671	1	37039932	p34.3
SNP_A-1950226	G	G	271	37	383	5	34.826	3.61E-09	rs1479599	5	76653699	q13.3
SNP_A-2201479	T	T	391	1	345	35	34.808	3.64E-09	rs692747	1	225663661	q42.13
SNP_A-2032932	G	G	285	39	358	4	34.778	3.70E-09	rs2197284	12	72210061	q21.1
SNP_A-1856530	G	G	365	5	307	43	34.56	4.13E-09	rs6414052	2	9233697	p25.1
SNP_A-2151560	A	A	408	0	305	27	34.437	4.40E-09	rs6942518	7	141811883	q34
SNP_A-2232095	G	G	338	30	406	0	34.432	4.4131E-09	rs12100834	14	103888129	q32.33
SNP_A-2252719	C	C	408	0	329	29	34.351	4.60E-09	rs9914076	17	72251995	q25.1
SNP_A-1842908	A	A	369	9	288	48	34.319	4.68E-09	rs326775	11	29573734	p14.1
SNP_A-2013922	C	C	382	6	325	45	34.011	5.4809E-09	rs2253584	11	94156462	q21
SNP_A-2225328	G	G	284	70	366	22	33.901	5.80E-09	rs12104808	2	101302375	q11.2
SNP_A-2208945	C	C	375	17	294	62	33.786	6.15E-09	rs916622	17	5915330	p13.2
SNP_A-2258209	G	G	342	2	330	40	33.693	6.45E-09	rs9503902	6	3994493	p25.2
SNP_A-1816118	G	G	416	0	356	30	33.588	6.81E-09	rs16854385	1	201496284	q32.1
SNP_A-1826878	G	G	343	37	382	2	33.488	7.17E-09	rs10845092	12	10294917	p13.2
SNP_A-1998094	C	C	342	0	292	30	33.371	7.61E-09	rs10828303	10	22643587	p12.2
SNP_A-2143372	A	A	310	30	393	1	33.135	8.60E-09	rs1930326	13	79974193	q31.1
SNP_A-1857484	G	G	328	4	312	44	32.936	9.5233E-09	rs17125945	12	60824357	q14.1
SNP_A-2146541	C	C	338	2	289	35	32.895	9.73E-09	rs6811944	4	73208961	q13.3
SNP_A-1709715	T	T	298	28	401	1	32.738	1.05E-08	rs2726713	8	50137139	q11.21
SNP_A-2079414	T	T	304	30	381	1	32.714	1.0678E-08	rs12286249	11	63972306	q13.1
SNP_A-2207018	G	G	273	37	386	6	32.592	1.1371E-08	rs16872191	6	12129457	p24.1
SNP_A-1986361	A	A	245	35	370	6	32.567	1.1513E-08	rs16868379	6	70717601	q13
SNP_A-2069757	T	T	336	22	284	74	32.528	1.1749E-08	rs1373548	12	44773389	q13.11
SNP_A-1862070	A	A	387	5	318	40	32.501	1.1914E-08	rs6545856	2	61453138	p15
SNP_A-2004351	A	A	299	43	373	7	32.158	1.42E-08	rs1347926	15	87824088	q26.1
SNP_A-2092768	A	A	416	0	348	28	32.114	1.45E-08	rs7919743	10	95098019	q23.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2031290	C	C	399	3	307	33	32.032	1.52E-08	rs16877370	4	10732844	p16.1
SNP_A-2242811	A	A	404	0	351	29	32.016	1.53E-08	rs17123044	1	62262078	p31.3
SNP_A-1889943	C	C	256	44	360	10	32.002	1.5404E-08	rs9486835	6	108666779	q21
SNP_A-2152072	T	T	321	13	281	59	31.996	1.54E-08	rs6922398	6	108339352	q21
SNP_A-2022746	A	A	392	0	341	29	31.94	1.59E-08	rs16903880	5	15529846	p15.1
SNP_A-1988216	G	G	327	3	317	41	31.887	1.6343E-08	rs6916787	6	154570849	q25.2
SNP_A-1879663	C	C	334	38	396	4	31.816	1.695E-08	rs627770	10	3563285	p15.2
SNP_A-2284656	G	G	363	5	320	42	31.788	1.7198E-08	rs16844422	4	3524291	p16.3
SNP_A-2285124	C	C	295	27	399	1	31.671	1.83E-08	rs16831942	3	162333689	q26.1
SNP_A-2069895	A	A	304	28	395	1	31.603	1.89E-08	rs1679375	12	74182832	q21.1
SNP_A-1981412	G	G	395	1	339	31	31.551	1.94E-08	rs3817322	5	41036428	p13.1
SNP_A-2066218	G	G	275	61	343	17	31.513	1.98E-08	rs2365106	2	88787365	p11.2
SNP_A-2060839	G	G	285	15	269	67	31.501	1.9935E-08	rs16975077	15	42894864	q21.1
SNP_A-1865616	A	A	296	28	383	1	31.426	2.07E-08	rs17141348	10	17656900	p12.33
SNP_A-2108442	C	C	302	14	272	62	31.409	2.09E-08	rs7575941	2	238449048	q37.3
SNP_A-2152368	A	A	338	14	274	56	31.216	2.309E-08	rs6493256	15	45054292	q21.1
SNP_A-1843086	T	T	340	2	316	36	31.161	2.3743E-08	rs8069772	17	16408705	p11.2
SNP_A-1889721	G	G	331	3	302	38	31.156	2.38E-08	rs16878786	6	49228275	p12.3
SNP_A-2103349	A	A	295	71	327	19	31.154	2.38E-08	rs1148117	11	122998271	q24.1
SNP_A-2043369	G	G	405	1	329	29	31.11	2.44E-08	rs2121943	16	10102934	p13.2
SNP_A-2223095	T	T	314	80	321	21	31.023	2.55E-08	rs10069462	5	149004044	q32
SNP_A-1956579	T	T	325	49	373	9	30.806	2.85E-08	rs1243986	10	8194237	p14
SNP_A-1824234	C	C	342	38	367	3	30.632	3.12E-08	rs7414683	1	12747788	p36.21
SNP_A-2173325	A	A	254	42	364	10	30.606	3.16E-08	rs12641338	4	3734797	p16.3
SNP_A-2158886	T	T	407	3	327	33	30.602	3.1683E-08	rs7918090	10	67759119	q21.3
SNP_A-1983151	G	G	352	0	319	29	30.601	3.17E-08	rs2900109	5	117360780	q23.1
SNP_A-1911042	A	A	364	8	319	47	30.573	3.22E-08	rs17743924	18	46909802	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2036154	T	T	382	4	334	38	30.494	3.3498E-08	rs10492187	12	16509479	p12.3
SNP_A-1733034	G	G	325	31	398	2	30.398	3.52E-08	rs1342778	1	90574425	p22.2
SNP_A-2233144	T	T	312	10	278	52	30.317	3.67E-08	rs1007653	9	79607567	q21.31
SNP_A-1968836	C	C	321	7	311	49	30.235	3.83E-08	rs462657	20	57294912	q13.32
SNP_A-2061537	T	T	373	5	344	42	30.22	3.86E-08	rs7792641	7	4236273	p22.2
SNP_A-2077900	T	T	280	22	400	0	30.082	4.14E-08	rs16859266	3	185992503	q27.1
SNP_A-1922915	A	A	403	1	354	30	29.812	4.76E-08	rs996489	8	139361784	q24.23
SNP_A-1886868	G	G	267	53	351	15	29.702	5.04E-08	rs2964953	7	47294601	p12.3
SNP_A-2035552	G	G	325	5	302	42	29.693	5.06E-08	rs4275079	6	142355023	q24.1
SNP_A-2090232	A	A	354	0	355	31	29.673	5.11E-08	rs7757359	6	101682103	q16.3
SNP_A-2170709	G	G	342	32	394	2	29.54	5.48E-08	rs6800393	3	60303640	p14.2
SNP_A-2104359	G	G	406	2	343	31	29.361	6.01E-08	rs4149797	16	2965553	p13.3
SNP_A-1839426	C	C	344	0	327	29	29.234	6.42E-08	rs7919445	10	2819670	p15.3
SNP_A-2081531	G	G	272	72	312	22	29.194	6.55E-08	rs9581249	13	24532208	q12.13
SNP_A-2207937	A	A	194	58	336	28	29.109	6.84E-08	rs7624756	3	73944942	p13
SNP_A-2189003	A	A	324	24	408	0	29.06	7.02E-08	rs7114749	11	34195229	p13
SNP_A-2155125	A	A	329	31	386	2	29.021	7.16E-08	rs3747227	22	43906810	q13.31
SNP_A-2068380	C	C	297	31	254	86	29.004	7.22E-08	rs13359413	5	35755837	p13.2
SNP_A-2074945	G	G	407	1	342	28	28.992	7.27E-08	rs16856662	1	228628404	q42.2
SNP_A-2020373	C	C	305	41	369	7	28.964	7.37E-08	rs2838392	21	44056387	q22.3
SNP_A-1981322	T	T	396	0	344	26	28.805	8.01E-08	rs10214132	5	38402287	p13.2
SNP_A-1899236	A	A	379	1	320	28	28.767	8.16E-08	rs6991830	8	51218518	q11.21
SNP_A-1947051	C	C	380	4	310	34	28.674	8.56E-08	rs11027565	11	23825835	p14.3
SNP_A-2201961	A	A	281	53	322	12	28.649	8.67E-08	---	8	37250448	p12
SNP_A-2078578	G	G	254	40	349	9	28.572	9.027E-08	---	2	121096310	q14.2
SNP_A-1987365	G	G	248	24	378	2	28.505	9.35E-08	rs1555401	6	117874028	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084377	A	A	285	25	257	79	28.485	9.44E-08	rs11102629	1	113681459	p13.2
SNP_A-1904037	G	G	391	1	347	29	28.436	9.69E-08	rs16935787	10	35215091	p11.21
SNP_A-1797038	G	G	347	1	329	31	28.409	9.82E-08	rs9290629	3	179064107	q26.32
SNP_A-2197176	T	T	351	19	278	60	28.362	1.0061E-07	rs16882757	7	143605626	q35
SNP_A-1965779	T	T	385	5	316	36	28.359	1.01E-07	rs3815675	2	169696362	q31.1
SNP_A-2188336	C	C	255	43	366	12	28.241	1.0709E-07	rs17150606	9	133392190	q34.2
SNP_A-1727212	T	T	402	0	315	23	28.233	1.0758E-07	rs10484574	6	163861121	q26
SNP_A-1850199	G	G	366	0	324	26	28.213	1.09E-07	rs6547285	2	80000879	p12
SNP_A-1933148	T	T	331	21	276	66	28.121	1.1395E-07	rs1897919	2	153710816	q23.3
SNP_A-2098412	C	C	417	1	362	28	28.085	1.16E-07	rs1227474	2	148715183	q23.1
SNP_A-2070168	G	G	357	1	308	28	28.079	1.1645E-07	rs16844233	1	195836317	q31.3
SNP_A-2265922	C	C	359	19	298	62	28.068	1.171E-07	rs11201902	10	87892545	q23.2
SNP_A-1811205	A	A	345	1	331	31	28.068	1.1715E-07	rs16934456	9	16318329	p22.3
SNP_A-1933345	A	A	374	26	418	0	28.062	1.1749E-07	rs1777604	1	112661920	p13.2
SNP_A-2013743	G	G	312	26	387	1	27.884	1.29E-07	rs6469632	8	117204707	q23.3
SNP_A-1744413	G	G	375	1	339	29	27.866	1.30E-07	rs9314945	13	27616793	q12.3
SNP_A-2271780	G	G	322	8	287	45	27.836	1.32E-07	rs674262	2	220301089	q35
SNP_A-1886767	C	C	411	1	321	25	27.683	1.43E-07	rs8076130	17	3161252	p13.3
SNP_A-2232368	A	A	391	3	321	31	27.664	1.4433E-07	rs6574596	14	25253292	q12
SNP_A-2215325	T	T	273	45	351	11	27.662	1.445E-07	---	8	139835886	q24.23
SNP_A-2272151	C	C	317	11	309	55	27.638	1.46E-07	rs11221237	11	127666125	q24.3
SNP_A-2310805	T	T	404	0	353	25	27.602	1.49E-07	rs6500267	16	48519950	q12.1
SNP_A-1876355	A	A	361	13	306	52	27.599	1.4928E-07	rs10099127	8	30544225	p12
SNP_A-2245290	T	T	282	40	375	9	27.544	1.54E-07	rs16853720	1	227576991	q42.2
SNP_A-1704827	T	T	397	1	272	22	27.521	1.55E-07	rs10483125	22	25196658	q12.1
SNP_A-2216534	C	C	331	21	270	64	27.491	1.5783E-07	rs7101539	11	20422573	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2019158	G	G	408	0	359	25	27.428	1.6303E-07	rs2836236	21	38535413	q22.13
SNP_A-2150760	G	G	250	70	302	24	27.356	1.69E-07	rs16974405	15	52336873	q21.3
SNP_A-2064663	T	T	333	9	324	50	27.239	1.7979E-07	rs1936763	13	56804649	q21.1
SNP_A-1660839	C	C	393	1	326	26	27.113	1.92E-07	rs1806162	11	31813539	p13
SNP_A-2087853	T	T	368	26	266	64	27.008	2.026E-07	rs6078963	20	13172651	p12.1
SNP_A-2110249	C	C	394	2	348	30	26.948	2.09E-07	rs11835869	12	126248350	q24.32
SNP_A-2135514	A	A	394	2	348	30	26.948	2.09E-07	rs17125357	14	88666033	q32.11
SNP_A-2280639	T	T	384	8	319	41	26.921	2.1189E-07	---	20	16955098	p12.1
SNP_A-1879006	A	A	353	9	286	42	26.768	2.29E-07	---	8	57186786	q12.1
SNP_A-2030970	G	G	411	3	362	32	26.656	2.431E-07	rs3772462	3	59921750	p14.2
SNP_A-1813020	C	C	294	32	362	4	26.603	2.4982E-07	rs12032150	1	228876969	q42.2
SNP_A-2084171	T	T	265	25	395	3	26.594	2.51E-07	rs12083030	1	169693050	q24.3
SNP_A-2255361	T	T	418	2	348	28	26.579	2.5295E-07	rs7753337	6	166686324	q27
SNP_A-2211939	G	G	369	21	300	62	26.364	2.83E-07	rs4757471	11	16966143	p15.1
SNP_A-1987870	T	T	345	5	309	37	26.34	2.86E-07	---	6	139502858	q24.1
SNP_A-1847090	A	A	323	7	326	46	26.293	2.93E-07	rs16859306	4	46156908	p12
SNP_A-1824757	G	G	394	0	333	23	26.26	2.98E-07	rs6706688	2	21524122	p24.1
SNP_A-1716923	A	A	339	3	331	35	26.26	2.98E-07	rs10485102	6	92324691	q15
SNP_A-1701519	G	G	384	4	285	29	26.079	3.28E-07	rs10502313	18	3310158	p11.31
SNP_A-2010479	T	T	302	24	258	70	25.962	3.48E-07	rs291715	11	41809196	p12
SNP_A-1868707	A	A	308	16	284	60	25.871	0.000000365	rs6871201	5	65423678	q12.3
SNP_A-1941688	G	G	393	1	342	26	25.83	3.73E-07	rs2727467	7	129105036	q32.2
SNP_A-2041729	C	C	250	104	317	51	25.778	3.83E-07	rs13267815	8	142640224	q24.3
SNP_A-1985176	T	T	400	0	345	23	25.772	3.84E-07	rs16875716	6	14897577	p23
SNP_A-2302347	T	T	402	0	332	22	25.732	3.92E-07	rs7701080	5	43668182	p12
SNP_A-2075797	G	G	356	26	407	1	25.729	3.9283E-07	rs17154678	10	43758377	q11.21
SNP_A-1805493	T	T	393	1	346	26	25.527	4.3634E-07	rs9309120	2	45095403	p21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1750195	G	G	340	10	256	40	25.503	4.42E-07	rs1373062	11	59900951	q12.2
SNP_A-2167154	C	C	399	5	303	31	25.496	4.43E-07	rs17119817	11	115938922	q23.3
SNP_A-1855122	T	T	305	23	393	1	25.441	4.56E-07	rs1882844	14	76402120	q24.3
SNP_A-2219753	T	T	323	11	293	49	25.437	4.5716E-07	rs16872701	5	74983739	q13.3
SNP_A-1952944	C	C	415	1	353	25	25.399	4.66E-07	rs13335905	16	68471479	q22.1
SNP_A-2259202	G	G	249	51	188	102	25.353	4.77E-07	rs9594037	13	85076105	q31.1
SNP_A-2094575	A	A	239	47	338	16	25.301	4.91E-07	rs7996205	13	94479706	q32.1
SNP_A-2027347	A	A	334	6	325	41	25.263	5.00E-07	rs263352	5	95900920	q15
SNP_A-1948199	T	T	362	4	319	33	25.181	5.22E-07	rs12088691	1	206808045	q32.2
SNP_A-2141942	A	A	362	0	334	24	25.105	5.43E-07	rs17088325	18	69619928	q22.3
SNP_A-2279438	C	C	338	4	328	36	25.089	5.47E-07	rs8037621	15	90776915	q26.1
SNP_A-2293856	C	C	322	52	370	14	25.081	5.50E-07	rs6693433	1	86388896	p22.3
SNP_A-2138144	C	C	324	20	420	0	25.075	5.51E-07	rs1461769	12	129032870	q24.33
SNP_A-2001165	G	G	351	27	286	70	25.058	5.5642E-07	rs1343888	10	57140925	q21.1
SNP_A-1989939	G	G	377	13	312	48	25.054	5.57E-07	rs17135299	7	52605668	p12.1
SNP_A-2163231	G	G	395	9	302	38	24.982	5.79E-07	rs16892741	8	120640027	q24.12
SNP_A-1948698	G	G	361	29	394	2	24.914	5.99E-07	rs7101380	11	76622653	q13.5
SNP_A-1886472	T	T	405	1	336	24	24.913	6.00E-07	rs10261788	7	66812368	q11.22
SNP_A-1950877	A	A	294	26	395	3	24.867	6.14E-07	rs8040267	15	37190484	q14
SNP_A-1848979	T	T	372	2	354	30	24.819	6.30E-07	rs6729375	2	71529299	p13.2
SNP_A-1947829	G	G	352	4	335	35	24.801	6.36E-07	rs17162165	1	26488151	p36.11
SNP_A-2190904	T	T	305	65	334	20	24.798	6.37E-07	rs3025003	6	43854449	p21.1
SNP_A-1962568	C	C	357	41	317	97	24.793	6.38E-07	rs644417	2	31408309	p23.1
SNP_A-2252612	C	C	410	0	337	21	24.726	6.61E-07	rs2982411	1	71222692	p31.1
SNP_A-2058221	G	G	265	43	361	13	24.637	6.92E-07	---	16	5945854	p13.3
SNP_A-1885187	T	T	272	26	394	4	24.622	6.97E-07	rs16893125	6	82180584	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2057702	G	G	310	10	308	50	24.621	6.98E-07	rs11742635	5	127816693	q23.2
SNP_A-1984555	A	A	379	9	364	46	24.606	7.03E-07	rs315785	5	169665910	q35.1
SNP_A-2312056	A	A	277	25	385	3	24.568	7.17E-07	rs2196559	6	81141904	q14.1
SNP_A-2060522	G	G	413	5	336	32	24.537	7.2888E-07	rs2123624	16	79704615	q23.2
SNP_A-2040853	G	G	356	0	351	25	24.507	7.40E-07	---	5	95378757	q15
SNP_A-2309029	G	G	390	2	350	28	24.449	7.63E-07	rs6668678	1	226016310	q42.13
SNP_A-2006218	T	T	287	21	391	1	24.406	7.80E-07	rs1709324	2	23677472	p24.1
SNP_A-2166292	C	C	305	39	362	8	24.403	7.81E-07	rs4381320	10	52193396	q11.23
SNP_A-1955254	C	C	411	1	318	22	24.368	7.96E-07	rs12499897	4	14822303	p15.33
SNP_A-1954294	C	C	289	19	384	0	24.357	8.00E-07	rs5490071	1	225606218	q42.13
SNP_A-1810537	A	A	275	39	362	10	24.316	8.18E-07	rs6132299	20	20364336	p11.23
SNP_A-2301702	T	T	266	60	307	19	24.212	8.63E-07	rs13361978	5	172589416	q35.1
SNP_A-2039823	G	G	368	8	304	38	24.104	9.12E-07	rs3114816	7	109015021	q31.1
SNP_A-2074483	T	T	336	4	327	35	24.097	9.16E-07	rs17168723	7	15128053	p21.1
SNP_A-2108609	C	C	249	55	306	18	23.995	9.66E-07	rs9813057	3	198698664	q29
SNP_A-1843958	G	G	324	8	332	46	23.959	9.84E-07	rs6746251	2	157468375	q24.1
SNP_A-1905440	T	T	326	30	294	80	23.95	9.89E-07	rs9820678	3	193699227	q28
SNP_A-2107506	A	A	353	3	340	32	23.932	9.98E-07	rs3774310	3	188923274	q27.3
SNP_A-1952086	G	G	272	28	381	5	23.818	1.06E-06	rs8109060	19	33782414	q12
SNP_A-1904573	C	C	354	34	370	4	23.789	1.08E-06	rs1395246	1	63859183	p31.3
SNP_A-2167662	G	G	397	5	354	34	23.786	1.0769E-06	rs6469145	8	108836735	q23.1
SNP_A-2271496	A	A	259	31	369	7	23.716	1.1166E-06	rs6686512	1	111269247	p13.3
SNP_A-1980063	G	G	294	28	380	4	23.711	1.1192E-06	rs419687	4	180008915	q34.3
SNP_A-1805355	A	A	297	21	393	1	23.696	1.13E-06	rs12319908	12	3903203	p13.32
SNP_A-2078552	A	A	344	4	319	33	23.65	1.1553E-06	rs7670796	4	134249963	q28.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2260163	T	T	306	14	274	52	23.591	1.1917E-06	rs17090343	4	61702378	q13.1
SNP_A-2010146	C	C	329	11	271	43	23.573	1.20E-06	rs11820281	11	38777996	p12
SNP_A-2274251	T	T	292	16	318	66	23.533	1.23E-06	rs7180290	15	40002826	q15.1
SNP_A-1906556	C	C	334	14	309	53	23.407	1.3113E-06	rs3131734	1	57921241	p32.2
SNP_A-1973899	T	T	331	37	358	6	23.386	1.33E-06	rs1512523	3	111829934	q13.13
SNP_A-2296749	G	G	357	15	305	51	23.381	1.33E-06	rs2057269	14	39608507	q21.1
SNP_A-1867932	C	C	307	23	365	1	23.373	1.33E-06	rs1880596	7	51610642	p12.1
SNP_A-2008428	T	T	341	5	348	38	23.28	1.4002E-06	rs6443098	3	7272636	p26.1
SNP_A-1937288	T	T	407	1	377	25	23.259	1.42E-06	---	9	105055150	q31.1
SNP_A-2070096	G	G	420	0	333	19	23.242	1.43E-06	rs597227	11	120899984	q23.3
SNP_A-2213302	G	G	414	0	346	20	23.218	1.4462E-06	---	9	76856953	q21.2
SNP_A-2238071	A	A	355	1	342	26	23.198	1.46E-06	rs7684353	4	102710542	q24
SNP_A-1798829	T	T	382	8	326	38	23.126	1.52E-06	rs729516	16	47809406	q12.1
SNP_A-2074884	G	G	392	6	345	35	23.105	1.5336E-06	rs2228064	10	45198056	q11.21
SNP_A-2162689	T	T	307	11	304	50	23.087	1.55E-06	---	15	49596463	q21.2
SNP_A-1840384	G	G	238	50	329	19	23.077	0.000001556	rs9292714	5	38711934	p13.1
SNP_A-2272135	G	G	396	6	316	32	23.01	0.000001612	rs16842511	1	194877591	q31.3
SNP_A-2286052	A	A	351	21	396	0	22.983	1.6342E-06	rs16977885	15	56072887	q21.3
SNP_A-1968782	A	A	355	5	324	34	22.974	1.64E-06	rs7267132	20	54508030	q13.31
SNP_A-2141436	C	C	390	6	334	34	22.936	1.6748E-06	rs856212	14	58308192	q23.1
SNP_A-1994006	T	T	340	12	310	48	22.936	1.68E-06	rs16907620	8	81442337	q21.13
SNP_A-1872889	G	G	408	0	363	21	22.92	1.6886E-06	rs16849976	3	141351793	q23
SNP_A-2218967	C	C	307	21	393	1	22.906	1.70E-06	rs7399104	12	87935777	q21.33
SNP_A-1971827	C	C	391	7	325	35	22.903	1.70E-06	rs16863265	1	167030989	q24.2
SNP_A-2205274	T	T	363	1	326	24	22.881	1.72E-06	rs1518472	4	73789545	q13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1900796	G	G	337	45	343	9	22.865	1.74E-06	rs713228	18	33531547	q12.2
SNP_A-2201135	C	C	391	3	327	27	22.831	1.77E-06	rs7796949	7	117453525	q31.31
SNP_A-2163721	G	G	354	20	416	0	22.824	1.7755E-06	rs2727113	15	98381534	q26.3
SNP_A-2243241	T	T	332	10	318	46	22.781	1.8156E-06	rs17831431	18	53293002	q21.31
SNP_A-2140830	T	T	408	0	348	20	22.761	0.000001835	rs7135679	12	124371260	q24.31
SNP_A-2239312	G	G	255	31	374	8	22.751	0.000001844	rs4747515	10	7646171	p14
SNP_A-2261529	A	A	368	0	361	23	22.737	1.8575E-06	---	14	51991954	q22.1
SNP_A-1991208	A	A	344	28	393	3	22.691	1.9023E-06	rs11563718	7	126344521	q32.1
SNP_A-1866172	T	T	367	21	408	0	22.681	1.91E-06	rs1407014	20	30258266	q11.21
SNP_A-2138863	G	G	305	41	360	10	22.613	1.98E-06	rs11853913	15	86503845	q25.3
SNP_A-1972462	A	A	390	6	338	34	22.586	2.0091E-06	rs2034736	3	40466445	p22.1
SNP_A-1718065	G	G	340	0	350	24	22.577	2.02E-06	-	13	74138660	q22.2
SNP_A-2135239	A	A	354	0	334	22	22.576	2.02E-06	rs17071534	13	47736889	q14.2
SNP_A-2305796	A	A	355	1	337	25	22.573	2.02E-06	rs1789521	18	31919593	q12.2
SNP_A-1645722	A	A	287	47	361	15	22.561	2.0356E-06	rs942591	13	32787277	q13.2
SNP_A-2155142	T	T	386	8	336	38	22.522	2.08E-06	rs1492902	1	169419215	q24.3
SNP_A-1936751	C	C	236	108	324	64	22.521	2.08E-06	rs7987859	13	28072007	q12.3
SNP_A-1788200	G	G	270	30	383	7	22.495	2.11E-06	rs1963880	8	130529193	q24.21
SNP_A-2290734	G	G	331	37	369	7	22.434	2.17E-06	rs16904982	8	134823188	q24.22
SNP_A-1876044	T	T	385	11	331	43	22.425	2.1847E-06	rs6843752	4	21258801	p15.31
SNP_A-2278804	C	C	389	5	316	30	22.397	2.22E-06	rs11102410	1	112440914	p13.2
SNP_A-2002469	A	A	302	40	364	10	22.386	2.23E-06	rs7976995	12	1247482	p13.33
SNP_A-1868307	C	C	342	22	407	1	22.38	2.24E-06	rs16928731	11	2815841	p15.4
SNP_A-1914058	C	C	340	2	304	26	22.377	2.24E-06	---	19	53999660	q13.33
SNP_A-2088157	C	C	396	4	348	30	22.375	2.24E-06	---	1	25970705	p36.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1795269	G	G	400	2	345	25	22.365	2.25E-06	rs4356530	17	5098539	p13.2
SNP_A-2129406	T	T	346	0	345	23	22.345	2.28E-06	rs4609947	18	64902614	q22.2
SNP_A-2097493	T	T	316	38	362	8	22.343	2.2799E-06	rs17152636	8	10764818	p23.1
SNP_A-1828013	T	T	411	1	363	23	22.32	2.3079E-06	rs16846728	1	170880948	q25.1
SNP_A-2277167	G	G	392	6	309	31	22.299	2.3336E-06	rs17042204	3	16405695	p24.3
SNP_A-2088132	A	A	390	10	335	41	22.295	2.34E-06	rs12729068	1	109968686	p13.3
SNP_A-1700971	G	G	314	2	317	29	22.217	2.44E-06	rs10515285	5	98363771	q21.1
SNP_A-2275105	A	A	401	3	358	28	22.199	2.46E-06	rs4144083	2	168453743	q24.3
SNP_A-2283553	A	A	372	8	317	37	22.186	2.47E-06	rs17111525	14	40707565	q21.1
SNP_A-2125933	C	C	355	1	343	25	22.167	2.50E-06	rs1434858	9	26231604	p21.2
SNP_A-1992121	T	T	344	22	288	60	22.132	2.55E-06	rs2442540	8	6260908	p23.1
SNP_A-1902655	T	T	399	5	328	30	22.095	2.60E-06	rs4281059	7	114266361	q31.2
SNP_A-1833716	C	C	400	2	364	26	22.091	2.60E-06	rs648425	1	78599229	p31.1
SNP_A-1985584	A	A	347	15	272	46	22.087	2.61E-06	rs12033808	1	217360229	q41
SNP_A-2275566	T	T	315	9	324	46	22.066	2.6349E-06	rs2593797	6	107419993	q21
SNP_A-2055103	C	C	310	18	392	0	22.064	2.64E-06	rs17015979	12	87646541	q21.33
SNP_A-1970675	T	T	387	13	332	46	22.06	2.64E-06	rs1123031	22	16437445	q11.21
SNP_A-2155188	G	G	287	21	279	67	22.025	2.6913E-06	rs17599248	5	144532286	q32
SNP_A-2219673	C	C	315	43	363	11	22.022	2.70E-06	rs6458375	6	44310330	p21.1
SNP_A-1864411	G	G	412	0	364	20	22.011	2.71E-06	rs17177752	10	50449270	q11.23
SNP_A-2307990	G	G	365	25	321	67	21.991	2.7392E-06	---	10	43659191	q11.21
SNP_A-2247590	T	T	340	6	309	35	21.987	2.74E-06	rs11705894	3	422069	p26.3
SNP_A-1870494	T	T	380	2	318	24	21.98	2.76E-06	rs7523514	1	21100526	p36.12
SNP_A-2262912	G	G	283	23	391	3	21.975	2.76E-06	rs11938182	4	57302705	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1833326	C	C	296	46	360	14	21.924	2.84E-06	rs7924263	10	77877107	q22.3
SNP_A-1972522	A	A	358	2	354	28	21.923	2.84E-06	rs17075340	3	43234393	p22.1
SNP_A-2246152	T	T	414	0	368	20	21.886	2.89E-06	rs17124157	14	51084046	q22.1
SNP_A-1816726	T	T	326	10	313	45	21.862	2.93E-06	rs812631	10	90066153	q23.31
SNP_A-1670878	G	G	293	51	242	102	21.862	2.93E-06	rs3935559	1	3736878	p36.32
SNP_A-2204384	A	A	291	61	358	24	21.833	2.97E-06	rs2188777	16	26777397	p12.1
SNP_A-2270723	G	G	395	3	330	26	21.797	3.03E-06	---	1	54311147	p32.3
SNP_A-1869762	A	A	336	4	311	31	21.789	3.0436E-06	rs16836270	2	137334754	q21.3
SNP_A-2302072	C	C	357	9	318	40	21.78	3.06E-06	rs10409928	19	3698890	p13.3
SNP_A-1830213	C	C	375	11	320	42	21.737	3.13E-06	rs4899192	14	65569935	q23.3
SNP_A-2007390	A	A	276	36	368	10	21.724	3.1479E-06	rs6041792	20	12967359	p12.1
SNP_A-1986380	G	G	280	32	382	8	21.717	3.16E-06	rs16869513	6	71624762	q13
SNP_A-1645524	A	A	309	17	406	0	21.675	3.23E-06	rs10508718	10	26699294	p12.1
SNP_A-2112142	A	A	279	31	371	7	21.67	3.24E-06	rs9931551	16	6588453	p13.2
SNP_A-2040037	G	G	346	4	334	32	21.643	3.28E-06	rs2444831	6	81397584	q14.1
SNP_A-2237767	A	A	401	1	348	22	21.635	3.2978E-06	rs6947217	7	69773744	q11.22
SNP_A-2224869	G	G	300	22	388	2	21.625	3.3144E-06	rs4758908	12	132022337	q24.33
SNP_A-2006482	C	C	329	5	336	36	21.53	3.4838E-06	rs363676	2	74717714	p13.1
SNP_A-2108987	C	C	404	2	361	25	21.518	3.50E-06	rs16995896	20	49357178	q13.2
SNP_A-2139295	T	T	365	13	286	42	21.444	3.64E-06	rs1442775	2	117073106	q14.1
SNP_A-2045360	T	T	293	29	363	5	21.439	3.65E-06	rs11200895	10	85908600	q23.1
SNP_A-1695099	T	T	367	7	330	36	21.438	3.65E-06	rs10489718	1	183165960	q31.1
SNP_A-2120652	T	T	296	22	380	2	21.432	3.67E-06	rs13314352	3	158158949	q25.31
SNP_A-1838124	G	G	231	37	343	13	21.389	3.75E-06	rs6858750	4	55931764	q12
SNP_A-2028932	T	T	353	3	324	28	21.382	3.76E-06	rs16972476	18	35776426	q12.3
SNP_A-1673944	T	T	314	16	271	51	21.349	3.83E-06	rs850399	7	144521478	q35
SNP_A-2191067	G	G	412	0	338	18	21.331	3.86E-06	rs9821834	3	95806980	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1792603	G	G	281	51	348	18	21.314	3.90E-06	rs10847569	12	127217800	q24.32
SNP_A-1815296	A	A	301	19	399	1	21.294	3.94E-06	rs11486857	7	40389052	p14.1
SNP_A-2255292	T	T	415	1	349	21	21.264	4.00E-06	rs4918713	10	96638821	q23.33
SNP_A-1971493	A	A	409	3	350	26	21.227	4.08E-06	rs10510301	3	5376491	p26.1
SNP_A-2209907	C	C	295	17	296	60	21.208	4.12E-06	rs11969423	6	39291545	p21.2
SNP_A-2219735	A	A	286	22	364	2	21.193	4.15E-06	rs16893114	5	64085652	q12.3
SNP_A-2088055	T	T	295	19	389	1	21.16	4.2245E-06	rs17093053	14	56818040	q22.3
SNP_A-1972386	A	A	418	0	346	18	21.157	4.23E-06	rs2063158	3	36823664	p22.3
SNP_A-2293925	C	C	378	8	313	35	21.157	4.23E-06	rs17030825	1	113226234	p13.2
SNP_A-2068350	T	T	352	22	397	1	21.152	4.24E-06	rs17109786	14	39302872	q21.1
SNP_A-1793151	C	C	322	24	295	67	21.149	4.25E-06	rs17828144	4	61631933	q13.1
SNP_A-2250359	A	A	283	31	369	7	21.101	4.36E-06	rs1442161	4	85630743	q21.23
SNP_A-2210458	G	G	386	0	356	20	21.085	4.39E-06	rs7542047	1	173256751	q25.2
SNP_A-1718735	T	T	269	15	285	59	21.084	4.40E-06	rs10506225	12	41941636	q12
SNP_A-2054920	T	T	306	56	225	97	21.076	4.41E-06	rs7178983	15	86107539	q25.3
SNP_A-1726252	C	C	398	0	349	19	21.072	4.42E-06	rs10484528	6	166795847	q27
SNP_A-2097827	T	T	348	4	320	30	21.05	4.47E-06	rs16898039	4	18733678	p15.31
SNP_A-2078025	G	G	246	32	368	10	21.009	4.57E-06	rs9661109	1	14508874	p36.21
SNP_A-2154449	T	T	322	20	399	1	21.008	4.57E-06	rs12345627	9	102089086	q31.1
SNP_A-2310623	A	A	412	0	363	19	20.995	4.61E-06	rs16898828	8	101945422	q22.3
SNP_A-1988496	T	T	342	30	370	4	20.978	4.6452E-06	rs3799647	6	166917094	q27
SNP_A-2291301	C	C	396	2	331	23	20.949	4.72E-06	rs16835244	1	33231509	p35.1
SNP_A-2163341	T	T	297	21	392	2	20.92	4.79E-06	---	1	50861684	p32.3
SNP_A-2165147	T	T	297	21	392	2	20.92	4.79E-06	rs1160432	4	179289198	q34.3
SNP_A-2166870	A	A	301	21	396	2	20.854	4.96E-06	rs5994039	22	15712688	q11.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1976364	A	A	421	1	361	21	20.847	4.97E-06	rs16861391	1	18075475	p36.13
SNP_A-2114490	C	C	396	2	350	24	20.726	5.30E-06	rs10045301	5	31511665	p13.3
SNP_A-2076919	A	A	319	43	370	12	20.725	5.30E-06	rs17093052	14	95163919	q32.13
SNP_A-1833986	C	C	379	7	306	32	20.714	5.33E-06	rs7575609	2	229256846	q36.3
SNP_A-2250546	T	T	248	46	353	19	20.709	5.35E-06	rs16943665	12	112976534	q24.21
SNP_A-2215576	T	T	418	0	354	18	20.697	5.38E-06	rs17122365	14	49843177	q21.3
SNP_A-2261033	T	T	413	5	358	30	20.693	5.39E-06	rs9885044	5	149231778	q32
SNP_A-2141989	T	T	386	18	312	50	20.663	5.48E-06	rs2500530	6	149361976	q25.1
SNP_A-2032582	A	A	391	3	342	26	20.654	5.50E-06	rs4943021	13	32412547	q13.1
SNP_A-2079775	C	C	349	1	361	25	20.645	5.53E-06	rs8063738	16	62112928	q21
SNP_A-1905899	A	A	328	8	311	39	20.622	5.5951E-06	rs6594302	5	107747061	q21.3
SNP_A-2185089	A	A	397	7	311	31	20.594	5.68E-06	rs6119314	20	31020744	q11.21
SNP_A-1677230	C	C	251	89	196	146	20.587	5.70E-06	rs4130554	2	242202382	q37.3
SNP_A-1789333	T	T	305	59	356	22	20.579	5.72E-06	rs6503019	17	7259283	p13.1
SNP_A-2243989	A	A	310	16	410	0	20.57	5.75E-06	rs17037654	2	88555986	p11.2
SNP_A-1900488	A	A	346	18	406	0	20.557	5.7867E-06	rs6534256	4	122487146	q27
SNP_A-1751983	T	T	402	0	285	15	20.539	5.84E-06	rs10483870	14	74061271	q24.3
SNP_A-1981973	G	G	319	33	379	7	20.535	5.86E-06	rs16896377	5	66513608	q12.3
SNP_A-2314509	T	T	408	2	364	24	20.532	5.86E-06	rs17016143	2	119942779	q14.2
SNP_A-1981428	C	C	290	18	393	1	20.516	5.91E-06	rs12074261	1	203483443	q32.1
SNP_A-2170354	A	A	402	0	363	19	20.491	5.99E-06	rs9842624	3	118582861	q13.31
SNP_A-2028987	A	A	421	1	367	21	20.491	5.99E-06	rs498871	11	105225667	q22.3
SNP_A-2222754	C	C	333	9	335	43	20.488	6.0007E-06	rs6416996	18	13516157	p11.21
SNP_A-1973833	G	G	422	0	362	18	20.448	6.13E-06	rs6782453	3	109203675	q13.12
SNP_A-1792130	A	A	327	25	387	3	20.435	6.17E-06	rs8073504	17	41625070	q21.31
SNP_A-2206533	T	T	347	7	353	39	20.43	6.19E-06	rs7955074	12	26176273	p12.1
SNP_A-2228009	G	G	266	32	369	9	20.428	6.19E-06	rs16940113	16	84537948	q24.1
SNP_A-2089529	A	A	300	52	249	101	20.425	6.20E-06	rs10952558	7	142816094	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043328	A	A	237	109	329	69	20.408	6.26E-06	rs157495	5	32123010	p13.3
SNP_A-1924848	T	T	394	6	357	33	20.392	6.31E-06	rs2797990	10	95947421	q23.33
SNP_A-2298806	C	C	217	123	249	63	20.387	6.32E-06	rs654499	11	94483155	q21
SNP_A-2282453	T	T	360	0	361	21	20.367	6.39E-06	rs6568927	6	116731095	q22.1
SNP_A-2093606	A	A	316	22	345	1	20.355	6.43E-06	rs4997473	2	236263620	q37.2
SNP_A-2106797	T	T	357	21	407	1	20.339	6.49E-06	rs16859754	1	230306350	q42.2
SNP_A-2042963	G	G	368	0	352	20	20.335	6.50E-06	rs16926898	9	1279180	p24.3
SNP_A-1849658	C	C	304	14	286	50	20.319	6.55E-06	---	11	36105454	p13
SNP_A-1810810	T	T	313	13	280	46	20.294	6.64E-06	rs17023044	4	96393254	q22.3
SNP_A-1902500	G	G	407	3	362	26	20.284	6.68E-06	rs16961582	19	33762729	q12
SNP_A-1985010	A	A	298	26	368	4	20.277	6.70E-06	rs633806	1	215483014	q41
SNP_A-2256706	A	A	420	0	343	17	20.275	6.71E-06	rs1226487	6	47100866	p12.3
SNP_A-1808281	A	A	317	1	305	23	20.248	6.80E-06	---	15	29946541	q13.3
SNP_A-2004453	T	A	178	160	200	108	20.228	6.8749E-06	rs5011255	15	98627999	q26.3
SNP_A-2148391	A	A	364	10	333	41	20.222	6.90E-06	rs10971163	9	32843105	p21.1
SNP_A-1972319	A	A	352	34	374	6	20.221	6.90E-06	rs17031971	3	34603533	p23
SNP_A-1977097	G	G	415	1	348	20	20.211	6.94E-06	rs1878403	1	186567942	q31.1
SNP_A-1897415	A	A	280	20	378	2	20.191	7.0093E-06	rs6120170	20	31268094	q11.21
SNP_A-1934834	A	A	388	4	316	26	20.185	7.03E-06	rs2779762	9	17171275	p22.2
SNP_A-2183487	T	T	398	0	365	19	20.183	7.04E-06	rs904552	11	36026784	p13
SNP_A-1962638	A	A	397	1	351	21	20.156	7.14E-06	rs17014708	2	34236840	p22.3
SNP_A-2130104	C	C	305	27	389	5	20.144	7.18E-06	rs7629057	3	45164457	p21.31
SNP_A-1926738	T	T	274	16	413	1	20.143	7.19E-06	rs2727219	15	98343576	q26.3
SNP_A-2065784	A	A	402	0	350	18	20.134	7.22E-06	rs16897352	8	100502644	q22.2
SNP_A-2166682	G	G	405	1	359	21	20.113	7.30E-06	rs17098497	10	92417973	q23.31
SNP_A-1726330	T	T	391	1	364	22	20.094	7.37E-06	rs10496109	2	64394225	p14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787357	G	G	297	19	373	1	20.087	7.40E-06	rs17036754	2	69676522	p13.3
SNP_A-1706271	A	A	303	33	399	9	20.063	7.49E-06	rs6713334	2	36878977	p22.2
SNP_A-1856341	G	G	312	32	377	7	20.02	7.66E-06	---	4	165273099	q32.3
SNP_A-2227650	T	T	269	35	271	91	19.997	7.7568E-06	rs17126961	8	18543876	p22
SNP_A-2225495	T	T	386	12	323	41	19.989	7.79E-06	rs12410125	1	228905120	q42.2
SNP_A-1871878	G	G	405	1	325	19	19.978	7.8325E-06	rs16977279	17	68044309	q24.3
SNP_A-1788107	A	A	346	2	329	25	19.971	7.86E-06	rs16918596	11	6818988	p15.4
SNP_A-2131246	C	C	294	22	393	3	19.97	7.87E-06	rs2379177	1	106350231	p21.1
SNP_A-2193082	G	G	402	6	345	31	19.968	7.87E-06	rs16955067	16	79927377	q23.2
SNP_A-1826731	C	C	357	23	408	2	19.929	8.04E-06	rs7550619	1	164353558	q24.2
SNP_A-2174822	G	G	408	0	339	17	19.927	8.05E-06	rs2386653	10	5713975	p15.1
SNP_A-1657283	G	G	342	0	351	21	19.891	8.1964E-06	rs921879	4	178129113	q34.2
SNP_A-2206931	A	A	369	15	310	46	19.85	8.38E-06	rs1469111	16	22079163	p12.1
SNP_A-2248083	T	T	369	9	341	39	19.849	8.3803E-06	rs16875964	7	32290244	p14.3
SNP_A-1851615	A	A	324	22	315	65	19.831	8.46E-06	rs3133748	8	96474764	q22.1
SNP_A-1974112	C	C	388	2	341	23	19.797	8.61E-06	rs571525	3	119645556	q13.32
SNP_A-1944787	G	G	297	65	238	114	19.784	8.67E-06	rs7926695	11	131514568	q25
SNP_A-2031717	T	T	371	3	351	27	19.733	8.90E-06	rs16838723	1	154304274	q23.1
SNP_A-2298060	T	T	364	0	341	19	19.729	8.92E-06	rs9353495	6	88509956	q15
SNP_A-1866637	A	A	401	5	347	29	19.718	8.98E-06	rs7833852	8	139361942	q24.23
SNP_A-2258488	G	G	391	9	332	36	19.716	8.99E-06	rs6035927	20	21618219	p11.22
SNP_A-2009614	G	G	321	19	395	1	19.701	9.05E-06	rs7687981	4	16344679	p15.32
SNP_A-2133741	A	A	360	18	404	0	19.691	9.10E-06	rs16959093	16	12268079	p13.13
SNP_A-1890351	C	C	297	47	371	17	19.686	9.12E-06	rs6795416	3	144346422	q23
SNP_A-2136714	A	A	317	11	318	46	19.673	9.19E-06	rs16886617	5	18848231	p14.3
SNP_A-1664730	C	C	390	2	345	23	19.657	9.2672E-06	rs1439735	2	210203125	q34
SNP_A-1947811	G	G	262	32	374	10	19.646	9.32E-06	rs17032574	2	106247099	q12.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2060032	A	A	335	3	343	29	19.636	9.37E-06	rs17006778	4	84682524	q21.23
SNP_A-2040175	C	C	372	14	312	44	19.6	9.55E-06	rs10917625	1	158361898	q23.3
SNP_A-2209195	T	T	402	0	360	18	19.595	9.57E-06	rs8177232	3	134958485	q22.1
SNP_A-1924821	A	A	352	20	407	1	19.556	9.77E-06	rs11254888	10	7015682	p14
SNP_A-1874957	T	T	374	4	299	25	19.527	9.92E-06	rs6760701	2	27239757	p23.3
SNP_A-1758111	T	T	341	17	402	0	19.526	9.92E-06	rs6880859	5	64074871	q12.3
SNP_A-2214790	A	A	405	3	372	26	19.522	9.95E-06	rs9298802	9	19886420	p22.1
SNP_A-1909450	G	G	332	24	395	3	19.514	9.99E-06	rs12771450	10	63140377	q21.2
SNP_A-2308109	G	G	362	0	343	19	19.512	1.00E-05	---	13	76669525	q22.3
SNP_A-2124961	G	G	338	4	306	28	19.498	0.00001007	rs620905	1	238117998	q43
SNP_A-1879062	T	T	334	24	397	3	19.496	0.000010083	rs9313466	5	168989088	q35.1
SNP_A-2024694	T	T	328	16	410	0	19.483	1.01E-05	rs7014982	8	5589093	p23.2
SNP_A-1857042	G	G	325	21	402	2	19.482	0.000010154	rs16958436	16	67453959	q22.1
SNP_A-2061843	T	T	244	60	217	119	19.477	0.000010182	rs12989324	2	41254388	p22.1
SNP_A-2171318	T	T	412	0	351	17	19.457	0.000010291	rs16961704	16	58750346	q21
SNP_A-2102567	C	C	312	24	371	3	19.452	0.000010317	rs13418573	2	205244019	q33.3
SNP_A-2163649	A	A	322	16	402	0	19.45	1.03E-05	rs4318394	2	112374502	q13
SNP_A-1865843	T	T	282	48	367	19	19.424	0.00001047	rs13136410	4	79417400	q21.21
SNP_A-2034263	A	A	298	24	388	4	19.417	1.05E-05	rs1558766	12	13603964	p13.1
SNP_A-2118173	C	C	353	1	355	23	19.406	0.000010566	rs7025844	9	8204946	p24.1
SNP_A-2250700	A	A	362	0	345	19	19.403	0.000010582	rs2783209	13	99863576	q32.3
SNP_A-1863189	G	G	279	25	377	5	19.355	1.09E-05	rs16956894	17	51650076	q23.2
SNP_A-2043985	T	T	412	0	353	17	19.35	1.09E-05	rs182523	12	27564085	p11.23
SNP_A-2140925	C	C	345	1	332	22	19.335	0.00001097	rs16916049	11	90794964	q14.3
SNP_A-2128586	C	C	353	17	299	49	19.332	0.000010987	rs10812362	9	26181311	p21.2
SNP_A-2304593	G	G	418	0	380	18	19.331	0.000010991	rs16981969	22	15916412	q11.1
SNP_A-2178412	G	G	391	7	321	31	19.291	1.12E-05	rs7751878	6	27095702	p22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1836216	G	G	298	22	387	3	19.29	0.000011232	rs17090670	4	184451069	q35.1
SNP_A-2301066	A	A	303	15	400	0	19.271	0.000011344	rs9349162	6	40725144	p21.1
SNP_A-1787232	G	G	370	8	327	35	19.269	0.000011351	rs812253	14	61097990	q23.1
SNP_A-1973324	G	G	292	18	276	56	19.233	1.16E-05	rs3911116	3	76856987	p12.3
SNP_A-1897960	A	A	188	158	273	117	19.223	1.16E-05	rs13096138	3	59926887	p14.2
SNP_A-2228160	A	A	326	16	402	0	19.22	0.000011646	rs7607536	2	172803264	q31.1
SNP_A-1909120	G	G	363	1	335	21	19.219	1.17E-05	---	2	173188958	q31.1
SNP_A-2070219	G	G	275	49	325	17	19.209	0.000011714	rs1885628	6	154355052	q25.2
SNP_A-2089129	T	T	395	15	297	41	19.197	1.18E-05	rs17103225	1	79650845	p31.1
SNP_A-2052904	T	T	339	9	310	38	19.189	0.000011837	rs7399629	13	21766628	q12.11
SNP_A-2013057	G	G	323	23	397	3	19.182	0.000011884	rs7803774	7	155465044	q36.3
SNP_A-2269550	C	C	366	0	372	20	19.18	0.000011898	rs17078011	8	6578161	p23.1
SNP_A-2235436	A	A	375	13	325	43	19.127	1.22E-05	rs981865	2	108258477	q12.3
SNP_A-2057337	A	A	343	23	261	53	19.11	1.23E-05	rs7728905	5	50870402	q11.2
SNP_A-2006728	T	T	246	60	210	114	19.102	0.000012391	rs6709132	2	136066304	q21.3
SNP_A-2058359	G	G	305	11	296	44	19.082	0.00001252	rs2306989	4	187894020	q35.2
SNP_A-2054104	T	T	357	17	298	48	19.039	0.000012807	rs16830056	2	134692563	q21.2
SNP_A-1876382	A	A	413	1	328	18	19.029	0.000012875	---	8	3807013	p23.2
SNP_A-1941944	A	A	413	1	328	18	19.029	0.000012875	rs7554652	1	12053835	p36.22
SNP_A-1823703	T	T	279	35	352	10	19.022	0.000012923	rs9905936	17	50739027	q22
SNP_A-1813528	C	C	248	44	342	18	18.994	1.31E-05	rs12101403	15	69593038	q23
SNP_A-1705123	T	T	242	48	355	23	18.927	1.36E-05	rs984492	12	19118443	p12.3
SNP_A-2060211	A	A	294	26	373	5	18.894	1.38E-05	rs4421141	5	86192546	q14.3
SNP_A-2003735	C	C	316	28	270	66	18.881	0.000013912	rs4284545	14	49307091	q21.3
SNP_A-1780656	G	G	306	68	310	24	18.87	1.40E-05	rs2840757	1	28653539	p35.3
SNP_A-2305066	G	G	381	11	318	38	18.867	0.000014018	rs3093559	6	31655771	p21.33
SNP_A-1843149	T	T	343	7	327	35	18.852	0.000014127	rs10993420	9	94812020	q22.32
SNP_A-2087234	G	G	261	105	232	180	18.789	1.46E-05	rs9316891	13	56491946	q21.1
SNP_A-2051385	T	T	352	0	347	19	18.77	0.000014747	rs287850	6	83509679	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2012492	A	A	409	1	349	19	18.737	0.000015007	rs7116350	11	80134162	q14.1
SNP_A-2221072	T	T	351	19	411	1	18.723	0.000015118	---	1	106624974	p21.1
SNP_A-2171641	A	A	391	9	322	34	18.715	0.00001518	rs11831926	12	17823911	p12.3
SNP_A-1796587	A	A	386	0	343	17	18.653	1.57E-05	rs7577659	2	169038126	q24.3
SNP_A-2193137	G	G	338	48	369	15	18.64	1.58E-05	rs2593091	8	38592505	p11.23
SNP_A-1818407	C	C	326	26	281	63	18.629	1.59E-05	rs7160410	14	98375794	q32.2
SNP_A-2151062	A	A	327	7	304	34	18.596	1.62E-05	---	9	103954612	q31.1
SNP_A-2066976	G	G	371	5	322	28	18.588	1.62E-05	---	14	70764530	q24.2
SNP_A-1922871	T	T	235	47	340	22	18.581	0.000016286	rs17082794	5	92338801	q15
SNP_A-2146094	G	G	362	0	342	18	18.563	1.64E-05	rs17096806	1	75572158	p31.1
SNP_A-1859995	T	T	291	21	274	60	18.562	0.00001645	rs6505342	17	28817841	q12
SNP_A-1808198	C	C	326	18	401	1	18.551	0.000016546	rs2545607	5	88598204	q14.3
SNP_A-2003896	G	G	387	5	351	29	18.515	0.000016855	rs7342489	14	83996307	q31.3
SNP_A-2073903	A	A	332	28	381	5	18.514	1.69E-05	rs744730	4	17168182	p15.32
SNP_A-2114233	C	C	298	54	331	19	18.507	0.000016932	rs7122583	11	106632506	q22.3
SNP_A-2241895	G	G	323	15	408	0	18.478	0.000017187	rs7651255	3	65108384	p14.1
SNP_A-2040710	G	G	293	41	276	92	18.461	0.000017343	rs17798885	18	20882881	q11.2
SNP_A-2062769	A	A	388	2	346	22	18.447	0.00001747	rs10919385	1	167096986	q24.2
SNP_A-2105405	T	T	313	25	374	4	18.446	1.75E-05	rs17118459	1	98637576	p21.3
SNP_A-1757337	G	G	348	0	368	20	18.439	0.000017541	rs948829	18	55534926	q21.32
SNP_A-2201054	G	G	267	19	393	3	18.428	1.76E-05	rs5749225	22	29899900	q12.2
SNP_A-1885771	G	G	324	22	293	59	18.409	1.78E-05	rs11217475	11	98279049	q22.1
SNP_A-2284508	G	G	413	1	359	19	18.379	1.81E-05	rs2203472	4	12722542	p15.33
SNP_A-2006971	T	T	354	16	416	0	18.363	1.83E-05	rs6435462	2	209072488	q34
SNP_A-1935066	A	A	396	2	356	22	18.291	1.90E-05	rs8067487	17	14978838	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2202742	G	G	306	20	378	2	18.283	1.90E-05	rs7357203	7	155748035	q36.3
SNP_A-2290218	C	C	410	2	351	21	18.277	0.000019103	rs10182182	2	7374086	p25.1
SNP_A-2228775	T	T	335	5	329	31	18.275	1.91E-05	rs17048675	4	137720357	q28.3
SNP_A-1850625	T	T	362	16	322	48	18.256	1.93E-05	rs4243121	16	75063352	q23.1
SNP_A-2231402	G	G	366	0	352	18	18.252	1.94E-05	rs6720890	2	176022193	q31.1
SNP_A-1832363	A	A	336	28	381	5	18.225	1.96E-05	rs4878159	9	28085988	p21.2
SNP_A-1952532	C	C	320	16	374	0	18.22	1.97E-05	---	9	78173291	q21.2
SNP_A-2237437	T	T	358	0	365	19	18.179	2.01E-05	rs2124145	4	79532467	q21.21
SNP_A-2074784	T	T	356	16	414	0	18.176	2.01E-05	rs2644142	1	224027820	q42.13
SNP_A-2007530	G	G	411	1	361	19	18.175	2.01E-05	rs6048532	20	23003327	p11.21
SNP_A-2122302	A	A	233	71	305	37	18.167	2.02E-05	rs10185592	2	206519687	q33.3
SNP_A-2012083	A	A	280	56	346	24	18.163	0.000020276	---	11	74600621	q13.4
SNP_A-2212452	T	T	402	2	364	22	18.151	2.04E-05	rs7299734	12	128320968	q24.33
SNP_A-1857799	A	A	370	0	358	18	18.151	2.04E-05	rs17080163	18	64868698	q22.1
SNP_A-1791369	T	T	320	26	274	62	18.147	2.05E-05	rs10916430	1	225586458	q42.13
SNP_A-1870967	G	G	343	37	371	9	18.142	2.05E-05	rs17549947	17	30841801	q12
SNP_A-2061556	A	A	390	4	361	27	18.139	0.000020531	rs10982271	9	114360572	q32
SNP_A-1994499	C	C	298	86	311	37	18.071	2.13E-05	rs2044534	8	105243079	q22.3
SNP_A-1939699	A	A	340	26	382	4	18.057	2.14E-05	rs17068955	5	167032842	q34
SNP_A-2304161	C	C	418	0	362	16	18.056	0.00002145	rs12287079	11	127879269	q24.3
SNP_A-2123980	G	G	290	14	384	0	18.052	2.15E-05	rs7518829	1	146900641	q21.2
SNP_A-2301741	C	C	357	19	403	1	18.002	2.21E-05	rs6093099	20	36943371	q11.23
SNP_A-2085990	C	C	337	15	414	0	17.994	0.000022155	rs6761059	2	127388373	q14.3
SNP_A-2139632	C	C	330	4	344	30	17.971	2.24E-05	rs11128122	3	69442979	p14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1992847	G	G	411	1	365	19	17.964	2.25E-05	rs17059209	8	28495861	p21.1
SNP_A-1987201	G	G	299	25	381	5	17.944	2.27E-05	---	6	109919489	q21
SNP_A-1931767	A	A	324	4	338	30	17.939	2.28E-05	rs16875849	4	10627880	p16.1
SNP_A-1896915	G	G	399	3	360	24	17.934	0.000022864	rs2089744	18	46781415	q21.1
SNP_A-1828548	T	T	394	0	365	17	17.927	2.30E-05	rs16855947	2	169497242	q24.3
SNP_A-1824855	C	C	325	15	398	0	17.923	2.30E-05	rs6876978	5	58114785	q11.2
SNP_A-1945329	C	C	260	104	228	174	17.883	2.35E-05	rs9316890	13	56491802	q21.1
SNP_A-2278247	T	T	371	9	325	35	17.876	2.36E-05	rs2476644	13	30155768	q12.3
SNP_A-2049468	T	T	364	16	416	0	17.875	2.36E-05	rs16858686	1	178936284	q25.3
SNP_A-1722304	G	G	385	1	343	19	17.871	2.36E-05	rs10483254	14	20091567	q11.2
SNP_A-2041632	A	A	269	39	350	14	17.849	0.000023913	rs16937062	8	49505986	q11.21
SNP_A-2005543	C	C	349	1	328	20	17.836	2.41E-05	rs17091043	10	115576927	q25.3
SNP_A-1935944	A	A	359	1	338	20	17.818	2.43E-05	rs1908704	5	18690209	p14.3
SNP_A-1926604	C	C	363	1	342	20	17.811	2.44E-05	rs6728776	2	174758850	q31.1
SNP_A-1963726	G	G	405	3	334	22	17.805	2.45E-05	rs1446328	2	70223844	p13.3
SNP_A-2113379	G	G	317	23	367	3	17.804	2.45E-05	rs6820050	4	6493378	p16.1
SNP_A-1984114	T	T	334	20	402	2	17.789	2.47E-05	rs17116671	5	153495005	q33.2
SNP_A-2268612	A	A	395	5	341	27	17.784	2.47E-05	rs10131532	14	43218705	q21.2
SNP_A-2087716	A	A	337	19	284	50	17.767	0.000024961	rs10973099	9	36826634	p13.2
SNP_A-2101610	A	A	335	15	406	0	17.752	2.52E-05	rs3097721	10	321620	p15.3
SNP_A-2133596	A	A	362	16	410	0	17.714	2.57E-05	rs1823095	2	113790840	q13
SNP_A-1925074	T	T	394	12	326	38	17.704	0.000025809	rs7701324	5	123741643	q23.2
SNP_A-2100082	C	C	358	2	347	23	17.678	2.62E-05	rs706892	6	112145333	q21
SNP_A-1955467	A	A	359	1	359	21	17.654	2.65E-05	rs6935909	6	113195541	q21
SNP_A-1874987	G	G	296	52	357	21	17.653	2.65E-05	rs11744750	5	61177420	q12.1
SNP_A-2291819	C	C	389	1	351	19	17.637	0.00002673	---	5	5345910	p15.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2216284	A	A	339	15	408	0	17.635	0.000026758	rs12042221	1	188455961	q31.2
SNP_A-2186507	T	T	265	51	318	20	17.633	2.68E-05	rs11033117	11	35396564	p13
SNP_A-1901119	C	T	201	127	198	164	17.629	2.68E-05	rs1021152	15	93694169	q26.2
SNP_A-2245893	T	T	356	16	315	47	17.626	0.000026886	rs4866298	5	17663889	p15.1
SNP_A-1946486	G	G	419	1	358	18	17.621	2.70E-05	rs2433015	11	54926976	q11
SNP_A-2202130	T	T	412	0	366	16	17.611	2.71E-05	rs7613694	3	118803258	q13.31
SNP_A-1814471	T	T	265	51	369	25	17.598	2.73E-05	rs4985684	17	5541638	p13.2
SNP_A-1979538	G	G	366	0	366	18	17.578	2.76E-05	rs10471079	4	158066769	q32.1
SNP_A-1899751	A	A	322	18	377	1	17.576	2.76E-05	rs2049101	3	123521083	q21.1
SNP_A-1841410	A	A	316	24	380	4	17.562	2.78E-05	rs1566407	12	24916198	p12.1
SNP_A-2235402	T	T	387	5	309	25	17.553	2.79E-05	rs16868375	5	39265072	p13.1
SNP_A-1783860	C	C	330	26	395	5	17.552	2.80E-05	rs1420086	16	8656045	p13.2
SNP_A-2142251	T	T	365	3	319	23	17.55	0.000027991	rs7929397	11	4094959	p15.4
SNP_A-2303961	A	A	340	16	382	0	17.549	0.000028	rs16922151	8	58499979	q12.1
SNP_A-1800769	G	A	192	162	244	156	17.545	2.81E-05	rs475639	11	85367433	q14.2
SNP_A-2233448	G	G	241	59	220	116	17.541	2.81E-05	rs1288671	1	88453937	p22.2
SNP_A-2031166	G	G	408	0	364	16	17.535	2.82E-05	rs814578	5	10620511	p15.2
SNP_A-2298505	G	G	370	0	372	18	17.491	0.000028864	rs7684885	4	144998733	q31.21
SNP_A-2015654	T	T	303	19	380	2	17.456	2.94E-05	rs2824371	21	17868598	q21.1
SNP_A-2184340	A	A	309	47	361	17	17.455	0.000029425	rs7094471	10	98725762	q24.1
SNP_A-2009782	G	G	267	97	291	47	17.454	2.94E-05	rs1961974	4	48020323	p12
SNP_A-1691746	C	C	346	20	298	52	17.451	2.95E-05	rs2041529	7	117340940	q31.31
SNP_A-2005245	T	T	370	10	311	35	17.446	2.96E-05	rs1396959	17	58356116	q23.3
SNP_A-1886729	G	G	357	1	361	21	17.444	2.96E-05	rs17084039	13	25875677	q12.13
SNP_A-1970654	A	A	376	26	313	59	17.436	2.97E-05	rs4339837	1	162255105	q23.3
SNP_A-1937877	T	T	331	15	394	0	17.434	2.97E-05	rs17776270	5	147661431	q32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2199901	T	C	182	166	210	120	17.412	3.01E-05	rs12879562	14	28090531	q12
SNP_A-1953095	A	A	364	0	347	17	17.406	3.02E-05	rs16893809	6	40683760	p21.1
SNP_A-1907225	C	C	364	0	347	17	17.406	3.02E-05	rs2853126	11	111669027	q23.1
SNP_A-2275090	C	C	335	15	398	0	17.406	3.02E-05	rs1025194	7	135385475	q33
SNP_A-2209655	A	A	420	0	378	16	17.398	0.000030318	rs16970461	17	30276183	q12
SNP_A-2149909	T	T	327	29	264	62	17.397	3.03E-05	rs17038354	2	49285804	p16.3
SNP_A-1803822	C	C	337	41	370	12	17.388	0.00003048	rs17600471	7	125521742	q31.33
SNP_A-1899400	T	T	328	28	388	6	17.383	3.06E-05	rs3816847	8	59678664	q12.1
SNP_A-1909707	T	T	350	0	354	18	17.368	3.08E-05	rs17002887	4	79319187	q21.21
SNP_A-2110088	C	C	353	5	348	30	17.362	3.09E-05	rs17137930	5	100992589	q21.1
SNP_A-2054314	A	A	420	0	355	15	17.357	3.10E-05	rs6089885	20	61428260	q13.33
SNP_A-1788977	A	A	336	4	347	29	17.35	3.11E-05	rs16948687	15	92401375	q26.2
SNP_A-2191425	G	G	290	26	257	63	17.348	3.11E-05	rs16857815	1	229094688	q42.2
SNP_A-1930058	T	T	323	17	310	52	17.348	0.00003112	rs17068038	13	45814328	q14.13
SNP_A-1798241	A	A	294	22	386	4	17.343	3.12E-05	rs11954795	5	127614708	q23.2
SNP_A-1828598	A	A	318	8	310	36	17.34	3.13E-05	rs2658072	5	10073372	p15.2
SNP_A-1962686	A	A	336	28	290	64	17.331	0.000031398	rs1439710	2	35712296	p22.3
SNP_A-2042034	A	A	322	14	408	0	17.326	3.15E-05	rs7033248	9	3105965	p24.2
SNP_A-2298127	G	G	300	18	396	2	17.319	3.16E-05	rs7513476	1	112785827	p13.2
SNP_A-2125370	T	T	303	23	378	4	17.309	3.18E-05	rs9864294	3	34382032	p23
SNP_A-2139610	G	G	304	48	371	19	17.302	3.19E-05	rs1631482	11	114092755	q23.2
SNP_A-2178613	C	C	378	12	336	40	17.297	3.20E-05	rs676069	1	33291170	p35.1
SNP_A-2303448	T	T	407	1	333	17	17.285	3.22E-05	rs1356535	3	117798780	q13.31
SNP_A-1934840	G	G	389	3	345	23	17.282	3.22E-05	rs6415692	8	39417993	p11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2037503	C	C	341	15	402	0	17.28	0.000032254	rs6052768	20	4618664	p13
SNP_A-1810688	C	C	347	1	336	20	17.279	3.23E-05	rs16917452	9	31836527	p21.1
SNP_A-2129253	G	G	305	39	354	12	17.272	3.24E-05	rs4442167	8	4230735	p23.2
SNP_A-1892154	G	G	382	8	341	33	17.241	3.29E-05	rs16908359	9	24413220	p21.3
SNP_A-1928765	G	G	420	0	382	16	17.221	3.33E-05	rs10996034	10	66208275	q21.3
SNP_A-1982107	T	T	391	1	361	19	17.214	3.34E-05	---	5	73438469	q13.3
SNP_A-2269127	A	A	324	40	364	12	17.212	3.34E-05	rs16927460	8	62603578	q12.3
SNP_A-1938869	A	A	400	0	364	16	17.195	3.37E-05	rs9925894	16	6586541	p13.2
SNP_A-2250392	G	G	270	74	206	116	17.181	3.40E-05	rs2269425	6	32231617	p21.32
SNP_A-2024065	A	A	318	48	346	16	17.159	3.44E-05	rs843943	3	124916556	q21.1
SNP_A-1730533	G	G	337	17	409	1	17.159	3.44E-05	rs2072642	6	167098357	q27
SNP_A-1964642	A	A	315	37	367	11	17.144	3.47E-05	rs17050308	2	118982047	q14.2
SNP_A-2044003	C	C	374	26	320	60	17.142	0.000034686	rs3815483	7	36234580	p14.2
SNP_A-1962985	G	G	420	0	384	16	17.134	3.48E-05	rs17032534	2	44849969	p21
SNP_A-2239525	G	G	329	17	399	1	17.134	3.48E-05	rs1947681	18	63729730	q22.1
SNP_A-1991405	C	C	318	14	398	0	17.111	3.53E-05	rs727186	7	135394404	q33
SNP_A-1802247	A	A	305	25	375	5	17.103	3.54E-05	rs6446934	4	74694639	q13.3
SNP_A-1869289	C	C	306	28	269	65	17.101	3.54E-05	rs12132296	1	6901825	p36.31
SNP_A-1983568	T	T	385	9	325	33	17.1	3.55E-05	rs17167924	5	134532200	q31.1
SNP_A-2095139	T	T	301	11	321	45	17.093	3.56E-05	rs16955027	16	79916804	q23.2
SNP_A-2313898	G	G	363	1	318	18	17.091	3.56E-05	---	4	85139685	q21.23
SNP_A-1940731	A	A	342	2	341	23	17.09	3.56E-05	rs17047918	3	799148	p26.3
SNP_A-2291121	G	G	287	89	219	133	17.086	3.57E-05	rs1109364	22	31181148	q12.3
SNP_A-1923419	T	T	346	8	342	36	17.073	3.60E-05	rs17069173	6	108444960	q21
SNP_A-2278438	A	A	404	2	367	21	17.072	3.60E-05	rs16898608	8	101671411	q22.3
SNP_A-1912408	T	T	346	2	362	24	17.055	3.63E-05	rs2897661	4	152402153	q31.3
SNP_A-1905996	C	C	350	18	397	1	17.019	0.00003701	rs2298296	1	20709548	p36.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1892247	C	C	368	10	304	34	17.005	3.73E-05	rs7874361	9	37894788	p13.2
SNP_A-2255601	C	C	398	2	344	20	16.999	3.74E-05	rs17288810	3	56557629	p14.3
SNP_A-2175920	T	T	380	16	412	0	16.983	0.000037721	rs17128857	11	123713645	q24.1
SNP_A-1921290	A	A	400	2	365	21	16.979	3.78E-05	rs1884596	20	21852139	p11.22
SNP_A-2073048	G	G	305	25	373	5	16.977	0.000037832	rs2336559	3	52861315	p21.1
SNP_A-1788523	G	G	285	51	345	21	16.963	3.81E-05	rs12425639	12	100982890	q23.2
SNP_A-1923695	C	C	311	19	380	2	16.945	3.85E-05	rs7524793	1	242962583	q44
SNP_A-1992446	A	A	364	16	394	0	16.94	3.86E-05	rs17141424	8	16330262	p22
SNP_A-1794042	A	A	246	44	342	20	16.929	3.88E-05	rs16934648	9	37938057	p13.2
SNP_A-1825603	A	A	323	29	269	63	16.921	3.90E-05	rs8055999	16	46488180	q12.1
SNP_A-1890986	C	C	319	9	307	37	16.902	3.94E-05	rs7613800	3	189286468	q27.3
SNP_A-2289842	A	A	392	2	359	21	16.898	3.94E-05	rs7959056	12	99374935	q23.1
SNP_A-1943818	C	C	322	30	276	66	16.898	3.94E-05	rs11175103	12	38762294	q12
SNP_A-2029658	G	G	416	2	362	20	16.89	3.96E-05	rs7834497	8	9261549	p23.1
SNP_A-1970985	A	A	362	18	407	1	16.87	4.00E-05	rs16992327	22	32150073	q12.3
SNP_A-2222400	C	C	329	23	296	58	16.86	4.02E-05	rs17008584	2	73144464	p13.2
SNP_A-2081291	G	G	391	11	319	35	16.843	4.06E-05	rs6787140	3	40631095	p22.1
SNP_A-1879506	A	A	371	29	381	5	16.83	4.09E-05	rs10850876	12	116543533	q24.22
SNP_A-1780283	T	T	341	7	307	31	16.8	4.15E-05	rs17011450	4	127987881	q28.1
SNP_A-2313748	G	G	285	37	346	12	16.793	4.17E-05	rs17015153	4	90473874	q22.1
SNP_A-2067874	G	G	286	34	363	11	16.791	0.000041729	---	1	162418008	q24.1
SNP_A-2116305	A	A	345	27	383	5	16.779	4.20E-05	rs1378337	4	14848424	p15.33
SNP_A-2197234	T	T	365	21	396	2	16.779	4.20E-05	rs10918914	1	165220834	q24.2
SNP_A-1890202	T	T	354	6	306	28	16.776	0.000042069	rs4856795	3	67834212	p14.1
SNP_A-2255457	C	C	303	15	411	1	16.76	4.24E-05	rs10732417	10	71805973	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2030573	G	G	287	27	371	7	16.712	4.35E-05	rs11229795	11	58610745	q12.1
SNP_A-2130958	A	A	302	30	370	8	16.708	0.000043605	rs1586825	14	46332937	q21.3
SNP_A-2010764	T	C	199	151	216	154	16.706	4.36E-05	rs2446699	5	27420404	p14.1
SNP_A-2085693	A	A	327	19	291	51	16.703	0.000043713	rs7603014	2	201945324	q33.1
SNP_A-1972557	T	T	383	3	366	24	16.699	4.38E-05	rs17077148	3	45058812	p21.31
SNP_A-1855637	T	T	404	0	332	14	16.658	0.000044767	rs2871015	22	17520729	q11.21
SNP_A-1909688	T	T	333	23	365	3	16.657	4.48E-05	rs7207176	17	63285488	q24.2
SNP_A-2171352	G	G	369	15	418	0	16.639	4.52E-05	rs6499748	16	53696935	q12.2
SNP_A-2082493	T	T	302	28	373	7	16.629	4.54E-05	rs11569334	20	44189670	q13.12
SNP_A-2097269	C	C	172	164	234	118	16.608	4.59E-05	rs6444074	3	186705895	q27.2
SNP_A-2252290	C	C	318	14	386	0	16.601	4.61E-05	rs9808207	2	30970935	p23.1
SNP_A-2257146	T	T	296	58	336	24	16.58	4.66E-05	rs8074779	17	75636789	q25.3
SNP_A-2239188	A	A	365	15	412	0	16.577	4.67E-05	rs16968440	17	71547286	q25.1
SNP_A-2084737	T	T	356	0	357	17	16.568	4.69E-05	rs9831890	3	98667087	q11.2
SNP_A-2087146	G	G	303	21	404	4	16.567	4.70E-05	rs11027591	11	23857193	p14.3
SNP_A-1970843	C	C	413	1	374	18	16.555	4.73E-05	rs12165367	22	25607484	q12.1
SNP_A-2048650	A	A	329	75	236	108	16.552	4.73E-05	rs7395908	11	5368320	p15.4
SNP_A-2201077	G	G	420	0	373	15	16.544	4.75E-05	rs10423953	19	16353438	p13.11
SNP_A-1838462	C	C	261	23	374	6	16.54	4.76E-05	rs17119515	14	47518079	q21.3
SNP_A-1867875	T	T	324	16	405	1	16.526	4.80E-05	rs2629445	12	54976115	q13.3
SNP_A-1858587	T	T	287	5	270	28	16.49	0.000048911	rs7680002	4	154082605	q31.3
SNP_A-2121767	T	T	405	1	368	18	16.487	4.90E-05	rs6597850	10	126388168	q26.13
SNP_A-2139534	G	G	392	2	367	21	16.474	4.93E-05	rs7895802	10	105853407	q25.1
SNP_A-2245265	C	C	418	0	373	15	16.466	4.95E-05	rs292552	7	134327702	q33
SNP_A-2129314	T	T	346	2	340	22	16.449	5.00E-05	rs17001395	4	77382752	q21.1
SNP_A-2055315	A	A	350	24	298	56	16.436	5.03E-05	rs2798658	1	115067596	p13.1
SNP_A-1911263	T	T	365	15	408	0	16.418	5.08E-05	rs10094485	8	30389166	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2270962	C	C	242	122	327	85	16.405	5.12E-05	rs6605333	3	42245192	p22.1
SNP_A-1973485	A	A	351	5	334	28	16.403	5.12E-05	rs17023747	3	86133575	p12.1
SNP_A-1975738	A	A	381	7	312	28	16.376	5.19E-05	rs1507056	1	181671422	q25.3
SNP_A-1992922	T	T	277	23	363	5	16.375	5.20E-05	---	8	31882962	p12
SNP_A-2296841	A	A	367	21	390	2	16.374	0.000051983	rs2839750	2	53040741	p16.2
SNP_A-1898369	C	C	352	6	360	32	16.372	0.000052057	rs890195	4	185740689	q35.1
SNP_A-2260850	C	C	321	9	306	36	16.35	5.27E-05	rs6790939	3	176784871	q26.31
SNP_A-2048011	A	A	248	40	260	96	16.344	5.28E-05	rs9378419	6	513603	p25.3
SNP_A-2292826	G	G	364	4	365	27	16.324	5.34E-05	rs2927510	10	127864810	q26.2
SNP_A-2017989	G	G	241	67	314	36	16.318	5.36E-05	rs2300359	21	31670702	q22.11
SNP_A-2077835	A	A	304	46	338	16	16.295	5.42E-05	rs10130168	14	70185320	q24.2
SNP_A-2086618	G	G	288	50	338	20	16.289	5.44E-05	rs11904054	2	2705099	p25.3
SNP_A-2120613	A	A	369	9	321	33	16.284	5.45E-05	rs17074749	13	30037657	q12.3
SNP_A-2236009	T	T	351	21	283	49	16.273	5.48E-05	rs5761235	22	24529417	q12.1
SNP_A-2002502	G	G	415	3	351	21	16.224	5.63E-05	rs16929205	10	73109589	q22.1
SNP_A-1828809	A	A	316	18	394	2	16.22	5.64E-05	rs7936052	11	74947412	q13.5
SNP_A-1803639	A	A	362	20	402	2	16.218	5.64E-05	rs11030143	11	27778508	p14.1
SNP_A-2151391	G	G	350	2	314	20	16.218	5.65E-05	rs17796180	6	136879460	q23.3
SNP_A-2118007	G	G	241	179	297	123	16.213	5.66E-05	rs4868294	5	172936597	q35.2
SNP_A-2022429	A	A	310	20	387	3	16.184	5.75E-05	rs2377974	10	50162941	q11.23
SNP_A-2083732	T	T	368	0	356	16	16.178	5.77E-05	rs15281115	12	87563305	q21.33
SNP_A-2012698	T	T	303	23	288	60	16.174	5.78E-05	rs6966352	7	83435413	q21.11
SNP_A-2249493	C	C	190	180	265	139	16.17	0.000057907	rs2706583	18	61842473	q22.1
SNP_A-2107224	C	C	189	177	270	140	16.17	5.79E-05	rs8094001	18	61847141	q22.1
SNP_A-2067731	G	G	393	11	318	34	16.167	5.80E-05	rs2306430	3	51369299	p21.31
SNP_A-1897588	C	C	402	2	383	21	16.156	5.83E-05	rs271520	18	28911107	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1971094	G	G	286	26	377	7	16.154	5.84E-05	rs17001378	22	38330610	q13.1
SNP_A-1650156	C	C	325	23	384	4	16.154	5.84E-05	rs10484890	6	11014032	p24.2
SNP_A-1924077	C	C	379	3	355	23	16.149	5.86E-05	rs1377061	15	71899161	q24.1
SNP_A-1819081	G	G	416	0	379	15	16.136	5.89E-05	rs17130360	1	88456772	p22.2
SNP_A-2193043	G	G	303	15	397	1	16.136	0.000058961	rs7975720	12	22399790	p12.1
SNP_A-2247784	A	A	362	28	375	5	16.132	0.000059063	rs8102530	19	19671078	p13.11
SNP_A-1833244	G	G	189	179	270	142	16.128	0.000059196	rs2541747	18	61838734	q22.1
SNP_A-1900734	G	G	189	179	270	142	16.128	0.000059196	rs9945830	18	61845429	q22.1
SNP_A-2286879	G	G	344	22	385	3	16.118	5.95E-05	rs11066175	12	111026714	q24.13
SNP_A-1980952	A	A	294	12	404	0	16.116	5.96E-05	rs6666244	1	201725888	q32.1
SNP_A-1810500	A	A	319	13	404	0	16.104	6.00E-05	rs11199741	10	85399060	q23.1
SNP_A-1753107	C	C	362	12	345	41	16.091	6.04E-05	rs1961544	21	19839174	q21.1
SNP_A-2167724	G	G	392	4	333	23	16.09	6.04E-05	rs9853116	3	15631636	p25.1
SNP_A-1872588	T	T	375	7	349	31	16.086	6.05E-05	rs10130378	14	70155455	q24.2
SNP_A-1977692	G	G	344	4	334	26	16.082	6.07E-05	rs17002462	4	78514706	q21.1
SNP_A-2169493	G	G	286	34	372	12	16.077	6.08E-05	rs678591	5	175045644	q35.2
SNP_A-1957811	G	G	300	28	276	66	16.076	6.08E-05	rs10840965	12	18197364	p12.3
SNP_A-2054148	G	G	272	32	323	9	16.072	6.10E-05	rs11191995	10	106055022	q25.1
SNP_A-1917575	C	C	326	16	397	1	16.062	6.13E-05	rs10954430	7	132873755	q33
SNP_A-1856230	G	G	350	4	355	27	16.058	6.14E-05	rs7569878	2	36470790	p22.3
SNP_A-2080939	G	G	340	4	345	27	16.031	6.23E-05	rs16946262	15	90363397	q26.1
SNP_A-2247969	G	G	281	45	331	17	16.029	0.000062376	rs3904679	1	75457218	p31.1
SNP_A-1934028	T	T	271	41	314	14	16.025	6.25E-05	rs297792	1	34345112	p34.3
SNP_A-2279475	A	A	334	4	311	25	16.021	6.26E-05	rs9860183	3	174443837	q26.31
SNP_A-1977047	T	T	389	11	338	36	16.02	6.27E-05	rs16860382	4	47411537	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1866361	G	G	248	50	339	25	16.02	6.27E-05	rs1833794	5	103166130	q21.2
SNP_A-2012450	C	C	402	2	366	20	16.013	6.29E-05	rs2240004	7	24515142	p15.3
SNP_A-2209112	G	G	239	43	332	20	16.01	6.30E-05	rs8066848	17	78337662	q25.3
SNP_A-2052864	T	T	347	17	395	1	16.008	6.31E-05	rs12077409	1	40254651	p34.2
SNP_A-2312251	T	T	322	16	391	1	16.006	6.32E-05	rs2420902	10	122800399	q26.12
SNP_A-1850491	T	T	412	0	354	14	15.96	6.47E-05	rs1719140	17	31454526	q12
SNP_A-1975941	C	C	268	34	331	11	15.959	6.47E-05	rs16893786	4	9804187	p16.1
SNP_A-1799216	T	T	261	41	354	18	15.931	6.57E-05	rs10930628	2	174697802	q31.1
SNP_A-2107389	T	T	381	7	331	29	15.93	6.57E-05	rs1385465	3	4062787	p26.1
SNP_A-1861721	A	A	371	9	316	32	15.93	6.57E-05	rs4702271	5	5544290	p15.32
SNP_A-2072414	T	T	406	0	375	15	15.915	6.62E-05	rs12066454	1	107137958	p13.3
SNP_A-2032729	A	A	337	27	390	6	15.908	6.65E-05	rs3889658	11	85908052	q14.2
SNP_A-1992970	A	A	361	17	325	47	15.905	6.66E-05	rs2976530	8	32632241	p12
SNP_A-1933040	G	G	336	8	315	33	15.899	6.68E-05	rs8021772	14	97309633	q32.2
SNP_A-2307913	T	T	333	3	330	24	15.888	6.72E-05	rs16975002	15	93625747	q26.2
SNP_A-1906208	T	T	414	0	358	14	15.863	6.81E-05	rs11064293	12	6606597	p13.31
SNP_A-1879866	A	A	418	0	362	14	15.843	6.88E-05	rs13361957	5	155086582	q33.2
SNP_A-2072468	G	G	298	12	402	0	15.828	0.000069366	rs748471	15	70053228	q23
SNP_A-2192102	C	C	373	5	336	26	15.818	0.000069731	rs6969085	7	103862916	q22.2
SNP_A-2059073	G	G	319	41	364	14	15.79	7.08E-05	rs17132684	11	73480663	q13.4
SNP_A-1794222	C	C	328	26	394	6	15.786	7.09E-05	rs4964398	12	104555814	q23.3
SNP_A-2244081	G	G	311	53	369	23	15.774	7.14E-05	rs11074535	16	22934703	p12.1
SNP_A-2243833	G	G	408	0	381	15	15.748	7.24E-05	rs16956487	18	43437894	q21.1
SNP_A-2146014	T	T	362	0	360	16	15.746	7.25E-05	rs11020497	11	87949324	q14.3
SNP_A-2113604	T	T	295	17	382	2	15.743	7.26E-05	rs4444195	13	97490651	q32.2
SNP_A-1937502	C	C	329	11	324	40	15.729	7.31E-05	---	5	167233933	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2001756	G	G	401	1	336	16	15.721	7.34E-05	rs7072455	10	63199029	q21.2
SNP_A-1927273	G	G	339	43	381	15	15.72	7.34E-05	---	1	171208371	q25.1
SNP_A-1916801	C	C	390	0	365	15	15.701	7.42E-05	---	8	87124770	q21.3
SNP_A-1920123	T	T	284	120	225	171	15.699	7.43E-05	rs7727405	5	171671315	q35.1
SNP_A-2127216	G	G	367	15	392	0	15.697	7.43E-05	rs2307444	15	87671627	q26.1
SNP_A-2211076	G	G	295	21	378	4	15.696	0.000074385	rs17127328	14	90917638	q32.12
SNP_A-1703013	T	T	394	0	369	15	15.693	7.45E-05	rs828256	2	26948819	p23.3
SNP_A-1933670	G	G	401	1	359	17	15.692	7.45E-05	rs17042317	2	113214568	q13
SNP_A-2130366	A	A	187	171	268	136	15.69	7.46E-05	rs2706584	18	61842312	q22.1
SNP_A-2274915	G	G	356	2	347	21	15.676	7.52E-05	---	9	14250138	p22.3
SNP_A-2068230	G	G	346	2	337	21	15.676	7.52E-05	rs7207631	17	49227078	q22
SNP_A-2105633	G	G	347	23	400	4	15.667	7.55E-05	rs2847698	11	65520706	q13.1
SNP_A-2062371	G	G	273	37	350	14	15.664	7.57E-05	rs8138745	22	24812585	q12.1
SNP_A-2267589	C	C	364	0	364	16	15.663	7.57E-05	rs1019331	12	22278064	p12.1
SNP_A-1869213	A	A	330	10	315	37	15.656	7.60E-05	rs10033193	4	148975025	q31.23
SNP_A-1914319	C	C	411	1	369	17	15.653	7.61E-05	rs9966157	18	7117725	p11.31
SNP_A-2177093	G	G	294	22	391	5	15.648	7.63E-05	rs9293317	5	82192914	q14.2
SNP_A-1699007	C	C	316	4	353	29	15.632	7.69E-05	rs10485307	6	85949880	q14.3
SNP_A-1981355	T	T	343	3	329	23	15.626	7.72E-05	rs3822460	5	39422101	p13.1
SNP_A-2088130	A	A	418	0	341	13	15.613	0.000007771	rs17039320	12	106368330	q23.3
SNP_A-1887167	C	C	394	16	392	0	15.609	7.79E-05	rs1146142	19	23321208	p12
SNP_A-1916825	G	G	366	14	416	0	15.601	7.82E-05	---	1	181873065	q25.3
SNP_A-2167346	T	T	227	187	281	131	15.597	7.84E-05	rs7565364	2	241834027	q37.3
SNP_A-2040379	A	A	313	25	390	6	15.593	7.85E-05	rs1062958	19	11477807	p13.2
SNP_A-1837920	C	C	406	0	383	15	15.592	7.86E-05	rs17208512	17	10195930	p13.1
SNP_A-2040977	G	G	282	58	321	25	15.592	7.86E-05	rs7970503	12	20247248	p12.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140856	G	G	233	59	307	31	15.576	7.92E-05	rs16842512	2	158739739	q24.1
SNP_A-2019081	T	T	338	30	394	8	15.55	8.04E-05	rs16995510	21	38100921	q22.13
SNP_A-1895295	G	G	367	19	295	45	15.541	8.07E-05	rs7501929	17	64691292	q24.3
SNP_A-2149359	A	A	382	4	382	26	15.536	8.10E-05	rs11228900	11	56610234	q11
SNP_A-2268734	G	G	412	0	364	14	15.535	8.10E-05	rs8022191	14	33046668	q13.1
SNP_A-2063461	T	T	394	2	328	18	15.535	8.10E-05	rs3214066	3	57850425	p14.3
SNP_A-1971681	C	C	363	9	314	32	15.528	8.13E-05	rs906665	3	8573690	p25.3
SNP_A-1994096	A	A	319	15	403	1	15.523	8.15E-05	rs16913165	8	85792471	q21.2
SNP_A-1660199	G	G	247	59	316	30	15.51	8.21E-05	rs2197252	17	55981259	q23.2
SNP_A-2169757	A	A	401	1	363	17	15.506	8.23E-05	rs826978	19	41935488	q13.12
SNP_A-1996398	A	A	337	13	410	0	15.494	8.28E-05	rs16911912	9	27883289	p21.2
SNP_A-2049786	G	G	358	0	362	16	15.49	8.29E-05	rs11051399	12	31396281	p11.21
SNP_A-2306567	G	G	411	1	350	16	15.459	8.43E-05	rs11065456	12	120049547	q24.31
SNP_A-1967593	T	T	326	12	308	40	15.445	8.49E-05	rs6054643	20	6906736	p12.3
SNP_A-1883084	A	A	311	7	339	35	15.442	8.51E-05	rs12048655	1	149659624	q21.3
SNP_A-1847015	A	A	305	39	364	14	15.429	8.57E-05	rs7320321	13	105089064	q33.2
SNP_A-2029105	T	T	420	0	374	14	15.422	8.60E-05	---	20	21020530	p11.23
SNP_A-2314652	G	G	373	7	318	28	15.419	8.61E-05	rs10906859	10	15287845	p13
SNP_A-1815052	A	A	368	22	397	3	15.415	8.63E-05	rs12639772	4	122197008	q27
SNP_A-2226139	A	A	243	47	320	22	15.415	8.63E-05	rs16841046	2	133359250	q21.2
SNP_A-2117521	A	A	271	25	388	8	15.401	8.70E-05	rs16966554	16	62359956	q21
SNP_A-2166687	A	A	310	6	295	29	15.389	8.75E-05	rs11205188	1	149866718	q21.3
SNP_A-1929439	A	A	354	24	305	55	15.378	8.80E-05	rs17147609	7	8154291	p21.3
SNP_A-1999849	T	T	297	19	377	3	15.377	8.81E-05	rs16935593	10	34951529	p11.21
SNP_A-2169364	G	G	247	111	224	182	15.373	8.82E-05	rs619819	4	130733550	q28.2
SNP_A-1829887	T	T	399	5	368	26	15.366	8.90E-05	rs2211737	8	36673363	p12
SNP_A-1837378	G	G	186	178	264	142	15.325	9.05E-05	rs1016330	18	61830178	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813036	C	C	328	6	326	30	15.32	0.000090739	rs3792788	5	150426809	q33.1
SNP_A-2109295	C	C	293	87	334	46	15.32	9.07E-05	rs11972345	7	146873198	q35
SNP_A-2038404	T	T	383	15	318	40	15.317	9.09E-05	rs1831792	13	63050808	q21.31
SNP_A-2276641	G	G	412	0	343	13	15.304	9.15E-05	rs9935803	16	66053236	q22.1
SNP_A-1965338	A	A	277	45	343	19	15.301	9.16E-05	---	2	151199856	q23.3
SNP_A-2252645	T	T	399	11	334	34	15.297	9.19E-05	rs6478071	9	114075422	q32
SNP_A-1898425	C	C	304	12	396	0	15.296	9.19E-05	rs257674	19	63172291	q13.43
SNP_A-1991975	T	T	350	16	407	1	15.293	9.20E-05	rs1987445	8	3916576	p23.2
SNP_A-1988229	G	G	339	9	338	36	15.285	9.24E-05	rs10499307	6	154972466	q25.2
SNP_A-2235117	T	T	300	18	289	51	15.27	9.32E-05	rs11151944	18	70150538	q22.3
SNP_A-1686296	G	G	312	32	378	10	15.247	9.43E-05	rs10510425	3	14106635	p25.1
SNP_A-2082329	C	C	312	40	375	15	15.235	9.49E-05	rs10119257	9	15542399	p22.3
SNP_A-1790169	A	A	408	2	367	19	15.221	9.56E-05	rs6540981	1	11511453	p36.22
SNP_A-2010391	T	T	326	2	342	22	15.218	9.58E-05	rs1394855	4	173349063	q34.1
SNP_A-2292746	A	A	337	5	325	27	15.202	9.66E-05	rs3756381	5	142422620	q31.3
SNP_A-2292054	A	A	319	31	354	8	15.186	9.74E-05	rs2303373	15	63978356	q22.31
SNP_A-2002801	T	C	215	143	192	160	15.184	9.75E-05	rs998314	12	63506634	q14.3
SNP_A-2129699	T	T	396	2	357	19	15.169	9.83E-05	rs7186843	16	10558202	p13.13
SNP_A-1822712	G	G	308	18	325	55	15.168	0.000098335	rs17029594	4	101129073	q23
SNP_A-1870560	C	C	374	10	332	34	15.166	9.84E-05	rs11225624	11	102617666	q22.3
SNP_A-2270577	A	A	358	0	370	16	15.166	9.85E-05	rs17001626	4	77477121	q21.1
SNP_A-2028238	C	C	398	2	380	20	15.144	9.96E-05	rs17144393	10	8813054	p14
SNP_A-2027260	C	C	310	28	380	8	14.839	0.0001	rs9269202	6	32557501	p21.32
SNP_A-2031071	C	C	422	0	369	13	14.597	0.0001	rs1863246	12	9410439	p13.31
SNP_A-2031556	A	A	314	48	274	88	14.486	0.0001	rs1822294	11	10190135	p15.4
SNP_A-2019244	T	T	401	3	365	21	14.789	0.0001	rs1041833	21	38910764	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2026027	G	G	404	2	352	18	14.738	0.0001	rs17106230	1	50651783	p32.3
SNP_A-2039222	A	A	281	49	268	98	14.819	0.0001	rs7404610	16	85387986	q24.1
SNP_A-2034648	T	T	366	4	357	25	15.131	0.0001	rs13438217	7	37003080	p14.1
SNP_A-2042357	T	T	353	27	384	6	14.54	0.0001	rs1769068	1	189675290	q31.2
SNP_A-2047274	C	C	272	86	258	150	14.524	0.0001	rs1900866	4	59496366	q12
SNP_A-2002780	T	T	368	2	337	19	14.861	0.0001	rs4509803	12	58600720	q14.1
SNP_A-1996100	G	G	405	1	362	16	14.665	0.0001	rs1360414	9	18153591	p22.2
SNP_A-2010160	G	G	292	22	302	60	14.443	0.0001	rs967914	4	133556757	q28.3
SNP_A-2018536	C	C	334	42	272	76	15.08	0.0001	rs762247	21	35249366	q22.12
SNP_A-2016236	C	C	331	15	393	1	14.507	0.0001	rs6518062	21	21354185	q21.1
SNP_A-2089664	A	A	333	27	366	6	14.729	0.0001	rs1032098	10	96959773	q23.33
SNP_A-2107666	G	G	348	2	338	20	14.785	0.0001	rs9966438	18	17834192	q11.2
SNP_A-2095495	T	T	388	12	334	36	14.893	0.0001	rs6657199	1	90850273	p22.2
SNP_A-2097871	T	T	317	13	308	42	14.845	0.0001	rs6888140	5	129097764	q23.3
SNP_A-2050476	A	A	358	4	357	25	14.681	0.0001	rs12327411	18	73618593	q23
SNP_A-2052975	T	T	319	65	264	106	14.764	0.0001	rs749053	14	54614229	q22.3
SNP_A-2061811	G	G	353	1	360	18	14.508	0.0001	rs16873007	4	22382528	p15.31
SNP_A-2059384	A	A	328	12	406	0	14.564	0.0001	rs9903537	17	27522062	q11.2
SNP_A-2064224	T	T	394	2	367	19	14.594	0.0001	rs7641266	3	35523770	p22.3
SNP_A-2065058	A	A	410	2	362	18	14.515	0.0001	rs17105423	14	36361111	q13.3
SNP_A-2128317	T	T	288	22	402	6	14.879	0.0001	rs16869716	6	71800193	q13
SNP_A-2127496	C	C	357	3	342	22	14.74	0.0001	rs9483390	6	132511503	q23.2
SNP_A-2128075	T	T	373	5	328	24	14.429	0.0001	rs6135672	20	16025705	p12.1
SNP_A-2115128	G	G	293	67	337	33	14.499	0.0001	rs7597220	2	2199903	p25.3
SNP_A-2117682	T	T	317	29	368	8	14.494	0.0001	rs2988013	9	37052647	p13.2
SNP_A-2167980	T	T	402	0	378	14	14.615	0.0001	rs16965684	18	30462220	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2163937	A	A	330	12	406	0	14.478	0.0001	rs2087478	2	196665645	q32.3
SNP_A-2161103	G	G	362	0	357	15	14.901	0.0001	rs16828443	2	148805335	q23.1
SNP_A-2150321	G	G	356	2	348	20	14.683	0.0001	rs7990224	13	66227913	q21.32
SNP_A-2152664	C	C	400	2	371	19	14.674	0.0001	rs16892872	8	120696169	q24.12
SNP_A-2141573	C	C	325	13	298	40	14.925	0.0001	rs11063046	12	4204214	p13.32
SNP_A-2168216	C	C	370	14	404	0	14.996	0.0001	rs1582679	7	131055110	q32.3
SNP_A-2168640	G	G	205	125	265	85	14.703	0.0001	rs11219139	11	122813292	q24.1
SNP_A-2182959	C	C	314	84	340	42	14.712	0.0001	rs2159457	14	71481829	q24.2
SNP_A-2194433	A	A	344	16	305	43	14.5	0.0001	---	2	129270455	q14.3
SNP_A-2195744	T	T	314	20	323	57	15.005	0.0001	rs6709385	2	12586341	p24.3
SNP_A-2223982	T	T	361	11	315	35	14.995	0.0001	rs11197676	10	118177008	q25.3
SNP_A-2213756	C	C	307	35	368	12	14.809	0.0001	rs16896071	5	66303099	q12.3
SNP_A-2211215	T	T	225	117	299	81	15.037	0.0001	rs6791019	3	42254957	p22.1
SNP_A-2212595	C	C	292	18	306	54	14.678	0.0001	rs17721089	8	10742848	p23.1
SNP_A-2208001	C	C	337	15	397	1	14.387	0.0001	rs557729	1	59306783	p32.1
SNP_A-2199816	G	G	322	12	400	0	14.61	0.0001	rs16947350	16	47987895	q12.1
SNP_A-2200023	T	T	341	13	398	0	14.873	0.0001	rs1873590	4	73018515	q13.3
SNP_A-2205589	A	A	280	80	353	47	14.93	0.0001	rs2424320	20	20209725	p11.23
SNP_A-1871711	G	G	298	18	385	3	14.585	0.0001	rs10248773	7	66940542	q11.22
SNP_A-1869273	C	C	316	14	409	1	14.72	0.0001	rs11574141	12	46521297	q13.11
SNP_A-1866282	A	A	404	0	357	13	14.437	0.0001	rs17805318	18	28092809	q12.1
SNP_A-1864110	G	G	359	11	326	36	14.802	0.0001	rs9971486	11	122737456	q24.1
SNP_A-1864185	C	C	204	162	273	121	14.91	0.0001	rs7651065	3	163605786	q26.1
SNP_A-1846670	T	T	340	30	357	7	14.664	0.0001	rs7736609	5	15383092	p15.1
SNP_A-1849461	T	T	366	0	340	14	14.762	0.0001	rs17073609	13	80400476	q31.1
SNP_A-1853804	A	A	404	2	337	17	14.41	0.0001	rs7121079	11	107400137	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1854168	G	G	326	18	374	2	14.698	0.0001	rs8035404	15	67540284	q23
SNP_A-1822471	A	A	270	48	227	87	14.962	0.0001	rs16950314	16	77936683	q23.1
SNP_A-1827383	A	A	383	11	324	34	14.99	0.0001	rs16977992	15	85142192	q25.3
SNP_A-1815091	C	C	267	25	372	8	14.74	0.0001	rs357847	4	59829428	q13.1
SNP_A-1815155	G	G	300	32	375	11	14.611	0.0001	rs10200190	2	171911763	q31.1
SNP_A-1820787	C	C	318	14	405	1	14.461	0.0001	rs13396829	2	119938834	q14.2
SNP_A-1840507	G	G	349	5	341	27	14.952	0.0001	rs7108227	11	19576451	p15.1
SNP_A-1841703	G	G	328	30	278	62	14.802	0.0001	rs12250085	10	55553150	q21.1
SNP_A-1840774	A	A	306	14	401	1	14.911	0.0001	rs6054973	20	7333958	p12.3
SNP_A-1843790	T	T	301	11	406	0	14.537	0.0001	rs16831539	2	200181834	q33.1
SNP_A-1829213	T	T	335	7	331	31	14.626	0.0001	rs4306971	4	128528341	q28.1
SNP_A-1791304	A	A	304	6	312	30	14.568	0.0001	rs2370096	16	22466298	p12.1
SNP_A-1788043	A	A	342	4	309	23	14.76	0.0001	rs17086877	13	69826291	q21.33
SNP_A-1794772	A	A	243	159	290	106	14.7	0.0001	rs1117177	1	89499307	p22.2
SNP_A-1809543	G	G	393	1	371	17	14.811	0.0001	---	18	8535894	p11.22
SNP_A-1802078	G	G	357	25	360	4	14.794	0.0001	rs17167667	7	133389828	q33
SNP_A-1801996	A	A	416	0	359	13	14.781	0.0001	rs17164360	5	127474809	q23.2
SNP_A-1695901	C	C	398	2	321	17	14.985	0.0001	rs6446122	3	60273061	p14.2
SNP_A-1758288	A	A	272	42	329	17	14.482	0.0001	rs714048	8	53235678	q11.23
SNP_A-1965733	T	T	369	13	340	40	14.936	0.0001	rs7581400	2	168221650	q24.3
SNP_A-1962517	G	G	337	29	262	56	14.671	0.0001	rs17008591	2	29877389	p23.2
SNP_A-1966768	A	A	382	2	349	19	14.918	0.0001	rs16833867	1	148958734	q21.3
SNP_A-1967142	C	C	392	2	369	19	14.412	0.0001	rs745988	2	225466285	q36.2
SNP_A-1971901	A	A	319	9	284	32	14.715	0.0001	rs17043579	3	17424255	p24.3
SNP_A-1975138	A	A	194	158	270	122	14.97	0.0001	rs13072199	3	163643799	q26.1
SNP_A-1974263	T	T	382	14	406	0	14.609	0.0001	rs16855311	1	176833566	q25.2
SNP_A-1957475	T	T	347	7	348	32	15.125	0.0001	rs6473722	8	53444710	q11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1955975	T	T	284	58	340	28	14.558	0.0001	rs4553317	10	33335956	p11.22
SNP_A-1904030	C	C	312	36	358	12	14.498	0.0001	rs8108302	19	34940204	q12
SNP_A-1895192	C	C	361	25	300	54	14.919	0.0001	rs657075	5	131458017	q23.3
SNP_A-1895290	C	C	416	0	378	14	15.119	0.0001	rs2738047	8	6715708	p23.1
SNP_A-1893975	G	G	259	47	314	20	14.963	0.0001	rs4772511	13	102369013	q33.1
SNP_A-1884029	G	G	351	1	352	18	14.772	0.0001	rs626090	1	174927796	q25.2
SNP_A-1881285	C	C	188	180	267	147	14.391	0.0001	rs2918440	5	85247669	q14.3
SNP_A-1880836	G	G	314	12	404	0	15.12	0.0001	rs16852896	3	144211971	q23
SNP_A-1928400	A	A	412	0	359	13	14.641	0.0001	rs3731556	3	48180659	p21.31
SNP_A-1928532	C	C	331	7	266	26	14.736	0.0001	rs4707582	6	90699933	q15
SNP_A-1920121	T	T	314	12	388	0	14.526	0.0001	rs10987061	9	125807258	q33.3
SNP_A-1924207	G	G	362	0	363	15	14.662	0.0001	rs9870625	3	81228683	p12.2
SNP_A-1914287	G	G	318	22	328	60	14.663	0.0001	rs12943688	17	50251811	q22
SNP_A-2268063	G	G	412	0	378	14	14.975	0.0001	rs17038962	2	39889957	p22.1
SNP_A-2259540	T	T	351	1	350	18	14.864	0.0001	rs6848931	4	189581594	q35.2
SNP_A-2262265	A	A	331	13	390	0	15.004	0.0001	rs9556487	13	94979598	q32.1
SNP_A-2280068	T	T	318	12	398	0	14.715	0.0001	rs16902499	5	72333889	q13.2
SNP_A-2235997	A	A	361	17	389	1	15.084	0.0001	rs17102959	1	79412333	p31.1
SNP_A-2236418	T	T	384	8	316	28	14.649	0.0001	rs2988003	9	37008949	p13.2
SNP_A-2238231	C	C	359	19	392	2	14.887	0.0001	rs16861869	1	18450008	p36.13
SNP_A-2240522	A	A	323	17	388	2	14.427	0.0001	rs12109343	5	114508714	q22.3
SNP_A-2231051	T	T	377	7	330	28	14.832	0.0001	rs17216782	3	56810018	p14.3
SNP_A-2255125	C	C	416	0	361	13	14.702	0.0001	rs16864645	2	224028870	q36.1
SNP_A-2253896	T	T	359	1	356	18	14.962	0.0001	rs1346780	2	175225747	q31.1
SNP_A-2248487	G	G	366	0	336	14	14.932	0.0001	rs6803943	3	184421998	q27.1
SNP_A-2288973	T	T	323	15	381	1	14.393	0.0001	rs2181643	14	95605237	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289626	T	T	322	12	410	0	14.972	0.0001	rs10195136	2	116271271	q14.1
SNP_A-2289719	G	G	281	31	267	71	15.028	0.0001	rs17120735	12	57071236	q14.1
SNP_A-2298869	G	G	283	25	373	7	15.103	0.0001	rs6101734	20	37925146	q12
SNP_A-2309664	A	A	356	14	390	0	15.034	0.0001	rs16922885	8	59088329	q12.1
SNP_A-2305505	G	G	305	77	236	114	14.597	0.0001	rs10202504	2	46232984	p21
SNP_A-2303250	C	C	312	16	396	2	14.238	2.00E-04	rs16941272	15	86459048	q25.3
SNP_A-2302041	G	G	292	54	328	24	13.578	2.00E-04	rs4662093	1	14123220	p36.21
SNP_A-2302456	G	G	341	7	347	31	13.994	2.00E-04	rs12258609	10	79645057	q22.3
SNP_A-2306421	C	C	416	0	383	13	13.879	2.00E-04	rs6723622	2	24701291	p23.3
SNP_A-2315008	G	G	299	67	282	120	13.862	2.00E-04	rs2422808	20	2564679	p13
SNP_A-2311775	T	T	322	0	352	16	14.332	2.00E-04	rs10018657	4	40142917	p14
SNP_A-2298014	C	C	288	18	359	3	13.909	2.00E-04	rs11897803	2	168210099	q24.3
SNP_A-2299494	C	C	328	14	397	1	13.674	2.00E-04	rs16942186	15	58241331	q22.2
SNP_A-2288032	A	A	320	14	299	41	13.915	2.00E-04	rs16910618	8	83622301	q21.13
SNP_A-2288486	C	C	380	4	359	23	13.962	2.00E-04	rs4562990	15	58614467	q22.2
SNP_A-2290375	C	C	319	17	380	2	14.277	2.00E-04	rs2698129	10	13971864	p13
SNP_A-2247670	C	C	311	17	309	49	14.237	2.00E-04	rs17610946	13	99030161	q32.3
SNP_A-2242260	C	C	345	17	288	42	14.277	2.00E-04	rs11141539	9	86609221	q21.33
SNP_A-2252078	T	T	285	57	223	91	14.209	2.00E-04	rs1269647	7	107486965	q31.1
SNP_A-2231056	T	T	353	33	288	62	13.716	2.00E-04	rs7156353	14	53410376	q22.2
SNP_A-2230307	C	C	340	20	311	49	13.48	2.00E-04	rs8037882	15	50404116	q21.2
SNP_A-2229198	T	T	402	0	357	13	14.366	2.00E-04	rs3731525	3	48188842	p21.31
SNP_A-2233369	G	G	404	4	370	22	13.641	2.00E-04	rs947906	11	119611296	q23.3
SNP_A-2233746	T	T	304	58	258	98	13.972	2.00E-04	rs7313368	12	128100360	q24.32
SNP_A-2231734	A	A	290	28	365	9	13.904	2.00E-04	rs11638444	15	79321875	q25.1
SNP_A-2232053	T	T	413	3	363	19	13.434	2.00E-04	rs10185225	2	69628836	p13.3
SNP_A-2236158	G	G	412	0	369	13	14.254	2.00E-04	rs17115689	10	105249628	q24.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2276000	G	G	356	0	342	14	14.281	2.00E-04	rs343702	6	80679092	q14.1
SNP_A-2279044	A	A	350	2	356	20	14.002	2.00E-04	rs1562197	6	166556412	q27
SNP_A-2279004	T	T	320	8	320	32	13.57	2.00E-04	rs16919173	10	19944727	p12.31
SNP_A-2278108	A	A	375	9	339	31	13.66	2.00E-04	rs237982	16	34533920	p11.1
SNP_A-2275184	T	T	375	11	345	35	13.726	2.00E-04	rs16843390	2	210345339	q34
SNP_A-2275672	T	T	329	45	304	86	13.49	2.00E-04	rs1784773	18	9066995	p11.22
SNP_A-2261348	C	C	397	1	343	15	14.114	2.00E-04	rs7854510	9	82426746	q21.32
SNP_A-2257416	T	T	250	104	221	165	14.261	2.00E-04	rs3850476	4	113168004	q25
SNP_A-2258555	A	A	343	1	339	17	14.044	2.00E-04	rs3008493	14	83970735	q31.3
SNP_A-2264899	A	A	338	12	400	0	13.937	2.00E-04	rs9861546	3	44472294	p21.32
SNP_A-2270480	G	G	283	41	268	84	14.065	2.00E-04	rs11247877	1	26234330	p36.11
SNP_A-2271607	C	C	289	13	308	44	13.722	2.00E-04	rs6984864	8	126914646	q24.13
SNP_A-1917596	C	C	340	10	318	34	13.821	2.00E-04	rs3889764	18	53351817	q21.31
SNP_A-1909737	T	T	336	4	319	23	13.806	2.00E-04	rs1356395	1	102782533	p21.1
SNP_A-1929053	G	G	280	32	345	11	14.179	2.00E-04	rs17136325	11	77565918	q14.1
SNP_A-1927324	T	T	344	12	400	0	13.701	2.00E-04	rs17093563	20	29790750	q11.21
SNP_A-1931024	A	A	352	0	344	14	14.042	2.00E-04	rs10975315	9	5834807	p24.1
SNP_A-1879993	T	T	378	8	339	29	13.618	2.00E-04	rs6047518	20	21550963	p11.22
SNP_A-1879508	G	G	381	7	329	27	14.223	2.00E-04	rs17154030	7	102890560	q22.1
SNP_A-1884792	T	T	306	30	363	9	14.371	2.00E-04	rs6886187	5	78766471	q14.1
SNP_A-1888147	G	G	405	1	359	15	13.73	2.00E-04	---	17	61776841	q24.2
SNP_A-1894723	A	A	361	45	285	75	13.728	2.00E-04	rs7875349	9	103739736	q31.1
SNP_A-1893146	T	T	391	1	366	16	13.934	2.00E-04	rs362899	6	146721963	q24.3
SNP_A-1904089	T	T	352	28	274	54	14.22	2.00E-04	rs937337	14	51858509	q22.1
SNP_A-1902365	C	C	311	15	286	42	13.83	2.00E-04	rs2724609	12	11738499	p13.2
SNP_A-1897905	G	G	350	2	328	18	13.463	2.00E-04	rs16964759	18	29391054	q12.1
SNP_A-1899350	A	A	369	5	351	25	13.778	2.00E-04	rs1219681	2	122964511	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1959027	C	C	410	0	354	12	13.654	2.00E-04	rs11009507	10	34065047	p11.22
SNP_A-1953739	T	T	347	3	352	22	13.695	2.00E-04	rs9294035	6	77641030	q14.1
SNP_A-1954668	C	C	403	5	330	22	13.923	2.00E-04	rs17131614	1	92422060	p22.1
SNP_A-1952687	A	A	317	45	321	95	14.203	2.00E-04	rs8084822	18	9086036	p11.22
SNP_A-1933299	C	C	304	44	295	89	13.623	2.00E-04	rs4891538	18	70088232	q22.3
SNP_A-1935239	G	G	337	33	271	61	13.487	2.00E-04	rs17124009	14	51028285	q22.1
SNP_A-1943658	A	A	358	0	350	14	14.042	2.00E-04	rs2221613	4	171745473	q33
SNP_A-1947076	C	C	374	12	338	36	13.634	2.00E-04	rs17113989	10	90643052	q23.31
SNP_A-1944844	T	T	330	12	398	0	14.195	2.00E-04	rs16860132	2	197679138	q33.1
SNP_A-1944074	A	A	400	0	367	13	13.916	2.00E-04	rs16855701	2	169375357	q24.3
SNP_A-1973142	G	G	278	84	264	144	13.451	2.00E-04	rs4855518	3	68941119	p14.1
SNP_A-1975161	C	C	330	4	300	22	13.675	2.00E-04	rs1826368	3	164432541	q26.1
SNP_A-1965830	G	G	273	69	242	118	14.253	2.00E-04	rs10490604	2	172139420	q31.1
SNP_A-1966266	T	T	302	20	364	4	13.431	2.00E-04	rs10177433	2	190725380	q32.2
SNP_A-1967399	G	G	317	39	362	14	14.239	2.00E-04	rs3769056	2	238447991	q37.3
SNP_A-1968365	T	T	410	0	348	12	13.883	2.00E-04	rs6093359	20	38588661	q12
SNP_A-1984162	C	C	269	27	349	9	13.601	2.00E-04	---	5	155205105	q33.2
SNP_A-1983481	A	A	299	85	257	133	13.696	2.00E-04	rs1875176	5	131230356	q23.3
SNP_A-1984998	A	A	358	0	360	14	13.662	2.00E-04	rs17143472	6	8213756	p24.3
SNP_A-1977593	T	T	313	21	374	4	14.312	2.00E-04	rs1269765	4	74915305	q13.3
SNP_A-1978131	T	T	326	14	401	1	13.921	2.00E-04	---	4	96039481	q22.3
SNP_A-1978574	A	A	316	16	400	2	14.197	2.00E-04	rs17046113	4	114783230	q26
SNP_A-1784887	T	T	320	2	332	20	13.64	2.00E-04	rs4393867	3	141580301	q23
SNP_A-1782165	T	T	388	4	346	22	14.121	2.00E-04	rs2275407	1	54365133	p32.3
SNP_A-1719339	T	T	391	1	383	17	14.226	2.00E-04	rs10490912	10	119810927	q26.11
SNP_A-1734490	A	A	369	1	356	16	13.463	2.00E-04	rs951853	13	43608507	q14.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1703885	A	A	306	44	347	17	14.256	2.00E-04	rs10510479	3	17706138	p24.3
SNP_A-1654081	T	T	188	124	255	89	14.358	2.00E-04	rs1057187	8	6250491	p23.1
SNP_A-1652606	G	G	402	0	348	12	13.614	2.00E-04	rs10489564	1	22841396	p36.12
SNP_A-1800773	A	A	315	21	299	53	13.89	2.00E-04	rs17154899	7	80474614	q21.11
SNP_A-1803850	G	G	325	73	351	35	14.19	2.00E-04	rs6840860	4	36852607	p14
SNP_A-1810007	C	C	401	3	330	18	13.515	2.00E-04	rs16889611	5	58662599	q11.2
SNP_A-1809269	G	G	349	3	341	21	13.455	2.00E-04	rs17072227	18	59756427	q21.33
SNP_A-1811585	T	G	193	171	249	165	13.518	2.00E-04	rs12615998	2	181888300	q31.3
SNP_A-1795151	C	C	341	1	339	17	13.953	2.00E-04	rs11923453	3	37668427	p22.3
SNP_A-1796892	T	T	418	0	379	13	14.088	2.00E-04	rs17019267	1	107768578	p13.3
SNP_A-1797488	C	C	396	16	357	43	14.202	2.00E-04	rs11243818	9	132436048	q34.13
SNP_A-1788649	A	A	299	23	273	55	14.256	2.00E-04	rs6778457	3	182699806	q26.33
SNP_A-1791980	T	T	357	5	339	25	13.793	2.00E-04	rs9483647	6	134436137	q23.2
SNP_A-1790400	C	C	355	23	380	4	14.174	2.00E-04	rs7574911	2	30412366	p23.1
SNP_A-1833316	G	G	313	47	375	21	13.845	2.00E-04	rs303606	9	103126844	q31.1
SNP_A-1838436	C	C	330	12	402	0	14.336	2.00E-04	rs6845612	4	38958167	p14
SNP_A-1817010	T	T	370	0	387	15	14.08	2.00E-04	---	3	170238592	q26.2
SNP_A-1827278	G	G	322	14	391	1	13.718	2.00E-04	rs17042418	2	113286564	q13
SNP_A-1828727	G	G	398	0	359	13	14.147	2.00E-04	rs1547114	13	51214899	q14.3
SNP_A-1825102	T	T	295	15	394	2	13.896	2.00E-04	---	4	139847201	q31.1
SNP_A-1823996	G	G	279	63	349	35	13.418	2.00E-04	rs9599403	13	68574335	q21.33
SNP_A-1856201	A	A	322	12	313	39	13.959	2.00E-04	rs10733100	1	118455136	p12
SNP_A-1856363	G	G	382	14	396	0	14.252	2.00E-04	rs4687883	3	120981705	q13.33
SNP_A-1859315	T	T	372	16	405	1	14.236	2.00E-04	rs1562462	3	136880575	q22.2
SNP_A-1863747	G	G	278	24	371	7	14.334	2.00E-04	rs7038622	9	126685479	q33.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1866385	G	G	333	23	323	57	13.835	2.00E-04	rs6591270	11	67189430	q13.2
SNP_A-1864982	A	A	297	23	278	56	14.119	2.00E-04	rs16854780	3	164130805	q26.1
SNP_A-1861813	A	A	191	179	264	142	14.338	2.00E-04	rs2918426	5	85231315	q14.3
SNP_A-1869094	T	T	310	16	392	2	14.171	2.00E-04	rs10512521	17	64445396	q24.2
SNP_A-1867269	G	T	222	134	207	199	13.662	2.00E-04	rs4438803	4	66336209	q13.1
SNP_A-1867497	T	T	344	18	372	2	13.703	2.00E-04	rs11108734	12	95804449	q23.1
SNP_A-2205435	T	T	302	76	330	38	13.776	2.00E-04	rs2226739	1	115797048	p13.1
SNP_A-2202107	C	C	309	11	404	0	14.102	2.00E-04	rs6944682	7	25654667	p15.2
SNP_A-2208412	T	T	348	4	321	23	14.37	2.00E-04	rs7529959	1	170139711	q25.1
SNP_A-2212548	G	G	314	16	392	2	13.958	2.00E-04	---	3	184590064	q27.1
SNP_A-2219333	T	T	338	8	303	29	13.547	2.00E-04	rs17031909	4	155971329	q32.1
SNP_A-2226009	G	G	414	0	377	13	14.027	2.00E-04	rs7974029	12	102140511	q23.2
SNP_A-2226095	A	A	402	12	343	35	14.321	2.00E-04	rs10831205	11	87441505	q14.2
SNP_A-2197172	C	C	368	0	362	14	13.965	2.00E-04	rs1526717	3	74063523	p13
SNP_A-2197262	T	T	345	33	294	64	13.444	2.00E-04	rs1219444	11	121308724	q24.1
SNP_A-2189420	A	A	334	14	399	1	13.481	2.00E-04	rs9842524	3	19005918	p24.3
SNP_A-2186778	C	C	394	2	347	17	13.5	2.00E-04	rs6964752	7	2387023	p22.3
SNP_A-2181391	A	A	374	18	406	2	13.798	2.00E-04	rs9553671	13	25380231	q12.13
SNP_A-2177362	C	C	366	0	381	15	14.142	2.00E-04	---	4	153149584	q31.3
SNP_A-2176821	A	A	311	21	397	5	13.742	2.00E-04	rs16997510	22	35657906	q12.3
SNP_A-2141438	T	T	266	140	322	94	14.257	2.00E-04	rs12610400	19	61015021	q13.43
SNP_A-2149496	C	C	335	3	325	21	13.56	2.00E-04	rs1469014	2	41078314	p22.1
SNP_A-2145227	A	A	365	5	343	25	14.012	2.00E-04	rs16867082	2	9716210	p25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2153173	C	C	348	24	393	5	14.319	2.00E-04	rs11580341	1	20945994	p36.12
SNP_A-2155985	C	C	217	111	305	83	13.946	2.00E-04	rs7626019	3	42245685	p22.1
SNP_A-2159349	C	C	291	31	344	10	13.696	2.00E-04	rs1919794	7	9106666	p21.3
SNP_A-2160154	T	T	340	2	352	20	13.699	2.00E-04	rs1394948	4	61903236	q13.1
SNP_A-2160717	T	T	345	3	344	22	13.997	2.00E-04	rs17114563	10	104239215	q24.32
SNP_A-2120345	T	C	151	147	228	130	13.692	2.00E-04	rs11694642	2	100416331	q11.2
SNP_A-2121638	A	A	340	82	279	123	13.734	2.00E-04	rs2422817	20	2571033	p13
SNP_A-2122209	A	A	355	13	322	38	13.777	2.00E-04	rs3005838	9	38644385	p13.1
SNP_A-2111869	T	T	305	63	239	97	13.806	2.00E-04	rs10887038	10	123756298	q26.13
SNP_A-2108213	A	A	219	105	193	167	13.917	2.00E-04	rs7984339	13	30407870	q12.3
SNP_A-2110880	T	T	422	0	368	12	13.529	2.00E-04	rs9935491	16	64560359	q22.1
SNP_A-2129671	G	G	385	23	342	52	13.516	2.00E-04	rs6969759	7	66804712	q11.22
SNP_A-2132153	A	A	378	6	350	26	13.494	2.00E-04	rs6014463	20	53731742	q13.31
SNP_A-2137227	C	C	281	25	304	66	13.438	2.00E-04	rs6573333	14	60378090	q23.1
SNP_A-2135283	T	T	381	9	326	30	14.066	2.00E-04	rs16848794	1	220987402	q42.12
SNP_A-2063497	G	G	308	30	274	64	14.284	2.00E-04	rs17585365	12	57089597	q14.1
SNP_A-2067417	T	T	281	35	250	70	13.452	2.00E-04	rs166136	5	3205957	p15.33
SNP_A-2070982	T	T	342	12	408	0	14.052	2.00E-04	rs16994288	4	37993336	p14
SNP_A-2074340	A	A	395	3	339	19	13.831	2.00E-04	rs1562263	11	25058532	p14.3
SNP_A-2055556	G	G	412	0	381	13	13.817	2.00E-04	rs16948963	16	77532715	q23.1
SNP_A-2051286	T	T	300	68	282	122	14.256	2.00E-04	rs1022585	20	2565003	p13
SNP_A-2097579	G	G	349	15	335	43	13.544	2.00E-04	rs942079	1	46724722	p33
SNP_A-2093994	G	G	284	30	365	11	13.452	2.00E-04	rs4752863	11	47692890	p11.2
SNP_A-2093573	G	G	339	39	361	13	13.671	2.00E-04	rs444597	22	20711025	q11.22
SNP_A-2103820	T	T	352	12	408	0	13.663	2.00E-04	rs7536198	1	44011625	p34.1
SNP_A-2100498	A	A	343	69	362	32	13.671	2.00E-04	rs12539201	7	146994608	q35
SNP_A-2102487	C	C	339	3	336	22	14.095	2.00E-04	rs7839739	8	60509380	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2087091	A	A	307	31	360	10	13.549	2.00E-04	rs11121718	1	11298401	p36.22
SNP_A-2087089	A	A	351	15	399	1	13.84	2.00E-04	rs274930	9	23473404	p21.3
SNP_A-2082147	C	C	348	28	336	64	13.568	2.00E-04	rs721009	6	16680780	p22.3
SNP_A-2082205	G	G	358	8	337	31	14.193	2.00E-04	rs16922725	10	23140293	p12.2
SNP_A-2084410	T	T	222	136	296	100	14.184	2.00E-04	rs7365656	1	89525158	p22.2
SNP_A-2018495	C	C	336	12	404	0	14.157	2.00E-04	rs2834602	21	35012300	q22.12
SNP_A-2018096	G	G	351	23	378	4	14.287	2.00E-04	rs16988933	21	32397686	q22.11
SNP_A-2014201	C	C	354	2	358	20	14.103	2.00E-04	rs17129883	11	96544282	q22.1
SNP_A-2011760	C	C	197	161	263	121	14.25	2.00E-04	rs6913061	6	46139120	p21.1
SNP_A-2008380	G	G	422	0	366	12	13.601	2.00E-04	rs7114554	11	21148024	p15.1
SNP_A-1991353	C	C	370	10	313	31	13.757	2.00E-04	rs782539	7	133717361	q33
SNP_A-2001090	T	T	407	1	342	14	13.43	2.00E-04	rs7085200	10	34812548	p11.21
SNP_A-2039007	A	A	260	100	277	53	13.698	2.00E-04	rs6096329	20	49276843	q13.2
SNP_A-2026441	C	C	321	9	316	34	13.998	2.00E-04	rs6504870	17	49353449	q22
SNP_A-2025206	A	A	410	0	375	13	13.965	2.00E-04	rs1021476	1	208765772	q32.3
SNP_A-2021454	C	C	377	33	389	9	13.727	2.00E-04	rs11107943	12	94126808	q22
SNP_A-2021510	A	A	409	3	338	18	13.451	2.00E-04	rs10269427	7	98119425	q22.1
SNP_A-2031647	A	A	345	3	340	22	14.206	2.00E-04	rs2248826	4	147663026	q31.22
SNP_A-2031278	G	G	253	49	304	22	14.041	2.00E-04	rs4627853	4	28466105	p15.1
SNP_A-2028545	T	T	281	125	235	179	13.616	2.00E-04	rs9527585	13	56508810	q21.1
SNP_A-2032434	G	G	336	2	387	21	12.838	3.00E-04	rs17750909	6	55908737	p12.1
SNP_A-2022351	A	A	297	19	271	47	13.063	3.00E-04	rs12695776	3	100016902	q12.1
SNP_A-2026261	T	T	406	0	364	12	13.159	3.00E-04	rs17071843	13	47975669	q14.2
SNP_A-2034095	A	A	272	92	248	148	12.85	3.00E-04	rs2017914	20	40766955	q12
SNP_A-2035543	A	A	377	5	354	24	13.151	3.00E-04	rs16898311	8	101469743	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041577	C	C	312	42	370	18	13.002	3.00E-04	rs17659820	7	47633750	p12.3
SNP_A-1998085	T	T	335	11	404	0	13.035	3.00E-04	rs424311	17	36573662	q21.2
SNP_A-1997687	G	G	364	12	400	0	12.966	3.00E-04	rs3893895	9	111884826	q31.3
SNP_A-2002298	C	C	312	26	305	61	13.067	3.00E-04	rs10493061	1	34773415	p34.3
SNP_A-1990840	G	G	336	14	399	1	13.393	3.00E-04	rs4150026	1	238379696	q43
SNP_A-1990763	C	C	332	10	313	33	12.839	3.00E-04	rs977641	7	103541198	q22.2
SNP_A-1995813	T	T	254	44	238	86	13.025	3.00E-04	rs12338165	9	9455911	p23
SNP_A-1995677	A	A	292	56	289	107	12.93	3.00E-04	rs17756142	9	6291578	p24.1
SNP_A-1996450	C	C	310	14	322	44	13.238	3.00E-04	rs16914219	9	29009023	p21.1
SNP_A-2006875	T	C	182	162	242	158	13.397	3.00E-04	rs4401183	2	181920771	q31.3
SNP_A-2010076	T	T	319	15	313	43	12.886	3.00E-04	rs6533738	4	115290625	q26
SNP_A-2015660	A	A	359	3	338	20	13.176	3.00E-04	rs2824386	21	17887960	q21.1
SNP_A-2013428	A	A	239	105	308	72	13.099	3.00E-04	rs7014818	8	58415293	q12.1
SNP_A-2018898	A	G	181	169	233	145	13.107	3.00E-04	rs2835424	21	36964409	q22.13
SNP_A-2083997	A	A	280	42	336	18	13.206	3.00E-04	rs2184931	1	32872554	p35.1
SNP_A-2081143	T	T	190	176	265	145	12.903	3.00E-04	rs11924705	3	163644318	q26.1
SNP_A-2091932	T	T	313	11	311	37	13.25	3.00E-04	rs10018144	4	22120961	p15.31
SNP_A-2103623	T	T	291	23	292	58	13.212	3.00E-04	rs6474330	8	41320405	p11.21
SNP_A-2092472	A	A	418	0	380	12	12.988	3.00E-04	---	14	65623833	q23.3
SNP_A-2095244	C	C	363	19	310	44	13.048	3.00E-04	rs10141959	14	81002102	q31.1
SNP_A-2094931	G	G	306	38	342	14	12.875	3.00E-04	rs11725123	4	174371023	q34.1
SNP_A-2097168	T	T	343	19	387	3	13.264	3.00E-04	rs2262497	1	178072445	q25.3
SNP_A-2051431	G	G	309	41	352	16	13.319	3.00E-04	rs17102005	14	64254123	q23.3
SNP_A-2053870	A	A	347	1	344	16	13.049	3.00E-04	rs2389252	13	94815726	q32.1
SNP_A-2048665	G	G	320	16	374	2	12.884	3.00E-04	---	3	169863260	q26.2
SNP_A-2048789	C	C	330	6	334	28	13.309	3.00E-04	rs17077361	6	116333644	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2048941	T	T	281	15	358	2	13.101	3.00E-04	rs6032287	20	43605638	q13.12
SNP_A-2056849	T	T	394	2	363	17	12.787	3.00E-04	rs16929939	10	73932359	q22.1
SNP_A-2063225	A	A	354	0	364	14	13.367	3.00E-04	rs11847920	14	104921090	q32.33
SNP_A-2134123	A	A	329	11	390	0	12.811	3.00E-04	rs9595550	13	46297498	q14.2
SNP_A-2136121	G	G	348	2	334	18	13.082	3.00E-04	rs17109259	1	83003422	p31.1
SNP_A-2132813	T	T	345	3	339	21	13.353	3.00E-04	rs17146940	7	22285984	p15.3
SNP_A-2126561	C	C	321	27	384	8	13.375	3.00E-04	---	1	171645779	q25.1
SNP_A-2112959	G	G	412	0	364	12	13.352	3.00E-04	rs9292430	5	31539616	p13.3
SNP_A-2121936	G	G	289	25	343	7	12.825	3.00E-04	rs4284821	2	221157914	q35
SNP_A-2115551	G	G	348	24	255	45	13.172	3.00E-04	rs1484106	16	83989463	q24.1
SNP_A-2159340	C	C	337	11	406	0	13.023	3.00E-04	rs10792084	11	54807466	q11
SNP_A-2164396	C	C	392	4	372	22	12.98	3.00E-04	rs4471068	8	12264620	p23.1
SNP_A-2149063	T	T	259	65	230	110	12.913	3.00E-04	rs11583797	1	81238922	p31.1
SNP_A-2147153	G	G	306	10	414	0	13.283	3.00E-04	rs7778437	7	70681425	q11.22
SNP_A-2152481	T	T	345	17	318	44	13.05	3.00E-04	rs2857783	6	29739567	p22.1
SNP_A-2143935	T	T	390	0	358	12	12.852	3.00E-04	rs16960481	17	62440461	q24.2
SNP_A-2177761	G	G	328	88	370	50	12.972	3.00E-04	rs751582	2	2706660	p25.3
SNP_A-2172021	T	T	335	11	408	0	13.163	3.00E-04	rs10086486	8	78142486	q21.11
SNP_A-2172222	G	G	227	125	203	193	13.338	3.00E-04	rs4870006	6	151673198	q25.1
SNP_A-2186359	G	G	359	1	375	17	13.233	3.00E-04	rs3003649	6	120777366	q22.31
SNP_A-2189953	T	T	418	0	382	12	12.922	3.00E-04	rs6481610	10	29826469	p11.23
SNP_A-2225645	C	C	293	49	360	24	13.05	3.00E-04	rs11780541	8	56319386	q12.1
SNP_A-2221970	T	T	323	3	342	22	12.929	3.00E-04	rs11691898	2	29662767	p23.2
SNP_A-2222408	G	G	298	24	373	7	13.002	3.00E-04	rs6824047	4	68656815	q13.2
SNP_A-2219189	C	C	231	137	311	105	13.15	3.00E-04	rs2808019	1	216833320	q41
SNP_A-2215800	G	G	297	17	375	3	13.046	3.00E-04	rs7243891	18	54285309	q21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213179	G	G	296	10	398	0	13.194	3.00E-04	rs7402359	15	99389091	q26.3
SNP_A-2210882	C	C	410	0	393	13	13.341	3.00E-04	rs17100805	14	32899937	q13.1
SNP_A-2209770	T	T	258	138	194	178	13.388	3.00E-04	rs10105518	8	31522759	p12
SNP_A-2199878	G	G	396	0	356	12	13.119	3.00E-04	rs2040359	8	49042823	q11.21
SNP_A-1867188	C	C	395	1	342	14	12.987	3.00E-04	rs11832651	12	114629349	q24.21
SNP_A-1870240	T	T	235	123	213	191	13.077	3.00E-04	rs6030766	20	41367492	q13.11
SNP_A-1862846	A	A	292	22	378	6	13.295	3.00E-04	rs1822710	10	63205599	q21.2
SNP_A-1864206	G	G	301	69	337	35	13.141	3.00E-04	rs8028882	15	66815710	q23
SNP_A-1857108	A	A	372	6	324	24	12.893	3.00E-04	rs7587948	2	7053378	p25.1
SNP_A-1855272	C	C	222	138	297	105	13.044	3.00E-04	rs7537417	1	216818213	q41
SNP_A-1850193	G	G	420	0	376	12	13.186	3.00E-04	rs11984525	8	102101965	q22.3
SNP_A-1845742	C	C	316	22	311	55	13.09	3.00E-04	rs10923035	1	88359113	p22.2
SNP_A-1818634	A	A	310	42	351	17	12.787	3.00E-04	rs2433246	8	3757524	p23.2
SNP_A-1819487	A	A	326	22	383	5	13.151	3.00E-04	rs16826845	1	22322362	p36.12
SNP_A-1819635	T	T	319	15	398	2	12.815	3.00E-04	rs17642438	15	89552862	q26.1
SNP_A-1837179	A	A	284	34	285	75	12.871	3.00E-04	rs7874309	9	80622508	q21.31
SNP_A-1838976	A	A	403	5	346	22	13.014	3.00E-04	rs6733293	2	17866827	p24.2
SNP_A-1843236	C	C	311	23	316	58	12.945	3.00E-04	rs1570032	20	31277762	q11.21
SNP_A-1842325	T	T	372	12	412	0	13.072	3.00E-04	rs1869058	2	106129045	q12.2
SNP_A-1830591	T	T	365	21	408	4	13.119	3.00E-04	---	16	81195719	q23.3
SNP_A-1831801	G	G	317	15	318	44	12.983	3.00E-04	rs17030420	4	155044307	q31.3
SNP_A-1790986	A	A	351	17	392	2	13.233	3.00E-04	rs13336072	16	34454657	p11.1
SNP_A-1799217	A	A	416	0	368	12	13.338	3.00E-04	rs12077144	1	157562565	q23.3
SNP_A-1795562	T	T	371	17	410	2	13.081	3.00E-04	rs10223920	7	130057119	q32.3
SNP_A-1792951	A	A	175	157	247	127	13.001	3.00E-04	rs7379261	5	75320765	q13.3
SNP_A-1811560	G	G	324	24	374	6	13	3.00E-04	rs7518551	1	110130033	p13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1645854	C	C	350	0	376	14	12.806	3.00E-04	rs10518135	4	76351278	q13.3
SNP_A-1672376	G	G	369	7	380	30	13.012	3.00E-04	rs10509635	10	93182910	q23.32
SNP_A-1687850	T	T	392	2	380	18	12.967	3.00E-04	rs10510287	3	4131186	p26.1
SNP_A-1721588	T	T	295	15	308	46	13.177	3.00E-04	rs10517898	4	167857136	q32.3
SNP_A-1725278	C	C	268	50	306	22	13.253	3.00E-04	rs743763	22	30783415	q12.3
SNP_A-1782839	A	A	324	10	327	35	12.797	3.00E-04	rs2587445	18	61671647	q22.1
SNP_A-1756961	G	G	353	9	340	32	13.012	3.00E-04	rs1475099	10	4212305	p15.1
SNP_A-1752153	C	T	189	165	232	156	12.933	3.00E-04	rs723599	11	112409954	q23.1
SNP_A-1981038	T	T	317	25	327	5	13.343	3.00E-04	rs16896571	5	27291525	p14.1
SNP_A-1967273	T	T	365	13	331	37	13.049	3.00E-04	rs1205590	1	151051978	q21.3
SNP_A-1967062	T	T	321	5	328	26	13.171	3.00E-04	rs1155046	2	222817379	q36.1
SNP_A-1966432	G	G	335	5	327	25	13.226	3.00E-04	rs13396759	2	199349980	q33.1
SNP_A-1971069	A	A	216	98	196	160	13.289	3.00E-04	rs2092662	22	35412839	q12.3
SNP_A-1944571	T	T	345	5	339	25	13.116	3.00E-04	rs6871869	5	125146590	q23.2
SNP_A-1943566	G	G	366	6	344	26	13.176	3.00E-04	rs16907396	11	10004263	p15.4
SNP_A-1942695	C	C	390	0	375	13	13.289	3.00E-04	rs6881021	5	52073512	q11.2
SNP_A-1933493	C	T	199	191	244	150	13.317	3.00E-04	rs4933648	10	92891080	q23.31
SNP_A-1938312	G	G	368	0	388	14	13.053	3.00E-04	rs17028001	4	153149138	q31.3
SNP_A-1938477	T	A	237	149	203	191	13.147	3.00E-04	rs1166206	16	74146007	q23.1
SNP_A-1954547	G	G	400	4	361	21	12.953	3.00E-04	rs1329568	9	37027976	p13.2
SNP_A-1954142	T	T	402	2	365	17	13.021	3.00E-04	---	19	36406472	q12
SNP_A-1951105	C	C	347	17	380	2	12.913	3.00E-04	rs1818976	19	24222331	p12
SNP_A-1950574	T	T	399	9	330	28	13.08	3.00E-04	rs4452640	6	38983730	p21.2
SNP_A-1950312	T	T	408	0	372	12	12.946	3.00E-04	rs16901496	8	127614849	q24.21
SNP_A-1949190	G	G	263	87	216	130	13.11	3.00E-04	rs4883261	12	7421154	p13.31
SNP_A-1957066	A	A	400	2	342	16	12.919	3.00E-04	---	3	18622708	p24.3
SNP_A-1901626	A	A	323	11	388	0	12.976	3.00E-04	---	20	17023413	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897191	C	C	328	88	282	134	13	3.00E-04	rs8077107	17	73124159	q25.3
SNP_A-1886291	C	C	387	5	345	23	13.237	3.00E-04	rs937531	12	129161348	q24.33
SNP_A-1882051	T	T	410	0	374	12	12.941	3.00E-04	rs10187411	2	58149375	p16.1
SNP_A-1929911	A	A	335	11	400	0	12.907	3.00E-04	rs3816602	10	127724319	q26.2
SNP_A-1927054	T	T	364	2	354	18	12.891	3.00E-04	rs7540461	1	195608515	q31.3
SNP_A-1928848	G	G	289	33	266	68	12.867	3.00E-04	rs1464859	7	69882859	q11.22
SNP_A-1923053	A	A	317	13	401	1	13.158	3.00E-04	rs516678	11	120544119	q23.3
SNP_A-1919522	C	C	414	0	372	12	13.135	3.00E-04	rs6797766	3	17885240	p24.3
SNP_A-1921922	G	G	343	11	410	0	12.926	3.00E-04	rs16934443	9	117111940	q33.1
SNP_A-1911199	C	C	366	0	361	13	12.949	3.00E-04	rs328113	18	42527123	q21.1
SNP_A-1906267	A	A	418	0	374	12	13.192	3.00E-04	rs6756415	2	133210494	q21.2
SNP_A-1918138	T	T	412	0	364	12	13.352	3.00E-04	rs17104608	14	36038981	q13.3
SNP_A-2268056	A	A	351	13	324	38	13.329	3.00E-04	rs11232536	11	80606592	q14.1
SNP_A-2266611	T	T	240	62	317	37	12.917	3.00E-04	rs9557290	13	99206337	q32.3
SNP_A-2258618	T	T	354	24	371	5	12.842	3.00E-04	rs6909717	6	47854941	p12.3
SNP_A-2257528	T	T	375	7	326	26	13.16	3.00E-04	rs883836	8	8190256	p23.1
SNP_A-2258861	C	C	356	2	359	19	13.241	3.00E-04	rs6660153	1	70164615	p31.1
SNP_A-2260729	T	T	271	75	257	131	13.235	3.00E-04	rs9547958	13	37038879	q13.3
SNP_A-2274218	A	A	370	0	359	13	13.161	3.00E-04	rs17087695	4	57917268	q12
SNP_A-2239818	G	G	353	23	295	49	13.184	3.00E-04	rs4504534	7	42271480	p14.1
SNP_A-2229772	T	T	421	1	364	14	13.025	3.00E-04	rs17108444	14	70264076	q24.2
SNP_A-2251228	T	T	335	5	340	26	13.323	3.00E-04	rs11064039	12	6107677	p13.31
SNP_A-2244020	A	A	347	11	414	0	12.905	3.00E-04	rs17008036	4	125592144	q28.1
SNP_A-2247680	C	C	328	10	342	36	12.793	3.00E-04	rs1373308	8	6294758	p23.1
SNP_A-2248715	G	G	348	2	349	19	13.32	3.00E-04	rs16932409	11	15970052	p15.2
SNP_A-2246289	G	G	359	3	361	21	12.977	3.00E-04	rs17033709	4	104770796	q24

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2291453	G	G	397	1	361	15	13.345	3.00E-04	rs17172458	7	55075412	p11.2
SNP_A-2298713	G	G	418	0	368	12	13.402	3.00E-04	rs6537573	10	49606424	q11.23
SNP_A-2299734	C	C	311	27	366	8	12.996	3.00E-04	rs2267433	22	40202272	q13.2
SNP_A-2312155	T	T	404	2	369	17	12.93	3.00E-04	rs2789328	1	18813568	p36.13
SNP_A-2313084	A	A	332	14	389	1	13.19	3.00E-04	rs16953991	15	68025422	q23
SNP_A-2313953	A	A	330	4	329	23	12.908	3.00E-04	rs7810177	7	138928138	q34
SNP_A-2306909	T	T	388	12	334	34	13.25	3.00E-04	rs16948934	15	92672296	q26.2
SNP_A-2308765	T	T	357	17	402	2	13.373	3.00E-04	rs16943999	16	74836502	q23.1
SNP_A-2310281	G	G	247	59	346	38	12.415	4.00E-04	rs649044	5	2436612	p15.33
SNP_A-2297410	T	T	295	35	257	67	12.601	4.00E-04	rs11124960	2	44127361	p21
SNP_A-2245641	C	C	269	23	372	8	12.499	4.00E-04	rs7225767	17	34296978	q12
SNP_A-2246144	T	T	333	17	403	3	12.377	4.00E-04	rs17590172	2	200357227	q33.1
SNP_A-2245116	C	C	325	13	306	38	12.775	4.00E-04	rs11263287	9	43905810	p12
SNP_A-2243021	T	T	366	0	350	12	12.336	4.00E-04	rs4458714	6	143627161	q24.2
SNP_A-2251647	A	A	366	10	338	32	12.59	4.00E-04	rs11022211	11	12127010	p15.3
SNP_A-2255585	T	T	352	2	354	18	12.367	4.00E-04	rs17042134	3	5275286	p26.1
SNP_A-2230709	T	T	309	25	365	7	12.769	4.00E-04	rs4863509	4	141041771	q31.1
SNP_A-2280691	A	A	321	67	308	28	12.609	4.00E-04	rs2469839	17	36244205	q21.2
SNP_A-2282868	T	T	267	79	260	138	12.561	4.00E-04	rs6658821	1	80274503	p31.1
SNP_A-2257093	G	G	355	13	338	38	12.587	4.00E-04	rs11978507	7	130741033	q32.3
SNP_A-2266777	A	A	242	42	330	22	12.663	4.00E-04	rs984447	15	51937309	q21.3
SNP_A-2264814	T	T	382	8	329	27	12.742	4.00E-04	rs16968853	15	37417688	q14
SNP_A-2266107	A	A	276	24	364	8	12.53	4.00E-04	rs7716372	5	98456084	q21.1
SNP_A-1914772	C	C	336	28	397	9	12.58	4.00E-04	rs9641522	7	114062821	q31.1
SNP_A-1912728	A	A	353	11	406	0	12.447	4.00E-04	rs17132782	5	110465393	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909666	G	G	401	9	342	28	12.423	4.00E-04	rs4252499	7	142126586	q34
SNP_A-1921712	T	T	282	28	288	66	12.564	4.00E-04	rs969599	8	18469011	p22
SNP_A-1919375	T	T	275	33	282	74	12.393	4.00E-04	rs2180322	6	52664707	p12.2
SNP_A-1920458	C	C	345	69	283	105	12.74	4.00E-04	rs10095515	8	5655483	p23.2
SNP_A-1926628	A	A	302	26	366	8	12.701	4.00E-04	---	12	53824552	q13.2
SNP_A-1926790	C	C	323	17	399	3	12.708	4.00E-04	rs673205	1	107667345	p13.3
SNP_A-1881890	A	A	314	10	396	0	12.394	4.00E-04	rs3890771	2	84771988	p11.2
SNP_A-1884476	C	C	270	96	247	153	12.587	4.00E-04	rs950699	4	79862951	q21.21
SNP_A-1888522	T	T	366	38	303	67	12.473	4.00E-04	rs7756254	6	3227962	p25.2
SNP_A-1874821	G	G	251	103	326	72	12.709	4.00E-04	rs8099000	18	13390714	p11.21
SNP_A-1874440	T	T	329	19	400	4	12.597	4.00E-04	rs879804	14	88518415	q32.11
SNP_A-1877156	C	C	323	35	296	70	12.758	4.00E-04	rs915117	10	121188614	q26.11
SNP_A-1897957	C	C	201	169	266	132	12.591	4.00E-04	rs10741729	11	17518689	p15.1
SNP_A-1959286	A	A	251	113	232	178	12.577	4.00E-04	rs9374021	6	108534117	q21
SNP_A-1948273	T	T	318	38	277	71	12.727	4.00E-04	rs7922799	10	12733766	p13
SNP_A-1939751	C	C	405	1	362	14	12.545	4.00E-04	rs7942510	11	21980410	p14.3
SNP_A-1969405	T	T	323	17	300	44	12.777	4.00E-04	rs17004109	21	22371265	q21.1
SNP_A-1971239	G	G	408	2	387	17	12.353	4.00E-04	rs16999471	22	47279215	q13.32
SNP_A-1966634	A	A	262	16	382	4	12.32	4.00E-04	rs16839485	2	207942987	q33.3
SNP_A-1967932	A	A	393	17	354	42	12.39	4.00E-04	rs16997087	20	16002982	p12.1
SNP_A-1968191	C	C	298	8	299	31	12.678	4.00E-04	rs2093419	20	23896300	p11.21
SNP_A-1981804	A	A	306	22	380	6	12.496	4.00E-04	rs16878181	5	59837400	q12.1
SNP_A-1979294	A	A	293	39	346	16	12.741	4.00E-04	rs17020454	4	146905884	q31.21
SNP_A-1982908	A	A	360	2	375	19	12.736	4.00E-04	rs17132800	5	110483101	q22.1
SNP_A-1783471	A	A	388	12	408	0	12.425	4.00E-04	rs7027128	9	127564917	q34.11
SNP_A-1728579	T	T	400	0	374	12	12.628	4.00E-04	rs6753563	2	20768217	p24.1
SNP_A-1734644	A	A	402	0	351	11	12.394	4.00E-04	rs10501789	11	91860473	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1731603	G	G	269	53	361	31	12.454	4.00E-04	rs3843777	20	23984782	p11.21
SNP_A-1738487	G	G	395	3	367	19	12.484	4.00E-04	rs10495788	2	33501430	p22.3
SNP_A-1693449	C	C	325	5	355	27	12.719	4.00E-04	rs10485310	6	105389176	q16.3
SNP_A-1676790	C	C	317	23	281	51	12.668	4.00E-04	rs4396488	15	91383349	q26.1
SNP_A-1807443	A	A	365	17	392	2	12.623	4.00E-04	rs7544913	1	33916170	p35.1
SNP_A-1809551	G	G	333	23	266	46	12.316	4.00E-04	rs11068945	12	117330384	q24.23
SNP_A-1810802	A	A	238	50	316	28	12.322	4.00E-04	rs4730073	7	104449822	q22.3
SNP_A-1810869	T	T	371	5	328	22	12.434	4.00E-04	rs4788667	16	71459210	q22.3
SNP_A-1803185	T	T	358	62	372	28	12.633	4.00E-04	rs4784481	16	53700450	q12.2
SNP_A-1795979	G	G	324	64	358	32	12.357	4.00E-04	rs10863568	1	217406474	q41
SNP_A-1831808	T	T	364	32	275	55	12.58	4.00E-04	rs11254889	10	7019601	p14
SNP_A-1829137	C	C	210	154	280	120	12.551	4.00E-04	rs6826026	4	157332302	q32.1
SNP_A-1840344	A	A	411	1	339	13	12.563	4.00E-04	rs321344	11	110448346	q23.1
SNP_A-1819631	G	G	407	1	358	14	12.771	4.00E-04	rs7710747	5	162885492	q34
SNP_A-1823568	A	A	408	0	382	12	12.615	4.00E-04	rs823431	6	17637430	p22.3
SNP_A-1855827	G	G	382	12	404	0	12.492	4.00E-04	rs4705228	5	145690839	q32
SNP_A-1864936	G	G	278	24	296	62	12.695	4.00E-04	rs16936657	11	42424471	p12
SNP_A-1865835	T	T	266	130	318	88	12.599	4.00E-04	rs13419936	2	228541693	q36.3
SNP_A-1866964	A	A	323	11	380	0	12.711	4.00E-04	rs7849574	9	119985792	q33.2
SNP_A-2207050	A	A	250	104	240	172	12.639	4.00E-04	rs2981503	3	126337326	q21.2
SNP_A-2207270	A	A	412	0	386	12	12.609	4.00E-04	rs868224	8	141687965	q24.3
SNP_A-2215850	G	G	197	165	258	126	12.767	4.00E-04	rs4737709	8	66251925	q13.1
SNP_A-2216212	A	A	413	1	370	14	12.518	4.00E-04	rs3746491	20	45234960	q13.12
SNP_A-2213201	C	C	407	1	391	15	12.566	4.00E-04	rs6747843	2	234446354	q37.1
SNP_A-2224322	T	T	220	132	299	103	12.342	4.00E-04	rs6541127	1	216789404	q41
SNP_A-2224454	G	G	397	21	389	3	12.76	4.00E-04	rs6650615	18	11883317	p11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225903	A	A	241	119	315	87	12.543	4.00E-04	rs13227663	7	135797492	q33
SNP_A-2191663	T	T	374	10	333	31	12.608	4.00E-04	rs6004906	22	24759109	q12.1
SNP_A-2192862	A	A	385	15	403	1	12.642	4.00E-04	rs16892417	8	106997496	q23.1
SNP_A-2168612	T	T	363	5	320	22	12.475	4.00E-04	rs8190887	8	30704196	p12
SNP_A-2169043	G	G	353	11	408	0	12.508	4.00E-04	rs1024036	3	47292669	p21.31
SNP_A-2177656	T	T	306	32	284	66	12.411	4.00E-04	rs16898397	5	68369792	q13.1
SNP_A-2178173	G	A	213	139	208	188	12.735	4.00E-04	rs1446146	2	4326943	p25.2
SNP_A-2176869	A	A	312	18	402	4	12.54	4.00E-04	rs7241477	18	7405260	p11.23
SNP_A-2182125	T	T	400	6	320	22	12.648	4.00E-04	rs6036400	20	23329786	p11.21
SNP_A-2180179	A	A	279	29	338	10	12.506	4.00E-04	---	3	178177306	q26.32
SNP_A-2167761	T	T	319	43	351	17	12.747	4.00E-04	rs7025416	9	18950696	p22.1
SNP_A-2161454	C	C	358	18	290	40	12.537	4.00E-04	rs874447	6	20539633	p22.3
SNP_A-2157265	C	T	232	172	223	183	12.365	4.00E-04	rs609744	18	2170338	p11.32
SNP_A-2154235	C	C	326	26	361	7	12.373	4.00E-04	rs616999	11	121608152	q24.1
SNP_A-2113354	G	G	406	0	376	12	12.749	4.00E-04	rs1497464	5	2791368	p15.33
SNP_A-2124385	G	G	410	2	364	16	12.35	4.00E-04	rs5460	19	54180660	q13.33
SNP_A-2057755	A	A	344	0	355	13	12.378	4.00E-04	---	3	118652203	q13.31
SNP_A-2057636	T	T	374	12	404	0	12.753	4.00E-04	rs16983147	20	21872897	p11.22
SNP_A-2048526	G	G	364	0	371	13	12.541	4.00E-04	rs6803834	3	75304301	p12.3
SNP_A-2096339	T	T	275	29	351	11	12.37	4.00E-04	rs137468	22	31944639	q12.3
SNP_A-2097865	A	A	309	43	272	78	12.475	4.00E-04	rs2188378	12	109894025	q24.11
SNP_A-2107242	A	A	310	28	386	10	12.319	4.00E-04	rs11902414	2	212841459	q34
SNP_A-2102750	G	G	395	1	358	14	12.347	4.00E-04	rs7131172	11	102907758	q22.3
SNP_A-2089318	C	C	362	0	375	13	12.343	4.00E-04	rs16985446	20	23458615	p11.21
SNP_A-2087826	T	T	247	51	333	29	12.715	4.00E-04	rs1402278	12	76231942	q21.2
SNP_A-2082821	A	A	269	77	326	46	12.348	4.00E-04	rs11747928	5	19022302	p14.3
SNP_A-2079928	C	C	292	26	377	9	12.606	4.00E-04	rs4487001	18	71797901	q23
SNP_A-2019173	A	A	353	11	414	0	12.69	4.00E-04	rs8130533	21	38627266	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2013898	T	T	379	5	317	21	12.489	4.00E-04	rs4486242	8	136362016	q24.22
SNP_A-2007963	T	T	311	35	359	13	12.597	4.00E-04	rs2826364	21	20833035	q21.1
SNP_A-1992234	G	G	292	42	265	79	12.478	4.00E-04	rs10503407	8	10266043	p23.1
SNP_A-2005016	G	G	345	3	340	20	12.402	4.00E-04	rs17121800	10	108700863	q25.1
SNP_A-2041432	A	T	197	171	241	167	12.337	4.00E-04	rs7996548	13	30540481	q12.3
SNP_A-2047500	T	T	370	14	407	1	12.313	4.00E-04	rs6877814	5	167770310	q34
SNP_A-2038677	G	G	353	21	382	4	12.518	4.00E-04	rs2310119	4	29497216	p15.1
SNP_A-2039768	T	T	323	25	307	57	12.541	4.00E-04	rs12876524	13	70484001	q21.33
SNP_A-2040178	T	T	286	24	351	7	12.571	4.00E-04	rs16860735	1	24273122	p36.11
SNP_A-2038349	T	T	339	3	353	21	12.378	4.00E-04	rs10770712	12	20761967	p12.2
SNP_A-2037731	A	A	305	75	257	115	12.437	4.00E-04	rs1487818	11	21885939	p14.3
SNP_A-2037166	G	G	351	1	360	16	12.572	4.00E-04	rs577954	1	100040464	p21.2
SNP_A-2021425	G	G	350	16	404	2	12.718	4.00E-04	rs4482039	11	123626372	q24.1
SNP_A-2020449	G	G	384	18	363	45	12.118	5.00E-04	rs233225	21	44752483	q22.3
SNP_A-2020905	T	T	405	1	374	14	12.098	5.00E-04	rs17112012	1	55542005	p32.3
SNP_A-2024963	C	C	370	2	374	18	12.306	5.00E-04	rs1886953	10	25520173	p12.1
SNP_A-2025626	C	C	365	23	385	5	12.1	5.00E-04	rs2230756	12	93144491	q22
SNP_A-2027516	A	A	344	12	341	37	12.12	5.00E-04	rs9906328	17	46826203	q21.33
SNP_A-2029526	G	G	312	18	349	3	12.088	5.00E-04	rs4845540	1	150138284	q21.3
SNP_A-2038671	C	C	348	18	391	3	12.201	5.00E-04	rs11160707	14	102444463	q32.32
SNP_A-2043362	C	T	229	141	208	204	12.085	5.00E-04	rs11131612	4	66353790	q13.1
SNP_A-1990137	A	A	337	27	351	7	12.001	5.00E-04	rs1881012	7	69782155	q11.22
SNP_A-2010430	C	C	310	14	394	2	11.942	5.00E-04	rs6827612	4	178835311	q34.3
SNP_A-2010865	T	T	321	15	380	2	12.009	5.00E-04	rs4866844	5	43995130	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015857	G	G	260	100	334	70	12.019	5.00E-04	rs2825018	21	19004030	q21.1
SNP_A-2016661	A	A	344	0	363	13	12.112	5.00E-04	rs2828628	21	24223324	q21.2
SNP_A-2016966	G	G	330	44	285	77	12.1	5.00E-04	rs2829871	21	26000862	q21.3
SNP_A-2084387	A	A	410	0	361	11	12.297	5.00E-04	rs9889952	17	51855276	q23.2
SNP_A-2084739	A	A	338	10	410	0	11.939	5.00E-04	rs17145676	11	82985330	q14.1
SNP_A-2102130	C	C	324	10	361	37	12.005	5.00E-04	---	3	3047361	p26.2
SNP_A-2102337	G	G	367	53	385	23	12.102	5.00E-04	rs4954262	2	136144535	q21.3
SNP_A-2094347	C	C	361	11	404	0	12.118	5.00E-04	rs6015712	20	58306720	q13.33
SNP_A-2048023	C	C	338	24	257	45	12.095	5.00E-04	rs11913192	22	47163714	q13.32
SNP_A-2057485	C	C	375	23	336	50	11.945	5.00E-04	rs898873	16	8163958	p13.2
SNP_A-2073617	T	T	273	39	344	18	12.265	5.00E-04	rs891925	5	168150963	q34
SNP_A-2072718	A	A	326	32	365	11	12.023	5.00E-04	rs222681	14	23087924	q11.2
SNP_A-2127166	T	T	418	0	377	11	12.014	5.00E-04	rs6445265	3	62357169	p14.2
SNP_A-2114869	C	C	280	42	348	20	12.157	5.00E-04	rs10241160	7	150313043	q36.1
SNP_A-2110619	T	T	274	56	325	29	12.091	5.00E-04	rs1886524	9	112781808	q32
SNP_A-2161384	T	T	355	11	398	0	12.136	5.00E-04	rs6452859	5	89297137	q14.3
SNP_A-2142255	G	G	267	101	253	163	12.044	5.00E-04	rs6787471	3	185402869	q27.1
SNP_A-2150768	A	A	414	0	369	11	12.153	5.00E-04	rs232818	1	58769432	p32.1
SNP_A-2147145	C	C	309	19	368	4	12.207	5.00E-04	rs353953	5	77134771	q14.1
SNP_A-2147673	G	G	273	79	249	129	12.212	5.00E-04	rs6515675	20	2567053	p13
SNP_A-2148272	A	A	348	16	384	2	12.024	5.00E-04	rs1393080	5	134705776	q31.1
SNP_A-2148615	G	G	351	23	371	5	12.12	5.00E-04	rs12038267	1	232411822	q42.3
SNP_A-2179034	A	A	373	11	310	30	11.986	5.00E-04	rs6959470	7	30243130	p15.1
SNP_A-2176580	G	G	388	2	377	17	11.98	5.00E-04	rs159274	17	29715070	q12
SNP_A-2170760	C	C	229	83	294	54	12.29	5.00E-04	rs7792518	7	143712383	q35
SNP_A-2172313	G	G	418	0	371	11	12.204	5.00E-04	rs10864525	1	11585919	p36.22
SNP_A-2195584	T	T	420	0	379	11	12.009	5.00E-04	rs17023147	1	211078979	q41

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2190041	T	T	348	18	311	43	12.127	5.00E-04	rs17091145	10	115724790	q25.3
SNP_A-2186588	G	G	223	125	209	197	12.164	5.00E-04	rs4909741	8	139253233	q24.23
SNP_A-2226849	C	C	331	51	264	80	12.008	5.00E-04	rs4151510	13	47843176	q14.2
SNP_A-2223651	C	C	319	17	377	3	11.975	5.00E-04	rs6842284	4	76074298	q13.3
SNP_A-2223383	A	A	308	68	238	98	12.187	5.00E-04	rs16857964	1	158881251	q23.3
SNP_A-2213943	T	T	396	10	348	30	12.112	5.00E-04	rs12324142	15	74201944	q24.2
SNP_A-2209567	T	T	265	51	322	26	12.138	5.00E-04	rs16871217	5	71036254	q13.2
SNP_A-2209265	G	G	321	17	340	48	11.944	5.00E-04	rs9391215	6	105156603	q21
SNP_A-2210923	A	A	332	10	406	0	12.032	5.00E-04	rs6038878	20	7496349	p12.3
SNP_A-2200124	T	T	329	15	390	2	12.037	5.00E-04	rs16935938	8	70559274	q13.2
SNP_A-1869717	T	T	367	11	408	0	12.042	5.00E-04	rs7006877	8	136151587	q24.22
SNP_A-1871720	T	T	206	80	289	57	12.192	5.00E-04	rs9455700	6	168950277	q27
SNP_A-1862529	A	A	409	3	370	18	11.958	5.00E-04	rs16956060	17	50993397	q23.1
SNP_A-1860912	G	G	318	12	297	35	11.966	5.00E-04	rs10972648	9	35956699	p13.3
SNP_A-1854535	A	A	268	100	312	62	12.204	5.00E-04	rs2196544	7	154355556	q36.2
SNP_A-1853754	A	A	272	26	291	65	12.309	5.00E-04	rs11034024	11	37181960	p12
SNP_A-1845986	G	G	300	64	307	29	12.152	5.00E-04	rs566541	9	135663356	q34.3
SNP_A-1844489	A	A	338	30	388	10	12.287	5.00E-04	rs13389202	2	70086072	p13.3
SNP_A-1821571	G	G	354	22	389	5	11.938	5.00E-04	rs17121758	14	85381926	q31.3
SNP_A-1816238	G	G	298	68	291	121	12.269	5.00E-04	rs2422809	20	2565701	p13
SNP_A-1815968	T	T	319	33	364	12	11.987	5.00E-04	rs16971750	16	71938606	q22.3
SNP_A-1840493	A	A	252	116	232	180	12.221	5.00E-04	rs646555	4	130790808	q28.2
SNP_A-1840613	G	G	330	10	410	0	12.222	5.00E-04	rs6497576	16	22089994	p12.1
SNP_A-1837657	T	T	276	26	374	10	12.26	5.00E-04	rs7697670	4	157229146	q32.1
SNP_A-1837720	C	C	216	186	266	138	12.293	5.00E-04	rs414264	5	172952573	q35.2
SNP_A-1831693	G	G	243	117	315	85	12.288	5.00E-04	rs12713280	2	54993027	p16.1
SNP_A-1831179	C	C	339	7	362	30	12.232	5.00E-04	rs11021219	11	94941605	q21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802802	G	G	405	3	381	19	12.291	5.00E-04	rs6798616	3	410713	p26.3
SNP_A-1801577	C	C	290	42	349	19	12.301	5.00E-04	rs2798743	9	15394061	p22.3
SNP_A-1804824	T	T	416	0	375	11	12.02	5.00E-04	rs17155189	8	8979688	p23.1
SNP_A-1805722	A	A	261	53	340	30	12.255	5.00E-04	rs7894089	10	126409143	q26.13
SNP_A-1808037	G	G	368	0	356	12	12.199	5.00E-04	rs16965370	15	31209759	q13.3
SNP_A-1812494	A	A	366	32	388	10	12.166	5.00E-04	rs1425889	7	49615436	p12.3
SNP_A-1813672	G	G	294	48	269	87	12.101	5.00E-04	rs2005022	20	46903575	q13.13
SNP_A-1677548	G	G	396	0	380	12	12.31	5.00E-04	rs1892445	1	245729550	q44
SNP_A-1671406	C	C	207	117	187	181	12.011	5.00E-04	rs10516862	4	91455565	q22.1
SNP_A-1752971	A	A	394	0	351	11	12.149	5.00E-04	rs10490618	2	38151293	p22.2
SNP_A-1983410	G	G	242	60	323	37	12.077	5.00E-04	rs2291628	5	127637532	q23.2
SNP_A-1984820	A	A	353	1	378	16	11.986	5.00E-04	rs2077681	6	3031099	p25.2
SNP_A-1979511	A	A	310	10	314	34	11.964	5.00E-04	rs1459852	4	157058182	q32.1
SNP_A-1977406	A	A	306	22	370	6	11.985	5.00E-04	rs10005234	4	65508800	q13.1
SNP_A-1980905	C	C	335	5	332	24	12.1	5.00E-04	rs6702906	1	201467405	q32.1
SNP_A-1967109	C	C	407	3	368	18	11.964	5.00E-04	rs6662869	1	150020537	q21.3
SNP_A-1963695	C	C	323	15	386	2	12.153	5.00E-04	rs4128633	2	69409843	p13.3
SNP_A-1974682	T	T	300	12	297	37	12.035	5.00E-04	---	3	146475001	q24
SNP_A-1939210	A	A	365	3	370	20	11.971	5.00E-04	rs11174151	12	60425168	q14.1
SNP_A-1937699	A	A	277	83	270	142	12.113	5.00E-04	rs9594819	13	42300786	q14.11
SNP_A-1937348	G	G	265	99	341	69	12.198	5.00E-04	rs169826	3	140765506	q23
SNP_A-1933248	G	G	283	83	268	138	12.056	5.00E-04	rs876535	3	68923672	p14.1
SNP_A-1948489	A	A	341	13	403	1	12.207	5.00E-04	rs9867869	3	66486358	p14.1
SNP_A-1898604	T	T	329	29	295	59	12.058	5.00E-04	rs5997090	22	25169094	q12.1
SNP_A-1900137	C	C	354	2	360	18	12.202	5.00E-04	rs16956256	17	51123878	q23.1
SNP_A-1895588	A	A	209	181	252	130	12.293	5.00E-04	rs11034878	11	38579595	p12
SNP_A-1877189	T	T	362	4	343	21	12.067	5.00E-04	rs16877292	8	30697824	p12
SNP_A-1875447	T	T	338	2	363	19	12.252	5.00E-04	rs1434954	4	20623176	p15.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1874103	C	C	235	65	320	42	12.263	5.00E-04	rs9622514	22	35671114	q12.3
SNP_A-1877936	G	G	285	9	388	0	12.036	5.00E-04	rs7707028	5	111768934	q22.2
SNP_A-1879847	T	T	319	17	381	3	12.145	5.00E-04	rs9371628	6	153107839	q25.2
SNP_A-1887487	T	T	406	2	364	16	12.2	5.00E-04	rs16941236	18	13824706	p11.21
SNP_A-1927595	T	T	341	5	338	24	12.106	5.00E-04	rs10503137	18	64817882	q22.1
SNP_A-1929764	G	G	290	32	270	66	12.218	5.00E-04	rs9322338	6	152292863	q25.1
SNP_A-1932136	T	T	318	16	291	41	12.156	5.00E-04	rs8017169	14	46325006	q21.3
SNP_A-1932235	T	T	273	89	263	149	12.133	5.00E-04	rs4712980	6	26463737	p22.1
SNP_A-1931187	A	A	354	0	346	12	12.069	5.00E-04	rs3007106	14	46437994	q21.3
SNP_A-1909382	T	C	188	168	246	166	12.044	5.00E-04	rs10189776	2	181855735	q31.3
SNP_A-1908329	T	T	301	65	295	117	12.241	5.00E-04	rs451743	11	21889104	p14.3
SNP_A-1907569	T	T	361	3	366	20	11.965	5.00E-04	rs7560081	2	62704890	p15
SNP_A-1912623	C	C	381	1	354	14	12.001	5.00E-04	rs11043886	12	8237144	p13.31
SNP_A-1911610	T	T	278	144	312	94	12.159	5.00E-04	rs10244229	7	54582532	p11.2
SNP_A-1917758	T	T	329	19	392	4	12.242	5.00E-04	rs1341552	1	228434720	q42.2
SNP_A-2265475	A	A	322	12	407	1	11.957	5.00E-04	rs7691921	4	114935493	q26
SNP_A-2271728	A	A	373	11	412	0	11.967	5.00E-04	rs2268637	6	39158896	p21.2
SNP_A-2271861	G	G	284	124	235	171	12.109	5.00E-04	rs17093914	14	74433394	q24.3
SNP_A-2256559	G	G	306	44	250	74	12.283	5.00E-04	rs6981452	8	37165208	p12
SNP_A-2262662	G	G	321	23	368	6	11.939	5.00E-04	rs16856233	3	172579984	q26.2
SNP_A-2283158	A	A	287	61	254	102	12.236	5.00E-04	rs4750833	10	132508509	q26.3
SNP_A-2275878	A	G	248	160	188	176	12.011	5.00E-04	rs7410918	1	224317536	q42.13
SNP_A-2278202	T	T	304	38	264	70	12.205	5.00E-04	rs11923552	3	183705456	q26.33
SNP_A-2241458	G	G	354	12	375	39	11.991	5.00E-04	rs1957325	14	84965914	q31.3
SNP_A-2238722	G	G	307	21	304	52	12.053	5.00E-04	rs17510039	2	185668463	q32.1
SNP_A-2236098	T	T	364	2	347	17	12.243	5.00E-04	rs11181012	12	40255795	q12
SNP_A-2235831	C	C	375	19	325	43	11.989	5.00E-04	rs17169886	7	34407948	p14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2254261	T	C	198	152	213	165	12.136	5.00E-04	rs10816010	9	8931155	p24.1
SNP_A-2297384	G	G	351	19	371	3	12.169	5.00E-04	rs9296709	6	53299101	p12.1
SNP_A-2295510	T	T	370	44	313	75	12.002	5.00E-04	rs11644114	16	17162085	p12.3
SNP_A-2295768	C	C	314	108	263	153	12.224	5.00E-04	rs7794120	7	55256357	p11.2
SNP_A-2310643	C	C	341	17	405	3	12.078	5.00E-04	rs7923605	10	3970337	p15.1
SNP_A-2312803	A	A	385	1	350	14	12.299	5.00E-04	rs6671413	1	10215950	p36.22
SNP_A-2306669	C	C	333	19	394	4	12.125	5.00E-04	---	4	7177013	p16.1
SNP_A-2294383	T	T	332	32	386	12	11.658	6.00E-04	rs16907215	11	9864874	p15.4
SNP_A-2288738	A	A	294	60	250	96	11.777	6.00E-04	rs2863725	11	46157456	p11.2
SNP_A-2254500	A	A	296	58	237	89	11.936	6.00E-04	rs568328	10	13121710	p13
SNP_A-2242396	A	A	300	22	302	54	11.805	6.00E-04	rs136611	22	44114820	q13.31
SNP_A-2245009	C	C	307	41	358	18	11.812	6.00E-04	rs2341615	6	168360698	q27
SNP_A-2249081	G	G	422	0	385	11	11.882	6.00E-04	rs16975300	18	1179386	p11.32
SNP_A-2248510	T	C	204	124	167	159	11.926	6.00E-04	rs7736970	5	17354984	p15.1
SNP_A-2238948	T	T	355	23	369	5	11.821	6.00E-04	rs6509615	19	34903661	q12
SNP_A-2240552	C	C	268	86	249	139	11.649	6.00E-04	rs4812631	20	40759541	q12
SNP_A-2279845	C	C	312	16	393	3	11.92	6.00E-04	rs4976403	5	136449090	q31.1
SNP_A-2265467	C	C	412	0	375	11	11.905	6.00E-04	rs9621599	22	31639512	q12.3
SNP_A-1910344	A	A	410	2	355	15	11.673	6.00E-04	rs11902626	2	127943782	q14.3
SNP_A-1896306	G	G	365	9	331	29	11.925	6.00E-04	rs17029894	3	31397018	p24.1
SNP_A-1890370	C	C	264	40	342	20	11.744	6.00E-04	rs6499591	16	71464505	q22.3
SNP_A-1902144	G	G	330	44	263	71	11.687	6.00E-04	rs7135417	12	126701115	q24.32
SNP_A-1900495	A	A	314	14	396	2	11.831	6.00E-04	rs1869320	1	21039641	p36.12
SNP_A-1903515	G	G	338	4	340	22	11.909	6.00E-04	rs16974057	18	36927318	q12.3
SNP_A-1951077	G	G	280	72	260	120	11.687	6.00E-04	rs2501870	1	158025642	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960584	A	A	417	1	363	13	11.836	6.00E-04	rs17132956	7	125376976	q31.33
SNP_A-1941566	G	G	338	46	372	20	11.789	6.00E-04	rs7810047	7	127946074	q32.1
SNP_A-1970683	C	C	297	35	350	14	11.895	6.00E-04	rs466019	22	16914156	q11.21
SNP_A-1964422	G	G	307	23	293	53	11.797	6.00E-04	rs4631686	1	14322780	p36.21
SNP_A-1980625	T	T	413	1	359	13	11.852	6.00E-04	---	1	200341536	q32.1
SNP_A-1985012	G	G	188	144	268	120	11.934	6.00E-04	rs330109	6	8491103	p24.3
SNP_A-1985388	T	T	318	12	395	1	11.72	6.00E-04	rs2000134	6	22413470	p22.3
SNP_A-1781298	T	T	261	73	330	46	11.738	6.00E-04	rs4578508	13	98096707	q32.2
SNP_A-1656259	A	A	309	83	338	46	11.831	6.00E-04	rs1364716	7	136220796	q33
SNP_A-1813643	G	G	318	14	398	2	11.723	6.00E-04	rs159322	2	201008965	q33.1
SNP_A-1813772	A	A	283	25	367	9	11.741	6.00E-04	rs9887913	1	55174401	p32.3
SNP_A-1813254	T	T	344	10	412	0	11.792	6.00E-04	rs1842908	11	18907713	p15.1
SNP_A-1808961	C	C	320	60	300	104	11.726	6.00E-04	rs11178295	12	69247103	q15
SNP_A-1803279	A	A	349	13	397	1	11.695	6.00E-04	rs10985612	9	122194957	q33.2
SNP_A-1792641	T	T	393	5	345	21	11.648	6.00E-04	rs6682578	1	89177535	p22.2
SNP_A-1787975	T	T	272	34	345	15	11.703	6.00E-04	rs10182925	2	29781856	p23.2
SNP_A-1786841	A	A	291	13	311	41	11.734	6.00E-04	rs7167441	15	95884503	q26.2
SNP_A-1832170	C	C	232	134	305	103	11.734	6.00E-04	rs10163683	18	53007600	q21.31
SNP_A-1830535	T	T	345	3	354	20	11.76	6.00E-04	rs3760556	18	54971080	q21.32
SNP_A-1836451	T	T	329	3	355	21	11.799	6.00E-04	rs9899296	17	63302865	q24.2
SNP_A-1836780	A	A	401	1	382	14	11.683	6.00E-04	rs11210904	1	43849900	p34.1
SNP_A-1843425	T	T	321	7	337	29	11.788	6.00E-04	rs9858143	3	76765445	p12.3
SNP_A-1821738	C	C	378	14	401	1	11.822	6.00E-04	rs6763169	3	384160	p26.3
SNP_A-1823887	C	T	212	140	202	184	11.678	6.00E-04	rs7716283	5	84438591	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1859170	T	T	370	16	402	2	11.811	6.00E-04	rs2177673	7	95879219	q21.3
SNP_A-1860640	T	T	377	11	414	0	11.9	6.00E-04	rs2514426	11	114286775	q23.2
SNP_A-1861883	C	C	358	40	360	14	11.789	6.00E-04	rs9533400	13	42596020	q14.11
SNP_A-1866017	T	T	380	34	348	66	11.647	6.00E-04	rs17499628	15	34791700	q14
SNP_A-1870613	A	A	342	10	406	0	11.688	6.00E-04	rs7105343	11	11184554	p15.3
SNP_A-2213115	C	C	268	14	389	3	11.763	6.00E-04	rs6540168	16	86680828	q24.2
SNP_A-2214877	T	T	207	121	291	97	11.866	6.00E-04	rs10917238	1	22557113	p36.12
SNP_A-2215306	T	T	355	41	291	69	11.78	6.00E-04	---	15	40497290	q15.1
SNP_A-2192592	A	A	347	17	401	3	11.647	6.00E-04	rs512920	1	74511289	p31.1
SNP_A-2172697	T	C	186	182	255	159	11.642	6.00E-04	rs13159024	5	85253325	q14.3
SNP_A-2173930	G	G	416	0	383	11	11.774	6.00E-04	rs3006934	1	239988343	q44
SNP_A-2170905	A	A	347	57	301	93	11.782	6.00E-04	rs1508729	3	3522685	p26.2
SNP_A-2177197	C	C	380	14	403	1	11.819	6.00E-04	rs3912444	16	21212772	p12.2
SNP_A-2182528	C	C	314	24	308	56	11.911	6.00E-04	rs17802978	9	4305908	p24.2
SNP_A-2149872	C	C	362	0	364	12	11.744	6.00E-04	rs2382286	9	11404732	p23
SNP_A-2142192	G	G	323	15	380	2	11.918	6.00E-04	rs7083119	10	80262503	q22.3
SNP_A-2160369	G	G	344	24	326	54	11.833	6.00E-04	rs9910447	17	31496575	q12
SNP_A-2126295	T	T	276	28	357	11	11.787	6.00E-04	rs17037442	4	159723181	q32.1
SNP_A-2137349	A	A	294	28	360	10	11.915	6.00E-04	rs923923	9	14754800	p22.3
SNP_A-2070539	G	G	282	18	385	5	11.714	6.00E-04	rs9891520	17	62600237	q24.2
SNP_A-2064477	T	T	371	17	378	2	11.825	6.00E-04	rs9920728	15	89417689	q26.1
SNP_A-2066593	T	T	337	31	289	59	11.842	6.00E-04	rs1555831	1	62490778	p31.3
SNP_A-2097509	T	T	377	11	408	0	11.729	6.00E-04	rs6432640	2	161326806	q24.2
SNP_A-2096874	G	G	343	19	400	4	11.888	6.00E-04	rs7009898	8	96888986	q22.1
SNP_A-2099943	C	C	231	137	303	105	11.909	6.00E-04	rs1873481	18	62060697	q22.1
SNP_A-2090561	C	C	337	3	327	19	11.735	6.00E-04	rs6745540	2	136298550	q21.3
SNP_A-2077711	C	C	302	16	377	3	11.765	6.00E-04	rs17044905	4	114027088	q25

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006924	T	T	348	2	345	17	11.656	6.00E-04	rs4241285	2	192639056	q32.3
SNP_A-1992372	T	T	329	13	375	1	11.708	6.00E-04	rs17119664	8	14430278	p22
SNP_A-1993122	C	C	322	16	401	3	11.749	6.00E-04	rs1000956	8	40836895	p11.21
SNP_A-2004273	A	A	321	39	347	15	11.673	6.00E-04	rs4777413	15	69675503	q23
SNP_A-1997934	T	T	367	11	400	0	11.807	6.00E-04	rs928179	9	122015264	q33.2
SNP_A-2000879	A	A	326	4	315	21	11.696	6.00E-04	rs4532864	1	243252640	q44
SNP_A-2043405	G	G	342	0	342	12	11.797	6.00E-04	rs8090916	18	59890849	q22.1
SNP_A-2045691	G	G	358	2	355	17	11.661	6.00E-04	rs10228188	7	19389035	p21.1
SNP_A-2040221	G	G	354	32	368	10	11.713	6.00E-04	rs6054393	20	661786	p13
SNP_A-2035432	G	G	280	80	330	48	11.666	6.00E-04	rs10216782	8	32354301	p12
SNP_A-2020812	A	A	352	16	291	37	11.848	6.00E-04	rs8133217	21	46887579	q22.3
SNP_A-2019880	A	A	414	0	377	11	11.9	6.00E-04	rs734198	21	41384893	q22.2
SNP_A-2021515	G	G	318	22	326	54	11.386	7.00E-04	rs13421583	2	146383366	q22.3
SNP_A-2023168	G	G	280	22	267	51	11.424	7.00E-04	rs2973962	5	119258697	q23.1
SNP_A-2030129	A	A	356	2	355	17	11.579	7.00E-04	rs6435077	2	202014480	q33.1
SNP_A-2030873	A	A	331	15	380	2	11.566	7.00E-04	rs9904357	17	12046678	p12
SNP_A-2030340	A	A	327	7	323	27	11.421	7.00E-04	rs16893076	5	24110799	p14.2
SNP_A-2005323	T	T	359	13	327	35	11.442	7.00E-04	rs8069028	17	74329058	q25.3
SNP_A-2003722	A	A	328	76	272	112	11.62	7.00E-04	rs814620	10	90412116	q23.31
SNP_A-1993307	T	T	382	10	357	31	11.582	7.00E-04	rs7844299	8	55124948	q11.23
SNP_A-2006171	T	T	280	30	348	12	11.41	7.00E-04	rs2710692	2	17696789	p24.2
SNP_A-2008252	T	T	258	110	335	81	11.506	7.00E-04	rs10500855	11	19518589	p15.1
SNP_A-2012608	C	C	262	136	289	87	11.474	7.00E-04	rs6967153	7	54576260	p11.2
SNP_A-2077500	A	A	328	88	356	50	11.49	7.00E-04	rs4535036	2	221137545	q35

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2091858	G	G	237	119	318	92	11.527	7.00E-04	rs1917366	7	123878437	q31.33
SNP_A-2090081	G	G	387	11	410	0	11.488	7.00E-04	rs16909971	8	140107823	q24.3
SNP_A-2103807	C	C	390	6	351	23	11.399	7.00E-04	rs16944651	16	83894004	q24.1
SNP_A-2098305	A	A	182	168	253	141	11.385	7.00E-04	rs17776	4	131888183	q28.3
SNP_A-2075331	C	C	408	0	385	11	11.491	7.00E-04	rs17046527	2	117445535	q14.1
SNP_A-2049344	A	A	264	158	213	205	11.519	7.00E-04	rs527346	12	3255015	p13.32
SNP_A-2049373	A	A	321	15	315	41	11.56	7.00E-04	rs6776063	3	180893044	q26.33
SNP_A-2052268	G	G	390	18	359	43	11.485	7.00E-04	rs430012	1	101675878	p21.2
SNP_A-2124078	T	T	344	10	404	0	11.565	7.00E-04	rs16865604	2	178381785	q31.2
SNP_A-2124088	A	A	375	11	400	0	11.561	7.00E-04	rs10979693	9	108956378	q31.3
SNP_A-2129211	C	C	391	27	360	56	11.407	7.00E-04	rs10751864	10	2312896	p15.3
SNP_A-2130484	G	G	358	2	359	17	11.501	7.00E-04	rs2942686	13	64278392	q21.31
SNP_A-2140515	C	C	363	27	311	53	11.579	7.00E-04	rs9607433	22	35955362	q13.1
SNP_A-2145271	C	C	322	12	391	1	11.424	7.00E-04	rs6446919	4	74558127	q13.3
SNP_A-2146522	C	T	206	158	230	184	11.436	7.00E-04	rs9614868	22	43086849	q13.31
SNP_A-2179875	C	C	337	5	346	24	11.484	7.00E-04	rs16860263	3	149460934	q24
SNP_A-2180606	T	T	303	47	335	21	11.496	7.00E-04	rs16835766	1	147074021	q21.2
SNP_A-2174250	A	A	402	2	355	15	11.388	7.00E-04	rs739763	17	29479160	q12
SNP_A-2185383	A	A	217	141	293	113	11.442	7.00E-04	rs11155338	6	144345925	q24.2
SNP_A-2218111	G	G	335	27	366	8	11.493	7.00E-04	rs6902317	6	47028034	p12.3
SNP_A-2200433	G	G	373	19	311	41	11.569	7.00E-04	rs2214762	7	119296194	q31.31
SNP_A-2199862	C	C	294	32	270	64	11.593	7.00E-04	rs6716436	2	206435635	q33.3
SNP_A-2201504	G	A	180	170	245	157	11.584	7.00E-04	rs7446072	5	84545996	q14.3
SNP_A-1870476	G	G	337	31	286	58	11.57	7.00E-04	rs16866417	2	7788630	p25.1
SNP_A-1865543	T	T	366	0	380	12	11.384	7.00E-04	rs7241870	18	60025790	q22.1
SNP_A-1858657	A	A	367	13	407	1	11.372	7.00E-04	rs7205016	16	34393084	p11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1854051	A	A	239	101	308	72	11.378	7.00E-04	rs2244977	5	152601853	q33.1
SNP_A-1855592	C	C	316	14	392	2	11.591	7.00E-04	rs16835040	1	149985712	q21.3
SNP_A-1824871	T	T	313	17	299	43	11.376	7.00E-04	rs10979176	9	107880953	q31.2
SNP_A-1823577	C	C	315	9	404	0	11.363	7.00E-04	rs6779333	3	155647840	q25.2
SNP_A-1823426	C	C	311	59	304	106	11.446	7.00E-04	rs1996372	4	130771299	q28.2
SNP_A-1827736	T	T	382	2	362	16	11.38	7.00E-04	rs16894178	5	61051585	q12.1
SNP_A-1826797	A	A	340	2	343	17	11.401	7.00E-04	rs6893103	5	164026314	q34
SNP_A-1821067	A	A	280	122	229	165	11.473	7.00E-04	rs534303	6	149652925	q25.1
SNP_A-1815430	A	A	256	64	339	41	11.558	7.00E-04	rs9384783	6	111442009	q21
SNP_A-1841107	A	A	368	6	282	20	11.377	7.00E-04	rs6778699	3	41745839	p22.1
SNP_A-1840744	T	T	215	165	284	132	11.603	7.00E-04	rs9401986	6	127978343	q22.33
SNP_A-1832753	G	G	401	1	361	13	11.39	7.00E-04	rs7716182	5	43926418	p12
SNP_A-1799987	T	T	321	23	389	7	11.448	7.00E-04	rs6022029	20	50708572	q13.2
SNP_A-1800435	A	A	309	23	280	50	11.408	7.00E-04	rs17045424	3	685110	p26.3
SNP_A-1810448	T	T	273	149	218	192	11.412	7.00E-04	rs2791559	1	215977198	q41
SNP_A-1812312	A	A	414	0	354	10	11.522	7.00E-04	rs10146749	14	21551607	q11.2
SNP_A-1701753	T	T	398	0	379	11	11.385	7.00E-04	rs3093432	1	204159336	q32.1
SNP_A-1986242	T	T	316	16	385	3	11.4	7.00E-04	---	6	65842965	q12
SNP_A-1979830	T	T	322	14	398	2	11.544	7.00E-04	rs17053500	4	168985418	q32.3
SNP_A-1977518	G	G	336	20	403	5	11.589	7.00E-04	rs3775781	4	70776397	q13.3
SNP_A-1968225	T	T	348	2	351	17	11.411	7.00E-04	rs10489840	1	155458040	q23.1
SNP_A-1973188	A	A	377	9	323	27	11.432	7.00E-04	rs16848541	1	172212949	q25.1
SNP_A-1955904	G	G	293	71	281	121	11.415	7.00E-04	rs12693604	2	192316938	q32.3
SNP_A-1903803	T	T	331	33	351	11	11.581	7.00E-04	rs4236016	6	22354583	p22.3
SNP_A-1902667	C	C	277	91	350	62	11.551	7.00E-04	rs7738617	6	100067168	q16.3
SNP_A-1900414	C	C	320	36	283	67	11.55	7.00E-04	rs2399106	3	107820260	q13.12
SNP_A-1890198	C	C	375	11	400	0	11.561	7.00E-04	rs4784275	16	51533865	q12.2
SNP_A-1893211	G	G	399	1	357	13	11.468	7.00E-04	rs12618556	2	21555242	p24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884630	A	A	359	45	326	80	11.385	7.00E-04	rs17060256	8	29411449	p12
SNP_A-1882900	C	C	388	6	347	23	11.51	7.00E-04	rs11826771	11	58265548	q12.1
SNP_A-1879868	T	T	378	10	340	30	11.59	7.00E-04	rs16977327	17	68203040	q24.3
SNP_A-1878960	T	A	200	170	239	173	11.372	7.00E-04	rs1478144	3	163729047	q26.1
SNP_A-1874497	C	C	272	52	247	91	11.55	7.00E-04	rs7768490	6	167165731	q27
SNP_A-1908098	C	A	222	140	195	187	11.496	7.00E-04	rs157640	20	52847946	q13.2
SNP_A-1905940	T	T	340	8	350	30	11.497	7.00E-04	rs4664865	2	157972824	q24.1
SNP_A-1906395	A	A	317	9	410	0	11.459	7.00E-04	rs8116793	20	7079781	p12.3
SNP_A-1923489	T	T	378	10	355	31	11.473	7.00E-04	rs9311462	3	51035468	p21.31
SNP_A-1925213	C	C	320	14	394	2	11.487	7.00E-04	rs17010813	4	127505188	q28.1
SNP_A-2265506	A	A	345	3	343	19	11.371	7.00E-04	rs10240279	7	105304036	q22.3
SNP_A-2268644	T	T	412	2	359	15	11.584	7.00E-04	---	3	52087014	p21.2
SNP_A-2271572	C	C	312	12	383	1	11.559	7.00E-04	rs16835850	2	137219713	q21.3
SNP_A-2279767	G	G	267	83	264	142	11.402	7.00E-04	rs8087306	18	9084245	p11.22
SNP_A-2278401	G	G	329	29	355	9	11.466	7.00E-04	rs17148215	9	131624439	q34.13
SNP_A-2283093	A	A	356	4	347	21	11.589	7.00E-04	rs17828395	18	48349460	q21.1
SNP_A-2282618	T	T	254	68	248	120	11.439	7.00E-04	rs443565	15	60575893	q22.2
SNP_A-2237917	C	C	257	105	243	167	11.585	7.00E-04	rs2654206	15	80199310	q25.2
SNP_A-2234761	A	A	414	6	388	24	11.567	7.00E-04	rs17114147	10	103394591	q24.32
SNP_A-2227975	A	A	410	0	383	11	11.605	7.00E-04	rs217779	5	37383243	p13.2
SNP_A-2232356	A	A	402	2	353	15	11.467	7.00E-04	rs4800336	18	17749666	q11.2
SNP_A-2242878	C	C	394	0	369	11	11.57	7.00E-04	rs17043438	2	52942471	p16.2
SNP_A-2253058	A	A	350	0	356	12	11.607	7.00E-04	rs17164893	7	11432887	p21.3
SNP_A-2299897	T	T	376	26	399	7	11.602	7.00E-04	rs1409707	9	84262297	q21.33
SNP_A-2298513	C	C	326	10	378	0	11.41	7.00E-04	rs935243	12	104026351	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2313767	A	A	412	0	385	11	11.602	7.00E-04	rs4647467	9	95041799	q22.32
SNP_A-2313690	T	T	367	11	366	34	11.144	8.00E-04	rs6119327	20	31208131	q11.21
SNP_A-2308625	C	C	286	64	269	109	11.166	8.00E-04	rs4140831	7	109622225	q31.1
SNP_A-2290644	A	A	258	66	320	40	11.164	8.00E-04	rs1471291	5	92635159	q15
SNP_A-2293278	A	A	389	11	347	31	11.307	8.00E-04	rs1009418	1	171761204	q25.1
SNP_A-2233694	C	C	228	122	305	95	11.2	8.00E-04	rs2479938	13	69677369	q21.33
SNP_A-2240472	G	G	360	0	380	12	11.199	8.00E-04	rs12041043	1	118780299	p12
SNP_A-2282628	C	C	308	62	305	111	11.24	8.00E-04	rs12416288	10	6996719	p14
SNP_A-2275224	G	G	380	16	396	2	11.214	8.00E-04	rs17012410	1	204905672	q32.2
SNP_A-2271644	A	A	335	15	306	38	11.242	8.00E-04	---	2	162954411	q24.2
SNP_A-2267308	C	C	339	29	363	9	11.326	8.00E-04	rs7932932	11	39908284	p12
SNP_A-1910819	T	T	356	0	372	12	11.308	8.00E-04	rs17042603	2	21710070	p24.1
SNP_A-1913554	A	A	364	0	353	11	11.169	8.00E-04	rs9938700	16	82065362	q23.3
SNP_A-1877224	G	G	289	59	297	111	11.325	8.00E-04	rs580940	3	62685640	p14.2
SNP_A-1880590	A	A	355	35	310	64	11.21	8.00E-04	rs10899121	11	75169851	q13.5
SNP_A-1896553	G	G	355	5	353	23	11.235	8.00E-04	rs16875449	8	108063754	q23.1
SNP_A-1961675	A	A	321	23	383	7	11.155	8.00E-04	rs405967	19	53284123	q13.32
SNP_A-1958406	A	A	310	18	368	4	11.149	8.00E-04	rs2127394	5	76795836	q13.3
SNP_A-1959846	C	C	329	39	336	80	11.303	8.00E-04	rs6748652	2	100198577	q11.2
SNP_A-1954497	T	T	358	20	291	41	11.213	8.00E-04	rs16882098	8	34369597	p12
SNP_A-1943083	G	G	290	34	376	16	11.228	8.00E-04	rs13175566	5	18486371	p15.1
SNP_A-1934517	A	A	326	14	394	2	11.226	8.00E-04	rs1893376	18	46917466	q21.1
SNP_A-1934777	G	G	348	34	271	57	11.35	8.00E-04	rs4959521	6	1118117	p25.3
SNP_A-1971109	T	T	271	85	179	101	11.264	8.00E-04	rs727563	22	40191877	q13.2
SNP_A-1971448	T	T	402	2	384	16	11.281	8.00E-04	rs1087894	3	4002766	p26.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1964237	G	G	329	35	336	74	11.334	8.00E-04	rs17437338	2	100124869	q11.2
SNP_A-1982034	C	C	373	45	337	79	11.143	8.00E-04	rs7536675	1	205340008	q32.2
SNP_A-1755448	G	G	398	0	387	11	11.154	8.00E-04	rs6575196	14	89945187	q32.12
SNP_A-1812544	G	G	347	1	367	15	11.251	8.00E-04	rs2294788	6	148903836	q24.3
SNP_A-1786948	A	A	298	40	280	76	11.274	8.00E-04	rs1027254	4	108475009	q25
SNP_A-1789867	C	C	288	130	326	86	11.272	8.00E-04	rs3848704	20	57574691	q13.32
SNP_A-1797451	A	A	332	16	308	40	11.186	8.00E-04	rs2144704	6	52664814	p12.2
SNP_A-1797217	G	G	326	14	396	2	11.298	8.00E-04	rs8179457	1	152436868	q22
SNP_A-1799868	A	A	342	6	341	25	11.2	8.00E-04	rs6429135	1	235849915	q43
SNP_A-1831547	T	T	265	61	260	110	11.352	8.00E-04	rs2255641	20	1461443	p13
SNP_A-1843891	G	G	369	13	403	1	11.176	8.00E-04	rs1958777	14	48986246	q21.3
SNP_A-1853642	T	T	274	28	277	63	11.268	8.00E-04	rs17012374	2	125756936	q14.3
SNP_A-1852543	G	G	231	139	209	205	11.329	8.00E-04	rs1019874	4	163199672	q32.2
SNP_A-1873816	A	A	277	23	303	59	11.263	8.00E-04	rs2416360	5	113368226	q22.3
SNP_A-2210894	G	G	396	4	353	19	11.25	8.00E-04	rs10998813	10	70900670	q22.1
SNP_A-2222923	G	G	333	37	276	64	11.305	8.00E-04	rs302864	17	54112583	q23.2
SNP_A-2192004	G	G	352	0	368	12	11.301	8.00E-04	rs16918682	8	58924560	q12.1
SNP_A-2194562	T	T	266	22	289	57	11.248	8.00E-04	rs6551449	3	90197024	p11.1
SNP_A-2171666	T	T	300	34	312	74	11.354	8.00E-04	rs12131061	1	223683043	q42.13
SNP_A-2140418	A	A	354	0	370	12	11.305	8.00E-04	rs3020824	4	55409970	q12
SNP_A-2139693	T	T	323	89	349	51	11.145	8.00E-04	rs11978828	7	136268687	q33
SNP_A-2160740	C	C	305	53	308	100	11.237	8.00E-04	rs7989438	13	75908264	q22.2
SNP_A-2159953	G	G	404	0	391	11	11.208	8.00E-04	rs306521	9	132562797	q34.13
SNP_A-2167469	T	T	355	5	336	22	11.221	8.00E-04	rs923193	2	180486573	q31.3
SNP_A-2129109	C	C	294	102	258	150	11.314	8.00E-04	rs815944	7	55289958	p11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123423	C	C	274	60	316	32	11.229	8.00E-04	rs16872023	4	21555757	p15.31
SNP_A-2135259	C	C	244	78	304	50	11.205	8.00E-04	rs335306	4	62210305	q13.1
SNP_A-2109819	A	A	315	41	326	84	11.23	8.00E-04	---	16	6006397	p13.3
SNP_A-2113848	T	T	378	0	361	11	11.344	8.00E-04	rs11831227	12	36789108	q12
SNP_A-2114347	A	A	384	12	373	35	11.239	8.00E-04	rs12703819	7	145643535	q35
SNP_A-2058059	G	G	354	0	374	12	11.187	8.00E-04	rs17051439	4	53213463	q12
SNP_A-2060282	G	G	387	11	402	0	11.265	8.00E-04	rs9310963	3	31270260	p24.1
SNP_A-2059327	T	T	328	4	325	21	11.29	8.00E-04	rs16928194	9	125307348	q33.3
SNP_A-2072671	G	G	311	13	294	36	11.22	8.00E-04	rs2881669	5	136211700	q31.1
SNP_A-2065156	C	C	331	33	383	13	11.155	8.00E-04	rs3890828	6	116046678	q22.1
SNP_A-2096118	C	C	356	18	375	3	11.187	8.00E-04	rs1504838	7	42587708	p14.1
SNP_A-2092940	G	G	297	47	325	21	11.196	8.00E-04	rs7044529	9	134793996	q34.3
SNP_A-2100742	G	G	389	11	402	0	11.209	8.00E-04	rs1479537	3	2616297	p26.3
SNP_A-2079093	A	A	422	0	372	10	11.186	8.00E-04	rs17127719	10	112416767	q25.2
SNP_A-2081890	A	G	189	141	202	162	11.287	8.00E-04	rs12607847	18	39100807	q12.3
SNP_A-2011257	C	C	369	13	405	1	11.24	8.00E-04	rs4958226	5	133175465	q31.1
SNP_A-1990259	C	C	326	38	327	77	11.175	8.00E-04	rs2159017	7	77960575	q21.11
SNP_A-2022407	T	T	305	23	297	53	11.246	8.00E-04	rs7068862	10	74726529	q22.2
SNP_A-2034364	T	T	364	0	386	12	11.15	8.00E-04	rs6715414	2	75210010	p12
SNP_A-2040258	C	C	336	24	385	7	11.311	8.00E-04	rs12252255	10	9284557	p14
SNP_A-2037835	T	T	237	119	313	91	11.248	8.00E-04	rs1539951	18	51072671	q21.2
SNP_A-2044470	A	A	285	73	359	47	11.165	8.00E-04	rs7017895	8	18258016	p22
SNP_A-2043176	C	C	301	11	397	1	11.285	8.00E-04	rs16955285	17	50302755	q22
SNP_A-2041546	C	C	239	89	305	61	11.187	8.00E-04	rs2353478	12	24895998	p12.1
SNP_A-2040194	A	A	363	9	332	28	10.946	9.00E-04	rs2041718	18	10102756	p11.22
SNP_A-2038751	C	C	300	58	288	102	10.996	9.00E-04	rs1359314	13	42286498	q14.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2020746	T	T	370	10	410	0	10.928	9.00E-04	rs7275401	21	46591690	q22.3
SNP_A-2025382	C	C	316	82	354	48	11.028	9.00E-04	rs7968423	12	89857298	q21.33
SNP_A-1990822	A	T	191	171	238	164	10.965	9.00E-04	rs342214	7	105918694	q22.3
SNP_A-1993402	T	T	260	102	315	69	10.99	9.00E-04	rs16921991	8	58386566	q12.1
SNP_A-2017963	G	G	308	26	344	8	11.052	9.00E-04	rs13433418	21	31594046	q22.11
SNP_A-2089878	G	G	356	38	319	69	10.964	9.00E-04	rs7114151	11	42367713	p12
SNP_A-2091485	G	G	414	2	373	15	11.115	9.00E-04	rs7870090	9	85632316	q21.33
SNP_A-2086841	A	A	297	47	312	20	11.041	9.00E-04	rs6478758	9	126678095	q33.3
SNP_A-2103201	A	A	347	1	348	14	10.996	9.00E-04	rs7917518	10	85020768	q23.1
SNP_A-2095308	T	T	371	13	399	1	10.982	9.00E-04	rs6989222	8	15471105	p22
SNP_A-2066609	T	T	380	0	373	11	11.044	9.00E-04	rs163204	12	61379915	q14.1
SNP_A-2067956	A	A	176	170	247	145	11.077	9.00E-04	rs2980248	8	76490475	q21.11
SNP_A-2071825	T	T	290	64	317	33	11.086	9.00E-04	rs16932405	11	15968818	p15.2
SNP_A-2061805	A	A	325	13	321	37	10.979	9.00E-04	rs4666983	2	185197069	q32.1
SNP_A-2050185	A	G	209	199	237	155	11.007	9.00E-04	rs2881270	8	31565252	p12
SNP_A-2110429	C	C	326	12	297	33	11.056	9.00E-04	rs16846320	2	162824507	q24.2
SNP_A-2109013	C	C	354	0	349	11	10.986	9.00E-04	rs12205704	6	47833773	p12.3
SNP_A-2117256	C	C	317	49	322	94	11.048	9.00E-04	rs1931064	1	97995875	p21.3
SNP_A-2132808	T	T	233	77	217	127	11.086	9.00E-04	rs16868637	4	19274132	p15.31
SNP_A-2132743	A	A	268	76	254	126	10.989	9.00E-04	rs6533835	4	79918137	q21.21
SNP_A-2131517	T	T	312	16	315	43	11.08	9.00E-04	---	4	111646628	q25
SNP_A-2127052	C	C	340	20	393	5	10.955	9.00E-04	rs12333519	7	66572039	q11.22
SNP_A-2127317	A	A	308	50	377	27	11.084	9.00E-04	rs4394609	1	22477824	p36.12
SNP_A-2155829	G	G	376	16	334	38	10.931	9.00E-04	rs553231	11	133686547	q25
SNP_A-2145465	C	C	331	77	370	44	11.127	9.00E-04	rs1001381	14	93388937	q32.13
SNP_A-2195436	A	A	410	4	369	19	11.109	9.00E-04	---	2	25701245	p23.3
SNP_A-2196300	A	A	328	10	315	31	10.927	9.00E-04	rs1460482	4	21178599	p15.31
SNP_A-2186305	C	C	310	32	369	13	10.972	9.00E-04	rs3931608	13	107206960	q33.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189382	C	C	335	43	343	17	10.929	9.00E-04	rs7918101	10	96459659	q23.33
SNP_A-2222558	C	C	332	16	395	3	11.053	9.00E-04	rs8003287	14	85481727	q31.3
SNP_A-2226456	T	T	305	111	255	153	11.069	9.00E-04	rs8055182	16	85385029	q24.1
SNP_A-2219311	T	T	329	9	406	0	10.943	9.00E-04	rs9353978	6	93772833	q16.1
SNP_A-2210385	T	T	395	9	345	27	11.078	9.00E-04	rs6488885	12	122644035	q24.31
SNP_A-2199903	C	C	342	10	386	0	11.117	9.00E-04	rs4412580	1	239347041	q43
SNP_A-1868720	T	T	319	25	372	8	11.06	9.00E-04	rs12074690	1	116294320	p13.1
SNP_A-1869340	T	T	340	12	403	1	11.125	9.00E-04	rs9385382	6	125990687	q22.31
SNP_A-1799184	C	C	331	9	339	31	10.947	9.00E-04	rs6049449	20	24086037	p11.21
SNP_A-1798343	A	A	354	0	351	11	10.925	9.00E-04	rs7775849	6	78968565	q14.1
SNP_A-1790698	A	A	378	8	340	26	11.016	9.00E-04	rs16941055	15	57214851	q22.2
SNP_A-1791483	T	T	331	9	408	0	10.932	9.00E-04	rs7561552	2	122655678	q14.3
SNP_A-1808756	A	A	192	162	258	132	11.025	9.00E-04	rs10146882	14	93794031	q32.13
SNP_A-1803495	T	T	319	9	396	0	11.003	9.00E-04	rs13336184	16	53899370	q12.2
SNP_A-1782929	C	C	296	28	286	60	11.098	9.00E-04	rs674757	8	142655235	q24.3
SNP_A-1685656	T	T	344	0	370	12	10.988	9.00E-04	rs10484807	6	110799158	q21
SNP_A-1971875	G	C	223	141	202	196	11.093	9.00E-04	rs1896822	3	16524898	p24.3
SNP_A-1970682	C	C	232	126	196	176	11.042	9.00E-04	rs462904	22	16901343	q11.21
SNP_A-1973154	A	A	375	25	342	52	10.942	9.00E-04	rs2128972	3	69510202	p14.1
SNP_A-1973305	A	A	299	9	294	30	10.952	9.00E-04	---	3	76371796	p12.3
SNP_A-1975031	C	C	306	18	299	45	11.064	9.00E-04	rs2088853	3	160351808	q25.32
SNP_A-1937809	C	C	329	9	298	28	11.076	9.00E-04	rs4016713	12	52784946	q13.13
SNP_A-1938559	T	T	206	120	261	87	11.032	9.00E-04	rs12699511	7	13342098	p21.2
SNP_A-1953989	T	T	252	54	285	27	10.971	9.00E-04	rs1378547	4	180711139	q34.3
SNP_A-1904163	T	T	334	12	393	1	11.029	9.00E-04	rs16975761	18	38066639	q12.3
SNP_A-1901526	A	A	341	19	376	4	10.959	9.00E-04	rs7561232	2	133240565	q21.2
SNP_A-1874908	A	A	335	9	317	29	11.018	9.00E-04	rs17123724	12	48202939	q13.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1908392	C	C	340	18	398	4	10.957	9.00E-04	rs7994297	13	32408096	q13.1
SNP_A-1905471	G	G	420	0	374	10	11.075	9.00E-04	rs16917065	11	91563799	q14.3
SNP_A-1930635	T	T	328	22	376	6	11.038	9.00E-04	rs9444240	6	85582214	q14.3
SNP_A-2272351	A	A	370	0	365	11	10.986	9.00E-04	rs16846805	4	72889792	q13.3
SNP_A-2256316	T	T	369	15	410	2	11.128	9.00E-04	rs13376651	1	206688886	q32.2
SNP_A-2276366	T	T	362	0	353	11	11.108	9.00E-04	rs853253	3	64298757	p14.1
SNP_A-2285860	C	C	284	54	273	97	11.038	9.00E-04	rs4537601	1	97945551	p21.3
SNP_A-2284672	A	A	338	4	339	21	11.107	9.00E-04	rs9323672	14	78687153	q31.1
SNP_A-2251235	C	C	352	0	374	12	11.124	9.00E-04	rs2245776	13	69659459	q21.33
SNP_A-2244101	C	C	285	109	316	68	10.969	9.00E-04	rs1498939	1	63284646	p31.3
SNP_A-2292463	C	C	360	2	350	16	11.008	9.00E-04	rs7626370	3	169892805	q26.2
SNP_A-2289743	G	G	331	9	408	0	10.932	9.00E-04	rs6508171	18	48637414	q21.2
SNP_A-2307306	T	T	391	9	371	29	11.051	9.00E-04	rs7171135	15	84280880	q25.3
SNP_A-2305501	G	G	417	3	375	17	11.075	9.00E-04	rs8038121	15	90775327	q26.1
SNP_A-2306350	T	T	346	2	342	16	10.773	0.001	rs17031315	4	155537682	q31.3
SNP_A-2293285	C	C	301	23	297	53	10.882	0.001	rs2274190	13	30695455	q12.3
SNP_A-2297003	T	T	413	1	387	13	10.893	0.001	rs16942398	15	87211486	q26.1
SNP_A-2244736	C	C	182	172	206	116	10.883	0.001	rs7185632	16	76987370	q23.1
SNP_A-2247108	G	G	337	9	414	0	10.898	0.001	rs4426771	4	15459250	p15.32
SNP_A-2245458	C	C	396	10	355	29	10.891	0.001	rs765030	14	89463462	q32.11
SNP_A-2254744	G	G	212	116	262	82	10.738	0.001	rs853789	2	169626995	q31.1
SNP_A-2239410	T	T	318	28	370	10	10.888	0.001	rs7023978	9	90978258	q22.2
SNP_A-2241524	C	C	312	16	326	44	10.886	0.001	rs424280	16	82298745	q23.3
SNP_A-2280676	G	G	332	26	287	51	10.823	0.001	rs505510	8	102991790	q22.3
SNP_A-2281518	A	A	321	5	342	24	10.838	0.001	rs6951316	7	63739771	q11.21
SNP_A-2277130	G	G	378	10	414	0	10.805	0.001	rs16940007	16	84511788	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2278417	T	T	277	79	264	130	10.86	0.001	rs2619569	3	2588613	p26.3
SNP_A-2268869	T	T	241	65	227	111	10.878	0.001	rs16851466	3	168995588	q26.1
SNP_A-2269381	C	C	280	30	357	13	10.819	0.001	rs1779565	14	83642260	q31.3
SNP_A-2265197	T	T	356	2	350	16	10.853	0.001	rs6828022	4	87775623	q21.3
SNP_A-2266378	A	A	275	37	262	72	10.817	0.001	rs9322291	6	151289758	q25.1
SNP_A-1924841	G	G	330	24	398	8	10.845	0.001	rs17413491	12	24306203	p12.1
SNP_A-1912875	A	A	369	17	403	3	10.799	0.001	rs8014553	14	97480360	q32.2
SNP_A-1884970	C	C	353	1	333	13	10.779	0.001	rs2850487	18	69844194	q22.3
SNP_A-1901775	T	T	358	30	334	60	10.787	0.001	rs2043873	2	135001473	q21.3
SNP_A-1900857	T	T	387	7	348	24	10.769	0.001	rs16848869	1	232216187	q42.3
SNP_A-1903915	C	C	405	1	350	12	10.829	0.001	rs16975226	18	37549779	q12.3
SNP_A-1897825	C	C	327	41	338	16	10.879	0.001	rs7924268	10	127086729	q26.13
SNP_A-1889684	T	T	301	9	320	32	10.863	0.001	rs16914467	11	88033488	q14.3
SNP_A-1956302	G	G	299	29	355	11	10.847	0.001	rs7562238	2	232227175	q37.1
SNP_A-1937053	T	T	243	31	331	15	10.841	0.001	rs1394825	5	102067327	q21.1
SNP_A-1970265	A	A	282	72	357	47	10.804	0.001	rs2835570	21	37361374	q22.13
SNP_A-1966051	A	A	258	68	332	44	10.918	0.001	rs17363057	2	179761678	q31.2
SNP_A-1986927	T	T	333	9	408	0	10.867	0.001	rs16873774	6	95609596	q16.1
SNP_A-1985816	A	A	374	10	410	0	10.813	0.001	rs16895425	6	42297280	p21.1
SNP_A-1645174	G	G	280	24	365	9	10.909	0.001	rs1537740	6	79974110	q14.1
SNP_A-1807275	T	T	372	10	406	0	10.765	0.001	rs17009828	2	74439944	p13.1
SNP_A-1805033	G	G	344	2	363	17	10.784	0.001	rs17068201	18	57163666	q21.33
SNP_A-1807705	G	G	309	11	391	1	10.768	0.001	rs6044923	20	17565531	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813604	A	A	418	0	380	10	10.852	0.001	rs10921292	1	189643674	q31.2
SNP_A-1787324	C	C	325	1	328	14	10.903	0.001	rs2162588	7	124663658	q31.33
SNP_A-1793422	C	C	312	82	353	49	10.761	0.001	rs17422332	1	100627779	p21.2
SNP_A-1868586	T	T	418	0	380	10	10.852	0.001	rs2298420	3	38298192	p22.2
SNP_A-1873005	T	T	348	12	405	1	10.899	0.001	rs16916587	8	52681230	q11.22
SNP_A-1863392	A	A	369	25	391	7	10.742	0.001	rs12059447	1	215076981	q41
SNP_A-1854496	A	A	409	1	356	12	10.744	0.001	rs16974789	18	37335287	q12.3
SNP_A-1854336	T	T	303	19	301	47	10.893	0.001	rs751060	5	38229443	p13.2
SNP_A-1856109	G	G	311	19	377	5	10.758	0.001	rs16822475	3	192623175	q28
SNP_A-1856644	C	C	320	8	327	29	10.867	0.001	rs13402277	2	55474204	p16.1
SNP_A-1851398	T	T	274	94	346	66	10.814	0.001	rs17746240	18	32224345	q12.2
SNP_A-1832547	A	A	259	157	210	202	10.741	0.001	rs7944560	11	8773852	p15.4
SNP_A-1815107	G	G	319	17	394	4	10.777	0.001	rs2276211	18	72709768	q23
SNP_A-1818397	C	C	360	2	354	16	10.853	0.001	rs17041311	4	111339215	q25
SNP_A-1820258	T	T	261	23	289	59	10.861	0.001	rs17041582	3	512682	p26.3
SNP_A-2209335	C	C	214	120	279	91	10.743	0.001	rs1385899	6	76993742	q14.1
SNP_A-2214474	T	T	307	17	285	41	10.743	0.001	rs2275279	1	228033829	q42.2
SNP_A-2225056	C	C	298	30	341	11	10.865	0.001	rs16997162	22	35399448	q12.3
SNP_A-2221247	G	G	342	18	364	48	10.869	0.001	rs12278864	11	84077677	q14.1
SNP_A-2221777	A	A	284	28	281	61	10.899	0.001	rs17032628	2	66982778	p14
SNP_A-2174429	G	G	306	60	306	108	10.801	0.001	rs585019	4	130772143	q28.2
SNP_A-2174600	A	A	374	20	386	4	10.836	0.001	rs6952478	7	132334314	q33
SNP_A-2178274	C	C	364	10	400	0	10.835	0.001	rs1357177	8	84346612	q21.13
SNP_A-2141041	G	G	416	0	380	10	10.801	0.001	rs16940016	16	23229946	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2144523	T	T	176	174	250	152	10.795	0.001	rs6972755	7	12459434	p21.3
SNP_A-2166053	G	G	318	16	300	40	10.757	0.001	rs9503930	6	4085809	p25.2
SNP_A-2124697	T	T	309	19	377	5	10.863	0.001	rs17058231	13	60043896	q21.2
SNP_A-2117519	C	C	376	10	414	0	10.861	0.001	rs6861923	5	4976555	p15.32
SNP_A-2120385	C	C	345	19	320	44	10.86	0.001	rs8024527	15	20688804	q11.2
SNP_A-2110884	A	A	205	143	279	117	10.862	0.001	rs10764274	10	21051062	p12.31
SNP_A-2057572	A	A	207	157	284	132	10.819	0.001	rs9815477	3	118889150	q13.31
SNP_A-2072481	C	C	331	9	402	0	10.772	0.001	rs974478	7	35987467	p14.2
SNP_A-2067637	A	A	370	10	406	0	10.822	0.001	rs1462882	8	32053536	p12
SNP_A-2064905	C	C	290	110	329	71	10.861	0.001	rs6057633	20	30790437	q11.21
SNP_A-2099801	A	A	291	45	353	23	10.874	0.001	rs13079772	3	190559625	q28
SNP_A-2104148	G	G	401	1	344	12	10.917	0.001	rs9900134	17	68825872	q25.1
SNP_A-2107345	G	G	341	9	327	29	10.77	0.001	rs17242578	14	19854271	q11.2
SNP_A-2086938	G	G	378	10	418	0	10.909	0.001	---	1	84988307	p22.3
SNP_A-2085407	G	G	343	25	367	7	10.888	0.001	rs14039900	2	168025498	q24.3
SNP_A-2083457	G	G	377	13	401	1	10.847	0.001	rs16993344	19	5986621	p13.3
SNP_A-2083504	C	C	306	18	287	43	10.801	0.001	rs16956111	16	54707079	q12.2
SNP_A-2077966	C	C	307	13	394	2	10.92	0.001	rs2668939	1	41875566	p34.2
SNP_A-2011567	A	A	335	9	412	0	10.909	0.001	rs17157735	11	62605274	q12.3
SNP_A-1994578	G	G	283	81	271	133	10.842	0.001	rs10505096	8	108251398	q23.1
SNP_A-1996107	T	T	371	5	341	21	10.849	0.001	rs2244328	9	18249823	p22.2
SNP_A-1997824	T	T	297	33	322	74	10.809	0.001	rs4510935	9	117364905	q33.1
SNP_A-2030509	G	G	337	9	412	0	10.846	0.001	rs10270799	7	80675452	q21.11
SNP_A-2035492	G	G	394	4	361	19	10.814	0.001	rs6726624	2	28819611	p23.2
SNP_A-2044654	A	A	319	41	277	71	10.795	0.001	rs12268338	10	74956812	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041026	C	C	309	93	345	57	10.622	1.10E-03	rs7647284	3	133415659	q22.1
SNP_A-2040291	T	T	315	67	276	104	10.574	1.10E-03	rs2794563	6	2553795	p25.2
SNP_A-2033050	G	G	408	0	380	10	10.594	1.10E-03	rs7116456	11	23911889	p14.3
SNP_A-2029277	A	A	324	58	254	84	10.589	1.10E-03	rs6911463	6	4547820	p25.1
SNP_A-2027111	A	A	364	0	404	12	10.664	1.10E-03	rs16910733	11	23145664	p14.3
SNP_A-2024159	C	C	342	22	384	6	10.689	1.10E-03	rs11183840	12	45994754	q13.11
SNP_A-2021648	A	-	215	131	183	183	10.631	1.10E-03	rs1492632	4	189344900	q35.2
SNP_A-1990254	G	G	334	42	362	18	10.706	1.10E-03	rs17439220	7	77863960	q21.11
SNP_A-2011736	G	G	316	26	346	8	10.685	1.10E-03	rs2492922	6	42247701	p21.1
SNP_A-2008010	A	A	401	3	371	17	10.647	1.10E-03	rs6486262	11	15699441	p15.2
SNP_A-2013244	G	G	385	13	405	1	10.714	1.10E-03	rs7814798	8	17312380	p22
SNP_A-2080145	C	C	329	21	314	48	10.716	1.10E-03	rs7320453	13	27679775	q12.2
SNP_A-2083784	T	T	347	15	346	40	10.606	1.10E-03	---	1	44791118	p34.1
SNP_A-2086148	A	A	339	77	360	42	10.689	1.10E-03	rs17138420	11	78868505	q14.1
SNP_A-2099093	G	G	304	20	279	45	10.687	1.10E-03	rs669118	18	8712062	p11.22
SNP_A-2064258	G	G	238	118	322	94	10.719	1.10E-03	rs1539950	18	51072604	q21.2
SNP_A-2075564	T	T	321	23	373	7	10.666	1.10E-03	rs17114354	12	73578213	q21.1
SNP_A-2061234	G	G	307	9	352	34	10.734	1.10E-03	rs12071289	1	155756813	q23.1
SNP_A-2116841	G	G	284	110	321	71	10.661	1.10E-03	rs11083788	19	51125731	q13.32
SNP_A-2118209	A	A	323	27	363	9	10.672	1.10E-03	rs10971563	9	33547023	p13.3
SNP_A-2127733	C	C	389	3	336	16	10.649	1.10E-03	rs17065613	8	985771	p23.3
SNP_A-2131023	G	G	294	14	297	39	10.61	1.10E-03	rs4394984	14	27129186	q12
SNP_A-2143833	G	G	335	9	402	0	10.646	1.10E-03	---	14	33276491	q13.1
SNP_A-2150709	C	C	230	128	302	100	10.671	1.10E-03	rs12781461	10	82915023	q23.1
SNP_A-2195619	A	A	332	2	332	16	10.606	1.10E-03	rs9657990	1	7926563	p36.23
SNP_A-2194826	G	G	263	27	377	13	10.732	1.10E-03	rs12183351	6	72351904	q13
SNP_A-2227239	C	C	304	36	360	16	10.632	1.10E-03	rs419695	4	167604122	q32.3
SNP_A-2214254	T	T	343	73	377	41	10.583	1.10E-03	rs7545834	1	54546381	p32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215640	A	A	305	63	358	36	10.726	1.10E-03	rs9258187	6	29803579	p22.1
SNP_A-2217087	A	A	403	3	373	17	10.642	1.10E-03	rs6560010	9	87483124	q21.33
SNP_A-2217355	A	A	406	0	376	10	10.653	1.10E-03	rs968032	20	58361874	q13.33
SNP_A-2208862	T	T	335	9	400	0	10.593	1.10E-03	rs7242067	18	54279498	q21.31
SNP_A-2207479	G	G	206	162	280	136	10.637	1.10E-03	rs7220992	17	66247287	q24.3
SNP_A-2212085	A	A	345	29	382	10	10.722	1.10E-03	rs4498257	5	43452780	p12
SNP_A-2200481	G	G	331	31	361	11	10.69	1.10E-03	rs17086916	13	28093457	q12.3
SNP_A-2201978	C	C	231	187	277	141	10.617	1.10E-03	rs4812258	20	59064296	q13.33
SNP_A-2202762	G	G	343	9	412	0	10.66	1.10E-03	rs618263	6	44676743	p21.1
SNP_A-1828238	A	A	343	13	292	32	10.636	1.10E-03	rs7640235	3	58643305	p14.2
SNP_A-1823359	G	G	408	2	354	14	10.59	1.10E-03	rs10732537	12	8869927	p13.31
SNP_A-1841287	G	G	315	15	393	3	10.681	1.10E-03	rs7789670	7	134947279	q33
SNP_A-1846413	T	T	257	75	328	50	10.682	1.10E-03	rs4912575	3	185706632	q27.1
SNP_A-1854981	G	G	373	17	401	3	10.569	1.10E-03	rs11808288	1	227242139	q42.2
SNP_A-1862677	G	C	216	188	230	166	10.686	1.10E-03	rs9616306	22	48150647	q13.33
SNP_A-1870922	T	T	384	10	416	0	10.69	1.10E-03	rs16976429	17	66655599	q24.3
SNP_A-1868449	G	G	323	45	363	21	10.724	1.10E-03	rs10939525	4	13590728	p15.33
SNP_A-1868094	G	G	345	9	412	0	10.599	1.10E-03	rs16827699	1	22945435	p36.12
SNP_A-1867603	G	G	335	9	400	0	10.593	1.10E-03	rs9559130	13	107118698	q33.3
SNP_A-1799703	T	T	406	2	379	15	10.629	1.10E-03	rs7703898	5	142955641	q31.3
SNP_A-1797688	G	G	386	10	418	0	10.687	1.10E-03	rs7534649	1	185912812	q31.1
SNP_A-1787603	A	A	374	10	406	0	10.708	1.10E-03	rs16961446	17	60646300	q24.1
SNP_A-1811758	T	T	278	16	364	4	10.581	1.10E-03	rs16949769	16	77766088	q23.1
SNP_A-1803491	G	G	313	11	391	1	10.613	1.10E-03	rs12302279	12	61413726	q14.2
SNP_A-1679432	T	T	247	139	306	104	10.622	1.10E-03	rs2221833	1	217471163	q41

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1722050	G	G	385	1	369	13	10.605	1.10E-03	-	16	80634320	q23.2
SNP_A-1988167	G	G	307	13	388	2	10.71	1.10E-03	rs17083966	6	153791065	q25.2
SNP_A-1981061	C	C	329	9	398	0	10.729	1.10E-03	rs16898305	5	29000881	p14.1
SNP_A-1969510	C	C	316	22	306	50	10.59	1.10E-03	rs2842008	1	159750302	q23.3
SNP_A-1941831	T	T	315	35	386	16	10.725	1.10E-03	rs17036142	4	106992340	q24
SNP_A-1891081	A	A	371	15	396	2	10.575	1.10E-03	rs17119757	8	14440301	p22
SNP_A-1894676	C	C	310	18	358	4	10.709	1.10E-03	rs1562356	11	3164015	p15.4
SNP_A-1903727	G	G	364	0	402	12	10.716	1.10E-03	rs10027838	4	118629572	q26
SNP_A-1912736	T	T	320	6	342	26	10.729	1.10E-03	rs7942093	11	64018362	q13.1
SNP_A-1917810	A	A	407	7	370	24	10.596	1.10E-03	rs17098148	14	60762952	q23.1
SNP_A-1908325	C	C	382	8	352	26	10.571	1.10E-03	rs11118629	1	217507807	q41
SNP_A-1930763	G	G	338	18	328	44	10.707	1.10E-03	rs2280479	12	51448905	q13.13
SNP_A-1932446	A	A	302	102	262	146	10.624	1.10E-03	rs3135093	4	2357534	p16.3
SNP_A-2263560	A	A	297	25	289	55	10.644	1.10E-03	---	8	126802296	q24.13
SNP_A-2275719	C	C	362	30	361	9	10.683	1.10E-03	rs5764076	22	42784346	q13.31
SNP_A-2282099	T	T	285	59	360	36	10.688	1.10E-03	rs209003	6	62892232	q11.1
SNP_A-2232328	G	G	304	50	270	84	10.641	1.10E-03	rs747513	14	73755728	q24.3
SNP_A-2248049	C	T	236	182	224	184	10.663	1.10E-03	rs6787987	3	96760311	q11.2
SNP_A-2242659	C	C	415	1	362	12	10.72	1.10E-03	rs17132433	4	2274886	p16.3
SNP_A-2241641	G	G	274	126	227	169	10.657	1.10E-03	rs4520719	13	56496046	q21.1
SNP_A-2295342	G	G	341	9	412	0	10.721	1.10E-03	rs3964884	10	51456143	q11.23
SNP_A-2294266	A	A	367	13	385	1	10.67	1.10E-03	---	19	37959375	q13.11
SNP_A-2306479	C	C	379	15	406	2	10.629	1.10E-03	rs7792937	7	150855016	q36.1
SNP_A-2304729	A	A	187	141	267	121	10.671	1.10E-03	rs380181	5	172956532	q35.2
SNP_A-2310793	C	C	365	27	309	51	10.695	1.10E-03	rs12003954	9	136198945	q34.3
SNP_A-2312591	C	C	357	1	345	13	10.491	1.20E-03	rs17097797	14	98313268	q32.2
SNP_A-2296276	T	T	246	124	317	95	10.569	1.20E-03	rs4800988	18	51070904	q21.2
SNP_A-2242798	T	T	344	24	377	7	10.497	1.20E-03	rs6882742	5	159790342	q33.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2245941	T	T	345	21	325	47	10.49	1.20E-03	rs4765359	12	123198401	q24.31
SNP_A-2231683	T	T	246	110	319	83	10.456	1.20E-03	---	7	13564218 3	q33
SNP_A-2240390	C	C	302	36	285	69	10.499	1.20E-03	rs4604247	6	91178246	q15
SNP_A-2274093	A	A	317	13	396	2	10.56	1.20E-03	rs1990513	2	210842605	q34
SNP_A-2277587	C	C	380	10	404	0	10.491	1.20E-03	rs17061338	3	59848083	p14.2
SNP_A-1927400	G	G	285	79	280	132	10.428	1.20E-03	rs324198	11	21963504	p14.3
SNP_A-1920976	G	G	220	62	206	106	10.496	1.20E-03	rs881729	18	57484139	q21.33
SNP_A-1919661	C	C	405	7	370	24	10.506	1.20E-03	rs1702217	10	132367305	q26.3
SNP_A-1910667	C	C	276	30	347	13	10.503	1.20E-03	rs7183419	15	98676967	q26.3
SNP_A-1906776	A	A	328	4	324	20	10.481	1.20E-03	rs6502807	17	4528593	p13.2
SNP_A-1915790	T	T	305	105	257	145	10.422	1.20E-03	rs16961675	17	17266676	p11.2
SNP_A-1891458	G	C	215	193	237	167	10.514	1.20E-03	rs1231463	9	129418683	q34.11
SNP_A-1882446	G	G	349	17	373	3	10.465	1.20E-03	rs7916138	10	54596668	q21.1
SNP_A-1942791	C	C	377	7	344	24	10.497	1.20E-03	rs6505347	17	28847221	q12
SNP_A-1934160	T	T	281	29	367	13	10.516	1.20E-03	rs9828305	3	40900533	p22.1
SNP_A-1960515	A	A	325	9	341	31	10.469	1.20E-03	rs17046464	4	115018743	q26
SNP_A-1951903	G	G	318	36	271	63	10.542	1.20E-03	rs16850409	1	14581191	p36.21
SNP_A-1949975	T	T	359	1	349	13	10.421	1.20E-03	rs11067069	12	113257839	q24.21
SNP_A-1948506	T	T	321	11	399	1	10.558	1.20E-03	rs12318283	12	112424461	q24.13
SNP_A-1974608	G	G	367	15	388	2	10.444	1.20E-03	rs16852701	3	144038239	q23
SNP_A-1975556	G	G	350	16	401	3	10.508	1.20E-03	rs924019	3	186276958	q27.2
SNP_A-1979580	T	T	241	81	224	130	10.509	1.20E-03	rs7678486	4	159498426	q32.1
SNP_A-1987168	T	T	306	30	286	60	10.531	1.20E-03	rs846974	6	108052999	q21
SNP_A-1985957	T	T	250	48	317	27	10.555	1.20E-03	rs17163098	1	218965550	q41

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1985308	C	C	253	67	297	39	10.532	1.20E-03	rs1580731	6	19481304	p22.3
SNP_A-1697354	G	G	400	0	376	10	10.496	1.20E-03	rs241291	1	225946964	q42.13
SNP_A-1652496	T	T	236	122	223	187	10.569	1.20E-03	rs269999	6	128110740	q22.33
SNP_A-1661670	T	T	348	10	343	31	10.448	1.20E-03	rs10486488	7	25729810	p15.2
SNP_A-1814079	G	G	332	36	356	14	10.512	1.20E-03	rs10970669	9	31998079	p21.1
SNP_A-1862793	T	T	349	9	414	0	10.531	1.20E-03	rs6434477	2	192232390	q32.3
SNP_A-1864790	C	C	245	103	230	160	10.471	1.20E-03	rs643541	4	130768282	q28.2
SNP_A-1853398	T	C	223	177	210	166	10.434	1.20E-03	rs2188783	17	65184676	q24.3
SNP_A-1846172	A	A	363	43	378	18	10.426	1.20E-03	rs1014737	6	41130695	p21.1
SNP_A-1829733	T	T	256	84	326	58	10.545	1.20E-03	rs2287584	5	31458764	p13.3
SNP_A-2200391	T	T	311	11	387	1	10.564	1.20E-03	rs7027009	9	134690140	q34.2
SNP_A-2204438	G	G	327	11	405	1	10.518	1.20E-03	rs3917485	7	94595123	q21.3
SNP_A-2218197	T	T	350	2	354	16	10.469	1.20E-03	rs16978283	18	40971481	q12.3
SNP_A-2224770	T	C	173	167	230	146	10.499	1.20E-03	rs1626391	13	98129569	q32.2
SNP_A-2195765	A	A	364	2	366	16	10.557	1.20E-03	rs1134070	6	127562222	q22.33
SNP_A-2197423	G	G	341	9	402	0	10.462	1.20E-03	---	4	109901023	q25
SNP_A-2182228	C	C	311	11	387	1	10.564	1.20E-03	rs11989216	8	108909893	q23.1
SNP_A-2149485	A	A	328	20	305	45	10.445	1.20E-03	rs16835146	3	125375040	q21.1
SNP_A-2143104	G	G	374	10	400	0	10.551	1.20E-03	rs7113200	11	93019243	q21
SNP_A-2156923	G	G	258	54	326	32	10.437	1.20E-03	rs16920456	12	33013480	p11.21
SNP_A-2154299	T	T	365	43	334	76	10.521	1.20E-03	rs307124	18	35881996	q12.3
SNP_A-2153316	C	C	256	104	242	162	10.541	1.20E-03	rs3850477	4	113181069	q25
SNP_A-2134347	T	T	363	1	378	14	10.548	1.20E-03	rs17053180	9	87435928	q21.33
SNP_A-2126576	T	T	325	13	404	2	10.5	1.20E-03	rs16925103	10	25195488	p12.1
SNP_A-2099052	A	A	399	13	413	1	10.522	1.20E-03	rs16850420	2	214181196	q34
SNP_A-2105303	A	A	242	68	286	40	10.53	1.20E-03	rs11230668	11	55209410	q11
SNP_A-1995581	T	T	281	53	279	97	10.466	1.20E-03	rs656414	9	2525695	p24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2024408	C	C	319	13	396	2	10.477	1.20E-03	rs1500700	3	98409238	q11.2
SNP_A-2026146	A	A	280	72	278	124	10.534	1.20E-03	rs7772505	6	99773026	q16.2
SNP_A-2020622	G	G	289	51	285	93	10.296	1.30E-03	rs1556329	21	45736814	q22.3
SNP_A-2040103	T	T	263	53	322	30	10.414	1.30E-03	rs17120701	12	57065848	q14.1
SNP_A-2015680	A	A	380	10	336	28	10.346	1.30E-03	rs1475854	21	18018805	q21.1
SNP_A-2005481	C	C	337	39	331	75	10.287	1.30E-03	rs7506596	18	13584999	p11.21
SNP_A-2101040	G	G	313	13	386	2	10.385	1.30E-03	rs12935938	17	68829578	q25.1
SNP_A-2095479	C	C	296	12	396	2	10.288	1.30E-03	rs17174558	12	32886096	p11.21
SNP_A-2084743	C	C	358	0	373	11	10.41	1.30E-03	rs17029602	4	154361257	q31.3
SNP_A-2080880	C	C	358	8	347	27	10.401	1.30E-03	rs9486046	6	105725669	q21
SNP_A-2059381	T	T	206	154	282	130	10.409	1.30E-03	rs9401988	6	127988966	q22.33
SNP_A-2058998	C	C	284	50	271	89	10.287	1.30E-03	rs9881429	3	195951288	q29
SNP_A-2075095	C	A	213	193	240	168	10.412	1.30E-03	rs10776910	9	134934905	q34.3
SNP_A-2126323	A	A	331	9	336	30	10.402	1.30E-03	---	9	22232055	p21.3
SNP_A-2135788	T	T	236	160	282	118	10.41	1.30E-03	rs10742809	11	5819108	p15.4
SNP_A-2131099	A	A	298	62	359	37	10.286	1.30E-03	rs11214457	11	112392326	q23.1
SNP_A-2131742	C	C	334	64	371	35	10.358	1.30E-03	rs17518342	1	215524681	q41
SNP_A-2120647	T	T	338	22	323	49	10.414	1.30E-03	rs13391425	2	34048121	p22.3
SNP_A-2158175	G	G	272	82	262	134	10.386	1.30E-03	rs534032	6	54538599	p12.1
SNP_A-2173862	T	T	363	1	357	13	10.287	1.30E-03	rs432800	13	92664850	q31.3
SNP_A-2171779	G	G	260	62	329	39	10.3	1.30E-03	rs11161189	15	23333359	q12
SNP_A-2193717	G	G	299	11	288	32	10.306	1.30E-03	---	14	53869191	q22.2
SNP_A-2214037	G	G	358	36	331	67	10.368	1.30E-03	rs10779456	1	218341452	q41
SNP_A-2200084	C	C	220	144	279	111	10.362	1.30E-03	rs10934410	3	118888107	q13.31
SNP_A-2199781	T	T	337	11	409	1	10.28	1.30E-03	rs29376	4	114560851	q26
SNP_A-1834010	T	T	328	10	325	31	10.31	1.30E-03	rs11769840	7	95843852	q21.3
SNP_A-1824727	T	T	348	0	367	11	10.283	1.30E-03	rs270096	8	3214326	p23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1819480	T	T	351	9	408	0	10.321	1.30E-03	rs12094972	1	53097313	p32.3
SNP_A-1818469	A	A	420	0	361	9	10.334	1.30E-03	rs16908474	9	92455531	q22.31
SNP_A-1853408	A	A	319	47	307	85	10.29	1.30E-03	rs991833	12	69246177	q15
SNP_A-1852717	A	A	286	64	342	38	10.406	1.30E-03	rs7039690	9	8510287	p24.1
SNP_A-1864466	G	G	383	23	332	46	10.318	1.30E-03	rs16942375	17	53202965	q23.2
SNP_A-1866457	G	G	346	20	316	44	10.311	1.30E-03	rs3926668	22	23819692	q11.23
SNP_A-1866562	C	C	331	11	405	1	10.374	1.30E-03	rs16858538	1	163834318	q24.1
SNP_A-1860078	T	T	333	11	405	1	10.303	1.30E-03	rs9396637	6	16151543	p22.3
SNP_A-1788589	G	G	253	113	240	174	10.393	1.30E-03	rs470506	12	127965990	q24.32
SNP_A-1790141	G	G	381	15	342	36	10.338	1.30E-03	rs6894984	5	4960084	p15.32
SNP_A-1695965	G	G	227	103	280	72	10.333	1.30E-03	rs9299542	10	79286268	q22.3
SNP_A-1985534	C	T	199	193	247	161	10.323	1.30E-03	rs9295695	6	26636229	p22.1
SNP_A-1988143	T	T	301	47	311	91	10.358	1.30E-03	rs1282444	6	153157438	q25.2
SNP_A-1980710	A	A	323	11	395	1	10.362	1.30E-03	rs10513089	5	11455654	p15.2
SNP_A-1959582	G	G	331	11	403	1	10.314	1.30E-03	rs6026852	20	57408113	q13.32
SNP_A-1945355	C	C	187	145	244	114	10.284	1.30E-03	rs7701077	5	85827641	q14.3
SNP_A-1947367	G	G	361	39	281	61	10.338	1.30E-03	rs11074830	16	26917990	p12.1
SNP_A-1879182	G	G	233	135	215	199	10.317	1.30E-03	rs4916078	1	60845462	p31.3
SNP_A-1892891	G	G	316	34	320	70	10.355	1.30E-03	rs1041857	14	21081056	q11.2
SNP_A-1902191	G	G	291	87	236	120	10.351	1.30E-03	rs2786619	1	217113185	q41
SNP_A-1907018	T	T	269	41	355	23	10.295	1.30E-03	rs3858847	13	32163824	q13.1
SNP_A-1905606	C	C	357	3	381	19	10.34	1.30E-03	rs11947396	4	88016644	q21.3
SNP_A-1923550	C	C	192	116	239	83	10.292	1.30E-03	rs2135382	18	60511242	q22.1
SNP_A-1929305	A	A	321	19	311	45	10.358	1.30E-03	rs17122692	12	58289000	q14.1
SNP_A-2276602	A	A	372	10	328	28	10.389	1.30E-03	rs3896537	19	59520927	q13.42
SNP_A-2269634	T	T	363	1	355	13	10.353	1.30E-03	rs17132783	5	110466338	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2236263	C	C	281	83	353	57	10.308	1.30E-03	rs2621462	4	96604676	q22.3
SNP_A-2230095	A	A	280	62	265	105	10.4	1.30E-03	rs17059190	6	99695609	q16.2
SNP_A-2252753	G	G	368	10	352	30	10.335	1.30E-03	rs16829591	2	134427050	q21.2
SNP_A-2251087	G	G	323	15	395	3	10.398	1.30E-03	rs17153283	7	105780436	q22.3
SNP_A-2305374	T	T	296	58	232	84	10.396	1.30E-03	rs17011474	3	22510871	p24.3
SNP_A-2311158	T	T	360	0	381	11	10.252	0.0014	rs9967476	18	51385421	q21.2
SNP_A-2242708	A	T	201	197	243	157	10.212	0.0014	rs4904317	14	85999269	q31.3
SNP_A-2231886	C	C	374	20	335	43	10.215	0.0014	rs580256	6	165593917	q27
SNP_A-1930930	A	A	309	27	385	11	10.21	0.0014	rs7896711	10	69101004	q21.3
SNP_A-1905809	T	T	306	10	409	1	10.202	0.0014	rs17172636	7	45972644	p13
SNP_A-1905085	A	A	342	26	317	53	10.171	0.0014	rs1719887	3	121067317	q13.33
SNP_A-1911934	A	A	301	7	345	29	10.149	0.0014	rs2817423	6	50932763	p12.3
SNP_A-1892314	C	C	409	1	374	12	10.158	0.0014	rs12254620	10	32556140	p11.22
SNP_A-1875033	T	T	339	11	411	1	10.269	0.0014	rs11984932	8	54993410	q11.23
SNP_A-1883832	C	C	327	31	368	12	10.167	0.0014	rs1191566	14	29039352	q12
SNP_A-1957988	T	T	358	0	383	11	10.143	0.0014	rs16927687	9	11508390	p23
SNP_A-1979395	T	T	295	23	362	8	10.219	0.0014	rs17025981	4	150527571	q31.23
SNP_A-1973075	G	G	368	12	405	1	10.23	0.0014	rs17045325	3	66964012	p14.1
SNP_A-1713245	T	T	394	4	377	19	10.152	0.0014	rs10483505	14	38593016	q21.1
SNP_A-1724872	A	A	323	49	293	83	10.198	0.0014	rs154152	5	14433062	p15.2
SNP_A-1780632	T	-	220	138	206	206	10.165	0.0014	rs2249922	14	51975831	q22.1
SNP_A-1791462	A	A	290	48	361	27	10.228	0.0014	rs7130414	11	130879435	q25
SNP_A-1859140	T	T	210	114	288	92	10.176	0.0014	rs11198725	10	120755161	q26.11
SNP_A-1846500	A	A	351	9	402	0	10.17	0.0014	rs7803433	7	97549058	q21.3
SNP_A-1817796	A	A	394	0	380	10	10.233	0.0014	rs241936	19	43002726	q13.13
SNP_A-1823559	A	A	350	22	382	6	10.209	0.0014	rs11065507	12	120149894	q24.31
SNP_A-1830573	C	C	303	43	351	21	10.157	0.0014	---	5	176070853	q35.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1831706	G	G	299	45	310	88	10.225	0.0014	rs11044150	12	18552294	p12.3
SNP_A-1844311	C	T	200	166	234	178	10.156	0.0014	rs10771755	12	30707044	p11.21
SNP_A-2203773	C	C	370	38	341	69	10.159	0.0014	rs10916113	1	223775680	q42.13
SNP_A-2227694	G	G	302	36	352	16	10.259	0.0014	rs161541	5	32169220	p13.3
SNP_A-2185690	T	T	404	0	351	9	10.22	0.0014	rs16938595	9	21935605	p21.3
SNP_A-2175763	T	T	318	18	395	5	10.175	0.0014	rs6760935	2	177257808	q31.1
SNP_A-2157300	T	T	337	11	339	33	10.217	0.0014	rs16824430	2	184106307	q32.1
SNP_A-2152978	C	C	270	26	353	11	10.242	0.0014	rs1511845	8	138971651	q24.23
SNP_A-2155033	A	A	320	8	412	0	10.159	0.0014	rs2665873	4	87147910	q21.23
SNP_A-2167545	C	C	358	26	382	8	10.262	0.0014	rs2884710	1	36891855	p34.3
SNP_A-2161409	C	C	391	7	345	23	10.249	0.0014	rs12247149	10	16728805	p13
SNP_A-2161035	T	T	406	4	364	18	10.223	0.0014	rs12712097	2	101452548	q11.2
SNP_A-2142941	G	G	327	11	395	1	10.218	0.0014	rs354135	12	30375079	p11.22
SNP_A-2142158	C	C	412	0	359	9	10.194	0.0014	rs17045252	2	23507004	p24.1
SNP_A-2132221	G	G	268	28	276	62	10.225	0.0014	rs17100980	14	62823597	q23.2
SNP_A-2137037	G	G	197	163	268	138	10.192	0.0014	rs13108253	4	157878674	q32.1
SNP_A-2066259	G	G	333	15	347	41	10.216	0.0014	rs10216497	8	68798494	q13.2
SNP_A-2056637	T	T	321	7	339	27	10.206	0.0014	rs6429868	2	141977117	q22.1
SNP_A-2007579	A	A	351	9	402	0	10.17	0.0014	rs6059458	20	31819320	q11.22
SNP_A-2017851	A	A	191	177	263	153	10.264	0.0014	rs2832907	21	30770217	q22.11
SNP_A-2016840	T	T	319	11	387	1	10.265	0.0014	---	21	25076241	q21.2
SNP_A-1995118	A	A	317	13	386	2	10.221	0.0014	rs16903924	8	130021318	q24.21
SNP_A-2000174	T	T	402	2	358	14	10.245	0.0014	rs564333	1	88750297	p22.2
SNP_A-2000380	C	C	303	19	392	6	10.249	0.0014	rs2185952	10	46555672	q11.22
SNP_A-2001640	C	C	382	22	379	5	10.214	0.0014	rs4335537	11	4162915	p15.4
SNP_A-2038214	A	A	266	82	339	57	10.251	0.0014	rs6742202	2	23628346	p24.1
SNP_A-2043218	C	C	246	158	300	120	10.228	0.0014	rs4150579	11	18313756	p15.1
SNP_A-2021350	G	G	334	4	355	21	10.207	0.0014	rs2312963	13	19461229	q12.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2016007	G	G	318	20	322	48	10.129	0.0015	rs3015838	21	19830637	q21.1
SNP_A-2008196	A	A	181	115	258	96	10.122	0.0015	rs240066	22	20617549	q11.22
SNP_A-2049020	T	T	290	110	240	148	10.133	0.0015	rs11487218	7	54915749	p11.2
SNP_A-2072070	C	C	339	3	348	18	10.03	0.0015	rs4891472	18	68124967	q22.3
SNP_A-2094574	G	G	362	0	389	11	10.101	0.0015	rs6444406	3	191095631	q28
SNP_A-2093587	T	C	186	182	248	160	10.049	0.0015	rs1837836	10	90620533	q23.31
SNP_A-2107527	T	T	308	16	388	4	10.028	0.0015	rs7255499	19	13893071	p13.12
SNP_A-2125579	A	A	296	32	322	12	10.131	0.0015	rs11120301	1	210898510	q41
SNP_A-2126724	T	T	383	3	367	17	10.136	0.0015	rs17167202	7	7200068	p21.3
SNP_A-2149902	A	A	238	60	311	39	10.053	0.0015	rs7770302	6	90858822	q15
SNP_A-2146531	T	T	315	15	302	38	10.108	0.0015	rs11776845	8	8641594	p23.1
SNP_A-2160256	A	A	361	15	328	36	10.036	0.0015	rs17117003	1	97794409	p21.3
SNP_A-2178016	C	C	337	45	313	79	10.081	0.0015	rs782257	1	72611080	p31.1
SNP_A-2192597	A	A	240	110	221	165	10.046	0.0015	rs429349	2	7117886	p25.1
SNP_A-2197045	C	C	318	34	375	15	10.136	0.0015	rs10028237	4	170852181	q33
SNP_A-2216993	G	G	219	117	210	182	10.071	0.0015	rs10756574	9	14533658	p22.3
SNP_A-2203609	A	A	278	70	355	47	10.052	0.0015	rs17161174	15	99443174	q26.3
SNP_A-1829908	T	T	405	1	374	12	10.043	0.0015	rs11259630	10	15447472	p13
SNP_A-1833180	A	A	329	19	381	5	10.035	0.0015	rs16937143	11	5877502	p15.4
SNP_A-1826010	T	T	374	12	407	1	10.1	0.0015	rs16964987	16	87375780	q24.3
SNP_A-1790759	A	A	326	14	362	2	10.077	0.0015	rs9582387	13	99839353	q32.3
SNP_A-1797077	A	A	412	0	361	9	10.138	0.0015	rs8083556	18	8083288	p11.23
SNP_A-1812242	C	C	324	18	306	42	10.063	0.0015	rs2676527	2	173573219	q31.1
SNP_A-1808275	C	C	413	1	382	12	10.028	0.0015	rs11844588	14	36166706	q13.3
SNP_A-1969594	A	A	320	26	316	56	10.072	0.0015	---	21	25217016	q21.2
SNP_A-1981751	A	A	382	4	367	19	10.083	0.0015	rs868078	5	58166656	q11.2
SNP_A-1952127	C	C	325	19	377	5	10.057	0.0015	rs6115022	20	2507521	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1938828	T	T	346	30	287	53	10.088	0.0015	rs7896232	10	86573114	q23.1
SNP_A-1940051	T	T	200	162	271	137	10.081	0.0015	rs12987697	2	241836237	q37.3
SNP_A-1877192	A	A	331	13	400	2	10.132	0.0015	rs13384312	2	123575735	q14.3
SNP_A-1876962	T	C	222	166	204	172	10.062	0.0015	rs5752562	22	26201369	q12.1
SNP_A-1890107	T	T	248	122	318	94	10.06	0.0015	rs968827	4	65629900	q13.1
SNP_A-1901789	G	G	348	18	312	40	10.039	0.0015	rs7299140	12	105237912	q23.3
SNP_A-1916064	A	A	295	113	255	157	10.06	0.0015	rs291122	5	58867629	q11.2
SNP_A-1904498	G	G	302	60	302	106	10.035	0.0015	rs7993521	13	97997943	q32.2
SNP_A-2234538	G	G	295	21	369	7	10.121	0.0015	rs8125534	20	55291318	q13.31
SNP_A-2253827	A	G	231	189	234	184	10.105	0.0015	rs17689617	7	40787764	p14.1
SNP_A-2283574	G	G	316	40	311	15	10.103	0.0015	rs7021313	9	119684897	q33.2
SNP_A-2280332	G	G	226	132	196	184	10.043	0.0015	rs6092524	20	55722808	q13.32
SNP_A-2309533	G	G	376	10	384	0	10.079	0.0015	rs747057	5	16838318	p15.1
SNP_A-2306386	G	G	403	3	366	16	9.953	1.60E-03	rs7196203	16	56166456	q13
SNP_A-2291673	G	G	409	1	380	12	9.975	1.60E-03	rs1299161	11	71964998	q13.4
SNP_A-2260263	C	C	308	102	338	64	10.014	1.60E-03	rs320631	17	28683620	q11.2
SNP_A-2253719	T	T	323	13	384	2	9.915	1.60E-03	rs17026877	4	98992260	q22.3
SNP_A-2256077	G	G	414	2	376	14	10	1.60E-03	rs14884445	11	15711852	p15.2
SNP_A-2237058	G	G	369	21	330	44	9.984	1.60E-03	rs17134377	7	3914513	p22.2
SNP_A-2240110	G	G	272	16	383	5	9.998	1.60E-03	rs17023814	1	119807964	p12
SNP_A-2240882	T	T	325	77	278	112	9.965	1.60E-03	rs1992964	3	54438165	p14.3
SNP_A-2228761	G	G	349	11	413	1	9.99	1.60E-03	---	9	104686069	q31.1
SNP_A-1918986	C	C	280	50	349	29	9.943	1.60E-03	rs2058945	7	132115339	q33
SNP_A-1911511	A	A	346	36	362	14	9.995	1.60E-03	rs7852882	9	119055201	q33.1
SNP_A-1914633	A	A	287	119	218	146	9.917	1.60E-03	rs11623084	14	99423413	q32.2
SNP_A-1928358	C	C	363	1	369	13	9.906	1.60E-03	rs4621078	18	65414946	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1927359	G	G	196	118	284	102	9.997	1.60E-03	rs6868474	5	134924354	q31.1
SNP_A-1923207	A	G	199	163	228	176	9.943	1.60E-03	rs10977415	9	8963301	p24.1
SNP_A-1920220	G	G	317	13	380	2	10.017	1.60E-03	rs16895741	5	66191340	q12.3
SNP_A-1898431	G	G	230	136	204	192	9.953	1.60E-03	rs7480312	11	121297288	q24.1
SNP_A-1934127	C	C	388	0	384	10	9.975	1.60E-03	rs4738529	8	57679595	q12.1
SNP_A-1936053	G	G	343	11	407	1	10.018	1.60E-03	rs17152343	10	12913282	p13
SNP_A-1959466	C	C	247	105	229	159	9.998	1.60E-03	rs2035794	4	130912944	q28.2
SNP_A-1971739	C	C	397	13	326	30	9.936	1.60E-03	rs17032929	3	10481883	p25.3
SNP_A-1975504	T	T	347	11	411	1	9.999	1.60E-03	rs1805608	3	182254675	q26.33
SNP_A-1808102	A	A	310	32	270	58	9.982	1.60E-03	rs11965549	6	131518221	q23.2
SNP_A-1792232	A	A	348	4	337	19	9.937	1.60E-03	---	12	8472071	p13.31
SNP_A-1821562	C	C	277	39	276	76	9.995	1.60E-03	rs16900160	5	82432595	q14.2
SNP_A-1834040	A	A	218	140	262	102	9.951	1.60E-03	rs1741177	14	34452970	q13.2
SNP_A-1835136	G	G	295	67	293	115	9.954	1.60E-03	rs10983142	9	116253821	q33.1
SNP_A-1840708	C	C	319	7	313	25	9.968	1.60E-03	rs6689316	1	31269569	p35.2
SNP_A-1837244	G	G	335	21	380	6	9.969	1.60E-03	rs9376079	6	135355976	q23.3
SNP_A-1847296	A	A	348	0	377	11	10.016	1.60E-03	rs7597367	2	238755062	q37.3
SNP_A-1861242	G	G	277	83	272	136	9.911	1.60E-03	rs6023772	20	53048355	q13.2
SNP_A-2213248	T	T	300	20	393	7	9.974	1.60E-03	rs7163265	15	23625311	q12
SNP_A-2223671	C	C	397	5	366	20	9.939	1.60E-03	rs17096287	1	75302471	p31.1
SNP_A-2185033	T	-	250	160	202	202	9.927	1.60E-03	rs10950124	7	67269738	q11.22
SNP_A-2188560	C	C	343	11	403	1	9.904	1.60E-03	rs12719455	5	132012215	q23.3
SNP_A-2172494	A	A	402	2	366	14	9.962	1.60E-03	---	15	89265552	q26.1
SNP_A-2169665	A	A	259	13	361	3	9.93	1.60E-03	rs2197797	5	118443389	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2155521	G	G	271	121	231	165	9.936	1.60E-03	rs581955	2	67601874	p14
SNP_A-2153233	G	G	368	0	364	10	9.974	1.60E-03	rs17087626	5	96964786	q15
SNP_A-2167826	A	A	280	34	344	16	9.951	1.60E-03	rs10750835	11	68486121	q13.3
SNP_A-2125759	C	C	267	37	365	21	10.006	1.60E-03	rs2148417	13	35331862	q13.3
SNP_A-2130595	G	G	418	0	375	9	9.908	1.60E-03	rs4469409	8	31701038	p12
SNP_A-2122278	T	T	399	3	362	16	9.965	1.60E-03	rs9653469	2	101568117	q11.2
SNP_A-2107873	A	A	347	3	335	17	10.006	1.60E-03	rs6428668	1	116980703	p13.1
SNP_A-2107109	T	T	289	71	264	112	9.973	1.60E-03	rs2075722	17	77113948	q25.3
SNP_A-2098922	A	A	333	25	393	9	9.974	1.60E-03	rs9990095	3	85493852	p12.1
SNP_A-2097364	G	C	251	163	210	208	9.932	1.60E-03	rs2338104	12	108357888	q24.11
SNP_A-2080858	T	A	195	129	166	152	9.914	1.60E-03	rs1076536	13	45294430	q14.13
SNP_A-2074180	A	A	403	3	391	17	9.977	1.60E-03	rs6546494	2	69406427	p13.3
SNP_A-2017407	T	T	301	69	297	117	9.976	1.60E-03	rs9978929	21	28371677	q21.3
SNP_A-1995651	T	T	309	59	380	36	9.983	1.60E-03	rs10491731	9	4532803	p24.2
SNP_A-1996078	T	T	381	13	325	31	9.906	1.60E-03	rs16935871	9	17663007	p22.2
SNP_A-1993716	G	G	254	146	199	181	9.918	1.60E-03	rs885047	10	7057126	p14
SNP_A-2022505	G	G	406	0	363	9	9.938	1.60E-03	rs10064820	5	39360549	p13.1
SNP_A-2024220	G	G	341	25	403	9	10.011	1.60E-03	rs4675634	2	207428980	q33.3
SNP_A-2023923	A	A	377	15	384	2	9.96	1.60E-03	rs2372219	2	214730516	q34
SNP_A-2040253	C	C	399	7	376	24	9.961	1.60E-03	rs9955415	18	21423824	q11.2
SNP_A-2036901	T	T	364	26	299	47	9.818	1.70E-03	rs12118621	1	99909080	p21.2
SNP_A-2028318	G	G	397	3	364	16	9.819	1.70E-03	rs2153865	9	118271831	q33.1
SNP_A-2030708	C	C	275	89	335	61	9.798	1.70E-03	rs13213621	6	120126009	q22.31
SNP_A-2002201	T	T	404	2	372	14	9.821	1.70E-03	rs532391	11	104428916	q22.3
SNP_A-2006727	A	G	213	203	247	167	9.866	1.70E-03	rs6430547	2	135446154	q21.3
SNP_A-2006752	A	A	401	3	366	16	9.884	1.70E-03	rs1368660	10	132626740	q26.3
SNP_A-2071281	A	A	216	52	223	99	9.881	1.70E-03	rs17017923	4	92276048	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2063791	T	T	359	31	375	11	9.852	1.70E-03	rs11118299	1	215978669	q41
SNP_A-2067347	A	A	293	43	335	21	9.802	1.70E-03	rs11178688	12	69893468	q15
SNP_A-2049738	C	C	254	96	327	71	9.875	1.70E-03	rs2171214	3	119355292	q13.32
SNP_A-2053691	C	C	238	120	310	94	9.878	1.70E-03	rs7618902	3	41482456	p22.1
SNP_A-2058211	G	G	356	2	351	15	9.889	1.70E-03	rs9876785	3	116564591	q13.31
SNP_A-2058962	C	C	280	44	346	24	9.835	1.70E-03	---	6	142144847	q24.1
SNP_A-2082951	G	G	416	0	377	9	9.81	1.70E-03	rs10901061	9	131388211	q34.13
SNP_A-2120137	C	C	216	128	200	190	9.859	1.70E-03	rs899940	17	30610953	q12
SNP_A-2117837	T	T	411	5	359	19	9.882	1.70E-03	rs16861358	3	115025006	q13.31
SNP_A-2127289	T	T	347	23	385	7	9.879	1.70E-03	rs4834796	4	120946037	q26
SNP_A-2136234	G	G	386	8	338	24	9.845	1.70E-03	rs9302914	17	65684617	q24.3
SNP_A-2133733	G	A	183	169	240	164	9.835	1.70E-03	rs7000848	8	76489433	q21.11
SNP_A-2138340	T	T	359	49	331	83	9.851	1.70E-03	rs9695992	9	132813268	q34.13
SNP_A-2181241	C	C	349	39	317	69	9.866	1.70E-03	rs4930081	11	2296398	p15.5
SNP_A-2189734	G	G	301	65	288	108	9.809	1.70E-03	rs324258	11	21925423	p14.3
SNP_A-2222545	T	T	336	26	315	53	9.857	1.70E-03	rs7558030	2	237980278	q37.3
SNP_A-2202627	G	G	345	15	405	3	9.838	1.70E-03	rs6857603	4	92898239	q22.1
SNP_A-2212107	T	T	196	98	269	77	9.82	1.70E-03	rs7382443	6	133284656	q23.2
SNP_A-1859173	T	T	326	8	406	0	9.831	1.70E-03	rs17152296	8	10656640	p23.1
SNP_A-1856787	A	A	322	8	402	0	9.853	1.70E-03	rs10038294	5	36949835	p13.2
SNP_A-1821474	A	A	304	10	395	1	9.872	1.70E-03	rs3218010	9	21988733	p21.3
SNP_A-1792773	A	A	210	150	269	119	9.805	1.70E-03	rs11735108	4	5687752	p16.2
SNP_A-1785421	C	C	379	9	338	26	9.846	1.70E-03	rs2952459	17	62981180	q24.2
SNP_A-1676352	G	G	344	0	379	11	9.85	1.70E-03	rs10519607	5	119130148	q23.1
SNP_A-1643403	A	A	347	1	324	12	9.889	1.70E-03	-	4	107131383	q24
SNP_A-1982412	C	C	327	11	383	1	9.86	1.70E-03	rs16902311	5	86001443	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1951449	G	A	201	177	240	174	9.846	1.70E-03	rs9375526	6	127978539	q22.33
SNP_A-1936600	C	C	351	13	414	2	9.832	1.70E-03	rs6815262	4	188457021	q35.2
SNP_A-1942826	C	C	291	13	401	3	9.807	1.70E-03	rs6962305	7	142019498	q34
SNP_A-1890681	A	A	405	1	380	12	9.861	1.70E-03	rs3737742	1	46613067	p33
SNP_A-1874087	A	A	416	0	377	9	9.81	1.70E-03	rs16984418	20	58881162	q13.33
SNP_A-1878734	A	A	376	12	401	1	9.867	1.70E-03	rs17096026	14	29280557	q12
SNP_A-1881564	A	A	377	37	397	15	9.82	1.70E-03	rs4461303	2	46393232	p21
SNP_A-1926154	C	C	294	106	258	150	9.832	1.70E-03	rs9929981	16	28154375	p11.2
SNP_A-2250614	A	A	345	13	408	2	9.862	1.70E-03	rs17035848	4	158464151	q32.1
SNP_A-2252162	G	G	336	22	391	7	9.831	1.70E-03	rs2269583	6	122199333	q22.31
SNP_A-2245090	G	G	385	9	344	26	9.819	1.70E-03	rs4243079	15	76463868	q25.1
SNP_A-2266622	T	T	375	9	416	0	9.861	1.70E-03	rs708248	16	52687571	q12.2
SNP_A-2290181	G	G	344	6	337	23	9.899	1.70E-03	rs2015824	19	58926183	q13.42
SNP_A-2305159	A	A	326	8	408	0	9.879	1.70E-03	rs7105650	11	85234807	q14.1
SNP_A-2312216	A	A	416	0	375	9	9.861	1.70E-03	rs7396111	11	11420739	p15.3
SNP_A-2271077	A	A	400	4	370	18	9.759	0.0018	rs17579575	8	21286513	p21.3
SNP_A-2271292	T	T	324	20	350	50	9.7	0.0018	rs4930932	12	30568532	p11.22
SNP_A-2259622	G	G	327	15	383	3	9.793	0.0018	rs6920118	6	78151876	q14.1
SNP_A-2262869	G	A	183	165	233	163	9.718	0.0018	rs7153862	14	77496143	q24.3
SNP_A-2278849	A	A	364	0	370	10	9.709	0.0018	rs11629867	15	46996085	q21.1
SNP_A-2255660	A	G	204	160	221	179	9.724	0.0018	rs4499887	6	80036419	q14.1
SNP_A-2236493	T	T	369	9	406	0	9.779	0.0018	rs1730702	2	168282447	q24.3
SNP_A-1927579	G	G	265	81	322	54	9.705	0.0018	rs17616779	8	8419784	p23.1
SNP_A-1920599	C	C	356	6	387	25	9.749	0.0018	rs7898272	10	72810822	q22.1
SNP_A-1921312	G	G	348	44	331	17	9.795	0.0018	rs12253880	10	57755166	q21.1
SNP_A-1914535	A	A	290	20	375	7	9.738	0.0018	rs17120989	12	57211497	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1907491	A	A	332	22	318	48	9.761	0.0018	rs3896090	9	30709889	p21.1
SNP_A-1878695	T	T	243	61	302	38	9.749	0.0018	rs7665392	4	187857834	q35.2
SNP_A-1875004	C	C	304	50	300	90	9.736	0.0018	rs1034217	1	97997443	p21.3
SNP_A-1895309	G	G	414	0	379	9	9.712	0.0018	rs17251606	12	91292185	q22
SNP_A-1900640	G	G	376	14	307	31	9.728	0.0018	rs6712107	2	14129252	p24.3
SNP_A-1945286	A	A	285	63	280	108	9.741	0.0018	rs6844942	4	66240958	q13.1
SNP_A-1937629	A	A	289	91	338	60	9.782	0.0018	rs1829995	7	16422731	p21.1
SNP_A-1950862	A	A	229	139	298	112	9.699	0.0018	rs13024335	2	214355482	q34
SNP_A-1961890	T	T	416	0	381	9	9.708	0.0018	rs681545	1	111379160	p13.3
SNP_A-1982395	T	T	238	120	210	170	9.724	0.0018	rs375536	5	84859033	q14.3
SNP_A-1979793	C	C	334	28	389	11	9.723	0.0018	rs1675022	4	167567624	q32.3
SNP_A-1985005	T	T	236	130	308	104	9.733	0.0018	rs2185503	6	8294510	p24.3
SNP_A-1798761	C	C	308	16	380	4	9.72	0.0018	rs7675958	4	119120643	q26
SNP_A-1857976	T	T	310	20	368	6	9.788	0.0018	rs2483423	13	38251581	q13.3
SNP_A-1864011	C	C	299	105	337	69	9.714	0.0018	rs12240301	10	1635025	p15.3
SNP_A-2205413	A	A	297	53	363	31	9.794	0.0018	rs2807241	10	25540538	p12.1
SNP_A-2206481	A	A	288	98	268	148	9.774	0.0018	rs7968144	12	71843667	q21.1
SNP_A-2223979	G	G	388	6	347	21	9.745	0.0018	rs7538366	1	242749493	q44
SNP_A-2183083	C	C	300	36	372	18	9.752	0.0018	rs6129503	20	38223823	q12
SNP_A-2194887	G	G	338	60	275	87	9.751	0.0018	rs7978994	12	97322134	q23.1
SNP_A-2175365	T	T	316	10	323	31	9.696	0.0018	rs942913	13	94375727	q32.1
SNP_A-2146843	G	G	330	8	408	0	9.761	0.0018	rs10986922	9	125637275	q33.3
SNP_A-2160973	A	A	322	20	382	6	9.792	0.0018	rs9957498	18	4380047	p11.31
SNP_A-2128945	G	G	255	107	327	81	9.79	0.0018	rs1415219	9	70776662	q21.11
SNP_A-2112708	T	T	355	1	365	13	9.774	0.0018	rs10093847	8	82664932	q21.13
SNP_A-2078307	G	G	292	80	336	50	9.751	0.0018	rs7896662	10	52547036	q11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2085462	G	G	284	20	311	51	9.784	0.0018	rs2126235	6	2685691	p25.2
SNP_A-2087031	C	C	369	7	269	19	9.721	0.0018	rs2267421	22	38673853	q13.1
SNP_A-2105271	G	G	351	11	405	1	9.701	0.0018	rs17064749	3	61267686	p14.2
SNP_A-2102236	C	C	343	39	371	17	9.695	0.0018	rs284055	1	185175421	q31.1
SNP_A-2063984	A	A	334	8	414	0	9.788	0.0018	rs17002980	4	79432132	q21.21
SNP_A-2074687	C	C	411	1	388	12	9.795	0.0018	rs11128097	3	68974220	p14.1
SNP_A-2075636	A	A	244	126	215	177	9.789	0.0018	rs10506678	12	73708472	q21.1
SNP_A-2018953	T	T	296	74	358	48	9.77	0.0018	rs2835583	21	37381595	q22.13
SNP_A-2013094	T	T	316	14	397	3	9.696	0.0018	rs7015423	8	2987440	p23.2
SNP_A-1995925	T	T	326	8	404	0	9.783	0.0018	rs16929184	9	12562122	p23
SNP_A-1989762	A	A	358	58	325	93	9.702	0.0018	rs2331003	7	44023105	p13
SNP_A-2031449	T	T	415	1	359	11	9.726	0.0018	rs9890403	17	38814140	q21.31
SNP_A-2030141	T	T	254	36	256	72	9.708	0.0018	rs1879609	18	73470121	q23
SNP_A-2021735	A	A	367	9	404	0	9.783	0.0018	rs3911141	14	87461923	q31.3
SNP_A-2040045	A	A	337	3	354	18	9.714	0.0018	rs16944454	16	80726765	q23.3
SNP_A-2044593	T	T	260	62	239	101	9.733	0.0018	rs1033953	13	94968596	q32.1
SNP_A-2022734	G	G	191	167	259	143	9.618	0.0019	rs555206	1	181574110	q25.3
SNP_A-2021129	T	T	229	121	200	170	9.663	0.0019	rs4350646	18	21115916	q11.2
SNP_A-2020963	G	G	349	49	315	81	9.613	0.0019	rs640663	11	119441502	q23.3
SNP_A-2024231	C	C	340	66	364	36	9.598	0.0019	rs8180271	4	16105176	p15.32
SNP_A-2027541	G	G	371	1	354	12	9.658	0.0019	rs11176600	12	65825559	q14.3
SNP_A-1992750	A	A	343	27	390	10	9.67	0.0019	rs17054669	8	25858365	p21.2
SNP_A-2018968	C	C	278	60	341	37	9.661	0.0019	rs2835661	21	37490777	q22.13
SNP_A-2017968	T	T	209	85	199	137	9.668	0.0019	rs13050344	21	31617135	q22.11
SNP_A-2076814	T	T	349	15	322	36	9.684	0.0019	rs11149662	16	83082170	q24.1
SNP_A-2070356	T	T	308	24	302	52	9.679	0.0019	rs17816450	13	34956038	q13.3
SNP_A-2052277	C	C	340	40	372	18	9.655	0.0019	rs4814404	20	15764772	p12.1
SNP_A-2103015	A	A	311	13	316	36	9.693	0.0019	rs7340804	4	170849139	q33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098090	A	A	290	28	284	58	9.668	0.0019	rs7447347	5	116462020	q23.1
SNP_A-2093198	T	T	284	74	272	120	9.645	0.0019	rs11736602	4	79929468	q21.21
SNP_A-2084855	T	T	270	26	362	12	9.6	0.0019	rs10217539	9	87481946	q21.33
SNP_A-2089743	T	T	267	131	228	176	9.624	0.0019	rs7934676	11	4355857	p15.4
SNP_A-2079142	A	A	359	11	413	1	9.672	0.0019	rs1720009	4	8454536	p16.1
SNP_A-2127463	C	C	261	75	339	53	9.671	0.0019	rs10918859	1	158900926	q23.3
SNP_A-2135065	G	G	380	12	397	1	9.635	0.0019	rs16998588	20	16948269	p12.1
SNP_A-2183035	A	A	360	0	368	10	9.655	0.0019	rs10143887	14	87445882	q31.3
SNP_A-2191070	G	G	283	37	340	18	9.679	0.0019	rs1731534	12	30289603	p11.22
SNP_A-2222530	C	C	344	4	339	19	9.68	0.0019	---	1	19827553	p36.13
SNP_A-2204778	T	T	255	61	246	104	9.657	0.0019	rs1843016	4	96590773	q22.3
SNP_A-2208533	C	C	311	9	304	28	9.619	0.0019	rs2936880	10	123365966	q26.13
SNP_A-1866844	C	C	332	6	346	24	9.662	0.0019	---	14	78619077	q31.1
SNP_A-1873786	A	A	344	36	371	15	9.62	0.0019	rs11624030	14	32623255	q13.1
SNP_A-1855571	C	C	418	2	361	13	9.605	0.0019	rs11824844	11	120797526	q23.3
SNP_A-1851345	G	G	419	1	330	10	9.625	0.0019	rs711557	3	3759464	p26.2
SNP_A-1819510	T	T	331	19	373	5	9.61	0.0019	rs10410450	19	21896903	p12
SNP_A-1817578	G	G	297	53	361	31	9.64	0.0019	rs7984692	13	69919103	q21.33
SNP_A-1814809	T	T	298	20	257	41	9.619	0.0019	rs318921	8	51082262	q11.21
SNP_A-1825877	C	C	320	18	385	5	9.676	0.0019	rs10054240	5	159898120	q33.3
SNP_A-1823863	T	T	271	67	352	46	9.606	0.0019	rs6852803	4	139743074	q28.3
SNP_A-1825576	C	C	271	51	345	31	9.648	0.0019	rs6478797	9	98495763	q22.33
SNP_A-1844084	G	G	348	2	349	15	9.672	0.0019	rs11192692	10	107804066	q25.1
SNP_A-1836803	A	A	342	8	416	0	9.609	0.0019	rs7538610	1	65101503	p31.3
SNP_A-1834585	C	C	416	0	385	9	9.609	0.0019	rs1146508	1	94741642	p21.3
SNP_A-1967875	C	C	240	150	199	195	9.679	0.0019	rs439150	20	15012634	p12.1
SNP_A-1964973	G	G	310	26	368	10	9.636	0.0019	rs11893424	2	135818453	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1951433	T	T	288	96	231	127	9.67	0.0019	rs916326	20	40445678	q12
SNP_A-1938256	G	G	274	142	229	185	9.676	0.0019	rs17829311	14	68134319	q24.1
SNP_A-1937230	T	T	332	18	320	42	9.621	0.0019	rs17092362	12	41583991	q12
SNP_A-1933454	T	T	307	59	250	86	9.596	0.0019	rs12622790	2	6248358	p25.2
SNP_A-1946549	A	A	399	1	382	12	9.633	0.0019	rs7870398	9	125533767	q33.3
SNP_A-1941760	A	A	220	194	264	150	9.628	0.0019	rs7078772	10	2312119	p15.3
SNP_A-1888917	T	T	379	9	412	0	9.665	0.0019	rs641928	10	13178056	p13
SNP_A-1904695	C	C	341	11	393	1	9.683	0.0019	rs9473165	6	47815573	p12.3
SNP_A-2239207	G	G	342	8	416	0	9.609	0.0019	rs353136	2	165968707	q24.3
SNP_A-2231297	A	A	210	200	234	142	9.681	0.0019	rs4499428	2	116698188	q14.1
SNP_A-2242269	A	A	386	12	403	1	9.63	0.0019	rs4271788	2	105243477	q12.1
SNP_A-2273340	A	A	347	17	398	4	9.678	0.0019	rs7286692	22	32466788	q12.3
SNP_A-2275080	A	A	362	8	350	26	9.684	0.0019	rs130027	16	3774674	p13.3
SNP_A-2280533	T	T	332	8	404	0	9.609	0.0019	rs425367	4	85659241	q21.23
SNP_A-2259932	C	C	220	146	294	122	9.645	0.0019	rs2789792	1	216720947	q41
SNP_A-2267762	T	T	364	0	372	10	9.658	0.0019	rs16862035	3	175777581	q26.31
SNP_A-2312677	G	G	230	122	202	172	9.66	0.0019	rs1860461	7	5826505	p22.1
SNP_A-2300858	G	G	318	44	364	22	9.676	0.0019	rs7515731	1	236564066	q43
SNP_A-2291455	A	A	351	1	367	13	9.585	0.002	rs6935817	6	65914994	q12
SNP_A-2264706	C	C	343	19	327	43	9.586	0.002	rs653064	1	39551094	p34.3
SNP_A-2262268	C	C	371	11	348	30	9.52	0.002	rs17116329	15	23696834	q12
SNP_A-2284885	A	A	395	1	380	12	9.578	0.002	rs1422999	5	147432354	q32
SNP_A-2286255	C	C	265	55	302	30	9.55	0.002	rs9592406	13	33760515	q13.2
SNP_A-2287284	T	T	362	0	376	10	9.505	0.002	rs1457814	4	161017651	q32.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2248045	G	G	324	10	409	1	9.557	0.002	rs9824459	3	179040348	q26.32
SNP_A-2229192	C	C	355	15	407	3	9.522	0.002	rs11113617	12	106873730	q23.3
SNP_A-2236608	G	G	387	9	414	0	9.515	0.002	rs838799	5	171167844	q35.1
SNP_A-1893805	A	A	412	0	383	9	9.566	0.002	rs2799148	9	38442973	p13.2
SNP_A-1895434	T	T	336	8	406	0	9.544	0.002	rs16850106	1	226134182	q42.13
SNP_A-1889755	T	T	315	15	319	39	9.568	0.002	rs7525887	1	165597271	q24.2
SNP_A-1891545	G	G	329	17	296	38	9.552	0.002	rs11925897	3	147659856	q24
SNP_A-1934999	C	C	236	124	224	186	9.506	0.002	rs2188151	3	50176928	p21.31
SNP_A-1964235	T	T	321	47	320	86	9.595	0.002	rs17023362	2	100061797	q11.2
SNP_A-1966157	G	G	352	2	357	15	9.536	0.002	rs1405945	2	183307972	q32.1
SNP_A-1972954	T	T	296	20	285	45	9.525	0.002	---	3	63578236	p14.2
SNP_A-1850180	T	T	340	8	412	0	9.572	0.002	---	1	189786806	q31.2
SNP_A-1850852	A	A	323	19	400	6	9.555	0.002	rs17071833	4	182846191	q34.3
SNP_A-1848409	T	T	354	2	359	15	9.538	0.002	rs17088666	4	58466110	q12
SNP_A-1844993	G	G	340	8	410	0	9.526	0.002	rs16900641	6	70076715	q13
SNP_A-1867645	T	T	418	0	389	9	9.558	0.002	rs333610	15	64099203	q22.31
SNP_A-1808219	C	C	410	0	383	9	9.52	0.002	rs6498607	16	16170651	p13.11
SNP_A-1809885	C	C	291	35	340	16	9.582	0.002	rs4517989	2	195141085	q32.3
SNP_A-1675650	A	A	250	146	299	109	9.565	0.002	rs2023387	6	7909352	p24.3
SNP_A-2210323	G	G	329	43	371	21	9.565	0.002	rs7854093	9	112297369	q32
SNP_A-2226169	A	A	326	12	319	33	9.596	0.002	rs1910130	18	49229300	q21.2
SNP_A-2183719	G	G	361	11	411	1	9.556	0.002	rs6785009	3	145016099	q24
SNP_A-2192187	C	C	353	13	406	2	9.517	0.002	rs4946781	6	107269290	q21
SNP_A-2181502	T	T	188	180	251	153	9.572	0.002	rs450614	3	122075028	q13.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2171238	G	G	245	117	261	73	9.584	0.002	rs277983	5	70964909	q13.2
SNP_A-2171766	G	G	393	9	420	0	9.507	0.002	rs6899575	6	42255598	p21.1
SNP_A-2134826	G	G	340	8	412	0	9.572	0.002	---	9	105059904	q31.1
SNP_A-2078701	A	A	393	9	420	0	9.507	0.002	rs4810925	20	35666949	q11.23
SNP_A-2095702	C	C	255	113	238	168	9.509	0.002	rs2903817	4	83894448	q21.22
SNP_A-2099513	C	C	355	13	353	35	9.567	0.002	rs17119426	12	51491710	q13.13
SNP_A-2072570	A	A	299	21	298	48	9.566	0.002	rs6571890	14	38604515	q21.1
SNP_A-2074825	A	A	328	10	415	1	9.584	0.002	rs17005442	4	83401892	q21.22
SNP_A-2068721	G	G	326	10	411	1	9.543	0.002	rs16844343	2	196745985	q32.3
SNP_A-2029087	A	A	336	8	408	0	9.59	0.002	rs2788619	10	7040770	p14
SNP_A-2020826	A	A	342	8	412	0	9.517	0.002	rs7123503	11	114627243	q23.3
SNP_A-2044954	T	T	332	8	400	0	9.515	0.002	rs7081857	10	2359856	p15.3
SNP_A-1997453	A	A	345	1	365	13	9.453	2.10E-03	rs16923444	9	103707118	q31.1
SNP_A-2052939	T	T	298	36	291	69	9.494	2.10E-03	rs10045386	5	26773215	p14.1
SNP_A-2057247	A	A	362	2	342	14	9.48	2.10E-03	rs12695918	3	149939325	q24
SNP_A-2078034	G	G	383	3	310	14	9.465	2.10E-03	rs10805000	4	7608947	p16.1
SNP_A-2134070	A	A	340	8	408	0	9.48	2.10E-03	rs1216960	13	46260389	q14.2
SNP_A-2137314	A	A	331	31	400	14	9.493	2.10E-03	rs6775003	3	96197722	q11.2
SNP_A-2137465	G	G	306	56	310	100	9.488	2.10E-03	rs12866529	13	75835110	q22.2
SNP_A-2118673	G	G	325	53	297	87	9.471	2.10E-03	rs10903528	10	1675508	p15.3
SNP_A-2115862	T	T	336	20	390	6	9.454	2.10E-03	rs2499690	6	34149396	p21.31
SNP_A-2157009	G	G	205	137	261	107	9.479	2.10E-03	rs13068491	3	150294958	q24
SNP_A-2144986	G	G	344	8	412	0	9.463	2.10E-03	rs1794841	6	112090115	q21
SNP_A-2171620	T	C	195	167	216	160	9.457	2.10E-03	rs1942803	18	69274982	q22.3
SNP_A-2171604	T	T	349	11	395	1	9.485	2.10E-03	rs7111497	11	86129095	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2173919	G	G	316	22	320	50	9.487	2.10E-03	rs17115956	5	153696556	q33.2
SNP_A-2171213	C	C	376	28	379	9	9.449	2.10E-03	rs6706862	2	127060663	q14.3
SNP_A-2196052	C	C	383	9	408	0	9.474	2.10E-03	rs9480510	6	151067946	q25.1
SNP_A-2187526	T	T	267	31	356	16	9.444	2.10E-03	rs6006506	22	42993929	q13.31
SNP_A-2222080	T	T	200	150	259	121	9.47	2.10E-03	rs11917591	3	58343489	p14.3
SNP_A-2219962	T	T	313	97	338	60	9.504	2.10E-03	rs11949123	5	136088164	q31.1
SNP_A-1678990	A	A	381	5	362	20	9.465	2.10E-03	rs10508970	10	53394770	q21.1
SNP_A-1671932	A	A	333	65	307	103	9.475	2.10E-03	rs10484171	14	43133559	q21.2
SNP_A-1798662	T	T	286	28	350	12	9.48	2.10E-03	rs17106443	1	51356723	p32.3
SNP_A-1797435	G	G	375	9	398	0	9.437	2.10E-03	rs6699151	1	68740418	p31.2
SNP_A-1847392	A	A	379	1	368	12	9.47	2.10E-03	rs9888445	12	62992131	q14.2
SNP_A-1832835	T	T	340	8	406	0	9.433	2.10E-03	rs1933618	1	205758299	q32.2
SNP_A-1823741	A	A	406	0	383	9	9.428	2.10E-03	rs11141919	9	87485886	q21.33
SNP_A-1819115	T	T	339	7	343	25	9.48	2.10E-03	rs16854721	2	216398014	q35
SNP_A-1820847	C	C	313	17	282	38	9.482	2.10E-03	rs2051020	6	73873395	q13
SNP_A-1965748	A	A	298	66	334	38	9.503	2.10E-03	rs2063958	2	168836166	q24.3
SNP_A-1979278	C	C	228	90	219	143	9.429	2.10E-03	rs1032296	4	145792293	q31.21
SNP_A-1977836	T	T	340	8	408	0	9.48	2.10E-03	rs17005533	4	83503111	q21.22
SNP_A-1903352	A	A	335	67	281	97	9.492	2.10E-03	rs879404	7	131187781	q32.3
SNP_A-1885512	T	C	203	155	217	181	9.504	2.10E-03	rs185025	5	132900041	q31.1
SNP_A-1874894	T	T	345	3	370	18	9.442	2.10E-03	rs4833941	4	125012176	q28.1
SNP_A-1906565	A	A	385	1	374	12	9.467	2.10E-03	rs16931976	11	5483201	p15.4
SNP_A-1921460	C	C	363	39	355	15	9.446	2.10E-03	rs13261399	8	137371774	q24.23
SNP_A-2230765	G	G	329	39	368	18	9.495	2.10E-03	rs1280831	12	70226623	q21.1
SNP_A-2233541	G	G	195	173	257	145	9.487	2.10E-03	rs9346333	6	70483200	q13
SNP_A-2233657	G	G	386	10	358	28	9.454	2.10E-03	rs7457045	7	106071396	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2286249	C	C	236	116	292	86	9.481	2.10E-03	rs2560309	5	121505722	q23.2
SNP_A-2283465	G	G	314	30	354	12	9.437	2.10E-03	rs7577175	2	135949164	q21.3
SNP_A-2273361	G	G	333	9	343	29	9.43	2.10E-03	rs5995341	22	35485820	q12.3
SNP_A-2279497	G	G	330	32	294	58	9.45	2.10E-03	rs16843885	1	168825787	q24.3
SNP_A-2291600	G	G	350	4	372	20	9.426	2.10E-03	rs1482226	11	97833196	q22.1
SNP_A-2294990	T	T	334	6	337	23	9.415	2.20E-03	rs7199853	16	68454736	q22.1
SNP_A-2297138	C	C	385	1	343	11	9.39	2.20E-03	rs6985773	8	37480293	p12
SNP_A-2305319	C	C	369	7	326	22	9.35	2.20E-03	rs6893841	5	126958571	q23.2
SNP_A-2274231	G	G	352	8	416	0	9.341	2.20E-03	rs6900860	6	148441096	q24.3
SNP_A-2284148	G	A	203	141	190	172	9.364	2.20E-03	rs164415	1	159122011	q23.3
SNP_A-2268608	T	T	291	61	289	105	9.335	2.20E-03	rs1840558	18	59427394	q21.33
SNP_A-2267156	G	G	344	18	345	43	9.357	2.20E-03	rs2958896	17	50225255	q22
SNP_A-2233220	G	G	379	43	345	73	9.336	2.20E-03	rs9295657	6	25527297	p22.2
SNP_A-2232082	T	T	275	75	331	49	9.41	2.20E-03	rs1858366	8	138996577	q24.23
SNP_A-2228751	T	T	287	107	256	152	9.347	2.20E-03	rs3129872	6	32515131	p21.32
SNP_A-2239899	G	G	422	0	356	8	9.37	2.20E-03	rs11834437	12	109942424	q24.11
SNP_A-2245603	T	T	302	26	377	11	9.403	2.20E-03	---	16	2309072	p13.3
SNP_A-2255754	G	G	214	154	283	129	9.336	2.20E-03	rs10828759	10	25468664	p12.1
SNP_A-2250963	T	T	385	11	364	30	9.389	2.20E-03	rs16920758	11	94021316	q21
SNP_A-1912345	C	C	356	26	362	8	9.39	2.20E-03	rs198199	16	24036955	p12.1
SNP_A-1912584	T	T	346	8	412	0	9.409	2.20E-03	---	12	99138995	q23.1
SNP_A-1874426	G	G	348	8	412	0	9.356	2.20E-03	---	1	217858460	q41
SNP_A-1875391	A	A	308	32	375	15	9.341	2.20E-03	rs16969466	19	39732161	q13.11
SNP_A-1898633	T	T	290	130	317	87	9.415	2.20E-03	rs7591791	2	23256981	p24.1
SNP_A-1900037	C	C	352	30	373	11	9.408	2.20E-03	rs2306511	17	30484480	q12
SNP_A-1896558	A	A	300	38	281	69	9.396	2.20E-03	rs16874977	6	85429826	q14.3
SNP_A-1896726	C	C	205	147	272	122	9.4	2.20E-03	rs2636743	4	106714185	q24
SNP_A-1975531	A	A	273	29	356	14	9.4	2.20E-03	rs2293201	3	184498721	q27.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1972873	C	C	410	0	389	9	9.376	2.20E-03	rs17065279	3	61709143	p14.2
SNP_A-1939939	A	A	349	11	330	30	9.337	2.20E-03	rs6677790	1	108959345	p13.3
SNP_A-1939761	G	G	330	24	395	9	9.388	2.20E-03	rs4316428	10	11303713	p14
SNP_A-1939141	C	C	231	135	295	107	9.36	2.20E-03	rs12686449	9	5344558	p24.1
SNP_A-1941941	G	G	350	18	368	4	9.339	2.20E-03	rs844683	7	70939919	q11.22
SNP_A-1947426	T	T	255	67	228	104	9.364	2.20E-03	rs6563574	13	37406150	q13.3
SNP_A-1961221	A	A	328	8	388	0	9.341	2.20E-03	rs16853416	3	170489463	q26.2
SNP_A-1840754	T	T	325	21	389	7	9.41	2.20E-03	rs7924536	11	12874326	p15.2
SNP_A-1839291	A	A	262	44	298	22	9.339	2.20E-03	rs2255280	5	39430746	p13.1
SNP_A-1848140	C	C	346	8	410	0	9.364	2.20E-03	rs6650134	10	23032969	p12.2
SNP_A-1851098	C	C	249	97	302	68	9.401	2.20E-03	rs12416899	11	25708845	p14.3
SNP_A-1854938	A	A	340	8	404	0	9.387	2.20E-03	rs17170436	7	33612205	p14.3
SNP_A-1859869	C	C	351	1	373	13	9.408	2.20E-03	rs17140042	1	43183719	p34.2
SNP_A-1859887	C	C	360	20	299	39	9.34	2.20E-03	---	1	110079652	p13.3
SNP_A-1862434	C	C	325	65	290	100	9.416	2.20E-03	rs7303836	12	128093286	q24.32
SNP_A-1793577	A	A	370	10	316	26	9.388	2.20E-03	rs6860483	5	38468095	p13.2
SNP_A-1646262	G	G	250	148	216	198	9.394	2.20E-03	rs10497215	2	161773525	q24.2
SNP_A-1680234	G	G	330	12	410	2	9.374	2.20E-03	rs1882205	5	30904296	p13.3
SNP_A-1780395	G	G	353	11	395	1	9.361	2.20E-03	rs7299181	12	73331995	q21.1
SNP_A-2192410	G	G	187	165	254	142	9.346	2.20E-03	rs1376974	3	188794235	q27.3
SNP_A-2176238	A	A	327	71	288	106	9.374	2.20E-03	rs1275659	5	52269416	q11.2
SNP_A-2165614	A	A	296	62	354	38	9.413	2.20E-03	rs10020928	4	173022485	q34.1
SNP_A-2109773	T	T	226	130	211	191	9.35	2.20E-03	rs2120372	4	91340901	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2135519	G	G	314	32	307	63	9.401	2.20E-03	rs7849404	9	8689997	p24.1
SNP_A-2082921	T	T	238	110	229	169	9.341	2.20E-03	rs17413793	18	9231386	p11.22
SNP_A-2056224	G	G	280	36	296	74	9.379	2.20E-03	rs4393213	10	66499981	q21.3
SNP_A-2067364	C	C	223	141	203	201	9.407	2.20E-03	rs7744164	6	18278503	p22.3
SNP_A-2065797	T	T	366	20	383	5	9.381	2.20E-03	rs2540244	2	39842076	p22.1
SNP_A-2074845	A	A	333	1	355	13	9.364	2.20E-03	rs17135796	7	53347138	p12.1
SNP_A-2002890	G	G	360	2	369	15	9.412	2.20E-03	rs7967028	12	82243357	q21.31
SNP_A-1995922	C	C	276	74	246	112	9.398	2.20E-03	rs10124086	9	12539675	p23
SNP_A-2017355	G	G	271	41	356	24	9.378	2.20E-03	rs2831138	21	28021938	q21.3
SNP_A-2008574	G	G	363	1	356	12	9.354	2.20E-03	rs7624966	3	29721595	p24.1
SNP_A-2047120	A	A	226	142	208	204	9.404	2.20E-03	rs256723	12	30914900	p11.21
SNP_A-2037140	G	G	334	8	392	0	9.271	0.0023	rs9549368	13	112964990	q34
SNP_A-2037126	G	G	296	36	329	77	9.292	0.0023	rs13417792	2	63358851	p15
SNP_A-2024237	C	C	293	73	330	44	9.3	0.0023	rs4602287	20	33831442	q11.22
SNP_A-2025293	T	T	304	28	309	59	9.26	0.0023	rs255574	5	129790761	q23.3
SNP_A-2033278	A	A	236	116	220	172	9.327	0.0023	rs13165859	5	27468915	p14.1
SNP_A-2018435	T	T	318	38	266	62	9.259	0.0023	rs8131582	21	34677115	q22.11
SNP_A-2013053	A	A	324	58	351	31	9.271	0.0023	rs4374942	7	154464455	q36.2
SNP_A-2074962	T	T	269	153	222	194	9.301	0.0023	rs187714	16	54264000	q12.2
SNP_A-2058775	C	C	256	90	326	66	9.28	0.0023	rs2568928	5	127515502	q23.2
SNP_A-2048436	G	G	369	11	409	1	9.264	0.0023	rs10041875	5	20333289	p14.3
SNP_A-2081048	C	C	344	8	406	0	9.326	0.0023	rs9316253	13	18204186	q11
SNP_A-2082972	G	G	364	22	409	7	9.269	0.0023	rs1907732	10	78362966	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2094160	G	G	327	17	361	45	9.263	0.0023	rs2715128	7	50516327	p12.2
SNP_A-2113784	G	G	304	28	309	59	9.26	0.0023	rs7234732	18	42158901	q21.1
SNP_A-2163051	G	G	303	15	329	41	9.264	0.0023	rs16924480	11	33585796	p13
SNP_A-2157233	G	G	350	8	410	0	9.258	0.0023	rs9426438	1	29566549	p35.3
SNP_A-2177079	G	G	315	87	274	124	9.322	0.0023	rs7811408	7	759081	p22.3
SNP_A-2169062	C	C	246	106	243	167	9.288	0.0023	rs988587	3	158536973	q25.32
SNP_A-2218799	A	A	249	95	246	152	9.291	0.0023	rs7695171	4	141058390	q31.1
SNP_A-2223681	T	T	329	17	291	37	9.262	0.0023	rs10149426	14	60693777	q23.1
SNP_A-2227471	T	T	365	49	315	77	9.305	0.0023	rs17412287	18	6394553	p11.31
SNP_A-2224909	G	G	364	0	349	9	9.266	0.0023	rs4772753	13	105549192	q33.2
SNP_A-1784576	A	A	317	83	268	116	9.254	0.0023	rs16885649	6	54617753	p12.1
SNP_A-1795439	T	T	345	33	384	14	9.258	0.0023	rs16999115	22	47156263	q13.32
SNP_A-1793855	C	C	340	8	400	0	9.295	0.0023	rs6431912	2	8048405	p25.1
SNP_A-1797277	A	A	367	1	362	12	9.294	0.0023	rs6552641	4	184451154	q35.1
SNP_A-1796223	T	T	316	8	325	27	9.297	0.0023	rs17111807	14	80956673	q31.1
SNP_A-1861392	C	C	258	152	296	110	9.32	0.0023	rs12035067	1	79253211	p31.1
SNP_A-1853250	G	G	316	48	312	86	9.303	0.0023	rs1034215	1	97996961	p21.3
SNP_A-1846617	C	C	376	12	349	31	9.319	0.0023	rs12216813	8	2634096	p23.2
SNP_A-1844896	C	C	395	7	369	23	9.294	0.0023	rs1915048	17	22021420	p11.2
SNP_A-1838702	G	G	376	4	358	18	9.33	0.0023	rs6657279	1	50520315	p32.3
SNP_A-1834973	G	G	412	0	393	9	9.327	0.0023	rs8010868	14	69156412	q24.1
SNP_A-1831484	C	C	346	8	406	0	9.273	0.0023	rs11933373	4	180137177	q34.3
SNP_A-1819872	C	C	294	84	311	49	9.255	0.0023	rs585335	12	99840463	q23.1
SNP_A-1819986	T	T	316	18	371	5	9.299	0.0023	rs1689940	15	99022396	q26.3
SNP_A-1826235	T	T	255	133	225	183	9.29	0.0023	rs6582190	12	72403662	q21.1
SNP_A-1978030	T	T	209	139	284	118	9.286	0.0023	rs7671248	4	91368867	q22.1
SNP_A-1978687	C	C	227	93	285	67	9.293	0.0023	rs1980026	4	120609246	q26

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1895023	T	T	340	8	400	0	9.295	0.0023	rs16912890	10	60385801	q21.1
SNP_A-1876696	A	G	217	151	212	196	9.281	0.0023	rs9530362	13	74126798	q22.1
SNP_A-1922387	G	G	320	14	391	3	9.326	0.0023	rs12592517	15	23227560	q12
SNP_A-2253530	T	T	327	9	339	29	9.307	0.0023	---	4	63662206	q13.1
SNP_A-2242876	T	T	350	70	311	105	9.282	0.0023	rs12423245	12	106434506	q23.3
SNP_A-2234604	C	C	208	156	270	128	9.304	0.0023	rs10122540	9	118368234	q33.1
SNP_A-2267520	G	G	239	123	313	99	9.324	0.0023	rs9293439	5	85088672	q14.3
SNP_A-2280633	G	G	214	146	280	120	9.28	0.0023	rs1599310	18	63626977	q22.1
SNP_A-2302871	G	G	277	55	353	35	9.313	0.0023	rs16981148	20	19738602	p11.23
SNP_A-2296608	A	A	261	109	244	162	9.287	0.0023	rs4520477	1	213031092	q41
SNP_A-2296368	C	C	222	118	296	96	9.185	2.40E-03	rs12895468	14	80025922	q31.1
SNP_A-2299289	A	A	330	10	405	1	9.25	2.40E-03	rs1685625	1	151071603	q21.3
SNP_A-2287621	C	C	294	66	354	42	9.195	2.40E-03	rs1879557	3	155139516	q25.2
SNP_A-2264768	G	G	340	2	353	15	9.245	2.40E-03	rs16830235	2	189318323	q32.2
SNP_A-2268764	G	G	328	26	355	9	9.187	2.40E-03	rs2580346	2	121718887	q14.2
SNP_A-2263388	A	A	334	18	364	46	9.178	2.40E-03	rs4414587	18	65516465	q22.2
SNP_A-2237530	G	G	402	0	387	9	9.241	2.40E-03	rs2010090	12	126152718	q24.32
SNP_A-2238028	C	C	297	91	263	131	9.226	2.40E-03	rs11090472	22	25826085	q12.1
SNP_A-2238514	T	T	368	14	331	33	9.21	2.40E-03	rs7589260	2	223276218	q36.1
SNP_A-2229935	T	T	349	21	378	6	9.233	2.40E-03	rs16950032	17	14468964	p12
SNP_A-2242313	C	C	183	181	253	161	9.233	2.40E-03	rs2060188	2	241313934	q37.3
SNP_A-2242135	A	A	242	98	227	149	9.223	2.40E-03	rs11715789	3	68863064	p14.1
SNP_A-1925869	G	G	283	133	319	93	9.213	2.40E-03	rs16953563	15	64473824	q22.31
SNP_A-1930991	C	C	326	10	399	1	9.218	2.40E-03	rs1012073	10	24192027	p12.2
SNP_A-1908725	T	T	394	12	341	29	9.22	2.40E-03	rs7616037	3	145186448	q24
SNP_A-1889486	A	A	328	14	397	3	9.207	2.40E-03	rs6589540	11	115713523	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1895395	T	T	350	8	333	25	9.181	2.40E-03	rs6555810	5	156390564	q33.3
SNP_A-1892818	A	A	346	8	404	0	9.227	2.40E-03	---	16	75482680	q23.1
SNP_A-1986745	G	G	211	139	275	113	9.178	2.40E-03	rs791856	6	86738560	q14.3
SNP_A-1971865	T	T	332	10	405	1	9.186	2.40E-03	rs6780774	3	16269998	p25.1
SNP_A-1971838	A	A	391	1	355	11	9.19	2.40E-03	rs10494488	1	167055774	q24.2
SNP_A-1959930	A	A	330	8	384	0	9.191	2.40E-03	rs1833397	5	39263109	p13.1
SNP_A-1956963	G	G	349	23	323	47	9.229	2.40E-03	rs10081556	8	50673552	q11.21
SNP_A-1828294	A	A	397	3	355	15	9.191	2.40E-03	rs681580	11	120919838	q23.3
SNP_A-1818428	C	C	313	41	295	73	9.247	2.40E-03	rs6854815	4	26143130	p15.2
SNP_A-1817982	T	T	364	22	349	47	9.247	2.40E-03	rs16843641	2	159743885	q24.2
SNP_A-1836029	A	A	378	6	349	21	9.233	2.40E-03	rs17157274	7	109179613	q31.1
SNP_A-1867762	G	G	330	50	355	25	9.246	2.40E-03	rs2467307	17	5109042	p13.2
SNP_A-1792734	G	G	334	10	409	1	9.228	2.40E-03	rs9397459	6	152357773	q25.1
SNP_A-1809646	G	G	274	74	304	44	9.184	2.40E-03	rs11660202	18	10357168	p11.22
SNP_A-1802058	T	C	176	122	178	158	9.179	2.40E-03	rs4385333	6	145131233	q24.2
SNP_A-1783188	C	C	246	110	257	67	9.201	2.40E-03	rs12368412	12	56860695	q14.1
SNP_A-1683482	C	C	400	0	385	9	9.242	2.40E-03	rs10484025	14	87824392	q32.11
SNP_A-2207563	C	T	202	164	220	174	9.233	2.40E-03	rs6909485	6	93229092	q16.1
SNP_A-2166259	G	G	332	10	407	1	9.239	2.40E-03	rs16930787	9	1173321	p24.3
SNP_A-2166672	A	A	399	1	361	11	9.23	2.40E-03	rs11992926	8	11548546	p23.1
SNP_A-2111166	T	T	279	29	270	58	9.194	2.40E-03	rs29265	6	29683602	p22.1
SNP_A-2117395	C	T	244	178	213	191	9.203	2.40E-03	rs12683067	9	79181153	q21.31
SNP_A-2130348	A	A	198	166	257	137	9.253	2.40E-03	rs11170195	12	51289829	q13.13
SNP_A-2078138	A	A	249	149	211	195	9.212	2.40E-03	rs2817690	10	98848753	q24.1
SNP_A-2088768	G	G	398	10	344	26	9.207	2.40E-03	rs16891948	8	120157149	q24.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2048324	A	A	304	12	303	33	9.197	2.40E-03	rs11232020	11	79660804	q14.1
SNP_A-2060858	T	T	268	36	339	19	9.216	2.40E-03	rs1881868	7	118047393	q31.31
SNP_A-2064821	G	G	276	108	253	157	9.219	2.40E-03	rs4132660	12	58619523	q14.1
SNP_A-1996162	T	T	384	2	372	14	9.19	2.40E-03	rs16937950	9	20186627	p21.3
SNP_A-2002158	T	T	396	4	357	17	9.205	2.40E-03	rs16924618	10	68972835	q21.3
SNP_A-1997781	C	C	298	66	286	108	9.212	2.40E-03	rs6478237	9	116272070	q33.1
SNP_A-2035472	C	C	410	2	365	13	9.233	2.40E-03	rs10838623	11	46836093	p11.2
SNP_A-2032784	A	A	297	17	288	40	9.118	2.50E-03	rs2841350	1	235281033	q43
SNP_A-2024094	T	T	348	0	376	10	9.14	2.50E-03	rs7759505	6	107151907	q21
SNP_A-2020561	T	T	403	1	369	11	9.105	2.50E-03	rs444789	21	45347689	q22.3
SNP_A-2019197	G	G	345	15	385	3	9.156	2.50E-03	rs16996348	21	38749096	q22.2
SNP_A-2091690	T	T	206	158	274	134	9.128	2.50E-03	rs2056075	12	99752343	q23.1
SNP_A-2079726	T	T	299	13	391	3	9.116	2.50E-03	---	1	116961150	p13.1
SNP_A-2098979	T	T	278	30	344	14	9.119	2.50E-03	rs1771179	13	28143376	q12.3
SNP_A-2102697	G	G	336	6	328	22	9.148	2.50E-03	rs3734267	6	34931110	p21.31
SNP_A-2122567	G	G	334	8	388	0	9.177	2.50E-03	rs6595709	5	125823204	q23.2
SNP_A-2147368	C	C	310	94	263	129	9.17	2.50E-03	rs1565029	11	11394617	p15.3
SNP_A-2199215	G	G	313	53	373	31	9.157	2.50E-03	rs17021431	3	84427280	p12.1
SNP_A-1660223	T	T	301	85	350	56	9.153	2.50E-03	rs10486366	7	19549491	p21.1
SNP_A-1800675	C	C	358	0	388	10	9.116	2.50E-03	rs11178667	12	69853423	q15
SNP_A-1812292	G	G	290	38	343	19	9.118	2.50E-03	rs3848290	16	65597836	q22.1
SNP_A-1797639	C	C	253	69	292	42	9.142	2.50E-03	rs11141862	9	87368995	q21.33
SNP_A-1790826	G	G	365	13	406	2	9.115	2.50E-03	rs2679117	15	63276741	q22.31
SNP_A-1944393	T	T	416	4	352	16	9.142	2.50E-03	rs16974823	15	83428583	q25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1941138	C	C	384	8	384	26	9.13	2.50E-03	rs10459601	15	72652462	q24.1
SNP_A-1969159	T	T	288	76	361	53	9.136	2.50E-03	rs208913	21	17708593	q21.1
SNP_A-1967792	G	G	307	95	227	115	9.11	2.50E-03	rs4268989	20	12221530	p12.1
SNP_A-1984007	T	T	384	4	347	17	9.164	2.50E-03	rs17111892	5	150638569	q33.1
SNP_A-1883908	C	C	229	107	300	84	9.14	2.50E-03	rs3804994	3	4725808	p26.1
SNP_A-1884516	A	A	403	1	367	11	9.162	2.50E-03	rs8051269	16	4644434	p13.3
SNP_A-1918135	A	A	295	23	367	9	9.173	2.50E-03	rs17146585	5	119760718	q23.1
SNP_A-1916877	A	A	316	42	372	22	9.106	2.50E-03	rs6852847	4	127263004	q28.1
SNP_A-1919872	A	A	331	3	341	17	9.127	2.50E-03	rs1977703	13	18804190	q12.11
SNP_A-2245723	C	G	196	180	227	159	9.154	2.50E-03	rs6974446	7	70150073	q11.22
SNP_A-2228433	A	A	221	141	208	206	9.126	2.50E-03	rs7372767	3	161181568	q25.33
SNP_A-2232678	T	T	371	11	407	1	9.153	2.50E-03	rs12067906	1	189163655	q31.2
SNP_A-2237281	T	T	313	7	414	0	9.143	2.50E-03	rs17064333	6	135621458	q23.3
SNP_A-2236804	C	C	390	14	400	2	9.122	2.50E-03	rs1505272	15	37344088	q14
SNP_A-2235700	G	G	343	1	373	13	9.157	2.50E-03	rs2525517	14	68068343	q24.1
SNP_A-2261964	G	G	254	94	300	64	9.161	2.50E-03	rs6133475	20	7640889	p12.3
SNP_A-2271660	C	C	397	17	385	3	9.151	2.50E-03	rs903451	7	97736583	q22.1
SNP_A-2264935	G	G	221	191	265	149	9.167	2.50E-03	rs1389663	3	22331934	p24.3
SNP_A-2283731	A	A	273	47	335	27	9.176	2.50E-03	rs7956041	12	40378217	q12
SNP_A-2279117	G	G	339	29	287	51	9.111	2.50E-03	rs12447678	16	13608932	p13.12
SNP_A-2291720	A	A	277	37	352	20	9.175	2.50E-03	rs16957364	17	43910744	q21.32
SNP_A-2309818	A	A	206	172	228	120	9.151	2.50E-03	rs3999074	10	65233653	q21.3
SNP_A-2306857	T	T	405	3	365	15	9.094	2.60E-03	rs6094101	20	43240886	q13.12
SNP_A-2275791	G	G	355	1	358	12	9.054	2.60E-03	rs7243154	18	11193236	p11.21
SNP_A-2272333	C	C	210	146	278	122	9.095	2.60E-03	rs9410425	9	88791865	q22.1
SNP_A-2270512	C	C	360	52	323	83	9.079	2.60E-03	rs6687031	1	72558211	p31.1
SNP_A-2231259	C	C	320	28	382	12	9.059	2.60E-03	rs7594501	2	191764106	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2245922	G	G	296	40	368	22	9.067	2.60E-03	rs926154	9	15497987	p22.3
SNP_A-2247991	T	T	282	94	224	122	9.047	2.60E-03	rs285737	15	91032010	q26.1
SNP_A-2247149	A	A	416	0	364	8	9.038	2.60E-03	rs1440465	2	164216017	q24.3
SNP_A-1919987	T	T	336	8	321	25	9.094	2.60E-03	rs17067243	18	56483767	q21.32
SNP_A-1916351	C	C	333	53	344	26	9.072	2.60E-03	rs2315334	4	14533398	p15.33
SNP_A-1980712	A	A	402	4	367	17	9.035	2.60E-03	rs31959	5	11503247	p15.2
SNP_A-1938964	G	G	312	50	311	89	9.072	2.60E-03	rs1483550	4	163283329	q32.2
SNP_A-1956223	A	A	296	68	370	46	9.041	2.60E-03	rs10078886	5	31463198	p13.3
SNP_A-1955926	T	T	382	0	375	9	9.06	2.60E-03	rs17116606	12	53600868	q13.2
SNP_A-1950905	C	C	380	0	373	9	9.06	2.60E-03	rs1006175	6	137796371	q23.3
SNP_A-1947882	A	A	304	12	368	2	9.043	2.60E-03	rs17008911	4	85721174	q21.23
SNP_A-1949305	T	T	377	11	409	1	9.036	2.60E-03	rs17091341	14	55889330	q22.3
SNP_A-1798931	G	A	215	147	205	193	9.058	2.60E-03	rs6440003	3	142576907	q23
SNP_A-1799027	A	A	285	75	356	52	9.065	2.60E-03	rs12503811	4	115443007	q26
SNP_A-1800900	C	C	333	21	391	7	9.103	2.60E-03	rs7329130	13	73422690	q22.1
SNP_A-1670934	C	C	294	96	272	142	9.038	2.60E-03	rs10501140	11	35451951	p13
SNP_A-1785305	G	G	411	1	377	11	9.089	2.60E-03	rs17034965	2	68242435	p14
SNP_A-1725858	C	C	317	15	329	39	9.062	2.60E-03	rs1919319	4	166094948	q32.3
SNP_A-1727190	G	G	360	8	345	25	9.071	2.60E-03	rs10488586	7	20357112	p21.1
SNP_A-1815850	G	A	218	148	212	202	9.068	2.60E-03	rs4976845	13	108622929	q33.3
SNP_A-2185201	C	C	355	41	323	15	9.055	2.60E-03	rs16959241	17	9866531	p13.1
SNP_A-2170357	G	G	342	62	294	92	9.061	2.60E-03	rs977162	3	20166510	p24.3
SNP_A-2221798	G	G	293	15	321	41	9.055	2.60E-03	rs8071383	17	2980836	p13.3
SNP_A-2166541	T	T	361	27	371	9	9.054	2.60E-03	rs12625025	20	55722148	q13.32
SNP_A-2111742	T	T	396	0	387	9	9.103	2.60E-03	rs10103245	8	50119082	q11.21
SNP_A-2137358	C	C	312	14	373	3	9.034	2.60E-03	rs6727854	2	158582356	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2104660	A	A	343	5	334	20	9.069	2.60E-03	rs6820779	4	1087745	p16.3
SNP_A-2049165	C	T	243	159	191	189	9.064	2.60E-03	rs11248546	10	125232273	q26.13
SNP_A-2010654	A	A	259	127	307	93	9.079	2.60E-03	rs183733	5	9430048	p15.31
SNP_A-2006935	C	C	287	53	341	31	8.985	2.70E-03	rs2667160	2	195793616	q32.3
SNP_A-2013491	C	C	323	25	386	10	8.967	2.70E-03	rs7015619	8	67852776	q13.1
SNP_A-2022461	G	G	272	28	362	14	9.012	2.70E-03	rs2255476	1	72901103	p31.1
SNP_A-2038152	G	G	379	21	404	6	9.009	2.70E-03	rs7546477	1	99864204	p21.2
SNP_A-2044118	G	G	313	19	374	6	8.981	2.70E-03	rs16851065	1	199886675	q32.1
SNP_A-2043358	A	A	326	40	332	76	8.974	2.70E-03	rs10005398	4	157504443	q32.1
SNP_A-2057967	C	C	380	0	375	9	9.012	2.70E-03	rs3777797	6	133626530	q23.2
SNP_A-2091566	A	A	337	27	393	11	8.974	2.70E-03	rs1897511	10	118176259	q25.3
SNP_A-2091816	A	A	310	32	275	57	8.97	2.70E-03	rs2124971	2	160877360	q24.2
SNP_A-2089608	C	C	395	1	365	11	9.005	2.70E-03	rs7208331	17	56055974	q23.2
SNP_A-2127267	G	G	294	28	313	61	8.996	2.70E-03	rs7232859	18	3556945	p11.31
SNP_A-2152701	C	C	332	12	400	2	9.005	2.70E-03	rs9555310	13	106440323	q33.3
SNP_A-2144813	A	A	324	38	329	73	9.005	2.70E-03	rs9931184	16	76320756	q23.1
SNP_A-2141323	C	C	354	34	376	14	8.991	2.70E-03	rs7529411	1	244298152	q44
SNP_A-2140805	C	A	183	165	229	163	8.967	2.70E-03	rs6971616	7	40930049	p14.1
SNP_A-2219976	C	C	320	2	364	16	8.989	2.70E-03	rs8057929	16	52818224	q12.2
SNP_A-2217066	C	C	347	45	376	22	9.014	2.70E-03	rs4766763	12	114318183	q24.21
SNP_A-2207734	T	T	359	11	389	1	9.016	2.70E-03	rs11574980	13	45577313	q14.13
SNP_A-2178280	T	T	304	48	318	90	9.02	2.70E-03	rs7187662	16	48171539	q12.1
SNP_A-2191535	G	G	311	7	406	0	9.024	2.70E-03	rs16823155	1	181148069	q25.3
SNP_A-1838629	T	T	212	210	253	165	8.996	2.70E-03	rs10279346	7	40927622	p14.1
SNP_A-1860702	C	C	346	52	319	85	9.001	2.70E-03	rs7797095	7	86212015	q21.12
SNP_A-1855839	G	G	320	10	385	1	9.032	2.70E-03	rs11862736	16	25811211	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1720837	A	A	377	11	336	28	9.011	2.70E-03	rs10509192	10	64762123	q21.3
SNP_A-1784266	G	G	413	9	418	0	9.011	2.70E-03	rs2878392	12	2970221	p13.33
SNP_A-1780906	C	C	319	43	332	82	8.983	2.70E-03	rs2736852	8	134507898	q24.22
SNP_A-1792985	G	G	412	2	375	13	8.973	2.70E-03	rs2348054	7	134187406	q33
SNP_A-1795200	C	C	378	18	356	40	9.004	2.70E-03	rs1793788	11	130591120	q25
SNP_A-1955508	G	G	310	14	369	3	8.977	2.70E-03	rs17091644	14	56075986	q22.3
SNP_A-1958401	A	A	216	192	257	149	8.971	2.70E-03	rs4573	6	26654787	p22.1
SNP_A-1940172	G	G	218	146	289	123	8.975	2.70E-03	rs1453281	7	47562018	p12.3
SNP_A-1942824	T	T	309	23	301	49	9.025	2.70E-03	rs7608253	2	64515587	p14
SNP_A-1942699	A	A	295	29	305	61	9.021	2.70E-03	rs2429542	17	36175982	q21.2
SNP_A-1966460	A	A	334	34	390	16	8.967	2.70E-03	rs188147	2	200609491	q33.1
SNP_A-1912530	T	T	278	130	233	169	9.006	2.70E-03	rs16933100	12	28656614	p11.22
SNP_A-1912440	C	C	403	1	373	11	8.991	2.70E-03	rs6009130	22	47735519	q13.32
SNP_A-1909639	G	G	410	2	373	13	8.977	2.70E-03	rs7083043	10	32101010	p11.22
SNP_A-1882992	A	A	282	26	345	11	8.988	2.70E-03	rs16866841	2	226805275	q36.3
SNP_A-1889170	G	G	330	28	348	10	9.004	2.70E-03	rs10427701	22	29798000	q12.2
SNP_A-1890948	A	A	362	8	317	23	8.989	2.70E-03	rs7300329	12	91886737	q22
SNP_A-2247709	G	G	313	39	301	71	8.998	2.70E-03	rs1019233	7	20861823	p15.3
SNP_A-2255893	A	A	288	38	365	21	8.986	2.70E-03	rs1258686	7	62745429	q11.21
SNP_A-2230696	G	G	282	86	277	137	9.034	2.70E-03	rs7004915	8	9650964	p23.1
SNP_A-2236109	G	G	379	9	339	25	9.001	2.70E-03	rs17587298	4	40390583	p14
SNP_A-2258943	G	G	235	177	278	136	8.97	2.70E-03	rs9406190	6	8630803	p24.3
SNP_A-2273023	G	G	401	3	392	16	8.977	2.70E-03	rs11030327	11	3913131	p15.4
SNP_A-2285175	C	C	324	12	390	2	8.989	2.70E-03	rs16927138	8	62357914	q12.2
SNP_A-2281466	C	C	250	136	217	183	9.01	2.70E-03	rs2172065	16	84961463	q24.1
SNP_A-2281788	G	G	418	0	366	8	9.032	2.70E-03	rs705476	10	3558208	p15.2
SNP_A-2294568	T	T	305	43	321	83	8.987	2.70E-03	rs4287668	18	45808351	q21.1
SNP_A-2309507	G	G	227	111	215	167	8.951	0.0028	rs1444889	5	38561123	p13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2303888	T	T	336	12	402	2	8.925	0.0028	rs16875080	6	85503901	q14.3
SNP_A-2282920	A	A	220	178	255	133	8.964	0.0028	rs3011382	10	122561234	q26.12
SNP_A-2267340	T	T	362	8	410	0	8.957	0.0028	rs7320382	13	51321099	q14.3
SNP_A-1895800	G	G	271	99	262	152	8.902	0.0028	rs1248679	10	79277783	q22.3
SNP_A-1894059	G	G	334	10	399	1	8.963	0.0028	rs12110748	6	3253608	p25.2
SNP_A-1900276	C	C	320	28	380	12	8.958	0.0028	rs2431301	8	140679763	q24.3
SNP_A-1875425	A	A	379	13	416	2	8.963	0.0028	rs803323	1	25175524	p36.11
SNP_A-1911522	C	C	296	74	293	121	8.902	0.0028	rs17712825	7	66586833	q11.22
SNP_A-1915571	G	G	187	167	258	148	8.958	0.0028	rs6487932	12	30737896	p11.21
SNP_A-1967681	C	C	264	90	254	140	8.949	0.0028	rs6695903	1	15731246	p36.13
SNP_A-1963890	G	G	301	19	302	44	8.921	0.0028	rs1526389	2	78481679	p12
SNP_A-1980069	C	C	237	171	273	127	8.959	0.0028	rs10492997	1	19514677	p36.13
SNP_A-1983006	T	T	291	9	331	31	8.944	0.0028	rs1457763	5	113717932	q22.3
SNP_A-1938415	G	G	278	144	231	183	8.916	0.0028	rs2526303	5	130531185	q23.3
SNP_A-1935695	G	G	325	3	318	16	8.917	0.0028	rs17084283	13	25990008	q12.13
SNP_A-1804802	A	A	344	0	343	9	8.911	0.0028	---	20	43326917	q13.12
SNP_A-1811505	C	C	374	0	371	9	8.965	0.0028	rs11175216	12	62641256	q14.2
SNP_A-1781012	G	G	296	68	299	115	8.91	0.0028	rs1372316	11	13726579	p15.2
SNP_A-1714308	A	A	353	43	387	21	8.948	0.0028	rs954057	2	135566826	q21.3
SNP_A-1648248	T	T	350	0	347	9	8.963	0.0028	rs9304445	18	49335127	q21.2
SNP_A-1702759	G	G	249	149	216	198	8.949	0.0028	rs1586601	8	118374596	q24.11
SNP_A-1700530	C	C	345	1	352	12	8.927	0.0028	rs588455	13	66939157	q21.33
SNP_A-1862107	A	A	319	7	412	0	8.931	0.0028	rs17091832	14	34914696	q13.2
SNP_A-1873887	T	T	338	10	403	1	8.945	0.0028	rs6485302	11	42109215	p12
SNP_A-1825905	T	T	259	95	261	153	8.939	0.0028	rs17698533	14	87881781	q31.3
SNP_A-1827319	G	G	351	63	377	35	8.924	0.0028	rs560634	19	7737953	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2185397	G	G	322	30	332	62	8.947	0.0028	rs815972	7	55264917	p11.2
SNP_A-2186306	T	T	257	47	331	29	8.917	0.0028	rs6799721	3	166063946	q26.1
SNP_A-2180859	G	G	319	93	349	59	8.933	0.0028	rs4686377	3	9852452	p25.3
SNP_A-2221277	G	G	366	8	412	0	8.903	0.0028	rs9369384	6	42864299	p21.1
SNP_A-2224185	C	C	277	145	308	102	8.957	0.0028	rs9616414	22	47752454	q13.32
SNP_A-2145829	T	T	297	69	364	46	8.925	0.0028	rs9572452	13	69913384	q21.33
SNP_A-2088699	C	C	392	4	313	15	8.913	0.0028	rs4234696	3	50634745	p21.31
SNP_A-2082031	A	A	340	10	405	1	8.936	0.0028	rs3746670	20	4558152	p13
SNP_A-2057345	C	C	338	38	271	59	8.958	0.0028	rs11039351	11	5842422	p15.4
SNP_A-2076721	A	A	315	39	372	20	8.935	0.0028	rs17209931	11	85488474	q14.2
SNP_A-2039807	C	C	340	2	336	14	8.932	0.0028	rs16928385	10	28206409	p12.1
SNP_A-2035765	C	C	337	63	283	91	8.931	0.0028	rs7551345	1	31500963	p35.2
SNP_A-2036448	T	T	252	94	210	128	8.933	0.0028	rs10240983	7	85012347	q21.11
SNP_A-2024108	A	A	246	118	306	90	8.959	0.0028	rs17406207	7	135727605	q33
SNP_A-2012946	T	T	266	84	267	137	8.891	2.90E-03	rs677909	11	85435237	q14.2
SNP_A-2018566	G	G	306	92	334	58	8.887	2.90E-03	rs17191809	21	35366649	q22.12
SNP_A-2017666	A	A	328	10	389	1	8.884	2.90E-03	rs16984180	21	29771486	q21.3
SNP_A-2009911	C	C	333	31	348	64	8.858	2.90E-03	rs1500498	4	78919395	q21.1
SNP_A-2004040	C	C	322	50	275	77	8.895	2.90E-03	rs6576569	15	24192203	q12
SNP_A-2072797	C	C	238	122	311	99	8.891	2.90E-03	rs11613673	12	24889776	p12.1
SNP_A-2072403	T	T	400	0	356	8	8.884	2.90E-03	rs17066950	13	45065165	q14.13
SNP_A-2070469	C	T	215	201	245	173	8.882	2.90E-03	rs12716852	16	76746239	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2058492	C	C	327	27	342	58	8.869	2.90E-03	rs10864552	1	12352966	p36.21
SNP_A-2052829	C	C	311	17	379	5	8.897	2.90E-03	rs10027377	4	54346832	q12
SNP_A-2051837	G	G	291	121	328	84	8.89	2.90E-03	rs2386937	20	59800328	q13.33
SNP_A-2083256	G	G	304	56	300	96	8.859	2.90E-03	rs9813535	3	18938756	p24.3
SNP_A-2079974	C	C	277	95	315	63	8.873	2.90E-03	rs1959176	14	32598416	q13.1
SNP_A-2092088	C	C	340	30	340	60	8.845	2.90E-03	rs12115314	9	14713386	p22.3
SNP_A-2096000	T	T	263	95	328	70	8.845	2.90E-03	rs2125714	5	100710302	q21.1
SNP_A-2167005	C	C	419	1	354	10	8.875	2.90E-03	rs17168462	5	134856204	q31.1
SNP_A-2162973	T	T	304	42	306	78	8.852	2.90E-03	rs1011365	15	25071628	q12
SNP_A-2135729	G	G	338	10	401	1	8.893	2.90E-03	rs1506942	1	162073554	q23.3
SNP_A-2113112	G	G	391	1	365	11	8.898	2.90E-03	---	13	45074613	q14.13
SNP_A-2222845	G	G	357	1	366	12	8.883	2.90E-03	---	13	18810679	q12.11
SNP_A-2204986	A	A	362	2	360	14	8.872	2.90E-03	rs11183051	12	44135240	q12
SNP_A-2206907	A	A	346	2	344	14	8.866	2.90E-03	rs12597747	16	27203565	p12.1
SNP_A-2169391	C	C	346	64	312	98	8.893	2.90E-03	rs17603668	4	37152106	p14
SNP_A-2174377	G	G	379	11	405	1	8.878	2.90E-03	rs2193199	7	103880843	q22.2
SNP_A-1869837	G	G	389	9	351	25	8.863	2.90E-03	rs17774635	19	37323334	q13.11
SNP_A-1809550	C	C	331	11	320	30	8.899	2.90E-03	rs508052	8	98593864	q22.1
SNP_A-1801380	C	C	321	79	260	106	8.853	2.90E-03	rs648787	1	61008261	p31.3
SNP_A-1787389	C	C	273	15	342	4	8.878	2.90E-03	rs746996	1	232521124	q42.3
SNP_A-1948501	G	G	349	1	358	12	8.874	2.90E-03	rs6571679	14	34255308	q13.1
SNP_A-1969947	C	C	187	161	243	133	8.89	2.90E-03	rs2832923	21	30809399	q22.11
SNP_A-1917367	C	C	183	145	256	128	8.848	2.90E-03	rs6819112	4	77924677	q21.1
SNP_A-1918464	G	G	363	13	396	2	8.883	2.90E-03	rs1527157	7	113514705	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1923500	G	G	263	29	334	14	8.844	2.90E-03	rs10858572	12	86153299	q21.32
SNP_A-1932021	A	A	299	53	362	32	8.856	2.90E-03	rs7958736	12	51254645	q13.13
SNP_A-1926313	T	T	335	31	392	14	8.842	2.90E-03	rs396402	4	167565648	q32.3
SNP_A-1874118	A	A	339	7	340	24	8.873	2.90E-03	rs1485128	2	151730921	q23.3
SNP_A-1887222	C	C	358	34	378	14	8.877	2.90E-03	rs2013727	2	13191692	p24.3
SNP_A-1893761	G	G	297	59	352	36	8.87	2.90E-03	rs16907133	8	80799140	q21.13
SNP_A-2261820	C	C	294	122	325	83	8.895	2.90E-03	rs10242065	7	135636152	q33
SNP_A-2261028	T	T	306	10	327	31	8.87	2.90E-03	rs1507609	18	9384998	p11.22
SNP_A-2242063	T	T	348	2	346	14	8.867	2.90E-03	rs10059586	5	107882842	q21.3
SNP_A-2243248	A	A	371	11	393	1	8.783	3.00E-03	rs16985785	19	59858220	q13.42
SNP_A-2249191	A	A	398	6	358	20	8.8	3.00E-03	rs11634262	15	66892287	q23
SNP_A-2238122	G	G	345	15	375	3	8.816	3.00E-03	rs11637526	15	62861185	q22.31
SNP_A-2232743	T	T	342	6	342	22	8.788	3.00E-03	rs7983604	13	109856843	q34
SNP_A-2271952	T	T	324	60	285	91	8.779	3.00E-03	rs35768	12	99087907	q23.1
SNP_A-2283856	A	A	305	31	318	64	8.824	3.00E-03	rs12171331	4	88076008	q21.3
SNP_A-2304265	G	G	224	186	262	142	8.83	3.00E-03	rs2747097	14	57531928	q23.1
SNP_A-2294638	C	C	201	171	237	129	8.791	3.00E-03	rs10210681	2	225860760	q36.2
SNP_A-2289809	G	G	278	40	287	77	8.782	3.00E-03	rs9643406	8	50670255	q11.21
SNP_A-1900432	G	G	374	8	416	0	8.8	3.00E-03	rs1291371	12	12997777	p13.1
SNP_A-1898139	C	C	271	91	331	65	8.806	3.00E-03	rs6887156	5	100729982	q21.1
SNP_A-1926468	C	C	307	55	374	34	8.83	3.00E-03	---	8	3236163	p23.2
SNP_A-1929307	C	C	313	107	345	71	8.818	3.00E-03	rs1023067	10	112102022	q25.2
SNP_A-1960881	A	A	331	13	341	35	8.827	3.00E-03	rs17094613	12	43086127	q12
SNP_A-1935808	C	C	396	14	396	2	8.824	3.00E-03	rs7694094	4	13003557	p15.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1938615	C	C	349	23	297	43	8.826	3.00E-03	rs12285071	11	82420713	q14.1
SNP_A-1786647	G	G	408	14	375	33	8.838	3.00E-03	---	1	54908760	p32.3
SNP_A-1808380	G	G	355	25	364	8	8.786	3.00E-03	rs6534252	4	122357707	q27
SNP_A-1814513	G	G	383	3	353	15	8.798	3.00E-03	rs9289221	3	124642104	q21.1
SNP_A-1700187	C	C	299	73	276	112	8.809	3.00E-03	rs1946303	7	132554692	q33
SNP_A-1674591	A	G	210	152	209	187	8.825	3.00E-03	rs10498620	14	87735656	q32.11
SNP_A-1873491	C	C	344	12	408	2	8.827	3.00E-03	rs16951224	18	45699106	q21.1
SNP_A-1848300	T	T	268	150	227	193	8.782	3.00E-03	rs11254908	10	7047094	p14
SNP_A-2188501	G	G	336	10	395	1	8.796	3.00E-03	rs7658698	4	145123469	q31.21
SNP_A-2191735	G	G	187	155	264	140	8.817	3.00E-03	rs4528908	3	149568220	q24
SNP_A-2207740	A	A	399	9	361	25	8.827	3.00E-03	rs11065386	12	119890210	q24.31
SNP_A-2110158	T	T	373	9	337	25	8.824	3.00E-03	rs7044778	9	77506162	q21.2
SNP_A-2121695	T	T	289	59	275	97	8.814	3.00E-03	rs4920901	5	115330403	q23.1
SNP_A-2130464	C	C	254	102	252	160	8.811	3.00E-03	rs957255	13	41599803	q14.11
SNP_A-2162786	G	G	313	33	327	67	8.79	3.00E-03	rs1958476	14	37797573	q21.1
SNP_A-2164843	A	A	332	24	385	9	8.833	3.00E-03	rs5745290	5	10736627	p15.2
SNP_A-2156241	A	A	323	11	338	32	8.778	3.00E-03	rs9318073	13	71893704	q21.33
SNP_A-2146956	G	G	312	52	322	94	8.812	3.00E-03	rs11524508	12	18524861	p12.3
SNP_A-2102922	T	T	213	131	198	190	8.779	3.00E-03	rs2730747	12	117585161	q24.23
SNP_A-2080119	A	A	284	34	360	18	8.785	3.00E-03	rs11199255	10	85320720	q23.1
SNP_A-2054413	G	G	271	25	364	12	8.789	3.00E-03	rs9499921	6	105243945	q21
SNP_A-2049285	G	G	344	10	405	1	8.815	3.00E-03	rs16933201	11	4453710	p15.4
SNP_A-2065183	T	T	240	112	226	166	8.785	3.00E-03	rs6428237	1	191155604	q31.3
SNP_A-2063605	G	G	397	7	383	23	8.78	3.00E-03	rs2785173	11	35112308	p13
SNP_A-2067643	C	C	367	1	380	12	8.785	3.00E-03	rs10493282	1	60462773	p31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2066528	C	C	372	24	332	46	8.773	3.10E-03	rs344902	2	139911793	q22.1
SNP_A-2072624	T	T	374	8	414	0	8.758	3.10E-03	rs17134987	6	2335711	p25.2
SNP_A-2026491	A	A	365	3	362	16	8.775	3.10E-03	rs5021590	4	188121231	q35.2
SNP_A-2022547	T	T	416	2	387	13	8.722	3.10E-03	rs16850573	2	214307187	q34
SNP_A-2045834	C	C	271	75	272	124	8.738	3.10E-03	rs10070137	5	65068283	q12.3
SNP_A-2125371	C	C	355	1	368	12	8.768	3.10E-03	rs16883239	8	113293800	q23.3
SNP_A-2108837	A	A	252	158	210	200	8.746	3.10E-03	rs1695969	15	85555170	q25.3
SNP_A-2181746	G	G	299	25	354	10	8.765	3.10E-03	rs4303156	10	118008490	q25.3
SNP_A-1869418	G	G	307	47	298	82	8.72	3.10E-03	rs17660776	18	46065372	q21.1
SNP_A-1867836	A	A	395	1	375	11	8.726	3.10E-03	rs17110420	14	25382609	q12
SNP_A-1839467	C	C	394	18	396	4	8.739	3.10E-03	rs17016730	1	106348252	p21.1
SNP_A-1735272	T	T	320	68	289	103	8.721	3.10E-03	rs2421528	5	159996571	q34
SNP_A-1780789	C	T	179	141	208	168	8.762	3.10E-03	rs6847487	4	91504007	q22.1
SNP_A-1788365	G	G	273	135	232	176	8.734	3.10E-03	rs5025419	3	32214253	p23
SNP_A-1937066	A	A	320	8	354	28	8.77	3.10E-03	rs17159549	7	84293127	q21.11
SNP_A-1937067	G	G	309	39	362	20	8.74	3.10E-03	rs3007682	1	148722612	q21.3
SNP_A-1969127	G	G	361	9	327	25	8.766	3.10E-03	rs2823901	21	16892745	q21.1
SNP_A-1927879	C	C	379	1	359	11	8.744	3.10E-03	rs11134804	5	156897522	q33.3
SNP_A-1927946	T	T	276	80	345	57	8.769	3.10E-03	rs10275303	7	133854762	q33
SNP_A-1915805	A	A	364	46	393	23	8.735	3.10E-03	rs11779853	8	14960422	p22
SNP_A-2230768	T	T	349	21	401	7	8.77	3.10E-03	rs16889286	6	24556783	p22.2
SNP_A-2235868	G	G	333	3	353	17	8.766	3.10E-03	rs6731071	2	26838342	p23.3
SNP_A-2250215	C	C	215	133	285	111	8.723	3.10E-03	rs6685657	1	76129461	p31.1
SNP_A-2248749	G	G	332	10	389	1	8.76	3.10E-03	rs16903599	5	37392668	p13.2
SNP_A-2265535	C	C	288	12	399	3	8.698	3.20E-03	rs9583332	13	108483649	q33.3
SNP_A-2263929	T	T	231	115	219	171	8.686	3.20E-03	rs10188228	2	163528924	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2260504	A	A	351	1	366	12	8.707	3.20E-03	rs1677128	12	21683322	p12.1
SNP_A-2288478	G	G	383	7	335	21	8.677	3.20E-03	rs4296532	3	39682202	p22.2
SNP_A-2304308	T	C	204	154	219	189	8.673	3.20E-03	rs11795353	9	34404339	p13.3
SNP_A-2309466	G	G	377	11	395	1	8.672	3.20E-03	rs6838812	4	14047154	p15.33
SNP_A-1899518	C	C	314	8	335	27	8.684	3.20E-03	rs4603392	12	24934221	p12.1
SNP_A-1882825	A	A	365	15	393	3	8.708	3.20E-03	rs17137406	10	15626596	p13
SNP_A-1884753	G	G	307	23	371	9	8.688	3.20E-03	rs7565023	2	163124980	q24.2
SNP_A-1879903	A	A	411	11	389	29	8.686	3.20E-03	rs17030886	1	7440107	p36.23
SNP_A-1987712	G	G	301	59	370	38	8.676	3.20E-03	rs9375929	6	133278693	q23.2
SNP_A-1987935	C	C	291	41	359	23	8.718	3.20E-03	rs17072149	6	143382964	q24.2
SNP_A-1977197	G	G	329	3	351	17	8.683	3.20E-03	rs10488922	4	57992354	q12
SNP_A-1792325	T	T	273	47	267	83	8.71	3.20E-03	rs1881535	11	61878199	q12.3
SNP_A-1802696	G	G	420	0	382	8	8.701	3.20E-03	rs17095801	14	97230425	q32.2
SNP_A-1802726	G	G	321	7	341	25	8.675	3.20E-03	rs6493998	15	29936000	q13.3
SNP_A-1737844	G	G	329	47	312	80	8.696	3.20E-03	rs10502813	18	39351157	q12.3
SNP_A-1829804	C	C	404	2	377	13	8.682	3.20E-03	rs10106319	8	104590191	q22.3
SNP_A-1825891	G	G	375	19	397	5	8.714	3.20E-03	rs10167952	2	29721156	p23.2
SNP_A-1820007	T	T	223	139	205	197	8.699	3.20E-03	rs6081862	20	19995559	p11.23
SNP_A-1875570	G	G	418	0	380	8	8.705	3.20E-03	rs16977717	17	69136688	q25.1
SNP_A-1855767	T	T	211	71	209	119	8.717	3.20E-03	rs10166912	2	173100257	q31.1
SNP_A-2177681	C	C	308	76	270	110	8.693	3.20E-03	rs4689472	4	6651133	p16.1
SNP_A-2171182	A	A	358	26	330	50	8.698	3.20E-03	rs12912051	15	75923034	q24.3
SNP_A-2171296	A	A	295	35	323	73	8.711	3.20E-03	rs1320495	1	223571515	q42.13
SNP_A-2205988	C	C	368	16	351	37	8.702	3.20E-03	rs2002321	7	153906333	q36.2
SNP_A-2204394	C	C	407	1	389	11	8.662	3.20E-03	rs4858833	3	47550572	p21.31
SNP_A-2132713	A	A	385	11	405	1	8.716	3.20E-03	---	1	170960340	q25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2131646	G	G	257	101	325	77	8.663	3.20E-03	rs7864693	9	29490946	p21.1
SNP_A-2148500	A	A	407	1	350	10	8.69	3.20E-03	rs8088539	18	14340608	p11.21
SNP_A-2142274	A	A	362	0	371	9	8.679	3.20E-03	rs16961583	18	27102092	q12.1
SNP_A-2045369	C	C	404	0	368	8	8.685	3.20E-03	---	5	27319545	p14.1
SNP_A-2040508	G	G	392	6	375	21	8.705	3.20E-03	rs1286943	14	89418102	q32.11
SNP_A-2025927	G	G	366	10	339	27	8.712	3.20E-03	rs11217398	11	119064341	q23.3
SNP_A-2006805	G	G	262	104	332	80	8.69	3.20E-03	rs2255518	10	135165726	q26.3
SNP_A-2005650	T	T	315	45	318	82	8.713	3.20E-03	rs4281815	18	45807493	q21.1
SNP_A-2069438	T	T	359	37	376	16	8.694	3.20E-03	rs10410399	19	19067500	p13.11
SNP_A-2064701	C	C	301	45	368	26	8.718	3.20E-03	rs6775958	3	198929894	q29
SNP_A-2049669	C	C	285	83	283	133	8.675	3.20E-03	rs1537929	13	68549853	q21.33
SNP_A-2058586	G	G	277	53	334	32	8.667	3.20E-03	rs10823804	10	73050910	q22.1
SNP_A-2060105	G	G	279	109	306	72	8.681	3.20E-03	rs1885346	11	35349331	p13
SNP_A-2081229	C	T	217	195	235	173	8.666	3.20E-03	rs164149	1	159070239	q23.3
SNP_A-2105430	G	G	267	37	345	21	8.692	3.20E-03	rs10190843	2	192405189	q32.3
SNP_A-2078714	C	C	390	24	359	47	8.657	0.0033	rs1867622	17	59690924	q23.3
SNP_A-2057315	T	T	418	0	384	8	8.616	0.0033	rs7548931	1	45435285	p34.1
SNP_A-2056852	G	G	397	11	415	1	8.655	0.0033	rs17034208	2	107461210	q12.3
SNP_A-2053240	C	C	332	10	385	1	8.654	0.0033	rs11175578	12	63551954	q14.3
SNP_A-2066343	G	G	344	14	397	3	8.608	0.0033	rs7197456	16	13845373	p13.12
SNP_A-2009201	G	G	307	19	393	7	8.651	0.0033	rs7431173	3	147189204	q24
SNP_A-1997450	A	A	263	83	232	120	8.634	0.0033	rs2319404	1	29441503	p35.3
SNP_A-1994515	G	G	416	0	382	8	8.619	0.0033	rs16871817	8	105849484	q22.3
SNP_A-2026092	G	G	319	37	379	19	8.631	0.0033	rs17790961	7	34699203	p14.3
SNP_A-2047350	C	C	305	115	260	152	8.635	0.0033	rs4453501	16	28167502	p11.2
SNP_A-2141218	A	A	378	20	363	43	8.622	0.0033	rs12192468	6	23739341	p22.3
SNP_A-2139709	C	C	311	45	356	24	8.654	0.0033	rs13415553	2	221243709	q35
SNP_A-2166387	G	G	344	10	399	1	8.661	0.0033	rs169147	14	56289873	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2108061	A	A	370	26	335	49	8.608	0.0033	rs12976706	19	48629080	q13.31
SNP_A-2110848	A	A	295	123	242	156	8.649	0.0033	rs10742355	11	4625467	p15.4
SNP_A-2116328	G	G	332	16	378	4	8.615	0.0033	rs6730870	2	104821371	q12.1
SNP_A-2201662	G	G	313	13	325	35	8.645	0.0033	rs16957269	16	10331058	p13.13
SNP_A-2208573	G	G	318	30	332	62	8.613	0.0033	rs6874766	5	93239563	q15
SNP_A-2208968	G	G	358	10	415	1	8.66	0.0033	rs2517509	6	31138203	p21.33
SNP_A-2210000	A	A	363	13	318	30	8.625	0.0033	rs761692	14	25085172	q12
SNP_A-2211956	T	T	224	98	209	147	8.636	0.0033	rs6050363	20	25072088	p11.21
SNP_A-2178767	C	C	414	0	380	8	8.622	0.0033	rs1461315	10	14164630	p13
SNP_A-1872331	T	C	219	177	211	171	8.638	0.0033	rs10950253	7	70181738	q11.22
SNP_A-1817043	G	G	387	11	403	1	8.613	0.0033	rs7124161	11	33652114	p13
SNP_A-1823575	T	T	349	1	366	12	8.648	0.0033	rs17057443	6	97663918	q16.1
SNP_A-1783097	A	A	326	42	294	70	8.63	0.0033	rs17130968	1	90267928	p22.2
SNP_A-1801335	T	T	365	1	349	11	8.643	0.0033	rs704508	6	63889269	q12
SNP_A-1812558	C	T	237	173	219	199	8.633	0.0033	rs4149513	2	100481244	q11.2
SNP_A-1796371	C	C	305	19	356	6	8.616	0.0033	rs4771684	13	109954774	q34
SNP_A-1788431	C	C	298	64	371	43	8.641	0.0033	rs9987001	7	133181300	q33
SNP_A-1978524	C	C	227	129	215	189	8.649	0.0033	rs1490901	4	112515402	q25
SNP_A-1963291	A	A	358	18	333	39	8.62	0.0033	rs2884114	2	53281919	p16.2
SNP_A-1969264	A	A	316	38	330	74	8.614	0.0033	rs2825559	21	19693752	q21.1
SNP_A-1969381	A	A	254	150	293	111	8.608	0.0033	rs2827009	21	22051268	q21.1
SNP_A-1959602	T	T	269	101	339	77	8.633	0.0033	rs1920750	12	89898474	q21.33
SNP_A-1950014	A	A	317	13	399	3	8.643	0.0033	rs1037671	4	62130125	q13.1
SNP_A-1887001	A	A	312	28	364	12	8.612	0.0033	rs10109933	8	6053806	p23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889783	A	A	414	0	380	8	8.622	0.0033	rs16841571	1	155819544	q23.1
SNP_A-1909902	G	G	310	54	315	95	8.618	0.0033	rs3934843	2	1848923	p25.3
SNP_A-1921783	T	T	335	33	398	16	8.637	0.0033	rs2049213	3	193503002	q28
SNP_A-2306717	G	G	392	8	351	23	8.657	0.0033	rs2193111	17	11381021	p12
SNP_A-2307399	T	T	299	27	343	11	8.614	0.0033	rs6036740	20	24261439	p11.21
SNP_A-2304396	G	G	254	162	286	118	8.637	0.0033	rs213199	6	33343733	p21.32
SNP_A-2290721	G	G	362	0	373	9	8.633	0.0033	rs6474622	9	11067950	p23
SNP_A-2267549	A	C	201	137	179	167	8.631	0.0033	rs12194972	6	47761199	p12.3
SNP_A-2269355	T	T	353	5	354	20	8.656	0.0033	rs16829618	1	185622663	q31.1
SNP_A-2286260	C	C	340	10	393	1	8.624	0.0033	rs7940889	11	61237872	q12.2
SNP_A-2285997	C	C	308	44	313	81	8.655	0.0033	rs6826826	4	32532226	p15.1
SNP_A-2245809	A	C	195	163	226	176	8.658	0.0033	rs2492589	9	2549581	p24.2
SNP_A-2246653	C	C	322	44	389	25	8.624	0.0033	rs312462	17	6854376	p13.1
SNP_A-2249973	T	T	323	83	265	111	8.624	0.0033	rs7820164	8	111280682	q23.2
SNP_A-2228461	C	C	331	19	386	6	8.629	0.0033	rs2093010	14	68423480	q24.1
SNP_A-2228332	T	T	259	111	329	87	8.58	3.40E-03	rs4309387	16	54441384	q12.2
SNP_A-2284976	G	G	287	131	323	93	8.566	3.40E-03	rs17279736	2	106215883	q12.2
SNP_A-2275500	G	G	388	6	354	20	8.581	3.40E-03	rs16876645	8	30170870	p12
SNP_A-2259235	T	T	292	50	295	89	8.557	3.40E-03	rs7221423	17	78551921	q25.3
SNP_A-2261533	A	G	203	179	215	159	8.554	3.40E-03	rs1923295	11	35399184	p13
SNP_A-1923206	A	A	342	14	393	3	8.553	3.40E-03	rs7540539	1	101581343	p21.2
SNP_A-1927747	A	A	361	35	334	62	8.564	3.40E-03	rs7093648	10	122516963	q26.12
SNP_A-1911710	G	G	310	36	349	17	8.564	3.40E-03	rs17827108	17	27088517	q11.2
SNP_A-1973487	T	T	323	13	405	3	8.599	3.40E-03	rs6804056	3	86156343	p12.1
SNP_A-1987955	A	A	347	7	371	25	8.602	3.40E-03	rs10484817	6	144299332	q24.2
SNP_A-1799516	G	G	305	65	269	97	8.557	3.40E-03	rs4307046	5	62764937	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1782342	C	C	333	3	359	17	8.557	3.40E-03	rs2801953	10	42242982	q11.21
SNP_A-1744843	G	G	263	85	259	135	8.575	3.40E-03	rs2142824	22	35176707	q12.3
SNP_A-1823143	T	T	224	140	293	117	8.564	3.40E-03	rs10770658	12	20478088	p12.2
SNP_A-1836278	A	A	308	44	349	23	8.595	3.40E-03	rs7906078	10	15374968	p13
SNP_A-1834486	T	T	297	27	283	53	8.573	3.40E-03	rs1389457	11	26439347	p14.2
SNP_A-1869770	G	G	332	22	388	8	8.564	3.40E-03	rs16966434	17	22998744	q11.2
SNP_A-2216901	G	G	291	65	288	108	8.6	3.40E-03	rs17613530	13	70446113	q21.33
SNP_A-2133976	A	G	211	157	221	195	8.56	3.40E-03	rs2627696	4	88924474	q22.1
SNP_A-2138413	A	A	353	1	372	12	8.6	3.40E-03	rs16872438	5	74499568	q13.3
SNP_A-2148588	C	C	353	15	377	3	8.599	3.40E-03	rs16840879	4	7832444	p16.1
SNP_A-2037515	G	G	342	4	344	18	8.558	3.40E-03	rs2532828	10	115760137	q25.3
SNP_A-2053257	A	A	349	1	368	12	8.593	3.40E-03	rs1082337	9	27581569	p21.2
SNP_A-2054608	G	G	384	8	416	0	8.575	3.40E-03	rs11975443	7	3766021	p22.2
SNP_A-2052287	C	C	290	120	249	159	8.566	3.40E-03	rs241548	14	55613128	q22.3
SNP_A-2047902	G	G	245	107	225	155	8.586	3.40E-03	rs6092797	20	57521589	q13.32
SNP_A-2058723	A	A	336	38	305	65	8.556	3.40E-03	rs1964012	1	229234490	q42.2
SNP_A-2079962	G	G	340	22	398	8	8.599	3.40E-03	rs17166783	7	12948733	p21.3
SNP_A-2079904	T	T	314	8	337	27	8.588	3.40E-03	rs497493	2	165115260	q24.3
SNP_A-2090239	G	G	342	22	400	8	8.587	3.40E-03	rs17094935	1	74384797	p31.1
SNP_A-2105229	C	C	414	0	382	8	8.578	3.40E-03	rs12101360	15	62056766	q22.31
SNP_A-2105557	G	G	388	8	418	0	8.528	3.50E-03	rs3851907	1	233181173	q43
SNP_A-2103849	G	G	330	30	394	14	8.509	3.50E-03	rs1711374	4	179334306	q34.3
SNP_A-2056624	T	T	198	168	264	146	8.502	3.50E-03	rs17505794	6	94824800	q16.1
SNP_A-2058813	A	A	239	167	283	129	8.544	3.50E-03	rs6967003	7	77485092	q21.11
SNP_A-2048322	T	T	348	16	355	39	8.514	3.50E-03	rs1791858	11	21229958	p15.1
SNP_A-2070274	C	C	336	34	367	15	8.545	3.50E-03	rs1384536	6	2475319	p25.2
SNP_A-2043900	A	A	325	17	385	5	8.505	3.50E-03	rs11122611	1	227256686	q42.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1993410	G	G	317	9	407	1	8.534	3.50E-03	---	8	58678451	q12.1
SNP_A-1991433	T	T	207	161	275	139	8.53	3.50E-03	rs1477524	7	136262203	q33
SNP_A-1997572	C	C	323	7	398	0	8.524	3.50E-03	rs7850670	9	107999746	q31.2
SNP_A-2005534	A	A	261	159	218	200	8.538	3.50E-03	rs331991	18	22797233	q11.2
SNP_A-2017848	C	C	188	172	258	154	8.516	3.50E-03	rs7281360	21	30753600	q22.11
SNP_A-2149679	G	G	325	7	400	0	8.515	3.50E-03	rs16942965	15	87634875	q26.1
SNP_A-2138134	C	C	263	159	220	200	8.506	3.50E-03	rs603446	11	116159645	q23.3
SNP_A-2142911	A	A	325	15	396	4	8.551	3.50E-03	rs17120960	1	60858788	p31.3
SNP_A-2144995	C	C	203	115	202	180	8.544	3.50E-03	rs10785884	10	82244470	q22.3
SNP_A-2167140	T	T	270	28	276	58	8.508	3.50E-03	rs10043893	5	34473003	p13.2
SNP_A-2134266	T	T	369	17	390	4	8.547	3.50E-03	rs3745222	19	47126313	q13.2
SNP_A-2123241	C	C	368	20	363	5	8.511	3.50E-03	rs998903	7	114257450	q31.2
SNP_A-2217361	G	G	346	44	350	20	8.503	3.50E-03	rs630084	11	60315621	q12.2
SNP_A-2220756	A	A	422	0	392	8	8.523	3.50E-03	rs934746	18	46420686	q21.1
SNP_A-2170322	G	G	219	147	285	123	8.522	3.50E-03	rs11941345	18	29843949	q12.1
SNP_A-2172314	G	G	370	0	387	9	8.509	3.50E-03	rs1928276	6	138806961	q23.3
SNP_A-1860342	G	G	412	0	382	8	8.536	3.50E-03	rs747592	5	4936606	p15.32
SNP_A-1866372	A	A	290	38	289	71	8.523	3.50E-03	rs17060718	3	59412702	p14.2
SNP_A-1856202	C	C	249	151	207	191	8.542	3.50E-03	rs10770084	11	10034616	p15.4
SNP_A-1853529	G	G	304	38	275	65	8.524	3.50E-03	rs7805729	7	21876667	p15.3
SNP_A-1849981	T	T	348	20	380	6	8.52	3.50E-03	rs16909523	12	13911517	p13.1
SNP_A-1726436	G	G	348	18	334	40	8.547	3.50E-03	rs7603501	2	114776027	q14.1
SNP_A-1802797	A	A	352	6	322	20	8.513	3.50E-03	rs10849349	12	5819156	p13.31
SNP_A-1987905	C	C	192	158	265	141	8.526	3.50E-03	rs955271	6	141810913	q24.1
SNP_A-1962846	C	C	337	9	380	30	8.53	3.50E-03	rs297130	2	39210965	p22.1
SNP_A-1948525	A	A	372	4	376	18	8.514	3.50E-03	rs9494534	6	136865786	q23.3
SNP_A-1937569	G	G	272	44	253	75	8.543	3.50E-03	rs12273845	11	40116743	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1935864	T	T	380	34	394	14	8.543	3.50E-03	rs17346334	1	11894660	p36.22
SNP_A-1916879	T	C	205	149	214	192	8.547	3.50E-03	rs6845536	4	145810388	q31.21
SNP_A-1931634	C	C	340	10	389	1	8.52	3.50E-03	rs8087214	18	53295793	q21.31
SNP_A-1930023	A	A	380	4	336	16	8.529	3.50E-03	rs11202908	10	90689000	q23.31
SNP_A-1898933	C	C	373	15	395	3	8.504	3.50E-03	rs8014351	14	51693389	q22.1
SNP_A-1887115	C	C	302	30	270	54	8.551	3.50E-03	rs17130405	1	68137627	p31.2
SNP_A-1883272	G	A	216	150	209	197	8.521	3.50E-03	rs4976844	13	108623067	q33.3
SNP_A-2262657	C	C	262	82	327	59	8.537	3.50E-03	rs1996105	8	57575677	q12.1
SNP_A-2230851	A	A	310	28	381	13	8.549	3.50E-03	rs17765246	3	55831278	p14.3
SNP_A-2249421	C	C	327	21	402	8	8.529	3.50E-03	rs11258523	10	13769973	p13
SNP_A-2296881	C	C	335	7	412	0	8.512	3.50E-03	rs17799613	5	149863508	q33.1
SNP_A-2305572	G	G	304	10	320	30	8.483	3.60E-03	rs13438266	7	13968901	p21.2
SNP_A-1891956	A	A	323	13	295	31	8.483	3.60E-03	rs7253679	19	34904135	q12
SNP_A-1892558	G	G	361	1	386	12	8.458	3.60E-03	rs12264616	10	19916494	p12.31
SNP_A-1895630	C	C	418	0	390	8	8.485	3.60E-03	rs3093132	19	15865482	p13.12
SNP_A-1929363	T	T	331	3	336	16	8.466	3.60E-03	rs16961603	18	27106378	q12.1
SNP_A-1919679	A	A	312	16	281	35	8.478	3.60E-03	rs4440398	5	117884188	q23.1
SNP_A-1906804	T	T	319	39	355	19	8.474	3.60E-03	rs575722	11	95264514	q21
SNP_A-1933782	C	C	329	53	279	79	8.464	3.60E-03	rs17703053	16	76377180	q23.1
SNP_A-1971075	A	A	251	45	324	28	8.45	3.60E-03	rs5995369	22	35691118	q12.3
SNP_A-1979368	A	A	290	34	347	17	8.47	3.60E-03	rs11725509	4	149669333	q31.23
SNP_A-1800169	G	G	321	11	406	2	8.453	3.60E-03	rs3101440	15	39076416	q15.1
SNP_A-1808768	C	C	411	1	362	10	8.451	3.60E-03	rs17053128	3	53528500	p21.1
SNP_A-1796153	C	C	333	7	408	0	8.479	3.60E-03	rs335951	5	16445206	p15.1
SNP_A-1788070	G	G	294	32	302	64	8.49	3.60E-03	rs490818	10	7439159	p14
SNP_A-1860327	A	A	326	34	372	16	8.475	3.60E-03	rs10967105	9	25867977	p21.2
SNP_A-1822995	C	C	396	8	359	23	8.462	3.60E-03	rs1508688	11	88281107	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172865	T	T	288	58	351	37	8.478	3.60E-03	rs1022373	4	125216668	q28.1
SNP_A-2177823	C	C	225	139	298	118	8.476	3.60E-03	rs754037	10	768091	p15.3
SNP_A-2199165	A	A	242	26	359	15	8.457	3.60E-03	rs16864497	2	6012703	p25.2
SNP_A-2188184	C	C	294	118	252	156	8.482	3.60E-03	rs241560	14	55620683	q22.3
SNP_A-2219856	T	T	274	36	272	68	8.487	3.60E-03	rs4918544	10	112377025	q25.2
SNP_A-2210450	T	T	323	13	401	3	8.476	3.60E-03	rs10432510	2	192212369	q32.3
SNP_A-2118148	A	A	390	8	353	23	8.482	3.60E-03	rs10845804	12	13591949	p13.1
SNP_A-2108013	G	G	325	7	398	0	8.473	3.60E-03	rs6477366	9	900162	p24.3
SNP_A-2137712	C	C	412	0	384	8	8.493	3.60E-03	rs742988	20	11412737	p12.2
SNP_A-2136682	T	T	370	44	387	21	8.477	3.60E-03	rs7069673	10	115773456	q25.3
SNP_A-2166916	C	C	360	12	349	31	8.482	3.60E-03	rs1862539	5	57489003	q11.2
SNP_A-2163070	C	C	307	63	305	105	8.478	3.60E-03	rs1818813	18	59464783	q21.33
SNP_A-2154994	A	A	331	25	353	55	8.458	3.60E-03	rs4668382	2	171976163	q31.1
SNP_A-2143510	A	A	380	8	408	0	8.498	3.60E-03	rs17018051	1	208332227	q32.3
SNP_A-2142150	T	T	422	0	394	8	8.48	3.60E-03	rs17016609	1	203385774	q32.1
SNP_A-2149752	A	A	194	158	257	135	8.48	3.60E-03	rs1957547	14	80673891	q31.1
SNP_A-2015317	T	C	201	153	201	171	8.487	3.60E-03	rs2823001	21	15290124	q11.2
SNP_A-2031268	C	C	380	8	406	0	8.456	3.60E-03	rs6445830	3	56866510	p14.3
SNP_A-2072911	T	T	308	36	360	18	8.466	3.60E-03	rs1848986	5	17556652	p15.1
SNP_A-2062473	A	A	340	12	392	2	8.499	3.60E-03	rs9494006	6	134992811	q23.2
SNP_A-2106178	A	A	412	4	366	16	8.487	3.60E-03	rs234518	15	95344169	q26.2
SNP_A-2021560	A	A	275	37	338	20	8.426	3.70E-03	rs6727129	2	197021150	q32.3
SNP_A-2036358	G	G	358	54	363	27	8.438	3.70E-03	rs17445853	14	30402433	q12
SNP_A-1999795	G	G	341	7	414	0	8.405	3.70E-03	rs16934246	10	33571016	p11.22
SNP_A-1995445	C	T	194	176	241	175	8.447	3.70E-03	rs2542476	8	140622515	q24.3
SNP_A-2164135	A	G	192	166	231	175	8.447	3.70E-03	rs1015886	7	78048341	q21.11
SNP_A-2204264	T	T	370	0	391	9	8.423	3.70E-03	rs17022783	12	93482788	q22
SNP_A-2195076	A	A	386	8	412	0	8.449	3.70E-03	rs17063524	9	77149201	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2171677	T	T	360	0	381	9	8.409	3.70E-03	rs9588960	13	90082102	q31.3
SNP_A-2170909	A	G	225	175	216	184	8.409	3.70E-03	rs13175997	5	17213258	p15.1
SNP_A-1861701	T	T	282	54	270	90	8.443	3.70E-03	rs6938971	6	70899341	q13
SNP_A-1863876	G	G	420	0	394	8	8.44	3.70E-03	rs997723	17	52520431	q23.2
SNP_A-1754013	G	G	272	118	309	83	8.446	3.70E-03	rs10258427	7	135604801	q33
SNP_A-1968790	T	T	416	0	390	8	8.445	3.70E-03	rs16980516	20	54945543	q13.31
SNP_A-1957874	C	C	308	44	358	24	8.424	3.70E-03	rs3892049	1	31242978	p35.2
SNP_A-1885391	T	T	318	44	357	23	8.404	3.70E-03	rs766902	2	53018939	p16.2
SNP_A-1880771	C	C	363	17	346	38	8.405	3.70E-03	rs10908236	11	69359824	q13.3
SNP_A-2301892	T	T	192	182	229	141	8.435	3.70E-03	rs9538146	13	58097462	q21.1
SNP_A-2308618	A	A	358	0	379	9	8.406	3.70E-03	rs17126215	12	50639845	q13.13
SNP_A-2314689	C	C	316	84	352	54	8.418	3.70E-03	rs2426559	20	53307954	q13.2
SNP_A-2234254	A	A	326	16	324	38	8.408	3.70E-03	---	10	83050823	q23.1
SNP_A-2261232	C	C	239	127	227	185	8.401	0.0038	rs9404480	6	96785334	q16.1
SNP_A-2283703	A	A	328	50	298	80	8.361	0.0038	rs17047682	1	214911420	q41
SNP_A-2290296	A	A	341	7	337	23	8.356	0.0038	rs12426244	12	89225420	q21.33
SNP_A-1885150	C	C	210	102	196	152	8.387	0.0038	rs1021632	10	4642819	p15.1
SNP_A-1899837	C	C	365	1	359	11	8.362	0.0038	rs9961966	18	13257454	p11.21
SNP_A-1903201	C	C	218	136	199	191	8.394	0.0038	rs7190612	16	10562878	p13.13
SNP_A-1901265	A	A	345	17	368	42	8.383	0.0038	rs470562	6	10594458	p24.3
SNP_A-1912935	G	G	358	14	405	3	8.369	0.0038	rs16834480	3	124826687	q21.1
SNP_A-1924618	A	A	219	101	271	75	8.357	0.0038	rs9314285	8	24359590	p21.2
SNP_A-1925469	G	G	361	1	355	11	8.362	0.0038	---	18	62470551	q22.1
SNP_A-1952250	A	A	396	6	366	20	8.398	0.0038	rs16845396	1	196368736	q32.1
SNP_A-1969135	A	A	258	106	245	157	8.361	0.0038	rs2824008	21	17034959	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974497	A	A	323	9	409	1	8.397	0.0038	rs3845424	1	177869477	q25.3
SNP_A-1979329	A	A	345	25	398	10	8.373	0.0038	rs10519852	4	148302817	q31.22
SNP_A-1661310	T	T	346	0	367	9	8.386	0.0038	rs9322424	6	96455205	q16.1
SNP_A-1660343	A	A	357	9	331	25	8.375	0.0038	rs10483157	22	28670346	q12.2
SNP_A-1712363	A	A	212	150	264	120	8.372	0.0038	rs2384121	10	54259206	q21.1
SNP_A-1681742	C	C	400	0	378	8	8.375	0.0038	rs10496616	2	124433912	q14.3
SNP_A-1692370	A	A	353	7	383	25	8.381	0.0038	rs10506702	12	72830291	q21.1
SNP_A-1814002	C	C	401	3	354	14	8.383	0.0038	rs3891458	18	28102725	q12.1
SNP_A-1815335	G	G	306	114	263	151	8.373	0.0038	rs2010492	19	10664395	p13.2
SNP_A-1819416	A	T	193	151	215	179	8.369	0.0038	rs7932915	11	44976758	p11.2
SNP_A-1831549	T	T	258	88	247	135	8.386	0.0038	rs12304432	12	81492100	q21.31
SNP_A-2201673	C	C	360	0	383	9	8.365	0.0038	rs16961075	18	26847015	q12.1
SNP_A-2201711	T	T	307	15	370	4	8.393	0.0038	rs6571017	6	102992323	q16.3
SNP_A-2201873	G	G	259	141	228	188	8.377	0.0038	rs395671	6	33661655	p21.31
SNP_A-2208189	C	A	203	161	223	185	8.365	0.0038	rs4516895	5	84504365	q14.3
SNP_A-2224849	C	T	198	162	222	178	8.357	0.0038	rs6071527	20	59176746	q13.33
SNP_A-2225483	A	A	323	37	394	20	8.374	0.0038	rs12464359	2	200979671	q33.1
SNP_A-2152591	A	A	272	20	352	8	8.399	0.0038	---	10	63904935	q21.2
SNP_A-2152146	A	A	304	16	383	5	8.393	0.0038	rs4389535	4	160579121	q32.1
SNP_A-2151707	C	C	336	34	349	67	8.365	0.0038	rs6581473	12	61889512	q14.2
SNP_A-2137817	A	A	304	22	308	48	8.38	0.0038	rs11843424	13	88732684	q31.2
SNP_A-2124868	A	A	352	38	311	63	8.392	0.0038	rs4258022	8	131602104	q24.22
SNP_A-2128505	G	G	401	11	407	1	8.359	0.0038	rs6021473	20	49879228	q13.2
SNP_A-2114448	C	C	321	7	388	0	8.362	0.0038	rs4634723	9	73135362	q21.13
SNP_A-2119697	A	A	202	154	264	130	8.373	0.0038	rs2793821	13	94629762	q32.1
SNP_A-2121442	G	G	336	30	398	14	8.365	0.0038	rs9595637	13	46752426	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015452	G	G	341	23	403	9	8.355	0.0038	rs926612	21	16028181	q21.1
SNP_A-2015568	C	C	246	108	235	161	8.368	0.0038	rs2824012	21	17036229	q21.1
SNP_A-2018964	G	G	298	68	364	46	8.358	0.0038	rs2040126	21	37471173	q22.13
SNP_A-2023858	T	T	362	12	327	29	8.388	0.0038	rs2505350	10	32688699	p11.22
SNP_A-2032660	T	T	258	110	329	87	8.366	0.0038	rs7003770	8	56981889	q12.1
SNP_A-2090157	T	T	319	27	340	58	8.382	0.0038	rs9906934	17	3133205	p13.3
SNP_A-2089505	A	A	362	0	385	9	8.369	0.0038	rs16993989	20	7702302	p12.3
SNP_A-2085279	C	C	364	0	387	9	8.372	0.0038	rs16935634	11	41345607	p12
SNP_A-2082956	A	A	391	17	408	4	8.39	0.0038	rs17080646	3	40729441	p22.1
SNP_A-2071977	A	A	356	0	379	9	8.359	0.0038	rs16969772	13	87774973	q31.2
SNP_A-2054805	T	A	206	162	223	187	8.34	3.90E-03	rs7205378	16	7223843	p13.2
SNP_A-2029730	T	T	299	15	312	38	8.33	3.90E-03	rs1555720	13	33943183	q13.2
SNP_A-2043939	T	T	313	53	319	93	8.325	3.90E-03	rs1392163	15	85583909	q25.3
SNP_A-2044515	T	T	259	97	236	140	8.33	3.90E-03	rs38895	7	116472265	q31.2
SNP_A-2018904	T	T	362	0	387	9	8.326	3.90E-03	rs16994399	21	37004809	q22.13
SNP_A-1989627	G	G	382	16	349	35	8.32	3.90E-03	rs16879966	7	38616496	p14.1
SNP_A-1991129	A	A	281	29	287	59	8.34	3.90E-03	---	7	123728421	q31.33
SNP_A-2001216	C	C	234	162	257	115	8.31	3.90E-03	rs4471324	10	68073195	q21.3
SNP_A-2115602	C	C	343	7	412	0	8.316	3.90E-03	rs16860759	1	165221254	q24.2
SNP_A-2114948	A	A	236	134	298	108	8.34	3.90E-03	rs17063255	18	53040806	q21.31
SNP_A-2133554	C	C	381	19	393	5	8.348	3.90E-03	rs1355478	13	30736560	q12.3
SNP_A-2131470	C	C	222	196	262	154	8.341	3.90E-03	rs4966009	15	97021019	q26.3
SNP_A-2152677	T	T	260	146	301	109	8.346	3.90E-03	rs216328	12	6016744	p13.31
SNP_A-2147436	G	G	401	19	413	5	8.339	3.90E-03	rs10150928	14	89449368	q32.11
SNP_A-2154348	G	G	279	71	314	44	8.316	3.90E-03	rs8069761	17	52859940	q23.2
SNP_A-2154734	G	G	386	2	371	13	8.343	3.90E-03	rs4873400	8	51034984	q11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187128	A	A	362	18	397	5	8.349	3.90E-03	rs6431110	2	130251973	q21.1
SNP_A-2189773	T	T	244	86	297	61	8.318	3.90E-03	rs4761594	12	93126497	q22
SNP_A-1841645	G	G	374	12	339	29	8.342	3.90E-03	rs11205875	1	51824547	p32.3
SNP_A-1859947	A	A	319	5	345	21	8.339	3.90E-03	rs8030672	15	66846138	q23
SNP_A-1846361	A	A	354	10	397	1	8.325	3.90E-03	rs12685495	9	81564276	q21.32
SNP_A-1796488	A	A	211	151	284	132	8.333	3.90E-03	rs6130713	20	42976996	q13.12
SNP_A-1649778	C	C	292	20	376	8	8.347	3.90E-03	rs2065775	13	88171974	q31.3
SNP_A-1732309	G	G	335	7	404	0	8.347	3.90E-03	rs2502119	1	197019597	q32.1
SNP_A-1976470	T	T	292	102	248	136	8.315	3.90E-03	rs16874916	4	23740673	p15.2
SNP_A-1988089	T	T	379	9	353	25	8.324	3.90E-03	rs6670024	1	227813335	q42.2
SNP_A-1988094	C	C	288	48	362	30	8.32	3.90E-03	rs649744	6	150819619	q25.1
SNP_A-1939307	C	C	224	196	264	154	8.314	3.90E-03	rs13122461	4	122544800	q27
SNP_A-1944193	C	T	214	154	216	198	8.334	3.90E-03	rs922105	1	89737678	p22.2
SNP_A-1926545	C	C	380	12	358	30	8.35	3.90E-03	rs472472	19	21277469	p12
SNP_A-1906542	A	A	341	25	367	9	8.351	3.90E-03	rs9501957	6	3190851	p25.2
SNP_A-1894907	C	C	388	8	408	0	8.325	3.90E-03	rs10184856	2	147156065	q22.3
SNP_A-1885453	C	C	230	114	307	95	8.309	3.90E-03	rs17299561	4	155123085	q31.3
SNP_A-1877209	A	A	300	102	253	135	8.344	3.90E-03	rs10921159	1	189156291	q31.2
SNP_A-2287937	T	T	379	13	394	2	8.338	3.90E-03	---	1	165518965	q24.2
SNP_A-2297120	G	G	303	45	318	84	8.308	3.90E-03	rs7072543	10	69193368	q21.3
SNP_A-2313137	T	T	332	34	282	56	8.349	3.90E-03	rs1385425	2	151753273	q23.3
SNP_A-2304741	C	C	299	29	387	15	8.327	3.90E-03	rs7802804	7	12712365	p21.3
SNP_A-2285654	C	C	322	46	389	27	8.351	3.90E-03	rs16857631	3	147143437	q24
SNP_A-2274906	A	A	366	10	411	1	8.343	3.90E-03	rs7750005	6	134943635	q23.2
SNP_A-2279559	A	A	373	17	388	4	8.338	3.90E-03	rs16963143	15	48064359	q21.2
SNP_A-2261740	A	A	337	7	406	0	8.339	3.90E-03	rs1527049	12	76312056	q21.2
SNP_A-2256709	T	T	318	36	325	69	8.332	3.90E-03	rs10762167	10	52889115	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2269881	G	G	274	138	313	101	8.314	3.90E-03	rs13356025	5	26602270	p14.1
SNP_A-2256056	A	A	368	0	350	8	8.315	3.90E-03	rs16866301	2	7568705	p25.1
SNP_A-2246700	C	C	337	15	404	4	8.345	3.90E-03	rs13382085	19	61406509	q13.43
SNP_A-2272215	G	G	371	15	333	33	8.275	4.00E-03	rs7723698	5	145433326	q32
SNP_A-2277750	T	T	338	50	287	75	8.27	4.00E-03	rs17136120	10	3966041	p15.1
SNP_A-2277891	C	C	400	0	382	8	8.289	4.00E-03	rs2442360	13	38196845	q13.3
SNP_A-2305358	A	A	365	27	325	49	8.269	4.00E-03	rs4804505	19	10450422	p13.2
SNP_A-2313004	T	T	330	68	283	97	8.289	4.00E-03	rs3020005	11	93392972	q21
SNP_A-2297945	T	T	374	2	361	13	8.291	4.00E-03	rs7295932	12	75033929	q21.2
SNP_A-2289826	A	A	361	37	334	64	8.267	4.00E-03	rs1909525	3	25133894	p24.2
SNP_A-1887517	A	A	405	11	407	1	8.261	4.00E-03	rs6050003	20	24753601	p11.21
SNP_A-1895858	C	C	336	2	352	14	8.272	4.00E-03	rs6693245	1	177376549	q25.3
SNP_A-1914273	T	T	346	14	389	3	8.287	4.00E-03	rs1942991	18	57744468	q21.33
SNP_A-1918472	C	C	217	149	285	127	8.274	4.00E-03	rs1397221	3	163261577	q26.1
SNP_A-1943990	T	T	236	120	309	99	8.291	4.00E-03	rs10756778	9	16663620	p22.2
SNP_A-1943445	A	A	262	100	331	77	8.299	4.00E-03	rs672784	3	74434751	p12.3
SNP_A-1937409	T	T	321	41	348	20	8.27	4.00E-03	rs1939869	11	115305528	q23.3
SNP_A-1953293	A	A	274	42	356	26	8.271	4.00E-03	rs11188203	10	96892143	q23.33
SNP_A-1947936	T	T	357	19	367	5	8.284	4.00E-03	rs17050385	3	9491586	p25.3
SNP_A-1950387	C	C	378	32	393	13	8.295	4.00E-03	rs1267858	6	6267977	p25.1
SNP_A-1727825	T	T	402	0	384	8	8.288	4.00E-03	rs10502696	18	34303561	q12.2
SNP_A-1783317	A	A	357	31	316	54	8.299	4.00E-03	rs736145	7	70697692	q11.22
SNP_A-1792793	G	G	364	28	368	10	8.296	4.00E-03	rs11248915	16	233916	p13.3
SNP_A-1857910	C	C	303	41	277	69	8.287	4.00E-03	rs7545719	1	4487637	p36.32
SNP_A-1860748	A	A	207	157	277	137	8.305	4.00E-03	rs3105377	7	68281653	q11.22
SNP_A-1834526	G	G	291	23	368	10	8.27	4.00E-03	rs9668480	12	29639626	p11.22
SNP_A-1817936	A	A	233	99	296	76	8.28	4.00E-03	rs1349696	7	133900233	q33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2191250	G	G	307	21	372	8	8.275	4.00E-03	rs17782650	5	100306992	q21.1
SNP_A-2183860	G	G	410	0	392	8	8.282	4.00E-03	rs4369194	1	178346926	q25.3
SNP_A-2195256	T	T	406	2	360	12	8.261	4.00E-03	rs763130	1	169158227	q24.3
SNP_A-2198718	C	C	290	64	237	89	8.276	4.00E-03	rs6817544	4	121938759	q27
SNP_A-2223032	G	G	335	7	402	0	8.306	4.00E-03	rs2228257	3	150263992	q24
SNP_A-2218722	T	T	347	3	383	17	8.279	4.00E-03	rs2993546	1	208615682	q32.3
SNP_A-2210079	G	G	297	37	334	18	8.267	4.00E-03	rs2415671	14	40655458	q21.1
SNP_A-2205938	C	C	315	19	393	7	8.264	4.00E-03	rs9690089	7	60875997	q11.1
SNP_A-2132013	A	A	335	7	400	0	8.265	4.00E-03	rs10062925	5	114147182	q22.3
SNP_A-2126036	T	T	224	112	197	155	8.289	4.00E-03	rs10756461	9	13175149	p23
SNP_A-2116831	G	G	401	7	380	22	8.279	4.00E-03	rs3971979	20	45895195	q13.13
SNP_A-2009787	T	T	256	110	250	166	8.27	4.00E-03	rs187115	11	35132735	p13
SNP_A-2060123	C	C	305	39	296	70	8.278	4.00E-03	rs6953290	7	7559362	p21.3
SNP_A-2073435	C	C	327	9	409	1	8.277	4.00E-03	rs5992333	22	17279043	q11.21
SNP_A-2076842	G	G	339	7	404	0	8.25	4.10E-03	rs13369667	18	582616	p11.32
SNP_A-2075310	C	C	347	19	394	6	8.248	4.10E-03	rs1678387	13	94515907	q32.1
SNP_A-2066720	G	G	368	26	362	52	8.226	4.10E-03	rs10096711	8	69121258	q13.2
SNP_A-2057093	C	C	303	103	330	68	8.237	4.10E-03	rs4396177	10	67951043	q21.3
SNP_A-2088914	G	G	329	15	346	38	8.236	4.10E-03	---	12	72398646	q21.1
SNP_A-2101226	C	C	356	54	379	29	8.245	4.10E-03	rs17429538	13	23525618	q12.12
SNP_A-2095818	G	G	390	8	406	0	8.243	4.10E-03	rs11250384	10	1322879	p15.3
SNP_A-1989909	A	A	375	15	326	32	8.22	4.10E-03	rs2023879	7	50812411	p12.1
SNP_A-2046110	T	T	212	112	215	177	8.257	4.10E-03	rs6901738	6	119308333	q22.31
SNP_A-2117236	G	G	264	152	297	111	8.256	4.10E-03	rs137866	22	48749841	q13.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113883	G	G	334	68	307	103	8.223	4.10E-03	rs11762504	7	66631828	q11.22
SNP_A-2128383	A	A	366	42	331	69	8.247	4.10E-03	rs6593903	1	200316507	q32.1
SNP_A-2133298	A	A	301	51	295	87	8.239	4.10E-03	rs1585399	5	168087889	q34
SNP_A-2158118	A	A	363	1	361	11	8.253	4.10E-03	rs17119093	14	83343365	q31.2
SNP_A-2167364	C	C	319	37	343	17	8.255	4.10E-03	rs6551551	4	61128836	q13.1
SNP_A-2212538	G	G	262	60	340	42	8.229	4.10E-03	rs17296933	19	53867776	q13.33
SNP_A-2212279	T	T	312	36	390	20	8.222	4.10E-03	rs3787152	20	56324804	q13.32
SNP_A-2218610	A	A	385	11	387	1	8.258	4.10E-03	rs7799581	7	114840161	q31.2
SNP_A-2219684	A	A	329	9	409	1	8.218	4.10E-03	rs10836083	11	33598811	p13
SNP_A-2194822	C	C	331	11	410	2	8.225	4.10E-03	rs11250671	10	1655047	p15.3
SNP_A-2193679	T	T	323	7	353	25	8.24	4.10E-03	rs12281950	11	134435410	q25
SNP_A-2174016	G	G	355	15	374	38	8.244	4.10E-03	rs17104921	10	92827241	q23.31
SNP_A-1816990	G	G	250	114	316	90	8.253	4.10E-03	rs7927687	11	98010959	q22.1
SNP_A-1824567	T	T	345	21	383	7	8.23	4.10E-03	rs17137388	10	15623865	p13
SNP_A-1833969	G	G	385	5	354	18	8.228	4.10E-03	rs2585118	15	55082355	q21.3
SNP_A-1829588	G	G	335	7	398	0	8.224	4.10E-03	rs1484208	15	44374236	q21.1
SNP_A-1797667	G	G	374	12	341	29	8.237	4.10E-03	rs11167989	5	146746956	q32
SNP_A-1798957	T	T	394	6	347	19	8.248	4.10E-03	rs7012388	8	10681970	p23.1
SNP_A-1791430	T	T	398	8	414	0	8.238	4.10E-03	rs7119921	11	46406259	p11.2
SNP_A-1814169	G	G	321	67	345	39	8.241	4.10E-03	rs1550890	8	3287743	p23.2
SNP_A-1720231	G	G	402	0	386	8	8.245	4.10E-03	rs10495651	2	16540158	p24.3
SNP_A-1671638	G	G	344	20	335	43	8.255	4.10E-03	rs9315234	13	18339404	q12.11
SNP_A-1948445	C	C	337	5	367	21	8.259	4.10E-03	rs1937052	20	26028882	p11.1
SNP_A-1959639	G	G	355	3	368	16	8.228	4.10E-03	rs1781590	13	66844643	q21.32
SNP_A-1912605	G	G	359	3	372	16	8.234	4.10E-03	rs7936161	11	115916659	q23.3
SNP_A-1910337	A	A	285	43	307	83	8.224	4.10E-03	rs17801909	18	45833153	q21.1
SNP_A-1930629	T	T	282	10	390	2	8.247	4.10E-03	rs7129932	11	50082004	p11.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1891997	A	A	327	49	291	77	8.234	4.10E-03	rs1667644	8	100739649	q22.2
SNP_A-2290410	G	G	404	2	393	13	8.218	4.10E-03	rs17144313	16	771465	p13.3
SNP_A-2311925	G	G	323	13	393	3	8.231	4.10E-03	rs7330474	13	78904811	q31.1
SNP_A-2276386	G	G	311	23	285	45	8.228	4.10E-03	rs10363441	4	158786368	q32.1
SNP_A-2281373	C	C	400	2	356	12	8.218	4.10E-03	rs727524	1	204895054	q32.2
SNP_A-2269697	G	G	312	52	376	32	8.234	4.10E-03	rs789779	15	34002472	q14
SNP_A-2265847	T	T	345	7	410	0	8.229	4.10E-03	rs7356706	5	131808054	q23.3
SNP_A-2266593	A	A	369	25	335	47	8.181	4.20E-03	rs2865108	7	66770889	q11.22
SNP_A-2244074	A	A	362	44	310	68	8.177	4.20E-03	rs16853946	1	14393898	p36.21
SNP_A-2230227	G	G	337	27	400	12	8.217	4.20E-03	---	11	81991272	q14.1
SNP_A-2314784	C	C	303	37	353	19	8.175	4.20E-03	rs17275450	18	66985314	q22.3
SNP_A-1902896	T	T	273	55	326	34	8.174	4.20E-03	rs7712927	5	10638111	p15.2
SNP_A-1888594	A	A	298	58	301	99	8.189	4.20E-03	rs1062748	2	241748731	q37.3
SNP_A-1883164	T	T	296	32	313	65	8.201	4.20E-03	---	4	82803608	q21.22
SNP_A-1879117	G	G	333	7	394	0	8.19	4.20E-03	rs1260749	6	109283510	q21
SNP_A-1927845	C	C	276	114	233	149	8.208	4.20E-03	rs205386	16	28031071	p11.2
SNP_A-1928032	C	C	311	33	316	64	8.177	4.20E-03	rs13241576	7	103110625	q22.1
SNP_A-1923582	G	G	332	30	350	12	8.189	4.20E-03	rs6049183	20	23787517	p11.21
SNP_A-1960568	G	G	313	19	389	7	8.203	4.20E-03	rs11834832	12	73424337	q21.1
SNP_A-1938999	C	C	245	87	314	66	8.201	4.20E-03	rs1996061	8	5633014	p23.2
SNP_A-1978640	G	G	343	7	343	23	8.18	4.20E-03	rs6696762	1	192468173	q31.3
SNP_A-1965095	C	C	348	12	390	2	8.186	4.20E-03	rs3953980	2	140495663	q22.1
SNP_A-1728601	T	T	368	4	357	17	8.209	4.20E-03	rs1588083	8	83074789	q21.13
SNP_A-1727497	C	C	315	17	347	43	8.207	4.20E-03	rs2497150	6	84842609	q14.2
SNP_A-1808629	A	A	349	7	414	0	8.215	4.20E-03	rs17630322	5	96394595	q15
SNP_A-1804831	G	G	299	65	303	109	8.215	4.20E-03	rs1869724	18	59423869	q21.33
SNP_A-1834753	G	G	312	32	280	56	8.182	4.20E-03	rs9326992	5	115510039	q23.1
SNP_A-1815078	T	T	245	123	314	100	8.212	4.20E-03	rs7667792	4	139981760	q31.1
SNP_A-1860983	G	G	242	66	340	52	8.201	4.20E-03	rs6858573	4	152946734	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2178948	C	C	353	1	353	11	8.196	4.20E-03	rs4073485	10	125808695	q26.13
SNP_A-2190511	G	G	278	130	241	171	8.203	4.20E-03	rs2801490	10	12479829	p13
SNP_A-2211021	C	C	285	129	323	93	8.208	4.20E-03	rs291075	1	76249469	p31.1
SNP_A-2167969	G	G	345	7	408	0	8.189	4.20E-03	rs551153	13	101598467	q33.1
SNP_A-2023879	G	G	299	69	296	112	8.191	4.20E-03	rs12705687	7	109621675	q31.1
SNP_A-2001647	T	T	268	40	333	23	8.19	4.20E-03	rs7935375	11	4879758	p15.4
SNP_A-2019046	C	C	260	146	221	187	8.205	4.20E-03	rs1709832	21	37960037	q22.13
SNP_A-2017854	C	C	187	177	249	155	8.213	4.20E-03	rs2027663	21	30792587	q22.11
SNP_A-2105891	G	G	359	1	359	11	8.198	4.20E-03	rs1303894	5	79877008	q14.1
SNP_A-2083250	T	T	366	10	405	1	8.198	4.20E-03	rs17128888	11	123742528	q24.1
SNP_A-2067622	A	G	207	157	215	187	8.193	4.20E-03	rs12707169	7	133841372	q33
SNP_A-2069577	G	G	248	50	330	34	8.182	4.20E-03	rs9352588	6	79080823	q14.1
SNP_A-2063682	G	G	221	105	291	85	8.156	0.0043	rs11088001	21	26780036	q21.3
SNP_A-2055193	G	T	190	174	238	172	8.132	0.0043	rs918058	2	206322208	q33.3
SNP_A-2100373	T	T	396	8	408	0	8.16	0.0043	rs12460798	19	42309276	q13.12
SNP_A-2000739	C	T	204	142	204	192	8.141	0.0043	rs6684472	1	223277764	q42.12
SNP_A-2027379	G	G	239	129	225	185	8.166	0.0043	rs2269026	20	17390609	p12.1
SNP_A-2121224	C	C	362	12	404	2	8.147	0.0043	rs4516177	15	48493781	q21.2
SNP_A-2184373	T	T	226	122	213	177	8.138	0.0043	rs2899313	22	37806523	q13.1
SNP_A-2171603	G	G	338	8	358	26	8.148	0.0043	rs1570212	6	65965297	q12
SNP_A-1858394	C	C	316	20	369	7	8.138	0.0043	rs4620486	1	184443621	q31.1
SNP_A-1848372	A	A	197	159	267	141	8.139	0.0043	rs7298007	12	30743294	p11.21
SNP_A-1804140	G	G	183	171	248	152	8.144	0.0043	rs11153113	6	108863061	q21
SNP_A-1812619	C	C	336	26	391	11	8.17	0.0043	rs6594522	5	110965487	q22.1
SNP_A-1736527	T	T	246	142	218	190	8.132	0.0043	rs9285221	13	57819611	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1663000	A	A	294	54	306	96	8.154	0.0043	rs1978910	4	163351868	q32.2
SNP_A-1645638	G	G	339	9	347	27	8.168	0.0043	rs10504838	8	88593353	q21.3
SNP_A-1686492	C	C	400	0	388	8	8.163	0.0043	rs1448486	15	25877344	q13.1
SNP_A-1682648	A	A	231	137	291	111	8.137	0.0043	rs1999334	21	45526659	q22.3
SNP_A-1944173	T	T	406	0	394	8	8.16	0.0043	rs4235154	4	48109092	p12
SNP_A-1923742	A	A	381	13	390	2	8.167	0.0043	rs871184	6	38396001	p21.2
SNP_A-1925065	T	T	325	29	311	55	8.158	0.0043	rs4677709	3	195912394	q29
SNP_A-1925830	T	C	212	158	220	196	8.133	0.0043	rs564461	6	128088406	q22.33
SNP_A-1878945	A	A	197	129	263	109	8.154	0.0043	rs17550571	3	80833283	p12.2
SNP_A-1885688	A	A	297	19	285	41	8.16	0.0043	rs6918717	6	104979422	q16.3
SNP_A-1897988	G	G	355	7	418	0	8.156	0.0043	rs6069155	20	53216742	q13.2
SNP_A-2229957	C	C	391	17	378	38	8.161	0.0043	rs12894731	14	70427418	q24.2
SNP_A-2237949	G	G	325	9	401	1	8.143	0.0043	rs6439527	3	136064202	q22.1
SNP_A-2266254	G	G	248	92	251	147	8.167	0.0043	rs9824637	3	175441550	q26.31
SNP_A-2269888	C	C	230	128	215	183	8.139	0.0043	rs9398527	6	120137008	q22.31
SNP_A-2259437	C	T	190	126	185	179	8.173	0.0043	rs10908268	15	25014703	q12
SNP_A-2280378	T	T	242	160	282	122	8.169	0.0043	rs7206992	17	60719139	q24.1
SNP_A-2274424	A	T	215	149	206	196	8.165	0.0043	rs4835366	4	148338491	q31.22
SNP_A-2276126	C	T	246	170	209	203	8.112	4.40E-03	rs2602381	2	234366324	q37.1
SNP_A-2278957	A	A	398	12	337	27	8.127	4.40E-03	rs2949761	7	142728779	q34
SNP_A-2282821	G	G	297	91	335	61	8.125	4.40E-03	rs3900909	1	194489503	q31.3
SNP_A-2270450	A	A	307	101	327	65	8.121	4.40E-03	rs3804469	6	6561561	p25.1
SNP_A-2272371	G	G	339	7	398	0	8.129	4.40E-03	rs2012190	17	8316042	p13.1
SNP_A-2245417	T	-	248	166	203	203	8.123	4.40E-03	rs7211982	17	15335097	p12
SNP_A-2299356	G	G	307	63	374	42	8.128	4.40E-03	rs17129234	14	93391975	q32.13
SNP_A-1896759	G	G	357	57	366	30	8.095	4.40E-03	rs17486081	2	217130923	q35
SNP_A-1879054	G	G	207	159	274	138	8.126	4.40E-03	rs4090714	7	136275024	q33
SNP_A-1923301	A	A	329	7	386	0	8.12	4.40E-03	rs8024410	15	58771812	q22.2
SNP_A-1910480	C	C	319	9	393	1	8.126	4.40E-03	rs2148518	13	74047647	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936492	A	A	316	12	289	29	8.101	4.40E-03	rs7615163	3	172323696	q26.2
SNP_A-1958327	A	A	340	6	320	20	8.093	4.40E-03	rs11131777	4	178350408	q34.3
SNP_A-1949311	T	A	210	194	240	174	8.13	4.40E-03	rs3851792	17	42414823	q21.32
SNP_A-1962651	T	T	353	7	414	0	8.123	4.40E-03	rs17014943	2	34377581	p22.3
SNP_A-1970217	T	T	389	7	334	20	8.117	4.40E-03	rs16993840	21	36347548	q22.12
SNP_A-1969190	A	A	305	25	296	50	8.094	4.40E-03	rs17768858	21	18254863	q21.1
SNP_A-1979330	C	C	341	27	402	12	8.099	4.40E-03	rs17022310	4	148302872	q31.22
SNP_A-1978886	T	T	315	11	318	30	8.11	4.40E-03	rs17012414	4	128694434	q28.1
SNP_A-1719685	T	T	370	10	405	1	8.093	4.40E-03	rs1178198	2	15246079	p24.3
SNP_A-1809964	A	A	230	182	275	145	8.12	4.40E-03	rs2295680	14	22444275	q11.2
SNP_A-1786654	A	A	229	137	215	195	8.105	4.40E-03	rs9387672	6	120034745	q22.31
SNP_A-1848415	G	G	288	18	379	7	8.115	4.40E-03	rs693517	9	14081127	p23
SNP_A-1847707	C	C	339	7	398	0	8.129	4.40E-03	rs525452	19	5916311	p13.3
SNP_A-1854943	A	A	333	3	348	16	8.118	4.40E-03	rs548324	2	20921785	p24.1
SNP_A-1862613	C	C	331	63	299	95	8.106	4.40E-03	rs16836480	4	5068373	p16.2
SNP_A-1872371	C	C	367	9	330	24	8.127	4.40E-03	rs9843787	3	98666131	q11.2
SNP_A-1816892	G	G	325	9	399	1	8.094	4.40E-03	rs1300266	3	101901284	q12.2
SNP_A-1822810	T	T	413	1	376	10	8.129	4.40E-03	rs10984311	9	97751698	q22.33
SNP_A-2184697	C	C	324	24	386	10	8.116	4.40E-03	rs1410346	13	105288295	q33.2
SNP_A-2207745	T	T	323	11	396	2	8.109	4.40E-03	rs7868036	9	16841897	p22.2
SNP_A-2205808	T	T	252	90	224	128	8.129	4.40E-03	rs1853920	13	58840169	q21.2
SNP_A-2204630	T	T	311	11	382	2	8.123	4.40E-03	rs6756270	2	178525401	q31.2
SNP_A-2222867	C	C	309	23	306	48	8.12	4.40E-03	rs12660923	6	73954502	q13
SNP_A-2115139	T	T	348	24	311	45	8.121	4.40E-03	rs1205218	20	18073441	p11.23
SNP_A-2020344	G	G	354	0	346	8	8.091	4.40E-03	rs17004585	21	43845096	q22.3
SNP_A-2020586	A	A	251	99	305	73	8.11	4.40E-03	rs2838830	21	45488655	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017375	G	G	315	39	308	70	8.117	4.40E-03	rs243700	21	28137133	q21.3
SNP_A-2008716	T	T	341	7	400	0	8.122	4.40E-03	rs4328779	3	56850548	p14.3
SNP_A-2101710	G	G	363	1	367	11	8.094	4.40E-03	rs17088179	8	23242782	p21.3
SNP_A-2105563	A	A	399	1	364	10	8.105	4.40E-03	rs16954821	15	27034826	q13.1
SNP_A-2083798	A	A	351	7	410	0	8.091	4.40E-03	rs17148958	7	125011069	q31.33
SNP_A-2077771	A	A	247	173	263	121	8.104	4.40E-03	rs6873648	5	154949246	q33.2
SNP_A-2091822	G	G	287	43	360	26	8.095	4.40E-03	rs12247775	10	52691629	q21.1
SNP_A-2050274	A	A	219	191	258	150	8.113	4.40E-03	rs1218346	10	14353061	p13
SNP_A-2050440	A	A	348	6	366	22	8.056	4.50E-03	rs7738882	6	145844718	q24.3
SNP_A-2099287	T	T	301	121	257	157	8.056	4.50E-03	rs8100239	19	49944944	q13.31
SNP_A-2017843	A	A	193	165	260	146	8.086	4.50E-03	rs1539784	21	30725081	q22.11
SNP_A-2004881	A	A	320	22	268	40	8.068	4.50E-03	rs17119547	10	107540165	q25.1
SNP_A-2001922	T	G	226	180	208	174	8.057	4.50E-03	rs1916409	10	65341921	q21.3
SNP_A-2110844	C	C	268	70	256	110	8.063	4.50E-03	rs11208538	1	65101310	p31.3
SNP_A-2127671	T	T	331	9	405	1	8.064	4.50E-03	rs214197	1	48355808	p33
SNP_A-2123520	G	G	170	148	225	125	8.082	4.50E-03	rs1025482	5	166825835	q34
SNP_A-2166421	T	T	290	70	284	112	8.059	4.50E-03	rs7994343	13	83660832	q31.1
SNP_A-2149091	T	T	258	74	269	125	8.064	4.50E-03	rs2977391	8	59257784	q12.1
SNP_A-2151911	C	C	337	11	412	2	8.085	4.50E-03	rs11952928	5	75567159	q13.3
SNP_A-2149822	T	T	338	4	375	19	8.069	4.50E-03	rs6573819	14	67731949	q24.1
SNP_A-2222862	A	A	317	17	324	40	8.083	4.50E-03	rs4762967	12	20563022	p12.2
SNP_A-2221521	C	C	283	67	336	44	8.085	4.50E-03	rs738902	22	20826733	q11.22
SNP_A-2214430	G	G	345	7	402	0	8.069	4.50E-03	rs17147124	11	83662736	q14.1
SNP_A-2190622	G	G	364	18	391	5	8.064	4.50E-03	rs788757	7	45823892	p13
SNP_A-2193554	T	T	282	136	313	97	8.066	4.50E-03	---	15	64400019	q22.31
SNP_A-2197360	A	C	206	158	223	193	8.082	4.50E-03	rs439192	4	112381796	q25
SNP_A-2172971	C	C	220	148	277	121	8.085	4.50E-03	rs1854980	13	91231958	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170652	T	T	331	9	341	27	8.054	4.50E-03	rs2176663	4	125340606	q28.1
SNP_A-2182483	T	T	355	1	359	11	8.089	4.50E-03	rs16962910	13	103106199	q33.1
SNP_A-1822984	G	G	410	2	370	12	8.072	4.50E-03	rs17119432	10	107494386	q25.1
SNP_A-1868294	A	A	354	2	378	14	8.073	4.50E-03	rs7673914	4	18063566	p15.32
SNP_A-1865710	G	G	399	1	366	10	8.053	4.50E-03	rs16844616	1	169194361	q24.3
SNP_A-1641999	T	T	261	57	342	40	8.076	4.50E-03	rs10514146	18	70734197	q22.3
SNP_A-1981249	C	C	357	53	385	29	8.062	4.50E-03	rs17252380	5	35508125	p13.2
SNP_A-1880839	T	T	228	80	286	58	8.089	4.50E-03	rs12484554	22	24072270	q11.23
SNP_A-1894966	G	G	329	15	386	4	8.061	4.50E-03	rs1332334	10	91092559	q23.31
SNP_A-2310987	T	T	280	70	347	49	8.06	4.50E-03	rs1436214	10	51764653	q11.23
SNP_A-2248762	C	C	367	21	302	38	8.084	4.50E-03	rs6922859	6	8729822	p24.3
SNP_A-2237630	C	C	307	17	353	5	8.077	4.50E-03	rs470727	11	63954613	q13.1
SNP_A-2261958	T	C	205	159	220	188	8.072	4.50E-03	rs3129206	6	33233440	p21.32
SNP_A-2275750	G	G	372	24	382	8	8.087	4.50E-03	rs1127047	10	3198512	p15.2
SNP_A-2261303	T	T	399	5	372	18	8.049	4.60E-03	rs2396037	2	224712936	q36.1
SNP_A-2259452	T	T	276	68	288	116	8.016	4.60E-03	rs17511739	9	88791653	q22.1
SNP_A-2257681	C	C	371	15	337	33	8.048	4.60E-03	rs6583002	1	107237385	p13.3
SNP_A-2304561	A	A	349	7	404	0	8.018	4.60E-03	rs4747540	10	7684255	p14
SNP_A-1889299	T	T	341	5	337	19	8.049	4.60E-03	rs870958	12	124338570	q24.31
SNP_A-1883201	G	G	330	84	292	118	8.025	4.60E-03	rs1424892	14	44277315	q21.2
SNP_A-1909438	C	C	249	113	322	92	8.036	4.60E-03	rs12734340	1	89775634	p22.2
SNP_A-1907273	C	C	353	17	373	41	8.038	4.60E-03	rs11814249	10	92807532	q23.31
SNP_A-1985185	G	G	244	170	274	126	8.04	4.60E-03	rs9476827	6	15567913	p22.3
SNP_A-1962707	T	T	245	107	310	84	8.043	4.60E-03	rs6714561	2	36151677	p22.3
SNP_A-1965540	G	G	251	111	324	90	8.013	4.60E-03	rs17808235	2	158949232	q24.1
SNP_A-1956406	G	G	326	16	399	5	8.015	4.60E-03	rs3769445	2	201137617	q33.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1940236	T	T	308	12	305	31	8.025	4.60E-03	rs16825770	3	176673127	q26.31
SNP_A-1682554	G	G	364	12	402	2	8.033	4.60E-03	rs10261711	7	9001039	p21.3
SNP_A-1729702	C	C	390	0	384	8	8.041	4.60E-03	rs7552328	1	201919216	q32.1
SNP_A-1734370	A	A	342	0	379	9	8.032	4.60E-03	rs10497596	2	183434808	q32.1
SNP_A-1742007	G	G	344	0	381	9	8.037	4.60E-03	rs597244	6	90949221	q15
SNP_A-1781797	G	G	198	162	264	142	8.011	4.60E-03	rs3113389	4	125123685	q28.1
SNP_A-1791400	C	C	296	26	364	12	8.034	4.60E-03	rs9834348	3	185656544	q27.1
SNP_A-1791053	T	T	255	115	245	169	8.023	4.60E-03	rs1881459	5	88877244	q14.3
SNP_A-1862431	G	G	256	98	231	139	8.027	4.60E-03	rs12943652	17	2476338	p13.3
SNP_A-1869686	A	A	366	16	306	32	8.032	4.60E-03	rs1215522	1	89794269	p22.2
SNP_A-1856664	A	A	259	101	318	76	8.047	4.60E-03	rs6456119	6	167118789	q27
SNP_A-1847525	T	T	290	62	316	36	8.013	4.60E-03	rs4504591	8	30191926	p12
SNP_A-1844456	G	G	351	39	302	62	8.027	4.60E-03	rs7574062	2	71628149	p13.2
SNP_A-1822996	T	T	333	15	390	4	8.041	4.60E-03	rs6842064	4	38564011	p14
SNP_A-1831322	G	C	210	152	210	192	8.027	4.60E-03	rs6483058	11	89903904	q14.3
SNP_A-1842915	A	A	401	11	378	28	8.046	4.60E-03	rs7107206	11	23542452	p14.3
SNP_A-2193198	T	T	336	6	354	22	8.02	4.60E-03	rs365424	17	36465434	q21.2
SNP_A-2185117	G	G	289	29	369	15	8.047	4.60E-03	rs883689	11	5408494	p15.4
SNP_A-2150136	C	C	241	123	305	99	8.035	4.60E-03	rs6943229	7	13346244	p21.2
SNP_A-2138834	G	G	343	29	317	53	8.043	4.60E-03	rs16997973	22	46663590	q13.31
SNP_A-2158911	C	C	276	90	346	68	8.018	4.60E-03	rs7701498	5	67550265	q13.1
SNP_A-2160940	A	A	277	47	343	29	8.017	4.60E-03	rs7546458	1	203186388	q32.1
SNP_A-2125009	G	G	359	55	351	27	8.031	4.60E-03	rs6767770	3	134832920	q22.1
SNP_A-2132127	T	C	232	166	201	187	8.045	4.60E-03	rs36081	5	148409197	q32
SNP_A-2131106	G	G	291	99	225	121	8.04	4.60E-03	rs2588844	18	35557196	q12.3
SNP_A-2120370	T	T	339	7	394	0	8.047	4.60E-03	rs17693234	4	119587355	q26

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2000560	C	C	335	9	409	1	8.045	4.60E-03	rs17010197	10	50507998	q11.23
SNP_A-2013562	C	C	318	68	290	102	8.044	4.60E-03	rs6473447	8	84551784	q21.13
SNP_A-2007504	A	A	224	138	210	196	8.029	4.60E-03	rs6081847	20	19976172	p11.23
SNP_A-2010300	A	A	357	1	363	11	8.037	4.60E-03	rs6536484	4	161220872	q32.1
SNP_A-2028374	T	T	378	10	411	1	8.031	4.60E-03	---	18	48171264	q21.1
SNP_A-2045914	A	A	344	2	368	14	8.048	4.60E-03	rs4266722	9	88880240	q22.1
SNP_A-2040623	C	C	408	8	414	0	8.039	4.60E-03	rs17107529	14	69519775	q24.2
SNP_A-2101347	A	A	306	16	346	42	8.043	4.60E-03	rs2112694	5	151635057	q33.1
SNP_A-2104442	C	C	188	170	252	150	8.039	4.60E-03	rs9354890	6	70561017	q13
SNP_A-2049862	C	C	384	28	382	10	8.039	4.60E-03	rs2009494	4	37521019	p14
SNP_A-2051553	T	T	304	24	292	48	8.029	4.60E-03	rs170069	7	44286374	p13
SNP_A-2059335	C	C	381	9	361	25	8.048	4.60E-03	rs2999066	3	129462984	q21.3
SNP_A-2063777	G	G	313	51	382	32	8.02	4.60E-03	rs11986722	8	127597922	q24.21
SNP_A-2074360	A	A	389	3	354	14	8.016	4.60E-03	rs1281351	9	18466171	p22.2
SNP_A-2071749	G	G	380	6	341	19	7.973	4.70E-03	rs2240883	16	3585910	p13.3
SNP_A-2107746	G	G	374	8	349	23	7.991	4.70E-03	rs11688464	2	220157960	q35
SNP_A-2010547	G	A	190	176	241	173	8.005	4.70E-03	rs7683009	4	189073244	q35.2
SNP_A-2007198	G	G	323	41	385	23	8.01	4.70E-03	rs4814698	20	1811216	p13
SNP_A-2016871	G	G	291	27	342	12	7.973	4.70E-03	rs8127091	21	25202236	q21.2
SNP_A-1989970	A	A	357	23	382	8	7.975	4.70E-03	rs2049409	7	54023957	p11.2
SNP_A-2135866	A	A	332	16	327	37	8.003	4.70E-03	---	5	58458870	q11.2
SNP_A-2161330	T	T	249	117	316	94	7.983	4.70E-03	rs995936	13	82963677	q31.1
SNP_A-2139396	G	G	366	10	397	1	8.004	4.70E-03	rs11205253	1	150044015	q21.3
SNP_A-2142656	T	T	196	182	244	150	7.993	4.70E-03	rs4698070	4	10236086	p16.1
SNP_A-2149214	A	A	351	1	359	11	7.98	4.70E-03	rs10782030	18	63927172	q22.1
SNP_A-2181333	A	A	340	60	315	93	7.993	4.70E-03	rs4877481	9	79136212	q21.31
SNP_A-2214371	C	C	279	71	293	41	8.008	4.70E-03	rs11886179	2	240173666	q37.3
SNP_A-2213827	C	C	201	163	222	116	8.008	4.70E-03	rs1620404	10	59997836	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2214628	A	A	403	3	368	14	7.983	4.70E-03	rs17170317	7	146224346	q35
SNP_A-1838668	G	G	413	1	382	10	7.978	4.70E-03	rs10155673	6	2341896	p25.2
SNP_A-1831105	G	G	324	20	344	46	7.99	4.70E-03	rs9860143	3	111191412	q13.13
SNP_A-1829164	T	T	294	42	296	76	7.994	4.70E-03	rs10167736	2	119361594	q14.2
SNP_A-1830674	C	C	302	102	272	142	8.004	4.70E-03	rs6429769	1	15713916	p36.13
SNP_A-1833762	G	T	203	177	229	175	8.007	4.70E-03	rs11077467	17	65374676	q24.3
SNP_A-1822373	C	C	416	0	361	7	7.984	4.70E-03	rs7615167	3	108996824	q13.12
SNP_A-1850458	A	A	341	13	332	32	8.005	4.70E-03	rs4301085	4	150711449	q31.23
SNP_A-1867189	A	A	317	15	370	4	7.987	4.70E-03	rs16945132	15	89327145	q26.1
SNP_A-1799746	C	C	266	120	232	160	7.99	4.70E-03	rs10745782	12	95975316	q23.1
SNP_A-1800116	C	C	183	165	215	125	7.998	4.70E-03	rs11087392	20	233349	p13
SNP_A-1758603	G	G	367	13	358	32	8.005	4.70E-03	rs10516102	5	173066470	q35.2
SNP_A-1934031	C	T	202	160	223	187	7.988	4.70E-03	rs17181079	3	87244991	p11.2
SNP_A-1950793	T	T	361	19	402	6	7.978	4.70E-03	rs10924446	1	242500645	q44
SNP_A-1984659	C	C	268	86	253	129	7.978	4.70E-03	rs414031	5	174292823	q35.2
SNP_A-1979082	C	C	335	21	326	44	7.994	4.70E-03	rs10013928	4	138750739	q28.3
SNP_A-1910319	C	C	299	69	368	48	7.998	4.70E-03	rs9295881	6	30525438	p21.33
SNP_A-1874826	T	T	351	69	318	102	7.996	4.70E-03	rs77938	5	131350393	q23.3
SNP_A-1903633	A	A	299	117	262	156	8.007	4.70E-03	rs7570552	2	119599561	q14.2
SNP_A-2309969	C	C	209	189	240	144	7.973	4.70E-03	rs1225074	3	133177403	q22.1
SNP_A-2288429	G	G	339	9	411	1	7.979	4.70E-03	rs6535981	4	155366791	q31.3
SNP_A-2288214	C	C	399	17	404	4	8.002	4.70E-03	rs4698380	4	15072380	p15.33
SNP_A-2242559	A	A	253	109	326	88	7.994	4.70E-03	rs7045259	9	36876065	p13.2
SNP_A-2255946	A	A	359	1	367	11	7.987	4.70E-03	rs16876171	7	9453262	p21.3
SNP_A-2254694	T	T	397	1	368	10	7.953	4.80E-03	rs2034444	3	54140928	p21.1
SNP_A-2230397	T	T	299	93	244	120	7.967	4.80E-03	rs12653237	5	131269677	q23.3
SNP_A-2273673	A	A	271	53	334	34	7.944	4.80E-03	rs17019101	2	60406034	p16.1
SNP_A-2273170	C	C	267	101	334	78	7.968	4.80E-03	rs16834011	2	154338458	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2297248	T	T	331	21	392	8	7.943	4.80E-03	rs11127111	2	89170082	p11.2
SNP_A-1883792	C	C	315	49	380	30	7.943	4.80E-03	rs7739209	6	7546775	p24.3
SNP_A-1909126	A	A	365	7	418	0	7.936	4.80E-03	rs10993301	9	94521213	q22.32
SNP_A-1935343	G	G	297	71	297	115	7.952	4.80E-03	rs11037654	11	43785335	p11.2
SNP_A-1821371	T	T	235	111	304	90	7.947	4.80E-03	rs6763183	3	149531404	q24
SNP_A-2213614	G	G	338	26	357	55	7.964	4.80E-03	rs9878394	3	90346746	p11.1
SNP_A-2206878	C	C	294	18	297	41	7.954	4.80E-03	rs7971786	12	53868717	q13.2
SNP_A-2212558	A	A	360	30	332	54	7.97	4.80E-03	rs6437370	2	241503587	q37.3
SNP_A-2177292	T	T	212	208	248	164	7.946	4.80E-03	rs708486	14	51810721	q22.1
SNP_A-2176831	G	G	333	27	217	37	7.966	4.80E-03	rs2173036	13	96775136	q32.1
SNP_A-2172872	T	T	276	138	304	98	7.957	4.80E-03	rs8011741	14	40887732	q21.1
SNP_A-2161209	G	G	330	14	361	3	7.95	4.80E-03	rs17140961	16	6688718	p13.2
SNP_A-2157451	A	A	343	7	394	0	7.955	4.80E-03	rs2325562	13	73245093	q22.1
SNP_A-2118292	G	G	231	191	270	150	7.961	4.80E-03	rs6963950	7	40815730	p14.1
SNP_A-2117851	C	C	376	0	374	8	7.958	4.80E-03	rs11967976	6	142914184	q24.2
SNP_A-2011082	G	G	333	11	402	2	7.947	4.80E-03	rs6861748	5	97720308	q21.1
SNP_A-2022957	G	G	289	81	357	59	7.95	4.80E-03	rs11005290	10	51777126	q11.23
SNP_A-2102816	T	T	254	92	304	66	7.963	4.80E-03	rs792442	1	208914683	q32.3
SNP_A-2095573	G	G	277	53	294	96	7.971	4.80E-03	rs6904538	6	145309153	q24.2
SNP_A-2098953	A	A	360	22	313	41	7.959	4.80E-03	rs6865592	5	176437098	q35.2
SNP_A-2085081	C	C	293	43	298	78	7.944	4.80E-03	rs10786775	10	105647306	q24.33
SNP_A-2086486	A	A	354	22	325	43	7.938	4.80E-03	rs6100034	20	36578767	q11.23
SNP_A-2081231	A	G	186	164	233	175	7.936	4.80E-03	rs6812192	4	91175026	q22.1
SNP_A-2075345	G	G	279	41	322	22	7.95	4.80E-03	rs16878287	5	80321921	q14.1
SNP_A-2063434	G	G	226	122	289	99	7.95	4.80E-03	rs11781560	8	78336915	q21.11
SNP_A-2068198	C	C	297	21	281	43	7.95	4.80E-03	rs1534357	6	46641731	p12.3
SNP_A-2059616	C	C	321	11	388	2	7.954	4.80E-03	rs285767	15	90987235	q26.1
SNP_A-2067885	G	A	185	177	234	162	7.92	4.90E-03	rs8181314	10	124030744	q26.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015754	C	C	399	3	366	14	7.929	4.90E-03	rs1735281	21	18431035	q21.1
SNP_A-1993220	A	A	354	6	357	21	7.912	4.90E-03	rs7017918	8	51693136	q11.21
SNP_A-2112205	C	C	341	7	390	0	7.92	4.90E-03	rs6692412	1	20306401	p36.12
SNP_A-2130444	A	A	308	18	295	39	7.921	4.90E-03	rs1281748	1	116319296	p13.1
SNP_A-2145263	C	C	394	2	360	12	7.934	4.90E-03	rs17059878	13	60930472	q21.2
SNP_A-2177470	C	C	401	3	339	13	7.905	4.90E-03	rs325069	6	48456083	p12.3
SNP_A-2183281	C	C	178	176	235	153	7.933	4.90E-03	rs4901508	14	53905296	q22.2
SNP_A-2223352	A	A	333	25	374	10	7.905	4.90E-03	rs740883	6	29683384	p22.1
SNP_A-2224464	G	G	260	116	297	83	7.909	4.90E-03	rs741262	2	10418317	p25.1
SNP_A-2226874	G	G	366	12	400	2	7.921	4.90E-03	rs11059289	12	126646002	q24.32
SNP_A-1828837	T	T	245	113	313	91	7.911	4.90E-03	rs4233289	1	22535761	p36.12
SNP_A-1873429	T	T	397	1	370	10	7.902	4.90E-03	---	9	89802791	q22.2
SNP_A-1848202	G	G	283	73	299	43	7.921	4.90E-03	rs2953753	3	131220081	q21.3
SNP_A-1702411	A	A	321	21	380	8	7.926	4.90E-03	rs1345541	12	104870045	q23.3
SNP_A-1702503	C	C	238	116	282	86	7.91	4.90E-03	rs958644	12	69383756	q15
SNP_A-1674267	G	G	323	39	288	64	7.934	4.90E-03	rs10483496	14	39090069	q21.1
SNP_A-1810550	C	C	341	11	410	2	7.907	4.90E-03	rs17170715	7	147006537	q35
SNP_A-1791350	A	A	331	11	398	2	7.903	4.90E-03	rs6719091	2	69383040	p13.3
SNP_A-1955932	A	A	351	3	347	15	7.935	4.90E-03	rs6901466	6	24874793	p22.2
SNP_A-1964063	C	C	345	13	409	3	7.934	4.90E-03	rs17022824	2	83105711	p12
SNP_A-1903949	T	T	315	63	279	93	7.904	4.90E-03	rs1679010	15	40247543	q15.1
SNP_A-2293866	C	C	232	94	308	76	7.917	4.90E-03	rs614023	3	74431277	p12.3
SNP_A-2277084	T	T	422	0	369	7	7.926	4.90E-03	rs16951193	17	15039707	p12
SNP_A-2259675	G	G	349	5	349	19	7.898	4.90E-03	rs17072521	6	111705347	q21
SNP_A-2269451	C	C	411	1	382	10	7.932	4.90E-03	rs7163467	15	33745714	q14
SNP_A-2250506	T	T	357	7	408	0	7.918	4.90E-03	rs11187631	10	95480038	q23.33
SNP_A-2231490	C	C	295	123	254	160	7.88	5.00E-03	rs7068827	10	86414305	q23.1
SNP_A-2265726	A	A	302	98	321	63	7.865	5.00E-03	rs6560621	9	77864854	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2267548	T	T	333	9	399	1	7.865	5.00E-03	rs9497540	6	146781527	q24.3
SNP_A-2282657	G	G	305	33	350	16	7.888	5.00E-03	rs7501465	17	18759684	p11.2
SNP_A-2294112	A	A	319	101	274	134	7.877	5.00E-03	rs4473347	2	29986544	p23.1
SNP_A-2290705	G	G	354	14	376	36	7.886	5.00E-03	rs4339853	1	237607234	q43
SNP_A-2311206	T	T	327	9	393	1	7.892	5.00E-03	rs271259	5	53208596	q11.2
SNP_A-1902901	A	A	312	92	285	131	7.868	5.00E-03	rs12706347	7	120676011	q31.31
SNP_A-1939009	G	G	242	106	240	162	7.863	5.00E-03	rs1482596	3	65043188	p14.1
SNP_A-1800038	A	A	404	8	402	0	7.883	5.00E-03	rs16850753	3	141927530	q23
SNP_A-1807002	T	T	295	71	357	49	7.878	5.00E-03	rs7513335	1	100570720	p21.2
SNP_A-1848761	A	A	392	12	365	29	7.888	5.00E-03	rs1847900	3	20632275	p24.3
SNP_A-1853669	G	G	296	46	305	83	7.88	5.00E-03	rs11914959	3	158099107	q25.31
SNP_A-1869801	G	G	303	19	369	7	7.89	5.00E-03	rs16988115	22	28666994	q12.2
SNP_A-1826152	G	G	310	14	359	39	7.88	5.00E-03	rs192379	5	117009211	q23.1
SNP_A-1824296	C	C	341	1	353	11	7.863	5.00E-03	rs1899024	2	190475218	q32.2
SNP_A-1825861	A	A	279	91	344	68	7.876	5.00E-03	rs17135179	5	100733753	q21.1
SNP_A-1833588	T	T	302	26	345	59	7.864	5.00E-03	rs4612367	8	118930460	q24.11
SNP_A-1832272	G	G	378	16	406	4	7.885	5.00E-03	rs9957884	18	29098190	q12.1
SNP_A-2214386	T	T	260	154	219	193	7.888	5.00E-03	rs4929914	11	8780964	p15.4
SNP_A-2220129	T	T	321	9	385	1	7.87	5.00E-03	rs1792555	11	15138367	p15.2
SNP_A-2183884	A	A	278	86	336	62	7.869	5.00E-03	rs2403583	11	20334676	p15.1
SNP_A-2187780	A	A	372	22	334	42	7.879	5.00E-03	rs16883315	4	11200445	p15.33
SNP_A-2186683	T	T	270	90	333	67	7.868	5.00E-03	rs6886884	5	67523084	q13.1
SNP_A-2139339	G	G	301	31	275	55	7.865	5.00E-03	rs11609218	12	85555151	q21.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141496	A	A	292	14	366	4	7.889	5.00E-03	rs3756417	5	43445638	p12
SNP_A-2139974	G	G	327	9	393	1	7.892	5.00E-03	rs1329522	6	47798538	p12.3
SNP_A-2120997	T	T	341	17	363	41	7.87	5.00E-03	rs16861797	1	165652991	q24.2
SNP_A-2001212	G	G	416	4	388	16	7.867	5.00E-03	rs4378283	10	67804815	q21.3
SNP_A-2006811	C	C	221	149	287	127	7.884	5.00E-03	rs4368343	2	161360158	q24.2
SNP_A-2037457	A	A	321	31	288	54	7.869	5.00E-03	---	16	77091468	q23.1
SNP_A-2062512	C	C	335	13	395	3	7.866	5.00E-03	rs10170897	2	191077191	q32.2
SNP_A-2064811	A	A	244	124	302	98	7.887	5.00E-03	rs2757592	6	7532193	p24.3
SNP_A-2052766	T	T	368	34	320	56	7.867	5.00E-03	rs2928445	10	58816782	q21.1
SNP_A-2083100	A	A	357	59	368	32	7.867	5.00E-03	rs891304	11	44488750	p11.2
SNP_A-2093300	T	T	274	42	260	72	7.872	5.00E-03	rs8023936	15	68862960	q23
SNP_A-2102959	T	T	362	0	366	8	7.828	5.10E-03	rs17046129	4	114789761	q26
SNP_A-2104369	C	G	206	164	225	189	7.853	5.10E-03	rs7768327	6	125087974	q22.31
SNP_A-2068345	G	G	224	140	207	195	7.835	5.10E-03	rs1495830	3	88839665	p11.1
SNP_A-2036521	A	A	254	86	250	134	7.859	5.10E-03	rs17819188	17	50913255	q23.1
SNP_A-2042468	T	T	288	80	349	57	7.856	5.10E-03	rs1022744	6	72096864	q13
SNP_A-1999278	A	A	280	22	339	9	7.859	5.10E-03	---	10	27674673	p12.1
SNP_A-1996606	A	A	286	34	301	67	7.855	5.10E-03	rs10508492	10	15744876	p13
SNP_A-2128205	C	C	375	19	373	5	7.844	5.10E-03	rs432770	22	17265521	q11.21
SNP_A-2125505	A	A	378	10	403	1	7.844	5.10E-03	---	3	43557137	p22.1
SNP_A-2136001	A	A	315	21	324	46	7.836	5.10E-03	rs1245416	14	26690888	q12
SNP_A-2147578	A	A	289	117	328	84	7.839	5.10E-03	rs7720449	5	170864007	q35.1
SNP_A-2150999	G	G	366	0	370	8	7.83	5.10E-03	rs842571	2	184118064	q32.1
SNP_A-2162796	G	G	263	53	257	89	7.853	5.10E-03	rs10050720	5	72058964	q13.2
SNP_A-2196964	G	G	409	1	384	10	7.836	5.10E-03	rs4054863	3	4928818	p26.1
SNP_A-2190836	A	A	223	141	208	198	7.839	5.10E-03	rs10885409	10	114798062	q25.2
SNP_A-2182181	G	G	332	18	390	6	7.853	5.10E-03	rs11125783	2	59423809	p16.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172931	C	C	392	4	366	16	7.842	5.10E-03	rs10153588	2	37234564	p22.2
SNP_A-2172342	G	G	335	9	401	1	7.857	5.10E-03	rs9995902	4	93646790	q22.3
SNP_A-2208858	T	T	326	64	347	37	7.827	5.10E-03	rs4540907	12	130266411	q24.33
SNP_A-2202991	G	G	327	63	263	85	7.848	5.10E-03	rs10779727	1	9612119	p36.22
SNP_A-1831335	A	A	408	0	361	7	7.832	5.10E-03	rs2500218	1	107549484	p13.3
SNP_A-1837784	G	G	249	115	243	171	7.857	5.10E-03	rs7649133	3	57746762	p14.3
SNP_A-1827268	C	C	290	72	287	115	7.831	5.10E-03	rs7001869	8	4752273	p23.2
SNP_A-1858424	G	G	336	4	379	19	7.859	5.10E-03	rs9854322	3	169260457	q26.1
SNP_A-1844440	C	C	353	1	330	10	7.859	5.10E-03	rs8100095	19	48117670	q13.31
SNP_A-1812759	T	T	258	138	216	174	7.83	5.10E-03	rs3847160	8	108525707	q23.1
SNP_A-1938106	G	G	297	73	260	104	7.839	5.10E-03	rs36993	5	1548763	p15.33
SNP_A-1944880	A	A	284	26	346	12	7.851	5.10E-03	rs6904523	6	27144991	p22.1
SNP_A-1944885	A	A	199	159	247	129	7.854	5.10E-03	rs9444993	6	93238769	q16.1
SNP_A-1956785	C	C	359	1	373	11	7.835	5.10E-03	rs17086792	6	156310052	q25.3
SNP_A-1953289	A	A	359	1	373	11	7.835	5.10E-03	rs7599610	2	5871611	p25.2
SNP_A-1889829	C	C	260	108	299	77	7.83	5.10E-03	rs3991716	16	56508486	q13
SNP_A-1904875	C	C	259	147	222	188	7.845	5.10E-03	rs5759415	22	21387444	q11.22
SNP_A-1912193	G	G	318	42	309	73	7.84	5.10E-03	rs11036358	11	41304985	p12
SNP_A-1916619	C	C	353	1	367	11	7.827	5.10E-03	rs6828253	4	88600430	q22.1
SNP_A-2309901	G	G	387	21	371	43	7.857	5.10E-03	rs4751732	10	121233404	q26.11
SNP_A-2293369	C	C	339	7	384	0	7.844	5.10E-03	rs9916690	17	68353174	q24.3
SNP_A-2284161	G	G	366	0	370	8	7.83	5.10E-03	rs3936919	1	167146096	q24.2
SNP_A-2229713	A	A	278	68	289	115	7.846	5.10E-03	rs7199856	16	57142273	q21
SNP_A-2234910	A	A	335	21	394	8	7.84	5.10E-03	rs17579600	11	18584994	p15.1
SNP_A-2239290	G	G	370	0	374	8	7.832	5.10E-03	rs16934426	12	29582405	p11.22
SNP_A-2253889	T	T	245	41	322	26	7.827	5.10E-03	rs7208031	17	69282933	q25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246919	C	C	422	0	375	7	7.801	5.20E-03	rs11129995	3	43191777	p22.1
SNP_A-2258851	A	A	311	33	332	66	7.797	5.20E-03	rs10884585	10	109741842	q25.1
SNP_A-2289419	A	A	198	158	223	115	7.796	5.20E-03	rs12017501	13	22229502	q12.12
SNP_A-1916904	G	G	369	35	375	15	7.804	5.20E-03	rs4982211	14	34328902	q13.1
SNP_A-1888124	C	C	307	59	373	39	7.795	5.20E-03	rs202072	6	13376190	p24.1
SNP_A-1875247	A	G	211	187	222	168	7.793	5.20E-03	rs4903279	14	74616336	q24.3
SNP_A-1877572	G	A	190	158	229	183	7.823	5.20E-03	rs7527013	1	220034320	q42.11
SNP_A-1956674	T	T	228	136	216	194	7.812	5.20E-03	rs13148977	4	91304716	q22.1
SNP_A-1955209	G	G	352	16	376	4	7.801	5.20E-03	rs6448194	4	10390330	p16.1
SNP_A-1958351	G	G	323	97	350	64	7.804	5.20E-03	rs194792	16	23729849	p12.1
SNP_A-1966895	A	A	238	114	295	89	7.798	5.20E-03	rs1983218	2	217162151	q35
SNP_A-1977622	C	C	362	2	396	14	7.819	5.20E-03	rs1246399	4	75668234	q13.3
SNP_A-1980783	C	C	198	140	266	122	7.796	5.20E-03	rs10462711	5	13938613	p15.2
SNP_A-1790913	A	A	304	14	378	4	7.799	5.20E-03	rs10409085	19	55189799	q13.33
SNP_A-1792595	G	G	301	21	354	8	7.804	5.20E-03	rs1550338	15	49246330	q21.2
SNP_A-1784282	C	C	422	0	375	7	7.801	5.20E-03	rs16970199	17	73043276	q25.3
SNP_A-1844566	C	C	385	3	385	15	7.819	5.20E-03	rs7790549	7	149527680	q36.1
SNP_A-1824795	C	C	333	83	356	52	7.809	5.20E-03	rs930099	14	80669264	q31.1
SNP_A-1821636	T	T	418	0	371	7	7.809	5.20E-03	rs6503971	17	55875821	q23.2
SNP_A-1839334	C	C	265	85	329	63	7.814	5.20E-03	rs244408	5	110049768	q22.1
SNP_A-2212550	A	A	349	41	327	69	7.798	5.20E-03	rs3132499	6	31315899	p21.33
SNP_A-2220763	G	G	289	87	339	61	7.814	5.20E-03	rs12211597	6	124847312	q22.31
SNP_A-2181332	A	A	335	13	393	3	7.807	5.20E-03	rs9596380	13	32321645	q13.1
SNP_A-2181682	T	T	372	42	397	21	7.794	5.20E-03	rs12218361	10	126060139	q26.13
SNP_A-2196211	C	C	337	9	401	1	7.801	5.20E-03	rs11161331	15	24489715	q12
SNP_A-2152416	C	C	271	119	230	154	7.796	5.20E-03	rs17523824	1	215851456	q41

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134378	C	C	370	12	400	2	7.807	5.20E-03	rs7571904	2	166481641	q24.3
SNP_A-1990804	C	C	335	9	399	1	7.81	5.20E-03	rs4149917	1	238350893	q43
SNP_A-2070672	G	G	300	52	374	34	7.808	5.20E-03	---	4	56727090	q12
SNP_A-2051129	C	C	235	173	275	135	7.821	5.20E-03	rs6490021	12	114391640	q24.21
SNP_A-2060395	A	A	328	40	313	69	7.808	5.20E-03	rs417418	5	116949767	q23.1
SNP_A-2083534	A	A	316	20	392	8	7.795	5.20E-03	rs16923215	8	59311258	q12.1
SNP_A-2088533	A	A	276	94	341	71	7.821	5.20E-03	rs7660347	4	43117557	p13
SNP_A-2084740	C	C	347	7	390	0	7.785	0.0053	rs16852656	1	174999641	q25.2
SNP_A-2059943	C	C	350	16	371	39	7.76	0.0053	rs4320186	4	66312359	q13.1
SNP_A-2048104	A	A	303	25	361	11	7.776	0.0053	rs2492791	1	48196347	p33
SNP_A-2001868	G	G	369	39	380	18	7.776	0.0053	rs273588	11	30838603	p14.1
SNP_A-2003188	A	A	355	1	371	11	7.78	0.0053	rs4381443	13	27160215	q12.2
SNP_A-2006783	A	A	364	48	332	76	7.775	0.0053	rs1491192	10	133792769	q26.3
SNP_A-2046568	A	A	232	104	279	77	7.779	0.0053	rs10863055	12	84598059	q21.31
SNP_A-2132850	T	T	309	29	306	56	7.777	0.0053	rs8022898	14	55658775	q22.3
SNP_A-2174202	A	A	365	17	364	4	7.79	0.0053	rs766156	1	7215758	p36.23
SNP_A-2174571	T	T	237	115	294	90	7.791	0.0053	rs10225840	7	135780530	q33
SNP_A-2227458	A	A	286	120	247	157	7.791	0.0053	rs7039216	9	123811801	q33.3
SNP_A-2225181	G	G	410	0	365	7	7.785	0.0053	rs9333546	6	43679359	p21.1
SNP_A-2219647	G	G	289	61	298	104	7.786	0.0053	rs1694329	13	75960412	q22.2
SNP_A-2214557	T	T	419	3	359	13	7.759	0.0053	rs9963226	18	3197370	p11.31
SNP_A-2211767	A	A	283	23	317	53	7.779	0.0053	rs12620026	2	148517651	q23.1
SNP_A-1822619	T	T	422	0	377	7	7.76	0.0053	rs9937229	16	78109371	q23.1
SNP_A-1852005	A	A	311	59	329	33	7.768	0.0053	rs1946487	5	151583767	q33.1
SNP_A-1866433	T	T	321	43	330	78	7.766	0.0053	rs6433337	2	172904267	q31.1
SNP_A-1783348	T	T	316	94	272	126	7.771	0.0053	rs16954581	17	43714501	q21.32
SNP_A-1758908	A	A	348	2	382	14	7.777	0.0053	rs10499110	6	121623366	q22.31
SNP_A-1780778	T	T	187	171	255	155	7.762	0.0053	rs251292	5	65226382	q12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1789838	C	C	277	27	341	13	7.773	0.0053	rs6427350	1	153879914	q23.1
SNP_A-1789228	T	T	369	7	414	0	7.776	0.0053	rs17065706	8	1091797	p23.3
SNP_A-1786220	C	C	205	179	237	137	7.768	0.0053	rs2675960	2	233617614	q37.1
SNP_A-1800648	C	C	299	63	262	92	7.778	0.0053	rs11703246	22	30505813	q12.3
SNP_A-1984614	A	G	220	192	232	180	7.774	0.0053	rs372474	5	172951212	q35.2
SNP_A-1988563	A	A	276	64	328	42	7.789	0.0053	rs3893527	6	29926847	p22.1
SNP_A-1967320	C	C	219	175	251	133	7.779	0.0053	rs6753112	2	232012660	q37.1
SNP_A-1961071	G	C	201	183	237	175	7.765	0.0053	rs11084995	19	3024830	p13.3
SNP_A-1874783	A	A	336	46	303	73	7.783	0.0053	rs623280	18	20198221	q11.2
SNP_A-1899718	C	C	279	47	361	31	7.787	0.0053	rs446820	14	77665874	q24.3
SNP_A-1932875	C	C	228	120	214	172	7.757	0.0053	rs7710990	5	29053217	p14.1
SNP_A-2263751	A	A	188	140	272	132	7.767	0.0053	rs11640912	16	75917420	q23.1
SNP_A-2287070	T	T	186	168	260	156	7.781	0.0053	rs453840	4	108245067	q25
SNP_A-2246970	C	C	261	85	214	112	7.763	0.0053	rs10447690	7	8222967	p21.3
SNP_A-2248378	C	C	404	8	345	21	7.783	0.0053	rs2116738	5	155393372	q33.2
SNP_A-2247369	A	A	317	21	372	8	7.788	0.0053	rs16918095	9	98789596	q22.33
SNP_A-2256006	C	C	218	142	282	120	7.748	5.40E-03	rs2504649	6	77172245	q14.1
SNP_A-2256208	G	G	378	10	399	1	7.75	5.40E-03	rs11019885	11	91618636	q14.3
SNP_A-2259296	C	C	267	83	260	128	7.754	5.40E-03	rs3744510	17	29520733	q12
SNP_A-2271133	T	T	233	115	227	171	7.727	5.40E-03	rs9373952	6	108004825	q21
SNP_A-2293022	A	A	247	155	283	117	7.749	5.40E-03	rs2647050	6	32777745	p21.32
SNP_A-1922096	C	C	327	15	332	36	7.743	5.40E-03	rs16924890	8	60484154	q12.1
SNP_A-1889836	A	A	250	48	317	31	7.752	5.40E-03	rs4493800	7	69877033	q11.22
SNP_A-1883342	A	G	178	164	226	162	7.741	5.40E-03	rs8087976	18	8705990	p11.22
SNP_A-1958344	G	G	286	58	299	101	7.747	5.40E-03	rs1356122	3	155666264	q25.2
SNP_A-1937376	A	C	187	159	216	168	7.724	5.40E-03	rs2715148	7	82094686	q21.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1988305	A	A	272	92	270	142	7.752	5.40E-03	rs17155270	7	27277572	p15.2
SNP_A-1988495	C	C	320	48	381	29	7.752	5.40E-03	rs3778422	6	166897575	q27
SNP_A-1985532	C	C	319	51	327	89	7.748	5.40E-03	rs7773938	6	26582023	p22.1
SNP_A-1982685	C	C	343	15	392	4	7.74	5.40E-03	---	5	100684490	q21.1
SNP_A-1801808	G	G	391	3	335	13	7.748	5.40E-03	rs1983539	3	9711741	p25.3
SNP_A-1803315	T	T	284	74	272	114	7.727	5.40E-03	rs17769598	17	65024330	q24.3
SNP_A-1795862	A	A	189	181	250	160	7.738	5.40E-03	rs3772505	3	59959164	p14.2
SNP_A-1799678	A	A	309	11	366	2	7.733	5.40E-03	rs6561300	13	45637626	q14.13
SNP_A-1783865	C	C	331	29	394	14	7.737	5.40E-03	rs1457717	5	111006302	q22.1
SNP_A-1848317	T	T	380	14	407	3	7.729	5.40E-03	rs12719416	5	129770771	q23.3
SNP_A-1836070	G	G	237	107	298	84	7.757	5.40E-03	rs2189216	4	105848975	q24
SNP_A-2226420	T	T	349	1	295	9	7.731	5.40E-03	rs8096783	18	46251633	q21.1
SNP_A-2224312	G	G	241	143	204	182	7.751	5.40E-03	rs6859132	5	168050195	q34
SNP_A-2170630	C	C	230	120	223	177	7.749	5.40E-03	rs11635196	15	35051474	q14
SNP_A-2175652	T	T	415	1	394	10	7.735	5.40E-03	rs1073097	15	66039856	q23
SNP_A-2184304	T	T	262	112	212	140	7.726	5.40E-03	rs11240666	1	200801881	q32.1
SNP_A-2132225	G	T	211	193	238	176	7.743	5.40E-03	rs12332452	5	29430683	p13.3
SNP_A-2153593	T	T	328	46	363	25	7.729	5.40E-03	rs2968271	5	22429328	p14.3
SNP_A-2044842	C	C	201	123	276	108	7.737	5.40E-03	rs237764	1	225728928	q42.13
SNP_A-2042405	A	A	336	46	360	24	7.737	5.40E-03	rs17208376	5	140376953	q31.3
SNP_A-2037421	C	C	397	13	390	2	7.729	5.40E-03	rs7616688	3	40232091	p22.1
SNP_A-2009860	A	A	351	17	366	40	7.748	5.40E-03	rs4487412	4	66313120	q13.1
SNP_A-2012779	T	C	210	204	245	171	7.731	5.40E-03	rs7794835	7	105992902	q22.3
SNP_A-2075688	G	G	377	15	336	32	7.756	5.40E-03	rs11906552	20	18678764	p11.23
SNP_A-2092077	A	A	269	63	357	47	7.728	5.40E-03	rs10003913	4	106800212	q24
SNP_A-2090342	G	G	303	47	380	30	7.745	5.40E-03	rs1450063	12	96813260	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2085168	G	G	212	156	277	135	7.698	5.50E-03	rs10798977	1	33806427	p35.1
SNP_A-2078315	C	C	300	108	258	142	7.707	5.50E-03	rs11844641	14	87878670	q31.3
SNP_A-2100399	A	A	280	72	267	111	7.704	5.50E-03	rs2346578	2	19035632	p24.2
SNP_A-2056617	G	G	316	34	363	17	7.7	5.50E-03	rs972	11	26641339	p14.2
SNP_A-2008947	A	A	316	12	319	31	7.704	5.50E-03	rs1461386	11	26382246	p14.2
SNP_A-2003483	C	C	287	83	353	61	7.722	5.50E-03	rs1008993	13	92693343	q31.3
SNP_A-2040386	C	C	420	0	377	7	7.723	5.50E-03	rs7874149	9	89784009	q22.2
SNP_A-2035149	G	G	281	33	335	17	7.711	5.50E-03	rs1759628	6	34305166	p21.31
SNP_A-2127804	G	G	234	134	207	179	7.697	5.50E-03	rs2895278	3	105493634	q13.11
SNP_A-2130475	C	C	333	9	393	1	7.723	5.50E-03	rs7848411	9	501094	p24.3
SNP_A-1838678	A	A	384	10	403	1	7.698	5.50E-03	rs2081301	2	53477137	p16.2
SNP_A-1819285	C	C	322	16	385	5	7.701	5.50E-03	---	6	107530943	q21
SNP_A-1846662	G	G	330	18	384	6	7.719	5.50E-03	rs461043	1	44750194	p34.1
SNP_A-1873364	A	A	310	14	382	4	7.691	5.50E-03	rs1603331	6	164961166	q27
SNP_A-1870538	T	T	306	10	402	2	7.71	5.50E-03	rs638148	10	42546047	q11.21
SNP_A-1736363	T	T	387	1	368	10	7.713	5.50E-03	rs10493012	1	22142321	p36.12
SNP_A-1802072	G	A	210	196	231	167	7.695	5.50E-03	rs11659972	18	2158420	p11.32
SNP_A-1966030	A	A	368	0	378	8	7.709	5.50E-03	rs16866200	2	178962292	q31.2
SNP_A-1965900	A	A	360	0	370	8	7.703	5.50E-03	rs16862384	2	174801611	q31.1
SNP_A-1970768	C	C	376	38	348	64	7.706	5.50E-03	rs738807	22	22558799	q11.23
SNP_A-1973163	G	G	412	0	371	7	7.698	5.50E-03	rs1498846	3	69684026	p14.1
SNP_A-1940932	C	C	290	20	358	8	7.692	5.50E-03	rs275898	13	63365550	q21.31
SNP_A-1941003	A	A	300	94	251	123	7.718	5.50E-03	rs8081803	17	2511759	p13.3
SNP_A-1921077	A	A	396	2	370	12	7.7	5.50E-03	rs7552217	1	102995219	p21.1
SNP_A-1911158	G	G	338	16	328	36	7.705	5.50E-03	rs11229005	11	56870720	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2294842	G	G	334	62	374	38	7.706	5.50E-03	rs557094	19	7738286	p13.2
SNP_A-2298656	A	A	402	0	361	7	7.717	5.50E-03	rs7102745	11	42022363	p12
SNP_A-2282143	T	T	273	69	334	48	7.713	5.50E-03	rs11571340	17	6848943	p13.1
SNP_A-2233931	A	A	405	1	386	10	7.697	5.50E-03	rs12416305	10	49418671	q11.22
SNP_A-2282031	C	C	288	58	292	98	7.681	5.60E-03	rs1487400	2	187830175	q32.1
SNP_A-2263434	G	G	384	8	312	20	7.671	5.60E-03	rs596698	9	130386318	q34.11
SNP_A-2300598	A	A	266	112	296	78	7.665	5.60E-03	rs4783500	16	22904931	p12.1
SNP_A-2305048	A	A	246	122	238	178	7.676	5.60E-03	rs6708276	2	144275882	q22.3
SNP_A-1908464	G	G	303	97	328	64	7.674	5.60E-03	rs7593101	2	241871575	q37.3
SNP_A-1918163	C	C	276	90	272	138	7.664	5.60E-03	rs820856	5	73997365	q13.3
SNP_A-1895136	G	G	410	2	384	12	7.68	5.60E-03	rs4441648	3	130701146	q21.3
SNP_A-1894578	G	G	321	11	378	2	7.678	5.60E-03	rs682234	11	99014102	q22.1
SNP_A-1902173	G	G	335	43	373	23	7.686	5.60E-03	rs11222954	11	131516723	q25
SNP_A-1940556	G	G	313	11	324	30	7.682	5.60E-03	rs11998864	9	27786645	p21.2
SNP_A-1795344	C	C	200	110	201	171	7.672	5.60E-03	rs11705567	22	42128385	q13.2
SNP_A-1788910	C	C	342	6	351	21	7.659	5.60E-03	rs6976902	7	4991689	p22.1
SNP_A-1790605	G	G	298	66	306	110	7.673	5.60E-03	rs11085784	19	11508141	p13.2
SNP_A-1816391	T	T	359	7	398	0	7.682	5.60E-03	rs16916576	8	95209580	q22.1
SNP_A-1844003	G	G	307	75	287	39	7.66	5.60E-03	rs4912608	5	140871379	q31.3
SNP_A-2157101	T	T	223	97	208	142	7.667	5.60E-03	rs6846361	4	152119204	q31.3
SNP_A-2183673	T	T	360	0	372	8	7.662	5.60E-03	rs4658830	1	239083145	q43
SNP_A-2192945	A	A	265	149	227	189	7.664	5.60E-03	rs882563	12	122735429	q24.31
SNP_A-2171802	C	C	273	91	266	138	7.675	5.60E-03	rs7136447	12	71953327	q21.1
SNP_A-2207509	A	A	220	78	211	121	7.667	5.60E-03	rs4395225	2	173019640	q31.1
SNP_A-2039378	A	A	324	20	332	44	7.691	5.60E-03	rs10862184	12	79614965	q21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043970	C	C	212	132	205	193	7.677	5.60E-03	rs4766591	12	108213346	q24.11
SNP_A-2047590	T	T	322	6	416	0	7.672	5.60E-03	---	12	31247316	p11.21
SNP_A-2031742	C	C	321	35	372	18	7.672	5.60E-03	rs10772078	12	33462170	p11.1
SNP_A-2013938	T	C	212	202	244	174	7.677	5.60E-03	rs4255117	8	140589040	q24.3
SNP_A-2049684	C	C	422	0	381	7	7.68	5.60E-03	rs7915201	10	129894967	q26.2
SNP_A-2051750	A	A	281	63	288	106	7.675	5.60E-03	rs11790496	9	2562011	p24.2
SNP_A-2077003	T	T	336	4	362	18	7.679	5.60E-03	rs16907970	9	118877479	q33.1
SNP_A-2071887	C	C	248	38	352	26	7.677	5.60E-03	rs903431	6	166136580	q27
SNP_A-2092759	C	C	348	22	384	8	7.675	5.60E-03	rs17096089	10	123188950	q26.13
SNP_A-2097570	G	G	392	4	345	15	7.669	5.60E-03	---	1	25041010	p36.11
SNP_A-2096633	T	T	378	12	404	2	7.689	5.60E-03	rs17122715	1	61902918	p31.3
SNP_A-2085085	G	G	345	9	405	1	7.678	5.60E-03	rs16917266	10	63893269	q21.2
SNP_A-2091450	G	G	332	90	356	58	7.68	5.60E-03	rs2572684	3	5909444	p26.1
SNP_A-2091530	G	G	350	4	378	18	7.658	5.70E-03	rs9492438	6	130376261	q22.33
SNP_A-2081028	G	G	367	9	340	24	7.657	5.70E-03	---	3	50510225	p21.31
SNP_A-2092674	C	C	386	6	355	19	7.638	5.70E-03	rs6938063	6	158552959	q25.3
SNP_A-2101309	-	G	161	161	211	137	7.656	5.70E-03	rs2210398	9	2333547	p24.2
SNP_A-2103524	T	G	220	200	240	180	7.636	5.70E-03	rs3936578	9	106561582	q31.2
SNP_A-2104037	C	C	340	20	383	7	7.629	5.70E-03	rs206015	6	32290737	p21.32
SNP_A-2066873	C	C	306	40	326	76	7.656	5.70E-03	rs4273666	6	65838683	q12
SNP_A-2063892	G	G	263	89	255	135	7.644	5.70E-03	rs1333532	13	58197484	q21.1
SNP_A-2059069	C	C	302	20	341	7	7.627	5.70E-03	rs11574530	12	51885607	q13.13
SNP_A-1990925	C	C	358	52	319	79	7.635	5.70E-03	rs2560656	7	111346798	q31.1
SNP_A-2203955	A	G	210	152	211	195	7.649	5.70E-03	rs9825150	3	163261368	q26.1
SNP_A-2220729	T	T	214	178	252	140	7.64	5.70E-03	rs2075222	2	70958926	p13.3
SNP_A-2217510	G	G	353	15	400	4	7.64	5.70E-03	rs10191351	2	117784583	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2177008	C	C	326	8	341	25	7.648	5.70E-03	rs6551452	3	90251394	p11.1
SNP_A-2196506	G	G	322	8	352	26	7.646	5.70E-03	rs6827845	4	163734845	q32.2
SNP_A-2154421	A	A	353	15	400	4	7.64	5.70E-03	rs7770130	6	159717541	q25.3
SNP_A-2146680	T	T	294	122	255	159	7.638	5.70E-03	rs4477688	16	82171973	q23.3
SNP_A-1868857	T	T	168	164	235	151	7.657	5.70E-03	rs8001889	13	64561369	q21.31
SNP_A-1851733	T	T	200	168	264	148	7.636	5.70E-03	rs9515971	13	91222210	q31.3
SNP_A-1850818	G	G	308	64	348	40	7.644	5.70E-03	rs13289616	9	77478449	q21.2
SNP_A-1858544	G	G	407	1	390	10	7.648	5.70E-03	rs1890648	1	31648690	p35.2
SNP_A-1801011	A	C	215	153	214	202	7.634	5.70E-03	rs1912108	18	59248451	q21.33
SNP_A-1805399	G	G	315	19	302	40	7.655	5.70E-03	rs10851634	15	56261931	q21.3
SNP_A-1807637	A	A	420	0	381	7	7.644	5.70E-03	rs13437956	7	151024482	q36.1
SNP_A-1968465	A	A	388	10	405	1	7.649	5.70E-03	rs16989639	20	43113435	q13.12
SNP_A-1900546	G	G	259	83	270	136	7.635	5.70E-03	rs6518854	22	33037796	q12.3
SNP_A-1883834	G	G	392	2	368	12	7.65	5.70E-03	rs7523248	1	83755698	p31.1
SNP_A-1885908	T	T	372	8	355	23	7.65	5.70E-03	rs12998596	2	9252223	p25.1
SNP_A-1916996	G	G	379	7	418	0	7.647	5.70E-03	rs1945136	18	13203140	p11.21
SNP_A-2299671	C	C	414	0	375	7	7.654	5.70E-03	rs11466804	5	156847875	q33.3
SNP_A-2285395	C	C	333	35	347	67	7.648	5.70E-03	rs1616442	18	45971027	q21.1
SNP_A-2273735	C	C	351	11	412	2	7.657	5.70E-03	rs16876401	5	5892722	p15.32
SNP_A-2251178	C	C	307	39	342	20	7.648	5.70E-03	rs1390489	1	148974176	q21.3
SNP_A-2250950	T	T	155	145	222	134	7.616	5.80E-03	rs642936	11	117525116	q23.3
SNP_A-2240891	A	A	207	149	274	130	7.625	5.80E-03	rs1036001	1	233163436	q43
SNP_A-2236609	G	G	353	5	361	19	7.607	5.80E-03	rs6846389	4	158808819	q32.1
SNP_A-1916697	T	T	340	30	344	58	7.619	5.80E-03	rs9393708	6	26470622	p22.1
SNP_A-1912773	T	A	207	161	220	190	7.619	5.80E-03	rs2690133	6	25361568	p22.2
SNP_A-1913801	C	C	416	0	379	7	7.61	5.80E-03	rs6430440	2	134264337	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909791	T	T	286	82	350	60	7.604	5.80E-03	rs17331092	7	48633002	p12.3
SNP_A-1905530	A	A	411	1	396	10	7.599	5.80E-03	rs11922494	3	106817870	q13.11
SNP_A-1889413	T	T	236	130	299	107	7.599	5.80E-03	rs10863047	12	84585483	q21.31
SNP_A-1883174	A	A	305	45	345	25	7.626	5.80E-03	rs1234515	11	47962636	p11.2
SNP_A-1974070	T	T	313	55	320	94	7.606	5.80E-03	rs12494360	3	118443575	q13.31
SNP_A-1972100	G	G	330	68	286	96	7.598	5.80E-03	rs2060565	3	25246269	p24.2
SNP_A-1956590	A	A	365	5	396	20	7.597	5.80E-03	rs11856068	15	69916180	q23
SNP_A-1953318	A	A	319	19	381	7	7.623	5.80E-03	rs11119896	1	208833299	q32.3
SNP_A-1810202	A	A	275	123	234	158	7.617	5.80E-03	rs16867617	5	15773106	p15.1
SNP_A-1806282	T	T	411	3	357	13	7.601	5.80E-03	rs16834553	1	149591934	q21.3
SNP_A-1790674	A	A	268	148	229	187	7.601	5.80E-03	rs2518796	3	50182079	p21.31
SNP_A-1790328	G	G	420	0	383	7	7.604	5.80E-03	rs11057106	12	16985077	p12.3
SNP_A-1741843	A	A	265	85	273	137	7.61	5.80E-03	rs10513920	18	61850394	q22.1
SNP_A-1867204	A	A	270	34	272	64	7.61	5.80E-03	rs8037172	15	57805779	q22.2
SNP_A-1823072	T	T	379	7	416	0	7.61	5.80E-03	rs10754233	1	194548444	q31.3
SNP_A-1827064	G	G	228	84	218	128	7.62	5.80E-03	rs759817	19	7943040	p13.2
SNP_A-2154398	C	C	177	167	233	145	7.616	5.80E-03	rs6767967	3	24683878	p24.2
SNP_A-2160392	C	C	301	63	307	105	7.619	5.80E-03	rs283977	13	75974751	q22.2
SNP_A-2159996	G	G	332	12	350	32	7.598	5.80E-03	rs9427858	1	190844936	q31.3
SNP_A-2129360	T	T	322	22	331	47	7.598	5.80E-03	rs10859398	12	91868451	q22
SNP_A-2133785	C	C	241	33	300	18	7.618	5.80E-03	rs169981	18	52238794	q21.2
SNP_A-2119721	C	C	389	25	399	9	7.613	5.80E-03	rs7839026	8	113613045	q23.3
SNP_A-2171332	T	T	258	70	257	113	7.606	5.80E-03	rs3923011	2	45941892	p21
SNP_A-2169430	A	A	310	24	383	11	7.625	5.80E-03	rs6782822	3	178639701	q26.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2226491	T	T	213	137	198	192	7.602	5.80E-03	rs9963419	18	50799053	q21.2
SNP_A-2002717	A	A	300	56	280	88	7.604	5.80E-03	rs4761935	12	49937423	q13.13
SNP_A-2032620	G	G	245	111	244	168	7.604	5.80E-03	rs10951660	7	41583575	p14.1
SNP_A-2021759	C	C	228	136	211	189	7.622	5.80E-03	rs6535383	4	83996319	q21.22
SNP_A-2025030	A	A	216	148	269	121	7.614	5.80E-03	rs10892755	11	98457727	q22.1
SNP_A-2042731	G	G	422	0	385	7	7.601	5.80E-03	rs16940166	17	39179622	q21.31
SNP_A-2071663	A	A	236	162	276	126	7.605	5.80E-03	rs9963077	18	32217202	q12.2
SNP_A-2094585	C	C	359	63	323	93	7.627	5.80E-03	rs4905592	14	96973226	q32.2
SNP_A-2098087	T	T	398	2	376	12	7.587	5.90E-03	rs1892017	10	85623914	q23.1
SNP_A-2088384	G	G	296	14	338	38	7.58	5.90E-03	---	3	152638081	q25.1
SNP_A-2059291	G	G	362	18	375	5	7.577	5.90E-03	rs2783572	10	29379758	p12.1
SNP_A-2052775	A	A	344	36	384	18	7.585	5.90E-03	rs2015441	8	126742286	q24.13
SNP_A-2046119	C	C	261	93	251	139	7.592	5.90E-03	rs585206	13	41587853	q14.11
SNP_A-2031732	G	G	206	158	269	137	7.582	5.90E-03	rs4569797	4	157874676	q32.1
SNP_A-1998061	A	A	301	33	387	19	7.586	5.90E-03	rs603328	9	132910598	q34.13
SNP_A-1991177	T	T	362	0	378	8	7.584	5.90E-03	rs10265406	7	125295154	q31.33
SNP_A-2225834	A	A	216	112	289	95	7.591	5.90E-03	rs1828187	5	138200119	q31.2
SNP_A-2203212	T	T	296	20	304	44	7.582	5.90E-03	rs16995978	22	45630535	q13.31
SNP_A-2207253	G	G	366	8	368	24	7.587	5.90E-03	rs16870220	5	2697862	p15.33
SNP_A-2169788	G	G	372	0	388	8	7.594	5.90E-03	rs11964151	6	138547941	q23.3
SNP_A-2190294	C	C	350	68	315	99	7.578	5.90E-03	rs17665285	5	168084887	q34
SNP_A-2154072	A	A	275	75	333	53	7.571	5.90E-03	rs1930893	13	69926153	q21.33
SNP_A-1839579	T	T	372	24	399	9	7.586	5.90E-03	rs2763237	6	168735179	q27
SNP_A-1829206	G	A	203	183	230	172	7.59	5.90E-03	rs1548882	7	12059465	p21.3
SNP_A-1855524	T	T	362	2	373	13	7.592	5.90E-03	rs510324	3	125585925	q21.2
SNP_A-1782585	G	A	193	161	220	176	7.591	5.90E-03	rs2093765	1	4895255	p36.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1757103	A	A	354	42	312	66	7.567	5.90E-03	rs10490456	2	32984467	p22.3
SNP_A-1643786	G	G	293	71	339	47	7.591	5.90E-03	rs1915337	3	110816930	q13.13
SNP_A-1794129	C	C	343	9	399	1	7.594	5.90E-03	rs16889829	6	79059234	q14.1
SNP_A-1802680	C	C	345	9	401	1	7.587	5.90E-03	rs16827827	2	150808777	q23.3
SNP_A-1808463	A	A	284	72	283	115	7.573	5.90E-03	rs606177	18	8715076	p11.22
SNP_A-1934710	A	A	270	148	304	110	7.592	5.90E-03	rs12707091	7	132643004	q33
SNP_A-1980991	G	G	305	25	359	11	7.575	5.90E-03	rs1428369	5	24496323	p14.2
SNP_A-1980409	A	A	352	2	363	13	7.58	5.90E-03	rs10512756	5	5025328	p15.32
SNP_A-1978220	G	G	349	1	373	11	7.572	5.90E-03	rs16836491	1	190891270	q31.3
SNP_A-1874600	A	A	368	0	384	8	7.59	5.90E-03	rs10888807	1	39639798	p34.3
SNP_A-2235158	G	G	262	88	253	133	7.577	5.90E-03	rs202817	5	157537262	q33.3
SNP_A-2241392	A	A	342	30	348	12	7.572	5.90E-03	rs8032941	15	46302144	q21.1
SNP_A-2255910	T	T	339	29	279	47	7.574	5.90E-03	rs6984624	8	9722567	p23.1
SNP_A-2282167	C	C	377	7	412	0	7.577	5.90E-03	rs16898071	8	124249338	q24.13
SNP_A-2289155	T	T	365	15	328	32	7.589	5.90E-03	rs17052856	9	87293533	q21.33
SNP_A-2296685	C	C	224	130	282	106	7.547	6.00E-03	rs2326825	6	6751170	p25.1
SNP_A-2286477	C	C	223	181	260	142	7.538	6.00E-03	rs2269375	17	75800151	q25.3
SNP_A-2258213	T	T	270	24	375	13	7.551	6.00E-03	rs10142960	14	101814505	q32.32
SNP_A-2250446	A	A	369	7	402	0	7.552	6.00E-03	rs7737076	5	61455233	q12.1
SNP_A-2231441	C	C	341	9	395	1	7.554	6.00E-03	rs925890	12	75146627	q21.2
SNP_A-1878588	G	G	293	77	316	48	7.548	6.00E-03	rs3986589	15	99441121	q26.3
SNP_A-1917637	C	C	314	32	366	16	7.548	6.00E-03	rs12651746	5	39288277	p13.1
SNP_A-1926686	T	T	370	6	383	21	7.562	6.00E-03	rs6116762	20	5285412	p12.3
SNP_A-1988379	T	T	227	137	209	189	7.536	6.00E-03	rs1937479	6	161225955	q26
SNP_A-1986879	C	C	359	9	415	1	7.541	6.00E-03	rs9353972	6	93751890	q16.1
SNP_A-1965776	G	G	214	138	284	120	7.554	6.00E-03	rs494874	2	169614813	q31.1
SNP_A-1956778	A	A	215	123	211	183	7.562	6.00E-03	rs2381553	2	144279712	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826470	A	A	298	62	362	42	7.543	6.00E-03	rs17470673	10	70319250	q22.1
SNP_A-1819260	C	C	239	115	300	92	7.543	6.00E-03	rs6755021	2	97959593	q11.2
SNP_A-2116934	T	G	183	145	223	187	7.558	6.00E-03	rs2726696	4	108844975	q25
SNP_A-2108964	T	T	333	19	395	7	7.536	6.00E-03	rs2900171	9	99331192	q22.33
SNP_A-2190821	C	C	412	0	379	7	7.538	6.00E-03	rs4366709	16	6366582	p13.2
SNP_A-2183255	A	A	322	36	334	68	7.544	6.00E-03	rs12373334	18	75886971	q23
SNP_A-2171267	G	G	272	80	337	59	7.548	6.00E-03	rs6809452	3	9799308	p25.3
SNP_A-2207865	A	A	366	0	384	8	7.549	6.00E-03	rs17107593	14	37708670	q21.1
SNP_A-2213774	G	G	373	7	406	0	7.546	6.00E-03	rs3870340	3	49511653	p21.31
SNP_A-1996258	C	C	359	1	385	11	7.545	6.00E-03	rs10118209	9	23511871	p21.3
SNP_A-2018326	G	G	302	14	368	4	7.549	6.00E-03	rs16990850	21	34065438	q22.11
SNP_A-2028316	C	C	209	149	272	128	7.54	6.00E-03	rs861615	1	181486938	q25.3
SNP_A-2054471	C	C	299	35	374	20	7.555	6.00E-03	rs1907860	3	165029125	q26.1
SNP_A-2051142	T	T	380	10	393	1	7.562	6.00E-03	rs7704802	5	139922300	q31.3
SNP_A-2076618	T	T	252	92	258	146	7.558	6.00E-03	rs7976773	12	5016038	p13.32
SNP_A-2080353	G	G	246	118	233	169	7.549	6.00E-03	rs11693523	2	13581959	p24.3
SNP_A-2096337	G	G	287	37	275	65	7.561	6.00E-03	rs9675615	18	60637216	q22.1
SNP_A-2063805	A	A	344	20	329	41	7.515	6.10E-03	rs11737428	4	5071158	p16.2
SNP_A-2051902	T	T	338	8	325	23	7.507	6.10E-03	rs721904	9	8149851	p24.1
SNP_A-2013200	C	C	341	9	393	1	7.508	6.10E-03	---	11	87971149	q14.3
SNP_A-1991806	G	G	374	10	385	1	7.518	6.10E-03	rs1440451	7	154306527	q36.2
SNP_A-1997223	T	T	227	161	273	129	7.517	6.10E-03	rs1388966	9	91412981	q22.31
SNP_A-2000536	C	C	385	7	418	0	7.529	6.10E-03	rs595730	1	179343984	q25.3
SNP_A-2213371	G	G	262	70	267	115	7.529	6.10E-03	rs9507893	13	26900724	q12.2
SNP_A-2216685	A	A	361	31	344	56	7.514	6.10E-03	rs11780227	8	22741639	p21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227300	A	A	331	13	379	3	7.527	6.10E-03	rs3775180	4	87336326	q21.3
SNP_A-2223904	C	C	328	32	399	17	7.524	6.10E-03	rs17728338	5	150458511	q33.1
SNP_A-2199780	A	A	349	5	359	19	7.529	6.10E-03	rs9993665	4	172389675	q34.1
SNP_A-2193165	A	A	409	1	398	10	7.509	6.10E-03	rs16836978	1	191155548	q31.3
SNP_A-2134627	T	T	393	5	357	17	7.535	6.10E-03	rs1036738	2	158542242	q24.1
SNP_A-2160077	T	A	218	148	208	206	7.527	6.10E-03	rs753255	4	56933574	q12
SNP_A-2166667	A	A	286	74	244	102	7.508	6.10E-03	rs935614	2	135766452	q21.3
SNP_A-2140688	C	C	342	22	403	9	7.506	6.10E-03	rs9309975	3	85480983	p12.1
SNP_A-2145215	G	G	345	13	395	3	7.533	6.10E-03	rs7152113	14	65422034	q23.3
SNP_A-1824317	G	G	185	167	245	147	7.517	6.10E-03	rs12692966	2	172220728	q31.1
SNP_A-1839173	T	T	363	1	352	10	7.527	6.10E-03	rs16848800	3	166114940	q26.1
SNP_A-1854457	C	C	360	44	374	22	7.521	6.10E-03	rs6669724	1	77463529	p31.1
SNP_A-1854295	G	A	209	155	212	192	7.511	6.10E-03	rs6548820	3	82627185	p12.2
SNP_A-1853873	T	T	271	69	243	101	7.526	6.10E-03	rs6794440	3	2275052	p26.3
SNP_A-1807539	A	A	416	0	383	7	7.532	6.10E-03	rs17126608	14	22640664	q11.2
SNP_A-1802549	C	C	262	146	304	112	7.52	6.10E-03	rs2038696	13	30512181	q12.3
SNP_A-1800432	G	C	180	164	221	161	7.529	6.10E-03	rs417474	9	111658125	q31.3
SNP_A-1805520	G	G	303	27	367	13	7.53	6.10E-03	rs7517389	1	227217074	q42.2
SNP_A-1797888	G	G	261	77	253	119	7.514	6.10E-03	rs1950279	14	87874519	q31.3
SNP_A-1787301	C	C	269	63	303	39	7.521	6.10E-03	rs582336	13	18639478	q12.11
SNP_A-1743151	A	A	300	84	288	126	7.528	6.10E-03	rs3886662	18	8561754	p11.22
SNP_A-1953569	C	C	324	6	410	0	7.515	6.10E-03	rs4246923	10	46531629	q11.22
SNP_A-1949510	T	T	389	1	378	10	7.516	6.10E-03	rs384440	17	10587584	p13.1
SNP_A-1949180	T	T	239	129	229	185	7.521	6.10E-03	rs9396834	6	18272052	p22.3
SNP_A-1963267	T	T	220	148	281	125	7.517	6.10E-03	rs13391006	2	52625828	p16.3
SNP_A-1963501	G	G	371	13	346	30	7.509	6.10E-03	rs10196963	2	60349259	p16.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1969362	G	G	396	2	376	12	7.535	6.10E-03	rs9982042	21	21833267	q21.1
SNP_A-1922686	G	G	327	41	279	63	7.514	6.10E-03	rs1233491	6	29569709	p22.1
SNP_A-1900542	A	A	377	13	365	31	7.512	6.10E-03	rs16891617	8	119956070	q24.12
SNP_A-2235576	G	G	321	21	311	43	7.516	6.10E-03	rs16856060	3	172458763	q26.2
SNP_A-2236980	A	A	271	97	329	73	7.508	6.10E-03	rs2025733	10	107969025	q25.1
SNP_A-2253735	C	C	390	28	401	11	7.52	6.10E-03	rs7921170	10	70802255	q22.1
SNP_A-2242193	A	A	236	126	303	105	7.516	6.10E-03	rs12734551	1	10325802	p36.22
SNP_A-2271969	A	A	418	0	385	7	7.529	6.10E-03	rs16941816	15	57916039	q22.2
SNP_A-2281119	T	T	342	22	403	9	7.506	6.10E-03	rs17152577	5	124642553	q23.2
SNP_A-2276532	T	T	316	16	373	5	7.529	6.10E-03	rs11804547	1	185584042	q31.1
SNP_A-2297238	T	T	404	2	384	12	7.527	6.10E-03	---	3	49418422	p21.31
SNP_A-2293061	G	G	279	133	224	160	7.526	6.10E-03	rs165400	5	143998172	q31.3
SNP_A-2294207	G	G	348	54	309	81	7.535	6.10E-03	rs250430	5	139921412	q31.3
SNP_A-2290302	C	C	289	77	290	122	7.484	6.20E-03	rs6722179	2	124994556	q14.3
SNP_A-2265303	T	T	267	101	333	79	7.491	6.20E-03	rs12367287	12	39376592	q12
SNP_A-2240707	G	G	349	19	329	39	7.487	6.20E-03	rs9783215	10	11305362	p14
SNP_A-1877562	C	C	281	141	240	178	7.499	6.20E-03	rs4839062	1	116520298	p13.1
SNP_A-1926919	G	G	300	32	271	55	7.499	6.20E-03	rs17038868	3	14098907	p25.1
SNP_A-1930114	T	T	213	207	249	165	7.504	6.20E-03	rs1922654	2	116703373	q14.1
SNP_A-1914295	A	A	311	27	344	58	7.489	6.20E-03	rs156466	5	8796390	p15.31
SNP_A-1914751	C	C	395	5	384	18	7.498	6.20E-03	rs2052208	7	19385486	p21.1
SNP_A-1905100	A	G	210	148	208	198	7.479	6.20E-03	rs7956536	12	108443236	q24.11
SNP_A-1972330	C	C	357	11	412	2	7.484	6.20E-03	rs11160577	3	35363086	p22.3
SNP_A-1967435	C	C	239	127	309	107	7.485	6.20E-03	rs672385	20	754677	p13
SNP_A-1983038	C	C	357	9	411	1	7.503	6.20E-03	rs12109985	5	114104913	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1947193	A	A	387	7	418	0	7.491	6.20E-03	rs4135356	3	12442613	p25.2
SNP_A-1671548	A	A	287	3	316	16	7.488	6.20E-03	rs10504984	8	98978052	q22.1
SNP_A-1794441	A	A	336	22	356	48	7.486	6.20E-03	rs17812685	12	103447278	q23.3
SNP_A-1795345	A	A	308	8	403	1	7.494	6.20E-03	rs2765980	10	11324270	p14
SNP_A-1806032	A	A	357	9	411	1	7.503	6.20E-03	rs6549186	3	69294645	p14.1
SNP_A-1845489	C	C	220	146	200	198	7.486	6.20E-03	rs7119000	11	10052816	p15.4
SNP_A-1869648	C	C	330	26	341	53	7.502	6.20E-03	rs2249739	21	17868941	q21.1
SNP_A-1860871	C	C	358	0	378	8	7.5	6.20E-03	rs16934753	9	16498701	p22.3
SNP_A-1838475	A	A	330	6	416	0	7.488	6.20E-03	rs266696	5	95823676	q15
SNP_A-1842431	G	G	410	0	379	7	7.501	6.20E-03	---	11	74649395	q13.4
SNP_A-1831884	T	T	379	7	410	0	7.501	6.20E-03	rs1106043	12	129366636	q24.33
SNP_A-1818321	G	G	264	72	250	110	7.497	6.20E-03	rs815216	4	168413460	q32.3
SNP_A-2158986	C	T	210	144	189	183	7.494	6.20E-03	rs7609503	2	82180365	p12
SNP_A-2170801	T	T	349	9	401	1	7.483	6.20E-03	rs16964995	15	35474329	q14
SNP_A-2203872	A	A	285	67	278	106	7.502	6.20E-03	rs2608049	8	129147984	q24.21
SNP_A-2212511	T	T	282	58	294	100	7.482	6.20E-03	rs17630450	4	42290609	p13
SNP_A-2013891	A	A	308	32	313	61	7.481	6.20E-03	rs4269493	8	135820298	q24.22
SNP_A-2018961	A	A	293	73	363	53	7.478	6.20E-03	rs2835611	21	37417902	q22.13
SNP_A-2017845	T	T	182	164	232	138	7.481	6.20E-03	rs1537095	21	30725570	q22.11
SNP_A-2065896	G	G	351	1	379	11	7.481	6.20E-03	rs17147651	4	70832957	q13.3
SNP_A-2081737	G	G	279	125	243	163	7.492	6.20E-03	rs895397	2	119693485	q14.2
SNP_A-2086743	G	G	414	0	383	7	7.496	6.20E-03	---	8	1847582	p23.3
SNP_A-2085559	C	C	297	13	392	4	7.499	6.20E-03	rs1095859	8	57707399	q12.1
SNP_A-2084348	C	C	207	155	271	135	7.452	0.0063	---	4	157870342	q32.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2049745	G	G	389	7	418	0	7.453	0.0063	rs16996800	22	46135396	q13.31
SNP_A-2057241	C	C	314	92	271	123	7.452	0.0063	rs12659534	5	168162396	q34
SNP_A-2015731	A	A	414	0	385	7	7.458	0.0063	rs9305836	21	18354018	q21.1
SNP_A-1992699	G	G	414	0	385	7	7.458	0.0063	rs6986589	8	23924548	p21.2
SNP_A-2217147	G	G	330	6	414	0	7.452	0.0063	rs17141299	7	103994116	q22.2
SNP_A-2144085	A	A	320	6	402	0	7.46	0.0063	rs10945786	6	162260239	q26
SNP_A-2142597	A	A	362	0	384	8	7.467	0.0063	rs11164386	1	102290118	p21.1
SNP_A-2127955	A	A	230	130	212	180	7.449	0.0063	rs9372547	6	120036016	q22.31
SNP_A-1832604	A	A	246	118	220	160	7.455	0.0063	rs7129973	11	88555218	q14.3
SNP_A-1831366	T	T	260	56	251	91	7.476	0.0063	rs7227646	18	56674795	q21.32
SNP_A-1864737	C	C	318	12	314	30	7.452	0.0063	rs16830581	3	160845617	q25.33
SNP_A-1852421	C	C	390	8	377	23	7.473	0.0063	rs10984561	9	119338131	q33.1
SNP_A-1803133	G	G	221	131	215	191	7.454	0.0063	rs112038111	8	12689731	p23.1
SNP_A-1794111	A	A	297	47	313	85	7.469	0.0063	rs17776288	16	26883719	p12.1
SNP_A-1799248	C	C	196	130	259	111	7.469	0.0063	rs8104912	19	33152104	q12
SNP_A-1787750	G	G	375	37	346	62	7.46	0.0063	rs4921702	8	20229590	p21.3
SNP_A-1788920	A	A	359	9	411	1	7.453	0.0063	rs2236208	20	54401300	q13.31
SNP_A-1718233	A	A	345	3	382	16	7.46	0.0063	rs7684854	4	138718545	q28.3
SNP_A-1936226	T	T	404	0	375	7	7.47	0.0063	rs16937602	9	19545619	p22.1
SNP_A-1953556	A	A	269	87	344	68	7.462	0.0063	rs12222455	11	83086089	q14.1
SNP_A-1989084	G	G	406	0	377	7	7.467	0.0063	rs16872384	7	19600110	p21.1
SNP_A-1914077	C	C	259	153	293	115	7.463	0.0063	rs10950076	7	66407425	q11.21
SNP_A-1911489	A	A	354	26	370	10	7.465	0.0063	rs12271738	11	35958140	p13
SNP_A-1899867	C	C	189	167	231	135	7.454	0.0063	rs9959583	18	20993778	q11.2
SNP_A-2235708	G	G	300	16	392	6	7.458	0.0063	rs8066895	17	47583528	q22
SNP_A-2247614	T	T	329	25	337	51	7.449	0.0063	rs3798465	6	73809830	q13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255694	T	T	324	30	385	15	7.47	0.0063	rs2490859	9	15380258	p22.3
SNP_A-2252762	C	C	313	47	377	29	7.464	0.0063	rs7690543	4	67885379	q13.2
SNP_A-2272272	A	T	185	177	243	171	7.471	0.0063	rs7914261	10	90619302	q23.31
SNP_A-2268717	C	C	366	12	349	29	7.453	0.0063	rs16992285	19	4110563	p13.3
SNP_A-2257410	T	T	264	74	244	110	7.465	0.0063	rs9535561	13	50513913	q14.3
SNP_A-2259103	C	C	316	80	283	113	7.461	0.0063	rs12692163	2	235934436	q37.2
SNP_A-2282662	T	T	350	0	372	8	7.45	0.0063	rs848225	2	150382172	q23.2
SNP_A-2283891	A	A	252	100	250	152	7.455	0.0063	rs3131751	1	57853194	p32.2
SNP_A-2289045	C	C	292	70	317	43	7.472	0.0063	rs7801950	7	115748734	q31.2
SNP_A-2295314	T	T	288	30	343	15	7.453	0.0063	rs7232172	18	23983703	q12.1
SNP_A-2301051	T	T	379	7	408	0	7.465	0.0063	rs7826024	8	37164161	p12
SNP_A-2305843	A	A	283	117	235	147	7.447	6.40E-03	rs12478344	2	151657256	q23.3
SNP_A-2274091	G	G	339	41	301	65	7.43	6.40E-03	rs12593770	15	62562055	q22.31
SNP_A-2274290	C	C	361	35	324	58	7.437	6.40E-03	rs4143999	14	89491246	q32.11
SNP_A-2256688	A	A	364	0	388	8	7.432	6.40E-03	rs17015528	2	34840885	p22.3
SNP_A-2247596	T	T	360	56	386	32	7.447	6.40E-03	rs9903532	17	58345634	q23.3
SNP_A-2228749	T	T	307	53	288	84	7.427	6.40E-03	---	2	53891535	p16.2
SNP_A-1893749	G	G	265	105	252	152	7.443	6.40E-03	rs4768729	12	45161741	q13.11
SNP_A-1879015	C	C	276	82	346	62	7.424	6.40E-03	rs17039652	4	161802109	q32.1
SNP_A-1920558	A	T	176	174	234	158	7.44	6.40E-03	rs3850539	1	58576891	p32.2
SNP_A-1926060	C	C	363	1	356	10	7.426	6.40E-03	rs1867412	18	63439628	q22.1
SNP_A-1974630	A	A	383	7	410	0	7.424	6.40E-03	rs10513199	3	144611284	q24
SNP_A-1953459	T	G	211	157	217	197	7.426	6.40E-03	rs11594020	10	95480563	q23.33
SNP_A-1955944	G	G	205	97	218	160	7.442	6.40E-03	rs2036485	15	80200243	q25.2
SNP_A-1946330	T	C	203	165	225	187	7.429	6.40E-03	rs2523399	6	29808058	p22.1
SNP_A-1750981	T	T	215	157	264	128	7.445	6.40E-03	rs1486410	12	114506922	q24.21
SNP_A-1669519	A	A	220	142	263	111	7.433	6.40E-03	rs10500658	11	5868586	p15.4
SNP_A-1788609	T	T	351	17	372	40	7.432	6.40E-03	rs7727761	5	115721065	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798510	G	G	280	40	324	22	7.427	6.40E-03	rs10960036	9	11617844	p23
SNP_A-1804315	A	A	278	90	342	68	7.424	6.40E-03	rs6585063	10	113067462	q25.2
SNP_A-1812213	G	G	363	1	356	10	7.426	6.40E-03	rs11012000	10	20689290	p12.31
SNP_A-1869531	T	T	260	44	259	77	7.42	6.40E-03	rs17823816	5	78384693	q14.1
SNP_A-1830582	G	G	379	5	370	18	7.435	6.40E-03	rs17673487	5	128989963	q23.3
SNP_A-1833772	A	A	221	109	213	161	7.441	6.40E-03	rs157643	20	52851126	q13.2
SNP_A-1841838	G	G	347	9	397	1	7.444	6.40E-03	rs7591129	2	169324749	q24.3
SNP_A-1821367	G	G	308	16	361	5	7.432	6.40E-03	rs1916239	3	176151802	q26.31
SNP_A-2137692	T	T	338	2	353	13	7.445	6.40E-03	rs17113085	14	27262968	q12
SNP_A-2120725	T	T	215	119	279	99	7.436	6.40E-03	rs1428013	5	5216011	p15.32
SNP_A-2169502	G	G	236	120	291	95	7.446	6.40E-03	rs620950	1	18011280	p36.13
SNP_A-2004105	T	T	257	73	299	49	7.421	6.40E-03	rs719964	15	37592863	q14
SNP_A-2023964	T	T	311	33	275	55	7.424	6.40E-03	rs17841962	3	31336629	p24.1
SNP_A-2044228	T	T	359	13	407	3	7.429	6.40E-03	rs638122	11	69053944	q13.3
SNP_A-2068172	A	A	228	138	289	115	7.431	6.40E-03	rs968323	20	56371439	q13.32
SNP_A-2069062	T	T	356	0	380	8	7.42	6.50E-03	rs1443063	4	128520178	q28.1
SNP_A-2077933	G	G	391	7	418	0	7.415	6.50E-03	rs8088570	18	23995051	q12.1
SNP_A-2103653	G	G	362	4	350	16	7.402	6.50E-03	rs343130	13	59097943	q21.2
SNP_A-2022913	T	T	251	119	208	150	7.405	6.50E-03	rs7952229	11	10222054	p15.4
SNP_A-2022401	G	G	400	10	407	1	7.42	6.50E-03	rs7932099	11	8259382	p15.4
SNP_A-2032563	G	G	279	45	353	29	7.409	6.50E-03	rs4910333	11	11370914	p15.3
SNP_A-1994670	G	G	324	6	404	0	7.406	6.50E-03	---	8	111736901	q23.2
SNP_A-2216223	T	T	232	128	300	108	7.416	6.50E-03	rs8072508	17	1654643	p13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2202623	A	A	415	1	365	9	7.393	6.50E-03	rs275753	15	37907672	q15.1
SNP_A-2117280	C	C	367	19	392	6	7.402	6.50E-03	rs9891758	17	68471230	q25.1
SNP_A-2144578	T	T	314	8	407	1	7.412	6.50E-03	rs864560	1	43180738	p34.2
SNP_A-2144984	G	A	213	149	206	198	7.419	6.50E-03	rs10954442	7	133464842	q33
SNP_A-2160727	T	T	195	161	258	142	7.417	6.50E-03	rs4659709	1	233225424	q43
SNP_A-2153520	A	A	324	32	357	15	7.4	6.50E-03	rs11898937	2	213516765	q34
SNP_A-1822475	A	A	322	12	399	3	7.404	6.50E-03	rs8099352	18	17809877	q11.2
SNP_A-1869606	G	G	387	13	377	31	7.416	6.50E-03	rs11977774	7	46107459	p13
SNP_A-1870851	G	G	256	98	252	148	7.415	6.50E-03	rs6672535	1	191112765	q31.3
SNP_A-1848731	T	T	275	55	245	83	7.406	6.50E-03	rs1553115	12	17541979	p12.3
SNP_A-1947032	A	A	339	29	396	14	7.407	6.50E-03	rs387873	4	167578381	q32.3
SNP_A-1956977	T	C	237	175	215	199	7.41	6.50E-03	rs10789898	11	111953400	q23.1
SNP_A-1925456	T	T	356	0	380	8	7.42	6.50E-03	---	2	103571817	q12.1
SNP_A-1905744	T	T	224	194	264	156	7.4	6.50E-03	rs11130742	3	59945272	p14.2
SNP_A-1906074	A	A	389	7	416	0	7.417	6.50E-03	rs6488918	12	123096842	q24.31
SNP_A-1911176	G	G	359	9	409	1	7.409	6.50E-03	rs17174953	14	35604215	q13.3
SNP_A-1910457	G	G	281	65	343	45	7.418	6.50E-03	rs7873893	9	9964453	p23
SNP_A-1910696	A	A	416	0	389	7	7.417	6.50E-03	rs16978547	18	42192305	q21.1
SNP_A-1909614	A	A	279	123	313	89	7.406	6.50E-03	rs7736704	5	55707498	q11.2
SNP_A-1888301	C	C	351	11	402	2	7.404	6.50E-03	rs12568393	1	67314160	p31.2
SNP_A-1897729	C	C	254	110	244	160	7.397	6.50E-03	rs10754104	1	191116183	q31.3
SNP_A-2250626	C	C	203	175	263	153	7.399	6.50E-03	rs9403303	6	141763811	q24.1
SNP_A-2278924	T	T	382	14	314	28	7.399	6.50E-03	rs4077656	8	129402637	q24.21
SNP_A-2308963	T	T	358	50	305	73	7.403	6.50E-03	rs3751529	15	95109334	q26.2
SNP_A-2295032	T	T	185	175	253	161	7.409	6.50E-03	rs12613470	2	181695220	q31.3
SNP_A-2300521	T	T	400	4	361	15	7.371	0.0066	rs17165922	7	93208650	q21.3
SNP_A-2286600	T	T	359	11	410	2	7.379	0.0066	rs7591997	2	149423506	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2256814	G	G	379	9	358	24	7.37	0.0066	rs4479454	2	1091472	p25.3
SNP_A-2246936	T	T	385	7	410	0	7.386	0.0066	rs327418	8	31953465	p12
SNP_A-1896646	C	C	394	16	366	34	7.389	0.0066	---	19	39512161	q13.11
SNP_A-1887232	C	C	341	13	385	3	7.374	0.0066	rs36796	5	109355147	q21.3
SNP_A-1886975	G	G	353	3	394	16	7.375	0.0066	rs7817004	8	54139976	q11.23
SNP_A-1883418	T	T	201	77	304	70	7.366	0.0066	rs1733866	7	130655283	q32.3
SNP_A-1874515	G	G	342	8	365	25	7.365	0.0066	rs17090855	8	13216746	p22
SNP_A-1931885	G	G	211	203	244	160	7.366	0.0066	rs616509	1	232841567	q42.3
SNP_A-1928985	T	G	190	174	236	174	7.371	0.0066	rs7460017	8	40222212	p11.21
SNP_A-1958558	C	C	308	40	327	75	7.371	0.0066	rs696014	3	64102128	p14.1
SNP_A-1943416	C	C	384	12	398	2	7.374	0.0066	rs7315627	12	2491387	p13.33
SNP_A-1933578	T	T	384	14	399	3	7.385	0.0066	rs11790425	9	93192698	q22.31
SNP_A-1976204	A	A	275	91	334	68	7.372	0.0066	rs2313733	4	15749690	p15.32
SNP_A-1964499	G	G	412	0	387	7	7.384	0.0066	rs10496448	2	113544921	q13
SNP_A-1985849	A	A	383	7	408	0	7.388	0.0066	rs486081	6	44991982	p21.1
SNP_A-1985627	T	T	278	90	272	136	7.386	0.0066	rs5000563	6	32512113	p21.32
SNP_A-1869566	G	G	384	14	399	3	7.385	0.0066	rs11155702	6	150466102	q25.1
SNP_A-1864586	A	A	244	162	285	127	7.373	0.0066	rs6507074	18	29818824	q12.1
SNP_A-1822383	G	G	308	110	336	76	7.389	0.0066	rs8054578	16	77874316	q23.1
SNP_A-1823338	A	A	211	143	279	125	7.38	0.0066	rs9816762	3	80922927	p12.2
SNP_A-1827878	G	G	369	39	350	66	7.368	0.0066	rs12408468	1	23190757	p36.12
SNP_A-1814174	C	C	389	7	414	0	7.382	0.0066	rs12320426	12	106166572	q23.3
SNP_A-1806731	G	G	324	12	401	3	7.392	0.0066	rs1193366	12	127309423	q24.32
SNP_A-1806981	G	G	310	20	374	8	7.373	0.0066	rs11563175	2	51630471	p16.3
SNP_A-1785058	T	T	287	27	306	56	7.37	0.0066	rs13330098	16	10237778	p13.2
SNP_A-2161121	T	T	394	4	355	15	7.388	0.0066	rs10245486	7	126211006	q32.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2161431	A	A	375	9	371	25	7.368	0.0066	rs2471579	7	77282189	q21.11
SNP_A-2139033	C	C	298	72	361	51	7.374	0.0066	rs9529745	13	69922412	q21.33
SNP_A-2107848	A	A	202	174	246	142	7.375	0.0066	rs432131	1	75833689	p31.1
SNP_A-2124230	T	T	313	15	393	5	7.384	0.0066	rs4655835	1	66526847	p31.2
SNP_A-2208023	A	A	359	5	352	18	7.368	0.0066	rs2417766	12	19153803	p12.3
SNP_A-2218407	G	A	184	182	246	168	7.371	0.0066	rs4901509	14	53905750	q22.2
SNP_A-2217870	A	A	375	15	329	31	7.383	0.0066	rs7847289	9	89468164	q22.2
SNP_A-2168704	G	G	290	76	293	121	7.369	0.0066	rs17241648	16	58917412	q21
SNP_A-2172965	C	C	343	1	375	11	7.367	0.0066	rs7024904	9	36000362	p13.3
SNP_A-2015342	G	G	396	10	401	1	7.375	0.0066	---	21	15411804	q21.1
SNP_A-2030937	A	A	391	7	416	0	7.38	0.0066	rs17034740	3	36285707	p22.3
SNP_A-2047743	G	G	288	102	253	137	7.39	0.0066	rs1781819	10	79295259	q22.3
SNP_A-2041392	C	C	391	7	416	0	7.38	0.0066	rs9317788	13	18425673	q12.11
SNP_A-2039380	G	G	277	123	239	159	7.389	0.0066	rs4727570	7	102728626	q22.1
SNP_A-2035097	A	A	265	145	301	109	7.392	0.0066	rs6875	2	97831498	q11.2
SNP_A-2104826	C	G	195	185	210	148	7.373	0.0066	rs10963383	9	17976621	p22.2
SNP_A-2092442	A	A	358	0	384	8	7.385	0.0066	rs7121916	11	88398239	q14.3
SNP_A-2084970	T	T	284	52	357	35	7.371	0.0066	rs2869214	4	9941902	p16.1
SNP_A-2056915	C	C	240	100	224	144	7.39	0.0066	rs4899588	14	75809787	q24.3
SNP_A-2053905	A	A	196	156	264	140	7.375	0.0066	rs782721	3	66421302	p14.1
SNP_A-2053729	T	T	327	37	334	68	7.36	6.70E-03	rs10005065	4	157504074	q32.1
SNP_A-2054367	T	T	336	48	292	72	7.353	6.70E-03	rs2067749	9	33120640	p21.1
SNP_A-2071474	C	C	359	21	375	7	7.344	6.70E-03	rs2418481	15	98497615	q26.3
SNP_A-2096341	T	T	304	10	386	2	7.359	6.70E-03	rs7786435	7	134190329	q33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169497	T	T	306	10	388	2	7.346	6.70E-03	rs12346083	9	32191106	p21.1
SNP_A-2189658	T	T	296	58	304	98	7.345	6.70E-03	rs3924889	16	78426000	q23.1
SNP_A-2219275	C	C	295	127	325	91	7.354	6.70E-03	rs6882257	5	170862039	q35.1
SNP_A-2224407	G	G	315	23	301	45	7.343	6.70E-03	rs7095488	10	91164155	q23.31
SNP_A-2128149	C	C	289	75	285	117	7.348	6.70E-03	rs11635094	15	58367563	q22.2
SNP_A-2118084	G	G	393	19	331	35	7.356	6.70E-03	rs3756815	6	24774173	p22.2
SNP_A-2121781	T	T	415	1	367	9	7.345	6.70E-03	rs6559653	9	69460624	q21.11
SNP_A-2144548	C	C	249	105	250	160	7.352	6.70E-03	rs10893268	11	123943822	q24.2
SNP_A-2146211	C	C	293	67	364	48	7.343	6.70E-03	rs2279797	5	31463785	p13.3
SNP_A-2148940	G	G	304	32	367	17	7.34	6.70E-03	rs11115332	12	75673660	q21.2
SNP_A-2167555	G	G	217	145	208	206	7.34	6.70E-03	rs11196205	10	114797037	q25.2
SNP_A-2158967	C	C	331	81	346	50	7.354	6.70E-03	rs17354870	11	9860504	p15.4
SNP_A-1747901	C	C	311	17	376	6	7.346	6.70E-03	rs10519537	5	117672585	q23.1
SNP_A-1657215	T	T	366	20	344	40	7.343	6.70E-03	rs2387105	20	60830023	q13.33
SNP_A-1804713	A	A	414	0	391	7	7.345	6.70E-03	rs9288703	2	158592876	q24.1
SNP_A-1827043	C	C	414	0	391	7	7.345	6.70E-03	rs1150571	6	11746423	p24.1
SNP_A-1861430	T	T	255	89	253	137	7.349	6.70E-03	rs163446	5	111901752	q22.2
SNP_A-1848556	A	A	239	67	239	109	7.356	6.70E-03	rs8006966	14	94914608	q32.13
SNP_A-1856089	T	T	286	84	353	63	7.358	6.70E-03	rs17331155	7	48633235	p12.3
SNP_A-1980609	A	A	293	73	288	114	7.361	6.70E-03	rs40687	5	9248233	p15.31
SNP_A-1980390	C	C	297	11	405	3	7.364	6.70E-03	rs7704914	5	4818956	p15.32
SNP_A-1959485	G	G	186	176	241	153	7.351	6.70E-03	rs1875199	5	85202493	q14.3
SNP_A-1932477	T	T	339	21	386	8	7.356	6.70E-03	rs9548544	13	38404002	q13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884483	A	A	222	140	288	120	7.358	6.70E-03	rs1940422	18	2086401	p11.32
SNP_A-1897516	G	G	322	14	386	4	7.365	6.70E-03	rs1993045	5	4598556	p15.32
SNP_A-2253964	-	G	195	195	188	124	7.355	6.70E-03	rs2312356	7	152520474	q36.2
SNP_A-2256982	A	A	216	132	287	115	7.342	6.70E-03	rs6700189	1	222566542	q42.12
SNP_A-2258860	T	T	323	65	347	39	7.355	6.70E-03	rs13161944	5	4724998	p15.32
SNP_A-2275206	A	A	194	180	239	149	7.343	6.70E-03	rs1884751	20	5345328	p12.3
SNP_A-2311487	A	A	409	3	363	13	7.362	6.70E-03	rs4595504	11	93010973	q21
SNP_A-2308868	G	G	372	14	385	3	7.336	6.80E-03	rs11229654	11	54961378	q11
SNP_A-2277404	C	C	293	69	289	109	7.327	6.80E-03	rs1862871	7	132672420	q33
SNP_A-2258748	A	A	265	141	232	182	7.318	6.80E-03	rs6934064	6	38934177	p21.2
SNP_A-2272075	C	C	207	133	206	198	7.316	6.80E-03	rs4955459	3	136150847	q22.1
SNP_A-2266318	C	C	414	4	375	15	7.335	6.80E-03	---	14	73465699	q24.3
SNP_A-1898097	T	T	326	18	332	40	7.316	6.80E-03	rs6801420	3	141846878	q23
SNP_A-1931131	C	C	233	137	280	108	7.315	6.80E-03	rs1520855	2	190107426	q32.2
SNP_A-1923382	C	C	307	49	322	26	7.321	6.80E-03	rs17272821	9	34858668	p13.3
SNP_A-1921368	T	T	263	79	309	55	7.319	6.80E-03	rs2523998	6	30012844	p21.33
SNP_A-1911361	G	G	310	40	291	67	7.324	6.80E-03	---	17	3082150	p13.3
SNP_A-1912843	C	C	392	30	365	53	7.318	6.80E-03	rs9959862	18	48479568	q21.1
SNP_A-1917536	C	C	384	0	363	7	7.333	6.80E-03	rs17109370	12	69847151	q15
SNP_A-1956869	G	G	286	42	334	24	7.327	6.80E-03	rs10113408	8	10316893	p23.1
SNP_A-1987613	G	G	272	148	229	183	7.315	6.80E-03	rs2780630	1	226236337	q42.13
SNP_A-1975142	T	T	241	123	229	175	7.317	6.80E-03	rs1478148	3	163719830	q26.1
SNP_A-1853395	T	T	316	10	400	2	7.334	6.80E-03	rs2664128	15	37781025	q14
SNP_A-1872132	C	C	290	84	260	118	7.338	6.80E-03	rs4969044	17	68491961	q25.1
SNP_A-1816239	A	A	318	12	391	3	7.316	6.80E-03	---	19	56248381	q13.41
SNP_A-1796964	G	G	229	165	254	122	7.32	6.80E-03	rs10100995	8	138671801	q24.23
SNP_A-2118126	T	T	341	25	344	50	7.325	6.80E-03	rs1354240	3	2437644	p26.3
SNP_A-2116820	G	G	299	57	355	37	7.335	6.80E-03	rs10948418	6	48625473	p12.3
SNP_A-2137865	T	T	303	21	373	9	7.333	6.80E-03	rs2552534	2	218530601	q35

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2132215	T	T	322	74	236	88	7.338	6.80E-03	rs1937863	10	5041532	p15.1
SNP_A-2214282	C	C	319	19	373	7	7.321	6.80E-03	rs1477408	16	67491131	q22.1
SNP_A-2201148	C	G	180	154	203	157	7.331	6.80E-03	rs2709832	4	152736999	q31.3
SNP_A-2189451	T	T	256	104	326	84	7.331	6.80E-03	rs4909995	11	11378255	p15.3
SNP_A-2077368	A	A	268	60	336	42	7.328	6.80E-03	rs6005255	22	25701464	q12.1
SNP_A-2078092	G	G	334	6	412	0	7.329	6.80E-03	rs10183709	2	31414452	p23.1
SNP_A-2071216	A	A	369	21	385	7	7.334	6.80E-03	rs2718418	3	115761666	q13.31
SNP_A-2074202	A	A	354	24	320	44	7.336	6.80E-03	rs609801	1	112037555	p13.2
SNP_A-2068637	G	G	306	72	288	108	7.331	6.80E-03	rs3133614	8	95690996	q22.1
SNP_A-2068768	C	C	254	78	303	55	7.319	6.80E-03	rs699499	7	41935212	p14.1
SNP_A-2052885	C	T	233	183	221	193	7.325	6.80E-03	rs10145984	14	46643032	q21.3
SNP_A-2033978	T	T	315	51	383	33	7.315	6.80E-03	rs1882146	12	89865891	q21.33
SNP_A-2037139	G	G	264	132	300	98	7.319	6.80E-03	rs3757573	7	44920804	p13
SNP_A-2000977	A	A	304	24	369	11	7.327	6.80E-03	rs281854	10	13004951	p13
SNP_A-1997359	G	G	324	96	285	129	7.295	6.90E-03	rs10491654	9	99219082	q22.33
SNP_A-2017432	C	C	293	69	301	113	7.293	6.90E-03	rs2831665	21	28518453	q21.3
SNP_A-2008325	T	C	205	171	226	184	7.296	6.90E-03	rs132034	22	43751992	q13.31
SNP_A-2049032	A	A	327	7	347	23	7.305	6.90E-03	rs7091038	10	19980850	p12.31
SNP_A-2067667	G	G	289	65	295	107	7.299	6.90E-03	rs1842627	8	84464701	q21.13
SNP_A-2076126	T	T	266	40	339	25	7.304	6.90E-03	rs12426838	12	59878490	q14.1
SNP_A-2093770	A	A	320	20	384	8	7.304	6.90E-03	rs1517860	2	104783007	q12.1
SNP_A-2190766	C	C	332	22	297	41	7.312	6.90E-03	rs17052966	8	24913085	p21.2
SNP_A-2188201	T	C	207	183	199	151	7.289	6.90E-03	rs9639160	7	13352629	p21.2
SNP_A-2207279	A	A	240	170	276	132	7.288	6.90E-03	rs4880987	10	2276134	p15.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2131218	T	C	194	142	196	178	7.303	6.90E-03	rs2241857	11	12772407	p15.2
SNP_A-2136960	G	G	344	18	361	41	7.302	6.90E-03	rs4599467	4	66271516	q13.1
SNP_A-2129725	A	A	197	125	261	107	7.306	6.90E-03	rs538768	6	102144575	q16.3
SNP_A-2130966	G	G	342	8	350	24	7.305	6.90E-03	rs17377726	3	78978925	p12.3
SNP_A-2126727	T	T	302	60	288	94	7.306	6.90E-03	rs1339397	1	211842820	q41
SNP_A-2117363	G	G	389	31	360	54	7.304	6.90E-03	rs6688257	1	151596652	q22
SNP_A-2158628	G	G	399	1	355	9	7.287	6.90E-03	rs16837911	1	158707633	q23.3
SNP_A-2149541	G	G	318	48	382	30	7.311	6.90E-03	rs7977147	12	89920065	q21.33
SNP_A-2141306	G	G	310	36	319	67	7.295	6.90E-03	rs17050727	4	121784432	q27
SNP_A-1796582	A	A	211	113	270	92	7.306	6.90E-03	rs12488167	3	33879937	p23
SNP_A-1786795	A	A	231	135	215	187	7.3	6.90E-03	rs13144206	4	91298968	q22.1
SNP_A-1805153	G	G	275	33	293	65	7.307	6.90E-03	rs1846198	4	126239744	q28.1
SNP_A-1814415	G	G	412	0	391	7	7.309	6.90E-03	rs17042366	3	5380140	p26.1
SNP_A-1814434	C	C	346	20	362	44	7.309	6.90E-03	rs7164330	15	35262404	q14
SNP_A-1812193	G	G	332	44	312	72	7.296	6.90E-03	rs6883058	5	5422685	p15.32
SNP_A-1780760	G	G	368	0	400	8	7.291	6.90E-03	rs17132044	7	47849468	p12.3
SNP_A-1839337	T	T	255	105	311	81	7.289	6.90E-03	rs10275475	7	29840866	p15.1
SNP_A-1834969	A	A	348	0	378	8	7.292	6.90E-03	rs157764	15	74573843	q24.3
SNP_A-1866920	G	G	384	18	389	5	7.301	6.90E-03	rs3809966	18	42931625	q21.1
SNP_A-1867651	T	T	249	119	316	98	7.297	6.90E-03	rs10277960	7	135685905	q33
SNP_A-1846850	C	C	356	58	328	88	7.306	6.90E-03	rs376230	5	132985549	q31.1
SNP_A-1973649	A	A	314	50	267	73	7.293	6.90E-03	---	3	101227074	q12.1
SNP_A-1965418	C	T	185	159	216	168	7.307	6.90E-03	rs727326	2	153290088	q23.3
SNP_A-1966763	C	C	393	3	351	13	7.287	6.90E-03	rs1521543	2	212736274	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977139	C	C	300	14	358	4	7.297	6.90E-03	---	4	55282208	q12
SNP_A-1959900	C	C	302	60	369	41	7.308	6.90E-03	rs202073	6	13376584	p24.1
SNP_A-1936958	A	A	266	98	333	77	7.306	6.90E-03	rs4559444	1	75085700	p31.1
SNP_A-1884098	C	C	228	120	214	170	7.311	6.90E-03	rs11919516	3	105459727	q13.11
SNP_A-1882063	A	A	359	41	321	65	7.31	6.90E-03	rs10237942	7	76884107	q11.23
SNP_A-2263064	G	G	300	86	264	118	7.297	6.90E-03	rs7023951	9	113860546	q32
SNP_A-2285001	T	T	378	12	350	28	7.291	6.90E-03	rs11163763	1	83727955	p31.1
SNP_A-2232807	G	G	274	64	339	45	7.303	6.90E-03	rs17597281	14	34852051	q13.2
SNP_A-2232894	T	T	404	0	385	7	7.278	7.00E-03	rs16931079	12	4031846	p13.32
SNP_A-2241652	C	C	269	97	336	76	7.275	7.00E-03	rs16937958	11	8361111	p15.4
SNP_A-2309124	G	G	298	42	313	77	7.272	7.00E-03	rs9583484	13	109764350	q34
SNP_A-2312533	T	T	364	36	346	62	7.276	7.00E-03	rs868256	4	4970228	p16.2
SNP_A-2312821	A	A	293	29	296	56	7.271	7.00E-03	rs6539124	12	103035249	q23.3
SNP_A-2294546	T	T	353	27	373	11	7.267	7.00E-03	---	16	87498110	q24.3
SNP_A-1912988	C	C	339	51	349	27	7.277	7.00E-03	rs1123630	17	44026815	q21.32
SNP_A-1908384	T	T	361	1	360	10	7.278	7.00E-03	rs2318152	3	98046579	q11.2
SNP_A-1932748	C	C	329	41	392	24	7.284	7.00E-03	rs7724788	5	110124838	q22.1
SNP_A-1941225	A	A	322	48	386	30	7.272	7.00E-03	rs515540	18	63640601	q22.1
SNP_A-1941956	C	C	402	2	392	12	7.269	7.00E-03	rs12325687	17	767075	p13.3
SNP_A-1955990	G	G	390	32	404	14	7.271	7.00E-03	rs11223991	11	134123615	q25
SNP_A-1986947	A	G	206	152	209	191	7.262	7.00E-03	rs6911299	6	96804847	q16.1
SNP_A-1986577	T	T	338	20	336	42	7.274	7.00E-03	rs16890994	6	80520025	q14.1
SNP_A-1848797	G	G	416	0	397	7	7.27	7.00E-03	rs11031699	11	32280693	p13
SNP_A-1863630	A	A	272	72	273	115	7.271	7.00E-03	rs17547773	2	216717478	q35
SNP_A-1865114	A	A	283	111	241	143	7.271	7.00E-03	rs10432042	17	62739160	q24.2
SNP_A-1834725	C	C	248	152	262	106	7.265	7.00E-03	rs12509527	4	23693598	p15.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1837630	A	A	284	50	307	91	7.277	7.00E-03	rs10456918	6	119275179	q22.31
SNP_A-1782736	C	C	287	81	352	60	7.281	7.00E-03	rs10944034	6	85408628	q14.3
SNP_A-1717383	T	T	390	4	382	16	7.263	7.00E-03	rs2309801	2	100661356	q11.2
SNP_A-1716005	T	T	287	63	333	41	7.279	7.00E-03	rs3906470	5	94547506	q15
SNP_A-1810994	C	C	314	8	401	1	7.28	7.00E-03	---	16	63805428	q21
SNP_A-1804046	C	C	341	25	368	10	7.265	7.00E-03	rs3859102	16	54425603	q12.2
SNP_A-2147379	G	G	391	7	410	0	7.274	7.00E-03	rs2806882	1	117144650	p13.1
SNP_A-2145556	C	C	355	63	323	93	7.275	7.00E-03	rs12028758	1	194254615	q31.3
SNP_A-2154005	A	A	250	82	236	122	7.277	7.00E-03	rs11654836	17	67306507	q24.3
SNP_A-2167512	A	A	186	170	255	157	7.268	7.00E-03	rs10194801	2	181758125	q31.3
SNP_A-2110611	T	T	381	13	347	29	7.266	7.00E-03	rs4657438	1	162131197	q23.3
SNP_A-2113005	A	A	345	9	387	1	7.267	7.00E-03	rs9477288	6	10035576	p24.3
SNP_A-2134980	C	C	352	62	317	91	7.284	7.00E-03	rs1996663	3	49853268	p21.31
SNP_A-2132129	C	C	359	1	397	11	7.272	7.00E-03	rs4374183	16	7787572	p13.2
SNP_A-2225308	T	T	391	7	410	0	7.274	7.00E-03	rs16891392	6	160711082	q25.3
SNP_A-2196255	T	T	299	69	365	49	7.269	7.00E-03	rs6956094	7	85414972	q21.11
SNP_A-2196064	G	G	331	21	325	43	7.265	7.00E-03	rs2896304	7	120708523	q31.32
SNP_A-2180830	G	A	223	153	186	182	7.278	7.00E-03	rs6067878	20	49705569	q13.2
SNP_A-2103511	A	A	223	121	290	102	7.27	7.00E-03	rs1920344	3	105412693	q13.11
SNP_A-2050078	T	T	348	20	337	41	7.273	7.00E-03	rs17127205	11	122642735	q24.1
SNP_A-2008038	T	T	393	7	412	0	7.273	7.00E-03	rs2256888	21	31556740	q22.11
SNP_A-2027372	A	A	341	1	377	11	7.269	7.00E-03	rs11898127	2	12176340	p24.3
SNP_A-2035958	C	C	242	156	185	177	7.244	7.10E-03	rs11125759	2	58825050	p16.1
SNP_A-2003428	G	G	334	8	327	23	7.241	7.10E-03	rs522371	13	79916470	q31.1
SNP_A-1991522	C	C	350	68	371	41	7.257	7.10E-03	rs2204607	7	141162878	q34
SNP_A-2100582	T	T	329	79	289	109	7.253	7.10E-03	rs1840358	8	14969668	p22
SNP_A-2092788	G	G	367	17	395	5	7.251	7.10E-03	rs17085573	9	82392864	q21.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098072	A	A	410	0	393	7	7.238	7.10E-03	rs7162128	15	53024871	q21.3
SNP_A-2175065	C	C	336	6	410	0	7.251	7.10E-03	rs9824223	3	58958779	p14.2
SNP_A-2198798	C	C	410	0	393	7	7.238	7.10E-03	rs6954520	7	138952955	q34
SNP_A-2215987	C	C	340	6	414	0	7.236	7.10E-03	rs7245775	19	7442221	p13.2
SNP_A-2203325	T	T	348	70	315	101	7.258	7.10E-03	rs11079533	17	59665907	q23.3
SNP_A-2126932	C	C	371	7	338	20	7.257	7.10E-03	rs907921	4	12675436	p15.33
SNP_A-2124354	T	T	326	6	398	0	7.252	7.10E-03	rs17081173	3	56511293	p14.3
SNP_A-2130139	A	A	227	137	212	190	7.235	7.10E-03	rs1193789	11	62798892	q12.3
SNP_A-2117257	G	G	391	7	408	0	7.239	7.10E-03	---	16	56558569	q13
SNP_A-2116955	A	A	298	68	350	46	7.249	7.10E-03	rs7100769	10	82334518	q22.3
SNP_A-2116168	C	C	315	63	349	39	7.259	7.10E-03	rs499126	11	94845770	q21
SNP_A-2165079	G	T	188	178	239	171	7.257	7.10E-03	rs4508560	2	181692691	q31.3
SNP_A-2162593	A	A	253	95	275	63	7.253	7.10E-03	rs10900408	1	145895756	q21.1
SNP_A-1806411	A	A	345	21	366	46	7.254	7.10E-03	rs2274913	1	70401236	p31.1
SNP_A-1795944	G	G	326	38	343	71	7.239	7.10E-03	rs7645334	3	176723013	q26.31
SNP_A-1795637	A	A	338	6	412	0	7.244	7.10E-03	rs4411873	3	7932815	p26.1
SNP_A-1783120	A	A	271	133	240	174	7.235	7.10E-03	rs1923294	11	35396392	p13
SNP_A-1866955	C	C	402	16	410	4	7.26	7.10E-03	rs12309292	12	7473380	p13.31
SNP_A-1854627	G	G	334	6	408	0	7.258	7.10E-03	rs7718721	5	160477293	q34
SNP_A-1978347	T	T	336	6	410	0	7.251	7.10E-03	rs17035075	4	106137398	q24
SNP_A-1973826	T	T	397	7	414	0	7.235	7.10E-03	rs17815011	3	109159106	q13.12
SNP_A-1974086	A	T	208	146	210	202	7.243	7.10E-03	rs9289082	3	118788316	q13.31
SNP_A-1971741	T	T	267	93	262	140	7.235	7.10E-03	rs1330372	1	166758901	q24.2
SNP_A-1969382	G	G	246	162	276	122	7.235	7.10E-03	rs2827010	21	22051380	q21.1
SNP_A-1957230	G	G	251	119	315	97	7.243	7.10E-03	rs10261789	7	135699370	q33
SNP_A-1959962	T	T	341	19	363	43	7.242	7.10E-03	rs16825480	2	146363281	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946287	G	G	222	146	209	203	7.243	7.10E-03	rs4740099	8	81168435	q21.13
SNP_A-1944292	T	T	395	7	412	0	7.236	7.10E-03	rs1338652	1	73584657	p31.1
SNP_A-1938808	A	A	301	113	261	147	7.25	7.10E-03	rs16852276	4	40343969	p14
SNP_A-1874659	C	C	322	34	361	17	7.241	7.10E-03	rs2248660	6	102254293	q16.3
SNP_A-1874412	A	A	254	96	256	148	7.26	7.10E-03	rs10922690	1	89844090	p22.2
SNP_A-1897840	G	G	406	6	385	19	7.24	7.10E-03	rs6438825	3	125249405	q21.1
SNP_A-1891066	G	C	193	151	209	179	7.253	7.10E-03	rs32222	5	127700211	q23.2
SNP_A-2304043	C	C	368	20	328	38	7.249	7.10E-03	rs11110972	12	100602899	q23.2
SNP_A-2248698	G	G	334	6	408	0	7.258	7.10E-03	rs1474257	15	77250927	q25.1
SNP_A-2251167	A	A	363	31	357	57	7.241	7.10E-03	rs7028949	9	33126516	p21.1
SNP_A-2230860	G	G	340	6	414	0	7.236	7.10E-03	rs7324027	13	68981421	q21.33
SNP_A-2240403	G	G	235	73	242	120	7.243	7.10E-03	rs11237414	11	77533005	q14.1
SNP_A-2282445	T	T	338	6	412	0	7.244	7.10E-03	rs7317615	13	75384073	q22.2
SNP_A-2256426	G	G	336	6	410	0	7.251	7.10E-03	rs11830656	12	30293396	p11.22
SNP_A-2259267	G	G	315	3	356	16	7.218	7.20E-03	rs9868569	3	32574943	p23
SNP_A-2275165	A	A	280	110	237	141	7.219	7.20E-03	rs1888286	9	116805605	q33.1
SNP_A-2239463	C	C	323	11	344	30	7.229	7.20E-03	rs1598326	18	6181618	p11.31
SNP_A-2240839	T	T	348	2	340	12	7.23	7.20E-03	rs4619256	13	101038509	q33.1
SNP_A-2252038	C	C	326	38	323	17	7.222	7.20E-03	rs10151870	14	73279644	q24.3
SNP_A-2307835	C	C	408	14	417	3	7.211	7.20E-03	rs11213020	11	108639700	q22.3
SNP_A-1892182	T	T	247	111	315	91	7.221	7.20E-03	rs4285547	16	76593310	q23.1
SNP_A-1898334	A	C	239	183	219	197	7.227	7.20E-03	rs8086342	18	29857021	q12.1
SNP_A-1884090	C	C	320	10	400	2	7.21	7.20E-03	rs10894389	11	130793417	q25
SNP_A-1885188	C	C	328	90	284	120	7.213	7.20E-03	rs4902961	14	71507030	q24.2
SNP_A-1906383	A	A	326	12	397	3	7.215	7.20E-03	rs17016021	4	143651991	q31.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1915508	C	T	187	183	241	167	7.225	7.20E-03	rs1782675	13	98124056	q32.2
SNP_A-1938607	G	G	338	8	348	24	7.214	7.20E-03	rs2441849	8	105376205	q22.3
SNP_A-1937381	A	A	320	14	319	33	7.215	7.20E-03	rs16963496	15	48323730	q21.2
SNP_A-1967956	C	C	288	110	250	144	7.215	7.20E-03	rs6111174	20	16480541	p12.1
SNP_A-1985826	T	T	236	134	294	110	7.228	7.20E-03	rs394754	6	42767957	p21.1
SNP_A-1985387	T	T	348	18	390	6	7.22	7.20E-03	rs16885768	6	22302411	p22.3
SNP_A-1983355	G	G	334	62	327	33	7.229	7.20E-03	rs7444765	5	125521415	q23.2
SNP_A-1866021	G	G	244	104	304	82	7.224	7.20E-03	rs768071	2	78551949	p12
SNP_A-1861480	A	A	296	84	353	61	7.212	7.20E-03	rs6940441	6	133298372	q23.2
SNP_A-1836215	A	A	244	122	236	176	7.224	7.20E-03	rs13269766	8	13883701	p22
SNP_A-1817731	G	A	202	138	198	194	7.218	7.20E-03	rs7692344	4	78248348	q21.1
SNP_A-1797758	A	A	398	8	353	21	7.223	7.20E-03	rs17111567	1	55248024	p32.3
SNP_A-1799366	G	G	291	117	321	83	7.231	7.20E-03	rs3765339	1	12263561	p36.22
SNP_A-1785443	G	G	326	20	357	7	7.215	7.20E-03	rs10197341	2	12450330	p24.3
SNP_A-1802198	G	A	185	159	219	171	7.22	7.20E-03	rs7355617	2	18191816 1	q31.3
SNP_A-1810502	T	T	277	79	278	124	7.212	7.20E-03	rs1170101	13	41674055	q14.11
SNP_A-2140605	C	C	389	5	338	16	7.221	7.20E-03	rs2101009	5	5203484	p15.32
SNP_A-2201740	G	G	376	0	361	7	7.22	7.20E-03	rs11175632	12	63719350	q14.3
SNP_A-2224498	C	C	321	17	384	6	7.213	7.20E-03	rs2656290	8	4133887	p23.2
SNP_A-2198504	T	T	296	56	308	96	7.222	7.20E-03	rs7534957	1	31370963	p35.2
SNP_A-2101459	T	T	279	29	358	16	7.234	7.20E-03	rs12062605	1	70172856	p31.1
SNP_A-2102254	A	A	360	60	327	89	7.21	7.20E-03	rs816206	12	116469025	q24.22
SNP_A-2063614	C	C	255	115	322	94	7.223	7.20E-03	rs4663195	2	236032584	q37.2
SNP_A-2024511	A	A	310	58	317	97	7.21	7.20E-03	---	2	134160219	q21.2
SNP_A-2022563	G	G	288	8	365	1	7.203	7.30E-03	rs7329916	13	56807657	q21.1
SNP_A-2032914	T	T	342	6	414	0	7.195	7.30E-03	rs16934355	9	116997213	q33.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2037547	C	C	166	154	202	122	7.207	7.30E-03	rs917829	5	144532779	q32
SNP_A-2067088	G	G	275	83	333	61	7.187	7.30E-03	rs989944	8	105898962	q22.3
SNP_A-2057132	A	A	279	49	252	76	7.205	7.30E-03	rs2813631	13	92909686	q31.3
SNP_A-2097610	T	T	399	7	414	0	7.199	7.30E-03	rs9307510	4	124050268	q27
SNP_A-2191728	C	C	335	27	397	13	7.195	7.30E-03	rs9524188	13	93196943	q31.3
SNP_A-2185386	C	C	393	7	408	0	7.202	7.30E-03	rs6101519	20	34690132	q11.23
SNP_A-2176121	G	G	393	7	408	0	7.202	7.30E-03	rs972821	8	130403196	q24.21
SNP_A-2222114	C	T	197	161	221	183	7.189	7.30E-03	rs4542562	14	61704441	q23.2
SNP_A-2218949	A	A	332	6	402	0	7.194	7.30E-03	rs16855881	1	228431424	q42.2
SNP_A-2217787	A	A	270	128	298	92	7.191	7.30E-03	rs11213980	11	111067902	q23.1
SNP_A-2161122	T	T	269	95	253	137	7.206	7.30E-03	rs1537510	9	119756092	q33.2
SNP_A-2155810	G	G	401	7	416	0	7.198	7.30E-03	rs6723799	2	25809875	p23.3
SNP_A-2120738	G	G	340	6	412	0	7.202	7.30E-03	---	1	74040291	p31.1
SNP_A-2123525	G	G	311	47	329	25	7.206	7.30E-03	rs8051913	16	64966474	q22.1
SNP_A-2136443	A	A	374	32	386	14	7.189	7.30E-03	rs17241197	16	81084782	q23.3
SNP_A-1782846	G	G	253	163	206	194	7.194	7.30E-03	rs7641861	3	141183572	q23
SNP_A-1757119	C	C	311	45	278	70	7.194	7.30E-03	rs10493483	1	71066856	p31.1
SNP_A-1816107	G	G	410	0	395	7	7.201	7.30E-03	rs4805378	19	34563653	q12
SNP_A-1819566	T	T	353	15	386	4	7.21	7.30E-03	rs8013004	14	40168033	q21.1
SNP_A-1843397	T	T	198	86	275	73	7.191	7.30E-03	rs7582848	2	39398243	p22.1
SNP_A-1864343	G	A	216	154	211	201	7.206	7.30E-03	rs11744184	5	27485581	p14.1
SNP_A-1852746	T	T	208	156	274	138	7.198	7.30E-03	rs12600739	17	23173454	q11.2
SNP_A-1850763	T	T	350	54	377	31	7.207	7.30E-03	rs3014881	1	150157988	q21.3
SNP_A-1846151	A	A	385	5	359	17	7.201	7.30E-03	rs6675269	1	220907001	q42.12
SNP_A-1938440	G	G	385	23	373	45	7.188	7.30E-03	rs4075496	7	69614100	q11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936209	C	C	216	116	212	172	7.188	7.30E-03	rs6080699	20	17382286	p12.1
SNP_A-2296107	A	A	397	7	412	0	7.2	7.30E-03	rs1481090	15	71607122	q24.1
SNP_A-2252731	A	A	363	1	405	11	7.196	7.30E-03	rs1540051	18	73178923	q23
SNP_A-2237451	G	G	416	0	401	7	7.198	7.30E-03	rs2513483	11	114271418	q23.2
SNP_A-2269912	A	A	394	6	352	18	7.207	7.30E-03	rs16912143	9	95261072	q22.32
SNP_A-2237029	G	G	414	0	401	7	7.164	7.40E-03	rs7833796	8	34813962	p12
SNP_A-2239620	A	A	391	7	404	0	7.168	7.40E-03	rs6083135	20	23401912	p11.21
SNP_A-2230496	C	T	213	155	215	201	7.166	7.40E-03	rs2648417	3	9527226	p25.3
SNP_A-2242554	C	C	300	36	343	19	7.172	7.40E-03	rs2014685	2	135089453	q21.3
SNP_A-2307124	G	G	338	6	408	0	7.174	7.40E-03	rs16846093	3	104470241	q13.11
SNP_A-1940711	T	T	318	16	365	5	7.174	7.40E-03	rs9313643	5	173034837	q35.2
SNP_A-1952405	T	T	319	23	346	50	7.17	7.40E-03	rs10829456	10	130326131	q26.2
SNP_A-1988650	G	A	201	161	224	190	7.166	7.40E-03	rs1497090	1	229966025	q42.2
SNP_A-1964958	G	G	312	48	327	85	7.175	7.40E-03	rs4954138	2	134967469	q21.3
SNP_A-1974455	G	G	227	141	216	198	7.176	7.40E-03	rs7644369	3	136153222	q22.1
SNP_A-1904583	A	A	405	7	418	0	7.162	7.40E-03	rs3777105	5	139230428	q31.2
SNP_A-1932972	A	A	336	6	406	0	7.18	7.40E-03	rs9846836	3	181315379	q26.33
SNP_A-1930682	G	G	330	6	398	0	7.166	7.40E-03	---	2	36511166	p22.2
SNP_A-1919591	T	T	259	95	251	141	7.175	7.40E-03	rs1430195	2	56042291	p16.1
SNP_A-1899755	C	T	213	155	215	201	7.166	7.40E-03	rs4702747	5	10938370	p15.2
SNP_A-1845420	C	C	335	65	300	94	7.174	7.40E-03	rs11021975	11	11640691	p15.3
SNP_A-1844423	G	G	359	7	385	23	7.184	7.40E-03	rs1038212	12	28916485	p11.22
SNP_A-1871221	A	A	354	16	376	38	7.179	7.40E-03	rs6551942	4	66368267	q13.1
SNP_A-1828415	T	T	340	6	410	0	7.167	7.40E-03	rs1902628	8	24847016	p21.2
SNP_A-1787321	G	G	412	0	399	7	7.165	7.40E-03	rs7038345	9	23285433	p21.3
SNP_A-2120433	T	T	419	3	346	12	7.163	7.40E-03	rs2484152	1	178714047	q25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2211763	C	C	312	48	383	31	7.179	7.40E-03	rs2914757	5	6310996	p15.32
SNP_A-2099119	C	C	275	87	330	64	7.162	7.40E-03	rs2553042	2	63143185	p15
SNP_A-2094895	T	T	355	1	358	10	7.179	7.40E-03	rs16893457	5	24542617	p14.2
SNP_A-2078061	C	C	403	5	377	17	7.17	7.40E-03	rs6107775	20	6207532	p12.3
SNP_A-2083051	T	T	367	9	407	1	7.173	7.40E-03	rs17061346	3	59848396	p14.2
SNP_A-2050329	T	T	413	3	373	13	7.173	7.40E-03	rs3787282	20	40137321	q12
SNP_A-2026467	A	A	224	120	223	179	7.178	7.40E-03	rs11259007	10	14401307	p13
SNP_A-1994190	G	G	361	35	389	17	7.153	7.50E-03	rs318284	8	90307295	q21.3
SNP_A-2002299	C	C	350	4	394	18	7.161	7.50E-03	rs643377	11	119412838	q23.3
SNP_A-2049955	T	T	316	14	372	4	7.147	7.50E-03	rs4846359	1	218698093	q41
SNP_A-2052666	T	T	336	6	404	0	7.145	7.50E-03	---	12	39995028	q12
SNP_A-2058692	A	A	284	66	290	108	7.15	7.50E-03	rs9325148	12	49957396	q13.13
SNP_A-2063086	G	G	285	35	350	20	7.159	7.50E-03	rs3875030	18	14333485	p11.21
SNP_A-2081024	G	G	390	2	349	11	7.157	7.50E-03	rs6576307	15	22216693	q11.2
SNP_A-2097417	C	C	256	114	276	78	7.152	7.50E-03	rs11058359	12	124836407	q24.31
SNP_A-2104863	T	T	283	133	241	167	7.143	7.50E-03	rs10271349	7	131399824	q32.3
SNP_A-2118390	C	C	205	199	237	157	7.148	7.50E-03	rs8077267	17	40411244	q21.31
SNP_A-2125911	A	A	369	1	374	10	7.14	7.50E-03	rs9360025	6	65441501	q12
SNP_A-2142586	A	A	336	84	300	116	7.139	7.50E-03	rs7762537	6	25442946	p22.2
SNP_A-1781145	C	C	270	150	232	188	7.149	7.50E-03	rs2741657	8	6799608	p23.1
SNP_A-1707293	C	C	382	4	378	16	7.14	7.50E-03	rs952253	10	120493891	q26.11
SNP_A-1843496	T	T	385	7	354	20	7.141	7.50E-03	rs466289	5	6052720	p15.32
SNP_A-1904169	C	C	293	43	352	26	7.139	7.50E-03	rs4439549	11	117285301	q23.3
SNP_A-1906265	C	C	332	6	400	0	7.159	7.50E-03	rs10242793	7	2827555	p22.2
SNP_A-1965121	T	T	382	22	365	43	7.152	7.50E-03	rs16845476	2	141708142	q22.1
SNP_A-1966708	T	T	360	8	355	23	7.16	7.50E-03	rs16843914	2	210603850	q34
SNP_A-1979110	C	C	288	72	335	49	7.151	7.50E-03	rs7692394	4	139578875	q28.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946134	T	T	357	3	379	15	7.139	7.50E-03	rs16964407	13	103688035	q33.1
SNP_A-1938413	A	A	342	6	412	0	7.16	7.50E-03	rs17012513	4	88424763	q22.1
SNP_A-1939417	C	C	223	177	255	137	7.158	7.50E-03	rs13432983	2	116862597	q14.1
SNP_A-2308543	C	C	319	45	286	70	7.147	7.50E-03	rs2150	11	20026460	p15.1
SNP_A-2301115	G	G	294	62	359	43	7.143	7.50E-03	rs17117547	1	58644210	p32.2
SNP_A-2232943	C	C	260	92	258	140	7.144	7.50E-03	rs268425	8	15041646	p22
SNP_A-2233820	A	A	366	0	406	8	7.146	7.50E-03	rs6713877	2	226912319	q36.3
SNP_A-2256377	G	G	293	63	300	104	7.145	7.50E-03	rs7712018	5	108064607	q21.3
SNP_A-2230679	C	C	394	6	354	18	7.133	0.0076	rs1434958	7	44386151	p13
SNP_A-2238342	G	G	299	123	256	156	7.116	0.0076	rs10258710	7	157288803	q36.3
SNP_A-2242552	C	C	281	75	340	54	7.117	0.0076	rs923128	3	56088596	p14.3
SNP_A-2294136	T	T	360	20	391	7	7.126	0.0076	rs1977586	1	154249768	q23.1
SNP_A-2304000	T	T	334	38	304	62	7.122	0.0076	rs7515535	1	36851489	p34.3
SNP_A-1981732	G	G	360	48	336	76	7.131	0.0076	rs17280328	5	57985672	q11.2
SNP_A-1907017	C	C	344	6	412	0	7.119	0.0076	rs512687	6	20157166	p22.3
SNP_A-1907322	C	C	339	53	362	30	7.128	0.0076	rs1154725	6	9522714	p24.3
SNP_A-1904405	C	C	412	0	401	7	7.129	0.0076	rs875231	2	11597317	p25.1
SNP_A-1933018	G	G	271	53	331	35	7.132	0.0076	rs9847998	3	85479859	p12.1
SNP_A-1896213	T	T	341	19	393	7	7.137	0.0076	rs12465442	2	173210248	q31.1
SNP_A-1880597	A	A	334	54	359	31	7.12	0.0076	rs2341689	1	237720505	q43
SNP_A-1842612	A	A	248	76	223	109	7.117	0.0076	rs17700763	4	138484959	q28.3
SNP_A-1848667	T	T	220	198	257	159	7.126	0.0076	rs198391	1	11810683	p36.22
SNP_A-1855630	G	T	197	139	199	189	7.119	0.0076	rs1333048	9	22115347	p21.3
SNP_A-1858342	T	T	305	45	308	78	7.125	0.0076	rs553104	12	10018611	p13.31
SNP_A-1780689	G	G	261	107	317	83	7.136	0.0076	rs10892258	11	118085075	q23.3
SNP_A-1783049	C	C	281	79	337	57	7.115	0.0076	rs1019142	16	7652980	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1728363	A	T	170	138	206	168	7.133	0.0076	rs6890246	5	111307298	q22.1
SNP_A-1788803	C	C	391	7	360	20	7.126	0.0076	rs16942559	16	85619722	q24.2
SNP_A-1792813	A	A	327	15	322	34	7.128	0.0076	rs11728753	4	159540012	q32.1
SNP_A-1810179	C	A	213	189	216	166	7.123	0.0076	rs505870	6	160741774	q25.3
SNP_A-1814069	C	C	247	105	310	84	7.117	0.0076	rs7186875	16	54441262	q12.2
SNP_A-1805924	A	A	395	7	406	0	7.131	0.0076	---	15	92341814	q26.2
SNP_A-2146249	A	A	390	6	373	19	7.119	0.0076	rs6710989	2	39317108	p22.1
SNP_A-2149243	T	T	394	0	383	7	7.136	0.0076	rs7828228	8	82158147	q21.13
SNP_A-2154828	C	C	227	129	294	110	7.123	0.0076	rs12488889	3	150249855	q24
SNP_A-2157199	G	G	312	104	277	139	7.121	0.0076	rs627238	18	39187966	q12.3
SNP_A-2160830	T	T	324	12	391	3	7.115	0.0076	rs6686569	1	95855454	p21.3
SNP_A-2216653	G	G	213	139	199	193	7.129	0.0076	rs1366302	3	161143977	q25.33
SNP_A-2175568	T	T	335	35	393	19	7.126	0.0076	rs12769140	10	33995436	p11.22
SNP_A-2173314	T	T	186	150	245	131	7.137	0.0076	rs926293	20	41377621	q13.11
SNP_A-2190994	T	T	325	29	374	14	7.124	0.0076	rs7990495	13	98720339	q32.3
SNP_A-2192670	A	A	265	151	226	188	7.131	0.0076	rs6432704	2	162581885	q24.2
SNP_A-2101067	G	G	366	2	395	13	7.129	0.0076	rs17083389	6	121662173	q22.31
SNP_A-2095681	C	A	196	146	205	185	7.118	0.0076	rs4574598	6	92364326	q16.1
SNP_A-2084604	A	A	245	77	224	112	7.127	0.0076	rs6506673	18	9448588	p11.22
SNP_A-2007372	A	A	391	7	402	0	7.133	0.0076	rs6109324	20	12186030	p12.1
SNP_A-2010817	T	T	309	97	279	133	7.122	0.0076	rs4703506	5	35207964	p13.2
SNP_A-2024939	G	G	378	24	346	44	7.117	0.0076	rs8060352	16	7782822	p13.2
SNP_A-2031140	T	T	303	19	298	40	7.132	0.0076	rs1771200	13	28135055	q12.3
SNP_A-2033377	T	T	312	16	312	36	7.107	7.70E-03	rs6911988	6	144422498	q24.2
SNP_A-2037119	T	T	305	19	275	37	7.114	7.70E-03	rs17782984	4	67016727	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2002238	C	C	354	2	383	13	7.1	7.70E-03	rs7926731	11	110599806	q23.1
SNP_A-1990335	T	T	314	14	304	32	7.11	7.70E-03	rs5745702	7	81000153	q21.11
SNP_A-2077846	G	G	342	6	408	0	7.091	7.70E-03	rs16840307	2	204582505	q33.2
SNP_A-2080149	T	T	397	7	406	0	7.096	7.70E-03	rs4778823	15	78649800	q25.1
SNP_A-2087069	G	G	224	122	224	182	7.1	7.70E-03	rs309308	2	7110210	p25.1
SNP_A-2073397	A	A	308	58	309	95	7.091	7.70E-03	rs1493773	12	90632082	q21.33
SNP_A-2056041	T	T	363	21	332	40	7.112	7.70E-03	rs16956548	15	44628880	q21.1
SNP_A-2125602	G	G	228	126	295	107	7.114	7.70E-03	rs6775599	3	80654082	p12.2
SNP_A-2115599	T	T	352	36	367	17	7.104	7.70E-03	rs826771	12	90156932	q21.33
SNP_A-1802775	A	A	183	143	234	120	7.108	7.70E-03	rs10779168	12	84452079	q21.31
SNP_A-1807528	A	A	251	113	245	165	7.09	7.70E-03	rs7934812	11	23373804	p14.3
SNP_A-1822109	T	T	338	6	404	0	7.103	7.70E-03	rs13436647	5	165238817	q34
SNP_A-1815486	G	G	316	36	374	20	7.105	7.70E-03	rs16879134	8	32309298	p12
SNP_A-1925573	A	A	342	6	408	0	7.091	7.70E-03	rs2056515	2	138792905	q22.1
SNP_A-1909811	T	T	322	8	403	1	7.106	7.70E-03	---	8	62567186	q12.3
SNP_A-1915453	A	A	280	66	257	33	7.109	7.70E-03	rs4959464	6	7933188	p24.3
SNP_A-2289346	G	G	384	8	362	22	7.1	7.70E-03	rs17103589	10	86269854	q23.1
SNP_A-2232561	T	T	265	129	230	166	7.11	7.70E-03	rs3825708	14	74270450	q24.3
SNP_A-2275345	A	A	338	22	314	42	7.111	7.70E-03	rs4497826	2	128588658	q14.3
SNP_A-2282232	G	G	335	9	337	25	7.081	7.80E-03	rs16996289	20	15564694	p12.1
SNP_A-2265954	G	G	343	17	406	6	7.09	7.80E-03	rs1638755	7	157052288	q36.3
SNP_A-2232815	C	C	330	68	281	93	7.072	7.80E-03	rs17032283	3	10056545	p25.3
SNP_A-2235241	C	C	229	79	236	128	7.087	7.80E-03	rs12641157	4	149344900	q31.23
SNP_A-2242615	C	C	336	74	363	47	7.068	7.80E-03	rs2521284	11	2298253	p15.5
SNP_A-2296282	A	A	297	27	370	14	7.078	7.80E-03	rs10951459	7	35957902	p14.2
SNP_A-2296499	T	T	276	42	291	77	7.084	7.80E-03	rs7236376	18	64175633	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2297150	G	G	288	20	369	9	7.09	7.80E-03	rs6424094	1	24431852	p36.11
SNP_A-2303619	A	A	218	136	283	117	7.08	7.80E-03	rs208168	15	24972469	q12
SNP_A-1913833	G	G	344	6	410	0	7.085	7.80E-03	rs8064757	17	13154826	p12
SNP_A-1874586	G	G	386	16	388	4	7.08	7.80E-03	rs10247246	7	104095116	q22.2
SNP_A-1885424	G	G	357	9	376	26	7.078	7.80E-03	rs17314575	4	157223219	q32.1
SNP_A-1886731	A	A	281	63	337	43	7.075	7.80E-03	rs1217562	18	53242291	q21.31
SNP_A-1887187	A	A	404	2	365	11	7.068	7.80E-03	rs578374	1	190615489	q31.3
SNP_A-1965008	T	T	275	93	340	72	7.083	7.80E-03	rs9287461	2	137710930	q22.1
SNP_A-1974136	T	T	338	6	402	0	7.068	7.80E-03	rs813883	3	120055773	q13.32
SNP_A-1957459	A	A	316	40	358	22	7.068	7.80E-03	rs16926253	10	70776460	q22.1
SNP_A-1955606	T	T	317	95	283	129	7.087	7.80E-03	rs11733214	4	31309798	p15.1
SNP_A-1855593	T	T	357	11	396	2	7.087	7.80E-03	rs6988739	8	52354055	q11.21
SNP_A-1791752	T	T	336	6	400	0	7.075	7.80E-03	rs10736285	10	121898842	q26.12
SNP_A-1783802	C	C	344	6	410	0	7.085	7.80E-03	rs17756565	20	23085509	p11.21
SNP_A-2120805	C	C	293	45	254	68	7.078	7.80E-03	rs327992	9	105138857	q31.1
SNP_A-2126246	C	C	305	95	274	130	7.084	7.80E-03	rs1154156	14	22075626	q11.2
SNP_A-2158757	A	A	347	19	286	34	7.071	7.80E-03	rs6003566	22	21884360	q11.23
SNP_A-2141217	A	A	343	39	284	58	7.085	7.80E-03	rs17124359	14	87783175	q31.3
SNP_A-2191833	G	G	328	8	409	1	7.076	7.80E-03	rs1334440	10	121818111	q26.12
SNP_A-2175927	C	C	312	8	389	1	7.07	7.80E-03	rs11888985	2	192860754	q32.3
SNP_A-2180815	C	C	334	28	352	56	7.083	7.80E-03	rs1393	8	9549119	p23.1
SNP_A-2210454	T	T	300	64	346	42	7.083	7.80E-03	rs2042494	2	159909731	q24.2
SNP_A-2203776	T	T	314	40	356	22	7.079	7.80E-03	rs6675203	1	217268012	q41
SNP_A-2073527	A	A	231	133	217	185	7.073	7.80E-03	rs14906691	10	98850750	q24.1
SNP_A-2084684	A	A	341	11	378	2	7.074	7.80E-03	rs3730697	22	19728466	q11.21
SNP_A-2094226	G	G	298	50	358	32	7.072	7.80E-03	rs2532844	10	119088888	q26.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1994071	T	T	300	66	308	108	7.075	7.80E-03	rs10093569	8	84317832	q21.13
SNP_A-1996109	G	G	378	36	393	17	7.084	7.80E-03	rs10511640	9	18282383	p22.2
SNP_A-2015647	A	A	338	6	402	0	7.068	7.80E-03	---	21	17852257	q21.1
SNP_A-2033740	T	T	208	150	275	133	7.082	7.80E-03	rs1231331	9	25708004	p21.2
SNP_A-2044813	C	C	290	20	371	9	7.07	7.80E-03	rs10880512	12	42184384	q12
SNP_A-2023884	A	A	291	63	289	101	7.086	7.80E-03	rs11625876	14	34318218	q13.1
SNP_A-2023845	G	G	287	37	343	21	7.09	7.80E-03	rs11255804	10	8747207	p14
SNP_A-2031657	A	A	352	2	350	12	7.06	7.90E-03	rs2784807	10	117300161	q25.3
SNP_A-2028871	A	A	389	5	367	17	7.058	7.90E-03	rs17416565	1	207057810	q32.2
SNP_A-2017979	G	G	310	38	385	23	7.065	7.90E-03	rs2833384	21	31642320	q22.11
SNP_A-2000499	G	G	364	20	393	7	7.047	7.90E-03	rs3886720	1	174543674	q25.2
SNP_A-2073647	G	G	323	9	340	26	7.054	7.90E-03	rs16933858	9	15968313	p22.3
SNP_A-2212121	G	G	385	29	357	51	7.063	7.90E-03	rs1534111	10	106679268	q25.1
SNP_A-2213068	G	G	343	39	323	65	7.054	7.90E-03	rs12514672	5	35224014	p13.2
SNP_A-2193047	C	C	347	1	393	11	7.062	7.90E-03	rs11207744	1	61643482	p31.3
SNP_A-2152228	A	A	387	7	394	0	7.063	7.90E-03	rs12078021	1	148970864	q21.3
SNP_A-2158927	A	A	400	4	371	15	7.053	7.90E-03	rs9967853	2	40018976	p22.1
SNP_A-2159582	A	A	385	13	355	29	7.063	7.90E-03	rs9329186	8	9244609	p23.1
SNP_A-2133088	A	A	350	6	416	0	7.066	7.90E-03	rs11891101	2	140548982	q22.1
SNP_A-1721435	C	C	288	62	303	105	7.056	7.90E-03	rs10505933	12	24129457	p12.1
SNP_A-1662794	A	A	371	9	341	23	7.048	7.90E-03	rs10495668	2	17893394	p24.2
SNP_A-1798480	A	A	308	20	393	9	7.05	7.90E-03	rs2191937	7	19457259	p21.1
SNP_A-1854439	C	C	347	3	371	15	7.058	7.90E-03	rs10440810	6	67065532	q12
SNP_A-1844872	T	T	401	7	408	0	7.061	7.90E-03	rs11562795	8	119316485	q24.12
SNP_A-1816898	T	T	255	129	224	168	7.046	7.90E-03	rs12512211	4	39439114	p14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826699	G	A	194	174	234	178	7.052	7.90E-03	rs1607688	12	102090201	q23.2
SNP_A-1842593	C	C	309	105	334	72	7.047	7.90E-03	rs9969246	7	138800621	q34
SNP_A-1956220	T	T	311	43	328	78	7.051	7.90E-03	rs13282123	8	32496606	p12
SNP_A-1959629	G	G	295	75	361	55	7.049	7.90E-03	rs9387592	6	98242896	q16.1
SNP_A-1962503	G	G	361	7	391	23	7.049	7.90E-03	rs17691570	2	28802268	p23.2
SNP_A-1983786	G	G	346	60	288	82	7.06	7.90E-03	rs3776232	5	142546019	q31.3
SNP_A-1877222	C	C	400	0	393	7	7.062	7.90E-03	rs731780	6	44301684	p21.1
SNP_A-1895127	C	C	239	131	230	186	7.047	7.90E-03	rs1750047	6	15859649	q25.3
SNP_A-2296783	C	C	296	124	257	159	7.06	7.90E-03	rs2965855	16	9205689	p13.2
SNP_A-2296040	C	C	324	50	348	28	7.057	7.90E-03	rs6734859	2	25291559	p23.3
SNP_A-2248818	G	G	312	54	319	91	7.047	7.90E-03	rs10974616	9	4532506	p24.2
SNP_A-2272606	T	T	283	139	315	103	7.049	7.90E-03	rs756928	17	65388939	q24.3
SNP_A-2258593	A	A	337	61	358	36	7.058	7.90E-03	rs3136703	1	117013627	p13.1
SNP_A-2283791	T	T	348	14	406	4	7.06	7.90E-03	rs16907728	9	91593003	q22.31
SNP_A-2275302	G	G	253	115	321	95	7.048	7.90E-03	rs12408544	1	89773035	p22.2
SNP_A-2275237	C	-	230	156	188	188	7.067	7.90E-03	rs12248552	10	8956837	p14
SNP_A-2258793	T	T	318	90	279	121	7.024	8.00E-03	rs17562236	1	75086046	p31.1
SNP_A-2267927	A	A	315	41	322	20	7.028	8.00E-03	rs16850172	1	226194742	q42.13
SNP_A-2248524	A	A	326	28	344	56	7.037	8.00E-03	rs12132466	1	225755752	q42.13
SNP_A-2232965	G	G	377	27	355	49	7.03	8.00E-03	rs17556941	18	30573110	q12.1
SNP_A-2298124	G	G	348	6	412	0	7.038	8.00E-03	rs653893	18	64820408	q22.1
SNP_A-2291077	T	T	311	41	379	25	7.037	8.00E-03	rs13150580	4	171467287	q33
SNP_A-1895369	C	C	411	1	377	9	7.027	8.00E-03	rs6501252	17	74324977	q25.3
SNP_A-1898351	C	G	180	162	212	158	7.026	8.00E-03	rs1214547	10	90614326	q23.31
SNP_A-1882235	C	C	350	6	414	0	7.032	8.00E-03	rs9388801	6	130892392	q23.1
SNP_A-1920804	C	C	346	6	410	0	7.044	8.00E-03	rs12549015	8	56575870	q12.1
SNP_A-1977405	G	G	352	6	416	0	7.027	8.00E-03	rs17085300	4	65470872	q13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944395	A	A	355	1	364	10	7.037	8.00E-03	rs12017991	13	82089301	q31.1
SNP_A-1941441	C	C	257	63	265	105	7.036	8.00E-03	rs6812007	4	9526489	p16.1
SNP_A-1840791	C	C	334	30	387	15	7.028	8.00E-03	rs3765455	20	19976830	p11.23
SNP_A-1834165	C	C	340	6	402	0	7.027	8.00E-03	rs2478822	1	204623446	q32.2
SNP_A-1859118	G	G	209	141	276	124	7.044	8.00E-03	rs17271883	19	5785212	p13.3
SNP_A-1792650	C	C	220	108	258	80	7.043	8.00E-03	rs10813115	9	29514697	p21.1
SNP_A-1790029	G	G	337	3	361	15	7.033	8.00E-03	rs1926930	6	157064230	q25.3
SNP_A-1673376	C	C	322	24	383	11	7.023	8.00E-03	rs10517446	4	59425955	q12
SNP_A-1784678	C	C	405	1	371	9	7.037	8.00E-03	rs6048170	20	22463237	p11.21
SNP_A-2133241	A	A	276	60	252	90	7.038	8.00E-03	rs9816944	3	18965531	p24.3
SNP_A-2123460	C	C	349	33	341	59	7.03	8.00E-03	rs3863194	5	153304038	q33.2
SNP_A-2119677	G	G	365	13	399	3	7.031	8.00E-03	rs16936810	11	19449534	p15.1
SNP_A-2164051	C	C	202	158	262	138	7.024	8.00E-03	rs2421790	1	70903828	p31.1
SNP_A-2180453	T	T	240	72	234	112	7.034	8.00E-03	rs13039782	20	4763305	p13
SNP_A-2168233	A	A	263	55	272	94	7.026	8.00E-03	rs4646457	7	98889731	q22.1
SNP_A-2171530	C	C	346	6	410	0	7.044	8.00E-03	---	2	115421016	q14.1
SNP_A-2218453	A	A	375	7	367	21	7.04	8.00E-03	rs1530962	5	8112876	p15.31
SNP_A-2070577	A	A	337	3	361	15	7.033	8.00E-03	rs17169611	5	135355726	q31.1
SNP_A-2058339	G	G	288	80	288	124	7.031	8.00E-03	rs7653345	3	21773445	p24.3
SNP_A-2061532	T	T	346	6	410	0	7.044	8.00E-03	rs6475502	9	21093359	p21.3
SNP_A-2103847	G	G	348	6	412	0	7.038	8.00E-03	rs10999625	10	72416877	q22.1
SNP_A-2082395	C	C	393	7	398	0	7.027	8.00E-03	rs7667922	4	487170	p16.3
SNP_A-2004124	G	G	339	25	362	52	7.038	8.00E-03	rs6493076	15	41105432	q15.2
SNP_A-2002857	A	T	189	163	225	177	7.016	8.10E-03	rs2673464	10	79086473	q22.3
SNP_A-2083487	G	G	303	29	365	15	7.005	8.10E-03	rs307106	18	35839036	q12.3
SNP_A-2095275	C	C	388	20	380	6	7.018	8.10E-03	rs9464797	6	15664265	p22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2063976	C	C	298	116	265	153	7.004	8.10E-03	rs4074250	10	87257985	q23.2
SNP_A-2069121	T	T	290	14	383	5	7.021	8.10E-03	rs16919532	11	93292359	q21
SNP_A-2213066	C	C	333	49	375	29	7.009	8.10E-03	rs2810569	1	41564590	p34.2
SNP_A-2169460	A	A	251	109	273	75	7.005	8.10E-03	rs27667	3	10352312	p25.3
SNP_A-2171798	G	G	316	22	388	10	7.019	8.10E-03	rs17118168	5	155012023	q33.2
SNP_A-2192243	T	T	346	6	408	0	7.01	8.10E-03	rs7014946	8	93858178	q22.1
SNP_A-2197837	C	C	364	20	348	40	7.006	8.10E-03	rs1499896	3	114405454	q13.2
SNP_A-2145203	A	A	398	8	378	22	7.005	8.10E-03	rs1591649	10	108933823	q25.1
SNP_A-2118992	C	C	350	2	350	12	7.004	8.10E-03	rs7768488	6	83898507	q14.1
SNP_A-2126150	G	G	337	61	314	92	7.015	8.10E-03	rs1928022	13	35684453	q13.3
SNP_A-2127035	A	A	316	8	345	25	7.012	8.10E-03	rs17055812	13	36948021	q13.3
SNP_A-1712895	G	G	259	133	230	174	7.016	8.10E-03	rs4132433	5	27462408	p14.1
SNP_A-1726144	T	T	199	159	265	143	7.002	8.10E-03	rs2709072	7	9351619	p21.3
SNP_A-1792719	C	C	288	68	348	48	7.001	8.10E-03	rs1991472	5	16609741	p15.1
SNP_A-1798081	C	C	349	5	352	18	7.01	8.10E-03	rs6594539	5	111151303	q22.1
SNP_A-1804048	C	T	227	183	224	192	7.011	8.10E-03	rs7386575	8	12731663	p22
SNP_A-1844416	T	T	289	75	348	54	7.015	8.10E-03	rs10758307	9	35491908	p13.3
SNP_A-1933723	C	T	238	174	207	195	7.007	8.10E-03	rs12595699	15	21699506	q11.2
SNP_A-1959248	T	T	270	100	263	147	7.002	8.10E-03	rs4527671	6	85124096	q14.3
SNP_A-1964052	A	A	288	36	327	19	7.013	8.10E-03	rs1365950	2	82572916	p12
SNP_A-1967699	G	G	264	144	299	109	7.018	8.10E-03	rs2179472	20	9741497	p12.2
SNP_A-1920750	G	G	419	1	385	9	7.015	8.10E-03	rs16981165	19	9492208	p13.2
SNP_A-1928669	A	A	290	122	254	158	7.011	8.10E-03	rs6504495	17	62710035	q24.2
SNP_A-1880500	T	T	354	2	354	12	7.006	8.10E-03	rs9957139	18	67530092	q22.3
SNP_A-1903037	G	G	232	172	266	134	7.021	8.10E-03	rs7043095	9	88833559	q22.1
SNP_A-1893346	C	C	339	83	364	54	7.009	8.10E-03	rs12199587	6	15057261	p23
SNP_A-2314289	C	C	341	29	369	13	7.01	8.10E-03	rs6461725	7	23503414	p15.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2232874	T	T	342	6	404	0	7.022	8.10E-03	rs947256	13	107144160	q33.3
SNP_A-2229570	G	G	270	76	347	59	7.008	8.10E-03	rs13047845	21	35156070	q22.12
SNP_A-2236957	C	C	321	19	345	43	7.021	8.10E-03	rs4565127	4	66354867	q13.1
SNP_A-2261827	C	C	344	6	406	0	7.016	8.10E-03	rs2498842	14	91420470	q32.12
SNP_A-2254401	A	A	280	70	275	109	6.982	8.20E-03	rs13285270	9	10160008	p23
SNP_A-1884389	T	C	203	159	212	184	6.993	8.20E-03	rs261771	6	120560384	q22.31
SNP_A-1886485	T	T	369	15	396	4	6.998	8.20E-03	rs2487990	10	105733788	q25.1
SNP_A-1926827	C	C	302	64	294	100	6.988	8.20E-03	rs9385919	6	100455488	q16.3
SNP_A-1932893	T	T	297	63	277	95	6.983	8.20E-03	rs1044762	6	72074574	q13
SNP_A-1931125	T	T	396	6	360	18	6.982	8.20E-03	rs7861791	9	122789125	q33.2
SNP_A-1916648	T	T	183	119	222	92	6.979	8.20E-03	rs11736034	4	180349213	q34.3
SNP_A-1905257	A	A	411	7	414	0	6.992	8.20E-03	rs11025825	11	20919625	p15.1
SNP_A-1963448	G	G	419	3	385	13	6.991	8.20E-03	rs12079216	1	116445740	p13.1
SNP_A-1977107	C	C	343	13	354	32	6.994	8.20E-03	rs10024153	4	54092586	q12
SNP_A-1943147	G	G	350	6	412	0	6.998	8.20E-03	rs16863238	3	152385820	q25.1
SNP_A-1835368	C	C	370	42	394	22	6.985	8.20E-03	rs17842279	10	3852320	p15.1
SNP_A-1823923	C	C	192	162	261	149	6.986	8.20E-03	rs447372	4	108211600	q25
SNP_A-1786788	T	T	381	13	353	29	6.979	8.20E-03	rs732509	1	54780013	p32.3
SNP_A-1781780	C	C	235	127	229	183	6.993	8.20E-03	rs527081	1	226224383	q42.13
SNP_A-1697587	C	C	390	0	387	7	6.991	8.20E-03	rs10487120	7	89765982	q21.13
SNP_A-2131717	G	G	356	34	393	17	6.999	8.20E-03	rs7766305	6	6550862	p25.1
SNP_A-2075703	T	T	354	14	410	4	6.979	8.20E-03	rs7742010	6	159719099	q25.3
SNP_A-2095469	T	T	309	51	317	87	6.983	8.20E-03	rs9453188	6	65884358	q12
SNP_A-2092349	T	T	219	141	269	115	6.997	8.20E-03	rs2870258	20	51490853	q13.2
SNP_A-2026998	G	G	362	18	376	40	6.997	8.20E-03	rs17751311	6	126248879	q22.32
SNP_A-2021987	G	G	237	165	281	133	6.999	8.20E-03	rs9933848	16	22869624	p12.1
SNP_A-2046699	T	T	247	113	208	144	6.993	8.20E-03	rs11700200	20	31124150	q11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2034621	C	C	330	8	407	1	6.982	8.20E-03	rs17035261	3	3684393	p26.2
SNP_A-2036742	A	A	209	123	213	187	6.994	8.20E-03	rs9467722	6	26460545	p22.1
SNP_A-2017104	G	G	286	58	329	37	6.974	8.30E-03	rs219653	21	26748294	q21.3
SNP_A-2093695	G	G	348	6	408	0	6.97	8.30E-03	rs17796594	19	16417740	p13.11
SNP_A-2106805	A	A	360	40	361	19	6.968	8.30E-03	rs9616619	22	48148741	q13.33
SNP_A-2082781	T	T	417	1	385	9	6.974	8.30E-03	rs3847629	11	35600517	p13
SNP_A-2058931	C	C	292	66	273	99	6.973	8.30E-03	rs2804672	10	38696893	p11.21
SNP_A-2139127	C	C	365	21	327	39	6.96	8.30E-03	rs6485967	11	49171864	p11.12
SNP_A-2146155	A	A	364	50	388	28	6.966	8.30E-03	rs3851919	1	16669641	p36.13
SNP_A-2164625	T	T	401	7	402	0	6.957	8.30E-03	rs6725812	2	35409380	p22.3
SNP_A-2175212	G	G	334	12	397	3	6.957	8.30E-03	rs10998172	10	69873240	q21.3
SNP_A-2204240	G	G	340	6	398	0	6.958	8.30E-03	rs7267882	20	853785	p13
SNP_A-2205075	C	C	328	24	355	51	6.976	8.30E-03	---	4	89509206	q22.1
SNP_A-2206100	C	C	349	7	343	21	6.964	8.30E-03	rs10734824	12	10306090	p13.2
SNP_A-1681692	G	G	336	0	382	8	6.969	8.30E-03	rs10491429	5	118211406	q23.1
SNP_A-1656089	T	T	312	86	349	59	6.976	8.30E-03	rs1073277	4	36901230	p14
SNP_A-1810213	G	G	348	6	408	0	6.97	8.30E-03	rs4338048	7	83947528	q21.11
SNP_A-1832581	G	G	340	6	398	0	6.958	8.30E-03	rs6430060	2	145133351	q22.3
SNP_A-1843834	A	A	212	144	279	127	6.958	8.30E-03	rs849826	1	154359419	q23.1
SNP_A-1837900	G	G	233	123	230	180	6.97	8.30E-03	rs4633293	1	186926566	q31.1
SNP_A-1858152	C	C	303	43	316	22	6.965	8.30E-03	rs10881101	12	46080727	q13.11
SNP_A-1951645	C	T	214	150	202	196	6.969	8.30E-03	rs11686880	2	100414747	q11.2
SNP_A-1985252	G	G	346	6	406	0	6.976	8.30E-03	rs2328103	6	17538157	p22.3
SNP_A-1891011	T	T	406	2	371	11	6.959	8.30E-03	rs1431482	10	118225556	q25.3
SNP_A-1898081	T	T	350	6	410	0	6.965	8.30E-03	rs9967255	18	29555593	q12.1
SNP_A-2242371	A	A	289	75	353	55	6.972	8.30E-03	rs4687321	3	193528684	q28

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2241996	G	G	408	0	407	7	6.958	8.30E-03	rs6691781	1	113422658	p13.2
SNP_A-2232641	G	G	207	139	283	127	6.961	8.30E-03	rs2372309	12	56616087	q14.1
SNP_A-2266597	C	C	402	14	381	31	6.966	8.30E-03	rs11016419	10	130345922	q26.2
SNP_A-2311045	C	C	341	27	321	49	6.967	8.30E-03	rs9680618	22	27891532	q12.1
SNP_A-2303283	A	A	236	156	278	124	6.964	8.30E-03	rs12541408	8	95654983	q22.1
SNP_A-2304976	T	T	251	155	216	194	6.962	8.30E-03	rs616352	13	29597738	q12.3
SNP_A-2292362	A	A	339	31	396	16	6.972	8.30E-03	rs2318452	4	67813854	q13.2
SNP_A-2294597	A	A	258	36	317	21	6.972	8.30E-03	rs8010566	14	89689735	q32.11
SNP_A-2274639	T	T	338	8	415	1	6.946	8.40E-03	rs4363588	11	21448759	p15.1
SNP_A-2237009	C	C	254	80	332	64	6.944	8.40E-03	rs3757100	6	8380882	p24.3
SNP_A-2248388	G	A	218	204	240	178	6.94	8.40E-03	rs7144888	14	93957830	q32.13
SNP_A-1905973	G	G	334	24	370	10	6.956	8.40E-03	rs16960453	15	46070428	q21.1
SNP_A-1924133	T	T	334	10	406	2	6.942	8.40E-03	rs275554	7	108271026	q31.1
SNP_A-1986357	G	G	189	171	255	157	6.937	8.40E-03	rs9294851	6	70514350	q13
SNP_A-1960570	C	C	231	131	295	111	6.942	8.40E-03	rs6501388	17	65893150	q24.3
SNP_A-1864340	C	C	232	168	259	127	6.936	8.40E-03	rs1662594	17	42347736	q21.32
SNP_A-1826983	C	C	284	60	357	43	6.944	8.40E-03	rs17738626	15	60613489	q22.2
SNP_A-1818235	A	A	270	28	284	56	6.952	8.40E-03	rs4658433	1	241466535	q44
SNP_A-1822239	A	A	276	128	305	93	6.946	8.40E-03	rs1491539	2	116947837	q14.1
SNP_A-1790570	G	G	344	6	402	0	6.947	8.40E-03	rs1371105	10	80367025	q22.3
SNP_A-1661250	A	A	359	33	339	57	6.953	8.40E-03	rs2900615	9	1140351 02	q33.1
SNP_A-1784118	G	G	353	47	328	74	6.938	8.40E-03	rs638145	10	7441884	p14
SNP_A-2227294	C	C	390	14	389	3	6.94	8.40E-03	rs7019602	9	94730683	q22.32
SNP_A-2182961	G	C	220	174	211	183	6.953	8.40E-03	rs10066764	5	141637503	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2188026	C	C	280	24	315	53	6.949	8.40E-03	rs6733529	2	139776005	q22.1
SNP_A-2187701	C	C	346	12	411	3	6.956	8.40E-03	rs12617742	2	16499143	p24.3
SNP_A-2164683	C	C	381	19	349	37	6.941	8.40E-03	rs11022541	11	12880948	p15.2
SNP_A-2165190	C	C	396	10	375	25	6.956	8.40E-03	rs5762201	22	26213009	q12.1
SNP_A-2141858	T	T	352	18	386	6	6.937	8.40E-03	rs17106611	14	77452901	q24.3
SNP_A-2125793	T	T	220	182	253	143	6.938	8.40E-03	rs6069163	20	53224665	q13.2
SNP_A-2076340	T	T	183	141	254	130	6.947	8.40E-03	rs1014684	18	61907915	q22.1
SNP_A-2087916	T	T	247	115	241	167	6.939	8.40E-03	rs12512494	4	139932854	q31.1
SNP_A-2067889	G	G	368	0	369	7	6.916	8.50E-03	rs9293988	6	75698671	q13
SNP_A-2066123	C	C	287	47	348	30	6.92	8.50E-03	rs6539502	12	79265878	q21.31
SNP_A-2014039	C	C	294	58	360	40	6.931	8.50E-03	rs2031212	9	8526034	p24.1
SNP_A-2006730	T	T	373	17	391	5	6.924	8.50E-03	rs4954423	2	136366893	q21.3
SNP_A-2001116	G	G	353	31	372	14	6.915	8.50E-03	rs2274888	10	44794346	q11.21
SNP_A-2023057	T	T	383	9	413	1	6.935	8.50E-03	rs11147021	12	131913385	q24.33
SNP_A-2026746	C	C	305	65	323	39	6.929	8.50E-03	rs7860074	9	88391228	q22.1
SNP_A-2029399	C	C	366	2	403	13	6.934	8.50E-03	rs9948074	18	68718990	q22.3
SNP_A-2118258	G	G	350	6	408	0	6.931	8.50E-03	rs1171002	13	35488180	q13.3
SNP_A-2115794	C	C	339	5	344	18	6.93	8.50E-03	---	10	64363943	q21.3
SNP_A-2112027	T	T	346	10	387	29	6.928	8.50E-03	rs10883450	10	101913411	q24.31
SNP_A-2144527	G	G	184	168	240	148	6.927	8.50E-03	rs1478155	3	163700474	q26.1
SNP_A-2138910	A	A	370	14	351	31	6.918	8.50E-03	rs188701	19	60868760	q13.42
SNP_A-2138587	G	G	392	8	355	21	6.925	8.50E-03	rs7624767	3	113221540	q13.2
SNP_A-2162330	C	C	212	156	275	137	6.922	8.50E-03	rs11941294	4	65707462	q13.1
SNP_A-2183502	G	G	332	8	407	1	6.932	8.50E-03	rs11562969	2	51772100	p16.3
SNP_A-2179306	T	T	315	93	338	62	6.932	8.50E-03	rs12041465	1	75321070	p31.1
SNP_A-2221781	A	A	358	10	339	25	6.925	8.50E-03	rs17113156	12	72876623	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783358	G	G	380	22	398	8	6.93	8.50E-03	rs17049981	2	120565336	q14.2
SNP_A-1697194	T	T	296	86	278	124	6.935	8.50E-03	rs1585398	21	21821589	q21.1
SNP_A-1811587	C	C	394	18	377	37	6.934	8.50E-03	rs1028312	1	30408392	p35.2
SNP_A-1816985	G	G	397	5	379	17	6.918	8.50E-03	rs17449755	10	94659511	q23.33
SNP_A-1871733	C	C	313	51	318	86	6.917	8.50E-03	rs294942	4	112409428	q25
SNP_A-1858922	T	T	355	13	381	33	6.932	8.50E-03	---	3	123962189	q21.1
SNP_A-1850587	G	G	337	15	407	5	6.917	8.50E-03	rs1248853	3	85106341	p12.1
SNP_A-1948487	G	G	356	14	410	4	6.915	8.50E-03	rs1890581	6	159749851	q25.3
SNP_A-1964720	C	C	322	40	388	24	6.934	8.50E-03	rs4528763	2	123167823	q14.3
SNP_A-1931140	T	T	232	114	303	97	6.92	8.50E-03	rs7783084	7	135789596	q33
SNP_A-1930326	G	G	288	30	333	15	6.924	8.50E-03	---	18	67259406	q22.3
SNP_A-1928763	C	C	368	0	369	7	6.916	8.50E-03	rs7985964	13	90516881	q31.3
SNP_A-1914120	T	T	231	165	272	132	6.929	8.50E-03	rs11873891	18	6495597	p11.31
SNP_A-1889960	C	T	186	176	237	171	6.917	8.50E-03	rs11133133	4	177467002	q34.2
SNP_A-2241494	A	A	289	75	358	56	6.93	8.50E-03	rs6822767	4	530099	p16.3
SNP_A-2279043	T	T	310	32	311	59	6.922	8.50E-03	rs7893991	10	114358151	q25.2
SNP_A-2286987	C	C	316	42	373	25	6.932	8.50E-03	rs4767761	12	117943016	q24.23
SNP_A-2281568	T	T	335	11	323	27	6.933	8.50E-03	rs5996436	22	21641410	q11.22
SNP_A-2292479	C	G	215	151	202	196	6.918	8.50E-03	rs10180423	2	100377530	q11.2
SNP_A-2313558	A	A	406	8	388	22	6.922	8.50E-03	rs529983	8	12942555	p22
SNP_A-2312925	G	G	193	149	229	117	6.898	0.0086	rs10733650	9	120864052	q33.2
SNP_A-2292521	C	C	336	8	411	1	6.914	0.0086	rs17162620	1	196386859	q32.1
SNP_A-2291682	G	G	399	1	371	9	6.91	0.0086	rs8028328	15	99118340	q26.3
SNP_A-2291003	C	C	348	52	327	81	6.898	0.0086	rs16834280	1	31386143	p35.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2241337	G	G	306	28	362	14	6.901	0.0086	rs7192610	16	54322776	q12.2
SNP_A-2237262	A	A	266	42	286	78	6.906	0.0086	rs1597813	9	28070109	p21.2
SNP_A-2249340	G	G	323	57	290	84	6.899	0.0086	rs7754623	6	167185795	q27
SNP_A-1974321	G	G	306	24	317	49	6.912	0.0086	rs10494529	1	177170897	q25.3
SNP_A-1974642	C	C	328	40	340	72	6.898	0.0086	rs16853827	3	144769499	q24
SNP_A-1986426	T	T	348	6	404	0	6.902	0.0086	rs16883059	6	73704516	q13
SNP_A-1982863	G	G	344	6	400	0	6.912	0.0086	rs17161896	5	108886123	q21.3
SNP_A-1950724	C	C	382	14	376	32	6.913	0.0086	---	14	45382428	q21.2
SNP_A-1958123	C	C	348	6	404	0	6.902	0.0086	rs6559361	9	88608220	q22.1
SNP_A-1934639	A	A	284	128	304	90	6.906	0.0086	rs923435	12	127669567	q24.32
SNP_A-1936701	G	G	358	16	307	31	6.896	0.0086	rs6816555	4	34174804	p15.1
SNP_A-1850087	C	C	306	40	381	25	6.906	0.0086	rs12408938	1	47218546	p33
SNP_A-1851708	C	C	231	103	267	75	6.913	0.0086	rs554580	9	1571178	p24.3
SNP_A-1848454	T	T	389	21	393	7	6.898	0.0086	rs246425	5	142966688	q31.3
SNP_A-1855137	C	C	321	57	288	84	6.911	0.0086	rs11627253	14	97002951	q32.2
SNP_A-1861693	C	C	364	58	332	86	6.897	0.0086	rs941039	19	43296954	q13.13
SNP_A-1790587	A	A	405	1	377	9	6.902	0.0086	rs17149964	7	24525388	p15.3
SNP_A-1755690	A	A	371	9	399	1	6.91	0.0086	rs10845098	12	10309191	p13.2
SNP_A-2202565	G	G	332	10	402	2	6.904	0.0086	rs2270092	19	43525474	q13.2
SNP_A-2175615	G	G	420	0	362	6	6.9	0.0086	rs4567318	1	119742581	p12
SNP_A-2172982	C	C	342	58	291	81	6.908	0.0086	rs11066735	12	112680876	q24.13
SNP_A-2145178	A	A	299	19	370	8	6.895	0.0086	rs6809861	3	191995960	q28
SNP_A-2026308	C	C	274	84	276	130	6.907	0.0086	rs9494089	6	135207211	q23.3
SNP_A-2037292	A	A	363	5	393	19	6.897	0.0086	rs17139565	5	115727376	q23.1
SNP_A-2002681	C	C	323	5	349	19	6.897	0.0086	rs1922757	12	41262659	q12
SNP_A-1995565	C	C	196	148	268	136	6.911	0.0086	rs10491696	9	2167423	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2055916	G	G	327	5	353	19	6.91	0.0086	rs11231948	11	79508769	q14.1
SNP_A-2079580	C	C	203	155	264	136	6.902	0.0086	rs10113727	18	70260408	q22.3
SNP_A-2094968	A	A	314	6	341	21	6.886	8.70E-03	rs10789869	11	111731373	q23.1
SNP_A-2068811	A	A	261	43	359	31	6.885	8.70E-03	rs16702247	15	97472219	q26.3
SNP_A-1994114	T	T	358	0	361	7	6.876	8.70E-03	rs16880855	8	87157084	q21.3
SNP_A-2000863	T	T	406	12	386	28	6.886	8.70E-03	rs3120118	1	240806430	q44
SNP_A-2043822	A	A	342	6	396	0	6.883	8.70E-03	rs2286880	4	15416835	p15.32
SNP_A-2043089	A	A	251	115	311	93	6.874	8.70E-03	rs208581	16	22890111	p12.1
SNP_A-2026514	C	C	335	29	353	57	6.878	8.70E-03	rs1828775	15	26812158	q13.1
SNP_A-2138347	C	C	379	25	398	10	6.874	8.70E-03	rs16825388	1	38831651	p34.3
SNP_A-2145834	C	C	296	30	358	16	6.879	8.70E-03	rs349203	4	60675160	q13.1
SNP_A-2113419	T	T	272	88	269	133	6.885	8.70E-03	rs5745347	1	75986541	p31.1
SNP_A-2113696	G	G	326	42	359	23	6.885	8.70E-03	rs466158	5	9583149	p15.31
SNP_A-2126513	G	G	251	115	317	95	6.878	8.70E-03	rs12452461	17	72336304	q25.2
SNP_A-2123669	G	G	352	10	380	28	6.874	8.70E-03	rs6434688	2	195134477	q32.3
SNP_A-2124122	G	G	300	64	306	104	6.874	8.70E-03	rs6963665	7	109617884	q31.1
SNP_A-2130159	C	C	324	96	354	66	6.883	8.70E-03	rs1696448	12	129006235	q24.33
SNP_A-2130866	G	G	413	1	385	9	6.892	8.70E-03	rs6592209	11	84240718	q14.1
SNP_A-2131921	T	T	344	6	398	0	6.878	8.70E-03	rs16948558	15	84477513	q25.3
SNP_A-2173019	T	T	369	29	322	48	6.873	8.70E-03	rs10215103	7	127394001	q32.1
SNP_A-2220646	C	C	311	17	291	35	6.889	8.70E-03	rs16945702	16	76038454	q23.1
SNP_A-1678492	C	C	207	183	254	154	6.885	8.70E-03	rs1584851	11	21265652	p15.1
SNP_A-1802380	C	C	352	28	349	11	6.888	8.70E-03	rs10972096	9	34399380	p13.3
SNP_A-1863595	C	C	235	107	300	88	6.877	8.70E-03	rs7903448	10	9848668	p14
SNP_A-1856195	A	A	326	8	397	1	6.874	8.70E-03	rs9574079	13	34991134	q13.3
SNP_A-1842482	G	G	392	10	356	24	6.884	8.70E-03	rs750400	10	4241459	p15.1
SNP_A-1832219	C	C	249	55	258	94	6.893	8.70E-03	rs6745099	2	100197959	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1989231	T	T	353	3	327	13	6.88	8.70E-03	rs17150318	7	24669361	p15.3
SNP_A-1977966	G	G	354	6	410	0	6.887	8.70E-03	rs1410511	1	190183844	q31.2
SNP_A-1885321	C	C	358	0	361	7	6.876	8.70E-03	rs2367421	3	62908835	p14.2
SNP_A-1917551	A	A	344	6	398	0	6.878	8.70E-03	rs4667151	2	187878799	q32.1
SNP_A-2245666	C	C	223	125	206	172	6.883	8.70E-03	rs7023064	9	134276505	q34.2
SNP_A-2238955	C	C	347	11	322	26	6.875	8.70E-03	rs4279515	7	84884856	q21.11
SNP_A-2270435	G	G	255	157	292	122	6.889	8.70E-03	rs1020466	9	22710921	p21.3
SNP_A-2263925	G	G	321	21	383	9	6.886	8.70E-03	rs1976996	3	129776713	q21.3
SNP_A-2297667	C	C	391	31	361	53	6.883	8.70E-03	rs10519162	15	75259926	q24.3
SNP_A-2302321	T	T	274	126	313	95	6.861	8.80E-03	rs7760870	6	17630965	p22.3
SNP_A-2263725	C	C	272	96	335	75	6.87	8.80E-03	rs1345617	5	156284081	q33.3
SNP_A-2267228	C	C	331	29	349	57	6.855	8.80E-03	rs12873209	13	70483880	q21.33
SNP_A-2286882	A	A	202	154	259	133	6.868	8.80E-03	rs7611969	3	188583359	q27.3
SNP_A-1937396	C	C	326	32	383	17	6.868	8.80E-03	rs7973611	12	89946865	q21.33
SNP_A-1941643	T	T	308	48	373	31	6.858	8.80E-03	rs10928445	2	133782826	q21.2
SNP_A-1826910	G	G	240	124	222	170	6.871	8.80E-03	rs10946813	6	26453120	p22.1
SNP_A-1825586	T	T	332	20	386	8	6.861	8.80E-03	rs7096807	10	17752749	p12.33
SNP_A-1866520	T	T	350	6	404	0	6.863	8.80E-03	rs16948284	15	91955565	q26.1
SNP_A-1807301	T	T	334	36	390	20	6.87	8.80E-03	rs4416501	4	78547458	q21.1
SNP_A-1812435	C	T	240	182	218	200	6.857	8.80E-03	rs7116296	11	14070335	p15.2
SNP_A-1790647	A	A	244	104	320	88	6.856	8.80E-03	rs6764070	3	164849354	q26.1
SNP_A-1796277	A	A	306	46	378	30	6.858	8.80E-03	rs17178946	14	71435520	q24.2
SNP_A-1710349	C	C	351	31	330	54	6.866	8.80E-03	rs2255014	10	7429570	p14
SNP_A-2227809	A	A	400	2	369	11	6.867	8.80E-03	rs2819504	1	224016105	q42.13
SNP_A-2219459	C	C	260	96	250	140	6.864	8.80E-03	rs12699560	7	13608502	p21.2
SNP_A-2187292	G	G	293	47	354	30	6.856	8.80E-03	rs11700112	20	9495018	p12.2
SNP_A-2144860	A	A	342	20	366	44	6.856	8.80E-03	rs11620298	13	70492689	q21.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2142542	C	C	257	73	293	49	6.866	8.80E-03	rs9447757	6	77498214	q14.1
SNP_A-2023668	T	T	272	136	306	102	6.857	8.80E-03	rs16961965	17	60698082	q24.1
SNP_A-2032789	T	T	217	107	187	141	6.865	8.80E-03	rs8086073	18	2421414	p11.32
SNP_A-2078110	C	C	187	179	249	163	6.869	8.80E-03	rs2116081	8	125766854	q24.13
SNP_A-2092507	G	G	333	23	384	10	6.841	8.90E-03	rs1324781	13	77612808	q22.3
SNP_A-2066271	T	T	239	87	313	71	6.848	8.90E-03	rs2799355	6	46295713	p21.1
SNP_A-2066178	T	T	326	24	383	11	6.833	8.90E-03	rs11197640	10	118121372	q25.3
SNP_A-2065585	G	G	207	125	290	116	6.846	8.90E-03	rs1522457	3	6639830	p26.1
SNP_A-2076758	A	A	325	11	315	27	6.841	8.90E-03	rs10734446	11	37117473	p12
SNP_A-2049082	C	C	241	117	305	97	6.847	8.90E-03	rs12106650	22	15545931	q11.1
SNP_A-1997707	A	A	405	3	377	13	6.85	8.90E-03	rs16917605	9	112795770	q32
SNP_A-2162521	G	G	341	69	303	97	6.843	8.90E-03	rs12794710	11	21894728	p14.3
SNP_A-2154809	G	G	353	53	372	30	6.852	8.90E-03	rs17820032	12	13139424	p13.1
SNP_A-2132072	T	T	234	184	271	147	6.847	8.90E-03	rs10953168	7	95501446	q21.3
SNP_A-2133442	A	A	348	28	366	12	6.849	8.90E-03	rs17028545	2	64313355	p14
SNP_A-2132993	G	G	231	133	299	115	6.846	8.90E-03	rs9660848	1	75926529	p31.1
SNP_A-2136749	C	C	287	113	251	147	6.85	8.90E-03	rs11234795	11	86149175	q14.2
SNP_A-2137398	A	A	364	2	370	12	6.853	8.90E-03	rs11937450	4	163743451	q32.2
SNP_A-2130179	C	C	328	28	386	14	6.84	8.90E-03	rs7908698	10	106129284	q25.1
SNP_A-2125032	G	G	411	1	385	9	6.851	8.90E-03	rs2819377	1	198359782	q32.1
SNP_A-2183041	T	C	188	136	202	188	6.845	8.90E-03	rs3803071	12	93201348	q22
SNP_A-2217739	T	T	334	12	393	3	6.85	8.90E-03	rs11729472	4	44338178	p13
SNP_A-2221628	G	G	316	38	361	21	6.834	8.90E-03	rs11785077	8	137184864	q24.23
SNP_A-2223562	C	C	317	101	276	132	6.839	8.90E-03	rs6828911	4	36297174	p14
SNP_A-1705609	T	T	392	0	397	7	6.852	8.90E-03	-	14	33978751	q13.2
SNP_A-1813546	C	C	387	9	361	23	6.846	8.90E-03	rs8051519	16	65267187	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813327	C	C	271	47	337	31	6.839	8.90E-03	---	12	95352978	q23.1
SNP_A-1804265	G	G	352	38	356	18	6.833	8.90E-03	rs897416	17	36847294	q21.2
SNP_A-1864042	A	A	359	19	320	36	6.841	8.90E-03	rs9302464	16	11545188	p13.13
SNP_A-1862857	A	A	257	85	249	127	6.853	8.90E-03	rs4870483	6	157181623	q25.3
SNP_A-1867691	G	G	216	116	206	166	6.852	8.90E-03	rs2913896	5	175854067	q35.2
SNP_A-1854814	A	A	360	6	414	0	6.839	8.90E-03	rs11569115	4	111286419	q25
SNP_A-1824812	C	C	334	12	393	3	6.85	8.90E-03	rs11562806	8	119250918	q24.12
SNP_A-1821182	A	A	324	10	390	2	6.844	8.90E-03	rs4412145	5	99205078	q21.1
SNP_A-1818697	A	A	380	6	371	19	6.847	8.90E-03	rs16966778	17	36813132	q21.2
SNP_A-1946662	C	C	236	88	313	73	6.835	8.90E-03	rs7243998	18	53093250	q21.31
SNP_A-1947315	G	G	261	125	307	97	6.85	8.90E-03	rs9568798	13	52512555	q14.3
SNP_A-1988642	T	T	306	112	267	145	6.849	8.90E-03	rs10495337	1	229907946	q42.2
SNP_A-1915492	A	A	333	29	357	13	6.843	8.90E-03	rs6538638	12	94333662	q22
SNP_A-1885099	A	A	299	17	348	6	6.839	8.90E-03	rs7115475	11	6566622	p15.4
SNP_A-1896555	G	G	348	6	400	0	6.834	8.90E-03	rs17005344	12	78081563	q21.2
SNP_A-2284624	C	C	231	135	299	117	6.841	8.90E-03	rs7548991	1	75949326	p31.1
SNP_A-2281814	A	A	336	10	404	2	6.838	8.90E-03	rs20668612	5	124630055	q23.2
SNP_A-2276973	T	T	281	23	370	12	6.844	8.90E-03	rs2988255	1	175384937	q25.2
SNP_A-2258178	T	T	279	89	276	134	6.85	8.90E-03	rs546093	11	97429607	q22.1
SNP_A-2307671	A	A	244	112	314	94	6.847	8.90E-03	rs80664670	17	72338324	q25.2
SNP_A-2297437	T	T	188	162	255	149	6.844	8.90E-03	rs396070	1	75833489	p31.1
SNP_A-2298540	T	T	325	87	291	119	6.843	8.90E-03	rs3743201	15	77061308	q25.1
SNP_A-2271491	A	A	255	49	260	84	6.816	9.00E-03	rs6660818	1	53569465	p32.3
SNP_A-2254561	G	G	375	15	396	4	6.815	9.00E-03	rs16998629	20	16980120	p12.1
SNP_A-1901148	G	G	358	10	388	28	6.82	9.00E-03	rs9446834	6	73848989	q13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889333	C	C	399	7	376	20	6.818	9.00E-03	rs945903	1	16693017	p36.13
SNP_A-1987030	T	T	303	33	331	65	6.813	9.00E-03	rs1506085	6	100961343	q16.3
SNP_A-1982879	G	G	328	8	397	1	6.823	9.00E-03	---	5	109357451	q21.3
SNP_A-1975985	A	G	210	204	237	169	6.827	9.00E-03	rs12501252	4	10337832	p16.1
SNP_A-1947052	T	T	338	32	378	16	6.821	9.00E-03	rs2685848	1	120109822	p12
SNP_A-1941396	G	G	251	169	286	132	6.825	9.00E-03	rs574937	19	6019553	p13.3
SNP_A-1812573	T	T	336	8	407	1	6.832	9.00E-03	---	16	66891931	q22.1
SNP_A-1808125	C	C	271	95	337	75	6.821	9.00E-03	rs9990365	3	185774757	q27.1
SNP_A-1643990	A	A	341	5	371	19	6.825	9.00E-03	rs2895910	12	81311725	q21.31
SNP_A-1780808	G	G	253	83	321	65	6.815	9.00E-03	rs13273714	8	70221448	q13.2
SNP_A-1727256	C	C	327	73	362	48	6.821	9.00E-03	rs10510781	3	56077845	p14.3
SNP_A-2224335	T	T	318	18	381	7	6.818	9.00E-03	rs17099838	14	61967521	q23.2
SNP_A-2223067	G	G	351	17	365	5	6.814	9.00E-03	rs6974443	7	151736178	q36.1
SNP_A-2204635	C	C	304	48	358	30	6.823	9.00E-03	rs9447089	6	74751120	q13
SNP_A-2208966	C	C	356	6	408	0	6.816	9.00E-03	rs4075113	8	10836597	p23.1
SNP_A-2176576	A	A	326	14	344	34	6.825	9.00E-03	rs2387305	10	1205166	p15.3
SNP_A-2125345	C	T	183	159	205	159	6.818	9.00E-03	rs2250152	7	50462341	p12.2
SNP_A-2125200	G	G	285	71	292	114	6.828	9.00E-03	rs957332	14	91173975	q32.12
SNP_A-2137412	C	C	236	112	307	95	6.827	9.00E-03	rs400689	5	160470059	q34
SNP_A-2116464	G	T	203	145	199	189	6.823	9.00E-03	rs1552859	12	43217168	q12
SNP_A-1994217	T	T	321	23	370	10	6.823	9.00E-03	rs6990398	8	91543044	q21.3
SNP_A-2033205	G	G	188	172	250	156	6.819	9.00E-03	rs4863762	4	138893467	q28.3
SNP_A-2024112	T	T	329	35	331	63	6.829	9.00E-03	rs7327778	13	103093501	q33.1
SNP_A-2045610	T	T	260	150	295	115	6.83	9.00E-03	rs2963429	5	157905977	q33.3
SNP_A-2056436	T	T	242	128	233	181	6.813	9.00E-03	rs8041905	15	59823892	q22.2
SNP_A-2059256	C	C	262	94	334	76	6.831	9.00E-03	rs1978887	2	127151516	q14.3
SNP_A-2070905	T	T	312	38	383	23	6.831	9.00E-03	rs10422163	19	58686614	q13.42

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2103870	G	G	241	113	238	166	6.818	9.00E-03	rs826378	3	24144730	p24.2
SNP_A-2078376	A	A	298	52	322	30	6.826	9.00E-03	rs11951891	5	156138714	q33.3
SNP_A-2084044	T	T	184	166	248	152	6.795	9.10E-03	rs10106681	8	58428893	q12.1
SNP_A-2091846	A	A	324	36	333	17	6.795	9.10E-03	rs7734088	5	7607315	p15.31
SNP_A-2089829	T	T	239	125	303	105	6.811	9.10E-03	rs3773950	3	191805877	q28
SNP_A-2092798	A	A	364	6	416	0	6.798	9.10E-03	rs11866961	16	75604661	q23.1
SNP_A-2057854	A	A	322	10	386	2	6.804	9.10E-03	rs4838689	10	135224177	q26.3
SNP_A-2040933	C	C	362	6	414	0	6.802	9.10E-03	rs11569105	4	111282313	q25
SNP_A-2031333	A	A	328	82	349	53	6.803	9.10E-03	rs17120564	8	14809851	p22
SNP_A-2000912	T	T	229	163	276	134	6.805	9.10E-03	rs4408237	10	54571725	q21.1
SNP_A-2111042	T	T	391	9	415	1	6.804	9.10E-03	rs7917268	10	77198003	q22.2
SNP_A-2129876	G	G	281	89	347	69	6.799	9.10E-03	rs9470265	6	36453955	p21.31
SNP_A-2128032	T	T	207	199	252	168	6.795	9.10E-03	rs861589	1	181470874	q25.3
SNP_A-2127962	G	G	342	8	413	1	6.808	9.10E-03	rs6566813	18	70358767	q22.3
SNP_A-2140810	G	G	324	36	333	17	6.795	9.10E-03	rs2696635	17	41625503	q21.31
SNP_A-2146784	A	A	312	4	339	17	6.811	9.10E-03	rs12424711	12	25166764	p12.1
SNP_A-2208717	T	T	209	159	274	142	6.794	9.10E-03	rs9564739	13	70210068	q21.33
SNP_A-2207396	A	A	334	34	345	63	6.805	9.10E-03	rs2176118	8	115330310	q23.3
SNP_A-2201267	T	T	261	91	336	74	6.798	9.10E-03	rs10847647	12	127554238	q24.32
SNP_A-2215470	G	G	421	1	397	9	6.798	9.10E-03	---	1	163865663	q24.1
SNP_A-2214272	G	A	215	155	212	202	6.81	9.10E-03	rs248426	5	150545917	q33.1
SNP_A-2213879	G	A	213	155	211	199	6.796	9.10E-03	rs9384389	6	156301448	q25.3
SNP_A-1780610	C	C	334	12	391	3	6.796	9.10E-03	rs1340013	9	1288487	p24.3
SNP_A-1782143	G	G	226	196	261	157	6.805	9.10E-03	rs7590908	2	2578648	p25.3
SNP_A-1802353	C	C	339	63	360	38	6.799	9.10E-03	rs2536242	7	85593071	q21.11
SNP_A-1786333	T	T	409	1	385	9	6.81	9.10E-03	rs16940315	15	56526938	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1815788	G	G	283	21	320	48	6.802	9.10E-03	rs7118944	11	34882570	p13
SNP_A-1828559	A	A	358	2	366	12	6.796	9.10E-03	rs17086743	4	66821087	q13.2
SNP_A-1835891	G	G	322	8	389	1	6.805	9.10E-03	rs16943291	16	74355880	q23.1
SNP_A-1939877	A	A	298	28	369	15	6.795	9.10E-03	rs12295488	11	44485362	p11.2
SNP_A-1956494	A	A	308	48	306	80	6.805	9.10E-03	---	10	69672114	q21.3
SNP_A-1955900	T	T	340	54	280	74	6.812	9.10E-03	rs13125325	4	24675021	p15.2
SNP_A-1970395	T	C	201	165	217	181	6.797	9.10E-03	rs2837121	21	39988096	q22.2
SNP_A-1965081	C	C	393	23	369	43	6.797	9.10E-03	rs344905	2	139911087	q22.1
SNP_A-1914387	T	T	207	145	264	124	6.802	9.10E-03	rs6808457	3	158435855	q25.31
SNP_A-1928602	A	A	218	136	270	112	6.808	9.10E-03	rs10110974	8	130078969	q24.21
SNP_A-1924800	A	A	301	107	264	140	6.812	9.10E-03	rs13085776	3	102988197	q12.3
SNP_A-2235152	G	G	370	12	367	29	6.811	9.10E-03	rs12681256	8	84387173	q21.13
SNP_A-2266270	G	G	224	130	290	112	6.793	9.10E-03	rs2673658	12	99822911	q23.1
SNP_A-2261629	G	G	345	1	364	10	6.794	9.10E-03	rs1254603	14	51847363	q22.1
SNP_A-2278010	C	C	273	127	224	154	6.809	9.10E-03	rs698467	9	106889342	q31.2
SNP_A-2285047	G	G	338	14	386	4	6.81	9.10E-03	rs2474121	1	85510059	p22.3
SNP_A-2299968	G	G	350	6	400	0	6.796	9.10E-03	rs6651180	8	99087571	q22.1
SNP_A-2296407	C	C	416	0	364	6	6.798	9.10E-03	rs4434245	4	14306161	p15.33
SNP_A-2294323	C	C	328	92	292	124	6.812	9.10E-03	rs3852737	16	81270604	q23.3
SNP_A-2305664	A	C	236	170	209	201	6.797	9.10E-03	rs2785665	1	154436090	q23.1
SNP_A-2314116	G	G	267	125	216	150	6.774	9.20E-03	rs12364202	11	43527981	p11.2
SNP_A-2278160	G	G	415	5	374	16	6.791	9.20E-03	rs16918796	10	65133452	q21.3
SNP_A-2264242	T	T	312	50	379	33	6.777	9.20E-03	rs1809578	4	103209753	q24
SNP_A-1910340	G	G	292	46	305	81	6.776	9.20E-03	rs17728885	18	45833522	q21.1
SNP_A-1899375	C	C	347	47	324	74	6.793	9.20E-03	rs244075	20	42686908	q13.12
SNP_A-1896769	A	A	311	7	326	22	6.774	9.20E-03	rs7716441	5	64030806	q12.3
SNP_A-1966081	T	T	307	63	370	44	6.788	9.20E-03	rs262302	2	180756967	q31.3
SNP_A-1949995	A	A	219	145	165	163	6.791	9.20E-03	rs12623884	2	166084772	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835723	G	G	362	6	334	18	6.774	9.20E-03	rs10213915	5	53898505	q11.2
SNP_A-1834717	C	C	270	66	329	47	6.78	9.20E-03	rs2929636	15	36816726	q14
SNP_A-1863857	A	A	201	91	200	140	6.79	9.20E-03	rs245170	5	127253506	q23.2
SNP_A-1794272	A	A	200	152	263	135	6.784	9.20E-03	rs6831986	4	185392899	q35.1
SNP_A-1812606	C	C	336	6	384	0	6.793	9.20E-03	rs7081546	10	42494477	q11.21
SNP_A-2150366	C	C	300	22	305	45	6.782	9.20E-03	rs7678633	4	59713	p16.3
SNP_A-2153054	T	T	196	142	273	133	6.778	9.20E-03	rs10116395	9	118368259	q33.1
SNP_A-2161835	T	T	353	49	318	74	6.782	9.20E-03	rs17797652	5	149085286	q32
SNP_A-2135959	G	G	401	19	408	6	6.778	9.20E-03	rs6540547	1	206238415	q32.2
SNP_A-2132140	C	C	383	13	409	3	6.789	9.20E-03	rs9426790	1	21998096	p36.12
SNP_A-2114727	A	A	361	1	382	10	6.774	9.20E-03	rs759931	12	21770270	p12.1
SNP_A-2015864	G	G	380	22	394	8	6.787	9.20E-03	rs8126906	21	19039253	q21.1
SNP_A-2040438	C	C	320	18	354	42	6.774	9.20E-03	rs2358545	3	128553834	q21.3
SNP_A-2036288	T	T	365	1	386	10	6.78	9.20E-03	rs9404154	6	102413675	q16.3
SNP_A-2071067	C	C	230	106	251	73	6.785	9.20E-03	rs6797646	3	62092077	p14.2
SNP_A-2074803	T	T	303	15	324	36	6.775	9.20E-03	rs8024046	15	48247458	q21.2
SNP_A-2061343	A	A	207	147	260	124	6.759	9.30E-03	rs7742201	6	86489649	q14.3
SNP_A-2096857	G	G	344	10	410	2	6.758	9.30E-03	rs1846372	6	156025169	q25.3
SNP_A-2078368	A	A	339	7	356	22	6.773	9.30E-03	rs2079495	7	25276568	p15.3
SNP_A-2119166	T	T	389	7	326	18	6.77	9.30E-03	rs2987346	13	28498415	q12.3
SNP_A-2122498	C	C	301	37	319	69	6.772	9.30E-03	rs17152281	7	105148473	q22.3
SNP_A-2132503	C	C	316	12	369	3	6.762	9.30E-03	rs1490997	2	179881363	q31.2
SNP_A-2159927	G	G	378	26	403	11	6.76	9.30E-03	rs11063333	12	4752896	p13.32
SNP_A-2213578	T	T	297	65	265	93	6.762	9.30E-03	rs10935363	3	141178433	q23
SNP_A-2214447	G	G	326	26	312	48	6.759	9.30E-03	rs17120184	14	47992012	q21.3
SNP_A-2173574	C	C	362	16	401	5	6.764	9.30E-03	rs1250031	2	216332385	q35
SNP_A-1788038	C	C	324	56	301	85	6.764	9.30E-03	rs8072674	17	24558691	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1857524	A	A	316	50	270	72	6.772	9.30E-03	rs7512286	1	204381497	q32.2
SNP_A-1847453	A	A	303	83	319	53	6.773	9.30E-03	rs12378217	9	37321605	p13.2
SNP_A-1840494	C	C	308	58	374	40	6.765	9.30E-03	rs2675255	3	8147650	p26.1
SNP_A-1826754	G	G	237	129	298	108	6.762	9.30E-03	rs6546753	2	72401974	p13.2
SNP_A-1953221	C	C	254	142	257	95	6.773	9.30E-03	rs9569215	13	54628380	q21.1
SNP_A-1981090	G	G	321	27	371	13	6.759	9.30E-03	rs13185289	5	30639352	p13.3
SNP_A-1915356	A	A	308	58	374	40	6.765	9.30E-03	rs1827135	8	129227418	q24.21
SNP_A-2279123	T	T	310	16	384	6	6.769	9.30E-03	---	4	94192166	q22.3
SNP_A-2231891	C	C	329	31	380	16	6.757	9.30E-03	rs9515552	13	88746965	q31.2
SNP_A-2231752	G	G	306	54	359	35	6.761	9.30E-03	rs1060547	16	75873651	q23.1
SNP_A-2297776	G	G	195	155	250	134	6.763	9.30E-03	rs6475207	9	18252127	p22.2
SNP_A-2301545	G	G	261	137	217	167	6.762	9.30E-03	rs2946360	15	84168262	q25.3
SNP_A-2295336	C	C	308	18	367	7	6.737	9.40E-03	rs1327401	9	19712760	p22.1
SNP_A-2301606	C	C	203	159	251	133	6.747	9.40E-03	rs3009959	6	128002956	q22.33
SNP_A-2240916	T	T	319	5	349	19	6.744	9.40E-03	rs17063047	13	74070265	q22.1
SNP_A-2253727	C	C	225	135	291	117	6.754	9.40E-03	rs9938028	16	75685331	q23.1
SNP_A-2253380	G	G	361	3	368	14	6.754	9.40E-03	rs16873285	5	75585993	q13.3
SNP_A-2243139	G	G	308	48	311	81	6.739	9.40E-03	rs2166221	10	69652304	q21.3
SNP_A-2285771	A	A	213	115	268	94	6.74	9.40E-03	rs4337490	2	161336818	q24.2
SNP_A-2268694	A	A	323	39	370	22	6.742	9.40E-03	rs12316574	12	44185771	q12
SNP_A-1914047	C	C	342	28	400	14	6.752	9.40E-03	rs16857041	1	228859196	q42.2
SNP_A-1913284	T	T	304	16	376	6	6.746	9.40E-03	rs10276193	7	102536852	q22.1
SNP_A-1927915	G	G	325	45	386	28	6.744	9.40E-03	rs12946841	17	50326276	q22
SNP_A-1927653	A	A	297	69	302	110	6.737	9.40E-03	rs12243326	10	114778805	q25.2
SNP_A-1886431	A	A	356	34	350	60	6.747	9.40E-03	rs6998052	8	98435114	q22.1
SNP_A-1844316	G	G	348	6	383	21	6.74	9.40E-03	rs5754968	22	20430136	q11.21
SNP_A-1869453	C	G	201	163	224	190	6.739	9.40E-03	rs1014811	14	90003124	q32.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1785580	T	T	294	126	324	92	6.74	9.40E-03	rs9314588	8	5814540	p23.2
SNP_A-1785719	C	C	358	6	406	0	6.745	9.40E-03	rs10033694	4	178948787	q34.3
SNP_A-1790113	T	T	285	55	292	92	6.749	9.40E-03	rs7405583	17	78531854	q25.3
SNP_A-1648988	C	C	201	149	273	137	6.745	9.40E-03	rs7858099	9	9964650	p23
SNP_A-2221282	G	G	352	2	362	12	6.739	9.40E-03	rs17010566	4	127282053	q28.1
SNP_A-2150006	G	G	323	93	344	62	6.741	9.40E-03	rs2238277	14	71504415	q24.2
SNP_A-2149479	A	A	305	23	350	10	6.739	9.40E-03	rs984397	11	20827493	p15.1
SNP_A-2145719	G	G	336	30	364	14	6.746	9.40E-03	rs11146061	10	134618899	q26.3
SNP_A-2145606	G	G	412	2	385	11	6.749	9.40E-03	rs1926558	10	111031163	q25.1
SNP_A-2130112	T	T	370	0	381	7	6.737	9.40E-03	rs10969465	9	2992755	p24.2
SNP_A-2121645	T	T	395	27	403	11	6.741	9.40E-03	rs7191950	16	25908200	p12.1
SNP_A-2118851	C	C	311	55	320	92	6.745	9.40E-03	rs7523406	1	31371040	p35.2
SNP_A-2102233	T	T	368	0	379	7	6.736	9.40E-03	rs16928111	12	24891286	p12.1
SNP_A-2040202	G	G	390	28	345	47	6.741	9.40E-03	rs17510687	11	67199237	q13.2
SNP_A-2032796	A	A	318	90	284	122	6.746	9.40E-03	rs1905386	2	126839666	q14.3
SNP_A-2016808	A	A	381	23	368	44	6.73	9.50E-03	rs2252966	21	24951825	q21.2
SNP_A-2010342	C	C	291	39	358	24	6.726	9.50E-03	rs4346606	4	166129396	q32.3
SNP_A-2001070	G	G	329	45	305	71	6.731	9.50E-03	rs7094704	10	29549596	p11.23
SNP_A-1997178	C	C	220	160	243	119	6.735	9.50E-03	rs10752652	9	89454105	q22.2
SNP_A-1999734	G	A	209	185	202	156	6.735	9.50E-03	rs1246762	10	30286238	p11.23
SNP_A-1996714	C	C	355	17	408	6	6.717	9.50E-03	rs2356216	10	17114584	p13
SNP_A-2080904	G	G	229	97	195	127	6.72	9.50E-03	rs9535058	13	48092584	q14.2
SNP_A-2090439	G	G	312	34	371	19	6.736	9.50E-03	rs2216029	12	96927691	q23.1
SNP_A-2061314	A	A	399	1	379	9	6.733	9.50E-03	rs2870302	20	52040803	q13.2
SNP_A-2059923	G	G	356	32	377	15	6.73	9.50E-03	rs8177906	16	79678854	q23.2
SNP_A-2047864	C	C	323	27	342	54	6.732	9.50E-03	rs29357	4	114567295	q26

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2067879	G	G	399	1	379	9	6.733	9.50E-03	rs4342598	8	9558531	p23.1
SNP_A-2118665	T	T	371	43	380	22	6.717	9.50E-03	rs11187341	10	94993660	q23.33
SNP_A-2111726	T	T	250	90	228	126	6.733	9.50E-03	rs287825	6	83455215	q14.1
SNP_A-2130124	T	T	337	63	297	89	6.724	9.50E-03	rs4762663	12	94960854	q23.1
SNP_A-2131857	C	C	303	41	318	74	6.73	9.50E-03	rs927890	9	26569586	p21.2
SNP_A-2135123	G	G	241	123	233	175	6.723	9.50E-03	rs13253295	8	13877219	p22
SNP_A-2143730	G	A	187	169	232	176	6.723	9.50E-03	rs9506015	13	28041558	q12.3
SNP_A-2156302	C	C	320	20	344	44	6.732	9.50E-03	rs17104915	10	92827157	q23.31
SNP_A-2156323	T	T	231	183	270	148	6.718	9.50E-03	rs10750016	11	112342950	q23.1
SNP_A-2163371	G	G	283	67	344	48	6.718	9.50E-03	rs1904444	10	115067346	q25.3
SNP_A-2220716	T	T	272	100	327	77	6.731	9.50E-03	rs2542971	18	41265162	q12.3
SNP_A-2214623	A	A	382	6	354	18	6.731	9.50E-03	rs16918487	9	32728787	p21.1
SNP_A-2172467	T	T	239	125	233	179	6.725	9.50E-03	rs1440048	2	182027210	q31.3
SNP_A-1664548	G	G	217	175	265	147	6.722	9.50E-03	rs4813709	20	4614157	p13
SNP_A-1799830	C	C	279	45	297	81	6.734	9.50E-03	rs7070661	10	19096317	p12.31
SNP_A-1812978	A	A	220	124	216	180	6.732	9.50E-03	rs2604543	4	14761398	p15.33
SNP_A-1872271	A	A	354	16	391	5	6.725	9.50E-03	rs2566894	11	94148351	q21
SNP_A-1854078	C	C	307	59	373	41	6.717	9.50E-03	rs17804159	18	70071393	q22.3
SNP_A-1826744	T	T	375	11	352	26	6.726	9.50E-03	rs7746988	6	35432719	p21.31
SNP_A-1825055	G	G	394	24	368	44	6.726	9.50E-03	rs17580584	12	115098978	q24.21
SNP_A-1895912	G	G	347	9	374	26	6.73	9.50E-03	rs626883	11	69139855	q13.3
SNP_A-1919888	A	A	329	35	350	66	6.728	9.50E-03	rs10503044	18	56389207	q21.32
SNP_A-1910730	G	T	184	158	223	177	6.732	9.50E-03	rs7846808	9	72257378	q21.13
SNP_A-1967959	G	G	323	21	381	9	6.722	9.50E-03	rs2152187	20	16567876	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1965130	G	G	353	31	327	53	6.735	9.50E-03	rs16845760	2	141908466	q22.1
SNP_A-1956034	T	T	290	70	348	50	6.718	9.50E-03	rs12279768	11	82491742	q14.1
SNP_A-1961226	T	T	331	31	345	59	6.718	9.50E-03	rs11533436	12	32957503	p11.21
SNP_A-1959126	C	C	221	141	284	122	6.733	9.50E-03	rs7732916	5	27571230	p14.1
SNP_A-2248124	A	A	264	46	317	29	6.733	9.50E-03	rs2057276	6	88922540	q15
SNP_A-2247802	C	C	237	129	228	182	6.733	9.50E-03	rs1847315	11	16365152	p15.1
SNP_A-2240819	C	C	314	52	324	88	6.718	9.50E-03	rs12614163	2	195549935	q32.3
SNP_A-2300456	G	G	351	17	404	6	6.734	9.50E-03	rs11183673	12	45637680	q13.11
SNP_A-2298709	T	T	407	1	387	9	6.726	9.50E-03	rs17108640	1	53683302	p32.3
SNP_A-2292778	T	T	392	6	364	18	6.712	9.60E-03	rs17088269	6	150141375	q25.1
SNP_A-2291322	C	C	266	88	328	68	6.705	9.60E-03	rs10834785	11	25728947	p14.3
SNP_A-2238798	A	A	347	1	370	10	6.708	9.60E-03	rs17027161	2	86496128	p11.2
SNP_A-2245338	T	T	284	56	328	36	6.701	9.60E-03	rs6728102	2	228939084	q36.3
SNP_A-2252788	T	T	267	89	342	72	6.701	9.60E-03	rs7566824	2	160616281	q24.2
SNP_A-2257490	T	T	364	6	410	0	6.7	9.60E-03	rs9385526	6	130284382	q22.33
SNP_A-2286095	A	A	422	0	374	6	6.713	9.60E-03	rs7610350	3	42817249	p22.1
SNP_A-1947452	G	G	216	202	252	164	6.71	9.60E-03	rs12541094	8	124640762	q24.13
SNP_A-1917008	A	A	375	39	347	63	6.714	9.60E-03	rs4284352	10	87861607	q23.2
SNP_A-1918883	T	T	252	98	242	142	6.709	9.60E-03	rs9563502	13	56842357	q21.1
SNP_A-1927155	C	C	362	6	408	0	6.704	9.60E-03	rs9398858	6	128266638	q22.33
SNP_A-1890460	A	A	322	20	401	9	6.71	9.60E-03	rs16881972	5	9152537	p15.31
SNP_A-1825426	A	A	215	165	246	128	6.71	9.60E-03	rs2290221	16	19131471	p12.3
SNP_A-1824326	T	T	285	83	261	117	6.702	9.60E-03	rs17263875	2	213281904	q34
SNP_A-1852672	A	A	311	45	315	77	6.702	9.60E-03	rs6708636	2	172910596	q31.1
SNP_A-1871852	G	G	184	170	243	153	6.716	9.60E-03	rs1175154	1	188961746	q31.2
SNP_A-1799390	G	G	307	57	371	39	6.706	9.60E-03	rs11195190	10	112320425	q25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2171007	G	G	264	90	318	68	6.702	9.60E-03	rs1365684	6	104602108	q16.3
SNP_A-2198701	C	C	249	119	243	171	6.715	9.60E-03	rs6910782	6	119295855	q22.31
SNP_A-2219422	C	C	269	147	305	113	6.699	9.60E-03	rs16989481	20	42968317	q13.12
SNP_A-2163768	A	A	373	31	388	14	6.713	9.60E-03	rs7484571	12	119223105	q24.23
SNP_A-2164504	G	A	217	201	234	176	6.704	9.60E-03	rs1612652	19	42169480	q13.12
SNP_A-2141723	C	C	264	40	327	25	6.701	9.60E-03	rs2125962	17	74647206	q25.3
SNP_A-2138190	G	G	305	13	376	4	6.713	9.60E-03	rs4790673	17	4524756	p13.2
SNP_A-2130181	G	G	329	17	362	40	6.702	9.60E-03	rs2018332	10	55632045	q21.1
SNP_A-2125920	C	G	209	157	217	199	6.701	9.60E-03	rs2617650	19	58585647	q13.42
SNP_A-2067323	A	A	356	6	351	19	6.709	9.60E-03	rs11100880	4	146748232	q31.21
SNP_A-2087641	A	T	223	183	222	188	6.717	9.60E-03	rs6430545	2	135436333	q21.3
SNP_A-2077778	C	C	294	36	355	21	6.712	9.60E-03	rs9634548	13	104945934	q33.2
SNP_A-1994564	C	C	422	0	374	6	6.713	9.60E-03	---	8	107895693	q23.1
SNP_A-2029001	C	C	267	125	295	91	6.701	9.60E-03	rs10901188	9	132450401	q34.13
SNP_A-2027007	C	C	200	144	255	123	6.714	9.60E-03	rs2924742	8	4898830	p23.2
SNP_A-2029538	C	C	219	201	255	163	6.696	9.70E-03	rs10897267	11	61913994	q12.3
SNP_A-2032538	C	C	288	132	317	97	6.697	9.70E-03	rs10997469	10	68416291	q21.3
SNP_A-2034766	T	T	386	0	401	7	6.681	9.70E-03	---	12	42899145	q12
SNP_A-2045253	C	C	331	17	324	36	6.685	9.70E-03	rs6428224	1	191096418	q31.3
SNP_A-2017973	C	C	327	39	387	23	6.698	9.70E-03	rs1016709	21	31624945	q22.11
SNP_A-2080708	C	C	277	85	264	124	6.697	9.70E-03	rs6012249	20	45766264	q13.12
SNP_A-2100988	G	G	348	4	358	16	6.681	9.70E-03	rs1892408	1	117401964	p13.1
SNP_A-2096996	T	C	195	175	233	179	6.693	9.70E-03	rs9268877	6	32539125	p21.32
SNP_A-2107788	A	A	294	38	359	23	6.69	9.70E-03	rs10058176	5	178029804	q35.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227189	G	G	348	48	325	75	6.693	9.70E-03	rs6102880	20	40572813	q12
SNP_A-2170582	C	C	229	125	285	103	6.68	9.70E-03	rs1479644	5	33206580	p13.3
SNP_A-2174309	G	C	204	142	202	198	6.681	9.70E-03	rs12116827	1	118144980	p12
SNP_A-1869749	G	G	239	131	231	185	6.695	9.70E-03	rs273449	9	79126270	q21.31
SNP_A-1863890	A	T	229	183	215	187	6.691	9.70E-03	rs7816730	8	118625383	q24.11
SNP_A-1828985	A	A	373	13	395	3	6.698	9.70E-03	rs16837768	3	128093832	q21.2
SNP_A-1889231	G	G	259	85	272	136	6.689	9.70E-03	rs7621469	3	53972317	p21.1
SNP_A-1916076	G	G	226	102	209	143	6.687	9.70E-03	rs10011243	4	185721239	q35.1
SNP_A-1948147	T	T	249	107	230	148	6.692	9.70E-03	rs4884589	13	64405062	q21.31
SNP_A-1966333	T	T	305	35	379	21	6.685	9.70E-03	rs7577996	2	195024250	q32.3
SNP_A-1974012	C	C	354	0	367	7	6.69	9.70E-03	rs260187	3	116137672	q13.31
SNP_A-1980775	T	C	239	173	212	204	6.697	9.70E-03	rs10513150	5	13757788	p15.2
SNP_A-2282842	T	G	224	196	226	180	6.689	9.70E-03	rs2962844	5	176266354	q35.2
SNP_A-2274511	T	T	266	104	321	81	6.698	9.70E-03	rs12402923	1	89691201	p22.2
SNP_A-2270659	G	G	420	0	374	6	6.682	9.70E-03	rs2379137	1	11481849	p36.22
SNP_A-2288102	A	A	300	64	308	104	6.686	9.70E-03	rs1198588	1	98264853	p21.3
SNP_A-2299556	T	T	323	31	280	50	6.689	9.70E-03	rs5752596	22	26317301	q12.1
SNP_A-2289150	A	A	327	57	334	32	6.668	9.80E-03	rs7078251	10	45142062	q11.21
SNP_A-2311391	C	C	366	0	381	7	6.665	9.80E-03	rs1942914	18	55875215	q21.32
SNP_A-2259850	A	A	347	25	321	45	6.678	9.80E-03	rs878282	4	6540529	p16.1
SNP_A-2279280	T	T	225	179	241	131	6.673	9.80E-03	rs4800731	18	22061516	q11.2
SNP_A-2230823	T	T	258	158	209	185	6.674	9.80E-03	rs17337467	11	121299396	q24.1
SNP_A-1984999	T	T	243	111	305	91	6.664	9.80E-03	rs9378540	6	8280374	p24.3
SNP_A-1984799	T	C	179	165	211	155	6.677	9.80E-03	rs2026446	6	2040233	p25.3
SNP_A-1951704	A	A	302	68	306	108	6.669	9.80E-03	rs1039275	8	129154095	q24.21
SNP_A-1933628	T	T	344	72	363	45	6.664	9.80E-03	rs2847212	11	60092540	q12.2
SNP_A-1911453	T	T	369	15	337	31	6.678	9.80E-03	rs16953488	18	47307552	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884110	T	T	326	92	276	118	6.668	9.80E-03	rs17199030	16	3862993	p13.3
SNP_A-1892638	G	G	307	113	337	81	6.671	9.80E-03	rs9948162	18	6543040	p11.31
SNP_A-1835152	T	T	311	13	382	4	6.676	9.80E-03	rs11029973	11	27336131	p14.1
SNP_A-1832839	T	T	295	75	281	111	6.678	9.80E-03	rs2039041	13	74134052	q22.1
SNP_A-1830391	C	C	376	0	391	7	6.673	9.80E-03	rs11181183	12	40521116	q12
SNP_A-1847629	C	C	311	33	381	19	6.673	9.80E-03	rs4351836	11	81901634	q14.1
SNP_A-1849549	T	T	314	42	378	26	6.679	9.80E-03	rs10008463	4	170687556	q33
SNP_A-1789545	G	G	366	16	330	32	6.663	9.80E-03	rs13312720	16	65752953	q22.1
SNP_A-1813055	A	A	359	35	320	56	6.669	9.80E-03	rs2289858	19	4053623	p13.3
SNP_A-1668833	A	G	172	168	239	167	6.673	9.80E-03	rs9309853	3	80207554	p12.2
SNP_A-1695337	C	C	370	30	398	14	6.663	9.80E-03	rs10515597	5	147361018	q33.1
SNP_A-2191825	C	C	223	129	283	109	6.664	9.80E-03	rs11123612	2	3225956	p25.3
SNP_A-2193306	A	A	300	56	315	95	6.665	9.80E-03	rs1460354	4	42412594	p13
SNP_A-2126537	T	T	340	4	350	16	6.67	9.80E-03	rs569134	13	36350364	q13.3
SNP_A-2127358	T	T	211	207	247	169	6.665	9.80E-03	rs1940664	18	2149851	p11.32
SNP_A-2146845	C	T	194	174	234	180	6.665	9.80E-03	rs11103226	9	136043087	q34.3
SNP_A-2157967	G	G	270	82	335	63	6.677	9.80E-03	rs10738397	9	15441866	p22.3
SNP_A-2107655	T	T	231	109	207	147	6.676	9.80E-03	rs937029	5	66806172	q13.1
SNP_A-2064295	C	C	369	43	325	65	6.673	9.80E-03	rs10170245	2	221014668	q35
SNP_A-2063485	C	C	346	14	390	4	6.666	9.80E-03	rs637342	10	35994757	p11.21
SNP_A-2062567	G	G	389	17	347	33	6.664	9.80E-03	rs11002049	10	78585584	q22.3
SNP_A-2014569	G	G	323	89	295	123	6.678	9.80E-03	rs7861295	9	135703683	q34.3
SNP_A-2012207	C	C	341	15	368	36	6.67	9.80E-03	rs4869890	6	157167688	q25.3
SNP_A-2044054	C	C	302	68	306	108	6.669	9.80E-03	rs7742281	6	155094833	q25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2042601	G	A	188	148	200	172	6.668	9.80E-03	rs573294	19	42102002	q13.12
SNP_A-2036979	T	T	349	37	320	60	6.664	9.80E-03	rs11257772	10	12485545	p13
SNP_A-2023947	C	C	250	116	311	95	6.668	9.80E-03	rs1442864	4	43087559	p13
SNP_A-2037907	C	C	312	48	299	77	6.66	9.90E-03	rs16917466	8	53279666	q11.23
SNP_A-2043660	T	T	277	73	345	55	6.662	9.90E-03	rs11953269	5	30253182	p13.3
SNP_A-2012230	A	G	229	183	220	192	6.649	9.90E-03	rs416879	6	160745249	q25.3
SNP_A-2063950	C	C	360	0	375	7	6.66	9.90E-03	rs7929706	11	122186945	q24.1
SNP_A-2072633	T	T	382	36	360	60	6.648	9.90E-03	rs2182689	9	90969920	q22.2
SNP_A-2105898	C	C	319	51	377	33	6.657	9.90E-03	rs2216982	7	131054756	q32.3
SNP_A-2081598	G	G	382	4	367	15	6.648	9.90E-03	rs11193085	10	108623596	q25.1
SNP_A-2086216	C	C	344	16	365	37	6.648	9.90E-03	rs7748098	6	103659979	q16.3
SNP_A-2089105	G	G	283	65	295	107	6.651	9.90E-03	rs10983132	9	116228994	q33.1
SNP_A-2153354	C	C	317	15	375	5	6.656	9.90E-03	rs7906180	10	19961109	p12.31
SNP_A-1646734	T	T	399	1	383	9	6.647	9.90E-03	rs10483227	22	43885150	q13.31
SNP_A-1814562	G	G	329	37	383	21	6.65	9.90E-03	rs10042020	5	59199583	q12.1
SNP_A-1808479	T	T	251	69	241	105	6.647	9.90E-03	rs11674810	2	198934154	q33.1
SNP_A-1802500	A	A	377	29	376	12	6.645	9.90E-03	rs12039933	1	177173504	q25.3
SNP_A-1789854	C	C	341	81	308	112	6.653	9.90E-03	rs3785349	16	19137163	p12.3
SNP_A-1869638	T	T	372	4	357	15	6.656	9.90E-03	rs16920278	8	57126439	q12.1
SNP_A-1866806	G	G	322	16	310	34	6.656	9.90E-03	rs1725825	12	130104264	q24.33
SNP_A-1840518	G	G	186	150	250	136	6.649	9.90E-03	rs9512143	13	25655811	q12.13
SNP_A-1890834	A	G	212	150	206	200	6.66	9.90E-03	rs6487842	12	29709471	p11.22
SNP_A-1895923	T	T	357	27	363	11	6.656	9.90E-03	rs967151	2	20551351	p24.1
SNP_A-1883442	A	A	183	181	244	166	6.652	9.90E-03	rs166724	18	26859490	q12.1
SNP_A-1908634	T	T	323	17	370	6	6.655	9.90E-03	rs17008292	4	85472189	q21.23
SNP_A-1932839	G	A	189	173	234	176	6.647	9.90E-03	rs6507970	18	45966788	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1951274	T	T	386	12	357	27	6.653	9.90E-03	rs16901734	8	127909223	q24.21
SNP_A-1948879	A	A	342	8	405	1	6.646	9.90E-03	rs17170439	7	146486763	q35
SNP_A-1959344	C	C	269	69	328	50	6.651	9.90E-03	rs6120843	20	33182654	q11.22
SNP_A-2232789	G	G	393	3	373	13	6.645	9.90E-03	rs2993016	9	70750866	q21.11
SNP_A-2234464	C	C	397	1	381	9	6.649	9.90E-03	rs11929453	3	46204712	p21.31
SNP_A-2255441	C	C	309	17	331	39	6.644	9.90E-03	rs7974014	12	3651362	p13.32
SNP_A-2281656	G	G	277	43	346	28	6.65	9.90E-03	rs602988	1	179317860	q25.3
SNP_A-2281527	G	G	244	124	302	102	6.638	0.01	rs548490	11	97422786	q22.1
SNP_A-2280003	C	C	252	116	248	168	6.639	0.01	rs2085102	4	184366786	q35.1
SNP_A-2274349	A	A	264	96	260	142	6.626	0.01	rs6976218	7	35129505	p14.2
SNP_A-2255826	C	C	296	74	300	116	6.642	0.01	rs12710293	19	15017473	p13.12
SNP_A-2244488	T	T	307	13	376	4	6.641	0.01	rs614590	11	118070570	q23.3
SNP_A-2230477	T	T	363	11	384	2	6.633	0.01	rs9927292	16	59297139	q21
SNP_A-2314798	C	C	333	51	353	29	6.628	0.01	rs738324	22	23792986	q11.23
SNP_A-2308924	T	T	273	45	248	70	6.634	0.01	rs6747216	2	183275291	q32.1
SNP_A-2297826	C	C	380	2	359	11	6.638	0.01	rs17104558	10	86794615	q23.1
SNP_A-1956499	A	A	397	9	413	1	6.639	0.01	rs4885962	13	55761955	q21.1
SNP_A-1951549	C	C	332	28	386	14	6.641	0.01	rs7128731	11	26649387	p14.2
SNP_A-1940773	G	G	315	29	371	15	6.631	0.01	rs1067373	2	44563192	p21
SNP_A-1979971	A	A	288	38	266	62	6.628	0.01	rs2196379	4	175459146	q34.1
SNP_A-1975962	G	G	220	138	284	120	6.63	0.01	rs6836916	4	9954061	p16.1
SNP_A-1924874	C	C	305	89	283	125	6.637	0.01	rs7186041	16	48051004	q12.1
SNP_A-1922969	C	C	309	109	264	138	6.629	0.01	rs4709815	6	164411255	q26
SNP_A-1909148	A	A	345	33	317	55	6.637	0.01	rs9563452	13	56533522	q21.1
SNP_A-1899132	A	A	345	17	371	39	6.628	0.01	rs12002327	9	1170114	p24.3
SNP_A-1827599	G	G	347	17	373	39	6.638	0.01	rs11151296	18	62497572	q22.1
SNP_A-1791107	C	C	342	16	375	5	6.631	0.01	rs10475528	5	168322553	q34
SNP_A-2146009	C	C	379	7	362	20	6.629	0.01	rs278956	4	40293042	p14
SNP_A-2184430	A	A	292	124	320	90	6.64	0.01	rs4141072	7	123944258	q31.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189957	G	G	359	5	397	19	6.64	0.01	rs10030679	4	176696749	q34.1
SNP_A-2169348	G	G	402	8	352	20	6.628	0.01	rs13005990	2	42214427	p21
SNP_A-2218693	C	C	409	1	393	9	6.641	0.01	rs9909180	17	31895171	q12
SNP_A-2217682	G	G	307	23	350	10	6.644	0.01	rs11997377	8	141468732	q24.3
SNP_A-2095523	A	A	334	8	395	1	6.633	0.01	rs17025790	2	62704705	p15
SNP_A-2072831	T	T	404	4	389	15	6.633	0.01	rs12079361	1	242690852	q44
SNP_A-2063894	T	T	400	4	385	15	6.635	0.01	rs7950254	11	108240280	q22.3
SNP_A-2067202	T	T	310	68	342	44	6.63	0.01	rs17100090	5	142527814	q31.3
SNP_A-2050942	G	G	265	101	264	150	6.639	0.01	rs10244108	7	54926546	p11.2
SNP_A-2057471	T	T	288	72	346	52	6.643	0.01	rs16901911	5	85083023	q14.3
SNP_A-2016760	T	T	364	16	399	5	6.639	0.01	rs17110599	11	109368091	q22.3
SNP_A-2017044	C	C	346	8	409	1	6.632	0.01	rs7282327	21	26462420	q21.3
SNP_A-2037826	T	T	249	167	211	203	6.637	0.01	rs1465544	12	114510549	q24.21
SNP_A-2023019	T	T	314	86	347	59	6.631	0.01	rs4943514	13	36928444	q13.3
SNP_A-2030552	G	G	212	142	199	195	6.626	0.01	rs9295187	6	162809095	q26
SNP_A-2022899	T	T	348	4	360	16	6.619	0.0101	rs17027304	4	99447987	q23
SNP_A-2033518	A	A	383	11	404	2	6.613	0.0101	rs16843557	3	137151879	q22.2
SNP_A-2044035	A	A	333	19	347	41	6.619	0.0101	rs13438394	7	87034981	q21.12
SNP_A-1994795	C	C	256	162	217	197	6.609	0.0101	rs1387434	8	118472448	q24.11
SNP_A-2070404	G	G	396	2	375	11	6.621	0.0101	rs4765557	12	123380255	q24.31
SNP_A-2096256	C	C	351	31	320	52	6.614	0.0101	rs7188467	16	81853370	q23.3
SNP_A-2087248	G	G	379	11	400	2	6.617	0.0101	rs6737027	2	28982456	p23.2
SNP_A-2083706	G	G	340	8	401	1	6.612	0.0101	rs3917832	1	166294003	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2146374	G	G	324	64	289	91	6.619	0.0101	rs6429718	1	15230620	p36.21
SNP_A-2147320	T	T	230	102	238	158	6.623	0.0101	rs980044	13	106702668	q33.3
SNP_A-2129595	A	A	264	62	272	102	6.615	0.0101	rs2959857	15	74248903	q24.2
SNP_A-1796430	C	C	220	140	265	113	6.622	0.0101	rs11236421	7	56508003	p11.2
SNP_A-1812163	G	G	394	26	373	47	6.616	0.0101	rs1286474	14	90123825	q32.12
SNP_A-1704263	T	T	387	11	366	26	6.622	0.0101	rs1914092	10	113035984	q25.2
SNP_A-1899268	T	T	358	0	375	7	6.623	0.0101	rs2503205	1	66151858	p31.2
SNP_A-1885033	A	A	327	9	309	23	6.611	0.0101	rs17023982	2	39707594	p22.1
SNP_A-1875919	G	G	315	41	364	24	6.618	0.0101	rs2166106	4	35572203	p15.1
SNP_A-1911479	A	A	278	60	359	45	6.624	0.0101	rs7696468	4	152950987	q31.3
SNP_A-1917281	T	T	392	22	365	41	6.616	0.0101	rs7927686	11	17376793	p15.1
SNP_A-1918823	A	A	255	103	238	144	6.62	0.0101	rs10013441	4	136132843	q28.3
SNP_A-1924119	G	G	280	88	282	134	6.625	0.0101	rs12676051	8	84290131	q21.13
SNP_A-1922243	A	G	205	159	215	191	6.609	0.0101	rs7681376	4	91479576	q22.1
SNP_A-1930530	G	G	344	2	358	12	6.625	0.0101	rs17154251	7	106856721	q22.3
SNP_A-2301674	T	T	258	152	294	118	6.624	0.0101	rs6755408	2	214218361	q34
SNP_A-2311955	G	G	356	28	391	13	6.624	0.0101	rs11058124	12	124291770	q24.31
SNP_A-2230954	C	C	343	1	370	10	6.612	0.0101	rs11988096	8	12988983	p22
SNP_A-2242221	T	T	277	87	211	103	6.622	0.0101	rs4424038	5	153100457	q33.2
SNP_A-2241203	A	A	309	9	408	2	6.603	1.02E-02	rs11819080	10	15671357	p13
SNP_A-2277595	T	T	410	0	370	6	6.593	1.02E-02	rs884927	1	200027379	q32.1
SNP_A-2312427	T	T	272	66	353	51	6.602	1.02E-02	rs11680715	2	8679057	p25.1
SNP_A-2309625	C	C	363	39	337	63	6.608	1.02E-02	rs1343625	6	24220716	p22.2
SNP_A-2298081	T	T	401	9	415	1	6.597	1.02E-02	rs16876760	4	24758859	p15.2
SNP_A-1893597	G	G	232	160	239	111	6.608	1.02E-02	rs973141	1	116545254	p13.1
SNP_A-1965220	G	A	201	161	210	180	6.596	1.02E-02	rs6721116	2	145989929	q22.3
SNP_A-1982847	G	A	198	150	201	181	6.604	1.02E-02	rs11952230	5	108046294	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1987767	C	C	370	0	389	7	6.601	1.02E-02	rs17064305	6	135574497	q23.3
SNP_A-1936683	A	A	298	72	351	51	6.598	1.02E-02	rs1944550	18	73144551	q23
SNP_A-1812383	G	G	332	34	327	15	6.599	1.02E-02	rs750210	2	45978492	p21
SNP_A-1801650	A	A	417	1	403	9	6.596	1.02E-02	rs17093756	14	57377777	q23.1
SNP_A-1794634	C	C	271	97	271	145	6.607	1.02E-02	rs17542916	5	17122654	p15.1
SNP_A-1789721	A	A	262	158	293	121	6.596	1.02E-02	rs1557063	10	124569760	q26.13
SNP_A-1819661	T	T	253	167	282	128	6.608	1.02E-02	rs11057458	12	123132065	q24.31
SNP_A-1839849	A	A	286	30	389	19	6.602	1.02E-02	rs160705	5	123603903	q23.2
SNP_A-1829869	A	A	342	8	403	1	6.606	1.02E-02	rs6843434	4	169382173	q32.3
SNP_A-1861422	C	G	236	180	212	194	6.594	1.02E-02	rs1986842	10	122256911	q26.12
SNP_A-2136599	G	G	294	48	362	32	6.608	1.02E-02	rs188014	13	49867924	q14.3
SNP_A-2113380	C	C	362	8	390	24	6.594	1.02E-02	rs10507313	13	22170145	q12.11
SNP_A-2114330	A	A	319	47	326	80	6.596	1.02E-02	rs4405320	11	63123634	q13.1
SNP_A-2119020	A	A	405	1	391	9	6.602	1.02E-02	rs7921175	10	119981748	q26.11
SNP_A-2166486	G	G	283	79	290	124	6.606	1.02E-02	rs7200337	16	82677316	q23.3
SNP_A-2204645	A	A	264	100	331	81	6.595	1.02E-02	rs1680686	14	33493678	q13.1
SNP_A-2210366	A	A	342	62	296	86	6.598	1.02E-02	rs10493577	1	76201244	p31.1
SNP_A-2188800	A	A	318	14	340	34	6.594	1.02E-02	rs1450511	18	20577181	q11.2
SNP_A-2184456	C	T	188	156	216	178	6.593	1.02E-02	rs589794	5	60551876	q12.1
SNP_A-2196139	C	C	290	68	285	105	6.6	1.02E-02	rs10971711	9	33805842	p13.3
SNP_A-2080823	G	G	360	26	332	46	6.605	1.02E-02	rs754479	14	94400761	q32.13
SNP_A-2079472	A	A	298	98	268	132	6.596	1.02E-02	rs4807569	19	1074378	p13.3
SNP_A-2074797	C	C	367	39	371	19	6.599	1.02E-02	rs870512	13	62121631	q21.31
SNP_A-2060898	G	G	306	106	275	141	6.594	1.02E-02	rs7528325	1	202025729	q32.1
SNP_A-2012874	T	T	184	176	245	161	6.603	1.02E-02	rs555156	11	84499629	q14.1
SNP_A-2010775	G	G	378	24	408	10	6.6	1.02E-02	rs2115120	5	29401304	p13.3
SNP_A-2009812	T	C	176	166	233	169	6.597	1.02E-02	rs911561	11	35355686	p13
SNP_A-2023729	G	G	415	1	401	9	6.597	1.02E-02	rs6054175	20	6298752	p12.3
SNP_A-2032052	T	T	388	6	364	18	6.582	0.0103	rs10426229	19	42076617	q13.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2042456	G	G	353	25	364	10	6.576	0.0103	rs17172861	7	47252783	p12.3
SNP_A-2014585	T	T	196	160	242	134	6.589	0.0103	rs2155046	11	100682646	q22.1
SNP_A-1996286	G	G	378	16	355	33	6.574	0.0103	---	9	24343310	p21.3
SNP_A-2065345	C	C	193	171	256	156	6.584	0.0103	rs2224237	14	93789068	q32.13
SNP_A-2091670	C	C	326	40	337	71	6.58	0.0103	rs10790965	11	127998557	q24.3
SNP_A-2173548	G	G	312	48	373	31	6.578	0.0103	---	13	96221171	q32.1
SNP_A-2173167	A	A	312	58	376	40	6.59	0.0103	rs938370	2	112127138	q13
SNP_A-2177258	C	C	360	0	379	7	6.59	0.0103	---	2	111504284	q13
SNP_A-2179199	T	T	182	148	243	133	6.587	0.0103	rs7315438	12	114354123	q24.21
SNP_A-2203061	T	T	333	39	314	64	6.578	0.0103	rs1485333	3	68026298	p14.1
SNP_A-2218873	G	G	334	30	396	16	6.583	0.0103	rs998864	5	167717782	q34
SNP_A-2141491	G	G	356	14	382	34	6.58	0.0103	rs10230949	7	92260526	q21.2
SNP_A-2119577	T	T	315	49	378	32	6.585	0.0103	rs1345683	5	110006141	q22.1
SNP_A-1861690	C	C	405	13	385	29	6.582	0.0103	rs2121435	2	121436178	q14.2
SNP_A-1861836	G	G	366	10	355	25	6.575	0.0103	rs16927014	8	62291565	q12.2
SNP_A-1853021	G	G	341	17	388	6	6.583	0.0103	rs1454590	8	14982009	p22
SNP_A-1842704	A	A	336	8	395	1	6.585	0.0103	rs977221	2	115510999	q14.1
SNP_A-1801990	T	T	222	140	286	122	6.575	0.0103	rs11768848	7	16636967	p21.1
SNP_A-1810230	T	T	420	0	380	6	6.577	0.0103	rs889731	16	81814943	q23.3
SNP_A-1810122	T	T	322	16	363	39	6.586	0.0103	rs3783728	14	63957957	q23.2
SNP_A-1943898	G	G	346	62	319	91	6.588	0.0103	rs6676073	1	194278083	q31.3
SNP_A-1961798	G	G	307	97	325	65	6.589	0.0103	rs10519477	2	1410597	p25.3
SNP_A-1979822	T	T	353	1	382	10	6.589	0.0103	rs17053323	4	168808484	q32.3
SNP_A-1898867	G	G	322	16	363	39	6.586	0.0103	rs6970194	7	70018597	q11.22
SNP_A-1873959	T	T	359	1	347	9	6.582	0.0103	rs7676547	4	159924157	q32.1
SNP_A-1880993	T	T	328	16	400	6	6.586	0.0103	rs404223	5	40911636	p13.1
SNP_A-1931029	A	G	223	193	213	171	6.579	0.0103	rs10909918	1	3231532	p36.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920995	C	C	301	109	335	79	6.586	0.0103	rs12703621	7	143733618	q35
SNP_A-1923650	A	A	397	3	379	13	6.587	0.0103	rs8104176	19	51373669	q13.32
SNP_A-1910994	T	T	338	12	387	3	6.569	0.0104	rs16960474	15	33230420	q14
SNP_A-1964689	G	G	293	77	295	119	6.558	0.0104	---	2	122421033	q14.3
SNP_A-1966052	C	C	309	59	373	41	6.563	0.0104	rs16866624	2	179762276	q31.2
SNP_A-1955816	G	G	393	9	405	1	6.561	0.0104	rs841162	1	244238256	q44
SNP_A-1952075	T	T	322	16	392	6	6.56	0.0104	rs16861813	2	174180059	q31.1
SNP_A-1935064	C	C	393	11	412	2	6.558	0.0104	rs781356	14	51946477	q22.1
SNP_A-1800844	C	C	326	42	390	26	6.571	0.0104	rs17060769	6	132140454	q23.2
SNP_A-1797879	G	G	319	13	388	4	6.572	0.0104	rs10214537	6	166909662	q27
SNP_A-1798788	T	T	265	89	338	72	6.563	0.0104	rs2036772	12	101020220	q23.2
SNP_A-1784982	C	C	321	43	331	75	6.56	0.0104	rs7634112	3	13508582	p25.1
SNP_A-1757357	A	A	313	73	356	50	6.564	0.0104	rs10491380	5	53905084	q11.2
SNP_A-1839808	G	G	233	131	223	183	6.559	0.0104	rs3806960	6	70564840	q13
SNP_A-1829089	T	T	235	129	294	108	6.572	0.0104	rs11233500	11	82559055	q14.1
SNP_A-1857138	A	A	340	8	399	1	6.572	0.0104	rs3950015	13	97637870	q32.2
SNP_A-1872443	T	T	401	15	414	4	6.571	0.0104	rs16867791	7	89257549	q21.13
SNP_A-2135515	C	C	354	12	405	3	6.567	0.0104	rs1565973	13	70178035	q21.33
SNP_A-2133780	G	G	376	42	392	22	6.564	0.0104	rs11186333	10	92595099	q23.31
SNP_A-2151255	G	G	328	20	347	43	6.563	0.0104	rs7824648	8	88880870	q21.3
SNP_A-2209856	A	A	389	9	401	1	6.562	0.0104	rs13331896	16	48539166	q12.1
SNP_A-2196830	A	A	379	1	367	9	6.572	0.0104	rs11114390	12	79194026	q21.31
SNP_A-2060693	C	C	240	178	276	142	6.562	0.0104	rs1992245	10	92889836	q23.31
SNP_A-1996431	A	A	399	1	387	9	6.563	0.0104	rs824411	9	28840822	p21.1
SNP_A-1994773	C	C	346	16	369	37	6.561	0.0104	rs12549176	8	117404404	q23.3
SNP_A-2005133	G	G	361	1	392	10	6.564	0.0104	rs6505350	17	28896866	q12
SNP_A-2041573	A	A	280	56	359	41	6.571	0.0104	rs4733372	8	32724930	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2037194	G	G	365	41	377	21	6.567	0.0104	rs17621519	1	224480716	q42.13
SNP_A-2033283	C	C	183	175	231	151	6.561	0.0104	rs2535668	6	94895734	q16.1
SNP_A-2297875	A	A	361	1	392	10	6.564	0.0104	rs16891647	8	42902832	p11.21
SNP_A-2307385	T	T	228	118	295	101	6.563	0.0104	rs4776709	15	62083994	q22.31
SNP_A-2305044	T	T	310	16	378	6	6.572	0.0104	rs6813071	4	17267896	p15.32
SNP_A-2311632	T	T	340	8	399	1	6.572	0.0104	rs17118160	14	82717509	q31.2
SNP_A-2283401	A	A	362	0	383	7	6.558	0.0104	rs12103309	16	4040269	p13.3
SNP_A-2264527	C	C	352	14	378	34	6.563	0.0104	rs17107613	14	77983851	q24.3
SNP_A-2239220	A	G	186	156	217	177	6.558	0.0104	rs10007992	4	90446622	q22.1
SNP_A-2238440	C	C	224	188	259	151	6.57	0.0104	rs11721321	3	123356123	q21.1
SNP_A-2228106	C	C	213	121	220	184	6.546	1.05E-02	rs9321961	6	144461218	q24.2
SNP_A-2254281	A	A	264	86	319	65	6.548	1.05E-02	rs4863588	4	139976994	q31.1
SNP_A-2282896	G	G	347	49	350	26	6.553	1.05E-02	rs4500362	1	82218024	p31.1
SNP_A-2304644	T	T	197	91	295	87	6.551	1.05E-02	rs2204919	4	98080957	q22.3
SNP_A-2294010	G	G	296	120	260	154	6.545	1.05E-02	rs879851	14	52565332	q22.1
SNP_A-2041180	G	G	269	119	235	153	6.544	1.05E-02	rs1970266	1	174720147	q25.2
SNP_A-2090614	T	T	225	101	232	156	6.543	1.05E-02	rs10040481	20	40770724	q12
SNP_A-2175997	C	C	341	67	318	98	6.55	1.05E-02	rs1472915	3	3528929	p26.2
SNP_A-2224543	T	T	420	0	382	6	6.543	1.05E-02	---	1	213784460	q41
SNP_A-2139657	C	C	278	90	277	135	6.541	1.05E-02	rs6812244	4	141063115	q31.1
SNP_A-1823215	C	C	263	83	259	125	6.551	1.05E-02	rs4072526	8	79537111	q21.12
SNP_A-1823534	C	C	414	0	376	6	6.552	1.05E-02	rs1923510	1	149189758	q21.3
SNP_A-1822825	C	C	309	35	338	18	6.549	1.05E-02	rs17084542	4	55335107	q12
SNP_A-1837894	T	T	283	73	334	52	6.541	1.05E-02	rs9483683	6	134709013	q23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1795619	G	G	290	116	323	85	6.553	1.05E-02	rs4658099	1	89681378	p22.2
SNP_A-1935735	C	C	351	15	411	5	6.554	1.05E-02	rs12326420	18	71036194	q22.3
SNP_A-1967884	T	T	222	134	279	113	6.553	1.05E-02	rs458032	20	15167500	p12.1
SNP_A-1986878	G	G	352	10	410	2	6.545	1.05E-02	rs16870549	6	93751833	q16.1
SNP_A-1932386	C	C	376	32	357	55	6.554	1.05E-02	rs3805678	5	131703106	q23.3
SNP_A-1928198	G	G	346	18	368	6	6.544	1.05E-02	rs7868594	9	16896384	p22.2
SNP_A-1900735	A	A	236	124	302	106	6.531	0.0106	rs12707307	7	135588343	q33
SNP_A-1894442	C	T	194	160	216	180	6.533	0.0106	rs10953517	7	105992104	q22.3
SNP_A-1938536	C	C	352	2	370	12	6.536	0.0106	rs6482213	10	22764104	p12.2
SNP_A-1786605	A	A	338	84	302	114	6.528	0.0106	rs937629	3	123347704	q21.1
SNP_A-1801931	T	T	295	69	305	111	6.529	0.0106	rs1886779	14	32728645	q13.1
SNP_A-1780600	G	G	293	71	295	111	6.527	0.0106	rs1986238	2	75811518	p12
SNP_A-1740473	C	C	374	0	397	7	6.539	0.0106	rs999399	9	19726356	p22.1
SNP_A-1673246	T	T	336	14	373	35	6.531	0.0106	rs10497621	2	184199986	q32.1
SNP_A-1837740	C	T	183	179	237	167	6.535	0.0106	rs6497126	15	92086173	q26.1
SNP_A-1837546	C	C	199	161	255	141	6.533	0.0106	rs1007740	10	68086926	q21.3
SNP_A-1828269	T	T	311	107	340	76	6.538	0.0106	rs1405123	7	148217048	q36.1
SNP_A-1863439	A	A	337	39	313	63	6.533	0.0106	rs751409	17	78558667	q25.3
SNP_A-1865563	T	T	341	29	351	55	6.536	0.0106	rs11856247	15	90012745	q26.1
SNP_A-2159697	A	A	209	159	272	142	6.528	0.0106	rs7184081	16	50341052	q12.1
SNP_A-2159365	T	T	311	57	373	39	6.534	0.0106	rs356073	5	173614182	q35.2
SNP_A-2123101	T	G	230	192	226	190	6.532	0.0106	rs3763115	5	131392080	q23.3
SNP_A-2119916	G	G	319	11	289	25	6.531	0.0106	rs17054023	6	142347759	q24.1
SNP_A-2225889	A	G	228	194	229	189	6.525	0.0106	rs745570	17	75396320	q25.3
SNP_A-2182009	T	T	258	66	246	100	6.534	0.0106	rs10846806	12	124021639	q24.31
SNP_A-2196526	C	C	344	10	400	2	6.527	0.0106	rs17011252	10	49697335	q11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2090705	G	G	304	8	328	24	6.525	0.0106	rs11241098	5	110486407	q22.1
SNP_A-2080436	A	A	248	102	248	152	6.538	0.0106	rs10832253	11	1321818	p15.5
SNP_A-2104635	T	T	281	63	343	45	6.539	0.0106	rs10815875	9	8431646	p24.1
SNP_A-2055682	G	G	318	12	363	3	6.529	0.0106	rs10764194	10	20391423	p12.31
SNP_A-2067959	C	C	376	14	352	30	6.527	0.0106	rs1998586	9	37789265	p13.2
SNP_A-2043016	A	A	381	9	391	1	6.524	0.0106	rs7528407	1	41457092	p34.2
SNP_A-2288007	G	G	189	149	229	121	6.524	0.0106	rs4526325	8	128680758	q24.21
SNP_A-2305253	A	A	359	29	377	13	6.53	0.0106	rs4095525	18	14361962	p11.21
SNP_A-2282700	C	C	360	46	388	26	6.526	0.0106	rs11147956	13	44209741	q14.12
SNP_A-2285887	G	G	362	0	385	7	6.525	0.0106	rs1236597	18	56996625	q21.32
SNP_A-2277530	A	A	207	203	232	158	6.537	0.0106	rs3785888	17	42360702	q21.32
SNP_A-2269532	A	A	396	4	356	14	6.524	0.0106	rs16863231	2	222657853	q36.1
SNP_A-2264949	A	A	350	6	384	0	6.525	0.0106	rs9400464	6	111501262	q21
SNP_A-2282967	T	T	358	6	392	0	6.513	1.07E-02	rs17030834	12	99877906	q23.1
SNP_A-2302024	T	T	231	139	220	192	6.518	1.07E-02	rs312335	4	18979159	p15.31
SNP_A-2303822	G	G	414	0	378	6	6.518	1.07E-02	rs940393	1	15011519	p36.21
SNP_A-2301016	C	C	386	34	363	57	6.519	1.07E-02	rs6459609	6	18434509	p22.3
SNP_A-2041142	G	G	422	0	386	6	6.507	1.07E-02	rs16989079	22	19749204	q11.21
SNP_A-2030315	C	C	366	2	386	12	6.51	1.07E-02	rs17084918	18	67518703	q22.3
SNP_A-2024949	T	T	420	0	384	6	6.51	1.07E-02	rs10182958	2	74440904	p13.1
SNP_A-2025918	C	C	289	35	370	22	6.522	1.07E-02	rs1338858	10	86811221	q23.2
SNP_A-2022498	G	G	346	8	403	1	6.512	1.07E-02	rs8181733	12	30181953	p11.22
SNP_A-2021802	C	C	334	22	396	10	6.513	1.07E-02	rs11769353	7	126683308	q32.1
SNP_A-2004347	T	T	389	9	399	1	6.522	1.07E-02	rs16839156	1	4475186	p36.32
SNP_A-1997831	A	A	300	70	363	51	6.521	1.07E-02	rs4836703	9	117628488	q33.1
SNP_A-2014314	C	C	267	25	290	52	6.515	1.07E-02	rs7853471	9	82461877	q21.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2065796	T	T	306	48	365	31	6.514	1.07E-02	rs39731	7	78074877	q21.11
SNP_A-2074355	G	G	406	2	350	10	6.507	1.07E-02	rs16841797	1	147584062	q21.2
SNP_A-2079801	A	A	238	74	311	59	6.513	1.07E-02	rs9542467	13	70147178	q21.33
SNP_A-2082879	C	C	279	77	347	59	6.516	1.07E-02	rs7825068	8	138876842	q24.23
SNP_A-2091149	A	A	362	6	384	20	6.523	1.07E-02	---	13	106770318	q33.3
SNP_A-2091839	G	G	377	19	376	6	6.512	1.07E-02	rs7163127	15	77029160	q25.1
SNP_A-2192274	A	A	210	132	204	188	6.511	1.07E-02	rs13405986	2	143995466	q22.2
SNP_A-2211050	G	T	230	192	227	191	6.518	1.07E-02	rs3763116	5	131391913	q23.3
SNP_A-2207368	C	T	188	158	218	178	6.508	1.07E-02	rs7945162	11	95046196	q21
SNP_A-2207671	T	T	346	10	402	2	6.52	1.07E-02	rs11058181	12	124466778	q24.31
SNP_A-2115568	C	C	319	13	386	4	6.515	1.07E-02	rs2511253	13	28136827	q12.3
SNP_A-2130763	G	G	214	168	251	135	6.517	1.07E-02	rs4861190	4	42221559	p13
SNP_A-2156531	A	A	340	14	366	34	6.509	1.07E-02	rs1453505	16	16878868	p12.3
SNP_A-2149414	G	G	361	29	350	52	6.521	1.07E-02	rs1867549	10	60275056	q21.1
SNP_A-1867139	T	T	175	163	248	158	6.515	1.07E-02	rs1466654	1	8310179	p36.23
SNP_A-1817052	A	A	270	118	216	140	6.512	1.07E-02	rs10948994	6	56292005	p12.1
SNP_A-1842940	A	A	293	67	299	107	6.517	1.07E-02	rs2065547	13	103009296	q33.1
SNP_A-1831944	C	C	258	48	289	89	6.52	1.07E-02	rs7610222	3	24332290	p24.2
SNP_A-1831536	A	A	402	2	385	11	6.519	1.07E-02	rs17157957	10	2296064	p15.3
SNP_A-1721852	C	C	367	19	354	38	6.522	1.07E-02	rs2415141	15	70579610	q24.1
SNP_A-1789029	C	C	403	17	363	33	6.509	1.07E-02	rs1912640	15	45774265	q21.1
SNP_A-1940045	G	G	247	155	280	120	6.516	1.07E-02	rs9616618	22	48148393	q13.33
SNP_A-1958334	T	T	339	5	356	18	6.522	1.07E-02	rs17118784	11	115194813	q23.3
SNP_A-1959802	A	A	348	24	374	10	6.512	1.07E-02	rs9370356	6	54977072	p12.1
SNP_A-1982985	C	C	308	38	328	70	6.508	1.07E-02	rs2162845	5	113016769	q22.2
SNP_A-1890373	A	A	364	18	386	6	6.517	1.07E-02	rs415230	20	52278805	q13.2
SNP_A-1928547	G	G	360	0	383	7	6.522	1.07E-02	rs4500706	16	8310626	p13.2
SNP_A-1886151	A	G	184	156	219	177	6.496	1.08E-02	rs2139404	2	100700112	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1887250	A	A	351	1	384	10	6.501	1.08E-02	rs12463525	2	214956052	q34
SNP_A-1955475	A	A	199	149	265	135	6.494	1.08E-02	rs10167103	2	127294974	q14.3
SNP_A-1954024	A	A	352	16	377	37	6.495	1.08E-02	rs10990158	9	102375661	q31.1
SNP_A-1938961	T	C	247	175	209	207	6.492	1.08E-02	rs6967341	7	144010934	q35
SNP_A-1792873	A	A	309	45	320	78	6.494	1.08E-02	rs1836559	18	39333539	q12.3
SNP_A-1813358	G	G	326	18	381	7	6.497	1.08E-02	rs7541048	1	224350231	q42.13
SNP_A-1780997	T	T	255	93	318	74	6.495	1.08E-02	rs17194382	2	158923532	q24.1
SNP_A-1842695	A	A	269	141	224	170	6.496	1.08E-02	rs10840105	11	8656238	p15.4
SNP_A-1841999	T	T	293	101	263	135	6.497	1.08E-02	rs10805874	5	72643737	q13.2
SNP_A-1821604	G	G	270	66	267	103	6.495	1.08E-02	rs343112	5	72916455	q13.2
SNP_A-1827206	T	T	331	15	327	33	6.499	1.08E-02	rs8031091	15	87635587	q26.1
SNP_A-1868756	T	T	244	56	258	96	6.502	1.08E-02	rs2061407	1	96204319	p21.3
SNP_A-1866332	C	C	264	92	226	120	6.504	1.08E-02	rs11167065	8	142573179	q24.3
SNP_A-1854637	T	T	274	90	323	67	6.502	1.08E-02	rs4407607	5	100700655	q21.1
SNP_A-1848659	G	G	234	116	236	172	6.497	1.08E-02	rs2971027	7	9780564	p21.3
SNP_A-2133531	A	A	382	20	365	39	6.501	1.08E-02	rs11901196	2	146350346	q22.3
SNP_A-2121530	G	G	343	71	365	45	6.492	1.08E-02	rs17182582	3	133555117	q22.1
SNP_A-2110541	C	C	222	192	251	151	6.504	1.08E-02	rs4669905	2	5929790	p25.2
SNP_A-2185040	C	C	198	170	260	154	6.5	1.08E-02	rs7710314	5	85811870	q14.3
SNP_A-2089921	C	C	265	157	224	190	6.5	1.08E-02	rs4980288	10	125228025	q26.13
SNP_A-2086295	G	G	354	30	348	54	6.5	1.08E-02	rs9458539	6	158192294	q25.3
SNP_A-2049196	T	T	260	48	320	32	6.502	1.08E-02	rs1447817	3	59659724	p14.2
SNP_A-2054040	A	A	245	109	230	152	6.502	1.08E-02	rs940183	3	120895816	q13.33
SNP_A-2010755	C	C	317	19	349	7	6.503	1.08E-02	rs2219842	5	25815576	p14.1
SNP_A-2007571	A	A	339	81	361	53	6.499	1.08E-02	rs1407256	20	30677308	q11.21
SNP_A-2022347	C	C	260	88	266	136	6.5	1.08E-02	rs491528	11	125002676	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246027	A	A	240	162	280	130	6.506	1.08E-02	rs2729908	11	19379056	p15.1
SNP_A-2229431	A	A	329	17	372	6	6.497	1.08E-02	rs12712003	2	4042716	p25.2
SNP_A-2231504	G	G	305	15	301	33	6.48	0.0109	rs11216041	11	96161682	q21
SNP_A-2255782	T	T	249	117	244	168	6.48	0.0109	rs10820661	9	104345544	q31.1
SNP_A-2292617	T	T	186	144	242	126	6.478	0.0109	rs537183	2	169600153	q31.1
SNP_A-2292140	C	C	267	91	295	63	6.486	0.0109	rs1028911	6	8651520	p24.3
SNP_A-2032288	T	T	399	1	391	9	6.481	0.0109	rs4776588	15	70322792	q23
SNP_A-2014128	T	T	348	28	379	13	6.479	0.0109	rs7862030	9	21330373	p21.3
SNP_A-1996373	G	G	387	1	379	9	6.484	0.0109	rs16923812	9	27448876	p21.2
SNP_A-1991994	A	A	328	32	394	18	6.48	0.0109	rs2680605	8	4133030	p23.2
SNP_A-2050910	T	T	387	9	395	1	6.482	0.0109	rs7717021	5	149938067	q33.1
SNP_A-2072185	A	A	279	141	230	168	6.489	0.0109	rs11067671	12	1145023358	q24.21
SNP_A-2095043	G	G	330	26	350	52	6.487	0.0109	rs7749636	6	12771149	p24.1
SNP_A-2184537	T	T	391	21	383	7	6.484	0.0109	rs7112171	11	8278378	p15.4
SNP_A-2190839	C	C	358	10	414	2	6.481	0.0109	rs17033748	3	35762893	p22.3
SNP_A-2199570	C	C	295	35	363	21	6.48	0.0109	rs10990559	9	102973034	q31.1
SNP_A-2177295	A	A	369	11	384	2	6.483	0.0109	rs17074869	13	50218564	q14.3
SNP_A-2220737	A	A	228	126	292	108	6.479	0.0109	rs4237989	12	123981415	q24.31
SNP_A-2109881	C	C	315	25	368	12	6.478	0.0109	rs9681359	3	128382446	q21.3
SNP_A-2108165	T	T	357	27	382	12	6.488	0.0109	rs2701959	8	1033773	p23.3
SNP_A-2152361	A	G	222	180	213	183	6.482	0.0109	rs12469941	2	135463659	q21.3
SNP_A-1848257	C	C	241	59	317	45	6.486	0.0109	rs175044	14	74541862	q24.3
SNP_A-1854971	C	C	335	9	383	27	6.481	0.0109	rs8015021	14	101379446	q32.31
SNP_A-1869623	C	C	286	60	303	101	6.485	0.0109	rs17050859	4	121808238	q27
SNP_A-1829126	C	C	205	151	274	138	6.475	0.0109	---	3	6652377	p26.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1837004	G	G	332	10	384	2	6.474	0.0109	rs6573820	14	67731966	q24.1
SNP_A-1658672	A	A	210	132	277	117	6.48	0.0109	rs2504988	6	77033275	q14.1
SNP_A-1679536	G	G	234	156	280	128	6.475	0.0109	rs2822963	21	15149921	q11.2
SNP_A-1938112	T	T	296	114	262	148	6.484	0.0109	---	18	36522022	q12.3
SNP_A-1947003	G	G	329	15	383	5	6.474	0.0109	rs1160188	11	84869209	q14.1
SNP_A-1894270	A	A	382	6	416	0	6.481	0.0109	---	14	64254258	q23.3
SNP_A-1906938	G	A	171	135	181	153	6.484	0.0109	rs1493742	11	26522071	p14.2
SNP_A-1909323	A	A	269	89	271	135	6.464	1.10E-02	rs1909838	14	32789264	q13.1
SNP_A-1911408	T	T	252	80	324	64	6.461	1.10E-02	rs11164167	13	112291800	q34
SNP_A-1935953	C	C	311	59	318	96	6.461	1.10E-02	rs10180781	2	204958325	q33.3
SNP_A-1933995	G	G	283	45	284	76	6.47	1.10E-02	rs17731873	15	93069073	q26.2
SNP_A-1980958	C	C	364	16	393	5	6.46	1.10E-02	rs17261751	5	21816665	p14.3
SNP_A-1782905	C	C	261	103	323	83	6.461	1.10E-02	rs1643081	7	133508767	q33
SNP_A-1722900	A	A	340	2	393	13	6.47	1.10E-02	rs10516677	4	83975689	q21.22
SNP_A-1803957	C	C	237	123	232	176	6.473	1.10E-02	rs9532984	13	41532693	q14.11
SNP_A-1795957	T	T	227	135	220	190	6.458	1.10E-02	rs4811469	20	51854019	q13.2
SNP_A-1838042	T	T	300	104	314	70	6.459	1.10E-02	rs320629	17	28678796	q11.2
SNP_A-1871855	T	T	199	167	261	151	6.464	1.10E-02	rs17544582	15	92037412	q26.1
SNP_A-1856514	C	C	224	142	217	199	6.468	1.10E-02	rs6111539	20	17379097	p12.1
SNP_A-2213906	T	T	338	2	358	12	6.462	1.10E-02	rs3948689	7	105390660	q22.3
SNP_A-2179765	A	A	364	0	391	7	6.461	1.10E-02	rs7863961	9	28416174	p21.1
SNP_A-2056006	T	T	414	2	399	11	6.464	1.10E-02	rs12115775	9	105248086	q31.1
SNP_A-1990273	G	G	326	88	349	59	6.461	1.10E-02	rs10495440	1	235601620	q43
SNP_A-2042389	G	G	364	0	391	7	6.461	1.10E-02	rs4072409	1	158090820	q23.3
SNP_A-2039321	G	G	358	22	335	41	6.473	1.10E-02	rs4944490	11	83799592	q14.1
SNP_A-2034821	T	T	287	69	294	110	6.47	1.10E-02	rs11089652	22	33016213	q12.3
SNP_A-2289113	C	C	353	65	365	39	6.464	1.10E-02	rs17792713	7	130920534	q32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2310070	T	T	251	113	243	161	6.473	1.10E-02	rs7798775	7	42921205	p14.1
SNP_A-2232125	G	G	334	10	386	2	6.467	1.10E-02	rs2163287	6	158011692	q25.3
SNP_A-2273520	C	C	326	42	388	26	6.465	1.10E-02	rs17088840	9	69983309	q21.11
SNP_A-2268071	T	T	418	0	386	6	6.446	0.0111	rs5743491	8	6715489	p23.1
SNP_A-2272095	G	G	308	58	338	36	6.456	0.0111	rs1322670	9	129839313	q34.11
SNP_A-2231118	A	A	271	95	325	73	6.445	0.0111	rs17640214	5	90838717	q14.3
SNP_A-2252824	T	T	336	68	310	98	6.449	0.0111	rs7379830	5	70975193	q13.2
SNP_A-2248013	G	G	407	11	356	24	6.443	0.0111	rs3002680	1	35257637	p34.3
SNP_A-2301098	T	T	229	139	289	119	6.455	0.0111	rs11914812	3	80629934	p12.2
SNP_A-2294648	G	G	356	8	411	1	6.444	0.0111	rs6765226	3	69295283	p14.1
SNP_A-2019477	T	G	202	162	221	191	6.452	0.0111	rs9980043	21	39991130	q22.2
SNP_A-2060268	G	G	300	54	264	78	6.457	0.0111	rs368039	4	111121455	p15.33
SNP_A-2058948	C	C	416	0	384	6	6.448	0.0111	rs16892695	8	120591283	q24.12
SNP_A-2075826	G	G	346	58	320	86	6.455	0.0111	rs9849434	3	10108710	p25.3
SNP_A-2176840	C	C	358	12	405	3	6.455	0.0111	rs10980080	9	96844302	q22.33
SNP_A-2197906	C	T	218	180	220	186	6.456	0.0111	rs12656759	5	131395509	q23.3
SNP_A-2215672	T	T	373	43	309	61	6.451	0.0111	rs12480690	20	19703487	p11.23
SNP_A-2227093	A	A	339	53	361	31	6.453	0.0111	rs1243698	14	20079312	q11.2
SNP_A-2152469	C	C	409	3	362	12	6.443	0.0111	rs6084677	20	4195774	p13
SNP_A-2118184	C	C	202	160	268	146	6.453	0.0111	rs2866104	15	77866999	q25.1
SNP_A-2132361	T	T	344	20	388	8	6.452	0.0111	rs17297964	4	121107375	q27
SNP_A-1858071	C	C	400	12	375	27	6.454	0.0111	rs11975441	7	155769605	q36.3
SNP_A-1850622	A	A	343	3	360	14	6.45	0.0111	rs11219282	11	98679357	q22.1
SNP_A-1839836	C	C	361	25	355	47	6.45	0.0111	rs2240567	17	12760195	p12
SNP_A-1819136	G	G	347	15	403	5	6.456	0.0111	rs260472	19	63499569	q13.43
SNP_A-1804235	C	C	358	2	380	12	6.449	0.0111	rs6914301	6	148403026	q24.3
SNP_A-1727933	G	T	149	113	178	154	6.442	0.0111	rs9312156	4	67381245	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946141	A	A	303	35	358	20	6.453	0.0111	rs17067132	3	39977032	p22.1
SNP_A-1918446	T	T	360	0	387	7	6.456	0.0111	rs16921826	9	641039	p24.3
SNP_A-1916384	C	C	344	22	406	10	6.455	0.0111	rs10777950	12	97756848	q23.1
SNP_A-1906803	C	C	315	33	381	19	6.444	0.0111	rs6434429	2	191621052	q32.2
SNP_A-1932989	T	T	313	17	389	7	6.448	0.0111	rs7906567	10	122912448	q26.12
SNP_A-1924702	A	A	233	135	225	189	6.456	0.0111	rs9866061	3	195056563	q29
SNP_A-1924780	G	G	384	6	416	0	6.448	0.0111	rs16918969	11	92845921	q21
SNP_A-1904146	C	C	334	44	389	27	6.451	0.0111	rs17081391	6	119898516	q22.31
SNP_A-1881040	G	G	360	0	387	7	6.456	0.0111	rs17019094	4	93384157	q22.2
SNP_A-1880709	A	A	257	149	277	109	6.45	0.0111	rs7026382	9	86107515	q21.33
SNP_A-1900138	T	T	322	44	327	75	6.441	0.0112	rs1586733	4	112606275	q25
SNP_A-1932694	C	C	411	9	417	1	6.439	0.0112	rs2461463	2	128424293	q14.3
SNP_A-1905726	G	G	340	8	370	24	6.441	0.0112	rs1453407	2	169116896	q24.3
SNP_A-1909471	C	C	316	82	272	108	6.437	0.0112	rs848577	1	12772106	p36.21
SNP_A-1935423	G	G	326	36	387	21	6.441	0.0112	rs1192285	2	84838142	p11.2
SNP_A-1980498	C	C	340	26	401	13	6.425	0.0112	rs275466	5	6892751	p15.31
SNP_A-1716409	A	A	268	120	248	162	6.429	0.0112	rs837846	2	130137131	q21.1
SNP_A-1782343	A	A	376	6	406	0	6.426	0.0112	---	5	55375458	q11.2
SNP_A-1712351	G	G	395	1	389	9	6.441	0.0112	rs2193931	5	150686290	q33.1
SNP_A-1795403	C	C	261	107	320	86	6.426	0.0112	rs7556550	1	89640065	p22.2
SNP_A-1790436	C	A	230	174	211	195	6.433	0.0112	rs2204221	8	123765319	q24.13
SNP_A-1858935	A	A	259	77	241	111	6.428	0.0112	rs1468115	17	47147884	q21.33
SNP_A-2154019	T	T	280	24	363	13	6.433	0.0112	rs7980126	12	85218697	q21.32
SNP_A-2159419	G	G	326	18	379	7	6.429	0.0112	rs3864014	3	77951152	p12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2195182	C	C	379	13	363	29	6.44	0.0112	---	5	176538691	q35.3
SNP_A-2187167	C	C	381	11	394	2	6.429	0.0112	rs10115550	9	125287788	q33.3
SNP_A-2175616	A	A	400	2	387	11	6.426	0.0112	rs610165	11	58237159	q12.1
SNP_A-2180334	A	A	336	48	284	68	6.43	0.0112	rs17133402	7	137273629	q34
SNP_A-2179858	C	C	278	140	310	106	6.436	0.0112	rs7005778	8	124656688	q24.13
SNP_A-2071476	C	C	272	56	340	40	6.438	0.0112	rs7591311	2	113412759	q13
SNP_A-2063003	C	C	283	59	341	41	6.441	0.0112	rs658446	18	53303141	q21.31
SNP_A-2060922	G	G	381	11	394	2	6.429	0.0112	rs17275444	2	72236000	p13.2
SNP_A-2080770	G	G	226	124	223	179	6.439	0.0112	rs295507	3	140764884	q23
SNP_A-2272810	T	T	322	16	388	6	6.434	0.0112	rs7636346	3	132913539	q22.1
SNP_A-2274056	C	C	212	130	200	180	6.432	0.0112	rs671946	11	73819188	q13.4
SNP_A-2276228	C	T	182	170	218	160	6.435	0.0112	rs1489912	3	160702818	q25.33
SNP_A-2276122	G	G	228	114	228	168	6.424	1.13E-02	rs4443226	4	6042701	p16.1
SNP_A-2283355	T	T	420	0	390	6	6.411	1.13E-02	rs613284	19	5432206	p13.3
SNP_A-2262126	C	C	344	18	399	7	6.412	1.13E-02	rs12104712	2	82556606	p12
SNP_A-2245465	T	T	294	62	349	43	6.425	1.13E-02	rs10810234	9	14748222	p22.3
SNP_A-2249745	G	G	236	134	299	115	6.419	1.13E-02	rs13043430	20	43064029	q13.12
SNP_A-2289966	C	C	298	32	271	53	6.415	1.13E-02	rs7114324	11	80330703	q14.1
SNP_A-2053900	G	G	360	0	389	7	6.423	1.13E-02	rs12341262	9	69542678	q21.11
SNP_A-2063741	G	G	313	31	293	53	6.416	1.13E-02	rs11062193	12	2310981	p13.33
SNP_A-2074451	A	A	188	176	250	162	6.412	1.13E-02	rs6558023	8	27787698	p21.1
SNP_A-2187806	C	C	283	55	269	85	6.417	1.13E-02	rs156661	5	115288214	q23.1
SNP_A-2188811	C	C	351	1	388	10	6.419	1.13E-02	rs10424037	19	39909324	q13.11
SNP_A-2198822	C	C	247	121	303	99	6.413	1.13E-02	rs1381488	8	108032486	q23.1
SNP_A-2217842	C	C	258	104	326	86	6.42	1.13E-02	rs12057038	9	29491683	p21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2206716	T	T	377	5	350	16	6.425	1.13E-02	rs16923584	8	59663937	q12.1
SNP_A-2153493	C	C	240	116	240	170	6.421	1.13E-02	rs367906	2	7090770	p25.1
SNP_A-2141728	C	C	350	8	403	1	6.421	1.13E-02	rs16913556	9	28710007	p21.1
SNP_A-2111759	T	T	330	50	384	32	6.42	1.13E-02	rs9320843	6	122229001	q22.31
SNP_A-1858546	T	T	324	32	388	18	6.42	1.13E-02	rs515034	1	198294310	q32.1
SNP_A-1868615	T	T	338	6	341	19	6.413	1.13E-02	rs17129609	11	96161663	q21
SNP_A-1834977	C	C	333	31	395	17	6.419	1.13E-02	rs2799347	13	52538172	q14.3
SNP_A-1812836	A	A	313	37	305	63	6.416	1.13E-02	rs2464260	12	125957754	q24.32
SNP_A-1958318	T	T	329	27	361	55	6.421	1.13E-02	rs732998	10	104887891	q24.33
SNP_A-1909082	G	G	235	133	224	184	6.424	1.13E-02	rs454481	3	140765401	q23
SNP_A-1907448	T	T	314	18	365	7	6.419	1.13E-02	rs290424	20	52104591	q13.2
SNP_A-1924549	T	T	294	58	312	98	6.414	1.13E-02	rs8083078	18	9140141	p11.22
SNP_A-1900558	G	G	272	98	271	145	6.422	1.13E-02	rs9395414	6	48947102	p12.3
SNP_A-1892709	T	T	346	18	401	7	6.403	0.0114	rs12089508	1	101940468	p21.2
SNP_A-1925583	T	T	363	21	386	8	6.406	0.0114	rs10865931	3	43191285	p22.1
SNP_A-1925879	T	T	368	22	327	39	6.401	0.0114	rs16856199	1	228460847	q42.2
SNP_A-1935636	C	C	283	79	351	61	6.404	0.0114	rs17331064	7	48632933	p12.3
SNP_A-1933837	C	C	265	117	320	94	6.402	0.0114	rs10777200	12	88675408	q21.33
SNP_A-1965580	G	G	296	74	359	55	6.409	0.0114	rs2292387	2	160560229	q24.2
SNP_A-1962907	T	T	204	158	265	141	6.401	0.0114	rs9309065	2	41299772	p22.1
SNP_A-1812851	T	T	321	43	383	27	6.406	0.0114	rs2145321	6	125630589	q22.31
SNP_A-1806030	G	G	271	19	351	9	6.397	0.0114	rs2280442	15	79027872	q25.1
SNP_A-1792336	G	G	188	174	250	160	6.403	0.0114	rs11694307	2	175412017	q31.1
SNP_A-1700915	G	G	345	43	361	23	6.403	0.0114	rs1391962	3	5312049	p26.1
SNP_A-1838832	C	C	312	58	321	95	6.406	0.0114	rs2589845	4	124966226	q28.1
SNP_A-2118101	G	G	364	0	395	7	6.397	0.0114	rs533522	18	70485643	q22.3
SNP_A-2148321	A	A	300	114	237	133	6.403	0.0114	rs11121821	1	11745110	p36.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2211589	C	C	318	50	263	69	6.406	0.0114	rs1564146	11	41659007	p12
SNP_A-2227187	A	A	412	4	405	15	6.409	0.0114	rs16999224	22	37401087	q13.1
SNP_A-2172366	A	A	285	59	357	43	6.406	0.0114	rs1923790	9	87162008	q21.33
SNP_A-2068732	G	G	316	12	308	28	6.407	0.0114	rs3737915	1	175623040	q25.2
SNP_A-2053539	C	C	360	8	413	1	6.395	0.0114	rs2572890	8	143903360	q24.3
SNP_A-2093153	G	G	308	50	331	29	6.405	0.0114	rs10116601	9	115690992	q33.1
SNP_A-2095545	A	A	357	7	386	22	6.404	0.0114	rs6037743	20	3996739	p13
SNP_A-2013517	T	T	267	103	265	151	6.408	0.0114	rs6472612	8	72807404	q13.3
SNP_A-2291118	G	G	357	25	389	11	6.406	0.0114	rs17105036	14	36224345	q13.3
SNP_A-2306401	T	T	190	172	251	157	6.396	0.0114	rs12682875	9	88767754	q22.1
SNP_A-2236687	T	T	287	75	281	113	6.401	0.0114	rs11051008	12	30686430	p11.21
SNP_A-2238992	T	T	260	78	309	57	6.383	0.0115	rs3104888	8	96690344	q22.1
SNP_A-2262099	T	T	418	0	390	6	6.38	0.0115	rs278213	19	36082303	q12
SNP_A-2262166	G	G	418	0	390	6	6.38	0.0115	rs17645358	15	90532323	q26.1
SNP_A-2303364	A	A	256	114	309	91	6.393	0.0115	rs11158445	14	62225157	q23.2
SNP_A-2303149	A	A	365	21	308	36	6.38	0.0115	rs17105811	14	76991802	q24.3
SNP_A-2006122	C	C	278	70	347	53	6.383	0.0115	rs6735529	2	8564982	p25.1
SNP_A-1997622	G	G	282	26	352	14	6.385	0.0115	rs17793873	9	109323876	q31.3
SNP_A-2003754	-	A	206	206	241	169	6.386	0.0115	rs8017164	14	53885533	q22.2
SNP_A-2032531	T	T	354	0	385	7	6.381	0.0115	rs6823074	4	129998199	q28.2
SNP_A-2037024	G	G	316	48	315	79	6.391	0.0115	rs11043936	12	18252910	p12.3
SNP_A-2046521	T	T	356	0	387	7	6.384	0.0115	---	4	99063254	q22.3
SNP_A-2093279	A	A	390	6	418	0	6.38	0.0115	rs1194040	12	125787579	q24.32
SNP_A-2201186	C	C	352	4	372	16	6.388	0.0115	rs7920038	10	22694436	p12.2
SNP_A-2146505	T	T	319	39	329	69	6.389	0.0115	rs17573792	9	119249888	q33.1
SNP_A-2142318	T	T	327	27	390	14	6.387	0.0115	rs9494187	6	135616823	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1843718	T	T	255	103	258	154	6.383	0.0115	rs17237642	5	9160918	p15.31
SNP_A-1819162	A	A	248	172	282	136	6.384	0.0115	rs1594050	16	75855148	q23.1
SNP_A-1869637	A	A	358	0	389	7	6.388	0.0115	rs16892371	5	63224996	q12.3
SNP_A-1855653	G	G	350	8	401	1	6.382	0.0115	rs1547310	6	11807938	p24.1
SNP_A-1709947	C	C	245	101	323	87	6.382	0.0115	rs3109798	3	152999894	q25.1
SNP_A-1680236	A	G	190	170	231	179	6.387	0.0115	rs10484702	6	145508627	q24.3
SNP_A-1670546	T	T	211	127	282	114	6.383	0.0115	rs4128620	11	133015280	q25
SNP_A-1654995	C	C	388	2	377	11	6.384	0.0115	rs10485135	6	54838797	p12.1
SNP_A-1786134	G	G	379	13	389	3	6.38	0.0115	rs9628174	22	49251680	q13.33
SNP_A-1972625	A	A	263	115	245	157	6.391	0.0115	rs11715034	3	51384640	p21.31
SNP_A-1930858	T	T	376	40	345	63	6.392	0.0115	rs17033243	2	106849924	q12.2
SNP_A-1929533	A	A	327	79	345	51	6.389	0.0115	rs4832849	4	36791715	p14
SNP_A-1905766	A	A	374	40	393	21	6.389	0.0115	rs10813049	9	29291676	p21.1
SNP_A-1912886	C	C	220	140	282	122	6.381	0.0115	rs2451576	6	77180387	q14.1
SNP_A-1890600	A	A	281	53	280	86	6.387	0.0115	rs11622790	14	57546588	q23.1
SNP_A-1889673	C	C	272	92	275	139	6.392	0.0115	rs1282970	3	113049928	q13.2
SNP_A-1887786	C	C	229	95	243	63	6.387	0.0115	rs6981769	8	23263573	p21.3
SNP_A-1879466	C	C	341	61	352	36	6.372	1.16E-02	rs9931907	16	79780797	q23.2
SNP_A-1895715	A	A	355	3	376	14	6.364	1.16E-02	rs3011203	1	38637076	p34.3
SNP_A-1899796	T	T	333	35	348	64	6.364	1.16E-02	rs17127810	1	85666530	p22.3
SNP_A-1899342	T	T	346	18	361	39	6.373	1.16E-02	rs686394	12	9966342	p13.31
SNP_A-1897785	T	T	292	16	304	36	6.369	1.16E-02	rs526169	4	173127007	q34.1
SNP_A-1969152	A	A	254	162	290	128	6.364	1.16E-02	rs2087861	21	17573647	q21.1
SNP_A-1790641	T	T	348	20	390	8	6.368	1.16E-02	rs7761315	6	81835757	q14.1
SNP_A-1795587	G	G	298	40	324	74	6.378	1.16E-02	rs6436669	2	227938680	q36.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783150	G	G	382	4	348	14	6.376	1.16E-02	rs6563631	13	38192730	q13.3
SNP_A-1725264	A	A	357	5	380	18	6.375	1.16E-02	rs7299616	12	81312239	q21.31
SNP_A-1847671	C	C	328	80	296	110	6.373	1.16E-02	rs12258754	10	90707272	q23.31
SNP_A-1865793	T	T	346	16	373	37	6.375	1.16E-02	rs1982916	4	177009216	q34.2
SNP_A-1840729	T	T	405	5	378	16	6.377	1.16E-02	rs6924008	6	11576045	p24.2
SNP_A-2157284	G	G	358	8	392	24	6.37	1.16E-02	rs4440700	9	38557913	p13.2
SNP_A-2115847	T	T	422	0	394	6	6.377	1.16E-02	rs9944374	16	27290062	p12.1
SNP_A-2113382	A	A	358	8	392	24	6.37	1.16E-02	rs17320405	13	22170244	q12.11
SNP_A-2127973	G	G	282	62	328	42	6.377	1.16E-02	rs12347113	9	117376115	q33.1
SNP_A-2205334	A	A	245	117	311	99	6.375	1.16E-02	rs4738897	8	62566348	q12.3
SNP_A-2207402	G	G	305	59	309	95	6.376	1.16E-02	rs6530994	8	12739903	p22
SNP_A-2214537	G	G	374	22	333	39	6.372	1.16E-02	rs395651	19	6441179	p13.3
SNP_A-2183402	T	T	219	131	216	188	6.371	1.16E-02	rs175102	11	60567333	q12.2
SNP_A-2088975	G	G	209	157	269	139	6.366	1.16E-02	rs9948507	18	62062341	q22.1
SNP_A-2058427	T	T	277	91	279	137	6.373	1.16E-02	rs7335730	13	105903870	q33.3
SNP_A-2047103	A	A	347	19	367	41	6.367	1.16E-02	rs17706574	8	115362153	q23.3
SNP_A-2044724	G	G	361	13	347	29	6.367	1.16E-02	rs6585580	10	121874092	q26.12
SNP_A-2040696	T	T	347	61	358	36	6.372	1.16E-02	rs2954759	17	15281908	p12
SNP_A-2026895	T	T	312	70	280	98	6.376	1.16E-02	rs6716692	2	151577947	q23.3
SNP_A-2021892	A	A	220	202	254	164	6.365	1.16E-02	rs6987643	8	118097727	q24.11
SNP_A-2008516	T	T	275	145	237	179	6.369	1.16E-02	rs4858753	3	20091908	p24.3
SNP_A-2008513	G	G	376	18	394	6	6.376	1.16E-02	rs7614599	3	19570414	p24.3
SNP_A-2308982	T	T	310	60	372	42	6.363	1.16E-02	rs3111577	16	83193286	q24.1
SNP_A-2314985	A	A	214	124	203	173	6.37	1.16E-02	rs6019639	20	35658300	q11.23
SNP_A-2233549	G	G	403	1	352	8	6.377	1.16E-02	rs4958224	5	133169328	q31.1
SNP_A-2234648	A	A	308	54	355	35	6.354	0.0117	rs1436573	4	96964543	q22.3
SNP_A-2282699	C	C	362	8	413	1	6.351	0.0117	rs11245246	10	126184034	q26.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2306170	C	C	346	22	370	46	6.36	0.0117	rs2956830	8	50608009	q11.21
SNP_A-1993647	A	A	298	24	310	48	6.349	0.0117	rs10112728	8	68736913	q13.2
SNP_A-2060827	G	G	336	22	394	10	6.354	0.0117	rs2471509	12	86961907	q21.32
SNP_A-2065780	G	G	304	8	332	24	6.362	0.0117	---	10	31029114	p11.23
SNP_A-2104577	A	A	220	134	286	118	6.354	0.0117	rs16890717	5	33121441	p13.3
SNP_A-2099729	C	C	344	72	316	102	6.356	0.0117	rs873745	2	45104824	p21
SNP_A-2099749	A	A	346	4	341	15	6.354	0.0117	rs16960505	15	46107025	q21.1
SNP_A-2197869	T	T	280	36	274	62	6.355	0.0117	rs7207107	17	14768612	p12
SNP_A-2193319	A	A	276	28	293	55	6.351	0.0117	rs3901982	7	18602015	p21.1
SNP_A-2169423	C	C	290	54	351	37	6.359	0.0117	rs10754873	1	15013961	p36.21
SNP_A-2180131	C	C	304	94	339	67	6.354	0.0117	rs6449959	5	67553319	q13.1
SNP_A-2209502	T	T	358	16	383	5	6.35	0.0117	rs2660353	1	25186852	p36.11
SNP_A-2138341	C	C	384	6	410	0	6.355	0.0117	rs6684175	1	208164770	q32.3
SNP_A-2152405	A	A	317	23	354	10	6.351	0.0117	---	13	68179827	q21.33
SNP_A-1839895	C	C	274	16	363	7	6.353	0.0117	rs2058090	17	12814209	p12
SNP_A-1823954	G	G	347	9	384	26	6.355	0.0117	rs1990016	7	16122404	p21.1
SNP_A-1825165	G	C	225	181	221	193	6.352	0.0117	rs8050741	16	81088547	q23.3
SNP_A-1866815	A	G	200	156	212	188	6.354	0.0117	rs1393027	1	207564694	q32.2
SNP_A-1852493	T	T	348	6	311	17	6.356	0.0117	rs2470592	15	50055305	q21.2
SNP_A-1805942	T	T	388	6	414	0	6.352	0.0117	rs17049831	2	59065410	p16.1
SNP_A-1802257	C	C	233	137	225	191	6.36	0.0117	rs9818840	3	195056633	q29
SNP_A-1972549	A	A	346	2	337	11	6.349	0.0117	rs17076900	3	44675111	p21.32
SNP_A-1979887	A	A	358	8	409	1	6.361	0.0117	rs3846271	4	171451123	q33
SNP_A-1988735	C	C	300	62	362	44	6.363	0.0117	rs1285452	7	90066132	p21.3
SNP_A-1954496	T	C	185	173	231	171	6.351	0.0117	rs6828210	4	80300802	q21.21
SNP_A-1951888	C	C	338	26	397	13	6.358	0.0117	rs259474	1	215148378	q41
SNP_A-1887843	C	C	213	167	257	139	6.354	0.0117	rs10876311	12	51273263	q13.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1882033	A	A	347	67	361	41	6.361	0.0117	rs7381811	6	6551226	p25.1
SNP_A-1912582	C	C	406	0	380	6	6.359	0.0117	rs9379904	6	26715651	p22.1
SNP_A-1928685	T	T	337	21	320	40	6.352	0.0117	rs4296524	22	30437634	q12.2
SNP_A-1888521	C	C	337	83	359	55	6.334	0.0118	rs2233967	6	31188807	p21.33
SNP_A-1988090	C	C	295	73	300	114	6.347	0.0118	rs1408505	6	150563377	q25.1
SNP_A-1987414	G	G	227	125	223	179	6.34	0.0118	rs7752256	6	120184114	q22.31
SNP_A-1986506	T	T	364	0	399	7	6.333	0.0118	rs2489350	1	221457327	q42.12
SNP_A-1968360	A	A	264	54	335	39	6.345	0.0118	rs17236831	20	38352341	q12
SNP_A-1802632	C	C	352	8	401	1	6.337	0.0118	rs12348671	9	2062470	p24.3
SNP_A-1785493	T	T	418	0	392	6	6.348	0.0118	rs6780716	3	27086908	p24.2
SNP_A-1714773	A	A	311	69	299	103	6.343	0.0118	rs10515812	5	159975706	q34
SNP_A-1721155	C	C	247	27	291	59	6.343	0.0118	rs10513436	3	153974577	q25.2
SNP_A-1844725	A	A	328	4	348	16	6.334	0.0118	rs17129660	11	96230216	q21
SNP_A-1871469	T	T	182	166	241	151	6.345	0.0118	rs11720160	3	8492932	p25.3
SNP_A-1826449	G	G	420	0	394	6	6.346	0.0118	rs11903672	2	53031259	p16.2
SNP_A-1835378	C	C	418	0	392	6	6.348	0.0118	rs328132	18	42517142	q21.1
SNP_A-1829426	A	A	202	144	264	128	6.348	0.0118	rs3768123	1	233225510	q43
SNP_A-2151682	C	C	420	0	394	6	6.346	0.0118	---	8	24666280	p21.2
SNP_A-2109925	C	C	318	60	300	90	6.338	0.0118	rs16899396	5	23340668	p14.2
SNP_A-2118946	G	G	230	126	219	175	6.337	0.0118	rs9594602	13	41110431	q14.11
SNP_A-2208711	A	A	385	11	394	2	6.335	0.0118	---	8	115823767	q23.3
SNP_A-2175050	A	A	256	144	292	112	6.345	0.0118	rs6017443	20	42961623	q13.12
SNP_A-2177259	G	G	359	7	390	22	6.344	0.0118	rs11127383	2	4742135	p25.2
SNP_A-2101750	T	T	194	170	254	154	6.339	0.0118	rs1463812	1	75949482	p31.1
SNP_A-2096713	A	A	354	2	380	12	6.346	0.0118	rs12271374	11	41453266	p12
SNP_A-2051602	G	G	245	167	285	135	6.333	0.0118	rs262354	7	103019119	q22.1
SNP_A-2004663	T	T	282	36	291	65	6.346	0.0118	rs11191580	10	104896201	q24.33
SNP_A-2291099	T	T	422	0	396	6	6.345	0.0118	rs16944153	12	113282577	q24.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2280944	A	A	370	0	405	7	6.343	0.0118	rs933937	11	12482035	p15.3
SNP_A-2276573	A	A	226	112	211	155	6.336	0.0118	rs2183081	14	54406501	q22.2
SNP_A-2259352	G	G	309	77	352	54	6.334	0.0118	rs11232103	11	79770063	q14.1
SNP_A-2234575	T	T	246	148	210	182	6.34	0.0118	rs1076915	22	48152289	q13.33
SNP_A-2236430	C	C	360	10	387	27	6.337	0.0118	rs10912092	1	184241145	q31.1
SNP_A-2245207	G	G	327	81	289	109	6.347	0.0118	rs10924862	1	243361749	q44
SNP_A-2243231	G	G	408	4	374	14	6.32	1.19E-02	rs1320448	10	105836064	q25.1
SNP_A-2252863	A	A	358	8	407	1	6.323	1.19E-02	rs7783464	7	7807665	p21.3
SNP_A-2254454	A	C	212	150	175	169	6.321	1.19E-02	rs3934973	2	239504952	q37.3
SNP_A-2232198	C	C	303	59	370	42	6.328	1.19E-02	rs2967874	16	83193225	q24.1
SNP_A-2307939	A	G	171	155	220	166	6.33	1.19E-02	rs6138575	20	25386952	p11.21
SNP_A-2014140	G	G	412	0	388	6	6.321	1.19E-02	rs492423	9	22754293	p21.3
SNP_A-2026100	A	A	289	131	320	98	6.329	1.19E-02	rs12127052	1	48293530	p33
SNP_A-2029737	G	G	412	0	388	6	6.321	1.19E-02	rs466456	22	16979683	q11.21
SNP_A-2029020	T	T	294	60	290	94	6.325	1.19E-02	rs843236	2	156309337	q24.1
SNP_A-2041629	C	C	380	22	359	41	6.322	1.19E-02	rs705575	1	64488278	p31.3
SNP_A-2035999	A	A	303	59	318	98	6.333	1.19E-02	rs9916431	17	59670386	q23.3
SNP_A-2054062	C	C	415	3	407	13	6.323	1.19E-02	rs1956681	14	57309830	q23.1
SNP_A-2090856	G	G	327	55	333	31	6.322	1.19E-02	rs4887606	16	34802728	p11.1
SNP_A-2079374	C	C	327	11	403	3	6.322	1.19E-02	rs238157	20	47289639	q13.13
SNP_A-2083422	C	C	276	40	335	25	6.322	1.19E-02	rs16862047	3	188593871	q27.3
SNP_A-2192637	T	T	399	23	374	42	6.32	1.19E-02	rs2048667	7	131218794	q32.3
SNP_A-2227822	G	G	200	126	166	156	6.326	1.19E-02	rs6820463	4	143701210	q31.21
SNP_A-2146188	C	C	335	15	385	5	6.329	1.19E-02	rs2158559	7	41081938	p14.1
SNP_A-2139959	C	C	228	106	231	159	6.326	1.19E-02	rs13210170	6	87247192	q14.3
SNP_A-1816868	G	G	322	16	316	34	6.329	1.19E-02	rs1643042	7	133470719	q33
SNP_A-1844679	A	A	361	1	404	10	6.324	1.19E-02	rs7253368	19	2736200	p13.3
SNP_A-1784658	G	G	276	30	324	16	6.329	1.19E-02	rs615783	15	69205557	q23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1986711	T	T	281	85	331	63	6.332	1.19E-02	rs4144150	6	85456857	q14.3
SNP_A-1955976	C	C	363	1	406	10	6.33	1.19E-02	rs2293441	12	52403532	q13.13
SNP_A-1933831	A	A	343	23	363	47	6.321	1.19E-02	rs2194119	4	78625459	q21.1
SNP_A-1939527	G	G	334	10	380	2	6.325	1.19E-02	rs4762794	12	19731735	p12.3
SNP_A-1894659	A	A	197	147	256	130	6.332	1.19E-02	rs6994734	8	6256850	p23.1
SNP_A-1926990	T	T	389	21	361	39	6.323	1.19E-02	rs30778	16	8888453	p13.2
SNP_A-1927771	G	G	213	193	252	160	6.312	0.012	rs2242193	1	151808576	q22
SNP_A-1932860	C	C	323	35	378	20	6.307	0.012	rs11682473	2	108487227	q12.3
SNP_A-1908122	A	A	299	57	348	38	6.308	0.012	rs9575502	13	83482367	q31.1
SNP_A-1881548	C	C	369	37	389	19	6.309	0.012	rs4561713	2	137275644	q21.3
SNP_A-1946588	C	C	335	85	298	114	6.313	0.012	rs11037036	11	42701654	p12
SNP_A-1948976	A	A	240	106	319	93	6.315	0.012	rs9995910	4	113412895	q25
SNP_A-1981100	C	C	370	0	407	7	6.312	0.012	rs1732944	5	30941353	p13.3
SNP_A-1982840	G	G	302	46	313	79	6.315	0.012	rs286809	5	107486536	q21.3
SNP_A-1982173	C	C	354	10	402	2	6.315	0.012	rs17748061	5	75867612	q13.3
SNP_A-1972659	G	G	422	0	398	6	6.313	0.012	rs358057	3	55040751	p14.3
SNP_A-1973829	G	G	234	118	308	104	6.313	0.012	rs697957	3	109190443	q13.12
SNP_A-1780969	G	G	392	0	370	6	6.305	0.012	rs16914081	8	51027783	q11.21
SNP_A-1677824	T	T	388	6	372	18	6.317	0.012	rs1005427	2	39805765	p22.1
SNP_A-1807120	G	G	282	84	322	60	6.31	0.012	rs6016360	20	38529666	q12
SNP_A-1862494	A	A	304	20	340	8	6.306	0.012	rs6014478	20	53766969	q13.31
SNP_A-1829297	G	G	335	31	395	17	6.317	0.012	rs11127139	2	28383476	p23.2
SNP_A-1831714	A	A	331	33	352	62	6.311	0.012	rs1516733	4	104608434	q24
SNP_A-1833243	C	C	314	16	339	37	6.307	0.012	---	17	2093142	p13.3
SNP_A-1840451	A	A	254	110	247	157	6.305	0.012	rs2000234	1	186793151	q31.1
SNP_A-1842559	T	T	295	121	257	153	6.31	0.012	rs7968121	12	98739347	q23.1
SNP_A-2141601	G	G	352	0	387	7	6.313	0.012	rs1805085	2	190752666	q32.2
SNP_A-2135782	A	A	329	15	340	34	6.306	0.012	rs2303732	5	43738644	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134364	G	G	336	78	364	52	6.315	0.012	rs6739715	2	139769167	q22.1
SNP_A-2225814	T	T	311	7	409	1	6.313	0.012	rs237712	20	47359776	q13.13
SNP_A-2222747	A	A	242	116	229	161	6.312	0.012	rs2584859	11	56964023	q12.1
SNP_A-2214450	T	T	326	34	394	20	6.315	0.012	rs16919819	12	32422806	p11.21
SNP_A-2207280	T	T	220	164	273	141	6.313	0.012	rs10879658	12	72376145	q21.1
SNP_A-2171098	G	G	383	21	404	8	6.31	0.012	rs17115612	14	44358756	q21.2
SNP_A-2174021	C	C	304	64	290	96	6.304	0.012	rs2767006	9	110673051	q31.3
SNP_A-2049973	G	G	422	0	398	6	6.313	0.012	rs4012230	10	50181630	q11.23
SNP_A-2067170	G	G	242	156	257	113	6.312	0.012	rs1225003	3	133109903	q22.1
SNP_A-2071468	C	C	269	91	332	72	6.306	0.012	rs17007298	3	20664340	p24.3
SNP_A-2010614	A	A	344	4	366	16	6.312	0.012	rs2964408	5	5310233	p15.32
SNP_A-2291569	C	C	185	149	248	136	6.308	0.012	rs6441502	3	163700530	q26.1
SNP_A-2298975	T	T	241	119	236	170	6.313	0.012	rs12276840	11	131853608	q25
SNP_A-2233720	G	G	344	22	402	10	6.312	0.012	rs11097893	4	106832696	q24
SNP_A-2227978	G	G	287	123	308	88	6.306	0.012	rs10735516	1	9441270	p36.22
SNP_A-2274365	G	G	339	13	402	4	6.306	0.012	---	9	13582277	p23
SNP_A-2269215	C	C	280	68	306	44	6.291	0.0121	rs11727057	4	24722700	p15.2
SNP_A-2230582	T	T	281	49	267	77	6.292	0.0121	rs31328	5	110805439	q22.1
SNP_A-2246853	G	G	294	72	360	54	6.302	0.0121	rs16874509	4	23672644	p15.2
SNP_A-2306054	G	G	297	29	314	56	6.293	0.0121	rs2254410	10	49908361	q11.23
SNP_A-2012689	C	C	321	47	325	25	6.3	0.0121	rs726473	7	80676731	q21.11
SNP_A-2029239	C	C	286	74	335	53	6.299	0.0121	rs271234	5	53110794	q11.2
SNP_A-2027293	G	G	348	4	345	15	6.292	0.0121	rs1957068	4	75101940	q13.3
SNP_A-2077046	G	G	315	5	400	0	6.294	0.0121	rs17052115	5	174930871	q35.2
SNP_A-2050044	A	A	297	71	363	53	6.298	0.0121	rs4868356	5	1735000372	q35.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181948	A	A	247	119	310	100	6.299	0.0121	rs9394115	6	11601590	p24.2
SNP_A-2182590	C	C	369	19	371	39	6.3	0.0121	rs17541655	12	39477383	q12
SNP_A-2202643	C	T	185	181	243	173	6.297	0.0121	rs11682163	2	3242915	p25.3
SNP_A-2112487	A	G	184	182	243	171	6.301	0.0121	rs7002237	8	18748794	p22
SNP_A-2141740	G	G	306	36	253	53	6.292	0.0121	rs10876831	12	54290778	q13.2
SNP_A-2146390	G	G	290	80	292	122	6.29	0.0121	rs930362	18	46377759	q21.1
SNP_A-1823609	T	T	344	22	298	38	6.292	0.0121	rs2117875	3	24561608	p24.2
SNP_A-1865163	G	G	390	6	412	0	6.289	0.0121	rs9902404	17	36854618	q21.2
SNP_A-1870109	C	T	157	139	211	161	6.297	0.0121	rs17294094	19	53412738	q13.32
SNP_A-1845429	C	C	245	107	297	85	6.294	0.0121	---	4	59453273	q12
SNP_A-1976478	T	T	379	29	356	50	6.297	0.0121	rs17191740	4	23840309	p15.2
SNP_A-1955973	C	C	267	95	284	64	6.295	0.0121	rs17035305	1	10550771	p36.22
SNP_A-1896836	A	A	313	95	335	65	6.293	0.0121	rs11630050	15	79353350	q25.1
SNP_A-1902111	G	G	253	115	239	159	6.299	0.0121	rs11027190	11	23364379	p14.3
SNP_A-1904109	C	C	337	19	398	8	6.29	0.0121	rs393130	11	8225525	p15.4
SNP_A-1910293	C	C	354	4	351	15	6.294	0.0121	rs16996862	20	15883216	p12.1
SNP_A-1927907	A	A	348	22	406	10	6.291	0.0121	rs10885916	10	118108810	q25.3
SNP_A-1926848	A	A	234	56	263	101	6.298	0.0121	rs3794679	16	83662089	q24.1
SNP_A-1923981	G	G	347	13	348	30	6.287	1.22E-02	rs1822487	5	112632510	q22.2
SNP_A-1905279	A	A	225	123	203	163	6.275	1.22E-02	rs10766982	11	22699340	p14.3
SNP_A-1898549	G	G	344	18	395	7	6.283	1.22E-02	rs10781905	13	23891574	q12.12
SNP_A-1898937	G	A	185	171	233	175	6.282	1.22E-02	rs12697870	5	76966048	q14.1
SNP_A-1846254	C	C	370	0	409	7	6.282	1.22E-02	rs2720165	12	56762728	q14.1
SNP_A-1824046	C	C	370	0	409	7	6.282	1.22E-02	rs16953995	18	47546484	q21.1
SNP_A-1807050	G	G	339	19	321	37	6.277	1.22E-02	rs11234759	11	86122450	q14.2
SNP_A-1644340	T	T	300	50	375	35	6.283	1.22E-02	rs990364	4	127899480	q28.1
SNP_A-2140559	G	G	311	43	267	63	6.289	1.22E-02	rs11174611	12	61384788	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2160331	T	T	343	21	364	44	6.275	1.22E-02	rs3767208	1	70405752	p31.1
SNP_A-2153920	G	G	296	46	307	79	6.276	1.22E-02	rs17124140	14	51080145	q22.1
SNP_A-2114454	G	G	345	21	364	8	6.288	1.22E-02	rs7102709	11	68598147	q13.3
SNP_A-2120157	A	A	370	0	409	7	6.282	1.22E-02	rs17087995	6	157412544	q25.3
SNP_A-2202344	C	C	331	65	295	91	6.277	1.22E-02	rs4974386	3	109253783	q13.12
SNP_A-2227877	A	A	258	138	282	102	6.284	1.22E-02	rs17197883	16	80080514	q23.2
SNP_A-2177923	G	G	190	176	253	163	6.287	1.22E-02	rs8056534	16	82096406	q23.3
SNP_A-2170156	C	C	320	40	340	72	6.275	1.22E-02	rs7637487	3	61257543	p14.2
SNP_A-2083852	G	G	309	103	275	135	6.277	1.22E-02	rs10787852	10	120422985	q26.11
SNP_A-2082671	A	A	305	29	291	51	6.285	1.22E-02	rs16978228	18	40749431	q12.3
SNP_A-2078683	G	G	329	7	322	20	6.282	1.22E-02	rs6904271	6	109822899	q21
SNP_A-2107475	T	T	267	43	328	28	6.276	1.22E-02	rs17346094	1	7297765	p36.23
SNP_A-2033263	T	A	201	167	224	188	6.282	1.22E-02	rs878469	18	18508034	q11.2
SNP_A-1990182	T	T	346	2	374	12	6.281	1.22E-02	rs3908607	7	75861996	q11.23
SNP_A-1990479	C	C	249	119	315	101	6.281	1.22E-02	rs181060	7	87754507	q21.13
SNP_A-2307023	G	G	294	122	324	90	6.282	1.22E-02	rs10917243	1	22577267	p36.12
SNP_A-2257031	G	G	298	18	343	7	6.28	1.22E-02	rs4730176	7	105815641	q22.3
SNP_A-2262639	G	G	192	176	254	162	6.283	1.22E-02	rs1492308	14	98445322	q32.2
SNP_A-2274631	G	G	349	17	372	38	6.277	1.22E-02	rs9671547	14	20273172	q11.2
SNP_A-2228991	A	A	249	119	312	100	6.261	0.0123	rs1643020	3	8823649	p25.3
SNP_A-2299443	G	G	281	85	344	66	6.266	0.0123	rs10823878	10	73343120	q22.1
SNP_A-2295729	G	G	300	68	305	107	6.271	0.0123	rs2036181	4	27937430	p15.1
SNP_A-1991588	A	-	218	152	207	207	6.261	0.0123	rs2692382	7	144055404	q35
SNP_A-2038530	G	-	218	152	207	207	6.261	0.0123	rs10030625	4	88976905	q22.1
SNP_A-2045151	C	C	345	39	371	21	6.262	0.0123	rs9262545	6	31101041	p21.33
SNP_A-2105977	A	A	332	32	394	18	6.27	0.0123	rs17009913	4	126797754	q28.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2080023	A	A	361	29	394	14	6.272	0.0123	rs11075069	16	12415505	p13.13
SNP_A-2084358	A	A	388	6	408	0	6.26	0.0123	rs7668704	4	5375833	p16.2
SNP_A-2051031	T	T	285	25	349	13	6.264	0.0123	rs16870040	6	93358992	q16.1
SNP_A-2055769	T	T	287	77	348	58	6.262	0.0123	rs7619783	3	21781436	p24.3
SNP_A-2065653	C	C	321	5	406	0	6.27	0.0123	rs10175802	2	29859100	p23.2
SNP_A-2169714	A	A	315	81	273	107	6.269	0.0123	rs12724890	1	44591398	p34.1
SNP_A-2198685	A	A	358	0	397	7	6.26	0.0123	rs11805090	1	66346890	p31.2
SNP_A-2198507	T	T	402	4	370	14	6.274	0.0123	rs16924620	9	105276633	q31.1
SNP_A-2136936	C	C	314	48	380	32	6.273	0.0123	rs286298	19	11656897	p13.2
SNP_A-1785064	G	G	382	6	402	0	6.264	0.0123	rs3828913	6	31573774	p21.33
SNP_A-1794666	G	G	285	67	281	103	6.272	0.0123	rs11028449	11	25114085	p14.3
SNP_A-1828663	G	G	257	41	323	27	6.26	0.0123	rs2200546	9	11827690	p23
SNP_A-1850601	G	G	210	118	216	178	6.266	0.0123	rs7595528	2	197685912	q33.1
SNP_A-1868187	G	G	301	53	283	81	6.267	0.0123	rs11770622	7	45970506	p13
SNP_A-1872309	A	A	214	142	282	128	6.273	0.0123	rs6597290	6	7917675	p24.3
SNP_A-1881990	A	A	404	4	372	14	6.27	0.0123	rs7170301	15	59569160	q22.2
SNP_A-1878021	A	A	331	83	363	57	6.261	0.0123	rs6132261	20	19962955	p11.23
SNP_A-1925674	A	G	201	141	192	188	6.263	0.0123	rs13120745	4	91375323	q22.1
SNP_A-1930966	A	A	251	165	213	199	6.269	0.0123	rs16949181	18	44199534	q21.1
SNP_A-1947573	T	T	372	42	382	22	6.261	0.0123	rs17065626	3	61919155	p14.2
SNP_A-1934352	T	T	312	26	365	13	6.267	0.0123	rs16936752	9	93143245	q22.31
SNP_A-1982052	C	T	219	189	229	187	6.273	0.0123	rs1217744	5	71281566	q13.2
SNP_A-1975240	A	A	337	9	327	23	6.253	0.0124	rs16852423	3	169760531	q26.2
SNP_A-1943139	G	G	358	12	382	30	6.255	0.0124	rs1039011	4	75734476	q13.3
SNP_A-1949495	-	A	178	178	234	162	6.255	0.0124	rs134933	22	25750344	q12.1
SNP_A-1930775	C	C	353	37	341	17	6.257	0.0124	rs11140903	9	85075224	q21.33
SNP_A-1894773	G	G	288	76	354	58	6.258	0.0124	rs2458343	11	105812443	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1791547	T	T	327	5	412	0	6.247	0.0124	rs17135490	7	100735302	q22.1
SNP_A-1806769	C	C	420	0	400	6	6.252	0.0124	rs11144102	9	68725574	q21.11
SNP_A-1814595	A	A	328	92	292	122	6.253	0.0124	rs1735538	3	129574800	q21.3
SNP_A-1780827	C	C	293	57	363	41	6.246	0.0124	rs4586276	13	28787466	q12.3
SNP_A-2135446	T	T	278	24	336	12	6.255	0.0124	rs4416102	18	73293058	q23
SNP_A-2113708	G	G	285	39	331	23	6.249	0.0124	rs12583237	13	31708018	q13.1
SNP_A-2214202	G	G	250	118	313	99	6.251	0.0124	rs3018579	11	98027750	q22.1
SNP_A-2212805	C	C	327	5	412	0	6.247	0.0124	rs1176728	11	113325300	q23.2
SNP_A-2076178	T	T	298	68	300	106	6.25	0.0124	rs964693	4	27923656	p15.1
SNP_A-2035078	T	T	302	104	264	134	6.254	0.0124	rs4269955	11	111719301	q23.1
SNP_A-2021172	A	A	390	16	413	5	6.247	0.0124	rs4326904	13	25376128	q12.13
SNP_A-2012437	A	A	315	7	344	22	6.246	0.0124	rs2697756	11	79653325	q14.1
SNP_A-2016433	G	G	338	12	375	3	6.252	0.0124	rs17393457	21	22744439	q21.1
SNP_A-2008123	C	C	376	16	372	34	6.258	0.0124	rs2214285	11	17337504	p15.1
SNP_A-2308357	T	T	220	144	209	197	6.247	0.0124	rs7427002	3	88860061	p11.1
SNP_A-2311860	C	C	340	16	369	37	6.253	0.0124	rs10426913	19	58472009	q13.42
SNP_A-2275494	A	A	334	0	371	7	6.247	0.0124	rs4892241	18	70386785	q22.3
SNP_A-2283761	C	C	355	59	326	86	6.258	0.0124	rs2029591	3	49621985	p21.31
SNP_A-2258994	T	T	289	27	361	15	6.249	0.0124	rs10401511	19	59112771	q13.42
SNP_A-2259546	G	G	333	87	296	116	6.243	1.25E-02	rs7076752	10	82831675	q22.3
SNP_A-2284332	G	G	373	39	346	62	6.232	1.25E-02	rs11189937	10	100770705	q24.2
SNP_A-2277432	C	C	300	102	326	72	6.232	1.25E-02	rs1743111	14	91190092	q32.12
SNP_A-2233883	G	G	311	27	368	14	6.241	1.25E-02	rs1273882	3	170602184	q26.2
SNP_A-2255634	C	C	346	10	390	2	6.246	1.25E-02	rs4243109	16	73639052	q22.3
SNP_A-2296293	T	T	204	112	243	87	6.243	1.25E-02	---	5	128282795	q23.3
SNP_A-2003858	T	T	209	191	244	156	6.234	1.25E-02	rs10340075	10	91960581	q23.31
SNP_A-2073314	T	C	231	167	207	201	6.238	1.25E-02	rs10447197	5	169560420	q35.1
SNP_A-2060422	T	T	228	158	247	117	6.233	1.25E-02	rs2237637	7	103018549	q22.1
SNP_A-2211137	T	T	252	86	244	126	6.243	1.25E-02	rs3799639	6	166924844	q27

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2208151	G	G	277	115	226	138	6.233	1.25E-02	rs13181236	5	13651086	p15.2
SNP_A-2208872	C	C	282	80	241	105	6.234	1.25E-02	rs12325385	16	8398216	p13.2
SNP_A-2114227	T	T	379	15	380	4	6.242	1.25E-02	rs9596364	13	50252187	q14.3
SNP_A-2121291	A	A	270	60	266	94	6.244	1.25E-02	rs1403503	12	97850981	q23.1
SNP_A-2117575	A	A	371	51	385	29	6.233	1.25E-02	rs16861130	3	114737348	q13.2
SNP_A-2135920	T	T	338	50	314	76	6.243	1.25E-02	rs10832947	11	18556122	p15.1
SNP_A-2133305	G	G	345	25	396	12	6.237	1.25E-02	rs12996371	2	173831278	q31.1
SNP_A-2130307	T	T	351	23	303	39	6.234	1.25E-02	rs12448944	16	75758986	q23.1
SNP_A-2156797	G	G	369	53	336	78	6.24	1.25E-02	rs6715897	2	230165903	q36.3
SNP_A-2156650	A	A	254	112	317	93	6.237	1.25E-02	rs7648599	3	158420918	q25.31
SNP_A-2158225	T	T	414	2	368	10	6.235	1.25E-02	rs1151917	1	147435769	q21.2
SNP_A-1724102	C	C	367	15	319	29	6.243	1.25E-02	rs715562	22	25942449	q12.1
SNP_A-1811357	C	C	290	44	287	73	6.238	1.25E-02	rs17676082	16	64390003	q22.1
SNP_A-1806986	C	C	327	37	316	62	6.239	1.25E-02	rs966811	17	18771012	p11.2
SNP_A-1786575	A	A	295	117	329	87	6.245	1.25E-02	rs1639375	4	23818964	p15.2
SNP_A-1798644	C	C	390	0	372	6	6.239	1.25E-02	rs16920808	8	57674036	q12.1
SNP_A-1866953	C	C	277	31	312	16	6.244	1.25E-02	rs11914797	3	17570621	p24.3
SNP_A-1860811	A	A	234	126	228	178	6.233	1.25E-02	rs10028815	4	79885992	q21.21
SNP_A-1850911	A	A	371	9	361	23	6.241	1.25E-02	rs12157495	22	39198076	q13.1
SNP_A-1855689	A	A	394	4	364	14	6.232	1.25E-02	rs16923179	10	67925329	q21.3
SNP_A-1827187	T	T	300	102	265	133	6.238	1.25E-02	rs10884115	10	106953950	q25.1
SNP_A-1887943	C	C	219	123	279	105	6.241	1.25E-02	rs1918695	2	84813866	p11.2
SNP_A-1908754	T	T	332	26	349	51	6.233	1.25E-02	rs17807127	18	65939579	q22.2
SNP_A-1948127	G	G	297	29	290	52	6.235	1.25E-02	rs17121253	13	112248461	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950154	A	A	277	83	343	65	6.239	1.25E-02	rs17134979	5	100723169	q21.1
SNP_A-1967165	C	C	265	93	264	138	6.242	1.25E-02	rs4674965	2	225747074	q36.2
SNP_A-1963397	G	A	212	190	220	172	6.237	1.25E-02	rs2033018	2	56701551	p16.1
SNP_A-1977704	T	T	328	36	385	21	6.232	1.25E-02	rs17395353	4	78550871	q21.1
SNP_A-1978588	G	G	217	145	208	200	6.233	1.25E-02	rs7679767	4	115491760	q26
SNP_A-1988185	A	A	313	25	360	12	6.236	1.25E-02	rs492982	6	153971268	q25.2
SNP_A-1984801	A	A	364	0	405	7	6.241	1.25E-02	rs1196388	6	2177807	p25.3
SNP_A-1965012	G	G	311	9	394	2	6.229	0.0126	rs7599664	2	137714625	q22.1
SNP_A-1975961	C	C	231	137	296	120	6.226	0.0126	rs4698000	4	9953736	p16.1
SNP_A-1956800	A	A	406	0	388	6	6.229	0.0126	rs17058926	8	28210400	p21.1
SNP_A-1937268	G	G	291	47	351	31	6.224	0.0126	rs2498856	9	106590826	q31.2
SNP_A-1907920	A	A	207	127	208	186	6.221	0.0126	rs9621915	22	33104784	q12.3
SNP_A-1932017	C	C	416	2	370	10	6.23	0.0126	rs752214	1	89980604	p22.2
SNP_A-1921772	G	G	352	20	390	8	6.218	0.0126	rs11908104	20	24977776	p11.21
SNP_A-1826966	C	C	247	83	299	63	6.226	0.0126	rs2819973	6	95355219	q16.1
SNP_A-1822553	A	A	238	104	237	153	6.224	0.0126	rs9315861	13	41204139	q14.11
SNP_A-1832384	A	A	422	0	404	6	6.22	0.0126	rs4238826	16	49740723	q12.1
SNP_A-2142504	T	C	187	141	190	172	6.22	0.0126	rs4757060	11	12799566	p15.2
SNP_A-2121041	C	C	224	138	204	182	6.221	0.0126	rs4745672	9	77727782	q21.2
SNP_A-2207271	T	T	408	10	388	24	6.224	0.0126	rs4899628	14	76471546	q24.3
SNP_A-2187020	G	G	344	52	318	78	6.221	0.0126	rs4879628	9	32878520	p21.1
SNP_A-2061515	G	G	242	104	289	81	6.222	0.0126	rs12670282	7	138259951	q34
SNP_A-2097306	C	C	238	98	233	143	6.228	0.0126	rs2036480	18	73583574	q23
SNP_A-1991357	A	A	370	28	319	45	6.229	0.0126	rs10488433	7	133782560	q33
SNP_A-1993343	G	G	350	12	387	3	6.224	0.0126	rs16921659	8	56434242	q12.1
SNP_A-2023579	A	A	277	59	338	42	6.231	0.0126	rs4240328	4	146614672	q31.21
SNP_A-2034480	A	G	234	184	217	195	6.218	0.0126	rs6442158	3	10218278	p25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253714	T	T	416	0	398	6	6.224	0.0126	rs11815940	10	6004102	p15.1
SNP_A-2241596	T	T	309	47	362	30	6.221	0.0126	rs17156525	7	81900509	q21.11
SNP_A-2244318	T	C	200	158	220	194	6.231	0.0126	rs4719481	7	16607837	p21.1
SNP_A-2233527	C	C	422	0	404	6	6.22	0.0126	rs16845434	1	222452853	q42.12
SNP_A-2287388	C	C	230	164	260	128	6.229	0.0126	rs4778803	15	78611464	q25.1
SNP_A-2281875	C	C	269	55	340	40	6.231	0.0126	rs11933135	4	84025589	q21.22
SNP_A-2244919	G	G	242	112	236	160	6.213	1.27E-02	rs12120477	1	80227185	p31.1
SNP_A-2254541	C	C	341	27	402	14	6.215	1.27E-02	rs12817979	12	8671404	p13.31
SNP_A-2254772	A	A	267	93	333	75	6.213	1.27E-02	rs12212601	6	123270976	q22.31
SNP_A-2298901	A	A	389	5	368	16	6.217	1.27E-02	rs17098042	10	120535580	q26.11
SNP_A-2293071	C	C	320	20	327	41	6.208	1.27E-02	rs2219261	12	60587781	q14.1
SNP_A-2038569	G	G	346	20	364	42	6.207	1.27E-02	rs10133904	14	37908373	q21.1
SNP_A-2037386	A	A	336	30	355	57	6.204	1.27E-02	rs1751027	13	94651871	q32.1
SNP_A-2031311	C	C	199	129	178	170	6.206	1.27E-02	rs12187932	5	176575757	q35.3
SNP_A-2003669	C	C	335	1	380	10	6.214	1.27E-02	rs4982166	14	33876472	q13.1
SNP_A-2002773	T	T	374	14	404	4	6.214	1.27E-02	rs2395442	10	78337126	q22.3
SNP_A-2011739	C	C	233	121	285	99	6.211	1.27E-02	rs423137	6	42768633	p21.1
SNP_A-2089271	T	T	386	12	352	26	6.213	1.27E-02	---	3	131266697	q21.3
SNP_A-2074405	G	G	253	97	317	79	6.214	1.27E-02	rs6057630	20	30782398	q11.21
SNP_A-2068019	T	T	328	4	352	16	6.212	1.27E-02	rs7097768	10	77052335	q22.2
SNP_A-2111903	A	A	316	14	389	5	6.213	1.27E-02	rs12491708	3	158211170	q25.31
SNP_A-2126999	G	G	262	104	259	151	6.205	1.27E-02	rs13149379	4	114408716	q26
SNP_A-2161381	A	A	291	35	289	61	6.204	1.27E-02	rs9544554	13	77090835	q22.3
SNP_A-1822714	G	G	208	162	265	143	6.211	1.27E-02	rs322458	3	122068005	q13.33
SNP_A-1828614	T	C	242	176	210	204	6.213	1.27E-02	rs10808271	7	132809573	q33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1849053	G	G	346	14	367	33	6.211	1.27E-02	rs3113927	4	75735250	q13.3
SNP_A-1745204	G	G	350	0	391	7	6.214	1.27E-02	rs1931347	13	106541900	q33.3
SNP_A-1924481	G	G	366	0	409	7	6.214	1.27E-02	rs265562	12	56772288	q14.1
SNP_A-1882472	T	T	322	20	387	9	6.214	1.27E-02	rs12082553	1	230919849	q42.2
SNP_A-1875479	G	G	224	154	192	190	6.208	1.27E-02	rs2239691	7	72913820	q11.23
SNP_A-1896288	G	A	213	153	210	204	6.214	1.27E-02	rs271128	6	133285984	q23.2
SNP_A-1946108	C	C	343	19	356	40	6.204	1.27E-02	rs13073510	3	168976003	q26.1
SNP_A-1959715	G	G	316	12	312	28	6.212	1.27E-02	rs10073578	5	113008008	q22.2
SNP_A-1950327	G	G	277	27	328	14	6.207	1.27E-02	rs2876709	13	75931802	q22.2
SNP_A-1971725	C	C	242	98	304	80	6.209	1.27E-02	rs1990772	3	9631299	p25.3
SNP_A-1986490	C	C	227	143	289	125	6.209	1.27E-02	rs2261333	6	77128094	q14.1
SNP_A-1891887	G	G	406	0	390	6	6.198	1.28E-02	rs11006644	10	61078772	q21.2
SNP_A-1889067	G	G	242	170	270	132	6.191	1.28E-02	rs9928186	16	5734215	p13.3
SNP_A-1918960	C	C	288	18	328	42	6.194	1.28E-02	rs768893	6	99166441	q16.2
SNP_A-1740391	A	A	383	17	375	35	6.193	1.28E-02	rs746665	3	15093737	p25.1
SNP_A-1666826	A	A	364	4	392	16	6.192	1.28E-02	rs2068633	12	81253988	q21.31
SNP_A-1679606	G	G	253	67	319	51	6.194	1.28E-02	rs2722623	3	165730653	q26.1
SNP_A-1798004	C	G	150	146	183	125	6.198	1.28E-02	rs10007915	4	106422912	q24
SNP_A-1853355	A	A	224	90	302	78	6.203	1.28E-02	rs4683198	3	46304282	p21.31
SNP_A-1853526	A	A	339	21	385	9	6.202	1.28E-02	rs10742839	11	5890620	p15.4
SNP_A-1859741	A	A	308	34	385	21	6.198	1.28E-02	rs12693329	2	183584741	q32.1
SNP_A-1863698	T	C	217	153	207	205	6.203	1.28E-02	rs6536515	4	161663217	q32.1
SNP_A-1871238	A	A	364	2	361	11	6.195	1.28E-02	rs16976761	17	67076892	q24.3
SNP_A-1827787	C	C	321	43	379	27	6.19	1.28E-02	rs11082427	18	40992739	q12.3
SNP_A-1815567	G	G	396	0	380	6	6.203	1.28E-02	rs10046680	8	51106775	q11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839100	A	A	360	6	392	20	6.202	1.28E-02	rs17040089	4	110500794	q25
SNP_A-2162678	T	T	382	16	367	33	6.193	1.28E-02	rs204019	16	13134742	p13.12
SNP_A-2135835	C	C	336	28	380	14	6.193	1.28E-02	rs16914629	8	92944445	q21.3
SNP_A-2121060	C	C	246	112	316	96	6.193	1.28E-02	rs1348515	11	98001115	q22.1
SNP_A-2121803	C	C	236	150	277	121	6.198	1.28E-02	rs4683778	3	141192315	q23
SNP_A-2188415	G	G	385	7	359	19	6.195	1.28E-02	rs17056971	8	27185803	p21.2
SNP_A-2074543	A	A	366	2	363	11	6.195	1.28E-02	rs7824076	8	72606787	q13.3
SNP_A-2078869	G	G	285	129	237	155	6.198	1.28E-02	rs12119303	1	215702945	q41
SNP_A-2015619	G	G	410	0	394	6	6.196	1.28E-02	rs2824265	21	17545940	q21.1
SNP_A-2005068	G	G	398	6	414	0	6.194	1.28E-02	rs1558217	17	11090972	p12
SNP_A-2033495	T	T	290	78	351	59	6.191	1.28E-02	rs1835668	3	152334152	q25.1
SNP_A-2036089	A	A	366	38	329	59	6.195	1.28E-02	rs17665544	3	71941680	p13
SNP_A-2043550	G	G	325	9	410	2	6.197	1.28E-02	rs2275150	3	161486150	q25.33
SNP_A-2232137	C	C	412	0	396	6	6.195	1.28E-02	rs9314310	8	25795903	p21.2
SNP_A-2237092	A	A	254	108	240	150	6.2	1.28E-02	rs912185	20	15984149	p12.1
SNP_A-2239001	C	C	327	35	395	21	6.186	0.0129	rs9306898	2	16878162	p24.2
SNP_A-2228452	T	T	271	47	327	31	6.181	0.0129	rs4793031	17	39223837	q21.31
SNP_A-2245861	A	A	225	137	203	179	6.18	0.0129	rs758069	2	241802618	q37.3
SNP_A-2267443	G	G	207	145	265	127	6.186	0.0129	rs12653531	5	27515509	p14.1
SNP_A-2292846	G	G	217	149	277	131	6.184	0.0129	rs12159113	22	48153554	q13.33
SNP_A-2290669	C	C	258	100	330	84	6.178	0.0129	rs10833310	11	20335244	p15.1
SNP_A-1991678	A	A	334	78	280	100	6.185	0.0129	rs2888493	7	146655654	q35
SNP_A-2100886	A	A	372	8	415	1	6.178	0.0129	rs7194464	16	34820192	p11.1
SNP_A-2070414	A	A	302	80	265	107	6.181	0.0129	rs913280	9	37473309	p13.2
SNP_A-2223422	G	G	329	5	410	0	6.179	0.0129	rs7677409	4	149626357	q31.23
SNP_A-2114747	C	C	268	54	264	86	6.188	0.0129	rs7836620	8	124850542	q24.13
SNP_A-2133694	A	A	358	10	389	27	6.182	0.0129	rs9320970	6	124373959	q22.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2130547	C	C	379	31	361	53	6.18	0.0129	rs11043765	12	18040976	p12.3
SNP_A-2155874	C	C	256	114	250	162	6.181	0.0129	rs6762782	3	123388347	q21.1
SNP_A-2141429	G	G	330	82	360	56	6.184	0.0129	rs17171730	7	40364987	p14.1
SNP_A-1836049	C	C	373	21	390	8	6.186	0.0129	rs2510165	11	104921016	q22.3
SNP_A-1858270	C	C	283	87	346	68	6.189	0.0129	rs11585077	1	159884224	q23.3
SNP_A-1707023	G	G	382	4	383	15	6.188	0.0129	rs10483506	14	38570380	q21.1
SNP_A-1782050	A	A	358	60	329	87	6.179	0.0129	rs11063691	12	5441709	p13.31
SNP_A-1905249	A	A	304	42	380	28	6.188	0.0129	rs6758689	2	72559113	p13.2
SNP_A-1883840	C	T	239	181	216	202	6.185	0.0129	rs1242744	14	22270010	q11.2
SNP_A-1874926	C	A	187	177	236	174	6.185	0.0129	rs6435162	2	203380849	q33.2
SNP_A-1892991	A	A	363	19	389	7	6.187	0.0129	rs8190892	8	30703530	p12
SNP_A-1947670	T	T	235	181	265	143	6.18	0.0129	rs4575596	17	68389374	q24.3
SNP_A-1938944	G	G	383	7	336	18	6.185	0.0129	rs16834151	1	149287456	q21.3
SNP_A-1959473	A	A	291	91	343	69	6.165	1.30E-02	rs10784014	12	58583969	q14.1
SNP_A-1956260	T	T	295	125	319	91	6.17	1.30E-02	rs9852703	3	114672058	q13.2
SNP_A-1891992	G	G	358	12	384	30	6.175	1.30E-02	rs16835842	2	195124831	q32.3
SNP_A-1904197	-	T	181	181	237	165	6.165	1.30E-02	rs1883799	20	56370153	q13.32
SNP_A-1901609	A	A	406	0	392	6	6.167	1.30E-02	rs650837	11	109201070	q22.3
SNP_A-1906965	C	C	365	23	344	42	6.171	1.30E-02	rs7080980	10	2999063	p15.3
SNP_A-1925095	A	A	336	4	362	16	6.175	1.30E-02	rs4333534	7	134257924	q33
SNP_A-1921575	G	G	318	20	381	9	6.168	1.30E-02	rs17107113	5	147031990	q32
SNP_A-1650966	C	C	330	60	287	83	6.174	1.30E-02	rs10508318	10	7054365	p14
SNP_A-1864850	T	T	356	10	387	27	6.174	1.30E-02	rs1559693	4	65221265	q13.1
SNP_A-1841036	G	G	281	73	295	117	6.174	1.30E-02	rs10865710	3	12328198	p25.2
SNP_A-1817414	G	G	394	4	366	14	6.174	1.30E-02	rs10949768	7	158626250	q36.3
SNP_A-1827914	G	G	312	6	340	20	6.163	1.30E-02	rs16894881	8	122278068	q24.12
SNP_A-2155357	G	G	394	6	408	0	6.166	1.30E-02	rs1176841	9	36779162	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2159261	T	T	375	9	331	21	6.163	1.30E-02	rs1223384	18	3534662	p11.31
SNP_A-2162121	A	A	404	0	390	6	6.167	1.30E-02	rs9655154	7	18158864	p21.1
SNP_A-2131808	G	G	221	191	255	155	6.169	1.30E-02	rs7499386	16	9256256	p13.2
SNP_A-2131822	T	T	409	3	372	12	6.176	1.30E-02	rs12256724	10	70635063	q22.1
SNP_A-2131392	G	G	213	147	274	130	6.17	1.30E-02	rs9697002	9	2243943	p24.2
SNP_A-2135760	A	T	190	180	237	175	6.17	1.30E-02	rs7721932	5	85269747	q14.3
SNP_A-2134477	A	A	387	3	352	12	6.168	1.30E-02	rs2780432	4	25863	p16.3
SNP_A-2137572	T	C	236	186	218	196	6.162	1.30E-02	rs717344	16	4979249	p13.3
SNP_A-2117553	G	G	287	31	352	18	6.166	1.30E-02	rs4570995	19	17144942	p13.11
SNP_A-2210891	G	G	404	0	390	6	6.167	1.30E-02	rs6766676	3	46966688	p21.31
SNP_A-2051457	T	C	227	171	206	192	6.173	1.30E-02	rs2345941	7	132794890	q33
SNP_A-2097337	G	G	392	6	406	0	6.167	1.30E-02	rs6056982	20	9824688	p12.2
SNP_A-2003991	A	A	242	48	317	35	6.169	1.30E-02	rs4906413	14	103593509	q32.33
SNP_A-2012334	C	C	408	0	394	6	6.166	1.30E-02	---	11	78643419	q14.1
SNP_A-2029665	A	A	340	32	301	51	6.174	1.30E-02	rs7235041	18	4522500	p11.31
SNP_A-2293395	C	C	396	0	382	6	6.171	1.30E-02	rs6887071	5	5882454	p15.32
SNP_A-2292515	A	A	287	83	330	60	6.174	1.30E-02	rs16837279	3	127414959	q21.2
SNP_A-2299272	A	C	207	153	210	198	6.175	1.30E-02	rs6068555	20	51516261	q13.2
SNP_A-2262424	T	T	291	63	305	103	6.172	1.30E-02	rs17270331	8	125015284	q24.13
SNP_A-2282267	C	C	417	1	374	8	6.174	1.30E-02	rs747104	3	108761579	q13.12
SNP_A-2246365	A	A	416	0	402	6	6.163	1.30E-02	rs11894663	2	141716261	q22.1
SNP_A-2253582	T	T	331	27	353	53	6.166	1.30E-02	rs7953994	12	25363835	p12.1
SNP_A-2256201	C	C	313	39	310	66	6.173	1.30E-02	rs7439916	4	157498279	q32.1
SNP_A-2233263	G	G	334	42	290	62	6.164	1.30E-02	rs528647	11	116029031	q23.3
SNP_A-2228934	G	G	353	3	382	14	6.152	1.31E-02	rs11614707	12	42024750	q12
SNP_A-2252816	C	C	222	94	266	72	6.15	1.31E-02	rs7303893	12	30350773	p11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247284	A	A	203	161	257	141	6.159	1.31E-02	rs7589644	2	2588044	p25.3
SNP_A-2299520	A	A	350	0	395	7	6.152	1.31E-02	rs1942664	11	124024143	q24.2
SNP_A-2293570	C	C	293	117	261	151	6.157	1.31E-02	rs2569213	5	171789813	q35.1
SNP_A-2308759	A	A	343	73	363	47	6.157	1.31E-02	rs1341247	1	66591290	p31.2
SNP_A-2305504	T	T	418	0	404	6	6.162	1.31E-02	rs17033997	3	35983786	p22.3
SNP_A-2029233	C	C	404	2	403	11	6.155	1.31E-02	rs11768011	7	14859615	p21.2
SNP_A-2099576	A	A	349	13	408	4	6.159	1.31E-02	rs2879160	4	33417920	p15.1
SNP_A-2080051	C	C	347	61	310	86	6.158	1.31E-02	rs3795375	1	229821669	q42.2
SNP_A-2224617	G	C	200	198	234	166	6.153	1.31E-02	rs3213788	2	45558694	p21
SNP_A-2186425	G	G	299	41	338	24	6.15	1.31E-02	rs12249434	10	118288696	q25.3
SNP_A-2197502	C	C	328	34	318	58	6.152	1.31E-02	rs1427190	8	112234375	q23.3
SNP_A-2120268	C	C	321	11	389	3	6.154	1.31E-02	rs16833081	1	232487383	q42.3
SNP_A-2112145	C	C	355	55	377	33	6.161	1.31E-02	rs11089887	22	37143176	q13.1
SNP_A-2131660	T	T	244	80	315	65	6.154	1.31E-02	rs2887286	1	1196054	p36.33
SNP_A-2154302	C	C	404	4	376	14	6.158	1.31E-02	rs12089111	1	210112640	q32.3
SNP_A-1826488	C	C	345	65	360	40	6.149	1.31E-02	rs1863178	2	53372590	p16.2
SNP_A-1822539	G	G	274	80	328	60	6.156	1.31E-02	rs17759529	2	162676520	q24.2
SNP_A-1816627	T	T	331	21	346	8	6.154	1.31E-02	rs328325	16	72413365	q22.3
SNP_A-1838427	C	C	278	82	284	126	6.151	1.31E-02	rs9883230	3	2035262	p26.3
SNP_A-1833912	C	C	209	181	242	146	6.156	1.31E-02	rs3107022	4	48458315	p12
SNP_A-1865295	T	T	319	15	404	6	6.151	1.31E-02	rs998191	10	84544582	q23.1
SNP_A-1857778	G	G	288	70	350	52	6.154	1.31E-02	---	18	45881032	q21.1
SNP_A-1729110	T	T	357	17	392	6	6.156	1.31E-02	rs10500756	11	12329846	p15.3
SNP_A-1926371	A	A	273	127	248	166	6.152	1.31E-02	rs9590634	13	41198025	q14.11
SNP_A-1897442	G	G	292	62	343	43	6.162	1.31E-02	rs2922480	8	134682698	q24.22
SNP_A-1951281	A	A	332	38	393	23	6.15	1.31E-02	rs16892009	6	39463457	p21.2
SNP_A-1939948	G	G	282	46	277	75	6.156	1.31E-02	rs7153171	14	71648449	q24.2
SNP_A-1940798	A	A	370	18	358	36	6.152	1.31E-02	rs11623545	14	70781903	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1981371	T	T	325	39	258	54	6.156	1.31E-02	rs16869479	5	40015071	p13.1
SNP_A-1979556	A	A	351	13	410	4	6.151	1.31E-02	rs17035841	4	158461029	q32.1
SNP_A-1981236	A	A	354	10	394	2	6.136	0.0132	rs16901858	5	35410331	p13.2
SNP_A-1971807	C	C	411	1	370	8	6.145	0.0132	rs17037952	3	13259062	p25.2
SNP_A-1969093	T	T	331	5	410	0	6.142	0.0132	rs238951	21	16484901	q21.1
SNP_A-1941386	T	T	238	148	272	116	6.14	0.0132	rs10991954	9	91333220	q22.31
SNP_A-1959065	G	G	403	5	384	16	6.142	0.0132	rs17141607	7	19375092	p21.1
SNP_A-1901487	G	G	286	92	240	116	6.138	0.0132	rs9394784	6	41423214	p21.1
SNP_A-1932338	C	C	341	41	371	23	6.142	0.0132	rs729356	17	15290054	p12
SNP_A-1913708	G	G	346	0	391	7	6.143	0.0132	rs2055456	3	79953597	p12.2
SNP_A-1735977	C	C	396	0	384	6	6.139	0.0132	rs10488638	7	154701891	q36.3
SNP_A-1790882	A	A	275	75	271	113	6.148	0.0132	rs1876215	4	83970991	q21.22
SNP_A-1806809	T	T	338	16	347	35	6.14	0.0132	rs2271717	17	3906480	p13.2
SNP_A-1826237	T	T	342	14	315	29	6.138	0.0132	rs1942462	18	68660804	q22.3
SNP_A-2163304	A	A	301	19	321	41	6.147	0.0132	rs4512017	4	35104400	p15.1
SNP_A-2167409	T	T	258	96	238	132	6.14	0.0132	rs4366138	9	107224616	q31.2
SNP_A-2138200	A	A	335	21	379	9	6.147	0.0132	rs7575368	2	181518306	q31.3
SNP_A-2151833	G	G	285	49	345	33	6.141	0.0132	rs7140781	14	64281211	q23.3
SNP_A-2134918	G	G	361	21	328	38	6.139	0.0132	rs4816104	20	96084	p13
SNP_A-2129106	C	C	226	140	217	193	6.143	0.0132	rs17808829	4	91309136	q22.1
SNP_A-2125073	A	A	201	179	236	146	6.149	0.0132	rs2211535	9	93042309	q22.31
SNP_A-2197627	A	A	387	33	365	55	6.144	0.0132	rs7623156	3	11670689	p25.3
SNP_A-2194315	C	C	331	29	319	51	6.136	0.0132	rs17090828	14	22889653	q11.2
SNP_A-2181967	A	A	225	171	259	137	6.142	0.0132	rs6460307	7	65505021	q11.21
SNP_A-2211616	C	C	314	52	327	87	6.146	0.0132	rs4946900	6	108522085	q21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2210367	G	G	243	105	299	85	6.136	0.0132	rs11145653	9	77852649	q21.2
SNP_A-2212265	T	T	260	108	259	157	6.147	0.0132	rs7778623	7	94722947	q21.3
SNP_A-2206300	G	G	338	32	398	18	6.14	0.0132	rs17024792	2	100882295	q11.2
SNP_A-2087634	T	T	333	5	412	0	6.136	0.0132	rs9657698	9	91643065	q22.31
SNP_A-2028317	A	T	193	161	216	180	6.144	0.0132	rs13331343	16	81998689	q23.3
SNP_A-2031521	C	C	338	32	398	18	6.14	0.0132	rs2108593	19	33590352	q12
SNP_A-2031937	C	C	388	14	416	4	6.139	0.0132	rs4848131	2	121411120	q14.2
SNP_A-2045541	T	T	382	6	394	0	6.14	0.0132	rs1376242	7	113361812	q31.1
SNP_A-1989664	G	G	346	66	370	42	6.138	0.0132	rs16834640	1	233457746	q43
SNP_A-2304554	C	C	286	22	355	11	6.149	0.0132	rs12331878	4	53762514	q12
SNP_A-2295766	C	C	362	56	386	34	6.143	0.0132	rs3791327	2	135037304	q21.3
SNP_A-2284640	A	A	338	66	288	88	6.139	0.0132	rs17292645	9	116582908	q33.1
SNP_A-2282044	G	G	340	76	309	105	6.122	1.33E-02	rs4814533	20	16597513	p12.1
SNP_A-2260744	C	C	374	30	367	53	6.131	1.33E-02	rs2589971	15	88696363	q26.1
SNP_A-2244119	G	G	229	131	274	106	6.127	1.33E-02	rs7758540	6	130194172	q22.33
SNP_A-2253537	G	G	201	161	261	145	6.128	1.33E-02	rs2133898	12	98441138	q23.1
SNP_A-2299330	C	C	406	6	418	0	6.132	1.33E-02	rs16899858	8	125697523	q24.13
SNP_A-2292551	C	C	267	45	328	30	6.124	1.33E-02	rs908602	3	6079780	p26.1
SNP_A-2305948	C	C	388	18	398	6	6.122	1.33E-02	rs11002433	10	79607214	q22.3
SNP_A-2310322	C	C	413	5	394	16	6.133	1.33E-02	rs2241309	3	10271133	p25.3
SNP_A-2314093	T	T	233	89	291	71	6.127	1.33E-02	rs10029269	4	136137977	q28.3
SNP_A-2034952	A	A	274	146	239	181	6.134	1.33E-02	rs2472562	8	6799659	p23.1
SNP_A-2079010	T	T	228	128	183	151	6.128	1.33E-02	rs637544	1	206906899	q32.2
SNP_A-2059941	T	T	305	11	369	3	6.131	1.33E-02	rs985043	7	93488389	q21.3
SNP_A-2073992	A	A	384	18	394	6	6.124	1.33E-02	rs4624663	4	38620442	p14
SNP_A-2076734	G	G	333	43	304	66	6.126	1.33E-02	rs17144383	16	7616817	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2066190	G	G	174	164	234	152	6.124	1.33E-02	rs11784930	8	125947767	q24.13
SNP_A-2063196	C	C	290	26	356	14	6.13	1.33E-02	rs6760006	2	202101658	q33.1
SNP_A-2226184	T	T	297	39	378	26	6.123	1.33E-02	rs156851	1	16560300	p36.13
SNP_A-2174294	T	T	280	68	291	109	6.124	1.33E-02	rs6073142	20	41660426	q13.12
SNP_A-2192458	G	G	309	45	311	75	6.134	1.33E-02	rs17046990	4	115608946	q26
SNP_A-2132424	A	A	272	76	275	117	6.132	1.33E-02	rs17379354	8	78270589	q21.11
SNP_A-2166344	G	G	322	6	352	20	6.132	1.33E-02	rs9306979	4	33494412	p15.1
SNP_A-2155520	G	G	322	46	384	30	6.129	1.33E-02	rs4579186	4	57856827	q12
SNP_A-1844059	C	C	305	53	316	88	6.128	1.33E-02	rs13319597	3	10101312	p25.3
SNP_A-1798543	T	T	273	97	336	78	6.13	1.33E-02	rs12494063	3	31195088	p24.1
SNP_A-1793046	A	A	361	9	389	25	6.125	1.33E-02	rs6052281	20	3994114	p13
SNP_A-1905205	T	T	176	150	223	129	6.129	1.33E-02	rs4751904	10	116180673	q25.3
SNP_A-1930460	G	G	225	143	288	126	6.127	1.33E-02	rs10479576	5	179840698	q35.3
SNP_A-1901888	T	T	231	115	221	161	6.123	1.33E-02	rs1886979	6	44012879	p21.1
SNP_A-1900569	A	A	288	76	347	57	6.129	1.33E-02	rs10882369	10	82688805	q22.3
SNP_A-1887255	A	A	247	115	308	96	6.131	1.33E-02	rs1890016	9	70723282	q21.11
SNP_A-1959990	G	G	395	17	387	5	6.134	1.33E-02	rs8182421	18	45597775	q21.1
SNP_A-1952994	C	C	309	59	374	42	6.132	1.33E-02	rs10965403	9	22612676	p21.3
SNP_A-1975139	A	A	201	167	261	151	6.135	1.33E-02	rs1031838	3	163719236	q26.1
SNP_A-1960071	T	T	307	13	358	4	6.113	0.0134	---	20	57422413	q13.32
SNP_A-1959500	A	A	283	137	246	170	6.116	0.0134	rs4501056	3	73031598	p13
SNP_A-1942631	G	G	370	14	396	4	6.114	0.0134	rs1015483	12	38069752	q12
SNP_A-1938455	C	C	323	41	333	71	6.121	0.0134	rs17053732	13	56562089	q21.1
SNP_A-1875877	C	C	315	43	316	72	6.118	0.0134	rs9470950	6	38992215	p21.2
SNP_A-1927148	C	T	207	163	219	195	6.118	0.0134	rs10143255	14	46642355	q21.3
SNP_A-1922957	A	A	331	7	347	21	6.114	0.0134	rs867948	12	58921609	q14.1
SNP_A-1912435	T	T	372	14	398	4	6.111	0.0134	rs4866310	5	17672912	p15.1
SNP_A-1794509	C	C	386	18	363	35	6.115	0.0134	rs2459343	10	125232065	q26.13
SNP_A-1788404	T	T	330	6	341	19	6.12	0.0134	rs4467541	4	150656562	q31.23
SNP_A-1804447	G	G	268	90	268	134	6.116	0.0134	rs10944779	6	65905532	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784392	A	G	203	197	233	169	6.117	0.0134	rs10051514	5	4940171	p15.32
SNP_A-1835108	G	G	298	122	263	155	6.11	0.0134	rs4487801	8	3344610	p23.2
SNP_A-1870934	A	A	358	22	383	9	6.11	0.0134	rs3783124	13	25356231	q12.13
SNP_A-2151935	C	C	368	8	407	1	6.111	0.0134	rs7189502	16	46630795	q12.1
SNP_A-2128824	T	T	241	177	277	143	6.11	0.0134	rs12726527	1	198230145	q32.1
SNP_A-2116053	G	G	257	139	230	178	6.117	0.0134	rs11264449	1	152948314	q22
SNP_A-2192618	A	A	257	159	214	188	6.112	0.0134	rs2415317	14	35679429	q13.3
SNP_A-2169494	A	A	378	0	368	6	6.113	0.0134	---	12	46691389	q13.11
SNP_A-2216165	C	T	207	205	228	162	6.111	0.0134	rs3861625	14	77513917	q24.3
SNP_A-2215141	A	A	350	40	347	67	6.115	0.0134	rs1294626	7	7194259	p21.3
SNP_A-2217912	G	G	304	104	338	76	6.113	0.0134	rs2909981	7	71329718	q11.22
SNP_A-2204165	C	C	327	15	369	5	6.117	0.0134	rs7548759	1	113347014	p13.2
SNP_A-2200754	G	G	266	140	297	107	6.111	0.0134	rs7388654	8	11803962	p23.1
SNP_A-2200560	G	G	340	30	392	16	6.113	0.0134	rs7376151	4	167576847	q32.3
SNP_A-2071949	G	G	237	111	224	154	6.115	0.0134	rs3824387	9	17616452	p22.2
SNP_A-2079653	T	T	212	146	200	198	6.111	0.0134	rs10256600	7	17596864	p21.1
SNP_A-2089387	A	A	358	0	348	6	6.119	0.0134	rs1070500	16	10186824	p13.2
SNP_A-2030020	C	C	237	117	299	99	6.118	0.0134	rs3005125	6	42568050	p21.1
SNP_A-1996607	A	A	288	44	295	75	6.121	0.0134	rs12766718	10	15745568	p13
SNP_A-2015114	T	T	264	100	266	148	6.11	0.0134	rs7483731	11	106223949	q22.3
SNP_A-2303690	C	C	244	118	241	169	6.12	0.0134	rs2722596	2	5852524	p25.2
SNP_A-2300451	G	G	186	178	240	160	6.121	0.0134	rs3734938	7	137881301	q34
SNP_A-2255546	G	G	359	9	387	25	6.118	0.0134	rs497480	2	166807076	q24.3
SNP_A-2228593	G	A	207	163	220	196	6.112	0.0134	rs588825	4	130857619	q28.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2234738	C	C	358	28	318	46	6.105	0.0135	rs4917161	7	48338356	p12.3
SNP_A-2246756	G	A	219	193	221	177	6.108	0.0135	rs10144454	2	45530624	p21
SNP_A-2259028	G	G	383	21	370	40	6.099	0.0135	rs506698	11	79328893	q14.1
SNP_A-2296545	A	A	289	59	343	41	6.098	0.0135	rs7141519	14	66594278	q23.3
SNP_A-2013130	C	C	237	87	314	74	6.107	0.0135	rs2171282	11	87512207	q14.2
SNP_A-2032651	A	A	323	7	413	1	6.099	0.0135	rs1536100	1	189907590	q31.2
SNP_A-2024673	A	A	258	52	323	37	6.103	0.0135	---	6	154688772	q25.2
SNP_A-2021186	A	A	404	6	414	0	6.103	0.0135	rs16875023	4	23784161	p15.2
SNP_A-2091460	A	A	249	97	311	79	6.097	0.0135	rs11973089	7	87715897	q21.13
SNP_A-2101850	C	C	268	78	262	116	6.109	0.0135	rs4940371	18	44195025	q21.1
SNP_A-2098512	T	T	256	92	307	71	6.096	0.0135	rs7606588	2	123137800	q14.3
SNP_A-2071012	A	A	270	124	298	92	6.101	0.0135	rs7179260	15	75923170	q24.3
SNP_A-2066102	A	A	400	6	410	0	6.104	0.0135	rs2454520	8	6454016	p23.1
SNP_A-2185116	C	C	330	8	365	1	6.103	0.0135	rs16929445	11	36808577	p12
SNP_A-2184627	T	T	366	22	391	9	6.096	0.0135	rs3860456	2	100908830	q11.2
SNP_A-2117038	C	C	333	5	410	0	6.106	0.0135	rs6558319	8	145327191	q24.3
SNP_A-2140340	A	A	299	35	333	19	6.102	0.0135	rs6680636	1	2945177	p36.32
SNP_A-1858390	G	G	257	111	253	159	6.102	0.0135	rs2511776	11	130708251	q25
SNP_A-1853364	A	A	415	1	376	8	6.097	0.0135	rs17122632	1	100656402	p21.2
SNP_A-1836691	T	T	257	111	253	159	6.102	0.0135	rs11014291	10	25238693	p12.1
SNP_A-1839569	G	G	412	0	402	6	6.103	0.0135	rs16946327	17	12476681	p12
SNP_A-1823174	G	G	285	77	291	119	6.102	0.0135	rs7799974	7	28171122	p15.1
SNP_A-1818234	T	T	404	4	378	14	6.102	0.0135	rs16943987	16	74802501	q23.1
SNP_A-1802748	T	T	394	0	384	6	6.108	0.0135	rs13312964	8	91019216	q21.3
SNP_A-1810619	A	A	324	20	315	39	6.103	0.0135	rs11575732	10	115321800	q25.3
SNP_A-1912879	A	A	245	87	324	74	6.101	0.0135	rs801286	2	195348647	q32.3
SNP_A-1908685	C	C	415	1	376	8	6.097	0.0135	rs10982004	9	113760277	q32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1874039	G	G	269	151	301	117	6.105	0.0135	rs6039875	20	10293462	p12.2
SNP_A-1895416	A	A	233	149	283	125	6.098	0.0135	rs1546198	5	2778974	p15.33
SNP_A-1954393	A	A	325	5	400	0	6.102	0.0135	rs4745281	9	68652193	q21.11
SNP_A-1965582	A	G	203	163	218	190	6.109	0.0135	rs6432570	2	160633821	q24.2
SNP_A-1978295	G	G	252	112	249	161	6.101	0.0135	rs10494706	1	191168513	q31.3
SNP_A-1987304	G	G	321	21	326	42	6.095	1.36E-02	rs17164503	6	115408562	q22.1
SNP_A-1951248	C	C	313	9	390	2	6.084	1.36E-02	rs351759	8	28084110	p21.1
SNP_A-1943501	G	G	326	26	345	51	6.088	1.36E-02	rs7117817	11	41089364	p12
SNP_A-1893863	G	G	353	13	410	4	6.092	1.36E-02	rs11956140	5	100760263	q21.1
SNP_A-1930356	C	C	305	117	331	85	6.09	1.36E-02	rs1514245	17	65846925	q24.3
SNP_A-1662444	T	T	369	11	377	27	6.094	1.36E-02	rs10483622	14	52126569	q22.1
SNP_A-1659796	A	A	303	97	341	71	6.09	1.36E-02	rs2827281	21	22499604	q21.1
SNP_A-1817848	A	A	292	54	301	89	6.094	1.36E-02	rs16925375	9	106157714	q31.2
SNP_A-1852761	G	C	190	152	210	182	6.087	1.36E-02	rs1398378	12	28642657	p11.22
SNP_A-1858389	G	G	270	132	235	165	6.087	1.36E-02	rs175114	11	60581773	q12.2
SNP_A-1863810	T	T	226	104	198	136	6.092	1.36E-02	rs3857944	8	125648969	q24.13
SNP_A-2166798	G	G	240	112	238	162	6.093	1.36E-02	rs11154835	6	136326169	q23.3
SNP_A-2118257	G	G	340	8	380	24	6.086	1.36E-02	rs7976015	12	18989836	p12.3
SNP_A-2132787	A	A	317	37	330	66	6.093	1.36E-02	rs17585412	14	51080939	q22.1
SNP_A-2169256	C	C	369	51	335	75	6.094	1.36E-02	rs1327905	20	20200186	p11.23
SNP_A-2217584	G	G	371	15	364	32	6.089	1.36E-02	rs13321422	3	13859816	p25.1
SNP_A-2226506	T	T	195	157	242	134	6.088	1.36E-02	rs685294	11	84413363	q14.1
SNP_A-2072013	G	G	319	61	292	88	6.086	1.36E-02	rs17366052	6	6026923	p25.1
SNP_A-2072700	G	G	319	29	281	47	6.083	1.36E-02	rs1924177	13	37566365	q13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2061837	C	C	255	111	227	145	6.094	1.36E-02	rs13426909	2	235294068	q37.1
SNP_A-2055116	G	G	316	22	364	10	6.084	1.36E-02	rs1652168	12	30289826	p11.22
SNP_A-2053762	A	A	341	15	334	32	6.084	1.36E-02	rs12299180	12	126047884	q24.32
SNP_A-2085724	T	T	292	114	316	82	6.093	1.36E-02	rs7584466	2	72023185	p13.2
SNP_A-2084495	T	T	286	40	365	27	6.094	1.36E-02	rs9838069	3	4911497	p26.1
SNP_A-2021642	G	G	222	148	211	201	6.09	1.36E-02	rs6803377	3	118763411	q13.31
SNP_A-2032711	G	G	280	54	281	87	6.093	1.36E-02	rs1834861	12	11385722	p13.2
SNP_A-2009328	A	G	176	168	207	149	6.095	1.36E-02	rs7612362	3	176495847	q26.31
SNP_A-2306004	C	C	199	161	255	143	6.084	1.36E-02	rs6921287	6	113512250	q21
SNP_A-2228195	T	T	329	9	410	2	6.091	1.36E-02	rs6475983	9	2726749	p24.2
SNP_A-2252944	G	G	394	6	402	0	6.075	0.0137	rs3787240	20	45233129	q13.12
SNP_A-2254718	G	G	402	6	410	0	6.074	0.0137	---	14	69611089	q24.2
SNP_A-2269419	A	A	412	0	404	6	6.074	0.0137	rs2815117	6	39297357	p21.2
SNP_A-2291451	T	T	378	12	363	27	6.073	0.0137	rs2417805	9	107646666	q31.2
SNP_A-2017857	G	G	193	173	245	153	6.071	0.0137	rs4816367	21	30848379	q22.11
SNP_A-1992220	G	G	296	34	326	18	6.082	0.0137	rs1567834	8	9672500	p23.1
SNP_A-1997501	T	T	362	10	400	2	6.075	0.0137	rs16924416	9	105135033	q31.1
SNP_A-2024894	T	T	303	39	336	22	6.079	0.0137	rs16937559	9	19475092	p22.1
SNP_A-2084174	C	C	261	59	330	44	6.075	0.0137	rs10919053	1	165774239	q24.2
SNP_A-2054875	T	T	268	62	300	108	6.074	0.0137	rs9875636	3	123429991	q21.1
SNP_A-2207118	T	T	302	26	389	15	6.08	0.0137	---	8	139106414	q24.23
SNP_A-2183797	C	C	352	12	380	30	6.073	0.0137	rs7215645	17	48900995	q22
SNP_A-2132022	G	G	359	19	334	36	6.072	0.0137	rs438876	1	41959943	p34.2
SNP_A-2131631	A	A	293	59	340	40	6.074	0.0137	rs7833825	8	135365471	q24.22
SNP_A-2115350	A	A	263	95	327	77	6.071	0.0137	rs11868422	17	198072	p13.3
SNP_A-2111190	A	A	313	33	312	58	6.072	0.0137	rs17090219	18	52342031	q21.2
SNP_A-2108057	T	T	291	27	323	13	6.077	0.0137	rs890848	19	8702963	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1866537	A	A	339	45	273	61	6.08	0.0137	rs2195108	20	17338095	p12.1
SNP_A-1866341	C	C	345	21	370	44	6.082	0.0137	rs11115448	12	81721596	q21.31
SNP_A-1867834	C	C	354	12	382	30	6.081	0.0137	rs17019384	1	209148956	q32.3
SNP_A-1850213	C	C	384	24	361	43	6.079	0.0137	rs17106180	10	87777969	q23.2
SNP_A-1818099	G	G	386	18	352	34	6.083	0.0137	rs11199302	10	122127705	q26.12
SNP_A-1816689	A	A	375	29	404	14	6.075	0.0137	rs1775585	1	90971137	p22.2
SNP_A-1826696	A	A	401	13	399	3	6.08	0.0137	rs4657519	1	162827900	q24.1
SNP_A-1839866	T	T	185	171	247	159	6.08	0.0137	rs9424179	10	5756561	p15.1
SNP_A-1837025	A	A	392	24	408	10	6.08	0.0137	rs16993428	19	6124690	p13.3
SNP_A-1830369	C	C	257	113	254	162	6.077	0.0137	rs12693637	2	192843917	q32.3
SNP_A-1781628	T	T	299	77	316	50	6.076	0.0137	rs610315	10	116121905	q25.3
SNP_A-1810934	G	G	328	18	371	7	6.083	0.0137	rs2544208	7	133427371	q33
SNP_A-1811051	C	C	217	137	259	111	6.081	0.0137	rs7894791	10	8631375	p14
SNP_A-1924705	T	T	318	94	346	66	6.081	0.0137	rs10775408	17	45682843	q21.33
SNP_A-1907533	G	G	398	16	415	5	6.075	0.0137	rs7204203	16	77041675	q23.1
SNP_A-1875540	G	G	309	23	386	12	6.071	0.0137	rs638261	9	99313775	q22.33
SNP_A-1965240	A	A	327	23	383	11	6.071	0.0137	rs17734682	2	146768377	q22.3
SNP_A-1975731	A	A	267	103	266	150	6.062	0.0138	rs7642926	3	192381542	q28
SNP_A-1976896	T	T	215	149	207	205	6.065	0.0138	rs1847118	4	40331931	p14
SNP_A-1980543	G	G	404	2	366	10	6.067	0.0138	rs12065020	1	200069306	q32.1
SNP_A-1938094	G	G	340	18	361	39	6.057	0.0138	rs1491709	4	72978601	q13.3
SNP_A-1903115	A	A	295	61	358	44	6.061	0.0138	rs2203817	3	118223951	q13.31
SNP_A-1912155	G	G	257	87	263	133	6.063	0.0138	rs10944941	6	67738476	q12
SNP_A-1920680	G	G	339	5	414	0	6.057	0.0138	---	18	57171424	q21.33
SNP_A-1926442	T	T	358	48	328	72	6.068	0.0138	rs17080201	5	179701004	q35.3
SNP_A-1787245	C	C	395	11	388	26	6.066	0.0138	rs10521099	16	13241312	p13.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1790922	G	G	230	138	289	119	6.066	0.0138	rs4340829	4	185425570	q35.1
SNP_A-1782005	G	G	337	5	412	0	6.064	0.0138	rs10237442	7	50127702	p12.2
SNP_A-1849780	T	T	333	13	364	32	6.059	0.0138	rs10931643	2	195135251	q32.3
SNP_A-1846214	A	A	232	156	257	119	6.069	0.0138	rs4703987	5	70800637	q13.2
SNP_A-1870865	G	G	296	58	357	41	6.064	0.0138	rs9924010	16	7338996	p13.2
SNP_A-2110929	G	G	274	142	298	106	6.058	0.0138	rs304389	5	121782624	q23.2
SNP_A-2164482	A	A	361	21	374	8	6.058	0.0138	rs2270126	16	7699339	p13.2
SNP_A-2163442	A	A	341	29	359	55	6.06	0.0138	rs1215446	13	79621156	q31.1
SNP_A-2153270	A	A	332	34	348	62	6.068	0.0138	rs16945656	18	3913759	p11.31
SNP_A-2151428	A	A	311	59	319	95	6.067	0.0138	rs11106285	12	90686410	q21.33
SNP_A-2189803	T	T	296	110	332	82	6.07	0.0138	rs11686713	2	72720193	p13.2
SNP_A-2198028	T	T	297	59	337	39	6.063	0.0138	rs6963373	7	92676356	q21.3
SNP_A-2168833	C	C	323	43	379	27	6.068	0.0138	rs11785702	8	108478599	q23.1
SNP_A-2048359	G	G	245	123	233	169	6.058	0.0138	rs1567675	2	2373887	p25.3
SNP_A-2040528	A	A	342	26	363	51	6.057	0.0138	rs17597799	4	163261473	q32.2
SNP_A-2300051	C	C	299	117	254	144	6.06	0.0138	rs17047376	2	118235156	q14.1
SNP_A-2271420	G	G	327	5	400	0	6.066	0.0138	rs16868802	7	94818987	q21.3
SNP_A-2284220	A	A	233	89	294	72	6.067	0.0138	rs2009152	4	89184151	q22.1
SNP_A-2231701	T	T	409	1	372	8	6.067	0.0138	rs13330069	16	2387029	p13.3
SNP_A-2276798	C	C	284	36	292	64	6.051	1.39E-02	rs2639281	3	81180245	p12.2
SNP_A-2313920	T	T	351	13	406	4	6.048	1.39E-02	rs17016393	1	207106482	q32.2
SNP_A-2017384	T	T	314	34	323	61	6.045	1.39E-02	rs9975542	21	28206871	q21.3
SNP_A-2055657	G	G	382	0	376	6	6.047	1.39E-02	rs454567	12	43622454	q12
SNP_A-2176842	G	G	350	56	363	33	6.057	1.39E-02	rs17782618	3	46415049	p21.31
SNP_A-2176833	T	T	306	116	324	82	6.046	1.39E-02	rs7158350	14	75016567	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2194073	T	T	289	127	254	160	6.046	1.39E-02	rs1896826	2	5941486	p25.2
SNP_A-2186624	A	A	355	13	321	27	6.056	1.39E-02	rs7210912	17	56468165	q23.2
SNP_A-2208370	G	G	347	47	294	66	6.056	1.39E-02	rs2008344	16	3681563	p13.3
SNP_A-2211958	G	G	305	49	319	83	6.048	1.39E-02	rs10484170	14	44263494	q21.2
SNP_A-2201566	T	C	203	165	219	189	6.048	1.39E-02	rs419097	9	111791298	q31.3
SNP_A-2205389	G	G	333	5	387	19	6.052	1.39E-02	rs1030528	8	40457269	p11.21
SNP_A-2223179	G	G	386	36	396	18	6.052	1.39E-02	rs7248022	19	61489972	q13.43
SNP_A-2156661	T	T	271	123	223	147	6.049	1.39E-02	rs7551781	1	153191498	q22
SNP_A-2120201	G	G	313	29	338	14	6.05	1.39E-02	rs7956853	12	129431340	q24.33
SNP_A-1832562	C	T	206	156	215	199	6.046	1.39E-02	rs473620	11	89890560	q14.3
SNP_A-1840912	G	G	328	14	351	33	6.05	1.39E-02	rs6922952	6	12499327	p24.1
SNP_A-1826291	T	T	250	120	314	102	6.05	1.39E-02	rs2440563	11	98067775	q22.1
SNP_A-1702517	C	C	390	0	384	6	6.047	1.39E-02	rs10492400	13	31280382	q13.1
SNP_A-1809630	G	G	266	146	303	115	6.045	1.39E-02	rs7718918	5	6319369	p15.32
SNP_A-1922155	T	G	238	172	211	207	6.054	1.39E-02	rs7189762	16	28126205	p11.2
SNP_A-1900978	A	G	186	174	229	171	6.048	1.39E-02	rs916732	13	31645122	q13.1
SNP_A-1893267	G	G	359	9	389	25	6.048	1.39E-02	rs585528	2	166798511	q24.3
SNP_A-1877989	T	T	369	21	382	8	6.053	1.39E-02	rs4917998	10	94827461	q23.33
SNP_A-1884758	A	A	236	124	225	171	6.05	1.39E-02	rs12470503	2	163522558	q24.2
SNP_A-1943550	A	A	331	39	392	24	6.047	1.39E-02	rs16929280	9	9384902	p23
SNP_A-1960737	T	T	329	19	344	40	6.053	1.39E-02	rs8112054	19	21035703	p12
SNP_A-1964254	C	C	319	91	291	123	6.051	1.39E-02	rs1374324	2	101072840	q11.2
SNP_A-1965432	G	G	326	34	342	62	6.036	0.014	rs1371393	2	153899364	q23.3
SNP_A-1975729	C	C	263	101	265	149	6.035	0.014	rs7628727	3	192381184	q28
SNP_A-1875264	G	G	243	83	255	131	6.042	0.014	rs6996558	8	84263445	q21.13
SNP_A-1896371	A	A	410	6	416	0	6.044	0.014	rs11199824	10	122949629	q26.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813474	A	A	408	6	414	0	6.044	0.014	rs12406311	1	196932608	q32.1
SNP_A-1803259	A	A	242	96	302	78	6.044	0.014	rs11732809	4	166080089	q32.3
SNP_A-1790255	G	G	322	12	408	4	6.042	0.014	rs6742441	2	45248160	p21
SNP_A-1873224	A	A	244	166	209	201	6.042	0.014	rs1800830	12	5408770	p13.31
SNP_A-1848039	C	C	357	37	343	61	6.033	0.014	rs8192674	2	165190394	q24.3
SNP_A-1846962	G	G	266	144	300	112	6.038	0.014	rs12596105	16	77807266	q23.1
SNP_A-1851389	A	A	370	16	322	30	6.037	0.014	rs2624664	3	45547792	p21.31
SNP_A-2114629	A	A	364	10	350	24	6.039	0.014	rs10082844	12	127491043	q24.32
SNP_A-2162309	C	C	412	6	418	0	6.043	0.014	rs11119916	1	202984698	q32.1
SNP_A-2161778	C	C	343	27	400	14	6.044	0.014	rs3844036	11	4606025	p15.4
SNP_A-2148678	G	G	237	131	299	113	6.037	0.014	rs7628552	3	84691044	p12.1
SNP_A-2185427	C	C	251	113	243	159	6.039	0.014	rs953846	18	74068941	q23
SNP_A-2191643	C	C	315	55	376	38	6.042	0.014	rs2016989	1	101947700	p21.2
SNP_A-2175502	T	T	334	32	304	52	6.035	0.014	rs7517484	1	41919549	p34.2
SNP_A-2168846	C	C	244	144	199	169	6.043	0.014	rs9525513	13	40959787	q14.11
SNP_A-2073348	C	C	187	175	235	153	6.041	0.014	rs317809	18	53509915	q21.31
SNP_A-2069751	G	G	303	49	296	78	6.043	0.014	rs1561335	12	66060010	q14.3
SNP_A-2087479	C	C	420	2	382	10	6.036	0.014	rs12149746	16	29740374	p11.2
SNP_A-2008876	C	C	272	90	328	70	6.035	0.014	rs16914560	11	25730150	p14.3
SNP_A-2044561	A	A	208	152	276	140	6.037	0.014	rs1837658	4	65714419	q13.1
SNP_A-2303848	T	T	414	6	420	0	6.043	0.014	rs17024473	2	100597620	q11.2
SNP_A-2298777	A	A	205	189	231	149	6.033	0.014	rs11723177	4	5667380	p16.2
SNP_A-2276151	G	A	206	148	204	198	6.044	0.014	rs6821114	4	145809994	q31.21
SNP_A-2279471	C	C	285	61	286	96	6.039	0.014	rs10212386	3	63188083	p14.2
SNP_A-2284350	G	G	276	78	313	55	6.033	0.014	rs3770978	2	207267094	q33.3
SNP_A-2271153	G	G	224	178	242	134	6.038	0.014	rs11196347	10	115235320	q25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2237900	A	A	285	49	352	34	6.034	0.014	rs10846652	12	123315121	q24.31
SNP_A-2239819	A	A	354	16	378	36	6.029	0.0141	rs9295661	6	25558005	p22.2
SNP_A-2235160	A	A	339	5	412	0	6.028	0.0141	rs872314	1	53499504	p32.3
SNP_A-2267131	T	T	270	150	234	184	6.028	0.0141	rs2175853	15	31323845	q13.3
SNP_A-2282323	C	C	308	52	326	88	6.03	0.0141	rs12702665	7	7642171	p21.3
SNP_A-2282627	G	G	357	13	412	4	6.027	0.0141	rs9343272	6	75895617	q13
SNP_A-2281036	A	A	322	24	382	12	6.025	0.0141	rs334728	1	61321028	p31.3
SNP_A-2297327	C	C	221	201	254	164	6.024	0.0141	rs10792346	11	61896645	q12.3
SNP_A-2040089	A	A	271	89	266	130	6.022	0.0141	rs1770889	1	76113187	p31.1
SNP_A-2023605	A	A	331	35	345	63	6.029	0.0141	rs10114624	9	90945766	q22.2
SNP_A-2097825	G	G	339	5	412	0	6.028	0.0141	rs11195828	10	113885848	q25.2
SNP_A-2094022	G	G	312	58	375	41	6.025	0.0141	rs201363	12	97747294	q23.1
SNP_A-2102509	A	A	266	98	254	138	6.028	0.0141	rs13148213	4	114393178	q25
SNP_A-2064343	T	T	224	82	217	121	6.029	0.0141	rs4794426	17	43522873	q21.32
SNP_A-2216621	A	A	275	61	285	99	6.03	0.0141	rs3099156	10	60284626	q21.1
SNP_A-2215804	T	T	185	137	250	126	6.031	0.0141	rs7695010	4	73862167	q13.3
SNP_A-2161878	G	A	194	166	218	178	6.029	0.0141	rs12286641	11	23269339	p14.3
SNP_A-2160360	G	G	365	1	379	9	6.027	0.0141	rs2556305	2	214438377	q34
SNP_A-2111822	C	C	351	55	380	34	6.028	0.0141	rs1329067	9	117501753	q33.1
SNP_A-2120254	C	C	339	17	407	7	6.03	0.0141	rs4776114	15	51201395	q21.3
SNP_A-2130596	A	A	267	103	249	141	6.024	0.0141	rs7523273	1	204365478	q32.2
SNP_A-1857592	G	G	319	39	365	23	6.026	0.0141	rs11987090	8	55547781	q11.23
SNP_A-1829000	A	A	238	150	284	124	6.022	0.0141	rs2045795	12	84563871	q21.31
SNP_A-1819509	T	T	270	30	280	56	6.024	0.0141	rs1353421	13	70081653	q21.33
SNP_A-1843360	G	G	359	15	341	31	6.023	0.0141	rs7096116	10	60283095	q21.1
SNP_A-1830300	T	T	286	60	275	91	6.023	0.0141	rs17594951	13	41213042	q14.11
SNP_A-1802455	G	G	364	22	387	9	6.029	0.0141	rs17140497	11	80042053	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1670251	C	C	387	3	391	13	6.026	0.0141	rs4133932	14	24813214	q12
SNP_A-1784874	C	C	335	21	360	44	6.03	0.0141	rs11246299	11	732508	p15.5
SNP_A-1892115	A	A	251	155	212	186	6.024	0.0141	rs1040729	14	62494673	q23.2
SNP_A-1900884	C	C	346	32	356	58	6.03	0.0141	rs11154661	6	132466247	q23.2
SNP_A-1904397	A	A	413	1	378	8	6.02	0.0141	rs2791508	1	86666419	p22.3
SNP_A-1888477	G	G	350	22	326	40	6.029	0.0141	rs4880121	9	136851666	q34.3
SNP_A-1931917	G	G	376	32	351	53	6.028	0.0141	rs17246486	11	121591743	q24.1
SNP_A-1975647	T	T	343	5	353	17	6.021	0.0141	rs16863803	3	190160686	q28
SNP_A-1974267	C	C	267	51	332	36	6.027	0.0141	rs1000716	3	126350729	q21.2
SNP_A-1978055	C	C	351	19	406	8	6.027	0.0141	---	4	92610025	q22.1
SNP_A-1934939	G	G	205	165	265	149	6.024	0.0141	rs12991269	2	129207214	q14.3
SNP_A-1950358	T	T	355	1	369	9	6.017	1.42E-02	rs662009	1	95802402	p21.3
SNP_A-1922642	C	C	247	121	302	100	6.016	1.42E-02	rs10019061	4	59447540	q12
SNP_A-1887132	C	C	333	5	404	0	6.017	1.42E-02	rs13336133	16	77887268	q23.1
SNP_A-1885635	A	A	361	9	357	23	6.015	1.42E-02	rs6651478	8	18983638	p22
SNP_A-1874855	G	G	302	106	274	140	6.017	1.42E-02	rs1268640	14	62500016	q23.2
SNP_A-1809489	G	G	373	3	377	13	6.017	1.42E-02	rs10783348	12	48993501	q13.12
SNP_A-1820038	A	A	350	40	337	65	6.018	1.42E-02	rs1111278	16	76260141	q23.1
SNP_A-1856158	A	A	313	53	318	86	6.013	1.42E-02	rs12374301	4	112225030	q25
SNP_A-1848172	T	T	231	137	224	190	6.013	1.42E-02	rs9843602	3	195056735	q29
SNP_A-2156615	A	A	408	2	372	10	6.012	1.42E-02	rs11186078	10	91973221	q23.31
SNP_A-2152673	C	C	355	55	384	34	6.016	1.42E-02	rs16826424	2	230567924	q36.3
SNP_A-2224327	G	G	317	93	276	120	6.016	1.42E-02	rs12278260	11	85344652	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2200851	A	A	333	5	404	0	6.017	1.42E-02	rs16931547	11	15486262	p15.2
SNP_A-2071704	G	G	230	136	222	188	6.012	1.42E-02	rs11710509	3	73618362	p13
SNP_A-2049299	T	G	211	157	208	196	6.013	1.42E-02	rs6827843	4	10364906	p16.1
SNP_A-2050621	A	A	230	114	284	94	6.008	1.42E-02	rs10281788	7	13045494	p21.3
SNP_A-2085470	G	G	294	48	343	31	6.009	1.42E-02	rs16843241	2	241751080	q37.3
SNP_A-2031854	A	A	344	6	359	19	6.012	1.42E-02	rs10245698	7	126516080	q32.1
SNP_A-2028424	G	G	304	32	288	54	6.008	1.42E-02	rs12082503	1	67201530	p31.2
SNP_A-2040179	G	G	386	0	382	6	6.016	1.42E-02	rs16919923	8	55127773	q11.23
SNP_A-2011572	G	G	264	128	298	98	6.019	1.42E-02	rs6907944	6	11588616	p24.2
SNP_A-1997943	T	T	322	44	334	24	6.014	1.42E-02	rs16911805	9	122333695	q33.2
SNP_A-2233301	A	A	285	121	299	85	6.019	1.42E-02	rs4886888	15	75685439	q24.3
SNP_A-2259041	A	A	308	60	319	97	5.996	0.0143	rs13293437	9	106157346	q31.2
SNP_A-2303117	G	G	223	143	214	196	5.996	0.0143	rs12503964	4	115383285	q26
SNP_A-2000643	T	T	286	126	250	158	6.004	0.0143	rs10508929	10	51841987	q11.23
SNP_A-2007144	T	T	249	109	248	158	6.003	0.0143	rs2573712	2	237726556	q37.3
SNP_A-2028300	A	A	365	7	366	20	6.004	0.0143	rs7091938	10	19981457	p12.31
SNP_A-2106279	T	T	339	5	410	0	5.999	0.0143	---	12	125304284	q24.31
SNP_A-2096803	G	G	261	105	261	153	5.999	0.0143	rs7226966	18	62068324	q22.1
SNP_A-2207424	A	A	256	92	253	135	6.007	0.0143	rs9589039	13	90345400	q31.3
SNP_A-2189134	A	A	282	66	357	51	6.002	0.0143	rs7979776	12	66491620	q15
SNP_A-2151183	A	A	342	8	367	23	5.995	0.0143	rs9402030	6	128602695	q22.33
SNP_A-2128532	T	T	276	36	358	24	6.006	0.0143	rs16849813	3	141276585	q23
SNP_A-1819977	C	C	356	44	368	24	6.001	0.0143	rs3171985	2	28583161	p23.2
SNP_A-1879742	G	G	319	9	315	23	6.001	0.0143	rs1508100	11	115842346	q23.3
SNP_A-1893023	C	C	322	44	333	75	5.999	0.0143	rs651069	11	75633449	q13.5
SNP_A-1924642	T	T	253	157	289	125	6.003	0.0143	rs589423	9	22711048	p21.3
SNP_A-1929853	G	G	173	171	237	163	6.001	0.0143	rs6965095	7	53060124	p12.1
SNP_A-1961036	T	C	198	166	220	184	6	0.0143	rs10900684	5	112704090	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1956888	C	C	337	27	392	14	5.998	0.0143	rs1613279	10	43780417	q11.21
SNP_A-1934179	C	C	319	97	289	129	6.006	0.0143	rs2605100	1	216032619	q41
SNP_A-1984393	C	C	312	56	321	91	5.998	0.0143	rs1862168	5	163127599	q34
SNP_A-1989430	T	T	329	19	380	8	5.994	0.0144	rs7785412	7	31720077	p14.3
SNP_A-1942021	T	T	323	9	398	2	5.991	0.0144	rs2606712	4	62142053	q13.1
SNP_A-1948591	T	T	416	6	418	0	5.986	0.0144	rs9825922	3	40590488	p22.1
SNP_A-1913958	G	G	294	104	326	76	5.987	0.0144	rs17045554	2	116619488	q14.1
SNP_A-1844053	T	T	252	104	252	152	5.992	0.0144	rs10732197	9	5849774	p24.1
SNP_A-1863727	A	A	412	6	414	0	5.986	0.0144	rs17123578	1	62580981	p31.3
SNP_A-1860708	G	G	349	19	326	36	5.989	0.0144	rs9357440	6	9600379	p24.3
SNP_A-1805078	G	A	192	168	219	175	5.987	0.0144	rs10041986	5	138452336	q31.2
SNP_A-1791562	G	G	361	1	377	9	5.983	0.0144	rs1347599	4	142596341	q31.21
SNP_A-1655743	G	G	320	26	355	53	5.985	0.0144	rs288326	2	183905879	q32.1
SNP_A-2123708	C	C	379	27	392	12	5.984	0.0144	rs2144975	14	50039198	q21.3
SNP_A-2112709	A	A	380	30	392	14	5.985	0.0144	rs625436	1	198293332	q32.1
SNP_A-2145164	G	G	362	0	360	6	5.984	0.0144	rs8191180	16	80663824	q23.3
SNP_A-2166879	C	C	329	73	359	49	5.985	0.0144	rs17485567	5	31468556	p13.3
SNP_A-2167896	A	A	248	102	220	134	5.992	0.0144	rs10198045	2	11453771	p25.1
SNP_A-2198399	T	T	408	6	410	0	5.986	0.0144	rs7870837	9	124678862	q33.3
SNP_A-2173447	G	G	367	19	387	7	5.988	0.0144	rs17061165	13	39817514	q14.11
SNP_A-2176706	C	C	360	8	387	23	5.984	0.0144	rs17647222	6	34988447	p21.31
SNP_A-2181854	G	G	357	13	379	31	5.986	0.0144	rs4793332	17	66605715	q24.3
SNP_A-2224439	T	T	277	73	287	115	5.993	0.0144	rs1346856	2	195691872	q32.3
SNP_A-2088122	A	A	341	5	412	0	5.993	0.0144	rs12563308	1	62781732	p31.3
SNP_A-2083854	A	A	331	5	400	0	5.993	0.0144	rs10119834	9	118879697	q33.1
SNP_A-2051102	C	C	376	0	374	6	5.984	0.0144	rs17126955	12	37838153	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072867	T	T	312	92	267	117	5.984	0.0144	rs12799307	11	68493638	q13.3
SNP_A-2071886	T	T	292	96	275	133	5.989	0.0144	rs12682291	8	56209626	q12.1
SNP_A-2027505	T	T	271	89	273	133	5.987	0.0144	rs6592177	11	83745645	q14.1
SNP_A-2032933	C	C	301	69	305	107	5.992	0.0144	rs924237	4	27937927	p15.1
SNP_A-2017437	G	G	293	77	298	118	5.991	0.0144	rs118736	21	28542240	q21.3
SNP_A-2014013	C	C	283	77	345	59	5.989	0.0144	rs4452851	9	5278908	p24.1
SNP_A-2000492	G	G	371	27	384	12	5.988	0.0144	rs6671463	1	173003394	q25.2
SNP_A-2003703	G	G	308	82	324	54	5.984	0.0144	rs1891431	10	90203400	q23.31
SNP_A-1996334	-	G	206	206	241	171	5.99	0.0144	rs7020191	9	26516327	p21.2
SNP_A-2304548	C	C	266	68	310	48	5.984	0.0144	rs676812	11	117431803	q23.3
SNP_A-2308796	G	G	320	48	382	32	5.991	0.0144	rs766771	4	188451901	q35.2
SNP_A-2290354	T	T	285	31	361	19	5.987	0.0144	rs1243507	14	94384186	q32.13
SNP_A-2288130	G	G	304	42	284	66	5.991	0.0144	rs6591243	11	55894030	q11
SNP_A-2259790	A	A	328	22	340	44	5.987	0.0144	rs9843992	3	64304857	p14.1
SNP_A-2261086	A	A	290	68	343	49	5.994	0.0144	rs2208981	20	12307879	p12.1
SNP_A-2236628	A	A	330	30	378	16	5.994	0.0144	rs7755882	6	120761581	q22.31
SNP_A-2238929	A	A	286	70	297	111	5.983	0.0144	rs11180001	12	120000137	q24.31
SNP_A-2244329	A	A	270	48	324	32	5.986	0.0144	rs892447	2	26321601	p23.3
SNP_A-2243605	C	C	312	64	274	88	5.99	0.0144	rs12246970	10	414200	p15.3
SNP_A-2261823	A	A	403	19	378	36	5.979	1.45E-02	rs7085996	10	68245644	q21.3
SNP_A-2260434	G	G	293	53	301	87	5.981	1.45E-02	rs10996891	10	67523940	q21.3
SNP_A-2291864	A	A	345	5	416	0	5.982	1.45E-02	rs7813624	8	28180868	p21.1
SNP_A-2314863	A	A	228	194	257	155	5.973	1.45E-02	rs11720652	3	14636424	p25.1
SNP_A-2310979	T	T	297	37	310	66	5.98	1.45E-02	rs10931508	2	153886164	q23.3
SNP_A-1992591	G	G	258	112	319	93	5.971	1.45E-02	rs923767	8	19691841	p21.3
SNP_A-2011714	G	G	161	125	248	130	5.972	1.45E-02	rs6458020	6	37831141	p21.2
SNP_A-2225629	G	G	325	21	350	44	5.976	1.45E-02	rs4772089	13	97946087	q32.2
SNP_A-2216825	A	A	357	13	410	4	5.976	1.45E-02	rs7578066	2	30888303	p23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209836	A	A	324	54	349	33	5.977	1.45E-02	rs12906915	15	31489514	q14
SNP_A-2177612	T	T	299	123	263	155	5.971	1.45E-02	rs949571	1	194044846	q31.3
SNP_A-2192481	C	C	357	9	389	25	5.971	1.45E-02	rs552161	2	166811553	q24.3
SNP_A-2139957	C	C	308	22	377	11	5.971	1.45E-02	rs4654669	1	225345163	q42.13
SNP_A-2112086	T	T	336	8	361	23	5.975	1.45E-02	rs10176638	2	171015646	q31.1
SNP_A-2127131	C	A	174	166	219	159	5.977	1.45E-02	rs6534608	4	76388831	q13.3
SNP_A-2136768	T	T	359	17	344	34	5.981	1.45E-02	rs17763310	16	10809655	p13.13
SNP_A-1791427	T	T	257	109	255	157	5.971	1.45E-02	rs8098648	18	53101627	q21.31
SNP_A-1789582	A	A	238	120	307	105	5.978	1.45E-02	rs426818	7	152456928	q36.2
SNP_A-1793015	C	C	350	26	357	49	5.981	1.45E-02	rs734706	12	46428418	q13.11
SNP_A-1871525	T	T	337	5	406	0	5.976	1.45E-02	rs16913256	11	13833706	p15.2
SNP_A-1849567	C	C	195	165	248	146	5.981	1.45E-02	rs13021632	2	116867725	q14.1
SNP_A-1910104	C	C	359	9	391	25	5.978	1.45E-02	rs6988862	8	48600111	q11.21
SNP_A-1930464	T	T	324	40	372	24	5.974	1.45E-02	rs4956136	4	109039695	q25
SNP_A-1952402	T	T	239	123	226	168	5.978	1.45E-02	rs9297647	8	122752621	q24.13
SNP_A-1988520	G	G	345	51	300	72	5.981	1.45E-02	rs515982	6	167956716	q27
SNP_A-1962289	C	C	222	144	214	198	5.974	1.45E-02	rs7592574	2	17170201	p24.2
SNP_A-1961999	C	C	304	30	349	61	5.96	0.0146	rs10495553	2	7356498	p25.1
SNP_A-1967886	G	G	289	79	295	121	5.965	0.0146	rs175310	20	15171632	p12.1
SNP_A-1950611	T	T	312	32	327	59	5.966	0.0146	rs17503704	7	154888937	q36.3
SNP_A-1937443	G	G	267	101	264	146	5.965	0.0146	rs2358	6	162619325	q26
SNP_A-1923776	A	A	296	56	346	38	5.961	0.0146	rs17121553	14	85250578	q31.3
SNP_A-1896439	T	T	329	5	396	0	5.969	0.0146	rs16839047	2	138113994	q22.1
SNP_A-1899038	T	T	313	49	346	30	5.959	0.0146	rs7592671	2	167750097	q24.3
SNP_A-1871504	C	C	256	84	311	65	5.963	0.0146	rs12104318	19	58339000	q13.42
SNP_A-1799253	T	T	341	5	410	0	5.964	0.0146	rs6566377	18	64487410	q22.1
SNP_A-1787607	A	A	339	5	408	0	5.97	0.0146	rs17099716	1	77105205	p31.1
SNP_A-1781896	G	G	326	28	383	15	5.959	0.0146	rs1545394	7	114054739	q31.1
SNP_A-2141667	A	A	318	102	282	132	5.963	0.0146	rs8048267	16	71647540	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2151896	C	C	244	126	239	177	5.964	0.0146	rs9837231	3	180732538	q26.33
SNP_A-2152456	T	T	266	78	222	100	5.966	0.0146	rs7105560	11	27401706	p14.1
SNP_A-2146179	G	G	246	108	249	159	5.963	0.0146	rs17012225	2	119607082	q14.2
SNP_A-2197693	G	G	336	34	354	62	5.965	0.0146	rs11934851	4	182020134	q34.3
SNP_A-2179138	T	C	205	187	219	169	5.967	0.0146	rs12705263	7	103919062	q22.2
SNP_A-2169451	C	C	269	87	277	133	5.958	0.0146	rs12770214	10	22911129	p12.2
SNP_A-2170656	C	C	277	87	281	131	5.963	0.0146	rs8075367	17	50918972	q23.1
SNP_A-2207506	G	G	294	42	353	27	5.96	0.0146	rs11236190	11	74044403	q13.4
SNP_A-2205399	A	A	303	33	357	19	5.959	0.0146	rs843257	9	102665633	q31.1
SNP_A-2214958	C	C	257	163	284	126	5.965	0.0146	rs1548836	12	12945501	p13.1
SNP_A-2015861	T	T	219	109	209	153	5.962	0.0146	rs2156200	21	19031172	q21.1
SNP_A-1990934	G	G	328	16	380	6	5.968	0.0146	rs1227170	7	112005670	q31.1
SNP_A-2026085	G	G	374	42	378	22	5.96	0.0146	rs11186298	10	92501484	q23.31
SNP_A-2058728	C	C	260	88	325	71	5.968	0.0146	rs4246096	7	154379051	q36.2
SNP_A-2105916	G	G	322	26	313	47	5.967	0.0146	rs17274369	7	24510498	p15.3
SNP_A-2297941	A	G	190	140	204	192	5.967	0.0146	rs563722	11	73806589	q13.4
SNP_A-2254043	G	G	217	151	279	135	5.96	0.0146	rs2742395	3	45733599	p21.31
SNP_A-2240371	C	C	355	49	337	25	5.967	0.0146	rs4983575	14	104060905	q32.33
SNP_A-2228093	G	G	361	17	390	6	5.965	0.0146	rs1927836	13	28607309	q12.3
SNP_A-2228589	C	C	273	81	325	61	5.966	0.0146	rs4670704	2	37536537	p22.2
SNP_A-2247477	G	G	330	12	332	28	5.948	0.0147	rs6494014	15	56564770	q21.3
SNP_A-2270107	G	G	230	172	237	123	5.947	0.0147	rs10868290	9	85229724	q21.33
SNP_A-2297148	G	G	204	156	265	141	5.951	0.0147	rs13187198	5	124843518	q23.2
SNP_A-2304095	T	T	232	92	299	77	5.955	0.0147	rs3822101	4	75673136	q13.3
SNP_A-2100894	T	T	242	168	277	135	5.95	0.0147	rs1372494	4	46959312	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082920	A	A	314	88	278	116	5.953	0.0147	rs12538804	7	7467159	p21.3
SNP_A-2077731	A	A	279	133	315	103	5.952	0.0147	rs7635061	3	129755179	q21.3
SNP_A-2077895	C	C	346	22	394	10	5.948	0.0147	rs1123595	2	190198621	q32.2
SNP_A-2057361	C	C	213	143	280	130	5.947	0.0147	rs1481153	1	234746223	q43
SNP_A-2054998	T	C	182	178	232	166	5.958	0.0147	rs1740733	10	38532383	p11.21
SNP_A-2075233	G	G	362	0	362	6	5.951	0.0147	rs1288178	6	113432209	q21
SNP_A-2062629	C	C	333	5	400	0	5.958	0.0147	rs10160264	11	97462791	q22.1
SNP_A-2033968	A	A	333	23	359	47	5.95	0.0147	rs17135807	11	77072900	q13.5
SNP_A-2041081	G	G	337	5	404	0	5.946	0.0147	rs16926614	9	262950	p24.3
SNP_A-2041961	G	G	358	58	325	83	5.95	0.0147	rs17620535	2	230193911	q36.3
SNP_A-2014049	C	C	358	2	402	12	5.952	0.0147	rs6477424	9	9856363	p23
SNP_A-2006992	C	C	374	8	405	1	5.953	0.0147	rs7604632	2	213506151	q34
SNP_A-2204803	C	C	342	36	325	59	5.955	0.0147	rs12352728	9	106237710	q31.2
SNP_A-2181844	T	T	261	97	309	75	5.952	0.0147	rs10871351	16	77080407	q23.1
SNP_A-2143219	T	T	224	122	203	161	5.955	0.0147	rs6982765	8	137088067	q24.23
SNP_A-2112037	A	A	412	0	412	6	5.957	0.0147	rs403322	1	83068302	p31.1
SNP_A-2112526	T	T	389	3	362	12	5.951	0.0147	rs8036851	15	45830750	q21.1
SNP_A-2108025	A	A	260	134	216	160	5.949	0.0147	rs10444780	14	106086257	q32.33
SNP_A-1805443	T	T	244	112	245	163	5.949	0.0147	rs1847029	3	123390184	q21.1
SNP_A-1842659	G	G	335	5	402	0	5.952	0.0147	rs7623124	3	147470976	q24
SNP_A-1833068	G	G	285	77	352	60	5.951	0.0147	rs6544486	2	42000458	p21
SNP_A-1815434	C	C	242	164	200	192	5.949	0.0147	rs17815112	2	155139802	q24.1
SNP_A-1827179	T	T	388	4	368	14	5.956	0.0147	rs619917	11	97088314	q22.1
SNP_A-1878597	A	A	310	8	333	23	5.957	0.0147	rs16874250	5	4966720	p15.32
SNP_A-1886014	G	G	342	26	365	51	5.949	0.0147	rs17165969	7	130987107	q32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889101	C	G	176	174	222	156	5.955	0.0147	rs811952	1	66628155	p31.2
SNP_A-1922948	G	G	297	57	315	95	5.957	0.0147	rs7998576	13	114059290	q34
SNP_A-1945317	T	T	305	33	323	61	5.95	0.0147	rs6676665	1	169077831	q24.3
SNP_A-1961922	A	A	242	116	241	167	5.955	0.0147	rs2564086	2	5895096	p25.2
SNP_A-1921198	A	A	274	80	261	115	5.94	1.48E-02	rs7021837	9	13844176	p23
SNP_A-1883370	A	A	314	66	299	97	5.935	1.48E-02	rs10089895	8	140653145	q24.3
SNP_A-1875019	C	C	383	1	354	8	5.942	1.48E-02	rs1377430	7	47560947	p12.3
SNP_A-1871377	A	A	184	182	243	169	5.935	1.48E-02	rs1511181	2	79828856	p12
SNP_A-1787814	T	C	215	201	235	179	5.936	1.48E-02	rs7792547	7	150661177	q36.1
SNP_A-1793180	C	T	207	159	210	192	5.938	1.48E-02	rs2881439	16	7223491	p13.2
SNP_A-1758408	T	T	324	42	299	65	5.942	1.48E-02	rs7779197	7	117340071	q31.31
SNP_A-2132749	T	T	260	72	221	95	5.938	1.48E-02	rs17077499	13	83403998	q31.1
SNP_A-2178294	C	C	319	35	366	20	5.943	1.48E-02	rs10873893	1	76731618	p31.1
SNP_A-2169171	G	G	315	47	384	32	5.94	1.48E-02	rs6135591	20	15822488	p12.1
SNP_A-2186448	A	A	383	31	346	50	5.938	1.48E-02	rs11199296	10	122113384	q26.12
SNP_A-2206740	G	G	415	1	384	8	5.94	1.48E-02	rs4872222	8	24249209	p21.2
SNP_A-2208901	G	G	361	53	337	79	5.942	1.48E-02	rs6465748	7	98505958	q22.1
SNP_A-2014047	C	C	356	2	400	12	5.946	1.48E-02	rs7341699	9	9856067	p23
SNP_A-2015656	C	C	339	29	359	55	5.935	1.48E-02	rs2849903	21	17869241	q21.1
SNP_A-2027318	A	A	354	16	380	36	5.942	1.48E-02	rs6739788	2	55774006	p16.1
SNP_A-2064634	G	G	304	62	313	99	5.935	1.48E-02	rs13296705	9	106175966	q31.2
SNP_A-2069109	C	C	337	67	345	41	5.946	1.48E-02	rs874651	11	11735950	p15.3
SNP_A-2048420	G	G	199	129	253	111	5.945	1.48E-02	rs2123590	7	61560772	q11.21
SNP_A-2084196	G	G	342	28	401	15	5.944	1.48E-02	rs7158821	14	89452604	q32.11
SNP_A-2092934	C	C	350	16	404	6	5.937	1.48E-02	rs757218	7	11346883	p21.3
SNP_A-2303190	A	A	337	11	399	3	5.937	1.48E-02	rs972201	13	66457730	q21.32
SNP_A-2309661	G	G	352	16	406	6	5.929	0.0149	rs7146630	14	93207300	q32.13
SNP_A-2279982	T	T	256	128	239	171	5.923	0.0149	rs287004	12	40313056	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2244511	A	A	321	7	401	1	5.924	0.0149	---	9	23667920	p21.3
SNP_A-2253793	C	T	181	153	213	175	5.932	0.0149	rs1355305	8	14516092	p22
SNP_A-2249528	A	A	307	45	372	30	5.933	0.0149	rs6043594	20	15811584	p12.1
SNP_A-2097054	T	T	326	16	328	34	5.923	0.0149	rs6533806	4	115974511	q26
SNP_A-2097343	G	A	188	158	210	174	5.927	0.0149	rs8005754	14	75746580	q24.3
SNP_A-2103293	A	A	335	73	358	48	5.924	0.0149	rs1009737	20	58268865	q13.33
SNP_A-2072043	A	A	341	23	395	11	5.924	0.0149	rs17096082	12	44217885	q12
SNP_A-2028960	G	G	360	42	390	24	5.934	0.0149	rs11253536	10	998627	p15.3
SNP_A-2209414	A	A	297	51	269	75	5.934	0.0149	rs12566267	1	159884826	q23.3
SNP_A-2209477	G	G	368	42	385	23	5.933	0.0149	rs906036	3	72100474	p13
SNP_A-2108562	T	T	352	18	366	38	5.934	0.0149	rs3935796	11	127896137	q24.3
SNP_A-2145072	C	C	262	108	326	90	5.931	0.0149	rs1543990	6	111042870	q21
SNP_A-2152829	A	A	339	21	348	42	5.927	0.0149	rs8039802	15	35251759	q14
SNP_A-1781129	C	C	356	64	327	91	5.93	0.0149	rs17395848	2	133116608	q21.2
SNP_A-1696564	C	C	310	78	354	56	5.926	0.0149	rs477627	20	48865480	q13.13
SNP_A-1798076	C	C	340	66	346	40	5.929	0.0149	rs2965004	1	215162221	q41
SNP_A-1814214	G	G	314	48	374	32	5.931	0.0149	rs12893741	14	70372615	q24.2
SNP_A-1817867	C	C	367	39	387	21	5.926	0.0149	rs1437256	1	117869655	p12
SNP_A-1837027	G	G	312	106	280	138	5.926	0.0149	rs10996854	10	67478039	q21.3
SNP_A-1920389	G	G	280	42	301	75	5.925	0.0149	rs11730109	4	66400390	q13.1
SNP_A-1905267	C	C	335	35	351	63	5.922	0.0149	rs17160672	7	31719351	p14.3
SNP_A-1986282	A	A	310	46	268	66	5.928	0.0149	rs1153930	1	220299854	q42.11
SNP_A-1947501	T	T	375	15	372	32	5.916	1.50E-02	rs12041396	1	176318441	q25.2
SNP_A-1906311	T	T	231	125	288	106	5.913	1.50E-02	rs227897	4	113200489	q25
SNP_A-1929797	G	G	340	14	407	5	5.915	1.50E-02	rs9955059	18	66884430	q22.2
SNP_A-1931943	T	T	376	8	405	1	5.913	1.50E-02	rs11035027	11	38944010	p12
SNP_A-1889605	G	G	374	8	403	1	5.916	1.50E-02	rs7982303	13	64818553	q21.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1830292	G	A	211	205	240	176	5.918	1.50E-02	rs3130232	6	33202918	p21.32
SNP_A-1844361	A	A	213	111	276	96	5.921	1.50E-02	rs10809565	9	11701989	p23
SNP_A-1839272	G	G	328	30	374	16	5.917	1.50E-02	rs4608753	4	30317605	p15.1
SNP_A-1870192	G	G	299	19	373	9	5.918	1.50E-02	rs12090325	1	213862464	q41
SNP_A-1865010	T	T	312	54	277	77	5.92	1.50E-02	rs1841575	15	51886958	q21.3
SNP_A-1849491	C	C	307	25	367	13	5.922	1.50E-02	rs12682088	8	127624112	q24.21
SNP_A-1852310	G	G	236	128	233	181	5.921	1.50E-02	rs11753672	6	6291965	p25.1
SNP_A-1789420	A	A	219	143	269	121	5.922	1.50E-02	rs1586736	18	61993649	q22.1
SNP_A-1782481	C	C	295	13	385	5	5.916	1.50E-02	rs445429	19	53285169	q13.32
SNP_A-2160270	C	C	249	121	245	171	5.922	1.50E-02	rs7001605	8	32466789	p12
SNP_A-2143393	A	G	197	161	207	177	5.916	1.50E-02	rs6572091	14	40956359	q21.1
SNP_A-2142987	A	A	332	32	330	56	5.911	1.50E-02	rs550137	6	145641712	q24.2
SNP_A-2147041	T	T	349	55	376	34	5.917	1.50E-02	rs6136060	20	17236277	p12.1
SNP_A-2118031	A	A	349	5	416	0	5.914	1.50E-02	rs6437746	3	96474778	q11.2
SNP_A-2131796	A	A	328	6	345	19	5.911	1.50E-02	rs283251	18	66016842	q22.2
SNP_A-2227891	G	G	303	17	319	37	5.919	1.50E-02	rs16926445	11	42107883	p12
SNP_A-2171573	C	C	291	31	367	19	5.921	1.50E-02	rs28948	17	28358672	q11.2
SNP_A-2025292	G	G	354	0	356	6	5.917	1.50E-02	rs7749889	6	91098350	q15
SNP_A-2022987	G	G	407	1	378	8	5.911	1.50E-02	rs11948492	5	145318370	q32
SNP_A-2019420	G	G	239	111	299	93	5.921	1.50E-02	rs6517547	21	39677864	q22.2
SNP_A-2073507	T	C	220	196	230	184	5.917	1.50E-02	rs12681643	8	31565475	p12
SNP_A-2053937	C	T	232	184	212	190	5.922	1.50E-02	rs276943	18	26862792	q12.1
SNP_A-2250745	C	C	211	147	279	135	5.916	1.50E-02	rs4424544	1	60645801	p31.3
SNP_A-2277104	T	T	390	10	361	23	5.917	1.50E-02	rs2699975	3	110453409	q13.13
SNP_A-2277884	T	T	350	62	323	89	5.911	1.50E-02	rs2666552	15	45685780	q21.1
SNP_A-2301792	C	C	360	8	389	23	5.918	1.50E-02	rs5021680	3	160758479	q25.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2310774	C	C	304	64	311	101	5.913	1.50E-02	rs358683	1	91170056	p22.2
SNP_A-2290960	G	G	371	35	390	18	5.922	1.50E-02	rs217632	14	61447527	q23.2
SNP_A-2288219	G	G	312	26	340	52	5.907	1.51E-02	rs11044016	12	18347045	p12.3
SNP_A-2309715	T	T	185	181	244	168	5.899	1.51E-02	rs1261086	18	51039823	q21.2
SNP_A-2267121	A	A	298	64	308	102	5.902	1.51E-02	rs506858	4	58446870	q12
SNP_A-2238896	C	C	300	70	307	109	5.906	1.51E-02	rs1996141	18	32178879	q12.2
SNP_A-2237466	G	G	316	24	372	12	5.906	1.51E-02	rs4270992	8	2632417	p23.2
SNP_A-2235646	A	A	365	1	385	9	5.91	1.51E-02	rs7578567	2	83579725	p11.2
SNP_A-2070255	A	A	404	16	415	5	5.91	1.51E-02	rs4346580	3	51191618	p21.31
SNP_A-2078414	G	G	319	97	347	69	5.9	1.51E-02	rs12435549	14	25596847	q12
SNP_A-2030768	T	T	371	11	368	26	5.909	1.51E-02	rs1996190	8	83633749	q21.13
SNP_A-1990554	A	A	372	40	381	21	5.904	1.51E-02	rs17163534	7	90323788	q21.13
SNP_A-2178413	C	C	389	19	407	7	5.902	1.51E-02	rs1835319	2	16507685	p24.3
SNP_A-2184819	C	A	200	160	210	184	5.902	1.51E-02	rs4918501	10	112138500	q25.2
SNP_A-2198939	T	T	232	124	299	109	5.908	1.51E-02	rs4310100	7	61635018	q11.21
SNP_A-2211988	G	G	195	173	255	159	5.905	1.51E-02	rs1962941	11	96877206	q22.1
SNP_A-2134953	T	T	198	114	274	106	5.903	1.51E-02	rs11236417	11	74768201	q13.4
SNP_A-2127678	T	T	268	114	302	86	5.902	1.51E-02	rs819652	1	233134513	q43
SNP_A-2129443	T	T	409	1	380	8	5.908	1.51E-02	rs6478815	9	127930433	q34.11
SNP_A-2160998	C	C	217	67	314	60	5.906	1.51E-02	rs7225419	17	30570582	q12
SNP_A-1782947	T	T	236	140	277	113	5.904	1.51E-02	rs17022939	12	93515203	q22
SNP_A-1784059	T	T	350	2	359	11	5.9	1.51E-02	---	4	62947625	q13.1
SNP_A-1783346	G	G	237	133	231	185	5.908	1.51E-02	rs17178251	17	66688474	q24.3
SNP_A-1651782	G	G	341	37	329	61	5.906	1.51E-02	rs9306937	4	36521236	p14
SNP_A-1670726	T	T	358	26	342	46	5.901	1.51E-02	rs2255945	13	49062249	q14.3
SNP_A-1807507	T	G	230	164	198	196	5.907	1.51E-02	rs2414346	15	52744472	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803705	C	C	315	31	363	17	5.902	1.51E-02	rs12190821	6	24276989	p22.2
SNP_A-1850064	C	C	292	62	346	44	5.899	1.51E-02	rs385628	4	167543776	q32.3
SNP_A-1855400	A	A	384	38	400	20	5.908	1.51E-02	rs7558431	2	221224908	q35
SNP_A-1827459	A	A	321	25	383	13	5.907	1.51E-02	rs11166770	8	138993825	q24.23
SNP_A-1892626	T	T	413	1	384	8	5.904	1.51E-02	rs11890915	2	18595616	p24.2
SNP_A-1881428	G	G	308	82	297	49	5.904	1.51E-02	rs4421839	12	102433819	q23.3
SNP_A-1921162	A	A	257	157	218	188	5.91	1.51E-02	rs10905076	10	7052437	p14
SNP_A-1922334	A	G	208	160	216	198	5.901	1.51E-02	rs7649685	3	82620799	p12.2
SNP_A-1922388	T	T	296	48	325	29	5.901	1.51E-02	rs10203097	2	132471215	q21.2
SNP_A-1982478	A	G	188	180	234	172	5.903	1.51E-02	rs702844	5	89410835	q14.3
SNP_A-1947381	T	T	214	156	273	139	5.889	0.0152	rs4490433	4	174872566	q34.1
SNP_A-1954683	C	C	271	125	242	160	5.893	0.0152	rs4435862	5	15772222	p15.1
SNP_A-1953763	T	T	222	136	212	186	5.894	0.0152	rs7644537	3	118763538	q13.31
SNP_A-1898251	C	C	225	145	286	128	5.89	0.0152	rs3784942	16	82268170	q23.3
SNP_A-1822426	T	T	272	26	347	15	5.888	0.0152	rs7159158	14	46915620	q21.3
SNP_A-1824275	T	T	336	32	390	18	5.89	0.0152	rs1858045	6	87321168	q14.3
SNP_A-1848515	T	T	329	35	391	21	5.892	0.0152	rs11108839	12	96037350	q23.1
SNP_A-1848432	C	C	368	44	378	24	5.894	0.0152	rs6507701	18	42216915	q21.1
SNP_A-1860574	A	A	335	11	395	3	5.897	0.0152	rs6097850	20	52271948	q13.2
SNP_A-1691458	C	C	342	34	336	58	5.896	0.0152	rs519504	1	228578000	q42.2
SNP_A-1785107	C	C	315	9	384	2	5.897	0.0152	rs9503909	6	4004541	p25.2
SNP_A-1758780	G	G	398	0	402	6	5.897	0.0152	rs10510971	3	68614485	p14.1
SNP_A-2159423	G	G	345	5	410	0	5.896	0.0152	rs755997	1	117180618	p13.1
SNP_A-2151588	T	T	324	16	348	36	5.897	0.0152	rs10990113	9	102308604	q31.1
SNP_A-2203934	C	C	293	25	370	14	5.892	0.0152	rs2412614	4	55602621	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2173104	A	A	338	26	299	43	5.896	0.0152	rs10968749	9	28742484	p21.1
SNP_A-2018186	C	T	201	159	216	192	5.893	0.0152	rs845017	21	32920185	q22.11
SNP_A-2020825	C	C	345	5	410	0	5.896	0.0152	rs4567502	11	114537776	q23.3
SNP_A-2043274	A	A	279	45	270	72	5.896	0.0152	rs17340963	4	13720965	p15.33
SNP_A-2042791	T	T	383	9	345	21	5.899	0.0152	rs7565911	2	125399794	q14.3
SNP_A-2086335	C	C	398	2	368	10	5.891	0.0152	rs10144170	14	40289373	q21.1
SNP_A-2074565	C	C	351	71	318	98	5.899	0.0152	rs11063667	12	5403395	p13.31
SNP_A-2250723	C	C	334	36	348	64	5.889	0.0152	rs10962297	9	16141623	p22.3
SNP_A-2250199	G	G	331	29	358	56	5.896	0.0152	rs10967964	9	27485920	p21.2
SNP_A-2254300	G	G	352	2	398	12	5.891	0.0152	rs10766347	11	16746222	p15.1
SNP_A-2263309	A	A	363	13	346	28	5.89	0.0152	rs7099015	10	102945942	q24.32
SNP_A-2264338	T	T	343	5	357	17	5.897	0.0152	rs17144974	5	118561398	q23.1
SNP_A-2280244	G	G	345	5	410	0	5.896	0.0152	rs12146806	12	49212971	q13.12
SNP_A-2283344	G	G	288	72	353	55	5.89	0.0152	rs10226177	7	133184207	q33
SNP_A-2306639	C	C	375	33	336	52	5.888	0.0152	rs163041	5	122540598	q23.2
SNP_A-2288814	T	T	376	8	348	20	5.888	0.0152	rs10813454	9	31082543	p21.1
SNP_A-2295541	C	C	330	78	307	109	5.892	0.0152	rs7888736	7	45803440	p13
SNP_A-2293932	G	G	220	148	282	132	5.886	1.53E-02	rs7689923	4	43118700	p13
SNP_A-2282206	G	G	266	144	301	113	5.881	1.53E-02	rs10848784	12	3058775	p13.33
SNP_A-2279060	T	T	351	5	416	0	5.881	1.53E-02	rs11067199	12	113502873	q24.21
SNP_A-2249882	G	A	234	184	213	193	5.882	1.53E-02	rs11039500	11	5875537	p15.4
SNP_A-2250936	C	C	408	2	378	10	5.876	1.53E-02	rs1525576	7	53034867	p12.1
SNP_A-2233818	G	G	303	63	359	45	5.876	1.53E-02	rs2426498	20	52230088	q13.2
SNP_A-2046491	A	A	317	51	331	85	5.886	1.53E-02	rs516286	11	104399381	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990348	G	G	239	125	292	104	5.879	1.53E-02	rs10486945	7	81417800	q21.11
SNP_A-2171159	A	G	206	160	218	198	5.885	1.53E-02	rs6129013	20	59459934	q13.33
SNP_A-2192182	G	G	321	7	399	1	5.887	1.53E-02	rs16886101	8	115634689	q23.3
SNP_A-2188896	T	T	374	10	404	2	5.882	1.53E-02	rs740996	7	156736135	q36.3
SNP_A-2189945	C	C	220	148	282	132	5.886	1.53E-02	rs2713285	4	134913061	q28.3
SNP_A-2214893	A	A	336	74	366	50	5.884	1.53E-02	rs2735400	16	76613442	q23.1
SNP_A-2140573	C	C	274	94	274	138	5.881	1.53E-02	rs1552124	1	215200962	q41
SNP_A-2125282	A	A	389	7	350	18	5.88	1.53E-02	rs16829292	2	233273128	q37.1
SNP_A-2111377	G	G	264	156	226	188	5.881	1.53E-02	rs2266985	22	21221876	q11.22
SNP_A-1806832	T	T	248	108	245	155	5.877	1.53E-02	rs3013813	10	47102635	q11.22
SNP_A-1788812	G	G	371	23	327	39	5.879	1.53E-02	rs7894582	10	115694448	q25.3
SNP_A-1790953	G	G	374	8	401	1	5.879	1.53E-02	rs6510606	19	1362326	p13.3
SNP_A-1871642	C	C	323	7	401	1	5.878	1.53E-02	rs10512583	17	67651131	q24.3
SNP_A-1844481	G	G	242	106	317	93	5.88	1.53E-02	rs7491984	13	82932721	q31.1
SNP_A-1856916	A	G	177	141	186	160	5.88	1.53E-02	rs10186231	2	242657167	q37.3
SNP_A-1827624	C	C	334	14	337	31	5.882	1.53E-02	---	4	100748818	q23
SNP_A-1843175	C	C	291	47	336	30	5.879	1.53E-02	rs7102635	11	31912785	p13
SNP_A-1834102	A	A	338	28	395	15	5.887	1.53E-02	rs443563	9	15561630	p22.3
SNP_A-1904223	T	T	403	1	376	8	5.876	1.53E-02	rs2298300	1	20720769	p36.12
SNP_A-1888176	T	T	310	22	377	11	5.881	1.53E-02	rs220928	6	15960369	p22.3
SNP_A-1874131	C	C	339	5	402	0	5.882	1.53E-02	rs7031006	9	28156400	p21.1
SNP_A-1925341	T	T	273	73	257	105	5.877	1.53E-02	rs9369470	6	12755098	p24.1
SNP_A-1925544	G	G	272	44	289	77	5.881	1.53E-02	rs541690	18	61010457	q22.1
SNP_A-1916111	T	T	329	35	285	53	5.88	1.53E-02	rs17109605	10	100135119	q24.2
SNP_A-1980499	G	G	290	56	338	38	5.879	1.53E-02	rs11958505	5	6927764	p15.31
SNP_A-1983534	A	A	352	68	321	95	5.881	1.53E-02	rs9327661	5	133030022	q31.1
SNP_A-1965777	C	A	201	169	225	189	5.878	1.53E-02	rs853772	2	169640162	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1969375	A	A	257	157	290	124	5.866	0.0154	rs2826984	21	22045027	q21.1
SNP_A-1988304	T	T	382	8	409	1	5.87	0.0154	rs11967737	6	158304731	q25.3
SNP_A-1948520	T	T	375	27	348	46	5.874	0.0154	rs2214873	7	41592151	p14.1
SNP_A-1942498	C	C	289	119	259	153	5.873	0.0154	rs1724932	7	2487598	p22.3
SNP_A-1905235	A	A	311	55	319	89	5.868	0.0154	rs17525479	4	169227941	q32.3
SNP_A-1924788	C	C	336	16	386	6	5.875	0.0154	rs1710746	1	105814037	p21.1
SNP_A-1877990	G	A	242	176	209	205	5.872	0.0154	rs517489	11	89869212	q14.3
SNP_A-1844830	T	T	248	122	310	104	5.872	0.0154	rs1925543	10	21001638	p12.31
SNP_A-1849204	A	A	354	16	406	6	5.865	0.0154	rs11953880	5	100783923	q21.1
SNP_A-1868212	G	G	243	109	318	96	5.871	0.0154	rs7998230	13	20138531	q12.11
SNP_A-1801563	C	C	254	164	216	196	5.874	0.0154	rs942679	1	153164139	q22
SNP_A-1781855	G	G	215	133	263	111	5.875	0.0154	rs2460177	5	90064161	q14.3
SNP_A-1696518	C	C	371	3	381	13	5.866	0.0154	rs1579014	10	60660947	q21.2
SNP_A-2113261	G	G	355	17	331	33	5.873	0.0154	rs5752616	22	26424465	q12.1
SNP_A-2120605	A	A	345	5	408	0	5.867	0.0154	rs6853995	4	70391165	q13.2
SNP_A-2123823	G	G	257	117	294	90	5.875	0.0154	rs1147134	15	48975828	q21.2
SNP_A-2140639	A	A	345	5	408	0	5.867	0.0154	rs2440483	3	131371119	q21.3
SNP_A-2163496	G	G	357	19	373	7	5.868	0.0154	rs13378627	13	34734115	q13.3
SNP_A-2225790	C	C	314	56	373	39	5.87	0.0154	rs298547	5	17412260	p15.1
SNP_A-1992293	A	A	246	118	245	169	5.876	0.0154	rs481616	8	12971390	p22
SNP_A-2019517	C	C	183	125	245	113	5.866	0.0154	rs760286	21	40083600	q22.2
SNP_A-2028864	T	T	343	19	373	41	5.865	0.0154	rs12962540	18	65515613	q22.2
SNP_A-2084061	A	A	329	39	386	24	5.865	0.0154	rs17583618	10	122496218	q26.12
SNP_A-2106467	A	A	301	103	271	135	5.871	0.0154	rs10038770	5	67732034	q13.1
SNP_A-2106803	A	A	377	43	383	23	5.872	0.0154	rs4852324	2	74114233	p13.1
SNP_A-2232715	A	A	215	145	206	198	5.867	0.0154	rs175048	14	74549647	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2248912	G	G	386	8	413	1	5.865	0.0154	rs1864918	10	118062542	q25.3
SNP_A-2277824	T	T	262	146	220	174	5.867	0.0154	rs4854292	2	912174	p25.3
SNP_A-2275340	T	T	414	2	384	10	5.868	0.0154	rs7430877	3	15633867	p25.1
SNP_A-2273111	C	C	268	142	300	110	5.866	0.0154	rs10932486	2	214210418	q34
SNP_A-2265478	G	G	222	146	213	199	5.865	0.0154	rs12511093	4	115489792	q26
SNP_A-2303316	G	G	345	5	408	0	5.867	0.0154	rs17161392	7	139236626	q34
SNP_A-2311316	C	C	204	166	261	149	5.869	0.0154	rs2180185	1	10180395	p36.22
SNP_A-2314625	G	G	336	26	352	50	5.873	0.0154	rs611162	9	13663752	p23
SNP_A-2314022	C	-	244	174	206	206	5.861	0.0155	rs2346910	3	16528828	p24.3
SNP_A-2312332	G	G	291	41	357	27	5.859	0.0155	rs9680627	22	42868237	q13.31
SNP_A-2293733	C	C	307	23	378	12	5.857	0.0155	rs7917246	10	67268247	q21.3
SNP_A-2249822	G	G	213	135	265	115	5.862	0.0155	rs9971207	10	86417483	q23.1
SNP_A-2251227	C	C	383	23	348	40	5.858	0.0155	rs2142716	1	30408227	p35.2
SNP_A-2254957	A	A	209	127	199	175	5.857	0.0155	rs9815034	3	168980146	q26.1
SNP_A-2229658	A	G	232	188	219	193	5.864	0.0155	rs3009947	1	215077550	q41
SNP_A-2097958	T	T	339	5	400	0	5.853	0.0155	rs6808151	3	54543601	p14.3
SNP_A-2082930	C	C	217	141	268	120	5.856	0.0155	rs7823874	8	117107615	q23.3
SNP_A-2082252	G	G	221	149	283	133	5.863	0.0155	rs10903516	10	1670786	p15.3
SNP_A-2067427	A	A	296	32	359	19	5.862	0.0155	rs759097	4	27014025	p15.2
SNP_A-2227601	C	T	238	180	211	199	5.862	0.0155	rs1316743	15	31333390	q13.3
SNP_A-2227215	T	T	358	16	303	29	5.854	0.0155	rs17165300	7	92634560	q21.3
SNP_A-2224006	A	A	381	7	365	19	5.861	0.0155	rs10423882	19	17834158	p13.11
SNP_A-2218751	A	A	368	18	351	35	5.855	0.0155	rs309430	15	83004074	q25.3
SNP_A-2201515	G	G	355	1	377	9	5.858	0.0155	rs6477267	9	8161142	p24.1
SNP_A-2190930	C	C	245	123	242	174	5.859	0.0155	rs9395129	6	45938081	p21.1
SNP_A-2185755	G	G	327	7	405	1	5.862	0.0155	rs12169677	22	48050609	q13.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2193274	C	C	286	118	316	88	5.864	0.0155	rs3811276	14	21739452	q11.2
SNP_A-2171301	C	C	396	22	363	39	5.863	0.0155	rs7107048	11	11974796	p15.3
SNP_A-2178466	C	C	212	144	201	195	5.854	0.0155	rs7144509	14	52093357	q22.1
SNP_A-2164470	A	A	337	5	398	0	5.858	0.0155	rs17090211	18	52325997	q21.2
SNP_A-2149672	A	A	302	22	367	11	5.863	0.0155	rs9452955	6	95558821	q16.1
SNP_A-2122908	A	A	313	51	366	34	5.854	0.0155	rs35271	5	82617924	q14.2
SNP_A-1802584	T	T	347	5	410	0	5.862	0.0155	rs16849509	1	158517807	q23.3
SNP_A-1810209	G	A	213	153	206	202	5.854	0.0155	rs11721154	3	194240682	q29
SNP_A-1813739	G	G	278	64	337	47	5.854	0.0155	rs12520298	5	143538755	q31.3
SNP_A-1786299	G	G	211	155	271	139	5.864	0.0155	rs1144343	1	76260779	p31.1
SNP_A-1845400	C	C	306	60	367	43	5.859	0.0155	rs16920144	9	3948783	p24.2
SNP_A-1836066	A	A	310	12	386	4	5.858	0.0155	rs17000250	20	52892353	q13.2
SNP_A-1880186	C	C	232	166	247	123	5.855	0.0155	rs1351304	4	37208360	p14
SNP_A-1889511	G	C	206	202	232	168	5.856	0.0155	rs378479	6	160707551	q25.3
SNP_A-1884391	G	G	353	1	375	9	5.855	0.0155	rs11112633	12	104544726	q23.3
SNP_A-1908335	T	T	344	50	359	29	5.857	0.0155	rs195640	16	69679057	q22.2
SNP_A-1919307	C	C	247	87	256	134	5.86	0.0155	rs6737282	2	25609054	p23.3
SNP_A-1888451	T	T	234	106	277	83	5.851	1.56E-02	rs6140583	20	8206564	p12.3
SNP_A-1876842	C	C	398	2	370	10	5.845	1.56E-02	rs10068456	5	149978749	q33.1
SNP_A-1942025	A	A	341	5	402	0	5.848	1.56E-02	rs604383	13	90908348	q31.3
SNP_A-1943465	A	A	243	123	234	170	5.848	1.56E-02	rs1437263	4	148239024	q31.22
SNP_A-1942008	C	C	302	66	301	101	5.847	1.56E-02	rs1885498	9	5326984	p24.1
SNP_A-1940216	C	C	388	28	405	13	5.847	1.56E-02	rs2980830	8	40243956	p11.21
SNP_A-1960910	T	T	315	17	373	7	5.847	1.56E-02	rs17081663	13	63539097	q21.31
SNP_A-1974387	T	T	325	25	364	12	5.851	1.56E-02	rs10914066	1	177391003	q25.3
SNP_A-1791500	G	G	200	164	264	152	5.843	1.56E-02	rs11967494	6	94822904	q16.1
SNP_A-1802603	A	A	351	5	414	0	5.853	1.56E-02	rs7951004	11	110318883	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800676	G	G	253	113	318	96	5.85	1.56E-02	rs7544735	1	217387308	q41
SNP_A-1805387	T	T	300	44	316	76	5.843	1.56E-02	rs580018	9	107967489	q31.2
SNP_A-1696506	A	A	237	161	279	133	5.845	1.56E-02	rs10133377	11	5836140	p15.4
SNP_A-2122345	C	C	254	108	322	92	5.85	1.56E-02	rs11597666	2	72375896	p13.2
SNP_A-2115937	G	C	180	176	234	168	5.849	1.56E-02	rs8013746	14	94544240	q32.13
SNP_A-2162325	C	C	292	26	352	14	5.85	1.56E-02	rs12516250	5	120695369	q23.1
SNP_A-2168564	A	A	281	85	348	68	5.853	1.56E-02	rs4797778	18	13457275	p11.21
SNP_A-2211971	G	G	347	5	363	17	5.844	1.56E-02	rs7699951	4	54306989	q12
SNP_A-2216649	G	G	349	11	409	3	5.845	1.56E-02	rs17757454	8	1987919	p23.3
SNP_A-2215615	C	C	239	153	282	126	5.844	1.56E-02	rs7815567	8	84504412	q21.13
SNP_A-2229916	A	A	311	95	286	128	5.853	1.56E-02	rs7843746	8	765025	p23.3
SNP_A-2081053	T	T	266	154	219	179	5.844	1.56E-02	---	3	105473274	q13.11
SNP_A-2093953	A	A	341	5	402	0	5.848	1.56E-02	rs7235393	18	70906685	q22.3
SNP_A-2028618	A	A	256	108	318	90	5.844	1.56E-02	rs12710221	19	23620564	p12
SNP_A-2022819	A	T	242	178	211	205	5.843	1.56E-02	rs9911460	17	77149278	q25.3
SNP_A-2038369	T	T	329	79	363	55	5.849	1.56E-02	rs7597534	2	156581827	q24.1
SNP_A-2000368	C	T	201	161	214	188	5.847	1.56E-02	rs7522860	1	153088354	q22
SNP_A-1997191	T	T	351	5	414	0	5.853	1.56E-02	rs3908476	10	18762765	p12.31
SNP_A-2007707	G	G	393	11	375	25	5.847	1.56E-02	rs6018800	20	45986181	q13.13
SNP_A-2248354	G	G	336	22	353	9	5.849	1.56E-02	rs3114745	7	109071015	q31.1
SNP_A-2247726	G	G	387	27	360	46	5.844	1.56E-02	rs17010429	2	31017625	p23.1
SNP_A-2270638	T	C	210	150	193	189	5.849	1.56E-02	rs12515718	5	162880970	q34
SNP_A-2277808	T	T	305	39	334	22	5.85	1.56E-02	rs8041604	15	63510635	q22.31
SNP_A-2278561	T	T	254	48	235	73	5.845	1.56E-02	rs10827646	10	19943201	p12.31
SNP_A-2296647	A	A	294	56	365	41	5.853	1.56E-02	rs2898934	11	3601633	p15.4
SNP_A-2312933	A	A	331	25	393	13	5.843	1.56E-02	rs6933067	6	41241500	p21.1
SNP_A-2307629	C	C	272	96	269	139	5.838	1.57E-02	rs309298	2	7137048	p25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2297276	T	T	398	22	376	40	5.832	1.57E-02	rs4751725	10	121229127	q26.11
SNP_A-2300940	T	T	405	1	380	8	5.836	1.57E-02	rs16944057	12	113249400	q24.21
SNP_A-2246742	T	T	345	5	406	0	5.839	1.57E-02	rs736624	7	98252853	q22.1
SNP_A-2242041	C	C	335	5	394	0	5.834	1.57E-02	rs6730988	2	206089087	q33.3
SNP_A-2238194	T	T	415	7	399	19	5.834	1.57E-02	rs6494976	15	69976660	q23
SNP_A-2104363	T	T	350	16	378	36	5.837	1.57E-02	rs1798891	12	123513238	q24.31
SNP_A-2088116	G	G	344	22	369	45	5.84	1.57E-02	rs1836852	8	31434691	p12
SNP_A-2051966	C	C	378	0	386	6	5.831	1.57E-02	rs17120784	12	39240653	q12
SNP_A-2216650	A	A	260	110	257	157	5.84	1.57E-02	rs6708828	2	194073165	q32.3
SNP_A-2172907	T	T	317	49	377	33	5.833	1.57E-02	rs462954	13	91169091	q31.3
SNP_A-2126179	A	A	371	11	338	24	5.831	1.57E-02	rs17073862	5	171035363	q35.1
SNP_A-2132526	C	C	390	12	349	25	5.84	1.57E-02	rs16872454	4	10385946	p16.1
SNP_A-1688950	G	G	319	29	376	16	5.835	1.57E-02	rs1401608	8	139352990	q24.23
SNP_A-1809157	C	C	322	62	308	92	5.831	1.57E-02	rs1791647	12	51062234	q13.13
SNP_A-1799992	A	A	256	112	303	89	5.831	1.57E-02	rs11893748	2	36624556	p22.2
SNP_A-1828885	G	G	226	176	262	144	5.836	1.57E-02	rs11056202	12	14885779	p12.3
SNP_A-1854784	T	T	278	26	290	50	5.838	1.57E-02	rs12657511	5	122977491	q23.2
SNP_A-1865998	G	G	342	24	400	12	5.834	1.57E-02	rs7656717	4	56011408	q12
SNP_A-1968630	T	T	279	143	304	108	5.833	1.57E-02	rs241792	20	50801385	q13.2
SNP_A-1978060	T	T	300	58	304	92	5.833	1.57E-02	rs1922233	4	92725524	q22.1
SNP_A-1977092	G	G	260	24	283	49	5.831	1.57E-02	rs17051581	4	53300491	q12
SNP_A-1950796	A	A	376	10	404	2	5.837	1.57E-02	rs12694468	2	220283710	q35
SNP_A-1950173	T	T	235	65	313	53	5.839	1.57E-02	rs1024697	16	6454040	p13.2
SNP_A-1953281	G	A	231	189	224	196	5.835	1.57E-02	rs3814667	10	13799982	p13
SNP_A-1874119	A	A	299	59	365	43	5.831	1.57E-02	rs9529788	13	70666116	q21.33
SNP_A-1907393	C	C	354	8	385	23	5.831	1.57E-02	rs17398876	8	108843901	q23.1
SNP_A-1926489	G	G	353	5	414	0	5.82	1.58E-02	rs11020496	11	87948954	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1891040	A	A	352	30	328	50	5.826	1.58E-02	rs11234958	11	86466364	q14.2
SNP_A-1952659	G	G	387	27	396	12	5.829	1.58E-02	rs1886024	1	19147274	p36.13
SNP_A-1947282	A	A	297	63	309	101	5.82	1.58E-02	rs13005095	2	199426034	q33.1
SNP_A-1966125	T	T	364	0	372	6	5.825	1.58E-02	rs2198729	2	182195680	q31.3
SNP_A-1975037	C	C	370	0	378	6	5.828	1.58E-02	rs3912727	3	160618075	q25.33
SNP_A-1871875	C	C	308	18	293	35	5.821	1.58E-02	rs8007927	14	56196742	q22.3
SNP_A-1817004	C	C	351	5	412	0	5.824	1.58E-02	rs4490372	3	76288204	p12.3
SNP_A-1843503	A	A	287	103	320	76	5.821	1.58E-02	rs3734772	6	170585305	q27
SNP_A-1789879	A	A	341	9	412	2	5.829	1.58E-02	---	10	113345210	q25.2
SNP_A-1801272	C	C	356	0	364	6	5.821	1.58E-02	rs17100445	12	63247930	q14.2
SNP_A-1655535	A	A	243	97	229	135	5.828	1.58E-02	rs10504879	8	90498217	q21.3
SNP_A-1782485	G	G	321	41	330	70	5.82	1.58E-02	rs6926634	6	72800435	q13
SNP_A-2131945	G	G	254	114	319	97	5.826	1.58E-02	rs4590233	6	74817301	q13
SNP_A-2195693	C	C	351	5	412	0	5.824	1.58E-02	rs11939770	4	128231584	q28.1
SNP_A-2190634	C	C	299	33	324	62	5.828	1.58E-02	rs2149773	13	113908334	q34
SNP_A-2218508	A	A	271	87	302	62	5.822	1.58E-02	rs1077613	5	172936057	q35.2
SNP_A-2214667	A	A	301	103	331	75	5.824	1.58E-02	rs11217524	11	119198081	q23.3
SNP_A-2208530	A	A	375	15	348	30	5.822	1.58E-02	rs1864459	2	26535548	p23.3
SNP_A-2205729	G	G	281	47	324	30	5.827	1.58E-02	rs7134685	12	60120633	q14.1
SNP_A-2067074	A	A	347	19	368	40	5.829	1.58E-02	rs2546197	5	95198037	q15
SNP_A-2011967	A	A	300	62	361	45	5.829	1.58E-02	rs4944584	11	72010579	q13.4
SNP_A-2009390	G	G	236	134	296	116	5.824	1.58E-02	rs6771152	3	187099681	q27.2
SNP_A-2005454	C	C	357	13	383	31	5.826	1.58E-02	rs2484754	1	39398057	p34.3
SNP_A-1990676	C	C	391	25	409	11	5.83	1.58E-02	rs1375670	7	96166593	q21.3
SNP_A-1994254	T	T	228	138	278	116	5.823	1.58E-02	rs1449243	8	93676222	q22.1
SNP_A-2046058	A	A	351	5	412	0	5.824	1.58E-02	rs16948352	18	26538420	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2022758	C	T	183	165	225	175	5.823	1.58E-02	rs4456913	4	6019363	p16.1
SNP_A-2022574	G	G	339	9	373	25	5.828	1.58E-02	rs11106356	12	90846436	q21.33
SNP_A-2033403	G	G	349	5	410	0	5.829	1.58E-02	rs12341212	9	7124581	p24.1
SNP_A-2230974	T	C	192	166	228	186	5.82	1.58E-02	rs312750	17	65855134	q24.3
SNP_A-2286419	G	A	195	171	225	181	5.828	1.58E-02	rs896706	10	130841593	q26.3
SNP_A-2265366	A	A	405	3	382	12	5.83	1.58E-02	rs11022526	11	12851050	p15.2
SNP_A-2267400	G	G	354	30	330	50	5.821	1.58E-02	rs6987050	8	94151469	q22.1
SNP_A-2268115	T	T	269	101	325	81	5.82	1.58E-02	rs62906	1	212798276	q41
SNP_A-2271604	G	G	376	8	350	20	5.816	1.59E-02	rs12076773	1	7577314	p36.23
SNP_A-2282271	A	A	210	142	175	171	5.818	1.59E-02	rs2469663	8	101679437	q22.3
SNP_A-2236229	C	C	343	5	402	0	5.815	1.59E-02	rs17063883	3	60689757	p14.2
SNP_A-2304816	A	A	247	145	287	117	5.809	1.59E-02	rs12334195	7	24128900	p15.3
SNP_A-2310648	A	A	226	140	218	192	5.813	1.59E-02	rs4793541	17	66739190	q24.3
SNP_A-2026105	C	C	302	98	304	64	5.819	1.59E-02	rs12137403	1	67149064	p31.2
SNP_A-2041270	G	G	297	73	302	112	5.812	1.59E-02	rs7632714	3	70783369	p13
SNP_A-2036121	A	A	315	53	370	36	5.812	1.59E-02	rs4737311	8	72282676	q13.3
SNP_A-2081996	A	A	320	26	384	14	5.812	1.59E-02	rs39028	7	88741417	q21.13
SNP_A-2102948	T	T	324	28	348	54	5.811	1.59E-02	rs4582335	5	127955022	q23.3
SNP_A-2094841	C	C	286	114	317	85	5.815	1.59E-02	rs2217383	5	24701275	p14.1
SNP_A-2206665	G	G	203	163	261	147	5.814	1.59E-02	rs625495	11	84395787	q14.1
SNP_A-2219648	A	A	355	37	307	55	5.818	1.59E-02	rs16908167	12	12538483	p13.2
SNP_A-2227432	G	G	324	42	385	27	5.81	1.59E-02	rs7443939	5	33265147	p13.3
SNP_A-2183839	G	G	200	134	187	181	5.816	1.59E-02	rs9985550	4	8407878	p16.1
SNP_A-2193284	G	G	345	11	403	3	5.813	1.59E-02	rs16963716	18	28540237	q12.1
SNP_A-2169904	T	T	239	155	274	124	5.812	1.59E-02	rs7372891	3	46125055	p21.31
SNP_A-2135467	C	C	398	0	408	6	5.811	1.59E-02	rs11252178	10	3931340	p15.1
SNP_A-2125165	T	T	237	119	225	163	5.811	1.59E-02	rs1954729	8	108185069	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1708627	A	A	302	46	324	80	5.81	1.59E-02	rs283905	2	79272438	p12
SNP_A-1785735	A	A	350	8	381	23	5.817	1.59E-02	rs16896641	6	43752778	p21.1
SNP_A-1818938	T	T	275	85	277	127	5.813	1.59E-02	rs17315193	4	157458055	q32.1
SNP_A-1853683	T	T	352	14	383	33	5.815	1.59E-02	rs12032155	1	70181610	p31.1
SNP_A-1850572	T	T	415	3	392	12	5.819	1.59E-02	rs4709857	6	164948407	q27
SNP_A-1984477	T	T	318	100	284	130	5.814	1.59E-02	rs279406	5	167064097	q34
SNP_A-1948637	C	C	334	50	358	30	5.812	1.59E-02	rs5753021	22	28854295	q12.2
SNP_A-1898254	C	C	215	205	244	166	5.812	1.59E-02	rs41006	2	8059946	p25.1
SNP_A-1926557	A	A	229	139	290	122	5.813	1.59E-02	rs9542253	13	69752150	q21.33
SNP_A-1876373	T	C	188	166	212	168	5.808	0.016	rs6963316	7	85677066	q21.11
SNP_A-1948624	A	A	273	97	274	142	5.802	0.016	rs11949240	5	17095902	p15.1
SNP_A-1847660	A	A	239	165	206	200	5.798	0.016	rs6874194	5	35737848	p13.2
SNP_A-1853900	C	C	337	5	394	0	5.8	0.016	rs8074241	17	59793035	q23.3
SNP_A-1787703	G	G	384	24	392	10	5.803	0.016	rs2306936	1	112958672	p13.2
SNP_A-1800894	A	A	280	80	345	63	5.804	0.016	rs7822022	8	138880104	q24.23
SNP_A-2163002	A	A	321	45	386	30	5.803	0.016	rs16958616	16	81373798	q23.3
SNP_A-2172576	C	C	342	14	405	5	5.798	0.016	rs13382079	19	61406170	q13.43
SNP_A-2175012	A	A	349	5	408	0	5.801	0.016	rs2273856	20	18975973	p11.23
SNP_A-2222767	C	C	226	122	271	99	5.799	0.016	rs17682853	5	157334473	q33.3
SNP_A-2069964	A	A	332	32	299	51	5.803	0.016	rs17116578	15	23880055	q12
SNP_A-2029117	A	A	336	6	378	20	5.804	0.016	rs9588472	13	111024447	q34
SNP_A-2014887	A	A	218	138	281	123	5.808	0.016	rs361306	11	103455066	q22.3
SNP_A-2311220	T	T	380	8	403	1	5.799	0.016	rs167997	15	64125701	q22.31
SNP_A-2299334	G	G	313	81	315	51	5.801	0.016	rs1526125	17	41167948	q21.31
SNP_A-2287771	G	G	406	0	347	5	5.805	0.016	rs2069115	2	118882519	q14.2
SNP_A-2287855	C	C	256	112	321	95	5.801	0.016	rs6065397	20	39931173	q12
SNP_A-2239196	G	T	209	169	198	172	5.8	0.016	rs1383616	15	71716238	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2240290	C	T	213	155	211	205	5.804	0.016	rs2777970	1	154401465	q23.1
SNP_A-2257891	A	A	403	1	380	8	5.799	0.016	rs16918779	10	65111042	q21.3
SNP_A-2274240	C	C	276	122	250	158	5.791	0.0161	rs2193596	14	74303854	q24.3
SNP_A-2289616	T	T	339	79	310	108	5.793	0.0161	rs12953059	17	53233479	q23.2
SNP_A-2311903	T	T	356	0	366	6	5.79	0.0161	rs9857346	3	117965655	q13.31
SNP_A-2304470	C	C	234	134	227	185	5.796	0.0161	rs9669686	12	93681971	q22
SNP_A-2016062	G	G	360	8	393	23	5.787	0.0161	rs2825986	21	20361776	q21.1
SNP_A-2009841	T	A	198	170	228	188	5.794	0.0161	rs6830089	4	61727843	q13.1
SNP_A-2006700	G	G	405	1	382	8	5.797	0.0161	rs3739128	2	131507260	q21.1
SNP_A-1997324	A	A	394	8	417	1	5.787	0.0161	rs2231671	9	97968258	q22.33
SNP_A-1997931	G	G	277	57	261	85	5.787	0.0161	rs953093	10	20867111	p12.31
SNP_A-2033427	C	C	349	7	356	20	5.787	0.0161	rs11145700	9	77957255	q21.2
SNP_A-2093089	A	A	358	0	368	6	5.791	0.0161	rs7467925	9	38436277	p13.2
SNP_A-2096362	G	G	353	5	412	0	5.792	0.0161	rs7185546	16	16960191	p12.3
SNP_A-2222179	A	A	366	56	384	34	5.791	0.0161	rs2278543	15	70864255	q24.1
SNP_A-2198778	T	T	360	46	299	63	5.796	0.0161	rs11119654	1	207557388	q32.2
SNP_A-2184689	A	A	382	10	408	2	5.788	0.0161	rs16954826	15	27035041	q13.1
SNP_A-2164812	C	C	325	41	384	26	5.792	0.0161	rs1870228	8	129212155	q24.21
SNP_A-2157885	T	T	353	5	412	0	5.792	0.0161	rs7108305	11	88432121	q14.3
SNP_A-2155410	A	A	335	7	411	1	5.794	0.0161	rs17035462	4	158236615	q32.1
SNP_A-2155602	T	T	297	39	348	24	5.788	0.0161	rs1432867	5	158586245	q33.3
SNP_A-2137996	T	T	394	12	370	26	5.788	0.0161	rs12698436	7	71646516	q11.23
SNP_A-2127997	A	A	359	19	329	35	5.787	0.0161	rs10507471	13	37852168	q13.3
SNP_A-2112519	G	G	317	105	284	136	5.795	0.0161	rs7913620	10	49791193	q11.23
SNP_A-1808969	A	A	339	11	395	3	5.788	0.0161	rs7016342	8	86945420	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1675756	C	C	190	136	260	128	5.791	0.0161	rs527498	3	8114779	p26.1
SNP_A-1729792	G	G	286	94	256	124	5.789	0.0161	rs4279912	10	67172329	q21.3
SNP_A-1855790	C	T	189	177	237	179	5.794	0.0161	rs7744028	6	127977204	q22.33
SNP_A-1847590	C	C	268	102	268	148	5.792	0.0161	rs6773838	3	192403238	q28
SNP_A-1851851	T	T	350	20	407	9	5.792	0.0161	rs1417889	1	74536988	p31.1
SNP_A-1872777	T	T	281	79	331	59	5.793	0.0161	rs11144764	9	75984703	q21.13
SNP_A-1816462	C	C	182	140	194	100	5.789	0.0161	rs1436878	6	81159044	q14.1
SNP_A-1831342	A	A	230	140	291	123	5.79	0.0161	rs1899671	18	46041400	q21.1
SNP_A-1947756	T	T	259	109	255	155	5.796	0.0161	rs2133918	4	118140150	q26
SNP_A-1973547	T	T	284	84	285	125	5.794	0.0161	rs2196083	3	89619236	p11.1
SNP_A-1886022	T	T	252	166	211	195	5.787	0.0161	rs10478764	5	126620000	q23.2
SNP_A-1899178	C	C	311	55	324	90	5.782	1.62E-02	rs2304365	8	53292766	q11.23
SNP_A-1891407	G	G	351	13	364	30	5.779	1.62E-02	rs830202	3	167137499	q26.1
SNP_A-1920570	C	C	322	14	381	5	5.78	1.62E-02	rs11012342	10	21124040	p12.31
SNP_A-1920023	G	G	318	18	384	8	5.778	1.62E-02	rs2128423	4	177540151	q34.2
SNP_A-1919466	A	A	358	8	391	23	5.78	1.62E-02	rs12243038	10	22783453	p12.2
SNP_A-1910479	G	G	313	21	272	36	5.777	1.62E-02	rs10977023	9	8378220	p24.1
SNP_A-1966328	G	G	257	109	253	155	5.784	1.62E-02	rs957845	2	194082918	q32.3
SNP_A-1963008	C	C	347	5	404	0	5.777	1.62E-02	rs6746735	2	45520379	p21
SNP_A-1937114	C	T	210	206	235	171	5.778	1.62E-02	rs7947910	11	112502623	q23.1
SNP_A-1935071	T	C	234	170	206	202	5.776	1.62E-02	rs506197	11	30212399	p14.1
SNP_A-1961089	T	T	329	31	338	56	5.784	1.62E-02	rs2278860	15	41446338	q15.3
SNP_A-1836163	G	G	187	165	252	156	5.782	1.62E-02	rs17045920	2	116900202	q14.1
SNP_A-1872597	G	G	348	0	358	6	5.785	1.62E-02	rs16998104	20	51494654	q13.2
SNP_A-1749887	C	C	348	54	380	34	5.777	1.62E-02	rs10510240	3	2879529	p26.2
SNP_A-1806478	T	T	345	5	402	0	5.781	1.62E-02	rs4478365	5	110673236	q22.1
SNP_A-1790497	A	A	203	195	231	157	5.782	1.62E-02	rs1822464	18	46002690	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137548	C	C	380	10	355	23	5.785	1.62E-02	rs5992952	22	16855069	q11.21
SNP_A-2192565	C	C	311	41	335	73	5.779	1.62E-02	rs17287442	2	172173528	q31.1
SNP_A-2223488	G	C	217	187	218	180	5.777	1.62E-02	rs11037948	11	44281483	p11.2
SNP_A-2217109	A	A	347	5	404	0	5.777	1.62E-02	rs1445466	16	58470237	q21
SNP_A-2203729	G	G	324	24	332	46	5.782	1.62E-02	rs920199	8	96970909	q22.1
SNP_A-2086329	C	C	338	42	320	66	5.779	1.62E-02	rs10199932	2	165519834	q24.3
SNP_A-2072184	T	C	193	165	213	175	5.779	1.62E-02	rs583338	18	39126231	q12.3
SNP_A-2054732	C	C	257	31	336	20	5.781	1.62E-02	rs7137130	12	122626861	q24.31
SNP_A-2058222	C	C	354	18	328	34	5.779	1.62E-02	rs9822277	3	16215860	p25.1
SNP_A-2026075	C	C	357	1	383	9	5.784	1.62E-02	rs4118143	7	29500379	p15.1
SNP_A-2022635	G	G	393	25	363	43	5.782	1.62E-02	rs17388019	9	119590229	q33.1
SNP_A-2035813	C	C	357	5	416	0	5.783	1.62E-02	rs647284	11	64937459	q13.1
SNP_A-2035089	G	G	219	137	282	122	5.782	1.62E-02	rs11919755	3	80630354	p12.2
SNP_A-2042560	A	A	353	11	411	3	5.785	1.62E-02	rs10930124	2	164976988	q24.3
SNP_A-2044078	T	T	363	55	339	81	5.786	1.62E-02	rs7551067	1	239932620	q44
SNP_A-2011052	A	A	283	75	331	55	5.784	1.62E-02	rs7705499	5	91867407	q14.3
SNP_A-2016874	T	T	383	33	360	54	5.776	1.62E-02	rs17000559	21	25219641	q21.2
SNP_A-2017440	A	A	187	179	247	167	5.779	1.62E-02	rs2831677	21	28547475	q21.3
SNP_A-2302649	C	C	345	5	402	0	5.781	1.62E-02	rs6688662	1	76554154	p31.1
SNP_A-2295494	T	T	257	51	309	35	5.784	1.62E-02	rs17138155	7	115076307	q31.2
SNP_A-2232459	C	C	310	14	367	5	5.779	1.62E-02	---	4	124245117	q27
SNP_A-2242710	T	T	399	21	404	8	5.782	1.62E-02	rs2749264	6	168733418	q27
SNP_A-2248177	T	T	227	141	219	193	5.776	1.62E-02	rs2018709	18	50687722	q21.2
SNP_A-2256747	T	T	349	5	406	0	5.772	1.63E-02	rs6834825	4	125488180	q28.1
SNP_A-2262946	A	A	351	5	408	0	5.768	1.63E-02	rs1942127	7	13503674	p21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017408	C	C	317	25	375	13	5.775	1.63E-02	rs2831466	21	28371806	q21.3
SNP_A-2016251	A	A	242	176	277	143	5.769	1.63E-02	rs2826684	21	21432224	q21.1
SNP_A-2044497	A	A	294	106	256	134	5.766	1.63E-02	rs4888082	16	78914954	q23.2
SNP_A-2046137	G	G	350	10	359	25	5.775	1.63E-02	rs1942418	18	45637241	q21.1
SNP_A-2043497	A	A	365	19	335	35	5.768	1.63E-02	rs17792227	1	211133950	q41
SNP_A-2052390	T	T	321	17	321	35	5.768	1.63E-02	rs9376134	6	136045899	q23.3
SNP_A-2064859	C	C	301	47	355	31	5.775	1.63E-02	rs6663895	1	238246603	q43
SNP_A-2192143	G	C	186	176	237	177	5.774	1.63E-02	rs9410430	9	88793646	q22.1
SNP_A-2115042	C	C	332	24	363	11	5.771	1.63E-02	rs4023899	19	59417647	q13.42
SNP_A-2114249	G	G	281	111	293	77	5.769	1.63E-02	rs1704675	14	91190224	q32.12
SNP_A-2145569	A	A	299	13	385	5	5.773	1.63E-02	rs6505097	17	24273564	q11.2
SNP_A-1800014	G	G	276	94	275	137	5.767	1.63E-02	rs4891639	18	61867908	q22.1
SNP_A-1830948	G	G	222	130	203	171	5.773	1.63E-02	rs6902041	6	162819340	q26
SNP_A-1951928	G	G	327	23	375	11	5.77	1.63E-02	rs16910051	10	58473972	q21.1
SNP_A-1935956	A	A	327	33	306	54	5.766	1.63E-02	rs1486082	1	72240560	p31.1
SNP_A-1976076	C	C	323	47	332	78	5.776	1.63E-02	rs6824284	4	12263723	p15.33
SNP_A-1982982	C	C	252	106	251	153	5.775	1.63E-02	rs367943	5	112837627	q22.2
SNP_A-1978636	C	C	270	92	272	136	5.771	1.63E-02	rs17590690	4	118244777	q26
SNP_A-1906746	A	A	309	15	308	32	5.768	1.63E-02	rs6651244	8	128286644	q24.21
SNP_A-1915479	T	T	345	15	377	5	5.771	1.63E-02	rs6592149	11	83237190	q14.1
SNP_A-1921759	A	A	370	0	382	6	5.767	1.63E-02	rs4673436	2	209680405	q34
SNP_A-1897460	A	A	273	119	255	159	5.773	1.63E-02	rs297571	8	96252193	q22.1
SNP_A-1931844	T	T	311	47	376	32	5.759	1.64E-02	rs6434632	2	194556255	q32.3
SNP_A-1984556	G	G	322	74	300	104	5.755	1.64E-02	rs876302	5	169666648	q35.1
SNP_A-1971945	G	G	329	89	299	119	5.76	1.64E-02	rs17006708	3	20201663	p24.3
SNP_A-1835657	C	C	258	106	252	150	5.762	1.64E-02	rs11125907	2	62251331	p15

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872640	A	A	343	5	398	0	5.757	1.64E-02	rs11049214	12	27938350	p11.22
SNP_A-1871865	A	A	187	175	247	163	5.759	1.64E-02	rs10240976	7	82465835	q21.11
SNP_A-1871781	C	C	321	9	323	23	5.756	1.64E-02	rs3843916	6	153894216	q25.2
SNP_A-1855154	C	C	311	13	322	30	5.762	1.64E-02	rs228465	1	79325955	p31.1
SNP_A-1804569	G	G	293	69	296	106	5.76	1.64E-02	rs1075811	10	49457630	q11.22
SNP_A-2160287	T	T	220	148	279	131	5.761	1.64E-02	rs17138489	16	5725308	p13.3
SNP_A-2120158	A	A	290	130	318	98	5.762	1.64E-02	rs12449967	17	72334876	q25.2
SNP_A-2188766	A	A	338	52	318	78	5.764	1.64E-02	rs250428	5	139925491	q31.3
SNP_A-2180892	A	G	198	172	228	186	5.764	1.64E-02	rs7492370	14	74670450	q24.3
SNP_A-2215145	C	C	330	24	347	47	5.755	1.64E-02	rs17156635	7	28168969	p15.1
SNP_A-2076742	G	G	248	94	295	73	5.764	1.64E-02	rs17120385	8	14733048	p22
SNP_A-2087408	G	G	213	147	203	199	5.758	1.64E-02	rs17276464	4	153386465	q31.3
SNP_A-2046002	A	A	296	50	291	79	5.764	1.64E-02	rs2607034	14	97425699	q32.2
SNP_A-2010804	T	T	239	171	271	137	5.756	1.64E-02	rs4621563	5	33685662	p13.3
SNP_A-2274353	T	T	322	74	300	104	5.755	1.64E-02	rs9907041	17	69236842	q25.1
SNP_A-2273443	C	C	278	68	332	50	5.76	1.64E-02	rs7787152	7	13466030	p21.2
SNP_A-2290855	C	C	232	126	300	112	5.757	1.64E-02	rs17779211	3	188600623	q27.3
SNP_A-2287677	C	C	321	33	373	19	5.745	1.65E-02	rs1401565	2	123781427	q14.3
SNP_A-2286728	T	T	333	39	292	58	5.746	1.65E-02	rs10802043	1	118829209	p12
SNP_A-2284726	G	G	207	145	239	115	5.752	1.65E-02	rs10892002	11	116010702	q23.3
SNP_A-2268015	T	T	150	120	249	135	5.749	1.65E-02	rs11042462	11	9626304	p15.4
SNP_A-2253034	G	G	379	39	353	61	5.744	1.65E-02	rs12331684	4	42631058	p13
SNP_A-2251983	T	T	315	35	280	54	5.744	1.65E-02	rs839307	5	171226678	q35.1
SNP_A-2006030	G	G	354	16	402	6	5.751	1.65E-02	rs7253544	19	58002524	q13.41
SNP_A-2037273	G	G	308	62	369	45	5.746	1.65E-02	rs14188878	4	37114896	p14
SNP_A-2081280	G	G	212	182	232	140	5.752	1.65E-02	rs3864922	12	16254589	p12.3
SNP_A-2096305	G	G	323	53	290	76	5.744	1.65E-02	rs10908319	1	37113309	p34.3
SNP_A-2070017	T	T	338	2	353	11	5.745	1.65E-02	rs2886527	3	61580779	p14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2062743	T	T	325	13	312	28	5.747	1.65E-02	---	4	72012612	q13.3
SNP_A-2214554	C	C	219	103	246	168	5.748	1.65E-02	rs7241214	18	22301872	q11.2
SNP_A-2211851	G	G	322	48	380	32	5.753	1.65E-02	rs7745447	6	122252672	q22.31
SNP_A-2169601	T	T	276	88	279	131	5.746	1.65E-02	rs383585	5	118173036	q23.1
SNP_A-2191237	G	G	351	11	407	3	5.746	1.65E-02	rs16921802	8	56501795	q12.1
SNP_A-2108038	T	T	219	143	215	199	5.748	1.65E-02	rs902890	12	128504182	q24.33
SNP_A-2139921	C	C	249	171	207	199	5.752	1.65E-02	rs10785876	9	134302321	q34.2
SNP_A-2142766	T	T	319	7	326	20	5.745	1.65E-02	rs11192655	10	83884946	q23.1
SNP_A-1807486	T	T	349	3	394	14	5.748	1.65E-02	rs9564193	13	64231540	q21.31
SNP_A-1720055	C	C	358	42	340	66	5.753	1.65E-02	rs3848643	19	17528970	p13.11
SNP_A-1782330	T	T	310	10	401	3	5.748	1.65E-02	rs17120956	14	48696306	q21.3
SNP_A-1664230	G	G	310	10	401	3	5.748	1.65E-02	rs176168	6	118548433	q22.31
SNP_A-1843662	T	T	320	36	352	20	5.746	1.65E-02	rs16930158	9	127747644	q34.11
SNP_A-1985879	C	C	241	123	298	104	5.747	1.65E-02	rs2889921	1	218728033	q41
SNP_A-1986786	A	A	257	67	257	103	5.745	1.65E-02	rs1535257	6	88951141	q15
SNP_A-1935854	A	A	211	107	222	164	5.754	1.65E-02	rs6507038	18	29284944	q12.1
SNP_A-1930221	A	A	367	15	342	30	5.75	1.65E-02	rs4256243	4	123092573	q27
SNP_A-1875358	A	A	314	52	328	86	5.75	1.65E-02	rs6919216	6	167161164	q27
SNP_A-1908046	G	G	320	28	352	14	5.74	0.0166	---	4	126002181	q28.1
SNP_A-1939253	C	C	355	13	383	31	5.74	0.0166	rs2442041	5	74029627	q13.3
SNP_A-1831896	G	G	351	5	406	0	5.74	0.0166	rs10096370	8	114623017	q23.3
SNP_A-1818915	G	G	232	128	226	178	5.734	0.0166	rs1367935	4	188110759	q35.2
SNP_A-1854179	A	A	225	111	297	99	5.737	0.0166	rs2744381	6	7532309	p24.3
SNP_A-1846063	A	A	399	3	380	12	5.738	0.0166	rs7942752	11	120763829	q23.3
SNP_A-1872154	T	T	331	13	331	29	5.735	0.0166	rs7974480	12	49084602	q13.12
SNP_A-1861695	G	G	388	10	346	22	5.737	0.0166	rs1473736	14	53626283	q22.2
SNP_A-2149743	C	C	353	5	408	0	5.736	0.0166	rs4518196	4	161193799	q32.1
SNP_A-2155535	T	T	321	21	359	45	5.738	0.0166	rs11043854	12	18139292	p12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2111145	G	G	354	30	360	14	5.738	0.0166	rs1064721	1	6215643	p36.31
SNP_A-2117948	C	C	362	54	335	79	5.74	0.0166	rs758937	7	31572276	p14.3
SNP_A-2130605	A	A	313	57	324	92	5.739	0.0166	rs2124141	4	11918295	p15.33
SNP_A-2186337	G	A	203	155	211	195	5.736	0.0166	rs4812254	20	59048972	q13.33
SNP_A-2180391	T	T	364	0	378	6	5.733	0.0166	rs16846893	4	72963446	q13.3
SNP_A-2207233	G	G	296	52	289	81	5.738	0.0166	rs2782991	13	75960658	q22.2
SNP_A-2206467	T	T	420	0	363	5	5.743	0.0166	---	2	5962144	p25.2
SNP_A-2074453	T	T	221	141	284	126	5.74	0.0166	rs12242002	10	35609612	p11.21
SNP_A-2055304	C	C	322	94	346	66	5.743	0.0166	rs892823	3	5907695	p26.1
SNP_A-2098478	A	A	285	75	291	115	5.742	0.0166	rs6535363	4	83919748	q21.22
SNP_A-2080840	A	A	209	143	258	122	5.743	0.0166	rs158914	5	60282166	q12.1
SNP_A-1991832	A	A	318	78	288	106	5.741	0.0166	rs2117522	7	157162431	q36.3
SNP_A-2252539	A	A	332	40	323	65	5.742	0.0166	rs1346732	2	137455435	q22.1
SNP_A-2253388	C	C	351	51	318	74	5.735	0.0166	rs2466321	8	118284918	q24.11
SNP_A-2247065	T	T	335	25	357	49	5.742	0.0166	rs8027733	15	41101610	q15.2
SNP_A-2246811	G	G	301	83	315	55	5.741	0.0166	rs651154	3	34809169	p23
SNP_A-2235992	G	G	204	154	272	144	5.736	0.0166	rs2543582	14	79143419	q31.1
SNP_A-2290952	A	A	291	69	359	53	5.736	0.0166	rs12995490	2	156536948	q24.1
SNP_A-2302925	A	A	199	157	254	140	5.74	0.0166	rs161792	3	153382402	q25.1
SNP_A-2304213	G	G	273	85	271	125	5.726	0.0167	rs2344914	20	35929819	q11.23
SNP_A-2237821	C	C	355	51	317	73	5.733	0.0167	rs17211962	5	135779080	q31.1
SNP_A-2240265	A	A	302	40	293	65	5.726	0.0167	rs17646732	14	83458057	q31.3
SNP_A-2234494	A	A	397	7	385	19	5.723	0.0167	rs4664525	2	152766010	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2244235	T	T	357	5	412	0	5.728	0.0167	rs11902752	2	75298256	p12
SNP_A-2277940	T	T	381	17	359	33	5.729	0.0167	rs1224661	15	45788757	q21.1
SNP_A-1994191	A	A	358	32	393	17	5.727	0.0167	rs7015077	8	90308622	q21.3
SNP_A-2000679	G	G	372	8	391	1	5.732	0.0167	rs2501839	1	209214667	q32.3
SNP_A-2016358	G	G	299	21	354	10	5.729	0.0167	rs17109239	11	108541206	q22.3
SNP_A-2047316	G	G	299	123	265	155	5.728	0.0167	rs6674167	1	160243083	q23.3
SNP_A-2021382	G	G	384	8	403	1	5.724	0.0167	rs6462571	7	3871097	p22.2
SNP_A-2077047	G	G	317	57	351	37	5.731	0.0167	rs2338018	1	148769444	q21.3
SNP_A-2075717	G	G	357	11	413	3	5.727	0.0167	rs2294569	20	39509852	q12
SNP_A-2201094	C	C	306	110	324	78	5.723	0.0167	rs107866	8	37275662	p12
SNP_A-2202381	G	G	245	69	243	105	5.725	0.0167	rs7117251	11	13874357	p15.2
SNP_A-2208879	A	A	404	14	416	4	5.726	0.0167	rs11002439	10	79619256	q22.3
SNP_A-2217048	T	T	331	5	382	0	5.724	0.0167	rs1456546	2	199671858	q33.1
SNP_A-2169932	G	G	229	137	276	114	5.726	0.0167	rs6475790	9	24288508	p21.3
SNP_A-2188899	A	A	224	150	200	190	5.732	0.0167	rs1825796	1	184912459	q31.1
SNP_A-2129234	G	G	385	19	397	7	5.723	0.0167	rs17416766	1	86758190	p22.3
SNP_A-1862102	G	G	345	5	398	0	5.724	0.0167	rs16845981	3	173843991	q26.31
SNP_A-1819725	A	A	276	66	287	105	5.73	0.0167	rs11973980	7	117155821	q31.31
SNP_A-1814874	T	T	253	93	311	75	5.724	0.0167	rs7513258	1	48538029	p33
SNP_A-1835149	T	T	303	55	316	90	5.728	0.0167	rs2039670	9	34400978	p13.3
SNP_A-1842560	C	C	333	7	405	1	5.73	0.0167	rs6729104	2	82693089	p12
SNP_A-1789624	T	T	354	24	360	10	5.73	0.0167	rs6438466	3	119847145	q13.32
SNP_A-1947563	C	C	304	62	312	98	5.727	0.0167	rs10889503	1	65101856	p31.3
SNP_A-1954844	T	T	304	18	366	8	5.73	0.0167	rs17106862	1	52060409	p32.3
SNP_A-1986821	T	T	355	5	410	0	5.732	0.0167	rs16883259	6	91370380	q15

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982632	G	G	286	56	275	85	5.722	0.0167	rs27027	5	97940427	q21.1
SNP_A-1928328	C	C	305	57	369	41	5.727	0.0167	rs791653	9	12480226	p23
SNP_A-1880015	C	C	367	1	397	9	5.726	0.0167	rs17095561	14	97088714	q32.2
SNP_A-1879555	G	G	411	3	392	12	5.728	0.0167	rs10800504	1	166882081	q24.2
SNP_A-1887234	T	T	328	94	352	66	5.728	0.0167	rs10951934	7	47690735	p12.3
SNP_A-1887547	G	G	368	54	341	79	5.723	0.0167	rs7556846	2	230178356	q36.3
SNP_A-1903761	G	G	357	5	412	0	5.728	0.0167	rs10476415	5	155814226	q33.3
SNP_A-1896365	G	G	341	5	394	0	5.732	0.0167	rs16962368	18	27580948	q12.1
SNP_A-1897432	C	C	264	68	286	112	5.715	1.68E-02	rs11633450	15	83108291	q25.3
SNP_A-1881556	A	A	245	175	276	140	5.714	1.68E-02	rs7950256	11	19872824	p15.1
SNP_A-1923660	G	G	401	19	413	7	5.715	1.68E-02	rs13331619	16	85408626	q24.1
SNP_A-1980241	A	A	207	163	265	147	5.714	1.68E-02	rs1026362	4	187181657	q35.1
SNP_A-1986336	C	C	207	141	265	125	5.718	1.68E-02	rs7760666	6	69678581	q12
SNP_A-1948390	A	A	307	63	368	46	5.713	1.68E-02	rs17018731	12	90001835	q21.33
SNP_A-1942487	C	T	209	199	232	174	5.72	1.68E-02	rs2696138	2	10621933	p25.1
SNP_A-1646162	T	T	220	116	270	96	5.717	1.68E-02	rs990965	4	27489847	p15.2
SNP_A-1705987	A	A	305	45	326	78	5.714	1.68E-02	rs283904	2	79272384	p12
SNP_A-1780608	G	G	303	55	365	39	5.722	1.68E-02	rs10965404	9	22612698	p21.3
SNP_A-1752845	C	C	254	96	263	145	5.715	1.68E-02	rs984696	4	148398104	q31.22
SNP_A-1729800	C	C	366	14	347	29	5.718	1.68E-02	rs1548831	7	31529965	p14.3
SNP_A-1820581	G	G	364	14	345	29	5.721	1.68E-02	rs11199825	10	122950845	q26.12
SNP_A-1863611	A	A	386	8	405	1	5.722	1.68E-02	rs16903298	5	36758177	p13.2
SNP_A-1870606	T	T	270	146	234	178	5.713	1.68E-02	rs11711241	3	9806970	p25.3
SNP_A-1868048	G	G	409	7	397	19	5.717	1.68E-02	rs7304805	12	92936666	q22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1847454	T	T	279	51	258	76	5.719	1.68E-02	---	4	34638482	p15.1
SNP_A-2154347	T	T	305	49	352	32	5.72	1.68E-02	rs4409934	12	123057306	q24.31
SNP_A-2160426	A	A	290	48	292	78	5.715	1.68E-02	rs2456948	7	112824414	q31.1
SNP_A-2159390	G	G	253	113	251	161	5.717	1.68E-02	rs894381	8	12951706	p22
SNP_A-2164658	A	A	261	79	335	65	5.722	1.68E-02	rs254227	5	115913473	q23.1
SNP_A-2162885	A	A	323	37	385	23	5.718	1.68E-02	rs1389219	5	24920151	p14.1
SNP_A-2196935	A	A	299	65	360	48	5.715	1.68E-02	rs11146436	10	133647972	q26.3
SNP_A-2178418	C	C	304	32	350	18	5.713	1.68E-02	rs919832	10	127215067	q26.13
SNP_A-2217943	C	C	322	78	283	103	5.72	1.68E-02	rs8009949	14	53281917	q22.1
SNP_A-2222814	G	G	331	87	291	113	5.716	1.68E-02	rs10997316	10	68127614	q21.3
SNP_A-2208453	A	A	328	40	341	69	5.718	1.68E-02	rs7157388	14	38574747	q21.1
SNP_A-2209534	C	C	272	82	335	65	5.72	1.68E-02	rs199782	20	22224650	p11.22
SNP_A-2073373	C	C	252	104	318	88	5.719	1.68E-02	rs7597717	2	78503360	p12
SNP_A-2058870	A	A	308	54	320	32	5.718	1.68E-02	rs1467375	14	76401158	q24.3
SNP_A-2104224	T	T	268	102	330	84	5.719	1.68E-02	rs1646716	7	133509716	q33
SNP_A-2038618	T	T	271	71	325	53	5.72	1.68E-02	rs10951074	7	25316904	p15.2
SNP_A-2019034	A	A	261	85	263	127	5.718	1.68E-02	rs2835850	21	37934847	q22.13
SNP_A-2007950	T	A	206	156	210	196	5.714	1.68E-02	rs1528641	11	14043034	p15.2
SNP_A-2010289	G	G	347	5	400	0	5.72	1.68E-02	rs16840024	1	5104594	p36.32
SNP_A-2002119	C	C	350	2	367	11	5.715	1.68E-02	rs7925554	11	88966566	q14.3
SNP_A-2271650	C	C	349	5	402	0	5.716	1.68E-02	rs6493050	15	40603893	q15.1
SNP_A-2229992	G	G	217	115	274	98	5.72	1.68E-02	rs1984610	2	214273765	q34
SNP_A-2306932	C	C	347	5	400	0	5.72	1.68E-02	rs3767070	1	37049479	p34.3
SNP_A-2296120	G	G	307	59	319	95	5.713	1.68E-02	rs17561584	16	7243575	p13.2
SNP_A-2294979	C	C	318	50	323	81	5.709	1.69E-02	rs17351902	5	121388402	q23.1
SNP_A-2301415	T	T	401	19	382	36	5.711	1.69E-02	rs2948087	3	20074219	p24.3
SNP_A-2241911	G	G	357	35	339	57	5.706	1.69E-02	rs10776947	9	134606636	q34.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2250081	C	C	272	138	228	164	5.709	1.69E-02	rs6717960	2	220630217	q35
SNP_A-2104297	C	C	350	6	375	19	5.711	1.69E-02	rs10829415	10	130168364	q26.2
SNP_A-2085676	A	A	303	57	351	39	5.707	1.69E-02	rs2708070	12	41164595	q12
SNP_A-2089340	T	T	351	5	404	0	5.712	1.69E-02	---	1	194666165	q31.3
SNP_A-2075387	C	T	218	184	221	187	5.709	1.69E-02	rs2426345	20	49702686	q13.2
SNP_A-2219699	A	A	380	36	346	56	5.702	1.69E-02	rs9997310	4	122986285	q27
SNP_A-2173245	C	C	228	140	290	124	5.704	1.69E-02	rs2125394	5	2290301	p15.33
SNP_A-2198283	A	A	355	11	388	28	5.702	1.69E-02	rs6061782	20	59748624	q13.33
SNP_A-2186568	G	G	314	58	341	37	5.707	1.69E-02	rs12711509	1	208200463	q32.3
SNP_A-2123290	C	T	208	202	235	173	5.702	1.69E-02	rs6757634	2	125058306	q14.3
SNP_A-1856298	G	G	232	152	197	183	5.703	1.69E-02	rs4780416	16	12199639	p13.13
SNP_A-1825203	C	C	376	14	357	29	5.705	1.69E-02	rs17037068	12	104311412	q23.3
SNP_A-1837815	G	G	330	18	396	8	5.708	1.69E-02	rs9434377	1	98882652	p21.3
SNP_A-1790040	A	T	193	139	198	192	5.71	1.69E-02	rs6533755	4	115383461	q26
SNP_A-1792522	G	G	333	43	320	68	5.702	1.69E-02	rs10759667	9	113807999	q32
SNP_A-1811796	T	T	346	64	324	92	5.705	1.69E-02	rs2126599	3	118445897	q13.31
SNP_A-1943108	G	G	344	18	373	39	5.704	1.69E-02	rs12640179	4	72977722	q13.3
SNP_A-1981205	C	T	220	166	211	199	5.705	1.69E-02	rs256322	5	34657929	p13.2
SNP_A-1969515	T	T	353	5	406	0	5.708	1.69E-02	rs2828586	21	24196787	q21.2
SNP_A-1965775	A	A	219	139	271	119	5.71	1.69E-02	rs563694	2	169599578	q24.3
SNP_A-1968889	T	T	295	127	257	157	5.709	1.69E-02	rs3924264	1	157991757	q23.3
SNP_A-1930440	A	A	398	2	376	10	5.711	1.69E-02	rs253314	5	16924264	p15.1
SNP_A-1913278	A	A	353	13	368	30	5.703	1.69E-02	rs9343005	6	73868784	q13
SNP_A-1929883	C	C	321	45	384	30	5.698	1.70E-02	rs2648849	8	129251833	q24.21
SNP_A-1900980	T	T	232	188	266	154	5.701	1.70E-02	rs11206457	1	55048118	p32.3
SNP_A-1966307	G	G	350	0	366	6	5.692	1.70E-02	rs4074881	2	192528681	q32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1943337	G	G	386	28	399	13	5.698	1.70E-02	rs16899160	6	31364646	p21.33
SNP_A-1791306	A	A	347	5	398	0	5.691	1.70E-02	rs16903793	5	37965236	p13.2
SNP_A-1821040	C	C	358	10	386	26	5.701	1.70E-02	rs1426474	7	135415516	q33
SNP_A-1862772	G	G	256	138	228	174	5.694	1.70E-02	rs10173329	2	16028334	p24.3
SNP_A-2149635	A	A	288	80	353	63	5.695	1.70E-02	---	5	100686116	q21.1
SNP_A-2143216	T	T	226	142	217	193	5.696	1.70E-02	rs1565971	3	88856873	p11.1
SNP_A-2194473	C	C	279	89	282	132	5.696	1.70E-02	rs533004	11	90003224	q14.3
SNP_A-2213388	A	A	384	26	381	11	5.692	1.70E-02	rs2615614	19	47499649	q13.2
SNP_A-2227335	C	C	360	0	376	6	5.701	1.70E-02	rs7397080	12	93895864	q22
SNP_A-2225009	A	A	376	8	393	1	5.693	1.70E-02	rs16896801	8	123232608	q24.13
SNP_A-2212055	A	A	263	103	263	149	5.697	1.70E-02	rs1343611	13	52520873	q14.3
SNP_A-2210403	C	C	273	41	353	29	5.691	1.70E-02	rs6713014	2	104646456	q12.1
SNP_A-2054017	G	G	374	12	391	3	5.696	1.70E-02	rs12433053	14	50906445	q22.1
SNP_A-2082686	A	A	299	29	350	16	5.7	1.70E-02	rs7327220	13	44926552	q14.13
SNP_A-2099866	G	G	358	10	386	26	5.701	1.70E-02	rs1021519	4	75734592	q13.3
SNP_A-2008753	A	A	388	10	410	2	5.7	1.70E-02	rs725423	3	62870718	p14.2
SNP_A-2043254	C	C	238	120	299	103	5.697	1.70E-02	rs3765044	12	83940967	q21.31
SNP_A-2248119	T	T	268	74	261	109	5.694	1.70E-02	rs17659787	18	34854041	q12.2
SNP_A-2232824	T	T	227	143	219	195	5.692	1.70E-02	rs1947186	4	190137818	q35.2
SNP_A-2237230	T	T	302	28	279	47	5.7	1.70E-02	rs16847456	3	138990700	q22.3
SNP_A-2258940	C	C	359	59	381	37	5.696	1.70E-02	rs7793325	7	147100227	q35
SNP_A-2273197	G	G	292	102	260	132	5.696	1.70E-02	rs6463180	7	43123429	p13
SNP_A-2277283	T	T	312	10	401	3	5.69	1.71E-02	rs7077534	10	90661790	q23.31
SNP_A-2239294	A	G	224	186	216	186	5.682	1.71E-02	rs5765956	22	43471196	q13.31
SNP_A-2232110	T	T	407	1	390	8	5.684	1.71E-02	rs1029654	19	37358469	q13.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041347	C	C	335	9	398	2	5.686	1.71E-02	rs7087342	10	1645794	p15.3
SNP_A-2046147	G	G	284	50	303	85	5.682	1.71E-02	rs10141214	14	45012753	q21.2
SNP_A-2022040	A	A	202	166	262	152	5.689	1.71E-02	rs7140480	14	79092585	q31.1
SNP_A-1992248	G	G	394	4	384	14	5.684	1.71E-02	rs12258501	10	2339567	p15.3
SNP_A-2104966	G	G	301	53	352	36	5.684	1.71E-02	rs12642125	4	61172250	q13.1
SNP_A-2093849	C	C	260	122	297	95	5.689	1.71E-02	rs4627421	17	7335005	p13.1
SNP_A-2078380	A	A	370	16	373	5	5.691	1.71E-02	rs16908621	10	57724376	q21.1
SNP_A-2048932	A	A	360	2	379	11	5.685	1.71E-02	rs1326015	20	54299566	q13.31
SNP_A-2068876	A	A	357	11	411	3	5.682	1.71E-02	rs178344	13	88716191	q31.2
SNP_A-2212741	C	C	219	199	252	164	5.682	1.71E-02	rs2178260	11	61825941	q12.3
SNP_A-2207538	A	A	332	4	349	15	5.682	1.71E-02	rs17071451	13	47661111	q14.2
SNP_A-2203077	A	A	249	157	280	124	5.687	1.71E-02	rs1225006	3	133108857	q22.1
SNP_A-2191601	G	G	286	70	347	53	5.686	1.71E-02	rs2374506	12	104512477	q23.3
SNP_A-2150079	G	G	355	15	382	34	5.684	1.71E-02	rs6585187	10	114521701	q25.2
SNP_A-2116645	T	T	370	48	388	28	5.686	1.71E-02	rs9793989	1	47208758	p33
SNP_A-2112821	G	A	231	177	213	199	5.685	1.71E-02	rs9135	17	3710682	p13.2
SNP_A-2128457	T	T	295	69	363	53	5.684	1.71E-02	rs1364315	16	81855981	q23.3
SNP_A-2137364	C	C	326	38	338	66	5.687	1.71E-02	rs17252027	13	50649706	q14.3
SNP_A-1857439	G	G	377	41	349	63	5.691	1.71E-02	rs573036	10	29445393	p11.23
SNP_A-1852099	G	G	363	5	416	0	5.688	1.71E-02	rs17033269	3	35480785	p22.3
SNP_A-1839549	G	G	348	72	317	99	5.689	1.71E-02	rs1233861	17	12455536	p12
SNP_A-1811668	G	G	342	26	362	50	5.683	1.71E-02	rs2777795	9	104751920	q31.1
SNP_A-1813198	G	G	304	100	272	130	5.686	1.71E-02	rs518113	2	23767150	p24.1
SNP_A-1801810	C	C	311	55	341	35	5.691	1.71E-02	rs7216075	17	29050492	q12
SNP_A-1946198	A	A	296	70	293	105	5.685	1.71E-02	rs4674515	2	199398128	q33.1
SNP_A-1949324	G	G	420	0	367	5	5.681	1.71E-02	rs10243157	7	126029121	q32.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1965075	G	G	384	36	357	57	5.683	1.71E-02	rs9287511	2	139869831	q22.1
SNP_A-1971737	G	G	319	51	379	35	5.683	1.71E-02	rs4656732	1	166736380	q24.2
SNP_A-1983816	G	G	340	56	347	33	5.688	1.71E-02	rs11167842	5	143425201	q31.3
SNP_A-1929865	A	A	231	137	289	119	5.688	1.71E-02	rs2352099	10	87674661	q23.2
SNP_A-1921671	A	A	405	1	388	8	5.685	1.71E-02	rs7951247	11	96978425	q22.1
SNP_A-1904250	A	A	320	88	353	63	5.68	0.0172	rs2233969	6	31188411	p21.33
SNP_A-1978461	G	G	361	7	393	21	5.672	0.0172	---	4	110496937	q25
SNP_A-1978489	G	G	246	146	212	178	5.679	0.0172	rs2236815	1	18795252	p36.13
SNP_A-1937120	G	G	354	2	373	11	5.676	0.0172	rs1190864	14	100138042	q32.2
SNP_A-1668745	A	A	276	124	306	94	5.675	0.0172	rs728527	14	61771045	q23.2
SNP_A-1840297	T	T	373	13	332	26	5.672	0.0172	rs7908658	10	65956546	q21.3
SNP_A-1830352	G	G	362	46	345	71	5.674	0.0172	rs7789583	7	82610444	q21.11
SNP_A-1820908	T	T	256	104	319	87	5.674	0.0172	rs7665846	4	56280173	q12
SNP_A-1855189	A	A	271	97	336	80	5.676	0.0172	rs1011927	3	182119446	q26.33
SNP_A-1871265	G	G	296	24	341	51	5.676	0.0172	rs8101906	19	48024719	q13.2
SNP_A-2110265	A	A	327	41	384	26	5.677	0.0172	rs10932644	2	216669371	q35
SNP_A-2145566	T	T	277	67	270	100	5.671	0.0172	rs12916690	15	58771562	q22.2
SNP_A-2144987	T	T	343	11	395	3	5.68	0.0172	rs12637416	3	69302498	p14.1
SNP_A-2165558	T	T	272	34	278	60	5.681	0.0172	rs1293035	11	62003172	q12.3
SNP_A-2157122	G	G	219	143	279	127	5.675	0.0172	rs12486767	3	171033461	q26.2
SNP_A-2182154	G	G	349	9	414	2	5.678	0.0172	rs1469483	18	19842110	q11.2
SNP_A-2215564	G	G	257	99	259	145	5.671	0.0172	rs3760030	16	5059873	p13.3
SNP_A-2090106	C	C	357	5	408	0	5.672	0.0172	rs2351823	7	9952913	p21.3
SNP_A-2088469	G	G	243	147	218	186	5.678	0.0172	rs939877	8	141417514	q24.3
SNP_A-2086225	C	C	282	74	259	103	5.679	0.0172	rs10119803	9	21656066	p21.3
SNP_A-2096841	T	T	319	49	326	80	5.674	0.0172	rs6747829	2	165293042	q24.3
SNP_A-2100737	A	T	188	180	230	170	5.679	0.0172	rs10862673	12	82362393	q21.31
SNP_A-1990751	A	A	283	95	256	126	5.68	0.0172	rs10487172	7	102996194	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1999320	G	G	353	5	404	0	5.68	0.0172	rs11015816	10	27815080	p12.1
SNP_A-2016735	A	A	346	14	405	5	5.675	0.0172	rs17398828	21	24484905	q21.2
SNP_A-2021312	C	C	284	76	352	60	5.676	0.0172	rs1562821	11	121909235	q24.1
SNP_A-2032718	A	A	300	44	300	72	5.672	0.0172	rs2473091	6	138393118	q23.3
SNP_A-2029625	G	G	307	15	297	31	5.676	0.0172	rs7698222	4	181770566	q34.3
SNP_A-2027647	G	G	327	41	384	26	5.677	0.0172	rs16973392	15	31708374	q14
SNP_A-2254891	G	G	347	43	325	21	5.673	0.0172	rs10795217	10	5017267	p15.1
SNP_A-2291344	C	C	353	15	380	34	5.676	0.0172	rs6771792	3	12276472	p25.2
SNP_A-2309289	C	C	314	22	314	42	5.677	0.0172	rs7109349	11	40073377	p12
SNP_A-2291240	A	A	377	45	350	68	5.665	1.73E-02	rs11750647	5	140843655	q31.3
SNP_A-2289345	T	T	237	129	223	173	5.664	1.73E-02	rs6569032	6	119298534	q22.31
SNP_A-2274864	A	A	302	52	316	86	5.669	1.73E-02	rs17781427	14	41340975	q21.1
SNP_A-2284340	G	G	359	5	410	0	5.668	1.73E-02	rs17012011	4	128312463	q28.1
SNP_A-2283469	T	T	280	30	346	18	5.668	1.73E-02	---	4	97136751	q22.3
SNP_A-2260382	G	G	361	5	412	0	5.665	1.73E-02	rs1664376	1	72725303	p31.1
SNP_A-2260620	A	A	387	7	377	19	5.664	1.73E-02	rs8025963	15	21256637	q11.2
SNP_A-2013016	A	A	398	2	378	10	5.667	1.73E-02	rs6464151	7	150743342	q36.1
SNP_A-2012791	T	T	323	99	288	128	5.667	1.73E-02	rs10501559	11	83730643	q14.1
SNP_A-2010373	C	C	331	7	399	1	5.666	1.73E-02	rs7672900	4	170673935	q33
SNP_A-2101844	G	G	342	18	340	36	5.661	1.73E-02	rs4793176	17	40433473	q21.31
SNP_A-2095764	A	A	345	5	394	0	5.667	1.73E-02	rs10033008	4	186306900	q35.1
SNP_A-2048201	C	C	315	41	331	71	5.661	1.73E-02	rs10933093	2	226157328	q36.3
SNP_A-2053278	C	C	363	5	414	0	5.661	1.73E-02	rs11005672	10	58589277	q21.1
SNP_A-2218606	G	C	210	158	213	201	5.664	1.73E-02	rs2813759	1	90280603	p22.2
SNP_A-2180487	T	T	346	2	365	11	5.664	1.73E-02	rs12608792	19	23774435	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2173489	C	C	320	42	366	26	5.665	1.73E-02	rs17834095	19	38667567	q13.11
SNP_A-2168536	C	C	314	52	374	36	5.665	1.73E-02	rs13369740	18	69000220	q22.3
SNP_A-2184839	T	T	332	36	392	22	5.665	1.73E-02	rs13231718	7	95245019	q21.3
SNP_A-2156528	C	C	214	208	245	171	5.663	1.73E-02	rs8045112	16	9242819	p13.2
SNP_A-2162200	G	C	199	147	194	184	5.662	1.73E-02	rs6542947	2	100458165	q11.2
SNP_A-2114851	T	T	304	20	351	9	5.666	1.73E-02	rs2450758	8	144509422	q24.3
SNP_A-1853822	A	A	261	75	261	113	5.663	1.73E-02	rs7759137	6	4407556	p25.1
SNP_A-1858384	C	T	230	176	192	178	5.665	1.73E-02	rs2130104	15	91801306	q26.1
SNP_A-1708607	G	G	388	10	384	24	5.662	1.73E-02	rs7204845	16	77683919	q23.1
SNP_A-1803393	A	C	218	190	224	184	5.668	1.73E-02	rs2210750	20	16572851	p12.1
SNP_A-1793978	G	G	338	18	404	8	5.664	1.73E-02	rs4433499	10	49998801	q11.23
SNP_A-1969924	A	A	304	24	328	48	5.665	1.73E-02	rs16986243	21	30507755	q22.11
SNP_A-1975500	G	G	256	92	325	77	5.667	1.73E-02	rs18005577	3	182150813	q26.33
SNP_A-1932267	G	G	278	86	269	123	5.669	1.73E-02	rs544068	11	97429337	q22.1
SNP_A-1926291	C	C	365	5	416	0	5.658	1.74E-02	rs16856526	1	228591942	q42.2
SNP_A-1908565	A	A	274	88	280	132	5.659	1.74E-02	rs9576371	13	37291541	q13.3
SNP_A-1897899	G	G	369	1	403	9	5.658	1.74E-02	rs17590614	6	143373357	q24.2
SNP_A-1969235	A	A	234	132	299	117	5.657	1.74E-02	rs2824957	21	18914694	q21.1
SNP_A-1983982	T	T	337	49	303	71	5.652	1.74E-02	rs17655812	5	149378055	q32
SNP_A-1942397	A	A	197	167	248	148	5.654	1.74E-02	rs719239	8	90606777	q21.3
SNP_A-1803050	T	T	315	95	334	66	5.657	1.74E-02	rs1858824	7	93026186	q21.3
SNP_A-1804794	A	A	331	27	397	15	5.653	1.74E-02	rs13402781	2	239013518	q37.3
SNP_A-1682980	A	A	365	19	359	37	5.652	1.74E-02	rs2332617	14	24185790	q12
SNP_A-1758363	T	T	342	6	390	20	5.653	1.74E-02	rs10519460	5	115780782	q23.1
SNP_A-1784446	G	G	209	199	229	155	5.66	1.74E-02	rs4780470	16	9498831	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1855855	T	T	247	121	245	171	5.652	1.74E-02	rs12716921	16	80464144	q23.2
SNP_A-1872480	A	A	420	0	369	5	5.651	1.74E-02	rs2202233	11	19339599	p15.1
SNP_A-1825831	A	T	208	206	239	173	5.658	1.74E-02	rs12591473	15	71754538	q24.1
SNP_A-1824764	G	G	267	91	264	132	5.654	1.74E-02	rs187994	5	6795168	p15.31
SNP_A-1830653	C	C	365	5	416	0	5.658	1.74E-02	rs17013370	2	77069483	p12
SNP_A-1833505	G	G	335	7	403	1	5.652	1.74E-02	rs16880186	6	88845934	q15
SNP_A-2225433	T	T	368	30	372	14	5.657	1.74E-02	rs7196247	16	25908920	p12.1
SNP_A-2056283	A	A	333	7	401	1	5.659	1.74E-02	rs1607497	22	26039739	q12.1
SNP_A-2099235	T	T	387	17	354	32	5.654	1.74E-02	rs829399	1	21743284	p36.12
SNP_A-2085614	A	A	212	132	281	121	5.66	1.74E-02	rs1507374	4	134912913	q28.3
SNP_A-1993241	A	A	349	5	398	0	5.659	1.74E-02	rs17263853	8	52472472	q11.22
SNP_A-2021276	A	A	367	53	342	78	5.653	1.74E-02	rs9882153	3	107221947	q13.11
SNP_A-2258245	A	A	401	21	402	8	5.657	1.74E-02	rs1886713	16	19930719	p12.3
SNP_A-2267643	G	G	314	46	335	79	5.652	1.74E-02	rs2644640	5	174788017	q35.2
SNP_A-2286248	A	A	340	28	361	53	5.659	1.74E-02	rs12212492	6	51967916	p12.2
SNP_A-2274364	A	A	365	5	416	0	5.658	1.74E-02	rs17158715	7	30025877	p15.1
SNP_A-2303727	A	A	358	56	326	80	5.655	1.74E-02	rs2519778	9	133789141	q34.2
SNP_A-2297127	G	G	347	59	351	35	5.649	1.75E-02	rs916766	16	19860948	p12.3
SNP_A-2267524	C	C	309	39	371	25	5.642	1.75E-02	rs1608096	3	193517626	q28
SNP_A-2265845	T	T	323	11	371	3	5.649	1.75E-02	rs17071182	5	164347216	q34
SNP_A-2264661	A	A	304	54	364	38	5.643	1.75E-02	rs719828	17	31489488	q12
SNP_A-2261637	G	G	331	31	375	17	5.641	1.75E-02	rs16973091	15	40418965	q15.1
SNP_A-2234521	A	A	347	9	410	2	5.644	1.75E-02	rs1731970	7	136558477	q33
SNP_A-2233297	G	G	378	12	393	3	5.646	1.75E-02	rs1768056	1	233216822	q43
SNP_A-2240556	G	G	323	93	345	65	5.643	1.75E-02	rs3743016	15	40077489	q15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235340	G	G	306	62	330	40	5.645	1.75E-02	rs7140044	13	23927295	q12.12
SNP_A-2019949	G	G	364	30	335	49	5.645	1.75E-02	rs2255764	21	41684027	q22.3
SNP_A-2007277	T	T	341	33	344	16	5.646	1.75E-02	rs6038678	20	6919610	p12.3
SNP_A-2077750	A	G	211	171	211	185	5.645	1.75E-02	rs1113599	12	76677660	q21.2
SNP_A-2102027	A	A	303	71	313	45	5.643	1.75E-02	rs4791114	17	63209035	q24.2
SNP_A-2059751	A	A	210	164	268	148	5.641	1.75E-02	rs12824366	12	51271560	q13.13
SNP_A-2060464	A	A	390	8	405	1	5.648	1.75E-02	rs11883018	19	47082164	q13.2
SNP_A-2072418	G	G	352	36	327	57	5.642	1.75E-02	rs168841	16	8865964	p13.2
SNP_A-2220169	G	G	338	30	397	17	5.645	1.75E-02	---	1	198276536	q32.1
SNP_A-2202049	A	A	342	70	313	97	5.644	1.75E-02	rs7648327	3	130053406	q21.3
SNP_A-2209944	C	C	209	127	271	113	5.65	1.75E-02	rs8052046	16	2424784	p13.3
SNP_A-2184502	C	C	403	1	388	8	5.649	1.75E-02	---	2	119720308	q14.2
SNP_A-2193995	C	C	311	51	378	36	5.642	1.75E-02	rs17115860	14	44706257	q21.2
SNP_A-2193346	C	C	396	8	411	1	5.645	1.75E-02	rs7102225	11	119165128	q23.3
SNP_A-2169011	G	G	207	171	255	149	5.641	1.75E-02	rs7314793	12	73381516	q21.1
SNP_A-2170566	C	C	338	28	389	15	5.646	1.75E-02	rs12561190	13	97293166	q32.2
SNP_A-2175795	G	G	372	38	382	20	5.641	1.75E-02	rs9925481	16	11004980	p13.13
SNP_A-1864931	C	C	248	104	274	76	5.645	1.75E-02	rs8000933	13	41496291	q14.11
SNP_A-1783722	A	A	236	118	304	104	5.647	1.75E-02	rs9395325	6	47962302	p12.3
SNP_A-1967685	A	A	362	0	382	6	5.643	1.75E-02	rs16995933	20	9377492	p12.2
SNP_A-1909505	C	C	357	5	406	0	5.644	1.75E-02	rs17046863	4	166888555	q32.3
SNP_A-1916152	A	G	199	165	223	191	5.644	1.75E-02	rs3762281	1	153117855	q22
SNP_A-1927518	C	C	398	8	413	1	5.644	1.75E-02	rs17364649	1	78464803	p31.1
SNP_A-1925880	G	G	318	20	299	37	5.649	1.75E-02	rs17078823	13	32703884	q13.1
SNP_A-1916527	-	G	185	185	242	172	5.631	1.76E-02	rs1181652	1	188912871	q31.2
SNP_A-1898295	C	C	260	146	279	109	5.633	1.76E-02	rs2359669	3	35527305	p22.3
SNP_A-1979328	A	A	338	24	390	12	5.635	1.76E-02	rs10519851	4	148300190	q31.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1980061	T	T	339	7	407	1	5.638	1.76E-02	rs168298	4	179976618	q34.3
SNP_A-1934194	T	T	235	117	300	102	5.634	1.76E-02	rs6469090	8	108116208	q23.1
SNP_A-1954839	C	C	325	29	314	50	5.633	1.76E-02	rs9725312	1	241364859	q44
SNP_A-1804421	A	A	324	80	285	105	5.631	1.76E-02	rs2994320	1	239967288	q44
SNP_A-1864636	T	T	271	51	323	35	5.639	1.76E-02	rs2049551	2	76481152	p12
SNP_A-1857339	G	G	361	51	385	31	5.631	1.76E-02	rs604782	1	33768052	p35.1
SNP_A-1842687	C	T	234	178	215	203	5.639	1.76E-02	rs7730159	5	13733956	p15.2
SNP_A-2172781	G	G	356	14	326	28	5.635	1.76E-02	rs7719232	5	15386338	p15.1
SNP_A-2183858	C	C	320	46	383	31	5.635	1.76E-02	rs4640726	4	57856787	q12
SNP_A-2217054	A	A	299	63	310	100	5.635	1.76E-02	rs1457690	5	123501287	q23.2
SNP_A-2119574	C	C	206	134	261	117	5.634	1.76E-02	rs7643155	3	179105286	q26.32
SNP_A-2159537	T	A	178	176	230	164	5.632	1.76E-02	rs6557346	6	154787261	q25.2
SNP_A-2065940	A	A	347	5	394	0	5.634	1.76E-02	rs1453715	12	60183681	q14.1
SNP_A-2049957	G	G	355	15	383	5	5.638	1.76E-02	rs7793209	7	20367724	p21.1
SNP_A-2049696	C	C	363	5	412	0	5.634	1.76E-02	rs10506114	12	33720732	p11.1
SNP_A-1997681	C	C	186	180	242	166	5.631	1.76E-02	rs7031902	9	111784692	q31.3
SNP_A-2237461	T	G	217	171	198	178	5.639	1.76E-02	rs6820437	4	18475113	p15.32
SNP_A-2292480	G	G	281	65	338	48	5.637	1.76E-02	rs10930969	2	182153463	q31.3
SNP_A-2308555	A	A	231	139	293	123	5.64	1.76E-02	rs7712875	5	55928141	q11.2
SNP_A-2253035	A	A	406	14	414	4	5.629	0.0177	rs12922753	16	77811220	q23.1
SNP_A-2286331	G	G	370	42	342	64	5.623	0.0177	rs237008	6	149808654	q25.1
SNP_A-2016594	T	T	365	5	414	0	5.631	0.0177	rs2828311	21	23887573	q21.2
SNP_A-2023491	G	G	302	58	294	88	5.624	0.0177	rs12854643	13	75885540	q22.2
SNP_A-2044453	G	G	390	2	372	10	5.63	0.0177	rs17069054	8	3971564	p23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086954	T	T	281	53	296	88	5.623	0.0177	rs13074282	3	9999699	p25.3
SNP_A-2153832	G	G	365	5	414	0	5.631	0.0177	rs13364133	8	92765741	q21.3
SNP_A-2107999	G	G	204	162	264	148	5.624	0.0177	rs7164271	15	93051824	q26.2
SNP_A-2132450	T	T	392	28	349	45	5.629	0.0177	rs12046987	1	65248881	p31.3
SNP_A-2215304	C	C	291	77	297	117	5.622	0.0177	rs6031580	20	42448695	q13.12
SNP_A-2208395	T	T	212	206	245	171	5.628	0.0177	rs12961600	18	29460378	q12.1
SNP_A-2174325	G	G	310	18	308	36	5.629	0.0177	rs4384003	8	1158023	p23.3
SNP_A-2170353	C	C	327	43	329	23	5.621	0.0177	rs4330937	1	158069992	q23.3
SNP_A-2168215	C	C	353	11	388	28	5.622	0.0177	rs496809	18	74857661	q23
SNP_A-2178008	C	C	329	13	370	32	5.625	0.0177	rs239243	6	101198986	q16.3
SNP_A-1870234	C	C	250	100	311	83	5.63	0.0177	rs723501	17	65787442	q24.3
SNP_A-1869466	C	C	400	2	382	10	5.623	0.0177	rs4654242	1	242841563	q44
SNP_A-1653594	A	A	245	105	318	92	5.621	0.0177	rs1114583	2	78567933	p12
SNP_A-1935118	T	G	185	169	194	148	5.628	0.0177	rs238117	18	3484891	p11.31
SNP_A-1944449	G	G	303	25	302	46	5.626	0.0177	---	4	73944671	q13.3
SNP_A-1980395	G	G	328	18	357	39	5.621	0.0177	rs26878	5	4956383	p15.32
SNP_A-1964824	C	C	412	4	404	14	5.629	0.0177	rs17262027	2	128139702	q14.3
SNP_A-1969723	C	C	365	5	414	0	5.631	0.0177	rs16979625	21	27311090	q21.3
SNP_A-1973311	A	A	342	8	341	21	5.628	0.0177	rs17014222	3	76592763	p12.3
SNP_A-1929816	A	A	317	97	281	125	5.621	0.0177	rs4028240	1	227888320	q42.2
SNP_A-1916888	G	G	292	68	358	52	5.612	0.0178	rs4763986	12	13475204	p13.1
SNP_A-1914771	G	G	357	5	404	0	5.617	0.0178	rs11132482	4	189087456	q35.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1912784	T	T	397	1	384	8	5.616	0.0178	rs6717030	2	11235366	p25.1
SNP_A-1889993	T	T	303	17	325	37	5.613	0.0178	rs826763	12	90145818	q21.33
SNP_A-1878803	A	A	333	31	394	18	5.62	0.0178	rs17009909	4	126797590	q28.1
SNP_A-1971684	T	T	238	176	275	145	5.62	0.0178	rs11131136	3	8594922	p25.3
SNP_A-1963017	A	A	322	54	323	85	5.618	0.0178	rs4141664	2	45728020	p21
SNP_A-1980494	C	C	272	98	272	142	5.615	0.0178	rs274715	5	6776429	p15.31
SNP_A-1981627	G	G	277	65	327	47	5.613	0.0178	rs26095	5	55622769	q11.2
SNP_A-1758970	G	G	386	10	404	2	5.62	0.0178	rs10014788	4	33549925	p15.1
SNP_A-1801942	T	T	235	131	229	181	5.614	0.0178	rs3777612	6	46073567	p21.1
SNP_A-1812430	C	C	188	124	231	103	5.613	0.0178	rs3761823	9	133116366	q34.2
SNP_A-2179885	G	G	264	140	288	106	5.618	0.0178	rs7719156	5	171599883	q35.1
SNP_A-2192158	C	C	191	171	251	159	5.618	0.0178	rs7816828	8	141257873	q24.3
SNP_A-2216732	T	T	285	105	313	77	5.619	0.0178	rs803022	14	51795384	q22.1
SNP_A-2227358	G	G	359	5	406	0	5.613	0.0178	rs11157746	14	50017298	q21.3
SNP_A-2137420	A	A	346	24	367	47	5.618	0.0178	rs12239301	1	67995192	p31.2
SNP_A-2119550	A	A	355	5	402	0	5.62	0.0178	rs12063868	1	165602885	q24.2
SNP_A-2165534	T	T	324	46	337	77	5.617	0.0178	rs1109106	5	168177820	q34
SNP_A-2086847	A	A	412	2	394	10	5.614	0.0178	rs6593439	10	42436213	q11.21
SNP_A-2088112	T	T	368	0	390	6	5.62	0.0178	rs435282	16	82335103	q23.3
SNP_A-2079506	C	C	287	131	253	163	5.619	0.0178	rs11103455	9	134764002	q34.3
SNP_A-2084469	G	G	396	10	414	2	5.613	0.0178	rs17168341	7	134406941	q33
SNP_A-2093898	G	G	357	5	404	0	5.617	0.0178	---	4	141231194	q31.1
SNP_A-2061673	T	T	331	39	348	68	5.613	0.0178	rs601003	18	64223744	q22.1
SNP_A-2070671	T	T	214	100	194	134	5.618	0.0178	rs1454692	3	192397659	q28
SNP_A-2038485	G	G	255	153	207	175	5.613	0.0178	rs1992495	10	6818093	p14
SNP_A-2013370	C	C	382	8	395	1	5.616	0.0178	rs7008825	8	42477309	p11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006726	G	G	339	13	376	4	5.617	0.0178	rs870278	10	132150617	q26.3
SNP_A-2001358	G	G	222	196	250	158	5.62	0.0178	rs6584037	10	97707062	q24.1
SNP_A-2262927	A	A	308	98	337	71	5.613	0.0178	rs3781709	11	34461287	p13
SNP_A-2251543	A	A	335	11	383	3	5.611	0.0178	rs6667214	1	230363221	q42.2
SNP_A-2234452	T	T	332	32	315	53	5.613	0.0178	rs932434	20	34126301	q11.23
SNP_A-2229638	C	C	331	39	348	68	5.613	0.0178	rs4901350	14	52683205	q22.1
SNP_A-2300821	G	G	327	29	380	16	5.617	0.0178	rs4319110	8	50363233	q11.21
SNP_A-2302302	G	G	187	147	252	138	5.61	1.79E-02	rs1993160	4	82637812	q21.21
SNP_A-2001423	G	G	219	157	244	122	5.607	1.79E-02	rs7914439	10	111266976	q25.1
SNP_A-2014531	A	A	305	57	344	38	5.61	1.79E-02	rs11224294	11	99954372	q22.1
SNP_A-2032916	A	A	257	103	326	88	5.604	1.79E-02	rs334353	9	98987920	q22.33
SNP_A-2031806	G	G	336	6	363	19	5.61	1.79E-02	rs11596224	10	21260140	p12.31
SNP_A-2063951	T	T	333	63	302	88	5.607	1.79E-02	rs4269911	11	42663442	p12
SNP_A-2068648	G	G	354	6	383	19	5.603	1.79E-02	rs1862555	5	91293683	q14.3
SNP_A-2069266	G	G	350	4	371	15	5.607	1.79E-02	rs10975894	9	6905049	p24.1
SNP_A-2056171	A	A	217	143	208	194	5.611	1.79E-02	rs3910791	6	48586661	p12.3
SNP_A-2079205	G	G	188	164	249	153	5.606	1.79E-02	rs7202781	16	77928684	q23.1
SNP_A-2146704	C	C	304	102	335	75	5.603	1.79E-02	rs4968748	17	58423232	q23.3
SNP_A-2110992	C	C	302	22	327	45	5.605	1.79E-02	rs10404394	19	51433408	q13.32
SNP_A-2112773	A	A	319	45	380	30	5.609	1.79E-02	rs7045283	9	27881840	p21.2
SNP_A-2126066	A	A	321	35	390	22	5.608	1.79E-02	rs7699371	4	121645460	q27
SNP_A-2209495	G	G	299	25	291	45	5.606	1.79E-02	rs6660454	1	101442347	p21.2
SNP_A-2210901	G	A	202	150	206	196	5.608	1.79E-02	rs7831120	8	81176544	q21.13
SNP_A-2203582	T	T	231	159	272	132	5.602	1.79E-02	rs36155	5	66195926	q12.3
SNP_A-2192095	A	A	271	93	261	131	5.605	1.79E-02	rs2205870	6	49017955	p12.3
SNP_A-1869221	C	C	251	155	260	112	5.608	1.79E-02	rs4854834	3	132941388	q22.1
SNP_A-1870637	T	C	178	130	184	174	5.61	1.79E-02	rs2693880	2	6177477	p25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1859796	C	C	353	17	409	7	5.609	1.79E-02	rs4884136	13	79116393	q31.1
SNP_A-1830145	C	C	362	56	335	81	5.603	1.79E-02	rs17729753	12	8910744	p13.31
SNP_A-1974417	C	T	202	168	222	190	5.605	1.79E-02	rs3849416	3	134344267	q22.1
SNP_A-1887296	G	G	353	41	373	23	5.608	1.79E-02	rs222567	10	109915120	q25.1
SNP_A-1896800	G	G	301	25	293	45	5.607	1.79E-02	rs2484191	10	27734770	p12.1
SNP_A-1887126	T	T	352	14	409	5	5.6	1.80E-02	rs2483491	10	27554881	p12.1
SNP_A-1878243	A	A	337	31	398	18	5.594	1.80E-02	rs16928514	11	36176296	p13
SNP_A-1876144	G	G	318	20	365	9	5.601	1.80E-02	rs10763581	10	60119600	q21.1
SNP_A-1905074	C	C	308	34	335	63	5.598	1.80E-02	rs17191351	15	58418368	q22.2
SNP_A-1965675	C	C	289	43	273	67	5.597	1.80E-02	rs2198225	2	165102103	q24.3
SNP_A-1984283	C	C	405	3	392	12	5.592	1.80E-02	rs2116732	5	159147091	q33.3
SNP_A-1953751	C	C	317	5	339	17	5.592	1.80E-02	rs17168587	7	14818549	p21.2
SNP_A-1952713	G	G	329	61	273	79	5.592	1.80E-02	rs4815390	20	25106241	p11.21
SNP_A-1825866	T	T	341	7	407	1	5.597	1.80E-02	rs17043720	2	53012717	p16.2
SNP_A-1828134	C	C	191	171	245	155	5.592	1.80E-02	rs2249061	1	188934227	q31.2
SNP_A-1862343	C	C	343	5	367	17	5.6	1.80E-02	rs11992951	8	50681173	q11.21
SNP_A-1864687	C	C	226	94	222	136	5.593	1.80E-02	rs10914766	1	33845021	p35.1
SNP_A-1845537	A	A	311	35	378	22	5.601	1.80E-02	rs16912372	9	107159008	q31.2
SNP_A-1732756	G	G	348	52	330	78	5.599	1.80E-02	rs10489841	1	155909159	q23.1
SNP_A-2206121	C	C	327	31	319	53	5.595	1.80E-02	rs17824109	4	2668635	p16.3
SNP_A-2112864	G	G	250	86	207	107	5.593	1.80E-02	rs9467161	6	24549942	p22.2
SNP_A-2166875	C	C	274	80	340	64	5.598	1.80E-02	rs1939230	11	126393062	q24.2
SNP_A-2163987	C	C	294	66	353	49	5.595	1.80E-02	rs16956119	17	51057888	q23.1
SNP_A-2095640	C	C	335	73	366	50	5.595	1.80E-02	rs9315655	13	38598767	q13.3
SNP_A-2048900	A	A	161	157	216	146	5.6	1.80E-02	rs1078572	2	2580817	p25.3
SNP_A-2074613	A	A	327	43	386	28	5.599	1.80E-02	rs1542634	16	87867072	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2033580	A	A	253	117	247	163	5.593	1.80E-02	rs4863483	4	139922636	q31.1
SNP_A-2047081	G	G	353	19	327	35	5.6	1.80E-02	rs4454229	7	117345661	q31.31
SNP_A-2018262	G	G	330	12	400	4	5.598	1.80E-02	rs2834136	21	33494661	q22.11
SNP_A-2003319	C	C	268	130	307	103	5.597	1.80E-02	rs913468	13	50516161	q14.3
SNP_A-2293169	A	A	204	196	235	161	5.6	1.80E-02	rs12694376	2	216572317	q35
SNP_A-2266197	G	G	271	97	320	76	5.593	1.80E-02	rs1430012	3	5582482	p26.1
SNP_A-2287255	C	C	362	0	386	6	5.585	1.81E-02	rs17105921	14	36545036	q13.3
SNP_A-2299644	A	A	355	59	326	84	5.586	1.81E-02	rs1217338	9	69277652	q21.11
SNP_A-2299632	T	T	276	44	338	30	5.588	1.81E-02	rs950426	15	79137794	q25.1
SNP_A-2295860	A	A	381	17	398	6	5.587	1.81E-02	rs17161647	7	98523864	q22.1
SNP_A-2307436	G	G	348	38	321	59	5.589	1.81E-02	rs11039509	11	48045891	p11.2
SNP_A-1991288	T	T	353	69	373	45	5.585	1.81E-02	rs1477226	7	130912619	q32.3
SNP_A-1991656	C	C	263	123	229	153	5.59	1.81E-02	rs826790	7	146465074	q35
SNP_A-2011701	C	C	353	9	414	2	5.585	1.81E-02	rs7745522	6	34073412	p21.31
SNP_A-2036918	T	T	165	123	226	114	5.591	1.81E-02	rs565843	4	13639457	p15.33
SNP_A-2038705	A	A	330	80	284	106	5.589	1.81E-02	rs663977	1	182933301	q31.1
SNP_A-2074731	C	C	328	38	390	24	5.582	1.81E-02	rs16924208	8	5968112	q12.1
SNP_A-2048058	T	T	263	35	292	66	5.589	1.81E-02	rs16850829	3	167913557	q26.1
SNP_A-2049781	C	C	272	88	274	130	5.584	1.81E-02	rs797078	3	110627233	q13.13
SNP_A-2061712	G	G	275	73	334	56	5.584	1.81E-02	rs7154637	14	34793317	q13.2
SNP_A-2096588	C	C	361	47	344	72	5.585	1.81E-02	rs4747952	10	6307181	p15.1
SNP_A-2097776	T	T	264	60	346	48	5.585	1.81E-02	rs2143739	6	168174	p25.3
SNP_A-2161107	T	T	268	86	255	121	5.583	1.81E-02	rs2875653	13	72903607	q22.1
SNP_A-2156318	T	T	341	9	400	2	5.583	1.81E-02	rs7535694	1	97802966	p21.3
SNP_A-2147520	T	T	293	105	321	77	5.585	1.81E-02	rs6757188	2	160669130	q24.2
SNP_A-2137988	T	T	345	7	411	1	5.584	1.81E-02	rs10283228	8	60007482	q12.1
SNP_A-2141245	C	C	238	146	219	189	5.587	1.81E-02	rs542926	11	30022024	p14.1
SNP_A-2126207	A	A	327	39	344	68	5.59	1.81E-02	rs11885631	2	165276860	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2201552	A	A	342	4	336	14	5.586	1.81E-02	rs6472664	8	50810643	q11.21
SNP_A-2210953	T	T	352	2	375	11	5.585	1.81E-02	rs2623858	8	68839922	q13.2
SNP_A-2211663	T	T	323	7	385	1	5.584	1.81E-02	rs17098132	1	76304652	p31.1
SNP_A-2222859	G	G	258	152	294	122	5.589	1.81E-02	rs11255780	10	5979834	p15.1
SNP_A-2183307	T	T	195	193	221	155	5.587	1.81E-02	rs1205030	6	3429796	p25.2
SNP_A-2189185	C	C	358	58	334	84	5.588	1.81E-02	rs2062135	3	65171347	p14.1
SNP_A-2188960	C	C	385	31	354	50	5.583	1.81E-02	rs7520276	1	202391148	q32.1
SNP_A-1744839	T	T	265	61	304	42	5.588	1.81E-02	rs10486462	7	26262315	p15.2
SNP_A-1644764	T	T	397	5	398	16	5.588	1.81E-02	rs10518752	15	52054483	q21.3
SNP_A-1804108	G	G	186	180	243	167	5.584	1.81E-02	rs9346956	6	163704615	q26
SNP_A-1792177	A	A	359	11	409	3	5.587	1.81E-02	rs4598716	12	19116850	p12.3
SNP_A-1798743	A	A	243	127	239	177	5.584	1.81E-02	rs6756471	2	34911231	p22.3
SNP_A-1815136	C	C	214	152	276	138	5.588	1.81E-02	rs2976428	8	24874922	p21.2
SNP_A-1831737	C	C	372	20	392	8	5.586	1.81E-02	rs893255	2	209015418	q34
SNP_A-1833370	T	T	281	41	254	62	5.588	1.81E-02	rs7752593	6	80005367	q14.1
SNP_A-1980719	G	G	235	169	274	140	5.588	1.81E-02	rs17221495	5	11650332	p15.2
SNP_A-1978298	T	T	218	144	283	131	5.588	1.81E-02	rs151402	4	103547664	q24
SNP_A-1924605	A	A	233	183	254	142	5.589	1.81E-02	rs10870505	12	131927283	q24.33
SNP_A-1879010	G	G	360	0	384	6	5.583	1.81E-02	rs7013972	8	29865635	p12
SNP_A-1902924	-	A	182	182	242	172	5.583	1.81E-02	rs10049853	4	32198089	p15.1
SNP_A-1894940	A	A	256	42	312	28	5.58	1.82E-02	rs1588173	2	17267746	p24.2
SNP_A-1924635	T	T	356	0	380	6	5.579	1.82E-02	rs17035047	3	3671098	p26.2
SNP_A-1951491	A	G	197	141	191	187	5.573	1.82E-02	rs2049957	6	166821731	q27
SNP_A-1935687	C	C	335	7	399	1	5.581	1.82E-02	rs1567872	4	188042412	q35.2
SNP_A-1936010	T	T	263	103	266	150	5.574	1.82E-02	rs926632	20	57318157	q13.32
SNP_A-1939796	G	G	403	1	392	8	5.577	1.82E-02	rs941789	20	54974819	q13.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1843746	C	C	321	45	283	65	5.577	1.82E-02	rs11887551	2	5957258	p25.2
SNP_A-1857661	T	T	404	8	415	1	5.573	1.82E-02	rs10306187	9	122234867	q33.2
SNP_A-1787970	A	A	413	1	402	8	5.574	1.82E-02	rs4083410	6	24625756	p22.2
SNP_A-1803851	G	G	334	4	355	15	5.574	1.82E-02	rs12697196	5	27964830	p14.1
SNP_A-1810759	C	C	378	0	404	6	5.574	1.82E-02	rs2566831	6	123008706	q22.31
SNP_A-1652930	C	C	275	97	274	140	5.575	1.82E-02	rs3918657	10	91600824	q23.31
SNP_A-1695431	A	A	312	30	339	57	5.578	1.82E-02	rs10515349	5	103130351	q21.2
SNP_A-1781243	G	G	298	124	325	93	5.58	1.82E-02	rs863035	1	155929754	q23.2
SNP_A-2176111	C	C	330	12	368	30	5.577	1.82E-02	rs8112064	19	48362135	q13.31
SNP_A-2176246	T	T	348	2	371	11	5.578	1.82E-02	---	2	213962339	q34
SNP_A-2224358	C	C	336	30	393	17	5.576	1.82E-02	rs10813820	9	324524	p24.3
SNP_A-2125685	T	T	267	63	288	104	5.577	1.82E-02	rs10021074	4	169831612	q32.3
SNP_A-2108085	C	C	308	34	386	22	5.573	1.82E-02	rs17281304	3	112805709	q13.2
SNP_A-2119764	A	A	345	21	371	43	5.574	1.82E-02	rs10103296	8	99373979	q22.2
SNP_A-2146220	-	A	184	184	243	173	5.573	1.82E-02	rs2181111	6	7569940	p24.3
SNP_A-2102955	G	G	287	113	305	81	5.578	1.82E-02	rs1693549	8	101744550	q22.3
SNP_A-2078282	T	T	239	103	304	88	5.579	1.82E-02	rs564214	11	125356265	q24.2
SNP_A-2089325	G	G	393	9	363	21	5.581	1.82E-02	rs11208515	1	64900051	p31.3
SNP_A-2071314	C	C	375	43	352	66	5.581	1.82E-02	rs16829328	2	151721167	q23.3
SNP_A-2028594	A	A	319	87	284	114	5.579	1.82E-02	rs9365388	6	162617303	q26
SNP_A-2014739	G	G	323	43	337	73	5.579	1.82E-02	rs486055	11	102155634	q22.2
SNP_A-1995105	A	A	335	5	359	17	5.579	1.82E-02	rs17232285	8	129599892	q24.21
SNP_A-2298767	C	C	333	17	385	7	5.573	1.82E-02	rs12083422	1	57761291	p32.2
SNP_A-2298019	C	C	415	1	404	8	5.573	1.82E-02	rs16951450	18	190576	p11.32
SNP_A-2292735	G	G	281	89	341	71	5.573	1.82E-02	rs2414937	15	65219730	q22.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2265052	T	-	232	166	204	204	5.578	1.82E-02	rs867750	18	34290188	q12.2
SNP_A-2264801	T	T	365	5	410	0	5.576	1.82E-02	rs7546822	1	25598365	p36.11
SNP_A-2264849	A	A	417	1	406	8	5.572	1.82E-02	rs17420901	11	30803823	p14.1
SNP_A-2268340	A	A	347	11	395	3	5.576	1.82E-02	rs36008	16	54292200	q12.2
SNP_A-2257400	T	T	265	53	317	37	5.578	1.82E-02	rs17026910	4	134931587	q28.3
SNP_A-2257514	A	A	349	43	362	24	5.58	1.82E-02	rs1494622	5	62491395	q12.1
SNP_A-2249218	A	A	339	73	370	50	5.58	1.82E-02	rs7467550	9	102742475	q31.1
SNP_A-2248416	C	C	363	1	401	9	5.576	1.82E-02	rs1923699	10	98139441	q24.1
SNP_A-2244041	G	G	322	16	399	7	5.577	1.82E-02	rs10169657	2	129849134	q21.1
SNP_A-2244667	C	C	322	40	342	70	5.578	1.82E-02	rs7800747	7	35162739	p14.2
SNP_A-2264632	A	A	387	15	338	28	5.567	0.0183	rs13428593	2	139842159	q22.1
SNP_A-2267217	T	T	289	95	265	127	5.57	0.0183	rs9847068	3	120907303	q13.33
SNP_A-2280785	C	T	200	186	222	170	5.563	0.0183	rs7232237	18	29578932	q12.1
SNP_A-2297906	T	T	199	135	194	188	5.567	0.0183	rs11933596	4	68410774	q13.2
SNP_A-2308577	C	C	318	44	330	74	5.563	0.0183	rs17072275	3	65048685	p14.1
SNP_A-2008833	A	A	339	7	403	1	5.568	0.0183	rs4677296	3	73643155	p13
SNP_A-2029896	C	C	361	1	399	9	5.572	0.0183	rs7236890	18	35771719	q12.3
SNP_A-2039908	T	T	279	121	316	94	5.569	0.0183	rs971251	2	141796376	q22.1
SNP_A-2069335	G	G	414	0	369	5	5.57	0.0183	rs227404	14	69561136	q24.2
SNP_A-2067280	G	A	200	170	222	186	5.563	0.0183	rs6706537	2	135452714	q21.3
SNP_A-2058030	C	G	205	203	231	167	5.565	0.0183	rs7617412	3	64537827	p14.1
SNP_A-2052714	C	C	232	136	222	184	5.568	0.0183	rs701175	1	229672503	q42.2
SNP_A-2097307	C	G	201	195	227	167	5.563	0.0183	rs7972346	12	108271491	q24.11
SNP_A-2149481	T	C	233	183	216	198	5.567	0.0183	rs2692681	3	135078316	q22.1
SNP_A-2141031	G	G	308	40	370	26	5.566	0.0183	---	22	16479346	q11.21
SNP_A-2153596	G	G	361	1	399	9	5.572	0.0183	rs2922867	8	6396720	p23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2117076	G	G	285	103	248	130	5.568	0.0183	rs134370	22	33891967	q12.3
SNP_A-2127735	A	A	334	26	394	14	5.567	0.0183	rs5760045	22	22480168	q11.23
SNP_A-2133984	T	T	320	36	376	22	5.563	0.0183	rs10823019	10	68720216	q21.3
SNP_A-2213464	A	A	381	7	352	18	5.563	0.0183	rs576366	19	5973592	p13.3
SNP_A-1688760	G	G	321	23	353	47	5.564	0.0183	rs10517658	4	158365817	q32.1
SNP_A-1655395	G	G	222	120	269	99	5.568	0.0183	rs6679031	1	237531268	q43
SNP_A-1801492	A	A	339	7	403	1	5.568	0.0183	rs4019611	11	114187729	q23.2
SNP_A-1785440	G	G	284	92	341	73	5.571	0.0183	rs17066538	6	137914611	q23.3
SNP_A-1862687	G	G	333	11	379	3	5.57	0.0183	rs3760280	17	51157187	q23.1
SNP_A-1827612	G	G	256	106	257	153	5.568	0.0183	rs2511646	8	105273361	q22.3
SNP_A-1919426	T	T	371	5	416	0	5.567	0.0183	rs9651887	12	125691107	q24.32
SNP_A-1931039	G	G	259	111	322	94	5.568	0.0183	rs9937007	16	16765833	p12.3
SNP_A-1876117	G	A	189	175	233	179	5.569	0.0183	rs10780227	9	78078631	q21.2
SNP_A-1882157	T	T	240	60	304	46	5.565	0.0183	rs1819033	7	45115027	p13
SNP_A-1876757	C	C	222	124	286	110	5.557	0.0184	rs10191101	2	97992583	q11.2
SNP_A-1892053	G	G	367	3	356	12	5.562	0.0184	rs6826731	4	72495727	q13.3
SNP_A-1922317	A	A	303	65	303	99	5.558	0.0184	rs611263	18	59441237	q21.33
SNP_A-1945508	C	C	307	55	367	39	5.562	0.0184	rs4862792	4	188576499	q35.2
SNP_A-1957731	T	C	237	177	204	196	5.556	0.0184	rs11067601	12	114346149	q24.21
SNP_A-1980238	T	T	252	104	252	150	5.56	0.0184	rs1499010	4	187136787	q35.1
SNP_A-1857149	C	C	311	55	323	89	5.555	0.0184	rs12953698	18	39277418	q12.3
SNP_A-1803901	A	A	322	10	335	25	5.562	0.0184	rs17102549	12	65163643	q14.3
SNP_A-2218734	T	T	364	0	390	6	5.559	0.0184	rs17125797	10	110910322	q25.1
SNP_A-2206889	T	T	273	93	270	134	5.56	0.0184	rs11728206	4	137946742	q28.3
SNP_A-2199470	T	T	309	27	311	49	5.554	0.0184	rs2712504	12	57431746	q14.1
SNP_A-2199406	G	G	236	112	222	152	5.559	0.0184	rs11138078	9	78962119	q21.31
SNP_A-2131296	C	C	375	25	385	11	5.556	0.0184	rs10887794	10	90005254	q23.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123301	G	G	268	144	235	177	5.558	0.0184	rs4708961	6	162845745	q26
SNP_A-2138270	C	C	341	7	405	1	5.562	0.0184	---	3	19947951	p24.3
SNP_A-2145478	G	G	249	109	313	93	5.562	0.0184	rs4641471	11	21239678	p15.1
SNP_A-2099701	C	C	298	20	368	10	5.56	0.0184	rs903576	3	124695623	q21.1
SNP_A-2091142	T	T	389	21	366	38	5.555	0.0184	rs12313609	12	97835067	q23.1
SNP_A-2086864	G	G	244	178	276	144	5.555	0.0184	rs4674033	2	216506080	q35
SNP_A-2036333	C	C	202	142	254	124	5.559	0.0184	rs196223	10	121483742	q26.11
SNP_A-2023012	G	G	348	64	320	90	5.558	0.0184	rs2017870	5	162905004	q34
SNP_A-2015230	A	A	333	27	397	15	5.562	0.0184	rs2822584	21	14631720	q11.2
SNP_A-2016568	A	A	278	92	338	74	5.556	0.0184	rs2828169	21	23753051	q21.2
SNP_A-2016818	G	G	362	0	388	6	5.557	0.0184	rs17110713	11	109453752	q22.3
SNP_A-1991528	A	A	221	171	232	126	5.555	0.0184	rs2097229	7	141543378	q34
SNP_A-2287972	G	G	336	14	389	5	5.555	0.0184	rs7446534	5	116461742	q23.1
SNP_A-2284994	C	C	341	7	405	1	5.562	0.0184	rs1179669	2	217605963	q35
SNP_A-2265499	T	T	322	26	380	14	5.562	0.0184	rs3784590	15	29110106	q13.3
SNP_A-2263450	T	T	297	65	300	100	5.558	0.0184	rs11628283	14	56032825	q22.3
SNP_A-2250797	T	T	226	134	223	187	5.547	1.85E-02	rs2269011	20	17363778	p12.1
SNP_A-2307767	G	G	341	11	387	3	5.546	1.85E-02	rs1799853	10	96692037	q23.33
SNP_A-2302938	C	C	325	17	375	7	5.545	1.85E-02	rs4757032	11	20057022	p15.1
SNP_A-2091660	T	T	221	147	215	201	5.544	1.85E-02	rs10860643	12	99728744	q23.1
SNP_A-2106286	G	G	304	52	369	37	5.549	1.85E-02	rs11174091	12	60276565	q14.1
SNP_A-2095484	T	T	288	22	297	43	5.55	1.85E-02	rs2129836	3	164219084	q26.1
SNP_A-2058682	A	A	240	106	308	92	5.548	1.85E-02	rs10777195	12	88657608	q21.33
SNP_A-2064352	G	G	330	12	398	4	5.549	1.85E-02	rs17098394	14	60994488	q23.1
SNP_A-2153645	A	A	211	195	235	155	5.544	1.85E-02	rs12404124	1	11808135	p36.22
SNP_A-2155871	A	A	305	87	279	117	5.549	1.85E-02	rs10881618	10	91412609	q23.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2118408	T	T	371	49	389	29	5.55	1.85E-02	rs2399486	3	114739028	q13.2
SNP_A-2182906	G	A	199	195	238	174	5.547	1.85E-02	rs11997560	8	97435182	q22.1
SNP_A-2171420	A	A	328	54	326	84	5.545	1.85E-02	rs10807747	7	1516573	p22.3
SNP_A-2211181	C	C	353	9	344	22	5.546	1.85E-02	rs2305610	3	31680653	p24.1
SNP_A-2226176	G	G	227	133	294	120	5.544	1.85E-02	rs288036	5	138238794	q31.2
SNP_A-1704145	T	T	312	74	271	97	5.55	1.85E-02	rs10485325	6	41417402	p21.1
SNP_A-1743349	A	A	358	0	384	6	5.552	1.85E-02	rs526895	6	128978935	q22.33
SNP_A-1739153	A	A	313	69	300	100	5.551	1.85E-02	rs10502860	18	41051796	q12.3
SNP_A-1859458	T	C	213	159	195	185	5.546	1.85E-02	rs2964758	5	6309302	p15.32
SNP_A-1848157	A	A	342	18	353	37	5.547	1.85E-02	rs3260222	5	125306885	q23.2
SNP_A-1841649	G	G	229	135	292	120	5.553	1.85E-02	rs7215329	17	14671928	p12
SNP_A-1962500	C	C	308	36	362	22	5.551	1.85E-02	rs10495764	2	28423201	p23.2
SNP_A-1956935	G	G	407	3	396	12	5.546	1.85E-02	rs12343676	9	105271030	q31.1
SNP_A-1949135	A	A	353	17	407	7	5.552	1.85E-02	rs16854658	3	171157108	q26.2
SNP_A-1925203	C	C	360	38	368	20	5.548	1.85E-02	rs12489702	3	17886543	p24.3
SNP_A-1925634	G	G	333	7	395	1	5.551	1.85E-02	rs8022309	14	61677035	q23.2
SNP_A-1927703	A	A	226	128	293	115	5.546	1.85E-02	rs4876693	8	118071304	q24.11
SNP_A-1909546	T	T	212	146	207	201	5.537	1.86E-02	rs6436832	2	229739760	q36.3
SNP_A-1907786	A	A	394	2	380	10	5.541	1.86E-02	rs16939736	18	42438616	q21.1
SNP_A-1903402	A	A	343	9	400	2	5.536	1.86E-02	rs10011532	4	20684255	p15.31
SNP_A-1902546	A	A	419	3	408	12	5.542	1.86E-02	rs918179	8	129143755	q24.21
SNP_A-1885176	T	T	304	56	364	40	5.54	1.86E-02	rs10173037	2	192616671	q32.3
SNP_A-1979651	G	G	291	59	269	85	5.536	1.86E-02	---	4	162923549	q32.2
SNP_A-1976461	C	C	250	116	248	164	5.536	1.86E-02	rs10020457	4	23639230	p15.2
SNP_A-1844064	A	A	347	1	385	9	5.542	1.86E-02	rs3774802	3	187740698	q27.3
SNP_A-1833235	A	A	390	22	399	9	5.535	1.86E-02	---	3	37563716	p22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872246	C	C	232	124	298	110	5.543	1.86E-02	rs7893529	10	14189709	p13
SNP_A-1873074	C	C	403	19	409	7	5.54	1.86E-02	rs1966480	19	11470869	p13.2
SNP_A-1744319	G	G	348	0	374	6	5.54	1.86E-02	rs7144267	5	86100453	q14.3
SNP_A-1810560	G	G	290	42	299	71	5.539	1.86E-02	rs969299	8	84379591	q21.13
SNP_A-2211706	G	G	378	10	392	2	5.542	1.86E-02	rs435340	14	44004257	q21.2
SNP_A-2208428	A	A	318	28	339	53	5.542	1.86E-02	rs9382665	6	56774326	p12.1
SNP_A-2176206	T	T	392	8	401	1	5.542	1.86E-02	rs17012997	1	202986446	q32.1
SNP_A-2146970	C	C	322	18	342	38	5.54	1.86E-02	rs4398767	6	129265160	q22.33
SNP_A-2140682	T	T	307	61	371	45	5.538	1.86E-02	rs9556617	13	96180371	q32.1
SNP_A-2063599	G	G	315	93	340	66	5.534	1.86E-02	rs12589331	14	70413084	q24.2
SNP_A-2061078	T	T	285	87	255	115	5.543	1.86E-02	rs11772635	7	21185042	p15.3
SNP_A-2106653	G	G	248	106	254	156	5.539	1.86E-02	rs4962418	10	126687076	q26.13
SNP_A-2085103	G	G	233	131	299	117	5.536	1.86E-02	rs10934683	3	125936073	q21.2
SNP_A-2005403	C	C	343	29	304	46	5.539	1.86E-02	rs17129649	10	113985799	q25.2
SNP_A-2000920	G	G	226	128	286	112	5.542	1.86E-02	rs2065092	10	4314728	p15.1
SNP_A-2287820	G	G	355	5	396	0	5.537	1.86E-02	rs17012257	1	204819245	q32.2
SNP_A-2233874	G	G	297	47	303	77	5.542	1.86E-02	rs6809606	3	59543698	p14.2
SNP_A-2258913	G	G	283	73	290	112	5.536	1.86E-02	rs6820577	4	121659425	q27
SNP_A-2257008	C	C	222	132	279	115	5.532	1.87E-02	rs701099	12	123765875	q24.31
SNP_A-2273791	G	G	366	0	394	6	5.533	1.87E-02	rs107696	19	43003463	q13.13
SNP_A-2232885	C	T	203	161	212	190	5.532	1.87E-02	rs2510777	4	95818127	q22.3
SNP_A-2237251	G	G	307	55	319	89	5.529	1.87E-02	rs2037694	7	53036554	p12.1
SNP_A-2289636	A	A	362	0	390	6	5.529	1.87E-02	rs356780	13	74374468	q22.2
SNP_A-2289762	T	T	236	132	229	181	5.525	1.87E-02	rs7178749	15	59841189	q22.2
SNP_A-2308779	T	T	181	169	241	159	5.527	1.87E-02	rs7813695	8	94974302	q22.1
SNP_A-1997444	C	C	344	54	316	78	5.531	1.87E-02	rs10521066	9	103401810	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017274	T	T	223	147	216	200	5.534	1.87E-02	rs2156292	21	27571833	q21.3
SNP_A-2012869	A	A	189	167	251	157	5.531	1.87E-02	rs542892	11	84468686	q14.1
SNP_A-2030678	T	T	382	8	364	20	5.531	1.87E-02	rs16826561	2	149784537	q23.2
SNP_A-2038062	T	T	221	135	210	182	5.529	1.87E-02	rs6854583	4	115411489	q26
SNP_A-2078900	G	C	193	167	225	185	5.527	1.87E-02	rs6573422	14	61715673	q23.2
SNP_A-2096870	G	G	405	9	396	22	5.534	1.87E-02	rs2427254	20	60157383	q13.33
SNP_A-2094971	A	A	311	39	371	25	5.526	1.87E-02	rs2710933	3	183714910	q26.33
SNP_A-2094919	T	T	263	93	264	136	5.534	1.87E-02	rs2799655	6	96439562	q16.1
SNP_A-2143563	C	C	316	42	322	70	5.526	1.87E-02	rs6805193	3	186380993	q27.2
SNP_A-2145935	C	C	339	7	401	1	5.533	1.87E-02	rs470954	12	127909761	q24.32
SNP_A-2131935	C	C	296	72	305	111	5.528	1.87E-02	rs12270338	11	93787112	q21
SNP_A-2169116	G	G	284	76	350	60	5.53	1.87E-02	rs12573579	10	56776159	q21.1
SNP_A-2192599	G	G	388	8	349	19	5.526	1.87E-02	rs2122282	1	74464024	p31.1
SNP_A-2192932	A	A	320	46	381	31	5.53	1.87E-02	rs10036206	5	90644934	q14.3
SNP_A-1814381	G	G	379	17	394	6	5.532	1.87E-02	rs6595427	5	122431933	q23.2
SNP_A-1788647	C	C	360	0	388	6	5.526	1.87E-02	rs6774840	3	193235741	q28
SNP_A-1744147	A	A	241	149	283	123	5.532	1.87E-02	rs2827003	21	22049820	q21.1
SNP_A-1860927	G	G	250	118	244	164	5.529	1.87E-02	rs7549131	1	80226517	p31.1
SNP_A-1976917	G	G	342	10	357	25	5.534	1.87E-02	rs16853060	4	41162963	p13
SNP_A-1981054	C	C	310	56	317	89	5.531	1.87E-02	rs16897990	5	28736678	p14.1
SNP_A-1981136	C	C	330	60	306	86	5.531	1.87E-02	rs400042	5	31728633	p13.3
SNP_A-1984869	G	G	340	26	400	14	5.532	1.87E-02	rs996221	1	215176829	q41
SNP_A-1976108	T	T	328	32	340	16	5.527	1.87E-02	rs16888169	4	12767566	p15.33
SNP_A-1899836	C	C	202	164	264	152	5.53	1.87E-02	rs12682832	9	70450245	q21.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1894703	C	C	333	23	400	12	5.527	1.87E-02	rs7718448	5	77826066	q14.1
SNP_A-1895280	G	G	345	43	369	25	5.526	1.87E-02	rs12596323	16	87804936	q24.3
SNP_A-1893626	A	A	241	101	226	138	5.53	1.87E-02	rs1017406	2	163468914	q24.2
SNP_A-1912800	C	C	304	54	321	89	5.533	1.87E-02	rs11716382	3	64111340	p14.1
SNP_A-1922174	A	A	267	81	262	118	5.531	1.87E-02	rs10029573	4	157487244	q32.1
SNP_A-1925277	T	T	332	14	383	5	5.516	1.88E-02	rs4908237	1	102500752	p21.1
SNP_A-1924411	A	A	273	93	328	74	5.52	1.88E-02	rs9863821	3	152489873	q25.1
SNP_A-1902711	A	A	337	21	392	10	5.524	1.88E-02	rs12492787	3	189531513	q28
SNP_A-1901680	C	C	223	111	287	97	5.519	1.88E-02	rs10989601	9	96031977	q22.32
SNP_A-1973540	C	C	291	79	291	117	5.524	1.88E-02	rs17800551	3	89400005	p11.1
SNP_A-1963680	A	A	283	127	310	96	5.519	1.88E-02	rs1373198	2	68499634	p14
SNP_A-1985080	T	T	286	124	249	153	5.517	1.88E-02	rs1146772	1	215661804	q41
SNP_A-1984250	T	T	410	0	369	5	5.516	1.88E-02	rs17056179	5	158119902	q33.3
SNP_A-1988886	A	A	227	129	287	113	5.52	1.88E-02	rs2041655	7	13140534	p21.2
SNP_A-1943749	A	A	322	88	353	63	5.519	1.88E-02	rs10137468	14	85112899	q31.3
SNP_A-1861002	A	A	199	161	262	150	5.521	1.88E-02	rs1332786	1	75847582	p31.1
SNP_A-1866718	G	A	232	188	220	196	5.519	1.88E-02	rs17631940	17	30842243	q12
SNP_A-1835829	C	C	367	47	379	27	5.521	1.88E-02	rs12055015	5	154072097	q33.2
SNP_A-1844277	C	C	335	31	394	18	5.524	1.88E-02	rs7048280	9	533703	p24.3
SNP_A-1821330	C	C	262	92	270	138	5.521	1.88E-02	rs6706696	2	181806561	q31.3
SNP_A-1781900	C	T	186	164	225	181	5.516	1.88E-02	rs12740439	1	230002129	q42.2
SNP_A-1781661	G	G	342	26	402	14	5.521	1.88E-02	rs9572719	13	70803518	q21.33
SNP_A-1791532	G	G	228	126	281	107	5.522	1.88E-02	rs9597820	13	58197720	q21.1
SNP_A-1790006	T	T	337	15	342	32	5.524	1.88E-02	rs2930806	4	89910336	q22.1
SNP_A-2192555	G	G	329	27	351	13	5.524	1.88E-02	rs1895944	12	106743492	q23.3
SNP_A-2206371	A	A	329	51	300	74	5.522	1.88E-02	rs9381884	6	13386767	p24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2047943	C	C	267	89	320	70	5.518	1.88E-02	rs1721804	10	95164808	q23.33
SNP_A-2067609	G	G	209	195	241	161	5.518	1.88E-02	rs356982	2	60710772	p16.1
SNP_A-2031991	C	C	313	103	344	76	5.516	1.88E-02	rs12586742	14	102399183	q32.32
SNP_A-2012866	C	C	233	101	293	85	5.522	1.88E-02	rs1826613	11	84463780	q14.1
SNP_A-2237674	G	G	275	75	344	60	5.519	1.88E-02	rs17740447	5	150748472	q33.1
SNP_A-2244621	T	T	305	27	382	16	5.522	1.88E-02	rs6056488	20	924269	p13
SNP_A-2235257	A	A	300	48	288	74	5.512	0.0189	rs2019397	2	36181137	p22.3
SNP_A-2239975	A	A	357	3	381	13	5.509	0.0189	rs17107382	1	82050699	p31.1
SNP_A-2264465	C	C	188	168	219	137	5.512	0.0189	rs924517	3	158464187	q25.31
SNP_A-2269861	A	A	388	8	395	1	5.507	0.0189	rs16843481	4	2897728	p16.3
SNP_A-2270406	C	C	334	20	317	37	5.514	0.0189	rs16963458	15	34654997	q14
SNP_A-2290054	A	A	287	129	256	162	5.507	0.0189	rs2868177	7	75234554	q11.23
SNP_A-1995442	C	C	200	158	232	128	5.512	0.0189	rs2468708	8	140620185	q24.3
SNP_A-2030486	C	C	362	6	395	19	5.512	0.0189	rs4921073	5	115540024	q23.1
SNP_A-2023841	A	A	363	1	405	9	5.506	0.0189	rs10993883	9	133879632	q34.2
SNP_A-2068145	C	C	255	111	254	158	5.513	0.0189	rs2380935	9	4078131	p24.2
SNP_A-2050201	T	T	289	59	295	93	5.509	0.0189	rs1265650	3	126055689	q21.2
SNP_A-2106195	C	C	372	12	381	3	5.508	0.0189	rs7423193	2	242438434	q37.3
SNP_A-2086424	A	A	365	1	407	9	5.511	0.0189	rs10994523	10	62242890	q21.2
SNP_A-2090320	T	T	386	8	393	1	5.507	0.0189	rs6538452	12	92671477	q22
SNP_A-2214274	G	G	283	71	347	55	5.508	0.0189	rs1367903	12	126768788	q24.32
SNP_A-2192483	C	C	267	101	268	146	5.513	0.0189	rs841528	6	65956249	q12
SNP_A-2192644	G	A	154	152	224	158	5.51	0.0189	rs9511128	13	23666205	q12.12
SNP_A-2176145	G	G	322	26	351	51	5.507	0.0189	rs1964052	1	159067082	q23.3
SNP_A-2111139	C	G	202	162	211	187	5.509	0.0189	rs6421389	10	90708507	q23.31
SNP_A-2146610	T	T	375	5	416	0	5.508	0.0189	rs2102615	13	62468593	q21.31
SNP_A-2160859	C	C	350	30	346	52	5.512	0.0189	rs17676896	7	20841810	p15.3
SNP_A-1804473	A	A	307	29	298	50	5.507	0.0189	rs4899863	14	84634803	q31.3
SNP_A-1807178	C	C	312	108	281	139	5.511	0.0189	rs1867750	2	119636685	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784801	T	T	166	146	225	137	5.51	0.0189	rs7591799	2	10621410	p25.1
SNP_A-1841163	G	G	191	135	246	120	5.511	0.0189	rs2972314	5	25822534	p14.1
SNP_A-1838701	G	G	248	174	213	207	5.511	0.0189	rs13428515	2	4317838	p25.2
SNP_A-1862620	G	G	324	56	370	38	5.508	0.0189	rs12427268	12	66491416	q15
SNP_A-1948478	T	T	289	59	295	93	5.509	0.0189	---	15	49155529	q21.2
SNP_A-1961535	C	C	351	1	391	9	5.515	0.0189	rs9882253	3	140541501	q23
SNP_A-1925082	T	T	318	56	282	78	5.507	0.0189	rs6931721	6	169939866	q27
SNP_A-1904235	T	T	419	1	412	8	5.503	0.019	rs17093760	14	57378051	q23.1
SNP_A-1890285	A	A	301	101	275	133	5.506	0.019	rs1502342	1	213765060	q41
SNP_A-1877827	G	G	329	37	346	20	5.498	0.019	rs6659859	1	14518962	p36.21
SNP_A-1981624	T	T	249	119	310	102	5.5	0.019	rs152344	5	55595641	q11.2
SNP_A-1963278	G	G	323	47	375	31	5.498	0.019	rs785289	2	52928666	p16.2
SNP_A-1861591	T	T	306	16	377	7	5.5	0.019	rs4860884	4	68721656	q13.2
SNP_A-1868920	A	A	274	94	337	77	5.499	0.019	rs9492414	6	130259804	q22.33
SNP_A-1869765	C	C	350	14	403	5	5.504	0.019	rs11119535	1	207098011	q32.2
SNP_A-1847733	G	G	364	6	374	18	5.505	0.019	rs12715965	4	176739687	q34.2
SNP_A-1838432	G	G	318	36	331	63	5.501	0.019	---	2	193591635	q32.3
SNP_A-1829261	C	C	390	12	399	3	5.503	0.019	rs6442508	3	15279745	p25.1
SNP_A-1823149	C	C	402	8	409	1	5.505	0.019	rs16952615	16	78783360	q23.2
SNP_A-1814717	T	T	364	0	394	6	5.503	0.019	rs11006039	10	59495478	q21.1
SNP_A-1797742	A	A	237	159	201	189	5.5	0.019	rs4651265	1	182232434	q25.3
SNP_A-2162122	C	C	252	96	322	82	5.498	0.019	rs2388639	16	53047294	q12.2
SNP_A-2148651	T	T	420	0	379	5	5.503	0.019	rs6741450	2	33284958	p22.3
SNP_A-2148437	G	G	276	88	334	70	5.497	0.019	rs7897163	10	18454226	p12.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2139460	C	C	240	118	240	168	5.501	0.019	rs17610219	4	148182469	q31.22
SNP_A-2109154	T	T	265	135	304	108	5.497	0.019	rs37575	5	58867115	q11.2
SNP_A-2134372	T	T	197	169	256	156	5.504	0.019	rs2962885	5	85836875	q14.3
SNP_A-2176179	T	T	360	0	390	6	5.498	0.019	rs17046040	4	166442731	q32.3
SNP_A-2175488	C	C	357	11	403	3	5.503	0.019	rs17121985	10	108798470	q25.1
SNP_A-2182764	C	C	245	125	303	107	5.498	0.019	rs513069	11	121519276	q24.1
SNP_A-2168405	A	A	396	12	405	3	5.501	0.019	rs3106318	8	24105570	p21.2
SNP_A-2054301	C	C	282	46	264	70	5.505	0.019	rs12795435	11	54803863	q11
SNP_A-2025124	G	G	278	128	305	97	5.502	0.019	rs11674963	2	116933899	q14.1
SNP_A-2030229	A	A	306	32	363	19	5.502	0.019	rs7351929	20	20612674	p11.23
SNP_A-2027008	G	G	327	37	350	66	5.504	0.019	rs2059107	4	78554922	q21.1
SNP_A-2036020	T	T	331	67	306	94	5.504	0.019	rs365909	2	147761145	q22.3
SNP_A-2045455	C	C	339	23	357	45	5.504	0.019	rs2029730	2	3467727	p25.3
SNP_A-1992119	T	T	297	39	331	23	5.504	0.019	---	8	6259638	p23.1
SNP_A-2005105	T	T	195	171	255	159	5.503	0.019	rs7501595	17	21345306	p11.2
SNP_A-2007741	A	A	279	109	321	85	5.504	0.019	rs2426245	20	49210581	q13.2
SNP_A-2293127	G	G	293	57	344	40	5.499	0.019	rs12455595	18	70838405	q22.3
SNP_A-2301771	G	G	280	88	343	71	5.502	0.019	rs4419389	3	176820775	q26.31
SNP_A-2255414	G	G	220	116	208	158	5.502	0.019	rs354271	9	95563215	q22.32
SNP_A-2256083	G	G	293	59	310	96	5.492	1.91E-02	rs4895183	5	118244217	q23.1
SNP_A-2236179	G	G	356	12	385	29	5.497	1.91E-02	rs2194531	14	78222138	q24.3
SNP_A-2281896	T	C	202	146	205	201	5.491	1.91E-02	rs2005470	8	140578679	q24.3
SNP_A-2010836	T	T	314	38	328	66	5.497	1.91E-02	rs2731979	5	38485966	p13.2
SNP_A-2013648	T	T	344	20	347	39	5.491	1.91E-02	rs4368946	8	98497864	q22.1
SNP_A-2015182	C	C	353	67	376	44	5.491	1.91E-02	rs9305211	21	14369853	q11.2
SNP_A-1990759	T	T	335	35	389	21	5.491	1.91E-02	rs6660991	1	238106248	q43
SNP_A-2039522	C	C	337	13	356	30	5.494	1.91E-02	rs17188985	8	13143078	p22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2025627	T	T	335	5	338	16	5.495	1.91E-02	rs538526	4	176559044	q34.1
SNP_A-2055061	C	C	300	92	310	62	5.488	1.91E-02	rs12572355	10	59248955	q21.1
SNP_A-2069939	A	A	349	19	367	39	5.497	1.91E-02	rs2331061	7	55287811	p11.2
SNP_A-2064434	G	G	241	165	211	201	5.488	1.91E-02	rs8045294	16	5062682	p13.3
SNP_A-2107121	A	A	182	158	235	143	5.488	1.91E-02	rs9459057	6	158382054	q25.3
SNP_A-2172751	G	G	279	65	294	104	5.492	1.91E-02	rs1758916	13	75969123	q22.2
SNP_A-2217926	G	G	357	9	414	2	5.494	1.91E-02	rs7090588	10	85707536	q23.1
SNP_A-2128387	C	C	352	14	405	5	5.497	1.91E-02	rs9864300	3	192922497	q28
SNP_A-2161177	G	G	323	25	317	45	5.497	1.91E-02	rs9464315	6	55975223	p12.1
SNP_A-1798626	-	C	164	164	220	154	5.49	1.91E-02	rs595158	11	60666157	q12.2
SNP_A-1805250	G	G	263	127	297	99	5.488	1.91E-02	rs784580	5	65219345	q12.3
SNP_A-1678158	A	A	350	40	345	65	5.492	1.91E-02	rs951318	6	1263711	p25.3
SNP_A-1844240	G	G	253	147	280	114	5.495	1.91E-02	rs1491108	9	106505164	q31.2
SNP_A-1973321	G	G	230	136	227	189	5.488	1.91E-02	rs264533	3	76808458	p12.3
SNP_A-1949983	A	A	207	139	267	125	5.491	1.91E-02	rs620729	6	11616657	p24.2
SNP_A-1940139	A	A	280	132	244	162	5.491	1.91E-02	rs2517263	8	17480023	p22
SNP_A-1909674	T	T	350	12	364	28	5.49	1.91E-02	rs7205254	16	15875743	p13.11
SNP_A-1921918	G	G	339	71	301	95	5.485	1.92E-02	rs11816901	10	111325851	q25.1
SNP_A-1875197	A	A	224	130	224	184	5.487	1.92E-02	rs1496367	5	7136536	p15.31
SNP_A-1892816	C	C	257	163	284	128	5.481	1.92E-02	rs7243368	18	22805864	q11.2
SNP_A-1901373	T	T	318	8	355	23	5.481	1.92E-02	rs1901322	2	199889630	q33.1
SNP_A-1898807	G	G	303	51	321	85	5.487	1.92E-02	rs7946768	11	98021239	q22.1
SNP_A-1949561	C	C	320	20	350	42	5.483	1.92E-02	rs17302965	15	58380811	q22.2
SNP_A-1976573	T	T	410	0	371	5	5.487	1.92E-02	rs16879531	4	27267204	p15.2
SNP_A-1978721	G	G	223	141	280	124	5.481	1.92E-02	rs1396539	4	121466121	q27

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1834385	A	A	302	64	366	48	5.484	1.92E-02	rs9415720	10	52543957	q11.23
SNP_A-1864326	C	C	389	19	393	7	5.48	1.92E-02	rs6777696	3	103428872	q12.3
SNP_A-1783667	T	T	340	14	391	5	5.487	1.92E-02	rs4027005	14	53401111	q22.2
SNP_A-1801367	G	G	322	26	378	14	5.483	1.92E-02	rs10735267	12	86849581	q21.32
SNP_A-1785335	G	G	308	42	324	72	5.484	1.92E-02	rs16948103	15	91835184	q26.1
SNP_A-2161104	A	A	253	111	314	94	5.482	1.92E-02	rs4741647	9	2170812	p24.3
SNP_A-2113775	G	G	252	102	237	139	5.483	1.92E-02	rs3802278	8	70733867	q13.3
SNP_A-2218165	T	T	253	107	320	92	5.487	1.92E-02	rs2281731	9	3845616	p24.2
SNP_A-2223661	T	T	396	14	398	4	5.482	1.92E-02	rs1678310	4	8311474	p16.1
SNP_A-2213132	C	C	345	21	373	43	5.48	1.92E-02	rs8038390	15	35251999	q14
SNP_A-2174043	T	T	272	52	338	38	5.486	1.92E-02	rs1947364	1	211632933	q41
SNP_A-2196628	T	T	404	4	402	14	5.483	1.92E-02	rs11231128	11	62047295	q12.3
SNP_A-2099280	T	T	217	141	279	127	5.487	1.92E-02	rs7210618	17	29165530	q12
SNP_A-2033077	A	A	289	79	292	118	5.485	1.92E-02	rs28149	4	114551772	q26
SNP_A-2045940	A	A	298	72	359	55	5.487	1.92E-02	rs1811647	9	13344300	p23
SNP_A-2008456	G	G	279	81	280	120	5.479	1.92E-02	rs1872898	11	21881475	p14.3
SNP_A-2237820	G	G	311	59	366	42	5.487	1.92E-02	rs2612383	18	71768713	q23
SNP_A-2229871	C	C	249	107	241	149	5.483	1.92E-02	rs6434605	2	194070109	q32.3
SNP_A-2255250	G	G	321	21	399	11	5.471	1.93E-02	rs5029939	6	138237416	q23.3
SNP_A-2281429	G	G	365	39	350	62	5.474	1.93E-02	rs10086142	8	6674382	p23.1
SNP_A-2276584	C	C	420	0	381	5	5.474	1.93E-02	rs12244093	10	110822575	q25.1
SNP_A-2309137	C	C	218	116	273	99	5.476	1.93E-02	rs8047798	16	79276587	q23.2
SNP_A-2000133	C	C	404	8	409	1	5.47	1.93E-02	rs718294	1	78276217	p31.1
SNP_A-2046271	G	G	268	94	265	135	5.476	1.93E-02	rs7623551	3	67089485	p14.1
SNP_A-2021596	G	G	304	54	353	37	5.471	1.93E-02	rs9470638	6	12086262	p24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098445	A	A	385	1	380	8	5.472	1.93E-02	rs16914122	8	51049599	q11.21
SNP_A-2085088	A	A	396	6	383	17	5.473	1.93E-02	---	14	21699992	q11.2
SNP_A-2195189	G	G	324	12	388	4	5.478	1.93E-02	rs11967411	6	76573772	q14.1
SNP_A-2184723	C	C	200	160	258	146	5.47	1.93E-02	rs2190921	7	123758078	q31.33
SNP_A-2129093	A	A	229	133	289	117	5.471	1.93E-02	rs9650258	8	78334849	q21.11
SNP_A-2163818	C	C	226	142	221	195	5.473	1.93E-02	rs10942413	5	85177678	q14.3
SNP_A-1786139	A	A	348	42	312	62	5.477	1.93E-02	rs8067181	17	29082971	q12
SNP_A-1805458	C	C	351	19	338	36	5.478	1.93E-02	---	16	6665969	p13.2
SNP_A-1744039	C	C	286	116	324	90	5.473	1.93E-02	rs10492146	12	14997289	p12.3
SNP_A-1642901	A	G	187	157	218	184	5.471	1.93E-02	rs1372522	4	91223674	q22.1
SNP_A-1848016	A	A	337	9	390	2	5.472	1.93E-02	rs9560306	13	88840699	q31.3
SNP_A-1858765	A	A	395	7	368	18	5.473	1.93E-02	rs7761914	6	28750488	p22.1
SNP_A-1815400	T	T	218	196	249	161	5.47	1.93E-02	rs1550527	2	101302533	q11.2
SNP_A-1816572	T	T	367	19	371	7	5.477	1.93E-02	rs4463102	4	40744022	p14
SNP_A-1986259	C	C	250	120	311	103	5.477	1.93E-02	rs10498837	6	66598820	q12
SNP_A-1949323	A	A	375	31	400	16	5.473	1.93E-02	rs2073390	22	22458124	q11.23
SNP_A-1961917	A	A	295	127	322	96	5.472	1.93E-02	rs16864209	2	5878691	p25.2
SNP_A-1936046	G	G	348	14	374	32	5.477	1.93E-02	rs9829331	3	177989891	q26.32
SNP_A-1902656	C	C	294	116	326	88	5.475	1.93E-02	rs9962908	18	11817239	p11.21
SNP_A-1894619	A	A	336	32	397	19	5.472	1.93E-02	rs648438	11	67860878	q13.2
SNP_A-1918090	T	T	345	23	387	11	5.479	1.93E-02	---	20	52338084	q13.2
SNP_A-1931458	C	C	335	87	303	115	5.467	1.94E-02	rs9269186	6	32556394	p21.32
SNP_A-1894715	C	C	196	172	250	156	5.466	1.94E-02	rs12458329	18	57885724	q21.33
SNP_A-1951303	C	C	351	7	411	1	5.464	1.94E-02	rs7311601	12	61516260	q14.2
SNP_A-1819142	C	C	326	44	340	74	5.469	1.94E-02	rs555146	1	65239428	p31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826342	A	A	321	75	286	100	5.463	1.94E-02	rs4682719	3	44201453	p21.33
SNP_A-1849742	C	C	394	14	351	27	5.467	1.94E-02	rs10788897	1	49031187	p33
SNP_A-1865414	T	T	210	158	270	144	5.462	1.94E-02	rs7547104	1	19202563	p36.13
SNP_A-1862487	A	A	334	72	313	101	5.465	1.94E-02	rs4867035	5	30437599	p13.3
SNP_A-1740679	G	G	334	64	319	93	5.461	1.94E-02	rs3856036	1	74887185	p31.1
SNP_A-1758661	A	A	205	171	256	152	5.463	1.94E-02	rs733046	4	32297668	p15.1
SNP_A-1800095	C	C	324	14	348	32	5.462	1.94E-02	rs9841424	3	167490451	q26.1
SNP_A-1799700	G	G	271	71	279	45	5.461	1.94E-02	rs12821507	12	5174553	p13.32
SNP_A-2139856	A	A	406	0	369	5	5.463	1.94E-02	rs11252980	10	5157499	p15.1
SNP_A-2147014	A	A	406	0	369	5	5.463	1.94E-02	rs11994254	8	22102774	p21.3
SNP_A-2123974	A	A	351	3	344	12	5.465	1.94E-02	rs9958946	18	64776690	q22.1
SNP_A-2135857	G	G	312	16	383	7	5.462	1.94E-02	rs12654455	5	126702768	q23.2
SNP_A-2108120	C	C	279	91	342	74	5.469	1.94E-02	rs2935706	10	123481658	q26.13
SNP_A-2109697	G	G	352	36	317	55	5.464	1.94E-02	rs173416	5	166324203	q34
SNP_A-2168749	A	A	304	18	389	9	5.464	1.94E-02	rs17047971	4	136886177	q28.3
SNP_A-2202439	A	A	250	100	234	136	5.469	1.94E-02	rs9592007	13	59139339	q21.2
SNP_A-2091152	A	A	228	140	220	190	5.467	1.94E-02	rs1155178	8	118108418	q24.11
SNP_A-2080346	G	G	355	11	399	3	5.464	1.94E-02	rs363411	10	119003622	q26.11
SNP_A-2106005	A	A	243	123	308	108	5.467	1.94E-02	rs6064607	20	56001130	q13.32
SNP_A-2103694	C	C	187	181	246	170	5.466	1.94E-02	rs1564996	3	151306822	q25.1
SNP_A-2074465	A	A	396	4	363	13	5.462	1.94E-02	rs7184148	16	20199361	p12.3
SNP_A-2042953	C	C	239	27	283	57	5.468	1.94E-02	rs11887064	2	76479886	p12
SNP_A-2006586	A	A	302	28	316	52	5.465	1.94E-02	rs4851084	2	105775080	q12.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2311099	A	A	345	5	380	0	5.466	1.94E-02	rs10949639	7	156575973	q36.3
SNP_A-2264427	A	A	292	94	253	119	5.468	1.94E-02	rs10891376	11	97550213	q22.1
SNP_A-2261920	A	A	351	7	411	1	5.464	1.94E-02	rs8822	8	55122566	q11.23
SNP_A-2254868	C	C	414	6	401	17	5.463	1.94E-02	rs10189426	2	234365490	q37.1
SNP_A-2254466	G	G	197	147	251	131	5.456	0.0195	rs10786772	10	105600316	q24.33
SNP_A-2249136	A	A	339	19	407	9	5.454	0.0195	rs6926847	6	100880966	q16.3
SNP_A-2270431	T	T	350	0	382	6	5.457	0.0195	rs9669852	13	97883413	q32.2
SNP_A-2016015	A	A	323	71	247	83	5.454	0.0195	rs2825708	21	19942535	q21.1
SNP_A-1992305	G	G	397	17	368	32	5.452	0.0195	rs10503446	8	13192073	p22
SNP_A-2025385	A	A	386	12	393	3	5.458	0.0195	rs9895704	17	7741807	p13.1
SNP_A-2053922	A	A	388	10	398	2	5.456	0.0195	rs16915319	11	26105829	p14.2
SNP_A-2100518	T	T	385	21	375	39	5.454	0.0195	rs9317119	13	59838907	q21.2
SNP_A-2096069	C	C	338	26	362	50	5.454	0.0195	rs13391078	2	220960611	q35
SNP_A-2203406	C	C	354	2	383	11	5.461	0.0195	rs6032689	20	44231964	q13.12
SNP_A-2184656	C	C	414	0	377	5	5.453	0.0195	rs936173	3	46893479	p21.31
SNP_A-2121046	T	T	240	168	211	205	5.458	0.0195	rs1574299	5	71235595	q13.2
SNP_A-2137160	C	C	346	22	380	10	5.458	0.0195	rs16896836	5	61234080	q12.1
SNP_A-2167309	A	A	231	169	258	134	5.453	0.0195	rs2966090	16	80086920	q23.2
SNP_A-2157084	G	G	269	93	311	71	5.459	0.0195	rs17739	1	220274688	q42.11
SNP_A-1804087	T	T	297	73	303	111	5.456	0.0195	rs12903325	15	48140569	q21.2
SNP_A-1783015	C	C	380	40	394	22	5.46	0.0195	rs10435898	9	98509354	q22.33
SNP_A-1710425	G	G	375	21	365	39	5.456	0.0195	rs6685118	1	202110238	q32.1
SNP_A-1844595	T	T	330	38	346	66	5.452	0.0195	rs703455	10	120135130	q26.11
SNP_A-1822419	G	G	244	110	303	93	5.453	0.0195	rs2749266	6	168733901	q27

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1836436	G	G	325	43	341	73	5.456	0.0195	rs2868215	4	82734508	q21.22
SNP_A-1831472	C	C	357	9	412	2	5.455	0.0195	rs9882442	3	175127187	q26.31
SNP_A-1841105	C	C	292	104	318	76	5.459	0.0195	rs2295778	10	102285826	q24.31
SNP_A-1952915	T	T	227	187	254	150	5.456	0.0195	rs11121828	1	11768720	p36.22
SNP_A-1933922	A	A	300	26	313	49	5.46	0.0195	rs1717744	7	37782536	p14.1
SNP_A-1972900	T	T	316	54	327	87	5.459	0.0195	rs9311842	3	62498262	p14.2
SNP_A-1963359	C	C	368	36	352	58	5.461	0.0195	rs1454425	2	55596778	p16.1
SNP_A-1882521	C	C	362	6	397	19	5.456	0.0195	rs6506299	18	5401968	p11.31
SNP_A-1886258	C	C	276	88	342	72	5.458	0.0195	rs1479107	12	13362314	p13.1
SNP_A-1877414	C	C	347	9	400	2	5.443	1.96E-02	rs6096615	20	49905800	q13.2
SNP_A-1880476	C	C	283	129	251	161	5.449	1.96E-02	rs309280	2	7147230	p25.1
SNP_A-1893059	G	G	362	6	374	18	5.443	1.96E-02	rs1417789	10	124528314	q26.13
SNP_A-1899764	G	G	362	0	396	6	5.446	1.96E-02	rs2786608	1	217118848	q41
SNP_A-1915368	C	C	388	20	404	8	5.447	1.96E-02	rs16898435	8	124574129	q24.13
SNP_A-1989519	G	G	352	14	403	5	5.445	1.96E-02	---	1	233112514	q43
SNP_A-1933611	G	G	297	123	319	91	5.451	1.96E-02	rs3896178	1	60774017	p31.3
SNP_A-1936309	A	A	334	22	393	11	5.445	1.96E-02	rs10858691	12	87128766	q21.32
SNP_A-1950648	T	T	414	2	404	10	5.451	1.96E-02	rs11127647	3	67708216	p14.1
SNP_A-1815144	A	G	209	155	208	200	5.446	1.96E-02	rs236504	17	65780331	q24.3
SNP_A-1692722	C	C	262	138	237	175	5.45	1.96E-02	rs1286231	1	115000189	p13.1
SNP_A-1650494	G	A	200	176	225	183	5.445	1.96E-02	rs1876496	8	57865530	q12.1
SNP_A-1716693	A	A	226	124	297	113	5.446	1.96E-02	rs1598486	18	63104358	q22.1
SNP_A-2166010	G	G	291	125	254	154	5.449	1.96E-02	rs11872913	18	11170760	p11.21
SNP_A-2163815	T	C	225	175	190	174	5.451	1.96E-02	rs2292175	15	48712287	q21.2
SNP_A-2148097	G	G	347	35	314	54	5.444	1.96E-02	rs16856470	1	202620986	q32.1
SNP_A-2144814	A	A	324	42	342	72	5.448	1.96E-02	rs17379561	1	98052160	p21.3
SNP_A-2114744	G	G	420	2	410	10	5.449	1.96E-02	rs7512516	1	53621041	p32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2183856	A	A	296	36	359	23	5.449	1.96E-02	rs9649417	7	78910299	q21.11
SNP_A-2190142	T	T	373	49	389	29	5.445	1.96E-02	rs17229266	5	157460864	q33.3
SNP_A-2169185	C	C	298	40	356	26	5.445	1.96E-02	rs11050084	12	29201569	p11.22
SNP_A-2170653	G	G	357	25	388	12	5.446	1.96E-02	rs2776478	14	48882022	q21.3
SNP_A-2182602	A	A	263	149	229	181	5.448	1.96E-02	rs10887874	10	82186537	q22.3
SNP_A-2208580	G	G	348	2	377	11	5.449	1.96E-02	rs536942	3	154297613	q25.2
SNP_A-2222523	A	A	202	148	264	136	5.447	1.96E-02	rs11611637	12	96187832	q23.1
SNP_A-2225744	A	A	307	37	361	23	5.451	1.96E-02	rs9283919	6	54222025	p12.1
SNP_A-2101016	T	T	231	59	242	96	5.451	1.96E-02	rs4707823	6	94890236	q16.1
SNP_A-2047776	G	G	336	14	385	5	5.447	1.96E-02	rs11159623	14	83497606	q31.3
SNP_A-2063404	G	G	360	0	394	6	5.443	1.96E-02	rs16934833	10	78893370	q22.3
SNP_A-2069143	T	T	249	89	244	128	5.444	1.96E-02	rs2187416	18	50793357	q21.2
SNP_A-1990329	G	G	345	9	398	2	5.449	1.96E-02	rs17155203	7	80766073	q21.11
SNP_A-2272850	C	C	320	100	287	129	5.448	1.96E-02	rs17157147	11	61825102	q12.3
SNP_A-2245934	T	T	190	172	247	159	5.442	1.97E-02	rs16847030	3	163479855	q26.1
SNP_A-2254191	G	G	328	20	322	38	5.44	1.97E-02	rs7370021	2	49528322	p16.3
SNP_A-2252938	G	G	344	26	402	14	5.436	1.97E-02	rs12118136	1	161544239	q23.3
SNP_A-2239393	C	C	313	77	278	102	5.435	1.97E-02	rs11162746	1	79765316	p31.1
SNP_A-2301398	A	A	319	17	336	36	5.436	1.97E-02	rs8082899	18	32083366	q12.2
SNP_A-2044832	C	C	283	137	248	168	5.439	1.97E-02	rs781365	14	51934459	q22.1
SNP_A-2038456	A	A	259	107	317	89	5.435	1.97E-02	rs1146036	2	158459313	q24.1
SNP_A-2088444	G	G	202	168	260	154	5.438	1.97E-02	rs10963545	9	18259232	p22.2
SNP_A-2217596	A	A	377	27	358	46	5.436	1.97E-02	rs17019407	3	300068	p26.3
SNP_A-2204953	A	A	295	73	304	112	5.438	1.97E-02	rs6827693	4	186130477	q35.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2201355	A	A	386	24	366	42	5.436	1.97E-02	rs10483372	14	29928163	q12
SNP_A-2168324	G	G	364	56	385	35	5.435	1.97E-02	rs11224295	11	99954513	q22.1
SNP_A-2185056	C	C	355	31	328	50	5.441	1.97E-02	rs6979185	7	116653329	q31.2
SNP_A-2152194	A	A	287	49	291	79	5.434	1.97E-02	rs1065144	17	78496746	q25.3
SNP_A-1718935	C	C	305	57	326	36	5.441	1.97E-02	rs2083414	2	127420088	q14.3
SNP_A-1673982	G	G	354	36	345	59	5.439	1.97E-02	rs10487260	7	93693060	q21.3
SNP_A-1793864	T	T	365	5	397	17	5.437	1.97E-02	rs2490320	10	92194667	q23.31
SNP_A-1843366	T	T	287	79	353	63	5.434	1.97E-02	---	3	25130875	p24.2
SNP_A-1837778	A	A	402	8	405	1	5.436	1.97E-02	rs7218038	17	32389341	q12
SNP_A-1837022	G	G	300	62	355	45	5.438	1.97E-02	rs4696687	4	8057265	p16.1
SNP_A-1868114	G	G	284	124	318	96	5.44	1.97E-02	rs879961	1	205849318	q32.2
SNP_A-1952575	T	T	260	94	257	135	5.436	1.97E-02	rs843605	4	121784489	q27
SNP_A-1934889	G	T	188	180	237	177	5.436	1.97E-02	rs2410709	5	85267229	q14.3
SNP_A-1964528	G	G	353	63	377	41	5.438	1.97E-02	rs1367420	2	114618514	q14.1
SNP_A-1972912	C	C	243	117	241	165	5.436	1.97E-02	rs486854	3	62699711	p14.2
SNP_A-1927566	C	C	238	174	268	140	5.441	1.97E-02	rs6971875	7	151153623	q36.1
SNP_A-1900455	C	C	223	135	219	187	5.439	1.97E-02	rs4241446	3	67229166	p14.1
SNP_A-1889701	G	G	336	22	395	11	5.434	1.97E-02	rs7156265	14	71812602	q24.2
SNP_A-1888099	G	G	387	33	384	16	5.425	1.98E-02	rs10838371	11	5557062	p15.4
SNP_A-1928601	A	A	323	37	341	65	5.431	1.98E-02	rs9310112	3	89343185	p11.1
SNP_A-1910629	C	C	264	106	263	151	5.429	1.98E-02	rs7615517	3	102317075	q12.2
SNP_A-1982549	A	A	226	110	287	95	5.426	1.98E-02	rs293052	5	94288398	q15
SNP_A-1980435	T	T	211	199	243	165	5.426	1.98E-02	rs755060	5	5472820	p15.32
SNP_A-1980668	G	G	281	41	320	76	5.432	1.98E-02	rs679416	5	10363797	p15.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939525	T	T	363	5	395	17	5.432	1.98E-02	rs4518265	4	129855598	q28.2
SNP_A-1946532	G	G	282	64	296	102	5.43	1.98E-02	rs12530317	6	133128774	q23.2
SNP_A-1951119	T	T	353	9	406	2	5.427	1.98E-02	rs1400440	2	18437752	p24.2
SNP_A-1957185	A	A	353	9	406	2	5.427	1.98E-02	rs16823593	3	155264405	q25.2
SNP_A-1868024	T	T	351	9	404	2	5.432	1.98E-02	rs11982855	7	80537077	q21.11
SNP_A-1850335	A	A	243	173	255	129	5.428	1.98E-02	rs10929838	2	5909595	p25.2
SNP_A-1837652	T	T	234	136	229	187	5.433	1.98E-02	rs11678082	2	13596223	p24.3
SNP_A-1837494	A	A	388	14	388	4	5.43	1.98E-02	rs2910633	5	33884502	p13.3
SNP_A-1843064	A	A	288	46	370	34	5.428	1.98E-02	rs1545635	3	29610482	p24.1
SNP_A-1815772	C	C	300	98	262	124	5.432	1.98E-02	rs2369373	3	133325486	q22.1
SNP_A-1794680	G	G	394	20	366	36	5.428	1.98E-02	rs12086988	1	58615754	p32.2
SNP_A-1645056	A	A	334	46	296	66	5.43	1.98E-02	rs10516148	5	177885526	q35.3
SNP_A-1757375	T	T	326	72	299	99	5.43	1.98E-02	rs4711162	6	11101065	p24.2
SNP_A-2147637	T	T	237	179	261	141	5.431	1.98E-02	rs10861733	12	106278492	q23.3
SNP_A-2160667	G	G	288	30	335	17	5.43	1.98E-02	rs4557395	5	151943465	q33.1
SNP_A-2160246	C	C	316	32	373	19	5.432	1.98E-02	rs4146082	2	161403032	q24.2
SNP_A-2196562	T	T	295	55	351	39	5.432	1.98E-02	rs1980730	13	36816173	q13.3
SNP_A-2226755	G	G	305	17	382	8	5.425	1.98E-02	rs11001525	10	77292491	q22.2
SNP_A-2091708	G	G	193	177	249	163	5.431	1.98E-02	rs17739370	4	178670578	q34.3
SNP_A-2086939	G	G	337	7	393	1	5.433	1.98E-02	rs16929978	9	9631475	p23
SNP_A-2095158	A	A	372	34	392	18	5.427	1.98E-02	rs1376349	7	127464579	q32.1
SNP_A-2036345	T	T	318	44	332	74	5.426	1.98E-02	rs10476598	5	93393037	q15
SNP_A-2301657	G	G	281	51	286	82	5.433	1.98E-02	rs3813115	18	69966043	q22.3
SNP_A-2237094	T	T	349	53	300	72	5.433	1.98E-02	rs2115151	4	124369976	q28.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2232948	G	G	246	168	202	192	5.43	1.98E-02	rs9870680	3	7504555	p26.1
SNP_A-2271527	G	A	197	195	232	168	5.43	1.98E-02	rs1175114	1	188937134	q31.2
SNP_A-2266335	T	T	300	56	319	35	5.424	1.99E-02	rs16889650	4	13703413	p15.33
SNP_A-2302572	A	A	267	129	233	159	5.417	1.99E-02	rs7708811	5	35323183	p13.2
SNP_A-2033545	A	A	380	10	388	2	5.417	1.99E-02	rs10918425	1	163022719	q24.1
SNP_A-2045587	A	A	371	25	367	45	5.421	1.99E-02	rs10101976	8	69946687	q13.2
SNP_A-2033051	A	A	348	4	348	14	5.417	1.99E-02	rs9299562	10	56990466	q21.1
SNP_A-1992394	G	G	205	155	262	140	5.421	1.99E-02	rs2034005	8	14715248	p22
SNP_A-2050946	T	T	355	7	413	1	5.42	1.99E-02	rs367587	4	53349084	q12
SNP_A-2195094	T	T	260	66	270	104	5.417	1.99E-02	rs11717225	3	105225874	q13.11
SNP_A-2187432	G	G	277	81	290	54	5.421	1.99E-02	rs4438288	16	18922935	p12.3
SNP_A-2182035	C	A	187	155	200	170	5.421	1.99E-02	rs9300546	13	98885720	q32.3
SNP_A-2149329	A	A	308	110	330	80	5.419	1.99E-02	rs10174913	2	116491397	q14.1
SNP_A-2117293	A	A	256	138	299	113	5.422	1.99E-02	rs9373560	6	148768439	q24.3
SNP_A-2124541	A	A	220	150	278	134	5.416	1.99E-02	rs9391137	6	96792640	q16.1
SNP_A-1729372	C	C	379	21	405	9	5.423	1.99E-02	rs2834681	21	35230806	q22.12
SNP_A-1800949	G	G	388	2	380	10	5.417	1.99E-02	rs3735083	7	149764571	q36.1
SNP_A-1801683	C	C	217	141	211	193	5.423	1.99E-02	rs2899039	4	56543227	q12
SNP_A-1818148	C	C	411	9	364	20	5.422	1.99E-02	rs2647998	16	50130291	q12.1
SNP_A-1827523	A	A	206	176	257	157	5.424	1.99E-02	rs10785646	12	45637114	q13.11
SNP_A-1828065	C	C	327	49	332	28	5.42	1.99E-02	rs10101725	8	19737256	p21.3
SNP_A-1843378	T	T	328	14	375	5	5.42	1.99E-02	rs2029425	8	127841380	q24.21
SNP_A-1866983	A	A	312	14	357	5	5.421	1.99E-02	rs3015210	9	69952302	q21.11
SNP_A-1862179	C	C	343	7	399	1	5.417	1.99E-02	rs17013246	4	129667779	q28.2
SNP_A-1865753	T	T	248	150	260	110	5.424	1.99E-02	rs10838750	11	5842822	p15.4
SNP_A-1967857	T	T	255	161	287	129	5.42	1.99E-02	rs10494316	1	154326642	q23.1
SNP_A-1925872	C	C	304	58	317	93	5.421	1.99E-02	rs4484675	8	140600968	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1880986	G	G	277	91	279	133	5.417	1.99E-02	rs4431240	4	36317550	p14
SNP_A-1875916	C	C	350	46	342	72	5.424	1.99E-02	rs6473455	8	84671102	q21.13
SNP_A-1895509	A	A	278	22	296	44	5.419	1.99E-02	rs10421785	19	46759870	q13.2
SNP_A-1898485	A	A	303	57	321	93	5.418	1.99E-02	rs1502376	3	26409299	p24.2
SNP_A-1944579	G	G	326	36	341	63	5.414	0.02	rs17147304	4	70474900	q13.2
SNP_A-1861410	T	T	342	4	342	14	5.414	0.02	rs5997025	22	24751494	q12.1
SNP_A-1853534	A	A	190	178	248	166	5.412	0.02	rs10174918	2	51141006	p16.3
SNP_A-1836724	A	A	387	17	398	6	5.415	0.02	rs1405576	7	113601596	q31.1
SNP_A-1804947	T	T	237	167	269	135	5.414	0.02	rs10807926	7	45391221	p13
SNP_A-1809158	T	T	309	105	324	74	5.411	0.02	rs17659868	7	47645841	p12.3
SNP_A-1792592	C	C	342	30	282	44	5.41	0.02	rs17442418	10	99767099	q24.2
SNP_A-1751749	T	T	316	70	294	98	5.414	0.02	rs248879	12	5080762	p13.32
SNP_A-1782872	A	A	340	26	375	13	5.409	0.02	rs7205245	16	5670141	p13.3
SNP_A-1673050	C	C	317	23	335	45	5.409	0.02	rs2102158	3	148047538	q24
SNP_A-1681456	A	A	400	0	367	5	5.411	0.02	rs10520118	15	37112639	q14
SNP_A-2117637	C	C	326	42	282	60	5.416	0.02	rs2453910	8	20152860	p21.3
SNP_A-2120755	C	C	322	10	401	3	5.41	0.02	rs16958259	16	81276991	q23.3
SNP_A-2156496	G	G	422	0	387	5	5.416	0.02	rs166201	12	15501051	p12.3
SNP_A-2166874	G	G	357	5	389	17	5.415	0.02	rs10827735	10	19976155	p12.31
SNP_A-2180168	C	C	260	118	293	91	5.41	0.02	rs17332173	8	58494945	q12.1
SNP_A-2168344	A	A	259	111	252	154	5.415	0.02	rs2357645	2	194072613	q32.3
SNP_A-2172548	A	A	337	5	367	17	5.412	0.02	rs1568376	2	76481953	p12
SNP_A-2221677	C	C	333	75	275	93	5.414	0.02	rs1389783	7	145811976	q35
SNP_A-2224060	C	C	281	77	310	54	5.412	0.02	---	22	49503757	q13.33
SNP_A-2204655	A	A	266	152	233	185	5.414	0.02	rs12369491	12	11781775	p13.2
SNP_A-2063594	G	G	376	44	389	25	5.41	0.02	rs11025849	11	20959597	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1995878	T	C	204	164	220	196	5.408	0.02	rs10959567	9	11134781	p23
SNP_A-2017704	G	G	404	2	396	10	5.413	0.02	rs363567	21	29956252	q21.3
SNP_A-2006820	A	A	271	133	222	154	5.409	0.02	rs7597971	2	167113679	q24.3
SNP_A-2024738	C	C	180	178	228	160	5.408	0.02	rs2208921	1	186412034	q31.1
SNP_A-2022856	T	T	322	36	325	61	5.411	0.02	rs16961112	17	18150876	p11.2
SNP_A-2040283	T	T	212	158	272	144	5.413	0.02	rs6495897	15	35346389	q14
SNP_A-2302220	G	G	330	14	377	5	5.413	0.02	rs6855428	4	93387131	q22.2
SNP_A-2314941	G	G	385	21	411	9	5.414	0.02	rs12409375	1	156646806	q23.2
SNP_A-2276260	T	T	276	26	301	51	5.409	0.02	rs12441108	15	44169610	q21.1
SNP_A-2280575	C	C	198	150	257	137	5.408	0.02	rs7624619	3	188580283	q27.3
SNP_A-2245413	A	A	396	4	365	13	5.41	0.02	rs3885745	3	42237556	p22.1
SNP_A-2245898	G	G	332	12	361	29	5.401	0.0201	rs1201872	6	34663687	p21.31
SNP_A-2241600	A	A	304	94	332	68	5.401	0.0201	rs2057115	14	85090042	q31.3
SNP_A-2266268	A	A	348	18	319	33	5.402	0.0201	rs6005496	22	26244586	q12.1
SNP_A-2261184	C	C	349	7	405	1	5.402	0.0201	rs336306	4	143377417	q31.21
SNP_A-2295082	C	C	304	62	316	98	5.399	0.0201	rs4731507	7	127943558	q32.1
SNP_A-2288877	G	G	262	104	303	81	5.406	0.0201	rs1016167	7	26264858	p15.2
SNP_A-2028185	C	C	301	63	363	47	5.402	0.0201	rs10014828	4	531182	p16.3
SNP_A-2012873	C	C	192	176	249	163	5.401	0.0201	rs595435	11	84479086	q14.1
SNP_A-2003071	C	C	236	158	195	183	5.404	0.0201	rs504403	12	119595757	q24.31
SNP_A-2073037	C	C	276	92	264	128	5.405	0.0201	rs843369	3	185379870	q27.1
SNP_A-2062165	C	C	256	96	315	79	5.4	0.0201	rs10977466	9	9055941	p23
SNP_A-2105339	G	G	366	52	388	32	5.399	0.0201	rs9987062	7	108002062	q31.1
SNP_A-2220865	C	C	368	0	406	6	5.401	0.0201	rs7340970	4	108408930	q25
SNP_A-2220422	A	A	332	14	379	5	5.407	0.0201	rs17142307	6	6501992	p25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213497	A	A	359	51	335	75	5.401	0.0201	rs9438883	1	25068145	p36.11
SNP_A-2115689	A	A	222	140	213	189	5.405	0.0201	rs4291477	1	65903096	p31.2
SNP_A-2127321	T	T	350	0	386	6	5.401	0.0201	---	4	45193209	p13
SNP_A-2131859	C	C	286	82	290	122	5.406	0.0201	rs7069698	10	82898268	q22.3
SNP_A-1650894	T	T	374	18	399	7	5.405	0.0201	rs1303755	5	29450336	p13.3
SNP_A-1795817	T	T	402	8	403	1	5.402	0.0201	rs11059649	12	127339533	q24.32
SNP_A-1788533	C	C	348	68	323	95	5.399	0.0201	rs1323772	9	83063306	q21.32
SNP_A-1788347	T	T	245	115	241	161	5.401	0.0201	rs11694545	2	1909505	p25.3
SNP_A-1806459	G	G	390	26	404	12	5.405	0.0201	rs6719593	2	232023832	q37.1
SNP_A-1802251	G	G	307	81	288	112	5.405	0.0201	rs947381	13	50057831	q14.3
SNP_A-1817471	G	G	329	83	344	56	5.403	0.0201	rs2270603	7	97503298	q21.3
SNP_A-1855075	C	C	272	96	273	139	5.405	0.0201	rs17508851	9	6761267	p24.1
SNP_A-1864129	T	T	317	15	376	6	5.405	0.0201	rs7004424	8	23391868	p21.3
SNP_A-1863634	C	C	361	9	414	2	5.405	0.0201	rs12617257	2	142625527	q22.2
SNP_A-1972261	G	G	288	34	288	58	5.406	0.0201	rs17029881	3	30985627	p24.1
SNP_A-1987084	G	G	352	4	381	15	5.403	0.0201	rs17064006	6	103945052	q16.3
SNP_A-1874180	G	G	333	21	384	10	5.407	0.0201	rs7087658	10	129146705	q26.2
SNP_A-1883163	G	G	398	8	399	1	5.401	0.0201	rs7361100	20	54325902	q13.31
SNP_A-1921779	T	T	258	106	325	91	5.399	0.0201	rs10776638	10	49590037	q11.23
SNP_A-1921354	G	G	225	143	219	195	5.394	2.02E-02	rs2733763	14	21337331	q11.2
SNP_A-1906034	T	T	379	5	412	0	5.398	2.02E-02	rs773021	9	74997756	q21.13
SNP_A-1883558	A	A	271	69	285	109	5.398	2.02E-02	rs6828448	4	10408127	p16.1
SNP_A-1880244	A	A	363	1	362	8	5.397	2.02E-02	rs2622913	1	47552091	p33
SNP_A-1880688	T	T	359	57	334	82	5.398	2.02E-02	rs2781007	9	83495622	q21.32
SNP_A-1878823	T	T	239	179	273	147	5.394	2.02E-02	rs4889384	16	80387976	q23.2
SNP_A-1986620	C	C	344	18	402	8	5.392	2.02E-02	rs7774156	6	81834733	q14.1
SNP_A-1939609	T	T	302	66	293	97	5.398	2.02E-02	rs17734913	6	123120389	q22.31
SNP_A-1948312	C	C	306	60	317	95	5.397	2.02E-02	rs9810436	3	55902605	p14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1953207	C	T	221	159	189	187	5.399	2.02E-02	rs10894818	11	133821432	q25
SNP_A-1846901	T	T	420	0	387	5	5.39	2.02E-02	rs6926516	6	8698372	p24.3
SNP_A-1741053	T	T	384	18	377	35	5.395	2.02E-02	rs10507266	12	114864528	q24.21
SNP_A-2135917	A	A	297	67	354	50	5.392	2.02E-02	rs7993619	13	94610746	q32.1
SNP_A-2127178	C	C	244	112	233	153	5.393	2.02E-02	rs4727688	7	107066089	q31.1
SNP_A-2168197	A	A	283	77	327	57	5.39	2.02E-02	rs939976	15	28003256	q13.2
SNP_A-2162638	G	G	213	149	206	202	5.391	2.02E-02	rs627865	3	161149934	q25.33
SNP_A-2162038	G	G	323	67	303	95	5.398	2.02E-02	rs12670040	7	136020504	q33
SNP_A-2152268	G	G	414	0	381	5	5.396	2.02E-02	rs4939940	18	45893306	q21.1
SNP_A-2226264	C	C	248	62	329	51	5.396	2.02E-02	rs12607337	18	72544197	q23
SNP_A-2227625	G	G	240	158	214	196	5.391	2.02E-02	rs7803390	7	41549284	p14.1
SNP_A-2180485	T	T	256	86	271	133	5.398	2.02E-02	rs7648111	3	116620856	q13.31
SNP_A-2185540	T	T	418	0	385	5	5.392	2.02E-02	rs16828100	2	151045725	q23.3
SNP_A-2102411	C	C	379	5	412	0	5.398	2.02E-02	rs17117020	5	154510115	q33.2
SNP_A-2095146	T	T	322	94	258	110	5.398	2.02E-02	rs2374544	12	104637875	q23.3
SNP_A-2093750	G	G	343	15	339	31	5.392	2.02E-02	rs12636420	3	45249919	p21.31
SNP_A-2085886	C	C	365	47	386	28	5.396	2.02E-02	rs17538708	10	80204581	q22.3
SNP_A-2069864	A	A	279	55	269	83	5.395	2.02E-02	rs6105564	20	16210545	p12.1
SNP_A-2006067	A	A	251	167	278	132	5.398	2.02E-02	rs1897199	10	122747061	q26.12
SNP_A-2010080	G	G	347	11	387	3	5.392	2.02E-02	rs7666328	4	116140909	q26
SNP_A-2024671	G	G	383	5	416	0	5.394	2.02E-02	rs7924490	11	114210277	q23.2
SNP_A-2289373	G	G	344	20	369	41	5.391	2.02E-02	rs11599265	10	20313775	p12.31
SNP_A-2297984	T	T	371	15	391	5	5.398	2.02E-02	rs2181016	6	4446339	p25.1
SNP_A-2262464	G	A	195	163	218	186	5.395	2.02E-02	rs2920206	4	4433279	p16.3
SNP_A-2268679	C	C	216	136	275	121	5.396	2.02E-02	rs6731773	2	166996621	q24.3
SNP_A-2287398	C	C	338	26	394	14	5.394	2.02E-02	rs9541348	13	67882435	q21.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2248732	T	T	201	125	198	176	5.398	2.02E-02	rs12614872	2	215621419	q35
SNP_A-2247663	G	G	260	156	227	189	5.393	2.02E-02	rs2283800	22	21223968	q11.22
SNP_A-2042204	A	A	305	21	322	42	5.385	2.03E-02	rs7854212	9	112394286	q32
SNP_A-1994240	T	T	181	175	237	163	5.386	2.03E-02	rs1443557	8	92964617	q21.3
SNP_A-2057844	C	C	249	101	250	146	5.384	2.03E-02	rs1001136	1	218722529	q41
SNP_A-2050678	C	C	259	105	253	147	5.386	2.03E-02	rs1505335	7	9364908	p21.3
SNP_A-2089583	G	G	422	0	389	5	5.388	2.03E-02	rs2855710	12	11921319	p13.2
SNP_A-2102199	G	G	324	66	350	44	5.383	2.03E-02	rs2484504	10	29344162	p12.1
SNP_A-2196564	G	G	259	111	320	94	5.384	2.03E-02	rs2030183	3	142973934	q23
SNP_A-2199011	C	C	326	38	320	62	5.385	2.03E-02	rs1882656	7	65557974	q11.21
SNP_A-2225083	G	G	264	102	325	85	5.385	2.03E-02	rs522643	11	125358428	q24.2
SNP_A-1740713	T	T	293	57	314	94	5.386	2.03E-02	rs6820536	4	157482715	q32.1
SNP_A-1787600	T	T	329	19	393	9	5.384	2.03E-02	rs2220197	12	30288849	p11.22
SNP_A-1850152	C	C	175	125	235	115	5.383	2.03E-02	rs151414	4	103495057	q24
SNP_A-1822610	T	T	299	31	300	54	5.39	2.03E-02	rs16827550	2	186884680	q32.1
SNP_A-1834415	T	T	364	44	343	67	5.385	2.03E-02	rs12437310	14	75712510	q24.3
SNP_A-1831967	A	A	317	75	346	52	5.389	2.03E-02	rs6930532	6	162937507	q26
SNP_A-1956718	A	A	355	9	406	2	5.382	2.03E-02	rs9509275	13	20014541	q12.11
SNP_A-1961884	T	T	358	6	395	19	5.387	2.03E-02	rs6548144	2	4781141	p25.2
SNP_A-1939249	T	T	293	27	297	49	5.389	2.03E-02	rs9257746	6	29414800	p22.1
SNP_A-1983196	G	G	341	7	395	1	5.388	2.03E-02	rs3330171	5	119103539	q23.1
SNP_A-1979931	C	C	316	14	329	31	5.39	2.03E-02	rs836324	4	173527424	q34.1
SNP_A-1978749	C	C	287	77	298	118	5.385	2.03E-02	rs17371804	4	122623077	q27
SNP_A-1966042	C	C	202	146	260	132	5.389	2.03E-02	rs2244492	2	179379811	q31.2
SNP_A-1965074	C	C	294	68	351	51	5.386	2.03E-02	rs1437299	2	139778262	q22.1
SNP_A-1895617	T	T	292	64	340	46	5.387	2.03E-02	rs7721045	5	53664613	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909511	C	C	308	94	336	68	5.385	2.03E-02	rs480245	9	38303350	p13.2
SNP_A-1917462	G	G	297	47	305	77	5.39	2.03E-02	rs11025413	11	20123244	p15.1
SNP_A-1913498	C	C	347	75	318	102	5.379	2.04E-02	rs7192444	16	80737839	q23.3
SNP_A-1921974	A	A	207	145	238	116	5.376	2.04E-02	rs4798684	18	885116	p11.32
SNP_A-1923985	G	G	370	30	387	15	5.377	2.04E-02	rs11096707	2	17003946	p24.2
SNP_A-1923470	A	A	248	112	310	96	5.377	2.04E-02	rs1499871	20	53128329	q13.2
SNP_A-1892817	C	C	345	7	399	1	5.377	2.04E-02	rs2681193	1	97065602	p21.3
SNP_A-1978316	T	T	352	0	390	6	5.376	2.04E-02	rs10516499	4	104569999	q24
SNP_A-1988749	C	C	211	153	267	137	5.375	2.04E-02	rs2938844	7	9400159	p21.3
SNP_A-1956931	T	T	272	92	293	65	5.374	2.04E-02	rs10221471	19	36621133	q12
SNP_A-1952583	A	A	273	89	281	133	5.376	2.04E-02	rs11175342	12	63006061	q14.2
SNP_A-1824503	A	A	394	10	400	2	5.374	2.04E-02	rs6684335	1	59801044	p32.1
SNP_A-1827706	G	G	290	60	348	44	5.374	2.04E-02	rs4908817	1	9179838	p36.22
SNP_A-1852331	T	T	338	6	329	17	5.377	2.04E-02	rs7625301	3	29888642	p24.1
SNP_A-1852173	C	C	391	15	411	5	5.378	2.04E-02	rs9533030	13	41670274	q14.11
SNP_A-1847485	A	A	280	94	254	124	5.373	2.04E-02	rs453826	5	39152577	p13.1
SNP_A-1845125	C	C	282	84	320	62	5.374	2.04E-02	rs10826295	10	60898447	q21.2
SNP_A-1814384	G	G	216	146	271	129	5.381	2.04E-02	rs13147209	4	134919514	q28.3
SNP_A-1723848	A	A	275	39	295	69	5.377	2.04E-02	rs10518070	4	71448883	q13.3
SNP_A-1717657	C	C	184	174	231	155	5.374	2.04E-02	rs982290	8	88160386	q21.3
SNP_A-2172616	T	T	354	30	345	51	5.377	2.04E-02	rs203958	8	51130788	q11.21
SNP_A-2096695	T	T	380	34	333	51	5.378	2.04E-02	rs10408343	19	9444804	p13.2
SNP_A-2049173	T	T	327	23	338	44	5.375	2.04E-02	rs6086852	20	9281616	p12.2
SNP_A-2070785	C	C	301	95	308	64	5.38	2.04E-02	rs6584896	10	110515342	q25.1
SNP_A-2003981	C	C	265	77	340	64	5.38	2.04E-02	rs4905917	14	99452945	q32.2
SNP_A-2017361	T	T	317	49	328	80	5.374	2.04E-02	rs243721	21	28053532	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2021214	A	A	288	120	317	91	5.376	2.04E-02	rs7753051	6	160498468	q25.3
SNP_A-2247738	A	A	365	41	394	24	5.381	2.04E-02	rs1327013	10	130463265	q26.2
SNP_A-2259369	G	G	316	36	381	23	5.375	2.04E-02	rs12079234	1	77473330	p31.1
SNP_A-2294949	G	G	353	17	374	36	5.381	2.04E-02	rs6687251	1	60736743	p31.3
SNP_A-2293175	A	A	235	159	265	127	5.375	2.04E-02	rs832502	12	93177610	q22
SNP_A-2310583	G	G	327	35	392	22	5.381	2.04E-02	rs7594399	2	232075903	q37.1
SNP_A-2302409	A	A	326	30	394	18	5.367	2.05E-02	rs2206979	6	131773895	q23.2
SNP_A-2259933	A	A	315	55	373	39	5.373	2.05E-02	rs12353950	1	65011109	p31.3
SNP_A-2262162	A	A	313	15	370	6	5.366	2.05E-02	rs17049985	4	139205076	q28.3
SNP_A-2278620	T	T	179	177	237	167	5.367	2.05E-02	rs314661	19	51864313	q13.32
SNP_A-2274554	A	A	163	141	219	131	5.368	2.05E-02	rs4144113	13	63669429	q21.31
SNP_A-2236474	A	A	252	134	286	106	5.369	2.05E-02	rs299620	5	34091777	p13.3
SNP_A-2104926	C	C	353	51	382	32	5.372	2.05E-02	rs2222310	4	12356043	p15.33
SNP_A-2104814	C	C	302	48	332	30	5.373	2.05E-02	rs5027576	4	22969784	p15.2
SNP_A-2157913	C	C	238	166	201	195	5.369	2.05E-02	rs4478531	8	31518041	p12
SNP_A-2120697	A	A	418	0	387	5	5.365	2.05E-02	rs9889031	16	8481372	p13.2
SNP_A-1652680	G	G	276	114	321	91	5.373	2.05E-02	rs721697	13	57155549	q21.1
SNP_A-1687834	C	C	326	16	362	36	5.369	2.05E-02	rs3755488	2	176146595	q31.1
SNP_A-1707733	A	A	289	105	329	81	5.369	2.05E-02	rs719851	14	31031224	q12
SNP_A-1808280	G	G	244	118	300	100	5.369	2.05E-02	rs2221744	16	60539744	q21
SNP_A-1787027	T	T	325	15	384	6	5.367	2.05E-02	rs3739033	2	135317092	q21.3
SNP_A-1841058	G	G	256	130	226	162	5.369	2.05E-02	rs7202234	16	11849823	p13.13
SNP_A-1954059	G	G	305	105	331	77	5.366	2.05E-02	rs10979229	9	107974635	q31.2
SNP_A-1979010	T	T	268	98	329	81	5.37	2.05E-02	rs17036514	4	135646294	q28.3
SNP_A-1879274	A	A	414	0	383	5	5.369	2.05E-02	rs16943645	15	88185865	q26.1
SNP_A-1923466	C	C	283	57	296	92	5.372	2.05E-02	rs4700832	5	178841338	q35.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1925625	T	T	366	0	406	6	5.372	2.05E-02	rs4797984	18	2465747	p11.32
SNP_A-1925851	G	G	253	87	270	60	5.364	0.0206	rs16991834	4	35829821	p14
SNP_A-1916657	T	T	190	154	242	138	5.359	0.0206	rs11070535	15	44739183	q21.1
SNP_A-1916229	A	A	306	20	372	10	5.362	0.0206	rs11053026	12	34017036	p11.1
SNP_A-1907882	C	C	216	152	223	109	5.359	0.0206	rs12719636	7	153840924	q36.2
SNP_A-1910253	G	G	256	114	255	161	5.361	0.0206	rs1014677	13	109362566	q34
SNP_A-1910014	C	C	231	187	259	151	5.358	0.0206	rs12458062	18	44622539	q21.1
SNP_A-1888879	C	C	397	19	397	7	5.364	0.0206	rs4897965	19	340805	p13.3
SNP_A-1903362	T	T	319	17	369	39	5.359	0.0206	rs17038919	3	1442650	p26.3
SNP_A-1949262	G	G	353	7	407	1	5.358	0.0206	rs2600111	20	57196894	q13.32
SNP_A-1943784	A	A	414	2	363	9	5.362	0.0206	rs16854657	2	168757865	q24.3
SNP_A-1829761	A	A	332	24	399	13	5.356	0.0206	rs301718	5	88267595	q14.3
SNP_A-1815446	G	G	318	46	355	29	5.357	0.0206	rs16992551	22	43321819	q13.31
SNP_A-1821901	A	A	333	85	360	60	5.358	0.0206	rs9694884	8	141251904	q24.3
SNP_A-1849198	A	A	332	12	376	30	5.36	0.0206	rs17169862	7	34383759	p14.3
SNP_A-1805606	T	T	308	50	317	81	5.364	0.0206	rs194913	6	82489502	q14.1
SNP_A-2115519	G	G	366	2	401	11	5.363	0.0206	rs11007101	10	28760790	p12.1
SNP_A-2108110	C	T	187	159	201	167	5.357	0.0206	rs10207154	2	34051404	p22.3
SNP_A-2132038	A	A	180	142	215	117	5.363	0.0206	rs4735300	8	95671019	q22.1
SNP_A-2142906	G	G	267	149	218	170	5.364	0.0206	rs807509	6	24690011	p22.2
SNP_A-2173222	A	A	310	18	362	8	5.362	0.0206	rs116719	17	72261926	q25.1
SNP_A-2194802	G	G	353	7	407	1	5.358	0.0206	rs8098728	18	8512581	p11.22
SNP_A-2193597	C	C	217	205	247	169	5.362	0.0206	rs9435130	1	9202193	p36.22
SNP_A-2183514	G	G	326	34	297	53	5.36	0.0206	rs955847	10	56145480	q21.1
SNP_A-2191205	G	G	235	117	292	100	5.362	0.0206	rs4529436	8	94709850	q22.1
SNP_A-2222772	T	T	252	128	274	96	5.359	0.0206	rs764497	4	24657958	p15.2
SNP_A-2215701	C	C	318	6	351	19	5.362	0.0206	rs41331	7	28465873	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2205942	A	A	357	1	358	8	5.358	0.0206	rs7690971	4	164661859	q32.2
SNP_A-2208449	A	A	393	29	370	48	5.363	0.0206	rs381879	5	132961027	q31.1
SNP_A-2211217	A	A	252	124	225	157	5.357	0.0206	rs6541205	1	215722625	q41
SNP_A-2087518	C	C	332	10	411	3	5.36	0.0206	rs1869875	3	152108804	q25.1
SNP_A-2074617	G	G	226	144	220	196	5.36	0.0206	rs11712956	3	141201328	q23
SNP_A-2048547	A	A	187	155	251	147	5.356	0.0206	rs197508	6	143139186	q24.2
SNP_A-2059109	C	C	322	90	296	120	5.36	0.0206	rs11867328	17	62776578	q24.2
SNP_A-2024002	C	C	343	29	292	44	5.362	0.0206	rs6745361	2	129903429	q21.1
SNP_A-2025219	G	G	290	68	352	52	5.364	0.0206	rs2246565	10	42217654	q11.21
SNP_A-2012884	T	T	236	182	265	147	5.359	0.0206	rs1320179	1	5167147	p36.32
SNP_A-2254140	A	A	328	12	388	4	5.361	0.0206	rs6766038	3	52421828	p21.1
SNP_A-2308713	A	A	304	62	313	97	5.358	0.0206	rs6833468	4	169732630	q32.3
SNP_A-2310357	T	T	347	9	396	2	5.363	0.0206	rs1538223	1	201405683	q32.1
SNP_A-2309291	T	T	248	96	250	140	5.35	0.0207	rs4234848	4	81207984	q21.21
SNP_A-2279640	T	T	288	82	349	65	5.355	0.0207	rs9549540	13	112247877	q34
SNP_A-2280483	G	A	205	183	212	170	5.349	0.0207	rs2979151	8	8295429	p23.1
SNP_A-2010189	G	T	195	157	202	178	5.352	0.0207	rs4532285	4	140080818	q31.1
SNP_A-2022221	T	T	270	86	329	69	5.353	0.0207	rs12696382	3	176825785	q26.31
SNP_A-2030679	A	A	261	107	260	152	5.355	0.0207	rs11835314	12	106412032	q23.3
SNP_A-2064915	A	A	329	3	357	13	5.352	0.0207	rs17002342	4	78312384	q21.1
SNP_A-2085530	C	C	250	74	321	61	5.351	0.0207	---	3	97796705	q11.2
SNP_A-2078371	T	T	332	4	361	15	5.352	0.0207	rs9363675	6	67703027	q12
SNP_A-2103061	G	G	330	16	401	7	5.356	0.0207	rs12024577	1	215532538	q41
SNP_A-2099733	C	C	208	154	251	131	5.351	0.0207	rs9857798	3	79798550	p12.3
SNP_A-2223226	G	G	405	17	414	6	5.355	0.0207	rs11062567	12	3188374	p13.32
SNP_A-2195780	A	A	327	17	371	7	5.351	0.0207	rs12401392	1	101607966	p21.2
SNP_A-2169074	T	T	230	106	231	153	5.355	0.0207	rs267196	6	7794334	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787906	G	G	270	126	314	102	5.352	0.0207	rs9527931	13	58512555	q21.2
SNP_A-1857202	C	C	376	42	352	64	5.352	0.0207	rs869159	2	9853723	p25.1
SNP_A-1832995	G	G	226	132	291	119	5.349	0.0207	rs968324	20	56371273	q13.32
SNP_A-1835197	C	C	317	53	373	37	5.352	0.0207	rs16937408	8	72206677	q13.3
SNP_A-1958190	G	G	359	9	392	24	5.35	0.0207	rs17112965	12	72695401	q21.1
SNP_A-1978920	G	G	326	22	381	11	5.348	0.0207	rs1395979	4	131282693	q28.2
SNP_A-1979961	A	A	239	129	233	177	5.354	0.0207	rs13144752	4	175319817	q34.1
SNP_A-1964288	A	G	193	163	220	186	5.355	0.0207	rs2310243	2	102336078	q11.2
SNP_A-1890504	A	A	248	92	319	79	5.354	0.0207	rs2275803	10	129761680	q26.2
SNP_A-1876032	C	C	354	48	329	71	5.356	0.0207	rs845559	7	55022169	p11.2
SNP_A-1909711	T	T	209	141	274	130	5.354	0.0207	rs10061469	5	72553904	q13.2
SNP_A-1928954	G	A	189	173	229	179	5.344	2.08E-02	rs34914	3	10432314	p25.3
SNP_A-1879098	C	C	377	23	390	10	5.342	2.08E-02	rs6506357	18	6016986	p11.31
SNP_A-1878665	T	T	317	15	374	6	5.347	2.08E-02	---	20	5841768	p12.3
SNP_A-1972578	C	C	219	145	282	132	5.341	2.08E-02	rs2742448	3	45739250	p21.31
SNP_A-1984390	C	C	366	44	390	26	5.347	2.08E-02	rs1898312	1	213462816	q41
SNP_A-1950538	T	T	291	91	333	69	5.345	2.08E-02	rs9861287	3	54134258	p21.1
SNP_A-1952528	T	T	203	129	261	115	5.339	2.08E-02	rs354842	4	142547963	q31.21
SNP_A-1815761	G	G	389	9	386	22	5.34	2.08E-02	rs4495116	4	6480719	p16.1
SNP_A-1853342	T	T	335	29	358	54	5.345	2.08E-02	rs3850190	3	173044310	q26.31
SNP_A-1860294	A	A	365	3	397	13	5.342	2.08E-02	rs11186601	10	93277180	q23.32
SNP_A-2196053	C	C	357	9	390	24	5.342	2.08E-02	rs7527438	1	108129086	p13.3
SNP_A-2212232	C	C	227	143	219	193	5.344	2.08E-02	rs2477725	1	117312087	p13.1
SNP_A-2161373	A	A	359	7	413	1	5.344	2.08E-02	rs7920755	10	109088926	q25.1
SNP_A-2126539	G	G	304	14	388	6	5.345	2.08E-02	rs11203417	1	17582911	p36.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2122929	C	C	242	124	238	172	5.339	2.08E-02	rs2881440	16	7231029	p13.2
SNP_A-2057655	C	C	362	26	397	13	5.345	2.08E-02	rs10963451	9	18094101	p22.2
SNP_A-2021998	A	A	334	80	362	56	5.343	2.08E-02	rs4648505	1	3428453	p36.32
SNP_A-2021804	A	G	183	143	214	194	5.347	2.08E-02	rs1399073	15	31331558	q13.3
SNP_A-2037036	A	A	298	68	307	105	5.346	2.08E-02	rs2146483	1	195627268	q31.3
SNP_A-2005907	C	C	315	37	328	64	5.346	2.08E-02	rs853918	10	120140454	q26.11
SNP_A-1997481	C	C	284	78	343	61	5.344	2.08E-02	rs1523677	9	104443405	q31.1
SNP_A-2286292	G	G	345	55	380	36	5.345	2.08E-02	rs575421	5	6638234	p15.31
SNP_A-2285569	G	G	261	105	263	151	5.34	2.08E-02	rs652008	8	103179097	q22.3
SNP_A-2265540	C	C	284	52	270	78	5.345	2.08E-02	rs7843772	8	72224650	q13.3
SNP_A-2275889	C	C	362	0	404	6	5.339	2.09E-02	rs1024675	7	51457401	p12.1
SNP_A-2272948	T	T	295	29	321	15	5.336	2.09E-02	rs12309119	12	53705326	q13.2
SNP_A-2237853	G	G	304	30	351	17	5.334	2.09E-02	rs9471494	6	41265322	p21.1
SNP_A-2308707	C	C	296	68	305	105	5.333	2.09E-02	rs2086091	3	163786008	q26.1
SNP_A-1996960	G	G	396	8	393	1	5.331	2.09E-02	rs17792380	9	79800981	q21.31
SNP_A-2022915	C	C	412	4	383	13	5.333	2.09E-02	rs11256902	10	10996778	p14
SNP_A-2070706	G	G	360	58	374	36	5.339	2.09E-02	rs10493295	1	60919958	p31.3
SNP_A-2105775	C	C	340	16	367	35	5.338	2.09E-02	rs17103253	1	47628985	p33
SNP_A-2085002	A	A	357	9	406	2	5.338	2.09E-02	rs166675	1	74607538	p31.1
SNP_A-2090670	T	T	205	129	278	122	5.337	2.09E-02	rs1564381	5	31545580	p13.3
SNP_A-2117576	C	C	420	0	391	5	5.336	2.09E-02	rs6687918	1	192525497	q31.3
SNP_A-2124686	G	G	260	102	252	142	5.337	2.09E-02	rs1567492	4	28218775	p15.1
SNP_A-2132628	C	C	267	133	233	163	5.333	2.09E-02	rs11764343	7	77514718	q21.11
SNP_A-2166570	T	T	407	7	384	18	5.333	2.09E-02	rs17141685	10	6828582	p14
SNP_A-2145423	A	A	293	15	383	7	5.332	2.09E-02	rs9905894	17	25937741	q11.2
SNP_A-2207391	C	C	304	26	373	15	5.333	2.09E-02	rs13416965	2	177147093	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2205668	G	G	278	90	339	73	5.339	2.09E-02	rs596844	7	18156604	p21.1
SNP_A-2196717	T	T	384	32	392	16	5.339	2.09E-02	rs4688766	3	131646921	q21.3
SNP_A-2183953	T	T	404	12	358	24	5.338	2.09E-02	rs12320582	12	113617156	q24.21
SNP_A-2170348	C	C	224	144	286	130	5.334	2.09E-02	rs10235993	7	46953836	p13
SNP_A-1841299	C	T	205	195	232	176	5.335	2.09E-02	rs9506534	13	20145165	q12.11
SNP_A-1793612	C	C	258	160	283	125	5.333	2.09E-02	rs532781	11	94665545	q21
SNP_A-1798126	A	A	378	2	374	10	5.334	2.09E-02	rs3211891	7	79934999	q21.11
SNP_A-1805026	G	G	242	124	285	101	5.332	2.09E-02	rs7656141	4	154876230	q31.3
SNP_A-1728747	G	G	309	17	384	8	5.335	2.09E-02	rs10497050	2	150095694	q23.1
SNP_A-1756309	A	A	401	1	404	8	5.334	2.09E-02	rs10495857	2	36207266	p22.3
SNP_A-1952851	G	G	287	57	283	87	5.338	2.09E-02	rs2631217	10	67962374	q21.3
SNP_A-1960590	G	G	219	149	278	134	5.334	2.09E-02	rs1025077	2	207199334	q33.3
SNP_A-1984016	A	A	342	8	368	22	5.339	2.09E-02	rs1432863	5	150977594	q33.1
SNP_A-1882082	C	C	337	33	296	50	5.339	2.09E-02	rs6025402	20	55149754	q13.31
SNP_A-1892390	T	T	293	11	382	4	5.332	2.09E-02	rs6938374	6	126565222	q22.32
SNP_A-1926736	T	T	416	0	387	5	5.339	2.09E-02	rs962841	8	142726810	q24.3
SNP_A-1927417	T	T	355	57	309	77	5.33	2.10E-02	rs17125571	10	110769683	q25.1
SNP_A-1904677	T	T	223	143	215	193	5.323	2.10E-02	rs12560681	13	68455672	q21.33
SNP_A-1911646	A	A	307	83	285	113	5.329	2.10E-02	rs8042059	15	76694914	q25.1
SNP_A-1895047	T	T	386	12	342	24	5.328	2.10E-02	rs1809885	3	55600202	p14.3
SNP_A-1898877	T	T	229	161	199	195	5.33	2.10E-02	rs2509	15	71646541	q24.1
SNP_A-1984357	C	G	195	165	220	186	5.327	2.10E-02	rs6556635	5	162178999	q34
SNP_A-1977381	G	G	267	27	283	51	5.324	2.10E-02	rs1489560	4	63914495	q13.1
SNP_A-1965179	T	T	217	151	209	203	5.324	2.10E-02	rs6707980	2	143964065	q22.2
SNP_A-1967526	G	G	193	177	251	165	5.324	2.10E-02	rs6085093	20	5250653	p12.3
SNP_A-1958385	C	C	325	27	354	52	5.33	2.10E-02	rs13126860	4	165768661	q32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802660	G	G	348	2	383	11	5.323	2.10E-02	rs6536071	4	156727987	q32.1
SNP_A-1814576	T	T	402	0	375	5	5.324	2.10E-02	rs17105058	14	67679820	q24.1
SNP_A-1813707	A	A	345	25	395	13	5.325	2.10E-02	rs7232965	18	70632585	q22.3
SNP_A-1789668	C	C	220	170	259	143	5.324	2.10E-02	rs135418	22	42990560	q13.31
SNP_A-1855523	G	G	274	68	344	54	5.328	2.10E-02	rs4753652	11	94446370	q21
SNP_A-1848692	T	T	243	173	265	135	5.329	2.10E-02	rs10416963	19	17623890	p13.11
SNP_A-1850216	T	T	219	143	274	126	5.328	2.10E-02	rs1486051	6	76986956	q14.1
SNP_A-1844530	G	A	227	165	203	201	5.324	2.10E-02	rs10094408	8	123763726	q24.13
SNP_A-1847010	A	A	277	113	302	84	5.328	2.10E-02	rs4548514	10	67951101	q21.3
SNP_A-2174996	A	A	347	15	408	6	5.325	2.10E-02	rs6414829	5	54003879	q11.2
SNP_A-2176603	A	A	198	196	219	155	5.33	2.10E-02	rs7231736	18	831321	p11.32
SNP_A-2211239	T	T	419	3	379	11	5.324	2.10E-02	rs1346448	5	173769678	q35.2
SNP_A-2121191	C	C	351	7	403	1	5.329	2.10E-02	rs6477021	9	5964573	p24.1
SNP_A-2110876	C	C	301	121	324	90	5.325	2.10E-02	rs3827784	6	6587404	p25.1
SNP_A-2095612	A	G	186	182	240	176	5.329	2.10E-02	rs4955692	3	171109081	q26.2
SNP_A-2098270	C	C	351	7	403	1	5.329	2.10E-02	rs1353603	4	143360620	q31.21
SNP_A-2064002	A	G	208	200	234	176	5.325	2.10E-02	rs11876331	18	20798754	q11.2
SNP_A-2066617	G	G	244	122	244	172	5.328	2.10E-02	rs11991621	18	69620005	q22.3
SNP_A-2055847	T	T	351	37	394	22	5.327	2.10E-02	rs17045293	12	77307042	q21.2
SNP_A-2053021	A	G	194	156	209	185	5.326	2.10E-02	rs4953938	2	135528580	q21.3
SNP_A-2030865	A	A	342	4	373	15	5.327	2.10E-02	rs2207007	6	103984685	q16.3
SNP_A-2038013	G	G	358	14	405	5	5.324	2.10E-02	rs9920394	15	30098102	q13.3
SNP_A-1996751	G	G	247	117	303	99	5.33	2.10E-02	rs7862783	9	70450716	q21.11
SNP_A-2006028	A	A	232	134	223	181	5.328	2.10E-02	rs7475474	10	122419759	q26.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2240989	T	T	407	3	406	12	5.324	2.10E-02	rs16903084	8	129620444	q24.21
SNP_A-2254577	G	G	277	119	236	144	5.326	2.10E-02	rs2504059	1	176422257	q25.2
SNP_A-2283561	C	C	217	183	254	154	5.323	2.10E-02	rs10822903	10	68155021	q21.3
SNP_A-2286332	G	G	207	87	291	81	5.321	2.11E-02	rs11650105	17	53943071	q23.2
SNP_A-2275943	G	G	385	5	412	0	5.315	2.11E-02	rs7533254	1	33850923	p35.1
SNP_A-2271274	T	T	235	169	254	130	5.321	2.11E-02	rs2279232	5	32136925	p13.3
SNP_A-2229806	T	T	282	112	257	145	5.317	2.11E-02	rs4736500	8	132661679	q24.22
SNP_A-2314142	T	T	326	60	358	40	5.315	2.11E-02	rs668136	3	40768669	p22.1
SNP_A-2292074	C	C	377	5	404	0	5.322	2.11E-02	rs537208	11	117251085	q23.3
SNP_A-2300014	C	C	345	47	327	71	5.318	2.11E-02	rs2413583	22	37984273	q13.1
SNP_A-2298181	T	T	217	205	248	170	5.314	2.11E-02	rs6588245	1	67323820	p31.2
SNP_A-1994192	A	A	322	30	388	18	5.315	2.11E-02	rs16893311	8	90321917	q21.3
SNP_A-2037092	A	A	211	149	200	198	5.322	2.11E-02	rs9353450	6	87893105	q15
SNP_A-2022415	T	T	259	61	251	91	5.321	2.11E-02	rs551421	9	75274831	q21.13
SNP_A-2019356	C	C	304	30	383	19	5.317	2.11E-02	rs999789	21	39348321	q22.2
SNP_A-2096432	G	G	283	69	355	55	5.322	2.11E-02	rs1703426	5	133213434	q31.1
SNP_A-2085941	G	G	224	144	217	195	5.319	2.11E-02	rs6000532	22	35729337	q12.3
SNP_A-2136639	T	T	374	14	370	4	5.322	2.11E-02	rs7899938	10	9553200	p14
SNP_A-2129371	G	G	315	97	287	127	5.315	2.11E-02	rs7168739	15	25744474	q13.1
SNP_A-2171226	A	A	351	9	384	24	5.321	2.11E-02	rs16831263	2	153197381	q23.3
SNP_A-2190285	C	A	215	195	228	182	5.318	2.11E-02	rs7335883	13	52508078	q14.3
SNP_A-1866650	G	G	276	60	344	46	5.32	2.11E-02	rs7117009	11	44511110	p11.2
SNP_A-1799021	A	A	366	54	340	78	5.316	2.11E-02	rs7570739	2	230178481	q36.3
SNP_A-1800025	T	T	369	33	347	53	5.322	2.11E-02	rs6807359	3	53154794	p21.1
SNP_A-1784766	T	T	264	74	284	118	5.318	2.11E-02	rs12466468	2	226208456	q36.3
SNP_A-1699865	G	G	383	3	382	12	5.32	2.11E-02	rs10521086	9	106117865	q31.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1682700	G	G	356	46	384	28	5.316	2.11E-02	rs6917477	6	30132218	p22.1
SNP_A-1955495	C	C	412	0	385	5	5.315	2.11E-02	rs17098969	14	31933477	q12
SNP_A-1949821	G	G	313	99	335	71	5.315	2.11E-02	rs916910	17	54959736	q23.2
SNP_A-1950097	A	A	267	95	267	137	5.317	2.11E-02	rs9822785	3	69637643	p14.1
SNP_A-1972552	A	A	259	61	251	91	5.321	2.11E-02	rs17279525	1	169380613	q24.3
SNP_A-1977882	C	C	264	104	265	149	5.318	2.11E-02	rs1545330	4	85785357	q21.23
SNP_A-1978951	G	G	334	20	404	10	5.318	2.11E-02	rs10518597	4	132739982	q28.3
SNP_A-1894006	T	T	243	149	210	180	5.32	2.11E-02	rs730354	5	41410981	p13.1
SNP_A-1883131	A	A	337	13	347	29	5.317	2.11E-02	rs4855642	3	109564561	q13.13
SNP_A-1879835	A	A	385	25	374	44	5.315	2.11E-02	rs6677524	1	204924169	q32.2
SNP_A-1927731	A	A	294	88	339	67	5.318	2.11E-02	rs10877333	12	58442313	q14.1
SNP_A-1929658	C	C	291	79	296	118	5.311	0.0212	rs6534682	4	129739684	q28.2
SNP_A-1921621	C	T	196	166	220	186	5.313	0.0212	rs918974	7	136228104	q33
SNP_A-1892399	C	C	356	4	389	15	5.314	0.0212	rs728659	18	22557970	q11.2
SNP_A-1893481	T	T	251	167	283	135	5.308	0.0212	rs268014	9	79729362	q21.31
SNP_A-1890850	A	A	222	144	215	195	5.307	0.0212	rs10205049	2	119616163	q14.2
SNP_A-1974514	A	A	210	136	259	117	5.309	0.0212	rs201676	3	139014623	q22.3
SNP_A-1951944	T	T	347	19	369	39	5.309	0.0212	rs6559312	9	88766580	q22.1
SNP_A-1955815	C	C	317	77	358	56	5.314	0.0212	rs3936222	8	56076558	q12.1
SNP_A-1757431	T	T	357	27	349	47	5.313	0.0212	rs4131714	5	18994882	p14.3
SNP_A-1715011	T	T	285	115	324	90	5.307	0.0212	rs10492145	12	15000323	p12.3
SNP_A-1813107	C	C	418	0	391	5	5.31	0.0212	rs6815823	4	13515096	p15.33
SNP_A-1845577	C	C	275	95	336	78	5.308	0.0212	rs1471383	10	67634469	q21.3
SNP_A-2186700	T	T	367	45	329	65	5.312	0.0212	rs2715143	7	50497651	p12.2
SNP_A-2195640	G	G	393	5	420	0	5.309	0.0212	rs2152628	10	113405602	q25.2
SNP_A-2178244	C	C	416	0	389	5	5.312	0.0212	rs4417692	2	12446265	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2201353	T	T	414	0	387	5	5.314	0.0212	rs4270114	15	59396856	q22.2
SNP_A-2222984	A	A	249	167	216	200	5.309	0.0212	rs10095975	8	31517852	p12
SNP_A-2138397	C	C	391	5	418	0	5.31	0.0212	rs2100454	2	55574074	p16.1
SNP_A-2159225	G	G	310	56	375	41	5.312	0.0212	rs10931393	2	189779466	q32.2
SNP_A-2153758	A	A	367	17	374	6	5.306	0.0212	rs16917085	11	91569604	q14.3
SNP_A-2038334	C	C	228	110	280	92	5.311	0.0212	rs11691543	2	193144676	q32.3
SNP_A-2010243	A	A	291	79	296	118	5.311	0.0212	rs905900	4	151210387	q31.23
SNP_A-2292504	C	C	252	112	317	97	5.31	0.0212	rs17276450	4	153386071	q31.3
SNP_A-2291494	T	T	311	59	321	93	5.311	0.0212	rs1565735	8	27481994	p21.1
SNP_A-2228812	C	C	271	99	321	79	5.309	0.0212	rs4686896	3	188816079	q27.3
SNP_A-2241603	A	A	281	87	287	129	5.311	0.0212	rs9380785	6	38913537	p21.2
SNP_A-2246821	T	T	199	153	264	144	5.3	2.13E-02	rs6790448	3	152558372	q25.1
SNP_A-2238789	C	C	352	18	408	8	5.299	2.13E-02	rs9671056	13	79077299	q31.1
SNP_A-2269193	G	G	363	7	415	1	5.302	2.13E-02	rs10017297	4	166846220	q32.3
SNP_A-2291612	A	A	330	12	388	4	5.304	2.13E-02	rs11683040	2	9399622	p25.1
SNP_A-2287744	G	G	246	100	306	84	5.302	2.13E-02	rs6886107	5	178984791	q35.3
SNP_A-2310467	G	G	243	113	309	99	5.301	2.13E-02	rs7539328	1	67444624	p31.2
SNP_A-2310626	G	G	285	101	326	78	5.299	2.13E-02	rs28233	5	68047469	q13.1
SNP_A-2015569	C	C	262	104	263	149	5.305	2.13E-02	rs2824050	21	17091368	q21.1
SNP_A-2001832	G	G	349	65	366	42	5.305	2.13E-02	rs224118	10	64113194	q21.2
SNP_A-2027203	C	C	350	16	379	35	5.298	2.13E-02	rs10990136	9	102338391	q31.1
SNP_A-2053411	A	A	352	18	408	8	5.299	2.13E-02	rs9995518	4	78556558	q21.1
SNP_A-2066602	C	C	260	144	235	181	5.3	2.13E-02	rs643621	13	29605853	q12.3
SNP_A-2076763	G	G	361	7	413	1	5.306	2.13E-02	rs7342569	14	66748771	q23.3
SNP_A-2138364	A	A	224	134	275	115	5.303	2.13E-02	rs4721135	7	1685463	p22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2150319	A	A	297	21	365	11	5.3	2.13E-02	rs9818328	3	70003238	p13
SNP_A-2150596	C	C	217	123	266	104	5.303	2.13E-02	rs259478	1	215133559	q41
SNP_A-2130702	T	T	213	115	204	158	5.305	2.13E-02	rs7077039	10	114779067	q25.2
SNP_A-2121606	C	C	249	117	305	99	5.298	2.13E-02	rs7820786	8	5595205	p23.2
SNP_A-2215696	A	A	258	160	291	129	5.304	2.13E-02	rs11124900	2	43043935	p21
SNP_A-2203635	C	C	320	44	336	74	5.302	2.13E-02	rs11816824	10	58365256	q21.1
SNP_A-2213014	A	A	304	48	370	34	5.302	2.13E-02	rs10947774	6	39085374	p21.2
SNP_A-2208049	G	G	344	20	371	41	5.3	2.13E-02	rs7145489	14	37904183	q21.1
SNP_A-1836695	C	C	363	7	415	1	5.302	2.13E-02	rs1436546	4	97104245	q22.3
SNP_A-1819210	T	T	308	52	315	83	5.305	2.13E-02	rs17017422	2	35934769	p22.3
SNP_A-1827580	T	T	294	106	323	79	5.299	2.13E-02	rs4394727	10	67951123	q21.3
SNP_A-1805704	C	C	280	54	316	36	5.306	2.13E-02	rs12539781	7	73013076	q11.23
SNP_A-1786962	C	C	301	103	325	75	5.305	2.13E-02	rs6597186	6	6023202	p25.1
SNP_A-1782912	C	C	331	33	330	56	5.305	2.13E-02	rs6754246	2	230361999	q36.3
SNP_A-1673256	C	C	387	7	366	18	5.298	2.13E-02	rs6934799	6	13288987	p24.1
SNP_A-1972959	T	T	318	52	330	84	5.299	2.13E-02	rs4688174	3	63613995	p14.2
SNP_A-1970433	A	A	318	50	379	35	5.298	2.13E-02	rs2837410	21	40357695	q22.2
SNP_A-1962447	A	A	320	100	286	128	5.303	2.13E-02	rs10495740	2	23343193	p24.1
SNP_A-1979043	A	A	349	7	399	1	5.299	2.13E-02	rs969984	4	137689842	q28.3
SNP_A-1894987	G	G	211	159	263	141	5.301	2.13E-02	rs487731	11	89969033	q14.3
SNP_A-1904752	A	G	222	188	222	190	5.3	2.13E-02	rs2181160	10	124071904	q26.13
SNP_A-1909585	C	C	324	40	371	25	5.302	2.13E-02	rs4539373	12	74042321	q21.1
SNP_A-1919104	C	C	228	132	225	183	5.298	2.14E-02	rs1622784	18	55603302	q21.32
SNP_A-1875223	G	G	306	30	385	19	5.297	2.14E-02	rs13314995	3	73481373	p13
SNP_A-1978059	G	G	266	72	259	105	5.29	2.14E-02	rs2204873	4	92724774	q22.1
SNP_A-1662256	C	C	389	1	394	8	5.296	2.14E-02	rs1631837	5	39281335	p13.1
SNP_A-1758598	G	G	278	124	313	97	5.293	2.14E-02	rs7035330	9	134158138	q34.3
SNP_A-1758863	C	C	289	87	271	119	5.295	2.14E-02	rs10484174	14	43099161	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787818	C	C	384	32	364	52	5.297	2.14E-02	rs11607985	11	117535008	q23.3
SNP_A-1841988	C	C	223	121	183	143	5.294	2.14E-02	rs11223389	11	132579837	q25
SNP_A-1844037	G	G	289	41	323	25	5.294	2.14E-02	rs1468370	7	146621047	q35
SNP_A-1839970	A	A	277	127	247	159	5.293	2.14E-02	rs1218831	13	26887215	q12.2
SNP_A-1853436	G	G	260	88	275	135	5.291	2.14E-02	rs7209177	17	36862543	q21.2
SNP_A-1856307	G	G	214	132	204	178	5.298	2.14E-02	rs2923123	11	10355094	p15.4
SNP_A-1864590	G	G	341	37	308	56	5.297	2.14E-02	rs16992880	22	43522709	q13.31
SNP_A-1859754	G	G	406	0	381	5	5.292	2.14E-02	rs1863548	12	113217726	q24.21
SNP_A-1872654	A	A	363	3	397	13	5.293	2.14E-02	rs1332433	9	25204441	p21.3
SNP_A-2211955	G	G	261	151	281	115	5.295	2.14E-02	rs4895047	3	105470908	q13.11
SNP_A-2203349	A	A	202	180	250	160	5.291	2.14E-02	rs7138703	12	45627188	q13.11
SNP_A-2220871	A	A	406	0	381	5	5.292	2.14E-02	rs16936324	10	36100911	p11.21
SNP_A-2183598	G	G	201	161	261	149	5.293	2.14E-02	rs9342396	6	94832358	q16.1
SNP_A-2119602	C	C	313	57	371	41	5.29	2.14E-02	rs1369992	4	96956331	q22.3
SNP_A-2113148	C	C	326	36	343	63	5.292	2.14E-02	rs1345546	12	104804400	q23.3
SNP_A-2128548	T	T	264	148	234	182	5.291	2.14E-02	rs11197620	10	118030561	q25.3
SNP_A-2145310	T	G	209	159	209	197	5.295	2.14E-02	rs9878602	3	71618028	p13
SNP_A-2165819	C	C	312	56	275	77	5.295	2.14E-02	rs6696140	1	84029489	p31.1
SNP_A-2084167	G	G	217	147	281	135	5.292	2.14E-02	rs1546518	8	56987448	q12.1
SNP_A-2031730	T	T	299	67	361	51	5.292	2.14E-02	rs12518136	5	104398469	q21.2
SNP_A-2293468	T	T	255	155	274	118	5.296	2.14E-02	rs4669010	2	15980188	p24.3
SNP_A-2241310	C	C	372	14	335	27	5.294	2.14E-02	rs1228833	1	30223029	p35.2
SNP_A-2239650	A	A	227	127	212	168	5.296	2.14E-02	rs1511354	4	23978789	p15.2
SNP_A-2237471	T	C	183	157	206	170	5.296	2.14E-02	rs10046536	7	130888980	q32.3
SNP_A-2229952	C	C	359	3	393	13	5.284	2.15E-02	rs1155494	18	59554904	q21.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2231386	A	A	420	0	395	5	5.282	2.15E-02	rs7148832	14	72103456	q24.2
SNP_A-2242700	A	A	230	80	292	66	5.285	2.15E-02	rs10225396	7	46933361	p13
SNP_A-2272452	C	C	373	47	392	28	5.285	2.15E-02	rs11032686	11	34401452	p13
SNP_A-2291167	C	C	414	0	389	5	5.287	2.15E-02	rs16971139	15	77681585	q25.1
SNP_A-2299635	C	C	390	10	360	22	5.288	2.15E-02	rs1870134	3	14195027	p25.1
SNP_A-2021716	-	G	176	176	203	143	5.286	2.15E-02	rs7127451	11	86328048	q14.2
SNP_A-2035939	C	C	362	36	371	19	5.284	2.15E-02	rs9475536	6	56008167	p12.1
SNP_A-2003315	A	A	338	22	393	11	5.288	2.15E-02	rs706603	13	49753024	q14.2
SNP_A-1995991	T	T	357	1	362	8	5.283	2.15E-02	rs12220850	10	13806417	p13
SNP_A-1989765	C	C	273	141	302	110	5.286	2.15E-02	rs2083364	7	44910999	p13
SNP_A-2017346	G	G	195	173	246	156	5.285	2.15E-02	rs1835648	21	27973181	q21.3
SNP_A-2084592	A	A	233	115	217	153	5.288	2.15E-02	rs4390438	13	24495837	q12.13
SNP_A-2076484	A	G	193	165	222	186	5.283	2.15E-02	rs651852	5	78444816	q14.1
SNP_A-2069275	A	A	300	24	300	44	5.288	2.15E-02	rs6769138	3	73906374	p13
SNP_A-2061598	C	C	210	208	242	174	5.287	2.15E-02	rs11191818	10	105581769	q24.33
SNP_A-2144778	C	C	337	25	385	13	5.287	2.15E-02	rs12950064	17	56706403	q23.2
SNP_A-2181758	T	T	299	43	348	28	5.282	2.15E-02	rs9482147	6	121723745	q22.31
SNP_A-1854412	G	G	320	10	393	3	5.287	2.15E-02	rs10732453	11	12405544	p15.3
SNP_A-1845405	C	C	241	145	196	166	5.287	2.15E-02	rs9841389	3	141185123	q23
SNP_A-1841821	G	G	307	59	317	93	5.288	2.15E-02	rs17813667	12	75692831	q21.2
SNP_A-1819768	G	G	202	166	262	154	5.29	2.15E-02	rs4921966	8	18742698	p22
SNP_A-1785615	T	T	401	15	386	30	5.286	2.15E-02	rs3804251	5	169654296	q35.1
SNP_A-1790106	C	C	215	141	204	188	5.283	2.15E-02	rs10898439	11	85537131	q14.2
SNP_A-1798701	C	C	228	116	283	99	5.289	2.15E-02	rs11957062	5	116582319	q23.1
SNP_A-1794414	C	C	382	36	391	19	5.283	2.15E-02	rs393332	6	5057464	p25.1
SNP_A-1805461	T	T	355	7	405	1	5.286	2.15E-02	rs1149832	13	49648652	q14.2
SNP_A-1805937	G	A	192	148	197	181	5.287	2.15E-02	rs9450273	6	86194607	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801250	G	G	393	17	381	33	5.287	2.15E-02	rs10913603	1	175377217	q25.2
SNP_A-1813850	T	T	328	26	359	13	5.289	2.15E-02	rs6486291	11	16443470	p15.1
SNP_A-1673624	G	G	300	50	322	84	5.286	2.15E-02	rs975618	6	65820177	q12
SNP_A-1962901	A	A	267	87	329	71	5.283	2.15E-02	rs6544381	2	41188155	p22.1
SNP_A-1968203	G	G	224	136	290	124	5.287	2.15E-02	rs926609	20	24371937	p11.21
SNP_A-1951201	T	T	272	64	340	50	5.288	2.15E-02	rs17658535	13	68610366	q21.33
SNP_A-1893232	G	G	317	45	336	76	5.287	2.15E-02	rs16979595	19	50169221	q13.31
SNP_A-1892758	G	G	399	7	378	18	5.284	2.15E-02	rs16899788	6	167401737	q27
SNP_A-1902383	G	G	303	117	327	87	5.283	2.15E-02	rs4906722	15	23364565	q12
SNP_A-1911808	T	T	220	152	275	135	5.284	2.15E-02	rs4748708	10	21057309	p12.31
SNP_A-1909799	A	A	311	33	322	58	5.282	2.15E-02	rs1569097	2	140607202	q22.1
SNP_A-1904654	T	T	350	24	325	41	5.286	2.15E-02	rs7151044	14	32726105	q13.1
SNP_A-1929061	T	T	274	46	271	73	5.282	2.15E-02	rs10967865	9	27284815	p21.2
SNP_A-1906747	C	C	229	189	252	150	5.276	2.16E-02	rs3844038	18	41267039	q12.3
SNP_A-1884557	G	G	311	43	294	66	5.281	2.16E-02	rs2572	14	72496043	q24.2
SNP_A-1960162	C	G	185	155	210	178	5.281	2.16E-02	rs217537	6	108618709	q21
SNP_A-1942671	T	T	242	124	231	167	5.279	2.16E-02	rs11745129	5	75294658	q13.3
SNP_A-1964238	G	G	327	19	338	38	5.278	2.16E-02	rs17352808	2	100125686	q11.2
SNP_A-1689226	T	A	220	170	213	199	5.281	2.16E-02	rs6668838	1	154815924	q23.1
SNP_A-1686698	C	C	215	175	260	152	5.281	2.16E-02	rs9316901	13	55431446	q21.1
SNP_A-1707693	A	A	297	101	335	77	5.28	2.16E-02	rs2178457	12	89846042	q21.33
SNP_A-1803879	C	C	317	67	302	96	5.274	2.16E-02	rs7839848	8	66089952	q12.3
SNP_A-1790117	A	A	292	116	325	89	5.278	2.16E-02	rs3753008	10	133635119	q26.3
SNP_A-1819823	C	C	304	62	364	46	5.282	2.16E-02	rs2524136	6	31372741	p21.33
SNP_A-1828227	G	G	337	19	399	9	5.279	2.16E-02	rs10959914	9	11535750	p23
SNP_A-1822671	T	T	422	0	397	5	5.281	2.16E-02	rs367873	16	78205653	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1860771	A	A	235	185	259	147	5.28	2.16E-02	rs4994644	22	25540530	q12.1
SNP_A-2220676	C	C	265	101	268	146	5.281	2.16E-02	rs12434656	14	86336181	q31.3
SNP_A-2138142	G	G	395	15	352	28	5.274	2.16E-02	rs10984823	9	119903724	q33.2
SNP_A-2164198	G	G	365	43	372	24	5.277	2.16E-02	rs9911585	17	65343602	q24.3
SNP_A-2126514	C	C	343	7	391	1	5.279	2.16E-02	rs4773939	13	95630065	q32.1
SNP_A-2121570	C	C	309	21	337	43	5.281	2.16E-02	rs7375203	4	179438500	q34.3
SNP_A-2057982	C	C	282	82	341	65	5.278	2.16E-02	rs2882788	6	66918281	q12
SNP_A-2051299	C	C	351	15	375	33	5.28	2.16E-02	rs1167537	12	26023917	p12.1
SNP_A-2098889	A	A	212	110	231	171	5.282	2.16E-02	rs7188465	16	12450175	p13.13
SNP_A-2010105	A	A	317	49	367	33	5.278	2.16E-02	rs6838795	4	119118018	q26
SNP_A-2009133	G	G	322	10	395	3	5.278	2.16E-02	rs6776091	3	134578452	q22.1
SNP_A-2011855	C	C	320	50	381	35	5.281	2.16E-02	rs4467744	6	76960856	q14.1
SNP_A-2001016	A	A	245	159	205	185	5.275	2.16E-02	rs718309	10	55451187	q21.1
SNP_A-2308129	C	C	306	58	371	43	5.277	2.16E-02	rs2997242	10	122494998	q26.12
SNP_A-2259576	T	T	252	94	240	130	5.28	2.16E-02	rs6997745	8	84640468	q21.13
SNP_A-2260322	A	A	358	4	393	15	5.27	2.17E-02	rs17141563	7	19347024	p21.1
SNP_A-2262968	G	G	261	101	320	84	5.267	2.17E-02	rs780226	1	229975486	q42.2
SNP_A-2291955	A	A	261	123	297	97	5.268	2.17E-02	rs10820860	9	91333158	q22.31
SNP_A-2014054	T	T	338	12	396	4	5.273	2.17E-02	rs2784598	9	10502307	p23
SNP_A-2039103	A	A	298	60	317	97	5.272	2.17E-02	rs2786107	1	194042434	q31.3
SNP_A-2032428	C	C	274	96	270	136	5.267	2.17E-02	rs10156534	9	2926864	p24.2
SNP_A-2081099	T	T	355	63	323	87	5.274	2.17E-02	rs7527274	1	176942448	q25.2
SNP_A-2054590	G	G	321	39	337	67	5.269	2.17E-02	rs17114692	5	152872144	q33.2
SNP_A-2063774	A	G	203	159	213	195	5.27	2.17E-02	rs4773797	13	93934421	q32.1
SNP_A-2063144	G	G	365	23	371	43	5.272	2.17E-02	rs4370388	6	148494695	q24.3
SNP_A-2064303	T	T	381	37	339	55	5.267	2.17E-02	rs12524063	6	32405288	p21.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113744	T	T	228	178	265	149	5.271	2.17E-02	rs9536344	13	52507861	q14.3
SNP_A-2123876	T	T	263	95	303	73	5.27	2.17E-02	rs1887272	9	131038703	q34.13
SNP_A-2132342	G	G	332	34	393	21	5.271	2.17E-02	rs11725914	4	32126804	p15.1
SNP_A-2155274	G	G	334	6	394	20	5.272	2.17E-02	rs1942869	18	55885586	q21.32
SNP_A-2159120	A	A	304	26	335	51	5.273	2.17E-02	rs16974655	18	37252288	q12.3
SNP_A-2202272	G	G	402	6	370	16	5.266	2.17E-02	---	16	74791685	q23.1
SNP_A-2177780	A	G	190	148	200	182	5.273	2.17E-02	rs1957151	14	45537691	q21.2
SNP_A-2175079	A	A	337	67	356	44	5.267	2.17E-02	rs1972238	1	154323464	q23.1
SNP_A-1859836	T	G	193	177	232	182	5.266	2.17E-02	rs1500825	4	118004722	q26
SNP_A-1863011	G	G	315	23	395	13	5.27	2.17E-02	rs17780227	18	55300960	q21.32
SNP_A-1866150	G	G	368	26	355	45	5.273	2.17E-02	rs2646397	10	8615616	p14
SNP_A-1854554	T	T	383	21	377	39	5.273	2.17E-02	rs10144981	14	52188951	q22.1
SNP_A-1853941	C	C	363	7	413	1	5.269	2.17E-02	rs3003703	1	88088748	p22.3
SNP_A-1853068	T	T	311	19	293	35	5.271	2.17E-02	rs7995488	13	46555865	q14.2
SNP_A-1838564	G	G	305	51	322	84	5.269	2.17E-02	rs6808829	3	188895485	q27.3
SNP_A-1836885	G	G	335	67	354	44	5.27	2.17E-02	rs16966598	17	23162249	q11.2
SNP_A-1807396	T	T	189	173	236	154	5.266	2.17E-02	rs1024022	11	25663566	p14.3
SNP_A-1801261	T	T	338	24	380	12	5.272	2.17E-02	rs6961104	7	25470878	p15.2
SNP_A-1665282	C	C	329	67	314	96	5.268	2.17E-02	rs1965169	10	49139213	q11.22
SNP_A-1652618	G	G	353	27	354	48	5.267	2.17E-02	rs10488475	7	17557760	p21.1
SNP_A-1744561	T	T	341	53	322	78	5.27	2.17E-02	rs10512087	9	77401745	q21.31
SNP_A-1963948	T	T	197	99	269	91	5.268	2.17E-02	rs10520240	2	79578790	p12
SNP_A-1978168	C	C	361	7	411	1	5.273	2.17E-02	rs17024738	4	97116474	q22.3
SNP_A-1982845	T	C	193	177	232	182	5.266	2.17E-02	rs7703883	5	108045161	q21.3
SNP_A-1941069	A	A	350	10	373	25	5.268	2.17E-02	rs9968159	3	126879111	q21.2
SNP_A-1900707	T	T	299	25	362	14	5.273	2.17E-02	rs809607	4	24461659	p15.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1924061	C	C	279	79	281	117	5.273	2.17E-02	rs2055316	3	196081	p26.3
SNP_A-1941227	C	C	279	65	275	97	5.263	0.0218	rs7669497	4	117567041	q26
SNP_A-1940475	C	C	218	152	278	138	5.26	0.0218	rs7197835	16	81272197	q23.3
SNP_A-1943556	C	C	362	0	410	6	5.262	0.0218	rs3808917	10	101980705	q24.31
SNP_A-1944547	C	C	416	0	393	5	5.258	0.0218	rs16922879	11	32122757	p13
SNP_A-1947044	T	T	358	6	376	18	5.262	0.0218	rs7740232	6	137545054	q23.3
SNP_A-1936269	T	T	367	3	403	13	5.259	0.0218	rs2406481	4	138643338	q28.3
SNP_A-1955868	A	A	410	0	387	5	5.262	0.0218	rs12085551	1	195900348	q31.3
SNP_A-1987893	A	A	194	160	246	144	5.258	0.0218	rs9389816	6	140995021	q24.1
SNP_A-1986855	G	G	290	80	292	118	5.262	0.0218	rs10498977	6	92951301	q16.1
SNP_A-1978022	C	A	196	168	221	185	5.263	0.0218	rs17192189	4	91132106	q22.1
SNP_A-1981657	T	T	337	31	390	18	5.265	0.0218	rs16886054	5	56021814	q11.2
SNP_A-1965272	T	T	391	5	414	0	5.26	0.0218	rs2081400	2	148431503	q22.3
SNP_A-1740387	C	C	328	22	363	45	5.261	0.0218	rs10492624	13	91359245	q31.3
SNP_A-1693286	T	T	342	54	331	81	5.265	0.0218	rs10509866	10	109579127	q25.1
SNP_A-1681258	T	T	392	4	367	13	5.26	0.0218	rs1993796	4	38541230	p14
SNP_A-1675894	A	A	329	61	354	40	5.261	0.0218	rs10509221	10	66471291	q21.3
SNP_A-1806100	G	G	273	67	282	104	5.258	0.0218	rs13179425	5	81870050	q14.2
SNP_A-1852045	T	T	328	26	269	39	5.26	0.0218	rs6745612	2	15701517	p24.3
SNP_A-2182768	T	T	326	42	388	28	5.265	0.0218	rs7555570	1	59732939	p32.1
SNP_A-2181097	A	A	339	9	382	2	5.261	0.0218	rs8049858	16	73480911	q22.3
SNP_A-2171585	C	C	278	20	336	10	5.264	0.0218	rs10207829	2	70340455	p13.3
SNP_A-2169211	C	C	357	61	375	39	5.264	0.0218	rs1832744	9	122258629	q33.2
SNP_A-2168652	C	C	281	87	306	62	5.259	0.0218	rs12112216	7	24284807	p15.3
SNP_A-2201453	C	C	367	3	403	13	5.259	0.0218	rs1262273	18	70224449	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2150434	A	A	355	21	375	9	5.264	0.0218	rs17007629	3	70778284	p13
SNP_A-2123811	A	A	334	34	395	21	5.258	0.0218	rs16932063	9	14605367	p22.3
SNP_A-2129590	T	T	273	109	242	138	5.266	0.0218	rs9405897	6	5997054	p25.1
SNP_A-2116541	C	C	212	154	269	139	5.259	0.0218	rs4432415	2	188371108	q32.1
SNP_A-2067883	C	C	272	96	268	136	5.259	0.0218	rs12357384	10	22909508	p12.2
SNP_A-2048383	T	T	344	70	367	47	5.265	0.0218	rs7924748	11	76128686	q13.5
SNP_A-2106237	G	G	410	0	387	5	5.262	0.0218	rs4790580	17	4013268	p13.2
SNP_A-2027230	G	G	337	75	359	51	5.262	0.0218	rs3888658	17	61903734	q24.2
SNP_A-2044055	G	G	315	53	330	86	5.264	0.0218	rs7919781	10	67520328	q21.3
SNP_A-2016878	C	C	385	33	356	52	5.262	0.0218	rs13050339	21	25244872	q21.2
SNP_A-2006930	C	C	357	11	387	27	5.259	0.0218	rs4474896	2	195141438	q32.3
SNP_A-2295261	A	G	224	192	223	189	5.263	0.0218	rs241256	1	4524885	p36.32
SNP_A-2285019	T	T	316	14	400	6	5.263	0.0218	rs2346069	3	89170752	p11.1
SNP_A-2228447	T	T	393	5	416	0	5.258	0.0218	rs6773258	3	139113445	q22.3
SNP_A-2239103	G	G	269	95	276	140	5.264	0.0218	rs4745488	9	75864590	q21.13
SNP_A-2263809	G	G	371	15	304	26	5.254	2.19E-02	rs1953220	14	89707470	q32.11
SNP_A-2000376	G	G	215	153	208	206	5.253	2.19E-02	rs2785663	1	154433831	q23.1
SNP_A-2004529	G	G	327	67	298	92	5.256	2.19E-02	rs2489037	10	102309908	q24.31
SNP_A-2125968	T	T	325	41	385	27	5.251	2.19E-02	---	6	125386212	q22.31
SNP_A-2137630	T	T	368	40	324	58	5.254	2.19E-02	rs10999893	10	73007164	q22.1
SNP_A-2134700	C	C	263	143	237	179	5.256	2.19E-02	rs10776899	9	134837125	q34.3
SNP_A-2146206	G	G	352	4	358	14	5.257	2.19E-02	rs17117934	1	98375168	p21.3
SNP_A-2153588	A	A	248	156	218	190	5.253	2.19E-02	rs7569069	2	12650172	p24.3
SNP_A-2222962	T	T	287	129	318	100	5.256	2.19E-02	rs867212	22	45383849	q13.31
SNP_A-2169638	G	G	371	11	407	3	5.254	2.19E-02	rs4906357	14	103213681	q32.33
SNP_A-2174501	T	T	365	3	401	13	5.254	2.19E-02	rs17141731	7	19423800	p21.1
SNP_A-2182512	C	C	329	51	317	77	5.253	2.19E-02	rs12653315	5	169403869	q35.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2177916	C	C	264	122	246	160	5.254	2.19E-02	rs6868681	5	19043387	p14.3
SNP_A-1793933	C	C	233	135	294	120	5.255	2.19E-02	rs392457	5	117002064	q23.1
SNP_A-1792567	C	C	325	45	380	30	5.253	2.19E-02	rs3861669	14	68558375	q24.1
SNP_A-1725304	A	A	236	128	214	164	5.252	2.19E-02	rs2826128	21	20588868	q21.1
SNP_A-1782700	T	T	321	31	345	57	5.254	2.19E-02	rs1814538	15	41547066	q15.3
SNP_A-1781857	T	T	260	106	316	88	5.252	2.19E-02	rs17477003	7	109957337	q31.1
SNP_A-1783562	C	C	284	50	277	77	5.251	2.19E-02	rs698235	3	22976396	p24.3
SNP_A-1949376	T	T	325	33	331	57	5.257	2.19E-02	rs10481377	8	5149620	p23.2
SNP_A-1940012	C	C	354	2	393	11	5.256	2.19E-02	rs11154199	6	124312571	q22.31
SNP_A-1946871	G	G	227	141	214	186	5.252	2.19E-02	rs324807	12	82432901	q21.31
SNP_A-1904529	G	G	356	8	386	22	5.256	2.19E-02	rs6588058	1	63865598	p31.3
SNP_A-1877395	C	C	275	111	236	136	5.25	2.19E-02	rs7093423	10	125853154	q26.13
SNP_A-1880165	G	G	256	102	324	88	5.243	2.20E-02	rs1997034	1	200850017	q32.1
SNP_A-1893684	G	G	341	15	398	6	5.243	2.20E-02	rs2923309	8	90232142	q21.3
SNP_A-1927627	G	G	223	145	278	128	5.244	2.20E-02	rs2333505	18	61993860	q22.1
SNP_A-1947956	A	A	281	29	288	52	5.244	2.20E-02	rs958492	5	94443714	q15
SNP_A-1691406	G	G	254	136	237	177	5.247	2.20E-02	rs723043	2	33516322	p22.3
SNP_A-1792006	C	C	382	24	366	42	5.246	2.20E-02	rs4263646	7	5579040	p22.1
SNP_A-1788403	C	C	338	82	361	57	5.248	2.20E-02	rs11576443	1	63324302	p31.3
SNP_A-1801850	G	G	285	127	255	159	5.242	2.20E-02	rs10248456	7	11789453	p21.3
SNP_A-1845199	T	T	277	71	347	57	5.243	2.20E-02	rs2412058	11	2597705	p15.5
SNP_A-1867170	G	G	249	105	251	151	5.247	2.20E-02	rs10007083	4	162629864	q32.2
SNP_A-1839995	A	A	332	12	337	27	5.246	2.20E-02	rs4941726	13	32453277	q13.1
SNP_A-2187807	A	A	245	111	305	95	5.245	2.20E-02	rs12501613	4	16966630	p15.32
SNP_A-2225244	G	G	355	47	317	67	5.248	2.20E-02	rs9917323	2	166871816	q24.3
SNP_A-2204816	C	C	197	125	253	111	5.248	2.20E-02	rs4804375	19	8866719	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2157294	A	A	283	85	347	69	5.245	2.20E-02	rs678583	11	126419401	q24.2
SNP_A-2164589	G	G	350	64	318	88	5.245	2.20E-02	rs31481	5	131425101	q23.3
SNP_A-2134950	A	G	213	201	235	181	5.246	2.20E-02	rs1254184	10	122580540	q26.12
SNP_A-2012276	C	C	277	129	247	161	5.244	2.20E-02	rs1783944	11	78106466	q14.1
SNP_A-2106605	G	G	246	84	252	126	5.242	2.20E-02	rs739566	16	19605038	p12.3
SNP_A-2053597	A	A	300	66	296	98	5.246	2.20E-02	rs9314136	5	94783440	q15
SNP_A-2062571	G	G	367	55	341	79	5.249	2.20E-02	rs17538716	5	147352648	q32
SNP_A-2259923	G	G	212	204	246	172	5.243	2.20E-02	rs12465802	2	136215080	q21.3
SNP_A-2243166	T	T	226	140	222	192	5.246	2.20E-02	rs1039533	1	238990513	q43
SNP_A-2289919	T	T	321	23	378	12	5.243	2.20E-02	rs17079387	13	33055583	q13.2
SNP_A-2302961	T	T	368	42	346	64	5.244	2.20E-02	rs11959796	5	17059405	p15.1
SNP_A-2311305	C	C	273	91	308	68	5.242	2.20E-02	rs3909658	4	13814167	p15.33
SNP_A-2314805	G	G	374	42	390	24	5.239	2.21E-02	rs3737656	1	200842317	q32.1
SNP_A-2303692	G	G	391	5	412	0	5.234	2.21E-02	rs7956191	12	14554682	p13.1
SNP_A-2251933	G	G	361	31	361	15	5.234	2.21E-02	rs12441549	15	99778547	q26.3
SNP_A-2239774	A	A	389	5	375	15	5.236	2.21E-02	rs17118701	14	83001154	q31.2
SNP_A-2237123	C	C	344	16	362	34	5.237	2.21E-02	rs9784550	4	66357177	q13.1
SNP_A-2261066	G	G	336	0	382	6	5.239	2.21E-02	rs4441406	2	142078300	q22.1
SNP_A-2056383	T	G	209	161	214	200	5.236	2.21E-02	rs2181212	1	154415324	q23.1
SNP_A-2096500	C	C	343	15	400	6	5.235	2.21E-02	rs7904193	10	25486251	p12.1
SNP_A-2077215	C	C	318	48	328	78	5.239	2.21E-02	rs4800573	18	20313668	q11.2
SNP_A-2080151	G	G	267	83	319	65	5.24	2.21E-02	rs6821770	4	7850876	p16.1
SNP_A-2009345	C	C	308	40	375	27	5.234	2.21E-02	rs7621839	3	178172583	q26.32
SNP_A-1996985	C	C	319	49	378	34	5.24	2.21E-02	rs17301434	9	80693084	q21.31
SNP_A-2041144	G	G	230	130	216	172	5.24	2.21E-02	rs6901152	6	143700705	q24.2
SNP_A-2027897	A	A	412	0	391	5	5.234	2.21E-02	rs7564880	2	217364467	q35

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2026198	C	C	402	0	381	5	5.241	2.21E-02	rs7625364	3	118179063	q13.31
SNP_A-2149661	A	A	391	5	412	0	5.234	2.21E-02	rs8038271	15	50531491	q21.2
SNP_A-2201999	T	T	253	95	313	79	5.234	2.21E-02	rs12978650	19	36067601	q12
SNP_A-2209969	A	A	339	23	318	40	5.236	2.21E-02	rs6494524	15	63622040	q22.31
SNP_A-2177003	A	A	335	33	355	59	5.24	2.21E-02	rs9556795	13	97152980	q32.2
SNP_A-1824697	T	T	271	39	372	30	5.238	2.21E-02	rs6990838	8	4449366	p23.2
SNP_A-1846988	A	A	256	112	312	94	5.241	2.21E-02	rs10221769	2	72390709	p13.2
SNP_A-1858434	G	G	312	44	374	30	5.241	2.21E-02	rs9635573	16	77129969	q23.1
SNP_A-1803790	G	G	325	5	336	16	5.241	2.21E-02	rs9318644	13	78982178	q31.1
SNP_A-1813427	T	T	331	9	372	2	5.239	2.21E-02	rs902396	9	84973922	q21.33
SNP_A-1808064	G	G	255	153	290	124	5.24	2.21E-02	rs10207133	2	119621883	q14.2
SNP_A-1809926	T	T	387	23	344	38	5.235	2.21E-02	rs16930701	10	74995314	q22.2
SNP_A-1739541	G	C	194	182	233	179	5.237	2.21E-02	rs1379023	2	41077498	p22.1
SNP_A-1962858	C	C	352	18	406	8	5.24	2.21E-02	rs2716734	2	39859372	p22.1
SNP_A-1930401	A	A	345	13	385	31	5.239	2.21E-02	rs11225755	11	102755298	q22.3
SNP_A-1904538	T	T	385	5	406	0	5.238	2.21E-02	rs7108580	11	36093458	p13
SNP_A-1910117	C	C	389	5	410	0	5.236	2.21E-02	rs7827845	8	56601376	q12.1
SNP_A-1912917	C	C	249	117	249	165	5.236	2.21E-02	rs957374	6	162613838	q26
SNP_A-1895419	G	G	296	42	324	74	5.236	2.21E-02	rs4705464	5	113021113	q22.2
SNP_A-1874080	G	G	422	0	401	5	5.229	2.22E-02	rs11917873	3	127410644	q21.2
SNP_A-1909788	C	C	395	5	416	0	5.232	2.22E-02	rs16950853	18	45449950	q21.1
SNP_A-1930829	C	C	273	135	310	108	5.228	2.22E-02	rs1498780	16	50168599	q12.1
SNP_A-1925832	C	C	360	10	385	25	5.23	2.22E-02	rs2288117	2	86216781	p11.2
SNP_A-1919706	A	A	269	89	331	73	5.229	2.22E-02	rs6546038	2	64028240	p14
SNP_A-1962818	T	T	217	131	292	124	5.232	2.22E-02	rs4670844	2	38400874	p22.2
SNP_A-1963927	G	G	312	38	330	66	5.227	2.22E-02	rs393580	2	79167689	p12
SNP_A-1982116	T	T	280	132	251	165	5.231	2.22E-02	rs10494916	1	205634254	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1662360	C	C	328	8	356	22	5.227	2.22E-02	rs3916105	12	57081630	q14.1
SNP_A-1849353	A	A	416	0	395	5	5.232	2.22E-02	rs16858356	1	229297240	q42.2
SNP_A-1849859	A	A	328	8	356	22	5.227	2.22E-02	rs2620951	10	117635217	q25.3
SNP_A-1870045	A	A	328	2	365	11	5.231	2.22E-02	rs503730	18	62357026	q22.1
SNP_A-1869155	G	G	338	28	398	16	5.23	2.22E-02	rs17645681	7	12972529	p21.3
SNP_A-1861623	G	G	307	51	366	36	5.229	2.22E-02	rs7333303	13	85757696	q31.1
SNP_A-2176827	A	A	359	13	358	28	5.232	2.22E-02	rs2209321	13	25386618	q12.13
SNP_A-2141529	T	T	416	0	395	5	5.232	2.22E-02	rs2878636	3	52851127	p21.1
SNP_A-2153746	T	T	316	92	283	119	5.229	2.22E-02	rs4338437	10	13227442	p13
SNP_A-2038100	C	C	418	0	397	5	5.231	2.22E-02	rs11214827	11	113405421	q23.2
SNP_A-2036234	G	G	275	83	272	120	5.23	2.22E-02	rs16846890	2	213287347	q34
SNP_A-1989919	G	G	256	104	261	151	5.232	2.22E-02	rs673982	7	51620356	p12.1
SNP_A-2081992	G	G	338	20	406	10	5.232	2.22E-02	rs2703076	13	49733839	q14.2
SNP_A-2058323	T	T	247	91	261	139	5.231	2.22E-02	rs741226	14	72445426	q24.2
SNP_A-2281441	C	C	316	34	388	22	5.231	2.22E-02	rs16942880	12	112483209	q24.13
SNP_A-2238345	A	A	231	97	252	152	5.227	2.22E-02	rs12454777	18	58425772	q21.33
SNP_A-2301645	G	G	418	0	397	5	5.231	2.22E-02	rs11879785	19	55528943	q13.33
SNP_A-2312358	T	T	200	168	256	154	5.234	2.22E-02	rs1541764	12	118063093	q24.23
SNP_A-2295650	C	C	349	7	395	1	5.231	2.22E-02	rs7198125	16	13496304	p13.12
SNP_A-2311407	A	A	261	161	226	192	5.219	0.0223	rs2133804	16	59674934	q21
SNP_A-2251096	G	G	361	31	345	51	5.22	0.0223	rs4760000	12	128731582	q24.33
SNP_A-2254543	T	T	384	4	361	13	5.219	0.0223	rs5758167	22	39722295	q13.2
SNP_A-2277354	G	G	223	145	214	194	5.22	0.0223	rs11187314	10	94930815	q23.33
SNP_A-2278753	G	G	376	18	373	35	5.222	0.0223	rs16886309	5	50141275	q11.1
SNP_A-2273714	A	A	342	18	394	8	5.221	0.0223	rs17117632	14	46315361	q21.3
SNP_A-2268859	T	T	347	5	385	17	5.225	0.0223	rs10003855	4	102332928	q24

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2049660	G	G	230	134	227	185	5.224	0.0223	rs1967880	9	69414492	q21.11
SNP_A-2046247	C	C	214	142	202	188	5.22	0.0223	rs3934154	5	88855273	q14.3
SNP_A-2032652	G	G	295	107	272	140	5.22	0.0223	rs9805634	13	52761605	q14.3
SNP_A-2153395	T	T	334	16	401	7	5.222	0.0223	rs7606525	2	19805683	p24.1
SNP_A-2122174	A	A	282	110	308	82	5.224	0.0223	rs2024648	22	23643798	q11.23
SNP_A-2112419	T	T	363	25	345	43	5.222	0.0223	rs2394022	10	65416007	q21.3
SNP_A-2224046	T	T	305	85	300	54	5.225	0.0223	rs12478509	2	121365036	q14.2
SNP_A-1843556	C	C	327	67	309	95	5.224	0.0223	rs10983427	9	116789586	q33.1
SNP_A-1655397	A	A	233	111	241	163	5.224	0.0223	rs3771361	2	199165327	q33.1
SNP_A-1676148	C	C	319	71	354	50	5.22	0.0223	rs3792446	3	7655588	p26.1
SNP_A-1732137	G	G	315	83	348	60	5.219	0.0223	rs720336	12	96259329	q23.1
SNP_A-1807950	A	A	367	17	381	35	5.221	0.0223	rs11175627	12	63691379	q14.3
SNP_A-1811910	G	G	308	26	375	15	5.223	0.0223	rs10892166	11	117111049	q23.3
SNP_A-1804971	G	G	317	25	382	14	5.224	0.0223	rs1337547	10	110533100	q25.1
SNP_A-1804724	A	A	238	184	268	150	5.221	0.0223	rs1347591	16	55426201	q13
SNP_A-1788010	A	A	328	52	280	70	5.221	0.0223	rs6483636	11	20042991	p15.1
SNP_A-1963498	A	A	243	67	263	109	5.22	0.0223	rs7597742	2	60187873	p16.1
SNP_A-1945634	G	G	259	111	259	157	5.221	0.0223	rs10756644	9	15066859	p22.3
SNP_A-1942278	A	A	325	27	356	52	5.225	0.0223	rs17648180	13	85173589	q31.1
SNP_A-1927949	A	A	324	46	338	76	5.22	0.0223	rs17072299	3	65054747	p14.1
SNP_A-1927565	A	A	215	149	276	136	5.222	0.0223	rs1519305	2	134647518	q21.2
SNP_A-1916518	G	G	267	73	330	58	5.224	0.0223	rs16922722	12	20227419	p12.2
SNP_A-1898798	G	G	342	18	394	8	5.221	0.0223	rs6781369	3	40022424	p22.1
SNP_A-1901388	G	G	220	150	280	136	5.211	0.0224	rs859369	1	172170833	q25.1
SNP_A-1891686	C	C	290	116	253	143	5.212	0.0224	rs10831360	11	94869496	q21
SNP_A-1875428	T	T	245	107	253	157	5.214	0.0224	rs663659	8	2801865	p23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1947790	G	A	218	180	204	178	5.214	0.0224	rs875153	1	56612291	p32.2
SNP_A-1969175	A	A	367	45	391	27	5.217	0.0224	rs2824432	21	17963050	q21.1
SNP_A-1984344	T	T	365	1	374	8	5.214	0.0224	rs13636636	5	161569355	q34
SNP_A-1794705	T	A	200	160	215	193	5.212	0.0224	rs309310	2	7108830	p25.1
SNP_A-1798900	C	C	225	125	284	110	5.212	0.0224	rs12122774	1	215876962	q41
SNP_A-1804174	C	C	354	12	412	4	5.216	0.0224	rs1037794	5	100699054	q21.1
SNP_A-1811881	T	T	249	157	280	126	5.212	0.0224	rs1471435	16	8942625	p13.2
SNP_A-1814253	C	C	265	83	338	70	5.213	0.0224	rs11601733	11	25729420	p14.3
SNP_A-1821624	T	T	312	74	290	102	5.213	0.0224	rs831425	12	102551059	q23.3
SNP_A-2217902	C	C	298	12	353	31	5.211	0.0224	rs11063830	12	5690894	p13.31
SNP_A-2198617	C	C	290	52	297	83	5.216	0.0224	rs1933565	1	205327147	q32.2
SNP_A-2118549	T	T	272	148	235	177	5.211	0.0224	rs4815451	20	2572033	p13
SNP_A-2125266	A	A	311	95	342	70	5.216	0.0224	rs7604766	2	29251428	p23.2
SNP_A-2154291	T	T	259	141	289	111	5.214	0.0224	rs329920	3	108859730	q13.12
SNP_A-2156754	C	C	327	27	381	15	5.212	0.0224	rs12957935	18	65836682	q22.2
SNP_A-2166418	T	T	204	160	264	148	5.211	0.0224	rs4823872	22	45426377	q13.31
SNP_A-2161528	T	T	384	30	397	15	5.212	0.0224	rs11860355	16	63054158	q21
SNP_A-2045021	G	A	219	201	233	185	5.216	0.0224	rs2843910	8	36112253	p12
SNP_A-1995546	C	C	307	53	322	86	5.213	0.0224	rs10752265	10	12519661	p13
SNP_A-2013833	A	A	253	105	301	85	5.218	0.0224	rs4339605	8	130181350	q24.21
SNP_A-2048410	G	G	279	89	330	70	5.217	0.0224	rs7327964	13	102784286	q33.1
SNP_A-2078458	C	C	299	77	293	111	5.211	0.0224	rs10877371	12	58639799	q14.1
SNP_A-2100568	G	G	222	140	218	192	5.217	0.0224	rs8012377	14	55261166	q22.3
SNP_A-2258087	G	G	325	97	290	124	5.214	0.0224	rs594445	18	32085187	q12.2
SNP_A-2250598	G	G	235	119	232	166	5.214	0.0224	rs12501198	4	139933099	q31.1
SNP_A-2244856	C	C	250	118	245	163	5.209	2.25E-02	rs12120142	1	80225868	p31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2245481	T	T	415	7	396	18	5.209	2.25E-02	rs3825869	15	70098664	q23
SNP_A-2268555	C	C	258	112	317	95	5.209	2.25E-02	rs4377918	8	82183255	q21.13
SNP_A-2268423	C	C	304	64	364	48	5.209	2.25E-02	rs764766	2	72685858	p13.2
SNP_A-2084902	G	G	395	5	414	0	5.207	2.25E-02	rs7833930	8	126001323	q24.13
SNP_A-2074807	A	A	304	50	370	36	5.208	2.25E-02	rs17071145	4	182638066	q34.3
SNP_A-2042387	T	T	416	0	397	5	5.206	2.25E-02	rs10890315	1	45031538	p34.1
SNP_A-2026252	T	T	208	146	205	201	5.206	2.25E-02	rs7918732	10	39034338	p11.1
SNP_A-2156326	A	A	312	22	361	11	5.204	2.25E-02	rs16902840	8	91159997	q21.3
SNP_A-2131831	G	G	346	18	398	8	5.205	2.25E-02	rs12485289	3	85100090	p12.1
SNP_A-2131952	A	A	342	46	286	62	5.205	2.25E-02	rs1997773	6	1060897	p25.3
SNP_A-2116628	A	A	271	149	234	178	5.206	2.25E-02	rs2244468	9	127294833	q33.3
SNP_A-2189235	T	T	412	0	393	5	5.208	2.25E-02	rs872431	10	16345087	p13
SNP_A-2184771	T	T	307	27	395	17	5.205	2.25E-02	rs7039190	9	134446258	q34.2
SNP_A-2178175	A	A	360	2	362	10	5.204	2.25E-02	---	10	19817075	p12.31
SNP_A-2205074	C	C	412	0	393	5	5.208	2.25E-02	rs6093562	20	40102950	q12
SNP_A-1815745	A	A	321	23	318	42	5.207	2.25E-02	rs17243943	11	27094036	p14.2
SNP_A-1841122	A	A	361	7	407	1	5.207	2.25E-02	rs17002607	4	78650500	q21.1
SNP_A-1840041	T	T	204	178	234	146	5.21	2.25E-02	rs6501584	17	68439421	q25.1
SNP_A-1838879	A	A	354	66	371	43	5.209	2.25E-02	rs7717311	5	180435974	q35.3
SNP_A-1838409	A	A	416	0	397	5	5.206	2.25E-02	rs1455607	14	97406870	q32.2
SNP_A-1866115	A	G	185	139	168	156	5.206	2.25E-02	rs10406151	19	57372222	q13.41
SNP_A-1869764	C	C	321	45	385	31	5.205	2.25E-02	rs276971	16	84786547	q24.1
SNP_A-1866810	G	G	249	121	246	168	5.209	2.25E-02	rs1479427	4	91233417	q22.1
SNP_A-1858782	A	A	298	26	301	47	5.206	2.25E-02	rs16859660	2	172315395	q31.1
SNP_A-1858379	C	C	285	121	253	151	5.207	2.25E-02	rs7033100	9	80087448	q21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800638	G	G	370	32	393	17	5.207	2.25E-02	rs10874607	1	102578342	p21.1
SNP_A-1799855	C	C	288	130	316	100	5.206	2.25E-02	rs1390762	16	49452675	q12.1
SNP_A-1792710	G	G	338	84	307	111	5.209	2.25E-02	rs387642	6	29753613	p22.1
SNP_A-1955826	T	T	332	40	292	58	5.205	2.25E-02	---	16	18700411	p12.3
SNP_A-1886617	C	C	311	31	375	19	5.203	2.25E-02	rs17595308	18	12351946	p11.21
SNP_A-1918870	A	A	257	111	257	157	5.208	2.25E-02	rs4843460	16	85382973	q24.1
SNP_A-1906341	A	A	217	169	253	141	5.205	2.25E-02	rs5745005	12	131821335	q24.33
SNP_A-1917539	T	T	379	25	361	43	5.203	2.26E-02	rs12123337	1	19607717	p36.13
SNP_A-1878540	C	C	290	74	286	108	5.2	2.26E-02	rs17100416	5	142955521	q31.3
SNP_A-1878047	G	G	328	16	393	7	5.196	2.26E-02	rs7092487	10	79479066	q22.3
SNP_A-1960415	T	T	351	15	377	33	5.2	2.26E-02	rs16994148	4	37839388	p14
SNP_A-1978031	A	A	224	140	219	191	5.199	2.26E-02	---	4	91383028	q22.1
SNP_A-1975393	T	T	328	28	290	44	5.196	2.26E-02	rs4429642	3	176811115	q26.31
SNP_A-1806158	G	G	200	150	256	136	5.202	2.26E-02	---	4	146342444	q31.21
SNP_A-1813998	C	C	358	64	364	40	5.199	2.26E-02	rs12601694	17	4921105	p13.2
SNP_A-1849403	C	C	312	110	279	139	5.201	2.26E-02	rs10123735	9	107226795	q31.2
SNP_A-1860463	C	C	304	62	315	97	5.198	2.26E-02	rs1702292	1	98236981	p21.3
SNP_A-2206719	G	G	272	34	347	23	5.197	2.26E-02	rs3810272	19	55433055	q13.33
SNP_A-2181083	C	T	208	162	215	199	5.197	2.26E-02	rs7731949	5	52223785	q11.2
SNP_A-2170253	A	A	239	107	306	94	5.196	2.26E-02	rs1029392	7	95242608	q21.3
SNP_A-2185019	T	T	340	20	349	39	5.195	2.26E-02	rs13399063	2	85953791	p11.2
SNP_A-2199513	C	C	223	139	217	189	5.2	2.26E-02	rs9687608	5	85177426	q14.3
SNP_A-2199641	C	C	253	139	230	176	5.197	2.26E-02	rs4672345	2	53466790	p16.2
SNP_A-2116170	C	C	327	43	342	72	5.196	2.26E-02	rs16876782	6	83276260	q14.1
SNP_A-2163920	T	T	353	49	385	31	5.199	2.26E-02	rs2694388	12	104481020	q23.3
SNP_A-2150899	C	C	330	40	388	26	5.202	2.26E-02	rs2296772	9	69970801	q21.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2021926	C	C	323	25	362	50	5.201	2.26E-02	rs11066958	12	113038177	q24.21
SNP_A-2031591	T	T	241	177	268	142	5.196	2.26E-02	rs1423971	16	57935351	q21
SNP_A-2037764	G	G	372	34	343	53	5.202	2.26E-02	rs8064845	17	52929662	q23.2
SNP_A-2039066	T	T	268	76	262	110	5.196	2.26E-02	rs4938535	11	110780460	q23.1
SNP_A-2012756	A	A	327	43	342	72	5.196	2.26E-02	rs7809688	7	103098529	q22.1
SNP_A-2010288	G	G	300	52	350	36	5.2	2.26E-02	rs7438004	4	159675648	q32.1
SNP_A-2052025	T	T	268	74	346	62	5.2	2.26E-02	rs6872579	5	139756023	q31.2
SNP_A-2237524	C	C	198	136	267	129	5.195	2.26E-02	rs6456218	6	170674075	q27
SNP_A-2236839	T	C	202	152	202	192	5.192	2.27E-02	rs40437	3	136133630	q22.1
SNP_A-2239833	G	G	232	134	228	184	5.195	2.27E-02	rs1075044	17	30047820	q12
SNP_A-2266860	G	G	269	87	326	70	5.188	2.27E-02	rs1426707	2	64530898	p14
SNP_A-2273278	T	T	283	87	288	128	5.188	2.27E-02	rs1900184	5	65118756	q12.3
SNP_A-2274715	G	G	281	81	280	118	5.188	2.27E-02	rs2134634	3	193798161	q28
SNP_A-2068871	C	C	299	63	364	48	5.191	2.27E-02	rs12538489	7	54874045	p11.2
SNP_A-2084783	A	A	303	53	326	88	5.19	2.27E-02	rs1574384	2	142214712	q22.1
SNP_A-2100168	A	A	248	104	317	91	5.195	2.27E-02	rs4468943	3	24999173	p24.2
SNP_A-2094257	A	A	332	34	350	60	5.188	2.27E-02	rs4840139	6	96465827	q16.1
SNP_A-2030242	C	C	217	145	208	194	5.193	2.27E-02	rs4971145	1	154422638	q23.1
SNP_A-2149788	C	C	204	142	272	134	5.192	2.27E-02	rs513870	6	11616840	p24.2
SNP_A-2114148	C	C	222	118	226	170	5.194	2.27E-02	rs17275182	4	184329209	q35.1
SNP_A-2198301	A	A	346	24	338	10	5.189	2.27E-02	rs9676843	19	44406471	q13.2
SNP_A-1844635	T	T	357	11	389	27	5.19	2.27E-02	---	2	178482332	q31.2
SNP_A-1856323	T	T	349	21	374	42	5.19	2.27E-02	rs971804	15	83345385	q25.3
SNP_A-1854770	T	C	203	153	209	199	5.188	2.27E-02	rs12499326	4	118019307	q26
SNP_A-1843534	T	T	284	136	311	105	5.194	2.27E-02	rs6965638	7	135820311	q33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802986	T	T	354	36	361	19	5.194	2.27E-02	rs16953850	16	53269805	q12.2
SNP_A-1985651	A	A	357	63	377	41	5.194	2.27E-02	rs2116264	6	33092766	p21.32
SNP_A-1961741	C	C	367	29	332	46	5.19	2.27E-02	rs1865956	19	61116501	q13.43
SNP_A-1956082	A	A	300	68	311	105	5.192	2.27E-02	rs11639486	15	94378745	q26.2
SNP_A-1897492	G	G	275	85	276	124	5.188	2.27E-02	rs17656058	2	70950220	p13.3
SNP_A-1901074	T	T	299	13	322	30	5.182	2.28E-02	rs17019285	1	107777486	p13.3
SNP_A-1911423	G	G	377	43	395	25	5.184	2.28E-02	rs8083132	18	19281033	q11.2
SNP_A-1934491	A	A	295	99	315	71	5.186	2.28E-02	rs1546326	8	31764724	p12
SNP_A-1962017	G	G	286	40	260	60	5.183	2.28E-02	rs798425	2	7933791	p25.1
SNP_A-1679142	T	T	387	3	392	12	5.187	2.28E-02	rs4953864	2	133901769	q21.2
SNP_A-1837086	T	T	377	7	360	18	5.185	2.28E-02	rs7557758	2	44651267	p21
SNP_A-1834641	T	T	276	114	237	139	5.181	2.28E-02	rs10279558	7	114456899	q31.2
SNP_A-1819441	C	C	380	24	346	40	5.185	2.28E-02	rs7944983	11	1552822	p15.5
SNP_A-1823089	A	A	387	5	404	0	5.186	2.28E-02	rs592526	11	93179168	q21
SNP_A-2197846	C	C	292	58	353	43	5.18	2.28E-02	rs7229482	18	62667595	q22.1
SNP_A-2194559	G	G	267	101	326	84	5.18	2.28E-02	rs1465099	16	77102849	q23.1
SNP_A-2181062	C	C	259	137	229	169	5.186	2.28E-02	rs4149570	12	6321851	p13.31
SNP_A-2177832	G	G	305	61	363	45	5.187	2.28E-02	rs2729706	2	160481210	q24.2
SNP_A-2209746	A	A	385	5	402	0	5.187	2.28E-02	rs2636889	9	114172664	q32
SNP_A-2128888	C	C	401	13	370	26	5.182	2.28E-02	rs7788297	7	29089527	p15.1
SNP_A-2128164	A	A	211	145	203	195	5.184	2.28E-02	rs10897704	11	80289783	q14.1
SNP_A-2029216	T	T	381	7	364	18	5.181	2.28E-02	rs13380712	16	25508683	p12.1
SNP_A-2036440	C	C	246	174	210	204	5.18	2.28E-02	rs2728928	3	9404959	p25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2008870	A	A	215	153	203	201	5.185	2.28E-02	rs4856219	3	82648593	p12.2
SNP_A-2003049	C	C	262	156	289	123	5.183	2.28E-02	rs7980016	12	114412048	q24.21
SNP_A-2003651	C	C	298	66	311	103	5.186	2.28E-02	rs1890223	14	29222157	q12
SNP_A-2087355	A	A	307	57	370	42	5.186	2.28E-02	rs2972192	5	72675502	q13.2
SNP_A-2063981	A	A	347	21	323	37	5.186	2.28E-02	---	11	32549131	p13
SNP_A-2231223	A	A	418	2	375	9	5.185	2.28E-02	rs1017441	1	118012709	p12
SNP_A-2244477	A	A	262	88	306	68	5.183	2.28E-02	rs10023055	4	65584543	q13.1
SNP_A-2304097	C	C	416	0	399	5	5.18	2.28E-02	rs4837697	9	119891914	q33.2
SNP_A-2288919	G	G	383	5	371	15	5.186	2.28E-02	rs11034248	11	37557347	p12
SNP_A-2292175	A	A	414	0	397	5	5.181	2.28E-02	rs3736449	16	77092401	q23.1
SNP_A-2291286	G	G	408	10	380	22	5.185	2.28E-02	rs13394891	2	139837302	q22.1
SNP_A-2290751	C	C	352	12	408	4	5.177	0.0229	rs12586849	14	83578368	q31.3
SNP_A-2309346	T	T	328	74	306	102	5.174	0.0229	rs253945	5	131358057	q23.3
SNP_A-2240564	A	A	338	12	392	4	5.178	0.0229	rs1934386	1	49036348	p33
SNP_A-2054316	C	C	420	0	403	5	5.178	0.0229	rs17732817	18	39398195	q12.3
SNP_A-2090259	A	A	284	130	303	97	5.173	0.0229	rs2730078	15	82112433	q25.2
SNP_A-2090401	A	A	304	66	311	101	5.174	0.0229	rs17803447	7	43364100	p13
SNP_A-2091989	G	G	310	16	371	7	5.173	0.0229	rs7223550	17	59532011	q23.3
SNP_A-2102819	A	A	334	28	392	16	5.177	0.0229	rs6826451	4	67769958	q13.2
SNP_A-2004759	C	C	299	107	331	81	5.177	0.0229	rs8055989	16	57603273	q21
SNP_A-1991415	G	G	292	120	319	91	5.174	0.0229	rs10262754	7	135646908	q33
SNP_A-2025471	C	C	283	121	310	92	5.173	0.0229	rs1426928	11	87535538	q14.2
SNP_A-2204702	C	C	403	5	420	0	5.178	0.0229	rs672511	1	24382141	p36.11
SNP_A-2222748	A	A	338	14	377	5	5.173	0.0229	rs7291177	12	10102308	p13.2
SNP_A-1822766	G	G	293	63	299	97	5.173	0.0229	rs1782812	1	98259523	p21.3
SNP_A-1821362	C	C	328	42	340	70	5.178	0.0229	rs10892118	11	98048428	q22.1
SNP_A-1862924	C	C	294	28	346	16	5.176	0.0229	rs17820776	17	51465847	q23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864176	A	A	261	109	323	93	5.175	0.0229	rs2689249	16	52639871	q12.2
SNP_A-1872850	A	A	237	133	298	118	5.177	0.0229	rs554393	13	101633794	q33.1
SNP_A-1871231	T	T	239	145	277	119	5.176	0.0229	rs434952	8	55254551	q11.23
SNP_A-1701963	G	G	394	2	398	10	5.176	0.0229	rs10521070	9	102536216	q31.1
SNP_A-1808917	C	C	344	76	317	103	5.176	0.0229	rs1202837	1	58077417	p32.2
SNP_A-1787169	A	A	299	53	282	78	5.179	0.0229	rs11232993	11	81521808	q14.1
SNP_A-1789823	A	A	293	75	350	58	5.178	0.0229	rs1035210	10	101335409	q24.2
SNP_A-1985725	C	C	230	136	228	188	5.179	0.0229	rs4302660	6	38953337	p21.2
SNP_A-1980393	C	C	331	37	348	64	5.178	0.0229	rs26877	5	4955915	p15.32
SNP_A-1935031	T	T	370	46	344	68	5.173	0.0229	rs7601880	2	222820660	q36.1
SNP_A-1945471	C	C	179	161	219	139	5.173	0.0229	rs9536792	13	54119999	q14.3
SNP_A-1955922	C	C	329	75	287	97	5.173	0.0229	rs2468699	8	140612740	q24.3
SNP_A-1961263	G	G	296	66	349	49	5.174	0.0229	rs9849881	3	142048828	q23
SNP_A-1950087	G	T	198	170	225	189	5.18	0.0229	rs11073381	15	93066016	q26.2
SNP_A-1912499	G	G	298	104	248	124	5.178	0.0229	rs9852954	3	134394290	q22.1
SNP_A-1919503	G	G	376	10	350	22	5.174	0.0229	rs7581085	2	151404720	q23.3
SNP_A-1897151	T	T	422	0	405	5	5.177	0.0229	rs17115375	15	23037710	q11.2
SNP_A-1878670	C	C	403	5	420	0	5.178	0.0229	rs10734450	11	38176187	p12
SNP_A-1895701	C	T	190	178	235	181	5.166	0.023	rs6850503	4	182183384	q34.3
SNP_A-1913942	A	A	253	107	255	153	5.167	0.023	rs2514631	8	105378279	q22.3
SNP_A-1906503	G	G	315	53	376	38	5.169	0.023	rs7171087	15	77761013	q25.1
SNP_A-1943230	T	T	340	28	355	51	5.167	0.023	rs17699096	13	96306889	q32.1
SNP_A-1935348	T	T	190	176	231	153	5.172	0.023	rs1999671	13	21766533	q12.11
SNP_A-1789159	G	G	362	32	366	16	5.171	0.023	rs995008	20	2286811	p13
SNP_A-1790008	C	C	384	4	363	13	5.168	0.023	rs16846383	1	170454765	q25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801618	C	C	282	40	343	27	5.171	0.023	rs1651088	16	16600001	p13.11
SNP_A-1731711	C	C	322	66	309	95	5.17	0.023	rs10512632	5	35310741	p13.2
SNP_A-1744593	T	T	364	4	374	14	5.166	0.023	rs10495509	2	4404110	p25.2
SNP_A-1862875	A	A	323	87	292	114	5.17	0.023	rs13264899	8	14240144	p22
SNP_A-1850974	C	C	238	122	299	107	5.168	0.023	rs549835	11	121505789	q24.1
SNP_A-1834353	C	C	197	149	259	139	5.168	0.023	rs11770440	7	151139807	q36.1
SNP_A-1831409	T	T	315	45	326	74	5.165	0.023	rs17376207	5	93571280	q15
SNP_A-2225971	C	C	264	88	274	132	5.165	0.023	rs6562058	13	59210620	q21.2
SNP_A-2206272	G	A	196	170	225	187	5.168	0.023	rs3915641	17	65862853	q24.3
SNP_A-2212009	G	G	195	175	248	160	5.169	0.023	rs1868056	4	181499399	q34.3
SNP_A-2178719	C	C	248	164	278	132	5.166	0.023	rs10850880	12	116546365	q24.22
SNP_A-2131894	G	G	345	5	385	17	5.166	0.023	rs462312	3	1598884	p26.3
SNP_A-2004616	G	G	288	120	321	93	5.167	0.023	rs8050676	16	22723494	p12.1
SNP_A-2018903	T	T	192	188	213	149	5.169	0.023	rs2251953	21	36988448	q22.13
SNP_A-2054007	A	A	245	83	301	67	5.168	0.023	rs1000003	3	99825597	q12.1
SNP_A-2048772	G	C	168	156	209	159	5.167	0.023	rs2439335	8	73752172	q13.3
SNP_A-2071428	C	C	346	48	354	28	5.17	0.023	rs9867284	3	32574240	p23
SNP_A-2071816	C	C	233	133	259	103	5.166	0.023	rs2384045	10	54205868	q21.1
SNP_A-2260492	T	T	328	46	289	65	5.172	0.023	rs6794153	3	56781243	p14.3
SNP_A-2261836	T	T	317	47	372	32	5.169	0.023	rs11811891	1	204702715	q32.2
SNP_A-2261797	T	T	342	66	299	87	5.161	2.31E-02	rs4798785	18	9190112	p11.22
SNP_A-2266832	A	A	222	146	282	132	5.16	2.31E-02	rs1024542	7	68348235	q11.22
SNP_A-2240647	T	T	393	21	411	9	5.16	2.31E-02	rs12572911	10	6489968	p15.1
SNP_A-2244687	A	A	279	87	284	128	5.161	2.31E-02	rs6706188	2	100198488	q11.2
SNP_A-2246378	A	A	310	112	277	141	5.16	2.31E-02	rs11107466	12	93127509	q22
SNP_A-2255809	T	T	398	0	383	5	5.162	2.31E-02	rs17167019	7	13142943	p21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2076451	A	A	277	77	337	61	5.161	2.31E-02	rs16930902	11	37915551	p12
SNP_A-2058622	G	G	193	175	247	161	5.162	2.31E-02	rs8044883	16	75915465	q23.1
SNP_A-2106172	A	A	216	136	277	123	5.157	2.31E-02	rs7937198	11	61525549	q12.3
SNP_A-2018922	C	C	396	6	368	16	5.162	2.31E-02	rs16994521	21	37129880	q22.13
SNP_A-1994725	A	A	228	110	284	94	5.161	2.31E-02	rs7823309	8	115055004	q23.3
SNP_A-1995086	G	G	318	8	404	2	5.162	2.31E-02	rs11256708	10	10694800	p14
SNP_A-2039550	G	G	385	5	400	0	5.161	2.31E-02	---	2	33660796	p22.3
SNP_A-2042622	C	C	393	21	411	9	5.16	2.31E-02	rs11067911	12	108601249	q24.11
SNP_A-2040880	C	C	347	65	369	43	5.157	2.31E-02	rs11258040	10	12953760	p13
SNP_A-2137620	C	C	348	22	369	43	5.159	2.31E-02	rs17082483	5	92057975	q15
SNP_A-2110339	G	G	270	90	259	125	5.158	2.31E-02	rs4612156	6	20990820	p22.3
SNP_A-2110432	T	T	278	84	322	64	5.165	2.31E-02	rs1952267	14	28959450	q12
SNP_A-2122537	G	G	409	3	377	11	5.159	2.31E-02	rs4749861	10	5715581	p15.1
SNP_A-2119684	C	C	220	132	206	174	5.161	2.31E-02	rs4832279	2	86506739	p11.2
SNP_A-2143207	C	C	342	12	396	4	5.164	2.31E-02	rs7927273	11	25638236	p14.3
SNP_A-2142302	A	A	211	201	240	166	5.159	2.31E-02	rs1909918	4	14148945	p15.33
SNP_A-2159519	T	T	346	8	378	22	5.161	2.31E-02	rs9573626	13	75179208	q22.2
SNP_A-1830425	C	C	237	83	307	71	5.159	2.31E-02	rs3099820	2	74325406	p13.1
SNP_A-1821150	G	G	311	59	323	93	5.158	2.31E-02	rs1732290	12	51059283	q13.13
SNP_A-1819127	G	G	248	118	308	102	5.16	2.31E-02	rs1241672	13	67736281	q21.33
SNP_A-1828350	C	C	314	12	364	4	5.164	2.31E-02	rs9288782	3	96033869	q11.2
SNP_A-1851174	A	A	239	115	300	100	5.163	2.31E-02	rs12699526	7	13357318	p21.2
SNP_A-1870417	G	G	383	5	344	14	5.157	2.31E-02	rs16902812	5	36237068	p13.2
SNP_A-1669501	A	A	387	5	402	0	5.16	2.31E-02	rs2921752	8	117876101	q24.11
SNP_A-1801358	T	T	364	2	368	10	5.163	2.31E-02	rs16832878	1	232311983	q42.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1958184	T	T	408	2	367	9	5.162	2.31E-02	rs16857089	2	170311679	q31.1
SNP_A-1967324	A	G	212	192	220	176	5.164	2.31E-02	rs4845390	1	151539447	q22
SNP_A-1905402	G	G	411	9	393	21	5.16	2.31E-02	rs1173586	1	53883233	p32.3
SNP_A-1901324	C	C	200	166	257	153	5.161	2.31E-02	rs10067069	5	107448775	q21.3
SNP_A-1898825	A	A	386	30	365	49	5.152	2.32E-02	rs13335962	16	9469503	p13.2
SNP_A-1899505	A	A	284	66	347	51	5.154	2.32E-02	rs17425708	5	38435479	p13.2
SNP_A-1923505	A	A	248	174	212	204	5.156	2.32E-02	rs11764592	7	41546026	p14.1
SNP_A-1929358	A	A	295	75	352	58	5.157	2.32E-02	rs13252799	8	32499495	p12
SNP_A-1975703	G	G	226	192	256	158	5.151	2.32E-02	rs234658	1	181583039	q25.3
SNP_A-1972956	G	G	318	52	332	84	5.156	2.32E-02	rs17652804	3	63612465	p14.2
SNP_A-1976717	C	C	303	59	366	44	5.153	2.32E-02	rs2337717	4	33045446	p15.1
SNP_A-1979214	C	C	343	3	381	13	5.153	2.32E-02	rs1874575	4	143413933	q31.21
SNP_A-1986659	A	A	351	19	377	39	5.151	2.32E-02	rs1355826	6	83518421	q14.1
SNP_A-1933316	G	G	275	93	318	72	5.157	2.32E-02	rs17535661	4	43133217	p13
SNP_A-1803255	C	C	403	5	418	0	5.154	2.32E-02	rs1463498	1	230465278	q42.2
SNP_A-1813083	G	G	287	53	351	39	5.15	2.32E-02	rs4954231	2	135850246	q21.3
SNP_A-1787912	T	T	276	36	318	22	5.156	2.32E-02	rs2806094	9	117887466	q33.1
SNP_A-1799468	T	T	291	79	295	117	5.154	2.32E-02	rs17422897	1	96342220	p21.3
SNP_A-1646424	T	T	304	46	375	33	5.156	2.32E-02	rs10518128	4	76171763	q13.3
SNP_A-1718835	C	C	276	124	253	159	5.152	2.32E-02	rs241557	14	54540461	q22.3
SNP_A-1860823	G	G	374	16	402	6	5.152	2.32E-02	rs3794284	12	2667332	p13.33
SNP_A-1853139	A	A	275	73	323	55	5.153	2.32E-02	rs4554493	8	49532144	q11.21
SNP_A-1817523	G	G	314	48	334	80	5.156	2.32E-02	rs6661049	1	230241294	q42.2
SNP_A-1831399	G	G	374	16	402	6	5.152	2.32E-02	rs17592094	13	39989489	q14.11
SNP_A-1838106	G	G	223	193	253	159	5.156	2.32E-02	rs562331	3	53484356	p21.1
SNP_A-1841529	C	C	274	64	278	98	5.157	2.32E-02	rs6024728	20	54252413	q13.31
SNP_A-1842265	T	T	401	5	416	0	5.155	2.32E-02	rs4849898	2	120977703	q14.2
SNP_A-2146501	C	C	300	60	349	43	5.153	2.32E-02	rs3845697	2	180624059	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2119036	T	T	373	13	394	4	5.157	2.32E-02	rs7610310	3	32858193	p23
SNP_A-2107819	C	C	316	82	337	57	5.152	2.32E-02	rs6687538	1	212594533	q41
SNP_A-2123509	G	G	251	107	317	93	5.152	2.32E-02	rs1111988	18	50796990	q21.2
SNP_A-2181704	A	A	412	0	397	5	5.156	2.32E-02	rs1599764	3	105715593	q13.11
SNP_A-2174256	G	G	274	44	319	29	5.156	2.32E-02	rs1504626	15	67486824	q23
SNP_A-2210862	G	G	416	0	401	5	5.155	2.32E-02	rs6795721	3	120171301	q13.32
SNP_A-2213554	C	C	353	17	393	7	5.15	2.32E-02	rs9495092	6	138865213	q23.3
SNP_A-2035349	A	A	353	7	395	1	5.156	2.32E-02	rs9316259	13	46641519	q14.2
SNP_A-2023566	A	A	391	7	351	17	5.156	2.32E-02	rs16879571	8	110524181	q23.1
SNP_A-2029805	G	G	278	82	274	118	5.157	2.32E-02	rs12180820	6	28424457	p22.1
SNP_A-1994162	A	A	337	15	390	6	5.151	2.32E-02	rs16880925	8	89390383	q21.3
SNP_A-2000947	T	T	401	5	416	0	5.155	2.32E-02	rs4747542	10	7690834	p14
SNP_A-2007989	A	A	335	19	339	37	5.151	2.32E-02	rs2829650	21	25523641	q21.2
SNP_A-2009102	A	A	342	76	312	102	5.155	2.32E-02	rs7789237	3	130119659	q21.3
SNP_A-2085466	G	G	292	70	352	54	5.151	2.32E-02	rs10937520	3	193190536	q28
SNP_A-2255576	G	G	410	8	381	19	5.151	2.32E-02	rs7585796	2	69146562	p13.3
SNP_A-2245701	A	A	262	90	322	74	5.155	2.32E-02	rs4907674	13	111900674	q34
SNP_A-2231020	C	C	416	0	401	5	5.155	2.32E-02	rs4363465	1	49052758	p33
SNP_A-2231344	G	G	331	81	357	57	5.152	2.32E-02	rs9610404	22	34858442	q12.3
SNP_A-2263403	A	A	403	5	418	0	5.154	2.32E-02	rs7968925	12	94302873	q22
SNP_A-2308533	G	G	410	0	395	5	5.157	2.32E-02	---	15	94320357	q26.2
SNP_A-2287975	A	A	277	71	281	107	5.151	2.32E-02	rs134932	22	25749919	q12.1
SNP_A-2289730	C	C	240	146	219	185	5.148	2.33E-02	rs4955522	3	136154221	q22.1
SNP_A-2304423	T	T	329	11	374	28	5.146	2.33E-02	rs154601	5	115855844	q23.1
SNP_A-2276284	C	G	190	162	212	178	5.143	2.33E-02	rs3826803	19	10744126	p13.2
SNP_A-2231194	C	C	340	28	398	16	5.143	2.33E-02	rs1373891	15	27395970	q13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2229355	A	A	322	36	383	23	5.147	2.33E-02	rs12586046	13	37234234	q13.3
SNP_A-2236949	C	C	228	142	287	127	5.142	2.33E-02	rs6468946	8	105760573	q22.3
SNP_A-2079385	G	G	318	42	365	27	5.143	2.33E-02	rs931809	5	31945420	p13.3
SNP_A-2106228	G	G	246	92	252	136	5.144	2.33E-02	rs16863336	3	152560616	q25.1
SNP_A-2059607	C	T	225	165	184	180	5.144	2.33E-02	rs5746497	22	16778183	q11.21
SNP_A-2071900	G	G	339	27	393	15	5.148	2.33E-02	rs12260518	10	95152767	q23.33
SNP_A-2012719	A	A	252	150	226	186	5.149	2.33E-02	rs4729053	7	92249802	q21.2
SNP_A-1994267	A	A	266	98	270	142	5.147	2.33E-02	rs10504929	8	94680796	q22.1
SNP_A-2222590	T	T	341	5	331	15	5.149	2.33E-02	rs16854531	3	171100582	q26.2
SNP_A-2182406	C	C	311	87	331	61	5.145	2.33E-02	rs2040307	11	83163162	q14.1
SNP_A-2178423	C	C	374	48	346	70	5.148	2.33E-02	rs17509502	3	10580733	p25.3
SNP_A-2190064	C	C	262	160	225	189	5.145	2.33E-02	rs237895	3	8782423	p25.3
SNP_A-2121802	C	C	263	89	315	71	5.148	2.33E-02	rs11657944	17	37243883	q21.2
SNP_A-2140537	A	A	346	16	372	6	5.143	2.33E-02	---	2	136184843	q21.3
SNP_A-2153646	T	T	279	121	255	155	5.144	2.33E-02	rs10072554	5	19042374	p14.3
SNP_A-1833312	T	T	202	142	187	185	5.146	2.33E-02	rs1837133	2	20004994	p24.1
SNP_A-1833500	G	G	281	117	234	138	5.147	2.33E-02	rs7527940	1	202025352	q32.1
SNP_A-1827426	T	T	323	39	377	25	5.148	2.33E-02	rs7569572	2	178847435	q31.2
SNP_A-1755422	C	C	363	13	379	29	5.143	2.33E-02	rs10504903	8	92325900	q21.3
SNP_A-1681452	C	C	355	43	384	26	5.149	2.33E-02	rs1109233	10	100264348	q24.2
SNP_A-1689861	A	A	311	37	338	66	5.147	2.33E-02	rs10484414	6	67123473	q12
SNP_A-1793751	G	G	201	169	258	156	5.145	2.33E-02	rs1265216	6	4464369	p25.1
SNP_A-1813102	G	G	228	132	287	117	5.146	2.33E-02	rs563170	3	80832607	p12.2
SNP_A-1814149	G	G	228	134	287	119	5.145	2.33E-02	rs10905411	10	8678685	p14
SNP_A-1805895	C	C	315	49	381	35	5.148	2.33E-02	rs11918377	3	185756411	q27.1
SNP_A-1934812	A	A	215	141	212	194	5.147	2.33E-02	rs6081840	20	19956581	p11.23
SNP_A-1938764	T	T	332	10	325	23	5.144	2.33E-02	---	3	66801488	p14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960753	C	C	239	123	300	108	5.148	2.33E-02	rs10850526	12	114397478	q24.21
SNP_A-1951454	G	G	353	15	408	6	5.144	2.33E-02	rs17082876	5	92415539	q15
SNP_A-1953181	C	C	295	25	354	14	5.142	2.33E-02	rs3218035	19	34997289	q12
SNP_A-1985498	T	T	253	109	256	156	5.145	2.33E-02	rs8180584	6	25353914	p22.2
SNP_A-1921427	G	G	355	11	372	26	5.147	2.33E-02	rs11594245	10	21693040	p12.31
SNP_A-1918064	C	C	292	76	354	60	5.145	2.33E-02	rs4903677	14	77494821	q24.3
SNP_A-1887322	G	G	305	49	315	29	5.147	2.33E-02	rs7254845	19	715046	p13.3
SNP_A-1883606	T	T	228	128	266	104	5.138	2.34E-02	rs2687984	4	39251987	p14
SNP_A-1895979	A	A	306	4	396	0	5.139	2.34E-02	rs11124483	2	35925953	p22.3
SNP_A-1919383	C	C	245	165	271	131	5.137	2.34E-02	rs7792492	7	133052571	q33
SNP_A-1950441	C	C	331	29	391	17	5.137	2.34E-02	rs7902923	10	61553990	q21.2
SNP_A-1958515	G	G	178	156	238	148	5.136	2.34E-02	rs1618598	10	29351434	p12.1
SNP_A-1959339	C	T	205	153	198	190	5.141	2.34E-02	rs9354907	6	70925359	q13
SNP_A-1677654	A	A	266	94	312	74	5.142	2.34E-02	rs10508281	10	4366236	p15.1
SNP_A-1642723	C	C	339	1	399	9	5.139	2.34E-02	rs9319816	18	67123249	q22.3
SNP_A-1829052	T	T	341	19	399	9	5.137	2.34E-02	rs1481528	3	100537919	q12.1
SNP_A-1826575	C	T	198	146	205	199	5.14	2.34E-02	rs6734144	2	103614063	q12.1
SNP_A-1826845	A	A	259	99	268	146	5.135	2.34E-02	rs11077288	16	8334875	p13.2
SNP_A-1853508	C	C	241	119	289	99	5.141	2.34E-02	rs10894623	11	132300779	q25
SNP_A-2157491	A	A	351	5	393	17	5.135	2.34E-02	rs4909764	8	139325100	q24.23
SNP_A-2151437	A	A	200	170	228	138	5.135	2.34E-02	rs9295564	6	22836767	p22.3
SNP_A-2121756	A	G	220	184	209	181	5.138	2.34E-02	rs11738059	5	148481947	q32
SNP_A-2120661	T	T	359	5	349	15	5.141	2.34E-02	rs17074837	13	30140334	q12.3
SNP_A-2192135	A	A	384	30	395	15	5.136	2.34E-02	rs12291717	11	115104280	q23.3
SNP_A-2176016	A	A	358	64	331	89	5.138	2.34E-02	rs16880831	8	111630681	q23.2
SNP_A-2214006	A	A	324	28	353	53	5.137	2.34E-02	rs17811708	8	117869446	q24.11
SNP_A-2214492	T	T	361	1	374	8	5.14	2.34E-02	rs16907076	9	90841610	q22.2
SNP_A-2216230	C	C	312	52	292	76	5.141	2.34E-02	rs10141001	14	51201951	q22.1
SNP_A-2210286	G	G	350	12	404	4	5.138	2.34E-02	rs10873028	14	48964500	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207205	T	T	267	101	329	85	5.138	2.34E-02	rs3913714	3	59582333	p14.2
SNP_A-2206165	G	A	202	164	211	187	5.138	2.34E-02	rs2699027	4	160707037	q32.1
SNP_A-2205333	G	G	341	81	312	108	5.14	2.34E-02	rs653791	1	182929561	q31.1
SNP_A-2201484	G	G	252	100	254	144	5.14	2.34E-02	rs11070682	15	47146912	q21.1
SNP_A-1995976	C	C	386	30	397	15	5.135	2.34E-02	rs12260389	10	13772842	p13
SNP_A-2030107	G	G	184	164	242	154	5.136	2.34E-02	rs9520975	13	108162688	q33.3
SNP_A-2070692	G	G	255	97	318	82	5.141	2.34E-02	rs1447149	11	119196279	q23.3
SNP_A-2062586	C	C	246	158	213	189	5.137	2.34E-02	rs6684354	1	42531043	p34.2
SNP_A-2053064	G	G	341	81	312	108	5.14	2.34E-02	rs654222	1	182929481	q31.1
SNP_A-2078607	G	G	276	90	330	72	5.136	2.34E-02	rs10000200	4	59630637	q12
SNP_A-2083359	C	C	300	58	320	94	5.136	2.34E-02	rs11685418	2	113411377	q13
SNP_A-2086050	A	A	340	8	372	22	5.14	2.34E-02	rs6778456	3	187443373	q27.2
SNP_A-2236304	A	G	193	143	190	182	5.139	2.34E-02	rs3845600	1	14941441	p36.21
SNP_A-2230959	G	G	207	161	267	149	5.14	2.34E-02	rs9409111	9	110707188	q31.3
SNP_A-2232155	G	G	246	122	226	158	5.138	2.34E-02	rs2074933	14	73511290	q24.3
SNP_A-2232518	C	C	272	118	312	94	5.137	2.34E-02	rs12340737	9	116462874	q33.1
SNP_A-2256264	G	G	325	35	353	63	5.142	2.34E-02	rs880386	1	55532285	p32.3
SNP_A-2250151	G	G	355	15	383	33	5.138	2.34E-02	rs17231486	10	66970080	q21.3
SNP_A-2260158	C	C	203	167	237	139	5.141	2.34E-02	rs2082365	7	26609185	p15.2
SNP_A-2272082	A	A	255	97	318	82	5.141	2.34E-02	rs4750489	10	14291898	p13
SNP_A-2243310	G	G	293	77	299	115	5.128	0.0235	rs10086880	8	4757537	p23.2
SNP_A-2233711	G	G	317	49	327	79	5.128	0.0235	rs11739264	5	174533811	q35.2
SNP_A-2235877	C	C	344	4	383	15	5.132	0.0235	rs6447883	4	8696994	p16.1
SNP_A-2239973	C	C	245	117	244	164	5.134	0.0235	rs3759733	14	76858591	q24.3
SNP_A-2291136	G	G	418	0	405	5	5.129	0.0235	rs16977353	15	55337841	q21.3
SNP_A-2086116	A	A	357	59	334	84	5.131	0.0235	rs11822653	11	76137152	q13.5

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100310	G	T	191	175	224	176	5.132	0.0235	rs2164787	13	72143745	q22.1
SNP_A-2051070	C	C	302	60	365	45	5.129	0.0235	rs12214409	6	128126976	q22.33
SNP_A-2059051	T	T	328	28	384	16	5.134	0.0235	rs1963397	5	24775874	p14.1
SNP_A-2060573	T	T	272	94	334	78	5.13	0.0235	rs802534	7	145356881	q35
SNP_A-2058476	C	C	253	105	316	90	5.134	0.0235	rs11169561	12	49472217	q13.12
SNP_A-2070065	T	T	410	0	397	5	5.131	0.0235	rs17006280	3	69775284	p14.1
SNP_A-2038337	C	C	307	53	319	85	5.133	0.0235	rs4282339	5	168188818	q34
SNP_A-2041758	T	T	346	10	356	24	5.13	0.0235	rs4624612	4	176950226	q34.2
SNP_A-1995842	C	C	184	178	244	170	5.134	0.0235	rs1343535	9	10004143	p23
SNP_A-1993692	C	C	316	40	337	69	5.132	0.0235	rs2912503	8	70109310	q13.2
SNP_A-2207005	G	G	353	1	366	8	5.134	0.0235	rs11012748	10	18451312	p12.33
SNP_A-2226377	T	T	264	128	231	157	5.13	0.0235	rs11803051	1	14624797	p36.21
SNP_A-2181642	A	A	391	5	404	0	5.133	0.0235	rs16920075	9	101050287	q31.1
SNP_A-2174020	T	T	405	5	418	0	5.129	0.0235	rs4659517	1	234717390	q43
SNP_A-2183167	C	C	342	28	400	16	5.132	0.0235	rs17042273	2	113192315	q13
SNP_A-2124784	G	G	348	46	334	70	5.128	0.0235	rs176632	10	114901069	q25.3
SNP_A-2157141	C	C	274	94	279	137	5.13	0.0235	rs7983188	13	50729287	q14.3
SNP_A-1849312	A	A	287	23	357	13	5.132	0.0235	rs2645870	12	57444305	q14.1
SNP_A-1869066	C	C	253	89	311	73	5.132	0.0235	rs12497088	3	27044816	p24.2
SNP_A-1822835	A	A	391	5	404	0	5.133	0.0235	rs1108210	1	224762222	q42.13
SNP_A-1758660	G	G	400	0	387	5	5.134	0.0235	rs10511213	3	104537798	q13.11
SNP_A-1716975	G	G	328	68	366	48	5.132	0.0235	rs1504476	10	66480364	q21.3
SNP_A-1814687	A	A	320	14	400	6	5.132	0.0235	rs882453	18	7307926	p11.23
SNP_A-1794919	G	G	307	95	341	71	5.132	0.0235	rs4459884	3	2121692	p26.3
SNP_A-1799540	G	G	359	51	334	74	5.129	0.0235	rs10782549	1	85593299	p22.3
SNP_A-1934445	G	C	202	196	229	171	5.134	0.0235	rs2002871	11	122566397	q24.1
SNP_A-1940144	T	T	274	92	278	134	5.132	0.0235	rs11790506	9	1310872	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1984301	A	A	290	70	305	109	5.133	0.0235	rs7718139	5	159908016	q34
SNP_A-1980805	C	C	289	121	322	94	5.13	0.0235	rs4702023	5	14297357	p15.2
SNP_A-1915592	C	C	249	121	309	105	5.131	0.0235	rs16755	18	11108427	p11.21
SNP_A-1912147	G	G	295	67	360	52	5.133	0.0235	rs13325144	3	140646238	q23
SNP_A-1904645	A	A	418	0	405	5	5.129	0.0235	rs7218683	17	8332878	p13.1
SNP_A-1894909	G	G	330	56	345	35	5.133	0.0235	rs1947555	3	138896601	q22.3
SNP_A-1882067	C	C	359	3	366	12	5.124	2.36E-02	rs882439	9	87261580	q21.33
SNP_A-1887298	C	C	406	10	380	22	5.122	2.36E-02	rs479180	20	47645512	q13.13
SNP_A-1877812	C	C	197	167	244	148	5.125	2.36E-02	rs13050624	21	31007539	q22.11
SNP_A-1925175	G	G	350	62	375	41	5.124	2.36E-02	rs1791847	11	21172421	p15.1
SNP_A-1927491	A	A	227	129	297	119	5.122	2.36E-02	rs13333735	16	76460409	q23.1
SNP_A-1986052	A	A	378	28	354	46	5.121	2.36E-02	rs10484881	6	52129832	p12.2
SNP_A-1961113	A	A	289	127	318	98	5.123	2.36E-02	rs11247168	15	98578034	q26.3
SNP_A-1954374	A	A	364	2	370	10	5.121	2.36E-02	rs12626103	20	11923843	p12.1
SNP_A-1809568	T	T	321	33	310	54	5.122	2.36E-02	rs9393325	6	22767176	p22.3
SNP_A-1823133	C	C	328	40	384	26	5.122	2.36E-02	rs2029809	3	149485843	q24
SNP_A-1828112	C	C	268	96	263	135	5.125	2.36E-02	rs9449885	6	85141132	q14.3
SNP_A-1820869	T	T	305	47	367	33	5.127	2.36E-02	rs16923328	8	59388605	q12.1
SNP_A-1841744	G	G	334	26	348	48	5.125	2.36E-02	rs1344364	5	49815219	q11.1
SNP_A-1840160	C	C	269	99	331	83	5.125	2.36E-02	rs10521213	17	13110583	p12
SNP_A-2111633	A	G	186	136	193	187	5.121	2.36E-02	rs980661	2	137860832	q22.1
SNP_A-2181666	T	C	202	166	208	182	5.124	2.36E-02	rs8083788	18	62842132	q22.1
SNP_A-1996673	C	C	413	5	403	15	5.123	2.36E-02	rs1556609	10	16394710	p13
SNP_A-2015530	T	T	301	65	296	96	5.125	2.36E-02	rs2823806	21	16736908	q21.1
SNP_A-2011177	C	C	359	7	388	20	5.121	2.36E-02	rs1073205	5	115689716	q23.1
SNP_A-2006838	A	A	223	141	287	129	5.121	2.36E-02	rs6433294	2	172194576	q31.1
SNP_A-2041131	C	C	255	159	286	128	5.125	2.36E-02	rs2295846	14	50292856	q22.1
SNP_A-2035560	T	T	338	78	314	106	5.125	2.36E-02	rs6560519	9	76276671	q21.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2021010	T	T	329	33	344	58	5.122	2.36E-02	rs11059876	12	127763498	q24.32
SNP_A-2100418	G	G	349	15	364	32	5.126	2.36E-02	---	1	75414150	p31.1
SNP_A-2087546	A	A	313	61	290	86	5.124	2.36E-02	rs10986432	9	124650194	q33.3
SNP_A-2089241	C	C	298	18	371	9	5.124	2.36E-02	rs6564850	16	79821899	q23.2
SNP_A-2236734	G	G	360	34	326	52	5.123	2.36E-02	rs6956225	7	137792501	q34
SNP_A-2252787	G	G	310	44	359	29	5.124	2.36E-02	rs17448997	5	120562786	q23.1
SNP_A-2270274	A	A	413	5	403	15	5.123	2.36E-02	rs16918808	10	65140918	q21.3
SNP_A-2265516	C	C	255	109	253	153	5.122	2.36E-02	rs12645191	4	5276365	p16.2
SNP_A-2278320	A	A	305	53	317	85	5.122	2.36E-02	rs542571	11	104417431	q22.3
SNP_A-2266686	T	T	322	74	288	98	5.117	2.37E-02	rs1202834	1	58072132	p32.2
SNP_A-2259018	T	T	314	52	373	37	5.117	2.37E-02	rs1920786	12	89883892	q21.33
SNP_A-2233005	T	T	349	55	312	76	5.116	2.37E-02	rs7173716	15	67910880	q23
SNP_A-2230711	T	T	317	51	333	83	5.116	2.37E-02	rs156499	4	156034830	q32.1
SNP_A-2229588	G	G	328	12	378	4	5.115	2.37E-02	rs17291954	4	62118102	q13.1
SNP_A-2296061	G	G	336	20	400	10	5.117	2.37E-02	rs2278587	2	143472394	q22.2
SNP_A-2311095	T	T	279	141	240	168	5.117	2.37E-02	rs344541	19	6638595	p13.3
SNP_A-2066431	T	T	341	11	358	26	5.113	2.37E-02	rs16830485	1	186078696	q31.1
SNP_A-2048543	T	T	251	115	238	154	5.114	2.37E-02	rs1328648	13	35621016	q13.3
SNP_A-1997756	T	T	284	50	353	37	5.116	2.37E-02	rs10982516	9	114925165	q33.1
SNP_A-2200858	G	G	248	142	217	173	5.117	2.37E-02	rs3217	4	10120919	p16.1
SNP_A-2200495	G	G	227	137	216	182	5.114	2.37E-02	rs12642497	4	162381649	q32.2
SNP_A-2161613	C	G	210	206	233	173	5.114	2.37E-02	rs17170046	7	34713094	p14.2
SNP_A-2164570	C	C	204	156	260	142	5.117	2.37E-02	rs6707346	2	116632838	q14.1
SNP_A-1839497	C	C	212	154	266	138	5.114	2.37E-02	rs6488722	12	14914758	p12.3
SNP_A-1837757	G	G	342	12	394	4	5.117	2.37E-02	rs693305	13	55564116	q21.1
SNP_A-1834383	G	G	316	54	377	39	5.114	2.37E-02	rs474533	6	156961729	q25.3
SNP_A-1813811	G	G	188	180	246	170	5.117	2.37E-02	rs4852511	2	79823545	p12
SNP_A-1805702	T	T	371	47	375	27	5.117	2.37E-02	rs7607353	2	72488881	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802852	T	T	302	44	360	30	5.118	2.37E-02	rs17227126	20	4403013	p13
SNP_A-1800594	C	C	305	63	316	98	5.115	2.37E-02	rs12115116	8	133430895	q24.22
SNP_A-1757969	C	C	287	115	324	90	5.114	2.37E-02	rs10492147	12	14996970	p12.3
SNP_A-1948754	C	C	308	54	323	87	5.115	2.37E-02	rs11253494	10	927047	p15.3
SNP_A-1946737	G	G	291	117	245	139	5.116	2.37E-02	rs7898677	10	128155254	q26.2
SNP_A-1980070	A	A	362	16	388	6	5.117	2.37E-02	rs2284441	1	198005149	q32.1
SNP_A-1972774	C	C	363	21	350	38	5.115	2.37E-02	rs7525115	1	170596601	q25.1
SNP_A-1968502	T	T	317	105	279	131	5.115	2.37E-02	rs3915736	20	44305031	q13.12
SNP_A-1926539	G	G	339	25	357	47	5.118	2.37E-02	rs17432027	5	143240906	q31.3
SNP_A-1919713	T	C	210	156	210	204	5.12	2.37E-02	rs2352199	13	91389873	q31.3
SNP_A-1909492	C	C	375	7	417	1	5.118	2.37E-02	rs8029187	15	42126242	q15.3
SNP_A-1885387	C	C	212	152	275	141	5.119	2.37E-02	rs11856273	15	78621198	q25.1
SNP_A-1892903	A	A	247	151	220	186	5.117	2.37E-02	rs10778455	12	104941496	q23.3
SNP_A-1909576	G	G	389	5	400	0	5.108	2.38E-02	rs16860597	4	47537162	p12
SNP_A-1918898	C	C	397	5	408	0	5.106	2.38E-02	rs9901612	17	51520028	q23.2
SNP_A-1924575	T	T	381	21	397	9	5.109	2.38E-02	rs17060993	8	26978029	p21.2
SNP_A-1966852	A	A	343	77	365	53	5.11	2.38E-02	rs10498040	2	216178631	q35
SNP_A-1969636	G	G	379	31	349	49	5.109	2.38E-02	rs2829984	21	26226123	q21.3
SNP_A-1980993	G	G	406	0	395	5	5.107	2.38E-02	rs16893488	5	24561616	p14.2
SNP_A-1953963	C	C	386	18	401	7	5.106	2.38E-02	rs13339044	16	76245186	q23.1
SNP_A-1952305	C	C	322	92	341	65	5.11	2.38E-02	rs7518922	1	48554327	p33
SNP_A-1960545	G	G	339	3	346	12	5.108	2.38E-02	rs13446739	7	118667349	q31.31
SNP_A-1956258	A	A	300	8	345	23	5.112	2.38E-02	rs11120588	1	212034348	q41
SNP_A-1722694	T	T	383	19	378	36	5.112	2.38E-02	rs740511	7	39196165	p14.1
SNP_A-1662102	C	C	397	5	408	0	5.106	2.38E-02	rs2250939	10	122542992	q26.12
SNP_A-1705183	C	C	235	159	276	134	5.106	2.38E-02	rs10486700	7	40754175	p14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802571	G	G	281	71	339	55	5.109	2.38E-02	rs7164968	15	23354702	q12
SNP_A-1812938	A	A	190	180	247	169	5.107	2.38E-02	rs6070411	20	56295416	q13.32
SNP_A-1787211	G	G	326	44	344	26	5.112	2.38E-02	rs10734471	11	39254691	p12
SNP_A-1819283	G	G	293	27	375	17	5.11	2.38E-02	rs698781	2	44654568	p21
SNP_A-1818002	G	G	222	134	286	122	5.11	2.38E-02	rs1385898	6	76989728	q14.1
SNP_A-1866709	C	C	261	151	297	123	5.107	2.38E-02	rs905488	2	68093676	p14
SNP_A-1862698	C	T	186	160	215	179	5.109	2.38E-02	rs9951893	18	58890230	q21.33
SNP_A-2167967	A	A	283	79	287	117	5.108	2.38E-02	rs10446793	4	61953297	q13.1
SNP_A-2140253	C	C	330	10	397	3	5.113	2.38E-02	rs17076761	18	62770969	q22.1
SNP_A-2134407	A	A	300	60	307	93	5.107	2.38E-02	rs12126772	1	195733901	q31.3
SNP_A-2225167	A	A	244	122	235	165	5.113	2.38E-02	rs17160322	1	144209331	q21.1
SNP_A-2185432	C	C	342	74	367	51	5.109	2.38E-02	rs7098827	10	133648418	q26.3
SNP_A-2191158	G	G	332	86	320	54	5.106	2.38E-02	rs11633610	15	52543476	q21.3
SNP_A-2007643	C	C	335	27	354	50	5.107	2.38E-02	rs6072758	20	40543716	q12
SNP_A-2058133	A	A	365	1	380	8	5.109	2.38E-02	rs7704701	5	36388728	p13.2
SNP_A-2055534	G	G	400	0	389	5	5.108	2.38E-02	rs16828515	2	232599480	q37.1
SNP_A-2066068	G	G	320	46	373	31	5.113	2.38E-02	rs9517416	13	98165797	q32.2
SNP_A-2085486	C	C	307	57	318	90	5.111	2.38E-02	rs9662729	1	236946326	q43
SNP_A-2104527	G	G	342	74	317	101	5.109	2.38E-02	rs10988439	9	129431773	q34.11
SNP_A-2266564	C	C	342	78	359	53	5.107	2.38E-02	rs38452	7	30346892	p14.3
SNP_A-2277632	A	A	273	147	302	116	5.112	2.38E-02	rs13281444	8	6508036	p23.1
SNP_A-2274605	A	A	293	65	288	96	5.107	2.38E-02	rs687804	11	85887204	q14.2
SNP_A-2285746	T	T	230	140	289	125	5.103	2.39E-02	rs3895392	13	113770904	q34
SNP_A-2265566	G	G	245	107	247	153	5.104	2.39E-02	rs7615225	3	163769016	q26.1
SNP_A-2255643	T	T	371	51	346	74	5.099	2.39E-02	rs6788550	3	144763390	q24

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255116	G	G	403	5	414	0	5.105	2.39E-02	rs17799141	19	49116022	q13.31
SNP_A-2312838	G	G	348	28	366	14	5.099	2.39E-02	rs1474864	1	183765246	q31.1
SNP_A-2101922	G	G	333	27	385	15	5.103	2.39E-02	rs12337203	9	29273813	p21.1
SNP_A-2091833	C	C	218	142	214	194	5.105	2.39E-02	rs931462	15	96151074	q26.2
SNP_A-2078026	G	G	403	5	414	0	5.105	2.39E-02	rs12006262	9	127958496	q34.11
SNP_A-2071760	A	A	257	107	258	152	5.105	2.39E-02	rs10889424	1	63675920	p31.3
SNP_A-2057184	G	G	322	64	286	86	5.101	2.39E-02	rs11603417	11	59134119	q12.1
SNP_A-2005469	G	G	353	65	326	90	5.101	2.39E-02	rs1555485	10	114902524	q25.3
SNP_A-2178961	C	C	347	73	319	99	5.103	2.39E-02	rs1543603	6	25521901	p22.2
SNP_A-2175469	C	C	256	108	310	90	5.103	2.39E-02	rs4286846	7	32828052	p14.3
SNP_A-2217940	C	C	403	5	414	0	5.105	2.39E-02	rs404109	19	59413443	q13.42
SNP_A-2113779	G	G	241	129	302	114	5.104	2.39E-02	rs4905203	14	93977997	q32.13
SNP_A-1853720	T	T	361	1	376	8	5.105	2.39E-02	rs16968112	17	38289805	q21.31
SNP_A-1818326	C	C	403	5	414	0	5.105	2.39E-02	rs10068247	5	143662647	q31.3
SNP_A-1800105	T	T	252	104	256	150	5.103	2.39E-02	rs644936	18	8321140	p11.23
SNP_A-1646110	T	T	273	77	346	64	5.103	2.39E-02	rs717694	4	156992822	q32.1
SNP_A-1753037	C	C	239	147	285	125	5.099	2.39E-02	rs722188	7	20381061	p21.1
SNP_A-1955936	T	T	411	11	396	24	5.103	2.39E-02	rs7180657	15	46168230	q21.1
SNP_A-1957607	C	C	287	75	342	58	5.1	2.39E-02	rs11724165	4	160800250	q32.1
SNP_A-1940586	A	A	265	95	333	81	5.103	2.39E-02	rs6422001	12	131325373	q24.33
SNP_A-1979267	A	A	211	155	270	142	5.104	2.39E-02	rs10917061	1	19244426	p36.13
SNP_A-1973392	A	A	230	140	289	125	5.103	2.39E-02	rs4856624	3	80704848	p12.2
SNP_A-1967116	G	G	401	5	412	0	5.105	2.39E-02	rs4674849	2	224710350	q36.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1966110	A	A	257	113	257	159	5.105	2.39E-02	rs10497572	2	181472532	q31.3
SNP_A-1893914	A	A	285	59	351	45	5.105	2.39E-02	rs9550117	13	112198903	q34
SNP_A-1885991	G	G	414	0	403	5	5.105	2.39E-02	rs9842335	3	44250330	p21.33
SNP_A-1885088	G	G	295	73	302	110	5.097	0.024	rs6865369	5	67732700	q13.1
SNP_A-1877500	C	C	260	92	323	77	5.096	0.024	rs270716	1	44723959	p34.1
SNP_A-1875342	C	C	336	32	341	55	5.098	0.024	rs494825	6	150446137	q25.1
SNP_A-1918199	G	G	271	57	340	44	5.092	0.024	rs9824142	3	76188244	p12.3
SNP_A-1913292	G	G	328	32	326	54	5.097	0.024	rs9994840	4	30906066	p15.1
SNP_A-1975463	C	C	237	85	310	74	5.098	0.024	rs765315	3	179856578	q26.32
SNP_A-1678190	C	C	326	76	358	54	5.098	0.024	rs1938684	11	69050036	q13.3
SNP_A-1790069	G	G	351	1	366	8	5.096	0.024	rs10256405	7	73416518	q11.23
SNP_A-1796074	T	T	244	120	308	106	5.095	0.024	rs11827640	11	11352817	p15.3
SNP_A-1829852	A	A	305	41	381	29	5.095	0.024	rs1787475	18	52846497	q21.31
SNP_A-1841440	C	C	226	126	221	173	5.095	0.024	rs1405246	8	5345291	p23.2
SNP_A-1854561	C	C	346	64	324	90	5.093	0.024	rs7530358	1	196992100	q32.1
SNP_A-1870964	G	G	358	10	387	25	5.092	0.024	rs1018411	1	14804705	p36.21
SNP_A-1871111	G	G	290	60	330	42	5.091	0.024	rs4758954	12	132044903	q24.33
SNP_A-2115528	A	A	309	105	328	76	5.092	0.024	rs7896430	10	63560965	q21.2
SNP_A-2122163	C	C	268	140	302	112	5.096	0.024	rs9576286	13	36986609	q13.3
SNP_A-2116558	T	T	230	118	237	171	5.095	0.024	rs7614439	3	77603996	p12.3
SNP_A-2148003	A	A	380	40	331	57	5.097	0.024	rs4980673	11	69104194	q13.3
SNP_A-2201777	A	A	268	82	274	122	5.092	0.024	rs175270	20	15146024	p12.1
SNP_A-2206161	A	A	297	71	306	108	5.094	0.024	rs33223	12	30929244	p11.21
SNP_A-2172710	A	A	295	71	355	55	5.092	0.024	rs1516493	3	192948683	q28
SNP_A-2184034	T	T	317	49	332	80	5.094	0.024	rs7226852	18	28289809	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2198158	G	G	270	96	276	140	5.093	0.024	rs883159	14	47428814	q21.3
SNP_A-2199292	G	G	298	102	315	73	5.096	0.024	rs12534088	7	42156612	p14.1
SNP_A-2197473	C	C	350	12	402	4	5.092	0.024	rs677807	2	21494680	p24.1
SNP_A-2008382	C	C	264	92	272	136	5.095	0.024	rs1377744	11	21149771	p15.1
SNP_A-1990347	C	C	277	91	339	75	5.094	0.024	rs4728499	7	81417220	q21.11
SNP_A-2029338	C	T	202	164	218	194	5.093	0.024	rs216903	12	5975760	p13.31
SNP_A-2069421	C	C	372	32	356	52	5.094	0.024	rs17151026	8	9970207	p23.1
SNP_A-2289854	-	T	181	181	236	170	5.095	0.024	rs502114	3	74427932	p12.3
SNP_A-2257685	A	A	291	25	284	44	5.095	0.024	rs9654060	4	73862392	q13.3
SNP_A-2286893	C	C	320	76	340	52	5.086	0.0241	rs6967330	7	105252402	q22.3
SNP_A-2309556	C	C	348	20	370	40	5.088	0.0241	rs2248713	1	17617965	p36.13
SNP_A-2071959	T	T	275	131	288	96	5.088	0.0241	rs10195236	2	42680674	p21
SNP_A-2083155	C	C	403	17	402	6	5.089	0.0241	rs7526063	1	233298039	q43
SNP_A-2028183	A	A	353	25	374	12	5.091	0.0241	rs10967401	9	26543975	p21.2
SNP_A-2027420	A	A	255	107	256	152	5.091	0.0241	rs934346	6	115564588	q22.1
SNP_A-2046130	C	C	321	33	336	58	5.086	0.0241	rs729136	12	23539875	p12.1
SNP_A-2003496	C	C	224	142	218	192	5.088	0.0241	rs6492827	13	95419148	q32.1
SNP_A-2184203	G	G	393	17	392	6	5.085	0.0241	rs4845046	1	207095719	q32.2
SNP_A-2173551	C	C	362	54	292	68	5.084	0.0241	rs2868093	20	42397212	q13.12
SNP_A-2218247	G	G	341	27	337	47	5.091	0.0241	rs1701706	12	54688471	q13.2
SNP_A-2222142	C	T	188	162	215	179	5.087	0.0241	rs9410431	9	88793671	q22.1
SNP_A-2149586	G	G	375	17	343	31	5.089	0.0241	rs2086546	11	13181900	p15.2
SNP_A-2144211	A	A	351	37	346	60	5.084	0.0241	rs9285082	13	30458544	q12.3
SNP_A-2121969	C	C	271	141	298	110	5.09	0.0241	rs2872046	2	112695121	q13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869362	C	C	294	98	271	129	5.089	0.0241	rs10845743	12	13347780	p13.1
SNP_A-1854265	A	A	243	99	313	87	5.085	0.0241	rs3936289	3	188237659	q27.3
SNP_A-1842720	C	T	213	157	209	205	5.088	0.0241	rs7321674	13	91399197	q31.3
SNP_A-1829692	G	G	283	77	333	59	5.088	0.0241	rs787152	2	144489423	q22.3
SNP_A-1830837	A	A	269	97	334	82	5.087	0.0241	rs2242153	6	43416866	p21.1
SNP_A-1820452	C	C	369	29	352	48	5.084	0.0241	rs11119951	1	209054185	q32.3
SNP_A-1822385	A	A	301	99	332	74	5.087	0.0241	rs4888946	16	77874931	q23.1
SNP_A-1648374	T	T	369	11	397	3	5.085	0.0241	rs10498383	14	41788498	q21.2
SNP_A-1657069	C	C	330	70	315	99	5.086	0.0241	rs2089352	3	62655629	p14.2
SNP_A-1973818	A	A	338	72	287	91	5.085	0.0241	rs2204260	3	108968587	q13.12
SNP_A-1971820	G	G	373	7	413	1	5.089	0.0241	rs3729585	3	14173390	p25.1
SNP_A-1980192	G	G	247	115	249	163	5.087	0.0241	rs2061023	4	184331659	q35.1
SNP_A-1941404	G	G	347	69	366	46	5.087	0.0241	rs12149530	16	75864204	q23.1
SNP_A-1945039	C	C	388	34	400	18	5.087	0.0241	rs6975351	7	32225874	p14.3
SNP_A-1935508	A	A	332	88	301	115	5.09	0.0241	rs17291890	2	5511001	p25.2
SNP_A-1937643	A	A	293	11	347	29	5.09	0.0241	rs7399020	12	10228022	p13.2
SNP_A-1960941	T	T	327	77	354	54	5.089	0.0241	rs4716560	7	155219329	q36.3
SNP_A-1954332	G	G	294	54	285	81	5.089	0.0241	rs432893	19	3094182	p13.3
SNP_A-1950274	C	C	285	129	317	101	5.091	0.0241	rs4456480	15	89853118	q26.1
SNP_A-1892172	G	G	269	115	260	156	5.084	0.0241	rs2544084	12	44281563	q12
SNP_A-1882186	C	C	402	0	393	5	5.082	2.42E-02	rs1015697	2	36871344	p22.2
SNP_A-1881555	G	G	316	36	388	24	5.083	2.42E-02	rs17505435	18	6536859	p11.31
SNP_A-1915396	T	T	217	145	203	189	5.077	2.42E-02	rs389625	1	186243024	q31.1
SNP_A-1915200	T	T	258	160	289	129	5.082	2.42E-02	rs11688940	2	127279414	q14.3
SNP_A-1905935	T	T	416	0	407	5	5.079	2.42E-02	rs2230592	3	49911612	p21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1929906	A	A	254	104	323	91	5.083	2.42E-02	rs6909459	6	115333820	q22.1
SNP_A-1981087	A	A	329	39	357	23	5.081	2.42E-02	rs1816571	5	30638173	p13.3
SNP_A-1978028	A	A	211	127	277	117	5.082	2.42E-02	rs1443795	4	91333293	q22.1
SNP_A-1988276	T	T	185	175	245	167	5.08	2.42E-02	rs1246182	6	157061429	q25.3
SNP_A-1661496	G	G	402	0	393	5	5.082	2.42E-02	rs2400445	3	136213509	q22.2
SNP_A-1676538	G	G	400	0	391	5	5.082	2.42E-02	rs742767	6	172752	p25.3
SNP_A-1756915	G	G	400	0	391	5	5.082	2.42E-02	rs10483197	22	36773791	q13.1
SNP_A-1804453	C	C	274	96	336	80	5.081	2.42E-02	rs10810668	9	16902435	p22.2
SNP_A-1811160	T	A	202	164	220	196	5.081	2.42E-02	rs277751	9	87004705	q21.33
SNP_A-1818872	T	T	323	39	388	26	5.081	2.42E-02	rs10153374	18	14717429	p11.21
SNP_A-1831471	C	C	375	11	403	3	5.077	2.42E-02	rs6473903	8	55082444	q11.23
SNP_A-1872642	C	C	176	174	234	166	5.082	2.42E-02	rs7997477	13	98170633	q32.2
SNP_A-2109843	A	A	280	60	276	90	5.078	2.42E-02	rs7705519	5	74092269	q13.3
SNP_A-2134448	T	T	260	76	270	116	5.084	2.42E-02	rs9287903	2	169505629	q24.3
SNP_A-2138373	C	C	298	56	357	41	5.077	2.42E-02	rs9402271	6	131077825	q23.1
SNP_A-2163678	T	C	197	173	228	188	5.079	2.42E-02	rs1431489	4	163174672	q32.2
SNP_A-2216706	G	G	254	100	323	87	5.078	2.42E-02	rs13117963	4	7868158	p16.1
SNP_A-2204469	A	A	251	171	197	185	5.082	2.42E-02	rs9911005	17	15353534	p12
SNP_A-2211952	T	T	203	137	276	132	5.078	2.42E-02	rs7113678	11	11964354	p15.3
SNP_A-2179778	G	G	319	37	380	24	5.083	2.42E-02	rs6743807	2	114321833	q14.1
SNP_A-2180196	C	C	272	130	298	100	5.079	2.42E-02	rs11130665	3	58597660	p14.2
SNP_A-2005067	G	G	407	5	416	0	5.079	2.42E-02	rs4335807	17	10936849	p12
SNP_A-1997293	A	A	288	82	350	66	5.08	2.42E-02	rs12550922	9	96394868	q22.33
SNP_A-2008133	T	T	396	0	387	5	5.083	2.42E-02	rs8130198	21	42503393	q22.3
SNP_A-2016654	A	A	370	8	366	20	5.081	2.42E-02	rs2828595	21	24200155	q21.2
SNP_A-2047025	T	T	361	9	328	20	5.084	2.42E-02	rs2809806	1	100747050	p21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043803	T	T	410	2	373	9	5.077	2.42E-02	rs3856677	3	27672507	p24.1
SNP_A-2039058	G	G	254	166	284	134	5.081	2.42E-02	rs2604 73	19	63489949	q13.43
SNP_A-2038807	A	A	310	14	343	5	5.08	2.42E-02	rs609725	3	43019028	p22.1
SNP_A-2025172	A	A	255	111	318	96	5.079	2.42E-02	rs7970553	12	102684098	q23.3
SNP_A-2077798	C	C	401	5	410	0	5.08	2.42E-02	rs17127243	8	18713108	p22
SNP_A-2308327	C	C	351	13	382	30	5.082	2.42E-02	rs17651026	15	25692912	q12
SNP_A-2305701	A	A	277	125	310	98	5.08	2.42E-02	rs4663748	2	238107399	q37.3
SNP_A-2294923	C	C	338	28	394	16	5.078	2.42E-02	rs11180768	12	74643059	q21.2
SNP_A-2300414	T	T	412	0	403	5	5.08	2.42E-02	rs16856524	1	202642884	q32.1
SNP_A-2275838	G	G	293	55	343	39	5.082	2.42E-02	rs16839198	1	4489266	p36.32
SNP_A-2242064	G	G	387	35	365	55	5.083	2.42E-02	rs11608072	11	117535296	q23.3
SNP_A-2244840	G	G	251	119	250	166	5.078	2.42E-02	rs10493658	1	80225727	p31.1
SNP_A-2244183	C	C	267	87	272	128	5.078	2.42E-02	rs4726540	7	141852546	q34
SNP_A-2247034	T	T	240	124	298	108	5.08	2.42E-02	rs4869276	5	95602398	q15
SNP_A-2280352	T	T	287	79	297	119	5.076	2.43E-02	rs716986	15	49767105	q21.2
SNP_A-2269131	T	C	178	176	235	171	5.076	2.43E-02	rs12645545	4	186842638	q35.1
SNP_A-2296569	G	G	224	172	240	132	5.07	2.43E-02	---	11	25714528	p14.3
SNP_A-2305738	G	G	313	107	282	136	5.071	2.43E-02	rs422472	15	90945082	q26.1
SNP_A-2096419	T	T	267	55	341	43	5.07	2.43E-02	rs17152660	10	13097266	p13
SNP_A-2098717	C	C	391	31	361	49	5.075	2.43E-02	rs17109144	14	70742159	q24.2
SNP_A-2075575	T	T	395	27	407	13	5.075	2.43E-02	rs9368745	6	32934211	p21.32
SNP_A-2075975	A	A	318	46	380	32	5.07	2.43E-02	rs17114704	1	96378159	p21.3
SNP_A-2062085	G	G	225	121	209	159	5.074	2.43E-02	rs9789387	2	69697839	p13.3
SNP_A-2020577	A	A	256	110	313	93	5.075	2.43E-02	rs4819035	21	45470143	q22.3
SNP_A-2006499	A	A	225	117	238	174	5.075	2.43E-02	rs2196334	2	79149958	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2004962	G	G	322	30	348	16	5.07	2.43E-02	rs1724045	10	108052853	q25.1
SNP_A-2173792	G	G	354	2	362	10	5.074	2.43E-02	rs319566	13	92631401	q31.3
SNP_A-2189754	C	C	338	30	356	54	5.071	2.43E-02	rs9324315	13	112295332	q34
SNP_A-2207182	G	G	354	2	362	10	5.074	2.43E-02	rs4931862	15	18427103	q11.2
SNP_A-2207341	C	C	351	3	360	12	5.071	2.43E-02	rs4731952	7	132559583	q33
SNP_A-2206830	T	T	209	133	205	183	5.072	2.43E-02	rs13273294	8	135426429	q24.22
SNP_A-2221793	T	T	254	116	314	100	5.07	2.43E-02	rs7858220	9	7262680	p24.1
SNP_A-2226689	C	C	258	112	257	157	5.076	2.43E-02	rs12642039	4	160289627	q32.1
SNP_A-2161626	A	G	209	157	210	202	5.071	2.43E-02	rs9805956	14	45565893	q21.2
SNP_A-2156166	C	C	250	148	221	181	5.076	2.43E-02	rs11661192	18	29457621	q12.1
SNP_A-2151569	T	T	394	12	356	24	5.071	2.43E-02	rs177369	14	72830195	q24.2
SNP_A-2148049	C	C	327	27	346	50	5.07	2.43E-02	rs10975076	9	5358980	p24.1
SNP_A-1868179	G	G	330	38	294	56	5.076	2.43E-02	rs17159756	10	652688	p15.3
SNP_A-1857648	A	A	361	7	399	1	5.075	2.43E-02	rs8063003	16	28064838	p11.2
SNP_A-1842326	G	G	296	18	367	9	5.073	2.43E-02	rs12064900	1	29658165	p35.3
SNP_A-1809936	A	A	313	25	332	12	5.075	2.43E-02	rs2109689	9	122609372	q33.2
SNP_A-1809868	G	G	341	7	377	1	5.074	2.43E-02	rs10846743	12	123835185	q24.31
SNP_A-1780310	A	A	342	12	392	4	5.07	2.43E-02	rs6925880	6	73040935	q13
SNP_A-1724296	G	G	254	96	323	83	5.075	2.43E-02	rs958848	4	89167664	q22.1
SNP_A-1738459	T	T	259	63	321	49	5.073	2.43E-02	rs10495344	1	231352079	q42.2
SNP_A-1644666	T	T	242	106	248	154	5.073	2.43E-02	rs764142	2	194531691	q32.3
SNP_A-1965589	A	A	379	35	395	19	5.071	2.43E-02	rs10484549	6	30134269	p21.33
SNP_A-1930345	T	T	266	44	301	79	5.071	2.43E-02	rs6814640	4	169637272	q32.3
SNP_A-1911313	G	G	270	88	330	72	5.07	2.43E-02	rs1024217	3	198590507	q29
SNP_A-1881501	G	G	245	115	309	101	5.076	2.43E-02	rs6961517	7	132588195	q33
SNP_A-1874003	C	C	284	112	316	86	5.076	2.43E-02	rs11214037	11	111278506	q23.1
SNP_A-1880240	C	C	328	28	329	49	5.074	2.43E-02	rs17266887	2	227382564	q36.3
SNP_A-1891965	C	C	295	49	330	32	5.072	2.43E-02	rs7645328	3	76968476	p12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893093	A	A	326	32	392	20	5.074	2.43E-02	rs2074018	11	2266210	p15.5
SNP_A-1899446	A	A	283	103	261	135	5.065	2.44E-02	rs3750207	8	144692227	q24.3
SNP_A-1919324	A	A	336	30	354	54	5.063	2.44E-02	rs1033643	20	40609029	q12
SNP_A-1926177	G	G	345	3	387	13	5.069	2.44E-02	rs17077853	18	63531155	q22.1
SNP_A-1984630	G	G	272	124	290	92	5.067	2.44E-02	rs870488	5	173545691	q35.2
SNP_A-1977884	C	C	293	67	306	104	5.063	2.44E-02	rs17009158	4	85837673	q21.23
SNP_A-1675025	T	T	276	62	347	49	5.063	2.44E-02	rs10518477	4	127270470	q28.1
SNP_A-1734718	G	G	349	43	329	65	5.066	2.44E-02	rs761562	20	8681438	p12.3
SNP_A-1809778	G	G	285	135	245	161	5.067	2.44E-02	rs10190539	2	225861662	q36.2
SNP_A-1786098	A	A	285	131	254	162	5.063	2.44E-02	rs2736860	8	134519012	q24.22
SNP_A-1864945	T	T	265	103	267	147	5.063	2.44E-02	rs1283772	2	156350156	q24.1
SNP_A-2145174	G	G	265	105	264	148	5.069	2.44E-02	rs7596052	2	43693477	p21
SNP_A-2132507	T	T	236	132	298	118	5.063	2.44E-02	rs3748577	1	10291672	p36.22
SNP_A-2133271	A	A	325	5	342	16	5.064	2.44E-02	rs4932715	19	23614833	p12
SNP_A-2130306	G	G	325	31	346	56	5.068	2.44E-02	rs12431131	13	49937752	q14.3
SNP_A-2122517	C	C	318	76	284	100	5.065	2.44E-02	rs7097203	10	82801181	q22.3
SNP_A-2217430	C	C	329	39	349	67	5.066	2.44E-02	rs1959351	14	52609999	q22.1
SNP_A-2010864	C	C	287	29	272	48	5.066	2.44E-02	rs6862256	5	43901209	p12
SNP_A-2010511	A	A	233	97	307	87	5.066	2.44E-02	rs3822303	4	186669737	q35.1
SNP_A-2021777	T	T	338	72	301	95	5.068	2.44E-02	rs4640493	22	43708323	q13.31
SNP_A-2045098	C	C	236	132	298	118	5.063	2.44E-02	rs4750200	10	6348652	p15.1
SNP_A-2053321	G	G	314	12	336	28	5.067	2.44E-02	rs9304377	18	45296554	q21.1
SNP_A-2076893	C	C	281	89	343	73	5.066	2.44E-02	rs310845	12	75983791	q21.2
SNP_A-2291053	G	G	261	47	282	80	5.068	2.44E-02	---	18	47954032	q21.1
SNP_A-2272137	C	C	213	157	272	144	5.064	2.44E-02	rs841374	1	19270891	p36.13
SNP_A-2247746	G	G	238	166	203	195	5.063	2.44E-02	rs579929	6	11749034	p24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2244717	T	T	186	148	243	137	5.055	2.45E-02	rs4323059	4	161261453	q32.1
SNP_A-2236766	C	C	349	1	366	8	5.059	2.45E-02	rs1203888	20	22494275	p11.21
SNP_A-2240492	T	C	214	188	222	184	5.061	2.45E-02	rs7485444	12	96752154	q23.1
SNP_A-2283213	C	C	368	44	386	26	5.058	2.45E-02	rs8029601	15	90082672	q26.1
SNP_A-2285821	G	G	213	141	207	191	5.059	2.45E-02	rs1353414	3	88859735	p11.1
SNP_A-2301813	T	T	311	59	279	81	5.057	2.45E-02	rs1478462	19	42838865	q13.12
SNP_A-2102318	C	C	336	30	398	18	5.061	2.45E-02	rs12418465	11	80583269	q14.1
SNP_A-2222464	G	G	330	40	348	68	5.062	2.45E-02	rs3739391	8	6407942	p23.1
SNP_A-2223472	A	A	397	5	404	0	5.056	2.45E-02	rs9753569	20	32004370	q11.22
SNP_A-2205392	T	T	315	53	374	38	5.059	2.45E-02	rs17084901	13	26397556	q12.13
SNP_A-2202303	C	C	331	37	350	64	5.06	2.45E-02	rs3799802	6	94160581	q16.1
SNP_A-2209062	C	C	329	23	382	12	5.059	2.45E-02	rs1673443	2	65705444	p14
SNP_A-2185164	A	A	406	0	399	5	5.056	2.45E-02	rs17077514	3	45269454	p21.31
SNP_A-2181187	C	C	334	12	358	28	5.062	2.45E-02	rs12938916	17	53221286	q23.2
SNP_A-2176605	G	G	218	114	204	152	5.062	2.45E-02	rs6838653	4	177763022	q34.2
SNP_A-2166410	C	C	269	145	292	112	5.059	2.45E-02	rs2426977	20	59205490	q13.33
SNP_A-1863531	G	G	392	4	375	13	5.06	2.45E-02	rs16941330	16	85072611	q24.1
SNP_A-1819338	C	C	323	21	389	11	5.057	2.45E-02	rs7464847	8	11830856	p23.1
SNP_A-1822818	A	A	367	17	405	7	5.058	2.45E-02	rs11082770	18	45429668	q21.1
SNP_A-1748707	G	G	284	82	289	121	5.058	2.45E-02	rs724211	12	70321877	q21.1
SNP_A-1717739	C	C	402	0	395	5	5.057	2.45E-02	rs1529563	2	218681802	q35
SNP_A-1755402	T	T	291	109	271	143	5.06	2.45E-02	rs4984391	15	92672584	q26.2
SNP_A-1752937	C	C	262	82	315	65	5.057	2.45E-02	rs7981959	13	18582332	q12.11
SNP_A-1647408	A	A	398	0	391	5	5.057	2.45E-02	rs10495292	1	227161100	q42.13
SNP_A-1964259	C	C	219	197	250	164	5.061	2.45E-02	rs13031025	2	101376029	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1951477	T	T	366	48	345	71	5.061	2.45E-02	rs10187195	2	100039843	q11.2
SNP_A-1958956	G	G	359	61	331	85	5.062	2.45E-02	rs6508877	19	44778442	q13.2
SNP_A-1943215	C	C	214	118	210	164	5.061	2.45E-02	rs3778241	6	70512716	q13
SNP_A-1917243	G	G	217	147	205	193	5.058	2.45E-02	rs1548807	14	74549335	q24.3
SNP_A-1887029	G	G	378	26	342	42	5.06	2.45E-02	rs4147864	1	94179259	p22.1
SNP_A-1911238	T	T	412	0	405	5	5.055	0.0246	rs16941021	18	20657295	q11.2
SNP_A-1943619	C	C	190	178	248	168	5.05	0.0246	rs1463095	4	89149800	q22.1
SNP_A-1948480	T	T	269	129	305	103	5.048	0.0246	rs7117996	11	339122	p15.5
SNP_A-1970625	A	A	278	130	241	157	5.055	0.0246	---	21	45829474	q22.3
SNP_A-1984063	A	G	181	163	200	158	5.055	0.0246	rs1544298	1	212652689	q41
SNP_A-1649428	C	C	335	63	367	43	5.055	0.0246	rs1775752	1	117676251	p12
SNP_A-1660109	G	G	284	118	321	93	5.05	0.0246	rs10514611	16	85736721	q24.1
SNP_A-1780401	T	T	233	187	265	155	5.05	0.0246	rs8105431	19	14795891	p13.12
SNP_A-1780614	G	A	226	180	211	193	5.052	0.0246	rs6693882	1	95857989	p21.3
SNP_A-1742099	G	G	349	47	340	72	5.055	0.0246	rs7681587	4	44826900	p13
SNP_A-1811153	G	G	310	52	329	85	5.052	0.0246	rs4803801	19	43317948	q13.13
SNP_A-1802351	T	T	200	170	253	155	5.049	0.0246	rs509062	20	56315644	q13.32
SNP_A-1832980	C	C	304	38	324	66	5.05	0.0246	rs1919335	8	35280653	p12
SNP_A-2165053	A	G	210	196	228	178	5.054	0.0246	rs2293424	19	52671965	q13.32
SNP_A-2163972	C	C	318	44	356	28	5.054	0.0246	rs7558504	2	194563662	q32.3
SNP_A-2153599	A	A	217	151	212	204	5.051	0.0246	rs7199748	16	7223826	p13.2
SNP_A-2111781	A	A	306	26	334	50	5.054	0.0246	rs1918456	2	57704053	p16.1
SNP_A-2123465	C	C	348	12	398	4	5.052	0.0246	rs11011957	10	20644383	p12.31
SNP_A-2137108	C	C	405	5	412	0	5.055	0.0246	rs6495541	15	79223619	q25.1
SNP_A-2179670	A	A	411	5	418	0	5.054	0.0246	rs17008714	2	123272285	q14.3
SNP_A-2184776	A	A	284	56	234	72	5.051	0.0246	rs7101558	11	114892659	q23.3
SNP_A-2192479	G	G	319	43	377	29	5.051	0.0246	rs1911513	6	79562355	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2194530	G	G	244	168	213	201	5.049	0.0246	rs11725773	4	48037263	p12
SNP_A-2216949	C	C	267	57	308	40	5.052	0.0246	rs2581655	18	71152131	q22.3
SNP_A-2086740	C	C	295	63	306	98	5.052	0.0246	rs495948	4	58469877	q12
SNP_A-2071706	T	T	189	177	240	162	5.05	0.0246	rs1555140	20	46819863	q13.13
SNP_A-2070727	G	G	320	46	382	32	5.054	0.0246	rs8136107	22	35691808	q12.3
SNP_A-2063488	C	C	319	43	377	29	5.051	0.0246	rs11829757	12	57087790	q14.1
SNP_A-2044463	C	C	409	5	416	0	5.055	0.0246	rs10089149	8	32048465	p12
SNP_A-2021468	C	C	376	38	350	58	5.054	0.0246	rs12933660	16	64692102	q22.1
SNP_A-2003749	A	A	327	39	347	67	5.055	0.0246	rs4898778	14	52599419	q22.1
SNP_A-1997930	A	A	393	23	374	40	5.053	0.0246	rs10513388	9	121896552	q33.2
SNP_A-1993109	A	A	377	31	356	50	5.054	0.0246	rs716398	8	40274016	p11.21
SNP_A-2311614	A	A	413	1	375	7	5.054	0.0246	rs7773704	6	8004016	p24.3
SNP_A-2292522	C	C	416	0	409	5	5.055	0.0246	rs734917	15	39940529	q15.1
SNP_A-2301539	G	G	339	83	360	58	5.045	0.0247	rs217242	11	1941487	p15.5
SNP_A-2309456	T	T	326	36	323	59	5.048	0.0247	rs9517668	13	98721841	q32.3
SNP_A-2280766	G	G	318	8	398	2	5.048	0.0247	rs10991325	9	104444359	q31.1
SNP_A-2279735	A	A	348	4	362	14	5.046	0.0247	rs426848	19	6593482	p13.3
SNP_A-2267477	C	C	346	76	366	52	5.043	0.0247	rs6439921	3	141648306	q23
SNP_A-2261221	C	C	399	23	380	40	5.046	0.0247	rs17820725	17	52051590	q23.2
SNP_A-2243787	G	G	371	9	406	2	5.043	0.0247	rs6712857	2	9640675	p25.1
SNP_A-2011490	G	G	339	79	309	105	5.044	0.0247	rs4700834	5	178841576	q35.3
SNP_A-2070481	G	G	275	139	296	106	5.042	0.0247	rs1732187	3	110782731	q13.13
SNP_A-2070555	G	G	206	134	254	116	5.046	0.0247	rs7157813	14	102533314	q32.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074025	C	C	314	28	308	48	5.042	0.0247	rs11923766	3	168975396	q26.1
SNP_A-2093628	G	G	240	126	239	175	5.044	0.0247	rs8010270	14	27949324	q12
SNP_A-2218157	C	C	349	19	405	9	5.042	0.0247	rs9974024	20	24345275	p11.21
SNP_A-2215918	T	T	368	54	341	77	5.047	0.0247	rs12633498	3	133136962	q22.1
SNP_A-2222610	G	G	289	75	354	60	5.045	0.0247	rs10044138	5	165217608	q34
SNP_A-2194666	G	A	210	158	212	204	5.048	0.0247	rs10953550	7	107065054	q31.1
SNP_A-2177882	C	C	252	96	267	145	5.042	0.0247	rs1518430	2	180814790	q31.3
SNP_A-2174254	C	C	285	55	326	38	5.046	0.0247	rs763086	22	34943557	q12.3
SNP_A-2110302	C	C	350	12	400	4	5.046	0.0247	rs9592959	13	73439823	q22.1
SNP_A-2110222	T	T	347	19	375	39	5.048	0.0247	rs967655	9	88793978	q22.1
SNP_A-2123323	G	G	314	56	375	41	5.045	0.0247	rs12548150	8	3190352	p23.2
SNP_A-2157732	A	A	406	2	371	9	5.043	0.0247	rs16907467	11	21074416	p15.1
SNP_A-1830404	T	T	409	7	396	18	5.045	0.0247	rs2616876	15	52011902	q21.3
SNP_A-1827097	C	C	356	8	373	21	5.045	0.0247	rs259039	5	79732760	q14.1
SNP_A-1817951	A	A	290	54	361	41	5.044	0.0247	rs9561558	13	93863575	q32.1
SNP_A-1807124	C	C	313	51	321	81	5.046	0.0247	rs12051058	16	59000229	q21
SNP_A-1798778	A	A	336	10	401	3	5.047	0.0247	rs2069723	12	66834861	q15
SNP_A-1758201	A	A	266	84	337	71	5.042	0.0247	rs2880170	4	60584817	q13.1
SNP_A-1975145	G	G	259	111	257	155	5.045	0.0247	rs10936294	3	163734636	q26.1
SNP_A-1953139	C	C	290	118	321	91	5.041	0.0247	rs6823684	4	30104157	p15.1
SNP_A-1943197	T	T	311	35	366	22	5.046	0.0247	rs12714584	3	84337910	p12.1
SNP_A-1942440	T	T	419	1	381	7	5.046	0.0247	rs17168373	5	134813951	q31.1
SNP_A-1917001	G	G	393	13	410	4	5.047	0.0247	rs17155965	7	81443353	q21.11
SNP_A-1916045	C	C	221	159	260	134	5.044	0.0247	rs649652	3	125946347	q21.2
SNP_A-1927494	G	G	323	43	340	72	5.047	0.0247	rs6588107	1	65111329	p31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932006	G	G	208	152	273	143	5.043	0.0247	rs1574272	7	68188898	q11.22
SNP_A-1887108	G	G	332	30	358	16	5.046	0.0247	rs2130784	10	122889375	q26.12
SNP_A-1875016	G	G	297	61	365	47	5.037	2.48E-02	rs595580	4	23700188	p15.2
SNP_A-1924139	A	A	272	150	301	119	5.035	2.48E-02	rs4973856	3	27065494	p24.2
SNP_A-1925063	T	T	243	121	301	105	5.041	2.48E-02	rs6696870	1	209393739	q32.3
SNP_A-1943929	G	G	331	17	336	34	5.035	2.48E-02	rs9915285	17	43831448	q21.32
SNP_A-1937064	C	C	410	2	375	9	5.036	2.48E-02	rs6502856	17	5098084	p13.2
SNP_A-1984617	C	C	258	108	321	93	5.04	2.48E-02	rs7736275	5	173000292	q35.2
SNP_A-1747843	G	G	381	19	406	8	5.036	2.48E-02	rs10483555	14	47880636	q21.3
SNP_A-1668642	T	T	228	122	298	112	5.037	2.48E-02	rs3886516	13	99276519	q32.3
SNP_A-1815121	A	A	326	16	385	7	5.035	2.48E-02	rs6549069	3	86211179	p12.1
SNP_A-1827344	A	A	353	15	404	6	5.04	2.48E-02	rs2008835	7	31765413	p14.3
SNP_A-1837271	T	T	360	2	370	10	5.037	2.48E-02	rs17070168	13	78210998	q31.1
SNP_A-1862761	G	G	290	120	265	153	5.038	2.48E-02	rs7185684	16	7221942	p13.2
SNP_A-1872474	C	C	341	45	314	66	5.039	2.48E-02	rs1020516	7	33377261	p14.3
SNP_A-2156229	A	A	406	8	381	19	5.036	2.48E-02	rs10794901	10	2341551	p15.3
SNP_A-2165443	A	A	360	2	370	10	5.037	2.48E-02	rs9401748	6	124857626	q22.31
SNP_A-2144712	C	C	302	66	360	50	5.036	2.48E-02	rs9520463	13	87831309	q31.2
SNP_A-2139232	G	G	320	12	357	29	5.038	2.48E-02	rs16842228	2	158561569	q24.1
SNP_A-2119881	C	C	303	49	356	34	5.04	2.48E-02	rs10999682	10	72540296	q22.1
SNP_A-2171356	A	A	229	135	285	119	5.039	2.48E-02	rs700621	5	138126329	q31.2
SNP_A-2178914	G	T	212	158	209	203	5.041	2.48E-02	rs9545193	13	79253962	q31.1
SNP_A-2193726	G	G	192	168	242	152	5.037	2.48E-02	rs10044618	5	87816924	q14.3
SNP_A-2209812	C	C	226	140	267	117	5.039	2.48E-02	rs17715303	6	36229446	p21.31
SNP_A-2093802	G	G	328	10	391	3	5.035	2.48E-02	rs17656278	4	48441627	p12
SNP_A-2094136	C	C	332	28	367	15	5.035	2.48E-02	rs6748368	2	37821038	p22.2
SNP_A-2060289	A	A	363	1	382	8	5.038	2.48E-02	rs6580575	5	148107835	q32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015413	G	G	295	9	397	3	5.037	2.48E-02	rs11911884	21	15762342	q21.1
SNP_A-2000987	G	G	251	97	234	130	5.036	2.48E-02	rs10825113	10	55250563	q21.1
SNP_A-2027362	G	G	349	15	379	33	5.036	2.48E-02	rs11196100	10	114520508	q25.2
SNP_A-2038894	T	T	297	119	319	89	5.035	2.48E-02	rs4766860	12	116450969	q24.22
SNP_A-2036722	T	T	353	17	347	33	5.039	2.48E-02	rs6059286	20	31421653	q11.21
SNP_A-2249639	A	A	286	56	283	85	5.035	2.48E-02	rs3821084	2	172163807	q31.1
SNP_A-2257963	T	T	290	78	296	116	5.039	2.48E-02	rs1490524	4	158906205	q32.1
SNP_A-2281138	T	T	282	64	336	48	5.04	2.48E-02	rs361165	4	153152305	q31.3
SNP_A-2295584	C	C	261	157	289	125	5.038	2.48E-02	rs11042068	11	8772175	p15.4
SNP_A-2292393	G	G	225	179	260	150	5.038	2.48E-02	rs3735802	8	141530367	q24.3
SNP_A-2291729	C	C	242	150	284	126	5.039	2.48E-02	rs11760055	6	148504292	q24.3
SNP_A-2288260	T	T	249	165	280	134	5.031	2.49E-02	rs8011350	14	69684461	q24.2
SNP_A-2267118	G	G	244	150	282	124	5.034	2.49E-02	rs17594870	8	8161043	p23.1
SNP_A-2271733	A	A	322	8	402	2	5.03	2.49E-02	rs17120194	1	99479908	p21.3
SNP_A-2255774	C	C	352	46	363	27	5.034	2.49E-02	rs9378127	6	33030437	p21.32
SNP_A-2243386	G	G	348	70	319	95	5.03	2.49E-02	rs321632	4	47859256	p12
SNP_A-2046722	C	C	234	130	293	115	5.032	2.49E-02	rs11152081	18	54364418	q21.31
SNP_A-2042255	A	C	209	199	231	177	5.034	2.49E-02	rs6038317	20	5813636	p12.3
SNP_A-2029232	G	G	326	36	385	23	5.03	2.49E-02	rs10210186	2	84766504	p11.2
SNP_A-2025377	T	T	357	1	376	8	5.032	2.49E-02	rs6880771	5	54093808	q11.2
SNP_A-2007396	C	C	418	0	413	5	5.03	2.49E-02	rs6042275	20	13579015	p12.1
SNP_A-2055890	T	T	326	44	386	30	5.03	2.49E-02	rs11183067	12	44180640	q12
SNP_A-2075786	G	G	415	5	420	0	5.03	2.49E-02	rs6932764	6	44637775	p21.1
SNP_A-2096285	T	T	402	0	397	5	5.031	2.49E-02	rs16832281	1	157403074	q23.3
SNP_A-2105320	C	C	406	0	401	5	5.031	2.49E-02	rs16917975	12	9118251	p13.31
SNP_A-2084170	G	G	213	127	279	117	5.032	2.49E-02	rs1525646	7	45371779	p13
SNP_A-2213598	T	T	391	31	370	50	5.032	2.49E-02	rs4945197	11	77056036	q13.5

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2184501	G	G	263	101	323	85	5.028	2.49E-02	rs2454161	1	17231220	p36.13
SNP_A-2176106	A	A	411	5	416	0	5.03	2.49E-02	rs7203124	16	19019657	p12.3
SNP_A-2172635	C	C	353	65	373	43	5.028	2.49E-02	rs12027713	1	25099252	p36.11
SNP_A-2173219	C	C	269	95	274	138	5.032	2.49E-02	rs13020350	2	192317626	q32.3
SNP_A-2142479	G	G	324	82	270	100	5.03	2.49E-02	rs922699	4	12245974	p15.33
SNP_A-2149552	G	G	415	5	420	0	5.03	2.49E-02	rs17008715	2	123272349	q14.3
SNP_A-2162730	T	T	187	161	227	139	5.027	2.49E-02	rs4961077	8	87180823	q21.3
SNP_A-2161811	T	T	394	22	368	38	5.033	2.49E-02	rs16999333	22	47246588	q13.32
SNP_A-1861225	C	C	258	106	324	92	5.03	2.49E-02	rs9930089	16	57765570	q21
SNP_A-1832122	C	C	397	5	402	0	5.031	2.49E-02	rs30134492	1	160089440	q23.3
SNP_A-1815513	C	C	356	12	406	4	5.028	2.49E-02	rs2020234	18	69105359	q22.3
SNP_A-1642173	C	C	299	103	335	79	5.034	2.49E-02	rs37192	5	142326644	q31.3
SNP_A-1643301	A	A	402	0	397	5	5.031	2.49E-02	rs10510062	10	121545212	q26.12
SNP_A-1696414	C	C	388	0	383	5	5.032	2.49E-02	rs280405	13	54492996	q21.1
SNP_A-1742147	A	A	310	90	340	66	5.033	2.49E-02	rs1913758	10	82009374	q22.3
SNP_A-1714741	C	C	310	88	294	120	5.034	2.49E-02	rs1219906	2	122840005	q14.3
SNP_A-1792441	C	C	411	5	416	0	5.03	2.49E-02	rs4630093	1	181079678	q25.3
SNP_A-1793479	G	G	236	178	265	145	5.031	2.49E-02	rs10891487	11	112374264	q23.1
SNP_A-1792936	G	G	314	46	330	76	5.03	2.49E-02	rs9962899	18	3907030	p11.31
SNP_A-1789008	G	G	386	6	389	17	5.028	2.49E-02	rs7139943	13	39733934	q14.11
SNP_A-1986243	G	G	306	54	326	88	5.031	2.49E-02	rs16896290	6	65885209	q12
SNP_A-1962098	A	T	208	158	212	202	5.034	2.49E-02	rs2110778	2	10699568	p25.1
SNP_A-1886198	G	G	243	111	242	156	5.029	2.49E-02	rs4798095	18	3429156	p11.31
SNP_A-1881434	A	A	418	0	413	5	5.03	2.49E-02	rs6042307	20	13621708	p12.1
SNP_A-1886808	G	G	301	35	354	22	5.022	2.50E-02	rs10150771	14	56744938	q22.3
SNP_A-1897727	A	A	217	161	247	131	5.022	2.50E-02	rs861606	1	181482280	q25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893347	A	A	380	40	345	59	5.027	2.50E-02	rs16911857	11	12923405	p15.2
SNP_A-1920675	G	G	315	103	332	74	5.024	2.50E-02	rs3117229	6	33164047	p21.32
SNP_A-1912881	G	G	264	76	315	59	5.025	2.50E-02	rs11549706	3	17106505	p24.3
SNP_A-1904544	A	A	351	65	329	91	5.026	2.50E-02	rs11088102	21	29228627	q21.3
SNP_A-1966706	C	C	317	49	381	35	5.025	2.50E-02	rs7593426	2	210559341	q34
SNP_A-1989490	A	A	214	150	273	137	5.021	2.50E-02	rs318572	7	34050005	p14.3
SNP_A-1977679	T	T	224	142	216	190	5.026	2.50E-02	rs9307224	4	78234018	q21.1
SNP_A-1954392	G	G	244	176	273	143	5.021	2.50E-02	rs6426714	1	19206907	p36.13
SNP_A-1954184	C	C	339	27	360	50	5.022	2.50E-02	rs11897760	2	118220594	q14.1
SNP_A-1959755	G	G	271	51	258	76	5.023	2.50E-02	rs7998948	13	19271628	q12.11
SNP_A-1805116	C	C	334	44	319	67	5.027	2.50E-02	rs757919	2	151668359	q23.3
SNP_A-1754936	C	C	317	29	351	55	5.023	2.50E-02	rs539620	6	87457843	q14.3
SNP_A-1816133	A	A	234	98	226	136	5.023	2.50E-02	rs12436651	14	20088121	q11.2
SNP_A-1836429	G	G	349	7	383	1	5.027	2.50E-02	rs3957815	12	79927662	q21.31
SNP_A-1859462	G	G	378	14	347	27	5.027	2.50E-02	rs11016421	10	130347804	q26.2
SNP_A-2151769	T	T	185	107	248	98	5.027	2.50E-02	rs7869857	9	1480268	p24.3
SNP_A-2121500	G	G	261	109	262	154	5.027	2.50E-02	rs10862244	12	80013763	q21.31
SNP_A-2121998	G	G	284	48	333	33	5.025	2.50E-02	rs4724219	7	43362188	p13
SNP_A-2107758	C	C	394	20	396	8	5.026	2.50E-02	rs176564	7	105406476	q22.3
SNP_A-2108535	A	A	259	103	261	147	5.022	2.50E-02	rs4964585	12	106405235	q23.3
SNP_A-2135929	G	G	296	62	364	48	5.026	2.50E-02	rs1506375	12	30375847	p11.22
SNP_A-2134880	C	C	336	22	383	11	5.027	2.50E-02	rs9321305	6	132035858	q23.2
SNP_A-2074513	G	G	278	90	335	73	5.025	2.50E-02	rs7980273	12	17102747	p12.3
SNP_A-2073357	A	A	381	9	416	2	5.027	2.50E-02	rs4340388	18	25592347	q12.1
SNP_A-1996758	C	C	269	151	298	120	5.025	2.50E-02	rs1981160	9	70792277	q21.11
SNP_A-2033212	C	C	335	83	361	59	5.023	2.50E-02	rs6665825	1	85667282	p22.3
SNP_A-2033483	T	T	348	2	358	10	5.027	2.50E-02	rs7653503	3	153405628	q25.1
SNP_A-2245237	G	G	340	46	343	73	5.024	2.50E-02	rs10862707	12	75773016	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2237248	G	G	285	69	353	55	5.027	2.50E-02	rs9262539	6	31098469	p21.33
SNP_A-2233846	T	T	272	70	343	57	5.024	2.50E-02	rs12913151	15	43760862	q21.1
SNP_A-2266503	G	G	319	11	402	4	5.027	2.50E-02	rs7997646	13	39602528	q14.11
SNP_A-2261814	A	A	403	15	409	5	5.025	2.50E-02	---	3	63375278	p14.2
SNP_A-2276536	T	T	324	8	404	2	5.022	2.50E-02	rs9994004	4	45293792	p13
SNP_A-2292779	A	A	302	114	325	85	5.027	2.50E-02	rs364583	8	37278504	p12
SNP_A-2298561	C	C	217	147	271	131	5.024	2.50E-02	rs1868998	8	40577154	p11.21
SNP_A-2273088	T	T	386	28	355	45	5.016	2.51E-02	---	3	106658336	q13.11
SNP_A-2238154	A	A	331	5	350	16	5.019	2.51E-02	rs6742504	2	240840734	q37.3
SNP_A-2256147	T	T	321	15	325	31	5.016	2.51E-02	rs16826199	3	157653145	q25.31
SNP_A-2249393	A	A	274	138	302	108	5.015	2.51E-02	rs473606	6	47916136	p12.3
SNP_A-2029433	T	T	279	39	295	67	5.016	2.51E-02	rs1553093	4	126214628	q28.1
SNP_A-2023937	A	A	370	16	357	31	5.015	2.51E-02	rs7935056	11	22296969	p14.3
SNP_A-2034061	A	A	355	25	374	12	5.016	2.51E-02	rs10924280	1	242141540	q44
SNP_A-2001158	T	C	193	167	216	180	5.019	2.51E-02	rs2939929	10	55406337	q21.1
SNP_A-1997526	C	C	231	135	224	182	5.017	2.51E-02	rs1491106	9	106563072	q31.2
SNP_A-2014473	G	G	285	79	340	62	5.017	2.51E-02	rs4317650	9	110463618	q31.3
SNP_A-2075663	C	C	251	105	237	141	5.015	2.51E-02	rs9495378	6	139564988	q24.1
SNP_A-2063333	G	G	340	24	364	46	5.016	2.51E-02	rs4956450	4	141858911	q31.21
SNP_A-2063671	T	T	230	138	226	188	5.015	2.51E-02	rs11856940	15	45298606	q21.1
SNP_A-2068075	G	G	296	54	360	40	5.018	2.51E-02	rs7433989	3	110568968	q13.13
SNP_A-2083824	T	T	228	76	286	62	5.019	2.51E-02	rs17284862	8	123813010	q24.13
SNP_A-2082196	A	A	304	54	324	88	5.015	2.51E-02	rs17763038	17	60676740	q24.1
SNP_A-2085731	G	G	391	27	371	45	5.02	2.51E-02	rs2213725	22	42599015	q13.2
SNP_A-2093900	A	A	330	16	389	7	5.017	2.51E-02	rs16950267	18	6549611	p11.31
SNP_A-2132725	T	T	260	106	323	91	5.015	2.51E-02	rs1171115	6	84286342	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2108307	C	C	360	30	350	50	5.015	2.51E-02	rs193858	7	105170508	q22.3
SNP_A-2153056	C	C	289	119	320	92	5.014	2.51E-02	rs6856111	4	37206719	p14
SNP_A-1862223	G	G	391	11	417	3	5.016	2.51E-02	rs17033738	3	35761535	p22.3
SNP_A-1872796	A	A	330	34	338	58	5.018	2.51E-02	rs2296753	9	90961319	q22.2
SNP_A-1873513	G	G	366	22	388	10	5.015	2.51E-02	rs7981921	13	56775905	q21.1
SNP_A-1817228	G	G	284	66	333	49	5.015	2.51E-02	rs629768	8	29199260	p12
SNP_A-1751745	T	T	331	5	350	16	5.019	2.51E-02	rs10516807	4	89777624	q22.1
SNP_A-1803163	A	A	197	165	240	144	5.014	2.51E-02	rs12619127	2	116897269	q14.1
SNP_A-1968954	C	C	321	23	395	13	5.015	2.51E-02	rs16998778	21	13718506	q11.2
SNP_A-1921359	A	A	290	46	291	73	5.016	2.51E-02	rs794783	6	15410151	p22.3
SNP_A-1931864	G	G	266	104	268	148	5.015	2.51E-02	---	5	31089541	p13.3
SNP_A-1930896	C	C	312	48	374	34	5.013	0.0252	rs1392391	5	173616520	q35.2
SNP_A-1927372	T	T	390	10	368	22	5.013	0.0252	rs996793	9	23666631	p21.3
SNP_A-1928951	C	T	206	158	209	197	5.012	0.0252	rs1451988	2	103681107	q12.1
SNP_A-1964327	A	A	211	151	206	204	5.008	0.0252	rs1901480	2	103711523	q12.1
SNP_A-1981833	G	G	271	97	328	80	5.008	0.0252	rs16893616	5	61011999	q12.1
SNP_A-1951678	G	A	225	165	201	199	5.01	0.0252	rs1145196	11	116077415	q23.3
SNP_A-1952274	T	T	224	122	288	110	5.011	0.0252	rs637858	11	125340677	q24.2
SNP_A-1952914	C	C	305	27	351	15	5.01	0.0252	rs2286218	8	1436803	p23.3
SNP_A-1952587	G	G	419	1	383	7	5.012	0.0252	rs1389813	3	141822237	q23
SNP_A-1943298	A	A	325	85	262	100	5.013	0.0252	rs4757728	11	18824693	p15.1
SNP_A-1780892	A	A	373	25	359	43	5.013	0.0252	rs442173	5	9562018	p15.31
SNP_A-1742881	C	C	300	90	338	68	5.007	0.0252	rs7735817	5	24597817	p14.2
SNP_A-1731621	G	G	276	96	255	127	5.008	0.0252	rs7595076	2	68350787	p14
SNP_A-1657347	A	A	340	58	373	39	5.009	0.0252	rs6022041	20	51978779	q13.2
SNP_A-1840479	C	T	211	159	211	203	5.009	0.0252	rs726799	17	13441121	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1866304	G	G	370	0	367	5	5.007	0.0252	rs9453055	6	95642984	q16.1
SNP_A-2142609	A	A	380	40	384	22	5.011	0.0252	rs1865151	12	93980119	q22
SNP_A-2137586	T	T	283	71	289	107	5.008	0.0252	rs7334087	13	72897205	q22.1
SNP_A-2180295	A	A	315	45	364	30	5.013	0.0252	rs16917643	8	53372167	q11.23
SNP_A-2182963	A	A	317	43	334	72	5.013	0.0252	rs11795240	9	9383744	p23
SNP_A-2185505	G	G	335	85	306	112	5.008	0.0252	rs10274639	7	156256929	q36.3
SNP_A-2188456	T	T	356	36	374	20	5.01	0.0252	rs9436483	1	54835957	p32.3
SNP_A-2227229	G	G	296	72	302	108	5.007	0.0252	rs17376111	1	160689296	q23.3
SNP_A-2203725	C	C	347	15	396	6	5.008	0.0252	rs12603583	17	75858832	q25.3
SNP_A-2088428	C	C	300	68	310	104	5.01	0.0252	rs7777600	7	50366880	p12.2
SNP_A-2088978	C	C	279	61	324	44	5.011	0.0252	rs2619685	15	49083307	q21.2
SNP_A-2068954	C	C	382	28	360	46	5.011	0.0252	rs1286495	14	90103602	q32.12
SNP_A-2065378	T	T	276	88	284	130	5.013	0.0252	rs2553685	8	68847578	q13.2
SNP_A-2049420	A	A	340	64	358	42	5.01	0.0252	rs16850791	1	14798396	p36.21
SNP_A-2010632	T	T	373	25	359	43	5.013	0.0252	rs4626310	5	6971362	p15.31
SNP_A-2046307	G	G	330	24	364	12	5.007	0.0252	rs688913	1	97410245	p21.3
SNP_A-2025146	A	A	394	4	379	13	5.01	0.0252	rs7552251	1	116442162	p13.1
SNP_A-2233837	T	T	335	41	280	56	5.007	0.0252	rs291111	1	203457921	q32.1
SNP_A-2307106	T	T	314	50	360	34	5.008	0.0252	rs2099298	5	119682494	q23.1
SNP_A-2290781	A	A	362	44	330	64	5.005	0.0253	rs16828119	1	41466191	p34.2
SNP_A-2263897	T	T	253	165	284	134	5.004	0.0253	rs17288506	7	105741609	q22.3
SNP_A-2271455	T	T	281	89	338	72	5.006	0.0253	rs1473047	5	90566107	q14.3
SNP_A-2027233	T	T	361	1	382	8	5.002	0.0253	rs11960452	5	100991004	q21.1
SNP_A-2034629	G	G	409	5	412	0	5.006	0.0253	rs1573022	1	81986161	p31.1
SNP_A-2035611	A	A	249	117	251	165	5.002	0.0253	rs2651314	3	148546494	q24
SNP_A-2008758	C	C	316	52	332	84	5.004	0.0253	rs2172950	3	63615268	p14.2
SNP_A-2013165	A	A	378	36	349	55	5.002	0.0253	rs4841169	8	9436786	p23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017939	G	G	361	37	353	19	5.003	0.0253	rs2833273	21	31409848	q22.11
SNP_A-1992070	G	G	348	10	413	3	5.003	0.0253	rs2725663	8	5505734	p23.2
SNP_A-2051598	G	G	417	5	420	0	5.006	0.0253	rs12075373	1	25620396	p36.11
SNP_A-2062289	G	G	215	145	278	134	5.005	0.0253	rs9831830	3	158446300	q25.31
SNP_A-2097283	A	A	335	27	356	50	5.004	0.0253	rs1422220	5	155992645	q33.3
SNP_A-2106071	G	G	247	123	308	108	5.004	0.0253	rs885062	7	45810821	p13
SNP_A-2202373	G	G	321	21	385	11	5.002	0.0253	rs2794612	1	14418577	p36.21
SNP_A-2212112	G	G	384	0	381	5	5.007	0.0253	rs17106000	14	68144981	q24.1
SNP_A-2214220	A	A	358	12	386	28	5	0.0253	rs12350715	9	24340222	p21.3
SNP_A-2176851	A	A	359	57	335	81	5.004	0.0253	rs1885334	10	116192319	q25.3
SNP_A-2170223	-	C	185	185	240	174	5.001	0.0253	rs1942555	18	63609146	q22.1
SNP_A-2137715	C	C	231	101	270	80	5.001	0.0253	rs9862736	3	192437800	q28
SNP_A-2131867	C	C	417	5	420	0	5.006	0.0253	rs10988347	9	98797556	q22.33
SNP_A-2109602	G	G	401	5	404	0	5.006	0.0253	rs2529729	17	12139691	p12
SNP_A-2119093	A	A	363	19	338	34	5.005	0.0253	rs17216650	3	56540901	p14.3
SNP_A-2161756	A	A	391	5	394	0	5.006	0.0253	rs13340817	11	21070819	p15.1
SNP_A-2163883	T	T	347	47	360	28	5.007	0.0253	rs6129032	20	59072251	q13.33
SNP_A-1844511	G	G	361	1	382	8	5.002	0.0253	rs17019300	4	93608819	q22.3
SNP_A-1834974	T	T	215	151	208	202	5.005	0.0253	rs2778012	1	154424706	q23.1
SNP_A-1832517	T	T	249	117	251	165	5.002	0.0253	rs11077513	17	66186754	q24.3
SNP_A-1697166	C	C	243	95	302	80	5.003	0.0253	rs2787952	1	243197558	q44
SNP_A-1691290	A	A	337	9	378	24	5.005	0.0253	rs10492421	13	106992153	q33.3
SNP_A-1806660	A	A	270	146	235	175	5.002	0.0253	rs6743358	2	105704260	q12.2
SNP_A-1798850	C	C	411	5	414	0	5.006	0.0253	rs10134588	14	90851888	q32.12
SNP_A-1937182	A	A	313	37	337	65	5.001	0.0253	rs11016416	10	130341275	q26.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1957502	A	A	376	40	348	60	5.006	0.0253	rs477725	19	42066106	q13.12
SNP_A-1925658	A	A	229	125	228	174	5.005	0.0253	rs10750286	11	123958703	q24.2
SNP_A-1897564	T	T	283	139	248	168	5.004	0.0253	rs10871427	16	81079031	q23.3
SNP_A-1900045	A	A	279	89	323	69	4.995	2.54E-02	rs10063903	5	100702874	q21.1
SNP_A-1895854	C	C	231	125	277	105	4.995	2.54E-02	rs2561193	5	65148485	q12.3
SNP_A-1924327	T	T	391	31	404	16	4.995	2.54E-02	rs2124018	7	54584144	p11.2
SNP_A-1926170	T	T	203	161	261	149	4.998	2.54E-02	---	18	63528516	q22.1
SNP_A-1943716	A	A	239	123	301	109	4.998	2.54E-02	rs7751379	6	133489548	q23.2
SNP_A-1838786	G	G	313	57	326	90	4.998	2.54E-02	rs16853894	1	176011342	q25.2
SNP_A-1823042	A	A	347	5	368	16	4.997	2.54E-02	rs17066881	18	56216463	q21.32
SNP_A-1872025	T	C	217	197	227	183	4.993	2.54E-02	rs2163533	8	124953339	q24.13
SNP_A-2151618	G	G	259	151	296	124	4.998	2.54E-02	rs10247439	7	102950247	q22.1
SNP_A-2195338	T	A	199	157	214	196	4.998	2.54E-02	rs683109	18	58733882	q21.33
SNP_A-2198478	C	C	373	11	397	3	4.995	2.54E-02	rs10083783	16	77535210	q23.1
SNP_A-2224637	C	C	336	44	352	26	4.995	2.54E-02	rs11710521	3	4541789	p26.1
SNP_A-2201018	T	T	358	2	370	10	4.994	2.54E-02	rs17032406	1	8277547	p36.23
SNP_A-2095879	T	T	334	16	393	7	4.999	2.54E-02	rs12554003	9	70839842	q21.12
SNP_A-2092226	A	A	282	74	350	60	4.997	2.54E-02	rs2117914	12	94768503	q23.1
SNP_A-2077784	G	G	318	40	370	26	4.998	2.54E-02	rs12646561	4	75657801	q13.3
SNP_A-2059089	A	A	327	43	385	29	4.993	2.54E-02	rs12313713	12	79278285	q21.31
SNP_A-2075500	C	C	267	77	257	47	4.999	2.54E-02	rs9376168	6	136306714	q23.3
SNP_A-2017984	T	T	265	125	245	161	4.996	2.54E-02	rs508288	21	31656623	q22.11
SNP_A-2025848	A	A	313	105	281	133	4.999	2.54E-02	rs3781214	10	63811969	q21.2
SNP_A-2270460	C	T	220	164	191	185	4.995	2.54E-02	rs4780718	16	16894078	p12.3
SNP_A-2284797	T	C	194	176	230	184	4.993	2.54E-02	rs843365	3	185383431	q27.1
SNP_A-2235104	C	C	398	14	380	4	4.993	2.54E-02	rs17579281	8	21263941	p21.3
SNP_A-2291253	T	C	185	163	218	178	4.999	2.54E-02	rs989547	15	61963259	q22.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2307772	T	T	405	3	381	11	4.986	2.55E-02	rs16947280	17	59370252	q23.3
SNP_A-2301845	T	T	277	41	345	29	4.992	2.55E-02	rs12621362	2	88643147	p11.2
SNP_A-2234751	G	G	321	47	383	33	4.99	2.55E-02	rs17515130	4	119106025	q26
SNP_A-2233715	G	G	323	45	383	31	4.989	2.55E-02	rs2407603	1	59757311	p32.1
SNP_A-2243888	C	C	295	49	346	34	4.991	2.55E-02	rs4473895	6	115275676	q22.1
SNP_A-2243479	C	C	269	99	268	140	4.987	2.55E-02	rs9374579	6	116275968	q22.1
SNP_A-2275212	G	G	413	7	402	18	4.988	2.55E-02	rs11157874	14	51611293	q22.1
SNP_A-2274706	A	A	314	18	335	37	4.987	2.55E-02	rs1580043	4	76130566	q13.3
SNP_A-2276974	G	G	235	159	206	192	4.99	2.55E-02	rs1418546	1	185969564	q31.1
SNP_A-2026020	A	A	377	11	401	3	4.991	2.55E-02	rs1538543	1	211795391	q41
SNP_A-2026537	T	T	339	11	313	23	4.988	2.55E-02	rs8038734	15	70598456	q24.1
SNP_A-2029633	G	G	201	151	264	142	4.99	2.55E-02	rs3922940	3	140880793	q23
SNP_A-2032305	C	C	305	63	361	47	4.987	2.55E-02	rs134734	22	24841924	q12.1
SNP_A-2030491	G	G	284	76	289	113	4.987	2.55E-02	rs7071218	10	90357870	q23.31
SNP_A-2044839	C	C	323	21	387	11	4.991	2.55E-02	rs12631294	3	149623768	q24
SNP_A-2006412	T	C	176	146	192	164	4.991	2.55E-02	rs965949	1	40823500	p34.2
SNP_A-1996285	A	A	354	12	382	28	4.986	2.55E-02	rs16908269	9	24340134	p21.3
SNP_A-2058597	T	T	253	163	220	194	4.989	2.55E-02	rs6724028	2	815247	p25.3
SNP_A-2051742	A	G	181	175	228	170	4.991	2.55E-02	rs731803	20	53941220	q13.31
SNP_A-2048199	C	C	276	88	336	72	4.991	2.55E-02	rs2134253	16	54321375	q12.2
SNP_A-2078706	T	T	314	52	330	84	4.992	2.55E-02	rs2533109	7	145820636	q35
SNP_A-2214756	C	C	399	3	375	11	4.993	2.55E-02	rs10928930	2	130215212	q21.1
SNP_A-2183756	G	G	366	34	341	53	4.988	2.55E-02	rs17120763	14	84660401	q31.3
SNP_A-2176448	G	G	215	143	278	132	4.993	2.55E-02	rs2598107	7	37746254	p14.1
SNP_A-2180791	A	A	345	73	308	96	4.99	2.55E-02	rs9827713	3	16758437	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2120955	G	G	296	56	309	89	4.987	2.55E-02	rs4952172	2	30799937	p23.1
SNP_A-2113625	A	A	216	152	210	204	4.991	2.55E-02	rs12405873	1	9423672	p36.22
SNP_A-2135320	C	C	335	19	363	39	4.992	2.55E-02	rs17203026	7	9007604	p21.3
SNP_A-1869140	T	T	281	131	304	100	4.986	2.55E-02	rs1129644	6	24761355	p22.2
SNP_A-1848871	C	C	321	47	383	33	4.99	2.55E-02	rs9559329	13	107862054	q33.3
SNP_A-1793520	A	A	357	21	398	10	4.992	2.55E-02	rs802745	6	128312943	q22.33
SNP_A-1787170	T	T	353	15	333	29	4.989	2.55E-02	rs7160791	14	76712325	q24.3
SNP_A-1645224	C	C	271	77	290	120	4.991	2.55E-02	rs1373376	6	92886263	q15
SNP_A-1952293	A	A	274	64	338	50	4.992	2.55E-02	rs780234	1	229999777	q42.2
SNP_A-1980597	T	T	202	138	190	182	4.989	2.55E-02	rs253647	5	9154276	p15.31
SNP_A-1967777	A	A	373	29	374	14	4.987	2.55E-02	rs2209357	1	154087222	q23.1
SNP_A-1926531	C	C	411	1	377	7	4.988	2.55E-02	rs11101010	10	50071220	q11.23
SNP_A-1902953	A	A	399	3	375	11	4.993	2.55E-02	rs6135707	20	16154469	p12.1
SNP_A-1883183	C	C	328	28	338	50	4.988	2.55E-02	rs11044000	12	18323182	p12.3
SNP_A-1880928	A	A	287	131	313	101	4.987	2.55E-02	rs208578	16	22891151	p12.1
SNP_A-1880941	C	C	260	100	260	142	4.989	2.55E-02	rs3019878	8	123539159	q24.13
SNP_A-1900053	T	T	267	153	296	122	4.984	2.56E-02	rs6071467	20	59069003	q13.33
SNP_A-1911320	G	G	370	0	369	5	4.98	2.56E-02	rs12542058	8	47166892	q11.1
SNP_A-1968922	G	G	350	34	375	19	4.98	2.56E-02	---	20	60769970	q13.33
SNP_A-1974529	G	G	415	5	416	0	4.982	2.56E-02	rs1720830	3	139635904	q22.3
SNP_A-1960615	T	T	275	123	312	98	4.983	2.56E-02	rs4028451	19	48422858	q13.31
SNP_A-1961599	C	C	409	5	410	0	4.982	2.56E-02	rs6901736	6	5812861	p25.1
SNP_A-1727763	G	G	348	42	342	66	4.982	2.56E-02	rs10492706	13	55615870	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1811437	G	G	296	46	320	78	4.984	2.56E-02	rs12361784	11	125060636	q24.2
SNP_A-1809319	T	T	203	159	256	144	4.98	2.56E-02	rs2199184	4	119072625	q26
SNP_A-1857220	T	T	230	128	224	174	4.983	2.56E-02	rs1380772	5	63764250	q12.3
SNP_A-1868418	C	C	403	5	404	0	4.982	2.56E-02	---	3	145544513	q24
SNP_A-1821940	T	T	309	11	313	25	4.981	2.56E-02	rs10795004	10	3123039	p15.2
SNP_A-2112871	T	T	386	0	385	5	4.981	2.56E-02	rs16914021	8	86700666	q21.2
SNP_A-2114393	T	T	405	5	406	0	4.982	2.56E-02	rs6478086	9	114352575	q32
SNP_A-2140047	C	C	253	95	264	66	4.983	2.56E-02	rs2526955	7	49234018	p12.3
SNP_A-2140452	A	A	417	5	418	0	4.982	2.56E-02	rs9938295	16	46556441	q12.1
SNP_A-2155673	A	A	417	1	383	7	4.981	2.56E-02	rs11122130	1	5900927	p36.31
SNP_A-2224635	C	C	401	5	402	0	4.982	2.56E-02	---	8	3774468	p23.2
SNP_A-2223624	T	T	384	26	386	12	4.986	2.56E-02	rs9503031	6	1793466	p25.3
SNP_A-2087316	C	C	417	5	418	0	4.982	2.56E-02	rs2488896	1	162978077	q24.1
SNP_A-2105441	A	A	252	152	223	185	4.982	2.56E-02	rs2846419	11	107981030	q22.3
SNP_A-2058841	C	C	290	80	287	115	4.98	2.56E-02	rs2346344	1	75158684	p31.1
SNP_A-2069479	G	G	226	74	308	66	4.984	2.56E-02	rs11950131	5	82930917	q14.3
SNP_A-2014381	A	A	264	154	230	184	4.984	2.56E-02	rs7469200	9	95900518	q22.32
SNP_A-2036336	T	T	327	91	299	119	4.986	2.56E-02	rs17509785	7	109551451	q31.1
SNP_A-2034022	C	C	385	15	378	30	4.986	2.56E-02	rs7940046	11	132998045	q25
SNP_A-2033789	A	A	399	9	387	21	4.983	2.56E-02	rs11086177	20	44784090	q13.12
SNP_A-2040204	G	G	329	33	353	59	4.983	2.56E-02	rs1979342	4	66740730	q13.2
SNP_A-2030717	G	G	338	20	398	10	4.982	2.56E-02	rs1417231	1	102548585	p21.1
SNP_A-2025055	G	G	381	7	415	1	4.983	2.56E-02	rs9313650	5	173106422	q35.2
SNP_A-2022608	T	T	223	143	215	191	4.985	2.56E-02	rs1420859	8	113387234	q23.3
SNP_A-2273501	T	T	315	13	375	5	4.981	2.56E-02	rs17627598	4	113569098	q25

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2285139	A	A	339	33	337	55	4.986	2.56E-02	rs2856311	12	11715607	p13.2
SNP_A-2261577	G	G	396	20	378	36	4.985	2.56E-02	rs1495371	3	55709713	p14.3
SNP_A-2233702	G	G	294	76	354	60	4.984	2.56E-02	rs1908217	16	53117358	q12.2
SNP_A-2233606	C	C	413	5	414	0	4.982	2.56E-02	rs10437533	10	4261872	p15.1
SNP_A-2295129	A	A	342	10	405	3	4.983	2.56E-02	---	4	29800995	p15.1
SNP_A-2295335	C	C	217	151	208	200	4.982	2.56E-02	rs8668	14	70209032	q24.2
SNP_A-2299617	G	G	394	24	405	11	4.975	2.57E-02	rs2280441	15	79027724	q25.1
SNP_A-2299686	G	G	410	6	388	16	4.977	2.57E-02	rs6499117	16	65822130	q22.1
SNP_A-2290189	C	C	385	35	365	55	4.978	2.57E-02	rs10997306	10	68119237	q21.3
SNP_A-2308205	G	G	232	134	270	110	4.976	2.57E-02	rs12662725	6	74558931	q13
SNP_A-2271085	T	T	325	45	385	31	4.974	2.57E-02	rs4497239	1	59757241	p32.1
SNP_A-2020223	T	T	237	133	296	118	4.974	2.57E-02	rs2284975	21	43060813	q22.3
SNP_A-2043774	C	C	320	14	343	31	4.976	2.57E-02	rs10201206	2	196802748	q32.3
SNP_A-2040635	A	A	294	60	360	46	4.975	2.57E-02	rs10917145	1	22157951	p36.12
SNP_A-2041153	A	A	306	54	363	39	4.976	2.57E-02	rs4402414	13	86569287	q31.2
SNP_A-2015540	G	G	359	29	360	14	4.978	2.57E-02	rs2823857	21	16816963	q21.1
SNP_A-2009738	G	G	201	161	260	150	4.975	2.57E-02	rs7665984	4	41298663	p13
SNP_A-1990048	C	C	365	53	381	33	4.975	2.57E-02	rs2243480	7	65043346	q11.21
SNP_A-2073381	G	A	210	160	213	203	4.974	2.57E-02	rs10984620	9	119474655	q33.1
SNP_A-2072017	A	A	297	125	324	96	4.975	2.57E-02	rs925356	2	214623911	q34
SNP_A-2089336	C	C	209	147	274	138	4.975	2.57E-02	rs4724420	7	45394200	p13
SNP_A-2206021	T	A	168	138	177	151	4.977	2.57E-02	rs17150651	7	77664301	q21.11
SNP_A-2153513	T	T	226	140	224	192	4.977	2.57E-02	rs1257169	2	134797594	q21.2
SNP_A-2161591	G	G	276	38	304	68	4.974	2.57E-02	rs1959760	14	47694010	q21.3
SNP_A-2166034	G	G	387	25	364	42	4.974	2.57E-02	rs4782029	16	17155517	p12.3
SNP_A-2107808	G	G	196	174	252	162	4.975	2.57E-02	rs1838182	8	92990662	q21.3
SNP_A-2131881	A	A	237	133	296	118	4.974	2.57E-02	rs7428379	3	75390047	p12.3
SNP_A-1843162	G	G	348	22	373	43	4.976	2.57E-02	rs16958782	16	81454350	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1852429	A	A	240	128	233	173	4.978	2.57E-02	rs4865010	4	56255890	q12
SNP_A-1787734	A	A	310	18	381	9	4.979	2.57E-02	rs4563220	2	152630346	q23.3
SNP_A-1789144	C	C	295	43	320	74	4.975	2.57E-02	rs6984001	8	95673845	q22.1
SNP_A-1784770	C	C	195	167	251	155	4.974	2.57E-02	rs9364602	6	161945367	q26
SNP_A-1652134	T	T	256	70	338	60	4.978	2.57E-02	rs9324307	13	111125916	q34
SNP_A-1667712	C	C	360	18	374	36	4.976	2.57E-02	rs3212692	5	52385549	q11.2
SNP_A-1953595	T	T	262	100	328	86	4.975	2.57E-02	rs860237	22	48050419	q13.33
SNP_A-1941896	G	G	377	15	381	5	4.975	2.57E-02	rs7355586	2	49873971	p16.3
SNP_A-1981107	A	A	216	152	209	203	4.976	2.57E-02	rs7724768	5	31131126	p13.3
SNP_A-1911296	C	C	311	85	332	60	4.976	2.57E-02	rs670528	6	52437151	p12.2
SNP_A-1915255	C	C	312	82	351	61	4.979	2.57E-02	rs1161473	13	28321507	q12.3
SNP_A-1923682	T	T	334	34	356	60	4.973	2.57E-02	rs10893626	11	126456118	q24.2
SNP_A-1923058	A	A	229	131	282	114	4.974	2.57E-02	rs706335	4	140879713	q31.1
SNP_A-1922931	C	C	332	86	306	114	4.975	2.57E-02	rs10481752	9	69364006	q21.11
SNP_A-1899490	C	C	256	142	270	106	4.977	2.57E-02	rs1145389	11	99182898	q22.1
SNP_A-1902040	T	G	183	171	229	177	4.975	2.57E-02	rs3849607	4	180924175	q34.3
SNP_A-1879689	G	G	366	48	381	29	4.97	0.0258	rs17090925	1	71371373	p31.1
SNP_A-1886531	G	G	221	109	220	154	4.971	0.0258	rs7329947	13	36997091	q13.3
SNP_A-1919882	G	G	342	28	361	51	4.968	0.0258	rs17049240	4	138306805	q28.3
SNP_A-1711818	G	G	333	17	373	37	4.968	0.0258	rs9320187	6	107186946	q21
SNP_A-1721003	T	T	281	69	301	109	4.97	0.0258	rs10505932	12	24129014	p12.1
SNP_A-1785939	A	A	233	135	289	119	4.967	0.0258	rs11736535	4	146497501	q31.21
SNP_A-2126136	G	G	294	110	258	136	4.971	0.0258	rs1928021	13	35671944	q13.3
SNP_A-2128160	G	G	393	7	359	17	4.966	0.0258	rs12352328	9	87885873	q22.1
SNP_A-2114040	A	A	213	155	273	143	4.97	0.0258	rs6801273	3	152545528	q25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140636	T	T	307	115	330	86	4.972	0.0258	rs11080209	17	28616992	q11.2
SNP_A-2147876	A	A	306	116	272	144	4.973	0.0258	rs1133398	1	11748897	p36.22
SNP_A-2202747	A	A	306	50	316	80	4.97	0.0258	rs2957461	8	106376404	q23.1
SNP_A-2215159	G	G	363	1	386	8	4.971	0.0258	rs10460389	2	196331470	q32.3
SNP_A-2063525	C	C	328	4	410	0	4.967	0.0258	rs641215	7	63248281	q11.21
SNP_A-2019259	A	A	263	97	329	83	4.967	0.0258	rs1893202	21	38982636	q22.2
SNP_A-2025220	G	G	237	133	234	182	4.966	0.0258	rs10053085	5	6895007	p15.31
SNP_A-2232343	G	G	299	123	266	152	4.967	0.0258	rs2162382	2	64433485	p14
SNP_A-2237356	T	T	273	93	333	77	4.968	0.0258	rs12504340	4	87258964	q21.23
SNP_A-2252898	T	T	249	163	281	133	4.968	0.0258	rs2599650	8	40614286	p11.21
SNP_A-2253519	C	C	334	10	395	3	4.97	0.0258	rs306163	2	6557068	p25.2
SNP_A-2293560	T	T	249	111	295	91	4.97	0.0258	rs9294279	6	84366650	q14.2
SNP_A-2294867	C	C	288	132	317	103	4.969	0.0258	rs12929266	16	49453732	q12.1
SNP_A-2263094	C	C	305	63	318	98	4.96	2.59E-02	rs10519582	15	24861760	q12
SNP_A-2030158	-	G	209	209	240	176	4.964	2.59E-02	rs3780453	9	98044206	q22.33
SNP_A-2029302	A	A	237	163	270	134	4.96	2.59E-02	rs1078334	17	78477536	q25.3
SNP_A-2028162	A	A	247	123	305	107	4.966	2.59E-02	rs1108615	3	172691089	q26.2
SNP_A-1993177	G	A	197	165	196	168	4.961	2.59E-02	rs10957378	8	50287903	q11.21
SNP_A-2006986	T	T	251	103	240	140	4.965	2.59E-02	rs6731471	2	212450327	q34
SNP_A-2064151	A	A	285	109	268	144	4.965	2.59E-02	rs6998971	8	84188140	q21.13
SNP_A-2065028	T	T	357	1	380	8	4.964	2.59E-02	rs17015510	3	24961698	p24.2
SNP_A-2060991	C	C	300	62	361	47	4.963	2.59E-02	rs7732658	5	82950420	q14.3
SNP_A-2050482	G	G	286	104	317	79	4.963	2.59E-02	rs11066923	12	112965673	q24.21
SNP_A-2091622	C	C	287	23	318	46	4.961	2.59E-02	rs7772410	6	31436834	p21.33
SNP_A-2215511	A	A	362	60	336	84	4.964	2.59E-02	rs2456899	1	159869247	q23.3
SNP_A-2200194	G	G	280	124	241	149	4.963	2.59E-02	rs2321538	2	134568258	q21.2
SNP_A-2211618	G	G	384	10	345	21	4.965	2.59E-02	rs750628	15	67691874	q23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175569	G	G	223	89	236	136	4.961	2.59E-02	rs10789078	1	40216380	p34.2
SNP_A-2169871	C	C	371	27	344	44	4.964	2.59E-02	rs3111483	5	171465102	q35.1
SNP_A-2152489	C	C	353	3	401	13	4.965	2.59E-02	rs13351019	4	13079918	p15.33
SNP_A-1791233	G	G	256	98	259	141	4.966	2.59E-02	rs2045439	18	56034781	q21.32
SNP_A-1671532	C	C	376	8	376	20	4.959	2.59E-02	rs10499612	7	38862611	p14.1
SNP_A-1841951	T	T	361	11	383	3	4.965	2.59E-02	rs16914038	10	61153045	q21.2
SNP_A-1827929	G	G	302	86	328	62	4.96	2.59E-02	rs9381143	6	42192733	p21.1
SNP_A-1923112	G	G	377	9	408	2	4.96	2.59E-02	rs16872468	5	35197620	p13.2
SNP_A-1926476	C	C	207	145	255	127	4.96	2.59E-02	rs7041077	9	2422932	p24.2
SNP_A-1880163	A	A	239	123	288	104	4.961	2.59E-02	rs11059345	12	126768540	q24.32
SNP_A-1891697	G	G	335	19	343	37	4.965	2.59E-02	rs7616711	3	96548708	q11.2
SNP_A-1973395	G	G	231	137	291	123	4.962	2.59E-02	rs11164295	3	80843337	p12.2
SNP_A-1964036	G	G	207	143	202	194	4.962	2.59E-02	rs10923444	1	118136311	p12
SNP_A-1963078	T	T	250	112	305	95	4.964	2.59E-02	rs7607076	2	47583216	p21
SNP_A-1941062	C	C	318	66	290	90	4.961	2.59E-02	rs668692	19	5420832	p13.3
SNP_A-1936708	T	T	284	124	250	152	4.961	2.59E-02	rs537136	12	3235061	p13.32
SNP_A-1958670	T	T	295	29	327	55	4.963	2.59E-02	rs3778818	7	136936298	q33
SNP_A-1961600	G	G	412	2	381	9	4.954	2.60E-02	rs16859876	1	158994694	q23.3
SNP_A-1934902	T	T	411	5	410	0	4.958	2.60E-02	rs17215946	3	6181901	p26.1
SNP_A-1933687	T	T	175	153	239	149	4.954	2.60E-02	rs10772814	12	14917124	p12.3
SNP_A-1986934	T	T	252	98	247	137	4.958	2.60E-02	rs6901148	6	96457716	q16.1
SNP_A-1884414	G	G	257	107	252	148	4.956	2.60E-02	rs17223410	4	160286964	q32.1
SNP_A-1928872	G	G	358	16	378	6	4.958	2.60E-02	rs12515480	5	42500191	p12
SNP_A-1912407	A	A	349	3	329	11	4.955	2.60E-02	rs10247858	7	14538932	p21.2
SNP_A-1910105	T	T	412	2	381	9	4.954	2.60E-02	rs11223354	11	132442892	q25
SNP_A-1858367	G	G	284	60	285	91	4.954	2.60E-02	rs12523231	5	45264593	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1865879	G	G	320	22	363	11	4.954	2.60E-02	rs1822426	17	27612321	q11.2
SNP_A-1696466	G	G	400	0	401	5	4.957	2.60E-02	rs7927154	11	11206921	p15.4
SNP_A-1739249	T	T	369	17	365	33	4.959	2.60E-02	rs2366979	5	38424713	p13.2
SNP_A-1749743	T	T	394	0	395	5	4.956	2.60E-02	rs10514711	3	44956768	p21.31
SNP_A-2130983	T	T	393	13	406	4	4.957	2.60E-02	rs949085	11	121321672	q24.1
SNP_A-2173152	C	C	206	142	199	191	4.957	2.60E-02	rs11713193	3	49899428	p21.31
SNP_A-2180172	G	G	241	165	243	119	4.954	2.60E-02	rs11761264	7	21685716	p15.3
SNP_A-2222985	T	T	329	25	333	45	4.957	2.60E-02	rs1273153	14	59016212	q23.1
SNP_A-2054796	C	C	298	70	356	54	4.955	2.60E-02	---	2	139781103	q22.1
SNP_A-2003773	C	C	298	120	326	92	4.955	2.60E-02	rs3802656	10	90965629	q23.31
SNP_A-2025826	T	T	232	66	244	104	4.956	2.60E-02	rs2210540	9	17158954	p22.2
SNP_A-2041684	G	G	324	94	338	66	4.959	2.60E-02	rs13392495	2	224689855	q36.1
SNP_A-2039656	A	A	397	23	380	40	4.959	2.60E-02	rs11817603	10	92807379	q23.31
SNP_A-2038224	A	A	326	34	364	20	4.953	2.60E-02	rs1593849	12	20319674	p12.2
SNP_A-2229404	C	C	341	81	311	107	4.957	2.60E-02	rs1795011	1	182937845	q31.1
SNP_A-2228993	C	C	388	22	379	9	4.954	2.60E-02	rs3934516	15	59391271	q22.2
SNP_A-2299502	A	A	210	148	275	139	4.957	2.60E-02	rs4128219	15	78613458	q25.1
SNP_A-2260035	G	G	205	161	263	149	4.95	2.61E-02	rs7558016	2	7651459	p25.1
SNP_A-1992486	G	G	186	180	241	169	4.952	2.61E-02	rs2410529	8	17285935	p22
SNP_A-2050446	C	C	323	87	272	106	4.951	2.61E-02	rs345767	15	31189953	q13.3
SNP_A-2057321	C	C	232	138	226	186	4.948	2.61E-02	rs1040148	15	45290444	q21.1
SNP_A-2101977	G	G	345	1	368	8	4.948	2.61E-02	rs17103071	14	74717702	q24.3
SNP_A-2095159	C	C	179	169	237	161	4.952	2.61E-02	rs6675284	1	63530414	p31.3
SNP_A-2109188	A	A	315	53	372	38	4.949	2.61E-02	---	4	182821213	q34.3
SNP_A-2152508	G	G	329	37	302	56	4.949	2.61E-02	rs13165692	5	30718381	p13.3
SNP_A-1782383	T	G	227	169	208	204	4.947	2.61E-02	rs2414347	15	52744634	q21.3
SNP_A-1786342	A	A	358	50	377	31	4.948	2.61E-02	rs2905760	6	30034440	p21.33
SNP_A-1865519	A	A	279	67	289	103	4.952	2.61E-02	rs13386177	2	199392363	q33.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1867191	T	T	285	115	320	90	4.951	2.61E-02	rs1538801	13	46804090	q14.2
SNP_A-1844477	G	G	312	94	339	69	4.949	2.61E-02	rs11163287	1	81602654	p31.1
SNP_A-1847166	G	G	317	31	360	18	4.949	2.61E-02	rs11139043	9	69357454	q21.11
SNP_A-1847427	T	T	380	8	359	19	4.949	2.61E-02	rs7153035	14	60331408	q23.1
SNP_A-1824826	A	A	324	44	382	30	4.947	2.61E-02	rs2622932	9	103166266	q31.1
SNP_A-1835430	G	G	401	3	379	11	4.947	2.61E-02	rs6439161	3	130463396	q21.3
SNP_A-1983071	C	C	359	7	394	20	4.951	2.61E-02	rs10519443	5	115500392	q23.1
SNP_A-1977002	C	C	319	47	335	77	4.947	2.61E-02	rs2173106	4	44762996	p13
SNP_A-1935780	C	C	189	173	249	165	4.946	2.61E-02	rs2339678	10	52520199	q11.23
SNP_A-1949557	C	C	279	69	302	110	4.947	2.61E-02	rs11016275	10	130181604	q26.2
SNP_A-1956934	C	C	195	159	251	147	4.944	2.62E-02	rs6461957	7	26430930	p15.2
SNP_A-1933900	A	G	234	182	216	204	4.94	2.62E-02	rs2052022	17	15345712	p12
SNP_A-1941198	G	G	264	30	312	18	4.94	2.62E-02	---	13	63448161	q21.31
SNP_A-1947423	A	A	370	18	338	32	4.942	2.62E-02	rs567621	6	18588998	p22.3
SNP_A-1983169	A	A	325	25	313	43	4.94	2.62E-02	rs17144660	5	118162313	q23.1
SNP_A-1968306	C	C	315	49	296	72	4.941	2.62E-02	rs16987685	20	36998249	q11.23
SNP_A-1881412	G	G	362	14	348	28	4.943	2.62E-02	rs11104989	12	87563035	q21.33
SNP_A-1888443	C	C	419	1	387	7	4.945	2.62E-02	rs911232	1	156887580	q23.2
SNP_A-1838726	T	A	224	194	223	189	4.94	2.62E-02	rs1951442	14	45456794	q21.2
SNP_A-1818266	C	T	229	191	214	188	4.946	2.62E-02	rs4525747	2	133475343	q21.2
SNP_A-1865820	T	T	257	113	227	141	4.941	2.62E-02	rs916570	6	30174010	p21.33
SNP_A-1799133	C	C	273	95	277	137	4.944	2.62E-02	rs1413128	13	58178900	q21.1
SNP_A-1809523	C	C	260	148	287	117	4.94	2.62E-02	rs877825	10	98956872	q24.1
SNP_A-1814192	G	G	259	83	323	69	4.944	2.62E-02	rs4794297	17	47131806	q21.33
SNP_A-1783323	G	G	288	42	338	28	4.945	2.62E-02	---	7	71042246	q11.22
SNP_A-1783936	T	T	343	27	366	50	4.941	2.62E-02	rs4945203	11	77087216	q13.5
SNP_A-2222458	A	A	338	70	369	49	4.945	2.62E-02	rs17712821	16	75870261	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213225	A	A	343	61	371	41	4.942	2.62E-02	rs7744451	6	53399535	p12.1
SNP_A-2207674	G	G	270	92	269	131	4.94	2.62E-02	rs1240117	8	90116543	q21.3
SNP_A-2169417	C	T	224	194	223	189	4.94	2.62E-02	rs11032739	11	34497717	p13
SNP_A-2093531	G	G	348	72	319	97	4.94	2.62E-02	rs12033154	1	31355178	p35.2
SNP_A-2099798	G	G	324	16	342	6	4.94	2.62E-02	rs725006	1	116440988	p13.1
SNP_A-2049006	G	G	386	8	365	19	4.941	2.62E-02	rs11568202	12	6185440	p13.31
SNP_A-2052364	C	C	199	167	254	154	4.94	2.62E-02	rs1952974	6	48204007	p12.3
SNP_A-2034443	G	G	353	25	393	13	4.941	2.62E-02	rs236711	20	57127454	q13.32
SNP_A-2035651	T	T	346	8	346	20	4.944	2.62E-02	rs2609204	4	75706275	q13.3
SNP_A-2022420	G	G	343	23	364	44	4.941	2.62E-02	rs11255734	10	8614080	p14
SNP_A-2032741	A	A	321	25	309	43	4.942	2.62E-02	---	2	171256307	q31.1
SNP_A-2269530	A	A	245	95	251	139	4.945	2.62E-02	rs177950	4	177784239	q34.2
SNP_A-2284573	C	C	207	183	246	158	4.945	2.62E-02	rs4610473	5	30404582	p13.3
SNP_A-2283614	G	G	285	27	327	15	4.945	2.62E-02	---	10	97657572	q24.1
SNP_A-2293242	C	C	338	8	376	22	4.945	2.62E-02	rs10241174	7	5999166	p22.1
SNP_A-2294305	C	C	308	14	378	6	4.936	0.0263	rs232130	17	61119807	q24.1
SNP_A-2288656	C	C	288	82	348	66	4.936	0.0263	rs12454981	18	66074947	q22.2
SNP_A-2237830	G	G	295	67	363	53	4.936	0.0263	rs17220900	8	106811978	q23.1
SNP_A-2032407	C	C	337	33	356	58	4.935	0.0263	rs7321248	13	76211602	q22.3
SNP_A-2030691	A	A	232	132	292	118	4.938	0.0263	rs288033	5	138241993	q31.2
SNP_A-2030519	T	T	393	9	362	20	4.938	0.0263	rs2377599	12	8880812	p13.31
SNP_A-2031574	A	A	365	23	366	10	4.935	0.0263	rs7200700	16	15603176	p13.11
SNP_A-2041490	G	G	321	33	385	21	4.934	0.0263	rs1621708	10	118447247	q25.3
SNP_A-2001410	G	G	298	54	291	81	4.934	0.0263	rs12569625	10	60087263	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2000926	G	G	362	58	338	82	4.937	0.0263	rs6601898	10	5108231	p15.1
SNP_A-2007146	T	T	325	31	385	19	4.939	0.0263	rs4416170	2	237869314	q37.3
SNP_A-2006617	T	A	215	203	234	182	4.937	0.0263	rs782394	10	130349442	q26.2
SNP_A-2050275	T	T	297	71	355	55	4.938	0.0263	rs521522	9	110699741	q31.3
SNP_A-2211882	C	C	300	70	358	54	4.935	0.0263	rs799488	14	34521161	q13.2
SNP_A-2204327	G	G	361	1	386	8	4.935	0.0263	rs2080987	19	43773827	q13.2
SNP_A-2223987	C	C	300	60	320	96	4.937	0.0263	rs4373023	3	34052227	p23
SNP_A-2223864	T	T	409	5	406	0	4.933	0.0263	rs1951960	14	61032784	q23.1
SNP_A-2141630	G	G	227	131	223	179	4.937	0.0263	rs10221582	2	215448896	q35
SNP_A-2156747	C	C	368	36	369	19	4.935	0.0263	rs11216422	11	98051843	q22.1
SNP_A-1784742	G	A	195	141	191	189	4.939	0.0263	rs685144	18	8336342	p11.23
SNP_A-1707481	G	G	343	3	391	13	4.933	0.0263	rs10519422	4	138739210	q28.3
SNP_A-1803801	T	T	337	79	364	56	4.939	0.0263	rs4839602	3	144779755	q24
SNP_A-1873172	C	C	379	39	360	60	4.938	0.0263	rs919757	5	170869179	q35.1
SNP_A-1849640	A	A	329	67	363	47	4.938	0.0263	rs1409391	10	14667831	p13
SNP_A-1859200	A	A	261	109	261	153	4.935	0.0263	rs1510183	16	9207447	p13.2
SNP_A-1856308	T	T	404	0	407	5	4.933	0.0263	rs221600	17	42618573	q21.32
SNP_A-1829069	C	C	367	9	396	2	4.935	0.0263	rs17002350	22	39936950	q13.2
SNP_A-1828596	G	G	360	62	374	40	4.936	0.0263	rs1631909	5	173617350	q35.2
SNP_A-1839869	G	G	321	47	372	32	4.933	0.0263	rs682982	18	63640822	q22.1
SNP_A-1898745	A	A	304	46	342	30	4.938	0.0263	rs1418687	6	71935685	q13
SNP_A-1883748	C	C	270	92	325	75	4.932	0.0264	rs9537556	13	56477392	q21.1
SNP_A-1948911	C	C	268	92	278	136	4.931	0.0264	rs2216924	2	66991594	p14
SNP_A-1826633	G	G	229	125	286	110	4.93	0.0264	rs918352	2	214910443	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1823686	A	A	182	172	239	163	4.931	0.0264	rs261996	5	95923591	q15
SNP_A-1818013	G	G	387	33	364	52	4.932	0.0264	rs662216	1	61008946	p31.3
SNP_A-1820504	A	A	310	60	371	45	4.932	0.0264	rs3772238	3	157544199	q25.31
SNP_A-1857230	C	C	316	36	358	22	4.933	0.0264	rs1495274	17	44432647	q21.32
SNP_A-1850566	T	T	299	71	307	107	4.933	0.0264	rs12190371	6	96769322	q16.1
SNP_A-1804506	T	T	363	21	373	9	4.931	0.0264	rs2288075	2	24325262	p23.3
SNP_A-1800335	C	C	324	14	336	30	4.931	0.0264	rs2577783	2	86052761	p11.2
SNP_A-1707419	G	G	328	4	373	15	4.931	0.0264	rs10514020	18	67535740	q22.3
SNP_A-1712569	G	G	400	0	403	5	4.932	0.0264	rs6119471	20	33500888	q11.22
SNP_A-1711040	T	T	259	91	331	79	4.927	0.0264	rs2882314	4	66691805	q13.2
SNP_A-1682760	C	C	331	67	365	47	4.929	0.0264	rs10496184	2	72656248	p13.2
SNP_A-1670610	A	A	190	178	243	165	4.931	0.0264	rs1502800	12	84978723	q21.31
SNP_A-2168119	T	T	248	92	296	74	4.928	0.0264	rs6085125	20	5286726	p12.3
SNP_A-2109079	T	T	266	86	319	69	4.927	0.0264	rs17359438	11	5398802	p15.4
SNP_A-2225884	G	G	227	139	288	126	4.928	0.0264	rs11767026	7	68234717	q11.22
SNP_A-2192706	C	C	188	138	259	135	4.932	0.0264	rs1029935	15	24955101	q12
SNP_A-2054146	G	G	322	40	385	27	4.927	0.0264	rs2301103	5	83466967	q14.3
SNP_A-2071899	G	G	276	56	281	87	4.927	0.0264	rs7602576	2	113415848	q13
SNP_A-2079083	G	G	334	8	353	21	4.933	0.0264	rs945905	1	16690664	p36.13
SNP_A-2013871	A	A	316	100	286	128	4.929	0.0264	rs2979025	8	134184919	q24.22
SNP_A-1994866	A	A	297	79	317	55	4.929	0.0264	rs2447160	8	120443654	q24.12
SNP_A-2043869	G	G	405	5	402	0	4.933	0.0264	rs4585955	1	22035341	p36.12
SNP_A-2035568	T	T	314	12	353	29	4.931	0.0264	rs30548	5	15083751	p15.2
SNP_A-2238856	C	C	302	68	341	49	4.928	0.0264	rs2910644	5	41301621	p13.1
SNP_A-2250643	C	C	269	93	324	76	4.928	0.0264	rs11129440	3	31195739	p24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247733	G	G	307	61	368	46	4.927	0.0264	rs11208868	1	66633903	p31.2
SNP_A-2275352	G	G	319	29	348	54	4.929	0.0264	rs1811618	3	88060490	p11.1
SNP_A-2292626	T	T	317	45	317	71	4.932	0.0264	rs10476597	5	93392928	q15
SNP_A-2310573	A	A	325	43	344	72	4.932	0.0264	rs16861911	3	188500652	q27.3
SNP_A-2301956	T	T	315	29	350	16	4.921	2.65E-02	rs9883476	3	198808132	q29
SNP_A-2289484	C	C	330	38	391	25	4.923	2.65E-02	rs17584106	10	122510144	q26.12
SNP_A-2280465	T	T	356	12	386	28	4.924	2.65E-02	rs16964596	15	49963936	q21.2
SNP_A-2280087	T	T	339	17	406	8	4.925	2.65E-02	rs8070348	17	14836713	p12
SNP_A-2248343	A	A	392	16	381	31	4.924	2.65E-02	rs17287176	5	141483936	q31.3
SNP_A-2253051	T	T	251	113	300	94	4.922	2.65E-02	rs484214	11	34423848	p13
SNP_A-2255115	C	C	336	4	416	0	4.92	2.65E-02	rs13410819	2	77971246	p12
SNP_A-2229156	A	A	280	58	297	93	4.924	2.65E-02	rs1585160	19	56750466	q13.41
SNP_A-2042232	T	T	240	74	290	58	4.923	2.65E-02	rs1382850	12	25690039	p12.1
SNP_A-2025952	T	C	164	138	203	171	4.924	2.65E-02	rs2110117	14	90002634	q32.12
SNP_A-2006219	G	G	229	187	235	139	4.926	2.65E-02	rs209573	1	40507729	p34.2
SNP_A-2009389	T	T	265	55	267	85	4.923	2.65E-02	rs7430319	3	186542742	q27.2
SNP_A-2062492	T	T	317	25	374	14	4.925	2.65E-02	rs7727683	5	20181089	p14.3
SNP_A-2051544	G	G	285	85	345	69	4.923	2.65E-02	rs12550655	8	55486710	q11.23
SNP_A-2183117	T	T	294	118	255	143	4.925	2.65E-02	rs7097084	10	109543387	q25.1
SNP_A-2176996	T	T	339	5	362	16	4.926	2.65E-02	rs7544887	1	182586464	q31.1
SNP_A-2207227	T	T	307	113	272	140	4.921	2.65E-02	rs1657256	7	154385280	q36.2
SNP_A-2110518	C	C	255	163	283	131	4.921	2.65E-02	rs1962451	7	135798047	q33
SNP_A-2167562	C	C	213	153	206	204	4.924	2.65E-02	rs4952479	2	41629645	p22.1
SNP_A-1783931	C	C	350	20	376	40	4.923	2.65E-02	rs1877380	3	9261736	p25.3
SNP_A-1782992	T	T	348	18	329	33	4.923	2.65E-02	rs1492469	4	108474355	q25

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801638	C	C	179	167	230	154	4.921	2.65E-02	rs9878472	3	85180035	p12.1
SNP_A-1864145	G	G	239	169	262	134	4.921	2.65E-02	rs1003136	5	127375714	q23.2
SNP_A-1837858	G	G	273	75	268	108	4.922	2.65E-02	rs1357943	7	144163552	q35
SNP_A-1831762	A	A	331	27	361	51	4.922	2.65E-02	---	2	186880567	q32.1
SNP_A-1949360	A	A	407	1	377	7	4.925	2.65E-02	rs2174866	15	51251512	q21.3
SNP_A-1940851	T	T	334	26	352	48	4.921	2.65E-02	rs8029892	15	77427879	q25.1
SNP_A-1970036	C	T	176	158	206	164	4.925	2.65E-02	rs4817457	21	32376672	q22.11
SNP_A-1988027	C	C	347	17	332	32	4.923	2.65E-02	rs844554	6	147944402	q24.3
SNP_A-1982275	C	C	341	15	373	33	4.925	2.65E-02	rs6151640	5	80002885	q14.1
SNP_A-1877100	C	C	318	68	352	48	4.926	2.65E-02	rs316776	4	25033433	p15.2
SNP_A-1901937	G	G	347	61	359	39	4.921	2.65E-02	rs6025572	20	55462913	q13.32
SNP_A-1911531	C	C	330	38	349	65	4.92	2.65E-02	rs7727515	5	152872497	q33.2
SNP_A-1927815	A	A	369	31	343	49	4.919	2.66E-02	rs2184331	10	71703304	q22.1
SNP_A-1897605	C	C	387	7	417	1	4.914	2.66E-02	rs8059228	16	10070946	p13.2
SNP_A-1879485	C	C	383	7	413	1	4.919	2.66E-02	rs16890089	8	40883800	p11.21
SNP_A-1943998	G	G	352	6	382	18	4.914	2.66E-02	rs392013	8	48112750	q11.21
SNP_A-1944071	T	T	402	12	385	25	4.915	2.66E-02	rs17097964	10	120438193	q26.11
SNP_A-1949860	G	G	306	110	333	83	4.918	2.66E-02	rs1189806	14	56577468	q22.3
SNP_A-1952948	T	T	255	95	256	136	4.917	2.66E-02	rs4567954	2	105189504	q12.1
SNP_A-1838500	G	G	320	4	396	0	4.916	2.66E-02	rs17166529	5	98359528	q21.1
SNP_A-1859881	A	A	253	93	309	77	4.915	2.66E-02	rs6432836	2	166240606	q24.3
SNP_A-1855814	G	G	339	5	337	15	4.915	2.66E-02	rs16920930	10	21037557	p12.31
SNP_A-1812546	T	T	402	14	388	28	4.915	2.66E-02	rs6687807	1	223418256	q42.13
SNP_A-1781350	A	A	373	9	344	20	4.914	2.66E-02	rs6760813	2	40544267	p22.1
SNP_A-1669775	G	G	351	31	348	52	4.914	2.66E-02	rs10498475	14	53602521	q22.3
SNP_A-2111130	C	C	345	73	366	50	4.916	2.66E-02	rs11076072	16	53710105	q12.2
SNP_A-2214201	C	C	295	71	306	108	4.914	2.66E-02	rs4909356	8	138289997	q24.23
SNP_A-2216792	A	A	208	136	281	131	4.915	2.66E-02	rs9917886	4	65719526	q13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2182366	C	C	401	21	411	9	4.918	2.66E-02	rs2248402	6	168735509	q27
SNP_A-2186265	G	G	264	88	272	130	4.917	2.66E-02	rs485125	11	70151456	q13.4
SNP_A-2198954	A	A	204	146	271	139	4.916	2.66E-02	rs1590392	6	93791795	q16.1
SNP_A-2051410	T	T	342	56	362	36	4.916	2.66E-02	rs10923995	1	116463055	p13.1
SNP_A-2065124	T	T	318	38	377	25	4.918	2.66E-02	rs12110025	5	5762270	p15.32
SNP_A-2071167	T	T	200	166	255	153	4.914	2.66E-02	rs9028	3	188571999	q27.3
SNP_A-2082894	G	G	323	89	294	116	4.914	2.66E-02	rs2929460	8	9108239	p23.1
SNP_A-2017853	A	A	226	112	274	94	4.915	2.66E-02	rs2832909	21	30776914	q22.11
SNP_A-2002309	G	G	338	10	397	3	4.914	2.66E-02	rs7934092	11	120148300	q23.3
SNP_A-2030598	C	C	404	14	390	28	4.914	2.66E-02	rs4759384	12	121881891	q24.31
SNP_A-2030320	T	T	243	127	295	109	4.915	2.66E-02	rs2024303	12	8165032	p13.31
SNP_A-2255691	C	C	318	74	310	46	4.914	2.66E-02	rs320442	1	210013687	q32.3
SNP_A-2253185	A	A	241	125	237	171	4.918	2.66E-02	rs2067833	6	53438315	p12.1
SNP_A-2246328	T	T	290	74	353	59	4.914	2.66E-02	rs4658958	1	228294628	q42.2
SNP_A-2244223	G	G	233	115	293	101	4.919	2.66E-02	rs13223397	7	13556034	p21.2
SNP_A-2266834	T	T	196	158	252	146	4.916	2.66E-02	rs589610	7	131825724	q32.3
SNP_A-2298887	A	A	361	5	332	14	4.919	2.66E-02	rs16971069	15	77628809	q25.1
SNP_A-2297301	G	G	407	15	387	29	4.916	2.66E-02	rs2074890	17	15495286	p12
SNP_A-2303569	T	T	330	88	301	115	4.919	2.66E-02	rs3755930	4	1226844	p16.3
SNP_A-2304467	C	C	417	1	387	7	4.914	2.66E-02	rs16998978	22	37202707	q13.1
SNP_A-2311902	A	A	280	42	274	66	4.913	2.67E-02	rs590429	12	10054850	p13.31
SNP_A-2253345	G	G	354	2	370	10	4.91	2.67E-02	rs1321723	6	85903221	q14.3
SNP_A-2230333	A	A	352	2	368	10	4.907	2.67E-02	rs10080206	5	173787444	q35.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238255	A	A	197	137	265	131	4.913	2.67E-02	rs10894834	11	133881535	q25
SNP_A-2026277	T	T	277	117	258	152	4.912	2.67E-02	rs17409588	5	31564384	p13.3
SNP_A-2023103	A	A	331	89	296	114	4.913	2.67E-02	rs9410395	9	88738482	q22.1
SNP_A-2075724	T	T	254	82	329	71	4.911	2.67E-02	rs1372632	18	4018927	p11.31
SNP_A-2196629	C	C	401	13	412	4	4.909	2.67E-02	rs13379409	14	90786027	q32.12
SNP_A-2188947	C	C	322	42	376	28	4.908	2.67E-02	rs13159978	5	80583639	q14.1
SNP_A-2221975	A	A	363	7	391	1	4.909	2.67E-02	rs17042851	12	75972431	q21.2
SNP_A-2138754	C	C	210	160	267	147	4.908	2.67E-02	rs921792	5	67501559	q13.1
SNP_A-1675369	C	C	357	41	348	64	4.912	2.67E-02	rs472040	4	12832815	p15.33
SNP_A-1806717	C	C	242	124	243	173	4.909	2.67E-02	rs2906438	7	9787173	p21.3
SNP_A-1785696	C	C	421	1	391	7	4.91	2.67E-02	rs929282	22	17496275	q11.21
SNP_A-1790978	C	C	357	13	379	29	4.909	2.67E-02	rs17704982	2	183806682	q32.1
SNP_A-1847938	A	A	275	147	295	113	4.913	2.67E-02	rs3098591	15	25608875	q12
SNP_A-1948676	C	T	174	154	208	168	4.911	2.67E-02	rs8181006	8	72360941	q13.3
SNP_A-1877656	G	G	231	133	295	121	4.909	2.67E-02	rs825672	5	138123542	q31.2
SNP_A-1874213	G	G	287	115	255	143	4.908	2.67E-02	rs817865	9	107223254	q31.2
SNP_A-1889483	A	A	309	61	370	46	4.908	2.67E-02	rs17193610	3	1538944	p26.3
SNP_A-1930914	T	T	340	20	398	10	4.911	2.67E-02	rs11939972	4	134513171	q28.3
SNP_A-1932357	T	T	255	111	313	95	4.901	2.68E-02	rs3784304	15	49025352	q21.2
SNP_A-1927725	C	C	254	116	315	101	4.901	2.68E-02	rs8083763	18	61945708	q22.1
SNP_A-1920200	C	C	344	16	401	7	4.902	2.68E-02	rs7023758	9	5857810	p24.1
SNP_A-1907513	T	T	349	7	363	19	4.904	2.68E-02	rs11026653	11	22539564	p14.3
SNP_A-1883320	A	A	383	11	403	3	4.901	2.68E-02	rs16949570	16	49855836	q12.1
SNP_A-1881356	C	C	236	116	243	167	4.907	2.68E-02	rs6583671	10	91787696	q23.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897751	T	G	236	180	206	198	4.904	2.68E-02	rs4727659	7	105951438	q22.3
SNP_A-1891549	T	T	315	55	324	86	4.904	2.68E-02	rs17276911	4	107691965	q24
SNP_A-1976706	C	C	342	10	401	3	4.901	2.68E-02	rs3900610	4	32334100	p15.1
SNP_A-1988106	G	G	383	37	361	57	4.901	2.68E-02	rs516651	1	227849391	q42.2
SNP_A-1966824	T	C	188	178	232	178	4.906	2.68E-02	rs1912211	2	214967894	q34
SNP_A-1963544	G	G	235	119	285	101	4.906	2.68E-02	rs2215870	2	63043993	p15
SNP_A-1842470	G	G	271	85	337	71	4.904	2.68E-02	rs244927	5	110100396	q22.1
SNP_A-1833401	T	T	329	5	352	16	4.903	2.68E-02	rs7513474	1	151427993	q22
SNP_A-1816833	A	G	211	203	237	181	4.904	2.68E-02	rs10754285	1	89828608	p22.2
SNP_A-1816210	G	G	384	0	389	5	4.905	2.68E-02	rs16917773	8	87874750	q21.3
SNP_A-2161781	T	T	256	86	267	129	4.906	2.68E-02	rs1943520	11	94871654	q21
SNP_A-2161837	C	C	261	161	227	191	4.907	2.68E-02	rs12631872	3	105494145	q13.11
SNP_A-2160608	A	A	304	56	361	41	4.905	2.68E-02	rs11195192	10	112326354	q25.2
SNP_A-2127106	G	G	241	119	284	98	4.906	2.68E-02	rs1559715	4	54914601	q12
SNP_A-2136183	T	T	291	73	300	110	4.901	2.68E-02	rs1557782	7	94743808	q21.3
SNP_A-2214379	A	A	286	98	265	129	4.906	2.68E-02	rs12917175	15	75605248	q24.3
SNP_A-2201524	T	T	393	7	361	17	4.907	2.68E-02	rs10223947	7	11528051	p21.3
SNP_A-2198247	G	T	205	153	208	202	4.903	2.68E-02	rs2380173	17	78502446	q25.3
SNP_A-2192633	G	G	223	129	281	115	4.907	2.68E-02	rs7900190	10	17198644	p13
SNP_A-2059252	A	A	343	19	362	8	4.907	2.68E-02	rs7540417	1	192507728	q31.3
SNP_A-2094135	A	A	289	75	299	113	4.901	2.68E-02	rs3843000	10	49467734	q11.22
SNP_A-2045887	T	T	305	115	274	144	4.902	2.68E-02	rs8097618	18	36536710	q12.3
SNP_A-2034905	C	C	303	15	331	33	4.906	2.68E-02	rs16938341	8	73813021	q13.3
SNP_A-2004142	G	G	334	4	412	0	4.902	2.68E-02	rs2675346	15	46199113	q21.1
SNP_A-2312641	A	A	362	46	335	67	4.904	2.68E-02	rs807535	6	24659708	p22.2
SNP_A-2302156	G	G	334	32	381	19	4.904	2.68E-02	rs9968204	3	25938544	p24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2280763	A	A	403	5	372	14	4.897	0.0269	rs7950949	11	10328253	p15.4
SNP_A-2282422	A	A	234	130	294	116	4.898	0.0269	rs10492972	1	10287378	p36.22
SNP_A-2274224	T	T	326	40	389	27	4.897	0.0269	rs11019633	11	91151708	q14.3
SNP_A-2004678	A	A	391	11	411	3	4.895	0.0269	rs8058288	16	46640236	q12.1
SNP_A-2026249	G	C	201	161	210	190	4.898	0.0269	rs6744599	2	10697611	p25.1
SNP_A-2094733	A	A	354	66	329	91	4.896	0.0269	rs6066563	20	46012126	q13.13
SNP_A-2065827	C	C	359	57	332	80	4.897	0.0269	rs17825567	16	52615272	q12.2
SNP_A-2131283	C	C	240	90	259	139	4.899	0.0269	rs12876308	13	109879675	q34
SNP_A-2128213	G	G	285	51	311	33	4.898	0.0269	rs848644	7	100865900	q22.1
SNP_A-2115990	C	C	383	29	327	43	4.897	0.0269	rs420812	15	65967183	q23
SNP_A-2155471	G	A	236	180	205	197	4.898	0.0269	rs2544165	7	133377698	q33
SNP_A-2150339	T	T	230	96	276	78	4.899	0.0269	rs11214112	11	111552666	q23.1
SNP_A-1844689	C	C	297	69	304	104	4.898	0.0269	rs12705680	7	109614905	q31.1
SNP_A-1799943	G	G	307	103	338	78	4.9	0.0269	rs298439	1	25939357	p36.11
SNP_A-1814008	G	G	332	18	346	36	4.9	0.0269	rs12960609	18	64851629	q22.1
SNP_A-1807538	G	G	242	164	245	119	4.898	0.0269	rs2255212	1	3280216	p36.32
SNP_A-1666244	C	C	213	137	281	129	4.895	0.0269	rs4075384	18	61990384	q22.1
SNP_A-1649830	C	C	291	49	319	83	4.896	0.0269	rs162307	5	119159171	q23.1
SNP_A-1683126	G	G	334	16	371	35	4.899	0.0269	rs10508094	13	101031414	q33.1
SNP_A-1733644	G	G	269	107	306	84	4.896	0.0269	rs721600	6	27406884	p22.1
SNP_A-1975554	T	T	316	20	370	10	4.899	0.0269	rs2377256	3	186224958	q27.2
SNP_A-1953685	C	C	340	24	395	13	4.894	0.0269	rs2468236	12	87055471	q21.32
SNP_A-1951698	C	C	394	6	349	15	4.897	0.0269	rs3107454	10	62716572	q21.2
SNP_A-1960489	A	A	269	81	263	115	4.896	0.0269	rs17448335	1	65907616	p31.2
SNP_A-1946942	G	C	208	162	214	200	4.894	0.0269	rs3772899	3	81816787	p12.2
SNP_A-1893536	G	G	379	1	408	8	4.895	0.0269	rs3850215	6	137700761	q23.3
SNP_A-1874518	A	A	301	53	347	37	4.898	0.0269	rs9554486	13	98103632	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1875799	T	T	375	7	403	1	4.896	0.0269	rs326285	3	97664874	q11.2
SNP_A-1884280	C	T	208	154	209	205	4.893	0.027	rs987280	5	85484360	q14.3
SNP_A-1901777	G	G	283	35	306	20	4.89	0.027	---	18	57550524	q21.33
SNP_A-1905859	T	T	274	96	278	138	4.892	0.027	rs2192264	7	54779474	p11.2
SNP_A-1912715	G	G	315	81	287	107	4.893	0.027	rs3740744	11	19498098	p15.1
SNP_A-1914162	C	C	188	144	251	137	4.889	0.027	rs17062983	6	134235209	q23.2
SNP_A-1928186	C	C	317	95	289	123	4.89	0.027	rs7822183	8	40203360	p11.21
SNP_A-1973430	G	G	212	148	264	132	4.892	0.027	rs13382071	3	82849385	p12.2
SNP_A-1974300	G	G	397	5	337	13	4.888	0.027	rs2241687	3	129273474	q21.3
SNP_A-1789287	G	G	238	172	196	194	4.89	0.027	rs7916423	10	81855167	q22.3
SNP_A-1849795	G	G	290	22	311	43	4.889	0.027	rs876477	4	20833197	p15.31
SNP_A-1856500	A	A	243	115	248	164	4.894	0.027	rs11998040	8	84221577	q21.13
SNP_A-1864291	C	C	344	20	402	10	4.892	0.027	rs17093416	8	20839113	p21.3
SNP_A-1870678	A	A	409	1	381	7	4.89	0.027	rs12039206	1	52281023	p32.3
SNP_A-1837365	T	T	398	2	371	9	4.893	0.027	rs1484359	5	161902631	q34
SNP_A-2138667	G	G	270	136	296	106	4.894	0.027	rs17420378	20	43062549	q13.12
SNP_A-2165911	T	T	282	82	345	67	4.89	0.027	rs3943706	7	38307999	p14.1
SNP_A-2113737	T	G	231	191	217	193	4.89	0.027	rs1446609	2	209943921	q34
SNP_A-2131712	C	C	311	55	328	88	4.891	0.027	rs322713	3	25270245	p24.2
SNP_A-2188292	C	C	355	55	364	34	4.891	0.027	rs9296691	6	52701783	p12.2
SNP_A-2072960	C	C	333	45	371	29	4.892	0.027	rs11250268	10	1149566	p15.3
SNP_A-2084952	C	C	334	16	389	7	4.888	0.027	rs7581318	2	242382611	q37.3
SNP_A-2023766	T	T	336	64	352	42	4.893	0.027	rs4563050	16	76987471	q23.1
SNP_A-2033880	A	A	212	112	285	105	4.889	0.027	rs12501692	4	113375706	q25
SNP_A-2282672	A	A	316	54	373	39	4.893	0.027	rs12628583	22	42314345	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2280997	A	A	357	31	347	51	4.894	0.027	rs2936041	1	219151168	q41
SNP_A-2263845	T	T	344	6	374	18	4.892	0.027	rs9851284	3	111515489	q13.13
SNP_A-2228166	G	G	264	54	257	81	4.889	0.027	rs3091627	20	44911112	q13.12
SNP_A-2256046	C	T	194	158	218	194	4.893	0.027	rs9450652	6	88059076	q15
SNP_A-2244219	C	C	212	152	273	141	4.892	0.027	rs11761839	7	138795388	q34
SNP_A-2299907	G	G	349	33	342	54	4.89	0.027	rs17721798	20	5321080	p12.3
SNP_A-2288532	C	C	333	37	349	63	4.894	0.027	rs11910666	21	22380025	q21.1
SNP_A-2299595	A	A	368	2	386	10	4.886	2.71E-02	rs11202215	10	88580861	q23.2
SNP_A-2297738	A	A	332	4	408	0	4.883	2.71E-02	rs6807392	3	171861111	q26.2
SNP_A-2306966	G	A	235	185	217	203	4.885	2.71E-02	rs6467552	7	133847728	q33
SNP_A-2251338	C	C	332	4	408	0	4.883	2.71E-02	rs1523528	15	59049369	q22.2
SNP_A-2262409	T	T	356	62	377	41	4.883	2.71E-02	rs17211908	14	22240100	q11.2
SNP_A-2286262	G	G	311	51	373	37	4.882	2.71E-02	rs9258223	6	29820154	p22.1
SNP_A-2275156	G	G	268	32	333	21	4.888	2.71E-02	rs2631382	6	153792336	q25.2
SNP_A-2276360	A	A	185	143	259	143	4.882	2.71E-02	rs4792347	17	13116856	p12
SNP_A-2043820	G	G	291	75	354	60	4.885	2.71E-02	rs2144523	1	87493178	p22.3
SNP_A-2031672	A	A	340	30	398	18	4.883	2.71E-02	rs17162012	7	140399494	q34
SNP_A-2000846	A	A	289	133	247	157	4.887	2.71E-02	rs2809985	1	238888762	q43
SNP_A-1993619	G	G	361	33	397	19	4.885	2.71E-02	rs908094	8	66373196	q13.1
SNP_A-1991192	A	A	349	49	330	72	4.884	2.71E-02	rs1468157	7	125950102	q32.1
SNP_A-2007949	C	T	182	170	220	170	4.886	2.71E-02	rs2049724	11	14034727	p15.2
SNP_A-2080890	G	G	217	153	206	200	4.884	2.71E-02	rs7608256	2	229736689	q36.3
SNP_A-2105778	C	C	337	25	396	14	4.886	2.71E-02	rs17795909	19	44875163	q13.2
SNP_A-2050564	A	A	352	18	379	37	4.886	2.71E-02	rs10997510	10	68535802	q21.3
SNP_A-2048821	A	G	218	202	234	186	4.883	2.71E-02	rs17103286	14	34954792	q13.2
SNP_A-2193176	T	T	184	174	241	165	4.887	2.71E-02	rs17322167	2	45609779	p21
SNP_A-2191863	G	G	294	76	298	112	4.882	2.71E-02	rs14908881	4	19046815	p15.31
SNP_A-2181363	T	T	252	108	256	154	4.882	2.71E-02	rs9375694	6	130398301	q22.33
SNP_A-2169596	C	C	246	108	311	95	4.883	2.71E-02	rs10848906	12	3638966	p13.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2133802	C	C	302	64	363	49	4.884	2.71E-02	rs6736919	2	139823425	q22.1
SNP_A-2130409	A	A	239	117	235	161	4.884	2.71E-02	rs10874816	1	94122006	p22.1
SNP_A-2156846	C	C	413	1	385	7	4.886	2.71E-02	rs12266536	10	36047394	p11.21
SNP_A-2156588	C	C	352	18	379	37	4.886	2.71E-02	rs764489	14	35559722	q13.2
SNP_A-1829372	T	T	324	42	298	62	4.884	2.71E-02	rs8137257	22	41554573	q13.2
SNP_A-1826214	A	A	287	75	297	113	4.887	2.71E-02	rs2432799	6	5412408	p25.1
SNP_A-1870793	A	G	174	168	219	163	4.885	2.71E-02	rs9269071	6	32548445	p21.32
SNP_A-1797850	T	T	377	9	404	2	4.886	2.71E-02	rs18667077	9	17452082	p22.2
SNP_A-1792332	C	C	356	14	385	31	4.882	2.71E-02	rs11965495	6	90719014	q15
SNP_A-1794049	G	G	294	124	260	152	4.884	2.71E-02	rs1295893	10	127742696	q26.2
SNP_A-1684898	G	G	272	82	283	123	4.883	2.71E-02	rs2038473	6	145566051	q24.3
SNP_A-1656151	G	G	400	0	407	5	4.884	2.71E-02	rs708503	14	50787839	q22.1
SNP_A-1671852	C	C	402	0	409	5	4.885	2.71E-02	rs4791580	17	14567504	p12
SNP_A-1941157	C	C	317	51	332	82	4.883	2.71E-02	rs11027260	11	23473340	p14.3
SNP_A-1928696	T	T	260	140	289	111	4.882	2.71E-02	rs10978948	9	107466567	q31.2
SNP_A-1922006	C	C	329	23	350	44	4.882	2.71E-02	rs12616055	2	78257225	p12
SNP_A-1914447	T	C	193	159	214	188	4.881	2.71E-02	rs7938730	11	38401344	p12
SNP_A-1912340	T	T	394	0	401	5	4.883	2.71E-02	rs1413048	13	38622000	q13.3
SNP_A-1919193	T	T	276	70	335	55	4.884	2.71E-02	rs17264828	3	252219	p26.3
SNP_A-1917951	A	A	312	66	330	44	4.884	2.71E-02	rs1637303	7	21100075	p15.3
SNP_A-1889427	T	T	284	132	251	161	4.887	2.71E-02	rs2745008	20	36854152	q11.23
SNP_A-1876106	T	T	417	5	410	0	4.887	2.71E-02	---	1	118123557	p12
SNP_A-1876573	C	C	369	1	398	8	4.881	2.71E-02	rs4722789	7	28181350	p15.1
SNP_A-1878810	C	C	260	110	260	154	4.879	2.72E-02	rs10027777	11	124949814	q24.2
SNP_A-1883680	G	G	358	6	390	18	4.877	2.72E-02	rs1956280	14	51611997	q22.1
SNP_A-1913852	G	G	259	143	291	115	4.881	2.72E-02	rs1868493	3	102247547	q12.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1907915	A	A	370	0	377	5	4.875	2.72E-02	rs1982405	4	190849006	q35.2
SNP_A-1922755	C	C	350	16	407	7	4.878	2.72E-02	rs2696074	15	42267001	q15.3
SNP_A-1983439	A	A	185	183	234	168	4.88	2.72E-02	rs2112698	5	128502242	q23.3
SNP_A-1710551	A	A	267	135	244	170	4.876	2.72E-02	rs1535279	6	51842984	p12.2
SNP_A-1781711	G	G	197	171	254	160	4.881	2.72E-02	rs6933981	6	123288753	q22.31
SNP_A-1797259	A	A	404	18	411	7	4.881	2.72E-02	rs7493767	14	72434969	q24.2
SNP_A-1799207	G	G	239	127	236	174	4.879	2.72E-02	rs720453	2	181977337	q31.3
SNP_A-1852031	G	G	250	112	252	158	4.879	2.72E-02	rs13321530	3	106028026	q13.11
SNP_A-1847009	G	G	211	157	268	144	4.878	2.72E-02	rs13018904	2	117048890	q14.1
SNP_A-1830437	G	G	334	4	410	0	4.878	2.72E-02	---	4	74927267	q13.3
SNP_A-2158862	T	T	297	85	321	61	4.877	2.72E-02	rs1458332	5	172323299	q35.1
SNP_A-2142230	A	A	213	123	218	176	4.875	2.72E-02	rs11106219	12	90529709	q21.33
SNP_A-2109858	G	G	318	86	288	112	4.88	2.72E-02	rs17836011	14	96966704	q32.2
SNP_A-2190335	A	A	242	88	232	122	4.88	2.72E-02	rs3991020	12	85744495	q21.32
SNP_A-2202833	T	T	414	2	387	9	4.875	2.72E-02	rs11946636	4	11620150	p15.33
SNP_A-2223767	C	C	301	53	312	84	4.875	2.72E-02	rs10776722	1	111540506	p13.2
SNP_A-2226401	G	A	191	151	195	177	4.876	2.72E-02	rs7707871	5	150458487	q33.1
SNP_A-2107330	A	A	208	150	261	135	4.876	2.72E-02	rs6475053	9	16422118	p22.3
SNP_A-2099428	C	C	304	38	348	24	4.879	2.72E-02	rs11778640	8	118112559	q24.11
SNP_A-2007466	T	T	339	35	309	53	4.876	2.72E-02	rs4814689	20	17978357	p11.23
SNP_A-2009430	C	C	308	36	361	23	4.88	2.72E-02	rs6797409	3	190829224	q28
SNP_A-2013576	T	T	256	126	278	96	4.876	2.72E-02	rs1121493	11	91311756	q14.3
SNP_A-1990433	T	T	298	46	325	29	4.881	2.72E-02	rs2373207	7	85620972	q21.11
SNP_A-2032565	C	C	350	10	409	3	4.875	2.72E-02	rs1475774	6	35727532	p21.31
SNP_A-2279118	G	G	354	62	328	86	4.878	2.72E-02	rs6975680	7	41576690	p14.1
SNP_A-2274476	C	C	354	46	317	65	4.881	2.72E-02	rs16978104	18	40418821	q12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251675	G	G	380	40	354	60	4.878	2.72E-02	rs1290281	1	82569474	p31.1
SNP_A-2231724	C	C	269	137	275	99	4.88	2.72E-02	rs891499	2	10064828	p25.1
SNP_A-2313040	G	G	320	56	263	71	4.877	2.72E-02	rs2080315	2	102562806	q11.2
SNP_A-2311083	A	A	214	140	270	126	4.879	2.72E-02	rs7894025	10	6349408	p15.1
SNP_A-2300467	G	G	368	18	373	35	4.881	2.72E-02	rs3213122	12	54649933	q13.2
SNP_A-2300141	A	A	308	30	307	51	4.875	2.72E-02	rs11968196	6	98900553	q16.2
SNP_A-2255346	G	G	305	91	269	115	4.87	2.73E-02	rs2764095	6	7274872	p24.3
SNP_A-2244162	G	G	250	124	205	143	4.873	2.73E-02	rs11208097	1	63207297	p31.3
SNP_A-2244700	G	G	247	115	236	154	4.869	2.73E-02	rs4650447	1	80196192	p31.1
SNP_A-2284342	T	T	292	76	350	60	4.869	2.73E-02	rs572652	10	107708922	q25.1
SNP_A-2258286	A	A	303	51	372	38	4.874	2.73E-02	rs11948763	5	28746813	p14.1
SNP_A-2266365	G	G	371	23	370	10	4.871	2.73E-02	rs585208	6	165884771	q27
SNP_A-2269506	T	T	358	2	376	10	4.875	2.73E-02	rs11174164	12	60442870	q14.1
SNP_A-2032044	G	G	350	8	392	22	4.874	2.73E-02	rs7443901	5	23905004	p14.2
SNP_A-2022050	G	G	364	0	371	5	4.873	2.73E-02	rs2090671	2	196816419	q32.3
SNP_A-2047474	A	A	267	103	267	145	4.871	2.73E-02	rs209416	6	83591448	q14.1
SNP_A-2045576	T	T	354	14	383	31	4.874	2.73E-02	rs17139253	5	115604038	q23.1
SNP_A-2038932	G	G	367	55	385	35	4.871	2.73E-02	rs11575575	7	50298417	p12.2
SNP_A-1989884	A	A	225	121	283	107	4.869	2.73E-02	rs1456893	7	50046933	p12.2
SNP_A-2015463	C	G	204	162	214	196	4.872	2.73E-02	rs373182	21	16242346	q21.1
SNP_A-2018012	C	C	312	56	324	88	4.871	2.73E-02	rs2250608	21	31792423	q22.11
SNP_A-2093356	C	C	246	122	308	108	4.87	2.73E-02	rs9561620	13	93986327	q32.1
SNP_A-2095998	T	T	253	141	268	106	4.874	2.73E-02	rs4813783	20	5812829	p12.3
SNP_A-2071869	A	A	352	16	409	7	4.871	2.73E-02	rs1769609	14	33472359	q13.1
SNP_A-2214297	C	C	268	154	294	122	4.87	2.73E-02	rs8100729	19	13484496	p13.13
SNP_A-2211925	C	C	267	101	266	142	4.871	2.73E-02	rs13020804	2	118301009	q14.1
SNP_A-2114146	G	G	328	4	402	0	4.87	2.73E-02	rs16957438	15	70980459	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134940	G	A	209	153	201	199	4.871	2.73E-02	rs9831534	3	189112077	q27.3
SNP_A-2157222	T	T	354	14	383	31	4.874	2.73E-02	rs980351	9	10731174	p23
SNP_A-2165237	T	T	279	85	311	63	4.871	2.73E-02	rs16962723	16	13710565	p13.12
SNP_A-1821004	C	C	251	117	300	98	4.869	2.73E-02	rs1499873	20	53131323	q13.2
SNP_A-1856118	T	T	249	115	248	160	4.874	2.73E-02	rs12371146	12	17651840	p12.3
SNP_A-1811658	T	T	278	88	341	73	4.874	2.73E-02	rs917908	14	91433539	q32.12
SNP_A-1753529	G	G	288	60	311	97	4.872	2.73E-02	rs10516439	4	100761552	q23
SNP_A-1696682	G	G	257	129	298	106	4.872	2.73E-02	rs2589998	7	137282267	q33
SNP_A-1665274	G	G	322	18	336	36	4.87	2.73E-02	rs10521015	5	34685333	p13.2
SNP_A-1978751	T	T	276	44	281	71	4.871	2.73E-02	rs692463	4	122666064	q27
SNP_A-1968866	G	G	360	54	376	34	4.874	2.73E-02	rs10485467	20	58267846	q13.33
SNP_A-1948681	C	C	224	138	286	126	4.873	2.73E-02	rs10943350	6	77162166	q14.1
SNP_A-1929522	G	G	352	16	409	7	4.871	2.73E-02	rs17115455	1	84954664	p22.3
SNP_A-1883742	T	T	336	4	356	14	4.875	2.73E-02	rs16935138	8	69898754	q13.2
SNP_A-1883293	G	G	288	78	351	63	4.872	2.73E-02	rs10759246	9	107505350	q31.2
SNP_A-1885686	T	T	222	130	208	170	4.869	2.73E-02	rs6704982	2	83412662	p11.2
SNP_A-1876212	C	C	392	8	373	19	4.873	2.73E-02	rs4148744	7	86795425	q21.12
SNP_A-1885152	A	A	190	172	244	160	4.864	2.74E-02	rs688956	5	89899035	q14.3
SNP_A-1900004	A	A	367	25	382	12	4.863	2.74E-02	rs2156042	1	115809085	p13.1
SNP_A-1930003	A	A	330	68	305	93	4.866	2.74E-02	rs7642932	3	69046950	p14.1
SNP_A-1911695	A	A	285	85	290	124	4.867	2.74E-02	rs10905061	10	6991458	p14
SNP_A-1948983	C	C	241	129	239	177	4.862	2.74E-02	rs1365625	4	175845399	q34.1
SNP_A-1672508	G	G	273	77	291	119	4.868	2.74E-02	rs10498976	6	92890101	q15
SNP_A-1784085	T	T	357	51	336	74	4.864	2.74E-02	rs4699892	5	66079396	q12.3
SNP_A-1806251	A	A	385	7	355	17	4.863	2.74E-02	rs7199857	16	68092189	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1792594	G	G	185	163	247	157	4.867	2.74E-02	rs8087158	18	43760334	q21.1
SNP_A-1846493	A	A	301	113	269	141	4.864	2.74E-02	rs9945882	18	36507202	q12.3
SNP_A-1868180	G	G	290	106	275	141	4.868	2.74E-02	rs17709473	8	94697309	q22.1
SNP_A-1861420	C	C	282	84	345	69	4.865	2.74E-02	rs16862162	2	174558712	q31.1
SNP_A-1825930	C	C	238	94	281	75	4.867	2.74E-02	rs11629609	15	66327585	q23
SNP_A-2187390	A	A	368	54	384	34	4.867	2.74E-02	rs2899412	15	45445823	q21.1
SNP_A-2069729	G	G	317	31	358	18	4.864	2.74E-02	rs11176702	12	66049817	q14.3
SNP_A-2068266	A	A	294	74	357	59	4.868	2.74E-02	rs12673410	7	109505472	q31.1
SNP_A-2068342	C	C	304	22	366	12	4.864	2.74E-02	rs4742801	9	95813824	q22.32
SNP_A-2047877	A	A	328	94	350	68	4.868	2.74E-02	rs253443	5	141774089	q31.3
SNP_A-2016427	C	C	348	12	390	4	4.867	2.74E-02	rs7277294	21	22714731	q21.1
SNP_A-2016830	A	A	340	10	397	3	4.866	2.74E-02	rs1023402	21	25031874	q21.2
SNP_A-2011604	A	A	366	18	336	32	4.864	2.74E-02	rs2282480	11	62987952	q12.3
SNP_A-1997002	A	A	253	79	310	64	4.863	2.74E-02	---	9	80945848	q21.31
SNP_A-2001360	G	G	353	21	361	9	4.868	2.74E-02	rs16911842	10	59580636	q21.1
SNP_A-2041136	G	G	277	141	292	106	4.868	2.74E-02	rs1504072	3	1162331	p26.3
SNP_A-2282879	T	C	198	170	225	191	4.864	2.74E-02	rs10807640	6	19233338	p22.3
SNP_A-2275890	C	C	188	182	244	172	4.866	2.74E-02	rs994564	8	17286849	p22
SNP_A-2276556	A	A	225	125	229	177	4.867	2.74E-02	rs1816662	8	105863506	q22.3
SNP_A-2233032	T	T	380	16	384	32	4.865	2.74E-02	rs16918254	8	53931766	q11.23
SNP_A-2293632	T	T	349	19	399	9	4.865	2.74E-02	rs11988733	8	30244043	p12
SNP_A-2308636	A	A	247	123	246	170	4.866	2.74E-02	rs7084327	10	91873776	q23.31
SNP_A-2312892	T	T	244	102	236	140	4.862	0.0275	rs4480940	2	213548060	q34
SNP_A-2281883	C	C	340	78	365	55	4.859	0.0275	rs16841819	2	139770878	q22.1
SNP_A-2000782	G	G	398	0	407	5	4.86	0.0275	rs4027083	1	230759644	q42.2
SNP_A-1997113	T	T	296	84	284	116	4.859	0.0275	rs354831	9	86300684	q21.33
SNP_A-2004325	A	A	267	97	264	136	4.859	0.0275	rs4493015	15	84761279	q25.3
SNP_A-2058896	G	G	364	16	342	30	4.862	0.0275	rs2705375	18	41392565	q12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2062286	C	C	198	172	255	161	4.86	0.0275	rs895924	11	131689549	q25
SNP_A-2075198	T	T	350	14	379	31	4.859	0.0275	rs16908259	9	24330549	p21.3
SNP_A-2094843	T	T	208	146	270	136	4.861	0.0275	rs6807438	3	45753627	p21.31
SNP_A-2102441	A	A	330	30	386	18	4.862	0.0275	rs1926457	13	35266395	q13.3
SNP_A-2105828	C	C	203	193	227	157	4.859	0.0275	rs6978435	7	156724270	q36.3
SNP_A-2177336	A	A	296	74	305	111	4.859	0.0275	rs12376699	9	36372790	p13.2
SNP_A-2177206	G	G	405	1	379	7	4.86	0.0275	rs7936473	11	64587243	q13.1
SNP_A-2176446	A	A	304	118	327	89	4.858	0.0275	rs3825364	12	2980134	p13.33
SNP_A-2214209	C	C	348	72	367	49	4.858	0.0275	rs17034864	2	68174354	p14
SNP_A-2160896	-	A	181	181	233	169	4.862	0.0275	rs4248	18	4016708	p11.31
SNP_A-2151228	T	T	262	154	292	124	4.862	0.0275	rs210772	4	27104442	p15.2
SNP_A-1829519	T	T	332	4	406	0	4.86	0.0275	rs6495461	15	78048881	q25.1
SNP_A-1838960	G	G	318	50	335	81	4.858	0.0275	rs12614495	2	172902347	q31.1
SNP_A-1863594	A	A	312	22	399	13	4.857	0.0275	---	17	68429991	q25.1
SNP_A-1783460	C	C	358	28	370	14	4.859	0.0275	rs1782392	1	94910254	p21.3
SNP_A-1660227	A	A	192	188	220	156	4.859	0.0275	rs2348424	5	151793999	q33.1
SNP_A-1651468	G	G	334	52	331	79	4.859	0.0275	rs10514876	5	58038502	q11.2
SNP_A-1942414	T	T	197	169	242	150	4.858	0.0275	rs7801387	7	103901938	q22.2
SNP_A-1976471	T	T	299	99	257	121	4.86	0.0275	rs10489103	4	23740810	p15.2
SNP_A-1988754	T	T	318	50	335	81	4.858	0.0275	rs16859582	1	230228383	q42.2
SNP_A-1920503	C	C	226	144	284	130	4.857	0.0275	rs11683554	2	237726167	q37.3
SNP_A-1920202	T	T	226	144	284	130	4.857	0.0275	rs2926876	10	14029305	p13
SNP_A-1923290	T	T	296	18	299	35	4.855	0.0276	rs352003	4	75210691	q13.3
SNP_A-1932467	G	G	320	8	390	2	4.851	0.0276	rs564528	7	71182658	q11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932008	T	T	224	162	255	133	4.852	0.0276	rs2351491	15	87199109	q26.1
SNP_A-1928447	G	G	265	139	301	113	4.851	0.0276	rs4697999	4	9951203	p16.1
SNP_A-1950541	G	G	380	0	389	5	4.854	0.0276	rs1474629	6	144703923	q24.2
SNP_A-1958878	T	T	249	109	221	137	4.855	0.0276	rs12139301	1	84029106	p31.1
SNP_A-1957971	C	C	269	153	233	181	4.853	0.0276	rs1329166	10	91842699	q23.31
SNP_A-1797432	T	T	345	25	369	47	4.853	0.0276	---	1	70367251	p31.1
SNP_A-1809826	G	A	202	166	201	177	4.854	0.0276	rs1622950	20	4106356	p13
SNP_A-1869163	G	G	298	72	306	108	4.852	0.0276	rs11675678	2	187651269	q32.1
SNP_A-1845135	T	T	327	15	335	31	4.854	0.0276	rs10931635	2	194813373	q32.3
SNP_A-1822950	G	G	326	38	340	64	4.852	0.0276	rs11808386	1	163454048	q24.1
SNP_A-1824465	T	T	176	166	230	156	4.851	0.0276	rs826285	19	42070872	q13.12
SNP_A-1821707	C	C	254	156	288	128	4.85	0.0276	rs555828	9	22723238	p21.3
SNP_A-1815790	C	C	337	79	303	103	4.85	0.0276	rs30574	7	31853771	p14.3
SNP_A-2140385	C	C	314	54	325	85	4.85	0.0276	rs17136716	5	113877249	q22.3
SNP_A-2162002	A	A	271	85	280	126	4.854	0.0276	rs10215690	7	120669030	q31.31
SNP_A-2127498	G	G	280	56	279	85	4.854	0.0276	rs318074	5	41483944	p13.1
SNP_A-2126905	C	C	271	59	324	44	4.851	0.0276	rs1330140	9	13323196	p23
SNP_A-2220283	T	T	251	111	252	156	4.856	0.0276	rs1982758	3	58524687	p14.2
SNP_A-2224943	G	G	280	40	268	62	4.855	0.0276	rs1031496	8	126660688	q24.13
SNP_A-2187889	C	C	329	17	349	35	4.856	0.0276	rs12797173	11	55263124	q11
SNP_A-2186695	T	T	353	5	380	16	4.854	0.0276	rs16971887	13	107550079	q33.3
SNP_A-2060877	T	C	178	156	211	173	4.855	0.0276	rs12594801	15	25034707	q12
SNP_A-2052264	G	G	356	12	388	28	4.856	0.0276	rs9999519	4	172135085	q33
SNP_A-2052559	T	T	281	87	287	127	4.851	0.0276	rs10871409	16	79812119	q23.2
SNP_A-2052959	C	C	365	49	380	30	4.852	0.0276	rs2450114	8	117692900	q23.3
SNP_A-1994352	A	A	356	12	388	28	4.856	0.0276	rs7843589	8	97544479	q22.1
SNP_A-1992985	C	C	229	141	224	190	4.855	0.0276	rs6998559	8	32991625	p12
SNP_A-2007595	G	G	334	10	384	26	4.853	0.0276	rs6020113	20	35736459	q11.23
SNP_A-2044132	T	T	326	36	381	23	4.855	0.0276	rs12712704	2	40814583	p22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2033503	A	A	290	58	309	93	4.852	0.0276	rs9451852	6	92659950	q16.1
SNP_A-2031055	G	G	314	52	332	84	4.854	0.0276	rs17729161	18	45888589	q21.1
SNP_A-2285522	A	A	413	1	387	7	4.853	0.0276	rs17140361	16	6489529	p13.2
SNP_A-2274020	C	C	326	36	381	23	4.855	0.0276	rs7714521	5	109758577	q22.1
SNP_A-2245381	C	C	413	1	387	7	4.853	0.0276	rs10135855	14	80764454	q31.1
SNP_A-2237064	C	C	167	147	236	148	4.846	2.77E-02	rs10817926	9	116562990	q33.1
SNP_A-2280265	T	T	287	67	358	54	4.848	2.77E-02	rs11135806	8	24433926	p21.2
SNP_A-2268858	C	C	248	108	289	87	4.849	2.77E-02	rs16895338	6	65267311	q12
SNP_A-2259819	T	T	366	0	375	5	4.848	2.77E-02	rs507269	18	57846829	q21.33
SNP_A-2033413	G	G	286	32	340	20	4.844	2.77E-02	rs4236089	6	46034552	p21.1
SNP_A-2021123	G	G	332	18	403	9	4.846	2.77E-02	rs12421071	11	121326266	q24.1
SNP_A-2043424	G	G	340	8	414	2	4.849	2.77E-02	rs4882086	11	48463528	p11.2
SNP_A-2006093	G	G	419	1	393	7	4.848	2.77E-02	rs1907223	10	122964688	q26.12
SNP_A-2004473	G	G	358	56	328	78	4.846	2.77E-02	rs10509737	10	101253118	q24.2
SNP_A-2051331	T	T	393	5	335	13	4.847	2.77E-02	rs7271565	20	17775622	p12.1
SNP_A-2059503	A	A	222	168	242	132	4.849	2.77E-02	rs1925953	1	68560702	p31.2
SNP_A-2107187	T	T	238	172	261	137	4.847	2.77E-02	rs4982709	14	22464539	q11.2
SNP_A-2093254	T	T	336	4	410	0	4.849	2.77E-02	rs4555960	6	116160769	q22.1
SNP_A-2170433	A	A	330	16	383	7	4.848	2.77E-02	rs9900598	17	62650403	q24.2
SNP_A-2224508	C	C	206	160	265	149	4.847	2.77E-02	rs2212449	11	112357242	q23.1
SNP_A-2109208	C	C	255	83	317	69	4.849	2.77E-02	rs1437277	8	57519288	q12.1
SNP_A-2108276	G	G	239	125	234	170	4.847	2.77E-02	rs7840632	8	3668188	p23.2
SNP_A-2120316	T	T	394	16	385	31	4.848	2.77E-02	rs17571062	19	36081417	q12
SNP_A-2164793	T	T	257	133	291	107	4.845	2.77E-02	rs7405450	17	77150886	q25.3
SNP_A-2143360	C	C	394	14	382	28	4.847	2.77E-02	rs8013771	14	58120529	q23.1
SNP_A-1826164	C	C	393	25	408	12	4.844	2.77E-02	rs9326161	2	1357950	p25.3
SNP_A-1828016	A	A	216	148	272	134	4.845	2.77E-02	rs2309823	2	100360075	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1830888	C	C	349	53	381	35	4.846	2.77E-02	rs17231134	10	34118979	p11.22
SNP_A-1853108	T	T	306	64	367	49	4.845	2.77E-02	rs12695695	3	140549347	q23
SNP_A-1873432	A	A	268	32	290	58	4.85	2.77E-02	rs17116051	14	44920193	q21.2
SNP_A-1862171	C	C	354	12	386	28	4.848	2.77E-02	rs10888871	1	54900962	p32.3
SNP_A-1863205	G	G	320	48	336	78	4.844	2.77E-02	rs130414	22	26813045	q12.1
SNP_A-1738875	G	G	384	18	378	34	4.848	2.77E-02	rs10493455	1	69222696	p31.1
SNP_A-1747845	G	G	377	23	373	41	4.844	2.77E-02	rs1439079	2	140275209	q22.1
SNP_A-1721514	A	G	223	175	213	199	4.846	2.77E-02	rs264968	2	103877967	q12.1
SNP_A-1976595	T	T	365	1	396	8	4.844	2.77E-02	rs985959	4	28014390	p15.1
SNP_A-1900076	G	G	368	0	377	5	4.849	2.77E-02	rs16926640	10	26511935	p12.1
SNP_A-1897559	G	G	263	103	263	145	4.848	2.77E-02	rs10954172	7	127457956	q32.1
SNP_A-1898589	G	G	306	100	275	127	4.846	2.77E-02	rs17014613	2	34203221	p22.3
SNP_A-1925413	T	T	185	171	242	162	4.84	2.78E-02	rs1980942	13	95374525	q32.1
SNP_A-1921741	C	C	334	80	303	105	4.843	2.78E-02	rs7762199	6	773201	p25.3
SNP_A-1913509	T	T	278	34	347	23	4.843	2.78E-02	rs1075781	4	1938916	p16.3
SNP_A-1976914	T	T	299	103	325	77	4.839	2.78E-02	rs3775257	4	41102496	p13
SNP_A-1986708	G	G	216	140	276	128	4.842	2.78E-02	rs1327756	6	85441054	q14.3
SNP_A-1971706	A	A	276	62	289	97	4.842	2.78E-02	rs2252575	3	9044468	p25.3
SNP_A-1933935	C	C	330	4	402	0	4.841	2.78E-02	rs11190404	10	101907038	q24.31
SNP_A-1939279	T	T	203	145	262	134	4.843	2.78E-02	rs9518213	13	100370742	q32.3
SNP_A-1746883	G	G	295	51	321	85	4.841	2.78E-02	rs9300945	13	102887610	q33.2
SNP_A-1697438	T	T	282	116	262	150	4.841	2.78E-02	rs10496792	2	138845284	q22.1
SNP_A-1837814	C	C	225	175	253	143	4.84	2.78E-02	rs12919692	16	85854891	q24.2
SNP_A-1838353	T	T	254	164	217	191	4.84	2.78E-02	rs9297736	8	127472832	q24.21
SNP_A-2161921	C	C	308	102	326	74	4.843	2.78E-02	rs17617521	5	153329452	q33.2
SNP_A-2097815	G	G	323	69	298	94	4.841	2.78E-02	rs11003396	10	54553872	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2089789	A	A	247	133	234	174	4.838	2.78E-02	rs7817858	8	80200188	q21.12
SNP_A-2055065	A	A	268	38	273	63	4.843	2.78E-02	rs11252262	1	207445581	q32.2
SNP_A-2074593	C	C	191	173	245	161	4.843	2.78E-02	rs10463395	5	147371778	q32
SNP_A-2064216	A	A	257	123	283	95	4.843	2.78E-02	rs264606	2	159713553	q24.2
SNP_A-1994317	A	A	318	34	367	21	4.838	2.78E-02	rs16917799	8	96587726	q22.1
SNP_A-2034428	G	A	209	195	223	175	4.841	2.78E-02	rs1644673	19	42170551	q13.12
SNP_A-2036495	G	G	209	143	197	187	4.839	2.78E-02	rs704191	12	21906289	p12.1
SNP_A-2263648	A	A	283	29	284	50	4.84	2.78E-02	rs17039268	1	12846905	p36.21
SNP_A-2271287	T	T	238	106	295	91	4.837	2.78E-02	rs16975742	17	65916223	q24.3
SNP_A-2034287	A	A	323	29	339	15	4.836	2.79E-02	rs7355094	1	26002974	p36.11
SNP_A-2019990	G	G	202	152	257	139	4.834	2.79E-02	rs7281619	21	41897987	q22.3
SNP_A-2012184	A	A	225	127	223	175	4.835	2.79E-02	rs647749	6	153158412	q25.2
SNP_A-2048594	T	T	221	149	216	200	4.834	2.79E-02	rs574951	11	115759054	q23.3
SNP_A-2077180	G	G	321	11	344	26	4.834	2.79E-02	rs12149751	16	64360386	q22.1
SNP_A-2168187	G	G	201	169	257	157	4.835	2.79E-02	rs10134615	14	93696941	q32.13
SNP_A-2167883	A	A	290	130	317	101	4.837	2.79E-02	rs1459920	3	67941732	p14.1
SNP_A-2155650	A	A	249	107	308	92	4.836	2.79E-02	rs12603818	17	46922748	q21.33
SNP_A-2145131	C	C	334	28	355	51	4.831	2.79E-02	rs7840970	8	103766788	q22.3
SNP_A-2126637	G	G	356	60	373	39	4.832	2.79E-02	rs17049773	2	58985200	p16.1
SNP_A-2123795	C	C	218	146	209	193	4.833	2.79E-02	rs1864868	2	241367119	q37.3
SNP_A-2204029	C	C	241	165	212	198	4.837	2.79E-02	rs4876460	8	113315426	q23.3
SNP_A-2182848	C	C	281	73	290	110	4.834	2.79E-02	rs1485351	12	30824877	p11.21
SNP_A-2193952	C	C	259	139	292	112	4.836	2.79E-02	rs12680736	8	143639778	q24.3
SNP_A-1818388	G	G	334	28	332	48	4.835	2.79E-02	rs11936536	4	101650781	q24
SNP_A-1862274	T	T	330	38	389	25	4.835	2.79E-02	rs16956240	13	98468980	q32.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864279	G	G	322	100	343	73	4.834	2.79E-02	rs12225388	11	83083527	q14.1
SNP_A-1703045	A	A	252	150	276	118	4.832	2.79E-02	rs1056116	17	45461899	q21.32
SNP_A-1693815	G	G	385	15	382	30	4.835	2.79E-02	rs10483895	14	76664858	q24.3
SNP_A-1669179	G	A	229	173	209	203	4.835	2.79E-02	rs6696736	1	182711413	q25.3
SNP_A-1796823	G	G	362	6	396	18	4.836	2.79E-02	rs9836021	3	175288740	q26.31
SNP_A-1958674	G	G	319	47	332	76	4.832	2.79E-02	rs4325320	11	125075965	q24.2
SNP_A-1922603	T	T	316	40	331	67	4.836	2.79E-02	rs730453	8	138166751	q24.23
SNP_A-1893431	A	A	293	25	363	15	4.833	2.79E-02	rs11200537	10	124043537	q26.13
SNP_A-1886928	G	G	381	7	405	1	4.827	2.80E-02	rs494479	5	31379276	p13.3
SNP_A-1918867	C	C	339	25	363	47	4.826	2.80E-02	rs17167557	7	88495383	q21.13
SNP_A-1960887	T	T	235	135	231	183	4.825	2.80E-02	rs6743271	2	200486660	q33.1
SNP_A-1956023	G	G	302	66	363	51	4.829	2.80E-02	rs11102462	1	112606811	p13.2
SNP_A-1969621	T	T	322	48	382	34	4.828	2.80E-02	rs2829770	21	25759354	q21.2
SNP_A-1969548	A	A	350	16	405	7	4.825	2.80E-02	rs16999651	21	24466507	q21.2
SNP_A-1985184	A	A	201	167	257	155	4.828	2.80E-02	rs2237150	6	15516507	p22.3
SNP_A-1791407	T	T	247	97	228	128	4.827	2.80E-02	---	2	56042875	p16.1
SNP_A-1787854	T	T	304	118	330	90	4.831	2.80E-02	rs11062450	12	2980308	p13.33
SNP_A-1805904	A	G	210	192	221	177	4.83	2.80E-02	rs10946715	6	24788269	p22.2
SNP_A-1802727	G	G	353	1	384	8	4.825	2.80E-02	rs609454	6	70957452	q13
SNP_A-1870473	T	T	198	184	227	153	4.825	2.80E-02	rs7866673	9	68587159	q13
SNP_A-1869889	T	T	287	105	299	75	4.825	2.80E-02	rs5754884	22	32903925	q12.3
SNP_A-1855645	T	T	314	54	317	83	4.828	2.80E-02	rs1506646	18	52284862	q21.2
SNP_A-1849412	C	C	242	126	225	163	4.83	2.80E-02	rs993845	12	72596016	q21.1
SNP_A-1817016	T	T	359	17	346	32	4.826	2.80E-02	rs7966980	12	77875734	q21.2
SNP_A-2208278	C	C	246	124	305	109	4.829	2.80E-02	rs4266895	1	218727854	q41
SNP_A-2214031	C	C	265	139	291	109	4.825	2.80E-02	rs7507534	19	45037758	q13.2
SNP_A-2127337	C	C	220	134	283	123	4.826	2.80E-02	rs4708236	6	76999407	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113436	A	A	230	130	284	114	4.829	2.80E-02	rs9285230	13	22239005	q12.12
SNP_A-2165923	T	T	338	24	357	45	4.83	2.80E-02	rs7323076	13	83030587	q31.1
SNP_A-2083245	C	C	245	123	238	166	4.831	2.80E-02	rs11909639	21	33161986	q22.11
SNP_A-1990022	G	G	256	138	279	107	4.83	2.80E-02	rs2123597	7	61524891	q11.21
SNP_A-2039363	T	T	272	76	270	110	4.825	2.80E-02	rs9590405	13	114017940	q34
SNP_A-2043214	T	T	229	159	206	196	4.826	2.80E-02	rs1825680	12	114533418	q24.21
SNP_A-2269967	G	G	220	134	199	169	4.826	2.80E-02	rs11098278	4	79903059	q21.21
SNP_A-2259624	A	A	350	16	405	7	4.825	2.80E-02	rs3797916	5	9216255	p15.31
SNP_A-2235491	T	T	375	45	391	27	4.829	2.80E-02	rs9989405	16	81381715	q23.3
SNP_A-2234053	T	T	289	71	333	53	4.825	2.80E-02	rs11754083	6	7968883	p24.3
SNP_A-2246457	C	C	373	49	349	71	4.826	2.80E-02	rs2161738	16	55099841	q12.2
SNP_A-2313666	G	G	388	24	371	41	4.827	2.80E-02	rs7422734	2	234097792	q37.1
SNP_A-2307040	A	A	360	22	376	10	4.827	2.80E-02	rs3785195	16	7690818	p13.2
SNP_A-2303820	C	C	273	97	277	139	4.828	2.80E-02	rs2673925	5	135733573	q31.1
SNP_A-2303012	A	A	202	196	234	166	4.83	2.80E-02	rs2543361	14	75663443	q24.3
SNP_A-2296703	A	A	301	61	307	93	4.826	2.80E-02	rs4484166	3	132031182	q21.3
SNP_A-2294831	C	C	337	85	304	110	4.828	2.80E-02	rs12604748	18	44517314	q21.1
SNP_A-2295895	T	T	279	47	340	34	4.829	2.80E-02	rs10877771	12	60652610	q14.1
SNP_A-2291553	G	G	215	161	262	142	4.824	0.0281	rs4103862	12	51277975	q13.13
SNP_A-2302930	G	G	273	85	334	70	4.822	0.0281	rs4744858	9	77908511	q21.2
SNP_A-2238446	T	T	310	34	308	56	4.823	0.0281	rs17067199	6	138554749	q23.3
SNP_A-2262088	G	G	235	87	236	126	4.82	0.0281	rs7677955	4	190499769	q35.2
SNP_A-2045157	T	T	339	3	358	12	4.824	0.0281	rs443719	2	142206030	q22.1
SNP_A-2020322	G	G	361	25	342	42	4.822	0.0281	rs2838300	21	43661787	q22.3
SNP_A-2003231	A	A	264	90	328	76	4.822	0.0281	rs883805	1	36547117	p34.3
SNP_A-2084854	T	T	307	21	388	12	4.821	0.0281	rs16918721	11	92629460	q21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2051779	G	G	330	60	354	40	4.822	0.0281	rs9530648	13	34979432	q13.3
SNP_A-2075674	T	T	290	74	299	111	4.821	0.0281	rs12087046	1	31369505	p35.2
SNP_A-2072786	A	A	381	11	397	3	4.82	0.0281	rs16854494	1	201539082	q32.1
SNP_A-2141034	A	A	360	0	371	5	4.82	0.0281	rs16868510	8	88509589	q21.3
SNP_A-2138042	T	T	385	7	409	1	4.824	0.0281	rs17033534	2	107009204	q12.3
SNP_A-2151628	C	C	267	119	315	99	4.82	0.0281	rs337519	12	61454874	q14.2
SNP_A-2111195	A	A	192	168	252	160	4.823	0.0281	rs2416419	5	115300810	q23.1
SNP_A-2118645	C	C	339	3	358	12	4.824	0.0281	rs2576928	15	54993969	q21.3
SNP_A-2126211	C	C	246	114	299	97	4.82	0.0281	rs700309	7	146530688	q35
SNP_A-2136640	G	G	263	31	324	20	4.823	0.0281	rs1276146	5	31007695	p13.3
SNP_A-2226698	T	T	333	41	385	27	4.822	0.0281	rs17060730	6	132131991	q23.2
SNP_A-2201549	C	C	249	117	311	103	4.82	0.0281	rs2529681	17	65776392	q24.3
SNP_A-2194503	C	C	305	75	290	104	4.825	0.0281	rs7490249	13	63948141	q21.31
SNP_A-2185321	C	C	339	3	358	12	4.824	0.0281	rs4393189	1	196330300	q32.1
SNP_A-2170928	T	T	376	12	346	24	4.822	0.0281	rs2451875	10	122870289	q26.12
SNP_A-1824998	C	C	300	38	366	26	4.822	0.0281	rs10965932	9	235706	p24.3
SNP_A-1853928	T	T	236	126	238	176	4.824	0.0281	rs2325898	20	2574587	p13
SNP_A-1869965	G	G	199	159	250	144	4.823	0.0281	rs2633673	3	87410666	p11.2
SNP_A-1787728	C	C	391	7	415	1	4.819	0.0281	rs13394205	2	17907655	p24.2
SNP_A-1791627	G	G	242	150	215	183	4.82	0.0281	rs11695103	2	71078680	p13.3
SNP_A-1792731	G	G	284	136	246	162	4.82	0.0281	rs7150111	14	90000121	q32.12
SNP_A-1989165	T	T	276	88	286	130	4.824	0.0281	rs2905309	7	22421782	p15.3
SNP_A-1982402	A	G	189	175	223	175	4.82	0.0281	rs2898534	5	85267170	q14.3
SNP_A-1979982	C	C	261	107	263	151	4.822	0.0281	rs17361947	4	175851100	q34.1
SNP_A-1972224	C	C	317	29	367	17	4.82	0.0281	rs11717088	3	29967737	p24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1954984	G	G	413	1	389	7	4.821	0.0281	rs1197069	17	55989666	q23.2
SNP_A-1919920	C	C	223	147	282	134	4.819	0.0281	rs17241313	16	57611910	q21
SNP_A-1923154	G	G	267	97	256	132	4.82	0.0281	rs7319633	13	109175464	q34
SNP_A-1931366	G	G	219	123	214	168	4.821	0.0281	rs10905431	10	8719221	p14
SNP_A-1933005	G	G	301	55	318	88	4.822	0.0281	rs6908994	6	31306688	p21.33
SNP_A-1888093	C	C	301	107	260	130	4.825	0.0281	rs169524	16	28009386	p11.2
SNP_A-1884907	G	G	380	36	394	20	4.82	0.0281	rs8078319	17	35882741	q21.2
SNP_A-1880311	T	T	346	2	366	10	4.819	0.0281	rs339798	13	71631235	q21.33
SNP_A-1879692	G	G	390	24	373	41	4.825	0.0281	rs17028958	1	112144737	p13.2
SNP_A-1903243	C	C	346	30	349	15	4.82	0.0281	rs2224507	10	105573156	q24.33
SNP_A-1904032	A	A	294	70	307	107	4.822	0.0281	rs4511539	16	23144982	p12.1
SNP_A-1903524	G	G	224	142	220	192	4.818	2.82E-02	rs5760628	22	23489514	q11.23
SNP_A-1900574	G	G	389	9	362	20	4.817	2.82E-02	rs2661472	1	69235867	p31.2
SNP_A-1880084	G	G	256	158	282	126	4.819	2.82E-02	rs559768	6	47917908	p12.3
SNP_A-1881164	G	G	246	120	237	161	4.818	2.82E-02	rs2056785	2	180797848	q31.3
SNP_A-1876610	C	C	292	72	297	107	4.816	2.82E-02	rs37060	16	57123805	q21
SNP_A-1931322	T	T	286	102	329	81	4.813	2.82E-02	rs11781985	8	8627193	p23.1
SNP_A-1908938	C	C	233	135	229	183	4.813	2.82E-02	rs11734306	4	189348343	q35.2
SNP_A-1958068	A	A	211	137	252	116	4.819	2.82E-02	rs7992982	13	42167205	q14.11
SNP_A-1948037	C	C	286	82	344	66	4.816	2.82E-02	rs3799338	6	164269103	q26
SNP_A-1984270	G	G	340	4	412	0	4.816	2.82E-02	rs3213105	5	158678277	q33.3
SNP_A-1717035	G	G	291	95	316	70	4.818	2.82E-02	rs1471013	11	11705272	p15.3
SNP_A-1847205	C	C	331	35	353	61	4.814	2.82E-02	rs11123997	2	104645954	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814792	G	G	370	42	349	63	4.813	2.82E-02	rs7116059	11	69837338	q13.3
SNP_A-2170966	A	A	324	16	375	7	4.816	2.82E-02	rs6854571	4	173211669	q34.1
SNP_A-2178074	G	G	228	186	253	151	4.813	2.82E-02	rs10101968	8	139562782	q24.23
SNP_A-2200711	T	T	360	14	387	5	4.819	2.82E-02	rs6953764	7	153621487	q36.2
SNP_A-2204370	A	A	354	6	388	18	4.813	2.82E-02	rs954122	10	113374511	q25.2
SNP_A-2207816	T	T	187	169	250	164	4.816	2.82E-02	rs12050973	16	7209418	p13.2
SNP_A-2136256	G	G	356	10	413	3	4.817	2.82E-02	rs10888287	1	244443457	q44
SNP_A-2133929	C	C	207	159	266	148	4.818	2.82E-02	rs4764407	12	18534382	p12.3
SNP_A-2152245	T	T	286	28	329	55	4.818	2.82E-02	---	18	32701978	q12.2
SNP_A-2164419	C	C	240	174	196	194	4.815	2.82E-02	rs957327	15	31333567	q13.3
SNP_A-2054843	C	C	293	59	290	88	4.817	2.82E-02	rs2282521	6	88712285	q15
SNP_A-1990969	T	T	331	33	345	57	4.817	2.82E-02	rs10487153	7	114283377	q31.2
SNP_A-1994630	A	A	264	150	295	121	4.818	2.82E-02	rs3019344	8	109792883	q23.1
SNP_A-1996390	T	T	398	2	375	9	4.814	2.82E-02	rs16911865	9	27829433	p21.2
SNP_A-2261171	G	G	306	64	271	85	4.815	2.82E-02	rs7210695	17	5077200	p13.2
SNP_A-2263949	A	A	253	103	309	87	4.813	2.82E-02	rs12652630	5	67479290	q13.1
SNP_A-2283762	C	C	362	26	323	41	4.818	2.82E-02	rs6700159	1	217807295	q41
SNP_A-2278389	A	A	253	107	260	154	4.815	2.82E-02	rs759519	12	106416291	q23.3
SNP_A-2235512	G	G	394	16	372	30	4.814	2.82E-02	rs945321	1	5618706	p36.31
SNP_A-2295231	G	G	246	176	209	203	4.813	2.82E-02	rs1740442	6	161167969	q26
SNP_A-2305808	A	A	404	2	381	9	4.809	2.83E-02	rs16947142	15	90993880	q26.1
SNP_A-2234417	C	C	288	74	297	111	4.808	2.83E-02	rs194348	16	10244231	p13.2
SNP_A-2231567	T	T	354	16	409	7	4.811	2.83E-02	rs11176964	12	66630101	q15
SNP_A-2251304	C	G	190	172	224	180	4.81	2.83E-02	rs7108358	11	10251416	p15.4

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2273231	G	G	288	114	318	88	4.812	2.83E-02	rs9510042	13	21677214	q12.11
SNP_A-2266238	C	C	354	16	409	7	4.811	2.83E-02	rs9318695	13	24122575	q12.12
SNP_A-1995718	C	C	225	139	272	120	4.808	2.83E-02	rs1928199	9	7260158	p24.1
SNP_A-1994120	C	C	242	96	282	76	4.808	2.83E-02	rs10107117	8	87623766	q21.3
SNP_A-2008916	A	G	223	177	206	190	4.813	2.83E-02	rs4928098	3	101696774	q12.2
SNP_A-2045565	T	T	314	34	343	61	4.81	2.83E-02	rs2128760	5	10650986	p15.2
SNP_A-2041677	T	C	177	157	196	158	4.809	2.83E-02	rs6777701	3	7128339	p26.1
SNP_A-2037702	A	A	326	34	390	22	4.811	2.83E-02	rs12477159	2	212700354	q34
SNP_A-2037306	C	C	324	44	343	73	4.809	2.83E-02	rs4675159	2	227934852	q36.3
SNP_A-2050768	C	C	361	9	393	23	4.807	2.83E-02	rs311581	2	86194618	p11.2
SNP_A-2061103	G	G	386	30	355	47	4.812	2.83E-02	rs17562317	5	169470737	q35.1
SNP_A-2098493	C	C	269	83	270	120	4.812	2.83E-02	rs9463163	6	46073713	p21.1
SNP_A-2155258	T	T	342	12	359	27	4.807	2.83E-02	rs12157518	22	27078596	q12.1
SNP_A-2158338	T	C	208	156	210	204	4.813	2.83E-02	rs6572335	14	45504335	q21.2
SNP_A-2139843	A	A	344	4	416	0	4.807	2.83E-02	rs6552642	4	184451369	q35.1
SNP_A-2131770	A	A	348	48	316	68	4.807	2.83E-02	rs2403901	11	24121054	p14.3
SNP_A-2117288	C	C	313	27	355	15	4.81	2.83E-02	---	8	87660010	q21.3
SNP_A-2114428	G	G	238	110	239	155	4.81	2.83E-02	rs1542531	3	163739066	q26.1
SNP_A-2208821	G	G	311	43	363	29	4.811	2.83E-02	rs1545669	4	181211332	q34.3
SNP_A-2223513	T	T	322	42	374	28	4.812	2.83E-02	rs7947046	11	61016327	q12.2
SNP_A-2174987	T	T	400	2	377	9	4.812	2.83E-02	rs842789	1	189659351	q31.2
SNP_A-2190252	A	A	202	172	240	148	4.811	2.83E-02	rs8072096	17	5941372	p13.2
SNP_A-1825126	G	G	333	19	334	36	4.81	2.83E-02	rs17071855	6	142918708	q24.2
SNP_A-1826060	C	C	419	3	403	11	4.807	2.83E-02	rs16824640	3	117453528	q13.31
SNP_A-1826463	C	C	312	46	368	32	4.812	2.83E-02	rs2479750	13	113200441	q34
SNP_A-1844257	T	T	320	32	303	51	4.808	2.83E-02	rs12030140	1	58149746	p32.2
SNP_A-1736411	T	T	336	26	376	14	4.811	2.83E-02	rs2019258	11	20073378	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1686756	G	G	342	60	323	85	4.809	2.83E-02	rs4712419	6	10288874	p24.3
SNP_A-1710966	A	A	392	0	405	5	4.81	2.83E-02	rs10511654	9	18424620	p22.2
SNP_A-1795041	A	G	193	161	216	188	4.812	2.83E-02	rs6793060	3	24671288	p24.2
SNP_A-1799417	C	C	397	11	413	3	4.81	2.83E-02	rs16887811	8	116916900	q23.3
SNP_A-1985395	T	T	295	21	349	11	4.809	2.83E-02	rs16886432	6	22652797	p22.3
SNP_A-1974848	A	A	232	136	229	185	4.81	2.83E-02	rs226751	3	153315051	q25.1
SNP_A-1962406	G	G	316	98	278	122	4.81	2.83E-02	rs6671600	1	112488911	p13.2
SNP_A-1956779	C	C	361	9	393	23	4.807	2.83E-02	rs1629426	12	67557550	q15
SNP_A-1939311	A	A	253	113	245	153	4.812	2.83E-02	rs1436330	3	106041195	q13.11
SNP_A-1913915	T	T	402	2	379	9	4.811	2.83E-02	rs4797759	18	13298547	p11.21
SNP_A-1919710	T	T	344	4	416	0	4.807	2.83E-02	rs16912230	9	27991003	p21.2
SNP_A-1877173	G	G	354	54	331	77	4.81	2.83E-02	rs815928	7	55242648	p11.2
SNP_A-1900022	A	A	288	46	283	71	4.808	2.83E-02	rs2162724	5	77997443	q14.1
SNP_A-1893388	G	G	247	113	249	159	4.806	2.84E-02	rs1872432	3	120857892	q13.33
SNP_A-1874076	G	G	326	30	348	54	4.801	2.84E-02	rs12910725	15	51627411	q21.3
SNP_A-1878957	A	A	247	137	229	175	4.804	2.84E-02	rs7142293	14	82595555	q31.2
SNP_A-1930350	T	T	353	5	382	16	4.803	2.84E-02	rs9299386	9	105220706	q31.1
SNP_A-1912828	T	T	326	6	335	17	4.803	2.84E-02	rs16823402	2	144603032	q22.3
SNP_A-1954773	T	T	175	147	240	144	4.804	2.84E-02	rs7677550	4	102447655	q24
SNP_A-1964838	A	A	309	27	295	45	4.801	2.84E-02	rs17048936	2	129459563	q14.3
SNP_A-1965575	C	C	387	9	410	2	4.803	2.84E-02	rs1229746	2	160319855	q24.2
SNP_A-1985976	C	C	395	1	373	7	4.802	2.84E-02	rs536818	6	49337946	p12.3
SNP_A-1983688	A	A	217	135	277	123	4.801	2.84E-02	rs9327827	5	138210227	q31.2
SNP_A-1987012	T	T	315	19	345	39	4.802	2.84E-02	rs4624874	6	100363740	q16.3
SNP_A-1795706	C	C	311	51	331	83	4.802	2.84E-02	rs17698667	3	63617760	p14.2
SNP_A-1806010	T	T	311	79	288	106	4.803	2.84E-02	rs6676015	1	192831583	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814379	G	C	181	173	223	169	4.801	2.84E-02	rs10237950	7	31288916	p14.3
SNP_A-1703479	A	A	315	27	338	50	4.801	2.84E-02	rs7859562	9	1500590	p24.3
SNP_A-1699325	C	C	225	125	294	116	4.803	2.84E-02	rs6825330	4	185744868	q35.1
SNP_A-1842976	G	G	350	20	406	10	4.806	2.84E-02	rs7567434	2	82700708	p12
SNP_A-1832376	A	A	257	105	258	148	4.805	2.84E-02	rs606105	18	11983038	p11.21
SNP_A-1815750	A	A	206	198	237	167	4.802	2.84E-02	rs9890878	17	5803018	p13.2
SNP_A-1821488	C	C	342	24	300	38	4.803	2.84E-02	rs169150	1	30109006	p35.2
SNP_A-1849740	C	C	359	9	391	23	4.801	2.84E-02	rs12018324	13	29073552	q12.3
SNP_A-1865490	C	C	406	8	389	19	4.801	2.84E-02	rs16990370	22	31106141	q12.3
SNP_A-2169546	G	G	238	78	245	117	4.803	2.84E-02	rs6811587	4	88278984	q21.3
SNP_A-2182803	A	A	325	3	344	12	4.801	2.84E-02	rs7147890	14	72442847	q24.2
SNP_A-2204345	G	G	194	154	252	144	4.801	2.84E-02	rs6459829	7	157333790	q36.3
SNP_A-2206995	G	G	332	8	402	2	4.806	2.84E-02	rs7199812	16	81878006	q23.3
SNP_A-2109432	G	G	202	162	247	143	4.803	2.84E-02	rs4235064	4	85011433	q21.23
SNP_A-2118969	G	G	349	21	355	9	4.802	2.84E-02	rs4789682	17	77691117	q25.3
SNP_A-2124974	A	A	292	66	351	51	4.806	2.84E-02	rs11650778	17	30158274	q12
SNP_A-2144701	T	T	341	29	360	52	4.804	2.84E-02	rs16898019	4	18716556	p15.31
SNP_A-2157421	T	T	235	61	240	94	4.804	2.84E-02	rs7587662	2	190312748	q32.2
SNP_A-2164789	T	T	341	5	343	15	4.803	2.84E-02	rs17131452	1	71008290	p31.1
SNP_A-2093299	C	C	240	126	241	175	4.802	2.84E-02	rs30781	16	8891770	p13.2
SNP_A-2094706	C	C	397	1	375	7	4.801	2.84E-02	rs11821483	11	122834939	q24.1
SNP_A-2091675	A	A	184	174	212	144	4.804	2.84E-02	rs475450	18	38037576	q12.3
SNP_A-2073832	A	A	345	71	304	92	4.806	2.84E-02	rs13288400	9	93714407	q22.32
SNP_A-2029115	C	C	408	2	385	9	4.805	2.84E-02	rs17150431	7	24698119	p15.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2009275	C	C	275	87	328	70	4.805	2.84E-02	rs585978	11	30051745	p14.1
SNP_A-2012187	G	G	281	53	265	77	4.806	2.84E-02	rs1479432	6	153707668	q25.2
SNP_A-2271744	C	C	373	47	346	68	4.806	2.84E-02	rs17009311	3	72168078	p13
SNP_A-2258526	C	C	308	98	327	71	4.803	2.84E-02	rs2297371	6	160495598	q25.3
SNP_A-2308505	G	G	263	95	274	140	4.805	2.84E-02	rs7533657	1	41102577	p34.2
SNP_A-2305297	C	C	250	118	312	104	4.802	2.84E-02	rs236511	17	65775691	q24.3
SNP_A-2290907	C	C	404	8	387	19	4.803	2.84E-02	rs11982596	7	156926430	q36.3
SNP_A-2292757	G	G	259	105	264	150	4.795	2.85E-02	rs1509332	4	148022367	q31.22
SNP_A-2314521	G	G	335	31	393	19	4.798	2.85E-02	rs2199112	4	55887423	q12
SNP_A-2256365	A	A	288	126	253	153	4.8	2.85E-02	rs6901838	6	56303235	p12.1
SNP_A-2264354	T	T	241	125	241	173	4.796	2.85E-02	rs12144259	1	80320107	p31.1
SNP_A-2272749	A	A	320	18	387	9	4.796	2.85E-02	rs1288736	14	87221749	q31.3
SNP_A-2280259	C	C	379	7	401	1	4.798	2.85E-02	rs12323472	14	54316012	q22.2
SNP_A-2250545	G	G	418	2	395	9	4.796	2.85E-02	rs2296840	1	148185120	q21.3
SNP_A-2241805	G	G	322	38	379	25	4.799	2.85E-02	rs16895362	6	34982153	p21.31
SNP_A-2008361	T	T	229	141	287	127	4.796	2.85E-02	rs883018	11	21025930	p15.1
SNP_A-2014243	C	C	195	173	248	160	4.799	2.85E-02	rs688697	11	97408057	q22.1
SNP_A-2025570	G	G	338	4	408	0	4.798	2.85E-02	rs1522861	2	79179418	p12
SNP_A-2033690	G	G	299	53	359	39	4.798	2.85E-02	rs415974	2	77549200	p12
SNP_A-2043867	A	A	321	37	389	25	4.798	2.85E-02	rs9709849	18	14724384	p11.21
SNP_A-2056184	A	A	293	51	326	34	4.798	2.85E-02	rs564605	9	40058671	p13.1
SNP_A-2057420	T	T	257	163	282	130	4.8	2.85E-02	rs10151301	14	28109185	q12
SNP_A-2099620	C	C	403	1	381	7	4.796	2.85E-02	rs17125440	14	51902506	q22.1
SNP_A-2159549	T	C	214	204	216	166	4.796	2.85E-02	rs573540	11	95664317	q21
SNP_A-2121620	G	G	295	57	306	36	4.8	2.85E-02	rs13226182	7	13389889	p21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2204979	C	C	242	124	305	111	4.798	2.85E-02	rs607193	11	128119098	q24.3
SNP_A-2202505	C	C	327	41	347	69	4.8	2.85E-02	rs4263106	2	227918404	q36.3
SNP_A-2216147	A	A	331	39	350	66	4.797	2.85E-02	rs10484089	14	51100819	q22.1
SNP_A-2182021	T	T	203	145	267	137	4.798	2.85E-02	rs17512701	5	53583570	q11.2
SNP_A-2172908	T	T	278	36	360	26	4.797	2.85E-02	rs7869788	9	9832282	p23
SNP_A-1851905	G	G	355	1	388	8	4.796	2.85E-02	rs6594609	5	111920136	q22.2
SNP_A-1851071	C	C	300	42	296	66	4.796	2.85E-02	rs1173200	5	4872803	p15.32
SNP_A-1847289	C	C	241	125	241	173	4.796	2.85E-02	rs3743761	16	75785385	q23.1
SNP_A-1817135	G	G	337	33	369	19	4.795	2.85E-02	rs11149752	16	73069512	q22.3
SNP_A-1834129	A	A	347	7	386	20	4.799	2.85E-02	rs17137842	10	15901948	p13
SNP_A-1698861	G	G	330	18	399	9	4.799	2.85E-02	rs10492670	13	106326717	q33.3
SNP_A-1784514	A	A	374	18	333	31	4.796	2.85E-02	rs11136428	8	1757869	p23.3
SNP_A-1758910	C	C	329	67	354	46	4.798	2.85E-02	rs2394132	10	66479115	q21.3
SNP_A-1786105	A	A	318	58	325	89	4.797	2.85E-02	rs12192108	6	132325558	q23.2
SNP_A-1985706	C	C	290	64	306	100	4.797	2.85E-02	rs17575638	6	37659302	p21.2
SNP_A-1968894	C	C	265	101	326	86	4.796	2.85E-02	rs2024675	20	58926895	q13.33
SNP_A-1966284	G	G	357	1	390	8	4.799	2.85E-02	rs16833049	2	191601756	q32.2
SNP_A-1970979	C	C	297	125	322	96	4.796	2.85E-02	rs858543	1	164198956	q24.2
SNP_A-1960138	A	A	206	150	265	139	4.797	2.85E-02	rs1917704	2	141581693	q22.1
SNP_A-1935255	C	C	391	9	414	2	4.8	2.85E-02	rs16842596	1	156509931	q23.2
SNP_A-1940240	A	G	191	145	205	195	4.798	2.85E-02	rs6583209	3	198622793	q29
SNP_A-1946830	C	C	215	165	252	140	4.795	2.85E-02	rs36024	16	54263892	q12.2
SNP_A-1947215	T	T	255	105	305	87	4.799	2.85E-02	rs9491694	6	127478793	q22.33
SNP_A-1928961	G	G	282	88	288	128	4.795	2.85E-02	rs17576594	4	148309846	q31.22
SNP_A-1885053	C	C	303	119	329	91	4.798	2.85E-02	rs6992364	8	135712158	q24.22
SNP_A-1889532	C	C	303	67	364	52	4.794	0.0286	rs17272241	4	161645359	q32.1
SNP_A-1887176	G	G	343	19	366	38	4.791	0.0286	rs17395192	12	26535198	p11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1895049	A	C	211	157	210	206	4.793	0.0286	rs10764785	10	130209737	q26.2
SNP_A-1927174	A	A	283	81	289	119	4.791	0.0286	rs2216508	3	176696650	q26.31
SNP_A-1932952	T	T	407	1	385	7	4.793	0.0286	rs16864954	2	224268429	q36.1
SNP_A-1908443	C	C	363	47	383	29	4.795	0.0286	rs12028479	1	18890443	p36.13
SNP_A-1943686	G	C	177	155	215	177	4.79	0.0286	rs6483645	11	20128523	p15.1
SNP_A-1943902	A	G	174	150	200	166	4.792	0.0286	rs11048580	12	26609096	p11.23
SNP_A-1939043	G	G	323	21	381	11	4.793	0.0286	rs328518	2	22185755	p24.1
SNP_A-1959978	A	A	333	19	348	8	4.789	0.0286	rs16945468	18	16857220	q11.1
SNP_A-1960582	A	A	278	122	307	95	4.792	0.0286	rs2190836	19	48373067	q13.31
SNP_A-1732786	G	G	303	31	333	57	4.794	0.0286	rs2206984	6	85031881	q14.3
SNP_A-1730951	T	T	324	78	295	103	4.792	0.0286	rs1841936	15	51948159	q21.3
SNP_A-1844518	C	C	271	55	289	89	4.792	0.0286	rs6029698	20	39532784	q12
SNP_A-2173087	A	A	229	121	287	107	4.794	0.0286	rs219245	7	150425820	q36.1
SNP_A-2172244	T	T	330	4	398	0	4.793	0.0286	rs7004492	8	24312019	p21.2
SNP_A-2201757	C	C	385	7	407	1	4.793	0.0286	rs10926764	1	239035834	q43
SNP_A-2114471	C	C	244	78	240	112	4.791	0.0286	rs4638198	10	12669374	p13
SNP_A-2115152	A	A	333	29	359	53	4.791	0.0286	rs17117815	10	106620676	q25.1
SNP_A-2133311	T	T	336	34	355	59	4.789	0.0286	rs11192207	10	106606056	q25.1
SNP_A-2165608	A	A	364	34	385	19	4.789	0.0286	rs1953978	14	19525147	q11.2
SNP_A-2094186	T	G	190	170	226	184	4.789	0.0286	rs1641147	2	10622631	p25.1
SNP_A-2048827	T	T	340	4	410	0	4.793	0.0286	rs5001924	2	167151869	q24.3
SNP_A-2076410	G	G	373	3	359	11	4.791	0.0286	rs6936667	6	12127516	p24.1
SNP_A-2024777	C	C	340	4	410	0	4.793	0.0286	rs10099920	8	23864643	p21.2
SNP_A-2015651	T	T	333	31	360	56	4.79	0.0286	rs384159	21	17865020	q21.1
SNP_A-2007855	T	T	311	29	300	48	4.794	0.0286	rs1182523	20	57812611	q13.33
SNP_A-1993370	G	G	272	96	330	80	4.789	0.0286	rs1440747	8	57580478	q12.1
SNP_A-2246839	A	A	391	7	413	1	4.789	0.0286	rs3112597	16	51218708	q12.2
SNP_A-2251040	G	G	262	146	294	118	4.792	0.0286	rs4769528	13	26281901	q12.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2273577	C	C	206	136	210	192	4.792	0.0286	rs957603	15	38796960	q15.1
SNP_A-2279649	T	T	312	74	276	96	4.794	0.0286	rs4767563	12	116451241	q24.22
SNP_A-2296339	T	T	315	47	333	77	4.792	0.0286	rs1241502	14	24681991	q12
SNP_A-2297788	A	A	310	42	349	27	4.783	0.0287	rs13327148	3	4499176	p26.1
SNP_A-2290814	G	G	324	42	387	29	4.785	0.0287	rs2648833	8	129243281	q24.21
SNP_A-2288021	T	T	389	29	369	47	4.786	0.0287	rs7899260	10	12091580	p14
SNP_A-2313124	A	A	197	153	244	136	4.784	0.0287	rs17640951	18	34354078	q12.2
SNP_A-2311662	C	C	342	70	320	96	4.784	0.0287	rs863854	12	101576479	q23.2
SNP_A-2275188	C	C	247	115	250	162	4.783	0.0287	rs10875649	12	46190264	q13.11
SNP_A-2282765	T	T	417	1	395	7	4.786	0.0287	rs2794997	1	52181615	p32.3
SNP_A-2286582	G	G	344	4	414	0	4.784	0.0287	rs2745761	20	8225943	p12.3
SNP_A-2002389	A	A	291	85	256	108	4.787	0.0287	rs7123712	11	128855477	q24.3
SNP_A-2021055	G	G	293	23	355	13	4.784	0.0287	rs738633	22	39741366	q13.2
SNP_A-2031741	G	G	333	17	394	8	4.785	0.0287	rs1001676	17	5567180	p13.2
SNP_A-2041088	T	T	415	1	393	7	4.787	0.0287	rs3176740	9	97519109	q22.33
SNP_A-2064076	G	G	267	77	262	110	4.783	0.0287	rs1787166	18	9611305	p11.22
SNP_A-2091092	A	A	351	51	302	68	4.787	0.0287	rs17660164	8	9227837	p23.1
SNP_A-2086578	G	G	318	96	273	117	4.785	0.0287	rs7099755	10	55697321	q21.1
SNP_A-2167924	C	C	323	61	277	79	4.788	0.0287	rs4568066	3	34234162	p23
SNP_A-2161131	A	A	348	18	377	37	4.788	0.0287	rs17713744	6	19029297	p22.3
SNP_A-2138859	C	C	265	153	292	122	4.784	0.0287	rs17319759	10	6002896	p15.1
SNP_A-2141430	T	T	344	24	311	39	4.786	0.0287	rs7740698	6	34012747	p21.31
SNP_A-2146511	G	G	332	4	400	0	4.788	0.0287	rs17138395	7	17715998	p21.1
SNP_A-2128036	T	T	311	87	350	66	4.788	0.0287	rs17299897	13	37900924	q13.3
SNP_A-2217636	G	G	366	16	380	6	4.787	0.0287	rs1511385	3	142389930	q23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2197631	-	G	193	193	230	168	4.785	0.0287	rs938830	8	97448268	q22.1
SNP_A-1866871	A	A	415	1	393	7	4.787	0.0287	rs16958035	16	67105950	q22.1
SNP_A-1820032	G	G	334	4	402	0	4.783	0.0287	---	18	69731170	q22.3
SNP_A-1780320	T	T	249	113	302	96	4.786	0.0287	rs792556	1	233731134	q43
SNP_A-1680572	G	G	214	182	242	150	4.783	0.0287	rs9605	5	179772913	q35.3
SNP_A-1653392	T	T	250	100	318	88	4.785	0.0287	rs989920	3	152998570	q25.1
SNP_A-1645270	C	A	224	178	215	199	4.786	0.0287	rs2078415	6	48441910	p12.3
SNP_A-1953359	A	A	202	162	258	150	4.787	0.0287	rs11207270	1	58774289	p32.1
SNP_A-1945667	G	G	320	88	341	63	4.787	0.0287	rs4976436	5	136794738	q31.1
SNP_A-1964047	T	T	251	115	313	101	4.787	0.0287	rs10496248	2	82336546	p12
SNP_A-1987009	T	T	268	82	265	117	4.783	0.0287	rs17826560	6	100302299	q16.3
SNP_A-1982200	T	C	188	164	212	176	4.783	0.0287	rs2061515	5	76844816	q13.3
SNP_A-1912568	G	G	377	23	344	38	4.787	0.0287	rs1012604	22	33516560	q12.3
SNP_A-1891409	G	G	370	34	363	55	4.785	0.0287	rs10044101	5	178145485	q35.3
SNP_A-1897505	G	G	255	87	262	128	4.786	0.0287	rs11212989	11	108591032	q22.3
SNP_A-1903189	G	G	244	172	202	194	4.788	0.0287	rs10864418	1	9424238	p36.22
SNP_A-1889387	A	A	337	21	397	11	4.786	0.0287	rs421787	13	43172394	q14.11
SNP_A-1885153	T	T	339	29	391	17	4.785	0.0287	---	6	82822555	q14.1
SNP_A-1971852	C	C	285	43	330	78	4.777	2.88E-02	rs4685252	3	15543867	p25.1
SNP_A-1974379	T	T	308	108	325	79	4.779	2.88E-02	rs2310230	3	133541937	q22.1
SNP_A-1972957	C	C	346	4	416	0	4.779	2.88E-02	rs17069191	3	63612599	p14.2
SNP_A-1973012	T	T	332	64	303	87	4.782	2.88E-02	rs796973	3	64914393	p14.1
SNP_A-1944252	G	G	302	68	363	53	4.779	2.88E-02	rs958700	15	86686322	q25.3
SNP_A-1951406	C	C	262	94	329	81	4.778	2.88E-02	rs9870018	3	6902311	p26.1
SNP_A-1960333	G	G	318	52	294	74	4.777	2.88E-02	rs946197	1	56314329	p32.2
SNP_A-1956928	C	C	222	124	267	105	4.782	2.88E-02	rs574288	3	197273307	q29

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1649718	C	C	363	5	394	16	4.778	2.88E-02	rs4143187	12	81305541	q21.31
SNP_A-1682656	G	G	289	73	267	99	4.779	2.88E-02	rs1482684	5	44524243	p12
SNP_A-1731781	G	G	332	10	384	26	4.778	2.88E-02	rs10498897	6	75270075	q13
SNP_A-1749737	G	G	386	4	381	13	4.777	2.88E-02	rs10484036	14	90696531	q32.12
SNP_A-1795774	T	T	362	56	380	36	4.78	2.88E-02	rs8180693	7	125312890	q31.33
SNP_A-1794595	A	A	316	50	325	79	4.782	2.88E-02	rs1469853	13	101165489	q33.1
SNP_A-1836850	G	G	368	44	380	26	4.777	2.88E-02	rs7138083	12	117917367	q24.23
SNP_A-1840220	G	G	219	141	275	127	4.779	2.88E-02	rs10823002	10	52869480	q21.1
SNP_A-1855417	G	G	256	104	252	144	4.78	2.88E-02	rs9356970	6	25365945	p22.2
SNP_A-2177078	G	G	331	35	354	20	4.777	2.88E-02	rs10077897	5	171772992	q35.1
SNP_A-2214169	C	C	243	105	254	154	4.782	2.88E-02	rs2224896	9	29460435	p21.1
SNP_A-2141082	G	G	376	0	391	5	4.778	2.88E-02	rs11181602	12	36660139	q12
SNP_A-2166018	A	A	365	1	400	8	4.781	2.88E-02	rs9307883	4	152923427	q31.3
SNP_A-2158223	T	T	396	2	375	9	4.777	2.88E-02	rs17036655	12	104005883	q23.3
SNP_A-2095145	C	C	190	176	246	166	4.782	2.88E-02	rs1996697	8	13886163	p22
SNP_A-2071342	A	A	328	14	396	6	4.779	2.88E-02	rs12328369	2	205554746	q33.3
SNP_A-2051363	A	A	234	188	264	156	4.779	2.88E-02	rs10894729	11	133087228	q25
SNP_A-2044815	A	A	379	5	354	14	4.778	2.88E-02	rs11806357	1	8460908	p36.23
SNP_A-2044695	T	T	334	32	394	20	4.779	2.88E-02	rs1025989	15	27391874	q13.1
SNP_A-2035024	A	A	352	14	377	5	4.78	2.88E-02	rs12696977	5	60320397	q12.1
SNP_A-2314356	A	A	395	25	408	12	4.778	2.88E-02	rs4313766	15	25421659	q12
SNP_A-2300476	C	C	242	124	235	167	4.78	2.88E-02	rs7289868	22	43574409	q13.31
SNP_A-2295439	C	C	366	0	381	5	4.773	2.89E-02	rs3181188	4	110978284	q25
SNP_A-2293267	T	T	237	133	294	118	4.773	2.89E-02	rs324859	1	96426532	p21.3
SNP_A-2293798	G	G	372	44	384	26	4.776	2.89E-02	---	7	28644807	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2292008	G	G	266	102	327	87	4.776	2.89E-02	rs193870	7	87712574	q21.13
SNP_A-2305629	G	G	345	25	402	14	4.776	2.89E-02	rs10026378	4	71388392	q13.3
SNP_A-2268556	T	T	314	50	323	79	4.773	2.89E-02	rs7112811	11	96027660	q21
SNP_A-2256137	T	T	359	1	394	8	4.771	2.89E-02	rs17592494	8	17842675	p22
SNP_A-2245927	C	C	231	137	220	180	4.776	2.89E-02	rs13140551	4	123313408	q27
SNP_A-2232827	A	A	184	176	244	170	4.771	2.89E-02	rs1569479	1	183605361	q31.1
SNP_A-2237398	C	C	335	3	356	12	4.772	2.89E-02	rs9830968	3	161895781	q25.33
SNP_A-2040618	G	G	351	17	375	35	4.771	2.89E-02	rs7535598	1	211001879	q41
SNP_A-2002454	G	G	306	104	332	78	4.774	2.89E-02	rs6590763	11	134127609	q25
SNP_A-2019092	T	T	339	31	363	17	4.771	2.89E-02	rs2836011	21	38132045	q22.13
SNP_A-2062092	T	T	284	130	254	160	4.776	2.89E-02	rs12132136	1	204809060	q32.2
SNP_A-2090348	G	G	326	68	320	98	4.772	2.89E-02	rs8077342	17	3867181	p13.2
SNP_A-2157802	G	G	358	10	413	3	4.772	2.89E-02	rs12123488	1	189072210	q31.2
SNP_A-2163413	T	T	341	1	374	8	4.772	2.89E-02	rs1509546	15	79285399	q25.1
SNP_A-2144888	A	A	347	23	372	44	4.776	2.89E-02	rs2848786	18	37281262	q12.3
SNP_A-2142898	A	A	230	128	288	114	4.773	2.89E-02	rs1490096	13	84714710	q31.1
SNP_A-2222363	C	C	334	4	358	14	4.771	2.89E-02	rs9588398	13	110775495	q34
SNP_A-1863893	T	T	385	33	402	18	4.774	2.89E-02	rs2021808	7	127463642	q32.1
SNP_A-1840213	T	T	400	2	379	9	4.774	2.89E-02	rs309388	4	123967717	q27
SNP_A-1782866	C	C	364	46	339	67	4.772	2.89E-02	rs2249296	1	86622285	p22.3
SNP_A-1782827	G	G	326	96	348	70	4.771	2.89E-02	rs241960	19	42976129	q13.12
SNP_A-1672056	C	C	363	21	347	37	4.774	2.89E-02	rs10502098	11	107211357	q22.3
SNP_A-1939255	C	C	296	100	264	126	4.774	2.89E-02	rs154238	3	10330584	p25.3
SNP_A-1934196	T	T	374	48	385	29	4.772	2.89E-02	rs1529779	15	92748167	q26.2
SNP_A-1963641	C	C	325	83	347	59	4.772	2.89E-02	rs726085	2	67642323	p14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1967643	A	A	392	28	402	14	4.774	2.89E-02	rs6140677	20	8597582	p12.3
SNP_A-1977160	T	T	368	0	383	5	4.774	2.89E-02	rs7692461	4	56167094	q12
SNP_A-1894484	C	C	324	38	345	65	4.771	2.89E-02	rs8087477	18	73044949	q23
SNP_A-1915238	T	T	338	4	406	0	4.774	2.89E-02	---	3	65091686	p14.1
SNP_A-1930141	G	G	408	4	403	13	4.776	2.89E-02	rs9292505	5	33726537	p13.3
SNP_A-1928573	A	A	352	12	386	28	4.773	2.89E-02	rs12249716	10	95398409	q23.33
SNP_A-1905162	A	A	238	126	295	111	4.768	2.90E-02	rs12273158	11	39557415	p12
SNP_A-1889784	C	C	367	39	376	22	4.768	2.90E-02	rs8050359	16	8116843	p13.2
SNP_A-1899090	G	G	240	108	239	151	4.766	2.90E-02	rs1025852	4	46241259	p12
SNP_A-1875899	A	A	267	99	268	140	4.77	2.90E-02	rs16868980	5	90020637	q14.3
SNP_A-1982024	C	C	341	21	401	11	4.767	2.90E-02	rs2607378	5	68015556	q13.1
SNP_A-1989011	C	C	299	71	309	107	4.77	2.90E-02	rs10251925	7	16971108	p21.1
SNP_A-1947170	C	C	306	88	294	56	4.766	2.90E-02	rs11059599	12	127259624	q24.32
SNP_A-1941038	G	G	406	2	385	9	4.769	2.90E-02	rs17271813	19	5406386	p13.3
SNP_A-1951848	G	G	267	103	270	146	4.767	2.90E-02	rs9953191	18	36488894	q12.3
SNP_A-1674309	G	A	217	181	220	194	4.767	2.90E-02	rs10509957	10	113718570	q25.2
SNP_A-1692460	A	A	312	76	297	105	4.769	2.90E-02	rs10501103	11	28801743	p14.1
SNP_A-1796058	G	G	330	4	396	0	4.769	2.90E-02	rs1545388	4	134135204	q28.3
SNP_A-1844162	T	T	211	139	191	175	4.767	2.90E-02	rs2614287	6	135734540	q23.3
SNP_A-1816960	A	A	255	77	333	67	4.766	2.90E-02	rs376690	9	6124926	p24.1
SNP_A-1828979	G	G	251	117	310	102	4.766	2.90E-02	rs501089	11	111007689	q23.1
SNP_A-2213274	G	G	338	32	356	56	4.77	2.90E-02	rs10484194	14	46560245	q21.3
SNP_A-2203976	G	G	298	118	266	146	4.766	2.90E-02	rs716193	14	32824348	q13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187324	G	G	285	77	289	113	4.768	2.90E-02	rs10801339	1	191286988	q31.3
SNP_A-2158267	G	G	330	10	333	23	4.769	2.90E-02	rs12684933	9	4084068	p24.2
SNP_A-2135766	G	G	328	32	371	19	4.767	2.90E-02	rs431225	4	167577693	q32.3
SNP_A-2112425	C	C	410	6	396	16	4.769	2.90E-02	rs12590846	14	105021165	q32.33
SNP_A-2085166	T	T	214	158	243	129	4.771	2.90E-02	rs7038730	9	18983912	p22.1
SNP_A-2078017	G	G	296	66	355	51	4.765	2.90E-02	rs7539751	1	202291776	q32.1
SNP_A-2099927	T	T	357	1	392	8	4.767	2.90E-02	rs291261	9	10037099	p23
SNP_A-2051665	C	C	333	25	388	14	4.767	2.90E-02	rs3887427	12	99145918	q23.1
SNP_A-2053981	G	G	238	124	225	163	4.769	2.90E-02	rs2463749	6	72974869	q13
SNP_A-2049192	C	C	286	72	300	110	4.77	2.90E-02	rs5995786	22	38589051	q13.1
SNP_A-2077038	A	A	275	93	325	75	4.77	2.90E-02	rs2050696	1	52806823	p32.3
SNP_A-2008505	A	A	333	25	366	48	4.767	2.90E-02	rs7621243	3	18823333	p24.3
SNP_A-1997792	A	A	367	53	379	33	4.768	2.90E-02	rs7858285	9	116618377	q33.1
SNP_A-2228906	G	G	358	0	373	5	4.768	2.90E-02	rs2728763	4	130973007	q28.2
SNP_A-2264842	C	C	316	74	335	51	4.766	2.90E-02	rs17634308	3	45107091	p21.31
SNP_A-2281894	C	C	357	1	392	8	4.767	2.90E-02	rs10229063	7	106693519	q22.3
SNP_A-2293101	G	G	332	8	400	2	4.77	2.90E-02	rs7901795	10	3942680	p15.1
SNP_A-2288665	A	A	241	127	301	113	4.769	2.90E-02	rs740743	12	125240060	q24.31
SNP_A-2311297	T	T	283	135	249	163	4.761	2.91E-02	rs9662290	1	9296607	p36.22
SNP_A-2279601	C	C	378	44	355	65	4.763	2.91E-02	rs2666970	6	343242	p25.3
SNP_A-2228322	G	G	317	27	326	48	4.761	2.91E-02	rs17160183	7	85078937	q21.11
SNP_A-2002124	G	G	225	179	253	147	4.761	2.91E-02	rs2510752	11	89853120	q14.3
SNP_A-2016253	C	C	234	176	262	144	4.761	2.91E-02	rs2156370	21	21440115	q21.1
SNP_A-2060323	G	G	360	18	356	34	4.759	2.91E-02	rs11007392	10	29355337	p12.1
SNP_A-2107436	C	C	273	53	350	42	4.764	2.91E-02	rs1281424	1	176536605	q25.2
SNP_A-2103581	A	A	332	14	400	6	4.76	2.91E-02	rs1894396	8	28696690	p21.1
SNP_A-2096949	C	C	344	4	412	0	4.761	2.91E-02	rs7216334	17	52856830	q23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2131114	G	G	249	121	245	165	4.763	2.91E-02	rs17350305	1	167108858	q24.2
SNP_A-2124616	A	A	188	162	244	152	4.759	2.91E-02	rs993951	9	6294401	p24.1
SNP_A-2153465	T	T	395	9	416	2	4.761	2.91E-02	rs17288100	3	6185929	p26.1
SNP_A-2138296	C	C	340	28	363	51	4.759	2.91E-02	rs2226133	6	73736298	q13
SNP_A-2189533	G	G	275	137	246	168	4.76	2.91E-02	rs7601545	2	213309400	q34
SNP_A-1826839	G	G	309	61	309	91	4.759	2.91E-02	rs554042	6	109186957	q21
SNP_A-1815579	G	G	305	63	364	48	4.763	2.91E-02	rs7539057	1	167980272	q24.3
SNP_A-1861986	G	G	352	12	371	27	4.761	2.91E-02	rs16896723	5	66737619	q13.1
SNP_A-1857224	C	C	409	1	389	7	4.76	2.91E-02	rs3848461	17	44402561	q21.32
SNP_A-1845225	A	A	238	128	295	113	4.764	2.91E-02	rs1415057	13	101724665	q33.1
SNP_A-1847889	G	G	297	71	358	56	4.763	2.91E-02	rs7076375	10	582926	p15.3
SNP_A-1793731	G	G	342	62	318	86	4.765	2.91E-02	rs9608	9	34988003	p13.3
SNP_A-1807664	T	T	245	107	243	149	4.762	2.91E-02	rs4694295	4	71408876	q13.3
SNP_A-1807083	T	T	311	105	326	76	4.761	2.91E-02	rs1424847	14	79077733	q31.1
SNP_A-1800509	G	G	336	32	354	56	4.762	2.91E-02	rs1134336	13	110347791	q34
SNP_A-1692512	T	T	250	100	321	89	4.761	2.91E-02	rs10513509	3	158391567	q25.31
SNP_A-1718773	T	T	390	0	407	5	4.763	2.91E-02	rs6475197	9	18060074	p22.2
SNP_A-1941909	G	G	295	121	255	145	4.763	2.91E-02	rs12142065	1	214589420	q41
SNP_A-1935302	C	C	221	135	273	119	4.76	2.91E-02	rs10028610	4	82675703	q21.21
SNP_A-1937451	G	G	348	10	401	3	4.76	2.91E-02	rs17170133	7	145663946	q35
SNP_A-1987076	G	G	231	117	289	103	4.761	2.91E-02	rs1934003	6	103165977	q16.3
SNP_A-1972580	T	T	263	151	287	119	4.762	2.91E-02	rs4683139	3	45771433	p21.31
SNP_A-1896842	T	T	326	18	393	9	4.763	2.91E-02	rs35389	5	33990637	p13.3
SNP_A-1910207	C	C	349	69	324	94	4.763	2.91E-02	rs10007790	4	28969543	p15.1
SNP_A-1931013	A	A	368	54	382	34	4.764	2.91E-02	rs10824215	10	53614883	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1931538	C	C	299	47	307	75	4.763	2.91E-02	rs7641766	3	57634200	p14.3
SNP_A-1920855	C	C	281	43	347	31	4.757	0.0292	rs17586307	2	231766524	q37.1
SNP_A-1878315	C	C	278	40	351	29	4.756	0.0292	rs1498359	1	210778874	q41
SNP_A-1965062	A	A	253	115	255	161	4.754	0.0292	rs17659751	2	139449677	q22.1
SNP_A-1937399	T	T	337	27	400	16	4.754	0.0292	rs11919076	3	96353479	q11.2
SNP_A-1957564	A	A	231	139	289	125	4.757	0.0292	rs6548717	3	80689467	p12.2
SNP_A-1726598	G	G	372	20	371	37	4.753	0.0292	rs10482903	21	20119296	q21.1
SNP_A-1748737	T	T	326	74	357	53	4.757	0.0292	rs1595314	2	140156217	q22.1
SNP_A-1782363	C	C	343	21	403	11	4.757	0.0292	rs1484736	18	66092446	q22.2
SNP_A-1808915	G	G	311	51	323	81	4.757	0.0292	rs9566655	13	40476109	q14.11
SNP_A-1810804	A	A	288	82	294	120	4.756	0.0292	rs9524537	13	94016015	q32.1
SNP_A-1791207	G	G	308	112	279	141	4.757	0.0292	rs11145629	5	157579192	q33.3
SNP_A-1872757	T	T	241	125	281	103	4.759	0.0292	rs4717501	7	62097086	q11.21
SNP_A-1826975	A	A	266	58	277	91	4.753	0.0292	rs11232464	11	80491777	q14.1
SNP_A-1824002	G	G	270	72	342	60	4.754	0.0292	rs8080344	17	51004571	q23.1
SNP_A-2189892	C	C	283	43	287	69	4.753	0.0292	rs11145117	9	76733622	q21.2
SNP_A-2193954	A	A	354	16	407	7	4.759	0.0292	rs3797918	5	9216336	p15.31
SNP_A-2174629	G	C	187	171	226	180	4.756	0.0292	rs8056547	16	6900777	p13.2
SNP_A-2219714	G	G	346	4	414	0	4.756	0.0292	rs17171037	7	147656175	q36.1
SNP_A-2157243	C	C	333	7	351	19	4.753	0.0292	rs2008097	5	16719407	p15.1
SNP_A-2124744	G	G	315	31	369	19	4.755	0.0292	rs778406	1	56415526	p32.2
SNP_A-2128487	C	C	224	136	268	116	4.753	0.0292	rs8084097	18	23354995	q12.1
SNP_A-2108529	C	C	375	41	377	23	4.756	0.0292	rs11829571	12	95872531	q23.1
SNP_A-2093519	T	C	232	174	205	201	4.755	0.0292	rs6602496	10	11435518	p14
SNP_A-2104883	G	A	182	176	225	169	4.757	0.0292	rs2406680	12	41194645	q12
SNP_A-2049409	G	G	280	56	338	42	4.757	0.0292	rs7139191	12	30391087	p11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2008041	T	T	355	3	343	11	4.755	0.0292	rs16932585	11	16105375	p15.1
SNP_A-2011345	A	A	341	51	358	32	4.758	0.0292	rs473490	11	59114519	q12.1
SNP_A-1994365	T	T	345	15	318	28	4.754	0.0292	rs16895377	8	98333370	q22.1
SNP_A-2039284	C	C	256	112	256	156	4.757	0.0292	rs11711042	3	166622649	q26.1
SNP_A-2235327	C	C	360	8	387	21	4.754	0.0292	rs2131425	8	18258603	p22
SNP_A-2246482	T	T	312	52	327	83	4.754	0.0292	rs11112634	12	104544783	q23.3
SNP_A-2261274	T	T	308	52	368	38	4.758	0.0292	rs8034011	15	92997089	q26.2
SNP_A-2312200	G	G	353	13	379	29	4.754	0.0292	rs12856544	13	105896357	q33.3
SNP_A-2314085	T	T	274	142	303	113	4.756	0.0292	rs1534991	1	11695518	p36.22
SNP_A-2291590	C	C	217	151	213	203	4.755	0.0292	rs9367197	6	44553424	p21.1
SNP_A-2296204	A	A	212	152	270	140	4.755	0.0292	rs7172094	15	78621699	q25.1
SNP_A-2296882	C	C	316	8	339	21	4.754	0.0292	rs7527096	1	24647382	p36.11
SNP_A-2298274	C	C	267	103	328	88	4.756	0.0292	rs11069386	13	99379711	q32.3
SNP_A-2294604	T	T	217	115	192	144	4.751	0.0293	rs6534998	4	135439213	q28.3
SNP_A-2305633	A	A	208	194	241	165	4.748	0.0293	rs4722631	7	26547565	p15.2
SNP_A-2303074	A	A	270	98	274	140	4.752	0.0293	rs11734539	4	181968784	q34.3
SNP_A-2302363	C	C	219	113	230	166	4.748	0.0293	rs3739075	2	26622072	p23.3
SNP_A-2270674	G	G	391	21	375	37	4.748	0.0293	rs17125551	14	52082297	q22.1
SNP_A-2270051	C	C	318	40	340	68	4.751	0.0293	rs2867559	7	70823875	q11.22
SNP_A-2274582	G	G	307	45	350	30	4.75	0.0293	rs11194894	10	111602656	q25.1
SNP_A-2281714	T	T	349	13	405	5	4.749	0.0293	rs6133609	20	8637441	p12.3
SNP_A-2283476	A	A	331	39	390	26	4.752	0.0293	rs3862864	10	59582876	q21.1
SNP_A-2284911	C	C	349	19	395	9	4.747	0.0293	rs2939316	5	39585791	p13.1
SNP_A-2254443	A	A	212	144	257	125	4.75	0.0293	rs6535918	4	154784184	q31.3
SNP_A-2238485	G	G	234	134	288	118	4.748	0.0293	rs11577282	1	222594357	q42.12
SNP_A-2037336	A	A	345	17	369	35	4.749	0.0293	rs6884819	5	4936953	p15.32
SNP_A-2027918	T	T	217	133	285	125	4.752	0.0293	rs354707	2	143720169	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2022416	G	G	282	138	305	107	4.747	0.0293	rs1164768	12	103533086	q23.3
SNP_A-2001424	C	C	243	125	242	172	4.75	0.0293	rs4429002	10	111379052	q25.1
SNP_A-2009107	C	C	338	4	404	0	4.751	0.0293	rs2713615	3	130756417	q21.3
SNP_A-2099542	C	T	165	143	187	153	4.751	0.0293	rs2701106	12	113160267	q24.21
SNP_A-2090079	T	T	330	66	360	46	4.752	0.0293	rs7019053	9	105693102	q31.2
SNP_A-2112109	C	C	232	188	257	153	4.751	0.0293	rs11648843	16	81545526	q23.3
SNP_A-2127280	G	G	230	40	309	31	4.749	0.0293	rs17028230	4	153232685	q31.3
SNP_A-2214574	G	G	310	24	378	14	4.749	0.0293	rs12434471	14	21230393	q11.2
SNP_A-2222836	T	T	276	136	293	103	4.749	0.0293	rs1290084	15	48941237	q21.2
SNP_A-2192377	G	G	331	21	389	11	4.753	0.0293	rs16849459	3	105125003	q13.11
SNP_A-1831212	A	A	370	20	358	36	4.749	0.0293	rs7847291	9	22999021	p21.3
SNP_A-1873369	A	A	267	107	247	139	4.753	0.0293	rs7817444	8	54722323	q11.23
SNP_A-1871622	C	C	250	172	278	140	4.748	0.0293	rs7521521	1	161469207	q23.3
SNP_A-1859856	G	G	349	13	405	5	4.749	0.0293	rs17053321	13	35475035	q13.3
SNP_A-1863859	A	A	323	93	297	121	4.749	0.0293	rs11593517	10	15521198	p13
SNP_A-1864285	T	T	263	147	236	180	4.748	0.0293	rs175115	11	60581790	q12.2
SNP_A-1848155	A	A	321	11	392	4	4.747	0.0293	rs7515500	1	20909515	p36.12
SNP_A-1845377	A	A	264	114	307	93	4.75	0.0293	rs497766	6	145595081	q24.2
SNP_A-1857796	G	G	349	13	405	5	4.749	0.0293	rs13386412	2	57853166	p16.1
SNP_A-1855249	A	A	403	13	384	26	4.749	0.0293	rs12780114	10	132356366	q26.3
SNP_A-1791416	T	T	338	4	404	0	4.751	0.0293	rs288690	13	106212476	q33.3
SNP_A-1784506	C	C	349	13	405	5	4.749	0.0293	rs470558	11	102171526	q22.2
SNP_A-1960896	A	A	348	4	374	14	4.752	0.0293	rs9344288	6	83347699	q14.1
SNP_A-1939087	C	C	321	59	304	84	4.75	0.0293	rs11788411	9	113922686	q32
SNP_A-1962909	T	C	205	191	213	167	4.752	0.0293	rs2098766	2	41380328	p22.1
SNP_A-1968504	C	C	307	59	371	45	4.748	0.0293	rs4809590	20	44518234	q13.12
SNP_A-1976112	A	A	348	4	416	0	4.752	0.0293	rs569684	4	12815802	p15.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977791	C	C	343	25	369	47	4.751	0.0293	rs17005057	4	82387567	q21.21
SNP_A-1977467	G	G	325	27	386	16	4.753	0.0293	rs2194891	4	67836824	q13.2
SNP_A-1879216	G	G	342	24	363	45	4.752	0.0293	rs943493	13	102056890	q33.1
SNP_A-1880777	G	G	254	156	285	127	4.75	0.0293	rs1031289	9	22721106	p21.3
SNP_A-1883559	G	G	348	4	416	0	4.752	0.0293	rs17055598	6	128669758	q22.33
SNP_A-1921079	G	G	368	0	385	5	4.749	0.0293	rs17002686	4	78724972	q21.1
SNP_A-1925264	A	A	189	173	246	164	4.743	2.94E-02	rs11802413	1	25506236	p36.11
SNP_A-1905737	A	A	241	121	243	169	4.743	2.94E-02	rs1893354	18	32142421	q12.2
SNP_A-1907311	A	A	243	101	309	89	4.744	2.94E-02	rs13217648	6	38794200	p21.2
SNP_A-1912069	G	G	289	35	347	23	4.744	2.94E-02	rs11847474	14	74789526	q24.3
SNP_A-1917609	T	T	310	98	261	117	4.746	2.94E-02	rs7373685	3	129589718	q21.3
SNP_A-1889534	A	A	315	39	339	67	4.741	2.94E-02	rs17668291	18	17977647	q11.2
SNP_A-1978078	G	G	356	8	383	21	4.744	2.94E-02	rs1450498	4	93833221	q22.3
SNP_A-1974480	G	G	358	0	375	5	4.743	2.94E-02	rs11928110	3	136798876	q22.2
SNP_A-1942448	G	G	315	51	375	37	4.741	2.94E-02	rs3893349	15	77760728	q25.1
SNP_A-1692232	T	T	297	103	318	76	4.745	2.94E-02	rs755648	10	7166318	p14
SNP_A-1654021	A	A	265	135	299	109	4.741	2.94E-02	rs10510591	3	27158409	p24.1
SNP_A-1788058	C	C	340	4	406	0	4.746	2.94E-02	rs6445216	3	61447265	p14.2
SNP_A-1806399	T	G	205	157	209	199	4.746	2.94E-02	rs7325116	13	91390556	q31.3
SNP_A-1857478	G	G	361	1	398	8	4.743	2.94E-02	rs2520675	5	10073635	p15.2
SNP_A-1870287	T	T	351	13	407	5	4.742	2.94E-02	rs16972357	13	107846335	q33.3
SNP_A-2187993	C	C	206	92	297	91	4.743	2.94E-02	rs7489580	13	22531483	q12.12
SNP_A-2174355	C	C	314	100	286	128	4.745	2.94E-02	rs12448685	16	8280125	p13.2
SNP_A-2179438	A	A	321	49	337	79	4.744	2.94E-02	rs1432579	3	64155460	p14.1
SNP_A-2224823	A	A	337	21	361	41	4.745	2.94E-02	rs9801310	7	131197102	q32.3
SNP_A-2218125	G	G	354	10	407	3	4.743	2.94E-02	---	14	61694778	q23.2
SNP_A-2126740	A	A	342	4	408	0	4.742	2.94E-02	rs9312903	5	16167428	p15.1
SNP_A-2080728	G	G	295	73	356	58	4.744	2.94E-02	rs16822581	2	160564184	q24.2
SNP_A-2082867	T	T	254	94	294	74	4.746	2.94E-02	rs2519015	1	805968	p36.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2049884	A	A	225	159	196	190	4.746	2.94E-02	rs9900295	17	75329032	q25.3
SNP_A-2013908	A	A	266	58	254	84	4.744	2.94E-02	rs585555	11	94053391	q21
SNP_A-1991714	T	T	300	102	254	122	4.742	2.94E-02	rs1406604	7	147376989	q36.1
SNP_A-2029014	A	A	300	32	354	20	4.746	2.94E-02	rs4657914	1	190932891	q31.3
SNP_A-2040431	G	G	270	98	331	83	4.745	2.94E-02	rs12380087	9	107982935	q31.2
SNP_A-2042035	C	C	297	41	330	72	4.742	2.94E-02	rs989121	13	76060418	q22.2
SNP_A-2228535	T	T	316	50	330	80	4.747	2.94E-02	rs12427892	13	46539754	q14.2
SNP_A-2269361	G	G	301	63	313	97	4.742	2.94E-02	rs6960164	7	109577142	q31.1
SNP_A-2268535	C	C	266	48	300	32	4.745	2.94E-02	rs10203191	2	83962856	p11.2
SNP_A-2305758	A	A	278	50	285	79	4.746	2.94E-02	rs17321133	12	93860732	q22
SNP_A-2314258	A	A	370	40	353	61	4.747	2.94E-02	rs2535960	7	152053747	q36.2
SNP_A-2304507	G	G	358	52	377	33	4.738	2.95E-02	rs1076790	20	12362259	p12.1
SNP_A-2299918	C	C	340	24	370	46	4.736	2.95E-02	rs1214212	12	126810932	q24.32
SNP_A-2286653	A	A	398	2	379	9	4.738	2.95E-02	rs701059	12	126485017	q24.32
SNP_A-2235146	C	C	364	22	405	11	4.737	2.95E-02	rs11168605	12	47178855	q13.11
SNP_A-2043465	C	C	326	14	392	6	4.738	2.95E-02	rs11824008	11	131574563	q25
SNP_A-2041282	G	G	326	14	392	6	4.738	2.95E-02	rs11191996	10	106055721	q25.1
SNP_A-2046192	C	C	375	13	388	28	4.74	2.95E-02	rs11114478	12	79383658	q21.31
SNP_A-2024294	T	T	205	129	256	114	4.739	2.95E-02	rs13232191	7	65430798	q11.21
SNP_A-2002017	C	C	269	147	236	176	4.741	2.95E-02	rs2359232	1	34439266	p34.3
SNP_A-2067058	G	G	234	164	256	130	4.737	2.95E-02	rs7901991	10	90301297	q23.31
SNP_A-2067276	T	T	228	134	222	180	4.738	2.95E-02	rs4524431	4	184834095	q35.1
SNP_A-2085964	A	A	232	136	290	122	4.737	2.95E-02	rs160405	5	138111975	q31.2
SNP_A-2102465	T	T	193	173	248	162	4.741	2.95E-02	rs3886182	5	67468547	q13.1
SNP_A-2136158	C	C	318	42	379	29	4.737	2.95E-02	rs11863214	16	15041876	p13.11
SNP_A-2110566	C	C	338	72	319	99	4.736	2.95E-02	rs2006655	13	18644610	q12.11
SNP_A-2110188	T	T	342	4	368	14	4.739	2.95E-02	rs1106079	3	111676716	q13.13
SNP_A-2139236	C	C	346	72	363	49	4.736	2.95E-02	rs138963	22	41910346	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2152477	C	C	297	65	310	100	4.737	2.95E-02	rs11917103	3	181146767	q26.33
SNP_A-2225493	A	A	336	28	359	51	4.74	2.95E-02	rs1211184	1	35557240	p34.3
SNP_A-2177638	C	C	284	28	315	53	4.741	2.95E-02	rs4908680	1	7692264	p36.23
SNP_A-2199025	C	C	269	75	331	61	4.738	2.95E-02	rs6658863	1	48392912	p33
SNP_A-1867538	G	G	292	26	362	16	4.736	2.95E-02	rs4856866	3	67590385	p14.1
SNP_A-1847657	A	A	383	29	347	45	4.74	2.95E-02	rs7699968	4	36863845	p14
SNP_A-1832640	A	A	218	128	216	176	4.739	2.95E-02	rs337841	5	78269997	q14.1
SNP_A-1802113	T	T	381	9	400	2	4.736	2.95E-02	rs3773796	3	132128116	q21.3
SNP_A-1808601	G	G	314	50	328	80	4.736	2.95E-02	rs2043475	17	28911274	q12
SNP_A-1783965	G	G	377	9	396	2	4.739	2.95E-02	rs7702739	5	64404559	q12.3
SNP_A-1960598	T	T	270	150	238	180	4.738	2.95E-02	rs7046875	9	127282461	q33.3
SNP_A-1961397	A	A	314	30	381	19	4.74	2.95E-02	rs3913154	4	190227617	q35.2
SNP_A-1967735	C	C	381	9	400	2	4.736	2.95E-02	rs10485740	20	10407613	p12.2
SNP_A-1885884	A	A	253	167	282	136	4.739	2.95E-02	rs2418881	1	186722946	q31.1
SNP_A-1904202	T	T	303	31	385	21	4.736	2.95E-02	rs10984951	9	120386336	q33.2
SNP_A-1907349	A	A	359	37	334	56	4.738	2.95E-02	rs1485334	3	68026220	p14.1
SNP_A-1907979	A	A	243	121	303	107	4.736	2.95E-02	rs2914756	5	6311496	p15.32
SNP_A-1909226	T	T	235	177	253	139	4.739	2.95E-02	rs9381497	6	47057506	p12.3
SNP_A-1921976	C	C	334	88	304	114	4.738	2.95E-02	rs491849	11	58218058	q12.1
SNP_A-1927197	G	G	344	4	410	0	4.738	2.95E-02	rs1560783	8	75966210	q21.11
SNP_A-1928245	C	C	345	17	406	8	4.731	2.96E-02	rs203885	6	28184865	p22.1
SNP_A-1925195	C	C	313	69	326	46	4.733	2.96E-02	rs11818158	10	44486274	q11.21
SNP_A-1890896	C	C	346	4	412	0	4.733	2.96E-02	rs17071538	6	110794444	q21
SNP_A-1879801	C	C	268	112	317	93	4.733	2.96E-02	rs904549	11	36058508	p13
SNP_A-1967225	C	C	387	27	389	13	4.73	2.96E-02	rs2288586	2	227480895	q36.3
SNP_A-1955765	T	T	327	41	388	28	4.732	2.96E-02	rs9621814	22	32662837	q12.3
SNP_A-1953222	G	G	200	168	258	158	4.731	2.96E-02	---	4	95909145	q22.3
SNP_A-1950010	T	T	273	45	312	30	4.734	2.96E-02	rs4803995	19	51910439	q13.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1807543	A	A	387	7	405	1	4.73	2.96E-02	rs16889617	4	13694073	p15.33
SNP_A-1785892	G	G	312	72	346	52	4.734	2.96E-02	rs274645	5	6839308	p15.31
SNP_A-1791169	C	C	236	130	297	117	4.73	2.96E-02	rs4851926	2	106201178	q12.2
SNP_A-1790920	A	A	210	156	269	145	4.733	2.96E-02	rs662150	1	215526795	q41
SNP_A-1799056	C	C	409	3	397	11	4.731	2.96E-02	rs1652430	2	137450450	q22.1
SNP_A-1843046	T	T	249	103	253	147	4.731	2.96E-02	rs4764927	12	98745880	q23.1
SNP_A-1816589	C	C	356	48	309	65	4.73	2.96E-02	rs17294604	2	5573645	p25.2
SNP_A-1847896	G	T	194	174	228	186	4.733	2.96E-02	rs11640711	16	82007595	q23.3
SNP_A-1854547	C	C	285	37	345	25	4.73	2.96E-02	rs3862391	11	66560671	q13.2
SNP_A-2199211	T	T	236	130	233	177	4.735	2.96E-02	rs9368373	6	22024631	p22.3
SNP_A-2199453	T	T	372	50	387	31	4.734	2.96E-02	rs6955063	7	139530612	q34
SNP_A-2204320	G	G	318	6	395	1	4.734	2.96E-02	---	14	33029132	q13.1
SNP_A-2140131	T	T	293	21	368	12	4.731	2.96E-02	rs828269	2	26881662	p23.3
SNP_A-2163043	C	C	341	61	342	38	4.73	2.96E-02	rs7222705	17	60864651	q24.1
SNP_A-2068634	G	G	202	102	267	93	4.735	2.96E-02	rs7762493	6	81991224	q14.1
SNP_A-2054521	C	C	320	48	333	77	4.733	2.96E-02	rs17313558	8	53319224	q11.23
SNP_A-2055791	G	G	306	106	279	135	4.731	2.96E-02	rs17654841	8	14862060	p22
SNP_A-2016738	C	C	287	79	348	64	4.73	2.96E-02	rs979914	21	24515826	q21.2
SNP_A-2009239	T	T	297	55	311	87	4.73	2.96E-02	rs659379	3	154957342	q25.2
SNP_A-2029787	C	C	314	98	328	70	4.731	2.96E-02	rs2241269	15	84079601	q25.3
SNP_A-2045899	A	A	275	91	336	76	4.734	2.96E-02	rs2128528	6	2589879	p25.2
SNP_A-2250346	C	A	229	177	204	194	4.73	2.96E-02	rs185257	3	136154983	q22.1
SNP_A-2282087	C	A	187	183	238	178	4.731	2.96E-02	rs690526	15	51794410	q21.3
SNP_A-2288841	T	T	328	8	334	20	4.731	2.96E-02	rs16915774	11	90552688	q14.3
SNP_A-2294409	G	C	195	175	228	186	4.728	2.97E-02	rs422224	5	32085050	p13.3
SNP_A-2296831	G	G	384	32	367	51	4.729	2.97E-02	rs10901198	9	132588803	q34.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259464	T	T	358	24	386	12	4.728	2.97E-02	rs3127536	1	184504536	q31.1
SNP_A-2237017	C	C	293	75	354	60	4.728	2.97E-02	rs16855239	1	228291376	q42.2
SNP_A-2239821	A	G	224	186	211	187	4.728	2.97E-02	rs3105748	6	160781131	q25.3
SNP_A-2229890	C	C	341	73	311	97	4.725	2.97E-02	rs470036	22	45893516	q13.31
SNP_A-2036779	G	G	281	89	287	129	4.727	2.97E-02	rs11248556	10	125252066	q26.13
SNP_A-2028517	T	T	370	0	389	5	4.726	2.97E-02	rs554888	3	96598427	q11.2
SNP_A-2004768	C	C	407	1	389	7	4.729	2.97E-02	rs17117578	10	106478637	q25.1
SNP_A-1992144	A	A	323	35	352	62	4.724	2.97E-02	rs17624022	8	6402090	p23.1
SNP_A-2052958	C	T	198	156	213	197	4.728	2.97E-02	rs2694084	2	4818691	p25.2
SNP_A-2064646	A	A	332	18	350	36	4.726	2.97E-02	rs12433409	14	70539173	q24.2
SNP_A-2094076	A	A	195	161	243	145	4.729	2.97E-02	rs11152332	18	57960485	q21.33
SNP_A-2084562	G	G	176	166	225	153	4.729	2.97E-02	rs4484748	9	4633573	p24.1
SNP_A-2129585	G	G	391	9	410	2	4.729	2.97E-02	rs17069524	8	2293385	p23.2
SNP_A-2214091	T	T	250	162	207	183	4.724	2.97E-02	rs2761887	14	53494802	q22.2
SNP_A-2195158	T	T	196	174	250	162	4.725	2.97E-02	rs2951012	7	154413093	q36.2
SNP_A-2185034	C	C	359	3	384	12	4.726	2.97E-02	rs6533361	4	109515151	q25
SNP_A-1870646	T	T	322	84	303	113	4.726	2.97E-02	rs17763873	17	66215284	q24.3
SNP_A-1864800	G	G	303	105	272	132	4.728	2.97E-02	rs2184483	1	116507566	p13.1
SNP_A-1821771	C	C	277	89	338	74	4.728	2.97E-02	rs12603181	17	51441559	q23.2
SNP_A-1825405	C	C	416	2	397	9	4.725	2.97E-02	rs16958140	16	81266662	q23.3
SNP_A-1822366	C	C	315	79	338	56	4.729	2.97E-02	rs12615739	2	216442597	q35
SNP_A-1842735	C	C	283	37	354	26	4.726	2.97E-02	rs4821456	22	34839769	q12.3
SNP_A-1829722	A	A	300	66	359	51	4.726	2.97E-02	rs9588040	13	109391019	q34
SNP_A-1793408	G	G	277	89	338	74	4.728	2.97E-02	rs2793093	1	228183808	q42.2
SNP_A-1790776	A	A	369	1	408	8	4.726	2.97E-02	rs12532261	7	131721284	q32.3
SNP_A-1788328	T	T	281	75	340	60	4.727	2.97E-02	rs9710177	19	44198621	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1812323	A	A	368	0	387	5	4.725	2.97E-02	rs4629723	6	116160841	q22.1
SNP_A-1803401	G	G	361	3	386	12	4.729	2.97E-02	rs11222070	11	129739526	q24.3
SNP_A-1783254	G	G	295	69	304	104	4.724	2.97E-02	rs957655	8	67572395	q13.1
SNP_A-1732267	G	G	393	7	411	1	4.727	2.97E-02	rs7603615	2	133742868	q21.2
SNP_A-1971644	A	A	393	7	411	1	4.727	2.97E-02	rs10510384	3	8045527	p26.1
SNP_A-1971566	T	T	229	127	291	115	4.727	2.97E-02	rs463149	3	6796860	p26.1
SNP_A-1986822	C	C	370	0	389	5	4.726	2.97E-02	rs16883261	6	91370661	q15
SNP_A-1989399	C	C	355	13	411	5	4.728	2.97E-02	rs17158629	7	29932019	p15.1
SNP_A-1886345	C	C	345	13	371	29	4.727	2.97E-02	rs11877854	18	60618044	q22.1
SNP_A-1885027	T	T	317	51	377	37	4.725	2.97E-02	rs7954757	12	21385935	p12.1
SNP_A-1882414	G	G	375	43	354	64	4.726	2.97E-02	rs17153204	10	6375737	p15.1
SNP_A-1893760	C	C	227	143	286	130	4.729	2.97E-02	rs12596008	16	7212848	p13.2
SNP_A-1904225	G	G	342	4	406	0	4.719	0.0298	---	22	38842800	q13.1
SNP_A-1926341	T	T	362	0	381	5	4.721	0.0298	rs12249604	10	18941732	p12.31
SNP_A-1966393	G	G	316	54	329	85	4.721	0.0298	rs11674328	2	197112120	q32.3
SNP_A-1950424	A	A	207	155	267	145	4.718	0.0298	rs623457	2	67593742	p14
SNP_A-1942835	C	C	390	16	402	6	4.722	0.0298	rs742928	20	56624736	q13.32
SNP_A-1938970	T	T	258	106	314	90	4.718	0.0298	rs17827323	4	59408876	q12
SNP_A-1725926	T	T	391	11	388	24	4.718	0.0298	rs10513414	9	120981753	q33.2
SNP_A-1802945	A	G	208	158	208	200	4.722	0.0298	rs13009175	2	145956668	q22.3
SNP_A-1809536	A	A	367	1	406	8	4.723	0.0298	rs7734622	5	125828300	q23.2
SNP_A-1820870	G	G	244	168	213	199	4.721	0.0298	rs11780923	8	5359978	p23.2
SNP_A-1866175	T	T	285	67	342	52	4.723	0.0298	rs17337503	13	74474385	q22.2
SNP_A-1873883	T	T	296	92	235	105	4.721	0.0298	rs1484369	9	106107847	q31.2
SNP_A-1856937	A	A	244	122	304	108	4.718	0.0298	rs10177513	2	190041033	q32.2
SNP_A-1844461	T	T	254	116	313	101	4.722	0.0298	rs236501	17	65778654	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227914	C	C	354	20	364	38	4.721	0.0298	rs180699	10	117728166	q25.3
SNP_A-2200496	A	A	305	65	312	98	4.722	0.0298	rs17524590	15	94477533	q26.2
SNP_A-2199758	A	A	196	172	250	160	4.718	0.0298	rs2736374	8	11151238	p23.1
SNP_A-2212335	C	C	400	10	367	21	4.72	0.0298	rs7180036	15	38906477	q15.1
SNP_A-2103991	C	C	347	19	372	38	4.723	0.0298	rs9355389	6	162594304	q26
SNP_A-2072611	A	A	227	191	258	160	4.719	0.0298	rs7178902	15	78577621	q25.1
SNP_A-2051502	C	C	292	76	353	61	4.722	0.0298	rs1465389	2	2133373	p25.3
SNP_A-1996674	A	A	344	76	365	53	4.718	0.0298	rs7090427	10	16423937	p13
SNP_A-2007005	A	A	233	179	266	150	4.719	0.0298	rs6435922	2	216502418	q35
SNP_A-2017477	A	A	366	0	385	5	4.724	0.0298	rs16982242	21	28673702	q21.3
SNP_A-2019387	T	T	362	46	378	28	4.719	0.0298	rs7410116	21	39461660	q22.2
SNP_A-2243764	G	G	421	1	403	7	4.721	0.0298	rs2179561	6	52278457	p12.2
SNP_A-2274769	A	A	356	26	328	42	4.721	0.0298	---	15	38012280	q15.1
SNP_A-2297740	A	A	410	6	398	16	4.719	0.0298	rs733803	20	31945322	q11.22
SNP_A-2303408	A	A	240	118	245	167	4.712	2.99E-02	rs335784	15	58126672	q22.2
SNP_A-2287390	C	T	184	168	228	182	4.714	2.99E-02	rs11982604	7	53105235	p12.1
SNP_A-2260376	A	A	304	100	331	75	4.715	2.99E-02	rs11793686	9	129679522	q34.11
SNP_A-2233039	C	C	272	98	333	83	4.718	2.99E-02	rs12192270	6	144003807	q24.2
SNP_A-2042691	T	C	192	164	218	186	4.716	2.99E-02	rs7614855	3	24956705	p24.2
SNP_A-2011543	G	G	320	102	289	129	4.715	2.99E-02	rs10501332	11	61858341	q12.3
SNP_A-2066815	A	A	331	13	383	5	4.715	2.99E-02	rs17044836	12	76962148	q21.2
SNP_A-2094495	C	C	251	83	252	120	4.714	2.99E-02	rs1536352	13	88153674	q31.2
SNP_A-2084922	T	T	380	28	364	46	4.718	2.99E-02	rs2941685	10	65410456	q21.3
SNP_A-2226818	C	C	185	167	237	155	4.718	2.99E-02	rs6996724	8	13304299	p22
SNP_A-2184864	T	T	198	126	175	157	4.717	2.99E-02	rs4855751	3	108642184	q13.12
SNP_A-2187598	A	A	319	85	294	112	4.715	2.99E-02	rs2270570	9	76026076	q21.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2173346	C	C	231	113	239	163	4.713	2.99E-02	rs3816528	3	158609992	q25.32
SNP_A-2128986	G	G	284	60	344	46	4.717	2.99E-02	rs17797837	18	20102747	q11.2
SNP_A-2110740	A	A	244	126	304	112	4.717	2.99E-02	rs2397670	6	100444677	q16.3
SNP_A-2113068	A	A	358	0	377	5	4.718	2.99E-02	rs13412111	2	83574448	p11.2
SNP_A-2114053	T	T	348	20	371	9	4.717	2.99E-02	rs26941	3	64111150	p14.1
SNP_A-2148979	T	T	232	120	240	172	4.713	2.99E-02	rs4650608	1	78950036	p31.1
SNP_A-1856181	A	A	231	181	248	142	4.712	2.99E-02	rs1678050	10	118916833	q26.11
SNP_A-1839052	G	G	339	15	351	31	4.716	2.99E-02	rs14820887	4	86910536	q21.23
SNP_A-1788382	C	C	232	120	222	160	4.716	2.99E-02	rs1991277	18	70264181	q22.3
SNP_A-1671302	T	T	326	50	332	78	4.718	2.99E-02	rs10504138	8	53200329	q11.23
SNP_A-1937515	T	T	339	57	357	37	4.716	2.99E-02	rs17231114	10	34112362	p11.22
SNP_A-1935706	A	A	235	155	272	130	4.712	2.99E-02	rs11025279	11	19809969	p15.1
SNP_A-1950854	C	C	342	26	401	15	4.715	2.99E-02	rs11845831	14	45437205	q21.2
SNP_A-1963693	A	A	321	47	336	76	4.713	2.99E-02	rs17036178	2	69023646	p13.3
SNP_A-1981237	A	A	329	63	355	43	4.717	2.99E-02	rs404220	5	35431002	p13.2
SNP_A-1927353	C	C	345	77	361	53	4.717	2.99E-02	rs11071923	15	64944769	q22.32
SNP_A-1889559	A	A	275	135	299	105	4.71	3.00E-02	rs4854498	2	68858695	p13.3
SNP_A-1875643	G	G	319	51	379	37	4.709	3.00E-02	rs12585125	13	98108307	q32.2
SNP_A-1934712	G	G	278	84	265	115	4.706	3.00E-02	rs766621	5	118094535	q23.1
SNP_A-1940576	C	C	323	89	339	63	4.712	3.00E-02	rs1675867	12	129006400	q24.33
SNP_A-1786496	C	C	338	48	308	68	4.711	3.00E-02	rs2631893	8	21167274	p21.3
SNP_A-1796910	G	G	336	4	398	0	4.708	3.00E-02	rs7868300	9	129263104	q34.11
SNP_A-1810604	A	A	345	25	400	14	4.708	3.00E-02	rs16954178	18	8784092	p11.22
SNP_A-1829563	A	A	335	71	310	96	4.712	3.00E-02	rs2901020	2	124030914	q14.3
SNP_A-2145523	A	A	312	66	263	83	4.71	3.00E-02	rs4733515	8	30784820	p12
SNP_A-2156709	G	G	329	11	400	4	4.711	3.00E-02	rs17386506	13	103886481	q33.2
SNP_A-2113058	G	G	346	4	410	0	4.711	3.00E-02	rs17029695	2	65096203	p14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172732	G	G	406	10	373	21	4.707	3.00E-02	rs17706989	16	77127458	q23.1
SNP_A-2190702	G	G	349	21	375	41	4.709	3.00E-02	rs10891729	11	114042950	q23.2
SNP_A-2212060	A	A	343	23	323	39	4.708	3.00E-02	rs4237324	10	71351772	q22.1
SNP_A-2206280	G	G	278	102	294	74	4.711	3.00E-02	rs2173143	8	28337658	p21.1
SNP_A-2089341	T	T	345	25	400	14	4.708	3.00E-02	rs12586076	13	37102852	q13.3
SNP_A-2095358	C	C	179	129	236	120	4.709	3.00E-02	rs10507207	12	104852278	q23.3
SNP_A-2095498	C	C	292	48	319	31	4.707	3.00E-02	rs911995	13	105830840	q33.3
SNP_A-2074855	T	T	377	9	354	20	4.708	3.00E-02	rs7242540	18	20643912	q11.2
SNP_A-2061917	T	T	195	137	257	129	4.71	3.00E-02	rs6997974	8	105758383	q22.3
SNP_A-2012074	T	T	349	9	383	23	4.707	3.00E-02	rs1073246	6	130047392	q22.33
SNP_A-1994629	G	G	237	129	298	116	4.709	3.00E-02	rs3019384	8	109706427	q23.1
SNP_A-2240979	A	A	309	53	369	39	4.709	3.00E-02	rs7206026	16	52987359	q12.2
SNP_A-2273211	C	C	369	33	384	18	4.711	3.00E-02	rs286928	11	34596076	p13
SNP_A-2303818	G	G	319	51	379	37	4.709	3.00E-02	rs6123272	20	51321745	q13.2
SNP_A-2311337	A	A	229	135	284	120	4.708	3.00E-02	rs2774008	13	75649333	q22.2
SNP_A-2301261	C	C	272	66	332	52	4.71	3.00E-02	rs1485919	3	31206283	p24.1
SNP_A-2229008	C	C	341	29	362	52	4.704	3.01E-02	rs7454934	6	93551093	q16.1
SNP_A-2002929	A	A	256	90	234	118	4.706	3.01E-02	rs4132165	12	90808542	q21.33
SNP_A-2018389	T	T	350	4	414	0	4.702	3.01E-02	rs9985040	21	34402201	q22.11
SNP_A-2017270	A	A	217	151	210	200	4.702	3.01E-02	rs235930	21	27558858	q21.3
SNP_A-2034339	A	A	255	113	255	157	4.703	3.01E-02	rs2851911	18	12034657	p11.21
SNP_A-2076683	C	C	290	64	340	48	4.706	3.01E-02	rs10810942	9	18270143	p22.2
SNP_A-2103946	C	C	254	116	251	159	4.703	3.01E-02	rs11084211	19	58152673	q13.41
SNP_A-2115088	G	G	350	4	414	0	4.702	3.01E-02	rs7114929	11	18174367	p15.1
SNP_A-2128524	T	T	307	51	365	37	4.702	3.01E-02	rs6766469	3	133466938	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2157712	G	G	333	37	334	60	4.706	3.01E-02	rs10000748	4	129440096	q28.2
SNP_A-2152195	C	C	322	14	386	6	4.705	3.01E-02	rs7735780	5	138977611	q31.2
SNP_A-2141110	A	A	350	4	414	0	4.702	3.01E-02	rs16839036	2	133242998	q21.2
SNP_A-2141907	C	C	207	115	227	87	4.703	3.01E-02	rs4730157	7	105528754	q22.3
SNP_A-1832708	G	G	381	33	396	18	4.701	3.01E-02	rs10164902	2	119452551	q14.2
SNP_A-1841153	A	A	350	4	414	0	4.702	3.01E-02	rs17052414	8	24612905	p21.2
SNP_A-1819004	A	A	315	17	348	36	4.702	3.01E-02	rs4339212	4	7661510	p16.1
SNP_A-1858194	C	C	235	81	299	69	4.704	3.01E-02	rs4378808	2	215186746	q34
SNP_A-1873493	G	G	267	95	273	137	4.704	3.01E-02	rs6556757	5	163823423	q34
SNP_A-1805697	C	C	263	103	316	86	4.703	3.01E-02	rs7141930	14	81109398	q31.1
SNP_A-1792203	C	C	241	93	296	78	4.704	3.01E-02	rs1162976	12	62948604	q14.2
SNP_A-1647820	T	T	278	84	285	123	4.704	3.01E-02	rs2063345	6	160769442	q25.3
SNP_A-1701429	G	G	289	55	314	90	4.702	3.01E-02	rs728758	6	99630256	q16.2
SNP_A-1934946	A	A	348	2	374	10	4.705	3.01E-02	rs16958460	18	43601121	q21.1
SNP_A-1977200	T	T	202	128	192	170	4.704	3.01E-02	rs1983453	4	58049320	q12
SNP_A-1976293	C	C	382	8	369	19	4.701	3.01E-02	rs16895671	4	17441979	p15.32
SNP_A-1985624	C	C	319	47	334	76	4.702	3.01E-02	rs2001097	6	32491836	p21.32
SNP_A-1971619	C	C	287	81	348	66	4.701	3.01E-02	rs6673493	1	166476305	q24.2
SNP_A-1969274	A	A	297	113	319	85	4.701	3.01E-02	rs2825628	21	19825394	q21.1
SNP_A-1909628	G	G	293	67	345	51	4.704	3.01E-02	rs9402178	6	130188954	q22.33
SNP_A-1905687	T	T	357	1	396	8	4.705	3.01E-02	rs17148490	7	124709417	q31.33
SNP_A-1886813	C	C	339	31	395	19	4.698	3.02E-02	rs16968855	19	39275498	q13.11
SNP_A-1972237	C	C	297	89	339	69	4.699	3.02E-02	rs10913582	1	168447242	q24.3
SNP_A-1973677	C	C	332	30	384	18	4.695	3.02E-02	rs554030	3	102483656	q12.3
SNP_A-1962643	A	A	352	4	416	0	4.699	3.02E-02	rs17014814	2	34312413	p22.3
SNP_A-1940400	G	G	299	29	323	53	4.7	3.02E-02	rs11189119	10	99057279	q24.1
SNP_A-1956049	G	G	259	103	266	148	4.698	3.02E-02	rs7618297	3	24633701	p24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1956584	C	C	364	0	385	5	4.698	3.02E-02	rs17172461	7	55078375	p11.2
SNP_A-1711270	G	G	342	8	408	2	4.7	3.02E-02	rs1396705	9	15722332	p22.3
SNP_A-1660161	T	T	335	67	320	94	4.696	3.02E-02	rs3798709	6	11109262	p24.2
SNP_A-1742915	A	A	267	127	249	163	4.697	3.02E-02	rs1162609	9	24576464	p21.3
SNP_A-1807874	A	A	306	114	273	141	4.697	3.02E-02	rs2530388	6	30075107	p21.33
SNP_A-1872142	A	A	360	8	389	21	4.697	3.02E-02	rs16845416	4	71984410	q13.3
SNP_A-1823812	C	C	379	19	392	8	4.696	3.02E-02	rs10019120	4	14428759	p15.33
SNP_A-1832641	C	C	357	13	385	29	4.697	3.02E-02	rs7439908	4	85298985	q21.23
SNP_A-2152443	C	C	314	50	333	81	4.7	3.02E-02	rs2518110	9	105379109	q31.2
SNP_A-2153975	A	A	246	108	303	93	4.7	3.02E-02	rs1332102	10	101314426	q24.2
SNP_A-2127992	G	G	350	12	386	28	4.697	3.02E-02	rs4658693	1	241565383	q44
SNP_A-2203531	A	A	319	49	377	35	4.7	3.02E-02	rs1001938	6	46035816	p21.1
SNP_A-2212559	G	G	404	2	387	9	4.696	3.02E-02	rs1872051	15	91557802	q26.1
SNP_A-2227443	G	G	337	7	336	18	4.699	3.02E-02	rs4300052	9	5839986	p24.1
SNP_A-2179475	A	A	193	173	242	158	4.699	3.02E-02	rs306416	13	25391476	q12.13
SNP_A-2179046	C	C	386	16	340	28	4.695	3.02E-02	rs6656230	1	26532766	p36.11
SNP_A-2095192	A	A	389	7	405	1	4.698	3.02E-02	rs318114	7	28873343	p15.1
SNP_A-2077212	A	A	234	128	292	114	4.7	3.02E-02	rs6535291	4	83283873	q21.22
SNP_A-2068457	C	C	324	86	290	110	4.699	3.02E-02	rs1523132	14	77838637	q24.3
SNP_A-2030878	G	G	206	162	262	150	4.695	3.02E-02	rs2026692	13	46426546	q14.2
SNP_A-2000370	A	A	286	82	347	67	4.699	3.02E-02	rs4661119	1	154119337	q23.1
SNP_A-1997217	C	C	296	64	353	49	4.697	3.02E-02	rs10512211	9	91183815	q22.31
SNP_A-1993530	A	A	248	110	242	150	4.696	3.02E-02	rs17801727	8	62845621	q12.3
SNP_A-1993719	C	C	334	32	392	20	4.699	3.02E-02	rs17142314	10	7058243	p14
SNP_A-2276203	A	A	364	0	385	5	4.698	3.02E-02	rs10803989	2	186380028	q32.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2283302	T	T	364	0	385	5	4.698	3.02E-02	rs12646827	4	59650934	q12
SNP_A-2288629	A	A	264	104	294	80	4.695	3.02E-02	rs3909594	15	58755653	q22.2
SNP_A-2288323	G	G	218	130	286	122	4.696	3.02E-02	rs7531369	1	22384467	p36.12
SNP_A-2307817	G	G	304	54	332	36	4.696	3.02E-02	rs10910003	1	3599086	p36.32
SNP_A-2307728	G	G	244	110	292	92	4.691	3.03E-02	rs702303	6	145618497	q24.2
SNP_A-2313813	C	C	213	129	282	122	4.693	3.03E-02	rs9547912	13	36969135	q13.3
SNP_A-2267012	C	C	341	11	370	26	4.692	3.03E-02	rs250212	5	50328352	q11.1
SNP_A-2233924	A	A	275	91	282	132	4.69	3.03E-02	rs671626	13	37275813	q13.3
SNP_A-2247691	T	T	359	35	331	53	4.69	3.03E-02	rs16879361	8	32403343	p12
SNP_A-1997676	G	G	291	129	319	101	4.694	3.03E-02	rs1004282	9	111329511	q31.3
SNP_A-2017935	G	G	385	19	398	8	4.692	3.03E-02	rs7281210	21	31407071	q22.11
SNP_A-2010037	T	T	339	3	364	12	4.69	3.03E-02	---	11	37824303	p12
SNP_A-2044870	C	C	316	96	341	71	4.694	3.03E-02	rs10978949	9	107466631	q31.2
SNP_A-2072001	G	G	304	58	366	44	4.693	3.03E-02	rs8178071	8	48977140	q11.21
SNP_A-2081469	C	C	312	58	324	90	4.691	3.03E-02	rs10256019	7	12708016	p21.3
SNP_A-2102605	T	T	321	25	393	15	4.694	3.03E-02	rs974053	8	18597019	p22
SNP_A-2174121	A	A	181	171	236	162	4.694	3.03E-02	rs11732621	4	120570486	q26
SNP_A-2123979	G	G	353	37	342	58	4.69	3.03E-02	rs1955127	2	100844716	q11.2
SNP_A-2131277	C	C	233	155	262	126	4.692	3.03E-02	rs1582588	16	57931256	q21
SNP_A-1838373	A	A	329	75	360	54	4.692	3.03E-02	rs6426025	1	37735682	p34.3
SNP_A-1822450	A	A	365	31	370	16	4.694	3.03E-02	rs17105051	14	36225514	q13.3
SNP_A-1863847	G	G	397	7	413	1	4.695	3.03E-02	rs10193802	2	40272588	p22.1
SNP_A-1811898	T	T	243	121	244	168	4.695	3.03E-02	rs7756217	6	123329002	q22.31
SNP_A-1791730	G	G	243	151	280	126	4.695	3.03E-02	rs1956881	14	22463909	q11.2
SNP_A-1789240	A	A	314	72	309	103	4.689	3.03E-02	rs16938769	8	75122296	q21.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1961549	T	T	358	10	409	3	4.693	3.03E-02	rs11133967	5	3009236	p15.33
SNP_A-1949198	C	C	277	55	297	89	4.69	3.03E-02	rs2158951	7	43540338	p13
SNP_A-1882263	G	G	248	166	278	136	4.691	3.03E-02	rs10869430	9	74465817	q21.13
SNP_A-1884406	A	A	317	47	332	76	4.692	3.03E-02	rs13386458	2	100523209	q11.2
SNP_A-1892867	G	G	234	98	307	89	4.693	3.03E-02	rs9364840	6	166642129	q27
SNP_A-1894306	T	T	243	121	244	168	4.695	3.03E-02	rs6905596	6	120793146	q22.31
SNP_A-1895083	G	G	341	17	400	8	4.694	3.03E-02	rs1455004	2	84500194	p11.2
SNP_A-1904933	G	T	207	159	211	201	4.693	3.03E-02	rs6596734	5	106612442	q21.3
SNP_A-1911256	C	C	289	59	349	45	4.694	3.03E-02	rs7747960	6	152883588	q25.2
SNP_A-1920337	A	A	238	98	296	84	4.69	3.03E-02	rs1477174	16	49432256	q12.1
SNP_A-1929670	T	T	224	144	218	192	4.685	0.0304	rs1840641	2	138518834	q22.1
SNP_A-1905158	G	G	311	49	327	79	4.687	0.0304	rs8099501	18	39364958	q12.3
SNP_A-1906524	T	T	240	118	291	101	4.686	0.0304	rs7784429	7	134453335	q33
SNP_A-1881358	T	T	306	42	334	72	4.686	0.0304	rs7625655	3	58312763	p14.3
SNP_A-1956116	C	C	310	54	323	85	4.688	0.0304	---	18	39279784	q12.3
SNP_A-1943732	G	G	235	109	234	152	4.685	0.0304	rs11207621	1	60665636	p31.3
SNP_A-1946974	C	C	180	172	236	164	4.684	0.0304	rs1288567	4	186604417	q35.1
SNP_A-1945050	T	T	255	123	298	102	4.685	0.0304	rs16837285	3	127416891	q21.2
SNP_A-1936438	G	G	382	30	362	48	4.687	0.0304	rs17598137	3	49866366	p21.31
SNP_A-1938074	A	A	332	6	409	1	4.686	0.0304	rs16926588	8	62001406	q12.2
SNP_A-1968896	G	G	212	156	271	145	4.688	0.0304	rs2426960	20	58927301	q13.33
SNP_A-1969390	A	A	335	5	341	15	4.688	0.0304	rs2154722	21	22254197	q21.1
SNP_A-1866271	C	C	238	126	299	113	4.685	0.0304	rs404420	2	70645181	p13.3
SNP_A-1822077	C	C	248	102	251	145	4.685	0.0304	rs3825393	12	108346094	q24.11
SNP_A-1836667	G	G	411	3	360	10	4.688	0.0304	rs17206162	17	8686622	p13.1
SNP_A-2126933	C	C	321	47	377	33	4.689	0.0304	rs1447815	3	59662653	p14.2
SNP_A-2129393	G	G	336	32	394	20	4.688	0.0304	rs17730982	8	134852184	q24.22
SNP_A-2118037	T	T	222	132	222	182	4.684	0.0304	rs1605586	6	87232480	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2159199	C	C	288	64	292	96	4.687	0.0304	rs11633504	15	94364237	q26.2
SNP_A-2164711	C	C	255	99	264	144	4.686	0.0304	rs9596839	13	53162396	q14.3
SNP_A-2164314	A	A	346	18	366	36	4.688	0.0304	rs2126999	16	8920965	p13.2
SNP_A-2147726	A	A	389	13	390	4	4.686	0.0304	rs902560	17	29324492	q12
SNP_A-2174511	C	C	304	110	270	136	4.684	0.0304	rs2184401	10	13226881	p13
SNP_A-2224038	A	A	359	17	383	7	4.689	0.0304	rs12114270	8	215763	p23.3
SNP_A-2213876	C	C	303	97	328	72	4.689	0.0304	rs2455308	5	40965270	p13.1
SNP_A-2217913	A	A	341	79	312	104	4.684	0.0304	rs17841201	15	81856385	q25.2
SNP_A-2066464	T	T	294	90	323	67	4.686	0.0304	rs6877485	5	72359464	q13.2
SNP_A-2062420	C	C	211	203	242	172	4.684	0.0304	rs11041427	11	7505405	p15.4
SNP_A-2060254	C	C	304	50	369	37	4.684	0.0304	rs17117846	12	54325648	q13.2
SNP_A-2054417	C	C	317	53	332	84	4.685	0.0304	rs1401072	3	117764397	q13.31
SNP_A-2048148	T	T	240	172	274	144	4.687	0.0304	rs3913446	4	7510020	p16.1
SNP_A-2022618	T	T	236	128	224	168	4.688	0.0304	rs9449475	6	83170215	q14.1
SNP_A-2021485	C	C	173	169	225	159	4.685	0.0304	rs1368999	9	28869870	p21.1
SNP_A-2011520	G	G	415	3	405	11	4.689	0.0304	rs226963	6	3669120	p25.2
SNP_A-2018169	T	T	330	40	389	27	4.688	0.0304	rs2833867	21	32831993	q22.11
SNP_A-1995838	G	G	286	68	343	53	4.688	0.0304	rs2890897	9	9963935	p23
SNP_A-1992053	A	G	227	183	218	200	4.685	0.0304	rs974997	8	5339167	p23.2
SNP_A-1991437	G	G	231	161	250	126	4.688	0.0304	rs832960	7	136306641	q33
SNP_A-2270579	C	C	271	77	333	63	4.687	0.0304	rs6844763	4	161293819	q32.1
SNP_A-2310051	A	A	231	125	237	177	4.688	0.0304	rs2077783	2	181977283	q31.3
SNP_A-2304666	C	C	405	11	415	3	4.689	0.0304	rs12042555	1	4369422	p36.32
SNP_A-2288316	A	A	302	38	333	67	4.689	0.0304	rs11231723	11	55497774	q11
SNP_A-2294390	T	T	405	11	415	3	4.689	0.0304	rs4654534	1	4386757	p36.32
SNP_A-2291259	A	A	206	152	257	137	4.684	3.05E-02	rs7354558	20	11020785	p12.2
SNP_A-2249249	A	A	248	46	308	34	4.679	3.05E-02	rs11692038	2	89075057	p11.2
SNP_A-2252983	A	C	204	172	212	184	4.683	3.05E-02	rs1486401	12	114508671	q24.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2000001	G	G	283	25	347	15	4.68	3.05E-02	rs3007211	1	36525712	p34.3
SNP_A-2044310	C	C	274	138	244	168	4.679	3.05E-02	rs7698402	4	34908026	p15.1
SNP_A-2045635	G	G	195	171	250	160	4.684	3.05E-02	rs6970653	7	140422695	q34
SNP_A-2046259	A	A	350	4	412	0	4.68	3.05E-02	rs17027814	2	102798626	q12.1
SNP_A-2047292	A	A	334	34	322	54	4.679	3.05E-02	rs7923239	10	2216705	p15.3
SNP_A-2106583	A	A	246	124	306	110	4.683	3.05E-02	rs17620154	13	100392540	q32.3
SNP_A-2089779	G	G	325	45	379	31	4.682	3.05E-02	rs6890800	5	110180038	q22.1
SNP_A-2088589	A	A	303	53	321	85	4.679	3.05E-02	rs17170220	7	33226384	p14.3
SNP_A-2091872	A	A	348	4	410	0	4.684	3.05E-02	rs6820677	4	114787275	q26
SNP_A-2219048	A	A	315	51	324	80	4.683	3.05E-02	rs7743593	6	111665682	q21
SNP_A-2214797	C	C	241	117	308	106	4.682	3.05E-02	rs9542425	13	70066447	q21.33
SNP_A-2170729	A	A	249	111	248	154	4.679	3.05E-02	rs39935	5	61849298	q12.1
SNP_A-2179293	G	G	363	43	349	65	4.679	3.05E-02	rs10967819	9	27250415	p21.2
SNP_A-2176877	G	G	197	115	268	110	4.682	3.05E-02	rs7552331	1	3277098	p36.32
SNP_A-2142976	T	T	279	91	340	76	4.683	3.05E-02	rs257933	5	128410949	q23.3
SNP_A-1829904	G	G	300	70	309	105	4.678	3.05E-02	rs2122521	15	94378219	q26.2
SNP_A-1843467	T	T	324	40	370	26	4.68	3.05E-02	rs2817248	6	24572552	p22.2
SNP_A-1821801	T	T	410	10	398	22	4.678	3.05E-02	rs2219618	15	51896429	q21.3
SNP_A-1822667	A	A	348	4	410	0	4.684	3.05E-02	rs17077216	6	116218421	q22.1
SNP_A-1825326	A	A	287	121	254	148	4.679	3.05E-02	rs7915809	10	81848610	q22.3
SNP_A-1856369	G	G	316	50	322	78	4.682	3.05E-02	rs12100401	13	60951280	q21.2
SNP_A-1935601	A	A	327	13	377	5	4.679	3.05E-02	rs7934730	11	120410442	q23.3
SNP_A-1947627	A	A	355	13	409	5	4.683	3.05E-02	rs7573145	2	163320186	q24.2
SNP_A-1940096	T	T	348	4	410	0	4.684	3.05E-02	rs389791	15	60539633	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1957528	C	C	353	13	381	29	4.684	3.05E-02	rs6892636	5	86961691	q14.3
SNP_A-1953435	A	A	336	34	357	59	4.681	3.05E-02	rs11253599	10	15744251	p13
SNP_A-1880977	C	C	384	32	360	50	4.682	3.05E-02	rs17147518	7	95683028	q21.3
SNP_A-1886375	G	G	193	171	249	161	4.679	3.05E-02	rs1521725	4	157907817	q32.1
SNP_A-1896774	A	A	317	45	380	32	4.679	3.05E-02	rs17083873	5	94016419	q15
SNP_A-1922211	C	G	185	157	203	173	4.68	3.05E-02	rs11893783	2	154557645	q23.3
SNP_A-1905657	G	G	314	50	336	32	4.674	3.06E-02	rs4242183	5	168633499	q35.1
SNP_A-1893025	T	T	346	18	380	8	4.677	3.06E-02	rs7119964	11	10382086	p15.4
SNP_A-1904156	A	A	327	37	380	24	4.673	3.06E-02	rs1319804	1	238649637	q43
SNP_A-1881208	T	T	210	160	265	147	4.677	3.06E-02	rs336506	2	105783237	q12.2
SNP_A-1948400	G	G	247	113	307	99	4.677	3.06E-02	rs9830798	3	18841543	p24.3
SNP_A-1950147	T	T	357	63	333	87	4.675	3.06E-02	rs7015381	8	4032708	p23.2
SNP_A-1955376	A	A	336	6	413	1	4.673	3.06E-02	rs2421054	5	158977077	q33.3
SNP_A-1960010	C	C	306	60	308	90	4.674	3.06E-02	rs17042591	2	113411572	q13
SNP_A-1973507	C	C	218	146	216	198	4.676	3.06E-02	rs4859044	3	87319480	p11.2
SNP_A-1981165	A	A	318	52	378	38	4.674	3.06E-02	rs696836	5	32770165	p13.3
SNP_A-1846061	A	A	364	0	387	5	4.674	3.06E-02	rs16965000	17	24671953	q11.2
SNP_A-1851603	A	A	309	49	365	35	4.673	3.06E-02	rs12456768	18	70830929	q22.3
SNP_A-1866248	C	G	188	174	229	181	4.673	3.06E-02	rs11160176	14	93950118	q32.13
SNP_A-1864101	T	T	350	10	399	3	4.674	3.06E-02	rs10062892	5	174212774	q35.2
SNP_A-1815950	T	T	281	77	294	116	4.675	3.06E-02	rs4867530	5	27707626	p14.1
SNP_A-1829382	T	T	376	16	386	6	4.677	3.06E-02	rs188953	3	51957291	p21.2
SNP_A-1811940	C	C	236	116	294	102	4.674	3.06E-02	rs12770412	10	35910720	p11.21
SNP_A-1810207	A	A	270	146	299	117	4.676	3.06E-02	rs1658190	18	4478582	p11.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800484	T	T	307	105	265	127	4.676	3.06E-02	rs563697	2	119130683	q14.2
SNP_A-1785193	G	G	357	9	393	23	4.675	3.06E-02	rs10946676	6	24252846	p22.2
SNP_A-1660525	A	A	341	1	380	8	4.674	3.06E-02	rs10498937	6	84840192	q14.2
SNP_A-2141945	C	C	364	0	387	5	4.674	3.06E-02	rs6820176	4	181865410	q34.3
SNP_A-2164544	C	C	375	21	361	37	4.675	3.06E-02	rs16824535	3	117395119	q13.31
SNP_A-2133052	A	A	357	13	411	5	4.676	3.06E-02	---	3	192462901	q28
SNP_A-2213964	G	G	299	59	287	85	4.673	3.06E-02	rs11634943	15	53045808	q21.3
SNP_A-2089305	C	C	279	57	258	80	4.677	3.06E-02	rs210225	10	42384252	q11.21
SNP_A-2054776	A	A	352	4	414	0	4.676	3.06E-02	rs7746203	6	79498898	q14.1
SNP_A-2053225	G	G	326	96	297	123	4.674	3.06E-02	rs1851722	9	104441197	q31.1
SNP_A-2057016	G	G	385	37	353	55	4.674	3.06E-02	rs919525	14	81561742	q31.1
SNP_A-2067203	G	G	302	48	365	35	4.674	3.06E-02	rs4696645	4	151540020	q31.23
SNP_A-2065205	A	A	211	145	210	198	4.674	3.06E-02	rs10110144	8	121074896	q24.12
SNP_A-2001618	C	C	344	26	368	48	4.673	3.06E-02	rs4481948	10	134196160	q26.3
SNP_A-2252872	A	A	197	165	251	153	4.673	3.06E-02	rs9383054	6	15505614	p22.3
SNP_A-2231709	G	G	306	54	327	87	4.675	3.06E-02	rs6781811	3	10096922	p25.3
SNP_A-2262233	C	C	267	99	271	141	4.676	3.06E-02	rs10190089	2	159075249	q24.1
SNP_A-2287489	T	T	285	85	346	70	4.672	3.06E-02	rs2726780	4	183558071	q34.3
SNP_A-2289848	A	A	219	191	252	162	4.675	3.06E-02	rs3845596	1	14934605	p36.21
SNP_A-2296898	A	A	262	86	253	119	4.675	3.06E-02	rs11192792	10	107995698	q25.1
SNP_A-2290195	G	G	315	29	361	17	4.67	3.07E-02	rs1542445	14	97957656	q32.2
SNP_A-2307534	G	G	199	153	252	140	4.668	3.07E-02	rs194422	16	47831489	q12.1
SNP_A-2284967	T	T	299	25	307	45	4.668	3.07E-02	rs372970	3	1599602	p26.3
SNP_A-2282097	G	G	260	102	322	88	4.67	3.07E-02	rs1719625	3	191232285	q28
SNP_A-2252361	T	T	352	4	382	14	4.667	3.07E-02	rs16970979	13	107165278	q33.3
SNP_A-1990502	T	T	237	175	271	147	4.667	3.07E-02	rs1208853	7	88549325	q21.13
SNP_A-1994350	G	G	348	10	389	25	4.672	3.07E-02	rs12675232	8	97543577	q22.1
SNP_A-2034894	A	A	317	67	285	89	4.672	3.07E-02	rs7193003	16	77416061	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2038073	G	G	350	2	378	10	4.67	3.07E-02	rs17165747	5	106736932	q21.3
SNP_A-2060469	T	T	336	80	307	105	4.667	3.07E-02	rs3820513	1	208977952	q32.3
SNP_A-2103191	C	C	330	36	352	62	4.671	3.07E-02	rs17295554	3	187417295	q27.2
SNP_A-2094063	A	A	238	38	299	27	4.67	3.07E-02	rs17005132	4	82697821	q21.21
SNP_A-2187144	C	C	287	81	292	118	4.669	3.07E-02	rs934155	2	216727040	q35
SNP_A-2188432	G	G	315	91	341	67	4.671	3.07E-02	rs12513842	5	136091081	q31.1
SNP_A-2185239	G	G	254	160	281	129	4.669	3.07E-02	rs650527	10	100303553	q24.2
SNP_A-2122705	C	C	303	67	362	52	4.671	3.07E-02	rs1513708	4	122642740	q27
SNP_A-2112508	G	G	263	53	329	41	4.668	3.07E-02	rs11665329	18	44079394	q21.1
SNP_A-2144305	C	C	333	37	353	63	4.667	3.07E-02	rs6067689	20	49295016	q13.2
SNP_A-2143548	A	A	271	147	237	175	4.667	3.07E-02	rs12043071	1	192666069	q31.3
SNP_A-2149062	A	A	344	4	404	0	4.669	3.07E-02	rs7516532	1	112767015	p13.2
SNP_A-2146738	T	T	405	1	391	7	4.667	3.07E-02	rs7487434	12	128464544	q24.33
SNP_A-1751411	C	C	379	23	399	11	4.671	3.07E-02	rs963933	7	155149375	q36.3
SNP_A-1727637	C	C	348	44	344	68	4.671	3.07E-02	rs2382591	7	61488653	q11.21
SNP_A-1805620	A	A	341	5	374	16	4.671	3.07E-02	rs6828394	4	166695685	q32.3
SNP_A-1806148	A	A	402	16	412	6	4.668	3.07E-02	rs16826683	1	160934676	q23.3
SNP_A-1812538	T	T	281	87	289	127	4.668	3.07E-02	rs16970288	19	40578969	q13.12
SNP_A-1792509	G	G	349	13	377	29	4.67	3.07E-02	rs11889339	10	99451007	q24.2
SNP_A-1792893	G	A	235	175	202	200	4.671	3.07E-02	rs4371519	3	96659060	q11.2
SNP_A-1832946	A	A	300	68	311	103	4.672	3.07E-02	rs1371435	2	209788460	q34
SNP_A-1840543	G	G	312	20	385	11	4.668	3.07E-02	rs6431594	2	239017165	q37.3
SNP_A-1973760	T	T	280	50	308	84	4.671	3.07E-02	rs2046704	3	105835477	q13.11
SNP_A-1963656	T	T	350	2	378	10	4.67	3.07E-02	rs10469953	2	67936239	p14
SNP_A-1950794	G	G	318	46	372	32	4.668	3.07E-02	rs17249006	4	102841965	q24
SNP_A-1944600	C	C	391	31	369	49	4.668	3.07E-02	rs11956288	5	170027339	q35.1
SNP_A-1880414	T	T	326	38	349	65	4.667	3.07E-02	rs4290780	3	113817729	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1917320	T	T	341	79	364	56	4.669	3.07E-02	rs17118063	8	13843629	p22
SNP_A-1919989	C	C	229	133	288	120	4.67	3.07E-02	rs2117837	2	237702244	q37.3
SNP_A-1930271	G	G	318	78	306	108	4.672	3.07E-02	rs2126796	8	54642650	q11.23
SNP_A-1921045	T	T	289	39	286	62	4.666	3.08E-02	rs16960091	17	62137923	q24.2
SNP_A-1914745	G	G	384	26	365	43	4.666	3.08E-02	rs10811322	9	20144688	p21.3
SNP_A-1906041	G	G	342	12	378	28	4.664	3.08E-02	rs282224	3	167154208	q26.1
SNP_A-1907765	C	C	341	49	352	30	4.662	3.08E-02	rs9836081	3	13656391	p25.1
SNP_A-1878355	C	C	199	163	258	154	4.662	3.08E-02	rs4849472	2	116896120	q14.1
SNP_A-1885892	A	A	301	65	365	51	4.662	3.08E-02	rs11249024	1	24272401	p36.11
SNP_A-1898405	T	T	413	1	399	7	4.664	3.08E-02	rs4924633	15	40305429	q15.1
SNP_A-1945665	G	G	251	101	308	86	4.666	3.08E-02	rs2173824	3	158560631	q25.32
SNP_A-1937416	C	C	305	33	346	20	4.665	3.08E-02	rs6506871	18	74745754	q23
SNP_A-1959765	C	C	301	65	365	51	4.662	3.08E-02	rs11172824	12	57598427	q14.1
SNP_A-1961602	A	A	270	144	235	171	4.662	3.08E-02	rs11680726	2	909085	p25.3
SNP_A-1961883	T	T	356	6	396	18	4.664	3.08E-02	rs6548143	2	4781034	p25.2
SNP_A-1982018	T	T	343	33	340	54	4.664	3.08E-02	rs40019	5	67978437	q13.1
SNP_A-1829447	T	T	254	130	225	159	4.666	3.08E-02	rs4768011	12	40584334	q12
SNP_A-1817142	A	A	195	167	250	156	4.667	3.08E-02	rs12510585	4	145550344	q31.21
SNP_A-1851346	A	A	340	28	365	51	4.661	3.08E-02	rs1872296	4	143589262	q31.21
SNP_A-1849611	C	C	284	86	288	124	4.662	3.08E-02	rs4796010	17	30172860	q12
SNP_A-1794878	C	C	340	82	360	58	4.667	3.08E-02	rs1543362	1	14664391	p36.21
SNP_A-1796675	C	C	397	7	411	1	4.665	3.08E-02	rs16865086	2	6462865	p25.2
SNP_A-1789216	T	T	396	2	381	9	4.663	3.08E-02	rs7245237	18	32157734	q12.2
SNP_A-1789944	C	C	252	142	279	113	4.666	3.08E-02	rs202536	20	1614253	p13
SNP_A-1809513	G	G	321	97	292	124	4.666	3.08E-02	rs9659735	1	36435005	p34.3
SNP_A-1806447	T	T	230	140	289	127	4.664	3.08E-02	rs9649959	8	129041903	q24.21
SNP_A-1666052	G	A	211	173	208	186	4.662	3.08E-02	rs6657576	1	187286544	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1699073	G	G	257	143	233	177	4.665	3.08E-02	rs1171381	1	187594601	q31.1
SNP_A-2158345	T	T	347	13	375	29	4.663	3.08E-02	rs17222142	4	103446392	q24
SNP_A-2158495	C	T	203	159	209	195	4.665	3.08E-02	rs6717417	2	229735140	q36.3
SNP_A-2198562	T	T	334	26	349	47	4.667	3.08E-02	---	2	226560732	q36.3
SNP_A-2173356	G	G	250	104	307	89	4.661	3.08E-02	rs9371062	6	18594907	p22.3
SNP_A-2218103	G	G	344	12	335	25	4.665	3.08E-02	rs1957842	14	53520034	q22.2
SNP_A-2227190	A	A	259	111	318	96	4.665	3.08E-02	rs10821629	10	61414253	q21.2
SNP_A-2102472	C	G	195	157	212	192	4.666	3.08E-02	rs4732421	7	81380918	q21.11
SNP_A-2087488	A	A	367	55	381	35	4.664	3.08E-02	rs6500718	16	5751661	p13.3
SNP_A-2053366	A	A	340	82	360	58	4.667	3.08E-02	rs8085163	18	12799304	p11.21
SNP_A-2067451	A	A	379	9	394	2	4.664	3.08E-02	rs10737088	10	14701682	p13
SNP_A-2072372	C	C	319	45	382	32	4.663	3.08E-02	rs1919874	6	122215387	q22.31
SNP_A-2232084	T	T	258	112	293	89	4.665	3.08E-02	rs1937860	10	5042471	p15.1
SNP_A-2272046	T	T	259	121	233	151	4.662	3.08E-02	rs7384340	7	113191515	q31.1
SNP_A-2282048	T	T	214	132	268	118	4.662	3.08E-02	rs746881	1	10281076	p36.22
SNP_A-2284174	A	A	348	4	408	0	4.661	0.0309	rs2897274	12	85230233	q21.32
SNP_A-2276768	A	A	393	9	408	2	4.657	0.0309	rs10160659	11	6622270	p15.4
SNP_A-2275777	C	C	321	43	382	30	4.657	0.0309	rs1845712	4	161512730	q32.1
SNP_A-2236625	T	T	192	160	242	146	4.661	0.0309	rs558825	6	20154765	p22.3
SNP_A-2252282	T	T	355	19	338	34	4.657	0.0309	rs11237664	11	69567347	q13.3
SNP_A-2306613	C	C	320	102	344	76	4.66	0.0309	rs12672696	7	153522400	q36.2
SNP_A-2294251	G	G	247	53	293	95	4.658	0.0309	rs10962289	9	16123597	p22.3
SNP_A-2106834	G	G	381	7	382	18	4.66	0.0309	rs3003146	20	62340180	q13.33
SNP_A-2104205	G	G	381	3	373	11	4.656	0.0309	rs4913419	12	66881043	q15
SNP_A-2038304	G	C	218	190	225	191	4.657	0.0309	rs2800788	1	161310310	q23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044357	C	A	214	208	236	180	4.657	0.0309	rs1934045	1	89819820	p22.2
SNP_A-2041044	G	G	276	110	248	138	4.657	0.0309	rs1975980	17	22419818	q11.1
SNP_A-2024142	A	A	348	4	408	0	4.661	0.0309	rs4458799	7	103472176	q22.2
SNP_A-2010064	T	T	242	116	309	105	4.657	0.0309	rs3796891	4	111767529	q25
SNP_A-2009582	C	C	294	64	292	94	4.656	0.0309	rs2969173	4	13870825	p15.33
SNP_A-2224837	G	G	319	39	350	24	4.66	0.0309	rs10044936	5	140633442	q31.3
SNP_A-2217213	T	C	178	170	216	164	4.657	0.0309	rs4442368	1	186741410	q31.1
SNP_A-2205954	C	C	206	150	262	138	4.656	0.0309	rs3098681	5	78187948	q14.1
SNP_A-2175313	C	C	193	151	253	143	4.658	0.0309	rs2876175	20	9820828	p12.2
SNP_A-2163134	T	T	207	137	250	118	4.658	0.0309	rs2065999	14	53726301	q22.2
SNP_A-2138797	G	G	324	32	395	21	4.659	0.0309	rs8054959	16	87808594	q24.3
SNP_A-2137720	A	A	287	53	265	75	4.658	0.0309	rs17090498	13	62507470	q21.31
SNP_A-1746434	C	A	209	191	229	185	4.661	0.0309	rs2030487	2	159290939	q24.1
SNP_A-1756044	G	G	241	159	214	192	4.66	0.0309	rs2260801	10	122424478	q26.12
SNP_A-1794114	A	A	211	149	199	193	4.659	0.0309	rs6840795	4	141104945	q31.1
SNP_A-1792313	A	A	292	64	310	100	4.657	0.0309	rs1994526	4	169759747	q32.3
SNP_A-1865807	C	C	341	25	394	14	4.659	0.0309	rs6944026	7	19178534	p21.1
SNP_A-1863448	G	G	320	42	345	71	4.657	0.0309	rs485056	1	226212121	q42.13
SNP_A-1868209	C	C	244	178	272	146	4.661	0.0309	rs11222958	11	131533007	q25
SNP_A-1822538	A	A	367	3	396	12	4.657	0.0309	rs8048373	16	27668057	p11.2
SNP_A-1828174	G	A	196	158	209	189	4.656	0.0309	rs6836932	4	57369371	q12
SNP_A-1840677	G	G	297	47	358	34	4.657	0.0309	rs4957150	5	41251802	p13.1
SNP_A-1958675	C	C	270	56	271	85	4.656	0.0309	rs330590	2	150794084	q23.3
SNP_A-1943582	T	T	365	1	408	8	4.659	0.0309	rs7012607	8	14559616	p22
SNP_A-1898990	A	A	333	81	310	108	4.661	0.0309	rs4631807	10	72636128	q22.1
SNP_A-1901495	G	G	349	17	408	8	4.661	0.0309	rs17011416	2	75656047	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897061	G	G	342	20	392	10	4.658	0.0309	rs17259747	6	1227532	p25.3
SNP_A-1895432	C	C	336	60	311	83	4.66	0.0309	rs6456125	6	167164429	q27
SNP_A-1910039	A	A	397	11	396	24	4.657	0.0309	rs11055183	12	13025639	p13.1
SNP_A-1924925	G	G	351	19	378	38	4.657	0.0309	rs648472	12	9982427	p13.31
SNP_A-1922601	A	A	334	62	296	82	4.654	0.031	rs11621139	14	51385352	q22.1
SNP_A-1909420	G	G	373	25	382	12	4.655	0.031	rs6559804	9	84294602	q21.33
SNP_A-1893312	T	T	246	136	211	161	4.653	0.031	rs10466817	12	9502064	p13.31
SNP_A-1941095	T	T	288	122	255	149	4.652	0.031	rs7259200	19	8449921	p13.2
SNP_A-1985037	C	C	210	156	270	146	4.653	0.031	rs10495129	1	215570863	q41
SNP_A-1969593	C	C	338	28	363	51	4.652	0.031	rs17770156	21	25189176	q21.2
SNP_A-1971492	A	A	272	92	265	127	4.654	0.031	rs2322977	3	5343801	p26.1
SNP_A-1833857	C	C	274	94	275	133	4.653	0.031	rs4357093	6	68924471	q12
SNP_A-1827198	T	T	267	75	270	110	4.651	0.031	rs2626018	3	124774156	q21.1
SNP_A-1824931	G	G	281	75	296	114	4.654	0.031	rs9783305	11	97966670	q22.1
SNP_A-1822074	G	G	384	24	371	41	4.651	0.031	rs7848406	9	32899259	p21.1
SNP_A-1867083	G	G	346	8	410	2	4.653	0.031	---	8	61809509	q12.2
SNP_A-1870349	C	C	399	5	378	14	4.651	0.031	rs6057648	20	30848541	q11.21
SNP_A-1782212	A	A	352	4	412	0	4.653	0.031	rs181916	5	53522418	q11.2
SNP_A-1741335	C	C	239	163	275	137	4.653	0.031	rs838824	9	107050545	q31.3
SNP_A-2136552	A	A	352	4	412	0	4.653	0.031	rs8044269	16	70191106	q22.2
SNP_A-2135611	C	C	226	178	261	151	4.653	0.031	rs2101582	6	26730713	p22.1
SNP_A-2112346	T	T	297	63	340	46	4.654	0.031	rs7762295	6	165104731	q27
SNP_A-2110777	C	C	183	119	215	97	4.652	0.031	rs10455163	6	89168129	q15
SNP_A-2139082	C	C	302	32	344	60	4.655	0.031	rs16938588	8	74259268	q21.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2143796	C	C	332	6	407	1	4.656	0.031	rs16909730	11	22568011	p14.3
SNP_A-2146822	A	A	323	19	317	35	4.654	0.031	rs1323570	13	75288340	q22.2
SNP_A-2151714	A	A	329	67	311	93	4.652	0.031	rs6559181	8	710491	p23.3
SNP_A-2166432	G	G	303	117	274	146	4.655	0.031	rs10468948	18	36501488	q12.3
SNP_A-2179263	T	T	319	17	332	34	4.653	0.031	rs17745313	18	58700029	q21.33
SNP_A-2194634	G	G	278	86	342	72	4.653	0.031	rs11708509	3	99558233	q12.1
SNP_A-2186943	G	G	298	74	315	51	4.655	0.031	rs687192	22	19301826	q11.21
SNP_A-2218662	C	C	280	124	256	156	4.654	0.031	rs6449314	4	17264706	p15.32
SNP_A-2041773	C	C	256	142	238	180	4.653	0.031	rs9783760	16	64946286	q22.1
SNP_A-2045661	C	C	202	194	222	156	4.653	0.031	rs1269639	7	107480340	q31.1
SNP_A-2096268	A	G	204	150	198	196	4.655	0.031	rs7406464	17	78484749	q25.3
SNP_A-2087872	G	G	361	1	404	8	4.651	0.031	rs1317115	8	139877413	q24.23
SNP_A-2073436	G	G	288	14	304	30	4.652	0.031	rs17132253	5	110023072	q22.1
SNP_A-2291513	A	A	246	142	288	120	4.651	0.031	rs10877047	12	56661856	q14.1
SNP_A-2275199	A	A	232	138	287	123	4.652	0.031	rs9393424	6	23740092	p22.3
SNP_A-2285759	C	C	193	175	250	166	4.65	0.031	rs6497537	16	21062418	p12.3
SNP_A-2267758	C	C	319	39	374	26	4.652	0.031	rs3810624	22	42965953	q13.31
SNP_A-2285903	G	G	304	58	316	90	4.646	3.11E-02	rs10924249	1	242096683	q44
SNP_A-2278256	C	C	356	4	416	0	4.646	3.11E-02	rs11026484	11	22246432	p14.3
SNP_A-2243356	G	G	354	4	414	0	4.65	3.11E-02	rs445633	1	238689763	q43
SNP_A-2235294	A	A	309	53	376	40	4.645	3.11E-02	rs881423	10	33467029	p11.22
SNP_A-2229242	C	C	241	155	222	194	4.648	3.11E-02	rs6996939	8	66062056	q12.3
SNP_A-2289905	C	C	381	35	360	54	4.647	3.11E-02	rs2239994	15	89609732	q26.1
SNP_A-2296429	G	G	362	0	387	5	4.648	3.11E-02	rs3024681	16	27282701	p12.1
SNP_A-2086811	A	A	195	175	251	165	4.649	3.11E-02	rs10280519	7	118403717	q31.31
SNP_A-2091122	T	T	340	58	325	83	4.648	3.11E-02	rs4803261	19	44755065	q13.2
SNP_A-2080701	C	C	277	91	280	130	4.645	3.11E-02	rs2911958	8	68849480	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2094760	C	C	256	130	244	170	4.647	3.11E-02	rs11174126	12	60344144	q14.1
SNP_A-2101521	G	G	343	51	358	32	4.65	3.11E-02	rs4077553	1	119842436	p12
SNP_A-2033912	C	C	320	84	276	104	4.646	3.11E-02	rs2602824	11	68511689	q13.3
SNP_A-2031893	G	G	356	4	416	0	4.646	3.11E-02	rs17010063	3	72776695	p13
SNP_A-2029647	A	A	288	76	332	58	4.649	3.11E-02	rs3737136	1	112772474	p13.2
SNP_A-2221906	T	T	334	32	354	56	4.647	3.11E-02	rs17814373	12	69271349	q15
SNP_A-2202730	T	T	417	3	409	11	4.649	3.11E-02	rs16924617	9	10527033	q31.1
SNP_A-2172734	T	T	347	11	378	26	4.647	3.11E-02	rs3807153	7	137875046	q34
SNP_A-2149416	A	A	276	84	335	69	4.649	3.11E-02	rs9829295	3	160960700	q25.33
SNP_A-2148331	A	A	246	90	258	134	4.648	3.11E-02	rs7630226	3	121390818	q13.33
SNP_A-2109409	G	G	247	165	282	138	4.645	3.11E-02	rs6602773	10	15047847	p13
SNP_A-2129286	A	A	356	4	416	0	4.646	3.11E-02	rs658709	20	3535400	p13
SNP_A-1718207	A	A	220	130	288	122	4.648	3.11E-02	rs925730	3	80491736	p12.2
SNP_A-1676794	G	G	313	37	343	65	4.647	3.11E-02	rs10513949	18	64222744	q22.1
SNP_A-1672526	T	T	280	50	348	38	4.648	3.11E-02	rs724417	12	31264161	p11.21
SNP_A-1645596	A	A	293	51	356	38	4.648	3.11E-02	rs2672662	2	181128504	q31.3
SNP_A-1795134	C	C	365	39	345	59	4.645	3.11E-02	rs12722527	10	6117334	p15.1
SNP_A-1816171	C	C	356	4	416	0	4.646	3.11E-02	rs11225508	11	96602243	q22.1
SNP_A-1830252	T	T	341	67	364	46	4.648	3.11E-02	rs13420750	2	156581099	q24.1
SNP_A-1962554	G	G	251	165	218	194	4.645	3.11E-02	rs12712311	2	31227206	p23.1
SNP_A-1980202	A	A	225	135	218	180	4.646	3.11E-02	rs907364	4	184654017	q35.1
SNP_A-1945385	G	G	261	109	320	94	4.645	3.11E-02	rs2667648	16	77138639	q23.1
SNP_A-1954817	T	T	354	4	414	0	4.65	3.11E-02	rs80872 79	18	33559406	q12.2
SNP_A-1951286	T	T	301	111	332	86	4.648	3.11E-02	rs687734	6	20146953	p22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893898	C	C	342	26	399	15	4.646	3.11E-02	rs12374312	4	72309145	q13.3
SNP_A-1903901	T	T	313	47	333	77	4.65	3.11E-02	rs1821443	12	81902432	q21.31
SNP_A-1902323	G	G	279	85	343	71	4.647	3.11E-02	rs2048647	18	35679521	q12.3
SNP_A-1900159	A	A	290	68	310	106	4.645	3.11E-02	rs6719292	2	204943551	q33.3
SNP_A-1898061	T	T	362	0	387	5	4.648	3.11E-02	rs6655960	1	101905378	p21.2
SNP_A-1882831	A	A	365	15	353	29	4.65	3.11E-02	rs16890992	5	62065583	q12.1
SNP_A-1908395	T	T	237	133	295	119	4.646	3.11E-02	rs10033637	4	125190912	q28.1
SNP_A-1923794	G	G	324	80	347	57	4.65	3.11E-02	rs8086329	18	29871047	q12.1
SNP_A-1930921	T	T	232	190	256	156	4.645	3.12E-02	rs6950288	7	140427443	q34
SNP_A-1904737	T	T	395	1	383	7	4.64	3.12E-02	rs2958780	8	30237813	p12
SNP_A-1915581	A	A	231	187	258	154	4.641	3.12E-02	rs13032664	2	33904128	p22.3
SNP_A-1899606	G	G	286	58	351	45	4.642	3.12E-02	rs5752412	22	25499550	q12.1
SNP_A-1936518	T	T	254	72	297	55	4.641	3.12E-02	rs9390815	6	102799962	q16.3
SNP_A-1984711	G	G	342	80	313	105	4.643	3.12E-02	rs3088050	5	176659241	q35.3
SNP_A-1835851	G	C	190	168	218	180	4.644	3.12E-02	rs9959300	18	22390915	q11.2
SNP_A-1856103	G	G	289	29	287	49	4.643	3.12E-02	rs1523588	18	28590715	q12.1
SNP_A-1670756	C	C	356	40	341	61	4.644	3.12E-02	rs190749	10	60000122	q21.1
SNP_A-1730595	T	C	208	194	231	183	4.644	3.12E-02	rs4275717	12	104948319	q23.3
SNP_A-2126994	T	T	322	46	376	32	4.641	3.12E-02	rs3901955	1	96385933	p21.3
SNP_A-2126132	C	T	223	191	222	192	4.643	3.12E-02	rs1024718	7	156726215	q36.3
SNP_A-2123837	C	G	208	160	205	195	4.642	3.12E-02	rs7628221	3	21711307	p24.3
SNP_A-2121435	C	C	336	14	400	6	4.643	3.12E-02	rs10981929	9	113632697	q32
SNP_A-2184131	G	G	268	130	240	160	4.642	3.12E-02	rs10244830	7	157481341	q36.3
SNP_A-2188418	C	C	231	139	290	126	4.643	3.12E-02	rs1330425	13	75649766	q22.2
SNP_A-2200176	T	T	290	106	254	130	4.64	3.12E-02	rs12916973	15	75595154	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2208623	A	A	215	153	209	203	4.64	3.12E-02	rs1372116	2	129687515	q21.1
SNP_A-2209817	C	C	304	36	364	24	4.645	3.12E-02	rs923697	1	101689619	p21.2
SNP_A-2021130	T	T	227	139	279	123	4.644	3.12E-02	rs7977987	12	63993841	q14.3
SNP_A-2042714	G	G	363	29	375	15	4.645	3.12E-02	rs1531815	6	2476099	p25.2
SNP_A-2080205	G	A	209	161	213	203	4.641	3.12E-02	rs12678797	8	10016329	p23.1
SNP_A-2087532	A	A	280	84	344	70	4.643	3.12E-02	rs10005303	4	90473983	q22.1
SNP_A-2060867	C	C	309	107	278	134	4.643	3.12E-02	rs7976110	12	122774698	q24.31
SNP_A-2057912	T	T	302	98	335	75	4.645	3.12E-02	rs9635816	18	5709511	p11.31
SNP_A-2230964	T	T	220	148	273	133	4.644	3.12E-02	rs9523177	13	90351314	q31.3
SNP_A-2283415	G	G	345	25	398	14	4.641	3.12E-02	rs17807056	4	56908873	q12
SNP_A-2274110	C	C	196	166	251	155	4.639	3.13E-02	rs1195064	15	60391666	q22.2
SNP_A-2264666	C	C	257	149	290	122	4.637	3.13E-02	rs4682810	3	46127505	p21.31
SNP_A-2263333	A	A	395	7	407	1	4.635	3.13E-02	rs1167461	2	36308627	p22.3
SNP_A-2234022	G	G	263	133	241	167	4.636	3.13E-02	rs16931576	8	66062218	q12.3
SNP_A-2298440	C	C	300	34	369	23	4.635	3.13E-02	rs310751	3	12248621	p25.2
SNP_A-2309804	T	T	312	44	362	30	4.636	3.13E-02	rs707974	6	31737478	p21.33
SNP_A-2072102	A	A	321	49	334	78	4.638	3.13E-02	rs4849482	2	116942210	q14.1
SNP_A-2081875	C	C	350	4	408	0	4.634	3.13E-02	rs12290768	11	83049339	q14.1
SNP_A-2033612	A	A	283	79	342	64	4.637	3.13E-02	rs9383934	6	152013451	q25.1
SNP_A-2021266	A	A	333	35	352	60	4.639	3.13E-02	rs12233216	2	104645975	q12.1
SNP_A-2012729	A	A	308	110	328	82	4.635	3.13E-02	rs4480567	11	83018663	q14.1
SNP_A-2004974	T	T	352	0	377	5	4.639	3.13E-02	rs11192880	10	108187260	q25.1
SNP_A-2221378	C	C	304	34	275	51	4.637	3.13E-02	rs16857583	2	11622101	p25.1
SNP_A-2220120	A	A	287	129	260	160	4.639	3.13E-02	rs11102404	1	112433957	p13.2
SNP_A-2122094	A	A	248	62	329	53	4.634	3.13E-02	rs1525645	7	45371709	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2117801	A	G	200	152	145	135	4.635	3.13E-02	rs10871017	13	67737117	q21.33
SNP_A-2125390	G	G	350	4	408	0	4.634	3.13E-02	rs765699	10	27775149	p12.1
SNP_A-2145605	C	C	381	29	393	15	4.636	3.13E-02	rs10131615	14	44591333	q21.2
SNP_A-1736209	A	A	271	131	306	106	4.638	3.13E-02	rs1822285	11	4196936	p15.4
SNP_A-1798213	T	T	340	8	402	2	4.636	3.13E-02	---	9	93185417	q22.31
SNP_A-1789973	T	T	292	120	313	91	4.637	3.13E-02	rs11109393	12	97111754	q23.1
SNP_A-1861508	G	G	283	79	342	64	4.637	3.13E-02	rs7339052	13	112273409	q34
SNP_A-1816998	T	T	397	15	385	29	4.634	3.13E-02	rs4778277	15	21864175	q11.2
SNP_A-1978812	T	T	324	12	330	26	4.639	3.13E-02	rs983597	4	125899519	q28.1
SNP_A-1978204	C	C	246	106	251	151	4.634	3.13E-02	rs664817	1	190825903	q31.3
SNP_A-1936207	A	A	340	8	402	2	4.636	3.13E-02	rs12719734	15	98931385	q26.3
SNP_A-1952032	G	G	214	154	273	143	4.634	3.13E-02	rs4714080	6	37652596	p21.2
SNP_A-1950175	G	G	335	7	357	19	4.638	3.13E-02	rs9547577	13	35894540	q13.3
SNP_A-1905860	G	G	259	61	308	46	4.634	3.13E-02	rs4143210	12	24938093	p12.1
SNP_A-1923458	T	C	233	181	208	198	4.639	3.13E-02	rs12299509	12	4276542	p13.32
SNP_A-1931818	T	T	307	59	322	92	4.633	3.14E-02	rs7498575	16	61681324	q21
SNP_A-1909425	C	C	257	113	256	156	4.633	3.14E-02	rs590974	18	64644387	q22.1
SNP_A-1882329	G	G	334	12	370	28	4.629	3.14E-02	rs16946582	17	12613363	p12
SNP_A-1956804	T	T	343	17	400	8	4.631	3.14E-02	rs7356451	4	147447816	q31.22
SNP_A-1943042	C	C	377	31	399	17	4.63	3.14E-02	rs17578360	11	58427129	q12.1
SNP_A-1978559	G	G	305	53	328	86	4.632	3.14E-02	rs10488905	4	114466787	q26
SNP_A-1976948	C	C	373	39	353	59	4.633	3.14E-02	rs12644472	4	42650018	p13
SNP_A-1987256	T	T	259	77	309	61	4.63	3.14E-02	rs12212827	6	113009255	q21
SNP_A-1828917	G	G	181	157	217	135	4.632	3.14E-02	rs10739208	9	9975322	p23
SNP_A-1842191	G	G	327	7	328	18	4.631	3.14E-02	rs6849489	4	143831799	q31.21
SNP_A-1862757	T	T	393	29	405	15	4.63	3.14E-02	rs12335848	9	128107517	q34.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798431	A	A	352	4	410	0	4.631	3.14E-02	rs7069743	10	107882504	q25.1
SNP_A-1809849	C	C	262	156	286	124	4.631	3.14E-02	rs2387092	10	6000215	p15.1
SNP_A-1748325	T	T	188	178	241	167	4.633	3.14E-02	rs952851	12	84979809	q21.31
SNP_A-2150701	A	A	366	0	393	5	4.628	3.14E-02	rs10507740	13	66365143	q21.32
SNP_A-2152403	T	T	309	113	334	86	4.631	3.14E-02	rs6805459	3	116483639	q13.31
SNP_A-2162801	C	C	261	109	262	152	4.631	3.14E-02	rs940182	3	120895788	q13.33
SNP_A-2125358	C	C	281	83	277	117	4.629	3.14E-02	rs1490875	4	19084841	p15.31
SNP_A-2122790	A	A	366	0	393	5	4.628	3.14E-02	rs16933906	9	15990812	p22.3
SNP_A-2114246	A	A	367	51	382	32	4.631	3.14E-02	rs13029887	2	237540706	q37.3
SNP_A-2199943	C	C	357	13	387	29	4.629	3.14E-02	rs7155220	14	87793806	q31.3
SNP_A-2202378	A	A	307	59	322	92	4.633	3.14E-02	rs1732291	12	51059373	q13.13
SNP_A-2205001	A	A	317	31	384	20	4.632	3.14E-02	---	7	48399176	p12.3
SNP_A-2174651	G	G	403	7	415	1	4.633	3.14E-02	rs2423186	20	7231182	p12.3
SNP_A-2016474	A	A	413	1	401	7	4.633	3.14E-02	rs928848	21	23168499	q21.2
SNP_A-2005527	C	C	211	207	242	176	4.631	3.14E-02	rs1539814	18	22364136	q11.2
SNP_A-2029928	G	T	169	161	215	163	4.631	3.14E-02	rs7605300	2	154367973	q23.3
SNP_A-2097428	C	C	337	31	391	19	4.632	3.14E-02	rs556820	3	102514225	q12.3
SNP_A-2063148	C	C	229	133	292	122	4.629	3.14E-02	rs2221541	12	56688732	q14.1
SNP_A-2060204	A	A	199	145	243	127	4.631	3.14E-02	rs200157	1	226924806	q42.13
SNP_A-2054418	T	T	310	44	380	32	4.631	3.14E-02	rs7456122	7	136729876	q33
SNP_A-2313971	A	A	253	113	257	159	4.633	3.14E-02	rs7903856	10	80365179	q22.3
SNP_A-2303369	G	G	317	83	352	62	4.633	3.14E-02	rs1696447	12	129006189	q24.33
SNP_A-2233830	G	G	405	7	417	1	4.632	3.14E-02	rs2996368	9	38512055	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2250924	C	C	348	2	378	10	4.629	3.14E-02	rs17069694	13	77853934	q22.3
SNP_A-2283750	T	T	366	0	393	5	4.628	3.14E-02	rs1481433	6	114066198	q21
SNP_A-2256384	A	A	328	14	390	6	4.627	0.0315	rs7139240	12	23540051	p12.1
SNP_A-2257393	T	C	230	186	218	200	4.623	0.0315	rs2296241	20	52219626	q13.2
SNP_A-2246465	T	T	281	31	299	55	4.626	0.0315	rs16962290	16	13555240	p13.12
SNP_A-2241129	G	G	202	166	255	153	4.627	0.0315	rs4546702	8	66283606	q13.1
SNP_A-2237925	C	C	374	8	342	18	4.628	0.0315	rs5753516	22	29945927	q12.2
SNP_A-2239219	G	G	308	54	375	41	4.626	0.0315	rs3900881	17	52172499	q23.2
SNP_A-2304779	T	T	343	13	393	5	4.627	0.0315	rs987060	5	97032060	q15
SNP_A-2314874	C	G	207	193	218	172	4.627	0.0315	rs4482037	11	128757809	q24.3
SNP_A-2299178	A	A	362	0	389	5	4.624	0.0315	rs11139459	9	81752056	q21.32
SNP_A-2301042	G	G	262	126	295	101	4.627	0.0315	rs10863308	1	213778542	q41
SNP_A-2297098	A	A	321	47	317	27	4.627	0.0315	rs10752975	1	183506448	q31.1
SNP_A-2294275	C	C	316	74	288	98	4.626	0.0315	rs2602948	1	77469445	p31.1
SNP_A-2061144	C	C	206	162	263	151	4.624	0.0315	rs3763619	9	70455356	q21.11
SNP_A-2055050	C	C	216	154	211	205	4.627	0.0315	rs6436831	2	229739695	q36.3
SNP_A-2097655	C	C	371	51	386	32	4.628	0.0315	rs1019382	10	113714187	q25.2
SNP_A-2040043	A	A	202	166	255	153	4.627	0.0315	rs1860630	4	23705674	p15.2
SNP_A-2011401	C	C	274	134	221	149	4.625	0.0315	rs6556583	5	161600915	q34
SNP_A-1989710	C	C	225	127	292	118	4.625	0.0315	rs29694	7	41612551	p14.1
SNP_A-2185302	T	T	302	108	267	133	4.624	0.0315	rs2965977	16	62179837	q21
SNP_A-2193722	G	G	385	9	398	2	4.625	0.0315	rs17008183	2	123073937	q14.3
SNP_A-2193592	C	C	261	87	277	131	4.624	0.0315	rs11245120	10	128414314	q26.2
SNP_A-2220132	A	A	370	52	387	33	4.624	0.0315	rs3103268	2	232810474	q37.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225005	T	T	210	138	209	189	4.626	0.0315	rs6437242	2	241793050	q37.3
SNP_A-2129635	C	C	330	18	361	37	4.624	0.0315	rs6552374	4	180879473	q34.3
SNP_A-2137085	A	A	198	126	206	182	4.625	0.0315	rs2709800	7	30286011	p15.1
SNP_A-2133284	A	A	346	2	376	10	4.625	0.0315	rs11212898	11	108431690	q22.3
SNP_A-2165261	C	T	222	198	226	188	4.626	0.0315	rs2512284	11	123591632	q24.1
SNP_A-2139504	A	A	345	17	402	8	4.623	0.0315	rs16969507	15	76192672	q25.1
SNP_A-1686860	G	G	284	62	356	50	4.628	0.0315	rs2202560	13	69342939	q21.33
SNP_A-1810466	T	T	290	66	306	102	4.626	0.0315	rs13001540	2	200762755	q33.1
SNP_A-1791588	G	G	235	185	257	149	4.628	0.0315	rs12910386	15	76259699	q25.1
SNP_A-1868958	T	T	209	161	265	149	4.626	0.0315	rs10077992	5	108056122	q21.3
SNP_A-1838582	A	A	228	140	280	124	4.624	0.0315	rs4583941	6	77191820	q14.1
SNP_A-1825464	A	A	259	49	260	76	4.625	0.0315	---	6	57159888	p12.1
SNP_A-1818485	C	C	285	81	293	119	4.627	0.0315	rs6561923	13	56562382	q21.1
SNP_A-1819332	G	G	293	77	302	114	4.627	0.0315	rs7162038	15	92234158	q26.2
SNP_A-1959462	C	C	356	48	321	67	4.627	0.0315	rs12983584	19	17503864	p13.11
SNP_A-1952911	C	C	328	14	390	6	4.627	0.0315	rs10466991	12	93542173	q22
SNP_A-1874847	G	G	205	159	257	145	4.624	0.0315	rs9482835	6	128096441	q22.33
SNP_A-1897741	T	T	346	4	347	13	4.626	0.0315	rs2808666	1	156374389	q23.2
SNP_A-1917062	C	A	193	169	219	183	4.628	0.0315	rs1415767	6	125101908	q22.31
SNP_A-1912894	T	T	383	31	354	48	4.624	0.0315	rs12418734	11	77058141	q13.5
SNP_A-1932153	G	G	268	40	346	30	4.623	0.0315	rs16961560	15	46835997	q21.1
SNP_A-1931102	C	C	315	79	300	108	4.62	3.16E-02	rs7388636	8	54683584	q11.23
SNP_A-1930850	A	A	307	93	283	121	4.62	3.16E-02	rs12520271	5	33651309	p13.3
SNP_A-1874105	C	C	396	22	406	10	4.62	3.16E-02	rs11250123	8	11130774	p23.1
SNP_A-1879723	G	G	243	117	291	99	4.622	3.16E-02	rs4849481	2	116941724	q14.1
SNP_A-1953640	A	A	404	2	391	9	4.623	3.16E-02	rs11079501	17	40705665	q21.31
SNP_A-1936099	C	C	387	33	400	18	4.622	3.16E-02	rs16896081	6	29919688	p22.1
SNP_A-1986591	A	A	196	174	252	164	4.62	3.16E-02	rs9294170	6	80870799	q14.1
SNP_A-1966116	C	C	353	17	381	35	4.623	3.16E-02	rs10497576	2	181949347	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1821167	G	G	414	2	401	9	4.619	3.16E-02	rs3107619	11	122271454	q24.1
SNP_A-1825933	A	A	286	38	280	60	4.62	3.16E-02	rs17454914	3	154244172	q25.2
SNP_A-1873888	T	T	264	158	231	187	4.619	3.16E-02	rs10978600	9	106547520	q31.2
SNP_A-1852144	G	A	197	169	221	189	4.619	3.16E-02	rs2726686	4	108856660	q25
SNP_A-1799613	C	C	389	33	402	18	4.621	3.16E-02	rs9867698	3	96350425	q11.2
SNP_A-1795655	T	T	360	0	387	5	4.623	3.16E-02	rs6596984	6	3497491	p25.2
SNP_A-1792850	A	A	295	75	303	111	4.62	3.16E-02	rs3731569	2	197826825	q33.1
SNP_A-1814010	A	A	365	39	307	53	4.618	3.16E-02	rs1591391	10	32990616	p11.22
SNP_A-1804068	G	G	335	25	363	47	4.618	3.16E-02	rs3783638	14	54418123	q22.2
SNP_A-1703053	T	T	280	70	352	58	4.619	3.16E-02	rs531111	6	109065176	q21
SNP_A-1782795	G	G	356	0	383	5	4.619	3.16E-02	rs2474772	20	25198163	p11.21
SNP_A-2141280	A	A	307	51	372	38	4.622	3.16E-02	rs4875370	8	4446460	p23.2
SNP_A-2144055	C	C	323	29	386	18	4.618	3.16E-02	rs3776739	5	53259509	q11.2
SNP_A-2148614	A	A	410	6	402	16	4.62	3.16E-02	rs270916	2	161432554	q24.2
SNP_A-2166441	G	G	358	4	416	0	4.62	3.16E-02	rs9558441	13	104439018	q33.2
SNP_A-2159947	A	A	361	59	381	39	4.621	3.16E-02	rs4667391	2	150556347	q23.3
SNP_A-2124035	A	G	229	191	215	191	4.621	3.16E-02	rs3127547	1	49134114	p33
SNP_A-2115062	C	C	284	86	291	125	4.617	3.16E-02	rs4811246	20	35929171	q11.23
SNP_A-2202296	C	C	332	4	386	0	4.621	3.16E-02	rs17091478	14	94388753	q32.13
SNP_A-2191737	A	A	239	117	242	164	4.619	3.16E-02	rs291260	9	10037170	p23
SNP_A-2193187	T	T	238	178	267	147	4.617	3.16E-02	rs7943322	11	131532819	q25
SNP_A-2183561	A	A	183	179	231	165	4.619	3.16E-02	rs7431408	3	77292893	p12.3
SNP_A-2003790	A	G	213	207	237	181	4.621	3.16E-02	rs6573466	14	62465413	q23.2
SNP_A-2003695	T	T	239	121	245	171	4.619	3.16E-02	rs4087541	10	90142120	q23.31
SNP_A-2016255	T	T	358	0	385	5	4.621	3.16E-02	rs8130364	21	21443245	q21.1
SNP_A-2016024	T	T	358	4	416	0	4.62	3.16E-02	rs9680445	21	19998366	q21.1
SNP_A-2042541	G	G	317	51	375	37	4.621	3.16E-02	rs2047894	4	147953589	q31.22
SNP_A-2041276	T	T	364	2	396	10	4.621	3.16E-02	rs7517554	1	157350032	q23.3
SNP_A-2030915	C	C	309	57	323	89	4.62	3.16E-02	rs6481109	10	56031482	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082594	A	A	360	0	387	5	4.623	3.16E-02	rs7105414	11	115215923	q23.3
SNP_A-2053503	G	G	296	120	267	149	4.62	3.16E-02	rs13095453	3	142557660	q23
SNP_A-2054046	A	A	219	195	252	166	4.623	3.16E-02	rs9908408	17	68372574	q24.3
SNP_A-2311829	T	T	358	4	416	0	4.62	3.16E-02	rs2251630	12	76599893	q21.2
SNP_A-2235490	G	G	300	58	312	90	4.622	3.16E-02	rs788160	2	172771822	q31.1
SNP_A-2229896	A	A	282	102	315	79	4.619	3.16E-02	rs9789512	2	129575392	q14.3
SNP_A-2244836	C	T	215	207	236	182	4.623	3.16E-02	rs6902214	15	51793355	q21.3
SNP_A-2259898	A	A	201	135	198	184	4.621	3.16E-02	rs4752223	10	120642218	q26.11
SNP_A-2055332	G	G	290	54	314	88	4.613	3.17E-02	rs3848110	15	53045063	q21.3
SNP_A-2071699	C	C	268	134	293	105	4.613	3.17E-02	rs486508	12	99821922	q23.1
SNP_A-2082010	T	T	312	44	382	32	4.613	3.17E-02	rs11930830	4	52816017	q11
SNP_A-2087544	C	C	364	16	348	30	4.615	3.17E-02	rs703682	12	93142840	q22
SNP_A-2099908	C	C	306	60	368	46	4.616	3.17E-02	rs17824827	14	64102031	q23.3
SNP_A-2023911	C	C	405	9	418	2	4.617	3.17E-02	rs873987	5	178535289	q35.3
SNP_A-2036736	C	C	289	77	295	113	4.617	3.17E-02	rs473287	11	58235881	q12.1
SNP_A-2036185	T	T	251	113	255	159	4.617	3.17E-02	rs11072440	15	31483405	q14
SNP_A-2001194	C	C	224	130	255	105	4.616	3.17E-02	rs2435875	10	57701356	q21.1
SNP_A-2224781	C	C	377	35	398	20	4.617	3.17E-02	rs4149244	8	27433079	p21.1
SNP_A-2219604	A	A	331	17	357	35	4.613	3.17E-02	rs13285858	9	2220334	p24.2
SNP_A-2114297	G	G	261	107	265	151	4.613	3.17E-02	rs7559302	2	205777109	q33.3
SNP_A-2121611	T	T	348	4	404	0	4.615	3.17E-02	rs16941060	12	109786582	q24.11
SNP_A-2115695	T	T	291	75	350	60	4.617	3.17E-02	rs10035923	5	165217561	q34
SNP_A-2164348	T	T	170	118	221	107	4.612	3.17E-02	rs5000509	13	80986874	q31.1
SNP_A-1657518	G	G	383	3	377	11	4.614	3.17E-02	rs10490900	10	29573281	p12.1
SNP_A-1809828	A	A	299	71	358	56	4.615	3.17E-02	rs6876913	5	154992079	q33.2
SNP_A-1797881	T	T	407	13	375	25	4.614	3.17E-02	rs10152810	15	70482294	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1846438	C	C	240	120	245	169	4.615	3.17E-02	rs3765475	6	161960927	q26
SNP_A-1860441	T	T	269	85	266	120	4.617	3.17E-02	rs12186330	4	157467019	q32.1
SNP_A-1838980	G	G	244	176	273	145	4.616	3.17E-02	rs7202693	16	57931708	q21
SNP_A-1967009	T	T	375	27	396	14	4.616	3.17E-02	rs17398519	2	221569940	q36.1
SNP_A-1971731	T	T	418	2	405	9	4.617	3.17E-02	rs7645643	3	10220198	p25.3
SNP_A-1973234	C	C	349	49	324	70	4.614	3.17E-02	rs17009353	3	72183368	p13
SNP_A-1983784	G	G	330	78	306	104	4.615	3.17E-02	rs17287641	5	142524348	q31.3
SNP_A-1978650	C	C	312	44	382	32	4.613	3.17E-02	rs11562874	4	119080848	q26
SNP_A-1982589	T	T	322	48	337	77	4.615	3.17E-02	rs42398	5	96146211	q15
SNP_A-1951118	T	T	383	5	364	14	4.617	3.17E-02	rs9860945	3	31015831	p24.1
SNP_A-1957009	A	A	313	45	374	32	4.614	3.17E-02	rs17828523	3	37581774	p22.3
SNP_A-1899191	C	C	382	40	391	23	4.616	3.17E-02	rs11539216	6	33025958	p21.32
SNP_A-1919667	A	A	242	128	241	175	4.616	3.17E-02	rs11850259	14	19715756	q11.2
SNP_A-1921100	G	G	352	4	408	0	4.608	3.18E-02	rs9403464	6	143569439	q24.2
SNP_A-1930531	A	A	236	174	271	147	4.61	3.18E-02	rs768172	7	95450354	q21.3
SNP_A-1928095	C	C	237	127	285	109	4.607	3.18E-02	rs2389137	13	93972032	q32.1
SNP_A-1916520	G	G	405	11	411	3	4.611	3.18E-02	rs10246667	7	119499288	q31.31
SNP_A-1911177	A	A	370	0	399	5	4.609	3.18E-02	rs16899741	5	81931487	q14.2
SNP_A-1898166	C	C	337	27	396	16	4.612	3.18E-02	rs2220292	12	128143785	q24.32
SNP_A-1903361	A	A	241	107	228	142	4.61	3.18E-02	rs9400836	6	115800405	q22.1
SNP_A-1884838	T	T	352	4	408	0	4.608	3.18E-02	---	16	84619254	q24.1
SNP_A-1957845	G	G	324	38	377	25	4.608	3.18E-02	rs10033219	5	59200750	q12.1
SNP_A-1944915	A	A	406	8	349	17	4.607	3.18E-02	rs878835	15	59811276	q22.2
SNP_A-1987245	A	A	276	144	292	110	4.61	3.18E-02	rs10916293	1	224738665	q42.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1963083	T	T	294	120	321	93	4.608	3.18E-02	rs195190	1	115449473	p13.1
SNP_A-1829395	A	A	353	5	390	16	4.607	3.18E-02	rs17013484	4	129852788	q28.2
SNP_A-1822344	C	C	336	32	392	20	4.61	3.18E-02	rs1398489	8	5636859	p23.2
SNP_A-1821345	G	G	349	21	405	11	4.608	3.18E-02	rs7585775	2	77489992	p12
SNP_A-1818348	G	G	371	39	358	60	4.61	3.18E-02	rs17153071	7	105651614	q22.3
SNP_A-1865235	G	G	350	4	406	0	4.612	3.18E-02	rs1546902	6	17592490	p22.3
SNP_A-1870404	A	A	385	23	345	37	4.608	3.18E-02	rs10782451	14	23554299	q11.2
SNP_A-1858796	G	G	350	4	406	0	4.612	3.18E-02	rs16955687	16	54290606	q12.2
SNP_A-1758893	G	G	261	139	299	115	4.607	3.18E-02	rs1030531	2	125132205	q14.3
SNP_A-2157841	C	C	365	47	347	69	4.608	3.18E-02	rs11123911	2	102220056	q11.2
SNP_A-2139736	G	G	228	138	284	124	4.608	3.18E-02	rs9559788	13	109846636	q34
SNP_A-2120894	G	G	183	179	240	172	4.61	3.18E-02	rs2627323	15	78808438	q25.1
SNP_A-2128583	T	T	227	119	221	161	4.611	3.18E-02	rs961328	2	67467097	p14
SNP_A-2131276	T	T	186	180	241	171	4.611	3.18E-02	rs6664119	1	67367916	p31.2
SNP_A-2219283	C	C	265	135	198	140	4.61	3.18E-02	rs541454	11	132578753	q25
SNP_A-2202969	A	A	349	21	405	11	4.608	3.18E-02	rs10863539	1	216800365	q41
SNP_A-2205351	G	G	349	21	405	11	4.608	3.18E-02	rs4142640	11	117109417	q23.3
SNP_A-2210038	A	A	350	4	406	0	4.612	3.18E-02	rs17023556	2	39418980	p22.1
SNP_A-2171457	G	G	352	4	408	0	4.608	3.18E-02	rs11128973	3	20831690	p24.3
SNP_A-2001011	C	C	337	27	396	16	4.612	3.18E-02	rs1277737	10	18614517	p12.32
SNP_A-2003922	A	A	266	94	267	133	4.61	3.18E-02	rs1075014	14	90600783	q32.12
SNP_A-2024610	C	C	352	4	408	0	4.608	3.18E-02	rs2739687	8	18029585	p22
SNP_A-2020694	G	G	399	7	352	16	4.609	3.18E-02	rs16978692	21	46182876	q22.3
SNP_A-2022249	C	C	310	106	275	131	4.61	3.18E-02	rs2186888	11	124472984	q24.2
SNP_A-2029373	G	G	272	66	247	89	4.611	3.18E-02	rs665973	1	60992803	p31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098376	A	A	203	167	256	154	4.607	3.18E-02	rs17481815	4	14088243	p15.33
SNP_A-2086376	A	A	350	2	339	9	4.607	3.18E-02	rs7248124	19	4218512	p13.3
SNP_A-2067935	G	G	372	38	354	58	4.608	3.18E-02	rs10108640	8	14957836	p22
SNP_A-2048490	A	A	341	81	312	106	4.611	3.18E-02	rs10114264	9	76298181	q21.13
SNP_A-2270181	T	T	301	115	271	143	4.607	3.18E-02	rs6448527	4	27300434	p15.2
SNP_A-2286701	A	A	232	108	294	96	4.611	3.18E-02	rs2043486	9	107952583	q31.2
SNP_A-2248164	G	G	233	135	232	184	4.607	3.18E-02	rs973110	2	75744845	p12
SNP_A-2250307	G	G	380	42	356	62	4.61	3.18E-02	rs6709842	2	240157640	q37.3
SNP_A-2253366	C	A	199	169	223	193	4.609	3.18E-02	rs10158279	1	65745717	p31.2
SNP_A-2231559	C	C	333	33	391	21	4.609	3.18E-02	rs2763049	6	2556705	p25.2
SNP_A-2235473	G	G	405	1	395	7	4.605	3.19E-02	rs12104985	2	148288800	q22.3
SNP_A-2244699	A	A	356	4	412	0	4.602	3.19E-02	rs17124990	14	88452623	q32.11
SNP_A-2285846	A	A	276	88	335	73	4.602	3.19E-02	rs7598396	2	73564283	p13.1
SNP_A-2273134	T	T	227	155	266	132	4.602	3.19E-02	rs797128	6	5276373	p25.1
SNP_A-2308081	G	G	331	87	306	114	4.603	3.19E-02	rs11036598	11	41820640	p12
SNP_A-2293245	G	G	307	61	320	94	4.605	3.19E-02	rs12101080	14	92632608	q32.13
SNP_A-2289928	T	T	280	84	339	69	4.601	3.19E-02	rs12191625	6	1215673	p25.3
SNP_A-2287969	G	G	322	94	292	120	4.605	3.19E-02	rs4974308	3	70749900	p13
SNP_A-2084948	C	C	232	176	247	137	4.606	3.19E-02	rs6986712	8	126397694	q24.13
SNP_A-2037038	A	A	234	124	237	173	4.604	3.19E-02	rs12892711	14	83156982	q31.2
SNP_A-2040747	T	T	354	4	410	0	4.605	3.19E-02	rs6795365	3	179256024	q26.32
SNP_A-2003253	G	G	399	7	409	1	4.604	3.19E-02	rs10490934	10	83861347	q23.1
SNP_A-1997262	A	A	409	1	399	7	4.604	3.19E-02	rs1004813	9	94820621	q22.32
SNP_A-2012389	G	G	222	146	216	194	4.605	3.19E-02	rs6460895	7	12025780	p21.3
SNP_A-2014080	G	G	376	42	391	25	4.602	3.19E-02	rs10501845	11	95586932	q21
SNP_A-2015863	A	A	216	148	215	201	4.605	3.19E-02	rs2212783	21	19036442	q21.1
SNP_A-2011450	T	T	354	4	410	0	4.605	3.19E-02	rs6871159	5	170249494	q35.1
SNP_A-2169698	T	T	357	51	330	72	4.602	3.19E-02	rs2288056	16	55076598	q12.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175170	A	A	252	110	315	97	4.606	3.19E-02	rs733936	4	11222848	p15.33
SNP_A-2186499	G	G	270	144	293	113	4.601	3.19E-02	rs1557191	14	51762335	q22.1
SNP_A-2188987	G	G	217	139	279	129	4.605	3.19E-02	rs6483468	11	95345679	q21
SNP_A-2218915	C	C	282	106	249	131	4.605	3.19E-02	rs12538423	7	102924162	q22.1
SNP_A-2215487	A	A	230	140	226	188	4.605	3.19E-02	rs6978581	7	116950844	q31.2
SNP_A-2129722	A	A	354	4	410	0	4.605	3.19E-02	rs16993677	20	46395764	q13.13
SNP_A-2115667	T	T	186	158	239	147	4.605	3.19E-02	rs2703025	3	54879807	p14.3
SNP_A-2113923	T	T	264	100	268	142	4.602	3.19E-02	rs7505953	18	36530073	q12.3
SNP_A-2115285	T	T	407	7	417	1	4.602	3.19E-02	rs3848860	22	24510745	q12.1
SNP_A-2146904	C	C	270	134	232	158	4.604	3.19E-02	rs2049418	1	34439847	p34.3
SNP_A-2165838	A	A	187	183	242	174	4.602	3.19E-02	rs7639345	3	154580659	q25.2
SNP_A-2164126	A	A	395	7	405	1	4.605	3.19E-02	rs2271993	15	75648426	q24.3
SNP_A-2161032	C	C	285	51	330	36	4.605	3.19E-02	rs12704812	7	94893353	q21.3
SNP_A-1788676	G	G	263	89	320	74	4.603	3.19E-02	rs11149616	16	82626126	q23.3
SNP_A-1859321	A	A	322	14	382	6	4.603	3.19E-02	rs16851687	2	214960033	q34
SNP_A-1849004	T	T	336	28	354	50	4.604	3.19E-02	rs684903	10	7438806	p14
SNP_A-1870270	C	C	415	1	405	7	4.603	3.19E-02	rs6757943	2	36461224	p22.3
SNP_A-1864663	T	T	306	64	363	49	4.605	3.19E-02	rs10912723	1	167989789	q24.3
SNP_A-1817958	G	G	389	29	364	46	4.606	3.19E-02	rs2578050	10	65423800	q21.3
SNP_A-1821361	A	A	286	80	350	66	4.605	3.19E-02	rs12541666	8	133398572	q24.22
SNP_A-1819388	C	C	214	104	275	93	4.604	3.19E-02	rs1634271	17	42542428	q21.32
SNP_A-1825339	G	G	272	120	255	155	4.601	3.19E-02	rs11251416	10	2689914	p15.3
SNP_A-1832847	T	T	369	15	359	5	4.606	3.19E-02	rs9327367	5	125151292	q23.2
SNP_A-1974987	A	A	356	4	412	0	4.602	3.19E-02	rs12487360	3	158201136	q25.31
SNP_A-1983864	T	T	275	89	334	74	4.603	3.19E-02	rs1416651	1	211848489	q41
SNP_A-1982394	A	A	249	121	248	166	4.603	3.19E-02	rs425542	5	84858536	q14.3
SNP_A-1946835	G	A	208	162	214	202	4.603	3.19E-02	rs9518907	13	87385138	q31.2
SNP_A-1933119	A	A	248	154	209	177	4.603	3.19E-02	rs10746451	1	203782119	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950906	C	C	202	154	260	144	4.604	3.19E-02	rs10420780	19	14592686	p13.12
SNP_A-1950895	A	A	245	141	225	177	4.604	3.19E-02	rs7047205	9	34961963	p13.3
SNP_A-1901143	G	G	405	7	415	1	4.603	3.19E-02	rs922650	10	44467053	q11.21
SNP_A-1928647	A	A	236	128	291	113	4.603	3.19E-02	rs612557	6	158865566	q25.3
SNP_A-1929352	T	T	353	11	386	26	4.603	3.19E-02	rs12288200	11	10167703	p15.4
SNP_A-1919903	C	C	219	151	277	139	4.602	3.19E-02	rs11172387	12	56618618	q14.1
SNP_A-1955434	A	A	358	0	387	5	4.597	3.20E-02	rs16925318	10	69756962	q21.3
SNP_A-1956529	C	C	360	0	389	5	4.599	3.20E-02	rs11825654	11	38631133	p12
SNP_A-1939802	T	T	266	104	325	89	4.601	3.20E-02	rs9567416	13	43806741	q14.11
SNP_A-1833058	C	C	322	36	384	24	4.601	3.20E-02	rs16847543	2	212719716	q34
SNP_A-1810794	A	A	206	132	266	122	4.599	3.20E-02	rs4425810	9	5212208	p24.1
SNP_A-1808093	A	A	229	141	226	190	4.597	3.20E-02	rs6561072	13	42173146	q14.11
SNP_A-2128368	G	G	339	27	398	16	4.601	3.20E-02	rs17011052	10	49092756	q11.22
SNP_A-2208032	G	G	325	11	390	4	4.597	3.20E-02	rs352014	4	75174635	q13.3
SNP_A-2180782	A	A	305	49	359	35	4.599	3.20E-02	rs10950616	7	16173062	p21.1
SNP_A-2013294	A	A	342	78	363	55	4.598	3.20E-02	rs7016551	8	24426768	p21.2
SNP_A-1991584	G	G	313	47	315	73	4.598	3.20E-02	rs1106719	1	243950754	q44
SNP_A-2037954	T	T	293	75	352	60	4.596	3.20E-02	rs991891	5	16609071	p15.1
SNP_A-2088758	C	C	233	133	230	180	4.597	3.20E-02	rs11690687	2	97920339	q11.2
SNP_A-2083130	G	G	310	32	362	20	4.597	3.20E-02	rs17331332	4	107165711	q24
SNP_A-2097179	A	A	337	3	366	12	4.598	3.20E-02	rs231751	2	204582227	q33.2
SNP_A-2103335	A	G	192	170	220	182	4.596	3.20E-02	rs12623151	2	229903037	q36.3
SNP_A-2292222	C	C	344	4	398	0	4.599	3.20E-02	rs16848440	3	165838403	q26.1
SNP_A-2312618	G	G	344	14	366	30	4.596	3.20E-02	rs1510050	18	66620776	q22.2
SNP_A-2311474	C	C	374	32	352	50	4.598	3.20E-02	rs17386174	15	75485622	q24.3
SNP_A-2280496	A	G	214	208	238	182	4.599	3.20E-02	rs10801757	1	89815101	p22.2
SNP_A-2243325	T	T	189	167	248	160	4.598	3.20E-02	rs545431	18	2162370	p11.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2237446	A	A	265	101	327	87	4.599	3.20E-02	rs6944993	7	152519346	q36.2
SNP_A-2239297	C	C	346	4	400	0	4.596	3.20E-02	rs4669340	2	8908074	p25.1
SNP_A-2285796	A	A	334	4	386	0	4.593	3.21E-02	rs16914125	8	51051444	q11.21
SNP_A-2267631	A	A	309	85	283	111	4.591	3.21E-02	rs1508855	5	10214876	p15.2
SNP_A-2262130	C	C	288	56	323	39	4.591	3.21E-02	rs16851520	3	169035414	q26.1
SNP_A-2308785	G	G	360	4	416	0	4.595	3.21E-02	rs16838879	1	192473247	q31.3
SNP_A-2289902	T	T	300	56	351	41	4.593	3.21E-02	rs11141641	9	86828773	q21.33
SNP_A-2057683	A	A	356	0	385	5	4.595	3.21E-02	rs1458492	9	73650688	q21.13
SNP_A-2065248	C	C	359	37	371	21	4.591	3.21E-02	rs1948570	15	84308721	q25.3
SNP_A-2073130	G	G	346	20	369	39	4.593	3.21E-02	rs10859609	12	92788058	q22
SNP_A-2030092	T	T	392	16	320	26	4.595	3.21E-02	rs1708108	3	39521362	p22.2
SNP_A-1992246	T	T	400	10	371	21	4.592	3.21E-02	rs10751868	10	2339357	p15.3
SNP_A-2016504	G	G	315	29	376	18	4.593	3.21E-02	rs2827828	21	23371766	q21.2
SNP_A-2018855	A	A	247	115	295	97	4.593	3.21E-02	rs8127992	21	36822288	q22.13
SNP_A-2186969	G	C	203	195	223	171	4.593	3.21E-02	rs7736055	5	141666833	q31.3
SNP_A-2195285	C	C	249	159	265	123	4.594	3.21E-02	rs3897584	11	112754935	q23.2
SNP_A-2196299	A	A	348	4	402	0	4.593	3.21E-02	rs17162712	1	196448789	q32.1
SNP_A-2202690	T	T	274	86	328	70	4.591	3.21E-02	rs4276230	3	31233590	p24.1
SNP_A-2215943	C	C	333	51	319	29	4.591	3.21E-02	rs160643	7	65002372	q11.21
SNP_A-2226778	A	A	256	102	245	137	4.593	3.21E-02	rs2945755	8	134756521	q24.22
SNP_A-2128526	A	A	247	119	250	166	4.591	3.21E-02	rs9321804	6	141578610	q24.1
SNP_A-1787419	C	C	362	48	380	30	4.591	3.21E-02	rs1675328	9	90701628	q22.2
SNP_A-1793723	G	G	239	179	263	145	4.595	3.21E-02	rs12075030	1	19159232	p36.13
SNP_A-1654605	G	G	366	26	340	42	4.594	3.21E-02	rs10500803	11	14613135	p15.2
SNP_A-1831012	G	G	348	22	372	42	4.595	3.21E-02	rs4783754	16	65916317	q22.1
SNP_A-1862469	T	T	255	77	295	59	4.591	3.21E-02	rs1626645	15	99062095	q26.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1851692	G	G	317	27	391	17	4.594	3.21E-02	rs12907715	15	66612521	q23
SNP_A-1855294	G	G	381	13	378	4	4.592	3.21E-02	rs3092120	20	45277983	q13.12
SNP_A-1961819	C	C	389	29	373	47	4.594	3.21E-02	rs10494124	1	111151586	p13.3
SNP_A-1961642	G	G	334	56	373	39	4.593	3.21E-02	rs2336219	19	50604246	q13.32
SNP_A-1986976	G	G	228	140	224	188	4.592	3.21E-02	rs1376499	6	98759316	q16.2
SNP_A-1969234	A	A	291	121	315	93	4.595	3.21E-02	rs386231	1	159057481	q23.3
SNP_A-1962204	G	G	243	125	304	112	4.594	3.21E-02	rs11674834	2	14459980	p24.3
SNP_A-1969118	G	G	202	148	255	135	4.595	3.21E-02	rs1375626	21	16725760	q21.1
SNP_A-1930165	T	T	303	65	315	99	4.592	3.21E-02	rs10849844	12	120014007	q24.31
SNP_A-1904853	C	C	360	4	416	0	4.595	3.21E-02	rs3916484	6	10966288	p24.2
SNP_A-1904162	G	G	312	40	336	68	4.593	3.21E-02	rs2995278	10	30583994	p11.23
SNP_A-1882065	T	T	325	37	389	25	4.595	3.21E-02	rs6427837	1	197372538	q32.1
SNP_A-1918350	G	G	252	118	312	104	4.589	3.22E-02	rs4411854	3	148529366	q24
SNP_A-1931836	C	C	243	149	289	129	4.586	3.22E-02	rs13163480	5	8619222	p15.31
SNP_A-1921103	A	A	262	134	284	104	4.587	3.22E-02	rs8031512	15	75934307	q24.3
SNP_A-1920569	G	G	342	16	376	34	4.59	3.22E-02	rs6440853	3	154419916	q25.2
SNP_A-1983597	C	C	337	33	395	21	4.586	3.22E-02	rs10494978	1	211014274	q41
SNP_A-1961112	A	A	252	118	312	104	4.589	3.22E-02	rs992072	17	65769803	q24.3
SNP_A-1957961	C	C	350	4	404	0	4.589	3.22E-02	rs6032295	20	43611553	q13.12
SNP_A-1949942	C	C	334	6	405	1	4.59	3.22E-02	rs9946267	18	10921941	p11.21
SNP_A-1942880	G	G	270	144	300	116	4.59	3.22E-02	rs6784028	3	134362410	q22.1
SNP_A-1824581	C	C	370	0	401	5	4.586	3.22E-02	rs2659633	12	56765419	q14.1
SNP_A-1823020	A	A	225	153	214	198	4.59	3.22E-02	rs7772820	6	144423362	q24.2
SNP_A-1818963	T	T	279	91	250	116	4.588	3.22E-02	rs4835943	5	127485468	q23.2
SNP_A-1820275	A	A	333	19	402	10	4.587	3.22E-02	rs11172742	12	57499753	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1821312	A	A	248	118	245	161	4.585	3.22E-02	rs9538651	13	59809523	q21.2
SNP_A-1693823	T	T	389	11	390	24	4.59	3.22E-02	rs10501226	11	40266315	p12
SNP_A-1783286	C	C	259	127	289	101	4.587	3.22E-02	rs12059907	1	240805958	q44
SNP_A-1783944	T	C	184	178	231	175	4.588	3.22E-02	rs12704648	7	92296990	q21.2
SNP_A-1796937	A	A	235	105	312	98	4.587	3.22E-02	rs509971	6	11675452	p24.2
SNP_A-2107928	T	T	350	4	404	0	4.589	3.22E-02	rs1290121	13	111656851	q34
SNP_A-2119625	G	G	326	42	385	29	4.586	3.22E-02	rs4869081	5	162765865	q34
SNP_A-2138547	T	T	350	4	404	0	4.589	3.22E-02	rs5998548	22	31317375	q12.3
SNP_A-2143723	A	A	352	4	406	0	4.586	3.22E-02	rs16882227	5	53434510	q11.2
SNP_A-2143378	A	A	327	93	300	120	4.585	3.22E-02	rs4849762	2	119634906	q14.2
SNP_A-2223307	C	C	271	79	285	119	4.589	3.22E-02	rs2895908	14	101009083	q32.31
SNP_A-2213985	G	G	344	8	404	2	4.589	3.22E-02	rs17134365	5	111694455	q22.2
SNP_A-2207572	T	T	226	134	275	117	4.59	3.22E-02	rs1391520	1	75886773	p31.1
SNP_A-2190014	T	T	376	30	392	16	4.589	3.22E-02	rs16892766	8	117699864	q23.3
SNP_A-2175814	C	C	366	22	361	39	4.59	3.22E-02	rs9348175	6	167081168	q27
SNP_A-2009483	A	A	334	6	405	1	4.59	3.22E-02	rs6437463	3	196403091	q29
SNP_A-1997264	G	G	417	3	370	10	4.588	3.22E-02	rs10512250	9	94842710	q22.32
SNP_A-1997996	C	C	227	139	222	186	4.587	3.22E-02	rs1966203	10	21097551	p12.31
SNP_A-2002854	T	T	216	172	260	152	4.586	3.22E-02	rs7314330	12	73381431	q21.1
SNP_A-2004004	C	C	395	9	406	2	4.586	3.22E-02	rs17107911	10	94541909	q23.33
SNP_A-2029205	C	C	219	141	207	183	4.59	3.22E-02	rs7912767	10	20339314	p12.31
SNP_A-2031593	T	A	184	172	219	171	4.586	3.22E-02	rs1778797	13	27350129	q12.2
SNP_A-2025958	G	G	341	27	400	16	4.59	3.22E-02	rs1663595	4	167575622	q32.3
SNP_A-2040217	G	G	261	95	329	83	4.587	3.22E-02	rs17270952	2	189830349	q32.2
SNP_A-2064996	A	A	344	8	404	2	4.589	3.22E-02	rs11249034	1	24285534	p36.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2080000	C	C	262	100	266	142	4.588	3.22E-02	rs16875715	8	108195366	q23.1
SNP_A-2266250	C	C	350	4	404	0	4.589	3.22E-02	rs16829259	2	233245926	q37.1
SNP_A-2272040	A	A	383	9	394	2	4.59	3.22E-02	rs17098460	10	120870651	q26.11
SNP_A-2239906	C	C	362	8	395	21	4.59	3.22E-02	rs6487254	12	22002520	p12.1
SNP_A-2228876	G	G	195	173	252	164	4.587	3.22E-02	rs2612558	18	41300541	q12.3
SNP_A-2247557	G	G	362	8	395	21	4.59	3.22E-02	rs12248190	10	22783472	p12.2
SNP_A-2254459	T	T	302	26	331	49	4.587	3.22E-02	rs4506547	10	129507762	q26.2
SNP_A-2232357	A	A	256	114	255	157	4.582	3.23E-02	rs7019268	9	83103043	q21.32
SNP_A-2234348	T	T	239	139	217	173	4.58	3.23E-02	rs7485263	12	103401097	q23.3
SNP_A-2260980	C	C	364	0	395	5	4.58	3.23E-02	rs990438	15	21873330	q11.2
SNP_A-2264050	A	A	228	120	291	109	4.583	3.23E-02	rs7582048	2	207782857	q33.3
SNP_A-2297768	C	C	353	63	370	42	4.581	3.23E-02	rs12357632	10	102944887	q24.32
SNP_A-2301231	A	A	294	70	285	99	4.585	3.23E-02	rs17221346	2	172165926	q31.1
SNP_A-2300127	C	T	229	191	221	197	4.583	3.23E-02	rs11629005	14	23930727	q11.2
SNP_A-2299046	G	G	314	18	303	33	4.584	3.23E-02	rs6769883	3	156565975	q25.31
SNP_A-2305737	C	C	309	43	287	63	4.58	3.23E-02	rs7709170	5	172340328	q35.1
SNP_A-2304642	G	G	375	37	359	57	4.585	3.23E-02	rs11684969	5	1914706	p15.33
SNP_A-2105559	C	C	235	185	263	153	4.585	3.23E-02	rs325095	12	124410184	q24.31
SNP_A-2094282	A	A	214	204	238	168	4.584	3.23E-02	rs4632265	19	13399543	p13.13
SNP_A-2072075	G	G	316	54	331	85	4.585	3.23E-02	rs13097853	3	16548144	p24.3
SNP_A-2058994	T	T	308	40	337	69	4.585	3.23E-02	rs1381675	6	77517862	q14.1
SNP_A-2040338	T	T	225	131	221	177	4.581	3.23E-02	rs1455769	15	92628889	q26.2
SNP_A-2036247	T	T	294	54	315	87	4.583	3.23E-02	---	8	4259320	p23.2
SNP_A-2034082	C	C	336	86	358	62	4.585	3.23E-02	rs1477280	5	160051326	q34
SNP_A-2032564	G	G	336	14	371	31	4.581	3.23E-02	rs17190515	8	13168721	p22
SNP_A-2177022	C	C	288	102	321	79	4.585	3.23E-02	rs11776804	8	84644233	q21.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2185773	T	T	347	53	305	71	4.581	3.23E-02	rs7129014	11	74931725	q13.5
SNP_A-2184356	T	T	341	21	395	11	4.581	3.23E-02	rs16862858	3	152012650	q25.1
SNP_A-2196741	G	G	264	100	329	87	4.582	3.23E-02	rs7460143	8	108100753	q23.1
SNP_A-2210483	A	A	193	165	244	152	4.582	3.23E-02	rs6762970	3	74825315	p12.3
SNP_A-2223267	G	G	368	0	399	5	4.584	3.23E-02	rs664150	18	75645386	q23
SNP_A-2145085	T	T	252	108	257	153	4.58	3.23E-02	rs1834471	11	127442283	q24.2
SNP_A-2151939	A	A	274	96	279	137	4.583	3.23E-02	rs4346897	7	15650788	p21.1
SNP_A-2162544	C	C	342	64	323	89	4.584	3.23E-02	rs11245517	10	126821431	q26.13
SNP_A-2165430	G	G	340	4	392	0	4.583	3.23E-02	rs1549980	11	74142446	q13.4
SNP_A-2157550	G	G	232	118	301	109	4.581	3.23E-02	rs9818865	3	84655178	p12.1
SNP_A-2156539	T	T	204	164	257	151	4.58	3.23E-02	rs1952975	6	48203805	p12.3
SNP_A-2155323	A	A	360	4	363	13	4.584	3.23E-02	rs17088392	13	71155237	q21.33
SNP_A-2122234	A	A	319	23	328	42	4.585	3.23E-02	rs17276827	4	153552694	q31.3
SNP_A-2113658	C	C	336	72	363	51	4.585	3.23E-02	rs2880848	13	18212519	q11
SNP_A-2131825	G	G	296	22	371	13	4.583	3.23E-02	rs1416492	1	188966863	q31.2
SNP_A-2133200	T	T	192	178	244	166	4.581	3.23E-02	rs9556998	13	98101783	q32.2
SNP_A-2133767	G	G	315	55	375	41	4.583	3.23E-02	rs10414630	19	15003380	p13.12
SNP_A-2135245	G	G	364	0	395	5	4.58	3.23E-02	rs1605471	11	89822821	q14.3
SNP_A-1793644	C	C	316	46	368	32	4.582	3.23E-02	rs1823437	8	84131211	q21.13
SNP_A-1713934	A	A	275	75	293	115	4.58	3.23E-02	rs9290978	3	192247053	q28
SNP_A-1842383	T	T	405	9	416	2	4.583	3.23E-02	rs17063760	9	77417514	q21.2
SNP_A-1863153	C	C	240	62	302	50	4.582	3.23E-02	rs806372	6	88913282	q15
SNP_A-1984978	C	C	297	65	359	51	4.583	3.23E-02	rs12664272	6	7540125	p24.3
SNP_A-1975395	C	C	361	5	400	16	4.582	3.23E-02	rs16826157	3	176894639	q26.31
SNP_A-1922121	T	T	402	16	386	30	4.581	3.23E-02	rs9465546	6	10319774	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1926335	G	G	271	97	330	82	4.582	3.23E-02	rs1600057	3	82815606	p12.2
SNP_A-1907556	A	A	243	107	304	94	4.582	3.23E-02	rs11757431	6	74813654	q13
SNP_A-1908800	A	A	343	1	388	8	4.583	3.23E-02	rs1930180	1	104077398	p21.1
SNP_A-1901975	G	G	258	112	224	136	4.585	3.23E-02	rs871269	5	150412581	q33.1
SNP_A-1892476	G	G	308	18	336	8	4.583	3.23E-02	rs16927744	9	11565768	p23
SNP_A-1901311	A	A	406	8	397	19	4.578	3.24E-02	rs10110925	8	35386210	p12
SNP_A-1898172	C	C	385	37	397	21	4.579	3.24E-02	rs7028354	9	82685513	q21.32
SNP_A-1886765	C	C	336	8	394	2	4.577	3.24E-02	rs4241913	4	190440393	q35.2
SNP_A-1906557	T	T	243	103	307	91	4.577	3.24E-02	rs921572	2	50245739	p16.3
SNP_A-1930415	C	C	269	95	320	78	4.579	3.24E-02	rs1863464	15	24489581	q12
SNP_A-1984954	T	C	230	190	221	199	4.578	3.24E-02	rs201061	6	6675511	p25.1
SNP_A-1981867	T	T	391	7	399	1	4.576	3.24E-02	rs16891119	5	62156572	q12.1
SNP_A-1947528	C	G	189	161	207	177	4.578	3.24E-02	rs10777318	12	90499930	q21.33
SNP_A-1960554	G	G	358	4	412	0	4.576	3.24E-02	rs2578129	4	95230234	q22.3
SNP_A-1864070	T	T	401	19	410	8	4.577	3.24E-02	rs792383	17	52785538	q23.2
SNP_A-1857099	C	C	299	35	355	23	4.576	3.24E-02	rs4326887	12	10267155	p13.2
SNP_A-1843805	T	T	356	4	410	0	4.579	3.24E-02	rs16993711	20	7415032	p12.3
SNP_A-1826490	G	G	328	18	389	9	4.578	3.24E-02	rs11061592	12	130529223	q24.33
SNP_A-1742611	C	C	295	107	274	138	4.575	3.24E-02	rs10493222	1	57292833	p32.2
SNP_A-1655541	G	G	378	20	370	36	4.578	3.24E-02	rs2060717	7	127934711	q32.1
SNP_A-1786826	G	G	362	32	369	17	4.577	3.24E-02	rs7683581	4	6321628	p16.1
SNP_A-1785980	C	C	385	37	397	21	4.579	3.24E-02	rs865443	1	117877619	p12
SNP_A-2135595	A	A	310	36	320	60	4.576	3.24E-02	rs7371892	3	56978121	p14.3
SNP_A-2157186	C	C	229	93	300	84	4.577	3.24E-02	rs9864830	3	86851806	p12.1
SNP_A-2165113	T	T	319	43	378	30	4.578	3.24E-02	rs17011337	4	127892641	q28.1
SNP_A-2166921	T	T	290	76	283	107	4.58	3.24E-02	rs13152937	5	23340125	p14.2
SNP_A-2151409	T	T	319	43	378	30	4.578	3.24E-02	rs7958227	12	96822193	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2144757	T	T	388	30	404	16	4.579	3.24E-02	rs17731193	20	57622421	q13.33
SNP_A-2144078	C	C	208	162	265	151	4.579	3.24E-02	rs7712025	5	121055833	q23.1
SNP_A-2215738	G	G	310	32	342	58	4.576	3.24E-02	rs606477	10	7439367	p14
SNP_A-2216563	C	C	245	125	241	169	4.579	3.24E-02	rs2696004	12	103539132	q23.3
SNP_A-2210444	C	C	243	151	285	129	4.577	3.24E-02	rs6936529	6	148507060	q24.3
SNP_A-2211590	C	C	326	12	407	5	4.576	3.24E-02	rs948125	11	126305721	q24.2
SNP_A-2198157	T	T	234	134	293	121	4.578	3.24E-02	rs825747	5	138164484	q31.2
SNP_A-2188548	T	T	260	94	295	73	4.578	3.24E-02	rs868	9	98991211	q22.33
SNP_A-2168864	A	A	333	83	307	109	4.577	3.24E-02	rs243864	16	54069823	q12.2
SNP_A-2037019	G	G	356	4	410	0	4.579	3.24E-02	rs2352121	7	10275533	p21.3
SNP_A-2042354	A	A	315	49	333	79	4.58	3.24E-02	rs17018692	3	81350224	p12.2
SNP_A-2002346	T	T	296	110	322	84	4.578	3.24E-02	rs10509322	10	71781854	q22.1
SNP_A-2017561	A	A	276	30	318	18	4.578	3.24E-02	rs16983193	21	29058444	q21.3
SNP_A-2075536	A	A	302	92	284	122	4.58	3.24E-02	rs13336562	16	78461848	q23.1
SNP_A-2064433	T	T	260	110	261	153	4.577	3.24E-02	rs10873068	14	52683456	q22.1
SNP_A-2092579	C	C	349	23	322	38	4.579	3.24E-02	rs7706060	5	140080790	q31.3
SNP_A-2106706	C	C	356	4	410	0	4.579	3.24E-02	rs16968634	13	105896063	q33.3
SNP_A-2103111	C	C	370	52	376	32	4.575	3.24E-02	rs6109426	20	12392139	p12.1
SNP_A-2100587	G	G	253	117	313	103	4.575	3.24E-02	rs17339549	2	79989700	p12
SNP_A-2088666	T	T	336	8	394	2	4.577	3.24E-02	---	4	88189112	q21.3
SNP_A-2300900	A	A	356	4	410	0	4.579	3.24E-02	rs12336181	9	2315825	p24.2
SNP_A-2292497	C	C	356	4	410	0	4.579	3.24E-02	rs6569655	6	130470001	q23.1
SNP_A-2228710	A	A	356	4	410	0	4.579	3.24E-02	rs16951491	16	73559633	q22.3
SNP_A-2230847	T	T	294	76	348	60	4.579	3.24E-02	rs9327224	5	121063906	q23.1
SNP_A-2255419	A	A	196	168	246	154	4.579	3.24E-02	rs9426534	1	225203155	q42.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251266	G	G	215	169	249	143	4.576	3.24E-02	rs12497104	3	8590207	p25.3
SNP_A-2244381	G	G	203	199	222	160	4.579	3.24E-02	rs282271	2	224747601	q36.1
SNP_A-2229528	G	G	388	32	366	50	4.574	3.25E-02	rs2069757	5	132026312	q23.3
SNP_A-2269900	C	C	362	4	416	0	4.57	3.25E-02	rs10217199	9	119245629	q33.1
SNP_A-2287510	G	G	329	21	381	11	4.571	3.25E-02	---	5	59540317	q12.1
SNP_A-2300595	T	T	318	32	305	51	4.57	3.25E-02	rs4631464	8	34054635	p12
SNP_A-2295589	C	C	193	159	244	146	4.572	3.25E-02	rs527158	20	56321619	q13.32
SNP_A-2308066	C	C	407	3	403	11	4.572	3.25E-02	rs7905314	10	29210183	p12.1
SNP_A-2090238	G	G	362	4	416	0	4.57	3.25E-02	rs4509295	8	56588619	q12.1
SNP_A-2088250	T	T	247	105	255	151	4.569	3.25E-02	rs2477868	1	229598992	q42.2
SNP_A-2061359	C	C	360	4	414	0	4.573	3.25E-02	rs6539696	12	81774070	q21.31
SNP_A-2016729	A	A	346	16	391	7	4.574	3.25E-02	rs7282675	21	24464614	q21.2
SNP_A-2011636	C	C	340	18	329	33	4.571	3.25E-02	rs2473662	6	23079718	p22.3
SNP_A-2045679	T	T	401	3	397	11	4.572	3.25E-02	rs162043	5	7942546	p15.31
SNP_A-2047183	C	C	338	8	396	2	4.571	3.25E-02	rs7228034	18	5698387	p11.31
SNP_A-2182577	T	T	356	0	387	5	4.571	3.25E-02	rs13384894	2	83622974	p11.2
SNP_A-2187826	C	C	208	134	200	178	4.573	3.25E-02	rs1902756	12	101481557	q23.2
SNP_A-2212965	G	G	325	45	341	73	4.573	3.25E-02	rs17066156	13	75831035	q22.2
SNP_A-2225788	G	G	348	4	400	0	4.57	3.25E-02	rs10921496	1	190798176	q31.3
SNP_A-2139436	T	T	407	1	399	7	4.575	3.25E-02	rs562929	1	36308872	p34.3
SNP_A-2160118	C	C	358	0	389	5	4.574	3.25E-02	rs2893319	13	107599411	q33.3
SNP_A-2126064	T	T	398	6	392	16	4.571	3.25E-02	rs16919682	11	29662649	p14.1
SNP_A-1794094	G	G	360	30	335	47	4.57	3.25E-02	rs11205743	1	50799486	p32.3
SNP_A-1804306	G	G	357	61	379	41	4.574	3.25E-02	rs7607490	2	12801718	p24.3
SNP_A-1804876	A	A	348	4	400	0	4.57	3.25E-02	rs7642133	3	105904161	q13.11
SNP_A-1744435	A	A	350	8	410	2	4.572	3.25E-02	rs2098979	2	214797714	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1728645	A	A	394	6	388	16	4.572	3.25E-02	rs9299385	9	103494341	q31.1
SNP_A-1782364	G	G	304	28	313	49	4.57	3.25E-02	rs10018670	4	99481886	q23
SNP_A-1845752	T	T	224	66	297	57	4.572	3.25E-02	rs2522236	7	24788397	p15.3
SNP_A-1845171	T	T	409	11	413	3	4.572	3.25E-02	rs9874679	3	9029865	p25.3
SNP_A-1862395	G	G	374	36	360	56	4.572	3.25E-02	rs16926600	10	71113156	q22.1
SNP_A-1869457	C	C	378	28	361	13	4.574	3.25E-02	rs4951447	1	209015433	q32.3
SNP_A-1951639	A	A	362	4	416	0	4.57	3.25E-02	rs11050264	12	29561035	p11.22
SNP_A-1944125	A	A	255	107	312	92	4.572	3.25E-02	rs842500	3	153252247	q25.1
SNP_A-1942167	A	A	328	42	387	29	4.572	3.25E-02	rs12227915	12	24935910	p12.1
SNP_A-1982343	G	G	343	21	397	11	4.573	3.25E-02	rs6452536	5	82581139	q14.2
SNP_A-1987560	T	C	179	169	207	159	4.573	3.25E-02	rs7766106	6	127496831	q22.33
SNP_A-1918363	C	C	345	25	396	14	4.573	3.25E-02	rs11917205	3	30545602	p24.1
SNP_A-1917196	G	G	362	4	416	0	4.57	3.25E-02	rs9559118	13	107099660	q33.3
SNP_A-1914454	G	G	263	159	229	187	4.573	3.25E-02	rs17114086	11	111955850	q23.1
SNP_A-1913210	C	C	419	1	411	7	4.572	3.25E-02	rs4894981	3	107323561	q13.11
SNP_A-1881947	C	C	258	100	250	136	4.57	3.25E-02	rs1370194	18	36512221	q12.3
SNP_A-1879944	C	C	403	7	411	1	4.574	3.25E-02	rs12120383	1	53777544	p32.3
SNP_A-1890014	G	G	237	133	233	179	4.574	3.25E-02	rs4945778	6	107933158	q21
SNP_A-1878261	C	T	241	181	211	209	4.567	3.26E-02	rs4950760	1	198727083	q32.1
SNP_A-1917766	T	T	378	36	364	56	4.569	3.26E-02	rs17269482	15	57092082	q22.1
SNP_A-1982467	A	A	217	147	212	196	4.565	3.26E-02	rs7705545	5	88868807	q14.3
SNP_A-1974416	T	C	198	172	222	188	4.565	3.26E-02	rs7630783	3	134343292	q22.1
SNP_A-1947596	T	T	247	95	305	81	4.565	3.26E-02	rs4703337	5	104734352	q21.3
SNP_A-1871372	A	A	372	28	342	44	4.568	3.26E-02	rs1056680	22	34327553	q12.3
SNP_A-1848514	T	T	319	45	380	32	4.567	3.26E-02	rs3766138	1	166504818	q24.2
SNP_A-1821032	G	G	326	44	344	72	4.566	3.26E-02	rs12436698	14	70761248	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784343	G	G	233	77	311	69	4.568	3.26E-02	rs6868487	5	87271124	q14.3
SNP_A-1646252	C	C	262	88	278	132	4.566	3.26E-02	rs4469023	4	145878061	q31.21
SNP_A-1661175	G	G	387	15	377	29	4.566	3.26E-02	rs1771363	1	34162047	p35.1
SNP_A-1709585	G	G	302	98	338	76	4.567	3.26E-02	rs10503463	8	13535677	p22
SNP_A-1789851	G	G	301	67	358	52	4.567	3.26E-02	rs17694839	20	15538487	p12.1
SNP_A-2135384	T	T	344	26	399	15	4.568	3.26E-02	rs11732298	4	107059283	q24
SNP_A-2135984	G	G	407	3	362	10	4.567	3.26E-02	rs12312811	12	115463295	q24.22
SNP_A-2122805	T	T	313	15	327	31	4.568	3.26E-02	rs1122667	3	61136786	p14.2
SNP_A-2149171	A	A	366	4	402	14	4.567	3.26E-02	rs10174013	2	62132095	p15
SNP_A-2226844	A	A	316	32	353	19	4.565	3.26E-02	rs404014	17	71925881	q25.1
SNP_A-2202397	G	G	294	118	268	148	4.567	3.26E-02	rs364716	1	39229203	p34.3
SNP_A-2206939	G	G	248	170	213	197	4.567	3.26E-02	rs4819519	22	18110557	q11.21
SNP_A-2035815	C	C	343	11	410	4	4.569	3.26E-02	rs6426618	1	20270466	p36.12
SNP_A-2023957	C	C	258	110	259	153	4.565	3.26E-02	rs1404829	7	144062333	q35
SNP_A-2005713	T	T	325	35	357	21	4.565	3.26E-02	rs2615883	10	117672154	q25.3
SNP_A-2050882	T	T	340	82	308	106	4.568	3.26E-02	rs7200813	16	25840300	p12.1
SNP_A-2053141	T	T	392	26	375	43	4.565	3.26E-02	rs10754705	1	236939807	q43
SNP_A-2066953	T	T	340	8	398	2	4.565	3.26E-02	rs16944795	17	56508780	q23.2
SNP_A-2076798	G	G	345	17	400	8	4.569	3.26E-02	rs8192081	4	140963786	q31.1
SNP_A-2102011	T	T	256	70	282	112	4.567	3.26E-02	rs2526191	5	128294089	q23.3
SNP_A-2097528	T	T	192	166	250	158	4.564	3.26E-02	rs2958163	18	51236410	q21.2
SNP_A-2299802	G	G	352	34	335	53	4.565	3.26E-02	rs17140654	6	5451840	p25.1
SNP_A-2289864	C	C	394	4	364	12	4.566	3.26E-02	rs6659764	1	243378452	q44
SNP_A-2278419	G	G	352	0	383	5	4.567	3.26E-02	rs6414953	5	88999906	q14.3
SNP_A-2257294	C	-	231	171	207	207	4.568	3.26E-02	rs4260625	5	68285092	q13.1
SNP_A-2241683	C	C	255	107	259	151	4.568	3.26E-02	rs4840106	6	100510235	q16.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2254359	A	A	201	137	199	187	4.564	0.0327	rs6687507	1	165281378	q24.2
SNP_A-2261027	G	G	279	55	333	41	4.561	0.0327	rs9447453	6	75935145	q14.1
SNP_A-2273172	C	C	312	54	327	85	4.562	0.0327	rs17009161	4	85849126	q21.23
SNP_A-2286638	A	A	388	22	396	10	4.562	0.0327	rs17115674	14	44409193	q21.2
SNP_A-2298269	G	G	213	135	276	126	4.563	0.0327	rs7771912	6	44610333	p21.1
SNP_A-2294685	C	C	354	8	414	2	4.561	0.0327	rs11941762	4	21662721	p15.31
SNP_A-2309501	A	A	263	103	311	85	4.563	0.0327	rs13214642	6	122204844	q22.31
SNP_A-2304189	G	G	387	29	397	15	4.563	0.0327	rs2267029	22	22442470	q11.23
SNP_A-2309837	C	C	303	111	326	84	4.56	0.0327	rs802535	7	145349150	q35
SNP_A-2313151	T	T	330	36	354	62	4.562	0.0327	rs4449111	2	33858700	p22.3
SNP_A-2092772	T	T	366	54	376	34	4.56	0.0327	rs6043596	20	15817271	p12.1
SNP_A-2094047	T	T	200	170	255	159	4.561	0.0327	rs154246	5	16655451	p15.1
SNP_A-2066433	C	T	199	153	209	199	4.561	0.0327	rs4897099	6	149617697	q25.1
SNP_A-2005972	T	T	260	150	230	180	4.564	0.0327	rs7250821	19	43065318	q13.13
SNP_A-2004357	T	T	374	44	369	25	4.56	0.0327	rs14280	15	89310738	q26.1
SNP_A-1996890	G	G	379	11	363	23	4.56	0.0327	rs17062312	9	76117762	q21.13
SNP_A-2026675	G	G	274	48	322	34	4.562	0.0327	rs11102769	1	114530891	p13.2
SNP_A-2205311	T	T	319	103	287	129	4.561	0.0327	rs1076573	16	3170889	p13.3
SNP_A-2209580	C	C	336	52	342	32	4.559	0.0327	rs10950412	7	12531712	p21.3
SNP_A-2227820	C	C	311	107	283	135	4.56	0.0327	rs1188349	1	30892750	p35.2
SNP_A-2148327	G	A	202	162	216	198	4.56	0.0327	rs11745418	5	111915028	q22.2
SNP_A-2141382	C	C	331	37	382	24	4.564	0.0327	rs4924116	15	35086443	q14
SNP_A-2159192	A	A	299	65	361	51	4.562	0.0327	rs11172823	12	57598380	q14.1
SNP_A-2156338	C	C	343	63	305	83	4.562	0.0327	rs9535661	13	50890162	q14.3
SNP_A-2154480	A	A	287	75	298	112	4.561	0.0327	rs1907678	9	104268028	q31.1
SNP_A-2163453	A	G	190	168	223	185	4.559	0.0327	rs12264692	10	126250236	q26.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123886	T	T	389	29	399	15	4.562	0.0327	rs16855587	3	110557627	q13.13
SNP_A-1812695	T	C	234	188	218	202	4.561	0.0327	rs1289452	11	134149492	q25
SNP_A-1652230	G	G	369	17	375	33	4.562	0.0327	rs3803221	13	23039724	q12.12
SNP_A-1825044	G	G	322	72	354	52	4.562	0.0327	rs7219691	17	60663086	q24.1
SNP_A-1944990	T	T	272	98	331	83	4.561	0.0327	rs10952921	7	87744919	q21.13
SNP_A-1940940	G	G	364	38	393	23	4.561	0.0327	rs7525488	1	244301598	q44
SNP_A-1957075	C	C	307	103	278	130	4.561	0.0327	rs12138644	1	167012320	q24.2
SNP_A-1988764	A	A	227	129	228	178	4.562	0.0327	rs10249024	7	9799568	p21.3
SNP_A-1915903	T	T	275	147	301	117	4.564	0.0327	rs764673	20	41987407	q13.12
SNP_A-1875487	T	T	289	131	257	159	4.56	0.0327	rs11188783	10	98228585	q24.1
SNP_A-1887483	C	C	370	0	403	5	4.564	0.0327	rs7333912	13	90672132	q31.3
SNP_A-1897633	A	A	314	44	373	31	4.56	0.0327	rs9524446	13	86516431	q31.2
SNP_A-1896671	T	G	168	162	217	163	4.559	3.28E-02	rs4512801	11	28289977	p14.1
SNP_A-1875096	G	G	290	72	347	57	4.555	3.28E-02	rs194330	16	10263191	p13.2
SNP_A-1879945	A	A	380	14	397	5	4.555	3.28E-02	rs7946458	11	112475543	q23.1
SNP_A-1907787	T	T	230	192	257	159	4.557	3.28E-02	---	18	45742623	q21.1
SNP_A-1919726	G	G	243	179	210	208	4.558	3.28E-02	rs7181150	15	37000183	q14
SNP_A-1989067	A	A	232	126	223	167	4.555	3.28E-02	rs17436053	7	18910468	p21.1
SNP_A-1974843	G	G	273	97	332	82	4.556	3.28E-02	rs2410776	3	153198922	q25.1
SNP_A-1971563	T	T	231	135	287	121	4.554	3.28E-02	rs164028	3	6792722	p26.1
SNP_A-1965904	C	C	308	18	365	9	4.558	3.28E-02	rs2083406	2	174932703	q31.1
SNP_A-1934600	C	C	306	56	314	86	4.558	3.28E-02	rs11720651	3	89343751	p11.1
SNP_A-1821042	A	A	238	136	264	108	4.554	3.28E-02	rs9527945	13	58608117	q21.2
SNP_A-1833046	A	A	314	56	374	42	4.556	3.28E-02	rs16937407	8	72206559	q13.3
SNP_A-1833656	C	C	340	24	362	12	4.555	3.28E-02	rs356612	16	16071245	p13.11
SNP_A-1846499	C	C	282	134	250	162	4.554	3.28E-02	rs6906206	6	24976059	p22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1782613	A	A	342	4	392	0	4.556	3.28E-02	rs7855497	9	72925231	q21.13
SNP_A-1757299	G	G	255	105	318	92	4.557	3.28E-02	rs10499194	6	137983207	q23.3
SNP_A-1803577	A	A	278	90	337	75	4.556	3.28E-02	rs2538007	5	128404705	q23.3
SNP_A-1785644	G	G	303	59	363	45	4.558	3.28E-02	rs16986926	2	19844121	p24.1
SNP_A-1795638	G	G	220	70	236	110	4.555	3.28E-02	rs36078	5	148410760	q32
SNP_A-2129882	G	G	277	111	312	88	4.556	3.28E-02	rs17577362	11	110787872	q23.1
SNP_A-2131170	T	T	368	2	404	10	4.557	3.28E-02	rs1905138	5	113177425	q22.3
SNP_A-2162563	G	G	314	56	374	42	4.556	3.28E-02	rs10009777	4	167536555	q32.3
SNP_A-2140689	G	G	226	130	228	180	4.555	3.28E-02	rs2062003	8	13791232	p22
SNP_A-2213780	C	C	347	39	329	59	4.556	3.28E-02	rs6133742	20	9671448	p12.2
SNP_A-2199711	T	T	281	77	338	62	4.554	3.28E-02	rs12194995	6	51918458	p12.2
SNP_A-2177705	G	G	311	49	374	36	4.555	3.28E-02	rs4423292	13	98115514	q32.2
SNP_A-2172790	T	T	287	125	258	154	4.557	3.28E-02	rs12186150	4	31325044	p15.1
SNP_A-2022152	T	T	281	141	308	112	4.557	3.28E-02	rs6807027	3	60067829	p14.2
SNP_A-2030138	T	C	185	183	233	173	4.557	3.28E-02	rs1366943	12	30433716	p11.22
SNP_A-2004344	T	T	342	12	370	4	4.555	3.28E-02	rs1252899	10	100065603	q24.2
SNP_A-2065676	A	A	240	106	240	148	4.557	3.28E-02	rs2103173	11	111715262	q23.1
SNP_A-2076334	A	A	358	4	410	0	4.554	3.28E-02	rs341474	9	38283902	p13.2
SNP_A-2071622	G	G	336	20	382	10	4.558	3.28E-02	rs12927909	16	7462588	p13.2
SNP_A-2057384	C	C	356	4	408	0	4.557	3.28E-02	rs16837598	4	5849146	p16.2
SNP_A-2093844	A	A	356	4	408	0	4.557	3.28E-02	rs17088022	9	84843487	q21.33
SNP_A-2298538	A	A	314	100	288	128	4.557	3.28E-02	rs3743198	15	77061040	q25.1
SNP_A-2291113	A	A	283	85	342	70	4.554	3.28E-02	rs1462778	4	98594268	q22.3
SNP_A-2233670	G	G	398	6	365	15	4.554	3.28E-02	rs12655006	5	126435501	q23.2
SNP_A-2256220	C	C	380	8	350	18	4.553	3.29E-02	rs12971997	19	23657340	p12
SNP_A-2248346	A	A	360	4	412	0	4.551	3.29E-02	rs2098543	12	14628739	p13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2292863	C	C	344	4	394	0	4.553	3.29E-02	rs2414946	15	65497574	q23
SNP_A-2307769	T	T	372	20	331	33	4.549	3.29E-02	rs1495672	10	29175611	p12.1
SNP_A-2104833	G	G	292	78	301	115	4.553	3.29E-02	rs175851	5	157567807	q33.3
SNP_A-2088733	T	T	291	79	350	64	4.549	3.29E-02	rs17170531	7	36025533	p14.2
SNP_A-2064875	A	A	243	123	301	109	4.548	3.29E-02	rs6437300	2	240852845	q37.3
SNP_A-2005275	T	T	391	9	400	2	4.552	3.29E-02	rs17127876	10	112480834	q25.2
SNP_A-2001311	C	C	311	57	371	43	4.548	3.29E-02	rs10826068	10	58968422	q21.1
SNP_A-1989960	T	T	265	85	272	124	4.55	3.29E-02	rs11769005	7	53440825	p12.1
SNP_A-2176323	T	T	312	58	326	90	4.55	3.29E-02	rs6419744	3	81089562	p12.2
SNP_A-2181288	T	T	330	84	307	111	4.55	3.29E-02	rs12476056	2	113766553	q13
SNP_A-2215171	T	T	255	165	282	134	4.553	3.29E-02	rs13223039	7	35203469	p14.2
SNP_A-2207109	G	G	283	87	290	126	4.55	3.29E-02	rs2438144	4	95798340	q22.3
SNP_A-2203505	C	C	308	60	323	93	4.553	3.29E-02	rs16828607	2	187782239	q32.1
SNP_A-2144973	A	A	339	15	368	32	4.549	3.29E-02	rs4053613	6	90711599	q15
SNP_A-2166836	G	G	296	42	360	30	4.553	3.29E-02	rs9963453	18	20297683	q11.2
SNP_A-2154881	A	A	405	9	414	2	4.549	3.29E-02	rs17107580	14	69535455	q24.2
SNP_A-2127217	G	G	199	173	242	154	4.551	3.29E-02	rs10904470	10	5378487	p15.1
SNP_A-2118204	A	A	291	69	305	105	4.55	3.29E-02	rs841531	6	65963051	q12
SNP_A-2110567	G	G	265	105	267	147	4.552	3.29E-02	rs11029819	11	27041285	p14.2
SNP_A-1797445	G	G	352	54	380	36	4.55	3.29E-02	rs7327863	13	35392802	q13.3
SNP_A-1787980	G	G	191	175	244	164	4.549	3.29E-02	rs2612552	18	41303903	q12.3
SNP_A-1806520	C	C	223	127	273	111	4.551	3.29E-02	rs1520589	3	80877860	p12.2
SNP_A-1752131	A	G	211	177	218	192	4.548	3.29E-02	rs10491443	5	52655585	q11.2
SNP_A-1784832	A	A	352	18	376	36	4.549	3.29E-02	rs11065270	12	119703582	q24.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1651658	G	G	360	42	386	26	4.549	3.29E-02	rs2319540	3	121214805	q13.33
SNP_A-1647220	T	T	373	1	367	7	4.549	3.29E-02	rs10505070	8	105946653	q22.3
SNP_A-1858820	T	T	337	23	366	44	4.551	3.29E-02	rs10100825	8	69951700	q13.2
SNP_A-1853011	G	G	254	78	320	66	4.553	3.29E-02	rs6442552	3	15897744	p25.1
SNP_A-1870176	G	G	386	36	365	55	4.55	3.29E-02	rs10822887	10	68124816	q21.3
SNP_A-1820652	G	G	282	84	291	123	4.553	3.29E-02	rs2433325	4	95798770	q22.3
SNP_A-1935551	A	G	238	184	212	204	4.552	3.29E-02	rs7199361	16	24976255	p12.1
SNP_A-1940062	C	C	292	78	301	115	4.553	3.29E-02	rs2813407	10	1509333	p15.3
SNP_A-1979712	T	T	360	4	412	0	4.551	3.29E-02	---	4	165313657	q32.3
SNP_A-1923950	G	G	324	62	353	43	4.553	3.29E-02	rs6582999	1	107209707	p13.3
SNP_A-1930174	G	G	360	4	412	0	4.551	3.29E-02	rs12954176	18	23662171	q12.1
SNP_A-1927433	C	C	360	4	412	0	4.551	3.29E-02	rs2465766	11	106417979	q22.3
SNP_A-1906101	G	G	346	8	404	2	4.549	3.29E-02	rs1896867	15	19886462	q11.2
SNP_A-1875233	A	A	280	68	297	105	4.55	3.29E-02	rs6463170	7	42981102	p14.1
SNP_A-1874599	G	G	360	0	393	5	4.553	3.29E-02	rs17141363	7	19280201	p21.1
SNP_A-1896188	A	A	330	24	396	14	4.551	3.29E-02	rs2471517	12	87034184	q21.32
SNP_A-1890911	G	G	346	14	408	6	4.553	3.29E-02	rs2579398	2	197813288	q33.1
SNP_A-1893482	T	T	362	4	414	0	4.548	3.30E-02	rs10414716	19	36871839	q12
SNP_A-1879318	A	A	420	2	411	9	4.547	3.30E-02	---	9	118750354	q33.1
SNP_A-1887839	G	G	420	2	411	9	4.547	3.30E-02	rs17018234	1	208498406	q32.3
SNP_A-1886238	A	A	304	110	280	140	4.543	3.30E-02	rs1437129	16	82262870	q23.3
SNP_A-1909853	A	A	377	43	353	63	4.544	3.30E-02	rs12094371	1	107095587	p13.3
SNP_A-1914990	G	G	358	60	325	81	4.548	3.30E-02	rs833523	18	44827549	q21.1
SNP_A-1922649	C	C	362	4	414	0	4.548	3.30E-02	rs17024881	3	86201639	p12.1
SNP_A-1967275	C	C	405	7	411	1	4.544	3.30E-02	rs6666943	1	151060327	q21.3
SNP_A-1974314	T	T	362	4	414	0	4.548	3.30E-02	rs784690	3	131030500	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1947294	A	A	403	7	409	1	4.544	3.30E-02	rs264676	3	65861112	p14.1
SNP_A-1938738	T	T	413	7	419	1	4.543	3.30E-02	rs328361	16	72364568	q22.3
SNP_A-1821157	C	C	203	167	257	155	4.544	3.30E-02	rs7839315	8	4947759	p23.2
SNP_A-1836554	T	T	244	178	210	206	4.545	3.30E-02	rs2109169	17	14427387	p12
SNP_A-1832590	T	T	323	17	374	8	4.544	3.30E-02	rs7506625	18	69813953	q22.3
SNP_A-1840816	A	A	411	7	417	1	4.543	3.30E-02	rs11225422	11	102161528	q22.2
SNP_A-1789852	G	G	349	21	403	11	4.548	3.30E-02	rs3853290	10	698360	p15.3
SNP_A-2118057	T	T	349	5	361	15	4.544	3.30E-02	rs11019260	11	90412393	q14.3
SNP_A-2132109	C	C	390	20	409	9	4.547	3.30E-02	rs9316052	13	43151109	q14.11
SNP_A-2167120	C	C	413	7	419	1	4.543	3.30E-02	rs8021829	14	100756991	q32.31
SNP_A-2161794	C	C	324	44	337	71	4.545	3.30E-02	rs16832105	2	200647813	q33.1
SNP_A-2147866	C	C	301	65	310	98	4.548	3.30E-02	rs9520222	13	106314248	q33.3
SNP_A-2146924	G	G	418	2	409	9	4.548	3.30E-02	rs16989809	22	30777330	q12.3
SNP_A-2151520	T	T	364	4	416	0	4.545	3.30E-02	rs17082856	13	67211675	q21.32
SNP_A-2149317	C	C	364	4	416	0	4.545	3.30E-02	rs6723616	2	235585554	q37.2
SNP_A-2211737	C	C	409	7	415	1	4.544	3.30E-02	rs17692477	18	35467838	q12.2
SNP_A-2220065	G	G	218	120	226	172	4.543	3.30E-02	---	4	57464325	q12
SNP_A-2181503	G	G	349	45	381	29	4.546	3.30E-02	rs16933854	8	69044487	q13.2
SNP_A-2179266	T	T	409	9	418	2	4.548	3.30E-02	rs16955410	15	27464659	q13.1
SNP_A-2177642	G	G	359	61	334	84	4.545	3.30E-02	rs11037018	11	42679163	p12
SNP_A-2196858	G	G	214	156	209	207	4.548	3.30E-02	rs10483301	14	25046977	q12
SNP_A-2196210	C	C	364	4	416	0	4.545	3.30E-02	rs3014597	1	201154188	q32.1
SNP_A-2000946	A	A	362	4	414	0	4.548	3.30E-02	rs6602255	10	7689249	p14
SNP_A-2017986	C	C	252	116	252	160	4.547	3.30E-02	rs542178	21	31658040	q22.11
SNP_A-2015841	G	G	206	138	203	187	4.545	3.30E-02	rs9974998	21	18905721	q21.1
SNP_A-2020416	G	G	364	4	416	0	4.545	3.30E-02	rs2070553	21	44441589	q22.3
SNP_A-2044233	G	G	334	8	390	2	4.547	3.30E-02	rs2418441	9	116154391	q33.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2067228	C	C	281	101	309	77	4.544	3.30E-02	rs13172733	5	142351873	q31.3
SNP_A-2073171	A	A	336	66	320	92	4.547	3.30E-02	rs16890354	5	32828931	p13.3
SNP_A-2074147	G	G	209	161	261	147	4.544	3.30E-02	rs7552841	1	55230773	p32.3
SNP_A-2074861	T	T	364	4	416	0	4.545	3.30E-02	rs12405350	1	213970546	q41
SNP_A-2054056	G	G	355	13	403	5	4.545	3.30E-02	rs497321	15	51191215	q21.3
SNP_A-2048538	C	C	373	35	392	20	4.543	3.30E-02	rs4149253	8	27452125	p21.1
SNP_A-2089292	G	G	417	1	411	7	4.543	3.30E-02	rs17156308	7	81702921	q21.11
SNP_A-2077131	T	A	194	152	208	194	4.544	3.30E-02	rs9353959	6	93648078	q16.1
SNP_A-2107128	A	A	297	123	268	152	4.547	3.30E-02	rs4708797	6	158978760	q25.3
SNP_A-2310454	C	C	397	1	391	7	4.546	3.30E-02	rs2481971	13	27466456	q12.2
SNP_A-2288138	G	G	356	0	389	5	4.548	3.30E-02	rs17024584	1	120223428	p12
SNP_A-2299526	T	T	395	7	401	1	4.545	3.30E-02	rs17026058	2	101856103	q11.2
SNP_A-2244885	C	C	244	118	246	164	4.545	3.30E-02	rs6424683	1	80226595	p31.1
SNP_A-2233472	G	G	303	115	331	89	4.546	3.30E-02	rs4903489	14	76311145	q24.3
SNP_A-2233188	C	C	379	31	380	16	4.547	3.30E-02	rs6771963	3	10484205	p25.3
SNP_A-2281271	T	T	401	7	407	1	4.545	3.30E-02	rs12351807	9	111088230	q31.3
SNP_A-2281792	T	T	236	134	295	121	4.542	3.31E-02	rs1555849	1	10334868	p36.22
SNP_A-2264670	G	G	227	135	280	120	4.539	3.31E-02	rs11682206	2	175120117	q31.1
SNP_A-2262841	A	A	372	12	350	24	4.539	3.31E-02	rs3766331	1	78715320	p31.1
SNP_A-2229269	A	A	226	144	283	131	4.543	3.31E-02	rs7811922	7	28131234	p15.1
SNP_A-2242744	C	C	288	80	298	118	4.542	3.31E-02	rs10158567	1	237614551	q43
SNP_A-2255815	G	G	319	45	340	74	4.542	3.31E-02	rs4741032	9	10398149	p23
SNP_A-2301401	A	A	299	61	359	47	4.54	3.31E-02	rs12474254	2	60977429	p16.1
SNP_A-2290865	A	A	265	139	293	111	4.541	3.31E-02	rs1395748	1	205864340	q32.2
SNP_A-2306809	G	G	284	76	351	63	4.54	3.31E-02	rs6506446	18	6824651	p11.31
SNP_A-2104666	C	C	338	72	318	98	4.543	3.31E-02	rs7072870	10	71050326	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2094868	C	C	353	17	408	8	4.538	3.31E-02	rs16869953	5	91038501	q14.3
SNP_A-2084279	G	G	318	104	286	130	4.542	3.31E-02	rs13012056	2	67384281	p14
SNP_A-2085889	G	G	311	55	329	87	4.539	3.31E-02	rs11106294	12	90710408	q21.33
SNP_A-2058912	T	T	271	45	283	73	4.539	3.31E-02	rs1019283	2	58577271	p16.1
SNP_A-2027751	G	G	353	17	408	8	4.538	3.31E-02	rs1150683	6	28263293	p22.1
SNP_A-1998592	C	C	324	38	349	65	4.542	3.31E-02	rs1556401	10	24734721	p12.1
SNP_A-2186025	G	G	342	28	384	16	4.541	3.31E-02	rs10877183	12	57567095	q14.1
SNP_A-2217217	C	C	296	106	267	133	4.539	3.31E-02	rs6988782	8	9647948	p23.1
SNP_A-2203466	G	G	284	18	302	36	4.542	3.31E-02	rs470393	12	127982170	q24.32
SNP_A-2142328	C	C	306	40	288	60	4.54	3.31E-02	rs11768246	7	110016928	q31.1
SNP_A-2140367	T	T	352	4	402	0	4.541	3.31E-02	rs4428236	4	179030717	q34.3
SNP_A-2131756	C	C	221	145	279	133	4.542	3.31E-02	rs4075523	1	93930494	p22.1
SNP_A-2124205	G	G	352	4	402	0	4.541	3.31E-02	---	2	36199686	p22.3
SNP_A-2112011	G	G	283	77	345	63	4.539	3.31E-02	rs11718794	3	13091061	p25.2
SNP_A-1796848	G	G	270	98	332	84	4.541	3.31E-02	rs7045170	9	37487684	p13.2
SNP_A-1805363	A	A	331	87	353	63	4.543	3.31E-02	rs5761843	22	25652295	q12.1
SNP_A-1803139	C	C	286	30	296	52	4.543	3.31E-02	rs9864430	4	183762589	q35.1
SNP_A-1643545	T	T	362	30	395	17	4.54	3.31E-02	rs10488241	7	12686266	p21.3
SNP_A-1651088	G	G	195	165	252	156	4.539	3.31E-02	rs643912	6	128000031	q22.33
SNP_A-1712973	A	A	220	182	257	157	4.538	3.31E-02	rs1977389	10	90438071	q23.31
SNP_A-1832373	T	T	383	15	345	27	4.539	3.31E-02	rs10774386	12	606363	p13.33
SNP_A-1870278	C	C	276	94	335	79	4.543	3.31E-02	rs6440735	3	152527430	q25.1
SNP_A-1846119	T	T	209	145	261	131	4.539	3.31E-02	rs7378098	4	118216646	q26
SNP_A-1939978	C	C	255	147	230	180	4.541	3.31E-02	rs2555269	12	118062776	q24.23
SNP_A-1946272	G	G	272	92	282	134	4.539	3.31E-02	rs3850134	18	70633746	q22.3
SNP_A-1942829	G	G	375	39	350	58	4.54	3.31E-02	rs489295	18	6967084	p11.31
SNP_A-1978540	C	C	256	110	313	95	4.542	3.31E-02	rs4834168	4	113333351	q25
SNP_A-1983824	T	T	342	6	361	17	4.542	3.31E-02	rs2042973	5	143745922	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1922814	C	C	349	73	321	97	4.539	3.31E-02	rs2352723	1	226598603	q42.13
SNP_A-1906461	T	T	352	4	402	0	4.541	3.31E-02	rs2051981	17	10775281	p12
SNP_A-1896160	G	G	242	106	237	145	4.538	3.31E-02	rs11125102	2	47037997	p21
SNP_A-1875917	G	G	299	23	334	12	4.536	0.0332	rs12386735	7	61829823	q11.21
SNP_A-1973543	A	A	289	71	295	105	4.537	0.0332	rs9866618	3	89402267	p11.1
SNP_A-1967737	C	T	195	171	224	188	4.535	0.0332	rs10494311	1	154007132	q23.1
SNP_A-1942818	A	A	308	72	276	94	4.537	0.0332	rs6574629	14	80661943	q31.1
SNP_A-1953511	C	C	358	52	373	33	4.535	0.0332	rs6085840	20	6978764	p12.3
SNP_A-1870339	C	C	283	123	298	92	4.537	0.0332	rs4756201	11	35219714	p13
SNP_A-1869797	G	G	338	76	350	52	4.534	0.0332	rs17208550	15	65004762	q22.33
SNP_A-1832711	A	A	287	83	346	68	4.534	0.0332	rs9426951	1	154115166	q23.1
SNP_A-1828102	G	G	327	41	346	68	4.534	0.0332	rs9360946	6	76629692	q14.1
SNP_A-1644622	A	A	300	102	281	133	4.535	0.0332	rs10489667	1	114135748	p13.2
SNP_A-1813959	G	G	346	0	379	5	4.536	0.0332	rs9593035	13	74482309	q22.2
SNP_A-2131657	A	A	312	54	370	40	4.537	0.0332	rs9287447	2	136821383	q21.3
SNP_A-2140953	T	G	195	171	224	188	4.535	0.0332	rs6985617	8	88485434	q21.3
SNP_A-2142172	C	C	304	64	366	50	4.535	0.0332	rs12918088	16	75872617	q23.1
SNP_A-2146230	C	C	272	94	334	80	4.533	0.0332	rs2707461	7	120581301	q31.31
SNP_A-2145303	A	A	241	119	233	159	4.537	0.0332	rs7682924	4	166095166	q32.3
SNP_A-2205180	T	G	218	178	211	191	4.537	0.0332	rs7914785	10	94943686	q23.33
SNP_A-2206508	G	G	257	109	311	93	4.537	0.0332	rs482736	6	72806741	q13
SNP_A-2216599	A	A	339	75	356	52	4.538	0.0332	rs11666461	19	57129299	q13.41
SNP_A-2213357	G	G	351	9	391	23	4.536	0.0332	rs3827855	10	25183825	p12.1
SNP_A-2189757	C	C	366	0	401	5	4.537	0.0332	rs2056786	2	180797898	q31.3
SNP_A-2176871	C	C	237	183	266	152	4.536	0.0332	rs1061628	1	12202265	p36.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169984	A	A	270	98	272	138	4.533	0.0332	rs7672780	4	92652646	q22.1
SNP_A-2004884	A	A	271	55	344	44	4.538	0.0332	rs4129721	16	77016847	q23.1
SNP_A-2003604	C	C	354	4	404	0	4.538	0.0332	rs4981601	14	19204326	q11.2
SNP_A-2013128	T	T	372	22	407	11	4.534	0.0332	rs966356	8	5143121	p23.2
SNP_A-2013375	A	A	224	142	211	183	4.535	0.0332	rs551076	11	89769654	q14.3
SNP_A-2029885	G	G	330	52	318	76	4.538	0.0332	rs16897183	5	67257328	q13.1
SNP_A-2023634	A	A	345	17	363	7	4.537	0.0332	rs6958922	7	27326395	p15.2
SNP_A-2034085	A	A	336	4	370	14	4.536	0.0332	rs10417672	19	48029945	q13.2
SNP_A-2062043	C	C	357	65	376	44	4.534	0.0332	rs11024671	11	18456332	p15.1
SNP_A-2072938	C	C	278	80	282	116	4.537	0.0332	rs1875529	5	98396954	q21.1
SNP_A-2091326	A	A	215	137	274	126	4.533	0.0332	rs11927031	3	84249639	p12.1
SNP_A-2080877	A	A	332	38	352	64	4.536	0.0332	rs9843093	3	106039315	q13.11
SNP_A-2093003	A	T	199	163	211	189	4.534	0.0332	rs10792520	11	80287535	q14.1
SNP_A-2100271	T	T	356	4	406	0	4.535	0.0332	rs7489249	12	54879298	q13.2
SNP_A-2290286	A	A	357	65	376	44	4.534	0.0332	rs10519152	15	60582927	q22.2
SNP_A-2241544	T	T	325	9	344	22	4.538	0.0332	rs16908791	8	82292397	q21.13
SNP_A-2228802	A	A	283	123	253	151	4.536	0.0332	rs273442	9	79120270	q21.31
SNP_A-2267687	A	A	330	90	354	66	4.534	0.0332	rs974529	2	137704261	q22.1
SNP_A-2279489	T	T	354	4	404	0	4.538	0.0332	rs11249921	8	9350993	p23.1
SNP_A-2275918	A	A	272	76	284	114	4.528	3.33E-02	rs9537612	13	56576854	q21.1
SNP_A-2268195	C	C	230	140	224	186	4.531	3.33E-02	rs7451257	6	66051700	q12
SNP_A-2269377	C	C	360	0	395	5	4.53	3.33E-02	rs2843124	6	63410822	q11.2
SNP_A-2258691	T	T	231	113	220	150	4.533	3.33E-02	rs2148014	6	67333511	q12
SNP_A-2229478	G	C	209	187	218	180	4.53	3.33E-02	rs4297045	8	9844234	p23.1
SNP_A-2307312	G	G	294	32	288	52	4.531	3.33E-02	rs7965555	12	87215059	q21.32
SNP_A-2304721	G	G	199	171	255	161	4.532	3.33E-02	rs10416843	19	8061859	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2302266	A	A	344	6	413	1	4.531	3.33E-02	rs7070997	10	21961081	p12.31
SNP_A-2102417	T	T	296	64	344	48	4.532	3.33E-02	rs6869605	5	150433059	q33.1
SNP_A-2095286	A	A	281	89	340	74	4.531	3.33E-02	rs475521	3	102504931	q12.3
SNP_A-2098202	T	T	348	4	353	13	4.529	3.33E-02	rs16908513	11	10875663	p15.3
SNP_A-2079608	C	C	210	88	215	129	4.533	3.33E-02	rs11932810	4	7332768	p16.1
SNP_A-2052912	A	A	314	56	327	87	4.529	3.33E-02	rs11126652	2	78218562	p12
SNP_A-2024508	C	C	339	83	304	106	4.532	3.33E-02	rs11872630	18	29295670	q12.1
SNP_A-2019743	T	T	263	101	317	85	4.53	3.33E-02	rs4818135	21	40753107	q22.2
SNP_A-2176898	T	T	358	4	408	0	4.532	3.33E-02	rs11015858	10	27866241	p12.1
SNP_A-2197900	A	A	260	94	253	129	4.53	3.33E-02	rs17244381	2	123771767	q14.3
SNP_A-2203756	A	A	353	15	384	32	4.531	3.33E-02	rs259024	5	79756542	q14.1
SNP_A-2130987	G	G	334	6	401	1	4.53	3.33E-02	rs293118	5	4692122	p15.32
SNP_A-2126774	T	T	259	101	299	81	4.528	3.33E-02	rs1027939	2	214628092	q34
SNP_A-1804622	C	C	333	11	366	26	4.528	3.33E-02	rs17079417	18	64418140	q22.1
SNP_A-1715497	A	A	360	4	410	0	4.529	3.33E-02	rs9325181	12	64951809	q14.3
SNP_A-1746563	A	A	395	3	393	11	4.532	3.33E-02	rs1347133	5	142162607	q31.3
SNP_A-1844177	C	C	304	20	371	11	4.529	3.33E-02	rs329311	5	133928010	q31.1
SNP_A-1839181	T	T	360	4	410	0	4.529	3.33E-02	rs4989560	1	194180930	q31.3
SNP_A-1840192	A	A	358	4	408	0	4.532	3.33E-02	rs17160546	7	85284715	q21.11
SNP_A-1847559	G	G	325	33	357	59	4.528	3.33E-02	rs6673013	1	191193156	q31.3
SNP_A-1959746	C	C	295	27	380	18	4.532	3.33E-02	rs276699	6	76512768	q14.1
SNP_A-1946548	C	C	358	4	408	0	4.532	3.33E-02	rs1584221	8	117997022	q24.11
SNP_A-1935336	T	C	184	166	223	181	4.533	3.33E-02	rs604711	6	11706267	p24.1
SNP_A-1935212	T	T	367	53	384	34	4.529	3.33E-02	rs4778807	15	78616570	q25.1
SNP_A-1966395	G	G	358	4	408	0	4.532	3.33E-02	rs2272405	2	197123486	q32.3
SNP_A-1880064	C	C	378	28	366	46	4.528	3.33E-02	rs2592295	12	116748624	q24.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1888609	C	C	360	4	410	0	4.529	3.33E-02	rs7076514	10	1653712	p15.3
SNP_A-1889130	G	A	217	193	214	178	4.532	3.33E-02	rs695271	22	32327285	q12.3
SNP_A-1895942	C	C	302	52	365	39	4.529	3.33E-02	rs11101580	10	134845613	q26.3
SNP_A-1905742	A	A	280	72	247	93	4.532	3.33E-02	rs11059715	12	127496584	q24.32
SNP_A-1922048	G	G	358	4	408	0	4.532	3.33E-02	rs10749177	10	117394381	q25.3
SNP_A-1930868	T	T	256	106	246	142	4.529	3.33E-02	rs9921579	16	28151838	p11.2
SNP_A-1910485	C	C	329	13	359	29	4.523	3.34E-02	rs12471006	2	196208335	q32.3
SNP_A-1912854	A	A	364	4	414	0	4.523	3.34E-02	rs7925246	11	22209477	p14.3
SNP_A-1900954	T	T	364	4	414	0	4.523	3.34E-02	rs17046858	4	166888365	q32.3
SNP_A-1880216	A	A	264	154	293	125	4.524	3.34E-02	rs7693881	4	122542355	q27
SNP_A-1878713	C	C	366	52	344	74	4.523	3.34E-02	rs11743128	5	149104298	q32
SNP_A-1966449	T	T	256	114	313	99	4.524	3.34E-02	rs10497836	2	200114224	q33.1
SNP_A-1973871	A	A	316	102	280	126	4.527	3.34E-02	rs1164067	3	110948709	q13.13
SNP_A-1969831	A	A	383	31	356	48	4.523	3.34E-02	rs2832049	21	29051148	q21.3
SNP_A-1985715	G	G	364	4	414	0	4.523	3.34E-02	rs10484930	6	38383454	p21.2
SNP_A-1989344	A	A	346	4	394	0	4.527	3.34E-02	rs10486595	7	28642059	p15.1
SNP_A-1989311	A	A	252	88	239	119	4.526	3.34E-02	rs10486549	7	27446135	p15.2
SNP_A-1986402	T	T	362	4	412	0	4.526	3.34E-02	rs1410672	6	72534676	q13
SNP_A-1978517	C	C	364	4	414	0	4.523	3.34E-02	rs159438	4	112342658	q25
SNP_A-1941169	T	T	287	49	274	72	4.527	3.34E-02	rs17374401	11	102560489	q22.3
SNP_A-1951155	C	C	307	109	336	84	4.527	3.34E-02	rs7941000	11	67221504	q13.2
SNP_A-1948271	G	G	268	102	272	144	4.524	3.34E-02	rs605636	18	11983138	p11.21
SNP_A-1846722	G	A	215	185	213	183	4.523	3.34E-02	rs2541390	2	217489526	q35
SNP_A-1852410	C	C	372	34	370	18	4.523	3.34E-02	rs9405429	6	8877889	p24.3
SNP_A-1854696	C	C	366	50	346	72	4.524	3.34E-02	---	2	36099153	p22.3
SNP_A-1827954	T	T	354	0	389	5	4.523	3.34E-02	rs17141406	6	5913241	p25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1825756	C	C	321	31	386	20	4.525	3.34E-02	rs11679513	2	85299844	p11.2
SNP_A-1716819	C	T	176	162	208	164	4.525	3.34E-02	rs2764617	13	31499347	q13.1
SNP_A-1645482	G	G	296	54	322	88	4.526	3.34E-02	rs389382	5	84718848	q14.3
SNP_A-1801871	G	G	294	80	288	112	4.527	3.34E-02	rs10783486	12	50649053	q13.13
SNP_A-1811485	C	C	318	46	379	33	4.526	3.34E-02	rs9372668	6	122230171	q22.31
SNP_A-2111952	A	G	201	193	225	173	4.526	3.34E-02	rs2717369	7	18820609	p21.1
SNP_A-2115512	T	T	246	138	223	171	4.524	3.34E-02	rs12698491	7	63814910	q11.21
SNP_A-2219028	T	T	257	161	285	131	4.524	3.34E-02	rs7689466	4	24774584	p15.2
SNP_A-2187520	A	A	263	83	318	68	4.524	3.34E-02	rs4244533	11	27965548	p14.1
SNP_A-2175501	C	C	238	108	239	151	4.527	3.34E-02	rs405086	5	13672952	p15.2
SNP_A-2181514	A	A	344	74	366	52	4.523	3.34E-02	rs7703260	5	141882084	q31.3
SNP_A-2020602	C	C	297	117	322	90	4.527	3.34E-02	rs2838873	21	45563781	q22.3
SNP_A-2033096	A	A	350	20	375	39	4.526	3.34E-02	rs327867	5	125245266	q23.2
SNP_A-2033721	T	T	264	82	319	67	4.526	3.34E-02	rs2203009	4	179694400	q34.3
SNP_A-2039152	A	A	288	56	299	87	4.525	3.34E-02	rs602761	18	61041723	q22.1
SNP_A-2047497	G	G	245	131	296	114	4.525	3.34E-02	rs12661091	6	122569516	q22.31
SNP_A-2042102	T	T	270	62	264	90	4.524	3.34E-02	rs1321678	1	86738305	p22.3
SNP_A-2041911	A	A	362	4	412	0	4.526	3.34E-02	rs16928693	12	25369492	p12.1
SNP_A-2013261	C	C	353	59	371	39	4.524	3.34E-02	rs6586846	8	19481847	p21.3
SNP_A-2016593	A	A	364	4	414	0	4.523	3.34E-02	rs2828306	21	23885777	q21.2
SNP_A-2012154	T	T	308	44	325	27	4.527	3.34E-02	rs4897028	6	149011085	q24.3
SNP_A-2004649	A	A	225	151	274	134	4.527	3.34E-02	rs4363867	16	25990397	p12.1
SNP_A-2047982	C	C	264	100	318	84	4.528	3.34E-02	rs7315570	12	26953037	p11.23
SNP_A-2076678	T	T	368	54	344	76	4.527	3.34E-02	rs17541277	9	89766300	q22.2
SNP_A-2066983	C	C	351	67	358	44	4.524	3.34E-02	rs9643188	8	125157817	q24.13
SNP_A-2068124	T	T	341	11	359	25	4.525	3.34E-02	rs7342995	18	62991705	q22.1
SNP_A-2069688	C	C	232	126	229	171	4.524	3.34E-02	rs13410843	2	181991927	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2069432	C	C	323	43	338	70	4.526	3.34E-02	rs1377940	4	184436770	q35.1
SNP_A-2077276	G	G	384	6	353	15	4.526	3.34E-02	rs183858	1	112390602	p13.2
SNP_A-2082885	A	A	265	99	319	83	4.526	3.34E-02	rs4643103	11	81855194	q14.1
SNP_A-2238018	C	C	279	137	307	109	4.525	3.34E-02	rs6589973	11	122568575	q24.1
SNP_A-2252826	A	A	346	4	394	0	4.527	3.34E-02	rs7310702	12	44535067	q12
SNP_A-2273855	G	G	342	8	398	2	4.525	3.34E-02	---	4	26187279	p15.2
SNP_A-2278818	G	G	345	11	410	4	4.52	3.35E-02	rs10519195	15	46950476	q21.1
SNP_A-2277958	G	G	273	23	344	14	4.522	3.35E-02	rs6775959	3	155977943	q25.2
SNP_A-2258920	A	A	298	44	319	73	4.518	3.35E-02	---	2	107366918	q12.3
SNP_A-2255098	C	C	240	98	261	149	4.522	3.35E-02	rs4810819	20	46622638	q13.13
SNP_A-2238636	A	A	222	144	280	132	4.519	3.35E-02	rs6760472	2	166996697	q24.3
SNP_A-2236137	T	T	331	23	369	45	4.521	3.35E-02	rs35628	16	16078607	p13.11
SNP_A-2308673	T	T	260	144	291	117	4.518	3.35E-02	rs4329950	17	11675071	p12
SNP_A-2104245	A	A	329	57	300	78	4.52	3.35E-02	rs1878639	2	131473087	q21.1
SNP_A-2064622	C	C	338	6	405	1	4.519	3.35E-02	rs4237693	11	42296333	p12
SNP_A-2075542	G	A	203	185	221	179	4.518	3.35E-02	rs1370711	3	10422415	p25.3
SNP_A-2049857	A	A	280	136	253	167	4.52	3.35E-02	rs6736779	2	165490651	q24.3
SNP_A-2009303	T	T	370	0	407	5	4.519	3.35E-02	rs1392207	3	172817502	q26.31
SNP_A-2022559	C	C	261	85	316	70	4.522	3.35E-02	rs133252	22	24131558	q11.23
SNP_A-2175145	G	G	233	133	289	119	4.52	3.35E-02	rs6565143	16	81750763	q23.3
SNP_A-2188846	T	T	316	102	338	76	4.519	3.35E-02	rs8053692	16	82173002	q23.3
SNP_A-2195957	G	G	350	4	398	0	4.521	3.35E-02	rs17170119	5	135702105	q31.1
SNP_A-2195376	C	C	350	62	325	85	4.52	3.35E-02	rs1097329	1	23077456	p36.12
SNP_A-2213844	C	C	279	119	310	94	4.521	3.35E-02	rs3768539	1	154873646	q23.1
SNP_A-2216536	T	T	327	43	386	30	4.521	3.35E-02	rs17154458	10	14108506	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225712	C	C	266	74	329	61	4.519	3.35E-02	rs555420	4	171439977	q33
SNP_A-2131213	A	A	213	147	207	195	4.521	3.35E-02	rs7963463	12	82621578	q21.31
SNP_A-2161545	A	A	237	175	268	146	4.518	3.35E-02	rs9409980	9	134656619	q34.2
SNP_A-2163396	A	A	352	4	400	0	4.518	3.35E-02	rs8068706	17	69907679	q25.1
SNP_A-1791447	T	T	366	2	404	10	4.518	3.35E-02	rs4349595	4	82874515	q21.22
SNP_A-1786528	C	C	329	17	380	8	4.52	3.35E-02	rs17171378	5	136737893	q31.1
SNP_A-1728369	A	A	253	95	322	84	4.521	3.35E-02	rs908439	2	78618636	p12
SNP_A-1729380	T	T	336	20	370	40	4.52	3.35E-02	rs10499211	6	139968882	q24.1
SNP_A-1825032	A	A	338	6	405	1	4.519	3.35E-02	rs11989770	8	82171015	q21.13
SNP_A-1819832	G	G	233	133	289	119	4.52	3.35E-02	rs3827908	14	20521583	q11.2
SNP_A-1843242	A	A	341	27	398	16	4.52	3.35E-02	rs4144545	13	93183362	q31.3
SNP_A-1833101	T	T	271	141	285	107	4.519	3.35E-02	rs13033107	2	33031034	p22.3
SNP_A-1831919	G	G	353	47	342	70	4.519	3.35E-02	rs6752351	2	106189451	q12.2
SNP_A-1847360	A	A	304	66	316	100	4.519	3.35E-02	rs312352	4	18938773	p15.31
SNP_A-1845249	G	G	341	27	398	16	4.52	3.35E-02	rs3861787	11	4604346	p15.4
SNP_A-1863407	T	T	269	93	334	80	4.519	3.35E-02	rs6561906	13	56463195	q21.1
SNP_A-1866344	G	G	265	123	299	99	4.518	3.35E-02	rs13026197	2	23200589	p24.1
SNP_A-1957888	T	T	313	47	374	34	4.52	3.35E-02	rs12886796	14	70371309	q24.2
SNP_A-1956039	A	A	274	92	336	78	4.518	3.35E-02	rs4143531	5	154958388	q33.2
SNP_A-1947083	C	C	272	96	334	82	4.523	3.35E-02	rs1341162	10	96800602	q23.33
SNP_A-1944188	G	G	293	117	254	140	4.522	3.35E-02	rs2860195	1	192671486	q31.3
SNP_A-1879782	G	G	366	4	416	0	4.52	3.35E-02	rs7846141	8	92789005	q21.3
SNP_A-1901737	A	A	251	105	258	150	4.519	3.35E-02	rs130021	16	3772472	p13.3
SNP_A-1917570	T	T	371	17	340	30	4.522	3.35E-02	rs16998424	20	51843411	q13.2
SNP_A-1931267	C	C	356	8	414	2	4.522	3.35E-02	rs12617281	2	142625645	q22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1929000	A	A	280	34	330	22	4.516	3.36E-02	rs1351887	18	66105008	q22.2
SNP_A-1928624	G	G	340	4	386	0	4.513	3.36E-02	rs10070252	5	55971172	q11.2
SNP_A-1918049	A	A	413	7	417	1	4.515	3.36E-02	rs17044722	2	53581234	p16.2
SNP_A-1905526	G	G	259	105	261	147	4.515	3.36E-02	rs1861586	12	106416608	q23.3
SNP_A-1876115	G	G	174	166	221	153	4.513	3.36E-02	rs661254	6	128081659	q22.33
SNP_A-1946356	C	C	235	139	203	165	4.513	3.36E-02	rs7608798	2	162715724	q24.2
SNP_A-1943205	T	T	356	4	404	0	4.513	3.36E-02	rs17112899	1	56022873	p32.2
SNP_A-1953489	T	T	320	40	362	26	4.514	3.36E-02	rs2634499	8	59828143	q12.1
SNP_A-1979607	G	G	338	8	371	21	4.514	3.36E-02	rs2348622	4	161045673	q32.1
SNP_A-1862467	A	A	306	62	319	95	4.516	3.36E-02	rs9470187	6	36058188	p21.31
SNP_A-1859868	C	C	329	17	346	34	4.512	3.36E-02	rs6058391	20	29743569	q11.21
SNP_A-1833456	T	T	413	7	417	1	4.515	3.36E-02	rs6749308	2	133396577	q21.2
SNP_A-1686016	G	G	224	126	292	118	4.515	3.36E-02	rs7762044	6	116348416	q22.1
SNP_A-1792821	C	C	405	7	409	1	4.515	3.36E-02	rs6797019	3	143032078	q23
SNP_A-1812847	G	G	354	4	402	0	4.515	3.36E-02	rs4483233	9	119566660	q33.1
SNP_A-1810965	G	G	403	7	407	1	4.515	3.36E-02	rs6422428	19	8132029	p13.2
SNP_A-1803526	C	C	394	16	380	30	4.514	3.36E-02	rs1567152	16	49636661	q12.1
SNP_A-2159599	C	C	405	1	401	7	4.515	3.36E-02	rs6092259	20	54182998	q13.31
SNP_A-2145692	G	G	356	8	391	21	4.516	3.36E-02	rs1333418	13	80517276	q31.1
SNP_A-2144596	G	G	276	68	287	103	4.514	3.36E-02	rs7216065	17	50115910	q22
SNP_A-2125169	T	T	314	46	338	76	4.515	3.36E-02	rs11140508	9	84156446	q21.33
SNP_A-2115502	T	T	283	65	304	102	4.514	3.36E-02	rs17124739	11	120429881	q23.3
SNP_A-2114538	T	T	354	40	329	59	4.516	3.36E-02	rs1859459	7	77347731	q21.11
SNP_A-2110875	C	C	344	22	402	12	4.514	3.36E-02	rs9995329	4	188407356	q35.2
SNP_A-2111410	T	T	401	1	397	7	4.515	3.36E-02	rs10447230	5	147675023	q32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2121154	C	C	387	9	394	2	4.517	3.36E-02	rs1694446	1	193509374	q31.3
SNP_A-2220218	C	C	415	1	411	7	4.515	3.36E-02	rs4626588	8	34652456	p12
SNP_A-2217018	A	A	283	115	251	141	4.513	3.36E-02	rs2045505	14	52036904	q22.1
SNP_A-2210482	C	C	305	57	356	42	4.513	3.36E-02	rs6460839	7	11559694	p21.3
SNP_A-2169526	C	C	370	4	420	0	4.515	3.36E-02	rs17005394	2	121393902	q14.2
SNP_A-2042123	A	A	248	158	265	123	4.517	3.36E-02	rs11576493	1	183989376	q31.1
SNP_A-2039932	C	C	307	55	325	87	4.513	3.36E-02	rs12213597	6	119375828	q22.31
SNP_A-1991913	C	C	327	93	348	68	4.516	3.36E-02	rs10503198	8	3013985	p23.2
SNP_A-1996971	C	C	411	9	418	2	4.514	3.36E-02	rs2082711	9	80338985	q21.31
SNP_A-1994902	G	G	387	29	364	46	4.514	3.36E-02	rs10505385	8	122051212	q24.12
SNP_A-2051550	A	A	354	4	402	0	4.515	3.36E-02	rs16823434	2	177195768	q31.1
SNP_A-2054846	A	A	364	2	402	10	4.514	3.36E-02	rs10006326	4	110538268	q25
SNP_A-2096386	G	G	222	142	284	132	4.515	3.36E-02	rs1027176	3	177932558	q26.32
SNP_A-2093801	C	C	416	2	409	9	4.514	3.36E-02	rs176468	7	105314365	q22.3
SNP_A-2091499	G	G	393	7	397	1	4.515	3.36E-02	---	2	151926488	q23.3
SNP_A-2086383	A	A	330	80	300	104	4.515	3.36E-02	rs604799	11	78190756	q14.1
SNP_A-2087551	A	A	387	7	391	1	4.516	3.36E-02	rs16883169	8	34853576	p12
SNP_A-2310839	G	G	207	151	241	127	4.515	3.36E-02	rs2748484	6	146375346	q24.3
SNP_A-2292241	G	G	247	107	302	92	4.515	3.36E-02	rs1500922	3	158535309	q25.32
SNP_A-2297718	A	A	359	59	377	39	4.517	3.36E-02	rs1863361	8	41488941	p11.21
SNP_A-2235550	C	C	318	100	343	75	4.517	3.36E-02	rs17713362	7	66604750	q11.22
SNP_A-2234192	C	C	403	9	410	2	4.515	3.36E-02	rs6137010	20	2038118	p13
SNP_A-2252396	C	C	222	148	215	195	4.513	3.36E-02	rs6505524	17	23221896	q11.2
SNP_A-2251659	T	T	413	7	417	1	4.515	3.36E-02	rs16873636	6	13261749	p24.1
SNP_A-2249607	T	T	382	24	342	38	4.516	3.36E-02	rs7541200	1	178059134	q25.3
SNP_A-2249018	C	C	255	75	316	62	4.517	3.36E-02	rs16909256	9	113614880	q32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246592	C	C	354	4	402	0	4.515	3.36E-02	rs6093910	20	42057434	q13.12
SNP_A-2235144	A	A	218	142	216	192	4.512	3.37E-02	rs10198266	2	227157204	q36.3
SNP_A-2280382	G	G	379	35	346	52	4.51	3.37E-02	rs12476852	2	234639174	q37.1
SNP_A-2306369	C	C	339	55	367	37	4.508	3.37E-02	rs2288013	16	56885243	q21
SNP_A-2303387	G	G	343	27	400	16	4.51	3.37E-02	rs10477467	5	110949248	q22.1
SNP_A-2088791	T	T	364	0	401	5	4.512	3.37E-02	rs8070569	17	12243754	p12
SNP_A-2081967	G	A	183	167	223	179	4.511	3.37E-02	rs4622543	17	61940872	q24.2
SNP_A-2050758	A	A	211	149	209	201	4.507	3.37E-02	rs4345596	8	136907982	q24.23
SNP_A-1996759	G	G	263	53	265	81	4.508	3.37E-02	rs12347831	9	70825563	q21.12
SNP_A-1995539	C	C	328	28	332	48	4.51	3.37E-02	rs10810324	9	1500848	p24.3
SNP_A-2038235	T	T	215	145	205	189	4.511	3.37E-02	rs12922654	16	59659261	q21
SNP_A-2028876	C	C	348	22	374	42	4.51	3.37E-02	rs1836841	11	131281509	q25
SNP_A-2026931	A	A	332	10	371	3	4.512	3.37E-02	rs7627798	3	164453808	q26.1
SNP_A-2178918	C	C	293	67	300	100	4.511	3.37E-02	rs2964677	5	116136300	q23.1
SNP_A-2184693	T	T	330	40	385	27	4.51	3.37E-02	rs1153014	7	62717701	q11.21
SNP_A-2211677	C	C	345	73	314	96	4.512	3.37E-02	---	7	55098046	p11.2
SNP_A-2211113	G	G	343	51	318	72	4.511	3.37E-02	rs266089	10	44189433	q11.21
SNP_A-2119951	G	G	358	4	406	0	4.51	3.37E-02	rs3828503	4	69977000	q13.2
SNP_A-1808798	A	A	259	101	267	145	4.509	3.37E-02	rs6797951	3	192403134	q28
SNP_A-1694711	C	T	226	176	212	202	4.511	3.37E-02	rs1035025	2	37923695	p22.2
SNP_A-1664974	A	A	317	69	310	98	4.508	3.37E-02	rs1504418	13	59257645	q21.2
SNP_A-1758296	C	C	350	16	362	32	4.51	3.37E-02	rs1182524	20	59065929	q13.33
SNP_A-1820957	T	T	329	61	349	41	4.512	3.37E-02	rs4952450	2	41405095	p22.1
SNP_A-1820789	G	G	337	19	404	10	4.508	3.37E-02	rs2333006	14	72427007	q24.2
SNP_A-1824841	T	T	366	50	341	71	4.509	3.37E-02	rs12444921	16	55060917	q12.2
SNP_A-1848653	G	G	342	26	395	15	4.508	3.37E-02	rs11784668	8	4134250	p23.2
SNP_A-1859718	T	T	246	174	209	199	4.511	3.37E-02	rs12491882	3	122812062	q13.33
SNP_A-1968656	C	C	358	4	406	0	4.51	3.37E-02	rs10485448	20	51353112	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889114	C	T	188	162	211	179	4.509	3.37E-02	rs12032866	1	216532555	q41
SNP_A-1897619	C	C	184	160	246	156	4.508	3.37E-02	rs373204	8	8808812	p23.1
SNP_A-1896147	T	T	245	111	247	155	4.511	3.37E-02	rs174436	12	32353939	p11.21
SNP_A-1918730	T	T	353	31	371	17	4.51	3.37E-02	rs11210796	1	43297069	p34.2
SNP_A-1920517	A	A	339	1	388	8	4.512	3.37E-02	rs154885	18	57012861	q21.32
SNP_A-1932093	C	C	352	70	326	94	4.505	3.38E-02	rs7252788	19	9204855	p13.2
SNP_A-1895319	G	G	316	106	284	132	4.504	3.38E-02	rs7206906	16	60732569	q21
SNP_A-1964101	T	T	346	22	404	12	4.505	3.38E-02	rs2364895	2	84499506	p11.2
SNP_A-1969882	A	A	218	138	241	109	4.507	3.38E-02	rs2186305	21	29838145	q21.3
SNP_A-1981668	A	A	314	20	317	37	4.507	3.38E-02	rs1017226	5	56189149	q11.2
SNP_A-1950172	G	G	343	27	367	49	4.503	3.38E-02	rs1358892	6	7778825	p24.3
SNP_A-1848742	T	T	362	4	410	0	4.504	3.38E-02	rs17067463	3	62941741	p14.2
SNP_A-1828072	G	G	345	21	397	11	4.503	3.38E-02	rs896993	11	81470868	q14.1
SNP_A-1817493	T	T	336	8	390	2	4.505	3.38E-02	rs16899303	5	81238902	q14.1
SNP_A-1757844	G	G	218	132	223	185	4.506	3.38E-02	rs1590380	13	72151955	q22.1
SNP_A-1785648	C	C	373	37	398	22	4.504	3.38E-02	rs11601884	11	44332520	p11.2
SNP_A-1785368	A	A	318	100	285	125	4.507	3.38E-02	rs11644135	16	6488428	p13.2
SNP_A-2108786	A	A	234	128	290	114	4.505	3.38E-02	rs10004744	4	83282595	q21.22
SNP_A-2142917	G	G	255	95	260	136	4.506	3.38E-02	rs7110726	11	29471258	p14.1
SNP_A-2152775	G	G	249	115	253	161	4.504	3.38E-02	rs11164835	1	93091114	p22.1
SNP_A-2226510	G	G	215	195	244	164	4.504	3.38E-02	rs6861510	5	134606540	q31.1
SNP_A-2224193	C	C	315	47	376	34	4.504	3.38E-02	rs8079641	17	75827015	q25.3
SNP_A-2186879	G	G	360	4	408	0	4.507	3.38E-02	rs4880913	10	1729001	p15.3
SNP_A-2191971	A	A	288	64	353	51	4.505	3.38E-02	rs6539663	12	75643907	q21.2
SNP_A-2174590	C	C	362	4	410	0	4.504	3.38E-02	rs9366956	6	38425163	p21.2
SNP_A-2026008	T	T	307	13	335	29	4.505	3.38E-02	rs7554031	1	207564121	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044863	G	G	322	8	374	2	4.507	3.38E-02	rs6571117	6	96749723	q16.1
SNP_A-2004656	T	T	336	24	379	13	4.503	3.38E-02	rs763584	16	26669722	p12.1
SNP_A-2003860	T	T	265	97	322	82	4.503	3.38E-02	rs699208	10	91962828	q23.31
SNP_A-2054480	C	T	172	154	211	171	4.503	3.38E-02	rs632113	10	96894047	q23.33
SNP_A-2061830	T	T	275	91	284	132	4.505	3.38E-02	rs10029931	4	145655223	q31.21
SNP_A-2055988	A	A	283	99	306	74	4.506	3.38E-02	rs1884984	1	34029323	p35.1
SNP_A-2068880	A	A	259	107	319	93	4.504	3.38E-02	rs6462354	7	32139723	p14.3
SNP_A-2096800	G	G	344	6	411	1	4.502	3.38E-02	rs11567719	5	35900181	p13.2
SNP_A-2296648	T	T	337	47	371	31	4.505	3.38E-02	rs2902951	15	77701933	q25.1
SNP_A-2298903	T	T	310	112	333	85	4.504	3.38E-02	rs241937	19	43002500	q13.13
SNP_A-2292856	A	A	275	91	329	75	4.506	3.38E-02	rs10754933	2	128557247	q14.3
SNP_A-2280888	A	A	246	46	240	70	4.505	3.38E-02	rs17234643	5	78619980	q14.1
SNP_A-2286102	A	A	285	131	252	158	4.507	3.38E-02	rs956563	15	24947621	q12
SNP_A-2275888	C	C	231	191	259	159	4.507	3.38E-02	rs4782541	16	82099727	q23.3
SNP_A-2269213	C	C	282	136	307	107	4.503	3.38E-02	rs1027005	3	132686571	q21.3
SNP_A-2234644	A	A	320	16	319	31	4.505	3.38E-02	rs927696	13	78769086	q31.1
SNP_A-2245578	G	G	350	8	406	2	4.504	3.38E-02	rs6731421	2	231005389	q37.1
SNP_A-2255855	C	C	343	27	367	49	4.503	3.38E-02	rs7118516	11	77057882	q13.5
SNP_A-2249185	C	T	188	182	235	179	4.502	0.0339	rs8000903	13	43858248	q14.11
SNP_A-2248333	G	G	340	4	376	14	4.5	0.0339	rs16901627	8	127736303	q24.21
SNP_A-2230680	G	G	293	43	306	70	4.5	0.0339	rs17284501	18	64227099	q22.1
SNP_A-2260718	T	T	340	2	376	10	4.5	0.0339	rs12281818	11	22511198	p14.3
SNP_A-2257168	T	T	195	81	201	121	4.5	0.0339	rs2866798	4	106832647	q24
SNP_A-2263453	G	G	381	17	363	31	4.499	0.0339	rs7530478	1	22874022	p36.12
SNP_A-2314661	T	T	333	21	372	42	4.497	0.0339	rs16989035	20	38478418	q12
SNP_A-2091346	G	G	407	5	392	14	4.501	0.0339	rs17718077	7	41254827	p14.1
SNP_A-2054081	G	G	364	4	412	0	4.501	0.0339	rs16958204	17	9208010	p13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2047794	A	A	306	60	366	46	4.502	0.0339	rs9994137	4	45764276	p13
SNP_A-2004805	C	C	384	34	360	52	4.498	0.0339	rs4917434	10	106698287	q25.1
SNP_A-2009229	C	C	304	58	318	90	4.502	0.0339	rs6806340	3	153110686	q25.1
SNP_A-2040990	G	G	348	4	394	0	4.501	0.0339	---	6	86942136	q14.3
SNP_A-2034844	G	G	203	153	262	144	4.497	0.0339	rs7202282	16	50340790	q12.1
SNP_A-2155070	G	G	243	99	247	141	4.502	0.0339	rs10419865	19	10633685	p13.2
SNP_A-2164852	C	C	367	3	404	12	4.499	0.0339	rs4919008	10	98138547	q24.1
SNP_A-2142783	G	G	336	0	371	5	4.5	0.0339	---	13	58443463	q21.1
SNP_A-2111365	G	G	246	124	304	110	4.499	0.0339	rs9883677	3	152293243	q25.1
SNP_A-2116220	A	A	258	112	312	96	4.501	0.0339	rs10423632	19	58325362	q13.42
SNP_A-2133971	A	A	364	4	412	0	4.501	0.0339	rs10965033	9	21481983	p21.3
SNP_A-2135149	C	C	391	21	381	37	4.5	0.0339	rs2099068	5	24493487	p14.2
SNP_A-1789930	T	T	286	128	257	157	4.5	0.0339	rs11770376	7	150956776	q36.1
SNP_A-1792957	A	A	317	43	374	30	4.498	0.0339	rs3134190	8	96669266	q22.1
SNP_A-1810562	A	A	246	122	304	108	4.501	0.0339	rs2843167	1	205901292	q32.2
SNP_A-1811136	G	C	180	142	183	167	4.5	0.0339	rs4749527	10	30409729	p11.23
SNP_A-1800336	A	A	262	98	268	140	4.497	0.0339	rs2990997	1	186851360	q31.1
SNP_A-1806348	C	C	250	112	252	156	4.5	0.0339	rs1105783	9	36307937	p13.2
SNP_A-1688828	C	C	385	17	403	7	4.499	0.0339	rs4075106	12	7441453	p13.31
SNP_A-1825090	G	G	308	60	320	92	4.498	0.0339	rs10860187	12	96231468	q23.1
SNP_A-1839747	A	A	249	141	220	170	4.497	0.0339	rs6918437	6	150589079	q25.1
SNP_A-1866509	T	T	314	102	288	130	4.497	0.0339	rs2744574	6	24601858	p22.2
SNP_A-1957234	A	G	189	169	225	185	4.502	0.0339	rs12331318	4	91127433	q22.1
SNP_A-1947676	A	A	370	0	409	5	4.497	0.0339	rs16947436	13	91786847	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1980296	C	C	366	4	414	0	4.499	0.0339	rs1358451	1	199138365	q32.1
SNP_A-1977538	T	T	344	26	397	15	4.499	0.0339	rs10518083	4	72313339	q13.3
SNP_A-1973488	C	C	366	4	414	0	4.499	0.0339	rs17024547	3	86179581	p12.1
SNP_A-1965654	C	C	367	3	404	12	4.499	0.0339	rs16848859	2	164405506	q24.3
SNP_A-1922759	C	C	345	25	368	46	4.498	0.0339	rs12321936	12	107229013	q23.3
SNP_A-1906272	C	C	370	0	409	5	4.497	0.0339	rs753418	13	111888787	q34
SNP_A-1899124	T	T	253	145	226	176	4.496	3.40E-02	rs2665322	16	84918772	q24.1
SNP_A-1882038	T	T	352	4	398	0	4.496	3.40E-02	rs8054280	16	72613065	q22.3
SNP_A-1879672	C	C	311	57	327	89	4.493	3.40E-02	rs4685334	3	16423594	p24.3
SNP_A-1969468	G	G	354	8	410	2	4.493	3.40E-02	rs2032205	21	23415399	q21.2
SNP_A-1971822	A	A	300	66	312	100	4.495	3.40E-02	rs3731124	3	14176404	p25.1
SNP_A-1941089	T	T	354	12	381	27	4.495	3.40E-02	rs7582905	2	153121718	q23.3
SNP_A-1955182	G	G	294	64	311	99	4.493	3.40E-02	rs11643521	16	75697639	q23.1
SNP_A-1959076	T	T	222	116	283	105	4.494	3.40E-02	rs6907703	6	77235069	q14.1
SNP_A-1953647	C	C	368	0	407	5	4.495	3.40E-02	rs6795076	3	79172088	p12.3
SNP_A-1848471	A	A	270	64	343	53	4.494	3.40E-02	rs7241937	18	6094283	p11.31
SNP_A-1855702	T	C	209	157	210	206	4.497	3.40E-02	rs10137112	14	45525836	q21.2
SNP_A-1837672	A	A	311	57	327	89	4.493	3.40E-02	rs11153778	6	119266115	q22.31
SNP_A-1662208	T	T	384	14	382	28	4.495	3.40E-02	rs10489670	1	154750798	q23.1
SNP_A-2142138	G	G	368	0	407	5	4.495	3.40E-02	rs11914905	3	160560293	q25.33
SNP_A-2153595	A	A	370	4	377	13	4.497	3.40E-02	rs1838505	15	56489057	q21.3
SNP_A-2159124	G	G	311	47	277	65	4.495	3.40E-02	rs17055998	5	157997922	q33.3
SNP_A-2218072	C	C	366	26	342	42	4.496	3.40E-02	rs4912087	1	19009089	p36.13
SNP_A-2043589	G	G	251	103	248	142	4.495	3.40E-02	rs2404061	11	25333379	p14.3
SNP_A-2027493	A	A	222	44	302	36	4.495	3.40E-02	rs4468382	12	58776632	q14.1
SNP_A-2086595	G	G	212	150	211	203	4.496	3.40E-02	rs9403208	6	100461656	q16.3
SNP_A-2082361	G	G	332	18	301	31	4.495	3.40E-02	rs7816219	8	5175604	p23.2
SNP_A-2078691	A	A	317	5	354	16	4.494	3.40E-02	rs2864105	19	56722302	q13.41

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098451	T	T	207	149	260	136	4.493	3.40E-02	rs11077460	17	65261700	q24.3
SNP_A-2104036	G	G	325	31	390	20	4.497	3.40E-02	rs1453013	5	114312438	q22.3
SNP_A-2299214	A	A	288	76	350	62	4.493	3.40E-02	rs6905275	6	85372323	q14.3
SNP_A-2296402	C	C	313	53	322	82	4.493	3.40E-02	rs1806081	5	9254631	p15.31
SNP_A-2232946	G	G	365	3	402	12	4.495	3.40E-02	rs6734475	2	10400996	p25.1
SNP_A-2250252	G	G	388	28	390	14	4.497	3.40E-02	rs7651293	3	142258996	q23
SNP_A-2246802	C	C	228	138	228	188	4.49	3.41E-02	rs7896224	10	10513853	p14
SNP_A-2243199	A	A	411	9	394	20	4.488	3.41E-02	rs11238075	11	79461549	q14.1
SNP_A-2235249	T	T	275	51	332	38	4.488	3.41E-02	rs11158289	14	60102143	q23.1
SNP_A-2261601	C	C	327	73	347	51	4.492	3.41E-02	rs13134676	4	16230616	p15.32
SNP_A-2259293	T	T	256	166	220	192	4.492	3.41E-02	rs6690493	1	12069792	p36.22
SNP_A-2287499	C	T	200	164	216	194	4.489	3.41E-02	rs1935961	10	95773232	q23.33
SNP_A-2297232	C	C	392	20	409	9	4.49	3.41E-02	rs11186419	10	82395063	q22.3
SNP_A-2104596	A	A	288	54	349	41	4.492	3.41E-02	rs9848804	3	188902018	q27.3
SNP_A-2106774	G	G	325	93	341	67	4.489	3.41E-02	rs7225810	17	28829097	q12
SNP_A-2097810	A	A	238	120	297	107	4.49	3.41E-02	rs6539882	12	84032666	q21.31
SNP_A-2096433	T	T	240	152	263	121	4.49	3.41E-02	rs1895950	12	106778064	q23.3
SNP_A-2090916	G	G	342	6	363	17	4.488	3.41E-02	rs7739370	6	14959081	p23
SNP_A-2050481	A	A	265	35	265	57	4.488	3.41E-02	rs17068391	13	77306469	q22.3
SNP_A-2070034	A	A	343	71	317	95	4.489	3.41E-02	rs393441	1	41950966	p34.2
SNP_A-2021165	A	A	348	72	361	49	4.49	3.41E-02	rs11952005	5	162751813	q34
SNP_A-2035086	C	C	246	152	221	185	4.491	3.41E-02	rs1191109	14	99421578	q32.2
SNP_A-2016312	C	C	352	20	346	36	4.491	3.41E-02	rs17734233	21	21881047	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2018512	A	A	397	9	359	19	4.487	3.41E-02	rs9976946	21	35129932	q22.12
SNP_A-2005181	T	C	197	173	226	190	4.49	3.41E-02	rs8078826	17	44302434	q21.32
SNP_A-2226328	T	T	322	48	339	77	4.488	3.41E-02	rs10476596	5	93392830	q15
SNP_A-2208283	T	T	310	38	340	66	4.488	3.41E-02	rs7806636	7	15252807	p21.1
SNP_A-2175495	C	C	356	14	382	30	4.491	3.41E-02	rs7736793	5	115536340	q23.1
SNP_A-2192884	T	T	286	136	311	107	4.489	3.41E-02	rs378441	7	158483765	q36.3
SNP_A-2195748	G	G	343	25	366	46	4.49	3.41E-02	rs1500704	3	98310507	q11.2
SNP_A-2185237	G	G	374	26	385	13	4.488	3.41E-02	rs1690786	1	215116385	q41
SNP_A-2190537	G	G	240	84	310	74	4.489	3.41E-02	rs4720750	7	7478515	p21.3
SNP_A-2139952	A	A	281	81	338	66	4.49	3.41E-02	rs10973177	9	37045109	p13.2
SNP_A-1658350	G	G	271	81	282	120	4.49	3.41E-02	rs353738	8	57752736	q12.1
SNP_A-1781255	G	G	275	95	275	133	4.488	3.41E-02	rs10822196	10	65166355	q21.3
SNP_A-1727196	G	G	210	118	195	153	4.488	3.41E-02	rs1951887	14	54094984	q22.3
SNP_A-1806256	C	C	218	144	218	196	4.489	3.41E-02	rs1660038	3	125834114	q21.2
SNP_A-1822925	C	C	356	8	412	2	4.489	3.41E-02	rs286249	19	11788751	p13.2
SNP_A-1816381	C	C	279	143	248	172	4.489	3.41E-02	rs2971974	7	133101853	q33
SNP_A-1863520	A	A	322	48	339	77	4.488	3.41E-02	rs10877965	12	61814976	q14.2
SNP_A-1935767	T	T	307	59	324	92	4.491	3.41E-02	rs247743	5	76336552	q13.3
SNP_A-1964873	T	T	258	148	274	114	4.488	3.41E-02	rs4954299	2	132924576	q21.2
SNP_A-1916607	T	T	302	58	316	90	4.49	3.41E-02	rs7313736	12	76268136	q21.2
SNP_A-1914747	A	A	325	35	383	23	4.488	3.41E-02	rs1712391	15	40272182	q15.1
SNP_A-1926548	A	A	318	38	326	62	4.491	3.41E-02	rs12717393	14	48497095	q21.3
SNP_A-1922734	G	G	353	39	369	23	4.484	3.42E-02	rs12064516	1	205846545	q32.2
SNP_A-1979286	A	A	340	6	405	1	4.484	3.42E-02	rs17019825	4	146280735	q31.21
SNP_A-1985675	A	A	282	126	312	100	4.487	3.42E-02	rs4646949	6	34953427	p21.31
SNP_A-1985021	A	A	254	74	305	59	4.484	3.42E-02	rs3005179	6	8625282	p24.3
SNP_A-1983687	A	A	230	136	283	121	4.487	3.42E-02	rs160404	5	138112168	q31.2
SNP_A-1982905	T	T	265	49	295	83	4.484	3.42E-02	rs11466749	5	110440484	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936377	T	T	334	62	322	88	4.484	3.42E-02	rs17596474	2	59813142	p16.1
SNP_A-1939109	T	T	241	123	303	111	4.487	3.42E-02	rs2518160	6	102006832	q16.3
SNP_A-1862321	A	C	209	157	208	204	4.482	3.42E-02	rs9351124	6	88047827	q15
SNP_A-1869103	C	C	223	157	195	187	4.487	3.42E-02	rs509152	12	119649269	q24.31
SNP_A-1803603	T	T	367	11	319	21	4.485	3.42E-02	---	8	126826070	q24.13
SNP_A-1789727	G	G	282	22	302	42	4.483	3.42E-02	rs16916513	8	95182419	q22.1
SNP_A-1719519	C	C	271	131	307	107	4.487	3.42E-02	rs7481346	11	79742618	q14.1
SNP_A-2161417	T	T	301	41	293	63	4.483	3.42E-02	rs11176448	12	65527538	q14.3
SNP_A-2136008	T	T	328	10	339	23	4.485	3.42E-02	rs16896173	6	65817762	q12
SNP_A-2113288	A	A	239	131	298	118	4.484	3.42E-02	rs4411986	4	83276980	q21.22
SNP_A-2209091	C	C	282	126	312	100	4.487	3.42E-02	rs3790018	13	50520669	q14.3
SNP_A-2225878	C	C	391	7	393	1	4.485	3.42E-02	rs9680823	22	31115535	q12.3
SNP_A-2011792	A	A	346	42	331	63	4.487	3.42E-02	rs4712104	6	55427700	p12.1
SNP_A-2036777	T	T	355	15	334	28	4.483	3.42E-02	rs16908434	9	24518128	p21.3
SNP_A-2029465	G	G	266	78	329	65	4.485	3.42E-02	rs8094429	18	6821878	p11.31
SNP_A-2031362	C	C	312	52	331	83	4.485	3.42E-02	rs12453488	17	28921210	q12
SNP_A-2074365	T	T	272	86	282	126	4.483	3.42E-02	rs7273511	20	8446416	p12.3
SNP_A-2059535	C	C	312	24	344	46	4.484	3.42E-02	rs7134655	12	22130328	p12.1
SNP_A-2088558	G	G	409	7	411	1	4.486	3.42E-02	rs2060546	12	94717924	q23.1
SNP_A-2096460	T	T	360	4	406	0	4.485	3.42E-02	rs17115592	10	105035718	q24.33
SNP_A-2230153	T	T	363	7	393	19	4.486	3.42E-02	rs7863150	9	10670025	p23
SNP_A-2244175	G	G	413	9	418	2	4.48	3.43E-02	rs8097053	18	19835198	q11.2
SNP_A-2247989	G	G	365	41	387	25	4.479	3.43E-02	rs2039142	9	36953222	p13.2
SNP_A-2249589	G	G	337	71	355	49	4.482	3.43E-02	rs11257350	10	11914760	p14
SNP_A-2252756	G	G	203	145	257	133	4.481	3.43E-02	rs10017744	4	82626638	q21.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2279708	G	G	342	56	318	78	4.48	3.43E-02	rs2913339	5	5457299	p15.32
SNP_A-2267639	A	A	288	130	311	101	4.481	3.43E-02	rs4698560	4	16967665	p15.32
SNP_A-2311415	T	T	335	25	382	14	4.479	3.43E-02	rs4508405	16	7904819	p13.2
SNP_A-2100000	G	G	413	9	418	2	4.48	3.43E-02	rs16968252	17	28716561	q11.2
SNP_A-2085223	C	C	210	150	209	203	4.478	3.43E-02	rs489096	11	30198307	p14.1
SNP_A-2067283	G	G	321	29	380	18	4.478	3.43E-02	rs6763067	3	54011645	p21.1
SNP_A-2028981	C	C	231	131	284	116	4.481	3.43E-02	rs4901560	14	54958286	q22.3
SNP_A-2021635	G	G	235	127	298	116	4.48	3.43E-02	rs7048037	9	533590	p24.3
SNP_A-1990781	G	G	340	28	399	17	4.477	3.43E-02	rs10487146	7	104198559	q22.3
SNP_A-2210166	T	T	308	54	328	86	4.479	3.43E-02	rs7002036	8	61486646	q12.1
SNP_A-2121741	T	T	203	167	258	156	4.481	3.43E-02	rs10248931	7	93781053	q21.3
SNP_A-2133258	C	C	413	9	418	2	4.48	3.43E-02	rs9882574	3	56919059	p14.3
SNP_A-2132511	T	G	211	201	227	177	4.481	3.43E-02	rs2466615	11	123600857	q24.1
SNP_A-2132497	C	C	207	143	210	198	4.481	3.43E-02	rs9877037	3	96740990	q11.2
SNP_A-1752711	C	C	225	163	204	200	4.478	3.43E-02	rs590833	11	30205341	p14.1
SNP_A-1806938	G	G	286	84	291	121	4.479	3.43E-02	rs336441	8	624073	p23.3
SNP_A-1808872	T	T	239	131	291	115	4.482	3.43E-02	rs4580655	4	104886878	q24
SNP_A-1863734	C	C	260	74	326	62	4.479	3.43E-02	rs4976326	5	135092388	q31.1
SNP_A-1840670	G	G	252	146	210	166	4.479	3.43E-02	rs1217814	5	71423062	q13.2
SNP_A-1831569	A	A	364	50	384	32	4.481	3.43E-02	rs11563496	7	126343766	q32.1
SNP_A-1956295	G	G	340	28	399	17	4.477	3.43E-02	rs13321334	3	95983166	q11.2
SNP_A-1971726	A	A	357	41	366	24	4.477	3.43E-02	rs10510414	3	9691403	p25.3
SNP_A-1929655	T	T	391	9	396	2	4.481	3.43E-02	rs7787503	7	89526797	q21.13
SNP_A-1913021	T	T	299	63	248	78	4.479	3.43E-02	rs6531330	4	32858207	p15.1
SNP_A-1905442	G	G	413	9	418	2	4.48	3.43E-02	rs9825359	3	56919338	p14.3
SNP_A-1910567	G	G	405	9	410	2	4.48	3.43E-02	rs11264123	1	35391711	p34.3
SNP_A-1910415	T	T	305	85	338	64	4.473	0.0344	rs8139236	22	16887050	q11.21
SNP_A-1906882	G	G	234	114	228	154	4.474	0.0344	rs6470250	8	125640928	q24.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1916145	T	T	252	118	297	99	4.475	0.0344	rs1031257	6	127987287	q22.33
SNP_A-1930235	A	A	328	14	384	6	4.476	0.0344	rs6749165	2	237186340	q37.3
SNP_A-1881955	A	A	298	70	360	56	4.476	0.0344	rs3788421	22	28701556	q12.2
SNP_A-1888215	T	T	409	11	395	23	4.474	0.0344	rs7214155	17	72107997	q25.1
SNP_A-1975688	A	A	263	105	320	90	4.472	0.0344	rs9290916	3	191236759	q28
SNP_A-1961807	G	G	405	17	387	31	4.473	0.0344	rs719875	2	2625028	p25.3
SNP_A-1950432	G	G	368	0	409	5	4.473	0.0344	---	2	194016931	q32.3
SNP_A-1948433	T	T	267	89	319	73	4.472	0.0344	rs10863537	1	216790798	q41
SNP_A-1937712	T	T	366	4	412	0	4.477	0.0344	rs16851045	3	142275540	q23
SNP_A-1829151	A	A	344	12	386	28	4.473	0.0344	rs3113925	4	75735092	q13.3
SNP_A-1850615	C	C	344	56	356	36	4.473	0.0344	rs12441009	15	91554868	q26.1
SNP_A-1803371	A	A	352	4	396	0	4.473	0.0344	rs6450059	5	51723806	q11.2
SNP_A-1786860	G	G	210	140	206	188	4.476	0.0344	rs2617890	7	136972868	q33
SNP_A-2215176	C	C	352	0	391	5	4.474	0.0344	rs7521495	1	70008606	p31.1
SNP_A-2189795	T	T	344	6	409	1	4.473	0.0344	rs7668660	4	75010751	q13.3
SNP_A-2190072	G	G	304	26	351	15	4.474	0.0344	rs10039413	5	75555114	q13.3
SNP_A-2010891	G	G	294	62	359	49	4.474	0.0344	rs6450226	5	53946883	q11.2
SNP_A-2034031	T	T	239	101	301	89	4.473	0.0344	rs2141408	8	90991278	q21.3
SNP_A-2067022	A	A	369	41	391	25	4.472	0.0344	rs10966462	9	24778834	p21.3
SNP_A-2073929	T	T	367	55	343	77	4.473	0.0344	rs7234029	18	12867060	p11.21
SNP_A-2059082	C	C	319	47	380	34	4.473	0.0344	rs12110693	6	122199969	q22.31
SNP_A-2087564	G	G	330	30	393	19	4.477	0.0344	rs12679253	8	127654555	q24.21
SNP_A-2299222	A	A	274	128	304	102	4.477	0.0344	rs4645116	3	42262787	p22.1
SNP_A-2289959	A	G	212	194	222	180	4.477	0.0344	rs7826398	8	37167909	p12
SNP_A-2276443	G	G	386	24	377	41	4.475	0.0344	rs3218446	7	151799859	q36.1
SNP_A-2287281	G	G	395	23	409	11	4.474	0.0344	rs9988487	1	74118825	p31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2274953	G	G	284	76	295	113	4.47	3.45E-02	rs1456231	3	67102900	p14.1
SNP_A-2272941	A	A	242	134	283	113	4.472	3.45E-02	rs7463601	8	12634940	p23.1
SNP_A-2243151	A	A	302	62	301	91	4.467	3.45E-02	rs8051889	16	61661084	q21
SNP_A-2230628	A	A	310	60	363	45	4.471	3.45E-02	rs7971075	12	37352685	q12
SNP_A-2231060	G	G	321	53	336	34	4.471	3.45E-02	rs2239260	14	71804095	q24.2
SNP_A-2290664	C	C	394	16	367	29	4.472	3.45E-02	rs17506661	1	178909818	q25.3
SNP_A-2301097	C	C	351	57	335	81	4.47	3.45E-02	rs12362105	11	76128556	q13.5
SNP_A-2310189	G	G	214	144	270	132	4.469	3.45E-02	rs7666197	4	161707177	q32.1
SNP_A-2091719	A	A	305	57	370	44	4.468	3.45E-02	rs13028398	2	100899355	q11.2
SNP_A-2056550	C	C	333	29	358	52	4.468	3.45E-02	rs3740390	10	104628470	q24.32
SNP_A-2055643	G	G	261	89	266	128	4.47	3.45E-02	rs1598161	2	55587804	p16.1
SNP_A-2054200	A	A	373	19	360	34	4.471	3.45E-02	rs1806011	5	9287139	p15.31
SNP_A-2016863	A	A	338	28	351	49	4.472	3.45E-02	---	21	25171566	q21.2
SNP_A-2189383	A	A	287	23	312	44	4.47	3.45E-02	rs745523	2	31276693	p23.1
SNP_A-2108399	C	C	222	124	287	115	4.472	3.45E-02	rs7717392	5	117995416	q23.1
SNP_A-2158839	G	G	268	144	299	117	4.469	3.45E-02	rs11651712	17	14564931	p12
SNP_A-1785955	C	C	277	145	246	174	4.469	3.45E-02	rs9686131	5	132922095	q31.1
SNP_A-1789792	C	C	212	202	240	170	4.468	3.45E-02	rs10749454	10	124019644	q26.13
SNP_A-1797551	C	C	344	20	388	10	4.47	3.45E-02	rs7374994	3	65020296	p14.1
SNP_A-1782881	A	A	311	57	362	42	4.468	3.45E-02	rs4733373	8	32725125	p12
SNP_A-1667758	A	A	298	102	334	80	4.471	3.45E-02	rs2979498	8	30432919	p12
SNP_A-1656569	T	T	396	6	394	16	4.472	3.45E-02	rs10484788	6	56363882	p12.1
SNP_A-1707639	A	A	339	61	324	86	4.468	3.45E-02	rs3087875	8	18395494	p22
SNP_A-1851687	A	A	241	163	209	191	4.47	3.45E-02	rs256897	7	153006778	q36.2
SNP_A-1848620	A	A	259	71	291	115	4.47	3.45E-02	rs2018533	5	2304369	p15.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1849239	C	C	270	90	275	129	4.472	3.45E-02	rs605181	1	58748407	p32.1
SNP_A-1866823	G	G	392	16	394	6	4.472	3.45E-02	rs3850004	12	128335410	q24.33
SNP_A-1819243	A	A	372	28	344	44	4.469	3.45E-02	rs7866669	9	100043216	q31.1
SNP_A-1972001	C	C	416	0	370	4	4.472	3.45E-02	rs974546	3	21631643	p24.3
SNP_A-1968895	G	G	209	159	267	149	4.47	3.45E-02	rs2024676	20	58926954	q13.33
SNP_A-1979533	A	T	196	164	215	189	4.471	3.45E-02	rs1521696	4	157876701	q32.1
SNP_A-1931101	G	G	266	150	235	179	4.47	3.45E-02	rs10851440	15	44751538	q21.1
SNP_A-1931264	C	C	259	101	325	89	4.471	3.45E-02	rs312719	17	65796889	q24.3
SNP_A-1926026	C	C	322	78	346	56	4.469	3.45E-02	rs2548606	5	53857458	q11.2
SNP_A-1876844	A	C	193	173	226	186	4.465	3.46E-02	rs1859964	17	66678166	q24.3
SNP_A-1899197	T	T	375	45	383	27	4.465	3.46E-02	rs2909341	18	31204286	q12.2
SNP_A-1893672	T	T	376	40	351	59	4.463	3.46E-02	rs10781028	9	71398497	q21.13
SNP_A-1942131	G	G	234	118	236	164	4.466	3.46E-02	rs10954928	8	33693168	p12
SNP_A-1950207	G	A	193	173	226	186	4.465	3.46E-02	rs7966849	12	21895465	p12.1
SNP_A-1860476	C	C	358	8	395	21	4.467	3.46E-02	rs13403523	2	177269085	q31.1
SNP_A-1848101	T	T	210	134	209	183	4.465	3.46E-02	rs315198	5	143322201	q31.3
SNP_A-1668694	A	A	324	78	348	56	4.464	3.46E-02	rs10507011	12	90997987	q21.33
SNP_A-1745021	C	C	250	110	311	97	4.467	3.46E-02	rs492947	6	145531666	q24.3
SNP_A-1732632	C	C	319	71	301	97	4.466	3.46E-02	rs1241598	14	23354039	q12
SNP_A-1786313	C	C	348	16	336	30	4.466	3.46E-02	rs11999461	9	121801492	q33.2
SNP_A-1812130	C	C	234	122	239	171	4.463	3.46E-02	rs12194012	6	54817810	p12.1
SNP_A-2162371	C	C	265	151	295	123	4.464	3.46E-02	rs1820026	19	13484707	p13.13
SNP_A-2108008	C	C	301	91	272	116	4.467	3.46E-02	rs6701070	1	202033404	q32.1
SNP_A-2135040	G	G	304	62	364	48	4.467	3.46E-02	rs7737921	5	82916457	q14.3
SNP_A-2178437	T	T	360	4	400	14	4.466	3.46E-02	rs7355269	2	62211725	p15
SNP_A-2171429	A	A	360	4	404	0	4.463	3.46E-02	rs1035151	12	66575178	q15

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2224528	T	T	330	36	390	24	4.463	3.46E-02	rs9613359	22	25777350	q12.1
SNP_A-2226891	A	A	330	36	390	24	4.463	3.46E-02	rs17647031	3	117585435	q13.31
SNP_A-2208010	A	A	191	177	246	168	4.467	3.46E-02	rs13061773	3	74669712	p12.3
SNP_A-2037869	C	C	201	167	257	157	4.465	3.46E-02	rs629648	6	128060200	q22.33
SNP_A-2023517	T	T	201	167	257	157	4.465	3.46E-02	rs1430271	2	83289865	p12
SNP_A-2059113	T	T	253	165	281	135	4.463	3.46E-02	rs7907314	10	117986140	q25.3
SNP_A-2060482	C	C	334	46	320	68	4.462	3.46E-02	rs1937905	10	5120610	p15.1
SNP_A-2070971	C	C	354	66	373	45	4.465	3.46E-02	rs1421320	7	154801369	q36.3
SNP_A-2098982	T	T	263	157	292	128	4.466	3.46E-02	rs7029452	9	72436883	q21.13
SNP_A-2272832	G	G	281	139	309	111	4.465	3.46E-02	rs885637	12	12139547	p13.2
SNP_A-2279360	C	C	379	11	384	24	4.458	3.47E-02	rs4873777	8	49146803	q11.21
SNP_A-2300756	C	C	245	115	294	98	4.458	3.47E-02	rs571120	7	54339086	p11.2
SNP_A-2295289	T	T	203	161	258	150	4.458	3.47E-02	rs4923279	1	48385765	p33
SNP_A-2088992	G	G	346	4	388	0	4.458	3.47E-02	rs1721989	11	49868260	p11.12
SNP_A-2078770	C	C	361	5	377	15	4.46	3.47E-02	rs9822518	3	104112490	q12.3
SNP_A-2067575	C	C	334	24	398	14	4.462	3.47E-02	rs2471507	12	86962133	q21.32
SNP_A-2049096	C	C	347	65	350	42	4.462	3.47E-02	rs908013	4	6321139	p16.1
SNP_A-2007612	G	G	267	99	324	84	4.461	3.47E-02	rs6071887	20	38054870	q12
SNP_A-2226648	C	C	364	4	408	0	4.458	3.47E-02	rs1922552	12	80660561	q21.31
SNP_A-2213482	C	C	380	12	360	24	4.459	3.47E-02	rs8042998	15	68862809	q23
SNP_A-2219663	T	T	313	39	336	66	4.462	3.47E-02	rs1922182	2	122600824	q14.3
SNP_A-2176899	T	T	262	108	322	94	4.458	3.47E-02	rs774345	9	98216425	q22.33
SNP_A-2194589	T	T	377	39	393	23	4.461	3.47E-02	rs7251341	19	58307803	q13.42
SNP_A-2108959	A	A	367	53	335	73	4.46	3.47E-02	rs633461	11	123751431	q24.1
SNP_A-2114142	A	A	364	4	408	0	4.458	3.47E-02	rs16901052	5	83652291	q14.3
SNP_A-2163355	T	T	295	75	305	111	4.458	3.47E-02	rs6790217	3	37924180	p22.3
SNP_A-2163759	T	T	292	72	271	97	4.46	3.47E-02	rs12818203	12	30024587	p11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2165544	T	T	242	112	307	101	4.46	3.47E-02	rs6832891	4	54897572	q12
SNP_A-1804072	T	T	338	6	401	1	4.46	3.47E-02	rs8114289	20	1951903	p13
SNP_A-1745634	G	G	208	142	274	136	4.458	3.47E-02	rs10507987	13	89240400	q31.3
SNP_A-1654193	G	G	367	35	357	55	4.46	3.47E-02	rs10485801	20	55216678	q13.31
SNP_A-1854259	C	T	211	167	204	190	4.46	3.47E-02	rs741273	14	88935677	q32.11
SNP_A-1859809	C	C	327	41	382	28	4.461	3.47E-02	rs17528679	14	98221659	q32.2
SNP_A-1818197	C	C	308	44	331	73	4.46	3.47E-02	rs2821446	9	6967843	p24.1
SNP_A-1827925	A	A	342	20	347	37	4.462	3.47E-02	rs10041869	5	127767599	q23.2
SNP_A-1832451	C	C	234	134	294	122	4.459	3.47E-02	rs10055224	5	56116958	q11.2
SNP_A-1935941	C	C	364	4	408	0	4.458	3.47E-02	rs901959	8	84558822	q21.13
SNP_A-1983052	G	G	265	27	325	17	4.459	3.47E-02	rs17137889	5	114857240	q22.3
SNP_A-1983812	T	T	252	118	252	162	4.459	3.47E-02	rs10515531	5	143346520	q31.3
SNP_A-1984440	A	A	311	109	332	82	4.46	3.47E-02	rs2545523	5	165446786	q34
SNP_A-1963214	A	A	261	85	271	125	4.458	3.47E-02	rs6718913	2	51131868	p16.3
SNP_A-1897774	G	G	353	13	397	5	4.459	3.47E-02	rs7756667	6	133323713	q23.2
SNP_A-1900579	C	C	271	73	324	58	4.462	3.47E-02	rs9512428	13	26331351	q12.13
SNP_A-1886947	C	C	353	7	383	19	4.46	3.47E-02	rs4579289	5	85973843	q14.3
SNP_A-1909254	C	T	225	179	207	193	4.461	3.47E-02	rs1406532	7	52521739	p12.1
SNP_A-1908014	C	C	333	27	357	49	4.457	3.48E-02	rs11922608	3	188719188	q27.3
SNP_A-1901150	T	T	356	0	397	5	4.457	3.48E-02	rs6684313	1	209358391	q32.3
SNP_A-1900383	C	C	299	119	324	92	4.453	3.48E-02	rs2730086	15	82136664	q25.2
SNP_A-1891557	C	C	193	175	247	165	4.454	3.48E-02	rs13208	1	203216557	q32.1
SNP_A-1890168	G	G	410	0	366	4	4.455	3.48E-02	rs17148344	11	85091468	q14.1
SNP_A-1967126	G	G	275	121	243	147	4.454	3.48E-02	rs2216460	2	225072992	q36.2
SNP_A-1977796	A	A	245	119	297	103	4.456	3.48E-02	rs1443536	4	82531344	q21.21
SNP_A-1940152	A	A	323	43	380	30	4.456	3.48E-02	rs1933483	6	76823944	q14.1
SNP_A-1951059	T	T	378	36	359	55	4.457	3.48E-02	rs11191548	10	104836168	q24.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1955353	T	T	321	47	382	34	4.457	3.48E-02	rs10041089	5	21049013	p14.3
SNP_A-1834906	A	A	415	7	415	1	4.457	3.48E-02	rs2275528	1	11133415	p36.22
SNP_A-1864068	A	A	284	112	259	141	4.455	3.48E-02	rs3751151	12	119904919	q24.31
SNP_A-1867487	A	A	348	4	390	0	4.456	3.48E-02	rs17099599	14	100210461	q32.2
SNP_A-1857806	A	A	356	8	410	2	4.455	3.48E-02	rs1392700	3	56927940	p14.3
SNP_A-1849696	C	T	178	170	223	171	4.453	3.48E-02	rs12116864	1	216640945	q41
SNP_A-1707451	T	T	390	12	387	25	4.457	3.48E-02	rs1594423	7	128313031	q32.1
SNP_A-1727729	A	A	319	27	357	51	4.453	3.48E-02	rs10516757	4	87163192	q21.23
SNP_A-1785476	A	A	333	27	357	49	4.457	3.48E-02	rs7123204	11	77138262	q13.5
SNP_A-2164954	G	G	307	61	311	91	4.454	3.48E-02	rs7683311	4	88749934	q22.1
SNP_A-2153878	C	C	349	17	381	35	4.455	3.48E-02	rs2466750	10	49910171	q11.23
SNP_A-2140555	A	A	380	40	355	59	4.454	3.48E-02	rs4947446	7	50592755	p12.2
SNP_A-2145093	G	G	219	135	274	122	4.455	3.48E-02	rs6814232	4	82546982	q21.21
SNP_A-2213499	T	T	257	79	331	69	4.457	3.48E-02	rs7169046	15	91161784	q26.1
SNP_A-2215937	C	C	251	109	315	97	4.453	3.48E-02	rs10014763	4	155096745	q31.3
SNP_A-2223994	A	A	211	129	252	110	4.456	3.48E-02	rs6482729	10	131010792	q26.3
SNP_A-1996204	A	A	260	68	259	99	4.453	3.48E-02	rs7026731	9	21509921	p21.3
SNP_A-1997058	C	C	415	7	415	1	4.457	3.48E-02	rs10512147	9	84150482	q21.33
SNP_A-2001271	T	T	220	160	191	189	4.456	3.48E-02	rs40430	10	78849351	q22.3
SNP_A-2025243	C	C	299	103	324	78	4.456	3.48E-02	rs1598745	8	15069647	p22
SNP_A-2033012	T	T	272	148	241	177	4.456	3.48E-02	rs2724635	12	11791240	p13.2
SNP_A-2061841	G	G	342	38	354	22	4.453	3.48E-02	rs71132734	12	39691763	q12
SNP_A-2075875	C	C	192	166	252	160	4.453	3.48E-02	rs7503865	17	68377634	q24.3
SNP_A-2099730	C	T	197	165	215	189	4.455	3.48E-02	rs983267	2	237589509	q37.3
SNP_A-2294849	C	C	366	4	410	0	4.455	3.48E-02	rs11015728	10	27709085	p12.1
SNP_A-2274745	G	G	411	7	411	1	4.457	3.48E-02	rs6025788	20	55814447	q13.32
SNP_A-2241621	G	G	304	66	310	98	4.457	3.48E-02	rs1544440	7	46839021	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253864	G	G	396	14	409	5	4.454	3.48E-02	rs2282091	10	106063769	q25.1
SNP_A-2234510	C	C	368	0	411	5	4.451	0.0349	rs11900288	2	115244451	q14.1
SNP_A-2235293	C	C	301	55	364	42	4.449	0.0349	rs7922015	10	52550903	q11.23
SNP_A-2298240	G	G	292	68	352	54	4.45	0.0349	rs709783	1	85306487	p22.3
SNP_A-2289022	G	G	255	145	283	117	4.45	0.0349	rs9951521	18	4443498	p11.31
SNP_A-2069458	C	C	357	13	401	5	4.449	0.0349	rs7796138	7	150926648	q36.1
SNP_A-2035921	G	G	327	27	380	16	4.449	0.0349	rs4836012	5	122829559	q23.2
SNP_A-1993117	C	C	266	148	293	119	4.449	0.0349	rs2722419	8	40609650	p11.21
SNP_A-2008246	C	C	350	58	329	81	4.45	0.0349	rs752275	11	19492086	p15.1
SNP_A-2016714	C	C	396	14	364	26	4.45	0.0349	rs1699648	21	24392162	q21.2
SNP_A-2182172	A	A	340	30	363	53	4.449	0.0349	rs6712443	2	152351557	q23.3
SNP_A-2108876	G	G	221	125	217	169	4.449	0.0349	rs1439982	12	72432928	q21.1
SNP_A-2134046	G	G	309	61	369	47	4.448	0.0349	rs9257745	6	29414635	p22.1
SNP_A-2129199	A	A	172	170	231	167	4.452	0.0349	rs1449995	3	36136859	p22.3
SNP_A-1752371	G	G	362	12	359	25	4.449	0.0349	rs2115105	16	12675120	p13.12
SNP_A-1679024	A	A	306	86	344	66	4.451	0.0349	rs773702	5	14337366	p15.2
SNP_A-1651160	G	G	289	61	313	97	4.45	0.0349	rs2057818	4	113311937	q25
SNP_A-1848957	C	C	271	45	280	72	4.451	0.0349	rs1764962	13	85157340	q31.1
SNP_A-1872557	G	G	352	0	393	5	4.452	0.0349	rs1527087	12	40033309	q12
SNP_A-1865403	C	C	265	133	298	108	4.448	0.0349	rs6685718	1	240807035	q44
SNP_A-1833661	A	A	352	4	394	0	4.451	0.0349	rs10835254	11	27974391	p14.1
SNP_A-1842601	T	T	265	101	264	140	4.449	0.0349	rs12465063	2	139704708	q22.1
SNP_A-1815274	T	T	355	45	374	28	4.449	0.0349	rs838313	12	113446198	q24.21
SNP_A-1952331	C	C	275	79	291	119	4.452	0.0349	rs7552600	1	154842094	q23.1
SNP_A-1946476	A	A	292	70	347	55	4.452	0.0349	rs936736	4	88904040	q22.1
SNP_A-1981000	A	A	286	22	355	13	4.451	0.0349	rs398536	5	24986100	p14.1
SNP_A-1981829	C	C	388	12	414	4	4.449	0.0349	rs10514913	5	60971948	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1892796	G	G	358	8	412	2	4.45	0.0349	rs2052650	15	93824498	q26.2
SNP_A-1894461	T	T	307	57	372	44	4.449	0.0349	rs9315226	13	33066454	q13.2
SNP_A-1895401	A	A	266	82	316	66	4.451	0.0349	rs2510	1	200893248	q32.1
SNP_A-1902776	C	C	353	5	369	15	4.449	0.0349	rs10976411	9	7558976	p24.1
SNP_A-1874915	C	C	218	150	212	198	4.45	0.0349	rs10512617	17	74205146	q25.3
SNP_A-1920323	T	C	208	158	210	204	4.45	0.0349	rs6909200	6	87941146	q15
SNP_A-1927091	G	G	230	130	287	117	4.449	0.0349	rs6854611	4	84645792	q21.23
SNP_A-1910698	T	T	320	46	331	73	4.447	3.50E-02	rs283841	2	79178115	p12
SNP_A-1891143	C	C	297	73	306	108	4.447	3.50E-02	rs11734670	4	109843986	q25
SNP_A-1863801	G	G	364	2	406	10	4.445	3.50E-02	rs17095030	14	97156543	q32.2
SNP_A-1861475	A	A	309	61	362	46	4.444	3.50E-02	rs17346	10	55053430	q21.1
SNP_A-1872697	G	G	192	178	247	169	4.447	3.50E-02	rs7191235	16	21066714	p12.3
SNP_A-1847997	C	C	303	41	365	29	4.445	3.50E-02	rs29586	16	8336492	p13.2
SNP_A-1856519	T	T	289	133	256	160	4.443	3.50E-02	rs1561199	18	36458761	q12.3
SNP_A-1853076	A	A	346	8	398	2	4.445	3.50E-02	rs17159219	7	83894744	q21.11
SNP_A-1642077	G	G	284	60	359	49	4.444	3.50E-02	rs10514150	18	70776824	q22.3
SNP_A-1689428	A	A	305	41	339	71	4.445	3.50E-02	rs10513584	3	163561576	q26.1
SNP_A-1728345	C	C	192	190	230	168	4.447	3.50E-02	rs1858964	17	68473769	q24.3
SNP_A-1743625	T	T	343	59	330	84	4.446	3.50E-02	rs10512041	9	73522657	q21.13
SNP_A-1741129	C	C	272	118	248	148	4.446	3.50E-02	rs10502151	11	111261782	q23.1
SNP_A-1794277	G	G	234	176	256	142	4.446	3.50E-02	rs9832624	3	67278514	p14.1
SNP_A-2117310	G	G	360	8	414	2	4.445	3.50E-02	rs1390393	3	88839314	p11.1
SNP_A-2145904	A	A	322	98	345	73	4.443	3.50E-02	rs11208853	1	66589566	p31.2
SNP_A-2150896	G	G	334	32	323	51	4.448	3.50E-02	rs808919	12	54934178	q13.3
SNP_A-2164417	C	C	413	9	416	2	4.446	3.50E-02	rs11068937	12	117319824	q24.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169837	T	T	263	107	323	93	4.446	3.50E-02	rs6930903	6	29089223	p22.1
SNP_A-2192677	C	C	382	26	349	41	4.444	3.50E-02	rs4763813	12	9753603	p13.31
SNP_A-2196843	C	C	318	30	332	52	4.444	3.50E-02	rs4285774	10	66242278	q21.3
SNP_A-2223269	T	T	257	65	321	53	4.447	3.50E-02	rs12591972	15	99443655	q26.3
SNP_A-2223345	T	T	241	129	300	116	4.447	3.50E-02	rs1348292	13	87403859	q31.2
SNP_A-2036702	A	A	250	104	260	150	4.446	3.50E-02	rs7607942	2	212722077	q34
SNP_A-2029102	C	C	413	9	416	2	4.446	3.50E-02	rs12498100	3	110611243	q13.13
SNP_A-2019267	C	C	241	129	300	116	4.447	3.50E-02	rs2836658	21	39041800	q22.2
SNP_A-2077919	A	A	269	93	268	130	4.446	3.50E-02	rs1579976	5	63448248	q12.3
SNP_A-2085548	A	A	278	86	284	124	4.447	3.50E-02	rs2309750	2	100200284	q11.2
SNP_A-2297874	C	C	221	199	249	167	4.447	3.50E-02	rs4410190	18	18274198	q11.2
SNP_A-2313747	C	C	265	105	322	90	4.446	3.50E-02	rs6924824	6	29118132	p22.1
SNP_A-2304840	T	T	236	130	234	176	4.443	3.50E-02	rs2254382	20	36813140	q11.23
SNP_A-2241276	A	A	237	175	211	209	4.443	3.50E-02	rs4681878	3	58582664	p14.2
SNP_A-2230007	A	A	358	10	390	24	4.443	3.50E-02	rs10458468	1	216209873	q41
SNP_A-2279085	A	A	284	86	307	63	4.445	3.50E-02	rs8028021	15	31341045	q13.3
SNP_A-2279023	A	A	329	27	363	15	4.444	3.50E-02	rs1039497	11	13852247	p15.2
SNP_A-2268754	G	G	258	102	266	146	4.446	3.50E-02	rs7310134	12	95977566	q23.1
SNP_A-2261714	T	T	260	94	326	82	4.447	3.50E-02	rs2075204	16	52658415	q12.2
SNP_A-2267303	T	T	290	70	311	49	4.44	3.51E-02	rs7923585	10	77119844	q22.2
SNP_A-2287523	T	C	215	201	212	168	4.442	3.51E-02	rs2350728	8	111253247	q23.2
SNP_A-2232105	T	T	288	126	249	149	4.442	3.51E-02	rs2548997	5	131863294	q23.3
SNP_A-2253040	A	A	322	90	287	113	4.441	3.51E-02	rs6495308	15	76694711	q25.1
SNP_A-2085821	A	A	338	14	394	6	4.438	3.51E-02	rs2034008	3	19357791	p24.3
SNP_A-2077882	A	A	302	26	319	47	4.439	3.51E-02	rs11046890	12	23370921	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2099783	T	T	231	139	288	126	4.442	3.51E-02	rs11015570	10	27474974	p12.1
SNP_A-2067017	T	T	227	47	321	41	4.442	3.51E-02	rs9534145	13	44908470	q14.13
SNP_A-2076576	G	G	297	61	355	47	4.442	3.51E-02	rs10219275	11	27956449	p14.1
SNP_A-2058811	C	C	234	172	262	142	4.442	3.51E-02	rs10881750	10	91859823	q23.31
SNP_A-2055578	A	A	221	133	216	178	4.442	3.51E-02	rs7894625	10	94952704	q23.33
SNP_A-2031229	C	C	365	7	397	19	4.439	3.51E-02	rs6482210	10	22757161	p12.2
SNP_A-2017611	G	G	407	3	368	10	4.44	3.51E-02	rs2832176	21	29398849	q21.3
SNP_A-2009309	C	C	314	28	348	52	4.44	3.51E-02	rs953883	3	173580319	q26.31
SNP_A-2005208	C	C	249	85	270	62	4.442	3.51E-02	rs7218226	17	50945696	q23.1
SNP_A-2004350	C	C	358	56	334	78	4.439	3.51E-02	rs2289352	15	87823841	q26.1
SNP_A-2210869	G	G	264	104	324	90	4.442	3.51E-02	rs7706559	5	14536164	p15.2
SNP_A-2162329	A	A	338	30	361	53	4.44	3.51E-02	rs4859648	4	77531841	q21.1
SNP_A-2107784	T	T	218	130	262	112	4.442	3.51E-02	rs11875168	18	72127143	q23
SNP_A-2129517	T	T	220	150	213	197	4.44	3.51E-02	rs12712179	2	103800584	q12.1
SNP_A-1791574	C	C	291	91	313	67	4.442	3.51E-02	rs1396980	8	131911818	q24.22
SNP_A-1806307	G	G	291	131	314	102	4.441	3.51E-02	rs93366	1	209982711	q32.3
SNP_A-1812703	C	C	359	3	398	12	4.442	3.51E-02	rs11101436	10	49589573	q11.23
SNP_A-1782732	A	A	307	55	322	86	4.441	3.51E-02	rs1599284	8	106265443	q23.1
SNP_A-1712057	T	T	322	14	359	31	4.441	3.51E-02	rs6940932	6	91038163	q15
SNP_A-1858243	A	G	194	146	194	188	4.443	3.51E-02	rs6942635	7	17761105	p21.1
SNP_A-1852274	T	T	346	6	409	1	4.439	3.51E-02	rs7644822	3	74661090	p12.3
SNP_A-1867042	C	C	358	0	401	5	4.438	3.51E-02	---	8	61582268	q12.1
SNP_A-1864867	C	C	245	117	294	100	4.44	3.51E-02	rs7308370	12	39689044	q12
SNP_A-1841541	A	A	422	0	378	4	4.441	3.51E-02	rs6095963	20	48523002	q13.13
SNP_A-1840462	A	A	307	55	322	86	4.441	3.51E-02	rs6774399	3	153113951	q25.1
SNP_A-1877106	T	T	343	27	398	16	4.441	3.51E-02	rs6700782	1	234588307	q43
SNP_A-1986104	G	G	320	14	344	30	4.44	3.51E-02	rs971199	6	54616360	p12.1
SNP_A-1988120	C	A	220	186	215	189	4.442	3.51E-02	rs1655281	1	227940775	q42.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939628	T	T	274	124	233	145	4.442	3.51E-02	rs546760	1	112091638	p13.2
SNP_A-1942318	T	T	202	166	258	156	4.437	3.52E-02	rs6479247	9	104376892	q31.1
SNP_A-1948915	G	G	235	133	295	121	4.437	3.52E-02	rs7592497	2	649958	p25.3
SNP_A-1976799	T	T	276	70	339	57	4.435	3.52E-02	rs1579804	4	36825672	p14
SNP_A-1971127	A	A	350	8	402	2	4.435	3.52E-02	rs17003421	22	41653523	q13.2
SNP_A-1876443	T	T	316	96	285	121	4.435	3.52E-02	rs2032161	18	9018510	p11.22
SNP_A-1887085	G	G	228	114	282	100	4.437	3.52E-02	rs6909216	6	53910847	p12.1
SNP_A-1888951	G	G	363	7	395	19	4.434	3.52E-02	rs7213007	17	9976389	p13.1
SNP_A-1896151	A	A	245	121	231	157	4.436	3.52E-02	rs3013713	6	120736258	q22.31
SNP_A-1894239	G	G	226	186	257	157	4.437	3.52E-02	rs2874705	6	164442532	q26
SNP_A-1899066	G	G	359	53	374	34	4.437	3.52E-02	rs3786313	18	30974357	q12.1
SNP_A-1907860	T	A	214	198	225	181	4.437	3.52E-02	rs2647962	12	114450963	q24.21
SNP_A-1918291	T	T	310	58	361	43	4.435	3.52E-02	rs7664501	4	175537497	q34.1
SNP_A-1912961	A	A	364	4	406	0	4.436	3.52E-02	rs6719009	2	11594447	p25.1
SNP_A-1925194	G	G	238	106	276	86	4.437	3.52E-02	rs12476783	2	39665801	p22.1
SNP_A-1837621	A	A	311	45	368	32	4.434	3.52E-02	rs1866260	3	32337429	p23
SNP_A-1840947	G	G	354	16	381	33	4.434	3.52E-02	rs34076	7	12738713	p21.3
SNP_A-1862135	G	G	254	114	256	158	4.435	3.52E-02	rs4244011	1	57841657	p32.2
SNP_A-1868591	C	C	360	62	373	41	4.436	3.52E-02	rs9261855	6	30491778	p21.33
SNP_A-1869538	C	C	335	29	323	47	4.433	3.52E-02	rs1932637	6	801224	p25.3
SNP_A-1694993	C	C	356	0	399	5	4.435	3.52E-02	rs9321206	6	130373374	q23.1
SNP_A-1652884	C	C	245	153	280	128	4.434	3.52E-02	rs1647686	2	106263203	q12.2
SNP_A-1727022	C	C	328	74	360	54	4.438	3.52E-02	rs10512274	9	98983039	q31.1
SNP_A-1810031	C	C	254	114	256	158	4.435	3.52E-02	rs9850529	3	150259309	q24
SNP_A-1800892	A	A	295	71	345	55	4.438	3.52E-02	rs6551878	4	65519355	q13.1
SNP_A-1794384	A	A	339	69	315	93	4.436	3.52E-02	rs11768743	7	129226032	q32.2
SNP_A-1792620	C	C	221	149	276	136	4.437	3.52E-02	rs2036645	4	134874657	q28.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796016	C	C	348	4	388	0	4.433	3.52E-02	rs17168623	5	134938281	q31.1
SNP_A-2134209	A	A	407	9	392	20	4.435	3.52E-02	rs11820600	11	78664629	q14.1
SNP_A-2114987	G	G	288	134	255	161	4.434	3.52E-02	rs7934652	11	132442824	q25
SNP_A-2151315	C	C	361	27	319	41	4.435	3.52E-02	rs13343453	19	57444616	q13.41
SNP_A-2142475	G	G	367	51	378	32	4.435	3.52E-02	rs601504	1	43272808	p34.2
SNP_A-2212394	C	C	248	136	271	107	4.433	3.52E-02	rs10835403	11	3947517	p15.4
SNP_A-2186211	C	C	359	51	370	32	4.437	3.52E-02	rs2061183	7	113851965	q31.1
SNP_A-2180273	T	T	305	113	277	141	4.434	3.52E-02	rs6910232	6	11010425	p24.2
SNP_A-2000753	C	C	357	3	396	12	4.437	3.52E-02	rs6669938	1	225355897	q42.13
SNP_A-1992746	A	A	296	120	261	145	4.437	3.52E-02	rs10503779	8	25799345	p21.2
SNP_A-2011658	A	A	339	71	296	90	4.434	3.52E-02	rs7744254	6	26529009	p22.1
SNP_A-2016035	C	C	287	79	299	117	4.434	3.52E-02	rs2825802	21	20099758	q21.1
SNP_A-2019562	G	G	263	103	326	90	4.435	3.52E-02	rs892954	11	112491180	q23.1
SNP_A-2040947	G	G	340	8	356	20	4.434	3.52E-02	rs16928679	9	12309485	p23
SNP_A-2095827	T	T	379	15	408	6	4.433	3.52E-02	rs16967400	17	27905787	q11.2
SNP_A-2083508	A	A	274	90	275	127	4.436	3.52E-02	rs12659444	5	118218789	q23.1
SNP_A-2089947	A	A	378	40	360	60	4.434	3.52E-02	rs7965805	12	96429531	q23.1
SNP_A-2251979	C	C	334	34	390	22	4.435	3.52E-02	---	8	13499218	p22
SNP_A-2235976	G	G	263	105	268	148	4.433	3.52E-02	rs10792468	11	79576466	q14.1
SNP_A-2236600	T	T	344	48	328	70	4.437	3.52E-02	rs17019729	1	107957706	p13.3
SNP_A-2281134	T	T	276	90	325	73	4.435	3.52E-02	rs4578586	15	51103779	q21.3
SNP_A-2256787	T	T	349	45	342	68	4.436	3.52E-02	rs11605035	11	86381667	q14.2
SNP_A-2258783	A	A	364	4	406	0	4.436	3.52E-02	rs17023566	2	83594141	p11.2
SNP_A-2303788	C	C	349	67	322	90	4.437	3.52E-02	rs17733538	5	168195597	q34
SNP_A-2306640	G	G	342	70	321	95	4.434	3.52E-02	rs8007035	14	49595202	q21.3
SNP_A-2290742	T	T	326	44	341	71	4.433	3.52E-02	rs17244601	15	65859435	q23
SNP_A-2297366	C	C	251	161	220	190	4.432	3.53E-02	rs8059982	16	6289394	p13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2302376	C	C	282	76	342	62	4.429	3.53E-02	rs17027132	3	31171698	p24.1
SNP_A-2314293	C	C	301	65	315	99	4.43	3.53E-02	rs4771666	13	109797253	q34
SNP_A-2265951	A	A	336	10	383	25	4.433	3.53E-02	rs16964507	15	49844296	q21.2
SNP_A-2269281	A	A	251	117	309	103	4.43	3.53E-02	rs2732248	18	71821121	q23
SNP_A-2271588	G	G	309	107	336	82	4.432	3.53E-02	rs7786094	7	138240478	q34
SNP_A-2278552	C	C	343	17	375	35	4.429	3.53E-02	rs4356943	4	186268549	q35.1
SNP_A-2275223	T	T	199	171	238	150	4.429	3.53E-02	rs655089	11	69157756	q13.3
SNP_A-2232055	G	G	206	138	198	182	4.429	3.53E-02	rs590656	6	71024433	q13
SNP_A-2253278	G	G	391	17	388	32	4.43	3.53E-02	rs9628605	22	47431296	q13.32
SNP_A-2246195	T	T	346	16	310	28	4.431	3.53E-02	rs12042157	1	4361454	p36.32
SNP_A-2098108	C	C	292	22	340	12	4.433	3.53E-02	rs7156551	14	75414324	q24.3
SNP_A-2070228	T	C	185	183	237	177	4.429	3.53E-02	rs1821851	2	3666407	p25.3
SNP_A-2066186	T	T	299	63	301	93	4.429	3.53E-02	rs343554	4	58457090	q12
SNP_A-2046392	C	C	350	6	413	1	4.43	3.53E-02	rs6893788	5	95360842	q15
SNP_A-2027622	G	G	337	33	391	21	4.429	3.53E-02	rs9912465	17	23654970	q11.2
SNP_A-2173755	C	C	354	10	386	24	4.43	3.53E-02	rs6812641	4	172031194	q33
SNP_A-2139499	C	C	353	17	404	8	4.433	3.53E-02	rs1552000	5	9160108	p15.31
SNP_A-2160436	A	A	375	17	346	30	4.431	3.53E-02	rs928371	15	39610017	q15.1
SNP_A-2114584	G	G	226	134	221	179	4.433	3.53E-02	rs12527475	6	148829289	q24.3
SNP_A-2119560	A	A	338	8	388	2	4.429	3.53E-02	rs280937	13	29054769	q12.3
SNP_A-2122458	T	T	284	84	292	122	4.43	3.53E-02	rs16876945	6	87147616	q14.3
SNP_A-2125904	G	G	261	95	327	83	4.432	3.53E-02	rs7979400	12	26834683	p11.23
SNP_A-1802654	T	T	257	99	312	84	4.431	3.53E-02	rs17677139	3	7816787	p26.1
SNP_A-1732530	C	C	283	115	315	91	4.429	3.53E-02	rs1107629	2	68920037	p13.3
SNP_A-1741515	A	A	337	7	388	20	4.432	3.53E-02	rs502309	9	2562909	p24.2
SNP_A-1783025	G	G	349	61	326	84	4.432	3.53E-02	rs444464	4	3780572	p16.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1655823	G	G	260	142	238	176	4.432	3.53E-02	rs1886777	1	65125309	p31.2
SNP_A-1840234	T	T	350	4	390	0	4.431	3.53E-02	rs16933112	9	36227241	p13.2
SNP_A-1819406	G	G	323	77	283	97	4.429	3.53E-02	rs4803470	19	46652551	q13.2
SNP_A-1916655	A	A	336	30	359	53	4.43	3.53E-02	rs1403343	15	36393834	q14
SNP_A-1890539	A	A	231	115	301	107	4.431	3.53E-02	rs2651316	3	148542032	q24
SNP_A-1889249	A	A	332	62	301	83	4.432	3.53E-02	rs16941684	17	42657685	q21.32
SNP_A-1979029	G	G	344	70	323	95	4.43	3.53E-02	rs12133885	1	194324225	q31.3
SNP_A-1936533	A	A	396	20	411	9	4.432	3.53E-02	rs12290352	11	38139808	p12
SNP_A-1933983	A	A	305	63	365	49	4.433	3.53E-02	rs10514149	18	70774707	q22.3
SNP_A-1947628	T	C	170	146	206	174	4.426	3.54E-02	rs6907771	6	42327272	p21.1
SNP_A-1889193	C	C	346	8	383	21	4.427	3.54E-02	rs17030657	4	155125317	q31.3
SNP_A-1899131	C	T	201	167	216	192	4.425	3.54E-02	rs4693498	4	83997511	q21.22
SNP_A-1902103	G	G	228	138	278	122	4.425	3.54E-02	rs12055559	6	77254913	q14.1
SNP_A-1925586	A	A	333	35	356	60	4.425	3.54E-02	---	4	165608018	q32.3
SNP_A-1930315	T	T	396	22	373	37	4.425	3.54E-02	rs17698883	3	117351248	q13.31
SNP_A-1817075	A	A	215	143	212	192	4.427	3.54E-02	rs11665456	18	34283162	q12.2
SNP_A-1859756	C	C	247	147	279	121	4.424	3.54E-02	rs575588	9	22707305	p21.3
SNP_A-1702123	G	G	323	25	362	48	4.425	3.54E-02	rs980720	4	82511458	q21.21
SNP_A-1678968	A	A	230	168	269	145	4.425	3.54E-02	rs2421608	2	117392678	q14.1
SNP_A-1782336	A	A	328	42	347	69	4.425	3.54E-02	rs1542550	16	7153618	p13.2
SNP_A-1808645	A	A	345	15	378	32	4.427	3.54E-02	rs1154842	9	10727004	p23
SNP_A-1814462	C	C	340	6	401	1	4.425	3.54E-02	rs7567003	2	26874898	p23.3
SNP_A-1797401	T	T	355	5	400	16	4.426	3.54E-02	rs17021996	4	148112424	q31.22
SNP_A-1789446	G	G	260	84	224	104	4.427	3.54E-02	rs1048650	3	13333204	p25.2
SNP_A-2156929	A	A	407	7	405	1	4.427	3.54E-02	rs9436867	1	69152984	p31.2
SNP_A-2174619	T	T	322	26	341	47	4.425	3.54E-02	rs4590108	4	70295215	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2186330	G	G	230	154	213	193	4.426	3.54E-02	rs7823154	8	87606086	q21.3
SNP_A-2185534	A	A	335	35	393	23	4.427	3.54E-02	rs12663807	6	40679852	p21.1
SNP_A-2189636	A	A	325	45	384	32	4.428	3.54E-02	rs8065041	17	67286965	q24.3
SNP_A-2190487	C	C	230	94	264	74	4.427	3.54E-02	rs4243136	16	72263281	q22.3
SNP_A-2197474	A	A	313	35	334	60	4.426	3.54E-02	rs530649	7	27975670	p15.1
SNP_A-2197998	A	A	331	89	293	111	4.425	3.54E-02	rs1296795	22	16396314	q11.21
SNP_A-2208178	T	T	359	47	382	30	4.423	3.54E-02	rs9650414	8	26010791	p21.2
SNP_A-2208904	C	C	391	7	389	1	4.424	3.54E-02	rs7728696	5	132486825	q31.1
SNP_A-2215296	C	C	250	144	228	178	4.424	3.54E-02	rs4688500	3	64651333	p14.1
SNP_A-2219419	C	C	325	69	365	51	4.425	3.54E-02	rs16939329	8	77726733	q21.11
SNP_A-2026923	T	T	335	35	393	23	4.427	3.54E-02	rs12657745	5	10638399	p15.2
SNP_A-2029729	T	T	207	143	174	166	4.426	3.54E-02	rs4882911	12	72168358	q21.1
SNP_A-2030639	G	G	416	0	374	4	4.424	3.54E-02	rs1456974	14	97574775	q32.2
SNP_A-2037351	A	A	377	17	361	31	4.425	3.54E-02	rs3855951	1	1836464	p36.33
SNP_A-2011044	C	C	224	136	221	183	4.426	3.54E-02	rs2438367	5	90079003	q14.3
SNP_A-2009285	T	T	348	0	391	5	4.424	3.54E-02	rs4279098	3	168443657	q26.1
SNP_A-2007783	T	T	256	104	308	88	4.423	3.54E-02	rs16910152	11	11771277	p15.3
SNP_A-2006858	G	G	317	21	363	11	4.428	3.54E-02	rs6751647	2	177538590	q31.1
SNP_A-1993281	G	G	340	6	401	1	4.425	3.54E-02	rs16917819	8	53487049	q11.23
SNP_A-2056984	T	T	333	35	356	60	4.425	3.54E-02	rs2223247	20	41367710	q13.11
SNP_A-2057930	A	A	366	0	411	5	4.427	3.54E-02	rs16926592	12	23728130	p12.1
SNP_A-2049707	C	A	191	155	205	185	4.426	3.54E-02	rs4532301	4	118244549	q26
SNP_A-2096245	C	C	253	101	314	88	4.427	3.54E-02	rs4521634	6	111951804	q21
SNP_A-2088591	A	A	378	16	353	29	4.426	3.54E-02	rs10422156	19	11299022	p13.2
SNP_A-2302882	G	C	196	156	207	191	4.425	3.54E-02	rs2047297	4	121869456	q27

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2244749	A	A	218	152	214	202	4.422	3.55E-02	rs7045097	9	6392856	p24.1
SNP_A-2233500	C	C	243	111	305	99	4.421	3.55E-02	rs6696752	1	11770201	p36.22
SNP_A-2283256	C	C	302	114	328	88	4.42	3.55E-02	rs10151137	6	9544230	p24.3
SNP_A-2270535	C	C	342	6	403	1	4.42	3.55E-02	rs16933349	9	116094854	q33.1
SNP_A-2098389	C	C	327	95	348	70	4.422	3.55E-02	rs2963455	5	157856884	q33.3
SNP_A-2008229	A	A	358	4	398	0	4.421	3.55E-02	rs16936577	11	19331993	p15.1
SNP_A-2011331	A	G	208	172	202	180	4.422	3.55E-02	rs7716435	5	147853590	q32
SNP_A-2014187	C	C	395	19	358	32	4.419	3.55E-02	rs7129943	11	96358495	q21
SNP_A-2040246	A	A	322	28	335	49	4.419	3.55E-02	rs7755292	6	85391817	q14.3
SNP_A-2045309	G	G	326	38	375	25	4.421	3.55E-02	rs17518769	1	166183748	q24.2
SNP_A-2032601	G	G	266	122	233	147	4.423	3.55E-02	rs2319727	1	146027927	q21.1
SNP_A-2032112	T	T	237	79	238	114	4.422	3.55E-02	rs2045876	12	10433099	p13.2
SNP_A-2201798	A	A	335	65	310	88	4.422	3.55E-02	rs904648	12	123299673	q24.31
SNP_A-2201970	C	C	232	188	262	158	4.423	3.55E-02	rs6077844	20	10527996	p12.2
SNP_A-2197476	G	G	178	162	239	159	4.42	3.55E-02	rs2871987	19	51867368	q13.32
SNP_A-2174010	C	C	253	145	285	119	4.419	3.55E-02	rs2341538	14	54964927	q22.3
SNP_A-2181943	T	T	260	160	289	131	4.422	3.55E-02	rs6673720	1	163719936	q24.1
SNP_A-2175527	C	C	345	37	353	21	4.421	3.55E-02	rs3739575	9	37482721	p13.2
SNP_A-2176707	C	-	204	150	203	203	4.423	3.55E-02	rs1962924	8	55425332	q11.23
SNP_A-2154990	A	A	245	125	297	109	4.422	3.55E-02	rs1506853	12	60234604	q14.1
SNP_A-2160328	C	C	362	26	371	13	4.423	3.55E-02	rs16841106	1	237432967	q43
SNP_A-2123337	G	G	356	8	408	2	4.421	3.55E-02	rs6787962	3	107174378	q13.11
SNP_A-1753095	G	G	382	6	382	16	4.419	3.55E-02	rs10501648	11	87249489	q14.2
SNP_A-1671248	C	C	264	86	281	129	4.421	3.55E-02	rs861085	5	102995021	q21.2
SNP_A-1869703	T	T	317	37	334	62	4.419	3.55E-02	rs4775719	15	45874910	q21.1
SNP_A-1855337	C	C	337	67	307	89	4.421	3.55E-02	rs12357769	10	65190374	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932636	T	T	267	99	327	85	4.421	3.55E-02	rs659875	1	212786497	q41
SNP_A-1917393	C	C	270	58	322	44	4.422	3.55E-02	rs2219109	3	177781268	q26.32
SNP_A-1918576	T	T	318	90	340	66	4.423	3.55E-02	rs17022944	1	210999603	q41
SNP_A-1906323	A	A	200	154	256	144	4.423	3.55E-02	rs550700	11	96328312	q21
SNP_A-1879148	A	A	301	61	366	48	4.42	3.55E-02	rs6596595	5	104399249	q21.2
SNP_A-1981055	C	C	343	57	364	38	4.419	3.55E-02	rs16897991	5	28736960	p14.1
SNP_A-1984234	A	A	387	21	379	37	4.42	3.55E-02	rs10045385	5	157755464	q33.3
SNP_A-1973208	C	C	314	94	289	121	4.422	3.55E-02	rs2568847	3	71404088	p13
SNP_A-1970982	C	C	293	99	265	125	4.418	0.0356	rs8136357	22	32121916	q12.3
SNP_A-1972654	G	G	304	102	270	126	4.416	0.0356	rs10510773	3	54786299	p14.3
SNP_A-1967688	A	A	277	75	275	107	4.415	0.0356	rs6056669	20	9455819	p12.2
SNP_A-1944458	C	C	304	64	364	50	4.418	0.0356	rs6972824	7	156972698	q36.3
SNP_A-1933306	C	C	182	168	242	164	4.415	0.0356	rs538534	19	42127605	q13.12
SNP_A-1934204	C	C	289	73	344	58	4.414	0.0356	rs7047812	9	9716090	p23
SNP_A-1954050	A	A	282	78	347	65	4.416	0.0356	rs1351516	15	58234912	q22.2
SNP_A-1874773	T	T	274	124	305	99	4.418	0.0356	rs4074575	7	276187	p22.3
SNP_A-1907582	A	A	221	135	276	122	4.418	0.0356	rs2033804	2	201047909	q33.1
SNP_A-1905096	C	C	316	70	301	43	4.414	0.0356	rs11021936	11	11546477	p15.3
SNP_A-1912712	C	C	332	6	391	1	4.416	0.0356	rs10237220	7	118671435	q31.31
SNP_A-1931956	T	T	218	118	215	161	4.415	0.0356	rs2315507	4	14650461	p15.33
SNP_A-1929311	A	A	362	4	402	0	4.416	0.0356	rs112507 41	10	1729576	p15.3
SNP_A-1924189	C	C	243	175	270	144	4.414	0.0356	rs6058166	20	33120371	q11.22
SNP_A-1919948	T	T	211	69	219	105	4.415	0.0356	rs4956409	4	141675827	q31.1
SNP_A-1848430	C	C	328	32	345	55	4.417	0.0356	rs11716028	3	45740752	p21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1663174	C	C	253	147	281	119	4.416	0.0356	rs6123609	20	37657010	q11.23
SNP_A-1653914	A	A	380	20	376	36	4.416	0.0356	rs781382	14	50900976	q22.1
SNP_A-1710519	G	G	394	8	391	19	4.415	0.0356	rs10515867	5	163094918	q34
SNP_A-1785817	T	T	248	82	291	65	4.417	0.0356	rs1877836	4	130432369	q28.2
SNP_A-1787545	G	G	344	4	382	0	4.415	0.0356	rs17100621	12	63419728	q14.3
SNP_A-1811417	T	T	337	33	359	57	4.418	0.0356	rs9322860	14	29914472	q12
SNP_A-2121549	C	C	344	6	405	1	4.415	0.0356	rs785267	2	190842835	q32.2
SNP_A-2116984	C	C	261	153	280	120	4.417	0.0356	rs6034860	20	17516891	p12.1
SNP_A-2114206	C	C	288	128	249	151	4.416	0.0356	rs13390359	2	159500814	q24.1
SNP_A-2133920	G	G	234	156	274	134	4.415	0.0356	rs6473756	8	53931790	q11.23
SNP_A-2140246	C	C	401	19	404	8	4.416	0.0356	rs6594004	1	201035279	q32.1
SNP_A-2150142	T	T	374	40	392	24	4.418	0.0356	rs7804649	7	110286519	q31.1
SNP_A-2184789	T	T	422	0	380	4	4.418	0.0356	rs1499742	15	85590430	q25.3
SNP_A-2220088	A	A	346	22	374	42	4.417	0.0356	rs1484998	20	29695950	q11.21
SNP_A-2223578	G	G	396	24	378	40	4.414	0.0356	rs4151342	14	60442812	q23.1
SNP_A-2037259	T	T	359	37	333	55	4.417	0.0356	rs7711492	5	164885303	q34
SNP_A-2008634	G	G	395	23	407	11	4.415	0.0356	rs6791790	3	40025279	p22.1
SNP_A-1993297	A	C	227	181	211	197	4.419	0.0356	rs6495537	10	5985678	p15.1
SNP_A-2092633	A	C	211	159	208	204	4.417	0.0356	rs11925916	3	85797067	p12.1
SNP_A-2064844	A	A	260	96	315	81	4.417	0.0356	rs4140922	12	106489079	q23.3
SNP_A-2063483	C	C	389	19	392	8	4.414	0.0356	rs1209075	14	94735334	q32.13
SNP_A-2283337	A	A	235	125	229	167	4.414	0.0356	rs2094799	13	83657934	q31.1
SNP_A-2280000	G	G	357	61	334	84	4.414	0.0356	rs7221995	17	3955101	p13.2
SNP_A-2272771	G	G	192	172	247	163	4.414	0.0356	rs7322877	13	79283633	q31.1
SNP_A-2231969	T	T	345	41	315	59	4.415	0.0356	rs2039369	20	61724265	q13.33
SNP_A-2250547	C	C	356	52	336	74	4.414	0.0356	rs968525	19	19320215	p13.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2314920	C	C	224	72	290	62	4.414	0.0356	rs6137955	20	2345519	p13
SNP_A-2297519	T	T	292	32	300	54	4.417	0.0356	rs12199650	6	52232503	p12.2
SNP_A-2300116	C	C	264	90	258	124	4.412	3.57E-02	rs5749787	22	33034806	q12.3
SNP_A-2250662	A	A	254	110	258	154	4.412	3.57E-02	rs628735	5	118125040	q23.1
SNP_A-2249844	A	A	395	5	353	13	4.413	3.57E-02	rs6705726	2	37615018	p22.2
SNP_A-2279831	G	A	230	178	205	197	4.41	3.57E-02	rs37026	16	55507635	q13
SNP_A-2269365	T	T	413	9	414	2	4.413	3.57E-02	rs6879837	5	171032737	q35.1
SNP_A-2268461	G	G	371	47	345	67	4.41	3.57E-02	rs2242655	6	31735428	p21.33
SNP_A-2081333	T	T	227	141	219	185	4.413	3.57E-02	rs2637808	4	71015368	q13.3
SNP_A-2001076	G	G	293	33	311	57	4.411	3.57E-02	rs561396	10	30537274	p11.23
SNP_A-2002053	C	C	276	92	333	77	4.412	3.57E-02	rs10509256	10	67487829	q21.3
SNP_A-2002072	A	A	395	17	379	31	4.409	3.57E-02	rs679598	11	79338595	q14.1
SNP_A-2014120	T	T	227	163	202	196	4.41	3.57E-02	rs6475402	9	20081810	p21.3
SNP_A-2203384	C	C	236	94	244	66	4.413	3.57E-02	rs2735985	8	127515680	q24.21
SNP_A-2211682	A	A	385	35	361	53	4.411	3.57E-02	rs2039978	10	29363850	p12.1
SNP_A-2183821	C	G	207	159	211	203	4.41	3.57E-02	rs349057	11	84503215	q14.1
SNP_A-2171428	G	G	366	40	336	58	4.409	3.57E-02	rs1873880	17	3398004	p13.2
SNP_A-2141425	A	A	224	132	209	169	4.412	3.57E-02	rs2821498	9	9767072	p23
SNP_A-1812831	C	C	204	124	258	112	4.411	3.57E-02	rs7799912	7	48403741	p12.3
SNP_A-1803198	T	T	234	182	260	150	4.409	3.57E-02	rs10881885	10	92870092	q23.31
SNP_A-1806278	C	C	274	148	301	119	4.413	3.57E-02	rs2280468	15	87182560	q26.1
SNP_A-1790485	G	G	283	65	286	96	4.411	3.57E-02	rs6981136	8	140637214	q24.3
SNP_A-1790788	A	A	251	65	308	52	4.411	3.57E-02	rs10823326	10	70689542	q22.1
SNP_A-1668000	G	G	387	3	391	11	4.411	3.57E-02	rs10511812	9	27687335	p21.2
SNP_A-1782166	C	C	195	163	248	152	4.411	3.57E-02	rs4709991	6	166269980	q27
SNP_A-1854884	G	G	259	109	262	152	4.411	3.57E-02	rs1378473	4	141193458	q31.1
SNP_A-1859273	G	G	315	47	339	77	4.412	3.57E-02	rs17024446	2	100573204	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1856040	T	T	355	7	387	19	4.412	3.57E-02	rs10843028	12	27985938	p11.22
SNP_A-1872096	G	G	362	10	399	3	4.412	3.57E-02	rs16917460	8	53278536	q11.23
SNP_A-1871397	T	T	317	31	329	53	4.411	3.57E-02	rs170654	4	65890922	q13.1
SNP_A-1815766	C	C	366	4	406	0	4.412	3.57E-02	---	6	17976089	p22.3
SNP_A-1821175	C	C	274	80	324	64	4.41	3.57E-02	rs2025330	9	21646683	p21.3
SNP_A-1827417	A	A	346	6	407	1	4.411	3.57E-02	rs14006616	19	38899057	q13.11
SNP_A-1830341	G	G	334	20	350	38	4.412	3.57E-02	rs17476034	11	50056843	p11.12
SNP_A-1914347	G	G	290	80	347	65	4.409	3.57E-02	rs6910043	6	3731552	p25.2
SNP_A-1915628	T	T	386	12	410	4	4.41	3.57E-02	rs206856	2	31529071	p23.1
SNP_A-1905332	G	G	190	162	251	157	4.414	3.57E-02	rs10958364	8	54527478	q11.23
SNP_A-1879940	A	A	269	83	332	70	4.412	3.57E-02	rs9999138	4	166079838	q32.3
SNP_A-1900983	A	A	242	126	242	172	4.41	3.57E-02	rs12493423	3	85484512	p12.1
SNP_A-1899173	T	T	357	27	333	43	4.408	3.58E-02	rs11041186	11	7088352	p15.4
SNP_A-1896243	A	A	283	77	343	63	4.404	3.58E-02	rs1939229	11	126393025	q24.2
SNP_A-1879916	C	T	189	181	227	175	4.406	3.58E-02	rs11792354	9	88793146	q22.1
SNP_A-1882100	T	G	190	166	215	181	4.405	3.58E-02	rs10176573	2	135491203	q21.3
SNP_A-1924415	G	G	247	45	251	71	4.404	3.58E-02	rs4748408	10	17793299	p12.33
SNP_A-1952183	G	G	413	5	402	14	4.407	3.58E-02	rs16951252	18	7101033	p11.31
SNP_A-1955854	G	G	229	109	299	101	4.408	3.58E-02	rs7978424	12	18576708	p12.3
SNP_A-1938658	C	C	417	5	406	14	4.405	3.58E-02	rs1797040	20	23855744	p11.21
SNP_A-1946046	A	A	347	23	371	43	4.407	3.58E-02	rs16851279	3	106748964	q13.11
SNP_A-1965673	C	C	257	159	226	188	4.408	3.58E-02	rs1371182	2	164924722	q24.3
SNP_A-1975315	A	A	345	25	370	46	4.408	3.58E-02	rs10513701	3	173548261	q26.31
SNP_A-1831949	G	G	274	54	324	40	4.405	3.58E-02	rs17081488	6	152017897	q25.1
SNP_A-1719709	T	T	218	132	285	125	4.406	3.58E-02	rs9312601	4	178062932	q34.2
SNP_A-1708560	G	G	220	178	254	152	4.408	3.58E-02	rs1587120	4	21156512	p15.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787559	T	T	347	23	371	43	4.407	3.58E-02	rs4561316	13	92455803	q31.3
SNP_A-1785375	G	G	366	54	344	76	4.405	3.58E-02	rs288831	20	52988657	q13.2
SNP_A-2148896	T	T	291	127	318	100	4.408	3.58E-02	rs8084294	18	34891116	q12.2
SNP_A-2156617	G	G	344	22	372	42	4.408	3.58E-02	rs5762916	22	27682773	q12.1
SNP_A-2161460	A	A	348	6	409	1	4.406	3.58E-02	rs6015225	20	56229934	q13.32
SNP_A-2166235	G	G	345	25	370	46	4.408	3.58E-02	rs17099235	14	32083454	q12
SNP_A-2135021	C	C	232	126	296	116	4.405	3.58E-02	rs1457122	5	6326004	p15.32
SNP_A-2175005	G	G	295	23	347	13	4.405	3.58E-02	rs10768850	11	42649133	p12
SNP_A-2171683	G	G	293	71	304	106	4.405	3.58E-02	rs652052	1	182933665	q31.1
SNP_A-2196228	A	A	384	36	344	52	4.405	3.58E-02	rs3823581	7	129611738	q32.2
SNP_A-2199449	A	A	272	98	329	83	4.406	3.58E-02	rs2283004	7	92705878	q21.3
SNP_A-2193390	G	G	417	5	406	14	4.405	3.58E-02	rs17100273	10	122252756	q26.12
SNP_A-2222713	A	A	363	59	379	39	4.408	3.58E-02	rs2517411	6	31068246	p21.33
SNP_A-2015842	G	G	243	103	305	91	4.408	3.58E-02	rs8127805	21	18914377	q21.1
SNP_A-1995403	A	A	357	29	313	43	4.406	3.58E-02	rs1398291	8	139409406	q24.23
SNP_A-2020739	C	C	269	91	274	130	4.409	3.58E-02	rs2839193	21	46522771	q22.3
SNP_A-20909111	A	G	195	149	210	202	4.408	3.58E-02	rs6084986	20	5007269	p12.3
SNP_A-2105081	A	A	252	164	211	185	4.404	3.58E-02	rs2119026	2	27222044	p23.3
SNP_A-2058527	A	A	362	8	414	2	4.408	3.58E-02	rs16857004	2	11094988	p25.1
SNP_A-2256989	C	C	370	4	410	0	4.408	3.58E-02	rs7308387	12	60052418	q14.1
SNP_A-2280514	G	G	296	116	268	144	4.405	3.58E-02	rs11052423	12	9731305	p13.31
SNP_A-2255353	C	C	264	130	243	163	4.408	3.58E-02	rs1437020	18	36448522	q12.3
SNP_A-2295676	T	T	362	2	406	10	4.407	3.58E-02	rs1609394	3	112636177	q13.13
SNP_A-2314738	C	C	404	14	415	5	4.406	3.58E-02	rs1609290	16	5331541	p13.3
SNP_A-2314978	G	G	263	91	329	79	4.4	3.59E-02	rs11489469	7	152188820	q36.2
SNP_A-2311958	C	C	319	97	345	73	4.402	3.59E-02	---	3	118726699	q13.31
SNP_A-2300771	G	G	185	183	238	174	4.4	3.59E-02	rs2259100	3	9549327	p25.3
SNP_A-2230228	A	A	376	12	341	23	4.404	3.59E-02	rs7540196	1	89173188	p22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235947	G	G	359	3	400	12	4.403	3.59E-02	rs9926939	16	82584041	q23.3
SNP_A-2282819	C	C	253	71	297	55	4.4	3.59E-02	rs17835169	3	104138957	q12.3
SNP_A-2258755	C	C	325	29	348	16	4.403	3.59E-02	rs16936750	9	93143011	q22.31
SNP_A-2266761	A	A	291	127	315	99	4.4	3.59E-02	rs10849538	12	6884868	p13.31
SNP_A-2057684	G	G	320	94	295	121	4.402	3.59E-02	rs7150889	14	28977399	q12
SNP_A-2044354	G	G	300	110	324	84	4.403	3.59E-02	rs4968168	17	423101	p13.3
SNP_A-2005277	G	G	185	183	238	174	4.4	3.59E-02	rs7206944	17	65357395	q24.3
SNP_A-2016567	T	T	320	94	295	121	4.402	3.59E-02	rs7280052	21	23749614	q21.2
SNP_A-2225165	A	A	334	8	382	2	4.403	3.59E-02	rs8014439	14	23257745	q11.2
SNP_A-2225807	T	T	379	25	359	41	4.401	3.59E-02	rs10211734	20	46009213	q13.13
SNP_A-2204973	C	C	171	169	232	168	4.4	3.59E-02	rs7200939	16	26009802	p12.1
SNP_A-2153228	T	T	205	103	275	97	4.404	3.59E-02	rs4931057	12	33156970	p11.21
SNP_A-2148730	T	T	196	166	249	155	4.4	3.59E-02	rs293002	5	58070723	q11.2
SNP_A-2146617	G	A	197	157	205	189	4.404	3.59E-02	rs2898093	13	54061244	q14.3
SNP_A-1711568	C	C	203	199	236	172	4.401	3.59E-02	rs9327458	5	127343698	q23.2
SNP_A-1836078	G	G	335	87	355	63	4.401	3.59E-02	rs17802770	9	114097931	q32
SNP_A-1856963	G	G	224	116	272	100	4.401	3.59E-02	rs10794776	10	1675758	p15.3
SNP_A-1936512	A	A	305	105	338	82	4.403	3.59E-02	rs987926	8	15667229	p22
SNP_A-1955095	G	G	348	14	404	6	4.403	3.59E-02	rs318306	8	90253692	q21.3
SNP_A-1951309	C	C	307	69	268	88	4.401	3.59E-02	rs7691887	4	4535623	p16.3
SNP_A-1953494	C	C	364	0	411	5	4.403	3.59E-02	rs17035430	1	116448289	p13.1
SNP_A-1909989	G	G	281	77	289	113	4.401	3.59E-02	rs11654929	17	72820946	q25.2
SNP_A-1917147	T	T	310	44	365	31	4.397	3.60E-02	rs11074316	15	25367436	q12
SNP_A-1889209	C	C	243	125	242	170	4.398	3.60E-02	rs6686600	1	80318922	p31.1
SNP_A-1951913	C	T	213	209	235	179	4.395	3.60E-02	rs6927944	6	55566203	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1957860	T	T	385	17	343	29	4.397	3.60E-02	rs6507006	18	29098078	q12.1
SNP_A-1958835	C	C	397	7	383	17	4.398	3.60E-02	rs11912378	22	41138001	q13.2
SNP_A-1936232	G	G	225	133	287	123	4.398	3.60E-02	rs1516584	3	80667437	p12.2
SNP_A-1944337	A	A	210	208	238	176	4.398	3.60E-02	rs7974845	12	109709360	q24.11
SNP_A-1983755	C	C	348	74	368	52	4.395	3.60E-02	rs168810	5	141773766	q31.3
SNP_A-1987015	C	C	267	79	338	68	4.396	3.60E-02	rs7751620	6	100459989	q16.3
SNP_A-1856060	T	C	214	200	228	182	4.398	3.60E-02	rs3851784	17	42395116	q21.32
SNP_A-1854361	A	A	373	33	397	19	4.396	3.60E-02	rs13175846	5	7477672	p15.31
SNP_A-1869236	C	C	341	21	389	11	4.397	3.60E-02	rs10883984	10	105972610	q25.1
SNP_A-1824099	A	A	230	96	241	141	4.399	3.60E-02	rs4685279	3	15940493	p25.1
SNP_A-1814950	A	A	221	199	250	168	4.399	3.60E-02	rs10997369	10	68155579	q21.3
SNP_A-1675241	C	C	393	1	397	7	4.396	3.60E-02	rs10496589	2	123448672	q14.3
SNP_A-1754584	C	C	280	68	302	106	4.396	3.60E-02	rs10518484	4	127456065	q28.1
SNP_A-1811346	T	T	205	111	231	173	4.396	3.60E-02	rs342147	12	61443372	q14.2
SNP_A-2141735	G	G	257	101	264	144	4.396	3.60E-02	rs1437019	18	36508304	q12.3
SNP_A-2144890	C	C	235	87	240	126	4.398	3.60E-02	rs7527606	1	163698270	q24.1
SNP_A-2165990	T	T	295	29	304	50	4.399	3.60E-02	rs7033350	9	100072199	q31.1
SNP_A-2163324	T	T	341	3	380	12	4.398	3.60E-02	rs11167810	5	142784880	q31.3
SNP_A-2133594	C	C	333	33	355	57	4.399	3.60E-02	rs1926146	10	129459229	q26.2
SNP_A-2109275	A	A	394	28	348	42	4.397	3.60E-02	rs640631	17	39441706	q21.31
SNP_A-2202150	C	C	362	52	384	34	4.397	3.60E-02	rs11002870	10	80640006	q22.3
SNP_A-2211829	A	A	360	4	398	0	4.397	3.60E-02	rs3745172	19	52577311	q13.32
SNP_A-2214722	G	G	342	22	396	12	4.399	3.60E-02	rs17044546	2	23124781	p24.1
SNP_A-2184329	G	G	298	58	368	46	4.398	3.60E-02	rs4745636	9	77289724	q21.2
SNP_A-2179031	C	C	237	131	297	119	4.395	3.60E-02	rs7672441	4	117828437	q26
SNP_A-2001923	C	C	289	73	301	109	4.397	3.60E-02	rs1447125	11	41279816	p12
SNP_A-1992187	C	C	352	62	372	42	4.399	3.60E-02	rs11906	8	8678669	p23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041697	C	C	325	21	371	11	4.396	3.60E-02	rs11021059	11	94534611	q21
SNP_A-2071438	G	G	260	136	300	114	4.395	3.60E-02	rs6986515	8	81170406	q21.13
SNP_A-2093114	C	C	217	139	273	127	4.395	3.60E-02	rs9554471	13	97882231	q32.2
SNP_A-2089177	C	C	340	6	399	1	4.396	3.60E-02	rs11052464	12	33167404	p11.21
SNP_A-2083415	T	T	258	68	266	102	4.396	3.60E-02	rs11925879	3	60239249	p14.2
SNP_A-2237195	C	C	365	33	372	18	4.397	3.60E-02	rs2729536	7	111377715	q31.1
SNP_A-2289608	C	C	408	14	393	27	4.398	3.60E-02	rs9796551	15	23362881	q12
SNP_A-2310645	G	G	329	37	389	25	4.399	3.60E-02	rs1422202	5	106558118	q21.3
SNP_A-2313466	C	C	264	156	290	126	4.393	0.0361	rs2679120	15	63284449	q22.31
SNP_A-2230608	T	T	350	68	323	91	4.391	0.0361	rs4472922	11	42694884	p12
SNP_A-2258336	C	C	244	126	303	113	4.394	0.0361	rs10951373	7	32883899	p14.3
SNP_A-2273147	C	C	355	67	374	46	4.393	0.0361	rs6969008	7	35307046	p14.2
SNP_A-2275147	G	G	267	95	319	79	4.39	0.0361	rs1308356	10	59597321	q21.1
SNP_A-2086433	T	T	257	115	284	90	4.391	0.0361	rs2585986	4	33079204	p15.1
SNP_A-2088065	A	G	210	160	211	205	4.394	0.0361	rs7047853	9	77345294	q21.2
SNP_A-2086527	T	T	391	17	405	7	4.393	0.0361	---	2	119292569	q14.2
SNP_A-2072727	G	G	317	47	376	34	4.391	0.0361	rs730918	16	24959552	p12.1
SNP_A-2057964	C	C	310	46	367	33	4.392	0.0361	rs11682914	2	210567539	q34
SNP_A-2055003	-	T	191	191	221	163	4.394	0.0361	rs2693808	8	5387422	p23.2
SNP_A-2171754	A	A	202	168	253	155	4.394	0.0361	rs12331240	4	95938721	q22.3
SNP_A-2199605	A	A	376	32	396	18	4.395	0.0361	rs6882530	5	56023174	q11.2
SNP_A-2209680	A	A	215	153	272	142	4.391	0.0361	rs1574273	7	68188797	q11.22
SNP_A-2201328	G	G	194	152	247	141	4.394	0.0361	rs1657305	7	154411555	q36.2
SNP_A-2206551	G	G	235	155	271	131	4.394	0.0361	rs4102886	15	92387926	q26.2
SNP_A-2111525	C	C	271	149	239	177	4.394	0.0361	rs16967810	15	37022888	q14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2110221	T	C	232	178	206	200	4.393	0.0361	rs34921	3	10438569	p25.3
SNP_A-2124860	C	C	314	56	329	87	4.393	0.0361	rs1975145	18	54082159	q21.31
SNP_A-2164975	A	A	328	42	383	29	4.392	0.0361	rs7791060	7	32170509	p14.3
SNP_A-2166855	T	T	328	42	383	29	4.392	0.0361	rs5691	1	71187084	p31.1
SNP_A-2153429	C	T	226	184	214	196	4.394	0.0361	rs9638695	7	13352568	p21.2
SNP_A-1810886	A	A	354	6	415	1	4.392	0.0361	rs7941833	11	44732907	p11.2
SNP_A-1782517	C	T	215	195	225	185	4.393	0.0361	rs1420138	7	29318741	p15.1
SNP_A-1783450	G	G	381	33	361	51	4.391	0.0361	rs815952	7	55336093	p11.2
SNP_A-1660403	C	C	330	70	358	50	4.394	0.0361	rs10500643	11	5470343	p15.4
SNP_A-1651282	C	C	373	15	400	6	4.394	0.0361	rs1050137	15	20551112	q11.2
SNP_A-1652246	C	C	287	115	322	92	4.392	0.0361	rs380319	6	9087681	p24.3
SNP_A-1704569	T	T	272	108	253	139	4.393	0.0361	rs901890	5	8231908	p15.31
SNP_A-1820479	G	G	290	78	298	114	4.391	0.0361	rs9915703	17	14542466	p12
SNP_A-1820541	A	A	276	88	328	72	4.39	0.0361	rs2535469	15	95362348	q26.2
SNP_A-1842713	C	C	260	104	256	142	4.393	0.0361	rs7492628	14	90616889	q32.12
SNP_A-1870579	C	C	276	138	242	164	4.392	0.0361	rs11819305	10	118898040	q26.11
SNP_A-1863441	G	G	257	87	310	72	4.392	0.0361	rs3450072	3	8817809	p25.3
SNP_A-1851619	T	T	265	85	323	71	4.391	0.0361	rs25506	3	35419722	p22.3
SNP_A-1845889	A	A	238	58	296	46	4.39	0.0361	rs7818693	8	104332465	q22.3
SNP_A-1967739	T	T	380	36	399	21	4.392	0.0361	rs10485741	20	10585057	p12.2
SNP_A-1943174	T	T	260	102	312	86	4.394	0.0361	rs3019916	8	108130232	q23.1
SNP_A-1940232	A	A	362	4	400	0	4.395	0.0361	---	3	152404603	q25.1
SNP_A-1952642	C	C	306	112	324	84	4.394	0.0361	rs10844372	12	9707169	p13.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1890132	G	G	385	9	372	20	4.391	0.0361	rs11118841	1	218296211	q41
SNP_A-1915843	A	A	309	59	367	45	4.393	0.0361	rs9516411	13	93877956	q32.1
SNP_A-1923590	C	C	342	6	401	1	4.391	0.0361	rs17087632	18	69277045	q22.3
SNP_A-1926116	A	A	235	89	241	129	4.385	3.62E-02	rs3787509	20	16656109	p12.1
SNP_A-1905710	G	G	347	23	382	12	4.388	3.62E-02	rs6431817	2	6745242	p25.2
SNP_A-1897764	C	C	372	10	332	20	4.387	3.62E-02	rs4752751	11	1690808	p15.5
SNP_A-1956858	G	G	302	120	271	147	4.389	3.62E-02	rs11082202	18	36464063	q12.3
SNP_A-1945934	A	A	254	116	312	102	4.387	3.62E-02	rs6829713	4	16966126	p15.32
SNP_A-1939079	A	A	319	49	380	36	4.389	3.62E-02	rs2099060	5	109753133	q22.1
SNP_A-1966407	G	G	325	13	363	5	4.388	3.62E-02	rs16863138	2	197891087	q33.1
SNP_A-1969192	T	T	344	6	403	1	4.387	3.62E-02	rs197531	21	18263986	q21.1
SNP_A-1984561	C	C	335	11	392	4	4.386	3.62E-02	rs1022038	5	169669316	q35.1
SNP_A-1852077	A	A	227	133	220	176	4.389	3.62E-02	rs4609653	12	101474537	q23.2
SNP_A-1822647	A	A	300	62	358	48	4.388	3.62E-02	rs1927551	13	35968420	q13.3
SNP_A-1713504	C	C	291	107	272	138	4.386	3.62E-02	rs3135095	4	2351439	p16.3
SNP_A-1728655	A	A	212	132	261	117	4.388	3.62E-02	rs2408612	5	125593322	q23.2
SNP_A-1789161	T	T	289	39	356	28	4.388	3.62E-02	rs10760634	9	129583425	q34.11
SNP_A-2156903	G	T	232	178	205	199	4.386	3.62E-02	rs2236947	3	50346436	p21.31
SNP_A-2125876	C	C	366	12	388	4	4.389	3.62E-02	rs7849276	9	28407572	p21.1
SNP_A-2126390	T	C	200	158	201	187	4.388	3.62E-02	rs956319	7	31747660	p14.3
SNP_A-2204103	C	C	392	14	362	26	4.388	3.62E-02	rs1976573	15	97367091	q26.3
SNP_A-2173532	C	T	229	181	206	194	4.388	3.62E-02	rs8016253	14	45508248	q21.2
SNP_A-2057123	G	G	322	98	340	72	4.389	3.62E-02	rs11666341	19	57293211	q13.41
SNP_A-2073739	G	G	310	52	326	82	4.387	3.62E-02	rs17465479	3	87611659	p11.2
SNP_A-2069110	G	G	314	100	329	73	4.388	3.62E-02	rs12128551	1	183638703	q31.1
SNP_A-2100693	C	C	340	8	388	2	4.389	3.62E-02	rs2874129	3	150135577	q24
SNP_A-2043258	T	T	368	48	347	69	4.386	3.62E-02	rs7183319	15	88896036	q26.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027813	C	C	267	155	236	184	4.387	3.62E-02	rs9893975	17	27026066	q11.2
SNP_A-2015706	C	C	232	186	263	157	4.389	3.62E-02	rs2824550	21	18212130	q21.1
SNP_A-2008254	T	T	235	167	260	136	4.389	3.62E-02	rs5753625	22	30179400	q12.2
SNP_A-2008368	G	G	314	42	367	29	4.39	3.62E-02	rs7649380	3	1334249	p26.3
SNP_A-2282079	T	T	344	6	403	1	4.387	3.62E-02	rs9310734	3	24250279	p24.2
SNP_A-2262878	C	C	364	24	382	12	4.389	3.62E-02	rs13279569	8	38460773	p12
SNP_A-2230595	T	T	244	116	303	103	4.389	3.62E-02	rs8011085	14	75123867	q24.3
SNP_A-2239280	T	T	267	55	350	46	4.387	3.62E-02	---	3	78446322	p12.3
SNP_A-2242781	A	A	290	122	318	96	4.386	3.62E-02	rs17622746	7	27763631	p15.1
SNP_A-2301499	C	C	319	49	380	36	4.389	3.62E-02	rs7042243	9	16711632	p22.2
SNP_A-2296682	T	T	217	149	269	135	4.389	3.62E-02	rs10451916	3	158434896	q25.31
SNP_A-2291825	C	C	372	12	394	4	4.383	3.63E-02	rs6900115	6	149333502	q25.1
SNP_A-2256296	T	T	393	19	382	34	4.382	3.63E-02	rs1867708	5	3638795	p15.33
SNP_A-2228941	C	C	358	8	408	2	4.383	3.63E-02	rs10922325	1	194599245	q31.3
SNP_A-2027419	C	C	370	52	345	73	4.383	3.63E-02	rs13016974	2	36091842	p22.3
SNP_A-2023744	A	A	297	63	310	96	4.381	3.63E-02	rs11051944	12	32377185	p11.21
SNP_A-2047299	G	G	206	150	270	144	4.384	3.63E-02	rs4650977	1	174509265	q25.2
SNP_A-2104776	G	G	285	53	328	38	4.382	3.63E-02	rs11196923	10	84773295	q23.1
SNP_A-2198758	C	T	202	168	220	196	4.382	3.63E-02	rs6532335	4	92932679	q22.1
SNP_A-2197811	T	T	349	37	337	57	4.384	3.63E-02	rs2018051	13	22717919	q12.12
SNP_A-2204299	A	A	398	22	400	10	4.385	3.63E-02	rs6797307	3	8576564	p25.3
SNP_A-2209379	G	G	369	39	383	23	4.385	3.63E-02	rs2186209	6	48932113	p12.3
SNP_A-2226231	A	A	350	54	310	72	4.383	3.63E-02	rs4276018	2	227918263	q36.3
SNP_A-2220839	C	C	349	11	408	4	4.382	3.63E-02	rs393412	19	53285853	q13.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2110113	T	C	210	160	209	203	4.382	3.63E-02	rs2030074	11	80321886	q14.1
SNP_A-1812526	C	C	313	17	321	33	4.384	3.63E-02	rs2211397	10	29590393	p11.23
SNP_A-1783655	T	T	301	67	361	53	4.381	3.63E-02	rs2977728	8	4827440	p23.2
SNP_A-1752835	T	T	336	0	381	5	4.383	3.63E-02	rs10498938	6	84842961	q14.2
SNP_A-1823135	C	C	342	8	390	2	4.384	3.63E-02	rs7667621	4	23049768	p15.2
SNP_A-1820459	G	G	210	142	205	189	4.383	3.63E-02	rs9354718	6	69089948	q12
SNP_A-1836823	A	A	321	49	338	78	4.383	3.63E-02	rs879537	3	188478797	q27.3
SNP_A-1847711	C	C	315	27	328	14	4.385	3.63E-02	rs32477	5	100160476	q21.1
SNP_A-1859238	G	G	229	137	225	183	4.382	3.63E-02	rs4553350	11	12716410	p15.2
SNP_A-1870929	G	G	231	141	213	177	4.382	3.63E-02	rs2384668	12	114513944	q24.21
SNP_A-1872134	-	C	182	182	228	168	4.381	3.63E-02	rs9967822	2	161518417	q24.2
SNP_A-1873426	G	G	363	7	397	19	4.382	3.63E-02	rs17548825	11	79455747	q14.1
SNP_A-1944305	G	G	221	123	221	169	4.381	3.63E-02	rs7744950	6	145233468	q24.2
SNP_A-1941351	C	C	297	69	357	55	4.381	3.63E-02	---	18	61791104	q22.1
SNP_A-1943152	G	G	264	154	283	121	4.383	3.63E-02	rs1046896	17	78278822	q25.3
SNP_A-1880018	C	C	324	96	345	71	4.383	3.63E-02	rs1658175	18	4473871	p11.31
SNP_A-1905558	C	C	198	148	245	133	4.381	3.63E-02	rs7164592	15	71063984	q24.1
SNP_A-1921855	C	C	302	34	325	59	4.384	3.63E-02	rs2688497	3	196965669	q29
SNP_A-1927726	A	A	337	43	317	63	4.385	3.63E-02	rs6970151	7	2955064	p22.2
SNP_A-1931715	G	G	392	20	405	9	4.38	3.64E-02	rs7843464	8	128231126	q24.21
SNP_A-1910135	T	C	214	200	229	183	4.376	3.64E-02	rs17737079	11	122558025	q24.1
SNP_A-1874661	G	G	380	22	382	10	4.38	3.64E-02	rs9668242	12	129517096	q24.33
SNP_A-1892580	T	T	369	7	380	18	4.38	3.64E-02	rs17117966	14	72120227	q24.2
SNP_A-1934861	C	C	405	9	404	2	4.378	3.64E-02	rs10198548	2	238450284	q37.3
SNP_A-1845640	C	C	377	7	340	16	4.378	3.64E-02	rs473706	7	99069402	q22.1
SNP_A-1821133	G	G	303	63	313	95	4.377	3.64E-02	rs10804857	3	176728529	q26.31
SNP_A-1758884	G	G	363	37	351	57	4.378	3.64E-02	rs724677	6	56167557	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2129620	T	T	337	79	312	104	4.378	3.64E-02	rs1958097	14	46792857	q21.3
SNP_A-2134794	C	C	348	6	407	1	4.377	3.64E-02	rs10000481	4	70017933	q13.2
SNP_A-2212483	T	T	351	15	376	6	4.377	3.64E-02	rs8026324	15	27010574	q13.1
SNP_A-2192573	G	G	362	16	401	7	4.377	3.64E-02	rs7541719	1	240843432	q44
SNP_A-2190822	A	A	246	114	248	158	4.379	3.64E-02	rs6776647	3	158470397	q25.31
SNP_A-2175651	G	G	375	25	346	40	4.38	3.64E-02	rs10119203	9	121892632	q33.2
SNP_A-2067298	C	C	271	97	331	83	4.378	3.64E-02	rs1037995	19	23098995	p12
SNP_A-2045627	C	C	329	21	375	11	4.38	3.64E-02	rs6885953	5	97694151	q21.1
SNP_A-2042698	T	T	264	28	324	18	4.38	3.64E-02	rs6928877	6	51440121	p12.2
SNP_A-2021496	C	C	351	11	410	4	4.376	3.64E-02	rs17049383	3	8655116	p25.3
SNP_A-2026984	G	G	372	48	351	69	4.379	3.64E-02	rs13087868	3	72180620	p13
SNP_A-2006439	A	A	340	82	361	59	4.376	3.64E-02	rs6546313	2	67683279	p14
SNP_A-2018892	A	A	288	78	296	114	4.379	3.64E-02	rs2249629	21	36932454	q22.13
SNP_A-1989611	C	C	276	136	302	108	4.378	3.64E-02	rs722336	7	38278145	p14.1
SNP_A-2000580	T	T	297	117	269	145	4.378	3.64E-02	rs7094791	10	51229942	q11.23
SNP_A-2273953	T	T	243	167	210	194	4.379	3.64E-02	rs6785203	3	136159208	q22.1
SNP_A-2312290	C	C	259	157	227	185	4.38	3.64E-02	rs11644188	16	84906069	q24.1
SNP_A-2306335	T	T	254	164	283	135	4.379	3.64E-02	rs8034122	15	91733751	q26.1
SNP_A-2307695	G	G	246	156	281	131	4.38	3.64E-02	rs11685085	2	119678201	q14.2
SNP_A-2300732	G	G	296	64	354	50	4.375	3.65E-02	rs7187443	16	81754558	q23.3
SNP_A-2298002	C	C	362	8	412	2	4.374	3.65E-02	rs5768165	22	46638717	q13.31
SNP_A-2277325	C	C	204	162	260	152	4.373	3.65E-02	rs11123350	2	116865668	q14.1
SNP_A-2034780	G	G	308	18	332	36	4.374	3.65E-02	rs16862069	2	174433013	q31.1
SNP_A-2069430	G	G	301	67	307	99	4.373	3.65E-02	rs6887976	5	113996634	q22.3
SNP_A-2075255	C	C	263	131	231	157	4.374	3.65E-02	rs6969722	7	12051677	p21.3
SNP_A-2099472	A	A	267	97	271	137	4.374	3.65E-02	rs529603	10	132068230	q26.3
SNP_A-2095360	G	G	174	172	225	163	4.372	3.65E-02	rs1595471	4	118431839	q26

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086514	G	G	221	181	249	151	4.374	3.65E-02	rs2717695	16	3090897	p13.3
SNP_A-2087516	A	A	324	30	347	53	4.372	3.65E-02	rs7774873	6	105025126	q16.3
SNP_A-2175074	G	G	416	6	389	15	4.373	3.65E-02	rs11824348	11	16871867	p15.1
SNP_A-2176886	T	T	385	9	384	2	4.374	3.65E-02	rs17149023	7	74842169	q11.23
SNP_A-2199833	C	C	254	92	307	77	4.372	3.65E-02	rs7818245	8	107303551	q23.1
SNP_A-2221721	G	G	350	6	409	1	4.373	3.65E-02	rs16953874	18	47514407	q21.1
SNP_A-2119009	A	A	262	96	262	134	4.374	3.65E-02	rs233928	6	132384438	q23.2
SNP_A-2145102	A	A	348	58	378	40	4.372	3.65E-02	rs6895045	5	1792087	p15.33
SNP_A-2147052	G	G	227	139	225	187	4.372	3.65E-02	rs10191219	2	214657470	q34
SNP_A-1726326	C	T	213	171	212	196	4.372	3.65E-02	rs366307	5	150575654	q33.1
SNP_A-1733762	G	G	281	67	349	55	4.374	3.65E-02	rs2249413	5	109113254	q21.3
SNP_A-1805495	A	A	290	132	307	101	4.374	3.65E-02	rs4144019	9	96030803	q22.32
SNP_A-1806475	G	G	338	24	400	14	4.375	3.65E-02	rs1219455	11	121314597	q24.1
SNP_A-1792881	A	A	274	124	251	155	4.373	3.65E-02	rs7096726	10	71106168	q22.1
SNP_A-1818389	G	G	272	92	277	131	4.373	3.65E-02	rs1961638	8	68857010	q13.2
SNP_A-1840933	T	T	219	141	283	133	4.374	3.65E-02	rs6925345	6	13243326	p24.1
SNP_A-1909389	C	C	326	24	386	14	4.374	3.65E-02	rs16892017	5	62943785	q12.1
SNP_A-1919121	C	C	333	15	397	7	4.374	3.65E-02	rs10117149	7	77718494	q21.11
SNP_A-1905364	C	C	290	74	350	60	4.369	3.66E-02	rs7122128	11	110107608	q23.1
SNP_A-1927241	G	G	241	113	291	97	4.37	3.66E-02	rs534621	6	145613858	q24.2
SNP_A-1922141	C	C	310	60	324	92	4.369	3.66E-02	rs6441441	3	163485729	q26.1
SNP_A-1890266	G	G	335	31	349	53	4.371	3.66E-02	rs17357858	7	105144158	q22.3
SNP_A-1874457	T	T	257	109	309	93	4.367	3.66E-02	rs1940735	11	112414065	q23.1
SNP_A-1873893	C	C	344	78	316	102	4.369	3.66E-02	rs12362057	11	131539251	q25
SNP_A-1879765	T	T	296	66	296	96	4.369	3.66E-02	rs312350	4	18939143	p15.31
SNP_A-1952738	C	C	217	91	217	129	4.37	3.66E-02	rs11951576	5	6784413	p15.31
SNP_A-1989308	C	T	202	198	233	177	4.369	3.66E-02	rs940525	7	27334062	p15.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1970568	A	A	224	184	251	153	4.367	3.66E-02	rs2838336	21	43896169	q22.3
SNP_A-1817737	C	C	256	112	314	98	4.367	3.66E-02	rs889785	16	26135788	p12.1
SNP_A-1825780	T	T	329	65	320	92	4.368	3.66E-02	rs10957333	8	66104003	q13.1
SNP_A-1866665	C	C	302	62	360	48	4.37	3.66E-02	rs9533810	13	43751819	q14.11
SNP_A-1795808	T	T	359	11	332	22	4.37	3.66E-02	rs6004842	22	24659853	q12.1
SNP_A-1707870	G	G	289	111	271	143	4.371	3.66E-02	rs4131413	3	111181939	q13.13
SNP_A-1701311	G	G	359	27	353	45	4.368	3.66E-02	rs2123149	15	42765072	q21.1
SNP_A-2164305	T	T	186	182	239	173	4.369	3.66E-02	rs4341430	10	68167094	q21.3
SNP_A-2117173	A	A	318	42	382	30	4.369	3.66E-02	rs8005401	14	55367122	q22.3
SNP_A-2129781	G	G	323	39	343	65	4.368	3.66E-02	rs9646822	2	195510668	q32.3
SNP_A-2206872	A	A	229	135	223	179	4.371	3.66E-02	rs8095055	18	32182513	q12.2
SNP_A-2205777	A	A	334	84	304	108	4.368	3.66E-02	rs2494069	1	107958895	p13.3
SNP_A-2168528	T	T	298	116	324	90	4.368	3.66E-02	rs13396538	2	157185034	q24.1
SNP_A-2197507	A	A	340	6	397	1	4.367	3.66E-02	rs10400347	11	120394755	q23.3
SNP_A-2082958	G	G	336	32	354	18	4.368	3.66E-02	rs4947984	7	54985525	p11.2
SNP_A-2072521	G	G	274	62	296	98	4.368	3.66E-02	rs1331478	6	12754666	p24.1
SNP_A-2060316	C	C	353	65	328	88	4.371	3.66E-02	rs637168	1	23039977	p36.12
SNP_A-2047941	G	G	401	3	366	10	4.367	3.66E-02	rs4459649	18	18971195	q11.2
SNP_A-2034321	A	A	352	6	411	1	4.368	3.66E-02	rs11193460	10	109206626	q25.1
SNP_A-2043121	T	T	348	8	396	2	4.371	3.66E-02	rs12355606	10	18537827	p12.33
SNP_A-2019396	A	-	238	178	210	210	4.37	3.66E-02	rs2150414	21	39536858	q22.2
SNP_A-1997127	T	T	360	56	379	37	4.37	3.66E-02	rs9314757	9	86818911	q21.33
SNP_A-1994516	G	G	224	132	224	180	4.37	3.66E-02	rs10505065	8	105851748	q22.3
SNP_A-2250656	C	C	260	104	264	146	4.368	3.66E-02	rs11151627	18	66817893	q22.2
SNP_A-2300688	A	A	324	86	288	108	4.371	3.66E-02	rs11724048	4	7790856	p16.1
SNP_A-2294428	T	T	249	97	242	132	4.367	3.66E-02	rs10020796	4	153877386	q31.3
SNP_A-2312245	G	G	352	56	362	36	4.364	3.67E-02	rs1061843	17	37211870	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255834	G	G	289	51	313	83	4.363	3.67E-02	rs12200580	6	123213557	q22.31
SNP_A-2238037	A	A	381	37	355	55	4.363	3.67E-02	rs1769441	14	81584922	q31.1
SNP_A-2284856	G	G	336	84	309	109	4.364	3.67E-02	rs2656283	8	4019020	p23.2
SNP_A-1991070	G	G	325	13	359	29	4.362	3.67E-02	rs1534528	7	120715973	q31.32
SNP_A-1991888	A	A	246	138	213	163	4.365	3.67E-02	rs6558562	8	1830399	p23.3
SNP_A-2040886	T	T	288	76	348	62	4.362	3.67E-02	rs7993042	13	73752182	q22.1
SNP_A-2064581	A	A	254	164	279	133	4.365	3.67E-02	rs2245251	10	93050437	q23.32
SNP_A-2095835	G	G	283	85	291	123	4.363	3.67E-02	rs2579399	2	197812007	q33.1
SNP_A-2106468	C	C	315	43	332	70	4.365	3.67E-02	rs12431261	13	109442991	q34
SNP_A-2203691	T	T	169	141	231	139	4.364	3.67E-02	rs6475552	9	21691674	p21.3
SNP_A-2114204	A	A	305	81	344	62	4.366	3.67E-02	rs1560846	8	77692021	q21.11
SNP_A-2154800	A	A	276	82	237	101	4.366	3.67E-02	rs42425	5	36214050	p13.2
SNP_A-1667050	G	G	309	89	292	118	4.366	3.67E-02	rs10503672	8	19997976	p21.3
SNP_A-1731553	G	G	391	1	397	7	4.366	3.67E-02	rs10495898	2	43573871	p21
SNP_A-1750001	G	G	280	70	348	58	4.364	3.67E-02	rs10513451	3	154888350	q25.2
SNP_A-1752115	G	G	366	36	356	56	4.364	3.67E-02	rs10499653	7	46886604	p13
SNP_A-1795917	C	C	181	179	228	166	4.367	3.67E-02	rs983394	7	37383603	p14.1
SNP_A-1790603	C	C	335	85	358	62	4.362	3.67E-02	rs7096997	10	112346697	q25.2
SNP_A-1813989	G	G	360	60	334	82	4.363	3.67E-02	rs11037023	11	42692458	p12
SNP_A-1807835	C	C	374	36	364	56	4.363	3.67E-02	rs11254072	10	16628371	p13
SNP_A-1872522	G	G	319	33	369	21	4.366	3.67E-02	rs13388525	2	180233887	q31.2
SNP_A-1872623	T	T	309	45	327	73	4.363	3.67E-02	rs10214278	5	93263435	q15
SNP_A-1863196	C	C	213	103	227	153	4.363	3.67E-02	rs9900575	17	36561201	q21.2
SNP_A-1846660	A	A	372	4	408	0	4.363	3.67E-02	rs16937526	8	72310739	q13.3
SNP_A-1970697	T	T	395	7	389	1	4.365	3.67E-02	rs17208994	22	17748415	q11.21
SNP_A-1985815	G	G	350	58	380	40	4.366	3.67E-02	rs3747751	6	41866561	p21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982813	G	G	244	126	243	171	4.365	3.67E-02	rs2445074	5	106915697	q21.3
SNP_A-1957329	C	C	268	32	281	55	4.365	3.67E-02	rs11264782	1	154433540	q23.1
SNP_A-1883077	G	G	340	2	341	9	4.364	3.67E-02	rs7908400	10	47097200	q11.22
SNP_A-1910608	A	A	319	27	387	17	4.363	3.67E-02	rs17502349	10	10506436	p14
SNP_A-1909474	C	C	213	151	205	197	4.359	3.68E-02	rs267184	6	7778428	p24.3
SNP_A-1918254	A	A	317	49	334	78	4.361	3.68E-02	rs2079373	7	31892770	p14.3
SNP_A-1922619	T	T	247	113	309	101	4.358	3.68E-02	rs1585804	17	69345596	q25.1
SNP_A-1923971	A	A	349	47	330	68	4.361	3.68E-02	rs12592407	15	56568387	q21.3
SNP_A-1900450	C	C	339	11	378	26	4.357	3.68E-02	rs450514	13	110099997	q34
SNP_A-1958048	A	A	240	124	238	168	4.361	3.68E-02	rs6075297	20	18129243	p11.23
SNP_A-1936555	A	A	379	23	376	40	4.361	3.68E-02	rs988766	16	56720980	q21
SNP_A-1940436	G	G	325	49	281	65	4.358	3.68E-02	rs7999935	13	19346857	q12.11
SNP_A-1978428	T	T	321	47	380	34	4.361	3.68E-02	rs220611	4	109595760	q25
SNP_A-1987963	T	T	259	89	245	119	4.358	3.68E-02	rs9285504	6	145126283	q24.2
SNP_A-1850571	C	T	219	169	200	192	4.358	3.68E-02	rs7331418	13	19778993	q12.11
SNP_A-1821894	A	A	321	47	380	34	4.361	3.68E-02	rs4833663	4	121946614	q27
SNP_A-1837732	G	G	298	56	352	42	4.36	3.68E-02	rs10954328	7	130915280	q32.3
SNP_A-1810107	A	A	282	8	399	3	4.361	3.68E-02	rs16873200	4	22563483	p15.31
SNP_A-1801572	T	T	406	14	415	5	4.362	3.68E-02	rs11067812	12	114774372	q24.21
SNP_A-1731115	C	C	360	42	347	63	4.361	3.68E-02	rs10520762	15	92992307	q26.2
SNP_A-1715235	A	A	312	90	342	68	4.361	3.68E-02	rs728465	5	142412670	q31.3
SNP_A-1664712	T	C	206	196	231	181	4.362	3.68E-02	rs726788	19	14604245	p13.12
SNP_A-2157010	A	A	328	26	375	15	4.362	3.68E-02	rs17208789	5	141798471	q31.3
SNP_A-2165665	G	G	282	136	295	103	4.362	3.68E-02	rs1058132	16	57103798	q21
SNP_A-2149946	T	T	231	131	285	117	4.359	3.68E-02	rs4072775	6	18188230	p22.3
SNP_A-2140660	C	C	276	120	317	99	4.358	3.68E-02	rs6471309	8	87456876	q21.3
SNP_A-2128651	T	T	316	42	335	69	4.361	3.68E-02	rs9568257	13	49031322	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123758	A	A	228	124	272	106	4.36	3.68E-02	rs500859	9	75297656	q21.13
SNP_A-2136304	A	A	250	104	259	149	4.358	3.68E-02	rs12017238	13	41209859	q14.11
SNP_A-2203041	A	A	315	19	345	9	4.357	3.68E-02	rs11709729	3	10889685	p25.3
SNP_A-2211612	G	G	354	16	383	33	4.362	3.68E-02	rs6771463	3	177971100	q26.32
SNP_A-2219956	G	G	236	106	296	94	4.358	3.68E-02	rs12884292	14	55808205	q22.3
SNP_A-2196152	C	C	406	14	415	5	4.362	3.68E-02	rs1706509	12	125744996	q24.32
SNP_A-2171954	A	A	206	152	261	141	4.358	3.68E-02	rs10964178	9	19476059	p22.1
SNP_A-2101707	T	T	270	152	238	180	4.358	3.68E-02	rs11853804	15	61315309	q22.2
SNP_A-2083469	A	A	326	90	300	116	4.361	3.68E-02	rs6670755	1	112444347	p13.2
SNP_A-2066140	T	T	343	47	319	67	4.358	3.68E-02	rs17825644	14	94013865	q32.13
SNP_A-2062854	G	G	246	124	305	111	4.36	3.68E-02	rs7376756	4	127907990	q28.1
SNP_A-2072031	C	C	209	153	268	144	4.359	3.68E-02	rs10991289	9	104363263	q31.1
SNP_A-2057757	A	A	302	66	316	100	4.359	3.68E-02	rs2552357	2	52514291	p16.3
SNP_A-2034600	G	G	318	14	368	6	4.361	3.68E-02	rs8072400	17	65481793	q24.3
SNP_A-2269641	A	A	250	120	250	164	4.361	3.68E-02	rs6950264	7	126366553	q32.1
SNP_A-2227957	C	C	204	142	259	131	4.362	3.68E-02	rs10829822	10	132546965	q26.3
SNP_A-2230720	G	G	299	69	359	55	4.361	3.68E-02	rs6854818	4	542862	p16.3
SNP_A-2292792	C	C	312	108	279	133	4.359	3.68E-02	rs897157	8	126740358	q24.13
SNP_A-2288803	C	C	299	57	312	88	4.358	3.68E-02	rs17199737	4	158953709	q32.1
SNP_A-2289849	C	C	331	29	358	52	4.361	3.68E-02	rs268391	8	15074417	p22
SNP_A-2300154	T	T	378	44	393	27	4.358	3.68E-02	rs17105725	10	87359244	q23.2
SNP_A-2299612	C	C	414	0	378	4	4.357	3.69E-02	rs11856090	15	79010261	q25.1
SNP_A-2228738	A	A	350	46	343	69	4.356	3.69E-02	rs4739959	8	84683102	q21.13
SNP_A-2229054	T	T	208	162	263	151	4.353	3.69E-02	rs7672552	4	23687877	p15.2
SNP_A-2244258	G	G	357	1	363	7	4.353	3.69E-02	rs10960465	9	12081983	p23
SNP_A-2261410	T	T	346	6	403	1	4.353	3.69E-02	rs17093183	8	20709014	p21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2285145	A	A	221	147	219	197	4.354	3.69E-02	rs3886608	7	41548715	p14.1
SNP_A-2031448	C	C	365	37	386	22	4.357	3.69E-02	rs1600705	1	234727786	q43
SNP_A-1992245	T	T	348	20	377	39	4.356	3.69E-02	rs10751867	10	2339064	p15.3
SNP_A-1996740	G	G	247	125	286	104	4.357	3.69E-02	rs7898283	10	17201246	p13
SNP_A-2003242	C	C	182	180	238	174	4.357	3.69E-02	rs7069727	10	83788449	q23.1
SNP_A-2069834	A	A	310	60	368	46	4.355	3.69E-02	rs17459885	12	30252146	p11.22
SNP_A-2174410	G	G	348	14	402	6	4.355	3.69E-02	rs11561896	7	145791421	q35
SNP_A-2122576	C	C	320	86	348	64	4.357	3.69E-02	rs7807392	7	75155212	q11.23
SNP_A-2150796	C	C	393	23	403	11	4.356	3.69E-02	rs11221232	11	127650074	q24.3
SNP_A-2161497	T	T	215	153	210	202	4.354	3.69E-02	rs9384411	6	156407169	q25.3
SNP_A-2155141	A	G	193	157	212	192	4.355	3.69E-02	rs1032472	9	28783694	p21.1
SNP_A-1663786	T	T	239	111	305	101	4.355	3.69E-02	rs10502992	18	50792586	q21.2
SNP_A-1680634	C	C	324	42	279	57	4.357	3.69E-02	rs10489494	1	63168678	p31.3
SNP_A-1744837	T	T	367	35	359	55	4.357	3.69E-02	rs10485802	20	55217196	q13.31
SNP_A-1753455	A	A	237	149	278	128	4.354	3.69E-02	rs1417315	13	57308332	q21.2
SNP_A-1790809	G	G	177	169	218	152	4.356	3.69E-02	rs10100077	8	50006930	q11.21
SNP_A-1785697	A	A	212	152	206	200	4.354	3.69E-02	rs2166337	5	13745279	p15.2
SNP_A-1845669	G	G	306	64	319	97	4.357	3.69E-02	rs1826214	1	208991808	q32.3
SNP_A-1845624	T	T	251	117	254	162	4.353	3.69E-02	rs2049303	8	3735937	p23.2
SNP_A-1871696	A	A	270	90	325	75	4.354	3.69E-02	rs16832990	2	191524552	q32.2
SNP_A-1869542	G	G	294	62	357	49	4.357	3.69E-02	rs9257725	6	29403873	p22.1
SNP_A-1870008	A	A	347	51	334	74	4.357	3.69E-02	rs4069937	2	101469515	q11.2
SNP_A-1988051	G	G	331	25	395	15	4.357	3.69E-02	rs16854007	1	227666666	q42.2
SNP_A-1986688	G	A	201	169	220	194	4.355	3.69E-02	rs6903593	6	85121967	q14.3
SNP_A-1985613	T	T	244	94	309	83	4.353	3.69E-02	rs1335914	1	217495627	q41
SNP_A-1978300	A	A	255	105	247	141	4.354	3.69E-02	rs2494148	1	191199314	q31.3
SNP_A-1944611	T	T	275	61	262	86	4.357	3.69E-02	rs6946289	7	53340306	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1951834	T	T	331	25	395	15	4.357	3.69E-02	rs9361485	6	79816451	q14.1
SNP_A-1948282	A	A	321	19	380	10	4.355	3.69E-02	rs17053795	4	169508723	q32.3
SNP_A-1902258	G	G	251	117	254	162	4.353	3.69E-02	rs7236963	18	36456498	q12.3
SNP_A-1900131	T	C	193	177	230	186	4.354	3.69E-02	rs10159180	1	153293397	q22
SNP_A-1889841	G	G	394	12	359	23	4.357	3.69E-02	rs16883109	4	29898872	p15.1
SNP_A-1889621	G	G	233	109	284	94	4.35	3.70E-02	rs7459315	7	76086023	q11.23
SNP_A-1900124	C	C	365	55	382	36	4.349	3.70E-02	rs16857578	1	228975966	q42.2
SNP_A-1925825	G	G	326	12	397	5	4.352	3.70E-02	rs6093909	20	42057381	q13.12
SNP_A-1969254	C	C	235	173	259	141	4.348	3.70E-02	rs2103500	21	19329426	q21.1
SNP_A-1963662	T	T	356	0	407	5	4.349	3.70E-02	rs6737954	2	67988135	p14
SNP_A-1857560	G	G	304	30	344	18	4.35	3.70E-02	rs9503347	6	294928	p25.3
SNP_A-1841311	A	A	317	99	335	73	4.35	3.70E-02	rs2530565	7	34476195	p14.3
SNP_A-1835416	T	T	346	60	325	83	4.352	3.70E-02	rs10277859	7	150824845	q36.1
SNP_A-1818672	A	A	293	17	321	35	4.351	3.70E-02	rs325931	1	111390544	p13.3
SNP_A-1792025	C	C	337	21	383	11	4.35	3.70E-02	rs12341214	9	27811861	p21.2
SNP_A-1796706	G	G	300	70	310	104	4.352	3.70E-02	rs11941943	4	168730224	q32.3
SNP_A-1690485	C	C	323	27	356	50	4.35	3.70E-02	rs345006	3	146434347	q24
SNP_A-1664522	G	G	315	87	348	66	4.349	3.70E-02	rs10491187	17	63947698	q24.1
SNP_A-2114700	G	G	325	25	341	45	4.348	3.70E-02	rs1112108	4	113331592	q25
SNP_A-2109505	A	A	293	65	304	98	4.351	3.70E-02	rs12881813	14	24313122	q12
SNP_A-2172228	A	A	364	4	398	0	4.349	3.70E-02	rs2928983	18	47656043	q21.1
SNP_A-2188875	A	A	241	129	236	172	4.35	3.70E-02	rs11623553	14	21345162	q11.2
SNP_A-2223309	G	G	323	11	360	26	4.353	3.70E-02	rs13229138	7	6004414	p22.1
SNP_A-2072401	A	A	313	25	320	44	4.352	3.70E-02	rs398702	12	69114046	q15
SNP_A-2053547	C	C	351	61	353	39	4.351	3.70E-02	rs9261198	6	30110921	p21.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101183	T	T	329	67	315	93	4.351	3.70E-02	rs11208257	1	63826322	p31.3
SNP_A-2106860	T	T	324	20	311	35	4.351	3.70E-02	rs13270617	8	92416397	q21.3
SNP_A-1990171	C	C	251	165	219	193	4.349	3.70E-02	rs1018945	7	74900399	q11.23
SNP_A-2017157	T	T	260	92	310	76	4.353	3.70E-02	rs2830468	21	27050077	q21.3
SNP_A-2012892	C	A	233	181	209	201	4.35	3.70E-02	rs7789785	7	129613867	q32.2
SNP_A-2025773	C	C	347	9	336	20	4.35	3.70E-02	rs9602431	13	83759840	q31.1
SNP_A-2036387	T	T	363	5	318	0	4.352	3.70E-02	rs2726602	8	59843406	q12.1
SNP_A-2041074	A	A	291	61	340	46	4.351	3.70E-02	rs11172831	12	57618799	q14.1
SNP_A-2276995	T	T	271	53	319	39	4.351	3.70E-02	rs883999	2	201028616	q33.1
SNP_A-2278636	T	T	244	126	300	112	4.345	3.71E-02	rs2900132	9	116489192	q33.1
SNP_A-2296232	C	C	264	140	240	172	4.347	3.71E-02	rs13362538	5	32828526	p13.3
SNP_A-2313522	G	G	355	51	317	69	4.347	3.71E-02	rs9989364	16	62551681	q21
SNP_A-2307635	C	C	218	116	250	94	4.346	3.71E-02	rs10905240	10	7948558	p14
SNP_A-2040790	C	C	341	75	361	53	4.346	3.71E-02	rs11777631	8	125929318	q24.13
SNP_A-2032233	A	A	290	72	333	55	4.347	3.71E-02	rs9504248	6	4716696	p25.1
SNP_A-2013042	G	G	403	15	384	28	4.346	3.71E-02	rs6597441	7	153841838	q36.2
SNP_A-2018060	A	A	193	171	242	158	4.347	3.71E-02	rs2833574	21	32246418	q22.11
SNP_A-2012077	A	A	255	123	251	165	4.348	3.71E-02	rs6569625	6	130099903	q22.33
SNP_A-2010179	G	G	319	39	339	65	4.347	3.71E-02	rs7695609	4	138244439	q28.3
SNP_A-2001579	C	C	259	153	290	126	4.344	3.71E-02	rs2799401	10	130002014	q26.2
SNP_A-2097647	T	T	257	151	222	176	4.345	3.71E-02	rs2240525	5	131343783	q23.3
SNP_A-2091054	C	C	277	135	247	163	4.344	3.71E-02	rs6891331	5	174078323	q35.2
SNP_A-2051716	G	G	349	73	320	96	4.345	3.71E-02	rs11204557	1	244402310	q44
SNP_A-2050773	C	C	201	127	200	174	4.346	3.71E-02	rs4814520	20	16564817	p12.1
SNP_A-2064465	C	C	343	15	378	32	4.347	3.71E-02	rs822022	1	152568312	q22
SNP_A-2221112	A	A	225	141	284	130	4.348	3.71E-02	rs7730339	5	95687493	q15
SNP_A-2219676	G	G	296	88	285	119	4.346	3.71E-02	rs13241368	7	57430579	p11.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189493	A	A	275	95	281	135	4.344	3.71E-02	rs10750687	11	103553612	q22.3
SNP_A-2196376	G	G	304	58	367	45	4.344	3.71E-02	rs11611582	12	57062327	q14.1
SNP_A-2194758	C	C	380	40	357	59	4.345	3.71E-02	rs6095326	20	46893183	q13.13
SNP_A-2110749	G	G	327	31	355	55	4.346	3.71E-02	rs11228349	11	68305044	q13.3
SNP_A-1801383	A	A	293	113	314	86	4.345	3.71E-02	rs1608443	18	907643	p11.32
SNP_A-1873048	T	T	195	173	250	164	4.347	3.71E-02	rs265767	3	1350581	p26.3
SNP_A-1860788	G	G	366	4	400	0	4.347	3.71E-02	rs1862617	5	56128342	q11.2
SNP_A-1965082	T	T	375	25	366	42	4.344	3.71E-02	rs344904	2	139911142	q22.1
SNP_A-1970262	A	A	378	10	413	3	4.348	3.71E-02	rs1012961	21	37238758	q22.13
SNP_A-1979007	C	C	336	66	300	86	4.346	3.71E-02	rs10754224	1	194244446	q31.3
SNP_A-1977883	C	C	297	65	305	97	4.345	3.71E-02	rs2868905	4	85826162	q21.23
SNP_A-1985124	C	C	272	52	290	34	4.344	3.71E-02	rs2516234	6	12701540	p24.1
SNP_A-1931118	C	C	225	189	257	161	4.345	3.71E-02	rs4961654	9	18486875	p22.2
SNP_A-1913629	A	A	335	35	391	23	4.347	3.71E-02	rs11998784	9	28865332	p21.1
SNP_A-1905260	A	A	333	25	397	15	4.345	3.71E-02	rs6703696	1	4488868	p36.32
SNP_A-1890473	T	T	313	47	361	33	4.344	3.71E-02	rs17130688	1	68614013	p31.2
SNP_A-1900096	A	A	352	6	409	1	4.34	3.72E-02	rs2480203	6	84794212	q14.3
SNP_A-1903547	T	T	247	121	306	108	4.342	3.72E-02	rs8072395	17	36380188	q21.2
SNP_A-1918003	A	A	303	45	316	72	4.343	3.72E-02	rs17582249	3	179680754	q26.32
SNP_A-1963882	G	G	362	8	410	2	4.341	3.72E-02	rs17013999	2	77467849	p12
SNP_A-1941241	T	T	322	60	290	80	4.34	3.72E-02	rs12471982	2	21297730	p24.1
SNP_A-1864580	A	A	328	6	330	16	4.341	3.72E-02	rs17144788	7	21428065	p15.3
SNP_A-1853203	C	T	217	205	232	184	4.341	3.72E-02	rs7174056	15	69293185	q23
SNP_A-1787138	C	C	341	15	405	7	4.339	3.72E-02	rs6709937	2	174722180	q31.1
SNP_A-1708042	T	T	328	72	304	96	4.34	3.72E-02	rs10490830	3	106769971	q13.11
SNP_A-1780291	G	G	277	75	310	56	4.34	3.72E-02	rs13396369	2	113727992	q13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116992	A	A	287	41	334	28	4.342	3.72E-02	rs1932055	1	70845683	p31.1
SNP_A-2125061	C	C	353	69	326	92	4.34	3.72E-02	rs17725929	2	210047947	q34
SNP_A-2154813	G	G	335	53	339	33	4.34	3.72E-02	rs7013226	8	125149660	q24.13
SNP_A-2160989	A	A	319	9	393	3	4.343	3.72E-02	rs1390269	6	65480452	q12
SNP_A-2152068	G	G	231	135	274	116	4.342	3.72E-02	rs6031579	20	42448522	q13.12
SNP_A-2138937	C	C	362	8	410	2	4.341	3.72E-02	rs2774180	13	88584289	q31.2
SNP_A-2217604	G	G	311	55	299	79	4.342	3.72E-02	rs10908338	1	37435353	p34.3
SNP_A-2222087	C	C	308	38	353	25	4.34	3.72E-02	rs878876	18	54590752	q21.31
SNP_A-2203540	G	G	372	42	381	25	4.343	3.72E-02	rs2461875	10	79661069	q22.3
SNP_A-2063954	G	G	331	7	363	19	4.341	3.72E-02	rs2020264	15	52816113	q21.3
SNP_A-2059591	C	C	217	145	278	136	4.34	3.72E-02	rs1391262	4	83020685	q21.22
SNP_A-2106500	G	G	257	101	321	89	4.343	3.72E-02	rs7198356	16	83777189	q24.1
SNP_A-2004300	A	A	388	28	371	45	4.34	3.72E-02	rs8023863	15	77423457	q25.1
SNP_A-2042060	G	G	223	147	220	196	4.343	3.72E-02	rs9952148	18	52998449	q21.31
SNP_A-2034291	C	C	240	126	239	171	4.339	3.72E-02	rs1421867	5	163190600	q34
SNP_A-2295892	C	C	332	24	392	14	4.342	3.72E-02	rs7923367	10	68842909	q21.3
SNP_A-2290995	A	A	304	28	303	47	4.343	3.72E-02	rs7037884	9	2203818	p24.2
SNP_A-2288666	T	T	247	121	306	108	4.342	3.72E-02	rs11160639	14	100920429	q32.31
SNP_A-2293373	A	A	223	117	285	107	4.341	3.72E-02	rs7234119	18	75332775	q23
SNP_A-2269956	G	G	349	17	396	8	4.34	3.72E-02	rs538996	8	26834071	p21.2
SNP_A-2231854	T	T	198	156	256	148	4.341	3.72E-02	rs6651480	8	18985621	p22
SNP_A-2241206	C	T	207	161	212	202	4.343	3.72E-02	rs13254175	8	10016182	p23.1
SNP_A-2235307	G	G	362	44	335	63	4.341	3.72E-02	rs228219	20	46235227	q13.13
SNP_A-2235022	C	C	367	53	342	74	4.335	0.0373	rs2063985	14	77813075	q24.3
SNP_A-2270407	C	C	354	14	408	6	4.336	0.0373	rs17122536	8	12868242	p22
SNP_A-2261501	C	C	400	14	387	27	4.337	0.0373	rs8044881	16	20333675	p12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2279330	T	T	374	12	394	4	4.338	0.0373	rs2560752	6	13573779	p23
SNP_A-2274716	T	T	203	163	260	154	4.335	0.0373	rs9933953	16	76467193	q23.1
SNP_A-2307965	A	A	301	55	313	85	4.337	0.0373	rs3753898	1	162147909	q23.3
SNP_A-2037683	A	A	281	121	257	151	4.335	0.0373	rs6984837	8	127970831	q24.21
SNP_A-2047701	G	G	260	108	312	92	4.338	0.0373	rs261124	5	4421462	p15.33
SNP_A-2019785	G	G	392	28	375	45	4.336	0.0373	rs2205139	21	40943988	q22.2
SNP_A-2003459	G	G	223	183	245	149	4.337	0.0373	rs4360643	10	86628627	q23.1
SNP_A-1996659	T	T	316	98	329	71	4.336	0.0373	rs480325	9	38303379	p13.2
SNP_A-2061505	A	A	319	47	335	75	4.337	0.0373	rs6990716	8	95729948	q22.1
SNP_A-2052648	A	A	245	79	245	113	4.337	0.0373	rs11063663	12	5395831	p13.31
SNP_A-2054112	G	G	388	24	372	40	4.337	0.0373	rs10798628	1	175384029	q25.2
SNP_A-2064129	G	G	272	82	330	68	4.335	0.0373	rs1489996	3	68899145	p14.1
SNP_A-2207817	G	G	345	71	310	92	4.337	0.0373	rs12786875	11	86168228	q14.2
SNP_A-2226635	C	C	339	27	358	48	4.337	0.0373	rs323222	6	77717106	q14.1
SNP_A-2194728	C	C	211	207	241	177	4.335	0.0373	rs6499330	16	69235286	q22.1
SNP_A-2195217	C	C	410	10	389	21	4.335	0.0373	rs3011362	10	122543184	q26.12
SNP_A-2172606	G	G	287	55	360	44	4.336	0.0373	rs10917139	1	22146844	p36.12
SNP_A-2177904	G	G	334	80	306	104	4.336	0.0373	---	3	64873952	p14.1
SNP_A-2149505	A	A	324	26	345	47	4.337	0.0373	rs619511	6	87494823	q14.3
SNP_A-2145857	A	A	261	109	263	151	4.337	0.0373	rs7615060	3	149307485	q24
SNP_A-2125883	C	C	343	79	315	103	4.337	0.0373	rs8035369	15	96707741	q26.3
SNP_A-2132454	C	C	398	4	378	12	4.335	0.0373	rs16932769	10	32216416	p11.22
SNP_A-2107986	C	C	368	54	383	35	4.337	0.0373	rs1335894	10	43551010	q11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1710900	C	C	323	27	391	17	4.336	0.0373	rs1374531	4	106982752	q24
SNP_A-1690467	C	C	378	20	376	36	4.336	0.0373	rs10521061	9	100710054	q31.1
SNP_A-1791246	C	C	245	131	294	114	4.335	0.0373	rs1507216	12	84041088	q21.31
SNP_A-1803438	G	G	300	28	366	18	4.337	0.0373	rs7188523	16	53870580	q12.2
SNP_A-1809314	G	G	300	62	315	95	4.334	0.0373	rs11854222	15	59224282	q22.2
SNP_A-1862351	G	G	275	95	335	81	4.338	0.0373	rs11887366	2	128681479	q14.3
SNP_A-1827005	G	G	338	72	361	51	4.337	0.0373	rs7026753	9	127934815	q34.11
SNP_A-1941604	T	T	346	50	382	34	4.338	0.0373	rs3134236	8	96679147	q22.1
SNP_A-1950680	C	C	415	7	403	17	4.338	0.0373	rs2274238	20	33553132	q11.22
SNP_A-1952811	C	C	351	19	375	37	4.336	0.0373	rs12781529	10	132543018	q26.3
SNP_A-1957082	C	C	215	207	244	176	4.337	0.0373	rs1731893	17	39368452	q21.31
SNP_A-1963691	A	A	226	142	281	129	4.335	0.0373	rs2312081	2	69022775	p13.3
SNP_A-1976915	G	G	261	91	322	78	4.336	0.0373	rs930758	4	41108108	p13
SNP_A-1979390	A	A	354	6	411	1	4.336	0.0373	rs974160	4	150442132	q31.23
SNP_A-1931424	C	C	321	51	313	75	4.337	0.0373	rs4736941	8	41170416	p11.21
SNP_A-1928173	T	T	325	45	382	32	4.335	0.0373	rs7873050	9	7502186	p24.1
SNP_A-1903073	C	C	262	148	234	178	4.337	0.0373	rs7958693	12	122687630	q24.31
SNP_A-1899940	G	G	336	8	375	21	4.334	3.74E-02	rs11704184	22	20667608	q11.22
SNP_A-1894447	T	C	230	186	213	197	4.334	3.74E-02	rs3846415	4	13829206	p15.33
SNP_A-1905671	G	G	286	60	340	46	4.334	3.74E-02	rs17711186	16	77599156	q23.1
SNP_A-1907418	C	C	306	48	345	33	4.332	3.74E-02	rs501109	6	117746313	q22.1
SNP_A-1978110	A	A	256	160	223	187	4.331	3.74E-02	rs600023	1	190567743	q31.3
SNP_A-1984068	T	T	317	71	284	92	4.33	3.74E-02	---	5	152480216	q33.1
SNP_A-1959469	C	C	335	25	399	15	4.334	3.74E-02	rs6897035	5	56030704	q11.2
SNP_A-1959619	A	A	324	38	341	63	4.333	3.74E-02	rs2471991	11	5398199	p15.4

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950076	A	A	350	10	367	23	4.331	3.74E-02	rs1845570	4	75718481	q13.3
SNP_A-1826508	G	G	336	30	361	53	4.333	3.74E-02	rs6028637	20	37816039	q12
SNP_A-1825561	T	T	416	0	382	4	4.332	3.74E-02	rs12550491	8	40738673	p11.21
SNP_A-1851882	A	A	333	11	372	26	4.332	3.74E-02	rs271461	18	29001233	q12.1
SNP_A-1791744	G	G	228	116	286	104	4.333	3.74E-02	rs7986543	13	113801546	q34
SNP_A-1796921	A	A	253	105	262	150	4.333	3.74E-02	rs1390750	3	83022744	p12.2
SNP_A-1797149	G	G	366	2	369	9	4.334	3.74E-02	rs17090112	4	61222559	q13.1
SNP_A-1734042	C	C	210	140	213	193	4.332	3.74E-02	rs6848993	4	61957627	q13.1
SNP_A-2115453	C	C	276	136	246	164	4.333	3.74E-02	rs7785231	7	44594977	p13
SNP_A-2142218	T	T	387	5	349	13	4.331	3.74E-02	rs16837853	2	137605592	q22.1
SNP_A-2165868	C	C	277	99	255	127	4.332	3.74E-02	rs7315502	12	123613088	q24.31
SNP_A-2155756	C	C	302	118	322	90	4.334	3.74E-02	rs629252	11	125362580	q24.2
SNP_A-2173460	G	G	390	16	367	29	4.33	3.74E-02	rs8030855	15	27702652	q13.1
SNP_A-2190149	A	A	350	10	367	23	4.331	3.74E-02	rs3118340	9	25175202	p21.3
SNP_A-2224639	C	C	314	58	319	37	4.332	3.74E-02	rs1963731	9	86674817	q21.33
SNP_A-2218105	G	G	321	11	343	25	4.333	3.74E-02	rs987235	14	53600030	q22.2
SNP_A-2220598	T	T	311	55	328	86	4.33	3.74E-02	rs11073852	15	83312985	q25.3
SNP_A-2074529	T	T	246	102	241	139	4.334	3.74E-02	rs7744304	6	32533465	p21.32
SNP_A-2103436	C	C	248	122	249	167	4.332	3.74E-02	rs4382127	5	27288223	p14.1
SNP_A-2094875	C	C	403	17	389	31	4.331	3.74E-02	rs12575741	11	35926252	p13
SNP_A-2090271	A	A	278	90	338	76	4.334	3.74E-02	rs3908571	9	70545247	q21.11
SNP_A-1997998	C	C	234	138	229	183	4.333	3.74E-02	rs10491053	10	21098139	p12.31
SNP_A-2040499	G	G	213	149	271	139	4.33	3.74E-02	rs2720488	8	17427496	p22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2040295	G	G	414	0	380	4	4.334	3.74E-02	rs11904988	20	5077356	p12.3
SNP_A-2039095	G	G	356	2	359	9	4.33	3.74E-02	rs16828611	1	23674069	p36.12
SNP_A-2301253	T	T	322	46	340	74	4.332	3.74E-02	rs10194748	2	75476567	p12
SNP_A-2279365	G	G	356	6	413	1	4.331	3.74E-02	rs4947082	6	111016193	q21
SNP_A-2266204	G	G	281	137	307	109	4.332	3.74E-02	rs11080490	18	11086618	p11.21
SNP_A-2228140	C	C	253	165	221	193	4.331	3.74E-02	rs2061188	4	27252990	p15.2
SNP_A-2241796	T	T	273	95	279	135	4.331	3.74E-02	rs11208722	1	65883022	p31.2
SNP_A-2255605	T	T	295	73	328	54	4.331	3.74E-02	rs9502134	6	4156533	p25.1
SNP_A-2271690	T	T	345	13	368	28	4.326	3.75E-02	rs17131061	1	70042397	p31.1
SNP_A-2261730	T	T	202	140	193	183	4.329	3.75E-02	rs650673	1	17941980	p36.13
SNP_A-2262016	A	A	330	38	390	26	4.327	3.75E-02	rs2161320	5	110083019	q22.1
SNP_A-2284334	G	G	352	68	371	47	4.329	3.75E-02	rs17185355	16	50440986	q12.1
SNP_A-2280063	A	A	325	97	297	123	4.328	3.75E-02	rs2898938	11	3788833	p15.4
SNP_A-2295942	G	G	288	132	258	160	4.329	3.75E-02	rs2499762	6	34056602	p21.31
SNP_A-2295310	T	T	344	6	399	1	4.329	3.75E-02	rs6935823	6	72006614	q13
SNP_A-2292996	A	A	420	0	386	4	4.329	3.75E-02	rs11888495	2	210994669	q34
SNP_A-2290703	A	A	256	56	316	44	4.327	3.75E-02	rs315552	1	84507304	p31.1
SNP_A-2038488	T	T	279	133	309	107	4.328	3.75E-02	rs17401966	1	10319737	p36.22
SNP_A-2036175	A	A	388	20	399	9	4.326	3.75E-02	rs8017913	14	29554531	q12
SNP_A-2015866	A	A	283	119	312	94	4.328	3.75E-02	rs11088696	21	19044324	q21.1
SNP_A-2082284	A	A	213	133	282	128	4.327	3.75E-02	rs4702551	5	8477283	p15.31
SNP_A-2095636	G	G	422	0	388	4	4.327	3.75E-02	rs1793065	11	105937838	q22.3
SNP_A-2055446	A	A	327	37	385	25	4.329	3.75E-02	rs17650849	12	43300253	q12
SNP_A-2179178	G	A	236	180	208	204	4.329	3.75E-02	rs2355351	2	170927016	q31.1
SNP_A-2167391	T	T	240	126	300	114	4.329	3.75E-02	rs4567005	8	94702409	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141045	T	-	236	176	200	200	4.328	3.75E-02	rs12036714	1	49377660	p33
SNP_A-2146824	C	C	294	74	354	60	4.327	3.75E-02	rs2610689	2	104053399	q12.1
SNP_A-1727621	C	C	337	65	366	46	4.326	3.75E-02	rs620504	18	2262846	p11.32
SNP_A-1706575	T	T	236	166	271	141	4.33	3.75E-02	rs711674	3	4340335	p26.1
SNP_A-1797697	C	C	356	14	410	6	4.33	3.75E-02	rs2086455	15	98482760	q26.3
SNP_A-1812671	A	A	259	109	320	96	4.328	3.75E-02	rs9262636	6	31133827	p21.33
SNP_A-1805524	T	T	294	74	354	60	4.327	3.75E-02	rs13140844	4	70089467	q13.2
SNP_A-1851632	A	A	240	126	300	114	4.329	3.75E-02	rs17149929	7	12179320	p21.3
SNP_A-1857523	G	G	420	0	386	4	4.329	3.75E-02	rs13004278	2	19849609	p24.1
SNP_A-1856969	A	A	259	155	286	126	4.326	3.75E-02	rs8039796	15	63285178	q22.31
SNP_A-1833365	C	C	365	1	373	7	4.326	3.75E-02	rs16909057	9	119634973	q33.2
SNP_A-1953909	C	C	266	104	315	87	4.327	3.75E-02	rs4487012	18	66977483	q22.3
SNP_A-1958851	T	T	356	14	410	6	4.33	3.75E-02	rs1867746	2	137244809	q21.3
SNP_A-1956347	G	G	319	101	342	76	4.327	3.75E-02	rs11814145	10	108345833	q25.1
SNP_A-1939178	A	A	203	195	239	171	4.329	3.75E-02	rs6910430	6	3799165	p25.2
SNP_A-1989253	C	C	272	114	314	94	4.327	3.75E-02	rs7807721	7	25222092	p15.3
SNP_A-1976141	C	C	209	147	211	201	4.329	3.75E-02	rs10433812	4	13828407	p15.33
SNP_A-1918578	T	T	309	53	370	40	4.33	3.75E-02	rs6916016	6	167601	p25.3
SNP_A-1913146	G	G	254	70	250	100	4.329	3.75E-02	rs1329179	10	91924433	q23.31
SNP_A-1894278	G	G	248	106	313	95	4.328	3.75E-02	rs6851971	4	56268992	q12
SNP_A-1874689	G	G	326	56	309	79	4.327	3.75E-02	rs701839	10	102945284	q24.32
SNP_A-1877302	G	G	324	86	303	113	4.323	3.76E-02	rs7035308	9	132851844	q34.13
SNP_A-1895510	A	A	182	160	216	138	4.323	3.76E-02	rs9293134	5	24560241	p14.2
SNP_A-1898700	T	T	398	20	409	9	4.322	3.76E-02	rs16894932	6	29523054	p22.1
SNP_A-1927408	G	G	281	87	341	73	4.322	3.76E-02	rs11145659	9	77885375	q21.2
SNP_A-1932501	T	T	269	153	296	124	4.322	3.76E-02	rs1862479	19	55721414	q13.33
SNP_A-1975709	C	C	347	23	373	43	4.322	3.76E-02	rs3773990	3	191744754	q28

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1976696	G	G	303	13	380	6	4.323	3.76E-02	rs10517244	4	32079843	p15.1
SNP_A-1938166	A	A	343	65	323	89	4.321	3.76E-02	rs17100500	5	142983922	q31.3
SNP_A-1953563	G	G	359	1	367	7	4.323	3.76E-02	rs7007557	8	62890489	q12.3
SNP_A-1809028	A	A	268	62	320	48	4.325	3.76E-02	---	15	54743606	q21.3
SNP_A-1793904	C	C	319	93	290	118	4.324	3.76E-02	rs6003360	22	21550334	q11.22
SNP_A-1684816	A	G	204	198	234	180	4.324	3.76E-02	rs2996268	6	48547455	p12.3
SNP_A-1720253	C	C	234	168	269	143	4.323	3.76E-02	rs325379	18	36559928	q12.3
SNP_A-1780363	A	A	355	11	412	4	4.323	3.76E-02	rs16974879	18	37366254	q12.3
SNP_A-2148987	C	C	321	101	344	76	4.322	3.76E-02	rs3790053	14	93488212	q32.13
SNP_A-2149888	A	A	318	98	280	120	4.323	3.76E-02	rs1657301	7	154409778	q36.2
SNP_A-2160389	C	C	354	8	400	2	4.324	3.76E-02	rs17061635	6	101831693	q16.3
SNP_A-2159441	C	T	195	167	223	193	4.324	3.76E-02	rs7982613	13	75068514	q22.2
SNP_A-2108950	C	T	187	175	230	182	4.325	3.76E-02	rs1500824	4	118004880	q26
SNP_A-2109747	A	G	199	169	222	194	4.325	3.76E-02	rs4406411	8	88477499	q21.3
SNP_A-2180625	A	A	309	39	367	27	4.323	3.76E-02	rs1114620	16	9171238	p13.2
SNP_A-2168248	A	A	274	124	241	149	4.323	3.76E-02	rs10859345	12	91514402	q22
SNP_A-2187952	T	T	315	19	372	10	4.324	3.76E-02	rs763578	9	2602434	p24.2
SNP_A-2196164	T	T	267	149	233	175	4.321	3.76E-02	rs610093	10	6002641	p15.1
SNP_A-2220222	A	A	193	161	254	156	4.322	3.76E-02	rs1554770	2	177596724	q31.1
SNP_A-2218027	T	T	283	101	312	78	4.323	3.76E-02	rs724171	17	2600902	p13.3
SNP_A-2056792	G	G	325	7	357	19	4.322	3.76E-02	rs11233811	11	83312749	q14.1
SNP_A-2059372	A	A	291	77	295	111	4.321	3.76E-02	rs10763382	10	51815899	q11.23
SNP_A-2052433	C	C	400	20	411	9	4.322	3.76E-02	rs8018145	14	20376406	q11.2
SNP_A-2048920	A	A	376	32	394	18	4.321	3.76E-02	rs6882818	5	56023338	q11.2
SNP_A-2096477	A	A	228	128	272	110	4.323	3.76E-02	rs2861814	2	68350265	p14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2093673	C	C	256	166	225	195	4.323	3.76E-02	rs304391	5	121781681	q23.2
SNP_A-2101338	A	A	267	127	308	106	4.324	3.76E-02	rs6998613	8	66236864	q13.1
SNP_A-2104251	T	T	242	58	317	49	4.322	3.76E-02	rs17563649	1	235451761	q43
SNP_A-2088213	C	C	285	67	297	101	4.323	3.76E-02	rs9523829	13	92364628	q31.3
SNP_A-2017435	G	G	189	179	241	169	4.321	3.76E-02	rs1997580	21	28538651	q21.3
SNP_A-2303086	C	C	354	4	400	14	4.322	3.76E-02	rs10187809	2	62076539	p15
SNP_A-2281485	A	A	293	21	379	13	4.324	3.76E-02	rs4107120	18	14336307	p11.21
SNP_A-2267986	A	A	356	38	337	57	4.321	3.76E-02	rs11641432	16	6301406	p13.2
SNP_A-2248242	C	C	225	193	250	160	4.324	3.76E-02	rs6436930	2	231077391	q37.1
SNP_A-2238942	A	A	306	54	367	41	4.325	3.76E-02	rs7734243	5	109700718	q22.1
SNP_A-2250035	G	G	290	72	307	109	4.32	3.77E-02	rs639688	11	85148541	q14.1
SNP_A-2266146	G	G	377	43	357	63	4.319	3.77E-02	rs11016397	10	130321307	q26.2
SNP_A-2265239	G	G	396	14	403	5	4.32	3.77E-02	rs11125090	2	46921369	p21
SNP_A-2269251	T	T	364	58	340	80	4.321	3.77E-02	rs7198570	16	20525969	p12.3
SNP_A-2291755	T	T	317	67	300	92	4.317	3.77E-02	rs7014520	8	51054533	q11.21
SNP_A-2016555	C	C	292	76	352	62	4.319	3.77E-02	rs200710	21	23735278	q21.2
SNP_A-2015306	A	A	327	3	368	12	4.319	3.77E-02	rs2822984	21	15219739	q11.2
SNP_A-2001735	T	C	192	178	231	185	4.321	3.77E-02	rs4316494	11	12621117	p15.2
SNP_A-2005178	T	T	332	30	391	19	4.316	3.77E-02	rs4362431	17	43291071	q21.32
SNP_A-2037759	T	T	196	180	237	161	4.319	3.77E-02	rs3742395	14	100383739	q32.2
SNP_A-2041788	G	G	346	12	362	26	4.32	3.77E-02	rs1201202	4	152198357	q31.3
SNP_A-2044160	T	T	293	39	311	65	4.319	3.77E-02	rs12335124	8	65398572	q12.3
SNP_A-2049642	G	G	406	0	374	4	4.318	3.77E-02	rs13209290	6	161323109	q26
SNP_A-2059459	A	T	221	199	227	189	4.319	3.77E-02	rs7952909	12	108271293	q24.11
SNP_A-2056944	T	T	262	90	277	133	4.319	3.77E-02	rs17032357	4	103539794	q24
SNP_A-2073385	C	G	213	177	205	183	4.32	3.77E-02	rs6987766	8	13040143	p22
SNP_A-2199060	A	A	314	96	292	124	4.319	3.77E-02	rs9591545	13	53374033	q14.3
SNP_A-2174525	A	A	193	119	242	106	4.32	3.77E-02	rs1158909	1	105264149	p21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2119063	C	C	245	117	243	159	4.317	3.77E-02	rs10749559	10	82070377	q22.3
SNP_A-2135485	A	A	243	127	242	172	4.319	3.77E-02	rs6988935	8	75374629	q21.11
SNP_A-1722062	G	G	350	0	403	5	4.318	3.77E-02	rs10492516	13	73330452	q22.2
SNP_A-1714991	G	G	219	131	226	184	4.318	3.77E-02	rs1470203	3	77236319	p12.3
SNP_A-1741365	C	C	307	93	342	72	4.321	3.77E-02	rs7776847	7	32828609	p14.3
SNP_A-1689657	G	G	277	121	312	98	4.318	3.77E-02	rs194825	7	103310749	q22.1
SNP_A-1788810	A	A	332	86	355	63	4.32	3.77E-02	rs12491013	3	65822120	p14.1
SNP_A-1809346	A	A	298	72	358	58	4.318	3.77E-02	rs17006246	2	70869463	p13.3
SNP_A-1813586	C	C	316	24	327	43	4.316	3.77E-02	rs7127090	11	67647865	q13.2
SNP_A-1802420	T	T	246	100	261	147	4.318	3.77E-02	rs12152503	3	83040472	p12.2
SNP_A-1853302	T	T	225	141	224	190	4.319	3.77E-02	rs1839492	3	162680493	q26.1
SNP_A-1864903	A	A	325	87	295	111	4.317	3.77E-02	rs2292085	15	95117827	q26.2
SNP_A-1945331	A	A	282	86	342	72	4.319	3.77E-02	rs4663855	2	238865301	q37.3
SNP_A-1962430	A	A	228	104	286	92	4.317	3.77E-02	rs1772635	1	13693531	p36.21
SNP_A-1893846	G	G	314	88	287	113	4.317	3.77E-02	rs12488374	3	70709179	p13
SNP_A-1895148	A	A	330	32	356	56	4.319	3.77E-02	rs12974655	19	14971530	p13.12
SNP_A-1878730	C	C	255	89	270	132	4.312	0.0378	rs1984082	13	58173507	q21.1
SNP_A-1913547	C	C	301	57	348	42	4.315	0.0378	rs221481	14	79169029	q31.1
SNP_A-1915862	T	T	350	18	405	9	4.316	0.0378	rs1642295	18	51580697	q21.2
SNP_A-1963391	C	C	225	183	253	153	4.314	0.0378	rs2194801	2	56645514	p16.1
SNP_A-1967843	A	A	272	122	304	98	4.316	0.0378	rs3789343	20	13446547	p12.1
SNP_A-1982961	A	A	342	22	372	42	4.315	0.0378	rs12087287	1	208687199	q32.3
SNP_A-1944118	C	C	357	65	372	44	4.312	0.0378	rs6537940	9	134785330	q34.3
SNP_A-1854624	A	A	226	120	228	166	4.312	0.0378	rs9565921	13	83657521	q31.1
SNP_A-1843486	A	A	211	153	270	144	4.314	0.0378	rs7958608	12	43286477	q12
SNP_A-1677394	C	T	210	180	209	181	4.313	0.0378	rs9302942	17	70485656	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1695691	G	G	270	76	287	115	4.314	0.0378	rs10507852	13	74703590	q22.2
SNP_A-1730581	A	A	230	170	208	206	4.312	0.0378	rs10518365	4	121995760	q27
SNP_A-1784051	A	A	375	19	342	32	4.315	0.0378	rs11200927	10	85974424	q23.1
SNP_A-2111707	G	G	328	74	358	54	4.315	0.0378	rs7318542	13	20146134	q12.11
SNP_A-2155677	G	G	321	31	342	54	4.315	0.0378	rs1525398	10	106679587	q25.1
SNP_A-2163420	G	G	237	65	244	98	4.315	0.0378	rs10455854	6	159426204	q25.3
SNP_A-2193067	T	T	347	51	365	33	4.312	0.0378	rs11641340	16	77109437	q23.1
SNP_A-2188365	G	G	228	50	306	42	4.315	0.0378	rs487972	6	153515366	q25.2
SNP_A-2208965	G	G	219	147	216	196	4.316	0.0378	rs1713669	8	96027813	q22.1
SNP_A-2206607	C	C	361	61	335	83	4.313	0.0378	rs17776317	12	5003864	p13.32
SNP_A-2201237	G	G	265	91	315	75	4.312	0.0378	rs2510596	11	106356732	q22.3
SNP_A-2063153	G	G	220	128	276	116	4.312	0.0378	rs7135063	12	56689179	q14.1
SNP_A-2087688	C	C	413	9	408	2	4.313	0.0378	rs6775553	3	110619136	q13.13
SNP_A-2086892	G	G	284	84	344	70	4.314	0.0378	rs759717	2	162683830	q24.2
SNP_A-2090781	C	C	292	118	321	93	4.315	0.0378	rs3095001	7	19978585	p21.1
SNP_A-2106033	G	G	380	4	412	0	4.313	0.0378	rs11859474	16	65112041	q22.1
SNP_A-2009851	T	T	357	3	365	11	4.314	0.0378	rs624415	11	35622003	p13
SNP_A-2006309	C	C	350	18	405	9	4.316	0.0378	rs2716736	2	39859598	p22.1
SNP_A-2006831	G	G	402	18	384	32	4.313	0.0378	rs4233828	2	170070814	q31.1
SNP_A-2291716	T	T	238	132	295	119	4.313	0.0378	rs6815145	4	185438603	q35.1
SNP_A-2295975	G	G	328	86	307	113	4.315	0.0378	rs1461214	15	86312021	q25.3
SNP_A-2310668	A	A	313	57	369	43	4.315	0.0378	rs9557021	13	98119056	q32.2
SNP_A-2272310	C	C	350	6	405	1	4.316	0.0378	rs16929326	11	36690851	p12
SNP_A-2279468	A	C	206	202	236	180	4.313	0.0378	rs8006520	14	41092873	q21.1
SNP_A-2276883	T	T	338	6	391	1	4.313	0.0378	rs16903877	5	15529181	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251898	T	T	292	124	302	92	4.315	0.0378	rs847846	6	35033349	p21.31
SNP_A-2251943	A	G	200	170	222	194	4.312	0.0378	rs874851	4	147520737	q31.22
SNP_A-2255284	T	T	227	155	256	128	4.312	0.0378	rs10761408	9	133990903	q34.2
SNP_A-2233718	C	C	290	78	350	64	4.314	0.0378	rs12636816	3	73907588	p13
SNP_A-2252048	C	C	211	139	211	189	4.308	3.79E-02	rs3823612	7	12031995	p21.3
SNP_A-2296726	C	C	353	3	398	12	4.311	3.79E-02	rs176638	15	87675617	q26.1
SNP_A-2007705	C	C	321	45	341	73	4.311	3.79E-02	rs5002650	20	45926354	q13.13
SNP_A-1992054	C	T	232	186	212	198	4.31	3.79E-02	rs2408057	8	5339373	p23.2
SNP_A-2036578	A	A	194	142	257	137	4.309	3.79E-02	rs489667	15	60958642	q22.2
SNP_A-2024743	C	C	363	19	395	9	4.31	3.79E-02	rs13249530	8	84416732	q21.13
SNP_A-2105910	C	C	330	16	400	8	4.31	3.79E-02	rs17033270	3	10646678	p25.3
SNP_A-2101557	A	A	249	121	308	108	4.31	3.79E-02	rs3847818	12	93274730	q22
SNP_A-2098958	G	G	309	59	325	91	4.308	3.79E-02	rs8141610	22	18244701	q11.21
SNP_A-2076564	G	G	305	43	317	69	4.311	3.79E-02	rs175145	22	15682795	q11.1
SNP_A-2061214	G	G	344	8	388	2	4.31	3.79E-02	rs2044234	2	86769638	p11.2
SNP_A-2216035	T	T	281	85	292	124	4.309	3.79E-02	rs11982449	7	133553145	q33
SNP_A-2169805	A	A	180	158	241	155	4.311	3.79E-02	rs6685120	1	18056446	p36.13
SNP_A-2161245	A	A	349	3	357	11	4.309	3.79E-02	rs7318836	13	25142193	q12.13
SNP_A-2110995	T	T	350	2	398	10	4.311	3.79E-02	rs2432786	6	5340833	p25.1
SNP_A-2132943	A	A	325	29	345	51	4.309	3.79E-02	rs17678734	6	12878829	p24.1
SNP_A-1712735	C	T	227	171	207	205	4.308	3.79E-02	rs6979945	7	81998176	q21.11
SNP_A-1668564	T	T	229	173	264	148	4.31	3.79E-02	rs4127470	11	62576508	q12.3
SNP_A-1651388	C	C	375	19	366	34	4.31	3.79E-02	rs10496873	2	142205971	q22.1
SNP_A-1654423	C	C	243	159	266	128	4.308	3.79E-02	rs267998	9	77967367	q21.31
SNP_A-1833384	G	G	327	43	346	70	4.31	3.79E-02	rs333224	2	108082184	q12.3
SNP_A-1818004	G	G	310	98	339	75	4.31	3.79E-02	rs12212312	6	3843012	p25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1853316	C	C	269	83	273	119	4.307	3.79E-02	rs7100029	10	10512847	p14
SNP_A-1850562	G	G	290	70	306	106	4.31	3.79E-02	rs6933878	6	158542115	q25.3
SNP_A-1845918	C	C	352	6	407	1	4.312	3.79E-02	rs16834613	1	189377429	q31.2
SNP_A-1867003	C	C	319	61	321	39	4.309	3.79E-02	rs1002169	7	2026414	p22.3
SNP_A-1961663	T	T	386	4	418	0	4.309	3.79E-02	rs16994185	19	7091801	p13.2
SNP_A-1987282	A	G	187	163	202	170	4.31	3.79E-02	rs986543	6	114059862	q21
SNP_A-1977182	T	T	255	97	308	82	4.312	3.79E-02	rs9992300	4	56952587	q12
SNP_A-1964527	T	T	413	3	380	10	4.308	3.79E-02	rs156723	2	114523014	q14.1
SNP_A-1974989	C	C	262	94	268	134	4.31	3.79E-02	rs1384542	3	158239362	q25.31
SNP_A-1974552	C	C	252	138	232	172	4.31	3.79E-02	rs9863029	3	141209688	q23
SNP_A-1920977	T	T	386	6	363	15	4.31	3.79E-02	rs644421	11	73709913	q13.4
SNP_A-1893642	A	A	364	22	391	11	4.309	3.79E-02	rs10119556	9	96631541	q22.33
SNP_A-1893144	A	A	309	45	324	28	4.309	3.79E-02	rs2041473	9	122619769	q33.2
SNP_A-1897780	G	G	363	59	377	39	4.304	3.80E-02	rs11563720	7	126342551	q32.1
SNP_A-1925479	A	A	276	82	276	116	4.306	3.80E-02	rs283980	13	75988010	q22.2
SNP_A-1913163	C	C	296	74	356	60	4.307	3.80E-02	rs10965393	9	22571260	p21.3
SNP_A-1970273	T	T	238	98	244	140	4.306	3.80E-02	rs702860	21	37930499	q22.13
SNP_A-1983205	T	T	310	58	366	44	4.306	3.80E-02	rs982605	5	119505036	q23.1
SNP_A-1952256	A	A	313	47	379	35	4.304	3.80E-02	rs4767879	12	111426790	q24.13
SNP_A-1935476	A	A	379	25	332	38	4.304	3.80E-02	rs7809215	7	138669332	q34
SNP_A-1756128	T	T	215	187	250	162	4.303	3.80E-02	rs4643108	11	110381337	q23.1
SNP_A-2132502	A	A	280	60	339	47	4.306	3.80E-02	rs9436816	1	68559269	p31.2
SNP_A-2137064	C	C	356	6	411	1	4.303	3.80E-02	rs11037868	11	44091183	p11.2
SNP_A-2123878	A	A	351	51	369	33	4.307	3.80E-02	rs4142117	6	39500696	p21.2
SNP_A-2119348	C	C	284	76	297	113	4.306	3.80E-02	rs9842824	3	156610	p26.3
SNP_A-2117906	T	T	244	96	232	128	4.306	3.80E-02	rs11117051	11	34882669	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2117163	T	T	330	92	301	117	4.304	3.80E-02	rs6014572	20	54007951	q13.31
SNP_A-2148285	G	G	248	158	221	189	4.304	3.80E-02	rs8034025	15	66843261	q23
SNP_A-2217843	A	A	390	20	377	35	4.306	3.80E-02	rs2302803	17	32708136	q12
SNP_A-2069278	T	T	282	76	350	64	4.306	3.80E-02	rs2268677	1	41211597	p34.2
SNP_A-2024541	G	G	322	44	344	72	4.306	3.80E-02	rs473518	18	18338672	q11.2
SNP_A-2047668	C	T	206	162	212	200	4.305	3.80E-02	rs3754932	2	202335320	q33.1
SNP_A-2002157	T	T	329	39	339	63	4.304	3.80E-02	rs7125582	11	96053431	q21
SNP_A-2009200	T	T	317	49	376	36	4.307	3.80E-02	rs1491799	11	29165952	p14.1
SNP_A-2011590	A	A	227	111	228	154	4.307	3.80E-02	rs543429	11	62825185	q12.3
SNP_A-2016367	G	G	269	95	275	135	4.304	3.80E-02	rs10502111	11	108547568	q22.3
SNP_A-2255895	T	T	200	164	253	153	4.304	3.80E-02	rs1033903	14	102758973	q32.32
SNP_A-2244625	G	T	214	208	237	183	4.306	3.80E-02	rs6559318	9	88798885	q22.1
SNP_A-2281705	G	G	349	39	354	62	4.303	3.80E-02	rs17044894	12	77027429	q21.2
SNP_A-2282447	T	T	344	6	397	1	4.3	3.81E-02	rs2297106	9	37010388	p13.2
SNP_A-2279405	G	G	295	121	267	149	4.299	3.81E-02	rs1542504	2	6502675	p25.2
SNP_A-2272495	G	G	227	141	225	189	4.3	3.81E-02	rs11646484	16	82048275	q23.3
SNP_A-2269585	G	G	352	14	369	29	4.301	3.81E-02	rs12030875	1	70162884	p31.1
SNP_A-2263562	C	C	261	95	311	79	4.301	3.81E-02	rs11709808	3	198802442	q29
SNP_A-2250522	T	T	250	118	253	163	4.302	3.81E-02	rs12745968	1	93113858	p22.1
SNP_A-2019060	A	G	177	173	228	172	4.301	3.81E-02	rs1005546	21	37990742	q22.13
SNP_A-2007619	A	A	354	12	387	27	4.301	3.81E-02	rs60290 85	20	38441479	q12
SNP_A-2034020	G	G	315	15	373	7	4.299	3.81E-02	rs7771026	6	101706465	q16.3
SNP_A-2068544	T	-	206	152	198	198	4.3	3.81E-02	rs10739491	9	117228270	q33.1
SNP_A-2065458	C	C	225	133	224	180	4.298	3.81E-02	rs6498962	16	63398452	q21
SNP_A-2071505	A	A	251	65	245	93	4.299	3.81E-02	rs2882466	12	29730659	p11.22
SNP_A-2071638	T	T	343	23	399	13	4.299	3.81E-02	rs705360	7	90447172	q21.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2057348	T	T	339	31	362	54	4.301	3.81E-02	rs790365	11	83323901	q14.1
SNP_A-2057391	C	C	349	19	296	30	4.298	3.81E-02	rs1410656	13	46440522	q14.2
SNP_A-2053857	G	G	272	54	313	39	4.302	3.81E-02	rs5996378	22	21433072	q11.22
SNP_A-2172808	A	A	370	18	392	8	4.3	3.81E-02	rs2618011	9	26319422	p21.2
SNP_A-2176177	C	C	182	162	243	159	4.3	3.81E-02	rs7993804	13	95610858	q32.1
SNP_A-2192432	C	C	216	128	220	178	4.299	3.81E-02	rs1960426	4	1264195	p16.3
SNP_A-2158542	A	A	339	81	314	106	4.299	3.81E-02	rs1327371	9	75294360	q21.13
SNP_A-2118912	T	T	186	182	241	175	4.299	3.81E-02	rs1018179	3	154580962	q25.2
SNP_A-2124667	C	C	330	28	315	45	4.302	3.81E-02	rs12506026	4	47769089	p12
SNP_A-2136164	A	A	230	136	231	185	4.303	3.81E-02	rs7011618	8	94964028	q22.1
SNP_A-2136041	A	A	217	147	214	196	4.302	3.81E-02	rs9914077	17	7981019	p13.1
SNP_A-1782230	A	A	344	6	397	1	4.3	3.81E-02	rs16994797	4	38643142	p14
SNP_A-1747719	T	T	318	70	356	52	4.298	3.81E-02	rs1413042	13	37500755	q13.3
SNP_A-1703373	A	A	247	129	217	155	4.299	3.81E-02	rs965009	6	54681571	p12.1
SNP_A-1688988	A	A	350	52	379	35	4.3	3.81E-02	rs35168	16	64749492	q21
SNP_A-1801252	T	T	264	100	322	86	4.301	3.81E-02	rs10521026	16	50995317	q12.1
SNP_A-1812124	C	C	408	12	392	24	4.301	3.81E-02	rs355954	16	65253955	q22.1
SNP_A-1867555	T	T	354	16	359	31	4.299	3.81E-02	rs9308729	2	117000702	q14.1
SNP_A-1937060	C	C	305	49	362	36	4.3	3.81E-02	rs2928240	5	5592552	p15.32
SNP_A-1955553	G	G	347	67	322	90	4.299	3.81E-02	rs6448604	4	28544288	p15.1
SNP_A-1986806	T	T	321	11	372	4	4.302	3.81E-02	rs12055442	6	90146944	q15
SNP_A-1930224	G	G	316	46	334	74	4.299	3.81E-02	rs1505160	14	85820804	q31.3
SNP_A-1876719	T	T	222	146	274	132	4.301	3.81E-02	rs321591	1	96430982	p21.3
SNP_A-1897390	C	C	284	84	291	121	4.295	3.82E-02	rs6588185	1	66244749	p31.2
SNP_A-1925335	C	C	311	55	365	41	4.294	3.82E-02	rs11250838	10	1892085	p15.3
SNP_A-1923230	A	A	279	141	250	170	4.294	3.82E-02	rs12094945	1	4843527	p36.32
SNP_A-1970812	C	C	352	12	385	27	4.294	3.82E-02	rs8139129	22	24823275	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1940473	G	G	296	24	314	44	4.297	3.82E-02	rs13391850	2	142339766	q22.1
SNP_A-1846357	A	A	353	65	375	45	4.296	3.82E-02	rs11253967	10	16471731	p13
SNP_A-1859485	C	C	351	11	406	4	4.295	3.82E-02	rs7616440	3	69351427	p14.1
SNP_A-1817192	G	G	358	50	374	32	4.296	3.82E-02	rs1821761	1	212593894	q41
SNP_A-1786423	T	T	307	59	323	91	4.295	3.82E-02	rs9390645	6	149317560	q25.1
SNP_A-1794005	G	G	393	25	375	41	4.296	3.82E-02	rs12610425	19	61921675	q13.43
SNP_A-1795996	G	G	310	46	365	33	4.295	3.82E-02	rs11111002	12	100656646	q23.2
SNP_A-2126603	G	G	249	169	216	196	4.296	3.82E-02	rs4633103	8	121185337	q24.12
SNP_A-2117949	A	A	210	144	247	123	4.296	3.82E-02	rs6804026	3	99372038	q12.1
SNP_A-2107841	A	A	257	165	225	193	4.295	3.82E-02	rs2237236	6	26559532	p22.1
SNP_A-2152035	G	G	211	135	265	123	4.295	3.82E-02	rs2662741	4	121569023	q27
SNP_A-2197980	G	G	360	6	415	1	4.295	3.82E-02	rs7914259	10	109202292	q25.1
SNP_A-2190686	C	C	360	6	415	1	4.295	3.82E-02	rs17787207	11	44892561	p11.2
SNP_A-2202809	A	A	334	28	387	17	4.295	3.82E-02	rs2222728	2	197259027	q32.3
SNP_A-2207931	C	C	297	21	360	12	4.296	3.82E-02	rs9870128	3	26253025	p24.2
SNP_A-2094891	G	G	248	154	219	183	4.296	3.82E-02	rs11710620	3	25167016	p24.2
SNP_A-2103163	C	C	318	78	350	58	4.296	3.82E-02	rs8115946	20	47158977	q13.13
SNP_A-2088403	A	A	222	168	264	148	4.295	3.82E-02	rs2970724	8	37013733	p12
SNP_A-2088317	G	G	191	187	225	163	4.295	3.82E-02	rs12823525	12	94433149	q22
SNP_A-2036785	G	G	385	23	393	11	4.298	3.82E-02	rs12683483	9	31710019	p21.1
SNP_A-2036211	A	A	405	11	397	23	4.296	3.82E-02	rs16842634	2	140193948	q22.1
SNP_A-2037662	C	C	182	160	223	143	4.296	3.82E-02	rs6742718	2	103625318	q12.1
SNP_A-2037928	C	C	360	6	415	1	4.295	3.82E-02	rs11193448	10	109205182	q25.1
SNP_A-2009721	A	A	360	6	415	1	4.295	3.82E-02	rs5743553	4	38629755	p14
SNP_A-2016262	T	T	262	154	278	120	4.297	3.82E-02	rs766090	21	21530192	q21.1
SNP_A-1992341	A	A	264	106	268	148	4.298	3.82E-02	rs4831501	8	13772865	p22
SNP_A-2253087	C	C	248	118	304	104	4.298	3.82E-02	rs2056999	6	24769490	p22.2
SNP_A-2231486	T	T	311	75	346	56	4.297	3.82E-02	rs12745080	1	167999586	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2240873	A	A	219	149	276	138	4.294	3.82E-02	rs1455137	4	146344273	q31.21
SNP_A-2281224	G	G	311	45	375	33	4.298	3.82E-02	rs2429953	17	67248230	q24.3
SNP_A-2307711	G	G	306	48	279	67	4.294	3.82E-02	rs13337529	16	47890098	q12.1
SNP_A-2301904	A	A	297	119	320	92	4.293	3.83E-02	rs890521	11	87535019	q14.2
SNP_A-2292150	C	C	340	56	357	37	4.291	3.83E-02	rs1392469	5	1797831	p15.33
SNP_A-2292800	G	G	371	47	347	67	4.292	3.83E-02	rs12045644	1	39753581	p34.3
SNP_A-2294013	G	G	337	31	360	54	4.291	3.83E-02	rs17129227	3	198237718	q29
SNP_A-2263423	C	C	337	27	365	49	4.29	3.83E-02	rs7931215	11	77183692	q13.5
SNP_A-2261504	G	G	297	73	308	108	4.291	3.83E-02	rs9303303	17	36435093	q21.2
SNP_A-2230025	C	C	354	14	406	6	4.289	3.83E-02	rs2200439	8	25972991	p21.2
SNP_A-1992259	G	G	291	79	351	65	4.291	3.83E-02	rs2251301	8	11156447	p23.1
SNP_A-2015354	A	A	322	32	353	19	4.294	3.83E-02	rs6517281	21	15484302	q21.1
SNP_A-2008506	C	C	324	46	381	33	4.292	3.83E-02	rs6809472	3	18823859	p24.3
SNP_A-2034460	A	A	341	29	398	18	4.294	3.83E-02	rs621854	18	8857754	p11.22
SNP_A-2024317	C	C	357	1	367	7	4.29	3.83E-02	rs1153720	2	175729659	q31.1
SNP_A-2104803	C	C	208	140	250	122	4.293	3.83E-02	rs7311429	12	128538249	q24.33
SNP_A-2093464	G	G	341	29	398	18	4.294	3.83E-02	rs17683020	7	12702351	p21.3
SNP_A-2053934	C	G	229	191	220	198	4.292	3.83E-02	rs911857	9	72226643	q21.13
SNP_A-2069657	A	G	204	162	215	201	4.294	3.83E-02	rs6972063	7	284803	p22.3
SNP_A-2200326	C	C	235	129	236	176	4.292	3.83E-02	rs2810696	13	23460950	q12.12
SNP_A-2184410	G	G	355	65	327	87	4.291	3.83E-02	rs12708713	16	10979960	p13.13
SNP_A-2177145	A	A	382	4	412	0	4.291	3.83E-02	rs2087349	15	91798745	q26.1
SNP_A-2182909	C	C	399	17	409	7	4.29	3.83E-02	rs6952600	7	82995612	q21.11
SNP_A-2147159	C	C	289	99	267	127	4.294	3.83E-02	rs9298878	9	26084889	p21.2
SNP_A-2107904	T	T	223	147	218	194	4.291	3.83E-02	rs1586393	12	128180389	q24.32
SNP_A-2115474	A	A	269	143	298	116	4.293	3.83E-02	rs7624209	3	135604567	q22.1
SNP_A-2131060	G	G	297	73	308	108	4.291	3.83E-02	rs4421623	1	98028306	p21.3
SNP_A-1792855	A	A	169	167	216	156	4.293	3.83E-02	rs1173663	1	241876435	q44

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1689751	C	C	340	24	344	42	4.291	3.83E-02	rs696467	12	76563264	q21.2
SNP_A-1661081	G	G	377	25	399	13	4.291	3.83E-02	rs1942839	11	100601423	q22.1
SNP_A-1738723	A	A	314	78	351	59	4.292	3.83E-02	rs1910964	5	24602129	p14.1
SNP_A-1756307	A	A	306	96	287	125	4.292	3.83E-02	rs987111	1	95155314	p21.3
SNP_A-1815625	T	T	239	123	296	110	4.291	3.83E-02	rs2305102	12	83942242	q21.31
SNP_A-1837080	C	T	211	191	214	176	4.291	3.83E-02	rs4985682	17	5599039	p13.2
SNP_A-1939016	C	C	234	130	236	178	4.293	3.83E-02	rs340419	5	178691515	q35.3
SNP_A-1975687	A	A	263	105	321	91	4.292	3.83E-02	rs2687656	3	191236564	q28
SNP_A-1986489	T	T	229	141	280	126	4.292	3.83E-02	rs2314211	6	77017577	q14.1
SNP_A-1922804	A	A	291	79	351	65	4.291	3.83E-02	rs9577820	13	112296262	q34
SNP_A-1921565	C	C	287	83	347	69	4.29	3.83E-02	rs10981115	9	111688201	q31.3
SNP_A-1879995	C	C	266	146	237	175	4.292	3.83E-02	rs1465801	2	100294578	q11.2
SNP_A-1882418	T	T	285	85	345	71	4.293	3.83E-02	rs11051641	12	31911523	p11.21
SNP_A-1873889	A	A	245	119	249	165	4.287	3.84E-02	rs7797620	7	112456220	q31.1
SNP_A-1915337	C	C	233	135	291	123	4.287	3.84E-02	rs10043478	5	138216610	q31.2
SNP_A-1906071	A	A	212	154	257	137	4.285	3.84E-02	rs2347565	4	160288806	q32.1
SNP_A-1905464	A	A	356	8	400	2	4.286	3.84E-02	rs1424544	7	136231260	q33
SNP_A-1986012	C	C	320	44	337	71	4.285	3.84E-02	rs2505283	6	51183239	p12.3
SNP_A-1973432	C	C	262	104	265	145	4.287	3.84E-02	rs10511097	3	83028451	p12.2
SNP_A-1954189	T	T	355	13	380	28	4.288	3.84E-02	rs633244	6	96549993	q16.1
SNP_A-1835333	G	G	388	4	418	0	4.286	3.84E-02	rs12595400	15	53652063	q21.3
SNP_A-1817020	C	C	283	43	303	71	4.289	3.84E-02	rs11740681	5	136734059	q31.1
SNP_A-1823093	G	G	292	62	293	91	4.286	3.84E-02	rs1451007	7	33481067	p14.3
SNP_A-1860816	A	A	338	30	380	18	4.288	3.84E-02	rs17683401	8	119741016	q24.12
SNP_A-1859935	A	A	309	49	331	79	4.286	3.84E-02	rs1938564	1	98184900	p21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1792279	T	T	386	32	370	50	4.285	3.84E-02	rs17032252	2	106134561	q12.2
SNP_A-2112952	G	G	276	90	331	75	4.286	3.84E-02	rs755723	13	21686211	q12.11
SNP_A-2117189	C	C	283	87	288	124	4.289	3.84E-02	rs11695839	2	226219486	q36.3
SNP_A-2147707	G	G	420	0	390	4	4.285	3.84E-02	rs7583480	2	7450012	p25.1
SNP_A-2162504	G	G	345	35	318	52	4.289	3.84E-02	rs359694	2	126841471	q14.3
SNP_A-2177527	T	T	276	90	339	77	4.286	3.84E-02	rs4952347	2	41139225	p22.1
SNP_A-2173196	A	A	327	59	300	80	4.289	3.84E-02	rs17063507	3	60518523	p14.2
SNP_A-2174569	G	G	344	28	329	45	4.288	3.84E-02	rs590557	2	31373046	p23.1
SNP_A-2200517	T	T	192	168	249	161	4.288	3.84E-02	rs17314018	2	83303843	p11.2
SNP_A-2208239	C	C	388	4	418	0	4.286	3.84E-02	rs235633	16	29652656	p11.2
SNP_A-2066203	T	T	420	0	390	4	4.285	3.84E-02	rs10274008	7	153601660	q36.2
SNP_A-2072282	A	A	232	128	290	116	4.288	3.84E-02	rs10893670	11	126711480	q24.2
SNP_A-2100225	G	G	420	0	390	4	4.285	3.84E-02	rs10923148	1	117055043	p13.1
SNP_A-2035725	T	T	386	32	370	50	4.285	3.84E-02	rs16856160	1	202393024	q32.1
SNP_A-2042121	C	C	239	123	241	169	4.287	3.84E-02	rs1436824	3	21169645	p24.3
SNP_A-2010743	G	G	215	201	239	167	4.289	3.84E-02	rs1000665	11	45242661	p11.2
SNP_A-2263679	G	G	311	29	347	17	4.287	3.84E-02	rs12936449	17	11460119	p12
SNP_A-2265288	A	A	313	27	346	50	4.287	3.84E-02	rs188576	3	11941535	p25.2
SNP_A-2292201	A	A	386	4	416	0	4.288	3.84E-02	rs7189012	16	85063607	q24.1
SNP_A-2296168	A	A	248	122	243	163	4.288	3.84E-02	rs4618385	4	189591587	q35.2
SNP_A-2309401	C	C	420	0	390	4	4.285	3.84E-02	rs7085980	10	114436330	q25.2
SNP_A-2310704	C	C	244	178	267	145	4.287	3.84E-02	rs2513486	11	114311601	q23.2
SNP_A-2310511	C	T	184	182	231	173	4.288	3.84E-02	rs4516626	3	85235677	p12.1
SNP_A-2311059	G	G	230	104	231	145	4.284	0.0385	rs11584623	1	209258412	q32.3
SNP_A-2312270	A	A	218	140	279	131	4.285	0.0385	rs6039313	20	8807642	p12.3
SNP_A-2307375	A	A	322	44	334	70	4.284	0.0385	rs209405	6	83600448	q14.1
SNP_A-2304054	G	G	262	106	266	148	4.284	0.0385	rs1361933	20	45902724	q13.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2295067	C	C	281	139	307	111	4.281	0.0385	rs1562306	2	113467611	q13
SNP_A-2288460	G	G	320	50	337	79	4.282	0.0385	rs10747495	1	98182626	p21.3
SNP_A-2262947	G	G	355	11	410	4	4.283	0.0385	rs6842825	4	56966104	q12
SNP_A-2261169	C	C	319	33	367	21	4.284	0.0385	rs6077153	20	7127994	p12.3
SNP_A-2283834	G	G	306	64	364	50	4.284	0.0385	rs9863517	3	24265684	p24.2
SNP_A-2285342	A	A	238	104	262	80	4.282	0.0385	rs7726935	5	133027881	q31.1
SNP_A-2279465	G	G	329	41	347	67	4.283	0.0385	rs11051126	12	30919354	p11.21
SNP_A-2272664	A	A	324	30	356	54	4.281	0.0385	rs4142791	1	91332059	p22.2
SNP_A-2232892	C	C	289	73	342	58	4.285	0.0385	rs6830266	4	178617547	q34.3
SNP_A-2249306	C	C	349	13	385	5	4.285	0.0385	rs17130733	1	68736194	p31.2
SNP_A-2015259	T	T	344	70	325	95	4.285	0.0385	rs1983537	21	14866830	q11.2
SNP_A-2041135	G	G	319	45	374	32	4.282	0.0385	rs7010386	8	53394440	q11.23
SNP_A-2045397	G	G	184	156	243	151	4.284	0.0385	rs4240658	8	10465830	p23.1
SNP_A-2035410	G	G	334	16	363	33	4.284	0.0385	rs17077516	13	22204806	q12.12
SNP_A-2031200	C	C	323	41	346	68	4.283	0.0385	---	14	85954870	q31.3
SNP_A-2082962	T	T	291	79	346	64	4.282	0.0385	rs12826226	12	21414787	p12.1
SNP_A-2060214	A	A	275	143	246	172	4.284	0.0385	rs12053126	2	100323164	q11.2
SNP_A-2210990	C	C	316	48	355	33	4.283	0.0385	rs511179	9	130422395	q34.11
SNP_A-2224603	C	C	364	54	344	76	4.283	0.0385	rs7596661	2	112742420	q13
SNP_A-2172030	T	T	340	32	388	20	4.282	0.0385	rs7477394	10	27125252	p12.1
SNP_A-2169085	G	G	351	15	362	30	4.283	0.0385	rs1421551	18	60098290	q22.1
SNP_A-2125134	G	G	380	22	407	11	4.282	0.0385	rs3885895	13	30136207	q12.3
SNP_A-1783949	G	G	314	108	336	82	4.284	0.0385	rs4782539	16	82097934	q23.3
SNP_A-1730429	C	C	385	15	408	6	4.285	0.0385	rs10497155	2	158078391	q24.1
SNP_A-1648944	A	A	387	15	385	29	4.284	0.0385	rs10485103	6	165974948	q27
SNP_A-1857839	A	A	333	81	299	103	4.284	0.0385	rs165757	22	15690057	q11.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1819562	G	G	300	22	367	13	4.282	0.0385	rs6507778	18	43369443	q21.1
SNP_A-1836753	C	C	368	14	357	27	4.284	0.0385	rs4595742	15	56245208	q21.3
SNP_A-1833620	G	G	247	51	296	38	4.284	0.0385	rs4360820	13	70827330	q21.33
SNP_A-1949261	T	T	271	143	300	116	4.283	0.0385	rs471336	3	16401431	p24.3
SNP_A-1937366	G	G	387	21	406	10	4.281	0.0385	rs1023926	5	31609897	p13.3
SNP_A-1975970	C	C	302	106	330	82	4.285	0.0385	rs2868939	4	9991190	p16.1
SNP_A-1963225	T	T	214	144	272	134	4.283	0.0385	rs9309208	2	51402360	p16.3
SNP_A-1980809	A	A	263	107	321	93	4.284	0.0385	rs6703590	1	201023390	q32.1
SNP_A-1911926	T	T	385	21	404	10	4.283	0.0385	rs5762906	22	27662789	q12.1
SNP_A-1878361	T	T	266	56	268	84	4.281	0.0385	rs386348	3	60408264	p14.2
SNP_A-1889432	A	A	242	108	249	153	4.283	0.0385	rs1256567	1	215653775	q41
SNP_A-1887904	G	G	251	159	278	130	4.283	0.0385	rs12876893	13	30300831	q12.3
SNP_A-1888605	A	A	384	28	401	15	4.279	3.86E-02	rs10116672	9	26694308	p21.2
SNP_A-1894163	T	G	179	161	205	167	4.276	3.86E-02	rs4539321	11	21375322	p15.1
SNP_A-1904657	A	A	205	161	262	152	4.278	3.86E-02	rs11142508	9	70461216	q21.11
SNP_A-1906651	A	A	245	107	251	151	4.28	3.86E-02	rs2570950	8	103953041	q22.3
SNP_A-1982989	G	G	321	49	380	36	4.277	3.86E-02	rs10519361	5	113050968	q22.2
SNP_A-1949791	C	C	351	51	378	34	4.278	3.86E-02	rs2185411	13	46869238	q14.2
SNP_A-1955558	G	G	318	28	326	48	4.28	3.86E-02	rs2222825	3	190753731	q28
SNP_A-1824133	G	-	206	152	196	196	4.279	3.86E-02	rs4345034	3	156385497	q25.2
SNP_A-1861033	G	G	279	89	285	127	4.281	3.86E-02	rs17585235	11	61852692	q12.3
SNP_A-1674106	C	C	213	137	279	131	4.278	3.86E-02	rs1074789	9	12742340	p23
SNP_A-1705371	A	A	319	83	303	111	4.277	3.86E-02	rs6762641	3	60573488	p14.2
SNP_A-1740019	C	C	325	17	370	36	4.28	3.86E-02	rs6841078	4	76224863	q13.3
SNP_A-1758418	A	A	269	133	303	109	4.279	3.86E-02	rs6427247	1	167567857	q24.2
SNP_A-1812877	G	G	382	14	371	27	4.278	3.86E-02	rs17080814	5	180489944	q35.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2126627	A	G	197	171	222	190	4.276	3.86E-02	rs10105587	8	88485574	q21.3
SNP_A-2115722	A	A	232	136	232	184	4.277	3.86E-02	rs2971148	7	9794318	p21.3
SNP_A-2123161	A	A	287	135	257	163	4.281	3.86E-02	rs13387555	2	225865926	q36.2
SNP_A-2108945	G	G	277	91	284	130	4.279	3.86E-02	rs2623820	8	68849890	q13.2
SNP_A-2163606	C	C	301	53	344	38	4.28	3.86E-02	rs768056	9	91345841	q22.31
SNP_A-2174238	G	G	335	11	376	26	4.277	3.86E-02	rs2280740	3	185576229	q27.1
SNP_A-2173545	G	G	292	68	355	55	4.28	3.86E-02	rs12536104	7	38408306	p14.1
SNP_A-2224596	T	C	219	165	180	176	4.28	3.86E-02	rs2842244	1	5737886	p36.31
SNP_A-2215384	A	A	292	40	337	27	4.28	3.86E-02	rs2240092	7	50873787	p12.1
SNP_A-2057308	T	T	252	108	249	147	4.278	3.86E-02	rs10036867	5	25660816	p14.1
SNP_A-2065267	A	A	213	155	208	204	4.279	3.86E-02	rs12699927	7	17784992	p21.1
SNP_A-2099842	G	G	277	125	290	94	4.276	3.86E-02	rs1977298	6	17636129	p22.3
SNP_A-2020214	T	T	251	119	310	106	4.279	3.86E-02	rs2284965	21	43018846	q22.3
SNP_A-1993655	T	T	277	91	284	130	4.279	3.86E-02	rs2553686	8	68847408	q13.2
SNP_A-2003738	A	A	322	78	293	101	4.278	3.86E-02	rs303526	10	90559703	q23.31
SNP_A-1998057	C	C	303	119	326	92	4.277	3.86E-02	rs10901196	9	132573367	q34.13
SNP_A-2238645	T	T	322	6	349	17	4.279	3.86E-02	rs6659716	1	61031203	p31.3
SNP_A-2283223	C	C	257	87	274	130	4.28	3.86E-02	rs9685837	4	188193615	q35.2
SNP_A-2291684	C	C	333	87	306	112	4.277	3.86E-02	rs1386580	1	218983956	q41
SNP_A-2298213	A	A	333	37	354	62	4.278	3.86E-02	rs4939921	18	45716326	q21.1
SNP_A-2310153	T	T	325	19	382	10	4.276	3.86E-02	rs935564	8	320846	p23.3
SNP_A-2274312	C	C	354	64	331	87	4.276	3.87E-02	rs10845764	12	13463448	p13.1
SNP_A-2275784	G	G	263	105	324	92	4.274	3.87E-02	rs11221789	11	129042497	q24.3
SNP_A-2239875	C	C	263	77	284	118	4.276	3.87E-02	rs7705406	5	31240468	p13.3
SNP_A-2240127	G	G	243	113	306	102	4.273	3.87E-02	rs2065168	6	126233426	q22.32
SNP_A-2255705	G	G	243	125	303	113	4.276	3.87E-02	rs7573518	2	132000119	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017000	G	G	389	5	384	14	4.275	3.87E-02	rs2829994	21	26236585	q21.3
SNP_A-2027993	C	C	408	14	413	5	4.275	3.87E-02	rs16881700	6	19203871	p22.3
SNP_A-2094938	T	T	288	82	297	119	4.272	3.87E-02	rs6090338	20	60797591	q13.33
SNP_A-2094534	A	A	332	78	309	103	4.273	3.87E-02	rs1436475	4	42949449	p13
SNP_A-2099011	T	T	304	32	328	56	4.276	3.87E-02	rs8039000	15	59470349	q22.2
SNP_A-2098657	T	T	272	40	268	62	4.273	3.87E-02	rs2130471	11	46069550	p11.2
SNP_A-2120333	T	T	192	130	197	183	4.276	3.87E-02	rs7031064	9	14445076	p22.3
SNP_A-1801818	C	C	307	57	314	86	4.273	3.87E-02	rs1389476	12	90623645	q21.33
SNP_A-1800679	C	C	379	41	356	60	4.275	3.87E-02	rs11235963	11	69868604	q13.3
SNP_A-1752503	T	T	375	23	374	40	4.275	3.87E-02	rs4358869	9	87026412	q22.1
SNP_A-1727691	T	T	396	2	403	9	4.275	3.87E-02	rs10517058	4	42788757	p13
SNP_A-1690659	T	T	280	122	260	154	4.275	3.87E-02	rs10502149	11	111245035	q23.1
SNP_A-1667090	A	A	321	55	368	40	4.276	3.87E-02	rs10504499	8	72086865	q13.3
SNP_A-1663720	A	A	280	122	260	154	4.275	3.87E-02	rs10502150	11	111245446	q23.1
SNP_A-1664182	A	A	337	5	386	16	4.272	3.87E-02	rs10516951	4	95873877	q22.3
SNP_A-1871441	T	T	254	168	262	128	4.275	3.87E-02	rs1780464	9	129355565	q34.11
SNP_A-1825686	A	A	234	136	292	124	4.272	3.87E-02	rs176382	5	138254666	q31.2
SNP_A-1830257	C	G	194	160	213	191	4.275	3.87E-02	rs8051237	16	84939020	q24.1
SNP_A-1955488	C	C	246	124	299	109	4.274	3.87E-02	rs12522240	5	86000448	q14.3
SNP_A-1987595	G	G	242	102	293	87	4.273	3.87E-02	rs265334	6	129591296	q22.33
SNP_A-1971567	G	G	240	116	297	103	4.276	3.87E-02	rs345213	3	6798232	p26.1
SNP_A-1932242	T	T	352	14	384	30	4.272	3.87E-02	rs305567	1	64691171	p31.3
SNP_A-1928062	C	C	284	72	301	109	4.272	3.87E-02	rs603377	11	117076061	q23.3
SNP_A-1931967	C	C	290	52	314	84	4.27	3.88E-02	rs1402778	2	82134065	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1919648	C	C	302	20	291	35	4.27	3.88E-02	rs17066897	18	56230118	q21.32
SNP_A-1899220	T	T	259	111	257	151	4.269	3.88E-02	rs7227668	18	60644712	q22.1
SNP_A-1878183	T	T	275	85	333	71	4.269	3.88E-02	rs17629798	17	30571045	q12
SNP_A-1967512	C	C	213	127	263	113	4.27	3.88E-02	rs7264576	20	4665456	p13
SNP_A-1984324	G	G	391	27	402	14	4.27	3.88E-02	rs1572738	1	213340282	q41
SNP_A-1980419	A	A	327	83	308	110	4.269	3.88E-02	rs1816235	5	5200032	p15.32
SNP_A-1829554	C	T	205	163	213	199	4.27	3.88E-02	rs1359563	6	54002749	p12.1
SNP_A-1841742	G	G	302	58	323	91	4.268	3.88E-02	rs10953259	7	97657758	q22.1
SNP_A-1826155	T	T	392	20	401	9	4.27	3.88E-02	rs900250	5	8036035	p15.31
SNP_A-1827430	C	C	306	56	367	43	4.268	3.88E-02	rs7681841	4	175537379	q34.1
SNP_A-1868862	C	G	233	189	218	202	4.271	3.88E-02	rs17663387	10	116578050	q25.3
SNP_A-1863172	A	A	318	50	335	79	4.271	3.88E-02	rs4634961	1	98199784	p21.3
SNP_A-1804675	C	C	360	6	413	1	4.268	3.88E-02	rs12256878	10	77331129	q22.2
SNP_A-1813302	G	G	209	145	264	134	4.269	3.88E-02	rs924825	3	154990915	q25.2
SNP_A-1793436	G	G	308	54	327	85	4.27	3.88E-02	rs6854094	4	19177691	p15.31
SNP_A-2120476	G	G	380	16	359	29	4.271	3.88E-02	rs12535283	7	87400102	q21.12
SNP_A-2129817	G	G	393	27	404	14	4.269	3.88E-02	rs10129671	14	45451570	q21.2
SNP_A-2130901	G	G	315	87	300	116	4.27	3.88E-02	rs7994531	13	41875439	q14.11
SNP_A-2151801	T	T	369	37	359	57	4.272	3.88E-02	rs4909954	11	10872044	p15.3
SNP_A-2223124	G	G	242	140	273	115	4.271	3.88E-02	rs2350137	14	59267022	q23.1
SNP_A-2201317	A	A	360	6	413	1	4.268	3.88E-02	rs8022938	14	66925080	q23.3
SNP_A-2203410	C	C	389	27	400	14	4.271	3.88E-02	rs10984435	9	119044794	q33.1
SNP_A-2203874	G	G	382	4	410	0	4.27	3.88E-02	rs16943898	12	113135728	q24.21
SNP_A-2188751	G	G	389	27	400	14	4.271	3.88E-02	rs6016500	20	39067902	q12
SNP_A-2188712	C	C	262	104	300	84	4.268	3.88E-02	rs11132327	4	186860392	q35.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098934	C	C	384	4	412	0	4.269	3.88E-02	rs2113340	7	133012835	q33
SNP_A-2092962	G	G	307	61	321	93	4.27	3.88E-02	rs833724	12	101579953	q23.2
SNP_A-2101876	C	C	384	4	412	0	4.269	3.88E-02	rs924829	17	70069117	q25.1
SNP_A-2077053	G	G	350	10	369	23	4.269	3.88E-02	rs568562	11	94500347	q21
SNP_A-2079405	A	A	335	87	353	63	4.268	3.88E-02	rs580891	11	65711257	q13.2
SNP_A-2080108	C	C	307	61	321	93	4.27	3.88E-02	rs1325382	13	107545226	q33.3
SNP_A-2085535	C	C	380	4	408	0	4.272	3.88E-02	rs10860391	12	97998971	q23.1
SNP_A-2090202	G	G	297	99	268	124	4.271	3.88E-02	rs10742602	11	41747049	p12
SNP_A-2252497	G	G	272	96	278	136	4.271	3.88E-02	rs6862878	5	163827779	q34
SNP_A-2244120	C	C	233	181	256	148	4.27	3.88E-02	rs9503063	6	1941657	p25.3
SNP_A-2231538	T	T	317	35	382	24	4.27	3.88E-02	rs17060323	8	29448065	p12
SNP_A-2284887	G	G	294	120	317	93	4.269	3.88E-02	rs1422672	5	158399979	q33.3
SNP_A-2270690	G	G	349	13	374	28	4.27	3.88E-02	rs1421540	18	60083845	q22.1
SNP_A-2309332	A	A	220	148	277	137	4.271	3.88E-02	rs2163617	2	55030698	p16.1
SNP_A-2267672	T	T	351	41	380	26	4.264	3.89E-02	rs11070264	15	38399153	q15.1
SNP_A-2279483	A	A	266	54	333	43	4.263	3.89E-02	rs6055170	20	7536116	p12.3
SNP_A-2231932	T	T	418	0	390	4	4.265	3.89E-02	rs1691907	10	29165925	p12.1
SNP_A-2235393	C	C	402	20	411	9	4.267	3.89E-02	rs11067936	12	108607652	q24.11
SNP_A-2079780	A	A	416	0	388	4	4.266	3.89E-02	rs6488944	12	123852069	q24.31
SNP_A-2026962	T	T	285	55	342	42	4.266	3.89E-02	rs3807823	7	8020428	p21.3
SNP_A-2017011	C	C	362	6	415	1	4.264	3.89E-02	rs10489659	1	55020630	p32.3
SNP_A-2003278	C	C	331	53	351	35	4.263	3.89E-02	rs7995855	13	43678160	q14.11
SNP_A-1995953	T	T	258	102	260	142	4.263	3.89E-02	rs1556421	9	13156139	p23
SNP_A-2177241	C	C	235	169	261	139	4.265	3.89E-02	rs2275403	1	19303019	p36.13
SNP_A-2212346	A	G	240	182	210	208	4.267	3.89E-02	rs6437870	3	96663820	q11.2
SNP_A-2209075	A	A	381	31	393	17	4.265	3.89E-02	rs2852221	11	120160234	q23.3
SNP_A-2214301	C	C	362	6	415	1	4.264	3.89E-02	rs11193449	10	109205223	q25.1
SNP_A-2220219	C	C	362	6	415	1	4.264	3.89E-02	rs17115086	14	44009629	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2152721	A	A	345	71	366	50	4.265	3.89E-02	rs7145819	14	50875702	q22.1
SNP_A-2145831	A	A	362	6	415	1	4.264	3.89E-02	rs17170834	7	36829121	p14.2
SNP_A-2159766	A	A	362	6	415	1	4.264	3.89E-02	rs9868347	3	190153747	q28
SNP_A-2116906	C	T	240	182	210	208	4.267	3.89E-02	rs13090887	3	96640233	q11.2
SNP_A-2115353	G	G	362	6	415	1	4.264	3.89E-02	rs1963276	9	8143933	p24.1
SNP_A-1787314	G	G	347	15	409	7	4.266	3.89E-02	rs3797936	5	9239073	p15.31
SNP_A-1741777	G	G	368	28	353	45	4.266	3.89E-02	rs1357520	1	235969630	q43
SNP_A-1754822	T	T	289	113	322	90	4.266	3.89E-02	rs2288627	2	222522966	q36.1
SNP_A-1860851	G	G	259	109	256	148	4.266	3.89E-02	rs10085132	5	173037224	q35.2
SNP_A-1848987	C	C	190	126	188	172	4.265	3.89E-02	rs10927757	1	15345355	p36.21
SNP_A-1827380	C	C	307	105	276	130	4.264	3.89E-02	rs1515881	16	26988411	p12.1
SNP_A-1824840	T	G	180	140	195	183	4.265	3.89E-02	rs7303990	12	26556243	p11.23
SNP_A-1820683	T	T	341	15	365	31	4.265	3.89E-02	rs11706420	3	58367451	p14.3
SNP_A-1838621	A	A	286	122	253	147	4.265	3.89E-02	rs10821487	9	89834687	q22.2
SNP_A-1970300	G	G	313	49	322	76	4.264	3.89E-02	rs1686193	1	161391892	q23.3
SNP_A-1975873	G	G	211	189	226	150	4.263	3.89E-02	rs7657964	4	5584399	p16.2
SNP_A-1973572	G	A	240	182	210	208	4.267	3.89E-02	rs1914881	3	96638064	q11.2
SNP_A-1958638	G	G	252	116	311	103	4.264	3.89E-02	rs10743498	12	24450637	p12.1
SNP_A-1899469	C	A	180	156	210	178	4.266	3.89E-02	rs13153071	5	112703850	q22.2
SNP_A-1889973	G	G	362	6	415	1	4.264	3.89E-02	rs17762315	5	76843333	q13.3
SNP_A-1923643	C	C	249	113	299	97	4.265	3.89E-02	rs332607	6	124765053	q22.31
SNP_A-1909578	G	G	362	6	415	1	4.264	3.89E-02	rs17013713	3	76187841	p12.3
SNP_A-1910713	C	C	242	170	272	142	4.259	0.039	rs6992026	8	27762454	p21.1
SNP_A-1880315	C	C	221	149	218	198	4.262	0.039	rs614767	11	78663186	q14.1
SNP_A-1953327	T	T	341	11	367	25	4.261	0.039	rs6731269	2	195134654	q32.3
SNP_A-1934886	T	T	339	49	285	63	4.262	0.039	rs10220371	14	87571605	q31.3
SNP_A-1946891	C	C	344	20	375	39	4.259	0.039	rs17665327	15	93246111	q26.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1967708	C	C	318	50	377	37	4.26	0.039	rs6087099	20	9934343	p12.2
SNP_A-1968969	C	C	298	122	270	150	4.263	0.039	rs2155971	21	14415232	q11.2
SNP_A-1978129	A	A	199	163	253	153	4.261	0.039	rs1472962	4	95949555	q22.3
SNP_A-1988380	C	C	332	14	380	6	4.263	0.039	rs1536324	1	228889962	q42.2
SNP_A-1831561	A	A	318	50	377	37	4.26	0.039	rs11233169	11	81943459	q14.1
SNP_A-1832922	T	T	296	108	265	133	4.262	0.039	rs10918268	1	162425197	q24.1
SNP_A-1828080	A	A	319	89	324	62	4.26	0.039	rs6999688	8	107886832	q23.1
SNP_A-1717407	T	T	290	102	330	82	4.26	0.039	rs766653	7	10425000	p21.3
SNP_A-1797344	G	G	353	41	382	26	4.259	0.039	rs10940159	5	67583032	q13.1
SNP_A-1804109	G	G	321	43	335	69	4.263	0.039	rs7527807	1	107846152	p13.3
SNP_A-1803591	T	T	343	3	353	11	4.262	0.039	rs1880563	19	41819915	q13.12
SNP_A-2115455	C	C	260	134	238	166	4.261	0.039	rs179106	14	22067673	q11.2
SNP_A-2118672	A	A	303	65	316	98	4.263	0.039	rs2985338	1	29190500	p35.3
SNP_A-2120914	G	G	295	67	358	54	4.263	0.039	rs3734586	6	7546719	p24.3
SNP_A-2166033	T	T	227	117	289	107	4.263	0.039	rs4772352	13	100391674	q32.3
SNP_A-2216083	C	C	344	20	375	39	4.259	0.039	rs1549736	2	218309894	q35
SNP_A-2227237	C	C	237	167	211	199	4.263	0.039	rs309297	2	7138414	p25.1
SNP_A-2205325	G	G	232	128	232	174	4.26	0.039	rs2293572	2	27640428	p23.3
SNP_A-2183512	C	C	208	164	243	141	4.261	0.039	rs7342740	16	5767066	p13.3
SNP_A-1989908	G	G	369	31	316	44	4.261	0.039	rs10486748	7	50800146	p12.1
SNP_A-2012728	T	T	312	110	331	83	4.262	0.039	rs1367980	11	83018046	q14.1
SNP_A-2032555	G	G	348	6	399	1	4.263	0.039	rs10967033	9	25658442	p21.2
SNP_A-2022449	T	C	203	163	209	193	4.263	0.039	rs10050320	4	31731975	p15.1
SNP_A-2034950	C	C	195	113	211	169	4.263	0.039	rs1422205	5	106568544	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2081216	G	G	195	141	185	183	4.262	0.039	rs3110202	12	82392548	q21.31
SNP_A-2107565	G	G	206	162	263	153	4.262	0.039	rs11077494	17	65928147	q24.3
SNP_A-2094834	C	C	313	109	283	135	4.262	0.039	rs450975	22	16690887	q11.21
SNP_A-2055388	C	C	209	161	265	151	4.259	0.039	rs6074247	20	11020272	p12.2
SNP_A-2245432	T	T	303	67	314	100	4.261	0.039	rs17136868	5	113989620	q22.3
SNP_A-2253885	A	A	399	17	387	31	4.262	0.039	rs2252549	1	39412805	p34.3
SNP_A-2276772	G	G	265	97	326	84	4.262	0.039	rs7033099	9	9959939	p23
SNP_A-2274079	C	C	302	64	309	95	4.259	0.039	rs7973610	12	37895910	q12
SNP_A-2281008	C	C	332	38	351	63	4.261	0.039	rs10044597	5	84143126	q14.3
SNP_A-2261837	T	T	303	67	314	100	4.261	0.039	rs11122381	1	228400842	q42.2
SNP_A-2297608	T	T	304	34	365	23	4.262	0.039	rs17103193	14	65531613	q23.3
SNP_A-2289763	A	A	350	18	403	9	4.262	0.039	rs10756253	9	11439567	p23
SNP_A-2292980	T	T	355	1	367	7	4.258	3.91E-02	rs6862329	5	120830204	q23.1
SNP_A-2303991	T	T	355	43	325	61	4.256	3.91E-02	rs6503851	17	53616980	q23.2
SNP_A-2266071	A	A	261	159	227	185	4.257	3.91E-02	rs2064342	20	44644956	q13.12
SNP_A-2249032	G	G	261	45	299	31	4.258	3.91E-02	rs2949938	17	62934459	q24.2
SNP_A-2059341	A	A	323	63	321	91	4.255	3.91E-02	rs1613631	12	51062202	q13.13
SNP_A-2073939	G	G	203	145	199	193	4.255	3.91E-02	rs6944358	7	5587419	p22.1
SNP_A-2092557	C	C	357	33	311	47	4.256	3.91E-02	rs7623683	3	2801203	p26.2
SNP_A-2103147	A	A	294	66	302	98	4.258	3.91E-02	rs2036182	4	27937396	p15.1
SNP_A-2088924	T	T	319	101	337	75	4.258	3.91E-02	rs8104554	19	56229928	q13.41
SNP_A-2014269	A	A	265	157	292	128	4.255	3.91E-02	rs7026124	9	72424532	q21.13
SNP_A-1989954	G	T	199	163	207	187	4.259	3.91E-02	rs1357961	7	52988628	p12.1
SNP_A-1991953	G	G	338	78	315	103	4.258	3.91E-02	rs2975357	8	3719275	p23.2
SNP_A-2001447	C	C	386	4	370	12	4.256	3.91E-02	rs6421366	10	115440504	q25.3
SNP_A-2171146	A	A	316	48	373	35	4.258	3.91E-02	rs4851581	2	102493267	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2226194	G	G	336	24	394	14	4.256	3.91E-02	rs16977497	17	68533240	q25.1
SNP_A-2220630	A	A	352	18	405	9	4.255	3.91E-02	rs1557075	13	23852953	q12.12
SNP_A-2152389	C	C	214	144	268	132	4.257	3.91E-02	rs7974004	12	31675348	p11.21
SNP_A-2141167	T	T	350	14	400	6	4.255	3.91E-02	rs1620255	8	16649761	p22
SNP_A-2130100	A	A	230	192	256	160	4.257	3.91E-02	rs9783823	17	39168895	q21.31
SNP_A-2126564	T	T	400	22	381	37	4.257	3.91E-02	rs17731603	20	6720066	p12.3
SNP_A-1800456	A	A	317	101	343	77	4.255	3.91E-02	rs4767206	12	112983073	q24.21
SNP_A-1798428	A	G	203	163	215	199	4.256	3.91E-02	rs10115327	9	119476473	q33.1
SNP_A-1792762	G	G	295	23	301	41	4.256	3.91E-02	rs1217750	5	71285196	q13.2
SNP_A-1691228	G	G	297	91	273	117	4.255	3.91E-02	rs198475	11	61301431	q12.2
SNP_A-1710143	C	C	362	40	389	25	4.257	3.91E-02	rs1219391	11	121304540	q24.1
SNP_A-1700255	G	G	354	40	352	62	4.258	3.91E-02	rs10489641	1	178914973	q25.3
SNP_A-1815972	G	G	317	101	343	77	4.255	3.91E-02	rs4101521	2	38382052	p22.2
SNP_A-1843248	C	C	302	28	338	52	4.255	3.91E-02	---	3	168993843	q26.1
SNP_A-1853418	G	G	252	112	308	98	4.255	3.91E-02	rs10018606	4	57979340	q12
SNP_A-1854628	T	T	336	24	394	14	4.256	3.91E-02	rs7675378	4	37513896	p14
SNP_A-1989195	C	C	398	0	372	4	4.256	3.91E-02	rs6960362	7	23715756	p15.3
SNP_A-1981659	C	C	366	32	382	18	4.257	3.91E-02	rs7730184	5	56022313	q11.2
SNP_A-1963674	T	T	230	132	285	119	4.257	3.91E-02	rs6546371	2	68454149	p14
SNP_A-1965398	G	G	294	34	366	24	4.257	3.91E-02	rs16830446	2	152587749	q23.3
SNP_A-1946389	T	T	350	46	367	29	4.256	3.91E-02	rs543030	19	6032667	p13.3
SNP_A-1884880	A	A	254	104	253	143	4.256	3.91E-02	rs13031728	2	167225074	q24.3
SNP_A-1885809	C	C	342	20	373	39	4.25	3.92E-02	rs4742095	9	5435990	p24.1
SNP_A-1959737	G	G	229	77	274	62	4.252	3.92E-02	rs2366178	18	66075437	q22.2
SNP_A-1966911	T	T	274	136	232	156	4.253	3.92E-02	rs6656583	1	149507266	q21.3
SNP_A-1973869	A	A	274	64	273	93	4.252	3.92E-02	rs10494512	1	174983337	q25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1856713	T	T	294	110	267	137	4.251	3.92E-02	rs6040341	20	11005774	p12.2
SNP_A-1845665	A	A	293	117	305	87	4.251	3.92E-02	rs1366083	5	143026361	q31.3
SNP_A-1863394	C	C	235	135	293	123	4.252	3.92E-02	rs9442961	6	74546353	q13
SNP_A-1866573	C	C	343	17	386	8	4.252	3.92E-02	rs4759331	12	52765366	q13.13
SNP_A-1837231	C	C	235	135	293	123	4.252	3.92E-02	rs7734159	5	84473276	q14.3
SNP_A-1680310	C	C	374	28	368	46	4.251	3.92E-02	rs2996255	6	48651807	p12.3
SNP_A-1680072	C	C	245	147	228	184	4.252	3.92E-02	rs7714938	5	22521472	p14.3
SNP_A-1799670	C	C	336	20	372	10	4.253	3.92E-02	rs1282275	1	111341613	p13.3
SNP_A-1812523	A	C	211	189	215	179	4.254	3.92E-02	rs7594278	2	46516244	p21
SNP_A-2116860	G	G	308	58	326	90	4.25	3.92E-02	rs880225	6	25510137	p22.2
SNP_A-2150421	C	C	345	75	313	97	4.25	3.92E-02	---	7	55098357	p11.2
SNP_A-2165574	T	T	380	4	406	0	4.251	3.92E-02	rs11176119	12	64950895	q14.3
SNP_A-2168426	G	G	230	134	228	180	4.254	3.92E-02	rs12465424	2	41574461	p22.1
SNP_A-2171609	G	G	343	13	377	5	4.25	3.92E-02	rs6706377	2	142108520	q22.1
SNP_A-2184463	A	A	289	31	342	20	4.254	3.92E-02	rs16966917	13	105045258	q33.2
SNP_A-2185999	G	G	371	47	342	66	4.254	3.92E-02	rs7513434	1	110898371	p13.3
SNP_A-2198877	G	G	267	99	267	137	4.254	3.92E-02	rs7626252	3	165168949	q26.1
SNP_A-2197167	C	C	286	76	349	63	4.254	3.92E-02	rs3818279	14	99453716	q32.2
SNP_A-2005082	C	C	289	89	286	60	4.254	3.92E-02	rs2191181	17	14669002	p12
SNP_A-2019004	T	T	406	0	380	4	4.251	3.92E-02	rs2835745	21	37737656	q22.13
SNP_A-2028883	G	G	293	57	345	43	4.253	3.92E-02	rs176600	6	63017985	q11.1
SNP_A-2082599	A	A	247	117	249	161	4.253	3.92E-02	rs11063200	12	4462602	p13.32
SNP_A-2096780	T	T	354	6	405	1	4.251	3.92E-02	rs11217807	11	119675240	q23.3
SNP_A-2059646	A	A	335	9	364	22	4.252	3.92E-02	rs9574041	13	76846919	q22.3
SNP_A-2059642	A	A	369	43	391	27	4.251	3.92E-02	rs1238553	11	121207450	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2055833	G	G	289	75	304	112	4.253	3.92E-02	rs8017309	14	41401326	q21.1
SNP_A-2058570	A	A	372	32	388	18	4.252	3.92E-02	rs10827556	10	36151776	p11.21
SNP_A-2050892	G	G	271	41	303	71	4.251	3.92E-02	rs10981637	9	112971799	q32
SNP_A-2237485	A	A	236	130	217	163	4.252	3.92E-02	rs1176387	1	116736533	p13.1
SNP_A-2240314	A	A	231	133	228	178	4.253	3.92E-02	rs7422720	2	202867850	q33.1
SNP_A-2229193	G	G	263	99	327	87	4.251	3.92E-02	rs2454162	1	17231246	p36.13
SNP_A-2260022	G	G	218	148	267	133	4.25	3.92E-02	rs497937	1	160709667	q23.3
SNP_A-2284553	G	G	277	143	242	168	4.25	3.92E-02	rs2971971	7	133101103	q33
SNP_A-2309255	T	T	226	90	296	82	4.254	3.92E-02	rs16860897	2	173503471	q31.1
SNP_A-2308514	C	C	318	30	373	19	4.246	3.93E-02	rs1998908	9	84326310	q21.33
SNP_A-2306716	C	C	342	46	342	70	4.249	3.93E-02	rs12321227	12	75773488	q21.2
SNP_A-2293499	G	G	235	135	233	181	4.249	3.93E-02	rs6720297	2	2360871	p25.3
SNP_A-2244211	C	C	352	14	402	6	4.249	3.93E-02	rs17104828	1	80618655	p31.1
SNP_A-2255625	A	A	235	133	293	121	4.247	3.93E-02	rs9822047	3	161276590	q25.33
SNP_A-2050538	T	T	340	82	312	106	4.247	3.93E-02	rs11521036	7	120684482	q31.31
SNP_A-2076942	C	C	329	57	325	83	4.247	3.93E-02	rs11179544	12	71781025	q21.1
SNP_A-2095783	G	G	245	161	217	191	4.249	3.93E-02	rs1959065	14	56077280	q22.3
SNP_A-2028830	G	G	332	20	395	11	4.247	3.93E-02	rs16934073	10	33467609	p11.22
SNP_A-2030989	A	A	412	0	386	4	4.247	3.93E-02	rs16947819	17	13247259	p12
SNP_A-2044885	G	G	335	61	358	42	4.248	3.93E-02	rs6707977	2	227976111	q36.3
SNP_A-2012199	T	T	364	42	353	63	4.248	3.93E-02	rs17105629	1	49511341	p33
SNP_A-2176617	G	G	281	85	344	72	4.247	3.93E-02	rs3742123	13	96286117	q32.1
SNP_A-2227478	C	C	281	45	321	31	4.246	3.93E-02	rs1503022	18	69045491	q22.3
SNP_A-2206681	G	G	326	42	337	67	4.247	3.93E-02	rs13435951	5	113021902	q22.2
SNP_A-2207780	T	T	261	109	262	150	4.249	3.93E-02	rs8086948	18	63308747	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2122479	T	T	234	136	233	183	4.249	3.93E-02	rs2143312	1	165287959	q24.2
SNP_A-2121660	A	A	353	9	384	22	4.249	3.93E-02	rs17622979	6	103689089	q16.3
SNP_A-2115065	A	A	393	27	371	43	4.248	3.93E-02	rs16988333	22	28877367	q12.2
SNP_A-2111331	A	A	217	149	275	139	4.247	3.93E-02	rs12472480	2	207224063	q33.3
SNP_A-1799498	C	C	237	125	298	114	4.249	3.93E-02	rs7028882	9	91357574	q22.31
SNP_A-1797441	C	C	345	77	319	101	4.249	3.93E-02	rs9871612	3	130053100	q21.3
SNP_A-1840749	A	A	293	31	281	49	4.246	3.93E-02	rs1401270	2	181068923	q31.3
SNP_A-1816417	C	C	295	89	254	108	4.249	3.93E-02	rs4782267	16	10126226	p13.2
SNP_A-1849939	C	C	375	15	396	6	4.248	3.93E-02	rs1483370	8	90289833	q21.3
SNP_A-1983689	G	G	235	133	293	121	4.247	3.93E-02	rs10515504	5	138250893	q31.2
SNP_A-1934989	T	T	378	0	354	4	4.247	3.93E-02	rs17072711	6	143865855	q24.2
SNP_A-1907895	C	C	312	102	284	128	4.25	3.93E-02	rs4796356	17	6662514	p13.1
SNP_A-1913649	C	C	252	116	308	102	4.244	3.94E-02	rs2738287	2	217175342	q35
SNP_A-1916539	C	C	278	84	336	70	4.245	3.94E-02	rs1900867	4	59568062	q12
SNP_A-1878409	T	T	325	45	380	32	4.242	3.94E-02	rs2420510	1	166520242	q24.2
SNP_A-1889746	T	T	269	153	293	123	4.243	3.94E-02	rs6903444	6	41122198	p21.1
SNP_A-1895601	G	G	363	15	348	28	4.241	3.94E-02	rs16941390	17	42405984	q21.32
SNP_A-1986014	T	T	284	128	261	159	4.243	3.94E-02	rs2397030	6	51238446	p12.3
SNP_A-1974976	C	C	328	24	350	44	4.245	3.94E-02	rs12497720	3	157846538	q25.31
SNP_A-1963914	C	C	212	156	207	205	4.242	3.94E-02	rs7565752	2	79139414	p12
SNP_A-1865019	G	G	245	157	269	127	4.245	3.94E-02	rs2723880	12	118051682	q24.23
SNP_A-1868440	G	G	313	43	364	30	4.243	3.94E-02	rs13102624	4	153351795	q31.3
SNP_A-1871167	G	G	325	45	380	32	4.242	3.94E-02	rs2071803	3	50382348	p21.31
SNP_A-1838551	C	C	290	46	350	34	4.244	3.94E-02	rs628908	1	206816397	q32.2
SNP_A-1831174	A	A	250	116	251	159	4.244	3.94E-02	rs2374240	2	41545137	p22.1
SNP_A-1832321	A	A	331	69	362	50	4.244	3.94E-02	rs4245353	13	49342272	q14.2
SNP_A-1791681	A	A	201	169	255	159	4.244	3.94E-02	rs995927	13	64235817	q21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1646674	A	A	247	129	283	107	4.242	3.94E-02	rs602295	1	60662610	p31.3
SNP_A-1752481	A	A	330	20	370	40	4.242	3.94E-02	rs9293381	5	84060531	q14.3
SNP_A-2118275	G	G	352	66	367	45	4.243	3.94E-02	rs2608819	4	39253997	p14
SNP_A-2149344	T	T	283	87	291	125	4.245	3.94E-02	rs606478	18	11982971	p11.21
SNP_A-2149829	G	G	347	19	373	37	4.243	3.94E-02	rs11201804	10	87567313	q23.2
SNP_A-2207822	G	G	274	14	298	30	4.246	3.94E-02	rs6567348	18	59283559	q21.33
SNP_A-2171248	C	C	388	4	414	0	4.246	3.94E-02	rs6863314	5	72047580	q13.2
SNP_A-2184256	G	G	358	6	409	1	4.244	3.94E-02	rs2090883	8	84284080	q21.13
SNP_A-2184801	C	A	210	164	206	196	4.246	3.94E-02	rs4285943	12	43691035	q12
SNP_A-2191053	C	G	207	155	204	202	4.242	3.94E-02	rs9369662	6	47258931	p12.3
SNP_A-2011994	G	G	374	10	403	3	4.242	3.94E-02	rs610280	11	73040645	q13.4
SNP_A-2015096	A	A	354	10	356	22	4.243	3.94E-02	rs7281785	21	9957781	p11.2
SNP_A-2012793	A	A	334	88	307	113	4.242	3.94E-02	rs6592176	11	83734936	q14.1
SNP_A-2090578	T	T	266	142	235	169	4.243	3.94E-02	rs11127532	2	909766	p25.3
SNP_A-2091528	A	A	315	9	383	3	4.243	3.94E-02	rs8060475	16	28076558	p11.2
SNP_A-2076350	C	C	351	7	389	19	4.244	3.94E-02	rs17168920	7	15440319	p21.1
SNP_A-2051504	A	G	200	198	227	171	4.246	3.94E-02	rs1340097	1	216038956	q41
SNP_A-2253541	G	G	247	65	250	96	4.242	3.94E-02	rs11891053	2	62222201	p15
SNP_A-2238700	G	G	285	77	298	114	4.245	3.94E-02	rs12536670	7	14235248	p21.2
SNP_A-2258922	C	C	231	135	286	122	4.242	3.94E-02	rs13084778	3	80654636	p12.2
SNP_A-2264462	T	C	193	145	201	197	4.241	3.94E-02	rs939293	4	57037083	q12
SNP_A-2290715	C	C	327	85	353	63	4.245	3.94E-02	rs2131506	18	1166216	p11.32
SNP_A-2296989	C	C	292	36	284	56	4.245	3.94E-02	rs1434302	9	28965706	p21.1
SNP_A-2294983	C	C	394	14	368	26	4.244	3.94E-02	rs17210273	22	18407130	q11.21
SNP_A-2298951	G	G	402	16	381	29	4.242	3.94E-02	---	22	47363409	q13.32
SNP_A-2301393	A	A	272	88	281	127	4.237	0.0395	rs11083054	18	50204369	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289856	C	C	365	35	345	53	4.24	0.0395	rs9885748	6	18479926	p22.3
SNP_A-2306131	C	C	368	54	381	35	4.239	0.0395	rs16958273	15	71881717	q24.1
SNP_A-2310024	T	T	360	6	411	1	4.24	0.0395	rs17299494	13	91609377	q31.3
SNP_A-2314587	C	C	321	17	344	34	4.241	0.0395	rs11142070	9	87896981	q22.1
SNP_A-2262945	A	A	376	36	391	21	4.241	0.0395	rs7778202	7	50886980	p12.1
SNP_A-2278383	A	A	406	6	385	15	4.238	0.0395	rs1038959	7	113195034	q31.1
SNP_A-2238545	A	A	223	133	229	185	4.238	0.0395	rs2325842	20	2293114	p13
SNP_A-2237712	C	C	403	17	411	7	4.241	0.0395	rs16961081	17	60623690	q24.1
SNP_A-2251704	C	C	234	188	261	157	4.239	0.0395	rs3003137	20	62301246	q13.33
SNP_A-2056000	G	A	197	163	210	188	4.238	0.0395	rs2181855	10	10137823	p14
SNP_A-2087460	C	C	226	144	282	132	4.239	0.0395	rs10106459	8	5202235	p23.2
SNP_A-2102235	G	A	201	163	215	197	4.241	0.0395	rs9586099	13	87407429	q31.2
SNP_A-2002147	T	T	292	78	302	114	4.241	0.0395	rs4753597	11	93739906	q21
SNP_A-2047759	G	G	405	17	413	7	4.24	0.0395	rs16960881	17	60609580	q24.1
SNP_A-2042597	G	G	323	93	340	68	4.241	0.0395	rs7941469	11	65656728	q13.2
SNP_A-2036202	T	T	355	15	381	31	4.24	0.0395	rs17025915	2	85253492	p11.2
SNP_A-2019516	A	A	228	128	287	117	4.238	0.0395	rs760285	21	40083524	q22.2
SNP_A-2170810	A	A	392	24	406	12	4.241	0.0395	rs749137	12	106304364	q23.3
SNP_A-2211692	A	A	238	124	240	170	4.238	0.0395	rs2042965	5	97872847	q21.1
SNP_A-2209980	T	T	354	12	389	27	4.238	0.0395	rs11645475	16	70380618	q22.2
SNP_A-2226025	G	G	294	60	294	88	4.238	0.0395	rs4972718	2	172901975	q31.1
SNP_A-2222164	G	G	353	49	339	71	4.238	0.0395	rs6721068	2	106843758	q12.2
SNP_A-2221728	G	G	393	21	378	36	4.239	0.0395	rs12600235	16	20352849	p12.3
SNP_A-2150145	C	C	357	11	410	4	4.238	0.0395	rs13150520	4	27824774	p15.2
SNP_A-2160237	C	C	322	38	354	24	4.24	0.0395	rs13124533	4	188412422	q35.2
SNP_A-2157673	G	G	360	6	411	1	4.24	0.0395	rs11193466	10	109207035	q25.1
SNP_A-1740053	T	T	385	15	406	6	4.238	0.0395	rs10495826	2	34922782	p22.3
SNP_A-1645540	T	T	332	18	373	37	4.238	0.0395	rs10497533	2	180201758	q31.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1683204	C	C	345	53	374	36	4.24	0.0395	rs10517008	4	23023080	p15.2
SNP_A-1709883	C	C	381	11	375	23	4.238	0.0395	rs1003063	6	9595662	p24.3
SNP_A-1791527	C	C	360	6	411	1	4.24	0.0395	---	4	17639368	q34.3
SNP_A-1787246	T	T	268	94	273	133	4.24	0.0395	rs1427985	12	20209455	p12.2
SNP_A-1796976	A	A	191	153	231	135	4.239	0.0395	rs12477836	2	36557994	p22.2
SNP_A-1792912	T	T	267	149	238	178	4.237	0.0395	rs1902757	12	101495278	q23.2
SNP_A-1795970	A	A	422	0	396	4	4.241	0.0395	rs7105029	11	17718456	p15.1
SNP_A-1812082	G	G	422	0	396	4	4.241	0.0395	rs16854861	1	176577264	q25.2
SNP_A-1808425	G	G	313	35	319	57	4.241	0.0395	rs7718854	5	128904019	q23.3
SNP_A-1862075	G	G	305	69	288	94	4.238	0.0395	---	1	155191682	q23.1
SNP_A-1845106	A	A	328	60	301	81	4.24	0.0395	rs1561136	16	9405329	p13.2
SNP_A-1859285	A	A	316	54	332	84	4.239	0.0395	rs7230413	18	45888880	q21.1
SNP_A-1951774	G	G	196	174	246	162	4.239	0.0395	rs1206726	6	132403009	q23.2
SNP_A-1903898	C	C	227	167	255	157	4.238	0.0395	rs9911967	17	42381910	q21.32
SNP_A-1901283	A	A	221	149	217	197	4.239	0.0395	rs9304191	18	34283363	q12.2
SNP_A-1874000	A	A	405	17	413	7	4.24	0.0395	rs765943	14	72455254	q24.2
SNP_A-1912397	C	C	323	59	309	83	4.238	0.0395	rs10827565	10	36284415	p11.21
SNP_A-1922711	G	G	344	26	369	47	4.24	0.0395	rs6433619	2	177590024	q31.1
SNP_A-1925532	C	G	197	173	223	189	4.235	3.96E-02	rs974251	2	229923416	q36.3
SNP_A-1905020	G	G	353	11	381	25	4.234	3.96E-02	rs705579	1	14898962	p36.21
SNP_A-1902616	C	C	211	141	211	191	4.233	3.96E-02	rs2048777	12	129464788	q24.33
SNP_A-1896894	A	A	254	116	313	103	4.233	3.96E-02	rs6806191	3	122643568	q13.33
SNP_A-1892892	C	C	257	165	283	135	4.233	3.96E-02	rs1941115	18	22868190	q11.2
SNP_A-1954981	G	G	262	96	315	81	4.235	3.96E-02	rs8096065	18	66967005	q22.3
SNP_A-1975197	C	C	233	109	291	97	4.237	3.96E-02	rs3912863	3	165980927	q26.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1975227	G	G	275	85	269	117	4.234	3.96E-02	rs9290318	3	168933271	q26.1
SNP_A-1865392	G	G	295	57	347	43	4.237	3.96E-02	rs9389049	6	133489461	q23.2
SNP_A-1828827	C	C	295	71	299	103	4.234	3.96E-02	rs12193274	6	73412184	q13
SNP_A-1794158	T	T	364	6	397	17	4.236	3.96E-02	rs16948141	18	5403815	p11.31
SNP_A-1655189	G	G	372	30	397	17	4.233	3.96E-02	rs10509440	10	83401211	q23.1
SNP_A-2159107	G	G	270	78	321	63	4.237	3.96E-02	rs2926052	5	162321566	q34
SNP_A-2127233	T	T	260	88	259	123	4.233	3.96E-02	rs7582695	2	202855457	q33.1
SNP_A-2179504	A	A	327	23	344	42	4.234	3.96E-02	rs12229182	12	27154899	p11.23
SNP_A-2197257	G	G	269	95	267	131	4.233	3.96E-02	rs17184988	2	123780306	q14.3
SNP_A-2024444	A	A	293	99	260	122	4.234	3.96E-02	rs10251103	7	114444515	q31.2
SNP_A-2003171	C	C	323	97	291	121	4.233	3.96E-02	rs10509427	10	82899282	q22.3
SNP_A-1991718	C	C	260	126	235	155	4.235	3.96E-02	rs1177948	7	147494062	q36.1
SNP_A-1990824	C	C	256	154	288	128	4.236	3.96E-02	rs10487285	7	105993899	q22.3
SNP_A-2018556	G	G	399	21	384	36	4.235	3.96E-02	rs2242886	21	35309676	q22.12
SNP_A-2093890	A	A	327	73	331	49	4.236	3.96E-02	rs2430338	14	91402603	q32.12
SNP_A-2092044	T	T	251	141	278	114	4.237	3.96E-02	rs10277413	7	55012673	p11.2
SNP_A-2078482	C	C	337	83	312	108	4.235	3.96E-02	rs10458992	11	125400607	q24.2
SNP_A-2072946	C	C	362	6	413	1	4.236	3.96E-02	rs16988320	4	37582519	p14
SNP_A-2066499	T	T	329	9	358	22	4.233	3.96E-02	rs17027362	4	135002038	q28.3
SNP_A-2246971	A	A	319	13	396	6	4.234	3.96E-02	rs9992243	4	174004579	q34.1
SNP_A-2292335	G	G	362	6	413	1	4.236	3.96E-02	rs17012147	4	128423993	q28.1
SNP_A-2307577	C	C	371	31	400	18	4.229	3.97E-02	rs16885510	5	55800618	q11.2
SNP_A-2229311	C	C	364	6	415	1	4.233	3.97E-02	rs16857905	2	170880051	q31.1
SNP_A-2264534	T	T	305	65	356	50	4.23	3.97E-02	rs1647311	8	4039629	p23.2
SNP_A-2261928	C	C	359	11	412	4	4.232	3.97E-02	rs10065492	5	169177077	q35.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2066260	A	A	364	6	415	1	4.233	3.97E-02	rs16833733	1	233001342	q43
SNP_A-2078041	G	G	384	34	391	19	4.232	3.97E-02	rs3888722	6	29846979	p22.1
SNP_A-2081344	C	C	345	23	373	43	4.23	3.97E-02	rs11263830	1	36014891	p34.3
SNP_A-2098138	G	G	364	6	415	1	4.233	3.97E-02	rs11853779	15	89630287	q26.1
SNP_A-2099937	G	G	364	6	415	1	4.233	3.97E-02	rs16871026	6	32923466	p21.32
SNP_A-2001418	G	G	364	6	415	1	4.233	3.97E-02	rs7076253	10	109223716	q25.1
SNP_A-2025674	C	C	290	98	336	80	4.23	3.97E-02	rs10878346	12	64607140	q14.3
SNP_A-2031461	A	A	236	134	294	122	4.232	3.97E-02	rs4941229	18	53796541	q21.31
SNP_A-2028832	A	A	289	133	313	105	4.232	3.97E-02	rs10445073	16	82656116	q23.3
SNP_A-2028803	G	G	322	20	356	10	4.23	3.97E-02	rs797754	12	195789	p13.33
SNP_A-2040046	G	G	364	6	415	1	4.233	3.97E-02	rs17157613	7	28999753	p15.1
SNP_A-2196779	A	A	364	6	415	1	4.233	3.97E-02	rs6672004	1	233868163	q43
SNP_A-2179824	A	A	280	116	319	95	4.231	3.97E-02	rs13249753	8	87582332	q21.3
SNP_A-2217528	T	T	216	142	274	132	4.231	3.97E-02	rs8099594	18	45245158	q21.1
SNP_A-2214836	A	A	312	44	284	62	4.23	3.97E-02	rs12261087	10	101242155	q24.2
SNP_A-2207258	T	T	332	38	390	26	4.232	3.97E-02	rs7678453	4	173100661	q34.1
SNP_A-2205792	G	G	359	11	412	4	4.232	3.97E-02	rs10929656	2	10461455	p25.1
SNP_A-2203866	A	A	226	136	226	184	4.232	3.97E-02	rs1678742	6	38923805	p21.2
SNP_A-2201196	G	G	268	102	273	143	4.23	3.97E-02	rs4737466	8	58780122	q12.1
SNP_A-2117709	A	A	204	182	237	157	4.231	3.97E-02	rs12620354	2	235088199	q37.1
SNP_A-2108652	T	T	248	116	249	159	4.232	3.97E-02	rs837875	2	129748369	q21.1
SNP_A-2114476	G	G	364	6	415	1	4.233	3.97E-02	rs2076856	1	20766481	p36.12
SNP_A-2158761	G	G	337	75	355	53	4.23	3.97E-02	rs1574399	10	1317085526	q26.3
SNP_A-2164538	A	A	269	79	338	68	4.23	3.97E-02	rs2459826	5	17506016	p15.1
SNP_A-2162855	C	C	364	6	415	1	4.233	3.97E-02	rs16928739	12	25386005	p12.1
SNP_A-2161220	C	C	300	40	345	27	4.232	3.97E-02	rs4582086	3	51085561	p21.31
SNP_A-2161061	A	A	325	79	296	102	4.232	3.97E-02	rs1474445	7	5370090	p22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2146377	T	T	272	148	297	119	4.229	3.97E-02	rs6730320	2	37716615	p22.2
SNP_A-2140899	G	G	309	61	320	92	4.23	3.97E-02	rs10931278	2	187894782	q32.1
SNP_A-1651004	C	C	196	152	261	149	4.232	3.97E-02	rs10516451	4	101084943	q23
SNP_A-1664908	C	C	268	134	246	166	4.233	3.97E-02	rs8040075	15	47320397	q21.1
SNP_A-1675009	T	T	171	163	210	146	4.23	3.97E-02	rs839177	12	85022246	q21.31
SNP_A-1716345	A	A	222	172	254	146	4.232	3.97E-02	rs248257	5	179518198	q35.3
SNP_A-1722648	G	G	260	138	239	171	4.231	3.97E-02	rs1329165	10	91520242	q23.31
SNP_A-1826008	C	C	244	108	304	96	4.229	3.97E-02	rs11214029	11	111266440	q23.1
SNP_A-1834184	A	A	302	44	294	66	4.231	3.97E-02	rs7401583	14	35199722	q13.2
SNP_A-1841929	A	A	236	134	294	122	4.232	3.97E-02	rs6032862	20	10306917	p12.2
SNP_A-1863924	G	G	269	101	327	87	4.231	3.97E-02	rs2690022	1	14953258	p36.21
SNP_A-1860135	C	C	359	11	412	4	4.232	3.97E-02	rs1146304	1	118781539	p12
SNP_A-1851128	C	C	334	12	382	28	4.23	3.97E-02	rs17033516	4	157062717	q32.1
SNP_A-1964279	T	T	372	48	348	68	4.229	3.97E-02	rs2310186	2	102201698	q11.2
SNP_A-1966931	C	C	220	112	204	144	4.23	3.97E-02	rs10494277	1	149552299	q21.3
SNP_A-1987699	C	C	262	116	308	98	4.232	3.97E-02	rs2255071	6	132922341	q23.2
SNP_A-1979557	A	A	359	11	412	4	4.232	3.97E-02	rs17035843	4	158461418	q32.1
SNP_A-1950366	A	A	283	45	314	30	4.231	3.97E-02	rs10792230	11	58815755	q12.1
SNP_A-1947841	C	A	190	170	223	185	4.231	3.97E-02	rs9362046	6	85164475	q14.3
SNP_A-1942141	C	C	408	14	411	5	4.231	3.97E-02	rs818961	1	20030006	p36.13
SNP_A-1889903	C	C	402	14	405	5	4.231	3.97E-02	rs6719419	2	16078520	p24.3
SNP_A-1896815	G	G	262	142	224	164	4.231	3.97E-02	rs4085361	11	106968105	q22.3
SNP_A-1878466	C	C	280	70	275	99	4.23	3.97E-02	rs2154305	10	5074852	p15.1
SNP_A-1881620	A	C	204	164	216	200	4.232	3.97E-02	rs6846031	4	178394297	q34.3
SNP_A-1913966	C	C	361	1	375	7	4.232	3.97E-02	rs16851408	3	142620408	q23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1914332	C	C	219	143	219	193	4.228	3.98E-02	rs12537389	7	67270541	q11.22
SNP_A-1919113	C	C	243	121	300	108	4.227	3.98E-02	rs581633	6	102163163	q16.3
SNP_A-1907356	A	A	193	131	260	128	4.226	3.98E-02	rs10081066	6	155611310	q25.3
SNP_A-1971916	A	A	341	39	351	23	4.226	3.98E-02	rs1877648	3	18560369	p24.3
SNP_A-1853266	A	A	408	0	384	4	4.227	3.98E-02	rs938758	16	5322000	p13.3
SNP_A-1864087	A	A	412	0	388	4	4.225	3.98E-02	rs17839493	16	31298621	p11.2
SNP_A-1840380	T	T	249	151	282	126	4.228	3.98E-02	rs1426033	3	141192788	q23
SNP_A-1834030	G	G	238	124	299	113	4.227	3.98E-02	rs16833	4	83976881	q21.22
SNP_A-1829178	G	G	367	47	386	30	4.228	3.98E-02	rs6489780	12	119691130	q24.31
SNP_A-1817175	A	A	257	109	258	150	4.226	3.98E-02	rs9445980	6	68987459	q12
SNP_A-1661063	T	T	263	87	279	129	4.226	3.98E-02	rs10518460	4	126622502	q28.1
SNP_A-1659702	G	G	377	25	397	13	4.228	3.98E-02	rs10512288	9	99874654	q31.1
SNP_A-1650870	G	G	255	91	248	124	4.227	3.98E-02	rs1480706	2	180911450	q31.3
SNP_A-1796133	T	T	255	129	236	162	4.228	3.98E-02	rs11719547	3	122797636	q13.33
SNP_A-1789832	C	C	286	128	311	101	4.225	3.98E-02	rs11113739	12	106992733	q23.3
SNP_A-2204569	T	T	296	86	330	66	4.228	3.98E-02	rs6768322	3	2877594	p26.2
SNP_A-2225366	A	A	273	95	320	78	4.227	3.98E-02	rs6558829	8	3818444	p23.2
SNP_A-2224648	A	A	265	141	295	115	4.228	3.98E-02	rs1016740	22	31288537	q12.3
SNP_A-2184408	T	T	291	121	262	148	4.226	3.98E-02	rs2105269	14	68816987	q24.1
SNP_A-2029770	A	A	296	34	333	61	4.226	3.98E-02	rs1461826	4	66749928	q13.2
SNP_A-2024718	T	T	386	4	410	0	4.226	3.98E-02	rs6135716	20	16181743	p12.1
SNP_A-2011253	G	G	362	16	356	30	4.228	3.98E-02	rs4958094	5	133029423	q31.1
SNP_A-2093045	G	G	292	76	298	110	4.225	3.98E-02	rs1233704	6	28274902	p22.1
SNP_A-2071635	G	G	284	78	288	112	4.228	3.98E-02	rs12429799	13	46192904	q14.13
SNP_A-2270159	G	G	198	116	224	180	4.225	3.98E-02	rs11178649	12	69819505	q15
SNP_A-2278183	G	G	384	4	408	0	4.227	3.98E-02	rs11176123	12	64963351	q14.3
SNP_A-2239039	C	C	300	60	361	47	4.225	3.98E-02	rs9943328	10	119120189	q26.11

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2239828	T	T	300	60	361	47	4.225	3.98E-02	rs8045844	16	81753726	q23.3
SNP_A-2301787	T	C	186	160	211	181	4.228	3.98E-02	rs6960279	7	4826071	p22.1
SNP_A-2310519	G	G	357	13	384	28	4.228	3.98E-02	rs9848688	3	98270901	q11.2
SNP_A-2287809	T	T	228	76	230	110	4.225	3.98E-02	rs4957819	5	108857094	q21.3
SNP_A-2307185	T	T	280	66	297	101	4.222	3.99E-02	rs1000937	2	161561005	q24.2
SNP_A-2238785	G	G	341	29	396	18	4.223	3.99E-02	rs17591685	13	26558912	q12.13
SNP_A-2238502	T	T	310	32	303	51	4.224	3.99E-02	rs10802870	1	236937619	q43
SNP_A-2229493	A	A	279	129	304	102	4.223	3.99E-02	rs7239555	18	44142122	q21.1
SNP_A-2243935	T	T	267	75	326	62	4.222	3.99E-02	rs701251	3	155085633	q25.2
SNP_A-2277125	G	G	265	99	329	87	4.222	3.99E-02	rs1782791	13	39876659	q14.11
SNP_A-2272914	A	A	416	0	392	4	4.223	3.99E-02	rs16836708	1	191030551	q31.3
SNP_A-2281904	T	T	396	4	420	0	4.221	3.99E-02	rs16962690	15	47729326	q21.2
SNP_A-2265222	C	C	324	38	343	63	4.222	3.99E-02	rs10979666	9	108880434	q31.3
SNP_A-2069988	G	A	220	180	204	186	4.221	3.99E-02	rs4920413	1	18107365	p36.13
SNP_A-2051044	G	G	280	84	338	70	4.222	3.99E-02	rs11234564	11	85547592	q14.2
SNP_A-2008665	A	A	225	185	254	156	4.222	3.99E-02	rs4683301	3	46906482	p21.31
SNP_A-1996133	G	G	245	119	248	164	4.221	3.99E-02	rs10429480	9	18749822	p22.1
SNP_A-2038247	T	C	193	171	224	188	4.224	3.99E-02	rs6803445	3	194039873	q29
SNP_A-2034719	G	G	420	0	396	4	4.221	3.99E-02	rs17036634	2	47632071	p21
SNP_A-2179689	T	T	386	26	389	13	4.223	3.99E-02	rs6504392	17	61462181	q24.1
SNP_A-2149583	T	T	239	183	267	153	4.223	3.99E-02	rs1897620	10	60566271	q21.1
SNP_A-2132877	A	A	238	78	244	114	4.224	3.99E-02	rs7749313	6	81786012	q14.1
SNP_A-1658256	T	T	332	36	350	60	4.22	3.99E-02	rs2247780	12	79602182	q21.31
SNP_A-1825814	C	C	232	140	201	165	4.22	3.99E-02	rs1040730	14	62494609	q23.2
SNP_A-1863053	A	A	279	61	343	49	4.222	3.99E-02	rs10935005	3	133581479	q22.1
SNP_A-1867958	G	G	330	88	348	64	4.224	3.99E-02	rs887489	17	60842973	q24.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982604	G	G	230	126	228	170	4.223	3.99E-02	rs27312	5	96531162	q15
SNP_A-1945681	C	C	348	22	371	41	4.222	3.99E-02	rs11018889	11	89538451	q14.3
SNP_A-1925907	G	G	418	0	394	4	4.222	3.99E-02	rs7083038	10	104142775	q24.32
SNP_A-1920845	G	G	340	8	343	19	4.22	3.99E-02	rs7741529	6	139361981	q24.1
SNP_A-1932605	T	T	288	128	313	101	4.219	4.00E-02	rs2542450	8	140654585	q24.3
SNP_A-1886119	A	A	336	8	339	19	4.217	4.00E-02	rs9385762	6	136864073	q23.3
SNP_A-1890819	C	C	328	16	394	8	4.216	4.00E-02	rs875440	4	167806562	q32.3
SNP_A-1936399	T	T	261	137	210	150	4.217	4.00E-02	rs12048557	1	204955173	q32.2
SNP_A-1936293	C	C	285	135	254	162	4.218	4.00E-02	rs7138925	12	114501848	q24.21
SNP_A-1954134	G	G	306	28	370	18	4.218	4.00E-02	rs11231649	11	63466592	q13.1
SNP_A-1960616	A	A	330	44	352	28	4.218	4.00E-02	rs2190843	19	48422999	q13.31
SNP_A-1840863	G	G	208	118	270	110	4.217	4.00E-02	rs17426830	4	38075821	p14
SNP_A-1659668	C	C	214	134	280	128	4.22	4.00E-02	rs10517927	4	168843414	q32.3
SNP_A-1668881	C	C	193	157	255	153	4.219	4.00E-02	rs2280002	4	96033717	q22.3
SNP_A-1712681	T	T	264	138	243	171	4.219	4.00E-02	rs1566753	6	54680871	p12.1
SNP_A-1718215	C	C	374	24	371	41	4.218	4.00E-02	rs1504037	3	6137218	p26.1
SNP_A-1738935	A	A	337	63	324	88	4.218	4.00E-02	rs1525628	7	122658617	q31.32
SNP_A-1743735	G	C	217	163	199	197	4.218	4.00E-02	rs4733164	8	33600595	p12
SNP_A-1786721	A	A	282	32	335	21	4.219	4.00E-02	rs4647756	11	47215555	p11.2
SNP_A-1793526	A	A	303	91	331	69	4.216	4.00E-02	rs8049649	16	26362052	p12.1
SNP_A-2136774	G	G	202	168	256	158	4.217	4.00E-02	rs6888688	5	170768471	q35.1
SNP_A-2127805	G	G	293	127	261	153	4.22	4.00E-02	rs17636399	2	105316337	q12.1
SNP_A-2129147	T	T	273	95	278	134	4.219	4.00E-02	rs6845267	4	58538955	q12
SNP_A-2115529	G	G	255	111	311	97	4.216	4.00E-02	rs7046606	9	21139963	p21.3
SNP_A-2165897	C	C	344	24	402	14	4.218	4.00E-02	rs16965665	15	35887965	q14
SNP_A-2167758	T	T	361	27	391	15	4.219	4.00E-02	rs1524170	1	79943530	p31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2156422	C	C	246	122	306	110	4.219	4.00E-02	rs1429974	2	21212422	p24.1
SNP_A-2199632	G	G	353	53	382	36	4.218	4.00E-02	rs3794399	13	27790892	q12.2
SNP_A-2225062	A	C	200	164	212	192	4.219	4.00E-02	rs2171871	3	68987784	p14.1
SNP_A-2225665	C	C	264	74	308	58	4.217	4.00E-02	rs17377128	2	6314072	p25.2
SNP_A-2212546	A	A	186	170	241	163	4.217	4.00E-02	rs7048584	9	1300475	p24.3
SNP_A-2046321	T	T	325	43	292	60	4.217	4.00E-02	rs4476539	3	107825453	q13.12
SNP_A-2045067	G	G	328	18	358	36	4.216	4.00E-02	rs9882890	3	167197110	q26.1
SNP_A-2027199	T	C	195	145	195	193	4.217	4.00E-02	rs10994008	10	61216947	q21.2
SNP_A-1990069	A	A	307	103	333	79	4.216	4.00E-02	rs7791163	7	66988670	q11.22
SNP_A-2048391	C	C	225	139	219	183	4.219	4.00E-02	---	18	38985999	q12.3
SNP_A-2053267	T	T	307	61	318	92	4.22	4.00E-02	rs1356350	3	29170015	p24.1
SNP_A-2054458	T	T	249	115	254	160	4.217	4.00E-02	rs855317	1	63781358	p31.3
SNP_A-2061297	A	T	203	155	204	198	4.217	4.00E-02	rs2709529	2	133281035	q21.2
SNP_A-2068496	C	C	314	36	353	23	4.219	4.00E-02	rs9953717	18	67394719	q22.3
SNP_A-2092456	T	T	332	12	350	26	4.219	4.00E-02	rs1233718	20	15485128	p12.1
SNP_A-2077473	C	C	317	99	285	123	4.218	4.00E-02	rs17442167	16	6489890	p13.2
SNP_A-2266289	A	A	312	56	373	43	4.216	4.00E-02	rs4805458	19	34820560	q12
SNP_A-2258583	T	C	206	156	207	203	4.219	4.00E-02	rs2961662	5	166456688	q34
SNP_A-2282440	T	T	270	108	241	133	4.218	4.00E-02	rs6094035	20	42833676	q13.12
SNP_A-2241207	T	T	308	60	324	92	4.219	4.00E-02	rs17120218	13	112212018	q34
SNP_A-2309699	A	A	296	74	307	109	4.217	4.00E-02	rs16924603	11	93894907	q21
SNP_A-2314563	T	T	384	26	375	43	4.218	4.00E-02	rs581957	5	15601576	p15.1
SNP_A-2294065	A	A	264	74	308	58	4.217	4.00E-02	rs12725080	1	35153076	p34.3
SNP_A-2294517	G	G	316	86	288	110	4.217	4.00E-02	rs2042369	1	15588550	p36.21
SNP_A-2242771	C	C	297	73	350	58	4.213	4.01E-02	rs7713313	5	150769366	q33.1
SNP_A-2084214	T	T	315	81	283	103	4.216	4.01E-02	rs10746941	9	74047481	q21.13
SNP_A-2064064	C	C	290	76	348	62	4.212	4.01E-02	rs9559673	13	109368996	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072542	T	T	356	58	375	39	4.215	4.01E-02	rs1573172	20	23209339	p11.21
SNP_A-1989811	A	A	218	140	214	186	4.214	4.01E-02	rs2918194	7	46959652	p13
SNP_A-2000592	A	A	335	57	310	78	4.215	4.01E-02	rs4915424	1	196994852	q32.1
SNP_A-2028587	G	G	337	3	349	11	4.213	4.01E-02	rs17122118	1	100447757	p21.2
SNP_A-2207043	C	C	402	20	409	9	4.214	4.01E-02	rs2248397	6	168735738	q27
SNP_A-2208877	C	C	353	39	389	25	4.212	4.01E-02	rs10922644	1	89611412	p22.2
SNP_A-2199586	G	G	352	18	373	35	4.215	4.01E-02	rs6747900	2	41827164	p21
SNP_A-2195387	C	C	264	90	320	76	4.212	4.01E-02	rs2454160	1	17230959	p36.13
SNP_A-2156120	C	C	316	12	379	5	4.215	4.01E-02	rs7321094	13	110482163	q34
SNP_A-2164847	G	G	307	115	331	89	4.212	4.01E-02	rs237744	20	47336183	q13.13
SNP_A-2147177	G	G	276	90	326	74	4.213	4.01E-02	---	7	46762544	p13
SNP_A-2143690	T	T	285	21	281	37	4.213	4.01E-02	rs1605748	13	63614805	q21.31
SNP_A-2115844	A	G	206	198	201	155	4.213	4.01E-02	rs10773815	12	129785395	q24.33
SNP_A-2118263	C	C	341	23	369	43	4.212	4.01E-02	rs12041193	1	36081853	p34.3
SNP_A-1729192	C	C	263	127	305	107	4.215	4.01E-02	rs9317039	13	57384740	q21.2
SNP_A-1784949	G	G	270	56	344	46	4.212	4.01E-02	rs3765129	16	16057402	p13.11
SNP_A-1711644	C	A	196	154	210	198	4.212	4.01E-02	rs10516928	4	95010700	q22.3
SNP_A-1661386	T	T	354	46	344	68	4.212	4.01E-02	rs10484087	14	50023173	q22.1
SNP_A-1653564	A	A	293	109	273	139	4.214	4.01E-02	rs396186	10	131667577	q26.3
SNP_A-1855233	G	G	322	100	343	75	4.216	4.01E-02	rs1822708	7	152495161	q36.2
SNP_A-1857617	G	G	257	105	313	91	4.212	4.01E-02	rs12634210	3	177157429	q26.31
SNP_A-1848891	T	T	330	48	293	65	4.215	4.01E-02	rs8073784	17	29652449	q12
SNP_A-1949616	C	C	316	34	331	57	4.215	4.01E-02	rs17141825	11	80614627	q14.1
SNP_A-1976618	G	G	319	51	378	38	4.215	4.01E-02	rs10517157	4	28981027	p15.1
SNP_A-1983768	A	A	305	47	280	66	4.212	4.01E-02	rs767187	5	142113769	q31.3
SNP_A-1984361	A	A	191	175	244	166	4.214	4.01E-02	rs828748	5	162265220	q34

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1891845	C	C	350	18	368	8	4.212	4.01E-02	rs2189452	7	120056906	q31.31
SNP_A-1930647	G	G	270	120	303	97	4.212	4.01E-02	rs282249	2	224757238	q36.1
SNP_A-1917960	A	A	322	46	337	73	4.212	4.01E-02	rs1905978	1	72277821	p31.1
SNP_A-1911488	A	G	197	173	225	191	4.209	0.0402	rs10773623	12	128250076	q24.32
SNP_A-1927549	A	A	207	157	259	145	4.207	0.0402	rs11223888	11	133908599	q25
SNP_A-1896971	G	G	333	21	400	12	4.211	0.0402	rs1505227	2	77490847	p12
SNP_A-1950294	T	T	313	47	377	35	4.209	0.0402	rs4657233	1	159584418	q23.3
SNP_A-1824759	T	T	254	162	281	133	4.209	0.0402	rs10131911	14	28103384	q12
SNP_A-1821262	C	C	318	64	343	45	4.211	0.0402	rs17101323	14	33014942	q13.1
SNP_A-1728845	C	C	245	105	311	95	4.209	0.0402	rs2903640	4	80989720	q21.21
SNP_A-1801154	A	A	218	150	215	199	4.209	0.0402	rs11185172	1	107998674	p13.3
SNP_A-2121561	T	T	258	96	317	83	4.207	0.0402	rs17400210	12	99642951	q23.1
SNP_A-2107791	T	T	271	119	249	149	4.208	0.0402	rs8051877	16	2002066	p13.3
SNP_A-2143364	G	G	362	6	411	1	4.209	0.0402	rs11193452	10	109205405	q25.1
SNP_A-2166065	A	A	227	95	218	128	4.209	0.0402	rs11954680	5	40077532	p13.1
SNP_A-2155079	A	A	223	147	280	136	4.209	0.0402	rs3775800	4	146457252	q31.21
SNP_A-2202625	C	C	362	6	411	1	4.209	0.0402	rs4953764	2	109782511	q13
SNP_A-2027167	C	C	328	20	389	11	4.208	0.0402	rs1477599	15	22881395	q11.2
SNP_A-2032285	G	G	222	148	275	135	4.209	0.0402	rs12521157	5	25905158	p14.1
SNP_A-2026301	C	C	382	4	404	0	4.208	0.0402	rs11173484	12	59157093	q14.1
SNP_A-1995692	C	C	249	121	299	105	4.209	0.0402	rs2381530	9	6976190	p24.1
SNP_A-2010154	C	C	378	4	400	0	4.21	0.0402	rs1913063	11	38871689	p12
SNP_A-2016116	G	G	339	73	367	53	4.209	0.0402	rs2142422	21	20691009	q21.1
SNP_A-2055390	G	G	266	82	279	121	4.208	0.0402	rs11710969	3	12318591	p25.2
SNP_A-2248638	C	C	248	104	284	84	4.21	0.0402	rs29162	18	9921497	p11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235025	C	C	379	41	395	25	4.21	0.0402	rs1028246	2	114317472	q14.1
SNP_A-2228731	T	T	279	71	313	53	4.21	0.0402	rs11223986	11	134132097	q25
SNP_A-2314649	C	C	395	25	379	41	4.21	0.0402	rs1342361	1	238877606	q43
SNP_A-2314366	T	T	228	136	227	183	4.208	0.0402	rs11097322	4	92977362	q22.1
SNP_A-2288598	A	A	331	37	347	61	4.204	4.03E-02	rs2632006	8	32316790	p12
SNP_A-2284115	C	C	412	0	390	4	4.204	4.03E-02	rs2223890	20	22171769	p11.22
SNP_A-2274297	G	A	217	195	216	180	4.206	4.03E-02	rs2426343	20	49702504	q13.2
SNP_A-2261358	A	A	271	125	246	154	4.203	4.03E-02	rs9963530	18	45777320	q21.1
SNP_A-2263097	C	C	233	125	288	112	4.205	4.03E-02	rs6847239	4	83283532	q21.22
SNP_A-2048413	C	C	281	135	305	107	4.203	4.03E-02	rs4663211	2	236538688	q37.2
SNP_A-2062472	A	A	308	48	319	75	4.205	4.03E-02	rs13381930	18	56436832	q21.32
SNP_A-2091914	A	A	256	90	318	78	4.204	4.03E-02	rs12054285	3	97829661	q11.2
SNP_A-2009658	C	C	354	42	372	26	4.206	4.03E-02	rs3796786	4	24681026	p15.2
SNP_A-1995843	G	G	192	178	245	169	4.205	4.03E-02	rs727756	9	10015975	p23
SNP_A-1994427	A	A	364	6	413	1	4.205	4.03E-02	rs16867579	8	102444443	q22.3
SNP_A-2003792	A	A	364	6	413	1	4.205	4.03E-02	rs7156345	14	62898372	q23.2
SNP_A-2025222	G	C	186	182	234	178	4.207	4.03E-02	rs4710625	6	67554551	q12
SNP_A-2047567	A	A	252	82	266	122	4.206	4.03E-02	rs1992119	4	148325711	q31.22
SNP_A-2212358	A	A	213	157	207	205	4.207	4.03E-02	rs6872375	5	13746277	p15.2
SNP_A-2214187	A	A	364	6	413	1	4.205	4.03E-02	rs11193447	10	109205151	q25.1
SNP_A-2169409	T	T	350	70	369	49	4.203	4.03E-02	rs8024817	15	91551260	q26.1
SNP_A-2171782	A	A	352	14	386	30	4.205	4.03E-02	rs6544404	2	41414196	p22.1
SNP_A-2158770	G	G	285	67	351	55	4.204	4.03E-02	rs1436851	3	41655754	p22.1
SNP_A-2157824	T	T	371	35	397	21	4.206	4.03E-02	rs1701858	20	37705857	q12
SNP_A-2162534	G	G	200	168	255	159	4.205	4.03E-02	rs13264388	8	54519001	q11.23
SNP_A-2143416	A	A	405	7	372	16	4.207	4.03E-02	rs7637875	3	40569268	p22.1
SNP_A-2144574	G	G	326	50	376	36	4.204	4.03E-02	rs7009099	8	53394337	q11.23
SNP_A-2140503	A	A	256	106	318	94	4.204	4.03E-02	rs2476973	10	102592116	q24.31
SNP_A-2147372	T	C	223	177	203	191	4.207	4.03E-02	rs7717417	5	141666716	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2146749	C	C	395	27	404	14	4.204	4.03E-02	rs1462811	1	38309433	p34.3
SNP_A-1798856	G	G	341	19	398	10	4.206	4.03E-02	rs4300850	2	197780286	q33.1
SNP_A-1714941	T	T	341	61	371	43	4.204	4.03E-02	rs10489391	1	207538250	q32.2
SNP_A-1662144	C	C	326	18	356	36	4.207	4.03E-02	rs10518132	4	76224622	q13.3
SNP_A-1667500	T	T	239	111	306	102	4.204	4.03E-02	rs10505864	12	20228452	p12.2
SNP_A-1682302	T	T	249	101	263	147	4.204	4.03E-02	rs1998574	13	72184990	q22.1
SNP_A-1814963	A	A	261	151	286	122	4.204	4.03E-02	rs12983168	19	33693476	q12
SNP_A-1843370	G	G	229	133	292	124	4.205	4.03E-02	rs13177415	5	138277839	q31.2
SNP_A-1847275	G	-	211	157	206	206	4.206	4.03E-02	rs2891979	8	122763933	q24.13
SNP_A-1854006	A	A	364	6	413	1	4.205	4.03E-02	rs7613828	3	85933936	p12.1
SNP_A-1954207	A	A	351	69	326	92	4.204	4.03E-02	rs11247351	15	96874455	q26.3
SNP_A-1956767	C	C	393	27	402	14	4.205	4.03E-02	rs3898730	15	67198506	q23
SNP_A-1965024	G	G	339	11	388	4	4.205	4.03E-02	rs3943484	2	138059524	q22.1
SNP_A-1896973	A	A	364	6	413	1	4.205	4.03E-02	rs10502601	18	28289587	q12.1
SNP_A-1881715	G	G	279	87	337	73	4.205	4.03E-02	rs10898148	11	83086000	q14.1
SNP_A-1878807	T	T	318	36	370	24	4.203	4.03E-02	rs1190055	6	105858444	q21
SNP_A-1881064	A	A	390	6	371	15	4.204	4.03E-02	rs17078435	8	6813700	p23.1
SNP_A-1914876	G	G	298	24	329	13	4.204	4.03E-02	rs6676882	1	233429772	q43
SNP_A-1917642	C	C	193	173	238	158	4.204	4.03E-02	rs11100870	4	146179619	q31.21
SNP_A-1911599	T	T	269	99	330	86	4.203	4.04E-02	rs6985798	8	23673824	p21.2
SNP_A-1905563	G	G	316	76	356	58	4.201	4.04E-02	rs1774644	10	112105656	q25.2
SNP_A-1909118	G	G	209	109	267	99	4.2	4.04E-02	rs6534429	4	80821339	q21.21
SNP_A-1925564	G	G	350	6	397	1	4.202	4.04E-02	rs6739848	2	241995541	q37.3
SNP_A-1882913	G	G	340	30	397	19	4.2	4.04E-02	rs8032547	15	27428127	q13.1
SNP_A-1962401	A	A	288	78	301	115	4.2	4.04E-02	rs1416203	1	112474335	p13.2
SNP_A-1984360	G	G	257	61	305	47	4.2	4.04E-02	rs1816785	5	162232537	q34
SNP_A-1977003	C	C	360	58	338	80	4.201	4.04E-02	rs7690944	4	44765392	p13
SNP_A-1946751	A	A	289	39	324	68	4.202	4.04E-02	rs581653	18	51366737	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839976	A	A	308	30	319	51	4.2	4.04E-02	rs7330358	13	74775077	q22.2
SNP_A-1823069	A	A	293	117	263	143	4.199	4.04E-02	rs10514486	16	78721310	q23.2
SNP_A-1668298	G	G	228	122	294	114	4.203	4.04E-02	rs4128355	6	115189749	q22.1
SNP_A-1806197	A	A	320	24	395	15	4.199	4.04E-02	rs7999	3	187853052	q27.3
SNP_A-1812201	G	A	179	173	221	169	4.2	4.04E-02	rs12708641	16	21066572	p12.3
SNP_A-2165611	T	T	416	0	394	4	4.202	4.04E-02	rs17154386	5	125683137	q23.2
SNP_A-2157208	T	T	286	50	339	37	4.203	4.04E-02	rs6563323	13	82550861	q31.1
SNP_A-2117086	A	A	188	164	248	160	4.203	4.04E-02	rs1929210	13	109083479	q33.3
SNP_A-2127526	T	T	339	15	397	7	4.2	4.04E-02	rs6846071	4	102759393	q24
SNP_A-2126990	C	C	244	168	218	200	4.203	4.04E-02	rs11740818	5	34736461	p13.2
SNP_A-2132558	C	C	336	18	385	9	4.203	4.04E-02	rs12257518	10	3930373	p15.1
SNP_A-2021381	A	A	328	34	331	55	4.203	4.04E-02	rs500566	6	145644112	q24.2
SNP_A-2016247	T	T	214	154	269	143	4.202	4.04E-02	rs2826681	21	21430148	q21.1
SNP_A-2081689	T	T	194	164	245	153	4.202	4.04E-02	rs4460209	6	42746542	p21.1
SNP_A-2057344	A	A	199	163	254	154	4.2	4.04E-02	rs7696176	4	185389539	q35.1
SNP_A-2231671	C	C	235	177	265	149	4.2	4.04E-02	rs6977284	7	109537504	q31.1
SNP_A-2251628	G	G	273	23	309	45	4.203	4.04E-02	rs12637817	3	124775794	q21.1
SNP_A-2251306	G	G	346	22	394	12	4.199	4.04E-02	rs1022651	6	112233736	q21
SNP_A-2253302	G	G	320	46	340	74	4.201	4.04E-02	rs2356086	2	159016048	q24.1
SNP_A-2293170	C	C	326	44	345	71	4.199	4.04E-02	rs10822996	10	52868890	q21.1
SNP_A-2307100	C	C	307	57	319	87	4.202	4.04E-02	rs12249828	10	884838	p15.3
SNP_A-2297987	G	G	300	122	320	94	4.199	4.05E-02	rs4886563	15	76314671	q25.1
SNP_A-2249383	T	T	340	58	323	81	4.197	4.05E-02	rs10995614	10	65186182	q21.3
SNP_A-2284033	G	G	353	1	369	7	4.195	4.05E-02	rs1838006	4	11675228	p15.33
SNP_A-2103106	G	G	211	157	267	147	4.198	4.05E-02	rs11731567	4	82627248	q21.21
SNP_A-2016191	G	G	269	85	325	71	4.197	4.05E-02	rs2826510	21	21067049	q21.1
SNP_A-2011731	A	A	368	52	386	34	4.197	4.05E-02	rs6924867	6	41198148	p21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2003207	C	C	337	31	396	20	4.198	4.05E-02	rs3011605	13	29009728	q12.3
SNP_A-2027046	G	G	382	22	365	37	4.196	4.05E-02	rs10040896	5	31967651	p13.3
SNP_A-2036017	G	G	227	131	229	179	4.195	4.05E-02	rs6659655	1	211309278	q41
SNP_A-2124648	A	A	213	151	259	135	4.197	4.05E-02	rs182996	4	60663042	q13.1
SNP_A-2120127	G	G	279	137	306	110	4.198	4.05E-02	rs11694048	2	159170389	q24.1
SNP_A-2144070	T	T	323	43	385	31	4.196	4.05E-02	rs1672989	19	40300708	q13.12
SNP_A-2199128	T	C	196	154	200	188	4.199	4.05E-02	rs11076300	16	57680049	q21
SNP_A-2187140	G	G	355	9	388	22	4.198	4.05E-02	rs17478346	13	108092458	q33.3
SNP_A-1813385	A	A	323	63	318	90	4.197	4.05E-02	rs10858890	12	88409634	q21.33
SNP_A-1797547	A	A	224	118	287	109	4.195	4.05E-02	rs4362037	1	199394013	q32.1
SNP_A-1678920	G	G	310	92	343	71	4.198	4.05E-02	rs1556501	9	76145743	q21.2
SNP_A-1826542	A	A	310	58	364	44	4.197	4.05E-02	rs9392070	6	5009357	p25.1
SNP_A-1955322	G	G	231	165	259	137	4.196	4.05E-02	rs1067367	2	44566556	p21
SNP_A-1948593	G	G	345	15	358	30	4.198	4.05E-02	rs11950842	5	155819816	q33.3
SNP_A-1978354	G	G	357	11	408	4	4.198	4.05E-02	rs17583579	4	106465108	q24
SNP_A-1887996	A	A	286	136	255	163	4.196	4.05E-02	rs7154776	14	65614033	q23.3
SNP_A-1919418	C	C	354	14	402	6	4.197	4.05E-02	rs2205938	20	40565306	q12
SNP_A-1885858	G	G	399	17	405	7	4.192	4.06E-02	rs1996842	11	122270523	q24.1
SNP_A-1883974	G	G	289	79	293	113	4.193	4.06E-02	rs4890275	18	36866452	q12.3
SNP_A-1899487	C	C	257	109	262	152	4.194	4.06E-02	rs7629468	3	179891272	q26.32
SNP_A-1977865	C	C	195	157	251	149	4.194	4.06E-02	rs1379975	4	84881771	q21.23
SNP_A-1984386	T	T	249	117	245	157	4.194	4.06E-02	rs2576270	1	213453353	q41
SNP_A-1964618	G	G	247	105	255	149	4.193	4.06E-02	rs6737733	2	118291698	q14.1
SNP_A-1961872	A	A	278	124	253	153	4.193	4.06E-02	rs13386451	2	4316049	p25.2
SNP_A-1959792	A	A	349	17	376	34	4.191	4.06E-02	rs17661230	5	18246975	p15.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946026	A	A	283	85	293	123	4.193	4.06E-02	rs7107545	11	1345412	p15.5
SNP_A-1937693	T	T	226	142	222	188	4.193	4.06E-02	rs2631806	16	59676871	q21
SNP_A-1827256	T	T	235	117	221	151	4.194	4.06E-02	rs13180704	5	112997160	q22.2
SNP_A-1823827	G	G	249	87	255	125	4.195	4.06E-02	rs11044840	12	19808650	p12.3
SNP_A-1842693	A	A	330	16	361	33	4.193	4.06E-02	rs17027267	3	89956003	p11.1
SNP_A-1832910	C	C	298	38	337	67	4.192	4.06E-02	rs17007527	2	122807350	q14.3
SNP_A-1854429	T	T	282	126	244	148	4.193	4.06E-02	rs1368852	11	130273474	q24.3
SNP_A-1873414	A	A	241	139	211	165	4.194	4.06E-02	rs2317730	8	137228639	q24.23
SNP_A-1701787	C	C	308	42	377	31	4.194	4.06E-02	rs2011035	13	107588891	q33.3
SNP_A-1666420	C	C	283	67	306	104	4.193	4.06E-02	rs1844986	12	31366772	p11.21
SNP_A-1723712	G	G	289	85	276	114	4.192	4.06E-02	rs323685	5	2657424	p15.33
SNP_A-1780867	T	T	315	51	327	79	4.194	4.06E-02	rs7982683	13	107050710	q33.3
SNP_A-1786302	T	T	275	141	244	168	4.192	4.06E-02	rs17393547	14	33123726	q13.1
SNP_A-1790594	T	T	263	103	267	73	4.192	4.06E-02	rs8100750	19	55775407	q13.33
SNP_A-2172213	A	A	223	135	213	175	4.191	4.06E-02	rs7873789	9	10607850	p23
SNP_A-2168926	T	T	382	38	388	22	4.194	4.06E-02	rs618915	1	33780190	p35.1
SNP_A-2178951	G	G	341	79	315	103	4.191	4.06E-02	rs1300114	1	32995265	p35.1
SNP_A-2227634	A	A	370	50	384	32	4.192	4.06E-02	rs17069779	3	64007263	p14.1
SNP_A-2209401	G	G	363	49	339	69	4.191	4.06E-02	rs2399153	22	15867847	q11.1
SNP_A-2144787	T	T	274	90	280	128	4.195	4.06E-02	rs2553681	8	68848813	q13.2
SNP_A-2114366	T	T	257	87	319	75	4.194	4.06E-02	rs6803573	3	65633892	p14.1
SNP_A-2129755	A	A	238	132	296	120	4.193	4.06E-02	rs11727475	4	185422594	q35.1
SNP_A-2035371	T	T	381	17	387	7	4.193	4.06E-02	rs11076140	16	54626872	q12.2
SNP_A-2040893	G	G	222	104	294	98	4.193	4.06E-02	rs6433342	2	172922850	q31.1
SNP_A-2028309	G	G	238	132	296	120	4.193	4.06E-02	rs4730205	7	106123200	q22.3
SNP_A-2032033	G	G	269	95	274	134	4.194	4.06E-02	rs9519858	13	105381445	q33.2
SNP_A-2030771	G	G	285	83	294	120	4.192	4.06E-02	rs7322370	13	58567008	q21.2
SNP_A-1995376	T	T	209	145	256	130	4.193	4.06E-02	rs4579564	8	138451412	q24.23
SNP_A-1990988	A	A	303	65	310	96	4.193	4.06E-02	rs2283053	7	116020970	q31.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2105847	C	C	345	61	313	81	4.194	4.06E-02	rs17220686	10	109370882	q25.1
SNP_A-2073255	G	G	351	25	369	13	4.192	4.06E-02	rs7003697	8	104043634	q22.3
SNP_A-2284185	A	A	283	85	293	123	4.193	4.06E-02	rs376857	5	73876395	q13.3
SNP_A-2276085	T	T	337	31	362	54	4.195	4.06E-02	rs7333428	13	45873366	q14.13
SNP_A-2264076	G	G	274	24	292	44	4.192	4.06E-02	rs11265739	9	65853919	q12
SNP_A-2263933	A	A	313	53	372	40	4.194	4.06E-02	rs791643	5	173037161	q35.2
SNP_A-2248135	C	C	200	160	260	154	4.194	4.06E-02	rs503342	8	103199536	q22.3
SNP_A-2243603	C	C	288	118	262	146	4.194	4.06E-02	rs8046353	16	19553632	p12.3
SNP_A-2294627	C	C	234	136	289	123	4.193	4.06E-02	rs4434479	6	96396524	q16.1
SNP_A-2310011	A	A	306	10	390	4	4.191	4.06E-02	rs2139308	2	134745994	q21.2
SNP_A-2313112	G	G	357	33	375	19	4.192	4.06E-02	rs11253253	10	611653	p15.3
SNP_A-2298853	C	C	311	111	277	135	4.188	0.0407	rs2682924	15	75650775	q24.3
SNP_A-2251639	C	C	224	128	231	179	4.19	0.0407	rs1078803	2	219432043	q35
SNP_A-2263280	T	T	340	18	389	9	4.189	0.0407	rs1960643	2	81046461	p12
SNP_A-2279693	C	C	294	128	316	100	4.189	0.0407	rs1040605	1	115471872	p13.1
SNP_A-2067910	G	G	244	126	240	168	4.187	0.0407	rs4839061	1	116520219	p13.1
SNP_A-2060641	C	C	271	147	293	117	4.19	0.0407	rs360757	3	13079266	p25.2
SNP_A-2084253	G	G	408	14	409	5	4.188	0.0407	rs4325130	1	115872553	p13.1
SNP_A-2078036	T	T	336	80	313	105	4.189	0.0407	rs2235585	20	17427763	p12.1
SNP_A-1997863	A	A	357	59	330	80	4.19	0.0407	rs1332457	9	119055063	q33.1
SNP_A-2008888	C	C	411	5	377	13	4.188	0.0407	rs161724	1	44450429	p34.1
SNP_A-2006965	C	C	335	35	387	23	4.188	0.0407	rs2663891	2	208398827	q33.3
SNP_A-2136602	G	G	313	55	324	84	4.19	0.0407	rs11100532	4	165223500	q32.3
SNP_A-2122828	G	G	358	6	405	1	4.188	0.0407	rs1637740	7	2010563	p22.3
SNP_A-2117380	C	T	191	173	224	184	4.188	0.0407	rs2920205	4	4433324	p16.3
SNP_A-2143601	T	T	343	5	369	15	4.189	0.0407	rs17754051	10	27021505	p12.1
SNP_A-2182376	G	G	242	128	296	114	4.19	0.0407	rs10866111	4	61728812	q13.1
SNP_A-2176590	T	T	239	121	238	164	4.188	0.0407	rs6496319	15	84648321	q25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170602	G	G	345	19	402	10	4.189	0.0407	rs17166659	7	131799399	q32.3
SNP_A-2195339	G	G	258	110	259	151	4.187	0.0407	rs9590630	13	41197559	q14.11
SNP_A-1787266	C	C	341	29	365	51	4.188	0.0407	rs12574073	11	127824688	q24.3
SNP_A-1758814	A	A	258	110	259	151	4.187	0.0407	rs10506606	12	69437921	q15
SNP_A-1850073	T	T	189	177	244	170	4.189	0.0407	rs7552562	1	163607737	q24.1
SNP_A-1833679	A	A	287	117	317	93	4.189	0.0407	rs1960253	2	231702078	q37.1
SNP_A-1832566	A	A	318	52	377	39	4.188	0.0407	rs17789341	8	62566886	q12.3
SNP_A-1844143	A	A	262	108	266	150	4.19	0.0407	rs10153423	18	62069508	q22.1
SNP_A-1938170	G	G	178	156	229	147	4.188	0.0407	rs4740715	9	3159845	p24.2
SNP_A-1942697	C	C	314	56	328	86	4.187	0.0407	rs6789156	3	10099120	p25.3
SNP_A-1957479	A	A	258	94	306	78	4.19	0.0407	rs11625574	14	43689563	q21.2
SNP_A-1950046	G	G	383	23	342	36	4.188	0.0407	rs11743342	5	153049554	q33.2
SNP_A-1977769	A	A	214	146	205	189	4.188	0.0407	rs10008633	4	80927587	q21.21
SNP_A-1980254	G	G	345	11	394	4	4.189	0.0407	rs1038598	4	188382567	q35.2
SNP_A-1926901	A	A	297	73	355	59	4.188	0.0407	rs7210298	17	54896409	q23.2
SNP_A-1913307	C	T	188	174	223	179	4.186	4.08E-02	rs7069291	10	119682325	q26.11
SNP_A-1892406	T	T	382	14	383	5	4.183	4.08E-02	rs11265845	9	89466963	q22.2
SNP_A-1884430	A	A	288	44	317	29	4.185	4.08E-02	rs311568	2	86206929	p11.2
SNP_A-1884652	G	G	281	47	339	35	4.186	4.08E-02	rs1544040	20	39936039	q12
SNP_A-1888264	T	T	216	172	244	144	4.185	4.08E-02	rs644631	13	30996486	q12.3
SNP_A-1874921	C	C	253	81	318	70	4.185	4.08E-02	rs2814990	6	34720357	p21.31
SNP_A-1876800	A	A	231	111	296	102	4.183	4.08E-02	rs13093434	3	66760063	p14.1
SNP_A-1988498	T	T	340	54	369	37	4.183	4.08E-02	rs3778412	6	166920790	q27
SNP_A-1974809	C	C	298	68	312	102	4.183	4.08E-02	rs1386290	3	151354157	q25.1
SNP_A-1961149	G	G	275	55	309	91	4.182	4.08E-02	rs10972022	9	34237364	p13.3
SNP_A-1933606	T	T	325	43	346	70	4.185	4.08E-02	rs16956471	15	29113362	q13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1832050	C	C	219	151	216	200	4.183	4.08E-02	rs17348805	8	4810178	p23.2
SNP_A-1827615	A	A	186	180	235	169	4.185	4.08E-02	rs2937084	5	85837488	q14.3
SNP_A-1821641	C	C	369	37	340	54	4.183	4.08E-02	rs4933938	10	85583522	q23.1
SNP_A-1846195	G	G	323	37	377	25	4.186	4.08E-02	rs6054709	20	6995285	p12.3
SNP_A-1715149	G	G	346	42	342	64	4.183	4.08E-02	rs4667879	2	167218684	q24.3
SNP_A-1731659	A	A	228	172	265	149	4.185	4.08E-02	rs1993998	2	117006861	q14.1
SNP_A-1788667	G	G	283	71	305	109	4.183	4.08E-02	rs10021219	4	186131125	q35.1
SNP_A-2171806	C	C	383	37	385	21	4.183	4.08E-02	rs7909343	10	53656768	q21.1
SNP_A-2182786	A	A	358	2	369	9	4.184	4.08E-02	rs9589150	13	90676413	q31.3
SNP_A-2182600	A	A	362	6	397	17	4.183	4.08E-02	rs17782499	12	4363654	p13.32
SNP_A-2179385	G	G	356	8	394	2	4.185	4.08E-02	rs3907716	16	69364695	q22.1
SNP_A-2208006	C	A	192	156	185	167	4.185	4.08E-02	rs11034748	11	38434774	p12
SNP_A-2212596	C	C	378	44	353	63	4.186	4.08E-02	rs6464286	7	152042863	q36.2
SNP_A-2202816	T	T	382	38	358	56	4.182	4.08E-02	rs10954844	8	32421634	p12
SNP_A-2154416	C	C	240	122	301	111	4.185	4.08E-02	rs562163	6	47931045	p12.3
SNP_A-2120124	T	T	307	107	327	81	4.183	4.08E-02	rs1412512	9	135599809	q34.3
SNP_A-2109490	A	A	388	4	408	0	4.184	4.08E-02	rs7556384	1	155448134	q23.1
SNP_A-2128503	A	A	380	18	398	8	4.183	4.08E-02	rs7207252	17	69710667	q25.1
SNP_A-2012870	T	T	194	152	250	144	4.183	4.08E-02	rs543740	11	84468782	q14.1
SNP_A-2032686	C	C	392	4	412	0	4.182	4.08E-02	rs17092304	20	33168733	q11.22
SNP_A-2019996	C	C	364	56	339	77	4.186	4.08E-02	rs3850709	21	41923546	q22.3
SNP_A-2036642	T	T	303	117	301	83	4.183	4.08E-02	rs2896345	7	123476373	q31.33
SNP_A-2086236	C	C	283	71	299	107	4.182	4.08E-02	rs17346797	8	123634453	q24.13
SNP_A-2069466	T	T	342	62	318	84	4.183	4.08E-02	rs17190580	15	56550970	q21.3
SNP_A-2070075	C	C	394	22	377	37	4.184	4.08E-02	rs17720022	8	139329738	q24.23
SNP_A-2282539	C	C	343	79	317	103	4.184	4.08E-02	rs4951495	1	207613509	q32.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282168	G	G	328	6	371	1	4.183	4.08E-02	rs7331715	13	41018119	q14.11
SNP_A-2271458	T	T	412	0	392	4	4.182	4.08E-02	rs17046085	1	213910886	q41
SNP_A-2254302	G	G	333	81	350	58	4.185	4.08E-02	rs4325639	18	9614796	p11.22
SNP_A-2229707	C	C	377	37	394	22	4.184	4.08E-02	rs2135319	3	72106390	p13
SNP_A-2235268	T	T	178	176	232	170	4.185	4.08E-02	rs3751052	11	9028716	p15.4
SNP_A-2292286	A	A	238	128	296	116	4.185	4.08E-02	rs9973392	2	3329427	p25.3
SNP_A-2300066	C	C	339	25	399	15	4.182	4.09E-02	rs1402065	14	71866598	q24.2
SNP_A-2271180	G	G	222	164	202	200	4.181	4.09E-02	rs2712500	12	57430714	q14.1
SNP_A-2269933	G	G	400	4	420	0	4.179	4.09E-02	rs12286824	11	124132052	q24.2
SNP_A-2283350	C	C	396	4	416	0	4.18	4.09E-02	rs16997040	22	35335850	q12.3
SNP_A-2276318	T	T	290	44	292	68	4.182	4.09E-02	rs11038884	11	5710573	p15.4
SNP_A-2050033	A	A	345	3	359	11	4.18	4.09E-02	rs312296	5	161973160	q34
SNP_A-2087604	C	C	289	131	257	157	4.18	4.09E-02	rs4886883	15	75675979	q24.3
SNP_A-2093465	G	G	311	33	335	57	4.179	4.09E-02	rs17332053	5	112944495	q22.2
SNP_A-2047207	C	C	289	79	347	65	4.182	4.09E-02	rs1260292	9	6075078	p24.1
SNP_A-2020494	G	G	374	34	396	20	4.181	4.09E-02	rs2838651	21	44948924	q22.3
SNP_A-2027672	G	G	238	126	296	114	4.181	4.09E-02	rs341135	6	158839757	q25.3
SNP_A-2109244	G	G	394	4	414	0	4.181	4.09E-02	rs17007780	3	70890313	p13
SNP_A-2109635	G	G	295	89	321	67	4.179	4.09E-02	rs7638751	3	135526531	q22.1
SNP_A-2114890	G	G	291	29	338	18	4.181	4.09E-02	rs619778	10	3634879	p15.2
SNP_A-2121294	A	A	418	0	398	4	4.18	4.09E-02	rs11240548	1	202364879	q32.1
SNP_A-2159334	C	C	390	14	366	26	4.182	4.09E-02	rs10918430	1	163034158	q24.1
SNP_A-2210462	A	A	414	0	394	4	4.181	4.09E-02	rs1547979	10	131070629	q26.3
SNP_A-2210830	A	A	286	34	367	25	4.182	4.09E-02	rs6490059	12	115271865	q24.21
SNP_A-2172867	C	C	333	57	300	76	4.18	4.09E-02	rs500095	4	12764614	p15.33
SNP_A-2197283	C	C	232	152	250	120	4.178	4.09E-02	rs4372467	11	127888014	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2191242	C	C	296	74	354	60	4.182	4.09E-02	rs8057403	16	81256171	q23.3
SNP_A-2186036	G	G	396	4	416	0	4.18	4.09E-02	rs6719118	2	121423874	q14.2
SNP_A-1793377	T	T	205	141	205	191	4.18	4.09E-02	rs2897161	1	221192803	q42.12
SNP_A-1712991	G	G	385	3	401	11	4.181	4.09E-02	rs9319288	13	24638848	q12.13
SNP_A-1758854	C	C	351	47	379	31	4.179	4.09E-02	rs10502292	18	918869	p11.32
SNP_A-1642669	T	G	207	167	205	189	4.182	4.09E-02	rs1961367	9	98508192	q31.1
SNP_A-1689530	C	C	298	50	369	39	4.182	4.09E-02	rs10513819	3	188712411	q27.3
SNP_A-1870561	C	C	262	156	290	128	4.181	4.09E-02	rs1491959	3	46095404	p21.31
SNP_A-1827970	A	A	265	65	332	54	4.182	4.09E-02	rs4938965	11	60123761	q12.2
SNP_A-1832820	G	G	361	5	389	15	4.18	4.09E-02	rs12123511	1	189815158	q31.2
SNP_A-1943890	A	C	190	156	189	169	4.182	4.09E-02	rs6738958	2	25804054	p23.3
SNP_A-1959276	T	T	273	61	282	92	4.18	4.09E-02	rs6722763	2	234064210	q37.1
SNP_A-1957364	T	T	345	21	363	39	4.179	4.09E-02	rs6488325	12	10804378	p13.2
SNP_A-1987141	G	G	223	133	276	120	4.181	4.09E-02	rs9320162	6	106958006	q21
SNP_A-1981344	C	C	351	19	379	37	4.182	4.09E-02	rs260326	5	39241949	p13.1
SNP_A-1875624	G	G	281	85	258	110	4.181	4.09E-02	rs2160206	2	58959570	p16.1
SNP_A-1887402	A	A	388	10	373	21	4.179	4.09E-02	rs11186413	10	92748486	q23.31
SNP_A-1893893	A	G	188	170	225	185	4.181	4.09E-02	rs6449528	5	60678104	q12.1
SNP_A-1913612	G	G	180	152	236	146	4.178	4.09E-02	rs10948268	6	46070430	p21.1
SNP_A-1911703	A	A	248	160	276	132	4.181	4.09E-02	rs7330546	13	58907635	q21.2
SNP_A-1912991	A	A	302	60	318	92	4.181	4.09E-02	rs8047356	16	80540600	q23.2
SNP_A-1925669	T	T	336	16	402	8	4.179	4.09E-02	rs16890136	4	13993498	p15.33
SNP_A-1927386	G	G	254	136	237	171	4.175	4.10E-02	rs4501550	8	92157388	q21.3
SNP_A-1900370	T	T	232	110	230	150	4.174	4.10E-02	rs4841371	8	10428766	p23.1
SNP_A-1898754	-	G	176	176	232	172	4.175	4.10E-02	rs629546	5	28967970	p14.1
SNP_A-1882173	C	C	314	24	387	15	4.175	4.10E-02	rs7167826	15	79503238	q25.2
SNP_A-1979346	A	A	239	131	297	119	4.174	4.10E-02	rs1517131	4	148840873	q31.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1983482	T	T	313	93	286	118	4.174	4.10E-02	rs630044	5	131286277	q23.3
SNP_A-1968501	A	A	283	99	278	134	4.175	4.10E-02	rs3915737	20	44304788	q13.12
SNP_A-1957715	T	T	235	135	290	122	4.176	4.10E-02	rs10923806	1	116181477	p13.1
SNP_A-1960421	T	T	224	144	222	192	4.175	4.10E-02	rs4771512	13	105358866	q33.2
SNP_A-1960919	T	T	298	118	316	90	4.176	4.10E-02	rs10822081	10	52441450	q11.23
SNP_A-1945854	A	A	282	78	292	114	4.177	4.10E-02	rs7681711	4	83954248	q21.22
SNP_A-1937972	C	C	331	39	389	27	4.176	4.10E-02	rs9709842	18	14724334	p11.21
SNP_A-1827945	G	G	422	0	402	4	4.178	4.10E-02	rs16973815	16	83039365	q24.1
SNP_A-1864004	C	C	324	78	349	57	4.176	4.10E-02	rs13118031	4	18456585	p15.32
SNP_A-1848539	A	A	367	1	385	7	4.177	4.10E-02	rs12203446	6	712905	p25.3
SNP_A-1855062	C	C	316	34	377	23	4.177	4.10E-02	rs1948731	2	155976896	q24.1
SNP_A-1799981	C	C	347	65	313	85	4.177	4.10E-02	rs11610488	12	112580320	q24.13
SNP_A-2178821	A	A	334	36	321	55	4.177	4.10E-02	rs17095231	14	26510973	q12
SNP_A-2178872	G	A	196	174	226	190	4.175	4.10E-02	rs2366447	4	73998081	q13.3
SNP_A-2182440	G	G	391	23	395	11	4.178	4.10E-02	rs2033099	8	129098496	q24.21
SNP_A-2199967	G	G	264	100	317	85	4.176	4.10E-02	rs1796740	6	89939568	q15
SNP_A-2205576	G	G	391	11	387	23	4.177	4.10E-02	rs3758139	8	6773630	p23.1
SNP_A-2167939	G	G	348	44	330	64	4.177	4.10E-02	rs3788504	22	31484951	q12.3
SNP_A-2045278	G	G	324	42	347	69	4.176	4.10E-02	rs698840	2	49547332	p16.3
SNP_A-2043478	A	A	257	121	297	101	4.177	4.10E-02	rs7816431	8	94698564	q22.1
SNP_A-1995876	G	A	204	166	217	199	4.175	4.10E-02	rs7873984	9	11132334	p23
SNP_A-2082109	T	T	297	85	339	67	4.178	4.10E-02	rs10957697	8	75250532	q21.11
SNP_A-2072545	C	C	315	53	374	40	4.178	4.10E-02	rs811304	15	28923081	q13.2
SNP_A-2287384	A	A	310	20	367	11	4.177	4.10E-02	rs7978046	12	108203456	q24.11
SNP_A-2244643	A	A	268	50	251	71	4.177	4.10E-02	rs17028071	4	100057252	q23
SNP_A-2292715	T	T	287	39	381	31	4.177	4.10E-02	rs3860110	5	134896238	q31.1
SNP_A-2308824	C	C	276	142	299	113	4.175	4.10E-02	rs10863305	1	213756548	q41

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2304826	T	T	230	134	282	120	4.178	4.10E-02	rs4679495	3	59537405	p14.2
SNP_A-2309739	G	G	212	202	239	171	4.173	4.11E-02	rs895520	2	101036455	q11.2
SNP_A-2298565	G	G	256	154	277	123	4.174	4.11E-02	rs5764804	22	44310576	q13.31
SNP_A-2254845	G	G	306	60	367	47	4.17	4.11E-02	rs10878917	12	39309270	q12
SNP_A-2237691	C	C	242	172	268	142	4.172	4.11E-02	rs2256090	1	38579281	p34.3
SNP_A-2240533	G	G	271	65	311	49	4.172	4.11E-02	rs1177565	3	127702671	q21.2
SNP_A-2231449	C	C	334	34	358	58	4.17	4.11E-02	rs17468883	5	165744747	q34
SNP_A-2233387	A	A	325	43	376	30	4.17	4.11E-02	rs2861412	19	12522178	p13.2
SNP_A-2285381	G	G	345	23	349	11	4.171	4.11E-02	rs9939857	16	34454744	p11.1
SNP_A-2278070	G	G	218	138	272	126	4.17	4.11E-02	rs10865036	2	100319113	q11.2
SNP_A-2049290	C	C	274	96	279	135	4.173	4.11E-02	rs8099793	18	70629026	q22.3
SNP_A-2078984	G	G	296	68	310	102	4.17	4.11E-02	rs6426503	1	224957746	q42.13
SNP_A-2103725	T	T	256	112	258	154	4.171	4.11E-02	rs233538	16	64852305	q22.1
SNP_A-1997474	G	G	286	76	298	112	4.172	4.11E-02	rs10820637	9	104239619	q31.1
SNP_A-2006544	C	C	298	70	307	103	4.173	4.11E-02	rs10751582	10	128484755	q26.2
SNP_A-2032753	C	C	284	78	297	115	4.172	4.11E-02	rs7019389	9	104241722	q31.1
SNP_A-2032501	C	C	280	52	312	86	4.174	4.11E-02	rs10996893	10	67525942	q21.3
SNP_A-2031258	G	G	254	82	319	71	4.171	4.11E-02	rs3006263	10	26198596	p12.1
SNP_A-2025617	C	C	321	47	376	34	4.171	4.11E-02	rs17681594	13	30060125	q12.3
SNP_A-2162184	C	C	253	115	257	159	4.174	4.11E-02	rs2950955	5	136789291	q31.1
SNP_A-2156786	C	C	250	128	273	101	4.174	4.11E-02	rs11034859	11	38549418	p12
SNP_A-2110669	C	C	349	19	406	10	4.173	4.11E-02	rs11817421	10	118111272	q25.3
SNP_A-2108594	T	T	319	103	337	77	4.173	4.11E-02	rs7037796	9	123935953	q33.3
SNP_A-2206859	A	A	334	6	377	1	4.173	4.11E-02	rs7110193	11	81328339	q14.1
SNP_A-2199955	A	A	179	157	243	157	4.172	4.11E-02	rs7483387	11	87450170	q14.2
SNP_A-2208105	C	C	241	85	307	75	4.171	4.11E-02	rs4509378	8	143486243	q24.3
SNP_A-2221084	G	G	299	63	360	50	4.174	4.11E-02	rs2066555	13	49507059	q14.2
SNP_A-2194238	T	T	218	132	214	176	4.173	4.11E-02	rs10956793	8	92179100	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1810646	C	C	238	130	237	175	4.173	4.11E-02	rs248276	5	165188563	q34
SNP_A-1689096	A	A	307	43	376	32	4.17	4.11E-02	rs2818939	9	14816616	p22.3
SNP_A-1689266	T	T	235	115	303	107	4.172	4.11E-02	rs1370687	4	166967982	q32.3
SNP_A-1646422	A	A	227	123	235	173	4.171	4.11E-02	rs10497423	2	175050237	q31.1
SNP_A-1755936	C	C	373	25	368	42	4.17	4.11E-02	rs10520706	15	90466083	q26.1
SNP_A-1784313	G	G	270	82	334	70	4.172	4.11E-02	rs7868364	9	123942032	q33.3
SNP_A-1859019	C	C	344	46	324	66	4.17	4.11E-02	rs7598676	2	132994595	q21.2
SNP_A-1845173	G	G	341	25	401	15	4.172	4.11E-02	rs17143339	5	117310133	q23.1
SNP_A-1865522	G	G	294	76	352	62	4.171	4.11E-02	rs6787683	3	152344939	q25.1
SNP_A-1819583	C	C	329	41	349	67	4.171	4.11E-02	rs9350602	6	76617218	q14.1
SNP_A-1837573	T	T	341	25	401	15	4.172	4.11E-02	rs16866181	2	7479050	p25.1
SNP_A-1938283	A	A	348	50	371	33	4.173	4.11E-02	rs2476506	13	21696746	q12.11
SNP_A-1955530	C	C	206	178	221	141	4.173	4.11E-02	rs12994778	2	208852522	q33.3
SNP_A-1968813	T	T	322	68	344	48	4.17	4.11E-02	rs10211746	20	55941028	q13.32
SNP_A-1966601	G	G	217	151	214	200	4.17	4.11E-02	rs10932150	2	206995237	q33.3
SNP_A-1971530	G	G	240	126	242	172	4.171	4.11E-02	rs10490889	3	6257028	p26.1
SNP_A-1980005	G	G	281	63	302	98	4.174	4.11E-02	rs6850091	4	177408795	q34.2
SNP_A-1884348	G	G	349	19	406	10	4.173	4.11E-02	rs16839210	3	133606466	q22.1
SNP_A-1894673	G	G	239	129	297	117	4.17	4.11E-02	rs6070329	20	55998520	q13.32
SNP_A-1964722	A	A	352	12	389	27	4.169	4.12E-02	rs17008586	2	123219747	q14.3
SNP_A-1957802	T	T	316	24	347	45	4.168	4.12E-02	rs2912617	6	48709549	p12.3
SNP_A-1960036	A	A	245	165	216	194	4.167	4.12E-02	rs10800728	1	197426804	q32.1
SNP_A-1951424	G	G	344	26	362	46	4.168	4.12E-02	rs2101793	4	70479178	q13.2
SNP_A-1937398	C	C	214	122	217	169	4.169	4.12E-02	rs6931445	6	120375210	q22.31
SNP_A-1940460	T	T	251	59	251	87	4.168	4.12E-02	rs16970834	13	107073983	q33.3
SNP_A-1821779	G	G	353	55	375	37	4.167	4.12E-02	rs17791761	9	18352486	p22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1823687	A	T	193	173	226	188	4.168	4.12E-02	rs2357036	8	114932522	q23.3
SNP_A-1850589	C	C	340	64	319	87	4.168	4.12E-02	rs5746449	22	16489510	q11.21
SNP_A-1783829	T	T	277	93	284	132	4.17	4.12E-02	rs2623828	8	68858285	q13.2
SNP_A-1781263	A	A	281	71	291	105	4.169	4.12E-02	rs13201563	6	66106533	q12
SNP_A-1780568	C	C	278	82	339	69	4.166	4.12E-02	rs1375422	4	59533907	q12
SNP_A-1651998	A	G	183	167	225	183	4.168	4.12E-02	rs1852730	5	88865941	q14.3
SNP_A-1685130	A	A	340	54	327	77	4.167	4.12E-02	rs2270279	4	13505894	p15.33
SNP_A-1675784	G	G	346	54	375	37	4.166	4.12E-02	rs10493372	1	64620420	p31.3
SNP_A-1787394	C	G	199	165	217	195	4.166	4.12E-02	rs11113400	12	106469024	q23.3
SNP_A-1786565	A	A	233	189	261	159	4.169	4.12E-02	rs1019484	5	159021469	q33.3
SNP_A-2187795	A	G	181	169	223	177	4.169	4.12E-02	rs585381	10	96909793	q23.33
SNP_A-2214341	A	A	367	43	387	27	4.168	4.12E-02	rs6683829	1	77463169	p31.1
SNP_A-2167765	C	C	198	152	258	146	4.17	4.12E-02	rs2241713	19	46561308	q13.2
SNP_A-2013085	T	T	272	134	244	162	4.168	4.12E-02	rs4876069	8	1433281	p23.3
SNP_A-2094230	G	G	238	118	296	106	4.166	4.12E-02	rs1490867	4	19001366	p15.31
SNP_A-2099178	T	T	222	182	253	155	4.167	4.12E-02	rs12936750	17	46022733	q21.33
SNP_A-2063508	A	A	250	106	258	150	4.169	4.12E-02	rs12826155	12	57094355	q14.1
SNP_A-2250762	G	G	285	73	346	60	4.168	4.12E-02	rs11222591	11	130748089	q25
SNP_A-2243127	T	T	258	72	338	64	4.167	4.12E-02	rs2505506	10	42965860	q11.21
SNP_A-2290345	C	C	330	92	350	68	4.169	4.12E-02	rs1710415	1	4482113	p36.32
SNP_A-2313896	C	C	296	68	352	54	4.168	4.12E-02	rs10006265	4	168685349	q32.3
SNP_A-2307847	G	G	285	115	262	144	4.17	4.12E-02	rs10904392	10	5058113	p15.1
SNP_A-2234402	A	A	232	138	231	185	4.163	4.13E-02	rs904033	4	78270550	q21.1
SNP_A-2239002	G	G	189	173	244	166	4.162	4.13E-02	rs1882708	16	21081441	p12.3
SNP_A-2265301	G	G	373	39	335	55	4.163	4.13E-02	rs7863291	9	94887538	q22.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2265392	C	C	295	91	305	65	4.163	4.13E-02	rs2715782	12	45605939	q13.11
SNP_A-2076285	T	T	311	53	361	39	4.164	4.13E-02	rs668667	11	60222063	q12.2
SNP_A-2074830	A	A	212	154	268	144	4.164	4.13E-02	rs1429368	2	141581821	q22.1
SNP_A-2050266	C	C	398	22	370	36	4.164	4.13E-02	rs6019910	20	47623094	q13.13
SNP_A-2097884	C	C	330	44	302	62	4.162	4.13E-02	rs12563944	1	158731962	q23.3
SNP_A-2105860	A	A	273	95	334	82	4.162	4.13E-02	rs8085007	18	4014459	p11.31
SNP_A-2016603	A	A	301	117	325	91	4.165	4.13E-02	rs2828394	21	23956856	q21.2
SNP_A-2006113	C	C	245	167	217	197	4.165	4.13E-02	rs7902280	10	123195271	q26.13
SNP_A-1991158	T	T	297	21	379	13	4.162	4.13E-02	rs2524909	7	124780279	q31.33
SNP_A-2029275	G	G	271	81	273	115	4.164	4.13E-02	rs2604230	11	128303864	q24.3
SNP_A-2045989	C	C	277	145	241	169	4.164	4.13E-02	rs205737	7	130118083	q32.3
SNP_A-2153441	A	A	234	180	264	152	4.164	4.13E-02	rs6088727	20	33177300	q11.22
SNP_A-2148308	C	C	182	178	234	170	4.164	4.13E-02	rs10027083	4	32198494	p15.1
SNP_A-2110430	T	T	288	58	298	88	4.162	4.13E-02	rs2670724	2	71401102	p13.2
SNP_A-2202950	C	C	223	139	225	189	4.165	4.13E-02	rs10915696	1	221184481	q42.12
SNP_A-2202557	C	C	339	65	294	82	4.165	4.13E-02	rs12255924	10	57756220	q21.1
SNP_A-2205483	T	T	204	160	263	153	4.162	4.13E-02	rs1700861	1	215635545	q41
SNP_A-2187358	C	C	342	8	347	19	4.162	4.13E-02	rs4389183	17	47078929	q21.33
SNP_A-2192758	G	G	261	97	320	84	4.163	4.13E-02	rs9555647	13	109364127	q34
SNP_A-2198147	A	A	240	166	272	140	4.165	4.13E-02	rs16860	8	26079823	p21.2
SNP_A-1809162	A	A	340	12	405	5	4.163	4.13E-02	rs16989055	4	33437993	p15.1
SNP_A-1697503	T	T	323	27	360	50	4.164	4.13E-02	rs345013	3	146494697	q24
SNP_A-1697615	C	C	372	30	395	17	4.163	4.13E-02	rs10494121	1	110686939	p13.3
SNP_A-1706883	T	G	219	183	216	194	4.164	4.13E-02	rs1376983	3	56171428	p14.3
SNP_A-1854937	C	C	281	89	339	75	4.165	4.13E-02	rs1130902	4	184187195	q35.1
SNP_A-1828361	G	G	391	27	371	43	4.163	4.13E-02	---	11	9419893	p15.4

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939725	G	G	348	8	374	20	4.165	4.13E-02	rs16912455	9	122844721	q33.2
SNP_A-1964811	T	T	317	25	373	15	4.163	4.13E-02	rs17678106	2	127052908	q14.3
SNP_A-1967633	T	T	356	20	303	31	4.165	4.13E-02	rs6055774	20	8299469	p12.3
SNP_A-1898959	G	G	282	34	337	23	4.163	4.13E-02	rs11116154	12	82891118	q21.31
SNP_A-1887336	T	T	381	41	360	60	4.165	4.13E-02	rs2743208	1	18763161	p36.13
SNP_A-1877411	T	T	295	67	277	91	4.163	4.13E-02	rs17737713	11	2240035	p15.5
SNP_A-1874263	C	C	246	154	222	186	4.164	4.13E-02	rs4708557	6	169157233	q27
SNP_A-1931178	A	A	362	60	330	80	4.165	4.13E-02	rs16942790	18	17369129	q11.2
SNP_A-1890934	A	A	230	140	286	128	4.159	4.14E-02	rs13218458	6	76990136	q14.1
SNP_A-1967842	C	C	279	119	279	85	4.158	4.14E-02	rs3789345	20	13419848	p12.1
SNP_A-1982462	T	T	259	89	302	72	4.16	4.14E-02	rs845464	1	206773409	q32.2
SNP_A-1944477	G	G	414	0	396	4	4.16	4.14E-02	rs11912803	22	24858762	q12.1
SNP_A-1955175	G	G	326	42	344	68	4.16	4.14E-02	rs7578083	2	196047572	q32.3
SNP_A-1835007	G	G	294	26	301	45	4.158	4.14E-02	rs195655	16	69604396	q22.2
SNP_A-1857008	T	G	186	184	236	178	4.158	4.14E-02	rs11250700	10	1678904	p15.3
SNP_A-1845338	G	G	330	38	386	26	4.161	4.14E-02	rs10876251	12	50905093	q13.13
SNP_A-1864842	T	T	311	59	365	45	4.158	4.14E-02	rs9867989	3	24266201	p24.2
SNP_A-1652712	C	C	396	4	414	0	4.16	4.14E-02	rs1938404	1	25962890	p36.11
SNP_A-1732752	C	C	274	76	343	65	4.161	4.14E-02	rs725751	6	94977986	q16.1
SNP_A-1807483	C	C	307	59	325	91	4.159	4.14E-02	rs6510997	19	18708608	p13.11
SNP_A-1803810	T	T	351	61	332	84	4.158	4.14E-02	rs9311335	3	43249983	p22.1
SNP_A-1786768	G	G	292	118	316	92	4.162	4.14E-02	rs1026514	1	218104114	q41
SNP_A-1798993	G	G	261	153	286	124	4.159	4.14E-02	rs6556114	5	173504283	q35.2
SNP_A-2174048	T	T	289	49	298	76	4.16	4.14E-02	rs1033408	1	173642579	q25.2
SNP_A-2202120	A	A	362	48	345	69	4.159	4.14E-02	rs1579103	13	58546807	q21.2
SNP_A-2222917	T	T	349	1	367	7	4.162	4.14E-02	rs17149214	7	24131135	p15.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2126713	C	C	335	29	359	51	4.161	4.14E-02	rs7730725	5	106119085	q21.3
SNP_A-2146279	A	A	304	112	277	139	4.159	4.14E-02	rs10130998	14	41956857	q21.1
SNP_A-2142364	C	C	390	26	391	13	4.16	4.14E-02	rs12024194	1	168455148	q24.3
SNP_A-2159142	A	A	270	88	334	76	4.158	4.14E-02	rs7598433	2	157276449	q24.1
SNP_A-2163817	T	T	420	0	402	4	4.158	4.14E-02	rs2092929	20	58007932	q13.33
SNP_A-2044945	T	T	242	124	303	113	4.158	4.14E-02	rs2036943	4	46717487	p12
SNP_A-2039873	T	C	187	183	236	180	4.16	4.14E-02	rs6432655	2	161531210	q24.2
SNP_A-2020290	T	T	194	190	230	168	4.159	4.14E-02	rs2839649	21	43480172	q22.3
SNP_A-1997174	T	T	347	21	376	40	4.158	4.14E-02	rs7032790	9	88765944	q22.1
SNP_A-2001416	C	C	289	125	260	152	4.159	4.14E-02	rs10458676	10	60179407	q21.1
SNP_A-2007847	A	A	303	57	362	44	4.16	4.14E-02	rs6417346	20	57403474	q13.32
SNP_A-2094166	C	C	282	80	348	68	4.159	4.14E-02	rs4794491	17	49687051	q22
SNP_A-2080004	T	T	222	118	289	111	4.161	4.14E-02	rs10937443	3	191811371	q28
SNP_A-2080691	C	C	412	0	394	4	4.161	4.14E-02	rs633605	2	111661472	q13
SNP_A-2089830	T	T	412	0	394	4	4.161	4.14E-02	rs9675034	17	10560597	p13.1
SNP_A-2051670	T	C	190	162	217	189	4.158	4.14E-02	rs6730262	2	64279345	p14
SNP_A-2072466	C	C	328	34	345	57	4.16	4.14E-02	rs1441073	4	58237327	q12
SNP_A-2266352	A	A	396	4	414	0	4.16	4.14E-02	rs7104611	11	18256168	p15.1
SNP_A-2264170	G	G	314	108	283	133	4.16	4.14E-02	rs1864346	1	155549518	q23.1
SNP_A-2278013	C	C	206	170	242	148	4.16	4.14E-02	rs2873804	9	133535198	q34.2
SNP_A-2275451	A	A	288	124	250	146	4.161	4.14E-02	rs2162174	11	127446026	q24.2
SNP_A-2231644	G	G	229	167	262	142	4.161	4.14E-02	rs3117016	6	33203494	p21.32
SNP_A-2243030	T	T	189	143	251	139	4.161	4.14E-02	rs11714466	3	129660224	q21.3
SNP_A-2251616	G	G	238	112	296	100	4.158	4.14E-02	rs593423	11	97422335	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2288901	T	C	187	183	236	180	4.16	4.14E-02	rs4815628	20	3839896	p13
SNP_A-2305718	G	G	305	65	361	51	4.155	4.15E-02	rs2734705	1	86664345	p22.3
SNP_A-2314452	C	C	295	39	369	29	4.154	4.15E-02	rs9930572	16	87817464	q24.3
SNP_A-2311523	G	G	345	61	359	41	4.156	4.15E-02	rs17166584	5	132697273	q31.1
SNP_A-2246841	A	A	346	4	367	13	4.157	4.15E-02	rs12429770	13	42812563	q14.11
SNP_A-2267040	A	A	359	3	375	11	4.154	4.15E-02	rs10134003	14	47974805	q21.3
SNP_A-2076757	T	T	228	192	256	162	4.157	4.15E-02	rs4659711	1	233228405	q43
SNP_A-2064497	A	A	274	58	290	90	4.156	4.15E-02	rs4988713	8	23668329	p21.2
SNP_A-2049405	T	T	364	2	377	9	4.154	4.15E-02	rs10772852	12	15502250	p12.3
SNP_A-2087560	G	G	240	130	277	109	4.156	4.15E-02	rs6473757	8	53931920	q11.23
SNP_A-2005774	A	A	332	38	353	63	4.154	4.15E-02	rs8088677	18	65213503	q22.2
SNP_A-2016199	G	G	182	174	242	172	4.157	4.15E-02	rs9983966	21	21138990	q21.1
SNP_A-2022438	G	G	344	24	400	14	4.155	4.15E-02	rs7177319	15	43919524	q21.1
SNP_A-2028040	A	A	341	23	295	35	4.154	4.15E-02	rs16974378	18	37159721	q12.3
SNP_A-2028603	C	C	379	23	360	38	4.157	4.15E-02	rs16989807	22	30773596	q12.3
SNP_A-2039393	C	C	290	72	300	106	4.157	4.15E-02	rs1180002	12	119998665	q24.31
SNP_A-2045498	C	C	368	54	345	75	4.156	4.15E-02	rs2847605	18	695598	p11.32
SNP_A-2134739	A	A	344	24	400	14	4.155	4.15E-02	rs11073267	15	35894105	q14
SNP_A-2109610	G	G	334	72	360	52	4.156	4.15E-02	rs1330228	1	106668757	p21.1
SNP_A-2226072	T	T	236	130	291	117	4.157	4.15E-02	rs6453167	5	75159406	q13.3
SNP_A-2171499	C	C	360	46	364	28	4.156	4.15E-02	rs2269089	10	33569839	p11.22
SNP_A-1834786	C	C	355	25	341	41	4.155	4.15E-02	rs710229	1	42006341	p34.2
SNP_A-1826770	C	C	213	149	207	195	4.154	4.15E-02	rs175057	14	74559385	q24.3
SNP_A-1822860	A	A	214	126	276	118	4.157	4.15E-02	rs906695	5	138167176	q31.2
SNP_A-1818616	T	T	374	16	405	7	4.155	4.15E-02	rs16923431	8	59471312	q12.1
SNP_A-1981860	T	T	321	39	377	27	4.154	4.15E-02	rs40290	5	61852899	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1898212	C	T	206	158	209	203	4.156	4.15E-02	rs2034221	5	13734326	p15.2
SNP_A-1892055	G	G	336	84	355	61	4.152	4.16E-02	rs10910097	1	2553592	p36.32
SNP_A-1881136	G	G	350	30	354	16	4.151	4.16E-02	rs2276008	22	20438590	q11.21
SNP_A-1882654	A	A	235	185	264	156	4.152	4.16E-02	rs298147	1	60550167	p31.3
SNP_A-1911390	C	C	340	58	315	79	4.153	4.16E-02	rs9605086	22	18574133	q11.21
SNP_A-1971779	A	A	416	2	378	8	4.152	4.16E-02	rs16863069	1	166858399	q24.2
SNP_A-1959330	C	C	235	185	264	156	4.152	4.16E-02	rs4370848	10	128075514	q26.2
SNP_A-1953809	A	G	179	157	216	182	4.15	4.16E-02	rs6510593	19	42325895	q13.12
SNP_A-1948972	G	A	216	192	219	185	4.151	4.16E-02	rs2222394	18	18502286	q11.2
SNP_A-1940048	G	G	249	97	260	140	4.152	4.16E-02	rs11078231	17	2392774	p13.3
SNP_A-1937377	C	C	330	34	354	58	4.15	4.16E-02	rs17710197	4	66754439	q13.2
SNP_A-1826777	C	C	353	69	370	48	4.15	4.16E-02	rs2310818	16	67830472	q22.1
SNP_A-1866829	C	C	295	99	279	129	4.15	4.16E-02	rs1266186	17	32499711	q12
SNP_A-1848612	C	C	306	48	281	67	4.153	4.16E-02	rs4739008	8	63860969	q12.3
SNP_A-1853269	A	C	226	176	196	188	4.153	4.16E-02	rs9803864	1	42548830	p34.2
SNP_A-1795118	A	A	316	48	380	36	4.151	4.16E-02	rs665088	10	84303976	q23.1
SNP_A-1786592	T	T	383	35	392	20	4.152	4.16E-02	rs568434	1	14268486	p36.21
SNP_A-1790476	A	A	262	154	232	182	4.15	4.16E-02	rs11787175	8	121166183	q24.12
SNP_A-1790152	T	T	277	139	229	155	4.151	4.16E-02	rs849749	1	224603480	q42.13
SNP_A-2179202	C	C	233	171	201	197	4.152	4.16E-02	rs8013742	14	95085817	q32.13
SNP_A-2176403	C	C	233	129	292	118	4.152	4.16E-02	rs2093154	20	59071337	q13.33
SNP_A-2196077	T	T	223	131	280	120	4.15	4.16E-02	rs11183343	12	44784254	q13.11
SNP_A-2221903	C	C	223	147	247	119	4.151	4.16E-02	rs2531755	3	45747746	p21.31
SNP_A-2120902	G	G	349	15	377	31	4.151	4.16E-02	rs10940987	5	32006173	p13.3
SNP_A-2122128	T	T	283	125	258	154	4.15	4.16E-02	rs1328570	9	75480786	q21.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2133125	C	C	278	76	284	110	4.152	4.16E-02	rs17016698	4	91523965	q22.1
SNP_A-2133265	A	A	364	6	409	1	4.151	4.16E-02	rs12614705	2	100581239	q11.2
SNP_A-2167822	C	C	354	56	316	74	4.15	4.16E-02	rs2385504	1	233325697	q43
SNP_A-2141755	G	G	268	144	291	115	4.15	4.16E-02	rs517226	6	47928485	p12.3
SNP_A-2139305	A	A	327	19	380	10	4.151	4.16E-02	rs1031372	16	8376285	p13.2
SNP_A-2044952	T	T	206	134	246	116	4.15	4.16E-02	rs9298007	8	49521444	q11.21
SNP_A-2031248	G	G	342	22	388	12	4.153	4.16E-02	rs180038	9	98593971	q22.33
SNP_A-2022007	C	C	271	95	302	74	4.153	4.16E-02	rs6826058	4	15307006	p15.33
SNP_A-2021764	G	G	354	62	330	84	4.152	4.16E-02	rs2047888	3	1093426	p26.3
SNP_A-2009693	G	G	359	11	408	4	4.153	4.16E-02	rs2879159	4	33417774	p15.1
SNP_A-2079915	T	T	331	23	341	41	4.152	4.16E-02	rs9620769	22	26827421	q12.1
SNP_A-2051219	G	G	259	143	286	116	4.152	4.16E-02	rs2254485	5	65143971	q12.3
SNP_A-2274284	G	G	247	121	250	166	4.151	4.16E-02	rs12429983	13	59125365	q21.2
SNP_A-2245121	T	T	349	59	368	40	4.15	4.16E-02	rs2252925	6	31074261	p21.33
SNP_A-2237371	C	C	317	105	289	131	4.153	4.16E-02	rs1388606	3	46133438	p21.31
SNP_A-2312413	C	C	369	23	330	36	4.153	4.16E-02	rs4256909	10	114083575	q25.2
SNP_A-2290179	G	A	229	177	205	199	4.15	4.16E-02	rs12911081	15	60503933	q22.2
SNP_A-2308191	C	C	311	25	322	44	4.149	4.17E-02	rs11767601	7	124463544	q31.33
SNP_A-2305949	G	G	312	40	379	29	4.146	4.17E-02	rs16843242	2	241751271	q37.3
SNP_A-2283868	G	G	326	8	331	19	4.148	4.17E-02	rs17023903	2	39665767	p22.1
SNP_A-2073592	G	G	346	24	372	44	4.146	4.17E-02	rs11207514	1	59956054	p32.1
SNP_A-2073181	A	A	315	55	331	85	4.147	4.17E-02	---	12	70079458	q15
SNP_A-2087056	A	A	361	31	352	16	4.147	4.17E-02	---	2	168374853	q24.3
SNP_A-2092416	T	C	191	145	189	183	4.148	4.17E-02	rs13019918	2	119806395	q14.2
SNP_A-2001569	C	C	262	90	313	75	4.146	4.17E-02	rs7083606	10	129409122	q26.2
SNP_A-2004760	A	A	253	117	253	159	4.148	4.17E-02	rs6500024	16	57790679	q21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2019268	G	G	346	26	368	14	4.146	4.17E-02	rs16996780	21	39046179	q22.2
SNP_A-2029470	C	C	312	96	342	74	4.146	4.17E-02	rs16870425	5	40901620	p13.1
SNP_A-2044570	T	T	332	38	388	26	4.149	4.17E-02	rs7604792	2	123206455	q14.3
SNP_A-2150449	A	A	234	174	205	203	4.146	4.17E-02	rs872107	2	68055490	p14
SNP_A-2133270	C	C	366	52	345	73	4.148	4.17E-02	rs13017326	2	36091893	p22.3
SNP_A-2136405	C	C	286	74	347	61	4.146	4.17E-02	rs10035976	5	100746891	q21.1
SNP_A-2137213	G	G	290	72	346	58	4.148	4.17E-02	rs6849346	4	58222351	q12
SNP_A-2202700	C	C	251	163	222	192	4.147	4.17E-02	rs424765	22	16860571	q11.21
SNP_A-2200943	C	C	261	109	248	142	4.147	4.17E-02	rs535834	11	132098373	q25
SNP_A-2209129	G	G	270	152	295	123	4.145	4.17E-02	rs8055861	16	31307402	p11.2
SNP_A-2188668	A	A	307	55	310	82	4.149	4.17E-02	rs1923580	10	84725425	q23.1
SNP_A-1813094	C	C	238	116	244	162	4.148	4.17E-02	rs312615	5	143346949	q31.3
SNP_A-1733134	G	G	211	139	275	133	4.147	4.17E-02	rs1543587	9	12741741	p23
SNP_A-1656967	C	C	283	59	359	49	4.147	4.17E-02	rs10505927	12	24070940	p12.1
SNP_A-1654235	T	T	220	130	285	123	4.146	4.17E-02	rs2714480	2	202553552	q33.1
SNP_A-1855018	G	G	326	36	391	25	4.148	4.17E-02	rs17060761	6	132138021	q23.2
SNP_A-1860778	C	C	282	84	288	120	4.149	4.17E-02	rs11996929	8	30294506	p12
SNP_A-1843133	A	A	346	24	402	14	4.146	4.17E-02	rs6481864	10	33968032	p11.22
SNP_A-1945585	A	A	356	54	358	34	4.149	4.17E-02	rs10831284	11	94307612	q21
SNP_A-1972116	A	A	346	24	402	14	4.146	4.17E-02	rs13070187	3	25720364	p24.2
SNP_A-1973159	A	A	327	79	347	57	4.147	4.17E-02	rs10510980	3	69603578	p14.1
SNP_A-1966340	G	G	273	61	299	97	4.149	4.17E-02	rs4622748	2	195491828	q32.3
SNP_A-1987484	G	G	355	21	364	38	4.147	4.17E-02	rs2611436	6	124057958	q22.31
SNP_A-1986194	T	T	324	42	373	29	4.147	4.17E-02	rs16900514	6	62669538	q11.1
SNP_A-1986983	A	A	311	55	370	42	4.149	4.17E-02	rs1295135	7	16082933	p21.1
SNP_A-1914687	G	G	332	38	388	26	4.149	4.17E-02	rs7237514	18	42147253	q21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1923706	A	A	304	18	347	9	4.146	4.17E-02	rs16982472	2	16589204	p24.3
SNP_A-1919540	A	A	386	4	402	0	4.144	4.18E-02	rs17208394	17	9899070	p13.1
SNP_A-1927412	A	A	261	95	266	134	4.143	4.18E-02	rs6566386	18	64636529	q22.1
SNP_A-1927338	G	G	392	28	405	15	4.142	4.18E-02	rs2240202	15	26184490	q13.1
SNP_A-1914559	G	G	368	52	347	73	4.145	4.18E-02	rs4309380	16	13523196	p13.12
SNP_A-1906793	G	G	334	86	309	111	4.145	4.18E-02	rs13004325	2	126881974	q14.3
SNP_A-1893265	A	A	237	131	292	118	4.142	4.18E-02	rs6849335	4	185422429	q35.1
SNP_A-1988411	G	G	250	66	262	100	4.143	4.18E-02	rs2187210	6	162643232	q26
SNP_A-1978107	C	C	267	75	292	116	4.143	4.18E-02	rs10516930	4	94914864	q22.3
SNP_A-1957789	A	A	353	53	317	71	4.141	4.18E-02	rs17440311	4	145616644	p15.33
SNP_A-1831738	C	C	268	102	318	86	4.142	4.18E-02	rs11960198	5	165443011	q34
SNP_A-1823051	C	C	331	39	350	64	4.142	4.18E-02	rs872683	2	64502097	p14
SNP_A-1858531	T	T	408	0	392	4	4.142	4.18E-02	rs1880830	4	9244564	p16.1
SNP_A-1809600	C	C	405	15	392	28	4.142	4.18E-02	rs1557941	7	38602587	p14.1
SNP_A-1804352	C	C	273	93	280	132	4.143	4.18E-02	rs7980781	12	44368918	q12
SNP_A-1798128	A	A	221	131	223	179	4.144	4.18E-02	rs4290027	1	38553622	p34.3
SNP_A-2177707	T	T	219	151	214	198	4.143	4.18E-02	rs4871822	8	121073845	q24.12
SNP_A-2174905	G	A	195	175	227	189	4.142	4.18E-02	rs1927763	13	106548762	q33.3
SNP_A-2136228	C	C	402	0	386	4	4.144	4.18E-02	rs444879	11	22600503	p14.3
SNP_A-2122114	A	G	194	176	226	186	4.144	4.18E-02	rs12206695	6	126297240	q22.32
SNP_A-2116397	G	G	279	75	269	103	4.143	4.18E-02	rs4390782	2	163690509	q24.3
SNP_A-2109806	T	T	237	131	292	118	4.142	4.18E-02	rs6813806	4	61737765	q13.1
SNP_A-2092233	A	A	308	56	367	43	4.145	4.18E-02	rs7138495	12	100517629	q23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2093381	T	T	376	36	356	54	4.142	4.18E-02	rs11780274	8	9558649	p23.1
SNP_A-2080821	G	G	328	92	301	117	4.145	4.18E-02	rs229006	16	19121804	p12.3
SNP_A-2084448	T	T	239	131	238	176	4.142	4.18E-02	rs8022542	14	82599949	q31.2
SNP_A-2239636	C	C	270	74	266	104	4.145	4.18E-02	rs7842539	8	84284145	q21.13
SNP_A-2229763	A	A	329	51	310	72	4.145	4.18E-02	rs1122551	8	33028233	p12
SNP_A-2251421	G	G	264	92	323	79	4.142	4.18E-02	rs11097700	4	101488285	q24
SNP_A-2312433	T	T	244	126	245	171	4.142	4.18E-02	rs100841	5	6758857	p15.31
SNP_A-2293618	T	T	304	28	349	17	4.144	4.18E-02	rs11237875	11	78904575	q14.1
SNP_A-2300596	T	T	332	32	391	21	4.144	4.18E-02	rs1745034	13	97590910	q32.2
SNP_A-2301268	C	C	386	14	385	5	4.139	0.0419	rs7512734	1	153385837	q22
SNP_A-2291818	C	C	237	173	249	135	4.138	0.0419	rs13189546	5	6389397	p15.32
SNP_A-2313369	A	A	394	4	410	0	4.141	0.0419	rs348246	13	41024651	q14.11
SNP_A-2309123	G	G	286	74	352	62	4.139	0.0419	rs7580615	2	215335539	q35
SNP_A-2302012	A	A	316	54	375	41	4.139	0.0419	rs11577233	1	59720536	p32.1
SNP_A-2244660	T	T	343	23	373	43	4.138	0.0419	rs7007453	8	54039563	q11.23
SNP_A-2245812	A	A	328	40	386	28	4.138	0.0419	rs1551636	4	55889916	q12
SNP_A-2233991	T	G	203	167	218	198	4.14	0.0419	rs11143894	9	74134904	q21.13
SNP_A-2286754	C	C	363	57	338	78	4.139	0.0419	rs10518978	15	56543465	q21.3
SNP_A-2276503	T	T	386	14	385	5	4.139	0.0419	rs11049722	12	28619402	p11.22
SNP_A-2090139	T	T	359	1	379	7	4.141	0.0419	rs1345358	12	96639686	q23.1
SNP_A-2101546	A	A	414	0	398	4	4.14	0.0419	rs4849323	2	114759687	q14.1
SNP_A-2070814	T	T	277	121	255	151	4.139	0.0419	rs10776745	1	112426477	p13.2
SNP_A-2057942	A	C	209	159	209	205	4.141	0.0419	rs9552937	13	22855313	q12.12
SNP_A-2044445	T	T	338	30	393	19	4.139	0.0419	rs10435604	8	62315228	q12.2
SNP_A-2039207	C	C	256	110	261	153	4.141	0.0419	rs12612846	2	2351594	p25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2030834	G	G	400	4	416	0	4.139	0.0419	rs16942821	17	53633643	q23.2
SNP_A-2002214	C	C	316	54	375	41	4.139	0.0419	rs10509306	10	70315703	q22.1
SNP_A-2001313	G	G	287	107	258	132	4.138	0.0419	rs7074418	10	87008714	q23.2
SNP_A-1999735	G	G	402	4	418	0	4.138	0.0419	rs10508755	10	30286286	p11.23
SNP_A-2011901	A	A	261	67	279	103	4.14	0.0419	rs7747367	6	89044847	q15
SNP_A-2019014	G	G	343	23	373	43	4.138	0.0419	rs6517420	21	37810056	q22.13
SNP_A-2115372	C	C	296	124	322	98	4.139	0.0419	rs4635643	3	73093234	p13
SNP_A-2121066	G	G	291	109	311	83	4.14	0.0419	rs7981822	13	30586396	q12.3
SNP_A-2132765	C	C	262	142	241	175	4.137	0.0419	rs1462031	13	50359721	q14.3
SNP_A-2129852	C	C	359	1	379	7	4.141	0.0419	rs7845343	8	52548990	q11.22
SNP_A-2138537	A	A	231	127	228	170	4.14	0.0419	rs6441129	3	158608530	q25.32
SNP_A-2158058	A	A	351	71	370	50	4.141	0.0419	rs11247281	15	99701852	q26.3
SNP_A-2199152	A	A	338	30	393	19	4.139	0.0419	rs17055278	18	70478617	q22.3
SNP_A-2199912	T	T	410	0	394	4	4.141	0.0419	rs7567828	2	44166313	p21
SNP_A-2215322	A	A	207	175	230	144	4.139	0.0419	rs1504020	2	125060107	q14.3
SNP_A-2218438	C	C	314	92	293	119	4.138	0.0419	rs4823569	22	45318663	q13.31
SNP_A-2219350	T	T	395	15	412	6	4.138	0.0419	rs2746542	1	17133874	p36.13
SNP_A-1791934	T	C	203	191	226	180	4.14	0.0419	rs7812444	8	96383240	q22.1
SNP_A-1804399	T	T	322	98	296	124	4.139	0.0419	rs7433570	3	28558884	p24.1
SNP_A-1803933	G	G	327	31	345	53	4.139	0.0419	rs8075722	17	3122408	p13.3
SNP_A-1801169	A	A	254	162	225	191	4.138	0.0419	rs3127556	1	49180045	p33
SNP_A-1814134	C	C	240	112	243	155	4.138	0.0419	rs1009586	3	106042312	q13.11
SNP_A-1706817	T	T	351	47	341	69	4.14	0.0419	rs2105942	20	42898216	q13.12
SNP_A-1738789	T	T	396	4	412	0	4.14	0.0419	rs764146	5	169059297	q35.1
SNP_A-1872616	G	G	396	4	412	0	4.14	0.0419	rs3969624	15	97405860	q26.3
SNP_A-1828328	T	T	202	164	257	155	4.139	0.0419	rs10095930	8	117043480	q23.3
SNP_A-1961844	T	C	203	167	218	198	4.14	0.0419	rs2034730	2	3375546	p25.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1882858	G	G	214	146	265	133	4.141	0.0419	rs2539824	7	104960632	q22.3
SNP_A-1905269	T	T	379	43	356	62	4.139	0.0419	rs2442773	3	11613889	p25.3
SNP_A-1926535	A	A	396	4	412	0	4.14	0.0419	rs4091524	10	57723862	q21.1
SNP_A-1925968	C	C	379	43	356	62	4.139	0.0419	rs4406819	11	11384682	p15.3
SNP_A-1906473	T	T	255	135	195	141	4.137	4.20E-02	rs9316426	13	48481847	q14.2
SNP_A-1877050	G	G	344	18	378	36	4.135	4.20E-02	rs9294265	6	83665958	q14.1
SNP_A-1934264	C	T	226	180	200	188	4.135	4.20E-02	rs871244	11	93592183	q21
SNP_A-1935001	T	T	362	6	399	17	4.137	4.20E-02	rs1874058	12	81345981	q21.31
SNP_A-1935090	A	A	362	6	399	17	4.137	4.20E-02	rs817137	1	190006686	q31.2
SNP_A-1984774	T	T	320	58	292	78	4.137	4.20E-02	rs1933642	1	214743727	q41
SNP_A-1984819	A	A	210	182	237	153	4.136	4.20E-02	rs2143378	6	2986845	p25.2
SNP_A-1965981	G	G	226	142	283	131	4.135	4.20E-02	rs1534681	2	177757518	q31.1
SNP_A-1968205	C	C	287	73	353	61	4.134	4.20E-02	rs4815271	20	24379225	p11.21
SNP_A-1822864	T	T	358	4	381	13	4.133	4.20E-02	rs16951716	16	78534146	q23.2
SNP_A-1825036	C	C	334	20	367	39	4.134	4.20E-02	rs7847832	9	88759876	q22.1
SNP_A-1820655	A	A	388	30	371	47	4.134	4.20E-02	rs16883305	6	20174037	p22.3
SNP_A-1842676	C	C	188	156	236	144	4.134	4.20E-02	rs2470536	3	15690160	p25.1
SNP_A-1844585	T	T	340	30	362	52	4.136	4.20E-02	rs4513316	2	197704411	q33.1
SNP_A-1734144	C	G	217	185	220	194	4.136	4.20E-02	rs726009	10	113718133	q25.2
SNP_A-1743605	C	C	252	136	228	166	4.134	4.20E-02	rs409492	14	54517146	q22.3
SNP_A-1744543	T	T	373	29	367	47	4.136	4.20E-02	rs155504	6	7896720	p24.3
SNP_A-1783591	G	G	422	0	406	4	4.137	4.20E-02	rs7626939	3	60847623	p14.2
SNP_A-1782355	A	A	250	162	278	134	4.133	4.20E-02	rs2922200	3	126850552	q21.2
SNP_A-1699673	G	G	241	109	305	99	4.136	4.20E-02	rs1403037	3	193326139	q28
SNP_A-2216299	G	G	361	59	380	40	4.134	4.20E-02	rs34533	12	96560222	q23.1
SNP_A-2200983	C	C	322	34	339	57	4.134	4.20E-02	rs7547288	1	47678312	p33
SNP_A-2185078	T	T	368	8	404	2	4.134	4.20E-02	rs7998658	13	29878547	q12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175427	G	A	204	188	225	183	4.136	4.20E-02	rs7328374	13	28039327	q12.3
SNP_A-2163864	A	A	304	58	356	44	4.134	4.20E-02	rs6781515	3	85546133	p12.1
SNP_A-2148417	C	C	263	137	291	111	4.136	4.20E-02	rs9549144	13	39749380	q14.11
SNP_A-2133019	T	T	362	0	348	4	4.137	4.20E-02	rs6029771	20	39731626	q12
SNP_A-2108519	A	A	328	38	349	63	4.134	4.20E-02	rs1335855	1	34317139	p34.3
SNP_A-2018300	G	G	266	80	333	69	4.137	4.20E-02	rs2254315	21	33649357	q22.11
SNP_A-2022662	T	T	248	108	290	90	4.137	4.20E-02	rs4908398	1	28360237	p35.3
SNP_A-2037168	A	C	192	176	226	184	4.134	4.20E-02	rs7961152	12	24872878	p12.1
SNP_A-2054807	G	G	231	131	231	177	4.137	4.20E-02	rs4963842	12	22727319	p12.1
SNP_A-2063236	A	A	290	46	339	33	4.137	4.20E-02	rs10493267	1	59770727	p32.1
SNP_A-2068962	A	A	293	75	301	109	4.135	4.20E-02	rs13301404	9	31647203	p21.1
SNP_A-2079185	C	C	294	72	345	57	4.136	4.20E-02	rs17175669	6	120044808	q22.31
SNP_A-2282147	T	T	378	18	340	30	4.133	4.20E-02	rs16968802	16	63861263	q21
SNP_A-2232003	G	G	313	55	329	85	4.136	4.20E-02	rs4324784	6	99369299	q16.2
SNP_A-2232312	A	A	282	122	256	150	4.134	4.20E-02	rs6828136	4	34926417	p15.1
SNP_A-2238425	A	A	251	111	257	155	4.136	4.20E-02	rs2849395	18	12034410	p11.21
SNP_A-2244646	C	C	324	12	385	5	4.137	4.20E-02	rs3751684	16	88190376	q24.3
SNP_A-2242716	T	T	283	85	286	120	4.136	4.20E-02	rs214439	6	9502075	p24.3
SNP_A-2300528	T	T	291	51	360	40	4.135	4.20E-02	rs17818796	22	19303226	q11.21
SNP_A-2289611	A	A	216	190	233	153	4.132	4.21E-02	rs899691	4	5872616	p16.2
SNP_A-2306451	T	T	370	52	344	72	4.13	4.21E-02	rs6667549	1	107717665	p13.3
SNP_A-2256076	T	T	288	82	341	67	4.13	4.21E-02	rs9788199	12	31912249	p11.21
SNP_A-2232130	T	T	335	11	380	4	4.132	4.21E-02	rs3899581	13	28476098	q12.3
SNP_A-2229259	A	C	208	158	203	199	4.13	4.21E-02	rs9643088	8	115451710	q23.3
SNP_A-2280904	A	G	220	190	216	188	4.131	4.21E-02	rs3109684	9	134837831	q34.3
SNP_A-2083685	G	G	184	174	235	165	4.132	4.21E-02	rs10889189	1	60737047	p31.3
SNP_A-2089390	T	T	347	75	320	98	4.132	4.21E-02	rs1858173	12	101130078	q23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2092343	A	A	261	103	270	146	4.13	4.21E-02	rs1370193	18	36512481	q12.3
SNP_A-2060855	G	G	317	51	374	38	4.132	4.21E-02	rs3860506	3	134026472	q22.1
SNP_A-2012991	G	A	180	136	188	182	4.132	4.21E-02	rs2707576	7	147076592	q35
SNP_A-2011047	G	G	278	88	339	75	4.129	4.21E-02	rs7731341	5	90559861	q14.3
SNP_A-2117478	G	G	250	172	276	142	4.132	4.21E-02	rs7875570	9	134764773	q34.3
SNP_A-2118405	C	C	328	90	346	66	4.13	4.21E-02	rs1458333	5	172323506	q35.1
SNP_A-2152964	G	G	313	55	372	42	4.132	4.21E-02	rs17680174	13	68801424	q21.33
SNP_A-2164051	T	T	335	47	320	68	4.132	4.21E-02	rs2955002	8	82771433	q21.13
SNP_A-2174969	T	T	259	147	233	177	4.132	4.21E-02	rs12541494	8	124498576	q24.13
SNP_A-2171048	T	T	347	75	320	98	4.132	4.21E-02	rs10215295	7	55098528	p11.2
SNP_A-2185653	A	A	343	25	359	13	4.133	4.21E-02	rs7180916	15	23781626	q12
SNP_A-2227345	C	C	307	61	323	93	4.132	4.21E-02	rs17278136	6	2649569	p25.2
SNP_A-1807867	G	G	359	43	366	26	4.131	4.21E-02	rs3905177	1	34614132	p34.3
SNP_A-1786202	T	T	282	120	303	93	4.132	4.21E-02	rs10898152	11	83098203	q14.1
SNP_A-1855182	C	C	314	56	366	42	4.13	4.21E-02	rs8092212	18	23668241	q12.1
SNP_A-1873571	G	G	307	73	305	103	4.13	4.21E-02	rs211436	6	133654685	q23.2
SNP_A-1830733	G	G	223	163	198	194	4.13	4.21E-02	rs11583756	1	4229423	p36.32
SNP_A-1973459	A	A	273	77	289	115	4.13	4.21E-02	rs9309947	3	84692693	p12.1
SNP_A-1980810	A	A	261	105	323	93	4.129	4.21E-02	rs6703594	1	201023419	q32.1
SNP_A-1949674	G	G	241	127	299	115	4.133	4.21E-02	rs6467475	7	132359056	q33
SNP_A-1900828	T	T	360	6	403	1	4.129	4.21E-02	rs1182658	9	19723645	p22.1
SNP_A-1901064	G	G	214	156	270	146	4.133	4.21E-02	rs2036936	18	34126301	q12.2
SNP_A-1894371	C	C	218	152	214	200	4.126	4.22E-02	rs9847400	3	190855699	q28

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1877358	C	C	303	67	359	53	4.127	4.22E-02	rs6460734	7	71403969	q11.22
SNP_A-1874738	C	C	208	150	204	198	4.126	4.22E-02	rs615577	11	30215565	p14.1
SNP_A-1905032	T	G	231	179	210	204	4.127	4.22E-02	rs2270133	17	58827057	q23.3
SNP_A-1924306	T	T	355	59	338	82	4.126	4.22E-02	rs4726863	7	146595183	q35
SNP_A-1981964	G	G	351	17	380	34	4.126	4.22E-02	rs1363933	5	66279477	q12.3
SNP_A-1834121	C	C	333	37	387	25	4.129	4.22E-02	rs4457887	13	82298113	q31.1
SNP_A-1843504	G	A	208	198	228	180	4.128	4.22E-02	rs9410414	9	88779411	q22.1
SNP_A-1819679	G	G	276	58	350	48	4.127	4.22E-02	rs10948423	6	4864499	p12.3
SNP_A-1817299	G	G	269	99	322	84	4.127	4.22E-02	rs2166280	4	32294737	p15.1
SNP_A-1865649	A	A	225	85	273	71	4.126	4.22E-02	rs1274381	10	92278646	q23.31
SNP_A-1797714	C	C	292	114	314	88	4.126	4.22E-02	rs35246	5	68048406	q13.1
SNP_A-1808754	G	G	286	60	343	47	4.129	4.22E-02	rs17097735	14	30648513	q12
SNP_A-2206563	T	T	219	149	169	157	4.126	4.22E-02	rs3997653	6	42864450	p21.1
SNP_A-2185927	G	G	247	111	258	158	4.128	4.22E-02	rs261900	12	32354282	p11.21
SNP_A-2183983	T	C	170	162	210	162	4.127	4.22E-02	rs273438	9	79147923	q21.31
SNP_A-2189450	T	T	342	6	377	17	4.129	4.22E-02	rs4236451	7	152338869	q36.2
SNP_A-2180080	C	C	190	162	250	158	4.128	4.22E-02	rs6793160	3	171017968	q26.2
SNP_A-2143550	A	A	284	36	305	61	4.126	4.22E-02	rs12526812	6	12871825	p24.1
SNP_A-2129823	A	G	199	173	208	178	4.128	4.22E-02	rs1587423	3	25144351	p24.2
SNP_A-2008860	G	G	201	169	251	157	4.126	4.22E-02	rs4680987	3	78594205	p12.3
SNP_A-2008847	C	C	304	48	330	32	4.127	4.22E-02	rs4856024	3	76046376	p12.3
SNP_A-2038552	C	C	273	87	284	126	4.129	4.22E-02	rs11020836	11	93948540	q21
SNP_A-2030408	A	A	221	113	298	110	4.125	4.22E-02	rs2164560	9	104786908	q31.1
SNP_A-2057605	G	G	199	161	255	153	4.127	4.22E-02	rs1428848	16	75919039	q23.1
SNP_A-2056340	G	G	235	143	275	123	4.128	4.22E-02	rs525928	6	143163270	q24.2
SNP_A-2050558	C	C	210	186	236	156	4.127	4.22E-02	rs7260675	20	45753145	q13.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2066842	C	A	233	177	207	205	4.129	4.22E-02	rs2478419	10	122250868	q26.12
SNP_A-2098020	G	G	262	106	321	93	4.128	4.22E-02	rs12605583	18	50988951	q21.2
SNP_A-2099638	C	C	381	41	395	25	4.127	4.22E-02	rs3760775	19	5792356	p13.3
SNP_A-2088620	C	C	289	77	301	113	4.127	4.22E-02	rs8043433	15	59820734	q22.2
SNP_A-2287397	T	T	273	135	250	166	4.127	4.22E-02	rs10071163	5	58445030	q11.2
SNP_A-2276311	C	C	344	74	341	49	4.129	4.22E-02	rs2053854	15	70911544	q24.1
SNP_A-2273158	G	G	401	3	378	10	4.127	4.22E-02	rs16928441	12	191614	p13.33
SNP_A-2268919	C	C	291	131	316	104	4.127	4.22E-02	rs208586	16	22888135	p12.1
SNP_A-2263257	A	A	350	36	376	22	4.128	4.22E-02	rs707915	6	31818947	p21.33
SNP_A-2228758	T	T	304	58	363	45	4.126	4.22E-02	rs7727099	5	22535261	p14.3
SNP_A-2228759	C	C	375	47	348	66	4.127	4.22E-02	rs11209151	1	67950955	p31.2
SNP_A-2239984	A	A	305	113	327	87	4.127	4.22E-02	rs10826259	10	60394488	q21.1
SNP_A-2247306	T	T	366	22	387	11	4.126	4.22E-02	rs11715069	3	61896985	p14.2
SNP_A-2305067	T	T	250	110	307	97	4.129	4.22E-02	rs4470706	4	115546105	q26
SNP_A-2299535	C	C	327	41	342	66	4.127	4.22E-02	rs17574227	9	119264126	q33.1
SNP_A-2248542	C	C	185	177	236	168	4.122	4.23E-02	rs265899	5	116915922	q23.1
SNP_A-2239536	C	C	351	71	326	94	4.125	4.23E-02	rs6499628	16	52161678	q12.2
SNP_A-2237590	T	T	400	4	390	12	4.122	4.23E-02	rs17103762	14	35538623	q13.2
SNP_A-2282979	T	T	320	62	290	82	4.121	4.23E-02	rs9932978	16	7819681	p13.2
SNP_A-2106405	C	C	390	4	404	0	4.122	4.23E-02	rs6577553	1	9131727	p36.22
SNP_A-2094208	G	G	266	138	287	109	4.123	4.23E-02	rs6546375	2	68479340	p14
SNP_A-2064468	A	A	234	60	256	96	4.121	4.23E-02	rs11256954	10	6220995	p15.1
SNP_A-2065713	C	C	187	169	229	153	4.125	4.23E-02	rs11683924	2	159993119	q24.2
SNP_A-2054488	T	T	377	17	369	31	4.124	4.23E-02	rs17828842	5	64886234	q12.3
SNP_A-2060474	A	A	404	0	390	4	4.122	4.23E-02	rs692885	15	47836718	q21.2
SNP_A-1989595	C	C	336	32	395	21	4.122	4.23E-02	rs3734953	7	37763462	p14.1
SNP_A-1992427	C	C	326	90	286	110	4.124	4.23E-02	rs17580758	8	15957345	p22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134102	G	G	390	4	404	0	4.122	4.23E-02	rs7864955	9	87254281	q21.33
SNP_A-2117403	C	C	280	88	333	73	4.124	4.23E-02	rs7193482	16	57271723	q21
SNP_A-2145657	G	G	311	55	354	40	4.123	4.23E-02	rs791656	9	12481250	p23
SNP_A-2181470	G	G	330	40	388	28	4.125	4.23E-02	rs1884133	22	26185519	q12.1
SNP_A-2176472	C	C	259	97	324	86	4.122	4.23E-02	rs999189	4	125180591	q28.1
SNP_A-2200753	C	C	232	116	222	152	4.125	4.23E-02	rs11049465	12	28256286	p11.22
SNP_A-1807571	C	C	219	195	241	161	4.124	4.23E-02	rs1438928	10	50713792	q11.23
SNP_A-1782110	A	A	237	175	209	205	4.121	4.23E-02	rs3849220	9	135707574	q34.3
SNP_A-1817148	C	C	290	80	297	115	4.122	4.23E-02	rs709389	5	98357615	q21.1
SNP_A-1816108	T	T	264	104	320	90	4.125	4.23E-02	rs17608359	14	40786307	q21.1
SNP_A-1844291	G	G	214	154	270	144	4.123	4.23E-02	rs6548846	3	82855528	p12.2
SNP_A-1838854	G	G	257	65	262	96	4.123	4.23E-02	rs4805207	19	42365573	q13.12
SNP_A-1966987	G	G	334	36	354	60	4.125	4.23E-02	rs10498074	2	220959784	q35
SNP_A-1949906	A	A	412	2	376	8	4.123	4.23E-02	rs10927191	1	240805728	q44
SNP_A-1937625	G	G	366	48	344	68	4.125	4.23E-02	rs17636048	9	119251655	q33.1
SNP_A-1946192	G	G	227	195	255	165	4.122	4.23E-02	rs557352	9	76554295	q21.2
SNP_A-1920741	-	T	182	182	236	176	4.123	4.23E-02	rs161881	12	124412527	q24.31
SNP_A-1911194	G	G	330	40	388	28	4.125	4.23E-02	rs1380251	1	217957570	q41
SNP_A-1912373	A	A	341	13	355	27	4.122	4.23E-02	rs3747961	1	94170442	p22.1
SNP_A-1874432	T	T	269	41	275	65	4.124	4.23E-02	rs7946299	11	116093059	q23.3
SNP_A-1876224	C	C	362	2	377	9	4.117	0.0424	rs4289807	8	34266892	p12
SNP_A-1879250	A	A	398	24	408	12	4.119	0.0424	rs7586119	2	26724877	p23.3
SNP_A-1881573	G	G	321	43	381	31	4.121	0.0424	rs2844615	6	31350938	p21.33
SNP_A-1887196	G	G	396	4	410	0	4.12	0.0424	rs7748724	6	7618834	p24.3
SNP_A-1901285	G	G	404	4	418	0	4.118	0.0424	rs4310111	7	2772052	p22.2
SNP_A-1902593	T	T	262	108	261	147	4.12	0.0424	rs7619900	3	192369380	q28
SNP_A-1909181	T	T	242	128	300	116	4.119	0.0424	rs10889961	1	41524267	p34.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1931376	T	T	300	28	303	47	4.119	0.0424	rs17086087	18	68287558	q22.3
SNP_A-1931716	C	C	266	104	267	143	4.119	0.0424	rs1942452	18	68723503	q22.3
SNP_A-1933048	C	C	420	0	406	4	4.117	0.0424	rs1551366	18	13359574	p11.21
SNP_A-1934697	T	T	367	41	322	56	4.12	0.0424	rs3138373	3	130631719	q21.3
SNP_A-1972612	T	T	301	59	319	91	4.12	0.0424	rs2131108	3	49640394	p21.31
SNP_A-1842183	G	G	322	82	354	62	4.118	0.0424	rs11899367	2	134627988	q21.2
SNP_A-1821891	G	G	334	28	362	50	4.119	0.0424	rs11115584	12	81994913	q21.31
SNP_A-1871864	T	T	301	33	325	57	4.121	0.0424	rs2058778	12	106464585	q23.3
SNP_A-1869423	G	G	228	94	290	84	4.121	0.0424	rs11786599	8	88353885	q21.3
SNP_A-1850929	T	T	339	23	369	43	4.119	0.0424	rs17121245	13	112232598	q34
SNP_A-1720983	G	G	236	162	274	140	4.12	0.0424	rs7127214	11	36308002	p13
SNP_A-1693507	T	T	200	96	207	139	4.119	0.0424	rs953380	4	46841355	p12
SNP_A-1811484	A	A	408	0	394	4	4.121	0.0424	rs16967099	15	36685468	q14
SNP_A-1793859	A	A	414	4	404	12	4.117	0.0424	rs2289875	16	27670611	p11.2
SNP_A-1786932	G	G	277	53	304	86	4.118	0.0424	rs2305130	5	114550120	q22.3
SNP_A-2222452	A	C	185	183	237	179	4.118	0.0424	rs10903532	10	1680721	p15.3
SNP_A-2220208	A	A	359	43	343	63	4.119	0.0424	rs16876542	4	24676275	p15.2
SNP_A-2185076	C	C	398	12	408	4	4.119	0.0424	rs2165303	1	41897112	p34.2
SNP_A-2152079	G	G	326	94	296	118	4.121	0.0424	rs4254565	20	1608099	p13
SNP_A-2154961	C	C	398	24	408	12	4.119	0.0424	rs1549504	12	106301450	q23.3
SNP_A-2156745	A	A	257	159	227	187	4.121	0.0424	rs6768747	3	73016009	p13
SNP_A-2156848	G	G	242	128	300	116	4.119	0.0424	rs12041455	1	41526641	p34.2
SNP_A-2116079	G	G	404	4	418	0	4.118	0.0424	rs2274930	13	41047812	q14.11
SNP_A-2017452	G	G	216	204	243	173	4.118	0.0424	rs2831705	21	28627373	q21.3
SNP_A-2031774	G	G	342	22	367	41	4.117	0.0424	rs1360609	13	103066944	q33.1
SNP_A-2036188	A	A	311	37	374	26	4.12	0.0424	rs1959650	14	19618933	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2093060	G	G	418	0	404	4	4.118	0.0424	rs16954997	15	27122593	q13.1
SNP_A-2104610	C	C	418	0	404	4	4.118	0.0424	rs248049	5	126517220	q23.2
SNP_A-2079038	T	T	367	13	397	5	4.118	0.0424	rs7340726	3	110821351	q13.13
SNP_A-2274651	T	T	201	167	257	159	4.12	0.0424	rs568675	6	128027478	q22.33
SNP_A-2277799	A	A	406	4	420	0	4.117	0.0424	rs1541658	5	166683377	q34
SNP_A-2272353	G	G	266	104	271	145	4.12	0.0424	rs1983503	4	185210909	q35.1
SNP_A-2246824	C	C	227	143	284	132	4.12	0.0424	rs3733023	3	173833708	q26.31
SNP_A-2246301	G	G	227	141	280	128	4.118	0.0424	rs10960779	9	12748881	p23
SNP_A-2234465	C	C	339	31	396	20	4.115	4.25E-02	rs2726139	4	108926035	q25
SNP_A-2275578	A	A	309	61	363	47	4.114	4.25E-02	rs286850	7	153547868	q36.2
SNP_A-2305369	G	G	269	153	239	181	4.114	4.25E-02	rs1473491	15	91819005	q26.1
SNP_A-2078762	C	C	422	0	408	4	4.117	4.25E-02	rs885205	8	118168688	q24.11
SNP_A-2088584	C	C	376	22	397	11	4.114	4.25E-02	rs11061403	12	130248171	q24.33
SNP_A-2084917	A	A	192	160	245	151	4.114	4.25E-02	rs4697708	4	9797458	p16.1
SNP_A-2053739	T	T	311	111	280	136	4.114	4.25E-02	rs2036293	3	46071389	p21.31
SNP_A-2075574	C	C	385	23	387	11	4.117	4.25E-02	rs7191772	16	58124917	q21
SNP_A-2046758	C	C	325	31	380	20	4.116	4.25E-02	rs6931616	6	71918979	q13
SNP_A-2018170	C	C	323	41	381	29	4.116	4.25E-02	rs2833869	21	32833578	q22.11
SNP_A-2011090	T	T	197	173	249	163	4.117	4.25E-02	rs6880477	5	100684431	q21.1
SNP_A-2000135	G	G	239	109	240	150	4.116	4.25E-02	rs2489720	10	42240890	q11.21
SNP_A-2115775	T	T	366	26	341	41	4.114	4.25E-02	rs10092934	8	43194744	p11.21
SNP_A-2119265	T	T	339	31	396	20	4.115	4.25E-02	rs13039230	20	6309948	p12.3
SNP_A-2121938	T	T	296	120	270	148	4.115	4.25E-02	rs4692524	4	31276409	p15.1
SNP_A-2132994	C	C	422	0	408	4	4.117	4.25E-02	rs7418811	1	172739185	q25.1
SNP_A-2160854	A	A	300	60	359	47	4.114	4.25E-02	rs2061808	2	218085390	q35
SNP_A-2170275	A	A	344	18	367	35	4.114	4.25E-02	rs1021767	5	28270663	p14.1
SNP_A-2217439	T	T	262	102	324	90	4.113	4.25E-02	rs708055	6	6464136	p25.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215465	T	T	383	35	365	53	4.115	4.25E-02	rs7026201	9	132427352	q34.13
SNP_A-2222664	G	G	315	55	374	42	4.117	4.25E-02	rs5747133	22	16286693	q11.1
SNP_A-2223695	G	G	295	125	321	99	4.115	4.25E-02	rs11128174	3	66789116	p14.1
SNP_A-2206285	G	G	300	22	321	41	4.115	4.25E-02	rs3014288	1	223903511	q42.13
SNP_A-2208765	C	C	361	1	383	7	4.114	4.25E-02	rs7048350	9	102190310	q31.1
SNP_A-1717019	C	C	231	119	297	111	4.114	4.25E-02	rs1381948	4	89294345	q22.1
SNP_A-1737607	T	T	214	178	254	158	4.114	4.25E-02	rs9328169	6	3365837	p25.2
SNP_A-1869644	G	G	294	70	294	100	4.113	4.25E-02	rs2036347	5	84158672	q14.3
SNP_A-1865580	G	G	380	40	377	23	4.114	4.25E-02	rs10850879	12	116544865	q24.22
SNP_A-1861185	G	A	191	175	227	185	4.117	4.25E-02	rs2341938	1	237872792	q43
SNP_A-1816016	C	C	251	109	308	96	4.116	4.25E-02	rs4627591	2	105919332	q12.2
SNP_A-1827590	T	T	300	84	327	63	4.116	4.25E-02	rs1568539	2	120151623	q14.2
SNP_A-1837664	T	T	275	67	298	104	4.117	4.25E-02	rs10752011	10	5383936	p15.1
SNP_A-1969383	C	C	237	177	268	150	4.113	4.25E-02	rs2827012	21	22052389	q21.1
SNP_A-1975104	C	C	329	9	393	3	4.116	4.25E-02	rs2135444	3	162799308	q26.1
SNP_A-1923833	T	T	339	31	396	20	4.115	4.25E-02	rs2040708	4	108945375	q25
SNP_A-1894038	C	C	214	152	270	142	4.114	4.25E-02	rs944464	14	31523612	q12
SNP_A-1896324	C	C	363	1	385	7	4.116	4.25E-02	rs659228	9	125501771	q33.3
SNP_A-1880652	T	T	185	175	236	166	4.113	4.25E-02	rs4484568	7	72632302	q11.23
SNP_A-1923529	T	T	335	87	307	111	4.111	4.26E-02	rs17357618	3	62789812	p14.2
SNP_A-1910034	A	A	324	6	334	16	4.113	4.26E-02	rs1920164	1	95874304	p21.3
SNP_A-1975426	G	G	335	33	356	56	4.113	4.26E-02	rs6443457	3	178607412	q26.32
SNP_A-1973389	G	G	222	134	272	120	4.109	4.26E-02	rs6780379	3	80643215	p12.2
SNP_A-1982236	G	G	342	12	405	5	4.113	4.26E-02	rs10514114	5	78296414	q14.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1978479	A	A	359	1	381	7	4.112	4.26E-02	rs9994891	4	111149057	q25
SNP_A-1986452	G	G	354	58	311	75	4.111	4.26E-02	rs930323	1	221172525	q42.12
SNP_A-1819261	C	C	258	162	229	191	4.109	4.26E-02	rs2926304	2	30887709	p23.1
SNP_A-1864264	T	T	203	149	257	139	4.112	4.26E-02	rs1120669	10	91019996	q23.31
SNP_A-1873785	A	A	321	29	387	19	4.11	4.26E-02	rs609782	18	68369906	q22.3
SNP_A-1854652	A	A	264	102	323	89	4.11	4.26E-02	rs7847480	9	86607457	q21.33
SNP_A-1853469	A	A	281	85	342	72	4.111	4.26E-02	rs9477153	6	16630805	p22.3
SNP_A-1679550	T	T	329	21	367	41	4.112	4.26E-02	rs10519679	4	144770980	q31.21
SNP_A-1703999	C	C	304	46	373	35	4.112	4.26E-02	rs1156251	4	64304990	q13.1
SNP_A-1787156	G	G	346	74	355	51	4.111	4.26E-02	rs7927314	11	56065574	q11
SNP_A-1803868	T	T	199	149	264	146	4.112	4.26E-02	rs7726370	5	85872663	q14.3
SNP_A-2208812	C	C	318	46	380	34	4.111	4.26E-02	rs12607452	18	41182167	q12.3
SNP_A-2225414	T	T	358	24	391	13	4.112	4.26E-02	rs6872507	5	135238694	q31.1
SNP_A-2217905	C	C	215	133	270	122	4.11	4.26E-02	rs2272265	7	55169149	p11.2
SNP_A-2171032	G	G	351	19	406	10	4.111	4.26E-02	rs17053752	6	100175327	q16.3
SNP_A-2177222	A	A	328	94	298	118	4.112	4.26E-02	rs7928968	11	2006875	p15.5
SNP_A-2156135	A	A	365	15	380	6	4.112	4.26E-02	rs1885444	14	50338872	q22.1
SNP_A-2164303	G	G	340	24	394	14	4.11	4.26E-02	rs7295430	12	87153679	q21.32
SNP_A-2166166	G	G	227	141	284	130	4.113	4.26E-02	rs9960523	18	9446982	p11.22
SNP_A-2138637	C	C	329	27	352	48	4.11	4.26E-02	rs2208166	6	87602887	q15
SNP_A-2137957	C	C	337	23	367	43	4.11	4.26E-02	rs581459	1	36044203	p34.3
SNP_A-2137645	T	T	318	46	380	34	4.111	4.26E-02	rs2118181	15	46703176	q21.1
SNP_A-2124831	C	C	284	82	292	118	4.109	4.26E-02	rs12332295	5	95743959	q15
SNP_A-2002102	G	G	219	179	252	154	4.11	4.26E-02	rs4344385	10	68073129	q21.3
SNP_A-2003128	C	C	348	46	318	64	4.112	4.26E-02	rs274132	1	36251071	p34.3
SNP_A-1995567	C	C	349	51	335	73	4.111	4.26E-02	rs7920524	10	12559581	p13
SNP_A-2008828	T	T	351	19	406	10	4.111	4.26E-02	rs4677259	3	73456561	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2042056	C	C	315	53	330	82	4.109	4.26E-02	rs981017	13	84761599	q31.1
SNP_A-2022481	C	C	230	136	260	112	4.111	4.26E-02	rs7817681	8	69052246	q13.2
SNP_A-2060670	C	C	252	114	312	102	4.111	4.26E-02	rs7582526	2	82308643	p12
SNP_A-2101547	T	C	209	171	205	187	4.111	4.26E-02	rs7753394	6	138126941	q23.3
SNP_A-2293050	G	G	322	92	350	70	4.111	4.26E-02	rs6598529	15	96933404	q26.3
SNP_A-2278743	T	T	246	124	245	167	4.112	4.26E-02	rs1555145	20	11952113	p12.1
SNP_A-2271911	G	A	194	176	228	188	4.109	4.26E-02	rs11042702	11	10244564	p15.4
SNP_A-2270193	G	G	327	67	320	94	4.111	4.26E-02	rs4531090	8	64549661	q12.3
SNP_A-2259899	C	C	355	3	373	11	4.11	4.26E-02	rs17034982	4	157905142	q32.1
SNP_A-2239358	C	C	272	148	241	175	4.111	4.26E-02	rs6705746	2	214503846	q34
SNP_A-2242969	C	C	194	176	248	168	4.105	4.27E-02	rs2037370	3	182069187	q26.33
SNP_A-2255021	G	G	278	82	283	117	4.106	4.27E-02	rs9538172	13	58188021	q21.1
SNP_A-2276035	G	G	352	62	333	85	4.107	4.27E-02	rs17265116	9	31620372	p21.1
SNP_A-2304603	G	G	352	6	389	17	4.109	4.27E-02	rs1861269	2	201952444	q33.1
SNP_A-2303899	A	A	281	129	247	153	4.109	4.27E-02	rs1080026	20	42846612	q13.12
SNP_A-2306821	A	A	285	79	346	66	4.109	4.27E-02	rs2306703	4	186953678	q35.1
SNP_A-2309447	G	G	366	42	382	26	4.107	4.27E-02	rs214544	6	18392695	p22.3
SNP_A-2092548	A	A	321	13	348	28	4.107	4.27E-02	rs1458491	9	73650648	q21.13
SNP_A-2085172	G	G	401	9	398	20	4.107	4.27E-02	rs7920034	10	6831198	p14
SNP_A-2059369	T	T	291	39	281	59	4.108	4.27E-02	rs10830715	11	90701357	q14.3
SNP_A-2052461	T	T	285	123	224	132	4.108	4.27E-02	rs1854448	9	117507038	q33.1
SNP_A-2074225	T	T	342	28	363	49	4.109	4.27E-02	rs16823186	3	115950619	q13.31
SNP_A-2074741	G	G	244	172	216	202	4.106	4.27E-02	rs4953394	2	46635829	p21
SNP_A-2026385	G	G	223	145	281	135	4.108	4.27E-02	rs7589111	2	132004620	q21.1
SNP_A-2023383	G	G	232	132	232	178	4.106	4.27E-02	rs6016963	20	41186657	q13.11
SNP_A-2044454	C	C	253	165	224	194	4.106	4.27E-02	rs6683156	1	3789598	p36.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2127026	T	T	197	171	249	161	4.109	4.27E-02	rs1991152	2	52535471	p16.3
SNP_A-2132556	A	A	374	34	394	20	4.107	4.27E-02	rs17089667	13	54045854	q14.3
SNP_A-2115155	G	G	412	10	399	21	4.107	4.27E-02	rs11651978	17	5965727	p13.2
SNP_A-2148734	T	T	367	55	344	76	4.106	4.27E-02	rs11641284	16	6714697	p13.2
SNP_A-2162846	C	C	279	55	285	83	4.108	4.27E-02	rs347181	7	145732604	q35
SNP_A-2153208	G	G	323	43	383	31	4.107	4.27E-02	rs9398455	6	98122073	q16.1
SNP_A-2159283	A	A	225	127	215	165	4.107	4.27E-02	rs6065482	20	40515646	q12
SNP_A-2196891	A	A	225	135	221	179	4.108	4.27E-02	rs12645681	4	162381769	q32.2
SNP_A-2225810	C	A	195	157	204	188	4.108	4.27E-02	rs1155422	4	156766278	q32.1
SNP_A-2202821	T	T	403	9	400	20	4.107	4.27E-02	rs17140230	7	66224203	q11.21
SNP_A-1804389	C	C	351	51	327	71	4.108	4.27E-02	rs7093269	10	3448842	p15.2
SNP_A-1808561	C	C	345	77	363	55	4.105	4.27E-02	rs17208578	15	65004801	q22.33
SNP_A-1685612	C	C	261	141	239	173	4.107	4.27E-02	rs699848	1	74443984	p31.1
SNP_A-1858072	C	C	343	27	359	47	4.109	4.27E-02	rs17792120	17	66183907	q24.3
SNP_A-1830880	C	C	225	127	222	170	4.107	4.27E-02	rs12189145	5	71554240	q13.2
SNP_A-1979568	A	A	290	66	303	99	4.109	4.27E-02	rs1490538	4	158939024	q32.1
SNP_A-1966609	T	T	239	97	303	87	4.107	4.27E-02	rs1559027	2	207414255	q33.3
SNP_A-1966401	A	A	227	125	273	109	4.107	4.27E-02	rs6434895	2	197654157	q33.1
SNP_A-1966058	G	G	281	87	288	124	4.105	4.27E-02	rs3942366	2	180112662	q31.2
SNP_A-1950066	G	G	321	47	341	75	4.107	4.27E-02	rs1420316	16	51602642	q12.2
SNP_A-1961313	A	A	337	45	359	29	4.108	4.27E-02	rs17129533	1	67119155	p31.2
SNP_A-1960028	A	A	268	98	324	84	4.107	4.27E-02	rs17677071	3	7816254	p26.1
SNP_A-1910364	A	A	366	44	331	61	4.108	4.27E-02	rs17564100	5	169795225	q35.1
SNP_A-1905104	T	T	292	20	368	12	4.109	4.27E-02	rs6492183	13	108780841	q33.3
SNP_A-1907411	G	A	184	166	213	175	4.108	4.27E-02	rs941695	20	58794076	q13.33
SNP_A-1877419	A	A	277	87	325	71	4.107	4.27E-02	rs1993110	10	102067915	q24.31
SNP_A-1886382	G	G	398	16	381	29	4.107	4.27E-02	rs753314	1	34324561	p34.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884823	G	G	200	146	231	123	4.105	4.27E-02	rs932717	13	30557791	q12.3
SNP_A-1882667	G	G	392	4	404	0	4.101	4.28E-02	rs1011112	18	41868683	q21.1
SNP_A-1879921	A	A	355	63	331	85	4.105	4.28E-02	rs7794679	7	92203999	q21.2
SNP_A-1955291	G	G	316	48	334	76	4.102	4.28E-02	rs2403054	12	81902512	q21.31
SNP_A-1934660	T	T	259	35	332	26	4.102	4.28E-02	rs17011893	4	87707284	q21.3
SNP_A-1938487	T	C	228	172	188	186	4.103	4.28E-02	rs1418323	10	30464672	p11.23
SNP_A-1939349	G	G	359	63	375	43	4.103	4.28E-02	rs4728160	7	128451123	q32.1
SNP_A-1945545	G	G	324	94	297	119	4.103	4.28E-02	rs7912259	10	7012861	p14
SNP_A-1943908	C	C	300	48	369	37	4.103	4.28E-02	rs17151071	8	9994082	p23.1
SNP_A-1979127	G	G	359	7	380	18	4.104	4.28E-02	rs17050546	4	139892603	q31.1
SNP_A-1986702	A	A	336	24	362	44	4.103	4.28E-02	rs10944025	6	85371590	q14.3
SNP_A-1842490	A	A	318	98	332	72	4.103	4.28E-02	rs2218500	1	72666662	p31.1
SNP_A-1853367	C	C	237	133	237	179	4.104	4.28E-02	rs2526747	3	50057918	p21.31
SNP_A-1851604	C	C	282	56	302	88	4.103	4.28E-02	rs17025133	12	94955864	q23.1
SNP_A-1869344	G	G	212	160	234	130	4.102	4.28E-02	rs11677035	2	5446561	p25.2
SNP_A-1704837	A	A	360	6	401	1	4.102	4.28E-02	rs1376835	14	39440105	q21.1
SNP_A-1643768	C	C	349	53	338	76	4.101	4.28E-02	rs9303490	17	64454072	q24.1
SNP_A-1661169	C	C	239	143	275	121	4.104	4.28E-02	rs10501199	11	38437691	p12
SNP_A-1658262	G	G	298	52	313	81	4.104	4.28E-02	rs2282038	9	468530	p24.3
SNP_A-1737896	C	C	281	37	300	62	4.105	4.28E-02	rs10497477	2	179053721	q31.2
SNP_A-1800066	T	A	189	173	228	186	4.102	4.28E-02	rs6862877	5	33059984	p13.3
SNP_A-2225280	A	A	328	76	339	53	4.102	4.28E-02	rs13361997	5	140843858	q31.3
SNP_A-2183531	G	G	255	119	226	144	4.103	4.28E-02	rs809097	3	59966696	p14.2
SNP_A-2148013	G	G	352	70	324	92	4.105	4.28E-02	rs1404889	7	53034619	p12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138328	G	A	212	204	231	181	4.102	4.28E-02	rs11977660	7	54936545	p11.2
SNP_A-2112115	C	C	222	140	280	130	4.103	4.28E-02	rs4869277	5	95641407	q15
SNP_A-2110533	T	T	264	104	323	91	4.105	4.28E-02	rs11252550	10	4502899	p15.1
SNP_A-2010510	-	T	183	183	237	177	4.105	4.28E-02	rs753359	4	186602681	q35.1
SNP_A-1992870	A	A	264	104	323	91	4.105	4.28E-02	rs17471230	8	29514956	p12
SNP_A-2068881	A	A	277	77	341	65	4.103	4.28E-02	---	3	174683883	q26.31
SNP_A-2055473	C	C	326	16	311	29	4.103	4.28E-02	rs9376835	6	145024814	q24.2
SNP_A-2088960	A	A	386	22	407	11	4.102	4.28E-02	rs9315024	13	30136546	q12.3
SNP_A-2091804	G	G	330	82	357	61	4.102	4.28E-02	rs7665617	4	124558801	q28.1
SNP_A-2091183	T	T	336	56	374	40	4.103	4.28E-02	rs10103716	8	72207410	q13.3
SNP_A-2260817	C	C	376	32	348	48	4.105	4.28E-02	rs4383094	15	79482027	q25.1
SNP_A-2235003	A	A	359	53	338	74	4.105	4.28E-02	rs4936336	11	110514584	q23.1
SNP_A-2235601	C	C	322	38	343	63	4.104	4.28E-02	rs17386534	13	103886721	q33.2
SNP_A-2230996	A	A	370	52	386	34	4.101	4.28E-02	rs6905117	6	41198227	p21.1
SNP_A-2248533	C	C	378	42	357	61	4.1	4.29E-02	rs12154200	6	40914908	p21.1
SNP_A-2260556	A	A	349	19	379	37	4.099	4.29E-02	rs3798751	6	11050950	p24.2
SNP_A-2261415	C	C	353	15	409	7	4.101	4.29E-02	rs7334027	13	96003976	q32.1
SNP_A-2260921	G	G	349	19	379	37	4.099	4.29E-02	rs12360242	10	132542494	q26.3
SNP_A-2272085	A	A	404	4	416	0	4.098	4.29E-02	rs6430874	2	132177071	q21.1
SNP_A-2276539	G	G	412	0	400	4	4.099	4.29E-02	rs17164343	7	142726099	q34
SNP_A-2277621	C	C	402	6	387	15	4.098	4.29E-02	rs4927234	1	48096816	p33
SNP_A-2284525	A	A	269	89	274	126	4.099	4.29E-02	rs17234869	2	156457151	q24.1
SNP_A-2292571	A	A	207	151	265	143	4.099	4.29E-02	rs7897642	10	10486715	p14
SNP_A-2290640	T	T	240	108	226	140	4.098	4.29E-02	rs9346456	6	63218825	q11.1
SNP_A-2088608	A	A	318	42	376	30	4.1	4.29E-02	rs2199458	4	88848895	q22.1
SNP_A-2080256	C	C	404	4	416	0	4.098	4.29E-02	rs7237964	18	25802597	q12.1
SNP_A-2092241	A	A	406	4	418	0	4.098	4.29E-02	rs7133408	12	13779460	p13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2061538	C	C	353	15	409	7	4.101	4.29E-02	rs1542364	12	53499968	q13.2
SNP_A-2074486	A	A	258	76	271	113	4.101	4.29E-02	---	16	75742532	q23.1
SNP_A-2005217	A	A	321	37	360	24	4.098	4.29E-02	rs10509904	10	111581759	q25.1
SNP_A-2026582	A	A	252	112	309	99	4.098	4.29E-02	rs10164177	18	63111650	q22.1
SNP_A-2031355	A	A	355	55	342	78	4.1	4.29E-02	rs2637333	10	28108621	p12.1
SNP_A-2108320	C	C	314	54	332	84	4.1	4.29E-02	rs17733502	5	168192959	q34
SNP_A-2135497	C	C	228	142	285	131	4.098	4.29E-02	rs9361003	6	76993550	q14.1
SNP_A-2124106	C	C	404	4	416	0	4.098	4.29E-02	rs543459	18	294139	p11.32
SNP_A-2129533	T	T	316	10	398	4	4.099	4.29E-02	rs12316084	12	78559603	q21.2
SNP_A-2144321	T	T	348	18	362	8	4.101	4.29E-02	rs4485305	15	90615950	q26.1
SNP_A-2146812	C	T	208	160	209	203	4.099	4.29E-02	rs6858558	4	70150303	q13.2
SNP_A-2150568	G	G	313	57	327	87	4.1	4.29E-02	rs17538164	10	69645683	q21.3
SNP_A-2161499	A	A	392	20	348	32	4.099	4.29E-02	rs522233	6	24107350	p22.2
SNP_A-2164948	G	G	281	87	342	74	4.099	4.29E-02	rs3748059	6	6845950	p25.1
SNP_A-2188062	A	A	394	26	393	13	4.098	4.29E-02	rs17041907	3	16144632	p25.1
SNP_A-2195739	A	A	343	25	401	15	4.098	4.29E-02	rs6799873	3	181934581	q26.33
SNP_A-2180973	T	T	406	4	418	0	4.098	4.29E-02	rs1251542	1	76152244	p31.1
SNP_A-2188699	G	G	335	23	365	43	4.1	4.29E-02	rs17250294	5	53269902	q11.2
SNP_A-2225507	T	T	420	0	408	4	4.097	4.29E-02	rs2545818	19	11784061	p13.2
SNP_A-2225087	G	A	195	157	210	194	4.099	4.29E-02	rs1782509	11	30205402	p14.1
SNP_A-2213442	G	G	353	15	409	7	4.101	4.29E-02	rs4666488	2	19608777	p24.1
SNP_A-2211281	C	C	187	169	201	133	4.099	4.29E-02	---	3	189220779	q27.3
SNP_A-2212184	G	G	386	32	398	18	4.099	4.29E-02	rs2033385	14	44675568	q21.2
SNP_A-1787851	C	C	398	18	386	32	4.099	4.29E-02	rs11590973	1	41595745	p34.2
SNP_A-1853420	C	C	287	49	301	77	4.099	4.29E-02	---	5	11610234	p15.2
SNP_A-1844169	C	C	418	0	406	4	4.098	4.29E-02	rs6585054	10	113041856	q25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1831613	T	T	248	98	317	89	4.099	4.29E-02	rs758163	12	1829210	p13.33
SNP_A-1828745	G	G	345	41	350	64	4.099	4.29E-02	rs7954976	12	49968170	q13.13
SNP_A-1972528	A	A	357	63	333	85	4.1	4.29E-02	rs4419357	3	43261045	p22.1
SNP_A-1947086	C	C	412	0	400	4	4.099	4.29E-02	rs6586644	8	17666025	p22
SNP_A-1939621	G	G	394	4	406	0	4.101	4.29E-02	rs150947	14	69608139	q24.2
SNP_A-1935731	T	C	203	159	209	199	4.1	4.29E-02	rs4659485	1	233471959	q43
SNP_A-1876006	C	C	299	69	310	102	4.098	4.29E-02	rs12658994	5	90100540	q14.3
SNP_A-1902620	G	G	217	205	244	174	4.098	4.29E-02	rs7624493	3	99462205	q12.1
SNP_A-1903023	C	C	216	128	215	173	4.1	4.29E-02	rs11599217	10	128556954	q26.2
SNP_A-1921069	T	T	367	51	381	33	4.1	4.29E-02	rs3103261	2	232819079	q37.1
SNP_A-1919279	T	T	303	61	297	87	4.096	4.30E-02	rs1018338	11	20700813	p15.1
SNP_A-1899330	G	G	303	115	276	142	4.096	4.30E-02	rs17388568	4	123686967	q27
SNP_A-1972837	T	T	291	61	299	91	4.094	4.30E-02	rs2856056	3	60600141	p14.2
SNP_A-1984155	G	G	353	65	332	88	4.097	4.30E-02	rs977776	5	154875106	q33.2
SNP_A-1978383	T	T	322	36	385	25	4.095	4.30E-02	rs17036506	4	107313531	q24
SNP_A-1828701	A	A	256	92	313	79	4.097	4.30E-02	rs4947376	7	51471327	p12.1
SNP_A-1826657	T	T	268	120	308	100	4.096	4.30E-02	---	8	87475660	q21.3
SNP_A-1839018	T	T	343	3	361	11	4.096	4.30E-02	rs1454377	2	33352052	p22.3
SNP_A-1808456	C	C	289	33	342	22	4.096	4.30E-02	rs235469	1	168250067	q24.3
SNP_A-1720497	T	T	289	51	349	39	4.096	4.30E-02	rs369910	6	92326085	q15
SNP_A-1784255	C	C	305	65	317	97	4.096	4.30E-02	rs33065	5	115799892	q23.1
SNP_A-1784631	A	A	363	5	395	15	4.096	4.30E-02	rs16840538	1	5300582	p36.31
SNP_A-2207093	G	G	255	99	258	138	4.096	4.30E-02	rs6450825	5	31082513	p13.3
SNP_A-2181924	A	A	320	46	382	34	4.096	4.30E-02	rs2510831	8	107575308	q23.1
SNP_A-2188916	G	G	344	74	365	53	4.094	4.30E-02	rs9878446	3	60296336	p14.2
SNP_A-2190764	C	C	390	14	387	5	4.095	4.30E-02	rs11111835	12	102807968	q23.3
SNP_A-2163565	A	A	331	9	328	20	4.094	4.30E-02	rs8182342	17	56016345	q23.2
SNP_A-2151593	G	G	284	82	345	69	4.097	4.30E-02	rs10417204	19	42726562	q13.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2129644	A	A	263	75	288	116	4.097	4.30E-02	rs6786469	3	72956499	p13
SNP_A-2124457	T	T	259	151	270	116	4.097	4.30E-02	rs4301249	5	121240053	q23.1
SNP_A-2036539	T	T	247	175	273	145	4.094	4.30E-02	rs41205	16	47860812	q12.1
SNP_A-2034023	G	G	191	155	233	139	4.095	4.30E-02	rs9367936	6	17144007	p22.3
SNP_A-2069343	C	G	198	158	215	201	4.095	4.30E-02	rs1348291	13	87403722	q31.2
SNP_A-2083849	T	T	295	25	329	47	4.096	4.30E-02	rs1592728	2	50168163	p16.3
SNP_A-2084802	G	C	222	194	218	188	4.097	4.30E-02	rs1974551	17	65574164	q24.3
SNP_A-2087002	A	A	249	105	260	150	4.096	4.30E-02	rs7623033	3	180674523	q26.32
SNP_A-2297680	T	T	390	32	402	18	4.097	4.30E-02	rs2923300	1	105273366	p21.1
SNP_A-2285338	C	C	253	105	310	92	4.095	4.30E-02	rs7938360	11	111045085	q23.1
SNP_A-2285101	A	A	422	0	410	4	4.097	4.30E-02	rs10518904	15	55317767	q21.3
SNP_A-2243844	G	G	364	6	405	1	4.096	4.30E-02	rs4569513	2	716030	p25.3
SNP_A-2229677	A	A	308	46	368	34	4.094	4.30E-02	rs4368185	16	75087709	q23.1
SNP_A-2239228	G	G	239	131	237	175	4.091	4.31E-02	rs11627587	14	82602610	q31.2
SNP_A-2246760	G	G	333	21	396	12	4.093	4.31E-02	rs7782729	7	28722350	p15.1
SNP_A-2260955	A	A	220	130	278	120	4.092	4.31E-02	rs214214	1	48340887	p33
SNP_A-2299674	T	T	280	88	284	124	4.091	4.31E-02	rs16972780	15	79253034	q25.1
SNP_A-2305410	T	T	238	182	263	151	4.09	4.31E-02	rs7836489	8	21460484	p21.3
SNP_A-2069497	A	A	267	103	323	89	4.092	4.31E-02	rs7617735	3	88615805	p11.1
SNP_A-2076811	A	A	314	40	336	66	4.091	4.31E-02	rs17153076	7	105652349	q22.3
SNP_A-2076383	G	G	361	61	334	82	4.09	4.31E-02	rs1439494	18	34595317	q12.2
SNP_A-2031752	C	C	292	40	322	68	4.092	4.31E-02	rs536947	12	10023206	p13.31
SNP_A-1992957	C	C	401	19	385	33	4.09	4.31E-02	rs16879301	8	32359677	p12
SNP_A-1994856	C	C	309	61	322	92	4.092	4.31E-02	rs1485306	8	120079442	q24.12
SNP_A-2007251	T	T	265	105	324	92	4.09	4.31E-02	rs4815798	20	5286936	p12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017347	C	C	214	180	248	156	4.092	4.31E-02	rs9975519	21	27979599	q21.3
SNP_A-2132584	T	T	340	82	314	106	4.093	4.31E-02	rs1347590	16	55405430	q13
SNP_A-2139522	G	G	311	57	370	44	4.093	4.31E-02	rs12780184	10	58973201	q21.1
SNP_A-2196648	G	G	292	76	288	106	4.09	4.31E-02	rs12003074	9	307417	p24.3
SNP_A-2194511	A	A	328	32	385	21	4.092	4.31E-02	rs618043	1	58664242	p32.2
SNP_A-2177680	C	C	308	54	313	81	4.093	4.31E-02	rs13317233	3	163806997	q26.1
SNP_A-2209486	A	A	202	166	258	158	4.091	4.31E-02	rs4075065	4	123041511	q27
SNP_A-2212644	C	C	367	53	346	74	4.091	4.31E-02	rs2224417	14	57374033	q23.1
SNP_A-2212577	A	A	278	74	292	110	4.09	4.31E-02	---	2	202693028	q33.1
SNP_A-2214360	C	C	280	72	293	107	4.091	4.31E-02	rs12263957	10	91297762	q23.31
SNP_A-1681966	C	C	285	113	322	92	4.093	4.31E-02	rs446710	6	9088625	p24.3
SNP_A-1803452	C	C	271	73	288	110	4.09	4.31E-02	rs3814837	14	91261103	q32.12
SNP_A-1798271	G	G	325	43	385	31	4.093	4.31E-02	rs16949533	17	14283144	p12
SNP_A-1837473	T	T	224	132	225	179	4.09	4.31E-02	rs1060736	9	111205674	q31.3
SNP_A-1873738	T	T	202	130	196	172	4.091	4.31E-02	rs10192752	2	85837800	p11.2
SNP_A-1873230	A	A	286	32	350	22	4.091	4.31E-02	rs614952	5	41676552	p13.1
SNP_A-1972117	A	A	356	0	346	4	4.092	4.31E-02	---	3	25721244	p24.2
SNP_A-1955691	G	G	409	13	393	25	4.09	4.31E-02	rs11042656	11	10171031	p15.4
SNP_A-1895723	C	C	265	105	324	92	4.09	4.31E-02	rs2066557	13	49508271	q14.2
SNP_A-1901633	C	C	253	165	213	185	4.089	4.32E-02	rs10166480	2	125240929	q14.3
SNP_A-1909697	G	G	305	89	286	116	4.087	4.32E-02	rs9905568	17	46275078	q21.33
SNP_A-1955908	A	A	352	70	369	49	4.088	4.32E-02	rs32585	5	149182361	q32
SNP_A-1942012	A	A	287	79	348	66	4.087	4.32E-02	rs460698	19	6912182	p13.2
SNP_A-1968102	G	G	304	36	322	60	4.088	4.32E-02	rs962879	1	155113379	q23.1
SNP_A-1989294	G	G	298	112	329	89	4.088	4.32E-02	rs10486483	7	26665680	p15.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864746	G	G	256	128	296	108	4.088	4.32E-02	rs2071286	6	32287874	p21.32
SNP_A-1864913	C	C	320	98	287	121	4.089	4.32E-02	rs2472866	6	5391550	p25.1
SNP_A-1852567	G	A	208	160	207	201	4.088	4.32E-02	rs4494464	14	45575599	q21.2
SNP_A-1847305	G	G	274	62	280	92	4.089	4.32E-02	rs793538	3	108542413	q13.12
SNP_A-1840233	G	G	353	13	384	28	4.086	4.32E-02	rs7039851	9	24389969	p21.3
SNP_A-1842427	T	T	212	206	240	176	4.086	4.32E-02	rs10919096	1	158994928	q23.3
SNP_A-1827280	A	A	278	142	305	115	4.087	4.32E-02	rs10422843	19	33891629	q12
SNP_A-1819787	A	A	257	91	303	75	4.088	4.32E-02	rs920882	13	42745352	q14.11
SNP_A-1796549	G	G	414	2	380	8	4.086	4.32E-02	rs17595410	3	49293269	p21.31
SNP_A-1797088	G	G	216	140	208	182	4.088	4.32E-02	rs546460	11	88781154	q14.3
SNP_A-1802060	C	C	309	37	337	63	4.086	4.32E-02	rs4735518	8	99060895	q22.1
SNP_A-1813682	A	A	236	114	240	158	4.088	4.32E-02	rs11187382	10	95067543	q23.33
SNP_A-1708759	C	C	314	88	298	116	4.086	4.32E-02	rs1943282	11	58387354	q12.1
SNP_A-1701225	C	C	234	116	245	165	4.086	4.32E-02	rs921298	6	156446979	q25.3
SNP_A-2214556	T	G	201	159	210	198	4.087	4.32E-02	rs17700151	2	137266882	q21.3
SNP_A-2227058	T	T	334	88	306	112	4.086	4.32E-02	rs198035	16	61707014	q21
SNP_A-2207441	C	T	196	158	204	188	4.087	4.32E-02	rs4688689	3	50010546	p21.31
SNP_A-2205117	A	A	386	24	376	40	4.088	4.32E-02	rs12697351	5	35838184	p13.2
SNP_A-2179503	C	C	339	29	365	51	4.087	4.32E-02	rs9969217	7	98536089	q22.1
SNP_A-2194434	G	G	311	57	325	87	4.089	4.32E-02	rs1572349	1	80249238	p31.1
SNP_A-2149347	C	C	302	64	356	50	4.089	4.32E-02	rs6831071	4	113809641	q25
SNP_A-2119105	C	C	330	2	345	9	4.087	4.32E-02	rs16850299	1	173583592	q25.2
SNP_A-2116786	C	C	339	29	365	51	4.087	4.32E-02	rs7340497	2	20718805	p24.1
SNP_A-2117093	A	A	324	32	354	56	4.086	4.32E-02	rs12578874	12	81554306	q21.31
SNP_A-2058538	C	C	274	92	280	130	4.088	4.32E-02	rs11752615	6	84437379	q14.2
SNP_A-2054121	G	G	333	77	303	99	4.087	4.32E-02	rs11103023	9	134615898	q34.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2078089	T	T	299	121	269	147	4.088	4.32E-02	rs10848803	12	3093017	p13.33
SNP_A-2308239	C	C	268	152	237	179	4.086	4.32E-02	rs9836538	3	7362400	p26.1
SNP_A-2313239	A	A	290	66	300	98	4.087	4.32E-02	rs11245462	10	126687952	q26.13
SNP_A-2281556	G	G	337	9	401	3	4.089	4.32E-02	rs1474187	12	88684099	q21.33
SNP_A-2276936	A	A	170	162	221	155	4.088	4.32E-02	rs12354259	1	90848484	p22.2
SNP_A-2274580	C	C	289	77	350	64	4.083	4.33E-02	rs6746840	2	106390688	q12.2
SNP_A-2274806	A	A	317	47	337	75	4.084	4.33E-02	rs16909797	10	58360697	q21.1
SNP_A-2286110	T	T	320	24	362	46	4.084	4.33E-02	rs7927259	11	36000682	p13
SNP_A-2245240	G	G	322	34	353	59	4.083	4.33E-02	rs11080426	18	10483841	p11.22
SNP_A-2239355	C	C	374	6	415	1	4.082	4.33E-02	rs6935666	6	135070565	q23.2
SNP_A-2232182	C	C	334	34	353	57	4.083	4.33E-02	rs727702	15	67793290	q23
SNP_A-2231357	A	A	204	162	259	153	4.085	4.33E-02	rs316202	5	96488981	q15
SNP_A-2081639	C	C	245	123	243	165	4.082	4.33E-02	rs10785939	10	91878874	q23.31
SNP_A-2056922	T	T	289	69	271	93	4.085	4.33E-02	rs11219381	11	123351092	q24.1
SNP_A-2072815	A	A	255	163	225	191	4.085	4.33E-02	rs17384795	7	100719716	q22.1
SNP_A-2016725	C	C	225	191	255	163	4.085	4.33E-02	rs1783383	21	24435961	q21.2
SNP_A-2006258	G	G	320	46	337	73	4.084	4.33E-02	rs207413	2	31450931	p23.1
SNP_A-2030151	A	A	325	29	275	41	4.082	4.33E-02	rs7030438	9	71477608	q21.13
SNP_A-2023916	C	C	314	100	341	77	4.083	4.33E-02	rs17359272	8	35918090	p12
SNP_A-2040105	T	T	287	125	257	151	4.084	4.33E-02	rs11733277	4	31309772	p15.1
SNP_A-2142249	G	G	322	28	350	16	4.084	4.33E-02	rs12042301	1	118067235	p12
SNP_A-2143283	G	G	292	74	353	61	4.082	4.33E-02	rs701262	3	155107196	q25.2
SNP_A-2164084	C	C	266	102	325	89	4.083	4.33E-02	rs411236	6	166892504	q27
SNP_A-2192178	G	G	216	154	272	144	4.084	4.33E-02	rs9641113	7	92612314	q21.3
SNP_A-2176037	T	T	213	121	261	107	4.083	4.33E-02	rs1350091	15	92557833	q26.2
SNP_A-2202291	C	C	227	133	284	122	4.085	4.33E-02	rs7292844	22	26218051	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1675555	G	G	380	4	372	12	4.085	4.33E-02	rs10515466	5	134371383	q31.1
SNP_A-1737403	C	C	312	36	373	25	4.083	4.33E-02	rs9294899	6	72011900	q13
SNP_A-1742767	G	G	299	99	279	127	4.082	4.33E-02	rs652531	11	97507483	q22.1
SNP_A-1821494	C	C	352	6	391	1	4.086	4.33E-02	rs10768611	11	5129362	p15.4
SNP_A-1830232	T	T	295	55	322	88	4.086	4.33E-02	rs259127	5	79094398	q14.1
SNP_A-1986939	C	C	322	34	353	59	4.083	4.33E-02	rs587041	6	96516095	q16.1
SNP_A-1962286	T	T	396	0	386	4	4.082	4.33E-02	rs2203534	2	17078132	p24.2
SNP_A-1973414	G	G	342	20	401	11	4.085	4.33E-02	rs998206	3	81804701	p12.2
SNP_A-1925975	G	A	226	186	216	198	4.083	4.33E-02	rs624319	6	160743311	q25.3
SNP_A-1886994	-	T	207	207	236	178	4.083	4.33E-02	rs6757796	2	125060416	q14.3
SNP_A-1904390	G	G	354	16	378	32	4.08	4.34E-02	rs11248555	10	125246563	q26.13
SNP_A-1897807	T	T	404	4	414	0	4.079	4.34E-02	rs8058702	16	69359737	q22.1
SNP_A-1924242	C	C	331	27	393	17	4.08	4.34E-02	---	4	103131316	q24
SNP_A-1963632	C	C	330	38	384	26	4.079	4.34E-02	rs6741192	2	67460925	p14
SNP_A-1984746	C	C	331	91	349	67	4.079	4.34E-02	rs10381143	5	180146484	q35.3
SNP_A-1985932	T	A	209	161	211	205	4.081	4.34E-02	rs9296538	6	47302408	p12.3
SNP_A-1947832	T	T	330	38	384	26	4.079	4.34E-02	rs16911966	9	27897621	p21.2
SNP_A-1944738	T	T	396	4	388	12	4.082	4.34E-02	rs16905635	9	22076883	p21.3
SNP_A-1944499	T	T	375	31	400	18	4.082	4.34E-02	rs4236625	7	127477646	q32.1
SNP_A-1818075	A	A	296	126	319	99	4.081	4.34E-02	rs7409138	19	23156405	p12
SNP_A-1824742	C	C	416	0	406	4	4.078	4.34E-02	rs7105044	11	122110819	q24.1
SNP_A-1848481	C	C	337	11	352	24	4.078	4.34E-02	rs2938236	8	3275090	p23.2
SNP_A-1852937	G	G	386	28	397	15	4.08	4.34E-02	rs7915333	10	49143941	q11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1862883	A	A	344	30	306	44	4.079	4.34E-02	rs17463300	9	70660570	q21.11
SNP_A-1718593	C	C	286	114	320	92	4.081	4.34E-02	rs7308665	12	100508969	q23.2
SNP_A-1714018	C	C	380	6	394	16	4.079	4.34E-02	rs10507531	13	43077466	q14.12
SNP_A-1706253	A	G	210	192	227	187	4.081	4.34E-02	rs1464413	3	119926370	q13.32
SNP_A-2201536	G	G	244	114	247	157	4.079	4.34E-02	rs12359343	10	97650562	q24.1
SNP_A-2207330	C	C	309	57	323	87	4.078	4.34E-02	rs3759595	14	49769368	q21.3
SNP_A-2226856	A	A	408	0	398	4	4.08	4.34E-02	rs3011667	10	106989536	q25.1
SNP_A-2222633	A	A	406	4	416	0	4.078	4.34E-02	rs3924993	15	22372938	q11.2
SNP_A-2173988	C	C	324	64	347	45	4.08	4.34E-02	rs10155960	7	132728289	q33
SNP_A-2192723	T	T	256	86	324	76	4.081	4.34E-02	rs8019537	14	21259146	q11.2
SNP_A-2189074	C	C	244	90	288	74	4.08	4.34E-02	rs7678401	4	106749484	q24
SNP_A-2152021	T	C	226	186	218	200	4.078	4.34E-02	rs12699517	7	13352190	p21.2
SNP_A-2034628	T	T	330	38	384	26	4.079	4.34E-02	rs4981719	14	19608948	q11.2
SNP_A-2005800	G	G	262	28	329	19	4.08	4.34E-02	rs4260153	18	69164242	q22.3
SNP_A-2012103	A	C	193	147	188	182	4.08	4.34E-02	rs2614286	6	135734364	q23.3
SNP_A-1991109	C	C	274	146	297	117	4.081	4.34E-02	rs4318999	7	122528972	q31.32
SNP_A-2002944	G	G	318	100	337	75	4.079	4.34E-02	rs7313175	12	92815609	q22
SNP_A-2073034	A	A	337	5	367	15	4.081	4.34E-02	rs7082774	10	95024432	q23.33
SNP_A-2073070	C	C	294	76	302	110	4.078	4.34E-02	rs10894590	11	99565104	q22.1
SNP_A-2075148	T	T	346	10	371	23	4.078	4.34E-02	rs16885146	6	75372267	q13
SNP_A-2063647	G	G	404	0	394	4	4.081	4.34E-02	rs7185144	16	8464394	p13.2
SNP_A-2079895	G	G	302	116	275	143	4.078	4.34E-02	rs8176318	17	38450800	q21.31
SNP_A-2099944	G	G	277	83	341	71	4.079	4.34E-02	rs6137596	20	22220385	p11.22
SNP_A-2101587	C	C	332	6	392	18	4.08	4.34E-02	rs17071936	5	169334643	q35.1
SNP_A-2107373	T	T	420	2	386	8	4.078	4.34E-02	rs11121007	1	7724554	p36.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238744	C	C	238	168	257	135	4.079	4.34E-02	rs13315042	3	103122354	q12.3
SNP_A-2240493	G	A	194	166	220	192	4.081	4.34E-02	rs2683192	17	69212508	q25.1
SNP_A-2242355	T	T	224	106	284	96	4.081	4.34E-02	rs6588750	10	125815367	q26.13
SNP_A-2251388	G	G	274	90	286	130	4.081	4.34E-02	rs2623819	8	68849759	q13.2
SNP_A-2287645	C	C	400	0	390	4	4.081	4.34E-02	rs1176558	1	153951822	q23.1
SNP_A-2274528	C	C	412	0	402	4	4.079	4.34E-02	rs16940555	15	85893737	q25.3
SNP_A-2276490	C	C	266	154	228	176	4.081	4.34E-02	rs11231073	11	61917900	q12.3
SNP_A-2262849	C	C	210	174	240	148	4.079	4.34E-02	rs222908	16	15406558	p13.11
SNP_A-2298641	T	T	293	71	302	104	4.08	4.34E-02	rs610262	1	182936036	q31.1
SNP_A-2301530	G	G	314	48	337	77	4.074	4.35E-02	rs8000837	13	37460315	q13.3
SNP_A-2300983	G	G	231	185	256	154	4.075	4.35E-02	rs6925091	6	158999751	q25.3
SNP_A-2296132	T	T	237	121	240	166	4.075	4.35E-02	rs6739095	2	88719326	p11.2
SNP_A-2272246	G	G	304	12	359	5	4.077	4.35E-02	rs7725087	5	2426878	p15.33
SNP_A-2285977	C	C	329	41	387	29	4.077	4.35E-02	rs17008057	2	72453301	p13.2
SNP_A-2235071	A	A	355	29	389	17	4.075	4.35E-02	rs892113	19	11136934	p13.2
SNP_A-2234764	C	G	188	158	201	177	4.076	4.35E-02	rs3943000	11	40610390	p12
SNP_A-2073264	G	G	238	128	240	174	4.077	4.35E-02	rs1041847	7	141394082	q34
SNP_A-2055734	T	T	253	95	254	132	4.076	4.35E-02	rs2904382	4	92677202	q22.1
SNP_A-2060945	A	A	266	156	291	127	4.075	4.35E-02	rs877138	11	112761718	q23.2
SNP_A-2054473	G	G	312	26	353	49	4.077	4.35E-02	rs381349	8	81614550	q21.13
SNP_A-2051850	A	A	303	13	370	6	4.077	4.35E-02	---	9	101461581	q31.1
SNP_A-2011135	A	A	300	48	351	35	4.075	4.35E-02	rs720402	5	109830098	q22.1
SNP_A-2034645	G	G	300	48	351	35	4.075	4.35E-02	rs10828713	10	25188982	p12.1
SNP_A-2033868	T	T	246	92	301	79	4.076	4.35E-02	rs3801831	7	26626710	p15.2
SNP_A-2025303	T	T	261	63	247	87	4.075	4.35E-02	rs10811726	9	22536002	p21.3
SNP_A-2193637	T	T	273	91	282	130	4.075	4.35E-02	rs7378179	4	145641813	q31.21
SNP_A-2181197	T	T	224	124	225	169	4.077	4.35E-02	rs9326982	5	115359017	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2220522	G	G	337	29	363	51	4.077	4.35E-02	rs3094035	6	30471115	p21.33
SNP_A-2209086	G	G	422	0	412	4	4.077	4.35E-02	rs169178	19	56074922	q13.41
SNP_A-2210808	A	A	229	123	289	113	4.076	4.35E-02	rs7451886	6	103186468	q16.3
SNP_A-2205852	G	G	384	38	362	56	4.077	4.35E-02	rs4792387	17	13560425	p12
SNP_A-1807594	A	A	288	120	257	145	4.078	4.35E-02	rs1880808	1	7448887	p36.23
SNP_A-1801587	C	C	260	106	266	148	4.075	4.35E-02	rs9844897	3	192366023	q28
SNP_A-1805154	T	T	292	54	361	43	4.077	4.35E-02	rs7913128	10	9906737	p14
SNP_A-1787233	G	G	281	125	255	153	4.076	4.35E-02	rs9285081	13	30307565	q12.3
SNP_A-1791003	G	G	344	12	383	27	4.075	4.35E-02	rs12336411	9	10104307	p23
SNP_A-1856260	T	C	206	160	206	198	4.074	4.35E-02	rs6925648	6	88044265	q15
SNP_A-1849118	T	T	410	4	420	0	4.078	4.35E-02	rs7220024	11	112343722	q23.1
SNP_A-1816982	G	G	422	0	412	4	4.077	4.35E-02	rs17075840	3	43595397	p22.1
SNP_A-1840726	C	C	286	82	347	69	4.074	4.35E-02	rs252742	5	77403521	q14.1
SNP_A-1967920	C	C	329	41	387	29	4.077	4.35E-02	rs6043593	20	15811524	p12.1
SNP_A-1970435	A	A	313	57	372	44	4.077	4.35E-02	rs2837422	21	40364677	q22.2
SNP_A-1923019	C	T	222	190	220	194	4.075	4.35E-02	rs4401144	18	18447666	q11.2
SNP_A-1926028	C	C	238	170	204	194	4.074	4.35E-02	rs1041516	10	121924104	q26.12
SNP_A-1919601	C	C	343	19	373	37	4.074	4.35E-02	rs10853589	18	45775158	q21.1
SNP_A-1901176	A	G	217	193	224	190	4.076	4.35E-02	rs9920378	15	21584543	q11.2
SNP_A-1879133	T	T	365	13	393	5	4.077	4.35E-02	rs16926052	9	106839464	q31.2
SNP_A-1887004	A	A	349	13	380	28	4.073	0.0436	rs9516766	13	96275492	q32.1
SNP_A-1884846	A	A	243	111	249	155	4.071	0.0436	rs12512791	4	189863883	q35.2
SNP_A-1897617	C	C	218	152	211	197	4.07	0.0436	rs16871229	8	105377855	q22.3
SNP_A-1895594	G	G	279	143	247	169	4.071	0.0436	rs513053	19	44332986	q13.2
SNP_A-1893639	C	C	321	45	340	72	4.071	0.0436	rs34428	5	107522936	q21.3
SNP_A-1982884	T	T	345	21	376	40	4.071	0.0436	rs10515410	5	109439221	q21.3
SNP_A-1933888	A	A	222	134	225	183	4.074	0.0436	rs1983841	6	87856604	q15

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950309	A	A	349	1	373	7	4.072	0.0436	rs6969582	7	74703031	q11.23
SNP_A-1816467	G	G	197	177	236	158	4.072	0.0436	rs650916	6	137991104	q23.3
SNP_A-1863238	C	C	344	34	392	22	4.074	0.0436	rs10877185	12	57584253	q14.1
SNP_A-1862367	A	A	223	125	218	166	4.073	0.0436	rs7869712	9	88821136	q22.1
SNP_A-1871391	G	G	287	73	300	108	4.072	0.0436	rs1441939	8	14626045	p22
SNP_A-1789086	A	A	294	114	274	144	4.072	0.0436	rs4666283	2	29985301	p23.1
SNP_A-1806838	T	T	304	56	361	43	4.072	0.0436	rs10843725	12	30388487	p11.22
SNP_A-1809179	T	T	305	41	335	69	4.073	0.0436	rs10961679	9	14706276	p22.3
SNP_A-1690315	G	G	236	164	213	197	4.072	0.0436	rs2078426	15	52669160	q21.3
SNP_A-2212250	A	A	225	111	201	137	4.072	0.0436	rs1226521	6	47133670	p12.3
SNP_A-2215240	T	T	277	31	274	50	4.071	0.0436	rs2648560	3	9393241	p25.3
SNP_A-2172900	C	C	267	101	270	140	4.072	0.0436	rs10978151	9	9979624	p23
SNP_A-2171612	T	T	342	80	362	58	4.071	0.0436	rs4567311	1	150587756	q21.3
SNP_A-2193767	G	G	360	62	374	42	4.07	0.0436	rs882727	9	98809676	q22.33
SNP_A-2192156	G	G	254	148	281	121	4.073	0.0436	rs1952517	14	20522832	q11.2
SNP_A-2196468	C	C	290	58	294	86	4.073	0.0436	rs4931251	12	30111943	p11.22
SNP_A-2191017	A	A	267	101	326	88	4.073	0.0436	rs2120998	4	32294215	p15.1
SNP_A-2120097	C	C	331	61	336	40	4.072	0.0436	rs6037845	20	4372600	p13
SNP_A-2031611	A	A	342	80	362	58	4.071	0.0436	rs17006285	2	70892541	p13.3
SNP_A-1997277	G	G	258	110	262	152	4.072	0.0436	rs1410783	9	95730976	q22.32
SNP_A-1993213	A	A	279	59	306	94	4.073	0.0436	rs2044778	8	51426828	q11.21
SNP_A-2072687	A	A	309	53	357	39	4.073	0.0436	rs2465810	12	69301547	q15
SNP_A-2074125	G	G	207	159	261	149	4.074	0.0436	rs9862709	3	80549699	p12.2
SNP_A-2069691	C	C	314	48	376	36	4.072	0.0436	rs11714139	3	133427335	q22.1
SNP_A-2105274	G	G	240	170	207	195	4.07	0.0436	rs7597885	2	53764626	p16.2
SNP_A-2093597	C	C	255	57	268	88	4.07	0.0436	rs1559905	8	82309140	q21.13
SNP_A-2098904	T	C	193	167	218	188	4.074	0.0436	rs2041343	7	2502984	p22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2081850	T	C	211	203	232	182	4.073	0.0436	rs2614780	15	48964128	q21.2
SNP_A-2088966	C	C	229	105	276	90	4.074	0.0436	rs847716	7	70026824	q11.22
SNP_A-2292689	G	G	269	123	290	96	4.072	0.0436	rs6807017	3	29466938	p24.1
SNP_A-2311966	G	G	234	126	235	171	4.073	0.0436	rs16843372	2	159495956	q24.1
SNP_A-2314278	C	C	274	118	308	96	4.068	4.37E-02	rs487752	9	126148659	q33.3
SNP_A-2255539	T	T	313	75	339	55	4.068	4.37E-02	rs7164426	15	84067909	q25.3
SNP_A-2267249	G	G	344	18	389	9	4.066	4.37E-02	rs16919644	8	82781278	q21.13
SNP_A-2265798	C	C	371	37	358	56	4.07	4.37E-02	rs710974	5	3591373	p15.33
SNP_A-2078738	G	G	337	77	360	56	4.07	4.37E-02	rs17096570	14	97700796	q32.2
SNP_A-2059187	G	G	245	125	244	168	4.069	4.37E-02	rs1375697	6	45932033	p21.1
SNP_A-1994195	G	G	205	163	260	154	4.069	4.37E-02	rs1487672	8	90544491	q21.3
SNP_A-2010044	T	C	190	166	218	186	4.069	4.37E-02	rs2726689	4	108855951	q25
SNP_A-2029656	C	T	236	180	210	208	4.069	4.37E-02	rs1888239	7	78035189	q21.11
SNP_A-2045106	A	A	368	16	395	7	4.067	4.37E-02	rs1356449	2	104820216	q12.1
SNP_A-2122401	G	G	342	10	367	23	4.067	4.37E-02	rs3094448	16	69868966	q22.2
SNP_A-2144935	A	A	246	118	307	107	4.07	4.37E-02	rs1372631	18	4016587	p11.31
SNP_A-2138305	A	A	301	121	319	93	4.067	4.37E-02	rs10923354	1	117864283	p12
SNP_A-2141227	T	T	341	7	362	18	4.069	4.37E-02	rs333846	2	117695424	q14.1
SNP_A-2204225	C	C	298	74	305	107	4.068	4.37E-02	rs7899691	10	24832177	p12.1
SNP_A-2199821	A	A	338	30	391	19	4.067	4.37E-02	rs10936921	3	178155116	q26.32
SNP_A-2202340	G	G	231	111	223	147	4.069	4.37E-02	rs2089722	16	82644639	q23.3
SNP_A-1680018	A	A	230	146	279	131	4.066	4.37E-02	rs10504244	8	59034735	q12.1
SNP_A-1700249	-	G	175	175	235	175	4.069	4.37E-02	rs950942	13	69329810	q21.33
SNP_A-1781149	G	G	246	118	307	107	4.07	4.37E-02	rs12424348	12	24880412	p12.1
SNP_A-1753413	C	C	307	53	322	82	4.067	4.37E-02	rs907752	12	69508257	q15
SNP_A-1870505	A	A	330	22	355	41	4.068	4.37E-02	rs17760230	10	20312981	p12.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1868123	C	C	254	114	311	101	4.067	4.37E-02	rs11249609	5	178362606	q35.3
SNP_A-1853515	A	A	312	54	369	41	4.068	4.37E-02	rs10834276	11	24075838	p14.3
SNP_A-1824595	G	G	187	183	239	175	4.07	4.37E-02	rs2807845	1	217384682	q41
SNP_A-1822705	G	G	326	34	338	56	4.07	4.37E-02	rs704471	3	61243200	p14.2
SNP_A-1826159	G	G	323	35	384	24	4.068	4.37E-02	rs4033035	1	77465104	p31.1
SNP_A-1839565	G	G	352	64	328	86	4.069	4.37E-02	rs1519252	17	12472410	p12
SNP_A-1948872	C	C	346	20	405	11	4.068	4.37E-02	rs1673442	2	65705529	p14
SNP_A-1956864	G	G	199	161	256	154	4.067	4.37E-02	rs951613	4	95929877	q22.3
SNP_A-1960409	T	T	268	98	327	85	4.068	4.37E-02	rs2030931	12	88710263	q21.33
SNP_A-1982897	G	G	314	36	375	25	4.069	4.37E-02	rs4391218	5	110066991	q22.1
SNP_A-1970494	T	T	330	90	296	112	4.07	4.37E-02	rs2838001	21	41568862	q22.3
SNP_A-1965832	C	C	315	55	328	84	4.069	4.37E-02	rs10515933	2	172150669	q31.1
SNP_A-1883010	A	A	357	11	391	25	4.066	4.37E-02	rs12496250	3	78187009	p12.3
SNP_A-1924737	C	C	221	145	217	191	4.067	4.37E-02	rs10159426	1	63004891	p31.3
SNP_A-1927944	A	A	225	117	282	106	4.068	4.37E-02	rs4588813	8	10396804	p23.1
SNP_A-1920532	T	T	242	126	297	113	4.064	4.38E-02	rs10209970	2	98081215	q11.2
SNP_A-1905790	A	G	216	198	227	187	4.066	4.38E-02	rs7587790	2	26625374	p23.3
SNP_A-1879974	C	C	227	127	284	116	4.065	4.38E-02	rs2161204	5	103269449	q21.2
SNP_A-1891203	T	T	324	30	375	19	4.063	4.38E-02	rs17339881	4	121794153	q27
SNP_A-1967359	G	G	281	61	324	46	4.064	4.38E-02	rs3821238	2	234531780	q37.1
SNP_A-1962997	A	G	206	204	224	170	4.065	4.38E-02	rs163513	2	45096875	p21
SNP_A-1843209	A	A	235	129	238	176	4.065	4.38E-02	rs17456106	2	181976482	q31.3
SNP_A-1816763	G	G	207	163	256	150	4.064	4.38E-02	rs978814	6	81016631	q14.1
SNP_A-1847853	C	C	219	119	263	103	4.063	4.38E-02	rs1482195	8	3507073	p23.2
SNP_A-1751221	G	G	381	19	405	9	4.065	4.38E-02	rs10503211	8	3469801	p23.2
SNP_A-1726352	C	C	237	147	281	129	4.064	4.38E-02	rs798525	7	2519969	p22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1709467	C	C	373	27	399	15	4.065	4.38E-02	rs2421084	2	125351734	q14.3
SNP_A-1711424	A	A	361	33	392	20	4.065	4.38E-02	rs7853840	9	28058081	p21.2
SNP_A-1798625	A	A	303	61	362	48	4.066	4.38E-02	rs7519522	1	162067276	q23.3
SNP_A-1794662	T	T	284	136	256	164	4.065	4.38E-02	rs2135999	2	41540652	p22.1
SNP_A-2200708	T	T	344	2	361	9	4.065	4.38E-02	rs4765775	12	4284387	p13.32
SNP_A-2216872	C	C	292	76	303	111	4.062	4.38E-02	rs11864374	16	16109386	p13.11
SNP_A-2227541	C	C	287	133	309	105	4.063	4.38E-02	rs7722731	5	128644255	q23.3
SNP_A-2190599	G	G	281	87	291	125	4.063	4.38E-02	rs9874979	3	168894481	q26.1
SNP_A-2192601	C	C	333	83	355	61	4.065	4.38E-02	rs11124232	2	240468848	q37.3
SNP_A-2195022	A	A	355	59	330	80	4.066	4.38E-02	rs17817873	9	104174238	q31.1
SNP_A-2139872	A	A	336	22	323	37	4.064	4.38E-02	rs11256103	10	9255068	p14
SNP_A-2119351	C	C	218	142	211	185	4.064	4.38E-02	rs10457419	6	121873961	q22.31
SNP_A-2124988	A	A	340	26	400	16	4.066	4.38E-02	rs7600297	2	191186058	q32.2
SNP_A-2126916	C	C	229	109	220	144	4.065	4.38E-02	rs2982705	6	152439972	q25.1
SNP_A-2040454	A	A	241	109	290	94	4.064	4.38E-02	rs4719072	7	70029344	q11.22
SNP_A-2031208	T	T	296	58	308	88	4.064	4.38E-02	rs872204	18	45824779	q21.1
SNP_A-1993286	G	G	244	112	302	100	4.064	4.38E-02	rs10095210	8	53891616	q11.23
SNP_A-1989879	T	T	250	170	221	199	4.065	4.38E-02	rs6957965	7	50014344	p12.2
SNP_A-2004381	G	G	249	155	271	125	4.065	4.38E-02	rs725458	15	91435937	q26.1
SNP_A-2060466	G	G	278	124	308	100	4.063	4.38E-02	rs9567986	13	47516171	q14.2
SNP_A-2070599	T	T	349	3	369	11	4.063	4.38E-02	rs11960646	5	117735272	q23.1
SNP_A-2093296	C	C	269	153	238	180	4.066	4.38E-02	rs6063499	20	48348329	q13.13
SNP_A-2094191	A	A	330	84	307	109	4.064	4.38E-02	rs11688203	2	126902407	q14.3
SNP_A-2276533	G	G	295	73	356	60	4.063	4.38E-02	rs11895522	2	104084721	q12.1
SNP_A-2313759	C	C	263	107	265	147	4.063	4.38E-02	rs6542396	2	118292418	q14.1
SNP_A-2295640	C	C	278	70	287	103	4.061	4.39E-02	rs2316671	6	122727927	q22.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284813	T	T	412	0	404	4	4.059	4.39E-02	rs16968968	16	63962866	q22.1
SNP_A-2237755	G	G	294	74	355	61	4.062	4.39E-02	rs11021127	11	94692946	q21
SNP_A-2238787	G	G	402	4	410	0	4.059	4.39E-02	rs6530777	8	14351769	p22
SNP_A-2229501	G	G	390	4	398	0	4.061	4.39E-02	rs11918106	3	23697181	p24.3
SNP_A-2094426	T	T	237	171	265	143	4.059	4.39E-02	rs2913360	5	5468877	p15.32
SNP_A-2103665	G	G	319	89	300	116	4.062	4.39E-02	rs7857957	9	84851166	q21.33
SNP_A-2100245	G	G	256	102	313	89	4.061	4.39E-02	rs4565335	6	29083766	p22.1
SNP_A-2081289	T	T	414	0	406	4	4.059	4.39E-02	rs6748634	2	102036078	q11.2
SNP_A-2084686	G	G	398	4	406	0	4.06	4.39E-02	rs1559538	14	78235361	q24.3
SNP_A-2083945	A	A	370	6	409	1	4.061	4.39E-02	rs9398855	6	128213712	q22.33
SNP_A-2085101	T	T	298	32	319	55	4.061	4.39E-02	rs7406829	17	77170499	q25.3
SNP_A-2011532	G	G	408	0	400	4	4.06	4.39E-02	rs4110195	11	61753218	q12.3
SNP_A-2018627	T	T	402	0	394	4	4.061	4.39E-02	rs16993108	21	35614841	q22.12
SNP_A-2020451	G	G	406	4	414	0	4.059	4.39E-02	rs17004655	21	44759519	q22.3
SNP_A-2109987	C	C	377	3	399	11	4.062	4.39E-02	rs235679	6	124304070	q22.31
SNP_A-2141080	C	T	209	207	225	171	4.06	4.39E-02	rs500000	8	102535133	q22.3
SNP_A-2147031	C	C	287	71	305	107	4.061	4.39E-02	rs1548459	7	117161188	q31.31
SNP_A-2148629	G	G	272	98	328	84	4.06	4.39E-02	rs332757	11	98111033	q22.1
SNP_A-2148650	G	G	412	0	404	4	4.059	4.39E-02	rs4636164	8	39133611	p11.23
SNP_A-2158325	A	A	253	97	316	86	4.06	4.39E-02	rs16838613	2	207392254	q33.3
SNP_A-2153283	C	C	404	4	412	0	4.059	4.39E-02	rs10016415	4	28889466	p15.1
SNP_A-2192128	C	C	392	10	381	21	4.06	4.39E-02	rs16854378	3	109471305	q13.13
SNP_A-2171037	C	C	232	132	231	177	4.061	4.39E-02	rs11853430	15	45285905	q21.1
SNP_A-2170335	T	T	288	128	314	102	4.062	4.39E-02	rs13138153	4	16968065	p15.32
SNP_A-2177632	C	C	355	11	389	25	4.06	4.39E-02	rs3742133	13	97955530	q32.2
SNP_A-2203843	G	G	266	94	328	82	4.06	4.39E-02	rs7085222	10	111946721	q25.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2204511	G	G	309	59	368	46	4.059	4.39E-02	rs590059	6	63096519	q11.1
SNP_A-2207892	C	C	307	111	279	137	4.059	4.39E-02	rs2744537	6	33270193	p21.32
SNP_A-1703543	C	C	349	27	358	46	4.06	4.39E-02	rs2010014	8	99024873	q22.2
SNP_A-1690229	A	A	398	0	390	4	4.061	4.39E-02	rs10490078	2	150847478	q23.3
SNP_A-1684740	G	G	351	43	342	64	4.059	4.39E-02	rs1885315	14	83905481	q31.3
SNP_A-1648830	A	A	266	136	298	112	4.06	4.39E-02	rs726789	19	14604003	p13.12
SNP_A-1730923	G	G	357	43	348	64	4.06	4.39E-02	rs7781339	7	130402043	q32.3
SNP_A-1816356	T	T	408	2	376	8	4.059	4.39E-02	rs16834469	1	149549653	q21.3
SNP_A-1835967	C	C	265	101	268	140	4.061	4.39E-02	rs6844817	4	171980218	q33
SNP_A-1964400	C	C	394	4	402	0	4.061	4.39E-02	rs266270	2	107596599	q12.3
SNP_A-1971657	T	T	248	128	282	106	4.062	4.39E-02	rs465632	3	8159528	p26.1
SNP_A-1978539	A	A	350	18	375	35	4.059	4.39E-02	rs10516582	4	113333201	q25
SNP_A-1960900	G	G	400	4	408	0	4.06	4.39E-02	rs10121452	9	31445133	p21.1
SNP_A-1933354	A	A	365	1	391	7	4.061	4.39E-02	rs12183323	6	113882154	q21
SNP_A-1940280	A	G	179	147	187	167	4.061	4.39E-02	rs10946675	6	24249899	p22.2
SNP_A-1892012	A	A	394	24	402	12	4.061	4.39E-02	rs11079629	17	61454243	q24.1
SNP_A-1908853	C	C	217	205	245	175	4.061	4.39E-02	rs2305482	17	35394453	q21.1
SNP_A-1929356	C	C	199	133	241	117	4.059	4.39E-02	rs4905446	14	95667710	q32.2
SNP_A-1927173	G	G	268	154	237	181	4.06	4.39E-02	rs496321	11	94526280	q21
SNP_A-1906313	C	C	408	4	416	0	4.058	4.40E-02	rs2847571	18	46627616	q21.1
SNP_A-1906294	C	C	314	86	288	110	4.057	4.40E-02	rs11986341	8	38942668	p11.23
SNP_A-1894046	G	G	351	19	404	10	4.057	4.40E-02	rs10959904	9	11527716	p23
SNP_A-1902119	T	T	422	0	414	4	4.058	4.40E-02	rs16924563	10	68950039	q21.3
SNP_A-1939206	G	G	328	36	391	25	4.055	4.40E-02	rs2178131	3	84137538	p12.1
SNP_A-1978844	G	G	220	142	223	193	4.056	4.40E-02	rs2390992	4	127462965	q28.1
SNP_A-1974372	G	G	420	0	412	4	4.058	4.40E-02	rs1554384	3	133380286	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1975121	T	T	410	4	418	0	4.058	4.40E-02	rs7531556	1	17750685	p36.13
SNP_A-1835119	A	A	377	15	390	6	4.057	4.40E-02	---	5	159928797	q34
SNP_A-1816123	G	G	282	62	344	50	4.057	4.40E-02	rs747611	20	1311295	p13
SNP_A-1854844	T	T	224	156	274	142	4.058	4.40E-02	rs17768206	6	141597194	q24.1
SNP_A-1855332	C	C	268	102	327	89	4.057	4.40E-02	rs921573	2	50245834	p16.3
SNP_A-1862031	A	A	276	92	332	78	4.055	4.40E-02	rs7444512	5	101585982	q21.1
SNP_A-1860516	A	G	220	202	227	187	4.056	4.40E-02	rs716534	3	111424797	q13.13
SNP_A-1747275	C	C	319	31	387	21	4.058	4.40E-02	rs10505881	12	22566137	p12.1
SNP_A-1731739	T	T	330	60	363	43	4.057	4.40E-02	rs9317500	13	21501577	q12.12
SNP_A-1758149	T	T	387	11	387	23	4.058	4.40E-02	rs10512658	3	126718651	q21.2
SNP_A-1792514	C	C	290	78	346	64	4.056	4.40E-02	rs615108	9	36208018	p13.2
SNP_A-1791935	T	T	340	28	387	17	4.057	4.40E-02	rs510340	6	74109531	q13
SNP_A-1807996	C	C	347	9	411	3	4.058	4.40E-02	rs10848757	12	2947480	p13.33
SNP_A-1813229	G	G	266	100	328	88	4.057	4.40E-02	rs759564	12	106231143	q23.3
SNP_A-2210546	C	C	422	0	414	4	4.058	4.40E-02	rs17075612	3	43382970	p22.1
SNP_A-2199792	G	G	393	21	404	10	4.055	4.40E-02	rs3779292	7	77426100	q21.11
SNP_A-2176906	G	G	245	107	309	97	4.057	4.40E-02	rs4534611	11	110945635	q23.1
SNP_A-2194217	G	G	337	83	359	61	4.057	4.40E-02	rs2239627	14	22705999	q11.2
SNP_A-2196398	A	A	286	116	314	92	4.056	4.40E-02	rs2251674	10	42925398	q11.21
SNP_A-2159552	A	A	324	44	384	32	4.056	4.40E-02	rs6911710	6	95478935	q16.1
SNP_A-2164258	G	G	225	137	275	123	4.058	4.40E-02	rs304381	5	121796441	q23.2
SNP_A-2113229	G	G	255	107	318	96	4.056	4.40E-02	rs7616271	3	188815629	q27.3
SNP_A-2121181	G	G	216	148	272	138	4.056	4.40E-02	rs2043760	2	85833650	p11.2
SNP_A-2135912	A	A	329	31	356	54	4.058	4.40E-02	rs7595960	2	234630798	q37.1
SNP_A-2020547	C	C	404	14	399	5	4.057	4.40E-02	---	21	45232658	q22.3
SNP_A-2033881	G	G	207	155	266	148	4.055	4.40E-02	rs7112850	11	14008775	p15.2
SNP_A-1996077	A	A	410	4	418	0	4.058	4.40E-02	rs2224451	9	17626754	p22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084500	G	C	206	160	202	194	4.058	4.40E-02	rs7620145	3	163238788	q26.1
SNP_A-2077163	A	A	322	30	344	52	4.055	4.40E-02	rs807525	6	24684016	p22.2
SNP_A-2079669	G	G	359	47	374	30	4.055	4.40E-02	---	14	96288681	q32.2
SNP_A-2093917	C	C	410	4	418	0	4.058	4.40E-02	rs8114989	20	46006752	q13.13
SNP_A-2071731	A	A	288	78	300	114	4.056	4.40E-02	rs4142753	2	119673046	q14.2
SNP_A-2073561	A	A	307	115	276	140	4.057	4.40E-02	rs1017234	16	82263320	q23.3
SNP_A-2059807	G	G	230	140	287	129	4.056	4.40E-02	rs13218818	6	76990244	q14.1
SNP_A-2231326	G	G	230	140	287	129	4.056	4.40E-02	rs12527444	6	76986401	q14.1
SNP_A-2236337	A	A	219	151	270	138	4.057	4.40E-02	rs1534835	14	79452128	q31.1
SNP_A-2241722	A	A	407	5	379	13	4.058	4.40E-02	rs8115360	20	30847547	q11.21
SNP_A-2287655	G	G	314	56	330	86	4.057	4.40E-02	rs6791810	3	10099444	p25.3
SNP_A-2287044	A	A	321	95	297	121	4.057	4.40E-02	rs4260245	2	122378485	q14.3
SNP_A-2264703	C	C	295	63	347	49	4.057	4.40E-02	rs9992459	4	125039350	q28.1
SNP_A-2267199	C	C	420	0	412	4	4.058	4.40E-02	rs2819386	1	198353682	q32.1
SNP_A-2300993	G	G	362	30	331	45	4.055	4.40E-02	rs2474362	1	61627310	p31.3
SNP_A-2311358	A	A	412	2	380	8	4.054	0.0441	rs954692	3	36141595	p22.3
SNP_A-2266908	C	C	357	1	383	7	4.052	0.0441	rs7438628	4	167911192	q32.3
SNP_A-2287126	C	C	377	31	383	17	4.052	0.0441	rs244777	5	35402012	p13.2
SNP_A-2285985	G	G	276	146	244	172	4.052	0.0441	rs12477464	2	67506890	p14
SNP_A-2274154	T	T	312	40	329	65	4.051	0.0441	rs1466612	6	98791187	q16.2
SNP_A-2250396	C	C	373	49	351	69	4.054	0.0441	rs10849181	12	508427	p13.33
SNP_A-2238761	C	C	259	149	225	173	4.054	0.0441	rs9945084	18	38976893	q12.3
SNP_A-2228981	G	G	343	23	391	13	4.051	0.0441	rs17392898	2	22759274	p24.1
SNP_A-2057316	G	G	353	19	339	33	4.052	0.0441	rs2792689	10	113830327	q25.2
SNP_A-2051956	G	G	214	126	262	112	4.054	0.0441	rs1046276	16	30822127	p11.2
SNP_A-2070941	C	C	328	40	384	28	4.053	0.0441	rs4248148	6	30850113	p21.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2069292	G	G	293	115	321	91	4.054	0.0441	rs4470469	3	141326834	q23
SNP_A-2085960	C	C	206	164	261	155	4.053	0.0441	rs13279803	8	124819702	q24.13
SNP_A-2090429	C	C	298	72	310	106	4.053	0.0441	rs6849318	4	85806502	q21.23
SNP_A-1990356	C	C	312	52	329	81	4.055	0.0441	rs12533606	7	81602288	q21.11
SNP_A-2013791	C	C	360	62	358	40	4.052	0.0441	rs7463141	8	125476282	q24.13
SNP_A-2045847	C	C	216	146	214	194	4.052	0.0441	rs10861072	12	77774776	q21.2
SNP_A-2023817	G	G	275	95	282	134	4.052	0.0441	rs1989838	7	22474407	p15.3
SNP_A-2134944	T	T	363	31	369	17	4.051	0.0441	rs578076	8	12924999	p22
SNP_A-2133892	C	C	349	73	324	96	4.054	0.0441	rs495062	9	117379362	q33.1
SNP_A-2162062	G	G	309	101	328	76	4.054	0.0441	rs2223749	20	52727160	q13.2
SNP_A-2168112	G	G	376	34	346	50	4.052	0.0441	rs12295525	11	19661808	p15.1
SNP_A-2141909	C	C	369	31	375	17	4.051	0.0441	rs641783	1	204428097	q32.2
SNP_A-2188588	A	A	249	109	253	151	4.054	0.0441	rs6920170	6	70961087	q13
SNP_A-2175724	A	A	337	31	392	20	4.053	0.0441	rs907454	8	138981239	q24.23
SNP_A-2181675	A	A	219	127	270	114	4.053	0.0441	rs9829033	3	80557125	p12.2
SNP_A-2171565	A	A	387	15	400	6	4.052	0.0441	rs9498	17	71819101	q25.1
SNP_A-2173410	G	G	300	102	277	129	4.053	0.0441	rs6882580	5	6662024	p15.31
SNP_A-2207422	A	A	352	54	336	76	4.051	0.0441	rs17612068	5	141863245	q31.3
SNP_A-1809342	T	T	336	32	361	55	4.054	0.0441	rs7831358	8	3869740	p23.2
SNP_A-1793370	G	G	383	31	389	17	4.052	0.0441	rs8094691	18	10926513	p11.21
SNP_A-1796316	T	T	317	79	330	56	4.053	0.0441	rs4325640	18	11107538	p11.21
SNP_A-1725610	C	C	190	160	251	157	4.052	0.0441	rs574793	6	94806773	q16.1
SNP_A-1703827	A	A	259	143	294	120	4.051	0.0441	rs63953	17	31803158	q11.2
SNP_A-1704327	C	C	259	143	294	120	4.051	0.0441	rs1450885	7	131297860	q32.3
SNP_A-1861421	T	T	410	10	399	21	4.053	0.0441	rs17119901	14	47770182	q21.3
SNP_A-1862098	A	A	353	15	407	7	4.054	0.0441	rs12430035	13	25000539	q12.13
SNP_A-1854007	T	T	289	79	345	65	4.052	0.0441	rs16944424	15	88784469	q26.1
SNP_A-1856904	A	A	224	132	278	120	4.053	0.0441	rs6822747	4	137721801	q28.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1845461	T	T	390	30	366	46	4.054	0.0441	rs9463119	6	12905482	p24.1
SNP_A-1844271	C	C	272	120	309	99	4.052	0.0441	rs17076450	8	6165620	p23.2
SNP_A-1839771	G	G	351	17	382	34	4.054	0.0441	rs1407496	6	19146316	p22.3
SNP_A-1837351	G	G	209	145	208	194	4.054	0.0441	rs1889276	6	72386809	q13
SNP_A-1983349	C	C	219	135	270	122	4.051	0.0441	rs3125161	1	20871652	p36.12
SNP_A-1987715	C	C	289	79	345	65	4.052	0.0441	rs1415858	6	133599134	q23.2
SNP_A-1933558	C	C	323	95	343	71	4.051	0.0441	rs11599482	10	85690695	q23.1
SNP_A-1933960	C	C	335	33	394	22	4.051	0.0441	rs757260	6	30223183	p21.33
SNP_A-1951020	C	C	335	33	394	22	4.051	0.0441	rs16953268	16	52844058	q12.2
SNP_A-1899214	C	C	271	145	291	115	4.052	0.0441	rs11637231	15	23653372	q12
SNP_A-1877849	T	T	327	41	349	67	4.052	0.0441	rs2256319	20	4652957	p13
SNP_A-1887994	G	G	215	125	218	172	4.053	0.0441	rs606846	7	51610221	p12.1
SNP_A-1889989	G	G	380	16	407	7	4.05	4.42E-02	rs7234036	18	13502994	p11.21
SNP_A-1916386	T	T	256	112	261	155	4.05	4.42E-02	rs654975	18	58418480	q21.33
SNP_A-1925706	G	G	355	1	381	7	4.05	4.42E-02	rs17078741	8	2711787	p23.2
SNP_A-1934034	A	A	287	81	294	116	4.047	4.42E-02	rs7929370	11	23377508	p14.3
SNP_A-1827296	A	A	256	108	313	95	4.048	4.42E-02	rs4700423	5	60996521	q12.1
SNP_A-1846664	T	T	418	2	386	8	4.047	4.42E-02	rs16872421	6	44782682	p21.1
SNP_A-1857845	A	A	326	42	373	29	4.047	4.42E-02	rs2518296	6	102233451	q16.3
SNP_A-1853779	C	C	294	74	301	107	4.048	4.42E-02	rs664805	18	53290005	q21.31
SNP_A-1854512	T	T	225	131	290	124	4.05	4.42E-02	rs9293941	6	74547065	q13
SNP_A-1866357	A	A	286	132	257	159	4.049	4.42E-02	rs2537710	17	44921585	q21.33
SNP_A-1867399	C	C	266	156	235	183	4.05	4.42E-02	rs4427378	1	210773840	q41
SNP_A-1702161	A	A	255	95	271	139	4.049	4.42E-02	rs10516971	4	96789440	q22.3
SNP_A-1782344	G	G	311	55	324	84	4.049	4.42E-02	rs6781696	3	43231709	p22.1
SNP_A-1792412	A	A	196	174	243	161	4.051	4.42E-02	rs4809605	20	44993488	q13.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1808322	G	G	313	109	336	84	4.049	4.42E-02	rs11204682	1	147408610	q21.2
SNP_A-1807864	C	C	269	67	274	98	4.05	4.42E-02	rs16894263	4	16730531	p15.32
SNP_A-2207254	C	C	238	132	236	176	4.05	4.42E-02	rs4856986	3	67198519	p14.1
SNP_A-2214469	C	C	318	50	334	78	4.048	4.42E-02	rs2980392	8	35298226	p12
SNP_A-2170066	G	G	378	14	343	25	4.048	4.42E-02	rs3920266	2	117939400	q14.1
SNP_A-2140390	C	C	418	2	386	8	4.047	4.42E-02	rs326769	11	29566056	p14.1
SNP_A-2150233	T	T	378	6	417	1	4.051	4.42E-02	rs1238878	1	154780254	q23.1
SNP_A-2125631	G	G	318	46	369	33	4.05	4.42E-02	rs16945825	18	3992200	p11.31
SNP_A-2124854	C	C	308	28	351	17	4.048	4.42E-02	rs1107802	1	231385898	q42.3
SNP_A-2129072	G	G	225	139	279	127	4.048	4.42E-02	rs2528593	2	159357416	q24.1
SNP_A-2081776	T	C	221	201	226	188	4.05	4.42E-02	rs7963923	12	104761216	q23.3
SNP_A-2067736	C	C	382	20	383	9	4.048	4.42E-02	rs2002581	22	37146564	q13.1
SNP_A-2059592	G	G	237	119	296	108	4.049	4.42E-02	rs1001974	19	45038875	q13.2
SNP_A-2253571	T	T	367	17	361	31	4.051	4.42E-02	rs3807573	7	5442801	p22.1
SNP_A-2274301	T	T	355	15	409	7	4.048	4.42E-02	rs12952208	17	5383312	p13.2
SNP_A-2284035	G	A	221	201	226	188	4.05	4.42E-02	rs7969076	12	92598510	q22
SNP_A-2269770	A	A	256	112	261	155	4.05	4.42E-02	rs1024653	17	58145550	q23.3
SNP_A-2265455	C	C	221	147	276	136	4.045	4.43E-02	rs4554121	4	32245056	p15.1
SNP_A-2255908	C	C	285	47	341	35	4.047	4.43E-02	---	6	90047470	q15
SNP_A-2246090	G	G	237	181	263	151	4.044	4.43E-02	rs6850140	4	27151479	p15.2
SNP_A-2231771	A	A	311	55	368	42	4.045	4.43E-02	rs4957734	5	107346815	q21.3
SNP_A-2293622	A	A	342	76	358	54	4.046	4.43E-02	rs17015218	1	206356310	q32.2
SNP_A-2054166	A	C	201	187	230	186	4.045	4.43E-02	rs1517661	12	41417800	q12
SNP_A-2075578	A	A	271	151	297	123	4.047	4.43E-02	rs10884942	10	112006916	q25.2
SNP_A-2090322	C	C	279	131	254	160	4.043	4.43E-02	rs16882093	5	9197644	p15.31
SNP_A-2099557	T	T	301	117	317	89	4.046	4.43E-02	rs7316431	12	2975009	p13.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2023560	T	T	300	56	311	85	4.046	4.43E-02	rs16959223	15	30908631	q13.3
SNP_A-2040791	G	G	311	55	368	42	4.045	4.43E-02	rs3869068	6	30112031	p21.33
SNP_A-2034964	C	C	291	97	284	130	4.044	4.43E-02	rs6582143	12	72013017	q21.1
SNP_A-2119467	C	C	231	183	257	153	4.044	4.43E-02	rs571643	11	89873308	q14.3
SNP_A-2149976	C	C	260	92	317	79	4.045	4.43E-02	rs10089434	8	3210534	p23.2
SNP_A-2144975	C	C	269	101	328	88	4.047	4.43E-02	rs11102772	1	114545887	p13.2
SNP_A-2166544	C	C	222	142	224	192	4.045	4.43E-02	rs11732312	4	144844453	q31.21
SNP_A-2164432	A	A	262	86	276	126	4.044	4.43E-02	rs11090066	22	40722695	q13.2
SNP_A-2166159	T	T	340	26	369	47	4.047	4.43E-02	—	5	74667018	q13.3
SNP_A-2205522	G	G	245	115	248	158	4.043	4.43E-02	rs12895061	14	33316845	q13.1
SNP_A-2206192	C	C	246	122	304	110	4.045	4.43E-02	rs6600202	16	2385364	p13.3
SNP_A-1796720	G	G	386	12	361	23	4.044	4.43E-02	rs3748478	20	10589575	p12.2
SNP_A-1682888	T	T	234	114	303	107	4.043	4.43E-02	rs1837171	4	166966144	q32.3
SNP_A-1870314	C	C	308	60	367	47	4.045	4.43E-02	rs2041141	12	1833253	p13.33
SNP_A-1827959	G	G	277	61	305	97	4.045	4.43E-02	rs11025571	11	20439377	p15.1
SNP_A-1820690	C	C	412	6	399	15	4.046	4.43E-02	rs2246310	20	50918996	q13.2
SNP_A-1820750	C	C	314	40	379	29	4.044	4.43E-02	rs11592111	10	126948601	q26.13
SNP_A-1954295	C	C	364	8	396	20	4.046	4.43E-02	rs10828309	10	22798204	p12.2
SNP_A-1952430	A	A	254	110	258	152	4.045	4.43E-02	rs9376365	6	139093669	q23.3
SNP_A-1960252	A	A	256	102	316	90	4.044	4.43E-02	rs1553329	6	55380223	p12.1
SNP_A-1979274	A	A	280	88	287	125	4.044	4.43E-02	rs4256191	4	145597616	q31.21
SNP_A-1914326	A	A	342	24	370	44	4.045	4.43E-02	rs163273	16	20580129	p12.3
SNP_A-1904061	G	G	299	61	290	86	4.043	4.43E-02	rs9953070	18	44406071	q21.1
SNP_A-1889359	G	G	375	29	390	16	4.045	4.43E-02	rs16884218	5	10200123	p15.2
SNP_A-1882803	G	C	208	162	212	204	4.045	4.43E-02	rs369674	6	88100121	q15
SNP_A-1878988	A	A	312	56	328	86	4.046	4.43E-02	rs16844995	1	162153963	q23.3
SNP_A-1880010	A	A	252	94	260	134	4.046	4.43E-02	rs414109	11	9700126	p15.4
SNP_A-1880014	T	T	244	118	249	163	4.044	4.43E-02	rs10894478	11	131348613	q25

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903942	G	G	185	181	239	175	4.04	4.44E-02	rs10095694	8	32619282	p12
SNP_A-1908441	T	T	402	4	408	0	4.04	4.44E-02	rs7904666	10	55544920	q21.1
SNP_A-1923572	T	T	310	60	325	91	4.04	4.44E-02	rs10068957	5	168205931	q34
SNP_A-1976440	C	C	312	14	389	7	4.043	4.44E-02	rs16873385	4	22921468	p15.2
SNP_A-1981634	A	A	281	125	314	102	4.04	4.44E-02	rs6450387	5	55710270	q11.2
SNP_A-1962725	A	A	239	127	298	116	4.042	4.44E-02	rs11124514	2	36533021	p22.2
SNP_A-1961556	T	T	356	26	333	41	4.042	4.44E-02	rs11102032	1	108813944	p13.3
SNP_A-1955264	T	T	339	31	394	20	4.043	4.44E-02	rs198246	14	56258944	q22.3
SNP_A-1817873	C	C	185	169	237	161	4.041	4.44E-02	rs7910754	10	60434150	q21.1
SNP_A-1823139	C	C	338	28	304	42	4.042	4.44E-02	rs4783597	16	65050679	q22.1
SNP_A-1824421	A	A	396	12	402	4	4.04	4.44E-02	rs6598902	1	27789851	p35.3
SNP_A-1830308	G	G	298	70	312	104	4.041	4.44E-02	rs17009114	4	85825249	q21.23
SNP_A-1868462	C	T	190	158	207	185	4.043	4.44E-02	rs339114	3	162591922	q26.1
SNP_A-1852411	G	G	347	1	373	7	4.04	4.44E-02	rs1330014	10	109562676	q25.1
SNP_A-1856120	G	G	323	27	339	47	4.041	4.44E-02	rs7793190	7	20180596	p21.1
SNP_A-1676590	G	G	321	81	306	108	4.04	4.44E-02	rs10509743	10	101854993	q24.31
SNP_A-1641749	G	G	400	0	394	4	4.04	4.44E-02	-	10	80218572	q22.3
SNP_A-1783264	C	C	388	32	369	49	4.04	4.44E-02	rs2523443	6	29523443	p22.1
SNP_A-1788996	C	C	382	40	358	58	4.042	4.44E-02	rs962508	7	50575539	p12.2
SNP_A-1788997	A	A	317	101	336	76	4.041	4.44E-02	rs4635693	3	5581978	p26.1
SNP_A-1787694	A	A	215	205	244	176	4.04	4.44E-02	rs808701	20	19672043	p11.23
SNP_A-2208333	C	C	400	4	406	0	4.04	4.44E-02	rs7843874	8	124654673	q24.13
SNP_A-2211922	T	C	210	186	208	176	4.04	4.44E-02	rs11078928	17	35317995	q21.1
SNP_A-2198407	T	T	292	32	356	22	4.043	4.44E-02	rs4689150	4	7759623	p16.1
SNP_A-2164918	A	A	245	141	285	121	4.043	4.44E-02	rs311387	8	55264176	q11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2159315	C	C	311	59	370	46	4.043	4.44E-02	rs7756629	6	63100657	q11.1
SNP_A-2158916	T	T	316	40	370	28	4.041	4.44E-02	rs12619303	2	220938102	q35
SNP_A-2144304	G	C	219	199	227	189	4.041	4.44E-02	rs893799	2	127180614	q14.3
SNP_A-2141440	G	G	279	139	251	167	4.041	4.44E-02	rs2086256	15	47345318	q21.1
SNP_A-2146440	C	C	341	9	403	3	4.041	4.44E-02	rs860378	2	19357215	p24.1
SNP_A-2121039	T	T	390	12	396	4	4.041	4.44E-02	rs16934465	9	117138409	q33.1
SNP_A-2120143	C	C	273	141	245	169	4.043	4.44E-02	rs256332	5	132926473	q31.1
SNP_A-2121788	A	A	368	44	340	62	4.042	4.44E-02	rs2157743	7	92412153	q21.3
SNP_A-2113399	T	T	352	64	368	44	4.04	4.44E-02	rs3825369	12	2979902	p13.33
SNP_A-2125373	G	G	226	160	248	130	4.041	4.44E-02	rs1570221	10	105646864	q24.33
SNP_A-2134032	G	G	234	186	259	155	4.043	4.44E-02	rs10765351	11	89936321	q14.3
SNP_A-2012491	G	G	339	31	394	20	4.043	4.44E-02	rs4476905	7	31946329	p14.3
SNP_A-2008613	C	C	252	140	208	156	4.042	4.44E-02	rs3732385	3	36847197	p22.3
SNP_A-2003208	G	G	339	31	394	20	4.043	4.44E-02	rs2989594	13	29009750	q12.3
SNP_A-2001224	A	A	302	68	315	101	4.039	4.44E-02	rs4117185	10	58058127	q21.1
SNP_A-2086405	G	G	398	4	404	0	4.04	4.44E-02	rs2089482	17	4558625	p13.2
SNP_A-2083861	A	A	371	15	347	27	4.042	4.44E-02	rs189062	2	137183010	q21.3
SNP_A-2077566	G	G	246	120	291	103	4.041	4.44E-02	rs2389803	4	120751114	q26
SNP_A-2293276	C	C	302	68	315	101	4.039	4.44E-02	rs585719	13	45954400	q14.13
SNP_A-2251711	G	G	194	174	242	162	4.043	4.44E-02	rs2013335	12	51528707	q13.13
SNP_A-2267578	A	A	340	30	364	52	4.042	4.44E-02	rs7584406	2	197704090	q33.1
SNP_A-2260353	G	G	398	4	404	0	4.04	4.44E-02	rs11064445	12	6864604	p13.31
SNP_A-2280437	T	C	184	154	214	190	4.04	4.44E-02	rs2427638	20	62371161	q13.33
SNP_A-2274741	A	T	196	174	215	181	4.04	4.44E-02	rs12818446	12	83517201	q21.31
SNP_A-2251215	A	A	406	4	412	0	4.039	4.45E-02	rs17131634	1	92644256	p22.1
SNP_A-2234114	G	G	406	4	412	0	4.039	4.45E-02	rs3936027	1	166918691	q24.2
SNP_A-2238126	A	A	414	0	408	4	4.039	4.45E-02	rs7905312	10	13786242	p13
SNP_A-2291865	C	C	412	4	418	0	4.039	4.45E-02	rs390406	19	44920811	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289103	A	A	408	4	414	0	4.039	4.45E-02	rs6876130	5	132628238	q31.1
SNP_A-2297789	G	G	299	59	356	46	4.036	4.45E-02	rs10826054	10	58937860	q21.1
SNP_A-2308569	G	G	295	125	265	151	4.037	4.45E-02	rs4082456	1	184888253	q31.1
SNP_A-2304067	A	A	418	0	412	4	4.039	4.45E-02	rs11571116	1	200860494	q32.1
SNP_A-2085083	T	T	223	149	252	124	4.039	4.45E-02	rs11131055	3	6842518	p26.1
SNP_A-2090757	C	C	412	4	418	0	4.039	4.45E-02	rs8015507	14	72918948	q24.3
SNP_A-2101595	G	G	414	4	420	0	4.038	4.45E-02	rs17025947	12	95710715	q23.1
SNP_A-2101755	A	A	243	175	270	146	4.036	4.45E-02	rs10746113	12	106965608	q23.3
SNP_A-2098786	G	G	366	54	345	75	4.039	4.45E-02	rs3888882	3	32472578	p23
SNP_A-2074479	C	C	230	168	207	201	4.038	4.45E-02	rs10887346	10	86413380	q23.1
SNP_A-2050591	C	C	226	142	284	132	4.037	4.45E-02	rs2367957	2	33858915	p22.3
SNP_A-2055779	C	C	298	68	314	102	4.038	4.45E-02	rs17278826	8	14718576	p22
SNP_A-2002154	C	C	422	0	416	4	4.038	4.45E-02	rs10509288	10	68916973	q21.3
SNP_A-2008101	A	A	260	52	342	44	4.036	4.45E-02	rs2249651	21	39640897	q22.2
SNP_A-2014256	T	T	265	99	263	135	4.037	4.45E-02	rs12275115	11	97610250	q22.1
SNP_A-2039387	A	A	375	43	354	62	4.038	4.45E-02	rs11016396	10	130320294	q26.2
SNP_A-2041414	T	T	338	32	395	21	4.037	4.45E-02	rs10201392	2	237838699	q37.3
SNP_A-2042882	G	G	409	11	385	3	4.036	4.45E-02	rs902364	1	39628584	p34.3
SNP_A-2122176	C	C	273	95	280	134	4.039	4.45E-02	rs782103	12	57122898	q14.1
SNP_A-2150216	C	C	410	4	416	0	4.039	4.45E-02	rs17142402	6	6577083	p25.1
SNP_A-2140125	C	C	287	135	312	108	4.039	4.45E-02	rs10786617	10	102825244	q24.31
SNP_A-2189218	G	G	410	12	416	4	4.039	4.45E-02	rs9358517	6	22332200	p22.3
SNP_A-2169726	A	A	328	34	354	58	4.039	4.45E-02	rs2025061	14	38480457	q21.1
SNP_A-2179501	G	G	324	24	359	45	4.037	4.45E-02	rs17821818	22	20659516	q11.22
SNP_A-2208355	C	C	422	0	416	4	4.038	4.45E-02	rs8041176	15	91017461	q26.1
SNP_A-2204916	T	T	198	162	256	156	4.039	4.45E-02	rs476366	6	128085744	q22.33
SNP_A-2202597	T	T	410	4	416	0	4.039	4.45E-02	rs516701	1	198281590	q32.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2214015	A	A	298	122	316	94	4.037	4.45E-02	rs1248627	10	79237105	q22.3
SNP_A-2213974	G	G	226	142	284	132	4.037	4.45E-02	rs17034643	1	10266368	p36.22
SNP_A-2216354	G	G	410	4	416	0	4.039	4.45E-02	rs7285546	22	41451046	q13.2
SNP_A-2219867	A	A	295	125	265	151	4.037	4.45E-02	rs7198698	16	48155763	q12.1
SNP_A-2227117	G	G	410	4	416	0	4.039	4.45E-02	rs265626	12	128633614	q24.33
SNP_A-2225203	G	G	410	4	416	0	4.039	4.45E-02	rs7096351	10	626122	p15.3
SNP_A-1788896	G	G	422	0	416	4	4.038	4.45E-02	rs1258058	1	46819339	p33
SNP_A-1791629	T	C	222	168	196	194	4.038	4.45E-02	rs5768984	22	45299295	q13.31
SNP_A-1790807	A	A	422	0	416	4	4.038	4.45E-02	rs1999861	20	22459936	p11.21
SNP_A-1797634	T	T	277	93	333	79	4.036	4.45E-02	rs6841252	4	65589328	q13.1
SNP_A-1794766	A	A	408	4	414	0	4.039	4.45E-02	rs12482609	21	31326674	q22.11
SNP_A-1809572	T	T	406	4	412	0	4.039	4.45E-02	rs2136440	2	69911149	p13.3
SNP_A-1812416	C	C	254	92	317	81	4.036	4.45E-02	rs1557492	22	20885043	q11.22
SNP_A-1804732	C	C	420	0	414	4	4.038	4.45E-02	rs1105263	3	43420133	p22.1
SNP_A-1752591	G	G	267	133	247	165	4.038	4.45E-02	rs1993511	12	13404769	p13.1
SNP_A-1744979	G	G	274	120	311	99	4.037	4.45E-02	rs10498336	14	36544282	q21.1
SNP_A-1657748	A	A	252	108	255	149	4.038	4.45E-02	rs943653	6	139494199	q24.1
SNP_A-1825555	C	C	329	59	353	41	4.039	4.45E-02	rs1122594	4	24591497	p15.2
SNP_A-1827647	C	C	414	4	420	0	4.038	4.45E-02	rs12052874	2	105534195	q12.2
SNP_A-1819029	C	C	295	125	265	151	4.037	4.45E-02	rs9471457	6	41060373	p21.1
SNP_A-1982492	C	C	195	99	236	84	4.036	4.45E-02	rs10514330	5	89937604	q14.3
SNP_A-1925653	G	G	412	4	418	0	4.039	4.45E-02	rs7919965	10	124941892	q26.13
SNP_A-1922435	A	A	201	157	252	146	4.036	4.45E-02	rs7634931	3	66741722	p14.1
SNP_A-1926139	A	A	359	3	381	11	4.038	4.45E-02	rs10976573	9	7774277	p24.1
SNP_A-1909712	G	G	406	4	412	0	4.039	4.45E-02	rs7739971	6	42067763	p21.1
SNP_A-1878586	C	C	262	156	230	182	4.038	4.45E-02	rs3772003	2	7062335	p25.1
SNP_A-1874281	G	G	312	46	334	74	4.036	4.45E-02	rs12471268	2	153290141	q23.3
SNP_A-1881714	A	A	298	60	362	48	4.037	4.45E-02	rs1532326	12	64203455	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1888746	C	C	420	0	414	4	4.038	4.45E-02	rs3772839	3	126021993	q21.2
SNP_A-1887989	C	C	404	4	410	0	4.039	4.45E-02	rs12060726	1	202983835	q32.1
SNP_A-1881920	A	A	243	97	241	133	4.033	4.46E-02	rs4306981	4	80281300	q21.21
SNP_A-1875151	T	T	351	29	347	47	4.034	4.46E-02	rs17727166	7	25379852	p15.2
SNP_A-1902330	T	T	279	89	283	125	4.033	4.46E-02	rs1545253	4	78688123	q21.1
SNP_A-1899778	T	T	343	9	405	3	4.035	4.46E-02	rs17064961	3	61454747	p14.2
SNP_A-1894145	T	T	378	40	361	59	4.033	4.46E-02	rs10999637	10	72448818	q22.1
SNP_A-1906309	G	G	324	38	275	51	4.035	4.46E-02	rs6059343	20	31531223	q11.22
SNP_A-1917100	G	G	206	104	223	155	4.035	4.46E-02	rs10876128	12	49734822	q13.12
SNP_A-1973652	A	A	244	106	233	139	4.032	4.46E-02	rs1021341	3	101268979	q12.1
SNP_A-1959799	T	T	318	42	316	64	4.035	4.46E-02	rs1510336	3	163325010	q26.1
SNP_A-1933395	G	G	253	107	264	152	4.032	4.46E-02	rs502716	20	874397	p13
SNP_A-1943452	A	A	337	15	354	30	4.035	4.46E-02	rs16914899	12	18990159	p12.3
SNP_A-1944333	T	T	312	52	367	39	4.033	4.46E-02	rs12882576	14	41389265	q21.1
SNP_A-1832903	G	G	219	191	251	165	4.034	4.46E-02	rs10883131	10	100310490	q24.2
SNP_A-1842995	T	T	217	123	196	152	4.034	4.46E-02	rs11174130	12	60357338	q14.1
SNP_A-1842538	C	C	377	43	356	62	4.035	4.46E-02	rs9831604	3	11613935	p25.3
SNP_A-1853960	C	C	343	25	399	15	4.034	4.46E-02	rs16883544	6	74058141	q13
SNP_A-1847394	G	G	317	53	329	81	4.033	4.46E-02	rs194937	6	82498741	q14.1
SNP_A-1870764	A	A	321	49	339	77	4.035	4.46E-02	rs752482	16	17178828	p12.3
SNP_A-1866480	A	A	316	46	376	34	4.033	4.46E-02	rs10831787	11	12299499	p15.3
SNP_A-1864111	T	T	246	96	304	84	4.034	4.46E-02	rs6586771	8	18738671	p22
SNP_A-1692376	C	C	190	158	245	151	4.033	4.46E-02	rs839594	3	31160066	p24.1
SNP_A-1703091	C	C	351	27	375	15	4.035	4.46E-02	rs816753	18	39113345	q12.3
SNP_A-1732972	G	G	274	74	341	63	4.035	4.46E-02	rs10499302	6	155999025	q25.3
SNP_A-1740429	C	C	331	65	323	91	4.033	4.46E-02	rs560494	2	169935587	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1758175	G	G	380	8	368	18	4.034	4.46E-02	rs1525499	7	109332266	q31.1
SNP_A-1805073	A	A	246	110	304	98	4.032	4.46E-02	rs1528502	7	84738892	q21.11
SNP_A-2220371	A	A	246	158	276	132	4.036	4.46E-02	rs9661504	1	202647324	q32.1
SNP_A-2210302	T	T	253	91	263	131	4.032	4.46E-02	rs588629	6	144649339	q24.2
SNP_A-2211665	T	T	406	16	391	29	4.033	4.46E-02	rs17606728	12	106240855	q23.3
SNP_A-2173438	G	G	281	125	259	155	4.033	4.46E-02	rs10004248	4	6013870	p16.1
SNP_A-2198333	C	C	384	36	366	54	4.032	4.46E-02	rs17452064	10	11282477	p14
SNP_A-2196511	G	G	321	49	339	77	4.035	4.46E-02	rs1521168	14	47544577	q21.3
SNP_A-2139680	T	T	244	122	299	109	4.035	4.46E-02	rs782903	15	59152970	q22.2
SNP_A-2144538	A	A	257	93	264	132	4.033	4.46E-02	rs1011275	2	53750489	p16.2
SNP_A-2038622	G	G	340	12	399	5	4.035	4.46E-02	rs7338604	13	47783811	q14.2
SNP_A-2029404	C	C	282	130	308	104	4.035	4.46E-02	rs763580	12	6063798	p13.31
SNP_A-2028978	C	C	221	143	276	132	4.032	4.46E-02	rs12571300	10	120754473	q26.11
SNP_A-2106888	A	A	214	146	275	139	4.034	4.46E-02	rs903077	5	133252303	q31.1
SNP_A-2299103	G	G	300	26	335	15	4.033	4.46E-02	rs11906953	20	41108655	q13.11
SNP_A-2233970	G	A	212	196	230	188	4.033	4.46E-02	rs2693809	8	5387568	p23.2
SNP_A-2231738	A	A	322	16	380	8	4.034	4.46E-02	rs10184975	2	14041476	p24.3
SNP_A-2252474	C	C	404	16	389	29	4.035	4.46E-02	---	1	226582432	q42.13
SNP_A-2253350	G	G	328	42	386	30	4.033	4.46E-02	rs16960037	16	81859618	q23.3
SNP_A-2233128	C	C	180	168	235	163	4.032	4.47E-02	rs913415	9	14454793	p22.3
SNP_A-2230567	T	T	376	32	386	18	4.032	4.47E-02	rs17097182	1	65615466	p31.2
SNP_A-2282609	C	C	247	169	275	141	4.031	4.47E-02	rs7227781	18	20390749	q11.2
SNP_A-2258842	A	A	243	171	210	196	4.029	4.47E-02	rs12949028	17	53180469	q23.2
SNP_A-2261481	T	T	248	100	300	86	4.032	4.47E-02	rs3804570	3	20167059	p24.3
SNP_A-2267128	A	A	256	110	298	92	4.03	4.47E-02	rs1522270	3	193479583	q28

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2288008	A	A	300	64	303	93	4.031	4.47E-02	rs17543807	3	19589284	p24.3
SNP_A-2314442	G	G	387	9	365	19	4.031	4.47E-02	rs10850852	12	116500495	q24.22
SNP_A-2054953	T	T	353	5	387	15	4.028	4.47E-02	rs17171495	7	35365984	p14.2
SNP_A-2070569	G	G	280	66	290	98	4.029	4.47E-02	rs12613103	2	187736813	q32.1
SNP_A-2000460	T	T	404	2	374	8	4.03	4.47E-02	rs7548427	1	165414419	q24.2
SNP_A-2150789	T	T	353	15	385	31	4.029	4.47E-02	rs9443711	6	80532039	q14.1
SNP_A-2113367	T	C	190	170	217	181	4.031	4.47E-02	rs11939691	4	7101749	p16.1
SNP_A-2208931	T	T	309	53	329	83	4.031	4.47E-02	rs6789124	3	141013592	q23
SNP_A-2209827	G	G	331	15	381	7	4.03	4.47E-02	rs2597856	8	56945514	q12.1
SNP_A-2203451	C	C	361	1	389	7	4.028	4.47E-02	rs12633472	3	86477938	p12.1
SNP_A-2221356	A	A	271	97	279	137	4.03	4.47E-02	rs2062090	11	108550308	q22.3
SNP_A-1789435	T	T	232	146	269	125	4.03	4.47E-02	rs12184246	1	47369161	p33
SNP_A-1755026	A	A	231	163	266	140	4.032	4.47E-02	rs718896	3	21235383	p24.3
SNP_A-1653510	G	G	294	56	363	45	4.03	4.47E-02	rs4130580	9	8169325	p24.1
SNP_A-1648666	T	T	200	150	261	145	4.03	4.47E-02	rs9302076	13	93853470	q32.1
SNP_A-1872907	T	T	213	155	211	205	4.03	4.47E-02	rs2156437	18	62868755	q22.1
SNP_A-1868864	G	G	293	57	327	41	4.028	4.47E-02	rs11695450	2	168566502	q24.3
SNP_A-1858158	T	T	303	17	308	32	4.03	4.47E-02	rs10254097	7	94936427	q21.3
SNP_A-1858522	T	T	308	60	323	91	4.029	4.47E-02	rs11944047	4	54190579	q12
SNP_A-1831343	C	C	244	80	289	65	4.031	4.47E-02	rs9304542	18	25460527	q12.1
SNP_A-1815224	A	A	325	69	282	86	4.028	4.47E-02	rs17649453	17	32226256	q12
SNP_A-1980324	T	T	249	163	278	136	4.029	4.47E-02	rs2047382	5	2784890	p15.33
SNP_A-1895752	C	C	345	29	377	17	4.031	4.47E-02	rs12827710	12	73130963	q21.1
SNP_A-1896099	T	T	207	143	202	188	4.029	4.47E-02	rs902967	17	1180365	p13.3
SNP_A-1896352	C	T	206	162	211	201	4.029	4.47E-02	rs3924208	1	231437261	q42.3
SNP_A-1891110	A	A	363	59	380	40	4.031	4.47E-02	rs9394524	6	38769909	p21.2
SNP_A-1879982	T	T	328	38	351	63	4.029	4.47E-02	rs17357657	4	140988964	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1887922	G	G	230	112	222	148	4.031	4.47E-02	rs4376017	3	3237478	p26.2
SNP_A-1878377	A	A	376	8	406	2	4.027	0.0448	rs11838953	13	27300826	q12.2
SNP_A-1912058	C	C	392	22	379	37	4.028	0.0448	rs12705112	7	77187712	q11.23
SNP_A-1988274	G	G	303	19	375	11	4.027	0.0448	rs7760620	6	156968018	q25.3
SNP_A-1967050	C	C	321	25	352	46	4.024	0.0448	rs10498121	2	222353045	q36.1
SNP_A-1936666	T	T	345	25	401	15	4.025	0.0448	rs1424151	16	80686853	q23.3
SNP_A-1821874	A	A	278	64	293	97	4.028	0.0448	rs17758091	14	96953831	q32.2
SNP_A-1843991	G	G	345	25	401	15	4.025	0.0448	rs17110270	12	70459657	q21.1
SNP_A-1848389	A	A	296	68	312	102	4.024	0.0448	rs1509541	4	58509869	q12
SNP_A-1873397	C	C	290	74	297	107	4.028	0.0448	rs12602581	17	28797566	q11.2
SNP_A-1734140	C	C	324	4	349	13	4.028	0.0448	rs1399044	4	157364841	q32.1
SNP_A-1785732	T	T	336	16	396	8	4.027	0.0448	rs6925408	6	29554549	p22.1
SNP_A-1798859	G	G	337	33	360	56	4.024	0.0448	rs11086852	20	40853580	q12
SNP_A-1813145	C	C	272	44	297	29	4.026	0.0448	rs7105659	11	36708908	p12
SNP_A-1809854	G	G	207	163	262	154	4.027	0.0448	rs6473835	8	54556406	q11.23
SNP_A-2227616	G	G	389	1	354	6	4.027	0.0448	---	8	52383099	q11.21
SNP_A-2207427	G	G	291	109	273	139	4.027	0.0448	rs7486860	12	130747834	q24.33
SNP_A-2184944	G	G	251	103	264	148	4.027	0.0448	rs987379	18	37702073	q12.3
SNP_A-2173198	T	T	233	163	206	192	4.025	0.0448	rs2600056	3	2019132	p26.3
SNP_A-2108035	G	G	276	84	278	118	4.025	0.0448	rs4937008	11	124888352	q24.2
SNP_A-2120554	T	T	330	12	387	5	4.026	0.0448	rs2388546	13	29939279	q12.3
SNP_A-2124221	C	C	351	61	334	84	4.027	0.0448	rs10282436	7	25646350	p15.2
SNP_A-2157436	G	A	219	203	230	188	4.026	0.0448	rs2282827	6	15545369	p22.3
SNP_A-2167451	A	A	272	78	334	66	4.028	0.0448	rs11080403	18	10302920	p11.22
SNP_A-1991779	T	T	218	150	274	140	4.027	0.0448	rs1861139	7	153449397	q36.2
SNP_A-1994440	C	C	215	203	245	175	4.026	0.0448	rs718263	8	103045541	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006917	A	A	345	25	401	15	4.025	0.0448	rs7561808	2	192233975	q32.3
SNP_A-2107405	A	A	257	107	320	96	4.026	0.0448	rs2299059	6	15484973	p22.3
SNP_A-2095210	G	G	252	170	222	198	4.024	0.0448	rs10507200	12	104708985	q23.3
SNP_A-2093608	C	C	338	66	349	45	4.024	0.0448	rs16895223	6	29734928	p22.1
SNP_A-2257996	T	T	312	50	374	38	4.027	0.0448	rs9819488	3	134026904	q22.1
SNP_A-2260495	G	G	348	56	377	39	4.027	0.0448	rs1489789	5	57334974	q11.2
SNP_A-2273248	C	C	245	129	234	166	4.024	0.0448	rs1338707	6	145229666	q24.2
SNP_A-2281458	A	A	267	153	293	125	4.023	4.49E-02	rs712177	5	142291693	q31.3
SNP_A-2230866	A	A	275	87	285	125	4.021	4.49E-02	rs590100	18	11982907	p11.21
SNP_A-2231581	A	A	216	154	210	200	4.021	4.49E-02	rs6888172	5	106506215	q21.3
SNP_A-2245764	T	T	234	130	294	120	4.021	4.49E-02	rs529443	1	225384366	q42.13
SNP_A-2241773	C	C	345	73	317	95	4.022	4.49E-02	rs1337167	1	194048092	q31.3
SNP_A-2094390	C	C	399	5	373	13	4.023	4.49E-02	rs9463749	6	52020257	p12.2
SNP_A-2070545	T	T	282	88	338	74	4.024	4.49E-02	rs11751952	6	105110313	q21
SNP_A-2070350	T	T	196	146	253	139	4.021	4.49E-02	rs10492199	12	66773366	q15
SNP_A-2067054	T	T	314	28	357	17	4.022	4.49E-02	rs7893337	10	83298892	q23.1
SNP_A-2062137	A	C	223	195	224	194	4.024	4.49E-02	rs13125675	4	40779551	p14
SNP_A-2017454	A	A	213	205	243	177	4.021	4.49E-02	rs1735326	21	28636914	q21.3
SNP_A-2026502	C	C	202	176	214	138	4.024	4.49E-02	rs10763075	10	55591988	q21.1
SNP_A-2019442	C	C	237	83	304	74	4.022	4.49E-02	rs551558	21	39843109	q22.2
SNP_A-2147395	A	A	344	4	371	13	4.024	4.49E-02	rs11843864	13	63082454	q21.31
SNP_A-2124417	G	A	223	195	224	194	4.024	4.49E-02	rs11731294	4	6024551	p16.1
SNP_A-2128777	T	T	232	98	209	123	4.022	4.49E-02	rs2708308	3	193818240	q28
SNP_A-2137609	A	A	267	153	293	125	4.023	4.49E-02	rs10447274	5	121238114	q23.1
SNP_A-2133598	T	T	278	122	246	146	4.023	4.49E-02	rs3885715	7	57020108	p11.1
SNP_A-2179755	A	A	386	30	386	16	4.022	4.49E-02	rs10099248	8	13040004	p22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2182078	C	C	382	8	412	2	4.021	4.49E-02	rs2140212	8	83684014	q21.13
SNP_A-2186851	A	A	318	78	308	106	4.023	4.49E-02	rs4873759	8	54634803	q11.23
SNP_A-2207598	C	C	323	45	383	33	4.022	4.49E-02	rs17204888	12	9966448	p13.31
SNP_A-2201314	T	T	299	65	358	52	4.023	4.49E-02	rs4927879	3	197365913	q29
SNP_A-2220909	C	C	237	131	293	119	4.024	4.49E-02	rs4431268	4	185421990	q35.1
SNP_A-1791804	G	G	362	44	317	59	4.022	4.49E-02	rs2011463	2	240270422	q37.3
SNP_A-1715065	C	C	312	38	345	65	4.023	4.49E-02	rs725901	18	62291136	q22.1
SNP_A-1780418	C	C	324	10	404	4	4.023	4.49E-02	rs17054099	5	156323558	q33.3
SNP_A-1657063	T	T	375	23	400	12	4.023	4.49E-02	rs172355	1	114020688	p13.2
SNP_A-1683354	T	T	311	29	324	16	4.022	4.49E-02	rs2891563	12	114270993	q24.21
SNP_A-1855346	T	T	359	59	351	37	4.021	4.49E-02	rs11702844	21	33681746	q22.11
SNP_A-1843348	T	T	262	52	275	81	4.021	4.49E-02	rs2463710	6	72923318	q13
SNP_A-1841835	C	C	216	154	210	200	4.021	4.49E-02	rs6436834	2	229740995	q36.3
SNP_A-1816122	A	A	260	136	229	161	4.024	4.49E-02	rs1173485	5	157502407	q33.3
SNP_A-1936244	T	T	271	77	328	64	4.021	4.49E-02	rs7111751	11	124580498	q24.2
SNP_A-1975843	T	T	345	73	317	95	4.022	4.49E-02	rs10516165	4	4627826	p16.2
SNP_A-1969319	G	G	356	12	382	26	4.023	4.49E-02	rs2019116	21	20698949	q21.1
SNP_A-1987188	C	C	287	83	343	69	4.023	4.49E-02	rs479744	6	109126725	q21
SNP_A-1890328	G	G	233	101	247	147	4.023	4.49E-02	rs4904639	14	89705456	q32.11
SNP_A-1882405	C	C	420	0	416	4	4.019	4.50E-02	rs8190568	9	96078525	q22.32
SNP_A-1921468	C	C	272	98	331	85	4.018	4.50E-02	rs4799084	18	75634606	q23
SNP_A-1921965	A	A	414	4	418	0	4.019	4.50E-02	rs12245264	10	70226776	q21.3
SNP_A-1979289	G	G	232	118	227	157	4.019	4.50E-02	rs7662091	4	146564053	q31.21
SNP_A-1965742	C	C	320	98	337	73	4.018	4.50E-02	rs2807562	1	14979335	p36.21
SNP_A-1935831	G	G	418	0	414	4	4.019	4.50E-02	rs8178707	8	42174630	p11.21
SNP_A-1938021	T	T	314	52	369	39	4.019	4.50E-02	rs16824639	1	160790975	q23.3
SNP_A-1944439	T	T	404	0	400	4	4.02	4.50E-02	rs10417246	19	12103729	p13.2
SNP_A-1954004	G	G	318	46	378	34	4.019	4.50E-02	rs9656085	7	103113049	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1820958	A	A	412	8	400	18	4.019	4.50E-02	rs17054615	3	54983131	p14.3
SNP_A-1833896	G	G	279	137	304	110	4.019	4.50E-02	rs6502743	17	3617632	p13.2
SNP_A-1835756	C	C	278	84	337	71	4.017	4.50E-02	rs16950465	18	45017811	q21.1
SNP_A-1854927	G	G	410	0	406	4	4.02	4.50E-02	rs11804052	1	29875884	p35.3
SNP_A-1851932	T	T	267	139	292	112	4.018	4.50E-02	rs12416156	10	8496654	p14
SNP_A-1693497	C	C	307	35	377	25	4.018	4.50E-02	rs1388193	13	88465617	q31.3
SNP_A-1695055	G	G	303	99	286	128	4.02	4.50E-02	rs918689	16	75977204	q23.1
SNP_A-1712235	A	A	236	166	212	198	4.02	4.50E-02	rs280734	2	35078924	p22.3
SNP_A-1753809	T	T	344	44	340	66	4.017	4.50E-02	rs10516232	4	11572038	p15.33
SNP_A-1790165	A	A	412	4	416	0	4.019	4.50E-02	rs10111051	8	10590882	p23.1
SNP_A-1793290	C	C	406	0	402	4	4.02	4.50E-02	rs16895564	5	66067800	q12.3
SNP_A-1802371	C	C	416	4	420	0	4.019	4.50E-02	rs16953104	16	52722874	q12.2
SNP_A-2200081	T	T	273	119	295	93	4.02	4.50E-02	rs4794079	17	45386399	q21.33
SNP_A-2184684	G	G	416	4	420	0	4.019	4.50E-02	rs10759413	9	110180520	q31.3
SNP_A-2191961	T	T	203	197	229	167	4.017	4.50E-02	rs986768	5	16332175	p15.1
SNP_A-2182412	A	A	410	4	414	0	4.019	4.50E-02	rs210900	6	11835941	p24.1
SNP_A-2172509	G	G	406	0	402	4	4.02	4.50E-02	---	6	164397206	q26
SNP_A-2173762	C	C	326	44	375	31	4.017	4.50E-02	rs10828257	10	18450618	p12.33
SNP_A-2136657	G	G	172	164	232	164	4.02	4.50E-02	rs1438866	2	148160650	q22.3
SNP_A-2124067	C	C	336	26	394	16	4.02	4.50E-02	rs13247935	7	136607637	q33
SNP_A-2113081	C	C	404	4	408	0	4.02	4.50E-02	rs16855775	2	169439446	q24.3
SNP_A-2151497	G	G	401	19	387	33	4.018	4.50E-02	rs6490095	12	115748599	q24.22
SNP_A-2142451	G	G	402	4	406	0	4.02	4.50E-02	rs16973455	19	44639337	q13.2
SNP_A-2156371	C	C	404	4	408	0	4.02	4.50E-02	rs1675084	11	61687193	q12.3
SNP_A-2039391	T	T	346	52	369	35	4.017	4.50E-02	rs11195768	10	113709954	q25.2
SNP_A-2040503	A	A	235	135	235	181	4.018	4.50E-02	rs10910376	1	230637591	q42.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2047035	A	A	414	0	410	4	4.019	4.50E-02	rs1654514	19	56091856	q13.41
SNP_A-2060486	C	C	217	193	235	157	4.018	4.50E-02	rs4754284	11	107363912	q22.3
SNP_A-2055302	G	G	235	135	235	181	4.018	4.50E-02	rs6039551	20	9622821	p12.2
SNP_A-2048817	T	T	274	90	282	128	4.019	4.50E-02	rs6441108	3	158254645	q25.31
SNP_A-2070097	C	C	306	62	365	49	4.018	4.50E-02	rs7668455	4	523399	p16.3
SNP_A-2102053	A	A	258	108	318	96	4.017	4.50E-02	rs9262635	6	31133458	p21.33
SNP_A-2102551	T	T	331	35	392	24	4.017	4.50E-02	rs16921974	8	58362727	q12.1
SNP_A-2241925	C	C	416	4	420	0	4.019	4.50E-02	rs8104917	19	38589007	q13.11
SNP_A-2244690	T	T	416	4	420	0	4.019	4.50E-02	rs10484008	14	88446316	q32.11
SNP_A-2228689	G	G	420	0	416	4	4.019	4.50E-02	rs6572845	14	51953386	q22.1
SNP_A-2238933	A	A	258	98	318	86	4.017	4.50E-02	rs4469056	4	155103401	q31.3
SNP_A-2234578	G	G	414	4	418	0	4.019	4.50E-02	rs291761	9	90773260	q22.2
SNP_A-2285087	T	T	420	0	416	4	4.019	4.50E-02	rs2733317	15	55306643	q21.3
SNP_A-2274863	A	A	268	72	278	106	4.018	4.50E-02	rs1913594	12	99725521	q23.1
SNP_A-2277430	A	A	254	166	278	136	4.02	4.50E-02	rs2928665	8	23476388	p21.2
SNP_A-2284132	G	G	365	5	401	15	4.014	4.51E-02	rs11206252	1	54109261	p32.3
SNP_A-2237363	G	G	293	27	347	17	4.015	4.51E-02	rs17165278	6	157746259	q25.3
SNP_A-2237134	A	A	349	11	390	4	4.016	4.51E-02	---	9	104373320	q31.1
SNP_A-2249842	T	T	298	54	367	43	4.015	4.51E-02	rs9814679	3	140852465	q23
SNP_A-2312243	G	G	337	75	312	98	4.016	4.51E-02	rs1519820	15	76364262	q25.1
SNP_A-2095731	G	G	255	85	318	74	4.014	4.51E-02	rs1340005	9	1295268	p24.3
SNP_A-2091987	A	A	284	94	248	114	4.015	4.51E-02	rs13095716	3	12328612	p25.2
SNP_A-2078922	A	A	382	10	399	3	4.014	4.51E-02	rs17067705	5	166241166	q34
SNP_A-2082782	C	C	382	10	399	3	4.014	4.51E-02	rs2153546	10	99306882	q24.2
SNP_A-2065730	C	C	315	55	372	42	4.015	4.51E-02	rs1389826	5	82627912	q14.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2050133	G	G	219	147	216	194	4.017	4.51E-02	rs7376847	4	167717505	q32.3
SNP_A-2055816	C	C	358	8	386	2	4.015	4.51E-02	rs6982160	8	60639227	q12.1
SNP_A-2057280	A	A	266	68	336	58	4.015	4.51E-02	rs2151236	13	40667660	q14.11
SNP_A-2062264	G	G	249	173	219	201	4.015	4.51E-02	rs619824	10	104571278	q24.32
SNP_A-2041204	A	A	239	123	225	157	4.016	4.51E-02	rs979444	8	59241922	q12.1
SNP_A-2034947	C	C	264	84	280	124	4.015	4.51E-02	rs2287034	2	102469106	q11.2
SNP_A-2035283	A	A	335	63	321	87	4.015	4.51E-02	rs2788175	10	115051438	q25.3
SNP_A-2007364	T	T	268	96	319	81	4.015	4.51E-02	rs6134318	20	11602336	p12.2
SNP_A-1989667	T	T	293	71	347	57	4.015	4.51E-02	rs6948900	7	40392235	p14.1
SNP_A-2159427	A	A	270	94	321	79	4.014	4.51E-02	rs1553833	18	62254329	q22.1
SNP_A-2167619	C	C	232	138	289	127	4.014	4.51E-02	rs4260030	15	71063448	q24.1
SNP_A-2164283	T	T	296	70	307	103	4.014	4.51E-02	rs11100528	4	165202726	q32.3
SNP_A-2143066	T	T	292	72	304	106	4.016	4.51E-02	rs17271095	15	59837790	q22.2
SNP_A-2173530	T	T	248	122	306	110	4.015	4.51E-02	rs13104183	4	113681238	q25
SNP_A-2193018	G	G	384	28	393	15	4.015	4.51E-02	rs219231	7	150379369	q36.1
SNP_A-2194522	A	A	236	134	235	179	4.015	4.51E-02	rs9404214	6	103080821	q16.3
SNP_A-2200179	A	A	332	36	354	60	4.014	4.51E-02	rs2291713	4	141903002	q31.21
SNP_A-2208266	A	A	380	42	394	26	4.013	4.51E-02	rs6046594	20	20004542	p11.23
SNP_A-1810431	A	A	316	42	341	69	4.016	4.51E-02	rs6546972	2	75473493	p12
SNP_A-1667894	G	G	368	18	371	33	4.016	4.51E-02	rs10508880	10	43809129	q11.21
SNP_A-1858140	A	A	281	43	351	33	4.013	4.51E-02	rs11064807	12	118361148	q24.23
SNP_A-1863779	T	C	199	153	209	203	4.016	4.51E-02	rs1345526	7	130909072	q32.3
SNP_A-1829625	G	G	298	24	363	15	4.014	4.51E-02	rs16972800	13	108078035	q33.3
SNP_A-1961038	G	G	328	32	353	55	4.014	4.51E-02	rs820769	2	57796041	p16.1
SNP_A-1945345	G	G	205	157	250	142	4.016	4.51E-02	rs9993306	4	32227267	p15.1
SNP_A-1988711	T	T	280	116	247	139	4.014	4.51E-02	rs7787432	7	8334969	p21.3
SNP_A-1983668	G	G	289	133	260	160	4.015	4.51E-02	rs1229718	5	136771691	q31.1
SNP_A-1985728	G	G	369	39	354	58	4.013	4.51E-02	rs4714203	6	39048774	p21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1922159	C	C	225	111	238	160	4.016	4.51E-02	rs7396950	11	68978264	q13.3
SNP_A-1918834	G	G	350	10	341	21	4.015	4.51E-02	rs17362758	1	186051218	q31.1
SNP_A-1881468	G	G	227	141	285	131	4.014	4.51E-02	---	4	112409749	q25
SNP_A-1886149	A	A	258	104	318	92	4.016	4.51E-02	rs10174656	2	78475229	p12
SNP_A-1888053	T	T	257	49	309	37	4.013	4.52E-02	rs709984	14	56476704	q22.3
SNP_A-1916133	T	T	341	63	327	87	4.012	4.52E-02	rs7151201	14	23799940	q11.2
SNP_A-1913342	G	A	232	188	217	203	4.01	4.52E-02	rs10928980	2	127181199	q14.3
SNP_A-1909646	C	C	219	151	275	141	4.012	4.52E-02	rs4816043	20	7999353	p12.3
SNP_A-1908930	T	T	255	105	218	124	4.012	4.52E-02	rs7515116	1	171175311	q25.1
SNP_A-1923772	G	G	389	21	380	36	4.009	4.52E-02	rs6025355	20	36451245	q11.23
SNP_A-1926351	C	C	281	71	293	105	4.013	4.52E-02	rs10210691	2	45576766	p21
SNP_A-1928239	T	T	221	141	221	189	4.013	4.52E-02	rs1835521	4	91440229	q22.1
SNP_A-1976635	A	A	346	20	403	11	4.012	4.52E-02	rs7677718	4	29427951	p15.1
SNP_A-1980434	A	A	211	201	243	175	4.01	4.52E-02	rs890747	5	5472363	p15.32
SNP_A-1941403	T	T	249	105	259	149	4.012	4.52E-02	rs2117380	4	73474331	q13.3
SNP_A-1958332	A	A	319	7	400	2	4.013	4.52E-02	rs7752694	6	89193824	q15
SNP_A-1829817	T	T	379	19	341	31	4.012	4.52E-02	rs17165857	7	93170440	q21.3
SNP_A-1819460	C	C	248	174	218	202	4.012	4.52E-02	rs4843329	16	84561740	q24.1
SNP_A-1660359	C	C	220	182	254	158	4.011	4.52E-02	rs2238147	12	109692557	q24.11
SNP_A-1781980	C	C	264	106	269	147	4.013	4.52E-02	rs2313909	3	68730612	p14.1
SNP_A-1749019	C	C	307	75	302	104	4.012	4.52E-02	rs1466011	5	61038537	q12.1
SNP_A-2212178	G	G	262	160	287	131	4.01	4.52E-02	rs4811465	20	51841188	q13.2
SNP_A-2225811	T	T	331	31	384	20	4.01	4.52E-02	rs17036007	12	103535048	q23.3
SNP_A-2184127	C	T	193	191	222	168	4.012	4.52E-02	rs8025352	15	86990938	q26.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2139333	T	T	340	28	363	49	4.01	4.52E-02	rs10932038	2	204651090	q33.2
SNP_A-2163377	T	T	247	159	221	189	4.011	4.52E-02	rs1957093	14	28069591	q12
SNP_A-2153567	A	G	180	164	218	178	4.01	4.52E-02	rs7415593	1	186219706	q31.1
SNP_A-1993720	G	G	275	113	304	90	4.013	4.52E-02	rs10504462	8	71028133	q13.3
SNP_A-2034716	A	A	331	49	311	69	4.013	4.52E-02	rs17198023	9	18184383	p22.2
SNP_A-2074828	G	G	241	177	209	203	4.011	4.52E-02	rs3748024	2	113062644	q13
SNP_A-2083501	A	G	199	171	221	193	4.013	4.52E-02	rs4686870	3	188500543	q27.3
SNP_A-2095349	T	C	231	189	217	201	4.01	4.52E-02	rs9732187	10	94945141	q23.33
SNP_A-2313056	C	C	242	100	237	135	4.012	4.52E-02	rs7476683	10	118447471	q25.3
SNP_A-2304159	A	A	336	18	361	35	4.01	4.52E-02	rs10429454	9	78136500	q21.2
SNP_A-2288302	C	T	223	199	226	192	4.012	4.52E-02	rs1022177	18	1036304	p11.32
SNP_A-2259000	C	C	256	158	231	189	4.01	4.52E-02	rs4285681	1	90378138	p22.2
SNP_A-2262886	T	T	279	33	341	23	4.009	4.52E-02	rs11124912	2	43134683	p21
SNP_A-2285957	T	T	345	1	373	7	4.008	0.0453	rs16942756	15	87486291	q26.1
SNP_A-2286055	G	G	348	12	407	5	4.009	0.0453	rs7995376	13	107581056	q33.3
SNP_A-2249676	T	T	240	96	258	142	4.006	0.0453	rs1530523	2	119616267	q14.2
SNP_A-2243621	T	T	261	155	287	127	4.009	0.0453	rs12346185	9	72425177	q21.13
SNP_A-2089807	T	C	207	163	212	202	4.007	0.0453	rs215935	6	85546335	q14.3
SNP_A-2085387	T	T	235	77	253	117	4.008	0.0453	rs13210630	6	98111850	q16.1
SNP_A-2043761	T	T	248	116	306	104	4.007	0.0453	rs6948197	7	54309831	p11.2
SNP_A-2005080	A	A	242	178	211	205	4.006	0.0453	rs2109168	17	14427317	p12
SNP_A-2009278	T	T	247	101	259	145	4.007	0.0453	rs1980722	1	4874378	p36.32
SNP_A-2157551	C	C	223	147	278	136	4.009	0.0453	rs12680655	8	135706519	q24.22
SNP_A-2150493	G	G	304	116	329	91	4.007	0.0453	rs85912	8	37274645	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2108137	T	T	259	101	273	75	4.007	0.0453	rs2093823	6	17852712	p22.3
SNP_A-2117433	C	C	249	113	310	102	4.006	0.0453	rs1675874	12	128984909	q24.33
SNP_A-2127718	T	T	285	51	265	71	4.006	0.0453	rs4736727	8	132036731	q24.22
SNP_A-2135702	T	T	315	93	346	72	4.006	0.0453	rs17120197	11	116350314	q23.3
SNP_A-2183138	C	C	227	89	238	130	4.006	0.0453	rs1392814	1	66257266	p31.2
SNP_A-2209786	C	C	199	133	250	122	4.008	0.0453	rs867019	10	84928166	q23.1
SNP_A-2205326	C	C	230	158	275	141	4.006	0.0453	rs12229918	12	64048325	q14.3
SNP_A-1739149	C	C	381	19	380	34	4.007	0.0453	rs10491935	9	78832588	q21.31
SNP_A-1658344	C	C	221	129	287	123	4.006	0.0453	rs4507084	2	202487643	q33.1
SNP_A-1683724	A	A	300	22	315	11	4.008	0.0453	rs10483732	14	59813909	q23.1
SNP_A-1802031	G	G	356	2	377	9	4.008	0.0453	rs2060791	3	77860949	p12.3
SNP_A-1800129	G	G	259	109	313	95	4.007	0.0453	rs11948659	5	87476253	q14.3
SNP_A-1793450	A	A	281	105	328	88	4.008	0.0453	rs12580750	12	88696135	q21.33
SNP_A-1797644	C	C	376	16	401	7	4.008	0.0453	rs1409692	9	32817589	p21.1
SNP_A-1838814	C	C	295	65	347	51	4.007	0.0453	rs12772984	10	29838186	p11.23
SNP_A-1858108	A	A	347	19	368	36	4.006	0.0453	rs159897	13	60331022	q21.2
SNP_A-1856614	G	G	291	71	350	58	4.007	0.0453	rs1400967	2	123205567	q14.3
SNP_A-1957804	G	G	297	67	356	54	4.008	0.0453	rs10854762	22	21389536	q11.22
SNP_A-1951417	A	A	337	85	311	109	4.008	0.0453	rs6416855	17	78529794	q25.3
SNP_A-1940291	A	A	305	101	285	129	4.009	0.0453	rs11197047	10	116818814	q25.3
SNP_A-1945662	C	C	348	46	347	69	4.007	0.0453	rs7817465	8	74710831	q21.11
SNP_A-1977803	T	T	246	122	301	109	4.006	0.0453	rs17499829	4	82655075	q21.21
SNP_A-1977868	C	C	319	19	366	10	4.007	0.0453	rs1847820	4	85251897	q21.23
SNP_A-1930320	G	G	360	60	335	81	4.008	0.0453	rs11758573	6	14238016	p23
SNP_A-1919412	C	C	258	112	312	98	4.008	0.0453	rs4972409	2	174352834	q31.1
SNP_A-1922250	A	A	362	60	337	81	4.003	4.54E-02	rs9807872	19	21629479	p12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1894221	A	A	311	59	320	88	4.003	4.54E-02	---	3	190702305	q28
SNP_A-1968270	T	T	299	123	317	95	4.003	4.54E-02	rs7550055	1	155591837	q23.1
SNP_A-1973372	A	A	296	28	301	47	4.003	4.54E-02	rs12630849	3	79547199	p12.3
SNP_A-1945106	G	G	205	163	250	148	4.005	4.54E-02	rs7727992	5	121058803	q23.1
SNP_A-1939180	T	T	352	48	378	32	4.003	4.54E-02	rs1971884	3	8567934	p25.3
SNP_A-1949043	T	T	191	171	241	161	4.005	4.54E-02	rs6549654	3	74873815	p12.3
SNP_A-1873543	T	T	284	80	348	68	4.005	4.54E-02	rs12708630	16	20115567	p12.3
SNP_A-1790520	C	C	337	85	308	108	4.002	4.54E-02	rs243866	16	54069038	q12.2
SNP_A-1802147	A	A	238	128	294	116	4.003	4.54E-02	rs1511812	4	189815772	q35.2
SNP_A-1804553	A	C	197	183	217	175	4.006	4.54E-02	rs2852911	11	96885650	q22.1
SNP_A-1813918	A	A	312	44	359	31	4.004	4.54E-02	rs2102626	3	118110221	q13.31
SNP_A-1689248	C	C	313	79	346	60	4.005	4.54E-02	rs3910579	10	80140025	q22.3
SNP_A-1644752	A	A	250	138	237	175	4.004	4.54E-02	rs457936	13	30358677	q13.1
SNP_A-1741915	A	A	290	84	285	115	4.004	4.54E-02	rs1449319	3	102092934	q12.2
SNP_A-1751427	C	C	335	57	364	40	4.003	4.54E-02	rs789785	15	33923353	q14
SNP_A-2225096	C	C	213	155	209	203	4.004	4.54E-02	rs12703771	7	139503202	q34
SNP_A-2170715	T	C	196	160	216	198	4.004	4.54E-02	rs1867868	2	113879213	q13
SNP_A-2130540	C	C	206	154	256	142	4.003	4.54E-02	rs7036108	9	104363681	q31.1
SNP_A-2113477	A	A	415	5	389	13	4.004	4.54E-02	rs2618461	8	11403101	p23.1
SNP_A-2139576	A	C	235	185	211	203	4.002	4.54E-02	rs2917080	3	120294717	q13.32
SNP_A-2140506	A	A	320	48	340	76	4.005	4.54E-02	rs11106296	12	90714223	q21.33
SNP_A-2143661	T	T	316	76	282	96	4.005	4.54E-02	rs9891023	17	5334928	p13.2
SNP_A-2012850	G	G	335	19	384	10	4.005	4.54E-02	rs6965592	7	120416510	q31.31
SNP_A-2024483	A	A	413	3	396	10	4.005	4.54E-02	rs3134437	11	122270699	q24.1
SNP_A-2089202	A	A	222	144	273	131	4.004	4.54E-02	rs2366777	5	89979327	q14.3
SNP_A-2064560	G	G	245	177	215	205	4.004	4.54E-02	rs9296436	6	44553024	p21.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235742	G	G	261	49	251	71	4.002	4.54E-02	rs6604066	1	92097352	p22.1
SNP_A-2229918	T	T	308	40	349	27	4.004	4.54E-02	rs12331980	4	170805469	q33
SNP_A-2231661	T	T	352	48	378	32	4.003	4.54E-02	rs2065170	1	170576889	q25.1
SNP_A-2275793	C	C	335	61	294	78	4.006	4.54E-02	rs3014299	1	223916626	q42.13
SNP_A-2273678	T	T	303	59	367	47	4.005	4.54E-02	rs2871005	22	17370780	q11.21
SNP_A-2259153	A	G	190	180	231	183	4.003	4.54E-02	rs11902209	2	79845250	p12
SNP_A-2287770	T	T	233	113	225	149	4.003	4.54E-02	rs6589991	11	122670975	q24.1
SNP_A-2305564	G	G	330	62	305	83	4.005	4.54E-02	rs12042881	1	77680464	p31.1
SNP_A-2308961	G	G	258	104	321	93	4.003	4.54E-02	rs4791573	17	14158697	p12
SNP_A-2311131	A	A	402	4	404	0	4	4.55E-02	rs16904725	8	133804168	q24.22
SNP_A-2309725	G	G	235	129	295	119	3.999	4.55E-02	rs2327290	20	10295418	p12.2
SNP_A-2269545	G	G	347	13	380	28	4.001	4.55E-02	rs8088979	18	38430116	q12.3
SNP_A-2229933	C	C	255	165	223	191	3.998	4.55E-02	rs6969314	7	37949613	p14.1
SNP_A-2240782	C	C	403	15	414	6	4	4.55E-02	rs714908	19	33606701	q12
SNP_A-2252684	C	C	418	4	420	0	4	4.55E-02	rs4711248	6	31015978	p21.33
SNP_A-2256259	G	A	230	192	218	198	3.999	4.55E-02	rs197926	17	42367086	q21.32
SNP_A-2254985	T	T	330	16	388	8	4.001	4.55E-02	rs16945349	17	11629252	p12
SNP_A-2070258	T	T	323	93	341	69	4	4.55E-02	rs10108636	8	3127122	p23.2
SNP_A-2050252	C	C	332	34	391	23	3.999	4.55E-02	rs12582634	12	80364259	q21.31
SNP_A-2090932	C	C	340	26	398	16	4.001	4.55E-02	rs2163194	15	52150269	q21.3
SNP_A-2083799	C	C	303	29	334	52	4.001	4.55E-02	rs12209564	6	74828799	q13
SNP_A-2080182	T	T	281	31	354	22	4.002	4.55E-02	rs3112574	16	51156459	q12.1
SNP_A-2097051	C	C	355	11	391	25	4.001	4.55E-02	rs948699	18	53843445	q21.31
SNP_A-2102792	T	T	359	3	383	11	4	4.55E-02	rs17079677	18	64584139	q22.1
SNP_A-2101038	T	T	404	4	406	0	4	4.55E-02	rs16849860	3	141309499	q23
SNP_A-2028801	A	A	280	78	292	114	4.002	4.55E-02	rs7699581	4	190180772	q35.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2047194	C	C	418	4	420	0	4	4.55E-02	rs7086618	10	70157269	q21.3
SNP_A-2007805	A	A	410	0	408	4	4	4.55E-02	rs2426614	20	54365833	q13.31
SNP_A-2004154	T	T	315	91	296	118	4.001	4.55E-02	rs2606143	15	49729747	q21.2
SNP_A-2159130	G	G	333	31	386	20	4	4.55E-02	rs16849258	3	166800478	q26.1
SNP_A-2136007	T	T	408	4	404	12	4	4.55E-02	rs6942419	7	21111845	p15.3
SNP_A-2171095	C	C	347	33	321	49	4.001	4.55E-02	rs10781238	9	74424166	q21.13
SNP_A-2224233	A	A	239	183	265	153	4.001	4.55E-02	rs7953249	12	119866444	q24.31
SNP_A-1758849	A	A	387	11	389	23	4	4.55E-02	rs4875767	8	2957838	p23.2
SNP_A-1784358	A	A	414	6	403	15	4	4.55E-02	rs10192117	2	135330811	q21.3
SNP_A-1739505	A	A	400	0	398	4	4	4.55E-02	rs10521473	9	74808385	q21.2
SNP_A-1652468	T	T	382	20	377	35	4.002	4.55E-02	rs2638017	3	113580059	q13.2
SNP_A-1696208	G	G	262	138	243	171	4	4.55E-02	rs2397170	6	54681993	p12.1
SNP_A-1806110	C	C	299	99	261	119	3.999	4.55E-02	rs11003389	10	54535967	q21.1
SNP_A-1798861	C	T	189	179	231	183	4	4.55E-02	rs41192	16	47835612	q12.1
SNP_A-1872910	T	T	299	69	353	55	4.002	4.55E-02	rs474186	9	110702021	q31.3
SNP_A-1872509	C	C	262	106	267	147	3.999	4.55E-02	rs1011814	5	44371577	p12
SNP_A-1869654	C	C	347	13	320	24	4.002	4.55E-02	rs4560743	7	158626108	q36.3
SNP_A-1869834	G	G	398	12	402	4	4	4.55E-02	rs7554647	1	27662065	p36.11
SNP_A-1860486	C	C	316	106	337	81	3.999	4.55E-02	rs11715472	3	142476409	q23
SNP_A-1859819	A	A	402	10	372	20	4.001	4.55E-02	rs10009160	4	37517782	p14
SNP_A-1849983	G	G	325	51	313	73	3.998	4.55E-02	rs1324860	13	25591147	q12.13
SNP_A-1842860	A	A	284	76	298	112	4.001	4.55E-02	rs9614258	22	42402008	q13.2
SNP_A-1836508	C	T	207	163	209	199	3.999	4.55E-02	rs11733857	4	40772640	p14
SNP_A-1950610	C	G	230	192	218	198	3.999	4.55E-02	rs2426318	20	49679139	q13.2
SNP_A-1957235	T	T	394	0	392	4	4	4.55E-02	rs9595445	13	45724714	q14.13
SNP_A-1956556	C	C	412	0	410	4	4	4.55E-02	rs16924415	10	68784394	q21.3
SNP_A-1939215	T	T	408	10	399	21	3.999	4.55E-02	rs6045905	20	19133770	p11.23
SNP_A-1939634	G	G	414	4	416	0	4	4.55E-02	rs10153458	19	36956270	q12
SNP_A-1975363	G	G	198	154	245	141	4.001	4.55E-02	rs961882	3	175443614	q26.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1972130	G	G	414	4	416	0	4	4.55E-02	---	1	168058924	q24.3
SNP_A-1966690	C	C	324	40	343	65	3.999	4.55E-02	rs17738962	2	209883574	q34
SNP_A-1962483	C	C	214	184	249	161	4.002	4.55E-02	rs351359	1	112752319	p13.2
SNP_A-1889220	C	C	298	12	333	27	4.002	4.55E-02	rs489945	15	32067495	q14
SNP_A-1880560	G	G	414	0	412	4	4	4.55E-02	rs1915197	15	53019380	q21.3
SNP_A-1930291	T	T	400	4	396	12	4	4.55E-02	rs10057455	5	6573414	p15.31
SNP_A-1917397	C	C	355	11	391	25	4.001	4.55E-02	rs30538	5	15098871	p15.2
SNP_A-1907635	C	C	352	12	411	5	3.996	4.56E-02	rs7721159	5	10945454	p15.2
SNP_A-1904750	T	T	239	121	246	168	3.997	4.56E-02	rs11128202	3	66850749	p14.1
SNP_A-1940821	G	G	310	104	326	78	3.995	4.56E-02	rs2613791	19	5099383	p13.3
SNP_A-1961436	A	A	301	45	357	33	3.996	4.56E-02	rs10066842	5	19040409	p14.3
SNP_A-1855972	C	C	288	72	306	108	3.997	4.56E-02	rs6902651	6	52492399	p12.2
SNP_A-1852705	T	T	301	29	311	49	3.995	4.56E-02	rs11562988	2	51745381	p16.3
SNP_A-1867552	T	T	338	50	357	33	3.996	4.56E-02	rs10805563	5	31265498	p13.3
SNP_A-1787153	T	T	393	25	372	40	3.995	4.56E-02	rs2447347	8	140701717	q24.3
SNP_A-1786306	C	C	276	94	282	132	3.997	4.56E-02	rs6778486	3	187710989	q27.3
SNP_A-1806274	G	G	359	61	378	42	3.995	4.56E-02	rs3782843	12	2983841	p13.33
SNP_A-1694723	C	C	363	39	355	59	3.995	4.56E-02	rs1013017	5	167575160	q34
SNP_A-1689564	T	T	393	9	394	20	3.998	4.56E-02	rs6941626	6	56546025	p12.1
SNP_A-1651454	G	G	206	142	213	197	3.996	4.56E-02	rs4550960	4	81030331	q21.21
SNP_A-1647656	C	C	375	27	399	15	3.997	4.56E-02	rs10494425	1	161990080	q23.3
SNP_A-1668450	C	C	268	74	338	64	3.998	4.56E-02	rs2709847	4	81001221	q21.21
SNP_A-1725366	A	A	322	28	359	51	3.995	4.56E-02	rs441785	4	66022271	q13.1
SNP_A-2220826	G	G	341	23	387	13	3.997	4.56E-02	rs16897170	4	10023683	p16.1
SNP_A-2191625	T	T	241	123	300	112	3.995	4.56E-02	---	14	56033028	q22.3
SNP_A-2136745	T	T	255	99	253	135	3.997	4.56E-02	rs4888535	16	75319157	q23.1
SNP_A-2128240	T	C	213	177	211	191	3.997	4.56E-02	rs10111014	8	94744668	q22.1
SNP_A-2124887	T	T	315	93	290	118	3.995	4.56E-02	rs11125997	2	64572008	p14

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2144835	C	C	304	64	363	51	3.996	4.56E-02	rs6565145	16	81755002	q23.3
SNP_A-2011148	T	T	359	1	389	7	3.998	4.56E-02	rs4527591	5	112483540	q22.2
SNP_A-2014490	G	G	216	152	273	143	3.995	4.56E-02	rs10501955	11	99586799	q22.1
SNP_A-2032888	A	A	241	63	300	52	3.996	4.56E-02	rs7694646	4	100416910	q23
SNP_A-2106521	T	T	316	48	331	75	3.996	4.56E-02	rs1170712	1	187587444	q31.2
SNP_A-2104538	A	A	339	31	361	53	3.997	4.56E-02	rs522202	6	87496898	q14.3
SNP_A-2090874	C	C	372	40	393	25	3.995	4.56E-02	rs4714455	6	41458799	p21.1
SNP_A-2239926	T	T	262	156	229	181	3.996	4.56E-02	rs1476730	17	53193675	q23.2
SNP_A-2231904	T	T	313	83	286	106	3.996	4.56E-02	rs8061200	16	69381006	q22.1
SNP_A-2233019	T	A	229	193	220	198	3.997	4.56E-02	rs2039385	10	110344709	q25.1
SNP_A-2270164	G	G	352	12	411	5	3.996	4.56E-02	rs16910598	8	83617490	q21.13
SNP_A-2264893	G	G	334	22	374	12	3.995	4.56E-02	rs12290883	11	84281431	q14.1
SNP_A-2310349	A	A	337	25	391	15	3.998	4.56E-02	rs2326345	16	83226111	q24.1
SNP_A-2287725	T	T	316	30	380	20	3.997	4.56E-02	rs7386698	8	17609398	p22
SNP_A-2267060	T	T	208	190	236	162	3.993	4.57E-02	rs6730157	2	135740820	q21.3
SNP_A-2282367	T	T	212	202	244	176	3.991	4.57E-02	rs6963245	7	154040324	q36.2
SNP_A-2235423	A	A	353	3	377	11	3.992	4.57E-02	rs4591540	4	145370649	q31.21
SNP_A-2250489	A	A	365	45	337	63	3.994	4.57E-02	rs7401258	14	59430906	q23.1
SNP_A-2248443	A	A	247	105	257	149	3.994	4.57E-02	rs17161607	5	108470727	q21.3
SNP_A-2092825	T	T	313	49	331	77	3.992	4.57E-02	rs7446237	5	107895457	q21.3
SNP_A-2053176	C	C	267	91	332	80	3.994	4.57E-02	rs6568968	6	117428781	q22.1
SNP_A-2070817	A	A	256	148	227	175	3.993	4.57E-02	rs4672344	2	53466769	p16.2
SNP_A-2005164	A	A	317	37	378	26	3.994	4.57E-02	rs1231222	17	36626567	q21.2
SNP_A-1993170	A	A	318	48	338	76	3.994	4.57E-02	rs12056729	8	50187447	q11.21
SNP_A-1995345	C	C	331	11	316	22	3.991	4.57E-02	rs1837695	8	137637459	q24.23
SNP_A-2148134	C	C	383	9	384	20	3.994	4.57E-02	rs12629794	3	31999282	p24.1
SNP_A-2188337	C	C	225	125	290	118	3.991	4.57E-02	rs9393423	6	23734153	p22.3
SNP_A-2192985	C	C	181	173	212	150	3.994	4.57E-02	rs1417958	6	2455494	p25.2
SNP_A-2182740	G	G	342	26	400	16	3.991	4.57E-02	rs17770335	9	23413452	p21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2219440	G	G	299	123	323	97	3.994	4.57E-02	rs17377597	1	9315748	p36.22
SNP_A-2209332	C	A	237	185	213	207	3.992	4.57E-02	rs9897669	17	51427891	q23.2
SNP_A-1689182	C	C	207	195	242	172	3.994	4.57E-02	rs1387381	16	83272419	q23.3
SNP_A-1686532	C	C	345	53	331	75	3.992	4.57E-02	rs7092384	10	8304796	p14
SNP_A-1686920	G	G	313	79	351	61	3.994	4.57E-02	rs6861112	5	16680499	p15.1
SNP_A-1787672	C	C	285	79	294	114	3.992	4.57E-02	rs7216404	17	24239828	q11.2
SNP_A-1790081	G	G	226	134	226	180	3.991	4.57E-02	rs2985941	13	45051601	q14.13
SNP_A-1859844	C	C	330	92	302	116	3.991	4.57E-02	rs4823125	22	42348074	q13.2
SNP_A-1861704	G	G	408	2	380	8	3.991	4.57E-02	rs3934333	10	9556869	p14
SNP_A-1845706	C	C	374	38	354	56	3.991	4.57E-02	rs3917729	1	166312788	q24.2
SNP_A-1840658	T	T	314	56	371	43	3.993	4.57E-02	rs2002028	11	68984613	q13.3
SNP_A-1815813	T	T	295	117	323	93	3.992	4.57E-02	rs7823650	8	117570161	q23.3
SNP_A-1957854	G	T	236	186	214	206	3.991	4.57E-02	rs2362755	3	24691672	p24.2
SNP_A-1954343	T	T	321	25	336	44	3.991	4.57E-02	rs6759814	2	163218268	q24.2
SNP_A-1938599	G	G	343	19	364	36	3.993	4.57E-02	rs443499	1	88567123	p22.2
SNP_A-1983837	G	G	270	90	278	128	3.993	4.57E-02	rs9324973	5	144304626	q31.3
SNP_A-1919123	T	T	333	29	345	49	3.993	4.57E-02	rs16968680	15	75206060	q24.3
SNP_A-1898187	G	G	327	43	385	31	3.992	4.57E-02	rs261339	15	56521781	q21.3
SNP_A-1903788	C	C	208	160	263	151	3.991	4.57E-02	rs4586243	12	89769388	q21.33
SNP_A-1901327	G	G	341	47	323	67	3.992	4.57E-02	rs7172930	15	56389096	q21.3
SNP_A-1879391	T	T	206	164	251	149	3.987	0.0458	rs2155411	11	84337570	q14.1
SNP_A-1912260	A	A	296	46	331	77	3.99	0.0458	rs3135376	6	32493448	p21.32
SNP_A-1927515	T	T	377	43	393	27	3.99	0.0458	rs1505807	3	133384268	q22.1
SNP_A-1988461	C	C	260	104	320	92	3.988	0.0458	rs1390466	6	165036714	q27
SNP_A-1955579	G	G	247	171	214	196	3.988	0.0458	rs9365421	6	162820554	q26

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1815653	C	C	245	175	213	201	3.991	0.0458	rs662141	10	13059519	p13
SNP_A-1859909	C	C	234	106	251	155	3.987	0.0458	rs6824412	4	27774165	p15.2
SNP_A-1788015	C	G	232	190	218	202	3.991	0.0458	rs12141751	1	234010319	q43
SNP_A-1793902	C	C	334	18	375	9	3.987	0.0458	rs6717055	2	202276067	q33.1
SNP_A-1805197	A	A	254	116	256	158	3.989	0.0458	rs10746132	12	75053018	q21.2
SNP_A-1814188	C	C	395	9	352	18	3.989	0.0458	rs6500824	16	6760961	p13.2
SNP_A-1808876	T	T	200	170	253	161	3.989	0.0458	rs823485	1	230978002	q42.2
SNP_A-1660743	C	C	246	154	226	188	3.988	0.0458	rs7455032	7	143899717	q35
SNP_A-1785156	A	A	314	90	282	112	3.989	0.0458	rs6501229	17	74045897	q25.3
SNP_A-1750745	T	T	230	172	208	206	3.988	0.0458	rs307810	5	180180911	q35.3
SNP_A-1752091	C	C	302	48	369	37	3.987	0.0458	rs3797819	5	108364201	q21.3
SNP_A-2216375	G	G	249	117	252	160	3.987	0.0458	rs910050	6	32423632	p21.32
SNP_A-2182677	C	C	246	176	215	203	3.989	0.0458	rs545013	19	7533641	p13.2
SNP_A-2174062	A	G	216	190	207	177	3.989	0.0458	rs7127228	11	127407910	q24.2
SNP_A-2172090	A	A	199	149	236	130	3.99	0.0458	rs10183142	2	142494620	q22.1
SNP_A-2198524	C	C	362	8	396	20	3.989	0.0458	rs17078563	13	22762836	q12.12
SNP_A-2145944	G	G	316	34	345	21	3.989	0.0458	rs11241539	5	119608393	q23.1
SNP_A-2129049	T	T	245	177	214	204	3.988	0.0458	rs7516730	1	73977912	p31.1
SNP_A-2107943	A	A	284	136	306	108	3.99	0.0458	rs536280	10	115065034	q25.3
SNP_A-2109686	C	C	393	27	377	43	3.99	0.0458	rs16910255	9	120836537	q33.2
SNP_A-2119508	G	G	317	7	396	2	3.988	0.0458	rs2332456	14	70284984	q24.2
SNP_A-2120658	C	C	388	22	405	11	3.988	0.0458	rs11842552	13	30140235	q12.3
SNP_A-1994454	T	T	264	132	216	146	3.988	0.0458	rs565338	8	104080736	q22.3
SNP_A-2013230	G	G	305	21	360	12	3.989	0.0458	rs17107208	1	52596703	p32.3
SNP_A-2067103	G	G	234	180	256	148	3.988	0.0458	rs6891528	5	172911511	q35.2
SNP_A-2092029	A	A	283	61	285	89	3.987	0.0458	rs11220261	11	125252679	q24.2
SNP_A-2086385	G	G	245	103	228	132	3.987	0.0458	rs12775779	10	29841854	p11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082266	C	C	226	132	194	154	3.99	0.0458	rs6834821	4	17055005	p15.32
SNP_A-2252510	G	T	233	189	217	203	3.991	0.0458	rs2900554	12	11025968	p13.2
SNP_A-2253454	G	G	308	54	323	83	3.988	0.0458	rs12254002	10	919133	p15.3
SNP_A-2287547	G	G	351	59	375	41	3.99	0.0458	rs2459811	5	17444228	p15.1
SNP_A-2257134	G	G	366	28	394	16	3.987	0.0458	rs13346080	19	47579332	q13.2
SNP_A-2292499	A	A	308	52	317	79	3.989	0.0458	rs2560614	5	116744499	q23.1
SNP_A-2291154	T	T	337	29	365	51	3.986	4.59E-02	rs4935649	10	57909670	q21.1
SNP_A-2286823	C	C	344	62	327	85	3.986	4.59E-02	rs2899632	15	56599161	q21.3
SNP_A-2274296	T	T	377	41	353	59	3.986	4.59E-02	rs4284353	10	87861649	q23.2
SNP_A-2277842	C	C	281	71	338	58	3.984	4.59E-02	rs11124988	2	44459933	p21
SNP_A-2066925	C	C	296	36	364	26	3.985	4.59E-02	---	22	43401796	q13.31
SNP_A-2069717	C	G	212	186	210	180	3.986	4.59E-02	rs3088241	11	125268956	q24.2
SNP_A-2061520	T	T	360	8	394	20	3.984	4.59E-02	rs12168968	22	34715747	q12.3
SNP_A-2060593	A	A	369	17	367	7	3.984	4.59E-02	rs3765944	1	119767986	p12
SNP_A-2004291	A	A	267	151	279	117	3.985	4.59E-02	rs793517	10	98977512	q24.1
SNP_A-2024950	G	G	331	29	378	18	3.985	4.59E-02	rs2955160	16	80689079	q23.3
SNP_A-2021103	A	A	308	58	365	45	3.986	4.59E-02	rs2738708	16	77080865	q23.1
SNP_A-2123382	T	T	329	87	297	109	3.984	4.59E-02	rs1348103	7	126985803	q32.1
SNP_A-2160141	T	T	258	162	283	133	3.987	4.59E-02	rs4953208	2	45349012	p21
SNP_A-2161735	C	C	239	125	243	171	3.985	4.59E-02	rs9290259	3	166260379	q26.1
SNP_A-2194334	A	A	351	7	376	18	3.985	4.59E-02	rs207145	1	55520164	p32.3
SNP_A-2222318	T	T	275	117	263	151	3.984	4.59E-02	rs4386973	8	75317480	q21.11
SNP_A-2224687	A	A	310	60	322	90	3.984	4.59E-02	rs4241952	4	135797511	q28.3
SNP_A-2213075	A	A	350	20	378	38	3.985	4.59E-02	rs17005990	4	83927201	q21.22
SNP_A-2210405	T	T	202	166	254	156	3.985	4.59E-02	rs6555954	5	170765610	q35.1
SNP_A-1813351	G	A	197	173	220	188	3.985	4.59E-02	rs565736	2	161486751	q24.2
SNP_A-1801947	T	T	210	144	268	136	3.985	4.59E-02	rs10218464	1	90578999	p22.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1793394	C	C	361	57	374	38	3.987	4.59E-02	rs7104461	11	72072094	q13.4
SNP_A-1791957	A	A	338	54	363	37	3.987	4.59E-02	rs3767145	1	21641108	p36.12
SNP_A-1863923	A	A	302	60	359	47	3.987	4.59E-02	rs7450548	6	162964656	q26
SNP_A-1870679	A	A	341	27	368	48	3.984	4.59E-02	rs2058177	17	66249013	q24.3
SNP_A-1852191	A	A	378	38	358	56	3.985	4.59E-02	rs7191857	16	52829875	q12.2
SNP_A-1853319	A	A	292	72	351	59	3.984	4.59E-02	rs1998022	14	43636337	q21.2
SNP_A-1837167	G	G	296	62	312	94	3.985	4.59E-02	rs13405503	2	199422091	q33.1
SNP_A-1835124	T	T	267	87	316	72	3.984	4.59E-02	rs759923	12	113065330	q24.21
SNP_A-1833053	C	C	306	36	376	26	3.985	4.59E-02	rs6484720	11	34406261	p13
SNP_A-1944356	G	G	292	12	340	28	3.986	4.59E-02	rs11171209	12	53664690	q13.2
SNP_A-1989440	G	G	228	184	255	155	3.985	4.59E-02	rs215634	7	32142388	p14.3
SNP_A-1964933	G	G	370	38	385	23	3.987	4.59E-02	rs16829733	2	134479332	q21.2
SNP_A-1876251	A	A	324	10	402	4	3.984	4.59E-02	rs328481	11	25950455	p14.3
SNP_A-1876762	G	G	344	6	360	16	3.983	4.60E-02	rs4529003	4	162803866	q32.2
SNP_A-1903066	C	C	267	103	270	142	3.981	4.60E-02	rs2043680	18	36511380	q12.3
SNP_A-1898543	C	C	266	140	236	166	3.982	4.60E-02	rs3822235	4	17371185	p15.32
SNP_A-1932288	C	C	258	98	304	82	3.981	4.60E-02	rs12614069	2	75087758	p12
SNP_A-1916199	G	G	322	38	280	52	3.982	4.60E-02	rs17341659	8	101523126	q22.2
SNP_A-1916255	A	A	402	4	402	0	3.98	4.60E-02	rs7795090	7	67712911	q11.22
SNP_A-1972358	G	G	414	4	414	0	3.981	4.60E-02	rs16843837	1	168796782	q24.3
SNP_A-1838532	A	A	303	117	328	92	3.981	4.60E-02	rs2056974	1	22154400	p36.12
SNP_A-1801966	T	T	297	73	309	107	3.981	4.60E-02	rs10747489	1	98030756	p21.3
SNP_A-1808782	A	A	416	0	416	4	3.981	4.60E-02	rs17052760	9	87191653	q21.33
SNP_A-1713780	T	T	324	24	393	15	3.98	4.60E-02	rs2184270	13	87653968	q31.2
SNP_A-1675938	C	C	402	0	402	4	3.98	4.60E-02	rs970426	16	6781297	p13.2
SNP_A-2174176	T	T	303	13	366	6	3.98	4.60E-02	rs17128718	1	66451598	p31.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2160692	C	C	285	51	302	80	3.981	4.60E-02	rs11647783	16	82379920	q23.3
SNP_A-2158713	C	C	309	59	326	90	3.981	4.60E-02	rs2638100	11	6926252	p15.4
SNP_A-2153387	A	A	319	23	340	12	3.983	4.60E-02	rs10878678	12	66543553	q15
SNP_A-2149077	G	G	402	4	402	0	3.98	4.60E-02	rs17101428	10	84907477	q23.1
SNP_A-2142211	A	A	329	9	311	19	3.982	4.60E-02	rs17118612	14	46962058	q21.3
SNP_A-2139791	T	T	278	90	337	77	3.98	4.60E-02	rs7607014	2	73641829	p13.1
SNP_A-2109906	T	T	349	5	356	14	3.981	4.60E-02	rs2038623	6	157355357	q25.3
SNP_A-2108340	G	G	410	4	410	0	3.981	4.60E-02	rs686955	12	3119895	p13.32
SNP_A-2028524	C	C	362	2	385	9	3.982	4.60E-02	rs3016594	18	2990857	p11.31
SNP_A-2043454	A	A	403	1	370	6	3.98	4.60E-02	rs17025986	1	110784174	p13.3
SNP_A-2034399	G	G	336	86	310	110	3.98	4.60E-02	rs17292696	3	59661326	p14.2
SNP_A-2018306	C	C	250	120	308	108	3.982	4.60E-02	rs2834209	21	33674664	q22.11
SNP_A-2069003	A	A	366	4	397	13	3.983	4.60E-02	rs4889048	16	78537214	q23.2
SNP_A-2081313	A	A	316	44	363	31	3.982	4.60E-02	rs10912297	1	184970496	q31.1
SNP_A-2097837	T	T	412	4	412	0	3.981	4.60E-02	rs7603729	2	65343157	p14
SNP_A-2102348	G	G	287	61	342	48	3.982	4.60E-02	rs4495107	4	54480763	q12
SNP_A-2247925	G	G	410	4	410	0	3.981	4.60E-02	rs7726886	5	161846701	q34
SNP_A-2236792	A	A	278	90	337	77	3.98	4.60E-02	rs17151496	10	12354709	p13
SNP_A-2298461	A	A	289	77	300	112	3.981	4.60E-02	rs11127582	3	77402128	p12.3
SNP_A-2301089	G	G	412	4	412	0	3.981	4.60E-02	rs16846351	1	223153447	q42.12
SNP_A-2300611	G	G	408	4	408	0	3.981	4.60E-02	rs8058588	16	22085711	p12.1
SNP_A-2306884	C	C	416	4	416	0	3.981	4.60E-02	rs16956181	18	10041028	p11.22
SNP_A-2313543	T	T	354	68	317	87	3.979	4.61E-02	rs17175892	17	65847254	q24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2299171	A	A	240	170	269	143	3.976	4.61E-02	rs962895	6	164414472	q26
SNP_A-2296042	G	G	365	1	397	7	3.978	4.61E-02	rs12208481	6	72003210	q13
SNP_A-2294221	G	G	307	33	328	56	3.979	4.61E-02	rs654551	6	87479339	q14.3
SNP_A-2238830	G	G	315	21	347	11	3.978	4.61E-02	rs17016859	4	91628543	q22.1
SNP_A-2248380	A	A	248	96	309	85	3.98	4.61E-02	rs17678541	14	40843491	q21.1
SNP_A-2258750	T	T	341	19	318	32	3.976	4.61E-02	rs16931131	12	4089626	p13.32
SNP_A-2100944	G	G	288	76	342	62	3.976	4.61E-02	rs2430624	12	15065706	p12.3
SNP_A-2104445	A	A	254	102	245	135	3.979	4.61E-02	rs7161385	14	52555486	q22.1
SNP_A-2098191	G	G	320	40	339	65	3.979	4.61E-02	rs12895374	14	35028019	q13.2
SNP_A-2079838	A	A	399	5	375	13	3.978	4.61E-02	rs7025426	9	27477349	p21.2
SNP_A-2011681	A	A	229	95	239	137	3.976	4.61E-02	rs2534812	6	30590972	p21.33
SNP_A-2010498	C	C	195	149	238	134	3.976	4.61E-02	rs793777	4	185689562	q35.1
SNP_A-2005950	G	G	355	61	330	82	3.977	4.61E-02	rs9325559	10	120811615	q26.11
SNP_A-2039143	G	G	261	109	318	96	3.979	4.61E-02	rs6909832	6	161830066	q26
SNP_A-2038600	C	C	360	2	383	9	3.979	4.61E-02	rs2204701	11	23887517	p14.3
SNP_A-2021386	G	G	213	147	210	194	3.978	4.61E-02	rs11655496	17	33929377	q12
SNP_A-2025424	C	C	268	68	276	100	3.978	4.61E-02	rs2348942	12	126823545	q24.32
SNP_A-2134983	A	A	277	91	278	126	3.977	4.61E-02	rs11735007	4	28162003	p15.1
SNP_A-2133484	T	T	318	24	285	37	3.978	4.61E-02	rs9599128	13	66142867	q21.32
SNP_A-2142714	G	G	345	65	326	88	3.976	4.61E-02	rs2313476	13	19649019	q12.11
SNP_A-2169647	G	G	320	40	339	65	3.979	4.61E-02	rs16873539	6	45682128	p21.1
SNP_A-2195078	T	T	277	93	336	80	3.977	4.61E-02	rs2793098	1	228180878	q42.2
SNP_A-2195251	G	-	240	182	208	208	3.976	4.61E-02	rs803926	9	116482922	q33.1
SNP_A-1684598	G	G	307	95	338	74	3.977	4.61E-02	rs2298581	18	667931	p11.32
SNP_A-1781920	T	T	326	94	295	117	3.978	4.61E-02	rs7115145	11	58356786	q12.1
SNP_A-1801428	C	C	335	33	392	22	3.977	4.61E-02	rs12781009	10	63107992	q21.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787973	C	C	263	149	235	177	3.979	4.61E-02	rs4808057	19	16888607	p13.11
SNP_A-1787705	A	A	276	76	284	110	3.977	4.61E-02	rs2890714	2	143961344	q22.2
SNP_A-1797474	C	C	302	116	274	142	3.976	4.61E-02	rs10817517	9	113578581	q32
SNP_A-1837926	C	C	331	37	381	25	3.978	4.61E-02	rs11212886	11	108425255	q22.3
SNP_A-1834779	C	C	306	64	365	51	3.979	4.61E-02	rs8050581	16	81755160	q23.3
SNP_A-1872207	T	T	295	47	360	36	3.978	4.61E-02	rs2911301	16	61181883	q21
SNP_A-1868969	A	A	314	52	328	80	3.977	4.61E-02	rs4356840	3	21775177	p24.3
SNP_A-1976288	A	A	273	145	245	173	3.979	4.61E-02	rs10939746	4	17361220	p15.32
SNP_A-1974292	T	T	324	48	291	65	3.979	4.61E-02	rs13099725	3	128410628	q21.3
SNP_A-1968476	C	C	256	166	224	192	3.979	4.61E-02	rs10494329	1	156377118	q23.2
SNP_A-1967758	T	T	294	68	358	56	3.977	4.61E-02	rs10494312	1	154046854	q23.1
SNP_A-1947022	A	A	315	35	301	53	3.977	4.61E-02	rs11030574	11	29042415	p14.1
SNP_A-1923889	A	A	306	64	365	51	3.979	4.61E-02	rs12103103	16	81754371	q23.3
SNP_A-1923473	A	A	369	41	392	26	3.976	4.61E-02	rs1908161	11	25657046	p14.3
SNP_A-1925981	A	A	282	60	292	90	3.976	4.61E-02	rs7965930	12	45045903	q13.11
SNP_A-1899861	G	G	313	91	297	119	3.978	4.61E-02	rs1080225	13	58546695	q21.2
SNP_A-1899199	C	C	335	33	392	22	3.977	4.61E-02	rs17652715	12	43378927	q12
SNP_A-1889927	G	G	357	13	330	24	3.98	4.61E-02	rs7546098	1	19874251	p36.13
SNP_A-1890688	T	T	284	138	309	111	3.977	4.61E-02	rs11245127	10	128422890	q26.2
SNP_A-1876980	C	C	386	0	386	4	3.979	4.61E-02	rs7705426	5	14299577	p15.2
SNP_A-1876199	T	T	400	8	390	18	3.973	4.62E-02	rs17063781	3	60636186	p14.2
SNP_A-1886132	A	A	296	124	320	98	3.975	4.62E-02	rs1261990	10	79237800	q22.3
SNP_A-1885964	G	G	259	133	232	160	3.973	4.62E-02	rs4801225	19	62684998	q13.43
SNP_A-1882543	T	T	358	18	374	34	3.973	4.62E-02	rs1526809	12	73690627	q21.1
SNP_A-1890425	A	A	240	88	226	116	3.973	4.62E-02	rs12374502	5	44132218	p12
SNP_A-1925490	A	A	321	37	286	52	3.975	4.62E-02	rs17278280	9	31976303	p21.1
SNP_A-1923080	C	T	206	164	214	202	3.974	4.62E-02	rs6478430	9	119496775	q33.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1928807	G	G	397	21	377	35	3.974	4.62E-02	rs10136661	14	77993962	q24.3
SNP_A-1928822	G	G	217	139	261	123	3.974	4.62E-02	rs3802268	8	12630632	p23.1
SNP_A-1945425	T	T	306	114	274	138	3.975	4.62E-02	rs12695150	3	107678003	q13.11
SNP_A-1953113	C	C	356	14	383	29	3.975	4.62E-02	rs17038761	2	49557901	p16.3
SNP_A-1951380	G	G	183	165	237	159	3.974	4.62E-02	rs6491899	13	104366383	q33.2
SNP_A-1981077	C	C	297	41	302	64	3.972	4.62E-02	rs4867190	5	29696192	p13.3
SNP_A-1860535	A	A	349	17	382	34	3.976	4.62E-02	rs17403010	2	36140049	p22.3
SNP_A-1853894	A	A	256	56	279	39	3.974	4.62E-02	rs11251146	10	2331027	p15.3
SNP_A-1841554	G	G	383	29	396	16	3.973	4.62E-02	rs2285291	8	17250959	p22
SNP_A-1790116	T	T	346	74	365	53	3.975	4.62E-02	rs10831742	11	12126901	p15.3
SNP_A-1812806	G	G	197	165	251	157	3.974	4.62E-02	rs614966	18	23837890	q12.1
SNP_A-1742775	A	A	282	120	313	97	3.974	4.62E-02	rs4345013	22	25706391	q12.1
SNP_A-1656625	C	C	212	190	247	167	3.975	4.62E-02	rs2073489	1	224038302	q42.13
SNP_A-2199297	C	C	346	12	403	5	3.973	4.62E-02	rs16918847	8	61424207	q12.1
SNP_A-2181586	C	C	234	136	291	125	3.974	4.62E-02	rs10732936	10	12673372	p13
SNP_A-2180442	T	T	376	6	409	1	3.974	4.62E-02	rs1863033	14	78275040	q24.3
SNP_A-2220802	G	G	218	140	270	128	3.973	4.62E-02	rs7515190	1	180671971	q25.3
SNP_A-2141719	A	A	244	176	211	201	3.975	4.62E-02	rs13002374	2	134162427	q21.2
SNP_A-2146667	C	C	300	66	304	44	3.975	4.62E-02	rs9349061	6	38322423	p21.2
SNP_A-2160635	G	G	240	124	243	169	3.976	4.62E-02	rs13104542	4	154726567	q31.3
SNP_A-2111259	C	C	212	154	204	198	3.975	4.62E-02	---	17	17366356	p11.2
SNP_A-2121716	C	C	286	72	289	103	3.974	4.62E-02	rs7751208	6	87596742	q15
SNP_A-2116954	A	A	316	88	293	113	3.973	4.62E-02	rs8007865	14	50896197	q22.1
SNP_A-2029441	C	C	346	12	403	5	3.973	4.62E-02	rs11872718	18	47727632	q21.1
SNP_A-2034276	C	C	263	73	303	57	3.973	4.62E-02	rs1963340	18	5442292	p11.31
SNP_A-2016486	A	A	296	22	294	38	3.974	4.62E-02	rs244179	21	23254346	q21.2
SNP_A-2013437	A	A	272	94	278	132	3.973	4.62E-02	rs4398899	8	59251382	q12.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1994686	T	T	320	22	358	12	3.976	4.62E-02	rs16882218	8	112647715	q23.3
SNP_A-2081503	G	G	261	107	321	95	3.975	4.62E-02	rs1038453	3	58619766	p14.2
SNP_A-2083143	C	C	336	32	391	21	3.975	4.62E-02	rs6431504	2	237783295	q37.3
SNP_A-2061406	A	G	206	164	214	202	3.974	4.62E-02	rs10192190	2	237585366	q37.3
SNP_A-2258961	T	T	313	53	330	82	3.973	4.62E-02	rs3804857	3	7653617	p26.1
SNP_A-2312953	G	G	249	119	253	163	3.973	4.62E-02	rs4952359	2	41529412	p22.1
SNP_A-2311100	A	A	389	29	402	16	3.969	4.63E-02	rs4717562	7	69826573	q11.22
SNP_A-2304046	A	A	228	122	225	163	3.972	4.63E-02	rs881502	17	71663961	q25.1
SNP_A-2258603	C	C	305	65	364	52	3.969	4.63E-02	rs16924700	8	60238953	q12.1
SNP_A-2261290	A	A	393	25	405	13	3.97	4.63E-02	rs7043125	9	101553307	q31.1
SNP_A-2275830	G	G	270	74	340	64	3.97	4.63E-02	rs10227362	7	2230040	p22.3
SNP_A-2286241	A	A	237	73	232	102	3.97	4.63E-02	rs10440526	4	190939136	q35.2
SNP_A-2282538	G	G	368	8	394	2	3.972	4.63E-02	rs7153139	14	46403821	q21.3
SNP_A-2246873	A	A	263	101	320	88	3.972	4.63E-02	rs667924	6	10592846	p24.3
SNP_A-2246397	G	G	238	128	238	172	3.971	4.63E-02	rs8008977	14	27945491	q12
SNP_A-2251864	A	A	305	65	364	52	3.969	4.63E-02	rs32504	5	55620174	q11.2
SNP_A-2097189	C	C	289	77	303	113	3.971	4.63E-02	rs4468012	9	83167309	q21.32
SNP_A-2000419	T	T	217	151	274	142	3.97	4.63E-02	rs4403608	1	160723175	q23.3
SNP_A-1999886	T	T	263	99	272	140	3.971	4.63E-02	rs1772636	1	13692825	p36.21
SNP_A-2012249	T	T	295	61	338	46	3.97	4.63E-02	rs2510033	11	77619419	q14.1
SNP_A-2033569	A	A	307	55	325	85	3.972	4.63E-02	rs7643749	3	174355430	q26.31
SNP_A-2046901	A	A	339	31	392	20	3.971	4.63E-02	rs7978244	12	61106231	q14.1
SNP_A-2044259	G	G	213	189	248	166	3.972	4.63E-02	rs487740	5	6571618	p15.31
SNP_A-2135175	G	G	213	151	271	143	3.971	4.63E-02	rs6471613	8	58556491	q12.1
SNP_A-2137101	G	G	221	143	222	192	3.972	4.63E-02	rs1555009	6	162811333	q26

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2221828	T	T	291	75	301	109	3.969	4.63E-02	rs7084413	10	23314154	p12.2
SNP_A-2226327	G	G	271	83	279	119	3.971	4.63E-02	rs2109424	12	4862873	p13.32
SNP_A-2214400	A	A	393	25	405	13	3.97	4.63E-02	rs2448246	14	101399588	q32.31
SNP_A-2203436	C	C	339	27	399	17	3.97	4.63E-02	rs17363245	5	113925780	q22.3
SNP_A-2187853	A	A	332	78	313	103	3.969	4.63E-02	rs17797834	19	48479157	q13.31
SNP_A-2190432	C	C	348	72	365	51	3.972	4.63E-02	rs17285278	16	81981328	q23.3
SNP_A-2184470	C	C	292	130	262	156	3.969	4.63E-02	rs12033437	1	19495200	p36.13
SNP_A-1650598	T	T	220	180	255	157	3.972	4.63E-02	rs4092003	21	16696707	q21.1
SNP_A-1687328	A	A	341	59	372	42	3.97	4.63E-02	rs10496753	2	137719793	q21.3
SNP_A-1781426	A	A	384	34	363	51	3.971	4.63E-02	rs2571444	2	218524622	q35
SNP_A-1783470	G	G	218	136	266	122	3.97	4.63E-02	rs2880143	4	61758822	q13.1
SNP_A-1810336	C	C	386	30	364	46	3.97	4.63E-02	rs630085	18	8297219	p11.23
SNP_A-1802124	T	T	264	92	255	123	3.97	4.63E-02	rs1521795	18	30287990	q12.1
SNP_A-1806138	C	C	241	175	269	147	3.972	4.63E-02	rs11898048	2	69039578	p13.3
SNP_A-1798992	C	C	221	201	244	168	3.97	4.63E-02	rs2279291	15	59009120	q22.2
SNP_A-1835857	T	T	278	84	332	70	3.97	4.63E-02	rs10756759	9	16530446	p22.3
SNP_A-1827185	G	G	411	3	396	10	3.97	4.63E-02	rs1146603	1	75951721	p31.1
SNP_A-1857611	A	A	291	75	298	108	3.972	4.63E-02	rs9577623	13	111582494	q34
SNP_A-1863430	T	T	280	84	288	120	3.971	4.63E-02	rs3971192	3	152530526	q25.1
SNP_A-1873719	G	G	402	16	389	29	3.969	4.63E-02	rs10512605	17	71723977	q25.1
SNP_A-1986746	G	G	319	29	338	50	3.97	4.63E-02	rs13200742	6	86838202	q14.3
SNP_A-1983335	T	T	328	40	382	28	3.969	4.63E-02	rs2408482	5	125045829	q23.2
SNP_A-1965492	C	T	198	172	223	193	3.97	4.63E-02	rs2691775	2	156259598	q24.1
SNP_A-1956266	C	C	322	28	382	18	3.972	4.63E-02	rs1951667	14	53719881	q22.2
SNP_A-1929372	A	A	266	148	297	123	3.97	4.63E-02	rs12616969	2	1710337712	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1926123	A	A	252	90	321	81	3.97	4.63E-02	rs17818883	3	100253968	q12.1
SNP_A-1906766	A	A	301	67	360	54	3.971	4.63E-02	rs3901856	6	118677207	q22.31
SNP_A-1909930	C	T	212	164	206	200	3.972	4.63E-02	rs7751410	6	122703037	q22.31
SNP_A-1893629	G	G	293	23	373	15	3.972	4.63E-02	rs3844411	16	81195315	q23.3
SNP_A-1902178	G	G	313	93	291	119	3.97	4.63E-02	rs6732978	2	64576986	p14
SNP_A-1890763	C	C	341	29	362	50	3.965	4.64E-02	rs17156624	7	82015406	q21.11
SNP_A-1906756	G	G	266	156	292	128	3.967	4.64E-02	rs7544174	1	233228996	q43
SNP_A-1928889	G	G	222	118	294	114	3.966	4.64E-02	rs10268714	7	81382552	q21.11
SNP_A-1961480	A	A	320	22	381	13	3.968	4.64E-02	rs11989518	8	77730209	q21.11
SNP_A-1952156	T	T	361	43	388	28	3.968	4.64E-02	rs959629	13	46721736	q14.2
SNP_A-1952827	C	C	315	25	365	15	3.966	4.64E-02	rs16954069	17	49458680	q22
SNP_A-1979313	C	C	363	5	401	15	3.966	4.64E-02	rs16843346	1	195274684	q31.3
SNP_A-1873280	A	A	221	149	277	139	3.966	4.64E-02	rs10808479	8	117125539	q23.3
SNP_A-1870271	C	C	304	118	326	92	3.968	4.64E-02	rs6501385	17	65806657	q24.3
SNP_A-1863458	G	G	294	46	306	72	3.969	4.64E-02	rs6998570	8	28729030	p21.1
SNP_A-1855739	A	A	404	16	391	29	3.968	4.64E-02	rs4328517	18	29136030	q12.1
SNP_A-1815658	G	G	197	145	197	195	3.965	4.64E-02	rs11514853	7	147450906	q36.1
SNP_A-1810805	C	C	266	156	292	128	3.967	4.64E-02	rs11671309	19	5420640	p13.3
SNP_A-1732271	T	G	215	179	210	190	3.969	4.64E-02	rs1808691	12	104955986	q23.3
SNP_A-1691864	G	G	260	140	296	118	3.967	4.64E-02	rs7790511	7	123595424	q31.33
SNP_A-1646616	A	A	232	118	243	167	3.967	4.64E-02	rs10497424	2	175042651	q31.1
SNP_A-2188086	G	G	278	120	245	143	3.967	4.64E-02	rs2253959	4	7822889	p16.1
SNP_A-2175494	C	C	244	126	242	168	3.967	4.64E-02	rs1355545	3	62577333	p14.2
SNP_A-2170544	A	A	319	89	290	112	3.969	4.64E-02	rs856966	20	60882911	q13.33
SNP_A-2174419	G	G	263	93	269	131	3.967	4.64E-02	rs4240251	4	36272066	p14
SNP_A-2209426	G	G	317	47	339	75	3.967	4.64E-02	rs10961844	9	1502561	p24.3
SNP_A-2044568	G	G	363	5	401	15	3.966	4.64E-02	rs16997135	20	50917265	q13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043434	A	A	335	7	337	17	3.967	4.64E-02	rs17041243	2	51226179	p16.3
SNP_A-2036341	C	C	235	173	264	146	3.966	4.64E-02	rs10158468	1	19147696	p36.13
SNP_A-2038222	A	A	305	63	321	95	3.966	4.64E-02	rs10895654	11	103715015	q22.3
SNP_A-2011649	C	C	360	54	340	32	3.966	4.64E-02	rs2817232	6	24646092	p22.2
SNP_A-2078093	C	C	381	41	391	25	3.966	4.64E-02	rs6538680	12	94786722	q23.1
SNP_A-2070173	G	G	355	49	372	32	3.965	4.64E-02	rs10832405	11	2605095	p15.5
SNP_A-2236634	C	C	246	168	275	141	3.969	4.64E-02	rs10173407	2	238650196	q37.3
SNP_A-2231287	G	G	358	28	324	42	3.966	4.64E-02	rs17779263	17	67763152	q24.3
SNP_A-2305285	T	T	234	134	291	123	3.967	4.64E-02	rs670603	8	36278313	p12
SNP_A-2313693	G	G	332	36	380	24	3.966	4.64E-02	rs1347664	2	209121235	q34
SNP_A-2313333	G	G	417	1	384	6	3.965	4.64E-02	rs4642072	3	127412766	q21.2
SNP_A-2313851	C	C	319	101	341	77	3.965	0.0465	rs272529	1	44720051	p34.1
SNP_A-2296332	C	C	300	68	359	55	3.964	0.0465	rs16825360	2	229467033	q36.3
SNP_A-2285769	C	C	227	131	231	179	3.965	0.0465	rs1779	7	679980	p22.3
SNP_A-2062095	A	A	354	18	346	32	3.964	0.0465	rs785205	1	21444645	p36.12
SNP_A-2054929	T	C	196	166	201	177	3.962	0.0465	rs10089402	8	113537043	q23.3
SNP_A-2051249	A	A	302	50	318	78	3.963	0.0465	rs12510610	4	42345633	p13
SNP_A-2054142	C	C	414	4	412	0	3.962	0.0465	rs17064122	5	174304656	q35.2
SNP_A-2012102	T	C	204	164	209	195	3.962	0.0465	rs2614285	6	135734311	q23.3
SNP_A-2007048	A	A	416	4	414	0	3.962	0.0465	rs6708287	2	224710786	q36.1
SNP_A-2008138	T	T	285	137	307	109	3.962	0.0465	rs2190454	11	17490211	p15.1
SNP_A-1997714	C	C	416	4	414	0	3.962	0.0465	rs16911401	9	113020159	q32
SNP_A-1994915	A	A	317	103	336	78	3.963	0.0465	rs2385922	8	122592919	q24.13
SNP_A-1996963	A	A	242	180	269	151	3.963	0.0465	rs7044051	9	79989372	q21.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207168	T	T	293	101	329	81	3.965	0.0465	rs4350588	16	61388944	q21
SNP_A-2221656	T	T	330	36	391	25	3.964	0.0465	rs10493536	1	77468248	p31.1
SNP_A-2189183	T	T	251	115	309	103	3.962	0.0465	rs6855352	4	28660867	p15.1
SNP_A-2112392	A	A	380	6	371	15	3.965	0.0465	rs3847906	12	61536040	q14.2
SNP_A-2152668	G	G	279	91	338	78	3.963	0.0465	rs10810593	9	16689008	p22.2
SNP_A-2141589	A	A	249	121	304	108	3.964	0.0465	rs831986	2	107833364	q12.3
SNP_A-1650756	G	G	281	121	315	99	3.964	0.0465	rs10502092	11	106912248	q22.3
SNP_A-1709163	T	T	305	93	339	73	3.964	0.0465	rs10516395	4	21379258	p15.31
SNP_A-1793860	A	A	418	4	416	0	3.962	0.0465	rs9378150	6	30977672	p21.33
SNP_A-1829367	C	C	336	26	358	46	3.962	0.0465	rs7015900	8	50693285	q11.21
SNP_A-1831120	A	A	324	74	348	54	3.962	0.0465	rs917722	7	121072419	q31.32
SNP_A-1832015	A	A	247	119	299	105	3.962	0.0465	rs878528	2	137912351	q22.1
SNP_A-1852782	G	A	226	172	201	199	3.965	0.0465	rs7653440	3	133241705	q22.1
SNP_A-1854264	G	G	311	53	328	82	3.962	0.0465	rs2195910	2	56244134	p16.1
SNP_A-1965710	G	G	402	2	376	8	3.964	0.0465	rs962091	2	167324212	q24.3
SNP_A-1935300	G	G	418	4	416	0	3.962	0.0465	rs2287786	16	24725309	p12.1
SNP_A-1917149	A	A	393	29	373	45	3.963	0.0465	rs2069327	6	48734929	p12.3
SNP_A-1901971	G	G	214	150	215	201	3.964	0.0465	rs12491489	3	118784125	q13.31
SNP_A-1897340	G	G	373	37	334	52	3.959	4.66E-02	rs11060965	12	129526881	q24.33
SNP_A-1888446	C	C	262	106	322	94	3.96	4.66E-02	rs10844387	12	32965120	p11.21
SNP_A-1919292	A	C	215	179	212	192	3.96	4.66E-02	rs1847661	1	215732200	q41
SNP_A-1913438	T	T	333	35	352	58	3.959	4.66E-02	rs12618369	2	13577602	p24.3
SNP_A-1906486	G	G	263	107	268	148	3.961	4.66E-02	rs1561201	18	36459373	q12.3
SNP_A-1905827	A	A	188	180	242	174	3.959	4.66E-02	rs1470569	3	77614616	p12.3
SNP_A-1908530	C	C	338	32	358	54	3.958	4.66E-02	rs6753135	2	47569335	p21
SNP_A-1932705	T	T	285	61	284	88	3.958	4.66E-02	rs11757081	6	33567398	p21.32
SNP_A-1938928	A	A	286	82	296	118	3.96	4.66E-02	rs12643478	4	10409371	p16.1
SNP_A-1953441	C	C	365	33	377	19	3.958	4.66E-02	rs1791204	18	27513817	q12.1
SNP_A-1958568	A	A	318	36	377	25	3.961	4.66E-02	rs16869750	5	90797966	q14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1968597	T	T	394	6	385	15	3.961	4.66E-02	rs6021120	20	49387119	q13.2
SNP_A-1856018	G	G	262	106	322	94	3.96	4.66E-02	rs9861636	3	161305369	q25.33
SNP_A-1870500	T	T	406	2	380	8	3.96	4.66E-02	rs6683993	1	7612519	p36.23
SNP_A-1813636	T	T	333	35	352	58	3.959	4.66E-02	rs6850028	4	70188903	q13.2
SNP_A-1806563	G	G	232	184	259	155	3.961	4.66E-02	rs12771003	10	122322335	q26.12
SNP_A-1648978	C	C	254	144	290	122	3.961	4.66E-02	rs1955639	14	56479707	q23.1
SNP_A-1746675	T	T	239	163	274	140	3.958	4.66E-02	rs1393749	3	30823330	p24.1
SNP_A-1719253	A	A	300	50	329	81	3.961	4.66E-02	rs881985	9	559992	p24.3
SNP_A-1752339	G	G	402	0	404	4	3.961	4.66E-02	rs1364401	7	136994917	q33
SNP_A-2151251	A	A	276	86	285	123	3.961	4.66E-02	rs207300	4	18772432	p15.31
SNP_A-2150915	T	T	309	95	284	120	3.961	4.66E-02	rs10200324	2	17190654	p24.2
SNP_A-2147045	C	C	221	189	248	160	3.959	4.66E-02	rs7044045	9	68584687	q13
SNP_A-2112451	G	G	288	132	258	158	3.96	4.66E-02	rs10776742	1	112423384	p13.2
SNP_A-2192742	C	C	266	94	323	81	3.961	4.66E-02	rs216905	12	5976516	p13.31
SNP_A-2182580	T	T	314	34	340	58	3.961	4.66E-02	rs16983598	19	57425764	q13.41
SNP_A-2219408	G	G	286	82	296	118	3.96	4.66E-02	rs10805247	4	10409218	p16.1
SNP_A-2205146	C	C	253	105	245	139	3.96	4.66E-02	rs10747857	12	58561904	q14.1
SNP_A-1991540	C	C	406	4	404	0	3.961	4.66E-02	rs17163405	7	141721866	q34
SNP_A-1992943	C	C	376	34	392	20	3.958	4.66E-02	---	8	32194354	p12
SNP_A-2005376	C	C	319	45	377	33	3.96	4.66E-02	rs1421058	10	113683950	q25.2
SNP_A-2040946	T	T	229	117	293	109	3.96	4.66E-02	rs639449	12	31302088	p11.21
SNP_A-2076457	A	A	240	124	237	165	3.96	4.66E-02	rs12998675	2	23138332	p24.1
SNP_A-2077875	G	G	404	4	402	0	3.961	4.66E-02	rs2101154	6	149262582	q25.1
SNP_A-2081051	C	C	286	80	345	67	3.96	4.66E-02	rs1327268	6	51280428	p12.3
SNP_A-2106581	C	C	304	66	363	53	3.961	4.66E-02	rs618283	4	23712023	p15.2
SNP_A-2263799	C	C	310	106	334	82	3.958	4.66E-02	---	16	74784985	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2258854	C	C	421	1	388	6	3.961	4.66E-02	rs736534	12	110727520	q24.12
SNP_A-2256525	T	T	254	142	229	171	3.961	4.66E-02	rs11876786	18	8334637	p11.23
SNP_A-2260108	C	C	292	74	351	61	3.96	4.66E-02	rs8020984	14	94000769	q32.13
SNP_A-2230541	A	A	249	103	253	143	3.961	4.66E-02	rs10763500	10	51902700	q11.23
SNP_A-2230031	G	G	300	48	340	34	3.959	4.66E-02	rs12618842	2	35557310	p22.3
SNP_A-2236900	C	C	301	113	276	140	3.96	4.66E-02	rs913033	10	91559667	q23.31
SNP_A-2236945	G	G	406	2	380	8	3.96	4.66E-02	rs11096832	4	36553147	p14
SNP_A-2241530	G	G	211	141	256	126	3.959	4.66E-02	rs1958715	14	19598047	q11.2
SNP_A-2243994	C	C	388	32	396	18	3.959	4.66E-02	rs1267649	7	139959037	q34
SNP_A-2309108	A	A	268	98	276	138	3.958	4.66E-02	rs6532293	4	92601207	q22.1
SNP_A-2299853	A	A	410	2	384	8	3.956	4.67E-02	rs3796040	2	38954733	p22.1
SNP_A-2253765	A	T	216	180	209	189	3.957	4.67E-02	rs817224	2	103528565	q12.1
SNP_A-2258334	A	A	312	86	329	63	3.956	4.67E-02	rs2925210	8	29147554	p12
SNP_A-2264078	T	T	315	35	385	25	3.954	4.67E-02	rs6590505	11	130145348	q24.3
SNP_A-2262375	C	C	238	114	291	101	3.957	4.67E-02	rs12866627	13	19916715	q12.11
SNP_A-2273814	G	G	293	67	314	102	3.954	4.67E-02	rs10837436	11	40542978	p12
SNP_A-2272868	C	C	191	179	243	171	3.956	4.67E-02	rs17249969	3	84440539	p12.1
SNP_A-2106908	G	G	241	129	297	117	3.957	4.67E-02	rs1649891	2	231163164	q37.1
SNP_A-2106992	C	C	298	56	322	88	3.957	4.67E-02	rs4469158	5	67024129	q13.1
SNP_A-2086623	A	A	405	15	414	6	3.956	4.67E-02	rs1278870	14	31451725	q12
SNP_A-2052950	A	A	369	33	381	19	3.956	4.67E-02	rs11615495	12	112949039	q24.21
SNP_A-2050015	A	A	329	27	387	17	3.955	4.67E-02	rs4862083	4	184000482	q35.1
SNP_A-2049959	T	T	293	51	286	74	3.955	4.67E-02	rs9586372	13	103516040	q33.1
SNP_A-2046624	T	T	283	47	293	73	3.955	4.67E-02	rs6111004	20	16204637	p12.1
SNP_A-2004701	G	G	312	44	308	26	3.957	4.67E-02	rs4377150	16	51216851	q12.2
SNP_A-1989743	C	C	201	189	240	170	3.957	4.67E-02	rs2024125	7	42931717	p14.1
SNP_A-2206303	T	T	262	140	237	169	3.954	4.67E-02	rs6050290	20	24989535	p11.21

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2168762	A	A	296	114	316	88	3.956	4.67E-02	rs2193701	2	159099735	q24.1
SNP_A-2112889	T	T	384	8	410	2	3.956	4.67E-02	---	2	233251924	q37.1
SNP_A-2119674	G	G	234	174	258	144	3.957	4.67E-02	rs3773181	3	14471933	p25.1
SNP_A-2136017	T	T	326	44	344	70	3.956	4.67E-02	rs17069328	13	49033205	q14.2
SNP_A-2133422	T	T	305	59	322	90	3.957	4.67E-02	rs9926529	16	62727653	q21
SNP_A-2148556	G	G	219	125	219	169	3.955	4.67E-02	rs4456868	3	118741783	q13.31
SNP_A-2149856	A	A	312	98	291	125	3.957	4.67E-02	rs4714188	6	38900142	p21.2
SNP_A-2160949	C	C	305	65	319	97	3.957	4.67E-02	rs3798398	6	117126249	q22.1
SNP_A-1729043	A	A	305	97	287	125	3.957	4.67E-02	rs10513376	9	119730871	q33.2
SNP_A-1727817	T	T	258	142	294	120	3.956	4.67E-02	rs7372094	3	46306863	p21.31
SNP_A-1870375	C	C	405	15	414	6	3.956	4.67E-02	rs4661202	1	153386057	q22
SNP_A-1871176	G	G	293	125	317	99	3.957	4.67E-02	rs1659390	10	79295413	q22.3
SNP_A-1843701	C	C	359	5	397	15	3.956	4.67E-02	rs17802789	15	87552739	q26.1
SNP_A-1971440	A	A	265	139	294	114	3.955	4.67E-02	rs6776332	3	3874791	p26.2
SNP_A-1959741	C	C	285	123	253	147	3.958	4.67E-02	rs2185196	1	89844603	p22.2
SNP_A-1933335	T	T	305	65	319	97	3.957	4.67E-02	rs941862	6	70877642	q13
SNP_A-1934054	T	T	263	107	320	94	3.957	4.67E-02	rs4322498	12	34237698	p11.1
SNP_A-1924334	G	G	301	63	306	92	3.958	4.67E-02	rs10744956	15	49056921	q21.2
SNP_A-1919571	C	C	246	164	209	185	3.956	4.67E-02	rs10268721	7	80352420	q21.11
SNP_A-1884211	A	A	319	95	291	119	3.958	4.67E-02	rs353823	9	86291366	q21.33
SNP_A-1899777	C	C	346	20	401	11	3.956	4.67E-02	rs17134562	7	51668343	p12.1
SNP_A-1892307	A	A	323	89	294	112	3.951	4.68E-02	rs11028415	11	25070842	p14.3
SNP_A-1888994	A	A	347	9	405	3	3.952	4.68E-02	rs12658669	5	86188147	q14.3
SNP_A-1919006	G	G	235	135	292	124	3.954	4.68E-02	rs1993007	14	80069466	q31.1
SNP_A-1940141	C	C	369	31	390	18	3.951	4.68E-02	rs16903497	5	14471419	p15.2
SNP_A-1941467	C	A	239	183	206	204	3.953	4.68E-02	rs12610691	19	18259335	p13.11
SNP_A-1943885	G	G	262	160	229	185	3.953	4.68E-02	rs10200936	2	29298297	p23.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960707	A	A	293	73	302	106	3.953	4.68E-02	rs4078378	1	241712896	q44
SNP_A-1841100	A	A	307	33	373	23	3.954	4.68E-02	rs17166578	5	98390917	q21.1
SNP_A-1838591	C	C	303	63	319	95	3.954	4.68E-02	rs3751585	15	49528348	q21.2
SNP_A-1817913	G	G	221	137	206	172	3.951	4.68E-02	rs820076	6	35141869	p21.31
SNP_A-1822143	T	T	299	51	366	40	3.954	4.68E-02	rs12365930	11	103698145	q22.3
SNP_A-1827101	T	T	209	149	210	200	3.952	4.68E-02	rs9656423	7	132782242	q33
SNP_A-1873401	T	T	310	102	283	127	3.954	4.68E-02	rs9875310	3	32323199	p23
SNP_A-1860156	G	G	370	48	385	31	3.951	4.68E-02	rs6926079	6	41198660	p21.1
SNP_A-1848739	G	G	283	85	342	72	3.954	4.68E-02	rs1369672	2	51952053	p16.3
SNP_A-1750241	T	T	365	11	386	24	3.952	4.68E-02	rs2253255	8	97479126	q22.1
SNP_A-1737355	C	C	367	29	365	47	3.953	4.68E-02	rs3767206	1	70085009	p31.1
SNP_A-1659524	A	A	374	22	374	38	3.951	4.68E-02	rs10490526	2	155438576	q24.1
SNP_A-1810291	T	T	277	67	290	100	3.952	4.68E-02	rs11009645	10	34441765	p11.22
SNP_A-1791698	G	G	340	70	311	91	3.953	4.68E-02	rs175095	8	3274026	p23.2
SNP_A-1787081	G	G	309	11	341	25	3.953	4.68E-02	rs2018558	15	55752290	q21.3
SNP_A-2120294	T	T	292	126	261	151	3.951	4.68E-02	rs711662	3	4438008	p26.1
SNP_A-2170864	A	A	228	128	229	173	3.953	4.68E-02	rs11136750	8	4399666	p23.2
SNP_A-2181250	C	C	303	117	275	143	3.952	4.68E-02	rs878507	19	16711733	p13.11
SNP_A-2199368	G	G	303	63	319	95	3.954	4.68E-02	rs2209313	20	1547142	p13
SNP_A-2187154	C	C	326	44	384	32	3.954	4.68E-02	rs1569263	7	54638595	p11.2
SNP_A-2183829	T	T	295	125	319	99	3.951	4.68E-02	rs387598	5	176449776	q35.2
SNP_A-2210244	C	C	249	159	212	180	3.952	4.68E-02	rs862480	14	41066681	q21.1
SNP_A-2218616	G	G	327	21	349	39	3.954	4.68E-02	rs12447331	16	63940334	q22.1
SNP_A-2008129	C	C	326	32	379	21	3.952	4.68E-02	rs7276454	21	42313907	q22.3
SNP_A-2009254	G	G	206	150	247	133	3.954	4.68E-02	rs1392799	3	158435447	q25.31
SNP_A-2046569	G	G	314	54	369	41	3.952	4.68E-02	rs11050837	12	30389079	p11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2038491	T	T	325	83	301	107	3.952	4.68E-02	rs7895198	10	98856285	q24.1
SNP_A-2048940	A	A	213	151	262	138	3.952	4.68E-02	rs2979684	8	24873358	p21.2
SNP_A-2049289	G	G	232	96	242	138	3.952	4.68E-02	rs792474	12	32325988	p11.21
SNP_A-2053434	A	A	296	86	272	110	3.953	4.68E-02	rs4677875	3	124323752	q21.1
SNP_A-2055460	T	T	270	146	280	112	3.953	4.68E-02	rs762085	14	24166172	q11.2
SNP_A-2075032	T	T	349	35	328	52	3.952	4.68E-02	rs2869472	4	10273367	p16.1
SNP_A-2100665	G	G	321	39	384	28	3.951	4.68E-02	rs7001339	8	70018061	q13.2
SNP_A-2264281	T	T	220	150	218	198	3.951	4.68E-02	rs13134991	4	112887734	q25
SNP_A-2269046	T	T	199	169	253	161	3.953	4.68E-02	rs11069568	13	104363291	q33.2
SNP_A-2253312	A	A	309	37	322	60	3.951	4.68E-02	rs1996506	2	186910839	q32.1
SNP_A-2250379	A	A	281	89	340	76	3.951	4.68E-02	rs12614459	2	134334939	q21.2
SNP_A-2249518	G	A	193	161	214	192	3.954	4.68E-02	rs1379188	3	66847308	p14.1
SNP_A-2234801	T	T	355	15	405	7	3.954	4.68E-02	---	5	112753534	q22.2
SNP_A-2295282	C	C	299	65	316	98	3.954	4.68E-02	rs4642255	4	98484327	q22.3
SNP_A-2312541	T	T	329	35	388	24	3.952	4.68E-02	rs11889456	2	84758341	p11.2
SNP_A-2311668	C	C	326	44	384	32	3.954	4.68E-02	rs16975794	15	94256555	q26.2
SNP_A-2249682	C	C	371	49	388	32	3.949	4.69E-02	rs1971883	3	8568038	p25.3
SNP_A-2246939	T	T	238	130	239	175	3.949	4.69E-02	rs4665969	2	27486604	p23.3
SNP_A-2260852	A	A	252	118	310	106	3.95	4.69E-02	rs2622351	4	80339019	q21.21
SNP_A-2275711	C	C	348	20	403	11	3.949	4.69E-02	rs9596608	13	51357325	q14.3
SNP_A-2096654	G	G	258	164	283	135	3.949	4.69E-02	rs12091558	1	239779951	q44
SNP_A-2098319	C	G	196	162	215	195	3.951	4.69E-02	rs6478429	9	119496642	q33.1
SNP_A-2050330	C	C	327	43	347	69	3.951	4.69E-02	rs6569153	6	98446490	q16.1
SNP_A-2032703	C	C	379	15	372	28	3.95	4.69E-02	rs4859372	4	35596913	p15.1
SNP_A-2032450	C	C	250	80	261	117	3.95	4.69E-02	rs7108208	11	30350934	p14.1
SNP_A-1989570	T	T	306	24	291	39	3.948	4.69E-02	rs7785477	7	36898257	p14.2
SNP_A-1996702	G	G	318	48	378	36	3.948	4.69E-02	rs7904146	10	17081169	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2004558	A	A	275	55	294	86	3.949	4.69E-02	rs644633	10	103040561	q24.32
SNP_A-2214619	T	T	232	186	253	153	3.948	4.69E-02	rs201064	10	11027558	p14
SNP_A-2209609	T	T	327	43	347	69	3.951	4.69E-02	rs16777	5	4927950	p15.32
SNP_A-2203767	G	G	220	146	272	134	3.948	4.69E-02	rs2726599	8	59881250	q12.1
SNP_A-2201803	G	G	374	48	389	31	3.948	4.69E-02	rs12029840	1	114243522	p13.2
SNP_A-2187552	G	G	281	41	271	61	3.951	4.69E-02	rs16912297	11	13144553	p15.2
SNP_A-2198736	A	A	342	80	360	58	3.95	4.69E-02	rs745218	18	9541028	p11.22
SNP_A-2117663	A	A	201	159	248	146	3.949	4.69E-02	rs9884601	4	23257871	p15.2
SNP_A-2131524	G	G	258	164	283	135	3.949	4.69E-02	rs10926979	1	239759182	q44
SNP_A-2125815	C	C	362	22	377	11	3.951	4.69E-02	rs17055510	5	157721619	q33.3
SNP_A-2156239	T	T	358	54	365	35	3.947	4.69E-02	rs3761789	6	24523115	p22.2
SNP_A-1656281	G	G	231	171	266	148	3.947	4.69E-02	rs7559913	2	4720062	p25.2
SNP_A-1655085	C	C	326	64	320	90	3.948	4.69E-02	rs2189344	7	11091856	p21.3
SNP_A-1653240	C	C	233	169	268	146	3.949	4.69E-02	rs1036756	1	33655919	p35.1
SNP_A-1748975	G	G	336	66	366	48	3.949	4.69E-02	rs10509222	10	66471358	q21.3
SNP_A-1718761	A	A	350	50	378	34	3.948	4.69E-02	rs10510212	3	1643488	p26.3
SNP_A-1848248	C	C	301	49	359	37	3.95	4.69E-02	rs1527877	6	108100857	q21
SNP_A-1957379	A	A	337	77	358	56	3.95	4.69E-02	rs6497035	15	91532308	q26.1
SNP_A-1968327	A	A	258	40	281	67	3.948	4.69E-02	rs11907082	20	37613135	q12
SNP_A-1983554	A	A	355	67	373	47	3.949	4.69E-02	rs328834	5	133809517	q31.1
SNP_A-1918882	C	C	240	118	244	162	3.947	4.69E-02	rs12616514	2	182029625	q31.3
SNP_A-1908039	T	T	361	17	394	8	3.948	4.69E-02	rs1400878	12	82111866	q21.31
SNP_A-1883677	C	C	349	15	383	31	3.947	4.69E-02	---	1	65352301	p31.3
SNP_A-1883322	T	T	334	32	361	55	3.949	4.69E-02	rs11225974	11	103065710	q22.3
SNP_A-1876562	C	C	382	30	399	17	3.947	0.047	rs6468747	8	102075581	q22.3
SNP_A-1896267	G	G	193	163	249	157	3.944	0.047	rs4970956	1	148329441	q21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1908924	C	C	300	58	362	46	3.944	0.047	rs6074503	20	12757182	p12.1
SNP_A-1917666	T	T	315	51	331	79	3.945	0.047	rs17753577	18	53527367	q21.31
SNP_A-1918154	T	T	274	40	320	28	3.944	0.047	rs11064699	12	118086386	q24.23
SNP_A-1923653	C	C	282	138	304	110	3.944	0.047	rs7430451	3	38770499	p22.2
SNP_A-1930830	C	C	235	109	301	101	3.946	0.047	rs6724852	2	215251333	q35
SNP_A-1929368	G	G	349	3	375	11	3.947	0.047	rs12060452	1	29919923	p35.3
SNP_A-1926446	C	C	257	145	233	175	3.944	0.047	rs11250695	10	1675231	p15.3
SNP_A-1978810	G	G	346	18	362	34	3.944	0.047	rs975107	4	125820398	q28.1
SNP_A-1972838	A	A	303	65	317	97	3.945	0.047	rs2856057	3	60600158	p14.2
SNP_A-1948631	A	A	303	67	315	99	3.945	0.047	---	14	85947005	q31.3
SNP_A-1939492	G	G	322	38	340	62	3.946	0.047	rs11021216	11	94927790	q21
SNP_A-1850065	C	C	225	141	222	186	3.945	0.047	rs1342560	1	186047404	q31.1
SNP_A-1829338	G	G	209	153	259	141	3.946	0.047	rs17745935	3	154991244	q25.2
SNP_A-1652926	A	A	202	148	205	201	3.944	0.047	rs10516864	4	91485442	q22.1
SNP_A-1659852	A	A	228	174	263	151	3.947	0.047	rs1372685	1	163737878	q24.1
SNP_A-1673132	T	T	382	14	381	27	3.945	0.047	rs10504986	8	99781080	q22.2
SNP_A-1793666	C	C	288	78	342	64	3.947	0.047	rs7777572	7	141709600	q34
SNP_A-1798573	C	C	347	3	373	11	3.944	0.047	rs10848350	12	130338562	q24.33
SNP_A-1811864	C	C	307	61	322	92	3.947	0.047	rs4316149	8	57695801	q12.1
SNP_A-2153933	G	G	331	27	389	17	3.945	0.047	rs2122691	1	105280447	p21.1
SNP_A-2147971	T	T	251	157	223	185	3.946	0.047	rs7857754	9	36728641	p13.2
SNP_A-2142991	A	A	213	157	267	147	3.947	0.047	rs12616974	2	192492042	q32.3
SNP_A-2125667	A	A	252	114	310	102	3.946	0.047	rs7651287	3	2893690	p26.2
SNP_A-2128965	C	C	244	90	261	133	3.946	0.047	rs2814038	1	100050527	p21.2
SNP_A-2122432	C	C	409	1	378	6	3.945	0.047	rs890242	11	35030628	p13
SNP_A-2195180	G	G	346	66	303	83	3.946	0.047	rs1574481	8	103796170	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175874	A	A	337	25	363	45	3.946	0.047	rs2318030	17	3232502	p13.2
SNP_A-2200114	G	G	378	6	409	1	3.945	0.047	rs9921634	16	48079935	q12.1
SNP_A-2210766	A	A	204	166	256	156	3.944	0.047	rs4240264	4	123041423	q27
SNP_A-2222168	G	G	366	4	399	13	3.944	0.047	rs17141650	7	19390078	p21.1
SNP_A-2031950	G	G	378	6	409	1	3.945	0.047	rs11173489	12	59163615	q14.1
SNP_A-2021599	T	T	337	9	393	3	3.945	0.047	rs16991533	20	5864712	p12.3
SNP_A-2053222	C	C	343	13	412	6	3.944	0.047	rs6493942	15	55750374	q21.3
SNP_A-2054966	A	A	409	1	378	6	3.945	0.047	rs11108517	5	167826310	q34
SNP_A-2073429	C	C	285	85	293	121	3.945	0.047	rs6792708	3	133382510	q22.1
SNP_A-2071457	A	A	360	24	334	38	3.946	0.047	rs936876	16	53798186	q12.2
SNP_A-2064241	A	A	350	2	328	8	3.944	0.047	rs4850697	2	197018655	q32.3
SNP_A-2103912	C	C	226	144	281	133	3.946	0.047	rs551422	5	117329735	q23.1
SNP_A-2274658	A	A	270	88	327	75	3.945	0.047	rs4106010	16	54324426	q12.2
SNP_A-2285841	A	A	302	68	361	55	3.946	0.047	rs12655973	5	90772293	q14.3
SNP_A-2262429	C	C	321	45	379	33	3.946	0.047	rs10954971	8	30313300	p12
SNP_A-2261176	G	G	238	120	301	111	3.947	0.047	rs7552206	1	215881293	q41
SNP_A-2265364	C	C	192	160	230	142	3.945	0.047	rs562594	20	24141691	p11.21
SNP_A-2250601	A	A	309	5	316	14	3.946	0.047	rs4375999	3	59797139	p14.2
SNP_A-2240134	G	G	250	160	223	189	3.946	0.047	rs2806943	13	52653599	q14.3
SNP_A-2300268	C	C	375	21	379	37	3.945	0.047	rs2240458	8	88870269	q21.3
SNP_A-2290557	C	C	239	99	250	142	3.947	0.047	rs16955288	17	50302974	q22
SNP_A-2236013	C	C	328	34	316	52	3.942	4.71E-02	rs569270	11	100352260	q22.1
SNP_A-2231953	C	C	241	117	297	105	3.943	4.71E-02	rs14226623	19	51122886	q13.32
SNP_A-2250503	T	T	408	0	412	4	3.942	4.71E-02	rs10152685	15	42746404	q21.1
SNP_A-2251956	T	T	218	118	284	112	3.942	4.71E-02	rs6088085	20	31113033	q11.21
SNP_A-2246363	T	T	269	151	296	124	3.941	4.71E-02	rs1609459	19	8945216	p13.2
SNP_A-2090608	G	G	335	29	356	50	3.941	4.71E-02	rs7738029	5	115304335	q23.1
SNP_A-2075633	A	A	410	4	406	0	3.942	4.71E-02	rs7657135	4	15857390	p15.32

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2058857	C	C	301	63	317	95	3.941	4.71E-02	rs10447236	5	115815122	q23.1
SNP_A-2048054	C	C	182	162	216	142	3.943	4.71E-02	rs2250371	8	14624508	p22
SNP_A-2022358	G	G	376	22	391	11	3.94	4.71E-02	rs1866804	1	210733139	q41
SNP_A-2000112	C	C	354	16	382	32	3.942	4.71E-02	rs344929	1	67845095	p31.2
SNP_A-2001077	C	C	353	59	330	80	3.942	4.71E-02	rs1930176	10	55996398	q21.1
SNP_A-2192221	G	G	246	166	221	197	3.943	4.71E-02	rs2283119	8	17982022	p22
SNP_A-2187895	C	C	318	70	362	54	3.941	4.71E-02	rs4093823	12	57077756	q14.1
SNP_A-2184852	C	C	313	107	287	133	3.943	4.71E-02	rs272041	2	116345018	q14.1
SNP_A-2136844	C	C	418	4	414	0	3.943	4.71E-02	rs16942602	18	22555679	q11.2
SNP_A-1808746	G	G	376	22	391	11	3.94	4.71E-02	rs12681485	8	1834095	p23.3
SNP_A-1664844	C	C	297	101	333	81	3.941	4.71E-02	rs4604073	4	122412254	q27
SNP_A-1642407	A	A	190	166	248	162	3.942	4.71E-02	rs715942	6	125016418	q22.31
SNP_A-1692794	C	C	398	0	402	4	3.941	4.71E-02	rs10496690	2	133657564	q21.2
SNP_A-1682374	C	C	398	0	402	4	3.941	4.71E-02	rs2041139	12	1771722	p13.33
SNP_A-1747419	C	C	402	0	406	4	3.941	4.71E-02	rs10490966	10	52056184	q11.23
SNP_A-1750993	G	G	394	0	398	4	3.94	4.71E-02	rs10517122	4	27335620	p15.2
SNP_A-1783608	C	C	414	4	410	0	3.942	4.71E-02	rs2073738	22	17545510	q11.21
SNP_A-1832423	G	G	359	1	393	7	3.943	4.71E-02	rs1424508	18	49569498	q21.2
SNP_A-1834203	C	C	270	88	287	129	3.941	4.71E-02	rs8045298	16	75218784	q23.1
SNP_A-1824044	A	A	351	9	409	3	3.942	4.71E-02	rs443465	19	53285699	q13.32
SNP_A-1820963	T	T	249	163	223	193	3.941	4.71E-02	rs1471616	17	30599233	q12
SNP_A-1815257	C	C	287	81	346	68	3.941	4.71E-02	rs10125601	9	111707628	q31.3
SNP_A-1933262	A	A	208	194	236	166	3.944	4.71E-02	rs4755115	11	96876054	q22.1
SNP_A-1948904	T	T	334	18	372	36	3.94	4.71E-02	rs4430358	1	107475426	p13.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950717	G	G	314	52	333	81	3.942	4.71E-02	rs4841004	8	8537743	p23.1
SNP_A-1951833	A	A	350	20	405	11	3.941	4.71E-02	rs17747706	12	61899529	q14.2
SNP_A-1957072	C	C	283	87	342	74	3.941	4.71E-02	rs167669	4	83234892	q21.22
SNP_A-1982036	G	G	226	142	281	131	3.94	4.71E-02	rs156756	5	70867397	q13.2
SNP_A-1923492	A	A	257	63	269	95	3.941	4.71E-02	rs1362694	5	103453507	q21.2
SNP_A-1920390	T	T	351	59	366	40	3.941	4.71E-02	rs17769754	16	75885362	q23.1
SNP_A-1918284	C	C	225	131	214	168	3.943	4.71E-02	rs17834427	18	54716681	q21.32
SNP_A-1917413	C	C	405	17	388	30	3.941	4.71E-02	rs948466	11	117471310	q23.3
SNP_A-1917156	C	C	264	136	221	153	3.943	4.71E-02	rs10736351	10	90167971	q23.31
SNP_A-1916677	G	G	336	26	367	47	3.941	4.71E-02	rs17654441	4	47563797	p12
SNP_A-1891257	T	T	282	140	253	167	3.942	4.71E-02	rs6672750	1	49225793	p33
SNP_A-1874845	G	G	262	82	317	69	3.94	4.71E-02	rs11137379	9	138303776	q34.3
SNP_A-1877676	G	G	330	88	304	112	3.941	4.71E-02	rs17478453	4	10000581	p16.1
SNP_A-1888363	A	A	297	69	310	102	3.941	4.71E-02	rs16896392	6	65962900	q12
SNP_A-1900023	C	C	259	147	229	173	3.937	4.72E-02	rs644740	11	65318044	q13.1
SNP_A-1921087	A	A	317	85	284	106	3.94	4.72E-02	rs1885397	14	54302848	q22.2
SNP_A-1924964	T	T	210	158	265	149	3.94	4.72E-02	rs4960463	6	8806911	p24.3
SNP_A-1983416	T	T	264	140	233	165	3.938	4.72E-02	rs331075	5	127749077	q23.2
SNP_A-1965680	T	T	320	44	343	71	3.94	4.72E-02	rs1509099	2	165453511	q24.3
SNP_A-1965420	A	A	278	92	286	130	3.939	4.72E-02	rs2304556	2	153299302	q23.3
SNP_A-1940056	T	G	205	165	215	201	3.94	4.72E-02	rs2991495	13	78624756	q31.1
SNP_A-1939734	G	G	278	92	286	130	3.939	4.72E-02	rs17165333	6	157832675	q25.3
SNP_A-1944848	C	C	311	59	368	46	3.938	4.72E-02	rs651370	6	63100946	q11.1
SNP_A-1835175	G	G	230	104	284	92	3.937	4.72E-02	rs7011660	8	30405716	p12
SNP_A-1832536	G	G	226	142	277	129	3.938	4.72E-02	rs4074856	4	140152121	q31.1
SNP_A-1841910	C	C	358	10	389	23	3.938	4.72E-02	rs1684835	5	19590628	p14.3
SNP_A-1856956	C	C	323	9	343	21	3.938	4.72E-02	rs17133266	5	110780209	q22.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869256	C	C	392	22	370	36	3.937	4.72E-02	rs6800306	3	43633849	p21.33
SNP_A-1866899	C	T	205	165	215	201	3.94	4.72E-02	rs1669417	2	4788216	p25.2
SNP_A-1758409	C	C	273	125	307	103	3.939	4.72E-02	rs1959675	14	36548832	q21.1
SNP_A-1659989	C	C	393	5	371	13	3.94	4.72E-02	rs10484061	14	97312581	q32.2
SNP_A-1675183	C	C	295	93	332	74	3.939	4.72E-02	rs208358	7	2517943	p22.3
SNP_A-1812039	G	G	273	97	280	136	3.938	4.72E-02	rs7633043	3	45286380	p21.31
SNP_A-1800126	C	A	197	173	224	192	3.937	4.72E-02	rs6714659	2	79845285	p12
SNP_A-1786897	T	T	339	9	395	3	3.939	4.72E-02	rs6851205	4	55138151	q12
SNP_A-2151929	A	A	307	47	319	73	3.938	4.72E-02	rs17234620	3	6467256	p26.1
SNP_A-2159243	A	A	248	122	300	108	3.94	4.72E-02	rs2041446	4	16969753	p15.32
SNP_A-2160023	T	A	193	153	206	194	3.939	4.72E-02	rs9474102	6	51804795	p12.2
SNP_A-2160054	G	G	366	16	368	30	3.94	4.72E-02	rs13263627	8	5487493	p23.2
SNP_A-2186041	C	C	326	42	348	68	3.94	4.72E-02	rs536223	3	175799617	q26.31
SNP_A-2196409	C	C	236	144	217	177	3.937	4.72E-02	rs2237701	7	107216101	q31.1
SNP_A-2168589	G	G	379	39	396	24	3.94	4.72E-02	rs1198394	1	43209431	p34.2
SNP_A-2169627	G	G	283	81	283	113	3.938	4.72E-02	rs1395624	6	54662173	p12.1
SNP_A-1992864	G	G	322	44	340	70	3.937	4.72E-02	rs1923394	10	4297011	p15.1
SNP_A-1992052	A	A	302	118	274	144	3.937	4.72E-02	rs974995	8	5339076	p23.2
SNP_A-2026436	G	G	279	89	289	127	3.937	4.72E-02	rs17811727	3	192589522	q28
SNP_A-2036690	G	G	392	22	370	36	3.937	4.72E-02	rs3888124	8	42404493	p11.21
SNP_A-2048678	T	T	382	40	360	58	3.939	4.72E-02	rs2130519	10	106556072	q25.1
SNP_A-2061544	C	T	195	173	223	189	3.937	4.72E-02	rs4609785	15	57622132	q22.2
SNP_A-2094440	C	C	245	101	248	140	3.939	4.72E-02	rs4850332	2	194071943	q32.3
SNP_A-2228105	A	A	293	75	352	62	3.938	4.72E-02	rs568161	10	107691979	q25.1
SNP_A-2238295	C	C	386	6	417	1	3.938	4.72E-02	rs594907	12	116571268	q24.22
SNP_A-2285542	A	A	351	61	361	41	3.94	4.72E-02	rs11242261	5	135056573	q31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289102	G	G	287	113	319	91	3.939	4.72E-02	rs6554840	5	14122216	p15.2
SNP_A-2294493	A	A	379	39	396	24	3.94	4.72E-02	rs13013673	2	165650499	q24.3
SNP_A-2310688	T	T	310	86	280	108	3.939	4.72E-02	rs11158106	14	56009873	q22.3
SNP_A-2307510	G	G	376	0	380	4	3.937	4.72E-02	rs2306850	12	53534580	q13.2
SNP_A-2305614	T	T	261	141	242	174	3.936	4.73E-02	rs4778000	15	90867745	q26.1
SNP_A-2314650	A	A	279	85	320	68	3.933	4.73E-02	rs12648836	4	56424518	q12
SNP_A-2300080	C	C	371	9	353	19	3.934	4.73E-02	rs9406868	9	25213373	p21.3
SNP_A-2270558	T	T	318	50	308	72	3.935	4.73E-02	rs1536136	13	48259434	q14.2
SNP_A-2092891	T	T	326	8	358	20	3.936	4.73E-02	rs7617876	3	182812072	q26.33
SNP_A-2103439	C	C	220	138	272	126	3.936	4.73E-02	rs2493588	13	101376071	q33.1
SNP_A-2067969	C	C	329	33	384	22	3.935	4.73E-02	rs1190053	6	105851881	q21
SNP_A-2038903	A	A	352	64	330	86	3.936	4.73E-02	rs17739309	2	126940575	q14.3
SNP_A-2040158	G	G	333	27	391	17	3.935	4.73E-02	rs2035508	1	101752289	p21.2
SNP_A-2039854	T	T	206	156	257	145	3.936	4.73E-02	rs11712517	3	136687232	q22.2
SNP_A-2030209	G	G	300	70	359	57	3.934	4.73E-02	rs13219624	6	34969777	p21.31
SNP_A-2000853	T	T	299	59	361	47	3.936	4.73E-02	rs6676375	1	239200926	q43
SNP_A-1998023	C	C	284	86	343	73	3.936	4.73E-02	rs9722212	9	129632578	q34.11
SNP_A-2008615	A	A	343	69	356	48	3.933	4.73E-02	rs1564100	11	23423031	p14.3
SNP_A-2169469	C	C	201	163	254	154	3.934	4.73E-02	rs9637968	6	11800050	p24.1
SNP_A-2186044	A	A	252	114	257	157	3.933	4.73E-02	rs1873555	2	43691316	p21
SNP_A-2208055	G	G	214	148	210	194	3.934	4.73E-02	rs11168513	14	37904698	q21.1
SNP_A-2205420	G	G	346	62	313	81	3.934	4.73E-02	rs7108541	11	2015930	p15.5
SNP_A-2153005	T	T	279	77	336	64	3.934	4.73E-02	rs16853221	2	167891998	q24.3
SNP_A-2164099	A	A	284	86	343	73	3.936	4.73E-02	rs1572783	1	19988453	p36.13
SNP_A-2120018	G	G	340	26	396	16	3.936	4.73E-02	rs1862798	16	81073862	q23.3
SNP_A-2116156	T	T	336	74	360	54	3.933	4.73E-02	rs12508370	4	12281647	p15.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2114839	A	A	198	162	252	154	3.934	4.73E-02	rs8098925	18	69257838	q22.3
SNP_A-1798501	C	C	278	68	333	55	3.934	4.73E-02	rs8181952	14	84634908	q31.3
SNP_A-1795348	A	A	264	100	324	88	3.934	4.73E-02	rs2894324	10	77612638	q22.2
SNP_A-1751281	C	C	327	65	362	48	3.933	4.73E-02	rs10503522	8	14784036	p22
SNP_A-1783720	G	G	262	48	328	38	3.934	4.73E-02	rs1031371	16	8376015	p13.2
SNP_A-1782033	T	C	186	178	233	183	3.935	4.73E-02	rs7677890	4	47212517	p12
SNP_A-1868167	T	T	234	136	233	181	3.933	4.73E-02	rs10196004	2	107248421	q12.3
SNP_A-1872330	T	T	335	13	325	25	3.935	4.73E-02	rs657657	10	105938379	q25.1
SNP_A-1871872	G	G	256	164	222	188	3.935	4.73E-02	rs9357290	6	36961348	p21.2
SNP_A-1863341	G	G	233	137	233	183	3.934	4.73E-02	---	10	20997482	p12.31
SNP_A-1832291	T	T	308	56	363	43	3.936	4.73E-02	rs10963561	9	18290883	p22.2
SNP_A-1942371	C	C	213	149	211	197	3.934	4.73E-02	rs9850286	3	96688212	q11.2
SNP_A-1961575	C	C	272	106	291	81	3.936	4.73E-02	rs1411406	1	205647110	q32.2
SNP_A-1966028	G	G	249	109	247	147	3.934	4.73E-02	rs334041	2	178922739	q31.2
SNP_A-1916934	G	G	400	10	413	3	3.934	4.73E-02	rs6702321	1	201399471	q32.1
SNP_A-1918370	C	C	283	115	309	91	3.933	4.73E-02	rs4858769	3	20149430	p24.3
SNP_A-1915325	A	A	287	75	303	111	3.935	4.73E-02	rs1202811	1	58092339	p32.2
SNP_A-1894873	T	T	327	69	303	91	3.934	4.73E-02	rs11727130	4	23251145	p15.2
SNP_A-1893804	C	C	266	104	269	143	3.93	4.74E-02	rs1565517	18	62011840	q22.1
SNP_A-1875046	C	C	207	161	258	150	3.931	4.74E-02	rs1821245	5	155513340	q33.2
SNP_A-1910503	G	G	312	50	372	38	3.93	4.74E-02	rs2258680	13	113210636	q34
SNP_A-1905115	C	C	278	66	338	54	3.93	4.74E-02	rs11920057	3	133585196	q22.1
SNP_A-1907121	A	A	342	28	367	49	3.93	4.74E-02	rs10932036	2	204650687	q33.2
SNP_A-1907589	T	T	232	190	258	160	3.932	4.74E-02	rs208591	16	22884639	p12.1
SNP_A-1922385	C	C	270	96	273	133	3.933	4.74E-02	rs1522723	18	59535960	q21.33
SNP_A-1821289	G	G	299	71	358	58	3.93	4.74E-02	rs9955895	18	61788542	q22.1
SNP_A-1828417	C	C	331	67	293	85	3.933	4.74E-02	rs13259019	8	19299555	p21.3
SNP_A-1849478	G	G	332	86	354	64	3.932	4.74E-02	rs10491113	17	30028246	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803980	C	C	245	123	304	112	3.931	4.74E-02	rs6544780	2	45181473	p21
SNP_A-2111282	G	G	283	131	252	156	3.93	4.74E-02	rs2338507	22	46722810	q13.31
SNP_A-2161536	A	A	356	62	375	43	3.932	4.74E-02	rs2730727	12	117731383	q24.23
SNP_A-2167544	T	T	250	96	262	138	3.931	4.74E-02	rs9583277	13	108131750	q33.3
SNP_A-2142162	T	T	277	53	340	42	3.93	4.74E-02	rs2017293	3	85561499	p12.1
SNP_A-2212593	C	C	232	190	258	160	3.932	4.74E-02	rs4821182	22	32493032	q12.3
SNP_A-2222312	C	C	232	190	258	160	3.932	4.74E-02	rs11639621	16	81545373	q23.3
SNP_A-2223342	G	G	337	81	350	58	3.931	4.74E-02	rs2164961	7	46934373	p13
SNP_A-2182965	T	T	334	88	305	111	3.932	4.74E-02	rs1556143	9	129102342	q34.11
SNP_A-2012504	C	C	212	146	191	177	3.933	4.74E-02	rs1391531	11	80289152	q14.1
SNP_A-2015845	T	T	253	107	308	94	3.93	4.74E-02	rs2223140	21	18919299	q21.1
SNP_A-2019036	C	C	310	108	284	134	3.931	4.74E-02	rs17814920	21	37937767	q22.13
SNP_A-2001445	T	T	221	191	248	162	3.932	4.74E-02	rs4918828	10	115241573	q25.3
SNP_A-1991093	A	A	323	43	379	31	3.931	4.74E-02	rs1006091	7	122136741	q31.32
SNP_A-2024567	T	T	293	71	304	104	3.931	4.74E-02	rs7647311	3	73461569	p13
SNP_A-2019550	A	T	176	172	230	176	3.93	4.74E-02	rs4539361	11	112488349	q23.1
SNP_A-2020348	C	C	245	171	274	144	3.93	4.74E-02	rs4818858	21	43907525	q22.3
SNP_A-2044803	A	A	342	28	367	49	3.93	4.74E-02	rs2152856	1	80900023	p31.1
SNP_A-2061418	C	C	305	57	360	44	3.931	4.74E-02	rs10506331	12	53332683	q13.2
SNP_A-2059855	A	A	351	1	385	7	3.931	4.74E-02	rs16859809	2	172428132	q31.1
SNP_A-2057461	C	C	346	12	401	5	3.932	4.74E-02	rs11850088	14	82069781	q31.1
SNP_A-2103562	G	G	244	138	289	121	3.93	4.74E-02	rs11116991	12	84604391	q21.31
SNP_A-2102876	C	C	332	54	364	38	3.931	4.74E-02	rs11177651	12	68085915	q15
SNP_A-2094808	T	T	299	71	358	58	3.93	4.74E-02	rs17657378	5	138005008	q31.2
SNP_A-2097282	A	A	327	89	346	66	3.93	4.74E-02	rs616710	1	91338346	p22.2
SNP_A-2090347	G	G	271	97	325	83	3.93	4.74E-02	rs13141833	4	179394760	q34.3
SNP_A-2271388	G	G	321	49	336	76	3.93	4.74E-02	rs417513	5	4316533	p15.33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2266334	T	T	202	160	249	147	3.931	4.74E-02	rs907021	16	9262257	p13.2
SNP_A-2260834	G	G	364	12	377	25	3.931	4.74E-02	rs11990608	8	97558505	q22.1
SNP_A-2257720	T	T	253	115	311	103	3.933	4.74E-02	rs6056891	20	9726729	p12.2
SNP_A-2276222	A	A	245	123	304	112	3.931	4.74E-02	rs7696083	4	121754052	q27
SNP_A-2296856	C	C	323	41	330	64	3.932	4.74E-02	rs4867947	5	169561981	q35.1
SNP_A-2291218	C	C	350	54	336	76	3.931	4.74E-02	rs6706247	2	223023893	q36.1
SNP_A-2291635	C	C	330	20	347	37	3.931	4.74E-02	rs1607542	8	78879014	q21.12
SNP_A-2289320	G	G	314	32	346	56	3.926	4.75E-02	rs11176716	12	66073037	q14.3
SNP_A-2276869	C	C	313	105	283	129	3.928	4.75E-02	rs998949	6	19283769	p22.3
SNP_A-2279100	G	G	320	102	342	78	3.926	4.75E-02	rs17118056	5	154954799	q33.2
SNP_A-2267811	T	T	331	35	357	59	3.929	4.75E-02	rs2281144	6	167062255	q27
SNP_A-2237723	G	G	307	61	311	89	3.926	4.75E-02	rs11067584	12	114315477	q24.21
SNP_A-2255461	C	C	192	178	244	170	3.929	4.75E-02	rs6662687	1	183611548	q31.1
SNP_A-2096572	T	T	245	97	254	138	3.928	4.75E-02	rs10018583	4	25207133	p15.2
SNP_A-2054863	T	T	298	72	357	59	3.926	4.75E-02	rs11108317	12	94780398	q23.1
SNP_A-2054162	T	C	179	177	231	175	3.928	4.75E-02	rs2730985	12	41416891	q12
SNP_A-2054496	G	G	327	37	388	26	3.928	4.75E-02	rs11066609	12	112473557	q24.13
SNP_A-2033622	A	A	172	154	231	153	3.929	4.75E-02	rs282270	2	224747493	q36.1
SNP_A-2025598	G	G	333	27	372	16	3.929	4.75E-02	rs9569841	13	33063186	q13.2
SNP_A-2006124	A	A	411	11	396	22	3.927	4.75E-02	rs7588402	2	9045665	p25.1
SNP_A-2186224	C	C	313	91	236	96	3.927	4.75E-02	rs6546726	2	26186767	p23.3
SNP_A-2214494	C	C	210	136	193	169	3.928	4.75E-02	rs7840624	8	2920034	p23.2
SNP_A-2202766	G	G	319	93	300	120	3.929	4.75E-02	rs6493511	15	49688897	q21.2
SNP_A-2166966	A	A	199	189	231	165	3.927	4.75E-02	rs1413809	6	19024544	p22.3
SNP_A-2114353	T	T	280	76	272	104	3.928	4.75E-02	rs6836670	4	148641978	q31.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134862	C	C	334	12	387	5	3.926	4.75E-02	rs11934067	4	96798734	q22.3
SNP_A-2127047	G	G	323	19	344	36	3.927	4.75E-02	rs9399791	6	103675507	q16.3
SNP_A-1807308	A	A	260	94	312	80	3.928	4.75E-02	rs12870733	13	58326056	q21.1
SNP_A-1810812	C	C	335	29	346	16	3.928	4.75E-02	rs7508955	20	46156315	q13.13
SNP_A-1792861	A	A	227	143	282	132	3.926	4.75E-02	rs12120042	1	10279591	p36.22
SNP_A-1797709	G	A	179	157	211	179	3.929	4.75E-02	rs595153	6	94226177	q16.1
SNP_A-1785738	G	G	358	62	377	43	3.929	4.75E-02	rs6926792	6	30093828	p21.33
SNP_A-1755224	T	T	260	134	297	113	3.926	4.75E-02	rs1179500	2	36698817	p22.2
SNP_A-1756126	T	T	205	77	292	76	3.926	4.75E-02	rs1827814	4	85313348	q21.23
SNP_A-1750243	T	T	228	116	289	107	3.926	4.75E-02	rs1405396	3	73986915	p13
SNP_A-1737868	T	T	252	148	288	126	3.927	4.75E-02	rs1869829	2	136088331	q21.3
SNP_A-1670518	G	G	217	151	270	140	3.928	4.75E-02	rs726603	12	44378810	q12
SNP_A-1857684	G	G	362	18	370	8	3.928	4.75E-02	rs7610333	3	30973753	p24.1
SNP_A-1832098	G	G	317	15	323	29	3.929	4.75E-02	rs17147033	7	123600691	q31.33
SNP_A-1842813	T	T	285	121	307	95	3.927	4.75E-02	rs7070724	10	1030138	p15.3
SNP_A-1907282	A	A	334	88	308	112	3.928	4.75E-02	rs10863963	1	208896482	q32.3
SNP_A-1890232	T	C	200	164	217	199	3.926	4.75E-02	rs11220786	11	126492478	q24.2
SNP_A-1975601	G	G	267	79	309	63	3.929	4.75E-02	rs12410630	1	181291095	q25.3
SNP_A-1954264	G	G	238	178	251	141	3.928	4.75E-02	rs4857328	3	99334165	q12.1
SNP_A-1949537	A	A	249	157	276	130	3.929	4.75E-02	rs10160375	11	117459460	q23.3
SNP_A-1940677	C	C	307	99	335	77	3.927	4.75E-02	rs3775256	4	41107223	p13
SNP_A-1933654	C	C	262	146	283	117	3.928	4.75E-02	rs2043614	10	51676508	q11.23
SNP_A-1969289	C	C	409	5	387	13	3.924	4.76E-02	rs2825778	21	20043042	q21.1
SNP_A-1971187	C	C	350	16	408	8	3.924	4.76E-02	rs6007994	22	45617340	q13.31
SNP_A-1983208	C	C	285	55	350	44	3.924	4.76E-02	rs719191	5	119510352	q23.1
SNP_A-1898720	G	G	304	54	357	41	3.923	4.76E-02	rs1060472	4	57100393	q12
SNP_A-1881825	A	A	331	9	385	3	3.925	4.76E-02	rs7756718	6	130837604	q23.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1906231	C	C	345	9	401	3	3.923	4.76E-02	rs17115761	1	57584881	p32.2
SNP_A-1915437	G	G	348	12	403	5	3.926	4.76E-02	rs2279055	17	71821156	q25.1
SNP_A-1924777	G	G	243	127	299	115	3.924	4.76E-02	rs13096142	3	46256748	p21.31
SNP_A-1933111	A	A	245	121	304	110	3.925	4.76E-02	rs7761904	6	122725755	q22.31
SNP_A-1830783	A	A	362	40	368	24	3.924	4.76E-02	rs1339400	1	211841681	q41
SNP_A-1827894	C	C	230	122	232	166	3.924	4.76E-02	rs10803724	2	10682921	p25.1
SNP_A-1851233	A	A	304	46	369	35	3.924	4.76E-02	rs7127735	11	102160267	q22.2
SNP_A-1847613	C	C	284	28	317	51	3.923	4.76E-02	rs4839317	1	113625871	p13.2
SNP_A-1703609	T	T	318	84	303	111	3.925	4.76E-02	rs967318	3	60572925	p14.2
SNP_A-1695633	C	C	321	29	356	52	3.925	4.76E-02	rs485963	6	87456261	q14.3
SNP_A-1757295	T	T	262	138	295	115	3.923	4.76E-02	rs10483951	14	78914479	q31.1
SNP_A-1785457	T	T	242	114	243	155	3.924	4.76E-02	rs887864	16	11066386	p13.13
SNP_A-1810947	C	C	412	4	406	0	3.923	4.76E-02	rs2123844	17	3961963	p13.2
SNP_A-1807751	T	T	318	104	288	128	3.925	4.76E-02	rs2483587	10	116293855	q25.3
SNP_A-1805241	C	C	376	42	352	60	3.925	4.76E-02	rs2529407	7	50531306	p12.2
SNP_A-2132085	T	T	418	4	412	0	3.924	4.76E-02	rs1360139	9	126646649	q33.3
SNP_A-2133060	C	C	352	14	388	6	3.925	4.76E-02	rs12452883	17	63888349	q24.2
SNP_A-2120965	T	T	309	55	371	43	3.925	4.76E-02	rs11122374	1	228360813	q42.2
SNP_A-2121793	A	A	342	72	316	94	3.924	4.76E-02	rs4473450	20	41676114	q13.12
SNP_A-2162970	T	T	299	67	311	99	3.923	4.76E-02	rs6847661	4	158935002	q32.1
SNP_A-2154850	G	G	315	37	323	59	3.922	4.76E-02	rs17012735	2	76605013	p12
SNP_A-2220645	A	A	343	19	377	37	3.924	4.76E-02	rs16897819	5	67752037	q13.1
SNP_A-2007373	A	A	406	0	412	4	3.923	4.76E-02	rs6033361	20	12193855	p12.1
SNP_A-2009521	G	G	287	75	233	87	3.925	4.76E-02	rs2980167	4	4416642	p16.3
SNP_A-2011363	C	C	339	81	306	102	3.925	4.76E-02	rs4958765	5	154071950	q33.2
SNP_A-1993522	A	A	264	100	307	83	3.926	4.76E-02	rs16927449	8	62596948	q12.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2032324	G	G	345	1	379	7	3.923	4.76E-02	rs16852867	3	170128424	q26.2
SNP_A-2042815	C	C	227	143	225	189	3.925	4.76E-02	rs6837393	4	175851192	q34.1
SNP_A-2051690	A	A	227	143	225	189	3.925	4.76E-02	rs6797720	3	81313429	p12.2
SNP_A-2055392	T	T	308	80	304	110	3.924	4.76E-02	rs10506250	12	43268257	q12
SNP_A-2056313	C	C	276	92	277	127	3.925	4.76E-02	rs11160020	14	91145530	q32.12
SNP_A-2064690	T	T	296	36	299	57	3.925	4.76E-02	rs17111159	12	71116708	q21.1
SNP_A-2229674	A	A	231	137	289	127	3.924	4.76E-02	rs17401943	7	111222976	q31.1
SNP_A-2231098	A	A	339	81	306	102	3.925	4.76E-02	rs4944551	11	85398735	q14.2
SNP_A-2266537	C	C	287	83	346	70	3.925	4.76E-02	rs2251521	10	109461321	q25.1
SNP_A-2269016	A	A	299	115	274	142	3.923	4.76E-02	rs12119179	1	67459436	p31.2
SNP_A-2258089	C	C	292	94	266	118	3.923	4.76E-02	rs4899737	14	78779263	q31.1
SNP_A-2258132	G	G	301	39	360	28	3.924	4.76E-02	rs6006678	22	42868894	q13.31
SNP_A-2259215	A	A	350	8	372	2	3.923	4.76E-02	rs2402132	14	91903909	q32.12
SNP_A-2288480	C	C	316	94	342	72	3.924	4.76E-02	rs2225614	9	24101280	p21.3
SNP_A-2295681	A	A	387	7	366	16	3.923	4.76E-02	rs2196693	2	140315990	q22.1
SNP_A-2290484	A	A	225	135	284	126	3.919	4.77E-02	rs13016055	2	151604161	q23.3
SNP_A-2303797	A	A	360	62	335	83	3.922	4.77E-02	rs6071498	20	59129793	q13.33
SNP_A-2307633	A	A	239	131	240	176	3.919	4.77E-02	rs4933557	10	91892368	q23.31
SNP_A-2262889	C	C	326	56	328	82	3.92	4.77E-02	rs12539387	7	12621048	p21.3
SNP_A-2274106	T	-	209	157	205	205	3.921	4.77E-02	rs2604541	4	14758307	p15.33
SNP_A-2232261	G	G	246	176	211	199	3.919	4.77E-02	rs7371671	2	17174382	p24.2
SNP_A-2252530	G	G	408	4	402	0	3.922	4.77E-02	rs7076439	10	93276822	q23.32
SNP_A-2066855	A	A	223	147	279	137	3.92	4.77E-02	rs10808877	8	53928945	q11.23
SNP_A-2072211	T	T	330	40	351	65	3.921	4.77E-02	rs1548609	7	50647601	p12.2
SNP_A-2048478	T	T	293	67	288	94	3.922	4.77E-02	rs10043180	5	35752263	p13.2
SNP_A-2048473	A	A	231	137	231	183	3.92	4.77E-02	rs7515197	1	165287774	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2094388	T	T	242	104	292	90	3.921	4.77E-02	rs9537680	13	56755082	q21.1
SNP_A-2101933	G	G	289	129	258	154	3.922	4.77E-02	rs10874118	1	80350968	p31.1
SNP_A-2080996	T	T	212	156	204	200	3.922	4.77E-02	rs1940159	11	95424092	q21
SNP_A-2078122	A	A	296	74	355	61	3.92	4.77E-02	rs11185024	1	107201441	p13.3
SNP_A-2037370	A	A	283	23	359	15	3.92	4.77E-02	rs17069337	5	167247202	q34
SNP_A-2011689	T	T	363	59	340	80	3.92	4.77E-02	rs3135366	6	32496687	p21.32
SNP_A-2219766	T	T	256	92	325	83	3.92	4.77E-02	rs4275850	16	50250537	q12.1
SNP_A-2214161	C	C	325	45	383	33	3.919	4.77E-02	rs7759564	6	54583664	p12.1
SNP_A-2210230	C	C	281	129	254	156	3.921	4.77E-02	rs10149327	14	41019623	q21.1
SNP_A-2181443	C	C	352	18	381	35	3.921	4.77E-02	rs36781	5	109317628	q21.3
SNP_A-2175772	G	G	398	18	406	8	3.921	4.77E-02	rs7763448	6	166675134	q27
SNP_A-2163085	G	G	280	88	286	124	3.921	4.77E-02	rs6936722	6	42999289	p21.1
SNP_A-2161395	A	A	242	178	270	150	3.921	4.77E-02	rs6090254	20	61224493	q13.33
SNP_A-2123021	A	A	273	107	315	89	3.922	4.77E-02	rs11178315	12	69274986	q15
SNP_A-2123736	A	A	388	8	412	2	3.922	4.77E-02	rs16938651	8	74501590	q21.11
SNP_A-2129351	A	A	239	131	240	176	3.919	4.77E-02	rs7941677	11	95507276	q21
SNP_A-1805849	G	G	315	3	414	0	3.922	4.77E-02	rs2941307	16	9226408	p13.2
SNP_A-1800630	G	G	317	49	368	36	3.92	4.77E-02	rs7414079	1	183690802	q31.1
SNP_A-1750267	G	G	398	0	404	4	3.921	4.77E-02	rs10513276	9	114517819	q33.1
SNP_A-1783302	T	T	398	0	404	4	3.921	4.77E-02	rs16872659	7	20867852	p15.3
SNP_A-1746723	A	A	322	80	306	106	3.92	4.77E-02	rs7785596	7	127114402	q32.1
SNP_A-1746478	C	C	363	27	367	45	3.921	4.77E-02	rs1886039	13	44521716	q14.13
SNP_A-1720061	G	G	344	56	333	79	3.921	4.77E-02	rs2818758	1	214179369	q41
SNP_A-1656107	C	C	363	29	393	17	3.919	4.77E-02	rs10269685	7	12686004	p21.3
SNP_A-1629174	G	G	262	92	325	81	3.921	4.77E-02	rs7034585	9	37497104	p13.2
SNP_A-1840852	A	A	289	81	348	68	3.92	4.77E-02	rs1001877	15	27996637	q13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1840279	G	G	327	13	392	6	3.921	4.77E-02	rs4988172	2	136458418	q21.3
SNP_A-1924574	T	T	239	131	240	176	3.919	4.77E-02	rs2150298	14	82598016	q31.2
SNP_A-1915935	G	G	296	74	355	61	3.92	4.77E-02	rs16852229	2	215297824	q35
SNP_A-1913357	G	G	335	33	360	56	3.919	4.77E-02	rs17089187	8	23310884	p21.3
SNP_A-1878610	A	A	340	28	365	49	3.921	4.77E-02	rs17007502	3	20738139	p24.3
SNP_A-1985095	G	G	218	200	235	163	3.921	4.77E-02	rs595877	6	11687079	p24.2
SNP_A-1980190	A	A	239	131	240	176	3.919	4.77E-02	rs747368	4	184326734	q35.1
SNP_A-1963924	A	A	239	131	240	176	3.919	4.77E-02	rs895757	2	79149273	p12
SNP_A-1936304	A	A	394	0	400	4	3.921	4.77E-02	rs4588812	8	91736071	q21.3
SNP_A-1938709	C	C	390	12	390	4	3.92	4.77E-02	rs1974102	20	48213325	q13.13
SNP_A-1946831	C	C	325	45	383	33	3.919	4.77E-02	rs1431485	10	118183206	q25.3
SNP_A-1971946	G	G	290	80	349	67	3.919	4.78E-02	rs6550413	3	20206523	p24.3
SNP_A-1973685	A	A	344	26	400	16	3.917	4.78E-02	rs6788864	3	102772279	q12.3
SNP_A-1981725	T	T	236	162	263	135	3.915	4.78E-02	rs10472063	5	57816626	q11.2
SNP_A-1879195	G	G	292	78	351	65	3.917	4.78E-02	rs745081	4	73046537	q13.3
SNP_A-1879701	G	G	307	107	277	131	3.918	4.78E-02	rs8073513	17	111099	p13.3
SNP_A-1884115	T	T	261	121	245	153	3.917	4.78E-02	rs12708716	16	11087374	p13.13
SNP_A-1885726	A	A	355	31	349	49	3.918	4.78E-02	rs196458	6	168935012	q27
SNP_A-1890787	C	C	361	33	351	51	3.918	4.78E-02	rs6005197	22	19678164	q11.21
SNP_A-1916334	T	T	382	6	411	1	3.915	4.78E-02	rs725574	12	92640900	q22
SNP_A-1917011	T	T	270	94	272	130	3.918	4.78E-02	rs17738824	15	85643188	q25.3
SNP_A-1831733	A	A	254	124	239	157	3.915	4.78E-02	rs6988980	8	76043325	q21.11
SNP_A-1834305	G	G	308	66	283	87	3.918	4.78E-02	rs4867173	5	29372002	p13.3
SNP_A-1848096	T	T	258	142	280	114	3.917	4.78E-02	rs10100706	8	9359190	p23.1
SNP_A-1856485	T	T	183	143	251	145	3.918	4.78E-02	rs1938378	1	194877897	q31.3
SNP_A-1864499	C	C	347	61	319	81	3.915	4.78E-02	rs1019977	18	17257904	q11.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1670357	A	A	263	139	243	171	3.918	4.78E-02	rs3929470	6	54680717	p12.1
SNP_A-1670193	G	G	233	135	231	179	3.918	4.78E-02	rs10492206	12	66454597	q15
SNP_A-1665056	C	C	278	68	303	105	3.917	4.78E-02	rs7328931	13	91273721	q31.3
SNP_A-1682790	C	C	258	140	291	117	3.919	4.78E-02	rs7499390	16	54558972	q12.2
SNP_A-1742991	C	C	323	27	379	17	3.918	4.78E-02	rs10508166	13	104169900	q33.2
SNP_A-2154981	T	T	218	200	243	169	3.917	4.78E-02	rs2427216	20	59647609	q13.33
SNP_A-2147270	A	A	329	21	362	40	3.917	4.78E-02	rs662616	13	78593828	q31.1
SNP_A-2171841	C	C	290	80	349	67	3.919	4.78E-02	rs6921876	6	108172532	q21
SNP_A-2198894	C	C	295	89	255	107	3.917	4.78E-02	rs7397680	12	18112831	p12.3
SNP_A-2211289	G	G	292	78	351	65	3.917	4.78E-02	rs2875855	16	82666152	q23.3
SNP_A-2207762	C	C	392	6	356	14	3.917	4.78E-02	rs10968093	9	27743227	p21.2
SNP_A-2205956	G	G	291	79	350	66	3.917	4.78E-02	rs5484	12	21422704	p12.1
SNP_A-2206224	C	C	392	8	416	2	3.919	4.78E-02	rs12945287	17	74749078	q25.3
SNP_A-1993014	C	C	346	66	369	47	3.915	4.78E-02	rs16882701	8	34642572	p12
SNP_A-2033501	G	G	191	179	244	172	3.918	4.78E-02	rs11687654	2	53301317	p16.2
SNP_A-2106487	T	T	292	78	351	65	3.917	4.78E-02	rs235893	1	168306429	q24.3
SNP_A-2076163	C	C	310	98	292	126	3.918	4.78E-02	rs4838635	10	49556068	q11.23
SNP_A-2062711	A	A	315	35	327	57	3.919	4.78E-02	rs10166594	2	202940491	q33.1
SNP_A-2252717	G	G	260	110	262	150	3.917	4.78E-02	rs12498847	4	160286512	q32.1
SNP_A-2251112	G	G	276	144	247	171	3.918	4.78E-02	rs6744496	2	129205786	q14.3
SNP_A-2248324	T	T	236	176	265	149	3.917	4.78E-02	rs3935844	5	33675439	p13.3
SNP_A-2242407	C	C	260	110	262	150	3.917	4.78E-02	rs6857434	4	160249727	q32.1
SNP_A-2280578	C	C	372	40	391	25	3.915	4.78E-02	rs1377106	11	40231636	p12
SNP_A-2262311	C	C	345	7	349	17	3.918	4.78E-02	rs344510	5	35064983	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2272048	C	C	338	28	363	49	3.913	4.79E-02	rs1355420	2	160738778	q24.2
SNP_A-2283905	A	A	252	110	259	153	3.913	4.79E-02	rs7923926	10	87847848	q23.2
SNP_A-2287619	G	G	331	29	376	18	3.913	4.79E-02	rs17018034	4	92389665	q22.1
SNP_A-2244230	T	T	334	36	354	22	3.913	4.79E-02	rs7914649	10	59155829	q21.1
SNP_A-2240457	G	G	326	70	316	96	3.913	4.79E-02	rs4582229	5	60884502	q12.1
SNP_A-2314673	A	A	301	55	354	42	3.914	4.79E-02	rs2900108	5	117354733	q23.1
SNP_A-2311734	T	T	303	67	312	98	3.915	4.79E-02	rs2600859	3	62509205	p14.2
SNP_A-2312620	C	C	308	40	358	28	3.915	4.79E-02	rs2925139	17	17949317	p11.2
SNP_A-2300110	A	A	232	126	286	114	3.914	4.79E-02	rs11224357	11	100026021	q22.1
SNP_A-2069357	T	T	286	64	300	96	3.913	4.79E-02	rs17696392	17	43782159	q21.32
SNP_A-2058195	C	C	256	76	271	113	3.914	4.79E-02	rs2622770	15	49758614	q21.2
SNP_A-2059856	T	T	270	94	327	81	3.913	4.79E-02	rs1563024	2	50225462	p16.3
SNP_A-2105230	A	A	334	34	391	23	3.912	4.79E-02	rs2132845	4	140944730	q31.1
SNP_A-2104668	T	C	188	166	207	175	3.913	4.79E-02	rs7752610	6	6904637	p25.1
SNP_A-2096628	G	G	253	149	222	174	3.913	4.79E-02	rs11631776	15	32429266	q14
SNP_A-2079699	G	G	364	48	357	29	3.913	4.79E-02	rs9393303	6	22609705	p22.3
SNP_A-2035286	G	G	248	110	260	156	3.914	4.79E-02	rs6544414	2	41527141	p22.1
SNP_A-2039704	G	G	311	7	384	2	3.914	4.79E-02	rs2385251	7	103870151	q22.2
SNP_A-1990628	G	G	279	89	325	73	3.915	4.79E-02	rs16840459	1	237136238	q43
SNP_A-1994315	T	T	328	40	369	27	3.913	4.79E-02	rs16917734	8	96550510	q22.1
SNP_A-2217266	G	G	205	163	257	153	3.913	4.79E-02	rs2113607	2	86508834	p11.2
SNP_A-2227949	A	A	245	125	247	169	3.914	4.79E-02	rs10872455	6	136317780	q23.3
SNP_A-2195710	G	G	334	34	391	23	3.912	4.79E-02	rs854420	14	24304777	q12
SNP_A-2176973	A	A	413	1	384	6	3.914	4.79E-02	rs654123	1	30563653	p35.2
SNP_A-2132935	A	A	415	1	386	6	3.912	4.79E-02	rs17123269	8	16496990	p22
SNP_A-2131190	T	T	245	125	247	169	3.914	4.79E-02	rs2304536	4	148238369	q31.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123398	T	T	211	157	205	203	3.913	4.79E-02	rs6833943	4	158908904	q32.1
SNP_A-1713133	A	A	357	45	348	66	3.912	4.79E-02	rs10494698	1	191384841	q31.3
SNP_A-1751817	C	C	396	6	389	15	3.915	4.79E-02	rs10494243	1	144186880	q21.1
SNP_A-1678782	G	G	342	26	357	45	3.913	4.79E-02	-	8	51311063	q11.21
SNP_A-1654387	G	G	195	165	251	159	3.912	4.79E-02	rs668527	6	128007556	q22.33
SNP_A-1857078	C	T	182	136	192	190	3.914	4.79E-02	rs683994	6	158849886	q25.3
SNP_A-1853308	A	A	373	29	346	44	3.915	4.79E-02	rs17526000	10	97017076	q24.1
SNP_A-1819619	A	A	350	18	379	35	3.914	4.79E-02	rs6809968	3	76430184	p12.3
SNP_A-1817489	C	C	223	195	249	165	3.913	4.79E-02	rs1004507	16	6396666	p13.2
SNP_A-1817085	G	G	284	74	346	62	3.913	4.79E-02	rs17238004	3	157589268	q25.31
SNP_A-1910060	A	A	379	25	389	13	3.915	4.79E-02	rs4674271	2	218885327	q35
SNP_A-1893422	T	T	289	71	303	105	3.915	4.79E-02	rs433900	16	82852587	q24.1
SNP_A-1900648	C	C	410	6	403	15	3.913	4.79E-02	rs1503306	4	5450670	p16.2
SNP_A-1938812	G	G	267	153	294	126	3.912	4.79E-02	rs4455270	3	73086747	p13
SNP_A-1936690	T	T	277	35	292	58	3.915	4.79E-02	rs10769784	11	7362974	p15.4
SNP_A-1934281	G	G	332	4	363	13	3.913	4.79E-02	rs7504721	18	68121139	q22.3
SNP_A-1959672	T	T	313	45	319	69	3.909	4.80E-02	rs2454962	13	84446757	q31.1
SNP_A-1975990	A	A	287	83	297	119	3.908	4.80E-02	rs6831297	4	10412923	p16.1
SNP_A-1897133	G	A	192	174	223	185	3.91	4.80E-02	rs4900037	14	89891231	q32.11
SNP_A-1895704	G	G	388	2	366	8	3.909	4.80E-02	rs1810378	7	38162129	p14.1
SNP_A-1884143	A	A	375	41	346	58	3.911	4.80E-02	rs1897477	2	1984430	p25.3
SNP_A-1909752	G	G	212	158	208	206	3.911	4.80E-02	rs999803	4	105053524	q24
SNP_A-1919012	A	A	332	32	317	49	3.909	4.80E-02	rs26927	5	66218232	q12.3
SNP_A-1920757	C	A	207	157	205	203	3.909	4.80E-02	rs7336560	13	37059492	q13.3
SNP_A-1815162	T	T	346	4	346	12	3.91	4.80E-02	rs7751840	6	7132245	p24.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1815571	A	A	296	74	308	108	3.911	4.80E-02	rs8070576	17	36434265	q21.2
SNP_A-1820471	A	A	337	23	353	41	3.908	4.80E-02	rs1067969	13	60315288	q21.2
SNP_A-1838180	A	A	245	175	264	142	3.908	4.80E-02	rs6969899	7	133054745	q33
SNP_A-1660257	G	G	266	124	307	105	3.91	4.80E-02	rs726051	13	37500998	q13.3
SNP_A-1677794	A	A	222	178	258	156	3.909	4.80E-02	rs719667	2	113437828	q13
SNP_A-1699523	C	T	177	173	231	177	3.912	4.80E-02	rs2358469	4	150168208	q31.23
SNP_A-1783769	C	C	287	83	297	119	3.908	4.80E-02	rs2964135	5	5451279	p15.32
SNP_A-1731799	C	C	316	74	310	102	3.912	4.80E-02	rs10486293	7	18380111	p21.1
SNP_A-1785918	A	A	251	121	250	162	3.911	4.80E-02	rs2731072	12	47203692	q13.11
SNP_A-2164714	A	A	286	136	256	162	3.91	4.80E-02	rs10885431	10	115087540	q25.3
SNP_A-2181932	C	C	232	122	286	110	3.91	4.80E-02	rs1511601	3	170126370	q26.2
SNP_A-2169320	C	C	273	105	278	76	3.909	4.80E-02	rs7102932	11	42824773	p12
SNP_A-2226986	C	C	188	178	243	173	3.909	4.80E-02	rs9821688	3	64806275	p14.1
SNP_A-2214749	T	T	405	13	395	25	3.91	4.80E-02	rs10431169	11	85785760	q14.2
SNP_A-1994652	T	T	310	52	316	78	3.91	4.80E-02	rs17385666	8	111181675	q23.2
SNP_A-2009032	T	T	349	61	321	81	3.909	4.80E-02	rs2331522	3	122299730	q13.33
SNP_A-2013554	A	A	287	55	345	43	3.909	4.80E-02	rs3847520	11	91161681	q14.3
SNP_A-2041648	C	C	399	7	378	16	3.91	4.80E-02	rs1390822	7	77999145	q21.11
SNP_A-2046812	A	A	240	168	213	197	3.909	4.80E-02	rs601194	16	56060714	q13
SNP_A-2099202	A	A	237	181	265	153	3.909	4.80E-02	rs7704598	5	167667985	q34
SNP_A-2104795	T	T	212	154	257	139	3.911	4.80E-02	rs4702974	5	97853674	q21.1
SNP_A-2063067	C	C	377	45	356	64	3.909	4.80E-02	rs10060095	5	152877600	q33.2
SNP_A-2063384	C	C	207	153	258	142	3.909	4.80E-02	rs10077716	5	121056050	q23.1
SNP_A-2250494	C	C	201	169	255	161	3.91	4.80E-02	rs4625954	2	55087196	p16.1
SNP_A-2285461	A	A	287	83	297	119	3.908	4.80E-02	rs2166596	4	140863237	q31.1
SNP_A-2281171	G	G	397	25	407	13	3.909	4.80E-02	rs6741506	2	16642363	p24.3
SNP_A-2281050	C	C	348	38	387	25	3.909	4.80E-02	rs11182579	12	43306428	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2275963	T	T	398	14	382	26	3.909	4.80E-02	rs7674006	4	41541035	p13
SNP_A-2270178	C	C	308	50	350	36	3.912	4.80E-02	rs10895777	11	96817135	q22.1
SNP_A-2259216	A	A	177	143	226	134	3.911	4.80E-02	rs1537778	10	25129056	p12.1
SNP_A-2250903	G	G	366	4	401	13	3.905	4.81E-02	rs17618099	1	190853200	q31.3
SNP_A-2236046	A	A	272	136	230	154	3.908	4.81E-02	rs13319916	3	54213098	p21.1
SNP_A-2300046	G	G	343	25	395	15	3.908	4.81E-02	rs16923301	9	737732	p24.3
SNP_A-2312949	T	T	178	176	231	171	3.908	4.81E-02	rs6071894	20	38065816	q12
SNP_A-2308978	G	G	205	161	257	151	3.906	4.81E-02	rs3805907	6	81030384	q14.1
SNP_A-2050486	A	A	315	95	293	121	3.906	4.81E-02	rs11619784	13	26897643	q12.2
SNP_A-2107546	A	G	204	166	216	200	3.905	4.81E-02	rs3888913	2	237562124	q37.3
SNP_A-2013952	T	T	344	26	368	46	3.907	4.81E-02	rs547243	11	94476263	q21
SNP_A-2010680	G	G	249	119	252	162	3.906	4.81E-02	rs4702015	5	14113165	p15.2
SNP_A-2005995	C	C	328	6	346	16	3.906	4.81E-02	rs1929684	10	121869552	q26.12
SNP_A-2217814	T	T	327	67	286	84	3.906	4.81E-02	rs6747870	2	135303501	q21.3
SNP_A-2208157	T	T	236	186	263	157	3.908	4.81E-02	rs2065108	20	33170483	q11.22
SNP_A-2210285	A	A	236	172	261	143	3.908	4.81E-02	rs2168443	3	46922091	p21.31
SNP_A-2167003	G	G	276	28	295	49	3.905	4.81E-02	rs4916329	1	170039832	q25.1
SNP_A-2160410	G	G	215	131	268	120	3.907	4.81E-02	rs6545334	2	53475139	p16.2
SNP_A-2142090	T	T	356	2	383	9	3.908	4.81E-02	rs4860663	4	66126340	q13.1
SNP_A-2141260	A	A	348	14	362	28	3.906	4.81E-02	rs9449519	6	83443389	q14.1
SNP_A-2133091	T	T	262	104	265	143	3.907	4.81E-02	rs2189208	4	114864543	q26
SNP_A-1807806	C	C	244	108	246	148	3.906	4.81E-02	rs10745698	12	93706540	q22
SNP_A-1753105	T	T	267	83	335	73	3.907	4.81E-02	rs774568	6	113561384	q21
SNP_A-1706519	G	G	326	24	393	15	3.905	4.81E-02	rs9301548	13	87631542	q31.2
SNP_A-1678634	T	T	334	12	377	27	3.908	4.81E-02	rs1603312	3	88682482	p11.1
SNP_A-1667190	C	C	280	100	262	128	3.907	4.81E-02	rs10486016	7	105774881	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1850293	G	G	354	12	409	5	3.908	4.81E-02	rs12444740	16	31845097	p11.2
SNP_A-1864804	T	T	253	95	314	84	3.905	4.81E-02	rs3007716	1	222432352	q42.12
SNP_A-1865081	C	C	316	54	333	83	3.905	4.81E-02	rs17733520	5	168193013	q34
SNP_A-1860715	A	A	246	120	305	109	3.907	4.81E-02	rs7005030	8	11407230	p23.1
SNP_A-1867951	T	T	229	133	233	181	3.905	4.81E-02	rs7424405	2	107248604	q12.3
SNP_A-1929786	A	A	268	102	325	89	3.907	4.81E-02	rs4413762	8	59432719	q12.1
SNP_A-1926631	G	G	327	41	346	66	3.908	4.81E-02	rs17636264	9	119261645	q33.1
SNP_A-1913877	C	C	296	110	317	85	3.905	4.81E-02	rs2162938	19	52888385	q13.32
SNP_A-1899153	A	G	186	180	234	182	3.906	4.81E-02	rs9473405	6	48574782	p12.3
SNP_A-1969137	G	G	272	94	281	133	3.908	4.81E-02	rs2824060	21	17104554	q21.1
SNP_A-1977830	T	T	323	13	328	26	3.905	4.81E-02	rs1443771	4	83310289	q21.22
SNP_A-1961024	C	C	245	115	251	159	3.908	4.81E-02	rs11778117	8	48124531	q11.21
SNP_A-1933778	A	A	343	25	395	15	3.908	4.81E-02	rs10813040	9	29259540	p21.1
SNP_A-1943595	C	C	358	12	388	26	3.907	4.81E-02	rs17108126	14	78257620	q24.3
SNP_A-1943180	G	G	332	90	297	111	3.907	4.81E-02	rs2074843	2	241727829	q37.3
SNP_A-1952573	A	A	388	26	404	14	3.904	0.0482	rs12553148	9	18026979	p22.2
SNP_A-1978426	C	C	369	1	407	7	3.904	0.0482	rs17038770	4	109557964	q25
SNP_A-1984961	T	T	358	48	351	29	3.902	0.0482	rs17142726	6	6942664	p25.1
SNP_A-1893052	G	G	353	9	409	3	3.902	0.0482	rs17172798	7	46789632	p13
SNP_A-1912957	C	C	228	138	229	185	3.902	0.0482	rs1317493	2	202884960	q33.1
SNP_A-1907778	A	A	410	4	402	0	3.903	0.0482	rs11807804	1	24375752	p36.11
SNP_A-1923055	C	C	331	13	396	6	3.905	0.0482	rs930814	3	95457618	q11.2
SNP_A-1866690	C	C	281	83	288	118	3.901	0.0482	rs10871408	16	79812037	q23.2
SNP_A-1863057	A	A	216	154	265	141	3.903	0.0482	rs11136837	8	5082418	p23.2
SNP_A-1837425	G	G	406	0	414	4	3.904	0.0482	rs9873674	3	53410766	p21.1
SNP_A-1815315	A	A	339	31	363	53	3.904	0.0482	rs12476641	2	78289802	p12
SNP_A-1816414	A	G	185	183	234	178	3.903	0.0482	rs2709441	2	5968216	p25.2
SNP_A-1670824	G	G	326	22	364	42	3.904	0.0482	rs10492622	13	91377184	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1653306	A	A	234	158	212	190	3.902	0.0482	rs1406720	7	143872411	q35
SNP_A-1682268	C	C	328	74	357	55	3.904	0.0482	rs2278528	2	20086344	p24.1
SNP_A-1702617	T	T	402	0	410	4	3.903	0.0482	rs10492259	12	113866269	q24.21
SNP_A-1746344	G	G	402	0	410	4	3.903	0.0482	rs765087	1	211115229	q32.3
SNP_A-1791012	T	T	367	15	347	27	3.905	0.0482	rs7753645	6	169891325	q27
SNP_A-2131516	C	C	335	33	390	22	3.903	0.0482	rs1438681	5	110988611	q22.1
SNP_A-2158636	C	C	400	16	389	29	3.904	0.0482	rs12128424	1	181124748	q25.3
SNP_A-2202729	A	A	284	40	301	65	3.904	0.0482	rs4357890	15	68477049	q23
SNP_A-2169535	A	A	333	37	355	61	3.902	0.0482	rs9648071	7	40777849	p14.1
SNP_A-2182405	C	C	322	32	388	22	3.903	0.0482	rs17720936	16	6611812	p13.2
SNP_A-2001215	G	G	355	5	395	15	3.903	0.0482	rs16909068	10	58035394	q21.1
SNP_A-2039965	C	C	354	14	383	29	3.904	0.0482	rs3851448	5	41661649	p13.1
SNP_A-2037716	A	A	330	92	346	68	3.903	0.0482	rs7571492	2	19861127	p24.1
SNP_A-2107164	G	G	330	36	354	60	3.903	0.0482	rs7120325	11	26005790	p14.2
SNP_A-2089720	T	T	267	57	273	85	3.902	0.0482	rs11194422	10	110894387	q25.1
SNP_A-2068938	A	A	212	136	215	185	3.905	0.0482	rs10736767	11	84314713	q14.1
SNP_A-2241719	C	C	333	37	355	61	3.902	0.0482	rs10441664	8	14082205	p22
SNP_A-2241720	G	G	353	9	409	3	3.902	0.0482	rs13411837	2	18722	p25.3
SNP_A-2258684	A	A	393	21	375	35	3.903	0.0482	rs12075867	1	3161113	p36.32
SNP_A-2271916	A	A	281	47	296	74	3.902	0.0482	rs991574	7	45023251	p13
SNP_A-2271808	T	T	356	66	329	87	3.904	0.0482	rs2114774	3	16687492	p24.3
SNP_A-2283152	A	A	333	37	355	61	3.902	0.0482	rs7201756	16	26845617	p12.1
SNP_A-2266968	T	T	367	1	405	7	3.901	4.83E-02	rs10277999	7	136646887	q33
SNP_A-2232136	T	T	260	98	312	84	3.899	4.83E-02	rs10996855	10	67479542	q21.3
SNP_A-2312763	A	A	336	34	393	23	3.901	4.83E-02	rs11160673	14	101740460	q32.32
SNP_A-2313726	C	C	388	26	367	41	3.899	4.83E-02	rs3132278	9	134586185	q34.2
SNP_A-2311318	A	A	356	8	371	19	3.899	4.83E-02	rs6664817	1	151497179	q22
SNP_A-2066626	T	T	326	10	355	23	3.899	4.83E-02	rs17112751	10	101969243	q24.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2071226	T	T	365	1	403	7	3.898	4.83E-02	rs395284	5	10043693	p15.2
SNP_A-2053028	A	A	341	81	359	59	3.901	4.83E-02	rs7025688	9	126585776	q33.3
SNP_A-2057466	T	T	233	147	263	123	3.901	4.83E-02	rs9548101	13	37390948	q13.3
SNP_A-2055284	G	G	402	10	413	3	3.898	4.83E-02	rs1356177	2	14540157	p24.3
SNP_A-2037899	A	A	272	92	280	130	3.9	4.83E-02	rs17072268	13	48281762	q14.2
SNP_A-2046313	C	C	260	98	268	138	3.901	4.83E-02	rs17182681	12	65560266	q14.3
SNP_A-2041167	C	C	218	142	275	133	3.9	4.83E-02	rs7015264	8	78468332	q21.11
SNP_A-2020337	G	G	216	196	243	167	3.9	4.83E-02	rs7283362	21	43798095	q22.3
SNP_A-2020180	C	C	404	10	415	3	3.898	4.83E-02	rs17115129	21	42856498	q22.3
SNP_A-2005647	A	A	219	143	207	181	3.898	4.83E-02	rs6507953	18	45535197	q21.1
SNP_A-2007942	A	A	208	156	264	148	3.9	4.83E-02	rs1528668	11	13994054	p15.2
SNP_A-2178206	G	G	331	33	356	56	3.899	4.83E-02	rs912129	13	98831653	q32.3
SNP_A-2185552	C	C	346	18	375	35	3.899	4.83E-02	rs16955222	18	9528612	p11.22
SNP_A-2188672	G	G	272	130	296	104	3.898	4.83E-02	rs1333348	13	26798534	q12.2
SNP_A-2203399	T	C	159	145	179	143	3.901	4.83E-02	rs6912551	6	62658688	q11.1
SNP_A-2211554	C	C	212	158	207	205	3.901	4.83E-02	rs10064315	5	68281215	q13.1
SNP_A-2217571	C	T	191	175	223	183	3.898	4.83E-02	rs1255332	14	52881630	q22.1
SNP_A-2144951	C	C	228	140	283	129	3.9	4.83E-02	rs1878615	2	104810445	q12.1
SNP_A-2131735	G	G	308	108	332	84	3.9	4.83E-02	rs17138731	17	32886650	q12
SNP_A-2130373	C	C	287	71	301	105	3.901	4.83E-02	rs13115884	4	127269929	q28.1
SNP_A-2124071	A	A	265	59	249	81	3.9	4.83E-02	rs2068260	5	115021230	q22.3
SNP_A-2115004	G	A	194	164	213	189	3.9	4.83E-02	rs6101193	20	59038519	q13.33
SNP_A-1797254	G	A	211	201	225	179	3.9	4.83E-02	rs10279584	7	28180218	p15.1
SNP_A-1798782	T	T	212	130	217	179	3.898	4.83E-02	rs17628530	6	119848000	q22.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1700610	C	C	358	42	381	27	3.898	4.83E-02	rs10495467	1	237555221	q43
SNP_A-1704895	T	T	399	1	372	6	3.898	4.83E-02	rs7093020	10	57388016	q21.1
SNP_A-1817435	G	G	332	84	308	108	3.9	4.83E-02	rs17358517	3	59660772	p14.2
SNP_A-1851074	C	C	336	34	393	23	3.901	4.83E-02	rs9866721	3	107490054	q13.11
SNP_A-1849836	C	C	365	51	323	67	3.899	4.83E-02	rs1321116	1	30387341	p35.2
SNP_A-1922301	G	G	364	4	399	13	3.901	4.83E-02	rs2481653	1	172775778	q25.1
SNP_A-1914686	T	T	200	198	230	172	3.9	4.83E-02	rs9536378	13	52728040	q14.3
SNP_A-1916041	G	G	275	63	345	53	3.9	4.83E-02	rs4801010	18	51779825	q21.2
SNP_A-1881202	A	A	289	81	298	116	3.899	4.83E-02	rs10117750	9	104278378	q31.1
SNP_A-1950858	A	A	366	44	382	28	3.898	4.83E-02	rs16872456	5	3915889	p15.33
SNP_A-1955985	G	G	266	154	293	127	3.898	4.83E-02	rs1451680	8	40610995	p11.21
SNP_A-1938098	G	G	313	109	334	84	3.901	4.83E-02	rs2173852	3	125902792	q21.2
SNP_A-1959326	G	G	370	52	348	72	3.895	4.84E-02	rs13017138	2	36091774	p22.3
SNP_A-1987642	C	C	374	0	382	4	3.896	4.84E-02	rs2133006	6	131033164	q23.1
SNP_A-1989145	A	A	315	37	361	25	3.895	4.84E-02	rs10227372	7	21575422	p15.3
SNP_A-1980598	A	A	333	17	395	9	3.894	4.84E-02	rs7722769	5	9154449	p15.31
SNP_A-1964629	G	G	284	84	288	118	3.894	4.84E-02	rs1559509	2	118572157	q14.1
SNP_A-1975553	G	G	317	39	345	65	3.897	4.84E-02	rs10911593	1	181090592	q25.3
SNP_A-1891418	T	T	271	81	318	66	3.897	4.84E-02	rs2659524	4	102506392	q24
SNP_A-1890630	A	A	216	140	212	184	3.896	4.84E-02	rs2723501	7	17627772	p21.1
SNP_A-1898759	A	A	171	165	227	163	3.897	4.84E-02	rs6777094	3	36951930	p22.3
SNP_A-1915596	T	T	298	72	309	105	3.895	4.84E-02	rs6826780	4	85837169	q21.23
SNP_A-1827432	C	C	270	132	297	107	3.896	4.84E-02	rs3809618	16	82728260	q24.1
SNP_A-1674565	A	A	307	61	319	91	3.895	4.84E-02	rs1791661	12	51060041	q13.13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1673474	A	A	397	5	344	12	3.896	4.84E-02	rs2250942	10	122542868	q26.12
SNP_A-1752879	T	T	259	75	330	66	3.895	4.84E-02	rs4131578	5	85375321	q14.3
SNP_A-1782375	G	G	417	3	406	10	3.897	4.84E-02	rs17034971	1	116203363	p13.1
SNP_A-2126824	C	C	401	1	374	6	3.896	4.84E-02	rs16994688	4	38443772	p14
SNP_A-2128654	T	T	208	198	236	170	3.896	4.84E-02	rs1731901	17	39354682	q21.31
SNP_A-2133081	A	A	355	9	411	3	3.897	4.84E-02	rs11877551	18	34545845	q12.2
SNP_A-2206492	T	T	380	0	388	4	3.898	4.84E-02	rs1317298	6	130977071	q23.1
SNP_A-2008058	T	T	228	194	254	164	3.897	4.84E-02	rs297366	11	16286125	p15.1
SNP_A-2018563	C	C	182	152	236	146	3.897	4.84E-02	rs9636889	21	35355470	q22.12
SNP_A-1995247	G	G	310	56	372	44	3.895	4.84E-02	rs2945733	8	134684932	q24.22
SNP_A-2024496	T	T	341	21	376	40	3.897	4.84E-02	rs8002020	13	45001343	q14.13
SNP_A-2031641	A	A	337	19	360	36	3.897	4.84E-02	rs17526839	3	25580105	p24.2
SNP_A-2029975	A	A	337	31	361	53	3.895	4.84E-02	rs7042626	9	108516857	q31.3
SNP_A-2028790	A	G	183	167	224	184	3.897	4.84E-02	rs9907418	17	66676814	q24.3
SNP_A-2039945	T	T	318	48	330	74	3.897	4.84E-02	rs10904633	10	6703232	p14
SNP_A-2040090	C	C	280	130	307	105	3.897	4.84E-02	rs2110177	4	27118329	p15.2
SNP_A-2050605	T	T	273	19	317	39	3.895	4.84E-02	rs2424737	20	25706656	p11.1
SNP_A-2065942	C	C	378	0	386	4	3.897	4.84E-02	rs17125038	12	60184407	q14.1
SNP_A-2104153	C	C	322	32	335	53	3.896	4.84E-02	rs9393713	6	26481657	p22.1
SNP_A-2099383	G	G	289	23	346	14	3.897	4.84E-02	rs4865159	4	57584865	q12
SNP_A-2297544	A	A	336	34	359	57	3.896	4.84E-02	rs7036787	9	111671420	q31.3
SNP_A-2290088	C	C	242	116	295	103	3.897	4.84E-02	rs12504525	4	44416672	p13
SNP_A-2291833	A	A	324	98	293	121	3.897	4.84E-02	rs2398428	12	127760446	q24.32
SNP_A-2228743	C	C	267	153	239	181	3.897	4.84E-02	rs36453	14	71404656	q24.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2261059	C	C	355	63	330	84	3.893	4.85E-02	rs13028756	2	55580422	p16.1
SNP_A-2286652	A	A	292	126	256	148	3.894	4.85E-02	rs6670619	1	204831917	q32.2
SNP_A-2285913	G	G	348	20	401	11	3.894	4.85E-02	rs16901065	8	127132968	q24.13
SNP_A-2274138	T	T	267	103	273	143	3.892	4.85E-02	rs13215804	6	28523551	p22.1
SNP_A-2288993	C	C	295	123	263	147	3.892	4.85E-02	rs17270640	15	59005595	q22.2
SNP_A-2297543	C	C	368	2	397	9	3.892	4.85E-02	rs11222236	11	130003366	q24.3
SNP_A-2301417	A	A	379	21	384	10	3.891	4.85E-02	rs7846359	8	12900672	p22
SNP_A-2080775	G	G	331	37	353	61	3.893	4.85E-02	rs10506877	12	81548422	q21.31
SNP_A-2081299	G	A	199	155	197	189	3.893	4.85E-02	rs1320026	3	148950756	q24
SNP_A-2081307	G	G	362	48	386	32	3.893	4.85E-02	rs4836822	9	120370590	q33.2
SNP_A-2063008	G	G	260	102	270	144	3.892	4.85E-02	rs9315868	13	41305759	q14.11
SNP_A-2049499	T	T	296	46	323	31	3.894	4.85E-02	rs10152995	15	33255119	q14
SNP_A-2053069	C	C	307	53	329	83	3.894	4.85E-02	rs2768364	10	12520245	p13
SNP_A-2025306	T	T	193	175	245	167	3.891	4.85E-02	rs2060681	4	140526464	q31.1
SNP_A-2018550	T	T	289	127	307	99	3.892	4.85E-02	rs2834721	21	35298730	q22.12
SNP_A-2013609	G	G	232	138	232	184	3.893	4.85E-02	rs6998580	8	94964119	q22.1
SNP_A-2007093	A	A	361	61	378	42	3.891	4.85E-02	rs10835979	11	4352761	p15.4
SNP_A-2213034	T	T	329	9	381	3	3.894	4.85E-02	rs11024885	11	18912802	p15.1
SNP_A-2215670	G	G	213	181	238	152	3.891	4.85E-02	rs1565839	14	50153775	q22.1
SNP_A-2214004	T	T	203	163	256	154	3.893	4.85E-02	rs10948962	6	55963505	p12.1
SNP_A-2188178	C	C	274	84	285	121	3.894	4.85E-02	rs7218454	17	38359611	q21.31
SNP_A-2190145	C	C	274	72	289	107	3.892	4.85E-02	rs1381763	3	149274395	q24
SNP_A-2191598	C	C	302	48	367	37	3.892	4.85E-02	rs1374361	2	199996240	q33.1
SNP_A-2185941	A	A	182	158	237	153	3.894	4.85E-02	rs4308319	3	146141283	q24
SNP_A-2172664	G	G	193	175	245	167	3.891	4.85E-02	rs1430205	5	87714341	q14.3
SNP_A-2128365	G	G	372	20	398	10	3.893	4.85E-02	rs17035363	1	116388765	p13.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2111312	C	C	257	139	224	162	3.894	4.85E-02	rs1108722	7	150869114	q36.1
SNP_A-2122504	T	T	300	70	313	103	3.892	4.85E-02	rs1351133	5	110988332	q22.1
SNP_A-2121345	T	T	351	5	391	15	3.892	4.85E-02	rs6820845	4	185235327	q35.1
SNP_A-2145767	T	T	183	121	186	168	3.891	4.85E-02	rs4507687	7	95766077	q21.3
SNP_A-2149631	A	A	282	140	304	112	3.894	4.85E-02	rs10952788	7	148176435	q36.1
SNP_A-2167073	A	A	319	103	341	79	3.893	4.85E-02	rs4765834	12	1599896	p13.33
SNP_A-2162388	C	C	288	68	289	97	3.892	4.85E-02	rs780762	9	31793850	p21.1
SNP_A-1642859	T	T	234	166	270	144	3.893	4.85E-02	rs6709870	2	155104436	q24.1
SNP_A-1797600	G	G	258	104	257	141	3.893	4.85E-02	rs16830291	3	120867830	q13.33
SNP_A-1809950	A	A	218	188	247	161	3.893	4.85E-02	rs630147	18	10118032	p11.22
SNP_A-1819139	T	T	315	95	341	73	3.892	4.85E-02	rs6880554	5	158969870	q33.3
SNP_A-1834242	C	C	338	32	391	21	3.892	4.85E-02	rs285034	13	97588194	q32.2
SNP_A-1845701	C	C	219	195	246	166	3.893	4.85E-02	rs4283554	3	13441117	p25.1
SNP_A-1865402	G	G	325	89	334	64	3.894	4.85E-02	rs6753004	2	54874374	p16.2
SNP_A-1908661	T	T	211	139	261	127	3.892	4.85E-02	rs11581303	1	202339810	q32.1
SNP_A-1921917	C	C	323	33	376	22	3.891	4.85E-02	rs7126236	11	128762904	q24.3
SNP_A-1889319	G	G	361	43	325	59	3.894	4.85E-02	rs9633889	11	48160560	p11.2
SNP_A-1964326	A	A	195	175	246	166	3.891	4.85E-02	rs1433309	2	103517801	q12.1
SNP_A-1949907	G	G	357	9	413	3	3.892	4.85E-02	rs16967491	15	36888988	q14
SNP_A-1951200	G	G	211	91	206	124	3.892	4.85E-02	rs882613	22	16340111	q11.21
SNP_A-1937495	G	G	337	33	392	22	3.892	4.85E-02	rs16913751	9	28843125	p21.1
SNP_A-1946581	G	G	205	181	238	158	3.891	4.85E-02	rs7702091	5	33234087	p13.3
SNP_A-1944201	T	T	314	56	369	43	3.892	4.85E-02	rs17223593	18	20887311	q11.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1879815	T	T	344	74	321	97	3.889	4.86E-02	rs751206	5	167340944	q34
SNP_A-1918498	C	C	383	17	368	30	3.89	4.86E-02	rs17612287	11	19909665	p15.1
SNP_A-1865359	T	T	279	33	293	55	3.891	4.86E-02	rs1355063	1	47760710	p33
SNP_A-1864614	G	G	409	1	382	6	3.889	4.86E-02	rs16942612	17	53492600	q23.2
SNP_A-1845243	T	T	212	158	206	204	3.89	4.86E-02	rs17424551	3	191331961	q28
SNP_A-1831841	C	C	401	5	381	13	3.888	4.86E-02	rs7897189	10	10288344	p14
SNP_A-1800176	G	G	334	84	307	107	3.888	4.86E-02	rs12122341	1	115367732	p13.1
SNP_A-1789478	A	A	273	69	311	53	3.889	4.86E-02	rs3771426	2	70869158	p13.3
SNP_A-2158143	G	G	314	38	344	64	3.89	4.86E-02	rs5768095	22	46577815	q13.31
SNP_A-2142926	G	G	359	3	389	11	3.889	4.86E-02	rs11012989	10	22748913	p12.2
SNP_A-2196102	G	G	336	22	397	13	3.888	4.86E-02	rs1908379	5	32994929	p13.3
SNP_A-2196638	C	C	388	30	384	16	3.887	4.86E-02	rs2139765	8	19201018	p21.3
SNP_A-2191851	C	C	315	15	394	8	3.889	4.86E-02	rs7578537	2	160406374	q24.2
SNP_A-2214794	G	G	264	86	327	75	3.89	4.86E-02	rs2078352	11	22323285	p14.3
SNP_A-2211310	G	G	332	20	371	39	3.89	4.86E-02	rs6772563	3	161933950	q25.33
SNP_A-2005799	T	T	346	12	399	5	3.89	4.86E-02	rs885093	18	69105721	q22.3
SNP_A-1996717	T	T	318	102	284	124	3.889	4.86E-02	rs1331977	9	69330123	q21.11
SNP_A-2036429	T	T	286	76	293	109	3.888	4.86E-02	rs7320909	13	79575903	q31.1
SNP_A-2064329	T	T	278	60	282	88	3.887	4.86E-02	rs7953275	12	57850194	q14.1
SNP_A-2306601	G	G	360	10	393	23	3.889	4.86E-02	rs9319649	18	72395179	q23
SNP_A-2273765	A	A	300	50	349	37	3.891	4.86E-02	rs11717234	3	66825847	p14.1
SNP_A-2276202	A	A	241	169	214	198	3.889	4.86E-02	rs253645	5	9153056	p15.31
SNP_A-2266599	T	T	288	110	265	137	3.888	4.86E-02	rs11075350	16	17438026	p12.3
SNP_A-2252347	C	C	345	15	391	7	3.889	4.86E-02	rs2467365	15	34540436	q14
SNP_A-2254040	A	A	354	68	372	48	3.89	4.86E-02	rs2122562	3	55136692	p14.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2244971	A	A	274	96	280	134	3.886	0.0487	rs782108	12	57119545	q14.1
SNP_A-2266180	G	G	387	17	372	30	3.887	0.0487	rs9395027	6	44552709	p21.1
SNP_A-2283197	G	G	296	68	353	55	3.885	0.0487	rs7808069	7	57035306	p11.1
SNP_A-2310069	T	T	338	26	319	41	3.886	0.0487	rs1372540	12	39611738	q12
SNP_A-2301356	G	G	304	64	320	96	3.886	0.0487	rs5750354	22	35711619	q12.3
SNP_A-2050207	C	C	281	85	292	122	3.886	0.0487	rs17534808	9	71209577	q21.13
SNP_A-2048632	A	A	273	95	275	131	3.886	0.0487	rs9563639	13	58187996	q21.1
SNP_A-2060480	A	A	269	91	310	74	3.885	0.0487	rs601487	3	34844620	p23
SNP_A-2090099	T	T	268	96	328	84	3.886	0.0487	rs2126747	10	67460870	q21.3
SNP_A-2106353	C	C	284	124	238	140	3.884	0.0487	rs9905797	17	2456111	p13.3
SNP_A-2105914	C	C	205	129	256	118	3.884	0.0487	rs2425628	20	42223466	q13.12
SNP_A-2098510	T	T	211	183	209	135	3.885	0.0487	rs7314022	12	111639221	q24.13
SNP_A-2037077	A	A	242	128	295	115	3.885	0.0487	rs7301316	12	18573866	p12.3
SNP_A-2044675	A	G	195	155	198	186	3.884	0.0487	rs941845	14	91123823	q32.12
SNP_A-2025447	C	C	296	52	310	80	3.885	0.0487	rs11720123	3	57670053	p14.3
SNP_A-2025866	T	T	238	150	212	178	3.887	0.0487	rs17261494	8	13843663	p22
SNP_A-2026918	G	G	296	68	353	55	3.885	0.0487	rs955806	4	127168031	q28.1
SNP_A-2005436	T	T	335	15	356	30	3.887	0.0487	rs5018094	10	114281287	q25.2
SNP_A-2010948	T	C	223	181	209	195	3.886	0.0487	rs468658	5	70889599	q13.2
SNP_A-2184294	T	T	289	51	345	39	3.887	0.0487	rs9562844	13	48282279	q14.2
SNP_A-2179964	-	A	185	185	235	177	3.885	0.0487	rs2150192	9	4477024	p24.2
SNP_A-2140527	C	C	353	39	381	25	3.886	0.0487	rs10972540	9	35631859	p13.3
SNP_A-2162244	C	C	241	125	243	169	3.887	0.0487	rs7999090	13	41080493	q14.11
SNP_A-2107911	C	C	234	122	229	161	3.887	0.0487	rs6008379	22	46477631	q13.31
SNP_A-2109280	C	C	347	23	374	42	3.886	0.0487	rs10493369	1	64933677	p31.3
SNP_A-1812956	A	A	173	171	220	162	3.886	0.0487	rs992157	2	218980286	q35

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783359	T	T	214	126	286	124	3.885	0.0487	rs6548715	3	80679798	p12.2
SNP_A-1830517	A	A	307	15	384	8	3.885	0.0487	rs11192968	10	108330433	q25.1
SNP_A-1839476	A	A	229	141	284	130	3.886	0.0487	rs10857934	1	112421327	p13.2
SNP_A-1817551	G	G	331	21	355	39	3.887	0.0487	---	11	32432060	p13
SNP_A-1846586	G	G	388	6	415	1	3.885	0.0487	rs16937430	8	72215363	q13.3
SNP_A-1854888	T	T	335	17	397	9	3.886	0.0487	rs16661295	2	173860596	q31.1
SNP_A-1904701	A	A	201	147	244	132	3.884	0.0487	rs6976643	7	77486180	q21.11
SNP_A-1929521	C	C	248	112	313	103	3.887	0.0487	rs1357396	2	176217776	q31.1
SNP_A-1875085	A	A	334	74	363	55	3.885	0.0487	rs2548644	5	53879284	q11.2
SNP_A-1883932	C	C	230	186	258	158	3.886	0.0487	rs258804	5	142514411	q31.3
SNP_A-1896214	C	C	270	54	338	44	3.887	0.0487	rs7329263	13	19690082	q12.11
SNP_A-1947662	C	C	220	150	215	195	3.886	0.0487	rs10778274	12	77774631	q21.2
SNP_A-1938810	A	A	302	58	321	89	3.887	0.0487	rs1611819	6	6979674	p25.1
SNP_A-1963692	G	G	222	136	239	107	3.884	0.0487	rs2312082	2	69023096	p13.3
SNP_A-1969303	T	T	304	90	287	117	3.886	0.0487	rs2226651	21	20272450	q21.1
SNP_A-1972525	A	A	359	63	334	84	3.883	4.88E-02	rs1320158	3	43260400	p22.1
SNP_A-1979790	T	T	339	29	384	18	3.882	4.88E-02	rs384197	4	167559949	q32.3
SNP_A-1987409	T	T	241	133	287	117	3.881	4.88E-02	rs9320695	6	119926543	q22.31
SNP_A-1961075	T	T	343	5	354	14	3.881	4.88E-02	rs11073089	15	33370324	q14
SNP_A-1893630	A	A	256	162	229	191	3.881	4.88E-02	rs4366914	2	120851885	q14.2
SNP_A-1928178	G	G	355	3	385	11	3.882	4.88E-02	rs9502823	6	1050674	p25.3
SNP_A-1868461	C	C	195	173	246	164	3.882	4.88E-02	rs10850239	12	112829316	q24.21
SNP_A-1871879	C	C	253	147	228	176	3.883	4.88E-02	rs9888360	12	123170704	q24.31
SNP_A-1820456	A	A	298	46	352	34	3.883	4.88E-02	rs18442258	12	28978712	p11.22
SNP_A-1823616	C	C	385	11	391	23	3.884	4.88E-02	rs11988485	8	97556177	q22.1
SNP_A-1840470	T	T	319	47	377	35	3.883	4.88E-02	rs16889509	4	9524595	p16.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1843403	G	G	259	153	279	123	3.882	4.88E-02	rs2255785	8	14670571	p22
SNP_A-1834521	G	G	283	83	293	119	3.883	4.88E-02	rs4083342	3	54742125	p14.3
SNP_A-1836281	T	T	289	55	354	44	3.884	4.88E-02	rs17207764	10	66817483	q21.3
SNP_A-1753349	T	T	279	123	259	153	3.882	4.88E-02	rs1246253	1	84419099	p22.3
SNP_A-1745754	C	C	385	11	391	23	3.884	4.88E-02	rs10520726	15	91650760	q26.1
SNP_A-1737331	A	A	394	0	404	4	3.882	4.88E-02	rs1323198	6	5831341	p25.1
SNP_A-1723934	C	C	390	12	388	24	3.883	4.88E-02	rs6030208	20	41711294	q12
SNP_A-1672826	A	A	216	134	224	186	3.883	4.88E-02	rs2405755	3	163438380	q26.1
SNP_A-1694639	C	C	384	14	385	27	3.882	4.88E-02	rs10501709	11	89539842	q14.3
SNP_A-1698269	G	G	398	0	408	4	3.883	4.88E-02	rs1959694	14	36555812	q21.1
SNP_A-1698377	C	C	284	116	319	95	3.882	4.88E-02	rs2041813	2	58829108	p16.1
SNP_A-1693405	A	A	398	0	408	4	3.883	4.88E-02	rs10500409	16	58775484	q21
SNP_A-1692106	C	C	398	0	408	4	3.883	4.88E-02	rs699532	1	90410862	p22.2
SNP_A-1687784	C	C	322	78	353	59	3.882	4.88E-02	rs2271383	2	160945406	q24.2
SNP_A-1688088	A	G	189	161	218	192	3.884	4.88E-02	rs10497746	2	196094935	q32.3
SNP_A-1814404	G	G	273	93	330	80	3.883	4.88E-02	rs10930397	2	170758531	q31.1
SNP_A-1791967	A	A	192	146	232	130	3.883	4.88E-02	rs250739	5	76081587	q13.3
SNP_A-1785352	G	G	373	33	383	19	3.882	4.88E-02	rs17039471	3	1469264	p26.3
SNP_A-2131198	G	G	362	2	391	9	3.884	4.88E-02	rs618481	18	2962981	p11.31
SNP_A-2156970	C	C	268	96	278	136	3.882	4.88E-02	rs10760063	9	119609017	q33.2
SNP_A-2144752	G	G	346	24	369	43	3.883	4.88E-02	rs12468338	2	33636580	p22.3
SNP_A-2145108	G	G	365	27	385	15	3.881	4.88E-02	rs13326400	3	40026460	p22.1
SNP_A-2198705	T	T	339	29	384	18	3.882	4.88E-02	rs17075073	8	5752660	p23.2
SNP_A-2220483	T	T	231	101	239	143	3.883	4.88E-02	rs12436338	14	56200540	q22.3
SNP_A-2000152	A	A	357	61	329	81	3.883	4.88E-02	rs2377717	1	31342356	p35.2
SNP_A-2046886	T	T	417	1	390	6	3.883	4.88E-02	rs10148992	14	78544014	q31.1
SNP_A-2038814	C	C	389	13	409	5	3.881	4.88E-02	rs16858481	1	229430948	q42.2
SNP_A-2098353	C	C	380	16	384	30	3.884	4.88E-02	rs16918258	8	53931810	q11.23

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2097920	G	G	260	138	283	111	3.882	4.88E-02	rs4551175	6	151363709	q25.1
SNP_A-2090456	T	T	272	98	279	137	3.882	4.88E-02	rs11159988	14	90600927	q32.12
SNP_A-2057062	A	A	299	121	324	96	3.883	4.88E-02	rs2870389	20	53142080	q13.2
SNP_A-2067479	G	G	308	82	316	58	3.883	4.88E-02	rs2165300	14	47994398	q21.3
SNP_A-2073640	A	A	417	1	390	6	3.883	4.88E-02	rs7084655	10	128505965	q26.2
SNP_A-2270858	A	A	364	56	382	38	3.881	4.88E-02	rs17149611	8	8202414	p23.1
SNP_A-2270764	C	C	320	38	345	63	3.881	4.88E-02	rs6817424	4	81355942	q21.21
SNP_A-2265602	C	C	304	66	318	98	3.88	4.89E-02	rs17787479	8	140579876	q24.3
SNP_A-2263777	A	G	194	174	226	190	3.877	4.89E-02	rs6430975	2	128534787	q14.3
SNP_A-2260625	G	G	321	71	329	49	3.879	4.89E-02	rs7109698	11	46629920	p11.2
SNP_A-2284152	G	G	307	63	364	50	3.88	4.89E-02	rs2414426	15	53793024	q21.3
SNP_A-2244140	A	A	387	33	397	19	3.878	4.89E-02	rs7171753	15	99879302	q26.3
SNP_A-2241229	T	T	330	38	350	62	3.879	4.89E-02	rs1513331	3	112883336	q13.2
SNP_A-2299126	G	G	379	41	357	59	3.879	4.89E-02	rs6593142	7	50572900	p12.2
SNP_A-2298392	A	A	283	135	306	108	3.879	4.89E-02	rs1652333	1	203858855	q32.2
SNP_A-2297031	G	G	336	12	387	5	3.877	4.89E-02	rs10977086	9	8416294	p24.1
SNP_A-2296051	A	A	380	22	393	11	3.88	4.89E-02	rs17045296	2	53964892	p16.2
SNP_A-2308148	C	C	233	135	291	125	3.88	4.89E-02	rs4234669	3	118851827	q13.31
SNP_A-2065607	C	C	321	41	340	66	3.879	4.89E-02	rs4351724	10	19556270	p12.31
SNP_A-2051496	G	G	299	117	274	144	3.879	4.89E-02	rs9304229	18	36501870	q12.3
SNP_A-2092488	G	G	384	34	398	20	3.88	4.89E-02	rs1698187	11	115101156	q23.3
SNP_A-1997573	A	A	272	96	329	83	3.88	4.89E-02	rs10512363	9	108002383	q31.2
SNP_A-1991244	T	T	265	81	275	117	3.878	4.89E-02	rs667745	1	240818952	q44
SNP_A-1993071	C	C	198	136	192	178	3.879	4.89E-02	rs481015	8	37194633	p12
SNP_A-2220476	C	C	304	66	318	98	3.88	4.89E-02	rs10865678	3	73814827	p13
SNP_A-2143788	T	T	270	142	292	114	3.88	4.89E-02	rs17461947	4	44419445	p13

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140381	T	T	343	17	317	29	3.879	4.89E-02	rs16891313	5	62274329	q12.1
SNP_A-2151654	A	A	266	108	258	142	3.877	4.89E-02	rs1245651	12	60887224	q14.1
SNP_A-2154546	C	C	331	27	387	17	3.878	4.89E-02	rs17099560	14	61679966	q23.2
SNP_A-2164498	C	C	215	139	199	173	3.88	4.89E-02	rs9948721	18	35171907	q12.2
SNP_A-2132359	C	C	297	63	310	94	3.878	4.89E-02	rs1502869	1	235112483	q43
SNP_A-2134220	A	A	280	88	289	125	3.877	4.89E-02	rs12644077	4	92769755	q22.1
SNP_A-2124095	C	C	325	39	375	27	3.878	4.89E-02	rs17441578	2	8374651	p25.1
SNP_A-1812277	C	C	229	139	284	128	3.88	4.89E-02	rs6752010	2	62770693	p15
SNP_A-1800580	A	A	349	9	403	3	3.877	4.89E-02	rs16912118	9	122535103	q33.2
SNP_A-1824316	C	C	192	158	243	149	3.878	4.89E-02	rs6548732	3	81079810	p12.2
SNP_A-1820326	C	C	318	96	336	72	3.88	4.89E-02	rs1033693	14	28194772	q12
SNP_A-1864439	C	C	386	22	399	11	3.877	4.89E-02	rs17317784	2	134510714	q21.2
SNP_A-1863678	A	A	400	20	386	34	3.879	4.89E-02	rs6481738	10	31468661	p11.22
SNP_A-1846005	C	C	308	62	323	93	3.878	4.89E-02	rs1442493	4	100678543	q23
SNP_A-1852141	T	T	229	139	284	128	3.88	4.89E-02	rs7945959	11	95501299	q21
SNP_A-1909001	C	C	245	163	276	138	3.877	4.89E-02	rs10733487	9	37481030	p13.2
SNP_A-1918588	A	A	286	28	286	46	3.88	4.89E-02	rs1001978	6	166556089	q27
SNP_A-1914141	T	T	369	1	409	7	3.878	4.89E-02	rs16904322	8	131705146	q24.22
SNP_A-1897786	A	A	304	66	318	98	3.88	4.89E-02	rs17005996	4	83927479	q21.22
SNP_A-1944396	A	A	304	66	318	98	3.88	4.89E-02	rs7569982	2	4362933	p25.2
SNP_A-1945527	A	A	212	148	190	178	3.877	4.89E-02	rs7688569	4	162921988	q32.2
SNP_A-1988622	A	A	346	62	318	82	3.88	4.89E-02	rs4649307	1	229819852	q42.2
SNP_A-1987766	C	C	238	126	229	163	3.879	4.89E-02	rs210949	6	135573332	q23.3
SNP_A-1970330	A	A	258	110	264	152	3.878	4.89E-02	rs2836503	21	38839154	q22.2
SNP_A-1967289	A	A	311	53	325	81	3.88	4.89E-02	rs11678266	2	230317051	q36.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1978675	T	T	336	16	390	8	3.876	4.90E-02	rs10033458	4	120400666	q26
SNP_A-1937278	G	G	207	163	259	153	3.874	4.90E-02	rs6006470	22	42712897	q13.31
SNP_A-1938275	G	G	237	171	209	199	3.877	4.90E-02	rs2206426	20	40719457	q12
SNP_A-1949364	A	A	268	108	287	83	3.875	4.90E-02	rs12440038	15	43494031	q21.1
SNP_A-1888218	C	C	350	16	406	8	3.876	4.90E-02	rs2422676	20	1940883	p13
SNP_A-1847686	C	G	206	158	206	202	3.874	4.90E-02	rs9655942	7	85657232	q21.11
SNP_A-1852537	T	T	283	115	265	145	3.875	4.90E-02	---	1	18174743	p36.13
SNP_A-1859178	A	T	203	167	216	198	3.874	4.90E-02	rs2815743	6	73148099	q13
SNP_A-1796011	G	G	356	10	389	23	3.877	4.90E-02	rs13397687	2	123371575	q14.3
SNP_A-1660133	A	G	217	185	217	193	3.874	4.90E-02	rs2031321	9	94371141	q22.32
SNP_A-1642787	T	T	351	51	379	35	3.875	4.90E-02	rs735866	17	64789847	q24.2
SNP_A-1751015	A	A	243	159	222	192	3.875	4.90E-02	rs9312021	3	8501809	p25.3
SNP_A-1782765	C	C	366	50	341	69	3.874	4.90E-02	rs16904682	8	133492836	q24.22
SNP_A-2110813	C	C	351	1	389	7	3.877	4.90E-02	rs1425526	4	143875941	q31.21
SNP_A-2122907	G	G	324	82	342	60	3.875	4.90E-02	rs7986395	13	28315053	q12.3
SNP_A-2167911	G	G	381	37	390	22	3.875	4.90E-02	rs17370182	9	81690872	q21.32
SNP_A-2163399	C	-	211	159	207	207	3.876	4.90E-02	rs1414116	13	79216636	q31.1
SNP_A-2156270	A	A	253	111	260	154	3.876	4.90E-02	rs17187323	15	71847131	q24.1
SNP_A-2159818	A	A	331	15	365	31	3.874	4.90E-02	rs7684087	4	21349650	p15.31
SNP_A-1997063	C	C	194	176	246	168	3.874	4.90E-02	rs1332891	9	84462815	q21.33
SNP_A-2034640	C	C	267	103	265	139	3.877	4.90E-02	rs11088595	21	17085329	q21.1
SNP_A-2028989	T	T	336	26	360	46	3.875	4.90E-02	rs976146	13	84735203	q31.1
SNP_A-2024626	C	C	356	2	385	9	3.875	4.90E-02	rs3815514	2	202080379	q33.1
SNP_A-2089998	C	C	231	129	224	168	3.874	4.90E-02	rs8011611	14	82605555	q31.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086536	C	C	229	137	284	126	3.874	4.90E-02	rs2138113	3	80673126	p12.2
SNP_A-2086046	G	G	283	83	345	71	3.875	4.90E-02	rs17649050	1	168445465	q24.3
SNP_A-2300344	T	T	225	197	251	167	3.874	4.90E-02	rs11071149	15	52958814	q21.3
SNP_A-2290811	G	G	344	60	359	41	3.875	4.90E-02	rs10817514	9	113574185	q32
SNP_A-2291566	G	G	364	16	383	7	3.876	4.90E-02	rs17385566	9	37153530	p13.2
SNP_A-2237638	T	T	204	136	264	130	3.876	4.90E-02	rs7586583	2	31128992	p23.1
SNP_A-2233202	C	C	367	1	407	7	3.875	4.90E-02	rs7941715	11	42424223	p12
SNP_A-2257955	C	T	218	202	222	182	3.874	4.90E-02	rs11016518	10	130546228	q26.3
SNP_A-2239911	C	T	194	164	217	193	3.872	4.91E-02	rs12441090	15	20457011	q11.2
SNP_A-2245428	G	G	357	49	372	32	3.872	4.91E-02	rs11866379	16	69399598	q22.1
SNP_A-2092418	A	A	250	120	253	163	3.873	4.91E-02	rs4952361	2	41548278	p22.1
SNP_A-2066787	T	T	354	10	387	23	3.871	4.91E-02	rs6718202	2	6842310	p25.2
SNP_A-2076794	A	A	220	144	277	135	3.873	4.91E-02	rs10898329	11	84304683	q14.1
SNP_A-2028580	C	C	250	120	253	163	3.873	4.91E-02	rs1396134	2	41529822	p22.1
SNP_A-2001623	G	G	364	56	373	37	3.872	4.91E-02	rs7925122	11	653463	p15.5
SNP_A-2003098	C	C	235	131	289	119	3.873	4.91E-02	rs2712542	12	126255667	q24.32
SNP_A-1990655	A	A	228	118	276	104	3.871	4.91E-02	rs1634045	7	95208504	q21.3
SNP_A-2012973	T	T	371	47	343	65	3.87	4.91E-02	rs644086	11	85883474	q14.2
SNP_A-2164512	A	A	359	5	401	15	3.872	4.91E-02	rs11173421	12	59033590	q14.1
SNP_A-2148968	A	A	307	57	328	88	3.873	4.91E-02	rs307311	5	84729376	q14.3
SNP_A-2138180	A	A	394	18	400	8	3.872	4.91E-02	rs16968981	18	33331212	q12.2
SNP_A-2116827	A	A	359	5	401	15	3.872	4.91E-02	rs17611274	2	221030240	q35
SNP_A-2219105	C	C	307	109	331	85	3.872	4.91E-02	rs2699971	3	110456382	q13.13
SNP_A-2217009	T	T	392	30	372	46	3.873	4.91E-02	rs2578043	10	65417797	q21.3
SNP_A-2210358	G	G	221	199	247	169	3.871	4.91E-02	rs6601662	8	11933744	p23.1
SNP_A-2209727	G	G	402	18	408	8	3.872	4.91E-02	rs2785061	17	29331645	q12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2197509	A	G	199	167	212	190	3.872	4.91E-02	rs1953057	1	149537889	q21.3
SNP_A-2196150	A	A	302	68	314	100	3.872	4.91E-02	rs343549	4	58455437	q12
SNP_A-1675109	T	T	287	61	359	51	3.872	4.91E-02	rs1976106	6	76920612	q14.1
SNP_A-1792041	C	C	298	68	313	101	3.873	4.91E-02	rs335789	15	58122959	q22.2
SNP_A-1873764	T	T	340	26	394	16	3.871	4.91E-02	rs10877178	12	57547968	q14.1
SNP_A-1831870	C	C	307	45	333	73	3.873	4.91E-02	rs12148542	15	93427212	q26.2
SNP_A-1874371	G	G	305	23	364	14	3.871	4.91E-02	rs2342772	6	150311303	q25.1
SNP_A-1890718	C	C	240	120	300	110	3.871	4.91E-02	rs10983334	9	116583296	q33.1
SNP_A-1915425	G	G	305	45	359	33	3.873	4.91E-02	rs1470266	15	69211686	q23
SNP_A-1915199	C	C	308	58	370	46	3.873	4.91E-02	rs1816847	5	119435264	q23.1
SNP_A-1960128	T	T	313	57	368	44	3.871	4.91E-02	rs208991	6	62923609	q11.1
SNP_A-1982240	A	A	263	107	267	147	3.872	4.91E-02	rs7709472	5	78350907	q14.1
SNP_A-1971655	A	A	281	141	303	113	3.873	4.91E-02	rs607390	3	8158799	p26.1
SNP_A-1982451	C	C	303	63	313	93	3.869	4.92E-02	rs12188167	5	87702061	q14.3
SNP_A-1989314	A	A	284	76	294	110	3.867	4.92E-02	rs10267854	7	27630343	p15.2
SNP_A-1950219	A	A	323	23	348	42	3.869	4.92E-02	rs7553966	1	212606180	q41
SNP_A-1936092	G	G	278	78	320	62	3.867	4.92E-02	rs12505693	4	65603642	q13.1
SNP_A-1926186	T	G	179	167	223	179	3.87	4.92E-02	rs4419450	4	73997988	q13.3
SNP_A-1929925	A	A	340	22	371	41	3.868	4.92E-02	rs4296830	5	91588733	q14.3
SNP_A-1875991	G	G	294	120	253	139	3.869	4.92E-02	rs2798121	1	48758917	p33
SNP_A-1889538	T	T	310	42	337	69	3.867	4.92E-02	rs17729993	18	17977937	q11.2
SNP_A-1884909	G	G	341	79	316	102	3.869	4.92E-02	rs1494057	2	3541180	p25.3
SNP_A-1843470	G	G	286	76	299	111	3.87	4.92E-02	rs4731992	7	133159352	q33
SNP_A-1842957	G	G	298	110	322	86	3.868	4.92E-02	rs7584056	2	224697888	q36.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1821305	A	A	352	16	408	8	3.869	4.92E-02	rs3917458	1	166428775	q24.2
SNP_A-1828466	C	C	335	27	364	48	3.869	4.92E-02	rs2207979	6	85629181	q14.3
SNP_A-1867894	G	G	359	49	374	32	3.87	4.92E-02	rs16892613	4	15608486	p15.32
SNP_A-1846712	C	C	324	46	340	72	3.87	4.92E-02	rs1948869	14	85817370	q31.3
SNP_A-1848537	T	T	191	161	249	157	3.868	4.92E-02	rs2965044	7	4747744	p22.1
SNP_A-1795877	A	A	326	44	382	32	3.867	4.92E-02	rs1947253	12	96823397	q23.1
SNP_A-1802642	C	C	298	68	355	55	3.867	4.92E-02	rs826733	8	59915262	q12.1
SNP_A-1660499	C	C	292	108	276	138	3.87	4.92E-02	rs726083	3	66944109	p14.1
SNP_A-1648334	C	C	375	27	395	15	3.87	4.92E-02	rs1931233	10	111236098	q25.1
SNP_A-1681868	C	C	266	106	300	86	3.868	4.92E-02	rs1446553	2	149412544	q23.1
SNP_A-2183082	G	G	301	109	278	136	3.87	4.92E-02	rs423932	13	31558137	q13.1
SNP_A-2174253	T	T	352	20	376	10	3.867	4.92E-02	rs9482188	6	122063581	q22.31
SNP_A-2209981	T	T	223	121	261	103	3.868	4.92E-02	rs11005044	10	57256208	q21.1
SNP_A-2200001	T	T	294	70	310	104	3.87	4.92E-02	rs12567502	1	8743086	p36.23
SNP_A-2118099	C	C	399	3	390	10	3.867	4.92E-02	rs9897106	17	9014028	p13.1
SNP_A-2123149	A	A	316	48	374	36	3.869	4.92E-02	rs791654	9	12480247	p23
SNP_A-2114579	A	A	351	19	376	36	3.87	4.92E-02	rs316689	1	84444665	p31.1
SNP_A-2138786	C	C	278	86	335	73	3.868	4.92E-02	rs41654	7	87699208	q21.12
SNP_A-2016317	A	A	322	88	344	66	3.87	4.92E-02	rs967429	21	21968086	q21.1
SNP_A-2016990	T	T	308	14	377	7	3.869	4.92E-02	rs7280059	21	26192901	q21.3
SNP_A-2003547	C	C	367	3	399	11	3.867	4.92E-02	rs4553462	13	103610007	q33.1
SNP_A-2001010	C	C	301	61	323	43	3.869	4.92E-02	rs7095247	10	18311751	p12.33
SNP_A-2075665	A	A	366	36	386	22	3.867	4.92E-02	rs11986487	8	1162965	p23.3
SNP_A-2066785	C	C	300	122	272	148	3.87	4.92E-02	rs139426	22	37885166	q13.1
SNP_A-2062936	C	C	298	42	348	30	3.87	4.92E-02	rs1016438	19	62282850	q13.43

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2063648	G	G	285	129	253	153	3.868	4.92E-02	rs1465157	14	41027451	q21.1
SNP_A-2049161	T	T	328	38	389	27	3.87	4.92E-02	rs1522314	12	80304722	q21.31
SNP_A-2093063	C	C	274	76	329	63	3.867	4.92E-02	rs11781433	8	123813918	q24.13
SNP_A-2250285	T	T	276	120	314	100	3.868	4.92E-02	rs4961193	8	87555284	q21.3
SNP_A-2268703	G	G	258	106	313	93	3.868	4.92E-02	rs13146986	4	80869407	q21.21
SNP_A-2272608	C	C	301	55	368	44	3.869	4.92E-02	rs7859012	9	86828477	q21.33
SNP_A-2281945	G	C	218	186	216	192	3.868	4.92E-02	rs7013981	8	16470404	p22
SNP_A-2274334	C	C	330	34	353	57	3.868	4.92E-02	rs10984022	9	118263223	q33.1
SNP_A-2298737	C	C	336	6	356	16	3.87	4.92E-02	rs6680110	1	240351059	q44
SNP_A-2295344	C	C	307	115	278	140	3.87	4.92E-02	rs9888117	10	99149953	q24.1
SNP_A-2291593	A	A	357	53	345	75	3.866	4.93E-02	rs936531	16	83033272	q24.1
SNP_A-2294162	C	C	338	32	360	54	3.864	4.93E-02	rs6906192	6	87587091	q15
SNP_A-2304420	T	T	213	179	239	151	3.866	4.93E-02	rs495529	1	162608363	q24.1
SNP_A-2273689	A	A	336	12	334	24	3.865	4.93E-02	rs4522548	2	192074514	q32.3
SNP_A-2282328	T	T	402	18	383	31	3.866	4.93E-02	rs1945413	11	21418450	p15.1
SNP_A-2262458	G	G	244	118	297	105	3.866	4.93E-02	rs522030	11	97422223	q22.1
SNP_A-2254977	A	A	266	88	329	77	3.864	4.93E-02	rs10460949	3	75318196	p12.3
SNP_A-2227990	G	G	323	93	339	69	3.865	4.93E-02	rs11189420	10	99642857	q24.2
SNP_A-2093773	C	C	265	121	239	147	3.864	4.93E-02	rs1966384	10	116617900	q25.3
SNP_A-2094789	A	A	287	57	306	88	3.867	4.93E-02	rs7574844	2	191254982	q32.2
SNP_A-2096516	T	T	288	80	287	111	3.864	4.93E-02	rs537202	18	216485	p11.32
SNP_A-2100120	T	T	239	127	296	116	3.865	4.93E-02	rs7171864	15	71014302	q24.1
SNP_A-2087406	G	G	291	65	346	52	3.866	4.93E-02	---	4	169212872	q32.3
SNP_A-2078266	T	T	247	169	208	188	3.864	4.93E-02	rs1944146	11	130195372	q24.3
SNP_A-2078715	G	G	326	30	345	51	3.866	4.93E-02	rs1698920	18	73496164	q23
SNP_A-2059424	A	A	312	54	365	41	3.866	4.93E-02	rs17741019	7	3230537	p22.2
SNP_A-2013083	T	C	207	159	209	205	3.864	4.93E-02	rs4129418	8	1214243	p23.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2046485	G	G	192	174	245	167	3.865	4.93E-02	rs2216308	2	51138663	p16.3
SNP_A-2041085	A	A	323	41	364	28	3.864	4.93E-02	rs10465658	1	217995086	q41
SNP_A-2113958	A	A	310	58	365	45	3.866	4.93E-02	rs176620	6	62997238	q11.1
SNP_A-2221202	C	C	413	3	404	10	3.864	4.93E-02	rs6758339	2	36461525	p22.3
SNP_A-2184730	C	C	268	90	275	127	3.865	4.93E-02	rs2476761	13	105311957	q33.2
SNP_A-2196257	C	C	395	21	366	34	3.866	4.93E-02	rs11021509	11	95639632	q21
SNP_A-1700694	T	T	294	50	366	40	3.867	4.93E-02	rs2490955	13	112103654	q34
SNP_A-1657117	A	A	314	72	310	100	3.864	4.93E-02	rs237315	17	12562626	p12
SNP_A-1750413	G	G	262	82	286	124	3.867	4.93E-02	rs977463	4	85837991	q21.23
SNP_A-1717879	T	T	369	15	379	29	3.865	4.93E-02	rs10486144	7	11304489	p21.3
SNP_A-1801982	T	T	276	90	333	77	3.865	4.93E-02	rs9486226	6	106499580	q21
SNP_A-1851527	A	A	325	37	347	61	3.864	4.93E-02	rs3772501	3	59953743	p14.2
SNP_A-1853905	T	T	376	44	357	63	3.866	4.93E-02	—	14	65476893	q23.3
SNP_A-1864444	T	T	383	31	370	48	3.864	4.93E-02	rs4350702	2	30048381	p23.1
SNP_A-1885759	C	C	402	10	411	3	3.864	4.93E-02	rs1838545	15	66527933	q23
SNP_A-1895321	A	A	350	2	379	9	3.866	4.93E-02	rs16948186	18	26330076	q12.1
SNP_A-1911641	A	A	276	90	333	77	3.865	4.93E-02	rs4262342	8	2068179	p23.3
SNP_A-1938050	T	T	274	140	243	165	3.864	4.93E-02	rs2463829	11	61845414	q12.3
SNP_A-1943253	G	G	274	94	331	81	3.866	4.93E-02	rs3019945	8	108060338	q23.1
SNP_A-1959070	A	A	322	46	343	73	3.865	4.93E-02	rs10959367	9	10907884	p23
SNP_A-1960776	C	C	205	147	198	190	3.866	4.93E-02	rs5750936	22	21025208	q11.22
SNP_A-1977298	C	C	325	7	398	2	3.865	4.93E-02	rs349182	4	60639350	q13.1
SNP_A-1969407	A	A	322	46	343	73	3.865	4.93E-02	rs2827240	21	22394009	q21.1
SNP_A-1973056	C	C	371	49	386	32	3.86	4.94E-02	rs10510950	3	65947474	p14.1
SNP_A-1948641	C	C	301	111	322	86	3.861	4.94E-02	rs852079	20	17084774	p12.1
SNP_A-1952941	A	A	345	57	316	76	3.861	4.94E-02	rs11022212	11	12127060	p15.3
SNP_A-1930469	T	T	384	6	409	1	3.862	4.94E-02	rs1454100	15	58572251	q22.2
SNP_A-1902495	C	C	339	25	389	15	3.861	4.94E-02	rs12776803	10	121555155	q26.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1881551	G	G	419	3	410	10	3.862	4.94E-02	rs3909402	5	167363846	q34
SNP_A-1863558	T	T	342	20	393	11	3.86	4.94E-02	rs6800625	3	191717029	q28
SNP_A-1857155	T	T	193	131	208	190	3.861	4.94E-02	rs7864535	9	72314064	q21.13
SNP_A-1788686	A	A	355	9	409	3	3.862	4.94E-02	rs11636015	15	44488509	q21.1
SNP_A-1696882	C	C	338	62	323	85	3.86	4.94E-02	rs462555	21	40090487	q22.2
SNP_A-1677404	T	A	217	185	219	195	3.861	4.94E-02	rs2058427	12	9638824	p13.31
SNP_A-2194679	C	C	269	77	337	67	3.863	4.94E-02	rs16922441	8	57013886	q12.1
SNP_A-2194361	G	G	322	28	308	44	3.861	4.94E-02	rs2232316	2	169583069	q24.3
SNP_A-2212287	T	T	229	179	259	153	3.861	4.94E-02	rs12027081	1	161846179	q23.3
SNP_A-2113234	T	T	419	3	410	10	3.862	4.94E-02	rs3909403	5	167363464	q34
SNP_A-2120392	G	G	340	24	363	43	3.861	4.94E-02	rs9692955	8	123720820	q24.13
SNP_A-2128374	G	G	302	60	319	91	3.86	4.94E-02	rs17327964	5	112757015	q22.2
SNP_A-2142979	G	G	266	86	261	117	3.86	4.94E-02	rs11176506	12	65650035	q14.3
SNP_A-2150506	A	A	356	12	409	5	3.862	4.94E-02	rs16972412	13	107871275	q33.3
SNP_A-2161817	C	C	248	114	307	103	3.86	4.94E-02	rs4142284	7	107534124	q31.1
SNP_A-2023419	C	C	411	1	386	6	3.86	4.94E-02	rs17137775	11	128133816	q24.3
SNP_A-2002871	C	C	258	112	316	100	3.861	4.94E-02	rs2812431	10	79219248	q22.3
SNP_A-1992566	G	A	223	183	215	199	3.86	4.94E-02	rs6586807	8	18983420	p22
SNP_A-2052262	C	G	169	161	208	162	3.861	4.94E-02	rs2055856	8	14598884	p22
SNP_A-2078496	G	G	419	3	410	10	3.862	4.94E-02	rs11846702	14	97064817	q32.2
SNP_A-2079660	C	C	333	31	350	52	3.861	4.94E-02	rs1215447	13	79617970	q31.1
SNP_A-2089681	C	C	317	39	354	26	3.862	4.94E-02	rs17036216	4	158774105	q32.1
SNP_A-2229068	-	C	183	183	235	177	3.863	4.94E-02	rs8013942	14	74781256	q24.3
SNP_A-2235499	C	C	256	110	262	152	3.863	4.94E-02	rs7655649	4	181466211	q34.3
SNP_A-2245086	A	A	308	58	324	88	3.863	4.94E-02	rs981126	1	80243815	p31.1

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2305228	A	A	245	87	293	73	3.861	4.94E-02	rs4471416	11	21550729	p15.1
SNP_A-2312022	C	C	417	3	408	10	3.863	4.94E-02	---	3	9719892	p25.3
SNP_A-2312116	-	G	168	168	229	171	3.863	4.94E-02	rs10935930	3	154587826	q25.2
SNP_A-2297823	G	G	342	80	353	57	3.863	4.94E-02	rs4434872	1	150587349	q21.3
SNP_A-2300117	A	A	226	124	260	104	3.86	4.95E-02	rs10787225	10	111954123	q25.2
SNP_A-2302172	G	G	336	10	410	4	3.859	4.95E-02	rs11638741	15	66521781	q23
SNP_A-2307524	G	G	241	121	301	111	3.859	4.95E-02	rs11073398	15	93214159	q26.2
SNP_A-2244958	G	G	373	37	343	53	3.859	4.95E-02	rs6484336	11	10483198	p15.4
SNP_A-2244293	G	G	235	125	296	116	3.859	4.95E-02	rs4951340	1	200968034	q32.1
SNP_A-2252172	A	A	357	9	411	3	3.858	4.95E-02	rs4632721	4	54572616	q12
SNP_A-2237098	A	A	263	99	315	85	3.858	4.95E-02	rs11681519	2	71050340	p13.3
SNP_A-2264056	G	A	193	173	208	174	3.858	4.95E-02	rs7741285	6	108203222	q21
SNP_A-2078589	G	G	274	32	302	56	3.858	4.95E-02	rs13066347	3	151351036	q25.1
SNP_A-2081770	A	A	262	158	234	186	3.86	4.95E-02	rs17799508	5	174369582	q35.2
SNP_A-2050567	G	G	390	6	415	1	3.858	4.95E-02	rs16937414	8	72208600	q13.3
SNP_A-1996451	G	G	355	27	394	16	3.86	4.95E-02	rs16914222	9	29009919	p21.1
SNP_A-1994354	G	G	319	21	372	12	3.86	4.95E-02	rs16894717	8	97628841	q22.1
SNP_A-2010400	T	T	362	4	399	13	3.857	4.95E-02	rs4342170	4	175031296	q34.1
SNP_A-2025809	C	C	234	134	292	124	3.859	4.95E-02	rs2103586	22	23698988	q11.23
SNP_A-2162903	T	T	350	72	365	51	3.857	4.95E-02	rs2571129	19	49591758	q13.31
SNP_A-2157929	G	G	362	4	399	13	3.857	4.95E-02	rs2333639	18	62681544	q22.1
SNP_A-2146286	T	T	223	199	249	169	3.859	4.95E-02	rs3816253	15	76245540	q25.1
SNP_A-2133682	T	T	280	138	306	112	3.858	4.95E-02	rs4078470	4	40146691	p14
SNP_A-2200818	T	T	229	137	288	128	3.858	4.95E-02	rs4522396	15	71063340	q24.1
SNP_A-2203075	G	G	358	48	330	66	3.858	4.95E-02	rs2517595	6	30192528	p21.33
SNP_A-2201715	C	C	203	147	196	190	3.858	4.95E-02	rs1533426	2	145952750	q22.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2197152	T	T	242	114	247	157	3.858	4.95E-02	rs6899867	6	74842670	q13
SNP_A-1644230	A	A	272	130	306	108	3.858	4.95E-02	rs1486932	1	76108735	p31.1
SNP_A-1801269	T	T	281	111	311	89	3.86	4.95E-02	rs298435	1	25942686	p36.11
SNP_A-1808010	T	T	362	4	399	13	3.857	4.95E-02	rs17601491	1	190098890	q31.2
SNP_A-1848840	A	A	267	151	231	173	3.859	4.95E-02	rs17124552	14	87884129	q31.3
SNP_A-1826030	A	A	340	14	369	29	3.857	4.95E-02	rs12343911	9	24449843	p21.3
SNP_A-1825520	T	T	348	74	365	53	3.859	4.95E-02	rs17185926	1	119185919	p12
SNP_A-1876969	G	G	305	65	362	52	3.858	4.95E-02	rs1960054	18	51750788	q21.2
SNP_A-1889574	C	C	384	36	389	21	3.86	4.95E-02	rs11883572	2	237873154	q37.3
SNP_A-1946188	T	T	268	100	276	140	3.86	4.95E-02	rs33612	5	82798333	q14.2
SNP_A-1963925	G	G	384	36	389	21	3.86	4.95E-02	rs10489820	1	117854582	p12
SNP_A-1983142	C	C	240	130	297	119	3.857	4.95E-02	rs17411921	5	117033876	q23.1
SNP_A-1937485	G	G	226	144	282	134	3.854	4.96E-02	rs553374	5	117329522	q23.1
SNP_A-1937337	G	G	323	47	381	35	3.856	4.96E-02	rs2119289	2	164323453	q24.3
SNP_A-1954348	G	G	349	17	373	33	3.856	4.96E-02	rs7049149	9	79896019	q21.31
SNP_A-1949151	T	T	339	27	352	46	3.856	4.96E-02	rs16859658	3	148878446	q24
SNP_A-1956379	A	A	311	53	371	41	3.856	4.96E-02	rs12187468	5	114049027	q22.3
SNP_A-1955486	G	G	357	33	382	20	3.853	4.96E-02	rs17774311	5	6356273	p15.32
SNP_A-1826264	T	T	231	79	224	108	3.856	4.96E-02	rs6126770	20	51217258	q13.2
SNP_A-1830707	G	G	295	55	346	42	3.854	4.96E-02	rs732317	4	73046279	q13.3
SNP_A-1859158	T	T	301	57	354	44	3.856	4.96E-02	rs1348665	16	58392588	q21
SNP_A-1855619	A	A	347	35	363	21	3.855	4.96E-02	rs6661789	1	234590466	q43
SNP_A-1809965	G	A	209	159	206	204	3.856	4.96E-02	rs4074720	10	114738487	q25.2
SNP_A-1791806	T	T	213	123	210	164	3.856	4.96E-02	rs8051129	16	7222984	p13.2

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1791917	G	G	358	12	411	5	3.856	4.96E-02	rs911125	20	23474288	p11.21
SNP_A-1790433	C	C	185	179	235	171	3.856	4.96E-02	rs4917464	10	107962518	q25.1
SNP_A-1728459	G	G	302	100	333	79	3.855	4.96E-02	rs722525	10	119764201	q26.11
SNP_A-1756737	G	G	369	21	401	11	3.854	4.96E-02	rs10486580	7	28022777	p15.1
SNP_A-1780661	C	C	299	65	307	95	3.855	4.96E-02	rs10027416	4	140900032	q31.1
SNP_A-2198967	C	C	359	7	390	18	3.855	4.96E-02	rs11954779	5	75669644	q13.3
SNP_A-2174955	T	C	178	160	212	176	3.855	4.96E-02	rs4704624	5	79516376	q14.1
SNP_A-2178644	C	C	318	76	347	57	3.854	4.96E-02	rs7856689	9	113344429	q32
SNP_A-2203254	G	G	388	16	407	7	3.854	4.96E-02	---	12	110209318	q24.12
SNP_A-2211894	A	A	347	71	326	94	3.857	4.96E-02	rs111111172	12	101031932	q23.2
SNP_A-2224432	A	A	273	93	281	131	3.856	4.96E-02	rs10029738	4	145655024	q31.21
SNP_A-2227654	C	C	268	98	275	137	3.856	4.96E-02	rs3740143	10	114214492	q25.2
SNP_A-2111919	C	C	306	60	312	88	3.854	4.96E-02	rs9521673	13	109707172	q34
SNP_A-2108864	T	T	252	82	270	122	3.855	4.96E-02	rs11221702	11	128778001	q24.3
SNP_A-2142761	A	A	251	155	283	131	3.854	4.96E-02	rs1417316	13	58408413	q21.1
SNP_A-2024960	C	C	362	42	372	26	3.856	4.96E-02	rs17113078	5	151677459	q33.1
SNP_A-2030144	A	A	221	197	248	168	3.854	4.96E-02	rs1007126	20	49302718	q13.2
SNP_A-2045128	T	T	247	117	303	105	3.855	4.96E-02	rs17269905	4	92538586	q22.1
SNP_A-2065647	A	A	380	40	353	57	3.854	4.96E-02	rs11605057	11	86381744	q14.2
SNP_A-2101743	A	A	292	96	313	73	3.854	4.96E-02	rs218674	17	6547657	p13.1
SNP_A-2102912	A	T	202	158	208	200	3.856	4.96E-02	rs136485	22	30916674	q12.3
SNP_A-2271700	C	C	329	31	346	18	3.855	4.96E-02	rs7300763	12	116062187	q24.22
SNP_A-2270614	A	A	358	12	411	5	3.856	4.96E-02	rs1893731	18	69105625	q22.3
SNP_A-2267213	A	A	226	144	282	134	3.854	4.96E-02	rs5769820	22	47747908	q13.32
SNP_A-2279788	G	G	358	12	411	5	3.856	4.96E-02	rs16838617	2	202699607	q33.1
SNP_A-2241362	G	G	370	0	382	4	3.855	4.96E-02	rs17121025	14	84871788	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238554	G	G	257	113	260	154	3.856	4.96E-02	rs1364405	7	136065414	q33
SNP_A-2252886	A	A	323	47	381	35	3.856	4.96E-02	rs1877109	7	103092446	q22.1
SNP_A-2256188	C	C	358	12	411	5	3.856	4.96E-02	rs17137865	16	5332297	p13.3
SNP_A-2253986	T	T	337	1	375	7	3.854	4.96E-02	rs7184248	16	68931104	q22.1
SNP_A-2254071	C	C	318	48	376	36	3.855	4.96E-02	rs13077592	3	105327818	q13.11
SNP_A-2290226	C	C	358	12	411	5	3.856	4.96E-02	rs7238633	18	65787044	q22.2
SNP_A-2307620	T	T	274	128	305	105	3.852	4.97E-02	rs2586532	17	4736083	p13.2
SNP_A-2230376	C	C	348	16	378	32	3.853	4.97E-02	rs1452144	3	134110326	q22.1
SNP_A-2273725	G	A	207	159	207	203	3.852	4.97E-02	rs4491418	14	45575579	q21.2
SNP_A-2100969	C	C	219	147	268	134	3.853	4.97E-02	rs4885674	13	79297493	q31.1
SNP_A-2106801	G	G	299	117	258	136	3.85	4.97E-02	rs7854636	9	125834210	q33.3
SNP_A-2105533	A	A	229	87	295	79	3.85	4.97E-02	rs12294925	11	25720495	p14.3
SNP_A-2046757	C	C	261	99	316	86	3.853	4.97E-02	rs17780667	10	104066221	q24.32
SNP_A-2046695	C	C	292	124	268	152	3.85	4.97E-02	rs1871045	19	50018608	q13.31
SNP_A-2028533	T	T	267	65	273	95	3.85	4.97E-02	rs17254830	9	24151849	p21.3
SNP_A-2030430	C	C	336	68	366	50	3.853	4.97E-02	rs16917748	11	28094790	p14.1
SNP_A-1991153	C	C	385	25	393	13	3.852	4.97E-02	rs17148257	7	124608703	q31.33
SNP_A-2160248	T	C	231	179	209	205	3.851	4.97E-02	rs13426115	2	103687817	q12.1
SNP_A-2156086	A	A	251	119	253	161	3.851	4.97E-02	rs35010	5	61792017	q12.1
SNP_A-2161427	T	T	326	6	346	16	3.851	4.97E-02	rs1159459	4	66921108	q13.2
SNP_A-2131460	T	C	189	175	225	183	3.852	4.97E-02	rs7690962	4	62595758	q13.1
SNP_A-2216164	T	G	202	158	207	199	3.852	4.97E-02	rs1614735	11	120998211	q23.3
SNP_A-2199432	C	C	249	111	311	101	3.851	4.97E-02	rs6593163	7	54315221	p11.2
SNP_A-2192139	T	T	176	118	233	113	3.852	4.97E-02	rs165039	15	44525649	q21.1
SNP_A-1750451	C	T	215	187	220	192	3.853	4.97E-02	rs10502172	11	112736795	q23.1
SNP_A-1749161	C	C	376	20	375	35	3.85	4.97E-02	rs2739352	21	21899267	q21.1
SNP_A-1680560	C	C	378	20	377	35	3.851	4.97E-02	rs236063	21	21898138	q21.1
SNP_A-1809701	G	C	185	139	197	195	3.852	4.97E-02	rs10774337	12	5496587	p13.31

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1810815	A	T	192	148	205	199	3.852	4.97E-02	rs4894198	2	177454911	q31.1
SNP_A-1814557	G	G	282	140	301	111	3.85	4.97E-02	rs703595	12	101577006	q23.2
SNP_A-1806462	G	G	393	25	401	13	3.851	4.97E-02	rs2302521	22	15998626	q11.1
SNP_A-1870218	A	A	376	42	386	26	3.853	4.97E-02	rs4390915	3	993544	p26.3
SNP_A-1832330	T	T	231	139	231	185	3.852	4.97E-02	rs169124	6	7792842	p24.3
SNP_A-1842141	G	G	274	66	289	99	3.852	4.97E-02	rs2932821	16	80863844	q23.3
SNP_A-1960376	G	G	335	29	358	50	3.85	4.97E-02	rs11043771	12	18046715	p12.3
SNP_A-1948704	A	A	389	7	397	17	3.85	4.97E-02	rs7007896	8	81107408	q21.13
SNP_A-1950801	A	A	349	39	331	57	3.851	4.97E-02	rs7974909	12	10133956	p13.2
SNP_A-1940642	C	C	243	171	216	200	3.85	4.97E-02	rs37027	16	55507529	q13
SNP_A-1966317	G	G	324	40	340	64	3.851	4.97E-02	rs1471772	2	193172893	q32.3
SNP_A-1875867	C	C	218	130	271	119	3.853	4.97E-02	rs10755901	8	108203756	q23.1
SNP_A-1878772	C	C	219	149	268	136	3.853	4.97E-02	rs11791652	9	88832350	q22.1
SNP_A-1922928	C	C	343	17	405	9	3.852	4.97E-02	rs16832000	2	136364984	q21.3
SNP_A-1921768	T	C	210	160	209	207	3.849	4.98E-02	rs9841810	3	197636365	q29
SNP_A-1877394	G	G	241	121	229	155	3.849	4.98E-02	rs2656275	8	55421807	q11.23
SNP_A-1884464	G	G	306	116	329	91	3.848	4.98E-02	rs973006	8	130586339	q24.21
SNP_A-1893390	A	A	280	62	293	93	3.85	4.98E-02	rs1350226	3	149422716	q24
SNP_A-1987866	T	T	350	6	372	16	3.847	4.98E-02	rs10499206	6	139311688	q24.1
SNP_A-1938347	T	T	236	120	290	108	3.848	4.98E-02	rs7017607	8	87263527	q21.3
SNP_A-1843780	C	C	301	53	336	38	3.849	4.98E-02	rs1291114	20	34934264	q11.23
SNP_A-1837586	C	C	259	109	317	97	3.847	4.98E-02	rs7676209	4	16969142	p15.32
SNP_A-1827166	T	T	374	48	351	67	3.85	4.98E-02	rs16924665	11	11737183	p15.3
SNP_A-1815374	T	T	358	12	390	26	3.848	4.98E-02	rs17111691	14	80834880	q31.1
SNP_A-1847887	G	G	307	111	328	86	3.848	4.98E-02	rs3848128	15	48679082	q21.2
SNP_A-1809216	C	C	225	145	223	191	3.849	4.98E-02	rs298733	1	221148986	q42.12

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1742973	C	C	268	82	288	122	3.85	4.98E-02	rs10497803	2	198228444	q33.1
SNP_A-1782592	A	A	318	92	295	117	3.849	4.98E-02	rs10988338	9	129191103	q34.11
SNP_A-1782024	C	C	332	76	309	99	3.848	4.98E-02	rs11026889	11	22978019	p14.3
SNP_A-2191956	A	A	312	56	327	85	3.847	4.98E-02	rs13332265	16	17809039	p12.3
SNP_A-2175137	C	C	358	54	372	36	3.849	4.98E-02	rs2355020	11	17471006	p15.1
SNP_A-2133896	T	T	310	102	289	129	3.849	4.98E-02	rs3765941	1	23384855	p36.12
SNP_A-2136500	A	A	308	112	282	138	3.85	4.98E-02	rs4933511	10	91560353	q23.31
SNP_A-2130433	T	T	358	12	390	26	3.848	4.98E-02	rs7215193	17	66920130	q24.3
SNP_A-2111609	G	G	328	82	356	62	3.847	4.98E-02	rs1161468	13	28324398	q12.3
SNP_A-2122894	C	C	346	12	397	5	3.849	4.98E-02	rs7771816	6	8827918	p24.3
SNP_A-2159706	G	G	287	39	342	28	3.849	4.98E-02	rs16927321	9	124110608	q33.3
SNP_A-2149235	G	G	370	30	368	48	3.847	4.98E-02	rs139072	22	42879680	q13.31
SNP_A-2149517	G	G	214	198	242	170	3.85	4.98E-02	rs663436	1	54426400	p32.3
SNP_A-1992433	C	C	278	86	286	122	3.849	4.98E-02	rs1872342	8	15988678	p22
SNP_A-1994188	T	T	269	47	263	69	3.847	4.98E-02	rs1351726	8	90271053	q21.3
SNP_A-1999065	T	T	356	14	387	29	3.847	4.98E-02	rs1748329	10	26987004	p12.1
SNP_A-2009046	G	G	365	53	338	72	3.848	4.98E-02	rs11932	3	123623825	q21.1
SNP_A-2037516	A	A	373	35	374	20	3.849	4.98E-02	rs10820393	9	103055050	q31.1
SNP_A-2106246	T	T	367	53	345	73	3.85	4.98E-02	rs1984968	14	95251335	q32.13
SNP_A-2078934	C	C	367	19	370	34	3.849	4.98E-02	rs10972429	9	35309634	p13.3
SNP_A-2068179	A	A	248	164	219	191	3.85	4.98E-02	rs11150195	16	78334242	q23.1
SNP_A-2069927	A	A	353	11	386	4	3.848	4.98E-02	rs1305377	3	101800618	q12.2
SNP_A-2074823	C	C	334	32	356	54	3.847	4.98E-02	rs7924690	11	40031169	p12
SNP_A-2070597	T	T	356	14	387	29	3.847	4.98E-02	rs12637368	3	164131613	q26.1
SNP_A-2051782	G	G	309	59	364	46	3.848	4.98E-02	rs9596166	13	49142151	q14.2
SNP_A-2277042	T	T	268	102	273	141	3.848	4.98E-02	rs11744363	5	144040681	q31.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282195	G	G	315	27	350	16	3.847	4.98E-02	rs11085841	19	13248250	p13.13
SNP_A-2270523	A	A	286	82	292	116	3.849	4.98E-02	rs2606136	15	49758825	q21.2
SNP_A-2251944	A	A	330	86	294	106	3.848	4.98E-02	rs7155312	14	75845696	q24.3
SNP_A-2312214	G	G	362	26	397	15	3.849	4.98E-02	rs17126180	12	50550223	q13.13
SNP_A-2310881	T	T	356	14	387	29	3.847	4.98E-02	rs1442316	15	99089921	q26.3
SNP_A-2290053	A	A	371	35	372	20	3.848	4.98E-02	rs4765523	12	126281672	q24.32
SNP_A-2300907	A	A	298	44	359	33	3.847	4.98E-02	rs12444741	16	49524320	q12.1
SNP_A-2291849	T	T	292	34	282	52	3.845	0.0499	rs17059224	13	60487747	q21.2
SNP_A-2312259	C	C	319	51	337	79	3.846	0.0499	rs740888	7	33314726	p14.3
SNP_A-2304847	T	T	406	12	402	4	3.846	0.0499	rs7764220	6	6341980	p25.1
SNP_A-2305707	A	A	282	100	308	78	3.844	0.0499	rs12617790	2	31102424	p23.1
SNP_A-2256282	T	T	211	157	267	149	3.845	0.0499	rs728486	7	90941320	q21.2
SNP_A-2244320	G	G	287	127	259	153	3.845	0.0499	rs6493735	15	53049743	q21.3
SNP_A-2265223	A	A	384	26	398	14	3.846	0.0499	rs7704706	5	12672289	p15.2
SNP_A-2265113	G	G	259	109	264	150	3.846	0.0499	rs10874746	1	93035992	p22.1
SNP_A-2260954	A	A	355	3	387	11	3.846	0.0499	rs1114454	13	77742279	q22.3
SNP_A-2281096	A	A	270	152	241	179	3.843	0.0499	rs17349222	1	165843527	q24.2
SNP_A-2062331	T	T	218	188	248	162	3.843	0.0499	rs1469372	3	16639513	p24.3
SNP_A-2079905	A	A	298	66	312	98	3.845	0.0499	rs17191359	14	95786943	q32.2
SNP_A-2093205	C	C	216	152	213	199	3.845	0.0499	rs618611	11	30196046	p14.1
SNP_A-2092774	A	A	326	44	346	70	3.846	0.0499	rs849422	7	106152415	q22.3
SNP_A-2047648	T	T	283	67	298	100	3.844	0.0499	rs4888770	16	76843781	q23.1
SNP_A-2030249	A	A	249	65	333	59	3.843	0.0499	rs3741060	11	107885191	q22.3
SNP_A-2000215	G	G	319	51	337	79	3.846	0.0499	rs1938567	1	98192149	p21.3

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2005412	G	G	278	66	331	53	3.846	0.0499	rs17464416	18	5226747	p11.31
SNP_A-2149810	A	A	390	14	344	24	3.844	0.0499	rs12295032	11	100037831	q22.1
SNP_A-2152320	C	A	192	176	226	186	3.844	0.0499	rs10766779	11	21233765	p15.1
SNP_A-2148852	C	C	326	44	346	70	3.846	0.0499	rs10173564	2	193161084	q32.3
SNP_A-2148675	G	G	365	1	407	7	3.846	0.0499	rs7115397	11	76656566	q13.5
SNP_A-2160506	G	A	200	168	214	192	3.846	0.0499	rs10403522	19	61853913	q13.43
SNP_A-2161674	A	A	344	24	390	14	3.844	0.0499	rs10777095	12	87132126	q21.32
SNP_A-2128091	T	C	174	150	176	150	3.845	0.0499	rs6055051	20	7415316	p12.3
SNP_A-2181047	A	A	201	167	256	160	3.845	0.0499	rs8180381	5	170776282	q35.1
SNP_A-2219327	C	C	332	12	381	5	3.846	0.0499	rs16911645	11	12800814	p15.2
SNP_A-2212841	T	T	280	86	337	73	3.846	0.0499	rs696676	1	75191184	p31.1
SNP_A-2200769	C	C	370	40	374	24	3.844	0.0499	rs7171902	15	64368453	q22.31
SNP_A-1783003	C	C	346	14	378	6	3.844	0.0499	rs16839536	1	4703953	p36.32
SNP_A-1724638	G	G	354	40	341	59	3.845	0.0499	rs10501147	11	36222594	p13
SNP_A-1646410	G	G	286	104	276	136	3.844	0.0499	rs10486392	7	20141347	p21.1
SNP_A-1794097	G	G	270	148	240	174	3.845	0.0499	rs11057355	12	122792583	q24.31
SNP_A-1855560	C	C	270	152	241	179	3.843	0.0499	rs17345107	1	165843319	q24.2
SNP_A-1861030	C	C	335	31	384	20	3.846	0.0499	rs9303344	17	49366410	q22
SNP_A-1861641	C	C	286	84	296	120	3.846	0.0499	rs7222529	17	50122753	q22
SNP_A-1823363	C	C	324	36	381	25	3.844	0.0499	rs1516142	2	145985987	q22.3
SNP_A-1951048	T	T	263	143	237	171	3.844	0.0499	rs12697018	5	63755052	q12.3
SNP_A-1978527	C	C	225	141	219	183	3.846	0.0499	rs1508218	4	112635327	q25
SNP_A-1901858	C	C	251	113	259	157	3.846	0.0499	rs4630332	12	58572619	q14.1
SNP_A-1884242	C	C	333	81	311	105	3.844	0.0499	rs1553497	17	28781096	q11.2
SNP_A-1932514	C	C	364	48	366	30	3.844	0.0499	rs9610750	22	20646692	q11.22

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1926944	A	A	248	122	304	110	3.845	0.0499	rs1389053	3	104493274	q13.11
SNP_A-1927250	A	A	365	1	407	7	3.846	0.0499	rs16902602	5	86577515	q14.3
SNP_A-1908432	G	G	349	1	389	7	3.846	0.0499	rs12685017	9	112793544	q32
SNP_A-1918481	G	G	278	106	286	78	3.842	5.00E-02	rs9879276	3	60928629	p14.2
SNP_A-1965324	G	G	345	69	363	49	3.843	5.00E-02	rs229336	2	149846879	q23.2
SNP_A-1944746	C	C	274	44	322	32	3.843	5.00E-02	rs2892599	11	90494970	q14.3
SNP_A-1821672	C	C	321	35	376	24	3.843	5.00E-02	rs13199684	6	69330377	q12
SNP_A-1838623	T	T	227	195	254	166	3.841	5.00E-02	rs7567073	2	211697137	q34
SNP_A-1834846	A	A	259	107	320	96	3.841	5.00E-02	rs7830310	8	81273011	q21.13
SNP_A-1786674	G	G	248	106	307	95	3.842	5.00E-02	rs2727682	12	118113616	q24.23
SNP_A-1786252	C	C	234	114	298	106	3.841	5.00E-02	rs11160180	14	93969013	q32.13
SNP_A-1659344	A	A	371	27	368	44	3.842	5.00E-02	rs4361405	4	11442970	p15.33
SNP_A-1666790	G	G	310	76	349	59	3.842	5.00E-02	rs6946775	7	11700313	p21.3
SNP_A-1661968	T	T	194	156	256	154	3.842	5.00E-02	rs6827711	4	61958056	q13.1
SNP_A-1683170	G	G	371	27	368	44	3.842	5.00E-02	rs10488986	4	11439004	p15.33
SNP_A-1689600	T	T	271	79	339	69	3.84	5.00E-02	rs1570843	6	84516116	q14.2
SNP_A-1699281	C	C	386	0	400	4	3.841	5.00E-02	rs1856558	9	16983249	p22.2
SNP_A-1706491	C	C	342	22	344	38	3.84	5.00E-02	rs950792	12	100431481	q23.2
SNP_A-1730731	T	T	379	17	379	31	3.841	5.00E-02	rs10496751	2	137606048	q21.3
SNP_A-2203318	A	A	349	3	342	10	3.84	5.00E-02	---	2	123781263	q14.3
SNP_A-2118978	G	G	354	14	385	29	3.84	5.00E-02	rs16857821	1	163382739	q24.1
SNP_A-2162349	G	C	193	191	228	174	3.841	5.00E-02	rs7137296	12	61895738	q14.2
SNP_A-2163953	G	G	229	117	232	160	3.842	5.00E-02	rs7923494	10	101027882	q24.2
SNP_A-2000554	G	G	337	85	357	63	3.842	5.00E-02	rs6425178	1	185097939	q31.1
SNP_A-2013199	C	C	363	1	405	7	3.843	5.00E-02	rs6995647	8	12632654	p23.1
SNP_A-2012976	A	A	266	98	273	137	3.843	5.00E-02	rs4493828	7	146061828	q35
SNP_A-2014856	A	C	208	158	200	198	3.84	5.00E-02	rs11600255	11	103197639	q22.3
SNP_A-2041894	C	C	224	164	201	195	3.84	5.00E-02	rs10247014	7	132888293	q33

Table 1

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2042826	A	G	193	167	213	185	3.842	5.00E-02	rs1374289	2	135528111	q21.3
SNP_A-2084099	C	C	257	73	313	61	3.841	5.00E-02	rs6573847	14	68174496	q24.1
SNP_A-2090554	T	T	297	123	316	96	3.841	5.00E-02	rs1967304	17	67802751	q24.3
SNP_A-2059254	G	G	185	167	234	158	3.84	5.00E-02	rs17484032	4	108476219	q25
SNP_A-2051619	A	A	378	6	401	1	3.84	5.00E-02	rs16930602	8	64769241	q12.3
SNP_A-2262783	G	G	356	12	388	26	3.842	5.00E-02	rs17025033	12	94902928	q23.1
SNP_A-2249101	G	G	304	58	320	88	3.84	5.00E-02	rs11754709	6	2657772	p25.2
SNP_A-2254663	T	T	295	75	307	109	3.843	5.00E-02	rs6959157	7	109576632	q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084457	actatccacccattca[C/T]gtaagtgagaaaactg	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 199248 // --- // --- // --- // ---	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1902305	tggccatctgttacca[A/G]tctcaggtgtatttta	A	G	Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), mRNA. /// ENST00000297161 // intron // 0 // --- // --- // --- // ---	BMPER	BMPER, Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), p14.3
SNP_A-1917221	tgttttagattttgtg[A/G]acatccaatttgtaag	A	G	10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // downstream // 223073 // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2147949	atggctcatcaccacc[A/G]gactcttgaggaggga	A	G	sapiens transferrin (TF), mRNA. /// ENST00000264998 //	TF	TF, Homo sapiens transferrin (TF), q22.1
SNP_A-2120324	agtcatcaacgtggga[C/G]agagcagcttgtgttg	C	G	9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 175641 //	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-1830896	taatgaaaacgctacc[A/G]cattgaatttccaata	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2118245	agtaaatgtgggccac[A/G]gaaaccacgttgtttg	A	G	CSRP2BP // 57325 // Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, mRNA. /// NM_177926 //	CSRP2BP	CSRP2BP, Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, p11.23
SNP_A-1757335	agctcttcacactctgcataagtaa[C/T]atacccccctattatgcacattcgct	C	T	NM_014917 // intron // 0 // - // - // - // -	-	- , rs10494062, -,p13.3
SNP_A-2211997	ccctgagctgatcagc[A/G]cagttttaattgttca	A	G	// 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// ENST00000355855 // upstream // 29315 // --- // --- // --- // ---	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-2207278	ccattccgtcctcaca[A/T]catccttagcagcaac	A	T	Homo sapiens replication factor C (activator 1) 1, 145kDa (RFC1), mRNA. /// ENST00000349703 // intron // 0 // --- // ---	RFC1	RFC1, Homo sapiens replication factor C (activator 1) 1, 145kDa (RFC1), p14
SNP_A-2065557	aattttaatgaagataa[C/G]taatttccttaaggta	C	G	10651 // Homo sapiens metaxin 2 (MTX2), transcript variant 1, mRNA. /// ENST00000249442 // downstream // 188835 // -	MTX2	MTX2, Homo sapiens metaxin 2 (MTX2), transcript variant 1, q31.1
SNP_A-1804680	gtcaggattcagttgg[A/G]aaaacagaactaacac	A	G	27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 329909 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2224642	tcaacactacagcaac[A/C]aagttattagctagta	A	C	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2024037	aaaagagataatgtga[A/G]tagtcatatatagcta	A	G	/// ENST00000236495 // upstream // 36970 // --- // --- // --- // ---	-	p33
SNP_A-2134872	atattatacctcattc[A/T]atctccccttttcctgg	A	T	1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 155733 // Hs.25674	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-2130903	atagaaacaataatca[A/G]aggcaaaatttcctgt	A	G	51705 // Homo sapiens endomucin (EMCN), mRNA. /// NM_000944 // downstream // 149959 // Hs.435512 //	EMCN	EMCN, Homo sapiens endomucin (EMCN), q24
SNP_A-1835766	tacgcagattaagctg[C/T]cactgtaatcaggata	C	T	113174 // Homo sapiens hypothetical protein BC012010 (LOC113174), mRNA. /// ENST00000300013 // intron // 0 // ---	LOC113174	LOC113174, Homo sapiens hypothetical protein BC012010 (LOC113174), p15.1
SNP_A-2075685	acatggcctggaggcc[C/T]gagtgtttgtacatga	C	T	29928 // Homo sapiens translocase of inner mitochondrial membrane 22 homolog (yeast) (TIMM22), mRNA. /// NM_001092 // downstream // 1065 // Hs.159306 // ABR // 29	TIMM22	TIMM22, Homo sapiens translocase of inner mitochondrial membrane 22 homolog (yeast) (TIMM22), p13.3
SNP_A-1844561	tataaattttcaaata[C/T]gcagaaaggttgaagg	C	T	// Homo sapiens hypothetical protein FLJ32440 (FLJ32440), mRNA. /// ENST00000287437 // intron // 0 // --- // --- // --- // ---	FLJ32440	FLJ32440, Homo sapiens hypothetical protein FLJ32440 (FLJ32440), q24.13
SNP_A-1797803	ggttttagagggtata[A/C]accttgcacacaaggg	A	C	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // --- // --- // --- // ---	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2045361	aagaagttgtgatcca[C/T]ataaacaaagagcata	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 198326 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1845418	tatagaaactagccat[C/T]acttaagcaatctccc	C	T	6332 // Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA. /// NM_002976 // upstream //	SCN7A	SCN7A, Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), q24.3
SNP_A-2307042	gctgttgtaaaagagc[A/C]aaacaatgaccatctg	A	C	Homo sapiens hypothetical protein FLJ23550 (FLJ23550), mRNA. /// ENST00000236160 // intron // 0 // --- // --- // --- // ---	FLJ23550	FLJ23550, Homo sapiens hypothetical protein FLJ23550 (FLJ23550), q24.3
SNP_A-1957729	ttttatgtgtattttc[A/G]ccatcctcaaaaggct	A	G	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-2143668	atgagaaaacagtaga[C/T]gctccaaatagtaagg	C	T	118980 // Homo sapiens sideroflexin 2 (SFXN2), mRNA. /// NM_017787 // upstream // 28850 // Hs.500897 // C10orf26 //	SFXN2	SFXN2, Homo sapiens sideroflexin 2 (SFXN2), q24.32
SNP_A-2040804	aacccattttaagacc[C/T]aatccaagtgtcattt	C	T	Homo sapiens retinitis pigmentosa 26 (autosomal recessive) (RP26), mRNA. /// ENST00000339098 // intron // 0 // --- // ---	CERKL	CERKL, Homo sapiens retinitis pigmentosa 26 (autosomal recessive) (RP26), q31.3
SNP_A-2273616	gactgagcctcagaaa[A/G]tgttttatagtgtctg	A	G	1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream //	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2183057	cagatttttctccagt[A/G]aaactgaaacctaaat	A	G	// 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream //	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1980555	atgacagagagataaa[C/T]gtggggttcacaagca	C	T	4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2246180	ctggtgaataatgaaa[C/G]agaagtagtggccaca	C	G	Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA. /// ENST00000285896 // intron // 0 // --- // ---	CNOT8	CNOT8, Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), q33.2
SNP_A-2244633	ctggagcttgctggag[C/T]cagcacatatgtccaa	C	T	ENST00000308464 // intron // 0 // --- // --- // --- // ---	-	q23.2
SNP_A-2264158	gaactgctgagaaccc[A/G]ggatgctgaagagcag	A	G	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2123363	agtgtcatattaagca[C/T]tattatgttctacatt	C	T	ENST00000329438 // intron // 0 // --- // --- // --- // --- /// ENST00000329662 // intron // 0 // --- // --- // --- // --- ///	-	q36.3
SNP_A-1750883	atggtctctacgtttctttgtaggc[C/T]aaatgggtattttgctccatttttta	C	T	7991 // tumor suppressor candidate 3 /// NM_139167 // upstream // 602944 // Hs.348641 // SGCZ // 137868 //	TUSC3	TUSC3 , rs10503537, tumor suppressor candidate 3 ,p22
SNP_A-1683814	ctctacctctaatagcctttattat[G/T]actttatgtttcatttgagtggata	G	T	// 301 // annexin A1 /// NM_006914 // upstream // 437318 // Hs.117956 // RORB // 6096 // RAR-related orphan receptor B	ANXA1	ANXA1 , rs1491442, annexin A1 ,q21.13
SNP_A-1916882	tgtttctgattagcaa[C/T]tgttgagtgctctggt	C	T	sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), mRNA. /// ENST00000258317 // CDS // 0 // --- // --- // --- // ---	NPL	NPL, Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), q25.3
SNP_A-1898521	tgcttgaacctgggaa[A/G]cagattgcagtgagct	A	G	ENST00000226258 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2284638	gatcagcattttggcc[A/G]caacaatttgaccaat	A	G	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-1939623	ttgatttcattcttcc[C/T]ccttttcttggacgga	C	T	Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- // --- ///	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-1855927	tcaatgtcgggacaca[A/C]gaaacatttaaaaagc	A	C	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2077946	accagccaaaccgtgg[A/G]caataggcaggaagca	A	G	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 250626 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-1946420	tttaaactgacagaca[A/G]tggaaaatcccaaagg	A	G	Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-2059153	aatcctcagacagagc[C/T]caggtaaagaggatgt	C	T	375061 // Homo sapiens hypothetical gene supported by BC009447 (MGC15887), mRNA. /// NM_001004342 //	MGC15887	MGC15887, Homo sapiens hypothetical gene supported by BC009447 (MGC15887), q42.2
SNP_A-1687462	ggacagaggtataaac[A/G]ggtctattctatctgg	A	G	2917 // glutamate receptor, metabotropic 7 /// NM_014674 // downstream // 338478 // - // - // - // --- /// NM_181874 //	GRM7	GRM7 , rs4241, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-2253987	cttgacttttttaaaca[C/T]gctcactgttctgttt	C	T	/// ENST00000297820 // upstream // 28828 // --- // --- // --- // ---	-	q21.33
SNP_A-1900843	tggagtgggaaatagc[A/G]gagatggataagttaa	A	G	Homo sapiens SH3-domain binding protein 3 (SH3BP3), mRNA. /// ENST00000263805 // intron // 0 // --- // --- // --- // ---	ZFP106	ZFP106, Homo sapiens SH3-domain binding protein 3 (SH3BP3), q15.1
SNP_A-2163765	caaaaatttcttaagt[A/C]acaggcaaaaaggtca	A	C	// 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1973768	attcccatggttttcc[A/G]gaaagacaaatgaacc	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2219138	cctgtatgacttcata[A/T]taatttgattctatct	A	T	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 1485561 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.1
SNP_A-1977549	ctataattgtttccaa[A/G]tggtcattgtcccttt	A	G	8671 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), mRNA. /// NM_000583 // downstream // 65906 // Hs.418497 // GC //	SLC4A4	SLC4A4, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), q13.3
SNP_A-1746044	aagaaaagaataaaagccaggaaga[C/G]acgaaactctttagaaggcatc tag	C	G	90871 // chromosome 9 open reading frame 123 /// NM_002839 // downstream // 386143 // Hs.323079 // PTPRD	C9orf123	C9orf123 , rs10491572, chromosome 9 open reading frame 123 ,p24.1
SNP_A-2243594	ctgctcagaagaaacc[A/G]caactgtagcagctct	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, mRNA. /// NM_030668 // intron // 0 // Hs.160871 // PTPRO // 5800 // Homo sapiens protein	PTPRO	PTPRO, Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, p12.3
SNP_A-2031537	aaaggtgttaatatca[A/C]catcaagaaactcact	A	C	/// ENST00000331815 // downstream // 566606 // --- // --- // ---	-	q13.13
SNP_A-1881130	ggcatccacaagttta[A/C]agcagggagagtaaat	A	C	Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA. /// ENST00000317931 // intron // 0 // --- // --- // --- // --- ///	L3MBTL4	L3MBTL4, Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), p11.31
SNP_A-2261889	gaaataagcataggca[A/G]cttgaattcctcagaa	A	G	2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 //	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2205177	ccagtaatttatgtaa[C/G]cagtgtcctattggtg	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 7972 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1874404	tctccatttattcaag[A/T]cttcttttatgtcctc	A	T	sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// ENST00000296212 // intron // 0 // --- // --- // --- // ---	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-1950226	tttcagaaaggtctgg[G/T]acatattggtggttct	G	T	Homo sapiens phosphodiesterase 8B (PDE8B), mRNA. /// ENST00000329238 // intron // 0 // --- // --- // --- // --- ///	PDE8B	PDE8B, Homo sapiens phosphodiesterase 8B (PDE8B), q13.3
SNP_A-2201479	ccaatgggaaaaccaa[G/T]ttggaaatgacagggc	G	T	// 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-2032932	aaataatcaaactgaa[A/G]aaagacaagcaaaatg	A	G	// 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1510102 // Hs.27214 // KCNC2 // 3747 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1856530	tcacagccccagacac[G/T]cgcccggtggaaaacg	G	T	129642 // Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), mRNA. /// NM_003887 // upstream // 63795 // Hs.467662 // DDEF2 // 8853 // Homo	OACT2	OACT2, Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), p25.1
SNP_A-2151560	atgttgaaactgaaaa[A/T]ttatgtctagttctta	A	T	receptor rearranged beta-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000361005 // intron // 0 // --- // --- // -	-	-, Human T-cell receptor rearranged beta-chain V-region (V-D-J) complete cds. ,q34
SNP_A-2232095	ctcaagctctcccaac[A/G]aagattctcagtacaa	A	G	ENST00000342537 // intron // 0 // --- // --- // --- // ---	-	q32.33
SNP_A-2252719	cttcggtcactctcta[C/T]ggagaaaaaagaagaa	C	T	sapiens hypothetical protein ET (ET), mRNA. /// ENST00000262771 // intron // 0 // --- // --- // --- // --- ///	ET	ET, Homo sapiens hypothetical protein ET (ET), q25.1
SNP_A-1842908	tagtagtatataaaaa[A/T]cattcacaaataaaat	A	T	FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-2013922	tgtgctttgagatgaa[C/T]gtgggcactggtatcc	C	T	Homo sapiens angiomotin like 1 (AMOTL1), mRNA. /// ENST00000317837 // intron // 0 // --- // --- // --- // --- ///	AMOTL1	AMOTL1, Homo sapiens angiomotin like 1 (AMOTL1), q21
SNP_A-2225328	cgtttcccaaactgaa[A/G]gaaatgccagatgtgc	A	G	// 6160 // Homo sapiens ribosomal protein L31 (RPL31), mRNA. /// NM_017546 // upstream // 25521 // Hs.30819 //	RPL31	RPL31, Homo sapiens ribosomal protein L31 (RPL31), q11.2
SNP_A-2208945	cccagccaggtacgta[C/T]gctcctgagtagccaa	C	T	ENST00000356513 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-2258209	cttttagaatacacac[A/G]agttcatgcagctgtt	A	G	Homo sapiens PRP4 pre-mRNA processing factor 4 homolog B (yeast) (PRPF4B), transcript variant 1, mRNA. /// NM_176800 // intron // 0 // Hs.159014 // PRPF4B // 8899 //	PRPF4B	PRPF4B, Homo sapiens PRP4 pre- processing factor 4 homolog B (yeast) (PRPF4B), transcript variant 1, p25.2
SNP_A-1816118	gttaccaggagaaccc[A/G]gaatctcttactgggc	A	G	10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 //	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-1826878	taacatatgttgcctc[A/G]ctagcattaactacag	A	G	GABARAPL1 // 23710 // Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), mRNA. ///	GABARAPL1	GABARAPL1, Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), p13.2
SNP_A-1998094	aaacacaagtggttgt[C/G]aatttgtgggcatgaa	C	G	// 55096 // Homo sapiens hypothetical protein FLJ10213 (FLJ10213), mRNA. /// NM_012071 // upstream // 1737 //	FLJ10213	FLJ10213, Homo sapiens hypothetical protein FLJ10213 (FLJ10213), p12.2
SNP_A-2143372	atgaccaagcccacaa[A/C]gtcaaatacatcactt	A	C	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1857484	tcactattgaaaagca[A/G]aaagtggcctgcctct	A	G	// 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// AF106069 // upstream // 116048 // Hs.434951 // USP15 //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2146541	atgctgatctattaca[A/C]atgaaatgccaacagt	A	C	// Homo sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// NM_053036 // upstream // 53595 //	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-1709715	cctgtaaattatctacaatagtata[C/T]agaaaaaaagttagaaattattctg	C	T	similar to RIKEN cDNA 2700038C09 gene (cDNA clone MGC:24600 IMAGE:4245342), complete cds /// NM_018967 // upstream // 737160 // Hs.388360 // SNTG1 // 54212 //	-	- , rs2726713, MRNA similar to RIKEN cDNA 2700038C09 gene (cDNA clone MGC:24600 IMAGE:4245342), complete cds ,q11.21
SNP_A-2079414	accccattgttcccaa[C/T]tgcattttaactgaaa	C	T	RPS6KA4 // 8986 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 4 (RPS6KA4), mRNA. ///	RPS6KA4	RPS6KA4, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 4 (RPS6KA4), q13.1
SNP_A-2207018	ccatgtgtcaatcaag[C/G]ccatgatctgatcaca	C	G	ENST00000355183 // intron // 0 // --- // --- // --- // ---	-	p24.1
SNP_A-1986361	taatgtgatagtaaaa[A/C]ttgaacaaatatagag	A	C	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // --- // ---	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-2069757	acacacttccagaaaa[C/T]gattcataaaataaca	C	T	9169 // Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA. /// NM_004719 //	SFRS2IP	SFRS2IP, Homo sapiens splicing factor, arginine,q13.11
SNP_A-1862070	tcatgcatatctgctc[A/C]aactctattattaaag	A	C	Homo sapiens ubiquitin specific protease 34 (USP34), mRNA. /// ENST00000263989 // intron // 0 // --- // --- // --- // ---	USP34	USP34, Homo sapiens ubiquitin specific protease 34 (USP34), p15
SNP_A-2004351	attctggtctctcaaa[A/T]cccagccctgccctcc	A	T	Homo sapiens Rhesus blood group, C glycoprotein (RHCG), mRNA. /// ENST00000268122 // intron // 0 // --- // --- // --- // ---	RHCG	RHCG, Homo sapiens Rhesus blood group, C glycoprotein (RHCG), q26.1
SNP_A-2092768	agaaatggtcaagaca[A/G]aactgaacttctaagg	A	G	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3,	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2031290	aaagggacccacttga[C/T]gaaacatataagtcct	C	T	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2242811	ctgccaaacaccatga[A/G]gcaaaaagctgggtca	A	G	Homo sapiens InaD-like protein (INADL), transcript variant 3, mRNA. /// NM_176878 // intron // 0 // Hs.478125 // INADL //	INADL	INADL, Homo sapiens InaD-like protein (INADL), transcript variant 3, p31.3
SNP_A-1889943	tgataggagctaacca[A/C]aaacttgtgacacctt	A	C	sapiens sorting nexin 3 (SNX3), transcript variant 3, mRNA. /// NM_152827 // intron // 0 // Hs.12102 // SNX3 // 8724 //	SNX3	SNX3, Homo sapiens sorting nexin 3 (SNX3), transcript variant 3, q21
SNP_A-2152072	attaaaacaacatcca[A/T]gaatttattttgaggc	A	T	Homo sapiens SEC63-like (S. cerevisiae) (SEC63), mRNA. /// ENST00000027474 // intron // 0 // --- // --- // --- // ---	SEC63	SEC63, Homo sapiens SEC63-like (S. cerevisiae) (SEC63), q21
SNP_A-2022746	aaaaattcatagtgca[A/G]gtcgctgtagcaaaaa	A	G	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream //	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.1
SNP_A-1988216	tcacgaaaagccaaag[A/G]aaagcattcaaagcta	A	G	Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3E), mRNA. /// ENST00000337049 // intron // 0 // --- // --- // --- //	PIP3-E	PIP3-E, Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), q25.2
SNP_A-1879663	tcttcagcggttaaaa[C/T]gttcttccttctgctg	C	T	10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 247956 //	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2284656	gatcagcttcctgttc[A/G]actgcatcgtccgagg	A	G	Homo sapiens hypothetical protein FLJ33718 (FLJ33718), mRNA. /// ENST00000322004 // CDS // 0 // --- // --- // --- // ---	FLJ33718	FLJ33718, Homo sapiens hypothetical protein FLJ33718 (FLJ33718), p16.3
SNP_A-2285124	gatctaatatgcaaaa[C/T]gtttatatggttcaaa	C	T	8706 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3 (B3GALT3), transcript variant 1, mRNA. /// NM_033167 // upstream // 27875 //	B3GALT3	B3GALT3, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3 (B3GALT3), transcript variant 1, q26.1
SNP_A-2069895	acacagctacagaaga[A/T]agataagtcaattact	A	T	Homo sapiens HIV-1 rev binding protein 2 (HRB2), mRNA. /// ENST00000229214 // intron // 0 // --- // --- // --- // --- ///	HRB2	HRB2, Homo sapiens HIV-1 rev binding protein 2 (HRB2), q21.1
SNP_A-1981412	ggttttcaggttcagc[A/G]ctaaggggtgacttta	A	G	Homo sapiens hypothetical protein FLJ40243 (FLJ40243), mRNA. /// ENST00000355152 // intron // 0 // --- // --- // --- // ---	FLJ40243	FLJ40243, Homo sapiens hypothetical protein FLJ40243 (FLJ40243), p13.1
SNP_A-2066218	aattttaccaaagcag[A/G]caagaaaggagaaaaa	A	G	9451 // Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA. /// NM_144563 // upstream // 43096 // Hs.469264 // RPIA // 22934 // Homo	EIF2AK3	EIF2AK3, Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), p11.2
SNP_A-2060839	aatgataacttttgaga[C/G]aggatcacattagact	C	G	140691 // Homo sapiens ring finger protein 36 (RNF36), transcript variant a, mRNA. /// NM_080745 // downstream //	RNF36	RNF36, Homo sapiens ring finger protein 36 (RNF36), transcript variant a, q21.1
SNP_A-1865616	tccatgttgtttgcac[A/G]gtattctcttggatga	A	G	338596 // Homo sapiens partial mRNA for alpha2,8-sialyltransferase (ST8SIA VI gene). /// ENST00000277639 //	ST8SIA6	ST8SIA6, Homo sapiens partial for alpha2,8-sialyltransferase (ST8SIA VI gene). ,p12.33
SNP_A-2108442	agctgcgttagagtta[A/C]gcaaagtctccacttg	A	C	Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA. /// ENST00000289175 // intron // 0 // ---	LRRFIP1	LRRFIP1, Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), q37.3
SNP_A-2152368	attaacatgaagctca[A/G]tgaaatagaattggga	A	G	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1843086	cagttcaacactgtga[G/T]tattggtatctgttat	G	T	Homo sapiens zinc finger protein 287 (ZNF287), mRNA. /// ENST00000268727 // intron // 0 // --- // --- // --- // ---	ZNF287	ZNF287, Homo sapiens zinc finger protein 287 (ZNF287), p11.2
SNP_A-1889721	tgataataaatggtaa[C/G]aaacttggagaaaaaa	C	G	/// ENST00000332660 // downstream // 205639 // --- // --- // ---	-	p12.3
SNP_A-2103349	agcaagggtggttctc[A/C]acactgtttcaaacag	A	C	ENST00000322282 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2043369	aactggcaacatcacc[A/G]cctaaatgaccccagg	A	G	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000330684 // intron // 0 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2223095	cgccagagcgtttgac[C/T]gccacgtggggtcatt	C	T	FLJ41603 // 389337 // Homo sapiens FLJ41603 protein (FLJ41603), mRNA. /// NM_133263 // upstream // 86013 //	FLJ41603	FLJ41603, Homo sapiens FLJ41603 protein (FLJ41603), q32
SNP_A-1956579	tttgtttcttggctgc[C/T]agctctctgggtgtac	C	T	2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1824234	taaacatttgtatata[C/T]ggtcaaatgactcttg	C	T	Homo sapiens hypothetical protein MGC35194 (MGC35194), mRNA. /// ENST00000288048 // intron // 0 // --- // --- // --- // ---	MGC35194	MGC35194, Homo sapiens hypothetical protein MGC35194 (MGC35194), p36.21
SNP_A-2173325	cacaagagcataacat[A/G]acaactaaaagtaata	A	G	285492 // Homo sapiens hypothetical protein FLJ35424 (FLJ35424), mRNA. /// ENST00000316915 // downstream //	FLJ35424	FLJ35424, Homo sapiens hypothetical protein FLJ35424 (FLJ35424), p16.3
SNP_A-2158886	attgtgggccttgcaa[A/T]ctactatactgagtca	A	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1983151	catgaagcctagcctg[A/G]aactttctttccttaa	A	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1911042	cctgtgcactgagaga[A/G]gagggtctgttctgtt	A	G	4089 // Homo sapiens SMAD, mothers against DPP homolog 4 (Drosophila) (SMAD4), mRNA. /// NM_016626 //	SMAD4	SMAD4, Homo sapiens SMAD, mothers against DPP homolog 4 (Drosophila) (SMAD4), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2036154	gttcgtcagaattaaa[C/T]gtagacagaaacagct	C	T	// 4257 // Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 1b, mRNA. /// NM_145792 // downstream // 100877 // Hs.389700 // MGST1	MGST1	MGST1, Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 1b, p12.3
SNP_A-1733034	atataacactctatatttaaaagga[C/G]taccataataaatgagaaaaaatga	C	G	KIAA1221 // 84146 // KIAA1221 protein /// NM_032186 // downstream // 273241 // Hs.173001 // KIAA1221 // 84146 //	KIAA1221	KIAA1221 , rs1342778, KIAA1221 protein ,p22.2
SNP_A-2233144	ctcagccctccctcac[C/T]gtaagaactctcagca	C	T	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1820590 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1968836	ctagtttctattccaa[C/G]cttcatctctacttca	C	G	// Homo sapiens endothelin 3 (EDN3), transcript variant 1, mRNA. /// NM_207034 // upstream // 13965 // Hs.1408 //	EDN3	EDN3, Homo sapiens endothelin 3 (EDN3), transcript variant 1, q13.32
SNP_A-2061537	aatgctgctactgcta[C/T]gtttccagcctgacca	C	T	221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // downstream //	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2077900	accagattgctcaaaa[C/T]acagatcacaaaatgg	C	T	64110 // Homo sapiens melanoma antigen, family F, 1 (MAGEF1), mRNA. /// NM_015303 // upstream // 40750 // ---	MAGEF1	MAGEF1, Homo sapiens melanoma antigen, family F, 1 (MAGEF1), q27.1
SNP_A-1922915	ttagattcaactacca[A/G]atggcctgttctcctg	A	G	ENST00000316225 // intron // 0 // --- // --- // --- // ---	-	q24.23
SNP_A-1886868	tgactgtgtttgagcc[A/G]ccttgcctccgttact	A	G	64759 // Homo sapiens tensin-like SH2 domain containing 1 (TENS1), mRNA. /// NM_022748 // upstream // 42124 //	TENS1	TENS1, Homo sapiens tensin-like SH2 domain containing 1 (TENS1), p12.3
SNP_A-2035552	aaatgtaagaagaatc[C/G]ataaagtaattgaaga	C	G	4829 // Homo sapiens neuromedin B receptor (NMBR), mRNA. /// ENST00000354295 // downstream // 240985 // ---	NMBR	NMBR, Homo sapiens neuromedin B receptor (NMBR), q24.1
SNP_A-2090232	acttgcacaacagaga[A/G]aaggagagtcacatag	A	G	10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// NM_022091 // upstream // 246233 // Hs.486031 // DJ467N11.1 // 63921 //	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-2170709	caagttctatcataga[A/G]gatctctcatccaacc	A	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2104359	agcagcgtgtcccgca[A/G]gtagccccagacctgg	A	G	Homo sapiens membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase (PKMYT1), transcript variant 1, mRNA. /// NM_182687 // CDS // 0 // Hs.77783 // PKMYT1 // 9088 // Homo sapiens m	PKMYT1	PKMYT1, Homo sapiens membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase (PKMYT1), transcript variant 1, p13.3
SNP_A-1839426	tagataacagtgaata[C/T]ggtgttgaagactcaa	C	T	5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 265128 // ---	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-2081531	acctgtgttccatgta[C/G]agaaaatggcagataa	C	G	55835 // Homo sapiens centromere protein J (CENPJ), mRNA. /// NM_030979 // upstream // 36068 // Hs.458280 //	CENPJ	CENPJ, Homo sapiens centromere protein J (CENPJ), q12.13
SNP_A-2207937	cccaaatttgagtaaa[A/C]ttatgcccagtgtaat	A	C	/// ENST00000319719 // upstream // 412136 // --- // --- // --- // -- /// ENST00000308537 // upstream // 188261 // --- // --- // ---	-	p13
SNP_A-2189003	cagtgtgtccagaata[A/G]cagcttagaggcagtt	A	G	Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// ENST00000298992 // intron	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-2155125	attcagagtagcataa[A/G]atttggctaaaagcca	A	G	ENST00000336156 // downstream // 5437 // --- // --- // --- // --- /// ENST00000251993 // downstream // 5437 // --- // --- // --- //	-	q13.31
SNP_A-2068380	acaaggactgcgtaga[C/T]gaaggtatgagcctttt	C	T	Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // --- // --- // --- // ---	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-2074945	acatcagttcagccac[A/G]caggtgatccaaccgg	A	G	27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 212045 // Hs.268774	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2020373	cctcagtttccagaaa[C/G]aagccagactcagtgc	C	G	// Homo sapiens hypothetical protein LOC284837 (LOC284837), mRNA. /// ENST00000343732 // CDS // 0 // ---	LOC284837	LOC284837, Homo sapiens hypothetical protein LOC284837 (LOC284837), q22.3
SNP_A-1981322	aaaatggaactgtgct[C/T]acacttccgtggagcc	C	T	Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, mRNA. /// NM_182799 // intron // 0 //	FLJ39155	FLJ39155, Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, p13.2
SNP_A-1899236	tggaaatggggaatac[A/G]attatattttagcagt	A	G	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 402102 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-1947051	tttaatacctgctata[C/T]gccagcctttaatcag	C	T	/// ENST00000336930 // upstream // 649348 // --- // --- // --- // -	-	p14.3
SNP_A-2201961	ccacagatgaaatgaa[A/G]tatgagagctgtttta	A	G	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2078578	accatggaggcacagc[A/G]actgcatctgggatag	A	G	// 84931 // Homo sapiens hypothetical protein FLJ14816 (FLJ14816), mRNA. /// NM_030381 // upstream // 174785 //	FLJ14816	FLJ14816, Homo sapiens hypothetical protein FLJ14816 (FLJ14816), q14.2
SNP_A-1987365	ctggtctcgaattcct[C/G]agcttaagttatccac	C	G	// Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), mRNA. /// NM_173674 //	ROS1	ROS1, Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084377	actataggctgtctac[A/C]agaacttggtccaaat	A	C	Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // intron // 0 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-1904037	tgggcacgcatgactc[A/G]agggcaaggaatgaaa	A	G	/// ENST00000298211 // upstream // 78912 // --- // --- // --- // --- /// ENST00000333415 // upstream // 79347 // --- // --- // --- // ---	-	p11.21
SNP_A-1797038	ggttctggccagggac[A/G]gagatctaccacaagc	A	G	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2197176	cattcaataagaatgc[C/T]aaaatgtgctacccca	C	T	Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// ENST00000360057 // intron // 0 // --- // --- // --- // --- ///	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-1965779	tcatcaggttacaaga[C/T]gagaagaaaggtgatg	C	T	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 11 (ABCB11), mRNA. ///	ABCB11	ABCB11, Homo sapiens ATP-binding cassette, sub-family B (MDR,q31.1
SNP_A-2188336	cagtctgtcgtgaaca[A/C]cctccaggcaggatca	A	C	11182 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6), mRNA. /// ENST00000291725 // upstream // 18418 // --- // --- // --- // ---	SLC2A6	SLC2A6, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6), q34.2
SNP_A-1727212	aagcggacacttcaaaatcaaacaa[C/T]gtagcaattgaaagtaaacactaaa	C	T	AB067801 // intron // 0 // Hs.153355 // QKI // 9444 // quaking homolog, KH domain RNA binding (mouse)	QKI	QKI , rs10484574, quaking homolog, KH domain RNA binding (mouse),q26
SNP_A-1850199	tatgtgtcctgctatc[A/G]ctcatgctaataattg	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // --- //	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1933148	ttcgttatttttggca[G/T]agttgtgatgattctt	G	T	ARL6IP6 // 151188 // Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), mRNA. ///	ARL6IP6	ARL6IP6, Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), q23.3
SNP_A-2098412	agagcaaaggatcaaa[A/C]aagacaaaggacagat	A	C	5000 // Homo sapiens origin recognition complex, subunit 4-like (yeast) (ORC4L), transcript variant 2, mRNA. /// NM_181742 // upstream // 103132 // Hs.470174 // ORC4L //	ORC4L	ORC4L, Homo sapiens origin recognition complex, subunit 4-like (yeast) (ORC4L), transcript variant 2, q23.1
SNP_A-2070168	acacatggaaaagcag[A/G]aacccagatgtatttg	A	G	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 378330 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3
SNP_A-2265922	gaaggagacttttccc[C/G]cagactgagaggactg	C	G	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-1811205	gtgcctcagtttacca[A/G]tcaagccattctgcct	A	G	// 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream //	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1933345	ttctaatcatctgtca[A/G]agtagtaagtggttaa	A	G	55917 // Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), mRNA. /// ENST00000271277 // intron // 0	DKFZp547A023	DKFZp547A023, Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), p13.2
SNP_A-2013743	tttgtcaacaagtgca[A/G]gccaagagtctgccta	A	G	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 521546 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1744413	ctgtggttaaggttgaatgaggtaa[A/G]attaaaagtaaaagtctgggccggg	A	G	AB018317 // intron // 0 // Hs.22201 // KIAA0774 // 23281 // KIAA0774	KIAA0774	KIAA0774 , rs9314945, KIAA0774,q12.3
SNP_A-2271780	gaccatacagctgggg[A/G]caacggcagcagctac	A	G	Homo sapiens serine/threonine kinase 11 interacting protein (STK11IP), mRNA. /// ENST00000295641 // intron // 0 // --- //	STK11IP	STK11IP, Homo sapiens serine q35
SNP_A-1886767	tgactgatgcacccga[C/T]gtccagcagagatgtc	C	T	ENST00000323164 // CDS // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-2232368	ctcacaattatggctg[A/G]acgcaaagggtaagca	A	G	// 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 733713 // Hs.211225 // NOVA1 // 4857 //	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2215325	cctcaatagcttaaaa[C/T]aaatctgatctatgtt	C	T	// Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000303045 // intron // 0 // --- // --- // --- // ---	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2272151	gacctaaagtaaagaa[C/G]gtcagcagtggcattt	C	G	// 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 167747 // Hs.369438 // ETS1 //	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.3
SNP_A-2310805	ggaagcctggacacca[C/T]gtgaacgcagcagctg	C	T	23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA. /// NM_017939 // upstream // 137452 // Hs.313917 //	ZNF423	ZNF423, Homo sapiens zinc finger protein 423 (ZNF423), q12.1
SNP_A-1876355	tctgaggggcctatga[A/G]aaaagaggagtctgaa	A	G	Homo sapiens RNA binding protein with multiple splicing (RBPMS), mRNA. /// ENST00000340497 // intron // 0 // --- // --	RBPMS	RBPMS, Homo sapiens RNA binding protein with multiple splicing (RBPMS), p12
SNP_A-2245290	ctggctgagacattgg[C/T]accagctgttctaaca	C	T	375061 // Homo sapiens hypothetical gene supported by BC009447 (MGC15887), mRNA. /// NM_001004342 //	MGC15887	MGC15887, Homo sapiens hypothetical gene supported by BC009447 (MGC15887), q42.2
SNP_A-1704827	ctataataaaatgctaactgtagaa[A/T]tgaggaggtatatgagtattcactg	A	T	Hermansky-Pudlak syndrome 4 /// NM_152840 // intron // 0 // Hs.441481 // HPS4 // 89781 // Hermansky-Pudlak syndrome	HPS4	HPS4 , rs10483125, Hermansky-Pudlak syndrome 4 ,q12.1
SNP_A-2216534	cctctaatgactgtta[C/T]agctgcatcccacaaa	C	T	Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), mRNA. /// ENST00000331079 // intron // 0 // --- // --- // --- // --- /// ENST00000330796 // intron //	HRMT1L3	HRMT1L3, Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2019158	tatcgaagcaatctgg[A/G]atttccacccttcatg	A	G	// 259234 // Homo sapiens Down syndrome critical region gene 10 (DSCR10), mRNA. /// NM_002243 // upstream //	DSCR10	DSCR10, Homo sapiens Down syndrome critical region gene 10 (DSCR10), q22.13
SNP_A-2150760	atgtgctcgcataaca[C/G]tatgttaaaggtacta	C	G	ENST00000311590 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-2064663	aattctccattatgaa[A/T]gtgaatgtccaattaa	A	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2891198 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1660839	tgtgtgatgggcacctgatctacac[C/G]aagagaacagggctgtctgcagaag	C	G	// paired box gene 6 (aniridia, keratitis) /// NM_001604 // upstream // 16465 // Hs.89506 // PAX6 // 5080 // paired box	PAX6	PAX6 , rs1806162, paired box gene 6 (aniridia, keratitis) ,p13
SNP_A-2087853	actggagatgtggtaa[C/T]agacaaacactccctt	C	T	-- /// ENST00000217206 // downstream // 77244 // --- // --- // --- // --- /// ENST00000262487 // upstream // 26581 // --- // --- // --	-	p12.1
SNP_A-2110249	aggaagttttattatg[A/C]aaaggcaaaatcctca	A	C	-- /// ENST00000355517 // downstream // 645896 // --- // --- //	-	q24.32
SNP_A-2135514	atattttaaaaatgca[A/G]acttattttgtgctcc	A	G	123016 // Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, mRNA. /// NM_198309 //	TTC8	TTC8, Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, q32.11
SNP_A-2280639	gaggtcataaatgcca[C/T]agatcaaaccagcccc	C	T	56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 200533 // Hs.315186 // PCSK2 //	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-1879006	tcttaacagaaaaaaa[A/G]tagaagttcacagatg	A	G	// Homo sapiens ribosomal protein S20 (RPS20), mRNA. /// NM_005372 // downstream // 1269 // Hs.533432 // MOS //	RPS20	RPS20, Homo sapiens ribosomal protein S20 (RPS20), q12.1
SNP_A-2030970	aaaggactatctttga[C/G]actctaagacgattct	C	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1813020	gtgggtctcgggaaga[C/T]gctgcactgcctctac	C	T	Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// ENST00000262861 // intron // 0 // --- // -- // --- // --- /// ENST00000308942 // intron // 0 // --- // --- //	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-2084171	actaggatctcaatca[C/T]taacatcattcaagtg	C	T	356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 //	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-2255361	cttgtatctgggaggc[A/T]ctcataattatgctga	A	T	Homo sapiens T, brachyury homolog (mouse) (T), mRNA. /// NM_175922 // downstream // 4830 // Hs.119062 //	T	T, Homo sapiens T, brachyury homolog (mouse) (T), q27
SNP_A-2211939	ccctgaagttgactgc[A/G]cctgttaataaccagt	A	G	Homo sapiens pleckstrin homology domain containing, family A member 2 (PLEKHA7), mRNA. /// ENST00000355661 // intron // 0 // --- // --- // --- // ---	PLEKHA7	PLEKHA7, Homo sapiens pleckstrin homology domain containing, family A member 2 (PLEKHA7), p15.1
SNP_A-1987870	tacttgtcaacagata[C/T]atggaattcagaatgc	C	T	Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // intron // 0 // --- // --- // --- // ---	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-1847090	tatcatcacagtttca[A/G]gttttgagggatcact	A	G	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA. /// ENST00000356504 // intron //	GABRA2	GABRA2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), p12
SNP_A-1824757	taaagaggtgctcagt[A/G]aatgatgaaacatgtc	A	G	// Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 245954 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1716923	tagttagcagctcccttgtgtattc[A/T]ctatgtatgtaaaatctgtttgctc	A	T	// 6885 // mitogen-activated protein kinase kinase kinase 7 /// NM_004440 // downstream // 1622046 // Hs.73962 // EPHA7	MAP3K7	MAP3K7 , rs10485102, mitogen-activated protein kinase kinase kinase 7 ,q15
SNP_A-1701519	ttagcttccttcagcacagctgaaa[C/G]ggtgttggagtgttctcagtcccaa	C	G	7050 // TGFB-induced factor (TALE family homeobox) /// NM_033546 // downstream // 41979 // Hs.511744 // MRLC2 //	TGIF	TGIF , rs10502313, TGFB-induced factor (TALE family homeobox) ,p11.31
SNP_A-2010479	gtttggaaatcaagga[C/T]tagaacaaagcccaaa	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1480913 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1868707	tcctcttacctgcacc[A/G]ctggaacccttccctt	A	G	// 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRNA. /// AF263744 // downstream // 12149 //	ERBB2IP	ERBB2IP, Homo sapiens erbb2 interacting protein (ERBB2IP), q12.3
SNP_A-1941688	ttggaaggatgatgta[G/T]gccacagccaaagcct	G	T	Homo sapiens ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) (UBE2H), transcript variant 1, mRNA. /// NM_182697 // intron // 0 // Hs.344165 // UBE2H // 7328 //	UBE2H	UBE2H, Homo sapiens ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) (UBE2H), transcript variant 1, q32.2
SNP_A-2041729	aacgtcatgaagtcac[C/T]gggggctgtctctagg	C	T	ENST00000358852 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1985176	tctctgggatgaatca[C/T]ctcatatgccactggg	C	T	9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 456929 // Hs.269059 // JARID2 //	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2302347	gctaagatttatagac[G/T]gagatccctggaaggc	G	T	Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA. /// NM_182977 // intron // 0 // Hs.482043 //	NNT	NNT, Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), p12
SNP_A-2075797	acatgtagagcttccc[A/G]cataactgccactaac	A	G	CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 434140 // Hs.522891 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1805493	gtccagagcaaagcaa[C/T]gtcttcaccatcagac	C	T	6496 // Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA. /// NM_016932 // downstream //	SIX3	SIX3, Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), p21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1750195	agcagtaactcaggagtatctaaag[A/G]aaggagggtagatggagaacaagaa	A	G	58475 // membrane-spanning 4-domains, subfamily A, member 7 /// NM_032597 // upstream // 38389 // Hs.28514 //	MS4A7	MS4A7 , rs1373062, membrane-spanning 4-domains, subfamily A, member 7 ,q12.2
SNP_A-2167154	caacacagtccgtggg[C/T]catgttcctccatgca	C	T	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1855122	tcaagagcttgaaccc[C/T]actgggacaatgaaga	C	T	145497 // Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), mRNA. /// ENST00000216453 //	C14orf166B	C14orf166B, Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), q24.3
SNP_A-2219753	ccttaattgaaagacc[A/T]gcaaatactttgtagc	A	T	COL4A3BP // 10087 // Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) binding protein (COL4A3BP), transcript variant 2, mRNA. /// NM_005713 // upstream //	COL4A3BP	COL4A3BP, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) binding protein (COL4A3BP), transcript variant 2, q13.3
SNP_A-1952944	tttcttcatgatgtta[C/T]gttatcaaaataaata	C	T	Homo sapiens WW domain containing E3 ubiquitin protein ligase 2 (WWP2), transcript variant 2, mRNA. /// NM_007014 // intron // 0 // Hs.408458 // WWP2 // 11060 // Homo sapiens	WWP2	WWP2, Homo sapiens WW domain containing E3 ubiquitin protein ligase 2 (WWP2), transcript variant 2, q22.1
SNP_A-2259202	gaaaaacaatatgaga[A/G]aatgacaacttgagaa	A	G	SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2094575	agaatacatcaacaaa[A/G]tggagaagaaggtgcc	A	G	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. ///	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-2027347	aaacatgagttgaaag[A/G]aagtttgaatggctat	A	G	5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// NM_173062 // upstream //	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin q15
SNP_A-1948199	tttagccatgtcaaga[G/T]aatataccttgcttag	G	T	// 56256 // Homo sapiens SERTA domain containing 4 (SERTAD4), mRNA. /// NM_018194 // upstream // 82647 //	SERTAD4	SERTAD4, Homo sapiens SERTA domain containing 4 (SERTAD4), q32.2
SNP_A-2141942	atctttaacaaatagt[A/G]acagtatgctcaaatc	A	G	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 936014 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2279438	gaggatagagaattga[C/T]gagttttgagtaaggc	C	T	Homo sapiens sialyltransferase 8B (alpha-2, 8-sialyltransferase) (SIAT8B), mRNA. /// ENST00000268164 //	ST8SIA2	ST8SIA2, Homo sapiens sialyltransferase 8B (alpha-2, 8-sialyltransferase) (SIAT8B), q26.1
SNP_A-2293856	gcagctgtaaatacta[C/T]gtaagttatcagtaag	C	T	255631 // Homo sapiens collagen, type XXIV, alpha 1 (COL24A1), mRNA. /// ENST00000302772 // upstream //	COL24A1	COL24A1, Homo sapiens collagen, type XXIV, alpha 1 (COL24A1), p22.3
SNP_A-2138144	atccaatgccacaaca[C/T]ggccccgcagtttca	C	T	// 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 139014 // Hs.31664 //	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2001165	aacatcttgggtataa[A/G]aattagctttctattg	A	G	65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 646280 // Hs.42650 // ZWINT	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1989939	ctgccatcattttaag[G/T]aatgtttcctggagag	G	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// ENST00000360955 // upstream // 118954 // --- // --- // --- // ---	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2163231	atttttgagatgcaaa[A/G]aactgcttcccctgaa	A	G	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2),	ENPP2	ENPP2, Homo sapiens ectonucleotide pyrophosphatase,q24.12
SNP_A-1948698	tttatagagacaggga[A/G]aaaataagtggaggaa	A	G	220032 // Homo sapiens GDPD domain containing protein (LOC220032), mRNA. /// ENST00000315938 // intron // 0 // ---	LOC220032	LOC220032, Homo sapiens GDPD domain containing protein (LOC220032), q13.5
SNP_A-1886472	tgactaaagaacccca[C/T]tggagacttaggaggc	C	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1950877	tttccaaggcactaaa[A/T]cttgtgtgactcaaaa	A	T	// 400360 // Homo sapiens FLJ39531 protein (FLJ39531), mRNA. /// ENST00000358555 // upstream // 73408 // --- // ---	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ39531), q14
SNP_A-1848979	tatgcagacctttaca[C/T]tccatcataactaata	C	T	Homo sapiens zinc finger protein 638 (ZNF638), mRNA. /// ENST00000264447 // intron // 0 // --- // --- // --- // --- ///	ZNF638	ZNF638, Homo sapiens zinc finger protein 638 (ZNF638), p13.2
SNP_A-1947829	tttacttagagcccaa[A/G]catctggtgacttttc	A	G	79947 // Homo sapiens dehydrodolichyl diphosphate synthase (DHDDS), transcript variant 1, mRNA. /// NM_205861 // downstream // 6224 // Hs.369385 // DHDDS //	DHDDS	DHDDS, Homo sapiens dehydrodolichyl diphosphate synthase (DHDDS), transcript variant 1, p36.11
SNP_A-2190904	catagcattgttataa[G/T]gattaaacaagttata	G	T	sapiens vascular endothelial growth factor (VEGF), mRNA. /// ENST00000324450 // intron // 0 // --- // --- // --- // --- ///	VEGF	VEGF, Homo sapiens vascular endothelial growth factor (VEGF), p21.1
SNP_A-1962568	cataacattggtgaaa[C/T]ctgacttcagtccagg	C	T	30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds. ,p23.1
SNP_A-2252612	cttccttcctagttgg[C/T]cacctgtacactccat	C	T	Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, mRNA. /// NM_198717 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens	PTGER3	PTGER3, Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, p31.1
SNP_A-2058221	aatcaacctgcattcc[A/G]ctggtaactacattaa	A	G	-- /// ENST00000314071 // upstream // 421911 // --- // --- // ---	-	p13.3
SNP_A-1885187	tgaattcatttgtaaa[C/T]catttatagtgtttat	C	T	/// ENST00000358773 // upstream // 259966 // --- // --- // --- // -- /// ENST00000357286 // upstream // 398588 // --- // --- // ---	-	q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2057702	aatatggtttgatcca[G/T]aatgaatatctactca	G	T	Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-1984555	taagttgcacaaggtc[A/T]cacagcaggagtgtaa	A	T	// Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// NM_004137 // downstream // 71835 // Hs.484099 // KCNMB1	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-2312056	ggacacatttagagaa[A/G]tgcaaaatgaactgga	A	G	// 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 29198 // Hs.436387 // BCKDHB	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-2060522	aatgacctcgataccc[A/G]agtagtgagcacagta	A	G	Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-2040853	aacccctaggatctgc[A/G]ctttgataacactttg	A	G	22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 373118 //	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2309029	gcttttctttctacac[A/G]acacacatacccaggt	A	G	23456 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 10 (ABCB10), nuclear gene encoding	ABCB10	ABCB10, Homo sapiens ATP-binding cassette, sub-family B (MDR,q42.13
SNP_A-2006218	gccccgactaatgcaa[C/T]cttaatttcccagggg	C	T	sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // --- // --- // --- // --- ///	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2166292	caaatcctagtttcac[C/T]atttaaccaatattag	C	T	29974 // Homo sapiens apobec-1 complementation factor (ACF), transcript variant 2, mRNA. /// NM_138933 //	ACF	ACF, Homo sapiens apobec-1 complementation factor (ACF), transcript variant 2, q11.23
SNP_A-1955254	tttggcttaggtcctc[C/T]gacaatgcagtgcttt	C	T	132864 // Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, mRNA. /// NM_182485 // downstream // 74260 // Hs.374216	CPEB2	CPEB2, Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, p15.33
SNP_A-1954294	tttgcaccgagcagac[C/T]ggtggccaatggagga	C	T	// 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1810537	gtgatttttagcaaag[A/G]aggaggcaggctgatg	A	G	ENST00000334388 // intron // 0 // --- // --- // --- // ---	-	p11.23
SNP_A-2301702	gcgcggcctggagcca[G/T]tctgtctgcatcttta	G	T	662 // Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 1 (BNIP1), transcript variant BNIP1,	BNIP1	BNIP1, Homo sapiens BCL2,q35.1
SNP_A-2039823	aacattcaaggccacc[A/G]agaaaaatgaaacaac	A	G	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 882588 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2074483	acatagaggtatgaaa[C/T]aatgaatttgtgttat	C	T	392636 // Homo sapiens FLJ16237 protein (FLJ16237), mRNA. /// ENST00000342526 // intron // 0 // --- // --- // --- // ---	FLJ16237	FLJ16237, Homo sapiens FLJ16237 protein (FLJ16237), p21.1
SNP_A-2108609	agctgggctgtcaaac[C/T]ggaatgacagaaaaaa	C	T	1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // upstream // 185413 //	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1843958	tagttccaaatatcaa[A/G]aagtgtgtgatctatg	A	G	2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// NM_000408 //	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-1905440	tggtaatggactccaa[C/T]atccagactgacttct	C	T	2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2107506	agctagcgttgtgcaa[A/G]tgtccgttccctgctt	A	G	sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), transcript variant 1, mRNA. /// NM_138931 // intron //	BCL6	BCL6, Homo sapiens B-cell CLL,q27.3
SNP_A-1952086	ctggcaattccagccc[A/G]ccgtggcttgtgaact	A	G	-- /// ENST00000360285 // downstream // 616093 // --- // --- // -- // --- /// ENST00000339882 // downstream // 616093 // --- //	-	q12
SNP_A-1904573	tggggcaccttctgga[C/G]cagctaagttgacaca	C	G	5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// NM_005012 // upstream // 92927 // Hs.436456 //	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2167662	caaccagcggaatgac[A/G]cagaagccgaagggaa	A	G	284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 257276 //	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2271496	gaccaaagataaagaa[A/G]tggtgtctctgataaa	A	G	// Homo sapiens receptor-interacting factor 1 (RIF1), mRNA. /// NM_178454 // downstream // 103096 // Hs.485606 //	RIF1	RIF1, Homo sapiens receptor-interacting factor 1 (RIF1), p13.3
SNP_A-1980063	aggtctttacccacaa[C/G]tcatttttctcagttg	C	G	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1270175 // --- // --- // --- ///	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1805355	gtccaacaggcacaca[A/G]taacacttggggtact	A	G	57097 // Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), mRNA. /// NM_001759 // upstream // 349996 // Hs.376071 // CCND2 // 894 // Homo sapiens cyclin	PARP11	PARP11, Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), p13.32
SNP_A-2078552	accatgcaattctgga[A/G]gcatatttttcccaag	A	G	57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // upstream //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2260163	gaaaatcttataagag[C/T]agcagtaatggcagag	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3884899 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2010146	aaagaggaagccaaca[C/T]cttgagtgcattttaa	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2201634 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2274251	tcctcctaaggctgaa[C/T]aggtcggcttgattct	C	T	Homo sapiens EH-domain containing 4 (EHD4), mRNA. /// ENST00000220325 // intron // 0 // --- // --- // --- // ---	EHD4	EHD4, Homo sapiens EH-domain containing 4 (EHD4), q15.1
SNP_A-1906556	tggtggtctctccaca[C/T]ggatgcgcgtgaaagg	C	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 452482	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1973899	tcaaatcaaacactca[C/T]atcaatctctctgaaa	C	T	/// ENST00000331815 // downstream // 263743 // --- // --- // ---	-	q13.13
SNP_A-2296749	gccaaatttttaattg[C/G]aaaattcatctctgaa	C	G	254170 // Homo sapiens F-box protein 33 (FBXO33), mRNA. /// ENST00000298097 // upstream // 637136 // --- // --- // --- // ---	FBXO33	FBXO33, Homo sapiens F-box protein 33 (FBXO33), q21.1
SNP_A-1867932	tcctagagaggataat[C/G]aggtaacagcagagct	C	G	23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 577793	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2008428	ccactctctgcttaaa[C/T]tgctccattaacactt	C	T	Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1937288	ttgaaactctcctcca[C/T]tgatgatattggtcag	C	T	19 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// NM_022109 //	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-2070096	acacatatttgcgttc[A/G]ccacatacagtacaca	A	G	Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// ENST00000260197 // intron // 0 // --- // --- // --- // ---	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q23.3
SNP_A-2213302	ccgcttaggagagccc[A/G]aaacgagcaggctgga	A	G	158471 // Homo sapiens chromosome 9 open reading frame 65 (C9orf65), mRNA. /// ENST00000286521 // upstream //	C9orf65	C9orf65, Homo sapiens chromosome 9 open reading frame 65 (C9orf65), q21.2
SNP_A-2238071	ctctgcactgagctaa[A/G]gaggtaagagtagaaa	A	G	5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// NM_017935 // upstream // 358532 //	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1798829	aatggagctgaaaaga[C/T]aaaagcagagctgaga	C	T	9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 60796 // Hs.458423	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-2074884	acatcacgctgaagac[A/G]ccccacggggactaca	A	G	sapiens arachidonate 5-lipoxygenase (ALOX5), mRNA. /// ENST00000265455 // CDS // 0 // --- // --- // --- // ---	ALOX5	ALOX5, Homo sapiens arachidonate 5-lipoxygenase (ALOX5), q11.21
SNP_A-2162689	attttcttgtttgtta[C/T]taaatgcagacaactt	C	T	Homo sapiens rabconnectin-3 (RC3), mRNA. /// ENST00000251076 // intron // 0 // --- // --- // --- // ---	DMXL2	DMXL2, Homo sapiens rabconnectin-3 (RC3), q21.2
SNP_A-1840384	tagcatttatgtaaat[C/G]aaaaccactgacacta	C	G	// Homo sapiens leukemia inhibitory factor receptor (LIFR), mRNA. /// NM_003999 // upstream // 169959 // Hs.120658 //	LIFR	LIFR, Homo sapiens leukemia inhibitory factor receptor (LIFR), p13.1
SNP_A-2272135	gaccgtaggggatgac[A/G]gataacaatgtagggg	A	G	56956 // Homo sapiens partial mRNA for LIM-homeobox 9 (LHX9 gene). /// NM_020204 // downstream // 246661 //	LHX9	LHX9, Homo sapiens partial for LIM-homeobox 9 (LHX9 gene). ,q31.3
SNP_A-2286052	ttaggctttggttcca[A/G]taagttctcgtgtatg	A	G	Homo sapiens aldehyde dehydrogenase 1 family, member A2 (ALDH1A2), transcript variant 2, mRNA. /// NM_003888 // intron // 0 // Hs.435689 // ALDH1A2 // 8854 // Homo sapiens	ALDH1A2	ALDH1A2, Homo sapiens aldehyde dehydrogenase 1 family, member A2 (ALDH1A2), transcript variant 2, q21.3
SNP_A-1968782	tttttctttcctattc[A/T]atttctatggtcaggt	A	T	Homo sapiens chromosome 20 open reading frame 43 (C20orf43), mRNA. /// ENST00000023939 // intron // 0 // --- //	C20orf43	C20orf43, Homo sapiens chromosome 20 open reading frame 43 (C20orf43), q13.31
SNP_A-2141436	atctgttttattgtgc[C/T]cattttacagatgagg	C	T	51339 // Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), mRNA. /// NM_014992 // upstream // 416960 // Hs.19156 // DAAM1 // 23002 // Homo	DACT1	DACT1, Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), q23.1
SNP_A-1994006	gtcttccatcccacac[C/T]gtagcaggagaggaga	C	T	7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 195912 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1872889	tctatcactgtgcaac[A/G]ctcattccttccaagc	A	G	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2218967	cctggtctgtgtctta[C/T]catctgcagaccacgt	C	T	4254 // Homo sapiens KIT ligand (KITLG), transcript variant a, mRNA. /// NM_000899 // upstream // 459064 // Hs.1048 //	KITLG	KITLG, Homo sapiens KIT ligand (KITLG), transcript variant a, q21.33
SNP_A-1971827	gaagcataaagatgac[C/T]gggtgccctgaatgac	C	T	// 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2205274	ccagtcacactcctta[C/T]aaatcagaggtaaaat	C	T	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// ENST00000286657 // intron // 0 // --- // --- // --- // ---	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1900796	aaaccccaaatcatac[A/G]acataacagtaggtta	A	G	/// ENST00000334919 // upstream // 131862 // --- // --- // --- // --- /// ENST00000322194 // downstream // 1637287 // --- // ---	-	q12.2
SNP_A-2201135	ccaagtgacatttaaa[A/C]tcagtagaggaaaaat	A	C	51691 // Homo sapiens LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM8), mRNA. /// NM_019644 // upstream // 5377 // Hs.371820 // ANKRD7 //	LSM8	LSM8, Homo sapiens LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM8), q31.31
SNP_A-2163721	caaaaatgatctttgc[A/G]ctgatctccagggcat	A	G	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-2243241	ctgcctgcagaacaca[A/T]tgaacaggaaatgcag	A	T	Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// ENST00000262095 // intron // 0 // ---	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-2140830	atctgaaatttacact[C/T]acttcttaccagcctc	C	T	ENST00000299308 // intron // 0 // --- // --- // --- // ---	-	q24.31
SNP_A-2239312	ctctttagccttctgg[A/G]aaaatgaatgaggaat	A	G	Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 //	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-2261529	gaaaggcagtattaaa[A/G]ttcacgatcaaaatct	A	G	ENST00000281741 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1991208	ctgagacttcataaaa[A/C]tatcatatgtgcttaa	A	C	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-1866172	tcccaggctcggggaa[C/T]tgaacctttcccacac	C	T	Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2), mRNA. /// ENST00000246229 // intron // 0 // --- // --- // --- // ---	PLAGL2	PLAGL2, Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2), q11.21
SNP_A-2138863	atccctctgccctaaa[A/G]aagtagacaatcgtat	A	G	Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), mRNA. /// U05012 // intron // 0 // Hs.410969 //	NTRK3	NTRK3, Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), q25.3
SNP_A-1972462	ctcctatcttgagagt[A/G]aaagcaagtccttcca	A	G	// 956 // Homo sapiens ectonucleoside triphosphate diphosphohydrolase 3 (ENTPD3), mRNA. /// NM_173656 // upstream // 31987 // Hs.407159 // ZNF619 // 285267 // Homo	ENTPD3	ENTPD3, Homo sapiens ectonucleoside triphosphate diphosphohydrolase 3 (ENTPD3), p22.1
SNP_A-1718065	tgtggcatatacttacacagacata[A/G]ataagatggagacctgccctcagtg	A	G	AF330045 // intron // 0 // Hs.5978 // LMO7 // 4008 // LIM domain only 7	LMO7	LMO7 , -, LIM domain only 7,q22.2
SNP_A-2135239	ttcaatatcttgtcca[A/G]agttattgctagcgtt	A	G	9445 // Homo sapiens integral membrane protein 2B (ITM2B), mRNA. /// NM_000321 // upstream // 39023 //	ITM2B	ITM2B, Homo sapiens integral membrane protein 2B (ITM2B), q14.2
SNP_A-2305796	gctgcgagtcctgagc[A/G]ccggaatgaaaacttg	A	G	55197 // Homo sapiens hypothetical protein FLJ10656 (P15RS), mRNA. /// NM_018170 // upstream // 18222 //	P15RS	P15RS, Homo sapiens hypothetical protein FLJ10656 (P15RS), q12.2
SNP_A-1645722	gggatttgttccataaagaataaac[A/C]agcaaagattgagattatacttagc	A	C	5983 // replication factor C (activator 1) 3, 38kDa /// NM_005584 // downstream // 1059067 // Hs.239506 //	RFC3	RFC3 , rs942591, replication factor C (activator 1) 3, 38kDa ,q13.2
SNP_A-2155142	attcagatgctcacaa[C/T]gccctaaggtctcttg	C	T	356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 //	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-1936751	ttctttagtcatcaac[C/T]atgaccttcccaccaa	C	T	2321 // Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mR /// NM_015932 // upstream // 59244 //	FLT1	FLT1, Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor,q12.3
SNP_A-1788200	gggagctaaagagtga[A/G]aacacatggacacata	A	G	// 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// NM_031415 // downstream //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2290734	gcaagcaaacctagaa[C/G]agtgctggaccactca	C	G	// 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 169844 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-1876044	tctgaataggctgaca[C/T]atccttacaaaaggag	C	T	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31
SNP_A-2278804	gagcttgggctggaga[A/C]cctgtactacatcttc	A	C	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 197095 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2002469	ctctgtcatttatgca[A/G]cagttatcaccagaat	A	G	Homo sapiens Rab6-interacting protein 2 (ELKS), transcript variant alpha, mRNA. /// NM_178037 // intron // 0 //	RAB6IP2	RAB6IP2, Homo sapiens Rab6-interacting protein 2 (ELKS), transcript variant alpha, p13.33
SNP_A-1868307	tcctcagtctgtccca[C/G]gttgccaccatttttc	C	G	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 //	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.4
SNP_A-1914058	tgtgtggattgcaggc[C/T]gaccacgtgtattatt	C	T	Homo sapiens branched chain aminotransferase 2, mitochondrial (BCAT2), mRNA. /// ENST00000316273 // intron // 0 // --- // --- // --- // ---	BCAT2	BCAT2, Homo sapiens branched chain aminotransferase 2, mitochondrial (BCAT2), q13.33
SNP_A-2088157	actgggtaaatttgag[C/T]aaatggtattctcttt	C	T	3925 // Homo sapiens stathmin 1/oncoprotein 18 (STMN1), transcript variant 1, mRNA. /// NM_005563 // upstream //	STMN1	STMN1, Homo sapiens stathmin 1,p36.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1795269	ggtgagtgtcagtcag[A/G]acatggagaactcaga	A	G	388325 // Homo sapiens DTFT5783 (UNQ5783), mRNA. /// NM_004703 // upstream // 27778 // Hs.536036 // RABEP1 //	UNQ5783	UNQ5783, Homo sapiens DTFT5783 (UNQ5783), p13.2
SNP_A-2129406	atacaagtctttgtta[C/T]gatcatttaaatacac	C	T	// 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2097493	agagaactggggacca[C/T]tgaggaaaggatcagg	C	T	54984 // Homo sapiens PIN2-interacting protein 1 (PINX1), mRNA. /// NM_173683 // downstream // 26255 // Hs.353115	PINX1	PINX1, Homo sapiens PIN2-interacting protein 1 (PINX1), p23.1
SNP_A-1828013	taagaatagcttccaa[C/T]tcagatctataaacaa	C	T	// 9910 // Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), mRNA. /// ENST00000309140 // upstream	RABGAP1L	RABGAP1L, Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), q25.1
SNP_A-2277167	gagatggtgccattgg[C/G]cattgctatcctagtt	C	G	Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000327152 // intron // 0 // --- // --- // --- // --- ///	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-2088132	actggggagactcaca[A/C]actctgggtggtagca	A	C	Homo sapiens glutathione S-transferase M5 (GSTM5), mRNA. /// ENST00000256593 // intron // 0 // --- // --- // --- // ---	GSTM5	GSTM5, Homo sapiens glutathione S-transferase M5 (GSTM5), p13.3
SNP_A-1700971	cagaagatacatacagctaatgaca[A/G]tctaagggagaatttcaggaaggat	A	G	NM_001270 // upstream // 25314 // Hs.311553 // CHD1 // 1105 // chromodomain helicase DNA binding protein 1	CHD1	CHD1 , rs10515285, chromodomain helicase DNA binding protein 1,q21.1
SNP_A-2275105	gagaagactcagatag[A/C]catagccattttcaat	A	C	8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 511982 // --- // --- // --- //	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2283553	gatactttgcagttat[A/G]aaaagaatgatgagtc	A	G	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 745261 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2125933	agttttactatttgtt[C/G]aaagtgtctgccactt	C	G	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 599081 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1992121	aaatttccttcagtga[C/T]actttctagttttcag	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 15572 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.1
SNP_A-1902655	tggctaacatgcaaca[C/T]tggcatactaggatac	C	T	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 907616 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-1833716	tacagggtttgccatg[C/T]caaaagataaacaaag	C	T	54810 // Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA. /// NM_000959 // upstream // 69520 // Hs.292843 //	GIPC2	GIPC2, Homo sapiens PDZ domain protein GIPC2 (GIPC2), p31.1
SNP_A-1985584	gcagatggaaggtggc[A/G]ctgcaagcatttcagg	A	G	Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA. /// ENST00000236452 // intron // 0 // --- // --- // --- // ---	FLJ22390	FLJ22390, Homo sapiens hypothetical protein FLJ22390 (FLJ22390), q41
SNP_A-2275566	gagacacagatgggga[G/T]attttccaagcaattc	G	T	// 55278 // Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), mRNA. /// NM_016487 // upstream // 36117 // Hs.486084 // C6orf203 //	QRSL1	QRSL1, Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), q21
SNP_A-2055103	aataacagcaacagca[A/C]aacacagcattttatt	A	C	4254 // Homo sapiens KIT ligand (KITLG), transcript variant a, mRNA. /// NM_000899 // upstream // 169828 // Hs.1048 //	KITLG	KITLG, Homo sapiens KIT ligand (KITLG), transcript variant a, q21.33
SNP_A-1970675	catctactgtggcaaa[C/T]acgtacacacaagcat	C	T	// Homo sapiens solute carrier family 25 (mitochondrial carrier), member 18 (SLC25A18), mRNA. /// ENST00000327451 // intron // 0 // --- // --- // --- // ---	SLC25A18	SLC25A18, Homo sapiens solute carrier family 25 (mitochondrial carrier), member 18 (SLC25A18), q11.21
SNP_A-2155188	attcagctactcaaaa[C/G]aaatacaccggtcaga	C	G	MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 586489 // Hs.314261 //	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q32
SNP_A-2219673	ccttaacaccaaagct[C/T]agcctgccagacttcc	C	T	2030 // Homo sapiens solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), mRNA. /// NM_004955 // downstream // 474 // Hs.25450 // SLC29A1 // 2030 // Homo	SLC29A1	SLC29A1, Homo sapiens solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), p21.1
SNP_A-1864411	tccactgtggaaactc[A/G]ctgagcccggcatttt	A	G	2074 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), mRNA. /// NM_000124 // upstream // 31676 // Hs.133444 //	ERCC6	ERCC6, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), q11.23
SNP_A-2307990	gcttcttgaaggttgg[A/G]atcggaggctcatcca	A	G	CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 533326 // Hs.522891 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2247590	ctgtcttcaatgctaa[C/T]acaaatgtcctgaaaa	C	T	Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1870494	tcgacaggccatacac[A/T]gtatatagcttgtgaa	A	T	Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA. /// ENST00000264211 // intron //	EIF4G3	EIF4G3, Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), p36.12
SNP_A-2262912	gaacaaattctggcca[A/G]tgattgcccggattga	A	G	ENST00000358277 // intron // 0 // --- // --- // --- // ---	-	q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1833326	tacagaaaaaagtgca[C/T]ataattgtctctgaaa	C	T	Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // intron // 0 // --- //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.3
SNP_A-1972522	ttcaggcaagaccttg[A/C]attcctggagcatttc	A	C	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 81853 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-2246152	ctggtctggtgatgta[C/T]attgagagccctacga	C	T	Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA. /// ENST00000356218 // intron // 0 // --- //	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-1816726	gttatcagttaataaa[C/T]tcagggaggcttgttc	C	T	Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // --- //	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-1670878	cccttcttgaagatgacgaggaaca[C/G]gagctggaagctgcagggaagcatc	C	G	NM_018836 // upstream // 648112 // Hs.25924 // SHREW1 // 55966 // transmembrane protein SHREW1	SHREW1	SHREW1 , rs3935559, transmembrane protein SHREW1,p36.32
SNP_A-2204384	ccagcgttgacagagc[A/G]gaggccagtatcctgg	A	G	HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 208132 // Hs.120831 // TNT //	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2270723	gacagcttaccttcac[A/G]gtactccttttacaga	A	G	FLJ32112 // 127428 // Homo sapiens hypothetical protein FLJ32112 (FLJ32112), mRNA. /// NM_201546 // downstream	FLJ32112	FLJ32112, Homo sapiens hypothetical protein FLJ32112 (FLJ32112), p32.3
SNP_A-1869762	tccttcatattagtca[A/G]agaaaacctatgatat	A	G	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2302072	gcgttaacagcgacta[C/T]gagacggacggcgagg	C	T	sapiens tight junction protein 3 (zona occludens 3) (TJP3), mRNA. /// ENST00000262968 // CDS // 0 // --- // --- // --- // ---	TJP3	TJP3, Homo sapiens tight junction protein 3 (zona occludens 3) (TJP3), p13.3
SNP_A-1830213	taatagggcccctcca[C/T]gtagtgtacttctact	C	T	MGC88374 // 440184 // Homo sapiens similar to CG32662-PA (MGC88374), mRNA. /// ENST00000310149 // upstream	MGC88374	MGC88374, Homo sapiens similar to CG32662-PA (MGC88374), q23.3
SNP_A-2007390	tcttaagaccatggaa[A/G]aagtaaaacaaactaa	A	G	Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000304791 // intron // 0 // --- //	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1986380	agtgatctggcagaaa[A/G]aattcaatagggataa	A	G	Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // 3UTR // 0 // Hs.4273 //	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-1645524	gaaatacattgcttaaacataataa[A/C]ataaaatcacaaaacccaattgaca	A	C	2572 // glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa) /// NM_019043 // upstream // 32408 //	GAD2	GAD2 , rs10508718, glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa) ,p12.1
SNP_A-2112142	aggattactgggagat[A/G]acaagaacattagttt	A	G	-- /// ENST00000314058 // upstream // 105432 // --- // --- // ---	-	p13.2
SNP_A-2040037	aacatttttcatttcc[A/G]aagcccagaaagcaac	A	G	BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 284878 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-2237767	ctctcttcttgctaca[A/G]atatttacttctgtat	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 268696 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2224869	cgtgcaggcatgacac[C/G]caaattcatgacgtgt	C	G	2802 // Homo sapiens golgi autoantigen, golgin subfamily a, 3 (GOLGA3), mRNA. /// NM_018223 // downstream // 5553 //	GOLGA3	GOLGA3, Homo sapiens golgi autoantigen, golgin subfamily a, 3 (GOLGA3), q24.33
SNP_A-2006482	ttttaaaataataatg[A/C]cagcataatctttatt	A	C	130951 // Homo sapiens hypothetical protein BC014602 (LOC130951), mRNA. /// ENST00000290536 // intron // 0 // ---	LOC130951	LOC130951, Homo sapiens hypothetical protein BC014602 (LOC130951), p13.1
SNP_A-2108987	agcttcaatctctgcc[C/T]ggatgatattgggcaa	C	T	3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 284127 // Hs.118695 // KCNG1	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2139295	atcctgcaatggaaaa[C/T]agaaaagaatgaagga	C	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2045360	aagaagttggataaat[G/T]atgacaagactttcac	G	T	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // downstream // 5309 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1695099	caaaacctttaactcctactatata[C/T]ataaaaacgtccccttctctcccac	C	T	hemicentin	FIBL-6	FIBL-6 , rs10489718, hemicentin,q31.1
SNP_A-2120652	agtccctcatggaccc[C/T]agagacaagaagaaag	C	T	FLJ16641 // 389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// ENST00000314241 // downstream //	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-1838124	tagaacagtggcttgc[A/G]cataatagatacacca	A	G	// Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 121573 // Hs.546432 // SRD5A2L // 79644 //	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-2028932	aaacttttgtgaaata[C/T]acctgataaaagttta	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1673944	gaaactagatactattatacagaca[C/T]tgacgattacagaggttaaggaggt	C	T	// 26047 // contactin associated protein-like 2 /// NM_022445 // upstream // 596604 // Hs.127548 // TPK1 // 27010 // thiamin	CNTNAP2	CNTNAP2 , rs850399, contactin associated protein like 2 ,q35
SNP_A-2191067	catagtaaaaatgtct[C/G]aaaatgtaaaatatca	C	G	/// ENST00000332119 // downstream // 331649 // --- // --- // ---	-	q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1792603	ggtaaagtccaggga[G/T]accaggcacaaactcc	G	T	/// ENST00000315208 // upstream // 407787 // --- // --- // --- //	-	q24.32
SNP_A-1815296	gtgtttaaaagaatta[A/G]aagtgatgagaagtgt	A	G	Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2255292	cttgtaaggtatctgg[C/T]atcattccataggtta	C	T	CYP2C19 // 1557 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 19 (CYP2C19), mRNA. /// NM_000771 // upstream // 49609 // Hs.282624 // CYP2C9 //	CYP2C19	CYP2C19, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 19 (CYP2C19), q23.33
SNP_A-1971493	gccttgcctctccgta[A/C]gtcctctgttaaaatg	A	C	// 9695 // Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), mRNA. /// ENST00000295399 // upstream // 171509 // --- // --- // --- // ---	EDEM1	EDEM1, Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), p26.1
SNP_A-2209907	ccccaaggaggaatca[C/G]gtaagggagatagaat	C	G	Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), mRNA. /// ENST00000297169 // intron // 0 // --- // ---	KCNK5	KCNK5, Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), p21.2
SNP_A-2219735	ccttaatctactacta[A/G]ccacctgtatcttcat	A	G	// Homo sapiens hypothetical protein FLJ36754 (FLJ36754), mRNA. /// ENST00000282964 // intron // 0 // --- // --- // --- // ---	FLJ36754	FLJ36754, Homo sapiens hypothetical protein FLJ36754 (FLJ36754), q12.3
SNP_A-2088055	actggctttctctgct[A/T]acacatgaccttacag	A	T	Homo sapiens chromosome 14 open reading frame 108 (C14orf108), mRNA. /// ENST00000261558 // intron // 0 // ---	C14orf108	C14orf108, Homo sapiens chromosome 14 open reading frame 108 (C14orf108), q22.3
SNP_A-1972386	ctgcttctgaacttcc[A/G]ggaaagagagaaataa	A	G	/// ENST00000301807 // downstream // 19651 // --- // --- // ---	-	p22.3
SNP_A-2293925	gcaggaaaatgcagaa[C/G]tgtttcatagtcccag	C	G	6566 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA. /// ENST00000285753 // upstream // 15387 // --- // ---	SLC16A1	SLC16A1, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), p13.2
SNP_A-2068350	acaagcttgccatgac[A/T]ggggagagctgataac	A	T	254170 // Homo sapiens F-box protein 33 (FBXO33), mRNA. /// ENST00000298097 // upstream // 331501 // --- // --- // --- //	FBXO33	FBXO33, Homo sapiens F-box protein 33 (FBXO33), q21.1
SNP_A-1793151	ggtagaagcaaattga[C/T]gatggtgaaatgtggc	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3814454 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2250359	cttagatttggtgtca[A/G]tcatggcctatgctcc	A	G	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2210458	ccccccttcttcttca[A/G]taatccctcccctcac	A	G	Homo sapiens pappalysin 2 (PAPPA2), transcript variant 1, mRNA. /// NM_021936 // 5UTR // 0 // Hs.187284 // PAPPA2 //	PAPPA2	PAPPA2, Homo sapiens pappalysin 2 (PAPPA2), transcript variant 1, q25.2
SNP_A-1718735	ggagaaatactttagagagggaaaa[G/T]agagacatatctcattctgcatttt	G	T	ADAMTS20 // 80070 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 /// NM_153026 // upstream // 671891 // Hs.6786 // PRICKLE1 //	ADAMTS20	ADAMTS20 , rs10506225, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 ,q12
SNP_A-2054920	aataaataaaagccaa[C/T]tggaggcaggcactct	C	T	FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-1726252	agacccagataaacacattaggtga[C/T]gccccaatttggagatagaccac aa	C	T	NM_021135 // intron // 0 // Hs.301664 // RPS6KA2 // 6196 // ribosomal protein S6 kinase, 90kDa, polypeptide 2	RPS6KA2	RPS6KA2 , rs10484528, ribosomal protein S6 kinase, 90kDa, polypeptide 2,q27
SNP_A-2097827	agagactgaaagagta[C/T]aggagatgcctgagga	C	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST00000359144 // downstream //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2078025	accagcttcacaagag[C/G]agaatgagacacagtt	C	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 611993 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2154449	attattcaagctaaaa[C/T]agtgtgtgtcttcatt	C	T	5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 735954 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-2310623	ggaagaggaaggagtc[A/C]aagatttctgaccaca	A	C	26986 // Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA. /// NM_002568 // upstream // 141307 //	PABPC1	PABPC1, Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), q22.3
SNP_A-1988496	aaaactgtgcatggca[C/T]gtgactttcccgtgat	C	T	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2291301	gcaatgatgctgactg[A/C]cacagtgaaggccgag	A	C	Homo sapiens ornithine decarboxylase-like (ODC-p), mRNA. /// ENST00000358680 // CDS // 0 // --- // --- // --- // --- ///	ODC-p	ODC-p, Homo sapiens ornithine decarboxylase-like (ODC-p), p35.1
SNP_A-2163341	atttttattttgttgg[C/T]attatagcatctatga	C	T	Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 2, mRNA. /// NM_007051 // intron // 0 // Hs.530402 // FAF1 // 11124 // Homo sapiens Fas (TNFRSF6)	FAF1	FAF1, Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 2, p32.3
SNP_A-2165147	caaagaaacaatgaca[A/T]ctctcaggaagagaaa	A	T	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 550458 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2166870	caaatttgaaacatac[A/G]aaatgatttatttgaa	A	G	9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream //	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1976364	ggaatcctcactgag[A/C]acataacttgtccctg	A	C	MGC15730 // 84966 // Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000355895 //	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-2114490	agggagaggaggatga[C/T]ggagggagtaaatata	C	T	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2076919	accaaataatttcta[A/G]ctgttcctcagggca	A	G	// 51218 // Homo sapiens chromosome 14 open reading frame 87 (C14orf87), mRNA. /// NM_020553 // upstream //	C14orf87	C14orf87, Homo sapiens chromosome 14 open reading frame 87 (C14orf87), q32.13
SNP_A-1833986	tacatagctacttcca[C/T]gttgcccagttaatat	C	T	FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000355115 //	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2250546	cttagtcataaggagag[G/T]ccctccacatgtgc	G	T	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 277922 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2215576	agagtcggataccagt[C/T]aacagtgattgtgatt	C	T	Homo sapiens chromosome 14 open reading frame 160 (C14orf160), mRNA. /// ENST00000261699 // intron // 0 // ---	C14orf160	C14orf160, Homo sapiens chromosome 14 open reading frame 160 (C14orf160), q21.3
SNP_A-2261033	gaaagaagcaaggagta[C/T]gccacaaaaatatgt	C	T	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA. /// ENST00000255266 // intron // 0 //	PDE6A	PDE6A, Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), q32
SNP_A-2141989	atcttatctatatga[A/T]cacttaagtacttttt	A	T	Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // --- // --- // --- // ---	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2032582	aaataaacatttcata[A/C]aacaatgcctatcct	A	C	// 23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream //	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-2079775	accctgacagtcatca[C/T]aatttgtatttctgaa	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1425258 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1905899	tggtcatttctgacaa[A/C]aaggccagaattaaca	A	C	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 364361 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-2185089	cagctttgtcctcaga[A/G]agaagccacccttgac	A	G	MAPRE1 // 22919 // Homo sapiens microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA. ///	MAPRE1	MAPRE1, Homo sapiens microtubule-associated protein, RP/EB family, member 1, p11.21
SNP_A-1677230	aagtaatgtacggttataacaaca[C/T]acacagaaataaaatatagaacaac	C	T	NM_024861 // upstream // 50190 // hs.193745 // FLJ22671 // 79919 // hypothetical protein FLJ22671	FLJ22671	FLJ22671 , rs4130554, hypothetical protein FLJ22671,q37.3
SNP_A-1789333	gggccagaagcccatc[C/T]ctccttgccaaatggt	C	T	Homo sapiens neuroligin 2 (NLGN2), mRNA. /// ENST00000302926 // intron // 0 // --- // --- // --- // ---	NLGN2	NLGN2, Homo sapiens neuroligin 2 (NLGN2), p13.1
SNP_A-2243989	ctgcttatcaatccca[A/G]tgcagctagttctgtc	A	G	FLJ10916 // 55258 // Homo sapiens hypothetical protein FLJ10916 (FLJ10916), mRNA. /// ENST00000358591 //	FLJ10916	FLJ10916, Homo sapiens hypothetical protein FLJ10916 (FLJ10916), p11.2
SNP_A-1900488	tggagccaacccagatc[A/G]ataaactgattcatct	A	G	79931 // Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), mRNA. /// NM_198179 // downstream // 120928 //	TNIP3	TNIP3, Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), q27
SNP_A-1751983	agagctacttaaactaaaagcaata[C/T]gggtgcaggaagtggtgtaatatt	C	T	NM_017791 // intron // 0 // Hs.267566 // C14orf58 // 55640 // chromosome 14 open reading frame 58	C14orf58	C14orf58, rs10483870, chromosome 14 open reading frame 58,q24.3
SNP_A-1981973	gagacttctaagaacc[A/G]gatgcccaaatgagaa	A	G	LOC375449 // 375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// NM_005582 // downstream // 264 //	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine,q12.3
SNP_A-2314509	ggaggtagattttgac[G/T]cgggtgactgatcat	G	T	sapiens secretin receptor (SCTR), mRNA. /// ENST00000019103 // intron // 0 // --- // --- // --- // ---	SCTR	SCTR, Homo sapiens secretin receptor (SCTR), q14.2
SNP_A-1981428	tggattcagttgtgaa[C/G]caacacctagggcagg	C	G	Homo sapiens polymeric immunoglobulin receptor (PIGR), mRNA. /// NM_005449 // intron // 0 // Hs.58831 // TOSO //	PIGR	PIGR, Homo sapiens polymeric immunoglobulin receptor (PIGR), q32.1
SNP_A-2170354	caagtagcttctccac[A/G]aaagagagggagagag	A	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2028987	aaagaaaaggataacc[A/G]ctgttgtatgaaatc	A	G	Homo sapiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4), mRNA. /// ENST00000282499 // intron // 0 // --- // ---	GRIA4	GRIA4, Homo sapiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4), q22.3
SNP_A-2222754	cgatgggaaatgaaaa[C/T]gcacagaggatatatc	C	T	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1973833	cctggtctgataaatg[A/G]acccagtcctggactt	A	G	56987 // Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// NM_198793 // downstream // 41162 //	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1792130	gggtgttagaagcaca[A/G]ctctgtagggctggag	A	G	284058 // Homo sapiens hypothetical protein LOC284058 (LOC284058), mRNA. /// ENST00000262419 // intron // 0 // ---	LOC284058	LOC284058, Homo sapiens hypothetical protein LOC284058 (LOC284058), q21.31
SNP_A-2206533	ccatcttcctcatctc[C/T]caacaactcctctaaa	C	T	79365 // Homo sapiens basic helix-loop-helix domain containing, class B, 3 (BHLHB3), mRNA. /// NM_005086 //	BHLHB3	BHLHB3, Homo sapiens basic helix-loop-helix domain containing, class B, 3 (BHLHB3), p12.1
SNP_A-2228009	ctacgaaccatggtgc[A/G]ctgaggccactgaggg	A	G	3394 // Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /// ENST00000268638 //	IRF8	IRF8, Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), q24.1
SNP_A-2089529	acttcaagccggtaaa[A/G]atggcagaggccgtg	A	G	/// ENST00000307248 // downstream // 7372 // --- // --- // ---	-	q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043328	aactggacagctcctc[A/G]gacctcatctcttccc	A	G	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // CDS // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1924848	ttatatcttaatgtca[C/T]gcttcattgtcagaaa	C	T	Homo sapiens phospholipase C, epsilon 1 (PLCE1), mRNA. /// ENST00000347778 // intron // 0 // --- // --- // --- // --- ///	PLCE1	PLCE1, Homo sapiens phospholipase C, epsilon 1 (PLCE1), q23.33
SNP_A-2298806	gcccatcttcttcttc[A/C]attgatcccatcatgg	A	C	Homo sapiens mRNA for KIAA0830 protein, partial cds. /// ENST00000278505 // intron // 0 // --- // --- // --- // ---	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds. ,q21
SNP_A-2282453	gagttgaaaaagagaa[A/T]gacgagaaggaggtag	A	T	Homo sapiens squamous cell carcinoma antigen recognized by T cells 2 (SART2), mRNA. /// ENST00000359564 // intron // 0 // --- // --- // --- // ---	SART2	SART2, Homo sapiens squamous cell carcinoma antigen recognized by T cells 2 (SART2), q22.1
SNP_A-2093606	agaagaagaagaagaa[A/G]aaagatggagcaatcg	A	G	Homo sapiens centaurin, gamma 2 (CENTG2), mRNA. /// ENST00000336665 // intron // 0 // --- // --- // --- // ---	CENTG2	CENTG2, Homo sapiens centaurin, gamma 2 (CENTG2), q37.2
SNP_A-2106797	agcctgtaatacaaca[C/T]tgctagtctgttgacc	C	T	// 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), mRNA. /// NM_173508 // upstream //	KCNK1	KCNK1, Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), q42.2
SNP_A-2042963	aactgaagagagaacc[A/G]ctgctttggtcatgtt	A	G	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1849658	tatggtgaaagttaca[A/C]aataaaacagtactga	A	C	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1810810	gtgcagctcatgacta[C/T]actaaaaatgggctgg	C	T	Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), mRNA. /// ENST00000264568 // intron // 0 // --- //	BMPR1B	BMPR1B, Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), q22.3
SNP_A-1902500	tggcctgaggtgagaa[A/G]cttgcagcctgcaaat	A	G	-- /// ENST00000360285 // downstream // 596408 // --- // --- // -- // --- /// ENST00000339882 // downstream // 596408 // --- //	-	q12
SNP_A-1985010	acaacacctacaaaac[A/G]gaataaagttttgtgg	A	G	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 252602 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2256706	ctttcagtagatcaag[A/G]accagggcaaagtcac	A	G	Homo sapiens hypothetical protein FLJ22684 (FLJ22684), mRNA. /// ENST00000259811 // intron // 0 // --- // --- // --- // ---	FLJ22684	FLJ22684, Homo sapiens hypothetical protein FLJ22684 (FLJ22684), p12.3
SNP_A-1808281	gtctttggtcttcagt[A/G]acacacccagatgctg	A	G	161725 // Homo sapiens chromosome 15 open reading frame 16 (C15orf16), mRNA. /// ENST00000307050 //	C15orf16	C15orf16, Homo sapiens chromosome 15 open reading frame 16 (C15orf16), q13.3
SNP_A-2004453	gcatggttaaaaagaa[A/T]aactgcaccaagaaag	A	T	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-2148391	atgggggactgttccc[A/G]attcagatatgctact	A	G	LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 //	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-1972319	ttgctatttggatact[A/G]aatgttttgtacatac	A	G	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-1977097	tttctgagaattttcc[A/G]aagagcatgttggagg	A	G	DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream //	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1897415	tgctgacacttccaga[A/G]catgaccacatataac	A	G	317716 // Homo sapiens breast cancer and salivary gland expression gene (BASE), mRNA. /// NM_178466 // upstream	BASE	BASE, Homo sapiens breast cancer and salivary gland expression gene (BASE), q11.21
SNP_A-1934834	ttctcttttgcttttc[A/T]ctgattctttcctgtc	A	T	Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST00000262360 // intron // 0 // --- // --	C9orf39	C9orf39, Homo sapiens chromosome 9 open reading frame 39 (C9orf39), p22.2
SNP_A-2183487	cagcagagatatgtga[C/T]aggagacttaactaaa	C	T	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1962638	aggataaagtctcata[A/G]tagcatctgtttcttg	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2130104	atacccacaacagtac[C/T]agaatggcagtgtatt	C	T	64866 // Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, mRNA. /// NM_022842 //	CDCP1	CDCP1, Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, p21.31
SNP_A-1926738	ttattgggatcagtga[C/T]attggcccgtgacatt	C	T	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-2065784	aatttcagtggttaaa[A/G]taacatatcaacaatt	A	G	Homo sapiens Cohen syndrome 1 (COH1), transcript variant 2, mRNA. /// NM_181661 // intron // 0 // Hs.191540 // COH1 //	COH1	COH1, Homo sapiens Cohen syndrome 1 (COH1), transcript variant 2, q22.2
SNP_A-2166682	caaattagtttctcac[A/G]aatctagctatggctt	A	G	-- /// ENST00000356117 // downstream // 28039 // --- // --- // ---	-	q23.31
SNP_A-1726330	tctctgtctcctagataataataaa[C/T]cccttgaaatcagaatccatgtcat	C	T	AL137337 // intron // 0 // Hs.272318 // DKFZp434G179 // 150992 // hypothetical protein DKFZp434G179	DKFZp434G179	DKFZp434G179 , rs10496109, hypothetical protein DKFZp434G179,p14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787357	gggaagctgcagatgc[A/G]cagacaactgtaactg	A	G	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA. /// ENST00000360555 // intron // 0 // --- // --- // --- // --- ///	AAK1	AAK1, Homo sapiens AP2 associated kinase 1 (AAK1), p13.3
SNP_A-1706271	accaactattctgagagatgctaaa[A/C]attttgctggcgggggaatggaata	A	C	9637 // fasciculation and elongation protein zeta 2 (zygin II) /// NM_053276 // upstream // 19472 // Hs.137415 // VIT // 5212	FEZ2	FEZ2 , rs6713334, fasciculation and elongation protein zeta 2 (zygin II) ,p22.2
SNP_A-1856341	tcacacagggctgtaa[C/G]gctccttcccccttcca	C	G	// 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// NM_012403 // downstream //	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.3
SNP_A-2227650	ctacatctttctcata[A/T]ctggcagcatttttct	A	T	Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2225495	ctaaaacttgaagaag[C/T]agttctgtaataggca	C	T	Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// ENST00000262861 // intron // 0 // --- // --- // --- // ---	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1871878	tagagctcaatgaagg[G/T]ccggtatctcctgtcc	G	T	6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 109375 // Hs.221127	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-1788107	gggagataggaatgta[A/G]caatttaaactaatgg	A	G	Homo sapiens olfactory receptor, family 6, subfamily A, member 2 (OR6A2), mRNA. /// NM_178168 // upstream //	OR6A2	OR6A2, Homo sapiens olfactory receptor, family 6, subfamily A, member 2 (OR6A2), p15.4
SNP_A-2131246	atagagcttcagatat[A/C]acattttcaaaactgc	A	C	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2018519 // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-2193082	catctacatggaagaa[C/G]agcatttccacagacg	C	G	sapiens giant axonal neuropathy (gigaxonin) (GAN), mRNA. /// ENST00000248272 // intron // 0 // --- // --- // --- // ---	GAN	GAN, Homo sapiens giant axonal neuropathy (gigaxonin) (GAN), q23.2
SNP_A-1826731	taacagcaaatcaata[C/G]aaattcacaaagactg	C	G	ENST00000294693 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2174822	cacaggacctcaggaa[A/G]ttacaggaggagcttg	A	G	CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 6862 // Hs.445899 //	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1
SNP_A-1657283	atttgtgcacaatagctcttgtaaa[C/G]tccctgtctgccacttcctgtatct	C	G	7424 // vascular endothelial growth factor C /// NM_021928 // downstream // 182871 // Hs.42194 // FLJ22649 // 60559 //	VEGFC	VEGFC , rs921879, vascular endothelial growth factor C ,q34.2
SNP_A-2206931	ccatgtaatgaggaga[A/G]cagctaccattgtttg	A	G	/// ENST00000299840 // downstream // 3488 // --- // --- // --- // --- /// ENST00000330898 // upstream // 5935 // --- // --- // --- // ---	-	p12.1
SNP_A-2248083	ctgtggagctggctaa[C/T]accaatgacaaataac	C	T	5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1851615	tattctgaaggtataa[A/G]gggaaaaatggccatt	A	G	LOC157657 // 157657 // Homo sapiens hypothetical protein LOC157657 (LOC157657), mRNA. /// ENST00000286688 //	LOC157657	LOC157657, Homo sapiens hypothetical protein LOC157657 (LOC157657), q22.1
SNP_A-1974112	atgagagttctgaatg[C/G]agagggctggtcagaa	C	G	// 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1944787	ttgtgccattcatttc[A/G]gaaaagtcacggccca	A	G	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2031717	aaagtagattaaaaca[C/T]agatgataaagctaat	C	T	Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA. /// ENST00000271529 // intron // 0 // --- // --- // --- // --- ///	IRTA2	IRTA2, Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), q23.1
SNP_A-2298060	gccatattccctccca[C/T]agttacaaagtatcat	C	T	55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 304270	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-1866637	tccccgtgaccaagca[A/T]tcattcctccaccttc	A	T	ENST00000316225 // intron // 0 // --- // --- // --- // ---	-	q24.23
SNP_A-2258488	cttttctcagattctc[A/G]gaaatcttcacatact	A	G	4821 // Homo sapiens NK2 transcription factor related, locus 2 (Drosophila) (NKX2-2), mRNA. /// NM_006192 // upstream	NKX2-2	NKX2-2, Homo sapiens NK2 transcription factor related, locus 2 (Drosophila) (NKX2-2), p11.22
SNP_A-2009614	gaaaaactgcactgtc[A/G]cttttggactggcaca	A	G	sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // intron // 0 // --- // --- // --- // --- ///	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2133741	atatcccactcagaca[A/G]cgtggttcttggtctt	A	G	ENST00000323433 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-1890351	tgatcccctagcagga[C/T]gtccatttcttcagta	C	T	9435 // Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2), mRNA. /// NM_173653 // downstream // 120340 // Hs.302257 // SLC9A9 // 285195 //	CHST2	CHST2, Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2), q23
SNP_A-2136714	atcactgtgtcattaa[A/G]caatgaaaaacataca	A	G	// 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1159868 // --- // ---	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1664730	gagttgctgtttctaagaaagtaaa[C/T]gagtgacaagtagactacaggacta	C	T	// microtubule-associated protein 2 /// NM_005048 // downstream // 641352 // Hs.159499 // PTHR2 // 5746 //	MAP2	MAP2 , rs1439735, microtubule-associated protein 2 ,q34
SNP_A-1947811	tttactgtccagaggc[A/G]acatggggtctgtgat	A	G	Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), mRNA. /// ENST00000283148 // intron // 0 // --- // --- // --- // ---	UXS1	UXS1, Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), q12.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2060032	aatctttgatttgcct[A/G]aagtttaatttggttt	A	G	10855 // Homo sapiens heparanase (HPSE), mRNA. /// NM_133636 // downstream // 3158 // Hs.480101 // HEL308 //	HPSE	HPSE, Homo sapiens heparanase (HPSE), q21.23
SNP_A-2040175	aaccaagtctgcctga[C/T]gctaaagacttaggtt	C	T	2215 // Homo sapiens Fc fragment of IgG, low affinity IIIb, receptor for (CD16) (FCGR3B), mRNA. /// NM_000569 // upstream // 29025 // Hs.372679 // FCGR3A // 2214 // Homo	FCGR3B	FCGR3B, Homo sapiens Fc fragment of IgG, low affinity IIIb, receptor for (CD16) (FCGR3B), q23.3
SNP_A-2209195	cccaggtcccttctca[C/T]accgtcgtggcccgaa	C	T	sapiens transferrin (TF), mRNA. /// ENST00000264998 //	TF	TF, Homo sapiens transferrin (TF), q22.1
SNP_A-1924821	ttatatcaacaaagaa[A/G]ctactgctgaactatc	A	G	/// ENST00000357074 // downstream // 228573 // --- // --- // --- /// ENST00000358765 // downstream // 228573 // --- // ---	-	p14
SNP_A-1874957	tctctagaaagaaaaa[C/T]cgtcagatgcttgatg	C	T	10669 // Homo sapiens cell growth regulator with EF hand domain 1 (CGREF1), mRNA. /// NM_152870 // upstream //	CGREF1	CGREF1, Homo sapiens cell growth regulator with EF hand domain 1 (CGREF1), p23.3
SNP_A-1758111	tttatacatttcatatcagtataaa[A/T]ctcatatcagtaaacagctctttga	A	T	NM_173829 // intron // 0 // Hs.438642 // FLJ36754 // 285672 // hypothetical protein FLJ36754	FLJ36754	FLJ36754 , rs6880859, hypothetical protein FLJ36754,q12.3
SNP_A-2214790	cctagtgtcttgagca[A/G]attggcatttcaaagc	A	G	// 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	MLLT3	MLLT3, Homo sapiens myeloid,p22.1
SNP_A-1909450	tgtattcttgattaga[A/G]catggttttttacaag	A	G	// Homo sapiens chromosome 10 open reading frame 107 (C10orf107), mRNA. /// ENST00000330194 // intron // 0 // ---	C10orf107	C10orf107, Homo sapiens chromosome 10 open reading frame 107 (C10orf107), q21.2
SNP_A-2308109	gcttgatacataggcc[A/G]gaaatctagacatttt	A	G	Homo sapiens MYC binding protein 2 (MYCBP2), mRNA. /// ENST00000357337 // intron // 0 // --- // --- // --- // ---	MYCBP2	MYCBP2, Homo sapiens MYC binding protein 2 (MYCBP2), q22.3
SNP_A-2124961	agttgatcaccattaa[A/G]gaatagtaatagaaat	A	G	Homo sapiens opsin 3 (encephalopsin, panopsin) (OPN3), mRNA. /// ENST00000063380 // intron // 0 // --- // --- // --- // ---	OPN3	OPN3, Homo sapiens opsin 3 (encephalopsin, panopsin) (OPN3), q43
SNP_A-1879062	tcttaagttgccataa[A/T]aacaacaaacccagtt	A	T	FLJ20364 // 54908 // Homo sapiens hypothetical protein FLJ20364 (FLJ20364), mRNA. /// NM_004946 // upstream //	FLJ20364	FLJ20364, Homo sapiens hypothetical protein FLJ20364 (FLJ20364), q35.1
SNP_A-2024694	aaaagtagaaaaagag[A/T]agcttaacaacaataa	A	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 687387 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1857042	tcacccattttaaggc[A/G]cactggaaaactgcag	A	G	ENST00000261778 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2061843	aatggatgaaattaaa[C/T]gcagacctacaataga	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2171318	caatattaagagtgcc[C/T]atgagaaaaaaaaatt	C	T	// 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 711354 // --- // --- // --- // -	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2102567	agattggagactatta[C/T]ggcaagtgaagtaact	C	T	// Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2163649	caaaaagtgcaagaac[A/G]attggtgaaacttttc	A	G	Homo sapiens c-mer proto-oncogene tyrosine kinase (MERTK), mRNA. /// ENST00000295408 // intron // 0 // --- // --	MERTK	MERTK, Homo sapiens c-mer proto-oncogene tyrosine kinase (MERTK), q13
SNP_A-1865843	tcccaaatgaggcaag[C/T]ctatgagcccaaagtt	C	T	Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 4, mRNA. /// NM_025074 // intron // 0 // Hs.369448 // FRAS1	FRAS1	FRAS1, Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 4, q21.21
SNP_A-2034263	atctccaccctcagaa[A/G]tcagcctggcaaacac	A	G	// 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 1447 //	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-2118173	agtaaaggaaaagata[C/G]attcatagtaagagat	C	G	// 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 102322 // Hs.446083 // PTPRD	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2250700	cttatagtccacttag[A/G]caatagatgtattctg	A	G	sapiens propionyl Coenzyme A carboxylase, alpha polypeptide (PCCA), mRNA. /// ENST00000310787 // intron //	PCCA	PCCA, Homo sapiens propionyl Coenzyme A carboxylase, alpha polypeptide (PCCA), q32.3
SNP_A-1863189	ttcctttgccttggaa[G/T]gggagatgaacttact	G	T	// Homo sapiens hypothetical protein FLJ38335 (FLJ38335), mRNA. /// ENST00000318698 // intron // 0 // --- // --- // --- // ---	FLJ38335	FLJ38335, Homo sapiens hypothetical protein FLJ38335 (FLJ38335), q23.2
SNP_A-2043985	ttggggatggtgtaac[A/T]aaagagtcagcttgtt	A	T	8496 // Homo sapiens PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), transcript variant 1, mRNA. /// NM_177444 // upstream // 4227 // Hs.172445 //	PPFIBP1	PPFIBP1, Homo sapiens PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), transcript variant 1, p11.23
SNP_A-2140925	atctgagtcaatttaa[C/G]ccttgctgtttggaat	C	G	-- /// ENST00000329885 // downstream // 527579 // --- // --- //	-	q14.3
SNP_A-2128586	ataatagtcaattcat[C/T]aaaagaacaattataa	C	T	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 649374 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2304593	gctctctagtggtccc[A/G]gagaagcaagtgtgag	A	G	23765 // Homo sapiens interleukin 17 receptor (IL17R), mRNA. /// ENST00000266136 // upstream // 68792 // --- // ---	IL17R	IL17R, Homo sapiens interleukin 17 receptor (IL17R), q11.1
SNP_A-2178412	cactccactcgcagac[G/T]gcgggccttcctccga	G	T	11039 // Homo sapiens SMA4 (SMA4), mRNA. /// NM_006780 // upstream // 94731 // Hs.484969 // SMA3 //	SMA4	SMA4, Homo sapiens SMA4 (SMA4), p22.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1836216	tactatcctctaggc[G/T]ccacaactgcagatag	G	T	152641 // Homo sapiens hypothetical protein FLJ30277 (FLJ30277), mRNA. /// NM_024949 // upstream // 38848 //	FLJ30277	FLJ30277, Homo sapiens hypothetical protein FLJ30277 (FLJ30277), q35.1
SNP_A-2301066	gccttcaagaacagta[A/G]agccccgcttctgagcc	A	G	UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-1787232	gggaacatgaaggagat[A/G]cccacctcgctgctgctt	A	G	// 5583 // Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// NM_181054 // upstream // 134002 // Hs.509554 //	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-1973324	ttagtgccttctgggcc[G/T]ctataataaatgaccca	G	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 986700 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds, p12.3
SNP_A-1897960	tgctgtaatttctcac[A/G]ggctccaaaaagcaat	A	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- //	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2228160	ctactatagctaatac[A/C]atgacttgaagttag	A	C	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 314613 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-1909120	tgtatccatctatac[A/G]cagttttcataatgt	A	G	mRNA for integrin alpha 6. /// NM_000210 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Homo sapiens integrin, alpha 6	ITGA6	ITGA6, Human for integrin alpha 6. ,q31.1
SNP_A-2070219	acacatttccttccca[A/G]caccaatgtgagacaa	A	G	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 212807 // Hs.146100	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-2089129	acttaattccagacaa[C/T]aatatgttctagttt	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-2052904	aagtcatgaagagaaa[C/T]agaagaaacttaagta	C	T	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 592441 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2013057	ctctttgctggtcaac[A/G]cggaccacctattcc	A	G	6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 466555 //	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-2269550	gacaaagcaccatgatt[C/G]accgggggcgacttggg	C	G	Homo sapiens acid acyltransferase-epsilon (LPAAT-e), mRNA. /// ENST00000285518 // intron // 0 // --- // --- // --- //	AGPAT5	AGPAT5, Homo sapiens acid acyltransferase-epsilon (LPAAT-e), p23.1
SNP_A-2235436	ctccctttctaactgg[A/C]agctgcattccagatg	A	C	SLC5A7 // 60482 // Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA. /// ENST00000264047 // downstream // 169518 // --- // --- // --- //	SLC5A7	SLC5A7, Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), q12.3
SNP_A-2057337	aatatatgtatagaaa[A/G]catttgacaaattcca	A	G	// Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA. /// NM_015946 // upstream // 1249129	ISL1	ISL1, Homo sapiens ISL1 transcription factor, LIM,q11.2
SNP_A-2006728	ggcagaggcagatggc[C/T]agtatcatcctgaaag	C	T	ENST00000283060 // intron // 0 // --- // --- // ---	-	q21.3
SNP_A-2058359	aatcacactgacaaac[A/G]gcgccatccaaactgt	A	G	sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /// ENST00000333644 // intron // 0 // --- // --- //	FAT	FAT, Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), q35.2
SNP_A-2054104	aagttcaggaattcag[G/T]aagtctggagtaagtc	G	T	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 150337 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1876382	tctgagtccaagctca[A/G]gttatctctgagaatg	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2469467 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1941944	ttggaggaagtcccttg[A/T]attttcctgaaccaagt	A	T	60672 // Homo sapiens hypothetical protein FLJ12438 (FLJ12438), mRNA. /// NM_001243 // upstream // 3865 //	FLJ12438	FLJ12438, Homo sapiens hypothetical protein FLJ12438 (FLJ12438), p36.22
SNP_A-1823703	taaaatatgtcagagc[C/T]atgacaggttcccagc	C	T	sapiens hepatic leukemia factor (HLF), mRNA. /// ENST00000226067 // intron // 0 // --- // --- // ---	HLF	HLF, Homo sapiens hepatic leukemia factor (HLF), q22
SNP_A-1813528	gtgtaaaatggtacaa[C/G]cacttggacaactga	C	G	79875 // Homo sapiens hypothetical protein FLJ13710 (FLJ13710), mRNA. /// NM_024817 // upstream // 146880 //	FLJ13710	FLJ13710, Homo sapiens hypothetical protein FLJ13710 (FLJ13710), q23
SNP_A-1705123	tttgtggataatatactattaaa[C/T]attgaaatgtcatttttcttcaaa	C	T	54477 // phosphoinositol 3-phosphate-binding protein-2 /// NM_033328 // downstream // 335055 // Hs.131288 //	PEPP2	PEPP2, rs9844492, phosphoinositol 3-phosphate-binding protein-2 ,p12.3
SNP_A-2060211	aatgaaccagtttgta[A/G]aatgttgttatgctt	A	G	/// ENST00000359457 // downstream // 188973 // --- // --- // ---	-	q14.3
SNP_A-2003735	tagaatcctggctcca[C/T]cattacttcataaata	C	T	Homo sapiens kelch domain containing 2 (KLHDC2), mRNA. /// ENST00000298307 // intron // 0 // --- // --- // ---	KLHDC2	KLHDC2, Homo sapiens kelch domain containing 2 (KLHDC2), q21.3
SNP_A-1780656	ggatcaccggaaatca[G/T]agttcaaaaccagcc	G	T	Homo sapiens chromosome condensation 1 (CHC1), mRNA. /// ENST00000344184 // intron // 0 // --- // --- // ---	CHC1	CHC1, Homo sapiens chromosome condensation 1 (CHC1), p35.3
SNP_A-2305066	gctgaaggagaaaggaa[A/G]gggagaatattagaga	A	G	7124 // Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA. /// NM_009588 //	TNF	TNF, Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), p21.33
SNP_A-1843149	tagtcaggttttcaa[C/T]actaatagtggtctg	C	T	Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA. /// ENST00000311678 // intron // 0 // --- // ---	C9orf3	C9orf3, Homo sapiens chromosome 9 open reading frame 3 (C9orf3), q22.32
SNP_A-2087234	actgatttgctacaa[A/G]cagtggcatatttaat	A	G	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2578495 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2051385	aaggggaatagaatac[A/T]cctatcaaagaaagca	A	T	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 149229 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2012492	tttccatccttatatc[A/T]gaatgtctagcacaca	A	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1647633 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2221072	ccttgtatgagagcaa[C/T]aaaagaagattccagg	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2293262 // --- // -	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p21.1
SNP_A-2171641	caatctcatggactct[A/C]aaatatctcattaagg	A	C	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1171620 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1796587	ggttactccgcagaat[A/G]acaactctcaataatc	A	G	27347 // Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA. ///	STK39	STK39, Homo sapiens serine threonine kinase 39 (STE20,q24.3
SNP_A-2193137	catctagtggaaaaga[G/T]ccccttgcacagccgt	G	T	389649 // Homo sapiens FLJ43582 protein (FLJ43582), mRNA. /// NM_006283 // upstream // 171433 // Hs.279245 //	FLJ43582	FLJ43582, Homo sapiens FLJ43582 protein (FLJ43582), p11.23
SNP_A-1818407	gttcttcaggtgccta[C/T]gctgggcttccaaatt	C	T	FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2151062	atgtgtcaggccttca[A/G]gaatttatacacttga	A	G	Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// ENST00000286398 // intron // 0 // --- // --- // --- // --- ///	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2066976	acaaacagcttcatcc[A/G]caccctgagggaagac	A	G	/// ENST00000355266 // upstream // 9369 // --- // --- // --- // ---	-	q24.2
SNP_A-1922871	ttagatctttgacaaa[C/T]tctccacatcaaacaa	C	T	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 605998 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-2146094	atgccttaatacagcc[A/G]cctgaaatttatttaa	A	G	204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// ENST00000294639 // intron // 0 // ---	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1859995	tcaggtttgtcaaaga[G/T]cagatcattgtagatg	G	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1808198	gtctttataagaggaa[C/T]gatcagagagtggtat	C	T	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1127083 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-2003896	cgataaacaacatcaa[C/G]caacatgtgttttcat	C	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2073903	acagtgtctggccata[A/G]caagtgctcagtgatc	A	G	sapiens quinoid dihydropteridine reductase (QDPR), mRNA. /// ENST00000281243 // intron // 0 // --- // --- // --- // ---	QDPR	QDPR, Homo sapiens quinoid dihydropteridine reductase (QDPR), p15.32
SNP_A-2114233	agggaagacagaaaat[C/G]aaaagctgtcctcaaa	C	G	// 2977 // Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// NM_152434 // downstream // 69787 //	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2241895	ctgatggcttgacaca[C/G]cacttatacctgtata	C	G	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 459979 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2040710	aacccacatgagaaac[A/G]cttcttgggactattt	A	G	/// ENST00000359604 // upstream // 425063 // --- // --- // --- // --- /// ENST00000344172 // upstream // 335806 // --- // --- // ---	-	q11.2
SNP_A-2062769	aatgtgagagacaaaa[A/C]atgaataagaaaaact	A	C	// 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2105405	agccaaactgtaggga[C/T]atgtagcaaatgggtt	C	T	FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 201658 //	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-1757337	agccagcgctaggatgagactctcc[A/G]caggaaacaccctcacagacatacc	A	G	NM_021127 // upstream // 181280 // Hs.96 // PMAIP1 // 5366 // phorbol-12-myristate-13-acetate-induced protein 1	PMAIP1	PMAIP1 , rs948829, phorbol-12-myristate-13-acetate-induced protein 1,q21.32
SNP_A-2201054	ccaaggtggcatggca[A/G]aaatcagcagcttccc	A	G	Homo sapiens hypothetical protein FLJ38628 (FLJ38628), mRNA. /// ENST00000326132 // intron // 0 // --- // --- // --- // ---	FLJ38628	FLJ38628, Homo sapiens hypothetical protein FLJ38628 (FLJ38628), q12.2
SNP_A-1885771	tgacaggacggacacc[A/G]ataagcaagtctgact	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 916424 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2284508	gatcacaacttaccac[A/G]actcattggcaaaatt	A	G	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 323076 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2006971	gtgaatgctcatagaa[C/T]agctaaaaactagcaa	C	T	200576 // Homo sapiens phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III (PIP5K3),	PIP5K3	PIP5K3, Homo sapiens phosphatidylinositol-3-phosphate,q34
SNP_A-1935066	ttctgatcattttctg[A/G]aaagccatttatttag	A	G	5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 // downstream //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2202742	ccacggaggcacaggc[A/G]cattgtgttgaggtgc	A	G	6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 183564 //	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-2290218	gcaaattgcatttttta[C/T]gccagtgagtatggcg	C	T	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 239181 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2228775	ctagagagaagcacca[A/T]tgaaattccaaagtgc	A	T	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1850625	tattaattccagcaaa[C/T]ctttacattgtatgaa	C	T	Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // intron // 0 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2231402	ctattgcctcatgttc[A/G]atgtcatcaaccaaaa	A	G	// Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 147351 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc ,q31.1
SNP_A-1832363	tacaaaaagattaaga[A/C]attatccaggcattgt	A	C	// Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // --- // --- // --- // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.2
SNP_A-1952532	tttctgatgactgaga[C/T]gtgtgaagctctgtgc	C	T	Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // intron // 0 // Hs.494261 // PSAT1 // 29968 // Homo sapiens	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.2
SNP_A-2237437	ctctcctcagaatcca[C/T]gcttgttcccatactc	C	T	Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 4, mRNA. /// NM_025074 // intron // 0 // Hs.369448 // FRAS1	FRAS1	FRAS1, Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 4, q21.21
SNP_A-2074784	acatattgcaaaacaa[C/T]gtatctggtgaattat	C	T	ENST00000357747 // intron // 0 // --- // --- // --- // ---	-	q42.13
SNP_A-2007530	accagctggatatggc[A/G]gccacaattcagagca	A	G	// Homo sapiens thrombomodulin (THBD), mRNA. /// NM_012072 // downstream // 4668 // Hs.97199 // C1QR1 //	THBD	THBD, Homo sapiens thrombomodulin (THBD), p11.21
SNP_A-2122302	agtgcatctcatgtgc[A/C]aggtcgtttcataggt	A	C	8828 // Homo sapiens neuropilin 2 (NRP2), transcript variant 6, mRNA. /// NM_003872 // downstream // 31327 //	NRP2	NRP2, Homo sapiens neuropilin 2 (NRP2), transcript variant 6, q33.3
SNP_A-2012083	ttaatgaggccagaag[A/C]agttggaatgaggatt	A	C	11309 // Homo sapiens solute carrier organic anion transporter family, member 2B1 (SLCO2B1), mRNA. /// NM_004041 // downstream // 53621 // Hs.503284 // ARRB1 //	SLCO2B1	SLCO2B1, Homo sapiens solute carrier organic anion transporter family, member 2B1 (SLCO2B1), q13.4
SNP_A-2212452	ccctgtgtttaaaaaa[A/T]ttagaatcgagtgcag	A	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1857799	tcactgtatagccaag[A/C]atcacttacaatagca	A	C	Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // --- //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1791369	gggtagagacagagca[G/T]ctaatcatgggacatc	G	T	// 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1870967	tcggttaatagtttga[A/G]gtccagcgtgcagctt	A	G	146857 // Homo sapiens hypothetical protein FLJ31952 (FLJ31952), mRNA. /// ENST00000360502 // upstream //	FLJ31952	FLJ31952, Homo sapiens hypothetical protein FLJ31952 (FLJ31952), q12
SNP_A-2061556	aatgctggttggtaga[A/G]agctgacaaagaaatg	A	G	// 9550 // Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), mRNA. /// ENST00000277323 // upstream // 13313 // --- // --- // --- // ---	ATP6V1G1	ATP6V1G1, Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), q32
SNP_A-1994499	gcttagcaacttaaaa[C/T]aatgcacatttaccat	C	T	Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // intron // 0 // Hs.117767 //	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1939699	ttgcaaaaattgaaac[A/T]atactgaacaatacac	A	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4153958 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2304161	gctccctaaaccatta[C/T]gctcactgctaaacct	C	T	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// ENST00000319397 // intron // 0 // --- // --- // --- // --- /// ENST00000345075 // intron //	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3
SNP_A-2123980	agttaatgtggtttag[C/G]aaaaataaaggatttg	C	G	Homo sapiens vacuolar protein sorting 45A (yeast) (VPS45A), mRNA. /// ENST00000259149 // intron // 0 // --- // -	VPS45A	VPS45A, Homo sapiens vacuolar protein sorting 45A (yeast) (VPS45A), q21.2
SNP_A-2301741	gcgcttccaaaaatca[A/C]cccactgagcaattga	A	C	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 16B (PPP1R16B), mRNA. /// ENST00000299824 // intron // 0 // --- // --- // --- // ---	PPP1R16B	PPP1R16B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 16B (PPP1R16B), q11.23
SNP_A-2085990	actctataaagtgtca[C/T]cttcatactttagaa	C	T	2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 //	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2139632	atcgcatattaaaaaa[A/C]ctttagctaagcagga	A	C	Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // intron // 0 // --- // --- // --- // ---	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. p14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1992847	tctttacagcaatagc[A/G]gaagtcaggattcggg	A	G	7976 // Homo sapiens frizzled homolog 3 (Drosophila) (FZD3), mRNA. /// NM_001440 // upstream // 119189 //	FZD3	FZD3, Homo sapiens frizzled homolog 3 (Drosophila) (FZD3), p21.1
SNP_A-1987201	gaaaagccactagcac[C/G]ctctctctggccacat	C	G	9841 // Homo sapiens KIAA0441 mRNA, partial cds. /// NM_173559 // downstream // 1268 // --- // FLJ25791 //	ZBTB24	ZBTB24, Homo sapiens KIAA0441 partial cds. ,q21
SNP_A-1931767	ttcccttactcttcca[A/C]caaggttctaagctct	A	C	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1896915	tgctcagcttcaccaa[C/G]tgtctactgtcaaagg	C	G	55520 // Homo sapiens elaC homolog 1 (E. coli) (ELAC1), mRNA. /// NM_005359 // upstream // 29196 // Hs.75862 //	ELAC1	ELAC1, Homo sapiens elaC homolog 1 (E. coli) (ELAC1), q21.1
SNP_A-1828548	taagcatgaccatgaa[C/T]tgcagaatatccaggc	C	T	// Homo sapiens nitric oxide synthase trafficker (NOSTRIN), mRNA. /// ENST00000343642 // intron // 0 // --- // --- // --- // ---	NOSTRIN	NOSTRIN, Homo sapiens nitric oxide synthase trafficker (NOSTRIN), q24.3
SNP_A-1824855	taaagcacaaatgctc[C/T]ccaatcataaagaaaa	C	T	Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1945329	ttgttaccttgattaa[A/C]gctctgaattcttctg	A	C	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2578351 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2278247	gagccttagagcagat[G/T]acatttcccataaaat	G	T	// 10208 // Homo sapiens chromosome 13 open reading frame 22 (C13orf22), mRNA. /// NM_001629 // upstream //	C13orf22	C13orf22, Homo sapiens chromosome 13 open reading frame 22 (C13orf22), q12.3
SNP_A-2049468	aagctggagaatggac[C/T]ctggaactctgatgca	C	T	CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 436532 // Hs.437444 // CACNA1E // 777 //	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-1722304	agagtcctacagattctgtgtttca[A/G]agggtaattttgattgtggtctaga	A	G	AB002358 // upstream // 96102 // Hs.416358 // SALL2 // 6297 // sal-like 2 (Drosophila)	SALL2	SALL2 , rs10483254, sal-like 2 (Drosophila),q11.2
SNP_A-2041632	aacgcctcaagcagaa[A/G]cagagtctgtgaccga	A	G	UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 //	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-2005543	tctctgatgtttgcaa[C/T]tgtttatgtgtgactc	C	T	// 79949 // Homo sapiens chromosome 10 open reading frame 81 (C10orf81), mRNA. /// ENST00000361048 //	C10orf81	C10orf81, Homo sapiens chromosome 10 open reading frame 81 (C10orf81), q25.3
SNP_A-1935944	ttcttaatcttaactg[A/G]aaaacagatgcaaaat	A	G	// 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1001846 // --- // ---	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1926604	ttattcttttaatggc[C/T]gacagtattcttttgt	C	T	29789 // Homo sapiens hypothetical protein PTD004 (PTD004), mRNA. /// NM_013341 // downstream // 6393 //	PTD004	PTD004, Homo sapiens hypothetical protein PTD004 (PTD004), q31.1
SNP_A-1963726	aactgaagagtccaca[A/G]actgacctaacactct	A	G	// 151516 // Homo sapiens hypothetical protein FLJ25084 (FLJ25084), mRNA. /// NM_006196 // upstream // 2506 //	FLJ25084	FLJ25084, Homo sapiens hypothetical protein FLJ25084 (FLJ25084), p13.3
SNP_A-2113379	aggccttggactgagc[A/G]ctagagagatggagag	A	G	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m /// NM_020416 // intron // 0 // Hs.479069 // PPP2R2C // 5522 // Ho	PPP2R2C	PPP2R2C, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m p16.1
SNP_A-1984114	tgacgcttcctggtga[C/T]agcttcttaggcgaaa	C	T	4238 // Homo sapiens microfibrillar-associated protein 3 (MFAP3), mRNA. /// NM_198321 // upstream // 55483 //	MFAP3	MFAP3, Homo sapiens microfibrillar-associated protein 3 (MFAP3), q33.2
SNP_A-2268612	gaatgtcagaaatcat[A/G]aagtaaaatatttcca	A	G	LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 824758 // Hs.307086 //	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-2087716	actgcttcctgggtga[A/T]cggggtggtgtagcct	A	T	9833 // Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA. /// NM_016734 // downstream // 1903	MELK	MELK, Homo sapiens maternal embryonic leucine zipper kinase (MELK), p13.2
SNP_A-2101610	agatgaggtgtcaaga[A/G]aggagaccaaggccac	A	G	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-2133596	atatcactaaccagaa[A/G]cactccagaaacatac	A	G	7849 // Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, mRNA. /// NM_013952 // upstream // 70089 //	PAX8	PAX8, Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, q13
SNP_A-1925074	ttatcagaaacacaga[C/T]ggaaaatgaaactact	C	T	-- /// ENST00000360683 // downstream // 762596 // --- // --- // -- // --- /// ENST00000345990 // downstream // 763654 // --- // ---	-	q23.2
SNP_A-2100082	agagtgcctgctatga[C/G]ctacagaaatgacagg	C	G	sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, mRNA. /// NM_002037 // intron // 0 //	FYN	FYN, Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, q21
SNP_A-1955467	tttggtatgtgctaag[A/C]agtggatgtctatgtg	A	C	/// ENST00000309379 // upstream // 1071618 // --- // --- // --- // ---	-	q21
SNP_A-1874987	tctctagggattcatc[A/G]ctgaaagttgcctctg	A	G	285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 460415 //	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-2291819	gcacagcctatcttaa[C/T]gttcacccctcttgg	C	T	170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // --- // --- // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2216284	cctcctccagagacat[A/G]agttaggtcatgaacc	A	G	// 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// NM_130782 // upstream // 403296 // Hs.440890 //	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.2
SNP_A-2186507	cagggacaaggaccgga[A/T]cggagcgggcccagca	A	T	Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // --- // --- 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 870902 // Hs.33368 // MCTP2 // 55784 //	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-1901119	tggatctcagcccaaa[C/T]gttgcagacctcataa	C	T		MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2245893	ctgggtgatgggaata[A/T]gaaaatatgatttcaa	A	T	/// ENST00000333744 // downstream // 24190 // --- // --- // ---	-	p15.1
SNP_A-1946486	ttaaaggaccattag[A/G]catagatcctagtggt	A	G	81328 // Homo sapiens olfactory receptor, family 4, subfamily A, member 15 (OR4A15), mRNA. /// ENST00000314706 //	OR4A15	OR4A15, Homo sapiens olfactory receptor, family 4, subfamily A, member 15 (OR4A15), q11
SNP_A-2202130	ccacatatagtgcaga[A/T]gaacgaaggtttgta	A	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1814471	gtgtgcaccagagagc[C/T]cttcattcagccatca	C	T	22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 113637 // Hs.513902 // NALP1 //	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-1979538	ggacagtagcactaca[C/G]aacatatgactctaaa	C	G	Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000274071 // intron // 0 // --- // --- // --- 846 // Homo sapiens calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism) (CASR), mRNA. /// NM_005213 // upstream // 5690 //	PDGFC	PDGFC, Homo sapiens platelet derived growth factor C (PDGFC), q32.1
SNP_A-1899751	tggaatgatacctgaa[A/G]tgtactgcctgtttcc	A	G		CASR	CASR, Homo sapiens calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism) (CASR), q21.1
SNP_A-1841410	taggactatgaaaaag[A/G]acacattaaatgtata	A	G	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2235402	ctccctactaaaggal[C/T]ccatgtaaaacacagt	C	T	// Homo sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// NM_001465 // upstream // 9640 // Hs.370503 //	FYB	FYB, Homo sapiens FYN binding protein (FYB-120/130) (FYB), p13.1
SNP_A-1783860	gggatgatttgccctc[C/T]gaacttttctctgagt	C	T	// 79091 // Homo sapiens hypothetical protein MGC2654 (MGC2654), mRNA. /// NM_000663 // upstream // 19901 //	MGC2654	MGC2654, Homo sapiens hypothetical protein MGC2654 (MGC2654), p13.2
SNP_A-2142251	atgaaaaggctgacaaa[A/T]tccaagcactgataag	A	T	Homo sapiens ribonucleotide reductase M1 polypeptide (RRM1), mRNA. /// ENST00000300738 // intron // 0 // --- // ---	RRM1	RRM1, Homo sapiens ribonucleotide reductase M1 polypeptide (RRM1), p15.4
SNP_A-2303961	gctcattcttctacca[A/G]ccacgccttcgctcac	A	G	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1800769	gtagaattgtatttaa[A/G]gttgataaggtaacag	A	G	Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // --- // --- // --- /// ENST00000356360 // intron // 0 // --- // --- // ---	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2233448	ctcagtcagcctaagc[C/G]atgagcacatttttt	C	G	8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 930666 // --- // --- // ---	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2031166	aaaggcagggactgcc[A/G]gattcagtttgagtc	A	G	ENST00000338956 // intron // 0 // --- // --- // ---	-	p15.2
SNP_A-2298505	gcccaagtaggatccc[A/G]ataaggaagtgtggg	A	G	2996 // Homo sapiens glycophorin E (GYPE), transcript variant 1, mRNA. /// NM_198682 // downstream // 150892 //	GYPE	GYPE, Homo sapiens glycophorin E (GYPE), transcript variant 1, q31.21
SNP_A-2015654	catcatgaccaatcca[A/T]tcactgttaacttttt	A	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// NM_006806 // downstream //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2184340	cagcgaaacacacaag[A/G]cccggtgtaattgagt	A	G	84458 // Homo sapiens ligand-dependent corepressor (MLR2), mRNA. /// NM_032440 // downstream // 17109 //	MLR2	MLR2, Homo sapiens ligand-dependent corepressor (MLR2), q24.1
SNP_A-2009782	gaaaaagtagagaaat[G/T]aagaacatcgtatttg	G	T	sapiens tec protein tyrosine kinase (TEC), mRNA. /// ENST00000258070 // intron // 0 // --- // --- // --- // ---	TEC	TEC, Homo sapiens tec protein tyrosine kinase (TEC), p12
SNP_A-1691746	ataagagggagcagtgctgtatga[C/T]gctaagacaaatatgggtagaattg g	C	T	51691 // LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) /// NM_033427 // upstream // 272876 //	LSM8	LSM8, rs2041529, LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) q31.31
SNP_A-2005245	ttggcagttccaatt[C/T]aagaccaggttaaggc	C	T	// 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // upstream //	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-1886729	tgactgaagatgtaaaa[A/G]tgagtatgataggaga	A	G	Homo sapiens cyclin-dependent kinase 8 (CDK8), mRNA. /// ENST00000255316 // intron // 0 // --- // --- // --- // ---	CDK8	CDK8, Homo sapiens cyclin-dependent kinase 8 (CDK8), q12.13
SNP_A-1970654	aagaatttgtaacaac[A/G]acgacagctagcatta	A	G	440699 // Homo sapiens FLJ25811 protein (FLJ25811), mRNA. /// ENST00000294818 // intron // 0 // --- // --- // --- // --- // 404203 // Homo sapiens protease inhibitor H (MGC21394), mRNA. /// NM_032566 // upstream // 10752 // Hs.244569 //	FLJ25811	FLJ25811, Homo sapiens FLJ25811 protein (FLJ25811), q23.3
SNP_A-1937877	ttgaatccacaataca[C/T]tgactgagtttaacct	C	T		SPINK6	SPINK6, Homo sapiens protease inhibitor H (MGC21394), q32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2199901	acaggtcattgtacac[C/T]atcagaaaaattgatt	C	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1953996 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1953095	tttcttggtgtagcat[A/G]aaattggaaatccaaa	A	G	UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-1907225	tggtttggcattgaaa[C/T]gagaagttattatgta	C	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2275090	gagaagaatgtgctaa[C/T]gtcttataaattttaa	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 266113 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2209655	cccatgtacaatcaaa[A/C]gcagaggcatccttga	A	C	LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 //	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-2149909	atgtcactctgaagac[C/T]aaaagtataattgaat	C	T	sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // intron // 0 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1803822	gtcaagatcccaacta[A/C]caggataatctttaat	A	C	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 1357917 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1899400	tggaactgtttataca[C/T]agctgaacaaatactt	C	T	Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // intron // 0 // --- // --- // --- // ---	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-1909707	tgtcaatactccaaaa[C/T]tctacaggcaggaaac	C	T	65008 // Homo sapiens mitochondrial ribosomal protein L1 (MRPL1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_032863 // upstream // 17126 // Hs.369448 //	MRPL1	MRPL1, Homo sapiens mitochondrial ribosomal protein L1 (MRPL1), nuclear gene encoding mitochondrial protein, q21.21
SNP_A-2110088	aggaagcggctaagca[C/G]aagttattgctttagg	C	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 725720 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2054314	aagttgggcttcccct[A/G]aagtggcgcttgcagg	A	G	Homo sapiens KIAA1510 protein (KIAA1510), mRNA. /// AB040943 // intron // 0 // Hs.271285 // KIAA1510 // 57642 //	KIAA1510	KIAA1510, Homo sapiens KIAA1510 protein (KIAA1510), q13.33
SNP_A-1788977	gggcacaagttactgt[A/G]aaagcaaaaatcagat	A	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 241124 // Hs.33368 // MCTP2 // 55784 // Homo	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2191425	catatctaagcaagac[A/G]ccaccactaacgggtt	A	G	57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 153236 // Hs.160373 // KIAA1383 // 54627 //	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1930058	ttcatgtgctcagtac[C/T]atcccattgaataaaa	C	T	/// ENST00000322896 // downstream // 775 // --- // --- // --- // ---	-	q14.13
SNP_A-1798241	gtaaagaagtagtagt[A/G]aaatcagaagacagtg	A	G	SLC12A2 // 6558 // Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters), member 2	SLC12A2	SLC12A2, Homo sapiens solute carrier family 12 (sodium q23.2
SNP_A-1828598	taagcccaggaagctg[A/G]atctgttgtggattaa	A	G	50834 // Homo sapiens taste receptor, type 2, member 1 (TAS2R1), mRNA. /// NM_199133 // downstream // 206073 //	TAS2R1	TAS2R1, Homo sapiens taste receptor, type 2, member 1 (TAS2R1), p15.2
SNP_A-1962686	tcctacaccctgagga[A/G]caggtacctgagaata	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2042034	aactacctcaaactaa[A/G]gcccctgcacaacaaa	A	G	// 9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 108684 // Hs.136829 // RFX3 //	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-2298127	gccatcctggttttca[A/G]tatgaaacaatgtgat	A	G	Homo sapiens suppression of tumorigenicity 7 like (ST7L), transcript variant 3, mRNA. /// NM_138727 // intron // 0 // Hs.201921 // ST7L // 54879 // Homo sapiens suppression of	ST7L	ST7L, Homo sapiens suppression of tumorigenicity 7 like (ST7L), transcript variant 3, p13.2
SNP_A-2125370	agtttaaagaccactg[G/T]acacaataattaattt	G	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2139610	atcgataaactgctta[A/G]agtatggaacattaaa	A	G	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2178613	cactctctcctggaaa[C/T]gcttcctccaggcttc	C	T	Homo sapiens hypothetical protein FLJ10759 (FLJ10759), mRNA. /// ENST00000291416 // intron // 0 // --- // --- // --- // ---	TRIM62	TRIM62, Homo sapiens hypothetical protein FLJ10759 (FLJ10759), p35.1
SNP_A-2303448	gctcaaaagatttcca[C/T]tcacagagggaatgtg	C	T	4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // upstream	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-1934840	ttctgaaaaactagaa[G/T]aatgcagatggtattg	G	T	/// ENST00000328274 // downstream // 9728 // --- // --- // --- //	-	p11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2037503	aacaacattgctggaa[C/G]ccatcacaagccagtc	C	G	Homo sapiens prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) /// NM_183079 // intron // 0 // Hs.472010 // PRNP // 5621 // Homo sapi	PRNP	PRNP, Homo sapiens prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia), p13
SNP_A-1810688	gtgcaccaaaacaaca[A/C]aagcactctaaagtga	A	C	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 538123 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-2129253	ataatttttaagctat[A/G]agacattaacactcta	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2045745 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1892154	tgcaaag[g/t]tcaca[C/G]ag[g/a]ccgtggcaggt	C	G	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 596885 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1928765	ttcagaatttctaac[A/G]aaatctctgaaactct	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1982107	gtcattcagaagttca[C/T]ctacagtactcatag	C	T	8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 //	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-2269127	gaattgctcctctaac[A/T]cataaaattactttc	A	T	MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// NM_020164 //	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-1938869	ttgaggctgatgcaga[A/C]actaaaaatgccagga	A	C	-- /// ENST00000314058 // upstream // 107344 // -- // -- // ---	-	p13.2
SNP_A-2250392	cttagcattgccattc[A/c]ttgccagacacggac	A	G	Homo sapiens palmitoyl-protein thioesterase 2 (PPT2), transcript variant 2, mRNA. /// NM_005155 // intron // 0 // Hs.332138 // PPT2 // 9374 // Homo sapiens palmitoyl-protein	PPT2	PPT2, Homo sapiens palmitoyl-protein thioesterase 2 (PPT2), transcript variant 2, p21.32
SNP_A-2024065	aaaagaggcaatgtga[A/G]agagagagagggggaa	A	G	Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, mRNA. /// NM_053028 // intron // 0 //	MYLK	MYLK, Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, q21.1
SNP_A-1730533	ggagagctgagcaccacggcgggagga[A/G]agtcgggggtcatggaaacca aatt	A	G	RNASET2 // 8635 // ribonuclease T2 /// NM_007045 // upstream // 223747 // Hs.180296 // FGFR1OP // 11116 //	RNASET2	RNASET2 , rs2072642, ribonuclease T2 ,q27
SNP_A-1964642	gagtgaaaacaagaaa[A/G]tcactcaggcccaaagg	A	G	51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 333956 // Hs.271977	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-2044003	aactgagcagtgaaa[C/G]taacatttgacttcc	C	G	Homo sapiens anillin, actin binding protein (scraps homolog, Drosophila) (ANLN), mRNA. /// ENST00000265748 // intron // 0 // -- // -- // ---	ANLN	ANLN, Homo sapiens anillin, actin binding protein (scraps homolog, Drosophila) (ANLN), p14.2
SNP_A-1962985	ttcttctccaatgcc[A/G]gctgtacttccatcta	A	G	Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // --- // -- // -- // ---	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-2239525	ctctttttaacaacta[A/G]ctgtggcaggaaacaa	A	G	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 762177	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1991405	accatttccagttga[C/T]ggagcacttttcata	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 275042 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1802247	gtatatctcttcacaa[A/G]ttattgtagttgtagg	A	G	// Homo sapiens alpha-fetoprotein (AFP), mRNA. /// NM_001133 // upstream // 17858 // Hs.168718 // AFM // 173	AFP	AFP, Homo sapiens alpha-fetoprotein (AFP), q13.3
SNP_A-1869289	tcctgggggagtttca[A/C]atgaaggcaactgaag	A	C	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.31
SNP_A-1983568	catggaaatctttgca[C/T]aatgttttgtgtgtt	C	T	ENST00000322410 // intron // 0 // --- // --- // ---	-	q31.1
SNP_A-2095139	agaattaaggaggaaat[A/T]caactggatgctaatt	A	T	sapiens giant axonal neuropathy (gigaxonin) (GAN), mRNA. /// ENST00000248272 // intron // 0 // --- // --- // ---	GAN	GAN, Homo sapiens giant axonal neuropathy (gigaxonin) (GAN), q23.2
SNP_A-2313898	ggagcctgatgtgtgcf[A/G]agttcccagctggggc	A	G	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1940731	ttgccttaatgttta[A/C]catccacacttattg	A	C	10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // downstream // 373050 // -- // -- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2291121	gcaatagcattaggca[A/G]aaaacgtggcatgtgt	A	G	254240 // Homo sapiens bactericidal/permeability-increasing protein-like 2 (BPIL2), mRNA. /// NM_012179 // upstream //	BPIL2	BPIL2, Homo sapiens bactericidal,q12.3
SNP_A-1923419	ttaggatgttatcaga[C/T]ctttgtacctgagaaa	C	T	11231 // Homo sapiens SEC63-like (S. cerevisiae) (SEC63), mRNA. /// NM_014028 // downstream // 25757 // Hs.226780	SEC63	SEC63, Homo sapiens SEC63-like (S. cerevisiae) (SEC63), q21
SNP_A-2278438	gagctcaagctttcta[A/G]gaaataggaacctcat	A	G	169166 // Homo sapiens hypothetical protein MGC39715 (MGC39715), mRNA. /// ENST00000311812 // intron // 0 // ---	MGC39715	MGC39715, Homo sapiens hypothetical protein MGC39715 (MGC39715), q22.3
SNP_A-1912408	tgtgcaagaataaatg[C/T]agagtgcaaaatgctc	C	T	ENST00000304527 // intron // 0 // --- // --- // ---	-	q31.3
SNP_A-1905996	tggtcgacgtggacca[C/T]gccttgctgcacctct	C	T	Homo sapiens PTEN induced putative kinase 1 (PINK1), mRNA. /// ENST00000289840 // intron // 0 // --- // --- // ---	PINK1	PINK1, Homo sapiens PTEN induced putative kinase 1 (PINK1), p36.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1892247	tgcaacagcccgagga[A/C]gcatacaaggcatggg	A	C	92014 // Homo sapiens mitochondrial carrier triple repeat 1 (MCART1), mRNA. /// NM_003028 // downstream // 14826 //	MCART1	MCART1, Homo sapiens mitochondrial carrier triple repeat 1 (MCART1), p13.2
SNP_A-2255601	cttgtggttccatttc[C/T]cttcattctgtcaatg	C	T	26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// NM_015224 // downstream // 71984 //	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2175920	cacatttttttcttgta[C/T]agtagtagcattaggg	C	T	// 283160 // Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), mRNA. ///	OR8D2	OR8D2, Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), q24.1
SNP_A-1921290	ttacattgtactagct[A/G]actttacattgtataa	A	G	// 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 167859 // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-2073048	acaggagtgtctctgc[G/T]ctggaaccaggacaca	G	T	375346 // Homo sapiens Similar to RIKEN cDNA 1810038N08 gene (MGC52022), mRNA. ///	MGC52022	MGC52022, Homo sapiens Similar to RIKEN cDNA 1810038N08 gene (MGC52022), p21.1
SNP_A-1788523	gggatagcattctcac[A/G]acatggtgccatgact	A	G	Homo sapiens nucleoporin 37kDa (NUP37), mRNA. /// ENST00000251074 // intron // 0 // --- // --- // --- // ---	NUP37	NUP37, Homo sapiens nucleoporin 37kDa (NUP37), q23.2
SNP_A-1923695	ttaggttctggcaata[C/T]gagaaactattaagtt	C	T	Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA. /// ENST00000327801 // intron // 0 // --- // ---	SMYD3	SMYD3, Homo sapiens SET and MYND domain containing 3 (SMYD3), q44
SNP_A-1992446	atctatgattggaaaa[A/C]attacatagataccta	A	C	4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 //	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22
SNP_A-1794042	ggtcagaaagacctga[A/G]agttttccaaagctgcg	A	G	sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// ENST00000262512 // intron // 0 // --- // --- // ---	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-1825603	taaatatccatcagca[A/G]agaaatgaataaagaa	A	G	5257 // Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. /// NM_145188 // downstream // 186205 // Hs.410111	PHKB	PHKB, Homo sapiens phosphorylase kinase, beta (PHKB), q12.1
SNP_A-1890986	tgatggctgctcccta[C/T]gacactctccccaacc	C	T	604 // Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), transcript variant 1, mRNA. ///	BCL6	BCL6, Homo sapiens B-cell CLL q27.3
SNP_A-2289842	gcaaaccacctaaaaa[A/G]ccatcaacagtggaat	A	G	Homo sapiens nuclear receptor subfamily 1, group H, member 4 (NR1H4), mRNA. /// ENST00000321046 // intron //	NR1H4	NR1H4, Homo sapiens nuclear receptor subfamily 1, group H, member 4 (NR1H4), q23.1
SNP_A-1943818	ttgtagggttgagtca[C/G]aggattgctcagtgaa	C	G	// Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), mRNA. /// ENST00000280871 // intron // 0 // --- // --- // --- // ---	SLC2A13	SLC2A13, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), q12
SNP_A-2029658	aaagagagtcggaagg[A/G]aatctaggagttgatg	A	G	// 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 189310 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-1970985	aagaagaatgtagcac[A/G]ctagggaatttattac	A	G	Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2222400	cgagatggagatgaga[C/T]gatgttcagtggtgta	C	T	Homo sapiens sideroflexin 5 (SFXN5), mRNA. /// ENST00000272433 // intron // 0 // --- // --- // --- // ---	SFXN5	SFXN5, Homo sapiens sideroflexin 5 (SFXN5), p13.2
SNP_A-2081291	acctggagagatgtta[A/G]ggacaccaggttacac	A	G	285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 80657 // --- //	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-1879506	tcttatttagcaataa[A/T]acctctcttctaaaag	A	T	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-1780283	ggataaaggccacctg[C/T]attaatctctcaaatg	C	T	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 144345 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2313748	ggagcaccatgtgagc[A/G]cctaccaaggtcatgc	A	G	166815 // Homo sapiens tigger transposable element derived 2 (TIGD2), mRNA. /// NM_198281 // downstream // 51568 //	TIGD2	TIGD2, Homo sapiens tigger transposable element derived 2 (TIGD2), q22.1
SNP_A-2067874	acaacccttttgagca[C/G]acgctgctgtttctct	C	G	223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // upstream // 18627 // Hs.2533 // ALDH9A1 // 223 // Human gamma-	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-2116305	aggtagagattacacc[A/G]agtgtagaagccccgg	A	G	// 132864 // Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, mRNA. /// NM_182485 // downstream // 100381 // Hs.374216	CPEB2	CPEB2, Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, p15.33
SNP_A-2197234	cattcacttttggctg[C/T]atggccagtgacagat	C	T	6846 // Homo sapiens chemokine (C motif) ligand 2 (XCL2), mRNA. /// ENST00000331499 // upstream // 68748 // --- // ---	XCL2	XCL2, Homo sapiens chemokine (C motif) ligand 2 (XCL2), q24.2
SNP_A-1890202	tgatcacactttgaca[C/T]tgaccatcactctctg	C	T	8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream //	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-2255457	cttgtcctttgactgc[C/T]gatgactgagtgtgtg	C	T	Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 1, mRNA. /// NM_018205 // intron // 0 // Hs.7778 // LRRC20 // 55222 // Homo sapiens leucine rich	LRRC20	LRRC20, Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 1, q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2030573	aaagctaaaggcacag[A/G]cacaatgatatctgac	A	G	MGC15937 // 92292 // Homo sapiens similar to RIKEN cDNA 0610008P16 gene (MGC15937), mRNA. /// NM_198947 //	MGC15937	MGC15937, Homo sapiens similar to RIKEN cDNA 0610008P16 gene (MGC15937), q12.1
SNP_A-2130958	atagaacaaggaccta[A/G]ctctcttcaattctat	A	G	140801 // Homo sapiens ribosomal protein L10-like (RPL10L), mRNA. /// NM_182830 // downstream // 46109 //	RPL10L	RPL10L, Homo sapiens ribosomal protein L10-like (RPL10L), q21.3
SNP_A-2010764	atatttgatgtaacaa[C/T]tgcctgaaagattttt	C	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 345973	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2085693	actccgtctcaacaaa[A/C]ataaaaagtgttaata	A	C	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), transcript variant E, mRNA. /// NM_001228 // intron // 0 // Hs.369736 // CASP8 // 841 //	CASP8	CASP8, Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), transcript variant E, q33.1
SNP_A-1972557	ttttttcctacccagg[C/T]aaagtcatgcttttg	C	T	7123 // Homo sapiens tetranectin (plasminogen binding protein) (TNA), mRNA. /// NM_178181 // downstream //	CLEC3B	CLEC3B, Homo sapiens tetranectin (plasminogen binding protein) (TNA), p21.31
SNP_A-1855637	tcaatacaatgttgaa[C/T]tgaagtggcgagagtg	C	T	// Homo sapiens goosecoid-like (GSCL), mRNA. /// NM_005984 // downstream // 16917 // Hs.111024 //	GSCL	GSCL, Homo sapiens goosecoid-like (GSCL), q11.21
SNP_A-1909688	tgtcaaggtttttctg[C/T]atgtggacaagacacc	C	T	Homo sapiens fetal Alzheimer antigen (FALZ), transcript variant 2, mRNA. /// NM_182641 // intron // 0 // Hs.444200 //	FALZ	FALZ, Homo sapiens fetal Alzheimer antigen (FALZ), transcript variant 2, q24.2
SNP_A-2171352	caatattgtcatgaaa[C/G]aaaggagcagctggat	C	G	10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 218238 // Hs.369907 //	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-2082493	acgctagtctccgccc[C/T]gccttttggtctttct	C	T	sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), transcript variant 2, mRNA. /// NM_001250 // intron // 0 // Hs.472860 // CD40 // 958 // Homo sapiens tumor	CD40	CD40, Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), transcript variant 2, q13.12
SNP_A-2097269	agacttttctcccaga[A/C]accttcattactattg	A	C	90407 // Homo sapiens similar to RIKEN cDNA 5730578N08 gene (MGC15397), mRNA. /// NM_139248 // downstream //	TMEM41A	TMEM41A, Homo sapiens similar to RIKEN cDNA 5730578N08 gene (MGC15397), q27.2
SNP_A-2252290	cttccctttcttcac[C/T]gctgaactgtgtctct	C	T	92291 // Homo sapiens calpain 13 (CAPN13), mRNA. /// BC010659 // downstream // 74057 // Hs.468058 // GALNT14	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1
SNP_A-2257146	ctttctctgggatgca[C/T]tgagtcagggaataga	C	T	ENST00000269336 // 5UTR // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2239188	ctcttgccccgggcca[A/G]tgcagacctggattta	A	G	Homo sapiens signal recognition particle 68kDa (SRP68), mRNA. /// ENST00000307877 // 3UTR // 0 // --- // --- // --- // ---	SRP68	SRP68, Homo sapiens signal recognition particle 68kDa (SRP68), q25.1
SNP_A-2084737	actatttacctcaaac[A/T]acctctaatcaatcat	A	T	/// ENST00000334709 // upstream // 866 // --- // --- // --- // ---	-	q11.2
SNP_A-2087146	actgatctttggcaca[C/G]tcaatggaaatataca	C	G	/// ENST00000336930 // upstream // 617990 // --- // --- // --- // -	-	p14.3
SNP_A-1970843	gcccggcgagaaccac[C/G]aacagtgtggtggaac	C	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 861336 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2048650	aagccacaactccaga[A/C]ataaatttgcccatat	A	C	390059 // Homo sapiens olfactory receptor, family 51, subfamily M, member 1 (OR51M1), mRNA. /// ENST00000328611 // downstream // 135 // --- // --- // --- // ---	OR51M1	OR51M1, Homo sapiens olfactory receptor, family 51, subfamily M, member 1 (OR51M1), p15.4
SNP_A-2201077	ccaagtacgaagctgc[A/G]attggaatctgggagt	A	G	Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), mRNA. /// ENST00000248070 // intron // 0 // --- // --- // --- // ---	EPS15L1	EPS15L1, Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), p13.11
SNP_A-1838462	tagaatcatttccaaa[A/C]acatagtgcttgctat	A	C	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 304537 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1867875	tcctaccttcagatta[C/T]aattctgcaaagtagg	C	T	sapiens citrate synthase (CS), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA. /// NM_198324 // intron // 0 // Hs.430606 // CS // 1431 // Homo	CS	CS, Homo sapiens citrate synthase (CS), nuclear gene encoding mitochondrial protein, transcript variant 1, q13.3
SNP_A-1858587	tcagagtaaattaaga[G/T]ggggtgctgctcttaac	G	T	Homo sapiens ADP-ribosylation factor interacting protein 1 (arfaptin 1) (ARFIP1), mRNA. /// ENST00000353617 // intron	ARFIP1	ARFIP1, Homo sapiens ADP-ribosylation factor interacting protein 1 (arfaptin 1) (ARFIP1), q31.3
SNP_A-2121767	agtgactcctttgcac[C/T]gtaagagcccaagagt	C	T	Homo sapiens KIAA0140 (KIAA0140), mRNA. /// ENST00000280780 // intron // 0 // --- // --- // --- // --- ///	FAM53B	FAM53B, Homo sapiens KIAA0140 (KIAA0140), q26.13
SNP_A-2139534	atcctttcttaataaa[A/G]caaatgacaccacaca	A	G	1308 // Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, mRNA. /// NM_130778 //	COL17A1	COL17A1, Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, q25.1
SNP_A-2245265	ctggctctgctggccc[C/T]gaactgaacctctcca	C	T	Homo sapiens HSPC049 protein (HSPC049), mRNA. /// ENST00000354475 // 3UTR // 0 // --- // --- // --- // ---	HSPC049	HSPC049, Homo sapiens HSPC049 protein (HSPC049), q33
SNP_A-2129314	atacaaatccacacca[A/T]gattagaggagtcttc	A	T	sapiens ADP-ribosyltransferase 3, mRNA (cDNA clone MGC:23844 IMAGE:4292261), complete cds. /// NM_001179 // intron // 0 // Hs.24976 // ART3 // 419 // Homo sapiens ADP-	ART3	ART3, Homo sapiens ADP-ribosyltransferase 3, (cDNA clone MGC:23844 IMAGE:4292261), complete cds. q21.1
SNP_A-2055315	aataagcaggaactca[A/G]taaatagaatgaatga	A	G	80143 // Homo sapiens hypothetical protein FLJ21168 (FLJ21168), mRNA. /// NM_000549 // upstream // 216861 //	FLJ21168	FLJ21168, Homo sapiens hypothetical protein FLJ21168 (FLJ21168), p13.1
SNP_A-1911263	tgtctggtggtgaaca[G/T]ggtgcctactaggaag	G	T	Homo sapiens RNA binding protein with multiple splicing (RBPMS), mRNA. /// ENST00000339877 // intron // 0 // --- // --	RBPMS	RBPMS, Homo sapiens RNA binding protein with multiple splicing (RBPMS), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270962	gacagtgttgggacaa[C/T]cagaaatttgaatata	C	T	22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// NM_014965 // downstream // 16081 // Hs.535711 //	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. p22.1
SNP_A-1973485	actaggtgatccagaa[A/G]gtggccagatgagtgg	A	G	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1975738	gcttttggaggaagcc[A/G]ctgggccctttatata	A	G	Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 //	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-1992922	tagaatagacaaatta[C/T]attttctctgcaaatt	C	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2296841	gccaagaagtaatccc[A/C]catacctacaacaaac	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 768028 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1898369	tgcttcaggaaccaaa[A/C]gcagaaggtaacagaa	A	C	sapiens interferon regulatory factor 2 (IRF2), mRNA. /// ENST00000303389 // intron // 0 // --- // --- // --- // ---	IRF2	IRF2, Homo sapiens interferon regulatory factor 2 (IRF2), q35.1
SNP_A-2260850	gaaactgagcacaaag[A/C]agttaagaaaactggc	A	C	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-2048011	aagcaagcgtccacga[A/G]tcagggtgctccaggg	A	G	Homo sapiens SEC5-like 1 (S. cerevisiae) (SEC5L1), mRNA. /// ENST00000230449 // intron // 0 // --- // --- // --- // ---	SEC5L1	SEC5L1, Homo sapiens SEC5-like 1 (S. cerevisiae) (SEC5L1), p25.3
SNP_A-2292826	gcagaaaaaccctatc[A/G]atcaatatacttagca	A	G	Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 //	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-2017989	gatgcgtgtttggcac[A/G]agatttccctaattgc	A	G	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2077835	accagacttaaaaaaa[A/C]caaagataatgctgca	A	C	mRNA for KIAA0227 gene, partial cds. /// ENST00000256367 // intron // 0 // --- // --- // --- // ---	TTC9	TTC9, Human for KIAA0227 gene, partial cds. ,q24.2
SNP_A-2086618	actgaagaaagacccc[A/G]aaatgaggccctcttc	A	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2120613	tcaggcagtattatga[A/G]gtgacaggaaatattt	A	G	Homo sapiens high-mobility group box 1 (HMGB1), mRNA. /// ENST00000341423 // intron // 0 // --- // --- // --- // ---	HMGB1	HMGB1, Homo sapiens high-mobility group box 1 (HMGB1), q12.3
SNP_A-2236009	ctcctgggccctggac[C/T]gatttttcgttaataa	C	T	Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST00000335473 // intron // 0 // --- // --- // --- // ---	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2002502	gggagtcttggctaaa[A/G]agcttccatcccacgg	A	G	Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, mRNA. /// ENST00000224721 // intron // 0 // --- // --- // --- // ---	CDH23	CDH23, Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, q22.1
SNP_A-1828809	taaggaagaatgttcc[A/G]attttcagcatgaaga	A	G	81544 // Homo sapiens hypothetical protein PP1665 (PP1665), mRNA. /// NM_001235 // upstream // 3406 //	PP1665	PP1665, Homo sapiens hypothetical protein PP1665 (PP1665), q13.5
SNP_A-1803639	gtcaaactcagcaaag[A/G]ctttcatgctgtcaag	A	G	// Homo sapiens brain-derived neurotrophic factor (BDNF), transcript variant 1, mRNA. /// NM_001709 // upstream // 80739 // Hs.502182 // BDNF // 627 // Homo sapiens brain-	BDNF	BDNF, Homo sapiens brain-derived neurotrophic factor (BDNF), transcript variant 1, p14.1
SNP_A-2151391	atgttcaattatagcc[A/G]caaataacatttaatt	A	G	Homo sapiens microtubule-associated protein 7 (MAP7), mRNA. /// ENST00000354570 // intron // 0 // --- // --- // --- // ---	MAP7	MAP7, Homo sapiens microtubule-associated protein 7 (MAP7), q23.3
SNP_A-2118007	aggttttgtgcaagac[C/G]caattccttcaggact	C	G	8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 30556 // Hs.425091 // FAM44B	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2022429	aaaaatagtttaaaca[A/G]gcatctaaacacaact	A	G	/// ENST00000323868 // upstream // 14303 // --- // --- // --- // ---	-	q11.23
SNP_A-2083732	aataaataatcacaaa[A/T]aagatcaatgtagact	A	T	// Homo sapiens KIT ligand (KITLG), transcript variant a, mRNA. /// NM_000899 // upstream // 86592 // Hs.1048 //	KITLG	KITLG, Homo sapiens KIT ligand (KITLG), transcript variant a, q21.33
SNP_A-2012698	aaagcactgtctatag[C/T]acaaatcatccctgac	C	T	NM_006080 // intron // 0 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // intron // 0 // --- // --- // --- // ---	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-2249493	cttaacaggcctccta[C/G]taagtagcattttcta	C	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 143318 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2107224	agcgtttaaagctgga[A/C]aaacttcaacaataaa	A	C	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 147986 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2067731	acaacagaagtggaaa[C/G]ggtccagggagtctca	C	G	Homo sapiens dedicator of cytokinesis 3 (DOCK3), mRNA. /// ENST00000266037 // intron // 0 // --- // --- // --- // ---	DOCK3	DOCK3, Homo sapiens dedicator of cytokinesis 3 (DOCK3), p21.31
SNP_A-1897588	tgtctctctttaaatg[C/T]aaaagtatttcaatta	C	T	Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // --- //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1971094	gtaagggaagccctcc[A/G]aatgtcttgaagccca	A	G	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), transcript variant 1, mRNA. /// NM_001003406 // intron // 0 // Hs.125116 // CACNA1I // 8911	CACNA1I	CACNA1I, Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), transcript variant 1, q13.1
SNP_A-1650156	ctcagagtgtatatagtagttctag[C/T]atcttaaaaaataacatctagatca	C	T	NM_004752 // upstream // 23948 // Hs.227098 // GCM2 // 9247 // glial cells missing homolog 2 (Drosophila)	GCM2	GCM2 , rs10484890, glial cells missing homolog 2 (Drosophila),p24.2
SNP_A-1924077	ttagtgtttctttggt[C/G]aaaaggttcagtacgc	C	G	27020 // Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, mRNA. /// NM_012428 // upstream // 186414 // Hs.187866 // SDFR1 // 27020 // Homo	SDFR1	SDFR1, Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, q24.1
SNP_A-1819081	gttgccctatctaaca[G/T]ggatcctaacagaacc	G	T	8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 933501 // --- // --- // --- //	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2193043	catctaaagatctaaa[G/T]atggctttaggtaaga	G	T	6489 // Homo sapiens sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8A), mRNA. /// NM_014802 // downstream // 93005 // Hs.271014 // KIAA0528 // 984	ST8SIA1	ST8SIA1, Homo sapiens sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8A), p12.1
SNP_A-2247784	ctgtgagcaagaggaa[A/G]cttcagcccacctggg	A	G	// 94039 // Homo sapiens zinc finger protein 101 (ZNF101), mRNA. /// NM_021030 // downstream // 11204 // Hs.466261	ZNF101	ZNF101, Homo sapiens zinc finger protein 101 (ZNF101), p13.11
SNP_A-1833244	tacactattagggtaa[A/G]actcttctgttcattc	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 139579 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1900734	tggaggtgtcatttcc[A/G]gagagaaaaatgtttc	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 146274 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2286879	gatggggagtgaagaa[A/G]taagcggcttctcaaa	A	G	Homo sapiens FLN29 gene product (FLN29), mRNA. /// ENST00000257604 // intron // 0 // --- // --- // --- // ---	FLN29	FLN29, Homo sapiens FLN29 gene product (FLN29), q24.13
SNP_A-1980952	tcatgagagaaagtca[A/G]gtaaacaaaagcgaca	A	G	23114 // Homo sapiens mRNA for KIAA0756 protein, partial cds. /// NM_005076 // upstream // 18109 // Hs.519220 //	NFASC	NFASC, Homo sapiens for KIAA0756 protein, partial cds. q32.1
SNP_A-1810500	gtgatttcaggcatca[A/G]ctgggactttggaaca	A	G	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 490178 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1753107	aggttattgttggggtgaacagacc[C/G]aacaccaggtcgtgggggtgacaa a	C	G	5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 1453519 // Hs.135892 // NCAM2 // 4685 // neural	PRSS7	PRSS7 , rs1961544, protease, serine, 7 (enterokinase) ,q21.1
SNP_A-2167724	caacccaggacactca[A/G]tcttcaagaagagagt	A	G	sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // intron // 0 // --- // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-1872588	tctagggcatagtaaa[A/T]acttcacacaagttag	A	T	10001 // Homo sapiens mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (MED6), mRNA. /// D86980 // upstream // 22803 // Hs.79170 // TTC9 // 23508 //	MED6	MED6, Homo sapiens mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (MED6), q24.2
SNP_A-1977692	cttcttcctttccttc[A/G]ctttcacaggtgtgga	A	G	901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 275379 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2169493	caagcctggttgctcc[G/T]gcactgaactgtggcc	G	T	3274 // Homo sapiens histamine receptor H2 (HRH2), mRNA. /// NM_006651 // upstream // 110572 // Hs.478930 // CPLX1	HRH2	HRH2, Homo sapiens histamine receptor H2 (HRH2), q35.2
SNP_A-1957811	ttttattggcaaaagc[A/G]gacaagagaaggaaaa	A	G	79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 108377 //	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-2054148	aagttccttgtcctcc[A/G]ccagccctctggtgat	A	G	119391 // Homo sapiens glutathione S-transferase omega 2 (GSTO2), mRNA. /// NM_033397 // downstream // 6862 //	GSTO2	GSTO2, Homo sapiens glutathione S-transferase omega 2 (GSTO2), q25.1
SNP_A-1917575	tgttttttcagcctca[C/T]gttcatgttgtgagga	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1856230	tcacaagtgatgagat[A/G]aaaattgtcaaccaag	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2080939	acctctgcctgcacaa[A/G]tgagaggcaatgagca	A	G	Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), mRNA. /// ENST00000318445 // intron // 0 // --- // --- // --- // ---	SLCO3A1	SLCO3A1, Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), q26.1
SNP_A-2247969	ctgtgcctacattcct[A/G]accatggaaattgtga	A	G	204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// ENST00000294639 // intron // 0 // ---	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1934028	ttctcactagcctctc[C/T]atgctgtgtcctctt	C	T	// Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// ENST00000270828 // intron // 0 // ---	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2279475	gaggatcttgctttta[A/G]gatggacaccaccaag	A	G	// 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 361254 // Hs.546345 //	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-1977047	aggcaaattgcacaca[C/T]gaagaaatttcacagc	C	T	Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA. /// ENST00000273859 // intron // 0 // --- // --- // --- // ---	ATP10D	ATP10D, Homo sapiens ATPase, Class V, type 10D (ATP10D), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1866361	tcccatttccaatcaa[G/T]aaattaagaatacagg	G	T	ENST00000359550 // intron // 0 // --- // --- // ---	-	q21.2
SNP_A-2012450	atcgttagctggtgc[C/T]ccctctggaaatgtca	C	T	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA. /// ENST00000342947 // intron // 0 // --- // --- // ---	DFNA5	DFNA5, Homo sapiens deafness, autosomal dominant 5 (DFNA5), p15.3
SNP_A-2209112	cccaggccaggctgac[A/G]agagctgcaggagacc	A	G	Homo sapiens tubulin-specific chaperone d (TBCD), mRNA. /// ENST00000355528 // intron // 0 // --- // --- // ---	TBCD	TBCD, Homo sapiens tubulin-specific chaperone d (TBCD), q25.3
SNP_A-2052864	aagtcagtataacgac[A/T]actccagaactgccac	A	T	Homo sapiens palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) (PPT1), mRNA. /// NM_012421 // upstream // 41503 // Hs.205627 // RLF // 6018	PPT1	PPT1, Homo sapiens palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) (PPT1), p34.2
SNP_A-2312251	ggacagtgagatgaca[C/T]aatccacatttagaaa	C	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-1850491	gtctcctgaataaaca[A/T]agaatgtgaccacaaa	A	T	ENST00000360174 // intron // 0 // --- // --- // ---	-	q12
SNP_A-1975941	tgtgagtggtggccta[C/T]ggaggattggagggta	C	T	/// ENST00000326756 // downstream // 316810 // --- // --- // ---	-	p16.1
SNP_A-1799216	gtaagtagaaaagtgt[C/T]aagaaaatcataagga	C	T	// 29789 // Homo sapiens hypothetical protein PTD004 (PTD004), mRNA. /// NM_013341 // downstream // 67441 //	PTD004	PTD004, Homo sapiens hypothetical protein PTD004 (PTD004), q31.1
SNP_A-2107389	agctacaggataaaaa[C/T]aagttaactgaactca	C	T	// 57633 // Homo sapiens leucine rich repeat neuronal 1 (LRRN1), mRNA. /// ENST00000319331 // downstream //	LRRN1	LRRN1, Homo sapiens leucine rich repeat neuronal 1 (LRRN1), p26.1
SNP_A-1861721	tcatctgcaccctcac[A/G]accgtcagctcccagc	A	G	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2072414	acagcacttggcagcc[A/T]caaaggtttggagctt	A	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2806246 // --- // -	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. .p13.3
SNP_A-2032729	aaataacatttctccta[A/T]gtgaacattatcttttg	A	T	Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000323418 // intron // 0 // --- // --- //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-1992970	accactgtcaagatca[A/G]aggagaaaaaagaacaa	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // intron // 0 // Hs.453951 // NRG1 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1933040	ttcggaaactgagctc[C/G]agacagggtcagtgtt	C	G	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2307913	gagagccgaacttaac[C/T]acagaatatagtgac	C	T	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 802480 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1906208	tggtgacataaactca[C/T]cttcacatatacaca	C	T	Homo sapiens G protein-coupled receptor 92 (GPR92), mRNA. /// ENST00000329858 // intron // 0 // --- // --- // ---	GPR92	GPR92, Homo sapiens G protein-coupled receptor 92 (GPR92), p13.31
SNP_A-1879866	tcttcccctctaagc[A/C]atcctgtacaggata	A	C	- /// ENST00000361117 // upstream // 557461 // --- // --- // ---	-	q33.2
SNP_A-2072468	acagcagtgctgagaa[A/G]cgctaaatctagacat	A	G	Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // --- // --- // --- // ---	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2192102	catcactgatatctac[A/C]caagagatacttgta	A	C	Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // --- // --- // ---	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-2059073	aatccctcaaaatgtg[C/G]agaatcactaatttag	C	G	26005 // Homo sapiens DKFZP586P0123 protein (DKFZP586P0123), mRNA. /// ENST00000313663 // intron // 0 // --- // --- // --- /// ENST00000313681 // intron // 0 // --- //	DKFZP586P012 3	DKFZP586P0123, Homo sapiens DKFZP586P0123 protein (DKFZP586P0123), q13.4
SNP_A-1794222	ggtcatctcctcccc[A/C]acatgaagcttgttgg	A	C	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2244081	ctgcttggctctcaat[A/G]atgatagctgctatt	A	G	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 52165 // Hs.183817 // USP31 // 57478 // 51124 // Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), mRNA. ///	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2243833	ctgctgcttgggacca[C/G]agaatacagcaggact	C	G	ENST00000256433 // upstream // 481161 // --- // --- // ---	IER3IP1	IER3IP1, Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), q21.1
SNP_A-2146014	atgcctcttattcct[A/T]actggccctcttctt	A	T	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-2113604	aggctatgcaatttg[C/T]acacgtataggttgtg	C	T	// 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_002271 // downstream // 16101 // Hs.513057	RANBP5	RANBP5, Homo sapiens RAN binding protein 5 (RANBP5), q32.2
SNP_A-1937502	ttgaaccaaatgaacc[A/C]ataaatagcattaaat	A	C	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4355049 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2001756	agaatataaggcaaag[A/G]agcttggtgcatcta	A	G	// 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf107), mRNA. /// BX641020 // upstream // 132436 // Hs.535297 // ARID5B // 84159 // Homo sapiens	C10orf107	C10orf107, Homo sapiens chromosome 10 open reading frame 107 (C10orf107), q21.2
SNP_A-1927273	ttcaaaacttcatata[A/G]caacttcttttacca	A	G	Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), mRNA. /// ENST00000357444 // intron // 0 // ---	RABGAP1L	RABGAP1L, Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), q25.1
SNP_A-1916801	tgtttccttccagaaac[C/T]gcaaagccacatggaa	C	T	254958 // Homo sapiens exonuclease GOR (GOR), mRNA. /// NM_033126 // downstream // 5037 // Hs.532044 // PSKH2	GOR	GOR, Homo sapiens exonuclease GOR (GOR), q21.3
SNP_A-1920123	ttaatcatgagaggac[C/T]atattctgcctagccc	C	T	92181 // Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), mRNA. /// ENST00000306184 // upstream	DC-UbP	DC-UbP, Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), q35.1
SNP_A-2127216	ataaatgaccacagga[A/G]gcaagcactggcccaat	A	G	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA. /// ENST00000268124 // intron // 0 // --- // --- // ---	POLG	POLG, Homo sapiens polymerase (DNA directed), gamma (POLG), q26.1
SNP_A-2211076	cccggccaaaaggccc[A/G]gcttgaatggaagaca	A	G	ENST00000282163 // intron // 0 // --- // --- // ---	-	q32.12
SNP_A-1703013	aatactctgcccatctaagatcta[C/T]atctgaaaagtccctttcatcacat	C	T	1058 // centromere protein A, 17kDa /// NM_002246 // downstream // 21581 // Hs.24040 // KCNK3 // 3777 //	CENPA	CENPA, rs828256, centromere protein A, 17kDa ,p23.3
SNP_A-1933670	ttctagtccaagtctc[A/G]attttccttcacaga	A	G	// Homo sapiens hypothetical protein FLJ40629 (FLJ40629), mRNA. /// ENST00000327581 // intron // 0 // --- // --- // ---	FLJ40629	FLJ40629, Homo sapiens hypothetical protein FLJ40629 (FLJ40629), q13
SNP_A-2130366	atactaaggaggggaga[A/C]tcataaagcagaaaag	A	C	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 143157 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2274915	gagaacacgtagagaa[C/G]agtccaagtgcactga	C	G	sapiens nuclear factor I/B (NFIB), mRNA. /// ENST00000339974 // intron // 0 // --- // --- // --- ///	NFIB	NFIB, Homo sapiens nuclear factor I,p22.3
SNP_A-2068230	acaagatcatcagaaa[A/G]acagaaaaatctgacc	A	G	56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 1635124 // Hs.463466 //	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-2105633	agccacgctataagag[A/G]aagtaaatgagaaaca	A	G	440044 // Homo sapiens FLJ16331 protein (FLJ16331), mRNA. /// NM_032325 // 3UTR // 0 // Hs.425178 //	FLJ16331	FLJ16331, Homo sapiens FLJ16331 protein (FLJ16331), q13.1
SNP_A-2062371	aatgtaaggccaata[G/T]aatagaagttttgtct	G	T	// 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 77605 // Hs.194766 // SEZ6L //	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2267589	gaatatttggaggaag[C/G]atggcacataaagaa	C	G	Homo sapiens sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8A), mRNA. /// ENST00000261197 // intron // 0 // --- // --- // --- // ---	ST8SIA1	ST8SIA1, Homo sapiens sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8A), p12.1
SNP_A-1869213	tcctggattgcagattt[A/G]aaaaagcagttcctat	A	G	90826 // Homo sapiens hypothetical protein BC004337 (LOC90826), mRNA. /// NM_024605 // upstream // 36033 //	LOC90826	LOC90826, Homo sapiens hypothetical protein BC004337 (LOC90826), q31.23
SNP_A-1914319	tgtgttccaggcgtta[C/T]gctaaagcatgtttcat	C	T	5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000217725 // upstream	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.31
SNP_A-2177093	cacctcaggcattgt[A/G]aaaataaaattatgtc	A	G	6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 191509 // Hs.355606	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1699007	taaatatggcaatagatgataata[C/T]aggatttctttgataagtctccaga	C	T	NM_002526 // upstream // 205525 // Hs.153952 // NT5E // 4907 // 5'-nucleotidase, ecto (CD73)	NT5E	NT5E, rs10485307, 5'-nucleotidase, ecto (CD73),q14.3
SNP_A-1981355	tctagggatacca[C/T]agtttgcaacatgagc	C	T	Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// ENST00000320816 // intron // 0 // --- // --- // --- ///	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-2088130	actgggaccaaaagag[A/G]aaacactgagggctc	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 145220 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1887167	tgagaaagtataccaa[C/T]gtagacccagctatcc	C	T	ENST00000339567 // intron // 0 // --- // --- // --- /// ENST00000343332 // intron // 0 // --- // --- // --- ///	-	p12
SNP_A-1916825	tgttctaacatttta[G/T]caccttctggccttt	G	T	Homo sapiens chromosome 1 open reading frame 26 (C1orf26), mRNA. /// ENST00000264138 // intron // 0 // --- // ---	C1orf26	C1orf26, Homo sapiens chromosome 1 open reading frame 26 (C1orf26), q25.3
SNP_A-2167346	caacaggcaacacaga[C/T]agtgattcttgagaga	C	T	Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. /// ENST00000272983 // intron // 0 // --- // ---	PPP1R7	PPP1R7, Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), q37.3
SNP_A-2040379	aaccagaggcgcctgc[A/G]gattctggagggtct	A	G	Homo sapiens likely ortholog of mouse signaling intermediate in Toll pathway-evolutionarily conserved (SITPEC), mRNA. /// ENST00000270517 // 3UTR // 0 // --- // --- // ---	SITPEC	SITPEC, Homo sapiens likely ortholog of mouse signaling intermediate in Toll pathway-evolutionarily conserved (SITPEC), p13.2
SNP_A-1837920	acgtgtttggtgagca[C/G]gtaggatagacccaat	C	G	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA. /// ENST00000252172 // intron // 0 // --- // --- // 121536 // Homo sapiens AE binding protein 2 (AEBP2),	MYH13	MYH13, Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), p13.1
SNP_A-2040977	aacctgtggaggtca[A/G]ccaaatagttcaggca	A	G	mRNA. /// NM_153207 // downstream // 682403 // Hs.504943	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140856	atctgaatcaactgta[A/G]actatacttaataata	A	G	90 // Homo sapiens activin A receptor, type I (ACVR1), mRNA. /// NM_173355 // upstream // 44141 // Hs.128427 //	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-2019081	aatagaacaacgataaa[G/T]attttaatgtgtgcag	G	T	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-1895295	tgccctcggtgtgaaa[C/G]ggcaatgtgtgtcccc	C	G	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 10 (ABCA10), mRNA. /// ENST00000269081 // intron // 0 // --- // --- // ---	ABCA10	ABCA10, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 10 (ABCA10), q24.3
SNP_A-2149359	atgtacaggatatatc[A/T]acatttactactcatc	A	T	390181 // Homo sapiens olfactory receptor, family 5, subfamily AK, member 2 (OR5AK2), mRNA. /// NM_001005210 // upstream // 95563 // Hs.199853 //	OR5AK2	OR5AK2, Homo sapiens olfactory receptor, family 5, subfamily AK, member 2 (OR5AK2), q11
SNP_A-2268734	gaatgtttgcaaaca[C/G]aactcgataatttgaa	C	G	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds., q13.1
SNP_A-2063461	aattaagttatatcga[C/T]agtttactgttctg	C	T	Homo sapiens sarcolemma associated protein (SLMAP), mRNA. /// ENST00000295952 // intron // 0 // --- // --- // ---	SLMAP	SLMAP, Homo sapiens sarcolemma associated protein (SLMAP), p14.3
SNP_A-1971681	gagccaggcctgcca[C/T]gatgtgctacagatga	C	T	138046 // Homo sapiens hypothetical protein LOC138046 (LOC138046), mRNA. /// ENST00000333552 // intron // 0 // ---	LOC138046	LOC138046, Homo sapiens hypothetical protein LOC138046 (LOC138046), q21.2
SNP_A-1994096	ttatcctggacccaaa[A/G]tgaaattatcataact	A	G	musashi homolog 2 (Drosophila) /// NM_170721 // intron // 0 // ---	LOC138046	MSI2 , rs2197252, musashi homolog 2 (Drosophila) ,q23.2
SNP_A-1660199	ccgggggccaacctttctctcccag[A/G]cacctagagcaatagtgcctattt	A	G	Hs.185084 // MSI2 // 124540 // musashi homolog 2	MSI2	MSI2 , rs2197252, musashi homolog 2 (Drosophila) ,q23.2
SNP_A-2169757	caagggagaaaaaggag[A/G]agaaatcaacaacaaa	A	G	ENST00000332454 // intron // 0 // --- // --- // ---	-	q13.12
SNP_A-1996398	ggcttcctgggggatat[A/C]agacaattcaacaaat	A	C	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 326124 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2049786	aaggaaaactgtaatc[A/G]agaacctctaagctat	A	G	58516 // Homo sapiens chromosome 12 open reading frame 14 (C12orf14), mRNA. /// NM_144973 // downstream // 32704	C12orf14	C12orf14, Homo sapiens chromosome 12 open reading frame 14 (C12orf14), p11.21
SNP_A-2306567	gctgtaagacggaggag[A/G]aactttgctgaaaggg	A	G	Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7), transcript variant 1, mRNA. /// NM_177427 // intron // 0 // Hs.507102 // P2RX7 // 5027 //	P2RX7	P2RX7, Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7), transcript variant 1, q24.31
SNP_A-1967593	cctgagaaaggcagaaa[C/T]agtttttcaaaaccat	C	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 904895 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1883084	tgaaatccccaacttg[A/C]aactccaattacttca	A	C	353131 // Homo sapiens late cornified envelope 1A (LCE1A), mRNA. /// NM_030663 // upstream // 4247 // Hs.111850 //	LCE1A	LCE1A, Homo sapiens late cornified envelope 1A (LCE1A), q21.3
SNP_A-1847015	tatcagggagattggc[A/G]aatgctacaaataagg	A	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 851035 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2029105	aaagaaatctgggaaa[C/T]tgctggaaatgaatgt	C	T	55857 // Homo sapiens chromosome 20 open reading frame 19 (C20orf19), mRNA. /// ENST00000334388 // upstream //	C20orf19	C20orf19, Homo sapiens chromosome 20 open reading frame 19 (C20orf19), p11.23
SNP_A-2314652	ggagtagggaattcaa[A/G]ggacaacatgaagata	A	G	// Homo sapiens N-myristoyltransferase 2 (NMT2), mRNA. /// ENST00000325585 // upstream // 37182 // --- // --- // ---	NMT2	NMT2, Homo sapiens N-myristoyltransferase 2 (NMT2), p13
SNP_A-1815052	gtgttcacacattcac[A/C]cttctccatagtgact	A	C	Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000264808 // intron // 0 // --- // --- // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-2226139	ctaacctgatgctct[A/G]acttccttggatagc	A	G	ENST00000344027 // intron // 0 // --- // --- // ---	-	q21.2
SNP_A-2117521	aggtgttggtatcaga[A/G]agatcttgatttgaat	A	G	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1178230 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2166687	caaattatcaaaagag[A/T]atctcgaaagcagcaa	A	T	Homo sapiens small proline-rich protein 2B (SPRR2B), mRNA. /// ENST00000360379 // intron // 0 // --- // --- // ---	SPRR2B	SPRR2B, Homo sapiens small proline-rich protein 2B (SPRR2B), q21.3
SNP_A-1929439	ttcagttcataggtca[A/C]ctgatcaagaagagcc	A	C	// Homo sapiens isiet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream //	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-1999849	tgggcctaactggaa[C/T]tgataatcttgcttac	C	T	Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// ENST00000354496 // intron // 0 // --- // --- /// ENST00000351738 // intron // 0 // --- // ---	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.21
SNP_A-2169364	caagcataataaaacat[C/G]atagtctggaactggg	C	G	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1829887	taataagcttaacata[C/T]atagataccccatgcaa	C	T	/// ENST00000297703 // upstream // 191792 // --- // --- // ---	-	p12
SNP_A-1837378	tacttccagagttagg[G/T]aaatcttagaaatt	G	T	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 131023 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813036	gtgggtgcctcccaca[C/T]ggtgtattcatcttgt	C	T	Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), mRNA. /// ENST00000361062 // intron // 0 // --- // --- // --- // ---	TNIP1	TNIP1, Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), q33.1
SNP_A-2109295	agctttcaacaacaac[C/T]gccctcatcaattgga	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2038404	aacactcttcaccaaa[C/T]gaataggaagcaaaaa	C	T	// 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 2163514 // Hs.391781 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-2276641	gagagtcacctcccaa[A/G]tccaggaagcaaaagg	A	G	Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 1 (ATP6V0D1), mRNA. /// ENST00000290949 // intron // 0 // --- // --- // --- // ---	ATP6V0D1	ATP6V0D1, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 1 (ATP6V0D1), q22.1
SNP_A-1965338	taccatgtactccata[A/C]tataatcttttaaatg	A	C	Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 731562 // Hs.302442	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2252645	cttcctttctctctcg[A/T]ccatgacttcaacatt	A	T	Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), mRNA. /// ENST00000357257 // intron // 0 // --- // --- // --- // ---	COL27A1	COL27A1, Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), q32
SNP_A-1898425	tgcttcctgaggttac[C/T]ggtgtacccgtgtgtg	C	T	Homo sapiens chromosome 19 open reading frame 18 (C19orf18), mRNA. /// ENST00000355486 // intron // 0 // --- //	C19orf18	C19orf18, Homo sapiens chromosome 19 open reading frame 18 (C19orf18), q13.43
SNP_A-1991975	tttaaactagctgaaa[G/T]atgtggagtgattagt	G	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2359904 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1988229	agagggcgtctttgga[A/G]aattccagcagttcag	A	G	154043 // Homo sapiens membrane associated guanylate kinase interacting protein-like 1 (MAGI1), mRNA. /// NM_014892 // upstream // 174159 // Hs.227602 // RBM16 //	MAGI1	MAGI1, Homo sapiens membrane associated guanylate kinase interacting protein-like 1 (MAGI1), q25.2
SNP_A-2235117	ctcccatgataaacca[C/T]taattcattaaccttc	C	T	1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // upstream // 40383 // Hs.465413 // CYB5 //	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-1686296	aagaaaatgccttcccaataatagg[A/G]agttgtactatggaagtaatatgga	A	G	// 131474 // coiled-coil-helix-coiled-coil-helix domain containing 4 /// NM_182629 // downstream // 24155 // - // - // -	CHCHD4	CHCHD4 , rs10510425, coiled-coil-helix-coiled-coil-helix domain containing 4 ,p25.1
SNP_A-2082329	acgatgtgcctggtta[C/T]gtaatgttgataatga	C	T	203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000318382 // upstream //	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1790169	ggggacagaggaagac[A/G]catcccgctagaccag	A	G	ENST00000294484 // intron // 0 // --- // --- // --- // ---	-	p36.22
SNP_A-2010391	acctggaataagaatc[A/T]gaataccaaattttag	A	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1963150 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2292746	gcacttctcatgttta[A/C]cagctcattggtaagt	A	C	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2292054	gacatttcttaggaca[A/G]gcaagaatacaagtct	A	G	Homo sapiens MEGF11 protein (MEGF11), mRNA. /// ENST00000288745 // intron // 0 // --- // --- // --- // ---	MEGF11	MEGF11, Homo sapiens MEGF11 protein (MEGF11), q22.31
SNP_A-2002801	agaacggtgataacaa[C/T]ggccacgggagtgttt	C	T	ENST00000229088 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2129699	atacagggcatttttta[C/T]acgactctctttcctc	C	T	Homo sapiens epithelial membrane protein 2 (EMP2), mRNA. /// ENST00000359543 // intron // 0 // --- // --- // --- // ---	EMP2	EMP2, Homo sapiens epithelial membrane protein 2 (EMP2), p13.13
SNP_A-1822712	taaaaaagacctagac[A/G]caacattctgctagga	A	G	Homo sapiens dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPP1), mRNA. /// ENST00000296414 // intron // 0 // --- // --- // --- // ---	DAPP1	DAPP1, Homo sapiens dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPP1), q23
SNP_A-1870560	tcgagtagtacattta[C/T]gtgatggagcagtaag	C	T	// 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2270577	gacagagggtttcctg[A/G]caaacatccaacttgt	A	G	Homo sapiens scavenger receptor class B, member 2 (SCARB2), mRNA. /// ENST00000264896 // intron // 0 // --- //	SCARB2	SCARB2, Homo sapiens scavenger receptor class B, member 2 (SCARB2), q21.1
SNP_A-2028238	aaactataaatggcta[C/G]aacgggagttatggag	C	G	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2027260	aaacatagggcagaaa[C/T]actagcttatgtctaa	C	T	DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 21659 // --- // --- // --- // ---	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-2031071	ctaccactttcggcct[C/G]aagtgacagtgttttt	C	G	/// ENST00000334227 // downstream // 31061 // --- // --- // ---	-	p13.31
SNP_A-2031556	aaaggttcagcctgct[A/G]actctggttttaccta	A	G	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2019244	taactcttacctacaa[C/T]taatctatgcatgaaa	C	T	sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 2, mRNA. /// ENST00000357391 // intron // 0 // --- // --- // --- // --- ///	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 2, q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2026027	aaaattaacacttcac[A/G]acacaagatattcctt	A	G	Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 2, mRNA. /// NM_007051 // intron // 0 // Hs.530402 // FAF1 // 11124 // Homo sapiens Fas (TNFRSF6)	FAF1	FAF1, Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 2, p32.3
SNP_A-2039222	aacagtgctgaagcac[A/G]cttcatgtgaacgttg	A	G	// 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 217118 // --- // --- // --- // --- //	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2034648	aaatgaaacgtgttgc[C/T]ctgaagcaaagtaatt	C	T	Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 //	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.1
SNP_A-2042357	aactcaaaagtgagat[G/T]aggaggatgcagctga	G	T	5997 // Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA. /// NM_015984 // downstream //	RGS2	RGS2, Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), q31.2
SNP_A-2047274	aagatatggcagacaa[A/C]gagttggtagatattc	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1678887 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2002780	gtaagactaccgaata[G/T]agtttatgatatttct	G	T	-- /// ENST00000354800 // downstream // 643471 // --- // --- // ---	-	q14.1
SNP_A-1996100	attggacctggccaca[C/G]agataacctgtaatca	C	G	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 310508 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2010160	gagtgattttgtttaa[G/T]gcttataacttgttat	G	T	57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // upstream //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2018536	cccatctggaagctac[C/T]gaatccagatctttgt	C	T	Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2016236	attaattataatgata[C/G]taaatccacagggtta	C	G	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2089664	acttccaaactgttca[A/G]atattcccagtatgat	A	G	// Homo sapiens chromosome 10 open reading frame 129 (C10orf129), mRNA. /// ENST00000327739 // intron // 0 // ---	C10orf129	C10orf129, Homo sapiens chromosome 10 open reading frame 129 (C10orf129), q23.33
SNP_A-2107666	agctcaaaaaagatgc[C/G]gagccctgacttgtat	C	G	57534 // Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), mRNA. /// NM_005257 // upstream // 169222 //	MIB1	MIB1, Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), q11.2
SNP_A-2095495	agacaactgaaaaatg[C/T]atgttgctttgtgtat	C	T	// 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 //	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-2097871	agagagaaaatagaca[C/T]tgaggtctccaaaagc	C	T	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 (ADAMTS19), mRNA. /// ENST00000274487 // intron // 0 // --- // --- // --- // ---	ADAMTS19	ADAMTS19, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 (ADAMTS19), q23.3
SNP_A-2050476	aaggatcatagagaca[A/G]agaagtaactactgta	A	G	// 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1222670 // Hs.514980 // SALL3	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2052975	aagtccagtgtcacaa[C/T]tgtacctctgagtagc	C	T	// 93487 // Homo sapiens chromosome 14 open reading frame 32 (C14orf32), mRNA. /// NM_002306 // upstream //	C14orf32	C14orf32, Homo sapiens chromosome 14 open reading frame 32 (C14orf32), q22.3
SNP_A-2061811	aatggagttaaaggaa[A/G]aatggaacatacagac	A	G	Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// ENST00000317327 // intron // 0 // --- // --- // --- // ---	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.31
SNP_A-2059384	aatctaaggcatccaa[A/C]ttattaagttttagta	A	C	Homo sapiens ras homolog gene family, member T1 (RHOT1), mRNA. /// ENST00000333942 // intron // 0 // --- // ---	RHOT1	RHOT1, Homo sapiens ras homolog gene family, member T1 (RHOT1), q11.2
SNP_A-2064224	aattcacacataaaaa[A/T]actaaccttaactcaa	A	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-2065058	aattgcaggtgaacca[A/G]gttcctagaatctcta	A	G	// Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), mRNA. /// ENST00000331299 // intron // 0 // --- // --- // --- // ---	SLC25A21	SLC25A21, Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), q13.3
SNP_A-2128317	ataagtcataagtcac[C/T]gatcaaacatatggtc	C	T	// 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream //	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-2127496	ataacagctaataaat[C/G]acttccaaattttaac	C	G	1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 147398 //	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2128075	ataagcatcattttga[C/T]aaaaagagaaagggat	C	T	C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000340000	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2115128	agggctgagtgacaat[C/G]aaacaaaggtcccttc	C	G	ENST00000321345 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-2117682	aggttcatccaggttg[C/T]agtatgtgtcagaatt	C	T	84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// NM_032226 // upstream // 57986 //	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-2167980	caacgtctataactca[C/T]cttatttttaatacag	C	T	sapiens dystrobrevin, alpha (DTNA), transcript variant 1, mRNA. /// NM_032975 // intron // 0 // Hs.58919 // DTNA //	DTNA	DTNA, Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2163937	caaaactcaggttgta[A/G]catctggaatgggtga	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), mRNA. /// ENST00000312428 // intron // 0 // --- // ---	DNAH7	DNAH7, Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), q32.3
SNP_A-2161103	atttgaaagcacctga[A/G]gcaaatgaatgaatat	A	G	5000 // Homo sapiens origin recognition complex, subunit 4-like (yeast) (ORC4L), transcript variant 2, mRNA. /// NM_181742 // upstream // 193284 // Hs.470174 // ORC4L //	ORC4L	ORC4L, Homo sapiens origin recognition complex, subunit 4-like (yeast) (ORC4L), transcript variant 2, q23.1
SNP_A-2150321	atgtctggggaaacaa[C/G]gatgaacaaaacaatg	C	G	Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2152664	attaatataaaagacc[A/C]actagtgaaagcttaa	A	C	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2),	ENPP2	ENPP2, Homo sapiens ectonucleotide pyrophosphatase,q24.12
SNP_A-2141573	atcttatctctgttaa[C/T]gttgccacaagttgat	C	T	57097 // Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), mRNA. /// NM_001759 // upstream // 48985 // Hs.376071 // CCND2 // 894 // Homo sapiens cyclin	PARP11	PARP11, Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), p13.32
SNP_A-2168216	caactgaacaagatta[A/C]caagccacatttttct	A	C	/// ENST00000251675 // downstream // 214835 // --- // --- // --- // --- /// ENST00000360855 // downstream // 214865 // --- // ---	-	q32.3
SNP_A-2168640	caagaagacatcctgg[A/G]agatgtggtttcatct	A	G	79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 320903	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2182959	cagattctgattcata[C/T]taattgtttaagaact	C	T	SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 19433 // Hs.509872 // RGS6 //	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2
SNP_A-2194433	catgattgcaagacca[A/G]tcatgtaggagaccaa	A	G	9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // upstream //	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-2195744	catgtacaaaaacaca[C/T]agtggaaccacattac	C	T	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2223982	cgggctctgaaaacaa[G/T]aatgataactcccata	G	T	/// ENST00000277891 // upstream // 361 // --- // --- // --- // --- /// ENST00000333401 // downstream // 12222 // --- // --- // ---	-	q25.3
SNP_A-2213756	ccgtttgcaaggagcc[C/T]ggacactttcttgata	C	T	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine q12.3
SNP_A-2211215	ccctaaagacagagaa[C/T]caggcttggaagccag	C	T	22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// NM_014965 // downstream // 25846 // Hs.535711 //	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. p22.1
SNP_A-2212595	cccttcagaatcgtga[C/T]ctgttacatcactagc	C	T	54984 // Homo sapiens PIN2-interacting protein 1 (PINX1), mRNA. /// NM_173683 // downstream // 48225 // Hs.353115	PINX1	PINX1, Homo sapiens PIN2-interacting protein 1 (PINX1), p23.1
SNP_A-2208001	cccaactagagctaaa[C/T]ccaggctgttccttag	C	T	3725 // Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), mRNA. /// NM_018291 // upstream //	JUN	JUN, Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), p32.1
SNP_A-2199816	ccaaacccattccgtc[A/G]acaaagcattgtctta	A	G	// Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// ENST00000299191 // CDS // 0 // ---	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-2200023	ccaaagtctagtcaat[C/T]accactctctgatgat	C	T	Homo sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// NM_053036 // upstream // 244041 //	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-2205589	ccagttgatcactgca[A/G]gtttacaaaatgcaat	A	G	Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- //	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1871711	tctaatctctacatca[C/G]agcaaaatccttttca	C	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1869273	tcctgggagtagagca[C/G]agtttggtccagcacc	C	G	FLJ20489 // 55652 // Homo sapiens hypothetical protein FLJ20489 (FLJ20489), mRNA. /// NM_015401 // upstream //	FLJ20489	FLJ20489, Homo sapiens hypothetical protein FLJ20489 (FLJ20489), q13.11
SNP_A-1866282	tcccatccttgaggca[A/C]atcactcacaaaccca	A	C	4225 // Homo sapiens meprin A, beta (MEP1B), mRNA. /// NM_022751 // downstream // 8668 // Hs.444314 // C18orf11	MEP1B	MEP1B, Homo sapiens meprin A, beta (MEP1B), q12.1
SNP_A-1864110	tccacagttgcaagac[A/G]gagaaaggagaagaag	A	G	79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 245067	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1864185	tccaccactgatgacc[A/C]accagagctttctttc	A	C	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1846670	tatattttgatattta[C/T]atttgatgctatgtag	C	T	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream //	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.1
SNP_A-1849461	tatggcaatcttggct[A/T]accttaaaattgaaat	A	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1853804	tcaaaaattataggca[A/G]taagtggcagggcagg	A	G	Homo sapiens cullin 5 (CUL5), mRNA. /// ENST00000299351 // intron // 0 // --- // --- // --- // ---	CUL5	CUL5, Homo sapiens cullin 5 (CUL5), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1854168	tcaaagaattctccaa[A/G]gccttctcaatttaac	A	G	6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 // downstream //	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-1822471	tttgagcagagtgaca[A/G]aagatgaccagaagtt	A	G	// 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 133151 // Hs.461453 // WWOX	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1827383	taactaattgcccttа[A/G]taaatttctttctgct	A	G	FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-1815091	gtgttccctccagcaa[C/T]gaatgtgagatcctgt	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2011949 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1815155	gtgttcttaggcggag[A/G]caatacctaagccagg	A	G	ENST00000356075 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1820787	gtttcccagaagaaag[C/G]ctgtttccggtaccag	C	G	sapiens secretin receptor (SCTR), mRNA. /// ENST00000019103 // intron // 0 // --- // --- // --- // ---	SCTR	SCTR, Homo sapiens secretin receptor (SCTR), q14.2
SNP_A-1840507	tagccatccgtgagcc[A/G]aggaaactgtacacag	A	G	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 115037 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1841703	taggcacttctcaaca[A/G]aaagggatacaagtag	A	G	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1840774	tagctagatgggacat[A/G]aagcagtggagagacg	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 477673 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1843790	tagttaaaaaatcaca[C/T]ggtgctgggttcacac	C	T	FLJ32063 // 150538 // Homo sapiens hypothetical protein FLJ32063 (FLJ32063), mRNA. /// NM_153689 // upstream //	FLJ32063	FLJ32063, Homo sapiens hypothetical protein FLJ32063 (FLJ32063), q33.1
SNP_A-1829213	taagtaagagattaga[C/T]atgagaggtaaagaag	C	T	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 684805 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-1791304	tacatttgggcatgac[A/G]cttttctaggagtaag	A	G	283846 // Homo sapiens mRNA for KIAA0220 gene, partial cds. /// NM_006043 // upstream // 266693 // Hs.115830 //	KIAA0220	KIAA0220, Homo sapiens for KIAA0220 gene, partial cds. p12.1
SNP_A-1788043	gggagagaaagtgcaa[A/G]taaaataaaacggtgc	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 1083808 //	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1794772	ttttatccctatgaat[A/G]agatttctaactcagc	A	G	115362 // Homo sapiens guanylate binding protein 5 (GBP5), mRNA. /// NM_198460 // upstream // 42331 // Hs.254338 //	GBP5	GBP5, Homo sapiens guanylate binding protein 5 (GBP5), p22.2
SNP_A-1809543	gtgagaggatcctgcc[A/G]aaaggtgctcagtggc	A	G	ENST00000327621 // CDS // 0 // --- // --- // --- // ---	-	p11.22
SNP_A-1802078	gtatacatttttaaaa[A/G]gcacaatatgctcata	A	G	// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// ENST00000285928 // intron // 0 // --- // --- // --- // ---	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1801996	gtataagccagatgca[A/G]taattgtgtgtatata	A	G	Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters), member 2	SLC12A2	SLC12A2, Homo sapiens solute carrier family 12 (sodium,q23.2
SNP_A-1695901	atcatcaaattaaaaattaattgcc[A/C]catatgttcaaataataacttatag	A	C	NM_002012 // intron // 0 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene	FHIT	FHIT , rs6446122, fragile histidine triad gene,p14.2
SNP_A-1758288	aaagcccatctgaattactaacatc[A/C]catccatatctatgttaagcagcag	A	C	NM_014682 // intron // 0 // Hs.151449 // ST18 // 9705 // suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ST18	ST18 , rs714048, suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein),q11.23
SNP_A-1965733	atgcaaaattgaatta[C/T]agtaaaatcacttgca	C	T	// 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 279889 // --- // --- // --- //	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-1962517	aaataacagctgcaac[A/G]gccagcaatgaatagg	A	G	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-1966768	caagagaactactgag[A/G]agtctgcatcagttcc	A	G	388697 // Homo sapiens mRNA for hornerin, partial cds. /// ENST00000316073 // upstream // 17112 // --- // --- // --- // ---	HRNR	HRNR, Homo sapiens for hornerin, partial cds. ,q21.3
SNP_A-1967142	tgagtttgacaaatag[C/G]aaggaagacaggctgg	C	G	Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // intron // 0 // --- // --- // --- // ---	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. ,q36.2
SNP_A-1971901	tgtgtttgaggatcac[A/G]acgctactgggttaaa	A	G	Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// ENST00000253692 // intron // 0 // --- // --- // --- // ---	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1975138	gtgttcaaaatgttcc[A/T]actaaccagagcagtt	A	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1974263	cctggggcaatagtaa[C/T]atgaatccacatagag	C	T	// 9857 // Homo sapiens centrosome-associated protein 350 (CAP350), mRNA. /// NM_002826 // upstream // 22059 //	CAP350	CAP350, Homo sapiens centrosome-associated protein 350 (CAP350), q25.2
SNP_A-1957475	ttttataaatctccat[C/T]acagatgccaaaccta	C	T	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1955975	tttgtctaacatactc[C/T]acagttagtattcttc	C	T	3688 // Homo sapiens integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript va /// NM_033666 // upstream // 48752 // Hs.429052 // ITGB1 // 36	ITGB1	ITGB1, Homo sapiens integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript va ,p11.22
SNP_A-1904030	tgggcaccggtggagg[C/T]catgcagtgcctgggg	C	T	83636 // Homo sapiens chromosome 19 open reading frame 12 (C19orf12), mRNA. /// NM_031448 // upstream // 42215 //	C19orf12	C19orf12, Homo sapiens chromosome 19 open reading frame 12 (C19orf12), q12
SNP_A-1895192	tgccccgaggcccctg[C/T]caacaaatgtcacttc	C	T	1437 // Homo sapiens colony stimulating factor 2 (granulocyte-macrophage) (CSF2), mRNA. /// NM_004199 //	CSF2	CSF2, Homo sapiens colony stimulating factor 2 (granulocyte-macrophage) (CSF2), q23.3
SNP_A-1895290	tgccctccactgctga[C/T]gcaattgtaatgatca	C	T	sapiens defensin, beta 1 (DEFB1), mRNA. /// ENST00000297439 // CDS // 0 // --- // --- // --- // ---	DEFB1	DEFB1, Homo sapiens defensin, beta 1 (DEFB1), p23.1
SNP_A-1893975	tgcatatttgttgtaa[A/G]tggcagctaaacattg	A	G	SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-1884029	tgaagcaagctacata[A/G]gaatactcaaaataca	A	G	Homo sapiens RAS protein activator like 2 (RASAL2), transcript variant 1, mRNA. /// NM_170692 // intron // 0 //	RASAL2	RASAL2, Homo sapiens RAS protein activator like 2 (RASAL2), transcript variant 1, q25.2
SNP_A-1881285	tctttatttctttcc[A/C]agagtctgcagtagat	A	C	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 705223 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1880836	tcttggtccacagcac[A/G]agaactctctttctct	A	G	ENST00000319822 // intron // 0 // --- // --- // --- // ---	-	q23
SNP_A-1928400	ttcacctcaggataaa[A/G]ttacatatgaaaatgg	A	G	sapiens cell division cycle 25A (CDC25A), transcript variant 2, mRNA. /// NM_001789 // intron // 0 // Hs.1634 // CDC25A //	CDC25A	CDC25A, Homo sapiens cell division cycle 25A (CDC25A), transcript variant 2, p21.31
SNP_A-1928532	ttcactctcggtgttg[C/T]acgttctatggttttg	C	T	Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // intron // 0 // --- // --- // --- // --- ///	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1920121	ttaatcatcatttcca[C/T]agagaagcagttgccc	C	T	Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // intron // 0 // --- // ---	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-1924207	ttagtttgagttttcc[A/G]aagcaaattccaagag	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1506932 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1914287	tgtgttattgtaaatg[A/G]cactgtttctaatttt	A	G	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 81392 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2268063	gaatcttgcagaatac[A/G]gcgtgggccatataag	A	G	Homo sapiens THUMP domain containing 2 (THUMPD2), mRNA. /// ENST00000295390 // intron // 0 // --- // --- // --- // ---	THUMPD2	THUMPD2, Homo sapiens THUMP domain containing 2 (THUMPD2), p22.1
SNP_A-2259540	gaaaacagtcacagaa[C/T]tgaaaagacacctggg	C	T	FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 //	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-2262265	gaaatcttactcctaa[A/C]tagaagtatcccagaa	A	C	Homo sapiens claudin 10 (CLDN10), transcript variant 1, mRNA. /// ENST00000257311 // intron // 0 // --- // --- // --- // ---	CLDN10	CLDN10, Homo sapiens claudin 10 (CLDN10), transcript variant 1, q32.1
SNP_A-2280068	gagggaagatcctgaa[C/T]catttcatcttcctat	C	T	ENST00000341845 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2235997	tcctgattagaaagta[A/T]gactattttgcaagca	A	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-2236418	ctcgctgtttgaaatc[C/T]cagggcaagatactga	C	T	Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-2238231	ctctgctgttctggaa[C/T]gggggttgggtctgcag	C	T	// Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000251296 // intron // 0 // ---	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-2240522	ctgaccacactgatga[A/G]gcaattcttaatgatc	A	G	Homo sapiens tripartite motif-containing 36 (TRIM36), mRNA. /// ENST00000282369 // intron // 0 // --- // --- // --- // ---	TRIM36	TRIM36, Homo sapiens tripartite motif-containing 36 (TRIM36), q22.3
SNP_A-2231051	ctatgtgccagagaaa[A/T]aacacgcaagaggaaa	A	T	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), mRNA. /// ENST00000338458 // intron // 0 // --- // --- // --- // --- /// ENST00000296315 // intron // 0 // ---	ARHGEF3	ARHGEF3, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), p14.3
SNP_A-2255125	cttgggtaaaatggca[C/T]ggtgattgggaatgaa	C	T	// 23704 // Homo sapiens potassium voltage-gated channel, Isk-related family, member 4 (KCNE4), mRNA. /// NM_003469 // downstream // 258297 // Hs.516726 // SCG2 //	KCNE4	KCNE4, Homo sapiens potassium voltage-gated channel, Isk-related family, member 4 (KCNE4), q36.1
SNP_A-2253896	cttgacaactacgtaa[C/T]cttaggcaagtttagt	C	T	151556 // Homo sapiens G protein-coupled receptor 155 (GPR155), mRNA. /// X86019 // downstream // 24063 //	GPR155	GPR155, Homo sapiens G protein-coupled receptor 155 (GPR155), q31.1
SNP_A-2248487	ctgtgtttccaatgac[A/G]atgccccacagccctc	A	G	Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), mRNA. /// ENST00000328913 //	MCF2L2	MCF2L2, Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), q27.1
SNP_A-2288973	gatttattatgaggaa[G/T]tggcttacacaattat	G	T	Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000329809 // intron // 0 // ---	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289626	gcaaaaatagtacata[C/T]accgtctgatgtgggt	C	T	// Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2289719	gcaaaaggtccaagtc[A/G]gaaaagcaatgcgaag	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 480969 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2298869	gccccaaggtggccac[A/G]caaagggtacttgata	A	G	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2309664	ggaaagattctgtaac[A/G]gcaggcatttgccatc	A	G	ENST00000360707 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2305505	gctgcaaagctgtcac[C/G]ctgggatcccacttca	C	G	Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // --- // --- // --- // ---	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-2303250	ctattaggttttctta[C/T]catttgcatatgtatc	C	T	Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), mRNA. /// U05012 // intron // 0 // Hs.410969 //	NTRK3	NTRK3, Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), q25.3
SNP_A-2302041	gcgtggtagatgaaca[A/G]gaattaaaaataaaga	A	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 226339 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2302456	gctaatctcaaattca[A/G]atcaaactgaacatag	A	G	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2306421	gctgggtgggtgccaa[C/T]gagcacgggtgagaga	C	T	8648 // Homo sapiens nuclear receptor coactivator 1 (NCOA1), transcript variant 1, mRNA. /// NM_147223 //	NCOA1	NCOA1, Homo sapiens nuclear receptor coactivator 1 (NCOA1), transcript variant 1, p23.3
SNP_A-2315008	ggagtttcatcctgga[C/G]ggtaaaaagagatcat	C	G	Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2311775	ggaattggaccgcacc[C/T]ctcattgtgggcagag	C	T	399 // Homo sapiens ras homolog gene family, member H (RHOH), mRNA. /// NM_017581 // upstream // 35480 //	RHOH	RHOH, Homo sapiens ras homolog gene family, member H (RHOH), p14
SNP_A-2298014	gccatacattttgcag[A/C]cctcgtggagcattaa	A	C	// 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 268338 // --- // --- // --- //	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2299494	gcccttgacaagctaa[A/C]tgagcaggaaaaggca	A	C	// 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 185312 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2288032	gattcaaaagggccca[A/G]tggaaagtaacagcta	A	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 707068 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2288486	ggcagtttagttttgt[C/G]aatttgagttttcagt	C	G	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2290375	gcaacattgtattcac[C/T]ggctggacaatatagc	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2247670	ctgtgaaagagggaaa[A/C]gaagcaatgaaaagta	A	C	// 9375 // Homo sapiens transmembrane 9 superfamily member 2 (TM9SF2), mRNA. /// NM_138280 // upstream //	TM9SF2	TM9SF2, Homo sapiens transmembrane 9 superfamily member 2 (TM9SF2), q32.3
SNP_A-2242260	ctgcaagtgatcctgg[C/G]atgtgcgcagatccat	C	G	2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 389046 // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2252078	cttccagaaatagctg[C/T]agaaggcctgttaata	C	T	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA. /// ENST00000351718 // intron // 0 // --- // --- // --- // ---	NRCAM	NRCAM, Homo sapiens neuronal cell adhesion molecule (NRCAM), q31.1
SNP_A-2231056	ctatgtggatatttaa[C/T]tggactggtttgcagg	C	T	652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // downstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2230307	ctatatcacaacaaaa[C/T]ccaggttcttagaagc	C	T	Homo sapiens myosin VA (heavy polypeptide 12, myoxin) (MYO5A), mRNA. /// ENST00000358212 // intron // 0 // --- // ---	MYO5A	MYO5A, Homo sapiens myosin VA (heavy polypeptide 12, myoxin) (MYO5A), q21.2
SNP_A-2229198	ctagctgtcatctctc[C/T]aacctttaagactgt	C	T	sapiens cell division cycle 25A (CDC25A), transcript variant 2, mRNA. /// NM_001789 // intron // 0 // Hs.1634 // CDC25A //	CDC25A	CDC25A, Homo sapiens cell division cycle 25A (CDC25A), transcript variant 2, p21.31
SNP_A-2233369	ctcaggtccaatgccg[G/T]cctcaaagtcaaaaaa	G	T	NS5ATP13TP2 // 220323 // Homo sapiens NS5ATP13TP2 protein (NS5ATP13TP2), mRNA. /// NM_014352 // upstream	NS5ATP13TP2	NS5ATP13TP2, Homo sapiens NS5ATP13TP2 protein (NS5ATP13TP2), q23.3
SNP_A-2233746	ctcatcactcttctaa[C/T]agagaaatgtttctct	C	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-2231734	ctcaaaagaaagcaaa[A/G]tacttaggcataaatc	A	G	sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), transcript variant 2, mRNA. /// NM_004513 // intron // 0 // Hs.459095 // IL16 // 3603 // Homo sapiens interleukin 16	IL16	IL16, Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), transcript variant 2, q25.1
SNP_A-2232053	ctcaagagatgatgaa[G/T]tgccataaaccaagag	G	T	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA. /// ENST00000360555 // intron // 0 // --- // --- // --- // --- ///	AAK1	AAK1, Homo sapiens AP2 associated kinase 1 (AAK1), p13.3
SNP_A-2236158	ctccttcgatgctgcc[A/G]gagtgattctcccaaa	A	G	Homo sapiens neuralized-like (Drosophila) (NEURL), mRNA. /// ENST00000224944 // intron // 0 // --- // --- // --- // ---	NEURL	NEURL, Homo sapiens neuralized-like (Drosophila) (NEURL), q24.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2276000	gaggagaaaaagtgcac[A/G]ctgaaacacatcactt	A	G	SH3BGRL2 // 83699 // Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA. /// NM_022726 // downstream // 2163 // Hs.101915 // ELOVL4 //	SH3BGRL2	SH3BGRL2, Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), q14.1
SNP_A-2279044	gaggaaggaaaaagaaa[A/G]ggccgtggagactccc	A	G	Homo sapiens T, brachyury homolog (mouse) (T), mRNA. /// NM_175922 // downstream // 134742 // Hs.119062 //	T	T, Homo sapiens T, brachyury homolog (mouse) (T), q27
SNP_A-2279004	gaggaagaagaaggata[C/T]cactatttgtcattac	C	T	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 200651 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2278108	gagccctagttcattaa[A/G]tgtcagttatgatcat	A	G	/// ENST00000331332 // downstream // 200944 // --- // --- // ---	-	p11.1
SNP_A-2275184	gagaagctggtgataa[C/T]acactgactgacaaa	C	T	Homo sapiens microtubule-associated protein 2 (MAP2), transcript variant 1, mRNA. /// NM_031846 // intron // 0 //	MAP2	MAP2, Homo sapiens microtubule-associated protein 2 (MAP2), transcript variant 1, q34
SNP_A-2275672	gagacataatccagacc[C/T]atttttttaaaagatg	C	T	4729 // Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), mRNA. /// ENST00000333526 // downstream // 56230 // --- // --- // --- // ---	NDUFV2	NDUFV2, Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), p11.22
SNP_A-2261348	gaaagcatggacagaa[C/T]gtgcaaactccacgga	C	T	FLJ46321 // 389763 // Homo sapiens FLJ46321 protein (FLJ46321), mRNA. /// NM_152573 // downstream // 400132	FLJ46321	FLJ46321, Homo sapiens FLJ46321 protein (FLJ46321), q21.32
SNP_A-2257416	cttgaatttactaa[C/T]agccagaagtatttac	C	T	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2258555	ctttctatcattca[A/G]gtttactgattatgc	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2264899	gaagagcgtttgcaca[A/G]aggtatatgccagtat	A	G	353274 // Homo sapiens zinc finger protein 445 (ZNF445), mRNA. /// NM_018651 // upstream // 99423 // Hs.529512 //	ZNF445	ZNF445, Homo sapiens zinc finger protein 445 (ZNF445), p21.32
SNP_A-2270480	gacagaatctgtgctc[A/G]agggtataaagcaca	A	G	DKFZP434L0117 // 64793 // Homo sapiens hypothetical protein DKFZp434L0117 (DKFZP434L0117), mRNA. /// NM_022778 // upstream // 10505 // Hs.63795 //	DKFZP434L0117	DKFZP434L0117, Homo sapiens hypothetical protein DKFZp434L0117 (DKFZP434L0117), p36.11
SNP_A-2271607	gaccacagagtaaata[A/C]ctggctggtcctctga	A	C	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-1917596	ttcggaggtttaactc[C/T]agccagtgcttcttc	C	T	ONECUT2 // 9480 // Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// NM_000140 //	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-1909737	tgtcaatgttcttctc[C/T]atcccaaatactgccc	C	T	118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26875 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 272483 // Hs.523446 // COL11A1 // 1301 //	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26875 IMAGE:4812035), complete cds. p21.1
SNP_A-1929053	ttcagctgccatgctc[A/G]actctgtggcaggggc	A	G	ENST00000340067 // intron // 0 // --- // --- // ---	-	q14.1
SNP_A-1927324	ttcaaaatttcaacgat[A/T]actgaatgagtcccgc	A	T	Homo sapiens TPX2, microtubule-associated protein homolog (Xenopus laevis) (TPX2), mRNA. /// ENST00000300403 // 5UTR // 0 // --- // --- /// 2315 // Homo sapiens melan-A (MLANA), mRNA. ///	TPX2	TPX2, Homo sapiens TPX2, microtubule-associated protein homolog (Xenopus laevis) (TPX2), q11.21
SNP_A-1931024	ttccagttgacagtca[A/G]gttttctggttgtgaa	A	G	ENST00000251879 // downstream // 75355 // --- // --- // --- // ---	MLANA	MLANA, Homo sapiens melan-A (MLANA), p24.1
SNP_A-1879993	tcttcctttccagcac[C/T]ggctttcccaacctga	C	T	4821 // Homo sapiens NK2 transcription factor related, locus 2 (Drosophila) (NKX2-2), mRNA. /// NM_006192 // upstream	NKX2-2	NKX2-2, Homo sapiens NK2 transcription factor related, locus 2 (Drosophila) (NKX2-2), p11.22
SNP_A-1879508	tctatttcatctcccc[A/G]caatgcaacaacttt	A	G	ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1884792	tgaatcaggtatgata[C/T]aaaaagttgtaatagc	C	T	Homo sapiens homer homolog 1 (Drosophila) (HOMER1), mRNA. /// ENST00000282260 // intron // 0 // --- // --- // ---	HOMER1	HOMER1, Homo sapiens homer homolog 1 (Drosophila) (HOMER1), q14.1
SNP_A-1888147	tgagccctccctctca[C/G]atcagaaatgcctgtt	C	G	Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1894723	tgccagctaagatctg[A/C]accaatcagtagacac	A	C	1539 // Homo sapiens cyclicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cyclicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1893146	tgcagaagtatttcag[C/T]agtctaagaatgtgta	C	T	sapiens glutamate receptor, metabotropic 1 (GRM1), mRNA. /// ENST00000355289 // intron // 0 // --- // --- // --- ///	GRM1	GRM1, Homo sapiens glutamate receptor, metabotropic 1 (GRM1), q24.3
SNP_A-1904089	tgggcatcaaggtttg[C/T]aaagtgctccaagtaa	C	T	Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // intron // 0 // --- // --- // ---	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1
SNP_A-1902365	tggcccatttttcaac[C/T]gaggacactgagcctc	C	T	Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), mRNA. /// ENST00000266427 // intron // 0 // --- // --- // ---	ETV6	ETV6, Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), p13.2
SNP_A-1897905	aacattctttattggcc[A/G]cagaatttcaaggcg	A	G	374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1899350	tggaaccggcagagaa[A/G]agccctttagaagtag	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1534583 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1959027	ttttctttttgggaaaac[C/T]gccatctcctttgctc	C	T	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 373448 // Hs.131489 // PARD3	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1953739	tttgagaaaacaaagaa[C/T]aaagtgttgaaggct	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 587637 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1954668	tttgctagatgatgaa[A/C]actgtgatgttaacct	A	C	11146 // Homo sapiens glomulin, FKBP associated protein (GLMN), transcript variant 2, mRNA. /// NM_053274 // downstream // 2008 // Hs.49105 // GLMN // 11146 // Homo	GLMN	GLMN, Homo sapiens glomulin, FKBP associated protein (GLMN), transcript variant 2, p22.1
SNP_A-1952887	tttcttagtcaaggaa[A/T]atttaacgtgcaaga	A	T	4729 // Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), mRNA. /// ENST00000333526 // downstream // 75271 // --- // --- // --- // --	NDUFV2	NDUFV2, Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), p11.22
SNP_A-1933299	ttaacagcagtgggaa[C/T]gtgttactgttagaat	C	T	Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // intron // 0 // Hs.465413 // CYB5 // 1528 //	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-1935239	ttctgcctaagtgtcc[A/G]cctcacagagctgtac	A	G	Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA. /// ENST00000356218 // intron // 0 // --- //	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-1943658	ttgtacaagctgaaaa[A/C]atattgactagccaac	A	C	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 359560 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1947076	tttaatataaattcta[A/C]attttgtgctatatc	A	C	Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), mRNA. /// ENST00000307717 // intron // 0 // --- // --- ///	AMSH-LP	AMSH-LP, Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), q23.31
SNP_A-1944844	ttgtgctgccttgtg[C/T]atatgatccactacac	C	T	ENST00000282272 // intron // 0 // --- // --- // ---	-	q33.1
SNP_A-1944074	ttgtcaactgcaaagc[A/C]ctcgtcggacatagta	A	C	Homo sapiens LAG1 longevity assurance homolog 6 (S. cerevisiae) (LASS6), mRNA. /// ENST00000305747 // intron // 0 // --- // --- // ---	LASS6	LASS6, Homo sapiens LAG1 longevity assurance homolog 6 (S. cerevisiae) (LASS6), q24.3
SNP_A-1973142	aatgaaagcacagaat[C/G]aatcaaaataaatgt	C	G	// Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // --- // --- // ---	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1975161	gatggctgcagcaaaac[C/T]acgatggcacatgat	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1965830	attttatacaattcac[C/G]cagcttaatcaaaaac	C	G	Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 // intron // 0 // --- // --- // ---	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-1966266	ctggccttgaacacaa[C/T]cttgaacacatataca	C	T	5378 // Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA. /// NM_005259 // downstream // 20559 // Hs.41565 // GDF8 // 2660 // Homo	PMS1	PMS1, Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), q32.2
SNP_A-1967399	ggttgatgaggtgaaa[A/G]agtgcttgcggcctca	A	G	Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA. /// ENST00000289175 // intron // 0 // ---	LRRFIP1	LRRFIP1, Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), q37.3
SNP_A-1968365	gagcctcctagagaaa[A/T]agatgcccaggaagtt	A	T	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534., q12
SNP_A-1984162	taatttgtctcccatc[A/C]aagtactaagcaggcc	A	C	-- /// ENST00000361117 // upstream // 438938 // --- // --- // ---	-	q33.2
SNP_A-1983481	aagcaggagaaggacaa[A/G]gtaatcatgaggaagt	A	G	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-1984998	actcctaaacagttta[A/C]agcagtcaaggctctg	A	C	9521 // Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA. /// NM_015948 // downstream	EEF1E1	EEF1E1, Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), p24.3
SNP_A-1977593	ttccttgctctcattc[C/T]acacaacagcaaggct	C	T	166824 // Homo sapiens Ras association (RalGDS/AF-6) domain family 6 (RASSF6), transcript variant 1, mRNA. ///	RASSF6	RASSF6, Homo sapiens Ras association (RalGDS/AF-6) domain family 6 (RASSF6), q13.3
SNP_A-1978131	agtttagagtaaaact[C/T]acagcttcaattata	C	T	Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), mRNA. /// ENST00000264568 // intron // 0 // --- //	BMPR1B	BMPR1B, Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), q22.3
SNP_A-1978574	tgcctcttatctcag[A/G]aagtgaagtcttacaa	A	G	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA.	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-1784887	ggcctggggtgagtca[C/T]gtagcctctctaagct	C	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1782165	ggcaagaggtaggaca[G/T]ggaggagctatagac	G	T	200008 // Homo sapiens hypothetical protein LOC200008 (LOC200008), mRNA. /// ENST00000311841 // intron // 0 // ---	LOC200008	LOC200008, Homo sapiens hypothetical protein LOC200008 (LOC200008), p32.3
SNP_A-1719339	aagaagacttctcattatcataaca[C/T]acccaagaatgtgttctatctccc	C	T	// 2834 // G protein-coupled receptor 10 /// NM_022063 // upstream // 44522 // Hs.11859 // C10orf84 // 63877 //	GPR10	GPR10 , rs10490912, G protein-coupled receptor 10 ,q26.11
SNP_A-1734490	aggcataactgacttcttattatg[A/C]aaataatctgggagaagaaatggat	A	C	NM_004128 // intron // 0 // Hs.58593 // GTF2F2 // 2963 // general transcription factor IIF, polypeptide 2, 30kDa	GTF2F2	GTF2F2 , rs951853, general transcription factor IIF, polypeptide 2, 30kDa,q14.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1703885	tatactacagaaaatccagcaggta[A/G]aaagtcacatcaggcagggataatc	A	G	NM_014744 // intron // 0 // Hs.115740 // TBC1D5 // 9779 // TBC1 domain family, member 5	TBC1D5	TBC1D5 , rs10510479, TBC1 domain family, member 5,p24.3
SNP_A-1654081	ttggatcctattaaaagctgagagt[G/T]aatgaataaacagataaaacagaga	G	T	// 285 // angiopoietin 2 /// NM_024596 // upstream // 25989 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein	ANGPT2	ANGPT2 , rs1057187, angiopoietin 2 ,p23.1
SNP_A-1652606	cagcaattagtaataaggggatcca[A/G]aatgttaggagcagacttttaaaaa	A	G	NM_015013 // intron // 0 // Hs.348515 // AOF2 // 23028 // amine oxidase (flavin containing) domain 2	AOF2	AOF2 , rs10489564, amine oxidase (flavin containing) domain 2,p36.12
SNP_A-1800773	gtagacaaacgccaca[A/G]tctgattttgtctcag	A	G	10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 501482 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1803850	gtcaaggaaggtcaga[G/T]aatgcatgagaaagaa	G	T	-- /// ENST00000345029 // upstream // 328010 // --- // --- // ---	-	p14
SNP_A-1810007	gtgataacggagctct[C/G]aagactggaaactggg	C	G	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000340635 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-1809269	gtgactagaatactga[G/T]aagtgggctctcttca	G	T	SERPINB10 // 5273 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10 (SERPINB10), mRNA. /// NM_002640 // upstream // 31816 //	SERPINB10	SERPINB10, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10 (SERPINB10), q21.33
SNP_A-1811585	gtgctgagaatttgat[G/T]acattgtagaattacc	G	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1795151	ggtgagaacggaagaa[A/C]aggatgtgacctaaat	A	C	Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /// ENST00000264741 // intron // 0 // --- // --- // --- // ---	ITGA9	ITGA9, Homo sapiens integrin, alpha 9 (ITGA9), p22.3
SNP_A-1796892	ggttccagtgactata[C/T]acgtagacttaggaac	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// NM_006113 // downstream // 57254 // Hs.267659 //	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p13.3
SNP_A-1797488	ggtttattataactca[C/T]atatagcccaatttac	C	T	// Homo sapiens FLJ46082 protein (FLJ46082), mRNA. /// ENST00000343036 // intron // 0 // --- // --- // --- // ---	FLJ46082	FLJ46082, Homo sapiens FLJ46082 protein (FLJ46082), q34.13
SNP_A-1788649	gggatgaggtattaga[A/C]cttagtgagcatcaga	A	C	6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ENST00000313571 // upstream // 509574	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-1791980	gggtggagagggaata[C/T]atagagttgagggagg	C	T	9519 // Homo sapiens TBP-like 1 (TBPL1), mRNA. /// NM_145176 // upstream // 20671 // Hs.486508 // SLC2A12 //	TBPL1	TBPL1, Homo sapiens TBP-like 1 (TBPL1), q23.2
SNP_A-1790400	ggggattatacaagga[C/T]atgaataccaagtggt	C	T	// 253558 // Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, mRNA. /// NM_182551 // upstream // 169408 // Hs.468048 // LYCAT //	LYCAT	LYCAT, Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, p23.1
SNP_A-1833316	tacactttaattagca[G/T]cagaatataattgtct	G	T	1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1838436	tagaatatgaggcctc[C/T]gagaggatgagaatga	C	T	51088 // Homo sapiens kelch-like 5 (Drosophila) (KLHL5), transcript variant b, mRNA. /// NM_015990 // downstream //	KLHL5	KLHL5, Homo sapiens kelch-like 5 (Drosophila) (KLHL5), transcript variant b, p14
SNP_A-1817010	gttatttattattgcc[C/T]aaactgcttgcatgtt	C	T	27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 46660 // Hs.165830	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-1827278	taaccttggacctcac[A/G]ccatagctattcacat	A	G	Homo sapiens interleukin 1, alpha (IL1A), mRNA. /// NM_000576 // downstream // 17004 // Hs.126256 // IL1B //	IL1A	IL1A, Homo sapiens interleukin 1, alpha (IL1A), q13
SNP_A-1828727	taagctgctgaatcca[G/T]tcttggtggagggttc	G	T	Homo sapiens WD repeat and FYVE domain containing 2 (WDFY2), mRNA. /// ENST00000267142 // intron // 0 // --- // ---	WDFY2	WDFY2, Homo sapiens WD repeat and FYVE domain containing 2 (WDFY2), q14.3
SNP_A-1825102	taaaggggctgaataa[A/T]gttaaattcacaagtc	A	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 447347 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-1823996	taaaatttgtagcata[A/G]gctagaaggaagggga	A	G	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1873762 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1856201	tcacaactgtaatacg[A/G]atagttctatacttat	A	G	// 10885 // Homo sapiens WD repeat domain 3 (WDR3), mRNA. /// NM_206996 // upstream // 15260 // Hs.528821 //	WDR3	WDR3, Homo sapiens WD repeat domain 3 (WDR3), p12
SNP_A-1856363	tcacaccacagaccca[A/G]aggaaaagagacccaa	A	G	// 89876 // Homo sapiens chromosome 3 open reading frame 15 (C3orf15), mRNA. /// NM_033013 // upstream // 316 //	C3orf15	C3orf15, Homo sapiens chromosome 3 open reading frame 15 (C3orf15), q13.33
SNP_A-1859315	tcagctgttccaaata[C/T]aaagccttagtaatta	C	T	// 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// NM_002718 // upstream // 286690 // Hs.518155 // PPP2R3A	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.2
SNP_A-1863747	tccaagatcttaggaa[A/G]tacaggcacacaacaa	A	G	// 23099 // Homo sapiens zinc finger protein 297B (ZNF297B), mRNA. /// AB082524 // upstream // 17020 //	ZNF297B	ZNF297B, Homo sapiens zinc finger protein 297B (ZNF297B), q33.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1866385	tccccaaacctgggcc[A/G]catcatcaaccagaaa	A	G	Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), mRNA. /// ENST00000349015 // CDS // 0 // --- // --- // --- // ---	ALDH3B2	ALDH3B2, Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), q13.2
SNP_A-1864982	tccagtaatggcagag[A/T]agcttgtatcaaatta	A	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1861813	tcatcttgctgaaata[A/G]agaggttctcattgtt	A	G	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 688869 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1869094	gtctcatttttcagta[C/T]taataaaacatccatg	C	T	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA. /// ENST00000269080 // intron //	ABCA8	ABCA8, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), q24.2
SNP_A-1867269	tccctgtcttcaatat[G/T]aacatctggtacacta	G	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1867497	tccgatacagtgctac[C/T]aaaagccattaaagtc	C	T	Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // intron // 0 // --- // --- // --- // --- ///	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2205435	ccagtgctggatacaa[C/T]agtgagcagaattctg	C	T	// Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 204149	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-2202107	ccacagtttgctgaac[C/T]ctggtcagtttgcaga	C	T	9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream //	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-2208412	cccaccatgtggcaaa[C/T]aaatgaggcttcagag	C	T	7292 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF /// NM_004905 // upstream // 38432 // Hs.120 // PRDX6 // 958	TNFSF4	TNFSF4, Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF q25.1
SNP_A-2212548	cccttaggcttcaccc[A/G]ggactagaacaggctg	A	G	Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), mRNA. /// ENST00000328913 //	MCF2L2	MCF2L2, Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), q27.1
SNP_A-2219333	cctgtgagtgtcagaa[C/T]aagtgcttgctattgt	C	T	// Homo sapiens fibrinogen, gamma polypeptide (FGG), transcript variant gamma-A, mRNA. /// NM_000509 // upstream // 79921 // Hs.546255 // FGG // 2266 // Homo	FGG	FGG, Homo sapiens fibrinogen, gamma polypeptide (FGG), transcript variant gamma-A, q32.1
SNP_A-2226009	ctaacaagggctcttg[C/G]agtgattggcagatac	C	G	FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream //	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-2226095	ctaacatgacaagtca[A/G]ctttctcagtcaggct	A	G	FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2197172	cattcaagtagcccaa[C/T]gtgccttaagctacc	C	T	/// ENST00000319719 // upstream // 530717 // --- // --- // --- // --- /// ENST00000308537 // upstream // 306842 // --- // --- // ---	-	p13
SNP_A-2197262	cattcagctcatctac[A/T]ctcccctctggtcaaa	A	T	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 182790 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-2189420	cagttgcggtgtcaga[A/G]gaatgctctttattta	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 449523 // --- // --- // --- //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2186778	caggggcaaacattta[C/T]ggatactgaaagccag	C	T	Homo sapiens IQ motif containing E (IQCE), mRNA. /// ENST00000325997 // intron // 0 // --- // --- // --- // --- ///	IQCE	IQCE, Homo sapiens IQ motif containing E (IQCE), p22.3
SNP_A-2181391	cagactatcaaaattg[A/T]aatgattaatataaca	A	T	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase,	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). ,q12.13
SNP_A-2177362	caccttcatgtggaaa[C/G]tgtacaggccccttttc	C	G	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 450434 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2176821	caccctgtgggaagaa[A/C]atgggcagaagagttg	A	C	Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// ENST00000262825 // intron // 0 // --- // --- // --- // ---	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-2141438	atctgttttcttgtta[C/T]gcagttccttatatac	C	T	Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), mRNA. /// ENST00000360133 //	NALP11	NALP11, Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), q13.43
SNP_A-2149496	atgtagatactttaaa[C/T]gaagtgttaggaagca	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2145227	atgcacaaattcctca[A/C]aacagaaattcacacc	A	C	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	YWHAQ, Homo sapiens tyrosine 3-monooxygenase,p25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2153173	attactaggtgtataa[C/T]caaaagaatataaatc	C	T	Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA. /// ENST00000264211 // intron //	EIF4G3	EIF4G3, Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), p36.12
SNP_A-2155985	attcctggttttcaaa[C/T]atgaaaggaaggaagg	C	T	22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// NM_014965 // downstream // 16574 // Hs.535711 //	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. p22.1
SNP_A-2159349	atttaagtttacatta[C/T]cattattgacttaacc	C	T	// 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 542027 // --- // --- // --- //	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2160154	atttcaaagaccccaa[G/T]tgaatatttatatatc	G	T	lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // --- // --- // --- // --- ///	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. ,q13.1
SNP_A-2160717	atttctaaaggagtga[C/T]taactcaaaacatttt	C	T	Homo sapiens ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) (ACTR1A), mRNA. /// ENST00000260680 // intron // 0 // --- // --- // --- // ---	ACTR1A	ACTR1A, Homo sapiens ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) (ACTR1A), q24.32
SNP_A-2120345	agtcatcctttgcccc[C/T]acacaaatgcatacac	C	T	164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // upstream // 31846 // --- // ---	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-2121638	agtgaatcacaggagc[A/G]agtgagttgcccagtg	A	G	117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 603 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2122209	agtgcaagggatctga[A/G]gcccacacgggcacac	A	G	253650 // Homo sapiens FLJ35740 protein (FLJ35740), mRNA. /// AB095935 // upstream // 34080 // Hs.535962 //	FLJ35740	FLJ35740, Homo sapiens FLJ35740 protein (FLJ35740), p13.1
SNP_A-2111869	aggatcagagagaaag[C/T]aagaaaataggagaca	C	T	54780 // Homo sapiens chromosome 10 open reading frame 86 (C10orf86), mRNA. /// NM_206861 // upstream // 15143 //	C10orf86	C10orf86, Homo sapiens chromosome 10 open reading frame 86 (C10orf86), q26.13
SNP_A-2108213	agctgaacacttgacc[A/G]gatgacctgcctacag	A	G	122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// ENST00000320096 // intron // 0 // ---	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2110880	aggactggtgtgagta[C/T]gatcagactgacattc	C	T	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 963932 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2129671	atacagctttccatca[C/G]tcacaagacaggcttg	C	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2132153	ataggtcttttgtata[A/G]cttctgtgttctgtgg	A	G	// 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 329599 // ---	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-2137227	atcagtcaatagaagc[A/C]gactcagaaaggacag	A	C	Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), mRNA. /// ENST00000261245 // intron // 0 // --- // ---	MNAT1	MNAT1, Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), q23.1
SNP_A-2135283	atattgttggtgatta[C/T]agtaaaatagccaaag	C	T	80232 // Homo sapiens WD repeat domain 26 (WDR26), mRNA. /// NM_152495 // upstream // 123512 // Hs.97338 //	WDR26	WDR26, Homo sapiens WD repeat domain 26 (WDR26), q42.12
SNP_A-2063497	tggatgctgtgttcaa[A/G]tcatggcaaagtgaga	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 462608 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2067417	acaaatatttgcagaa[A/T]gaagctcaattaaaac	A	T	153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 443211 // Hs.424156 // IRX1 //	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-2070982	acactctgcaagaagg[C/T]aatagaatgaggtatt	C	T	// 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-2074340	acatacagataaagaa[A/G]tcaaaggttgaaaaca	A	G	ENST00000336930 // 3UTR // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-2055556	aataatcaacatgcgc[A/G]acatccctaatgtcct	A	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2051286	aagggcacaagaaata[C/T]gtgattttgacaacat	C	T	Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2097579	agagaagtcagatcac[A/G]aaaagccttgagtggt	A	G	// Homo sapiens hypothetical protein FLJ32011 (FLJ32011), mRNA. /// ENST00000294445 // 3UTR // 0 // --- // --- // --- // ---	FLJ32011	FLJ32011, Homo sapiens hypothetical protein FLJ32011 (FLJ32011), p33
SNP_A-2093994	agaagctacaaagcca[C/G]aagaggacaagtgaaa	C	G	Homo sapiens hypothetical protein FLJ23598 (FLJ23598), mRNA. /// ENST00000298861 // 5UTR // 0 // --- // --- // --- // ---	FLJ23598	FLJ23598, Homo sapiens hypothetical protein FLJ23598 (FLJ23598), p11.2
SNP_A-2093573	agaagaaataggccca[C/G]agagaagcaaggcagt	C	G	ENST00000358271 // intron // 0 // --- // --- // --- // --- /// ENST00000358972 // intron // 0 // --- // --- // --- // ---	-	q11.22
SNP_A-2103820	agcacctagcatatta[C/T]aggtaatgaatgaatg	C	T	Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), transcript variant 3, mRNA. /// NM_174972 // intron // 0 // Hs.132001 // ST3GAL3	ST3GAL3	ST3GAL3, Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), transcript variant 3, p34.1
SNP_A-2100498	agataagtaagaccta[A/T]atcatctattgtacaa	A	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2102487	agattcttttaaaaaa[C/T]gagatcttgcctgaac	C	T	767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 313859 // --- // --- // ---	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2087091	actgatacagttacca[A/G]tgccctttgttgagtc	A	G	29914 // Homo sapiens transitional epithelia response protein (TERE1), mRNA. /// ENST00000240179 // downstream //	TERE1	TERE1, Homo sapiens transitional epithelia response protein (TERE1), p36.22
SNP_A-2087089	actgatacagaacaca[A/G]tgacctttcatttatt	A	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 206701 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2082147	acgaatttccacttat[C/T]actcaagaataaccat	C	T	Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // intron // 0 // --- // --- // --- // ---	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3
SNP_A-2082205	acgagaactaaagcca[C/G]cttagcttgagatgtc	C	G	5305 // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), mRNA. /// NM_173081 // upstream // 116673 // Hs.137270 // ARMC3 // 219681 //	PIP5K2A	PIP5K2A, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), p12.2
SNP_A-2084410	actatatggaatacca[G/T]gacagtgattaaggca	G	T	115362 // Homo sapiens guanylate binding protein 5 (GBP5), mRNA. /// NM_198460 // upstream // 16480 // Hs.254338 //	GBP5	GBP5, Homo sapiens guanylate binding protein 5 (GBP5), p22.2
SNP_A-2018495	gaatacaaagttagca[C/G]tagtaacatctggtag	C	G	Homo sapiens chloride intracellular channel 6 (CLIC6), mRNA. /// ENST00000360731 // 3UTR // 0 // --- // --- // --- // ---	CLIC6	CLIC6, Homo sapiens chloride intracellular channel 6 (CLIC6), q22.12
SNP_A-2018096	aactatatggaagaga[A/G]gaagcatagttcctcc	A	G	30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 //	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2014201	atacaacttgagatga[C/T]gaaatgatttttttt	C	T	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 777907 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2011760	ttaggaataggataca[C/T]gggacccaaacacagc	C	T	Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// ENST00000185206 // intron // 0 // --- // --- // --- // ---	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-2008380	aaaggcatcggtggac[A/G]acctggggacatctgc	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1991353	tctgccccagggaaga[C/T]taaggcaagccagggt	C	T	ENST00000342384 // intron // 0 // --- // --- // --- // --- /// ENST00000328742 // intron // 0 // --- // --- // --- // --- ///	-	q33
SNP_A-2001090	cctttctatttccata[C/T]ggccaacagccccaga	C	T	Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// ENST00000354496 // intron // 0 // --- // --- // --- // --- /// ENST00000351738 // intron // 0 // --- //	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.21
SNP_A-2039007	aacaggatttggccca[A/G]agacatgttctgtttg	A	G	3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 203792 // Hs.118695 // KCNG1	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2026441	aaacaaacaaacaaaa[C/T]gcctccttcatctcaa	C	T	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 979754 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2025206	aaaataggtaaatgta[A/G]cccacgcaagaaagta	A	G	51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 //	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-2021454	aaaaaaggagagataa[C/T]tggacacaatggctca	C	T	Homo sapiens clone A34.1 transmembrane protein vezatin mRNA, complete cds. /// ENST00000261219 // intron // 0 // --- // --- // --- // ---	VEZATIN	VEZATIN, Homo sapiens clone A34.1 transmembrane protein vezatin complete cds. ,q22
SNP_A-2021510	aaaaaataagaggtcc[A/G]aagttgaagactgaaa	A	G	DKFZp761L1417 // 222865 // Homo sapiens hypothetical protein DKFZp761L1417 (DKFZp761L1417), mRNA. /// NM_003496 // upstream // 1339 // Hs.203952 // TRRAP //	DKFZp761L1417	DKFZp761L1417, Homo sapiens hypothetical protein DKFZp761L1417 (DKFZp761L1417), q22.1
SNP_A-2031647	aaagtaataatgccta[A/G]aagccataaagaaaaa	A	G	ENST00000335472 // intron // 0 // --- // --- // --- // ---	-	q31.22
SNP_A-2031278	aaagggaagcttgaag[A/G]ctaaaggcaaggtgat	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1933209 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2028545	aaactgatgattaacc[C/T]atgcttggagaatctg	C	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2595359 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2032434	aaagtttctgaaaaaa[G/T]ttcaagctccttagca	G	T	// Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA. /// ENST00000265030 // upstream // 60403 // --- // ---	BMP5	BMP5, Homo sapiens bone morphogenetic protein 5 (BMP5), p12.1
SNP_A-2022351	aaaaataagaaaactg[A/C]aggctgtccaggtcct	A	C	Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// ENST00000326840 // intron // 0 // --- // -	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1
SNP_A-2026261	aaaattgttctgagaa[C/T]tacctcctcatcaatc	C	T	Homo sapiens chromosome condensation 1-like (CHC1L), mRNA. /// ENST00000344532 // intron // 0 // --- // --- // --- // ---	CHC1L	CHC1L, Homo sapiens chromosome condensation 1-like (CHC1L), q14.2
SNP_A-2034095	aaatcatattccaaat[A/G]agcatcaaaaataata	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2035543	aaatgtaaatcttcaa[A/G]ccactgacttcataat	A	G	25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream //	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041577	aacgagatgctaagaa[C/T]gtgtccaaagtctgtg	C	T	Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // --- // --- // ---	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3
SNP_A-1998085	aacctgcttctgttca[C/T]ctgactgaggacaaa	C	T	84616 // Homo sapiens keratin associated protein 4-4 (KRTAP4-4), mRNA. /// AJ406935 // downstream // 3701 //	KRTAP4-4	KRTAP4-4, Homo sapiens keratin associated protein 4-4 (KRTAP4-4), q21.2
SNP_A-1997687	aagatctgacctgact[C/G]actccatcttgcttct	C	G	Homo sapiens sushi domain containing 1 (SUSD1), mRNA. /// ENST00000297886 // intron // 0 // --- // --- // --- ///	SUSD1	SUSD1, Homo sapiens sushi domain containing 1 (SUSD1), q31.3
SNP_A-2002298	ctcagtcgggggaaaaa[C/G]agaaaatagagattag	C	G	MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-1990840	ggcagatacctggaaa[C/G]agaaccagctgcacaa	C	G	9156 // Homo sapiens exonuclease 1 (EXO1), transcript variant 2, mRNA. /// NM_003686 // downstream // 608 //	EXO1	EXO1, Homo sapiens exonuclease 1 (EXO1), transcript variant 2, q43
SNP_A-1990763	atctgaattatccaaa[C/G]caatgaatgtgattcc	C	G	5001 // Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, mRNA. /// NM_002553 // upstream // 98784 // Hs.432948 // ORC5L //	ORC5L	ORC5L, Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, q22.2
SNP_A-1995813	caatcggccacaacca[C/T]tgcaatacatatcagc	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 374600 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1995677	agcacaatggtttaga[A/C]gccaagtgtgtctgac	A	C	// 90865 // Homo sapiens chromosome 9 open reading frame 26 (NF-HEV) (C9orf26), mRNA. /// NM_001001875 // ---	C9orf26	C9orf26, Homo sapiens chromosome 9 open reading frame 26 (NF-HEV) (C9orf26), p24.1
SNP_A-1996450	aatacctctcaggtta[C/T]gtttataggtcaccta	C	T	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2006875	tgaaatggcttaattia[C/T]catgacctcctaata	C	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2010076	attcttcttttctaa[C/T]tgtcttcacacttat	C	T	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 586590 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2015660	ttctagcacctttgag[A/C]atttacttttatggagc	A	C	Homo sapiens BTG family, member 3 (BTG3), mRNA. /// ENST00000348354 // 3UTR // 0 // --- // --- // --- ///	BTG3	BTG3, Homo sapiens BTG family, member 3 (BTG3), q21.1
SNP_A-2013428	aaaatttagaaacctg[A/C]atatacgcaagtgttg	A	C	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2018898	cctttgggccaagaaa[A/G]ctgggatgggaactgtc	A	G	23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 190151 //	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-2083997	actagaatttccaggga[A/G]tcaacccacagattgg	A	G	5928 // Homo sapiens retinoblastoma binding protein 4 (RBBP4), mRNA. /// NM_030786 // upstream // 42584 //	RBBP4	RBBP4, Homo sapiens retinoblastoma binding protein 4 (RBBP4), p35.1
SNP_A-2081143	acctgatttaactata[C/T]ggctcaaaaaatatt	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2091932	agaaacaatttcataa[C/T]cagttctgacatttag	C	T	Homo sapiens, Similar to RIKEN cDNA 3830613O22 gene, clone IMAGE:5551209, mRNA, partial cds. /// ENST00000282943 // intron // 0 // --- // --- // --- ///	GPR125	GPR125, Homo sapiens, Similar to RIKEN cDNA 3830613O22 gene, clone IMAGE:5551209, partial cds. p15.31
SNP_A-2103623	agcacaccagcatctc[C/T]ctgtgcgaggacccct	C	T	6422 // Homo sapiens secreted frizzled-related protein 1 (SFRP1), mRNA. /// NM_016099 // upstream // 146833 //	SFRP1	SFRP1, Homo sapiens secreted frizzled-related protein 1 (SFRP1), p11.21
SNP_A-2092472	agaaagtgacaaatca[A/G]tatgcaatgcatggga	A	G	MGC88374 // 440184 // Homo sapiens similar to CG32662-PA (MGC88374), mRNA. /// ENST00000310149 // upstream	MGC88374	MGC88374, Homo sapiens similar to CG32662-PA (MGC88374), q23.3
SNP_A-2095244	agaattgattgggtaa[A/C]tagttcagagaaatct	A	C	85439 // Homo sapiens stonin 2 (STN2), mRNA. /// NM_005065 // downstream // 5544 // Hs.181300 // SEL1L //	STN2	STN2, Homo sapiens stonin 2 (STN2), q31.1
SNP_A-2094931	agaatgatttcagat[A/G]acgatcttctttttt	A	G	51809 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA. /// ENST00000340153 // downstream // 122983 // --- ///	GALNT7	GALNT7, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), q34.1
SNP_A-2097168	agacttcattatgaaa[A/T]cttgccaaggcctat	A	T	777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // upstream // 112093 // Hs.437444 // CACNA1E // 777 // Homo sapiens	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2051431	aaggggaagaaatgg[A/G]acccaatatgaacgtc	A	G	ENST00000356612 // intron // 0 // --- // --- // ---	-	q23.3
SNP_A-2053870	aagtgtgttggttgaa[A/C]agttttcatttttgct	A	C	10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// NM_182848 //	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2048665	aagccccacactgcc[A/G]gcgaatagtgctggag	A	G	27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 421992 // Hs.165830	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-2048789	aagcccaacactgaaa[C/T]ggattaaacttgattt	C	T	222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 35745 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2048941	aagcctcagtgtctca[C/T]gcctggactgttgagg	C	T	Homo sapiens serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin) (SPINLW1), transcript variant 2, mRNA. /// NM_020398 // intron // 0 // Hs.121084 // SPINLW1	SPINLW1	SPINLW1, Homo sapiens serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin) (SPINLW1), transcript variant 2, q13.12
SNP_A-2056849	aatagggaaagtacat[G/T]agcatatgcattcatc	G	T	Homo sapiens calcium binding atopy-related autoantigen 1 (CBARA1), mRNA. /// ENST00000361114 // intron // 0 // --- //	CBARA1	CBARA1, Homo sapiens calcium binding atopy-related autoantigen 1 (CBARA1), q22.1
SNP_A-2063225	aatgtttgtttgatac[A/G]gtaacactttgttaat	A	G	ENST00000325438 // intron // 0 // --- // --- // --- // ---	-	q32.33
SNP_A-2134123	tgcctttcccaatcca[A/G]tcagctgtggtgggct	A	G	// Homo sapiens esterase D/formylglutathione hydrolase (ESD), mRNA. /// NM_000621 // downstream // 8016 //	ESD	ESD, Homo sapiens esterase D q14.2
SNP_A-2136121	atcaataactgaaaaa[G/T]atgttcatcaggatcc	G	T	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 833521 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2132813	atataacgtgatgcat[G/T]accgcactgaccagga	G	T	ENST00000222607 // intron // 0 // --- // --- // --- // ---	-	p15.3
SNP_A-2126561	ataaaatgctaagaaa[C/G]ctgaagcattactttt	C	G	Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), mRNA. /// ENST00000251507 // intron // 0 // ---	RABGAP1L	RABGAP1L, Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), q25.1
SNP_A-2112959	aggcatgtgcacaaac[A/G]ctcacaagatgccacc	A	G	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2121936	agtgaggtggttcagc[A/G]gccaacaggctaacac	A	G	// 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 766701 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2115551	aggggttagagcaggc[A/G]agagcccagtccctcc	A	G	MGC22001 // 197196 // Homo sapiens hypothetical protein MGC22001 (MGC22001), mRNA. /// ENST00000316859 //	MGC22001	MGC22001, Homo sapiens hypothetical protein MGC22001 (MGC22001), q24.1
SNP_A-2159340	atttaagtcattctaa[C/T]gcataagcaagttcca	C	T	// 79097 // Homo sapiens tripartite motif-containing 48 (TRIM48), mRNA. /// NM_001005274 // upstream // 59787 // -	TRIM48	TRIM48, Homo sapiens tripartite motif-containing 48 (TRIM48), q11
SNP_A-2164396	caaaatgatgaacaca[C/T]ctgctaataatcataa	C	T	Homo sapiens deubiquitinating enzyme DUB4 (DUB4), mRNA. /// NM_201402 // upstream // 230942 // Hs.531448 //	-	-, Homo sapiens deubiquitinating enzyme DUB4 (DUB4), p23.1
SNP_A-2149063	atggtttggctaggat[C/T]aaactcagctttctct	C	T	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 739181 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2147153	atggaattgataccac[C/G]ggctttcctggatctc	C	G	WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// NM_031468 // downstream // 15986 // Hs.333274 // CALN1 //	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-2152481	attaagaacttgaaag[C/T]aaaggtagctgcattt	C	T	sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, mRNA. /// NM_206810 // intron // 0 //	MOG	MOG, Homo sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, p22.1
SNP_A-2143935	atgagcaggtacaggc[C/T]cgtctgcacacgtgta	C	T	Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), mRNA. /// ENST00000262138 // intron // 0 // --- // --- // --- // ---	CACNG4	CACNG4, Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), q24.2
SNP_A-2177761	cacgtctcctgcaaga[C/G]agttttagacatgggg	C	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2172021	caatggaaattccaac[C/T]gatgactgagaatttg	C	T	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 67606 // Hs.437966 // PXMP3 //	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2172222	caatgtgaatgaagga[C/G]atgggattggatgagc	C	G	Homo sapiens A kinase (PRKA) anchor protein (gravin) 12 (AKAP12), transcript variant 1, mRNA. /// NM_144497 // intron // 0 // Hs.371240 // AKAP12 // 9590 // Homo sapiens A	AKAP12	AKAP12, Homo sapiens A kinase (PRKA) anchor protein (gravin) 12 (AKAP12), transcript variant 1, q25.1
SNP_A-2186359	caggctgtacaaataa[A/G]attttgaagacagaag	A	G	// 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2189953	cataaatttttgaata[C/T]aggcatcaaatcagtt	C	T	sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-2225645	ctaaacattgagtaca[C/T]gtagacacaaagaaag	C	T	ENST00000327381 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2221970	cgaaaggaaacaagac[A/T]cgaggtggccttctgg	A	T	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki 1) (ALK), p23.2
SNP_A-2222408	cgagattggccactaa[A/G]ttagtgaacttcacta	A	G	339967 // Homo sapiens hypothetical protein LOC339967 (LOC339967), mRNA. /// ENST00000334830 // intron // 0 // ---	LOC339967	LOC339967, Homo sapiens hypothetical protein LOC339967 (LOC339967), q13.2
SNP_A-2219189	cctgtcaggaagtgaa[C/T]gagaatctacattagg	C	T	25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // --- // --- // --- // --- ///	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2215800	cctcatgctatgcacc[A/G]aggcctgctcattgta	A	G	// 23327 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), mRNA. /// ENST00000256830 // downstream // 70523 // --- // --- // --- // ---	NEDD4L	NEDD4L, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), q21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213179	ccgcacagagtcacgc[A/G]atatggtctctaattg	A	G	Homo sapiens leucine-rich repeat kinase 1 (LRRK1), mRNA. /// ENST00000284395 // intron // 0 // --- // --- // --- // ---	LRRK1	LRRK1, Homo sapiens leucine-rich repeat kinase 1 (LRRK1), q26.3
SNP_A-2210882	ccccttgacaatgaaa[C/T]ccttaaggcagtgggt	C	T	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-2209770	cccattgggctttcaa[C/T]aaacaccacatggcac	C	T	3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1002568 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2199878	ccaaacttgaatgttg[G/T]agctcatggttcgtgt	G	T	Homo sapiens MCM4 minichromosome maintenance deficient 4 (S. cerevisiae) (MCM4), transcript variant 1, mRNA. /// NM_182746 // intron // 0 // Hs.460184 // MCM4 //	MCM4	MCM4, Homo sapiens MCM4 minichromosome maintenance deficient 4 (S. cerevisiae) (MCM4), transcript variant 1, q11.21
SNP_A-1867188	tccctgctctaaaaaa[C/T]gatgtggctcctacgc	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1870240	tcctttcctcatgaaa[G/T]cttcacaggaaaatca	G	T	11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 115705 // Hs.526879 // PTPRT //	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-1862846	tcattcttcatttcca[A/G]atttagatatagataa	A	G	// 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf107), mRNA. /// BX641020 // upstream // 125866 // Hs.535297 // ARID5B // 84159 // Homo sapiens	C10orf107	C10orf107, Homo sapiens chromosome 10 open reading frame 107 (C10orf107), q21.2
SNP_A-1864206	tccacccagattacca[C/G]aacagcttcctggcca	C	G	10391 // Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA. /// NM_006305 // downstream // 43550 //	CORO2B	CORO2B, Homo sapiens coronin, actin binding protein, 2B (CORO2B), q23
SNP_A-1857108	tcaccgaaataaggaa[A/C]acttctaacacttaga	A	C	Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1855272	tcaagctggataaaga[C/G]gcaaaaccttcaagga	C	G	25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // --- // --- // --- // --- ///	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-1850193	tatgtgtattctcatc[A/G]ccaaagatccaaacaa	A	G	7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	YWHAZ	YWHAZ, Homo sapiens tyrosine 3-monooxygenase,q22.3
SNP_A-1845742	tataggtttcaattaa[C/T]gttctacctttctgac	C	T	8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 835842 // --- // --- // --- //	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1818634	gttgaagcatgataga[A/G]aagagagagaaggagc	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2518956 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1819487	gttgggtttcattcca[A/G]gcaaaaaaaatgttaa	A	G	54361 // Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), mRNA. /// ENST00000290167 // upstream // 107605 // --- // --- // --- // --- /// ENST00000354898	WNT4	WNT4, Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), p36.12
SNP_A-1819635	gttgtaggctcttcaa[C/T]agctactagactcatc	C	T	// Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// ENST00000331504 // upstream // 176191 // --- // ---	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-1837179	tactgtttctatcata[A/G]tactgtgcttgatatg	A	G	// 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 805649 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1838976	tagagactgacagaat[A/G]aataccatttcttgct	A	G	// Homo sapiens hypothetical protein FLJ40869 (FLJ40869), mRNA. /// ENST00000317402 // intron // 0 // --- // --- // --- // ---	FLJ40869	FLJ40869, Homo sapiens hypothetical protein FLJ40869 (FLJ40869), p24.2
SNP_A-1843236	tagtcctcactcagcc[C/T]catgccagaagtatca	C	T	Homo sapiens chromosome 20 open reading frame 71 (C20orf71), mRNA. /// ENST00000344897 // intron // 0 // --- //	C20orf71	C20orf71, Homo sapiens chromosome 20 open reading frame 71 (C20orf71), q11.21
SNP_A-1842325	taggtaggttaggaca[C/T]tgcttgctgtttttg	C	T	NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 //	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-1830591	taatcatctgtaggga[C/T]tcaccaactttctcct	C	T	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1831801	taattcccatacttca[C/G]attaattgccagaggt	C	G	285533 // Homo sapiens hypothetical protein LOC285533 (LOC285533), mRNA. /// NM_003013 // downstream // 15042	RNF175	RNF175, Homo sapiens hypothetical protein LOC285533 (LOC285533), q31.3
SNP_A-1790986	ggggtatattcaacac[A/G]catgggttttataatc	A	G	/// ENST00000331332 // downstream // 280207 // --- // --- // ---	-	p11.1
SNP_A-1799217	gtaagttagagttgcc[A/T]gagagaatctcctgaa	A	T	// 57823 // Homo sapiens SLAM family member 7 (SLAMF7), mRNA. /// NM_002348 // upstream // 16456 // Hs.403857 //	SLAMF7	SLAMF7, Homo sapiens SLAM family member 7 (SLAMF7), q23.3
SNP_A-1795562	ggtgctacttttttact[C/T]accctcaatttggaga	C	T	136259 // Homo sapiens Kruppel-like factor 14 (KLF14), mRNA. /// ENST00000310992 // upstream // 181004 // --- // ---	KLF14	KLF14, Homo sapiens Kruppel-like factor 14 (KLF14), q32.3
SNP_A-1792951	ggtacacgtgcaggag[A/G]atgcgcaggtctgtta	A	G	// 134359 // Homo sapiens hypothetical protein FLJ35779 (FLJ35779), mRNA. /// ENST00000282199 // upstream //	FLJ35779	FLJ35779, Homo sapiens hypothetical protein FLJ35779 (FLJ35779), q13.3
SNP_A-1811560	gtgctcttctgggcac[A/G]caaaacaatgaatatc	A	G	1435 // Homo sapiens colony stimulating factor 1 (macrophage) (CSF1), transcript variant 4, mRNA. ///	CSF1	CSF1, Homo sapiens colony stimulating factor 1 (macrophage) (CSF1), transcript variant 4, p13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1645854	tctgactcttccaactccataaata[A/C]attctgaaaagacatgaaagaaggt	A	C	25849 // DKFZP564O0823 protein /// NM_025064 // 5UTR // 0 // - // - // - // -	DKFZP564O0823	DKFZP564O0823 , rs10518135, DKFZP564O0823 protein ,q13.3
SNP_A-1672376	gcaaatcataatttgcatttggaaa[A/G]tattttaataatgttcacaaggtaa	A	G	// 5507 // protein phosphatase 1, regulatory (inhibitor) subunit 3C /// NM_025235 // upstream // 39736 // Hs.280776 //	PPP1R3C	PPP1R3C , rs10509635, protein phosphatase 1, regulatory (inhibitor) subunit 3C ,q23.32
SNP_A-1687850	tccttaatatgctgccctattgac[C/T]aagttactatcactagttaatgtaa	C	T	6419 // SET domain and mariner transposase fusion gene /// NM_020873 // downstream // 266286 // Hs.126085 // LRRN1	SETMAR	SETMAR , rs10510287, SET domain and mariner transposase fusion gene ,p26.1
SNP_A-1721588	ctcttacacatatgtttataaataa[C/T]actagtctctatggtgtctgagtta	C	T	7092 // tolloid-like 1 /// NM_016950 // downstream // 494090 // Hs.159425 // SPOCK3 // 50859 // sparc/osteonectin, cwcv	TLL1	TLL1 , rs10517898, tolloid-like 1 ,q32.3
SNP_A-1725278	tgtctgtcttagttggctcaggctg[C/T]cacaacaaaataccacagactaggt	C	T	solute carrier family 5 (sodium/glucose cotransporter), member 1	SLC5A1	SLC5A1 , rs743763, solute carrier family 5 (sodium,q12.3
SNP_A-1782839	ggcagagatacattac[A/G]cttctcattctaaaaa	A	G	Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // intron // 0 // Hs.130306 // CDH7 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1756961	atctaaaatgagattcattacaaaa[A/G]tgtatgttaataaagaacaccatta	A	G	1316 // core promoter element binding protein /// NM_031436 // upstream // 610121 // Hs.250469 // AKR1CL2 // 83592 //	COPEB	COPEB , rs1475099, core promoter element binding protein ,p15.1
SNP_A-1752153	gagtgtccagttgaaagagccagct[C/T]cacaaccagacacacccaagttcca	C	T	NM_000615 // intron // 0 // Hs.78792 // NCAM1 // 4684 // neural cell adhesion molecule 1	NCAM1	NCAM1 , rs723599, neural cell adhesion molecule 1,q23.1
SNP_A-1981038	ggatttcttgctctta[A/T]ccacacacaactaatt	A	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 217094	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1967273	agaaaggctacagata[C/T]cacctcatctcaggaa	C	T	Homo sapiens ubiquitin associated protein 2-like (UBAP2L), mRNA. /// ENST00000271877 // intron // 0 // --- // --- // --- // ---	UBAP2L	UBAP2L, Homo sapiens ubiquitin associated protein 2-like (UBAP2L), q21.3
SNP_A-1967062	gtccttttaatagttg[C/T]atggtattctcttgta	C	T	5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 72733 // Hs.42146 // PAX3 //	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-1966432	acttgctataggatac[A/G]cacacccaatttaata	A	G	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 609750 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1971069	tcctgaacttctttga[A/C]cttgggtagccttcct	A	C	Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// ENST00000300105 // intron // 0 // --- // --- // --- // ---	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3
SNP_A-1944571	ttgtgaaagaagtaaa[G/T]tcagcatctacgtaca	G	T	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1943566	ttgtaaccagcattta[C/G]cgtcaaggaccaggga	C	G	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1942695	ttgggatactgtggca[C/T]actaaatataaagtgt	C	T	3670 // Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA. /// NM_015946 //	ISL1	ISL1, Homo sapiens ISL1 transcription factor, LIM,q11.2
SNP_A-1933493	ttctactcataaacca[C/T]tcaccacttctgacac	C	T	/// ENST00000318847 // downstream // 11284 // --- // --- // ---	-	q23.31
SNP_A-1938312	ttgacgttagattac[A/G]gaaatttcataccaaa	A	G	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 450880 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-1938477	ttgacttttttcactat[A/T]agggacaacatttctt	A	T	ENST00000258173 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1954547	tttgccgggcctgaac[G/T]gtgtcagcattgaggg	G	T	// Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // upstream	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-1954142	catattttatcttcca[C/T]gaaaaattcttccagg	C	T	// 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000283950 // downstream // 69877 // --- //	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-1951105	atagccctttgtgcc[C/G]agtctattactaaacc	C	G	// 399655 // Homo sapiens zinc finger protein 539 (ZNF539), mRNA. /// NM_004876 // downstream // 119709 // Hs.434406	ZNF539	ZNF539, Homo sapiens zinc finger protein 539 (ZNF539), p12
SNP_A-1950574	tttcatccatctcatc[C/T]cgtgcaaacaagttgg	C	T	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // CDS // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1950312	tttcagatgaggaaac[C/T]gcatcttcaaaagtta	C	T	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1949190	tttatgggacagaatg[A/G]aattccaaataaaatg	A	G	Homo sapiens scavenger receptor cysteine-rich type 1 protein M160 (M160), mRNA. /// ENST00000313599 // intron	M160	M160, Homo sapiens scavenger receptor cysteine-rich type 1 protein M160 (M160), p13.31
SNP_A-1957066	ttttaattggattttc[A/C]ctcacgtcacttaaga	A	C	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 66313 // --- // --- // --- // ---	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1901626	tggcaactgttttcag[A/G]acaccaatgcagttgc	A	G	56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 132218 // Hs.315186 // PCSK2 //	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897191	tgctctatttcacaca[C/T]ctctgacaatttgacc	C	T	// 10801 // Homo sapiens MLL septin-like fusion (MSF), mRNA. /// NM_018996 // upstream // 432430 // Hs.80618 //	SEPT9	SEPT9, Homo sapiens MLL septin-like fusion (MSF), q25.3
SNP_A-1886291	tgacctatttacacac[C/T]gaggagggatgtggaa	C	T	// 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 10536 // Hs.31664 //	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1882051	tcttttggttggaata[C/T]aggtctccattggaaa	C	T	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 148656 // Hs.411433	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-1929911	ttcatgaagagtttca[A/G]aataacatttcaaact	A	G	Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 //	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-1927054	ttatttgtagcataac[C/T]ataggtcaaggctgga	C	T	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 150528 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3
SNP_A-1928848	ttcagaggttcgagca[C/G]tcactctgtatgcccc	C	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 159581 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1923053	ttagcataggcttcac[A/C]acagaatccaaggaga	A	C	Homo sapiens tectorin alpha (TECTA), mRNA. /// ENST00000264037 // CDS // 0 // --- // --- // --- // ---	TECTA	TECTA, Homo sapiens tectorin alpha (TECTA), q23.3
SNP_A-1919522	ttaaggaaaggtgcta[C/T]ggttattatttcttct	C	T	9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 479199 //	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1921922	ttactccttcaaactc[A/G]cacagctagtaatgtg	A	G	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1911199	tgtctgcgtgtcctac[C/T]gtacctgattaaaaca	C	T	Homo sapiens sialyltransferase 8E (alpha-2, 8-polysialyltransferase) (SIAT8E), mRNA. /// ENST00000315087 // intron // 0 // --- // --- // --- // ---	ST8SIA5	ST8SIA5, Homo sapiens sialyltransferase 8E (alpha-2, 8-polysialyltransferase) (SIAT8E), q21.1
SNP_A-1906267	tggtgaggtgcacacc[A/G]accctctctttgcca	A	G	Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-1918138	ttaaactagtggaact[G/T]agatttcagatttagc	G	T	7080 // Homo sapiens thyroid transcription factor 1 (TITF1), mRNA. /// NM_003317 // downstream // 17227 // Hs.94367 //	TITF1	TITF1, Homo sapiens thyroid transcription factor 1 (TITF1), q13.3
SNP_A-2268056	gaatcttctgtattta[A/G]aaaacaattttccaat	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2120063 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2266611	gaagtccctgctgaac[C/T]aggagcttcatgctag	C	T	Homo sapiens citrate lyase beta like (CLYBL), transcript variant 1, mRNA. /// NM_206808 // intron // 0 // Hs.130690 //	CLYBL	CLYBL, Homo sapiens citrate lyase beta like (CLYBL), transcript variant 1, q32.3
SNP_A-2258618	cttttgacatatcata[G/T]gtggacttatttttt	G	T	// 221393 // Homo sapiens G protein-coupled receptor 115 (GPR115), mRNA. /// NM_181744 // upstream // 2816 //	GPR115	GPR115, Homo sapiens G protein-coupled receptor 115 (GPR115), p12.3
SNP_A-2257528	ctttgattctcacagt[C/T]actgctttttgttcaa	C	T	/// ENST00000330777 // downstream // 22420 // --- // --- // ---	-	p23.1
SNP_A-2258861	ctttttatacactaac[C/T]ggcaaattatttgatc	C	T	Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // --- // --- // --- // ---	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2260729	gaaacgactcaagcaa[A/T]taaaggagaataacag	A	T	Homo sapiens periostin, osteoblast specific factor (POSTN), mRNA. /// ENST00000350926 // intron // 0 // --- // --- // --- // ---	POSTN	POSTN, Homo sapiens periostin, osteoblast specific factor (POSTN), q13.3
SNP_A-2274218	gacttctgtaccttca[A/G]caagggtggctagagc	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 99789 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2239818	ctgaaattgaacccaa[C/G]catctttagagctttc	C	G	2737 // Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// NM_024054 // downstream // 450634 // Hs.214247 // C7orf25	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-2229772	tgagacctgctactac[C/T]atacagatccttagcc	C	T	// Human mRNA for KIAA0227 gene, partial cds. /// NM_033141 // downstream // 670 // Hs.437214 // MAP3K9 //	TTC9	TTC9, Human for KIAA0227 gene, partial cds. ,q24.2
SNP_A-2251228	cttcaaactaagacac[C/T]gcatatagaattctcc	C	T	// Homo sapiens von Willebrand factor (VWF), mRNA. /// NM_001769 // upstream // 72139 // Hs.114286 // CD9 // 928	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2244020	ctgcttcctataggcc[A/G]ccaaaagctacaggat	A	G	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 909632 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2247880	ctgtgattggcagtgc[C/T]aagggtcaggtgggac	C	T	Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2248715	ctgttcctcagaaaaa[A/G]gtagaaactggtaaag	A	G	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.2
SNP_A-2246289	ctggtggtctttctaa[C/G]ccaacctggatatgat	C	G	1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 97433 //	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2291453	gcaattctctgggaaa[C/G]attgtgcaggctgtga	C	G	1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 64875 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri.p11.2
SNP_A-2298713	gcccagggattacaga[C/G]agcaagggatggaaat	C	G	sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// ENST00000360890 // intron // 0 // --- // --- // ---	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-2299734	gccgtgacacgaccac[C/T]ggccttctggattgtg	C	T	sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000216254 // intron // 0 // --- // --- // ---	ACO2	ACO2, Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-2312155	ggacagatcgcttaca[C/T]tgcctggagcagaaca	C	T	5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // downstream // 5630 //	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-2313084	ggagaaagtggtccga[A/G]gtgtggatcagagaga	A	G	7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// ENST00000318987 // downstream // 103920 // --- // --- // --- // ---	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2313953	ggagctcaaaacccac[A/G]aggaatccctcttctt	A	G	Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // --- // ---	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-2306909	aagcaaatagaagaca[G/T]gctacatttaattcaa	G	T	Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // --- // --- // --- /// ENST00000310362 // intron // 0 // --- // ---	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2308765	gctttgagtcctgaaa[C/T]aaacttgagggataat	C	T	85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 32175 // Hs.461389 // CNTNAP4 // 85445 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2310281	ggaaccatggatgacc[A/G]ggatccacgtgtgttt	A	G	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 362672 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2297410	gccactgctcaataaa[C/T]aatagctgtcttatta	C	T	Homo sapiens leucine-rich PPR-motif containing (LRPPRC), mRNA. /// ENST00000260665 // intron // 0 // --- // --- // ---	LRPPRC	LRPPRC, Homo sapiens leucine-rich PPR-motif containing (LRPPRC), p21
SNP_A-2245641	ctgggccagagctgcc[C/T]ggaggtctcctctccc	C	T	Homo sapiens LIM and SH3 protein 1 (LASP1), mRNA. /// ENST00000318008 // intron // 0 // --- // --- // ---	LASP1	LASP1, Homo sapiens LIM and SH3 protein 1 (LASP1), q12
SNP_A-2246144	ctggtctgacgaatca[C/T]agtatagacaaaagag	C	T	FLJ32063 // 150538 // Homo sapiens hypothetical protein FLJ32063 (FLJ32063), mRNA. /// NM_153689 // upstream //	FLJ32063	FLJ32063, Homo sapiens hypothetical protein FLJ32063 (FLJ32063), q33.1
SNP_A-2245116	ctggcccaagttaca[C/T]gtgtccaatttctccc	C	T	/// ENST00000355344 // downstream // 182156 // --- // --- // ---	-	p12
SNP_A-2243021	ctgccccacagttac[C/T]ggacaccagacaaaag	C	T	Homo sapiens androgen-induced 1 (AIG1), mRNA. /// ENST00000305853 // intron // 0 // --- // --- // --- ///	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-2251647	cttcaggatgaaacac[A/G]gtgacgcctggctggg	A	G	Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), mRNA. /// ENST00000256194 // intron // 0 // --- // ---	MICAL2	MICAL2, Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), p15.3
SNP_A-2255585	cttgtggcagagctac[C/T]acatacttaatagctt	C	T	9695 // Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), mRNA. /// ENST00000295399 // upstream // 70304 // --- // --- // ---	EDEM1	EDEM1, Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), p26.1
SNP_A-2230709	ctatgaaggcctgcaa[C/T]ggctgatcttggtta	C	T	/// ENST00000356642 // downstream // 522164 // --- // --- // ---	-	q31.1
SNP_A-2280691	gaggtctgacccagag[A/T]actcaacaacaggata	A	T	147184 // Homo sapiens hypothetical protein MGC21518 (MGC21518), mRNA. /// ENST00000301665 // 5UTR // 0 // ---	MGC21518	MGC21518, Homo sapiens hypothetical protein MGC21518 (MGC21518), q21.2
SNP_A-2282868	gataaataagcaaaaaa[A/T]catataatgcaactct	A	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2257093	ctttctcatcatcatc[A/G]cagaaaatcaatgtta	A	G	5420 // Homo sapiens podocalyxin-like (PODXL), mRNA. /// ENST00000322985 // upstream // 42452 // --- // --- // ---	PODXL	PODXL, Homo sapiens podocalyxin-like (PODXL), q32.3
SNP_A-2266777	gaagtgtcaccaaaaat[A/T]gttaatcagataacat	A	T	256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 94942 // FLJ39531 // 400360 // Homo sapiens FLJ39531 protein	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2264814	gaagagaagataaaaat[A/T]gtgcagaaalaacagt	A	T	(FLJ395311), mRNA. /// NM_003246 // upstream // 242879 //	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ395311), q14
SNP_A-2266107	gaaggctcgttagacc[A/G]actgcctatgggaaat	A	G	1105 // Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /// ENST00000284049 // upstream // 93986 // Homo sapiens forkhead box P2 (FOXP2),	CHD1	CHD1, Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), q21.1
SNP_A-1914772	tgttacctatttttgc[A/C]atgtttatacttttgt	A	C	transcript variant 1, mRNA. /// NM_148900 // downstream //	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-1912728	tgtgctaggttcagca[A/G]tagtgactgaaatact	A	G	Homo sapiens WD repeat domain 36 (WDR36), mRNA. /// ENST00000323652 // intron // 0 // --- // --- // ---	WDR36	WDR36, Homo sapiens WD repeat domain 36 (WDR36), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909666	tgtcaacttcgcctc[A/G]ccatcattgccacact	A	G	Homo sapiens transient receptor potential cation channel, subfamily V, member 5 (TRPV5), mRNA. /// ENST00000265310 // CDS // 0 // --- // --- // ---	TRPV5	TRPV5, Homo sapiens transient receptor potential cation channel, subfamily V, member 5 (TRPV5), q34
SNP_A-1921712	ttacggtggacttcc[C/T]attgttcttttcagt	C	T	Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-1919375	ttaagatctttacca[C/T]acaaatactgacaaca	C	T	/// 28978 // Homo sapiens transmembrane protein 14A (TMEM14A), mRNA. /// NM_000846 // downstream // 58433 //	TMEM14A	TMEM14A, Homo sapiens transmembrane protein 14A (TMEM14A), p12.2
SNP_A-1920458	ttaattaigttggagc[A/C]caagtagtcagaaagt	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 620997 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1926628	ttattgaatataaaaa[A/G]atcagagagcattaa	A	G	441639 // Homo sapiens olfactory receptor, family 9, subfamily K, member 2 (OR9K2), mRNA. /// NM_001005280	OR9K2	OR9K2, Homo sapiens olfactory receptor, family 9, subfamily K, member 2 (OR9K2), q13.2
SNP_A-1926790	ttattgtgtgcacc[C/T]ggagaacttacaagca	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// NM_006113 // downstream // 158487 // Hs.267659 //	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p13.3
SNP_A-1881890	tctttttattatttttg[A/T]atctcggcgactgaag	A	T	ENST00000306670 // intron // 0 // --- // --- // ---	-	p11.2
SNP_A-1884476	tgaagtgggtgctcaa[C/T]gtattaattaatagga	C	T	Homo sapiens annexin A3 (ANXA3), mRNA. /// ENST00000264908 // intron // 0 // --- // --- // ---	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1888522	tgaggagcttgagttat[C/T]accacactgaacttct	C	T	Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// ENST00000324987 // intron // 0 // --- // ---	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-1874821	tctcgcacatttttc[A/G]aaatgctttgaccaga	A	G	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1874440	tctcccatccaaacaa[C/T]tacagcaggttccgcc	C	T	123016 // Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, mRNA. /// NM_198309 //	TTC8	TTC8, Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, q32.11
SNP_A-1877156	tctgctggctctcccc[C/T]catcctgggaatgcag	C	T	ENST00000357356 // intron // 0 // --- // --- // ---	-	q26.11
SNP_A-1897957	tgctgtaagttgaaga[C/T]gcctgctagaggtgac	C	T	Homo sapiens mRNA for AIE-75, complete cds. /// NM_153676 // intron // 0 // Hs.502072 // USH1C // 10083 // 28962 // Homo sapiens osteopetrosis associated transmembrane protein 1 (OSTM1), mRNA. /// NM_003269 // upstream // 59838 // Hs.157688 // NR2E1 // 7101 // Homo	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. p15.1
SNP_A-1959286	ttttgatgaagttctct[A/G]atactatttcacgtat	A	G		OSTM1	OSTM1, Homo sapiens osteopetrosis associated transmembrane protein 1 (OSTM1), q21
SNP_A-1948273	tttaggacaaaggagc[C/T]cattaccatcttgga	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 190883 // Hs.154329 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 //	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-1939751	ttgcaaatcagacata[C/T]gtgacactccttttc	C	T		NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1969405	tcttttttattctatc[C/T]gacaatctgccttta	C	T		C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-1971239	aggaaaagagggtctcc[A/G]agctgtcaagtgggggc	A	G	ENST00000336769 // intron // 0 // --- // --- // ---	-	q13.32
SNP_A-1966634	aacctgttttcagtca[A/G]tccagtgtatcaaaga	A	G	8609 // Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA. /// NM_004379 // upstream // 277205 //	KLF7	KLF7, Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), q33.3
SNP_A-1967932	aataggaatgaatttta[A/G]cagtgatttgtcaca	A	G	C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000340000 1473 // Homo sapiens cystatin D (CST5), mRNA. ///	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1968191	aggacttagggcagca[C/T]ctgacacagaacagaa	C	T	NM_080920 // downstream // 17387 // Hs.355394 // GGTLA4	CST5	CST5, Homo sapiens cystatin D (CST5), p11.21
SNP_A-1981804	atgcagactgaattaa[A/G]atggcaccctaaggga	A	G	DEPDC1B // 55789 // Homo sapiens DEP domain containing 1B (DEPDC1B), mRNA. /// ENST00000282876 //	DEPDC1B	DEPDC1B, Homo sapiens DEP domain containing 1B (DEPDC1B), q12.1
SNP_A-1979294	caacaatttaattgca[A/G]ctttctcagaaaatc	A	G	Homo sapiens methylmalonic aciduria (cobalamin deficiency) type A (MMAA), mRNA. /// ENST00000281317 // intron // 0 //	MMAA	MMAA, Homo sapiens methylmalonic aciduria (cobalamin deficiency) type A (MMAA), q31.21
SNP_A-1982908	ctagtttgtataaaa[A/G]taaggcacaagtataa	A	G	Homo sapiens WD repeat domain 36 (WDR36), mRNA. /// ENST00000323652 // intron // 0 // --- // --- // ---	WDR36	WDR36, Homo sapiens WD repeat domain 36 (WDR36), q22.1
SNP_A-1783471	ggcatcagggcacag[A/G]ccaactgagccacggg	A	G	138428 // Homo sapiens chromosome 9 open reading frame 115 (C9orf115), mRNA. /// NM_144965 // intron // 0 //	C9orf115	C9orf115, Homo sapiens chromosome 9 open reading frame 115 (C9orf115), q34.11
SNP_A-1728579	gatggcatttcctatctgtgtccca[C/T]ggctccgggtttctgaatgtcacca	C	T	388 // ras homolog gene family, member B /// NM_022460 // downstream // 33879 // Hs.288410 // FLJ14249 // 64342 //	RHOB	RHOB , rs6753563, ras homolog gene family, member B ,p24.1
SNP_A-1734644	caacaacggttcctgtaagtgaaggt[A/C]atttagacatcagaagaatccaataa	A	C	NM_012124 // upstream // 2216114 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1, rs10501789, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1731603	gactttcagacagaggaaacagtac[A/G]tgcagaggccacaggccagagc ctg	A	G	79953 // chromosome 20 open reading frame 39 /// NM_080920 // upstream // 22270 // Hs.355394 // GGTLA4 //	C20orf39	C20orf39 , rs3843777, chromosome 20 open reading frame 39 ,p11.21
SNP_A-1738487	aaaagacagctccaagcagtgcaaa[C/G]ataatctggactctactcccttctt	C	G	NM_000627 // intron // 0 // Hs.241257 // LTBP1 // 4052 // latent transforming growth factor beta binding protein 1	LTBP1	LTBP1 , rs10495788, latent transforming growth factor beta binding protein 1,p22.3
SNP_A-1693449	ttaactttcacaataacttgtaaaa[C/T]agtcttgcattgtacagatggggta	C	T	57531 // HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 /// NM_007073 // downstream // 204890 // Hs.221660 // BVES // 11149 // blood vessel	HACE1	HACE1 , rs10485310, HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 ,q16.3
SNP_A-1676790	ccaccctccagctcccacacgcaca[C/G]cattttccatagcacatgaaacac c	C	G	NM_020211 // upstream // 21148 // Hs.271277 // RGMA // 56963 // RGM domain family, member A	RGMA	RGMA , rs4396488, RGM domain family, member A,q26.1
SNP_A-1807443	gtctgcaacacatcac[A/C]gggccttagaaaatgt	A	C	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-1809551	gtgagaggtgctggaa[A/G]taggccagcctataaa	A	G	// 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 12141 // --- //	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1810802	gtgcagccagtttgga[A/C]aacagtctagcagtat	A	C	Homo sapiens SFRS protein kinase 2 (SRPK2), transcript variant 2, mRNA. /// NM_182692 // intron // 0 // Hs.285197 //	SRPK2	SRPK2, Homo sapiens SFRS protein kinase 2 (SRPK2), transcript variant 2, q22.3
SNP_A-1810869	gtgcagtgaccagagg[C/T]atcattagaagaggaa	C	T	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA. /// ENST00000268489 // intron // 0 // --- // --- // --- // ---	ATBF1	ATBF1, Homo sapiens AT-binding transcription factor 1 (ATBF1), q22.3
SNP_A-1803185	cagactggcatctgca[C/T]gataacccaagagcta	C	T	10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 214723 // Hs.369907 //	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1795979	ggtggtagtgggtgca[C/G]aatcagggaggtgttg	C	G	FLJ22390 // 64757 // Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA. /// NM_021958 // upstream //	FLJ22390	FLJ22390, Homo sapiens hypothetical protein FLJ22390 (FLJ22390), q41
SNP_A-1831808	taattccgcttcttca[C/T]cttttgggtttatacc	C	T	/// ENST00000357074 // downstream // 224654 // --- // --- // --- // --- /// ENST00000358765 // downstream // 224654 // --- // ---	-	p14
SNP_A-1829137	taaggtgagaggacaa[C/T]ggaattgaaacctggc	C	T	// Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 708067 // Hs.148162 // PDGFC // 56034 //	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1840344	tagcatggatacaaac[A/C]atcagaagagatccat	A	C	MGC50104 // 341032 // Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), mRNA. ///	MGC50104	MGC50104, Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), q23.1
SNP_A-1819631	gttgtagcatatgtcg[A/G]atttttttaaggctga	A	G	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 6608 // Hs.54642 // MAT2B // 27430 // Homo	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1823568	taaaagtgtgctataa[A/G]tatgaatgtaaaattt	A	G	Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), mRNA. /// ENST00000229922 // intron // 0 // -	CAP2	CAP2, Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), p22.3
SNP_A-1855827	tcaatgaagcaagagc[A/G]acaagatgactgatct	A	G	Homo sapiens POU domain, class 4, transcription factor 3 (POU4F3), mRNA. /// ENST00000265271 // downstream //	POU4F3	POU4F3, Homo sapiens POU domain, class 4, transcription factor 3 (POU4F3), q32
SNP_A-1864936	tccaggtatagcaaac[A/G]cccagttacccaaatg	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 865638 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1865835	tcccaaatactggctt[A/T]aaacaagtgccccaga	A	T	ENST00000358349 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-1866964	tccctcaatggataaa[A/G]acatcaaaataaccaa	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 244916 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2207050	ccatgttctgaaataa[A/T]gcaatggagagcaacg	A	T	Homo sapiens solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8), mRNA. ///	SLC12A8	SLC12A8, Homo sapiens solute carrier family 12 (potassium q21.2
SNP_A-2207270	ccattccccaacctcc[A/G]ctgcgcaggccaagca	A	G	Homo sapiens eukaryotic translation initiation factor 2C, 2 (EIF2C2), mRNA. /// ENST00000220592 // intron // 0 // --- // ---	EIF2C2	EIF2C2, Homo sapiens eukaryotic translation initiation factor 2C, 2 (EIF2C2), q24.3
SNP_A-2215850	cctcattgtgccgtgc[A/G]ataaatgagaagttgc	A	G	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 425705 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-2216212	cctccgaggaagggaa[A/G]ctcattgggatggatg	A	G	Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 //	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12
SNP_A-2213201	ccgcagtcctaaacaa[C/T]aggatgtcttcagccc	C	T	Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), mRNA. /// NM_019076 // intron // 0 // Hs.546397 // UGT1A8 // 54576 // Homo sapiens UDP	UGT1A10	UGT1A10, Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), q37.1
SNP_A-2224322	cgtaacacccgactaa[C/T]gcagaagaaaagttta	C	T	25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // --- // --- // --- // --- ///	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2224454	cgtaggctatttggaa[A/G]atgattagaattcata	A	G	Homo sapiens metallophosphoesterase 1 (MPPE1), mRNA. /// NM_023075 // intron // 0 // Hs.288147 // MPPE1 // 65258 //	MPPE1	MPPE1, Homo sapiens metallophosphoesterase 1 (MPPE1), p11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225903	ctaaatgcaaagacaa[A/G]aaatatgctgtattcc	A	G	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 678130 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2191663	catattatgaagagga[A/T]ctcctggcagggtgca	A	T	84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 131081 // Hs.194766 // SEZ6L //	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2192862	catcctgagctggcag[A/G]aacataatccacttct	A	G	// 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// NM_181354 // upstream // 741762 //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2168612	caagaaccaggatcta[C/T]ggcaccgtcaccctcg	C	T	sapiens glutathione reductase (GSR), mRNA. /// ENST00000221130 // intron // 0 // --- // --- // --- // ---	GSR	GSR, Homo sapiens glutathione reductase (GSR), p12
SNP_A-2169043	caagagtctttacatc[A/G]gaagttctcatcaaga	A	G	Homo sapiens kinesin family member 9 (KIF9), mRNA. /// NM_182902 // intron // 0 // Hs.373947 // KIF9 // 64147 //	KIF9	KIF9, Homo sapiens kinesin family member 9 (KIF9), p21.31
SNP_A-2177656	cacggcttgcctgttc[G/T]cctctagcacaaagtc	G	T	ENST00000359815 // intron // 0 // --- // --- // --- // ---	-	q13.1
SNP_A-2178173	cactatgaaaattccc[A/G]caaagtctgccctttg	A	G	7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2176869	caccgcccctgaagag[A/G]aagtcctttgtttggt	A	G	5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000217725 // upstream	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-2182125	cagagggaacagtaca[G/T]gcaaaggctctgaagt	G	T	Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, beta (NAPB), mRNA. /// ENST00000246011 // intron // 0 // --- // --- // --- // ---	NAPB	NAPB, Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, beta (NAPB), p11.21
SNP_A-2180179	cagaaacccatccgta[A/C]agcagggcaccggccg	A	C	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-2167761	caaccctctggactca[A/T]gtgtcttttgccttag	A	T	Homo sapiens chromosome 9 open reading frame 138 (C9orf138), mRNA. /// ENST00000286333 // intron // 0 // --- //	C9orf138	C9orf138, Homo sapiens chromosome 9 open reading frame 138 (C9orf138), p22.1
SNP_A-2161454	atttgccttctgctga[C/T]ggtgtcctgcctcagg	C	T	sapiens E2F transcription factor 3 (E2F3), mRNA. /// ENST00000346618 // intron // 0 // --- // --- // --- // ---	E2F3	E2F3, Homo sapiens E2F transcription factor 3 (E2F3), p22.3
SNP_A-2157265	attgacatgtgattat[C/T]acctaaagcccatagt	C	T	METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream //	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-2154235	attatgagtgtagaaa[C/T]gttggtgcaggaaata	C	T	BRCC2 // 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 423502 // Hs.444075 //	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-2113354	aggcctgtgaccggga[A/G]ggggctgagtccaagc	A	G	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 7916 // Hs.282089 //	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2124385	agttcaacgtggacaa[A/G]gaagcaggggagaggc	A	G	sapiens glycogen synthase 1 (muscle) (GYS1), mRNA. /// ENST00000323798 // CDS // 0 // --- // --- // --- // --- ///	GYS1	GYS1, Homo sapiens glycogen synthase 1 (muscle) (GYS1), q13.33
SNP_A-2057755	aatatgtgggttatca[A/G]taacaggtcgctggaa	A	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2057636	aatatgccaaaggacc[C/T]acaagctgcaaagacc	C	T	// 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 188617 // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-2048526	aagcatggcttgagaa[A/G]ctcaaaactctctggg	A	G	/// ENST00000321014 // upstream // 42981 // --- // --- // --- // ---	-	p12.3
SNP_A-2096339	agaccatcctagctaa[C/T]gcagtgaaatccaaaa	C	T	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // downstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2097865	aggtgggcttcaccca[A/G]accttgcactggggtg	A	G	23316 // Homo sapiens mRNA for KIAA0293 gene, partial cds. /// ENST00000331096 // downstream // 56071 // --- // ---	CUTL2	CUTL2, Homo sapiens for KIAA0293 gene, partial cds. ,q24.11
SNP_A-2107242	agctaaaatgcttaac[A/C]aagagattagaacata	A	C	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // --- // --- // --- // --- /// ENST00000260943 // intron //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2102750	agatttgctgagaata[A/G]cttcccctcaaaagaa	A	G	// 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2089318	acttaggcagtgttca[C/T]ggtaaaggcttcttct	C	T	10047 // Homo sapiens cystatin 8 (cystatin-related epididymal specific) (CST8), mRNA. /// NM_080610 // downstream //	CST8	CST8, Homo sapiens cystatin 8 (cystatin-related epididymal specific) (CST8), p11.21
SNP_A-2087826	actggaccttaaatat[C/T]agcagacaatgtcact	C	T	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 495723 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2082821	acgtactaaaaggcaa[A/G]actttaagatcatgtc	A	G	// 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1333939 // --- // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2079928	accettcatcccctag[A/C]aagcactattctagcc	A	C	9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 524575 // --- // --- // ---	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds. q23
SNP_A-2019173	ctcccaggactgtaga[A/T]gattggcattgactca	A	T	// 3772 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15), transcript variant 2, mRNA. /// NM_170736 // downstream // 31648 //	KCNJ15	KCNJ15, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15), transcript variant 2, q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2013898	tggtacatgcatagaa[C/T]agattccaacatttgt	C	T	// 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// NM_006558 // upstream // 176882 // Hs.444558 //	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.22
SNP_A-2007963	aagaaagctcggggcg[C/T]acatggaaatcaagct	C	T	4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000331037 // upstream //	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-1992234	cctaatcatctatcat[C/G]acactgagagctctgc	C	G	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2005016	agttattgaagcagcc[A/G]cccggaaatgccagat	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2041432	aaccttatgatttaca[A/T]cccacttactattcac	A	T	MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 //	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2047500	aagatgcatgcacaaa[A/T]gttttagtacaataaa	A	T	Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // --- // --- // --- // ---	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2038677	aacagagagagtaaag[A/G]agaatgccccaaagtt	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 902098 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2039768	aacattaaattttgca[G/T]caccttacttggcata	G	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 426098 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2040178	aaccaagtggagatga[C/T]acaaaaacgaaaactc	C	T	163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 14065 // Hs.221375 //	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-2038349	tttcctacacaagcaa[C/T]gtcccagaagaaaagc	C	T	Homo sapiens solute carrier organic anion transporter family, member 1C1 (SLCO1C1), mRNA. /// ENST00000266509 // intron // 0 // --- // --- // --- // ---	SLCO1C1	SLCO1C1, Homo sapiens solute carrier organic anion transporter family, member 1C1 (SLCO1C1), p12.2
SNP_A-2037731	aacaaggtctaaaaca[A/G]tagtgaaaattggtgc	A	G	// 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 285354 // Hs.154329 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2037166	aacaaaattaaacata[C/G]aggcaaaaagatatgg	C	G	sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) p21.2
SNP_A-2021425	aaaaaagattacaacc[A/G]ccaacatgtgggagct	A	G	// Homo sapiens olfactory receptor, family 8, subfamily G, member 1 (OR8G1P), mRNA. /// NM_001005198 // CDS // 0 // Hs.448172 // OR8G5 // 219865 // Homo sapiens olfactory	OR8G1P	OR8G1P, Homo sapiens olfactory receptor, family 8, subfamily G, member 1 (OR8G1P), q24.1
SNP_A-2020449	tcagctgtgcgtgccc[A/G]cggacgtgcagagaag	A	G	Homo sapiens chromosome 21 open reading frame 29 (C21orf29), mRNA. /// ENST00000323084 // intron // 0 // --- //	C21orf29	C21orf29, Homo sapiens chromosome 21 open reading frame 29 (C21orf29), q22.3
SNP_A-2020905	aattattcatgaaaag[C/T]cattccttccaggctg	C	T	PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 1129955 // Hs.405156 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.3
SNP_A-2024963	aaaataaattggatta[C/T]gtgatctctaaaatcc	C	T	Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// ENST00000280625 // intron // 0 // --- // --- // --- // ---	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-2025626	aaaatgacaacttcaa[C/T]atttccaaaaaagaca	C	T	Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // CDS // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-2027516	aaaccaataggcttta[A/G]agagaaggtgtcaatt	A	G	// 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 236470 // Hs.463466 // CA10 //	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33
SNP_A-2029526	aaagacgtgccacaca[G/T]aagcatgaaggtaagg	G	T	57115 // Homo sapiens peptidoglycan recognition protein 4 (PGLYRP4), mRNA. /// AF242518 // upstream // 4189 //	PGLYRP4	PGLYRP4, Homo sapiens peptidoglycan recognition protein 4 (PGLYRP4), q21.3
SNP_A-2038671	aacagagaccccgata[C/T]aaccaaacacaaagac	C	T	7187 // Homo sapiens TNF receptor-associated factor 3 (TRAF3), transcript variant 2, mRNA. /// NM_145725 // downstream // 2589 // Hs.510528 // TRAF3 // 7187 // Homo	TRAF3	TRAF3, Homo sapiens TNF receptor-associated factor 3 (TRAF3), transcript variant 2, q32.32
SNP_A-2043362	aactggattgtttata[C/T]actagagtaacagaaa	C	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1990137	gtgaccgagggcagcc[A/G]attttatgcaccttaa	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 260285 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2010430	atttcaagaattgtca[C/T]gtgaacagtggaatac	C	T	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 96571 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2010865	tggttgttatacagca[C/T]cactctttttagtgca	C	T	23530 // Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA. /// NM_182977 //	NNT	NNT, Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015857	tgaagcacttgcttac[A/G]attttgatatttgtgg	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 147887 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2016661	cagaaaatgaatttaa[A/G]tagcagctcaacagag	A	G	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 520410 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016966	tgaatatctctgtctc[A/G]ctgcactgcaccactc	A	G	Homo sapiens junctional adhesion molecule 2 (JAM2), mRNA. /// ENST00000312957 // intron // 0 // --- // --- // --- // ---	JAM2	JAM2, Homo sapiens junctional adhesion molecule 2 (JAM2), q21.3
SNP_A-2084387	actatagttgtttgag[A/T]ccccaaagtcctggtg	A	T	// Homo sapiens hypothetical protein FLJ38335 (FLJ38335), mRNA. /// ENST00000318698 // intron // 0 // --- // --- // --- // ---	FLJ38335	FLJ38335, Homo sapiens hypothetical protein FLJ38335 (FLJ38335), q23.2
SNP_A-2084739	actatttagagtccca[A/G]gttactttacatgata	A	G	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2102130	agatgtgttctgaaaa[C/T]gtcggtgttcccatct	C	T	Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 //	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2102337	agattatgtttgctta[C/G]atatttgaaagagtct	C	G	sapiens KIAA0029 mRNA, partial cds. /// NM_015361 // intron // 0 // Hs.412462 // R3HDM // 23518 // Homo sapiens R3H	R3HDM	R3HDM, Homo sapiens KIAA0029 partial cds. ,q21.3
SNP_A-2094347	agaagtccaaagtcaa[C/T]gtgtcggtggggccac	C	T	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 954245 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2048023	aagcaaggctagcaga[C/T]gtgcaggtagatggaa	C	T	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.32
SNP_A-2057485	aatatctatgaggaag[A/C]acaggccaatgctttt	A	C	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2073617	acagtatgaggtgaga[C/T]gcccccacggtttggag	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2072718	acagcgtgactgatgc[A/G]aagagagcgagagcac	A	G	85446 // Homo sapiens mRNA for KIAA1762 protein, partial cds. /// BX161435 // upstream // 7147 // Hs.15098 // THTPA //	ZFHX2	ZFHX2, Homo sapiens for KIAA1762 protein, partial cds. ,q11.2
SNP_A-2127166	ataaatcattgagctg[C/T]aggcttagaattcatg	C	T	55079 // Homo sapiens zinc finger protein 312 (ZNF312), mRNA. /// NM_183393 // downstream // 1893 // Hs.127013 //	ZNF312	ZNF312, Homo sapiens zinc finger protein 312 (ZNF312), p14.2
SNP_A-2114869	agggcactgtcctaga[C/T]ggagtggccaagaaag	C	T	Homo sapiens ankyrin repeat and SOCS box-containing 10 (ASB10), mRNA. /// ENST00000275838 // intron // 0 // --- // ---	ASB10	ASB10, Homo sapiens ankyrin repeat and SOCS box-containing 10 (ASB10), q36.1
SNP_A-2110619	aggacataagtcatca[C/T]aagatatgtagaaacg	C	T	57864 // Homo sapiens thymic stromal co-transporter (TSCOT), mRNA. /// NM_003408 // downstream // 101921 //	TSCOT	TSCOT, Homo sapiens thymic stromal co-transporter (TSCOT), q32
SNP_A-2161384	atttgcagggactaat[C/T]agtgtgtcttaattat	C	T	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 428150 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-2142255	atgaaaaggtatcctc[A/G]cctccaactttgtttc	A	G	55324 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA. /// ENST00000292808 // downstream // 8374 // --- // --- // --- // --- ///	ABCF3	ABCF3, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), q27.1
SNP_A-2150768	atgtgctgacatttat[A/G]actgttgtttggactc	A	G	4070 // Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), mRNA. /// ENST00000330286 //	TACSTD2	TACSTD2, Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), p32.1
SNP_A-2147145	atggaattatatacag[C/G]catttaacttattttt	C	G	6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// NM_003664 // downstream // 199136 // Hs.532091	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-2147673	atggcacagaatactc[A/G]ataatgataataatta	A	G	Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2148272	atgggcagtgggacac[A/G]atctcagaggtggctc	A	G	Homo sapiens H2A histone family, member Y (H2AFY), transcript variant 1, mRNA. /// NM_004893 // intron // 0 //	H2AFY	H2AFY, Homo sapiens H2A histone family, member Y (H2AFY), transcript variant 1, q31.1
SNP_A-2148615	atggtagcaactcaga[C/G]ctgcggaatctgagtc	C	G	1130 // Homo sapiens Chediak-Higashi syndrome 1 (CHS1), transcript variant 1, mRNA. /// NM_002508 // downstream //	LYST	LYST, Homo sapiens Chediak-Higashi syndrome 1 (CHS1), transcript variant 1, q42.3
SNP_A-2179034	cactgctacccagaac[A/G]atggggtgcattctca	A	G	Homo sapiens caspase recruitment domain family, member 4 (CARD4), mRNA. /// ENST00000222823 // intron // 0 // --- // ---	CARD4	CARD4, Homo sapiens caspase recruitment domain family, member 4 (CARD4), p15.1
SNP_A-2176580	cacccagtgtaagcac[A/G]gagatagatgtgttat	A	G	Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), mRNA. /// NM_207454 // downstream // 210185 // Hs.514090	CCL1	CCL1, Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), q12
SNP_A-2170760	caagtttaacatacaa[A/C]aatgttgctcaaggga	A	C	Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// ENST00000360057 // intron // 0 // --- // --- // --- // --- ///	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-2172313	caattaaaggcaatcc[A/G]ccagaacaggtgagag	A	G	26232 // Homo sapiens F-box protein 2 (FBXO2), mRNA. /// NM_183413 // upstream // 62779 // Hs.519716 // FBXO44 //	FBXO2	FBXO2, Homo sapiens F-box protein 2 (FBXO2), p36.22
SNP_A-2195584	catggtcagtgtacta[C/T]aaaatttccacataaa	C	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// ENST00000281894 // intron // 0 // --- // --- // --- // ---	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2190041	cataactgaatgatca[C/T]gataagagtagtcggc	C	T	// Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA. /// ENST00000358967 // downstream // 57852 // --- //	ADRB1	ADRB1, Homo sapiens adrenergic, beta-1-, receptor (ADRB1), q25.3
SNP_A-2186588	cagggagtccgtgaga[G/T]agtgggtttctttaca	G	T	51059 // Homo sapiens hypothetical protein LOC51059 (LOC51059), mRNA. /// ENST00000160713 // upstream //	LOC51059	LOC51059, Homo sapiens hypothetical protein LOC51059 (LOC51059), q24.23
SNP_A-2226849	ctaatagttccccaga[C/T]acattgtgttgtgtga	C	T	sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA. /// ENST00000267163 // intron // 0 // --- // --- // --- // ---	RB1	RB1, Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), q14.2
SNP_A-2223651	cggagtcatgaagtgg[C/T]agagctggaaccaggg	C	T	sapiens betacellulin (BTC), mRNA. /// ENST00000311727 // intron // 0 // --- // --- // ---	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-2223383	cgctgacttgcctgct[A/G]aaaagctttgacctca	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2213943	cctaacatattttagt[G/T]aatagcatgtaaagca	G	T	Homo sapiens chromosome 15 open reading frame 27 (C15orf27), mRNA. /// ENST00000305457 // intron // 0 // --- //	C15orf27	C15orf27, Homo sapiens chromosome 15 open reading frame 27 (C15orf27), q24.2
SNP_A-2209567	cccatctttcacaaca[C/T]ctgtctacattcagtt	C	T	// 64087 // Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), mRNA. /// NM_004291 // upstream // 14496 // Hs.1707 // CART // 9607 // Homo	MCCC2	MCCC2, Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), q13.2
SNP_A-2209265	cccagtctgtaaaata[C/G]agtaggaatgtctgac	C	G	// 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 508482 // --- // --- // --- //	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q21
SNP_A-2210923	ccccttttccctctgaa[A/T]ctcagggtcaggcaat	A	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 315282 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2200124	ccaaatctcaacttta[C/T]agtaaagcacacagtt	C	T	Homo sapiens sulfatase 1 (SULF1), mRNA. /// ENST00000260128 // intron // 0 // --- // --- // --- // ---	SULF1	SULF1, Homo sapiens sulfatase 1 (SULF1), q13.2
SNP_A-1869717	tccttcaattcattca[C/T]gtgacctcatttttcc	C	T	57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // upstream // 357113 // --- // ---	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-1871720	tctaatgaaataatga[C/T]gttagtgggttggggt	C	T	64094 // Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 //	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. q27
SNP_A-1862529	ttaaacactcggcact[A/C]aacgatctctgggtga	A	C	221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 // upstream // 139079 // Hs.463483 // MMD // 23531 // Homo	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-1860912	tcatacgaccactagc[A/G]caatcaagacatggta	A	G	Homo sapiens olfactory receptor, family 2, subfamily S, member 2 (OR2S2), mRNA. /// NM_019897 // upstream //	OR2S2	OR2S2, Homo sapiens olfactory receptor, family 2, subfamily S, member 2 (OR2S2), p13.3
SNP_A-1854535	tcaaattgagaaatca[A/T]acaagctctggaagat	A	T	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-1853754	tcaaaaactacttcac[A/C]atgtgcctgattcata	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 605598 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1845986	tatatactgaccttga[A/G]ccacacaatagtgccc	A	G	3933 // Homo sapiens lipocalin 1 (tear prealbumin) (LCN1), mRNA. /// NM_014582 // upstream // 574 // Hs.512150 //	LCN1	LCN1, Homo sapiens lipocalin 1 (tear prealbumin) (LCN1), q34.3
SNP_A-1844489	tataaagtgtggtgac[A/G]agaaagcagggccagg	A	G	4084 // Homo sapiens MAX dimerization protein 1 (MAD), mRNA. /// NM_152792 // downstream // 13368 // Hs.516253	MXD1	MXD1, Homo sapiens MAX dimerization protein 1 (MAD), p13.3
SNP_A-1821571	gtttgtatctcaccga[A/G]aaaatgtcctacttcc	A	G	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1816238	gttactggtcctcaca[A/G]ctgattggagagggca	A	G	Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1815968	aaacaaacttcttcca[C/T]ctgattctacttcctg	C	T	388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 202759 // --- // ---	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-1840493	tagccatacatgacta[A/G]cagtaattgaaatggg	A	G	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1840613	tagcctcaacctggcc[A/G]cattctacccatgtga	A	G	ENST00000330898 // intron // 0 // --- // --- // --- // ---	-	p12.1
SNP_A-1837657	tactttatttaatttc[C/T]actgtgtctaaagaac	C	T	sapiens cathepsin O (CTSO), mRNA. /// ENST00000281527 // intron // 0 // --- // --- // --- // --- /// ENST00000356616 // intron	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1837720	tactttgatagggtca[A/C]cctggtcttacctgac	A	C	8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 14580 // Hs.425091 // FAM44B	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1831693	taattatgtctgaaag[A/G]atttccttgcttttc	A	G	ENST00000343628 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-1831179	taatgctccaagtctg[C/T]acccttagcaagtgaa	C	T	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 200160 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802802	gtatggagtattataa[C/G]attactgtaacaatag	C	G	Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1801577	gtaggtgtgaaataaa[C/T]gctagtaccctcccct	C	T	158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// NM_003084 // upstream // 18671 //	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-1804824	gtcagtggaatctctc[C/T]agctagtgtgtaaagg	C	T	PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// ENST00000250275 // upstream // 23582 // --- // --- // --- // ---	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-1805722	gtcccagtgtgtgggag[A/G]atccaaatctgggaga	A	G	Homo sapiens KIAA0140 (KIAA0140), mRNA. /// ENST00000280780 // intron // 0 // --- // --- // --- // ---	FAM53B	FAM53B, Homo sapiens KIAA0140 (KIAA0140), q26.13
SNP_A-1808037	gtcttctgaacacaac[A/G]aatttctcctcaatga	A	G	ENST00000320930 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1812494	gtggccatcctgggcc[A/G]ccaaacagagccctgt	A	G	Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000340652 // intron // 0 // --- // --- // --- // ---	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-1813672	gtgtaccaaggcagaa[A/G]gtatcctactgatatg	A	G	57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// NM_006420 // upstream // 68259 // Hs.62578 // ARFGEF2	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-1677548	tactttctatgaggtttaggaga[G/T]aatctatttctagcctctccagt	G	T	KIAA1720 // 80851 // KIAA1720 protein	KIAA1720	KIAA1720, rs1892445, KIAA1720 protein,q44
SNP_A-1671406	acccccagcttcaccctaaccacatc[A/C]aagctctcggtcccagcatgatgaa	A	C	80730 // KIAA1680 protein /// NM_007351 // downstream // 122162 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680, rs10516862, KIAA1680 protein, q22.1
SNP_A-1752971	aaactaaaatcaaattacaaatccag[A/G]ccattgtatggtgaacgttagagag	A	G	AK095462 // intron // 0 // Hs.9905 // FLJ32954 // 151393 // hypothetical protein FLJ32954	FLJ32954	FLJ32954, rs10490618, hypothetical protein FLJ32954,p22.2
SNP_A-1983410	ctttgctccacaaggc[A/G]aaggttgagacccaca	A	G	sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 // CDS // 0 // --- // --- // ---	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-1984820	catcatgccaagtggat[A/G]aagccagacacaaaa	A	G	Homo sapiens receptor (TNFRSF)-interacting serine-threonine kinase 1 (RIPK1), mRNA. /// ENST00000259808 // intron // 0 // --- // --- // ---	RIPK1	RIPK1, Homo sapiens receptor (TNFRSF)-interacting serine-threonine kinase 1 (RIPK1), p25.2
SNP_A-1979511	atttaacatgaaatc[A/C]atcaatataaaatgt	A	C	Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), mRNA. /// ENST00000264424 // intron // 0 // ---	GUCY1B3	GUCY1B3, Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), q32.1
SNP_A-1977406	atcttccttattcca[A/T]ctggccttttcccag	A	T	/// ENST00000360919 // upstream // 363492 // --- // --- // ---	-	q13.1
SNP_A-1980905	ctgctcatggattgga[C/T]gtgagaagagcagcaa	C	T	10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 // PGLYRP3 // 114771 // Homo sapiens peptidoglycan recognition protein 3 (PGLYRP3), mRNA. ///	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-1967109	gagacaagttagacaa[A/C]gtaagactaaatagt	A	C		PGLYRP3	PGLYRP3, Homo sapiens peptidoglycan recognition protein 3 (PGLYRP3), q21.3
SNP_A-1963695	tgaagctggggaatgal[C/T]gttgtggactgagtga	C	T	ANTXR1 // 84168 // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, mRNA. /// NM_053034 //	ANTXR1	ANTXR1, Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, p13.3
SNP_A-1974682	aagagcacatggctaa[G/T]aagaatttgagcaat	G	T	-- /// ENST00000356397 // upstream // 790055 // --- // ---	-	q24
SNP_A-1939210	ttgatatttctgaaga[A/G]gagtaggtagactttt	A	G	// Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // --- // --- // --- // ---	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-1937699	ttgaagcttgtctccaa[A/G]tcaatactgactccta	A	G	// 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 57739 //	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-1937348	ttgaaaggtagataaa[A/G]ctgaaattacataga	A	G	Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// ENST00000339837 // intron // 0 // --- // ---	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-1933248	ttctaacaaaagtttcc[A/G]catatctagagctgaa	A	G	// Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // --- // --- // --- // ---	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1948489	tttagtgatgataaca[A/G]ccataataaaagcaag	A	G	// Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// ENST00000354883 // intron // 0 // ---	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-1898604	tgcttggcccagctga[C/T]agcgaggcagggcagg	C	T	LOC57168 // 57168 // Homo sapiens similar to aspartate beta hydroxylase (ASPH) (LOC57168), mRNA. /// NM_152842 // 221938 // Homo sapiens monocyte to macrophage	LOC57168	LOC57168, Homo sapiens similar to aspartate beta hydroxylase (ASPH) (LOC57168), q12.1
SNP_A-1900137	tggactggtcatagca[A/C]aatggatgaaccaaaa	A	C	differentiation-associated 2 (MMD2), mRNA. /// NM_012329 //	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-1895588	tgcctcaatctcccaa[A/C]tagtggaactacaggc	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2003233 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1877189	tctgcttagctaagga[C/T]gaacaaaaacagcct	C	T	sapiens glutathione reductase (GSR), mRNA. /// ENST00000221130 // intron // 0 // --- // --- // ---	GSR	GSR, Homo sapiens glutathione reductase (GSR), p12
SNP_A-1875447	tctctggaaaataaga[G/T]ggttgaatgacctcca	G	T	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, p15.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1874103	tctcattccagccaga[C/T]gggcctctgggcacct	C	T	// 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// NM_178552 // downstream // 40565 // Hs.124502	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-1877936	tctggttccaggtctc[G/T]catgaggttgcactca	G	T	// Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), mRNA. /// ENST00000261486 // intron // 0 // --- // --- // --- // ---	EPB41L4A	EPB41L4A, Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), q22.2
SNP_A-1879847	tcttcccaatattaaa[C/T]tgacccaaacagtttc	C	T	2099 // Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// NM_133650 // upstream // 57739 // Hs.12967 // SYNE1 //	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.2
SNP_A-1887487	tgttttctcggaagta[G/T]agcagcgtgagaaatc	G	T	4161 // Homo sapiens melanocortin 5 receptor (MC5R), mRNA. /// NM_000529 // downstream // 49918 // Hs.248144	MC5R	MC5R, Homo sapiens melanocortin 5 receptor (MC5R), p11.21
SNP_A-1927595	ttcattagtcataaaa[C/T]ttaccccagaactttg	C	T	Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // --- //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1929764	ttcatcataaaataac[A/G]gtaacaacaacgaaca	A	G	Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// ENST00000206249 // intron // 0 // --- // --- // --- // --- ///	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.1
SNP_A-1932136	ttcctcagcttttcag[C/T]ccagaaatgacagtat	C	T	140801 // Homo sapiens ribosomal protein L10-like (RPL10L), mRNA. /// NM_182830 // downstream // 54040 //	RPL10L	RPL10L, Homo sapiens ribosomal protein L10-like (RPL10L), q21.3
SNP_A-1932235	ttcctccttaattcaa[G/T]atgttacattctttag	G	T	// 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 69996 // Hs.143080 //	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-1931187	ttccattagcggctgc[A/G]attttcccctaggtt	A	G	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1909382	tgtattaggacacgta[C/T]gtacccaatactgaac	C	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1908329	tgtactgaattttgca[C/T]gaataatggtttcaaa	C	T	// 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 282189 // Hs.154329 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1907569	tgtaaatttaagctca[A/T]gaatagtccaaagctc	A	T	200728 // Homo sapiens transmembrane protein 17 (TMEM17), mRNA. /// NM_015252 // upstream // 139882 //	TMEM17	TMEM17, Homo sapiens transmembrane protein 17 (TMEM17), p15
SNP_A-1912623	tgtgccgaatttcaaa[C/T]ggaatgcttccagctc	C	T	FLJ16353 // 440077 // Homo sapiens FLJ16353 protein (FLJ16353), mRNA. /// NM_018088 // downstream // 27989 //	FLJ16353	FLJ16353, Homo sapiens FLJ16353 protein (FLJ16353), p13.31
SNP_A-1911610	tgtgaaagagggtaca[C/T]gttgtgaaaataaatc	C	T	MGC33530 // 222008 // Homo sapiens hypothetical protein MGC33530 (MGC33530), mRNA. /// NM_014302 //	MGC33530	MGC33530, Homo sapiens hypothetical protein MGC33530 (MGC33530), p11.2
SNP_A-1917758	ttaaaacagcaaacta[C/T]acaactctcagacctt	C	T	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2265475	gaagccatcatgaaaa[A/G]gagaaaagagtttcag	A	G	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA.	CAMK2D	CAMK2D, Homo sapiens calcium,q26
SNP_A-2271728	gaccaggcctggctac[A/C]gaccccagctagcatc	A	C	Homo sapiens glucagon-like peptide 1 receptor (GLP1R), mRNA. /// ENST00000229900 // intron // 0 // --- // --- // --- // ---	GLP1R	GLP1R, Homo sapiens glucagon-like peptide 1 receptor (GLP1R), p21.2
SNP_A-2271861	gacccaaagggcactc[A/G]atctaaaccaaattag	A	G	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), mRNA. /// ENST00000334220 // intron // 0 // --- // --- // --- // --- ///	DLST	DLST, Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), q24.3
SNP_A-2256559	ctttcaaactttcagc[G/T]gaccttcatctgccct	G	T	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2262662	gaaattcccaagtcac[A/G]actacaaacctgcttg	A	G	sapiens mRNA for KIAA0551 protein, partial cds. /// ENST00000284483 // intron // 0 // --- // --- // --- // --- ///	TNIK	TNIK, Homo sapiens for KIAA0551 protein, partial cds. q26.2
SNP_A-2283158	gataatcatttttata[A/G]agcacatggtcaagtt	A	G	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 272137 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2275878	gagactcagcaaggta[A/G]gaggatgggaaggtga	A	G	Homo sapiens marapsin 2 (MPN2), mRNA. /// ENST00000329666 // intron // 0 // --- // --- // --- // ---	MPN2	MPN2, Homo sapiens marapsin 2 (MPN2), q42.13
SNP_A-2278202	gagcctgagctagaaa[C/T]caaactgctatagtta	C	T	6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// AB023173 // upstream // 315294 //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2241458	aatttgtttaggtaca[A/G]aagcagtgctttccca	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2238722	ctcttaaattctttag[A/G]acaaaatcacttcatt	A	G	// 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. /// ENST00000302277 // downstream //	C2orf10	C2orf10, Homo sapiens similar to C630007C17Rik protein (LOC91752), q32.1
SNP_A-2236098	ctccttaacagcctaa[A/T]catttccactcaggtt	A	T	29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 // downstream //	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12
SNP_A-2235831	ctcctcttcttattca[C/T]gtgcaaatgtttaccc	C	T	Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 //	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2254261	ctgatttttagaataa[C/T]agatgtgtttatgagc	C	T	5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 207206 // Hs.446083 // PTPRD // 5789 // Homo	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2297384	gccactcttgcctgaa[C/G]cttttgtcacctgc	C	G	Homo sapiens ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (ELOVL5), mRNA. /// ENST00000304434 // intron // 0 // --- // -	ELOVL5	ELOVL5, Homo sapiens ELOVL family member 5, elongation of long chain fatty acids (FEN1,p12.1
SNP_A-2295510	gcatctccgcgtggt[G/T]aaaccccatcgtgcat	G	T	Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // intron // 0 // --- // --- // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2295768	gcatgccigaacaact[C/T]aggacttcatatgcca	C	T	Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // --- // --- // --- // ---	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2310643	ggaagagggcgaccca[C/T]gccatactcacggtgc	C	T	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 888089 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2312803	ggactgagagatgcaa[A/G]atgtgatataaggagg	A	G	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-2306669	gctgtcaaatgaaaaa[C/G]ttgtgctgaagcagg	C	G	80273 // Homo sapiens GrpE-like 1, mitochondrial (E. coli) (GRPEL1), mRNA. /// ENST00000310074 // downstream //	GRPEL1	GRPEL1, Homo sapiens GrpE-like 1, mitochondrial (E. coli) (GRPEL1), p16.1
SNP_A-2294383	gcaggtggaatgaga[C/T]aaagagtgggtgaagt	C	T	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2288738	gattgtaccagtacca[A/G]cttctagtttgata	A	G	51317 // Homo sapiens BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA. /// NM_052854 // upstream // 98680 //	PHF21A	PHF21A, Homo sapiens BRAF35,p11.2
SNP_A-2254500	cttgcctgaggtcaca[A/G]tgcaaattacagtgaa	A	G	83643 // Homo sapiens coiled-coil domain containing 3 (CCDC3), mRNA. /// NM_021980 // upstream // 59745 //	CCDC3	CCDC3, Homo sapiens coiled-coil domain containing 3 (CCDC3), p13
SNP_A-2242396	ctgcactctggcgcga[A/G]tcccacagctgccacg	A	G	Homo sapiens SMC1 structural maintenance of chromosomes 1-like 2 (yeast) (SMC1L2), mRNA. /// AJ504806 // intron // 0 // Hs.334176 // SMC1L2 // 27127 //	SMC1L2	SMC1L2, Homo sapiens SMC1 structural maintenance of chromosomes 1-like 2 (yeast) (SMC1L2), q13.31
SNP_A-2245009	ctggcataaaaatagat[C/T]acatagaccatcagaa	C	T	79981 // Homo sapiens FERM domain containing 1 (FRMD1), mRNA. /// NM_214462 // downstream // 165444 //	FRMD1	FRMD1, Homo sapiens FERM domain containing 1 (FRMD1), q27
SNP_A-2249081	ctgtttcctacaagcc[A/G]cagtgttatgcttgta	A	G	ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 83053 // Hs.464442 // C18orf2	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-2248510	ctgtgtttttggagc[C/T]aggaacttcacaaagg	C	T	10409 // Homo sapiens brain abundant, membrane attached signal protein 1 (BASP1), mRNA. /// ENST00000322611 // downstream // 25049 // --- // --- // --- ///	BASP1	BASP1, Homo sapiens brain abundant, membrane attached signal protein 1 (BASP1), p15.1
SNP_A-2238948	ctctccaggcttca[A/T]cactgtctttaaat	A	T	83636 // Homo sapiens chromosome 19 open reading frame 12 (C19orf12), mRNA. /// NM_031448 // upstream // 5672 //	C19orf12	C19orf12, Homo sapiens chromosome 19 open reading frame 12 (C19orf12), q12
SNP_A-2240552	ctgaccatttcctta c[C/T]ggttatcttccttcg	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2279845	gaggcctgtgggaga[C/T]ggcttagagaaagag	C	T	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc q31.1
SNP_A-2265467	gaagccaggccgcctа[C/T]ctggctagtcctaga	C	T	Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 //	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-1910344	tgtccaggtatgtccc[A/G]aaccagccaactgaa	A	G	5624 // Homo sapiens protein C (inactivator of coagulation factors Va and VIIIa) (PROC), mRNA. /// NM_017969 //	PROC	PROC, Homo sapiens protein C (inactivator of coagulation factors Va and VIIIa) (PROC), q14.3
SNP_A-1896306	tgctaaacaacacaac[A/G]catattctgaaagtag	A	G	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1890370	tgatccgtagtggagta[C/G]cagagagtggaacagg	C	G	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA. /// ENST00000268489 // intron // 0 // --- // --- // ---	ATBF1	ATBF1, Homo sapiens AT-binding transcription factor 1 (ATBF1), q22.3
SNP_A-1902144	tggcatttccacctcc[A/G]cgtcatcctgcagt	A	G	- /// ENST00000355517 // downstream // 193131 // --- // --- // -	-	q24.32
SNP_A-1900495	tggagcccagttaca[A/G]acaagtgatatggatg	A	G	Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA. /// ENST00000264211 // intron //	EIF4G3	EIF4G3, Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), p36.12
SNP_A-1903515	gaaatatactctcaga[A/G]gtcaaaccattctcgt	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1951077	tttccatcaccttcac[A/G]ataaaatccaatctct	A	G	Homo sapiens hypothetical protein FLJ12770 (FLJ12770), mRNA. /// ENST00000289918 // 3UTR // 0 // --- // --- // ---	FLJ12770	FLJ12770, Homo sapiens hypothetical protein FLJ12770 (FLJ12770), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960584	tttttcatgttagtac[A/G]gatagtttacatatat	A	G	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 1213151 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1941566	ttggaaaatacagcaa[G/T]gttttttttgtttttg	G	T	METTL2 // 55798 // Homo sapiens methyltransferase like 2 (METTL2), mRNA. /// NM_181725 // downstream // 209146 //	METTL2	METTL2, Homo sapiens methyltransferase like 2 (METTL2), q32.1
SNP_A-1970683	ttcctctgcaaggcca[C/G]aagacactgctaagaa	C	G	55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 95807	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-1964422	tgaacctgtactagag[A/G]aggcataaccaaaaca	A	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 425899 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1980625	atgaagacaatgctaa[C/T]atcgacctcactgttc	C	T	plasma membrane calcium-pumping ATPase (PMCA4) mRNA, complete cds. /// ENST00000357681 // intron // 0 // --- // --- // --- // --- /// ENST00000357588 // intron // 0 // --- // --- // --	ATP2B4	ATP2B4, Human plasma membrane calcium-pumping ATPase (PMCA4) complete cds. ,q32.1
SNP_A-1985012	acaggaattcagcaga[A/G]aagggaaagaaagagc	A	G	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1513833	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1985388	caaactctcagctaca[G/T]gaatgaacagtgaaat	G	T	Homo sapiens prolactin (PRL), mRNA. /// NM_138574 // upstream // 264314 // Hs.97124 // PWWP1 // 154150 // Homo	PRL	PRL, Homo sapiens prolactin (PRL), p22.3
SNP_A-1781298	ggatgtctctgcaaga[A/T]aattaaacttccacct	A	T	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 109461 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-1656259	tgacttccagaaaaaaaagtattta[A/G]tagcaattacgtgttttgttatgtt	A	G	// 1129 // cholinergic receptor, muscarinic 2 /// NM_002825 // downstream // 107588 // Hs.44 // PTN // 5764 // pleiotrophin	CHRM2	CHRM2 , rs1364716, cholinergic receptor, muscarinic 2 ,q33
SNP_A-1813643	gtgtaatttcttatca[C/G]tgagtttcatgaagat	C	G	// 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 363236 //	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1813772	gtgtagggtgcgctgg[A/G]aatgttcgggtgcagc	A	G	LOC199964 // 199964 // Homo sapiens hypothetical protein LOC199964 (LOC199964), mRNA. /// NM_057176 //	LOC199964	LOC199964, Homo sapiens hypothetical protein LOC199964 (LOC199964), p32.3
SNP_A-1813254	gtggtctggatcacaa[C/T]actatttatcttcagt	C	T	84867 // Homo sapiens cDNA FLJ33604 fis, clone BRAMY2015251, highly similar to PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.4 /// NM_032781 // upstream // 137748 // Hs.79092 // PTPN5 // 84	PTPN5	PTPN5, Homo sapiens cDNA FLJ33604 fis, clone BRAMY2015251, highly similar to PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.4 p15.1
SNP_A-1808961	gtgaatgtgggtttga[C/T]agctgaattatgtctc	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-1803279	gtattgccaactgagg[A/G]agtgcatctgagctca	A	G	92399 // Homo sapiens mitochondrial ribosome recycling factor (MRRF), nuclear gene encoding mitochondrial protein, transcript variant 2, /// NM_199176 // downstream // 67297 //	MRRF	MRRF, Homo sapiens mitochondrial ribosome recycling factor (MRRF), nuclear gene encoding mitochondrial protein, transcript variant 2, q33.2
SNP_A-1792641	tctctcttaaagagct[A/T]aaagtctatgctgaat	A	T	// 494115 // Homo sapiens kynurenine aminotransferase III (KAT3), mRNA. /// NM_018284 // downstream // 6857 //	LOC494115	LOC494115, Homo sapiens kynurenine aminotransferase III (KAT3), p22.2
SNP_A-1787975	gggagaagaagagaca[G/T]attagagatgcagagc	G	T	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki 1) (ALK), p23.2
SNP_A-1786841	ggctttgcatcatgta[A/G]aaaaacaaactcaatt	A	G	SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream //	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1832170	taatttctttctatga[C/T]agagtgacaagccatg	C	T	// 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream //	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1830535	taatcactttgtgagt[C/T]actatgggtttaacta	C	T	Homo sapiens similar to signal peptidase complex (18kD) (LOC90701), mRNA. /// ENST00000299714 // intron // 0 // ---	SEC11L3	SEC11L3, Homo sapiens similar to signal peptidase complex (18kD) (LOC90701), q21.32
SNP_A-1836451	tactccaagtaagtta[G/T]agcacaccaagagtgt	G	T	Homo sapiens fetal Alzheimer antigen (FALZ), transcript variant 2, mRNA. /// NM_182641 // intron // 0 // Hs.444200 //	FALZ	FALZ, Homo sapiens fetal Alzheimer antigen (FALZ), transcript variant 2, q24.2
SNP_A-1836780	tactgaggatttaaag[A/T]atgtagcagttgttct	A	T	Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), transcript variant 3, mRNA. /// NM_174972 // intron // 0 // Hs.132001 // ST3GAL3	ST3GAL3	ST3GAL3, Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), transcript variant 3, p34.1
SNP_A-1843425	tagtgacctgggaaca[C/T]ggcctggttgaattca	C	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 895158 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1821738	gttttaaatcccataa[C/G]atagtttgaattaaaa	C	G	Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1823887	taaaatgtgcttatta[C/T]aagagtgttttgggaa	C	T	10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 //	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1859170	tcagcctttggcccta[C/T]attggcattcgtgagg	C	T	// 401388 // Homo sapiens FLJ42280 protein (FLJ42280), mRNA. /// NM_006304 // downstream // 83515 // Hs.489201	FLJ42280	FLJ42280, Homo sapiens FLJ42280 protein (FLJ42280), q21.3
SNP_A-1860640	tcagttttcttatgta[C/T]gaagtgaaaataataa	C	T	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-1861883	tcatgaacagtgtcct[C/T]aacatgtcatggacat	C	T	// 29103 // Homo sapiens DnaJ (Hsp40) homolog, subfamily D, member 1 (DNAJD1), mRNA. /// NM_145261 // downstream // 16438 // Hs.230601 // TIM14 // 131118 //	DNAJD1	DNAJD1, Homo sapiens DnaJ (Hsp40) homolog, subfamily D, member 1 (DNAJD1), q14.11
SNP_A-1866017	tcccactattttcaga[C/T]taaagattggatttta	C	T	Homo sapiens hypothetical protein HH114 (HH114), mRNA. /// ENST00000338183 // intron // 0 // --- // --- // --- // ---	HH114	HH114, Homo sapiens hypothetical protein HH114 (HH114), q14
SNP_A-1870613	tcgattcctaggctca[A/G]catgaaagcctctcct	A	G	// 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 64443 // Hs.501911 //	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2213115	ccgagtcaggcaacga[A/C]ggcacagagaggttag	A	C	ENST00000318224 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2214877	cctatatctattaaag[A/T]aggtgaatcaacaata	A	T	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2215306	cctcaagtcccactaa[C/T]gtacctgtttggatcc	C	T	Homo sapiens SH3-domain binding protein 3 (SH3BP3), mRNA. /// ENST00000263805 // intron // 0 // --- // --- // --- // ---	ZFP106	ZFP106, Homo sapiens SH3-domain binding protein 3 (SH3BP3), q15.1
SNP_A-2192592	gtcccttatcataaaa[A/G]ggccatccacatttta	A	G	Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // intron // 0 // --- // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-2172697	caattgtgagacaata[C/T]gaatgagccacgtggc	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 710879 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2173930	cacacagtgcacagta[C/G]aaactccagacatgct	C	G	// Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// NM_181690 // intron // 0 //	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44
SNP_A-2170905	caataactggcctgca[A/G]aaataataactgtact	A	G	// 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream //	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2177197	cacctgccaaaggaaa[C/G]taaccacaaagcagag	C	G	Homo sapiens crystallin, mu (CRYM), mRNA. /// ENST00000219599 // upstream // 14990 // --- // --- // --- // ---	CRYM	CRYM, Homo sapiens crystallin, mu (CRYM), p12.2
SNP_A-2182528	cagatatctcgtatta[C/T]ctcttgggatgctgtt	C	T	169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 174532 // Hs.444915 //	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2149872	atgtcaatgaaactga[C/T]gacactgaacctttaa	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2323421 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2142192	atgaaaaagccactgc[A/G]gacatcccagcctcgg	A	G	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2160369	atttcagtgattcccc[A/G]ggattggttactatga	A	G	6362 // Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), mRNA. /// NM_002983 // upstream // 54975 // Hs.514107 // CCL3 //	CCL18	CCL18, Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), q12
SNP_A-2126295	ataaaaatttgaatca[C/T]tcaatcagttaccact	C	T	59350 // Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), mRNA. /// ENST00000340501 // downstream // 165748 // --- // --- // --- //	LGR7	LGR7, Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), q32.1
SNP_A-2137349	atcataaatgaatcaa[A/G]tagctagaaaataaaa	A	G	ENST00000324457 // intron // 0 // --- // --- // --- // ---	-	p22.3
SNP_A-2070539	acacctcagttctgtc[A/G]ctctgctttagtaaac	A	G	ENST00000358691 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2064477	aattcccaaaaaataa[C/T]gccctgctatttgcca	C	T	// Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// ENST00000331504 // upstream // 41018 // --- // ---	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2066593	acaaaaactatgtgaa[C/T]atggtctttctctctc	C	T	163782 // Homo sapiens hypothetical protein LOC163782 (LOC163782), mRNA. /// ENST00000354381 // intron // 0 // ---	LOC163782	LOC163782, Homo sapiens hypothetical protein LOC163782 (LOC163782), p31.3
SNP_A-2097509	agagaagacagcctta[C/T]gacaatggggacagag	C	T	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 150994 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2096874	agactccaggtttgta[C/G]catcaatggtgactta	C	G	/// ENST00000359064 // upstream // 250412 // --- // --- // --- // --- /// ENST00000332041 // downstream // 261162 // --- // --- // ---	-	q22.1
SNP_A-2099943	agagtcatgaaactta[C/G]aaccggtgatacctaa	C	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 361542 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2090561	acttgtgaaattacta[C/T]agaactgattcatctc	C	T	sapiens KIAA0029 mRNA, partial cds. /// NM_015361 // intron // 0 // Hs.412462 // R3HDM // 23518 // Homo sapiens R3H	R3HDM	R3HDM, Homo sapiens KIAA0029 partial cds. q21.3
SNP_A-2077711	accactgcttgaggac[A/C]ctgaatttgatttttc	A	C	HDCMA18P // 51574 // Homo sapiens HDCMA18P protein (HDCMA18P), mRNA. /// ENST00000308878 // downstream	HDCMA18P	HDCMA18P, Homo sapiens HDCMA18P protein (HDCMA18P), q25

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006924	tgtgactctattggca[C/T]aaccatcactcaaatg	C	T	8436 // Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), mRNA. /// NM_016192 // downstream // 1199 // Hs.144513 // TMEFF2 //	SDPR	SDPR, Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), q32.3
SNP_A-1992372	gagtaatctggagtga[A/T]gtgaacacgcatacat	A	T	Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1993122	gtaaaagccatgagaa[C/G]catcatcattttcttt	C	G	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // --- // --- // --- // ---	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-2004273	tactcacaagataaaa[A/G]cacaaacaaggaatac	A	G	Homo sapiens hypothetical protein FLJ13710 (FLJ13710), mRNA. /// ENST00000357769 // intron // 0 // --- // --- // --- // ---	FLJ13710	FLJ13710, Homo sapiens hypothetical protein FLJ13710 (FLJ13710), q23
SNP_A-1997934	cattagccagtacata[C/T]ggggttaggtttagga	C	T	Homo sapiens chromosome 9 open reading frame 18 (C9orf18), mRNA. /// ENST00000331384 // intron // 0 // --- // --	C9orf18	C9orf18, Homo sapiens chromosome 9 open reading frame 18 (C9orf18), q33.2
SNP_A-2000879	gctacacacattgtcc[A/G]acccagcatagtctct	A	G	Homo sapiens CGI-49 protein (CGI-49), mRNA. /// ENST00000271981 // intron // 0 // --- // --- // --- // ---	CGI-49	CGI-49, Homo sapiens CGI-49 protein (CGI-49), q44
SNP_A-2043405	aactgggaatttcacc[A/G]cagcaccgttgatgtc	A	G	SERPINB8 // 5271 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), transcript variant 1, mRNA. /// NM_198833 // downstream // 83262 // Hs.368077 // SERPINB	SERPINB8	SERPINB8, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), transcript variant 1, q22.1
SNP_A-2045691	aagacaatactattgg[A/G]aatgagaaatgccatg	A	G	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 119290 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-2040221	aaccacaaaccaggta[A/G]gttaagacaactgaaa	A	G	140809 // Homo sapiens chromosome 20 open reading frame 139 (C20orf139), mRNA. /// NM_033129 // upstream //	C20orf139	C20orf139, Homo sapiens chromosome 20 open reading frame 139 (C20orf139), p13
SNP_A-2035432	aaatggggaaacaaag[A/G]aacacatgaagaaagc	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2020812	tcaccttcaggaagca[A/G]agctgatgaaggacaa	A	G	Homo sapiens HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) (HRMT1L1), transcript variant 2, mRNA. /// NM_206962 // intron // 0 // Hs.154163 // HRMT1L1 // 3275 //	HRMT1L1	HRMT1L1, Homo sapiens HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) (HRMT1L1), transcript variant 2, q22.3
SNP_A-2019880	tcatgaaccacaggaa[A/T]gcttagccagggactc	A	T	1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // upstream // 382325 // Hs.397800 // DSCAM //	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2021515	aaaaaatacaagagcc[A/G]ccttgaaataatgttt	A	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 1271718 // --- // -	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-2023168	aaaacatacaatagaa[C/G]tccatcactgctgagg	C	G	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2030129	aaagcaacaacagtaa[A/G]acaagacaaagatggt	A	G	// Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (ALS2CR12), mRNA. /// ENST00000286190 // intron // 0 // --- // --- // --- // ---	ALS2CR12	ALS2CR12, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (ALS2CR12), q33.1
SNP_A-2030873	aaaggaacgctaagag[A/C]agcacttggaaaatat	A	C	// 6416 // Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /// ENST00000353533 //	MAP2K4	MAP2K4, Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), p12
SNP_A-2030340	aaagcatgaaaatgta[A/G]aattagattggaattt	A	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000317394 // downstream //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-2005323	atatatatattctcat[G/T]aggaagtgccgtgcac	G	T	Homo sapiens ubiquitin specific protease 36 (USP36), mRNA. /// ENST00000312010 // intron // 0 // --- // --- // --- // ---	USP36	USP36, Homo sapiens ubiquitin specific protease 36 (USP36), q25.3
SNP_A-2003722	gtaccaagcaaaaaac[A/G]gacaatttgatctttg	A	G	// Homo sapiens lipase, gastric (LIPF), mRNA. /// NM_004190 // upstream // 2080 // Hs.523130 // LIPF // 8513 // Homo	LIPF	LIPF, Homo sapiens lipase, gastric (LIPF), q23.31
SNP_A-1993307	ttccctatccacttca[C/T]acaatcctttgcattt	C	T	Homo sapiens lysophospholipase I (LYPLA1), mRNA. /// ENST00000316963 // intron // 0 // --- // --- // --- // --- ///	LYPLA1	LYPLA1, Homo sapiens lysophospholipase I (LYPLA1), q11.23
SNP_A-2006171	tggttgagaatagaga[G/T]agttccaaggcatgga	G	T	Homo sapiens visinin-like 1 (VSNL1), mRNA. /// ENST00000295156 // intron // 0 // --- // --- // --- // ---	VSNL1	VSNL1, Homo sapiens visinin-like 1 (VSNL1), p24.2
SNP_A-2008252	tgggaatgattatagt[G/T]accttgcagaatcacc	G	T	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 172899 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2012608	tataaggaaatccata[C/T]tagaatactaaatgaa	C	T	MGC33530 // 222008 // Homo sapiens hypothetical protein MGC33530 (MGC33530), mRNA. /// NM_014302 //	MGC33530	MGC33530, Homo sapiens hypothetical protein MGC33530 (MGC33530), p11.2
SNP_A-2077500	accacattgctttcac[A/G]gaacccaattctataa	A	G	// 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 746332 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2091858	agaaaatggccttcaa[A/G]gctaaagaatatcata	A	G	// 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 167477 // --- // --- // --- // ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2090081	acttgaaccaaagcaa[A/G]gctcctaaaatatggaa	A	G	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 586163	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2103807	agcaccccgttggacc[C/T]gattgaaggagaatgc	C	T	MGC22001 // 197196 // Homo sapiens hypothetical protein MGC22001 (MGC22001), mRNA. /// ENST00000316859 // --- /// ENST00000357636 // upstream // 744314 // --- // --- // --- // --- /// ENST00000357643 // upstream // 744959 // --- // --- // ---	MGC22001	MGC22001, Homo sapiens hypothetical protein MGC22001 (MGC22001), q24.1
SNP_A-2098305	agagatggcatcttga[A/C]ctttagtaattccac	A	C	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	-	q28.3
SNP_A-2075331	acatgaaagaatttcaa[C/T]ccaagcagctacctct	C	T	Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2049344	aagctctgggttcgcc[A/G]gcgatggctgaaactt	A	G	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA. /// ENST00000263966 // intron // 0 // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2049373	aagctgaaatattga[A/G]tatcttctgatgcttt	A	G	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 256784 // --- // --- // --- // ---	USP13	USP13, Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), q26.33
SNP_A-2052268	aagtaaggagataggg[A/G]aaggtgtattaacatg	A	G	Homo sapiens phosphodiesterase 11A (PDE11A), mRNA. /// ENST00000286063 // intron // 0 // --- // --- // --- // ---	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2124078	agttactctgcagtta[C/T]atagcagtccaagagt	C	T	Homo sapiens chromosome 9 open reading frame 5 (C9orf5), mRNA. /// ENST00000223608 // intron // 0 // --- // --- // ---	PDE11A	PDE11A, Homo sapiens phosphodiesterase 11A (PDE11A), q31.2
SNP_A-2124088	agttactggcagagcc[A/C]agtttagaacttcagg	A	C	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // /// ENST00000355561 // upstream // 2304 // --- // --- // --- // ---	C9orf5	C9orf5, Homo sapiens chromosome 9 open reading frame 5 (C9orf5), q31.3
SNP_A-2129211	ataatttgacttcata[C/T]gtagctcttctcagg	C	T		IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2130484	atactcactgtaagac[A/G]acatttcctctgctct	A	G		-	q21.31
SNP_A-2140515	atctcctctggaata[C/T]gcttccagcccaatttt	C	T	Homo sapiens ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2), mRNA. /// ENST00000249071 // intron // 0 // --- // --- // --- // --- 26057 // Homo sapiens ankyrin repeat domain 17 (ANKRD17), transcript variant 2, mRNA. /// NM_032217 // upstream // 68707 // Hs.518804 // ANKRD17 // 26057 //	RAC2	RAC2, Homo sapiens ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2), q13.1
SNP_A-2145271	atgcacatatggagga[C/T]ggtctgtggagaatt	C	T		ANKRD17	ANKRD17, Homo sapiens ankyrin repeat domain 17 (ANKRD17), transcript variant 2, q13.3
SNP_A-2146522	atgctgagatgttcga[C/T]cttacccgagggaaa	C	T	LDOC1L // 84247 // Homo sapiens leucine zipper, down-regulated in cancer 1-like (LDOC1L), mRNA. ///	LDOC1L	LDOC1L, Homo sapiens leucine zipper, down-regulated in cancer 1-like (LDOC1L), q13.31
SNP_A-2179875	cacttataactgata[A/C]ctaaaatgtccagct	A	C	/// ENST00000356128 // upstream // 218462 // --- // --- // --- // ---	-	q24
SNP_A-2180606	cagaagcacaaatgga[C/T]aggtttgccttaaaa	C	T	148523 // Homo sapiens hypothetical protein BC017397 (LOC148523), mRNA. /// NM_144697 // downstream // 1447	C1orf51	C1orf51, Homo sapiens hypothetical protein BC017397 (LOC148523), q21.2
SNP_A-2174250	cacactgacagccaca[A/G]atatataatgatgatg	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2185383	caggacaatgaggatg[A/T]aactgcaagaaagata	A	T	Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA. /// NM_002656 // intron // 0 //	PLAGL1	PLAGL1, Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, q24.2
SNP_A-2218111	cctgcctccatgcagc[G/T]ctcatctggaggactt	G	T	Homo sapiens G protein-coupled receptor 116 (GPR116), mRNA. /// ENST00000283296 // intron // 0 // --- // --- // --- // ---	GPR116	GPR116, Homo sapiens G protein-coupled receptor 116 (GPR116), p12.3
SNP_A-2200433	ccaaccctcacctta[C/G]ttgaatgaatctaca	C	G	ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 1819506	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-2199862	ccaaactgccttcccc[C/G]ctcctagccaaagtc	C	G	Homo sapiens neuropilin 2 (NRP2), transcript variant 6, mRNA. /// NM_003872 // intron // 0 // Hs.471200 // NRP2 // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 3550 // --- // --- // --- // ---	NRP2	NRP2, Homo sapiens neuropilin 2 (NRP2), transcript variant 6, q33.3
SNP_A-2201504	ccaatgtgaatatgac[A/G]aatttcaaaggacaag	A	G		COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1870476	tcgaagtcaaaatggc[A/G]ccctcagctgaaaata	A	G	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 653725 // --- // --- 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // downstream // 341780 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1865543	tccatgcctataaaca[C/T]tgagatgtggcaccca	C	T		C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1858657	tcagatactgagcaaa[A/G]gtgtatgtcacagtca	A	G		-	p11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1854051	tcaaacaggtctcttc[A/G]ctgtttgttgtaggat	A	G	56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 248646 // Hs.519693 //	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-1855592	tcaataacattgatat[C/G]aacccttcctactcaa	C	G	PGLYRP3 // 114771 // Homo sapiens peptidoglycan recognition protein 3 (PGLYRP3), mRNA. ///	PGLYRP3	PGLYRP3, Homo sapiens peptidoglycan recognition protein 3 (PGLYRP3), q21.3
SNP_A-1824871	taaagcacttaaaccc[A/T]caaagttattgtctat	A	T	/// ENST00000333948 // upstream // 587715 // --- // --- // --- //	-	q31.2
SNP_A-1823577	taaaagttgctctggc[A/C]gatttagtgaatgaat	A	C	4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // upstream // 636819 // Hs.307734 // MME // 4311	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN ,q25.2
SNP_A-1823426	taaaagccaactgaac[C/T]aactcccaatggctaa	C	T	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1827736	taacttcagcaaaaaa[G/T]ggaaaatacacagatg	G	T	285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 586250 //	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-1826797	taacaggtgtaagaaa[A/G]tgggatttagattagg	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 1147430 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1821067	gtttcttattagacttt[A/T]aaaagagcctgttctg	A	T	10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 52717 // Hs.269775 //	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1815430	gtgtttgttttataca[A/C]gttaatgctgtgtttt	A	C	Homo sapiens brix domain containing 1 (BXDC1), mRNA. /// ENST00000356691 // intron // 0 // --- // --- // --- // ---	BXDC1	BXDC1, Homo sapiens brix domain containing 1 (BXDC1), q21
SNP_A-1841107	tagcttcctgaactgc[A/G]attggcccgtgaggag	A	G	ENST00000301831 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-1840744	tagctaatttcaattc[C/T]ctgccagacagtttca	C	T	/// ENST00000341548 // downstream // 8763 // --- // --- // --- //	-	q22.33
SNP_A-1832753	tacaaggaaggaaaag[G/T]aaatatccatttagtg	G	T	23530 // Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA. /// NM_182977 //	NNT	NNT, Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), p12
SNP_A-1799987	gtacataattaggccc[C/T]ataaatgtatcaccat	C	T	55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 466641 // Hs.473082 // ZFP64 // 55734 // Homo	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1800435	gtactctgactgtgac[A/T]ccatattttaaacaag	A	T	10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // downstream // 259012 // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1810448	gtgattctgcctgtga[C/T]ggtgattgatgatatt	C	T	LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1812312	gtggatgttctcaaac[A/T]gctacagcaattttag	A	T	/// ENST00000339800 // upstream // 57186 // --- // --- // --- // ---	-	q11.2
SNP_A-1701753	ttcgtaaaatcatcttgtagggaaa[C/T]atagaagcactttaacttgaaaact	C	T	interleukin 24 /// NM_181339 // intron // 0 // Hs.411311 // IL24 // 11009 // interleukin 24	IL24	IL24 , rs3093432, interleukin 24 ,q32.1
SNP_A-1986242	tcatacatattgacaa[A/T]gacatggcaaaataat	A	T	/// ENST00000310012 // upstream // 225161 // --- // --- // --- //	-	q12
SNP_A-1979830	ctcccaaatatgccaa[G/T]ctcaaattactgaatg	G	T	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1977518	cattacttccatttaa[A/G]tagtctgtttattgtg	A	G	Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA. /// ENST00000310613 // intron // 0 // --- // --- // --- // ---	SULT1B1	SULT1B1, Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), q13.3
SNP_A-1968225	tgttttgaaatcacaa[C/T]catatgacaagcactg	C	T	Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), mRNA. /// ENST00000295798 // intron // 0 // --- // ---	SPTA1	SPTA1, Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), q23.1
SNP_A-1973188	tcttcaccctagaaag[A/G]agcatgtaaaagggcc	A	G	7143 // Homo sapiens tenascin R (restrictin, janusin) (TNR), mRNA. /// ENST00000263525 // upstream // 105361 // --- // ---	TNR	TNR, Homo sapiens tenascin R (restrictin, janusin) (TNR), q25.1
SNP_A-1955904	tttgtcagcatcttgt[A/G]aaattagatggggagg	A	G	// 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 51430 // Hs.118183 // FLJ22833 //	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-1903803	tgggataatatataag[C/T]cagattctaggactgg	C	T	6659 // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA. /// NM_000948 // downstream // 40876 //	SOX4	SOX4, Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), p22.3
SNP_A-1902667	tggctaagcaacatcg[C/T]aattttcatggttgct	C	T	ENST00000329966 // intron // 0 // --- // --- // --- // ---	-	q16.3
SNP_A-1900414	tggagatctgcagata[C/T]gtcatttagcctctgc	C	T	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 751148 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.12
SNP_A-1890198	tgatcacaaaacagac[A/C]cagaagagcacttaac	A	C	80205 // Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), mRNA. /// AF150735 // downstream //	CHD9	CHD9, Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), q12.2
SNP_A-1893211	tgcagagaaaacctca[C/G]ggcctcagcatcagca	C	G	// Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 277074 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884630	tgaatacatgattaca[A/G]tgagacaaaatgaaga	A	G	1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 147345 // Hs.417962 // DUSP4 // 1846 // Homo	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-1882900	tgaaaggggtgcagac[A/C]gaagataaatggctac	A	C	10249 // Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // upstream // 9525 //	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-1879868	tcttcccggcacgtag[C/T]atccacagcctgacat	C	T	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-1878960	tcttaaagagaatgca[A/T]agagttgttattacag	A	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1874497	tctccctcagagccga[C/G]tatgggcagagtgtcc	C	G	// 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1908098	tgtacagaagtgcaaa[A/C]atatggaccatccaac	A	C	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 146832 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1905940	tggtcccagggtatta[G/T]gaggctctctgaagtt	G	T	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5) (GALNT5), mRNA. /// ENST00000259056 // intron // 0 // --- // --- // --- // ---	GALNT5	GALNT5, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5) (GALNT5), q24.1
SNP_A-1906395	tggtgctaaattatca[A/G]tctgcctcttaaactc	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 731850 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1923489	ttaggctatctaaagt[G/T]aacacctacaaccaac	G	T	Homo sapiens dedicator of cytokinesis 3 (DOCK3), mRNA. /// ENST00000266037 // intron // 0 // --- // --- // --- // ---	DOCK3	DOCK3, Homo sapiens dedicator of cytokinesis 3 (DOCK3), p21.31
SNP_A-1925213	ttatccatttgtgttc[C/T]actaaggaggataaag	C	T	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 734660 // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2265506	gaagcccgccactgta[A/C]ggttcccgcccttgag	A	C	FLJ23834 // 222256 // Homo sapiens hypothetical protein FLJ23834 (FLJ23834), mRNA. /// NM_006754 // downstream	FLJ23834	FLJ23834, Homo sapiens hypothetical protein FLJ23834 (FLJ23834), q22.3
SNP_A-2268644	gaatgtgaccactaaa[C/T]gtgtctaaattatttg	C	T	Homo sapiens DKFZP434C245 protein (DKFZP434C245), mRNA. /// ENST00000296484 // intron // 0 // --- // --- // --- // ---	WDR51A	WDR51A, Homo sapiens DKFZP434C245 protein (DKFZP434C245), p21.2
SNP_A-2271572	gaccaatactggcaga[C/T]ggtggttattggagaa	C	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2279767	gaggccaggaatttac[C/G]atcagcctaggcaaca	C	G	4729 // Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), mRNA. /// ENST00000333526 // downstream // 73480 // --- // --- // --- // ---	NDUFV2	NDUFV2, Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), p11.22
SNP_A-2278401	gagctaggttgaagcc[A/G]ctgcccagtattgaaa	A	G	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1), transcript variant 1, mRNA. /// ENST00000266110 // intron // 0 // --- // --- // --- // ---	RAPGEF1	RAPGEF1, Homo sapiens Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1), transcript variant 1, q34.13
SNP_A-2283093	gataagtctgtgtaat[A/G]acaagatagatcataa	A	G	sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.1
SNP_A-2282618	gagtttccctttcaga[G/T]aaggattggaatgtgt	G	T	// 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 150909 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2237917	ctctgactctgacaag[C/T]agcgttgggaagaggc	C	T	84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 10316 //	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2234761	ctccagtcatgccaac[A/G]aaaatgagatcatacc	A	G	Homo sapiens split hand/foot malformation (ectrodactyly) type 3 (SHFM3), mRNA. /// ENST00000252129 // intron // 0 //	SHFM3	SHFM3, Homo sapiens split hand,q24.32
SNP_A-2227975	ctaccttatatttcca[A/G]ctatcaaacataagaa	A	G	Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 2, mRNA. /// NM_153485 // intron // 0 // Hs.481942 //	NUP155	NUP155, Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 2, p13.2
SNP_A-2232356	ctcacaaggcaagtca[A/G]aaattccagggagctg	A	G	57534 // Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), mRNA. /// NM_005257 // upstream // 253748 //	MIB1	MIB1, Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), q11.2
SNP_A-2242878	ctgccactggagagga[A/C]aattaagagtttgtta	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 866298 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2253058	cttctctcagataaaa[A/G]gaataagttggcaatg	A	G	ENST00000262042 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-2299897	gcctagatacttctac[C/T]caattacaccagggtg	C	T	64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 251950 // Hs.494312 //	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2298513	gcccaagtttaaacaa[C/G]tagtaggtggcagatg	C	G	Homo sapiens KIAA1033 protein (KIAA1033), mRNA. /// ENST00000311317 // intron // 0 // --- // --- // --- // --- ///	KIAA1033	KIAA1033, Homo sapiens KIAA1033 protein (KIAA1033), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2313767	ggagcagatagctact[A/G]acttgtataaatcatc	A	G	Homo sapiens Fanconi anemia, complementation group C (FANCC), mRNA. /// ENST00000289081 // intron // 0 // --- // --- // 149954 // Homo sapiens chromosome 20 open reading frame 186 (C20orf186), mRNA. /// NM_080574 // upstream // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 275384 // Hs.89576 // IMMP2L // 83943 // Homo sapiens 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 309640 // 63931 // Homo sapiens mitochondrial ribosomal protein S14 (MRPS14), nuclear gene encoding mitochondrial protein, mRNA. /// AL049689 // upstream // 7442 // Hs.156369 // TNN 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 1232730 // 10885 // Homo sapiens WD repeat domain 3 (WDR3), mRNA. /// NM_206996 // upstream // 340423 // Hs.528821 // /// ENST00000357074 // downstream // 247536 // --- // --- // --- /// ENST00000358765 // downstream // 247536 // --- // --- 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1239785 // Hs.199068 // CAMK1G Homo sapiens interferon induced with helicase C domain 1 (IFIH1), mRNA. /// ENST00000263642 // intron // 0 // --- // --- // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 3331922 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 431902 // --- // --- // --- Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2 Homo sapiens diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA. /// ENST00000228027 // intron // 0 // --- // --- // --- 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA. /// ENST00000354276 // intron // 0 // --- // --- // --- /// Homo sapiens WD repeat domain 41 (WDR41), mRNA. /// ENST00000329238 // intron // 0 // --- // --- // --- /// 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 159945 FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 4089 // Homo sapiens SMAD, mothers against DPP homolog 4 (Drosophila) (SMAD4), mRNA. /// NM_016626 // 94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 67936 // --- // --- // --- // --- sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000216254 // intron // 0 // --- // --- // --- // 57633 // Homo sapiens leucine rich repeat neuronal 1 (LRRN1), mRNA. /// ENST00000319331 // downstream //	FANCC	FANCC, Homo sapiens Fanconi anemia, complementation group C (FANCC), q22.32
SNP_A-2313690	ggagatttgggaaatgt[A/T]aatgaaagcacagtga	A	T		C20orf186	C20orf186, Homo sapiens chromosome 20 open reading frame 186 (C20orf186), q11.21
SNP_A-2308625	gctttcattacagaat[C/T]gttgattggtagatca	C	T		DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2290644	gcaagacagacagctc[A/T]ctctcagggcacgtag	A	T		ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-2293278	gcagagggacacaaag[A/T]aatttagggagtact	A	T		MRPS14	MRPS14, Homo sapiens mitochondrial ribosomal protein S14 (MRPS14), nuclear gene encoding mitochondrial protein, q25.1
SNP_A-2233694	ctcatatgagagagca[C/T]aaacaaaaagtgaagga	C	T		KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2240472	ctgacagttcaaaata[C/G]tgtcttaaggaagct	C	G		WDR3	WDR3, Homo sapiens WD repeat domain 3 (WDR3), p12
SNP_A-2282628	gagtttctctttctg[A/C]aaccagtagcacttg	A	C		-	p14
SNP_A-2275224	gagaaggcatgcctac[A/G]caacagatactcaagg	A	G		PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2271644	gaccacgggcctgaaa[A/T]cacaaataaatcaagt	A	T		IFIH1	IFIH1, Homo sapiens interferon induced with helicase C domain 1 (IFIH1), q24.2
SNP_A-2267308	gaatagaataaaatga[C/T]gctgattagtttctt	C	T		RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1910819	tgtctaatcatggaaa[C/T]agcaatgtgtcctagc	C	T		KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1913554	tgtgtaaagtggctt[A/G]aagatgcaggtaaaat	A	G		CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1877224	tctgctgaatttcac[A/G]gctaattcttgacaga	A	G		CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1880590	tctlgccacccacaga[A/G]ataacctatttgaaga	A	G		DGAT2	DGAT2, Homo sapiens diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), q13.5
SNP_A-1896553	tgctacttttcaaatac[G/T]caatttgtgctgtaga	G	T		STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1961675	caacctccaaatggct[A/G]actaaaggtgtgagat	A	G		PLA2G4C	PLA2G4C, Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), q13.32
SNP_A-1958406	ttttcctaagaaacaa[A/G]tgccaaagtatgaaaa	A	G		WDR41	WDR41, Homo sapiens WD repeat domain 41 (WDR41), q13.3
SNP_A-1959846	ttttgtatttgtaaaa[C/T]ggcatcgatagtgttg	C	T		LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1954497	tttgccatcattaaaa[C/T]atagacttcaatgtca	C	T		FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1943083	ttggtatattgttta[A/G]tcctccatttccgta	A	G		CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p15.1
SNP_A-1934517	ttctctaggaatggag[A/G]atgggaacacataaat	A	G		SMAD4	SMAD4, Homo sapiens SMAD, mothers against DPP homolog 4 (Drosophila) (SMAD4), q21.1
SNP_A-1934777	ttctcttgcaagttte[A/G]atccaggaaaggaacc	A	G		FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1971109	ggctgtctcaaataac[C/T]aactaacacggtttct	C	T		ACO2	ACO2, Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-1971448	agtctttcaaaagcca[C/T]gtgtttcttaagctgg	C	T		LRRN1	LRRN1, Homo sapiens leucine rich repeat neuronal 1 (LRRN1), p26.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1964237	acattaatgctagaaa[C/G]cttacattcagaatag	C	G	sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // --- // --- // --- // ---	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1982034	tgggcatagtcattgc[C/T]cctcttacacaccaga	C	T	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 805449 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1755448	ttctaataccaccatctatgtggca[A/G]gtaatgcttagaaagtgaggtaacc	A	G	KIAA2010 /// NM_032560 // intron // 0 // Hs.334657 // KIAA2010 // 55671 // KIAA2010	KIAA2010	KIAA2010 , rs6575196, KIAA2010 ,q32.12
SNP_A-1812544	gtggcctctctgtaca[C/G]ccagtcaggaagtgta	C	G	Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// ENST00000229686 // intron // 0 // --- // --- // --- // ---	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-1786948	gggaaaaataggaaga[A/G]gcaaagtgaagaaaaa	A	G	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 417418 //	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1789867	gggctgtcccagcgaa[C/T]gggaatgtgcagtccc	C	T	116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_183244 // upstream // 38639 // Hs.473218 // PHACTR3 // 116154 //	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.32
SNP_A-1797451	ggtttagaatattcac[A/C]atttgatccagttgga	A	C	// 28978 // Homo sapiens transmembrane protein 14A (TMEM14A), mRNA. /// NM_000846 // downstream // 58326 //	TMEM14A	TMEM14A, Homo sapiens transmembrane protein 14A (TMEM14A), p12.2
SNP_A-1797217	ggttgctaaggctctc[A/G]gaatctaatactattt	A	G	ENST00000314835 // intron // 0 // --- // --- // --- // ---	-	q22
SNP_A-1799868	gtacactaaaaattca[A/G]caattctgggagaaaa	A	G	FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream //	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1831547	taattaagattcttaa[A/T]tcaaaatgttaaattc	A	T	PTPNS1L2 // 128646 // Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), mRNA. /// ENST00000359801 // upstream //	PTPNS1L2	PTPNS1L2, Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), p13
SNP_A-1843891	tagttatcacaggagc[A/G]agggtgtggcctggat	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1772704 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1853642	tatttttgatgagtag[C/T]aaaagatggataaatt	C	T	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 367842 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1852543	tatttagctttacaga[C/G]cttgtcattaagcact	C	G	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1873816	tctcaggaaaaagagc[A/C]cagaggtgaagcacca	A	C	YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 357689 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.3
SNP_A-2210894	ccccttgctgtttctt[C/G]aaaacacaggcacatc	C	G	Homo sapiens transmembrane 4 superfamily member 15 (TM4SF15), mRNA. /// ENST00000263561 // intron // 0 // --- //	TM4SF15	TM4SF15, Homo sapiens transmembrane 4 superfamily member 15 (TM4SF15), q22.1
SNP_A-2222923	cgcacggctttcttgc[A/G]cagttaaacaagctgc	A	G	Homo sapiens testis expressed sequence 14 (TEX14), transcript variant 2, mRNA. /// NM_198393 // intron // 0 //	TEX14	TEX14, Homo sapiens testis expressed sequence 14 (TEX14), transcript variant 2, q23.2
SNP_A-2192004	catcacactgcactga[G/T]tattgcatcttctagc	G	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2194562	catgcactatttacct[C/T]aaccattcattcgtaa	C	T	// 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // downstream // 583052 // Hs.123642	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-2171666	caatctgaaaagtcta[C/T]aaactgtacgattcca	C	T	Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 //	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-2140418	atctcattccatgtca[A/C]tattagctccttttac	A	C	sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), mRNA. /// ENST00000288135 // intron // 0 // --- // --- // --- // ---	KIT	KIT, Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), q12
SNP_A-2139693	atcggttctcaacata[C/T]gatccctaaaataaga	C	T	// 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2160740	atttctaatttaagac[C/T]gaacgtacttccaaaa	C	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 553025 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2159953	atttatctttagttgt[A/G]aaacatgttaagttag	A	G	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA. /// NM_022779 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD	DDX31	DDX31, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, q34.13
SNP_A-2167469	caacatcagttttacc[C/T]aagggctgttttcatt	C	T	151126 // Homo sapiens zinc finger protein 533 (ZNF533), mRNA. /// NM_152520 // upstream // 220070 // Hs.470791 //	ZNF533	ZNF533, Homo sapiens zinc finger protein 533 (ZNF533), q31.3
SNP_A-2129109	ataattcccaataata[A/C]acagtgttggcaaagg	A	C	// 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// NM_030796 // downstream // 22558 // Hs.488307 //	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123423	agtgtctattgtgtga[C/G]atggagagaaaaggcc	C	G	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31
SNP_A-2135259	atattgtcattttagg[C/T]aatgaagagagggata	C	T	lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // --- // --- // --- // --- ///	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds, q13.1
SNP_A-2109819	aggaacaacatataca[A/G]aagattggatacaaca	A	G	-- /// ENST00000314071 // upstream // 361368 // --- // --- // ---	-	p13.3
SNP_A-2113848	aggctggtctgtgaga[G/T]gattaaaaccaagagc	G	T	// 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), mRNA. /// ENST00000266483 // downstream // 2716607 // ---	ALG10	ALG10, Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), q12
SNP_A-2114347	agggacaattgcctcc[A/G]caaagttaacagcact	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2058059	aatatttggtataaag[A/G]caccatgacagaatgg	A	G	LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA. /// ENST00000295213 // downstream	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q12
SNP_A-2060282	aatgaaggagttggac[G/T]gattgctccactctta	G	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2059327	aatcggcttgatgtta[C/T]gtgttttatgatttcc	C	T	Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), mRNA. /// BC003044 // intron // 0 // Hs.495138 // MAPKAP1 // 79109 // Homo sapiens mitogen-	MAPKAP1	MAPKAP1, Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), q33.3
SNP_A-2072671	acagcctggcaatagc[A/G]cgaggctccatctcaa	A	G	// 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc q31.1
SNP_A-2065156	aattggaaaaagccat[C/T]aacaatgcgtttgtgc	C	T	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 322711 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2096118	agacatctgttgactg[C/G]agttggcttattcttt	C	G	2737 // Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// NM_024054 // downstream // 134406 // Hs.214247 // C7orf25	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-2092940	agaacaatacccgatca[A/G]agagttgaggggttac	A	G	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2100742	agatagccgtaataca[A/G]aaactgatgtaagcca	A	G	Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 //	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.3
SNP_A-2079093	acccagatctctctca[A/G]tccaaagcccaggatg	A	G	27250 // Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA. /// NM_014456 // upstream // 204819 // Hs.232543 //	PDCD4	PDCD4, Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, q25.2
SNP_A-2081890	accttgtcaaccctcg[A/G]cattttcaaaacttta	A	G	// Homo sapiens synaptotagmin IV (SYT4), mRNA. /// ENST00000354821 // downstream // 126468 // --- // --- // --- //	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2011257	gagggtcttgagtcta[C/T]gacccaggatacagct	C	T	// 56951 // Homo sapiens chromosome 5 open reading frame 15 (C5orf15), mRNA. /// ENST00000231482 // downstream //	C5orf15	C5orf15, Homo sapiens chromosome 5 open reading frame 15 (C5orf15), q31.1
SNP_A-1990259	acctggtcttcagata[A/C]aatttcatctatgaaa	A	C	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2022407	aaaaatagattaaata[G/T]gttgcataaattgtga	G	T	Homo sapiens tetratricopeptide repeat domain 18 (TTC18), mRNA. /// ENST00000340329 // intron // 0 // --- // --- // --- // ---	TTC18	TTC18, Homo sapiens tetratricopeptide repeat domain 18 (TTC18), q22.2
SNP_A-2034364	aaatctaaagtcatcc[G/T]cttaaaactgtaaagg	G	T	Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // intron // 0 // Hs.200262	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-2040258	aaccacatgggcaaaa[A/C]gtaaaaaatttacact	A	C	GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 //	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2037835	aacaatagtatctata[C/T]ctgaaattctaactct	C	T	Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // --- // --- // --- // --- ///	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2044470	aagaaaagacaagttg[A/T]aactaagtatcataat	A	T	9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// NM_000015 //	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-2043176	aactgcagcaaatgca[A/C]actcatgaagactgac	A	C	// 84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 30448 // Hs.153504 //	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2041546	gcataatacacacacc[C/T]gcttttcttcccagct	C	T	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2040194	aaccaatcaaccaatc[A/C]accatccaaccaatga	A	C	9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 153185 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2038751	aacagatcgtcctata[C/T]ggggtagccaacgcta	C	T	// 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 72027 //	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2020746	tggacacgtgccagca[A/T]tcacgggctagcagga	A	T	Homo sapiens pericentrin 2 (kendrin) (PCNT2), mRNA. /// ENST00000291695 // intron // 0 // --- // --- // --- // --- ///	PCNT2	PCNT2, Homo sapiens pericentrin 2 (kendrin) (PCNT2), q22.3
SNP_A-2025382	aaaatcagcaaaaaga[C/T]ggactgagatacttag	C	T	196477 // Homo sapiens hypothetical protein MGC26598 (MGC26598), mRNA. /// NM_004950 // downstream // 2636 //	MGC26598	MGC26598, Homo sapiens hypothetical protein MGC26598 (MGC26598), q21.33
SNP_A-1990822	gttgattctgtcaacc[A/T]caaaataaaatgtacg	A	T	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 181181 // Hs.32942 // PIK3CG // 5294 // Homo	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-1993402	attgacaaagagacat[C/T]agagagttttgaatct	C	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2017963	ctgtggctcaggcagc[A/G]gactgtgatttccaac	A	G	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2089878	acttctcaatattaaa[A/G]ctttgaacttctctct	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 922396 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2091485	agaaaaaatggattcc[A/G]caaggaagtgggtgac	A	G	/// ENST00000297820 // upstream // 28122 // --- // --- // --- // ---	-	q21.33
SNP_A-2086841	actgactgcttccaaa[A/T]ctaccacccaagcgtg	A	T	// 23099 // Homo sapiens zinc finger protein 297B (ZNF297B), mRNA. /// AB082524 // upstream // 24404 //	ZNF297B	ZNF297B, Homo sapiens zinc finger protein 297B (ZNF297B), q33.3
SNP_A-2103201	agcaactatttctgag[A/G]attttccttgccccag	A	G	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 868470 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2095308	agaatttagtagctta[C/T]ctatcttacagtactt	C	T	Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA. /// NM_006765 // intron // 0 //	TUSC3	TUSC3, Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, p22
SNP_A-2066609	cccaacaagaacagat[C/T]actaattgagcctgcc	C	T	ENST00000228705 // intron // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-2067956	acaactatgtgaaggc[A/G]cagagactcggggcca	A	G	Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// ENST00000354370 // intron // 0 // --- // ---	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2071825	acagactgagaacttc[C/T]ataattaaaggtaaag	C	T	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.2
SNP_A-2061805	aatggaggttaggtgt[A/G]aagaatagtactgcca	A	G	NUP35 // 129401 // Homo sapiens nucleoporin 35kDa (NUP35), mRNA. /// NM_194250 // upstream // 92124 //	NUP35	NUP35, Homo sapiens nucleoporin 35kDa (NUP35), q32.1
SNP_A-2050185	aaggactatctttcac[A/G]agcactcccagcagat	A	G	3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 960075 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2110429	aggaatttacttctgg[C/T]ccactttacttgcata	C	T	SLC4A10 // 57282 // Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA. /// NM_001935 // upstream // 67948 // Hs.368912 //	SLC4A10	SLC4A10, Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), q24.2
SNP_A-2109013	agcttcatttaagaac[A/C]acctcctgcatgaaat	A	C	// 221393 // Homo sapiens G protein-coupled receptor 115 (GPR115), mRNA. /// NM_181744 // upstream // 23984 //	GPR115	GPR115, Homo sapiens G protein-coupled receptor 115 (GPR115), p12.3
SNP_A-2117256	aggtggaacaaaccaa[C/T]gcttagattaatgagt	C	T	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2132808	atataaccggtcacca[C/T]tgcaaaactaaattta	C	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 657372 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2132743	atataaagatgaccag[A/G]aacacaagaatctaaa	A	G	306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 136574 // Hs.146551 // BMP2K //	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-2131517	atagcacagataacaa[C/T]acaagcttacaacttt	C	T	3281 // Homo sapiens heat shock factor binding protein 1 (HSBP1), mRNA. /// NM_001977 // upstream // 108301 //	HSBP1	HSBP1, Homo sapiens heat shock factor binding protein 1 (HSBP1), q25
SNP_A-2127052	ataaataagcaaatcc[A/C]agtatacaatacttta	A	C	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2127317	ataaattactcattca[A/G]ataggattgtgtataa	A	G	9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000354898 // upstream // 82661 // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2155829	attccgtaaggaccac[A/G]cagtccaaacaagagc	A	G	// Homo sapiens hypothetical protein FLJ90231 (FLJ90231), mRNA. /// ENST00000299136 // intron // 0 // --- // --- // --- // ---	FLJ90231	FLJ90231, Homo sapiens hypothetical protein FLJ90231 (FLJ90231), q25
SNP_A-2145465	atgcaggcaggcctgg[A/C]aaactattggtttatc	A	C	145270 // Homo sapiens proline rich membrane anchor 1 (PRIMA1), mRNA. /// NM_138344 // upstream // 66074 //	PRIMA1	PRIMA1, Homo sapiens proline rich membrane anchor 1 (PRIMA1), q32.13
SNP_A-2195436	catgggatgtgagaga[A/G]taaataaccacctgaa	A	G	Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB //	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-2196300	catgtgttttacatag[A/G]atttatgacagtactt	A	G	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31
SNP_A-2186305	tatcctttattaaaca[C/T]gcatgctaaatacctc	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 450835 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189382	cagttgactacaaaca[C/T]gaggatttattttag	C	T	Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 18 (CYP2C18), mRNA. /// ENST00000285979 // intron // 0 // --- // --- // --- /// ENST00000339022 // intron // // 23768 // Homo sapiens fibronectin leucine rich	CYP2C18	CYP2C18, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 18 (CYP2C18), q23.33
SNP_A-2222558	cgagtaaggaaggctaa[C/G]ttaatcaggaagaaatg	C	G	transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2226456	ctaagattgatgtagc[C/T]agtcaacaagtcaatg	C	T	// 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 214161 // --- // --- // --- //	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2219311	ccigtgacaacaaaca[C/T]aactgagtactact	C	T	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2419205 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2210385	cccccagaacttcaca[C/T]aatcattcaagtcggt	C	T	Homo sapiens general transcription factor IIH, polypeptide 3, 34kDa (GTF2H3), mRNA. /// ENST00000228955 // intron // 0 // --- // --- // --- // 200150 // Homo sapiens hypothetical protein FLJ40773	GTF2H3	GTF2H3, Homo sapiens general transcription factor IIH, polypeptide 3, 34kDa (GTF2H3), q24.31
SNP_A-2199903	ccaaagaattgaggcca[C/G]tcagatgcccttaac	C	G	(FLJ40773), mRNA. /// ENST00000314833 // upstream //	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773), q43
SNP_A-1868720	tcctcttccactacca[C/T]tgagccattgtctttc	C	T	// Homo sapiens solute carrier family 22 (organic cation transporter), member 15 (SLC22A15), mRNA. /// ENST00000295687 // intron // 0 // --- // --- // --- // ---	SLC22A15	SLC22A15, Homo sapiens solute carrier family 22 (organic cation transporter), member 15 (SLC22A15), p13.1
SNP_A-1869340	tcctggttaatacttc[C/T]agtcatttttggtgag	C	T	51020 // Homo sapiens chromosome 6 open reading frame 74 (C6orf74), mRNA. /// NM_012259 // upstream // 121879 //	C6orf74	C6orf74, Homo sapiens chromosome 6 open reading frame 74 (C6orf74), q22.31
SNP_A-1799184	gtaagtgaaaaatgaa[C/G]aaggccacagaacagg	C	G	79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1798343	gtaaagtctgccagca[A/C]ctatggctcacagata	A	C	endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 278789 // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-1790698	ggggcttatgataaca[A/G]ggaaagatggtcctgg	A	G	9133 // Homo sapiens cyclin B2 (CCNB2), mRNA. /// NM_004998 // downstream // 1051 // Hs.370392 // MYO1E //	CCNB2	CCNB2, Homo sapiens cyclin B2 (CCNB2), q22.2
SNP_A-1791483	gggtatgtaaaacaca[C/T]tggctctgcaagcttct	C	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1843416 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1808756	gtgaagccagtctgtc[A/C]catggaaattctgtag	A	C	Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, mRNA. /// ENST00000304338 // intron // 0 // --- // --- // --- // ---	KIAA1622	KIAA1622, Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, q32.13
SNP_A-1803495	tctgccgttagttcca[C/T]aaataaaatgggacact	C	T	10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 15803 // Hs.369907 //	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1782929	ggcagatgaaagctga[C/G]agttgaataaatgag	C	G	ENST00000358852 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1685656	atcttaaaaaatactataatttca[C/T]aattgcaatgcacattgacattatt	C	T	// solute carrier family 22 (organic cation transporter), member 16	SLC22A16	SLC22A16 , rs10484807, solute carrier family 22 (organic cation transporter), member 16,q21
SNP_A-1971875	agctggaaaatcaggt[C/G]acattctgcagtgatg	C	G	Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // --- // --- // ---	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1970682	tcactagcttaacatc[A/C]cgagcggtcaccggta	A	C	55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 82994	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-1973154	agcatttaactgctag[A/G]accagactctgaagag	A	G	Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // intron // 0 // --- // --- // --- // ---	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. ,p14.1
SNP_A-1973305	gcctgtttcactcccaa[A/T]cgtgcctgcaaagccc	A	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 501509 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds, p12.3
SNP_A-1975031	aggaagtgctggcctc[C/T]gaagcacaggggccggc	C	T	64747 // Homo sapiens hypothetical protein FLJ14153 (FLJ14153), mRNA. /// ENST00000264266 // downstream //	MFSD1	MFSD1, Homo sapiens hypothetical protein FLJ14153 (FLJ14153), q25.32
SNP_A-1937809	ttgaataaggcaggaa[C/T]gacctcacagcatcaa	C	T	3221 // Homo sapiens homeo box C4 (HOXC4), transcript variant 1, mRNA. /// NM_153633 // downstream // 49316 //	HOXC4	HOXC4, Homo sapiens homeo box C4 (HOXC4), transcript variant 1, q13.13
SNP_A-1938559	ttgagaattggcagca[C/T]aggtattctgaaagtt	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1953989	tttgatactactagc[C/T]atgtcacctaaactct	C	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1972399 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1904163	cttccttcctaatca[C/T]agtccaaggaagaatt	C	T	// 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 510552 //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1901526	tggatttcatcaaaa[A/G]gatgagtaaaatgcct	A	G	Homo sapiens hypothetical protein MGC29643 (MGC29643), mRNA. /// ENST00000345008 // intron // 0 // --- // --- // --- // ---	LYPDC1	LYPDC1, Homo sapiens hypothetical protein MGC29643 (MGC29643), q21.2
SNP_A-1874908	tctctaattaataatc[A/G]ccacctgtagtgccca	A	G	Homo sapiens spermatogenesis associated, serine-rich 2 (SPATS2), mRNA. /// ENST00000321898 // intron // 0 // --- // -	SPATS2	SPATS2, Homo sapiens spermatogenesis associated, serine-rich 2 (SPATS2), q13.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1908392	tgtactttcttaaaga[C/G]cagagttgatcagctg	C	G	// 23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream //	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-1905471	tggtacaatgcagtga[A/G]gtaccaggccacttag	A	G	/// ENST00000359050 // upstream // 164200 // --- // --- // --- // -- /// ENST00000339373 // downstream // 307188 // --- // --- //	-	q14.3
SNP_A-1930635	ttccacaaaacatgaa[C/T]cttcactctctgaaat	C	T	// Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 634314 // Hs.153952 // NT5E //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2272351	gacctgatgttgccaa[A/C]tcaaattacttgtttg	A	C	8671 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), mRNA. /// NM_000583 // downstream // 82656 // Hs.418497 // GC //	SLC4A4	SLC4A4, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), q13.3
SNP_A-2256316	ctttagttcaaacttc[C/T]acatgctgacttgcaa	C	T	Homo sapiens synaptotagmin XIV (SYT14), mRNA. /// ENST00000271745 // intron // 0 // --- // --- // --- // ---	SYT14	SYT14, Homo sapiens synaptotagmin XIV (SYT14), q32.2
SNP_A-2276366	gagagcctaaagaaaa[C/T]gggacatgaaagatga	C	T	// 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 177616	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2285860	gatgagatttgtcaaa[C/G]ttaatagaaaatccac	C	G	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2284672	gatcaggctctgaaag[A/C]attttaggtcttgata	A	C	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2251235	cttcaaagaaacagaa[C/G]caacagtgtgtgtgtg	C	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 1250640 //	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2244101	ctgcttgtcctcagtg[C/T]ataggaatataatgat	C	T	84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 241802 // Hs.7353 // APG4C //	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2292463	gcactagcttcatgaa[C/T]aagtgactggtgctgg	C	T	27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 392447 // Hs.165830	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-2289743	gcaaaatacttatgaa[G/T]cagaaaagctaaaaga	G	T	sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-2307306	gcttagaaatcagaca[C/T]gccttctccaaatccc	C	T	64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 141725 //	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-2305501	tcacctggcataacac[A/G]ggcttcattcatagct	A	G	Homo sapiens sialyltransferase 8B (alpha-2, 8-sialyltransferase) (SIAT8B), mRNA. /// ENST00000268164 //	ST8SIA2	ST8SIA2, Homo sapiens sialyltransferase 8B (alpha-2, 8-sialyltransferase) (SIAT8B), q26.1
SNP_A-2306350	gctgggcattaggaga[A/T]ctctaacctcccgtga	A	T	Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 1, mRNA. /// ENST00000260019 // intron // 0 // --- // ---	DCHS2	DCHS2, Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 1, q31.3
SNP_A-2293285	gcagaggggaaggaga[C/T]atggtccctgttatta	C	T	Homo sapiens beta 3-glycosyltransferase-like (B3GTL), mRNA. /// ENST00000343307 // intron // 0 // --- // --- // --- // ---	B3GTL	B3GTL, Homo sapiens beta 3-glycosyltransferase-like (B3GTL), q12.3
SNP_A-2297003	gccaatgacttaccaa[C/T]tcaagtaccacaaaga	C	T	sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an /// NM_001135 // intron // 0 // Hs.2159 // AGC1 // 176 // Homo sapiens a	AGC1	AGC1, Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an ,q26.1
SNP_A-2244736	ctggataagtgaggta[C/T]agcaggacacactgca	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2247108	ctgtcacacattccta[C/G]tactaatgctacagta	C	G	sapiens CD38 antigen (p45) (CD38), mRNA. /// ENST00000226279 // intron // 0 // --- // --- // --- // ---	CD38	CD38, Homo sapiens CD38 antigen (p45) (CD38), p15.32
SNP_A-2245458	aagccacagaggaccc[C/T]ggcctaattagaattc	C	T	Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000316738 // intron // 0 // ---	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-2254744	cttggaaagatagtaa[A/G]caagaaagtaacttta	A	G	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 11 (ABCB11), mRNA. ///	ABCB11	ABCB11, Homo sapiens ATP-binding cassette, sub-family B (MDR q31.1
SNP_A-2239410	ctctttctttcataaa[C/T]tgcccagtcttgggca	C	T	6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 77413 // Hs.175905 // AUH //	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2241524	ctgagttcctataaga[C/T]agagatcagctcttag	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2280676	gaggtcgccagaaaag[A/G]agagctcagaatgaga	A	G	Homo sapiens neurocalcin delta (NCALD), mRNA. /// ENST00000311028 // intron // 0 // --- // --- // --- // --- ///	NCALD	NCALD, Homo sapiens neurocalcin delta (NCALD), q22.3
SNP_A-2281518	gagtccaatcagtcca[A/G]cctatttttggttata	A	G	7697 // Homo sapiens zinc finger protein 138 (clone pHZ-32) (ZNF138), mRNA. /// ENST00000359735 // downstream //	ZNF138	ZNF138, Homo sapiens zinc finger protein 138 (clone pHZ-32) (ZNF138), q11.21
SNP_A-2277130	gagatggcaagaatcc[A/G]cttcccgcatattgaa	A	G	sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /// ENST00000268638 // intron // 0 // --- // --	IRF8	IRF8, Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2278417	gagctatccagataaa[C/T]gtccatccactgaaat	C	T	Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 //	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.3
SNP_A-2268869	gaattatatctgaaac[C/T]aggtctcgatgaatag	C	T	Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2269381	gaattttataaaagga[C/G]agtaaattacagactt	C	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2265197	gaagattctaaaagca[C/T]caaagtcacacttatg	C	T	5602 // Homo sapiens mitogen-activated protein kinase 10 (MAPK10), transcript variant 4, mRNA. /// NM_002753 // upstream // 137228 // Hs.25209 // MAPK10 // 5602 // Homo	MAPK10	MAPK10, Homo sapiens mitogen-activated protein kinase 10 (MAPK10), transcript variant 4, q21.3
SNP_A-2266378	gaaggtgctgggggaa[A/G]aagtggcactttgttt	A	G	Homo sapiens formyltetrahydrofolate synthetase domain containing 1 (FTHFSDC1), mRNA. /// ENST00000265365 // intron // 0 // --- // --- // --- // ---	MTHFD1L	MTHFD1L, Homo sapiens formyltetrahydrofolate synthetase domain containing 1 (FTHFSDC1), q25.1
SNP_A-1924841	ttatatcgttggctac[A/G]gagacttcaaatttgg	A	G	6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // upstream // 312299 // Hs.505007 // SOX5 // 6660 // Homo	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-1912875	tgtgcttgctccctcc[A/G]ctttcacagtctatag	A	G	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-1884970	tgaatgatttcctttа[C/T]gactctgcaggggtag	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 1160280 // Hs.465407 // NETO1 // 81832 //	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1901775	tggcaccttaaccaca[C/T]tgaattgcttttcccc	C	T	Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase (MGAT5), mRNA. /// ENST00000281923 // intron // 0 // --- // --- // --- // ---	MGAT5	MGAT5, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase (MGAT5), q21.3
SNP_A-1900857	tggagttaaacacaaa[C/T]tgagtagaatttttaa	C	T	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), transcript variant 1, mRNA. /// ENST00000272000 // intron //	LYST	LYST, Homo sapiens Chediak-Higashi syndrome 1 (CHS1), transcript variant 1, q42.3
SNP_A-1903915	tatctgagcctctgta[C/T]gtgatgtttctctgcc	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1897825	tgctggcagttcaaga[C/T]ggtcttttcttccctc	C	T	Homo sapiens FLJ40536 protein (FLJ40536), mRNA. /// ENST00000316750 // upstream // 180917 // --- // --- // --- // ---	-	-, Homo sapiens FLJ40536 protein (FLJ40536), q26.13
SNP_A-1889684	tgataagcataactaa[A/T]gatttcagtgggcaag	A	T	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-1956302	tttgtgttgatgttca[A/G]atttgtcccagatttg	A	G	10316 // Homo sapiens neuromedin U receptor 1 (NMUR1), mRNA. /// NM_152614 // upstream // 55942 // Hs.98104 //	NMUR1	NMUR1, Homo sapiens neuromedin U receptor 1 (NMUR1), q37.1
SNP_A-1937053	ttcttttctctgctac[C/T]ctggccaccttattgt	C	T	// 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 162099 // Hs.369430 // PAM //	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-1970265	gttgcttttctgggta[A/G]aagtgctaatactcca	A	G	Homo sapiens Down syndrome critical region gene 5 (DSCR5), transcript variant 1, mRNA. /// NM_153682 // intron // 0 // Hs.408790 // DSCR5 // 51227 // Homo sapiens Down	DSCR5	DSCR5, Homo sapiens Down syndrome critical region gene 5 (DSCR5), transcript variant 1, q22.13
SNP_A-1966051	caataaactataagtg[A/C]atcatcaaacatcacc	A	C	285025 // Homo sapiens hypothetical protein FLJ39502 (FLJ39502), mRNA. /// NM_178123 // downstream // 37860 //	FLJ39502	FLJ39502, Homo sapiens hypothetical protein FLJ39502 (FLJ39502), q31.2
SNP_A-1986927	taaattcgagtagtta[C/T]cagtgcctgtatttat	C	T	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 522538 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1985816	aaagcccatcattaaa[A/C]agaacacatttggcct	A	C	55173 // Homo sapiens mitochondrial ribosomal protein S10 (MRPS10), nuclear gene encoding mitochondrial protein, mRNA. /// NM_018415 // downstream // 6563 // Hs.485392 //	MRPS10	MRPS10, Homo sapiens mitochondrial ribosomal protein S10 (MRPS10), nuclear gene encoding mitochondrial protein, p21.1
SNP_A-1645174	ttttccagaaaacttgtctacactc[A/G]catctccacttttctgaaccctcatt	A	G	9324 // high mobility group nucleosomal binding domain 3 /// NM_138730 // upstream // 34059 // Hs.77558 // HMGN3 //	HMGN3	HMGN3 , rs1537740, high mobility group nucleosomal binding domain 3 ,q14.1
SNP_A-1807275	gtctctgtggaaggaa[C/T]aaaagtcagctacctg	C	T	Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, mRNA. /// NM_033323 // intron // 0 // Hs.469033 // SLC4A5 //	SLC4A5	SLC4A5, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, p13.1
SNP_A-1805033	gtcatctgctgttaat[C/G]aaacagttttagactg	C	G	28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 550537 // --- // --- // --- // -	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.33
SNP_A-1807705	gtctgtcgtcgttccc[A/G]ctgcagctggcttgag	A	G	Homo sapiens mRNA for KIAA1398 protein, partial cds. /// NM_004587 // intron // 0 // Hs.472213 // RRBP1 // 6238 //	RRBP1	RRBP1, Homo sapiens for KIAA1398 protein, partial cds. p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813604	gtgtaagttccctgta[A/G]gtctgaaccaagccta	A	G	5997 // Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA. /// NM_015984 // downstream //	RGS2	RGS2, Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), q31.2
SNP_A-1787324	gggaagatcatttttc[C/T]cagtcaataaagcctga	C	T	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 499833 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1793422	ggtaggtgctaaagag[C/G]aatgttaggactcta	C	G	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // intron // 0 // --- // --- // --- ///	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-1868586	tcctctccaaaactca[C/T]gttgaaacttcatctc	C	T	SLC22A13 // 9390 // Homo sapiens solute carrier family 22 (organic cation transporter), member 13 (SLC22A13), mRNA. /// NM_004803 // upstream // 24239 // Hs.165559 //	SLC22A13	SLC22A13, Homo sapiens solute carrier family 22 (organic cation transporter), member 13 (SLC22A13), p22.2
SNP_A-1873005	tcatgagattgtgaa[C/T]tgtgataagattaact	C	T	// 137902 // Homo sapiens hypothetical protein FLJ25471 (FLJ25471), mRNA. /// NM_052937 // downstream // 211472	FLJ25471	FLJ25471, Homo sapiens hypothetical protein FLJ25471 (FLJ25471), q11.22
SNP_A-1863392	tcatttttctcttctt[A/G]aaagcagtatattggc	A	G	7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 658635 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1854496	tcaaatgttctttcag[A/G]cacccaaaaaacttagc	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1854336	tcaaaatacaagtcta[C/T]gtgtttattgtctcat	C	T	2668 // Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, mRNA. /// NM_199234 // upstream // 358093 // Hs.248114 // GDNF // 2668 // Homo	GDNF	GDNF, Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, p13.2
SNP_A-1856109	tcaatttttggagatc[A/G]ctggtctctaacttat	A	G	152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 30509 // Hs.478682 // C3orf6 // 152137 //	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-1856644	tcacagtttaaggaa[C/T]ggttgagaaaatgtatt	C	T	ENST00000263632 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-1851398	tattccaggttaaaga[C/T]aggagtgagtctaaaa	C	T	ENST00000359247 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-1832547	tacaaatcatattcaa[A/T]tgtgtttccttcctgc	A	T	sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 //	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-1815107	gtgttccttcagctcc[A/G]aggaggctctcgaactc	A	G	Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) mRNA, complete cds. /// NM_007345 // CDS // 0 //	ZNF236	ZNF236, Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) complete cds. q23
SNP_A-1818397	gttcttcaatgccccg[A/C]aatgtgttaatctcc	A	C	sapiens epidermal growth factor (beta-urogastrone) (EGF), mRNA. /// NM_024090 // intron // 0 // Hs.412939 // ELOVL6 //	EGF	EGF, Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), q25
SNP_A-1820258	gtttacgagttcatca[C/T]agaataaaattcgtat	C	T	10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // downstream // 86584 // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2209335	cccagttctcctctc[C/T]agaaattctaagtgct	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1234925	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2214474	cctacttagcctgagt[A/T]aaataagcatctgcat	A	T	7257 // Homo sapiens translin-associated factor X (TSNAX), mRNA. /// NM_018662 // upstream // 35467 // Hs.13318 //	TSNAX	TSNAX, Homo sapiens translin-associated factor X (TSNAX), q42.2
SNP_A-2225056	cgtgtcctgggaaga[C/T]ggtgtgcgatgagatg	C	T	Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// ENST00000300105 // intron // 0 // --- // --- // --- // ---	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3
SNP_A-2221247	cctttagaatgtgggaa[G/T]aggcctccttcacag	G	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2221777	cctttcatcatcaac[A/G]acactccattctaat	A	G	// 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_0190002 // upstream // 553315 // Hs.353022 // ETAA16 //	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2174429	cacagaatagtttaq[G/T]gcccccagacatttca	G	T	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2174600	cacagatattagtgaa[A/G]acccaattaaataaca	A	G	54927 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA. /// NM_021807 // upstream // 60770 // Hs.321273 // SEC8L1 // 60412 // Homo	CHCHD3	CHCHD3, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), q33
SNP_A-2178274	cactcacacacactca[C/T]tcacttttctcttatta	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1431379 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2141041	atctgccatttcacccc[A/G]caggaattgacccagt	A	G	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA. /// ENST00000343070 // intron // 0 // --- // --- // --- /// ENST00000307331 // intron	SCNN1B	SCNN1B, Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2144523	atgatatttcagagcc[C/T]agtgtaaaatcactcc	C	T	Homo sapiens scinderin (SCIN), mRNA. /// ENST00000341757 // intron // 0 // --- // --- // --- // --- ///	SCIN	SCIN, Homo sapiens scinderin (SCIN), p21.3
SNP_A-2166053	caaatacacaaactac[A/G]aaaaataaggattgac	A	G	// 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream //	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.2
SNP_A-2124697	agttctctcaccacaa[C/T]gaggaagtatatgtgt	C	T	Homo sapiens tudor domain containing 3 (TDRD3), mRNA. /// ENST00000196169 // intron // 0 // --- // --- // --- // ---	TDRD3	TDRD3, Homo sapiens tudor domain containing 3 (TDRD3), q21.2
SNP_A-2117519	aggtgttggagaaata[C/T]ggctttttccctacgc	C	T	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 217026 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-2120385	agtcatgtacaagaca[C/G]caaaaagaatacaaag	C	G	ENST00000358578 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2110884	aggactgtacagacaa[A/G]tatcatacaagaaaag	A	G	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 63542 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-2057572	aatatgaatgctttaa[A/C]aatgacactattaaaa	A	C	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2072481	acagcatatgaagggc[C/T]ctggaaatacacactg	C	T	Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // --- // --- // --- // ---	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-2067637	acaacaaatgaataca[A/G]acactcaacgtgaact	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2064905	aattgacctgtttaaa[C/G]tcatgtagacaggagt	C	G	// Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // --- // --- // --- // ---	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21
SNP_A-2099801	agagtaatagtattag[A/T]aaaatgtgtcggttgc	A	T	FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 272293 //	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-2104148	agcagagaagtcaact[A/G]aagtcagtaaaacttg	A	G	23580 // Homo sapiens CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4), mRNA. /// NM_019064 // downstream // 19535 // Hs.435719 // SDK2 // 54549 // Homo	CDC42EP4	CDC42EP4, Homo sapiens CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4), q25.1
SNP_A-2107345	agctaatgtccaacac[A/G]atctctggtcgcagtc	A	G	Homo sapiens cyclin B1 interacting protein 1 (CCNB1IP1), transcript variant 3, mRNA. /// NM_182849 // CDS // 0 //	CCNB1IP1	CCNB1IP1, Homo sapiens cyclin B1 interacting protein 1 (CCNB1IP1), transcript variant 3, q11.2
SNP_A-2086938	actgagcacacgctcg[A/G]ccccggttggatggac	A	G	117178 // Homo sapiens synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP), mRNA. /// NM_012152 //	SSX2IP	SSX2IP, Homo sapiens synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP), p22.3
SNP_A-2085407	actcattttaagcaac[G/T]acactgacatgatggc	G	T	// 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 83737 // --- // --- // --- // ---	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2083457	actaagcgaaagtccc[A/G]agaaacaaaactctga	A	G	Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, mRNA. /// NM_000635 // intron // 0 // Hs.465709 // RFX2 // 5990 //	RFX2	RFX2, Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, p13.3
SNP_A-2083504	actaagtgaaaggagc[C/T]gagactgggcaggctg	C	T	// 221223 // Homo sapiens hypothetical protein FLJ31547 (FLJ31547), mRNA. /// NM_138736 // upstream // 76570 //	FLJ31547	FLJ31547, Homo sapiens hypothetical protein FLJ31547 (FLJ31547), q12.2
SNP_A-2077966	accagccctggctcta[C/T]cattcatccacagatg	C	T	59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 412619 // Hs.32966 // GUCA2B // 2981 // Homo	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-2011567	gtacaacagagttact[A/G]aacacatgggctttga	A	G	283238 // Homo sapiens hypothetical protein MGC34821 (MGC34821), mRNA. /// ENST00000327600 // downstream //	MGC34821	MGC34821, Homo sapiens hypothetical protein MGC34821 (MGC34821), q12.3
SNP_A-1994578	ctacagtaccaggggа[A/G]gtatgttcaggaataa	A	G	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1996107	actaagaaaaccagca[C/T]gaataggaataaaaat	C	T	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 214276 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1997824	ccccaaatcatgcaat[C/T]agtaaaaggcaatata	C	T	23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 108034 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2030509	aaagcctctgctcttc[A/G]agatgaaccacatacg	A	G	10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 300644 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-2035492	aaatggtggaagctac[A/G]gcagcgagtccatcct	A	G	5500 // Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), transcript variant 1, mRNA. /// NM_206876 // upstream // 66654 // Hs.468018 // PPP1CB	PPP1CB	PPP1CB, Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), transcript variant 1, p23.2
SNP_A-2044654	aagaaagaaggaaata[A/G]atatgaaaccaatatg	A	G	Homo sapiens ubiquitin specific protease 54 (USP54), mRNA. /// ENST00000339859 // intron // 0 // --- // --- // --- // ---	USP54	USP54, Homo sapiens ubiquitin specific protease 54 (USP54), q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041026	aaccgcaggaacactc[C/T]gagaggaaaaaggcaa	C	T	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 174511 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2040291	aaccacgaactcatac[G/T]gatatcaacaaatgat	G	T	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 13351 //	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2033050	aaatacaatagtaaca[A/G]cagatgctatgaatct	A	G	/// ENST00000336930 // upstream // 563294 // --- // --- // --- //	-	p14.3
SNP_A-2029277	aaagaagtgtttcttg[A/C]aggtctccagtgcacc	A	C	C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 //	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2027111	aaacagcttggttttc[A/G]acaatgactgtatcta	A	G	/// ENST00000336930 // upstream // 1329519 // --- // --- // --- //	-	p14.3
SNP_A-2024159	aaaagatgggaaacaa[C/T]ctcactgctctttgac	C	T	MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 //	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-2021648	aaaaaatttctaagac[A/C]actcatgaaatctgaa	A	C	132625 // Homo sapiens zinc finger protein 42 (ZFP42), mRNA. /// NM_173553 // downstream // 42676 // Hs.276429	ZFP42	ZFP42, Homo sapiens zinc finger protein 42 (ZFP42), q35.2
SNP_A-1990254	atttacactgttttct[A/G]aactccagtttcatag	A	G	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2011736	gccctatcagatgggc[A/G]ccattattcctatttt	A	G	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A), mRNA. /// ENST00000053469 // intron // 0 // --- //	GUCA1A	GUCA1A, Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A), p21.1
SNP_A-2008010	gacaaatttaatatca[A/G]agtagtatttggtttg	A	G	55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // downstream // 250459 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.2
SNP_A-2013244	cccagacagtgaagta[A/G]aaacctagaagttcac	A	G	9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 128292 //	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. ,p22
SNP_A-2080145	accgtatgtatgaatt[C/G]aatcttaaaagacaag	C	G	Homo sapiens PABP1-dependent poly A-specific ribonuclease subunit PAN3 (PAN3), mRNA. /// ENST00000282391 // intron // 0 // --- // --- // --- // ---	PAN3	PAN3, Homo sapiens PABP1-dependent poly A-specific ribonuclease subunit PAN3 (PAN3), q12.2
SNP_A-2083784	actaccacatcactaa[C/T]tactgctgctgttggt	C	T	Homo sapiens hypothetical protein FLJ22353 (FLJ22353), mRNA. /// ENST00000246355 // intron // 0 // --- // --- // --- // ---	FLJ22353	FLJ22353, Homo sapiens hypothetical protein FLJ22353 (FLJ22353), p34.1
SNP_A-2086148	actctgaatgaactct[A/G]aagtttagtctcacaa	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 381976 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2099093	agaggacaaattcctc[A/G]agtcctgggagcagac	A	G	Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000306329 // intron // 0 // --- // --- // --- // --- ///	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-2064258	aattcacttaacatac[A/G]atgagcccatttcagg	A	G	Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // --- // --- // --- // --- ///	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2075564	acaatttagagtactg[C/T]acgctgttggcatgga	C	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 141950 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2061234	aatgcatattttgtga[A/G]tattgaaggacttaga	A	G	Homo sapiens interferon-inducible protein X (IFIX), transcript variant b1, mRNA. /// NM_152501 // intron // 0 // Hs.224645 //	PYHIN1	PYHIN1, Homo sapiens interferon-inducible protein X (IFIX), transcript variant b1, q23.1
SNP_A-2116841	aggtctctacacatga[C/G]aggagccaggtcatta	C	G	339345 // Homo sapiens nanos homolog 2 (Drosophila), mRNA (cDNA clone IMAGE:5270224), partial cds. /// NM_002516 // downstream // 8900 // Hs.375439 // NOVA2 //	NANOS2	NANOS2, Homo sapiens nanos homolog 2 (Drosophila), (cDNA clone IMAGE:5270224), partial cds. ,q13.32
SNP_A-2118209	agtaaatacatggaaa[A/G]gtagctgtgttcaggg	A	G	ENST00000354752 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-2127733	ataactgaagtagcaa[C/T]ggctttgaagtcagat	C	T	ENST00000359307 // intron // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-2131023	atagaataatcaaaga[G/T]aactatggaatgaaga	G	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 992651 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2143833	atgagagtctccagcc[A/G]atgccctactctcttc	A	G	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2150709	atgtgccacatttcac[C/T]aagccacaccaagact	C	T	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q23.1
SNP_A-2195619	catggtgctttgggtt[A/G]aaattttgctctcaaa	A	G	Homo sapiens tumor necrosis factor receptor superfamily, member 9 (TNFRSF9), mRNA. /// ENST00000054670 // intron // 0 // --- // --- // --- // ---	TNFRSF9	TNFRSF9, Homo sapiens tumor necrosis factor receptor superfamily, member 9 (TNFRSF9), p36.23
SNP_A-2194826	catgcgaagccaatac[A/G]aggtcatggcggagca	A	G	79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 301544	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-2227239	ctacaaaaagaaaaga[C/T]taatgtcagagaagta	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 425146 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2214254	cctacactaaagaagc[G/T]gcttcactctttccac	G	T	Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /// NM_018070 // intron // 0 // Hs.175551 //	SSBP3	SSBP3, Homo sapiens single stranded DNA binding protein 3 (SSBP3), p32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215640	cctcagggtatgggga[A/C]ctaaagctcgtgagga	A	C	3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 1595 //	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-2217087	cctcttcctgccttga[A/G]ctggaaccttcccacca	A	G	Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2217355	cctgaagctggcagatt[A/C]agcaaggtaaacaatg	A	C	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 899091 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2208862	cccagatgcacttgac[G/T]ccattctgtccggagc	G	T	// 23327 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), mRNA. /// ENST00000256830 // downstream // 64712 // --- // --- // ---	NEDD4L	NEDD4L, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), q21.31
SNP_A-2207479	ccattgtttgatgcc[C/G]aaagtgctgaatgcaa	C	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 559511 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2212085	ccctgccagcaggaag[A/G]catagggacagaatcc	A	G	MGC42105 // 167359 // Homo sapiens hypothetical protein MGC42105 (MGC42105), mRNA. /// NM_019846 // upstream	MGC42105	MGC42105, Homo sapiens hypothetical protein MGC42105 (MGC42105), p12
SNP_A-2200481	ccaacgtaccatcagc[A/G]cataaaagatgtttgc	A	G	2321 // Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mR /// NM_015932 // upstream // 37794 //	FLT1	FLT1, Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor,q12.3
SNP_A-2201978	ccacagcaggaggatcc[C/G]ccatccggctcaggcc	C	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 196669 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2202762	ccacggtgaggatcc[A/G]gcatctgacctaaaa	A	G	// 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-1828238	taagaggtagaaaaat[A/C]attgggaactgacggg	A	C	131177 // Homo sapiens family with sequence similarity 3, member D (FAM3D), mRNA. /// NM_198463 // downstream //	FAM3D	FAM3D, Homo sapiens family with sequence similarity 3, member D (FAM3D), p14.2
SNP_A-1823359	taaaagacctaaaata[A/G]ccaaatctattctgaa	A	G	// Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // ---	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31
SNP_A-1841287	taggaagagactgggc[A/G]cttatcagacaccaca	A	G	389558 // Homo sapiens HWKM1940 (UNQ1940), mRNA. /// NM_145808 // downstream // 121485 // Hs.43297 // MTPN //	UNQ1940	UNQ1940, Homo sapiens HWKM1940 (UNQ1940), q33
SNP_A-1846413	tatatgtgacataaaa[C/T]tgaccactttaccac	C	T	8646 // Homo sapiens chordin (CHRD), transcript variant 2, mRNA. /// NM_177979 // downstream // 116313 // Hs.166186	CHRD	CHRD, Homo sapiens chordin (CHRD), transcript variant 2, q27.1
SNP_A-1854981	tcaacttcagcatgta[A/G]gacacatgtaataact	A	G	Homo sapiens calpain 9 (nCL-4) (CAPN9), mRNA. /// ENST00000271971 // intron // 0 // --- // --- // ---	CAPN9	CAPN9, Homo sapiens calpain 9 (nCL-4) (CAPN9), q42.2
SNP_A-1862677	tcattcaaaattatac[C/G]aagctttgtaaagaaa	C	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 683153 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1870922	catgtgaaatcttgga[A/T]gtcatacaacagatga	A	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 967823 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1868449	tcctcccttcagtgaa[A/G]ttaagaatttaaact	A	G	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1868094	tcctatctctgacac[A/G]cttcacacatgagaaa	A	G	Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // intron // 0 // Hs.523329 // EPHB2 // 2048 //	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-1867603	tccgtatcttgatgag[A/G]ccccaaactcaggtag	A	G	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 539097 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1799703	gtaatttttaaagagt[C/T]acctgatgagtgcata	C	T	2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 191339 // Hs.122926 // NR3C1 //	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1797688	ggtttgcatcaaactc[A/G]catccacaatatgctt	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2223042 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1787603	gggacaaaatatgagt[A/G]aagacctaagacaatt	A	G	Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// ENST00000262406 // intron // 0 // --- // --- // ---	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-1811758	gtgcttagggcggaca[C/T]agaaatcactggaca	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1803491	gtatttatgttcga[G/T]tatttaaacttcctgat	G	T	ENST00000228705 // intron // 0 // --- // --- // ---	-	q14.2
SNP_A-1679432	ccaagtagagccaagtaaaattgc[C/T]gaatcccctaaatattacaagtc	C	T	NM_012414 // intron // 0 // Hs.197289 // RAB3-GAP150 // 25782 // rab3 GTPase-activating protein, non-catalytic subunit (150kD)	RAB3-GAP150	RAB3-GAP150 , rs2221833, rab3 GTPase-activating protein, non-catalytic subunit (150kD),q41

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1722050	aaaataataagctttctaatacta[C/G]agagtcataaagattgagatgaatag	C	G	55839 // uncharacterized bone marrow protein BM039 /// NM_020188 // downstream // 154912 // Hs.6879 // DC13 //	BM039	BM039 , -, uncharacterized bone marrow protein BM039, q23.2
SNP_A-1988167	ctgtgtgggatgcaaa[A/G]acttacaaaatatggt	A	G	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 776794 // Hs.146100	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-1981061	gacataacaatggaat[C/G]attatggctttagatt	C	G	/// ENST00000354793 // downstream // 1522633 // --- // --- // ---	-	p14.1
SNP_A-1969510	tcaagtgcaaatatgal[C/G]aaaagaagatgtggga	C	G	MGC48998 // 339512 // Homo sapiens hypothetical protein MGC48998 (MGC48998), mRNA. /// NM_005613 // upstream	MGC48998	MGC48998, Homo sapiens hypothetical protein MGC48998 (MGC48998), q23.3
SNP_A-1941831	ttggactgatgtacaa[C/T]tctcatctctaatg	C	T	Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // --- // --- // --- // ---	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-1891081	tgatgtaaatgaaggca[A/G]gagtagaacattctag	A	G	Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1894676	tgccagaggctctctgt[C/G]aagttcacttaccaaa	C	G	114879 // Homo sapiens oxysterol binding protein-like 5 (OSBPL5), transcript variant 2, mRNA. /// NM_020896 // upstream // 20899 // Hs.436166 // OSBPL5 // 114879 //	OSBPL5	OSBPL5, Homo sapiens oxysterol binding protein-like 5 (OSBPL5), transcript variant 2, p15.4
SNP_A-1903727	tgggaggatagcctgat[G/T]ccagggaaatccaggt	G	T	// 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 683643 // Hs.480596 // NDST3 //	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1912736	tglgctccaaaaatcgal[A/T]ggagatgaattaaaag	A	T	// 55867 // Homo sapiens solute carrier family 22 (organic anion/cation transporter), member 11 (SLC22A11), mRNA. ///	SLC22A11	SLC22A11, Homo sapiens solute carrier family 22 (organic anion q13.1
SNP_A-1917810	ttaaaagaatgtgaca[A/G]cttgatgtgggtttgt	A	G	SLC38A6 // 145389 // Homo sapiens solute carrier family 38, member 6 (SLC38A6), mRNA. /// ENST00000267488 //	SLC38A6	SLC38A6, Homo sapiens solute carrier family 38, member 6 (SLC38A6), q23.1
SNP_A-1908325	tgtactctgttcctal[C/T]aagttgggaatccat	C	T	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 755354 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-1930763	ttccactgtggctcac[A/G]gagatgctacctgcac	A	G	// Homo sapiens cytokeratin 2 (HUMCYT2A), mRNA. /// ENST00000332411 // CDS // 0 // --- // --- // ---	HUMCYT2A	HUMCYT2A, Homo sapiens cytokeratin 2 (HUMCYT2A), q13.13
SNP_A-1932446	ttcctgcccatgtgac[A/G]acttattagagaaa	A	G	Homo sapiens mRNA for KIAA1643 protein, partial cds. /// ENST00000290974 // intron // 0 // --- // --- // --- ///	ZFYVE28	ZFYVE28, Homo sapiens for KIAA1643 protein, partial cds. .p16.3
SNP_A-2263560	gaaccagttggatgaa[A/C]agtttttgccttctta	A	C	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2275719	gagaccacaggacaca[C/T]cgcaagtgcttgtaaa	C	T	// Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB //	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-2282099	gagtggttttggaaa[C/T]aggatcacacaaggac	C	T	// Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // --- // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2232328	actaaggttaggaaac[A/G]gcacacagtggtggag	A	G	C14orf45 // 80127 // Homo sapiens chromosome 14 open reading frame 45 (C14orf45), mRNA. /// NM_005589 //	C14orf45	C14orf45, Homo sapiens chromosome 14 open reading frame 45 (C14orf45), q24.3
SNP_A-2248049	ctgtgctttagccac[C/T]gactgaggcacagctt	C	T	/// ENST00000330649 // upstream // 790906 // --- // --- // --- //	-	q11.2
SNP_A-2242659	ctgcatagccagtgcc[C/G]aatggtattttggaa	C	G	Homo sapiens mRNA for KIAA1643 protein, partial cds. /// ENST00000290974 // intron // 0 // --- // --- // ---	ZFYVE28	ZFYVE28, Homo sapiens for KIAA1643 protein, partial cds. .p16.3
SNP_A-2241641	ctgatagatatttacc[A/G]aacatttcaggtaaga	A	G	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2582595 // --- // --- // --- ///	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2295342	gcatcatccaatagca[C/G]tacaggagtcaggact	C	G	/// ENST00000314664 // upstream // 41547 // --- // --- // ---	-	q11.23
SNP_A-2294266	gcagggggagagaagtc[A/C]aacacttgaaaaacag	A	C	ENST00000311695 // intron // 0 // --- // --- // ---	-	q13.11
SNP_A-2306479	gctggtctggacaagt[C/T]attgttgtcaagcca	C	T	Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // --- // --- // --- ENST00000287878 // intron //	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-2304729	gctctggagtgaaacc[A/C]ccctgcgctttatcc	A	C	8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 10621 // Hs.425091 // FAM44B	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2310793	ggaagcccagaccaaa[C/T]ggaccctcagtggcca	C	T	// Homo sapiens BTB (POZ) domain containing 14A (BTBD14A), mRNA. /// ENST00000277554 // intron // 0 // --- // ---	BTBD14A	BTBD14A, Homo sapiens BTB (POZ) domain containing 14A (BTBD14A), q34.3
SNP_A-2312591	ggacgaaggtgaacaa[A/C]aatggccaatataacc	A	C	FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2296276	gcattgcttcagagac[A/T]attttttccataaata	A	T	Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // --- // --- // --- ///	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2242796	ctgcatttctctacac[C/T]acctctgagcctgcct	C	T	10744 // Homo sapiens pituitary tumor-transforming 2 (PTTG2), mRNA. /// NM_004219 // downstream // 2019 //	PTTG2	PTTG2, Homo sapiens pituitary tumor-transforming 2 (PTTG2), q33.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2245941	ctgggttgatttctgc[C/T]aggaatcccgcaggct	C	T	// 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 //	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2231683	ctatttttcctaatta[C/T]acatccaccacagtga	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 522821 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2240390	ctgacaatcacctcta[C/T]gagagcagcttggatg	C	T	60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 103828 // Hs.485968 //	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2274093	gacttatgtggatatt[A/T]aacacttaagatttgg	A	T	// Homo sapiens hypothetical protein FLJ23861 (FLJ23861), mRNA. /// ENST00000281772 // intron // 0 // --- // --- // --- // ---	FLJ23861	FLJ23861, Homo sapiens hypothetical protein FLJ23861 (FLJ23861), q34
SNP_A-2277587	gagcaccatctttggg[C/G]caaaagcctggggaag	C	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1927400	ttcaaagataagtgga[A/G]taaacaagaaaggcta	A	G	// 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 207789 // Hs.154329 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1920976	cagacatacacatcag[A/G]atttcctgacaggaac	A	G	// 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// NM_173557 // downstream // 147444 // Hs.465316	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.33
SNP_A-1919661	ttaaggtctgtaaaaa[C/T]gggaaggattttaggc	C	T	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 413341 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1910667	tgtcctgtaaatggga[C/T]gtgtgcttttcagcag	C	T	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-1906776	tggttagagccgtgtc[A/G]cttcaccgtacactgc	A	G	Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), mRNA. /// ENST00000301396 // intron // 0 // --- // ---	PELP1	PELP1, Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), p13.2
SNP_A-1915790	tgttgaaaattatcac[G/T]cctctctctgtgtccc	G	T	55090 // Homo sapiens mediator subunit 25 (MED25), mRNA. /// ENST00000328591 // upstream // 38625 // --- // ---	MED9	MED9, Homo sapiens mediator subunit 25 (MED25), p11.2
SNP_A-1891458	tgattccaaaatgtcg[C/G]agctaacgcaggttct	C	G	LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 //	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-1882446	tgaaaagtggcagaga[C/G]agactgtaaacactga	C	G	4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 654198 // Hs.232819 // PCDH15 // 65217 //	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1942791	ttgggctgatgaatga[C/T]gccacctgatcggctt	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1934160	ttctcatcctctcttc[C/T]attcatccttaaacat	C	T	1499 // Homo sapiens catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA. /// ENST00000301828 // downstream // 122239 // --- // --- // --- // --- ///	CTNNB1	CTNNB1, Homo sapiens catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), p22.1
SNP_A-1960515	tttttcacacttcaaa[A/C]tatctaaactattcca	A	C	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA.	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-1951903	tttctaccactcaagc[A/G]catggtctttccacca	A	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 684310 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1949975	tttcaatgcagttttc[C/T]aggaaagagcccagca	C	T	Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA. /// NM_000192 // intron // 0 // Hs.381715 // TBX5 // 6910 //	TBX5	TBX5, Homo sapiens T-box 5 (TBX5), transcript variant 2, q24.21
SNP_A-1948506	tttagtgggagacaaa[C/T]ggaaagcaagtaaaca	C	T	64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 292806 // Hs.7482 // RBM19 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-1974608	aagaaaagttagacca[A/G]gacagagtcaatagag	A	G	Homo sapiens procollagen C-endopeptidase enhancer 2 (PCOLCE2), mRNA. /// ENST00000295992 // intron // 0 // ---	PCOLCE2	PCOLCE2, Homo sapiens procollagen C-endopeptidase enhancer 2 (PCOLCE2), q23
SNP_A-1975556	gctggatctgtgcctg[A/G]aagtgggttgaggccg	A	G	23355 // --- /// ENST00000287546 // downstream // 23870 // --- // --- // --- /// ENST00000335012 // downstream // 6539 //	KIAA0804	KIAA0804, --- ,q27.2
SNP_A-1979580	gataagctatgtgtta[C/T]gattttctacatatta	C	T	Homo sapiens hypothetical protein FLJ11155 (FLJ11155), mRNA. /// ENST00000296529 // intron // 0 // --- // --- // ---	FLJ11155	FLJ11155, Homo sapiens hypothetical protein FLJ11155 (FLJ11155), q32.1
SNP_A-1987168	tacatgaatttcctca[C/T]tgaacctccacaaata	C	T	Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// ENST00000317357 // downstream // 36166 // --- //	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-1985957	aaggcaaggtatggag[C/T]caaatagatacaggaa	C	T	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 661694 // Hs.497822 // DUSP10 // 11221 //	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1985308	tgccatatgctccaca[C/T]tgcgtcttatcccacc	C	T	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 464292 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1697354	taacagtaatatattctatagtctc[A/G]aatagctaggatattgaatgtttcc	A	G	cDNA FLJ40168 fis, clone TESTI2016410. /// NM_021205 // downstream // 103341 // Hs.20252 // RHOU // 58480 // ras	-	- , rs241291, Homo sapiens cDNA FLJ40168 fis, clone TESTI2016410. ,q42.13
SNP_A-1652496	cttcccaatggatcattaactttac[G/T]aaatcatttcttgcattaagtaaca	G	T	AK097903 // intron // 0 // Hs.380210 // C6orf190 // 387357 // chromosome 6 open reading frame 190	C6orf190	C6orf190 , rs269999, chromosome 6 open reading frame 190,q22.33
SNP_A-1661670	ctgtttggttcattcacataaagta[C/T]ctaaaataaagacaggagtgccaag	C	T	9603 // nuclear factor (erythroid-derived 2)-like 3 /// NM_022150 // upstream // 719433 // Hs.60473 // C7orf9 //	NFE2L3	NFE2L3 , rs10486488, nuclear factor (erythroid-derived 2)-like 3 ,p15.2
SNP_A-1814079	gtgtccctcctcttca[A/G]ctgtttggaatagttt	A	G	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 376571 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-1862793	tcattcgtgagatcca[C/T]tactcctttgcagcag	C	T	// 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 135978 // Hs.118183 // FLJ22833	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-1864790	tccagcttgacttaga[A/C]atctttctgtatatat	A	C	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1853398	tattttcctatagaaa[C/T]tgtaccatttggaaga	C	T	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 133609 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1846172	tatatcagtggactta[A/T]cccttcaggatccatt	A	T	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2 (APOBEC2), mRNA. /// ENST00000244669 // intron // 0 // --- // --- // --- // ---	APOBEC2	APOBEC2, Homo sapiens apolipoprotein B editing enzyme, catalytic polypeptide-like 2 (APOBEC2), p21.1
SNP_A-1829733	taagtttttgtagaac[C/T]ggagaagtttcaataa	C	T	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // CDS // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2200391	ccaaccagaagtcaag[C/T]cccatccacactagca	C	T	1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 132258 // ---	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2
SNP_A-2204438	ccagctctctcgaaat[A/G]aatagagtgagaattc	A	G	Homo sapiens paraoxonase 1 (PON1), mRNA. /// ENST00000222381 // intron // 0 // --- // --- // --- // ---	PON1	PON1, Homo sapiens paraoxonase 1 (PON1), q21.3
SNP_A-2218197	cctgctacagatatag[C/T]ctagaaaaaatgaata	C	T	// 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 487147 // Hs.135642 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2224770	cgtgaaatttaagtaa[C/T]tggtccaaggccatat	C	T	// 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 142323 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2195765	catgtacatttttatg[A/G]atactatcacatatca	A	G	84870 // Homo sapiens thrombospondin, type I, domain containing 2 (THSD2), mRNA. /// NM_032784 // downstream	THSD2	THSD2, Homo sapiens thrombospondin, type I, domain containing 2 (THSD2), q22.33
SNP_A-2197423	cattccatcgtcaagg[A/G]atgaaagctcagtaag	A	G	Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, mRNA. /// NM_033625 // intron // 0 // Hs.438227 //	RPL34	RPL34, Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, q25
SNP_A-2182228	cagagtaatacatggc[C/T]ctttctttcttcttct	C	T	284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 330434 //	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2149485	atgtagagagtcaaca[A/C]atcattgtattgaagt	A	C	sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // --- // ---	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.1
SNP_A-2143104	atgaatgtgggttcta[C/G]actcaggtggagccaa	C	G	56935 // Homo sapiens FN5 protein (FN5), mRNA. /// NM_024116 // downstream // 83774 // Hs.355750 //	FN5	FN5, Homo sapiens FN5 protein (FN5), q21
SNP_A-2156923	attcttgagttgaaaa[C/G]agcctctggagtaatg	C	G	5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 72548 //	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-2154299	attatggctgattata[G/T]ctcctactcatttttt	G	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2153316	attagaaaagtaaaca[C/T]gatgaaacacaaagta	C	T	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2134347	atatgctgactaccta[C/T]ctgtttaaattgtttc	C	T	Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2126576	ataaaatgtgtgtatc[C/T]attaaagtaagatttt	C	T	Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA. /// ENST00000358336 // intron // 0 // --- // --- // --- /// ENST00000320152 // intron // 0 // --- // --- // --	PRTFDC1	PRTFDC1, Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), p12.1
SNP_A-2099052	agaggaagctttgcaa[A/T]tgaaaaaaaaatactc	A	T	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2105303	agcattgtttcattaa[A/C]tgtcatcttgttataa	A	C	/// ENST00000333984 // upstream // 41057 // --- // --- // --- // --	-	q11
SNP_A-1995581	cttaatttcaaaatta[C/T]gttcatatgtgccaat	C	T	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2024408	aaaagctgtacacata[C/T]aaaattttgtgtaaat	C	T	ENST00000338994 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2026146	aaaattcacactacaa[A/G]tgagttcttattttac	A	G	// 84553 // Homo sapiens chromosome 6 open reading frame 168 (C6orf168), mRNA. /// ENST00000305402 //	C6orf168	C6orf168, Homo sapiens chromosome 6 open reading frame 168 (C6orf168), q16.2
SNP_A-2020622	aaattcaactggactc[A/G]agcgacttacagatca	A	G	Homo sapiens collagen, type XVIII, alpha 1 (COL18A1), transcript variant 2, mRNA. /// NM_030582 // intron // 0 //	COL18A1	COL18A1, Homo sapiens collagen, type XVIII, alpha 1 (COL18A1), transcript variant 2, q22.3
SNP_A-2040103	aaccaaatcgactaca[C/T]agcccagtatagtatt	C	T	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 486357 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2015680	atgagacacttaataa[A/G]tatttgttgaggcact	A	G	// 54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// ENST00000359578 //	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-2005481	gattagataacttgta[C/T]gaaatgaaaaaaaatt	C	T	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-2101040	agatcaaggtggtccc[A/G]ctatgtggtgaagtgg	A	G	23580 // Homo sapiens CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4), mRNA. /// NM_019064 // downstream // 15829 // Hs.435719 // SDK2 // 54549 // Homo	CDC42EP4	CDC42EP4, Homo sapiens CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4), q25.1
SNP_A-2095479	agacaacagcatcttc[C/T]ctattggccaacttgc	C	T	Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // intron // 0 // Hs.164384 // PKP2	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-2084743	actatttatttcagac[A/C]aggcaagtctaaacac	A	C	KIAA1727 // 85462 // Homo sapiens KIAA1727 protein (KIAA1727), mRNA. /// NM_015271 // upstream // 174903 //	KIAA1727	KIAA1727, Homo sapiens KIAA1727 protein (KIAA1727), q31.3
SNP_A-2080880	acctctcaaacatcta[C/T]cagctatcttggtttg	C	T	Homo sapiens popeye domain containing 3 (POPDC3), mRNA. /// ENST00000254765 // intron // 0 // --- // --- // --- // ---	POPDC3	POPDC3, Homo sapiens popeye domain containing 3 (POPDC3), q21
SNP_A-2059381	aatctaagcgtttata[A/T]ctggtctctcaatttt	A	T	ENST00000341548 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-2058998	aatccattcttaatga[C/T]gtcttccgtgttcggt	C	T	55341 // Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA. /// NM_152531 // downstream // 319339	FLJ11301	FLJ11301, Homo sapiens hypothetical protein FLJ11301 (FLJ11301), q29
SNP_A-2075095	acatccttgctgtcaa[A/C]tccctgcatgaaacac	A	C	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2126323	ataaaacataatctct[A/G]aacttaaggaccttca	A	G	1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 232784 // Hs.72901 // CDKN2B	CDKN2B	CDKN2B, Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3
SNP_A-2135788	atcaaagtcaacatta[G/T]gtttggtcttggcagt	G	T	ENST00000316998 // CDS // 0 // --- // --- // --- // ---	-	p15.4
SNP_A-2131099	atagacagacataaaa[A/G]taggacactgggtctc	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2131742	atagctacaggatgct[C/T]actctgtcaatagagt	C	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 210935 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2120647	agtccctactccatca[C/T]tcatttcctatttctt	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2158175	attggcaacagatgga[G/T]aagcaataaatgtaag	G	T	// 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream //	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-2173862	aatttgaagcctctgg[A/T]caacccacgtcaaaaa	A	T	2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 12861 // Hs.444329 // GPC6 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2171779	caatgaagaggcagcc[A/G]ctgaaatctgcatagc	A	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 128471 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2193717	catcttgtcctccaaa[A/G]cttgagctccaccgaa	A	G	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2214037	cctaaggacacaaggc[A/G]aaaccaaccacctagc	A	G	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 37596 // Hs.497822 // DUSP10 // 11221 // Homo	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2200084	ccaaatataccaagaa[C/T]gaacaatcagtaaata	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2199781	ccaaacagaagcatat[G/T]agttggagtattatag	G	T	sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 //	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26
SNP_A-1834010	tacatataccatgaaa[C/T]actaccgagccataaa	C	T	401388 // Homo sapiens FLJ42280 protein (FLJ42280), mRNA. /// NM_006304 // downstream // 118882 // Hs.489201	FLJ42280	FLJ42280, Homo sapiens FLJ42280 protein (FLJ42280), q21.3
SNP_A-1824727	taaagagagatgatta[C/T]agcactaaagtttcac	C	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1819480	gttgggtggtaaacca[C/T]tcttcactgttcttag	C	T	Homo sapiens hypothetical protein FLJ10948 (FLJ10948), mRNA /// ENST00000358358 // intron // 0 // --- // --- // ---	ECHDC2	ECHDC2, Homo sapiens hypothetical protein FLJ10948 (FLJ10948), p32.3
SNP_A-1818469	gttcttggtcttccac[A/G]agaaaggaagctgtc	A	G	ENST00000340222 // 3UTR // 0 // --- // --- // ---	-	q22.31
SNP_A-1853408	tattttctagtccctga[A/G]gattagaaatctgaaaa	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA /// ENST00000261266 // intron // 0 // --- // --	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-1852717	tatttcacgattgtaa[A/G]tgtgacaatgtgtac	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1864466	aattcacaaacaatgc[A/G]aaagccaaatgtaatc	A	G	51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 25333 // --- // ---	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-1866457	tcccacctgtgcagag[A/G]agaaaactgaggcaga	A	G	ENST00000358431 // intron // 0 // --- // --- // ---	-	q11.23
SNP_A-1866562	tccccaaaatacctg[C/G]cagatgtagtgtaaac	C	G	5451 // Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), mRNA. /// NM_002697 // upstream //	POU2F1	POU2F1, Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), q24.1
SNP_A-1860078	tcagtacttttcactc[A/T]ctgaatctctaaaat	A	T	84062 // Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 //	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3
SNP_A-1788589	gggatcactaggatc[A/G]actgttcatccccgat	A	G	Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// ENST00000355128 // intron // 0 // --- // --- // ---	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-1790141	ggggaatgcatattcca[G/T]aaaataattcactatt	G	T	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 233497 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1695965	ggggcagaggcaagacattcccac[A/G]cctcctgggctagcctcagcatgt	A	G	// 6229 // ribosomal protein S24 /// NM_020338 // upstream // 980205 // Hs.438767 // RAI17 // 57178 // retinoic acid induced	RPS24	RPS24 , rs9299542, ribosomal protein S24 .q22.3
SNP_A-1985534	aattcaatctaattac[C/T]gagttaccaaagcaga	C	T	// 696 // Homo sapiens butyrophilin, subfamily 1, member A1 (BTN1A1), mRNA. /// NM_006353 // upstream // 10322 //	BTN1A1	BTN1A1, Homo sapiens butyrophilin, subfamily 1, member A1 (BTN1A1), p22.1
SNP_A-1988143	gcatcaaggggccgaaa[A/T]gaacttctaatgtatt	A	T	80177 // Homo sapiens myc target 1 (MYCT1), mRNA. /// NM_194435 // upstream // 6609 // Hs.53973 // VIP // 7432 //	MYCT1	MYCT1, Homo sapiens myc target 1 (MYCT1), q25.2
SNP_A-1980710	taatttgtaaatgggc[A/G]agttcttctggaaccc	A	G	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // --- // --- // ---	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1959582	ttttggacacgtgcaaa[C/G]ctcactcggatacgca	C	G	1908 // Homo sapiens endothelin 3 (EDN3), transcript variant 1, mRNA. /// NM_207034 // downstream // 73672 // Hs.1408	EDN3	EDN3, Homo sapiens endothelin 3 (EDN3), transcript variant 1, q13.32
SNP_A-1945355	ttgttagcgtctcctg[C/T]agtttttctactaac	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1285195 // --- // --	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1947367	ttacaatgatggaaa[A/G]ctggaagcaatctagc	A	G	HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 67539 // Hs.120831 // TNT //	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-1879182	tcttactaaaatttta[A/G]ggttgactacagggat	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 414539 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1892891	tgcaccctgccctttg[A/G]acacataatctcatta	A	G	6297 // Homo sapiens sal-like 2 (Drosophila) (SALL2), mRNA. /// ENST00000317492 // upstream // 16861 // --- // ---	SALL2	SALL2, Homo sapiens sal-like 2 (Drosophila) (SALL2), q11.2
SNP_A-1902191	tggccaagctgcaaag[C/G]agtgggtttaatgac	C	G	Homo sapiens MAP/microtubule affinity-regulating kinase 1 (MARK1), mRNA. /// ENST00000294888 // intron // 0 // --- // --	MARK1	MARK1, Homo sapiens MAP q41
SNP_A-1907018	tggttgccattaaaa[A/T]ctcctgaaaggctttt	A	T	Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // intron // 0 // Hs.369263 //	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-1905606	tggtaggactgtaaaa[C/T]gtacaatgatttttgg	C	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript v /// NM_006264 // intron // 0 //	PTPN13	PTPN13, Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1,q21.3
SNP_A-1923550	gaagcatagcaaggca[C/T]attccacagagtggg	C	T	221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1929305	ttcagtatttatgatc[A/C]aaattattatgcatat	A	C	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 7 (SLC16A7), mRNA. /// ENST00000261187 // intron // 0 // --- // --- // ---	SLC16A7	SLC16A7, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 7 (SLC16A7), q14.1
SNP_A-2276602	gagaggttgctgagac[A/C]gtcggagagacagcgg	A	C	353514 // Homo sapiens leukocyte Ig-like receptor 9 (LIR9), transcript variant 2, mRNA. /// NM_181986 // upstream //	LIR9	LIR9, Homo sapiens leukocyte Ig-like receptor 9 (LIR9), transcript variant 2, q13.42
SNP_A-2269634	gacaaatttctctaca[C/T]gacttacaataccgct	C	T	Homo sapiens WD repeat domain 36 (WDR36), mRNA. /// ENST00000323652 // intron // 0 // --- // --- // ---	WDR36	WDR36, Homo sapiens WD repeat domain 36 (WDR36), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2236263	ctcctttgcttcttca[C/T]agagaaaaaaatattt	C	T	Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // --- // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2230095	ctataatggtgatgac[A/G]agaggctgtggtactc	A	G	26235 // Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA. /// ENST00000229971 // upstream //	FBXL4	FBXL4, Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), q16.2
SNP_A-2252753	cttctaaatgacttaa[C/G]ctgacctaaaatatgt	C	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 415850 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2251087	cttattgaaacacaga[A/G]ctctctaactaactgg	A	G	10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 261155 // Hs.489615 // PBEF1 // 10135 // Homo	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-2305374	gctgatacttcaaaca[C/T]atattacctgactaaa	C	T	ENST00000255320 // intron // 0 // --- // --- // --- // ---	-	p24.3
SNP_A-2311158	ggaagtgcaataatta[C/T]accaatatcagacaaa	C	T	Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // --- // --- // --- // --- ///	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2242708	tagacagatttaatga[A/T]gtaatataatggtgat	A	T	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2231886	ctcaaatgaagggtga[C/T]gatgagaacatgacgc	C	T	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1632340 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1930930	ttccaggcaccttacc[A/G]cagtcaggttaaggaa	A	G	29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// NM_021800 //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1905809	tggtcacagccaaagg[A/T]cctgctttgcccacag	A	T	/// ENST00000321536 // upstream // 621567 // --- // --- // --- // -	-	p13
SNP_A-1905085	tgggtgacttaaaaaa[A/T]tactggaaataggccg	A	T	Homo sapiens glycogen synthase kinase 3 beta, mRNA (cDNA clone MGC:16182 IMAGE:3637163), complete cds. /// NM_002093 // intron // 0 // Hs.445733 // GSK3B // 2932 //	GSK3B	GSK3B, Homo sapiens glycogen synthase kinase 3 beta, (cDNA clone MGC:16182 IMAGE:3637163), complete cds. ,q13.33
SNP_A-1911934	tgtgactaatgcttca[A/T]tgaacatacaggggca	A	T	7021 // Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta) (TFAP2B), mRNA. /// ENST00000344788 // downstream // 13129 // --- //	TFAP2B	TFAP2B, Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta) (TFAP2B), p12.3
SNP_A-1892314	tgcaactggaaaccac[C/T]gatgtgagatgtgggt	C	T	80314 // Homo sapiens enhancer of polycomb homolog 1 (Drosophila) (EPC1), mRNA. /// ENST00000331754 //	EPC1	EPC1, Homo sapiens enhancer of polycomb homolog 1 (Drosophila) (EPC1), p11.22
SNP_A-1875033	tctctatggatttgcc[C/T]agtctgaaaatttctt	C	T	Homo sapiens regulator of G-protein signalling 20 (RGS20), mRNA. /// NM_003702 // intron // 0 // Hs.368733 // RGS20 //	RGS20	RGS20, Homo sapiens regulator of G-protein signalling 20 (RGS20), q11.23
SNP_A-1883832	tgaagaatatttccag[C/T]ctcatctaggacaata	C	T	5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000335192 // downstream // 707226 // ---	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-1957988	ttttcacacttcaaag[C/T]attgccacttagcatc	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2427079 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1979395	ttactgcaaggcagca[C/T]attctctcttatccac	C	T	4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // upstream // 806443 // --- // --- // --- // --- /// ENST00000355292	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1973075	aaatagacaaatattc[A/G]gaaaacatacaaattc	A	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-1713245	actatttttcaaataggctgataa[A/T]tccaccaaaaggaaatatatcaaaa	A	T	145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs10483505, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1724872	ccacacctagttgtttctaacaaca[A/C]gtaagacaagagggacacggagaca	A	C	NM_007118 // intron // 0 // Hs.367689 // TRIO // 7204 // triple functional domain (PTPRF interacting)	TRIO	TRIO , rs154152, triple functional domain (PTPRF interacting),p15.2
SNP_A-1780632	ggatcaaaatatgccc[G/T]caagattcctctcccc	G	T	ENST00000281741 // CDS // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1791462	gggtatccccatgcca[A/G]cagaggagaggtgttt	A	G	399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 155912 // Hs.299419 //	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds. q25
SNP_A-1859140	tcagcctcttcctaga[C/T]ggctgggcttctgagg	C	T	143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// NM_199461 // upstream //	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11
SNP_A-1846500	tatattcagagtaaca[A/G]aacagggtgcttttcc	A	G	168620 // Homo sapiens class II bHLH protein MIST1 (MIST1), mRNA. /// NM_015379 // upstream // 6580 //	MIST1	MIST1, Homo sapiens class II bHLH protein MIST1 (MIST1), q21.3
SNP_A-1817796	gttcctctaccagaga[A/C]gcacagatccagaaag	A	C	7560 // Human Kox5 mRNA for zinc finger protein, partial. /// ENST00000333201 // downstream // 16218 // --- // --- // --- // --	ZNF13	ZNF13, Human Kox5 for zinc finger protein, partial. ,q13.13
SNP_A-1823559	taaaagtgctttctgc[A/G]agagggtgggattcag	A	G	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 2, mRNA. ///	CAMKK2	CAMKK2, Homo sapiens calcium,q24.31
SNP_A-1830573	taatcagtttctgttc[C/T]ctgaagacagtctggt	C	T	TM4SF17 // 26262 // Homo sapiens transmembrane 4 superfamily member 17 (TM4SF17), transcript variant 2, mRNA. /// NM_002115 // downstream // 169626 // Hs.411695	TM4SF17	TM4SF17, Homo sapiens transmembrane 4 superfamily member 17 (TM4SF17), transcript variant 2, q35.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1831706	taattattgataggat[A/G]aatgaaaatgaagttg	A	G	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-1844311	tataaaaaatcatgta[C/T]gtgaagactatcccga	C	T	Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2203773	ccagagcagccaatca[A/C]gagaaagcgttctaat	A	C	Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 //	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-2227694	ctacattccataaaaa[G/T]aatctttaacactgta	G	T	Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA. /// ENST00000265070 // intron // 0 // --- //	GOLPH3	GOLPH3, Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3), p13.3
SNP_A-2185690	caggaggttgtgaccc[A/T]cagcaaattctggcag	A	T	4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// AF211119 // upstream // 21532 //	MTAP	MTAP, Homo sapiens methylthioadenosine phosphorylase (MTAP), p21.3
SNP_A-2175763	cacattctagtgtgtc[A/T]aagatgtgtgatcaca	A	T	10651 // Homo sapiens metaxin 2 (MTX2), transcript variant 1, mRNA. /// ENST00000249442 // downstream // 229640 // -	MTX2	MTX2, Homo sapiens metaxin 2 (MTX2), transcript variant 1, q31.1
SNP_A-2157300	attgactgcataaaaa[C/T]tttacatatggatagg	C	T	// 129401 // Homo sapiens nucleoporin 35kDa (NUP35), mRNA. /// NM_194250 // upstream // 1182886 // Hs.159528 //	NUP35	NUP35, Homo sapiens nucleoporin 35kDa (NUP35), q32.1
SNP_A-2152978	attacagtgataataa[C/G]aatagtgattttcctt	C	G	-- /// ENST00000276737 // downstream // 242367 // --- // --- //	-	q24.23
SNP_A-2155033	attcactgaaagtttc[A/G]ctattttgacacctac	A	G	ENST00000318116 // intron // 0 // --- // --- // --- // ---	-	q21.23
SNP_A-2167545	caacattggaggtggg[C/T]attgctattcccttga	C	T	1441 // Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, mRNA. /// NM_000760 // upstream // 277642 // Hs.524517 // CSF3R //	CSF3R	CSF3R, Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, p34.3
SNP_A-2161409	atttgcatttccctaa[C/T]ggctttgatgctggac	C	T	Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, mRNA. /// NM_012425 // intron // 0 // Hs.524161 //	RSU1	RSU1, Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, p13
SNP_A-2161035	atttcttggctgagca[C/T]aaattcatttggtcaa	C	T	Homo sapiens cellular repressor of E1A-stimulated genes 2 (CREG2), mRNA. /// ENST00000324768 // intron // 0 // --- // ---	CREG2	CREG2, Homo sapiens cellular repressor of E1A-stimulated genes 2 (CREG2), q11.2
SNP_A-2142941	atgaatagctacaaaa[G/T]tgtcattcacttggct	G	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 546120 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2142158	atctttttacattatc[A/C]ctgacaactctgttac	A	C	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 2228836 // --- // --- // --- // --	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-2132221	atagtaaaggtgatga[C/G]agaagggaagaagaag	C	G	Homo sapiens ras homolog gene family, member J (RHOJ), mRNA. /// ENST00000316754 // intron // 0 // --- // --- // --- // ---	RHOJ	RHOJ, Homo sapiens ras homolog gene family, member J (RHOJ), q23.2
SNP_A-2137037	atcagctctacttcta[A/G]aatgttgatatccttc	A	G	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 161695 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2066259	aattttatcctagagg[A/G]ccatttacagaagaga	A	G	Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// ENST00000297769 // intron // 0 // --- // --- // --- // --- ///	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2056637	aatagcaacagcaaac[G/T]atgacaggttttcaat	G	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2007579	tatatagagcaggtca[A/G]atatgtcaccatagac	A	G	Homo sapiens zinc finger protein 341 (ZNF341), mRNA. /// AK027550 // intron // 0 // Hs.516989 // ZNF341 // 84905 //	ZNF341	ZNF341, Homo sapiens zinc finger protein 341 (ZNF341), q11.22
SNP_A-2017851	ctgtcatctccatagc[A/C]aattggtagctatttt	A	C	254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 4018	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-2016840	tgtcctattaccacct[C/T]aatagcaactcctaga	C	T	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 647844	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1995118	tcatttagacctgact[A/G]agctaccctctcttca	A	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2000174	cttgaattattattta[C/T]gctcattactacttta	C	T	// 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 1227026 // --- // --- // -	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2000380	ctagtgaactgttata[C/T]agtaattgcgcatcac	C	T	ENST00000342241 // intron // 0 // --- // --- // --- // ---	-	q11.22
SNP_A-2001640	attctaactcatttaa[C/T]acaacaatcatatgat	C	T	6240 // Homo sapiens ribonucleotide reductase M1 polypeptide (RRM1), mRNA. /// ENST00000300738 //	RRM1	RRM1, Homo sapiens ribonucleotide reductase M1 polypeptide (RRM1), p15.4
SNP_A-2038214	aacacattctgggtca[A/C]atatttaggatggata	A	C	sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2043218	aactgccctattccaa[C/T]actgatgcttttgtag	C	T	Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA. /// ENST00000265963 // intron // 0 // --- // --- // --- // ---	GTF2H1	GTF2H1, Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), p15.1
SNP_A-2021350	aaaaaactcttgagag[A/G]atcacatcatactgac	A	G	ENST00000261630 // intron // 0 // --- // --- // --- // ---	-	q12.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2016007	cattaacagccttcaa[A/G]attttccttcactac	A	G	/// ENST00000331037 // downstream // 888531 // --- // --- // ---	-	q21.1
SNP_A-2008196	agggaaaggaaatggc[A/C]gacaggaaatggcaag	A	C	Homo sapiens protein phosphatase 1F (PP2C domain containing) (PPM1F), mRNA. /// ENST00000263212 // intron	PPM1F	PPM1F, Homo sapiens protein phosphatase 1F (PP2C domain containing) (PPM1F), q11.22
SNP_A-2049020	aagccttctcaacata[C/T]attttcttccaagat	C	T	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri, p11.2
SNP_A-2072070	acagagtggtcagaaaa[C/T]gcttctgctaccattt	C	T	// 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 1209501 // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2094574	agaatacatatctaca[C/G]tcttacctacataata	C	G	Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST00000264731 // 3UTR // 0 // --- // --- // --- // ---	TP73L	TP73L, Homo sapiens tumor protein p73-like (TP73L), q28
SNP_A-2093587	agaagaacatttggaa[C/T]caaggaggtacagggt	C	T	118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// NM_020799 // upstream // 9462 //	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31
SNP_A-2107527	agctagtagtccctttt[A/T]aaaggaagtgacatca	A	T	Homo sapiens putative NFkB activating protein (FLJ20241), mRNA. /// ENST00000318003 // intron // 0 // --- // --- // ---	FLJ20241	FLJ20241, Homo sapiens putative NFkB activating protein (FLJ20241), p13.12
SNP_A-2125579	agtttcagtggctttc[A/C]atttcctgtttgatct	A	C	Homo sapiens SET and MYND domain containing 2 (SMYD2), mRNA. /// ENST00000313573 // CDS // 0 // --- // ---	SMYD2	SMYD2, Homo sapiens SET and MYND domain containing 2 (SMYD2), q41
SNP_A-2126724	ataaacctgcaagaaa[C/T]gaatcctgggcccaga	C	T	C1GALT1 // 56913 // Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), mRNA. /// NM_019005 // upstream // 185279 //	C1GALT1	C1GALT1, Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), p21.3
SNP_A-2149902	atgtcactaaatccig[A/T]actgcaaaaccaccgca	A	T	Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // intron // 0 // --- // --- // --- // ---	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2146531	atgctgaggtttgagg[C/T]atgaatgatcccatca	C	T	// 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// NM_004225 // downstream // 39348 // Hs.379414 // MFHAS1	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-2160256	atttcactattgcatt[A/C]aaattctaagattat	A	C	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2178016	taatgatatcagttta[C/T]cccacatctgttgtc	C	T	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 150879 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2192597	catccaggagttatga[A/T]tatttcagacacggcctc	A	T	Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2197045	cattatgcttaattat[C/G]aattacaaagtatact	C	G	Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA. /// ENST00000336047 // intron // 0 // --- // ---	NEK1	NEK1, Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), q33
SNP_A-2216993	cctctgtgatcttcac[C/G]aatacacactgcaatgc	C	G	4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 73378 // Hs.21388 // ZDHHC21	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2203609	ccagacacgttgccca[A/G]aggcgccatcagacct	A	G	79705 // Homo sapiens leucine-rich repeat kinase 1 (LRRK1), mRNA. /// NM_014918 // downstream // 90282 // Hs.110488	LRRK1	LRRK1, Homo sapiens leucine-rich repeat kinase 1 (LRRK1), q26.3
SNP_A-1829908	taataagttctgaaaa[C/T]ggtaaatgaaaggaag	C	T	ENST00000344513 // intron // 0 // --- // --- // ---	-	p13
SNP_A-1833180	tacacccgtagcagc[A/C]aagtttctaatcaagt	A	C	119679 // Homo sapiens olfactory receptor, family 52, subfamily J, member 3 (OR52J3), mRNA. /// NM_001005165 // downstream // 14465 // --- // OR52E4 // 390081 // Homo	OR52J3	OR52J3, Homo sapiens olfactory receptor, family 52, subfamily J, member 3 (OR52J3), p15.4
SNP_A-1826010	taaatggtgacacttc[G/T]cagtgacaatcagcct	G	T	FLJ40448 // 339059 // Homo sapiens hypothetical protein FLJ40448 (FLJ40448), mRNA. /// NM_030928 // upstream //	FLJ40448	FLJ40448, Homo sapiens hypothetical protein FLJ40448 (FLJ40448), q24.3
SNP_A-1790759	gggggacaaggatgaa[A/G]gctgtgtcagtgaagg	A	G	sapiens propionyl Coenzyme A carboxylase, alpha polypeptide (PCCA), mRNA. /// ENST00000310787 // intron //	PCCA	PCCA, Homo sapiens propionyl Coenzyme A carboxylase, alpha polypeptide (PCCA), q32.3
SNP_A-1797077	ggttctgtgaagact[A/G]aatgaggtgatattat	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1812242	gtggataattggaaatt[C/G]aacaaatttaaaattt	C	G	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 4 (RAPGEF4), mRNA. /// ENST00000264111 // intron // 0 // --- // --- // --- // --- // ENST00000354762 // intron // 0 // ---	RAPGEF4	RAPGEF4, Homo sapiens Rap guanine nucleotide exchange factor (GEF) 4 (RAPGEF4), q31.1
SNP_A-1808275	gtctttggaggctaa[C/T]gctggtaattggcttc	C	T	ENST00000358001 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1969594	tatgattaatatgtaa[A/G]agtctctaatgagaaa	A	G	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 507069	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1981751	actcagtttggagaac[A/G]aatggtatggttatcc	A	G	Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1952127	tttctcacttatctat[C/T]aaactgtccaaaccag	C	T	Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1938828	ttgaggaggttgaatg[C/T]aaactcttaggaattc	C	T	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 262115 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-1940051	ttgcagctgcattcta[C/T]gagtcttcaccaacct	C	T	Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. /// ENST00000272983 // intron // 0 // --- // -	PPP1R7	PPP1R7, Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), q37.3
SNP_A-1877192	tctgcttatgtgccca[A/T]gcagaaaaaaaattat	A	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 923359 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1876962	tctgcctccgccccaa[C/T]gaatcctctggtttat	C	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 267451 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1890107	tgatattaaatcttaa[C/T]gctactctctcatgactt	C	T	/// ENST00000360919 // upstream // 242392 // --- // --- // --- // -	-	q13.1
SNP_A-1901789	tggcactagttttccc[A/G]cctccagctctcaaca	A	G	255394 // Homo sapiens hypothetical protein MGC40368 (MGC40368), mRNA. /// ENST00000299045 // intron // 0 // ---	MGC40368	MGC40368, Homo sapiens hypothetical protein MGC40368 (MGC40368), q23.3
SNP_A-1916064	tgttgctaaatttcag[A/G]cactattctttaagtc	A	G	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000340635 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-1904498	tggggaggcaagatta[A/G]gagtaaaatcaatagc	A	G	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 10697 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2234538	ctccacgctcctcctc[A/G]cagacgagactggcat	A	G	// Homo sapiens bone morphogenetic protein 7 (osteogenic protein 1) (BMP7), mRNA. /// NM_012444 // upstream //	BMP7	BMP7, Homo sapiens bone morphogenetic protein 7 (osteogenic protein 1) (BMP7), q13.31
SNP_A-2253827	cttgaagcagattttc[A/G]caagtacttcctataa	A	G	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 714266	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2283574	gatagaaatccaggca[C/G]agccattgatactgac	C	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 545811 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2280332	gaggggaggtcattaa[G/T]ctgcctaaggtttccc	G	T	56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 4371 // Hs.517155 // TMEPAI //	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2309533	ggaaaccccaactaaa[A/G]gtggcctaatttatgc	A	G	Homo sapiens myosin X (MYO10), mRNA. /// ENST00000274203 // intron // 0 // --- // --- // --- // ---	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-2306386	gctggggcagcaggaa[A/G]acgccaaaagaaaaga	A	G	Homo sapiens G protein-coupled receptor 114 (GPR114), mRNA. /// AK160368 // CDS // 0 // Hs.187884 // GPR114 //	GPR114	GPR114, Homo sapiens G protein-coupled receptor 114 (GPR114), q13
SNP_A-2291673	gcacacagaatgaaac[A/G]gagaaaaagagagaag	A	G	Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA. /// ENST00000334456 // 3UTR // 0 // --- // ---	PDE2A	PDE2A, Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), q13.4
SNP_A-2260263	gaaaatgtgactggtc[C/T]gaaataagacatgctg	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-2253719	cttgaaacatttgata[C/T]agtagacctctaacat	C	T	285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// ENST00000295268 // intron // 0 // ---	MGC46496	MGC46496, Homo sapiens hypothetical protein MGC46496 (MGC46496), q22.3
SNP_A-2256077	ctttacaggagccaaa[A/G]tactgccttgttgcta	A	G	55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // downstream // 238048 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.2
SNP_A-2237058	ctctatttctggtcac[A/G]acaccatcgtcctctg	A	G	Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // --- // --- // --- // --- ///	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2240110	ctgaagtagctctgcc[A/G]atttctgtgttgaagt	A	G	// 3283 // Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), mRNA. /// ENST00000235547 // downstream //	HSD3B1	HSD3B1, Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), p12
SNP_A-2240882	ctgagaatttattcca[C/T]ataccagagagggctg	C	T	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-2228761	ctagagaaatagctac[A/G]gacttgcaaaacagtt	A	G	sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// ENST00000297693 // intron // 0 // --- //	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-1918986	ttaacctcctccacta[A/C]atccttagcttccaaa	A	C	Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA. /// ENST00000262570 //	CHCHD3	CHCHD3, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), q33
SNP_A-1911511	tgtctttccacccctg[A/G]aactcatttttctgaa	A	G	Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1914633	tgttaagttgtggcca[A/G]tatctccaagacgaac	A	G	sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // --- // ---	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-1928358	tcccagtccaaccgta[A/C]caaaaaacagtatcag	A	C	C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1927359	ttcaaacctaggcagc[G/T]ctttctgattctagaa	G	T	// 4762 // Homo sapiens neurogenin 1 (NEUROG1), mRNA. /// NM_004887 // downstream // 9920 // Hs.483444 // CXCL14	NEUROG1	NEUROG1, Homo sapiens neurogenin 1 (NEUROG1), q31.1
SNP_A-1923207	ttagctcccatttata[A/G]acggacacacaggatt	A	G	5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 239352 // Hs.446083 // PTPRD // 5789 // Homo	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1920220	ttaatgaagacagcac[A/G]gtccatgagcatctca	A	G	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine q12.3
SNP_A-1898431	tgcttcctgtcagatc[A/G]gagtgcaactcaagtg	A	G	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 194226 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-1934127	ttctcagttatttaca[C/T]gcttacctggagaata	C	T	5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 158452 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1936053	ttcttagtaagcaacc[A/G]cctagttctccaatac	A	G	// 57118 // Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 //	CAMK1D	CAMK1D, Homo sapiens calcium p13
SNP_A-1959466	ttttgcctgtctggaa[A/C]tctcttccacatgatt	A	C	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1971739	gatccctcagccagaa[C/T]gtttaagagttcaagt	C	T	491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 15337 // Hs.268942 // ATP2B2	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-1975504	gcttgacttggtctca[C/T]gctaccattccacact	C	T	6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ENST00000313571 // upstream // 64443	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-1808102	gtcttgccttttgca[A/G]ctttaagattgatcag	A	G	Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, mRNA. /// ENST00000263049 // intron // 0 // --- // --- // --- // ---	AKAP7	AKAP7, Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, q23.2
SNP_A-1792232	gggttcaagatggctg[A/C]acgatatggagggtgg	A	C	ENST00000341827 // intron // 0 // --- // --- // --- // ---	-	p13.31
SNP_A-1821562	gtttgtaggtttgata[C/T]gataatcacagaaaaa	C	T	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, mRNA. /// NM_003401 // intron // 0 // Hs.171190 // XRCC4 // 7518 // Homo sapiens X	XRCC4	XRCC4, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, q14.2
SNP_A-1834040	tacatatgatatgtat[A/G]aatgtaagatatgtat	A	G	11177 // Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 2, mRNA. /// NM_013448 // upstream // 38366 // Hs.509140 // BAZ1A //	BAZ1A	BAZ1A, Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 2, q13.2
SNP_A-1835136	taccctgctaccagaa[A/G]gatacctaaaaatccc	A	G	5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // downstream //	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1
SNP_A-1840708	tagcgtatcatcaaca[C/T]gggctggtggtgccag	C	T	9698 // Homo sapiens pumilio homolog 1 (Drosophila) (PUM1), mRNA. /// NM_024522 // downstream // 52117 //	PUM1	PUM1, Homo sapiens pumilio homolog 1 (Drosophila) (PUM1), p35.2
SNP_A-1837244	tacttacacaaatctg[A/G]atggtaacatctttta	A	G	Homo sapiens HBS1-like (S. cerevisiae) (HBS1L), mRNA. /// ENST00000257985 // intron // 0 // --- // --- // --- // ---	HBS1L	HBS1L, Homo sapiens HBS1-like (S. cerevisiae) (HBS1L), q23.3
SNP_A-1847296	tatccaggccatgacc[A/G]aggccatgtgggaagc	A	G	Homo sapiens selenocysteine lyase (SCLY), mRNA. /// ENST00000254663 // CDS // 0 // --- // --- // --- // ---	SCLY	SCLY, Homo sapiens selenocysteine lyase (SCLY), q37.3
SNP_A-1861242	tcatatttaaatgttc[A/G]agataatgtctcaata	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 347241 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2213248	ccgcctccttactcca[C/T]gttggttcttgcaaac	C	T	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 420423 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2223671	cggatgcccgagtcgg[C/G]aagaaaggctggaggg	C	G	LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 //	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2185033	cagcttgtacatgtga[G/T]actttttcagcctccat	G	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2188560	cagtgagttcaaagac[C/T]ggtcaattgagattat	C	T	10111 // Homo sapiens RAD50 homolog (S. cerevisiae) (RAD50), transcript variant 1, mRNA. /// NM_133482 //	RAD50	RAD50, Homo sapiens RAD50 homolog (S. cerevisiae) (RAD50), transcript variant 1, q23.3
SNP_A-2172494	caattccaaagtttca[A/G]tctcattggaattaca	A	G	4122 // Homo sapiens mannosidase, alpha, class 2A, member 2 (MAN2A2), mRNA. /// ENST00000360468 //	MAN2A2	MAN2A2, Homo sapiens mannosidase, alpha, class 2A, member 2 (MAN2A2), q26.1
SNP_A-2169665	caaggaaagtgaagga[A/G]aaaatgatcaacatga	A	G	Homo sapiens Dmx-like 1 (DMXL1), mRNA. /// ENST00000311085 // intron // 0 // --- // --- // --- // ---	DMXL1	DMXL1, Homo sapiens Dmx-like 1 (DMXL1), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2155521	attcatttcttatcaa[A/G]agctacccatatctag	A	G	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 579115 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-2153233	attactgccacatgaa[A/G]aacatttaagcatggc	A	G	55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 420086 // --- // ---	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-2167826	caacctccactctaac[A/T]ccacttccacgctgac	A	T	IGHMBP2 // 3508 // Homo sapiens immunoglobulin mu binding protein 2 (IGHMBP2), mRNA. /// NM_198923 //	IGHMBP2	IGHMBP2, Homo sapiens immunoglobulin mu binding protein 2 (IGHMBP2), q13.3
SNP_A-2125759	tactaagtgtacacta[C/T]gtgtgctgataggttg	C	T	Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 //	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-2130595	atactgactaaaatcc[A/G]ggaagaatgacattta	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2122278	agtgcagtatgcaatg[C/T]actatgtttaatctc	C	T	389012 // Homo sapiens FLJ42986 protein (FLJ42986), mRNA. /// NM_004834 // upstream // 204944 // Hs.431550 //	FLJ42986	FLJ42986, Homo sapiens FLJ42986 protein (FLJ42986), q11.2
SNP_A-2107873	agctccagcgcaaatg[A/G]aaagacaggaagacca	A	G	// Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), mRNA. /// ENST00000295608 // upstream //	CD2	CD2, Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), p13.1
SNP_A-2107109	agcggagataaggaca[C/T]tcagacctgtttccct	C	T	Homo sapiens fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus) (FSCN2), mRNA. /// ENST00000334850 // intron // 0 // --- // --- // ---	FSCN2	FSCN2, Homo sapiens fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus) (FSCN2), q25.3
SNP_A-2098922	agagctgttggtaata[A/C]attgttctaccaaagg	A	C	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2097364	tctaaaattagatagt[C/G]gttatggcctcacaac	C	G	Homo sapiens potassium channel tetramerisation domain containing 10 (KCTD10), mRNA. /// ENST00000228495 // intron // 0 // --- // --- // --- // ---	KCTD10	KCTD10, Homo sapiens potassium channel tetramerisation domain containing 10 (KCTD10), q24.11
SNP_A-2080858	acctctaggaaaattaa[A/T]attggagctgaagaac	A	T	283514 // Homo sapiens similar to seven in absentia 2 (LOC283514), mRNA. /// ENST00000332325 // intron // 0 // ---	LOC283514	LOC283514, Homo sapiens similar to seven in absentia 2 (LOC283514), q14.13
SNP_A-2074180	acataaatgattgaaa[A/G]gaatgagttaaacat	A	G	ANTXR1 // 84168 // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, mRNA. /// NM_053034 //	ANTXR1	ANTXR1, Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, p13.3
SNP_A-2017407	gactcacactgtgca[C/T]agcataaaatctgatt	C	T	// 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-1995651	gttagagactcttgaa[G/T]ggataagaacaccaag	G	T	Homo sapiens solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	SLC1A1	SLC1A1, Homo sapiens solute carrier family 1 (neuronal p24.2
SNP_A-1996078	tcaaagagccgagtga[C/T]actgccaaatactacc	C	T	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// ENST00000315856 // intron // 0 // --- // --- // ---	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1993716	cactatgttaaaccccc[A/G]agagacagcaaagaag	A	G	/// ENST00000357074 // downstream // 187129 // --- // --- // --- // --- /// ENST00000358765 // downstream // 187129 // --- // ---	-	p14
SNP_A-2022505	aaaaatccatccatgc[A/G]aaaagaagtctaggct	A	G	sapiens complement component 9 (C9), mRNA. /// ENST00000263408 // intron // 0 // --- // --- // ---	C9	C9, Homo sapiens complement component 9 (C9), p13.1
SNP_A-2024220	aaaagcaaggtgacag[A/G]agagagcacataaaaa	A	G	Homo sapiens malate dehydrogenase 1B, NAD (soluble) (MDH1B), mRNA. /// ENST00000260972 // intron // 0 // --- // ---	MDH1B	MDH1B, Homo sapiens malate dehydrogenase 1B, NAD (soluble) (MDH1B), q33.3
SNP_A-2023923	aaaagaatggaagaaa[A/G]agatatcagtccttcc	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2040253	aaccacagggagaaat[C/G]aagcctcgttagaata	C	G	6760 // Homo sapiens synovial sarcoma translocation, chromosome 18 (SS18), mRNA. /// X79201 // downstream //	SS18	SS18, Homo sapiens synovial sarcoma translocation, chromosome 18 (SS18), q11.2
SNP_A-2036901	aaatttggagcaatca[C/T]gacttaaaccaggagt	C	T	ENST00000287474 // intron // 0 // --- // --- // ---	-	p21.2
SNP_A-2028318	aaactcacaagagaaa[G/T]aatacaattagaaaat	G	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 346719 // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2030708	aaagctgggttaaatc[C/T]gaagtatcagggtcag	C	T	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2002201	taaaatagacttaaca[A/T]ctccataaatttgtg	A	T	Homo sapiens CARD only protein (COP), mRNA. /// NM_033293 // intron // 0 // Hs.2490 // CASP1 // 834 // Homo	COPI	COPI, Homo sapiens CARD only protein (COP), q22.3
SNP_A-2006727	tgactggtgaagttac[A/G]ggcccctgagttaa	A	G	Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-2006752	tcttaaaatatttata[A/C]catttgccaattgat	A	C	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 153906 // Hs.128575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2071281	acacttcctcattttg[A/C]atattaataataagaa	A	C	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2063791	aattagcctgggctta[C/T]ggatttaagaagaag	C	T	LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream // 7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// NM_003667 // upstream // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // ENST00000301831 // intron // 0 // --- // --- // ---	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2067347	acaaataaaaatcataaa[A/G]gatgcaatatacaa	A	G		TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-2049738	aagctttagtcatga[C/T]agaaaggaaaggagc	C	T		IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-2053691	aagtgggaaggtaga[C/G]aaagatagaaactacc	C	G		-	p22.1
SNP_A-2058211	aatcaacatggtagac[A/G]gacattatactgaatt	A	G	26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream // 4829 // Homo sapiens neuromedin B receptor (NMBR), mRNA. /// ENST00000354295 // downstream // 30809 // --- // ---	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2058962	aatccataaaacatca[A/C]aattgttccttaala	A	C		NMBR	NMBR, Homo sapiens neuromedin B receptor (NMBR), q24.1
SNP_A-2082951	acgtgatgcagttccc[C/G]cgactcaaaaactcca	C	G	ENST00000357304 // intron // 0 // --- // --- // ---	-	q34.13
SNP_A-2120137	agtcagacaattgcaa[A/C]tcagagagctaaatctc	A	C	162394 // Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA. /// ENST00000299977 // intron // 0 // --- // ---	MGC19764	MGC19764, Homo sapiens hypothetical protein MGC19764 (MGC19764), q12
SNP_A-2117837	aggttggtggatatca[C/T]gaggcagaaaggaga	C	T	ATP6V1A // 523 // Homo sapiens ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A (ATP6V1A), mRNA. /// ENST00000273398 // downstream // 11420 // --- // --- // ---	ATP6V1A	ATP6V1A, Homo sapiens ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A (ATP6V1A), q13.31
SNP_A-2127289	ataaatgtctctaaca[C/T]aatacttagcacatct	C	T	8654 // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, mRNA. /// NM_033437 //	PDE5A	PDE5A, Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, q26
SNP_A-2136234	atcaatctagcaaac[A/G]aattactggcctcaaa	A	G	sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // 3UTR // 0 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2133733	atatccatgggtcac[A/G]cagtattatttgtgt	A	G	Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// ENST00000354370 // intron // 0 // --- // ---	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2138340	atccagctgtcttttca[C/T]gaagccatatattaaa	C	T	Homo sapiens tuberous sclerosis 1 (TSC1), mRNA. /// ENST00000298552 // intron // 0 // --- // --- // ---	TSC1	TSC1, Homo sapiens tuberous sclerosis 1 (TSC1), q34.13
SNP_A-2181241	cagaccacgttgatga[C/T]gaattagctctaatgg	C	T	10077 // Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, mRNA. /// NM_005705 //	PHEMX	PHEMX, Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, p15.5
SNP_A-2189734	cataaaaaagtcgata[A/G]aatgattcttccaac	A	G	4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 245870 // Hs.154329 // 10920 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, mRNA. /// NM_006710 // downstream // 190791 // Hs.531713 // COPS8 // 10920 /	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2222545	cgaggtcggcctcata[C/T]cgcacagttcagactc	C	T		COPS8	COPS8, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, q37.3
SNP_A-2202627	ccacctctgatgaac[C/G]attactgccatctcac	C	G	MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// NM_183049 // upstream // 6206 // Homo sapiens ribosomal protein S12 (RPS12).	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2212107	cctgccggcccttca[C/T]tacccttcctagactc	C	T	mRNA. /// NM_172104 // upstream // 319550 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1859173	tcagccttttataac[C/T]agactgatgctcttcc	C	T	83595 // Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), mRNA. /// NM_017884 // downstream // 3245 //	SOX7	SOX7, Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), p23.1
SNP_A-1856787	tcacattactatcca[A/G]cagttgtcaggaaat	A	G	25836 // Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, mRNA. /// NM_015384 //	NIPBL	NIPBL, Homo sapiens Nipped-B homolog (Drosophila) (NIPBL), transcript variant A, p13.2
SNP_A-1821474	gtttgggaggaggagt[A/G]acaagacaaggatat	A	G	1029 // Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 1, mRNA. /// NM_058197 // upstream // 23695 // Hs.512599 //	CDKN2A	CDKN2A, Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 1, p21.3
SNP_A-1792773	ggtaaggagcaaaatc[A/G]ctctgctgtaagatt	A	G	Homo sapiens Ellis van Creveld syndrome 2 (limbin) (EVC2), mRNA. /// ENST00000344938 // intron // 0 // --- // --- // ---	EVC2	EVC2, Homo sapiens Ellis van Creveld syndrome 2 (limbin) (EVC2), p16.2
SNP_A-1785421	ggctatttggattgaa[A/C]ccaaaaaactcaactct	A	C	Homo sapiens phosphatidylinositol transfer protein, cytoplasmic 1 (PITPNC1), transcript variant 2, mRNA. /// NM_012417 // intron // 0 // Hs.231295 // PITPNC1 // 26207 // NM_182761 // downstream // 82416 // Hs.434682 //	PITPNC1	PITPNC1, Homo sapiens phosphatidylinositol transfer protein, cytoplasmic 1 (PITPNC1), transcript variant 2, q24.2
SNP_A-1676352	cattgatgtaagctctcagagaacc[A/G]gatctcactccttttggattacacat	A	G	LOC340069 // 340069 // hypothetical protein LOC340069	LOC340069	LOC340069 , rs105196607, hypothetical protein LOC340069,q23.1
SNP_A-1643403	tgtaaatcaaatgatagtttaatac[A/G]aggcaagagctgcaaagacatctga	A	G	NM_024751 // intron // 0 // Hs.126119 // FLJ13273 // 79807 // hypothetical protein FLJ13273	FLJ13273	FLJ13273 , -, hypothetical protein FLJ13273,q24
SNP_A-1982412	atagtgataatacaga[A/C]taacctaacatttgta	A	C	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000247655 // downstream // 49106 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1951449	tttcctcagctatgta[A/G]agtctgctgatgagct	A	G	/// ENST00000341548 // downstream // 8567 // --- // --- // --- //	-	q22.33
SNP_A-1936600	ttcttggcacaacata[A/C]aacagaaggaatttgg	A	C	4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 436885 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1942826	ttggggacgtggaaaa[A/C]ggaggcattagcaggt	A	C	Human T-cell receptor rearranged beta-chain V-region (V-D-J) mRNA, complete cds. /// NM_002769 // downstream //	-	-, Human T-cell receptor rearranged beta-chain V-region (V-D-J) complete cds. q34
SNP_A-1890681	tgatgactgagagggc[A/G]gactgcatggttccca	A	G	2166 // Homo sapiens fatty acid amide hydrolase (FAAH), mRNA. /// NM_147192 // upstream // 71621 // Hs.375623 //	FAAH	FAAH, Homo sapiens fatty acid amide hydrolase (FAAH), p33
SNP_A-1874087	tctcatgtttggtctg[A/G]aaaacaggatgaacat	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 379803 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1878734	tctgttctagttaaaa[A/C]acgtcagataaggaac	A	C	Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000331968 // intron // 0 // --- // --- // --- // ---	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-1881564	tctttctttaaagcaa[A/G]tgacccacttctaaaa	A	G	5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// NM_001430 // upstream // 42982 // Hs.468410 //	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-1926154	ttattaaattaacaca[A/C]atgcttttctctttat	A	C	23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 24170 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2250614	cttagttgcaaataga[A/C]taccaatcaatgatgt	A	C	2743 // Homo sapiens glycine receptor, beta (GLRB), mRNA. /// NM_000826 // upstream // 35330 // Hs.32763 // GRIA2 //	GLRB	GLRB, Homo sapiens glycine receptor, beta (GLRB), q32.1
SNP_A-2252162	cttccatcttgcaaat[A/G]atgcccagcccttact	A	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2245090	ctggccaggtgcaata[C/G]ctcacgcctgtaatcc	C	G	// 1381 // Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), mRNA. /// NM_004136 // upstream // 53813 //	CRABP1	CRABP1, Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), q25.1
SNP_A-2266622	gaagtccttctgccca[A/T]atcctggctttatcag	A	T	ENST00000355787 // intron // 0 // --- // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2290181	gcaaatgtattaccac[A/G]atcggcatcagcttca	A	G	// 91662 // Homo sapiens NACHT, leucine rich repeat and PYD containing 12 (NALP12), mRNA. /// NM_144687 //	NALP12	NALP12, Homo sapiens NACHT, leucine rich repeat and PYD containing 12 (NALP12), q13.42
SNP_A-2305159	gctgaccccaccttat[A/G]acccacaaagtgccag	A	G	54843 // Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, mRNA. /// NM_032379 // upstream //	SYTL2	SYTL2, Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, q14.1
SNP_A-2312216	ggacaggatagtagca[A/G]aggaagaatatagccc	A	G	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2271077	gacatagagacatcta[A/C]ggaaaacccaaagtgt	A	C	11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2271292	gacattaatgcctgga[G/T]agtgacctgatggctc	G	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 739573 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2259622	gaaaactaggaatcag[A/G]aacattaatctggcaa	A	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 76791 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2262869	gaacaaagaaataaac[A/G]gaggagaaaggacagc	A	G	57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 283047 //	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-2278849	cccattccattctgtg[A/T]aggaagaaaccctgag	A	T	Homo sapiens rai-like protein (RaLP), mRNA. /// ENST00000332408 // intron // 0 // --- // --- // --- // ---	RaLP	RaLP, Homo sapiens rai-like protein (RaLP), q21.1
SNP_A-2255660	cttgttactgtccaca[A/G]atatgtgtgtggttgc	A	G	9324 // Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, mRNA. /// NM_004242 // upstream // 35245 // Hs.77558 // HMGN3 //	HMGN3	HMGN3, Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, q14.1
SNP_A-2236493	ctcggtgaacaggtta[A/T]aaaccactgaatctta	A	T	// 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 340686 // --- // --- // --- //	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-1927579	ttcaacaggaaaatat[A/G]aggttgcactgtccat	A	G	137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// ENST00000330777 // upstream // 143185 // --- // --- // --- // ---	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-1920599	ttaatttgaggcaaca[C/T]atttgtaaatgttttg	C	T	SLC29A3 // 55315 // Homo sapiens solute carrier family 29 (nucleoside transporters), member 3 (SLC29A3), mRNA. /// NM_022124 // upstream // 15875 // Hs.546421 // CDH23 //	SLC29A3	SLC29A3, Homo sapiens solute carrier family 29 (nucleoside transporters), member 3 (SLC29A3), q22.1
SNP_A-1921312	ttacattttcaagtac[G/T]atcaataacaacattt	G	T	// 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 32039 // Hs.42650 //	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1914535	tgttaaagctgaatga[A/G]caattaaattttccag	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 340708 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1907491	tgtaaagtttcagtag[A/G]atgctttggagagtgg	A	G	FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1878695	tctgttattgaaatga[G/T]aatgatagtaatcatg	G	T	ENST00000333644 // intron // 0 // --- // --- // ---	-	q35.2
SNP_A-1875004	tcictataaaatctcc[C/T]cttttgcagtcaaggaa	C	T	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1895309	tgcctgacattacta[C/G]ataggcagtttgcatt	C	G	694 // Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), mRNA. /// NM_001004330 // upstream //	BTG1	BTG1, Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), q22
SNP_A-1900640	tggaggccgaggttac[A/G]atgagcaaactaaca	A	G	// 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 594202 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1945286	ttgttaataggcagaa[A/G]tccagaaaggaaaaaaa	A	G	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1937629	ttgaagagacaaagaa[A/T]atcataagtaacagaa	A	T	Homo sapiens ankyrin repeat and MYND domain containing 2 (ANKMY2), mRNA. /// ENST00000306999 // intron // 0 // ---	ANKMY2	ANKMY2, Homo sapiens ankyrin repeat and MYND domain containing 2 (ANKMY2), p21.1
SNP_A-1950862	tttccaactgaagcta[A/C]attgtggctgcatatt	A	C	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1961890	gtagtaatgaagactc[C/T]aataattgtcctgtgg	C	T	128338 // Homo sapiens hypothetical protein MGC54289 (MGC54289), mRNA. /// ENST00000286692 // intron // 0 // ---	MGC54289	MGC54289, Homo sapiens hypothetical protein MGC54289 (MGC54289), p13.3
SNP_A-1982395	gggtggcaagctgcta[C/T]agaaccaggaagagct	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 316587 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1979793	ttccatgctaaggaga[C/T]aagtaatttttaag	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 461644 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1985005	cccaaatctgtatttta[C/T]agcacaaattactcat	C	T	9521 // Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA. /// NM_015948 // downstream	EEF1E1	EEF1E1, Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), p24.3
SNP_A-1798761	gtaactataatgaaag[C/G]ctatgtgtcataaatg	C	G	// 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 192572 // Hs.480596 // NDST3 //	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1857976	tcacttggcaggtca[C/T]atactgaaattggagt	C	T	341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// ENST00000342700 //	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-1864011	tccacacacatatgca[A/C]atctgtacatacacac	A	C	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2205413	ccagtgcaacggtgat[A/G]agagatgggaccigta	A	G	Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// ENST00000280625 // intron // 0 // --- // --- // ---	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-2206481	ccatctgctgtaccaa[A/C]aaatctagagacggct	A	C	// 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1876496 // Hs.27214 // KCNC2 // 3747 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2223979	cgggctactgcacccaa[C/G]taagcttgtgctccaa	C	G	Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA. /// ENST00000327801 // intron // 0 // --- // ---	SMYD3	SMYD3, Homo sapiens SET and MYND domain containing 3 (SMYD3), q44
SNP_A-2183083	cagcaaaatcaatgaa[C/T]ttcaaaacctcatgga	C	T	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2194887	catgctatgagctagg[A/G]aatcagcttaattgga	A	G	NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1472538 // ---	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2175365	ctgaaaccaaggaaga[C/T]gagagaagaaaacccca	C	T	10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. ///	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2146843	atgctttcatcacaaa[G/T]aatatatatcagtaa	G	T	Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // intron // 0 // --- // ---	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-2160973	atttcttaagatcaaa[A/C]accatacctcatttag	A	C	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 509912 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2128945	ataatgtaatgataaa[A/G]caagggtagagaggca	A	G	ENST00000354500 // intron // 0 // --- // --- // ---	-	q21.11
SNP_A-2112708	aggcagcattaacaa[C/T]gagtcctgaggtta	C	T	/// ENST00000311489 // downstream // 36748 // --- // --- // ---	-	q21.13
SNP_A-2078307	accatactgtgcacaa[A/G]gaagcattatgggacc	A	G	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2085462	actccacaagaccccc[A/G]atggtggagatggcgc	A	G	56897 // Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, mRNA. /// NM_020135 // upstream // 24974 // Hs.236828 // WRNIP1 // 56897 // Homo	WRNIP1	WRNIP1, Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, p25.2
SNP_A-2087031	actgagtaggtggtga[C/T]ggctttacagaaatag	C	T	Homo sapiens GRB2-related adaptor protein 2 (GRAP2), mRNA. /// ENST00000344138 // intron // 0 // --- // --- // --- // ---	GRAP2	GRAP2, Homo sapiens GRB2-related adaptor protein 2 (GRAP2), q13.1
SNP_A-2105271	agcattcttcctgcta[C/G]acccaaagaactctgc	C	G	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2102236	agattaataactaccc[A/C]caaatgtcttatgaat	A	C	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1485651 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2063984	aattatgaaaatgtaa[A/T]gcagattcaagaaaca	A	T	Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 4, mRNA. /// NM_025074 // intron // 0 // Hs.369448 // FRAS1	FRAS1	FRAS1, Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 4, q21.21
SNP_A-2074687	acatatccttcaccca[C/T]tctttgatggagttgt	C	T	// Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // --- // --- // --- // ---	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2075636	attcagcgtaaagtat[A/C]agagacattcttttca	A	C	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 11691 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2018953	tacacaatgtcaaaaa[C/T]gaaaaattagcaaacc	C	T	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA. /// NM_001001894 // intron // 0 //	TTC3	TTC3, Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, q22.13
SNP_A-2013094	ccctcatccactttta[C/T]agtgaccattcgcaaa	C	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // CDS // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1995925	tctcaaactgagatta[A/T]cttactgaacataaat	A	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3480811 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1989762	atatttgcttttaaca[A/G]atagctctgtgggcct	A	G	Homo sapiens SNARE protein Ykt6 (YKT6), mRNA. /// ENST00000223369 // intron // 0 // --- // --- // --- // ---	YKT6	YKT6, Homo sapiens SNARE protein Ykt6 (YKT6), p13
SNP_A-2031449	aaaggtaggtacacaa[C/T]caatcaaaagtttaaa	C	T	ENST00000341011 // intron // 0 // --- // --- // --- // ---	-	q21.31
SNP_A-2030141	aaagcaactcagtcaa[C/T]aaggtgaggccaccac	C	T	// 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1371142 // Hs.514980 // SALL3	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2021735	aaaaacagagaaatca[A/G]tgaggtgcattttgtg	A	G	2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 //	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2040045	aaccaaaaagaatttg[A/G]aaagcaataatttagt	A	G	HSD17B2 // 3294 // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// NM_005792 //	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-2044593	aagaaacctagaaaaa[C/T]tgatgatctaagtcac	C	T	Homo sapiens claudin 10 (CLDN10), transcript variant 1, mRNA. /// ENST00000257311 // intron // 0 // --- // --- // --- // ---	CLDN10	CLDN10, Homo sapiens claudin 10 (CLDN10), transcript variant 1, q32.1
SNP_A-2022734	aaaaattatgagcaaa[A/G]aaagcagtgaaggaga	A	G	Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 //	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-2021129	aaaaaaaatcctctca[C/T]attctaggcaaagctt	C	T	ENST00000355656 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2020963	ctgggcaagggtttgc[A/G]cagaagagagatggag	A	G	5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 336857 //	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2024231	aaaagcacattcactc[C/T]atcttctccaaagttg	C	T	FLJ39653 // 202020 // Homo sapiens hypothetical protein FLJ39653 (FLJ39653), mRNA. /// NM_001290 // downstream	FLJ39653	FLJ39653, Homo sapiens hypothetical protein FLJ39653 (FLJ39653), p15.32
SNP_A-2027541	aaaccacccacgtgtc[A/G]cagcatccacatcaag	A	G	23426 // Homo sapiens mRNA for GRIP1 protein. /// NM_018448 // upstream // 123857 // Hs.546407 // TIP120A //	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. ,q14.3
SNP_A-1992750	aagagcagtcctgaac[A/G]ctggtatcctgtctta	A	G	64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 346586 // Hs.146339 //	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2018968	aatattcatcagaacc[C/T]atgacaatttgctaag	C	T	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA. /// NM_001001894 // intron // 0 //	TTC3	TTC3, Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, q22.13
SNP_A-2017968	ctacagcgttctacca[C/T]ggactccaccaaggaa	C	T	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2076814	accaaaagttggttca[A/T]tgaaaagatcaacaaa	A	T	Homo sapiens KIAA1609 protein (KIAA1609), mRNA. /// ENST00000343629 // intron // 0 // --- // --- // --- // ---	KIAA1609	KIAA1609, Homo sapiens KIAA1609 protein (KIAA1609), q24.1
SNP_A-2070356	acaccagtgtttaaga[C/T]agcaaaagattgaatt	C	T	Homo sapiens neurobeachin (NBEA), mRNA. /// ENST00000310336 // intron // 0 // --- // --- // --- // ---	NBEA	NBEA, Homo sapiens neurobeachin (NBEA), q13.3
SNP_A-2052277	aagtaaggttacaact[C/T]agtcttttgcctttct	C	T	-- /// ENST00000340000 // upstream // 150938 // --- // --- // ---	-	p12.1
SNP_A-2103015	agcaaaggcaattcaa[A/G]gaaacaaatatagtct	A	G	Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA. /// ENST00000336047 // intron // 0 // --- // ---	NEK1	NEK1, Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), q33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098090	agagaggctcaaagag[A/G]aagataatagattagt	A	G	-- /// ENST00000329863 // downstream // 680400 // --- // --- //	-	q23.1
SNP_A-2093198	agaaccagaattatca[C/T]aggtgaagtaaaccag	C	T	306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 125243 // Hs.146551 // BMP2K //	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-2084855	actcaaattcacaata[A/T]atggtctgataagggt	A	T	Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2089743	acttccctgttctgga[C/T]gtctcttttatcacct	C	T	// 143496 // Homo sapiens olfactory receptor, family 52, subfamily B, member 4 (OR52B4), mRNA. /// NM_003141 // downstream // 6846 // Hs.532357 // TRIM21 // 6737 // Homo	OR52B4	OR52B4, Homo sapiens olfactory receptor, family 52, subfamily B, member 4 (OR52B4), p15.4
SNP_A-2079142	acccaggacctagcac[A/G]cagtgtctgtagagtc	A	G	94031 // Homo sapiens serine protease HTRA3 (HTRA3), mRNA. /// NM_003501 // downstream // 31981 // Hs.479122	HTRA3	HTRA3, Homo sapiens serine protease HTRA3 (HTRA3), p16.1
SNP_A-2127463	ataacacatacctcta[C/T]atccctcagaaagttt	C	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2135065	atattctagttatttg[C/G]aagaatgttggtcaaa	C	G	56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 207362 // Hs.315186 // PCSK2 //	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-2183035	cagatttgtcgttgcc[A/G]atttcagttgcagttc	A	G	2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 //	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2191070	catagtaaagcattca[A/G]tactaactattatgaa	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 460644 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2222530	cgagggcactatgacg[C/G]ccgggccagagtcctc	C	G	// Homo sapiens hypothetical protein LOC255104 (LOC255104), mRNA. /// ENST00000294543 // CDS // 0 // ---	LOC255104	LOC255104, Homo sapiens hypothetical protein LOC255104 (LOC255104), p36.13
SNP_A-2204778	ccaggcatagaataaa[C/T]ttaattgtagcttaga	C	T	Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // --- // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2208533	cccacggtgcaagcca[C/G]gtacatgatcatcttc	C	G	2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // upstream // 18059 // Hs.533683 // FGFR2 // 22	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.13
SNP_A-1866844	tcccgtgttgtgaatg[C/G]aaatggcaatggtgta	C	G	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-1873786	tctcagcattttgtcc[A/G]ctatatatgcttgggt	A	G	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-1855571	tcaataaaataaatta[C/T]ggtagccaacagtgct	C	T	6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// ENST00000329573 // upstream // 58744 // --- // --- // --- // ---	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q23.3
SNP_A-1851345	tattcattgtatctcc[A/G]gaacctagcatactta	A	G	// 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream //	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-1819510	gttggtcacagaggta[C/T]gtcacaataccaataa	C	T	7594 // Homo sapiens zinc finger protein 43 (HTF6) (ZNF43), mRNA. /// NM_178523 // upstream // 150542 // Hs.148374 //	ZNF43	ZNF43, Homo sapiens zinc finger protein 43 (HTF6) (ZNF43), p12
SNP_A-1817578	gttccaacttattcac[A/G]cactcattattttact	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 990996 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1814809	gtgtgtggaaatagag[C/T]cccaccataccaagca	C	T	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 265846 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-1825877	taaatgagatcaaccc[A/C]aagtttgtagctacta	A	C	// 10744 // Homo sapiens pituitary tumor-transforming 2 (PTTG2), mRNA. /// NM_004219 // downstream // 109797 //	PTTG2	PTTG2, Homo sapiens pituitary tumor-transforming 2 (PTTG2), q33.3
SNP_A-1823863	taaaatgggtataaaa[A/T]gcagatttaagaggca	A	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 551474 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1825576	taaatatacccactca[C/T]ggtgtggttggagagc	C	T	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // --- // --- // --- // ---	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1844084	tagttggagtttctgg[A/G]atttatcatttatttt	A	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1836803	tactgatatggttcca[A/G]tgcatcagaccaacgg	A	G	3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 37496 //	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-1834585	actcaggaacaggtac[A/C]atacttggcccatgaa	A	C	Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), mRNA. /// NM_152369 // upstream // 256314 //	F3	F3, Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), p21.3
SNP_A-1967875	agcttccccttgcacc[C/T]cctataatgacattga	C	T	-- /// ENST00000299455 // upstream // 145954 // --- // --- // ---	-	p12.1
SNP_A-1964973	tatggtcactaaatga[A/G]taacaaggaaaataac	A	G	Homo sapiens zinc finger, RAN-binding domain containing 3 (ZRANB3), mRNA. /// ENST00000264159 // intron // 0 // --- // -	ZRANB3	ZRANB3, Homo sapiens zinc finger, RAN-binding domain containing 3 (ZRANB3), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1951433	tttcctattatagctg[C/T]aatggtaaccaactct	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1938256	ttgaccctgatggaga[A/G]aactctactctatcct	A	G	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// ENST00000342389 // intron // 0 // --- // --- // --- // ---	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-1937230	ttgaaaatatgaattg[A/T]actgcaaaagctagac	A	T	// 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 450288	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-1933454	ttctaccataggcaga[G/T]atgcagtggctaaaat	G	T	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 183384 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-1946549	tttaaataggtgggaa[A/G]tgatccatttttctct	A	G	Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), mRNA. /// BC003044 // intron // 0 // Hs.495138 // MAPKAP1 // 79109 // Homo sapiens mitogen-	MAPKAP1	MAPKAP1, Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), q33.3
SNP_A-1941760	ttggaattctgagcta[A/C]gagagcctgcagttgg	A	C	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1888917	tgaggtggtagactaa[A/T]attcgtacttgctacc	A	T	83643 // Homo sapiens coiled-coil domain containing 3 (CCDC3), mRNA. /// NM_021980 // upstream // 3399 //	CCDC3	CCDC3, Homo sapiens coiled-coil domain containing 3 (CCDC3), p13
SNP_A-1904695	tgggggcagcagatga[C/G]agttacagtgaaattc	C	G	// 221393 // Homo sapiens G protein-coupled receptor 115 (GPR115), mRNA. /// NM_181744 // upstream // 42184 //	GPR115	GPR115, Homo sapiens G protein-coupled receptor 115 (GPR115), p12.3
SNP_A-2239207	ctcttgctttttagcc[G/T]ggatgcagttggtcaa	G	T	Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), mRNA. /// NM_021007 // intron // 0 // Hs.470470 //	SCN1A	SCN1A, Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), q24.3
SNP_A-2231297	ctattcccagttctta[A/T]ggcagtctgaaccctg	A	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2242269	ctgcaagtttctttttc[A/C]cacattgctgtttccc	A	C	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 73241 // Hs.129701 //	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2273340	gactccgtctcaaaac[A/G]aaataagaatattagc	A	G	Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2275080	gagaagaacttaaaag[A/C]aacaaagtatggagcc	A	C	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), mRNA. /// ENST00000262367 //	CREBBP	CREBBP, Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), p13.3
SNP_A-2280533	gaggtacagaggtgtc[C/T]agttacttccccaaag	C	T	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2259932	gaaaagtaaattaaaa[C/T]tggccatagttcatga	C	T	25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // --- // --- // --- // --- ///	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2267762	gaatcatgggctaata[G/T]aagtcaccaagaggaa	G	T	22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// NM_207015 // upstream // 519688 // Hs.416922 //	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. q26.31
SNP_A-2312677	ggactagaatgggtgc[A/G]aggtggaataggctag	A	G	sapiens JTV1 gene (JTV1), mRNA. /// ENST00000223029 // intron // 0 // --- // --- // --- // ---	JTV1	JTV1, Homo sapiens JTV1 gene (JTV1), p22.1
SNP_A-2300858	gcctggtttagaggca[G/T]taatttcctaatgaga	G	T	// Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319953 // downstream // 61465 // --	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-2291455	gcaattctgaaatcca[A/G]tagaacagacattaaa	A	G	/// ENST00000310012 // upstream // 153132 // --- // --- // --- // -	-	q12
SNP_A-2264706	gaagacagtaggtcaa[C/G]aacagagccattcttg	C	G	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA. /// NM_033044 // intron // 0 // Hs.472475 // MACF1 // 23499 // Homo sapiens	MACF1	MACF1, Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, p34.3
SNP_A-2262268	attggaaatggctgaa[A/C]accaagttgcaaatct	A	C	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 491946 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-2284885	gatccagagatacata[A/C]attttctaagttacac	A	C	Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRNA. /// ENST00000256084 // intron // 0 // --- // --	SPINK5	SPINK5, Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), q32
SNP_A-2286255	gatgccatttcacaca[C/T]gaacaaaattatcgat	C	T	5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 450873 // Hs.115474 // RFC3 // 5983 // Homo	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-2287284	gatgtgcacattgggt[A/T]aactggcccagaatga	A	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1645005 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2248045	ctgtgcttgtttcttc[A/G]aaattcatcaataaaa	A	G	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2229192	ctagctggaatgagga[A/C]aaatttgggcatcaga	A	C	// 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2236608	ctctaaagtagtgagc[A/G]gaaaaataatcaagtt	A	G	// 23291 // Homo sapiens F-box and WD-40 domain protein 11 (FBXW11), transcript variant 1, mRNA. /// NM_033644 // downstream // 53317 // Hs.484138 // FBXW11 // 23291 //	FBXW11	FBXW11, Homo sapiens F-box and WD-40 domain protein 11 (FBXW11), transcript variant 1, q35.1
SNP_A-1893805	tgcagtttgacatgtg[A/C]atggtccatgtaatat	A	C	/// ENST00000340614 // upstream // 25498 // --- // --- // --- // ---	-	p13.2
SNP_A-1895434	tgccgtacttgacata[C/T]agtactcaataaatgt	C	T	9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 375509 // Hs.300834 // GALNT2	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13
SNP_A-1889755	tgataattccctgaaa[C/T]tgtcctgctttcttag	C	T	ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+ q24.2
SNP_A-1891545	tgattctggattctgc[A/G]ctttttaattccaata	A	G	Homo sapiens phospholipid scramblase 2 (PLSCR2), mRNA. /// ENST00000296039 // intron // 0 // --- // --- // --- // --- ///	PLSCR2	PLSCR2, Homo sapiens phospholipid scramblase 2 (PLSCR2), q24
SNP_A-1934999	ttctgagctattacca[A/C]ctctggaggagtcaag	A	C	NM_004186 // intron // 0 // Hs.32981 // SEMA3F // 6405 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), mRNA. /// ENST00000002829 // intron // 0 // --- // --- // --- // ---	SEMA3F	SEMA3F, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), p21.31
SNP_A-1964235	tctgaatgaaaagctc[C/T]actatttaaactccca	C	T	sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // --- // --- // --- // ---	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1966157	agaacaggaagaagcc[A/G]atgcaaaggcatggag	A	G	5136 // Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), transcript variant 1, mRNA. /// NM_001003683 // upstream // 95363 // Hs.416061 // PDE1A	PDE1A	PDE1A, Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), transcript variant 1, q32.1
SNP_A-1972954	aagctaagggaaagca[C/T]tgaaggatttttgagc	C	T	132204 // Homo sapiens synaptoporin (SYNPR), mRNA. /// ENST00000295894 // downstream // 600 // --- // --- // --- // ---	SYNPR	SYNPR, Homo sapiens synaptoporin (SYNPR), p14.2
SNP_A-1850180	tatgtgtaagctacct[C/T]agacggccataataaa	C	T	// Homo sapiens Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro) (SSA2), mRNA. /// NM_197962 // downstream // 10451 // Hs.458283 // GLRX2 //	SSA2	SSA2, Homo sapiens Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A q31.2
SNP_A-1850852	tattaggtgtaccaga[A/G]tcagagaaattcagtg	A	G	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1848409	tatgaacattgataaa[C/T]tgatatgagagcaatt	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 648631 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1844993	tataatttaaactcac[A/G]acataagaataaaaca	A	G	sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // --- // --- // --- // ---	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q13
SNP_A-1867645	tccgtgggaaggatgg[C/T]ataagtgatgcatgtg	C	T	Homo sapiens MEGF11 protein (MEGF11), mRNA. /// ENST00000288745 // intron // 0 // --- // --- // --- // ---	MEGF11	MEGF11, Homo sapiens MEGF11 protein (MEGF11), q22.31
SNP_A-1808219	gtctttccatttttga[C/G]gaggagaagaaggagt	C	G	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA. ///	ABCC6	ABCC6, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p13.11
SNP_A-1809885	gtgagtaggtgtgtta[C/T]ctcttttatactattg	C	T	/// ENST00000359634 // upstream // 1206360 // --- // --- // --- // --- /// ENST00000359181 // upstream // 1206360 // --- // --- // --	-	q32.3
SNP_A-1675650	aaaatacatatacacaaatatatgc[A/T]catatacatttcctattgaaaagat	A	T	NM_022085 // intron // 0 // Hs.430169 // TXNDC5 // 81567 // thioredoxin domain containing 5	TXNDC5	TXNDC5 , rs2023387, thioredoxin domain containing 5,p24.3
SNP_A-2210323	cccccaaaactttgca[A/G]cctggatacaactgtg	A	G	Homo sapiens chromosome 9 open reading frame 99 (C9orf99), mRNA. /// ENST00000338786 // intron // 0 // --- // --	HSDL2	HSDL2, Homo sapiens chromosome 9 open reading frame 99 (C9orf99), q32
SNP_A-2226169	ctaacgcaataataaa[A/G]tgttgcctaaatttat	A	G	sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-2183719	cagcatcctgtgtttg[G/T]attgctaaacctggca	G	T	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. ///	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-2192187	catcagcagaaggaca[C/T]ggtgaccacagaggtc	C	T	55278 // Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), mRNA. /// NM_016487 // upstream // 186820 // Hs.486084 // C6orf203 // 51250 //	QRSL1	QRSL1, Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), q21
SNP_A-2181502	cagacttgatgaccaa[A/T]cctgttcttaatcctg	A	T	// 2960 // Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA. /// ENST00000283875 // downstream // 90423 // --- // --- // --- // --	GTF2E1	GTF2E1, Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), q13.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2171238	caatatattatgttaa[C/G]ggtgtagatttctggaa	C	G	Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), mRNA. /// ENST00000340941 // intron // 0 // --- // --- // --- /// ENST00000323375 // intron // 0 // --- // ---	MCCC2	MCCC2, Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), q13.2
SNP_A-2171766	caatgaaatgcaaaggc[A/G]cacaagtaggctccag	A	G	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A), mRNA. /// ENST00000053469 // 3UTR // 0 // --- // 19 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// NM_022109 //	GUCA1A	GUCA1A, Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A), p21.1
SNP_A-2134826	atatttagaagtcactc[A/G]agcacatatgtatcat	A	G		ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-2078701	accattctgtgggaaa[A/C]ttgttctgtgaaac	A	C	10904 // Homo sapiens bladder cancer associated protein (BLCAP), mRNA. /// NM_181689 // downstream // 81447 //	BLCAP	BLCAP, Homo sapiens bladder cancer associated protein (BLCAP), q11.23
SNP_A-2095702	agacaccaagcaggaat[C/T]ctatgttcaagaggt	C	T	79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000354971 // upstream // 2214 // --- // --- //	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2099513	agagggccttcctaga[C/T]gccttcagagcctgag	C	T	Homo sapiens keratin 4 (KRT4), mRNA. /// ENST00000293774 // intron // 0 // --- // --- // ---	KRT4	KRT4, Homo sapiens keratin 4 (KRT4), q13.13
SNP_A-2072570	acagccagctcccaca[A/G]attaagctatttcct	A	G	Homo sapiens Sec23 homolog A (S. cerevisiae) (SEC23A), mRNA. /// ENST00000307712 // intron // 0 // --- // --- // ---	SEC23A	SEC23A, Homo sapiens Sec23 homolog A (S. cerevisiae) (SEC23A), q21.1
SNP_A-2074825	acatcaaatcaaagtc[A/C]atacaagcattctggg	A	C	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), p21.22
SNP_A-2068721	acaatagatgtcattc[A/G]aattaccctctgtcct	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), mRNA. /// ENST00000312428 // intron // 0 // --- // --- /// ENST00000357074 // downstream // 203485 // --- // ---	DNAH7	DNAH7, Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), q32.3
SNP_A-2029087	aaagaaaaggaggcaac[A/C]atagaaaggtatttttc	A	C	/// ENST00000358765 // downstream // 203485 // --- // ---	-	p14
SNP_A-2020826	cattttctgccaac[A/C]agagtcattgaaaacc	A	C	Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // intron // 0 // --- // ---	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2044954	aagaacatggagagta[G/T]agagaatgccaaacgca	G	T	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1997453	tcccttgataataac[A/C]agaaaaactgggaaaaa	A	C	1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2052939	aagtcatttttctatct[C/T]actcatctccctctac	C	T	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 143251 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2057247	aatatagtgtatcgag[A/G]ctaatttctgtgaaat	A	G	Homo sapiens angiotensin II receptor, type 1 (AGTR1), transcript variant 1, mRNA. /// NM_009585 // intron // 0 //	AGTR1	AGTR1, Homo sapiens angiotensin II receptor, type 1 (AGTR1), transcript variant 1, q24
SNP_A-2078034	accagctttggctcc[A/G]gcgttgcacggatttc	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron //	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2134070	aaggagcatacagaaa[A/G]cttcccatgatggggc	A	G	sapiens esterase D/formylglutathione hydrolase (ESD), mRNA. /// ENST00000267160 // intron // 0 // --- // --- // ---	ESD	ESD, Homo sapiens esterase D q14.2
SNP_A-2137314	atcagttgggaaccg[A/G]aaggaaacagagaata	A	G	/// ENST00000330649 // upstream // 1353495 // --- // --- // ---	-	q11.2
SNP_A-2137465	atcatatgaagacaaa[A/G]ttggtaagattagcac	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 479871 // --- // --- // --- // ---	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2118673	agtacaaagtctctgc[A/G]cctataaacttagcca	A	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2115862	agggtgggggtgtgga[C/T]gcttcacggtgggcac	C	T	Homo sapiens glutamate receptor, metabotropic 4 (GRM4), mRNA. /// ENST00000266007 // intron // 0 // --- // --- // --- // ---	GRM4	GRM4, Homo sapiens glutamate receptor, metabotropic 4 (GRM4), p21.31
SNP_A-2157009	attctttaaaaaatc[G/T]aaagttggctggtccg	G	T	6596 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member	SMARCA3	SMARCA3, Homo sapiens SWI,q24
SNP_A-2144986	atgatttcattcatgc[A/G]aaattctagaaaaggc	A	G	sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, mRNA. /// NM_002037 // intron // 0 //	FYN	FYN, Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, q21
SNP_A-2171620	caatctactcacggaga[C/T]aaacatcagatcaatt	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 591068 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2171604	caatcgaactgattggt[C/T]attaaatttggatct	C	T	10873 // Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006680 // upstream //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2173919	cacacagtagaagctc[A/G]ataaacatgagttctt	A	G	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10) (GALNT10), transcr /// NM_017540 // intron // 0 // Hs.34421 //	GALNT10	GALNT10, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10) (GALNT10), transcr q33.2
SNP_A-2171213	caatataattagtaga[C/T]aaagatgttaaatcag	C	T	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1671569 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2196052	catgtcttctaggtga[C/T]cttgctactgtgtccc	C	T	// 389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// AB033035 // upstream // 149949 //	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-2187526	cagtaaagttcacaga[C/T]caatggagcaagtgag	C	T	// 64098 // Homo sapiens parvin, gamma (PARVG), mRNA. /// NM_022141 // downstream // 65994 // Hs.546422 //	PARVG	PARVG, Homo sapiens parvin, gamma (PARVG), q13.31
SNP_A-2222080	cgaaggaatctgtgaa[C/T]tatggtcacatggcta	C	T	Homo sapiens PX domain containing serine/threonine kinase (PXK), mRNA. /// ENST00000302779 // intron // 0 // --- // --- //	PXK	PXK, Homo sapiens PX domain containing serine p14.3
SNP_A-2219962	ccttatctcctattac[G/T]cagtctgcctcatgtc	G	T	// 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1678990	atgattaagttaaacaaactctagg[A/G]aaaatgtcacattaaaataatgaca	A	G	NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // protein kinase, cGMP-dependent, type I	PRKG1	PRKG1 , rs10508970, protein kinase, cGMP-dependent, type I,q21.1
SNP_A-1671932	tacaaaaatataactgaacaaagag[A/G]aatatatattcactacagaagccag	A	G	DKFZP434F1017 // 84075 // hypothetical protein DKFZp434F1017	DKFZP434F1017	DKFZP434F1017 , rs10484171, hypothetical protein DKFZp434F1017,q21.2
SNP_A-1798662	gtaacatctcaggata[C/T]agtacacaagtaactt	C	T	CDKN2C // 1031 // Homo sapiens cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (CDKN2C), transcript variant 1, mRNA. /// NM_078626 // downstream // 204397 //	CDKN2C	CDKN2C, Homo sapiens cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (CDKN2C), transcript variant 1, p32.3
SNP_A-1797435	ggtttaccaagtacac[A/G]atcatgtcactggtga	A	G	55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 1197461 // Hs.479658 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-1847392	tatccctagatcacct[A/C]agccagagtcctagaa	A	C	ENST00000333722 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-1832835	tacaatatacattgac[C/T]attgtgtcatttgact	C	T	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 387158 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1823741	taaaatcatgaaataa[A/G]gaagtgaacatcacag	A	G	Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1819115	gttgcgtgattgctga[C/T]aaacacagtgctgttt	C	T	2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 271717 // Hs.203717	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-1820847	gtttcctggaacaaaa[C/T]gatgaaatccaggaga	C	T	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // --- ///	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-1965748	atgtagggtccaagag[A/G]acgacaaggatcgagg	A	G	Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA. /// ENST00000355999 //	STK39	STK39, Homo sapiens serine threonine kinase 39 (STE20 q24.3
SNP_A-1979278	tgttatccaaaaccaa[C/T]ggtatgagatttctac	C	T	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 372844	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1977836	cattttataaaagcta[C/T]atggatgtcatggtgc	C	T	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1903352	tgggaaatgaagaagc[A/C]ataatttagttttgtc	A	C	/// ENST00000251675 // downstream // 82164 // --- // --- // --- // --- /// ENST00000360855 // downstream // 82194 // --- // ---	-	q32.3
SNP_A-1885512	tgacaatacaatcatg[C/T]catagcatactaaaca	C	T	ENST00000360575 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1874894	tctctaagattaatga[C/T]gtgcttggacataaat	C	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 329664 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-1906565	tggtggtgctagggga[A/G]atgaagaggaaagtct	A	G	390066 // Homo sapiens olfactory receptor, family 52, subfamily D, member 1 (OR52D1), mRNA. /// NM_017481 // downstream // 1907 // Hs.189184 // UBQLN3 // 50613 //	OR52D1	OR52D1, Homo sapiens olfactory receptor, family 52, subfamily D, member 1 (OR52D1), p15.4
SNP_A-1921460	ttacccacgtcttcag[C/T]atgattagatattggt	C	T	-- /// ENST00000328955 // upstream // 1406375 // --- // --- // ---	-	q24.23
SNP_A-2230765	ctatgagagatgttaa[A/G]tatgtgggcctggcag	A	G	Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA. /// ENST00000266674 // intron // 0 // --- // --- // --- // ---	LGR5	LGR5, Homo sapiens G protein-coupled receptor 49 (GPR49), q21.1
SNP_A-2233541	ctcagttcaaaatcta[G/T]ctctactgattgtgca	G	T	Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // --- //	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-2233657	ctcatagacactcaac[A/G]cttcctcatacaccat	A	G	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 28479 // Hs.32942 // PIK3CG // 5294 // Homo	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2286249	gatgccattagaaaga[C/G]agtgaagagtatagca	C	G	// Homo sapiens FLJ32921 protein (FLJ32921), mRNA. /// ENST00000296600 // intron // 0 // --- // --- // --- // ---	FLJ32921	FLJ32921, Homo sapiens FLJ32921 protein (FLJ32921), q23.2
SNP_A-2283465	gatactactacccaaa[C/G]cttctgtgaatttttt	C	G	ENST00000283060 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-2273361	gactcctggttcaccc[A/G]ctctggctttagcttg	A	G	Homo sapiens RAB, member of RAS oncogene family-like 4 (RABL4), mRNA. /// ENST00000340630 // intron // 0 // --- // ---	RABL4	RABL4, Homo sapiens RAB, member of RAS oncogene family-like 4 (RABL4), q12.3
SNP_A-2279497	gaggatgcctgtgctc[A/G]caaaggtagatctttc	A	G	Homo sapiens dynamin 3 (DNM3), mRNA. /// ENST00000358155 // intron // 0 // --- // --- // --- // --- ///	DNM3	DNM3, Homo sapiens dynamin 3 (DNM3), q24.3
SNP_A-2291600	gcacaagattctgata[C/G]agatacttttgttta	C	G	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 2066821 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2294990	gcatacagccaggtag[C/T]cactatcataatcaag	C	T	Homo sapiens WW domain containing E3 ubiquitin protein ligase 2 (WWP2), transcript variant 2, mRNA. /// NM_007014 // intron // 0 // Hs.408458 // WWP2 // 11060 // Homo sapiens	WWP2	WWP2, Homo sapiens WW domain containing E3 ubiquitin protein ligase 2 (WWP2), transcript variant 2, q22.1
SNP_A-2297138	gccacagcggaaaata[C/T]gtttcttgctgtggat	C	T	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2305319	gctgagggtctaactg[C/G]atatgttttaaatcag	C	G	LOC133619 // 133619 // Homo sapiens hypothetical protein MGC12103 (LOC133619), mRNA. /// ENST00000330542 //	LOC133619	LOC133619, Homo sapiens hypothetical protein MGC12103 (LOC133619), q23.2
SNP_A-2274231	gacttctttccatagc[A/G]ctctgattatgctgtt	A	G	// 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream //	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2284148	gatatgcagtggaatc[A/G]agagacagaagaggga	A	G	117157 // Homo sapiens SH2 domain-containing molecule EAT2 (EAT2), mRNA. /// NM_144624 // upstream // 77302 // -	EAT2	EAT2, Homo sapiens SH2 domain-containing molecule EAT2 (EAT2), q23.3
SNP_A-2268608	gaatgtcaaaaacata[C/T]cactgagcaaaagaag	C	T	SERPINB13 // 5275 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), mRNA. /// NM_002974 // downstream // 28080	SERPINB13	SERPINB13, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), q21.33
SNP_A-2267156	gaataatgccaccttc[A/G]agggaataatttcaaa	A	G	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 107948 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2233220	ctcagcttagccgttc[A/G]agcccggggttgtgtc	A	G	ENST00000332168 // intron // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2232082	ctcaagcagccaggta[G/T]gaagcaaaaatgggtt	G	T	-- /// ENST00000276737 // downstream // 217441 // --- // --- //	-	q24.23
SNP_A-2228751	ctagacttcaagatga[A/T]caactcaggccaagag	A	T	56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream //	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-2239899	ctgaaccctactaacc[A/G]ggtatcttcatgcatt	A	G	Homo sapiens mRNA for KIAA0293 gene, partial cds. /// ENST00000261726 // intron // 0 // --- // --- // --- // ---	CUTL2	CUTL2, Homo sapiens for KIAA0293 gene, partial cds. ,q24.11
SNP_A-2245603	ctgggcagcctcaaaa[C/T]gagcccctagccaggt	C	T	sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA. /// ENST00000301732 // intron // 0 // --- //	ABCA3	ABCA3, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), p13.3
SNP_A-2255754	cttgttgtggtttgga[A/G]tcaaataaccttcatc	A	G	THNSL1 // 79896 // Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), mRNA. /// NM_020752 // upstream //	THNSL1	THNSL1, Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), p12.1
SNP_A-2250963	cttatgtaacatgaca[C/T]tgacccttttgtatag	C	T	143689 // Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// NM_130847 // upstream // 119873 // Hs.503594 //	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-1912345	tgtgattgcttgagag[C/T]cagactgcctagattt	C	T	Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 //	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1
SNP_A-1912584	tgtgccagttttagca[C/T]acttctagcatttctt	C	T	64431 // Homo sapiens ARP6 actin-related protein 6 homolog (yeast) (ACTR6), mRNA. /// NM_152317 // downstream //	ACTR6	ACTR6, Homo sapiens ARP6 actin-related protein 6 homolog (yeast) (ACTR6), q23.1
SNP_A-1874426	tctcccagaaattgac[A/G]gctccagaagacaaaa	A	G	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 404701 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-1875391	tctctgcattaattca[A/G]ctctccctcttccaac	A	G	ENST00000328648 // intron // 0 // --- // --- // --- // --- /// ENST00000359497 // intron // 0 // --- // --- // --- // --- ///	-	q13.11
SNP_A-1898633	tgcttgtattctacta[A/T]catgatgtgatccaat	A	T	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1978813 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1900037	tggacctgcccggcca[C/T]gcggatgaggtagggc	C	T	Homo sapiens Notchless gene homolog (Drosophila) (FLJ10458), mRNA. /// ENST00000360831 // CDS // 0 // --- //	FLJ10458	FLJ10458, Homo sapiens Notchless gene homolog (Drosophila) (FLJ10458), q12
SNP_A-1896558	tgctagaaaggtttgc[A/C]agtactgattctggga	A	C	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 447467 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1896726	tgctatgcaagatgaa[C/T]atcaccaaggcacaca	C	T	Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-1975531	cctgtctttctgttca[A/T]gtgtctcagtggagtt	A	T	Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), mRNA. /// ENST00000328913 //	MCF2L2	MCF2L2, Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), q27.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1972873	aacctgtgtgtaaaga[C/T]cctcgggctccatttg	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1939939	ttgcactgactcaaga[A/C]acagagaaataattca	A	C	// 55119 // Homo sapiens hypothetical protein FLJ10330 (FLJ10330), mRNA. /// NM_173532 // upstream // 17683 // ---	FLJ10330	FLJ10330, Homo sapiens hypothetical protein FLJ10330 (FLJ10330), p13.3
SNP_A-1939761	ttgcaaatttcttcca[C/G]acatcttctctgaata	C	G	Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// ENST00000354440 // intron // 0 // --- // ---	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1939141	ttgatacttttctgc[C/T]ccaccattcttggaaa	C	T	6013 // Homo sapiens relaxin 1 (H1) (RLN1), mRNA. /// NM_018465 // downstream // 3415 // Hs.534185 // C9orf46 //	RLN1	RLN1, Homo sapiens relaxin 1 (H1) (RLN1), p24.1
SNP_A-1941941	ttggaggaacaatcag[A/G]ataggtcccccatatc	A	G	Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // --- // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-1947426	tttacagatgaagcaa[C/T]tgaagccaaaagtagt	C	T	7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// NM_016617 // upstream // 415838 // Hs.524969 // Ufm1 //	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-1961221	ttttttatgaaagaca[A/G]aaggattccagagaag	A	G	2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. /// NM_032487 // downstream // 477952 // Hs.135411	EVI1	EVI1, Homo sapiens ecotropic viral integration site 1 (EVI1), q26.2
SNP_A-1840754	tagctacaccaattca[C/T]cctcaaagtttcgagg	C	T	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- // --- ///	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-1839291	tagagtagagttatga[A/C]ctgtatcttattcaca	A	C	Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// ENST00000320816 // intron // 0 // --- // --- // --- // ---	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1848140	tatcttcacatgaata[A/C]ctaatagacatctcag	A	C	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), mRNA. /// ENST00000280452 // intron // 0 // --- // --- // --- // ---	PIP5K2A	PIP5K2A, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), p12.2
SNP_A-1851098	tattatttgaaagtta[C/T]gtacactgtgtataca	C	T	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 828311	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1854938	tcaactctgggcatac[A/G]gccccaagcctgcatc	A	G	168667 // Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), mRNA. /// ENST00000311067 // downstream // 70904 // --- // --- // --- // --- ///	BMPER	BMPER, Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), p14.3
SNP_A-1859869	tcagggttgtcttggg[A/C]aagccctaaaggctcc	A	C	6513 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /// ENST00000270929 // upstream // 90125 // --- // --- // --- // ---	SLC2A1	SLC2A1, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), p34.2
SNP_A-1859887	tcaggtacacaggtaa[C/G]aggacagcccctggtg	C	G	1435 // Homo sapiens colony stimulating factor 1 (macrophage) (CSF1), transcript variant 4, mRNA. /// NM_172211 // upstream // 85847 // Hs.173894 // CSF1 //	CSF1	CSF1, Homo sapiens colony stimulating factor 1 (macrophage) (CSF1), transcript variant 4, p13.3
SNP_A-1862434	tcatgtggttgcctga[C/T]ggtagatggtggagac	C	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-1793577	ggtatattaataagca[A/G]atagactagtagaaaa	A	G	Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, mRNA. /// NM_182799 // intron // 0 //	FLJ39155	FLJ39155, Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, p13.2
SNP_A-1646262	agaagagttattgttttaaacctca[A/G]gatatatttaggaagacatttgagc	A	G	5937 // RNA binding motif, single stranded interacting protein 1 /// NM_004180 // upstream // 422485 // Hs.146847 // TANK	RBMS1	RBMS1 , rs10497215, RNA binding motif, single stranded interacting protein 1 ,q24.2
SNP_A-1680234	ttcttcccatataccaaatctatta[C/G]caaatcttataaatttttctccttgt	C	G	NM_004932 // upstream // 335001 // Hs.32963 // CDH6 // 1004 // cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	CDH6 , rs1882205, cadherin 6, type 2, K-cadherin (fetal kidney),p13.3
SNP_A-1780395	ggatacaatcaacaaa[G/T]aaaactcaaactgata	G	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 388168 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2192410	catcatgcaccttcaa[A/G]aggctgcataaccaac	A	G	// 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 75172 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2176238	caccagaagctaggaa[A/G]acagcatgagaaagag	A	G	Homo sapiens integrin, alpha 1 (ITGA1), mRNA. /// ENST00000282588 // intron // 0 // --- // --- // --- // ---	ITGA1	ITGA1, Homo sapiens integrin, alpha 1 (ITGA1), q11.2
SNP_A-2165614	caaaggaattcaggaa[A/G]aggaagactagtggtt	A	G	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1636572 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2109773	aggaaatgcaatcata[C/T]aaggtgtgcagaaagt	C	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 107945 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2135519	atatttaagaatgcc[A/G]ccatcataaatgttgg	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2082921	acgtcttagctc[C/T]agtgtatttattagat	C	T	Homo sapiens ankyrin repeat domain 12 (ANKRD12), mRNA. /// ENST00000262126 // intron // 0 // --- // --- // ---	ANKRD12	ANKRD12, Homo sapiens ankyrin repeat domain 12 (ANKRD12), p11.22
SNP_A-2056224	aatactacgaattggc[A/G]catcaaaataaaaattg	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2067364	acaaataatcatggta[C/T]gtaagatgacaacatt	C	T	7172 // Homo sapiens thiopurine S-methyltransferase (TPMT), mRNA. /// ENST00000309983 // upstream // 15240 // Homo sapiens hypothetical protein MGC33926	TPMT	TPMT, Homo sapiens thiopurine S-methyltransferase (TPMT), p22.3
SNP_A-2065797	aatttcatgaaaagta[C/T]ctactctgtcttaaaa	C	T	(MGC33926), mRNA. /// ENST00000281961 // intron // 0 // ---	MGC33926	MGC33926, Homo sapiens hypothetical protein MGC33926 (MGC33926), p22.1
SNP_A-2074845	acatcaataatattta[A/G]gcaacagggaccatct	A	G	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1037219 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2002890	catgtaagaatgaaag[A/G]aaaatgaattggagca	A	G	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1513541 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1995922	taagagaaaaaaggaa[A/C]agctgcggtaagaaga	A	C	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3458364 //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2017355	atggcatagccaaaaa[G/T]tcaatggtagaagtaa	G	T	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT // NM_145180 // upstream // 285634 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2008574	tttcaccaaataaaaac[A/G]atagctttctcgccca	A	G	// Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2047120	gctcacagtaggtctc[A/G]ctaccagatgggggctc	A	G	65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 116185 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2037140	aacaaaataaaaataca[C/G]tacttaggcagaagca	C	G	Homo sapiens cullin 4A (CUL4A), mRNA. /// ENST00000326335 // intron // 0 // --- // --- // ---	CUL4A	CUL4A, Homo sapiens cullin 4A (CUL4A), q34
SNP_A-2037126	aacaaaagcctttggc[G/T]acattgactgcacctc	G	T	// Homo sapiens hypothetical protein LOC51057 (LOC51057), mRNA. /// ENST00000272321 // intron // 0 // ---	LOC51057	LOC51057, Homo sapiens hypothetical protein LOC51057 (LOC51057), p15
SNP_A-2024237	aaaagcacgttagcta[C/G]agagagagggatgtaa	C	G	Homo sapiens chromosome 20 open reading frame 104 (C20orf104), mRNA. /// ENST00000026952 // intron // 0 // ---	PHF20	PHF20, Homo sapiens chromosome 20 open reading frame 104 (C20orf104), q11.22
SNP_A-2025293	aaaatatgttgactaa[C/T]cataactgaatacaga	C	T	3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// ENST00000305031 //	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3
SNP_A-2033278	aaatagaagccatata[A/C]aagtgtacaaacact	A	C	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 394484	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2018435	ggggcccttattactaa[C/T]ataacaaagcccatgt	C	T	9992 // Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2), mRNA. /// NM_000219 // downstream // 66110 // Hs.121495 // KCNE1 // 3753 // Homo	KCNE2	KCNE2, Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2), q22.11
SNP_A-2013053	caacgctgctcctccca[A/G]tgacacagaggaacgt	A	G	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2074962	acatcatcagttccta[C/T]gtcacctcctcagaga	C	T	Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // intron // 0 // --- // --- // ---	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-2058775	aatcattaatcattaa[C/T]cagttaaaacaagattt	C	T	Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters), member 2	SLC12A2	SLC12A2, Homo sapiens solute carrier family 12 (sodium q23.2
SNP_A-2048436	aagcataaactcacc[A/G]atacatattatttcaa	A	G	1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // upstream // 458179 // --- // --- // ---	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2081048	acctgaatggcctga[C/G]aaactcagcttctgt	C	G	// 7278 // Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, mRNA. /// NM_006001 // downstream // 441817 //	TUBA2	TUBA2, Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, q11
SNP_A-2082972	acgtgccctcaaatga[C/G]ataaagcagccaaata	C	G	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 //	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2094160	agaaggctctgcccat[A/G]aggcctggacctacct	A	G	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2113784	aggctgccaaggtgtc[A/G]cagggaatgctagcag	A	G	// 147339 // Homo sapiens chromosome 18 open reading frame 25 (C18orf25), mRNA. /// ENST00000321319 //	C18orf25	C18orf25, Homo sapiens chromosome 18 open reading frame 25 (C18orf25), q21.1
SNP_A-2163051	atttttacctgcaaga[A/G]gtgggagatttccaaa	A	G	ENST00000265654 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-2157233	attgacaaggcttagc[A/G]gcagggaaacagtgta	A	G	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 92622 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-2177079	cacctccgtgttttcc[A/G]catattgtctcccagt	A	G	Homo sapiens centaurin, alpha 1 (CENTA1), mRNA. /// ENST00000265846 // intron // 0 // --- // --- // --- // --- ///	CENTA1	CENTA1, Homo sapiens centaurin, alpha 1 (CENTA1), p22.3
SNP_A-2169062	caagagtgttcactga[A/C]ctagcggtaagcagtg	A	C	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2218799	cctgggatctgccagc[A/G]atacacatgaccatag	A	G	/// ENST00000356642 // downstream // 505545 // --- // --- // ---	-	q31.1
SNP_A-2223681	ttcagagtgaaggaga[C/T]gcttcatggagggcag	C	T	SLC38A6 // 145389 // Homo sapiens solute carrier family 38, member 6 (SLC38A6), mRNA. /// ENST00000267488 //	SLC38A6	SLC38A6, Homo sapiens solute carrier family 38, member 6 (SLC38A6), q23.1
SNP_A-2227471	ctacagaaggatatgc[C/T]agtcctgtgcttttat	C	T	91133 // Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA. /// ENST00000317931 // upstream //	L3MBTL4	L3MBTL4, Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), p11.31
SNP_A-2224909	cgtgctatgtccttgc[A/G]ccattcataggtgact	A	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 390907 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1784576	ggcctagctgcttctg[A/T]cagaaccaacattttg	A	T	// 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream //	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1795439	ggtgcagcctggtgaa[C/T]actttcttcccgcaag	C	T	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.32
SNP_A-1793855	ggtcaaaataaatgga[C/T]gctagtcttggctgtc	C	T	LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 //	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-1797277	ggttgggctcagaacc[A/G]ctctactgcctaacct	A	G	152641 // Homo sapiens hypothetical protein FLJ30277 (FLJ30277), mRNA. /// NM_024949 // upstream // 38763 //	FLJ30277	FLJ30277, Homo sapiens hypothetical protein FLJ30277 (FLJ30277), q35.1
SNP_A-1796223	ggtgtgaccagggcaa[A/T]gaggagaatgtagcag	A	T	85439 // Homo sapiens stonin 2 (STN2), mRNA. /// NM_005065 // downstream // 50973 // Hs.181300 // SEL1L //	STN2	STN2, Homo sapiens stonin 2 (STN2), q31.1
SNP_A-1861392	tcatcaggagtagtta[C/T]gaaagatgataatttt	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-1853250	tattttaactacttga[A/G]aagtttgagcagtgag	A	G	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1846617	tatatttccaaaaaca[C/T]cagtgagtgagtttat	C	T	// 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 148694 //	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-1844896	tataatcttatgagac[C/T]gccatcgtaacatgat	C	T	-- /// ENST00000356807 // downstream // 292292 // --- // --- //	-	p11.2
SNP_A-1838702	tagacatacacagaga[A/G]aaagaaaatacagaaa	A	G	// 1996 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) (ELAVL4), mRNA. /// ENST00000323186 // downstream // 141241 // --- // --- // --- //	ELAVL4	ELAVL4, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D) (ELAVL4), p32.3
SNP_A-1834973	tacccacctaaatgca[A/G]cgtgaacacacatcta	A	G	Homo sapiens KIAA0247 (KIAA0247), mRNA. /// ENST00000342745 // intron // 0 // --- // --- // --- // ---	KIAA0247	KIAA0247, Homo sapiens KIAA0247 (KIAA0247), q24.1
SNP_A-1831484	taatgttgcatttagg[C/T]catattgctacagtaa	C	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1398437 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1819872	gttgtgtatcctaaag[C/T]atcacctgtactgcag	C	T	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-1819986	gttgttggctaaataa[C/T]attccacattcaattt	C	T	140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 15222 // Hs.31845 // ASB7 //	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3
SNP_A-1826235	taaattctaattccca[G/T]gtataaatcacactga	G	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1316501 // Hs.27214 // KCNC2	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1978030	ttagcacagtgctcaa[A/T]aacgtttggttgatct	A	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 135911 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1978687	ctcagcagacaacctg[A/C]acattacttcacagag	A	C	2169 // Homo sapiens fatty acid binding protein 2, intestinal (FABP2), mRNA. /// ENST00000274024 // upstream // 8325 //	FABP2	FABP2, Homo sapiens fatty acid binding protein 2, intestinal (FABP2), q26

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1895023	tgcccagaatagtgag[C/T]attatgtgcctagata	C	T	// 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 290099 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1876696	tctgcaccagatacccf[A/G]actcaatagatgtgat	A	G	/// ENST00000325796 // downstream // 581278 // --- // --- // ---	-	q22.1
SNP_A-1922387	ttagaaactgaatttgt[A/G]atgatcttaaacagca	A	G	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_ 130838 // intron // 0 // Hs.22543 // UBE3A // 7337 // Homo sap	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2253530	ctctctctatagata[C/T]acagttgaccctagaa	C	T	/// ENST00000360919 // upstream // 2210086 // --- // --- // ---	-	q13.1
SNP_A-2242876	ctgccactgagtccaa[G/T]aactggcctggaagct	G	T	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 79044 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2234604	ctccagaactatggga[C/G]aataagttctgtttt	C	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 443122 // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2267520	gaatatgcagaggcca[A/G]taatctagaaatttat	A	G	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 546226 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2280633	gaggtcaggtgaataa[A/G]gtggacgaggcaaaaa	A	G	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 864930	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2302871	gctagatggccgctgc[A/G]accactgagatagaac	A	G	/// ENST00000246019 // downstream // 13488 // --- // --- // ---	-	p11.23
SNP_A-2296608	gccaaaaagccaaatg[A/G]caaatgatagatattt	A	G	7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // upstream // 45959 // Hs.232072 // USH2A //	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2296368	gcatttaccacactta[C/T]cacctcctgaccaggg	C	T	// 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // downstream //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2299289	gccctcctttgcctca[A/G]agtcagaaagaacaca	A	G	10456 // Homo sapiens HS1 binding protein (HAX1), mRNA. /// NM_080429 // upstream // 35062 // Hs.259048 // AQP10 //	HAX1	HAX1, Homo sapiens HS1 binding protein (HAX1), q21.3
SNP_A-2287621	gattaacttctagtca[C/T]ctcccagatctcagcc	C	T	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 182376 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2264768	gaagactcaagctcaa[A/G]taagactgagcatcac	A	G	51454 // Homo sapiens GULP, engulfment adaptor PTB domain containing 1 (GULP1), mRNA. /// NM_016315 // downstream // 32171 // Hs.470887 // GULP1 // 51454 //	GULP1	GULP1, Homo sapiens GULP, engulfment adaptor PTB domain containing 1 (GULP1), q32.2
SNP_A-2268764	gaattaagattgctac[A/G]caactgatgcaatagg	A	G	Homo sapiens transcription factor CP2-like 1 (TFCP2L1), mRNA. /// ENST00000263707 // intron // 0 // --- // --- // ---	TFCP2L1	TFCP2L1, Homo sapiens transcription factor CP2-like 1 (TFCP2L1), q14.2
SNP_A-2263388	gaacatgacatatttc[A/C]aaatttgtatgagaaa	A	C	C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2237530	ctctctaagccctttta[G/T]cctcatgggggaggggg	G	T	- /// ENST00000355517 // downstream // 741528 // --- // --- // ---	-	q24.32
SNP_A-2238028	ctctgattctctcacc[C/T]cactctttgtggcct	C	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 642735 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2238514	ctctgtatttcctgaa[A/T]gaatggtggcctgcc	A	T	Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-2229935	ctagtttcatacttc[C/T]attgttgatcatgatg	C	T	HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 275520 // Hs.48384	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-2242313	ctgcacacgttctatc[A/C]cacaagcttgctagat	A	C	2859 // Homo sapiens G protein-coupled receptor 35 (GPR35), mRNA. /// NM_198998 // downstream // 21895 //	GPR35	GPR35, Homo sapiens G protein-coupled receptor 35 (GPR35), q37.3
SNP_A-2242135	ctgcaaaaatacaaaa[A/C]attctcataccttattt	A	C	// 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// NM_182522 // downstream // 544 // Hs.187873 //	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-1925869	ttatggctcttctgaf[A/G]atggtaccatgatga	A	G	Homo sapiens mitogen-activated protein kinase kinase 1 (MAP2K1), mRNA. /// ENST00000307102 // intron // 0 // --- // ---	MAP2K1	MAP2K1, Homo sapiens mitogen-activated protein kinase kinase 1 (MAP2K1), q22.31
SNP_A-1930991	ttccagtcatttggcf[A/C]ctgttagctctgtgac	A	C	// 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000298035 // downstream // 422189 // --- // --- // ---	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.2
SNP_A-1908725	tgtaggtaaaagacaf[C/T]ctctcaagaatctttc	C	T	205428 // Homo sapiens hypothetical protein MGC33365 (MGC33365), mRNA. /// ENST00000315691 // intron // 0 // ---	MGC33365	MGC33365, Homo sapiens hypothetical protein MGC33365 (MGC33365), q24
SNP_A-1889486	tgagttgcctgagagat[A/G]accccatggcctgtaa	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1895395	tgccgagaagataatg[C/T]catgaagaagtgttca	C	T	Homo sapiens hepatitis A virus cellular receptor 1 (HAVCR1), mRNA. /// ENST00000339252 // intron // 0 // --- // --- // --- // ---	HAVCR1	HAVCR1, Homo sapiens hepatitis A virus cellular receptor 1 (HAVCR1), q33.3
SNP_A-1892818	tgcacatcaacttttca[A/G]gtgagtttggcaacat	A	G	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 332219 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1986745	gttatcttcaggttagt[A/G]ttgtcactgtggaagt	A	G	// 10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 329251 // --- // --- // --- // ---	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3
SNP_A-1971865	atgatcccttactctca[C/T]gaagaccaataatgt	C	T	GALNTL2 // 117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// NM_206831 // downstream // 4498 // Hs.388087 // 2CSL2 // 92344 // Homo sapiens NTKL-binding protein 1	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-1971838	aaatttgcgccatgaa[A/G]attcctacagttatg	A	G	(FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1959930	tttgtgcaaaccagaa[A/G]tccaaccaagagttat	A	G	// Homo sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// NM_001465 // upstream // 7677 // Hs.370503 //	FYB	FYB, Homo sapiens FYN binding protein (FYB-120 p13.1
SNP_A-1956963	ttttaagtgaaagatg[A/G]aatatcccaaatgtat	A	G	-- /// ENST00000342478 // downstream // 141798 // --- // --- // ---	-	q11.21
SNP_A-1828294	taagatacaaagaaata[A/G]cacccagtcttactaa	A	G	Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// ENST00000260197 // intron // 0 // --- // --- // --- // ---	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q23.3
SNP_A-1818428	gttcttcctgtctccc[C/T]gcttaggtccaaagct	C	T	// 3516 // Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, mRNA. /// NM_005349 // downstream // 33583 //	RBPSUH	RBPSUH, Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, p15.2
SNP_A-1817982	gttctactgcatgtca[C/T]agaggctaaggtttta	C	T	-- /// ENST00000263635 // upstream // 87377 // --- // --- // ---	-	q24.2
SNP_A-1836029	tactacaaaataaaagt[A/C]acaggccaatgaagag	A	C	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 717996 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1867762	tcctagaataagtca[A/G]agattatcaaagccct	A	G	388325 // Homo sapiens DTFT5783 (UNQ5783), mRNA. /// NM_004703 // upstream // 17275 // Hs.536036 // RABEP1 //	UNQ5783	UNQ5783, Homo sapiens DTFT5783 (UNQ5783), p13.2
SNP_A-1792734	ggtaagaatgcgaagg[A/G]cagctttaagagtca	A	G	Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// ENST00000206249 // intron // 0 // --- // --- // --- // ---	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.1
SNP_A-1809646	gtgagcaggtggaggat[A/G]cggaagagggtgaggg	A	G	9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 407597 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-1802058	gtatacaggaattaca[C/T]atcagcatcctggtat	C	T	Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// ENST00000282749 // intron // 0 // --- // --- // --- // ---	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1783188	ggcagggaccacacat[C/T]agcatcagcaatacat	C	T	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 223377 // --- // --- // --- // ---	-	-, Human endogenous retrovirus env , q14.1
SNP_A-1683482	gctgacctcggcaggtgtgtgtcta[C/T]ctcagaaactgctgagttctgctat	C	T	NM_005197 // intron // 0 // Hs.211773 // C14orf116 // 55453 // chromosome 14 open reading frame 116	C14orf116	C14orf116 , rs10484025, chromosome 14 open reading frame 116,q32.11
SNP_A-2207563	ccatttccactatatac[C/T]aagtagccaaaaatat	C	T	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1875464 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2166259	caaatcattggcactc[A/G]agagtttcaagaattc	A	G	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2166672	caaattagaaaggaag[A/G]agtcaaattatcttg	A	G	2626 // Homo sapiens GATA binding protein 4 (GATA4), mRNA. /// ENST00000304233 // downstream // 72287 // --- // ---	GATA4	GATA4, Homo sapiens GATA binding protein 4 (GATA4), p23.1
SNP_A-2111166	agggagagttccagag[G/T]agggatctgcacaaag	G	T	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA. /// NM_021905 // intron // 0 // Hs.167017 // GABBR1 // 2550 // Homo sapiens	GABBR1	GABBR1, Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, p22.1
SNP_A-2117395	aggtggttaggctgc[C/T]agtccaggtgaactgg	C	T	/// ENST00000335028 // upstream // 54620 // --- // --- // --- // ---	-	q21.31
SNP_A-2130348	atactaaatatctaac[A/G]gtacaagtcaaacatg	A	G	Homo sapiens keratin 6 irs3 (K6IRS3), mRNA. /// ENST00000305748 // intron // 0 // --- // --- // --- // ---	K6IRS3	K6IRS3, Homo sapiens keratin 6 irs3 (K6IRS3), q13.13
SNP_A-2078138	accaggtcctcaggcca[A/G]ggatgttagggggacca	A	G	Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2088768	actgtgtggtcaaatc[A/G]catgcaaggagcagtag	A	G	Homo sapiens collectin sub-family member 10 (C-type lectin) (COLEC10), mRNA. /// ENST00000332843 // intron // 0 // ---	COLEC10	COLEC10, Homo sapiens collectin sub-family member 10 (C-type lectin) (COLEC10), q24.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2048324	aagcagcaagataaaa[A/G]tgacctgtaacataga	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1174275 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2060858	aatgatagctagaaca[A/T]ctaaatgtctgaaggc	A	T	ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 570705 //	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-2064821	aaaacatgctcttggg[A/G]acactatttctacaga	A	G	-- /// ENST00000354800 // downstream // 624668 // --- // --- //	-	q14.1
SNP_A-1996162	gtgtattagctaggcc[C/T]gacataagaaaatggc	C	T	// 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	MLLT3	MLLT3, Homo sapiens myeloid,p21.3
SNP_A-2002158	ttttttcttcaagaaa[C/T]cccactctatacataa	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1997781	acaaagcctccttttg[A/C]atggattaggaaaaca	A	C	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2035472	aaatggtcagaaagaa[C/T]gatcaggttggagact	C	T	sapiens mRNA for MEGF7, partial cds. /// ENST00000256991 // 3UTR // 0 // --- // --- // --- // ---	LRP4	LRP4, Homo sapiens for MEGF7, partial cds. ,p11.2
SNP_A-2032784	aaataagaatgagatc[A/C]aaatcccaaaactgaa	A	C	FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream //	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2024094	aaaagataaaaacaga[G/T]tcaagagaaagtatca	G	T	Homo sapiens reticulon 4 interacting protein 1 (RTN4IP1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000252638 // intron // 0 // --- // --- // --- // ---	RTN4IP1	RTN4IP1, Homo sapiens reticulon 4 interacting protein 1 (RTN4IP1), nuclear gene encoding mitochondrial protein, q21
SNP_A-2020561	tgcacaataaatgtaa[C/T]gcgctggaatcatccc	C	T	Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, mRNA. /// NM_015833 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosin	ADARB1	ADARB1, Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, q22.3
SNP_A-2019197	ggcagtctggctaaga[A/G]gttcacaccatcattc	A	G	sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-2091690	tagtttccaaatgcac[C/T]gtagacttttcatac	C	T	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2079726	accctccacaggaacc[C/T]gagctccacaggactc	C	T	3321 // Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA. /// ENST00000342231 // upstream //	IGSF3	IGSF3, Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), p13.1
SNP_A-2098979	agagctttctgaacct[C/T]agatttttaatttaa	C	T	Homo sapiens chromosome 13 open reading frame 12 (C13orf12), mRNA. /// ENST00000255315 // intron // 0 // --- //	C13orf12	C13orf12, Homo sapiens chromosome 13 open reading frame 12 (C13orf12), q12.3
SNP_A-2102697	agatttccagaaaggc[A/G]aaagagaccgccaaac	A	G	Homo sapiens chromosome 6 open reading frame 107 (C6orf107), mRNA. /// ENST00000266004 // intron // 0 // --- //	C6orf107	C6orf107, Homo sapiens chromosome 6 open reading frame 107 (C6orf107), p21.31
SNP_A-2122567	agtgcttaaatatatg[A/G]aaatacactcagcttt	A	G	Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000285689 // intron // 0 // --- // --- // --- // ---	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2147368	atggagctcatgtaaa[C/T]tctgagcccctactta	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2199215	cattttagtgcctatg[G/T]agataattgcaaatag	G	T	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 664169 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1660223	agtattcaaaaaacatttagaacta[C/T]gtaaatacttgttgaaaagtgaaag	C	T	NM_152774 // intron // 0 // Hs.487670 // MGC42090 // 256130 // hypothetical protein MGC42090	MGC42090	MGC42090 , rs10486366, hypothetical protein MGC42090,p21.1
SNP_A-1800675	gtagaaatgtgagaga[A/C]ccatggagaattttct	A	C	7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// NM_003667 // upstream //	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-1812292	tgaatttgagcaccac[A/G]ctcgtggaataatcgt	A	G	// Homo sapiens hypothetical protein FLJ37464 (FLJ37464), mRNA. /// ENST00000338718 // intron // 0 // --- // --- // --- // ---	FLJ37464	FLJ37464, Homo sapiens hypothetical protein FLJ37464 (FLJ37464), q22.1
SNP_A-1797639	ggtttcttgccagaac[C/T]acctcctcgcagaatc	C	T	Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1790826	gggggcactcatcggc[A/G]gacagtggggaagctg	A	G	sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA. /// ENST00000261883 // CDS // 0 // --- // --- // --- // ---	CILP	CILP, Homo sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), q22.31
SNP_A-1944393	ttgtctataaagtacc[C/T]atcttccctacacgtg	C	T	sapiens phosphodiesterase 8A (PDE8A), transcript variant 4, mRNA. /// NM_173457 // intron // 0 // Hs.9333 // PDE8A //	PDE8A	PDE8A, Homo sapiens phosphodiesterase 8A (PDE8A), transcript variant 4, q25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1941138	ttgctgaagtcttata[C/T]cagatatactatgacc	C	T	Homo sapiens AT rich interactive domain 3B (BRIGHT- like) (ARID3B), mRNA. /// ENST00000346246 // intron // 0 // --- // -	ARID3B	ARID3B, Homo sapiens AT rich interactive domain 3B (BRIGHT- like) (ARID3B), q24.1
SNP_A-1969159	tgagtggtggaggtta[C/T]ggtagactccccgaca	C	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1967792	ctagccagagtcaggc[A/G]agaccaggccagatgt	A	G	// 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 //	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1984007	tttaataagccgctta[C/T]agagaaaactcagcat	C	T	// Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 3 (SLC36A3), mRNA. ///	SLC36A3	SLC36A3, Homo sapiens solute carrier family 36 (proton,q33.1
SNP_A-1883908	tgaagagaatattgac[C/T]gggtgcttccaaaagg	C	T	mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 //	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. p26.1
SNP_A-1884516	tgaagttgcagttttc[A/C]aactttcagggccaga	A	C	Homo sapiens mahogunin, ring finger 1 (MGRN1), mRNA. /// ENST00000262370 // intron // 0 // --- // --- // --- // ---	MGRN1	MGRN1, Homo sapiens mahogunin, ring finger 1 (MGRN1), p13.3
SNP_A-1918135	ttaaactagagtataa[A/G]gaaagatgagtttctc	A	G	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1916877	tgtttctgactccaaa[A/T]tctatgctctactcac	A	T	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 492476 // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1919872	ttaataaaacctatgc[A/G]agtgaatggcaagtac	A	G	7278 // Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, mRNA. /// NM_006001 // upstream // 150254 //	TUBA2	TUBA2, Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, q12.11
SNP_A-2245723	ctggggactccaaata[C/G]agggagacaagaaggg	C	G	// Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // --- // --- // --- // ---	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-2228433	ctacttcaaagactca[A/G]tctacttctttagagg	A	G	// 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// NM_000882 // upstream // 7763 //	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2232678	ctcactacatctgtta[C/T]acaatgatttatctct	C	T	// 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 112927 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2237281	ctctccaaacttccat[A/T]aaaactctgtaggctt	A	T	4602 // Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA. /// NM_017651 //	MYB	MYB, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), q23.3
SNP_A-2236804	ctctactagactgcaa[C/T]ctcttcgatgacagcc	C	T	// 400360 // Homo sapiens FLJ39531 protein (FLJ39531), mRNA. /// NM_003246 // upstream // 316479 // Hs.164226 //	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ39531), q14
SNP_A-2235700	ctcctcagcctccaga[A/G]tagtcaccacatctgg	A	G	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// NM_133509 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-2261964	gaaatacagtggaaaa[A/G]ctcttgaagttcagtg	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 170742 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2271660	gaccactgttgcacac[A/C]actatgtctggctagt	A	C	55971 // Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), mRNA. /// NM_002523 // upstream //	BAIAP2L1	BAIAP2L1, Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), q22.1
SNP_A-2264935	gaagaggatgagctac[G/T]cagagaatagattaca	G	T	79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2283731	gatagcttgttttaag[A/G]agggatgagatgtttt	A	G	PDZRN4 // 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 //	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12
SNP_A-2279117	gaggaattatgggaaa[C/G]aggcgagtttacaaaa	C	G	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 704946 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-2291720	gcacacggtggccaca[A/G]aggtccttatgcttac	A	G	8631 // Homo sapiens src family associated phosphoprotein 1 (SCAP1), mRNA. /// NM_002145 // downstream // 64276 //	SCAP1	SCAP1, Homo sapiens src family associated phosphoprotein 1 (SCAP1), q21.32
SNP_A-2309818	ggaaagttatgttgtg[A/C]aaagcactgtggaaag	A	C	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2306857	gctgtggaacagagac[C/T]gtaattcctttcatgt	C	T	// Homo sapiens protease inhibitor 3, skin-derived (SKALP) (PI3), mRNA. /// NM_198139 // upstream // 28202 // Hs.1968	PI3	PI3, Homo sapiens protease inhibitor 3, skin-derived (SKALP) (PI3), q13.12
SNP_A-2275791	gagacctcaaagcaaa[A/G]cacagggccatgaggg	A	G	/// ENST00000321719 // upstream // 406359 // --- // --- // --- // -	-	p11.21
SNP_A-2272333	gacctgacaatggggga[C/T]gcaagtgacctctgtg	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2270512	gacagacccacccaca[C/T]gttgtactgtgcatct	C	T	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 98010 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2231259	ctattcagagagaaca[C/T]attggtaagattttgg	C	T	Homo sapiens signal transducer and activator of transcription 4 (STAT4), mRNA. /// ENST00000260949 // intron // 0 // --- // -	STAT4	STAT4, Homo sapiens signal transducer and activator of transcription 4 (STAT4), q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2245922	ctgggttaacagaaat[C/G]atctcttaagggatta	C	G	Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA. /// NM_021144 // intron // 0 // Hs.493516 // PSIP1 //	PSIP1	PSIP1, Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), p22.3
SNP_A-2247991	ctgtgctaaaagacac[C/T]gagaaagattcactct	C	T	// 400451 // Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), mRNA. /// NM_004965 // upstream // 24032 // Hs.356285 // HMGN1 // 3150 // Homo	LOC400451	LOC400451, Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), q26.1
SNP_A-2247149	ctgtcacttttgatag[A/G]aatgcacaagaaagtt	A	G	90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 695482 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.3
SNP_A-1919987	ccaagaggaacatata[A/T]caggtcctggtggttt	A	T	/// ENST00000331305 // downstream // 19459 // --- // --- // --- // --- /// ENST00000330861 // downstream // 19459 // --- // ---	-	q21.32
SNP_A-1916351	tgttgtgggattagaa[A/C]tgagttggggagaggc	A	C	// 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1980712	acacgaatgatacata[A/G]gttgagagccattgaa	A	G	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // --- // --- // --- // ---	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1938964	ttgagtagttctaaat[G/T]ataagcatctagaagg	G	T	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1956223	tttgtgtaacccttca[A/T]gtttgacccagtacat	A	T	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-1955926	tttgtcattcttctct[A/T]aatgtatccttttctt	A	T	LOC118430 // 118430 // Homo sapiens small breast epithelial mucin (LOC118430), mRNA. /// ENST00000308796 //	LOC118430	LOC118430, Homo sapiens small breast epithelial mucin (LOC118430), q13.2
SNP_A-1950905	tttccacaagtcagga[C/T]gttgttctagggatca	C	T	3459 // Homo sapiens interferon gamma receptor 1 (IFNGR1), mRNA. /// NM_175747 // downstream // 59811 //	IFNGR1	IFNGR1, Homo sapiens interferon gamma receptor 1 (IFNGR1), q23.3
SNP_A-1947882	tttactttggtggcag[A/G]aaaagtcagatggcag	A	G	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1949305	tttattaaaatgtgaa[C/T]aaaagcagagtatctc	C	T	57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 226934 //	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-1798931	gtaagagacaaaaggc[A/G]ccaatgagaagattca	A	G	92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// NM_006506 // upstream // 111717 // Hs.15999 //	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-1799027	gtaagcccgtcctact[A/G]agaacataaaggaaat	A	G	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 434208 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1800900	gtagaggccctcactg[A/C]atatttaaggaaagat	A	C	Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // intron // 0 // Hs.373857 //	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-1670934	ttctatttttttttttttatcaaag[C/T]attgtgtaattcgttcatcaagaaa	C	T	NM_015430 // intron // 0 // Hs.55044 // DKFZP586H2123 // 25891 // DKFZP586H2123 protein	DKFZP586H2123	DKFZP586H2123 , rs10501140, DKFZP586H2123 protein,p13
SNP_A-1785305	ggctagggcattgtga[C/G]aaatccggctagaatc	C	G	10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mRNA. /// NM_006333 // upstream //	C1D	C1D, Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, p14
SNP_A-1725858	attataatatgttccaataggatta[C/T]gttctctttgggccaacaagtatta	C	T	23520 // acidic (leucine-rich) nuclear phosphoprotein 32 family, member C /// NM_017923 // upstream // 982656 // Hs.136900 // FLJ20668 // 55016 // hypothetical protein	ANP32C	ANP32C , rs1919319, acidic (leucine-rich) nuclear phosphoprotein 32 family, member C ,q32.3
SNP_A-1727190	atgctatcaatcagagaaaataaga[C/G]actataatccttttatgtttttgca	C	G	3696 // integrin, beta 8 /// NM_178559 // upstream // 108348 // Hs.310735 // ABCB5 // 340273 // ATP-binding cassette,	ITGB8	ITGB8 , rs10488586, integrin, beta 8 ,p21.1
SNP_A-1815850	gttaataagcatcaga[A/G]gtgagcttcaaaccca	A	G	ENST00000358401 // intron // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-2185201	caggaacccacaggca[C/G]agcgaaaacagccctc	C	G	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant a, mRNA. /// NM_201432 // intron // 0 // Hs.462214 //	GAS7	GAS7, Homo sapiens growth arrest-specific 7 (GAS7), transcript variant a, p13.1
SNP_A-2170357	caagtaggctatgatc[A/G]acgagatctgctagac	A	G	Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // --- // --- // --- // ---	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-2221798	ccttttctcattaatg[A/G]aacataacacttttaa	A	G	8390 // Homo sapiens olfactory receptor, family 1, subfamily G, member 1 (OR1G1), mRNA. /// ENST00000328890 //	OR1G1	OR1G1, Homo sapiens olfactory receptor, family 1, subfamily G, member 1 (OR1G1), p13.3
SNP_A-2166541	caaatggattgtgaaa[C/T]gggtgactgcagagac	C	T	56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 3711 // Hs.517155 // TMEPAI //	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2111742	aggataagatgcatag[A/T]caagttaatgaacact	A	T	6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 122541 // --- // ---	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-2137358	atcataagaaaatcca[C/T]gtgtttcccagactcc	C	T	// Homo sapiens activin A receptor, type I (ACVR1), mRNA. /// NM_173355 // upstream // 201524 // Hs.128427 // UPP2 //	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2104660	agcagtccaaatcatt[A/G]aatacctaacagagat	A	G	285498 // Homo sapiens hypothetical protein LOC285498 (LOC285498), mRNA. /// ENST00000358000 // intron // 0 // ---	LOC285498	LOC285498, Homo sapiens hypothetical protein LOC285498 (LOC285498), p16.3
SNP_A-2049165	aagctaattctgactc[C/T]gacctttcatcgaagt	C	T	2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream //	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-2010654	aaatcccaattcgaat[A/C]atctctttcaacggta	A	C	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2006935	tctctcttcaaagtat[C/T]actggtaatcaggaac	C	T	-- /// ENST00000359634 // upstream // 553829 // --- // --- // --- // --- /// ENST00000359181 // upstream // 553829 // --- // --- // -	-	q32.3
SNP_A-2013491	cctcactagaaacagg[C/G]aacagccactagtcca	C	G	Homo sapiens serum/glucocorticoid regulated kinase-like (SGKL), transcript variant 2, mRNA. /// NM_013257 // intron //	SGKL	SGKL, Homo sapiens serum q13.1
SNP_A-2022461	aaaaatattctgaata[A/G]caaagaaacagtgaat	A	G	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 440902 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2038152	aacacagtacaaatgc[A/G]gagttctcaaatatgt	A	G	Homo sapiens palmdelphin (PALMD), mRNA. /// ENST00000263174 // intron // 0 // --- // --- // --- // ---	PALMD	PALMD, Homo sapiens palmdelphin (PALMD), p21.2
SNP_A-2044118	aacttgtaacccaccc[A/G]gaatggcagtcctgtg	A	G	Homo sapiens chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA. /// ENST00000255409 // intron // 0 // --- // ---	CHI3L1	CHI3L1, Homo sapiens chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), q32.1
SNP_A-2043358	aactggatgacatgaa[A/C]tgtggggtagcagaca	A	C	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 535926 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2057967	aatattgtacaagata[C/T]gcttctgaaaatttac	C	T	Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, mRNA. /// NM_004100 // intron // 0 //	EYA4	EYA4, Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, q23.2
SNP_A-2091566	agaaaaatcaccctct[A/G]aaagcttcactagtta	A	G	/// ENST00000277891 // upstream // 1110 // --- // --- // --- // --- /// ENST00000333401 // downstream // 12971 // --- // --- // ---	-	q25.3
SNP_A-2091816	agaaaatcagcgcaca[A/G]agatgccaagagaatc	A	G	Homo sapiens integrin, beta 6 (ITGB6), mRNA. /// ENST00000283249 // intron // 0 // --- // --- // --- // ---	ITGB6	ITGB6, Homo sapiens integrin, beta 6 (ITGB6), q24.2
SNP_A-2089608	acttcagtaaaaggga[C/G]agtagtaggtcaattt	C	G	Homo sapiens protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D), mRNA. /// ENST00000305921 // intron // 0 // --- // --- // --- // ---	PPM1D	PPM1D, Homo sapiens protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D), q23.2
SNP_A-2127267	ataaatgggaaatgta[G/T]gatttcataaaattac	G	T	Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // intron // 0 // Hs.19872 // DLGAP1 // 9229 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2152701	attaatctagaaatgg[C/T]aaagaactcttcaacc	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 1217472 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2144813	atgatgtgaggtagta[A/C]attaattagctagatt	A	C	ENST00000268533 // intron // 0 // --- // --- // ---	-	q23.1
SNP_A-2141323	atctgtgaagtaatga[C/T]atgtatcctaatgtta	C	T	NM_001001966 // downstream // 5991 // --- // OR5AT1 // 284532 // Homo sapiens olfactory receptor, family 5,	-	q44
SNP_A-2140805	atctgaaaaaatgaaa[A/C]aggaaggagagatgtg	A	C	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 571981	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2219976	ccttatggcaccacat[C/T]aatgctctgtggaaaa	C	T	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// ENST00000357652 // upstream // 101442 // --- // ---	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2217066	cctcttcatgtgaaca[C/T]gcatatttatcccaat	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2207734	cccaaaaagagaaata[C/T]tattggcttagttagg	C	T	// Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase U) (CPB2), transcript variant 1, mRNA. /// NM_016413 // upstream // 144 // Hs.512937 // CPB2 // 1361	CPB2	CPB2, Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase U) (CPB2), transcript variant 1, q14.13
SNP_A-2178280	cactcacagcttatag[C/T]cctgcaataatttcct	C	T	Homo sapiens zinc finger protein 423 (ZNF423), mRNA. /// ENST00000262383 // intron // 0 // --- // --- // --- // ---	ZNF423	ZNF423, Homo sapiens zinc finger protein 423 (ZNF423), q12.1
SNP_A-2191535	catatgcagacaaagc[A/G]ctatatatttcagagg	A	G	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // --- // ---	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-1838629	tagacaatcgggtctg[C/T]agaaagagttttcatt	C	T	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 574408	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1860702	tcataaatatctctca[C/T]gaacaaattagagtct	C	T	// Homo sapiens hypothetical protein FLJ31340 (FLJ31340), mRNA. /// ENST00000297222 // intron // 0 // --- // --- // --- // ---	FLJ31340	FLJ31340, Homo sapiens hypothetical protein FLJ31340 (FLJ31340), q21.12
SNP_A-1855839	tcaatgagacacagag[A/G]agattaaattgaaaaa	A	G	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1720837	tggttaagtaaataaataaagttaca[A/G]ccatgtctgtttccaatgtatga	A	G	CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 3269158 // Hs.499861 //	CTNNA3	CTNNA3, rs10509192, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1784266	ggcccagagaatcttc[A/G]ctgtcatatttgtca	A	G	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33
SNP_A-1780906	ggatgaaggtttagaac[C/T]catcatgtctgagcc	C	T	10397 // Homo sapiens N-myc downstream regulated gene 1 (NDRG1), mRNA. /// NM_003033 // downstream // 32429 //	NDRG1	NDRG1, Homo sapiens N-myc downstream regulated gene 1 (NDRG1), q24.22
SNP_A-1792985	ggtacattgcaaaaca[C/G]ataaaacaaaacattg	C	G	340351 // Homo sapiens hypothetical protein LOC340351 (LOC340351), mRNA. /// ENST00000275763 // intron // 0 // ---	LOC340351	LOC340351, Homo sapiens hypothetical protein LOC340351 (LOC340351), q33
SNP_A-1795200	ggtgagcgggggaggac[C/T]attctgcctaactagg	C	T	399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 444227 // Hs.299419 //	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds. ,q25
SNP_A-1955508	ttggtgaagagagcc[A/G]cagtccgaacaatggg	A	G	57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 40278 //	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-1958401	ttttccataaggttgca[A/G]taatcaggactgtact	A	G	Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), mRNA. /// ENST00000328219 // 3UTR //	HMGN4	HMGN4, Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), p22.1
SNP_A-1940172	ttgcatcaatgttac[A/G]ggagatatgggtgat	A	G	64759 // Homo sapiens tensin-like SH2 domain containing 1 (TENS1), mRNA. /// NM_022748 // upstream // 309541 //	TENS1	TENS1, Homo sapiens tensin-like SH2 domain containing 1 (TENS1), p12.3
SNP_A-1942824	ttgggggacccagatcc[A/T]ccttgttttttgattt	A	T	29094 // Homo sapiens HSPC159 protein (HSPC159), mRNA. /// ENST00000335402 // upstream // 29063 // --- // ---	HSPC159	HSPC159, Homo sapiens HSPC159 protein (HSPC159), p14
SNP_A-1942699	ttgggatcaacttttag[A/C]aattaaaaaagaatcag	A	C	Homo sapiens keratin 25B (KRT25B), mRNA. /// ENST00000335552 // intron // 0 // --- // --- // --- // ---	KRT25B	KRT25B, Homo sapiens keratin 25B (KRT25B), q21.2
SNP_A-1966460	tgtaaataaaaggaac[A/G]gactactggctgggca	A	G	// Homo sapiens hypothetical protein FLJ38973 (FLJ38973), mRNA. /// ENST00000319974 // intron // 0 // --- // --- // ---	FLJ38973	FLJ38973, Homo sapiens hypothetical protein FLJ38973 (FLJ38973), q33.1
SNP_A-1912530	tgtgcattatttcatc[C/T]acacaggtaactgac	C	T	FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 536786 //	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1912440	tgtgcacgtccaccac[C/T]gaacatcactctatgc	C	T	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 268025 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.32
SNP_A-1909639	tgtcaacaagtcttac[A/G]aggcctgacaggagcc	A	G	6935 // Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA. /// NM_018287 // downstream // 34221 // Hs.499264 // ARHGAP12 // 94134 //	TCF8	TCF8, Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), p11.22
SNP_A-1882992	tgaaataatacacttttc[A/C]aatttgtactgggggc	A	C	ENST00000358349 // intron // 0 /// --- // --- // --- // ---	-	q36.3
SNP_A-1889170	tgagtcctgtgaggta[A/G]gaccaccattatacag	A	G	FLJ20618 // 55000 // Homo sapiens hypothetical protein FLJ20618 (FLJ20618), mRNA. /// NM_134269 // upstream //	FLJ20618	FLJ20618, Homo sapiens hypothetical protein FLJ20618 (FLJ20618), q12.2
SNP_A-1890948	tgatggagcagcctaa[A/G]aagtcaagcagtcct	A	G	8411 // Homo sapiens early endosome antigen 1, 162kD (EEA1), mRNA. /// NM_021104 // downstream // 93105 //	EEA1	EEA1, Homo sapiens early endosome antigen 1, 162kD (EEA1), q22
SNP_A-2247709	ctgtgaagtacaggac[A/G]ggccttgttatcactg	A	G	221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream //	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-2255893	ctttaaagaaattacc[A/G]atgatttatcttacta	A	G	ENST00000345030 // intron // 0 /// --- // --- // ---	-	q11.21
SNP_A-2230696	ctatgaacataggtag[A/G]aacacttttatatgg	A	G	Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// ENST00000310430 // intron // 0 // --- // --- // --- // ---	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2236109	ctccttactcatctgc[A/G]actcatctggtcctgg	A	G	54502 // Homo sapiens RNA-binding protein (FLJ20273), mRNA. /// NM_024677 // upstream // 202259 // Hs.479612 //	FLJ20273	FLJ20273, Homo sapiens RNA-binding protein (FLJ20273), p14
SNP_A-2258943	cttttctctgatagac[G/T]atatgtctgtgatgt	G	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1374133	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2273023	gactagtgtcaggtga[C/G]gctagacactggtctt	C	G	Homo sapiens stromal interaction molecule 1 (STIM1), mRNA. /// ENST00000300737 // intron // 0 // --- // --- // ---	STIM1	STIM1, Homo sapiens stromal interaction molecule 1 (STIM1), p15.4
SNP_A-2285175	gatctatttccgtcaa[A/C]ctgaaaggactaaca	A	C	157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000355465 // upstream //	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-2281466	gagtcataataaacac[C/T]gtatactatgccacca	C	T	2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 31522 // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-2281788	gagtgacttacggtcc[A/G]ggaagagtacatctgc	A	G	10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 253033 //	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2294568	gcagtctgaatttaca[C/T]tgacagaaagcaaatt	C	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2309507	ggaaacatggaagaaa[A/G]tccaagtctctctgat	A	G	sapiens leukemia inhibitory factor receptor (LIFR), mRNA. /// ENST00000263409 // intron // 0 // --- // --- // ---	LIFR	LIFR, Homo sapiens leukemia inhibitory factor receptor (LIFR), p13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2303888	gctcatatttacaaaa[C/T]tgaaaggaaaggatga	C	T	sapiens mRNA for TBX18 protein, partial. /// ENST00000330469 // intron // 0 // --- // --- // --- // --- ///	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2282920	gataaatttgacaaaa[A/G]tgcctgctctttgggg	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-2267340	gaatagatggtaaata[G/T]agaaacggtgactcaa	G	T	ENST00000356159 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1895800	tgcctgcctgagtgga[A/G]aagttgactctcaggc	A	G	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1894059	tgcatctccaggtgcc[G/T]cctctgctatgacaca	G	T	Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// ENST00000355144 // intron // 0 // --- // ---	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-1900276	tggagaatggtcctga[C/T]ggccaactgtgtacag	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 14223 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1875425	tctctgctcacgggga[A/T]cgggacgtcaagatga	A	T	864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 118954 //	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-1911522	tgtctttctgctcaac[C/T]gtaaaagccctttaga	C	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1915571	tgttctatttacagcc[A/G]attcaaaaaaccttaa	A	G	Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-1967681	ctaaaaccaccaggga[C/T]gcttgtgaagtatgca	C	T	6248 // Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), mRNA. /// ENST00000320153 // downstream // 7473 // --- // --- // --- // --- /// ENST00000345034	RSC1A1	RSC1A1, Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), p36.13
SNP_A-1963890	atcccaacaggatttc[A/G]ccaaaacagcaatctg	A	G	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1980069	tgcctactccacgtta[C/T]acaaatacacctcctc	C	T	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // ---	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-1983006	gcccaactctgaacta[C/T]aaagaatggttaaagg	C	T	YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 7983 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.3
SNP_A-1938415	ttgactggcatcacgc[A/G]aactcagtgtgctagg	A	G	3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// NM_181705 // upstream // 3350	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3
SNP_A-1935695	ttctgtcttgggaacc[A/G]gcctcgaggacttaaa	A	G	1024 // Homo sapiens cyclin-dependent kinase 8 (CDK8), mRNA. /// NM_006646 // upstream // 39879 // Hs.82318 //	CDK8	CDK8, Homo sapiens cyclin-dependent kinase 8 (CDK8), q12.13
SNP_A-1804802	gtcagtctgattccaa[A/G]gtctgtgatcttttaa	A	G	// Homo sapiens secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA. /// NM_003833 // downstream // 28613 // Hs.278489 // MATN4 // 8785 // Homo	SLPI	SLPI, Homo sapiens secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), q13.12
SNP_A-1811505	gtgctccatagccaca[C/G]gcagccagagcctact	C	G	Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), mRNA. /// ENST00000355086 // intron // 0 // --- //	SRGAP1	SRGAP1, Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), q14.2
SNP_A-1781012	ggatgattaactgtgc[A/G]ctttagaaagattctt	A	G	// 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream // 214235 //	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-1714308	atttaccaatgaaaaaatagaggcc[A/G]cagctctgctttaagccagctagtg	A	G	NM_030923 // intron // 0 // Hs.374353 // DKFZP566N034 // 81615 // hypothetical protein DKFZp566N034	DKFZP566N034	DKFZp566N034 , rs954057, hypothetical protein DKFZp566N034,q21.3
SNP_A-1648248	gggccattacaaccataaatcctga[C/T]actactgagcaaaattcatcaaaat	C	T	8932 // methyl-CpG binding domain protein 2 /// NM_005215 // downstream // 25852 // Hs.172562 // DCC // 1630 // deleted	MBD2	MBD2 , rs9304445, methyl-CpG binding domain protein 2 ,q21.2
SNP_A-1702759	tccaccacagaccatccattgcaga[A/G]gcagcacttaactgggtggacaag a	A	G	90390 // thyroid hormone receptor associated protein 6 /// NM_173851 // downstream // 233088 // Hs.179082 //	THRAP6	THRAP6 , rs1586601, thyroid hormone receptor associated protein 6 ,q24.11
SNP_A-1700530	atatagcactttattatactgaaac[C/T]gttatattgattcaccatgggagtg	C	T	5101 // protocadherin 9 /// NM_020866 // downstream // 1133570 // Hs.106808 // KLHL1 // 57626 // kelch-like 1	PCDH9	PCDH9 , rs588455, protocadherin 9 ,q21.33
SNP_A-1862107	tcatgccttccttacc[A/G]atgctgtaattttcct	A	G	5687 // Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA. /// NM_020529 // downstream // 25777 // Hs.81328 // NFKBIA // 4792 // Homo	PSMA6	PSMA6, Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), q13.2
SNP_A-1873887	tctcagtatccacaag[C/T]cctaaacttcaccaat	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1180894 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1825905	taaatgatttgtataa[C/T]ggtttgggaaacacat	C	T	54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 74895 // Hs.365690 // KCNK10 //	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-1827319	taacggccagctctcc[G/T]gagagaaaattcctga	G	T	Homo sapiens CD209 antigen-like (CD209L), transcript variant 3, mRNA. /// NM_214677 // intron // 0 // Hs.421437 //	CLEC4M	CLEC4M, Homo sapiens CD209 antigen-like (CD209L), transcript variant 3, p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2185397	caggacagaaagtgtg[A/G]aaagacagcacaatgc	A	G	Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // --- // --- // --- // ---	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2186306	caggctctgcaaaata[C/T]ctgaagcactgatttt	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2180859	cagaatgacacctacc[A/G]ggcataggaacgttaa	A	G	Homo sapiens tubulin tyrosine ligase-like family, member 3 (TTLL3), mRNA. /// ENST00000310252 // 3UTR // 0 // --- // ---	TTLL3	TTLL3, Homo sapiens tubulin tyrosine ligase-like family, member 3 (TTLL3), p25.3
SNP_A-2221277	cctttagtgggagcaa[A/G]acaacgcagtgtggca	A	G	FLJ38717 // 401261 // Homo sapiens FLJ38717 protein (FLJ38717), mRNA. /// ENST00000356304 // downstream //	FLJ38717	FLJ38717, Homo sapiens FLJ38717 protein (FLJ38717), p21.1
SNP_A-2224185	cggtctgcagctcaga[C/G]accttttaggggtagcc	C	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 284960 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.32
SNP_A-2145829	atgccatatgaaaagg[G/T]agttcaggggcccata	G	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 996715 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2088699	actgtggcattcaaag[C/T]ctctgcagtccagccc	C	T	// Homo sapiens mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), mRNA. /// ENST00000357955 // intron // 0 // --- // --- // --- // --- ///	MAPKAPK3	MAPKAPK3, Homo sapiens mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), p21.31
SNP_A-2082031	acctttccttgggga[A/G]gagaaatccatggtat	A	G	146 // Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), mRNA. /// NM_000311 // upstream // 56917 //	ADRA1D	ADRA1D, Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), p13
SNP_A-2057345	aatatattccatatga[C/T]gatgagaagaatgtat	C	T	// Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), mRNA. /// NM_001005167 // upstream // 6959 // Hs.534693 // OR52E6 // 390078 // Homo sapiens	OR52E8	OR52E8, Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), p15.4
SNP_A-2076721	acattttggctaagta[A/C]attcttataagggaaa	A	C	8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 144989 // Hs.503510 // EED // 8726 // Homo	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2039807	aacattaggctcaaaa[C/T]cctgcaggtccctctg	C	T	Homo sapiens armadillo repeat containing 4 (ARMC4), mRNA. /// ENST00000305242 // intron // 0 // --- // --- // --- // ---	ARMC4	ARMC4, Homo sapiens armadillo repeat containing 4 (ARMC4), p12.1
SNP_A-2035765	aaatgtggtagaaata[A/C]catgaatgtgttctag	A	C	Homo sapiens putative S1 RNA binding domain protein (PS1D), mRNA. /// ENST00000263699 // intron // 0 // --- // ---	PS1D	PS1D, Homo sapiens putative S1 RNA binding domain protein (PS1D), p35.2
SNP_A-2036448	aaattctggagtcgat[A/T]accctttttcaggatg	A	T	/// ENST00000354196 // upstream // 905528 // --- // --- // --- // --- /// ENST00000355224 // upstream // 905528 // --- // --- // ---	-	q21.11
SNP_A-2024108	aaaagataatatttca[A/G]ctgacttttggtaaca	A	G	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 608243 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2012946	tcattttaggagacaa[C/T]tcctctatcacctttc	C	T	Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // --- // --- // --- // --- /// ENST00000356360 // intron // 0 // --- // ---	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2018566	aacagttgcatgtgca[C/G]aatcagcacaatcctc	C	G	RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 23138 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2017666	tctaaagaaccataaa[A/G]aggtcattggtttgca	A	G	// 571 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 1 (BACH1), transcript variant 1, mRNA. /// NM_001186 // downstream // 131146 //	BACH1	BACH1, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 1 (BACH1), transcript variant 1, q21.3
SNP_A-2009911	tgatgcaataatttaa[A/C]ctttcctttgaagggg	A	C	// 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13), mRNA. /// NM_144571 // downstream // 84943 // Hs.183085 // CNOT6L // 246175 //	CXCL13	CXCL13, Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13), q21.1
SNP_A-2004040	ttttaaatctttaaaa[C/G]aaaacagtgaagtggc	C	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 987315 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-2072797	acagctcttgcatttc[C/T]actatttggtatatgt	C	T	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2072403	acagcactcacaccca[C/T]gttgtgcatccaaaat	C	T	ENST00000298738 // intron // 0 // --- // --- // --- // ---	-	q14.13
SNP_A-2070469	acaccctcagtccata[C/T]gttcacaactcaatca	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2058492	aatcagaaccattggc[C/T]gatgacctcaggcttg	C	T	Homo sapiens vacuolar protein sorting 13D (yeast) (VPS13D), transcript variant 1, mRNA. /// ENST00000356315 // intron // 0 // --- // --- // --- /// ENST00000358136 // intron // 81608 // Homo sapiens FiP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 81537 // Hs.407755 //	VPS13D	VPS13D, Homo sapiens vacuolar protein sorting 13D (yeast) (VPS13D), transcript variant 1, p36.21
SNP_A-2052829	aagtcagaggcataat[C/G]aagagttatttaggtc	C	G		FIP1L1	FIP1L1, Homo sapiens FiP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-2051837	aaggtctgtgcggtga[A/G]aatatgagtgagggaa	A	G	Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // --- // ---	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2083256	actaaactaaaagaa[C/G]agattccaatggtatt	C	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 382361 // --- // --- // --- //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2079974	acccttaccaaagaa[A/C]ctgatcttaccaatta	A	C	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6), complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-2092088	agaaactcacaattcc[C/T]aagttaatcctctcac	C	T	// Homo sapiens cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis) (CER1), mRNA. /// ENST00000276911 // upstream // 716 // --- // --- // --- ///	CER1	CER1, Homo sapiens cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis) (CER1), p22.3
SNP_A-2096000	agacagtgagcaaaaa[C/T]ggcaccttcgcaaacc	C	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 443433 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2167005	caacaacatatgctgai[C/T]attcatgtaataaacc	C	T	140947 // Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// NM_006161 // downstream // 42362 //	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1
SNP_A-2162973	atttgttaataccaa[G/T]caacatcagttaata	G	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2135729	atcaaacggaccaaca[C/G]aacagtgataccgtag	C	G	4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // upstream // 15944 // Hs.357630 // LMX1A //	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-2113112	aggccagtgatgaggg[C/G]aagtcaaaccaagaag	C	G	ENST00000298738 // intron // 0 // --- // --- // ---	-	q14.13
SNP_A-2222845	cgcaaaaagtgtttga[A/G]attaaagtcttaccac	A	G	7278 // Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, mRNA. /// NM_006001 // upstream // 156743 //	TUBA2	TUBA2, Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, q12.11
SNP_A-2204986	ccagggtcccaggcaa[A/G]agcaaatacacatcct	A	G	/// ENST00000338636 // upstream // 274519 // --- // --- // --- // --- /// ENST00000334344 // upstream // 362509 // --- // --- // ---	-	q12
SNP_A-2206907	ccatggtcacaccaac[A/G]aggcttcatgtttcag	A	G	197370 // Homo sapiens non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA. /// NM_000418 // upstream // 55440 // Hs.513457 // IL4R // 3566	NSMCE1	NSMCE1, Homo sapiens non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), p12.1
SNP_A-2169391	caagcatgaagtagac[C/T]ggtatgttggagtaac	C	T	--- /// ENST00000345029 // upstream // 28511 // --- // --- // ---	-	p14
SNP_A-2174377	cacagaaataaagctc[A/G]gaatcatatatctcta	A	G	Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // --- // --- // ---	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1869837	tcctcctgtgcctcc[A/G]agagaagatctccaat	A	G	57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 791350 // --- // ---	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q13.11
SNP_A-1809550	gtgagaggtatgtgaa[C/T]attgtggccaaaggg	C	T	85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 131719 // Hs.377155 // LYRIC //	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-1801380	gtaggatattgtttaa[C/T]gtcacaaagctagagg	C	T	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 251740 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1787389	gggaaggccaccacaa[A/C]accaaggaaaacatccc	A	C	sapiens nidogen (enactin) (NID), mRNA. /// ENST00000264187 // intron // 0 // --- // --- // --- ///	NID	NID, Homo sapiens nidogen (enactin) (NID), q42.3
SNP_A-1948501	tttagtgctgtaaaga[C/G]aatgaaaaggaagctt	C	G	// Homo sapiens cofilin 2 (muscle) (CFL2), transcript variant 1, mRNA. /// NM_138638 // upstream // 2523 // Hs.180141 //	CFL2	CFL2, Homo sapiens cofilin 2 (muscle) (CFL2), transcript variant 1, q13.1
SNP_A-1969947	agcacaaaatataccaa[C/G]tacgtaaattcagagt	C	G	337972 // Homo sapiens keratin associated protein 19-5 (KRTAP19-5), mRNA. /// NM_181612 // downstream // 26448	KRTAP19-5	KRTAP19-5, Homo sapiens keratin associated protein 19-5 (KRTAP19-5), q22.11
SNP_A-1917367	tgtttctgtttggtc[C/T]aagaaggatgaaagaa	C	T	Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // intron // 0 // --- // --- // ---	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-1918464	ttaaatatacttaaaaa[G/T]tctttggctattagaa	G	T	// 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 134298 // Hs.282787 // FOXP2 /	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1923500	ttaggctggtgcaaaa[C/G]taattgtaatttcaga	C	G	H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 722985 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1932021	ttcctagagtaggacа[A/G]ataatcttatccagga	A	G	121391 // Homo sapiens keratin 6 irs4 (K6IRS4), mRNA. /// NM_080747 // downstream // 10995 // Hs.147040 // K6IRS2 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. ///	K6IRS4	K6IRS4, Homo sapiens keratin 6 irs4 (K6IRS4), q13.13
SNP_A-1926313	ttattagtattcagca[C/T]aataccagtgggcac	C	T	BC013983 // downstream // 463620 // Hs.481133 // SPOCK3 // Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 200497 //	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1874118	tctcattgccattatc[A/T]atctttttttctaggg	A	T		RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1887222	tgagaacagactaata[C/T]aattaccatttggtga	C	T	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1531762 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1893761	tgcagtgtgagtggg[G/T]acgtagcacagctggt	G	T	11075 // Homo sapiens stathmin-like 2 (STMN2), mRNA. /// NM_012258 // downstream // 39661 // Hs.234434 // HEY1 //	STMN2	STMN2, Homo sapiens stathmin-like 2 (STMN2), q21.13
SNP_A-2261820	gaaataaaacccatga[C/T]tcaaatctctaaacct	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 516790 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2261028	gaaagaagaggtacca[C/T]tggacagctggtgac	C	T	Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), mRNA. /// ENST00000262120 // intron // 0 // --- // --	TWSG1	TWSG1, Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), p11.22
SNP_A-2242063	ctgatttacacagcgc[C/T]caaagattggttggac	C	T	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 228580 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-2243248	ctgcctgcctgttgc[A/G]gagacccagctacatg	A	G	10859 // Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 (LILRB1), mRNA. /// NM_006847 // upstream // 8044 // Hs.67846 // LILRB4 // 11006 // H	LILRB1	LILRB1, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 (LILRB1), q13.42
SNP_A-2249191	ctgtttctccattct[A/G]aaatctaaaatggga	A	G	Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member A (ANP32A), mRNA. /// ENST00000267918 // intron // 0 // --- // --- // --- // ---	ANP32A	ANP32A, Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member A (ANP32A), q23
SNP_A-2238122	ctctgccaggacctga[A/G]ctgagcttccaagatt	A	G	ENST00000268043 // downstream // 33704 // --- // --- // --- // --	-	q22.31
SNP_A-2232743	ctcactctgcatgac[C/T]ggctccaatagaagca	C	T	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2271952	gaccccactacataaa[C/T]accagaactgaaaatt	C	T	DKFZp434M0331 // 55592 // Homo sapiens hypothetical protein DKFZp434M0331 (DKFZp434M0331), mRNA. /// NM_022496 // upstream // 8426 // Hs.115088 // ACTR6 //	DKFZp434M0331	DKFZp434M0331, Homo sapiens hypothetical protein DKFZp434M0331 (DKFZp434M0331), q23.1
SNP_A-2283856	gatagtgactgtcttc[A/T]cctattgggttatggg	A	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript v /// NM_006264 // intron // 0 //	PTPN13	PTPN13, Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1 q21.3
SNP_A-2304265	gctcctcttttaaca[A/G]tgacagagaaaggaaa	A	G	C14orf37 // 145407 // Homo sapiens chromosome 14 open reading frame 37 (C14orf37), mRNA. /// ENST00000281555	C14orf37	C14orf37, Homo sapiens chromosome 14 open reading frame 37 (C14orf37), q23.1
SNP_A-2294638	gcagtgcaatataata[C/T]taaatggcttcctata	C	T	55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 128164 // --- // --- //	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. ,q36.2
SNP_A-2289809	gcaaacacagcctcaa[C/G]ctagccagaaaaact	C	G	– /// ENST00000342478 // downstream // 145095 // --- // --- //	-	q11.21
SNP_A-1900432	tggagatgtgaaggaa[A/G]tacaggtgggtaagaa	A	G	55507 // Homo sapiens G protein-coupled receptor, family C, group 5, member D (GPRC5D), mRNA. /// NM_015987 // downstream // 21294 // Hs.294133 // HEBP1 // 50865 //	GPRC5D	GPRC5D, Homo sapiens G protein-coupled receptor, family C, group 5, member D (GPRC5D), p13.1
SNP_A-1898139	tgctgttattgcactg[C/T]ataatttgctataata	C	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 463113 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1926468	ttattcatggaagaaa[C/T]attgtgataaaggagt	C	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1929307	ttcagtcaacactgac[C/T]gcgtaccaagcactgg	C	T	10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream //	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-1960881	tttttgaccattaaaa[A/C]aaatctctttcaaat	A	C	DKFZp434K2435 // 84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// NM_006159 // downstream // 102205 // Hs.505326 // NELL2	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-1935808	ttctgttataagtccat[C/T]attagacttgcatcat	C	T	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 42061 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1938615	ttgagagctgaaagga[C/G]gccaaagaaagactgg	C	G	Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA. /// ENST00000260056 // intron // 0 // --- // ---	RAB30	RAB30, Homo sapiens RAB30, member RAS oncogene family (RAB30), q14.1
SNP_A-1786647	ggcttgagggcaggta[A/G]ccatgtctagttctct	A	G	Homo sapiens tetratricopeptide repeat domain 4 (TTC4), mRNA. /// ENST00000294374 // intron // 0 // --- // --- // --- // ---	TTC4	TTC4, Homo sapiens tetratricopeptide repeat domain 4 (TTC4), p32.3
SNP_A-1808380	gtgaaaacaaaacagg[G/T]atttttatatcagagg	G	T	79625 // Homo sapiens hypothetical protein FLJ23191 (FLJ23191), mRNA. /// NM_024873 // downstream // 52465 //	FLJ23191	FLJ23191, Homo sapiens hypothetical protein FLJ23191 (FLJ23191), q27
SNP_A-1814513	gtgtgccttaaagaaa[G/T]gaagaggagattggaa	G	T	Homo sapiens adenylate cyclase 5 (ADCY5), mRNA. /// ENST00000309879 // intron // 0 // --- // --- // ---	ADCY5	ADCY5, Homo sapiens adenylate cyclase 5 (ADCY5), q21.1
SNP_A-1700187	agaagtaattaaccaagagacgata[A/C]ctttagtaaaaagaatactctctttt	A	C	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1 , rs1946303, SEC8-like 1 (S. cerevisiae),q33
SNP_A-1674591	cttttctcttcctgatagggttaca[A/G]attcccccagttgctctaggaactg	A	G	NM_005197 // intron // 0 // Hs.211773 // C14orf116 // 55453 // chromosome 14 open reading frame 116	C14orf116	C14orf116 , rs10498620, chromosome 14 open reading frame 116,q32.11
SNP_A-1873491	tctcaatatccagaga[C/G]agcctgttggtcctgg	C	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1848300	tatcttttgctgtata[C/T]gaaatttggccaaatc	C	T	/// ENST00000357074 // downstream // 197161 // --- // --- // --- // --- /// ENST00000358765 // downstream // 197161 // --- // ---	-	p14
SNP_A-2188501	cagtgacttccaactg[G/T]cagtatttgtatcctc	G	T	2996 // Homo sapiens glycophorin E (GYPE), transcript variant 1, mRNA. /// NM_198682 // downstream // 26156 //	GYPE	GYPE, Homo sapiens glycophorin E (GYPE), transcript variant 1, q31.21
SNP_A-2191735	catattgtagacttaa[A/G]attaaattgcccataa	A	G	/// ENST00000356128 // upstream // 111176 // --- // --- // --- // ---	-	q24
SNP_A-2207740	cccaaaaatgcatgat[A/G]aatagtggccattatt	A	G	Homo sapiens transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), albumin proximal factor (TCF1), mRNA. /// ENST00000257555 // intron // 0 // --- // --- // --- // ---	TCF1	TCF1, Homo sapiens transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), albumin proximal factor (TCF1), q24.31
SNP_A-2110158	aggaagggagcaaaaa[A/T]ggagcagccttcgggc	A	T	9630 // Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// NM_002072 // downstream // 58592 // Hs.269782 // GNAQ // 2776 // Homo	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-2121695	agtgacaataccaaat[G/T]atggccatgatacaga	G	T	Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000274462 // intron // 0 // --- // --- // --- // --- ///	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1
SNP_A-2130464	taagagcataatgcta[C/T]agtgcgcttccaagac	C	T	Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 //	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2162786	attttgattgattcaa[C/G]gttttgttaatatgaa	C	G	161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream //	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2164843	caaacccaccgcagac[A/G]ctcccagacttacccg	A	G	sapiens death-associated protein (DAP), mRNA. /// ENST00000338956 // intron // 0 // --- // --- // --- // --- ///	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2156241	ttaaaaagtaattgaa[A/C]acacttgccacgtctc	A	C	1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // upstream // 554796 // Hs.129452 // DACH1 // 1602 // Homo	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-2146956	atggaaaggagcagta[A/G]catttgggtgttgtca	A	G	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-2102922	caaacacttaagtccc[C/T]ggcctaaggtcacaca	C	T	// 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 266918 // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2080119	accggcctatgttaga[A/G]tatttaatttccaaag	A	G	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 568518 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2054413	aagtttagagtgaaca[C/G]agaatgaatcatgatt	C	G	57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 595824 // --- // --- // --- // ---	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q21
SNP_A-2049285	aagctcagtgccaaca[C/G]tctgtttagaatttgt	C	G	119774 // Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), mRNA. /// NM_001005171 // upstream // 12997 // --- // OR52K1 //	OR52K2	OR52K2, Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), p15.4
SNP_A-2065183	aattggagaagaattg[C/T]aactcactctctcaaa	C	T	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 630747 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2063605	aattacattcccttaa[A/G]taatagtgcataaaat	A	G	8050 // Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), mRNA. /// NM_001001392 // upstream	PDHX	PDHX, Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), p13
SNP_A-2067643	atcaaaagatttttca[C/T]gggcctggaagaatag	C	T	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 797228 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2066528	aatttttttattggaa[C/G]aaaacttgttgtactt	C	G	/// ENST00000355063 // upstream // 500913 // --- // --- // --- // ---	-	q22.1
SNP_A-2072624	acagccctgtcatcca[C/T]gtgcttccggtgaatc	C	T	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 231435 // ENST00000333644 // intron // 0 // --- // --- // ---	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2026491	aaacaaagtcaaaagc[A/C]agagtcctggaggtta	A	C		-	q35.2
SNP_A-2022547	aaaaatctgttcaggc[C/T]attgtagctcagtctg	C	T	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2045834	aagacataaacaggca[C/G]aaaatacaaatggcaa	C	G	Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // intron // 0 // --- // --- // ---	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2125371	agtttaaagtgtgaaa[C/T]gttaatgctaatttta	C	T	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.3
SNP_A-2108837	agctgttggtcaagca[A/G]ggctcttactagagg	A	G		FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2181746	cagagagttctcaatg[A/G]aaccactatatatatt	A	G	Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // intron // 0 //	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-1869418	tcctgtctgctcacca[A/G]gccatggtcatcaaag	A	G	Homo sapiens CXXC finger 1 (PHD domain) (CXXC1), mRNA. /// ENST00000285106 // CDS // 0 // --- // --- // --- // --- // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 604396 // Hs.211225 // NOVA1 // 4857 //	CXXC1	CXXC1, Homo sapiens CXXC finger 1 (PHD domain) (CXXC1), q21.1
SNP_A-1867836	tcctacacaaaggaac[A/G]gtccatctgaaatctg	A	C		NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1839467	tagatacccacttagta[C/T]ggacacacctctctt	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2016540 // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds., p21.1
SNP_A-1735272	ccatttacgatttagaaatatggt[C/T]agatgcaataaggtttaacttgccc	C	T	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // ATPase, Class V, type 10B	ATP10B	ATP10B , rs2421528, ATPase, Class V, type 10B,q34
SNP_A-1780789	ggatctatacccaaaag[C/T]aggagagacaaatcca	C	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 271051 // --- // --- // --- // ---	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1788365	gggaggtcaaatattc[A/G]agaccttttgtaatct	A	G	23171 // Homo sapiens glycerol-3-phosphate dehydrogenase 1-like (GPD1L), mRNA. /// NM_178868 // upstream // 40922 // NM_152754 // intron // 0 // Hs.201340 // SEMA3D // 223117 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), mRNA. /// ENST00000284136 // intron // 0 // --- // --- // --- // ---	GPD1L	GPD1L, Homo sapiens glycerol-3-phosphate dehydrogenase 1-like (GPD1L), p23
SNP_A-1937066	ttctttcttatgta[A/G]aatcagcttttatgag	A	G		SEMA3D	SEMA3D, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), q21.11
SNP_A-1937067	ttcttttcttctaac[A/G]ctgtccactaatta	A	G	117145 // Homo sapiens C-terminal modulator protein (CTMP), transcript variant 1, mRNA. /// NM_176853 //	CTMP	CTMP, Homo sapiens C-terminal modulator protein (CTMP), transcript variant 1, q21.3
SNP_A-1969127	ctagagccaatgatga[C/G]taaaaagtacttaatt	C	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1927879	ttcaagtggtaacccl[C/G]aaaccaccacacggaa	C	G	Homo sapiens a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19), transcript variant 1, mRNA. /// NM_033274 // CDS // 0 // Hs.483944 // ADAM19 // 8728 //	ADAM19	ADAM19, Homo sapiens a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19), transcript variant 1, q33.3
SNP_A-1927946	ttcaatatggtcaga[C/T]ctcagctaaaagactg	C	T	669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 //	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1915805	tgttgaaatgttagta[A/G]aatcagcttaaggtgc	A	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 481679 // Hs.426324 // TUSC3 // NM_001503 // intron // 0 // Hs.512001 // GPLD1 // 2822 // Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, mRNA. /// ENST00000230036 // intron // 0 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2230768	ctatgagagtccacaa[C/T]gcagaaatgatgtcat	C	T		GPLD1	GPLD1, Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, p22.2
SNP_A-2235868	ctcctgaagtcctcac[G/T]catttgttcaaacctac	G	T	Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), mRNA. /// ENST00000302909 // intron // 0 // --- // ---	KCNK3	KCNK3, Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), p23.3
SNP_A-2250215	cttacttgctgtttgt[C/T]aacagagagtaagctt	C	T	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2248749	ctgttctcacttccac[A/G]ggccatcaagaatatg	A	G	Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 2, mRNA. /// NM_153485 // intron // 0 // Hs.481942 //	NUP155	NUP155, Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 2, p13.2
SNP_A-2265535	gaagccgctcgagctg[A/C]aaaatgagtattgtgc	A	C	ENST00000251041 // intron // 0 // --- // --- // ---	-	q33.3
SNP_A-2263929	gaactagaacaattac[C/T]agggataatgaggggc	C	T	90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 8389 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2260504	gaaacagatatgaagg[A/G]aaaagctatttaaagc	A	G	Homo sapiens lactate dehydrogenase B (LDHB), mRNA. /// ENST00000350669 // intron // 0 // --- // --- // --- // ---	LDHB	LDHB, Homo sapiens lactate dehydrogenase B (LDHB), p12.1
SNP_A-2288478	gattgaactccagcta[A/G]gtttgggggtgatgaa	A	G	// 4336 // Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), mRNA. /// NM_182934 // downstream	MOBP	MOBP, Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), p22.2
SNP_A-2304308	gctcctgtttttgttc[C/T]ccatctccctttctcc	C	T	Homo sapiens chromosome 9 open reading frame 25 (C9orf25), mRNA. /// ENST00000297620 // intron // 0 // --- // ---	C9orf25	C9orf25, Homo sapiens chromosome 9 open reading frame 25 (C9orf25), p13.3
SNP_A-2309466	ggaaacacccatgtag[C/G]attcttcaatgtctct	C	G	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1899518	tggaagccctgcactc[C/T]atcccccgatacctca	C	T	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-1882825	tgaaagcataaactgt[A/C]aatcctgtttttctct	A	C	Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // --- // --- // --- // ---	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-1884753	tgaatatttctacaca[A/G]taaatgcataagtaca	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1879903	tcttcctaagcgatga[A/G]catctcaatttgctgc	A	G	ENST00000303646 // intron // 0 // --- // --- // --- // ---	-	p36.23
SNP_A-1987712	tccttgagcaattcac[A/G]ctgcagtcagaagaat	A	G	6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 325513 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1987935	aggttgtataacttca[C/T]aggaaaagcttcataa	C	T	3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 40752 // Hs.112783 // AIG1 // 51390 // Homo	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-1977197	gcaggacagctttgca[C/G]acaaaaggctaagatg	C	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 174875 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1792325	gggttgatgttcttac[C/T]cattttacacatgaag	C	T	Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// ENST00000301776 // intron // 0 // --- // --- // --- // ---	ASRGL1	ASRGL1, Homo sapiens asparaginase like 1 (ASRGL1), q12.3
SNP_A-1802696	gtatgagttgcaccaa[A/G]cctctggagaaagtc	A	G	FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-1802726	gtatgcacagagagga[A/G]caaaatgctgagagtg	A	G	161725 // Homo sapiens chromosome 15 open reading frame 16 (C15orf16), mRNA. /// ENST00000307050 //	C15orf16	C15orf16, Homo sapiens chromosome 15 open reading frame 16 (C15orf16), q13.3
SNP_A-1737844	gatacttttatcctcatactataaa[A/G]gaagagtttattctgatcatgcaat	A	G	// 26040 // SET binding protein 1 /// NM_020783 // upstream // 241826 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs10502813, SET binding protein 1 ,q12.3
SNP_A-1829804	taataaatgatgaaga[C/T]atgaaataaggcagta	C	T	Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // intron // 0 // Hs.117767 //	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1825891	taaatgagtgttgaaa[C/G]tgttcctatttcccag	C	G	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-1820007	gttgtttactgggtga[C/T]aaattaggaaactttt	C	T	Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- //	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1872570	gaacagctggacccat[A/G]atctggcttctccagc	A	G	54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 121470 // Hs.464079	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-1855767	tcaatccgtcaatcaa[C/T]aaggacaagaaaggaa	C	T	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 17620 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-2177681	cacgggttggctctga[C/T]gtcctttcctctgtga	C	T	// 5522 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m /// NM_020416 // upstream // 59051 // Hs.479069 // PPP2R2C	PPP2R2C	PPP2R2C, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m ,p16.1
SNP_A-2171182	caatagtcgaagacat[A/G]aaaacagatcatttcc	A	G	84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// NM_032808 // upstream // 147504 //	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-2171296	caatatgcccaatgca[A/G]tagtatttaataagta	A	G	Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 //	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-2205988	ccatatctatcctcca[C/T]atattttgtaggctct	C	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2204394	ccagctacctcactga[C/T]gtggagttctaactgg	C	T	54859 // Homo sapiens hypothetical protein FLJ20211 (FLJ20211), mRNA. /// NM_006574 // downstream // 28161 //	FLJ20211	FLJ20211, Homo sapiens hypothetical protein FLJ20211 (FLJ20211), p21.31
SNP_A-2132713	atataaaagtttataa[A/G]gttagagcattggcta	A	G	Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), mRNA. /// ENST00000357444 // intron // 0 // ---	RABGAP1L	RABGAP1L, Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), q25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2131646	atagccagatgtagag[G/T]aagtgaaatttgtgcc	G	T	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2148500	atgggtgtatgggaag[A/G]aaatactcaaaatgct	A	G	/// ENST00000342224 // downstream // 26964 // --- // --- // ---	-	p11.21
SNP_A-2142274	atgaaaatgcaacagg[A/G]atagagacaaaaattc	A	G	1823 // Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, mRNA. /// NM_004948 // upstream // 105275	DSC1	DSC1, Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, q12.1
SNP_A-2045369	aagaataaaaaaggaa[A/C]tctgcatcacattgct	A	C	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 245114	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2040508	aaccagtttttggaag[C/G]attataaatagaagtc	C	G	Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000316738 // intron // 0 // ---	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-2025927	aaaatgtcattggtgc[A/G]gagttcattcgtgccc	A	G	Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // intron // 0 // Hs.334846 // PVRL1 //	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2006805	tctactttcctagcaa[A/G]cttccagtgtacaatg	A	G	ENST00000333815 // intron // 0 // --- // --- // --- // --- /// ENST00000352388 // intron // 0 // --- // --- // --- // --- ///	-	q26.3
SNP_A-2005650	aacggcattactacga[G/T]gtaaatagcaatgcca	G	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2069438	acacaagcccactgga[C/T]gtttggcctgacagtg	C	T	ENST00000318596 // intron // 0 // --- // --- // --- // ---	-	p13.11
SNP_A-2064701	aattctgataaaaaag[A/C]aagatgagcttagagt	A	C	Homo sapiens mRNA for KIAA0226 protein, partial cds. /// ENST00000273582 // intron // 0 // --- // --- // --- // ---	KIAA0226	KIAA0226, Homo sapiens for KIAA0226 protein, partial cds. ,q29
SNP_A-2049669	gggtttaaatacgagt[C/T]tgtgaaattcaagctt	C	T	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1849280 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2058586	aatcaggcaactgtta[A/G]agaaaagatttttaga	A	G	Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, mRNA. /// NM_052836 // intron // 0 // Hs.546421 // CDH23 //	CDH23	CDH23, Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, q22.1
SNP_A-2060105	aatgaaacaatgggaa[A/G]caaggaaatggggctt	A	G	Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // --- // ---	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-2081229	acctgctagagtcata[C/T]gttcggggaattaagt	C	T	LOC284680 // 284680 // Homo sapiens hypothetical protein LOC284680 (LOC284680), mRNA. /// ENST00000290009 //	LOC284680	LOC284680, Homo sapiens hypothetical protein LOC284680 (LOC284680), q23.3
SNP_A-2105430	agccaaattcatatta[A/G]ccatttccggaatcca	A	G	FLJ22833 // 64859 // Homo sapiens hypothetical protein FLJ22833 (FLJ22833), mRNA. /// ENST00000307849 //	FLJ22833	FLJ22833, Homo sapiens hypothetical protein FLJ22833 (FLJ22833), q32.3
SNP_A-2078714	accattgactataaga[A/C]acactgttattttatg	A	C	Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), mRNA. /// ENST00000258991 // intron // 0 // --- // ---	HT008	HT008, Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), q23.3
SNP_A-2057315	aatatatgaaccacaa[C/T]aaatgtatgaacgaac	C	T	57643 // Homo sapiens mRNA for KIAA1511 protein, partial cds. /// NM_032756 // upstream // 26353 // Hs.162717 //	ZSWIM5	ZSWIM5, Homo sapiens for KIAA1511 protein, partial cds. ,p34.1
SNP_A-2056852	aatagggacattgaga[A/G]gattaatgaggatctg	A	G	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2053240	aagtctttgggtgtga[C/T]ggtaaacaattgctca	C	T	ENST00000229088 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2066343	aattttctttcattac[C/G]agcatctaagcgtcct	C	G	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 941387 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-2009201	ccaaagaagagcctga[A/G]taacaaaacaatccta	A	G	// --- /// ENST00000356397 // upstream // 75852 // --- // --- // ---	-	q24
SNP_A-1997450	tcaggtctctttttcc[A/G]tgaaatgcctgttcat	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // intron // 0 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-1994515	tggatggaaaagccca[A/G]cataactagtaccaag	A	G	23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2026092	aaaattaggtcatagt[C/G]acaagaacatactcaa	C	G	404744 // Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // upstream // 157532 //	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-2047350	aagatccgtttcagaa[C/T]ttctctgcagacatct	C	T	23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 37297 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2141218	atctggtggtcaataa[A/G]ctttttatttatttat	A	G	PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-2139709	atcgtcatttagcaga[C/T]gaagaactgagactca	C	T	// 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 852496 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2166387	caaatgaacagctttc[A/G]aaatgatcttggttaa	A	G	C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA (cDNA clone IMAGE:4791744), partial cds. /// NM_017799 // downstream // 105118 //	C14orf101	C14orf101, Homo sapiens chromosome 14 open reading frame 101, (cDNA clone IMAGE:4791744), partial cds. q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2108061	agctctctacagccaa[A/G]tcctctggaaaaccca	A	G	83639 // Homo sapiens testis-specific protein TES101RP (MGC4766), mRNA. /// NM_014400 // downstream // 27699 //	TEX101	TEX101, Homo sapiens testis-specific protein TES101RP (MGC4766), q13.31
SNP_A-2110848	aggactgaaggcctcc[A/C]cgtggatttccagtct	A	C	Homo sapiens Dresden-G-protein-coupled receptor (D-GPCR), mRNA. /// ENST00000326310 // intron // 0 // --- // ---	OR51E1	OR51E1, Homo sapiens Dresden-G-protein-coupled receptor (D-GPCR), p15.4
SNP_A-2116328	aggtagcagggctcca[C/G]ctacagaagttatagg	C	G	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 324819 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2201662	ccacaaacgagccaca[C/G]gataagaactgtggct	C	G	2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// NM_024997 // upstream // 100899 // Hs.513343 // ATF7IP2 // 80063 //	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.13
SNP_A-2208573	cccactcaatccagta[C/G]ctgagattacaatcca	C	G	83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2208968	cccagcctgaacttca[A/G]gaggaagattttatag	A	G	// 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2210000	ccccacctaaacctga[A/G]ataaactggcttattt	A	G	// 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 901833 // Hs.211225 // NOVA1 // 4857 //	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2211956	ccctgacattaacaca[C/T]ggcattacaggagcat	C	T	30813 // Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, mRNA. /// NM_199425 // upstream // 61321 // Hs.274264 // VSX1 //	VSX1	VSX1, Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, p11.21
SNP_A-2178767	cactgaagttgagtga[C/T]gaaaaggcacctgaaa	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1872331	tctagactgtcataca[C/T]tggaaatggaatcatg	C	T	// Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // --- // --- // --- // ---	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-1817043	gttattttaatgcttc[A/G]ctttctaatgaacttt	A	G	// Homo sapiens hypothetical protein MGC34830 (MGC34830), mRNA. /// ENST00000321505 // 3UTR // 0 // ---	MGC34830	MGC34830, Homo sapiens hypothetical protein MGC34830 (MGC34830), p13
SNP_A-1823575	taaaagttgaaagtta[C/T]atgaaatctatgagaa	C	T	Homo sapiens KIAA1900 (KIAA1900), mRNA. /// ENST00000334273 // intron // 0 // --- // --- // --- // ---	KIAA1900	KIAA1900, Homo sapiens KIAA1900 (KIAA1900), q16.1
SNP_A-1783097	ggcagctttttaatgg[A/T]acatttcctgatagat	A	T	// 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 //	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-1801335	gtaggacaggggcata[C/T]gaaggcactgccaatc	C	T	// 202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 835178 // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q12
SNP_A-1812558	gtggccttatgccttg[C/T]agcagggcgcctctca	C	T	Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// ENST00000264249 // intron // 0 // --- // --- // --- // ---	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1796371	ggtgttctgctgggca[C/T]aggagtgtagctgcta	C	T	ENST00000257309 // intron // 0 // --- // --- // --- // --- /// ENST00000360467 // intron // 0 // --- // --- // --- // --- ///	-	q34
SNP_A-1788431	gggagtgcataataaa[C/G]cttggagtgcatgata	C	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1978524	gccaaagggactgata[C/T]actttccgttcaaaat	C	T	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 594681 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1963291	aaattaacaacactca[A/G]caacctggtgcaaatt	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 526850 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1969264	caagttcagtgtggta[A/G]aactttaaaaaatcac	A	G	5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 //	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, q21.1
SNP_A-1969381	caaaataggaagtggc[A/G]aaataggcagatcata	A	G	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 99326 // --- // --- // --- // --- ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. ,q21.1
SNP_A-1959602	ttttggaggttaatac[C/T]ggaacagtcttttgcc	C	T	Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 // intron // 0 // --- // --- // --- // ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-1950014	tttcacaaattcctaa[A/G]tgtattgtccaatatg	A	G	lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // --- // --- // --- // --- ///	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-1887001	tgacttgccaatttaa[A/C]acatctcactatttat	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 222674 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889783	tgatacagagacttac[A/G]gcacctgatttttcat	A	G	sapiens interferon, gamma-inducible protein 16 (IFI16), mRNA. /// AF208043 // intron // 0 // Hs.380250 // IFI16 // 3428	IFI16	IFI16, Homo sapiens interferon, gamma-inducible protein 16 (IFI16), q23.1
SNP_A-1909902	tgtcagaagttcacgc[A/G]agcctgaaaatcccgt	A	G	ENST00000321345 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1921783	ttactaattcactaaa[C/T]gtctagatgttgatgt	C	T	Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2306717	gctgtcctgaagacgc[A/G]gatcacagcaggtggc	A	G	// Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000343478 // intron // 0 // --- // --- // --- // ---	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-2307399	gcttatacctcctaaa[A/T]tatgataactacaaga	A	T	79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-2304396	gctcgttcattgccca[A/G]cagaaactgatagaag	A	G	Homo sapiens vacuolar protein sorting 52 (yeast) (VPS52), transcript variant 2, mRNA. /// NM_080564 // CDS // 0 //	VPS52	VPS52, Homo sapiens vacuolar protein sorting 52 (yeast) (VPS52), transcript variant 2, p21.32
SNP_A-2290721	gcaagatggccaaata[C/G]aactctctaggtatca	C	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1986639 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2267549	gaatattagccatcag[A/C]atatttgtggaaaaaa	A	C	222611 // Homo sapiens G protein-coupled receptor 111 (GPR111), mRNA. /// NM_153838 // upstream // 360 //	GPR111	GPR111, Homo sapiens G protein-coupled receptor 111 (GPR111), p12.3
SNP_A-2269355	gaatttgtagaataga[C/T]catttaaaggaatgga	C	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1932893 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2286260	gatgcccacccccaga[C/T]cagataagctccagtg	C	T	Homo sapiens chromosome 11 open reading frame 11 (C11orf11), mRNA. /// ENST00000257215 // intron // 0 // --- //	C11orf11	C11orf11, Homo sapiens chromosome 11 open reading frame 11 (C11orf11), q12.2
SNP_A-2285997	gatgatatttttgcta[C/T]attgggctaaataaat	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2245809	ctggggtcctaaataa[A/C]agtgaaatgcagtcta	A	C	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2246653	ctgtaatctccttttc[C/T]agcttttccaaatctg	C	T	Homo sapiens arachidonate 12-lipoxygenase (ALOX12), mRNA. /// ENST00000251535 // CDS // 0 // --- // --- // --- // ---	ALOX12	ALOX12, Homo sapiens arachidonate 12-lipoxygenase (ALOX12), p13.1
SNP_A-2249973	cttacattagattcag[A/T]cacactccattgtcca	A	T	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-2228461	cgtctgtactgatctt[C/T]aaccaataaaatctca	C	T	sapiens actinin, alpha 1 (ACTN1), mRNA. /// ENST00000193403 // intron // 0 // --- // --- // --- // ---	ACTN1	ACTN1, Homo sapiens actinin, alpha 1 (ACTN1), q24.1
SNP_A-2228332	ctactgccttctcaga[C/T]gtgagctcttcatcac	C	T	// Homo sapiens hypothetical protein FLJ31547 (FLJ31547), mRNA. /// ENST00000319165 // intron // 0 // --- // --- // --- // ---	FLJ31547	FLJ31547, Homo sapiens hypothetical protein FLJ31547 (FLJ31547), q12.2
SNP_A-2284976	gatccctgtttataca[C/G]acggtggaaaagtaaa	C	G	Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), mRNA. /// ENST00000283148 // intron // 0 // --- // --- // --- // ---	UXS1	UXS1, Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), q12.2
SNP_A-2275500	gagacaaaactgataa[A/G]attcagggatgaacta	A	G	10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 190715 // Hs.334587 // RBPMS //	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-2259235	gaaaaacccaagtgta[C/T]gtaggctgtgcagttc	C	T	ENST00000320865 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2261533	gaaaggcatggatgga[A/G]gatgacgtttggattc	A	G	6506 // Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// NM_015430 // downstream // 10772 // Hs.55044 //	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-1923206	ttagctcccacttaca[A/T]ctgagaacatgaggta	A	T	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 162249 // --- // --- // --- //	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-1927747	ttcaagatcagagtca[A/G]taagtgataaaactag	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-1911710	tgtgaagcaagatgaa[G/T]tctccctgaaggctta	G	T	RAB11FIP4 // 84440 // Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), mRNA. /// NM_018405 // downstream // 114489 // Hs.462729 //	RAB11FIP4	RAB11FIP4, Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), q11.2
SNP_A-1973487	gtacaagttgaaatta[A/T]ctcaggcctgaggtct	A	T	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // –	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1987955	ctcttctcgcattcct[A/C]aaagattctaatgttc	A	C	5325 // Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA. /// NM_002656 //	PLAGL1	PLAGL1, Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, q24.2
SNP_A-1799516	gtaatgtaacagaatc[A/G]caattttaaagtcctt	A	G	// 3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. /// ENST00000315260 //	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1782342	ggcaatggcaataaac[A/C]aaacacattttcactc	A	C	ENST00000358040 // intron // 0 // --- // --- // --- // --- /// ENST00000345581 // intron // 0 // --- // --- // --- // --- ///	-	q11.21
SNP_A-1744843	gcacttcatcttggtaaggagcaca[A/G]tggagcgtccagacagccagaggt	A	G	// eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67kDa /// NM_006078 // downstream // 26436 //	EIF3S7	EIF3S7 , rs2142824, eukaryotic translation initiation factor 3, subunit 7 zeta, 66,q12.3
SNP_A-1823143	taaaacactgggacca[C/T]gtaggaattctatcta	C	T	Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), mRNA. /// U36798 // intron // 0 // Hs.386791 //	PDE3A	PDE3A, Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), p12.2
SNP_A-1836278	tactattctgtctaaa[A/T]cgtcgatcccagcctc	A	T	ENST00000344513 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-1834486	taccaaaaccctacca[C/T]tgactgccagtttgta	C	T	Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// ENST00000256737 // intron // 0 // --- // --- // --- // ---	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1869770	tccttcatgcgggaca[A/G]taataataataataat	A	G	Homo sapiens lectin, galactoside-binding, soluble, 9 (galectin 9) (LGALS9), transcript variant short, mRNA. /// NM_009587 // intron // 0 // Hs.81337 // LGALS9 // 3965 // Homo sapiens	LGALS9	LGALS9, Homo sapiens lectin, galactoside-binding, soluble, 9 (galectin 9) (LGALS9), transcript variant short, q11.2
SNP_A-2216901	cctctgcttctcagga[A/G]agggaaagagagagct	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 463986 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2133976	atatcttagctctgtc[A/G]ctatagagacctaaaa	A	G	1834 // Homo sapiens dentin sialophosphoprotein (DSPP), mRNA. /// NM_004407 // upstream // 10350 // Hs.128556 //	DSPP	DSPP, Homo sapiens dentin sialophosphoprotein (DSPP), q22.1
SNP_A-2138413	atccagtttaatggcc[A/G]gaagaatgcaggcttg	A	G	ENST00000274361 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2148588	atggtacaggtaggaa[C/G]agagtccagaggggac	C	G	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2037515	aacaacccagggcaga[A/G]gaatctttgtgttcag	A	G	// Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA. /// ENST00000358967 // downstream // 93199 // --- //	ADRB1	ADRB1, Homo sapiens adrenergic, beta-1-, receptor (ADRB1), q25.3
SNP_A-2053257	aagtgaaagaatgaag[A/C]aagatctaccatgcaa	A	C	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 24404 // Hs.493639 // C9orf72 // 203228 // Homo	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2054608	aataaaaaaatttgca[A/G]tctgccactttgcaaa	A	G	Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // --- // --- // --- // ---	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2052287	aagtaagtgtgccgac[A/C]gggccagggtattgga	A	C	3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 41828 // Hs.105103 //	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-2047902	aagcaaagaagaattc[A/G]agcaaaaatcaaattt	A	G	116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_183244 // upstream // 91741 // Hs.473218 // PHACTR3 // 116154 //	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.32
SNP_A-2058723	aatcatgaaatcaaaa[A/G]tcaaaacaggtcgggt	A	G	57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 13434 // Hs.160373 // KIAA1383 // 54627 //	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-2079962	acccttgtgtatctaa[G/T]ggttcataaacttgaa	G	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2079904	acccttacaggtccca[C/T]agttgaggtaggaata	C	T	55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 59580 // Hs.411881 // GRB14 //	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-2090239	acttgcagatttttca[A/G]aggatgttatgtcttt	A	G	sapiens fucose-1-phosphate guanylyltransferase (FPGT), mRNA. /// ENST00000263417 // 3UTR // 0 // --- // --- // --- // ---	FPGT	FPGT, Homo sapiens fucose-1-phosphate guanylyltransferase (FPGT), p31.1
SNP_A-2105229	agcattatttttttca[C/G]tcctgtttcacaagaa	C	G	Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // --- // --- // --- // ---	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-2105557	agccacagacatatcc[A/G]atacagagctaggctt	A	G	sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-2103849	agcacgatggagaacc[A/G]cccgactacagacgga	A	G	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 595566 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2056624	aatagatttgatgtca[C/T]aagtaataggattatt	C	T	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1307334 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2058813	aatcatttcatgagac[A/G]agagagggtgtgatct	A	G	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2048322	aagcagattttggctt[C/T]aagatggtctgtaagt	C	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2070274	acaccaacaagcaata[C/G]aaaagctgaattcctc	C	G	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 91827 //	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2043900	aacttctagagatgaa[A/G]accacaagggcttaga	A	G	10753 // Homo sapiens calpain 9 (nCL-4) (CAPN9), mRNA. /// NM_032800 // downstream // 22915 // Hs.520494 //	CAPN9	CAPN9, Homo sapiens calpain 9 (nCL-4) (CAPN9), q42.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1993410	agaggctcataaaaag[G/T]ccttgagctcacaaaa	G	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1991433	aaaatagagagccaaa[C/T]gttttcttaccagaag	C	T	// 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-1997572	tgcctatgctccaaaa[C/T]tacctctgcaagtttc	C	T	/// ENST00000333948 // upstream // 468922 // --- // --- // --- // ---	-	q31.2
SNP_A-2005534	ttgacatgaaggactc[A/G]ctcctctgccatttcc	A	G	Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // --- // --- // --- // ---	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-2017848	ttatctgttccattcc[C/T]attttcctcctcaatg	C	T	254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 20635	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-2149679	atgtatccattaccca[C/G]atttaagaaataatat	C	G	Homo sapiens hypothetical protein FLJ10719 (FLJ10719), mRNA. /// ENST00000300027 // intron // 0 // --- // --- // --- // ---	FLJ10719	FLJ10719, Homo sapiens hypothetical protein FLJ10719 (FLJ10719), q26.1
SNP_A-2138134	atccaatcagttaggg[C/T]cattaatagctaccaa	C	T	Homo sapiens zinc finger protein 259 (ZNF259), mRNA. /// ENST00000227322 // intron // 0 // --- // --- // --- // ---	ZNF259	ZNF259, Homo sapiens zinc finger protein 259 (ZNF259), q23.3
SNP_A-2142911	atgaataactgaagaa[A/G]gagaggagcttaaaaa	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 401213 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2144995	atgatttcttcatttc[C/T]atctcagtaatgcagt	C	T	Homo sapiens transmembrane 4 superfamily member 14 (TM4SF14), mRNA. /// ENST00000265450 // intron // 0 // --- //	TM4SF14	TM4SF14, Homo sapiens transmembrane 4 superfamily member 14 (TM4SF14), q22.3
SNP_A-2167140	caacacactacactaa[C/T]aaatatcactgttaaa	C	T	26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000331766 // upstream // 218798 // --- // ---	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-2134266	atatgcacaaacactg[C/T]agctggtgacctgtgt	C	T	ARHGEF1 // 9138 // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 1 (ARHGEF1), transcript variant 2, mRNA. /// NM_198977 // downstream // 22876 // Hs.278186	ARHGEF1	ARHGEF1, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 1 (ARHGEF1), transcript variant 2, q13.2
SNP_A-2123241	agtgtaagctgccaat[C/T]accacatcctcttttt	C	T	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 916527 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-2217361	cctgaaggaatgtaga[G/T]cttctgggaaatggtg	G	T	Homo sapiens membrane-spanning 4-domains, subfamily A, member 10 (MS4A10), mRNA. /// ENST00000308287 // intron // 0 // --- // --- // --- // ---	MS4A10	MS4A10, Homo sapiens membrane-spanning 4-domains, subfamily A, member 10 (MS4A10), q12.2
SNP_A-2220756	ccttgaggtcatgcca[A/G]agaaacttggacttat	A	G	Homo sapiens mitogen-activated protein kinase 4 (MAPK4), mRNA. /// ENST00000269463 // intron // 0 // --- // --- // --- // ---	MAPK4	MAPK4, Homo sapiens mitogen-activated protein kinase 4 (MAPK4), q21.1
SNP_A-2170322	caagtactcaatatac[A/G]ctttcatttttccttg	A	G	Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // --- // --- // --- // --- ///	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-2172314	caattaaaggcagtga[C/G]taattcaacagatatt	C	G	ENST00000342260 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1860342	tcagtgcatgattctc[A/G]ctcacattactgtgcc	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 256975 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1866372	tcccattttatgacta[A/G]gaacactgagcctttg	A	G	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 300290 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-1856202	tcacaactgtgacaca[C/G]aaaaataattacctag	C	G	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1853529	tattttgtgcatatca[G/T]ggtcctggtacatact	G	T	DNAH11 // 8701 // Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// NM_018719 //	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-1849981	tatgtccttagtttga[A/T]gcatagaataagattt	A	T	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), mRNA. /// ENST00000279593 // intron // 0 // --- // --- // --- // ---	GRIN2B	GRIN2B, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), p13.1
SNP_A-1726436	caaacaaacaaatattccatgttag[A/G]aagataaccattagagtaatcctgc	A	G	NM_005721 // intron // 0 // Hs.433512 // ACTR3 // 10096 // ARP3 actin-related protein 3 homolog (yeast)	ACTR3	ACTR3 , rs7603501, ARP3 actin-related protein 3 homolog (yeast),q14.1
SNP_A-1802797	gtatggaccgtggatg[A/G]aatgatgctcagggaa	A	G	Homo sapiens transmembrane protein 16B (TMEM16B), mRNA. /// ENST00000327087 // intron // 0 // --- // --- // --- // ---	TMEM16B	TMEM16B, Homo sapiens transmembrane protein 16B (TMEM16B), p13.31
SNP_A-1987905	ttaatgctataatcta[C/T]atgacagtattacttt	C	T	/// ENST00000343481 // downstream // 171041 // --- // --- // ---	-	q24.1
SNP_A-1962846	atccctatactatata[C/T]cacatttctgttattg	C	T	Homo sapiens son of sevenless homolog 1 (Drosophila) (SOS1), mRNA. /// ENST00000263879 // intron // 0 // --- // ---	SOS1	SOS1, Homo sapiens son of sevenless homolog 1 (Drosophila) (SOS1), p22.1
SNP_A-1948525	tttagttaacaagagg[A/G]agcttagacttgcaga	A	G	Homo sapiens microtubule-associated protein 7 (MAP7), mRNA. /// ENST00000354570 // intron // 0 // --- // --- // --- // ---	MAP7	MAP7, Homo sapiens microtubule-associated protein 7 (MAP7), q23.3
SNP_A-1937569	ttgaactgccagctcc[A/G]gattcattttccttcc	A	G	Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// ENST00000278198 // intron // 0 // --- // --- // --- // ---	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1935864	ttcgttccttagga[C/T]gtattcccacatgtga	C	T	4879 // Homo sapiens natriuretic peptide precursor B (NPPB), mRNA. /// NM_138346 // downstream // 10847 //	NPPB	NPPB, Homo sapiens natriuretic peptide precursor B (NPPB), p36.22
SNP_A-1916879	tgtttctgataaagtg[C/T]atcttgccactgacac	C	T	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 390939	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1931634	ttccctaatgacttca[A/C]aataggtgtcttgaaa	A	C	// 9480 // Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// NM_000140 // downstream // 71947	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-1930023	ttcatggtgatgatg[A/T]aagaattaataaatgc	A	T	sapiens actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA. /// ENST00000307717 // intron // 0 // --- // --- // --- // ---	ACTA2	ACTA2, Homo sapiens actin, alpha 2, smooth muscle, aorta (ACTA2), q23.31
SNP_A-1898933	tgcttttctctcctc[C/T]acttactatatcgt	C	T	22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 110792 // Hs.306831 //	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-1887115	tgagaaaaatggtcag[C/G]agaacgctggcagaa	C	G	55970 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), mRNA. /// NM_004675 // downstream // 86041 // Hs.194695 // DIRAS3 // 9077 // Homo	GNG12	GNG12, Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), p31.2
SNP_A-1883272	tgaaatttagcagaaaa[A/G]ttaatactcaagaaat	A	G	ENST00000358401 // intron // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-2262657	gaaattccaccacatc[C/T]aggaatgcaacaagca	C	T	5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 54534 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2230851	ctatgccaagttcaca[A/G]tcttgaacaactgc	A	G	Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // --- // --- // --- // ---	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2249421	cttaaatacaggtcta[C/T]ggggtctcacagggga	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2296881	gccaagccaatgaaga[C/T]ccttggctagggaaag	C	T	6208 // Homo sapiens ribosomal protein S14 (RPS14), mRNA. /// ENST00000312037 // upstream // 53996 // --- // ---	RPS14	RPS14, Homo sapiens ribosomal protein S14 (RPS14), q33.1
SNP_A-2305572	gctgcactcttaaatg[G/T]cagcattccccagtta	G	T	Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // intron // 0 //	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-1891956	tgatttgtatttgag[A/G]aaattgaggattatct	A	G	83636 // Homo sapiens chromosome 19 open reading frame 12 (C19orf12), mRNA. /// NM_031448 // upstream // 6146 //	C19orf12	C19orf12, Homo sapiens chromosome 19 open reading frame 12 (C19orf12), q12
SNP_A-1892558	tgcaatgaaattcaat[C/G]aaatgtgctcaagaat	C	G	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 228884 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1895630	tgcctccagctgaaca[C/T]gtgaccgatgtgcaga	C	T	sapiens cytochrome P450, family 4, subfamily F, polypeptide 2 (CYP4F2), mRNA. /// ENST00000221700 // intron // 0 // --- // --- // --- // ---	CYP4F2	CYP4F2, Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 2 (CYP4F2), p13.12
SNP_A-1929363	ttcagtgacattaaac[C/T]gtagcatatggccaca	C	T	1823 // Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, mRNA. /// NM_004948 // upstream // 109561	DSC1	DSC1, Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, q12.1
SNP_A-1919679	ttaagtaaactggatg[A/G]agctaatctttctac	A	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1906804	tggttatacagaaata[C/T]acattagtgcttatta	C	T	Homo sapiens myotubularin related protein 2 (MTMR2), transcript variant 1, mRNA. /// NM_201278 // intron // 0 //	MTMR2	MTMR2, Homo sapiens myotubularin related protein 2 (MTMR2), transcript variant 1, q21
SNP_A-1933782	ttctatctcattataa[C/T]agcatgttccttga	C	T	57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000268533 // downstream // 43865 // --- // ---	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1971075	aaaatgtgggatgaaa[A/G]cacacaaggccctta	A	G	// 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// NM_178552 // downstream // 20561 // Hs.124502	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-1979368	actgtgtgaatgaaaa[A/C]acaacaaggttctat	A	C	Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // intron // 0 // --- // --- // --- // --- // ENST00000355292 // intron // 0 // --- //	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1800169	gtaccctaaatgtctc[A/G]aacagtatcagacaca	A	G	Homo sapiens homolog of yeast INO80 (INO80), transcript variant 1, mRNA. /// NM_032196 // intron // 0 // Hs.292949 //	INO80	INO80, Homo sapiens homolog of yeast INO80 (INO80), transcript variant 1, q15.1
SNP_A-1808768	gtgaagctgtgcgaga[C/T]gacaaagactgttgta	C	T	Homo sapiens calcium channel, voltage-dependent, L type, alpha 1D subunit (CACNA1D), mRNA. /// M76558 // intron // 0 // Hs.476358 // CACNA1D // 776 // Human neuronal DHP-	CACNA1D	CACNA1D, Homo sapiens calcium channel, voltage-dependent, L type, alpha 1D subunit (CACNA1D), p21.1
SNP_A-1796153	ggtgtcagtttccaga[C/T]ggtgagagaggcctcc	C	T	90441 // Homo sapiens zinc finger protein 622 (ZNF622), mRNA. /// ENST00000332432 // upstream // 214276 // --- // ---	ZNF622	ZNF622, Homo sapiens zinc finger protein 622 (ZNF622), p15.1
SNP_A-1788070	gggagagcaagtggc[A/G]attcagctctagctct	A	G	ENST00000358765 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-1860327	tcagtgattattgta[A/G]ggctacatggatatt	A	G	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 962708 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1822995	taaaaatctatgatcg[C/G]atgatatatttttgaaa	C	G	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172865	caattttcctaaagtc[C/T]cgccaaattccagggg	C	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 534156 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2177823	cacgttctcatgttca[C/T]gtgggagctaaccact	C	T	22982 // Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // upstream // 42573 // --- // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-2199165	cattttacaaacagca[A/C]caataacaacaaattg	A	C	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 48986 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2188184	cagtcctatcaactta[C/T]aaacatgctgttcttt	C	T	3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 34273 // Hs.105103 //	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-2219856	ccttagatggtcaacc[A/T]gaatcctcaggctgag	A	T	27250 // Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA. /// NM_014456 // upstream // 244561 // Hs.232543 //	PDCD4	PDCD4, Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, q25.2
SNP_A-2210450	ccccctacattttct[C/T]acttaagactcttcac	C	T	4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 155999 // Hs.118183 // FLJ22833	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-2118148	agtaaagacactgtaa[A/G]tctcaaaaatactcca	A	G	// 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 13462 //	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-2108013	agctctagagagatac[A/G]aacttaacgctgaaga	A	G	Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), mRNA. /// ENST00000223955 // intron // 0	DMRT1	DMRT1, Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), p24.3
SNP_A-2137712	atcatggagaagtata[C/T]gtatgatttgtttatg	C	T	-- /// ENST00000358396 // downstream // 326143 // --- // --- //	-	p12.2
SNP_A-2136682	atcactgatggaaaga[C/T]gtctcttagagatata	C	T	// Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA. /// ENST00000358967 // downstream // 106518 // ---	ADRB1	ADRB1, Homo sapiens adrenergic, beta-1-, receptor (ADRB1), q25.3
SNP_A-2166916	caacaaaaagcaatca[A/C]aaacaggttcttttta	A	C	10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 674712	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-2163070	atttttagtccatcaa[C/T]gccccattagtctatt	C	T	ENST00000345651 // intron // 0 // --- // --- // --- // ---	-	q21.33
SNP_A-2154994	attcacctggcagcac[A/T]agttgacgtgtgacct	A	T	9874 // Homo sapiens tousled-like kinase 1 (TLK1), mRNA. /// ENST00000359766 // upstream // 133613 // --- // --- // --- // ---	TLK1	TLK1, Homo sapiens tousled-like kinase 1 (TLK1), q31.1
SNP_A-2143510	atgactatgtatgtaa[A/C]cagctcaatggttttt	A	C	sapiens mRNA for KIAA0205 gene, partial cds. /// ENST00000331274 // intron // 0 // --- // --- // --- // ---	LPGAT1	LPGAT1, Homo sapiens for KIAA0205 gene, partial cds. ,q32.3
SNP_A-2142150	atcttttgccaagaaa[A/T]ggtcctgagtgttttg	A	T	Homo sapiens polymeric immunoglobulin receptor (PIGR), mRNA. /// NM_013371 // intron // 0 // Hs.128395 // IL19 //	PIGR	PIGR, Homo sapiens polymeric immunoglobulin receptor (PIGR), q32.1
SNP_A-2149752	atgtattaaaatgcaa[A/G]cacattacttggatga	A	G	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA. /// ENST00000298171 // intron // 0 // --- // --- // --- // ---	TSHR	TSHR, Homo sapiens thyroid stimulating hormone receptor (TSHR), q31.1
SNP_A-2015317	agagccttccaaacca[C/T]agaaaggaattcagac	C	T	8204 // Homo sapiens nuclear receptor interacting protein 1 (NRIP1), mRNA. /// ENST00000318948 // upstream // 27740	NRIP1	NRIP1, Homo sapiens nuclear receptor interacting protein 1 (NRIP1), q11.2
SNP_A-2031268	aaagggaaacatatca[A/C]cccagtggctactggc	A	C	ENST00000338458 // intron // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-2072911	acaggaaatcccatga[C/T]aatcaatactcacaaa	C	T	/// ENST00000354660 // downstream // 36447 // --- // --- // ---	-	p15.1
SNP_A-2062473	aatgtagtctttctga[A/T]atttatgtccctggtt	A	T	ALDH8A1 // 64577 // Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 287418 //	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2
SNP_A-2106178	agccccagttcctcca[A/G]gaaatctatctcatct	A	G	SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream //	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-2021560	aaaaaatcagacctgg[A/G]cagtagttaagtagta	A	G	ENST00000260983 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2036358	aaattcctcatttgca[A/G]cctgttttcactcttt	A	G	// 23256 // Homo sapiens sec1 family domain containing 1 (SCFD1), transcript variant 2, mRNA. /// NM_016106 //	SCFD1	SCFD1, Homo sapiens sec1 family domain containing 1 (SCFD1), transcript variant 2, q12
SNP_A-1999795	gctgaaattcagctcc[A/G]actatcaacttctgta	A	G	Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000265371 // intron // 0 // --- // --- // --- // --- ///	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1995445	tcagcacagtgtagga[C/T]gcaattctcagtgtct	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 71471 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2164135	caaaaggcaatatcat[A/G]aacataggaaacacag	A	G	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2204264	ccagccagattttaaa[C/T]aacttcatctcgtctt	C	T	Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // intron // 0 // --- // --- // --- // ---	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2195076	catggaactgcccaca[A/G]gttcatatttttttcc	A	G	Homo sapiens vacuolar protein sorting 13A (yeast) (VPS13A), transcript variant B, mRNA. /// NM_033305 // intron // 0 // Hs.459790 // VPS13A // 23230 // Homo sapiens	VPS13A	VPS13A, Homo sapiens vacuolar protein sorting 13A (yeast) (VPS13A), transcript variant B, q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2171677	gtttatttataacatc[C/T]attgatcagtaagca	C	T	407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 715973 // Hs.24115 // C13orf25 //	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2170909	caataagaaacaatca[A/G]agctctcatttattaa	A	G	4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 9107 // --- // FLJ34047 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1861701	tcatctgaaacactc[C/T]aaatagagataagacc	C	T	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // --- //	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-1863876	gatttcaatgggacaa[C/G]atgcccacaggatcta	C	G	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA. /// ENST00000337714 // intron // 0 // --- // ---	AKAP1	AKAP1, Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), nuclear gene encoding mitochondrial protein, transcript variant 1, q23.2
SNP_A-1754013	aaaggtactctggttgaccttctg[G/T]atctattcactcctaagttacaac	G	T	1129 // cholinergic receptor, muscarinic 2 /// NM_145808 // upstream // 526640 // Hs.21321 // MTPN // 136319 //	CHRM2	CHRM2 , rs10258427, cholinergic receptor, muscarinic 2 ,q33
SNP_A-1968790	tttggtttctccctga[C/T]cacgggccgttagcaa	C	T	TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream //	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31
SNP_A-1957874	tttaatttgtgttcc[C/T]aaatgtgttgctgga	C	T	9698 // Homo sapiens pumilio homolog 1 (Drosophila) (PUM1), mRNA. /// NM_024522 // downstream // 78708 //	PUM1	PUM1, Homo sapiens pumilio homolog 1 (Drosophila) (PUM1), p35.2
SNP_A-1885391	tgacaaaattataagc[C/T]attgcagagtcatat	C	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 789830 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1880771	tcttggctctaggccg[C/T]atcaatccaatctctg	C	T	// Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream // 242470 //	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-2301892	gcggtcccagccacaa[C/T]gttgcagccagtggtg	C	T	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2308618	gcttcatctgactat[A/C]actttttctagatat	A	C	Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, mRNA. /// NM_020328 // intron // 0 //	ACVR1B	ACVR1B, Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, q13.13
SNP_A-2314689	ggagtcagactgcta[C/T]atgtgcttaccgttca	C	T	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 606840 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2234254	ctcatttttcaaaggaa[A/G]cctccatctgtaatga	A	G	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q23.1
SNP_A-2261232	gaaagatagatttcta[C/G]taagccaaacctatc	C	G	10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// NM_015323 //	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-2283703	gatagccctttgtgggg[A/G]catttataaagttca	A	G	Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// ENST00000350220 // intron // 0 // --- // --- // --- //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2290296	gcaacaccagtgaaagg[A/G]agaaaacttttatttt	A	G	490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 673108 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1885150	tgaattaggtagatag[A/C]caattggaaatcttct	A	C	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 215607 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1899837	tggaatttgagaagaa[C/T]ggggacagtttgatca	C	T	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1903201	tggcttctgggtccca[C/T]catgtgctcttggttg	C	T	Homo sapiens epithelial membrane protein 2 (EMP2), mRNA. /// ENST00000359543 // intron // 0 // --- // --- // ---	EMP2	EMP2, Homo sapiens epithelial membrane protein 2 (EMP2), p13.13
SNP_A-1901265	tggatggatctcatcc[A/G]atcaactgaagacctg	A	G	ENST00000319549 // intron // 0 // --- // --- // --- // ---	-	p24.3
SNP_A-1912935	tgtggaacctcagtca[A/G]aatacagagaagagga	A	G	Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, mRNA. /// NM_053028 // intron // 0 //	MYLK	MYLK, Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, q21.1
SNP_A-1924618	ttatagagaattttta[A/T]gaagcatgaagaaata	A	T	Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// ENST00000175238 // intron // 0 // --- // ---	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-1925469	tttccagggaaggcaa[A/G]catttctgggatgtcaa	A	G	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 48355 // --- // --- // --- // ---	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1952250	ttctcctatcatcca[A/G]tagcatctgttttctg	A	G	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 910749 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q32.1
SNP_A-1969135	tgcacaaatgagccac[A/G]gtggagtctttggtaa	A	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974497	ccttccccataaaaca[A/G]tggctttctcttctta	A	G	51278 // Homo sapiens immediate early response 5 (IER5), mRNA. /// ENST00000294850 // downstream // 77848 // --- // -1 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 78228 // Hs.378893 //	IER5	IER5, Homo sapiens immediate early response 5 (IER5), q25.3
SNP_A-1979329	tctgaaggccagtaaa[A/G]caattgggatctccag	A	G		NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1661310	ctcctggtaagattatgaataaaga[C/T]ccctcaatgataactgtgcttcaga	C	T	10690 // fucosyltransferase 9 (alpha (1,3) fucosyltransferase) /// NM_024641 // downstream // 354013 // Hs.46903 //	FUT9	FUT9 , rs9322424, fucosyltransferase 9 (alpha (1,3) fucosyltransferase) ,q16.1
SNP_A-1660343	gtcgtcagtctagtgttaaagataa[A/G]attatgtatgtttaagagggcaga	A	G	myotubularin related protein 3 /// NM_153050 // intron // 0 // Hs.412833 // MTMR3 // 8897 // myotubularin related protein 3	MTMR3	MTMR3 , rs10483157, myotubularin related protein 3 ,q12.2
SNP_A-1712363	ttcaatgttacctatgtttagata[A/T]aaaaatactgttgtgttacagttgc	A	T	// mannose-binding lectin (protein C) 2, soluble (opsonic defect) /// NM_033056 // downstream // 666257 // Hs.232819	MBL2	MBL2 , rs2384121, mannose-binding lectin (protein C) 2, soluble (opsonic defect) ,q21.1
SNP_A-1681742	atccatttggaagcaaggcatagga[C/T]gtaagtagaaggcaattaaaaaa at	C	T	7247 // translin /// NM_130773 // upstream // 444097 // Hs.437463 // caspr5 // 129684 // caspr5 protein ///	TSN	TSN , rs10496616, translin ,q14.3
SNP_A-1692370	atgtgaactatgtggtaatgaataa[A/C]gtctttctgagaaacatgaatggag	A	C	29953 // thyrotropin-releasing hormone degrading ectoenzyme /// NM_032662 // downstream // 142071 // -1 // -1	TRHDE	TRHDE , rs10506702, thyrotropin-releasing hormone degrading ectoenzyme ,q21.1
SNP_A-1814002	gtgtcagtttagtga[C/T]gctgcttaaagcaaa	C	T	Homo sapiens chromosome 18 open reading frame 11 (C18orf11), mRNA. /// ENST00000269209 // CDS // 0 // --- // -1	C18orf11	C18orf11, Homo sapiens chromosome 18 open reading frame 11 (C18orf11), q12.1
SNP_A-1815335	gtgtttattattgcac[A/G]gtgattacatgtcaag	A	G	3609 // Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, mRNA. /// NM_004516 // downstream // 6952 // Hs.465885 // ILF3 // 3609 // Homo	ILF3	ILF3, Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, p13.2
SNP_A-1819416	gttgggactccatcct[A/T]aggaaaacagggtgtac	A	T	LOC90139 // 90139 // Homo sapiens tetraspanin similiar to uroplakin 1 (LOC90139), mRNA. /// NM_006034 // upstream	LOC90139	LOC90139, Homo sapiens tetraspanin similiar to uroplakin 1 (LOC90139), p11.2
SNP_A-1831549	taattaaggatctcca[C/T]tcaaaaaacacaggaa	C	T	FLJ22789 // 84190 // Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// NM_152588 // upstream //	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-2201673	ccacaaaggaagatca[C/G]taggtaagagtggcat	C	G	sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 //	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2201711	ccacaacttctaggaaa[C/T]cctgattttcatgat	C	T	2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 369244 // Hs.98262 // GRIK2 // 2898 // Homo	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2201873	ccacactaggtgtaac[C/G]ggtcttcctctgggtt	C	G	// Homo sapiens BCL2-antagonist/killer 1 (BAK1), mRNA. /// NM_207497 // downstream // 206 // Hs.520075 // FLJ43752 //	BAK1	BAK1, Homo sapiens BCL2-antagonist,p21.31
SNP_A-2208189	cccaatgtactcataa[A/C]ccgacttcgacaatta	A	C	10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 //	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2224849	cgtgatgagaattcaa[C/T]gcagtcattgcgaagg	C	T	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 84219 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2225483	ctaaaacctgttggcf[A/G]aacatagatatctgcc	A	G	// 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 333942 //	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-2152591	attaagtgatgatgac[A/G]aacttgtaaccctcca	A	G	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, mRNA. /// NM_199451 // intron // 0 // Hs.22653 //	ZNF365	ZNF365, Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, q21.2
SNP_A-2152146	attaaaattgtcattc[A/G]cagggtggtttttta	A	G	Homo sapiens mRNA for KIAA0313 gene, partial cds. /// ENST00000264431 // intron // 0 // --- // --- // --- // ---	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-2151707	atgttgttaaaaggca[C/T]ctctttaatcctgtac	C	T	552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 349448 //	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2137817	atcattataaaagaag[A/G]cttcactcagagaaac	A	G	SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2124868	agttgaagaattagca[A/G]tgagagaaatgtaca	A	G	50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 339788 // Hs.106015 // DDEF1 // 50807 // Homo	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-2128505	ataataatcaggcaag[A/G]cacagtatttcaggca	A	G	57167 // Homo sapiens sal-like 4 (Drosophila) (SALL4), mRNA. /// NM_022088 // downstream // 322004 // Hs.473082	SALL4	SALL4, Homo sapiens sal-like 4 (Drosophila) (SALL4), q13.2
SNP_A-2114448	agggagaaggcgta[C/T]gcaaatgactgacagc	C	T	// 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 120501 // --- // --- // ---	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2119697	agtattatgctttgtc[A/C]acttatttcttaaata	A	C	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. ///	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), q32.1
SNP_A-2121442	agtctttgtttctac[A/G]attcacaggaaattaa	A	G	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015452	gtcattaagtgcttct[A/G]aaggttctttcaaagc	A	G	Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // intron // 0 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds. q21.1
SNP_A-2015568	aagtgttacactaaac[A/C]aggtaattctcatata	A	C	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2018964	acgcttagcgattaca[G/T]tcatgtgtcactgggg	G	T	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA. /// NM_001001894 // intron // 0 //	TTC3	TTC3, Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, q22.13
SNP_A-2023858	aaaagaaattctcaca[C/T]gaagccaaatacctga	C	T	80314 // Homo sapiens enhancer of polycomb homolog 1 (Drosophila) (EPC1), mRNA. /// NM_145023 // upstream //	EPC1	EPC1, Homo sapiens enhancer of polycomb homolog 1 (Drosophila) (EPC1), p11.22
SNP_A-2032660	aaataaatgaaatgta[C/T]cccagttgaacaacag	C	T	sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA. /// ENST00000276497 // intron // 0 // - // --- // --- // --- /// ENST00000359619 // intron // 0 // --- // --- //	LYN	LYN, Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), q12.1
SNP_A-2090157	acttgaggacagaata[C/T]gtttgattcattttca	C	T	8383 // Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), mRNA. /// NM_002550 // downstream	OR1A1	OR1A1, Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), p13.3
SNP_A-2089505	acttcaaatattgcaa[A/G]taagccaccagaaaat	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 109329 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2085279	actcatagtcctttca[C/T]tatgtgtagctggtat	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1944502 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2082956	acgtgcaagatcacgg[A/G]aaacactcagcactga	A	G	// 285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 179003 // ---	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-2071977	acagagctgatatacc[A/T]gaaaaagttctaaaaa	A	T	// 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2054805	aataaaccttgttgtc[A/T]attagctttgcccttа	A	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2029730	aaagaggaatggatac[C/T]aaaaatccttaagaca	C	T	5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 633541 // Hs.115474 // RFC3 // 5983 // Homo	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-2043939	aacttctgtttcctca[C/T]gtatccaccaattttt	C	T	FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2044515	aagaaaatctttggaa[C/T]tgaaaacctcaactgg	C	T	7982 // Homo sapiens suppression of tumorigenicity 7 (ST7), transcript variant b, mRNA. /// NM_018412 // downstream //	ST7	ST7, Homo sapiens suppression of tumorigenicity 7 (ST7), transcript variant b, q31.2
SNP_A-2018904	ggctgactcgctgacc[C/T]aagtcatggcgtcctg	C	T	sapiens single-minded homolog 2 (Drosophila) (SIM2), transcript variant SIM2, mRNA. /// NM_009586 // intron // 0 // Hs.146186 // SIM2 // 6493 // Homo sapiens single-minded	SIM2	SIM2, Homo sapiens single-minded homolog 2 (Drosophila) (SIM2), transcript variant SIM2, q22.13
SNP_A-1989627	ggatttaaatattcaa[C/G]attagaaaagatcatg	C	G	Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA. /// NM_080631 // intron // 0 //	VPS41	VPS41, Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, p14.1
SNP_A-1991129	atggaagaatctctga[A/C]agcccaagtttcctac	A	C	// 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 17461 // --- // --- // --- // --	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2001216	aacatttattttagaa[A/C]ctgaaatctttgtgag	A	C	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2115602	agggtacaggatgagc[C/T]gagcctttagagacag	C	T	6846 // Homo sapiens chemokine (C motif) ligand 2 (XCL2), mRNA. /// ENST00000331499 // upstream // 69168 // --- // ---	XCL2	XCL2, Homo sapiens chemokine (C motif) ligand 2 (XCL2), q24.2
SNP_A-2114948	agggcatggtaggaca[A/G]catgacgaccgagatg	A	G	// 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream //	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2133554	atatcaatgaactata[C/T]acattctacggtttgt	C	T	Homo sapiens beta 3-glycosyltransferase-like (B3GTL), mRNA. /// ENST00000343307 // intron // 0 // --- // --- // --- // ---	B3GTL	B3GTL, Homo sapiens beta 3-glycosyltransferase-like (B3GTL), q12.3
SNP_A-2131470	atagcaaacaatacta[C/T]cagcttgccctctggc	C	T	sapiens insulin-like growth factor 1 receptor (IGF1R), mRNA. /// ENST00000268035 // intron // 0 // --- // --- // --- // ---	IGF1R	IGF1R, Homo sapiens insulin-like growth factor 1 receptor (IGF1R), q26.3
SNP_A-2152677	attaatatgtacttaa[C/T]actctggaggtgaggg	C	T	sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2147436	atggagtatcatgtcc[A/G]ccctgttaccaaaatg	A	G	Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000316738 // intron // 0 // ---	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-2154348	attatgtggtcctaag[A/G]ctgaaatgaggccacg	A	G	Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 //	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-2154734	attcaaatggacttca[C/G]taacattcatggataa	C	G	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 218568 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187128	caggtccaccaaaagc[A/G]cagcagggcagggtgc	A	G	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2189773	cataaaagaacttgga[A/T]gaatttccagagaatt	A	T	Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // intron // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-1841645	taggattttctatatg[G/T]aaggttatgtcttctt	G	T	Homo sapiens oxysterol binding protein-like 9 (OSBPL9), transcript variant 1, mRNA. /// NM_148909 // intron // 0 // Hs.21938 // OSBPL9 // 114883 // Homo sapiens oxysterol	OSBPL9	OSBPL9, Homo sapiens oxysterol binding protein-like 9 (OSBPL9), transcript variant 1, p32.3
SNP_A-1859947	tcaggtgcatttacca[A/T]acacatataatatttg	A	T	// 10391 // Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA. /// NM_006305 // downstream // 13122 //	CORO2B	CORO2B, Homo sapiens coronin, actin binding protein, 2B (CORO2B), q23
SNP_A-1846361	tatatggagtcttagc[A/G]aagcttcctctgtcct	A	G	7088 // Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), mRNA. /// ENST00000355495 // upstream // 31126 // --- // --- // --- // ---	TLE1	TLE1, Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), q21.32
SNP_A-1796488	ggttaagaaatgactg[A/G]aaggattctcttatga	A	G	ENST00000217074 // intron // 0 // --- // --- // --- // ---	-	q13.12
SNP_A-1649778	tccaaaatatgttatcggaatatat[C/T]acaaccttaggacttcatgaattac	C	T	// 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 1577247 // Hs.450919 // GPC5 //	SLITRK5	SLITRK5 , rs2065775, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1732309	agctactaatagcagagctaccctc[A/G]aaactataatggagtttgcctctcc	A	G	PTPRC // 5788 // protein tyrosine phosphatase, receptor type, C /// NM_003822 // upstream // 265430 // Hs.183123 //	PTPRC	PTPRC , rs2502119, protein tyrosine phosphatase, receptor type, C ,q32.1
SNP_A-1976470	ttatcattgactatac[C/T]accaattcaaatagtc	C	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 464697	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1988089	caattttaaaagtata[C/T]gcactgatgcaaggac	C	T	Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// ENST00000357180 // intron // 0 // --- // --- // --- // ---	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2
SNP_A-1988094	aactatgtaaccacaa[C/T]gtaggttaagatacaa	C	T	389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// AB033035 // upstream // 398276 //	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-1939307	ttgatctgcctgttga[C/T]ctaatgggctccatct	C	T	79931 // Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), mRNA. /// NM_198179 // downstream // 63274 //	TNIP3	TNIP3, Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), q27
SNP_A-1944193	ttgtcatctcacgtaa[C/T]ctaattttccttacat	C	T	163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 8147 // Hs.546355 // TA-LRRP //	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-1926545	ttattctatgtagtga[C/T]atgctttggttatttt	C	T	Human Kox8 mRNA for zinc finger protein, partial. /// ENST00000357774 // intron // 0 // --- // --- // --- // --- ///	ZNF15L1	ZNF15L1, Human Kox8 for zinc finger protein, partial. ,p12
SNP_A-1906542	tggtgggttcttagca[A/G]cagcttcaagagagga	A	G	7280 // Homo sapiens tubulin, beta polypeptide (TUBB), mRNA. /// NM_178012 // upstream // 17981 // Hs.300701 //	TUBB2	TUBB2, Homo sapiens tubulin, beta polypeptide (TUBB), p25.2
SNP_A-1894907	tgccattaagaaacaa[C/T]tcagaggtttaacaag	C	T	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 2044417 // --- // -	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1885453	tgacaacagtggtcca[C/T]gctgtgctggtgagca	C	T	6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 390047 //	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1877209	tctgcttccttttttga[A/G]attataccagtcacaa	A	G	// 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 120291 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2287937	gattatcttccagtta[C/T]atttttggtcttaccc	C	T	ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+,q24.2
SNP_A-2297120	gccacagaagcgccaa[C/G]ttctgtcgatgggcaa	C	G	29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// NM_021800 //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2313137	ggagaacttgtaatga[C/T]aacctaaaatatcacc	C	T	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 178145 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2304741	gctctggcttccccca[A/C]gaatgccaaatagaaa	A	C	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2285654	gatgaagtcacgttga[A/C]ctgggtttgatttcac	A	C	// --- /// ENST00000356397 // upstream // 121619 // --- // --- // -	-	q24
SNP_A-2274906	gagaacacactgacac[A/T]gcaaggggaccatcac	A	T	ALDH8A1 // 64577 // Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 336594 //	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2
SNP_A-2279559	aattatattcatttaa[A/T]cagtctctaggagtct	A	T	Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), mRNA. /// ENST00000284509 // intron // 0 // --- // -	ATP8B4	ATP8B4, Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), q21.2
SNP_A-2261740	gaaagtgcttatagca[A/G]aactctagaactaaca	A	G	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 415609 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2256709	ctttcagtctctgaag[A/T]atgagactttcccact	A	T	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 //	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2269881	gacaatatacttgccc[A/G]agagctcaattagaaa	A	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA /// NM_016279 // downstream // 314196 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2256056	ctttacaaatgcagag[A/G]aatttatggacttgt	A	G	// 9781 /// Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 433800 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2246700	ctgtacaccataaata[C/T]gtatcttcttgtttt	C	T	// 79149 // Homo sapiens zinc finger protein 495 (ZNF495), mRNA. /// ENST00000358992 // upstream // 10390 // --- // ---	ZSCAN5	ZSCAN5, Homo sapiens zinc finger protein 495 (ZNF495), q13.43
SNP_A-2272215	gacctatgggctccag[A/G]caagtgctgctcccac	A	G	Homo sapiens SH3 domain containing ring finger 2 (SH3RF2), mRNA. /// ENST00000359120 // intron // 0 // --- // ---	SH3RF2	SH3RF2, Homo sapiens SH3 domain containing ring finger 2 (SH3RF2), q32
SNP_A-2277750	gagcaggtgccctcaa[C/T]tgggagacttgatacag	C	T	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 892385 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2277891	gagccaaacaaaggaaa[C/G]agaaaggccccaggtt	C	G	341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// ENST00000342700 //	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2305358	gctgagttggagccaaa[A/C]atccaggaaaagctgaa	A	C	// Human phosphodiesterase mRNA, complete cds. /// NM_006202 // downstream // 9116 // Hs.89901 // PDE4A //	PDE4A	PDE4A, Human phosphodiesterase complete cds. p13.2
SNP_A-2313004	ggactttggcaaagaa[G/T]agtggaaaagaaagttg	G	T	/// ENST00000315765 // upstream // 1238 // --- // --- // --- /// ENST00000334665 // upstream // 25684 // --- // --- // ---	-	q21
SNP_A-2297945	gccagtgtaaatccta[C/T]agacgtcaatatgaga	C	T	4676 // Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA. /// NM_139207 // upstream // 269212 //	NAP1L4	NAP1L4, Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), q21.2
SNP_A-2289826	gcaaacagcatgtgca[A/C]atatccagaacaggaa	A	C	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 622577 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1887517	tgagactgggcattca[A/T]aaagaagagaatcat	A	T	C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000262490	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1895858	tgcctggttgggagc[A/C]atacatccaagtcaca	A	C	Homo sapiens xenotropic and polytropic retrovirus receptor (XPR1), mRNA. /// ENST00000271566 // intron // 0 // --- // ---	XPR1	XPR1, Homo sapiens xenotropic and polytropic retrovirus receptor (XPR1), q25.3
SNP_A-1914273	tgtgttatcaagttac[A/T]cttagtgcatgagttt	A	T	220441 // Homo sapiens ring finger protein 152 (RNF152), mRNA. /// NM_012327 // downstream // 117972 // Hs.157031	RNF152	RNF152, Homo sapiens ring finger protein 152 (RNF152), q21.33
SNP_A-1918472	ttaaatatatttgtcc[C/T]gataacaccttgtgt	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1943990	ttgtattattacttca[C/T]aaggctaaccagccag	C	T	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1943445	ttggtttgtcccctaa[A/G]atagttttcattgca	A	G	ENST00000263665 // intron // 0 // --- // --- // ---	-	p12.3
SNP_A-1937409	ttgaaatgattcctca[C/T]tccttacttacaact	C	T	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // upstream // 72971 // Hs.282871 // CYP2C8	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1953293	tttgaaaaatcacaac[A/T]ctgtctttcacagtgc	A	T		CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-1947936	tttagaacatagccca[C/T]aattaaccactcattt	C	T	ENST00000354427 // intron // 0 // --- // --- // ---	-	p25.3
SNP_A-1950387	tttcaggctaaaatc[C/T]gaaatcaaattatttg	C	T	2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// NM_173675 // downstream // 241562 //	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1
SNP_A-1727825	tgaagtacgaacaacaatttcagaa[C/T]tccttggtcatgtatttagcaaat	C	T	5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 905970 // Hs.435976 // BRUNOL4 // 56853 //	PIK3C3	PIK3C3, rs10502696, phosphoinositide-3-kinase, class 3 , q12.2
SNP_A-1783317	ggcagtggtccccataa[A/G]tgcctgtcaacttgat	A	G	Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-1792793	ggtaagtattgggga[A/G]tattgttataaatgct	A	G	Homo sapiens hypothetical protein DKFZp761D0211 (DKFZP761D0211), mRNA. /// ENST00000354222 // intron //	C16orf9	C16orf9, Homo sapiens hypothetical protein DKFZp761D0211 (DKFZP761D0211), p13.3
SNP_A-1857910	tcacttcccaccaataa[C/T]gcgttaatcatcatc	C	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1860748	tcataagaaatcttga[A/G]gcctatattcatttgg	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1834526	taccaaatgttaata[A/G]aagcagagattgtaga	A	G	Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // intron // 0 // Hs.401954 // ARG99 // 83857 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1817936	gttctaacaatccata[A/T]gtcttggagtttgac	A	T	669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 //	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2191250	catatacccacagaac[A/G]gtatcaatacatgggt	A	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 40123 // Hs.308628 // ST8SIA4	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2183860	cagccaacataggcta[A/G]caaaaaagccaggcca	A	G	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // intron // 0 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2195256	catggcaagtcttagg[C/T]ccagtcggatgtgaaa	C	T	// Homo sapiens LOC92346 (LOC92346), mRNA. /// ENST00000314608 // intron // 0 // --- // --- // --- // ---	LOC92346	LOC92346, Homo sapiens LOC92346 (LOC92346), q24.3
SNP_A-2198718	catttcctggaaagca[C/T]gtgtttcctatttagg	C	T	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 317370 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-2223032	cgcatctagatgtagt[C/G]aacaacccagtatttc	C	G	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	SMARCA3	SMARCA3, Homo sapiens SWI q24
SNP_A-2218722	cctggctctttgtaag[A/T]caagtaatttaagatt	A	T	Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// ENST00000271754 // intron // 0 //	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-2210079	gagagcatttctctgg[A/G]atgaagaaaggaagat	A	G	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 693154 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2205938	ccatataagagcaaaa[C/T]agaaggacagggagag	C	T	// --- /// ENST00000355326 // downstream // 1116104 // --- // --- // --- // --- /// ENST00000332323 // downstream // 1320048 //	-	q11.1
SNP_A-2132013	ataggcccttacctta[A/C]cccaaatcactcttta	A	C	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-2126036	agttttgaagtgctaa[C/T]ataatacccatggaga	C	T	Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319217 // intron // 0 // --- // --- // --- // ---	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2116831	aggtctccagcttcac[A/G]atccttaaactagaac	A	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 46428 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2009787	aataaagtttattctc[C/T]caatgacgatgataac	C	T	Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // intron // 0 // Hs.502328 // CD44 // 960 //	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-2060123	aatgaaagacttttaaa[C/T]gtatgtgagttccaag	C	T	ENST00000297227 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-2073435	acaggtgcctggacta[C/T]gtgttggaggagctga	C	T	Homo sapiens proline dehydrogenase (oxidase) 1 (PRODH), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000334029 // CDS // 0 // --- // --- // --- // --- ///	PRODH	PRODH, Homo sapiens proline dehydrogenase (oxidase) 1 (PRODH), nuclear gene encoding mitochondrial protein, q11.21
SNP_A-2076842	accaaacagcagatac[A/G]ctttcttttcaagcgc	A	G	1068 // Homo sapiens centrin, EF-hand protein, 1 (CETN1), mRNA. /// NM_199167 // upstream // 4382 // Hs.274959 //	CETN1	CETN1, Homo sapiens centrin, EF-hand protein, 1 (CETN1), p11.32
SNP_A-2075310	acatctttgcaagcaa[C/T]cttaattggtttctta	C	T	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. ///	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2066720	acaaaactttcaggtc[G/T]aattgaatccaagaac	G	T	Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-2057093	aatataaactttgtta[C/T]cataagctccatcaag	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2088914	actgtttcttgactcc[A/G]gatatttaaaggagaa	A	G	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1321517 // Hs.27214 // KCNC2	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2101226	agatcccaggtaagaa[C/T]ggcttgctcaatttca	C	T	// 400110 // Homo sapiens FLJ46358 protein (FLJ46358), mRNA. /// NM_153023 // upstream // 107269 // Hs.131017 //	FLJ46358	FLJ46358, Homo sapiens FLJ46358 protein (FLJ46358), q12.12
SNP_A-2095818	agacagacagatgtca[A/G]cacacacaaccgtcaa	A	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1989909	cacagaggactgggaa[A/G]gaatgctgtgatttaa	A	G	// 2887 // Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // upstream // 177044 // Hs.164060 // GRB10 // 2887 // Homo	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.1
SNP_A-2046110	aagactctcaaattaa[C/T]tcaattgacaaagaca	C	T	25842 // Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), mRNA. /// NM_153255 // upstream // 10355 // Hs.486315 // MCMDC1 // 254394 //	ASF1A	ASF1A, Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), q22.31
SNP_A-2117236	aggtgctgggattcat[A/G]aacagaggaaaactga	A	G	400935 // Homo sapiens FLJ41993 protein (FLJ41993), mRNA. /// ENST00000341280 // intron // 0 // --- // --- // --- // ---	FLJ41993	FLJ41993, Homo sapiens FLJ41993 protein (FLJ41993), q13.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113883	aggctgtgcctgggta[A/G]cctcttggtggcctga	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2128383	ataagttagaaacaca[A/G]aggcagattctggaac	A	G	26254 // Homo sapiens opticin (OPTC), mRNA. /// M83363 // upstream // 10839 // Hs.343522 // ATP2B4 // 493 // Human	OPTC	OPTC, Homo sapiens opticin (OPTC), q32.1
SNP_A-2133298	atatatatatatcctc[A/G]agagaaaattctcccct	A	G	Homo sapiens slit homolog 3 (Drosophila) ENST00000332966 // intron // 0 // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2158118	attggagctggcttca[A/G]atttcttctcagtctg	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2167364	caacagggtgaagaga[C/T]aacctaccagatggga	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3311357 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2212538	ccctagcacctgagj[C/G]aaccaggctgtgagtt	C	G	126147 // Homo sapiens hypothetical protein BC018697 (LOC126147), mRNA. /// ENST00000270235 // intron // 0 // ---	LOC126147	LOC126147, Homo sapiens hypothetical protein BC018697 (LOC126147), q13.33
SNP_A-2212279	ccctggatctggaca[G/T]acaaaggaatgacaag	G	T	PRO1085 mRNA, complete cds. /// NM_020673 // intron // 0 // Hs.529044 // RAB22A // 57403 // Homo sapiens RAB22A,	-	-, Homo sapiens PRO1085 complete cds, q13.32
SNP_A-2218610	cctggcagaggtcatg[A/G]aaaagagtctgtgagt	A	G	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 333816 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-2219684	ccttaaccaccatgca[A/G]atggcctctgtattc	A	G	ENST00000265654 // intron // 0 // --- // --- // ---	-	p13
SNP_A-2194822	catgcctttgcgtgga[C/T]gtgttttcattcctcc	C	T	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2193679	catcttgaagcaaaac[C/T]gccatgaagacctatg	C	T	ENST00000360397 // upstream // 264499 // --- // --- // ---	-	q25
SNP_A-2174016	cacacatttaagtgtc[A/G]cgggttaggacaaat	A	G	/// ENST00000318847 // downstream // 75123 // --- // ---	-	q23.31
SNP_A-1816990	gttatttaagatgtca[A/G]taagttctggaaatat	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1184514 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1824567	taaacttttggattca[G/T]atttgctaagtgaata	G	T	Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // --- // --- // ---	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-1833969	tacatactcgcacctg[C/G]aaaaccaacagatgat	C	G	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // intron // 0 // Hs.511504 // TCF12 // 6938 //	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-1829588	taagtgttctggcacat[C/G]atatttcctaagaaccc	C	G	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1797667	ggtttgactgccctacj[A/G]catctactcgaggtca	A	G	// 202374 // Homo sapiens serine/threonine kinase 32A (STK32A), mRNA. /// NM_001387 // downstream // 3610 //	STK32A	STK32A, Homo sapiens serine,q32
SNP_A-1798957	gtaagagtcaaactgt[A/T]aaaatgtatgtcgttt	A	T	Homo sapiens PIN2-interacting protein 1 (PINX1), mRNA. /// ENST00000314787 // intron // 0 // --- // --- // --- ///	PINX1	PINX1, Homo sapiens PIN2-interacting protein 1 (PINX1), p23.1
SNP_A-1791430	gggtataaagggatag[A/T]ccactactgaccagca	A	T	Homo sapiens hypothetical protein FLJ20294 (FLJ20294), mRNA. /// ENST00000314845 // intron // 0 // --- // --- // ---	FLJ20294	FLJ20294, Homo sapiens hypothetical protein FLJ20294 (FLJ20294), p11.2
SNP_A-1814169	gtgtctatattatga[C/G]agatattagtacatag	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2988737 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1720231	aaagccaaccaggttgaacccaaag[A/G]actgtgtcaggttagagttgtacg c	A	G	4613 // v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) /// NM_006316 // upstream // 436574 // - // - // - /// NM_030797 // downstream // 178256	MYCN	MYCN , rs10495651, v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) p24.3
SNP_A-1671638	catatcatgatctcaccaaattcac[C/G]agtttactgtaatttggaaacatac	C	G	NM_003453 // intron // 0 // Hs.315241 // ZNF198 // 7750 // zinc finger protein 198	ZNF198	ZNF198 , rs9315234, zinc finger protein 198,q12.11
SNP_A-1948445	tttagtcaaagatgaa[C/G]acacacaattattatt	C	G	FLJ38374 // 284800 // Homo sapiens hypothetical protein FLJ38374 (FLJ38374), mRNA. /// ENST00000246000 //	FLJ38374	FLJ38374, Homo sapiens hypothetical protein FLJ38374 (FLJ38374), p11.1
SNP_A-1959639	ttttggcagaaaagta[C/G]aaagacttaaagtgag	C	G	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 144070 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-1912605	tgtgcccaggaccccaa[A/G]gagaccacctctggg	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1910337	gaatgaatggtgaaa[A/G]ccagagtgaaaaaact	A	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1930629	ttccaatttcagaccc[G/T]ctctttgtgaacacat	G	T	Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// ENST00000335238 // intron // 0 // --- // --- // ---	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1891997	tgcaaaaagcatcaga[A/G]tacagttaaatgactg	A	G	Homo sapiens Cohen syndrome 1 (COH1), transcript variant 1, mRNA. /// NM_181661 // intron // 0 // Hs.191540 // COH1 //	COH1	COH1, Homo sapiens Cohen syndrome 1 (COH1), transcript variant 1, q22.2
SNP_A-2290410	gcaacccctgcttgac[A/G]cctgccggagaagaga	A	G	ENST00000293892 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-2311925	ggacaacctgcttgcg[C/G]agaggagctacccact	C	G	64062 // Homo sapiens chromosome 13 open reading frame 10 (C13orf10), mRNA. /// ENST00000327303 // upstream //	C13orf10	C13orf10, Homo sapiens chromosome 13 open reading frame 10 (C13orf10), q31.1
SNP_A-2276386	gagagctctgaccaga[A/G]gaaagtgaggttcagg	A	G	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 143666 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-2281373	gagtcaaagagaaaga[A/C]caaagggacctagagt	A	C	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1250403 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2269697	ttctaggctggtggta[C/G]ccttgattttacttttt	C	G	MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. ///	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2265847	gaaggaagtgagccaa[C/T]tctcatgtccctgaga	C	T	ENST00000337752 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2266593	gaagtcatgccctgca[A/C]cataaagttagcatct	A	C	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2244074	ctgcttgcttaatcct[A/G]acaaacttggtagagg	A	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 497017 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2230227	ctatagattctgttga[A/G]attctcaagatgggga	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3504743 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2314784	ggagtgaccatcccac[C/T]gtgaaccccaacaaaa	C	T	CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 69848	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1902896	tggctcttctagaaca[G/T]tccagctctaccacct	G	T	ENST00000338956 // intron // 0 // --- // --- // --- // ---	-	p15.2
SNP_A-1888594	tgaggcacccttgggt[A/G]acaagccacttcaaaa	A	G	130916 // Homo sapiens hypothetical protein MGC61716 (MGC61716), mRNA. /// ENST00000310397 // intron // 0 // ---	MGC61716	MGC61716, Homo sapiens hypothetical protein MGC61716 (MGC61716), q37.3
SNP_A-1883164	tgaaatgcttaatctc[C/T]atttcccaagcaatta	C	T	// 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // upstream	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1879117	tcttacaaagctaaac[A/G]caatcttcccatatga	A	G	Homo sapiens armadillo repeat containing 2 (ARMC2), mRNA. /// ENST00000237512 // intron // 0 // --- // --- // --- // ---	ARMC2	ARMC2, Homo sapiens armadillo repeat containing 2 (ARMC2), q21
SNP_A-1927845	ttcaagtatcagatta[C/G]agaggaaacgagaggt	C	G	Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1928032	ttcaattaagatgaaa[C/T]gttagaatgtatcttt	C	T	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1923582	ttagggtatggaggat[A/G]agaaagcgataatcaa	A	G	1470 // Homo sapiens cystatin SA (CST2), mRNA. /// NM_001900 // downstream // 17055 // Hs.121489 // CST5 //	CST2	CST2, Homo sapiens cystatin SA (CST2), p11.21
SNP_A-1960568	tttttcatcatgctca[A/G]aagctagcactctaaa	A	G	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 295826 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1938999	ttgagtctatatagca[C/T]ctcacagttcagatcc	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 643466 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1978640	tttatatgcacatttc[A/G]atttttcataagatca	A	G	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1943316 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1965095	cactaggccttttctga[C/T]attttcaacaataagc	C	T	ENST00000357839 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1728601	ggacattttaacaacattcattcta[C/T]caatctataaacatacctttttatt	C	T	64089 // sorting nexin 16 /// NM_152836 // upstream // 270392 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 ///	SNX16	SNX16 , rs1588083, sorting nexin 16 ,q21.13
SNP_A-1727497	cttatggttgttgtgtgactctaaa[C/T]gtttacttgaacatgctagcgagcc	C	T	NM_014895 // intron // 0 // - // - // - // -	-	- , rs2497150, -,q14.2
SNP_A-1808629	gtgaaccaaattagta[A/T]tacaatgtagtagcaa	A	T	4012 // Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA. /// NM_153234 // downstream // 58736 //	LNPEP	LNPEP, Homo sapiens leucyl q15
SNP_A-1804831	gtcagtgggtggcgaa[A/G]atgagattcatccctt	A	G	SERPINB13 // 5275 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), mRNA. /// NM_002974 // downstream // 31605	SERPINB13	SERPINB13, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), q21.33
SNP_A-1834753	taccagattcagaaaa[A/G]caattccaaaaatcac	A	G	// Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// ENST00000274458 // intron // 0 // --- // --- // --- // ---	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-1815078	gtgttcattttaataa[C/T]tagacacaggctgcat	C	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 312788 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-1860983	tcatagacttgtccca[A/G]taaaaagtcagctgac	A	G	// 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// ENST00000340515 // downstream // 17365 // --- //	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2178948	cactgcacccatggaa[A/C]aatgctgagcctcca	A	C	51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// ENST00000346248 // intron //	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-2190511	cataccagaaaaaaatc[C/G]caggtaaactgtacat	C	G	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-2211021	cggatacatacactca[C/T]cctgtatttttcaacc	C	T	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2167969	caacggtcctgcatc[A/G]aaaatgaaagtttcat	A	G	Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // --- // ---	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-2023879	aaaagaacttaagcaa[A/G]atttgaatgaccaa	A	G	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 275934 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2001647	tttgccacataaatac[C/T]acatactgataatcg	C	T	Homo sapiens olfactory receptor, family 51, subfamily A, member 7 (OR51A7), mRNA. /// NM_001004748 // intron // 0 // --- // OR51A2 // 401667 // Homo sapiens olfactory receptor,	OR51A7	OR51A7, Homo sapiens olfactory receptor, family 51, subfamily A, member 7 (OR51A7), p15.4
SNP_A-2019046	cttggagtaactaaac[A/C]agcaaacctctggcac	A	C	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2017854	tttccagttttaaca[A/C]cagcttcaaagatct	A	C	// Homo sapiens keratin associated protein 19-4 (KRTAP19-4), mRNA. /// NM_181611 // downstream // 3474 // --- //	KRTAP19-4	KRTAP19-4, Homo sapiens keratin associated protein 19-4 (KRTAP19-4), q22.11
SNP_A-2105891	agccatatactcaagga[G/T]aaaagagctcatgtat	G	T	// 167555 // Homo sapiens AASA9217 (UNQ9217), mRNA. /// NM_001004441 // downstream // 13042 // Hs.519404 // DP58	UNQ9217	UNQ9217, Homo sapiens AASA9217 (UNQ9217), q14.1
SNP_A-2083250	actaaacgcgtagtaa[C/T]caagacttcatttttt	C	T	// 283160 // Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), mRNA. ///	OR8D2	OR8D2, Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), q24.1
SNP_A-2067622	acaacaaacgtcatgc[A/G]ctgttgtttggtcaaa	A	G	669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 //	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-2069577	acacacacacacagat[G/T]aaaacttgtatttttc	G	T	endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 391047 // --- // --- // ---	-	-, Human endogenous retrovirus env q14.1
SNP_A-2063682	aattactgggatgtac[A/G]ataaatgtatgtttga	A	G	Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // intron // 0 // --- // --- // ---	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2055193	aataactggagccaca[G/T]tatttttaaatggcct	G	T	ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // downstream // 16165 // Hs.271903 // ALS	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2100373	agataaagaaaatcat[G/T]atctgaatctgaatca	G	T	// Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA. /// ENST00000304239 // intron // 0 // --- // --- // ---	FLJ32191	FLJ32191, Homo sapiens hypothetical protein FLJ32191 (FLJ32191), q13.12
SNP_A-2000739	ggcacttggtttgtat[C/T]gtcagtctctataagc	C	T	3707 // Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), mRNA. /// NM_000447 // upstream // 87929 //	ITPKB	ITPKB, Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), q42.12
SNP_A-2027379	aaacattaacaaaaaa[A/G]tcagtctgctggtcag	A	G	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // --- // ---	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1
SNP_A-2121224	agtctgggtgacacaa[C/T]aaaaccctgtctcaaa	C	T	2553 // Homo sapiens GA binding protein transcription factor, beta subunit 2, 47kDa (GABPB2), transcript variant beta-1, mRNA. /// NM_016654 // upstream // 59090 // Hs.511316 //	GABPB2	GABPB2, Homo sapiens GA binding protein transcription factor, beta subunit 2, 47kDa (GABPB2), transcript variant beta-1, q21.2
SNP_A-2184373	cagcgcccggccgaggt[G/T]aatttttagtgagtca	G	T	// Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G (APOBEC3G), mRNA. /// ENST00000337976 // intron // 0 // --- // --- // --- // ---	APOBEC3G	APOBEC3G, Homo sapiens apolipoprotein B editing enzyme, catalytic polypeptide-like 3G (APOBEC3G), q13.1
SNP_A-2171603	caatcgaaatacataa[A/G]tcagattatgttgctc	A	G	/// ENST00000310012 // upstream // 102829 // --- // --- // ---	-	q12
SNP_A-1858394	tcagactaatccacca[C/T]tggcttccctggctcct	C	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 753851 // --- // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1848372	tatgaaatatgatacc[A/G]gatattagaggctggg	A	G	10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // upstream // 3276 // Hs.523470 // IPO7 //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-1804140	gtcacatgaactcaca[A/G]ctgagggataggagc	A	G	Homo sapiens lactation elevated 1 (LACE1), mRNA. /// ENST00000258002 // intron // 0 // --- // --- // ---	LACE1	LACE1, Homo sapiens lactation elevated 1 (LACE1), q21
SNP_A-1812619	gtggctctgaatccca[C/T]atagtacaaaagctaa	C	T	134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream //	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-1736527	tgtttcgaagatattatctgcgatt[G/T]aaatttttttctattggatgcagt	G	T	CDNA clone IMAGE:5277680, partial cds /// NM_030932 // downstream // 326690 // Hs.122164 // DIAPH3 // 81624 //	-	-, rs9285221, CDNA clone IMAGE:5277680, partial cds ,q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1663000	attcttaagggaggctattaggaac[A/C]catttttgctcaagtaaatgataaa	A	C	follistatin-like 5	FSTL5	FSTL5 , rs1978910, follistatin-like 5,q32.2
SNP_A-1645638	gacaattaagtgaaaattgatgcta[C/G]agtgaattgattcaatgataatttt	C	G	FLJ35775 // 138009 // hypothetical protein FLJ35775 /// NM_173538 // downstream // 241744 // Hs.246284 //	FLJ35775	FLJ35775 , rs10504838, hypothetical protein FLJ35775 ,q21.3
SNP_A-1686492	gaaaaagacattcctaccaccaata[A/C]cttaattagcttcatgcaaaaagag	A	C	oculocutaneous albinism II (pink-eye dilution homolog, mouse)	OCA2	OCA2 , rs1448486, oculocutaneous albinism II (pink-eye dilution homolog, mouse),q13.1
SNP_A-1682648	ctttgttttctgcaggttcaccatc[A/G]ctctccaaatgtgggtttcttttga	A	G	NM_153755 // intron // 0 // - // - // - // -	-	- , rs1999334, -,q22.3
SNP_A-1944173	ttgtcagttgaaaaca[C/T]attttcaggcatctac	C	T	sapiens tec protein tyrosine kinase (TEC), mRNA. /// ENST00000258070 // intron // 0 // --- // --- // --- // ---	TEC	TEC, Homo sapiens tec protein tyrosine kinase (TEC), p12
SNP_A-1923742	ttagtaagaatgaaaa[A/G]tcaggtgagtggtcac	A	G	Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // --- // --- // --- // ---	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-1925065	ttatcactcatagaga[A/T]tcatgagacatattag	A	T	55341 // Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA. /// NM_152531 // downstream // 358233	FLJ11301	FLJ11301, Homo sapiens hypothetical protein FLJ11301 (FLJ11301), q29
SNP_A-1925830	ttatggacctttataa[C/T]gcacaatgatgaatta	C	T	ENST00000309493 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-1878945	tcttaaacataaacac[A/T]cttgacctaaaagaca	A	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1111532 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1885688	tgacagaatctttgga[A/C]gggctgaagaaccagg	A	C	// 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 331301 // --- // --- // --- // ---	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q16.3
SNP_A-1897988	tgctgtatgcttagcc[A/G]caaactccaattgctg	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 515628 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2229957	catgttcttctcttat[C/G]aagcaaactccacttc	C	G	4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 //	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2237949	ctctgagccacacggc[A/G]accaaggctggagctt	A	G	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // --- // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2266254	gaaggggttggatgag[G/T]atggcacctgttattt	G	T	Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000304853 // intron // 0 // --- // --- // --- // --- ///	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. ,q26.31
SNP_A-2269888	gacaatatgttaagca[C/T]tatagaggacaaagaa	C	T	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2259437	gaaaaatgggcaaaga[C/T]taagaacactttgtaa	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2280378	gaggggtgaataggat[C/T]agagcaatgcgtctgg	C	T	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 236967 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2274424	gactttctctagtggg[A/T]aataaatggccacctg	A	T	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 113902 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2276126	gagagactcagtgtaa[C/T]gagcacccacttatcc	C	T	Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), mRNA. /// NM_019076 // intron // 0 // Hs.546397 // UGT1A8 // 54576 // Homo sapiens UDP	UGT1A10	UGT1A10, Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), q37.1
SNP_A-2278957	gaggaaattgaggcct[A/G]aggaaatgaaacatca	A	G	ENST00000307248 // downstream // 94687 // --- // --- // --- // ---	-	q34
SNP_A-2282821	gataaagaatataata[C/G]agaatggcatcagcaa	C	G	// 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_019049 // upstream // 13409 //	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-2270450	gacagaagacagaagc[A/G]gagctttagatggagg	A	G	sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // --- // --- // --- // ---	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-2272371	gacctgcctggaactc[A/G]agggagaggagtcctc	A	G	ENST00000299734 // intron // 0 // --- // --- // --- // ---	-	p13.1
SNP_A-2245417	ctgggaagttttccaa[C/T]accctcactcatgcat	C	T	284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// NM_145301 // downstream // 11207 //	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-2299356	gccctgcagctgccga[G/T]aggtgcaaggagatgc	G	T	145270 // Homo sapiens proline rich membrane anchor 1 (PRIMA1), mRNA. /// NM_138344 // upstream // 63036 //	PRIMA1	PRIMA1, Homo sapiens proline rich membrane anchor 1 (PRIMA1), q32.13
SNP_A-1896759	tgctattctgttaacc[A/G]aacctttcatctctgt	A	G	// Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	SMARCAL1	SMARCAL1, Homo sapiens SWI,q35
SNP_A-1879054	tcttaagggatttaga[A/G]tcaacaactactaatt	A	G	// 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-1923301	ttaggaagaatgaccc[A/C]aaattcacagattaag	A	C	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1910480	tgtccctctgcctccc[C/T]aaacaagaaaatctct	C	T	/// ENST00000325796 // downstream // 662429 // --- // --- // ---	-	q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936492	ttcttgacctgatgct[A/G]aaaatcacctcgaaat	A	G	sapiens mRNA for KIAA0551 protein, partial cds. /// ENST00000284483 // intron // 0 // --- // --- // --- ///	TNIK	TNIK, Homo sapiens for KIAA0551 protein, partial cds. q26.2
SNP_A-1958327	tttccatgcatttta[A/T]gtgtgactgaagaaac	A	T	7424 // Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA. /// NM_018248 // upstream // 255769 //	VEGFC	VEGFC, Homo sapiens vascular endothelial growth factor C (VEGFC), q34.3
SNP_A-1949311	ttattaagcatctat[A/T]acatgcccagtgcatt	A	T	ENST00000341671 // intron // 0 // --- // --- // ---	-	q21.32
SNP_A-1962651	aggatcaagcctggga[C/T]aatttccactcaagaa	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1970217	acaaaataaatttcca[C/T]gctgcttaagcacctc	C	T	Homo sapiens chromosome 21 open reading frame 18 (C21orf18), mRNA. /// ENST00000344232 // intron // 0 // --- //	C21orf18	C21orf18, Homo sapiens chromosome 21 open reading frame 18 (C21orf18), q22.12
SNP_A-1969190	agaaaaggaaaagatc[A/C]agaacagattctgaaa	A	C	54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 284158	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-1979330	cttggtctaccagata[C/T]ccactggccatttttg	C	T	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 78283 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1978886	ttttaatactagcctg[A/T]cactgactatacagat	A	T	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 850898 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-1719685	ggtgtccaccaccactatagtgta[C/T]gcctgcctaatttttttgcatttttt	C	T	PRO2958 mRNA, complete cds. /// NM_015909 // downstream // 82701 // Hs.413771 // NAG // 51594 //	-	-, rs1178198, Homo sapiens PRO2958 mRNA, complete cds. p24.3
SNP_A-1809964	gtgagttccgatctga[A/G]atgatacgtacatcgc	A	G	sapiens mRNA; cDNA DKFZp547I166 (from clone DKFZp547I166). /// NM_018107 // CDS // 0 // Hs.4997 //	RBM23	RBM23, Homo sapiens cDNA DKFZp547I166 (from clone DKFZp547I166). q11.2
SNP_A-1786654	ggcttgcaacagctgc[A/G]attccatcttgactat	A	G	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1848415	tatgaaccttttgggggt[A/G]aaataaatctcaaaca	A	G	sapiens nuclear factor I/B (NFIB), mRNA. /// ENST00000339974 // intron // 0 // --- // --- // --- // ---	NFIB	NFIB, Homo sapiens nuclear factor I p23
SNP_A-1847707	tatctagggaaagggc[C/G]cagatactgcctcttc	C	G	Homo sapiens RAN binding protein 3 (RANBP3), transcript variant RANBP3-a, mRNA. /// NM_007322 // intron // 0 //	RANBP3	RANBP3, Homo sapiens RAN binding protein 3 (RANBP3), transcript variant RANBP3-a, p13.3
SNP_A-1854943	tcaactgaaaatcaat[A/C]aggaaaaacattgaaaa	A	C	Homo sapiens hypothetical protein FLJ21820 (FLJ21820), mRNA. /// ENST00000237822 // intron // 0 // --- // --- // ---	FLJ21820	FLJ21820, Homo sapiens hypothetical protein FLJ21820 (FLJ21820), p24.1
SNP_A-1862613	tcattagttcctggta[A/C]taaacattccatttttc	A	C	4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream //	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1872371	tctagagtgtatctaa[C/T]ggtgggggcagattca	C	T	/// ENST00000334709 // upstream // 1822 // --- // --- // ---	-	q11.2
SNP_A-1816892	gttattacaaatagca[G/T]tacctccttttttaag	G	T	84873 // Homo sapiens G protein-coupled receptor 128 (GPR128), mRNA. /// NM_006070 // upstream // 9675 //	GPR128	GPR128, Homo sapiens G protein-coupled receptor 128 (GPR128), q12.2
SNP_A-1822810	taaaaaccagtcataca[A/T]gacaaacactccacat	A	T	Homo sapiens chromosome 9 open reading frame 156 (C9orf156), mRNA. /// ENST00000259459 // intron // 0 // --- //	C9orf156	C9orf156, Homo sapiens chromosome 9 open reading frame 156 (C9orf156), q22.33
SNP_A-2184697	tcaaatatctccaaat[C/G]aaattcatggtaattt	C	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 651804 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2207745	cccaaaacaggtatac[C/T]ctgaactgaagagact	C	T	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2205808	ccatacctcttctcaa[C/T]tcaaccccatcctta	C	T	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2204630	ccaggacttgaagata[C/T]aaggacagaagaaaga	C	T	Homo sapiens phosphodiesterase 11A (PDE11A), mRNA. /// ENST00000286063 // intron // 0 // --- // --- // ---	PDE11A	PDE11A, Homo sapiens phosphodiesterase 11A (PDE11A), q31.2
SNP_A-2222867	cgcaagctacagcata[A/C]gtcagtgtgtctctc	A	C	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // ---	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-2115139	agggctgcatagaaaat[C/T]aggtgatcacaacaac	C	T	Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, mRNA. /// NM_177926 // intron // 0 // Hs.488051 //	CSRP2BP	CSRP2BP, Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, p11.23
SNP_A-2020344	gtagcgttcaccaagg[A/G]aattcaactctggtta	A	G	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA. /// ENST00000291560 // intron // 0 // --- // --- // ---	HSF2BP	HSF2BP, Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), q22.3
SNP_A-2020586	gaaacttcaaactgta[A/C]atgaaaaatttcatgc	A	C	// 104 // Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, mRNA. /// NM_015833 // downstream // 17753 // Hs.474018 // ADARB1 // 104 // Homo	ADARB1	ADARB1, Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017375	cacaaggatgagaaag[A/G]agttttacagtcttac	A	G	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 170439 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2008716	cccactttctccatca[C/T]ggcagtcacttacaag	C	T	ENST00000338458 // intron // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-2101710	agatgcagcccaatca[G/T]ctatgcagagagggtg	G	T	Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /// ENST00000256397 // intron // 0 // --- // --- // --- // ---	LOXL2	LOXL2, Homo sapiens lysyl oxidase-like 2 (LOXL2), p21.3
SNP_A-2105563	agccacagctttctca[A/G]ccgtacttcctgttct	A	G	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2083798	actaccattaaaggca[A/G]gtagcctctcaagagg	A	G	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 847244 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-2077771	accagaaacatgtgaa[A/C]gttccagtgtcttggt	A	C	-- /// ENST00000361117 // upstream // 694797 // --- // --- // ---	-	q33.2
SNP_A-2091822	agaaaatcctaaccac[A/G]ctggctttaaatttcc	A	G	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 //	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q21.1
SNP_A-2050274	aaggagagcaagtgta[A/C]cacatggcgggcacag	A	C	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2050440	aaggataatttagtga[A/G]accataaacaacatat	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 143423 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.3
SNP_A-2099287	agaggcaggatgaaaa[A/T]ttcaggggtctccaga	A	T	sapiens B-cell CLL/lymphoma 3 (BCL3), mRNA. /// ENST00000164227 // intron // 0 // --- // --- // --- // ---	BCL3	BCL3, Homo sapiens B-cell CLL,q13.31
SNP_A-2017843	gttactcattaatttc[A/G]cagtctgccagaagtt	A	G	284827 // Homo sapiens keratin associated protein 13-4 (KRTAP13-4), mRNA. /// NM_181623 // upstream // 9436 // ---	KRTAP13-4	KRTAP13-4, Homo sapiens keratin associated protein 13-4 (KRTAP13-4), q22.11
SNP_A-2004881	ctgcttagaggagcaa[A/G]ccaacacacatgacac	A	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2001922	ctgttgcaaagacaga[G/T]cccatttagctgtatt	G	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2110844	atgtgaagtggttaca[C/G]tggtttagtcacagca	C	G	3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 37303 //	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-2127671	ataactaacaagtcca[C/T]tgaattataaactggt	C	T	/// ENST00000236495 // upstream // 44616 // --- // --- // --- // --	-	p33
SNP_A-2123520	agtgtgctatagagga[A/G]caaggagtggaggagg	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3946951 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2166421	atgtactgaagacaga[G/T]atatttcactaaaatg	G	T	114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream //	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-2149091	atggtttttgtcaaga[C/T]aatggcaggaccaaga	C	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2151911	atgtttgtagtgtggc[C/T]gaaactcagaacacag	C	T	ENST00000322285 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2149822	atgtatttttttaattg[C/T]aggtcatcctcaaaaa	C	T	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-2222862	cgcaacacttagatag[A/G]actttctgtactgatg	A	G	Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), mRNA. /// U36798 // intron // 0 // Hs.386791 //	PDE3A	PDE3A, Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), p12.2
SNP_A-2221521	cctttcttgccttcca[C/T]gacaattacatttta	C	T	ENST00000331019 // upstream // 29805 // --- // --- // --- // --- /// ENST00000333289 // upstream // 47997 // --- // --- // --- // --	-	q11.22
SNP_A-2214430	cctactctcatttccc[A/G]agaacatttaaagaca	A	G	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2190622	catactccaccataag[A/G]acaactagaagctcca	A	G	/// ENST00000321536 // upstream // 770319 // --- // --- // --- // -	-	p13
SNP_A-2193554	catctgtgtatccaaa[C/T]ggacattttgtgcgtg	C	T	Homo sapiens hypothetical protein MGC4562 (MGC4562), mRNA. /// ENST00000319194 // CDS // 0 // --- // --- // --- // ---	MGC4562	MGC4562, Homo sapiens hypothetical protein MGC4562 (MGC4562), q22.31
SNP_A-2197360	cattcattgcgctcta[A/C]agtgtctatctctgac	A	C	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 461075 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-2172971	tgagaaaactgcagca[C/T]tgataagtcgaatcca	C	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170652	caagttaacaagtatt[A/T]aaggaaacatgcatat	A	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 658094 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2182483	acactctcagctaata[C/T]tacctcaaagccaggc	C	T	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1
SNP_A-1822984	taaaaatcatatcctc[A/G]aattgcttataatcta	A	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1868294	tcctcaggcagaagaa[A/G]aatgaatacaaattga	A	G	G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// NM_153686 // upstream //	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32
SNP_A-1865710	tccattgctcactgaa[C/G]ggtgatgcttgggtag	C	G	LOC92346 // 92346 // Homo sapiens LOC92346 (LOC92346), mRNA. /// NM_002642 // upstream // 49474 //	LOC92346	LOC92346, Homo sapiens LOC92346 (LOC92346), q24.3
SNP_A-1641999	ggaagtcaaaagatatttcaagtaa[C/T]attgtaactcagatagtgatgctca	C	T	NM_017757 // intron // 0 // Hs.272792 // ZNF407 // 55628 // zinc finger protein 407	ZNF407	ZNF407 , rs10514146, zinc finger protein 407,q22.3
SNP_A-1981249	cagaaaactactttaa[C/T]tccagcattcccttag	C	T	5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 145621 // Hs.298863 // FLJ23577	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1880839	tcttggtcttcaccag[C/T]agagccgccatccaca	C	T	91355 // Homo sapiens hypothetical protein DKFZp434O0213 (DKFZp434O0213), mRNA. /// ENST00000215872 // 3UTR // 0 // --- // --- // --- // ---	DKFZp434O0213	DKFZp434O0213, Homo sapiens hypothetical protein DKFZp434O0213 (DKFZp434O0213), q11.23
SNP_A-1894966	tgcccaactgctccgg[A/G]acacagccaatagctg	A	G	Homo sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), mRNA. /// NM_000235 // upstream // 90987 // Hs.127445 // LIPA // 3988 // Homo sapiens lipase	LIPA	LIPA, Homo sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), q23.31
SNP_A-2310987	ggaagggaggttagaa[C/T]tgggggctaagttggt	C	T	ENST00000358195 // intron // 0 // --- // --- // --- // --- /// ENST00000282635 // 5UTR // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2248762	ctgttctcggttacac[C/T]catctttcatctatgt	C	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1275114	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2237630	ctctctctccctctcc[C/T]gctggtgtgtgtttca	C	T	RPS6KA4 // 8986 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 4 (RPS6KA4), mRNA. ///	RPS6KA4	RPS6KA4, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 4 (RPS6KA4), q13.1
SNP_A-2261958	gaaatacagagaggcc[C/T]gctgccagctagaatc	C	T	// 1302 // Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA. ///	COL11A2	COL11A2, Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, p21.32
SNP_A-2275750	gagacccacaaaggac[A/G]gtatgctcaagaatgt	A	G	Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// ENST00000224949 // CDS // 0 // --- // --- // --- // ---	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2261303	gaaagcaagttaatgg[C/T]ccatgtcatagaacta	C	T	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // --- // --- // --- // ---	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2259452	gaaaaattaatacttg[C/T]agcacactttgcctct	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2257681	ctttgcttcctttcaa[C/T]gttcttgcttattgtt	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2905673 // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p13.3
SNP_A-2304561	gctctccatctgaata[A/C]cttcaccacctcactg	A	C	Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 //	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-1889299	tgagtgcttttataag[C/T]agagaaagaagtacca	C	T	65985 // Homo sapiens acetoacetyl-CoA synthetase (AACS), mRNA. /// ENST00000316519 // downstream // 185829 // ---	AACS	AACS, Homo sapiens acetoacetyl-CoA synthetase (AACS), q24.31
SNP_A-1883201	tgaaatgtgttttgca[G/T]gtagaaatatgagtca	G	T	// 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-1909438	tgtattctaggatcca[C/T]gcagctcttttcaggt	C	T	// 23507 // Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA. /// NM_032270 // upstream //	TA-LRRP	TA-LRRP, Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), p22.2
SNP_A-1907273	tggttttcactctcca[C/T]ggccaagtctagtcat	C	T	/// ENST00000318847 // downstream // 94832 // --- // --- // ---	-	q23.31
SNP_A-1985185	caatgaggccagcaac[A/G]ctctttagaaaaaaca	A	G	Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // --- // ---	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-1962707	gactgagaataagaga[C/T]acctcaaaaatcaatt	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1965540	accaaacatcaaactc[C/G]ccgtgctttttgcag	C	G	130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // ---	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-1956406	tttgttcaaccactac[A/G]gcaccgtaagatatgt	A	G	Homo sapiens DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA. /// ENST00000360760 // intron // 0 // ---	DNAPTP6	DNAPTP6, Homo sapiens DNA polymerase-transactivated protein 6 (DNAPTP6), q33.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1940236	ttgcattacacttcaa[C/T]caaaaaattatggctca	C	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1682554	ataaagaactattcctgaaattaga[G/T]tacctaatgaattgtagattigaaa	G	T	NDUFA4 // 4697 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa /// NM_152745 // downstream // 464112 // Hs.343660 // NXPH1 // 30010 // neurexophilin 1	NDUFA4	NDUFA4 , rs10261711, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa ,p21.3
SNP_A-1729702	ctttagaaagacagaattttcaatc[C/T]attggctgttgtatttaagaagctt	C	T	4194 // Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse) /// NM_006338 // upstream // 87302 // Hs.26312 // LRRN5 // 10446 // leucine rich repeat neuronal	MDM4	MDM4 , rs7552328, Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse) ,q32.1
SNP_A-1734370	agttgtaaggaagttctttgttcc[A/G]ctagacatttatttaagagaacaaa	A	G	NM_005019 // intron // 0 // Hs.416061 // PDE1A // 5136 // phosphodiesterase 1A, calmodulin-dependent	PDE1A	PDE1A , rs10497596, phosphodiesterase 1A, calmodulin-dependent,q32.1
SNP_A-1742007	ctcaattgaggagcaataaacctca[A/G]tcataggacattcatttttatttt	A	G	BTB and CNC homology 1, basic leucine zipper transcription factor 2	BACH2	BACH2 , rs597244, BTB and CNC homology 1, basic leucine zipper transcription factor 2,q15
SNP_A-1781797	ggatttggaaaaggca[A/G]cctttagattggaaaa	A	G	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 441173 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-1791400	gggtaggcatgggaaaa[A/C]ctttccccagaattag	A	C	8646 // Homo sapiens chordin (CHRD), transcript variant 2, mRNA. /// NM_177979 // downstream // 66225 // Hs.166186	CHRD	CHRD, Homo sapiens chordin (CHRD), transcript variant 2, q27.1
SNP_A-1791053	ggggtctctttaaata[C/T]gctgtatacgcacaaa	C	T	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 848043 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1862431	tcatggtgtatttggc[A/G]attatgtgttaaccat	A	G	Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // --- // --- // --- // ---	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-1869686	tcctatggcatgccc[A/G]agtcacactctggttt	A	G	// 23507 // Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA. /// NM_032270 // upstream //	TA-LRRP	TA-LRRP, Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), p22.2
SNP_A-1856664	tcacatacagaatgag[A/G]aaatatcacagatttt	A	G	// 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1847525	tatccttcaagacccaa[A/T]ataaagtgttctgtga	A	T	10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 169659 // Hs.334587 // RBPMS //	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-1844456	tataaagcagcatccc[A/G]ccgattcctaaaatag	A	G	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// ENST00000258104 // intron // 0 // --- // --- // --- // ---	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-1822996	taaaaatctatgtgca[C/T]gaacaaatgaataatc	C	T	51274 // Homo sapiens Kruppel-like factor 3 (basic) (KLF3), mRNA. /// NM_030956 // downstream // 33251 // Hs.120551	KLF3	KLF3, Homo sapiens Kruppel-like factor 3 (basic) (KLF3), p14
SNP_A-1831322	taatggttagaaatga[C/G]gatagttctattgaac	C	G	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1842915	tagtagtctttcaagg[A/G]caataaaatattgccct	A	G	/// ENST00000336930 // upstream // 932731 // --- // --- // --- // ---	-	p14.3
SNP_A-2193198	catctcaagttgttag[C/T]attctttgccactgct	C	T	// 85294 // Homo sapiens keratin associated protein 2-4 (KRTAP2-4), mRNA. /// ENST00000306271 // upstream //	KRTAP2-4	KRTAP2-4, Homo sapiens keratin associated protein 2-4 (KRTAP2-4), q21.2
SNP_A-2185117	caggaaaacaaggtga[A/G]aattcccgtcttatt	A	G	ENST00000317283 // CDS // 0 // --- // --- // ---	-	p15.4
SNP_A-2150136	atgtcctgaactccatt[C/T]agtgaacattcccctt	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2138834	atccctacagcaccgcd[A/G]aagggacgtcatagac	A	G	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2158911	attgtgtatgccttga[C/T]gtgagagaattccaaa	C	T	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 7953 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2160940	atttctgtaaagaaga[A/C]aactgagatttttgata	A	C	1939 // Homo sapiens ligatin (LGTN), mRNA. /// NM_003582 // upstream // 10902 // Hs.164267 // DYRK3 // 8444 // Homo	LGTN	LGTN, Homo sapiens ligatin (LGTN), q32.1
SNP_A-2125009	agttgcagtagttaaa[A/G]cagtgtggtgtcacgt	A	G	Homo sapiens topoisomerase (DNA) II binding protein 1 (TOPBP1), mRNA. /// ENST00000260810 // intron // 0 // --- // ---	TOPBP1	TOPBP1, Homo sapiens topoisomerase (DNA) II binding protein 1 (TOPBP1), q22.1
SNP_A-2132127	ataggtactataaaag[C/T]catttgctaaaggga	C	T	Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// ENST00000323829 // intron // 0 // --- // --- // ---	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-2131106	atagacaggaagaggc[A/G]gattcaagagatgatt	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2120370	agtcatgattcaaaag[C/T]attagaacagcccaaa	C	T	Homo sapiens protease, serine, 12 (neurotrypsin, motopsin) (PRSS12), mRNA. /// ENST00000296498 // intron // 0 // --- // ---	PRSS12	PRSS12, Homo sapiens protease, serine, 12 (neurotrypsin, motopsin) (PRSS12), q26

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2000560	atggagagaccagtga[C/G]gtcaaggccattgaaa	C	G	Homo sapiens choline acetyltransferase (CHAT), transcript variant N2, mRNA. /// NM_020984 // intron // 0 // Hs.302002 //	CHAT	CHAT, Homo sapiens choline acetyltransferase (CHAT), transcript variant N2, q11.23
SNP_A-2013562	caacttctgttcccaa[C/G]aaaaatgaacaagagt	C	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1636551 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2007504	attttattgtaatgct[A/G]aaagctaatgtttcct	A	G	51126 // Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, mRNA. /// NM_016100 // downstream // 13622 // Hs.368783 // NAT5	NAT5	NAT5, Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, p11.23
SNP_A-2010300	cccatttcatttccca[A/G]ctgaggaggacttata	A	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1441784 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2028374	aaactccaagtgctaa[A/T]acactcaatgttcgct	A	T	sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.1
SNP_A-2045914	aagaccagactggcca[A/C]tatggagaaaacctgt	A	C	Homo sapiens src homology 2 domain containing transforming protein C3 (SHC3), mRNA. /// ENST00000277153 // intron // 0 // --- // --- // --- // ---	SHC3	SHC3, Homo sapiens src homology 2 domain containing transforming protein C3 (SHC3), q22.1
SNP_A-2040623	aaccattgatatttta[C/T]gcttggtgcttttact	C	T	ENST00000355599 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2101347	agatctgaaactgtaa[A/G]actactgaaagaaaac	A	G	2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA.	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease q33.1
SNP_A-2104442	agcaggactttatgta[C/T]gcatgcttcatatttt	C	T	Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // --- //	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-2049862	aaggaaatatccccac[C/T]gaataaatttataggt	C	T	FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ11017), mRNA. /// NM_018302 // downstream	FLJ11017	FLJ11017, Homo sapiens hypothetical protein FLJ11017 (FLJ11017), p14
SNP_A-2051553	aagggttcacagcaca[C/T]tccagggatatgacaa	C	T	Homo sapiens KIAA1068 protein (KIAA1068), mRNA. /// ENST00000354528 // intron // 0 // --- // --- // --- ///	NUDCD3	NUDCD3, Homo sapiens KIAA1068 protein (KIAA1068), p13
SNP_A-2059335	aatcgtatacatacta[C/T]aaccaaaatctgaaaa	C	T	Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // --- // ---	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-2063777	aattagcatgactatc[C/G]caccttt catgaggct	C	G	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2074360	acatacatccctttgc[A/C]aagcaataacagcatt	A	C	// Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 //	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.2
SNP_A-2071749	acagacagttcaccca[C/G]aggattcactcgctgt	C	G	ENST00000294008 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-2107746	agctcagagagatgaa[C/G]tgacttgttcaaagtt	C	G	ENST00000265327 // intron // 0 // --- // --- // --- // ---	-	q35
SNP_A-2010547	cttacagttttgctaa[A/G]ttaaatgacagatgct	A	G	// 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 1053108 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2007198	aggtttgcaccaagaa[A/G]aagagataaagaagag	A	G	55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 //	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-2016871	cagttcctacaataaa[C/G]cagtgcattgacaggg	C	G	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 521849	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1989970	aatcagccagggtggc[A/C]aagttattgctctcat	A	C	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 360400 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-2135866	atcaacacacatttaa[A/G]gcatatcagttttacc	A	G	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-2161330	atttgatttctttgaa[C/T]acaataggctttcctt	C	T	/// ENST00000357497 // downstream // 119817 // --- // --- // --- // --- /// ENST00000359402 // downstream // 119870 // --- // ---	-	q31.1
SNP_A-2139396	atcctgttctgcatgc[A/G]cagaggtgatgctact	A	G	PGLYRP3 // 114771 // Homo sapiens peptidoglycan recognition protein 3 (PGLYRP3), mRNA. ///	PGLYRP3	PGLYRP3, Homo sapiens peptidoglycan recognition protein 3 (PGLYRP3), q21.3
SNP_A-2142656	atgaagaaattgattg[C/T]aaaaattcgtattctt	C	T	Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2149214	atgtaagagagtttga[A/G]taagtgaagtataaga	A	G	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 564735	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2181333	cagacgaaagaaccac[A/G]gggtagagatgggaga	A	G	/// ENST00000335028 // upstream // 99561 // --- // --- // --- // ---	-	q21.31
SNP_A-2214371	cctacctcttccaaga[C/T]gcccaggaagtgcacc	C	T	9759 // Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /// NM_207483 // upstream // 62583 // Hs.516794 //	HDAC4	HDAC4, Homo sapiens histone deacetylase 4 (HDAC4), q37.3
SNP_A-2213827	cctaaactcagatagc[C/T]agaaagttgttgggag	C	T	7019 // Homo sapiens transcription factor A, mitochondrial (TFAM), mRNA. /// NM_012251 // downstream // 171933 //	TFAM	TFAM, Homo sapiens transcription factor A, mitochondrial (TFAM), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2214628	cctagatttataacaa[A/G]gacttatttccaattt	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1838668	tagacactttccacac[A/G]agggctgagtaacttt	A	G	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 225250 //	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-1831105	taatgcaaccaccttc[A/G]aaaatgatttggtgtt	A	G	/// ENST00000331815 // downstream // 902265 // --- // --- // ---	-	q13.13
SNP_A-1829164	taaggttaactatact[C/T]aggctgctgatctatt	C	T	// Homo sapiens engrailed homolog 1 (EN1), mRNA. /// NM_006770 // upstream // 54379 // Hs.67726 // MARCO //	EN1	EN1, Homo sapiens engrailed homolog 1 (EN1), q14.2
SNP_A-1830674	taatcccattggcaaa[C/G]acagagaaatccaaag	C	G	ENST00000320153 // intron // 0 // --- // --- // --- // ---	-	p36.13
SNP_A-1833762	tacagtaaatgccacc[G/T]atacttcttggacgga	G	T	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 323609 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1822373	gttttgttccagaaaa[C/T]tacttctcggatacag	C	T	Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// ENST00000325839 // intron // 0 // --- // --- // --- // ---	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1850458	tattaaaagacagaaa[A/G]gacaaactatacactg	A	G	ENST00000335031 // intron // 0 // --- // --- // --- // ---	-	q31.23
SNP_A-1867189	tccctgctctactcct[A/G]actggttaacaagaaa	A	G	ENST00000328153 // intron // 0 // --- // --- // --- // ---	-	q26.1
SNP_A-1799746	gtacaaataaggttaa[C/T]aggaaaatcaagttta	C	T	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 125720 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1800116	gtaccaggctgggttc[C/G]aagtgcacaagggagt	C	G	85364 // Homo sapiens zinc finger, CCHC domain containing 3 (ZCCHC3), mRNA. /// NM_006943 // upstream // 20890 //	ZCCHC3	ZCCHC3, Homo sapiens zinc finger, CCHC domain containing 3 (ZCCHC3), p13
SNP_A-1758603	ggaatcatgacccccagctcttaag[A/G]aactcataatctagtagaggggact	A	G	80315 // cytoplasmic polyadenylation element binding protein 4	CPEB4	CPEB4 , rs10516102, cytoplasmic polyadenylation element binding protein 4,q35.2
SNP_A-1934031	ttctcactcaagtcta[C/T]ggaaacaaggaaataa	C	T	IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p11.2
SNP_A-1950793	tttcattttcttttac[G/T]attctgcctgagcttt	G	T	Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA. /// ENST00000327801 // intron // 0 // --- // ---	SMYD3	SMYD3, Homo sapiens SET and MYND domain containing 3 (SMYD3), q44
SNP_A-1984659	gggaaatgtaattgac[A/C]caaatgtggccaggat	A	C	4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream //	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-1979082	atgttaagtttattta[C/T]catcagagaaggataa	C	T	// 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 3270990 // --- // -	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1910319	tgtccagagattaatg[C/T]aacaaactgtctccaa	C	T	/// ENST00000316561 // upstream // 36258 // --- // --- // --- // ---	-	p21.33
SNP_A-1874826	tctcgctcaataaaga[C/T]ctgcaggtgaattcgc	C	T	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-1903633	tgggagaaagggcttc[A/G]actgtggtttcagaca	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 80024 // --- // --- // --- // ---	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2309969	ggaaatgacatgcaaa[C/T]aaggatgaccatcaca	C	T	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2288429	gattcttcatccttga[A/G]aatggaggtagtcagt	A	G	6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 146341 //	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-2288214	gattccatttcaaaaa[C/T]aaattcatcctcatat	C	T	// Homo sapiens C1q and tumor necrosis factor related protein 7 (C1QTNF7), mRNA. /// ENST00000295297 // intron // 0 // --- // --- // --- // ---	C1QTNF7	C1QTNF7, Homo sapiens C1q and tumor necrosis factor related protein 7 (C1QTNF7), p15.33
SNP_A-2242559	ctgcaggctagccagg[A/G]catattctcaggataa	A	G	Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-2255946	ctttaaccttcatttc[A/G]attcctccaggtctca	A	G	// 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 888623 // --- // --- // --- //	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2254694	cttgcttcgcaaatta[C/T]agcacaatgttacagc	C	T	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2230397	ctatcaacagaatcaa[C/T]aatctacagaatggga	C	T	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2273673	gactgcaactctaggt[A/G]aacatcccttctgttt	A	G	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2273170	gactcacagctaagtg[A/C]agtatttttcaaactt	A	C	56475 // Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), mRNA. /// NM_052917 // upstream // 215516 // Hs.470277 // GALNT13 // 114805 //	RPRM	RPRM, Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2297248	gccacccaactgaggc[G/T]ccaggatttctgcac	G	T	ENST00000354893 // intron // 0 // --- // --- // ---	-	p11.2
SNP_A-1883792	tgaagaaatgtaaagc[C/T]atgatgtgcatctcaa	C	T	Homo sapiens chromosome 6 open reading frame 151 (C6orf151), mRNA. /// ENST00000342415 // intron // 0 // --- // ---	C6orf151	C6orf151, Homo sapiens chromosome 6 open reading frame 151 (C6orf151), p24.3
SNP_A-1909126	tgtatccatttttagc[A/G]aagttttccaagccta	A	G	2203 // Homo sapiens fructose-1,6-bisphosphatase 1 (FBP1), mRNA. /// NM_032823 // upstream // 47336 // Hs.434253 // ---	FBP1	FBP1, Homo sapiens fructose-1,6-bisphosphatase 1 (FBP1), q22.32
SNP_A-1935343	ttctgctttttctggaa[A/G]atagccatcgaacaag	A	G	// Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), mRNA. /// ENST00000278353 // intron // 0 // ---	HSD17B12	HSD17B12, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), p11.2
SNP_A-1821371	gtttgcttctagacaa[G/T]atgtgtgacagtatgt	G	T	/// ENST00000356128 // upstream // 147992 // --- // --- // ---	-	q24
SNP_A-2213614	ccgtctttcaatcctg[A/G]caattcgtagttact	A	G	/// ENST00000334663 // downstream // 42354 // --- // --- // ---	-	p11.1
SNP_A-2206878	ccatggcacacgtttta[C/G]ctgttttaatcagta	C	G	441639 // Homo sapiens olfactory receptor, family 9, subfamily K, member 2 (OR9K2), mRNA. /// NM_001005280	OR9K2	OR9K2, Homo sapiens olfactory receptor, family 9, subfamily K, member 2 (OR9K2), q13.2
SNP_A-2212558	ccctatctaacccaa[A/G]gcctttcttctactg	A	G	// Homo sapiens kinesin family member 1A (K1F1A), mRNA. /// NM_000030 // upstream // 24565 // Hs.144567 // AGXT // ---	KIF1A	KIF1A, Homo sapiens kinesin family member 1A (KIF1A), q37.3
SNP_A-2177292	cacctgtgaaatgtca[C/T]atgtatggagacacca	C	T	Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// ENST00000306051 // intron // 0 // --- // --- // ---	PTGDR	PTGDR, Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), q22.1
SNP_A-2176831	gccagaagactcagca[A/G]atgttcattccacat	A	G	Homo sapiens muscleblind-like 2 (Drosophila) (MBNL2), transcript variant 3, mRNA. /// NM_144778 // intron // 0 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 925428 // --- // --- // ---	MBNL2	MBNL2, Homo sapiens muscleblind-like 2 (Drosophila) (MBNL2), transcript variant 3, q32.1
SNP_A-2172872	caatttctggaatga[C/T]attaagttcttattaa	C	T		LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2161209	atttgagaacaggcttg[C/G]aggacagcaggtggga	C	G	– /// ENST00000314058 // upstream // 5167 // --- // --- // –	-	p13.2
SNP_A-2157451	tctgcctcacttaccc[A/C]cacctcacatgtactt	A	C	Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // intron // 0 // Hs.373857 // ---	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2118292	agtaacagcccataag[G/T]cgtgaattatgtggtc	G	T	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 686300	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2117851	aggttgtggttatgta[C/G]gttgttatactgagc	C	G	GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126), mRNA. /// NM_198569 //	GPR126	GPR126, Homo sapiens G protein-coupled receptor 126 (GPR126), q24.2
SNP_A-2011082	atcatataggcattgc[A/G]cagccaatcaaaaaca	A	G	285704 // Homo sapiens RGM domain family, member B (RGMB), mRNA. /// ENST00000308338 // downstream //	RGMB	RGMB, Homo sapiens RGM domain family, member B (RGMB), q21.1
SNP_A-2022957	aaaacaatttggacgc[C/G]caaggagaataagatg	C	G	ENST00000358195 // intron // 0 // --- // --- // ---	-	q11.23
SNP_A-2102816	agatttttgggaaaata[C/T]cattccatttgggagga	C	T	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), mRNA. /// ENST00000261461 // intron // 0 // --- // --- // ---	PPP2R5A	PPP2R5A, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), q32.3
SNP_A-2095573	agacaatcacttctc[A/G]ctgtatctccacatag	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 678988 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2098953	agagctctctgtgaa[A/T]gacagcaataaaggaa	A	T	Homo sapiens zinc finger protein 346 (ZNF346), mRNA. /// ENST00000358149 // intron // 0 // --- // --- // ---	ZNF346	ZNF346, Homo sapiens zinc finger protein 346 (ZNF346), q35.2
SNP_A-2085081	actcacttggtcggag[C/G]aggcactgtgaatcac	C	G	Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. /// ENST00000224950 // CDS	OBFC1	OBFC1, Homo sapiens oligonucleotide q24.33
SNP_A-2086486	actcttttcttttgca[A/G]tcatttactctatcc	A	G	Homo sapiens KIAA1219 protein (KIAA1219), mRNA. /// ENST00000262879 // intron // 0 // --- // --- // ---	KIAA1219	KIAA1219, Homo sapiens KIAA1219 protein (KIAA1219), q11.23
SNP_A-2081231	acctgctatgtgaaag[A/G]catttagttaaagctg	A	G	Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // --- // --- // ---	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2075345	acatgaaattgggcac[C/G]agggaagctcacctac	C	G	Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 2 (RASGRF2), mRNA. /// ENST00000265080 // intron // 0 // --- // --- // ---	RASGRF2	RASGRF2, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 2 (RASGRF2), q14.1
SNP_A-2063434	aattaaggaaggcttaj[A/G]atgtaagcttaaacaa	A	G	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 262035 // Hs.437966 // PXMP3 // ---	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2068198	acaagagcagatgggat[C/G]agcaagaatgaagaac	C	G	Homo sapiens cytochrome P450, family 39, subfamily A, polypeptide 1 (CYP39A1), mRNA. /// ENST00000275016 // intron // 0 // --- // --- // ---	CYP39A1	CYP39A1, Homo sapiens cytochrome P450, family 39, subfamily A, polypeptide 1 (CYP39A1), p12.3
SNP_A-2059616	aatctctatgtgtctc[C/T]gaatttttcttctgtg	C	T	// Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451). mRNA. /// ENST00000327355 // intron // 0 // --- // --- // ---	LOC400451	LOC400451, Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), q26.1
SNP_A-2067885	acaacctcacacacaa[A/G]aaaaglactgcgaggga	A	G	Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // --- //	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015754	tagttttgttaggag[C/G]catattatataatctg	C	G	54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 107986	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-1993220	tggaagaaagtctggc[A/G]gacagcaacttctcaa	A	G	Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000276467 // intron // 0 // --- // --- // --- // --- ///	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2112205	aggattgctgacggga[C/T]gcacgctgttcctctc	C	T	127733 // Homo sapiens UBX domain containing 3 (UBXD3). mRNA. /// NM_144623 // upstream // 98313 // Hs.205178 //	UBXD3	UBXD3, Homo sapiens UBX domain containing 3 (UBXD3), p36.12
SNP_A-2130444	atactatctaaaaggg[A/C]caaggttcacatttgt	A	C	// Homo sapiens solute carrier family 22 (organic cation transporter), member 15 (SLC22A15), mRNA. /// ENST00000295587 // intron // 0 // --- // --- // --- // ---	SLC22A15	SLC22A15, Homo sapiens solute carrier family 22 (organic cation transporter), member 15 (SLC22A15), p13.1
SNP_A-2145263	cattcagaaaaattctg[C/T]aatttttggccttgggc	C	T	64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 43178 // Hs.391781 // PCDH20	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2177470	cacgaaatgttacaa[C/G]aagatatgaaaaaggc	C	G	/// ENST00000332660 // downstream // 977831 // --- // --- // ---	-	p12.3
SNP_A-2183281	cagcacaaaggacaat[C/T]aataaataggatcgata	C	T	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2223352	cgctccagccatgctg[A/T]actactcacttctct	A	T	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA. /// NM_021905 // intron // 0 // Hs.167017 // GABBR1 // 2550 // Homo sapiens	GABBR1	GABBR1, Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, p22.1
SNP_A-2224464	cgtagtatatatcaa[C/G]taactgcatttgtgtt	C	G	Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, mRNA. /// NM_002149 // intron // 0 // Hs.467696 //	HPCAL1	HPCAL1, Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, p25.1
SNP_A-2226874	ctaatattctgaccta[A/G]ctgcctccaagttct	A	G	-- /// ENST00000355517 // downstream // 248244 // --- // --- // ---	-	q24.32
SNP_A-1828837	taaggaccactagaaa[G/T]gttgttttcaaaact	G	T	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-1873429	tctcaacttcctccta[C/T]aaattcacatttaag	C	T	// 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 351774 // --- // --- // --- // ---	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-1848202	tatcttctttagggac[A/G]catctactcgagtctt	A	G	7200 // Homo sapiens thyrotropin-releasing hormone (TRH), mRNA. /// ENST00000302649 // downstream // 40603 // --- // ---	TRH	TRH, Homo sapiens thyrotropin-releasing hormone (TRH), q21.3
SNP_A-1702411	gcaccttagataaatcgtcctat[A/G]aggtagctcaagacaccatgtagt	A	G	NM_014840 // downstream // 89547 // --- // --- // --- // ---	-	- , rs1345541, -,q23.3
SNP_A-1702503	gccatcccttaagcggcctctcta[A/C]cttcatactaaaatatctataaagc	A	C	protein tyrosine phosphatase, receptor type, R /// NM_130846 // intron // 0 // Hs.198288 // PTPRR // 5801 //	PTPRR	PTPRR , rs958644, protein tyrosine phosphatase, receptor type, R ,q15
SNP_A-1674267	ttatatattttaagtcttctaca[A/G]attgttctaaacttgacaaaactagt	A	G	145581 // leucine rich repeat and fibronectin type IiI domain containing 5	LRFN5	LRFN5 , rs10483496, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1810550	gtgcaaaataaattcc[A/C]gaactattcggccacg	A	C	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1791350	gggtactcaactgaac[A/G]atgcagagaagaccct	A	G	Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 1, mRNA. /// ENST00000303714 // intron // 0 // --- // ---	ANTXR1	ANTXR1, Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 1, p13.3
SNP_A-1955932	tttgtccacctccaaa[A/C]agaataactcctctac	A	C	81688 // Homo sapiens chromosome 6 open reading frame 62 (C6orf62), mRNA. /// NM_015895 // upstream // 8345 //	C6orf62	C6orf62, Homo sapiens chromosome 6 open reading frame 62 (C6orf62), p22.2
SNP_A-1964063	taaagttgattatatg[C/G]aagatttttgtaaaa	C	G	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1903949	tgggattgtttgggaa[C/T]agcacgaggaacttc	C	T	Homo sapiens vacuolar protein sorting 39 (yeast) (VPS39). mRNA. /// AB018313 // intron // 0 // Hs.88025 // VPS39 //	VPS39	VPS39, Homo sapiens vacuolar protein sorting 39 (yeast) (VPS39), q15.1
SNP_A-2293866	gcagctgtgcagcccc[A/C]actggtgaagtcacct	A	C	ENST00000263665 // intron // 0 // --- // --- // --- // ---	-	p12.3
SNP_A-2277084	gagatgcaatttaaa[C/T]aggtttgtcatggaa	C	T	5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 // downstream //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2259675	gaaaacttctggtcc[A/G]cacagatgagaactgt	A	G	KIAA1919 // 91749 // Homo sapiens KIAA1919 (KIAA1919), mRNA. /// NM_002912 // downstream // 21624 // Hs.232021	KIAA1919	KIAA1919, Homo sapiens KIAA1919 (KIAA1919), q21
SNP_A-2269451	atagagaaatttggca[C/G]aacttttccagaaac	C	G	MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. ///	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2250506	cttaggtcagagacta[G/T]gtgttcctcacacttt	G	T	ENST00000347778 // intron // 0 // --- // --- // ---	-	q23.33
SNP_A-2231490	ctatttaaggaattga[C/T]ggctgatccacaggc	C	T	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 103306 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-2265726	gaagctgtgtccgag[A/G]aaaaccctgacagag	A	G	Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // intron // 0 // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2267548	gaataltagcaagaaa[A/T]aatttgagcttctct	A	T	sapiens glutamate receptor, metabotropic 1 (GRM1), mRNA. /// ENST00000355289 // intron // 0 // --- // --- // --- // --- ///	GRM1	GRM1, Homo sapiens glutamate receptor, metabotropic 1 (GRM1), q24.3
SNP_A-2282657	gagtttggcttcccag[A/G]ctctctcgtttcctct	A	G	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA. /// ENST00000356398 // intron // 0 // --- // --- // --- ///	PRPSAP2	PRPSAP2, Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), p11.2
SNP_A-2294112	gcaggcagatatggcc[A/G]gaacagagtaataata	A	G	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.1
SNP_A-2290705	gcaagataagcatgaa[A/G]tcagaatccaggcata	A	G	Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // --- // --- // --- // ---	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2311206	ggaagttctgaggcca[C/T]ggaacgaggtgtatt	C	T	NDUFS4 // 4724 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA. /// NM_019087 // downstream	NDUFS4	NDUFS4, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), q11.2
SNP_A-1902901	tggctctttcaaaaca[A/T]acctgaatataattgg	A	T	10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 394783 // Hs.476604 // ADAMTS9	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-1939009	ttgagtcttgcttga[A/G]agtagtgaatttttttt	A	G		ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-1800038	gtacatggtacttcaa[A/C]atatatcacctgaagt	A	C	// 287015 // Homo sapiens tripartite motif-containing 42 (TRIM42), mRNA. /// NM_018155 // upstream // 215856 //	TRIM42	TRIM42, Homo sapiens tripartite motif-containing 42 (TRIM42), q23
SNP_A-1807002	gtctcataattcttac[C/T]acagatatccaatttg	C	T	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // intron // 0 // --- // --- // --- // --- ///	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-1848761	tatgatagcggttatc[A/G]ccactgccatgagtat	A	G	151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream //	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1853669	tatttttgttacagcc[A/G]cccggatggactaagg	A	G	FLJ16641 // 389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// ENST00000314241 // downstream //	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-1869801	tccttcccacagaaat[C/G]ataagccttctctcg	C	G	Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, mRNA. /// NM_153050 // intron // 0 //	MTMR3	MTMR3, Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, q12.2
SNP_A-1826152	taaattaatctggcaa[C/G]agttaaactgagttt	C	G	– /// ENST00000329863 // downstream // 133209 // --- // --- // ---	-	q23.1
SNP_A-1824296	taaacccagaaggcca[A/C]gagcaaaaatcgtgat	A	C	Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA. /// ENST00000342075 // intron // 0 // --- // --- // ---	PMS1	PMS1, Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), q32.2
SNP_A-1825861	taaatgaccagcatga[A/G]gcctaatgagagtatt	A	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 466884 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1833588	tacagctacaaagtcc[G/T]gctctcaatttctga	G	T	Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// ENST00000333324 // intron // 0 // --- // --- // --- // ---	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.11
SNP_A-1832272	taatttatctatttc[A/G]atatttgcacatata	A	G	Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // --- // ---	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2214386	cctaccttctactta[C/T]taaaggctgaggcctc	C	T	sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 //	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2220129	ccttcagaagagagat[C/T]aaggtcaagacctcaa	C	T	797 // Homo sapiens calcitonin-related polypeptide, beta (CALCB), mRNA. /// ENST00000324229 // downstream //	CALCB	CALCB, Homo sapiens calcitonin-related polypeptide, beta (CALCB), p15.2
SNP_A-2183884	cagccacaacccgagg[A/C]acgcctggaagccatca	A	C	10553 // Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), mRNA. /// ENST00000227256 // upstream	HTATIP2	HTATIP2, Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), p15.1
SNP_A-2187780	cagtagctgcataaatt[A/G]acaagttcacttaga	A	G	9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1845173 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2198683	catttcccaagaatag[C/T]agcttcatgactctat	C	T	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 35134 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2139339	atcctggcagaggggaa[A/G]atgtgaactcggcaac	A	G	H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1321133 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141496	atcttaatgtacaata[A/G]aacagccaggcccaca	A	G	Homo sapiens chemokine (C-C motif) ligand 28 (CCL28), transcript variant 1, mRNA. /// NM_148672 // intron // 0 //	CCL28	CCL28, Homo sapiens chemokine (C-C motif) ligand 28 (CCL28), transcript variant 1, p12
SNP_A-2139974	atctactccaccaaag[A/G]caattattggcttag	A	G	221393 // Homo sapiens G protein-coupled receptor 115 (GPR115), mRNA. /// NM_181744 // upstream // 59219 //	GPR115	GPR115, Homo sapiens G protein-coupled receptor 115 (GPR115), p12.3
SNP_A-2120997	agtctcagattcagga[A/T]acaaatgatattgagt	A	T	ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+ q24.2
SNP_A-2001212	attcattattgccaaa[A/G]atttctagaggacatg	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2006811	ttggtgccatctcttt[C/G]aaaagcaattgaaaat	C	G	NM_016836 // upstream // 184346 // Hs.470412 // RBMS1 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2037457	aacaacacaacagcaa[A/G]gcagactagcatggtt	A	G	3628 // Homo sapiens inositol polyphosphate-1-phosphatase (INPP1), mRNA. /// NM_017694 // upstream // 49014 //	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2062512	aatgtatgcgtccctc[C/T]aaaattcatatgttgg	C	T	// Homo sapiens desmoplakin (DSP), mRNA. /// NM_152551 // upstream // 3238 // Hs.13366 // C6orf151 // 154007 // Homo	INPP1	INPP1, Homo sapiens inositol polyphosphate-1-phosphatase (INPP1), q32.2
SNP_A-2064811	aattctttcctctac[A/G]ggacaaagtgaaacac	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1025756 //	DSP	DSP, Homo sapiens desmoplakin (DSP), p24.3
SNP_A-2052766	aagtcaatcatagtca[C/T]tcctcatagtcacagt	C	T	60529 // Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // upstream // 200433 // Hs.436055 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2083100	acgttctgctggtcaa[A/T]ggagtcacgtggctcc	A	T	55075 // Homo sapiens uveal autoantigen with coiled-coil domains and ankyrin repeats (UACA), mRNA. /// ENST00000322954 // upstream // 20111 // --- // --- // --- // ---	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds. .p11.2
SNP_A-2093300	agaacgccctggaaaa[C/T]atccacccgccagcaa	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA.	UACA	UACA, Homo sapiens uveal autoantigen with coiled-coil domains and ankyrin repeats (UACA), q23
SNP_A-2102959	agcaaactcagaataa[C/T]tgaaattgcaatagca	C	T	Homo sapiens T-cell lymphoma breakpoint associated target 1, mRNA. /// ENST00000355094 // intron // 0 // --- //	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-2104369	agcagctacttaacat[C/G]atggttcatttgaaaa	C	G	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 565674	TCBA1	TCBA1, Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), q22.31
SNP_A-2068345	acaagctgtgtagagg[A/G]caaacacaaggttaag	A	G	221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 //	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2036521	aaattgagaaacatag[A/G]aaaatctagagataaca	A	G	79627 // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA. /// NM_024882 // downstream // 84006 //	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-2042468	aactcagcactgtgac[C/T]agaatatatttttttag	C	T	ENST00000341414 // downstream // 32349 // --- // --- // --- // ---	OGFRL1	OGFRL1, Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), q13
SNP_A-1999278	ggctttgtctctcacc[A/T]cgtgtgctttctgcaa	A	T	Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // --- // --- // --- // ---	-	p12.1
SNP_A-1996606	cctggaattggttagg[A/G]acagattacttcttg	A	G	8214 // Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA. /// ENST00000292697 // upstream	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-2128205	ataaggctgaatgaag[C/T]actcccagggcaactt	C	T	Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA. /// ENST00000350459 // intron // 0 // --- // --- // --- // ---	DGCR6	DGCR6, Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), q11.21
SNP_A-2125505	agtttatggctcacca[A/G]gaggcatttgttccc	A	G	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 554353 // Hs.211225 // NOVA1 // 4857 // Homo	FLJ10375	FLJ10375, Homo sapiens hypothetical protein FLJ10375 (FLJ10375), p22.1
SNP_A-2136001	atcaagatccctcacac[A/G]ggaaggatgaggcaac	A	G	8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // downstream // 129401 // Homo sapiens nucleoporin 35kDa (NUP35), mRNA. /// NM_194250 // upstream // 1171129 // Hs.159528 // 167465 // Homo sapiens zinc finger protein 366 (ZNF366), mRNA. /// NM_002270 // upstream // 89290 // Hs.482497 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // downstream // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2147578	atggatgtctcagctc[A/C]agcagaggaggcagtc	A	C		FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-2150999	atgtggtttagcactat[A/G]aaattctgttgaggat	A	G		NUP35	NUP35, Homo sapiens nucleoporin 35kDa (NUP35), q32.1
SNP_A-2162796	atttgcaaatctgac[A/G]atactgtatattatgc	A	G		ZNF366	ZNF366, Homo sapiens zinc finger protein 366 (ZNF366), q13.2
SNP_A-2196964	cattatacataacatt[C/G]aacttctatggtggta	C	G		ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. .p26.1
SNP_A-2190836	catagagttaatcagc[A/G]agacaagaaatgacaa	A	G		TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.2
SNP_A-2182181	cagaggtcaatagtga[C/G]tggcgatggccatag	C	G		BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172931	cacaaaacattcatca[C/T]tctcaggttattctaa	C	T	// Homo sapiens hypothetical protein FLJ38348 (FLJ38348), mRNA. /// ENST00000281932 // intron // 0 // --- // --- // --- // ---	FLJ38348	FLJ38348, Homo sapiens hypothetical protein FLJ38348 (FLJ38348), p22.2
SNP_A-2172342	caattaatggctcaac[A/G]acacaataacaatata	A	G	Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-2208858	cccagatgaaaatcaa[C/T]tgaaaatacagatggt	C	T	GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream //	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2202991	ccactctggaccccac[A/G]gaagacacctatggtg	A	G	5293 // Homo sapiens phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD), mRNA. /// NM_005026 // upstream // 33965 // Hs.518451 // PIK3CD // 5293 // Homo	PIK3CD	PIK3CD, Homo sapiens phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD), p36.22
SNP_A-1831335	taatgtaatgtcacaa[A/G]atggcagatagatgat	A	G	Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000294649 // intron // 0 // --- // --- // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p13.3
SNP_A-1837784	tacttttctaggtgac[A/G]gagatgaaaaaacagg	A	G	MGC33692 // 414918 // Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692), mRNA. ///	MGC33692	MGC33692, Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692), p14.3
SNP_A-1827268	taaccttcagacaaaa[C/T]ggcaaaaagcttgggc	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1524207 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1858424	tcagagaaacaggcag[G/T]ctagagtgactgaggc	G	T	Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// ENST00000309027 // intron // 0 // --- // --- // --- // ---	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.1
SNP_A-1844440	tataaagaactagcta[A/C]aactcaataacaaaag	A	C	Homo sapiens pregnancy specific beta-1-glycoprotein 5 (PSG5), mRNA. /// ENST00000342951 // intron // 0 // --- // ---	PSG5	PSG5, Homo sapiens pregnancy specific beta-1-glycoprotein 5 (PSG5), q13.31
SNP_A-1812759	gtgggagagataatga[C/T]gctcagaaatcaattt	C	T	Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 //	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-1938106	ttgacacgcagcagac[A/G]gccacggtgtgtgaga	A	G	Homo sapiens hypothetical protein FLJ12443 (FLJ12443), mRNA. /// ENST00000283415 // intron // 0 // --- // --- // --- // ---	FLJ12443	FLJ12443, Homo sapiens hypothetical protein FLJ12443 (FLJ12443), p15.33
SNP_A-1944880	ttgtggaccagaaaga[A/T]gcagatgtttctggat	A	T	11039 // Homo sapiens SMA4 (SMA4), mRNA. /// NM_006780 // upstream // 144020 // Hs.484969 // SMA3 //	SMA4	SMA4, Homo sapiens SMA4 (SMA4), p22.1
SNP_A-1944885	ttgtggacttttgaga[A/G]tctatggaaattttca	A	G	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1885141 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1956785	ttttaaatatggccta[C/T]cctgtattacataggc	C	T	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 881147 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1953289	tttgaaaaagttccca[A/G]taacaatgacattttt	A	G	6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 190078 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1889829	tgatacgttcaaatta[C/T]gcacatcagatattgc	C	T	Homo sapiens cyclic nucleotide gated channel beta 1 (CNGB1), mRNA. /// ENST00000251102 // intron // 0 // --- // ---	CNGB1	CNGB1, Homo sapiens cyclic nucleotide gated channel beta 1 (CNGB1), q13
SNP_A-1904875	tgggtaaatctgaaaa[C/T]gcacttggcccttctt	C	T	rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // --- // --- // --- //	-	-, Human clone rev16,q11.22
SNP_A-1912193	tgtgatagagtatcgg[G/T]agttataggtattgag	G	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1985124 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1916619	tgtttatcatgtgcca[C/G]gtatcgtttatcatat	C	G	Homo sapiens short-chain dehydrogenase/reductase 9 (SCDR9), mRNA. /// ENST00000302219 // intron // 0 // --- // ---	SCDR9	SCDR9, Homo sapiens short-chain dehydrogenase,q22.1
SNP_A-2309901	ggaaatatataactcc[A/G]caagtttttttgctt	A	G	6001 // Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, mRNA. /// ENST00000313060 // downstream // 24162 // --- // --- // --- // --- ///	RGS10	RGS10, Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, q26.11
SNP_A-2293369	gcagatctctgggaaa[C/G]agtgagtgttttaggc	C	G	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-2284161	gatatgctgagcaaaa[G/T]gatgattcacatctgg	G	T	92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream // 370559 // --- // ---	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2229713	ctagtcattagtcata[A/C]ctcatttttctcccaga	A	C	Homo sapiens KIAA1007 protein (KIAA1007), transcript variant 1, mRNA. /// NM_206999 // intron // 0 // Hs.460923 //	CNOT1	CNOT1, Homo sapiens KIAA1007 protein (KIAA1007), transcript variant 1, q21
SNP_A-2234910	ctccatgtcaaaaaaa[A/G]aagaatgtgggaactc	A	G	// Homo sapiens hypothetical protein FLJ39441 (FLJ39441), mRNA. /// ENST00000333429 // intron // 0 // --- // --- // --- // ---	FLJ39441	FLJ39441, Homo sapiens hypothetical protein FLJ39441 (FLJ39441), p15.1
SNP_A-2239290	ctctttaaatgtccac[A/G]aaatgagtgaatcaat	A	G	Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // intron // 0 // Hs.401954 // ARG99 // 83857 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2253889	cttgacaaaaatccaa[A/T]aaagagctcaatcctt	A	T	// Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA. /// ENST00000321800 // intron // 0 // --- // --- // --- // ---	FLJ40319	FLJ40319, Homo sapiens hypothetical protein FLJ40319 (FLJ40319), q25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246919	ctgtatactatggata[A/C]tagagcacacattatg	A	C	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 124469 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-2258851	ctttttagattgctgc[A/C]gagaaagtgaggcact	A	C	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2289419	gattttcccacaataa[A/C]aacatcacttaacaat	A	C	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1055315 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-1916904	tgtttcttcaaactaa[A/G]cctcagtttctttata	A	G	Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 2, mRNA. /// NM_013448 // intron // 0 // Hs.509140 // BAZ1A // 11177 // Homo sapiens	BAZ1A	BAZ1A, Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 2, q13.1
SNP_A-1888124	tgagcccagctggtta[C/T]acttttttgagcctg	C	T	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495 // intron // 0 // Hs.484678 // TBC1D7 // 51256 //	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-1875247	tctctctggagggccc[A/G]gatctatgaccttact	A	G	// 79696 // Homo sapiens chromosome 14 open reading frame 140 (C14orf140), mRNA. /// NM_033116 //	C14orf140	C14orf140, Homo sapiens chromosome 14 open reading frame 140 (C14orf140), q24.3
SNP_A-1877572	tctggctagaagtaag[A/G]cctactatggcttgtt	A	G	FLJ35728 // 164127 // Homo sapiens hypothetical protein FLJ35728 (FLJ35728), mRNA. /// NM_001748 // upstream //	FLJ35728	FLJ35728, Homo sapiens hypothetical protein FLJ35728 (FLJ35728), q42.11
SNP_A-1956674	ttttaaaaaattatga[C/T]ggagtaagtcaagatg	C	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 71760 // --- // --- // --- // --	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1955209	tttggcctatttgcag[A/G]aatgagccagggtggt	A	G	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1958351	ttttcccataggatta[A/G]ccagggtctgtttctg	A	G	LOC63928 // 63928 // Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA. ///	LOC63928	LOC63928, Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), p12.1
SNP_A-1966895	tgatcagtggttccta[A/C]ctttggagatcattga	A	C	// Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	SMARCAL1	SMARCAL1, Homo sapiens SWI q35
SNP_A-1977622	tctgtggttcttcctg[A/C]aacacctccatcttac	A	C	2069 // Homo sapiens epiregulin (EREG), mRNA. /// NM_001657 // upstream // 7654 // Hs.270833 // AREG // 374	EREG	EREG, Homo sapiens epiregulin (EREG), q13.3
SNP_A-1980783	ggctggaaaagctaca[C/G]tggcccccaaggacct	C	G	Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1790913	gggggtgggggccgga[A/T]gtgtcaatgactaaag	A	T	Homo sapiens vaccinia related kinase 3 (VRK3), mRNA. /// ENST00000316763 // intron // 0 // --- // --- // --- // ---	VRK3	VRK3, Homo sapiens vaccinia related kinase 3 (VRK3), q13.33
SNP_A-1792595	ggtaaaggagtcttca[C/G]atgattccagcgttta	C	G	// 388121 // Homo sapiens FLJ41287 protein (FLJ41287), mRNA. /// NM_031226 // downstream // 42634 // Hs.511367	FLJ41287	FLJ41287, Homo sapiens FLJ41287 protein (FLJ41287), q21.2
SNP_A-1784282	ggcccagcgctctgaa[C/T]gccacttttcctggct	C	T	10801 // Homo sapiens MLL septin-like fusion (MSF), mRNA. /// NM_018996 // upstream // 513313 // Hs.80618 // TNRC6C	SEPT9	SEPT9, Homo sapiens MLL septin-like fusion (MSF), q25.3
SNP_A-1844566	tataacaaatgtacca[C/T]atgaatgcaaaatgtt	C	T	285971 // Homo sapiens hypothetical protein MGC33584 (MGC33584), mRNA. /// ENST00000286137 // intron // 0 // ---	MGC33584	MGC33584, Homo sapiens hypothetical protein MGC33584 (MGC33584), q36.1
SNP_A-1824795	taaagatgaagcatta[A/C]acctaagattttattt	A	C	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA. /// ENST00000298171 // intron // 0 // --- // --- // --- // ---	TSHR	TSHR, Homo sapiens thyroid stimulating hormone receptor (TSHR), q31.1
SNP_A-1821636	gtttgtggtgcacagt[C/T]aagtgttggatcacta	C	T	Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA. /// ENST00000083182 // 3UTR // 0 // --- // --- // --- // ---	APPBP2	APPBP2, Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), q23.2
SNP_A-1839334	tagagtctaatcccaa[C/T]acttgtgaatctgggc	C	T	91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-2212550	cccttagtactggggc[A/G]acactcactgcatctc	A	G	253018 // Homo sapiens HLA complex group 27 (HCG27), mRNA. /// NM_002117 // downstream // 28608 // Hs.534125	HCG27	HCG27, Homo sapiens HLA complex group 27 (HCG27), p21.33
SNP_A-2220763	ccttgagtaagctgga[A/G]cctatttgtgtttcat	A	G	ENST00000355094 // intron // 0 // --- // --- // --- // ---	-	q22.31
SNP_A-2181332	cagacctttgctact[A/G]agcaccttgagtgtcc	A	G	23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream //	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-2181682	cagagagaaccctgga[C/T]gccgggacactcattt	C	T	GALNAC4S-6ST // 51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// NM_000274	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-2196211	catgtggtggaaatac[C/T]gctctggtggaactcc	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, mRNA. /// NM_021912 // intron // 0 // Hs.302352 // GABRB3 // 2562 // Homo sapiens	GABRB3	GABRB3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, q12
SNP_A-2152416	attaactaaaacaata[C/T]gcttgaaagtgtttga	C	T	// 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134378	atatggaaatagaata[C/G]gtcacttattttaaaa	C	G	2591 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) (GALNT3), mRNA. /// NM_024753 // downstream // 8620 // Hs.310672 //	GALNT3	GALNT3, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) (GALNT3), q24.3
SNP_A-1990804	cgttttagttatgtcc[C/T]gagctgtgattaaagg	C	T	Homo sapiens exonuclease 1 (EXO1), transcript variant 2, mRNA. /// NM_003686 // intron // 0 // Hs.498248 // EXO1 //	EXO1	EXO1, Homo sapiens exonuclease 1 (EXO1), transcript variant 2, q43
SNP_A-2070672	acacgatgtttctccc[A/G]agtcagtctcctaaat	A	G	Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000257287 // intron // 0 // --- // --- // --- // ---	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-2051129	aagggaataacaaaca[A/C]ctgctaagagaataag	A	C	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2060395	aatgaattcaagtcag[A/C]aaataagcaatgaaag	A	C	-- /// ENST00000329863 // downstream // 192653 // --- // --- //	-	q23.1
SNP_A-2083534	actaatacaaataaag[A/C]cctgagtgtacactta	A	C	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2088533	actgtcctccaatgtg[A/T]ataaggtttccattat	A	T	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 617727 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2084740	actatttaggatgtta[A/C]aattcttaattctgat	A	C	Homo sapiens RAS protein activator like 2 (RASAL2), transcript variant 1, mRNA. /// NM_170692 // intron // 0 //	RASAL2	RASAL2, Homo sapiens RAS protein activator like 2 (RASAL2), transcript variant 1, q25.2
SNP_A-2059943	aatcttctgagacctc[C/T]atgggcttgccaactg	C	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2048104	aagcacaaagctaaga[A/G]gagtcagtcatccctc	A	G	/// ENST00000341422 // downstream // 145965 // --- // --- // ---	-	p33
SNP_A-2001868	gaattgctttctaggg[G/T]acaacattcagatcct	G	T	758 // Homo sapiens chromosome 22 open reading frame 1 (C22orf1), mRNA. /// NM_001584 // upstream // 279987 //	C22orf1	C22orf1, Homo sapiens chromosome 22 open reading frame 1 (C22orf1), p14.1
SNP_A-2003188	ttgtatttgaaaaaaa[A/C]tcctggcaccccagtc	A	C	MGC9850 // 219404 // Homo sapiens hypothetical protein MGC9850 (MGC9850), mRNA. /// NM_015972 // downstream	MGC9850	MGC9850, Homo sapiens hypothetical protein MGC9850 (MGC9850), q12.2
SNP_A-2006783	gtctagagaattcact[A/G]tgatcttctattctgt	A	G	ENST00000298622 // intron // 0 // --- // --- // --- // ---	-	q26.3
SNP_A-2046568	aagagattacttagga[A/T]cccaaaaccttataga	A	T	8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 172484 //	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2132850	atataagggctaaaca[C/T]ataccatgaccattag	C	T	Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// ENST00000267460 // intron // 0 // --- // --- // --- // ---	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2174202	cacactatggaaaccc[A/C]aaagccggagcaatgg	A	C	ENST00000303646 // intron // 0 // --- // --- // --- // ---	-	p36.23
SNP_A-2174571	cacagagtaccagtca[C/T]aggaatcatagcattg	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 661168 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2227458	ctacagaaaaatgtgc[A/C]aatgtatttttagtag	A	C	// Homo sapiens crumbs homolog 2 (Drosophila) (CRB2), mRNA. /// NM_004789 // upstream // 41642 // Hs.445265 //	CRB2	CRB2, Homo sapiens crumbs homolog 2 (Drosophila) (CRB2), q33.3
SNP_A-2225181	cgttcaattgtacaac[A/G]cctgctgtcctgtttg	A	G	Homo sapiens polymerase (DNA directed), eta (POLH), mRNA. /// ENST00000303499 // intron // 0 // --- // --- // --- // ---	POLH	POLH, Homo sapiens polymerase (DNA directed), eta (POLH), p21.1
SNP_A-2219647	ccttaaacatcctcac[A/G]acacttacgttatttc	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 605173 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2214557	cctagacattatagta[C/T]aaagacacttgacaat	C	T	Homo sapiens myomesin 1 (skelemin) 185kDa (MYOM1), mRNA. /// X69090 // intron // 0 // Hs.464469 // MYOM1 // 8736	MYOM1	MYOM1, Homo sapiens myomesin 1 (skelemin) 185kDa (MYOM1), p11.31
SNP_A-2211767	ccctctaaagctctat[A/T]actttacaatcacctt	A	T	sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000241416 // intron // 0 // --- // --- // --- // ---	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q23.1
SNP_A-1822619	ttgagtttccagacaa[A/T]agaagcagagctgtag	A	T	// 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 305839 // Hs.461453 // WWOX	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1852005	tattgccctggtgaag[A/G]accactgttagaaaag	A	G	2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA.	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease,q33.1
SNP_A-1866433	tccccacagtctgaaa[G/T]ctacagtccttctaat	G	T	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 213610 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-1783348	ggcataaaagaaagta[C/T]taagtgcagttcaact	C	T	Homo sapiens src family associated phosphoprotein 1 (SCAP1), mRNA. /// ENST00000336915 // intron // 0 // --- // ---	SCAP1	SCAP1, Homo sapiens src family associated phosphoprotein 1 (SCAP1), q21.32
SNP_A-1758908	tacagcaggtcactaaaagaactca[A/G]gaatctaaagagtgagtatggccat	A	G	AK091554 // 5UTR // 0 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	C6orf170	C6orf170 , rs10499110, chromosome 6 open reading frame 170,q22.31
SNP_A-1780778	ggatctaaggttgaaa[A/T]catctaatccctaggt	A	T	57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 31758 //	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1789838	gggctggcaaggcaaa[C/G]aggtgtcaggccacag	C	G	ENST00000304823 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1789228	gggcatctggataaaa[C/T]cgtgtctcgatgtatt	C	T	/// ENST00000358493 // upstream // 160941 // --- // --- // --- // -- /// ENST00000329590 // downstream // 113680 // --- // --- //	-	p23.3
SNP_A-1786220	ggctggtgtggaaatg[A/C]atcacccggtcgcgcc	A	C	Homo sapiens neuronal guanine nucleotide exchange factor (NGEF), mRNA. /// ENST00000264051 // intron // 0 // --- // ---	NGEF	NGEF, Homo sapiens neuronal guanine nucleotide exchange factor (NGEF), q37.1
SNP_A-1800648	gtagaaaatcctcaaa[A/C]tccacaaagtaagtat	A	C	Homo sapiens mRNA for KIAA0645 protein, partial cds. /// ENST00000266091 // intron // 0 // --- // --- // --- // ---	DEPDC5	DEPDC5, Homo sapiens for KIAA0645 protein, partial cds. ,q12.3
SNP_A-1984614	ctatttgtttttgca[A/G]tctgctatttttcagg	A	G	8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 15941 // Hs.425091 // FAM44B	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1988563	aatataaaaacactta[A/G]acataaaacagcatgt	A	G	Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p22.1
SNP_A-1967320	caagtggaaagcacac[C/T]ggatactttcacttgt	C	T	Homo sapiens hypothetical protein FLJ12584 (FLJ12584), mRNA. /// ENST00000349938 // intron // 0 // --- // --- // --- // ---	FLJ12584	FLJ12584, Homo sapiens hypothetical protein FLJ12584 (FLJ12584), q37.1
SNP_A-1961071	tttttgtatttttcta[C/G]agatggtatttcacca	C	G	// Homo sapiens amino-terminal enhancer of split (AES), transcript variant 2, mRNA. /// NM_198970 // upstream //	AES	AES, Homo sapiens amino-terminal enhancer of split (AES), transcript variant 2, p13.3
SNP_A-1874783	tctcctttctcctgca[A/G]atgtgtggagtttccc	A	G	// Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, mRNA. /// NM_018030 // intron // 0 // Hs.370725 // OSBPL1A // 114876	OSBPL1A	OSBPL1A, Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, q11.2
SNP_A-1899718	tggaatccgtagacac[C/T]gatggagaagctgtca	C	T	// 57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 113316 //	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-1932875	ttcctttcttaataaa[A/C]cataactctcaccttt	A	C	/// ENST00000354793 // downstream // 1470297 // --- // --- // -	-	p14.1
SNP_A-2263751	gaacctggacagaata[A/T]gccaccatactgaggc	A	T	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // CDS // 0 // Hs.188746 // ADAMTS18 // 170692 // Ho	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-2287070	gatgtaccactctttc[A/T]ctgaagaataataaat	A	T	Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// ENST00000285311 // intron // 0 // --- // --- // --- // ---	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-2246970	ctgtatgagttgttat[C/G]aagacgtaatataata	C	G	3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream //	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-2248378	ctgtgtgcagggaata[C/T]agcagtgaccaaaata	C	T	// --- /// ENST00000361117 // upstream // 250671 // --- // --- // -	-	q33.2
SNP_A-2247369	ctgtcctgggcccaca[A/G]tggcattcagggatag	A	G	// 8693 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), mRNA. /// NM_024642 // downstream // 98667 // Hs.47099 //	GALNT4	GALNT4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), q22.33
SNP_A-2256006	ctttaataagtggtac[C/T]gggaaactgaataacc	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1056422	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2256208	ctttagagtaagaaaa[A/G]atgatagttgaggata	A	G	/// ENST00000359050 // upstream // 109363 // --- // --- // --- // -- /// ENST00000339373 // downstream // 252351 // --- // --- //	-	q14.3
SNP_A-2259296	gaaaaagagtacttaa[A/C]aattgcattctttgtg	A	C	40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, mRNA. /// NM_001094 // upstream // 13069 // Hs.368417 // ACCN1 //	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, q12
SNP_A-2271133	gacatcatgtctttga[C/T]aagtattgctgttagt	C	T	ENST00000317357 // intron // 0 // --- // --- // --- // ---	-	q21
SNP_A-2293022	gcagaatctttcatca[A/G]tcataggctgacatta	A	G	// 3119 // Homo sapiens major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA. /// NM_020056 // upstream // 39454 // Hs.534320 // HLA-DQA2 // 3118 //	HLA-DQB1	HLA-DQB1, Homo sapiens major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), p21.32
SNP_A-1922096	ttactgtggaattgaa[C/T]gccagtggcccccagc	C	T	767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 288633 // --- // --- // ---	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1889836	tgatactcacatgcag[A/G]cagagttgagtaccac	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 165407 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1883342	tcctatgctcagtcca[A/G]taacttccagttccag	A	G	23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000357520 // downstream // 64458 // --- // --- // --- // --	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1958344	ttttcccaattttgca[C/G]acaccctgtagaatat	C	G	4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // upstream // 618395 // Hs.307734 // MME // 4311	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN q25.2
SNP_A-1937376	ttgaaataataggcaa[A/C]aaacactgatccacat	A	C	CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1989305	taaatgggcccaaaga[A/G]gtaggctttaatctag	A	G	ENST00000339492 // downstream // 27363 // --- // --- // --- // ---	-	p15.2
SNP_A-1988495	tggcacagaagacaaa[C/T]gctggggaggaaaagg	C	T	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1985532	cacagagagctgcaaa[C/T]actttgagaggtaggg	C	T	11120 // Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, mRNA. /// NM_078476 // downstream // 4179 // Hs.519635 // BTN2A1 // 11120 //	BTN2A1	BTN2A1, Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, p22.1
SNP_A-1982685	ccttgaccaaacccac[A/C]attttcatattggaga	A	C	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 417621 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1801808	gtagtgggagagcaga[C/G]ggggtggagcttggat	C	G	Homo sapiens hypothetical protein FLJ22405 (FLJ22405), mRNA. /// ENST00000296003 // intron // 0 // --- // --- // --- // ---	FLJ22405	FLJ22405, Homo sapiens hypothetical protein FLJ22405 (FLJ22405), p25.3
SNP_A-1803315	gtattgtctcttttaa[C/T]actcactcctgcttca	C	T	Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // intron // 0 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1795862	ggtggcttactaggca[A/G]tatttgctccataaaa	A	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1799678	gtaatttgcaaactaa[A/G]gccatcaccaactaat	A	G	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA. /// ENST00000323076 // intron // 0 // --- // ---	LCP1	LCP1, Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), q14.13
SNP_A-1783865	ggccaagtaatgataa[C/T]tgttaacatcggctgg	C	T	134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream //	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-1848317	tatgaaaaaaagctca[C/T]tattactaatcattag	C	T	3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// ENST00000305031 //	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3
SNP_A-1836070	tactacccccagatta[A/G]cagcctagcaggtact	A	G	80319 // Homo sapiens CXXC finger 4 (CXXC4), mRNA. /// NM_017628 // upstream // 575661 // Hs.367639 // FLJ20032	CXXC4	CXXC4, Homo sapiens CXXC finger 4 (CXXC4), q24
SNP_A-2226420	ctaagataccatcaac[A/T]gtaagatgtctcagaa	A	T	// 220134 // Homo sapiens chromosome 18 open reading frame 24 (C18orf24), mRNA. /// NM_002747 // upstream //	C18orf24	C18orf24, Homo sapiens chromosome 18 open reading frame 24 (C18orf24), q21.1
SNP_A-2224312	cgtaaagatcagcagt[A/G]aactgaagtcaaatca	A	G	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2170630	caagtgtggagcaaca[C/G]gtaactaaattttaat	C	G	Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // intron // 0 // Hs.510989 // MEIS2 // 4212 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2175652	cacatggtaatgttaa[C/T]tgacatggccaaactc	C	T	8554 // Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), mRNA. /// ENST00000341418 // downstream //	PIAS1	PIAS1, Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), q23
SNP_A-2184304	cagccttgaatgcaaa[C/T]agtcagcaaacaactt	C	T	284573 // Homo sapiens hypothetical protein FLJ40343 (FLJ40343), mRNA. /// NM_005686 // upstream // 11874 //	FLJ40343	FLJ40343, Homo sapiens hypothetical protein FLJ40343 (FLJ40343), q32.1
SNP_A-2132225	atagtaacccagaaaa[G/T]ggaaagattagtatga	G	T	-- /// ENST00000354793 // downstream // 1092831 // --- // ---	-	p13.3
SNP_A-2153593	attagcttcctgtgac[A/T]gcctgtacaaatgggt	A	T	Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// ENST00000284308 // intron // 0 // --- // --- // --- // ---	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-2044842	aagaaattcacagcac[C/T]attttgaagttatttt	C	T	Homo sapiens RAB4A, member RAS oncogene family (RAB4A), mRNA. /// ENST00000284615 // intron // 0 // --- // ---	RAB4A	RAB4A, Homo sapiens RAB4A, member RAS oncogene family (RAB4A), q42.13
SNP_A-2042405	aactcacaacccaaga[A/G]tctattttaaaatgca	A	G	// 9752 // Homo sapiens protocadherin alpha 9 (PCDHA9), transcript variant 2, mRNA. /// NM_018909 // downstream //	PCDHA9	PCDHA9, Homo sapiens protocadherin alpha 9 (PCDHA9), transcript variant 2, q31.3
SNP_A-2037421	aacaaatttttttca[C/T]aagcacattaaacttg	C	T	Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), mRNA. /// ENST00000302541 // intron // 0 // --- // ---	MYRIP	MYRIP, Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), p22.1
SNP_A-2009860	cagagttcatttctgc[A/T]acgaattttacagtaa	A	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2012779	gccaaagtcctggcaa[C/T]ggcctcagggcccgac	C	T	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 106973 // Hs.32942 // PIK3CG // 5294 // Homo	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-2075688	acatggctaaattctc[A/G]gaagcaggagcaccca	A	G	Homo sapiens histidyl-tRNA synthetase 2 (HARS2), mRNA. /// ENST00000262550 // intron // 0 // --- // --- // --- // ---	HARS2	HARS2, Homo sapiens histidyl-tRNA synthetase 2 (HARS2), p11.23
SNP_A-2092077	agaaactatgccatca[A/C]ggagcattatgctatt	A	C	27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // upstream // 47383 // Hs.480452 // PPA2 // 27068 // Homo sapiens	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-2090342	tttccctgtcagcatc[C/G]gacctcaaactctact	C	G	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 963664 // --- // --- // --- // ---	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2085168	actcagcttcagcaac[A/G]ggagatttctaccag	A	G	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2078315	accatagacaagagca[C/T]acatttctctttccc	C	T	54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 71784 // Hs.365690 // KCNK10 //	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-2100399	agataaaatacgtgctg[A/G]acctcaaaatgataaa	A	G	57665 // Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA. /// NM_001002006 // upstream //	RDH14	RDH14, Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), p24.2
SNP_A-2056617	aatagatgtgctaag[A/G]atcatttggaagaat	A	G	Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// ENST00000256737 // 3'UTR // 0 // --- // --- // ---	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2008947	gaggatgagcaataca[A/G]tcacaatccctcctc	A	G	Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// ENST00000256737 // intron // 0 // --- // --- // ---	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2003483	tccccagatcgcagcc[C/T]gctccagtactgggc	C	T	Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // --- // --- // ---	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2040386	aaccagatacattcac[C/T]gtcgtattatcatcac	C	T	// 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 332992 // --- // --- // ---	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-2035149	aaatgcccctaaacac[A/G]atgccctttccaccc	A	G	2914 // Homo sapiens glutamate receptor, metabotropic 4 (GRM4), mRNA. /// NM_145899 // upstream // 7462 //	GRM4	GRM4, Homo sapiens glutamate receptor, metabotropic 4 (GRM4), p21.31
SNP_A-2127804	atacctgagaggaag[A/G]ctcaccaggaaagaaa	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2130475	atactcaatatcgata[C/T]aaaaggttcactctgg	C	T	Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-1838678	tagacagagtatacta[A/G]aaacctcactaaaaaa	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 331632 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1819285	gttggacgagggact[C/T]aaatttggaaacaggc	C	T	// 57107 // Homo sapiens chromosome 6 open reading frame 210 (C6orf210), mRNA. /// ENST00000339644 // upstream //	C6orf210	C6orf210, Homo sapiens chromosome 6 open reading frame 210 (C6orf210), q21
SNP_A-1846662	tatatttttcaaagac[A/G]gcatcaaccatatctt	A	G	Homo sapiens hypothetical protein FLJ10597 (FLJ10597), mRNA. /// ENST00000335497 // intron // 0 // --- // --- // ---	FLJ10597	FLJ10597, Homo sapiens hypothetical protein FLJ10597 (FLJ10597), p34.1
SNP_A-1873364	tctcaaaggatagag[A/G]aagaatttacagtgac	A	G	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 999589 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1870538	tcgaggaaatttcagtc[A/T]cagagaagctgagtaa	A	T	7558 // Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), mRNA. /// NM_014753 // upstream // 52218 //	ZNF11B	ZNF11B, Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), q11.21
SNP_A-1736363	gacatttattacaagtgaacaaata[C/T]gtgggttggtgtacatcagggctga	C	T	/// 9923 // KIAA0478 gene product /// NM_030761 // upstream // 203387 // Hs.302428 // WNT4 // 54361 // wingless-type	KIAA0478	KIAA0478, rs10493012, KIAA0478 gene product p36.12
SNP_A-1802072	gtatacatgtaaaata[A/G]attcatatgccttttc	A	G	METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream //	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1966030	acaggtttgaactga[A/G]agccagagaaatctc	A	G	Homo sapiens oxysterol binding protein-like 6 (OSBPL6), transcript variant 1, mRNA. /// ENST00000357080 // intron // 0 // --- // --- // --- /// ENST00000190611 // intron // 0 // --- //	OSBPL6	OSBPL6, Homo sapiens oxysterol binding protein-like 6 (OSBPL6), transcript variant 1, q31.2
SNP_A-1965900	ctcatgaatttgagct[A/G]aaagaagtttccaaaa	A	G	Homo sapiens hypothetical protein PTD004 (PTD004), mRNA. /// ENST00000344357 // intron // 0 // --- // --- // ---	PTD004	PTD004, Homo sapiens hypothetical protein PTD004 (PTD004), q31.1
SNP_A-1970768	ccttgtgacagtacta[C/T]ccctagtatcagagga	C	T	// 66035 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 11 (SLC2A11), mRNA. /// AJ271290 // downstream // 6522 // Hs.531906 // SLC2A11 //	SLC2A11	SLC2A11, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 11 (SLC2A11), q11.23
SNP_A-1973163	tcttggttctcattca[A/G]ggctgacttttgtcccc	A	G	23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 187297 // Hs.166017 //	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds., p14.1
SNP_A-1940932	ttgctatataggtgaa[C/T]tgtaigtcacaagggt	C	T	/// ENST00000355561 // upstream // 915146 // --- // --- // ---	-	q21.31
SNP_A-1941003	ttgctcatatgaagaat[A/G]aaacaaggttaagtca	A	G	Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // --- // --- // ---	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-1921077	ttacagtaaaatatat[A/G]accgcggtgccacaag	A	G	118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 59797 // Hs.523446 // COL11A1 // 1301 //	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds. p21.1
SNP_A-1911158	tgtctgattacgtgac[A/G]ccacctcaggtatggt	A	G	Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 3 (P2RX3), mRNA. /// ENST00000263314 // CDS //	P2RX3	P2RX3, Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 3 (P2RX3), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2294842	gcagtttctgatata[C/G]caggtcctgagcctcc	C	G	Homo sapiens CD209 antigen-like (CD209L), transcript variant 3, mRNA. /// NM_214677 // intron // 0 // Hs.421437 //	CLEC4M	CLEC4M, Homo sapiens CD209 antigen-like (CD209L), transcript variant 3, p13.2
SNP_A-2298656	gcccagagcagagtgc[A/G]agatagaggtgcagcc	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1267746 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2282143	gagtgtctattacaca[C/T]aagagtcctggaatag	C	T	Homo sapiens arachidonate 12-lipoxygenase (ALOX12), mRNA. /// ENST00000251535 // intron // 0 // --- // --- // ---	ALOX12	ALOX12, Homo sapiens arachidonate 12-lipoxygenase (ALOX12), p13.1
SNP_A-2233931	ctcatgcaatatttttc[A/T]atgcacaggatttttac	A	T	// Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), mRNA. /// ENST00000249601 // intron // 0 // ---	ARHGAP22	ARHGAP22, Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), q11.22
SNP_A-2282031	gagtggctattattca[A/C]cctactagaaggagtt	A	C	151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 //	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-2263434	gaacatttaccgaaaac[A/G]ggaagccctgacccca	A	G	sapiens argininosuccinate synthetase (ASS), transcript variant 1, mRNA. /// NM_054012 // intron // 0 // Hs.160786 //	ASS	ASS, Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, q34.11
SNP_A-2300598	gcctgcaagaaatatc[A/G]aggatttcagacctt	A	G	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 81937 // Hs.183817 // USP31 // 57478 //	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2305048	gctgaacttgctgccc[A/G]gagaccttcagttaat	A	G	// Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // ---	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.3
SNP_A-1908464	tgtagacgggtgaggaa[A/G]tagaagttgacgaact	A	G	5510 // Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. /// ENST00000272983 //	PPP1R7	PPP1R7, Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), q37.3
SNP_A-1918163	ttaaactggacactca[C/G]agggaactggcttaaa	C	G	8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// NM_000521 // upstream //	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1895136	tgccccaaatagtcta[C/G]aaagtgttgtttagcc	C	G	Homo sapiens WD repeat domain 10 (WDR10), transcript variant 4, mRNA. /// NM_018262 // intron // 0 // Hs.477537 //	WDR10	WDR10, Homo sapiens WD repeat domain 10 (WDR10), transcript variant 4, q21.3
SNP_A-1894578	tgccacccaccatgtac[A/G]aagaacctttcacctc	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 181371 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1902173	tggccaaatacaccct[A/G]aatattgacacaggtg	A	G	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-1940556	ttgccgccaaggaaaa[A/G]tgcctccaaattacat	A	G	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 229480 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-1795344	ggtgatggcctggagt[C/T]acatggcagggaatgc	C	T	Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), mRNA. /// ENST00000360835 // upstream // 80274 //	SCUBE1	SCUBE1, Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), q13.2
SNP_A-1788910	gggcaacatagtaagga[A/C]cttcatctctaaaac	A	C	26100 // Homo sapiens WIPI49-like protein 2 (DKFZP434J154), transcript variant 1, mRNA. /// NM_016003	WIPI-2	WIPI-2, Homo sapiens WIPI49-like protein 2 (DKFZP434J154), transcript variant 1, p22.1
SNP_A-1790605	ggggcgggattcgaac[A/G]cgcagattcctggatc	A	G	51295 // Homo sapiens likely ortholog of mouse signaling intermediate in Toll pathway-evolutionarily conserved (SITPEC), mRNA. /// NM_001299 // upstream // 2438 //	SITPEC	SITPEC, Homo sapiens likely ortholog of mouse signaling intermediate in Toll pathway-evolutionarily conserved (SITPEC), p13.2
SNP_A-1816391	gttagatgaaaagtaa[C/T]aggatgagatggttgt	C	T	Homo sapiens cadherin 17, LI cadherin (liver-intestine) (CDH17), mRNA. /// ENST00000027335 // 3'UTR // 0 // --- // ---	CDH17	CDH17, Homo sapiens cadherin 17, LI cadherin (liver-intestine) (CDH17), q22.1
SNP_A-1844003	tagttctgaaaagttg[C/G]aaggcatcatgacct	C	G	// Homo sapiens protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, mRNA. /// NM_032009 // 3'UTR // 0 // Hs.368160 // PCDHGA2 // 56113 // Homo	PCDHGA2	PCDHGA2, Homo sapiens protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, q31.3
SNP_A-2157101	attgaaatgagaccaa[C/T]tacagccctacagtgg	C	T	sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), mRNA. /// ENST00000356913 // intron // 0 // --- // --- // --- /// ENST00000357115 // intron //	LRBA	LRBA, Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), q31.3
SNP_A-2183673	cagcatacattttgtc[G/T]gaatttatgttgtc	G	T	200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream //	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2192945	catctttattgtaa[A/G]ccaattgaagacattt	A	G	// Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), mRNA. /// ENST00000330342 // intron // 0 // --- // --- // --- ///	ATP6V0A2	ATP6V0A2, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), q24.31
SNP_A-2171802	caatgaatttttcaga[C/T]tccattaggcactact	C	T	// 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1766836 // Hs.27214 // KCNC2 // 3747 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2207509	ccatttaggcttcagc[A/T]ctgctggagtcctttc	A	T	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 98237 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-2039378	aacatagaaatttgca[A/C]caaatatctggcaatt	A	C	Homo sapiens myogenic factor 5 (MYF5), mRNA. /// ENST00000228644 // intron // 0 // --- // --- // ---	MYF5	MYF5, Homo sapiens myogenic factor 5 (MYF5), q21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043970	aactgaaccattaaa[C/T]agaaccctccagggc	C	T	121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// AF425596 // upstream // 22569 // Hs.528316 // FOXN4 //	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2047590	gaatttatcttgtagg[C/T]aatagtggaccattaa	C	T	// 58516 // Homo sapiens chromosome 12 open reading frame 14 (C12orf14), mRNA. /// ENST00000354978 //	C12orf14	C12orf14, Homo sapiens chromosome 12 open reading frame 14 (C12orf14), p11.21
SNP_A-2031742	aaagtaggtgaatag[A/C]aagtctttaacttt	A	C	Homo sapiens synaptotagmin X (SYT10), mRNA. /// ENST00000228567 // intron // 0 // --- // --- // ---	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-2013938	ccaaaggaggctttcc[C/T]agattagacatgactg	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 104946	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2049684	aagcttgggaatgtac[C/T]gatgggggtgtctgca	C	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2051750	aaggtcagaaaggaa[A/T]gtcttacatctgttc	A	T	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2077003	accaacagtaattaat[G/T]aggccttacaacccct	G	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1). mRNA. /// ENST00000332944 // upstream // 952367 // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2071887	acagagagaggcctaa[C/T]gatgaatacctcacgt	C	T	10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 176233 // --- // ---	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-2092759	agaaatggatggaacat[A/C]aaagaaaggcccaaaat	A	C	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-2097570	agagaaggggcctgcca[G/T]ctgagggcatccattg	G	T	864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 253468 //	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2096633	agacggaactggcctc[C/T]atcctatgcgaggtcc	C	T	// Homo sapiens beta-amyloid binding protein precursor (BBP), mRNA. /// NM_005799 // upstream // 17252 //	BBP	BBP, Homo sapiens beta-amyloid binding protein precursor (BBP), p31.3
SNP_A-2085085	actcagaaaaaagagcc[A/G]ggacaaaatatgtcgg	A	G	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, mRNA. /// NM_199451 // intron // 0 // Hs.22653 //	ZNF365	ZNF365, Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, q21.2
SNP_A-2091450	agaaaaaaaaaagcgtg[A/G]aggagagaatctgctg	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 968632 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2091530	agaaaaagcatgggaa[G/T]attaggcgattagacag	G	T	/// ENST00000354350 // upstream // 5166 // --- // --- // --- /// ENST00000355158 // upstream // 5166 // --- // --- // ---	-	q22.33
SNP_A-2081028	acctgaagagcttcca[A/G]agctgcctgtggctaa	A	G	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 2 (CACNA2D2), transcript variant 2, mRNA. ///	CACNA2D2	CACNA2D2, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.31
SNP_A-2092674	agaaatctaagctcta[C/T]gtgtttctttgtag	C	T	Homo sapiens serine active site containing 1 (SERAC1), mRNA. /// ENST00000265129 // intron // 0 // --- // --- // ---	SERAC1	SERAC1, Homo sapiens serine active site containing 1 (SERAC1), q25.3
SNP_A-2101309	agatctagaaatttca[A/G]gatgatggtgtacgtg	A	G	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2103524	agcaattcccggtcca[G/T]actttctcaacctccgt	G	T	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2104037	agcagaaagaagagcca[C/T]aaatccccaggggcgaa	C	T	Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), mRNA. /// ENST00000316427 // intron // 0 // --- // --- // ---	NOTCH4	NOTCH4, Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), p21.32
SNP_A-2066873	acaaaatggactaaga[C/G]aaatagtaagctccga	C	G	/// ENST00000310012 // upstream // 229443 // --- // --- // ---	-	q12
SNP_A-2063892	aattatacaggcttaa[A/G]gaaatttgggggatg	A	G	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // sapiens integrin, beta 7 (ITGB7), mRNA. ///	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2059069	aatccctagcagagga[C/T]gtgcaggataactaga	C	T	ENST00000267082 // intron // 0 // --- // --- // ---	ITGB7	ITGB7, Homo sapiens integrin, beta 7 (ITGB7), q13.13
SNP_A-1990925	cacacaagaggcctc[C/G]aatctcattggctctt	C	G	9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000342288 // upstream // 328531 // --- // ---	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-2203955	ccagatcttcttcta[A/G]gacgaagacaggtgat	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2220729	ccttgagatttggaga[G/T]cggtggtctcggtctc	G	T	sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 13 (CLECSF13), mRNA. /// ENST00000272367 // intron // 0 // --- // --- // ---	CLEC4F	CLEC4F, Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 13 (CLECSF13), p13.3
SNP_A-2217510	cctgactccaggggaa[C/G]atcacctctcacttc	C	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2177008	cacctatctaaggagc[C/G]cagattataacgaggt	C	G	// 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // downstream // 637422 // Hs.123642	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-2196506	catgtttgtaaagaaa[A/G]tagggctaatgaggaa	A	G	56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// NM_138386 // downstream // 672585 // Hs.332844 //	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2154421	attattataaccccaa[A/T]tcaattacttctttgc	A	T	FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream //	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2146680	atgctgttggagttaa[C/T]tgtaagtagaaagttg	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1868857	tcctgaattgatatga[A/T]acttttcttagaagac	A	T	PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // downstream //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.31
SNP_A-1851733	tattctttctgcttta[C/T]gcaattcatttctcaa	C	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1850818	tattagcattaggtat[A/G]acagaaaaagaataaa	A	G	Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// ENST00000286545 // intron // 0 // --- // --- // --- // ---	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-1858544	tcagaggatggccaga[A/G]gatgaggagagcagag	A	G	347735 // Homo sapiens tumor differentially expressed 2-like (TDE2L), mRNA. /// NM_022164 // upstream // 62516 //	TDE2L	TDE2L, Homo sapiens tumor differentially expressed 2-like (TDE2L), p35.2
SNP_A-1801011	gtagatgatctattag[A/C]aacaaagtgtctgcca	A	C	9525 // Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA. /// NM_080474 // upstream // 125922 //	VPS4B	VPS4B, Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), q21.33
SNP_A-1805399	gtccaatctgataaaa[G/T]aaaaagcatccagcca	G	T	sapiens aquaporin 9 (AQP9), mRNA. /// ENST00000219919 // intron // 0 // --- // --- // --- // ---	AQP9	AQP9, Homo sapiens aquaporin 9 (AQP9), q21.3
SNP_A-1807637	gtctggtatttgcact[A/G]acatcaaggaagagac	A	G	51422 // Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// NM_145292 // upstream // 66677 // Hs.131311 // GALNTL5 //	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-1968465	gaggcctggaccatca[A/G]aggctagagaaaagaa	A	G	Homo sapiens serine/threonine kinase 4 (STK4), mRNA. /// ENST00000262978 // intron // 0 // --- // --- // --- // ---	STK4	STK4, Homo sapiens serine,q13.12
SNP_A-1900546	tggagctgtgaggcaa[A/G]tagcacatcttgcatg	A	G	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1883834	tgaagaatcaaagaaa[C/G]aggattttatgctaag	C	G	// 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1585797 // Hs.24212 // LPHN2	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1885908	tgacatccttataaaa[C/T]agtccaaacttctcca	C	T	129642 // Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), mRNA. /// NM_003887 // upstream // 45269 // Hs.467662 // DDEF2 // 8853 // Homo	OACT2	OACT2, Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), p25.1
SNP_A-1916996	tgtttgatgaaaaagc[A/G]gagcctctgaaagcag	A	G	// 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, mRNA. /// NM_032142 //	Cep192	Cep192, Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, p11.21
SNP_A-2299671	gccggccaattccccc[C/T]gcaccaaattgcatcg	C	T	Homo sapiens a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19), transcript variant 1, mRNA. /// NM_033274 // CDS // 0 // Hs.483944 // ADAM19 // 8728 //	ADAM19	ADAM19, Homo sapiens a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19), transcript variant 1, q33.3
SNP_A-2285395	gatctgttcccttcaa[C/G]tggcagtttatatgtt	C	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2273735	gactgctgagaaacta[C/T]gaagttgcttaagttg	C	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2251178	cttatttgtgttagaa[A/C]atactaaaaccagccc	A	C	388697 // Homo sapiens mRNA for hornerin, partial cds. /// ENST00000316073 // upstream // 32554 // --- // --- // --- // ---	HRNR	HRNR, Homo sapiens for hornerin, partial cds. ,q21.3
SNP_A-2250950	cttatggcagctacca[C/T]atatcccaaggcaaat	C	T	Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), mRNA. /// ENST00000324727 // intron // 0 // --- // ---	SCN4B	SCN4B, Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), q23.3
SNP_A-2240891	ctgagacagacttgat[A/G]aatctgagtttgggtt	A	G	55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 12404 //	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. q43
SNP_A-2236609	ctctaaagtcctacta[C/G]agcacatatatatgag	C	G	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 166117 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-1916697	tgtttcacttacctaa[C/T]gcattcgtgatttatt	C	T	// 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 76881 // Hs.143080 //	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-1912773	tgtgctctctgcaaag[A/T]cagcaagtcaatattt	A	T	-- /// ENST00000244644 // upstream // 7878 // --- // --- // --- // ---	-	p22.2
SNP_A-1913801	tgtgtccaaaggcaga[C/G]tccattttgtctctta	C	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 578563 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909791	tgtcacagtaagatca[C/T]atggagtaacctttt	C	T	ABCA13 // 154664 // Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // downstream // 168650 // --- // --- // --- //	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-1905530	tggtactgtattgatc[A/G]ctaaattcattcatat	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// NM_170662 // downstream //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1889413	tgagttaggtgaaaaa[C/T]gtgcagactgagtgct	C	T	8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 185060 //	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1883174	tgaaatggccaaatga[A/G]ataatgcattaaaacc	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 // intron // 0 // --- // ---	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2
SNP_A-1974070	ttcagcatccatgtaa[C/T]actacctaccattgtc	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1972100	gtaggattggctacac[A/G]ctgttctcctcttgac	A	G	Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// ENST00000264330 // intron // 0 // --- // ---	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-1956590	tttgtttgctaccaaa[A/G]tatgtatccctgagca	A	G	Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000261864 // intron // 0 // --- // --- // --- // --- ///	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-1953318	tttgaaaattgcacag[A/T]atttcagtgggtagct	A	T	51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 //	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-1810202	gtgatcttgttgaaca[A/G]acaggatgcagtagct	A	G	Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1
SNP_A-1806282	gtccttaaaactcaac[C/T]agctgaagcacaaaga	C	T	353133 // Homo sapiens late cornified envelope 1C (LCE1C), mRNA. /// NM_178349 // upstream // 5586 // Hs.375103 //	LCE1C	LCE1C, Homo sapiens late cornified envelope 1C (LCE1C), q21.3
SNP_A-1790674	ggggctgggcacaatc[A/G]agggttctgtggggat	A	G	NM_004186 // intron // 0 // Hs.32981 // SEMA3F // 6405 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), mRNA. /// ENST00000002829 // intron // 0 // --- // --- // --- // ---	SEMA3F	SEMA3F, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), p21.31
SNP_A-1790328	ggggagtgggggcacc[A/G]aattcccttcattgtc	A	G	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 332786 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1741843	ttacatcatctgaaataggcgagtc[A/G]agatagaaaagatttttgataata	A	G	1005 // cadherin 7, type 2 /// NM_021153 // downstream // 469896 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2	CDH7	CDH7 , rs10513920, cadherin 7, type 2 ,q22.1
SNP_A-1867204	tccctggaaacaaaaa[A/G]gaatatgcacaaatca	A	G	663 // Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 2 (BNIP2), mRNA. /// NM_182777 //	BNIP2	BNIP2, Homo sapiens BCL2 q22.2
SNP_A-1823072	taaaaatttgaggata[C/T]gttcttccaatatttg	C	T	// 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_019049 // upstream // 72350 //	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-1827064	taaccagcagggaaga[A/G]tccactccctgagcct	A	G	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), mRNA. /// ENST00000341177 // intron // 0 // --- // --- // --- // --- ///	ELAVL1	ELAVL1, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), p13.2
SNP_A-2154398	attattacattcccaa[C/T]tcacttcttactcaga	C	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 172561	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2160392	actatttgccatatac[C/T]ctgagtattacagaat	C	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 619512 // --- // --- // --- // ---	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2159996	atttatgtaagtgtaa[A/G]gaaattggaatgttca	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 320079 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2129360	atacaagaaaacacag[A/T]attcaagcaacaaaaa	A	T	8411 // Homo sapiens early endosome antigen 1, 162kD (EEA1), mRNA. /// NM_021104 // downstream // 111391 //	EEA1	EEA1, Homo sapiens early endosome antigen 1, 162kD (EEA1), q22
SNP_A-2133785	atatcctgagtcgtcc[C/T]aattcttagacctttt	C	T	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 182259 // Hs.114412 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2119721	agtattctaagtccaa[C/T]tgcactgcaaccatct	C	T	Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // intron // 0 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2171332	caatattccaaagcaa[A/T]cttaaagagaaattca	A	T	Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // --- // --- // --- // ---	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-2169430	caagccagaaagctgg[A/C]aggttttattaattat	A	C	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2226491	ctaagcatcttgatttt[C/T]aaataaacacacctaa	C	T	80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 247040 //	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-2002717	ttgatggtgagggtgc[A/G]agcctttggcagttct	A	G	// Homo sapiens hypothetical protein from clone 643 (LOC57228), mRNA. /// ENST00000307274 // intron // 0 // ---	LOC57228	LOC57228, Homo sapiens hypothetical protein from clone 643 (LOC57228), q13.13
SNP_A-2032620	aaataaagtcataca[A/G]gatgaactcctttgt	A	G	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2021759	aaaaacagtaccaaaa[C/G]ggtcaatttcaggca	C	G	Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- ///	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2025030	aaaataatcacattga[A/G]atttgttagatiag	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 737746 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2042731	aactctagcatatgtc[A/G]gtcaggagacaaatt	A	G	// Homo sapiens mesenchyme homeo box 1 (MEOX1), transcript variant 2, mRNA. /// NM_004527 // upstream //	MEOX1	MEOX1, Homo sapiens mesenchyme homeo box 1 (MEOX1), transcript variant 2, q21.31
SNP_A-2071663	acagaatcctcagacc[A/G]aaattccctcgcccct	A	G	ENST00000359247 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2094585	agaatacctaattgac[C/T]agaaggattgaccaga	C	T	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 555533 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2098087	agagaggccaagatca[A/T]tcataatgtgggtgag	A	T	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 265324 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2088384	actgtactaccaacac[A/G]ctctctccacctt cat	A	G	Homo sapiens immunoglobulin superfamily, member 10 (IGSF10), mRNA. /// ENST00000358179 // CDS // 0 // --- // ---	IGSF10	IGSF10, Homo sapiens immunoglobulin superfamily, member 10 (IGSF10), q25.1
SNP_A-2059291	aatcgaccattatgtc[A/G]caggataaacagccaa	A	G	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 238272 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2052775	aagtcaattgtaaaaa[A/G]aactgtatgagaagat	A	G	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2046119	aagactctttgtcca[C/T]aagtgcccaccttcc	C	T	Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. ///	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2031732	aaagtaggaaagagta[G/T]aatcaggtcaatgaaa	G	T	NM_016205 // downstream // 165693 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1998061	gacgtcgtcttgacca[A/G]ctctctctttgca	A	G	8328 // Homo sapiens growth factor independent 1B (potential regulator of CDKN1A, translocated in CML) (GFI1B), mRNA. /// NM_001402 // upstream // 13788 //	GFI1B	GFI1B, Homo sapiens growth factor independent 1B (potential regulator of CDKN1A, translocated in CML) (GFI1B), q34.13
SNP_A-1991177	gttatcattgagaaaa[C/T]tgacagatttgatta	C	T	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 1131329 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-2225834	ctaaatactgcaatgc[A/G]caatgccaggatagct	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- /// ENST00000302763 // intron // 0 // --- ///	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-2203212	ccacttaatagttgac[C/T]gacagaaataaatggt	C	T	// Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // intron // 0 // --- // ---	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2207253	ccattccaacttcctc[A/G]cagcgcctggtgaagg	A	G	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 101422 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2169788	caaggaggcgtggccac[A/G]ggcctgccctgcatca	A	G	64065 // Homo sapiens PERP, TP53 apoptosis effector (PERP), mRNA. /// NM_020340 // upstream // 21983 //	PERP	PERP, Homo sapiens PERP, TP53 apoptosis effector (PERP), q23.3
SNP_A-2190294	cataattacaatgaga[C/T]gtcttatcttaagcc	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // ---	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2154072	atgcccaaatccagtc[A/G]catttcttactagatt	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 983946 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1839579	tagatcattggtgaa[C/T]acaaataaacctccag	C	T	Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // intron // 0 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC rela	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. q27
SNP_A-1829206	taagtaacttccactc[A/G]cttgaatgtaatacaa	A	G	// 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000353474 // downstream //	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-1855524	tcaagttccctgtaaa[C/T]actggtgttatcttt	C	T	sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // --- // ---	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.2
SNP_A-1782585	ggcacctcatggtcca[A/G]tcagttgacacatag	A	G	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1757103	accacatcaccacctccatctaata[A/G]caactgcctccaacagttttggacc	A	G	NM_017735 // intron // 0 // Hs.26090 // FLJ20272 // 55622 // hypothetical protein FLJ20272	FLJ20272	FLJ20272 , rs10490456, hypothetical protein FLJ20272,p22.3
SNP_A-1643786	acccactttatggctagatgggtcc[A/G]aaagcatgcagttcattataggtag	A	G	25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 439684 // Hs.317659 // DPPA4 // 55211 //	PVRL3	PVRL3 , rs1915337, poliovirus receptor-related 3 ,q13.13
SNP_A-1794129	ggtcaggtataccatg[A/C]ataacagttgttaata	A	C	endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 369458 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-1802680	gtatgagatttagtgc[C/T]gaggctcctgtgagac	C	T	// 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 341443	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-1808463	gtgaaagaattagggc[A/T]atctttaagaagtgga	A	T	Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000306329 // intron // 0 // --- // --- // --- // --- ///	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1934710	ttctctgtatttaaaa[A/G]cttcatggaggtagac	A	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1980991	aggagtataattgaag[C/G]acctgggtttggcaac	C	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000317394 // downstream //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-1980409	ttgtactcactaagaa[A/G]aggaatccatagatca	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 168253 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1978220	gtaaaatcttcagaag[A/G]aaaggaaaatgttttg	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 366413 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1874600	tctcctatctcagtaa[A/G]tagaatgtccaatcgg	A	G	Homo sapiens bone morphogenetic protein 8a (BMP8A), mRNA. /// ENST00000331593 // intron // 0 // --- // --- // --- // ---	BMP8A	BMP8A, Homo sapiens bone morphogenetic protein 8a (BMP8A), p34.3
SNP_A-2235158	ctccccagctcacact[C/G]aaaaactatttgttgg	C	G	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 189949 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2241392	ctgagtaaggttgaca[A/G]taagtttctagtactc	A	G	Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters), member 1	SLC12A1	SLC12A1, Homo sapiens solute carrier family 12 (sodium,q21.1
SNP_A-2255910	ctttaaatcagccaaa[C/T]atttttttaatctctc	C	T	8658 // Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// NM_012331 // upstream // 226673 // Hs.490981 // MSRA //	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2282167	gagtgtggaatgaatg[A/C]atgatataagtttata	A	C	MGC21654 // 93594 // Homo sapiens unknown MGC21654 product (MGC21654), mRNA. /// NM_032899 // upstream //	MGC21654	MGC21654, Homo sapiens unknown MGC21654 product (MGC21654), q24.13
SNP_A-2289155	gatttgaacctagaac[A/T]gatttgaacacctaca	A	T	1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream //	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2296685	gccaaagctaatgtac[A/C]aatactttcttgagga	A	C	// 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 150957	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-2286477	gatgcttgttaatatc[C/T]aaattgcaaatcccag	C	T	sapiens N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH), mRNA. /// ENST00000326317 // intron // 0 // --- // ---	SGSH	SGSH, Homo sapiens N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH), q25.3
SNP_A-2258213	cttttagagagactaa[C/T]aaattccttgcctttg	C	T	ENST00000358648 // intron // 0 // --- // --- // --- // --- /// ENST00000360114 // intron // 0 // --- // --- // --- // ---	-	q32.32
SNP_A-2250446	cttaggaaaactagta[A/T]ggaagctcttgctcat	A	T	285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 182602 //	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-2231441	ctattggtctgagtaa[C/T]aatgctgctctttaga	C	T	4676 // Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA. /// NM_139207 // upstream // 381910 //	NAP1L4	NAP1L4, Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), q21.2
SNP_A-1878588	tctgtgtctcacacac[A/G]actcctgagttttggc	A	G	79705 // Homo sapiens leucine-rich repeat kinase 1 (LRRK1), mRNA. /// NM_014918 // downstream // 92335 // Hs.110488	LRRK1	LRRK1, Homo sapiens leucine-rich repeat kinase 1 (LRRK1), q26.3
SNP_A-1917637	ttaaaaaattccacag[C/T]catagctatttccctt	C	T	// Homo sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// NM_001465 // upstream // 32845 // Hs.370503 //	FYB	FYB, Homo sapiens FYN binding protein (FYB-120 p13.1
SNP_A-1926686	ttattgcaggaaacac[G/T]ggtttatgtctaaagc	G	T	Homo sapiens hypothetical protein MGC35023 (MGC35023), mRNA. /// ENST00000318405 // downstream // 39043 // --- //	-	-, Homo sapiens hypothetical protein MGC35023 (MGC35023), p12.3
SNP_A-1988379	taaccatgtactagta[C/T]gtcaagcattttgtca	C	T	5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 157209 // Hs.390428 // MAP3K4 //	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-1986879	ggaagaatcatagtgc[C/T]aaatttcaaactggat	C	T	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2398262 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1965776	ggaagctattgtggtc[A/G]aataaaggtttggagg	A	G	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 11 (ABCB11), mRNA. ///	ABCB11	ABCB11, Homo sapiens ATP-binding cassette, sub-family B (MDR q31.1
SNP_A-1956778	ttttaaataatcatca[A/G]atgcccccagagcttt	A	G	// Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // ---	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826470	taacaacaaatcatac[A/G]gagccatggctttctt	A	G	ENST00000358844 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1819260	gttggaaatatatatg[C/G]acctagcactagagca	C	G	mRNA for KIAA0257 gene, partial cds. /// ENST00000186436 // intron // 0 // --- // --- // --- // ---	RW1	RW1, Human for KIAA0257 gene, partial cds. q11.2
SNP_A-2116934	aggtgaaaactgctca[G/T]ctagctaagtacattc	G	T	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 47452 //	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-2108964	agcttatgtttacaga[A/T]cacatattatgtgcca	A	T	8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 332500 // Hs.279522 // NR4A3 //	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-2190821	catagaggacaggtga[C/T]gtgaacagacaccaat	C	T	// --- /// ENST00000314071 // upstream // 1183 // --- // --- // ---	-	p13.2
SNP_A-2183255	cagcaatgctgccaga[A/G]cccaaatgcattagtt	A	G	10907 // Homo sapiens thioredoxin-like 4A (TXNL4A), mRNA. /// NM_024805 // upstream // 8375 // Hs.532987 // C18orf22 //	TXNL4A	TXNL4A, Homo sapiens thioredoxin-like 4A (TXNL4A), q23
SNP_A-2171267	caatatctaagagaca[A/G]taagaatggccaaatg	A	G	Homo sapiens transcriptional adaptor 3 (NGG1 homolog, yeast)-like (TADA3L), transcript variant 3, mRNA. /// NM_133480 // intron // 0 // Hs.386390 // TADA3L // 10474 //	TADA3L	TADA3L, Homo sapiens transcriptional adaptor 3 (NGG1 homolog, yeast)-like (TADA3L), transcript variant 3, p25.3
SNP_A-2207865	ctaaggctgttttgaa[A/G]tgaacttgggctaaca	A	G	115669 // human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). /// NM_001049 // upstream // 38285 // Hs.248160 // SSTR1 // 6751 // Homo	TTC6	TTC6, human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). q21.1
SNP_A-2213774	cctaaaaactctgaaa[C/G]aacagctctctattag	C	G	sapiens dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1), mRNA. /// ENST00000308775 // intron // 0 // --- // --- // --- // ---	DAG1	DAG1, Homo sapiens dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1), p21.31
SNP_A-1996258	aggaagccattttata[C/G]ctggtggataagggtt	C	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 168234 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2018326	gatgctcacagctgca[C/G]atctcaaggcagagtg	C	G	// 29980 // Homo sapiens downstream neighbor of SON (DONSON), transcript variant 2, mRNA. /// NM_145794 //	DONSON	DONSON, Homo sapiens downstream neighbor of SON (DONSON), transcript variant 2, q22.11
SNP_A-2028316	aaactcaatttcctgc[A/C]accaaacaaataacga	A	C	80267 // Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA. /// NM_022083 // downstream // 4987 //	C1orf22	C1orf22, Homo sapiens chromosome 1 open reading frame 22 (C1orf22), q25.3
SNP_A-2054471	aagtttcctatctaac[C/T]gacactaaaaattaat	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2051142	aagggacaggaattaa[C/T]aaggatggagtagggt	C	T	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 3 (APBB3), transcript variant 5, mRNA. /// NM_133173 // intron // 0 // Hs.529449 // APBB3 // 10307 //	APBB3	APBB3, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 3 (APBB3), transcript variant 5, q31.3
SNP_A-2076618	acatttggagatttgc[C/T]ctcgaggaagaacaga	C	T	3741 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), mRNA. /// ENST00000333731 // upstream // 3670 // --- // --- // --- // --- ///	KCNA5	KCNA5, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), p13.32
SNP_A-2080353	acctaccggtctcaag[A/G]aaatttctgttcaata	A	G	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1141495 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2096337	agaccatccatcccac[A/G]gcatctgattccttgg	A	G	221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2063805	aattagctgcagagag[A/G]aactggcttttcttgg	A	G	4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream //	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2051902	aaggtgatctcttaca[C/T]agtggcctggacctttt	C	T	// 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 157417 // Hs.446083 // PTPRD	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2013200	gtatttctgtacagaa[A/C]attggtttgtgtatag	A	C	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-1991806	tcatgatgagattata[C/G]ctgatctgacgtgaga	C	G	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// ENST00000287907 // intron // 0 // --- // ---	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-1997223	ccaaccactgcccctа[C/T]agatgagatgagtatt	C	T	4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 151458 //	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-2000536	aaaggagaaagtcaga[C/T]gcagagggcatagagg	C	T	6004 // Homo sapiens regulator of G-protein signalling 16 (RGS16), mRNA. /// NM_033345 // downstream // 3465 //	RGS16	RGS16, Homo sapiens regulator of G-protein signalling 16 (RGS16), q25.3
SNP_A-2213371	ccggcacacttggaga[A/G]ggggctggttagttag	A	G	Homo sapiens general transcription factor IIIA (GTF3A), mRNA. /// ENST00000241462 // intron // 0 // --- // --- // --- // ---	GTF3A	GTF3A, Homo sapiens general transcription factor IIIA (GTF3A), q12.2
SNP_A-2216685	cctctcccatctatgg[A/G]aatatttgctgccatc	A	G	Homo sapiens phosphatidylethanolamine-binding protein 4 (PEBP4), mRNA. /// ENST00000256404 // intron // 0 // --- // --- // --- // ---	PEBP4	PEBP4, Homo sapiens phosphatidylethanolamine-binding protein 4 (PEBP4), p21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227300	ctacaaccaacaatcg[A/C]aagagtgacatcaaca	A	C	Homo sapiens mitogen-activated protein kinase 10 (MAPK10), transcript variant 4, mRNA /// NM_002753 // intron // 0 // Hs.25209 // MAPK10 // 5602 // Homo sapiens	MAPK10	MAPK10, Homo sapiens mitogen-activated protein kinase 10 (MAPK10), transcript variant 4, q21.3
SNP_A-2223904	cgggagccttttgcaa[C/T]ggtcctactaagagct	C	T	10318 // Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), mRNA. /// NM_006058 // upstream // 17667 //	TNIP1	TNIP1, Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), q33.1
SNP_A-2199780	ccaaacagaaagcata[A/G]tagaatgtttcttcca	A	G	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1003762 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2193165	catctatggttataga[A/G]atatgatgtggtagaa	A	G	/// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 630691 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2134627	atatgtggtaaactgc[C/T]aggaaggtacccacc	C	T	sapiens activin A receptor, type I (ACVR1), mRNA. /// ENST00000263640 // intron // 0 // --- // --- // --- // ---	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-2160077	atttattgcatatag[A/T]cctctggagtccctaa	A	T	KIAA0635 // 9662 // Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000264222 // downstream // 265555 // ---	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-2166667	caaattaccctgaata[A/G]tgtgtgtaggctccctc	A	G	Homo sapiens zinc finger, RAN-binding domain containing 3 (ZRANB3), mRNA. /// ENST00000264159 // intron // 0 // --- // --- //	ZRANB3	Homo sapiens zinc finger, RAN-binding domain containing 3 (ZRANB3), q21.3
SNP_A-2140688	atctctgaataggagg a[C/T]aaaagatggcatttag	C	T	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // --- //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2145215	atgcaatttgttcatc[A/G]ctgctatctcaaatt	A	G	ENST00000310149 // downstream // 127267 // --- // --- // --- // ---	-	q23.3
SNP_A-1824317	taaacctacaagagacc[A/G]atgtgaattcagcctc	A	G	Homo sapiens cytochrome b reductase 1 (CYBRD1), mRNA. /// ENST00000321348 // intron // 0 // --- // --- // ---	CYBRD1	CYBRD1, Homo sapiens cytochrome b reductase 1 (CYBRD1), q31.1
SNP_A-1839173	tagagcttagagaaca[G/T]gaggaagattatcact	G	T	/// Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 3410532	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1855457	tcaagtctaactgagaa[C/G]tcaaaaaaatttaggt	C	G	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-1854295	tcaaagtaagcaatcc[A/G]aaaacaatgactgca	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2464264 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1853873	tcaaaagatcagaaag[C/T]ccagctatcactgat	C	T	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 313037 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1807539	gtctggaaggcagtca[A/T]cttcaaaggcatcaga	A	T	64403 // Homo sapiens cadherin-like 24 (CDH24), mRNA. /// NM_022478 // upstream // 45789 // Hs.155912 // CDH24 //	CDH24	CDH24, Homo sapiens cadherin-like 24 (CDH24), q11.2
SNP_A-1802549	gtatctcacattttta[C/T]agatttcaacagaga	C	T	MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 //	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-1800432	gtactctctatgcagc[C/G]aagaacaaaaagtcat	C	G	158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 80476 //	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-1805520	gtccagctgagcagaa[A/G]cgtctgtgtcacactg	A	G	Homo sapiens calpain 9 (nCL-4) (CAPN9), mRNA. /// ENST00000271971 // CDS // 0 // --- // --- // --- // ---	CAPN9	CAPN9, Homo sapiens calpain 9 (nCL-4) (CAPN9), q42.2
SNP_A-1797888	ggttttggccatgaa[A/G]gattcattatgttact	A	G	54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 67633 // Hs.365690 // KCNK10 //	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-1787301	gggaagacagaaaggc[A/C]agggaccattctgac	A	C	ENST00000343130 // intron // 0 // --- // --- // --- // --- ENST00000338506 // intron // 0 // --- // --- // --- // ---	-	q12.11
SNP_A-1743151	aggtgactgaaaatggcaggttaa[A/C]atatatttgtgaattacaaaaatgc	A	C	23255 // KIAA0802 /// NM_002845 // downstream // 164902 // Hs.154151 // PTPRM // 5797 // protein tyrosine phosphatase,	KIAA0802	KIAA0802, rs3886662, KIAA0802 ,p11.22
SNP_A-1953569	tttgaattgtcagaggc[C/T]agaggtcggttagc	C	T	ENST00000342241 // intron // 0 // --- // --- // --- // ---	-	q11.22
SNP_A-1949510	tttatggcaaaccac[C/T]gggcgccaggctctgt	C	T	LOC388335 // 388335 // Homo sapiens similar to RIKEN cDNA A730055C05 gene (LOC388335), mRNA. ///	LOC388335	LOC388335, Homo sapiens similar to RIKEN cDNA A730055C05 gene (LOC388335), p13.1
SNP_A-1949180	tttatggcccgtaatg[C/T]agtgtatcttggtaaa	C	T	// Homo sapiens thiopurine S-methyltransferase (TPMT), mRNA. /// ENST00000309983 // upstream // 8789 // --- // --- //	TPMT	TPMT, Homo sapiens thiopurine S-methyltransferase (TPMT), p22.3
SNP_A-1963267	aggatcaatttgggtc[C/T]caaagagctgagagga	C	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1182941 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1963501	tggagagtaggctac[C/G]agctcgggggccagtgg	C	G	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1969362	tctagctagaacatcc[A/G]gaatagaacacatagt	A	G	4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000338221 // upstream //	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-1922686	ttagagagatgagaaa[C/G]agagtcagatgaagag	C	G	116511 // Homo sapiens MAS1 oncogene-like (MAS1L), mRNA. /// ENST00000306877 // upstream // 6051 // --- // --- //	MAS1L	MAS1L, Homo sapiens MAS1 oncogene-like (MAS1L), p22.1
SNP_A-1900542	tggagctggggagaaa[A/G]ctaagctcctgtctgg	A	G	401474 // Homo sapiens sterile alpha motif domain containing 12 (SAMD12), mRNA. /// NM_002546 //	SAMD12	SAMD12, Homo sapiens sterile alpha motif domain containing 12 (SAMD12), q24.12
SNP_A-2235576	ctcctaccactgtgga[A/G]gaatagaacaaagaaa	A	G	sapiens mRNA for KIAA0551 protein, partial cds. /// ENST00000284483 // intron // 0 // --- // --- // --- // --- ///	TNIK	TNIK, Homo sapiens for KIAA0551 protein, partial cds. ,q26.2
SNP_A-2236980	ctctatctcattgtcc[A/G]gcagagagcctgatat	A	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2253735	cttgaaagccattttta[C/T]cctctttgtggcaggg	C	T	sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA. /// NM_033497 // intron // 0 // Hs.370365 // HK1 // 3098 // Homo	HK1	HK1, Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, q22.1
SNP_A-2242193	ctgcaaatgaacatta[A/C]atcagatgaaataatg	A	C	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, mRNA. /// AB017133 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, p36.22
SNP_A-2271969	gacccccaatacatta[A/G]aagccacgtgaattta	A	G	6189 // Homo sapiens ribosomal protein S3A (RPS3A), mRNA. /// NM_001006 // downstream // 67402 // Hs.356572	RPS3A	RPS3A, Homo sapiens ribosomal protein S3A (RPS3A), q22.2
SNP_A-2281119	gagtacaatggagaga[C/T]gactgagcatgaagtc	C	T	// 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2276532	gagagggatggtccaa[C/T]tgggagcagaggtgga	C	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1894272 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2297238	gccaccatacgcagcc[C/T]gccttctgtttctgaa	C	T	sapiens ras homolog gene family, member A (RHOA), mRNA. /// ENST00000265538 // intron // 0 // --- // --- // --- // ---	RHOA	RHOA, Homo sapiens ras homolog gene family, member A (RHOA), p21.31
SNP_A-2293061	gcagacaatcatatgc[A/G]ctgaactgatttctta	A	G	MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 1120603 // Hs.314261 //	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q31.3
SNP_A-2294207	gcagggacatcacagc[A/G]aaacacatggcacttg	A	G	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 3 (APBB3), transcript variant 5, mRNA. /// NM_133173 // CDS // 0 // Hs.529449 // APBB3 // 10307 //	APBB3	APBB3, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 3 (APBB3), transcript variant 5, q31.3
SNP_A-2290302	gcaacacctttaggc[C/T]gagaatgtcttgatgg	C	T	Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2265303	gaagcactaatgaaaa[C/T]tgaaaacacattatac	C	T	1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 211831 // Hs.143434	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2240707	ctgactgacacattcc[A/G]cagcagaatacatgtg	A	G	Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// ENST00000354440 // intron // 0 // --- //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1877562	tctggcgcttaggtat[A/C]aatatatgagctttta	A	C	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-1926919	ttatttcagctcattc[A/G]aaaaggcctctttggg	A	G	// 131474 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 4 (CHCHD4), mRNA. ///	CHCHD4	CHCHD4, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 4 (CHCHD4), p25.1
SNP_A-1930114	ttcattaccaactacc[C/T]atagctacaaattcaa	C	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1914295	tgtgttcacactgtaa[A/G]aattccaggaaacatg	A	G	4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1914751	tgttaccaacaaaatg[C/G]agtgaactattttccc	C	G	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 122839 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1905100	tgggtgatggctggaa[A/G]tccctgcgttccttgg	A	G	89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // downstream //	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-1972330	ccttacagacaccctg[A/C]agtataggtatgctca	A	C	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1967435	acaaaggttctgaggc[C/T]caaggttgcttggtgc	C	T	113278 // Homo sapiens chromosome 20 open reading frame 54 (C20orf54), mRNA. /// ENST00000217254 //	C20orf54	C20orf54, Homo sapiens chromosome 20 open reading frame 54 (C20orf54), p13
SNP_A-1983038	ggaagatgtttccatt[C/T]aacattatcattctct	C	T	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1947193	tttaatgggcagatca[A/G]agaaaacattggctgg	A	G	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, mRNA. /// NM_138711 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens	PPARG	PPARG, Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, p25.2
SNP_A-1671548	aatgaatcattctgggacaggcaga[A/G]agtcttcaattaggggaatagctca	A	G	matrilin 2 /// NM_030583 // intron // 0 // Hs.153647 // MATN2 // 4147 // matrilin 2	MATN2	MATN2 , rs10504984, matrilin 2 ,q22.1
SNP_A-1794441	ggtccgtacttgagac[A/G]cactacagcttatttc	A	G	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // --- // --- // --- // ---	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-1795345	ggtgatggctggggtt[A/C]aacaagttccaacatg	A	C	Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// ENST00000354440 // intron // 0 // --- //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1806032	gtcctagtcctgacta[A/T]gcagaagagctgtagc	A	T	56203 // Homo sapiens leiomodin 3 (fetal) (LMOD3), mRNA. /// AB023230 // downstream // 7464 // Hs.371681 // FRMD4B	LMOD3	LMOD3, Homo sapiens leiomodin 3 (fetal) (LMOD3), p14.1
SNP_A-1845489	tatagactagggagaa[C/T]agagaaaattgaaaat	C	T	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1869648	tccttagcttcacttc[C/T]gaacattcaaagaatt	C	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// NM_006806 // downstream //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1860871	tcatacactatgctag[A/C]ccccacaaagttaatt	A	C	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.3
SNP_A-1838475	tagaatctaggggcca[A/G]aagcaatcaattaaga	A	G	5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// NM_173062 // upstream //	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin q15
SNP_A-1842431	taggtgaaaatgtgaa[A/G]ctcagggcacagcaag	A	G	11309 // Homo sapiens solute carrier organic anion transporter family, member 2B1 (SLCO2B1), mRNA. /// NM_004041 // downstream // 4847 // Hs.503284 // ARRB1 //	SLCO2B1	SLCO2B1, Homo sapiens solute carrier organic anion transporter family, member 2B1 (SLCO2B1), q13.4
SNP_A-1831884	taattgaaaggtttga[C/T]gtggctccctgtaatg	C	T	Homo sapiens piwi-like 1 (Drosophila) (PIWIL1), mRNA. /// ENST00000245255 // intron // 0 // --- // --- // --- // ---	PIWIL1	PIWIL1, Homo sapiens piwi-like 1 (Drosophila) (PIWIL1), q24.33
SNP_A-1818321	gttctgtccacaatcc[A/G]gcatcgaccctggctt	A	G	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc,q32.3
SNP_A-2158986	attgttatgctataac[C/T]gggtgctgtgagctgt	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2170801	caagttttggctctac[C/T]atacttttatttttt	C	T	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 294333 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2203872	ccagagtgacagttca[A/G]acttattttgccttgc	A	G	/// ENST00000356718 // upstream // 51455 // --- // --- // --- // ---	-	q24.21
SNP_A-2212511	cccttacatatttgac[C/T]ctgaataaacgttgaa	C	T	Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // --- // --- // --- // --- ///	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2013891	tgtggagcagagaaca[A/G]tggggagaaggtaaga	A	G	57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // upstream // 25824 // --- // ---	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2018961	tatttaaatttagcac[A/G]aggtcataggtatttt	A	G	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, mRNA. /// NM_001001894 // intron // 0 //	TTC3	TTC3, Homo sapiens tetratricopeptide repeat domain 3 (TTC3), transcript variant 1, q22.13
SNP_A-2017845	taagtaaccttttagtg[C/T]aagcatacagtttacc	C	T	284827 // Homo sapiens keratin associated protein 13-4 (KRTAP13-4), mRNA. /// NM_181623 // upstream // 8947 // ---	KRTAP13-4	KRTAP13-4, Homo sapiens keratin associated protein 13-4 (KRTAP13-4), q22.11
SNP_A-2065896	aatttctcttaagtct[C/G]acagtgacctaaaatt	C	G	27284 // Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA. /// NM_005420 // downstream // 54739 // Hs.479898 // SULT1E1 // 6783 // Homo sapiens	SULT1B1	SULT1B1, Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), q13.3
SNP_A-2081737	accttccgagcagcaa[A/G]gggttaaaacccaggc	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 // upstream // 4129 // Hs.20805 // TSAP6 // 55240 // Homo	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2086743	actgaattttagaaca[C/G]tcattcaagcagcaga	C	G	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA. /// ENST00000339765 // intron // 0 // --- // --- // --- // --- /// ENST00000349830 // intron //	ARHGEF10	ARHGEF10, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), p23.3
SNP_A-2085559	actccatcatctcagc[C/T]caaaatttccttaagc	C	T	5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 186256 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2084348	actatacagcctctca[C/G]gtaagggttctaggta	C	G	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 170027 // Hs.148162 // PDGFC,	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2049745	aagcttttctcigcct[A/G]aatttgcataatggtc	A	G	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // 54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 185003	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2057241	aatatagtatatccta[C/T]ggaccagacacaatgc	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // ---	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2015731	ctgcaaattgagaatg[A/C]acagcaaagtgtaaaa	A	C	6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 283013 // Hs.528304 // ADAM28 // 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// NM_018682 // upstream // 254472 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 764898 // Hs.523446 // COL11A1 // 1301 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // sapiens tyrosinase (oculocutaneous albinism IA) (TYR), mRNA. /// ENST00000263321 // intron // 0 // --- // --- // --- // --- 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 61666 // --- // --- // --- // --- 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 892577 // Hs.269560 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 163505 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 101810 // Hs.120831 // TNT // ENST00000360285 // intron // 0 // --- // --- // --- // --- ENST00000339882 // intron // 0 // --- // --- // --- // --- 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa (CSTF1), mRNA. /// ENST00000217109 // intron // 0 // --- // --- // --- // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 4185320 // Hs.146858 // PCDH10 // 57575 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 256130 // Homo sapiens hypothetical protein MGC42090 (MGC42090), mRNA. /// NM_000982 // upstream // 215518 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // --- ENST00000355656 // intron // 0 // --- // --- // --- // --- Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // --- // --- // --- // --- Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // ---	TYR CDH20 MAN1A1 OLFM3 PARK2 DBC1 FLJ23749 HS3ST4 LZTS1 CSTF1 SLC7A11 SLC24A2 DLG2 MGC42090 AUTS2 LOC143458 - CA10 KCNQ5	TYR, Homo sapiens tyrosinase (oculocutaneous albinism IA) (TYR), q14.3 CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.32 MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31 OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds. p21.1 PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26 LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2 STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2 DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1 FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1 HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1 q12 LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3 CSTF1, Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa (CSTF1), q13.31 SLC7A11, rs7684854, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11, q28.3 SLC24A2, Homo sapiens solute carrier family 24 (sodium,p22.1 DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1 MGC42090, Homo sapiens hypothetical protein MGC42090 (MGC42090), p21.1 AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.21 LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13 q11.2 CA10, Homo sapiens carbonic anhydrase X (CA10), q22 KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-2040085	atgaggaggggaaaaaa[A/T]atttggatgcacatg	A	T			
SNP_A-2142597	atgaactaaatttggg[A/C]atgacaaagacagaat	A	C			
SNP_A-2127955	ataaggaggaaaaaaga[A/G]aactcaatgcttcaga	A	G			
SNP_A-1832604	tacaacaatgtcaaca[A/G]agccacttactcaaa	A	G			
SNP_A-1831366	taatgtatcaaatatg[A/T]aatggattaaggaata	A	T			
SNP_A-1864737	tccagcggaagaaaaa[C/G]gtcaatgtagttgttt	C	G			
SNP_A-1852421	tatttaatctccataa[C/T]ctttctatgatgtagg	C	T			
SNP_A-1803133	gtattcactcataccа[C/G]aagaaccaatttttgc	C	G			
SNP_A-1794111	gacaaacagaaaaaaaa[A/G]tgtctgttctcatttag	A	G			
SNP_A-1799248	gtaataaaagacttcа[C/T]aggacttgatgtgctg	C	T			
SNP_A-1787750	gggaccaccagtgaca[A/G]gggcaggtctgtgagg	A	G			
SNP_A-1788920	gggcaactaggaaac[A/G]caaagtgaggccgcat	A	G			
SNP_A-1718233	aatatatcttgcctattcctataca[A/G]tctttacattgaattcattcacc	A	G			
SNP_A-1936226	ttcttcagtggtgtaa[C/T]agaaatttagtgtaa	C	T			
SNP_A-1953556	tttgaattagtattac[A/T]acaagccagtggcctg	A	T			
SNP_A-1989084	agtgcaggataagacc[A/G]attcatgaaacaatat	A	G			
SNP_A-1914077	tgtgtgggaaaacca[C/T]ggagtcttgggcccag	C	T			
SNP_A-1911489	tgtcttaaataaca[A/G]tgtgatggaaattatt	A	G			
SNP_A-1899867	tggacaagctactcag[C/T]atccttcggcttggt	C	T			
SNP_A-2235708	ctcctcataaataaaa[G/T]gtaaggtctaatctta	G	T			
SNP_A-2247614	ctgtcttccaataa[C/T]aggctttactgctttt	C	T			

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255694	ctgttcatttcctta[A/T]catttatgaccagag	A	T	158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// NM_003084 // upstream // 32474 //	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-2252762	cttctaactagttgaa[C/T]acagcaaaggtgatgg	C	T	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2272272	gacctcctctgtcagg[A/T]acacctagtttaaggc	A	T	118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// NM_020799 // upstream // 10693 //	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31
SNP_A-2268717	gaatgttgggattaat[C/G]atgggagacttggtgg	C	G	Homo sapiens cAMP responsive element binding protein 3-like 3 (CREB3L3), mRNA. /// ENST00000252587 // intron // 0 // --- // --- // --- /// ENST00000078445 // intron // 0 // --- // ---	CREB3L3	CREB3L3, Homo sapiens cAMP responsive element binding protein 3-like 3 (CREB3L3), p13.3
SNP_A-2257410	ctttgaatgtcaggaa[C/T]cttttcttctgtagt	C	T	Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), mRNA. /// ENST00000242850 // intron // 0 // ---	GUCY1B2	GUCY1B2, Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), q14.3
SNP_A-2259103	gaaaaaaaaaggatga[C/T]catatggaaattttcag	C	T	SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream //	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-2282662	gagtttggattgacc[A/T]aaagcttacattacta	A	T	27249 // Homo sapiens chromosome 2 open reading frame 25 (C2orf25), mRNA. /// NM_153041 // downstream // 158058	C2orf25	C2orf25, Homo sapiens chromosome 2 open reading frame 25 (C2orf25), q23.2
SNP_A-2283891	gatagttgtgatatca[A/T]cctgtcctcaaagca	A	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 384435	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-2289045	gatttccatgatttta[C/T]ggttcttagagttgaa	C	T	858 // Homo sapiens caveolin 2 (CAV2), transcript variant 2, mRNA. /// NM_001233 // downstream // 6189 // Hs.212332 //	CAV2	CAV2, Homo sapiens caveolin 2 (CAV2), transcript variant 2, q31.2
SNP_A-2295314	gcatcaggaaaagattg[C/T]acaagtggcttcaatt	C	T	Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // --- // ---	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2301051	gccttatgctataacc[A/T]acagagaattagatgg	A	T	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2305843	gctgctagtgacaaga[A/G]gctcactactgggtg	A	G	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 274162 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2274091	gacttatggtaaggaa[A/G]gtcagaccaaagactg	A	G	9325 // Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), mRNA. /// NM_001029 // upstream // 110176 //	TRIP4	TRIP4, Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), q22.31
SNP_A-2274290	gacttgctgatctgaa[C/T]gagaatcctggacttg	C	T	90141 // Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// NM_018319 // upstream // 789 //	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-2256688	ctttcagctcatttaa[A/G]atgccaaaagttatg	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2247596	ctgtcttcatccaaga[C/T]gctatcacctcttact	C	T	// 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // upstream //	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-2228749	ctagacttactatata[C/T]taaaccatgtcttaaa	C	T	Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 2, mRNA. /// NM_016115 // intron // 0 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin	ASB3	ASB3, Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 2, p16.2
SNP_A-1893749	tgcagtggttcaatgg[A/G]agatcatttttattt	A	G	// 54407 // Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA. /// ENST00000256689 // upstream //	SLC38A2	SLC38A2, Homo sapiens solute carrier family 38, member 2 (SLC38A2), q13.11
SNP_A-1879015	tcttaacctttatgac[C/T]aatgttagcttgacct	C	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 860547 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1920558	ttaatttacatctgta[A/T]agtgctttgaagtgta	A	T	115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream //	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-1926060	tactgacatataaggaa[C/T]gcagaatggttgtgag	C	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 1052279	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1974630	gttcttgcttcatcc[A/G]agttaatcttccttgca	A	G	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. ///	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-1953459	ttgaagatatgggaa[G/T]ggaaaagtctacatac	G	T	ENST00000347778 // intron // 0 // --- // --- // ---	-	q23.33
SNP_A-1955944	tttgtcccatacagtc[A/G]aacagagttctaagtg	A	G	84208 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 9383 //	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-1946330	tttaaaatcccaacca[C/T]aggagaatctttatgt	C	T	3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 6074 //	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-1750981	agttttctgcactcaaaatataa[C/T]ggcatttgtgacttggaaacttcc	C	T	// 23389 // thyroid hormone receptor associated protein 2 /// NM_005996 // upstream // 973703 // Hs.129895 // TBX3 //	THRAP2	THRAP2, rs1486410, thyroid hormone receptor associated protein 2 ,q24.21
SNP_A-1669519	agcaaatttaaatatgaaataaa[A/G]gtttaaggactctcaatgattc	A	G	// 10346 // tripartite motif-containing 22 /// NM_173525 // upstream // 322521 // Hs.278221 // MGC34805 // 160298 //	TRIM22	TRIM22 , rs10500658, tripartite motif-containing 22 ,p15.4
SNP_A-1788609	gggatctaggtctta[C/T]catttctgtgccacag	C	T	COMMD10 // 51397 // Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// NM_020796 //	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798510	gtaaatgtgtccattc[A/G]aaatgggaaaaatgt	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2536533 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1804315	gtcactcatttagtaat[A/G]tagtagagcaacagtg	A	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-1812213	gtggagtaagctgaac[A/G]aacttctgtgagtg	A	G	// 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // downstream //	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-1869531	tcctgtttaacaataa[C/T]atataccgcataacat	C	T	Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000255189 // intron // 0 // --- // --- // --- ///	DMGDH	DMGDH, Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, q14.1
SNP_A-1830582	taatcatataaataga[A/G]caaatagtttagcaaa	A	G	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 (ADAMTS19), mRNA. /// ENST00000274487 // intron // 0 // --- // --- // ---	ADAMTS19	ADAMTS19, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 (ADAMTS19), q23.3
SNP_A-1833772	tacagtacaaacatca[A/G]gcatgaatatgtatta	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 150012 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1841838	taggcctttactgtac[A/G]ctggaaagagagggca	A	G	Homo sapiens LAG1 longevity assurance homolog 6 (S. cerevisiae) (LASS6), mRNA. /// ENST00000305747 // intron // 0 // --- // --- // ---	LASS6	LASS6, Homo sapiens LAG1 longevity assurance homolog 6 (S. cerevisiae) (LASS6), q24.3
SNP_A-1821367	gtttgctgttctaatg[A/G]aaaaagctaacgattt	A	G	22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// NM_207015 // upstream // 145467 // Hs.416922 //	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. q26.31
SNP_A-2137692	atcatgctcaaaagta[C/T]gaaattcatgggaatt	C	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1126433 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2120725	agtcctagagagtgga[C/T]ggtctcctagttcag	C	T	170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // --- // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2169502	caagccttttattcta[C/G]aaggctgtgcctgagt	C	G	MGC15730 // 84966 // Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000355895 //	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-2004105	tatttaaaaataccca[C/T]atattgcaaacataga	C	T	FLJ39531 // 400360 // Homo sapiens FLJ39531 protein (FLJ39531), mRNA. /// NM_003246 // upstream // 67704 //	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ39531), q14
SNP_A-2023964	aaaagacaggaaaagaa[G/T]gtgaacagaaagagtc	G	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2044228	aacttctaaagaatc[A/T]gaaggcatcgctctgt	A	T	// 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 111110 // Hs.523852 //	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-2068172	acaagacgtaaagaga[A/C]gttctgaaattaaagt	A	C	Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA. /// ENST00000244040 // 3UTR // 0 // --- //	RAB22A	RAB22A, Homo sapiens RAB22A, member RAS oncogene family (RAB22A), q13.32
SNP_A-2069062	acaatgtatacatgaa[C/T]tgaaacatcacactgc	C	T	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 676642 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2077933	accagcatccaggaaa[A/G]gttaaaatgaagaatg	A	G	Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // --- // ---	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2103653	agcacagagatgctaa[A/G]caacagctagaccttg	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2022913	aaaacaaggaaatttg[C/T]aatcttctttataag	C	T	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2022401	aaaaatagaattaggc[A/G]acaaaacactattgga	A	G	// Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// NM_030906 // downstream // 110612 // Hs.501833	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-2032563	aaataaaatttaaaaa[A/G]atggctgtaatgctgt	A	G	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-1994670	ccaaccagtccctggc[A/G]cttgccaaaatcagag	A	G	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-2216223	cctccggatcctgtcc[A/T]ctcataccaggtatcc	A	T	Homo sapiens SET and MYND domain containing 4 (SMYD4), mRNA. /// ENST00000305513 // intron // 0 // --- // ---	SMYD4	SMYD4, Homo sapiens SET and MYND domain containing 4 (SMYD4), p13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2202623	ccacctctgggtattat[A/T]gggctgaaaaacaact	A	T	sapiens putative G protein coupled receptor (GPR), mRNA. /// ENST00000299092 // intron // 0 // --- // --- // --- // ---	GPR	GPR, Homo sapiens putative G protein coupled receptor (GPR), q15.1
SNP_A-2117280	aggtggagatctgaga[C/T]ggccctaagaattat	C	T	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- /// 6513 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /// ENST00000270929 // upstream // 87144 // --- // --- // --- // ---	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q25.1
SNP_A-2144578	atgatcccatttactc[G/T]catttccagtgaccca	G	T		SLC2A1	SLC2A1, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), p34.2
SNP_A-2144984	atgatttcatctcaca[A/G]atctttttttctctt	A	G	FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2160727	atttctaagcagagaaa[C/T]aaggccggttggaaa	C	T	sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-2153520	attagcatcctacttaa[A/G]cacagtaatgatgtcc	A	G	2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 180085 // Hs.374243 //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1822475	gttttttccaaggattat[A/G]ctgctactaataatactg	A	G	57534 // Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), mRNA. /// NM_005257 // upstream // 193537 //	MIB1	MIB1, Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), q11.2
SNP_A-1869806	tcctccctctgctccc[G/T]atcttcctgtggtttc	G	T	/// ENST00000321536 // upstream // 486752 // --- // --- // --- // ---	-	p13
SNP_A-1870851	tcggcccaaaactgat[A/G]atacacatgaatggtt	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 587908 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1848731	tatgagtgggaagaaat[G/T]aacaacaaacgtatta	G	T	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 889688 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1947032	tttaataactccaatg[A/T]atttgatgaaacacaa	A	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 450887 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1956977	ttttaataaagcactc[C/T]gaatatttcaaatgtg	C	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-1925456	ttatcttacaaaaata[C/T]catactgcttttcta	C	T	/// ENST00000360991 // downstream // 924664 // --- // --- // ---	-	q12.1
SNP_A-1905744	tggtattggctaaaca[C/T]tgttcctaaagtcaat	C	T	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1906074	tggtctctgtcagaaac[A/G]aaactctgcccttcca	A	G	144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 //	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-1911176	tgtctgcaggttaagt[A/G]actagcctaaggtaag	A	G	BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 //	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.3
SNP_A-1910457	tgtccccctttccaca[A/G]cagttcttttgacttca	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 883142 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1910696	tgtccttcactcgttc[A/G]cttcctcactaggcc	A	G	ENST00000269439 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-1909614	tgtcaagaaccaaagg[A/G]aatctatgaaatccca	A	G	// 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 142555 //	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-1888301	tgagctgaaggtattat[C/T]aacaatcttagacaaa	C	T	23169 // Homo sapiens solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual	SLC35D1	SLC35D1, Homo sapiens solute carrier family 35 (UDP-glucuronic acid p31.2
SNP_A-1897729	tgctgcttctattccaa[C/T]gttatactggttgaat	C	T	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 591326 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2250626	cttagtttggattgc[C/G]cttctgcaaaatgagg	C	G	/// ENST00000343481 // downstream // 218143 // --- // --- // ---	-	q24.1
SNP_A-2278924	gaggaaagccacagtt[C/T]aaaaggagactcatac	C	T	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2308963	cctagagatatcttgg[A/T]cagcagcttcgctggg	A	T	145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// ENST00000344738 // downstream //	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-2295032	gcatactgtcagccta[G/T]aagacaaactcagcac	G	T	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. ///	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2300521	gcctgagaaatattgta[C/T]cagggattacagagaaa	C	T	2791 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 11 (GNG11), mRNA. /// NM_005868 // downstream // 58564 // Hs.489132 // BET1 // 10282 // Homo	GNG11	GNG11, Homo sapiens guanine nucleotide binding protein (G protein), gamma 11 (GNG11), q21.3
SNP_A-2286600	gatggagagatctaga[C/T]gctggtgccccgtlgt	C	T	26122 // Homo sapiens enhancer of polycomb homolog 2 (Drosophila) (EPC2), mRNA. /// ENST00000258484 //	EPC2	EPC2, Homo sapiens enhancer of polycomb homolog 2 (Drosophila) (EPC2), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2256814	ctttccagctcacctc[A/G]catcctgggtcccaca	A	G	Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000308624 // intron // 0 // --- // --- // ---	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2246936	ctgtatattaaccata[C/T]gttctgacaagagttc	C	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1896646	tgctagtatagaaata[A/C]ctgtgtatattatcgc	A	C	Homo sapiens KIAA0355 (KIAA0355), mRNA. /// ENST00000299505 // intron // 0 // --- // --- // ---	KIAA0355	KIAA0355, Homo sapiens KIAA0355 (KIAA0355), q13.11
SNP_A-1887232	tgagaacattaagaaa[C/G]aaagcaaaacagaact	C	G	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-1886975	tgacttctggcttcta[C/G]gtttgtcagtaggag	C	G	2831 // Homo sapiens G protein-coupled receptor 7 (GPR7), mRNA. /// ENST00000331251 // downstream // 123746 // ---	GPR7	GPR7, Homo sapiens G protein-coupled receptor 7 (GPR7), q11.23
SNP_A-1883418	tgaacagcgttggccca[C/T]aggaagctattgacac	C	T	Homo sapiens podocalyxin-like (PODXL), mRNA. /// ENST00000322985 // intron // 0 // --- // --- // ---	PODXL	PODXL, Homo sapiens podocalyxin-like (PODXL), q32.3
SNP_A-1874515	tctccctgtaataaaa[A/G]tgtttctgggctccag	A	G	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// NM_024767 // intron // 0 // Hs.134296 //	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-1931885	ttccgtctcaatgccc[A/G]ctaaaactggcctttt	A	G	56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// NM_080738 // upstream // 42154 //	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-1928985	ttcagccattgaaaca[G/T]agaaatcctgtactat	G	T	56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 317422 //	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1958558	ttttctaagtactttc[C/T]ataaactaaactcact	C	T	// Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // --- // --- // --- // ---	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-1943416	ttggtttaaagaaatc[A/C]aatcagaatagaaaaa	A	C	1) L-type voltage-dependent calcium channel a1 subunit (hHT) mRNA, complete cds. /// NM_000719 // intron // 0 // Hs.335817 // CACNA1C // 775 // Homo sapiens calcium	-	-, Homo sapiens (clone hHT-1) L-type voltage-dependent calcium channel a1 subunit (hHT) complete cds. .p13.33
SNP_A-1933578	ttctagatctcagaca[C/T]gctttcttactattc	C	T	65268 // Homo sapiens mRNA for KIAA1760 protein, partial cds. /// NM_006648 // downstream // 31657 // Hs.522291 //	WNK2	WNK2, Homo sapiens for KIAA1760 protein, partial cds. .q22.31
SNP_A-1976204	tccattcagtttctg[A/G]aataataccatagact	A	G	Homo sapiens prominin 1 (PROM1), mRNA. /// ENST00000265014 // intron // 0 // --- // --- // ---	PROM1	PROM1, Homo sapiens prominin 1 (PROM1), p15.32
SNP_A-1964499	ataaagccataggtaa[C/G]ggtgcaacaacacga	C	G	Homo sapiens interleukin 1 family, member 10 (theta) (IL1F10), transcript variant 1, mRNA. /// NM_173161 // intron // 0 // Hs.306974 // IL1F10 // 84639 // Homo sapiens	IL1F10	IL1F10, Homo sapiens interleukin 1 family, member 10 (theta) (IL1F10), transcript variant 1, q13
SNP_A-1985849	ctttagattgaaagaa[A/G]aaaatgaaagatgcag	A	G	// 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-1985627	acctctaccttgaaacc[C/T]gatgctttaaagacca	C	T	56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream //	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1869566	tccttaaactagaaca[A/G]cagcatcgcctcctcc	A	G	154064 // Homo sapiens retinoic acid early transcript 1L (RAET1L), mRNA. /// NM_024518 // downstream // 11755 //	RAET1L	RAET1L, Homo sapiens retinoic acid early transcript 1L (RAET1L), q25.1
SNP_A-1864586	tccagagtcgaaaaaa[A/T]gtagaattcactaggt	A	T	Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // --- // --- // --- // ---	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-1822383	gcttatgagtttcatc[A/G]aaggcatgtttcaaac	A	G	51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 70784 // Hs.461453 // WWOX ///	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1823338	taaaagaaatttatc[A/G]cttgcttcagcatatt	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1201176 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1827878	taagaaaatgctcaa[A/G]agagatacagacaaa	A	G	7798 // Homo sapiens leucine zipper protein 1 (LUZP1), mRNA. /// NM_000864 // downstream // 74128 // Hs.121482	LUZP1	LUZP1, Homo sapiens leucine zipper protein 1 (LUZP1), p36.12
SNP_A-1814174	gtgtctattcaaggcc[A/C]attgataactttag	A	C	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 346978 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1806731	gtctagacacagtcgg[C/G]cagtgttcaatactag	C	G	/// ENST00000315208 // upstream // 316164 // --- // --- // --- // ---	-	q24.32
SNP_A-1806981	gtctcaggattacata[A/G]gaatttaggaaattg	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2178298 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1785058	aatacaaaccattaca[C/T]accgcagtttcaattc	C	T	2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// NM_024997 // upstream // 194179 // Hs.513343 // ATF7IP2 // 80063 //	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2161121	atttgaaatttttcaa[C/T]ctgtccatcactgtt	C	T	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2161431	atttgcccaaagtcac[A/G]cagctactaagaagca	A	G	57157 // Homo sapiens putative homeodomain transcription factor 2 (PHTF2), mRNA. /// NM_012301 // downstream //	PHTF2	PHTF2, Homo sapiens putative homeodomain transcription factor 2 (PHTF2), q21.11
SNP_A-2139033	atcctaccagttttga[C/T]attgtgtacagtgagt	C	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 987687 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2107848	agctccaaaggtcaaa[A/G]ttaaagggaaatcctt	A	G	// 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 68614 //	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2124230	agttatagagcagcta[C/T]attcaaatttgtttga	C	T	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // --- // ---	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2208023	cccaacttcaaacatg[A/C]atcagtgtaaaatctt	A	C	CAPZA3 // 93661 // Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA. /// NM_019012 // upstream // 20192 // Hs.188614 // PLEKHA5 //	CAPZA3	CAPZA3, Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), p12.3
SNP_A-2218407	cacatgaaataagaga[A/G]gggcaattctccaaag	A	G	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2217870	cctgcacagagataaa[A/T]ataacagcggtacagg	A	T	// 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 17147 // --- // --- // --- // --	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-2168704	caagaatatacctgga[A/G]ctcttaagattcaaca	A	G	// 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 878420 // --- // --- // --- // -	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2172965	cacaaaatcaaataga[A/C]ctcctcaacctgcaag	A	C	8434 // Homo sapiens reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA. /// ENST00000320491 // upstream // 6498 // --- // --- // --- // --- ///	RECK	RECK, Homo sapiens reversion-inducing-cysteine-rich protein with kazal motifs (RECK), p13.3
SNP_A-2015342	agctgtgtttgtggca[A/G]tgactttcagctgaga	A	G	29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 612581 // Hs.473370 // USP25 // 29761 // Homo sapiens	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds. ,q21.1
SNP_A-2030937	aaaggaattatgaccc[A/G]gagctaccttcttaag	A	G	21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 475124 // Hs.475902	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2047743	aagattgaaatagcag[A/G]agatttcttattaaat	A	G	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2041392	aacctgtcctcaaacc[A/C]ctgggaaggcaaaggc	A	C	ENST00000343130 // intron // 0 // --- // --- // --- // --- /// ENST00000338506 // intron // 0 // --- // --- // --- // --- ///	-	q12.11
SNP_A-2039380	aacatagagctgaggc[A/G]aaaagcaaatacattt	A	G	ENST00000343529 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2035097	aaatgcatatggtctc[A/G]actgaatgtttttaca	A	G	mRNA for KIAA0257 gene, partial cds. /// ENST00000186436 // 3UTR // 0 // --- // --- // --- // ---	RW1	RW1, Human for KIAA0257 gene, partial cds. ,q11.2
SNP_A-2104826	agcataattttaaatg[C/G]attcccttgcctatcc	C	G	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 487478 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2092442	agaaaggttaatgcag[A/G]cataaggagagtagag	A	G	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-2084970	actcacaagcaacaaa[C/T]acactgggcaagcaag	C	T	/// ENST00000326756 // downstream // 179095 // --- // --- // ---	-	p16.1
SNP_A-2056915	aatagtacctacttta[C/T]aaggatgtgtgtagat	C	T	C14orf118 // 55668 // Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // downstream // 70903 // Hs.410231 //	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-2053905	aagtgttggagtactg[A/G]caagataagaacaaat	A	G	// Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// ENST00000354883 // intron // 0 // ---	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2053729	aagtggtaaataaata[C/T]attggcactctgcaat	C	T	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 536295 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2054367	aagttgttatgactca[C/T]actctgtctatagtaa	C	T	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// ENST00000199168 // intron // 0 // --- // --- // --- // ---	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-2071474	acagaaaggacattga[C/T]ggaaaaactggtgaaa	C	T	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-2096341	agaccatgaatagcca[C/T]atcaaatcaatcctga	C	T	340351 // Homo sapiens hypothetical protein LOC340351 (LOC340351), mRNA. /// ENST00000275763 // intron // 0 // ---	LOC340351	LOC340351, Homo sapiens hypothetical protein LOC340351 (LOC340351), q33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169497	caagccttctgttttg[C/T]agaaactggtcatttc	C	T	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 183544 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-2189658	cagttttatggctttg[G/T]acatatcattgattta	G	T	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 706355 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-2219275	cctgtctgcctgctaa[C/T]tggggtgcagaacttg	C	T	8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // downstream //	FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-2224407	cgtactcagggaggca[C/G]ataaaagccgagacca	C	G	3434 // Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 1, mRNA. /// NM_012420 // upstream // 264 // Hs.252839 //	IFIT1	IFIT1, Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 1, q23.31
SNP_A-2128149	ataaggacaaagagat[C/G]atctccaccagccatt	C	G	// 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 59080 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2118084	agtaaaagtttgatag[C/G]cctggaacctggaaag	C	G	Homo sapiens TRAF and TNF receptor associated protein (TTRAP), mRNA. /// ENST00000341060 // intron // 0 // --- // ---	TTRAP	TTRAP, Homo sapiens TRAF and TNF receptor associated protein (TTRAP), p22.2
SNP_A-2121781	agtgactgtagcaaca[A/T]ccctaaggcaactgtt	A	T	sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2144548	atgatcaggacagagc[C/T]gaggtaagtttgagtt	C	T	219858 // Homo sapiens olfactory receptor, family 8, subfamily B, member 12 (OR8B12), mRNA. /// NM_001005194 // upstream // 1404 // Hs.339298 // OR8A1 //	OR8B12	OR8B12, Homo sapiens olfactory receptor, family 8, subfamily B, member 12 (OR8B12), q24.2
SNP_A-2146211	atgctaaagaggaaaa[C/T]ccatacattgtgagcc	C	T	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2148940	atggttaacacatcac[C/G]gtacatccatactgtg	C	G	Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), mRNA. /// ENST00000334822 // intron // 0 // ---	ZDHHC17	ZDHHC17, Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), q21.2
SNP_A-2167555	caacatttataactac[C/G]agcagtatgtaagaga	C	G	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.2
SNP_A-2158967	attgttaatggtgaca[A/C]aatatcctaaatcaca	A	C	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1747901	tggtctccagcatgactgtagaaca[C/T]tgaaggaactagactgagtgaagaa	C	T	// 57556 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A /// NM_173666 // downstream // 578867 // Hs.14822 // FLJ33977 // 285605 //	SEMA6A	SEMA6A , rs10519537, sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A ,q23.1
SNP_A-1657215	cctgttgcccctagatacttcagca[C/T]gtatttcctaagaatgggatatact	C	T	1002 // cadherin 4, type 1, R-cadherin (retinal) /// NM_173644 // downstream // 1496605 // Hs.335319 // FLJ33860 //	CDH4	CDH4 , rs2387105, cadherin 4, type 1, R-cadherin (retinal) ,q13.33
SNP_A-1804713	gtcagggagaggtaca[A/G]aatccagagcagccta	A	G	// Homo sapiens activin A receptor, type I (ACVR1), mRNA. /// NM_173355 // upstream // 191004 // Hs.128427 // UPP2 //	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-1827043	taaccaccagagctca[A/C]gccagatttatggaaa	A	C	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 405536 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-1861430	tcatcatgaaaaagac[G/T]accttatgttcaggat	G	T	// Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 216715 // Hs.158932 // APC //	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1848556	tatgaccaattatgat[A/G]actgaaaactgttaag	A	G	79789 // Homo sapiens calmin (calponin-like, transmembrane) (CLMN), mRNA. /// NM_024633 //	CLMN	CLMN, Homo sapiens calmin (calponin-like, transmembrane) (CLMN), q32.13
SNP_A-1856089	tcaattttaaaatgta[C/T]gtagccagagatgcaa	C	T	ABCA13 // 154664 // Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // downstream // 168883 // --- // --- // --- //	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-1980609	gaggagaaaatgagac[A/G]aaatatgcatttacac	A	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1980390	gtctgcctgacccagt[C/G]aaacaccagagacctc	C	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 374625 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1959485	ttttgctaacaaaaaa[C/G]tttcagaagaatttcg	C	G	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 660047 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1932477	ttcctgctttgcagtg[C/T]atttactcactttatc	C	T	341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream //	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884483	tgaagtgtgagcataa[A/G]ctgtgaactccaagag	A	G	METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream //	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1897516	tgctgatagttacaga[A/G]aagaaaaatggcatca	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 595025 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-2253964	ctgactcttggtgca[C/G]gtgttacttccagtta	C	G	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2256982	ctttcctctctctca[A/C]aagtctcacgtctca	A	C	3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 105 //	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q42.12
SNP_A-2258860	ctttttataatcttta[C/T]gcagaagatgaaaag	C	T	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 468583 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-2275206	gagaaggaggaggagaa[A/G]tggactaggaatgtc	A	G	Homo sapiens hypothetical protein MGC35023 (MGC35023), mRNA. /// ENST00000318405 // downstream // 98959 // --- //	-	-, Homo sapiens hypothetical protein MGC35023 (MGC35023), p12.3
SNP_A-2311487	ggaatctgaataaca[A/G]tgatgactggaaatg	A	G	56935 // Homo sapiens FN5 protein (FN5), mRNA. /// NM_024116 // downstream // 92044 // Hs.355750 //	FN5	FN5, Homo sapiens FN5 protein (FN5), q21
SNP_A-2308868	gctttgtacctaacaa[A/G]gacaatgctgagattt	A	G	81328 // Homo sapiens olfactory receptor, family 4, subfamily A, member 15 (OR4A15), mRNA. /// ENST00000314706 //	OR4A15	OR4A15, Homo sapiens olfactory receptor, family 4, subfamily A, member 15 (OR4A15), q11
SNP_A-2277404	gagcaaaaggccaaac[A/C]atgtagcctaggtgtg	A	C	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2258748	ctttggtaaaacttc[A/G]aaacaggcagtctgtg	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2272075	gaccctggattaacg[A/C]agttagatgccttgg	A	C	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2266318	gaaggtattggaggaac[C/T]caaactagtgaagaaa	C	T	Homo sapiens zinc finger protein 410 (ZNF410), mRNA. /// ENST00000324593 // intron // 0 // --- // --- // --- ///	ZNF410	ZNF410, Homo sapiens zinc finger protein 410 (ZNF410), q24.3
SNP_A-1898097	tgctgtggtccaagac[C/T]atgtctggtgatgattt	C	T	// 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// NM_152616 // upstream // 32701 // Hs.343487 // TRIM42 //	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1931131	ttccatctggaatttta[C/T]ggactaaacagaagt	C	T	COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 24239 //	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-1923382	ttaggaggctgctcat[C/G]agacttttcagctac	C	G	/// ENST00000340783 // downstream // 20816 // --- // --- // ---	-	p13.3
SNP_A-1921368	ttaccacacatacaac[G/T]gaattaaacttttaca	G	T	Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1911361	tgtcttacggcctaa[C/G]cacaaacgagcccgtt	C	G	8383 // Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), mRNA. /// NM_002550 // downstream	OR1A1	OR1A1, Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), p13.3
SNP_A-1912843	cctgtaaatcttgcac[C/G]ctgtcatcccttccaa	C	G	sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.1
SNP_A-1917536	tgttttcttttgcaa[C/T]gttatctcccagcaca	C	T	7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// NM_003667 // upstream //	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-1956869	tttaactactgcaga[C/G]tactggctccatttcc	C	G	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1987613	agctcagaaatttccc[A/G]cagatctgggctgagt	A	G	9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 273354 // Hs.300834 // GALNT2	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. , q42.13
SNP_A-1975142	ttctcatacagtcttac[C/T]ggatttcagcacaggt	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1853395	tatttccctcatca[C/T]tctatgctttttaa	C	T	Homo sapiens fibrous sheath interacting protein 1 (FSIP1), mRNA. /// ENST00000350221 // intron // 0 // --- // --- // ---	FSIP1	FSIP1, Homo sapiens fibrous sheath interacting protein 1 (FSIP1), q14
SNP_A-1872132	aatgcaatgctacaag[A/C]agctttcaaggccgtt	A	C	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q25.1
SNP_A-1816239	gttactggtggaagaca[A/G]ggtaccaggagggagt	A	G	43849 // Homo sapiens kallikrein 12 (KLK12), transcript variant 2, mRNA. /// NM_145895 // upstream // 18572 //	KLK12	KLK12, Homo sapiens kallikrein 12 (KLK12), transcript variant 2, q13.41
SNP_A-1796964	ggttctaagtggaaga[C/G]agaagcagaatagaga	C	G	// --- /// ENST00000328955 // upstream // 106348 // --- // --- // ---	-	q24.23
SNP_A-2118126	agtaaacgttcaggac[C/T]cagcagttgcatttta	C	T	CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 150445 // Hs.298705 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2118820	agtaccttctaaagct[C/G]aatatgcacatacaac	C	G	/// ENST00000332660 // downstream // 808441 // --- // --- // ---	-	p12.3
SNP_A-2137865	atcattctcaaatgaa[C/T]tactgtgaccccagtg	C	T	sapiens tensin (TNS), mRNA. /// ENST00000335713 // intron // 0 // --- // --- // --- /// ENST00000017887 // intron // 0 // ---	TNS	TNS, Homo sapiens tensin (TNS), q35

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2132215	atagtaaaataacaaa[C/T]agtgcagacaaggcag	C	T	1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 5325 // Hs.498513 // AKR1C2 // 16	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste ,p15.1
SNP_A-2214282	cctacagtctaacta[C/T]gtggtaggctgaggca	C	T	ENST00000261778 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-2201148	ccaagtgcaattcaaa[C/G]ttctgtggcctaaaag	C	G	ENST00000340515 // intron // 0 // --- // --- // ---	-	q31.3
SNP_A-2189451	cagttggcttccttcca[C/T]agtgagtgatccaaga	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // --- // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4),	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2077368	accacacaacctcatta[A/G]aaagtctattgaac	A	G	mRNA. /// NM_002430 // downstream // 767356 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2078092	accaggccaagcagtc[A/G]caagttcaagagccca	A	G	30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds, p23.1
SNP_A-2071216	acactgtttcttaatc[A/G]ctgtattagaagatta	A	G	Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // ---	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2074202	acataaccatacccag[A/C]atatgaaattggtgg	A	C	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // intron // 0 // Hs.414110 // KCND3 // DKFZP4341116 // 25962 // Homo sapiens DKFZP4341116	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2068637	acaataaatgaagaag[C/G]attgatagaaattggaa	C	G	protein (DKFZP4341116), transcript variant 2, mRNA. /// NM_015496 // upstream // 56132 // Hs.202238 //	DKFZP4341116	DKFZP4341116, Homo sapiens DKFZP4341116 protein (DKFZP4341116), transcript variant 2, q22.1
SNP_A-2068768	acaatatcacttctgg[C/G]caatttgtggttatac	C	G	sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// ENST00000265526 // intron // 0 // --- // --- // ---	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-2052885	aagtcatatgcatttat[C/T]caggcttgactgggat	C	T	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2033978	aaatcacaggctgaaa[C/T]gatgttttttttc	C	T	Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 // intron // 0 // --- // --- // ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2037139	aacaaaagttccatga[A/G]acattagtgaatcccc	A	G	Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, mRNA. /// ENST00000355752 // intron // 0 // --- // --- // --- /// ENST00000360042 // intron	TBRG4	TBRG4, Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, p13
SNP_A-2000977	attggccaaatgttca[A/G]tatataaacttatgac	A	G	Homo sapiens coiled-coil domain containing 3 (CCDC3), mRNA. /// ENST00000281144 // intron // 0 // --- // --- // ---	CCDC3	CCDC3, Homo sapiens coiled-coil domain containing 3 (CCDC3), p13
SNP_A-1997359	ctctaagcatcttcaa[A/G]caatcagtgccatttt	A	G	8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 444610 // Hs.279522 // NR4A3 //	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-2017432	aaccccataacataa[C/G]gcacatagcactttcc	C	G	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2008325	aaggaaatgaggattc[C/T]aggctcctgcctcac	C	T	112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// NM_153645 // upstream // 128271 //	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-2049032	aagcctgttctccag[A/G]cctccaagtgtttctg	A	G	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 164528 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2067667	acaacaagtgttaatg[G/T]atatgtcaaaggggat	G	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1549468 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2076126	acattcattcataaa[G/T]tattgcttagttcta	G	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2093770	agaagaggaaaaaaaa[A/C]cctaatgtgtatagtg	A	C	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 286455 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2190766	catagaatgaaggggg[C/T]aattcaaagcattaga	C	T	4747 // Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRNA. /// NM_024940 // upstream // 185119 //	NEFL	NEFL, Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), p21.2
SNP_A-2188201	cagtcctggactcatc[C/T]aaaatatcctatcatat	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2207279	ccattccgtttgcttc[A/G]cttcctcactcattcg	A	G	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2131218	atagagatgaacatga[C/T]atagaccagacctggt	C	T	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- // --- ///	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2136960	atcagcaacagtgtta[G/T]aaagttttgtacctgt	G	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2129725	atacagtatgtagtat[A/G]aagcaaagacaaaaat	A	G	Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2130966	atagaacagggaaatc[A/G]attaatcaaatctagg	A	G	Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // intron // 0 // Hs.13640 // ROBO1 // 6091 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.3
SNP_A-2126727	ataaacgacgataatg[G/T]cagaatccagaatgtt	G	T	3776 // Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), mRNA. /// NM_016121 // upstream //	KCNK2	KCNK2, Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), q41
SNP_A-2117363	aggtggtaatagtgtc[A/G]cctccatctgttgatc	A	G	Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (KCNN3),	KCNN3	KCNN3, Homo sapiens potassium intermediate,q22
SNP_A-2158628	attgtatggatgaagc[A/G]agctcatctctgtgaa	A	G	Homo sapiens olfactomedin-like 2B (OLFML2B), mRNA. /// ENST00000294794 // intron // 0 // --- // --- // --- // ---	OLFML2B	OLFML2B, Homo sapiens olfactomedin-like 2B (OLFML2B), q23.3
SNP_A-2149541	atgtagctttgagtct[A/G]aagtttgtagggcagg	A	G	1833 // Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// NM_007035 // downstream // 26674 //	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2141306	atctgtctccaggaga[A/G]aagaatgcattactcc	A	G	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 163043 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1796582	ggttactagagtcaag[A/G]aagagtagggggtggg	A	G	Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// ENST00000307296 // intron // 0 // --- //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-1786795	ggctttcctatcaata[A/T]ctaagggatgaagata	A	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 66012 // --- // --- // --- // --	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1805153	gtcattaaatctttaa[G/T]ctccaacatctcattt	G	T	57182 // Homo sapiens mRNA for KIAA1223 protein, partial cds. /// ENST00000281131 // upstream // 250464 // --- // --- //	KIAA1223	KIAA1223, Homo sapiens for KIAA1223 protein, partial cds. ,q28.1
SNP_A-1814415	gtgtgatagcagacct[C/G]aagtgatataatcaac	C	G	// 9695 // Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), mRNA. /// ENST00000295399 // upstream // 175158 // --- // --- // --- // ---	EDEM1	EDEM1, Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), p26.1
SNP_A-1814434	gtgtgatctttgacaa[A/C]catttattctctccag	A	C	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 82408 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-1812193	gtggagggaaggggcc[A/G]acccaaaaatgcacca	A	G	ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 50434 // --- // --- //	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1780760	ggatcctgttgctcca[A/G]attgaaccaagatagg	A	G	ENST00000348904 // intron // 0 // --- // --- // --- // ---	-	i p12.3
SNP_A-1839337	tagagtctggacaaca[C/T]ctgtttacactggcct	C	T	55033 // Homo sapiens FK506 binding protein 14, 22 kDa (FKBP14), mRNA. /// NM_032639 // upstream // 662 //	FKBP14	FKBP14, Homo sapiens FK506 binding protein 14, 22 kDa (FKBP14), p15.1
SNP_A-1834969	tacccacatcaataaa[A/C]cagtacaaaaacaccc	A	C	Homo sapiens zinc finger protein 291 (ZNF291), mRNA. /// ENST00000324767 // intron // 0 // --- // --- // --- // --- ///	ZNF291	ZNF291, Homo sapiens zinc finger protein 291 (ZNF291), q24.3
SNP_A-1866920	tccctagtcaaggaca[A/G]agcagtggttttatca	A	G	84064 // Homo sapiens haloacid dehalogenase-like hydrolase domain containing 2 (HDHD2), mRNA. /// NM_016097 // downstream // 3788 // Hs.130917 // IER3IP1 //	HDHD2	HDHD2, Homo sapiens haloacid dehalogenase-like hydrolase domain containing 2 (HDHD2), q21.1
SNP_A-1867651	tccgtgtaacttaacc[C/T]atcctgattaatggaa	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 566543 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1846850	tatcacaaccaggtaa[C/T]tgacatgtataaaatg	C	T	/// ENST00000360575 // upstream // 9395 // --- // --- // --- // --- /// ENST00000231482 // upstream // 100735 // --- // --- // --- // -	-	q31.1
SNP_A-1973649	cagggattcgagtata[A/G]catctttccccgttcc	A	G	Homo sapiens hypothetical protein MGC4308 (MGC4308), mRNA. /// NM_182909 // intron // 0 // Hs.104672 // DOC1 //	MGC4308	MGC4308, Homo sapiens hypothetical protein MGC4308 (MGC4308), q12.1
SNP_A-1965418	tcatacacgtaaatct[C/T]aatctggaaggaagat	C	T	Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 //	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1966763	catcttcagaggcaaa[C/T]ggtggatcatgagaat	C	T	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // --- // --- // --- // --- /// ENST00000260943 // intron //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977139	tttacactggatgtcc[A/C]agggcagaaaacaggc	A	C	// 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /// NM_000222 // upstream // 82881 // Hs.479754 // KIT // 3815	PDGFRA	PDGFRA, Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), q12
SNP_A-1959900	ttttgtctgccataac[C/T]atgatactttactagt	C	T	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495 // intron // 0 // Hs.484678 // TBC1D7 // 51256 //	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-1936958	ttctttggtttgttcc[A/G]atcaagtagtttattt	A	G	LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 //	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-1884098	tgaagcctaacacaaa[C/T]ctgctcttagtttcat	C	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1882063	tcttttgtgtatatgg[A/C]attgcgactactgcaa	A	C	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA. /// ENST00000248594 // intron // 0 // --- // --- // --- // ---	PTPN12	PTPN12, Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), q11.23
SNP_A-2263064	gaacacagaaagaaaa[A/G]tagacagcccttcagg	A	G	ENST00000288466 // intron // 0 // --- // --- // --- // ---	-	q32
SNP_A-2285001	ataataaaagcaaaaa[C/T]ttctaacacatattta	C	T	// 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1558054 // Hs.24212 // LPHN2	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2232807	ctcactgttctatata[C/G]cataaaaaaagtcagc	C	G	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA. /// ENST00000261479 // intron // 0 // --- // --- // --- // ---	PSMA6	PSMA6, Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), q13.2
SNP_A-2232894	ctcagaagccaaatga[G/T]aagttgaaactgtaat	G	T	57097 // Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), mRNA. /// NM_001759 // upstream // 221353 // Hs.376071 // CCND2 // 894 // Homo sapiens cyclin	PARP11	PARP11, Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), p13.32
SNP_A-2241652	ctgataggaaaataac[A/C]atgcttcagggacaca	A	C	// Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// NM_030906 // downstream // 8883 // Hs.501833 //	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-2309124	gctttttgtaaaacc[G/T]gctcctttgaagtgca	G	T	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2312533	ggacctcagaggggga[C/T]gaatggctgactacca	C	T	D4S234E // 27065 // Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// NM_016930 // upstream // 308381 //	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.2
SNP_A-2312821	ggactgcagtttgaga[A/G]agacagcgaaggagct	A	G	Homo sapiens nuclear transcription factor Y, beta (NFYB), mRNA. /// NM_000980 // upstream // 126305 // Hs.337766 //	NFYB	NFYB, Homo sapiens nuclear transcription factor Y, beta (NFYB), q23.3
SNP_A-2294546	gcagtcggggacttca[A/T]gtggttccctttgggc	A	T	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 3 (CBFA2T3), transcript variant 2, mRNA. /// NM_005187 // intron // 0 // Hs.513811 // CBFA2T3	CBFA2T3	CBFA2T3, Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 3 (CBFA2T3), transcript variant 2, q24.3
SNP_A-1912988	tgtggaccggtaacag[C/T]agttccaccaggatgc	C	T	3215 // Homo sapiens homeo box B5 (HOXB5), mRNA. /// NM_018952 // downstream // 1298 // Hs.98428 // HOXB6 //	HOXB5	HOXB5, Homo sapiens homeo box B5 (HOXB5), q21.32
SNP_A-1908384	tgtacttggaaaatag[C/T]agtgaacatgacaaaa	C	T	ENST00000338994 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-1932748	ttccttctttaacaca[C/T]tccaaaatgccagtat	C	T	Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000296626 // CDS // 0 // --- // --- // --- // ---	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1941225	ttgctggatgttctgc[A/C]ctagccatatctttcc	A	C	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 851306	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1941956	ttggaggcaaagcgga[C/T]gtttgatttgtagctt	C	T	Homo sapiens nucleoredoxin (NXN), mRNA. /// ENST00000336868 // intron // 0 // --- // --- // --- // ---	NXN	NXN, Homo sapiens nucleoredoxin (NXN), p13.3
SNP_A-1955990	tttgtctatgcagctg[G/T]caagattacactcact	G	T	ENST00000360397 // intron // 0 // --- // --- // --- // ---	-	q25
SNP_A-1986947	tctttctgacatactg[A/G]caaatttccctctctt	A	G	10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// NM_015323 //	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-1986577	acccaccaaaatggaa[C/T]caaagtgaaaatatct	C	T	SH3BGRL2 // 83699 // Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA. /// NM_022726 // downstream // 161230 // Hs.101915 //	SH3BGRL2	SH3BGRL2, Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), q14.1
SNP_A-1848797	tatgatctctggtata[C/G]ctacaaaacaaacttt	C	G	5954 // Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA. /// NM_000378 //	RCN1	RCN1, Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), p13
SNP_A-1863630	tccaacaagtatattc[A/G]caccattgttttgtct	A	G	// Homo sapiens hypothetical protein FLJ10116 (FLJ10116), mRNA. /// NM_018441 // downstream // 11140 // Hs.281680	DSU	DSU, Homo sapiens hypothetical protein FLJ10116 (FLJ10116), q35
SNP_A-1865114	tccagttactactgaa[A/G]ctttgatgatctattc	A	G	5718 // Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, mRNA. /// NM_002816 // downstream // 25335 // Hs.4295 //	PSMD12	PSMD12, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, q24.2
SNP_A-1834725	taccagaaatgacaag[C/T]actttgaagaccttct	C	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 511772	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1837630	tacttacaaatatca[A/C]attatgattctaacag	A	C	// Homo sapiens minichromosome maintenance deficient domain containing 1 (MCMDC1), mRNA. /// ENST00000243218 // intron // 0 // --- // --- // --- ///	MCMDC1	MCMDC1, Homo sapiens minichromosome maintenance deficient domain containing 1 (MCMDC1), q22.31
SNP_A-1782736	ggcagaaaatatgtct[C/T]aatgtgttcagctggc	C	T	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 426269 // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1717383	aaaatatgctgtaagtaaggtgac[C/T]ccacagagtttgtttggctgcatg	C	T	9486 // carbohydrate sulfotransferase 10 /// NM_024065 // upstream // 139483 // Hs.406178 // PDCL3 // 79031 //	CHST10	CHST10, rs2309801, carbohydrate sulfotransferase 10, q11.2
SNP_A-1716005	aaatatttgaagcagcttacaataa[C/T]gtatatactaatagacaatcagaat	C	T	79772 // hypothetical protein FLJ22344 /// NM_152548 // upstream // 253615 // Hs.276287 // FLJ25333 // 153643 //	FLJ22344	FLJ22344, rs3906470, hypothetical protein FLJ22344, q15
SNP_A-1810994	ctaagtcactgttgta[C/G]cctagcaagttatttc	C	G	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 209001 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q21
SNP_A-1804046	tgaaaggagaaaataa[C/T]aggttataaactgttg	C	T	// Homo sapiens carboxylesterase 1 (monocyte/macrophage serine esterase 1) (CES1), mRNA. /// NM_016280 //	CES1	CES1, Homo sapiens carboxylesterase 1 (monocyte,q12.2
SNP_A-2147379	atggagcttgccactc[A/G]aagtgtggtttgagga	A	G	914 // Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), mRNA. /// NM_020440 // upstream // 20076 //	CD2	CD2, Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), p13.1
SNP_A-2145556	atgcatactgacttga[C/T]atgcatgagttattt	C	T	Homo sapiens hypothetical protein FLJ20054 (FLJ20054). mRNA. /// NM_144977 // intron // 0 // Hs.497279 // FAM31B //	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-2154005	attatatctttttcaa[A/G]gtggtgaaaatcaaat	A	G	--- /// ENST00000355156 // upstream // 239996 // --- // --- // ---	-	q24.3
SNP_A-2167512	caacatgggaattaa[A/G]ggagacatgacagata	A	G	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2110611	aggacagtgccttgcat[G/T]gtagtaggcactcaag	G	T	sapiens retinoid X receptor, gamma (RXRG), mRNA. /// ENST00000271387 // intron // 0 // --- // --- // --- ///	RXRG	RXRG, Homo sapiens retinoid X receptor, gamma (RXRG), q23.3
SNP_A-2113005	aggccaaatggatgccc[A/G]aggaactctaaccctc	A	G	Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), mRNA. /// ENST00000359382 // intron // 0 // --- // --- // --- ///	OFCC1	OFCC1, Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), p24.3
SNP_A-2134980	atattcaggccaatgcc[C/G]cagtaaggactggtaa	C	G	Homo sapiens TRAF interacting protein (TRIP), mRNA. /// ENST00000331456 // intron // 0 // --- // --- // ---	TRIP	TRIP, Homo sapiens TRAF interacting protein (TRIP), p21.31
SNP_A-2132129	atagtagaaacacat[C/T]aagggataggcctggg	C	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2225308	cgtttactgtggcaac[G/T]gcatgtaccaatgcat	G	T	6582 // Homo sapiens solute carrier family 22 (organic cation transporter), member 2 (SLC22A2), transcript variant 1, mRNA. /// NM_153191 // upstream // 60709 // Hs.436385 //	SLC22A2	SLC22A2, Homo sapiens solute carrier family 22 (organic cation transporter), member 2 (SLC22A2), transcript variant 1, q25.3
SNP_A-2196255	catgtgtgagaagtgc[A/T]cccaagtctatgacct	A	T	/// ENST00000354196 // upstream // 502903 // --- // --- // --- /// ENST00000355224 // upstream // 502903 // --- // --- // ---	-	q21.11
SNP_A-2196064	catgtgaaagaaaccac[C/G]agaaagttaaagtgg	C	G	10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream //	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.32
SNP_A-2180830	cagaatccaaacaact[A/G]acagtaacaaggattg	A	G	Homo sapiens mRNA for KIAA0611 protein, partial cds. /// ENST00000311637 // intron // 0 // --- // --- // --- ///	ATP9A	ATP9A, Homo sapiens for KIAA0611 protein, partial cds. .q13.2
SNP_A-2103511	agcaatgtgctagac[A/G]ctttaaattaaactg	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2050078	aaggaatttgaagaaaa[C/T]aaagtagttatgta	C	T	79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 150346	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2008038	gcaatttttggtttaa[C/T]tcgtgtatttatgag	C	T	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2027372	aaacatggtttaatag[A/G]acacaatttctaagat	A	G	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2035958	aaattaaaggataaaa[C/T]gaagttgagaagttt	C	T	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-2003428	agcacaatctcagaga[A/G]aacaggaagaggtgag	A	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1991522	gttgtatggtgttca[C/T]attaaagggaatgtag	C	T	Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// ENST00000312952 // intron // 0 // --- // --- ///	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2100582	agatacagaaattaaa[G/T]gtgagccatcatcaca	G	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 472433 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2092788	agaaatgtccagcaga[A/G]ggaattagatatgaa	A	G	FLJ46321 // 389763 // Homo sapiens FLJ46321 protein (FLJ46321), mRNA. /// NM_152573 // downstream // 434014	FLJ46321	FLJ46321, Homo sapiens FLJ46321 protein (FLJ46321), q21.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098072	agagaggaccttacat[A/G]acctgacggagctgaa	A	G	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2175065	cacagtcagtcttccaa[C/T]agagttggccctctgtg	C	T	200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 754213 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2198798	catttctggcttggaa[A/C]ctagaagtggaaactc	A	C	28996 // Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// NM_030984 // upstream //	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-2215987	cctccagggaacggac[C/T]gtaagctgcaacagct	C	T	// Homo sapiens rho/rac guanine nucleotide exchange factor (GEF) 18 (ARHGEF18), mRNA. /// ENST00000319670 //	ARHGEF18	ARHGEF18, Homo sapiens rho p13.2
SNP_A-2203325	ccacttgttctcaaaa[G/T]atcctattgatttggc	G	T	Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), mRNA. /// ENST00000258991 // intron // 0 // --- // --- //	HT008	HT008, Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), q23.3
SNP_A-2126932	ataaaggcagaggcta[A/C]ataaaagtaaacaatt	A	C	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 370182 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2124354	agttatttgcagagca[C/T]ataaaggaaccaaaaag	C	T	26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// NM_015224 // downstream // 118320 //	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2130139	atacccgacacatggg[A/G]atcaattccctttttac	A	G	114571 // Homo sapiens solute carrier family 22 (organic anion/cation transporter), member 9 (SLC22A9), mRNA. ///	SLC22A9	SLC22A9, Homo sapiens solute carrier family 22 (organic anion q12.3
SNP_A-2117257	aggtggaaccagaacc[A/G]aatcctgaggaggccg	A	G	Homo sapiens cyclic nucleotide gated channel beta 1 (CNGB1), mRNA. /// ENST00000251102 // CDS // 0 // --- // --- //	CNGB1	CNGB1, Homo sapiens cyclic nucleotide gated channel beta 1 (CNGB1), q13
SNP_A-2116955	aggtgaacatccatac[A/G]ccatactttctctc	A	G	Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // intron // 0 // --- // --- // ---	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2116168	aggtaagtcttttaa[C/T]aagtaatgttggaatg	C	T	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 295995 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2165079	caaacttaggaatgat[G/T]acgaacgaagaaaacc	G	T	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. ///	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2162593	atttctataaatgaa[A/C]taatacctgcgttctt	A	C	2209 // Homo sapiens Fc fragment of IgG, high affinity Ia, receptor for (CD64) (FCGR1A), mRNA. /// ENST00000271699 // downstream // 182796 // --- // --- // --- //	FCGR1A	FCGR1A, Homo sapiens Fc fragment of IgG, high affinity Ia, receptor for (CD64) (FCGR1A), q21.1
SNP_A-1806411	gtcctttaatgcaga[A/G]tatcccagatcatata	A	G	Homo sapiens splicing factor, arginine/serine-rich 11 (SFRS11), mRNA. /// ENST00000235399 // intron // 0 // --- // -	SFRS11	SFRS11, Homo sapiens splicing factor, arginine p31.1
SNP_A-1795944	ggtgggtcagactagt[G/T]acatctcagtgatcag	G	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1795637	ggtgcttcagataaca[A/G]ctcaaatattacatga	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 229701 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1783120	ggcaggacacgactcc[A/G]gatcctcgggctgaat	A	G	Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // ---	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-1866955	tccctcaaaaatgttc[C/T]aacactctagcatct	C	T	Homo sapiens scavenger receptor cysteine-rich type 1 protein M160 (M160), mRNA. /// ENST00000313599 // intron	M160	M160, Homo sapiens scavenger receptor cysteine-rich type 1 protein M160 (M160), p13.31
SNP_A-1854627	tcaacaattatttacc[A/G]aattcaaacagaagga	A	G	23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 176156 // Hs.87083 //	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds, q34
SNP_A-1978347	tgaagcacttctgtag[C/T]cactgaaattctgtag	C	T	80319 // Homo sapiens CXXC finger 4 (CXXC4), mRNA. /// NM_017628 // upstream // 287238 // Hs.367639 // FLJ20032	CXXC4	CXXC4, Homo sapiens CXXC finger 4 (CXXC4), q24
SNP_A-1973826	gtttcgatgttgattal[C/T]ctttgctattgagta	C	T	56987 // Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// NM_198793 // downstream // 85731 //	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1974086	agaccagttgctgga[A/T]aactcagaagggagac	A	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1971741	ctgaagtacatcctta[C/T]gttcctagatttcatg	C	T	ENST00000286050 // intron // 0 // --- // --- // ---	-	q24.2
SNP_A-1969382	aggctcttcacaatac[A/G]actccacttatgttcc	A	G	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 99438 // --- // --- // --- // --- ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds., q21.1
SNP_A-1957230	ttttactggtcaatat[A/G]agaagctttccataat	A	G	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 580008 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1959962	ttttgtaacagtaa[C/T]gaatctgtagttta	C	T	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 1251633 // --- // -	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946287	tttaaaagcaagttta[A/G]ctgcctaaatgtatga	A	G	Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1944292	ttgtcccttaggagta[C/T]aaactcatttcctctga	C	T	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1124456 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1938808	ttgaggaacttaatga[A/G]gaacataatcatttgcc	A	G	Homo sapiens RNA-binding protein (FLJ20273), mRNA. /// ENST00000319592 // intron // 0 // --- // --- // ---	FLJ20273	FLJ20273, Homo sapiens RNA-binding protein (FLJ20273), p14
SNP_A-1874659	tctcctctgtttctta[A/C]attgcaactatataca	A	C	Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1874412	tctcccaactctctaa[A/G]taagatagaaattgtcc	A	G	Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // --- // -	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1897840	tgctggctaactgtag[A/G]ccatttgaaaaatgtg	A	G	54763 // Homo sapiens ropporin, rhophilin associated protein 1 (ROPN1), mRNA. /// NM_003947 // upstream // 46870 //	ROPN1	ROPN1, Homo sapiens ropporin, rhophilin associated protein 1 (ROPN1), q21.1
SNP_A-1891066	tgatggttccacaagga[C/G]gaggcgcatgacaatag	C	G	Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-2304043	gctccagaaccatgag[C/T]caaataagtctttct	C	T	Homo sapiens choline phosphotransferase 1 (CHPT1), mRNA. /// ENST00000229266 // intron // 0 // --- // --- // ---	CHPT1	CHPT1, Homo sapiens choline phosphotransferase 1 (CHPT1), q23.2
SNP_A-2248698	ctgttccagagaaaac[A/G]cgaggactggtctggt	A	G	5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // upstream // 80766 // Hs.459035 //	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-2251167	cttatttgaccaggag[A/T]catgttttccattaa	A	T	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// ENST00000199168 // intron // 0 // --- // --- // ---	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-2230860	ctatgcctttcaagta[A/G]gccatgacaaaaaaaa	A	G	// 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000360501 // downstream // 74237 // --- //	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2240403	ctgacacaacagatac[A/G]ctctatatttgttgaa	A	G	79053 // Homo sapiens asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase) (ALG8), mRNA. /// ENST00000299626 // upstream // 4658 // --- // --- //	ALG8	ALG8, Homo sapiens asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase) (ALG8), q14.1
SNP_A-2282445	gagttctctccacaa[C/T]gcatggctctagagt	C	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 28834 // --- // --- // ---	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2256426	ctttatgataaatgcc[A/G]aagccaggtagcataa	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 464437 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2259267	gaaaaagaaaatctca[A/G]attccacacatggtca	A	G	Homo sapiens dynein, cytoplasmic, light intermediate polypeptide 1 (DNCLI1), mRNA. /// ENST00000273130 //	DNCLI1	DNCLI1, Homo sapiens dynein, cytoplasmic, light intermediate polypeptide 1 (DNCLI1), p23
SNP_A-2275165	gagaagccaactacaa[A/G]agcccatcgagtccat	A	G	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2239463	ctctttgtggtttcct[C/G]aaatggcactgctta	C	G	Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA. /// ENST00000317931 // intron // 0 // --- // --- // ---	L3MBTL4	L3MBTL4, Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), p11.31
SNP_A-2240839	ctgagaaccttaataa[C/T]tcctgccttcccagca	C	T	Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), mRNA. /// ENST00000355866 // intron //	ITGBL1	ITGBL1, Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), q33.1
SNP_A-2252038	cttccacagcacacctc[C/T]acaccacctccaagca	C	T	Homo sapiens chromosome 14 open reading frame 43 (C14orf43), mRNA. /// ENST00000286523 // intron // 0 // --- // - // 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box	C14orf43	C14orf43, Homo sapiens chromosome 14 open reading frame 43 (C14orf43), q24.3
SNP_A-2307835	gcttctacattagaca[C/T]gatcagccgaagaagg	C	T	polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1892182	tgcaaatccgttgtca[C/T]ctccttaaaaaatcct	C	T	KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// NM_005752 // upstream // 20682 //	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1898334	tactgatttactcagg[A/C]atgaaatatgtaacgc	A	C	Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // --- // --- // ---	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-1884090	tgaagcccatgcaaaa[C/T]gctgcctttgggatgc	C	T	399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 241930 // Hs.299419 //	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds. q25
SNP_A-1885188	tgaattccaaaccaca[C/T]ctatccctagcttcc	C	T	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1906383	tggtgccctttcataa[A/T]gcagaaagtgttgag	A	T	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1915508	tgttcggtcccttaa[C/T]gcaaattctggcaaca	C	T	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 136810 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-1938607	ttgagagatttgagca[G/T]ataaaattaaaaactt	G	T	9699 // Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // downstream // ---	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1937381	ttgaaatagagcagt[A/G]gtatgagaactaactg	A	G	sapiens histidine decarboxylase (HDC), mRNA. /// ENST00000267845 // intron // 0 // --- // --- // --- // ---	HDC	HDC, Homo sapiens histidine decarboxylase (HDC), q21.2
SNP_A-1967956	gttgcacctggtggga[C/T]agttacacctcaatt	C	T	Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000355755 // intron // 0 // --- // ---	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1985826	ctaaattggcagagtat[G/T]atcatctaaagccaaa	G	T	23304 // Homo sapiens chromosome 6 open reading frame 133 (C6orf133), mRNA. /// NM_000322 // downstream // 4361	UBR2	UBR2, Homo sapiens chromosome 6 open reading frame 133 (C6orf133), p21.1
SNP_A-1985387	tgttaaacaggtctaa[A/T]tcacaatgaatgacaa	A	T	6659 // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA. /// NM_000948 // downstream // 93048 // ---	SOX4	SOX4, Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), p22.3
SNP_A-1983355	accatatctgaatgta[C/G]gctgttagaagcagctc	C	G	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // ---	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1866021	tcccactcccctgccac[A/G]aacatttctaaagga	A	G	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // ---	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1861480	tcatccaagcgtatggg[A/T]catggtctttaaaat	A	T	// 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 305834 // Hs.102408 // ---	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1836215	tactatccgacatcaa[A/G]tcttactgcagacatt	A	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 413534 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1817731	gttcccttcagaataa[A/G]taacagctcaactccc	A	G	Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1797758	ggtttgtggagtctct[A/G]acctgtatcctcctgc	A	G	Homo sapiens mRNA for KIAA1057 protein, partial cds. /// ENST00000294383 // intron // 0 // --- // --- // --- // ---	USP24	USP24, Homo sapiens mRNA for KIAA1057 protein, partial cds., p32.3
SNP_A-1799366	gtaatatttaagata[A/G]gtaccgattcaaaggt	A	G	Homo sapiens vacuolar protein sorting 13D (yeast) (VPS13D), transcript variant 1, mRNA. /// ENST00000356315 // intron // 0 // --- // --- // --- /// ENST00000358136 // intron	VPS13D	VPS13D, Homo sapiens vacuolar protein sorting 13D (yeast) (VPS13D), transcript variant 1, p36.22
SNP_A-1785443	ggctcaaatcttggaa[C/G]tgtccactggtgtagc	C	G	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream // ---	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1802198	gtatatacctatgcct[A/G]aatttttccatcattg	A	G	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), mRNA. /// ENST00000035383 // intron // 0 // --- // --- // --- // ---	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1810502	gtgatttcatcatcaa[C/T]cgaaatgagacatttt	C	T	Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // ---	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2140605	atctctaagtaataaaa[C/G]ccacttcatgtaactt	C	G	170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // --- // --- // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2201740	ccacaagtgcagtcca[A/G]gaaagatgtagcctgt	A	G	11197 // Homo sapiens WNT inhibitory factor 1 (WIF1), mRNA. /// ENST00000229088 // downstream // 161000 // ---	WIF1	WIF1, Homo sapiens WNT inhibitory factor 1 (WIF1), q14.3
SNP_A-2224498	cgtatcaccatttttta[C/T]agctgccacactatta	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2142593 // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2198504	catttatcacagccta[C/T]gaagtgggaaatgaga	C	T	79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 30547 // ---	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2101459	agatgaaagtctaaca[C/T]tgccttttaaagataa	C	T	Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // --- // --- // --- // ---	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2102254	tgatcgctcagattca[A/C]gatccagacttttaa	A	C	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // ---	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2063614	aattaccaaaaatgta[C/T]gctgtggcagacggca	C	T	SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // ---	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-2024511	aaaaggagttgcaccc[A/G]agacaatctatctagg	A	G	401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 682681 // Hs.115903 // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2022563	aaaaatgaacaaacgg[A/G]atcacatcaagttaca	A	G	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2894206 // --- // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2032914	aaataatagagatcca[A/T]ccttagggagccatttg	A	T	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // ---	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2037547	aacaactagtgaaaag[C/T]aaatagttctggttac	C	T	MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 585996 // Hs.314261 //	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q32
SNP_A-2067088	acaaacttggaaccaa[A/G]agacaaactccaggcc	A	G	23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2057132	aatataagcagaaaaa[A/G]tgcttttgtcttttat	A	G	Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // --- // --- // --- // ---	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2097610	agagaatattacgtga[C/T]agctatagcagagaaa	C	T	FLJ35630 // 166379 // Homo sapiens hypothetical protein FLJ35630 (FLJ35630), mRNA. /// NM_002006 // upstream //	FLJ35630	FLJ35630, Homo sapiens hypothetical protein FLJ35630 (FLJ35630), q27
SNP_A-2191728	catattgctgctatgc[C/T]atagacacctttgggc	C	T	Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // --- // --- // --- // ---	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2185386	caggacacacctata[A/C]aaaatctgaaacaaaa	A	C	Homo sapiens Src-like-adaptor 2 (SLA2), transcript variant 1, mRNA. /// NM_175077 // intron // 0 // Hs.517020 // SLA2 //	SLA2	SLA2, Homo sapiens Src-like-adaptor 2 (SLA2), transcript variant 1, q11.23
SNP_A-2176121	caccacagctaaaaaa[G/T]ccatttaaatatgaca	G	T	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2222114	cgaatatgtcaaaata[C/T]actatgaaaggccaga	C	T	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 539259 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2218949	cctggtcaatgtgaca[A/G]tcaaggagcagtatgg	A	G	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2217787	cctgattcttccagac[A/T]gagttagtctttctcc	A	T	Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // --- // --- //	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine,q23.1
SNP_A-2161122	atttgaacaaatcata[C/T]gtctgatctcttttc	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 474616 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2155810	attcccttatggttta[G/T]gattgtctagtccaca	G	T	// Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // upstream // 1721 // Hs.307720 //	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-2120738	agtcctcactacctga[A/G]cgctgtgaacacacat	A	G	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1580090 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2123525	agtgtgcttacacaaa[C/G]aaatctggatcgtata	C	G	sapiens cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA. /// ENST00000341529 // intron // 0 // --- // ---	CDH5	CDH5, Homo sapiens cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), q22.1
SNP_A-2136443	atcacatggagtccaa[A/G]tgacccttgacaatcc	A	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1782846	ggcagagcaaggaaga[A/G]tagacctgagagatga	A	G	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1757119	atttctgtctagttttcatggggag[C/T]ccttaagtcattggcaaacaattca	C	T	9406 // zinc finger protein 265 /// NM_173808 // downstream // 174878 // Hs.479888 // NEGR1 // 257194 // neuronal	ZNF265	ZNF265 , rs10493483, zinc finger protein 265 ,p31.1
SNP_A-1816107	gttaccaaatgtgccc[A/G]gattcctgctccctgg	A	G	// 7386 // Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), mRNA. /// ENST00000304863 // upstream // 167699 // --- // --- // --- // ---	UQCRFS1	UQCRFS1, Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), q12
SNP_A-1819566	gttggttggccaacaa[C/T]gaggtggtggtggttt	C	T	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 205729 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1843397	tagtgaagtgatggaa[G/T]atgatcaaaaaggtaa	G	T	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// ENST00000341681 // intron // 0 // --- // --- // --- // --- /// ENST00000263881 // intron //	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-1864343	tccactcattttcaac[A/G]cgactattgagaggac	A	G	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 411150	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1852746	tatttcatcgcttatc[C/T]acaaccgtataagaca	C	T	4843 // Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, mRNA. /// NM_153292 // upstream // 21772 // Hs.462525 // NOS2A //	NOS2A	NOS2A, Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, q11.2
SNP_A-1850763	tattacttcagctata[C/T]aaaattattgttgaga	C	T	// 6280 // Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA. /// NM_005621 //	S100A9	S100A9, Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), q21.3
SNP_A-1846151	tatatcaagggcaaag[A/C]attttgtgatttatga	A	C	Homo sapiens WD repeat domain 26 (WDR26), mRNA. /// ENST00000295024 // intron // 0 // --- // --- // --- // ---	WDR26	WDR26, Homo sapiens WD repeat domain 26 (WDR26), q42.12
SNP_A-1938440	ttgacttatactgggc[A/G]attactgctgtccttt	A	G	Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000345497 // intron // 0 // --- // --- // --- // ---	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936209	ttcttcagcagttgaa[C/G]ctaaagactgggtgca	C	G	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // --- // ---	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1
SNP_A-2296107	ctatctccccataaaa[A/C]tagacagttcaaacag	A	C	ENST00000331090 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2252731	cttcgtgtcaaacctc[A/G]gactttcacttaataa	A	G	2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1662340 // Hs.514980 // SALL3 //	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2237451	ctctcctctcctccac[A/G]ctattgtagcacactg	A	G	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2269912	gacaatctctgtaaga[A/C]aatcacaggttgataa	A	C	2176 // Homo sapiens Fanconi anemia, complementation group C (FANCC), mRNA. /// NM_000264 // downstream //	FANCC	FANCC, Homo sapiens Fanconi anemia, complementation group C (FANCC), q22.32
SNP_A-2237029	ctctattatctatccc[G/T]ctgcctaatttattta	G	T	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2239620	ctgaaaatggataaaa[A/G]cacttggaagctctgt	A	G	140880 // Homo sapiens cystatin 11 (CST11), transcript variant 2, mRNA. /// NM_130794 // upstream // 20430 //	CST11	CST11, Homo sapiens cystatin 11 (CST11), transcript variant 2, p11.21
SNP_A-2230496	ctatccagctaccca[C/T]ggtcctactgactttc	C	T	375323 // Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), mRNA. /// ENST00000287585 //	LOC375323	LOC375323, Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), p25.3
SNP_A-2242554	ctgcaggcaagtcatg[C/T]agtcaccctgactctg	C	T	81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // intron // 0 // --- // --- // --- // --- /// ENST00000281924 // intron // 0 // --- // ---	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-2307124	gcttaaaatctataaa[G/T]cagtgtgtaaatgcaa	G	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1940711	ttgccttctcacatat[C/T]agtgcaggtgcaggtc	C	T	91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream //	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-1952405	tttctctttgaaccaa[G/T]gaattttggaaatatg	G	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1988650	tttcacccacttgtag[A/G]catagctgtggggcac	A	G	KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 90460 //	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1964958	cctggaaaaacacaga[C/G]agtgctgctgccttat	C	G	Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase (MGAT5), mRNA. /// ENST00000281923 // intron // 0 // --- // --- // --- // ---	MGAT5	MGAT5, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase (MGAT5), q21.3
SNP_A-1974455	agtccacctgggagaa[A/G]ctctcatctgcagcaa	A	G	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // CDS // 0 // --- // --- // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-1904583	tggggcagctttagca[A/C]cttgccagggctctag	A	C	Homo sapiens neuregulin 2 (NRG2), transcript variant 2, mRNA. /// NM_013983 // intron // 0 // Hs.408515 // NRG2 //	NRG2	NRG2, Homo sapiens neuregulin 2 (NRG2), transcript variant 2, q31.2
SNP_A-1932972	ttcgagctctcaaaac[A/G]gaagggaaatagaatt	A	G	51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// NM_016559 // upstream // 78160 //	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-1930682	ttccacattcagtgtg[C/G]aattgtttttctgta	C	G	Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // --- // --- // --- // ---	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1919591	ttaaggcatgacatta[C/T]acatttctaacaagct	C	T	Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, mRNA. /// NM_004105 // intron // 0 // Hs.76224 // EFEMP1 // 2202 //	EFEMP1	EFEMP1, Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, p16.1
SNP_A-1899755	tggaatgcactttcca[C/T]cttgctgcaaggacag	C	T	// Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 86589 // Hs.314543 // CTNND2	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1845420	tatagaaagcctggta[C/T]gactgactccaggcat	C	T	374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // upstream // 40566 // --- // --- // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-1844423	tataaactctttaagc[A/G]atcctgatatgatttc	A	G	FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 276915 //	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1871221	tctaaaagcgattttc[A/C]aaataggtagtatagg	A	C	2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 3992 // Hs.479853 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1828415	taagatttgaacagga[G/T]gatgtatgtatcagtc	G	T	4741 // Homo sapiens neurofilament 3 (150kDa medium) (NEF3), mRNA. /// NM_006158 // downstream // 19224 //	NEF3	NEF3, Homo sapiens neurofilament 3 (150kDa medium) (NEF3), p21.2
SNP_A-1787321	gggaagataaaataga[C/G]gttgttgacattcttt	C	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 394672 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2120433	agtcattgagaatcat[C/T]ataataagctccacaa	C	T	CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 214295 // Hs.437444 // CACNA1E // 777 //	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage dependent, alpha 1E subunit (CACNA1E), q25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2211763	ccctcgtccatagaaaa[C/T]ctcgggttcagtgggag	C	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2099119	agaggaccttcccata[C/T]gcccatcttatcagg	C	T	Homo sapiens EH domain binding protein 1 (EHBP1), mRNA. /// ENST00000263991 // intron // 0 // --- // --- // ---	EHBP1	EHBP1, Homo sapiens EH domain binding protein 1 (EHBP1), p15
SNP_A-2094895	agaatgacctaattaa[C/T]tggcatttggcaaat	C	T	Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000264463 // intron // 0 // --- // --- // ---	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-2078061	accaggaagtaaaca[C/T]gtggaccacttgtgt	C	T	/// Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// ENST00000341547 // upstream // 76694 // --- // ---	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2083051	acgtgtgcagataaca[C/T]agaagtaaaataccag	C	T	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2050329	aaggagctcagactgt[C/T]aagtaatgggggaagcc	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// ENST00000356100 /// 3UTR // 0 // --- // --- // ---	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2026467	aaacaaactatccccac[A/G]cttgtaatttttgta	A	G	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1994190	ctattcaacaaaacattt[A/G]aaatgaatcacaaact	A	G	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 898631 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2002299	acaaattaaatagcac[C/T]acaaggaagtgatcag	C	T	5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 308193 //	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2049955	aaggaagagttgcaccc[A/T]cagtaacttaaatca	A	T	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 394237 // Hs.497822 // DUSP10 // 11221 //	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2052666	ctctgtctgcatgagt[C/T]accattcttgatgact	C	T	1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // downstream // 244667 //	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2058692	gaaaaaggagtaacag[A/G]attagatttttggaaaa	A	G	57228 // Homo sapiens hypothetical protein from clone 643 (LOC57228), mRNA. /// NM_016187 // downstream // 3694 //	LOC57228	LOC57228, Homo sapiens hypothetical protein from clone 643 (LOC57228), q13.13
SNP_A-2063086	aatgttctctggatc[A/G]agtaggtttcagtcac	A	G	/// ENST00000342224 // downstream // 34087 // --- // --- // ---	-	p11.21
SNP_A-2081024	acctgaagaaaactat[G/T]aagaaagtctgtagtt	G	T	// Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 255415 // Hs.451286 // C15orf2 //	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-2097417	agagaaaatatatcaca[C/G]actactggaaaggaa	C	G	--- /// ENST00000345111 // upstream // 917845 // --- // --- // ---	-	q24.31
SNP_A-2104863	agcatagctggaaaga[C/T]gcctcggaaaacatgg	C	T	DKFZp434G0625 // 91584 // Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), mRNA. /// ENST00000251675 // upstream // 29374 // --- // --- // ---	DKFZp434G0625	DKFZp434G0625, Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), q32.3
SNP_A-2118390	agtaagatagaagcgg[C/T]agtcctggcttccagc	C	T	10882 // Homo sapiens complement component 1, q subcomponent-like 1 (C1QL1), mRNA. /// NM_024819 // downstream // 44988 // Hs.463148 // FLJ22955 // 79877 //	C1QL1	C1QL1, Homo sapiens complement component 1, q subcomponent-like 1 (C1QL1), q21.31
SNP_A-2125911	agtttaacgttgaa[A/G]acttttgccaaacttt	A	G	/// ENST00000237253 // downstream // 211811 // --- // --- // ---	-	q12
SNP_A-2142586	atgaacctttacagc[A/C]ccctctgtggcagtc	A	C	ENST00000332168 // intron // 0 // --- // --- // ---	-	p22.2
SNP_A-1781145	ggatggaaacgtcctc[C/T]accactaaggaaaaca	C	T	// Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /// ENST00000297435 // upstream // 16412 // --- // ---	DEFA4	DEFA4, Homo sapiens defensin, alpha 4, corticostatin (DEFA4), p23.1
SNP_A-1707293	atggcagttttctaaaatagatata[C/T]atgagtaaaagagaaccacacaaag	C	T	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa	EIF3S10	EIF3S10, rs952253, eukaryotic translation initiation factor 3, subunit 10 theta, 150,q26.11
SNP_A-1843496	tagtgattattatac[G/T]gatttttccattgtta	G	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1904169	tgggcccccaaagaca[A/C]agaccagctggtgac	A	C	Homo sapiens mosaic serine protease (MSP), mRNA. /// ENST00000278940 // intron // 0 // --- // --- // --- ///	MSP	MSP, Homo sapiens mosaic serine protease (MSP), q23.3
SNP_A-1906265	tggtgaggcacagga[C/T]ggaacggcagggccctt	C	T	Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// ENST00000356408 // intron // 0 // ---	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-1965121	atgtgtggtaagacta[C/T]ggaaagtcatctcgta	C	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1966708	cttataccttataac[G/T]gaagcataattagaaa	G	T	ENST00000331169 // intron // 0 // --- // --- // ---	-	q34
SNP_A-1979110	gggtgccagtaaagaa[C/T]agattcaactagagca	C	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 715673 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946134	ttgttttaaatgaaa[C/T]ttcttgtgcttgtcca	C	T	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-1938413	ttgactggaggcaatc[A/C]accttgtacaaccttc	A	C	4299 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	MLLT2	MLLT2, Homo sapiens myeloid q22.1
SNP_A-1939417	ttgatgctttcttttct[A/C]aattgttaattcaaat	A	C	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2308543	gctttatgcctgggcc[C/T]gcagagacagagatga	C	T	Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-2301115	gccttccaggctccaa[A/G]tcctggcttcaggga	A	G	115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream //	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-2232943	ctcagacctacacctc[C/T]ccatttctcactctct	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 400455 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2233820	ctcatctaagttctga[A/C]cctcaaattggttccc	A	C	ENST00000358349 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-2256377	ctttatccaaaagta[C/G]agctgaacggattgtg	C	G	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 46815 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-2230679	ctatctttctactta[C/G]agaattattgtgagaa	C	G	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 (DDX56), mRNA. /// ENST00000258772 // intron // 0 // --- // ---	DDX56	DDX56, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 (DDX56), p13
SNP_A-2238342	ctctggctggtgtggat[C/G]aagccctaactgaga	C	G	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2242552	ctgcaggattgggctc[C/T]ctctggccagtctggc	C	T	Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // --- // --- // ---	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2294136	gcaggcctagtacata[A/T]ggaatggattcagata	A	T	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 46472 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. ,q23.1
SNP_A-2304000	gctccaagtttcttca[A/T]ggaaaggactgggtta	A	T	1441 // Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, mRNA. /// NM_000760 // upstream // 237276 // Hs.524517 // CSF3R //	CSF3R	CSF3R, Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, p34.3
SNP_A-1981732	ccacctgaagaaattat[C/G]gccagcaaggtgatga	C	G	Homo sapiens RAB3C, member RAS oncogene family (RAB3C). /// ENST00000282878 // intron // 0 // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1907017	tggttgcccatgtggc[C/T]ctgaactagatagaaa	C	T	ENST00000324607 // downstream // 51837 // --- // --- // --- /// ENST00000357722 // downstream // 64012 // --- // --- // ---	-	p22.3
SNP_A-1907322	tgtaaaaaacactaaa[A/C]cattagtaggcagaat	A	C	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 482222	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1904405	tggggaaatccacctc[C/T]aattcctaaccaactc	C	T	1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // upstream //	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-1933018	ttcgccatgataaccca[A/G]gctggccttgaactcc	A	G	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // --	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1896213	tgcgggtctcaaaaa[C/T]atctcaaaccaccagta	C	T	// Human mRNA for integrin alpha 6. /// NM_000210 // downstream // 13739 // Hs.133397 // ITGA6 // 3655 // Homo	ITGA6	ITGA6, Human for integrin alpha 6. q31.1
SNP_A-1880597	tcttgcccagtttcac[A/T]gtatattgtatgaaca	A	T	Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // --- // --- // ---	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-1842612	taggtttcagtgtgtgca[A/G]aagactcatacaatca	A	G	// 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 3005210 // --- // -	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1848667	aaacccatgctatctg[C/T]aaggtaggcctatgtt	C	T	Homo sapiens chloride channel 6 (CLCN6), transcript variant CIC-6a. mRNA. /// NM_021735 // intron // 0 // Hs.193043 //	CLCN6	CLCN6, Homo sapiens chloride channel 6 (CLCN6), transcript variant CIC-6a, p36.22
SNP_A-1855630	tcaataattcgacatt[G/T]aaacatctcctcaaaa	G	T	1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 116076 // Hs.72901 // CDKN2B	CDKN2B	CDKN2B, Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3
SNP_A-1858342	tcagacacagagatgt[C/T]aaaaggtgttaaataa	C	T	// Homo sapiens myeloid inhibitory C-type lectin-like receptor (MICL), transcript variant 2, mRNA. /// NM_138337 // intron // 0 // Hs.190519 // CLEC12A // 160364 // Homo sapiens	CLEC12A	CLEC12A, Homo sapiens myeloid inhibitory C-type lectin-like receptor (MICL), transcript variant 2, p13.31
SNP_A-1780689	ggatcagtcaagctca[A/G]agcaagattgaataac	A	G	11181 // Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), mRNA. /// ENST00000264029 //	TREH	TREH, Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), q23.3
SNP_A-1783049	catccaaaagcagtga[C/G]atgaccattcaagagc	C	G	Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // intron // 0 // Hs.527984 //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1728363	tcttctgtcatgcagctgacaatcc[A/T]agtgggagtgacagtgaagaaccag	A	T	9315 // chromosome 5 open reading frame 13 /// NM_022140 // downstream // 269617 // Hs.104746 // EPB41L4A // 64097	C5orf13	C5orf13 , rs6890246, chromosome 5 open reading frame 13, q22.1
SNP_A-1788803	gggattgaaggagcctg[C/G]agaacagaatcacaag	C	G	// 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 448854 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.2
SNP_A-1792813	ggtaataaaatcatca[A/C]cttaatatgggaatg	A	C	// 55314 // Homo sapiens hypothetical protein FLJ11155 (FLJ111155), mRNA. /// ENST00000296529 // downstream //	FLJ111155	FLJ11155, Homo sapiens hypothetical protein FLJ111155 (FLJ111155), q32.1
SNP_A-1810179	gtgatctcaggataaa[A/C]cccctggcaagacag	A	C	Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-1814069	gtgtccccacctatca[A/C]gtctggatgtataga	A	C	// Homo sapiens hypothetical protein FLJ31547 (FLJ31547), mRNA. /// ENST00000319165 // intron // 0 // --- // --- // --- // ---	FLJ31547	FLJ31547, Homo sapiens hypothetical protein FLJ31547 (FLJ31547), q12.2
SNP_A-1805924	gtcccttaaggtgaa[A/G]taacctgggaatgttt	A	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 300685 // Hs.33368 // MCTP2 // 55784 // Homo	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2146249	atgctaatgagaagac[A/G]aatgactgaaaattag	A	G	6654 // Homo sapiens son of sevenless homolog 1 (Drosophila) (SOS1), mRNA. /// NM_003618 // downstream //	SOS1	SOS1, Homo sapiens son of sevenless homolog 1 (Drosophila) (SOS1), p22.1
SNP_A-2149243	atgtaagtagaaacca[C/T]atgcggaacctgggtt	C	T	55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// NM_001444 // upstream // 197179 // Hs.408061 // FABP5 //	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-2154828	attcaagtaattctta[A/C]aactgccattttctat	A	C	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	SMARCA3	SMARCA3, Homo sapiens SWI q24
SNP_A-2157199	attgaatgcaggctta[A/G]atagttccctctacct	A	G	Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1347501 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2160830	attctcccgagttta[G/T]actggagctcatttta	G	T	// 25950 // Homo sapiens RWD domain containing 3 (RWDD3), mRNA. /// ENST00000354428 // downstream //	RWDD3	RWDD3, Homo sapiens RWD domain containing 3 (RWDD3), p21.3
SNP_A-2216653	cctctcagtccgctaa[A/G]tgtgaacttccccagc	A	G	// 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// NM_000882 // upstream // 45354 //	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2175568	cacatgacctagtga[C/T]gtctggtaacaaaaga	C	T	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 443059 // Hs.131489 // PARD3	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2173314	cacaagacctaggaga[C/T]agtagctgcacaataa	C	T	11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 125834 // Hs.526879 // PTPRT //	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-2190994	cataggagtttcacaa[C/T]tgctatacagtgggtg	C	T	// Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), mRNA. /// ENST00000355700 // intron // 0 // ---	PHGDHL1	PHGDHL1, Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), q32.3
SNP_A-2192670	catccatttgcctgggt[A/G]aaattgttaaaatatt	A	G	Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA. /// ENST00000272716 // intron // 0 // --- // --- // --- // ---	SLC4A10	SLC4A10, Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), q24.2
SNP_A-2101067	agatcacataaaaggc[A/G]aattgcttcattatcc	A	G	Homo sapiens chromosome 6 open reading frame 170 (C6orf170), mRNA. /// ENST00000314282 // intron // 0 // --- //	C6orf170	C6orf170, Homo sapiens chromosome 6 open reading frame 170 (C6orf170), q22.31
SNP_A-2095681	agacacagtggagaaac[A/C]atacagacatggcat	A	C	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1010698 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2084604	actatgtctgttagta[A/G]gagtctgctgagaggc	A	G	// 57045 // Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), mRNA. /// NM_006788 // upstream //	TWSG1	TWSG1, Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), p11.22
SNP_A-2007372	tgcttaagagtctagg[A/G]caatttggtgatacta	A	G	// 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 //	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-2010817	tcagaaaatgtgagca[C/T]gtcccgtgagactcaa	C	T	Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // --- // --- // --- // ---	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2024939	aaaataaagagattta[C/G]accctgaagagagatc	C	G	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2031140	aaaggcacacatctag[C/T]aaagagcagagccaag	C	T	Homo sapiens chromosome 13 open reading frame 12 (C13orf12), mRNA. /// ENST00000255315 // intron // 0 // --- //	C13orf12	C13orf12, Homo sapiens chromosome 13 open reading frame 12 (C13orf12), q12.3
SNP_A-2033377	aaatagctaccacccaa[C/T]catagccactcactaa	C	T	5325 // Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA. /// NM_002656 // upstream // 51262 // Hs.444975 // PLAGL1 // 5325 // Homo	PLAGL1	PLAGL1, Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, q24.2
SNP_A-2037119	aacaaaagactatcaa[C/T]gaaaccactgaaact	C	T	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2002238	tttatagatttttatg[C/T]actttgaaatgagagt	C	T	// 341032 // Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), mRNA. ///	MGC50104	MGC50104, Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), q23.1
SNP_A-1990335	agtatacataactgac[A/T]ctgcccaaattactga	A	T	sapiens hepatocyte growth factor (hepapoietin A; scatter factor) (HGF), mRNA. /// ENST00000222390 // intron // 0 // ---	HGF	HGF, Homo sapiens hepatocyte growth factor (hepapoietin A; scatter factor) (HGF), q21.11
SNP_A-2077846	accagagaccctctca[A/G]tcccatatgagtcgga	A	G	1493 // Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA. /// NM_012092 // upstream //	CTLA4	CTLA4, Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), q33.2
SNP_A-2080149	accgtcaccttccact[G/T]aatgtaggactgatgg	G	T	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2087069	actgagtttcagagac[A/G]acttgaaaggcgatga	A	G	Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2073397	acaggtcccagagcta[A/C]gactattgtaacgaac	A	C	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 557285 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2056041	aatacatcctatctga[C/T]aaactaattacagtgt	C	T	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2125602	agtttccattagacaa[C/G]ggctggagatctatta	C	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 932331 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2115599	agggtacacaaagttc[C/T]ccagttggtcactggg	C	T	// Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 82135 // Hs.156316 // DCN //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1802775	gtatgctgcacataat[A/T]atgactgaagaagtac	A	T	8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 318464 //	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1807528	gtctgcttgtaacgaa[A/G]taagatttttgaatct	A	G	/// ENST00000336930 // upstream // 1101379 // --- // --- // --- //	-	p14.3
SNP_A-1822109	gttttctcttctttaa[A/T]cacctctcttcacttg	A	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2359933 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1815486	gtgtttttccttttaag[A/G]ccaaagacagcaaatt	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1925573	ttatgaatctctctac[A/C]agaagaaagaacccat	A	C	3176 // Homo sapiens histamine N-methyltransferase (HNMT), mRNA. /// NM_001001664 // upstream // 300198 //	HNMT	HNMT, Homo sapiens histamine N-methyltransferase (HNMT), q22.1
SNP_A-1909811	tgtcaccaaaactctt[C/T]aacatgactatagatt	C	T	157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-1915453	tgttcctcagagacca[A/G]tggctggtaagtaatg	A	G	Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA. /// NM_152700 // CDS // 0 // --- // --- // 0 // --- /// ENST00000358251 // intron // 0 // --- // --- // --- // -	TXNDC5	TXNDC5, Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, p24.3
SNP_A-2289346	gattttaagacttctc[C/G]actatcctaaggccac	C	G	// 54462 // Homo sapiens KIAA1128 (KIAA1128), mRNA. /// ENST00000359979 // downstream // 146113 // --- // --- // --- //	KIAA1128	KIAA1128, Homo sapiens KIAA1128 (KIAA1128), q23.1
SNP_A-2232561	tggcacaacgactgac[C/T]agtctgagaatcgttc	C	T	Homo sapiens chromosome 14 open reading frame 111 (C14orf111), mRNA. /// ENST00000238591 // intron // 0 // ---	C14orf111	C14orf111, Homo sapiens chromosome 14 open reading frame 111 (C14orf111), q24.3
SNP_A-2275345	gagaatatagactctg[A/G]attgatttttaaaaca	A	G	Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), mRNA. /// ENST00000259253 // intron // 0 // --- // --- // --- // ---	UGCGL1	UGCGL1, Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), q14.3
SNP_A-2282232	gagttaaatccaccac[A/G]gagttactagatcact	A	G	-- /// ENST00000340000 // upstream // 331016 // --- // --- // ---	-	p12.1
SNP_A-2265954	gaaggaggcccctaga[A/G]cagagtatggcatctg	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2232815	ctcacttagatgatga[C/G]agagggtttatccacc	C	G	Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// ENST00000287647 // intron // 0 // --- // -	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-2235241	ctcccgccagggaaac[A/C]agacagaggcccaggt	A	C	// Homo sapiens Rho GTPase activating protein 10 (ARHGAP10), mRNA. /// ENST00000336498 // intron // 0 // ---	ARHGAP10	ARHGAP10, Homo sapiens Rho GTPase activating protein 10 (ARHGAP10), q31.23
SNP_A-2242615	ctgcagtgaagtccta[C/T]aggatatggccctgct	C	T	10077 // Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, mRNA. /// NM_005705 //	PHEMX	PHEMX, Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, p15.5
SNP_A-2296282	gcattggacaaaatcc[A/G]acatccattcatgaaa	A	G	// 989 // Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), mRNA. /// AF118079 // upstream // 269223 // --- // --- // 0 // Homo sapiens PRO1854 mRNA,	SEPT7	SEPT7, Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), p14.2
SNP_A-2296499	gcatttgctgcgaaga[G/T]aaagaaatgaagggac	G	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 316274	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2297150	gccacaggtccgcagc[A/G]agttcgtggcgggcag	A	G	// Homo sapiens hypothetical protein LOC90529 (LOC90529), mRNA. /// ENST00000350501 // intron // 0 // --- // --- // --- // --- // ---	LOC90529	LOC90529, Homo sapiens hypothetical protein LOC90529 (LOC90529), p36.11
SNP_A-2303619	gctcaccaaaaaaattc[A/G]aaggaaaaagctaagga	A	G	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-1913833	tgtgtcctgtgcattg[A/G]aaatggacaacagagg	A	G	60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 184905 // Hs.462270	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-1874586	tctcctagaatgtaaa[A/G]tgttatagagaaaat	A	G	// 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// NM_018682 // upstream // 153472 // --- // --- // ---	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1885424	tgacaaatataagcca[A/G]agactattaactgcta	A	G	// 0 // --- // --- // --- // ENST00000356616 // intron // 51046 // Homo sapiens sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase) (SIAT8C), mRNA. /// NM_004852 // upstream // 11624 // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 90632 // --- // --- // --- // ---	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1886731	tgactgaaggatgcca[A/G]gacagtttcaagggtc	A	G		ST8SIA3	ST8SIA3, Homo sapiens sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase) (SIAT8C), q21.31
SNP_A-1887187	tgagaaatgacataaa[A/C]tacatctcaccca	A	C		SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1965008	aggcctacctttccac[C/T]tgtcatgtaacttct	C	T	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1974136	ccacgttgttagtctt[C/T]aagaccatgcacaata	C	T	152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1957459	tttagttgtctttcaa[A/G]taatctgtatatcaltt	A	G	sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA. /// NM_033497 // intron // 0 // Hs.370365 // HK1 // 3098 // Homo	HK1	HK1, Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, q22.1
SNP_A-1955606	tttggttttattgcgat[C/T]agtaaagaaagaagatt	C	T	// 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1855593	tcaataacctgaacac[G/T]gaacaagtgtggaatg	G	T	// 54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// NM_144651 // downstream // 40643 // Hs.444882	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-1791752	gggtcttattaggagc[C/T]acatacagtggagaga	C	T	SEC23IP // 11196 // Homo sapiens SEC23 interacting protein (SEC23IP), mRNA. /// NM_000982 // downstream // 205361 // 22918 // Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), mRNA. /// NM_013248 // upstream // 193864 // Hs.516933 // NXT1 // 29107 // Homo	SEC23IP	SEC23IP, Homo sapiens SEC23 interacting protein (SEC23IP), q26.12
SNP_A-1783802	ggccaaagtcctgaaa[C/T]gtggtctccatacacc	C	T		C1QR1	C1QR1, Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), p11.21
SNP_A-2120805	agtcctcatctcttta[C/T]gccacaatgctacatt	C	T	Homo sapiens CDW92 antigen (CDW92), mRNA. /// NM_080546 // intron // 0 // Hs.494700 // CDW92 // 23446 //	CDW92	CDW92, Homo sapiens CDW92 antigen (CDW92), q31.1
SNP_A-2126246	ataaaaagtctaacaa[A/C]aatttatatgtgtatg	A	C	ENST00000299064 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2158757	attgtctggttgactg[A/G]agttagggaagtgggt	A	G	sapiens breakpoint cluster region (BCR), transcript variant 1, mRNA. /// NM_021574 // intron // 0 // Hs.517461 // BCR // 613	BCR	BCR, Homo sapiens breakpoint cluster region (BCR), transcript variant 1, q11.23
SNP_A-2141217	atctggtgcgcagcaa[A/G]gctagcaaacaatgct	A	G	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // intron // 0 // Hs.365690 // KCNK10 // 54207 // Homo sapiens	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-2191833	catcaaaaaaaacaaaaa[A/G]gtgaatgttggcaaga	A	G	SEC23IP // 11196 // Homo sapiens SEC23 interacting protein (SEC23IP), mRNA. /// NM_000982 // downstream // 286092 //	SEC23IP	SEC23IP, Homo sapiens SEC23 interacting protein (SEC23IP), q26.12
SNP_A-2175927	caccaaaagaaggtaa[C/T]gacagaatagcaatcc	C	T	Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // intron // 0 // --- // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-2203776	ccagagcaggggaggga[C/T]gaatgtaccatctact	C	T	// 79762 // Homo sapiens hypothetical protein FLJ14146 (FLJ14146), mRNA. /// NM_017898 // upstream // 42059 //	FLJ14146	FLJ14146, Homo sapiens hypothetical protein FLJ14146 (FLJ14146), q41
SNP_A-2073527	acagtaaggggaatggga[A/C]ctctctgtgcatcaat	A	C	Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2084684	actaattcctctgctg[A/C]aatgctctccctctga	A	C	ENST00000342608 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-2094226	agaaggtagctttgga[A/G]ccaaaccaagaaaggt	A	G	Homo sapiens PDZ domain containing 8 (PDZK8), mRNA. /// ENST00000298474 // intron // 0 // --- // --- // --- // ---	PDZK8	PDZK8, Homo sapiens PDZ domain containing 8 (PDZK8), q26.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1994071	tatttccttagtaaac[C/T]caatggtcaggcatga	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1402599 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1996109	agaatttgcctaccac[C/G]atagtttcttgttaac	C	G	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 181716 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2015647	gaaacacctggaatat[A/G]acctcagatttccttt	A	G	Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000284878 // intron // 0 // --- // ---	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2033740	aaatatgtttccccaa[A/T]tctctgcatggcttaa	A	T	286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 1122681 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2044813	aagaaatgcccaacat[C/G]actaatcgttagagaa	C	G	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip /// NM_025003 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 /	ADAMTS20	ADAMTS20, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip q12
SNP_A-2023884	aaaagaagaaacacaa[A/G]ctgagctagacattta	A	G	Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 2, mRNA. /// NM_013448 // intron // 0 // Hs.509140 // BAZ1A // 11177 // Homo sapiens	BAZ1A	BAZ1A, Homo sapiens bromodomain adjacent to zinc finger domain, 1A (BAZ1A), transcript variant 2, q13.1
SNP_A-2023845	aaaagaaatcttctct[A/G]accttccaactctaaa	A	G	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2031657	aaagtaatcccatgga[A/C]aaagagcttattaaat	A	C	Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// ENST00000355044 // intron // 0 // --- // --- // --- // --- ///	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2028871	aaactttactctttct[A/C]acccatgaatactgat	A	C	Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // --- // --- // --- // --- ///	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2017979	tgaaaggaattttaaa[A/G]cccagctattgtagat	A	G	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2000499	tgagcagggaaatatc[A/G]cccaagaagtctatca	A	G	89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2073647	acagtcacaattaaaa[A/G]tgctttctaataacga	A	G	203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream // 440266	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2212121	ccctgcctgctacaga[A/G]cacacaggcagatggg	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2213068	ccgactttccaggcac[A/G]gctagtttcttcctag	A	G	Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // --- // --- // --- // --- ///	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2193047	catctaacacctgcct[C/T]aactaagtaggaggaa	C	T	4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB037860 // downstream // 39233 // Hs.191911 // NFIA //	NFIA	NFIA, Homo sapiens nuclear factor I p31.3
SNP_A-2152228	attaaaggcaaaggga[A/G]gaaatacatctgggct	A	G	388697 // Homo sapiens mRNA for hornerin, partial cds. /// ENST00000316073 // upstream // 29242 // --- // --- // --- // ---	HRNR	HRNR, Homo sapiens for hornerin, partial cds. ,q21.3
SNP_A-2158927	attgtgtggagaaggg[A/G]caaagtactcaggaag	A	G	// 80745 // Homo sapiens THUMP domain containing 2 (THUMPD2), mRNA. /// NM_021097 // downstream // 235068	THUMPD2	THUMPD2, Homo sapiens THUMP domain containing 2 (THUMPD2), p22.1
SNP_A-2159582	atttactcacacggca[A/G]atattactgagcatct	A	G	// 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 206250 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2133088	atatagaaataacact[A/C]acctgatttgcatagc	A	C	// 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000357839 // upstream // 28108 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1721435	ctgaattcatcccctcaatggaata[C/T]ctttgggccatctgaaaactacaca	C	T	NM_152989 // intron // 0 // Hs.87224 // SOX5 // 6660 // SRY (sex determining region Y)-box 5	SOX5	SOX5 , rs10505933, SRY (sex determining region Y)-box 5,p12.1
SNP_A-1662794	atacacctaacaagttaagatatca[A/G]agtacaattggaaaagtatagaaaa	A	G	NM_024624 // intron // 0 // Hs.424559 // SMC6L1 // 79677 // SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	SMC6L1	SMC6L1 , rs10495668, SMC6 structural maintenance of chromosomes 6-like 1 (yeast),p24.2
SNP_A-1798480	gtaaatgatgggcagg[A/T]aaagagggttgaagat	A	T	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 51066 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1854439	tcaaatgaattaatag[C/G]catttgatatgcaaat	C	G	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 460858	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1844872	tataatccaaataaac[C/T]gtcaattctattgtca	C	T	2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// NM_207506 // downstream // 142923 // Hs.492653 //	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.12
SNP_A-1816898	gttattactgccaatc[C/T]ctaccaggaaaggttg	C	T	201895 // Homo sapiens hypothetical protein LOC201895 (LOC201895), mRNA. /// ENST00000295958 // intron // 0 // ---	LOC201895	LOC201895, Homo sapiens hypothetical protein LOC201895 (LOC201895), p14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826699	taacagaattcaaacc[A/G]cattagaagcatcata	A	G	FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream //	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-1842593	taggttgtatattgtc[A/C]aagactcttctctgtc	A	C	Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // --- // ---	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-1956220	tttgtgtaaatttcta[C/T]ccaactctgaaaatgt	C	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1959629	ttttggattgtggaag[A/G]cttaatatcacaaata	A	G	253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream //	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-1962503	aagccttaatcaagtg[C/G]acagtgcttgtatcat	C	G	5500 // Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), transcript variant 1, mRNA. /// NM_206876 // upstream // 83997 // Hs.468018 // PPP1CB	PPP1CB	PPP1CB, Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), transcript variant 1, p23.2
SNP_A-1983786	ttcttaaaagcagcat[C/G]acataacgtttcatac	C	G	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1877222	tctgcttctttgcttg[C/G]aaggcttctcagaatg	C	G	Homo sapiens solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), mRNA. /// ENST00000313248 // intron // 0 // --- // --- // --- // --- ///	SLC29A1	SLC29A1, Homo sapiens solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), p21.1
SNP_A-1895127	tgcccattgtggtcaa[C/T]agagaaggaagtggac	C	T	Homo sapiens synaptojanin 2 (SYNJ2), mRNA. /// AF039945 // intron // 0 // Hs.434494 // SYNJ2 // 8871 // Homo sapiens	SYNJ2	SYNJ2, Homo sapiens synaptojanin 2 (SYNJ2), q25.3
SNP_A-2296783	gccaacatgcacagca[C/G]cttgaagatggatttg	C	G	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 47450 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2296040	gcattagaacctgaga[C/T]ccccagatgtttctgc	C	T	5443 // Homo sapiens proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-melanocyte	POMC	POMC, Homo sapiens proopiomelanocortin (adrenocorticotropin,p23.3
SNP_A-2248818	ctgttgaatagcaaga[C/G]aaacccatgtgcccca	C	G	Homo sapiens solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	SLC1A1	SLC1A1, Homo sapiens solute carrier family 1 (neuronal p24.2
SNP_A-2272606	gacgcaatgtgcttga[C/T]gatcaaaagtggtaag	C	T	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 337872 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2258593	cttttctttttttct[A/G]aacagcttcattgaga	A	G	sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), mRNA. /// ENST00000235470 // intron // 0 // --- // --- //	CD2	CD2, Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), p13.1
SNP_A-2283791	gatagggaccctctta[C/T]agtgactgtgcatccc	C	T	sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), mRNA. /// ENST00000303641 // intron // 0 // --- // ---	ROR2	ROR2, Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), q22.31
SNP_A-2275302	gagaagttcgtcaggt[A/G]aatggtagcaaatctg	A	G	// 23507 // Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA. /// NM_032270 // upstream //	TA-LRRP	TA-LRRP, Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), p22.2
SNP_A-2275237	gagaagggcccattga[A/C]aatgtgagttgtaagt	A	C	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2258793	cttttgtggctaataa[C/T]taatagaagtttgata	C	T	LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 //	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2267927	gaatctaaagctactg[A/C]ataataaaaactcatg	A	C	9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 314949 // Hs.300834 // GALNT2	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. ,q42.13
SNP_A-2248524	ctgttaacccacaata[A/C]aatacacagtacagca	A	C	5867 // Homo sapiens RAB4A, member RAS oncogene family (RAB4A), mRNA. /// NM_006542 // downstream //	RAB4A	RAB4A, Homo sapiens RAB4A, member RAS oncogene family (RAB4A), q42.13
SNP_A-2232965	ctcagagaatcagcca[A/G]gcatattttagtttaa	A	G	sapiens dystrobrevin, alpha (DTNA), transcript variant 1, mRNA. /// NM_032975 // intron // 0 // Hs.58919 // DTNA //	DTNA	DTNA, Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, q12.1
SNP_A-2298124	gccatcctgattttca[A/G]gtctattgttgctata	A	G	Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // --- //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-2291077	gcaataagatgtgtac[C/T]agttctccattgcctg	C	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 81374 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1895369	tgcccttgtggttaca[C/T]gacacctgagtctacg	C	T	Homo sapiens ubiquitin specific protease 36 (USP36), mRNA. /// ENST00000312010 // intron // 0 // --- // --- // --- // ---	USP36	USP36, Homo sapiens ubiquitin specific protease 36 (USP36), q25.3
SNP_A-1898351	tgcttcacacaaagta[C/G]atactcaatacatatt	C	G	118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// NM_020799 // upstream // 15669 //	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31
SNP_A-1882235	tgaaaaactgtgagta[C/T]ccaaagtgtgaaaata	C	T	KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 309791 // Hs.486470	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1
SNP_A-1920804	ttacaatctcatttaa[C/T]cctgcaaaaccctaa	C	T	ENST00000327381 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-1977405	cgagatatttgcaaag[A/G]cagtagagatcctctt	A	G	/// ENST00000360919 // upstream // 401420 // --- // --- // --- //	-	q13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944395	ttgtctatgactgaaa[A/G]catttttactttaaca	A	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1941441	ttgcttgccccatagc[A/C]aatcatgtctgtctct	A	C	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, mRNA. /// NM_001001290 // intron // 0 // Hs.444612 //	SLC2A9	SLC2A9, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, p16.1
SNP_A-1840791	tagctatagaacatta[C/T]gattatgacttaatag	C	T	51126 // Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, mRNA. /// NM_016100 // downstream // 14280 // Hs.368783 // NAT5	NAT5	NAT5, Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, p11.23
SNP_A-1834165	tacatcttgagagacc[C/T]ggattctgctattctg	C	T	Homo sapiens plexin A2 (PLXNA2), mRNA. /// ENST00000264296 // intron // 0 // --- // --- // --- // ---	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1859118	tcagcctaccagagga[A/G]taacctttgggtgctt	A	G	sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), mRNA. /// ENST00000286955 // intron // 0 // --- // ---	FUT6	FUT6, Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), p13.3
SNP_A-1792650	ggtaaattgtcataaa[C/G]ttaatgcttcttagat	C	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1790029	ggggaaagaacaacac[A/G]aagtttccaggccttc	A	G	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 126969 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1673376	gtagcagagaacaatcagttgatat[C/T]aaaagcattatttttatctattaaa	C	T	POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 1533874	POLR2B	POLR2B , rs10517446, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12
SNP_A-1784678	ggcctctcctctgcca[C/T]gaagtgggtaatctgg	C	T	/// ENST00000304952 // downstream // 30484 // --- // --- // ---	-	p11.21
SNP_A-2133241	atatataatacctata[A/G]acaaacaacttttacc	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 409136 // --- // --- // --- //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2123460	agtgtctttcacctgc[C/T]atgattctgaggcctc	C	T	// 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// NM_000827 // downstream //	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2119677	agtattaataagaagc[A/G]acagcaataactattt	A	G	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 241954 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2164051	aaagttaacattgtta[C/T]gtgtaaattcgaatct	C	T	1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 286555 // Hs.19904 // CTH // 1491 // Homo	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-2180453	cagaaccatgacgaca[C/T]ccatgttccatcagcc	C	T	9770 // Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), transcript variant 1, mRNA. ///	RASSF2	RASSF2, Homo sapiens Ras association (RalGDS,p13
SNP_A-2168233	caactgacgaattgac[A/C]atttttattcagtgt	A	C	// 221785 // Homo sapiens zinc finger protein 498 (ZNF498), mRNA. /// NM_000777 // downstream // 743 // Hs.150276 //	ZNF498	ZNF498, Homo sapiens zinc finger protein 498 (ZNF498), q22.1
SNP_A-2171530	caatccaggtcagata[C/T]gcaggttgctgattag	C	T	// Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2218453	cctggaatgtgcggga[A/G]agctggggtagcagag	A	G	4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2070577	acacctgctgctggaa[A/T]cactgggaacttcact	A	T	// 26223 // Homo sapiens F-box and leucine-rich repeat protein 21 (FBXL21), mRNA. /// NM_002302 // upstream //	FBXL21	FBXL21, Homo sapiens F-box and leucine-rich repeat protein 21 (FBXL21), q31.1
SNP_A-2058339	aatcaattttatgacc[A/G]aattcttacttgatgt	A	G	79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2061532	aatgctgatttttgta[A/T]gttcattttgtatcct	A	T	3456 // Homo sapiens interferon, beta 1, fibroblast (IFNB1), mRNA. /// NM_002177 // downstream // 37623 // Hs.73010 //	IFNB1	IFNB1, Homo sapiens interferon, beta 1, fibroblast (IFNB1), p21.3
SNP_A-2103847	agcaccttgcagtcaa[A/G]cacccagggaccacat	A	G	// Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase q22.1
SNP_A-2082395	acgcagagccttgagg[C/G]acgggtgatggggttc	C	G	sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /// ENST00000310340 // intron // 0 // --- // --- // --- // --- ///	GPI7	GPI7, Homo sapiens hypothetical protein FLJ20265 (FLJ20265), p16.3
SNP_A-2004124	cttctaaattaaagga[A/G]actattggccgggcga	A	G	Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), mRNA. /// ENST00000326693 // intron //	UBR1	UBR1, Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), q15.2
SNP_A-2002857	cttttcaagccaaccc[A/T]ctgtgtaacctctatg	A	T	3778 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // upstream // 19067 // Hs.144795 //	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2083487	actaaggtcattattc[A/G]cttttcttccccctct	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2095275	agaattgggttagagg[A/C]ccaacttagcagggtt	A	C	Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 // intron // 0 //	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2063976	aattatctgagcacaa[C/T]ctagtgtatgttgcaa	C	T	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 946986 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-2069121	acaattacctctcgaa[C/T]agagcccaattaactg	C	T	/// ENST00000315765 // upstream // 101851 // --- // --- // --- // -- /// ENST00000334665 // upstream // 126297 // --- // --- // ---	-	q21
SNP_A-2213066	ccgacttcaagcccca[C/T]gagaaatccccagccg	C	T	1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 268923 // --- // --- // --- // ---	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2
SNP_A-2169460	caagccccttagggtc[A/C]cagtcagtcacattgg	A	C	Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // intron // 0 // Hs.268942 // ATP2B2 // 491 //	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2171798	caatgaatggggtagc[A/G]agattatccttgttca	A	G	-- /// ENST00000361117 // upstream // 632020 // --- // --- // ---	-	q33.2
SNP_A-2192243	catcaggattgataaa[C/T]gctcattgagtaactg	C	T	/// ENST00000328621 // upstream // 106863 // --- // --- // --- // -	-	q22.1
SNP_A-2197837	cattgagaatcagaaa[A/C]cagctgtatattcttt	A	C	25871 // Homo sapiens DKFZP434F2021 protein (DKFZP434F2021), mRNA. /// NM_033254 // upstream //	C3orf17	C3orf17, Homo sapiens DKFZP434F2021 protein (DKFZP434F2021), q13.2
SNP_A-2145203	atgcaattatattcac[A/T]aatgccacaaaaataa	A	T	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2118992	agtagaatattaaaag[C/G]ctttcaggtctgacag	C	G	Homo sapiens KIAA1117 (KIAA1117), mRNA. /// ENST00000237163 // intron // 0 // --- // --- // --- // --- ///	KIAA1117	KIAA1117, Homo sapiens KIAA1117 (KIAA1117), q14.1
SNP_A-2126150	ggcactgattttgtaa[A/G]gcagagaaagaagcat	A	G	Homo sapiens hypothetical protein FLJ20449 (FLJ20449), mRNA. /// ENST00000218554 // intron // 0 // --- // --- // --- // ---	FLJ20449	FLJ20449, Homo sapiens hypothetical protein FLJ20449 (FLJ20449), q13.3
SNP_A-2127035	aaaaattaagcaatag[A/G]aagtgagtgtgaatac	A	G	CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 //	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1712895	ctttctaaatagtacatagcctttta[A/G]agttacatggatttaggtagaaata	A	G	Clone IMAGE:4825049, mRNA, partial cds /// NM_016279 // upstream // 378233 // Hs.272212 // CDH9 // 1007 // cadherin	-	- , rs4132433, Clone IMAGE:4825049, mRNA, partial cds ,p14.1
SNP_A-1726144	tcttagtctccagattcttcctata[A/T]aatgaaatatctacaaaaagtgcag	A	T	NDUFA4 // 4697 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa /// NM_152745 // downstream // 814692 // Hs.343660 // NXPH1 // 30010 // neurexophilin 1	NDUFA4	NDUFA4 , rs2709072, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa ,p21.3
SNP_A-1792719	ggtaacttatcaatga[C/T]gtaatactcagaactc	C	T	Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-1798081	gtaaaatatttttgag[C/G]atgttcttcaaatata	C	G	9315 // Homo sapiens chromosome 5 open reading frame 13 (C5orf13), mRNA. /// NM_053000 // upstream // 372819 //	C5orf13	C5orf13, Homo sapiens chromosome 5 open reading frame 13 (C5orf13), q22.1
SNP_A-1804048	gtcacaatccatagaa[C/T]gaacactaccaacggt	C	T	91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 121573 //	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-1844416	tataaactagaaagca[C/T]ggctagaaaaaatatc	C	T	ENST00000360406 // intron // 0 // --- // --- // --- // --- /// ENST00000356803 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-1933723	ttctataatgaaactg[C/T]aatggtgaacacatga	C	T	// Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 772602 // Hs.451286 // C15orf2 //	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-1959248	ttttgagtatttcaaa[A/T]catcctaaatttgtaa	A	T	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 141737 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1964052	gttagataatggctaa[A/T]gctaaaaaatacaaaa	A	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1967699	gatatccgtcacatca[A/G]gcatttattatttctt	A	G	Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-1920750	ttacaactgcagtcat[A/G]aagaaagtgctaattt	A	G	79088 // Homo sapiens zinc finger protein 426 (ZNF426), mRNA. /// ENST00000338852 // downstream // 1211 // --- // ---	ZNF426	ZNF426, Homo sapiens zinc finger protein 426 (ZNF426), p13.2
SNP_A-1928669	ttcacttttttctgg[A/G]aacgcctgggcccaac	A	G	5718 // Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, mRNA. /// NM_002816 // downstream // 54460 // Hs.4295 //	PSMD12	PSMD12, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, q24.2
SNP_A-1880500	tcttgatatttcttga[C/T]atgttgatacccttg	C	T	// 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 614626 // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1903037	tggctgtaccttacag[A/G]aagatcaaactcagtg	A	G	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1893346	tgcagcacaatagaca[C/T]aataaaaccttgcttg	C	T	9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 297245 // Hs.269059 // JARID2 //	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2314289	ggaggccagaatatac[C/T]attaacaaaatcttta	C	T	340277 // Homo sapiens hypothetical protein MGC72075 (MGC72075), mRNA. /// ENST00000344962 // intron // 0 // ---	MGC72075	MGC72075, Homo sapiens hypothetical protein MGC72075 (MGC72075), p15.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2232874	ctcagaaatgctaaga[C/T]ataactcagatttgga	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 513635 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2229570	ctaggtctacacagcc[G/T]caaactgcattcagta	G	T	Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2236957	ctctatagaaaatgtg[C/T]atatgaattccttttc	C	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2261827	gaaataaaataggaca[C/G]tcagttatgatgggct	C	G	Homo sapiens fibulin 5 (FBLN5), mRNA. /// ENST00000342058 // intron // 0 // --- // --- // --- // --- ///	FBLN5	FBLN5, Homo sapiens fibulin 5 (FBLN5), q32.12
SNP_A-2254401	cttgcattttgtgata[A/G]gagagtatcatattga	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1078697 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1884389	tgaagtagagtggaga[C/T]ggaaagcactagggct	C	T	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1886485	tgactaactctgttgc[C/T]aactgaaaaaataata	C	T	sapiens STE20-like kinase (yeast) (SLK), mRNA. /// ENST00000192055 // intron // 0 // --- // --- // --- // --- ///	SLK	SLK, Homo sapiens STE20-like kinase (yeast) (SLK), q25.1
SNP_A-1926827	ttatttaatataacag[C/G]attctacatcattaaa	C	G	PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 19019 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1932893	ttcctttgcctgtgtg[C/T]agcaacagttggtagt	C	T	79627 // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA. /// NM_024882 // downstream // 106296 //	OGFRL1	OGFRL1, Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), q13
SNP_A-1931125	ttccatctctaagaaa[C/T]tgactactctaggtgt	C	T	Homo sapiens RAB GTPase activating protein 1 (RABGAP1), mRNA. /// ENST00000317419 // intron // 0 // ---	RABGAP1	RABGAP1, Homo sapiens RAB GTPase activating protein 1 (RABGAP1), q33.2
SNP_A-1916648	tgtttattagttcagt[G/T]aatttatcatttggct	G	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1610473 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1905257	tgggttggagaacata[A/T]cttgagattattactt	A	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1963448	ttacaatatggctgga[A/G]ctctcagacgagaagt	A	G	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-1977107	tgaagagttttgaatt[C/T]aatggtttctactcta	C	T	Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// ENST00000306932 // intron // 0 // --- // --- // --- // --- ///	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1943147	ttggtcattaggttgc[A/G]cccaacgatgaagctg	A	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // CDS // 0 // --- // --- // --- // --- ///	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1835368	tacctccattggtgaa[C/T]gccatttatctctgtc	C	T	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 1006106 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1823923	taaaattaggtcatga[C/T]atcaggaaaatttata	C	T	Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// ENST00000285311 // intron // 0 // --- // --- // --- // ---	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1786788	ggctttccatgtggaa[C/T]tgcaccaaatccttac	C	T	Homo sapiens thioesterase, adipose associated (THEA), transcript variant 2, mRNA. /// NM_015547 // intron // 0 //	THEA	THEA, Homo sapiens thioesterase, adipose associated (THEA), transcript variant 2, p32.3
SNP_A-1781780	ggatttctttttttcat[C/G]aatgagtaaaaaccca	C	G	9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 285308 // Hs.300834 // GALNT2	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13
SNP_A-1697587	taaagtcagagtagtgtgaaaatca[C/T]caacttataaaatacctcagtatga	C	T	CLDN12 // 9069 // claudin 12 /// NM_012395 // upstream // 184759 // Hs.57856 // PFTK1 // 5218 // PFTAIRE protein	CLDN12	CLDN12 , rs10487120, claudin 12 ,q21.13
SNP_A-2131717	atagcgaaaacattgg[A/G]atgttgcttctgagat	A	G	sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // --- // --- // --- // ---	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-2075703	acatggcttgcctgaa[C/T]gtctccctgaggctgt	C	T	FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream //	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2095469	agacaacaaaaaagaa[G/T]gggcaactgaaagaat	G	T	/// ENST00000310012 // upstream // 183768 // --- // --- // --- // -	-	q12
SNP_A-2092349	agaaagctgctaaaaa[C/T]actgatgcccaaacct	C	T	C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 //	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-2026998	aaacagacacagtaga[A/G]cgaaaggacagtaaaa	A	G	Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA. /// ENST00000355470 // intron // 0 // --- // --- // --- // ---	NCOA7	NCOA7, Homo sapiens nuclear receptor coactivator 7 (NCOA7), q22.32
SNP_A-2021987	aaaaagaagcttcaga[G/T]tcatgccttttttatt	G	T	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 117244 // Hs.183817 // USP31 // 57478 //	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2046699	aagagctccccaccaa[C/T]gtacctttgttttcaa	C	T	// Homo sapiens chromosome 20 open reading frame 185 (C20orf185), mRNA. /// ENST00000342109 // intron // 0 // ---	C20orf185	C20orf185, Homo sapiens chromosome 20 open reading frame 185 (C20orf185), q11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2034621	aaatgaaaaacaggaa[C/T]gtgctctgctagtggt	C	T	// 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream //	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2036742	aaatttaattttggag[A/G]catccactaataaaaa	A	G	// 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 66804 // Hs.143080 //	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-2017104	ggttagagttttgcca[A/G]cattctccaagcacaa	A	G	116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000356027 // downstream //	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2093695	agaagacgccatcttc[A/G]cctctgcagtgtgtga	A	G	Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), mRNA. /// ENST00000248070 // intron // 0 // --- // --- // --- // ---	EPS15L1	EPS15L1, Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), p13.11
SNP_A-2106805	agcctgtctgaggacc[A/G]gggttgccgggacaga	A	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 681247 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2082781	acggttcactaaagaa[G/T]ctgagaagagccattt	G	T	DKFZP586H2123 // 25891 // Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, mRNA. /// NM_001001991 // upstream // 96362 //	DKFZP586H2123	DKFZP586H2123, Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, p13
SNP_A-2058931	aatccagcgtttccaa[C/T]gtatataattctctga	C	T	ENST00000277668 // intron // 0 // --- // --- // --- // ---	-	p11.21
SNP_A-2139127	atcctcagaggtagca[C/T]gaaatttggctttgcc	C	T	Homo sapiens folate hydrolase (prostate-specific membrane antigen) 1 (FOLH1), mRNA. /// ENST00000356696 // intron // 0 // --- // --- // --- // --- /// ENST00000256999 // intron // 0 // --- //	FOLH1	FOLH1, Homo sapiens folate hydrolase (prostate-specific membrane antigen) 1 (FOLH1), p11.12
SNP_A-2146155	atgcgatcatatttaa[A/G]tctgtcaactatcctg	A	G	/// ENST00000338067 // downstream // 20426 // --- // --- // --- // --- /// ENST00000359891 // downstream // 23005 // --- // ---	-	p36.13
SNP_A-2164625	caaacacactttgaat[A/T]atggaatttctagggt	A	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2175212	cacataaaaacacaga[C/G]aatcatttggattttg	C	G	sapiens KIAA0083 mRNA, partial cds. /// ENST00000358410 // intron // 0 // --- // --- // --- // --- /// ENST00000357404 // intron	DNA2L	DNA2L, Homo sapiens KIAA0083 partial cds. q21.3
SNP_A-2204240	ccagccaaactggtgc[A/G]gaccagaagcaaagtc	A	G	51378 // Homo sapiens angiopoietin 4 (ANGPT4), mRNA. /// ENST00000262924 // upstream // 8823 // --- // --- // --- // --- ///	ANGPT4	ANGPT4, Homo sapiens angiopoietin 4 (ANGPT4), p13
SNP_A-2205075	ccaggtgatacatatg[C/T]aagttagtgtatgaga	C	T	9429 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), mRNA. /// ENST00000237612 // upstream // 72305 // --- // --- // --- // ---	ABCG2	ABCG2, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), q22.1
SNP_A-2206100	ccatcaagaccaataa[C/T]gaagaattggaagtgt	C	T	GABARAPL1 // 23710 // Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), mRNA. ///	GABARAPL1	GABARAPL1, Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), p13.2
SNP_A-1681692	acaaaaaatagtagtcttacgttca[A/G]gaagaattcataattcctgaagttt	A	G	// 57556 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A /// NM_173666 // downstream // 40046 // Hs.14822 // FLJ33977 // 285605 //	SEMA6A	SEMA6A , rs10491429, sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A ,q23.1
SNP_A-1656089	gttttactgttttacattcatcata[C/T]aaaagaatcatacagtattggtgta	C	T	57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs1073277, KIAA1239 protein,p14
SNP_A-1810213	gtgatgaaatcaccca[A/G]tatggaatttaatgag	A	G	10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // upstream // 478968 // --- // --- // --- // --- //	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-1832581	tacaaattactcaaaa[A/G]ttcaaaaagcttgaaa	A	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 21703 // --- // ---	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1843834	tagttacatttcagac[A/T]cttgaattattaatga	A	T	Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // intron // 0 // --- // --- // --- // ---	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1
SNP_A-1837900	tagaaaagtagagaaa[A/G]acctcagaggtatcag	A	G	Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000294697 // intron // 0 // --- // --- // --- // ---	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1858152	tcagaaataaagccac[C/T]atctacagccatctgt	C	T	MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 //	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-1951645	tttccttatcaaacta[C/T]gccgtcacctcagctt	C	T	164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // upstream // 30262 // --- // ---	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-1985252	gtgttcttggaataaa[A/G]ttcaacccccacttct	A	G	Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), mRNA. /// ENST00000229922 // intron // 0 // -	CAP2	CAP2, Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), p22.3
SNP_A-1891011	tgatggggaaaaaaca[A/T]gtcattggtttcactt	A	T	ENST00000277891 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1898081	caaagcagcacttaga[C/T]ggaaatgtggaaggct	C	T	374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2242371	ctgcacctctttttgg[A/G]caagttctttatgtgt	A	G	Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2241996	ctgattcaatgtgaaa[A/G]gggattacaaaaggag	A	G	260425 // Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // upstream // 223040 // Hs.486189 // MAGI-3 // 260425 //	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-2232641	ctcacgacccttttagc[A/G]catcctaaaagacctc	A	G	10106 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2), mRNA. /// ENST00000310189 // upstream //	CTDSP2	CTDSP2, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2), q14.1
SNP_A-2266597	gaagtcattccgctca[C/T]gctggggaccaggggg	C	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2311045	ggaaggtggtcagata[C/T]ggggggctctggataa	C	T	// 83999 // Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, mRNA. /// NM_153379 // downstream // 2657 // Hs.229335 // KREMEN1	KREMEN1	KREMEN1, Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, q12.1
SNP_A-2303283	gctatgggtatggacc[A/G]gaattttagagtgtca	A	G	DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, mRNA. /// NM_015496 // upstream // 20119 // Hs.202238 //	DKFZP434I116	DKFZP434I116, Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, q22.1
SNP_A-2304976	gctgaaaactggacat[G/T]aggatggaaatgcatg	G	T	KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000241471 //	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-2292362	gcacggaatattcaga[A/G]aagagaaagtagctag	A	G	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2294597	gcagtgaatatgcagt[A/G]aatattgtggtatgga	A	G	Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), mRNA. /// ENST00000282146 // intron // 0 // --- // -	KCNK13	KCNK13, Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), q32.11
SNP_A-2274639	gagaaacacatgaatg[C/T]cagtgcaatgtggtaa	C	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- ///	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2237009	ctctatggggtagaga[C/T]gctaggccggcactgc	C	T	51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1624054	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2248388	tggtaaagttttcaca[A/G]cggtggatgacagagg	A	G	// 5265 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran /// NM_001002236 // upstream // 31048 // Hs.525557 // SERPI	SERPINA1	SERPINA1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran ,q32.13
SNP_A-1905973	tggtcctctaccatta[C/G]ataataaagggtcttt	C	G	SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 216717 // Hs.511265 // SEM	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN ,q21.1
SNP_A-1924133	ttagttctgtaattta[G/T]ctaaaatttgtgtgga	G	T	4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 1626583 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1986357	gttggatactgtgcta[A/G]atcttagggctaaagg	A	G	Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // --- //	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1960570	tttttcatcctttata[C/T]ggacatgggtgattat	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 205374 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1864340	tccactcagcttcttg[C/T]agcacttactctggga	C	T	ENST00000341671 // intron // 0 // --- // --- // --- // ---	-	q21.32
SNP_A-1826983	taacatttggaagcac[C/T]ggagtaaccccatccc	C	T	// 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 113313 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-1818235	gttctgcaagatgaag[A/G]aagttctggagattgg	A	G	3192 // Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA. /// NM_004501 // upstream //	HNRPU	HNRPU, Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, q44
SNP_A-1822239	gttttgcagcatggga[A/T]ggatattggataggcc	A	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1790570	ggggcctaggcatctg[G/T]attccctttaaggcct	G	T	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-1661250	ggggatgcataaaaagcatacttga[A/T]gaaataacaattgagactgtcctaa	A	T	NM_021208 // intron // 0 // Hs.23367 // C9orf27 // 58483 // chromosome 9 open reading frame 27	C9orf27	C9orf27 , rs2900615, chromosome 9 open reading frame 27,q33.1
SNP_A-1784118	ggccagttctgaaatc[A/G]atgctttgaaaatagc	A	G	ENST00000358765 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-2227294	ctacaacagttataca[C/T]gcattattttctctct	C	T	Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA. /// ENST00000277198 // intron // 0 // --- // ---	C9orf3	C9orf3, Homo sapiens chromosome 9 open reading frame 3 (C9orf3), q22.32
SNP_A-2182961	cagattctggcacaaa[C/G]ctggtctttagggaat	C	G	80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 32686 //	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2188026	cagtcactaaaacaga[C/T]ggaaataaaggcaaca	C	T	/// ENST00000355063 // upstream // 636701 // --- // --- // --- //	-	q22.1
SNP_A-2187701	cagtacgtgcacatga[A/C]gtgtccatctcatggt	A	C	4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 153894 // Hs.467769 //	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2164683	caaacagaaggcagag[A/C]atagactggacaggtg	A	C	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- // --- ///	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2165190	caaagaacttttaaaa[C/T]ggatcttatatcttct	C	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 255811 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2141858	atcttggactaacaaa[C/T]gctgaggtggagtctg	C	T	Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// ENST00000238561 // intron // 0 // --- // --- // --- // ---	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-2125793	agtttgcttattctta[C/T]aaacttttccagatag	C	T	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 523551 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2076340	acattgccataggaac[C/T]aataatttaagtatgc	C	T	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 208760 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2087916	actggatgtagtcagc[G/T]aaatttttcttatggc	G	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 361694 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2067889	acaacctcatttttcc[A/G]aagtcattctatacta	A	G	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2066123	aatttgtccagcagca[C/G]gaaaagtaacttgaga	C	G	sapiens hypothetical protein FLJ90579 (FLJ90579), mRNA. /// ENST00000298820 // intron // 0 // --- // --- // --- // ---	FLJ90579	FLJ90579, Homo sapiens hypothetical protein FLJ90579 (FLJ90579), q21.31
SNP_A-2014039	ccatccttatttacct[C/G]aaggaactctaataag	C	G	Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2006730	taatctactatctcta[C/T]ggatttgtctattttg	C	T	Homo sapiens UBX domain containing 2 (UBXD2), mRNA. /// ENST00000272638 // intron // 0 // --- // --- // --- // ---	UBXD2	UBXD2, Homo sapiens UBX domain containing 2 (UBXD2), q21.3
SNP_A-2001116	caaaaatagcctgctc[C/G]gaaggctgtcttagga	C	G	Homo sapiens Ras association (RalGDS/AF-6) domain family 4 (RASSF4), transcript variant 2, mRNA. /// NM_032023 //	RASSF4	RASSF4, Homo sapiens Ras association (RalGDS,q11.21
SNP_A-2023057	aaaacagaacaatgta[C/T]agactgtattactgct	C	T	ENST00000318139 // 3UTR // 0 // --- // --- // --- // ---	-	q24.33
SNP_A-2026746	aaacaatttttcttga[C/T]gtaaggcaaagtattc	C	T	Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// ENST00000252329 // intron // 0 // --- //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2029399	aaagacaattcataaa[C/T]gatgtgacttacatgg	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 35076 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2118258	agtaaattgtccatgc[A/G]ctagccttctggttgc	A	G	Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 //	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds. q13.3
SNP_A-2115794	agggtgagctgagaac[C/G]caggacactggcccat	C	G	// Homo sapiens early growth response 2 (Krox-20 homolog, Drosophila) (EGR2), mRNA. /// NM_030759 // upstream //	EGR2	EGR2, Homo sapiens early growth response 2 (Krox-20 homolog, Drosophila) (EGR2), q21.3
SNP_A-2112027	aggatgcatactacaa[C/T]ctgaaactttggtcaa	C	T	Homo sapiens chromosome 10 open reading frame 69 (C10orf69), mRNA. /// ENST00000266059 // intron // 0 // --- //	SPFH1	SPFH1, Homo sapiens chromosome 10 open reading frame 69 (C10orf69), q24.31
SNP_A-2144527	atgatcaaaaccacca[A/G]taatcagagtagagca	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2138910	atccctgtgtcgtaga[A/C]ctgccgtgcatggagg	A	C	Homo sapiens U2 (RNU2) small nuclear RNA auxiliary factor 2 (U2AF2), mRNA. /// ENST00000308924 // intron // 0 // --- //	U2AF2	U2AF2, Homo sapiens U2 (RNU2) small nuclear RNA auxiliary factor 2 (U2AF2), q13.42
SNP_A-2138587	atcccaaagaaaaaaa[C/G]ttacatgacatctgca	C	G	29114 // Homo sapiens neuronal protein (NP25), mRNA. /// ENST00000273368 // downstream // 6120 // --- // --- // --- // ---	TAGLN3	TAGLN3, Homo sapiens neuronal protein (NP25), q13.2
SNP_A-2162330	attttatggggcagaa[A/C]gcatagtagggtttaa	A	C	/// ENST00000360919 // upstream // 164830 // --- // --- // --- //	-	q13.1
SNP_A-2183502	cagcagataaccctga[A/G]gcccaaagattgctag	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2036669 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2179306	cactgtctcaaaagac[G/T]caaaagtatttaagta	G	T	Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// ENST00000359730 // intron // 0 // --- // --- // --- // --- ///	LHX8	LHX8, Homo sapiens LIM homeobox 8 (LHX8), p31.1
SNP_A-2221781	ccttttcatttgccca[A/G]tcttgatcacaacact	A	G	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 843540 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783358	ggcataacagaagtaa[A/G]ggaaattttaggtcta	A	G	Homo sapiens erythrocyte membrane protein band 4.1 like 5 (EPB41L5), mRNA. /// ENST00000263713 // intron // 0 // --- // -- // --- // --- /// ENST00000331393 // intron // 0 // --- // --- // ---	EPB41L5	EPB41L5, Homo sapiens erythrocyte membrane protein band 4.1 like 5 (EPB41L5), q14.2
SNP_A-1697194	attcgtcttttcattcacttaacaa[C/T]gtttgcagagcataaatttttaatt	C	T	NM_004540 // intron // 0 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	NCAM2	NCAM2 , rs1585398, neural cell adhesion molecule 2,q21.1
SNP_A-1811587	gtgctgagatatcagt[A/C]acatttttggaaaagg	A	C	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 934465 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1816985	gttattgtttagaaag[G/T]attctatcagtgtttt	G	T	Homo sapiens SEC15-like 1 (S. cerevisiae) (SEC15L1), mRNA. /// ENST00000260762 // intron // 0 // --- // --- // --- // ---	SEC15L1	SEC15L1, Homo sapiens SEC15-like 1 (S. cerevisiae) (SEC15L1), q23.33
SNP_A-1871733	tctaatggagaccttg[C/T]atgattatgtaagtta	C	T	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 488707 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1858922	tcagcaccactgtaaa[C/T]gcacatggctcacatg	C	T	Homo sapiens HSPB (heat shock 27kDa) associated protein 1 (HSPBAP1), mRNA. /// ENST00000306103 // intron // 0 // ---	HSPBAP1	HSPBAP1, Homo sapiens HSPB (heat shock 27kDa) associated protein 1 (HSPBAP1), q21.1
SNP_A-1850587	tattaagttttcctaa[A/G]tcagagatgcatacat	A	G	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // –	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1948487	tttagtgagtagttac[A/G]gatctcattttacaat	A	G	FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream //	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-1964720	agctgtttcacgtggg[C/G]cagatgtctgagtagc	C	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1331271 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1931140	ttccatgaaaaggcac[G/T]ggtcattttcttacat	G	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 670234 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1930326	ttaaaagaagaaacga[C/G]ataacaattatacctc	C	G	CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream //	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1928763	ttcagaattggctgga[C/G]acagaccctgagatct	C	G	407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 281194 // Hs.24115 // C13orf25 //	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1914120	tgtgtgtcataaataa[C/T]attgcatttacaaata	C	T	/// ENST00000262227 // upstream // 283116 // --- // --- // --- // -- /// ENST00000314319 // upstream // 331595 // --- // --- // ---	-	p11.31
SNP_A-1889960	tgatagggctagaata[C/T]tattcacctcgtcttt	C	T	Homo sapiens WD repeat domain 17 (WDR17), transcript variant 1, mRNA. /// NM_181265 // intron // 0 // Hs.532056 //	WDR17	WDR17, Homo sapiens WD repeat domain 17 (WDR17), transcript variant 1, q34.2
SNP_A-2241494	ctgagtggtccgatga[A/G]catttgaaaacgggca	A	G	54872 // Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /// NM_000283 // upstream // 79274 //	GPI7	GPI7, Homo sapiens hypothetical protein FLJ20265 (FLJ20265), p16.3
SNP_A-2279043	gaggaagctgtataaa[G/T]aatttgccaaggaaaa	G	T	Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// ENST00000281221 // intron // 0 // --- // --- // --- // ---	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2286987	gatggtggatcacaca[C/T]atcagaagtttgaatc	C	T	Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // intron // 0 // --- // --- // --- // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2281568	gagtcctaaggtacaa[C/T]agatacaatacaatag	C	T	Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// NM_080764 // upstream //	-	-, Human clone rev16 q11.22
SNP_A-2292479	gcactatgctggtgaa[C/G]ctttgctgaaaattac	C	G	Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // intron // 0 // --- // --- // --- // ---	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-2313558	ggagataaggcagaaa[A/G]tgtaaccttctccca	A	G	KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 42688 //	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2312925	ggacttattcccagaa[A/G]cgattgcctcattttc	A	G	sapiens complement component 5 (C5), mRNA. /// ENST00000223642 // intron // 0 // --- // --- // --- // ---	C5	C5, Homo sapiens complement component 5 (C5), q33.2
SNP_A-2292521	gcactcccacttaaaa[C/T]gagatcgtctttgaag	C	T	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 928872 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q32.1
SNP_A-2291682	gcacacagtccctcaa[G/T]cacatatagctctttt	G	T	140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 111166 // Hs.31845 // ASB7 //	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3
SNP_A-2291003	gcaagtgctgccctga[C/G]gaattcacgcacacag	C	G	79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 15367 //	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2241337	ctgaggtaggtctccc[A/G]ctggatgcccccaacc	A	G	6530 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // downstream //	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-2237262	ctctcattatttccaa[A/G]gctttctatctgattc	A	G	// Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // --- // --- // --- // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.2
SNP_A-2249340	cttaaacactgttaaa[G/T]actttccttctcaatt	G	T	ENST00000341806 // intron // 0 // --- // --- // --- // ---	-	q27
SNP_A-1974321	cttaaattggaaaaat[C/G]aaccaacaatgttaat	C	G	Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), mRNA. /// ENST00000258326 // intron // 0 // --- // ---	ACBD6	ACBD6, Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), q25.3
SNP_A-1974642	ttgtataactttgtga[C/T]agatcagaagggaaga	C	T	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. ///	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium q24
SNP_A-1986426	atgccaagtattttaa[C/T]ctggcatcatctcatt	C	T	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // --- ///	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-1982863	ctagttaatgtacagc[A/G]ctctccattctagcct	A	G	/// ENST00000356209 // upstream // 112652 // --- // --- // --- // --- /// ENST00000330461 // upstream // 66172 // --- // --- // --- //	-	q21.3
SNP_A-1950724	tttcattccatcccag[A/C]actgttccattccccc	A	C	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1958123	ttttcatacaacatta[C/G]atgatattttacttttt	C	G	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1934639	ttctctgaggtggagc[A/C]gacctttggtgtcgac	A	C	ENST00000315208 // intron // 0 // --- // --- // --- // ---	-	q24.32
SNP_A-1936701	ttcttgttgagagtga[C/G]agaaggaagggacaag	C	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1850087	tatgtgattggagtta[A/C]taacaatttgtatact	A	C	Homo sapiens cytochrome P450, family 4, subfamily X, polypeptide 1 (CYP4X1), mRNA. /// ENST00000334540 // intron // 0 // --- // --- // --- // ---	CYP4X1	CYP4X1, Homo sapiens cytochrome P450, family 4, subfamily X, polypeptide 1 (CYP4X1), p33
SNP_A-1851708	tattcttgagaatttc[C/T]agtctcttatgccttg	C	T	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1848454	tatgaaggttgcataa[C/T]attccattgtttggaa	C	T	2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 202386 // Hs.122926 // NR3C1 //	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1855137	tcaagagttaactgta[C/G]atagttttactcctgt	C	G	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 585258 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-1861693	tcatctctgtaaagtg[C/T]aatctgacaatctgac	C	T	Homo sapiens mRNA for KIAA0545 protein, partial cds. /// ENST00000222345 // intron // 0 // --- // --- // --- // ---	SIPA1L3	SIPA1L3, Homo sapiens for KIAA0545 protein, partial cds. ,q13.13
SNP_A-1790587	ggggcctggtataggg[A/G]attttaaagatttaca	A	G	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA. /// ENST00000342947 // intron // 0 // --- // --- // --- // ---	DFNA5	DFNA5, Homo sapiens deafness, autosomal dominant 5 (DFNA5), p15.3
SNP_A-1755690	gagtaatttcacatgataagtttat[A/G]aagtaaatatatcaaaacaaaagga	A	G	3824 // killer cell lectin-like receptor subfamily D, member 1 /// NM_007334 // upstream // 42493 // Hs.41682 // KLRD1 //	KLRD1	KLRD1 , rs10845098, killer cell lectin-like receptor subfamily D, member 1 ,p13.2
SNP_A-2202565	ccacctatgcaagtca[C/G]aggacagccaagttct	C	G	Homo sapiens chromosome 19 open reading frame 15 (C19orf15), mRNA. /// ENST00000341782 // intron // 0 // --- //	C19orf15	C19orf15, Homo sapiens chromosome 19 open reading frame 15 (C19orf15), q13.2
SNP_A-2175615	cacatggaaaaaggga[C/G]atgaacgcgagcaatg	C	G	3283 // Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), mRNA. /// ENST00000286193 // downstream //	HSD3B1	HSD3B1, Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), p12
SNP_A-2172982	cacaaacaacctggca[C/T]gaaggagtgtgtctaa	C	T	64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 36391 // Hs.7482 // RBM19 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-2145178	atgcaatagagaaata[A/G]cattaaagcaaggaca	A	G	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 143957 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-2026308	aaaatttccattttaa[C/T]atgatattgcctgaga	C	T	ALDH8A1 // 64577 // Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 73018 //	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.3
SNP_A-2037292	aacaaaggaattaagc[A/G]gaacaagaaggtaagt	A	G	COMMD10 // 51397 // Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// NM_020796 //	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-2002681	ctctaatgttgaaata[C/T]gtgttataatgtatgt	C	T	// Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// ENST00000345127 // intron // 0 // --- // --- // --- // ---	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-1995565	tctgttgaccagaata[C/G]ctaatagatagtgctg	C	G	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SMARCA2	SMARCA2, Homo sapiens SWI p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2055916	aatacacataacaaga[A/G]aagggcatggtggttt	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1022240 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2079580	acccgcacgaggtgaa[C/T]agaagttgtgaacagg	C	T	ENST00000343998 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-2094968	agaatgctcaggagcc[A/G]agggacaaattataag	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2068811	acaatcaagcagatag[A/G]cacagacttcctgggt	A	G	Homo sapiens desmuslin (DMN), transcript variant B, mRNA. /// NM_145728 // intron // 0 // Hs.207106 // DMN // 23336 //	DMN	DMN, Homo sapiens desmuslin (DMN), transcript variant B, q26.3
SNP_A-1994114	agtgattggacttgaa[C/T]cttcagatcccttcca	C	T	85481 // Homo sapiens protein serine kinase H2 (PSKH2), mRNA. /// NM_152565 // upstream // 23165 // Hs.436360 //	PSKH2	PSKH2, Homo sapiens protein serine kinase H2 (PSKH2), q21.3
SNP_A-2000863	aggccatgttgaaata[C/T]ccttgatatcaccagt	C	T	-- /// ENST00000308105 // upstream // 35548 // --- // --- // --- // ---	-	q44
SNP_A-2043822	aacttcagaaagactg[A/G]aatggaaatgagcatt	A	G	683 // Homo sapiens bone marrow stromal cell antigen 1 (BST1), mRNA. /// NM_001775 // upstream // 39365 //	BST1	BST1, Homo sapiens bone marrow stromal cell antigen 1 (BST1), p15.32
SNP_A-2043089	aactgataaaaccgca[A/G]tgcacccttgtttagg	A	G	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 96757 // Hs.183817 // USP31 // 57478 //	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2026514	aaacaaatcctgagaa[C/G]catataggagtgaatg	C	G	/// ENST00000328146 // upstream // 21228 // --- // --- // --- // ---	-	q13.1
SNP_A-2138347	atccaggagagtgagg[C/G]aaatgtatagctgact	C	G	5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 //	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-2145834	atgccatattttgggg[A/C]aatttttttctgagac	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2857681 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2113419	aggcgagtggcccaaa[C/T]gaatgatgagtgatat	C	T	Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// ENST00000263187 // intron // 0 // --- // --- // --- // ---	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-2113696	aggctctgaagagcag[G/T]caaaggcaaggcagag	G	T	9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// NM_019599 // downstream // 99096 // Hs.533930 // TAS2R1	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2126513	ataaaatagactgctc[A/G]atatttcattacactc	A	G	6427 // Homo sapiens splicing factor, arginine/serine-rich 2 (SFRS2), mRNA. /// NM_024311 // downstream // 49949 //	SFRS2	SFRS2, Homo sapiens splicing factor, arginine q25.2
SNP_A-2123669	agtgttcaaaaccgat[A/G]agaataaatgggaaac	A	G	ENST00000354860 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2124122	agttagacagaagaaa[G/T]ctcacacttgaaattt	G	T	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 279725 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2130159	ataccgttcgccttaa[C/T]tcagcatatggccact	C	T	121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 165649 // Hs.31664 //	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2130866	atacttttaatgaacc[A/G]atttgacagctcagct	A	G	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2131921	ataggactttgcatac[C/T]agcctcttttgccctg	C	T	64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 338358 //	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-2173019	cacaaactagtaagga[A/T]gtttcttggcattttt	A	T	27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // downstream //	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2220646	ccttgaaatgtgaaca[C/G]catcaatgtgatccct	C	G	// 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // upstream // 11942 // Hs.188746 // ADAMTS	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-1678492	tttagagcagctttattcataacca[C/T]ccaaacttggaagcaataaaaatgt	C	T	NM_006157 // intron // 0 // Hs.376489 // NELL1 // 4745 // NEL like 1 (chicken)	NELL1	NELL1 , rs1584851, NEL-like 1 (chicken),p15.1
SNP_A-1802380	gtatcagaaaagactc[C/T]aggcagaaggaagtgc	C	T	Homo sapiens chromosome 9 open reading frame 25 (C9orf25), mRNA. /// ENST00000297620 // intron // 0 // --- // ---	C9orf25	C9orf25, Homo sapiens chromosome 9 open reading frame 25 (C9orf25), p13.3
SNP_A-1863595	tccaaatctggaagaa[C/T]catttatggaaaaaca	C	T	-- /// ENST00000242916 // upstream // 407531 // --- // --- // ---	-	p14
SNP_A-1856195	tcacaacgaagcatca[A/G]atttgcttaatgcaaa	A	G	Homo sapiens neurobeachin (NBEA), mRNA. /// ENST00000310336 // intron // 0 // --- // --- // --- // ---	NBEA	NBEA, Homo sapiens neurobeachin (NBEA), q13.3
SNP_A-1842482	taggtggaacttgcag[A/G]accctgctactaaccc	A	G	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 616967 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1832219	taatttggtagatgat[C/G]aataaatgcttatttt	C	G	3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 160563	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1989231	agaaagtagttatgaa[C/T]gccatgggtaccgctc	C	T	Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, mRNA. /// NM_145321 // intron // 0 // Hs.520259 // OSBPL3 // 26031 // Homo sapiens oxysterol	OSBPL3	OSBPL3, Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, p15.3
SNP_A-1977966	tagttgagaatgaacc[G/T]agtacattaaatatac	G	T	// 79577 // Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), mRNA. /// NM_003783 // upstream //	HRPT2	HRPT2, Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), q31.2
SNP_A-1885321	tgaatttctgtatcag[C/G]agggagaggctagtat	C	G	8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 72741 // Hs.127013 // CADPS // 8618 // Homo	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1917551	tgtttttgctgtgatg[A/T]aaaaacacaaaaagta	A	T	151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 //	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-2245666	ctgggcgcggagaaga[C/T]cagatgcccagcgatg	C	T	// 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream //	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-2238955	ctcttcccctactata[A/C]ccccgataggctgcag	A	C	/// ENST00000354196 // upstream // 1033019 // --- // --- // --- // --- /// ENST00000355224 // upstream // 1033019 // --- // --- // -	-	q21.11
SNP_A-2270435	gacagaaataagatgt[A/G]aaaattctgtatgcta	A	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 969184 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2263925	gaactactgacctcac[A/G]atctgctcacctcagt	A	G	// Homo sapiens putative GR6 protein (GR6), mRNA. /// ENST00000356020 // upstream // 1443 // --- // --- // --- // --- ///	GR6	GR6, Homo sapiens putative GR6 protein (GR6), q21.3
SNP_A-2297667	cttaccgagttgtgaa[C/T]ctggaacagccattgt	C	T	// 81698 // Homo sapiens chromosome 15 open reading frame 5 (C15orf5), mRNA. /// ENST00000312493 // upstream	C15orf5	C15orf5, Homo sapiens chromosome 15 open reading frame 5 (C15orf5), q24.3
SNP_A-2302321	gctaagaaggtggggc[C/T]atgtagtgtttgaagt	C	T	Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), mRNA. /// ENST00000229922 // intron // 0 // -	CAP2	CAP2, Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), p22.3
SNP_A-2263725	gaacctctagccaaaa[C/G]aagtccaacaaggcca	C	G	Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), mRNA. /// ENST00000274532 // intron	TIMD4	TIMD4, Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), q33.3
SNP_A-2267228	gaatacatttattcaa[C/T]cctcattaaattttaa	C	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 426219 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2286882	gatggggcagagaaca[A/T]gaaaggaggttcagga	A	T	64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 286048 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1937396	ttgaaatccacttaaa[C/T]tgcaaattgttcttta	C	T	Homo sapiens keratocan (KERA), mRNA. /// ENST00000266719 // 3UTR // 0 // --- // --- // --- // ---	KERA	KERA, Homo sapiens keratocan (KERA), q21.33
SNP_A-1941643	ttggaaccaacctaaa[C/T]gtccatgaatgataga	C	T	// Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1826910	taacatctgataacaa[A/G]caggtcagaatggtgc	A	G	// 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 59379 // Hs.143080 //	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-1825586	taaatatatacagtga[C/T]gttatttgactattat	C	T	Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA. /// ENST00000259259 // intron // 0 // --- // --- // --- // ---	STAM	STAM, Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), p12.33
SNP_A-1866520	tccccatatttgacac[C/T]gtcttctctcatactt	C	T	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 403284 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1807301	gtctcttcatttcaaa[G/T]gctgagaaatcaagac	G	T	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 242627 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1812435	gtggcagtgaaaaata[C/T]atcagcgactaacatg	C	T	Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-1790647	ggggctgaactctaca[A/G]aaccacaggggctgag	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1796277	ggtgtgggaaaaacca[A/G]taggctggtgatatcc	A	G	SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 65742 // Hs.509872 // RGS6 //	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2
SNP_A-1710349	aaaatacctgtttcggagaatgaac[C/T]ataaaactatccggagtgggtcggc	C	T	AB046837 // intron // 0 // Hs.29299 // SFMBT2 // 57713 // Scm-like with four mbt domains 2	SFMBT2	SFMBT2 , rs2255014, Scm-like with four mbt domains 2,p14
SNP_A-2227809	ctaccattataacatc[A/G]agtgtttttcttaatt	A	G	ENST00000357747 // intron // 0 // --- // --- // --- // ---	-	q42.13
SNP_A-2219459	cctgttaaagccatca[A/C]ccaattactgaggata	A	C	ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2187292	caggtggattacgatc[C/G]agcacagatggtcctc	C	G	sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // CDS // 0 // Hs.32539 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2144860	atgattaattcagcca[A/T]taagcatcaacagtta	A	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 417410 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2142542	atgaacagtatcttga[C/G]cattgttctggaagga	C	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 730453 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2023668	aaaactgttgcgatga[C/T]gcatgcacgtttgaat	C	T	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 258024 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2032789	aaataagacattttaa[G/T]agagagactatattca	G	T	METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream //	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-2078110	accagggaacaggtaa[C/T]gtacagtacagtgcta	C	T	Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// ENST00000325064 // intron // 0 // --- // --- // --- // --- ///	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2092507	agaaagttatttttca[A/G]tcatgtataggaagcc	A	G	1910 // Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, mRNA. /// NM_003991 // upstream //	EDNRB	EDNRB, Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, q22.3
SNP_A-2066271	aattttattgcttatc[A/T]gacaaaagcaaatgat	A	T	59084 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	ENPP5	ENPP5, Homo sapiens ectonucleotide pyrophosphatase p21.1
SNP_A-2066178	aatttgtttaaatcaa[C/T]ggctctcttatctttt	C	T	ENST00000333254 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2065585	aatttaccagtatgac[A/G]ctcatgtttactgaaa	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 238246 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2076758	acatttttgttatcca[A/G]tacagagttgggttta	A	G	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 541111 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2049082	aagcgctggactaaga[C/T]caaaggaggaaaaatt	C	T	9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // downstream //	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-1997707	aagcagttgccaacac[A/C]ataccaatatgccaat	A	C	57864 // Homo sapiens thymic stromal co-transporter (TSCOT), mRNA. /// NM_003408 // downstream // 87959 //	TSCOT	TSCOT, Homo sapiens thymic stromal co-transporter (TSCOT), q32
SNP_A-2162521	attttccaggcccata[A/G]gtggaagaaactgccc	A	G	// 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 276565 // Hs.154329 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2154809	attcaagaggtatccc[A/G]accctagcaggaaaag	A	G	Homo sapiens germ cell associated 1 (GSG1), mRNA. /// NM_031289 // intron // 0 // Hs.240053 // GSG1 // 83445 //	GSG1	GSG1, Homo sapiens germ cell associated 1 (GSG1), p13.1
SNP_A-2132072	atagggccaagaatag[C/T]cgagataatcttaaag	C	T	// Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// ENST00000265631 // intron // 0 // ---	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-2133442	atatattattcaaaag[A/G]cagttattttaaaaga	A	G	// Homo sapiens pellino homolog 1 (Drosophila) (PELI1), mRNA. /// ENST00000358912 // upstream // 30146 // --- // ---	PELI1	PELI1, Homo sapiens pellino homolog 1 (Drosophila) (PELI1), p14
SNP_A-2132993	atatacatttgtcaga[A/G]ctattagaaatgtata	A	G	Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// ENST00000235701 // intron // 0 // --- // --- // --- // ---	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN p31.1
SNP_A-2136749	atcacttgaatcaatc[A/C]atcagaaattatagtt	A	C	10873 // Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006680 // upstream //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-2137398	atcatacctgacaagt[A/G]aaactcttgcagcatc	A	G	56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// NM_138386 // downstream // 663979 // Hs.332844 //	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2130179	atacctagaattaaca[C/T]atgacccaataatttc	C	T	ENST00000312902 // intron // 0 // --- // --- // --- // --- /// ENST00000239104 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2125032	agttgccatgccctgg[A/G]aattgattaggcccta	A	G	Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST00000295624 // intron // 0 // --- // --- // --- // --- ///	NAV1	NAV1, Homo sapiens neuron navigator 1 (NAV1), q32.1
SNP_A-2183041	cagattttaccactca[C/T]agcatcaggtatgcaa	C	T	Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // intron // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-2217739	cctgatgaatcccaga[A/T]catgaaattactagat	A	T	386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000331273 // upstream // 46710 // --- // --- // --- // --- ///	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2221628	cctttgctcttaaacc[A/G]cagcctggatgtacca	A	G	/// ENST00000328955 // upstream // 1593285 // --- // --- // --- // --- ///	-	q24.23
SNP_A-2223562	cggaatcctcctaact[A/C]actcaagatcaaatca	A	C	-- /// ENST00000345029 // upstream // 883443 // --- // --- // --- // ---	-	p14
SNP_A-1705609	tgaatataccatgtggcttttgtct[C/T]aattaactagcactctaattcttga	C	T	4792 // nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha /// NM_032594 // upstream // 14536 // Hs.62813 // INSM2 // 84684 //	NFKBIA	NFKBIA , -, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha ,q13.2
SNP_A-1813546	gtgtaaataatttgca[C/T]ggctgttcggtcctgc	C	T	// Homo sapiens chemokine-like factor super family 4 (CKLFSF4), transcript variant 1, mRNA. /// NM_181521 // intron // 0 // Hs.325825 // CKLFSF4 // 146223 // Homo	CKLFSF4	CKLFSF4, Homo sapiens chemokine-like factor super family 4 (CKLFSF4), transcript variant 1, q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813327	gtggtggaaactgatg[C/G]cagagtgcctgggttg	C	G	5128 // Homo sapiens PCTAIRE protein kinase 2 (PCTK2), mRNA. /// ENST00000261211 // upstream // 56287 // --- // ---	PCTK2	PCTK2, Homo sapiens PCTAIRE protein kinase 2 (PCTK2), q23.1
SNP_A-1804265	gtcacgcaggagggag[A/G]cgtggagcacggattg	A	G	Homo sapiens keratin, hair, acidic, 8 (KRTHA8), mRNA. /// ENST00000246646 // CDS // 0 // --- // --- // --- // ---	KRTHA8	KRTHA8, Homo sapiens keratin, hair, acidic, 8 (KRTHA8), q21.2
SNP_A-1864042	tccacactgcataaca[A/C]tggaaggaacaatcat	A	C	9516 // Homo sapiens lipopolysaccharide-induced TNF factor (LITAF), mRNA. /// ENST00000344649 // upstream // 81525	LITAF	LITAF, Homo sapiens lipopolysaccharide-induced TNF factor (LITAF), p13.13
SNP_A-1862857	tcattcttgttagcta[A/C]gggactattgtgtagg	A	C	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 9576 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1867691	tcctaaaccataaagc[A/G]aaggtaatatgacccc	A	G	Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), mRNA. /// ENST00000261942 // intron // 0	ETEA	ETEA, Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), q35.2
SNP_A-1854814	tcaaccagcttgcaaa[A/T]ttgtcattgcactggt	A	T	sapiens epidermal growth factor (beta-urogastrone) (EGF), mRNA. /// ENST00000265171 // intron // 0 // --- // --- // --- // ---	EGF	EGF, Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), q25
SNP_A-1824812	taaagatgtattccca[C/G]aggaacaaagaaatgt	C	G	2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// NM_207506 // downstream // 208490 // Hs.492653 //	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.12
SNP_A-1821182	gtttgaatttcttaac[A/G]ctcatattactatcct	A	G	/// ENST00000342005 // upstream // 315186 // --- // --- // --- // --- /// ENST00000331523 // upstream // 155072 // --- // --- // ---	-	q21.1
SNP_A-1818697	gttgacaaagaagctc[A/C]actcacttcctgccat	A	C	3881 // Homo sapiens keratin, hair, acidic, 1 (KRTHA1), mRNA. /// NM_003770 // downstream // 17203 // Hs.159403	KRTHA1	KRTHA1, Homo sapiens keratin, hair, acidic, 1 (KRTHA1), q21.2
SNP_A-1946662	tttaacacaagtgaaa[C/T]tgcattttaattatta	C	T	// 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream //	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1947315	tttacaaagtggcata[A/G]agatccaacctactac	A	G	Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // intron // 0 // --- // --- // --- // ---	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1988642	gtggcacttttgaaaa[C/T]gatttgtctaattgga	C	T	KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 148539 //	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1915492	tgttcctttatctcca[A/T]ctttatttcatacact	A	T	55591 // Homo sapiens clone A34.1 transmembrane protein vezatin mRNA, complete cds. /// NM_017599 // downstream // 136248 // Hs.24135 // VEZATIN // 55591 // Homo sapiens	VEZATIN	VEZATIN, Homo sapiens clone A34.1 transmembrane protein vezatin complete cds. ,q22
SNP_A-1885099	tgaatgttgtttttag[A/G]atggctgctccatatc	A	G	FLJ32752 // 144132 // Homo sapiens hypothetical protein FLJ32752 (FLJ32752), mRNA. /// NM_144666 // downstream	FLJ32752	FLJ32752, Homo sapiens hypothetical protein FLJ32752 (FLJ32752), p15.4
SNP_A-1896555	tgctagaaaaacagtc[A/G]gaaaaatagaaatgca	A	G	Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // --- // --- // --- // --- ///	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-2284624	gatcagataaacagta[C/T]agttggccatactctg	C	T	34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 14581 // Hs.78948 // RABGGTB // 58	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN p31.1
SNP_A-2281814	gagtgagattcagtta[A/G]cagaacaaccattatt	A	G	// 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2276973	gagatctctgccctct[C/T]agaacttgtgtcatgt	C	T	FLJ35530 // 400798 // Homo sapiens FLJ35530 protein (FLJ35530), mRNA. /// NM_018037 // upstream // 41020 //	FLJ35530	FLJ35530, Homo sapiens FLJ35530 protein (FLJ35530), q25.2
SNP_A-2258178	cttttacatttcagga[C/T]cttgtctgcttctatc	C	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1663232 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2307671	gcttccaacaaatata[A/T]cacagaaatgataaga	A	T	6427 // Homo sapiens splicing factor, arginine/serine-rich 2 (SFRS2), mRNA. /// NM_024311 // downstream // 51969 //	SFRS2	SFRS2, Homo sapiens splicing factor, arginine q25.2
SNP_A-2297437	gccactgttccataca[A/T]ccctttgggccaggcc	A	T	// 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 68814 //	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2298540	cacctccgttccagag[A/T]ctcagcttccctcctg	A	T	Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 //	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-2271491	gaccaaagaaagatgg[A/T]agtgagagggaaccaa	A	T	7804 // Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, mRNA. /// NM_004631 // upstream // 63623 // Hs.444637 //	LRP8	LRP8, Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, p32.3
SNP_A-2254561	cttgctatattcttaa[A/G]agttgagtactactgg	A	G	56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 175511 // Hs.315186 // PCSK2 //	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-1901148	tggatctttacatcac[A/G]atattggacataattc	A	G	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // --- ///	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889333	tgagtggtggttatca[C/T]gcttctccatcagggg	C	T	ENST00000359891 // 3UTR // 0 // --- // --- // --- // --- /// ENST00000356241 // 3UTR // 0 // --- // --- // --- // ---	-	p36.13
SNP_A-1987030	tatacagcaccataaa[C/T]ttaatgtacgtataca	C	T	sapiens single-minded homolog 1 (Drosophila) (SIM1), mRNA. /// ENST00000262901 // intron // 0 // --- // --- // --- // ---	SIM1	SIM1, Homo sapiens single-minded homolog 1 (Drosophila) (SIM1), q16.3
SNP_A-1982879	taccaagcaacaagac[A/G]aaagagccaataatta	A	G	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-1975985	agatgagacataagaa[A/G]ggagaaaacttgactt	A	G	Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1947052	tttaatactaaatgac[C/T]cctgttaagaattcct	C	T	ENST00000344859 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-1941396	ggaagcatttgacaac[C/G]ctttaaaaattgcaac	C	G	Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, mRNA. /// NM_000635 // intron // 0 // Hs.465709 // RFX2 // 5990 //	RFX2	RFX2, Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, p13.3
SNP_A-1812573	tgccttaagtccttgg[C/T]atttataatcaatgct	C	T	Homo sapiens hypothetical protein FLJ13291 (FLJ13291), mRNA. /// ENST00000263997 // 3UTR // 0 // --- // --- // --- // ---	FLJ13291	FLJ13291, Homo sapiens hypothetical protein FLJ13291 (FLJ13291), q22.1
SNP_A-1808125	gtcttggcaagccatc[C/G]gaggcaggcttcctga	C	G	sapiens EphB3 (EPHB3), mRNA. /// ENST00000330394 // intron // 0 // --- // --- // --- // ---	EPHB3	EPHB3, Homo sapiens EphB3 (EPHB3), q27.1
SNP_A-1643990	ccataattgtgtcagcccattctta[A/G]taaatctaattacatgtatgtgtat	A	G	BC029120 // intron // 0 // Hs.436140 // FLJ22789 // 84190 // hypothetical protein FLJ22789	FLJ22789	FLJ22789 , rs2895910, hypothetical protein FLJ22789,q21.31
SNP_A-1780808	ggatctgaagacaccc[A/G]cttctaagtcattcat	A	G	// 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 327638 // Hs.491941	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-1727256	ttcactctgtctttaaagttttgca[C/T]tagaaatgggcttcagggtcttctt	C	T	AB002376 // intron // 0 // Hs.476384 // CAST // 26059 // CAZ-associated structural protein	CAST	CAST , rs10510781, CAZ-associated structural protein,p14.3
SNP_A-2224335	ctggattagacacttc[C/T]agtacctataataaaa	C	T	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 276179 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2223067	cgcattgtacctccac[A/G]ccatcagcctaacagg	A	G	7516 // Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), mRNA. /// ENST00000021776 // downstream // 154182 // --- // --- // --- //	XRCC2	XRCC2, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), q36.1
SNP_A-2204635	ccaggagaaatatatg[C/T]caaacaatgaaaaccc	C	T	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2208966	cccagcctcctgacct[C/G]agagcctacagtctgt	C	G	Homo sapiens chromosome 8 open reading frame 21 (C8orf21), mRNA. /// ENST00000304437 // intron // 0 // --- // --	C8orf21	C8orf21, Homo sapiens chromosome 8 open reading frame 21 (C8orf21), p23.1
SNP_A-2176576	cacccagtagttttaa[A/G]tatcttcatctgctgc	A	G	ENST00000324599 // intron // 0 // --- // --- // --- // ---	-	p15.3
SNP_A-2125345	agttgttcgttgtaga[C/T]ggaaagtcttttctgc	C	T	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2125200	agttggtgaaaaatga[C/G]gtaaatgcttttttt	C	G	Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // ---	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2137412	atcatagattcttaat[C/T]aggccaagaggaaatt	C	T	23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 183390 // Hs.87083 //	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. q34
SNP_A-2116464	aggtatggtagcacaa[G/T]actggttgttctgtac	G	T	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-1994217	aattagaaggaaaaca[G/T]gtgcctaaaagattta	G	T	793 // Homo sapiens calbindin 1, 28kDa (CALB1), mRNA. /// ENST00000265431 // upstream // 378761 // --- // --- // --- // ---	CALB1	CALB1, Homo sapiens calbindin 1, 28kDa (CALB1), q21.3
SNP_A-2033205	aaatactatgcagaga[A/G]gtaataagagctccaa	A	G	// 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 3413718 // --- // -	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2024112	aaaagatacaaacata[C/T]gtaagctataagaaat	C	T	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2045610	aagaattgggttggaa[C/T]gagaagcatggaaaat	C	T	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 558664 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2056436	aatagaacggtggtca[C/T]agtaatggcgagatct	C	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2059256	aatccttcgctaggga[C/T]gagcacacgagggtcc	C	T	sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // intron // 0 //	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2070905	acactcagtacacttg[A/T]agggtttctctccact	A	T	// Homo sapiens hypothetical protein BC001610 (LOC91661), mRNA. /// ENST00000340310 // intron // 0 // --- // --- // --- // —	LOC91661	LOC91661, Homo sapiens hypothetical protein BC001610 (LOC91661), q13.42

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2103870	agcacgtttgctcttg[G/T]agcctcttggcacaaa	G	T	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// X04707 // intron // 0 // Hs.187861 // THRB // 7068 //	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2078376	accatcaaggacaata[A/G]taaaagaatcaaaaca	A	G	6444 // Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, mRNA. /// NM_000337 // downstream // 13091 // Hs.387207 // SGCD	SGCD	SGCD, Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, q33.3
SNP_A-2084044	actagagtgatgtttc[C/T]agaggcccaggaacat	C	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2091846	agaaaatgattagtca[A/G]atgttttcaaatgtgc	A	G	sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020546 // intron // 0 // Hs.481545 // ADCY2 // 108 //	ADCY2	ADCY2, Homo sapiens for KIAA1060 protein, partial cds. ,p15.31
SNP_A-2089829	acttctaaaaactgag[G/T]cctctccacagaatag	G	T	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // intron // 0 // Hs.478673 // IL1RAP // 3556 // Homo sapiens	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-2092798	agaaatgtgtccaaaa[A/T]aggagtggcatttgtt	A	T	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 454200 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2057854	aatattatgatgagca[A/G]agatagaccagggaaa	A	G	ENST00000298743 // intron // 0 // --- // --- // --- // ---	-	q26.3
SNP_A-2040933	aaccctctgtcaaaag[C/G]cctacctggacgttcc	C	G	sapiens epidermal growth factor (beta-urogastrone) (EGF), mRNA. /// ENST00000265171 // intron // 0 // --- // --- // --- // ---	EGF	EGF, Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), q25
SNP_A-2031333	aaagggcagtctgaac[A/T]aggaaaaattacatat	A	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 632250 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2000912	atcatttgccaatatc[A/T]cttggtttgttcattt	A	T	4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 679141 // Hs.232819 // PCDH15 // 65217 //	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2111042	aggagaatgggctgcc[C/T]aataataatgccaatc	C	T	83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000356343 // upstream //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-2129876	atacatgacagaggca[A/G]gattttaattcagagg	A	G	Homo sapiens ets variant gene 7 (TEL2 oncogene) (ETV7), mRNA. /// ENST00000339796 // intron // 0 // --- // --- // --- // ---	ETV7	ETV7, Homo sapiens ets variant gene 7 (TEL2 oncogene) (ETV7), p21.31
SNP_A-2128032	ataagcaaaattaaaa[C/T]gagactgattttccac	C	T	80267 // Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA. /// NM_022083 // downstream // 20951	C1orf22	C1orf22, Homo sapiens chromosome 1 open reading frame 22 (C1orf22), q25.3
SNP_A-2127962	ataagagggaatggca[A/G]cagctctcttggggaa	A	G	Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), mRNA. /// ENST00000323246 // intron	CNDP1	CNDP1, Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), q22.3
SNP_A-2140810	atctgaaaacgtaagt[A/G]acctgaatttacaggc	A	G	284058 // Homo sapiens hypothetical protein LOC284058 (LOC284058), mRNA. /// ENST00000262419 // intron // 0 // ---	LOC284058	LOC284058, Homo sapiens hypothetical protein LOC284058 (LOC284058), q21.31
SNP_A-2146784	atgcttctttccccat[A/G]acttctaggaatctat	A	G	Homo sapiens cancer susceptibility candidate 1 (CASC1), mRNA. /// ENST00000320267 // intron // 0 // --- // --- // --- // ---	CASC1	CASC1, Homo sapiens cancer susceptibility candidate 1 (CASC1), p12.1
SNP_A-2208717	cccagaagaggatacc[G/T]agtcatctcagaaacc	G	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 700031 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2207396	ccattgccaacaacag[A/G]aaattatcatcactag	A	G	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2201267	ccaatacaagtgaaaa[C/T]tgtagtgtccttaaaa	C	T	/// ENST00000315208 // upstream // 71349 // --- // --- // --- // ---	-	q24.32
SNP_A-2215470	cctcactattctttga[C/G]ataggaaacaacaagg	C	G	5451 // Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), mRNA. /// NM_002697 // upstream //	POU2F1	POU2F1, Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), q24.1
SNP_A-2214272	cctacagcatttatga[A/G]gcaggctttgattgtc	A	G	26112 // Homo sapiens DKFZP434C171 protein (DKFZP434C171), mRNA. /// ENST00000355417 // intron // 0 // --- // --- // --- // --- /// ENST00000356749 // intron // 0 // --- // ---	DKFZP434C171	DKFZP434C171, Homo sapiens DKFZP434C171 protein (DKFZP434C171), q33.1
SNP_A-2213879	cctaaatcaagtagga[A/G]agaggaattgtcaaat	A	G	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 889751 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1780610	ggatattgagagctga[C/T]gccttctacccaaagg	C	T	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1782143	ggcaagaaacatgtcc[A/G]ggaaagtgaacaccaa	A	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-1802353	gtatcaactcttatga[C/T]gtagcctgagaggtca	C	T	/// ENST00000354196 // upstream // 324804 // --- // --- // --- // --- /// ENST00000355224 // upstream // 324804 // --- // --- // ---	-	q21.11
SNP_A-1786333	ggctgtgttcccatta[C/T]aggtcttacagaagtg	C	T	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1815788	gttaaggccatgggaa[G/T]aagagtgacccaagga	G	T	Homo sapiens likely ortholog of mouse monocyte macrophage 19 (MMRP19), mRNA. /// ENST00000278359 // intron // 0 // --- // --- // --- // ---	MMRP19	MMRP19, Homo sapiens likely ortholog of mouse monocyte macrophage 19 (MMRP19), p13
SNP_A-1828559	taagcatttctaagca[A/G]cttccctctataagca	A	G	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-1835891	tacgttcagagaaatc[A/G]ctctaaataaaacatc	A	G	/// ENST00000332049 // upstream // 64335 // --- // --- // --- // --- /// ENST00000355617 // upstream // 64335 // --- // --- // --- // ---	-	q23.1
SNP_A-1939877	ttgcacagcattgctc[A/C]cagtctgtggttattt	A	C	60529 // Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // upstream // 197045 // Hs.436055 //	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds. p11.2
SNP_A-1956494	tttgttggtcctccaa[A/G]gtgtgtttcccaaatg	A	G	220202 // Homo sapiens atonal homolog 7 (Drosophila) (ATOH7), mRNA. /// NM_022129 // downstream // 40309 //	ATOH7	ATOH7, Homo sapiens atonal homolog 7 (Drosophila) (ATOH7), q21.3
SNP_A-1955900	tttgtcagaaaaaaaa[A/T]catttgtgccaattag	A	T	DKFZp761B107 // 91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. ///	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), p15.2
SNP_A-1970395	aggataaaggcattga[C/T]taattctagattctta	C	T	B3GALT5 // 10317 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5), transcript variant 1, mRNA. /// NM_033171 // downstream //	B3GALT5	B3GALT5, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5), transcript variant 1, q22.2
SNP_A-1965081	ctgtttccctttctag[C/T]attagctcactgcatt	C	T	/// ENST00000355063 // upstream // 501619 // --- // --- // --- // ---	-	q22.1
SNP_A-1914387	tgtgttgttaatacta[C/T]ctcaaatgatttaatc	C	T	79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 201454 //	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-1928602	ttcacttaatgccaaa[A/C]ataacaaagtacagtc	A	C	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1924800	ttatatagtaaaacac[A/G]caagaacagtttaagc	A	G	Homo sapiens hypothetical protein MGC15606 (MGC15606), mRNA. /// ENST00000273347 // intron // 0 // --- // --- // --- // ---	FAM55C	FAM55C, Homo sapiens hypothetical protein MGC15606 (MGC15606), q12.3
SNP_A-2235152	ctccccagaatgctac[A/G]gctcttctttctttct	A	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1471940 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2266270	gaagggtgagaataga[C/G]aggaagggacaaataa	C	G	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2261629	gaaagtaacatcaata[A/G]aactatgaacaagaat	A	G	// 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// NM_000956 // upstream // 3500 //	PTGDR	PTGDR, Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), q22.1
SNP_A-2278010	gagccagttgtggtga[C/T]gctgtaagttaaggat	C	T	// 58499 // Homo sapiens zinc finger protein 462 (ZNF462), mRNA. /// NM_002874 // upstream // 235773 // Hs.521640 //	ZNF462	ZNF462, Homo sapiens zinc finger protein 462 (ZNF462), q31.2
SNP_A-2285047	gatcctgggacaaagg[A/G]agctgaagcatgtgtt	A	G	Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // --- // ---	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-2299968	gcctatcctggcatcc[A/G]aatgctgcacagctgg	A	G	Homo sapiens matrilin 2 (MATN2), transcript variant 1, mRNA. /// NM_030583 // intron // 0 // Hs.189445 // MATN2 //	MATN2	MATN2, Homo sapiens matrilin 2 (MATN2), transcript variant 1, q22.1
SNP_A-2296407	gcatttcacattatgg[C/T]ccactatacgcatgca	C	T	// 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2294323	gcaggtagaaaaataa[C/G]gcctggtaagatgcca	C	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2305664	gctgccaaaaaggaga[A/C]accagagattagcata	A	C	/// ENST00000318905 // downstream // 23255 // --- // --- // --- // --- /// ENST00000304745 // downstream // 23255 // --- // ---	-	q23.1
SNP_A-2314116	ggaggacatggaatcc[A/G]atggaatctgacccag	A	G	55761 // Homo sapiens tetratricopeptide repeat domain 17 (TTC17), mRNA. /// ENST00000039989 // downstream //	TTC17	TTC17, Homo sapiens tetratricopeptide repeat domain 17 (TTC17), p11.2
SNP_A-2278160	gagcctagaacacaaa[A/G]actgtctcctcctcgc	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2264242	gaacttaagaaccagc[C/T]ctttctgtatttcctt	C	T	Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// ENST00000322953 // intron // 0 // --- // ---	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1910340	ccatggctggctctga[G/T]ctatcattatgagtga	G	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1899375	tggaactagatgtccc[C/T]ggatacaaatccaggg	C	T	sapiens adenosine deaminase (ADA), mRNA. /// ENST00000359372 // intron // 0 // --- // --- // --- // --- ///	ADA	ADA, Homo sapiens adenosine deaminase (ADA), q13.12
SNP_A-1896769	tgctattggtaaggca[A/G]gattttacgtgatcag	A	G	ENST00000274299 // intron // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-1966081	cctatctcgtaattta[C/T]gaaggaacgaggttta	C	T	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4,q31.3
SNP_A-1949995	tttcaattgttaaata[A/G]ccacacatgcagaggc	A	G	6323 // Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), mRNA. /// NM_021007 // downstream //	SCN1A	SCN1A, Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835723	tacgactccccatccc[A/G]acttcagagaaagtct	A	G	112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-1834717	taccactttagctgaa[C/T]gccacaaatattgttc	C	T	FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream //	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-1863857	tccaatattcaaggta[A/G]cttttctggttcttac	A	G	ENST00000308464 // intron // 0 // --- // --- // --- // ---	-	q23.2
SNP_A-1794272	ggtcatttgatttaac[A/G]gatggatccctgccaa	A	G	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-1812606	gtggctcaggcctgtg[C/T]ataattccagcacttt	C	T	7558 // Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), mRNA. /// NM_014753 // upstream // 103788 //	ZNF11B	ZNF11B, Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), q11.21
SNP_A-2150366	atgtcttgaataatac[C/T]cccacaagcacaggga	C	T	Homo sapiens zinc finger protein 595 (ZNF595), mRNA. /// ENST00000339368 // intron // 0 // --- // --- // --- // ---	ZNF595	ZNF595, Homo sapiens zinc finger protein 595 (ZNF595), p16.3
SNP_A-2153054	attaccacacacttta[C/T]ggtttacaaaaacaga	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 443147 // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2161835	atttgtcggtagtgac[G/T]aaaatattcaagtcaa	G	T	FLJ41603 // 389337 // Homo sapiens FLJ41603 protein (FLJ41603), mRNA. /// NM_133263 // upstream // 4771 //	FLJ41603	FLJ41603, Homo sapiens FLJ41603 protein (FLJ41603), q32
SNP_A-2135959	atcaacttctgagcta[C/G]agtgagtaggagataa	C	G	50486 // Homo sapiens putative lymphocyte G0/G1 switch gene (G0S2), mRNA. /// NM_005525 // upstream // 9530 //	G0S2	G0S2, Homo sapiens putative lymphocyte G0,q32.2
SNP_A-2132140	ataggtcaccagtcaa[C/T]gttccctgagtgctga	C	T	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// ENST00000337517 // intron // 0 // --- // --- // --- // ---	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2114727	agggatgataagaaaa[A/G]tatttagctaggtaca	A	G	3945 // Homo sapiens lactate dehydrogenase B (LDHB), mRNA. /// NM_004982 // downstream // 38886 // Hs.102308	LDHB	LDHB, Homo sapiens lactate dehydrogenase B (LDHB), p12.1
SNP_A-2015864	gagtgggaagaacaca[A/G]catgaagtcagacgtc	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 112664 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2040438	aaccaggaagtgctga[C/T]aggttgctttcccttc	C	T	131601 // Homo sapiens seven transmembrane domain orphan receptor (TPRA40), mRNA. /// NM_016372 //	GPR175	GPR175, Homo sapiens seven transmembrane domain orphan receptor (TPRA40), q21.3
SNP_A-2036288	aaattcaggttttata[A/T]gaaatagtagtgcttt	A	T	Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2071067	acactgcacacacttc[C/T]atctctcctaagcctc	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2074803	acatatttgggctgaa[A/T]atttacaattcctcag	A	T	79895 // Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), mRNA. /// NM_003645 // upstream // 14256 //	ATP8B4	ATP8B4, Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), q21.2
SNP_A-2061343	aatgccataagttaag[A/G]ataatcacaaatggct	A	G	10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 80340 // --- // --- // --- // ---	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3
SNP_A-2096857	agactcatgaaaagct[G/T]aaatgttcatgaatat	G	T	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 1166030 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2078368	accatcaaatgttatt[A/T]aagagagctataaaaa	A	T	64111 // Homo sapiens chromosome 7 open reading frame 9 (C7orf9), mRNA. /// ENST00000222674 // upstream //	C7orf9	C7orf9, Homo sapiens chromosome 7 open reading frame 9 (C7orf9), p15.3
SNP_A-2119166	aatattgagaactgaa[C/T]ctgctcttgctgaggt	C	T	ENST00000255289 // CDS // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-2122498	agtgctcatgggagga[A/C]aaagaacacaaatagg	A	C	57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// NM_152749 // upstream // 37494 // Hs.489603 //	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. q22.3
SNP_A-2132503	atagtgctgcaaggaa[C/T]gtatgaatgcatgtgt	C	T	Homo sapiens SEC14 and spectrin domains 1 (SESTD1), mRNA. /// ENST00000335289 // intron // 0 // --- // --- // --- // ---	SESTD1	SESTD1, Homo sapiens SEC14 and spectrin domains 1 (SESTD1), q31.2
SNP_A-2159927	atttatccagtgggca[A/G]ccgtagaatccctggt	A	G	26290 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA. /// NM_002235 // upstream // 36476 // Hs.306190 //	GALNT8	GALNT8, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), p13.32
SNP_A-2213578	ccgtcccaagcaatta[A/T]actgcctagaaggcaa	A	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2214447	aaaaaagaatcaaaac[A/G]aatagcatgaaagccc	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 778470 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2173574	cacaattacttttctc[C/T]caatgtgttataccaa	C	T	2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 206088 // Hs.203717	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-1788038	gggagactgtggcaaa[C/T]ggattgcttgatccca	C	T	399687 // Homo sapiens myosin XVIIIA (MYO18A), transcript variant 2, mRNA. /// NM_078471 // upstream // 27135 //	MYO18A	MYO18A, Homo sapiens myosin XVIIIA (MYO18A), transcript variant 2, q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1857524	tcactcagctaagaag[A/G]aggatcacaatgaaaa	A	G	4179 // Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, mRNA. /// NM_172357 // downstream // 24244 // Hs.510402 // MCP // 417	MCP	MCP, Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, q32.2
SNP_A-1847453	tatcctatcttacatc[A/C]caatctcaggataaag	A	C	Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// ENST00000359025 // intron // 0 // --- //	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-1840494	tagccataccactgaa[C/T]attgatttaaccaaga	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 444536 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1826754	taacagcctgccagag[G/T]aggttaacaataggat	G	T	ENST00000272427 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-1953221	tttctttgctcacgca[C/T]ataagcctgtgttgtt	C	T	// 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 714929 // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1981090	actggtgagttgttta[G/T]gttttcttccatatac	G	T	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1915356	tgttccacaaaccagc[A/G]agatgagtgttatacc	A	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2279123	gaggaatttccttta[G/T]agaatttgagtcgttt	G	T	Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-2231891	ctcaaatggtagaaga[C/T]gaaagagcaagaggga	C	T	SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2231752	ctcaaaatattactta[G/T]agaagcaagtgagaac	G	T	22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 278 //	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2297776	gccaggcaaaccctac[A/G]acttcattttagataa	A	G	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 211972 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2301545	atagctttattccaca[C/G]ggttgttttaaggtag	C	G	64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 29107 //	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-2295336	gcatcatatgacaaaa[C/T]aaaaaagaagatgacc	C	T	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	SLC24A2	SLC24A2, Homo sapiens solute carrier family 24 (sodium p22.1
SNP_A-2301606	gcgattcaaaattatc[A/C]aacacatttcaaatac	A	C	ENST00000309493 // downstream // 62923 // --- // --- // --- //	-	q22.33
SNP_A-2240916	ctgagacttattcttg[C/T]atcatttttttagctct	C	T	/// ENST00000325796 // downstream // 639811 // --- // --- // ---	-	q22.1
SNP_A-2253727	cttgaaactgttagaa[A/C]aaggtggaggccacat	A	C	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 534870 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2253380	cttctgtctcactcca[A/G]ctggggctctcagaac	A	G	ENST00000322285 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2243139	ctgcctacactgaagt[A/G]aatttccctggaatct	A	G	84665 // Homo sapiens myopalladin (FLJ14437), mRNA. /// NM_032578 // downstream // 10529 // Hs.55205 // MYPN //	MYPN	MYPN, Homo sapiens myopalladin (FLJ14437), q21.3
SNP_A-2285771	gatgactaaagtcaca[A/G]aagttatataagtcat	A	G	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 161006 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2268694	gaatgttaattcccag[A/G]aggaaaaaataagatg	A	G	/// ENST00000338636 // upstream // 223988 // --- // --- // --- // -- /// ENST00000334344 // upstream // 311978 // --- // --- // ---	-	q12
SNP_A-1914047	tgtgtgctttgtatat[A/C]aaatagcatcctcaat	A	C	Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// ENST00000262861 // intron // 0 // --- // -- // --- // --- /// ENST00000308942 // intron // 0 // --- // --- //	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1913284	tgtgggattggtggtc[C/T]accctggtagtttcca	C	T	Homo sapiens peptidase (mitochondrial processing) beta (PMPCB), mRNA. /// ENST00000249269 // intron // 0 // --- // --	PMPCB	PMPCB, Homo sapiens peptidase (mitochondrial processing) beta (PMPCB), q22.1
SNP_A-1927915	ttcaataactgttgga[G/T]cccaaagcttaaagta	G	T	// 84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 6927 // Hs.153504 //	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-1927653	ttcaaccttgaaggat[A/G]aaccatgtaaatgaag	A	G	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.2
SNP_A-1886431	tgacgctgctatctac[A/C]gacaggtgggagttag	A	C	85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 290469 // Hs.377155 // LYRIC //	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-1844316	tataaaaagaagtata[C/G]gtcttgatcaggtggg	C	G	23759 // Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 1, mRNA. /// NM_148175 // downstream // 53034 // Hs.438587 // PPIL2 // 23759 // Homo	PPIL2	PPIL2, Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 1, q11.21
SNP_A-1869453	tcctgtgcttaagtaa[C/G]tagtactgtcttcact	C	G	805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // downstream //	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q32.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1785580	ggctcatttcctgata[C/T]caaatggactcaatgt	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 461940 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1785719	ggctctcagcctacta[C/T]atatatgaattaagat	C	T	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 210047 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1790113	ggggaagtggtgtaga[C/T]ggtctaggtcctcttg	C	T	ENST00000320865 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1648988	ctctctgaagcttccgacatctttt[C/G]aaaacctccttaaaacacttccata	C	G	7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 955913 // Hs.323079 // PTPRD // 5789 // protein	TYRP1	TYRP1 , rs7858099, tyrosinase-related protein 1 ,p23
SNP_A-2221282	cctttataattgccag[A/G]aaataaacatacatag	A	G	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 511525 // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2150006	atgtcattaactgtga[C/G]aagttgtactttccca	C	G	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2149479	atgtagactgagcact[A/G]aaggccaagcaccacc	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2145719	atgccaacttatgtac[A/G]agtgtgtgtgcgtgtc	A	G	255352 // Homo sapiens chromosome 10 open reading frame 93 (C10orf93), mRNA. /// NM_032422 // upstream //	C10orf93	C10orf93, Homo sapiens chromosome 10 open reading frame 93 (C10orf93), q26.3
SNP_A-2145606	atgcatctataactta[A/G]atgtttatgcagaagg	A	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2130112	atacccagtgagggaa[C/T]actttgaccaatggga	C	T	// 9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 221894 // Hs.136829 // RFX3 //	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-2121645	agtgaatctattaata[C/T]gagtgatctggggaca	C	T	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2118851	agtactagaacccagg[A/C]attctgtcttgcagct	A	C	79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 30470 //	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2102233	agattaagtgagataa[C/T]agaaagtgcctaggat	C	T	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2040202	aaccaatgaacaatgc[A/G]ccatcctagagctaca	A	G	// Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), mRNA. /// ENST00000349015 // upstream // 484 // --- // --- // --- // --- /// ENST00000339095 // downstream	ALDH3B2	ALDH3B2, Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), q13.2
SNP_A-2032796	aaataagagcataacc[A/G]cacctggcggcatata	A	G	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1450572 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2016808	tcaaggaaagtgacaa[A/G]aaggcttattctaact	A	G	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 772260	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2010342	gtgagaatggacaagt[A/C]aatagggcttaggcag	A	C	ENST00000356562 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2001070	acgctgatggactaca[G/T]attcaacctgccttct	G	T	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 68434 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-1997178	ccgccagaggagtggc[C/T]aagttcgtgtgcaggg	C	T	10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 3088 // --- // --- // --- // ---	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-1999734	ggacaccaaaatgcta[A/G]caatgattgtatttgg	A	G	6840 // Homo sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // upstream // 221502 // Hs.499209 //	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-1996714	catcatgtgctagaca[C/G]tactaccaatactttg	C	G	Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // --- // ---	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-2080904	acctctctggttaagg[A/G]aaaaaaggaaggcagt	A	G	1102 // Homo sapiens chromosome condensation 1-like (CHC1L), mRNA. /// NM_020377 // upstream // 86108 //	CHC1L	CHC1L, Homo sapiens chromosome condensation 1-like (CHC1L), q14.2
SNP_A-2090439	gttctcaattctgagc[A/G]cttctctccttctgca	A	G	NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1078095 // ---	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2061314	aatgccactcaaggca[A/C]aaccctgaagtccttg	A	C	Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), mRNA. /// ENST00000262592 // intron // 0 // --- // ---	BCAS1	BCAS1, Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), q13.2
SNP_A-2059923	aatcttcattataggg[A/G]attcagtgtttggctt	A	G	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH), mRNA. /// ENST00000315467	GCSH	GCSH, Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH), q23.2
SNP_A-2047864	aagcaaaaaggttcag[C/T]catctggatgcttcac	C	T	sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 //	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2067879	acaacctactactagc[A/G]agtagcctctaaagtg	A	G	Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// ENST00000310430 // intron // 0 // --- // --- // --- // ---	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2118665	agtacaaaaagacata[C/T]agtaaaactcagcctc	C	T	// 26509 // Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // downstream // 62517 // Hs.500572 // FER1L3 // 26509 //	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-2111726	aggataaaattagtag[C/T]acgcaagaagatttga	C	T	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 203693 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2130124	ataccccctctatagga[C/T]acttcccgtgattgga	C	T	4048 // Homo sapiens leukotriene A4 hydrolase (LTA4H), mRNA. /// NM_005230 // upstream // 129821 // Hs.46523 //	LTA4H	LTA4H, Homo sapiens leukotriene A4 hydrolase (LTA4H), q23.1
SNP_A-2131857	ataggaaaattacaaa[A/C]tgacccctggctagga	A	C	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 261099 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2135123	atattgaaatctttaa[G/T]taagtgtcattgatct	G	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 407052 // --- // --- // --- //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2143730	atgagaatacttagga[A/G]agacaagaaagatggc	A	G	2321 // Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mR /// NM_015932 // upstream // 89693 //	FLT1	FLT1, Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor q12.3
SNP_A-2156302	attctatggttacaaa[C/G]acaacctttagtctct	C	G	/// ENST00000318847 // downstream // 75207 // --- // --- // ---	-	q23.31
SNP_A-2156323	attctattttcttcca[A/T]atatacgtaacacttt	A	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-2163371	atttttttgaggagctg[A/G]actcccagtgggcttg	A	G	// 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2220716	ccttgagaagagagtc[C/T]aatggtcacttaggct	C	T	SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 193466 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2214623	cctagattcctcaggg[A/T]ccaattctgtgctgat	A	T	138474 // Homo sapiens TAF1-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa (TAF1L), mRNA. /// NM_212558 // upstream // 44710 //	TAF1L	TAF1L, Homo sapiens TAF1-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa (TAF1L), p21.1
SNP_A-2172467	caattcacatttatag[C/T]cagtgttcaaacataa	C	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1664548	tgccagattaaattatccattgacc[A/G]atttatgtcattaaacttaaatgct	A	G	5621 // prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) /// NM_000678 // upstream // 389498 // Hs.557 // ADRA1D // 146 // adrenergic	PRNP	PRNP , rs4813709, prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) ,p13
SNP_A-1799830	gtacacaagtgaggaa[C/G]tgatctctgccccatc	C	G	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 1049061 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1812978	gtggggtatgtggcat[A/G]aggggtttggacagaa	A	G	132864 // Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, mRNA. /// NM_182485 // downstream // 13355 // Hs.374216	CPEB2	CPEB2, Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, p15.33
SNP_A-1872271	tctagaactttaaaaa[A/C]atagatgtgggccaga	A	C	Homo sapiens angiomotin like 1 (AMOTL1), mRNA. /// ENST00000317837 // intron // 0 // --- // --- // --- // --- ///	AMOTL1	AMOTL1, Homo sapiens angiomotin like 1 (AMOTL1), q21
SNP_A-1854078	tcaaacctatttcccg[A/C]acctccagtcatatgg	A	C	// 29090 // Homo sapiens HSPC154 protein (HSPC154), mRNA. /// NM_001914 // downstream // 119 // Hs.465413 //	C18orf55	C18orf55, Homo sapiens HSPC154 protein (HSPC154), q22.3
SNP_A-1826744	taacagcatattccaa[C/T]gaagaaagaaagcata	C	T	Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, mRNA. /// NM_177435 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens	PPARD	PPARD, Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, p21.31
SNP_A-1825055	taaaggcagtagtgcc[A/G]cctacatttgcaatac	A	G	Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// ENST00000281928 // intron // 0 // --- // -	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-1895912	tgcctgttacacccaa[A/G]gcaggtgggagtcaat	A	G	// 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 25199 // Hs.523852 //	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-1919888	ctttgtcacttaaaaa[A/T]ttctccttatgatcca	A	T	4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000299766 // upstream // 198645 // --- // ---	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1910730	tgtcctttgaagagga[G/T]acctcagagagtgtgc	G	T	7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 203453 //	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-1967959	attctccttgcttggc[A/G]ccttgccaataaatgc	A	G	55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 90753 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1965130	ttaaatcatttcataa[C/G]ctctagacctaagaat	C	G	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1956034	tttgtcttcttctgga[A/T]acagagtgatggcatt	A	T	27314 // Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA. /// NM_015885 // upstream // 54091	RAB30	RAB30, Homo sapiens RAB30, member RAS oncogene family (RAB30), q14.1
SNP_A-1961226	ttttttattctttaga[C/T]agagctcacgctgttg	C	T	5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 16571 //	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-1959126	ttttgaatctgcaata[C/T]cctaaagagacacaaa	C	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 496799	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2248124	ctgtggcccattccta[A/T]gttcctggctggaatc	A	T	// Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, mRNA. /// NM_016083 // upstream //	CNR1	CNR1, Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, q15
SNP_A-2247802	ctgtgagggatgttta[C/T]gtgaagactaatttta	C	T	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2240819	ctgagaaatacatcta[A/C]atttgctaggaatgca	A	C	-- /// ENST00000359634 // upstream // 797510 // --- // --- // --- // --- /// ENST00000359181 // upstream // 797510 // --- // --- // -	-	q32.3
SNP_A-2300456	gcctcttttcttaaac[A/G]caccattcacatgcat	A	G	// 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 118077	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-2298709	gcccaggcctggagca[C/T]gggcctgttcctcgtg	C	T	// 63948 // Homo sapiens DMRT-like family B with proline-rich C-terminal, 1 (DMRTB1), mRNA. /// NM_147193 //	DMRTB1	DMRTB1, Homo sapiens DMRT-like family B with proline-rich C-terminal, 1 (DMRTB1), p32.3
SNP_A-2292778	gcacttgtatgtacca[C/T]taatttactactttat	C	T	Homo sapiens nucleoporin 43kDa (NUP43), transcript variant 2, mRNA. /// NM_198887 // intron // 0 // Hs.510375 // NUP43	NUP43	NUP43, Homo sapiens nucleoporin 43kDa (NUP43), transcript variant 2, q25.1
SNP_A-2291322	gcaatgccatcaatga[C/G]taaatacagctatact	C	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 808209	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2238798	ctcttagaggaatcag[A/T]atgttatattccttac	A	T	65055 // Homo sapiens chromosome 2 open reading frame 23 (C2orf23), mRNA. /// NM_018433 // upstream // 83973 //	C2orf23	C2orf23, Homo sapiens chromosome 2 open reading frame 23 (C2orf23), p11.2
SNP_A-2245338	ctggcttcaaactata[C/T]aaaacgttacagtaat	C	T	3667 // Homo sapiens insulin receptor substrate 1 (IRS1), mRNA. /// NM_032276 // downstream // 1251988 //	IRS1	IRS1, Homo sapiens insulin receptor substrate 1 (IRS1), q36.3
SNP_A-2252788	cttctaattctcatag[C/T]cctgctatcccctaca	C	T	4065 // Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /// NM_007366 // downstream // 6486 // Hs.410477 // PLA2R1	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2
SNP_A-2257490	ctttgagttaatagcc[C/T]actgtgaagaagtaaa	C	T	/// ENST00000354350 // upstream // 97045 // --- // --- // --- // --- /// ENST00000355158 // upstream // 97045 // --- // --- // --- // ---	-	q22.33
SNP_A-2286095	gatgatttctgagcca[A/G]tagtccaagacctttt	A	G	sapiens likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA. /// ENST00000321331 // intron // 0 // --- // --- //	HIG1	HIG1, Homo sapiens likely ortholog of mouse hypoxia induced gene 1 (HIG1), p22.1
SNP_A-1947452	tttacagtagtctgga[A/G]gataatgtgaaaaagc	A	G	114907 // Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, mRNA. /// NM_148177 // upstream //	FBXO32	FBXO32, Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, q24.13
SNP_A-1917008	tgtttgcaaagaaata[A/G]aatctctggatgacat	A	G	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-1918883	ttaacatggttaacaa[C/T]atcctgaatgacatat	C	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2928906 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1927155	ttattttgcatattga[A/C]taacaagtggccttta	A	C	5796 // Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), mRNA. /// ENST00000309493 // upstream	PTPRK	PTPRK, Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), q22.33
SNP_A-1890460	tgatctcccttgctga[A/C]actggatattatatct	A	C	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1825426	taaataagaaataaac[A/G]gggaagtgaggtaatg	A	G	// Homo sapiens B/K protein (LOC51760), mRNA. /// ENST00000261375 // intron // 0 // --- // --- // --- // --- ///	LOC51760	LOC51760, Homo sapiens B,p12.3
SNP_A-1824326	taaacctcacttaata[C/T]gttcatgttttcatta	C	T	2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 414946 // Hs.374243 //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1852672	tatttatttctagata[A/G]acttatgtgcttccct	A	G	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 207281 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-1871852	tctacaatcctgacca[A/G]agatggattagtcata	A	G	64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 314836 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1799390	gtaatcattctagcta[A/G]taagttacagatcatt	A	G	ENST00000265274 // intron // 0 // --- // --- // --- // --- /// ENST00000360069 // intron // 0 // --- // --- // --- // --- ///	-	q25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2171007	caatacactgaatagt[A/G]aacaaaggatttgtga	A	G	// 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1979029 // Hs.98262 // GRIK2	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2198701	catttcctaatatcta[C/T]catgtacaaggcacta	C	T	// Homo sapiens minichromosome maintenance deficient domain containing 1 (MCMDC1), mRNA. /// ENST00000243218 // intron // 0 // --- // --- // --- // --- ///	MCMDC1	MCMDC1, Homo sapiens minichromosome maintenance deficient domain containing 1 (MCMDC1), q22.31
SNP_A-2219422	cctgtgtcactgcaga[C/T]agggatgattgcaaag	C	T	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	YWHAB	YWHAB, Homo sapiens tyrosine 3-monooxygenase,q13.12
SNP_A-2163768	caaaacaaaacaaaaa[A/T]acacaggatgcccaga	A	T	Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B), mRNA. /// ENST00000308366 // intron // 0 // --- //	PLA2G1B	PLA2G1B, Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B), q24.23
SNP_A-2164504	caaaattctcttatcc[A/G]aaaatacgaatcaaat	A	G	// 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 91742 // Hs.444992 //	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-2141723	atcttctcctgctgac[C/T]gggatgtgggctcctt	C	T	339221 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 7 (ENPP7), mRNA. ///	ENPP7	ENPP7, Homo sapiens ectonucleotide pyrophosphatase q25.3
SNP_A-2138190	atccacaggcaaacaa[C/G]aaggcaagacagccac	C	G	Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), mRNA. /// ENST00000301396 // intron // 0 // --- // ---	PELP1	PELP1, Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), p13.2
SNP_A-2130181	atacctagttcttaga[A/G]cctgcttggccaattt	A	G	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2125920	agttttaatgcaaaga[C/G]ctttttggagcaggt	C	G	/// ENST00000355509 // upstream // 7434 // --- // --- // --- // ---	-	q13.42
SNP_A-2067323	acaaagtgagaaagaa[A/G]gtaaaagatgaatgca	A	G	4086 // Homo sapiens SMAD, mothers against DPP homolog 1 (Drosophila) (SMAD1), transcript variant 1, mRNA. /// NM_001003688 // upstream // 12308 // Hs.519005 // SMAD1	SMAD1	SMAD1, Homo sapiens SMAD, mothers against DPP homolog 1 (Drosophila) (SMAD1), transcript variant 1, q31.21
SNP_A-2087641	actgctgagataacag[A/T]attttcttcttgtata	A	T	Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-2077778	accagaaagagaaatg[C/T]agtgcccagagaaggg	C	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 994165 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1994564	gaggagcaagtctcac[A/C]cagaaatatccttgta	A	C	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 435206 // Hs.369675 // ANGPT1 // 284 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2029001	aaagaaaatcaacatg[C/T]aagccacagcatatac	C	T	// Homo sapiens FLJ46082 protein (FLJ46082), mRNA. /// ENST00000343036 // intron // 0 // --- // --- // ---	FLJ46082	FLJ46082, Homo sapiens FLJ46082 protein (FLJ46082), q34.13
SNP_A-2027007	aaacagactaatacaa[C/G]tgctgtcattaatgaa	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1377650 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2029538	aaagactagagcaaca[C/T]attaaaaagggaaggt	C	T	Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// ENST00000301776 // intron // 0 // --- // --- // ---	ASRGL1	ASRGL1, Homo sapiens asparaginase like 1 (ASRGL1), q12.3
SNP_A-2032538	aaataaaataaagtag[C/T]aagacctctgtgatta	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2034766	aaatgaatttgggtta[C/T]gtaaaggaagacaaaa	C	T	84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// ENST00000266534 // intron // 0 // --- // --- // --- // ---	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-2045253	aagaaggagaggataa[C/T]gactaaagatgcagca	C	T	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 571561 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2017973	caccgaaagagaaatg[A/C]aaagaatgaccttagt	A	C	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2080708	acctcattggcctgga[C/G]atttgggagccatgca	C	G	Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// ENST00000359930 // intron // 0 // --- // --- // --- // ---	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.12
SNP_A-2100988	agatatttagccctga[C/G]taattaccctggattc	C	G	Homo sapiens immune costimulatory protein B7-H4 (B7-H4), mRNA. /// ENST00000359008 // intron // 0 // --- // --- // --- // ---	B7-H4	B7-H4, Homo sapiens immune costimulatory protein B7-H4 (B7-H4), p13.1
SNP_A-2096996	agactgcagtgctaac[C/T]atgcaagctacagtga	C	T	DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 3283 // --- // --- // --- // --- ///	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-2107788	agctcagtccagagca[A/G]aactgagggtcttccc	A	G	57396 // Homo sapiens CDC-like kinase 4 (CLK4), mRNA. /// NM_005649 // downstream // 41333 // Hs.484324 //	CLK4	CLK4, Homo sapiens CDC-like kinase 4 (CLK4), q35.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227189	ctaatttattctgcac[A/G]atgaatagagagaaat	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2170582	caagtggaaaaaattg[C/T]aggacatcataaactg	C	T	FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2174309	cacacttattgaaaag[C/G]ctatttctattacatt	C	G	Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), mRNA. /// ENST00000359885 // intron // 0 // --- // --- // --- // ---	GDAP2	GDAP2, Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), p12
SNP_A-1869749	tccttcaggtctccaa[G/T]ccaatgttactccatt	G	T	/// ENST00000335028 // upstream // 109503 // --- // --- // --- // -	-	q21.31
SNP_A-1863890	tccaatctgaagccaa[A/T]gtagaaaccgtagctc	A	T	90390 // Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), mRNA. /// NM_000127 // downstream //	THRAP6	THRAP6, Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), q24.11
SNP_A-1828985	taaggcgctgtgactt[A/G]aagagactgcaaagcc	A	G	Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 6 (CHCHD6), mRNA. /// ENST00000290913 // intron // 0 // --- // --- // --- // ---	CHCHD6	CHCHD6, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 6 (CHCHD6), q21.2
SNP_A-1889231	tgagtgaagctctttc[A/G]cagacctgaatcttaa	A	G	58515 // Homo sapiens selenoprotein K (SELK), mRNA. /// NM_018398 // upstream // 159416 // Hs.369421 //	SELK	SELK, Homo sapiens selenoprotein K (SELK), p21.1
SNP_A-1916076	tgttgctccccttcaa[A/G]tccatgacattcatct	A	G	sapiens interferon regulatory factor 2 (IRF2), mRNA. /// ENST00000303389 // intron // 0 // --- // --- // --- // ---	IRF2	IRF2, Homo sapiens interferon regulatory factor 2 (IRF2), q35.1
SNP_A-1948147	tttagcaagtaccaga[A/T]accgcaaatcacagct	A	T	/// ENST00000343695 // downstream // 25105 // --- // --- // ---	-	q21.31
SNP_A-1966333	tcaaagtaaaattaga[C/T]cagtacagtttatatt	C	T	/// ENST00000354860 // upstream // 56812 // --- // --- // --- // ---	-	q32.3
SNP_A-1974012	ttctgtatttcctcca[C/T]tattgtgtttcctcca	C	T	Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // -	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-1980775	agtcctttgacctaag[C/T]atagtatccggttctt	C	T	Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-2282842	gataaaggtaacatat[G/T]aatgatgcacaaaaca	G	T	Homo sapiens receptor associated protein 80 (RAP80), mRNA. /// ENST00000323774 // intron // 0 // --- // --- // --- // ---	RAP80	RAP80, Homo sapiens receptor associated protein 80 (RAP80), q35.2
SNP_A-2274511	gacttttttattttga[A/T]ctgtgcttttgtatta	A	T	163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 54624 // Hs.546355 // TA-LRRP //	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2270659	gacagcacttgaatag[A/G]aatcaatttgcatcat	A	G	ENST00000294484 // intron // 0 // --- // --- // --- // ---	-	p36.22
SNP_A-2288102	gattcactgaatgaga[A/T]tagtagcccacaaatc	A	T	FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 574381 //	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2299556	gccgaatgtctgatcc[C/T]cctcacctcctgcctc	C	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 151519 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2289150	gatttctttttaaaca[A/C]atgagaatttacaaga	A	C	// 79290 // Homo sapiens olfactory receptor, family 13, subfamily A, member 1 (OR13A1), mRNA. /// NM_000698 // upstream // 47630 // Hs.89499 // ALOX5 // 240 // Homo	OR13A1	OR13A1, Homo sapiens olfactory receptor, family 13, subfamily A, member 1 (OR13A1), q11.21
SNP_A-2311391	ggaatcaaaacttata[C/T]gtggattttcagatgt	C	T	4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 45860 // --- // ---	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-2259850	gaaaagctgatgccca[A/G]taagaggactggttaa	A	G	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 1, m /// ENST00000264959 // intron // 0 // --- // --- // --- // ---	PPP2R2C	PPP2R2C, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 1, m ,p16.1
SNP_A-2279280	gaggagataatatagc[C/T]gaagttaatttccatg	C	T	H.sapiens TAFII105 mRNA, partial. /// ENST00000269142 //	TAF4B	TAF4B, H.sapiens TAFII105 partial. ,q11.2
SNP_A-2230823	ctatgcaaaagaagta[C/T]agatgcttggaagggt	C	T	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 192118 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-1984999	ccttctgttcttttag[C/T]aaatcaaggtattcac	C	T	9521 // Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA. /// NM_015948 // downstream	EEF1E1	EEF1E1, Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), p24.3
SNP_A-1984799	ctcactaagaatcaaa[C/T]gaatggttattttctc	C	T	Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // --- // --- // --- // ---	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-1951704	tttcctttcttaacca[A/T]gctaaatggactggag	A	T	/// ENST00000356718 // upstream // 45344 // --- // --- // --- // ---	-	q24.21
SNP_A-1933628	ttctaggcccacgctt[C/T]aaaaggacacagcttc	C	T	// 54860 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), mRNA. /// NM_174939 // upstream // 52580 // Hs.372650 // MGC39681 // 283197 //	MS4A12	MS4A12, Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), q12.2
SNP_A-1911453	cataatgtaatacata[C/T]accatgaggtaactac	C	T	51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 813604 //	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884110	tgaagccttattcaga[G/T]caccctttctggttcc	G	T	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), mRNA. /// ENST00000262367 //	CREBBP	CREBBP, Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), p13.3
SNP_A-1892638	tgcaatttcatacgta[A/G]caaatttaattcagtt	A	G	/// ENST00000262227 // upstream // 235673 // --- // --- // --- // --- /// ENST00000314319 // upstream // 284152 // --- // --- // ---	-	p11.31
SNP_A-1835152	taccctcacccacag[C/T]ccctaattgttacatg	C	T	// Homo sapiens NY-REN-41 antigen (NY-REN-41), mRNA. /// ENST00000317945 // intron // 0 // --- // --- // --- // --- ///	NY-REN-41	NY-REN-41, Homo sapiens NY-REN-41 antigen (NY-REN-41), p14.1
SNP_A-1832839	tacaatatcttgaaag[C/T]atcatcttaaggttta	C	T	/// ENST00000325796 // downstream // 576024 // --- // --- // ---	-	q22.1
SNP_A-1830391	taatattaaaatctac[A/C]agtttctattaaattt	A	C	PDZRN4 // 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 //	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12
SNP_A-1847629	tatctaaccagtgtct[C/G]acatacagaaaggtgt	C	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3415105 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1849549	tatgggattctccaat[G/T]aggatggtccttgacc	G	T	57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// NM_012224 // downstream // 1603 // Hs.481181 //	SH3MD2	SH3MD2, Homo sapiens SH3 multiple domains 2 (SH3MD2), q33
SNP_A-1789545	gggccttacccttcc[A/G]gagagcctgatttagt	A	G	Homo sapiens F-box and leucine-rich repeat protein 8 (FBXL8), mRNA. /// ENST00000258200 // intron // 0 // --- // ---	FBXL8	FBXL8, Homo sapiens F-box and leucine-rich repeat protein 8 (FBXL8), q22.1
SNP_A-1813055	gtgggtgttcagaccc[A/G]aaggcagaactgtcag	A	G	Homo sapiens mitogen-activated protein kinase kinase 2 (MAP2K2), mRNA. /// ENST00000262948 // intron // 0 // --- // -	MAP2K2	MAP2K2, Homo sapiens mitogen-activated protein kinase kinase 2 (MAP2K2), p13.3
SNP_A-1668833	ctacagaaggccaatgtattaaaga[A/G]tcctgaaaatgtcagtatatgcaga	A	G	2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_002941 // upstream // 647592 // Hs.301198 // ROBO1 // 6091 //	GBE1	GBE1 , rs9309853, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-1695337	cacttgtaaaacaataggattaaga[C/T]agagtgagatttttaaaacactttt	C	T	NM_006846 // upstream // 111058 // Hs.331555 // SPINK5 // 11005 // serine protease inhibitor, Kazal type 5	SPINK5	SPINK5 , rs10515597, serine protease inhibitor, Kazal type 5,q33.1
SNP_A-2191825	catattttggctgtga[C/T]attgtaaacagtgtca	C	T	Homo sapiens allantoicase (ALLC), transcript variant 2, mRNA. /// NM_018436 // intron // 0 // Hs.97899 // ALLC //	ALLC	ALLC, Homo sapiens allantoicase (ALLC), transcript variant 2, p25.3
SNP_A-2193306	catctcgtggtagcca[A/G]agttacttctaaaatg	A	G	Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // --- // --- // --- // --- ///	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2126537	tagaaagatactttcc[C/T]atacaatcatgcactg	C	T	Homo sapiens SMAD, mothers against DPP homolog 9 (Drosophila) (SMAD9), mRNA. /// BC011559 // intron // 0 //	SMAD9	SMAD9, Homo sapiens SMAD, mothers against DPP homolog 9 (Drosophila) (SMAD9), q13.3
SNP_A-2127358	ataaattgtctaagcc[C/T]gcaaaatatagggtaa	C	T	METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream //	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-2146845	atgctttcccaggtgc[C/T]cacttgtttcaggagc	C	T	// 157922 // Homo sapiens calmodulin regulated spectrin-associated protein 1 (CAMSAP1), mRNA. /// NM_016172 //	CAMSAP1	CAMSAP1, Homo sapiens calmodulin regulated spectrin-associated protein 1 (CAMSAP1), q34.3
SNP_A-2157967	attgcttaagtacata[A/G]tataggaaaaatctgt	A	G	Homo sapiens small nuclear RNA activating complex, polypeptide 3, 50kDa (SNAPC3), mRNA. /// ENST00000360381 // intron // 0 // --- // --- // --- // --- ///	SNAPC3	SNAPC3, Homo sapiens small nuclear RNA activating complex, polypeptide 3, 50kDa (SNAPC3), p22.3
SNP_A-2107655	agctattgtggcaaaa[G/T]aaagggagataaagta	G	T	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 752046 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2064295	aattcagctggtctga[C/T]ggtgaacactcaagat	C	T	EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 623455 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2063485	aattaatatatggtga[C/G]tatcttcccacattat	C	G	8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 24394 //	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2062567	aatgtcacaaaaccct[A/G]acacagtgaaacaatt	A	G	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 //	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2014569	agattcctcttctcac[C/G]acatgaagctcccctc	C	G	5047 // Homo sapiens progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin /// NM_001001676 // upstream // 77430 // Hs.532679 // LCN9 //	PAEP	PAEP, Homo sapiens progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin ,q34.3
SNP_A-2012207	cattttttcagctccat[C/T]acgatctatgggacca	C	T	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 23511 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2044054	aacttgctactgctct[C/G]accttatgcccatttc	C	G	154043 // Homo sapiens membrane associated guanylate kinase interacting protein-like 1 (MAGI1), mRNA. /// NM_014892 // upstream // 51792 // Hs.227602 // RBM16 //	MAGI1	MAGI1, Homo sapiens membrane associated guanylate kinase interacting protein-like 1 (MAGI1), q25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2042601	aactccatgaaaacaa[A/G]gacttatttttgtctg	A	G	// 388536 // Homo sapiens hypothetical protein LOC388536 (MGC62100), mRNA. /// NM_003419 // downstream // 39694	MGC62100	MGC62100, Homo sapiens hypothetical protein LOC388536 (MGC62100), q13.12
SNP_A-2036979	aaattttgagtctttta[C/T]agaatagctgttcatg	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-2023947	aaaagacaagttttca[C/T]agagtgacattactat	C	T	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 587729 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2037907	aacaatgctgttacat[A/C]ataccctgggtttgtt	A	C	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2043660	aacttaactcacgaca[C/T]agaatggaatttttta	C	T	// --- /// ENST00000354793 // downstream // 270332 // --- // ---	-	p13.3
SNP_A-2012230	gaccacacagagagac[A/G]agctgggtgtttctta	A	G	Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-2063950	aattatcatagaaaaa[C/G]aaacaaaacgacagca	C	G	Homo sapiens Cbl-interacting protein Sts-1 (STS-1), mRNA. /// ENST00000284273 // 3UTR // 0 // --- // --- // --- // ---	STS-1	STS-1, Homo sapiens Cbl-interacting protein Sts-1 (STS-1), q24.1
SNP_A-2072633	acagcctaagtgtgta[C/T]gcagctaggtttgtgt	C	T	6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 85751 // Hs.175905 // AUH //	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2105898	agccatattttagatc[C/T]actggaaggggtttgg	C	T	/// ENST00000251675 // downstream // 215189 // --- // --- // --- // --- /// ENST00000360855 // downstream // 215219 // --- // ---	-	q32.3
SNP_A-2081598	accttacaagaaaagc[A/G]atcaggggtcaccctt	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2086216	actctgctttatgatg[C/T]caaagcagtgggcaaa	C	T	// 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1036900 // Hs.98262 // GRIK2	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2089105	acttaatatgtgcttc[A/G]ctgtggcctggatctc	A	G	Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // intron // 0 // --- // ---	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1
SNP_A-2153354	attagaagctagttaa[A/C]caaggtctactccttg	A	C	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 184269 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1646734	tatcataaagaaatacccatttgtaa[C/T]agaaggagaagtccctgtgaggatc	C	T	BC053595 // intron // 0 // Hs.454533 // KIAA0930 // 23313 // KIAA0930 protein	KIAA0930	KIAA0930 , rs10483227, KIAA0930 protein,q13.31
SNP_A-1814562	gtgtgcttgtatcatc[A/G]agtcaacccaattaat	A	G	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000340635 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q12.1
SNP_A-1808479	gtgaaagatgtgacca[C/T]agaaaagcagtgctga	C	T	5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 1025576 //	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1802500	gtatcctgagtttacc[A/G]ggaaaaacacattcta	A	G	Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), mRNA. /// ENST00000258326 // intron // 0 // --- // ---	ACBD6	ACBD6, Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), q25.3
SNP_A-1789854	agtgatcaatttgtaa[A/C]actgttgtctggagtc	A	C	// Homo sapiens B/K protein (LOC51760), mRNA. /// ENST00000261375 // intron // 0 // --- // --- // --- // --- ///	LOC51760	LOC51760, Homo sapiens B,p12.3
SNP_A-1869638	tccttagacttcaagc[C/T]agttggttgccttaag	C	T	6224 // Homo sapiens ribosomal protein S20 (RPS20), mRNA. /// ENST00000317182 // upstream // 110 // --- // --- // ---	RPS20	RPS20, Homo sapiens ribosomal protein S20 (RPS20), q12.1
SNP_A-1866806	tcccgccccgccttac[A/G]gatgagttttcctgag	A	G	Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// ENST00000261654 // intron // 0 // --- // --- // --- // ---	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-1840518	tagccatgcagtaaaa[A/G]atagttttggactaat	A	G	Homo sapiens ring finger protein (C3H2C3 type) 6 (RNF6), transcript variant 2, mRNA. /// ENST00000339626 // intron // 0 // --- // --- // --- // ---	RNF6	RNF6, Homo sapiens ring finger protein (C3H2C3 type) 6 (RNF6), transcript variant 2, q12.13
SNP_A-1890834	tgatgccaataccctc[A/G]attaatgttcaactgt	A	G	Homo sapiens ARG99 protein (ARG99), mRNA. /// ENST00000256062 // intron // 0 // --- // --- // --- // ---	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1895923	tgcctgttttccaatc[C/T]catccggtcaattctc	C	T	23369 // Homo sapiens pumilio homolog 2 (Drosophila) (PUM2), mRNA. /// NM_015317 // upstream // 79260 //	PUM2	PUM2, Homo sapiens pumilio homolog 2 (Drosophila) (PUM2), p24.1
SNP_A-1883442	tgaacataaatttcaa[A/T]gtatttcgatgtaaat	A	T	sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 //	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-1908634	tgtagcttaggaaaca[C/T]agaaggaattacacat	C	T	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1932839	ttcctttaaagctata[A/G]taagagaccagaaagc	A	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1951274	tttcccgcgtctcata[C/T]actcaacactcaacaa	C	T	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 588071 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1948879	tttatcagctaattaa[A/G]gcaaaacaaattgcca	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1959344	ttttgcaagaaggcat[C/G]aagtgctgtagtgggc	C	G	Homo sapiens chromosome 20 open reading frame 31 (C20orf31), mRNA. /// ENST00000262875 // intron // 0 // --- //	C20orf31	C20orf31, Homo sapiens chromosome 20 open reading frame 31 (C20orf31), q11.22
SNP_A-2232789	ctcactgggcctgagc[A/G]ctgaaagagagggccg	A	G	ENST00000354500 // intron // 0 // --- // --- // --- // ---	-	q21.11
SNP_A-2234464	ctccacacccttaccc[C/T]ggaatgttcatcccac	C	T	2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 14020 //	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-2255441	cttgtcctaagttgca[C/T]agctagtaaatggcag	C	T	Homo sapiens hypothetical protein MGC4266 (MGC4266), mRNA. /// ENST00000333750 // intron // 0 // --- // --- // --- // ---	MGC4266	MGC4266, Homo sapiens hypothetical protein MGC4266 (MGC4266), p13.32
SNP_A-2281656	gagtctgccttgacac[A/G]ggaggaaccaagtggc	A	G	6004 // Homo sapiens regulator of G-protein signalling 16 (RGS16), mRNA. /// NM_033345 // downstream // 29589 //	RGS16	RGS16, Homo sapiens regulator of G-protein signalling 16 (RGS16), q25.3
SNP_A-2281527	gagtccaggaagcaaa[G/T]aatttgtttatgcctt	G	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1656411 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2280003	gaggcttcaggagata[C/T]acgatcatggtggaag	C	T	1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 153132 // Hs.183850 // DCTD //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-2274349	gacttgtggagtcaga[A/G]cttcagtcatcaccat	A	G	57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 316007 // Hs.424711 //	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2255826	cttgtttttagagagc[C/G]aagtgttagacatctt	C	G	126402 // Homo sapiens hypothetical protein FLJ40365 (FLJ40365), mRNA. /// NM_012114 // upstream // 6542 //	FLJ40365	FLJ40365, Homo sapiens hypothetical protein FLJ40365 (FLJ40365), p13.12
SNP_A-2244488	ctggacggaaatgtaa[A/T]gggaatgaaggaaagc	A	T	11181 // Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), mRNA. /// ENST00000264029 //	TREH	TREH, Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), q23.3
SNP_A-2230477	ctatcattgttggata[A/T]atgggttggttccagg	A	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 1258147 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2314798	ggagtgaggagccaca[C/T]aggcccaccgctggtt	C	T	ENST00000358431 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2308924	gcttttaacacctaaa[C/T]agaggagcacagtaat	C	T	5136 // Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), transcript variant 1, mRNA. /// NM_001003683 // upstream // 62682 // Hs.416061 // PDE1A	PDE1A	PDE1A, Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), transcript variant 1, q32.1
SNP_A-2297826	gccagggtacaaagaa[C/G]tagaagtaaccataga	C	G	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 483616 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-1956499	tttgttgtcatggcaa[A/C]tctgtaagaaatctca	A	C	// 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 1848504 // --- // -	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1951549	tttcctgagggaaata[C/G]aaagacacatattagc	C	G	ENST00000340797 // intron // 0 // --- // --- // --- // ---	-	p14.2
SNP_A-1940773	ttgcgcaatgtatcac[A/G]gccctttcacatggac	A	G	Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // --- // --- // --- // ---	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1979971	gtgaatcagagcatca[A/C]aaagtccctgtgagtt	A	C	10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// NM_012180 // downstream // 73393 // Hs.76917 // FBXO8 //	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-1975962	gagatctgttccctct[C/G]acacaatcctttactg	C	G	/// ENST00000326756 // downstream // 166936 // --- // --- // ---	-	p16.1
SNP_A-1924874	ttatatgccaagtagt[C/T]aagaatgctcagtgat	C	T	MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// NM_015069 //	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-1922969	ttagcaagactttctg[C/T]aaataagaatctcgga	C	T	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 449678 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-1909148	tgtatcctttaactaa[A/T]caattttgtctgaaaa	A	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2620071 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1899132	tggaaagatgaaggac[A/G]ctacttgaagctcctt	A	G	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1827599	taactgcatcacaccc[G/T]aacaatttactgcatg	G	T	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 75376 // --- // --- // --- // ---	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1791107	ggggtgctgagatgga[C/T]agtttcggggagactt	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2146009	atgcctcccgggccaa[C/T]gtttttccaatccatg	C	T	Homo sapiens RNA-binding protein (FLJ20273), mRNA. /// ENST00000319592 // intron // 0 // --- // --- // --- // --- ///	FLJ20273	FLJ20273, Homo sapiens RNA-binding protein (FLJ20273), p14
SNP_A-2184430	cagctaaaaacaacaa[A/G]cttccactatagcatc	A	G	2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 233298 // --- // --- // --- //	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189957	cataacaaatgtgaca[C/G]gttaacacaagtacaa	C	G	ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // downstream // 422766 // Hs.126838	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.1
SNP_A-2169348	caagcagtaccttcac[A/G]gtaagtcctgtgcagg	A	G	27436 // Homo sapiens echinoderm microtubule associated protein like 4 (EML4), mRNA. /// ENST00000294964 //	EML4	EML4, Homo sapiens echinoderm microtubule associated protein like 4 (EML4), p21
SNP_A-2218693	cctggcggtcctctta[C/T]gtccttactgtgcagc	C	T	LOC414059 // 414059 // Homo sapiens similar to TBC1 domain family, member 3, centromeric (LOC414059), mRNA. /// NM_032258 // upstream // 13020 // Hs.105891 // TBC1D3	LOC414059	LOC414059, Homo sapiens similar to TBC1 domain family, member 3, centromeric (LOC414059), q12
SNP_A-2217682	cctgagtggccgtgac[A/G]gcagtgaccattggtg	A	G	sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // --- // --- // --- // --- /// ENST00000301226 // intron //	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2095523	agacaagcagaatagg[A/G]cagatacccacacaca	A	G	200728 // Homo sapiens transmembrane protein 17 (TMEM17), mRNA. /// NM_015252 // upstream // 140067 //	TMEM17	TMEM17, Homo sapiens transmembrane protein 17 (TMEM17), p15
SNP_A-2072831	acagctggtactgcca[C/T]gtttttgatggcctaa	C	T	Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA. /// ENST00000327801 // intron // 0 // --- // ---	SMYD3	SMYD3, Homo sapiens SET and MYND domain containing 3 (SMYD3), q44
SNP_A-2063894	aattatacatatatac[C/T]gcatgaacacatgtaa	C	T	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// ENST00000322536 // intron // 0 // --- // ---	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2067202	acaaagccttccttga[C/T]catcccagttcaaagt	C	T	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2050942	aaggctacacttggga[A/G]gaatgtttacaaactg	A	G	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-2057471	aatatctaacagagaa[A/T]ctgctaacaaaagtgg	A	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 540577 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2016760	cctttggaatatttca[A/T]ctttatgtccactggg	A	T	LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 566461 // --- // --- // --- //	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-2017044	cccccgatagccaagg[C/T]cccattatcattgccc	C	T	sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // intron // 0 // Hs.434980 // APP // 351 // Homo	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3
SNP_A-2037826	aacaatagagaactaa[C/T]tcactaacctgttatc	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2023019	aaaacactagtcctac[A/T]ggattaggagcccatc	A	T	CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 //	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2030552	aaagcgctctcaaatg[C/G]aacatagcagggaacc	C	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2022899	aaaacaacttgtggaa[A/T]aagagagaattacatc	A	T	// 285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// NM_021159 // upstream // 91811 //	MGC46496	MGC46496, Homo sapiens hypothetical protein MGC46496 (MGC46496), q23
SNP_A-2033518	aaatataagtgtagga[A/G]aaaagttgttactatg	A	G	// 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// NM_002718 // upstream // 15386 // Hs.518155 // PPP2R3A //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.2
SNP_A-2044035	aacttgcattatcaaa[A/G]gataccatcaaaaaat	A	G	Homo sapiens Rap2-binding protein 9 (RPIB9), mRNA. /// ENST00000338056 // intron // 0 // --- // --- // --- // --- ///	RPIB9	RPIB9, Homo sapiens Rap2-binding protein 9 (RPIB9), q21.12
SNP_A-1994795	ccttttactctaact[C/G]aggataactctgagag	C	G	SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 129763 // Hs.492612 // THRAP6 //	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2070404	acacccaaacaggacg[A/G]cactggggtcctccag	A	G	Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /// ENST00000355191 // intron // 0 // --- // --- // --- // ---	NCOR2	NCOR2, Homo sapiens nuclear receptor co-repressor 2 (NCOR2), q24.31
SNP_A-2096256	agaccacatggggtaa[C/T]gggcctccatgtctct	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2087248	actgcaaacctggata[A/G]catgttactgtactaa	A	G	Homo sapiens speedy homolog 1 (Drosophila) (SPDY1), mRNA. /// ENST00000334056 // intron // 0 // --- // --- // --- // ---	SPDY1	SPDY1, Homo sapiens speedy homolog 1 (Drosophila) (SPDY1), p23.2
SNP_A-2083706	actacacttcactacc[A/G]gcactgatttcacctg	A	G	sapiens selectin P (granule membrane protein 140kDa, antigen CD62) (SELP), mRNA. /// ENST00000263686 // intron // 0 // --- // --- // --- // ---	SELP	SELP, Homo sapiens selectin P (granule membrane protein 140kDa, antigen CD62) (SELP), q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2146374	atgctcaaatccacta[A/G]taagtggctgtccatt	A	G	Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // --- // --- // --- // ---	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-2147320	atggagaggctcacaa[C/T]gtggagagttgcttct	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 955127 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2129595	atacagaatacactca[A/T]atcccttggaaggata	A	T	Homo sapiens chromosome 15 open reading frame 27 (C15orf27), mRNA. /// ENST00000305457 // intron // 0 // --- //	C15orf27	C15orf27, Homo sapiens chromosome 15 open reading frame 27 (C15orf27), q24.2
SNP_A-1796430	ggtgtttgttacaatc[C/T]caaaagtaggatcacg	C	T	ENST00000354205 // intron // 0 // --- // --- // --- // ---	-	p11.2
SNP_A-1812163	gtggagcgaggcactg[A/G]agtcctatggttatga	A	G	Homo sapiens mRNA; cDNA DKFZp667H0525 (from clone DKFZp667H0525). /// ENST00000357056 // intron // 0 // --- //	TTC7B	TTC7B, Homo sapiens cDNA DKFZp667H0525 (from clone DKFZp667H0525). ,q32.12
SNP_A-1704263	gagtaaattacgctcccaatgaaca[A/T]ctcttcactattacttaagactgat	A	T	ADRA2A // 150 // adrenergic, alpha-2A-, receptor /// NM_020918 // downstream // 541105 // Hs.42586 //	ADRA2A	ADRA2A , rs1914092, adrenergic, alpha-2A-, receptor ,q25.2
SNP_A-1899268	tggaaattttagatca[C/T]ggttgccctcttttcc	C	T	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // --- // ---	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1885033	tgaatggcagaaatgg[A/G]aggacagaagaaaaat	A	G	8491 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// NM_152390 // upstream // 97116 // Hs.40808 // MGC33926 // 130733 //	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-1875919	tctgaaatcagtgtca[G/T]cagagttttttttttc	G	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1911479	tgtcttgtgctgtgct[A/G]agaacacaaaatgacc	A	G	Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// ENST00000263985 // intron // 0 // --- // --- // --- // ---	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-1917281	tgttttcaccccaaga[C/T]ccatttttctctaggtc	C	T	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 8 (ABCC8), mRNA. ///	ABCC8	ABCC8, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p15.1
SNP_A-1918823	ttaacagcttcttttg[A/G]aggatagatgttttac	A	G	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1924119	ttagttccagctctta[C/G]gcggaatgcttccagc	C	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1374898 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1922243	ttacttggtgcaataa[A/G]tcagcgtatttatttt	A	G	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 246620 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1930530	ttccaactgcagttaa[A/G]atcaaaccaccaagac	A	G	55973 // Homo sapiens B-cell receptor-associated protein 29 (BCAP29), mRNA. /// NM_000441 // upstream // 38310 //	BCAP29	BCAP29, Homo sapiens B-cell receptor-associated protein 29 (BCAP29), q22.3
SNP_A-2301674	gcgcccgttgaaaaca[C/T]aggtttgtcctgaact	C	T	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2311955	ggacaagcctggatga[C/G]ctgaggagtgagggag	C	G	65985 // Homo sapiens acetoacetyl-CoA synthetase (AACS), mRNA. /// ENST00000316519 // downstream // 139029 // ---	AACS	AACS, Homo sapiens acetoacetyl-CoA synthetase (AACS), q24.31
SNP_A-2230954	ctatgggatgacacag[C/T]aaaaagaccctcatta	C	T	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2, mRNA. /// NM_182643 // intron // 0 // Hs.134296 //	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2, p22
SNP_A-2242221	ctgcaactagcatcag[C/T]atggaaatggaccagc	C	T	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // --- // ---	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2241203	ctgaggacagtcacca[A/G]gacctgtttgtatgtg	A	G	Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // --- // --- // --- // ---	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-2277595	gagcacctcacaaaaa[C/T]caatcctcccaacaat	C	T	7832 // Homo sapiens BTG family, member 2 (BTG2), mRNA. /// NM_002023 // downstream // 14035 // Hs.519168	BTG2	BTG2, Homo sapiens BTG family, member 2 (BTG2), q32.1
SNP_A-2312427	ggaccagacttagaga[G/T]gaatgaggctgcagaa	G	T	LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 //	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-2309625	ggaaagacacaaagta[C/G]acaagcaattttgctt	C	G	PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.2
SNP_A-2298081	gccatcacattcactc[C/T]cttcttatgttgaaaa	C	T	// Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// NM_153825 // downstream // 40034 //	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-1893597	tgcagggtaatttgca[A/G]aatctcagaatcaggg	A	G	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-1965220	gataactctacatcaa[A/G]aaatagcagaaaacta	A	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 878281 // --- // ---	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1982847	gatctttgggtgtgca[A/G]aaagaagagaaagaca	A	G	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 65128 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1987767	ttagaaagtctatcaa[C/T]gtgaaaggtgaagaga	C	T	sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA. /// ENST00000339290 // intron // 0 // ---	MYB	MYB, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), q23.3
SNP_A-1936683	tggaacactgaaaacc[A/G]gcggcagaatggcaca	A	G	2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1696712 // Hs.514980 // SALL3 //	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-1812383	gtggcacaacttcacc[A/G]ctgaattagtttaatc	A	G	Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // --- // --- // --- // ---	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-1801650	gtagtagagaccaggc[A/C]aaaggggtttggattc	A	C	ENST00000339762 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1794634	ggtctatccttccaac[C/T]gagtgttccggaacag	C	T	4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 99711 // --- // FLJ34047 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1789721	gggctcatttgatttc[A/G]ctactaaagctggggt	A	G	ENST00000327131 // downstream // 22609 // --- // --- // --- // --- /// ENST00000260742 // upstream // 3424 // --- // --- // --- // ---	-	q26.13
SNP_A-1819661	gttgtatctgtctcga[C/T]ggcgttgtgtcaacgt	C	T	// 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 //	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-1839849	tagattctggttggcc[A/G]aggactgaagagtttc	A	G	--- /// ENST00000360683 // downstream // 624856 // --- // --- // --- // --- /// ENST00000345990 // downstream // 625914 // --- // ---	-	q23.2
SNP_A-1829869	taataagagaattgca[A/T]attagaagcacgatgt	A	T	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1861422	tcatcatcatcaacaa[C/G]agtaaacatttcttga	C	G	6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 152226 // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2136599	tttagacatagaaaaa[A/G]aggcccagaagagtta	A	G	NM_198989 // downstream // 447392 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.3
SNP_A-2113380	ctgtgaattattcttc[C/G]caaacagtgtttaaga	C	G	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 995958 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2114330	agggaattttacagat[A/G]aatcatgttcttttgt	A	G	Homo sapiens HRAS-like suppressor 3 (HRASLS3), mRNA. /// ENST00000356525 // intron // 0 // --- // --- // --- // --- ///	HRASLS3	HRASLS3, Homo sapiens HRAS-like suppressor 3 (HRASLS3), q13.1
SNP_A-2119020	agtagaccgaggacta[A/G]gtggaaaggggaaaaa	A	G	255082 // Homo sapiens cancer susceptibility candidate 2 (CASC2), mRNA. /// NM_201377 // downstream // 24429 //	CASC2	CASC2, Homo sapiens cancer susceptibility candidate 2 (CASC2), q26.11
SNP_A-2166486	caaatgccattaaaaa[C/G]ctggctggtgatgaag	C	G	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, mRNA. /// NM_201268 // intron // 0 // Hs.75890 // MBTPS1 // 8720 //	MBTPS1	MBTPS1, Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, q23.3
SNP_A-2204645	tttacctcgttaaagt[A/C]aaaatgcatacatata	A	C	112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 478227 //	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2210366	tttggagaagagagaa[A/T]ttactataaacagaac	A	T	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2188800	cagtggcttcctataa[A/G]ctcaaatgcctacaaa	A	G	/// ENST00000359604 // upstream // 119363 // --- // --- // --- // --- /// ENST00000344172 // upstream // 30106 // --- // --- // --- //	-	q11.2
SNP_A-2184456	cagctaagtgagaacc[C/T]gagcagaaagcccacc	C	T	MGC40405 // 257415 // Homo sapiens hypothetical protein MGC40405 (MGC40405), mRNA. /// ENST00000314437 //	MGC40405	MGC40405, Homo sapiens hypothetical protein MGC40405 (MGC40405), q12.1
SNP_A-2196139	catgtgccagtcacta[C/T]gctaaatgctgtacat	C	T	5646 // Homo sapiens mRNA for trypsinogen IV a-form. /// NM_002771 // downstream // 16614 // Hs.435699 // PRSS3 //	PRSS3	PRSS3, Homo sapiens for trypsinogen IV a-form. p13.3
SNP_A-2080823	acctcgcgccccgacc[A/G]acgggactcgcgggct	A	G	145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 221558 // Hs.87889 // DICER1	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2079472	accccggttttgtata[A/C]gcctggattgtagaac	A	C	ENST00000355033 // intron // 0 // --- // --- // --- // --- /// ENST00000356605 // intron // 0 // --- // --- // --- // --- ///	-	p13.3
SNP_A-2074797	acatatttctgaaact[C/T]actcaccactgataaa	C	T	// 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 1234337 // Hs.391781 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-2060898	aatgatctaagctgct[A/G]aaactcatatctcaaa	A	G	81788 // Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK), mRNA. /// NM_018203 //	SNARK	SNARK, Homo sapiens likely ortholog of rat SNF1,q32.1
SNP_A-2012874	gtgtctcttggaatta[C/T]gtgtactgtaaatgag	C	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2010775	agtttttctaagagta[C/G]attttacgctcttgcc	C	G	-- /// ENST00000354793 // downstream // 1122210 // --- // ---	-	p13.3
SNP_A-2009812	ggcttaagttctgaca[C/T]agccacttagctctct	C	T	Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // --- // ---	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-2023729	aaaacttgtgtcccca[A/G]atgagatacattaaat	A	G	// Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// ENST00000341547 // upstream // 167914 // --- // ---	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2032052	aaagtgagaccaaata[C/T]cacaccaggtgctgaa	C	T	ENST00000330692 // intron // 0 // --- // --- // --- // ---	-	q13.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2042456	aactcagagcagtgac[A/G]catgggctcaaatgca	A	G	64759 // Homo sapiens tensin-like SH2 domain containing 1 (TENS1), mRNA. /// NM_022748 // upstream // 306 //	TENS1	TENS1, Homo sapiens tensin-like SH2 domain containing 1 (TENS1), p12.3
SNP_A-2014585	tttttgtttgttttac[C/T]atagcaaagtctgacc	C	T	5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 144931 // Hs.159003 //	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-1996286	ctccatatcttgggaa[G/T]gtaaccacagagaata	G	T	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 526975 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2065345	aattgtcaaaagatac[C/T]gaaaagttcaacttaa	C	T	Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, mRNA. /// ENST00000304338 // intron // 0 // --- // --- // --- // ---	KIAA1622	KIAA1622, Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, q32.13
SNP_A-2091670	agaaaagacagcggct[C/T]aagtcaatggtgggcg	C	T	2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// NM_002017 // upstream // 70682 // Hs.504281 // FLI1 // 2313 // Homo	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3
SNP_A-2173548	cacaatggctttcttg[A/G]atcagcaatgtatgga	A	G	Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // --- // -	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-2173167	cacaacaagcctatga[A/G]gcatagtttaccatca	A	G	/// ENST00000295345 // upstream // 90010 // --- // --- // --- // --	-	q13
SNP_A-2177258	cacctggggccgcagg[C/G]acagtttggaggacaa	C	G	Homo sapiens acyl-Coenzyme A oxidase-like (ACOXL), mRNA. /// ENST00000283065 // intron // 0 // --- // --- // --- // ---	ACOXL	ACOXL, Homo sapiens acyl-Coenzyme A oxidase-like (ACOXL), q13
SNP_A-2179199	cactgggccaagaagg[C/T]caacaaggtggtgcca	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2203061	ccactgcaaaataaag[A/T]actggaacaaaatggt	A	T	8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream //	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-2218873	cctggggccctgatag[G/T]acacctttggtaggca	G	T	Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // --- // --- // --- // ---	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2141491	atcttaatccaatcca[A/G]ctaatcttgtcctcct	A	G	1021 // Homo sapiens cyclin-dependent kinase 6 (CDK6), mRNA. /// NM_152703 // downstream // 143493 // Hs.489118	CDK6	CDK6, Homo sapiens cyclin-dependent kinase 6 (CDK6), q21.2
SNP_A-2119577	agtatgacaggatcag[A/T]ccaggaggcttgcatg	A	T	ENST00000334037 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1861690	tcatctctctcctaca[C/T]ggtgagctccatgagg	C	T	sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 //	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-1861836	tcatctttctgaggaa[A/G]ctgaaagacaaatact	A	G	// 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000355465 // upstream //	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-1853021	tatttgattcctggac[A/G]agatatttgcagtgga	A	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 460092 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1842704	tagtaactaaatggta[A/G]aatgtaactattaata	A	G	// Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1801990	gtataacttgctgaat[G/T]aagcagaacctattca	G	T	10551 // Homo sapiens anterior gradient 2 homolog (Xenopus laevis) (AGR2), mRNA. /// NM_176813 //	AGR2	AGR2, Homo sapiens anterior gradient 2 homolog (Xenopus laevis) (AGR2), p21.1
SNP_A-1810230	gtgatgacatgagtgc[A/T]atttttttaattccat	A	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1810122	gtgatcaattatgagc[C/T]actgtcttaaaagcac	C	T	Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydr /// ENST00000216605 // intron // 0 // --- // --- // --- // ---	MTHFD1	MTHFD1, Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydr q23.2
SNP_A-1943898	ttgtatattctatacc[A/G]caatgtagctatggca	A	G	Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_144977 // intron // 0 // Hs.497279 // FAM31B //	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-1961798	actcacagcaaattgt[A/G]aatattggaaatggtc	A	G	sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_175719 // intron // 0 // Hs.467554 // TPO //	TPO	TPO, Homo sapiens thyroid peroxidase (TPO), transcript variant 5, p25.3
SNP_A-1979822	aactgcaataactagg[C/T]cctaaattccttaact	C	T	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1898867	tgcttttaactattca[G/T]atggatgtacagggtt	G	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 23843 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1873959	tctcatacagtggctc[C/T]gaaggcacaatatttt	C	T	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), mRNA. /// ENST00000307765 // intron // 0 // --- // --- // --- // --- /// ENST00000342048 // intron //	LGR7	LGR7, Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), q32.1
SNP_A-1880993	tcttgttaagattgat[G/T]agtattttcaagtcaa	G	T	84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream //	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1
SNP_A-1931029	ttccagtttgagaccc[A/G]ctgggttggacatagc	A	G	Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, mRNA. /// NM_022114 // intron // 0 //	PRDM16	PRDM16, Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, p36.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920995	ttacagatgagtgacc[C/T]agatcaccaagaggtc	C	T	Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// ENST00000360057 // intron // 0 // --- // --- // --- // --- ///	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-1923650	ttaggtctaaaaagaa[A/G]catttatcatctattc	A	G	374918 // Homo sapiens insulin growth factor-like family member 1 (IGFL1), mRNA. /// ENST00000328308 //	IGFL1	IGFL1, Homo sapiens insulin growth factor-like family member 1 (IGFL1), q13.32
SNP_A-1910994	tgtctccaaaacctca[C/T]agaaacatcatcattt	C	T	ENST00000311061 // intron // 0 // --- // --- // --- // ---	-	q14
SNP_A-1964689	cagtcaggccactgaa[A/G]gaatctcagcaaatcc	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2078061 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1966052	tctttttccttccgga[C/G]agtctcagtaattatt	C	G	285025 // Homo sapiens hypothetical protein FLJ39502 (FLJ39502), mRNA. /// NM_178123 // downstream // 37262 //	FLJ39502	FLJ39502, Homo sapiens hypothetical protein FLJ39502 (FLJ39502), q31.2
SNP_A-1955816	tttgtataggtaaata[C/G]gaaaatattcttcata	C	G	343170 // Homo sapiens olfactory receptor, family 5, subfamily AY, member 1 (OR5AY1), mRNA. /// NM_012353 //	OR5AY1	OR5AY1, Homo sapiens olfactory receptor, family 5, subfamily AY, member 1 (OR5AY1), q44
SNP_A-1952075	tttctattttaactca[A/T]cttctttcactgatgt	A	T	/// ENST00000357595 // downstream // 213663 // --- // --- // ---	-	q31.1
SNP_A-1935064	ttctgatcagtaggtc[C/T]aggataaggcataaga	C	T	5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // downstream // 81407 // --- // --- // --- // --- ///	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1
SNP_A-1800844	gtagagaatgcaggga[A/C]cataaaatctttagcc	A	C	5169 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3), mRNA. ///	ENPP3	ENPP3, Homo sapiens ectonucleotide pyrophosphatase,q23.2
SNP_A-1797879	ggttttgctgtcagca[C/G]gtggagagcatccctg	C	G	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1798788	gtaactctgagagaac[C/T]actctatgtggtgcag	C	T	Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA. /// ENST00000327680 // 5UTR // 0 // --- // --- // --- // ---	FLJ20641	FLJ20641, Homo sapiens hypothetical protein FLJ20641 (FLJ20641), q23.2
SNP_A-1784982	ggcgatttcagatgaa[A/C]cctgcaagaggcacag	A	C	Homo sapiens histone deacetylase 11 (HDAC11), mRNA. /// ENST00000295757 // intron // 0 // --- // --- // --- // ---	HDAC11	HDAC11, Homo sapiens histone deacetylase 11 (HDAC11), p25.1
SNP_A-1757357	ggagattggagtggggagaaactac[A/G]gcaagttaagaatagagtctgggcc	A	G	11082 // endothelial cell-specific molecule 1 /// NM_052870 // downstream // 73530 // Hs.297325 // SNAG1 // 112574 //	ESM1	ESM1 , rs10491380, endothelial cell-specific molecule 1 ,q11.2
SNP_A-1839808	tagattataggtagag[C/G]ataactcatcaccaca	C	G	55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// NM_001858 // upstream // 68329	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1829089	taaggtagccatagaa[C/T]tgattgaactgttctt	C	T	Homo sapiens pre-mRNA cleavage complex II protein Pcf11 (PCF11), mRNA. /// ENST00000298281 // intron // 0 // --- // ---	PCF11	PCF11, Homo sapiens pre- cleavage complex II protein Pcf11 (PCF11), q14.1
SNP_A-1857138	tcacctacgaagttga[A/G]taagttatttcgcctg	A	G	Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // --- // --- // --- // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-1872443	tctagcagcaatctta[C/T]gaaagcattatttaaa	C	T	FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// NM_152706 // upstream //	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-2135515	atattttaaaagggta[C/T]ccatatactcaagaat	C	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 732064 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2133780	atatcctcctcatata[A/G]caggcaatggctacaa	A	G	sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, mRNA. /// NM_019860 // intron // 0 // Hs.73739 // HTR7 //	HTR7	HTR7, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, q23.31
SNP_A-2151255	atgttacctagaaaat[A/G]aaatgcagggttataa	A	G	168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 73258 //	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2209856	ccccaaattagaagac[A/G]gatgaatctatttgct	A	G	23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA. /// NM_017939 // upstream // 118236 // Hs.313917 //	ZNF423	ZNF423, Homo sapiens zinc finger protein 423 (ZNF423), q12.1
SNP_A-2196830	cattactttctgcttc[A/G]agcccacattccagaa	A	G	ENST00000328569 // intron // 0 // --- // --- // --- // ---	-	q21.31
SNP_A-2060693	aatgagccttcaccac[C/T]aattgaacctatcaat	C	T	/// ENST00000318847 // downstream // 12528 // --- // --- // ---	-	q23.31
SNP_A-1996431	gtgttcctctcttctc[A/T]caaccagagactcatt	A	T	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1994773	tttggtcctttctatc[A/C]caaatcatgattttaa	A	C	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 321849 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-2005133	atttttataggagcaa[A/G]attactctgggaataa	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2041573	aacgagaatacagtaa[A/G]tggcccagggtacatc	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-gamma, mRNA. /// NM_013957 // intron // 0 // Hs.453951 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-gamma, p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2037194	aacaaacaaatagcag[A/G]aaccaaataaccactc	A	G	89780 // Homo sapiens wingless-type MMTV integration site family, member 3A (WNT3A), mRNA. /// ENST00000340510 // downstream // 11913 // --- // --- // --- // --- ///	WNT3A	WNT3A, Homo sapiens wingless-type MMTV integration site family, member 3A (WNT3A), q42.13
SNP_A-2033283	aaatagaagtgtttaa[A/C]agactatgacactctc	A	C	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1236400 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2297875	gccagtaagcagacac[A/G]aaatgatcagtagcat	A	G	Homo sapiens hook homolog 3 (Drosophila) (HOOK3), mRNA. /// ENST00000307602 // intron // 0 // --- // --- // --- // ---	HOOK3	HOOK3, Homo sapiens hook homolog 3 (Drosophila) (HOOK3), p11.21
SNP_A-2307385	gcttagtgcttttgta[G/T]gtgtgccctggagcct	G	T	Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // --- // --- // --- // ---	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-2305044	gctgaactgagaaaga[G/T]agtggagtttggtatt	G	T	Homo sapiens leucine aminopeptidase 3 (LAP3), mRNA. /// ENST00000226299 // intron // 0 // --- // --- // --- // ---	LAP3	LAP3, Homo sapiens leucine aminopeptidase 3 (LAP3), p15.32
SNP_A-2311632	ggaatgtcagacttcc[C/T]agtaatctctttcatt	C	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2283401	gataccatccaagtca[A/C]atggtttgtttcagct	A	C	Homo sapiens adenylate cyclase 9 (ADCY9), mRNA. /// ENST00000294016 // intron // 0 // --- // --- // --- ///	ADCY9	ADCY9, Homo sapiens adenylate cyclase 9 (ADCY9), p13.3
SNP_A-2264527	gaagaacttaaaccca[A/C]agactccattttcaaa	A	C	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// ENST00000332068 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2239220	ctcttggctattataa[A/G]taatgatacgatgaac	A	G	166815 // Homo sapiens tigger transposable element derived 2 (TIGD2), mRNA. /// NM_198281 // downstream // 78820 //	TIGD2	TIGD2, Homo sapiens tigger transposable element derived 2 (TIGD2), q22.1
SNP_A-2238440	ctctggtgcccaaaga[C/T]aggcatgctcagactg	C	T	942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // downstream // 33451 // Hs.171182 // CD86 //	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q21.1
SNP_A-2228106	ctactaatgtttgaaa[C/T]gtcaaaaatcccggtg	C	T	83443 // Homo sapiens splicing factor 3b, subunit 5, 10kDa (SF3B5), mRNA. /// NM_003764 // upstream // 52144 //	SF3B5	SF3B5, Homo sapiens splicing factor 3b, subunit 5, 10kDa (SF3B5), q24.2
SNP_A-2254281	cttgcaaagcagaaac[A/T]acagtcatagcagcag	A	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 317554 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2282896	gataaatgaccttacc[A/G]actggagcctcagttt	A	G	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 48123 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2304644	gctctgaaggaaaaca[C/T]tctgcttagtagtttc	C	T	// 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA. /// NM_183003 // upstream // 100173 // --- // --- // 0 // --- /// ENST00000295266 //	PDHA2	PDHA2, Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), q22.3
SNP_A-2294010	gcaggagaatgattaa[G/T]aacccaatgaggtcca	G	T	80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // downstream // 17758 // ---	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2041180	aacctcacagatctga[A/G]cttatttattatttaa	A	G	Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2090614	acttgttcaagccact[C/T]aggaggtagctatgga	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2175997	caccaactaccaaata[C/T]gggatgagggagaaat	C	T	// 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream //	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2224543	cgtattggctgtatca[C/T]tagcatgcattttgta	C	T	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 499258 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2139657	atcgcttggaatgcca[C/T]tggagaggcaagatgg	C	T	/// ENST00000356642 // downstream // 500820 // --- // --- // ---	-	q31.1
SNP_A-1823215	taaaaccatatgctca[C/G]tagtaaaatatttttt	C	G	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 1462231 // Hs.437966 // PXMP3 //	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-1823534	taaaagtcaaggatgg[C/T]cagtaagtccctacag	C	T	49860 // Homo sapiens chromosome 1 open reading frame 10 (C1orf10), mRNA. /// ENST00000271816 // upstream //	C1orf10	C1orf10, Homo sapiens chromosome 1 open reading frame 10 (C1orf10), q21.3
SNP_A-1822825	taaaaactcaaggtca[C/T]acagggagttgatggt	C	T	// 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /// NM_000222 // upstream // 29982 // Hs.479754 // KIT // 3815	PDGFRA	PDGFRA, Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), q12
SNP_A-1837894	tagaaaagccagttaa[C/T]ctctctgacagtggct	C	T	ALDH8A1 // 64577 // Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 571216 //	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1795619	taaagagagagtaggc[A/G]catgctctattcacaa	A	G	163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 64447 // Hs.546355 // TA-LRRP //	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-1935735	ttctgtgatatttaga[C/T]gacacagaatcaaatg	C	T	284273 // Homo sapiens zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), mRNA. /// ENST00000322371 // upstream // 88998 // --- // --- // --- // ---	ZADH2	ZADH2, Homo sapiens zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), q22.3
SNP_A-1967884	attctcaggaaaatca[C/T]tattggtttctacaac	C	T	/// ENST00000340000 // upstream // 748210 // --- // --- // --- // -	-	p12.1
SNP_A-1986878	tagaaatcagaattat[A/G]agtaggctcaacctct	A	G	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2398205 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1932386	ttcctgagaattcata[C/T]atgttttcaggtgtgt	C	T	Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // --- // --- // --- // ---	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-1928198	ttcacagcaaaattaa[C/G]aggaaggtacacagac	C	G	54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 228650 // Hs.435381 // C9orf39 //	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1900735	tggaggtgtcctcagg[A/G]agagtttcatttcatc	A	G	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 468981 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1894442	tgccaaattggcttta[C/T]aatccatgcttgaaaa	C	T	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 107771 // Hs.32942 // PIK3CG // 5294 // Homo	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-1938536	ttgagaataaacacca[C/G]taggaaccaataaatg	C	G	9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // downstream //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-1786605	ggcttctgatttctgc[A/G]caataaatttatattt	A	G	942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // downstream // 25032 // Hs.171182 // CD86 //	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q21.1
SNP_A-1801931	gtataaaagttgacca[C/T]atatgacagaatcctg	C	T	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-1780600	ggatattagggagatg[A/G]agagaatgctcagaac	A	G	Homo sapiens chromosome 2 open reading frame 3 (C2orf3), mRNA. /// ENST00000321027 // intron // 0 // --- // ---	C2orf3	C2orf3, Homo sapiens chromosome 2 open reading frame 3 (C2orf3), p12
SNP_A-1740473	atgcaaattgattaaatctaattaa[A/C]tgattataaacaaaacagtgcaatc	A	C	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	SLC24A2	SLC24A2 , rs999399, solute carrier family 24 (sodium,p22.1
SNP_A-1673246	tcaaatcaaaaacattctctataaa[C/T]tatgacccacgagtctttcaaacat	C	T	NM_138285 // intron // 0 // Hs.180591 // LOC129401 // 129401 // mitotic phosphoprotein 44	LOC129401	LOC129401 , rs10497621, mitotic phosphoprotein 44,q32.1
SNP_A-1837740	tactttggctatgtca[C/T]ctgtcttttgacctgc	C	T	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 533892 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1837546	tacttggacctgatgc[C/T]aaaagaaggttcatgc	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1828269	taagagttactagcaa[C/T]tggttttgaattttac	C	T	136051 // Homo sapiens hypothetical protein DKFZp762I137 (DKFZp762I137), mRNA. /// ENST00000316286 // intron // 0	DKFZp762I137	DKFZp762I137, Homo sapiens hypothetical protein DKFZp762I137 (DKFZp762I137), q36.1
SNP_A-1863439	tccaaaacgtgaagac[A/T]gagaggctcagcatct	A	T	ENST00000320865 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1865563	tccatggcagtaagta[C/T]gttgcttaccagagta	C	T	9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 185205 //	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2159697	atttagcagcctctgt[A/C]aaaaacttgaattata	A	C	HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 102524 // --- // --- // ---	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2159365	atttaatatggttaga[C/T]ggattgatattcttta	C	T	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 470026 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-2123101	agtggtcacttgtacc[G/T]gggagtgaataattct	G	T	23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2119916	agtcaagtgaaattac[A/G]aagtataaattatcac	A	G	4829 // Homo sapiens neuromedin B receptor (NMBR), mRNA. /// ENST00000354295 // downstream // 233721 // ---	NMBR	NMBR, Homo sapiens neuromedin B receptor (NMBR), q24.1
SNP_A-2225889	ctaaatctgtcaccca[A/G]gagttgaggagcctaa	A	G	57332 // Homo sapiens chromobox homolog 8 (Pc class homolog, Drosophila) (CBX8), mRNA. /// NM_003655 //	CBX8	CBX8, Homo sapiens chromobox homolog 8 (Pc class homolog, Drosophila) (CBX8), q25.3
SNP_A-2182009	cagaggaaggcagaga[C/T]cctgacccaagaggaa	C	T	Homo sapiens BRI3 binding protein (BRI3BP), mRNA. /// ENST00000341446 // intron // 0 // --- // --- // --- // --- ///	BRI3BP	BRI3BP, Homo sapiens BRI3 binding protein (BRI3BP), q24.31
SNP_A-2196526	catgttttctatacaa[A/C]aaaggccttggcagag	A	C	ENST00000312002 // intron // 0 // --- // --- // --- // ---	-	q11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2090705	actttaccatagaaac[A/G]ctcttccatcaaatgt	A	G	Homo sapiens WD repeat domain 36 (WDR36), mRNA. /// ENST00000323652 // intron // 0 // --- // --- // --- // ---	WDR36	WDR36, Homo sapiens WD repeat domain 36 (WDR36), q22.1
SNP_A-2080436	acctagcagaccagga[A/G]tagcaggaaacatccc	A	G	54472 // Homo sapiens toll interacting protein (TOLLIP), mRNA. /// NM_003957 // upstream // 45889 // Hs.170819 //	TOLLIP	TOLLIP, Homo sapiens toll interacting protein (TOLLIP), p15.5
SNP_A-2104635	agcagtatctagtcca[C/T]tgccttgtggatacaa	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2055682	aataatgtatgaaatc[A/G]cacagttactaagtac	A	G	Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // intron // 0 // --- // --- // --- // --- ///	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-2067959	acaactatttgagtaa[A/C]caggctatagattagc	A	C	EXOSC3 // 51010 // Homo sapiens exosome component 3 (EXOSC3), transcript variant 2, mRNA. /// NM_016042 //	EXOSC3	EXOSC3, Homo sapiens exosome component 3 (EXOSC3), transcript variant 2, p13.2
SNP_A-2043016	aactgacggtctgcac[A/G]ggtgaaggtttgtgag	A	G	1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 161425 // --- // --- // --- // ---	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2
SNP_A-2288007	gattattgtatgaaga[A/G]gcattccaatatctga	A	G	POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, complete cds. /// ENST00000311492	POU5F1P1	POU5F1P1, Homo sapiens POU 5 domain protein (POU5FLC20) complete cds. ,q24.21
SNP_A-2305253	gctgagatttaacaca[A/T]ctttggaactcaactt	A	T	/// ENST00000342224 // downstream // 5610 // --- // --- // --- // ---	-	p11.21
SNP_A-2282700	gagttttcagtgcaaa[C/G]actttcacattcttcg	C	G	8848 // Homo sapiens transforming growth factor beta 1 induced transcript 4 (TGFB1I4), transcript variant 1, mRNA. /// NM_006022 // upstream // 300762 // Hs.507916 //	TGFB1I4	TGFB1I4, Homo sapiens transforming growth factor beta 1 induced transcript 4 (TGFB1I4), transcript variant 1, q14.12
SNP_A-2285887	gatgaggaatgtattg[A/G]aacaaaggtgactctt	A	G	28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 383496 // --- // --- // --- // ---	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.32
SNP_A-2277530	gagcaatgcaaaccag[A/G]accccaaatctaccaa	A	G	Homo sapiens golgi SNAP receptor complex member 2 (GOSR2), transcript variant A, mRNA. /// NM_054022 // intron // 0 // Hs.463278 // GOSR2 // 9570 // Homo sapiens golgi	GOSR2	GOSR2, Homo sapiens golgi SNAP receptor complex member 2 (GOSR2), transcript variant A, q21.32
SNP_A-2269532	gacaaagaaaaaatca[A/G]tagaattgtctggtcc	A	G	5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 232259 // Hs.42146 // PAX3 //	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-2264949	gaagagggtaaccaca[A/G]agctaaaattcatcat	A	G	// 117247 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), mRNA. /// ENST00000243236 // upstream // 25878 // --- // ---	SLC16A10	SLC16A10, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), q21
SNP_A-2282967	gataacctaatcagac[C/T]gaattaaatgaagcag	C	T	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2302024	gcgtgctacttggtaa[A/T]ccagatgtccactgaa	A	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 952345 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2303822	gctcagtcactgtcac[A/G]gctctcaatatcccaa	A	G	ENST00000303864 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2301016	gccttagaaggaagca[C/T]gatatttcctgaaggg	C	T	// Homo sapiens DEK oncogene (DNA binding) (DEK), mRNA. /// NM_182757 // upstream // 61064 // Hs.148741 //	DEK	DEK, Homo sapiens DEK oncogene (DNA binding) (DEK), p22.3
SNP_A-2041142	aacctatccactcaac[A/G]cttggcttgtttctcc	A	G	400892 // Homo sapiens FLJ42953 protein (FLJ42953), mRNA. /// ENST00000330423 // downstream // 327 // --- // ---	FLJ42953	FLJ42953, Homo sapiens FLJ42953 protein (FLJ42953), q11.21
SNP_A-2030315	aaagcataatatgtat[C/G]acatgtatctagatag	C	G	// 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 603237 // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2024949	aaaataaagtcttgtg[G/T]acccatgaaaatgcat	G	T	Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, mRNA. /// NM_033323 // intron // 0 // Hs.469033 // SLC4A5 //	SLC4A5	SLC4A5, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, p13.1
SNP_A-2025918	aaaatgtcaacatgaa[A/C]ccccttgttagtcata	A	C	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 500222 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-2022498	aaaaatcatgtattcc[A/G]ccaggtagagtggctc	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 352994 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2021802	aaaaaccaactctcac[C/T]attcttgttcaacata	C	T	// 168850 // Homo sapiens hypothetical protein LOC168850 (LOC168850), mRNA. /// NM_024523 // downstream //	LOC168850	LOC168850, Homo sapiens hypothetical protein LOC168850 (LOC168850), q32.1
SNP_A-2004347	gatattatcacactaa[C/T]gcaaaaggtcagcatg	C	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1997831	tcatagtccaaacacg[A/G]aagtgaagcagcaagc	A	G	7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 70881 //	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-2014314	tcatggtaatgagtga[C/G]ctcttctgtgagttca	C	G	FLJ46321 // 389763 // Homo sapiens FLJ46321 protein (FLJ46321), mRNA. /// NM_152573 // downstream // 365001	FLJ46321	FLJ46321, Homo sapiens FLJ46321 protein (FLJ46321), q21.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2065796	aatttcatcccttcaa[C/T]tagaggttgccattca	C	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2074355	acatacataaaccaac[A/G]agcagatgacaccttc	A	G	Homo sapiens cathepsin K (pycnodysostosis) (CTSK), mRNA. /// ENST00000271651 // intron // 0 // --- // --- // --- // ---	CTSK	CTSK, Homo sapiens cathepsin K (pycnodysostosis) (CTSK), q21.2
SNP_A-2079801	accctgatgtataaca[A/G]tatgtcgttccctaca	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 762921 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2082879	acgtcatgcctaagac[C/T]gacttgataatccata	C	T	/// ENST00000276737 // downstream // 337176 // --- // --- // ---	-	q24.23
SNP_A-2091149	actttggtgtgtcaca[A/G]gtacttcaaatttcag	A	G	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 887477 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2091839	agaaaatgaatgtggc[A/G]aaaggcccagcttgtc	A	G	// Homo sapiens cathepsin H (CTSH), transcript variant 2, mRNA. /// NM_004390 // upstream // 4687 // Hs.148641 //	CTSH	CTSH, Homo sapiens cathepsin H (CTSH), transcript variant 2, q25.1
SNP_A-2192274	catcagtaggggttag[A/G]atatactgatgattct	A	G	// Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // ---	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.2
SNP_A-2211050	cccgctgtactctgct[G/T]aatgaggctagaaaga	G	T	23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2207368	ccattgacaggaggta[C/T]taaagagtcctgtgga	C	T	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 95569 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2207671	ccattttagctcctaa[C/T]tggggtggagggtgaa	C	T	ENST00000299308 // intron // 0 // --- // --- // --- // ---	-	q24.31
SNP_A-2115568	aggggtttgaaaataa[C/T]gcctcatattcttcat	C	T	Homo sapiens chromosome 13 open reading frame 12 (C13orf12), mRNA. /// ENST00000255315 // intron // 0 // --- //	C13orf12	C13orf12, Homo sapiens chromosome 13 open reading frame 12 (C13orf12), q12.3
SNP_A-2130763	atacttcaagaataag[A/G]aagaatcaagacatcc	A	G	// 389206 // Homo sapiens FLJ43965 protein (FLJ43965), mRNA. /// ENST00000344852 // upstream // 225936 // --- // ---	FLJ43965	FLJ43965, Homo sapiens FLJ43965 protein (FLJ43965), p13
SNP_A-2156531	attctctttccttcaa[A/G]taagatgccccatgca	A	G	// 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000327792 // downstream // 526930 // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2149414	atgtactatcagacaa[G/T]aaagacaaaaagaatt	G	T	// 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 400844 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1867139	tccctgaggtgctgaa[G/T]ctcatcagttgatggc	G	T	50651 // Homo sapiens DNb-5 mRNA, partial cds. /// ENST00000341781 // upstream // 257384 // --- // --- // --- // ---	DNB5	DNB5, Homo sapiens DNb-5 partial cds. p36.23
SNP_A-1817052	gttattttgcatgcag[A/G]agttttcacacctgtc	A	G	81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// NM_183380 // downstream // 138750	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-1842940	tagtatacatgccctg[A/C]agaattcctggaattg	A	C	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1
SNP_A-1831944	taattgcagggagaag[C/T]agttcactccactaat	C	T	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // --- // --- // --- // ---	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1831536	taattaacagagagta[A/T]gagggaacactttgtg	A	T	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1721852	ccataatgtaggctcccataactga[C/T]gtatagtaaccactccaggggaagt	C	T	NM_005744 // intron // 0 // Hs.181461 // ARIH1 // 25820 // ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	ARIH1	ARIH1 , rs2415141, ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila),q24.1
SNP_A-1789029	gggcacggaaagaata[C/T]ggcagcttttctcaaa	C	T	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1940045	ttgcagctcagcatca[C/G]ggaagagctggctcct	C	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 680899 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1958334	ttttccattcgtcaga[G/T]atttctcttttctaag	G	T	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1959802	ttttgtaatggagaaa[A/C]ataagtagaattatct	A	C	3062 // Homo sapiens hypocretin (orexin) receptor 2 (HCRTR2), mRNA. /// ENST00000306858 // downstream //	HCRTR2	HCRTR2, Homo sapiens hypocretin (orexin) receptor 2 (HCRTR2), p12.1
SNP_A-1982985	ttgattatatactaaa[C/T]gaggggtagattattc	C	T	// 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 709146 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-1890373	tgatcctaactaagtc[A/G]cctccccagagcttac	A	G	5203 // Homo sapiens prefoldin 4 (PFDN4), mRNA. /// NM_177959 // upstream // 246859 // Hs.473133 // DOK5 //	PFDN4	PFDN4, Homo sapiens prefoldin 4 (PFDN4), q13.2
SNP_A-1928547	ttcactgaaactttac[A/G]cccatggatgagcaag	A	G	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1886151	tgaccatgggcccaag[A/G]agatctggctacctcc	A	G	79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 279599 // Hs.156832 // NPAS2 //	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1887250	tgagaacttaacatta[A/G]aatcagaatacaaatg	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1955475	tttggtcaatacagcc[A/G]acacccacaaggtcat	A	G	2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 //	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1954024	tttgatcagagataga[A/T]cttgtgtagtggtctt	A	T	5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 449379 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-1938961	ttgagtagtaggaaga[C/T]gactggctcaatgtca	C	T	27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 1240683 //	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-1792873	ggtaatggaaaactgc[A/G]acagacaaatccaggc	A	G	// Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1201928 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1813358	gtggtggtcttagtaa[G/T]aaagcttctgctttga	G	T	339501 // Homo sapiens marapsin 2 (MPN2), mRNA. /// NM_003395 // downstream // 65723 // Hs.149504 // WNT9A	MPN2	MPN2, Homo sapiens marapsin 2 (MPN2), q42.13
SNP_A-1780997	ggatgatctcttataa[C/T]tgcatgaggtatggag	C	T	130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // ---	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-1842695	tagtaacataaaatga[A/G]tcacaaaaatgttcat	A	G	9866 // Homo sapiens mRNA for KIAA0298 protein, partial cds. /// NM_000990 // upstream // 4677 // Hs.523463 //	TRIM66	TRIM66, Homo sapiens for KIAA0298 protein, partial cds. ,p15.4
SNP_A-1841999	tagggacgcttggtta[A/T]aattacatgtgcccaa	A	T	MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-1821604	gtttgtctgattaaca[A/G]atgaagaaaatgagat	A	G	// 84135 // Homo sapiens Src-associated protein SAW (FLJ12787), mRNA. /// ENST00000296792 // downstream //	FLJ12787	FLJ12787, Homo sapiens Src-associated protein SAW (FLJ12787), q13.2
SNP_A-1827206	taacctccaagttaac[C/T]gaaaatgttgattgca	C	T	Homo sapiens hypothetical protein FLJ10719 (FLJ10719), mRNA. /// ENST00000300027 // intron // 0 // --- // --- // --- // ---	FLJ10719	FLJ10719, Homo sapiens hypothetical protein FLJ10719 (FLJ10719), q26.1
SNP_A-1868756	tcctcttgtttctcat[C/T]aaccaagaaaagtggc	C	T	/// ENST00000359165 // upstream // 420131 // --- // --- // --- // -	-	p21.3
SNP_A-1866332	tcccattacaatgccc[C/T]caacctgcctgtgtcc	C	T	ENST00000355548 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1854637	tcaacacagtgccatc[A/T]ctaatcattgcaatat	A	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 433786 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1848659	tatgagcagagtaaca[A/G]tgcattaaaaccacaa	A	G	// 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 239409 // --- // --- //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-2133531	atatcaacattataac[A/G]gccatctactaaagat	A	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 1238698 // --- // -	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-2121530	agtgaaataagagcaa[C/G]gaaagggctgagttaa	C	G	sapiens acid phosphatase, prostate (ACPP), mRNA. /// ENST00000336375 // intron // 0 // --- // --- // --- // --- ///	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-2110541	aggacagaaacaatga[C/T]gtaaaggttccttgca	C	T	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 131899 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2185040	cagcttgttatgatac[C/T]cttctgcgatatggca	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1269424 // --- // -	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2089921	acttctctggacttca[C/T]atctttgcgaatttac	C	T	2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream //	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-2086295	actctgtctctttcca[A/G]tccattctgtctgctc	A	G	ENST00000356060 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2049196	aagctagaggcagaga[G/T]atcattcagcaacgag	G	T	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 53268 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2054040	aagttagtagatgtca[A/G]ccaatgttcagatttt	A	G	10063 // Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, /// NM_033364 // upstream // 8747 // Hs.341906 // C3orf15 // 8	COX17	COX17, Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, q13.33
SNP_A-2010755	cctagttcaggtaagc[C/G]cagtggagaccagagg	C	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1100890 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2007571	gaggaagactgtctca[A/G]aaacaaccctgtcctc	A	G	FLJ33706 // 284805 // Homo sapiens hypothetical protein FLJ33706 (FLJ33706), mRNA. /// ENST00000341639 //	FLJ33706	FLJ33706, Homo sapiens hypothetical protein FLJ33706 (FLJ33706), q11.21
SNP_A-2022347	taacattacagaattc[A/C]atttcttctaaaactt	A	C	Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA. /// ENST00000278916 // intron // 0 // --- // ---	CHEK1	CHEK1, Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246027	ctggtaggggtgagcc[A/G]ggagtcttgtcttctt	A	G	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 312432 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2229431	ctaggccgctgtaaca[A/G]agtaccacaagctgag	A	G	-- /// ENST00000331540 // downstream // 12447 // --- // --- // ---	-	p25.2
SNP_A-2231504	ctatttagagaggaca[C/G]aggcataaactgttct	C	G	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 395307 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2255782	cttgtttctaagtgtc[C/T]aaagtctctgttactt	C	T	SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 555 // --- // OR13F1	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2292617	gcactgctctgaccca[C/T]ggaaagaatgggcgtt	C	T	57818 // Homo sapiens glucose-6-phosphatase, catalytic, 2 (G6PC2), mRNA. /// NM_003742 // downstream // 4802 //	G6PC2	G6PC2, Homo sapiens glucose-6-phosphatase, catalytic, 2 (G6PC2), q31.1
SNP_A-2292140	gcacccaagcacacaa[C/T]tatttttgtttgttag	C	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1353416	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2032288	aaagttacattaaaaa[C/T]ctgaccagtcattcaa	C	T	Homo sapiens poly (ADP-ribose) polymerase family, member 6 (PARP6), mRNA. /// NM_020214 // intron // 0 // Hs.270244	PARP6	PARP6, Homo sapiens poly (ADP-ribose) polymerase family, member 6 (PARP6), q23
SNP_A-2014128	cagctaaaaaggagaa[G/T]atgtgagctgagaaca	G	T	55958 // Homo sapiens kelch-like 9 (Drosophila) (KLHL9), mRNA. /// NM_018847 // upstream // 5470 // Hs.522029 //	KLHL9	KLHL9, Homo sapiens kelch-like 9 (Drosophila) (KLHL9), p21.3
SNP_A-1996373	cagacaaggaaacaga[C/G]actcagatctcctagt	C	G	Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// ENST00000262244 // intron // 0 // --- // --- // --- // ---	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-1991994	gcatggctagcaaaat[A/G]agtaaaacttaaggct	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2143450 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2050910	aaggcgataattgcaa[A/T]tgttattcttatcgca	A	T	11346 // Homo sapiens mRNA for KIAA1029 protein, partial cds. /// NM_007286 // upstream // 62379 // Hs.435228 //	SYNPO	SYNPO, Homo sapiens for KIAA1029 protein, partial cds. ,q33.1
SNP_A-2072185	acagatgagaaacttg[A/C]aggagtcagtccacaa	A	C	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2095043	agaatgtaattgcata[C/G]aatatagccttaaata	C	G	// 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 55379 // Hs.436996 //	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-2184537	cagctatatctaggaa[C/T]gaagtcctctttagtt	C	T	// Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// NM_030906 // downstream // 91616 // Hs.501833	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-2190839	catagagttgctctca[C/T]aaatgactgccatgac	C	T	Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_016300 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2199570	ccaaaaaggagatgaa[C/T]aaatgaaaattcttat	C	T	1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2177295	cacctgtgatggaaga[A/C]taaggccacaggatag	A	C	NM_198989 // downstream // 96752 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.3
SNP_A-2220737	ccttgagcgtcttcac[A/G]gtccctggcctcagaa	A	G	Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 37 (DHX37), mRNA. /// ENST00000308736 // intron // 0 // --- // ---	DHX37	DHX37, Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 37 (DHX37), q24.31
SNP_A-2109881	aggaaccaacaagaga[C/T]gatgaggtccccaggg	C	T	PLXNA1 // 5361 // Homo sapiens plexin A1 (PLXNA1), mRNA. /// ENST00000332739 // downstream // 143520 // ---	PLXNA1	PLXNA1, Homo sapiens plexin A1 (PLXNA1), q21.3
SNP_A-2108165	agctcttgatgatgaa[C/T]atgccccggaatgcat	C	T	ENST00000359307 // intron // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-2152361	attaacagtaattaca[A/G]aggacctattgtgttc	A	G	Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-1848257	tatctttccttgaacc[C/T]agcagctcgccatctt	C	T	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), mRNA. /// ENST00000266126 // intron // 0 // --- // --- // --- // ---	EIF2B2	EIF2B2, Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), q24.3
SNP_A-1854971	tcaactgttagagata[C/T]gaaataagatggaaca	C	T	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), transcript variant 4, mRNA. /// NM_178587 // intron // 0 // Hs.368264 // PPP2R5C	PPP2R5C	PPP2R5C, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), transcript variant 4, q32.31
SNP_A-1869623	tccttactctagcttg[C/T]acctcagtgtcccttа	C	T	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 186849 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1829126	taaggtctacaccttg[A/C]aaagcccttgtaaccg	A	C	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 225699 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1837004	tactgggagtatcatg[A/G]atgtatttttttaattg	A	G	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-1658672	gatttcatacttgaaacttagctga[A/C]gaattccccactcatttaatcacta	A	C	HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 255343 // Hs.129882 // IMPG1 //	HTR1B	HTR1B , rs2504988, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-1679536	tttctcactattcttgaacctatta[A/G]aagaggaaaaagcaaacatgttgga	A	G	// 8204 // nuclear receptor interacting protein 1 /// NM_022136 // upstream // 272327 // Hs.221851 // SAMSN1 // 64092 //	NRIP1	NRIP1 , rs2822963, nuclear receptor interacting protein 1 ,q11.2
SNP_A-1938112	ttgacactggctttga[G/T]taggctcttaataaat	G	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1947003	tttaagttgcatataa[A/G]tgttatgatgttgcat	A	G	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1894270	tgcattcttcttgaac[A/G]ctccctggctctaggg	A	G	ENST00000356612 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1906938	tggttctgaacatacc[A/G]aaacacttaatgtttg	A	G	Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// ENST00000256737 // intron // 0 // --- // --- // --- // ---	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1909323	tgtatgtgtaggctca[A/G]tcttgaagacagcaat	A	G	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-1911408	tgtcttccaggagcaa[A/T]catctcaacaagcaaa	A	T	ENST00000359749 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1935953	ttcttaattgcaacca[C/T]gttaactgatacaaac	C	T	29851 // Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// NM_205863 // upstream // 277904 // Hs.271903 //	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.3
SNP_A-1933995	ttctcacaggtcttga[A/G]atcttgactactatga	A	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 245806 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1980958	caaagatcttataaaa[C/T]gaaagtggatttttaa	C	T	Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// ENST00000284308 // intron // 0 // --- // --- // --- // ---	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1782905	ggcagagtcagtaaga[C/T]gaggcaagctcacaca	C	T	FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1722900	ggtttatccaaaaagacagatatca[A/G]ctgcaacttctattcacccttcaag	A	G	58478 // E-1 enzyme /// NM_024906 // downstream // 63747 // Hs.379191 // SCD4 // 79966 // stearoyl-CoA desaturase 4	MASA	MASA , rs10516677, E-1 enzyme ,q21.22
SNP_A-1803957	gtcaatcccttctata[C/T]gaggcaatttattcta	C	T	Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 //	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-1795957	ggtgggttcctgatta[C/T]catactttaaatactg	C	T	7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000355985 // upstream // 225965 // --- // ---	ZNF217	ZNF217, Homo sapiens zinc finger protein 217 (ZNF217), q13.2
SNP_A-1838042	tagaaatataggatgc[C/T]aaagtcgttcattaga	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-1871855	tctacaattctcagga[C/T]ccagggatgtttaagg	C	T	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 485131 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1856514	tcacagcaagcatttc[C/T]atagcacttactacat	C	T	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // --- // ---	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1
SNP_A-2213906	cctaacaaagactcac[C/T]ccttgggcaagcccta	C	T	// Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, mRNA. /// NM_182715 // upstream // 43652 //	SYPL	SYPL, Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, q22.3
SNP_A-2179765	cacttgctacaataca[A/G]cgacaataatttatcc	A	G	// Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // --- // --- // --- // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2056006	aatacagtctctacaa[G/T]acatagttcagaaaag	G	T	ENST00000343170 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1990273	cgataataatctcaga[A/G]atagcttcttatgtgt	A	G	FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream //	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2042389	aactcaataaactcaa[A/G]atatacacatacttac	A	G	sapiens myelin protein zero (Charcot-Marie-Tooth neuropathy 1B), mRNA (cDNA clone MGC:10453 IMAGE:3926008), complete cds. /// NM_000530 // intron // 0 // Hs.93883 // MPZ // 4359 // Homo sapiens my	MPZ	MPZ, Homo sapiens myelin protein zero (Charcot-Marie-Tooth neuropathy 1B), (cDNA clone MGC:10453 IMAGE:3926008), complete cds. q23.3
SNP_A-2039321	aacataagatccataa[A/G]ctcttaaaaatttatt	A	G	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2034821	aaatgactctgattgc[G/T]ctttggagaatgtaat	G	T	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2289113	gatttctgactgttga[C/T]ccaaatatgaccctct	C	T	/// ENST00000251675 // downstream // 349411 // --- // --- // --- // --- /// ENST00000360855 // downstream // 349441 // --- // ---	-	q32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2310070	ggaaattggtttgcta[C/T]gtgagttggacaaagg	C	T	// 64983 // Homo sapiens mitochondrial ribosomal protein L32 (MRPL32), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000223324 // downstream // 170514 // ---	MRPL32	MRPL32, Homo sapiens mitochondrial ribosomal protein L32 (MRPL32), nuclear gene encoding mitochondrial protein, p14.1
SNP_A-2232125	ctcaaggtggcccaac[A/G]catcacatatggcgag	A	G	Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA. /// NM_153746 // intron // 0 // Hs.187459	ZDHHC14	ZDHHC14, Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), q25.3
SNP_A-2273520	gactctttgacctgca[A/C]aatttaaactgagtga	A	C	// Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// ENST00000324072 // intron // 0 // --- // --- // --- // ---	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11
SNP_A-2268071	gaatcttgtgtctcaa[C/T]tggaagaggtaaagaa	C	T	389610 // Homo sapiens HARL2754 (UNQ2754), mRNA. /// NM_005218 // downstream // 22 // Hs.32949 // DEFB1 //	XRG5a	XRG5a, Homo sapiens HARL2754 (UNQ2754), p23.1
SNP_A-2272095	gacccttgactttata[A/G]ataacataatctagtg	A	G	Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // --- // --- // --- // ---	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-2231118	ctattaaactaaggca[A/G]caaacattatgttcta	A	G	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 2106082 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-2252824	cttctagaaagggtca[C/T]gatacatgtagagtta	C	T	Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), mRNA. /// ENST00000340941 // intron // 0 // --- // --- // --- // --- /// ENST00000323375 // intron // 0 // --- // ---	MCCC2	MCCC2, Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), q13.2
SNP_A-2248013	ctgtgctcgcagagaa[A/G]tcctctgttatcaggc	A	G	79830 // Homo sapiens zinc finger, MYM domain containing 1 (ZMYM1), mRNA. /// NM_024772 // downstream // 7090 //	ZMYM1	ZMYM1, Homo sapiens zinc finger, MYM domain containing 1 (ZMYM1), p34.3
SNP_A-2301098	gccttcatatggcaca[C/T]tcttagagtagaataa	C	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 908183 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2294648	gcagtgcctgagacgt[C/G]aatcagccctcaacaa	C	G	56203 // Homo sapiens leiomodin 3 (fetal) (LMOD3), mRNA. /// AB023230 // downstream // 6826 // Hs.371681 // FRMD4B	LMOD3	LMOD3, Homo sapiens leiomodin 3 (fetal) (LMOD3), p14.1
SNP_A-2019477	catgttcttccagcac[G/T]attcttttgtccctct	G	T	B3GALT5 // 10317 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5), transcript variant 1, mRNA. /// NM_033171 // downstream //	B3GALT5	B3GALT5, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5), transcript variant 1, q22.2
SNP_A-2060268	aatgaagatctccaat[A/G]agaagcatctattatc	A	G	9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1924163 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2058948	aatccaggtcgaccaa[A/C]ctcaatcatgatgctg	A	C	4856 // Homo sapiens nephroblastoma overexpressed gene (NOV), mRNA. /// NM_006209 // downstream // 47226 //	NOV	NOV, Homo sapiens nephroblastoma overexpressed gene (NOV), q24.12
SNP_A-2075826	acatgtgcaggcctca[A/G]aaccatcttgtggatg	A	G	Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// NM_173472 // intron // 0 // Hs.190413	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-2176840	cacccttgctcaaaat[C/T]agttggccatacatgg	C	T	84278 // Homo sapiens hippocampus abundant gene transcript-like 2 (HIATL2), mRNA. /// NM_001333 //	HIATL2	HIATL2, Homo sapiens hippocampus abundant gene transcript-like 2 (HIATL2), q22.33
SNP_A-2197906	cattgattcatgatta[C/T]gtggtttgttgttgtc	C	T	23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2215672	cctcagtgagaccaga[C/T]aggagaagactgtgat	C	T	/// ENST00000246019 // downstream // 48603 // --- // --- // ---	-	p11.23
SNP_A-2227093	ctaattaatacacaca[A/G]gaattagagagatggt	A	G	RNASE9 // 390443 // Homo sapiens ribonuclease-like protein 9 (h461), mRNA. /// ENST00000328444 // downstream //	RNASE9	RNASE9, Homo sapiens ribonuclease-like protein 9 (h461), q11.2
SNP_A-2152469	attaacttccctcaga[A/C]ctatcctcagggctct	A	C	// Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), mRNA. /// NM_000311 // upstream // 419295 // Hs.472010 //	ADRA1D	ADRA1D, Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), p13
SNP_A-2118184	agtaaaggtgttccta[C/G]gagaatctagggctga	C	G	KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 57376 //	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2132361	atagtatttccctgta[C/T]gtatgcttaagtgtag	C	T	8654 // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, mRNA. /// NM_033437 //	PDE5A	PDE5A, Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, q27
SNP_A-1858071	tcacttttgggtcata[C/T]ggatattttaacaata	C	T	6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 161994 //	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-1850622	tattaattagtattac[A/C]gatttgagacacattt	A	C	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 516116 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1839836	agggattcttacctaa[A/C]cacatggtcaagattc	A	C	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA. /// ENST00000340825 // intron // 0 // --- // --- // --- // --- ///	KIAA0672	KIAA0672, Homo sapiens KIAA0672 gene product (KIAA0672), p12
SNP_A-1819136	gttgctatgagccaga[A/G]gttctttttttgttt	A	G	ENST00000355486 // intron // 0 // --- // --- // --- // ---	-	q13.43
SNP_A-1804235	gtcacctgactgataa[A/C]aaagaaatcactctgc	A	C	// 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream //	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-1727933	tgtggctttttacctatgagagtga[G/T]aggagtccccattgtctttgtttt	G	T	CENPC1 // 1060 // centromere protein C 1 /// NM_004439 // upstream // 842356 // Hs.201920 // EPHA5 // 2044 // EphA5	CENPC1	CENPC1 , rs9312156, centromere protein C 1 q13.2

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946141	ttgtttttattcacca[A/G]acagaactctaaagaa	A	G	Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), mRNA. /// ENST00000302541 // intron // 0 // --- // ---	MYRIP	MYRIP, Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), p22.1
SNP_A-1918446	ttaaatagccagaata[C/T]agtcacacaaactagt	C	T	Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-1916384	tgttgttcacctccca[C/T]gtataaatgagaacac	C	T	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1
SNP_A-1906803	tggttataattagtat[C/G]aattttcaaaagctca	C	G	sapiens glutaminase (GLS), mRNA. /// ENST00000320717 // intron // 0 // --- // --- // --- // --- /// ENST00000338435 // intron //	GLS	GLS, Homo sapiens glutaminase (GLS), q32.2
SNP_A-1932989	ttcgatcattcagtaa[G/T]tatgtattgggtccct	G	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-1924702	ttataggtctagaagc[A/T]atgagaagaattgaga	A	T	3280 // Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), mRNA. /// ENST00000351516 //	HES1	HES1, Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), q29
SNP_A-1924780	ttatataccatatcaa[C/G]cttattcatgtgatta	C	G	FLJ25393 // 159989 // Homo sapiens hypothetical protein FLJ25393 (FLJ25393), mRNA. /// NM_181645 // downstream	FLJ25393	FLJ25393, Homo sapiens hypothetical protein FLJ25393 (FLJ25393), q21
SNP_A-1904146	tgggccagataactac[C/G]ggagatgatgttcctt	C	G	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1881040	tcttgtttgtaatcaa[C/G]aacttgtctaaatacc	C	G	2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000360030 // upstream //	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.2
SNP_A-1880709	tcttggagacaggaac[A/G]caattgcttcttcagt	A	G	81689 // Homo sapiens HESB like domain containing 2 (HBLD2), mRNA. /// ENST00000339137 // upstream // 35016	HBLD2	HBLD2, Homo sapiens HESB like domain containing 2 (HBLD2), q21.33
SNP_A-1900138	tggactggtgcgggga[C/T]gtgacatactgagaca	C	T	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 685554 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1932694	ttccttccaacaaaga[C/T]gattaagaagacagca	C	T	Homo sapiens mSin3A-associated protein 130 (SAP130), mRNA. /// ENST00000357702 // intron // 0 // --- // --- // --- // ---	SAP130	SAP130, Homo sapiens mSin3A-associated protein 130 (SAP130), q14.3
SNP_A-1905726	tggtattatgaggatt[G/T]aacaaatagtatatgt	G	T	27347 // Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA. ///	STK39	STK39, Homo sapiens serine threonine kinase 39 (STE20 q24.3
SNP_A-1909471	cctgctcaatgtgaac[C/G]ggaaaggaaaggggat	C	G	// 65121 // Homo sapiens hypothetical protein similar to preferentially expressed antigen of melanoma (LOC65121), mRNA. /// AL049680 // downstream // 46628 // Hs.451982 //	LOC65121	LOC65121, Homo sapiens hypothetical protein similar to preferentially expressed antigen of melanoma (LOC65121), p36.21
SNP_A-1935423	ttctggatgtgattta[A/G]gtccctttcacccgtg	A	G	LOC200383 // 200383 // Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), mRNA. ///	LOC200383	LOC200383, Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), p11.2
SNP_A-1980498	aaagaggtttatggct[C/T]acatacctgcatttta	C	T	11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 556594 //	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1716409	ttcttaaataaaacaatgcataaat[A/T]ataagttaaaaaaggaataataaaa	A	T	9394 // heparan sulfate 6-O-sulfotransferase 1 /// NM_032144 // upstream // 693373 // Hs.440748 // RAB6C //	HS6ST1	HS6ST1 , rs837846, heparan sulfate 6-O-sulfotransferase 1 ,q21.1
SNP_A-1782343	ggcaatggcaatgtta[A/G]gtaaataaacagccta	A	G	3572 // Homo sapiens interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST), transcript variant 1, mRNA. /// NM_175767 // upstream // 67568 // Hs.532082 // IL6ST //	IL6ST	IL6ST, Homo sapiens interleukin 6 signal transducer (gp130, oncostatin M receptor) (IL6ST), transcript variant 1, q11.2
SNP_A-1712351	tgcttctgctgctgtccgaatatca[A/G]ccacttatttttctattcttaatag	A	G	// solute carrier family 36 (proton/amino acid symporter), member 3	SLC36A3	SLC36A3 , rs2193931, solute carrier family 36 (proton,q33.1
SNP_A-1795403	ggcagagactaagtac[C/T]gactaattgttgacct	C	T	163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 105760 // Hs.546355 // TA-LRRP	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-1790436	ggggcaagttctacga[A/C]gtcttttgtcgccctt	A	C	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 97851 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1858935	gtgaaataatcacaaa[A/G]cagggaatgaggtatc	A	G	Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // --- // --- // --- // --- ///	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-2154019	attatatgtctaaaaa[G/T]gtaatagcaaccaaag	G	T	H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1657587 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2159419	atttaattaccttcaa[A/G]tgaaagccccaacact	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 777928 // Hs.13640 //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2195182	catggaggtgtgatag[C/T]ataagatttatgtgaa	C	T	Homo sapiens nuclear receptor binding SET domain protein 1 (NSD1), transcript variant 1, mRNA. /// NM_022455 // intron // 0 // Hs.208961 // NSD1 // 64324 // Homo sapiens nuclear	NSD1	NSD1, Homo sapiens nuclear receptor binding SET domain protein 1 (NSD1), transcript variant 1, q35.3
SNP_A-2187167	caggtctcctgcaaaa[C/T]gcccagaaatgacctt	C	T	Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), mRNA. /// BC003044 // intron // 0 // Hs.495138 // MAPKAP1 // 79109 // Homo sapiens mitogen-	MAPKAP1	MAPKAP1, Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), q33.3
SNP_A-2175616	cacatggaaataataa[A/T]tattctggatgatgaa	A	T	Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // intron // 0 // Hs.145384 // GLYAT //	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-2180334	cagaaatctctgccta[A/G]cattattcatgtgtgg	A	G	// 6718 // Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), mRNA. /// ENST00000242375 // downstream //	AKR1D1	AKR1D1, Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), q34
SNP_A-2179858	cactttacaggcaaaa[C/T]ctcatgtactccttac	C	T	114907 // Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, mRNA. /// NM_148177 // upstream //	FBXO32	FBXO32, Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, q24.13
SNP_A-2071476	acagaaaggcacagga[C/T]gagagtggtctgggtg	C	T	27178 // Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, mRNA. /// NM_014439 //	IL1F7	IL1F7, Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, q13
SNP_A-2063003	aatgttaagagataaa[C/T]cccagtccctgctcat	C	T	// 9480 // Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// NM_000140 // downstream // 64599	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-2060922	aatgatgacgaataaa[C/G]agaaaggaatcatcaa	C	G	8291 // Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// NM_019885 // downstream // 32022 // Hs.91546 // CYP26B1	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-2080770	acctcccccataggaa[G/T]accacataaaactacc	G	T	Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// ENST00000339837 // intron // 0 // --- //	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-2272810	gactaacatctgcaaa[C/T]tgatctttcaaaaacc	C	T	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2274056	gacttagccaatgcaa[A/C]aaggtaagaaaacaca	A	C	283209 // Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), mRNA. /// NM_005472 // downstream // 24618 //	PGM2L1	PGM2L1, Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), q13.4
SNP_A-2276228	gagagaggccactgaa[C/T]gggtgtctggcacatt	C	T	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // --- // --- // --- // ---	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2276122	gagagacctttgaaag[A/G]caggagcctagacctt	A	G	// Homo sapiens FLJ46481 protein (FLJ46481), mRNA. /// ENST00000324058 // intron // 0 // --- // --- // --- // ---	FLJ46481	FLJ46481, Homo sapiens FLJ46481 protein (FLJ46481), p16.1
SNP_A-2283355	gatacaggcgatgaca[C/T]tgatgaaccttgagga	C	T	148066 // Homo sapiens zinc and ring finger 4 (ZNRF4), mRNA. /// NM_153375 // downstream // 76979 // Hs.515575	ZNRF4	ZNRF4, Homo sapiens zinc and ring finger 4 (ZNRF4), p13.3
SNP_A-2262126	gaaatcaaaggttata[A/C]acgcatttttgactca	A	C	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2245465	ctgggactgtgcttga[C/T]gaaggcctgcacactc	C	T	ENST00000324457 // intron // 0 // --- // --- // --- // ---	-	p22.3
SNP_A-2249745	cttaatcttgagttta[A/G]gggatgaaacataaag	A	G	Homo sapiens serine/threonine kinase 4 (STK4), mRNA. /// ENST00000262978 // intron // 0 // --- // --- // --- // ---	STK4	STK4, Homo sapiens serine q13.12
SNP_A-2289966	gcaaagctgaggtcta[C/T]gctcagatgtgtctgt	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1844174 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2053900	aagtgttgagtttttc[A/G]atgtgatcaaattaaa	A	G	// Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // upstream // 25902 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2063741	aattagagcatcaaaa[C/G]agaggagacattaaca	C	G	1) L-type voltage-dependent calcium channel a1 subunit (hHT) mRNA, complete cds. /// NM_000719 // intron // 0 // Hs.335817 // CACNA1C // 775 // Homo sapiens calcium	-	-, Homo sapiens (clone hHT-1) L-type voltage-dependent calcium channel a1 subunit (hHT) complete cds. p13.33
SNP_A-2074451	acatagaaagcaggac[A/G]actatttaacaggtat	A	G	286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780), mRNA. /// ENST00000354914 // intron // 0 // ---	MGC45780	MGC45780, Homo sapiens hypothetical protein MGC45780 (MGC45780), p21.1
SNP_A-2187806	cagtaggtccaggcta[C/T]gaggcaaatgattctt	C	T	1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 10539 // Hs.406191 //	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-2188811	cagtgggacagaagga[C/T]aacttctcatcactcc	C	T	// 55900 // Homo sapiens zinc finger protein 302 (ZNF302), mRNA. /// NM_018675 // downstream // 41342 // Hs.436350	ZNF302	ZNF302, Homo sapiens zinc finger protein 302 (ZNF302), q13.11
SNP_A-2198822	catttcttcatcttca[C/G]cttttgctcaaccgt	C	G	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2217842	cctgcaaggcttccgc[C/T]agtgataaaaatgtac	C	T	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2206716	ccatgatcagaaatat[C/T]agttgattatagttaa	C	T	Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // intron // 0 // --- // --- // --- // ---	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2153493	attagcaattgctagg[C/T]cagtccctttcacact	C	T	Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2141728	atcttctctgaactac[C/T]gaagcatctaatttga	C	T	158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2111759	aggataatgccaaacg[C/T]acaaatggtagctatt	C	T	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1858546	tcagaggattgcagaa[C/T]ctaatccagaaggaag	C	T	1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 54797 //	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-1868615	tcctctctaaatagca[G/T]gaatatttttactacta	G	T	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 395288 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-1834977	tacccacgtcttctgc[A/C]agcatctttgcaaatg	A	C	10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 13985 // --- // --- // --- // --	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1812836	gtgggcacttttaaaa[A/G]gttttgcagaggagga	A	G	-- /// ENST00000355517 // downstream // 936492 // --- // --- //	-	q24.32
SNP_A-1958318	ttttccatatttgtca[C/T]ggagtttcaatgactt	C	T	Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), mRNA. /// ENST00000343289 // intron // 0 // --- // --- // --- // ---	NT5C2	NT5C2, Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), q24.33
SNP_A-1909082	tgtatcactgttagga[G/T]aaatcgtattgatttc	G	T	Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// ENST00000339837 // intron // 0 // --- //	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-1907448	tgtaaagagtcccagt[C/T]aatcccgaggtagcaa	C	T	Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), mRNA. /// ENST00000262592 // intron // 0 // --- // ---	BCAS1	BCAS1, Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), q13.2
SNP_A-1924549	ttatacctttcgggaa[A/T]ctgagcctgacaaaga	A	T	Homo sapiens ankyrin repeat domain 12 (ANKRD12), mRNA. /// ENST00000262126 // intron // 0 // --- // --- // --- // ---	ANKRD12	ANKRD12, Homo sapiens ankyrin repeat domain 12 (ANKRD12), p11.22
SNP_A-1900558	tggagctttttagttc[A/G]atagacctgacttagt	A	G	/// ENST00000332660 // downstream // 486812 // --- // --- // ---	-	p12.3
SNP_A-1892709	atgatatgtacactga[C/T]gtaggccatacataga	C	T	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 521374 // --- // --- // --- //	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-1925583	ttatgaattaatctac[A/T]cttattagcatttaaa	A	T	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 124961 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1925879	ttatgggaactataac[A/T]gagtaaaaatgtcctt	A	T	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1935636	ttctgtatagagacaa[A/C]catgaaagaaagctgg	A	C	ABCA13 // 154664 // Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // downstream // 168581 // --- // --- // --- //	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-1933837	ttctattactccaata[C/T]agtagtcgcttatttg	C	T	490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 123096 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1965580	gacatgatgatcttca[A/G]gattggagtctatcta	A	G	sapiens lymphocyte antigen 75 (LY75), mRNA. /// ENST00000263636 // intron // 0 // --- // --- // --- // ---	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2
SNP_A-1962907	atgctctgtgatataa[C/T]tggttacttttgtct	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-1812851	gtgggcatccctggtc[A/T]ctggcctatgctgggc	A	T	TPD52L1 // 7164 // Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, mRNA. /// NM_001003396 //	TPD52L1	TPD52L1, Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, q22.31
SNP_A-1806030	gtcctaggggcagctc[A/G]aaggtaggcaggttcc	A	G	Homo sapiens KIAA1199 (KIAA1199), mRNA. /// D42039 // 3UTR // 0 // Hs.513070 // MESDC2 // 23184 // Homo sapiens	KIAA1199	KIAA1199, Homo sapiens KIAA1199 (KIAA1199), q25.1
SNP_A-1792336	gggttgcccagtctgc[A/G]agagggaagagcttgg	A	G	3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 1464 //	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q31.1
SNP_A-1700915	taattagaaataaatggaaagatat[A/G]tatgcatctttgtggtcacataaag	A	G	2917 // glutamate receptor, metabotropic 7 /// NM_014674 // downstream // 75407 // - // - // - // - /// NM_181874 // upstream	GRM7	GRM7 , rs1391962, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-1838832	tagactccattagaga[C/T]gggtggctttttgtttt	C	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 283714 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2118101	agtaaaatggggataa[G/T]aaggataaggtaagca	G	T	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // --- ///	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-2148321	atgggctgtgttttga[A/G]ccaccttcaatctcct	A	G	57085 // Homo sapiens angiotensin II receptor-associated protein (AGTRAP), mRNA. /// NM_005957 // downstream //	AGTRAP	AGTRAP, Homo sapiens angiotensin II receptor-associated protein (AGTRAP), p36.22

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2211589	ccctcagccatagtca[C/T]cttgagagttttgaat	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1631102 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2227187	ctaatttattcctacc[A/G]agtaaaacatggctca	A	G	PGEA1 // 25776 // Homo sapiens PKD2 interactor, golgi and endoplasmic reticulum associated 1 (PGEA1), transcript variant 2, mRNA. /// NM_015373 // downstream // 6738 //	PGEA1	PGEA1, Homo sapiens PKD2 interactor, golgi and endoplasmic reticulum associated 1 (PGEA1), transcript variant 2, q13.1
SNP_A-2172366	caattacccaaggaca[A/T]taactggcacacctgt	A	T	1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream //	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2068732	acaatagcctacagga[A/G]actccacacaggtatt	A	G	ENST00000324778 // intron // 0 // --- // --- // --- // ---	-	q25.2
SNP_A-2053539	aagtgctaacatctgg[A/C]aaacagtgtaggatct	A	C	Homo sapiens GPI anchored molecule like protein (GML), mRNA. /// ENST00000343427 // upstream // 20815 // --- // ---	GML	GML, Homo sapiens GPI anchored molecule like protein (GML), q24.3
SNP_A-2093153	agaacatgtcagagga[A/G]cctctggatttcttga	A	G	50514 // Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA. /// NM_002581 // upstream // 304633 //	DEC1	DEC1, Homo sapiens deleted in esophageal cancer 1 (DEC1), q33.1
SNP_A-2095545	agacaaggctttgaac[A/G]caagtagttctgtgaa	A	G	/// ENST00000355503 // upstream // 52887 // --- // --- // --- // --	-	p13
SNP_A-2013517	ttctactggcttctaa[A/T]caaaacaagaaactag	A	T	2138 // Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, mRNA. /// NM_172059 //	EYA1	EYA1, Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, q13.3
SNP_A-2291118	gcaatagcagcagacc[A/G]cgagtagccttgattt	A	G	// Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), mRNA. /// ENST00000331299 // intron // 0 // --- // --- // --- // ---	SLC25A21	SLC25A21, Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), q13.3
SNP_A-2306401	gctggggtggcaccaa[C/T]gagcctgaaagctaca	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2236687	ctctaatactctaata[A/T]gcacagatttttttt	A	T	Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2238992	ctcttccttcggccaa[A/T]acagccagattaggca	A	T	/// ENST00000359064 // upstream // 51770 // --- // --- // --- // -- /// ENST00000332041 // downstream // 459804 // --- // --- // --- // --	-	q22.1
SNP_A-2262099	gaaatatgtggtaaga[C/T]gcagaaatataatgcc	C	T	/// ENST00000354623 // downstream // 341498 // --- // --- // --- // --- /// ENST00000283950 // upstream // 249898 // --- // ---	-	q12
SNP_A-2262166	gaaatcagccgttaca[A/G]aagtcaaggctctttg	A	G	SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), mRNA. /// ENST00000318445 // downstream // 24548 // --- // --- // --- // --	SLCO3A1	SLCO3A1, Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), q26.1
SNP_A-2303364	gctattccaaaagttc[A/C]caagtattgcagatga	A	C	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 18543 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2303149	gctatcaaaagcctca[A/G]caggactaccatgaca	A	G	Homo sapiens chromosome 14 open reading frame 133 (C14orf133), mRNA. /// ENST00000327028 // intron // 0 // ---	C14orf133	C14orf133, Homo sapiens chromosome 14 open reading frame 133 (C14orf133), q24.3
SNP_A-2006122	tccctaggagaaccga[C/T]agggctgtctcacctg	C	T	LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 //	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-1997622	cacacatttcttaagc[A/G]cctatgggcagaggct	A	G	5774 // Homo sapiens protein tyrosine phosphatase, non-receptor type 3 (PTPN3), mRNA. /// ENST00000262539 // upstream // 18585 // --- // --- // --- // --- /// ENST00000332925	PTPN3	PTPN3, Homo sapiens protein tyrosine phosphatase, non-receptor type 3 (PTPN3), q31.3
SNP_A-2003754	gaaagaaagggcatgc[A/G]agttcagaacctgtct	A	G	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2032531	aaataaaaggcatcca[C/T]gagggaaaaattaaga	C	T	// 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream // 90376 // Hs.12420 // PHF17 // 79960 // Homo sapiens PHD	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-2037024	aataatgttagactta[A/G]gccacaagtcttggtc	A	G	// 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 52831 //	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-2046521	aagagatacagaaaga[C/T]taaattttgccagaaa	C	T	285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// ENST00000295268 // intron // 0 // ---	MGC46496	MGC46496, Homo sapiens hypothetical protein MGC46496 (MGC46496), q22.3
SNP_A-2093279	agaacctgtgctcaaa[A/G]tcaccagtgtgtgtac	A	G	/// ENST00000355517 // downstream // 1106667 // --- // --- // --	-	q24.32
SNP_A-2201186	ccaagttataggcatg[C/T]caactctgttaagcac	C	T	Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // intron // 0 //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-2146505	atgctgaattttaacc[C/T]gagttccaggtcctct	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 980820 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2142318	atgaaacgagcagtaa[C/T]gacgacccaggtcact	C	T	4602 // Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA. /// NM_017651 //	MYB	MYB, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1843718	tagtgtctgccaagaa[A/T]ctcatgtttgcagaag	A	T	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1819162	gcaaagagaacattgg[A/G]aaaaaaatggaatcaa	A	G	22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 18781 //	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-1869637	tccttagaccatgaag[A/G]agtttatggagacttg	A	G	3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. /// ENST00000315260 //	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.3
SNP_A-1855653	tcaatagaaataaaga[C/G]aagtagagctggcagg	C	G	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 467051 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-1709947	ctgctgtggaataaactaggaagaa[C/T]gtttgttaagcagcattgaggaacc	C	T	NM_033050 // downstream // 79334 // Hs.279575 // GPR91 // 56670 // G protein-coupled receptor 91	-	- , rs3109798, - ,q25.1
SNP_A-1680236	aaggaaagcccctaaaaagcttcat[A/G]actacaaaattggtcacaaggaaga	A	G	// 7957 // epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) /// NM_007124 // downstream // 360093 // Hs.250607 // UTRN // 7402 // utrophin (homologous to	EPM2A	EPM2A , rs10484702, epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) ,q24.3
SNP_A-1670546	tgtctgttgccaacgcccatgatca[C/T]tccactgtatcaacatcttgcactg	C	T	4978 // opioid binding protein/cell adhesion molecule-like /// NM_174927 // downstream // 232889 // Hs.97541 // SPAS1 //	OPCML	OPCML , rs4128620, opioid binding protein,q25
SNP_A-1654995	aagtcaaaagtaacagaaaatacta[C/T]gtgaaatgattctaataagcaatac	C	T	AK055204 // intron // 0 // Hs.258095 // C6orf143 // 222584 // chromosome 6 open reading frame 143	C6orf143	C6orf143 , rs10485135, chromosome 6 open reading frame 143,p12.1
SNP_A-1786134	ggctggccagccacca[A/G]ctccgcaaagggacac	A	G	Homo sapiens hypothetical protein 384D8_6 (384D8-2), mRNA. /// NM_152299 // CDS // 0 // Hs.180903 // 384D8-2 //	384D8-2	384D8-2, Homo sapiens hypothetical protein 384D8_6 (384D8-2), q13.33
SNP_A-1972625	ctgtttcctagctcca[A/G]tcagccttttgatcag	A	G	Homo sapiens dedicator of cytokinesis 3 (DOCK3), mRNA. /// ENST00000266037 // intron // 0 // --- // --- // --- // ---	DOCK3	DOCK3, Homo sapiens dedicator of cytokinesis 3 (DOCK3), p21.31
SNP_A-1930858	ttccagcactttctta[C/T]gaaaatttgcaaacag	C	T	// 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-1929533	ttcataatgaaagata[A/G]ccttcttctgtcatat	A	G	-- /// ENST00000345029 // upstream // 388902 // --- // --- // ---	-	p14
SNP_A-1905766	tggtatttgctgttct[A/G]aatctttgagggattg	A	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1912886	tgtgctttatgtgtaa[C/T]atctcatgttgtaaag	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1048280	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1890600	tgatgaaagtcacaga[A/G]tcccttagaactaaaa	A	G	145407 // Homo sapiens chromosome 14 open reading frame 37 (C14orf37), mRNA. /// ENST00000267485 // intron	C14orf37	C14orf37, Homo sapiens chromosome 14 open reading frame 37 (C14orf37), q23.1
SNP_A-1889673	tgataacttctgcagg[A/C]caaaactagcttttgc	A	C	257068 // Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 2 (PLCXD2), mRNA. /// NM_145753 // upstream // 35572 // Hs.477114 // PHLDB2	PLCXD2	PLCXD2, Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 2 (PLCXD2), q13.2
SNP_A-1887786	tgagatctgacaccaa[C/T]acatagttactgaact	C	T	Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /// ENST00000256397 // intron // 0 // --- // --- // --- // ---	LOXL2	LOXL2, Homo sapiens lysyl oxidase-like 2 (LOXL2), p21.3
SNP_A-1879466	tcttattagatactta[C/T]cacaattcctaattct	C	T	Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-1895715	tgcctcttataggtca[A/G]ctctgatgtcaccagc	A	G	5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 //	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-1899796	tggaattatattctga[C/T]gactggtgaaaaagta	C	T	23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// NM_012137	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-1899342	tggaaccactagcttc[C/T]cataatctatattaat	C	T	Homo sapiens INPE5792 (UNQ5792), mRNA. /// ENST00000339766 // intron // 0 // --- // --- // --- // ---	CLEC2A	CLEC2A, Homo sapiens INPE5792 (UNQ5792), p13.31
SNP_A-1897785	tgctggagaatcaaac[C/T]aatagaagtcttaagg	C	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1741094 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-1969152	agctaaggcctgtatc[A/G]aaggacttacaactct	A	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1790641	ggggctcttccgcttc[G/T]ctcttcactcttctcc	G	T	ENST00000358773 // intron // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-1795587	ggtgctcctgctaaag[A/G]agaagatatagaactt	A	G	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 //	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783150	ggcaggattcctgaaa[A/G]cctaaagctagaccag	A	G	341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// ENST00000342700 //	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-1725264	gttttgtttcccagaaaatacaaac[A/G]gagagagttggtaatagtaaaatgg	A	G	BC029120 // intron // 0 // Hs.436140 // FLJ22789 // 84190 // hypothetical protein FLJ22789	FLJ22789	FLJ22789 , rs7299616, hypothetical protein FLJ22789,q21.31
SNP_A-1847671	tatctaccccaactca[C/G]aactaatatgtgccaa	C	G	ENST00000307717 // intron // 0 // --- // --- // --- // ---	-	q23.31
SNP_A-1865793	tcccaaaaacatcgta[A/T]gaaaacatccaatatt	A	T	Homo sapiens glycoprotein M6A (GPM6A), transcript variant 1, mRNA. /// NM_201591 // intron // 0 // Hs.75819 // GPM6A //	GPM6A	GPM6A, Homo sapiens glycoprotein M6A (GPM6A), transcript variant 1, q34.2
SNP_A-1840729	tagctaaggaatgcaa[C/T]atttccccttgaaaa	C	T	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 235158 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2157284	attgacggcttcgagc[A/G]cttcaccaagaagatg	A	G	// Homo sapiens FLJ35740 protein (FLJ35740), mRNA. /// ENST00000313339 // intron // 0 // --- // --- // --- // ---	FLJ35740	FLJ35740, Homo sapiens FLJ35740 protein (FLJ35740), p13.2
SNP_A-2115847	agggtggatgccgata[C/T]ggaatgggcaggaatt	C	T	3566 // Homo sapiens interleukin 4 receptor (IL4R), mRNA. /// NM_021798 // upstream // 31162 // Hs.210546 // IL21R //	IL4R	IL4R, Homo sapiens interleukin 4 receptor (IL4R), p12.1
SNP_A-2113382	tcccccataatgaccc[A/G]ggatgtctcttaagcc	A	G	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 996057 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2127973	ataagagtcagtcttc[A/G]aatgtgtttaagatgc	A	G	23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 119244 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2205334	ccagtctagtagtatg[A/C]acagaaacttgtggct	A	C	157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-2207402	ccattgccatggaaag[G/T]agtggtagcgctgggg	G	T	91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 113333 //	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-2214537	cctagaatcctgacac[A/G]ggcagccagagttccg	A	G	92359 // Homo sapiens crumbs homolog 3 (Drosophila) (CRB3), transcript variant 3, mRNA. /// NM_139161 //	CRB3	CRB3, Homo sapiens crumbs homolog 3 (Drosophila) (CRB3), transcript variant 3, p13.3
SNP_A-2183402	cagcactgctcgttaa[C/T]agccccaaactggaaa	C	T	923 // Homo sapiens CD6 antigen (CD6), mRNA. /// NM_014207 // upstream // 59210 // Hs.58685 // CD5 // 921 //	CD6	CD6, Homo sapiens CD6 antigen (CD6), q12.2
SNP_A-2088975	acttaaaatgcattca[C/G]tatttcctcagagaga	C	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 363186 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2058427	aatcacgagaatttga[C/T]gataaattggatatgg	C	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 36229 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3
SNP_A-2047103	aagataaagtattaaa[A/G]tcagcttgtcattagg	A	G	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2044724	aagaaagtaactttac[A/G]atgaagacctcaaaca	A	G	SEC23IP // 11196 // Homo sapiens SEC23 interacting protein (SEC23IP), mRNA. /// NM_000982 // downstream // 230111 //	SEC23IP	SEC23IP, Homo sapiens SEC23 interacting protein (SEC23IP), q26.12
SNP_A-2040696	aacccacacacttaca[G/T]gcggattccagagact	G	T	Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000312177 // CDS // 0 // --- // --- // --- // ---	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-2026895	aaacactacaaataac[A/T]cttagtctgcaaaatg	A	T	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 353471 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2021892	aaaaactctttgattc[A/G]atatcgacttctatta	A	G	// Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// ENST00000297345 // intron // 0 // --- // --- // --- // ---	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2008516	gaaccgaaatgaatta[C/T]gggacctccagctagt	C	T	Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // --- // --- // --- // ---	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-2008513	agcccagattatgaag[A/G]ctacaacaaggaccta	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// NM_144715 // downstream // 325558 // Hs.257224 // EFHB //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2308982	gcttttcagttccaaa[C/T]ttgcagctgcgtttca	C	T	Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), mRNA. /// ENST00000262428 // intron // 0 // --- // --- // --- // ---	COTL1	COTL1, Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), q24.1
SNP_A-2314985	ggagttggcgagggga[A/G]gtgttccaaaggcacc	A	G	10904 // Homo sapiens bladder cancer associated protein (BLCAP), mRNA. /// NM_181689 // downstream // 72798 //	BLCAP	BLCAP, Homo sapiens bladder cancer associated protein (BLCAP), q11.23
SNP_A-2233549	ctcagttctcccaaca[G/T]gcctgagacttccatg	G	T	// 56951 // Homo sapiens chromosome 5 open reading frame 15 (C5orf15), mRNA. /// ENST00000231482 // downstream //	C5orf15	C5orf15, Homo sapiens chromosome 5 open reading frame 15 (C5orf15), q31.1
SNP_A-2234648	ctccagatcaaaacaa[A/G]atgcctctcttcagtt	A	G	8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 153878 //	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2282699	gagttttcagtctgca[C/T]tcagaatagatataac	C	T	Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), mRNA. /// ENST00000224892 // intron // 0 // --- // --- // --- // ---	LHPP	LHPP, Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), q26.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2306170	gctggatgcattaacg[C/T]aaagtgaatatacctg	C	T	-- /// ENST00000342478 // downstream // 207341 // --- // --- //	-	q11.21
SNP_A-1993647	agttgaaaacagggga[A/G]agaaggaaggcattca	A	G	Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// ENST00000297769 // intron // 0 // --- // --- // --- // --- ///	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2060827	aatgataaacacctat[G/T]aatatcactgattggt	G	T	Homo sapiens centrosome protein cep290 (Cep290), mRNA. /// ENST00000309041 // intron // 0 // --- // --- // --- // ---	Cep290	Cep290, Homo sapiens centrosome protein cep290 (Cep290), q21.32
SNP_A-2065780	aatttcagctggcaaa[A/G]cacttatggaatggaa	A	G	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// ENST00000280633 // upstream // 70451 // --- // --- // --- // ---	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2104577	agcaggtcaagttcaa[A/C]ctctagtgccagcaaa	A	C	FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2099729	agaggttgccaaaaga[C/G]agtctgaggggaaatg	C	G	6496 // Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA. /// NM_016932 // downstream //	SIX3	SIX3, Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), p21
SNP_A-2099749	agaggttttggtctcc[A/G]ctcacgttaatctttt	A	G	SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 253314 // Hs.511265 // SEM	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN q21.1
SNP_A-2197869	cattgatacccaagtc[C/T]aataataatattcacc	C	T	// 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2193319	catctctcaccacaaa[A/T]tctgtatttttatgta	A	T	Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, mRNA. /// NM_058177 // intron // 0 // Hs.196054 //	HDAC9	HDAC9, Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, p21.1
SNP_A-2169423	caagccacataaacac[C/T]gcagcttgtgatgctt	C	T	ENST00000303864 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2180131	cagaaaatctacttta[C/T]agcagttgtacgttaa	C	T	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 4899 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2209502	cccatccctatactca[C/T]gccccttctcaacatg	C	T	864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 107626 //	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2138341	atccagctttggcttc[C/T]cttcagagctttcatt	C	T	7779 // Homo sapiens solute carrier family 30 (zinc transporter), member 1 (SLC30A1), mRNA. /// NM_002497 // downstream // 59740 // Hs.153704 // NEK2 // 4751 // Homo	SLC30A1	SLC30A1, Homo sapiens solute carrier family 30 (zinc transporter), member 1 (SLC30A1), q32.3
SNP_A-2152405	ctaattaagggttcca[A/G]actagatgaatcattt	A	G	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1479254 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1839895	tgttacccaggctgga[A/C]cactgctctctctcag	A	C	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA. /// ENST00000340825 // intron // 0 // --- // --- // --- // --- ///	KIAA0672	KIAA0672, Homo sapiens KIAA0672 gene product (KIAA0672), p12
SNP_A-1823954	taaaattgaacaagga[C/G]gattatgtttaaatca	C	G	ENST00000335259 // intron // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-1825165	aggccatgcttacacc[C/G]gcattgccaacagtgt	C	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1866815	tcccggcaaaaaatga[A/G]ccctcccactacacca	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, mRNA. /// NM_172362 // intron // 0 // Hs.527656 // KCNH1 //	KCNH1	KCNH1, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, q32.2
SNP_A-1852493	tatttacttactgcta[C/T]agagagaaactacaag	C	T	// 123169 // Homo sapiens senescence downregulated leo1-like (LOC123169), mRNA. /// NM_002748 // upstream //	LOC123169	LOC123169, Homo sapiens senescence downregulated leo1-like (LOC123169), q21.2
SNP_A-1805942	gtccgcttgagcaaca[C/T]agtttcacttctaagg	C	T	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-1802257	gtatatgacagtttca[A/C]atggatcacactttaa	A	C	3280 // Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), mRNA. /// ENST00000351516 //	HES1	HES1, Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), q29
SNP_A-1972549	tggaggtgctgaaatc[A/C]catacttcgttttatg	A	C	Homo sapiens zinc finger protein 35 (clone HF.10) (ZNF35), mRNA. /// ENST00000358588 // intron // 0 // --- // --- // --- // ---	ZNF35	ZNF35, Homo sapiens zinc finger protein 35 (clone HF.10) (ZNF35), p21.32
SNP_A-1979887	tcagtcttatcacaaa[A/T]aagtagtttgaggaag	A	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 65210 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1988735	gtgaacgaaataatgt[C/G]aaactgaaaatgttct	C	G	// 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 441493 // --- // --- // --- //	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1954496	tttgccatatttgcta[C/T]cagatatgttggcagt	C	T	152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 //	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1951888	tttctacaatcttctc[C/T]aatcacttcccagcca	C	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 587238 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1887843	tgagatgtcatgcaga[C/T]tctactgtccctctcc	C	T	Homo sapiens keratin protein K6irs (K6IRS2), mRNA. /// ENST00000293745 // intron // 0 // --- // --- // --- // ---	K6IRS2	K6IRS2, Homo sapiens keratin protein K6irs (K6IRS2), q13.13

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1882033	tcttttgcttttcgca[A/G]taaattttgctggtgg	A	G	sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // --- // --- // --- // ---	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-1912582	tgtgccagttatcaca[C/T]gattgtgtcccagccc	C	T	29777 // Homo sapiens activator of basal transcription 1 (ABT1), mRNA. /// NM_024639 // downstream // 28847 //	ABT1	ABT1, Homo sapiens activator of basal transcription 1 (ABT1), p22.1
SNP_A-1928685	ttcagaaaccagcaca[C/T]tagttaccccagaacc	C	T	9681 // Homo sapiens mRNA for KIAA0645 protein, partial cds. /// ENST00000327423 // upstream // 1149 // --- // --- // ---	DEPDC5	DEPDC5, Homo sapiens for KIAA0645 protein, partial cds. ,q12.2
SNP_A-1888521	tgaggagctgctccta[C/G]atgagaccctggatct	C	G	29113 // Homo sapiens chromosome 6 open reading frame 15 (C6orf15), mRNA. /// NM_014068 // upstream // 1795 //	C6orf15	C6orf15, Homo sapiens chromosome 6 open reading frame 15 (C6orf15), p21.33
SNP_A-1988090	tgtttctgtatctgaa[C/T]taattggtgatattcc	C	T	ENST00000359407 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-1987414	accattgtagtaacaa[A/G]catcagacattactga	A	G	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1986506	tttccatttttagtg[C/T]aatttggcagattcaa	C	T	ENST00000310269 // intron // 0 // --- // --- // --- // ---	-	q42.12
SNP_A-1968360	acacattggacagagc[A/G]agaatgtcacactgtc	A	G	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. ,q12
SNP_A-1802632	gtatctttgagtgtga[C/T]aaagaaaaaagctctg	C	T	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SMARCA2	SMARCA2, Homo sapiens SWI,p24.3
SNP_A-1785493	ggctcactgagaacaa[C/T]tgagtgtgtagacaag	C	T	FLJ32685 // 152110 // Homo sapiens hypothetical protein FLJ32685 (FLJ32685), mRNA. /// ENST00000358592 //	FLJ32685	FLJ32685, Homo sapiens hypothetical protein FLJ32685 (FLJ32685), p24.2
SNP_A-1714773	caaagtgtgatgtcacctatttata[A/T]ccctccaagggcttcccaagacctc	A	T	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // ATPase, Class V, type 10B	ATP10B	ATP10B , rs10515812, ATPase, Class V, type 10B,q34
SNP_A-1721155	gggcacatatttttggctctggaaa[C/T]aaagcttcaagccctaaaagtatgg	C	T	5028 // purinergic receptor P2Y, G-protein coupled, 1 /// NM_002886 // upstream // 226815 // Hs.98643 // RAP2B //	P2RY1	P2RY1 , rs10513436, purinergic receptor P2Y, G-protein coupled, 1 ,q25.2
SNP_A-1844725	tataagcattatttca[A/G]tcatttttttagagttc	A	G	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 463841 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-1871469	tctaacctctgctcta[A/T]gcctgactcattgtac	A	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 789818 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p25.3
SNP_A-1826449	taacaaaggtgtattg[C/G]atttacactgaactct	C	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 777510 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1835378	tacctccgtttccccc[C/T]gaaggtatcgctacct	C	T	Homo sapiens sialyltransferase 8E (alpha-2, 8-polysialyltransferase) (SIAT8E), mRNA. /// ENST00000315087 // intron // 0 // --- // --- // --- // ---	ST8SIA5	ST8SIA5, Homo sapiens sialyltransferase 8E (alpha-2, 8-polysialyltransferase) (SIAT8E), q21.1
SNP_A-1829426	taagtgaaatagtgga[A/G]gggataacagagttgg	A	G	sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-2151682	atgttggtgctaggga[C/G]atattgatgcattgaa	C	G	// 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream //	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-2109925	aggaactgaaatatga[C/T]gttggtggaggagaac	C	T	1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 1152446 //	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.2
SNP_A-2118946	agtagaaaaatagaat[A/G]agttctccatttcttc	A	G	ENST00000251030 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-2208711	cccagaactagtagaa[A/G]taagttgcaattaaag	A	G	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // upstream // 1305349 // Hs.91381 // CSMD3 // 114788 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2175050	cacagtataaaaatac[A/G]ctaatatcctgagcta	A	G	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	YWHAB	YWHAB, Homo sapiens tyrosine 3-monooxygenase,q13.12
SNP_A-2177259	cacctggggcctcact[A/G]agagctgggagaagaa	A	G	sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2101750	agatgcctacatatca[C/T]tctatttgtgtggatt	C	T	34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 14425 // Hs.78948 // RABGGTB // 58	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN p31.1
SNP_A-2096713	agactaagttaagaaa[A/G]gaaagtcatccaggag	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1836843 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2051602	aaggtaagaaatgtga[A/G]cacctaaagcagacta	A	G	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2004663	cttgcataattacaca[C/T]tgaaaatttgctacaa	C	T	Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), mRNA. /// ENST00000343289 // intron // 0 // --- // --- // --- // ---	NT5C2	NT5C2, Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), q24.33
SNP_A-2291099	gcaataccttgacaga[C/T]ggttaggacagccaat	C	T	Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA. /// NM_000192 // intron // 0 // Hs.381715 // TBX5 // 6910 //	TBX5	TBX5, Homo sapiens T-box 5 (TBX5), transcript variant 2, q24.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2280944	gaggtttaaactggcc[A/G]gcatctgcctggcttc	A	G	Homo sapiens parvin, alpha (PARVA), mRNA. /// ENST00000334956 // intron // 0 // --- // --- // --- // ---	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.3
SNP_A-2276573	gagaggtaggagagag[A/G]acttcactgcaaaagg	A	G	sapiens GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA. /// ENST00000254299 // intron // 0 // --- // ---	GCH1	GCH1, Homo sapiens GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), q22.2
SNP_A-2259352	gaaaaagtcatatgaa[G/T]cttgctacagaattta	G	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1283534 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2234575	ctccactggctcctca[C/T]gcgtacgagaagaccg	C	T	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 684795 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2236430	ctcggaatctaatacg[C/T]atctgctatcattttc	C	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 551375 // --- // --- // --- //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2245207	ctggctaaataaaagg[G/T]atacacccttgtcaca	G	T	sapiens ELYS transcription factor-like protein TMBS62 (ELYS), mRNA. /// ENST00000283201 // intron // 0 // --- // ---	-	-, Homo sapiens ELYS transcription factor-like protein TMBS62 (ELYS), q44
SNP_A-2243231	ctgcctgagccctaga[A/G]aaactgaagttggcag	A	G	1308 // Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, mRNA. /// NM_130778 //	COL17A1	COL17A1, Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, q25.1
SNP_A-2252863	cttctatataaggaac[A/T]gtcttgaatattgact	A	T	ENST00000223145 // intron // 0 // --- // --- // ---	-	p21.3
SNP_A-2254454	cttgcccagtgattct[A/C]aactgtgcttccagag	A	C	51665 // Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA. /// ENST00000264607 //	ASB1	ASB1, Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), q37.3
SNP_A-2232198	ctcaatacatacttcc[C/T]gaataaatgaagggca	C	T	Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), mRNA. /// ENST00000262428 // intron // 0 // --- // --- // --- // ---	COTL1	COTL1, Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), q24.1
SNP_A-2307939	gcttctgggtaactga[A/G]gaccggtgggcccgcc	A	G	Homo sapiens KIAA0980 protein (KIAA0980), mRNA. /// ENST00000278886 // intron // 0 // --- // --- // ---	KIAA0980	KIAA0980, Homo sapiens KIAA0980 protein (KIAA0980), p11.21
SNP_A-2014140	tgactcttcactgtgg[A/G]accatcaaaaattcct	A	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 925812 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2026100	aaaattagttgggcag[A/T]caactaaagctggtcc	A	T	/// ENST00000341422 // downstream // 48782 // --- // --- // ---	-	p33
SNP_A-2029737	aaagaggactgggcac[A/G]aagtatatgcctggac	A	G	Homo sapiens tubulin, alpha 8 (TUBA8), mRNA. /// ENST00000316027 // intron // 0 // --- // --- // --- // ---	TUBA8	TUBA8, Homo sapiens tubulin, alpha 8 (TUBA8), q11.21
SNP_A-2029020	aaagaaacaacatgag[G/T]caaatttagaaaataa	G	T	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 697122 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2041629	aacgcccagatcataa[C/T]gaattttatgagtgtc	C	T	MGC35130 // 148581 // Homo sapiens hypothetical protein MGC35130 (MGC35130), mRNA. /// NM_020925 // upstream	MGC35130	MGC35130, Homo sapiens hypothetical protein MGC35130 (MGC35130), p31.3
SNP_A-2035999	aaattaaggttatttc[A/G]agactaagaacataac	A	G	Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), mRNA. /// ENST00000258991 // intron // 0 // --- // ---	HT008	HT008, Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), q23.3
SNP_A-2054062	aagttattactgaacc[C/T]atcttatgaatgaggc	C	T	ENST00000339762 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-2090856	actttcagacaacaca[A/G]gcattctcatgataga	A	G	FLJ43980 // 124149 // Homo sapiens FLJ43980 protein (FLJ43980), mRNA. /// ENST00000331332 // upstream //	FLJ43980	FLJ43980, Homo sapiens FLJ43980 protein (FLJ43980), p11.1
SNP_A-2079374	accccaggctgcatac[C/T]ggttccagtccatggc	C	T	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 (DDX27), mRNA. /// ENST00000338362 // intron // 0 // --- // ---	DDX27	DDX27, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 (DDX27), q13.13
SNP_A-2083422	actaagaactgaggac[C/T]gcacacttccttgtaa	C	T	64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 275536 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2192637	catccatgcatgcaaa[A/T]attcattttggaacaa	A	T	/// ENST00000251675 // downstream // 51151 // --- // --- // --- // --- /// ENST00000360855 // downstream // 51181 // --- // ---	-	q32.3
SNP_A-2227822	ctaccattttctgggc[A/G]ccttctaatgacaagt	A	G	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2146188	atgcgtagccatgact[C/T]agccatcccctcaacc	C	T	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 420092	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2139959	atctaccttgagaaag[C/G]aatagtagatctaagc	C	G	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-1816868	gttatgtggccaacac[A/G]acactaggaagtatgg	A	G	FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1844679	tataagaagcgaggca[A/G]gtacacattaacgcgg	A	G	// Homo sapiens small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha (SGTA), mRNA. /// NM_003249 // upstream // 306 // Hs.78769 // THOP1 // 7064 // Homo	SGTA	SGTA, Homo sapiens small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha (SGTA), p13.3
SNP_A-1784658	ggcctcctctgaccac[A/G]ccagtaggaatgaaga	A	G	// 54839 // Homo sapiens hypothetical protein FLJ20156 (FLJ20156), mRNA. /// ENST00000260382 // downstream //	FLJ20156	FLJ20156, Homo sapiens hypothetical protein FLJ20156 (FLJ20156), q23

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1986711	aatggggtggatatca[C/T]agtccttcctgacttt	C	T	ENST00000330469 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1955976	tttgtctaactttcaa[C/G]gaggtctttagttggc	C	G	Homo sapiens KIAA1536 protein (KIAA1536), mRNA. /// ENST00000262059 // intron // 0 // --- // --- // --- // --- ///	KIAA1536	KIAA1536, Homo sapiens KIAA1536 protein (KIAA1536), q13.13
SNP_A-1933831	ttctatgttacagtag[A/C]agttgtatgtgttaag	A	C	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 164626 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1939527	ttgattcaactacacc[A/G]aaccactgacaattct	A	G	// 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 166890 // Hs.504943	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.3
SNP_A-1894659	tgccagacaaggacat[A/C]aacaggatttgttcat	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 19630 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.1
SNP_A-1926990	ttatttgaaaacatga[C/T]gagtagaacaatattt	C	T	23589 // Homo sapiens calcium regulated heat stable protein 1, 24kDa (CARHSP1), mRNA. /// NM_003470 // downstream	CARHSP1	CARHSP1, Homo sapiens calcium regulated heat stable protein 1, 24kDa (CARHSP1), p13.2
SNP_A-1927771	ttcaagccctggcaaa[A/G]gtccagacacccagga	A	G	Homo sapiens hypothetical protein FLJ32934 (FLJ32934), mRNA. /// ENST00000324761 // intron // 0 // --- // --- // --- // ---	FLJ32934	FLJ32934, Homo sapiens hypothetical protein FLJ32934 (FLJ32934), q22
SNP_A-1932860	ttcctttcagttgtaa[C/T]ctttctgtgattctaa	C	T	SULT1C2 // 27233 // Homo sapiens sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), mRNA. /// NM_014635 // upstream // 36922 // Hs.436505 // GCC2 // 9648 // Homo	SULT1C2	SULT1C2, Homo sapiens sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), q12.3
SNP_A-1908122	tgtacagtaaaagtac[A/G]gaagtacagtattata	A	G	114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream //	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-1881548	tctttcttatgaacac[C/T]aattaatcttaggttt	C	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-1946588	tttaaatggaatcaca[C/T]tatttgtaaccatcca	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 588455 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1948976	tttatctatctagaac[A/G]cagttaagaacaagaa	A	G	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1981100	ccaaggacaccactta[C/T]gcagttttcccacatg	C	T	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1982840	catttagtttataaga[A/G]catctgcttctaatac	A	G	Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// ENST00000359660 // intron // 0 // --- // --	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1982173	tttatttctcctagca[C/T]gtacccatttacctgg	C	T	Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA. /// ENST00000274364 // intron // 0 // ---	IQGAP2	IQGAP2, Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), q13.3
SNP_A-1972659	ggcacgaacaacatac[A/G]gaaattaatgactgtc	A	G	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-1973829	aggatttgagcattta[G/T]gtaaagtgcagagctt	G	T	56987 // Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// NM_198793 // downstream // 54394 //	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1780969	ggatgaggcagtgata[A/G]gattgtgcagaggctg	A	G	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 211367 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-1677824	gataccccagtagcaattaacatac[G/T]gattaaccagatcttggcttctaaa	G	T	8491 // mitogen-activated protein kinase kinase kinase kinase 3 /// NM_152390 // upstream // 61863 // Hs.40808 //	MAP4K3	MAP4K3 , rs1005427, mitogen-activated protein kinase kinase kinase kinase 3 ,p22.1
SNP_A-1807120	gtctcctcgagcctgt[C/G]aaagagacgaaggaga	C	G	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1862494	tcatgtttctgcctca[A/G]caaaataccaactgct	A	G	// 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 364826 // ---	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-1829297	taagtatcttaaggtc[A/G]actctgagttatatac	A	G	sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, mRNA. /// NM_199194 // intron // 0 // Hs.258314 // BRE // 9577 // Homo	BRE	BRE, Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, p23.2
SNP_A-1831714	taattcaaaacttcaa[A/G]tgtaagattggggctg	A	G	1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 259795 //	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24
SNP_A-1833243	acttaggcaaagtaaa[C/G]tagatgcatcactggt	C	G	sapiens hypothetical protein FLJ14069 (FLJ14069), mRNA. /// NM_017575 // intron // 0 // Hs.448342 // C17orf31 // 23293	-	-, Homo sapiens hypothetical protein FLJ14069 (FLJ14069), p13.3
SNP_A-1840451	tagccacttttttgtta[A/C]aagcaaaagcaaaaga	A	C	// 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 497439 // ---	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1842559	taggttcaagggtaga[C/T]atgcataacgtgcagg	C	T	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, mRNA. /// ENST00000329257 // intron //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, q23.1
SNP_A-2141601	atcttcaagaatagaa[A/G]ccattaagatacaaat	A	G	sapiens growth differentiation factor 8 (GDF8), mRNA. /// ENST00000260950 // CDS // 0 // --- // --- // --- // ---	GDF8	GDF8, Homo sapiens growth differentiation factor 8 (GDF8), q32.2
SNP_A-2135782	atcaaaggtcacttca[A/G]atatacacacagaact	A	G	Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA. /// NM_182977 // intron // 0 // Hs.482043 //	NNT	NNT, Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134364	atatgctttatagggt[G/T]aattcagaaaacaaaa	G	T	/// ENST00000355063 // upstream // 643539 // --- // --- // --- // ---	-	q22.1
SNP_A-2225814	ctaaagttgaatccca[C/T]tggatccatctgagtt	C	T	/// ENST00000328175 // upstream // 8613 // --- // --- // --- // ---	-	q13.13
SNP_A-2222747	cgatggaatgcataaa[A/G]gatggggctgtgatag	A	G	29015 // Homo sapiens solute carrier family 43, member 3 (SLC43A3), mRNA. /// NM_199329 // upstream // 12924 //	SLC43A3	SLC43A3, Homo sapiens solute carrier family 43, member 3 (SLC43A3), q12.1
SNP_A-2214450	cctactgagtctttcc[G/T]gataaaaggtatcaag	G	T	636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // downstream // 728 // Hs.505202 // BICD1 // 636 // Homo	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2207280	ccattcctatttaaca[C/T]tgaatccagaaattaa	C	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1344018 // Hs.27214 // KCNC2	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2171098	caatagaatcagtggc[A/G]aagatctggacaatag	A	G	// 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-2174021	cacaccaaaacgagta[A/C]aaaagctcctttctaa	A	C	4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream //	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2049973	aaggaagcatcctcac[A/G]cttttcagaatgccct	A	G	ENST00000323868 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2067170	acaaagcaaagggaga[A/G]aaagaatcagctggtg	A	G	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2071468	acagaaagcattacca[C/T]taaagcacatacacaa	C	T	151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream //	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2010614	atgaagatgttttatg[A/G]acctactttccacttg	A	G	170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // --- // --- // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2291569	gcacaaatggtagata[C/T]agagaaagaaatccaa	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2298975	gccccccaaagagtca[C/T]tcacatcaaagatctt	C	T	Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // intron // 0 // ---	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-2233720	ctcatatttgtggaaa[A/G]agatttgttaaatata	A	G	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000265154 // intron // 0 // --- // --- // --- // ---	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24
SNP_A-2227978	ctaccttcagcaaata[G/T]aatggaacaagacgtt	G	T	80176 // Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), mRNA. /// NM_025106 // downstream	SSB1	SSB1, Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), p36.22
SNP_A-2274365	gactttaacacagaac[A/G]aatggttgcttctact	A	G	8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 495330 // Hs.370359	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2269215	gaatttaagaagccaa[A/C]cttcaaactatgacag	A	C	// Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// NM_153825 // downstream // 76193 //	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-2230582	ctatctatagagctga[C/T]aaagaaatacctaatc	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA. /// ENST00000282356 // intron // 0 // ---	CAMK4	CAMK4, Homo sapiens calcium q22.1
SNP_A-2246853	ctgtagggcaagggag[A/G]aaattggtcaggcttt	A	G	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 532726	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2306054	gctggaatccagttgc[A/G]ctcccaaatccagcat	A	G	ENST00000332853 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2012689	gggtgaatcaggagaa[C/T]gtttctccaatcaacc	C	T	10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 299365 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-2029239	aaagaagctaatctga[C/T]gatgtacacagtttgt	C	T	// 4724 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA. /// NM_019087 // downstream // 105577 //	NDUFS4	NDUFS4, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), q11.2
SNP_A-2027293	aaacatcaataattaa[A/G]ccccttttgttctaagc	A	G	sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA. /// ENST00000296031 // intron // 0 // --- // --- // --- // ---	CXCL1	CXCL1, Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), q13.3
SNP_A-2077046	accaactagaaaacaa[A/G]cacttgcatgaatgtg	A	G	94081 // Homo sapiens sideroflexin 1 (SFXN1), mRNA. /// NM_022304 // upstream // 111447 // Hs.247885 // HRH2 //	SFXN1	SFXN1, Homo sapiens sideroflexin 1 (SFXN1), q35.2
SNP_A-2050044	aaggaatgacgtgtcc[A/G]attgcaaacacatctc	A	G	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 583836 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181948	cagagctgagcttctc[A/G]caccattagagtttga	A	G	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 260703 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2182590	cagatcatattcccac[C/T]agtcttccttgcagga	C	T	1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 111040 // Hs.143434	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2202643	ccacctgcaggatgga[C/T]gctctgagatattcca	C	T	Homo sapiens allantoicase (ALLC), transcript variant 2, mRNA. /// NM_018436 // intron // 0 // Hs.97899 // ALLC //	ALLC	ALLC, Homo sapiens allantoicase (ALLC), transcript variant 2, p25.3
SNP_A-2112487	aggcacaaattgaggc[A/G]aatttttctcccttta	A	G	sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) mRNA, complete cds. /// NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and	PSD3	PSD3, Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) complete cds. p22
SNP_A-2141740	atcttctgataaggaa[A/G]ggaaaatccagagaaa	A	G	/// ENST00000309675 // upstream // 26165 // --- // --- // --- // ---	-	q13.2
SNP_A-2146390	atgctcacctgtctct[A/G]aaatcatgactctgtc	A	G	Homo sapiens mitogen-activated protein kinase 4 (MAPK4), mRNA. /// ENST00000269463 // intron // 0 // --- // --- // --- // ---	MAPK4	MAPK4, Homo sapiens mitogen-activated protein kinase 4 (MAPK4), q21.1
SNP_A-1823609	taaaataacataacta[G/T]attctctctcagttct	G	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 50291 // Hs.187861 // THRB // 7068 //	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1865163	tccagtttgtagtgta[A/G]gccaatttctgtggtg	A	G	8687 // Homo sapiens keratin, hair, acidic, 8 (KRTHA8), mRNA. /// NM_002278 // downstream // 14970 // Hs.41752 //	KRTHA8	KRTHA8, Homo sapiens keratin, hair, acidic, 8 (KRTHA8), q21.2
SNP_A-1870109	tccttgtcttgggtaa[C/T]acagcatgaaaaattt	C	T	Homo sapiens caspase recruitment domain family, member 8 (CARD8), mRNA. /// ENST00000357778 // intron // 0 // --- // ---	CARD8	CARD8, Homo sapiens caspase recruitment domain family, member 8 (CARD8), q13.32
SNP_A-1845429	tatagaaatgtcacac[C/T]atagaagacagttcaa	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1635794 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1976478	tgaggggagtacatac[G/T]cagatcagcctggctc	G	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 365061	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1955973	tttgtcggtctctgtg[A/C]agggtttctattatac	A	C	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA. /// ENST00000270774 // intron // 0 // --- // --- // --- // ---	PEX14	PEX14, Homo sapiens peroxisomal biogenesis factor 14 (PEX14), p36.22
SNP_A-1896836	tgctcaataatccatg[A/C]atgactttagggtgga	A	C	sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), transcript variant 2, mRNA. /// NM_004513 // intron // 0 // Hs.459095 // IL16 // 3603 // Homo sapiens interleukin 16	IL16	IL16, Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), transcript variant 2, q25.1
SNP_A-1902111	tggcattccatggtaa[A/G]ggtctatcccagcttg	A	G	/// ENST00000336930 // upstream // 1110804 // --- // --- // --- // ---	-	p14.3
SNP_A-1904109	tgggcatggtgctctc[C/T]cccttcaaaggcagcc	C	T	sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// ENST00000332914 // intron // 0 // --- // --- // --- // --- ///	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-1910293	tgtccaccatttttatc[C/T]ctgtgattagtacaca	C	T	-- /// ENST00000340000 // upstream // 32494 // --- // --- // --- // ---	-	p12.1
SNP_A-1927907	ttcaataacaacatca[A/G]cttaattttggccttc	A	G	ENST00000333254 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1926848	ttatttactctcaata[A/C]cagcatcagatgaaat	A	C	Homo sapiens mRNA for KIAA0513 protein, partial cds. /// ENST00000357662 // intron // 0 // --- // --- // --- // --- ///	KIAA0513	KIAA0513, Homo sapiens for KIAA0513 protein, partial cds. q24.1
SNP_A-1923981	ttagtgcaggacacac[C/G]acaggaatattaacgg	C	G	sapiens mutated in colorectal cancers (MCC), mRNA. /// ENST00000359932 // intron // 0 // --- // --- // --- // --- ///	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-1905279	tgggttgtttcagaag[A/G]caaaatcagacccgtt	A	G	/// ENST00000336930 // upstream // 1575843 // --- // --- // --- // ---	-	p14.3
SNP_A-1898549	tgcttgataacctgga[A/G]cacctattaaatatcc	A	G	SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// NM_178540 //	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-1898937	tgcttttgattctag[A/G]ctaaattatccaatat	A	G	Homo sapiens orthopedia homolog (Drosophila) (OTP), mRNA. /// ENST00000306422 // intron // 0 // --- // --- // --- // ---	OTP	OTP, Homo sapiens orthopedia homolog (Drosophila) (OTP), q14.1
SNP_A-1846254	tatatctggatagcaa[C/T]aatactcaactctgat	C	T	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 125410 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-1824046	taaacaagagtaacga[A/C]atcattcatacccaga	A	C	51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 574672 //	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-1807050	gtctccactatcaaac[A/G]aaatgaacttgtatat	A	G	10873 // Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006680 // upstream //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-1644340	gacatggaatactttgttggataga[G/T]agtaaacatcctcttttttccttgag	G	T	27152 // PDZ domain containing 6 /// NM_024582 // downstream // 1026573 // Hs.25201 // FATJ // 79633 // fat-like	PDZK6	PDZK6 , rs990364, PDZ domain containing 6 ,q28.1
SNP_A-2140559	atctccttagccacaa[A/G]aaaggctgctggcttt	A	G	ENST00000228705 // intron // 0 // --- // --- // --- // ---	-	q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2160331	cttcctaatggctttc[A/T]cagagtaagaaagatg	A	T	Homo sapiens splicing factor, arginine/serine-rich 11 (SFRS11), mRNA. /// ENST00000235399 // intron // 0 // --- // ---	SFRS11	SFRS11, Homo sapiens splicing factor, arginine p31.1
SNP_A-2153920	attatactacacagga[C/G]atttctataggagaat	C	G	Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA. /// ENST00000356218 // intron // 0 // --- // ---	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-2114454	agggagacaaaattca[A/G]cccatagcaactgtca	A	G	Homo sapiens two pore segment channel 2 (TPCN2), mRNA. /// ENST00000294309 // intron // 0 // --- // --- // --- // ---	TPCN2	TPCN2, Homo sapiens two pore segment channel 2 (TPCN2), q13.3
SNP_A-2120157	agtcagataaagccca[A/G]ctgtgcatacaagtta	A	G	Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-2202344	ccaccagccagtgtaa[C/G]aagtggctgatttggg	C	G	sapiens CD47 antigen (Rh-related antigen, integrin-associated signal transducer) (CD47), transcript variant 2, mRNA. /// ENST00000360645 // intron // 0 // --- // --- // --- // ---	CD47	CD47, Homo sapiens CD47 antigen (Rh-related antigen, integrin-associated signal transducer) (CD47), transcript variant 2, q13.12
SNP_A-2227877	ctaccgaggagaaaaa[A/G]gtaccagtgtattgtg	A	G	Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, mRNA. /// NM_198390 // intron // 0 //	CMIP	CMIP, Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, q23.2
SNP_A-2177923	cactaaggtgaggata[C/G]attgaattatccttcg	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2170156	caaggtcaaaattatc[A/C]aaaggcatttttcct	A	C	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2083852	actacggtttcacagc[A/G]gagtaaactgaagctc	A	G	2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 11074 //	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-2082671	acgggaatataagagc[A/C]aacatgatctcagcct	A	C	Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000282030 // intron // 0 // --- // --- // --- // ---	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2078683	accattcaccaagata[C/G]agaatataaggaggag	C	G	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 6 (PPIL6), mRNA. /// ENST00000327404 // intron // 0 // --- // ---	PPIL6	PPIL6, Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 6 (PPIL6), q21
SNP_A-2107475	agacatagagtatagc[C/T]cagcttcataaacata	C	T	ENST00000303646 // intron // 0 // --- // --- // --- // ---	-	p36.23
SNP_A-2033263	aaatagaaaatccaga[A/T]atcctgcagtctaatt	A	T	64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 259259 // Hs.546282 // RBBP8	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-1990182	taagatcttttaaatg[C/T]aatcaaattcaaagga	C	T	// 22932 // Homo sapiens POM (POM121 homolog, rat) and ZP3 fusion (POMZP3), transcript variant 2, mRNA. /// NM_152992 // downstream // 21962 // Hs.488877 // POMZP3	POMZP3	POMZP3, Homo sapiens POM (POM121 homolog, rat) and ZP3 fusion (POMZP3), transcript variant 2, q11.23
SNP_A-1990479	ggagacccataagagc[C/G]aataatgtagttccag	C	G	79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream //	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.13
SNP_A-2307023	gctgttgagaatcaga[C/G]gaatggataataagga	C	G	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2257031	ctttctacagctccta[G/T]atctgataaacaactt	G	T	10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 296360 // Hs.489615 // PBEF1 // 10135 // Homo	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-2262639	gaaattcagaatgcac[A/G]atgcccaaaagggaaa	A	G	FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2274631	gagaaacaacacaggc[A/G]aggttatggtatcaag	A	G	// 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, mRNA. /// NM_194431 //	RNASE4	RNASE4, Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, q11.2
SNP_A-2228991	ctagcaagtccggaaa[A/T]aggcactatacattac	A	T	// Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 72912 // Hs.375684 // RAD18 //	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-2299443	gccctgttgatgtctc[A/G]ctaactatctactgta	A	G	5660 // Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA. /// NM_004273 // upstream // 51006 // Hs.158304 // CHST3 //	PSAP	PSAP, Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), q22.1
SNP_A-2295729	gcatgatctaactgtc[A/G]agccagtaatgatttt	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2461884 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1991588	tccacatcctctgtgt[A/T]aaggtacttctacaaa	A	T	27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 1196213 //	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-2038530	aacagaaaagtggaca[A/G]agacatagtggaatag	A	G	1758 // Homo sapiens dentin matrix acidic phosphoprotein (DMP1), mRNA. /// NM_004967 // upstream // 101007 //	DMP1	DMP1, Homo sapiens dentin matrix acidic phosphoprotein (DMP1), q22.1
SNP_A-2045151	aagaagagagctacaa[C/T]ataaaatataaataca	C	T	135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2105977	agccattctttaagac[A/G]gtaatgtgagatgtta	A	G	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 27226 // --- // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2080023	accgaccacagattac[A/C]aatactcaaaaaagtg	A	C	ENST00000323433 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-2084358	actatactgaatctaa[A/G]tggttactttggttgt	A	G	Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // --- // --- // --- // ---	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-2051031	aaggcttacgtcctcc[C/T]aaacattgcactccaa	C	T	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2005364 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2055769	aataatttctgtcaca[C/T]tatggatgcccttgct	C	T	79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2065653	aatttagtctgaaaaa[C/G]agagatgtgatttcag	C	G	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki 1) (ALK), p23.2
SNP_A-2169714	caaggaagtcttaaga[A/G]aggagtgacatttgct	A	G	Homo sapiens hypothetical protein FLJ10597 (FLJ10597), mRNA. /// ENST00000335497 // intron // 0 // --- // --- // --- // ---	FLJ10597	FLJ10597, Homo sapiens hypothetical protein FLJ10597 (FLJ10597), p34.1
SNP_A-2198685	catttcccagagtgac[A/G]aattatactccaaagg	A	G	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // --- // ---	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2198507	catttatcagactgta[C/T]actttagtcttaaggg	C	T	ENST00000343170 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2136936	atcagatgagtgtcag[C/G]aacatagaagccacat	C	G	/// ENST00000344893 // upstream // 145 // --- // --- // --- // ---	-	p13.2
SNP_A-1785064	ggcggggccacgttca[G/T]aagagaaaattctagc	G	T	10866 // Homo sapiens HLA complex P5 (HCP5), mRNA. /// NM_005931 // upstream // 68 // Hs.211580 // MICB // 4277 //	HCP5	HCP5, Homo sapiens HLA complex P5 (HCP5), p21.33
SNP_A-1794666	ggtctcagatgggtat[C/G]agaaagttgttggaaa	C	G	/// ENST00000278194 // downstream // 452512 // --- // --- // ---	-	p14.3
SNP_A-1828663	taagctaaagagaatg[G/T]aaagagatatgtggaa	G	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2746379 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1850601	tattaatattttagat[C/G]agacttatgttaacca	C	G	// Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// ENST00000282272 // intron // 0 // ---	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-1868187	tcctcaacaatgctaa[A/G]ggaaaagtccaaaaca	A	G	/// ENST00000321536 // upstream // 623705 // --- // --- // --- // -	-	p13
SNP_A-1872309	tctagacaatggcatc[A/G]cgtcccatctgtaccc	A	G	Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA. /// ENST00000358251 // intron // 0 // --- // --- // --- // ---	TXNDC5	TXNDC5, Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, p24.3
SNP_A-1881990	tcttttctttatacca[A/T]ctacttagcttccaag	A	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1878021	tctgtaatatgtgaaa[A/C]tatccagttagttagt	A	C	51126 // Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, mRNA. /// NM_016100 // downstream // 405 // Hs.368783 // NAT5 //	NAT5	NAT5, Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, p11.23
SNP_A-1925674	ttatgatgacacaaca[A/G]aaagaaagataggtac	A	G	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 142367 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1930966	ttccaggtccccttttc[A/G]cttcctgtgctgttgc	A	G	-- /// ENST00000332560 // upstream // 59396 // --- // --- // --- //	-	q21.1
SNP_A-1947573	tttacccgattcaaga[A/T]aattccagccagccat	A	T	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1934352	ttctccgggcaggcaa[G/T]tcgaggacacaagggc	G	T	Homo sapiens mRNA for KIAA1760 protein, partial cds. /// NM_006648 // intron // 0 // Hs.522291 // WNK2 // 65268 //	WNK2	WNK2, Homo sapiens for KIAA1760 protein, partial cds. q22.31
SNP_A-1982052	cacaatgctctggaac[C/T]ctcttattaaggccac	C	T	9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 157371 // Hs.335079 // MAP1B // 4131 // Homo sapiens	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-1975240	ttaaaaccctgacatc[A/C]aataatcaaggaaatt	A	C	27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 524721 // Hs.165830	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-1943139	ttggtcagcatccctg[A/G]agaagtcttcctacac	A	G	374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 269578 // Hs.34198 // FLJ44796 // 401209 //	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-1949495	tttattgcctgggctc[A/G]ctttcctcatggacac	A	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 718476 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1930775	ttccacttctgcacca[C/T]acccaaaaggctcaag	C	T	// 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 //	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1894773	tgccaggtgctgtgcc[G/T]aacactttaaatatat	G	T	AASDHPPT // 60496 // Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), mRNA. /// NM_000855 // downstream // 250677 // Hs.503756 // GUCY1A2 // 2977 //	AASDHPPT	AASDHPPT, Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1791547	gggtcactgtttctca[C/T]gcaaagaaaggcaaac	C	T	Homo sapiens EMI domain containing 2 (EMID2), mRNA. /// ENST00000313669 // intron // 0 // --- // --- // --- // ---	EMID2	EMID2, Homo sapiens EMI domain containing 2 (EMID2), q22.1
SNP_A-1806769	gtctaggctctgcccc[A/C]accaatgtgtgtaacc	A	C	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), mRNA. /// ENST00000265382 // intron // 0 // --- // --- // --- // --- /// ENST00000312722 // intron //	PIP5K1B	PIP5K1B, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), q21.11
SNP_A-1814595	gtgtggagttccgtgc[A/G]atgtggagccaggcag	A	G	Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // --- // ---	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-1780827	ggatctggcatggtcc[C/T]aacacaaagaaatgat	C	T	ENST00000255289 // intron // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-2135446	atatttgagtcacgga[G/T]gtgcagagttgcttct	G	T	// 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1548205 // Hs.514980 // SALL3	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2113708	aggctcttagacatag[A/G]aaaataaatttgtatg	A	G	// Homo sapiens hypothetical protein CG003 (13CDNA73), mRNA. /// ENST00000261575 // intron // 0 // --- // --- // --- // ---	13CDNA73	13CDNA73, Homo sapiens hypothetical protein CG003 (13CDNA73), q13.1
SNP_A-2214202	cctaatttttgattac[A/G]gaagtatctatgacaa	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1167723 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2212805	ccctttaagagtgaag[A/C]ctggccgccaaactgg	A	C	9177 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3B (HTR3B), mRNA. /// NM_000869 // upstream //	HTR3B	HTR3B, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3B (HTR3B), q23.2
SNP_A-2076178	acattcgaagagtcta[C/T]gcctatggcttaaggc	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2475658 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2035078	aaatgcaggatcacac[C/T]ggattttacagctgac	C	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-2021172	aaaaaaactgttgtac[A/G]aactctgcagattgag	A	G	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase,	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). ,q12.13
SNP_A-2012437	agcacaaagatctctc[A/G]ctgtctgtagtctgcc	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1166796 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2016433	ctttcctttgcctgtc[A/G]ctccattctgtgatat	A	G	// 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-2008123	cttgctcatctgtaaa[C/T]tcccactccaacagtg	C	T	ENST00000338965 // intron // 0 // --- // --- // --- // ---	-	p15.1
SNP_A-2308357	gcttgtctgtctcttg[C/T]agtgctttgctagatg	C	T	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 586070	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2311860	ggaatttttaaaagcc[C/T]atgtcagatggggaga	C	T	Homo sapiens vomeronasal 1 receptor 4 (VN1R4), mRNA. /// NM_174980 // upstream // 9279 // --- // --- // 0 // --- ///	VN1R4	VN1R4, Homo sapiens vomeronasal 1 receptor 4 (VN1R4), q13.42
SNP_A-2275494	gagaatttttgagaac[A/G]aaggcactgaggaggt	A	G	Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), mRNA. /// ENST00000323246 // intron	CNDP1	CNDP1, Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), q22.3
SNP_A-2283761	gataggaggagccaca[C/T]ggtagagtgctttgaa	C	T	sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // --- // --- // --- // ---	BSN	BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-2258994	cttttgtctctaggc[C/T]actatttttccatttg	C	T	Homo sapiens calcium channel, voltage-dependent, gamma subunit 7 (CACNG7), mRNA. /// ENST00000222212 // intron // 0 // --- // --- // --- // ---	CACNG7	CACNG7, Homo sapiens calcium channel, voltage-dependent, gamma subunit 7 (CACNG7), q13.42
SNP_A-2259546	gaaaacatccagaaat[C/G]aagctaactgactgta	C	G	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2284332	gatatttattggttac[A/G]agagtagagacagggc	A	G	Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // --- // --- // --- // --- ///	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2277432	gagcaaatagaagatc[C/T]gaccagtgctgcacct	C	T	Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // ---	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2233883	ctcatcttttctctgg[A/G]aaacaccttcaaagcc	A	G	2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. /// NM_032487 // downstream // 365231 // Hs.135411	EVI1	EVI1, Homo sapiens ecotropic viral integration site 1 (EVI1), q26.2
SNP_A-2255634	cttgtgttagttatta[A/C]catttgtagattttct	A	C	Homo sapiens zinc and ring finger 1 (ZNRF1), mRNA. /// ENST00000335325 // intron // 0 // --- // --- // --- // --- ///	ZNRF1	ZNRF1, Homo sapiens zinc and ring finger 1 (ZNRF1), q22.3
SNP_A-2296293	gcattggctacagaga[G/T]agtgttgaagaatgac	G	T	2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-2003858	actagcattactctaa[C/T]acatgaagcaccaagt	C	T	-- /// ENST00000356117 // downstream // 485431 // --- // --- //	-	q23.31
SNP_A-2073314	acagggtgaagaggac[C/T]catttattgaagcaac	C	T	2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 91133 //	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2060422	aatgacaaatttctca[C/T]gattatcacaaagttt	C	T	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2211137	cccgtcattgacctac[G/T]aaaggaagaaagaaat	G	T	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2208151	cccaatagtaatgagc[A/G]cctcttaatgcctaca	A	G	// 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 //	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2208872	cccagattaaacagaa[A/C]tgacttgatcaaccta	A	C	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2114227	agggaagaacttgcta[C/T]tactaacacagaaact	C	T	NM_198989 // downstream // 63129 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.3
SNP_A-2121291	agtcttagagctttta[A/T]gaacctaggctagtgg	A	T	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1
SNP_A-2117575	aggttaatttcccaca[A/G]taagtggcttttgagg	A	G	Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2135920	atcaaccatatacata[C/T]gataggccgaataaag	C	T	Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA. /// ENST00000320750 // intron // 0 // --- // --- // --- // ---	UEV3	UEV3, Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), p15.1
SNP_A-2133305	atatatatcataaaaa[C/G]gtgtcccaatgtgtaa	C	G	Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), mRNA. /// NM_016653 // intron // 0 // Hs.444451 // ZAK // 51776 // Homo sapiens sterile	ZAK	ZAK, Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), q31.1
SNP_A-2130307	atacgggtatcatcca[C/T]actctaaacctagaaa	C	T	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 608525 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2156797	attctgtttttagttc[A/G]agggccattgtttatt	A	G	Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // --- // --- // --- // ---	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3
SNP_A-2156650	attctgctaacatact[A/G]agaggtgtgaatcagt	A	G	79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 216391 //	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2158225	attggctaaaaggtct[A/T]aagcacaacctttgac	A	T	Homo sapiens GPP34-related protein (GPP34R), mRNA. /// ENST00000271732 // intron // 0 // --- // --- // --- // ---	GOLPH3L	GOLPH3L, Homo sapiens GPP34-related protein (GPP34R), q21.2
SNP_A-1724102	agctcctcacctgaattccagaaat[C/T]agtggggtgaaccgcacacaggtag	C	T	// 1413 // crystallin, beta A4 /// NM_002430 // downstream // 526371 // Hs.268515 // MN1 // 4330 // meningioma (disrupted	CRYBA4	CRYBA4 , rs715562, crystallin, beta A4 ,q12.1
SNP_A-1811357	tatttcaaaagaaacc[A/C]aatggccttaccatat	A	C	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 793576 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1806986	gtctcaggtgttacag[C/T]agcacaaagtggacaa	C	T	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA. /// ENST00000356398 // intron // 0 // --- // --- // --- // --- ///	PRPSAP2	PRPSAP2, Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), p11.2
SNP_A-1786575	ggcttcgaacagccat[A/T]agtgcactggaagatg	A	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 386406	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1798644	gtaacagagcttagga[A/C]atgtggaagaaaatta	A	C	5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 152893 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1866953	tccctattctacagca[C/G]cataacatatttggtg	C	G	Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// ENST00000253692 // intron // 0 // --- // --- // --- // ---	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1860811	tcataatctatgtgga[A/G]acttgaggtaggtatg	A	G	Homo sapiens annexin A3 (ANXA3), mRNA. /// ENST00000264908 // intron // 0 // --- // --- // --- // ---	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1850911	tattataattttacaa[A/G]tcacttttcatgtaca	A	G	Homo sapiens megakaryoblastic leukemia (translocation) 1 (MKL1), mRNA. /// ENST00000355630 // intron // 0 // --- // ---	MKL1	MKL1, Homo sapiens megakaryoblastic leukemia (translocation) 1 (MKL1), q13.1
SNP_A-1855689	tcaatatcataacaca[A/C]aagtatctacgtaatt	A	C	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1827187	taacctatatccaaga[C/T]gtttcttctcattaaa	C	T	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1887943	tgagcaaggctatttg[C/G]agatgggccttgaagg	C	G	200383 // Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), mRNA. /// ENST00000272375 // intron // 0 // ---	LOC200383	LOC200383, Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), p11.2
SNP_A-1908754	tgtaggtcccattcac[C/T]gtacagaattttaata	C	T	Homo sapiens rotatin (RTTN), mRNA. /// ENST00000255674 // intron // 0 // --- // --- // --- // ---	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-1948127	tttagattgtgtagcc[A/G]gcaatttttgctact	A	G	Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // ---	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950154	tttcactctttctcaa[A/G]aatccatgatagtgtt	A	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 456300 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1967165	aatctacaaacacata[C/G]agtgactcactagctc	C	G	55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 14478 // --- // --- // ---	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1963397	acaaggcataggggat[A/G]acatctaagcaaagac	A	G	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 1596480 //	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-1977704	cttcagcagctttgag[A/T]ctaagcctcactcttg	A	T	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 239214 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1978588	aatattcaaaatgaga[A/G]accataacatactgga	A	G	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 385455 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1988185	aatgatggcaagaaaa[A/C]gtctgtgcatattcag	A	C	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 596591 // Hs.146100	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-1984801	cttcctacctgaacga[A/C]gatagaaaatgatgat	A	C	Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // --- // --- // --- // ---	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-1965012	gaaccttgaccaatga[A/G]aaacaagattcaggag	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1975961	tgagtgatgacctcaa[C/T]agtgacttcagtcagc	C	T	/// ENST00000326756 // downstream // 167261 // --- // --- // ---	-	p16.1
SNP_A-1956800	ttttaaatggaactgc[A/G]gaaaaatctattgtga	A	G	55140 // Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), mRNA. /// NM_006228 // upstream //	ELP3	ELP3, Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), p21.1
SNP_A-1937268	ttgaaacagtatcctg[A/G]aatgggagattgaccc	A	G	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1907920	tgtaatgactagccca[A/G]aaacaaacagtcgtaa	A	G	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1932017	ttcctagaattaagga[C/T]gtgagataaacagcag	C	T	// 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// NM_018103 // upstream // 18021 //	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1921772	ttactaatactagtaa[C/G]agacacaggaaagttc	C	G	Homo sapiens acetyl-Coenzyme A synthetase 2 (AMP forming)-like (ACAS2L), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000323482 // intron // 0 // --- // --- // --- // ---	ACAS2L	ACAS2L, Homo sapiens acetyl-Coenzyme A synthetase 2 (AMP forming)-like (ACAS2L), nuclear gene encoding mitochondrial protein, p11.21
SNP_A-1826966	taacattgagttcata[C/T]atcttaaaagcaacat	C	T	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 776915 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1822553	gtttttggaggatgga[A/T]ctctcatggattacgt	A	T	ENST00000281496 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-1832384	tacaaaacacactata[A/T]aatgctctcttatctc	A	T	Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// ENST00000251020 // intron // 0 // --- // --- // --- // ---	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-2142504	atgaacaaaaatattc[C/T]cccacagtgctttcca	C	T	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- // --- ///	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2121041	agtctccagatggtta[C/T]agcagcatcaaaaaca	C	T	Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // intron // 0 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2207271	ccattccccactttga[C/T]gaaacagtaaccattt	C	T	C14orf166B // 145497 // Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), mRNA. ///	C14orf166B	C14orf166B, Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), q24.3
SNP_A-2187020	cagctactgaactccc[A/G]gctcctctacagcctg	A	G	LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 //	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-2061515	aatgctgaagttggaa[A/G]tcaaagtgtatgaagt	A	G	56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // upstream // 8231 // Hs.133512 // ZC3HAV1 // 56829 // Homo	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-2097306	agagaaaactagagaa[C/G]agagttgcagaatctt	C	G	// 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1257689 // Hs.514980 // SALL3	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-1991357	taatatatgttaataa[A/G]tgaatgcatcaaaaaa	A	G	// Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // upstream //	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1993343	tagacagcaaattgga[A/G]gaagaggaaagtggag	A	G	ENST00000327381 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2023579	aaaactctgagacagt[A/C]aatgttcgttgtttta	A	C	54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 //	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-2034480	aaatctgaagtggtcc[A/G]aaaggatttgggatag	A	G	Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), mRNA. /// ENST00000256458 // intron // 0 // --- // ---	IRAK2	IRAK2, Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), p25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253714	cttgaaaatctttcca[C/T]aaatgaatgagtgaat	C	T	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-2241596	ctgatacacttattga[A/T]cagagcaaaacccatt	A	T	CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2244318	ctggaagatattcaaa[C/T]cgtctctatgcttacg	C	T	Homo sapiens anterior gradient 2 homolog (Xenopus laevis) (AGR2), mRNA. /// ENST00000223274 // CDS // 0 // --- // --- //	AGR2	AGR2, Homo sapiens anterior gradient 2 homolog (Xenopus laevis) (AGR2), p21.1
SNP_A-2233527	ctcagtgtttagttaa[C/G]aggatgatagtggaca	C	G	7044 // Homo sapiens endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfa /// NM_152608 // downstream // 24286 // Hs.520192 // FLJ35382	LEFTY2	LEFTY2, Homo sapiens endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfa ,q42.12
SNP_A-2287388	gatgtgttcagcccca[C/T]gtgccaggctaaatgc	C	T	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2281875	gagtgattgtaataag[C/T]atggttataaagtgct	C	T	Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- // --- // --- ///	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2244919	gcaagaggatacaatg[G/T]aggaggaaaagggaag	G	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2254541	cttgctaaaactttcc[A/C]aattgtggtctcctac	A	C	57379 // Homo sapiens activation-induced cytidine deaminase (AICDA), mRNA. /// ENST00000229335 //	AICDA	AICDA, Homo sapiens activation-induced cytidine deaminase (AICDA), p13.31
SNP_A-2254772	cttggaagtggaaata[A/G]gacttcagtctgataa	A	G	SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 98415 // --- // --- // --- // --	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31
SNP_A-2298901	gccccacttggaaacc[A/G]ctgatttgctttatca	A	G	143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// NM_199461 // upstream //	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11
SNP_A-2293071	gcagacactcaacacc[C/T]atgaaagcaggcagga	C	T	// Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // --- // --- // --- // --- ///	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2038569	aacagaacagctttta[A/G]gggagacactctatat	A	G	// 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream //	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2037386	aacaaatggcttcaat[A/G]ataaggggaaaatgag	A	G	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. ///	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2031311	aaagggatatgcacag[C/T]agctcatgtctggaat	C	T	Homo sapiens nuclear receptor binding SET domain protein 1 (NSD1), transcript variant 1, mRNA. /// NM_022455 // intron // 0 // Hs.208961 // NSD1 // 64324 // Homo sapiens nuclear	NSD1	NSD1, Homo sapiens nuclear receptor binding SET domain protein 1 (NSD1), transcript variant 1, q35.3
SNP_A-2003669	aatatagaatcacaaa[A/C]ctttagtcccaaaagt	A	C	112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 95433 //	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2002773	gcttgtgcaactcaaa[C/T]ccagatgggcccccac	C	T	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 //	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2011739	atcttatgaatgaagg[C/T]cagaaaaaggggaga	C	T	23304 // Homo sapiens chromosome 6 open reading frame 133 (C6orf133), mRNA. /// NM_000322 // downstream // 3685	UBR2	UBR2, Homo sapiens chromosome 6 open reading frame 133 (C6orf133), p21.1
SNP_A-2089271	acttagagaagcaaaa[C/T]ctaacatgagtcgcaa	C	T	/// ENST00000299623 // downstream // 32628 // --- // --- // --- // --- /// ENST00000321602 // downstream // 34102 // --- // ---	-	q21.3
SNP_A-2074405	acatactacacataca[A/G]ctttgggggttttaag	A	G	// Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // --- // --- // --- // ---	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21
SNP_A-2068019	acaactggtcactgca[A/T]tgaccactgaaactaa	A	T	83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000356343 // upstream //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-2111903	aggatccctgatcaat[A/G]agcatacttttgctgc	A	G	389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// ENST00000356539 // intron // 0 // --- // --- // --- // ---	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-2126999	ataaagttataatttc[A/G]caaaacagaagggaga	A	G	sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 //	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26
SNP_A-2161381	tttctgtagacaacaa[A/G]cactaagttgttttag	A	G	Homo sapiens sciellin (SCEL), transcript variant 1, mRNA. /// NM_144777 // intron // 0 // Hs.115166 // SCEL // 8796 //	SCEL	SCEL, Homo sapiens sciellin (SCEL), transcript variant 1, q22.3
SNP_A-1822714	taaaaaagaggtaact[A/G]aagctcagaaaggttt	A	G	// 2960 // Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA. /// ENST00000283875 // downstream // 83400 // --- // --- // --- // --	GTF2E1	GTF2E1, Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), q13.33
SNP_A-1828614	taagccctgtgcagtg[C/T]attttgtttctagttt	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1849053	tatgcatttttcaagc[A/G]gatgaataaagtaaaa	A	G	374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 268804 // Hs.34198 // FLJ44796 // 401209 //	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-1745204	ctcgagatctgatggttttatattc[A/G]cttcattctcattatcacttgtctg	A	G	apoptosis related protein APR-4 mRNA, partial cds. /// NM_002312 // downstream // 16666 // Hs.166091 // LIG4 //	-	- , rs1931347, Homo sapiens apoptosis related protein APR-4 mRNA, partial cds. ,q33.3
SNP_A-1924481	ttataatttgacctca[G/T]gtacacttcagtttga	G	T	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 134970 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-1882472	tgaaaatataacctca[C/T]aacttcagccaaacaa	C	T	Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), mRNA. /// ENST00000040877 // intron // 0 // --- // --- // --- // ---	TARBP1	TARBP1, Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), q42.2
SNP_A-1875479	tctctgggcaagtaga[A/G]gagggtcctttagttc	A	G	sapiens mRNA; cDNA DKFZp686F06102 (from clone DKFZp686F06102); complete cds. /// NM_000501 // intron // 0 // Hs.252418 // ELN // 2006 // Homo sapiens elastin	ELN	ELN, Homo sapiens cDNA DKFZp686F06102 (from clone DKFZp686F06102); complete cds. ,q11.23
SNP_A-1896288	tgctaaaaagaacagc[A/G]ataacccttttctgtt	A	G	// 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 318222 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1946108	ttgttttgctaataaa[C/G]agagttgtagcctgac	C	G	Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-1959715	ttttggtagagatgac[A/G]gcttactattttgccc	A	G	// 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 717907 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-1950327	tttcagcaattcctct[A/G]aaaatcagaaacttgg	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 576563 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-1971725	cttcagaaagaataaa[C/T]gcaataagtttatttc	C	T	// 375323 // Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), mRNA. /// NM_022485 // upstream //	LOC375323	LOC375323, Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), p25.3
SNP_A-1986490	acatataggatttttta[C/T]acctgaagccaagaat	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1100573	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1891887	tgatttgtggaggaac[A/G]gcctgtgttttgtttt	A	G	PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // upstream // 286414 // Hs.499705 //	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.2
SNP_A-1889067	tgagtaggggtttcag[A/G]agcatgccagatgagt	A	G	-- /// ENST00000314071 // upstream // 633550 // --- // --- // ---	-	p13.3
SNP_A-1918960	ttaacccctagcacct[C/T]agaatatgaccttatt	C	T	// 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream //	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-1740391	gccagcttcagaaacaagggtgaaa[A/T]gtataacatctggagttgccaggct	A	T	NM_022340 // intron // 0 // Hs.173002 // ZFYVE20 // 64145 // zinc finger, FYVE domain containing 20	ZFYVE20	ZFYVE20 , rs746665, zinc finger, FYVE domain containing 20,p25.1
SNP_A-1666826	gttgtctgaaaagctagcaattatc[A/G]gaagactgaatttaacatttatata	A	G	NM_014167 // intron // 0 // Hs.90527 // HSPC128 // 29080 // HSPC128 protein	HSPC128	HSPC128 , rs2068633, HSPC128 protein,q21.31
SNP_A-1679606	ccaaagggaaataatatatacaaac[C/G]caatgatgtatttatctgttcagaa	C	G	// LOC401099 (LOC401099), mRNA /// NM_001041 // downstream // 286947 // Hs.429596 // SI // 6476 // sucrase-	-	- , rs2722623, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-1798004	gtaaaaccaactgcaa[C/G]ccaaacatgattccaa	C	G	80319 // Homo sapiens CXXC finger 4 (CXXC4), mRNA. /// NM_017628 // upstream // 1724 // Hs.367639 // FLJ20032 //	CXXC4	CXXC4, Homo sapiens CXXC finger 4 (CXXC4), q24
SNP_A-1853355	tattttcaatagtttc[A/G]aaagcaaggcttatgt	A	G	1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 //	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1853526	tattttgtgaaaaagc[A/T]gacacctgggaggttc	A	T	390082 // Homo sapiens olfactory receptor, family 52, subfamily E, member 5 (OR52E5), mRNA. /// NM_001003443 // upstream // 34533 // --- // OR56A3 //	OR52E5	OR52E5, Homo sapiens olfactory receptor, family 52, subfamily E, member 5 (OR52E5), p15.4
SNP_A-1859741	tcagggaccttcagag[A/G]aaggagagactgaact	A	G	2487 // Homo sapiens frizzled-related protein (FRZB), mRNA. /// NM_013436 // downstream // 30377 // Hs.516633 //	FRZB	FRZB, Homo sapiens frizzled-related protein (FRZB), q32.1
SNP_A-1863698	tccaactgtccaacta[C/T]gtttgcctgcacagtc	C	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 999439 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-1871238	ttatataaagacacca[A/G]tgaaaagtcaatatga	A	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1389116 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1827787	taacttgggtgacaga[C/T]agctttaagtgtctta	C	T	// 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 465889 // Hs.135642 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1815567	gttaaactagacttgc[A/G]acactagaataaacta	A	G	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 290359 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839100	tagagcacaaatacaa[A/G]aagtcacttaatagtt	A	G	Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 //	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-2162678	attttcttgaaaaaag[C/T]aatagtttggtaagta	C	T	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 230756 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-2135835	atcaaatgctggggta[A/C]aatgctaaaattagat	A	C	SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 464891 // Hs.354013 //	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2121060	agtctccttaaaccaa[C/T]gtgtgtaacaatttta	C	T	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1194358 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2121803	agtgagaactacaagg[C/G]catcttgtctagcacc	C	G	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2188415	cagtgaaatgtgagaa[C/G]tcatgaaaaaagaaaa	C	G	81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // upstream // 13960 // Hs.201058 // STMN4 //	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-2074543	acataggatcaaaata[A/G]gaagtaacttcacctc	A	G	2138 // Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, mRNA. /// NM_172059 //	EYA1	EYA1, Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, q13.3
SNP_A-2078869	acccaacagctgagta[G/T]gtctatttagaaagcc	G	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 32671 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2015619	gtcttcaagcataatc[A/G]aaatcctagatatatt	A	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2005068	tggtcacattgctcac[G/T]gtcttcatgtcccttc	G	T	388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000342036 // upstream // 421291 // --- // ---	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-2033495	aaatagttgatgttgc[C/T]acttgagggagagtac	C	T	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- // --- // --- ///	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2036089	aaattagcaaatctga[A/G]agtgtgtctgtcaccc	A	G	60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 24778 // Hs.528665 // PROK2 //	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2043550	aactgtgacatctttа[A/G]gcaaaatagtcaatgg	A	G	Homo sapiens KIAA1374 protein (KIAA1374), mRNA. /// ENST00000326448 // intron // 0 // --- // --- // --- // --- ///	KIAA1374	KIAA1374, Homo sapiens KIAA1374 protein (KIAA1374), q25.33
SNP_A-2232137	ctcaagtagctcacaa[C/T]gttcctgaaaacttca	C	T	Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// ENST00000256409 // intron // 0 // --- // --- // --- // ---	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2237092	ctctcaacttggttta[A/T]gatgctgccagcatat	A	T	C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000340000	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2239001	ctcttcgaggtgtaac[C/T]atggtaatgagatcag	C	T	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-2228452	ctacttcctttaaaca[C/T]caggcttatggtttca	C	T	4356 // Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA. /// ENST00000335243 // downstream // 6116 // --- // --- // --- // ---	MPP3	MPP3, Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), q21.31
SNP_A-2245861	ctgggtcagaacccgc[A/G]atgggagaatggtcca	A	G	Homo sapiens PAS domain containing serine/threonine kinase (PASK), mRNA. /// ENST00000234040 // intron // 0 // -	PASK	PASK, Homo sapiens PAS domain containing serine,q37.3
SNP_A-2267443	gaatatacatgaacac[G/T]ggaaaacaatgttgac	G	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 441078	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2292846	gcagaaacataggaca[A/G]tatttctccagaaaga	A	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 686060 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2290669	gcaagacttgtgcaag[C/T]agtggatcttagacac	C	T	10553 // Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), mRNA. /// ENST00000227256 // upstream	HTATIP2	HTATIP2, Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), p15.1
SNP_A-1991678	ggttttgactcttcac[A/G]gatttctggatatctc	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2100886	agatatctaggcaacc[A/G]caggcattttaatggg	A	G	FLJ43980 // 124149 // Homo sapiens FLJ43980 protein (FLJ43980), mRNA. /// ENST00000331332 // upstream //	FLJ43980	FLJ43980, Homo sapiens FLJ43980 protein (FLJ43980), p11.1
SNP_A-2070414	acacccactgaagcaa[A/G]aactcctagaattacc	A	G	64425 // Homo sapiens RNA polymerase I associated factor 53 (PAF53), mRNA. /// ENST00000344067 // downstream //	PAF53	PAF53, Homo sapiens RNA polymerase I associated factor 53 (PAF53), p13.2
SNP_A-2223422	cgctggcctcagtaaa[G/T]gcaccagtgggaataa	G	T	Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // intron // 0 // --- // --- // --- // --- /// ENST00000355292 // intron // 0 // --- //	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-2114747	agggatgggaaacaaa[C/T]gaatacgatacaggat	C	T	ENST00000334705 // intron // 0 // --- // --- // --- // ---	-	q24.13
SNP_A-2133694	atatccaactatttgc[A/G]gaatccaaacaacttt	A	G	ENST00000355094 // intron // 0 // --- // --- // --- // ---	-	q22.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2130547	atactctcatcatcaa[C/G]tcttttgtcagggtgt	C	G	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1388685 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2155874	attcctagtggataca[C/T]tctggtcctacgtaaa	C	T	942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // downstream // 65675 // Hs.171182 // CD86 //	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q21.1
SNP_A-2141429	atctgtttccatgtga[C/G]tacactgtgatacatt	C	G	Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1836049	tactacagaaaataaa[C/T]taaaaactgtcagcaa	C	T	59082 // Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), mRNA. /// NM_000829 // upstream // 65000 //	ICEBERG	ICEBERG, Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), q22.3
SNP_A-1858270	tcagaagggattccca[C/T]gagagctcctctgaac	C	T	sapiens regulator of G-protein signalling 5 (RGS5), mRNA. /// ENST00000313961 // intron // 0 // --- // --- // --- // ---	RGS5	RGS5, Homo sapiens regulator of G-protein signalling 5 (RGS5), q23.3
SNP_A-1707023	gcctattatgagaacttgcagatta[G/T]acagtttactcaatctactgaaggt	G	T	145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs10483506, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1782050	ggcaaattggtaatcc[A/C]agttctaaatcaaagt	A	C	Homo sapiens FLJ44874 protein (FLJ44874), mRNA. /// NM_002527 // upstream // 31818 // Hs.99171 // NTF3 // 4908	-	-, Homo sapiens FLJ44874 protein (FLJ44874), p13.31
SNP_A-1905249	tgggttgatggatgcc[A/G]caatccactatggcac	A	G	ENST00000272427 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-1883840	tgaagaatgaattgca[C/T]ccgtgttgggtttaga	C	T	/// ENST00000357217 // downstream // 33024 // --- // --- // ---	-	q11.2
SNP_A-1874926	tctctacccttatatc[A/C]ctttctttggtgtggc	A	C	// Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (ALS2CR13), mRNA. /// ENST00000303116 // intron // 0 // --- // --- // --- // --- ///	ALS2CR13	ALS2CR13, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (ALS2CR13), q33.2
SNP_A-1892991	tgcactcattctaaaa[A/G]taaatgttgtttccaa	A	G	sapiens glutathione reductase (GSR), mRNA. /// ENST00000221130 // intron // 0 // --- // --- // --- // ---	GSR	GSR, Homo sapiens glutathione reductase (GSR), p12
SNP_A-1947670	tttactaagtagttca[C/T]agagctggcatcccat	C	T	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-1938944	ttgagtaaagaatgaa[C/G]gaatgaaagactgaga	C	G	49860 // Homo sapiens chromosome 1 open reading frame 10 (C1orf10), mRNA. /// NM_178438 // upstream // 9628 //	C1orf10	C1orf10, Homo sapiens chromosome 1 open reading frame 10 (C1orf10), q21.3
SNP_A-1959473	ttttgccttttcatga[A/G]gagatagttgcactga	A	G	/// ENST00000354800 // downstream // 660222 // --- // --- // ---	-	q14.1
SNP_A-1956260	tttgtgtctttcaatt[C/T]aagctagcagtatttc	C	T	152185 // Homo sapiens hypothetical protein AY099107 (LOC152185), mRNA. /// ENST00000295872 // intron // 0 // ---	LOC152185	LOC152185, Homo sapiens hypothetical protein AY099107 (LOC152185), q13.2
SNP_A-1891992	tgcaaaaaagaagatg[A/G]acatcctgacaagtat	A	G	ENST00000354860 // intron // 0 // --- // --- // ---	-	q32.3
SNP_A-1904197	tgggcctctatctcca[C/T]gacaacaaaataaaaa	C	T	Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA. /// ENST00000244040 // 3UTR // 0 // --- // -	RAB22A	RAB22A, Homo sapiens RAB22A, member RAS oncogene family (RAB22A), q13.32
SNP_A-1901609	tggcaacacataagtc[A/G]cagtgatactcattga	A	G	LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 399440 // --- // --- // --- //	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-1906965	tggttgaaagatgttc[C/T]agggctatttttatct	C	T	5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 444521 // ---	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1925095	ttatcagctgttttaa[A/G]ccttataatcctatgg	A	G	// 340351 // Homo sapiens hypothetical protein LOC340351 (LOC340351), mRNA. /// NM_018295 // upstream // 32155 //	LOC340351	LOC340351, Homo sapiens hypothetical protein LOC340351 (LOC340351), q33
SNP_A-1921575	ttacctgaaactgctc[A/G]ctcttctatcctcatc	A	G	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA. /// ENST00000333010 // intron // 0 // --- // --- // --- // --- ///	KIAA0555	KIAA0555, Homo sapiens KIAA0555 gene product (KIAA0555), q32
SNP_A-1650966	gtagtcccaacatcccagtaaagaa[A/C]catgcatacagaaggcgattggaga	A	C	57713 // Scm-like with four mbt domains 2 /// AK093639 // upstream // 481187 // - // - // - // Homo sapiens cDNA	SFMBT2	SFMBT2 , rs10508318, Scm-like with four mbt domains 2 ,p14
SNP_A-1864850	tccaggatggtaaaga[A/T]gccaatgtctgcctct	A	T	/// ENST00000360919 // upstream // 651027 // --- // --- // --- // -	-	q13.1
SNP_A-1841036	tagctgtattttccat[C/G]aagacaaaacagcatc	C	G	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, mRNA. /// NM_138711 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens	PPARG	PPARG, Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, p25.2
SNP_A-1817414	gttcagtcagttggga[A/G]cttaggatttcatttt	A	G	7434 // Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), mRNA. /// ENST00000262178 // upstream //	VIPR2	VIPR2, Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), q36.3
SNP_A-1827914	taagaaatcacttgga[A/G]agcaaaccaactgagc	A	G	6641 // Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), mRNA. /// NM_021021 // upstream // 384804 // Hs.371902 //	SNTB1	SNTB1, Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), q24.12
SNP_A-2155357	attcatcaccaaatat[A/G]aaaaaccatcataata	A	G	9833 // Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA. /// NM_016734 // downstream //	MELK	MELK, Homo sapiens maternal embryonic leucine zipper kinase (MELK), p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2159261	atttaacaagatagac[A/T]atattttggcccaaaa	A	T	Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // intron // 0 // Hs.19872 // DLGAP1 // 9229 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2162121	attttaagttttcagg[A/G]actcatttttctcaat	A	G	// 221823 // Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), mRNA. /// NM_014707 // upstream // 149745 // Hs.196054 // HDAC9 // 9734 // Homo	PRPS1L1	PRPS1L1, Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), p21.1
SNP_A-2131808	atagctgggattctac[A/G]gaaagcagcattttct	A	G	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 98017 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2131822	atagctgtttaaagga[C/T]ggtgtgaatggtgcca	C	T	Homo sapiens suppressor of var1, 3-like 1 (S. cerevisiae) (SUPV3L1), mRNA. /// ENST00000347315 // intron // 0 // --- //	SUPV3L1	SUPV3L1, Homo sapiens suppressor of var1, 3-like 1 (S. cerevisiae) (SUPV3L1), q22.1
SNP_A-2131392	atagatgcacagagat[A/G]agtgaggtgctgggtt	A	G	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2
SNP_A-2135760	atcaaagaggaatgaa[A/T]gatttgtccagtggat	A	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 727301 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2134477	atatggtcaaaagtta[A/C]aggtatgttgggcaaa	A	C	152687 // Homo sapiens zinc finger protein 595 (ZNF595), mRNA. /// ENST00000339368 // upstream // 23459 // --- // ---	ZNF595	ZNF595, Homo sapiens zinc finger protein 595 (ZNF595), p16.3
SNP_A-2137572	atcatcgtgaaaacga[C/T]ccagcaaggcaggatc	C	T	ENST00000251170 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-2117553	aggttaaattacacac[A/G]caggtcgagtttctgt	A	G	Homo sapiens myosin IXB (MYO9B), mRNA. /// ENST00000319396 // intron // 0 // --- // --- // --- // ---	MYO9B	MYO9B, Homo sapiens myosin IXB (MYO9B), p13.11
SNP_A-2210891	ccccttgccctgacac[A/G]aaaaccaagaaagcac	A	G	Homo sapiens hypothetical protein MGC23918 (MGC23918), mRNA. /// ENST00000292314 // intron // 0 // --- // --- // --- // ---	CCDC12	CCDC12, Homo sapiens hypothetical protein MGC23918 (MGC23918), p21.31
SNP_A-2051457	aaggggtctactttaa[C/T]atagcacgtggtctgt	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2097337	agagaaacaagtttca[A/G]aaatgaacagtagtca	A	G	57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2003991	actgccttaaaacaat[A/G]aggtgtgttaatcaac	A	G	122402 // Homo sapiens tudor domain containing 9 (TDRD9), mRNA. /// ENST00000339063 // downstream // 4754 // --- // ---	TDRD9	TDRD9, Homo sapiens tudor domain containing 9 (TDRD9), q32.33
SNP_A-2012334	tataatgtgttcaatg[C/T]cacgctggtgaggtga	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 156890 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2029665	aaagagatcattttga[A/G]actttaagatttaatg	A	G	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 652365 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2293395	gcagatggaaagataa[C/T]gtaagacaccttcctg	C	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2292515	gcactccacgccaaaa[A/C]gttaaaagaggtctgc	A	C	Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 32776 // Hs.434435 // ALDH1L1 // 10840 // Homo	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2299272	gccctccaagtatgga[A/C]ataaacaaggtagact	A	C	C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 //	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-2262424	gaaatgcttctgcaga[C/T]tctcaaaataaataga	C	T	/// ENST00000297628 // upstream // 32296 // --- // --- // --- // ---	-	q24.13
SNP_A-2282267	gagttaccacactggg[C/G]caggattagaattctt	C	G	Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// ENST00000325839 // intron // 0 // --- // --- // --- // ---	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-2246365	ctggttcactagactg[A/T]cacaccacaaagggaa	A	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2253582	cttcttgtccatttat[A/T]acctgaacacttttt	A	T	4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /// NM_006152 // downstream // 211574 //	LRMP	LRMP, Homo sapiens lymphoid-restricted membrane protein (LRMP), p12.1
SNP_A-2256201	ctttagactttggaca[C/T]gtgagttaatacttga	C	T	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 542090 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2233263	ctcaggactgggattc[A/G]ctccgcaggtgctggg	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2228934	ctagatgtgagacacg[C/G]aatcaaaagaggtcat	C	G	// 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 9529 //	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2252816	cttctactgacccaca[A/C]aatggtttttatccat	A	C	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 521814 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247284	ctgtccatacattgcc[A/G]cattatataagaattc	A	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2299520	gccctttccctcccca[A/G]gtattcttcctgatcc	A	G	Homo sapiens cytosolic sialic acid 9-O-acetylesterase homolog (CSE-C), mRNA. /// ENST00000263593 // intron // 0	CSE-C	CSE-C, Homo sapiens cytosolic sialic acid 9-O-acetylesterase homolog (CSE-C), q24.2
SNP_A-2293570	gcagcatcattgtgag[C/G]agaaggtcacaaaggt	C	G	ENST00000358068 // intron // 0 // --- // --- // --- // ---	-	q35.1
SNP_A-2308759	gctttgagactgttct[A/G]aaactaggcttgtggt	A	G	5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 120006 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2305504	gctgcaaagagaagac[C/T]gcttcatgggctcaga	C	T	21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 173203 // Hs.475902	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2029233	aaagaagcagaagcac[C/T]gaagatgagcaaagcc	C	T	1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 //	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-2099576	agaggtaaaacacctg[A/G]attatattttggaaag	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2080051	accgatgccagaagga[C/T]ggtgcacccatacaga	C	T	Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// ENST00000272005 // CDS // 0 // --- // --- // --- // ---	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2224617	cgtcatgctgaaaaga[C/G]aaagatcaaatattaa	C	G	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // --- // --- // --- // ---	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2186425	cagggaaaacaaagaa[A/G]gaatgactgcagactt	A	G	5406 // Homo sapiens pancreatic lipase (PNLIP), mRNA. /// ENST00000277891 // downstream // 61240 // --- // --- // --- // --	PNLIP	PNLIP, Homo sapiens pancreatic lipase (PNLIP), q25.3
SNP_A-2197502	cattcctggccctgaa[C/T]agctcctaaagaagag	C	T	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.3
SNP_A-2120268	agtcagtgggaggtga[C/T]gagacaaggcacacag	C	T	sapiens nidogen (enactin) (NID), mRNA. /// ENST00000264187 // intron // 0 // --- // --- // --- // --- ///	NID	NID, Homo sapiens nidogen (enactin) (NID), q42.3
SNP_A-2112145	aggattaggcctgaac[C/G]gtggaattccaggcag	C	G	1454 // Homo sapiens casein kinase 1, epsilon (CSNK1E), transcript variant 1, mRNA. /// NM_001894 // upstream //	CSNK1E	CSNK1E, Homo sapiens casein kinase 1, epsilon (CSNK1E), transcript variant 1, q13.1
SNP_A-2131660	gcagaaaagacccaaa[C/T]aaagtggcaccaagga	C	T	Homo sapiens calcium binding protein Cab45 precursor (Cab45), mRNA. /// NM_016547 // intron // 0 // Hs.42806 //	Cab45	Cab45, Homo sapiens calcium binding protein Cab45 precursor (Cab45), p36.33
SNP_A-2154302	attatggctttcccca[C/T]gacagtttcagcgttc	C	T	5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// ENST00000331583 // upstream //	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q32.3
SNP_A-1826488	taacaacctgactcca[A/C]atttttttgttccctt	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 436179 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1822539	gtttttgcaattacaa[C/G]gtgatcttttgttgaa	C	G	Homo sapiens dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP4), mRNA. /// ENST00000360534 // intron // 0 // --- // --- // --- // ---	DPP4	DPP4, Homo sapiens dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP4), q24.2
SNP_A-1816627	tgcctttggaatgggc[C/T]gccaagcatcagaaat	C	T	388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 677518 // --- // --	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-1838427	tagaatagtgtaggca[A/C]aggaaacagtatgaat	A	C	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 552827 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1833912	tacataaaagatatca[C/T]caccttctgatacttc	C	T	ENST00000358350 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-1865295	tccatcaacctttaca[A/T]cctctaatggaggaat	A	T	ENST00000332738 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1857778	tcactgggggccaaaa[G/T]ccacatactatgcatg	G	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1729110	atcagaacttgctgaattaagcccc[A/T]gcttttgaaatgtcttgcatattga	A	T	NM_032867 // intron // 0 // Hs.128196 // FLJ14966 // 84953 // hypothetical protein FLJ14966	FLJ14966	FLJ14966 , rs10500756, hypothetical protein FLJ14966,p15.3
SNP_A-1926371	ttattatgtgcagata[A/C]taccttaaaagttact	A	C	ENST00000281496 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-1897442	tgctgactccaaatta[C/G]agaataaacataagaa	C	G	6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 29354 // Hs.374257 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-1951281	tttccctactcagtgc[A/G]atttgacccttattgt	A	G	Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // --- //	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-1939948	ttgcactgtagccaag[A/G]agaaaagtaaaaccga	A	G	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1940798	ttgcgtaacttcttaa[A/G]agcaaggaatcccttc	A	G	/// ENST00000356854 // downstream // 10948 // --- // --- // ---	-	q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1981371	aaaccaggccacacaa[C/T]aggagtacagagacca	C	T	1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 700718 // Hs.199248 // PTGER4 //	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1979556	attttcagtaaatccc[A/T]atttgcagcctgaagc	A	T	2743 // Homo sapiens glycine receptor, beta (GLRB), mRNA. /// NM_000826 // upstream // 38452 // Hs.32763 // GRIA2 //	GLRB	GLRB, Homo sapiens glycine receptor, beta (GLRB), q32.1
SNP_A-1981236	tttggagaaattctaa[A/C]tcccaaatgattatgt	A	C	5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 243415 // Hs.298863 // FLJ23577	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1971807	gtgtagtggacggaca[C/G]agaggcttcagccacg	C	G	9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 73675 //	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-1969093	tcctgtatgataggga[A/T]catggctttgtgaatt	A	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1941386	ttgcttcccaccaaaa[A/T]tgcgtatcctgaatct	A	T	// Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 231219 //	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-1959065	ttttgaaaggaggaag[C/G]atcgactgatagacgt	C	G	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 133233 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1901487	tggatttcacagtgca[C/G]aactcactggaggtgt	C	G	Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), mRNA. /// ENST00000229454 // intron // 0 // --- // ---	NCR2	NCR2, Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), p21.1
SNP_A-1932338	ttcctctttagccaaa[A/C]ataaatgaggagtggc	A	C	// Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000312177 // intron // 0 // --- // --- // --- // ---	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-1913708	tgtgtatccattcaac[A/G]gaataccacacagcca	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 231846 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1735977	ataatctgaatgaaaggatgggcaa[C/T]gtgactcttcactctgtcataagtc	C	T	2020 // engrailed homolog 2 /// NM_053043 // upstream // 180538 // Hs.368420 // MGC20460 // 92454 // hypothetical	EN2	EN2 , rs10488638, engrailed homolog 2 ,q36.3
SNP_A-1790882	ggggggtgccacagtg[A/G]atttcacactcaaggg	A	G	Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- // --- // ---	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-1806809	gtctataggtctatta[C/T]attgggcatttttcaa	C	T	Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-1826237	taaattctagaatcac[C/T]gagaacaactgaaatc	C	T	Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // intron // 0 // Hs.465407 // NETO1 // 81832 // Homo sapiens	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2163304	atttttgtttttaaca[A/G]ctttctcagtatctac	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2167409	caacagtgtgtgaata[C/T]gccttcttctccaaat	C	T	// 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 51888 //	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2138200	atccacatatatttac[A/T]agtattgattacaaca	A	T	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2151833	atgtttcctggggacc[A/G]gagagaaacgcaaaag	A	G	/// ENST00000247226 // downstream // 401 // --- // --- // --- // --- /// ENST00000267516 // downstream // 401 // --- // --- // --- // ---	-	q23.3
SNP_A-2134918	atattatttactcttc[A/G]aaaaggagatcctgcc	A	G	140850 // Homo sapiens defensin, beta 127 (DEFB127), mRNA. /// ENST00000202526 // downstream // 8280 // --- // ---	DEFB127	DEFB127, Homo sapiens defensin, beta 127 (DEFB127), p13
SNP_A-2129106	ataattccataaacac[C/T]gtcttcttggttttga	C	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 76180 // --- // --- // --- // ---	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2125073	agttgctggctggaca[A/G]tgatggcctgttgtcc	A	G	Homo sapiens mRNA for KIAA1760 protein, partial cds. /// NM_006648 // intron // 0 // Hs.522291 // WNK2 // 65268 //	WNK2	WNK2, Homo sapiens for KIAA1760 protein, partial cds. ,q22.31
SNP_A-2197627	cattctctgatacagc[A/T]caagaggtcaatgtcc	A	T	Homo sapiens vestigial like 4 (Drosophila) (VGLL4), mRNA. /// ENST00000273038 // intron // 0 // --- // --- // --- // ---	VGLL4	VGLL4, Homo sapiens vestigial like 4 (Drosophila) (VGLL4), p25.3
SNP_A-2194315	gagcctctggtcattg[C/G]aaaaggggcaccaatc	C	G	// Homo sapiens solute carrier family 22 (organic cation transporter), member 17 (SLC22A17), transcript variant 1, mRNA. /// NM_016609 // intron // 0 // Hs.373498 // SLC22A17	SLC22A17	SLC22A17, Homo sapiens solute carrier family 22 (organic cation transporter), member 17 (SLC22A17), transcript variant 1, q11.2
SNP_A-2181967	cagagctggttttctc[A/G]cttcatccaggtcctc	A	G	/// ENST00000246872 // downstream // 10869 // --- // --- // ---	-	q11.21
SNP_A-2211616	ccctcataaaaaacta[C/T]gtcatccatggaaaag	C	T	28962 // Homo sapiens osteopetrosis associated transmembrane protein 1 (OSTM1), mRNA. /// NM_003269 // upstream // 71870 // Hs.157688 // NR2E1 // 7101 // Homo	OSTM1	OSTM1, Homo sapiens osteopetrosis associated transmembrane protein 1 (OSTM1), q21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2210367	cccccacctgtgtaga[G/T]gtacatgggtctttca	G	T	Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // intron // 0 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2212265	ccctgggaaactagta[C/T]gccatgatatcacaaa	C	T	5445 // Homo sapiens paraoxonase 2 (PON2), mRNA. /// AF001601 // upstream // 14035 // Hs.530077 // PON2 // 5445	PON2	PON2, Homo sapiens paraoxonase 2 (PON2), q21.3
SNP_A-2206300	ccatccgggatgtcca[A/G]gttcagatacactcat	A	G	// 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 97416 // Hs.156832 // NPAS2 //	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-2087634	actgctctttgttcaa[C/T]ctgggatagaagcgtt	C	T	sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), mRNA. /// ENST00000303641 // intron // 0 // --- // ---	ROR2	ROR2, Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), q22.31
SNP_A-2028317	aaactcaatttgcaat[A/T]ataggctaaggagatt	A	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2031521	aaagggtggaaacagcc[C/G]aaattgatggaagaat	C	G	-- /// ENST00000360285 // downstream // 424031 // --- // --- // -- // --- /// ENST00000339882 // downstream // 424031 // --- //	-	q12
SNP_A-2031937	aaagtcctgacttcac[C/T]gctacaaaatctatgc	C	T	sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 //	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-2045541	aagaatgtaaagtcac[A/T]gcttcttccacttttc	A	T	// 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 287191 // Hs.282787 // FOXP2 /	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1
SNP_A-1989664	ccccaagaactcttaa[A/G]tgattttatgagatgg	A	G	/// ENST00000294915 // upstream // 12932 // --- // --- // --- // ---	-	q43
SNP_A-2304554	gctctccagctgtgaa[C/T]gtttaaatgctataag	C	T	Homo sapiens sec1 family domain containing 2 (SCFD2), mRNA. /// ENST00000329818 // intron // 0 // --- // --- // --- // ---	SCFD2	SCFD2, Homo sapiens sec1 family domain containing 2 (SCFD2), q12
SNP_A-2295766	gcatgccagtaaaagg[C/G]agagctcactgggggc	C	G	Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase (MGAT5), mRNA. /// ENST00000281923 // intron // 0 // --- // --- // --- // ---	MGAT5	MGAT5, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase (MGAT5), q21.3
SNP_A-2284640	gatcagccatgctgac[A/G]gcaaagacaaacaagg	A	G	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2282044	gagtgggatcttctca[A/G]tacatttgtttggtgg	A	G	55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 61116 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2260744	gaaacgtagtcccgag[C/G]aagacctcaaaggact	C	G	23766 // Homo sapiens GABA-A receptor-associated protein mRNA, complete cds. /// NM_001004309 // upstream // 183 //	GABARAPL3	GABARAPL3, Homo sapiens GABA-A receptor-associated protein complete cds. ,q26.1
SNP_A-2244119	ctgctttaggtatatc[A/G]aaattgcttgtttaga	A	G	ENST00000345007 // CDS // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-2253537	cttcttctggctaaaa[A/G]tgcctgctgttttaac	A	G	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, mRNA. /// ENST00000329257 // intron //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, q23.1
SNP_A-2299330	gccctgaatttggcat[C/T]atgaacttgcactctt	C	T	Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// ENST00000325064 // intron // 0 // --- // --- // --- // --- ///	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2292551	gcactcttttcctcat[C/T]agcaaggccccagatg	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 798296 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2305948	gctgctgtttctaata[C/T]gttattttgacacaca	C	T	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2310322	ggaacgcaggagagca[C/T]ggatgagagaagggag	C	T	sapiens mRNA for KIAA0218 gene, partial cds. /// ENST00000287652 // intron // 0 // --- // --- // --- // ---	TATDN2	TATDN2, Homo sapiens for KIAA0218 gene, partial cds. ,p25.3
SNP_A-2314093	ggaggaagtgtaagta[G/T]ggctatcagtcatata	G	T	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2034952	aaatgatcacaggctc[A/C]aggatatgcatgtgct	A	C	// Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /// ENST00000297435 // upstream // 16463 // --- // ---	DEFA4	DEFA4, Homo sapiens defensin, alpha 4, corticostatin (DEFA4), p23.1
SNP_A-2079010	acccactcatactcac[A/T]ccccacactcgttac	A	T	Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // --- // --- // --- // --- ///	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2059941	aatcttctcagcagtt[C/T]aaatcccttcattatc	C	T	10282 // Homo sapiens BET1 homolog (S. cerevisiae) (BET1), mRNA. /// NM_000089 // upstream // 180606 //	BET1	BET1, Homo sapiens BET1 homolog (S. cerevisiae) (BET1), q21.3
SNP_A-2073992	acagttctgacacata[A/G]gggatccacttgtttc	A	G	81793 // Homo sapiens toll-like receptor 10 (TLR10), mRNA. /// NM_006068 // downstream // 30828 // Hs.366986 // TLR6	TLR10	TLR10, Homo sapiens toll-like receptor 10 (TLR10), p14
SNP_A-2076734	acatttttaaaaacaa[C/G]tctccacttctaccct	C	G	Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // intron // 0 // Hs.527984 //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2066190	aattttaaacacagag[A/G]aattagataaaggaaa	A	G	9788 // Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// NM_152412 // upstream // 106954 // Hs.175350 //	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2063196	aatgtttctgaggaga[C/G]aaaagttacaaatatt	C	G	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA. /// ENST00000332624 // intron // 0 // --- // --- // --- // ---	ALS2CR3	ALS2CR3, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), q33.1
SNP_A-2226184	ctaactaaaatgttct[C/T]aacgcactaaatgaaa	C	T	ENST00000344168 // intron // 0 // --- // --- // --- // ---	-	p36.13
SNP_A-2174294	cacactgttaggcaat[C/T]aatctgcagaactgtt	C	T	Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA. /// ENST00000262601 // intron // 0 // --- // ---	C20orf9	C20orf9, Homo sapiens chromosome 20 open reading frame 9 (C20orf9), q13.12
SNP_A-2192458	catcattcaggaacgc[A/G]gactcttcccaacatg	A	G	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 268269 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2132424	atagtctagttatagc[A/G]cagcattaaataaatg	A	G	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 195709 // Hs.437966 // PXMP3 //	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2166344	caaatctctccaaaaa[A/G]ttgcccaatgtatgta	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2155520	attcatttctgttatc[A/G]gacaatctcaggcaga	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 39348 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1844059	tagttgatgtacaata[A/C]acttcatgtacttaaa	A	C	Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// NM_173472 // intron // 0 // Hs.190413	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-1798543	gtaaattgataatgtc[C/T]catgaaccgaggaata	C	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1793046	ggtacgttgcataata[A/C]agaaagatgtgtacta	A	C	/// ENST00000355503 // upstream // 55512 // --- // --- // --- // ---	-	p13
SNP_A-1905205	tgggttattggacaca[C/T]agtcctggaatatcct	C	T	KIAA1914 // 84632 // Homo sapiens KIAA1914 (KIAA1914), transcript variant 1, mRNA. /// NM_032550 // upstream //	KIAA1914	KIAA1914, Homo sapiens KIAA1914 (KIAA1914), transcript variant 1, q25.3
SNP_A-1930460	ttccaaaccaagcgga[G/T]tatttcaaaaatggcc	G	T	9945 // Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA. /// NM_015455 // upstream	GFPT2	GFPT2, Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), q35.3
SNP_A-1901888	tggcagcaggcacttc[C/T]ctgggtgctcttgaca	C	T	ENST00000327200 // 3UTR // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-1900569	tggaggaaatgaattc[A/G]atgcttttggcaagtg	A	G	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1887255	tgagaacttgttagaa[A/G]tgctgattcataggcc	A	G	ENST00000354500 // intron // 0 // --- // --- // --- // ---	-	q21.11
SNP_A-1959990	ttttgttaattagaac[A/G]caaatgttgaatgtgg	A	G	10449 // Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding mi /// AB032945 // downstream // 5409 // Hs.445218 // MYO5B // 46	ACAA2	ACAA2, Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding mi ,q21.1
SNP_A-1952994	tttcttctcttcataa[C/T]tcaaaaggaacacatg	C	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 1067429	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1975139	ccagtggtatgggcca[A/G]aaacagtcaggtagat	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1960071	ttttgtttattttaca[C/T]ggcatttattaaacat	C	T	1908 // Homo sapiens endothelin 3 (EDN3), transcript variant 1, mRNA. /// NM_207034 // downstream // 87972 // Hs.1408	EDN3	EDN3, Homo sapiens endothelin 3 (EDN3), transcript variant 1, q13.32
SNP_A-1959500	ttttgctattttaaca[A/T]ggagaaagtctgcaaa	A	T	55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // upstream //	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-1942631	ttgggaccaactgaga[C/G]aatgaccaccttcttc	C	G	ENST00000313553 // intron // 0 // --- // --- // --- // ---	-	q12
SNP_A-1938455	ttgacttgactgacat[A/C]ataaggacaattcttt	A	C	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2648638 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1875877	tctgaaaatggcaaag[A/C]aaatacaattacccta	A	C	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1927148	ttattttgagttttca[C/T]atcaacttctaatata	C	T	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1922957	ttagcaaattacaaaa[A/G]agagctagagattgta	A	G	-- /// ENST00000354800 // downstream // 322582 // --- // --- // -	-	q14.1
SNP_A-1912435	tgtgcacattgtctaa[C/T]atctaatttaggtaat	C	T	/// ENST00000333744 // downstream // 15167 // --- // --- // ---	-	p15.1
SNP_A-1794509	ggtcctgggttttaaa[C/T]tcctggttcacttgtc	C	T	2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream //	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1788404	gggagtatttagccca[C/T]gaaaatcagcaaatgc	C	T	ENST00000335031 // intron // 0 // --- // --- // --- // ---	-	q31.23
SNP_A-1804447	gtcagaatagctattg[A/G]aaagtccaaagataac	A	G	/// ENST00000310012 // upstream // 162594 // --- // --- // --- // -	-	q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784392	ggcccgatggcctgag[A/G]agcttatccttgcctt	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 253410 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1835108	taccctataccacaag[G/T]cgtcaagcagagtcgg	G	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2931870 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1870934	tcggtacaagggagta[A/G]cactgagggtggccta	A	G	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase,	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). ,q12.13
SNP_A-2151935	atgttttaggaaatga[A/C]ctcaaaaggaagagat	A	C	5257 // Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. /// NM_145188 // downstream // 43590 // Hs.410111	PHKB	PHKB, Homo sapiens phosphorylase kinase, beta (PHKB), q12.1
SNP_A-2128824	ataatgaatgaataga[C/T]gttaaaatgtcagatg	C	T	1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 118962 //	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2116053	aggtaaaacattttaa[C/G]atcttgagtgtctgaa	C	G	Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (S /// ENST00000355014 // intron // 0 // --- // -- // --- // --- ///	SEMA4A	SEMA4A, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A (S ,q22
SNP_A-2192618	catccataatagatgc[A/G]aggtcctgttggtcca	A	G	BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 //	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.3
SNP_A-2169494	caagcctgtgtcagga[A/G]gagctattttcagtga	A	G	1290 // Homo sapiens collagen, type V, alpha 2 (COL5A2), mRNA. /// NM_000393 // upstream // 6861 // Hs.445827 //	COL5A2	COL5A2, Homo sapiens collagen, type V, alpha 2 (COL5A2), q13.11
SNP_A-2216165	cctccctcattgacac[C/T]gtacaaggttctgccc	C	T	57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 265273 //	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-2215141	cctatttataggtaga[A/C]aaagcaatgcacgagg	A	C	C1GALT1 // 56913 // Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), mRNA. /// NM_019005 // upstream // 191088 //	C1GALT1	C1GALT1, Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), p21.3
SNP_A-2217912	cctgcagactgtggac[A/G]gctaagtgttaacggc	A	G	83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // upstream // 141279 // --- // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2204165	ccagcagccctttaaa[C/T]agtttgtctcaaatgt	C	T	ENST00000359964 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-2200754	ccaagagagaagacca[A/G]ctctgcttaagcggtg	A	G	1508 // Homo sapiens cathepsin B (CTSB), transcript variant 1, mRNA. /// NM_147782 // upstream // 40918 // Hs.520898 //	CTSB	CTSB, Homo sapiens cathepsin B (CTSB), transcript variant 1, p23.1
SNP_A-2200560	ccaactgacttcaaca[A/G]gactcaaagcaagcac	A	G	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 452421 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2071949	acagagcaggaaataa[A/G]agagagatgaggacac	A	G	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// ENST00000315856 // intron // 0 // --- // --- // --- // ---	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2079653	accctactctactaga[C/T]tataacttactcattc	C	T	196 // Homo sapiens aryl hydrocarbon receptor (AHR), mRNA. /// NM_015132 // downstream // 8834 // Hs.487648 //	AHR	AHR, Homo sapiens aryl hydrocarbon receptor (AHR), p21.1
SNP_A-2089387	acttatatgaagttca[A/G]aaaagggcaaaactaa	A	G	2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// NM_024997 // upstream // 245133 // Hs.513343 // ATF7IP2 // 80063 //	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2030020	aaagatgtggaaagaa[C/T]gccaagacatattgtt	C	T	55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // upstream // 40289 // Hs.485392 // TRERF1 // 55809 // Homo	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-1996607	aaaagagtcttgttgg[A/G]aagctctcaagaatag	A	G	Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // --- // --- // --- // ---	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-2015114	ggaaggatctggacac[C/T]gattacttaaagtaac	C	T	Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// ENST00000347596 // intron // 0 // ---	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2303690	gctcacttctgtaata[C/T]cacacattagaaggca	C	T	6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 209165 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2300451	gcctctttctccatca[A/G]tcatatccctggtggt	A	G	Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 4 (ATP6V0A4), transcript variant 1, mRNA. /// NM_130840 // intron // 0 // Hs.98967 // ATP6V0A4 // 50617	ATP6V0A4	ATP6V0A4, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 4 (ATP6V0A4), transcript variant 1, q34
SNP_A-2255546	cttgtgatcagaaaaa[G/T]aagttgtgacagaatt	G	T	Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) mRNA, complete cds. /// NM_002977 // downstream // 73243 // Hs.2319 // SCN9A // 6335 // Homo	SCN1A	SCN1A, Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) complete cds. q24.3
SNP_A-2228593	ctagaacaactgcagg[A/G]ataaattgggaaacct	A	G	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2234738	ctccagggtgatgtgg[C/T]caattcaaaagcacat	C	T	Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // intron // 0 // --- // --- // --- // ---	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-2246756	ctgtactggatttttc[A/G]catccatcttcatttt	A	G	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // --- // --- // --- // ---	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2259028	ctttttttcattcacct[C/G]aatagctactgcaaag	C	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 842364 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2296545	gcattttatgaaccag[A/G]aacagttagggacttg	A	G	Homo sapiens gephyrin mRNA, complete cds. /// NM_020806 // intron // 0 // Hs.208765 // GPHN // 10243 //	GPHN	GPHN, Homo sapiens gephyrin complete cds. q23.3
SNP_A-2013130	aagaaaaagctgttac[C/T]cccacctgtgagtgat	C	T	Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // --- // ---	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-2032651	aaataaatatttgatg[A/C]aatgagaaataaaaat	A	C	Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), mRNA. /// ENST00000256767 // intron // 0 // --- // ---	HRPT2	HRPT2, Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), q31.2
SNP_A-2024673	aaaagtaagggccatc[A/G]cttgctattcctatct	A	G	Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3E), mRNA. /// ENST00000265198 // intron // 0 // --- // --- // --- //	PIP3-E	PIP3-E, Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), q25.2
SNP_A-2021186	aaaaaaagactgggaa[A/G]ttcataagaaacagat	A	G	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 421209	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2091460	agaaaaaaatacatca[A/G]taagtccatcacctag	A	G	79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream //	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.13
SNP_A-2101850	agatggagaaaattca[C/G]tctaaatctatgagga	C	G	-- /// ENST00000332560 // upstream // 63905 // --- // --- // --- //	-	q21.1
SNP_A-2098512	agagcagcaccaagga[C/T]aagttgggctcagcag	C	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1361294 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2071012	acactgaagaatataa[A/C]agacagagacaaaaac	A	C	84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// NM_032808 // upstream // 147640 //	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-2066102	aatttgtaaaccttat[A/G]ataacacgaaagcagg	A	G	Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2185116	caggaaaacaaagaca[C/G]gaggctgagtgtttac	C	G	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 232215 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2184627	cagctcccacagttct[A/T]aaaggatcctattgtt	A	T	// 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 70881 // Hs.156832 // NPAS2 //	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-2117038	aggtgagaagctgggg[C/T]cacctaatcgctgggc	C	T	ENST00000326134 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2140340	atctcagagcctgcac[A/G]gagactcagacacacc	A	G	140625 // Homo sapiens actin-related protein M2 (ARPM2), mRNA. /// ENST00000355271 // upstream // 217752 // --- // ---	ARPM2	ARPM2, Homo sapiens actin-related protein M2 (ARPM2), p36.32
SNP_A-1858390	tcagacggacattgga[A/G]cccctgtcaggatcag	A	G	399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 327096 // Hs.299419 //	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds. q25
SNP_A-1853364	tattttcagaattcta[A/G]ctttgttgcaagcctt	A	G	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // intron // 0 // --- // --- // --- // --- ///	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-1836691	tactgaaatttcatga[C/T]gcccttagcacctcag	C	T	Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA. /// ENST00000358336 // intron // 0 // --- // --- // --- /// ENST00000320152 // intron // 0 // --- // --- // ---	PRTFDC1	PRTFDC1, Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), p12.1
SNP_A-1839569	tgtcaggcccaatagg[A/G]acaggacttgaggtct	A	G	ENST00000313495 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-1823174	taaaacataaggagaa[A/G]agctgctaagctggtt	A	G	221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 54262	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1818234	atgattatataaataa[C/T]tggacagcatttgttc	C	T	85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 66176 // Hs.461389 // CNTNAP4 // 85445 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1802748	gtatgccggttaaaac[G/T]gaatcacacaaaaaag	G	T	Homo sapiens Nijmegen breakage syndrome 1 (nibrin) (NBS1), mRNA. /// ENST00000265433 // intron // 0 // --- // ---	NBS1	NBS1, Homo sapiens Nijmegen breakage syndrome 1 (nibrin) (NBS1), q21.3
SNP_A-1810619	gtgcaaggaaagtcac[A/C]aagatcctttccattt	A	C	Homo sapiens hyaluronan binding protein 2 (HABP2), mRNA. /// ENST00000351270 // intron // 0 // --- // --- // --- // ---	HABP2	HABP2, Homo sapiens hyaluronan binding protein 2 (HABP2), q25.3
SNP_A-1912879	tgtgcttgtgaataac[A/C]actgtactcaagtcag	A	C	-- /// ENST00000359634 // upstream // 998798 // --- // --- // --- // --- /// ENST00000359181 // upstream // 998798 // --- // --- //	-	q32.3
SNP_A-1908685	tgtaggcaagaagcaa[C/G]aatagatgctaaaatt	C	G	ENST00000288466 // intron // 0 // --- // --- // --- // ---	-	q32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1874039	tctcatgaatatgtta[A/G]gcataagaagcaaaac	A	G	// 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // downstream // 57397 // Hs.167317 // SNAP25 // 6616 //	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-1895416	tgccgctttgttttag[A/G]agatgaagaattcttt	A	G	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 20310 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-1954393	tttgcatatagtgtat[A/C]ataaattgttgtaata	A	C	Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000265382 // intron // 0 // --- // --- // --- // ---	PIP5K1B	PIP5K1B, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), q21.11
SNP_A-1965582	ttctagaaatggttca[A/G]tctatgtttatgtttt	A	G	Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // --- // ---	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-1978295	aaaaattacacacaga[A/G]aaagtgacattaatag	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 643656 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1987304	tatgagcagaaacaca[C/G]tggctcattgactatt	C	G	222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 960827 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1951248	tttccccctacaaaca[C/G]atggagaaattttatg	C	G	Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), mRNA. /// ENST00000256398 // intron // 0 // --- // --- // ---	ELP3	ELP3, Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), p21.1
SNP_A-1943501	ttgtaaagagtatgta[A/G]gggctttggaaacagc	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2200745 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1893863	tgcatacagcaatata[C/G]gcagaaaacatttatg	C	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 493394 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1930356	ttcatttctttgccat[C/T]atcaggttagatgtgg	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 159149 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1662444	atatttaaaagtcaaaattctgtca[C/T]caataatatttaagcagttctaaat	C	T	mRNA for KIAA1705 protein, partial cds. /// NM_001202 // downstream // 279926 // Hs.68879 // BMP4 // 652 // bone	-	- , rs10483622, Homo sapiens mRNA for KIAA1705 protein, partial cds. ,q22.1
SNP_A-1659796	gctccatgtaaaggactttacatct[A/C]actttgtgttgaatgtacggtcaca	A	C	C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 90300 // Hs.352631 //	C21orf42	C21orf42 , rs2827281, chromosome 21 open reading frame 42 ,q21.1
SNP_A-1817848	gttccttcactgatac[A/G]cacatttttttttctt	A	G	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1852761	tatttcattatttgct[C/G]aaaattatgccttttt	C	G	FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 550743 //	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1858389	tcagacggacaccgca[A/G]tccacgctccttttta	A	G	923 // Homo sapiens CD6 antigen (CD6), mRNA. /// NM_014207 // upstream // 44770 // Hs.58685 // CD5 // 921 //	CD6	CD6, Homo sapiens CD6 antigen (CD6), q12.2
SNP_A-1863810	tccaagtcgtgtcatc[C/T]attgaagctaagcaac	C	T	Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// ENST00000325064 // intron // 0 // --- // --- // --- // --- ///	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2166798	caaattggacccaaaa[A/G]gcatagttttgtctga	A	G	Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA. /// NM_002603 // intron // 0 // Hs.527119 //	PDE7A	PDE7A, Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, q23.3
SNP_A-2118257	agtaaattgtattaca[A/G]aatttcattgtcaggg	A	G	CAPZA3 // 93661 // Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA. /// NM_019012 // upstream // 184159 // Hs.188614 // PLEKHA5	CAPZA3	CAPZA3, Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), p12.3
SNP_A-2132787	atataacaaagtagaa[A/G]cttccctattatacac	A	G	Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA. /// ENST00000356218 // intron // 0 // --- // ---	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-2169256	caagcaagaaggagcc[C/T]gaagtcattctcgcac	C	T	Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-2217584	cctgagagcgtaggac[A/G]aggcactccaggggca	A	G	Homo sapiens wingless-type MMTV integration site family, member 7A (WNT7A), mRNA. /// ENST00000285018 // intron // 0 // --- // --- // --- // --- /// ENST00000355174 // intron // 0 // --- // --- // --- // ---	WNT7A	WNT7A, Homo sapiens wingless-type MMTV integration site family, member 7A (WNT7A), p25.1
SNP_A-2226506	ctaagccatttgtaag[C/T]actctgttgtctctgt	C	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2072013	acagaggctatgccac[A/G]ctataaataagctgaa	A	G	51299 // Homo sapiens neuritin 1 (NRN1), mRNA. /// NM_000129 // downstream // 62394 // Hs.335513 // F13A1 //	NRN1	NRN1, Homo sapiens neuritin 1 (NRN1), p25.1
SNP_A-2072700	acagccttttagagca[A/G]aaaaagatataaaata	A	G	7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// NM_016617 // upstream // 255623 // Hs.524969 // Ufm1 //	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2061837	aatggatcgttgcaga[C/T]gtcgaatgttggggat	C	T	10123 // Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA. /// NM_014521 // upstream // 348618 // Hs.516777 //	ARL7	ARL7, Homo sapiens ADP-ribosylation factor-like 7 (ARL7), q37.1
SNP_A-2055116	aataacataaacaaga[A/G]aaggcaagactacacc	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 460867 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2053762	aagtgtaaaagaatga[A/G]taaaagcagaaggtcc	A	G	-- /// ENST00000355517 // downstream // 846362 // --- // --- //	-	q24.32
SNP_A-2085724	actcctatgaagcaaa[C/T]gtggccacctccagtt	C	T	8291 // Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// NM_019885 // downstream // 244837 // Hs.91546 //	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-2084495	actatctgtccctttg[C/T]aggaagtttgcagcct	C	T	// Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // downstream //	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. p26.1
SNP_A-2021642	aaaaaattgtatcagc[C/G]aagagaaacttccctt	C	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2032711	aggtgacagaagagcc[A/G]aaagagactctatcag	A	G	5545 // Homo sapiens proline-rich protein BstNI subfamily 4 (PRB4), mRNA. /// NM_199353 // downstream // 10302 //	PRB4	PRB4, Homo sapiens proline-rich protein BstNI subfamily 4 (PRB4), p13.2
SNP_A-2009328	aattcaggtttggcca[A/G]gttgagctaaggtgtt	A	G	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-2306004	gctggaaaaatctatt[C/G]aaataggtgcaaattg	C	G	/// ENST00000309379 // upstream // 754909 // --- // --- // --- // -	-	q21
SNP_A-2228195	ctactcagaagtaata[C/T]cttttgctcttatttt	C	T	169522 // Homo sapiens potassium channel, subfamily V, member 2 (KCNV2), mRNA. /// NM_014878 // downstream //	KCNV2	KCNV2, Homo sapiens potassium channel, subfamily V, member 2 (KCNV2), p24.2
SNP_A-2252944	cttctcacctgatgga[A/G]taaataaaccccagat	A	G	Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 //	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12
SNP_A-2254718	cttgctttgaccataa[A/G]aataacttcagacctt	A	G	Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // intron // 0 // Hs.337696 // SLC8A3 // 6547 //	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-2269419	gaatttttacttctgc[A/G]cttagaagaaggcagg	A	G	Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), mRNA. /// ENST00000297169 // intron // 0 // --- // ---	KCNK5	KCNK5, Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), p21.2
SNP_A-2291451	gcaattctagtgagca[C/T]cctaaagtgaaatgtc	C	T	9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 315356 // --- // ---	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-2017857	aacttcatcaactaca[A/G]taatttgccttttcca	A	G	337973 // Homo sapiens keratin associated protein 19-6 (KRTAP19-6), mRNA. /// NM_181614 // downstream // 6909	KRTAP19-6	KRTAP19-6, Homo sapiens keratin associated protein 19-6 (KRTAP19-6), q22.11
SNP_A-1992220	agatgcaggttgacac[A/G]ggcttgagttccaagg	A	G	Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// ENST00000310430 // 3UTR // 0 // --- // --- // --- // ---	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-1997501	atcaagcagcttcata[A/T]aattgactctaacctt	A	T	Homo sapiens CDW92 antigen (CDW92), mRNA. /// NM_080546 // intron // 0 // Hs.494700 // CDW92 // 23446 //	CDW92	CDW92, Homo sapiens CDW92 antigen (CDW92), q31.1
SNP_A-2024894	aaaagtttaagtgaga[C/T]aacatgtaacaattca	C	T	SLC24A2 // 25769 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	SLC24A2	SLC24A2, Homo sapiens solute carrier family 24 (sodium,p22.1
SNP_A-2084174	actaggatttaaataa[C/G]aaatattgcagaaaac	C	G	// 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant 2, mRNA. ///	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+ q24.2
SNP_A-2054875	aataaaggcatttcca[C/T]gttccacaagtgaggc	C	T	942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // downstream // 107319 // Hs.171182 // CD86 //	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q21.1
SNP_A-2207118	ccattaagttctcaac[A/T]ctacagctgaggagtt	A	T	-- /// ENST00000276737 // downstream // 107604 // --- // --- //	-	q24.23
SNP_A-2183797	cagcattaaagcagaa[C/T]ttacctgagtaactct	C	T	56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 1309041 // Hs.463466 //	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-2132022	ataggcgttggagtta[C/G]gagcaatttttgcggg	C	G	59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 328242 // Hs.32966 // GUCA2B // 2981 // Homo	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-2131631	atagccaaccatggac[A/C]aatggatgtgctcttc	A	C	// 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 712127 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2115350	aggggattttgaaggc[A/C]gcaaagccattattct	A	C	Homo sapiens rabphilin 3A-like (without C2 domains) (RPH3AL), mRNA. /// ENST00000323434 // intron // 0 // --- // -	RPH3AL	RPH3AL, Homo sapiens rabphilin 3A-like (without C2 domains) (RPH3AL), p13.3
SNP_A-2111190	aggagatgacccttga[A/G]atgggctttataggat	A	G	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 79022 // Hs.114412 // TXNL1	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2108057	agctctcctgtgcaga[C/T]acctgtgcctacgaga	C	T	sapiens olfactory receptor, family 2, subfamily Z, member 1 (OR2Z1), mRNA. /// ENST00000324060 // CDS // 0 // --- // ---	OR2Z1	OR2Z1, Homo sapiens olfactory receptor, family 2, subfamily Z, member 1 (OR2Z1), p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1866537	tccccatgcttcatta[A/T]attatattgtgatttt	A	T	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // --- // ---	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-1866341	tcccattcatgttcag[C/T]aggaaaataaaaacat	C	T	160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// ENST00000321196 // intron // 0 // --- // --- // --- // ---	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1867834	tcctacaataataata[C/T]cgtgcttaaattatac	C	T	SCIRP10 // 29937 // Homo sapiens secreted protein of unknown function (SPUF), mRNA. /// NM_001674 //	SCIRP10	SCIRP10, Homo sapiens secreted protein of unknown function (SPUF), q32.3
SNP_A-1850213	tatgtgtgctgcccca[C/T]caaactgtgcactaca	C	T	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-1818099	gttctccaaaatccta[A/G]cccacagaattgagca	A	G	6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 23020 // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-1816689	gttatatctttctccc[A/G]aacacacgtattctca	A	G	343472 // Homo sapiens BarH-like 2 (Drosophila) (BARHL2), mRNA. /// NM_016620 // downstream // 121743 // Hs.173001	BARHL2	BARHL2, Homo sapiens BarH-like 2 (Drosophila) (BARHL2), p22.2
SNP_A-1826696	taacagaatcaggtga[A/G]atctcttggattcctt	A	G	ENST00000354422 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-1839866	tagattgtaaacttcc[A/T]attgcattaaatctgg	A	T	79754 // Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA. /// ENST00000357700 //	ASB13	ASB13, Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), p15.1
SNP_A-1837025	tactggtaaatggata[A/T]gttttgaactgaaaat	A	T	Homo sapiens bubblegum related protein (BGR), mRNA. /// ENST00000252669 // intron // 0 // --- // --- // --- // ---	BGR	BGR, Homo sapiens bubblegum related protein (BGR), p13.3
SNP_A-1830369	taatatgcttttcata[C/T]cacaggtgttgatttc	C	T	Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // intron // 0 // --- // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-1781628	ggattgatgctctaaa[A/T]cgttttgtggagaatc	A	T	84632 // Homo sapiens KIAA1914 (KIAA1914), transcript variant 1, mRNA. /// NM_032550 // intron // 0 // Hs.501106 //	KIAA1914	KIAA1914, Homo sapiens KIAA1914 (KIAA1914), transcript variant 1, q25.3
SNP_A-1810934	gtgcatgaggccatac[G/T]ccactcctcagtctgt	G	T	FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1811051	gtgccaggcactgtga[A/C]ctcctgatcctttcag	A	C	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1924705	ttataggtgtacatca[A/T]catacctggctaattt	A	T	1277 // Homo sapiens collagen, type I, alpha 1 (COL1A1), mRNA. /// NM_153229 // upstream // 23989 // Hs.224630 //	COL1A1	COL1A1, Homo sapiens collagen, type I, alpha 1 (COL1A1), q21.33
SNP_A-1907533	tgtaaatgattcaaga[G/T]atcccatcatatgcaa	G	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1875540	tctctgtgcttcagta[G/T]ccccatctggaataag	G	T	8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 349917 // Hs.279522 // NR4A3 //	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-1965240	aatagggatatagata[A/G]agatatttttcacagc	A	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 1656729 // --- // -	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1975731	tactaaagttaatatg[A/C]cagctagtggtaaagc	A	C	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 529539 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1976896	ggtggcagatgtagaa[C/T]tcatatccaggttccc	C	T	Homo sapiens RNA-binding protein (FLJ20273), mRNA. /// ENST00000319592 // intron // 0 // --- // --- // --- // --- ///	FLJ20273	FLJ20273, Homo sapiens RNA-binding protein (FLJ20273), p14
SNP_A-1980543	ttgcccagggacagaa[A/G]atcccaattagatatc	A	G	2331 // Homo sapiens fibromodulin (FMOD), mRNA. /// NM_201348 // upstream // 107234 // Hs.76494 // PRELP //	FMOD	FMOD, Homo sapiens fibromodulin (FMOD), q32.1
SNP_A-1938094	ttgacacaaaagaaga[A/G]agtatgtctaatggag	A	G	sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// ENST00000273951 // intron // 0 // --- // --- // ---	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-1903115	tggcttaatgtctttc[A/G]actgtatgaatttata	A	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1912155	tgtgagtgttttagag[A/G]cctatattgttattct	A	G	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 1133802	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1920680	gagaaactaatgccac[A/G]ctaaaaactctgagct	A	G	28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 558295 // --- // --- // --- // -	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.33
SNP_A-1926442	ttattcagatgtagca[C/T]attgacatgaatctga	C	T	Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA. /// ENST00000253778 // intron // 0 // --- // -	GFPT2	GFPT2, Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), q35.3
SNP_A-1787245	tgtaccaagacaagga[C/T]gctatagctagggtag	C	T	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 337326 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1790922	gggggtgtttgtgtac[G/T]acgtcagtgcattttt	G	T	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase q35.1
SNP_A-1782005	ggcaaagggaagaata[A/G]aagcatcaatggcttg	A	G	Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA. /// ENST00000357364 // intron // 0 // --- //	ZNFN1A1	ZNFN1A1, Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), p12.2
SNP_A-1849780	tatgtaattcaaataa[C/T]gtgttagaaacatcat	C	T	ENST00000354860 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1846214	tatatcctgctgtttg[A/T]atttttcctcaaaact	A	T	Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA. /// ENST00000358731 // intron // 0 // --- // --- // --- // ---	BDP1	BDP1, Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), q13.2
SNP_A-1870865	tcggctccagtcaacc[A/G]ggtgagtaggaggctt	A	G	Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // intron // 0 // Hs.527984 //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2110929	aggacttggtgcctga[A/G]cgatgaagggcagggg	A	G	Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), mRNA. /// ENST00000261367 // intron // 0 // --- // -	SNCAIP	SNCAIP, Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), q23.2
SNP_A-2164482	caaaattagaaatata[A/G]taacttacatgcacta	A	G	Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // intron // 0 // Hs.527984 //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2163442	tgtagccaccttaatc[A/G]atgatcttagctagat	A	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2153270	attactgttttagtac[A/G]gaggaatgtaagggac	A	G	// 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 43624 // Hs.19872 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2151428	atgttcatgcacatca[A/G]agaaccctttttaag	A	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 611613 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2189803	cataaacacattccta[C/T]ggacaataacatacaa	C	T	Homo sapiens mRNA for KIAA0919 protein, partial cds. /// ENST00000272427 // intron // 0 // --- // --- // --- // --- ///	SEC15L2	SEC15L2, Homo sapiens for KIAA0919 protein, partial cds. ,p13.2
SNP_A-2198028	cattgctgggaaaaga[C/T]aactggaagaacatat	C	T	FLJ20097 // 55610 // Homo sapiens hypothetical protein FLJ20097 (FLJ20097), mRNA. /// NM_001742 // downstream	FLJ20097	FLJ20097, Homo sapiens hypothetical protein FLJ20097 (FLJ20097), q21.3
SNP_A-2168833	caagactactacaaaa[A/C]catcattcctagagga	A	C	Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 //	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2048359	aagcaggaaacaatag[G/T]agatactcagataatt	G	T	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2040528	aaccatagtcaaaagg[A/G]cataattgctgtgcat	A	G	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2300051	gcctcacaaaatataa[A/C]cttccaccttcctttt	A	C	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2271420	gacatttatgtgcaca[A/G]gccaaagatccagctt	A	G	51666 // Homo sapiens ankyrin repeat and SOCS box-containing 4 (ASB4), transcript variant 2, mRNA. /// NM_016116 // downstream // 7265 // Hs.127735 // ASB4 //	ASB4	ASB4, Homo sapiens ankyrin repeat and SOCS box-containing 4 (ASB4), transcript variant 2, q21.3
SNP_A-2284220	gatattaaaaatggct[A/T]aaatgccaggcatggt	A	T	56955 // Homo sapiens matrix, extracellular phosphoglycoprotein with ASARM motif (bone) (MEPE), mRNA. /// NM_020203 // downstream // 59030 // Hs.189587	MEPE	MEPE, Homo sapiens matrix, extracellular phosphoglycoprotein with ASARM motif (bone) (MEPE), q22.1
SNP_A-2231701	ctcaaaaaatgaaaac[C/T]gagctacaggtttaat	C	T	// Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA. /// NM_001761 // upstream //	ABCA3	ABCA3, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), p13.3
SNP_A-2276798	gagataattattccaa[A/C]aaagagtgaatgaatc	A	C	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1458494 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2313920	ggagcggaaggacacc[C/T]ataagagaaccaaacc	C	T	Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // --- // --- // --- // --- ///	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2017384	agataattaaattcta[C/T]cttgtgctaaaactgg	C	T	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 100701 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2055657	aatgtataatttagcc[A/G]cactttattctttact	A	G	4753 // Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// NM_001004329 // downstream // 73882 // Hs.302764 //	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2176842	cacccttgtatatacc[G/T]aattggctctggtata	G	T	1234 // Homo sapiens chemokine (C-C motif) receptor 5 (CCR5), mRNA. /// NM_003965 // upstream // 8634 //	CCR5	CCR5, Homo sapiens chemokine (C-C motif) receptor 5 (CCR5), p21.31
SNP_A-2176833	caccctctatttgca[C/T]aacaccacctgagaag	C	T	122953 // Homo sapiens jun dimerization protein 2 (JDP2), mRNA. /// NM_006399 // upstream // 41973 // Hs.509964 //	JDP2	JDP2, Homo sapiens jun dimerization protein 2 (JDP2), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2194073	catgacatagcacaaa[C/T]agttctggactaaatg	C	T	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 120203 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2186624	cagggattagaaagat[A/G]ataactacagtagtcc	A	G	Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), mRNA. /// AK025510 // intron // 0 // Hs.463702 //	BCAS3	BCAS3, Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), q23.2
SNP_A-2208370	cccacattcgcctcac[A/G]ggtgacacctcgcatc	A	G	Homo sapiens TNF receptor-associated protein 1 (TRAP1), mRNA. /// ENST00000246957 // intron // 0 // --- // --- // --- // ---	TRAP1	TRAP1, Homo sapiens TNF receptor-associated protein 1 (TRAP1), p13.3
SNP_A-2211958	tcttggtcttctataa[A/G]gctgagggtaaatata	A	G	// 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-2201566	ccaattctctttatac[C/T]gggcattcttaccatc	C	T	7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), mRNA. /// NM_022486 //	UGCG	UGCG, Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), q31.3
SNP_A-2205389	ccagtgagagatggaa[A/G]ctcggacccgagtgca	A	G	// 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 82365 //	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-2223179	cgccgagcagatctca[C/G]gtggacacagattcag	C	G	79149 // Homo sapiens zinc finger protein 495 (ZNF495), mRNA. /// ENST00000254165 // upstream // 58501 // --- // ---	ZSCAN5	ZSCAN5, Homo sapiens zinc finger protein 495 (ZNF495), q13.43
SNP_A-2156661	attctgctgcttcgtg[C/T]accctgaacccaaaca	C	T	Homo sapiens transcriptional activator of the c-fos promoter (CROC4), mRNA. /// ENST00000320269 // intron // 0 // --- // ---	CROC4	CROC4, Homo sapiens transcriptional activator of the c-fos promoter (CROC4), q22
SNP_A-2120201	agtcaggaagagaatg[A/G]aaacggaatgccagat	A	G	Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // --- // --- // --- // ---	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-1832562	tacaaatgccaaagaa[C/T]gttctcagttgaacat	C	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1840912	tagctcttaccttcaa[A/G]gatattaaaattagca	A	G	1906 // Homo sapiens endothelin 1 (EDN1), mRNA. /// NM_002948 // upstream // 123001 // Hs.381219 // RPL15 //	EDN1	EDN1, Homo sapiens endothelin 1 (EDN1), p24.1
SNP_A-1826291	taaattgtaagccaac[C/T]cgtttgcaggataaaa	C	T	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1127698 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1702517	gcatgtttgattttgttctatgaaa[C/T]atggatttgctcagaagaatcctcc	C	T	// klotho /// NM_015032 // downstream // 130225 // Hs.168625 // APRIN // 23047 // androgen-induced	KL	KL , rs10492400, klotho ,q13.1
SNP_A-1809630	gtgagcacaagtcaac[A/G]gagatttggctcactc	A	G	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1922155	ttacttagtattgagc[G/T]agctgttgcttaatat	G	T	Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1900978	tggatactattgaatc[A/G]aattttcaaacattta	A	G	ENST00000318671 // intron // 0 // --- // --- // --- // ---	-	q13.1
SNP_A-1893267	tgcagataattgagtc[C/G]cccagaattatgcagg	C	G	Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) mRNA, complete cds. /// NM_002977 // downstream // 81808 // Hs.2319 // SCN9A // 6335 // Homo	SCN1A	SCN1A, Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) complete cds. q24.3
SNP_A-1877989	tctgtaaattcttcta[C/T]agtcacttagattccc	C	T	Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // 3UTR // 0 // Hs.150595 // CYP26A1 // 1592 //	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-1884758	tgaatcaaacggaaga[A/C]gttcctaggaatgttg	A	C	90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 2023 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1943550	ttgtaacaattgcacc[A/G]aagatcatgtttgcat	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 303591 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1960737	tttttctgaaagtagg[G/T]acaaactcatattcca	G	T	80264 // Homo sapiens zinc finger protein 430 (ZNF430), mRNA. /// ENST00000261560 // downstream // 2210 // --- // ---	ZNF430	ZNF430, Homo sapiens zinc finger protein 430 (ZNF430), p12
SNP_A-1964254	tttggatgtatttata[C/T]ggcaccctctcatgcc	C	T	4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// NM_000993 // upstream // 4429 //	NPAS2	NPAS2, Homo sapiens neuronal PAS domain protein 2 (NPAS2), q11.2
SNP_A-1965432	ttttgatattccctga[C/G]cttcttgaatatatgg	C	G	ARL6IP6 // 151188 // Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), mRNA. ///	ARL6IP6	ARL6IP6, Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), q23.3
SNP_A-1975729	gacactattccttcac[A/C]atgatgaaagttgata	A	C	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 529181 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1875264	tctctcttagaaccct[C/G]agagcaaccatgccct	C	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1348212 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1896371	tgctaagcagaatgca[A/G]tattctaaaatctgaa	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813474	gtggttgttatagata[A/C]aaatattggagactag	A	C	2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 54403 // Hs.33446 // NR5A2 //	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-1803259	gtattgagttcattaa[A/T]ggttattatcatcgtg	A	T	ENST00000356562 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1790255	ggggagattatcctgc[A/G]aactgttgaccttcct	A	G	10736 // Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA. /// NM_018079 // downstream //	SIX2	SIX2, Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), p21
SNP_A-1873224	tctatttagaaacacg[A/G]atttacttagaagtca	A	G	Homo sapiens FLJ44874 protein (FLJ44874), mRNA. /// NM_002527 // upstream // 64757 // Hs.99171 // NTF3 // 4908	-	-, Homo sapiens FLJ44874 protein (FLJ44874), p13.31
SNP_A-1848039	tatctgtatttcagaa[C/T]gtgaagtctcactggg	C	T	Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST00000263915 // intron // 0 // --- // ---	GRB14	GRB14, Homo sapiens growth factor receptor-bound protein 14 (GRB14), q24.3
SNP_A-1846962	tatcagaagttatcta[C/G]gttacttgaagatgaa	C	G	51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 3734 // Hs.461453 // WWOX //	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1851389	tattccagaggattca[A/T]gttacttggattaatc	A	T	Homo sapiens leucyl-tRNA synthetase 2, mitochondrial (LARS2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000265537 // intron // 0 // --- // --- // --- // ---	LARS2	LARS2, Homo sapiens leucyl-tRNA synthetase 2, mitochondrial (LARS2), nuclear gene encoding mitochondrial protein, p21.31
SNP_A-2114629	agggagtgagtgtcaa[A/G]gcgcaggtcccaccct	A	G	/// ENST00000315208 // upstream // 134544 // --- // --- // --- // -	-	q24.32
SNP_A-2162309	attttatcttcctgac[C/T]atcttaggaaaacttc	C	T	Homo sapiens mRNA for KIAA0456 protein, partial cds. /// ENST00000295713 // intron // 0 // --- // --- // --- // ---	SRGAP2	SRGAP2, Homo sapiens for KIAA0456 protein, partial cds. ,q32.1
SNP_A-2161778	atttgtatcttaaaag[C/T]acagagctgagacttc	C	T	55128 // Homo sapiens ring finger protein 137 (RNF137), mRNA. /// NM_001004751 // upstream // 11572 // --- //	TRIM68	TRIM68, Homo sapiens ring finger protein 137 (RNF137), p15.4
SNP_A-2148678	atggtcaaatggtaac[A/G]gactagaaaatctatg	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 400405 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.1
SNP_A-2185427	caggaccacaggaaga[C/T]gagggcccacgatgag	C	T	// 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 772322 // Hs.514980 // SALL3 //	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2191643	catattaacagaaaca[C/T]gacaagcactttctcc	C	T	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 528606 // --- // --- // --- //	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2175502	cacatctccgtttaca[C/T]agaaaaatgctctttt	C	T	59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 368636 // Hs.32966 // GUCA2B // 2981 // Homo	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-2168846	caagactcctgcttga[C/G]acagtggagcaaaaag	C	G	28984 // Homo sapiens response gene to complement 32 (RGC32), mRNA. /// ENST00000341475 // downstream //	RGC32	RGC32, Homo sapiens response gene to complement 32 (RGC32), q14.11
SNP_A-2073348	acaggtaagaaaatca[C/T]gttcatttcagaattg	C	T	Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA. /// ENST00000357493 // intron // 0 // --- // -	ATP8B1	ATP8B1, Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), q21.31
SNP_A-2069751	gtggtcaactgagtaa[A/G]taacatgtaaatattt	A	G	// 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// NM_003583 // upstream // 269011 // Hs.173135 //	TIP120A	TIP120A, Homo sapiens TBP-interacting protein (TIP120A), q14.3
SNP_A-2087479	actgcccagatggtgc[C/T]aatggcagttcaaagg	C	T	sapiens major vault protein (MVP), transcript variant 2, mRNA. /// NM_017458 // intron // 0 // Hs.513488 // MVP //	MVP	MVP, Homo sapiens major vault protein (MVP), transcript variant 2, p11.2
SNP_A-2008876	atctgctcacctagga[A/C]agatgctgcttgctgc	A	C	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 807006	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2044561	aagaaacaggcctacc[A/G]acaacttgaatttagc	A	G	/// ENST00000360919 // upstream // 157873 // --- // --- // --- //	-	q13.1
SNP_A-2303848	gctcagtgttatataa[C/T]tgctaaagctaatgac	C	T	9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 40337 //	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-2298777	gcccatacaagcccca[A/G]gttcagccaaagctga	A	G	ENST00000344938 // intron // 0 // --- // --- // --- // ---	-	p16.2
SNP_A-2276151	gagagagaacacccac[A/G]agtgtccaaaacctat	A	G	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 390545	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2279471	gaggatctgggataca[A/C]aacacagcccatctac	A	C	8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 351989 // Hs.127013 // CADPS // 8618 // Homo	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2284350	gatatttgaaagatag[C/G]agaaataggagaaatg	C	G	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// ENST00000264377 // intron // 0 // --- //	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2271153	gacatcgtcaaaagag[A/G]cattgttagcaaatga	A	G	// 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2237900	ctctgacccccctggaa[A/C]gctgtgatgacatcag	A	C	144347 // Homo sapiens hypothetical protein LOC144347 (LOC144347), mRNA. /// ENST00000338359 // intron // 0 // ---	LOC144347	LOC144347, Homo sapiens hypothetical protein LOC144347 (LOC144347), q24.31
SNP_A-2239819	ctgaaattgaagtgac[A/C]ctcatctttgttgaag	A	C	ENST00000332168 // intron // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2235160	ctccccaggcacagcc[A/G]agaggaaaggagcaga	A	G	Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, mRNA. /// NM_004631 // intron // 0 // Hs.444637 // LRP8 //	LRP8	LRP8, Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, p32.3
SNP_A-2267131	ctggcccaggttttca[C/T]gtctgtgtgccttact	C	T	ENST00000300172 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2282323	gagttattgctcttag[A/C]actggactagctgttc	A	C	ENST00000297227 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-2282627	gagtttctctgctttg[A/G]caaactaactgtagta	A	G	Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, mRNA. /// NM_004370 // intron // 0 //	COL12A1	COL12A1, Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, q13
SNP_A-2281036	gagtaagaagttctaa[A/G]tggtagctatgattaa	A	G	sapiens nuclear factor I/A (NFIA), mRNA. /// AB037860 // intron // 0 // Hs.191911 // NFIA // 4774 // Homo sapiens	NFIA	NFIA, Homo sapiens nuclear factor I p31.3
SNP_A-2297327	gccacgtctcgcataa[A/C]catatttggtacaggc	A	C	Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// ENST00000301776 // intron // 0 // --- // --- // --- // ---	ASRGL1	ASRGL1, Homo sapiens asparaginase like 1 (ASRGL1), q12.3
SNP_A-2040089	aaccaaagctgaatcc[A/G]cagttcatgttctttg	A	G	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2023605	aaaactgagatgaaga[A/G]aaactcaatgatcttc	A	G	6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 109905 // Hs.175905 // AUH	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2097825	agagactctgcacaaa[A/G]tcctcgggctctcaac	A	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2094022	agaagctgccagtagg[A/G]acttagaactgtagta	A	G	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1
SNP_A-2102509	agattgaccgacatac[A/G]cattgcacaaagcact	A	G	sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 //	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-2064343	aattcatacttttttc[C/T]agccccactgctgctg	C	T	Homo sapiens chromobox homolog 1 (HP1 beta homolog Drosophila) (CBX1), mRNA. /// ENST00000225603 // intron //	CBX1	CBX1, Homo sapiens chromobox homolog 1 (HP1 beta homolog Drosophila) (CBX1), q21.32
SNP_A-2216621	cctctcaaaccaacca[A/G]ggcaccagatggagtt	A	G	// 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 391274 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-2215804	cctcatgcttggagca[C/T]taaatgaggcttcatc	C	T	9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// NM_173827 // downstream // 424672 // Hs.356697 // FLJ38991 //	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-2161878	atttgtgagtttggaa[A/G]aagaaactggaggcac	A	G	/// ENST00000336930 // upstream // 1205844 // --- // --- // --- //	-	p14.3
SNP_A-2160360	atttcaggttacaaaa[A/G]atagacatagagttgt	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2111822	aggatagttggtggct[C/T]acttcaaaaaggcccc	C	T	23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 244882 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2120254	agtcagtccagagccc[C/T]ggcaaaagagatcttt	C	T	FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2130596	atactgactacataac[A/G]cgttatacttaggggg	A	G	4179 // Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, mRNA. /// NM_172357 // downstream // 8225 // Hs.510402 // MCP // 4179	MCP	MCP, Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, q32.2
SNP_A-1857592	tcactcgggtgagccc[A/G]gcatgtctcaagcttg	A	G	64321 // Homo sapiens SRY (sex determining region Y)-box 17 (SOX17), mRNA. /// ENST00000297316 // downstream //	SOX17	SOX17, Homo sapiens SRY (sex determining region Y)-box 17 (SOX17), q11.23
SNP_A-1829000	taaggctgccataaca[A/G]actatgataaattaga	A	G	8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 206672 //	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1819509	gttggtcacaaataaa[C/T]tacaccagcttgttgc	C	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 828446 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1843360	tagtctttctctctcc[A/G]ctcctgcccttgtggt	A	G	// 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 392805 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1830300	taatatatgggtcaaa[C/T]tagaaaaaaacaggca	C	T	ENST00000281496 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-1802455	gtatccagatagtaca[C/G]cagaaaccattcccag	C	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1555524 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1670251	gattgttctggcaagtacttcccta[C/T]gttaaaaaggagctgtgagagtggg	C	T	4857 // neuro-oncological ventral antigen 1 /// NM_006489 // downstream // 92004 // Hs.292511 // NOVA1 // 4857 // neuro-	NOVA1	NOVA1 , rs4133932, neuro-oncological ventral antigen 1 ,q12
SNP_A-1784874	ggccttctttcactca[C/T]cacatcccttgggggc	C	T	64787 // Homo sapiens EPS8-like 2 (EPS8L2), mRNA. /// NM_006755 // upstream // 4924 // Hs.438678 // TALDO1 //	EPS8L2	EPS8L2, Homo sapiens EPS8-like 2 (EPS8L2), p15.5
SNP_A-1892115	tgcaaagcataatagc[A/G]acatatttctgaatat	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-1900884	tggagttgcttctgaa[C/T]ctcttaaccaagacag	C	T	1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 192654 //	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-1904397	tggggaaacagcaaag[A/G]aggtgttcctagtttc	A	G	Homo sapiens chloride channel, calcium activated, family member 1 (CLCA1), mRNA. /// ENST00000234701 // intron // 0 // --- // --- // --- // --- /// ENST00000353619 // intron // 0 // --- //	CLCA1	CLCA1, Homo sapiens chloride channel, calcium activated, family member 1 (CLCA1), p22.3
SNP_A-1888477	tgaggacatcaacttc[A/G]actttcttccaccccc	A	G	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), mRNA. /// ENST00000341163 // intron // 0 // --- // --- // --- // --- /// ENST00	AGPAT2	AGPAT2, Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), q34.3
SNP_A-1931917	ttcctaaagttctgaa[A/G]tccttgaccatcgaag	A	G	// 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 439911 // Hs.444075 // STS-1 //	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-1975647	gctgccttattatcac[C/T]gaaacagctttggcct	C	T	4026 // Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), mRNA. /// ENST00000312675 // downstream // 85717 // --- // --- // --- // --	LPP	LPP, Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), q28
SNP_A-1974267	gcccagcttcgacccc[C/T]gagtctgctcccactc	C	T	Homo sapiens solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8), mRNA. ///	SLC12A8	SLC12A8, Homo sapiens solute carrier family 12 (potassium q21.2
SNP_A-1978055	catctttttaaatgtg[A/C]aaaatcaacgctcaaa	A	C	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1934939	ttctgacccaagtcca[G/T]ctgtcagtaacagccg	G	T	9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // upstream //	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-1950358	tttcaggaaaattaaa[A/T]gagaccaaaaatgcag	A	T	// 25950 // Homo sapiens RWD domain containing 3 (RWDD3), mRNA. /// ENST00000354428 // downstream //	RWDD3	RWDD3, Homo sapiens RWD domain containing 3 (RWDD3), p21.3
SNP_A-1922642	ttagactgcacatgca[A/C]atttgtcaatgaaggt	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1630061 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1887132	tgagaaactgaagcca[C/T]gttctttgcccaaggc	C	T	51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 83736 // Hs.461453 // WWOX //	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1885635	tgacactaggacctca[A/C]ctctactgtacacgtg	A	C	23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 214036 // Hs.434255 // PSD3 //	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-1874855	tctcgtcttgcttttg[A/G]actggaatttacacca	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-1809489	gtgagacaactctgac[A/G]ggggattctgacttga	A	G	51474 // Homo sapiens epithelial protein lost in neoplasm beta (EPLIN), mRNA. /// ENST00000341247 // upstream //	EPLIN	EPLIN, Homo sapiens epithelial protein lost in neoplasm beta (EPLIN), q13.12
SNP_A-1820038	gttatgatagaggaaa[A/G]agggttagaaggtggc	A	G	ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // upstream // 233629 // Hs.188746 // ADAM	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip ,q23.1
SNP_A-1856158	tcacaaatcagtatga[A/G]gaaattaactattgcc	A	G	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 304309 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1848172	tatcttcctctttccc[C/T]gattcaacatcattaa	C	T	3280 // Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), mRNA. /// ENST00000351516 //	HES1	HES1, Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), q29
SNP_A-2156615	attctgcaaatagagc[A/G]attttatattaccaga	A	G	-- /// ENST00000356117 // downstream // 472791 // --- // --- //	-	q23.31
SNP_A-2152673	attaatatgcataaaa[C/T]cgcagttgttctaaag	C	T	sapiens KIAA0045 mRNA, partial cds. /// ENST00000283943 // intron // 0 // --- // --- // --- // ---	TRIP12	TRIP12, Homo sapiens KIAA0045 partial cds. ,q36.3
SNP_A-2224327	cgtaactcacaaacac[A/G]cttccaaactctgttt	A	G	MGC34732 // 220047 // Homo sapiens hypothetical protein MGC34732 (MGC34732), mRNA. /// NM_007166 //	MGC34732	MGC34732, Homo sapiens hypothetical protein MGC34732 (MGC34732), q14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2200851	ccaagatgtgggtgct[A/G]aaatgggctagggctt	A	G	55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // downstream // 463638 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.2
SNP_A-2071704	acagaatttctgtgta[A/G]ggtaatgaaaaggtta	A	G	ENST00000308537 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-2049299	aagctccatcaaagga[G/T]taggtatatctcttat	G	T	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2050621	aaggcaagaaatacaa[A/C]ttagatgacttaggaa	A	C	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2085470	actccaccaacctcac[A/G]agtttctaacacccag	A	G	130916 // Homo sapiens hypothetical protein MGC61716 (MGC61716), mRNA. /// ENST00000310397 // 3UTR // 0 // ---	MGC61716	MGC61716, Homo sapiens hypothetical protein MGC61716 (MGC61716), q37.3
SNP_A-2031854	aaagtcaagtagtaca[A/G]aataatgtacagtgaa	A	G	2918 // Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// NM_176814 // downstream // 88227 //	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-2028424	aaactcgtgcagctca[A/G]taataagacaaataat	A	G	Homo sapiens solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member	SLC35D1	SLC35D1, Homo sapiens solute carrier family 35 (UDP-glucuronic acid p31.2
SNP_A-2040179	aaccaagttacctgtg[A/G]aaaggaagcccgaagt	A	G	Homo sapiens lysophospholipase I (LYPLA1), mRNA. /// ENST00000316963 // CDS // 0 // --- // --- // --- // --- ///	LYPLA1	LYPLA1, Homo sapiens lysophospholipase I (LYPLA1), q11.23
SNP_A-2011572	gtcaggctcccaacaa[A/G]gacatgaaggagcctt	A	G	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 247729 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-1997943	gctcatcctgaagagg[C/T]aagagtgaaggcaaaa	C	T	H.sapiens mRNA HTPCRX15 for olfactory receptor. /// ENST00000335302 // intron // 0 // --- // --- // --- // ---	OR1J2	OR1J2, H.sapiens HTPCRX15 for olfactory receptor. ,q33.2
SNP_A-2233301	ctcaggcagcctgcca[A/T]cgtcgaccacctgggg	A	T	// 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 6985 // Hs.132344 //	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2259041	ctttttttctcaaggtg[A/G]actcactaacatcgaa	A	G	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2303117	gctataggagaaagga[C/G]gaacaagaaatacatt	C	G	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 493930 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2000643	cagtgtccctattgca[C/T]tgaattgtgtaaacct	C	T	ENST00000358195 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2007144	aatcaaaaagaaacag[A/T]catggggttatgttgc	A	T	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-2028300	aaactcaaatcccaga[A/C]tatctcttcccatttc	A	C	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 163921 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2106279	tctctttctcctcaca[C/T]agttaagcacttgcac	C	T	-- /// ENST00000345111 // upstream // 449968 // --- // --- // ---	-	q24.31
SNP_A-2096803	agactattctaatcct[A/G]aaaacttcaccaatga	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 369169 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2207424	ccattggcaactaaca[A/C]gaattgtacaaaacca	A	C	407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 452675 // Hs.24115 // C13orf25 //	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2189134	cagttagaaacatcta[A/C]actgggtgttaagtag	A	C	// 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 151210 //	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-2151183	atgtgttttatttcag[A/G]aaaggaaatctctaac	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), mRNA. /// ENST00000282833 // intron // 0 // --- // ---	PTPRK	PTPRK, Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), q22.33
SNP_A-2128532	ataatacccagctaaa[C/T]gccctcactagtcatc	C	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1819977	gttgttgctgctcggg[A/C]caaagcaacctcttcc	A	C	2355 // Homo sapiens FOS-like antigen 2 (FOSL2), mRNA. /// ENST00000265539 // downstream // 32065 // --- // --- // --- // ---	FOSL2	FOSL2, Homo sapiens FOS-like antigen 2 (FOSL2), p23.2
SNP_A-1879742	tcttcatgcccagaag[C/G]ctctccaacagtcccc	C	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1893023	tgcactgattctatca[C/T]attttcaaacttttcc	C	T	7481 // Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), mRNA. /// NM_004705 // downstream // 105203 // Hs.503315 // PRKRIR // 5612 //	WNT11	WNT11, Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), q13.5
SNP_A-1924642	ttatagatgttgctaa[C/T]tggatccaaacgggtt	C	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 969057 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1929853	ttcatctctaccataa[C/G]tgtaacaataaatgac	C	G	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1324233 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1961036	tttttggttcatggaa[C/T]acatatttcggcctgt	C	T	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1956888	ttttaactttcccatc[C/T]aataaatttaccaatt	C	T	CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 412100 // Hs.522891 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1934179	ttctcatgttcatcca[C/T]tggacagttggctctc	C	T	LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1984393	acttggcggtacagca[C/T]aagggaacagccccac	C	T	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 248715 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1989430	tgagacttaatttttta[C/T]gtaatatgtcttggat	C	T	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1942021	ttggataacagactga[C/T]agttttatttgcataa	C	T	lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // --- // --- // --- // --- ///	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. ,q13.1
SNP_A-1948591	tttataaacagaatga[C/T]atgatgtctgaaattt	C	T	285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 40050 // --- //	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-1913958	tgtgtgagtagcattc[G/T]caatgaaatgtagtcc	G	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1844053	tagttgatgcttacta[C/T]agagacgtactataat	C	T	2315 // Homo sapiens melan-A (MLANA), mRNA. /// ENST00000251879 // downstream // 90322 // --- // --- // --- // --	MLANA	MLANA, Homo sapiens melan-A (MLANA), p24.1
SNP_A-1863727	tccaagactgtttcaa[A/G]ttccaaatacatggat	A	G	// 163782 // Homo sapiens hypothetical protein LOC163782 (LOC163782), mRNA. /// NM_003368 // upstream // 33719 //	LOC163782	LOC163782, Homo sapiens hypothetical protein LOC163782 (LOC163782), p31.3
SNP_A-1860708	tcataaatcttcagga[C/G]agaccgttaagatcac	C	G	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 404557	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1805078	gtcatgattgtttagg[A/G]cagcctgtaactagtg	A	G	Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), mRNA. /// ENST00000265195 //	SIL1	SIL1, Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), q31.2
SNP_A-1791562	gggtcagattcaacta[C/G]cacctcctggctaatc	C	G	// 27309 // Homo sapiens zinc finger protein 330 (ZNF330), mRNA. /// NM_000585 // upstream // 319018 // Hs.311958 //	ZNF330	ZNF330, Homo sapiens zinc finger protein 330 (ZNF330), q31.21
SNP_A-1655743	gtctttatctctttaactttagccc[A/G]aatgactgggataaaagacaagaaa	A	G	NM_001463 // CDS // 0 // Hs.128453 // FRZB // 2487 // frizzled-related protein	FRZB	FRZB , rs288326, frizzled-related protein,q32.1
SNP_A-2123708	agtgttgaagtaggaa[C/T]agaaaaaagaaagtca	C	T	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 1, mRNA. /// NM_198794 // intron // 0 // Hs.130491 // MAP4K5 // 11183 //	MAP4K5	MAP4K5, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 1, q21.3
SNP_A-2112709	aggcagcactttgccc[A/G]cttattccatgtaagg	A	G	1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 55775 //	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2145164	atgcaagtgtatgaac[A/G]agtgaaaaatggaaaa	A	G	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// ENST00000199936 // intron // 0 // --- //	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-2166879	caaatttggctctaaa[C/G]tcttctgaggccaaat	C	G	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2167896	caaccttcacatttac[A/G]acctcagtttcatcat	A	G	1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // downstream //	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-2198399	catttaattttgtgat[C/T]ataagttacacgtgaa	C	T	OLFML2A // 169611 // Homo sapiens olfactomedin-like 2A (OLFML2A), mRNA. /// ENST00000331715 // downstream //	OLFML2A	OLFML2A, Homo sapiens olfactomedin-like 2A (OLFML2A), q33.3
SNP_A-2173447	cacaagtgtctttcaa[A/G]gagaagtgaaaaccct	A	G	57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream //	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2176706	cacccctttttctaac[C/T]ccaatcgactttgtgg	C	T	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), mRNA. /// ENST00000353125 // intron // 0 // --- // --- // --- // --- /// ENST00000360359 // intron // 0 // ---	ANKS1	ANKS1, Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), p21.31
SNP_A-2181854	cagagcagtgcagata[G/T]cttccttcttgagaaa	G	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 917939 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2224439	cgtagcatttaacaca[C/T]ggcagtgtaacaatgc	C	T	-- /// ENST00000359634 // upstream // 655573 // --- // --- // --- // --- /// ENST00000359181 // upstream // 655573 // --- // --- //	-	q32.3
SNP_A-2088122	tctttccagtcttcca[A/G]ctcaattcgtaaaaca	A	G	Homo sapiens angiopoietin-like 3 (ANGPTL3), mRNA. /// ENST00000294618 // intron // 0 // --- // --- // --- // --- ///	ANGPTL3	ANGPTL3, Homo sapiens angiopoietin-like 3 (ANGPTL3), p31.3
SNP_A-2083854	actacgtgtaagtaga[A/G]tcatacagcatctcct	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 954585 // --- // --	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2051102	agatcctttggaggtc[A/C]atcctggagtcattgt	A	C	144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000331366 // upstream // 252453 // --- // --- // --- // ---	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072867	acagcttgagggtcga[C/T]actgggcttgcagctg	C	T	IGHMBP2 // 3508 // Homo sapiens immunoglobulin mu binding protein 2 (IGHMBP2), mRNA. /// NM_198923 //	IGHMBP2	IGHMBP2, Homo sapiens immunoglobulin mu binding protein 2 (IGHMBP2), q13.3
SNP_A-2071886	acagagagagagtgaa[C/T]gcatgaatgaacgtag	C	T	ENST00000327381 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2027505	aaaccaagctgatttc[C/T]acccaatagcccttga	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2032933	aaataatcacagcata[C/T]ctttatcaagtctcca	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2461387 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2017437	gtcataataggcgaca[A/G]gtattccttaaaaaga	A	G	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2014013	ttgtttgtagatgtta[C/T]gatcctatatctagaa	C	T	3641 // Homo sapiens insulin-like 4 (placenta) (INSL4), mRNA. /// NM_005059 // downstream // 10960 // Hs.127032	INSL4	INSL4, Homo sapiens insulin-like 4 (placenta) (INSL4), p24.1
SNP_A-2000492	aggggctgaggggacc[A/G]atattttggcacattt	A	G	// 64326 // Homo sapiens constitutive photomorphogenic protein (COP1), transcript variant 2, mRNA. /// NM_022457 // upstream // 95367 // Hs.523744 // RFWD2 // 64326 // Homo	RFWD2	RFWD2, Homo sapiens constitutive photomorphogenic protein (COP1), transcript variant 2, q25.2
SNP_A-2003703	agaacacataaataag[A/G]agcaaatttctccaca	A	G	Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // --- //	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-1996334	taatggatgatgaaag[A/G]agaagctgtgaacaga	A	G	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 314358 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2304548	gctctccaagccccca[C/T]gtttacctcttatagc	C	T	3587 // Homo sapiens interleukin 10 receptor, alpha (IL10RA), mRNA. /// NM_183247 // upstream // 21173 //	IL10RA	IL10RA, Homo sapiens interleukin 10 receptor, alpha (IL10RA), q23.3
SNP_A-2308796	gctttgctaagtaata[A/G]ggataccagtatgaat	A	G	4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 431765 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2290354	gcaacataatagacaa[C/T]agacaaacaagataat	C	T	145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 238133 // Hs.87889 // DICER1	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2288130	gattcaggaacaaaaa[A/G]tcaactaaggctatga	A	G	219477 // Homo sapiens olfactory receptor, family 8, subfamily J, member 1 (OR8J1), mRNA. /// NM_001005204 //	OR8J1	OR8J1, Homo sapiens olfactory receptor, family 8, subfamily J, member 1 (OR8J1), q11
SNP_A-2259790	gaaaagattcctggga[A/G]atgaagaaagagagct	A	G	// 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 171516	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2261086	gaaagacacacagatt[A/G]aataattgtaaaagag	A	G	// 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 //	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-2236628	ctctaacaagacagga[A/G]ctaaagagatttgcaa	A	G	// 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2238929	ctcttccaacccttta[A/T]gaataatcgtgtaaga	A	T	8638 // Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, mRNA. /// NM_003733 // upstream // 60636 // Hs.118633 // OASL // 8638 // Homo	OASL	OASL, Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, q24.31
SNP_A-2244329	ctggaaggaagaacac[A/G]gccattccggagggtc	A	G	ENST00000288676 // intron // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-2243605	ctgctcagtcttgcta[C/T]gtgaactgtattttca	C	T	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-2261823	gaaataaaaggacata[A/T]gacagtaacttgaatt	A	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2260434	gaaacacaattcctac[A/G]ctgccccctctttccc	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2291864	gcacaggtgttcacag[A/G]aaatgtgccttgtccc	A	G	55140 // Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), mRNA. /// NM_006228 // upstream //	ELP3	ELP3, Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), p21.1
SNP_A-2314863	ggagtggggatgctgc[A/G]gagttaaatggcaagg	A	G	80852 // Homo sapiens mRNA for KIAA1719 protein, partial cds. /// NM_016474 // upstream // 31849 // Hs.517820 //	GRIP2	GRIP2, Homo sapiens for KIAA1719 protein, partial cds. ,p25.1
SNP_A-2310979	ggaagggaagggaata[C/T]ccaacagaagtctgag	C	T	ARL6IP6 // 151188 // Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), mRNA. ///	ARL6IP6	ARL6IP6, Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), q23.3
SNP_A-1992591	agttattacaaaaaca[A/G]actgtgacacaaaaat	A	G	55790 // Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), mRNA. ///	ChGn	ChGn, Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), p21.3
SNP_A-2011714	cggtcatctagctcag[C/G]acagtgacttctctcc	C	G	266727 // Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), mRNA. /// NM_021943 // upstream // 64470 // Hs.36959 // TEX27 //	MDGA1	MDGA1, Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), p21.2
SNP_A-2225629	ctaaacacatcagcaa[C/G]gacgaaacaaatcagc	C	G	Homo sapiens serine/threonine kinase 24 (STE20 homolog, yeast) (STK24), mRNA. /// ENST00000261573 // intron // 0 //	STK24	STK24, Homo sapiens serine,q32.2
SNP_A-2216825	cctctgaggaatgtac[A/C]cgtcatgctctaagat	A	C	Homo sapiens calpain 13 (CAPN13), mRNA. /// ENST00000295055 // intron // 0 // --- // --- // --- // --- ///	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209836	ccccaaagaacataga[A/G]gtcaatttgaaggaaa	A	G	ENST00000358682 // intron // 0 // --- // --- // --- // ---	-	q14
SNP_A-2177612	cacggactaaacacca[C/T]aagctgttgtatgcaa	C	T	Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, mRNA. /// ENST00000256772 // intron //	CRB1	CRB1, Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, q31.3
SNP_A-2192481	catcatttcccagaca[C/T]tgagtaacttcaaatg	C	T	Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) mRNA, complete cds. /// NM_002977 // downstream // 68766 // Hs.2319 // SCN9A // 6335 // Homo	SCN1A	SCN1A, Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) complete cds. q24.3
SNP_A-2139957	atctacctacctatcc[C/T]atcatatctatctcta	C	T	// 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-2112086	aggatgtaaaaaagca[C/T]agtatgtccaaaaaac	C	T	Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-2127131	ataaatattactcaaa[A/C]aagtctgatttctgtg	A	C	// Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 373208 // Hs.48297 // RCHY1 // 25898 //	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-2136768	atcactttatctgcca[C/T]tggatacaaaagcagt	C	T	ENST00000299866 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-1791427	gggtagtttttgagca[A/T]tgctattcagtggcta	A	T	// 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream //	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1789582	gggcgcccgagtccta[A/G]gctctgttctgttacc	A	G	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-1793015	ggtaccctgcatctga[C/T]gtcaccgaatgctgga	C	T	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 3 (RAPGEF3), mRNA. /// ENST00000171000 // intron // 0 // --- // --- // --- // ---	RAPGEF3	RAPGEF3, Homo sapiens Rap guanine nucleotide exchange factor (GEF) 3 (RAPGEF3), q13.11
SNP_A-1871525	tctaagaaagaacaga[G/T]tcaaatgctgagtgga	G	T	MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream //	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-1849567	tatgggcttgagagta[C/G]aagacatggttgaaga	C	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1910104	tgtcatccctaattca[C/T]agtgtggcctttacac	C	T	ENST00000297423 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-1930464	ttccaaagacaaccta[C/T]tagaagcagtaagttt	C	T	9061 // Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), mRNA. ///	PAPSS1	PAPSS1, Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), q25
SNP_A-1952402	tttctctttattacac[C/T]acctgaactaaactgg	C	T	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 1110549 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1988520	gctgccaccggcgcac[G/T]ctgcatgccaggcaac	G	T	// 8635 // Homo sapiens ribonuclease T2 (RNASET2), mRNA. /// NM_194429 // downstream // 532240 // Hs.487175	RNASET2	RNASET2, Homo sapiens ribonuclease T2 (RNASET2), q27
SNP_A-1962289	agaatcttgtatccat[C/T]actggccaaagaagta	C	T	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1961999	ccagtaactgtgggaa[C/T]gttatcaaagctctga	C	T	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 221593 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1967886	agctttagagctccca[A/G]tagggtcaccagatgc	A	G	/// ENST00000340000 // upstream // 744078 // --- // --- // --- //	-	p12.1
SNP_A-1950611	tttcatcttcaggcag[C/T]aaaccatctttaaaat	C	T	// 92454 // Homo sapiens hypothetical protein MGC20460 (MGC20460), mRNA. /// ENST00000321736 // upstream //	MGC20460	MGC20460, Homo sapiens hypothetical protein MGC20460 (MGC20460), q36.3
SNP_A-1937443	ttgaaatttgggggaa[A/G]tccaaaaagatggaca	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1923776	ttagtacataaaattc[A/G]aatctgggaccattat	A	G	23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1896439	tgctacaaaactttgc[C/T]cgaatggagctggatt	C	T	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1899038	tggaaaatgtagaaaa[G/T]tgtttaagacatacag	G	T	ENST00000328983 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1871504	tctaactggtgtgaga[C/T]gtaagccttattttat	C	T	Homo sapiens zinc finger protein 347 (ZNF347), mRNA. /// ENST00000334197 // intron // 0 // --- // --- // --- // ---	ZNF347	ZNF347, Homo sapiens zinc finger protein 347 (ZNF347), q13.42
SNP_A-1799253	gtaataaaccttcaca[C/T]gtatcctcaaacctta	C	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 4497 //	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1787607	gggacaaagagttagc[A/G]aaggcctgatagtgat	A	G	81849 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000318803 // intron // 0 // --- // --- // --- // ---	ST6GALNAC5	ST6GALNAC5, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-1781896	ggcaaaaatagatgcc[A/G]catgagttgaaaggat	A	G	// 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream //	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2141667	atcttcccaaaccgca[A/G]tcttttcaaaactgac	A	G	// Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA. /// NM_207385 // downstream // 70498 // Hs.371893	ATBF1	ATBF1, Homo sapiens AT-binding transcription factor 1 (ATBF1), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2151896	atgtttggcactaata[C/T]atctcaaaaacaagtg	C	T	59345 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA. /// NM_004301 // upstream // 30872 // Hs.435326 // ACTL6A // 86 // Homo	GNB4	GNB4, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), q26.33
SNP_A-2152456	attaactgtaagacaa[C/T]agacattgataatgat	C	T	// 91057 // Homo sapiens NY-REN-41 antigen (NY-REN-41), mRNA. /// NM_018362 // downstream // 70994 // Hs.91393 //	NY-REN-41	NY-REN-41, Homo sapiens NY-REN-41 antigen (NY-REN-41), p14.1
SNP_A-2146179	atgcgggtttgtgtcc[A/G]ctcagcctggctgcct	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. ///	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2197693	cattctgtgatatctc[A/G]aaactgtaattgggca	A	G	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2179138	cactggatgccactga[C/T]gtgctctggtaaaacc	C	T	Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // --- // --- // --- // ---	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-2169451	caagcccacagtagta[C/G]aggaaaaagttctgag	C	G	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), mRNA. /// ENST00000280452 // intron // 0 // --- // --- // --- // ---	PIP5K2A	PIP5K2A, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), p12.2
SNP_A-2170656	caagttacatcaaaat[C/T]acctgagtgcttatta	C	T	221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 //	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-2207506	ccatttagcaggttga[G/T]gatgttttcttctatt	G	T	10714 // Homo sapiens polymerase (DNA-directed), delta 3, accessory subunit (POLD3), mRNA. /// NM_015424 // downstream // 40719 // Hs.432379 // CHRDL2 // 25884 //	POLD3	POLD3, Homo sapiens polymerase (DNA-directed), delta 3, accessory subunit (POLD3), q13.4
SNP_A-2205399	ccagtgagtccaaaaa[A/T]tgaattttgattactt	A	T	// 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 159407 // Hs.3232 // CYLC2 //	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-2214958	cctatcttagtggccg[A/C]aggtggctcccaggaa	A	C	9052 // Homo sapiens retinoic acid induced 3 (RAI3), mRNA. /// ENST00000308109 // downstream // 25190 // --- // --- // ---	GPCR5A	GPCR5A, Homo sapiens retinoic acid induced 3 (RAI3), p13.1
SNP_A-2015861	tctctattgatgaaaa[C/T]gtgaatagtttcaaac	C	T	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 120745 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-1990934	gattttaaactagcat[C/G]atctcattgatttcat	C	G	Homo sapiens hypothetical protein FLJ13576 (FLJ13576), mRNA. /// ENST00000312814 // intron // 0 // --- // --- // --- // ---	FLJ13576	FLJ13576, Homo sapiens hypothetical protein FLJ13576 (FLJ13576), q31.1
SNP_A-2026085	aaaattagcatgcctg[C/G]aattcacaacctagta	C	G	sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, mRNA. /// NM_019860 // intron // 0 // Hs.73739 // HTR7 //	HTR7	HTR7, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, q23.31
SNP_A-2058728	aatcatgacttactat[A/C]aactctagtctgtatc	A	C	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2105916	agccatcccagcaagc[A/G]ccgaaagtctgggtta	A	G	51678 // Homo sapiens membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (MPP6), mRNA. /// NM_004403 // downstream // 717 // Hs.520708 // DFNA5 //	MPP6	MPP6, Homo sapiens membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (MPP6), p15.3
SNP_A-2297941	gccagtggggcagaaa[A/G]gttttgtgtaaacaca	A	G	283209 // Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), mRNA. /// NM_005472 // downstream // 37217 //	PGM2L1	PGM2L1, Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), q13.4
SNP_A-2254043	cttgagctcccaattc[A/G]ctttcctttgaagccc	A	G	8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 38347 // Hs.413095	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-2240371	ctgacaaatcccaaca[C/T]aaacccccagctgtat	C	T	ENST00000342537 // intron // 0 // --- // --- // --- // ---	-	q32.33
SNP_A-2228093	ctactaagtgactaat[A/G]agtgggtagtgcacac	A	G	ENST00000255289 // intron // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-2228589	ctagaaattatcaaac[C/T]gtacacttacaatggg	C	T	25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 245857 // Hs.369574 // CDC42EP3 // 10602 //	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-2247477	ctgtctcctaaaactc[A/G]cttgaatccatttta	A	G	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2270107	gacacagcaaagatga[A/G]caatgtgaccttagta	A	G	// 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 //	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-2297148	gccacaggtaataggc[A/G]gatacccagatagaca	A	G	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2304095	gctccatgctgcccaa[C/T]gatgcaccataaaata	C	T	2069 // Homo sapiens epiregulin (EREG), mRNA. /// NM_001657 // upstream // 2752 // Hs.270833 // AREG // 374	EREG	EREG, Homo sapiens epiregulin (EREG), q13.3
SNP_A-2100894	agatatctgtggcaac[C/T]actttgtaagtgaatg	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), mRNA. /// ENST00000295454 // intron // 0	GABRB1	GABRB1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082920	acgtctgttttaccca[A/G]gtgaggccatctgtat	A	G	Homo sapiens replication protein A3, 14kDa (RPA3), mRNA. /// ENST00000223129 // intron // 0 // --- // --- // --- // ---	RPA3	RPA3, Homo sapiens replication protein A3, 14kDa (RPA3), p21.3
SNP_A-2077731	accactgtgggcaact[A/G]agaacacagtccaggc	A	G	2624 // Homo sapiens GATA binding protein 2 (GATA2), mRNA. /// NM_007354 // downstream // 19642 // Hs.194283	GATA2	GATA2, Homo sapiens GATA binding protein 2 (GATA2), q21.3
SNP_A-2077895	accagatgtctttcaa[A/C]ggatgactgattaaac	A	C	FLJ12519 // 84128 // Homo sapiens hypothetical protein FLJ12519 (FLJ12519), mRNA. /// NM_014585 // downstream	FLJ12519	FLJ12519, Homo sapiens hypothetical protein FLJ12519 (FLJ12519), q32.2
SNP_A-2057361	aatatattttagtata[A/C]gtatgacctgtgcaat	A	C	57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 366247 // --- // ---	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-2054998	aataaatctgaaagtc[C/T]atctaggccacaagga	C	T	7587 // H.sapiens ZNF37A mRNA for zinc finger protein. /// ENST00000351773 // downstream // 80115 // --- // --- // --- // ---	ZNF37A	ZNF37A, H.sapiens ZNF37A for zinc finger protein. p11.21
SNP_A-2075233	acatctggaacaatgg[C/G]attcatataaatgaag	C	G	/// ENST00000309379 // upstream // 834950 // --- // --- // --- // ---	-	q21
SNP_A-2062629	aatgtccaaaagttaa[C/T]aaaatagcaaatgaag	C	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1696416 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2033968	aaatcacaagcttaaa[A/T]ggcctgtcaagttatt	A	T	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000360355 // intron // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-2041081	aacctaacctcttcaa[C/G]ataagcagcagaacca	C	G	157983 // Homo sapiens chromosome 9 open reading frame 66 (C9orf66), mRNA. /// NM_203447 // upstream // 98 //	C9orf66	C9orf66, Homo sapiens chromosome 9 open reading frame 66 (C9orf66), p24.3
SNP_A-2041961	aactaatgactgaata[C/G]gattctagtaatgtgg	C	G	Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // --- // --- // --- // ---	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3
SNP_A-2014049	gtggctgcttacttaa[C/T]atttttaaagctatc	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 775052 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2006992	aatgaaagcaatgcta[C/T]attttgtctaatgctt	C	T	2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 190699 // Hs.374243 //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2204803	ccaggccccagagtaa[C/T]gaaggcaaggcttaaa	C	T	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2181844	cagagcaggatttaga[C/T]actctgcagagactgc	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2143219	atgacaagtactttaa[C/T]aactatgtttctgttt	C	T	KHDRBS3 // 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// ENST00000355849 // downstream // 359039 // ---	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.23
SNP_A-2112037	aggatgctagagccaa[A/G]cctcaagggagcctag	A	G	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 898401 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2112526	aggcacatgaatgcta[C/T]ataaacctaaacctcc	C	T	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // intron // 0 // Hs.511265 // SEMA6D // 80031 // Ho	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN ,q21.1
SNP_A-2108025	agctctagtgttctca[A/G]tcagtgtcatcacctt	A	G	mRNA for IgM heavy chain complete sequence. /// ENST00000359542 // intron // 0 // --- // --- // --- // --- ///	IGHM	IGHM, Human for IgM heavy chain complete sequence. ,q32.33
SNP_A-1805443	gtccacccactttgaa[C/T]tgaaagcctcccagaa	C	T	942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // downstream // 67512 // Hs.171182 // CD86 //	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q21.1
SNP_A-1842659	tagtaaaaagatgtga[C/G]cttcttttcttggaca	C	G	57088 // Homo sapiens phospholipid scramblase 4 (PLSCR4), mRNA. /// NM_020359 // downstream // 162804 //	PLSCR4	PLSCR4, Homo sapiens phospholipid scramblase 4 (PLSCR4), q24
SNP_A-1833068	tacacaggaccttaca[A/G]attgtttacttaatgt	A	G	/// ENST00000294964 // upstream // 192473 // --- // --- // --- // ---	-	p21
SNP_A-1815434	gtgttttaaattctga[C/T]ctcaattgtttagaca	C	T	// 114805 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), mRNA. /// NM_052917 // downstream // 3806 //	GALNT13	GALNT13, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), q24.1
SNP_A-1827179	taacctaactaagaca[A/T]aataaccaatcatctt	A	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1321939 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1878597	tctgtgtgaatcaatc[A/C]gaaagctgtaagtaga	A	C	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 226861 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1886014	tgaccaaaatgtattg[A/G]atactcagctatggga	A	G	/// ENST00000251675 // downstream // 282838 // --- // --- // --- // --- /// ENST00000360855 // downstream // 282868 // --- // ---	-	q32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889101	tgagtattcttgtcct[C/G]actttacagataagaa	C	G	5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 83141 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1922948	ttagcaaaggtgaaga[G/T]aaggcagttgaactta	G	T	7027 // Homo sapiens transcription factor Dp-1 (TFDP1), mRNA. /// NM_000705 // upstream // 698776 // Hs.434202 //	TFDP1	TFDP1, Homo sapiens transcription factor Dp-1 (TFDP1), q34
SNP_A-1945317	ttgttacattcacctc[G/T]aggaatatgaaacacc	G	T	Homo sapiens dynamin 3 (DNM3), mRNA. /// ENST00000358155 // intron // 0 // --- // --- // --- // --- ///	DNM3	DNM3, Homo sapiens dynamin 3 (DNM3), q24.3
SNP_A-1961922	ggccagccaaaacttc[A/G]cggggagaggaagaag	A	G	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 166593 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1921198	ttacatcaggaccaca[A/G]atgagaagaggacaag	A	G	8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 233431 // Hs.370359	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1883370	tgaacacatggctttc[A/G]atgcccagggattttc	A	G	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 40841 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1875019	tctctatcccattaac[C/G]attttatcttcttcat	C	G	64759 // Homo sapiens tensin-like SH2 domain containing 1 (TENS1), mRNA. /// NM_022748 // upstream // 308470 //	TENS1	TENS1, Homo sapiens tensin-like SH2 domain containing 1 (TENS1), p12.3
SNP_A-1871377	tctaaatctgatgaaa[A/G]ccattaagccacagat	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // --- //	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1787814	gggacctggcaatgac[C/T]ggttatcagtagatac	C	T	// 349136 // Homo sapiens hypothetical protein LOC349136 (LOC349136), mRNA. /// NM_144727 // downstream // 3528	LOC349136	LOC349136, Homo sapiens hypothetical protein LOC349136 (LOC349136), q36.1
SNP_A-1793180	ggtagacagcaggccg[C/T]cgatcagcacttgtta	C	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1758408	aaacatacacatatacatacaatta[C/T]ctctctgacaaaaactgcagcatat	C	T	51691 // LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) /// NM_033427 // upstream // 272007 //	LSM8	LSM8 , rs7779197, LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) ,q31.31
SNP_A-2132749	atataaaggatttgag[C/T]agcatccagtgtgtct	C	T	114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream //	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-2178294	cactcacgtattcata[C/T]aattactgtgaaatta	C	T	256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // --- // --- // --- // --	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-2169171	caagatggaagcagaa[A/G]tgcaggataaaggtga	A	G	-- /// ENST00000340000 // upstream // 93222 // --- // --- // --- //	-	p12.1
SNP_A-2186448	cagggaacaagacaca[A/C]aggtgcctgctctctc	A	C	6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 8699 // --- // --- //	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2206740	ccatgattttgagttc[A/G]aagcttctaagaagga	A	G	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 1, mRNA. /// NM_021777 // intron // 0 // Hs.528304 // ADAM28 // 10863 // Homo sapiens	ADAM28	ADAM28, Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 1, p21.2
SNP_A-2208901	cccagcaatcagttca[A/G]tcattggaagctccca	A	G	/// ENST00000330888 // upstream // 9617 // --- // --- // --- // ---	-	q22.1
SNP_A-2014047	tatgcacttataaaca[C/T]ggttatgtgcctctga	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 774756 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2015656	catacatacatacata[A/C]gggttgatatttaggg	A	C	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// NM_006806 // downstream //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2027318	aaacatctattaaccg[A/T]aagtcatgatccttca	A	T	57223 // Homo sapiens KIAA1387 protein (KIAA1387), mRNA. /// NM_033109 // downstream // 112 // Hs.388733 //	KIAA1387	KIAA1387, Homo sapiens KIAA1387 protein (KIAA1387), p16.1
SNP_A-2064634	aattctattgaatgtg[C/G]aaaattgtgagcctgt	C	G	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2069109	acaattaaagaacctg[C/T]accaatgcatgggacc	C	T	55031 // Homo sapiens ubiquitin specific protease 47 (USP47), mRNA. /// ENST00000250515 // upstream // 32117	USP47	USP47, Homo sapiens ubiquitin specific protease 47 (USP47), p15.3
SNP_A-2048420	aagcagtgtttccaaa[C/G]tgtccaatcataaaca	C	G	// --- /// ENST00000355326 // downstream // 431329 // --- // --- // --- // --- /// ENST00000332323 // downstream // 635273 // ---	-	q11.21
SNP_A-2084196	actaggctttcaattg[C/G]agatttagacttggag	C	G	Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000316738 // intron // 0 // ---	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-2092934	agaacaaggtatcttc[C/T]actaattcccttcaaa	C	T	ENST00000262042 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-2303190	gctatcctgatgcctg[A/G]cagaaaccaaaataca	A	G	Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2309661	ggaaagatatgcacaa[G/T]ataacattacagaaag	G	T	Homo sapiens KIAA1409 (KIAA1409), mRNA. /// ENST00000344699 // intron // 0 // --- // --- // --- // --- ///	KIAA1409	KIAA1409, Homo sapiens KIAA1409 (KIAA1409), q32.13
SNP_A-2279982	gaggctgtagagaaaa[C/T]gacatgtttatgcact	C	T	// 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 //	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2244511	ctggactctgttctca[A/G]ggtcttgttgttctaa	A	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 12185 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2253793	cttgaacctttagaac[C/T]gaaaatgaattaaatc	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 926009 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2249528	cttaactagaagtatc[A/G]atccttcctctgacac	A	G	-- /// ENST00000340000 // upstream // 104126 // --- // --- // ---	-	p12.1
SNP_A-2097054	agactggggtttaatc[C/T]aatatattcattctga	C	T	7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) (UGT8), mRNA. /// NM_022569 // downstream // 132022 // Hs.309539 // NDST4	UGT8	UGT8, Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) (UGT8), q26
SNP_A-2097343	agagaaacagcccacc[A/G]ggacaaacaagtcaat	A	G	// 55668 // Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // downstream // 7696 // Hs.410231 // C14orf118	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-2103293	agcaagcagacaaata[A/C]atcacagtaattgtat	A	C	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 992100 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2072043	acagagtagccataat[A/G]aactaaatactagcta	A	G	-- /// ENST00000338636 // upstream // 191874 // --- // --- // --- // --- /// ENST00000334344 // upstream // 279864 // --- // --- //	-	q12
SNP_A-2028960	aaagaaaaataatatc[A/G]agtaggcctgacccaa	A	G	23560 // Homo sapiens GTP binding protein 4 (GTPBP4), mRNA. /// ENST00000354890 // downstream // 30070 // --- //	GTPBP4	GTPBP4, Homo sapiens GTP binding protein 4 (GTPBP4), p15.3
SNP_A-2209414	cccatagcatccagta[A/C]agtgcctgacaaatgg	A	C	sapiens regulator of G-protein signalling 5 (RGS5), mRNA. /// ENST00000313961 // intron // 0 // --- // --- // --- // ---	RGS5	RGS5, Homo sapiens regulator of G-protein signalling 5 (RGS5), q23.3
SNP_A-2209477	cccatcagtcttggtc[G/T]cagaatctatcccatg	G	T	60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 183572 // Hs.528665 // PROK2 //	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2108562	agctggcagtgcctta[A/T]cctaaaagaaagcatc	A	T	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// ENST00000319397 // intron // 0 // --- // --- // --- // --- /// ENST00000345075 // intron //	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3
SNP_A-2145072	atgcaaaggattgtta[C/G]accccagaattggaat	C	G	Homo sapiens cyclin-dependent kinase (CDC2-like) 11 (CDK11), mRNA. /// ENST00000230146 // intron // 0 // --- // ---	CDC2L6	CDC2L6, Homo sapiens cyclin-dependent kinase (CDC2-like) 11 (CDK11), q21
SNP_A-2152829	attaatttgctttatg[A/G]aaacagaattttaata	A	G	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 71763 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-1781129	ggatgcttgacagact[C/T]aatgccctcatctgtg	C	T	Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-1696564	actcagtggtagcaccctctctaaa[C/T]cttgccacagtccccactactccct	C	T	NM_000961 // intron // 0 // Hs.302085 // PTGIS // 5740 // prostaglandin I2 (prostacyclin) synthase	PTGIS	PTGIS , rs477627, prostaglandin I2 (prostacyclin) synthase,q13.13
SNP_A-1798076	gtaaaataggtactct[C/T]agaattatgtgtcaac	C	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 573395 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1814214	gtgtctgaagtgaggg[A/G]agtattatagaggact	A	G	4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 //	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-1817867	gttcctttaaaacaaa[C/T]agtagcataacgatta	C	T	Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// ENST00000328500 // intron // 0 // --- //	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1837027	tactggtacagaaacc[A/G]acaaatagaccaatgg	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1920389	ttaatgttacacatta[A/G]gtaacctctaggaata	A	G	2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 36115 // Hs.479853 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1905267	tgggttggtcttgata[C/T]aggatgatattcagat	C	T	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1986282	gaaatgcagaagctca[A/C]acctcaactcacctac	A	C	Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), mRNA. /// ENST00000360391 // intron // 0 // --- //	TP53BP2	TP53BP2, Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), q42.11
SNP_A-1947501	tttacattcagttatc[A/T]actttaatgtcgattg	A	T	Homo sapiens tudor domain containing 5 (TDRD5), mRNA. /// AK092142 // intron // 0 // Hs.197354 // TDRD5 // 163589 //	TDRD5	TDRD5, Homo sapiens tudor domain containing 5 (TDRD5), q25.2
SNP_A-1906311	tggtgatggcttgacg[A/T]attttttttttgtttt	A	T	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1929797	gttcctttcaattgtg[G/T]aagataagtcttaata	G	T	/// ENST00000357663 // downstream // 26829 // --- // --- // ---	-	q22.2
SNP_A-1931943	ttcctaatacactcca[C/T]tatattgtgtttggtg	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2367648 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1889605	tgataaacatatgagc[G/T]catgtttctttttggt	G	T	// 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // downstream // 958235 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1830292	taatatatatataaac[A/G]acattctcatggtcta	A	G	COL11A2 // 1302 // Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA. ///	COL11A2	COL11A2, Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, p21.32
SNP_A-1844361	tataaaagtagactcc[A/G]caaagttcttcaccct	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2620678 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1839272	tagagtaaaatagcac[A/G]acacttctatcagagg	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 81709 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1870192	tcctttatgctagtaa[A/G]taaaaccaatatcagt	A	G	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 577262 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-1865010	tccagtcaacaattaa[C/T]atggctggactcaaac	C	T	256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 44591 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1849491	tatggcccagcaaggc[C/T]gcatttatggccattt	C	T	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1852310	tattgttgattggaaa[C/G]actggctcatatttaa	C	G	2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// NM_173675 // downstream // 217574 //	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1
SNP_A-1789420	gggcccattctttacc[A/G]atggcaccatgtagct	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 294494 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1782481	ggcacagaggcagaaa[A/C]cgaggcacagagaggt	A	C	Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA. /// ENST00000354276 // intron // 0 // --- // --- // --- // --- ///	PLA2G4C	PLA2G4C, Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), q13.32
SNP_A-2160270	atttcacttaacaata[C/G]ctggcaaatattatgt	C	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2143393	atgaccatgaaaaatc[A/G]ataaggaagaacttcc	A	G	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 994055 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2142987	atgaatccattcatac[A/G]ctcttttatcttcata	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 346429 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2147041	atggaagaggattcaa[C/T]acaatcttggtgaagg	C	T	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // --- // ---	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-2118031	agtaaaaacctaaaac[A/T]gcctattgattcactt	A	T	/// ENST00000330649 // upstream // 1076439 // --- // --- // --- //	-	q11.2
SNP_A-2131796	atagctgatatataga[A/G]atttagagagtatttt	A	G	Homo sapiens rotatin (RTTN), mRNA. /// ENST00000255674 // intron // 0 // --- // --- // --- // ---	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-2227891	ctacctacaaaagaaa[A/G]tctatcaggtgccaag	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1182226 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2171573	caatcctccaaaagaa[C/T]gccacagtaccacaaa	C	T	124912 // Homo sapiens sperm acrosome associated 3 (SPACA3), mRNA. /// NM_183377 // downstream // 5549 //	SPACA3	SPACA3, Homo sapiens sperm acrosome associated 3 (SPACA3), q11.2
SNP_A-2025292	aaaatatgttcccact[C/G]acactgaccaacaggt	C	G	60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 183724 // Hs.485968 //	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2022987	aaaacacatctggtcc[A/G]atatcttcttatacaa	A	G	Homo sapiens SH3 domain containing ring finger 2 (SH3RF2), mRNA. /// ENST00000287018 // intron // 0 // --- // -	SH3RF2	SH3RF2, Homo sapiens SH3 domain containing ring finger 2 (SH3RF2), q32
SNP_A-2019420	accttacgtccattag[A/G]atggttagtattacaa	A	G	sapiens tryptophan rich basic protein (WRB), mRNA. /// ENST00000333781 // intron // 0 // --- // --- // --- // ---	WRB	WRB, Homo sapiens tryptophan rich basic protein (WRB), q22.2
SNP_A-2073507	acagtaaaagaaggat[C/T]agacagatggagatgt	C	T	3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 959852 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2053937	aagttaaacttactag[C/T]agaatgcacatagtcc	C	T	sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 //	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2250745	cttatatttaaatacc[A/C]aggcaccaattttgag	A	C	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 614200 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2277104	gagatgctgcaggaca[C/T]tatggcagagttgcac	C	T	27136 // Homo sapiens microrchidia homolog (mouse) (MORC), mRNA. /// NM_138815 // downstream // 41922 //	MORC	MORC, Homo sapiens microrchidia homolog (mouse) (MORC), q13.13
SNP_A-2277884	tgggttgtaaagagga[C/T]agtccattttaaaaga	C	T	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2301792	gcggatccttctctgg[C/T]cagtgattcccttcat	C	T	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // --- // --- // --- // ---	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2310774	ggaagcattgtttata[C/G]actgaattaccagttg	C	G	Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, mRNA. /// NM_032186 // intron // 0 // Hs.173001 // ZNF644 // 84146 // Homo sapiens zinc	ZNF644	ZNF644, Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, p22.2
SNP_A-2290960	gcaagtcagtcaatag[C/G]caagaaattgttcaat	C	G	SNAPC1 // 6617 // Homo sapiens small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA. /// NM_031914 // upstream // 84767 // Hs.404139 // SYT14L //	SNAPC1	SNAPC1, Homo sapiens small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), q23.2
SNP_A-2288219	gattcccagccccacg[C/G]atatgtttgggtgcta	C	G	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-2309715	ggaaaggaagacagtg[C/T]cacagctatgagaaag	C	T	80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 6270 //	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-2267121	gaataaggttctattc[A/C]atattcacaccagcaa	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 629391 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2238896	ctcttcaggcaggaaa[C/T]attactagagagaagg	C	T	ENST00000359247 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2237466	ctctcctgcactgacc[A/G]aaccccgcagaaaggc	A	G	// 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 150373 //	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-2235646	ctcctatcctaaccag[A/C]agataagatgataaga	A	C	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2070255	acacatttttttgtcc[A/G]acaaacagaacacatc	A	G	Homo sapiens dedicator of cytokinesis 3 (DOCK3), mRNA. /// ENST00000266037 // intron // 0 // --- // --- // --- // ---	DOCK3	DOCK3, Homo sapiens dedicator of cytokinesis 3 (DOCK3), p21.31
SNP_A-2078414	accatccaacttcaaa[G/T]aaatctcagtttgtca	G	T	// 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 390158 // Hs.211225 // NOVA1 // 4857 //	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2030768	aaagcttcttcgaaga[C/T]ctgaaagtaaaattaa	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 718516 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1990554	gcattgaacaaaaagc[A/G]aatgatccttacaggg	A	G	sapiens mRNA for KIAA0834 protein, partial cds. /// NM_012395 // intron // 0 // Hs.430742 // PFTK1 // 5218 //	PFTK1	PFTK1, Homo sapiens for KIAA0834 protein, partial cds. ,q21.13
SNP_A-2178413	cactccagaacccagc[C/T]gcaagatgcctgacag	C	T	4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 145352 // Hs.467769 //	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2184819	cagctggatacaggga[A/C]agtcactcacacactc	A	C	10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream //	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-2198939	catttgcatattctac[A/T]acagtgtctgaacact	A	T	// --- /// ENST00000355326 // downstream // 357083 // --- // --- // --- // --- /// ENST00000332323 // downstream // 561027 // ---	-	q11.21
SNP_A-2211988	ccctgagcagtcttca[A/G]agattttcacatgaga	A	G	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1110831 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2134953	atattcaatgcatata[A/T]aagcacttggatgtac	A	T	408 // Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, mRNA. /// NM_020251 // upstream // 76073 //	ARRB1	ARRB1, Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, q13.4
SNP_A-2127678	ataactaatgagttaa[C/T]gtttactaggcttaat	C	T	55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 41327 //	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. ,q43
SNP_A-2129443	atacaatgtatacaaa[C/T]gaagccaggagcgcct	C	T	203245 // Homo sapiens chromosome 9 open reading frame 90 (C9orf90), mRNA. /// NM_052901 // upstream // 9937 //	C9orf90	C9orf90, Homo sapiens chromosome 9 open reading frame 90 (C9orf90), q34.11
SNP_A-2160998	atttcttcatacttga[C/T]gttgtacaagtgcaat	C	T	146861 // Homo sapiens transmembrane protein 21A (TMEM21A), mRNA. /// NM_144975 // upstream // 23621 //	AMAC1	AMAC1, Homo sapiens transmembrane protein 21A (TMEM21A), q12
SNP_A-1782947	ggcagattccatctaa[C/T]gtggccatctgtctgc	C	T	Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // intron // 0 // --- // --- // --- // ---	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-1784059	ggccagcttcacggta[C/T]aggaacttgaagcttt	C	T	/// ENST00000360919 // upstream // 2924667 // --- // --- // --- //	-	q13.1
SNP_A-1783346	ggcagttttgatggag[C/G]ctcaagagatacagtc	C	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1000698 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1651782	atggatgtctttctatatattcaga[A/G]ctgttaaaagcatgtgtctgttttc	A	G	NM_153241 // downstream // 348493 // Hs.176497 // MGC42157 // 201824 // hypothetical protein MGC42157	MGC42157	MGC42157 , rs9306937, hypothetical protein MGC42157,p14
SNP_A-1670726	gctaagtcattaggactcaaaccta[C/T]tacattccttagctagagtccatct	C	T	// 79621 // hypothetical protein FLJ11712 /// NM_153290 // downstream // 516496 // Hs.511834 // FAM10A4 // 145165 //	FLJ11712	FLJ11712 , rs2255945, hypothetical protein FLJ11712 ,q14.3
SNP_A-1807507	gtctgctataaatgaa[G/T]aattctcaggaagctg	G	T	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803705	gtcaaatctctttaga[C/T]tacgtggttaattgac	C	T	Homo sapiens doublecortin domain containing 2 (DCDC2), mRNA. /// ENST00000274754 // intron // 0 // --- // --- // --- // ---	DCDC2	DCDC2, Homo sapiens doublecortin domain containing 2 (DCDC2), p22.2
SNP_A-1850064	tatgtgacaataagaa[A/C]aagattacagatccaa	A	C	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 485492 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1855400	tcaaggttaaaattac[A/G]agaggggctgaattc	A	G	// 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 833695 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-1827459	taactcaaaagtccac[A/G]atccaaactctcatct	A	G	-- /// ENST00000276737 // downstream // 220193 // --- // --- //	-	q24.23
SNP_A-1892626	tgcaattgagaagtga[C/T]acttatgtttaagatt	C	T	// 3790 // Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA. /// NM_020905 // downstream // 62004 // Hs.288880 // RDH14 //	KCNS3	KCNS3, Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), p24.2
SNP_A-1881428	tctttcctatatagaa[G/T]tgctgagaagtggctg	G	T	374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// NM_017564 // upstream // 136400 // Hs.408249 //	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.3
SNP_A-1921162	ttacatagggtaatca[A/G]taattcagtcttatca	A	G	/// ENST00000357074 // downstream // 191818 // --- // --- // --- // --- /// ENST00000358765 // downstream // 191818 // --- // ---	-	p14
SNP_A-1922334	ttacttttgacaatgc[A/G]gacacctgggtaatcc	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2470650 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1922388	ttagaaactttgtggg[C/T]agtattctgctaatat	C	T	/// ENST00000357025 // upstream // 223954 // --- // --- // --- //	-	q21.2
SNP_A-1982478	ttatttatctgttcca[A/G]tgatgggcatctaggt	A	G	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 314452 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1947381	tttacacagagcagaa[C/T]ttccttaacgctaata	C	T	// 10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// ENST00000296508 // downstream // 37216 // --- // --- // ---	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-1954683	tttgctatcccctgga[C/G]aaatgtgtgaattctt	C	G	Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1
SNP_A-1953763	tttgagaatagatcta[C/T]atggtacaggaaggaa	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1898251	tgcttactggaacaaa[C/T]agctaacccatcagac	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1822426	gtttttagatacacaa[A/T]gaagacaggaaaatgg	A	T	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000357362 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1824275	taaaccaggtgcttac[C/T]ctttcacatatccatg	C	T	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-1848515	tatgaattaagcttat[C/T]agggagttgtattaac	C	T	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 187754 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1848432	tatgaagacaacgtca[C/T]actcttcttggcatgt	C	T	ENST00000269439 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-1860574	tcagttggctgaagaa[A/G]agatacaccaggactt	A	G	5203 // Homo sapiens prefoldin 4 (PFDN4), mRNA. /// NM_177959 // upstream // 253716 // Hs.473133 // DOK5 //	PFDN4	PFDN4, Homo sapiens prefoldin 4 (PFDN4), q13.2
SNP_A-1691458	atttctagattcaggatttaatcaa[C/T]gtgggagaagcagttgctttaacta	C	T	NM_022051 // intron // 0 // Hs.130946 // EGLN1 // 54583 // egl nine homolog 1 (C. elegans)	EGLN1	EGLN1 , rs519504, egl nine homolog 1 (C. elegans),q42.2
SNP_A-1785107	ggcgtgctggttcaga[C/G]ctttgtgcctttgcta	C	G	Homo sapiens PRP4 pre-mRNA processing factor 4 homolog B (yeast) (PRPF4B), transcript variant 1, mRNA. /// NM_176800 // intron // 0 // Hs.159014 // PRPF4B // 8899 //	PRPF4B	PRPF4B, Homo sapiens PRP4 pre- processing factor 4 homolog B (yeast) (PRPF4B), transcript variant 1, p25.2
SNP_A-1758780	tgagagttactttgagctcgaggta[G/T]aatttaatgttctcagaagactaaa	G	T	NM_182522 // downstream // 99503 // Hs.187873 // FLJ25161 // 151647 // hypothetical protein FLJ25161	FLJ25161	FLJ25161 , rs10510971, hypothetical protein FLJ25161,p14.1
SNP_A-2159423	atttaattccctgcaa[A/G]ccaaactgttaaacaa	A	G	Homo sapiens prostaglandin F2 receptor negative regulator (PTGFRN), mRNA. /// ENST00000256643 // intron // 0 // --- //	PTGFRN	PTGFRN, Homo sapiens prostaglandin F2 receptor negative regulator (PTGFRN), p13.1
SNP_A-2151588	atgttgagtatttttc[C/T]aaatctttgttggaca	C	T	5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 516436 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-2203934	ccagatcaagaaggca[C/T]tcccatttacaatacc	C	T	3815 // Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), mRNA. /// NM_002253 // downstream // 182956 // Hs.479756 // KDR //	KIT	KIT, Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2173104	cacaaataggcacaca[A/G]tctatgctatattgta	A	G	158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2018186	tagaaaaatgtctgac[C/T]gtatcaaggattacca	C	T	56683 // Homo sapiens chromosome 21 open reading frame 59 (C21orf59), mRNA. /// NM_017835 // upstream // 13401 //	C21orf59	C21orf59, Homo sapiens chromosome 21 open reading frame 59 (C21orf59), q22.11
SNP_A-2020825	gatgaatggctgattg[C/G]aaggctgattggagga	C	G	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 12459	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.3
SNP_A-2043274	aactgctgtaagaata[A/G]actaaaatactgtata	A	G	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2042791	aactctctttagtatc[C/T]ctttatgtttttggag	C	T	// 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 10700 // Hs.21975 // CNTNAP5 // 129684 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2086335	actcttaagggaacac[C/T]gagagctgatcatatt	C	T	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 327069 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2074565	acataggttatgtctg[C/T]atgaaggaaccagctg	C	T	Homo sapiens FLJ44874 protein (FLJ44874), mRNA. /// NM_002527 // upstream // 70132 // Hs.99171 // NTF3 // 4908	-	-, Homo sapiens FLJ44874 protein (FLJ44874), p13.31
SNP_A-2250723	cttatatcagtaaata[C/T]gtgctctatctgagta	C	T	// 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream //	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2250199	cttactgttcctccag[G/T]ataggagatgtccctt	G	T	Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// ENST00000262244 // intron // 0 // --- // --- // --- // ---	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-2254300	cttgcaagttcgctca[C/G]gtgattgtggcaggtc	C	G	10944 // Homo sapiens small acidic protein (SMAP), mRNA. /// NM_175058 // downstream // 19569 // Hs.12332 //	SMAP	SMAP, Homo sapiens small acidic protein (SMAP), p15.1
SNP_A-2263309	gaacataaaggaggcc[A/G]aagggctgtcagcaga	A	G	3195 // Homo sapiens T-cell leukemia, homeobox 1 (TLX1), mRNA. /// NM_006562 // downstream // 30781 // Hs.37128 //	TLX1	TLX1, Homo sapiens T-cell leukemia, homeobox 1 (TLX1), q24.32
SNP_A-2264338	gaacttgttcccaaca[C/T]tgaagagtttttagaa	C	T	Homo sapiens Dmx-like 1 (DMXL1), mRNA. /// ENST00000311085 // CDS // 0 // --- // --- // --- // ---	DMXL1	DMXL1, Homo sapiens Dmx-like 1 (DMXL1), q23.1
SNP_A-2280244	gagggccagaggagtc[A/G]ctaacaaagagttact	A	G	ENST00000228360 // intron // 0 // --- // --- // --- // ---	-	q13.12
SNP_A-2283344	gatacagcgactttaa[A/G]taatcattttgcagaa	A	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2306639	gctgtatattgaaaga[C/T]gtggagttaggatgtg	C	T	Homo sapiens PR-domain zinc finger protein 6 isoform A (PRDM6) mRNA, partial cds; alternatively spliced. /// ENST00000359091 // intron // 0 // --- // --- // --- // --- ///	PRDM6	PRDM6, Homo sapiens PR-domain zinc finger protein 6 isoform A (PRDM6) partial cds; alternatively spliced. ,q23.2
SNP_A-2288814	gattgttggtggtatg[C/T]atatcttcatttgaaa	C	T	/// ENST00000360120 // upstream // 161500 // --- // --- // --- //	-	p21.1
SNP_A-2295541	gcatctgcagtgttgc[C/T]aggaaaagagctctga	C	T	3486 // Homo sapiens insulin-like growth factor binding protein 3 (IGFBP3), mRNA. /// ENST00000275521 //	IGFBP3	IGFBP3, Homo sapiens insulin-like growth factor binding protein 3 (IGFBP3), p13
SNP_A-2293932	gcaggaaactacaaga[C/G]caattcttcttcataa	C	G	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 618870 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2282206	gagtgttgtgaccta[A/G]ataagatacttattct	A	G	Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.33
SNP_A-2279060	gaggaaggtcaataaa[A/T]ggtgcatagtcatacc	A	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2249882	cttacacagtattagg[A/G]atttattagctcaacc	A	G	119679 // Homo sapiens olfactory receptor, family 52, subfamily J, member 3 (OR52J3), mRNA. /// NM_001005165 // downstream // 12500 // --- // OR52E4 // 390081 // Homo	OR52J3	OR52J3, Homo sapiens olfactory receptor, family 52, subfamily J, member 3 (OR52J3), p15.4
SNP_A-2250936	cttatgctattataca[C/G]atattaattcttctag	C	G	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1349490 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2233818	ctcatctaaccacaga[C/G]gtactttccaccaggt	C	G	1591 // Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, mRNA /// NM_002623 // upstream // 27959 // Hs.91161 // PFDN4 // 520	CYP24A1	CYP24A1, Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-2046491	aagagagggatgaata[A/C]aagaagatgtggggct	A	C	838 // Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), mRNA. /// NM_033295 // downstream //	CASP5	CASP5, Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990348	ctgcccaatcttgctg[A/G]agaaaattacacacca	A	G	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2171159	caataggctgggaata[A/G]ctgaagaaaaattagt	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 215031 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2192182	catcagcaattctttc[A/G]aaaaaatcaagtggta	A	G	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2188896	cagtgtaagttaaaac[G/T]gaagaaggatctcacc	G	T	// 10049 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA. /// NM_005494 // downstream // 27867 // Hs.490745 // DNAJB6	DNAJB6	DNAJB6, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, q36.3
SNP_A-2189945	cataaattactgaatg[A/C]cacttttccaaattat	A	C	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2214893	cctatattttatcatc[A/G]agtatctatttccgca	A	G	KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// NM_005752 // upstream // 550 //	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-2140573	atctcctttcaaatga[C/G]gataacaacatctgct	C	G	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 534654 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2125282	agttgtcttttccatc[A/C]aaaacatactggccct	A	C	9470 // Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// NM_025202 // upstream //	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-2111377	aggaggaaccgcgatc[A/G]agtgtgagttgtgtaa	A	G	rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// NM_206953 // intron // 0 // Hs.30743 // PRAME	-	-, Human clone rev16,q11.22
SNP_A-1806832	gtctatcttgagtcca[C/T]tattaagttcaatttt	C	T	-- /// ENST00000342900 // downstream // 262173 // --- // --- // -- // --- /// ENST00000321814 // upstream // 23450 // --- // --- //	-	q11.22
SNP_A-1788812	gggattgcacctgaac[G/T]catacctgtgctgggt	G	T	// Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA. /// ENST00000358967 // downstream // 27510 // --- //	ADRB1	ADRB1, Homo sapiens adrenergic, beta-1-, receptor (ADRB1), q25.3
SNP_A-1790953	ggggtactcctgaccc[A/G]gagtgaatggaggcca	A	G	Homo sapiens DAZ associated protein 1 (DAZAP1), transcript variant 2, mRNA. /// NM_170711 // intron // 0 //	DAZAP1	DAZAP1, Homo sapiens DAZ associated protein 1 (DAZAP1), transcript variant 2, p13.3
SNP_A-1871642	agcacaaggagctaaa[C/G]aaatagaagtccaata	C	G	6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 502553 // Hs.221127	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-1844481	tataaagtctaaatta[C/G]agttagtagcattaat	C	G	/// ENST00000357497 // downstream // 150773 // --- // --- // --- // --- /// ENST00000359402 // downstream // 150826 // --- // ---	-	q31.1
SNP_A-1856916	tcaccacgccgagatc[A/G]ccagcctgcccagaaa	A	G	FLJ40712 // 401044 // Homo sapiens FLJ40712 protein (FLJ40712), mRNA. /// NM_178530 // upstream // 4427 //	FLJ40712	FLJ40712, Homo sapiens FLJ40712 protein (FLJ40712), q37.3
SNP_A-1827624	taactggaaggggtga[A/C]gaaatgtgactaaggc	A	C	Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7), mRNA. /// NM_032149 //	ADH7	ADH7, Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7), q23
SNP_A-1843175	tagtcatcttcagaca[C/T]atttccaattgtggta	C	T	5080 // Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), mRNA. /// NM_001604 // upstream // 130615 //	PAX6	PAX6, Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), p13
SNP_A-1834102	tacatccaatgaggca[A/T]tcttcaacctttaaaa	A	T	Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000359391 // CDS // 0 // --- // ---	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1904223	tgggcgggcagcgtga[C/T]gtctcacccactgctt	C	T	Homo sapiens PTEN induced putative kinase 1 (PINK1), mRNA. /// ENST00000289840 // intron // 0 // --- // --- // --- // ---	PINK1	PINK1, Homo sapiens PTEN induced putative kinase 1 (PINK1), p36.12
SNP_A-1888176	tgagcctgcttcctac[G/T]ggtagaaagttggaga	G	T	84062 // Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 //	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3
SNP_A-1874131	tctcatttaaccataa[C/G]aaatgcatccggtagg	C	G	// Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // --- // --- // --- // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1925341	ttatctatttctgatc[C/T]aagtgtgacagaacaa	C	T	// 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 71430 // Hs.436996 //	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-1925544	ttatgaaattctcata[A/G]gcaaagaaaaagaaca	A	G	// 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1916111	tgttggaaaaacagaa[C/T]tgtctgacttattgtg	C	T	Homo sapiens chromosome 10 open reading frame 33 (C10orf33), mRNA. /// ENST00000238999 // intron // 0 // --- //	C10orf33	C10orf33, Homo sapiens chromosome 10 open reading frame 33 (C10orf33), q24.2
SNP_A-1980499	gtgcaggagaatataa[C/G]aagtttttttgattcat	C	G	11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 521581 //	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1983534	aaactacagaaataca[A/G]cgttggaggcttttca	A	G	/// ENST00000360575 // upstream // 53868 // --- // --- // --- // --- /// ENST00000231482 // upstream // 56262 // --- // --- // --- // ---	-	q31.1
SNP_A-1965777	tagatgattaatataa[A/C]cctctctctgctcaag	A	C	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 11 (ABCB11), mRNA. ///	ABCB11	ABCB11, Homo sapiens ATP-binding cassette, sub-family B (MDR q31.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1969375	ggaagatactcagatg[A/G]acagattacttcaggg	A	G	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 93085 // --- // --- // --- // --- ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. ,q21.1
SNP_A-1988304	ataaaatatagataga[C/T]agtattatgcacctac	C	T	Homo sapiens sorting nexin 9 (SNX9), mRNA. /// ENST00000252631 // intron // 0 // --- // --- // --- // --- ///	SNX9	SNX9, Homo sapiens sorting nexin 9 (SNX9), q25.3
SNP_A-1948520	tttagtgtggtcacag[A/T]ctgctcaaacacttaa	A	T	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1942498	ttggctgtcagtctaa[C/T]gtctgttctttcaaag	C	T	80727 // Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), mRNA. /// ENST00000258796 // downstream //	TTYH3	TTYH3, Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), p22.3
SNP_A-1905235	tgggttctcaaaatgc[A/G]gcagatctgtcacaac	A	G	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1924788	ggagtcattagagagg[C/T]cacagcttgagaaaaa	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 1482325 // --- // --	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-1877990	tctgtaaattgctttg[A/G]aactatagccatttta	A	G	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1844830	tataatagggaaaata[C/T]ggaaaacagccggagt	C	T	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 112966 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1849204	tatgctctttgatgag[A/G]agttcagattaggttg	A	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 517054 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1868212	tcctcaatgagatgaa[C/G]agagggcaagtgctta	C	G	Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, mRNA. /// NM_175605 // intron // 0 //	TTC10	TTC10, Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, q12.11
SNP_A-1801563	gtaggtgatttgcctg[A/C]agttatacaacttgta	A	C	Homo sapiens Rhesus blood group, B glycoprotein (RHBG), mRNA. /// ENST00000255013 // intron // 0 // --- // --- // --- // ---	RHBG	RHBG, Homo sapiens Rhesus blood group, B glycoprotein (RHBG), q22
SNP_A-1781855	ggattttgattaaaga[C/G]taccaactttcagtta	C	G	Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1696518	ataaagagaagaggttattttggct[C/T]atgcttctacaaactgtacaaggag	C	T	// 84457 // phytanoyl-CoA hydroxylase interacting protein-like /// BC036453 // upstream // 194036 // Hs.311205 // FAM13C1	PHYHIPL	PHYHIPL , rs1579014, phytanoyl-CoA hydroxylase interacting protein-like ,q21.2
SNP_A-2113261	aggccgcagaagagaa[A/G]gccgtgtggggatgga	A	G	CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 44355 //	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2120605	agtcccactggagaag[A/G]agctcaaaattggaga	A	G	ENST00000359915 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2123823	agttaaacaaagagtg[A/G]aagaatattccaggca	A	G	84888 // Homo sapiens putative intramembrane cleaving protease (SPPL2A), mRNA. /// NM_007347 // upstream // 12410 // Hs.413366 // AP4E1 // 23431 // Homo sapiens	SPPL2A	SPPL2A, Homo sapiens putative intramembrane cleaving protease (SPPL2A), q21.2
SNP_A-2140639	atctctcaaataaatg[A/G]ataaaattgtggtata	A	G	/// ENST00000321602 // upstream // 58106 // --- // --- // --- // --- /// ENST00000355466 // upstream // 94570 // --- // --- // --- // ---	-	q21.3
SNP_A-2163496	caaaaaactcttatta[A/G]caagagacaaatagct	A	G	Homo sapiens neurobeachin (NBEA), mRNA. /// ENST00000310336 // intron // 0 // --- // --- // --- // ---	NBEA	NBEA, Homo sapiens neurobeachin (NBEA), q13.3
SNP_A-2225790	ctaaagtcatgaccaa[C/T]ttcaaattatatatat	C	T	ENST00000328167 // upstream // 127076 // --- // --- // --- // ---	-	p15.1
SNP_A-1992293	cagaactccatttaga[A/C]ctcctgcagaagtctc	A	C	KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 13853 //	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2019517	cccatagatatgcaca[C/G]aaagcattttgtgaaa	C	G	ENST00000328060 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-2028864	aaactttaagaattac[C/T]ggcagatatacctctg	C	T	C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2084061	actagatcgtatttcc[A/G]agaaagggagactttt	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2106467	agcctacaatcgtggc[A/G]gaaaatgaagtggggc	A	G	5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 101879 // Hs.132225 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2106803	agcctgtccccgaagc[A/G]cttgaccaggagaaac	A	G	// 1716 // Homo sapiens deoxyguanosine kinase (DGUOK), nuclear gene encoding mitochondrial protein, transcript variant 5, mRNA. /// NM_080917 // downstream // 16490 //	DGUOK	DGUOK, Homo sapiens deoxyguanosine kinase (DGUOK), nuclear gene encoding mitochondrial protein, transcript variant 5, p13.1
SNP_A-2232715	tgtttcttcagcacta[A/T]gtagcttattttctag	A	T	8892 // Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), mRNA. /// NM_014381 // downstream // 3592 // Hs.279843 // MLH3 // 27030 // Homo	EIF2B2	EIF2B2, Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2248912	ctgttggggctgacaa[A/G]gtttttttttgttttt	A	G	2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 //	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-2277824	gagcatctagacgcat[C/T]atcctgagagtgcccg	C	T	54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 233868 // ---	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2275340	gagaatagctagatga[C/T]cttgtgttggacaaaa	C	T	sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // intron // 0 // --- // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2273111	gactattggcaaccac[C/G]agaagttaggagaaag	C	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2265478	gaagccatgatataac[A/G]gagaggtgaaaagagg	A	G	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 387423 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2303316	gctatgttacagacag[C/G]atttgaaacaggagcc	C	G	64761 // Homo sapiens zinc finger CCCH type domain containing 1 (ZC3HDC1), mRNA. /// ENST00000263549 //	ZC3HDC1	ZC3HDC1, Homo sapiens zinc finger CCCH type domain containing 1 (ZC3HDC1), q34
SNP_A-2311316	ggaatagcaagggata[C/G]caaggttaggtgaata	C	G	10277 // Homo sapiens ubiquitination factor E4B (UFD2 homolog, yeast) (UBE4B), mRNA. /// AF043117 //	UBE4B	UBE4B, Homo sapiens ubiquitination factor E4B (UFD2 homolog, yeast) (UBE4B), p36.22
SNP_A-2314625	ggagtaaggatagaga[A/G]gaaggcagatacaacc	A	G	8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 413855 // Hs.370359	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2314022	ggagctgggcgctcaa[C/T]tagactaggcatcttc	C	T	Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // --- // --- // --- // ---	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-2312332	ggacatggccaccgtc[A/G]cgggggaagtggttgg	A	G	// Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB //	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-2293733	gcagcgggtgagagaa[A/C]gtgtgcaggaagtgaa	A	C	// 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2249822	cttaatttaaaatcca[A/G]ctgtgtgcacagtccc	A	G	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 106484 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.1
SNP_A-2251227	cttcaaacgtggctca[C/T]cctttcctgatgctgt	C	T	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 934300 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-2254957	cttggcccattcccaa[A/G]tcttccataatttttt	A	G	Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2229658	ctagtacttatatacc[A/G]attgttcaaatcacta	A	G	7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 658066 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2097958	agagagagaggccata[C/T]accattacagcgggaa	C	T	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2082930	acgtgaaatttttgtg[C/T]accacttagaaaacaa	C	T	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 618638 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-2082252	acgaggctcagagaac[A/G]atgtctggctagcagt	A	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2067427	acaaatcactttccaa[A/G]gtattcgtgtccactg	A	G	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3385289 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2227601	ctacataaacctcaaa[C/T]cttccagaaaaatgaa	C	T	ENST00000355802 // upstream // 57063 // --- // --- // --- // --- /// ENST00000358682 // upstream // 57079 // --- // --- // --- // ---	-	q13.3
SNP_A-2227215	ctaattttcagataaa[C/T]acaattgaaaagctga	C	T	FLJ20097 // 55610 // Homo sapiens hypothetical protein FLJ20097 (FLJ20097), mRNA. /// NM_001742 // downstream	FLJ20097	FLJ20097, Homo sapiens hypothetical protein FLJ20097 (FLJ20097), q21.3
SNP_A-2224006	cggggcacaggaagac[A/G]aaaggatgccccaggc	A	G	Homo sapiens ribosomal protein L18a (RPL18A), mRNA. /// ENST00000222247 // intron // 0 // --- // --- // --- // ---	RPL18A	RPL18A, Homo sapiens ribosomal protein L18a (RPL18A), p13.11
SNP_A-2218751	cctggctttccccca[A/G]tctccttgcttctcac	A	G	// Homo sapiens neuromedin B (NMB), transcript variant 2, mRNA. /// NM_021077 // upstream // 1268 // Hs.386470 //	NMB	NMB, Homo sapiens neuromedin B (NMB), transcript variant 2, q25.3
SNP_A-2201515	ccaatgttatctttct[A/G]aaagtctaatgtggcc	A	G	// 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 146126 // Hs.446083 // PTPRD	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2190930	catagcgctaagacca[C/T]taagcctgaacttttg	C	T	// 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream //	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-2185755	caggataattagagga[A/G]aaaatacaacgtgtca	A	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 583115 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2193274	aatggcttgaatgacc[C/T]ctatttctatgccact	C	T	Human T-cell receptor rearranged alpha-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000250499 //	-	-, Human T-cell receptor rearranged alpha-chain V-region (V-D-J) complete cds. ,q11.2
SNP_A-2171301	caatatgctcatatcc[C/T]gagggtctgagcaggc	C	T	Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA. /// NM_015881 // intron // 0 // Hs.292156 // DKK3 //	DKK3	DKK3, Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), p15.3
SNP_A-2178466	cactcctaagaccaaa[C/T]tgaaagtaagaacttc	C	T	ENST00000321662 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2164470	caaaatgttgtggttc[A/G]atgtgcatttttcatc	A	G	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 95056 // Hs.114412 // TXNL1	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2149672	atgtatcatatcttcc[A/C]attaatctttcctaag	A	C	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 573313 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2122908	agtggctctctgatac[A/G]attttccaaaatgtac	A	G	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, mRNA. /// NM_003401 // intron // 0 // Hs.171190 // XRCC4 // 7518 // Homo sapiens X	XRCC4	XRCC4, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, q14.2
SNP_A-1802584	gtatctggaagcctaa[C/T]ctctctgtcagcaatc	C	T	Homo sapiens activating transcription factor 6 (ATF6), mRNA. /// ENST00000263291 // intron // 0 // --- // --- // --- // ---	ATF6	ATF6, Homo sapiens activating transcription factor 6 (ATF6), q23.3
SNP_A-1810209	gtgatgaaacgtgtcc[A/G]ctatgaagtacagtcc	A	G	LOC151963 // 151963 // Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), mRNA. /// NM_020386 // upstream // 200934 // Hs.36761 // HRASLS //	LOC151963	LOC151963, Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), q29
SNP_A-1813739	gtgtagccagttaaac[A/G]aggggtgttttggtca	A	G	81555 // Homo sapiens golgi membrane protein SB140 (SMAP-5), mRNA. /// ENST00000274496 // upstream // 8346	SMAP-5	SMAP-5, Homo sapiens golgi membrane protein SB140 (SMAP-5), q31.3
SNP_A-1786299	ggctgtgcatttacta[C/G]acacgaagtaaaaact	C	G	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-1845400	tatactttgacaccca[C/T]ctgtatagtatcccag	C	T	Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000324333 // intron // 0 // --- // --- // --- // --- ///	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1836066	tactaccagtaataca[A/G]ctacaatggtaaacca	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 191239 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1880186	tcttctggctttaaa[C/G]agtttatgtctatcta	C	G	ENST00000345029 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-1889511	tgagttgtgccttcta[C/G]atccctctaaggaaag	C	G	6582 // Homo sapiens solute carrier family 22 (organic cation transporter), member 2 (SLC22A2), transcript variant 1, mRNA. /// NM_153191 // upstream // 57178 // Hs.436385 //	SLC22A2	SLC22A2, Homo sapiens solute carrier family 22 (organic cation transporter), member 2 (SLC22A2), transcript variant 1, q25.3
SNP_A-1884391	tgaagtagcaatgaga[C/G]gacttttaccttggt	C	G	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1908335	tgtactgatctcatga[C/T]atatactatacattca	C	T	Homo sapiens hydrocephalus inducing (HYDIN), mRNA. /// ENST00000288168 // intron // 0 // --- // --- // --- // --- ///	HYDIN	HYDIN, Homo sapiens hydrocephalus inducing (HYDIN), q22.2
SNP_A-1919307	ttaagaccaaggacaa[C/T]agagatgttgggggaa	C	T	Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB //	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-1888451	tgaggaatgcaggggg[A/T]ataatccctagaggtt	A	T	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-1876842	tctgccaaagagggca[C/T]gtgagaaggcagtgag	C	T	Homo sapiens mRNA for KIAA1029 protein, partial cds. /// ENST00000314840 // intron // 0 // --- // --- // --- // --- ///	SYNPO	SYNPO, Homo sapiens for KIAA1029 protein, partial cds. ,q33.1
SNP_A-1942025	ttggataatcagggaa[A/G]aagtggcatttcagca	A	G	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1943465	ttgtaaaaaaaggaga[A/G]gtgatttggagaattt	A	G	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 14435 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1942008	ttggagtttgacagag[C/G]aataaaaaacaaaaca	C	G	Homo sapiens relaxin 1 (H1) (RLN1), mRNA. /// ENST00000223862 // intron // 0 // --- // --- // --- // --- ///	RLN1	RLN1, Homo sapiens relaxin 1 (H1) (RLN1), p24.1
SNP_A-1940216	ttgcatgcctgtcgtg[A/C]attgtagacatctcaa	A	C	// 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 295678 //	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1960910	tttttgataccttaca[G/T]ccatcttgtaattctg	G	T	/// ENST00000355561 // upstream // 741599 // --- // --- // --- // ---	-	q21.31
SNP_A-1974387	gtaaggttttgtacca[C/T]tgacagaatgtaaatt	C	T	Homo sapiens xenotropic and polytropic retrovirus receptor (XPR1), mRNA. /// ENST00000271566 // intron // 0 // --- // ---	XPR1	XPR1, Homo sapiens xenotropic and polytropic retrovirus receptor (XPR1), q25.3
SNP_A-1791500	gggtattatccactcc[A/G]agctgaatgctctgtt	A	G	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1309230 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1802603	gtatcttaggattacc[A/G]aaataatatatgtggt	A	G	MGC50104 // 341032 // Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), mRNA. ///	MGC50104	MGC50104, Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800676	gtagaaattaagatgc[A/G]ctgtgtatgtaaaata	A	G	FLJ22390 // 64757 // Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA. /// NM_021958 // upstream //	FLJ22390	FLJ22390, Homo sapiens hypothetical protein FLJ22390 (FLJ22390), q41
SNP_A-1805387	gtccaataataagaga[C/T]gaaaaagttaaacgcc	C	T	/// ENST00000333948 // upstream // 501179 // --- // --- // --- //	-	q31.2
SNP_A-1696506	atcaaaactgcatttttactcccta[A/C]atttacacaaaaatgtattctaatt	A	C	// 10346 // tripartite motif-containing 22 /// NM_173525 // upstream // 354967 // Hs.278221 // MGC34805 // 160298 //	TRIM22	TRIM22 , rs1013377, tripartite motif-containing 22 ,p15.4
SNP_A-2122345	agtgccaggtagaggc[C/T]cttaggtagctcattc	C	T	ENST00000272427 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-2115937	agggttcaacaagccc[C/G]ccacatgatcctaata	C	G	145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 78079 // Hs.87889 // DICER1 //	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2162325	attttatgctctgtca[C/T]cttttgaatgctttac	C	T	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2168564	caagaaagctactaga[A/G]caaatagatgaattca	A	G	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-2211971	ccctgactgtgggcac[A/G]aaactgagaccatatc	A	G	// 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 41694 // Hs.407755 //	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-2216649	cctctcagctaaggtc[A/G]ctcttccctcctcacc	A	G	Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// ENST00000262113 // intron // 0 // --- // --- // --- // ---	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.3
SNP_A-2215615	cctcaggaattcatga[A/C]gcttaggaagagcata	A	C	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1589179 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2222916	cgcacctggagtcaac[A/G]cagggtgctgcttgtc	A	G	// 157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA. /// ENST00000262109 // upstream //	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3
SNP_A-2081053	acctgacaactttga[C/T]ccaaagccttctgata	C	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2093953	agaagccagcagccac[A/G]agcgccggggtgcccc	A	G	55628 // Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // downstream // 72 // --- // --- //	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-2028618	aaactggatacacaca[A/G]tcttccaaaattgagc	A	G	ENST00000339567 // intron // 0 // --- // --- // --- // --- /// ENST00000343332 // intron // 0 // --- // --- // --- // --- ///	-	p12
SNP_A-2022819	aaaacaaaaagcccttt[A/T]aaactgtgagcatttc	A	T	Homo sapiens nuclear protein localization 4 (NPL4), mRNA. /// ENST00000331134 // intron // 0 // --- // --- // --- // ---	NPL4	NPL4, Homo sapiens nuclear protein localization 4 (NPL4), q25.3
SNP_A-2038369	aacactactactaaaa[C/T]ctgggtcattttctag	C	T	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 424632 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2000368	cattttagtcaagtcc[C/T]atctcccctgccataa	C	T	391104 // Homo sapiens von Hippel-Lindau tumor suppressor-like (VHLL), mRNA. /// NM_005998 //	VHLL	VHLL, Homo sapiens von Hippel-Lindau tumor suppressor-like (VHLL), q22
SNP_A-1997191	gaaactgtctatcccc[A/T]aatccttttttctacc	A	T	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, mRNA. /// NM_201572 // intron // 0 // Hs.59093 // CACNB2 // 783 //	CACNB2	CACNB2, Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, p12.31
SNP_A-2007707	aatgtaaacttaatga[A/G]agcagcagtcatgttt	A	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 137414 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2248354	ctgtgtcttcttctaa[A/G]agttgtatgattttag	A	G	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 826594 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2247726	ctgtgacacacaaaag[G/T]cttatgcccctggtct	G	T	92291 // Homo sapiens calpain 13 (CAPN13), mRNA. /// BC010659 // downstream // 27367 // Hs.468058 // GALNT14	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1
SNP_A-2270638	gacagcaaccgaattc[C/T]cagttctttttttga	C	T	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2086 // Hs.54642 // MAT2B // 27430 // Homo	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2277808	gagcatcaaaaaaaca[C/T]tgggaagcacttacct	C	T	57722 // Homo sapiens likely ortholog of mouse neighbor of Punc E11 (NOPE), mRNA. /// NM_130434 // downstream //	NOPE	NOPE, Homo sapiens likely ortholog of mouse neighbor of Punc E11 (NOPE), q22.31
SNP_A-2278561	gagctgagaagagcaa[C/T]tgggctcctgtgccct	C	T	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 202177 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2296647	gccaaacatacctgcc[A/C]ctgtgtttctcccata	A	C	/// ENST00000333132 // upstream // 4894 // --- // --- // --- // ---	-	p15.4
SNP_A-2312933	ggacttcatcagaaat[A/G]acatctatccatttag	A	G	54209 // Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA. /// NM_024807 //	TREM2	TREM2, Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), p21.1
SNP_A-2307629	gcttcatccgaaaatg[C/T]acatcctgggtgactt	C	T	9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 2143 // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2297276	gccaccgtgttcctga[C/T]gtagctgtcacatgat	C	T	6001 // Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, mRNA. /// ENST00000313060 // downstream // 19885 // --- // --- // --- // --- ///	RGS10	RGS10, Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, q26.11
SNP_A-2300940	gcctgtgggaaagcta[C/T]gttttaattattgttg	C	T	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 5056 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2246742	ctgtactagagactca[C/T]agactactgcagacat	C	T	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA. /// AF110377 // intron //	TRRAP	TRRAP, Homo sapiens transformation q22.1
SNP_A-2242041	ctgattgcttacagta[C/T]aggactttcttcaaaa	C	T	// Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2238194	ctctgctattcatgat[C/T]agtcaaggattcctag	C	T	Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000261864 // intron // 0 // --- // --- // --- // --- ///	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2104363	agcagctaagttgata[C/T]ccatctggtgatgagt	C	T	9612 // Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /// NM_005505 // downstream // 273818 //	NCOR2	NCOR2, Homo sapiens nuclear receptor co-repressor 2 (NCOR2), q24.31
SNP_A-2088116	actgggctgagaatta[A/G]agtcaggagcaaatct	A	G	3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1090636 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2051966	gctcctggacctccta[C/T]cacaggtaagtcagat	C	T	1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 347770 // Hs.143434	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2216650	cctctcagcttgacta[A/G]acttcaggcgggtttc	A	G	/// ENST00000354860 // upstream // 1007897 // --- // --- // --- //	-	q32.3
SNP_A-2172907	gtatgtgccaaagaaa[C/T]gctataagccatgagt	C	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2126179	ataaaaaagcattaca[A/G]tagggattgcaacctg	A	G	8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // downstream //	FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-2132526	atagtggggttccaga[A/C]aatggaatagagacaa	A	C	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1688950	cccgagccagtcaaggtcagaaccc[A/G]aggctcaattttaatcccaagtcat	A	G	// 169044 // collagen, type XXII, alpha 1 /// NM_015912 // upstream // 217287 // Hs.13497 // LOC51059 // 51059 //	COL22A1	COL22A1 , rs1401608, collagen, type XXII, alpha 1 ,q24.23
SNP_A-1809157	gtgacatttctagatc[C/T]cagtctttaaattggt	C	T	Homo sapiens keratin, hair, basic, 4 (KRTHB4), mRNA. /// ENST00000257951 // intron // 0 // --- // --- // --- // ---	KRTHB4	KRTHB4, Homo sapiens keratin, hair, basic, 4 (KRTHB4), q13.13
SNP_A-1799982	gtacataacagggatc[A/G]aaactcagtttatggg	A	G	Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // --- // --- // --- // ---	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1828885	taaggataaagttcaa[C/G]gatttaatttggtttt	C	G	sapiens Dombrock blood group (DO), mRNA. /// ENST00000228936 // intron // 0 // --- // --- // --- // ---	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-1854784	tcaacattttccatca[C/T]attaaaaaagtgaaag	C	T	ENST00000360683 // intron // 0 // --- // --- // --- // --- /// ENST00000345990 // intron // 0 // --- // --- // --- // ---	-	q23.2
SNP_A-1865998	tcccacctgttatgta[A/G]gaataaaaacacatgc	A	G	3791 // Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 41929 // Hs.546432 // SRD5A2L // 79644 //	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-1968630	tgggttatggctagct[G/T]ctgaaaccagtttcaa	G	T	55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 559454 // Hs.473082 // ZFP64 // 55734 // Homo	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1978060	atattatgtgtaacct[C/T]aaaagtcactggactt	C	T	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1977092	tcaactgcactgcccc[A/G]agaagatggacagcag	A	G	64854 // Homo sapiens ubiquitin specific protease 46 (USP46), mRNA. /// ENST00000356681 // upstream // 2745 //	USP46	USP46, Homo sapiens ubiquitin specific protease 46 (USP46), q12
SNP_A-1950796	tttcattttggtggaa[A/T]ccgtaggtctcagtta	A	T	3623 // Homo sapiens inhibin, alpha (INHA), mRNA. /// NM_052902 // upstream // 4391 // Hs.22410 // STK11IP //	INHA	INHA, Homo sapiens inhibin, alpha (INHA), q35
SNP_A-1950173	tttcactgttcctgat[A/T]aatgtgaatcaaattt	A	T	/// ENST00000314058 // upstream // 239845 // --- // --- // --- //	-	p13.2
SNP_A-1953281	tttctttttttgcctc[A/G]cacagatatcgctagg	A	G	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1874119	tctcattgccttggga[A/G]gaatcaaatccttatt	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 843983 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1907393	tgtaaaattaagatga[C/T]aagatggtaagtatga	C	T	284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 264442 //	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-1926489	ttattccagtcagcac[A/G]ctttattatttaaatt	A	G	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1891040	tgatggtagttaaaca[A/C]ctttgtgaatatatta	A	C	Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// ENST00000340353 // intron // 0 // --- // --- // --- // ---	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-1952659	tttctgggaagaacgc[A/G]aggcatgtgctaaggt	A	G	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1947282	tttaattttattgcac[A/T]aatatgctatggtgac	A	T	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 533696 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1966125	catgtgctaatttgca[C/T]gcttgtgggcacccta	C	T	Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), mRNA. /// ENST00000233573 // intron // 0 // --- // --- // --- // ---	ITGA4	ITGA4, Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), q31.3
SNP_A-1975037	tgcataggtaaataga[C/T]ggatagtgataggacc	C	T	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // --- // --- // --- // ---	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-1871875	tctacacctcctattc[A/C]gaaccacattcctaaa	A	C	// 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA (cDNA clone IMAGE:4791744), partial cds. /// NM_017799 // downstream // 11987 // Hs.497253 //	C14orf101	C14orf101, Homo sapiens chromosome 14 open reading frame 101, (cDNA clone IMAGE:4791744), partial cds. q22.3
SNP_A-1817004	gttatttatcagactg[A/C]aaaagaagccatatag	A	C	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 417917 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1843503	tagtgatttgaagaga[A/G]taggttatgtggttct	A	G	Homo sapiens KIAA1838 (KIAA1838), mRNA. /// ENST00000262196 // intron // 0 // --- // --- // --- // --- ///	KIAA1838	KIAA1838, Homo sapiens KIAA1838 (KIAA1838), q27
SNP_A-1789879	gggctgtggtttgtca[A/G]taggctcctggaggga	A	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-1801272	gtagcttcaccctgcc[C/T]gatggaaaggctgtgt	C	T	29110 // Homo sapiens TANK-binding kinase 1 (TBK1), mRNA. /// NM_178169 // upstream // 42630 // Hs.346527 //	TBK1	TBK1, Homo sapiens TANK-binding kinase 1 (TBK1), q14.2
SNP_A-1655535	attgaatgagtgcatcacgagacac[A/C]aaactccattagagttactataggt	A	C	8767 // receptor-interacting serine-threonine kinase 2 /// NM_005941 // upstream // 1202146 // Hs.90800 // MMP16 //	RIPK2	RIPK2 , rs10504879, receptor-interacting serine-threonine kinase 2 ,q21.3
SNP_A-1782485	ggcacagatgtctaca[A/G]aatgaggaaaattaaa	A	G	Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // --- // --- // --- // --- /// ENST00000349908 // intron //	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-2131945	ataggagttaagctag[G/T]aaatgtgaaaggaaaa	G	T	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2195693	catgtaaactgaaaca[C/G]aaaggtgcattttata	C	G	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 388048 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2190634	ccacatgcatttccca[C/T]acagcacattgtcttg	C	T	Homo sapiens RAS p21 protein activator 3 (RASA3), mRNA. /// ENST00000357860 // intron // 0 // --- // --- // --- // --- ///	RASA3	RASA3, Homo sapiens RAS p21 protein activator 3 (RASA3), q34
SNP_A-2218508	cctggagcctccggaa[A/G]agaccagctcagatga	A	G	8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 31096 // Hs.425091 // FAM44B	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2214667	cctagccctggctgga[A/G]ataagagcctcaacct	A	G	5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 93436 //	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2208530	cccacgggctaatggg[A/T]cagaaccctgttaaat	A	T	85465 // Homo sapiens selenoprotein I (SELI), mRNA. /// NM_145038 // upstream // 887 // Hs.393714 // MGC16372 //	SELI	SELI, Homo sapiens selenoprotein I (SELI), p23.3
SNP_A-2205729	ccataaggatgaaaca[A/G]caaaagactggcacta	A	G	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2067074	acaaactgtcctttcg[A/C]attagagatgctctat	A	C	// Homo sapiens glutaredoxin (thioltransferase) (GLRX), mRNA. /// NM_175616 // upstream // 15895 // Hs.8373 // FIS	GLRX	GLRX, Homo sapiens glutaredoxin (thioltransferase) (GLRX), q15
SNP_A-2011967	ctgggatttgctttaa[A/C]atatttcagcgaagca	A	C	Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA. /// ENST00000334456 // intron // 0 // --- // ---	PDE2A	PDE2A, Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), q13.4
SNP_A-2009390	gttccctttgctgaag[A/G]atcatggtgctgtgtt	A	G	10644 // Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2), mRNA. /// NM_004593 // downstream // 17568 //	IMP-2	IMP-2, Homo sapiens IGF-II binding protein 2 (IMP-2), q27.2
SNP_A-2005454	catcagcagtcacaaa[C/T]ctttaatctggatcca	C	T	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA. /// ENST00000289890 // intron // 0 // --- // --- // --- // --- /// ENST00000356138 // intron	MACF1	MACF1, Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, p34.3
SNP_A-1990676	ggttggtcagttgtta[C/T]atatttgtgtatagcc	C	T	7979 // Homo sapiens split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA. /// ENST00000248566	SHFM1	SHFM1, Homo sapiens split hand,q21.3
SNP_A-1994254	aaggaggttcttctac[G/T]gctaatactccaggta	G	T	/// ENST00000328621 // upstream // 288819 // --- // --- // --- //	-	q22.1
SNP_A-2046058	aagactactgaggtta[A/G]aaggatatgttaaata	A	G	1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream //	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2022758	aaaaattctccagaga[C/T]gagaagtttcctcctg	C	T	// Homo sapiens FLJ46481 protein (FLJ46481), mRNA. /// ENST00000324058 // intron // 0 // --- // --- // --- // ---	FLJ46481	FLJ46481, Homo sapiens FLJ46481 protein (FLJ46481), p16.1
SNP_A-2022574	aaaaatgaatctgtgc[A/G]acctagggaaagtcaa	A	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 771639 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2033403	aaataggagaattcaa[A/G]ctaactaatgtctgat	A	G	Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // --- // --- // --- // ---	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2230974	ctatggtagtccatta[C/T]agcagcataagacgat	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 167358 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2286419	gatgctggaaatagag[A/G]agaattgcccatgtgc	A	G	4255 // Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), mRNA. /// ENST00000248179 //	MGMT	MGMT, Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), q26.3
SNP_A-2265366	gaagcagtcctgaaca[A/G]aagtgtttttatcttt	A	G	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- // --- ///	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2267400	gaatagtaaagaatgg[A/G]aaacccaatgagatat	A	G	-- /// ENST00000327715 // upstream // 159595 // --- // --- // ---	-	q22.1
SNP_A-2268115	gaatgaaatggataga[G/T]agctgaatggatgaat	G	T	Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2271604	gaccacacttggagaa[C/G]agggctcttttacacc	C	G	ENST00000303635 // intron // 0 // --- // --- // --- // ---	-	p36.23
SNP_A-2282271	gagttaccttgcttca[A/G]gaaaggatcacaagtt	A	G	169166 // Homo sapiens hypothetical protein MGC39715 (MGC39715), mRNA. /// ENST00000311812 // intron // 0 // ---	MGC39715	MGC39715, Homo sapiens hypothetical protein MGC39715 (MGC39715), q22.3
SNP_A-2236229	ctcctttaattttaaa[C/G]tcattatcagagagca	C	G	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2304816	gctctgttttattgac[A/G]gaaatgggcaaaatga	A	G	// Homo sapiens neuropeptide Y (NPY), mRNA. /// NM_016447 // upstream // 257341 // Hs.533355 // MPP6 //	NPY	NPY, Homo sapiens neuropeptide Y (NPY), p15.3
SNP_A-2310648	ggaagaggttcagagc[A/G]aagtggtggaaaagcc	A	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1051414 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2026105	aaaattataggaatct[C/T]aagaagccacaaagaa	C	T	Homo sapiens mesoderm induction early response 1 (MI-ER1), mRNA. /// ENST00000355977 // intron // 0 // --- // --- // -	MI-ER1	MI-ER1, Homo sapiens mesoderm induction early response 1 (MI-ER1), p31.2
SNP_A-2041270	aacctcttgaaacagc[A/G]aacaggacttcttaaa	A	G	4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 683195 // Hs.166017 // MITF //	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-2036121	aaattataaggtgtac[A/G]aaactattctattaca	A	G	Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, mRNA. /// NM_172059 // intron // 0 //	EYA1	EYA1, Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, q13.3
SNP_A-2081996	acctttggggtctaga[A/C]tatgactgaatatgag	A	C	FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// NM_152706 // upstream //	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-2102948	agcaaacatcatttta[C/T]ctactaaatagctctg	C	T	2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-2094841	agaatctgactttata[C/T]aacttctttccttct	C	T	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 2215191 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2206665	ccatgacttctaattc[A/G]cggagtttcataagaa	A	G	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2219648	ccttaaacattaagta[A/G]acacaccttctgttaa	A	G	Homo sapiens dual specificity phosphatase 16 (DUSP16), mRNA. /// ENST00000298573 // intron // 0 // --- // --- // --- // ---	DUSP16	DUSP16, Homo sapiens dual specificity phosphatase 16 (DUSP16), p13.2
SNP_A-2227432	ctacacgccgaggcct[A/G]aagaagaggaaacaat	A	G	FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2183839	cagcatttgtgatgaa[A/G]tcttttgcaaggggt	A	G	Homo sapiens serine protease HTRA3 (HTRA3), mRNA. /// ENST00000307358 // intron // 0 // --- // --- // --- // ---	HTRA3	HTRA3, Homo sapiens serine protease HTRA3 (HTRA3), p16.1
SNP_A-2193284	catctcctaagatcac[A/G]gactgcaccttaattt	A	G	Homo sapiens mRNA for KIAA1384 protein, partial cds. /// ENST00000359358 // intron // 0 // --- // --- // --- // --- ///	KLHL14	KLHL14, Homo sapiens for KIAA1384 protein, partial cds. q12.1
SNP_A-2169904	caaggccaaactctca[C/T]gatgaccaggaagtag	C	T	2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 93677 //	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-2135467	atatttgctcttcttg[C/T]attttttcatgatta	C	T	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 927086 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2125165	agttgggaacttaaaa[C/T]gaatcaagtcataggt	C	T	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1708627	gctacatatgtaagcaataaaggta[A/T]ctatcttaatgggtatacagctatt	A	T	5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 1550910 // Hs.285782 // LRRTM4 // 80059 // leucine-rich	REG1B	REG1B , rs283905, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-1785735	ggctctctccagcaga[A/G]gaaatctaatcccggc	A	G	Homo sapiens mitochondrial ribosomal protein S18A (MRPS18A), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000211302 // intron // 0 // --- // --- // --- // ---	MRPS18A	MRPS18A, Homo sapiens mitochondrial ribosomal protein S18A (MRPS18A), nuclear gene encoding mitochondrial protein, p21.1
SNP_A-1818938	gttgatgttcttttct[C/T]aaggcttcatggacta	C	T	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 582314 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1853683	tatttttagtgaaca[G/T]atctgcaactgatgag	G	T	Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // --- // --- // --- // ---	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-1850572	tattaagtaagatcag[G/T]aagacctgtgttaaaa	G	T	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 986830 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1984477	ttcttaattatgatga[A/T]gcaggagggtgaaaca	A	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4185213 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1948637	tttataatacccaata[C/T]gacataaatgctatgt	C	T	// Homo sapiens hypothetical protein MGC26710 (MGC26710), mRNA. /// ENST00000336726 // intron // 0 // ---	HORMAD2	HORMAD2, Homo sapiens hypothetical protein MGC26710 (MGC26710), q12.2
SNP_A-1898254	tgcttacttctatgtg[C/T]atttctagttaagttc	C	T	LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 //	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-1926557	ttattctctccttgta[A/T]cctctgttaacatctt	A	T	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 1157949 //	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1876373	tctgagtaccaacaac[C/T]cctcattcacttccaa	C	T	/// ENST00000354196 // upstream // 240809 // --- // --- // --- // -- /// ENST00000355224 // upstream // 240809 // --- // --- // ---	-	q21.11
SNP_A-1948624	tttataagctcttgaa[A/G]gggttaacaactagaa	A	G	4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 126463 // --- // FLJ34047 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1847660	tatctacagagcaatg[A/C]aatttttttggagaca	A	C	Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // --- // --- // --- // ---	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-1853900	tcaaaaggcaggaatg[A/C]aagagacaaatgtgtg	A	C	/// ENST00000332935 // upstream // 82721 // --- // --- // --- // ---	-	q23.3
SNP_A-1787703	gggacaggtctccctc[A/G]atgggttagaatacag	A	G	sapiens ras homolog gene family, member C (RHOC), mRNA. /// ENST00000339083 // intron // 0 // --- // --- // --- // ---	RHOC	RHOC, Homo sapiens ras homolog gene family, member C (RHOC), p13.2
SNP_A-1800894	gtagaggaagcagtca[A/C]atacgcaattgtttca	A	C	-- /// ENST00000276737 // downstream // 333914 // --- // --- //	-	q24.23
SNP_A-2163002	attttgtttttggtca[A/G]agatgtcaagatgcat	A	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2172576	caattctgggagtata[C/T]agcacacaggaccccc	C	T	// 79149 // Homo sapiens zinc finger protein 495 (ZNF495), mRNA. /// ENST00000358992 // upstream // 10051 // --- // ---	ZSCAN5	ZSCAN5, Homo sapiens zinc finger protein 495 (ZNF495), q13.43
SNP_A-2175012	cacagtaaaataatgg[A/G]acatgacaaacttttg	A	G	C20orf79 // 140856 // Homo sapiens chromosome 20 open reading frame 79 (C20orf79), mRNA. /// NM_020689 //	C20orf79	C20orf79, Homo sapiens chromosome 20 open reading frame 79 (C20orf79), p11.23
SNP_A-2222767	cgatgtcagaaaagtc[A/C]agggtttctcattcca	A	C	9685 // Homo sapiens enthoprotin (ENTH), mRNA. /// ENST00000296951 // upstream // 115727 // --- // --- // --- // ---	ENTH	ENTH, Homo sapiens enthoprotin (ENTH), q33.3
SNP_A-2069964	acacaggtattttcaa[A/G]gcagtatttcttcgtg	A	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 675167 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-2029117	aaagaaatgtaaccaa[A/G]gaggaattagggaggg	A	G	MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2014887	tactttgtttgaattc[A/G]ccaaatatgtttttct	A	G	Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // intron // 0 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2311220	ggaagtttggatagtc[C/T]agatggcgatttggga	C	T	Homo sapiens MEGF11 protein (MEGF11), mRNA. /// ENST00000288745 // intron // 0 // --- // --- // --- // ---	MEGF11	MEGF11, Homo sapiens MEGF11 protein (MEGF11), q22.31
SNP_A-2299334	gccctgaccaatcata[A/G]taccttttctacctctg	A	G	FLJ25168 // 147081 // Homo sapiens hypothetical protein FLJ25168 (FLJ25168), mRNA. /// NM_004382 // upstream //	FLJ25168	FLJ25168, Homo sapiens hypothetical protein FLJ25168 (FLJ25168), q21.31
SNP_A-2287771	gattactgtcctcaga[C/G]aggtcaggtcagctct	C	G	51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 433484 // Hs.271977	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-2287855	gattagtactgcaaaa[A/C]ctacaagcctgtgatg	A	C	84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream //	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-2239196	ctcttgctattcagat[G/T]accaccccactcatct	G	T	ENST00000287226 // intron // 0 // --- // --- // --- // ---	-	q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2240290	ctgaatgtgatttaaa[C/T]ttcattgtcagaggtg	C	T	83417 // Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // upstream // 20522 // --- // --- // --- // ---	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1
SNP_A-2257891	ctttgtacacacagga[A/G]cattgagaccattgtt	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2274240	gacttgaacacaccaa[A/C]aaaacattgtttggga	A	C	sapiens (clone zap113) mRNA, 3' end of cds. /// ENST00000238571 // intron // 0 // --- // --- // --- // ---	YLPM1	YLPM1, Homo sapiens (clone zap113) 3' end of cds. ,q24.3
SNP_A-2289616	gcaaaaagcctagcta[C/T]attgcgcccctgcttt	C	T	51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 55847 // --- // ---	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-2311903	ggacaaatatctatca[C/T]ctttttcaggttcaat	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2304470	gctctagtcatcacaa[C/T]catgttccaggcagca	C	T	57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // upstream // 135179 // --- // ---	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2016062	acttgtttattcttca[A/G]tgaaataccgaaactt	A	G	/// ENST00000331037 // downstream // 357392 // --- // --- // ---	-	q21.1
SNP_A-2009841	aacaagaagtataaca[A/T]tcattctgctacacct	A	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3910364 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2006700	acaggggtctcgcca[C/G]tgctcaagggagattc	C	G	FLJ38377 // 205147 // Homo sapiens hypothetical protein FLJ38377 (FLJ38377), mRNA. /// NM_015320 // upstream //	FLJ38377	FLJ38377, Homo sapiens hypothetical protein FLJ38377 (FLJ38377), q21.1
SNP_A-1997324	gtggcctggcctagtc[A/G]cttgactcattttgtt	A	G	Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA. /// NM_052820 // intron // 0 // Hs.113094 // CORO2A // 7464 // Homo sapiens coronin, actin	CORO2A	CORO2A, Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, q22.33
SNP_A-1997931	aaccacattcacatac[A/G]tgccataagtccctga	A	G	ENST00000358221 // upstream // 18705 // --- // --- // --- // --- /// ENST00000356179 // upstream // 21097 // --- // --- // --- // ---	-	,p12.31
SNP_A-2033427	aaataggggtggttga[C/T]actgcagatgtaaaaa	C	T	2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 81509 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2093089	agaacagtagttacca[A/G]aaaccagggagggaat	A	G	/// ENST00000340614 // upstream // 32194 // --- // --- // --- // ---	-	p13.2
SNP_A-2096362	agacccacaaggctaa[A/G]gttctcattgtgtttg	A	G	// 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000327792 // downstream // 608253 // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2222179	cgacaaagatattcac[A/G]caggaacagatttggg	A	G	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 267695 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2198778	catttctctgcaaaaa[C/T]attcctatgcttgagg	C	T	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, mRNA. /// NM_172362 // intron // 0 // Hs.527656 // KCNH1 //	KCNH1	KCNH1, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, q32.2
SNP_A-2184689	cagctctgttcaagaa[A/G]tgttattgtagttgct	A	G	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2164812	caaaccagacagtagc[C/G]agaggagagtttaatc	C	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2157885	attgctatctcaaata[A/T]ctccttttttagtcag	A	T	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// ENST00000357667 // intron // 0 // --- // --- // --- // ---	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-2155410	attcatgcagtctaaa[A/G]tgcagtttgttttgag	A	G	Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000274071 // intron // 0 // --- // --- // --- // ---	PDGFC	PDGFC, Homo sapiens platelet derived growth factor C (PDGFC), q32.1
SNP_A-2155602	attccacctgtgcttc[C/T]ctttggtgcagaagag	C	T	153830 // Homo sapiens hypothetical protein FLJ31951 (FLJ31951), mRNA. /// NM_145049 // upstream // 36631 //	FLJ31951	FLJ31951, Homo sapiens hypothetical protein FLJ31951 (FLJ31951), q33.3
SNP_A-2137996	atccaaaaagtagata[C/T]actccagatgtccatt	C	T	ENST00000359626 // intron // 0 // --- // --- // --- // --- /// ENST00000343721 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2127997	ctacacctttatctat[A/T]agcaatttatggatgt	A	T	51569 // Homo sapiens ubiquitin-fold modifier 1 (Ufm1), mRNA. /// ENST00000239878 // downstream // 17031 // --- //	Ufm1	Ufm1, Homo sapiens ubiquitin-fold modifier 1 (Ufm1), q13.3
SNP_A-2112519	aggcacagtgagtcag[C/G]aagggcctgtccatgt	C	G	ENST00000265453 // intron // 0 // --- // --- // --- // --- /// ENST00000298124 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-1808969	gtgaattactaaagat[A/T]aaactagtagactgat	A	T	254958 // Homo sapiens exonuclease GOR (GOR), mRNA. /// NM_033126 // downstream // 184387 // Hs.532044 //	GOR	GOR, Homo sapiens exonuclease GOR (GOR), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1675756	gatgaggatgtggatacattggaac[C/T]cttgcgcaccgttggtggaaatgta	C	T	2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 403732 // Hs.279943 // LMCD1 // 29995 // LIM	GRM7	GRM7 , rs527498, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-1729792	gtatccatatctgtactatacttca[C/G]ggaacctatccaaaggaaataatat	C	G	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs4279912, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-1855790	tcaatctctataaata[C/T]atcgtgcaccgaactc	C	T	/// ENST00000341548 // downstream // 9902 // --- // --- // --- //	-	q22.33
SNP_A-1847590	tatcggctggccgttc[C/T]atacataggcaacttt	C	T	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 551235 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1851851	tattgagactctgtta[C/T]gtgccaagcacttaaa	C	T	Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // intron // 0 // --- // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-1872777	tctatacaagatgtaa[C/T]tagttaatgaagagaa	C	T	Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// ENST00000265283 // intron // 0 // --- // ---	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin,q21.13
SNP_A-1816462	gttagctgtttcagtc[C/T]attttaatttcatgtt	C	T	// 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 46338 // Hs.436387 // BCKDHB	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1
SNP_A-1831342	taatgtaccaactttg[A/G]attctgtttgtgtgtt	A	G	Homo sapiens hypothetical protein FLJ32743 (FLJ32743), mRNA. /// ENST00000303601 // intron // 0 // --- // --- // --- // ---	CCDC11	CCDC11, Homo sapiens hypothetical protein FLJ32743 (FLJ32743), q21.1
SNP_A-1947756	tttactgaattaccaa[C/T]gctagatatgttgcta	C	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-1973547	tgagatttgtttgaca[C/T]acagtgaacccttcaa	C	T	2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // downstream // 5264 // Hs.123642 //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1886022	tgaccaaaggagatag[C/T]ccttgatgtttcctgt	C	T	84466 // Homo sapiens MEGF10 protein (MEGF10), mRNA. /// ENST00000327728 // upstream // 112472 // --- // --- // --- // -	MEGF10	MEGF10, Homo sapiens MEGF10 protein (MEGF10), q23.2
SNP_A-1899178	tggaaataagcagata[C/T]acaatgaggaagaaaa	C	T	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1891407	tgattattcacagcaa[A/G]cttcatgtaaatggta	A	G	// Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 99547 // --- // --- // --- // ---	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1920570	ttaatttcaaaataac[A/C]actgtgaattcagaaa	A	C	sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1920023	ttaatatagcaacagc[A/G]ctttaagttagtattt	A	G	Homo sapiens ankyrin repeat and SOCS box-containing 5 (ASB5), mRNA. /// ENST00000296525 // intron // 0 // --- // ---	ASB5	ASB5, Homo sapiens ankyrin repeat and SOCS box-containing 5 (ASB5), q34.2
SNP_A-1919466	ttaagcccagacagta[A/C]aaagccaccgggaata	A	C	9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // downstream //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-1910479	tgtccctcatatacac[A/G]cccaggcttagagaaa	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1966328	tgagcaagaaataatc[A/G]tctgtgtactaagtca	A	G	/// ENST00000354860 // upstream // 998144 // --- // --- // --- //	-	q32.3
SNP_A-1963008	ctttgacagagcggta[A/C]caccaggacaatgtac	A	C	10736 // Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA. /// NM_018079 // downstream //	SIX2	SIX2, Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), p21
SNP_A-1937114	ttctttttatgagaac[C/T]gttcatgtaaaagaat	C	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 75684	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-1935071	ttctgatctaaagaag[C/T]cattgttgtgtttcta	C	T	2488 // Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), mRNA. /// NM_152316 // upstream //	FSHB	FSHB, Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), p14.1
SNP_A-1961089	tttttgtgataatcag[C/T]ccaaactatgacaact	C	T	// Homo sapiens hypothetical protein FLJ35867 (FLJ35867), mRNA. /// ENST00000267817 // intron // 0 // --- // --- // --- // ---	FLJ35867	FLJ35867, Homo sapiens hypothetical protein FLJ35867 (FLJ35867), q15.3
SNP_A-1836163	tactagtctaattcgg[A/G]aaactaagagaaaccg	A	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1872597	tctagggtatgtcaaa[A/G]tgtccacaagccctgt	A	G	C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 //	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-1749887	gattaatgttttgctctgataaaaa[C/T]agattttggttcttaagggaaatct	C	T	contactin 4	CNTN4	CNTN4 , rs10510240, contactin 4,p26.2
SNP_A-1806478	gtcggaatagaagaaa[C/T]aacctgtgccacagct	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA. /// ENST00000282356 // intron // 0 // ---	CAMK4	CAMK4, Homo sapiens calcium q22.1
SNP_A-1790497	ggggcatacctgggtc[A/G]agaattattatcataa	A	G	4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// NM_145020 // downstream // 4874 // Hs.132701 //	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. ,q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137548	atcatccccagtttta[C/T]ggatgacaaggttttg	C	T	55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 36720	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2192565	catccacggccaccag[C/G]aggtgaaaaacaccca	C	G	// 80067 // Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 // downstream //	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-2223488	cgcttgtactcgggac[C/G]gcttggtcaaggctgc	C	G	sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // intron // 0 // Hs.436055 // ALX4 // 60529 //	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds. ,p11.2
SNP_A-2217109	cctcttcttctgtgaa[A/G]tgatggtgtcccagaa	A	G	// 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 431245 // --- // --- // --- //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2203729	ccagagaatataggct[A/G]aattggggtcttcatc	A	G	/// ENST00000359064 // upstream // 332335 // --- // --- // --- // -- /// ENST00000332041 // downstream // 179239 // --- // --- //	-	q22.1
SNP_A-2086329	actcttaacctcataa[C/T]gaattccaaaaagaag	C	T	ENST00000342193 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2072184	acagatgacttgagaa[C/T]aaaaaaggcaaggcac	C	T	Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1409236 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2054732	aataaaatgaaaatga[C/G]caataacctcaggagt	C	G	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (DDX55), mRNA. /// ENST00000238146 // intron // 0 // --- // ---	DDX55	DDX55, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (DDX55), q24.31
SNP_A-2058222	aatcaaccttcctaac[C/T]gtctggactcttggtc	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000339732 // intron // 0 // --- // --- // --- // --- ///	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-2026075	aaaattagaactggct[C/T]acctcaatgagtattt	C	T	/// ENST00000333076 // upstream // 188307 // --- // --- // --- // -- /// ENST00000242140 // upstream // 188307 // --- // --- // ---	-	p15.1
SNP_A-2022635	aaaaatgcttagagaa[A/G]tgattactcctagtca	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 640479 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2035813	aaatgttaaggcacaa[C/T]ggatgctcagaaaacg	C	T	440044 // Homo sapiens FLJ16331 protein (FLJ16331), mRNA. /// NM_031904 // 3UTR // 0 // Hs.362974 // FKSG44 //	FLJ16331	FLJ16331, Homo sapiens FLJ16331 protein (FLJ16331), q13.1
SNP_A-2035089	aaatgcataaaaggaa[A/G]gactggtgacacgaag	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 908603 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2042560	aactcattgtacctaa[A/C]ctgtttgtacaaacaa	A	C	55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 197852 // Hs.411881 // GRB14	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-2044078	aacttggaacaattca[A/T]acaaaaagggcgaaga	A	T	// Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// ENST00000355875 // intron // 0 // ---	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44
SNP_A-2011052	ttgaaagcaacaaggg[A/T]aatatgtcccttcact	A	T	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1077392 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-2016874	ggtgaagaaaagttaa[C/T]ccagttggagaccaga	C	T	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 504444	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2017440	aaagacagacactatg[A/C]aacccgttgttttttt	A	C	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2302649	gctacccctttatggc[C/T]acagacagctccctcc	C	T	256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // --- // --- // --- // --	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-2295494	gcatctcaaagactgt[C/T]aaaaatcattttgctc	C	T	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 97670 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-2232459	ctcacatacctacaaa[C/T]gaagtaatagagttgg	C	T	Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q27
SNP_A-2242710	ctgcatctgagaaaaa[A/T]caagtcagtctgtttc	A	T	Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // intron // 0 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC rela	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. ,q27
SNP_A-2248177	ctgtggggtcaatttc[C/T]agtgaaccttgaaaat	C	T	Homo sapiens RAB27B, member RAS oncogene family (RAB27B), mRNA. /// ENST00000262094 // intron // 0 // --- // -	RAB27B	RAB27B, Homo sapiens RAB27B, member RAS oncogene family (RAB27B), q21.2
SNP_A-2256747	ctttcatgctaatgcc[C/T]ctttaatgtttccatt	C	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 805668 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2262946	gaacaagagtcttaca[A/G]cagagaagtagtttct	A	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017408	tgttggtgcttctagt[A/C]aattctttaggaataa	A	C	// 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2016251	ctgttcctcagatata[A/G]atgctagaggagatgg	A	G	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2044497	aagaaaagtggcacaa[A/G]ctgggtggcctaaaac	A	G	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 217401 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-2046137	aagactgaggattggg[A/G]atatttaaatgaagat	A	G	sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // CDS // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2043497	aactgtagtaacttga[A/T]gttggcttacagagag	A	T	ENST00000312751 // intron // 0 // --- // --- // --- // ---	-	q41
SNP_A-2052390	aagtacctgattgata[C/T]agaaaatgtgttaaca	C	T	54806 // Homo sapiens Abelson helper integration site (AHI1), mRNA. /// NM_002604 // upstream // 168644 //	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3
SNP_A-2064859	aattgaacttttcatg[C/T]actcactggatttctg	C	T	Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// ENST00000341258 // intron // 0 // --- // --- // --- // ---	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43
SNP_A-2192143	catcagaaataatgat[C/G]agaagattcgaatgct	C	G	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2115042	agggcctggaaccccc[C/G]actgtggagctgctgt	C	G	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA. /// ENST00000245620 // intron // 0 // --- // --- // --- // --- /// ENST000003	LILRB3	LILRB3, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), q13.42
SNP_A-2114249	agggaagattagaaaa[A/G]gagggattatagagag	A	G	Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // ---	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2145569	atgcatatagaatcaa[A/G]gcttctctgatttttta	A	G	Homo sapiens PHD finger protein 12 (PHF12), mRNA. /// ENST00000268756 // intron // 0 // --- // --- // --- // ---	PHF12	PHF12, Homo sapiens PHD finger protein 12 (PHF12), q11.2
SNP_A-1800014	gtacatcatcttccaa[A/G]gaatctcattactgca	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 168753 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1830948	taatgacaaatcccaa[A/G]ttcaggataatagtta	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1951928	tttctactggaaccac[A/G]aaaaactaattcttac	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 682946 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1935956	ttcttaattggttaat[A/G]atgccatgtgggcagt	A	G	Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// ENST00000306821 // intron // 0 // --- // --- // --- // --- ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1976076	agctttgggctttcaa[C/T]agactttcatgaaggt	C	T	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 781895 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1982982	ctgaattttggtcaca[C/T]tgatcttttagattag	C	T	83942 // Homo sapiens serine/threonine kinase 22D (spermiogenesis associated) (STK22D), mRNA. ///	STK22D	STK22D, Homo sapiens serine q22.2
SNP_A-1978636	aaattctttctctaga[C/T]cataaagttgtgcaat	C	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-1906746	tggttaatggagacaa[A/C]ttcaattcaaatatgt	A	C	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 210650 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1915479	tgttccttatctgggt[C/T]aattgtgtctgcccaa	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1921759	ttactaagaggccaaa[A/G]gagatcaagtatatgg	A	G	// 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 433883 //	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1897460	tgctgagaagagggag[A/G]aaacttcagaacacta	A	G	// 79666 // Homo sapiens pleckstrin homology domain containing, family F (with FYVE domain) member 2 (PLEKHF2), mRNA. /// NM_177965 // downstream // 74176 //	PLEKHF2	PLEKHF2, Homo sapiens pleckstrin homology domain containing, family F (with FYVE domain) member 2 (PLEKHF2), q22.1
SNP_A-1931844	ttccgagtactttcca[C/T]tgaagcacagatacgt	C	T	/// ENST00000354860 // upstream // 524807 // --- // --- // --- // ---	-	q32.3
SNP_A-1984556	ccacatcttcattttc[A/G]aatctgaatacgttaa	A	G	// Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// NM_004137 // downstream // 71097 // Hs.484099 // KCNMB1	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-1971945	tactgggaggttccta[A/G]cagagatagggtagct	A	G	Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // intron // 0 // --- // --- // --- // ---	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1835657	taccttgttacacata[C/T]cccgtcccttgacact	C	T	// Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 //	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872640	tctagtacaaagatta[A/G]aatcaaaacagtcaaa	A	G	57542 // Homo sapiens mRNA for KIAA1340 protein, partial cds. /// NM_198964 // downstream // 63934 // Hs.89626 //	KLHDC5	KLHDC5, Homo sapiens for KIAA1340 protein, partial cds. p11.22
SNP_A-1871865	tctacacacattcagg[A/T]catgaatcgaggctat	A	T	// Homo sapiens mRNA for KIAA0559 protein, partial cds. /// AB002329 // downstream // 172038 // Hs.528721 // SEMA3E	PCLO	PCLO, Homo sapiens for KIAA0559 protein, partial cds. q21.11
SNP_A-1871781	tctaattcttatctta[C/T]gttgtatggattatgg	C	T	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 673643 // Hs.146100	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-1855154	tcaagatagtggatga[C/T]ggagaattcttataag	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-1804569	gtcagcagaggacaga[A/G]agcatagatacaagac	A	G	// Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), mRNA. /// ENST00000249601 // intron // 0 // ---	ARHGAP22	ARHGAP22, Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), q11.22
SNP_A-2160287	atttcagaactaacac[C/T]gtctgggtttgagtaa	C	T	-- /// ENST00000314071 // upstream // 642457 // --- // --- // ---	-	p13.3
SNP_A-2120158	agtcagatacaagaac[A/G]gcccacaagcaccact	A	G	6427 // Homo sapiens splicing factor, arginine/serine-rich 2 (SFRS2), mRNA. /// NM_024311 // downstream // 48521 //	SFRS2	SFRS2, Homo sapiens splicing factor, arginine,q25.2
SNP_A-2188766	cagtggcaaagaaaga[A/C]aagcattgaaaagcac	A	C	// Homo sapiens solute carrier family 35, member A4 (SLC35A4), mRNA. /// ENST00000323146 // intron // 0 // --- //	SLC35A4	SLC35A4, Homo sapiens solute carrier family 35, member A4 (SLC35A4), q31.3
SNP_A-2180892	cagaatgtaatcttac[A/G]aggctgatctttttc	A	G	Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// ENST00000303575 // 3UTR // 0 // --- // --- // --- // ---	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2215145	cctatttatttataga[C/T]gtcattttggttatgc	C	T	221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 56415	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2076742	acatttttattagcca[C/G]agtcatccatagtttc	C	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 709053 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2087408	actgcatctgaagcac[A/G]gtaacattctctgtca	A	G	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 213553 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2046002	aagaccttgtcttaaa[A/G]aagagaatgtgtccag	A	G	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2010804	ttgccttctgtacaaa[C/T]gtggctgtctgtgagt	C	T	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // --- // --- // --- // ---	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-2274353	gacttgtgtcagaggc[C/T]ctttctcttagttgtt	C	T	54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 21316 // Hs.464079	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-2273443	gactctgaccatagca[C/T]caggagaaaatagtgg	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2290855	gcaaggattttcccaa[C/T]gaacctgaagcccagg	C	T	64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 268784 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2287677	gattaatgacagacta[C/T]attactgatttttcc	C	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 717667 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2286728	gatggcagcatagaag[C/T]acaagtttctagtccc	C	T	// 10885 // Homo sapiens WD repeat domain 3 (WDR3), mRNA. /// NM_206996 // upstream // 389333 // Hs.528821 //	WDR3	WDR3, Homo sapiens WD repeat domain 3 (WDR3), p12
SNP_A-2284726	gatcatagcacatgta[C/G]atttggtgtcaggtga	C	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2268015	gaatctggcataaacc[C/T]agaggtggagaaatca	C	T	7465 // Homo sapiens WEE1 homolog (S. pombe) (WEE1), mRNA. /// ENST00000299613 // downstream // 59579 // --- //	WEE1	WEE1, Homo sapiens WEE1 homolog (S. pombe) (WEE1), p15.4
SNP_A-2253034	cttctctaaatcccag[A/G]cctgaatttttttcag	A	G	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 131228 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2251983	cttccaaaggcaacac[A/T]cccaccagtcactact	A	T	Homo sapiens F-box and WD-40 domain protein 11 (FBXW11), transcript variant 1, mRNA. /// NM_033644 // intron // 0 // Hs.484138 // FBXW11 // 23291 // Homo sapiens	FBXW11	FBXW11, Homo sapiens F-box and WD-40 domain protein 11 (FBXW11), transcript variant 1, q35.1
SNP_A-2006030	aacaaaccttatggca[C/G]actttaaagatatcca	C	G	ENST00000331416 // downstream // 73137 // --- // --- // --- // --	-	q13.41
SNP_A-2037273	aacaaagagggatgca[A/G]taaaaggtgaagtctg	A	G	-- /// ENST00000345029 // upstream // 65721 // --- // --- // --- //	-	p14
SNP_A-2081280	acctggaattgaacag[G/T]acaactgaactctgca	G	T	ENST00000344941 // intron // 0 // --- // --- // --- // ---	-	p12.3
SNP_A-2096305	agaccagctaaccccc[A/G]cagaccacagatacag	A	G	sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// ENST00000296212 // intron // 0 // --- // --- // --- // ---	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2070017	acacagttcagaaaat[C/T]aagagacaagggaact	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2062743	aatgtgaaggtgcctg[C/T]atgaggccgagaggaa	C	T	sapiens rap2 interacting protein x (RIPX), mRNA. /// ENST00000226328 // intron // 0 // --- // --- // --- // ---	RIPX	RIPX, Homo sapiens rap2 interacting protein x (RIPX), q13.3
SNP_A-2214554	cctagacatagacaaa[C/T]ttgctggcaggcagct	C	T	Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // — // --- // — // ---	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-2211851	ccctctgtagctggcc[A/G]ctagcataaattgatg	A	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2169601	caagctgtataactga[A/T]cttgttacactttgct	A	T	// 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2191237	catatacacgagtcag[C/G]cattaaaaataggctc	C	G	ENST00000327381 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2108038	tcagaggccaggatga[G/T]gacttccgattttatt	G	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2139921	atctacacagctgcac[C/G]gagcctggcgagcagc	C	G	// 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream //	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-2142766	atgaagctttagaata[C/T]gtggcagcagaattct	C	T	ENST00000332738 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1807486	gtctgccatatcaata[C/T]gctagattattttcca	C	T	/// ENST00000355561 // upstream // 49156 // --- // --- // --- // ---	-	q21.31
SNP_A-1720055	gtcgcttttccttccacctgatttc[C/T]cagtctggataatccaaatacacaa	C	T	NM_024656 // intron // 0 // Hs.418795 // FLJ22329 // 79709 // hypothetical protein FLJ22329	FLJ22329	FLJ22329 , rs3848643, hypothetical protein FLJ22329,p13.11
SNP_A-1782330	ggcaatgactgaatat[G/T]aacttccatagcctga	G	T	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1482764 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1664230	ttctagatgtacgatgattataaaa[C/G]atacacttaaaaatggaaataccaa	C	G	// phospholamban /// NM_012107 // upstream // 320266 // - // // - // - /// NM_138459 // downstream // 473115 // Hs.289008 //	PLN	PLN , rs176168, phospholamban ,q22.31
SNP_A-1843662	tagtggtcttggcaga[G/T]tagtacccctctctgg	G	T	ST6GALNAC6 // 30815 // Homo sapiens sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytrans /// NM_175040 // downstream // 2076 // Hs.3972 // ST6GALN	ST6GALNAC6	ST6GALNAC6, Homo sapiens sialytransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialytrans ,q34.11
SNP_A-1985879	gaacaattggttttaa[C/T]tacaatgtcaattgaa	C	T	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 424177 // Hs.497822 // DUSP10 // 11221 //	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-1986786	agtcactgaattagaa[A/C]tgaaacttcccattta	A	C	// Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, mRNA. /// NM_016083 // upstream //	CNR1	CNR1, Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, q15
SNP_A-1935854	ttctgttgttagatga[A/G]gtattctataaatgtc	A	G	374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1930221	ttcattctcatcttca[A/G]cagttcatcaaatagc	A	G	Homo sapiens exosome component 9 (EXOSC9), mRNA. /// ENST00000357078 // intron // 0 // --- // --- // --- // --- ///	EXOSC9	EXOSC9, Homo sapiens exosome component 9 (EXOSC9), q27
SNP_A-1875358	tctctgataattaaaa[A/G]tgccaggcctgtgcct	A	G	// 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1908046	tgtacaacttttgcc[A/G]caacctcagaaaaatc	A	G	57182 // Homo sapiens mRNA for KIAA1223 protein, partial cds. /// ENST00000281131 // upstream // 12901 // --- // --- // ---	KIAA1223	KIAA1223, Homo sapiens for KIAA1223 protein, partial cds. q28.1
SNP_A-1939253	ttgatcattatgatga[A/C]actatgctatttaaaa	A	C	sapiens hexosaminidase B (beta polypeptide) (HEXB), mRNA. /// ENST00000261416 // intron // 0 // --- // --- // --- // ---	HEXB	HEXB, Homo sapiens hexosaminidase B (beta polypeptide) (HEXB), q13.3
SNP_A-1831896	taattgaatatactgg[G/T]aaccttggaaggatca	G	T	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-1818915	gttgatgatcctgtta[G/T]acatttttttatttatt	G	T	ENST00000333644 // intron // 0 // --- // --- // --- // ---	-	q35.2
SNP_A-1854179	tcaaagagaaactact[A/G]aaattcacacatttgt	A	G	// Homo sapiens desmoplakin (DSP), mRNA. /// NM_152551 // upstream // 3122 // Hs.13366 // C6orf151 // 154007 // Homo	DSP	DSP, Homo sapiens desmoplakin (DSP), p24.3
SNP_A-1846063	tatatatatatatctc[A/G]cagtttctttatccac	A	G	6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// ENST00000329573 // upstream // 25047 // --- // --- // --- // ---	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q23.3
SNP_A-1872154	tctactgaagtcaata[C/T]agttggtcttgctctg	C	T	ENST00000354215 // intron // 0 // --- // --- // --- // ---	-	q13.12
SNP_A-1861695	tcatctcttatcatca[G/T]ctaggcatcatatcat	G	T	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2149743	atgtatgttaaagaaa[C/T]cttactgcagtagaac	C	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1468857 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2155535	attccaaaagaggctc[C/T]aacaagaaagcagcct	C	T	79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 166449 //	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2111145	aggagaggaactgaac[A/G]gagtaattattctact	A	G	Homo sapiens isoprenylcysteine carboxyl methyltransferase (ICMT), transcript variant 2, mRNA. /// NM_012405 // 3UTR // 0 // Hs.515688 // ICMT // 23463 // Homo sapiens	ICMT	ICMT, Homo sapiens isoprenylcysteine carboxyl methyltransferase (ICMT), transcript variant 2, p36.31
SNP_A-2117948	aggtttggttcttctc[C/T]actagtggtcggggat	C	T	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2130605	atactgagcaggctac[A/G]aaagctttccaggcat	A	G	9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1127323 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2186337	caggctgctggtatgc[A/G]aggccacttgtagctc	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 211993 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2180391	cagaacaaatcatcca[G/T]ccaaatttttcattta	G	T	8671 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), mRNA. /// NM_000583 // downstream // 9002 // Hs.418497 // GC // 2638	SLC4A4	SLC4A4, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), q13.3
SNP_A-2207233	ccattcagcagaagca[A/G]tactttgaattttgat	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 605419 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2206467	ccatctgcagtaggaa[A/T]gcggaggacgccttct	A	T	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 99545 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2074453	acatagaaataatgac[C/T]ctggatttagtgacag	C	T	1390 // Homo sapiens cAMP responsive element modulator (CREM), transcript variant 5, mRNA. /// NM_001881 // downstream // 67721 // Hs.200250 // CREM // 1390 // Homo	CREM	CREM, Homo sapiens cAMP responsive element modulator (CREM), transcript variant 5, p11.21
SNP_A-2055304	aataagcaaacacaaa[C/G]gtaaagcaataaaaaa	C	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 970381 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2098478	agagcacattagtggt[A/G]aataccaggaagaaaa	A	G	ENST00000319540 // intron // 0 // --- // --- // --- // ---	-	q21.22
SNP_A-2080840	acctcgtttgctgagc[A/G]ctttctcttatgaatc	A	G	// Homo sapiens hypothetical protein LOC91942 (LOC91942), mRNA. /// ENST00000296597 // intron // 0 // ---	LOC91942	LOC91942, Homo sapiens hypothetical protein LOC91942 (LOC91942), q12.1
SNP_A-1991832	tatcctaattggagag[A/G]accaacaattaacagc	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2252539	cttcctgggaaaaaca[A/T]tgtttcactgacaaat	A	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q22.1
SNP_A-2253388	cttctgtgactgcaag[C/G]aagtggctacctatcc	C	G	SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 317293 // Hs.492612 // THRAP6 //	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2247065	ctgtatttttagatc[C/T]ctgaagacatcaaaaa	C	T	Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), mRNA. /// ENST00000326693 // intron //	UBR1	UBR1, Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), q15.2
SNP_A-2246811	ctgtagcaggttccag[A/G]atggtcagatcctcca	A	G	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2235992	agtgatttgtaggcca[A/G]aagaaaggttctgttt	A	G	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2290952	gcaagtattgaaatcc[A/T]cttagaaaagtcagga	A	T	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 469511 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2302925	gctaggaacagagaac[A/T]gactatagtgactaaa	A	T	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2304213	gctccgtggccggctc[A/G]ctgtgggaccctggcc	A	G	Homo sapiens catenin, beta like 1 (CTNNBL1), mRNA. /// ENST00000347721 // intron // 0 // --- // --- // --- // --- ///	CTNNBL1	CTNNBL1, Homo sapiens catenin, beta like 1 (CTNNBL1), q11.23
SNP_A-2237821	ctctgaaatgccatcc[A/C]aacataaatatagttg	A	C	57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 58106 // --- // --- // --- // ---	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2240265	ccatcaagagaaatct[A/G]aaattggagtacttat	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2234494	ctccaccacaagtaca[A/T]atgcataaaacaaaaa	A	T	Homo sapiens calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 2, mRNA. /// ENST00000327479 // intron // 0 // --- // --- // --- // ---	CACNB4	CACNB4, Homo sapiens calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 2, q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2244235	ctggaaactccgagaa[C/T]tcctcagtgatatgcc	C	T	Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // intron // 0 // Hs.200262	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-2277940	ggagcaattacctccc[C/T]catctggctccttagg	C	T	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1994191	taagggaagaaaacag[A/T]aatgtcaaacaatttg	A	T	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 899958 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2000679	accagcctggcagcaa[G/T]gtcctcttcctctcat	G	T	FLJ32796 // 149647 // Homo sapiens hypothetical protein FLJ32796 (FLJ32796), mRNA. /// NM_018664 // downstream	FLJ32796	FLJ32796, Homo sapiens hypothetical protein FLJ32796 (FLJ32796), q32.3
SNP_A-2016358	gtcagccaatgtgttc[A/G]ctgcactttgacagac	A	G	// 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2047316	aagatcagaataaacc[A/G]caaagaagtctgtctc	A	G	// 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 185878 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-2021382	aaaaaagaaccaaaca[G/T]atatccaggaactaat	G	T	Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // --- // --- // --- ///	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2077047	accaactcaaagaatg[A/G]aaggattctagaaaca	A	G	Homo sapiens S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA. /// ENST00000358003 // intron // 0 // --- // --- // --- // ---	S100A10	S100A10, Homo sapiens S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), q21.3
SNP_A-2075717	acatgggcctctttaa[A/G]cacaggcaagtttggc	A	G	Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// ENST00000244003 // intron // 0 // --- // ---	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-2201094	ccaagtcaccgagaga[C/G]agcaattacatcagaa	C	G	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2202381	ccaccatcatcttaaa[C/G]acccagaatggctccc	C	G	MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream //	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-2208879	cccagattccagcctc[A/G]gagaactatttttga	A	G	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2217048	cctcttagtattgcct[C/T]agctgtgttccacaca	C	T	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 287872 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-2169932	caaggcctgaatcaaa[G/T]ctcagagacttgaagc	G	T	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 472173 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2188899	cagtgtacacattgca[A/G]tatttcttgaataaat	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1222689 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2129234	ataattttaagatgtc[A/G]gaaaaggatactttga	A	G	Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), mRNA. /// ENST00000263723 // 3UTR // 0 // --- // --- // --- // ---	CLCA4	CLCA4, Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), p22.3
SNP_A-1862102	tcatgcctcccatctg[A/G]acaccatgttgtatag	A	G	Homo sapiens KIAA1363 protein (KIAA1363), mRNA. /// ENST00000273512 // intron // 0 // --- // --- // --- // ---	KIAA1363	KIAA1363, Homo sapiens KIAA1363 protein (KIAA1363), q26.31
SNP_A-1819725	gttgtcatttggttca[A/G]agaagtttttttatttc	A	G	83992 // Homo sapiens cortactin binding protein 2 (CTTNBP2), mRNA. /// ENST00000160373 // upstream //	CTTNBP2	CTTNBP2, Homo sapiens cortactin binding protein 2 (CTTNBP2), q31.31
SNP_A-1814874	gtgtgttacaggatat[A/T]aagtaacatgagaagc	A	T	Homo sapiens spermatogenesis associated 6 (SPATA6), mRNA. /// ENST00000254448 // intron // 0 // --- // --- // --- // ---	SPATA6	SPATA6, Homo sapiens spermatogenesis associated 6 (SPATA6), p33
SNP_A-1835149	tacccttagcactata[C/T]ccatgttaactgtaaa	C	T	Homo sapiens chromosome 9 open reading frame 25 (C9orf25), mRNA. /// ENST00000297620 // intron // 0 // --- // ---	C9orf25	C9orf25, Homo sapiens chromosome 9 open reading frame 25 (C9orf25), p13.3
SNP_A-1842560	taggttcacacctttc[C/T]agtgctaagtggacag	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1789624	gggctaaatgcagcaa[C/T]agacataaagttagca	C	T	// 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1947563	tttaccatttttataa[A/C]tcacttgccaatgttg	A	C	3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 37849 //	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-1954844	tttgcttccagattag[C/T]acactacaatttagcc	C	T	H.sapiens mRNA for NRD2 convertase. /// NM_002525 // upstream // 3966 // Hs.444934 // NRD1 // 4898 // Homo	NRD1	NRD1, H.sapiens for NRD2 convertase. p32.3
SNP_A-1986821	cttgacttcttgaagc[C/T]gacattcttgttgtat	C	T	6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 16752 // Hs.485968 // MAP3K7 //	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q15

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982632	cgacatgcatgagtcg[C/G]agcccttcagctttgc	C	G	285704 // Homo sapiens RGM domain family, member B (RGMB), mRNA. /// ENST00000308338 // downstream //	RGMB	RGMB, Homo sapiens RGM domain family, member B (RGMB), q21.1
SNP_A-1928328	ttcaccaccacttgaa[C/T]taagtctcatctctca	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3398915 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1880015	tcttctaaaaatcaaa[C/T]tgttgtctttttggt	C	T	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 671021 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-1879555	tcttcaacactggtga[A/G]gattccaagagatatt	A	G	// 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1887234	tgagaaccactgccta[C/T]atgttcattaatataa	C	T	Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // --- // --- // --- // ---	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3
SNP_A-1887547	tgagagaactccaaga[A/G]ggatgtcgaaactggg	A	G	Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // --- // --- // --- // ---	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3
SNP_A-1903761	tgggagtatacaaaag[C/G]aagagttcatggggtg	C	G	Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, mRNA. /// NM_000337 // intron // 0 // Hs.387207 // SGCD // 6444 //	SGCD	SGCD, Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, q33.3
SNP_A-1896365	tcaactcctcttgaac[A/G]ctgccacaagatttgc	A	G	9331 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 (B4GALT6), mRNA. /// NM_014939 // downstream // 82954 // Hs.202001 //	B4GALT6	B4GALT6, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6 (B4GALT6), q12.1
SNP_A-1897432	tgctgacctcttccta[C/T]actgctatctgccccc	C	T	23478 // Homo sapiens signal peptidase complex (18kD) (SPC18), mRNA. /// D86966 // upstream // 18620 // Hs.79347	SEC11L1	SEC11L1, Homo sapiens signal peptidase complex (18kD) (SPC18), q25.3
SNP_A-1881556	tctttcttctgacact[A/G]aagtctttccctgggg	A	G	Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1923660	ttaggtgaaatggacc[A/G]agtaccttgaaagata	A	G	// 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 237758 // --- // --- // --- //	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1980241	gtcttttcattttctc[A/G]cactgctgaataaata	A	G	Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron //	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-1986336	aaacccagtagtttca[C/G]agatcagaattttcca	C	G	sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // --- // --- // --- // ---	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1948390	tttaggttattttgcc[A/G]gataataatcaactat	A	G	sapiens lumican (LUM), mRNA. /// ENST00000266718 // intron // 0 // --- // --- // --- // ---	LUM	LUM, Homo sapiens lumican (LUM), q21.33
SNP_A-1942487	ttggctggagttgggc[C/T]gaagaggaagcaggtt	C	T	4953 // Homo sapiens ornithine decarboxylase 1 (ODC1), mRNA. /// NM_024894 // downstream // 39559 // Hs.222494	ODC1	ODC1, Homo sapiens ornithine decarboxylase 1 (ODC1), p25.1
SNP_A-1646162	ggaaataaagcttatttttctgtaa[C/T]taatatagtcttcttcatgagcctc	C	T	5099 // BH-protocadherin (brain-heart) /// NM_020860 // downstream // 711961 // Hs.278894 // STIM2 // 57620 //	PCDH7	PCDH7 , rs990965, BH-protocadherin (brain-heart) ,p15.2
SNP_A-1705987	tttaaaacaaataacaactgacaaa[A/G]ttctctcataaaaaaatatttattgc	A	G	5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 1550856 // Hs.285782 // LRRTM4 // 80059 // leucine-rich	REG1B	REG1B , rs283904, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-1780608	ggatattctttcaacc[A/G]ctgttcatgtgttcct	A	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 1067407	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1752845	tgtgcagctctagaatgaatgggaa[C/T]gtctattgatccagtgtctgagagc	C	T	NM_031956 // intron // 0 // Hs.378893 // NYD-SP14 // 83894 // NYD-SP14 protein	NYD-SP14	NYD-SP14 , rs984696, NYD-SP14 protein,q31.22
SNP_A-1729900	ggactattcttatcctcccttttcaa[C/G]ttaaactatataactaaattccttct	C	G	5137 // phosphodiesterase 1C, calmodulin-dependent 70kDa /// NM_006658 // downstream // 39625 // Hs.227011 //	PDE1C	PDE1C , rs1548831, phosphodiesterase 1C, calmodulin-dependent 70kDa ,p14.3
SNP_A-1820581	gtttcaaagaggaaaa[A/G]gaagaagacatctctt	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-1863611	tccaaatgtttccttc[A/C]cgtcatctctcatgtc	A	C	// 6507 // Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), mRNA. /// ENST00000265113 // downstream // 33986 // --- // --- // ---	SLC1A3	SLC1A3, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), p13.2
SNP_A-1870606	tcgatgtcaccactac[G/T]gagatgccttctctca	G	T	Homo sapiens transcriptional adaptor 3 (NGG1 homolog, yeast)-like (TADA3L), transcript variant 3, mRNA. /// NM_133480 // intron // 0 // Hs.386390 // TADA3L // 10474 //	TADA3L	TADA3L, Homo sapiens transcriptional adaptor 3 (NGG1 homolog, yeast)-like (TADA3L), transcript variant 3, p25.3
SNP_A-1868048	tcctatacgttagctg[C/G]aatgcccaacaatgga	C	G	// 8738 // Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// NM_003805 // downstream // 189674 // Hs.38533 // CRADD	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1847454	tatcctatggccaaga[C/T]tccagtcatgaagggg	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2154347	attatgtgggaaacca[C/T]tgagcatccattcctc	C	T	144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 //	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2160426	atttcatgctcttatc[A/C]aatttttatcattacc	A	C	54329 // Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA. /// NM_002711 // downstream // 283923 //	GPR85	GPR85, Homo sapiens G protein-coupled receptor 85 (GPR85), q31.1
SNP_A-2159390	atttaatgagaagggg[G/T]agtatgtcattaacta	G	T	KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 33537 //	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2164658	caaacacctctttgcc[A/C]aagtgctacctgtacg	A	C	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA. /// ENST00000343348 // intron // 0 // --- // --- // --- // ---	SEMA6A	SEMA6A, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), q23.1
SNP_A-2162885	attttggcattaatgg[A/T]accttgatgaggaaca	A	T	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1996315 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2196935	cattagtgccagttga[A/G]aaaaaagttgtttgat	A	G	sapiens BCL2/adenovirus E1B 19kDa interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein,	BNIP3	BNIP3, Homo sapiens BCL2 q26.3
SNP_A-2178418	cactccagcccgggga[C/G]gtgtgctctgatcagc	C	G	Homo sapiens FLJ40536 protein (FLJ40536), mRNA. /// ENST00000316750 // upstream // 309255 // --- // --- // --- // ---	-	-, Homo sapiens FLJ40536 protein (FLJ40536), q26.13
SNP_A-2217943	gtgttttaaatgtgta[C/T]gtggatgagtaagcta	C	T	652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // downstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.1
SNP_A-2222814	cgattggaaccaaaga[G/T]aatatgctagcacagt	G	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2208453	tgacagttattgcctc[A/G]agtaattaataatcta	A	G	Homo sapiens Sec23 homolog A (S. cerevisiae) (SEC23A), mRNA. /// ENST00000307712 // intron // 0 // --- // --- // --- // ---	SEC23A	SEC23A, Homo sapiens Sec23 homolog A (S. cerevisiae) (SEC23A), q21.1
SNP_A-2209534	cccatctcccctaaag[A/C]cattcagccattgctt	A	C	// 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 540370 // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-2073373	acaggtagggagaatc[C/T]cacatctctgcaatca	C	T	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2058870	aatccaataccaccac[A/C]cagaggtaacatcttg	A	C	145497 // Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), mRNA. /// ENST00000216453 //	C14orf166B	C14orf166B, Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), q24.3
SNP_A-2104224	agcagatagatattca[G/T]tagaaaagggctggta	G	T	FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2038618	aacagaatgtatttttt[A/T]aaaaacagtgagctct	A	T	64111 // Homo sapiens chromosome 7 open reading frame 9 (C7orf9), mRNA. /// ENST00000222674 // upstream //	C7orf9	C7orf9, Homo sapiens chromosome 7 open reading frame 9 (C7orf9), p15.2
SNP_A-2019034	aagaacaagtatatgt[A/G]aagtaaaccctgacat	A	G	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2007950	gcaggcatgaaaatca[A/T]ggcttctactttagac	A	T	Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-2010289	tgcctaagtctgggaa[A/G]tcataatcttaatatg	A	G	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2002119	atccgatgtgtttttc[C/T]ctggtatttccttagt	C	T	50507 // Homo sapiens NADPH oxidase 4 (NOX4), mRNA. /// NM_153696 // upstream // 65547 // Hs.511922 // PSMAL //	NOX4	NOX4, Homo sapiens NADPH oxidase 4 (NOX4), q14.3
SNP_A-2271650	gaccactattggtcca[C/T]ggcctgttaacagaaa	C	T	Homo sapiens synaptosomal-associated protein, 23kDa (SNAP23), transcript variant 2, mRNA. /// NM_003825 // intron // 0 // Hs.511149 // SNAP23 // 8773 // Homo sapiens	SNAP23	SNAP23, Homo sapiens synaptosomal-associated protein, 23kDa (SNAP23), transcript variant 2, q15.1
SNP_A-2229992	ctataaagatttagca[A/G]tatatgaagcattata	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2306932	gctgtgttaaaacaac[C/T]ggtcactgatgcctca	C	T	sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// ENST00000296212 // intron // 0 // --- // --- // --- // ---	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2296120	gcattcagacagagga[A/G]acatccagaaatgact	A	G	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2294979	gcatacaagctaagca[C/G]aaaaaaccctttattt	C	G	153443 // Homo sapiens hypothetical protein FLJ25286 (FLJ25286), mRNA. /// ENST00000339397 // intron // 0 // --- //	p49	p49, 153443 q23.1
SNP_A-2301415	gccttttcaggggtaa[C/T]gcatgcttaggtttgc	C	T	Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // --- // --- // --- // ---	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-2241911	ctgatggtttgaccac[C/G]aaatcagcacaacact	C	G	1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 48754 // --- //	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2250081	cttacgggctgtagta[C/T]agttcctgcagatctc	C	T	EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 239004 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2104297	agcagcaggctctgca[C/T]tcagggctttgctgtt	C	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2085676	actccgaaatgcaggg[A/G]aagtcctaagagaatt	A	G	// Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// ENST00000345127 // intron // 0 // --- // --- // --- // ---	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2089340	acttagtatactatac[A/T]gcctcttcggttaaca	A	T	56956 // Homo sapiens partial mRNA for LIM-homeobox 9 (LHX9 gene). /// NM_020204 // downstream // 35235 //	LHX9	LHX9, Homo sapiens partial for LIM-homeobox 9 (LHX9 gene), q31.3
SNP_A-2075387	acatgaatgcattgat[C/T]agaaaagtaaaaagta	C	T	Homo sapiens mRNA for KIAA0611 protein, partial cds. /// ENST00000311637 // intron // 0 // --- // --- // --- // --- ///	ATP9A	ATP9A, Homo sapiens for KIAA0611 protein, partial cds. ,q13.2
SNP_A-2219699	ccttaactctgactca[A/G]catacttgccctggtt	A	G	308 // Homo sapiens annexin A5 (ANXA5), mRNA. /// NM_152399 // downstream // 51414 // Hs.27524 // FLJ30834	ANXA5	ANXA5, Homo sapiens annexin A5 (ANXA5), q27
SNP_A-2173245	cacaactaccattgga[C/T]ctggcagtctcattac	C	T	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 508983 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2198283	cattgttagaaaagcc[A/G]gctacggtactgcctc	A	G	Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // --- // ---	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2186568	cagggagcttttatcc[A/G]gatagctgaacacagg	A	G	7779 // Homo sapiens solute carrier family 30 (zinc transporter), member 1 (SLC30A1), mRNA. /// NM_002497 // downstream // 24047 // Hs.153704 // NEK2 // 4751 // Homo	SLC30A1	SLC30A1, Homo sapiens solute carrier family 30 (zinc transporter), member 1 (SLC30A1), q32.3
SNP_A-2123290	agtgtagctcatggca[C/T]atttgttcatcttttc	C	T	Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1856298	tcacacaaaaattaaa[A/G]cattgtgaagggtgta	A	G	ENST00000323433 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-1825203	taaagtattatataga[C/G]agttggccccagaatt	C	G	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1837815	tacttttttcttaccac[A/G]cagatatacccacaaaa	A	G	Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA. /// NM_152238 // intron // 0 // Hs.197015 // SNX7 //	SNX7	SNX7, Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, p21.3
SNP_A-1790040	ggggaaagtgtggaaa[A/T]gggtgtttctactgct	A	T	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 493754 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1792522	ggtaaaacatgtaata[C/G]catgtaaaagtactta	C	G	ENST00000288466 // intron // 0 // --- // --- // --- // ---	-	q32
SNP_A-1811796	gtgcttgaccttaaat[C/T]aatgcttaaggtatgc	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1943108	ttggtatttagtttca[C/G]gcaatctttcacctgg	C	G	sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// ENST00000273951 // intron // 0 // --- // --- // --	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-1981205	acatttacagaaccaa[C/T]ttcatttatgttttaa	C	T	26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000331766 // upstream // 403724 // --- // --	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-1969515	accaaatcctgaattg[C/T]atcttacccatttgat	C	T	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 493873 // --- // --	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1965775	aatgtatgatgtaaag[A/C]attttaaccacttctg	A	C	57818 // Homo sapiens glucose-6-phosphatase, catalytic, 2 (G6PC2), mRNA. /// NM_003742 // downstream // 5377 //	G6PC2	G6PC2, Homo sapiens glucose-6-phosphatase, catalytic, 2 (G6PC2), q24.3
SNP_A-1968889	gtattcttcccaatgc[C/T]gcattcagttacatga	C	T	NM_004550 // intron // 0 // Hs.173611 // NDUFS2 // 4720 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) (NDUFS2), mRNA. /// ENST00000289897 // intron // 0 // --- // --- // --- // ---	NDUFS2	NDUFS2, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) (NDUFS2), q23.3
SNP_A-1930440	ttccaaaactgaaaca[A/C]tatccccattaaacag	A	C	Homo sapiens myosin X (MYO10), mRNA. /// ENST00000274203 // intron // 0 // --- // --- // --- // ---	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1913278	tgtgggatattactca[A/C]gaaatccttgccctgg	A	C	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // --- ///	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-1929883	ttcatctgtgtttttc[C/T]atgaagtgtttaagtg	C	T	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1900980	tggatactgagagaca[A/T]ctgtatttatttcctc	A	T	Homo sapiens 24-dehydrocholesterol reductase (DHCR24), mRNA. /// ENST00000234746 // intron // 0 // --- // --- // --- // ---	DHCR24	DHCR24, Homo sapiens 24-dehydrocholesterol reductase (DHCR24), p32.3
SNP_A-1966307	ttctgcttttgcgtc[A/G]acacaagacattaccc	A	G	sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), mRNA. /// ENST00000304141 // intron // 0 // --- // --- // --- // ---	SDPR	SDPR, Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), q32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1943337	ttggttacactttcaa[A/G]tcactggtaatccctt	A	G	3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 65593	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-1791306	gggtaatggatcagga[A/G]acctgtgtggaaatca	A	G	2668 // Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, mRNA. /// NM_199234 // upstream // 93886 // Hs.248114 // GDNF // 2668 // Homo	GDNF	GDNF, Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, p13.2
SNP_A-1821040	gtttctgtcacttgca[C/T]ctgaacaagtcctgat	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 296154 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1862772	tcattcctagaaaaag[A/G]aggagatttctcagaa	A	G	10408 // N-cym=DNA-binding transcriptional activator homolog {oncogene} [human, Kelly neuroblastoma cell line, mRNA, 778 nt]. /// ENST00000311168 // downstream //	MYCNOS	MYCNOS, N-cym=DNA-binding transcriptional activator homolog {oncogene} [human, Kelly neuroblastoma cell line, 778 nt]. ,p24.3
SNP_A-2149635	atgtatacttggaacc[A/T]ctttgatacctgtgca	A	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 419247 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2143216	atgacaagctttaatg[C/T]atgcagggcagcactg	C	T	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 582882	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2194473	catgcaaacttgtttc[C/T]caaccaactgactaag	C	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2213388	ccggcccagttccagg[A/G]aagtggattgaaaaca	A	G	284338 // Homo sapiens hypothetical LOC284338 (MGC70924), mRNA. /// ENST00000341747 // intron // 0 // ---	MGC70924	MGC70924, Homo sapiens hypothetical LOC284338 (MGC70924), q13.2
SNP_A-2227335	ctacaaggaactcaca[C/T]aaatcagtaagaaaaa	C	T	Homo sapiens 13kDa differentiation-associated protein (DAP13), mRNA. /// ENST00000327772 // intron // 0 // --- // ---	DAP13	DAP13, Homo sapiens 13kDa differentiation-associated protein (DAP13), q22
SNP_A-2225009	cgtggtcaaaaaaaag[A/G]acattatcttgaacat	A	G	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 630562 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2212055	ccctgcaagtatttca[A/G]gccaaatccaacaatt	A	G	Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // intron // 0 // --- // --- // --- // ---	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2210403	ccccaaggggtcaaaa[C/T]ggtgttgcaaagtctg	C	T	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 149904 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2054017	aagttagagaaccctc[A/G]aggggctaggtatgag	A	G	// 81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA. /// NM_152330 // upstream // 119160 //	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-2082686	acgggcagagcagtcc[A/G]cggagccagaaaagag	A	G	83548 // Homo sapiens component of oligomeric golgi complex 3 (COG3), mRNA. /// ENST00000310862 //	COG3	COG3, Homo sapiens component of oligomeric golgi complex 3 (COG3), q14.13
SNP_A-2099866	agagtagttacaatga[A/G]ccatgggaaatgacgc	A	G	374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 269462 // Hs.34198 // FLJ44796 // 401209 //	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-2008753	gaacacttagcaggta[A/G]gggagctcagtaacat	A	G	8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 34624 // Hs.127013 // CADPS // 8618 // Homo	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2043254	aactgctccataacta[C/T]agcctagagaaagaaa	C	T	Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// ENST00000256007 // 5UTR // 0 // --- // -	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-2248119	ctgtggccaaatgtca[A/T]tcctaagagcctgcac	A	T	/// ENST00000334919 // upstream // 1454356 // --- // --- // --- // --- /// ENST00000322194 // downstream // 314793 // --- // --- //	-	q12.2
SNP_A-2232824	ctcacttccaatagga[C/T]gaatttaggtattggt	C	T	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 102021 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-2237230	ctctcatattgataag[C/T]aggtaaaatcatgttt	C	T	8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream //	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-2258940	ctttttcttcatgaca[C/T]tactagatccctttgt	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2273197	gactcagaatgccaac[A/G]ctgtgctttctcaggc	A	G	23072 // Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// ENST00000322220 // downstream //	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p13
SNP_A-2277283	gagattcccacatggg[A/T]caccactgtaggctat	A	T	Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), mRNA. /// ENST00000307717 // intron // 0 // --- // --- // --- // --- ///	AMSH-LP	AMSH-LP, Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), q23.31
SNP_A-2239294	ctctttaaccgaagcc[A/G]cctttaactccatcgt	A	G	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, mRNA. /// ENST00000352766 // intron // 0 // --- // --- // --- // --- /// ENST00000336995 // intron // 0 // --- //	ARHGAP8	ARHGAP8, Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, q13.31
SNP_A-2232110	ctcaaggagcttccaa[C/T]ctatttgcaaggcaga	C	T	57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 826485 // --- // ---	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q13.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041347	aacctggatacactga[C/T]gtgctaatagtttact	C	T	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2046147	aagactgcccttacca[A/G]catacaaatgagtgat	A	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2022040	aaaaagaggaatctca[A/G]gggcagacaacaatct	A	G	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-1992248	tctgcttactggatcc[A/G]ataaagcataaaatca	A	G	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2104966	agcatcatgtttaaaa[A/G]ctgttcatataactca	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3354771 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2093849	agaagatggatttaga[C/T]gttgctaggtgagggg	C	T	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA. /// ENST00000322644 // intron // 0 // --- // --- // --- // ---	POLR2A	POLR2A, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), p13.1
SNP_A-2078380	accatcaattcatgaa[A/C]catttctactaccact	A	C	// 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 62829 // Hs.42650 //	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2048932	aagcctattaaagtga[A/G]taactttccaagattc	A	G	4159 // Homo sapiens melanocortin 3 receptor (MC3R), mRNA. /// NM_080821 // upstream // 67863 // Hs.143736 //	MC3R	MC3R, Homo sapiens melanocortin 3 receptor (MC3R), q13.31
SNP_A-2068876	acaatctaataatgct[A/T]aaaagttaaacatcaa	A	T	SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2212741	cccttgcagtgaaata[C/T]gtgatagaaccactac	C	T	404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 35555 //	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2207538	ccatttcaagagacag[A/C]attttgcataatcact	A	C	9445 // Homo sapiens integral membrane protein 2B (ITM2B), mRNA. /// ENST00000310929 // upstream // 54440	ITM2B	ITM2B, Homo sapiens integral membrane protein 2B (ITM2B), q14.2
SNP_A-2203077	ccactgcagagcacca[A/G]tgccatgtgaggttga	A	G	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2191601	catatgtatactcaca[A/G]gcatatacgtaggcac	A	G	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2150079	atgtccattggctgaa[G/T]aataggtaaacaaaat	G	T	143187 // Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// NM_030756 // upstream // 178500 // Hs.501080 // TCF7L2 //	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2116645	aggtcagtagacacca[C/T]gtattgaggtgtcaat	C	T	Homo sapiens cytochrome P450, family 4, subfamily X, polypeptide 1 (CYP4X1), mRNA. /// ENST00000334540 // intron // 0 // --- // --- // --- // ---	CYP4X1	CYP4X1, Homo sapiens cytochrome P450, family 4, subfamily X, polypeptide 1 (CYP4X1), p33
SNP_A-2112821	aggcagtgtggcccga[A/G]gcttaaaaagttactc	A	G	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1, alpha (CAMKK1), transcript variant 2, mRNA. ///	CAMKK1	CAMKK1, Homo sapiens calcium,p13.2
SNP_A-2128457	ataataaatgtgtgca[C/T]agtttgacagccatat	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2137364	taacccatctttgtcc[C/T]ctacactagatttcaa	C	T	// 2974 // Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), mRNA. /// NM_145019 // upstream // 44850 //	GUCY1B2	GUCY1B2, Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), q14.3
SNP_A-1857439	tcactagcattgagta[A/G]ctggaggttgccagca	A	G	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 172637 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-1852099	tattggcataaagact[A/G]aaggcatacagttatt	A	G	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1839549	aacgttgtgagaaatc[A/G]cttcaaacctttctc	A	G	ENST00000313495 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-1811668	gtgctgggctcctatc[A/G]aagggtgacagtcagc	A	G	sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// ENST00000297693 // intron // 0 // --- //	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-1813198	gtggtcagaggtgccc[A/G]caacaaatgcacttct	A	G	sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // --- // --- // --- // --- ///	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1801810	gtagtggggaaggaga[C/T]atgaggggctctgttc	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1946198	tttaaaaaattgctgt[A/G]aaataaggaagaaata	A	G	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 561602 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1949324	tttattacatttggca[A/G]cccaagttataaagct	A	G	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1965075	acagccctattataga[A/G]gtcacacgatgatggg	A	G	/// ENST00000355063 // upstream // 542875 // --- // --- // --- // -	-	q22.1
SNP_A-1971737	ggagaggtaccgaaac[A/G]atcattctccttgctc	A	G	ENST00000286050 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1983816	cacatattagctgaga[A/G]atatgttatttgaaca	A	G	57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 93831 //	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1929865	ttcatctgaaggatcc[A/G]caaatgatctgtaatg	A	G	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-1921671	ttacgaattaagtact[A/G]aaggtctccgagctat	A	G	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1212050 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1904250	tgggctagtggttgtg[A/G]agacaataaacctcca	A	G	29113 // Homo sapiens chromosome 6 open reading frame 15 (C6orf15), mRNA. /// NM_014068 // upstream // 2191 //	C6orf15	C6orf15, Homo sapiens chromosome 6 open reading frame 15 (C6orf15), p21.33
SNP_A-1978461	gtgagtgttcattttc[A/G]ccattactggcaactg	A	G	Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 //	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-1978489	atgggcactgagaggg[A/G]aatcgaagatgattgg	A	G	Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // intron // 0 // Hs.113253 // PAX7 //	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-1937120	ttctttttcatactta[G/T]gatttctgctaccttc	G	T	57596 // Homo sapiens brain-enriched guanylate kinase-associated protein (KIAA1446), mRNA. /// NM_020836 // upstream // 32158 // Hs.211751 // KIAA1446 // 57596 //	KIAA1446	KIAA1446, Homo sapiens brain-enriched guanylate kinase-associated protein (KIAA1446), q32.2
SNP_A-1668745	gctggagaccttggaaaatccacttt[A/C]acttcctgaagactcagtttcctcc	A	C	glycoprotein beta 5	GPB5	GPB5 , rs728527, glycoprotein beta 5,q23.2
SNP_A-1840297	tagcatacttttcaaa[C/T]acaaagccactcacgg	C	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1830352	taatatgaagaaagca[G/T]agaggcatatataatg	G	T	27445 // Homo sapiens mRNA for KIAA0559 protein, partial cds. /// AB002329 // downstream // 27429 // Hs.528721 //	PCLO	PCLO, Homo sapiens for KIAA0559 protein, partial cds. ,q21.11
SNP_A-1820908	gtttctacttctttcc[C/T]cacttaattctgaatt	C	T	Homo sapiens phosducin-like 2 (PDCL2), mRNA. /// ENST00000295645 // intron // 0 // --- // --- // --- // ---	PDCL2	PDCL2, Homo sapiens phosducin-like 2 (PDCL2), q12
SNP_A-1855189	tcaagattcagactct[A/G]aagtttgacaccacag	A	G	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA. /// ENST00000357559 // intron // 0 // --- // --- // --- // --- /// ENST00000305586 // intron // 0 // --- //	FXR1	FXR1, Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), q26.33
SNP_A-1871265	tctaaaatttgcctaa[A/G]tctcttcttctgcctt	A	G	ENST00000356802 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2110265	aggaataagcttgtag[A/G]catagaactttgtaga	A	G	sapiens hypothetical protein FLJ10116 (FLJ10116), mRNA. /// ENST00000236976 // intron // 0 // --- // --- // --- // ---	DSU	DSU, Homo sapiens hypothetical protein FLJ10116 (FLJ10116), q35
SNP_A-2145566	atgcatagttcttaga[C/T]acaacagcttagaggt	C	T	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2144987	atgatttccatattcc[A/T]gattgatctttttgt	A	T	Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // 3UTR // 0 // --- // --- // --- // ---	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. p14.1
SNP_A-2165558	caaagctcttagaaaa[G/T]ttgtcctactatctta	G	T	Homo sapiens hypothetical protein MGC5395 (MGC5395), mRNA. /// ENST00000257247 // intron // 0 // --- // --- // --- // ---	MGC5395	MGC5395, Homo sapiens hypothetical protein MGC5395 (MGC5395), q12.3
SNP_A-2157122	attgaaccaccattac[A/G]aaaaaatcttttcagc	A	G	ENST00000344471 // intron // 0 // --- // --- // --- // --- /// ENST00000339441 // intron // 0 // --- // --- // --- // ---	-	q26.2
SNP_A-2182154	cagaggggatgagttg[A/G]actcagaggggaaagg	A	G	Homo sapiens chromosome 18 open reading frame 17 (C18orf17), mRNA. /// ENST00000304621 // intron // 0 // --- //	C18orf17	C18orf17, Homo sapiens chromosome 18 open reading frame 17 (C18orf17), q11.2
SNP_A-2215564	cctcagattttgttca[A/G]gttgactgagcaccca	A	G	146556 // Homo sapiens hypothetical protein MGC45438 (MGC45438), mRNA. /// NM_019109 // upstream // 1948 //	MGC45438	MGC45438, Homo sapiens hypothetical protein MGC45438 (MGC45438), p13.3
SNP_A-2090106	acttgaatgctgttac[A/C]caagtttggaaagact	A	C	// 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 411758 // --- // --- //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-2088469	actgtattctgtcccc[A/G]cgccatacgtataagc	A	G	sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // --- // --- // --- // --- /// ENST00000301226 // intron //	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2086225	actctggagccataga[C/G]actgggagctgaacct	C	G	338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 136569 // Hs.193268 // MTAP //	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2096841	agactcagaaaacagc[A/T]acgataaagccttgga	A	T	Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST00000263915 // intron // 0 // --- // ---	GRB14	GRB14, Homo sapiens growth factor receptor-bound protein 14 (GRB14), q24.3
SNP_A-2100737	agatagcataagtaca[A/T]atcaaaaattactgta	A	T	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1394505 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1990751	aggtctaggatttta[A/G]aagttgctacacagta	A	G	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1999320	ggatgccatccctcaa[A/G]aaagtcccatgcctta	A	G	22931 // Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA. /// ENST00000329227 // upstream //	RAB18	RAB18, Homo sapiens RAB18, member RAS oncogene family (RAB18), p12.1
SNP_A-2016735	aatcgtgtcctgttac[A/C]gaataaaacagtttct	A	C	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 781991 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2021312	aacttttatttagagc[C/T]gcacttctcaaacttt	C	T	BRCC2 // 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 122419 // Hs.444075 //	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-2032718	aaataacagatctaaa[A/G]tgtggattgatttaag	A	G	64065 // Homo sapiens PERP, TP53 apoptosis effector (PERP), mRNA. /// ENST00000342131 // downstream //	PERP	PERP, Homo sapiens PERP, TP53 apoptosis effector (PERP), q23.3
SNP_A-2029625	aaagagacatctgagc[A/G]aacttcacctgggaga	A	G	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 3031826 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2027647	aaaccatattaaacaa[C/G]ttctgattcaaaacaa	C	G	ENST00000358682 // intron // 0 // --- // --- // --- // ---	-	q14
SNP_A-2254891	cttggatgtaaacctg[A/G]cactgttagcagagca	A	G	1645 // Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogena /// NM_205845 // downstream // 4699 // Hs.498513 // AKR1C2 /	AKR1C1	AKR1C1, Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogena ,p15.1
SNP_A-2291344	gcaatggatgtatcag[C/T]aagcacaatgtggtct	C	T	6854 // Homo sapiens synapsin II (SYN2), transcript variant IIb, mRNA. /// NM_133625 // downstream // 68587 //	SYN2	SYN2, Homo sapiens synapsin II (SYN2), transcript variant IIb, p25.2
SNP_A-2309289	ggaaaagatgagtaaa[C/G]actaggagcctgaagg	C	G	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 3497015 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2291240	gcaatctgagtgggaa[A/T]cacaccagagctcaga	A	T	// Homo sapiens protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, mRNA. /// NM_032009 // intron // 0 // Hs.368160 // PCDHGA2 // 56113 // Homo	PCDHGA2	PCDHGA2, Homo sapiens protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, q31.3
SNP_A-2289345	gattttaagactctta[C/T]gaatctacaggaatca	C	T	25842 // Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), mRNA. /// NM_153255 // upstream // 556 // Hs.486315 // MCMDC1 // 254394 // Homo	ASF1A	ASF1A, Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), q22.31
SNP_A-2274864	gagaaattagatgaga[A/T]gaaacagggttaaggt	A	T	Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2284340	gatatttcctttgttc[A/G]ctcacactaaataatc	A	G	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 468927 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2283469	gatactagaagacaac[A/T]ggtagcctctgctgcc	A	T	5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA. /// NM_183003 // upstream // 1044379 // --- // --- // 0 // --- /// ENST00000295266 //	PDHA2	PDHA2, Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), q22.3
SNP_A-2260382	gaaacaaattgagacc[A/G]cttaagtaaataagga	A	G	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 265102 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2260620	tagaatggggcatgaa[A/T]gagctaaacatgcttt	A	T	283685 // Homo sapiens hypothetical protein FLJ36144 (FLJ36144), mRNA. /// NM_005664 // upstream // 105277 //	FLJ36144	FLJ36144, Homo sapiens hypothetical protein FLJ36144 (FLJ36144), q11.2
SNP_A-2013016	cgtacttgcccctctc[A/G]aatttgatctgtgctt	A	G	Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // --- // --- // --- // --- /// ENST00000287878 // intron //	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-2012791	ttcttttgatgccaaa[C/T]gtcatatctcctccac	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2010373	aaaaaagaaaaatgac[C/T]cagctatatgccacct	C	T	57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// NM_012224 // downstream // 15224 // Hs.481181	SH3MD2	SH3MD2, Homo sapiens SH3 multiple domains 2 (SH3MD2), q33
SNP_A-2101844	agatggacagaaaaga[A/G]atatcaacctatcagg	A	G	10882 // Homo sapiens complement component 1, q subcomponent-like 1 (C1QL1), mRNA. /// NM_024819 // downstream // 22759 // Hs.463148 // FLJ22955 // 79877 //	C1QL1	C1QL1, Homo sapiens complement component 1, q subcomponent-like 1 (C1QL1), q21.31
SNP_A-2095764	agacactgaggccacc[A/G]gaaagggcagagcatg	A	G	2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream //	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1
SNP_A-2048201	aagcactgacaggcca[C/T]tgcgcaggcagacagc	C	T	ENST00000272907 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-2053278	aagtgaacgaatttaa[C/T]atcaacaataataaaa	C	T	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 798251 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2218606	cctggcagaaatcata[C/G]agtatgggctagaatg	C	G	// 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 //	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-2180487	cagaactatcttgtca[G/T]gaagatgtgaaaaggt	G	T	ENST00000339567 // intron // 0 // --- // --- // --- // --- /// ENST00000343332 // intron // 0 // --- // --- // --- // --- ///	-	p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2173489	cacaatcagacacaca[C/T]ggaagaatccaaaaga	C	T	sapiens peptidase D (PEPD), mRNA. /// ENST00000244137 // intron // 0 // --- // --- // --- // ---	PEPD	PEPD, Homo sapiens peptidase D (PEPD), q13.11
SNP_A-2168536	caagaaaattcaacta[C/T]agatcagtatctctga	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 316306 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2184839	cagctgggattccata[G/T]gaacagtggcaccatt	G	T	Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // --- // ---	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-2156528	attctcttgtctaaaa[A/C]cctgattgcttccaat	A	C	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 84580 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2162200	attttacctttataa[C/G]tatgcagttctatgtt	C	G	9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// ENST00000307888 // upstream //	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-2114851	agggcacagggtgaga[C/T]cagctttcgtcctgag	C	T	116447 // Homo sapiens topoisomerase (DNA) I, mitochondrial (TOP1MT), nuclear gene encoding mitochondrial protein, mRNA. /// NM_024035 // downstream //	TOP1MT	TOP1MT, Homo sapiens topoisomerase (DNA) I, mitochondrial (TOP1MT), nuclear gene encoding mitochondrial protein, q24.3
SNP_A-1853822	tcaaaacatcaacaaa[A/G]atatctatagccaatg	A	G	C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 //	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-1858384	tcagacctggaggcga[C/T]ggtcgacccaatgttt	C	T	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 249025 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1708607	tgttggaacctactgccactcaaga[A/G]aaattcttccctaatctgtgtgggc	A	G	KIAA1576 protein	KIAA1576	KIAA1576 , rs7204845, KIAA1576 protein,q23.1
SNP_A-1803393	gtatttcagtatttac[A/C]gacatgttcagttgac	A	C	55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 85778 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1793978	ggtcacagggagggaa[C/G]catttgaggctgaaag	C	G	196740 // Homo sapiens chromosome 10 open reading frame 72 (C10orf72), mRNA. /// ENST00000332853 //	C10orf72	C10orf72, Homo sapiens chromosome 10 open reading frame 72 (C10orf72), q11.23
SNP_A-1969924	cattatcagtctcata[A/C]aagatttaataacaat	A	C	26285 // Homo sapiens claudin 17 (CLDN17), mRNA. /// NM_199328 // downstream // 441 // Hs.162209 // CLDN8 //	CLDN17	CLDN17, Homo sapiens claudin 17 (CLDN17), q22.11
SNP_A-1975500	ctaaaacacttttcca[C/G]atacaggcagatttgt	C	G	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA. /// ENST00000357559 // intron // 0 // --- // --- // --- // --- /// ENST00000305586 // intron // 0 // --- //	FXR1	FXR1, Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), q26.33
SNP_A-1932267	ttcctctcaatatgta[A/G]gtatgtgtcttaaaca	A	G	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1662962 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1926291	ttattagctaacacat[C/T]atgattttagcaaggt	C	T	27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 248507 // Hs.268774	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1908565	tgtagcactatgtata[A/G]taggaaagacatggca	A	G	Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // --- // --- // --- // --- ///	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-1897899	tgctggtcaatcagac[A/G]aataattaaagcaatg	A	G	3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 50359 // Hs.112783 // AIG1 // 51390 // Homo	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-1969235	gaaagagagccctttc[A/G]acaggatgattccaat	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 237223 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-1983982	tgatagttgctatgca[C/T]tgagctaggcaccaca	C	T	Human mRNA for KIAA0194 gene, partial cds. /// ENST00000261804 // intron // 0 // --- // --- // --- // ---	KIAA0194	KIAA0194, Human for KIAA0194 gene, partial cds. ,q32
SNP_A-1942397	ttggccttggtttgaa[A/G]actgtttccattctac	A	G	8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA. /// ENST00000326299 // upstream	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-1803050	gtattagaataagata[C/T]gacttctctgaaaatg	C	T	7980 // Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), mRNA. /// ENST00000356305 // upstream // 82143	TFPI2	TFPI2, Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), q21.3
SNP_A-1804794	gtcagtcattctaaca[A/T]ctttatcaagtaggtc	A	T	// Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, mRNA. /// NM_003894 // upstream //	PER2	PER2, Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, q37.3
SNP_A-1682980	aattagggaggatataattaaagaa[A/G]taagcaagataaatctttattcatc	A	G	// 4857 // neuro-oncological ventral antigen 1 /// NM_006489 // downstream // 719428 // Hs.292511 // NOVA1 // 4857 //	NOVA1	NOVA1 , rs2332617, neuro-oncological ventral antigen 1 ,q12
SNP_A-1758363	atctaattttgacaggtagatggaa[C/T]tgttactttagattttggcaaattt	C	T	COMMD10 // 51397 // COMM domain containing 10 /// NM_020796 // downstream // 77631 // Hs.443012 // SEMA6A	COMMD10	COMMD10 , rs10519460, COMM domain containing 10 ,q23.1
SNP_A-1784446	tttgtacaatgccaca[A/G]atctttgtttctcaat	A	G	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 340592 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1855855	tcaatgatccactcta[A/T]gaaatatgttttcccc	A	T	Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // --- // --- // --- // --- ///	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-1872480	tctagccttttgtggg[A/C]atttggtatctaggtt	A	C	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 351889 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1825831	taaatgaaaagaccag[A/T]agttgacaagtacatg	A	T	ENST00000287226 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-1824764	taaagagtgaaaaccc[A/G]aagtagagaaacaata	A	G	Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// ENST00000230859 // intron // 0 // --- // --- // --- // ---	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1830653	taatccaggcttctaa[C/T]tctggccctctgattc	C	T	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1833505	tacagatggccaagaa[A/G]tcacttacatcactat	A	G	// 81833 // Homo sapiens sperm acrosome associated 1 (SPACA1), mRNA. /// NM_033181 // downstream // 64360 //	SPACA1	SPACA1, Homo sapiens sperm acrosome associated 1 (SPACA1), q15
SNP_A-2225433	ctaaaaagaaatgagc[G/T]gagaagacatggagaa	G	T	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2056283	aatactgaaccaaaga[A/T]gccacacataaaagaa	A	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 429081 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2099235	agaggatgggtagaga[G/T]atggtgcttaaaagga	G	T	5909 // Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1), mRNA. /// NM_032236 // downstream // 7110 //	RAP1GA1	RAP1GA1, Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1), p36.12
SNP_A-2085614	actcccagtattatca[A/T]gggattaaaggctcat	A	T	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1993241	tttaggtatgttaaaa[A/G]tgcaaattgtttacat	A	G	// Homo sapiens hypothetical protein FLJ25471 (FLJ25471), mRNA. /// ENST00000356297 // intron // 0 // --- // --- // --- // ---	FLJ25471	FLJ25471, Homo sapiens hypothetical protein FLJ25471 (FLJ25471), q11.22
SNP_A-2021276	aaaaaaattagagcat[A/G]atgatactgcaaaagt	A	G	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 152835 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-2258245	cttttataactctagc[A/G]gcatatgtgtaaacca	A	G	51704 // Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA. /// NM_001502 // downstream // 297679 // Hs.53985 // GP2 // 2813 // Homo	GPRC5B	GPRC5B, Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), p12.3
SNP_A-2267643	gaatcaattttatcaa[A/G]tgtgtaggtacaatgt	A	G	4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream //	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-2286248	gatgccattacatgac[A/G]ggcagtgcttccacga	A	G	Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 //	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2274364	gactttaaatgtgatc[A/C]gaccttatgtctcttc	A	C	222166 // Homo sapiens hypothetical protein Ells1 (Ells1), mRNA. /// NM_147128 // upstream // 71286 // Hs.487869 //	Ells1	Ells1, Homo sapiens hypothetical protein Ells1 (Ells1), p15.1
SNP_A-2303727	gctcagagggcgtaaa[A/G]gcggtttccaccttta	A	G	Homo sapiens vav 2 oncogene (VAV2), mRNA. /// S76992 // intron // 0 // Hs.369921 // VAV2 // 7410 // VAV2=VAV	VAV2	VAV2, Homo sapiens vav 2 oncogene (VAV2), q34.2
SNP_A-2297127	gccacagagagcagta[A/G]gtggcctccatctggt	A	G	51704 // Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA. /// NM_001502 // downstream // 367450 // Hs.53985 // GP2 // 2813 // Homo	GPRC5B	GPRC5B, Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), p12.3
SNP_A-2267524	gaatatgctgggacac[C/G]cttgaagccagcacag	C	G	Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2265845	gaaggaagtagaccca[C/T]tgagacaggagggttc	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 1468332 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2264661	gaagacaaagtccctc[A/G]agtcccttcctacatc	A	G	6362 // Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), mRNA. /// NM_002983 // upstream // 47888 // Hs.514107 // CCL3 //	CCL18	CCL18, Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), q12
SNP_A-2261637	gaaagtaatattctaa[A/G]agcccattgtcagatc	A	G	Homo sapiens glucosidase, alpha; neutral C (GANC), mRNA. /// ENST00000318010 // intron // 0 // --- // --- // --- // ---	GANC	GANC, Homo sapiens glucosidase, alpha; neutral C (GANC), q15.1
SNP_A-2234521	ctccacctcagatgtg[A/G]caacacaaagctcttt	A	G	Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // --- // --- // --- // ---	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2233297	ctcaggcaaggaagtc[A/G]aaaggagaggagtacc	A	G	sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-2240556	ctgacccagaagtttc[A/G]cgggtagtttgaggtg	A	G	123745 // Homo sapiens FLJ45651 protein (FLJ45651), mRNA. /// NM_178034 // downstream // 69684 // Hs.380225	FLJ45651	FLJ45651, Homo sapiens FLJ45651 protein (FLJ45651), q15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235340	ctccctgacctagcca[A/G]tgagagcgaagtgatt	A	G	sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA. /// ENST00000218883 // CDS // 0 // --- // ---	PARP4	PARP4, Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), q12.12
SNP_A-2019949	gtcagatacaacatac[A/G]cacaagtcactctaat	A	G	sapiens myxovirus (influenza virus) resistance 2 (mouse) (MX2), mRNA. /// ENST00000330714 // intron // 0 // --- // --- //	MX2	MX2, Homo sapiens myxovirus (influenza virus) resistance 2 (mouse) (MX2), q22.3
SNP_A-2007277	tgattatatcttatca[C/T]tacttttgtcccaaga	C	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 892021 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2077750	tctgggttctgataaa[A/G]ggttataaggttttat	A	G	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 50005 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2102027	agatgtataattaaga[A/G]cttgtgaacagataca	A	G	DKFZP586L0724 // 25926 // Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA. /// NM_004459 // upstream // 43207 // Hs.444200 // FALZ // 2186 // Homo	DKFZP586L0724	DKFZP586L0724, Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), q24.2
SNP_A-2059751	ccttgctctttagggc[A/G]atctcctcgtactggg	A	G	Homo sapiens keratin protein K6irs (K6IRS2), mRNA. /// ENST00000293745 // CDS // 0 // --- // --- // --- // ---	K6IRS2	K6IRS2, Homo sapiens keratin protein K6irs (K6IRS2), q13.13
SNP_A-2060464	aatgacagctgacaca[A/G]aagagacacttagtat	A	G	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 1 (ARHGEF1), transcript variant 2, mRNA. /// NM_198977 // intron // 0 // Hs.278186 // ARHGEF1 // 9138 //	ARHGEF1	ARHGEF1, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 1 (ARHGEF1), transcript variant 2, q13.2
SNP_A-2072418	acagcagaaatgctac[A/G]gagaaaaagccagcag	A	G	Homo sapiens calcium regulated heat stable protein 1, 24kDa (CARHSP1), mRNA. /// ENST00000311052 // intron //	CARHSP1	CARHSP1, Homo sapiens calcium regulated heat stable protein 1, 24kDa (CARHSP1), p13.2
SNP_A-2220169	ccttcataataaactc[A/G]agaaacactttatcaa	A	G	1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 72571 //	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2202049	ccacagggccacactc[A/G]gagatgtgctggtatt	A	G	7879 // Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA. /// NM_014049 // upstream // 27746 //	RAB7	RAB7, Homo sapiens RAB7, member RAS oncogene family (RAB7), q21.3
SNP_A-2209944	ccccacaatcctggaa[A/C]ctctagacaaccccta	A	C	sapiens cyclin F (CCNF), mRNA. /// ENST00000293968 //	CCNF	CCNF, Homo sapiens cyclin F (CCNF), p13.3
SNP_A-2184502	cagctagagctgcata[C/T]gtttcttgccacgagg	C	T	Homo sapiens dudulin 2 (TSAP6), mRNA. /// NM_018234 // intron // 0 // Hs.20805 // TSAP6 // 55240 // Homo sapiens	TSAP6	TSAP6, Homo sapiens dudulin 2 (TSAP6), q14.2
SNP_A-2193995	catgaataatctcgta[C/T]agcctttccaaagaga	C	T	ENST00000267430 // intron // 0 // --- // --- // --- // ---	-	q21.2
SNP_A-2193346	catctctgccgtcaaa[C/T]gcacctctctgtccca	C	T	5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 60483 //	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2169011	caagaggtaatctgaa[A/G]acaggtctttctttga	A	G	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 338647 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2170566	caagtgcatatgctaa[A/C]ggttgcatctggtgga	A	C	// 5911 // Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA. /// NM_002271 // upstream // 110783	RAP2A	RAP2A, Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), q32.2
SNP_A-2175795	cacattgcacatattc[A/G]ctcatttaattcttgt	A	G	ENST00000261657 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-1864931	tccaggtaagagatca[C/T]ggtgacttgcactaag	C	T	160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // upstream //	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-1783722	ggcattgggatgtcac[A/G]atcgggggtgattttc	A	G	FLJ41841 // 401263 // Homo sapiens FLJ41841 protein (FLJ41841), mRNA. /// ENST00000244795 // upstream //	FLJ41841	FLJ41841, Homo sapiens FLJ41841 protein (FLJ41841), p12.3
SNP_A-1967685	ggagagcttatttcca[A/G]acttgcaggttagcta	A	G	Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 //	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2
SNP_A-1909505	tgtatttagcaggcga[C/T]gaagagccagtgaaag	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 58765 // --- // --- // --- // ---	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1916152	tgttggagtaataggg[A/G]aaaggggcatgaacaa	A	G	Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA. /// ENST00000295688 // intron // 0	CCT3	CCT3, Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), q22
SNP_A-1927518	ttcaaattaaggatat[C/T]aaggcactaataaggt	C	T	54810 // Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA. /// NM_000959 // upstream // 203946 // Hs.292843 //	GIPC2	GIPC2, Homo sapiens PDZ domain protein GIPC2 (GIPC2), p31.1
SNP_A-1925880	ttatgggaatgccccg[A/G]acctgcagtcagaaac	A	G	Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, mRNA. /// NM_178006 // intron // 0 // Hs.507704 // STARD13 // 90627 // Homo sapiens START	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.1
SNP_A-1916527	tgtttacaggcaagcc[A/G]ctactctaaaaactac	A	G	64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 363711 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1898295	tgcttatagaaaaaaa[C/T]agccaactgaattgaa	C	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1979328	ataaattactttaaca[A/T]ctggcacaataggctc	A	T	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 75601 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1980061	catcttggattgcttg[C/T]ataaaacagtaaaatg	C	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1237878 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1934194	ttctcattgaagtgaa[G/T]gttgtctcttcactct	G	T	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1954839	tttgcttcatctaagc[A/C]cacattaaataggcta	A	C	3192 // Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA. /// NM_004501 // upstream // 11215 // Hs.166463 // HNRPU // 3192 //	HNRPU	HNRPU, Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, q44
SNP_A-1804421	gtcagaaattttcaaa[A/G]caatcaaacactgctt	A	G	// Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// ENST00000355875 // intron // 0 // ---	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44
SNP_A-1864636	tccagattgttagaat[A/T]aatggacatatttcca	A	T	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1857339	tcacgtccggctaaag[C/G]aaggaggctctagaag	C	G	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-1842687	tagtaaatgaaataca[C/T]gacaggctttgttagt	C	T	1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000284293 // upstream //	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-2172781	caatttctgaaactga[A/G]tcaaaaataaaaacc	A	G	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream //	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.1
SNP_A-2183858	cagccaacaatcaata[C/T]gtattttcaggcaaag	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 39308 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2217054	cctcttatctgattta[A/C]agtgttgaaagatgaa	A	C	-- /// ENST00000360683 // downstream // 522240 // --- // --- // -- // --- /// ENST00000345990 // downstream // 523298 // --- //	-	q23.2
SNP_A-2119574	agtatgacactatcac[C/T]cttaacaacaaccaac	C	T	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2159537	atttacccaaataaaa[A/T]caagtcatcctaccaa	A	T	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // upstream // 17248 // Hs.146100 //	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-2065940	ctggtccctgatgaca[A/G]caaattggaaattgct	A	G	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2049957	aaggaagataaaaaca[A/G]acatatccaattattg	A	G	3696 // Homo sapiens integrin, beta 8 (ITGB8), mRNA. /// NM_178559 // upstream // 92561 // Hs.404102 // ABCB5 //	ITGB8	ITGB8, Homo sapiens integrin, beta 8 (ITGB8), p21.1
SNP_A-2049696	agagcataagcctcag[A/C]agtttttatggaactc	A	C	341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 345751 // Hs.102971 // ALG10	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-1997681	aacctgttcatataaa[C/T]cctcctcaaagtaaac	C	T	7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), mRNA. /// NM_022486 //	UGCG	UGCG, Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), q31.3
SNP_A-2237461	ctctcctgagtctgga[G/T]agagtttagaaggata	G	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST00000359144 // downstream //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.32
SNP_A-2292480	gcactatggagtgtga[A/G]ctaaactgtaggttag	A	G	Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), mRNA. /// ENST00000233573 // intron // 0 // --- // --- // --- // --- ///	ITGA4	ITGA4, Homo sapiens integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4), q31.3
SNP_A-2308555	gctttattgtgatgct[A/C]actttattgggatagt	A	C	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 130588 // --- // --- //	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-2253035	cttctctaagctgaac[A/G]agtgggaattccattg	A	G	51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 7688 // Hs.461453 // WWOX //	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2286331	gatgcgtgcttaagcc[A/G]gccacgagaatggctc	A	G	MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2), transcript variant 1, mRNA. /// NM_145342 // downstream // 34310 // Hs.269775 // MAP3K7	MAP3K7IP2	MAP3K7IP2, Homo sapiens mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2), transcript variant 1, q25.1
SNP_A-2016594	cctgaactgtatttga[C/T]gcattctggtgaggga	C	T	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 184659 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2023491	aaaactacagggtaag[A/G]aaagtatcagactgca	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 530301 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2044453	aagaaaaccaaataca[C/G]aaagcctcaaggacat	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2304916 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086954	actgagccactccatg[G/T]cagagctggtataatc	G	T	// Homo sapiens 30 kDa protein (LOC55831), mRNA. /// ENST00000245046 // intron // 0 // --- // --- // --- // ---	LOC55831	LOC55831, Homo sapiens 30 kDa protein (LOC55831), p25.3
SNP_A-2153832	attagtttaatggaga[G/T]tcccttgtatttcact	G	T	SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 286187 // Hs.354013 //	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2107999	agctctaacgttctat[G/T]aatactttcgctgatg	G	T	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 228557 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2132450	atagtgaaagagatac[C/T]gagcttagtctattga	C	T	Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // upstream // 76653 // Hs.10862 // AK3L2 //	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-2215304	cctcaaggtgtgataa[C/T]caaaactatctccaga	C	T	3172 // Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 3, mRNA. /// NM_000457 // upstream // 14643 // Hs.116462 // HNF4A // 3172 // Homo	HNF4A	HNF4A, Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 3, q13.12
SNP_A-2208395	cccaccactttcataa[G/T]tctaactaccatcacc	G	T	374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2174325	cacacttgaccaaata[C/G]acctaatagatatcta	C	G	/// ENST00000358493 // upstream // 227167 // --- // --- // --- // -- /// ENST00000329590 // downstream // 179906 // --- // --- //	-	p23.3
SNP_A-2170353	caagtagctgggatta[A/C]aaagatgtgccaccac	A	C	// Homo sapiens myelin protein zero (Charcot-Marie-Tooth neuropathy 1B), mRNA (cDNA clone MGC:10453 IMAGE:3926008), complete cds. /// NM_000530 // downstream // 17608 // Hs.93883 // MPZ // 4359 //	MPZ	MPZ, Homo sapiens myelin protein zero (Charcot-Marie-Tooth neuropathy 1B), (cDNA clone MGC:10453 IMAGE:3926008), complete cds. ,q23.3
SNP_A-2168215	caactgaaagaccgca[C/T]tcattaatttatattt	C	T	Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST00000339709 // intron // 0 // --- // --- // --- // --- ///	SALL3	SALL3, Homo sapiens sal-like 3 (Drosophila) (SALL3), q23
SNP_A-2178008	cactacctttttcctta[C/T]agatttgcctaatctg	C	T	Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// ENST00000324696 // intron // 0 // --- // --- // --- // --- /// ENST00000262902 // intron // 0 // --- //	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-1870234	gtgctgcccatgttaa[C/T]tagtgtctaccctacc	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 99666 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1869466	tcctgtgggcacaagg[C/T]acatgttacacctgca	C	T	Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA. /// ENST00000327801 // intron // 0 // --- // ---	SMYD3	SMYD3, Homo sapiens SET and MYND domain containing 3 (SMYD3), q44
SNP_A-1653594	ataagacagataacctgatacaaaa[A/G]tgggcaaaatgtttgaatagaaagt	A	G	5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 846405 // Hs.285782 // LRRTM4 // 80059 // leucine-rich	REG1B	REG1B , rs1114583, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-1935118	ttctgatttttgtaca[G/T]aagcaagacctatgcc	G	T	7050 // Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, mRNA. /// NM_174886 // downstream // 36487 // Hs.373550 // TGIF //	TGIF	TGIF, Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, p11.31
SNP_A-1944449	ttgtctctttatatcc[A/G]gaaaataaggcctttg	A	G	// 9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// NM_173827 // downstream // 342168 // Hs.356697 // FLJ38991 //	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-1980395	attagggctgcccttg[A/G]agtttttcaccttctg	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 237198 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1964824	tttacagattatgttg[C/T]acaaaacacttgtggc	C	T	ENST00000355119 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1969723	aaagtctgttgatcag[A/C]aggagacacagtcctg	A	C	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 996482 // Hs.505079 // C21orf94	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-1973311	tgtcgattactaaata[A/G]atagaactatggaaaa	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 722476 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1929816	ttcatcctggtcaatg[A/T]agggcaagcttatatt	A	T	54583 // Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// NM_005999 // upstream // 82814 //	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2
SNP_A-1916888	tgtttctgcttggcaa[C/G]acatccggaatataca	C	G	283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 130207	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-1914771	tgttacctattataca[A/G]tgactttatttttaaa	A	G	// 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 1067320 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1912784	tgtgctcttttaggag[G/T]atctggggaagaatct	G	T	130813 // Homo sapiens hypothetical protein FLJ25143 (FLJ25143), mRNA. /// NM_152391 // upstream // 10772 //	FLJ25143	FLJ25143, Homo sapiens hypothetical protein FLJ25143 (FLJ25143), p25.1
SNP_A-1889993	tgatagtgttattatc[C/T]aatgaatcacagctga	C	T	// Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 71021 // Hs.156316 // DCN //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1878803	tctgttgtatagacta[A/T]taaactgtgcagtata	A	T	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 27062 // --- //	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1971684	tccttaagcgaagtga[C/T]actggtcatatattgt	C	T	29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// NM_015931 // downstream // 41395 //	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-1963017	agctacctacaggtaa[A/G]ggtcaaccacacttcc	A	G	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // --- // --- // --- // ---	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-1980494	aacctgcgtgcaaaaa[C/T]gctgagacctatcacc	C	T	Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// ENST00000230859 // intron // 0 // --- // --- // --- // ---	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1981627	caaggtcctagtccta[G/T]cccaaccacagactca	G	T	// 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 57826 //	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-1758970	agaaagcaagattgaagacagcttc[A/G]ataagaaagttaaaagaattgcttg	A	G	PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_015230 // downstream // 2414877 // Hs.427719 //	PCDH7	PCDH7 , rs10014788, BH-protocadherin (brain-heart) ,p15.1
SNP_A-1801942	gtataaactcatggaa[C/T]ctacttatagtctctg	C	T	Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 //	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-1812430	gtggcaggtgggccga[C/G]agcgtgggtcaccagt	C	G	29989 // Homo sapiens odorant binding protein 2B (OBP2B), mRNA. /// ENST00000238389 // upstream // 2182 // --- // --- //	OBP2B	OBP2B, Homo sapiens odorant binding protein 2B (OBP2B), q34.2
SNP_A-2179885	cactttcaacttataa[A/G]tacttagcatctacaa	A	G	Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), mRNA. /// ENST00000306184 // intron // 0 // --- // --- // -	DC-UbP	DC-UbP, Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), q35.1
SNP_A-2192158	catcagagacactata[A/C]gaagattacagaacga	A	C	sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // --- // --- // --- // --- /// ENST00000301226 // intron //	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2216732	ttacaccaaaattaca[A/T]tgctccctccagtgac	A	T	22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 8797 // Hs.306831 //	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-2227358	ctacaatatcagtaca[C/G]taatgtgctgtgcagg	C	G	Homo sapiens mitogen-activated protein kinase kinase kinase 5 (MAP4K5), transcript variant 1, mRNA. /// NM_198794 // intron // 0 // Hs.130491 // MAP4K5 // 11183 //	MAP4K5	MAP4K5, Homo sapiens mitogen-activated protein kinase kinase kinase 5 (MAP4K5), transcript variant 1, q21.3
SNP_A-2137420	ccaaaacctggatcat[A/G]atctttccacacactg	A	G	Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), mRNA. /// ENST00000305296 // intron // 0 // --- // --- // --- // ---	GNG12	GNG12, Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), p31.2
SNP_A-2119550	agtatcttggagctca[A/G]aattgctctttggagt	A	G	ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+ q24.2
SNP_A-2165534	caaagcgtcctagaac[C/T]ggttagaaaatatttt	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2086847	actgacttaaaatcca[A/G]agacacaaataaatta	A	G	Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), mRNA. /// ENST00000359467 // intron // 0 // --- // --- // --- // ---	ZNF11B	ZNF11B, Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), q11.21
SNP_A-2088112	actgggccgcttttga[C/T]aagttgctaagcctct	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2079506	acccctcgtttccttc[C/T]aggagctcacagtctg	C	T	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2084469	actatcctgaagtaaa[A/G]tactagttttgttagt	A	G	LOC346673 // 346673 // Homo sapiens STRA8 (LOC346673), mRNA. /// NM_013316 // downstream // 97951	LOC346673	LOC346673, Homo sapiens STRA8 (LOC346673), q33
SNP_A-2093898	agaagcactattttac[A/G]caggaggccaaacatt	A	G	/// ENST00000356642 // downstream // 332741 // --- // --- // ---	-	q31.1
SNP_A-2061673	aatggaaagctttaga[C/T]gagtcctttaaagttt	C	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 268163	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2070671	acacgatgttcacatc[A/T]cattctcttcaaatta	A	T	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 545656 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-2038485	aacacttctgttggac[A/G]cctttggagatgggtt	A	G	5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // upstream // 220807 // Hs.498570 //	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-2013370	aaataaacttgtagca[C/G]agagtataacaggaat	C	G	Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA. /// ENST00000342228 // intron // 0 // --- // --- // --- // ---	SLC20A2	SLC20A2, Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), p11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006726	ccagggagcagagtca[C/G]ggctggggcgtcttta	C	G	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 630029 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2001358	ccctctatctctggat[A/G]aagtgacttccagagg	A	G	/// ENST00000298762 // upstream // 16810 // --- // --- // --- // ---	-	q24.1
SNP_A-2262927	gaacaacgtgcaggac[A/G]agtggaagagcaactg	A	G	sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // intron // 0 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13
SNP_A-2251543	cttcagaacttctctc[A/T]ccctcttttcagcctt	A	T	Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // intron // 0 // --- //	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2
SNP_A-2234452	ctccacaaaggaaaac[C/T]ctgtagcatagcctaa	C	T	// 51230 // Homo sapiens chromosome 20 open reading frame 104 (C20orf104), mRNA. /// NM_016558 // upstream //	PHF20	PHF20, Homo sapiens chromosome 20 open reading frame 104 (C20orf104), q11.23
SNP_A-2229638	ctagtaatctactcaa[C/T]tgtcagtgattcaaca	C	T	Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // intron // 0 // --- // DDHD1 // 80821 // Homo	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2300821	gcctgggtgacaggac[A/G]agatacaataaaaaaa	A	G	-- /// ENST00000342478 // downstream // 452117 // --- // --- //	-	q11.21
SNP_A-2302302	gctaactagttttcca[A/G]aaatagtcatgacata	A	G	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 67586 //	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2001423	taaaatcagaaaagta[A/G]gtaagtatatttgaga	A	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2014531	agattatgaaggagaa[A/G]tctattttgtaactct	A	G	// 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // downstream // 221689 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2032916	aaataatagatacaaa[A/C]gaatgccagtcctcat	A	C	Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBR1), mRNA. /// ENST00000262458 // intron // 0 // --- // --- // --- // ---	TGFBR1	TGFBR1, Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBR1), q22.33
SNP_A-2031806	aaagtatgacaaagac[A/G]caccataattctcaat	A	G	sapiens nebulette (NEBL), transcript variant 2, mRNA. /// ENST00000311725 // intron // 0 // --- // --- // --- // ---	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 2, p12.31
SNP_A-2063951	aattatcatttggtaa[C/T]catcatagtaattaat	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 626667 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2068648	acaataacgaaaaata[A/G]gtgtttataggtgatc	A	G	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1651116 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-2069266	acaatttgaaattctc[A/G]agttagtcttactgaa	A	G	Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // --- // --- // --- // ---	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2056171	aatacctgagtaaat[A/T]aactgaggtgttttat	A	T	/// ENST00000332660 // downstream // 847253 // --- // --- // ---	-	p12.3
SNP_A-2079205	acccataaaacacaga[C/G]agcagtcaggcatggt	C	G	// 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 125152 // Hs.461453 // WWOX	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2146704	atgcttaagtctatta[C/T]gtaaaatgatacagtg	C	T	// 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // upstream //	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-2110992	aggagaacatctgatg[C/G]aagaggttggtttgtg	C	G	374918 // Homo sapiens insulin growth factor-like family member 1 (IGFL1), mRNA. /// NM_152795 // upstream //	IGFL1	IGFL1, Homo sapiens insulin growth factor-like family member 1 (IGFL1), q13.32
SNP_A-2112773	aggcaggctgttcagc[A/G]aaagcatgattgagtg	A	G	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 324675 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2126066	agttttggccacagga[A/G]taggagaacgtagtga	A	G	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 24071 // --- //	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-2209495	cccatccagcaagagc[A/G]catctggagagagggg	A	G	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 23253 // --- // --- // --- // ---	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2210901	ccccttggtaatgatc[A/G]agttctcacccggttg	A	G	Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-2203582	ccagaatgttctcaac[A/T]caggatctctgggatt	A	T	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine,q12.3
SNP_A-2192095	catcactcttgtttac[A/G]acccaacttaataaac	A	G	/// ENST00000332660 // downstream // 415959 // --- // --- // ---	-	p12.3
SNP_A-1869221	tcctggcaatgctgaa[A/C]acaaagccagtttttc	A	C	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1870637	tcgcagcatcacccaa[C/T]accaccatgtttacca	C	T	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 112503 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1859796	tcagggctagcctacg[A/C]aacatagtgagaccct	A	C	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1830145	taatagatattttaca[C/T]gagtgagatataacaa	C	T	// Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // --- // ---	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31
SNP_A-1974417	ccctaatgaggggggca[C/T]agattgtgagttaaag	C	T	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 540187	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-1887296	tgagaagctactaaga[A/G]ataaaattaaacaaca	A	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1896800	tgctcaaacagtagga[A/G]aaatggaatcgaaaaa	A	G	ENST00000329227 // intron // 0 // --- // --- // --- // ---	-	p12.1
SNP_A-1887126	tgagaaacccaaatgc[C/T]gaatttagtagcctta	C	T	Homo sapiens acyl-Coenzyme A binding domain containing 5 (ACBD5), mRNA. /// ENST00000325451 // intron // 0 // --- // ---	ACBD5	ACBD5, Homo sapiens acyl-Coenzyme A binding domain containing 5 (ACBD5), p12.1
SNP_A-1878243	tctgtcataagcatga[A/C]ggtcatcaaatgcttt	A	C	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1876144	tctgaccaatttcggc[A/G]aagtcaaatcaaatgg	A	G	7019 // Homo sapiens transcription factor A, mitochondrial (TFAM), mRNA. /// NM_012251 // downstream // 293697 //	TFAM	TFAM, Homo sapiens transcription factor A, mitochondrial (TFAM), q21.1
SNP_A-1905074	tgggtgaatatgtcca[C/T]gtggaagagaaactat	C	T	// 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 8275 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-1965675	gtgtaaaattcaagca[A/C]ctttcctcttccccta	A	C	55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 72737 // Hs.411881 // GRB14 //	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1984283	cgcaggctgtgctttg[C/T]aaggggttgatagaat	C	T	// Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 129227 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1953751	tttgagaactggtgaa[C/T]gtgagcactctaaatt	C	T	1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 //	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-1952713	tttctgtatatgtcac[A/G]gccttgccatttttga	A	G	30813 // Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, mRNA. /// NM_199425 // upstream // 95474 // Hs.274264 // VSX1 //	VSX1	VSX1, Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, p11.21
SNP_A-1825866	taaatgacttcacaaa[C/T]ggagatcaagtgtcgt	C	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 796052 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1828134	taagactgcctttaaa[C/G]ttcatgcaatactgtt	C	G	64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 342355 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1862343	tcatgtacttagtgac[A/C]atttgtatatcttctt	A	C	-- /// ENST00000342478 // downstream // 134177 // --- // --- //	-	q11.21
SNP_A-1864687	tccagcatgaccctag[C/T]cctcaagttactgaca	C	T	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-1845537	tatagatatggagaca[A/G]gagttggaaacagggt	A	G	Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// ENST00000262560 // intron // 0 // --- // --- // --- // ---	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-1732756	actggatgaaattccacatacaacc[A/G]atggaaaaaataattaaagcttgga	A	G	4332 // myeloid cell nuclear differentiation antigen /// NM_003126 // upstream // 35879 // Hs.418378 // SPTA1 //	MNDA	MNDA , rs10489841, myeloid cell nuclear differentiation antigen ,q23.1
SNP_A-2206121	ccatcaccaggagaaa[C/G]cagtttgagttcatca	C	G	Homo sapiens chromosome 4 open reading frame 8 (C4orf8), mRNA. /// ENST00000324666 // intron // 0 // --- // ---	C4orf8	C4orf8, Homo sapiens chromosome 4 open reading frame 8 (C4orf8), p16.3
SNP_A-2112864	aggcataggtcctttc[A/G]aaatgcagtgcctgtg	A	G	NM_001503 // intron // 0 // Hs.512001 // GPLD1 // 2822 // Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, mRNA. /// ENST00000230036 // intron // 0 // --- // --- // --- // ---	GPLD1	GPLD1, Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, p22.2
SNP_A-2166875	caaatttgcagaccca[C/G]gcatacctccaggtgt	C	G	283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream //	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2163987	caaaagaaacactcaa[C/T]tgttcctcaccagggg	C	T	221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 //	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-2095640	agacacacaggctttg[A/C]atggcatataggtttc	A	C	10186 // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /// ENST00000344021 // downstream // 76525 // --- // -	LHFP	LHFP, Homo sapiens lipoma HMGIC fusion partner (LHFP), q13.3
SNP_A-2048900	aagccgtgggtcagaa[A/G]agctggaaggggagca	A	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2074613	acatataagagcgtta[A/G]ctggattgtttgtaac	A	G	Homo sapiens ankyrin repeat domain 11 (ANKRD11), mRNA. /// ENST00000301030 // intron // 0 // --- // --- // --- // ---	ANKRD11	ANKRD11, Homo sapiens ankyrin repeat domain 11 (ANKRD11), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2033580	aaatatatctctcata[A/G]ctaagtggctgtggga	A	G	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 371912 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2047081	aagagtttttaagaca[A/G]agagaactgtgactgc	A	G	// 83992 // Homo sapiens cortactin binding protein 2 (CTTNBP2), mRNA. /// ENST00000160373 // upstream //	CTTNBP2	CTTNBP2, Homo sapiens cortactin binding protein 2 (CTTNBP2), q31.31
SNP_A-2018262	tctgttgttttctata[A/G]gttagattgcccattg	A	G	116448 // Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), mRNA. /// NM_207584 // upstream // 29440 //	OLIG1	OLIG1, Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), q22.11
SNP_A-2003319	ttgcaaaccagacaga[A/C]agatcccctcttgatc	A	C	Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), mRNA. /// ENST00000242850 // intron // 0 // ---	GUCY1B2	GUCY1B2, Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), q14.3
SNP_A-2293169	gcagagaatatggcaa[A/G]aactgaccaaatcaat	A	G	2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 446020 // Hs.203717	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-2266197	gaagggatttattcag[G/T]aaaggtatctaacaag	G	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1295594 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2287255	gatgtgacaaggcaaa[C/T]taaatgtatacaaggt	C	T	// Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), mRNA. /// ENST00000331299 // intron // 0 // --- // --- // --- // ---	SLC25A21	SLC25A21, Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), q13.3
SNP_A-2299644	gccgctgaattgggaa[A/G]ctctgaaggagtctct	A	G	sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2299632	gttttggatacttttt[C/T]cagttgattctcttat	C	T	// 59274 // Homo sapiens mesoderm development candidate 1 (MESDC1), mRNA. /// NM_173528 // upstream // 75905 // ---	MESDC1	MESDC1, Homo sapiens mesoderm development candidate 1 (MESDC1), q25.1
SNP_A-2295860	gcatgggcccaaccta[A/G]ctcataattgttttgt	A	G	ENST00000330888 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2307436	gcttatctagatagga[A/G]actagaagaactgcac	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 // intron // 0 // --- // ---	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2
SNP_A-1991288	catgagacctgattca[C/T]gttcacaaaatcttca	C	T	/// ENST00000251675 // downstream // 357326 // --- // --- // --- // --- /// ENST00000360855 // downstream // 357356 // --- // ---	-	q32.3
SNP_A-1991656	gtaaaaggaggaaatg[A/C]ataggaaaaggcatga	A	C	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2011701	tatgaaagaatgttca[C/T]cacaactttactcaga	C	T	// Homo sapiens motilin (MLN), mRNA. /// NM_000841 // downstream // 24195 // Hs.429018 // GRM4 // 2914 // Homo	MLN	MLN, Homo sapiens motilin (MLN), p21.31
SNP_A-2036918	aaatttggtgattaga[C/T]cttgaacttaaagctt	C	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2038705	aacagaggctgtggag[A/G]atagtctttgtgtcca	A	G	83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 64344 // Hs.432458 // PRG4 //	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2074731	acatatggtgttggac[C/T]aacaaattcatctgct	C	T	ENST00000356808 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2048058	aagcaatcactatagc[C/T]aagctcagggtcaccg	C	T	/// ENST00000354335 // downstream // 110167 // --- // --- // ---	-	q26.1
SNP_A-2049781	aaggaaaacctctaca[A/C]tgctaatggtaatgta	A	C	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2061712	aatggaagtcatgtca[C/G]tctcctgttttggttt	C	G	Homo sapiens mRNA for KIAA0391 gene, partial cds. /// ENST00000250377 // intron // 0 // --- // --- // --- // --- ///	KIAA0391	KIAA0391, Homo sapiens for KIAA0391 gene, partial cds. q13.2
SNP_A-2096588	agacctttctcttaga[A/C]cgagcgtgactttctg	A	C	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA. /// ENST00000317224 //	PFKFB3	PFKFB3, Homo sapiens 6-phosphofructo-2-kinase,p15.1
SNP_A-2097776	agagaccgcagggagc[C/T]gaggactgaaggagag	C	T	56940 // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// ENST00000307499 // upstream //	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3
SNP_A-2161107	atttgaaaggaaatgg[A/T]aaactcgcttttttt	A	T	// 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream //	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2156318	attctattgcctctga[C/T]actactctaatccaga	C	T	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2147520	atggatcaaattaaaa[C/T]agtgttggtcctgtta	C	T	Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // --- // -	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-2137988	atcatttttcttctgt[C/T]aaagtggcaaaattat	C	T	ENST00000356808 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2141245	atctgtaactacctga[C/T]gagcccaattagttgc	C	T	3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 188002 // Hs.36975 // FSHB //	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-2126207	ataaaaacagcatttc[A/G]agaagaggcaaagaaa	A	G	Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST00000263915 // intron // 0 // --- // ---	GRB14	GRB14, Homo sapiens growth factor receptor-bound protein 14 (GRB14), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2201552	ccaattcagataatca[A/C]ctttcacagcacacca	A	C	-- /// ENST00000342478 // downstream // 4707 // --- // --- // ---	-	q11.21
SNP_A-2210953	cccgaagtttgctgca[C/T]attgaattcacttgaa	C	T	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 186985 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2211663	tagtttactgaaggta[C/T]gacattcacatccttg	C	T	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2222859	cgcaacaagcattttg[A/G]attcagacgtattttc	A	G	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-2183307	cagcacagtcatgtaa[C/T]tataatacaacacagg	C	T	63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 238057	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-2189185	cagttatggctgcaag[C/G]aaggtcatcataagtg	C	G	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 522942 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-2188960	cagtgtctctccttcc[C/T]gcaggcctggatggat	C	T	85414 // Homo sapiens prostein protein (Prostein), mRNA. /// NM_022731 // downstream // 26924 // Hs.213061 // NUCKS	PCANAP6	PCANAP6, Homo sapiens prostein protein (Prostein), q32.1
SNP_A-1744839	atgcagattgacagccctttaata[C/T]gaaataaatcaggcaggagaaggag	C	T	AK056484 // intron // 0 // Hs.446652 // LOC340281 // 340281 // hypothetical protein LOC340281	LOC340281	LOC340281 , rs10486462, hypothetical protein LOC340281,p15.2
SNP_A-1644764	acaacaatgaatagcactgtagatg[A/T]atttttctatgaggcgtgtcatcag	A	T	NM_182758 // upstream // 286568 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	FLJ38736	FLJ38736 , rs10518752, hypothetical protein FLJ38736,q21.3
SNP_A-1804108	gtcacaggtaaagctg[A/G]atttcaatttatttaa	A	G	Homo sapiens PARK2 co-regulated (PACRG), mRNA. /// ENST00000230292 // intron // 0 // --- // --- // --- // --- ///	PACRG	PACRG, Homo sapiens PARK2 co-regulated (PACRG), q26
SNP_A-1792177	gggttaatgtccttac[A/G]agaagaataagagaaa	A	G	CAPZA3 // 93661 // Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA. /// NM_019012 // upstream // 57145 // Hs.188614 // PLEKHA5 //	CAPZA3	CAPZA3, Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), p12.3
SNP_A-1798743	gtaacgtgtagaggta[A/T]aaaccatctttctgt	A	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1815136	gtgttctgaatataaa[C/T]gtgctttccatcctta	C	T	// Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRNA. /// NM_024940 // upstream // 223282 //	NEFL	NEFL, Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), p21.2
SNP_A-1831737	taattcactctcttaa[C/T]atctgtaaaagaaaaa	C	T	Homo sapiens phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III (PIP5K3),	PIP5K3	PIP5K3, Homo sapiens phosphatidylinositol-3-phosphate,q34
SNP_A-1833370	tacagaagagaaagaa[A/T]gtgaaataaacaggtt	A	T	9324 // Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, mRNA. /// NM_004242 // upstream // 4193 // Hs.77558 // HMGN3 //	HMGN3	HMGN3, Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, q14.1
SNP_A-1980719	agataccaatgtatag[G/T]cactgttcggaaatag	G	T	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // --- // --- // --- // ---	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1978298	gcagatttgccactaa[C/T]gaaatagtaaagagat	C	T	Homo sapiens solute carrier family 39 (zinc transporter), member 8 (SLC39A8), mRNA. /// ENST00000265515 //	SLC39A8	SLC39A8, Homo sapiens solute carrier family 39 (zinc transporter), member 8 (SLC39A8), q24
SNP_A-1924605	ttatagaagtttacca[A/C]gcgtgatctaaggtgt	A	C	ENST00000357997 // intron // 0 // --- // --- // --- // --- /// ENST00000337516 // intron // 0 // --- // --- // --- // ---	-	q24.33
SNP_A-1879010	tcttaacattacataa[G/T]tcaaccaagtattgta	G	T	MGC8721 // 51669 // Homo sapiens hypothetical protein MGC8721 (MGC8721), mRNA. /// ENST00000330733 //	MGC8721	MGC8721, Homo sapiens hypothetical protein MGC8721 (MGC8721), p12
SNP_A-1902924	tggctgactctatcca[A/C]ctttggttatacttct	A	C	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1894940	tgccattttattgtga[A/C]tagttctatagatatc	A	C	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1924635	ttatagatctttgcaa[A/T]tgaaagacactggtaa	A	T	// 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream //	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-1951491	tttcctcctgctggcc[A/G]aaggcggcaacaggag	A	G	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1935687	ttctgtcttagtttta[C/T]ggctgctgttcagtgg	C	T	ENST00000333644 // intron // 0 // --- // --- // --- // ---	-	q35.2
SNP_A-1936010	ttcttagaacactgga[C/T]ggcaagatacttcttt	C	T	sapiens endothelin 3 (EDN3), transcript variant 1, mRNA. /// NM_207034 // intron // 0 // Hs.1408 // EDN3 // 1908 // Homo	EDN3	EDN3, Homo sapiens endothelin 3 (EDN3), transcript variant 1, q13.32
SNP_A-1939796	ttgcaagagaagcaga[G/T]gtgaaagagaaggaaa	G	T	TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream //	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1843746	tagtgttagaaggcaa[C/T]gccaggactctgactc	C	T	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 104431 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1857661	tcactgaacaggaaaa[G/T]gaatcaaatccacatt	G	T	Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 2 /// ENST00000223423 // 3UTR // 0 // --- // -	PTGS1	PTGS1, Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G,q33.2
SNP_A-1787970	gggagaaagcgttgta[A/C]atccttctcattcaag	A	C	Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Hom	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding ,p22.2
SNP_A-1803851	gtcaaggaattagaaa[A/G]tggcagagttcagaca	A	G	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 890399	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1810759	gtgcagactcatgtga[C/T]ggtcacctttgaaaa	C	T	57515 // Homo sapiens tumor differentially expressed 2 (TDE2), mRNA. /// NM_181795 // upstream // 6868 //	TDE2	TDE2, Homo sapiens tumor differentially expressed 2 (TDE2), q22.31
SNP_A-1652930	aagcaatattcaaataaattagtca[C/T]tcaatcactaattcatttatttaac	C	T	NM_016195 // downstream // 401557 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs3918657, M-phase phosphoprotein 1,q23.31
SNP_A-1695431	gatattctatagcctatgagcatta[A/T]aaaatgataaattggtcaggggttt	A	T	// 1946 // ephrin-A5 /// NM_031438 // upstream // 155678 // Hs.434289 // NUDT12 // 83594 // nudix (nucleoside	EFNA5	EFNA5 , rs10515349, ephrin-A5 ,q21.2
SNP_A-1781243	ggatggtgggcaagta[A/G]agtggtctgaagaatg	A	G	9447 // Homo sapiens absent in melanoma 2 (AIM2), mRNA. /// NM_021189 // upstream // 24739 // Hs.365689 // IGSF4B //	AIM2	AIM2, Homo sapiens absent in melanoma 2 (AIM2), q23.2
SNP_A-2176111	caccacacgagggaga[A/C]taccagtatgactatc	A	C	Homo sapiens pregnancy specific beta-1-glycoprotein 5 (PSG5), mRNA. /// ENST00000342951 // intron // 0 // --- // ---	PSG5	PSG5, Homo sapiens pregnancy specific beta-1-glycoprotein 5 (PSG5), q13.31
SNP_A-2176246	caccagacattctgca[A/T]attgtgactatgccaa	A	T	// 22807 // Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), mRNA. /// NM_024532 // upstream //	ZNFN1A2	ZNFN1A2, Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), q34
SNP_A-2224358	cgtaatccagtcataa[C/T]agtgtttcattctatt	C	T	Homo sapiens dedicator of cytokinesis 8 (DOCK8), mRNA. /// ENST00000287364 // intron // 0 // --- // --- // --- // ---	DOCK8	DOCK8, Homo sapiens dedicator of cytokinesis 8 (DOCK8), p24.3
SNP_A-2125685	agtttcttaagaggga[G/T]gcaatgggtgttcaaa	G	T	Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000261509 // intron // 0 // --- // --- // --- // --- ///	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3
SNP_A-2108085	agctctgaggaaaccc[C/T]ggaattaagccagttg	C	T	Homo sapiens CD96 antigen (CD96), transcript variant 2, mRNA. /// NM_198196 // intron // 0 // Hs.142023 // CD96 //	CD96	CD96, Homo sapiens CD96 antigen (CD96), transcript variant 2, q13.2
SNP_A-2119764	agtatttatttgcctc[A/G]catttatgtcacatga	A	G	Homo sapiens hypothetical protein FLJ13955 (FLJ13955), mRNA. /// ENST00000341166 // intron // 0 // --- // --- // --- // ---	FLJ13955	FLJ13955, Homo sapiens hypothetical protein FLJ13955 (FLJ13955), q22.2
SNP_A-2146220	atgctaacaacttgta[A/C]atagttctgtgtgagt	A	C	654 // Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000305775 // downstream // 3824 // --- // --	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-2102955	agcaaacgcgctgcgc[A/G]aaaggtaggtttccaa	A	G	// 169166 // Homo sapiens hypothetical protein MGC39715 (MGC39715), mRNA. /// NM_002568 // downstream // 39769	MGC39715	MGC39715, Homo sapiens hypothetical protein MGC39715 (MGC39715), q22.3
SNP_A-2078282	accataaggtccccaa[C/T]gcagtcaatggaattg	C	T	Homo sapiens cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA. ///	CDON	CDON, Homo sapiens cell adhesion molecule-related q24.2
SNP_A-2089325	acttagggattcactg[C/G]aagatttcttgaaaga	C	G	KIAA1573 // 57685 // Homo sapiens KIAA1573 protein (KIAA1573), mRNA. /// NM_020925 // downstream // 29289 //	KIAA1573	KIAA1573, Homo sapiens KIAA1573 protein (KIAA1573), p31.3
SNP_A-2071314	acacttgctgaaacaa[C/T]tgcccatgattctcat	C	T	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 210251 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2028594	aaactgctggctacag[A/G]aaatgactgctgttaa	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2014739	gtgaaacagtttagaa[A/G]aaaggacagtaatctc	A	G	sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), mRNA. /// ENST00000279441 // CDS // 0 // --- // --- // --- // ---	MMP10	MMP10, Homo sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), q22.2
SNP_A-1995105	aggccccttgcagtga[A/G]tagtctttgggcagca	A	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2298767	gcccagtttcctctta[C/T]attaaatgatgggatt	C	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 292532	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-2298019	gccatactaaagaata[C/T]ggactcacataaaatg	C	T	Homo sapiens ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), mRNA. /// ENST00000261601 // intron // 0 // --- // --- // --- // ---	USP14	USP14, Homo sapiens ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), p11.32
SNP_A-2292735	ctcactttggtttcag[C/G]caagagaaatggtacc	C	G	Homo sapiens SMAD, mothers against DPP homolog 3 (Drosophila) (SMAD3), mRNA. /// ENST00000327367 //	SMAD3	SMAD3, Homo sapiens SMAD, mothers against DPP homolog 3 (Drosophila) (SMAD3), q22.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2265052	gaagatagcaacttga[C/T]agatataatctggaga	C	T	/// ENST00000334919 // upstream // 890503 // --- // --- // --- // --- /// ENST00000322194 // downstream // 878646 // --- // --- // ---	-	q12.2
SNP_A-2264801	gaagagaaagagttac[C/T]gagaactgctatccac	C	T	26119 // Homo sapiens LDL receptor adaptor protein (ARH), mRNA. /// NM_020379 // upstream // 29740 // Hs.197043 //	ARH	ARH, Homo sapiens LDL receptor adaptor protein (ARH), p36.11
SNP_A-2264849	gaagagagcccttaaa[A/C]tcagtcaggaccagac	A	C	758 // Homo sapiens chromosome 22 open reading frame 1 (C22orf1), mRNA. /// NM_001584 // upstream // 245207 //	C22orf1	C22orf1, Homo sapiens chromosome 22 open reading frame 1 (C22orf1), p14.1
SNP_A-2268340	gaatgcatagaaagaa[A/T]tagttcagaaatctct	A	T	Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // intron // 0 // --- // --- // --- // --- ///	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-2257400	ctttgaataattaagc[A/T]agaatggattacaaga	A	T	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2257514	ctttgatgaagaaatt[A/T]aaaaaagtctatataa	A	T	// 3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. /// ENST00000315260 //	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.1
SNP_A-2249218	ctgtttttatacatca[A/G]taattgacaagcaaat	A	G	// 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 82565 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m ,q31.1
SNP_A-2248416	ctgtgtgtcctgccta[C/T]agccacagcatcttct	C	T	sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- // --- /// ENST00000357947 // intron //	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2244041	ctgcttctgcagctgc[A/G]aagctacttatctgca	A	G	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2244667	ctggagggacctagac[C/T]atagcagagaagaagt	C	T	57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 282773 // Hs.424711 //	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2264632	gaagaatgcccttctc[A/T]ctgacagaactgtgag	A	T	/// ENST00000355063 // upstream // 570547 // --- // --- // --- // ---	-	q22.1
SNP_A-2267217	gaatacatcaacaaaa[C/T]gacaaaaatctttgac	C	T	Homo sapiens chromosome 3 open reading frame 15 (C3orf15), mRNA. /// ENST00000273390 // intron // 0 // --- // ---	C3orf15	C3orf15, Homo sapiens chromosome 3 open reading frame 15 (C3orf15), q13.33
SNP_A-2280785	gaggtggaagctttca[C/T]gttctgtgtttgttgt	C	T	ENST00000269197 // CDS // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2297906	gccagtccatccgggga[G/T]cttggagggtcagcct	G	T	55236 // Homo sapiens hypothetical protein FLJ10808 (FLJ10808), mRNA. /// NM_000406 // downstream // 24190 //	FLJ10808	FLJ10808, Homo sapiens hypothetical protein FLJ10808 (FLJ10808), q13.2
SNP_A-2308577	gctttcaagacagaga[A/C]taacaacaaatgactt	A	C	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 400280 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2008833	ctaagagagtcgtccc[A/G]cttcctgcttgggcct	A	G	ENST00000308537 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-2029896	aaagatataattatac[A/C]cactatccacaaaagc	A	C	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2039908	aacattggtttacata[C/T]ggtaatacacttgatc	C	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2069335	acacaaacatccttca[C/G]ctcattgaaaactgtt	C	G	ENST00000355599 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2067280	acaaagtaaatactca[A/G]tgagggttggtcatga	A	G	Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 //	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-2058030	aatatttccactcttg[C/G]agaacaaaaagagccc	C	G	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // H	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-2052714	aagtattttgttcaat[C/G]agtgaaaacatgaatg	C	G	Homo sapiens hypothetical protein FLJ11383 (FLJ11383), transcript variant 1, mRNA. /// NM_024938 // intron // 0 //	PCNXL2	PCNXL2, Homo sapiens hypothetical protein FLJ11383 (FLJ11383), transcript variant 1, q42.2
SNP_A-2097307	atagcattttgtacaa[C/G]ttacagttatgaaact	C	G	121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// AF425596 // upstream // 80714 // Hs.528316 // FOXN4 //	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2149481	atgtagacttgccctc[C/T]aagtggcaacaaaatt	C	T	Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA. /// ENST00000285208 // intron // 0 // --- // ---	RAB6B	RAB6B, Homo sapiens RAB6B, member RAS oncogene family (RAB6B), q22.1
SNP_A-2141031	atctgccacaagagat[A/G]atacttcatttatgag	A	G	Homo sapiens ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1 (ATP6V1E1), mRNA. /// ENST00000253413 // intron // 0 // --- // --- // --- // ---	ATP6V1E1	ATP6V1E1, Homo sapiens ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1 (ATP6V1E1), q11.21
SNP_A-2153596	attagcttgtggttgg[A/G]atttgatggttttctg	A	G	Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// NM_001147 // intron // 0 // Hs.490892 //	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2117076	aggtgagtttcatgag[C/G]atgtgaccagtctgtg	C	G	HMG2L1 // 10042 // Homo sapiens high-mobility group protein 2-like 1 (HMG2L1), transcript variant 3, mRNA. /// NM_014250 // upstream // 86083 // Hs.197086 // HMG2L1 //	HMG2L1	HMG2L1, Homo sapiens high-mobility group protein 2-like 1 (HMG2L1), transcript variant 3, q12.3
SNP_A-2127735	ataactgaattcccca[A/G]ggtcacaagatacaag	A	G	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	SMARCB1	SMARCB1, Homo sapiens SWI q11.23
SNP_A-2133984	atatcttattaaattc[C/T]caattgtctcaggcta	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2213464	ccgggtgtggcaggcc[A/G]ccgacttgagcagaag	A	G	Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, mRNA. /// NM_000635 // intron // 0 // Hs.465709 // RFX2 // 5990 //	RFX2	RFX2, Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, p13.3
SNP_A-1688760	tttttcacttactcctttccataaa[A/G]aagtgtaacaatggagtacgttata	A	G	NM_016205 // intron // 0 // Hs.43080 // PDGFC // 56034 // platelet derived growth factor C	PDGFC	PDGFC , rs10517658, platelet derived growth factor C,q32.1
SNP_A-1655395	actctttccttaagacaataaaga[A/G]gttatagggattggagacctttatg	A	G	formin 2 /// NM_000740 // downstream // 417595 // Hs.7138 // CHRM3 // 1131 // cholinergic receptor, muscarinic 3 ///	FMN2	FMN2 , rs6679031, formin 2 ,q43
SNP_A-1801492	gtagggccagagaatg[A/C]agttagtatgggttgc	A	C	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-1785440	ggctcaaagtcaggca[C/G]gtaatgttccggtcac	C	G	167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 315540 //	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3
SNP_A-1862687	cagacacactcactgc[G/T]cctcattatagactca	G	T	Homo sapiens hypothetical protein FLJ10970 (FLJ10970), mRNA. /// ENST00000299377 // intron // 0 // --- // --- // --- // ---	FLJ10970	FLJ10970, Homo sapiens hypothetical protein FLJ10970 (FLJ10970), q23.1
SNP_A-1827612	taactgctcttcttgg[A/G]aaatgaatttctattc	A	G	Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // intron // 0 // Hs.117767 //	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1919426	ttaagcaccaaacaca[G/T]tacaggacatttggat	G	T	// --- /// ENST00000345111 // upstream // 63145 // --- // --- // ---	-	q24.32
SNP_A-1931039	ttccataacacgtaag[A/G]cattccatgtgcaaga	A	G	// 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000327792 // downstream // 413895 // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-1876117	tctgacactgagggca[A/G]tgagaaatcttggctt	A	G	/// ENST00000277082 // upstream // 1934 // --- // --- // --- // ---	-	q21.2
SNP_A-1882157	tctttttatgtgtga[G/T]gataacacaagatcta	G	T	10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream //	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13
SNP_A-1876757	tctgcagggcttggga[C/T]gcctcagaaaactaac	C	T	Human mRNA for KIAA0257 gene, partial cds. /// NM_144992 // upstream // 169588 // Hs.269977 //	RW1	RW1, Human for KIAA0257 gene, partial cds. q11.2
SNP_A-1892053	tgcaaacaatagctca[C/G]aaaactttccgccaca	C	G	ENST00000351898 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1922317	agagcacaagtggacc[A/G]gaacctggaaaaatgt	A	G	SERPINB13 // 5275 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), mRNA. /// NM_002974 // downstream // 14237	SERPINB13	SERPINB13, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), q21.33
SNP_A-1945508	ttgttcattaacttca[A/C]ctgttccaggtaaaag	A	C	4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 556363 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1957731	ttttatgttaatgctc[C/T]accaggtgattcatgt	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1980238	agatattctacagaca[G/T]gtttagaggaaattag	G	T	Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron //	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-1857149	tcacctagtgtagtat[C/T]agccatacggaaagag	C	T	// Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1258049 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1803901	gtcaagttattccaaa[A/G]ttaatgcaattaccag	A	G	Homo sapiens mRNA for GRIP1 protein. /// ENST00000286445 // intron // 0 // --- // --- // --- // --- ///	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. q14.3
SNP_A-2218734	cctggctggaaataca[A/T]cacaggtgagccatag	A	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2206889	ccatggcttttaggtg[C/T]aagttataatgaacaa	C	T	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2199470	catttttcccccaaga[A/T]gtaacactctcaatca	A	T	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 120459 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2199406	cattttgtacatctag[C/G]actggcaacaaaactt	C	G	/// ENST00000335028 // upstream // 273654 // --- // --- // --- // ---	-	q21.31
SNP_A-2131296	atagagttagtttaca[C/T]accccatatcacccct	C	T	5728 // Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /// NM_018363 // downstream // 19444 // Hs.149849 // C10orf59	PTEN	PTEN, Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), q23.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123301	agtgtagtggaataga[A/G]ctccattgggaacact	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA. /// NM_013987 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, q26
SNP_A-2138270	atccagaaatgggaac[C/T]ggtgtggtcaagtaaa	C	T	Homo sapiens hypothetical protein FLJ25200 (FLJ25200), mRNA. /// ENST00000295824 // intron // 0 // --- // --- // --- // ---	EFHB	EFHB, Homo sapiens hypothetical protein FLJ25200 (FLJ25200), p24.3
SNP_A-2145478	atgcaggtaggtaata[A/G]tatcttcctcacagag	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2099701	agaggtgttctgagaa[C/T]ggtgctgtgaaaagga	C	T	111 // Homo sapiens adenylate cyclase 5 (ADCY5), mRNA. /// ENST00000309879 // upstream // 45541 // --- // --- // --- // ---	ADCY5	ADCY5, Homo sapiens adenylate cyclase 5 (ADCY5), q21.1
SNP_A-2091142	tgagcagaggatgaaa[C/T]tgggaagtcacccatc	C	T	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1
SNP_A-2086864	actgacttttcagatc[A/G]aaggccctttccaaat	A	G	2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 379783 // Hs.203717	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-2036333	aaattccaccatacat[C/T]acaaggactaaaatta	C	T	ENST00000354225 // intron // 0 // --- // --- // --- // ---	-	q26.11
SNP_A-2023012	aaaacaccttgtaaaa[C/G]gcaacatacggccagt	C	G	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 26120 // Hs.54642 // MAT2B // 27430 // Homo	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2015230	acctgttaattagaag[A/T]acagtagtcaccacat	A	T	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 13 (ABCC13), transcript variant 1,	ABCC13	ABCC13, Homo sapiens ATP-binding cassette, sub-family C (CFTR q11.2
SNP_A-2016568	acattaaaacatccaa[A/G]tagctcattgtagaat	A	G	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream //	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016818	tggccttggtaagaaa[A/G]ctggccttcatctttg	A	G	LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 652122 // --- // --- // --- //	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-1991528	gatattaacatagtta[A/T]aaaagagccaagtgct	A	T	/// ENST00000356506 // downstream // 61572 // --- // --- // --- // --- /// ENST00000332013 // downstream // 27120 // --- // ---	-	q34
SNP_A-2287972	gattatgtgtcattca[A/G]atttttcggcactgta	A	G	-- /// ENST00000329863 // downstream // 680678 // --- // --- //	-	q23.1
SNP_A-2284994	gatcctaactcctgag[A/C]ccagagccaaggaggt	A	C	7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 44096 // --- // --- // --- // ---	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-2265499	agagcagagtaactga[C/T]acttcccaccatcctc	C	T	Homo sapiens transient receptor potential cation channel, subfamily M, member 1 (TRPM1), mRNA. /// ENST00000220192 // intron // 0 // --- // --- // --- // --- ///	TRPM1	TRPM1, Homo sapiens transient receptor potential cation channel, subfamily M, member 1 (TRPM1), q13.3
SNP_A-2263450	gaaccaaaatgaacca[C/T]gttacacaaatgaagt	C	T	57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 83439 //	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2250797	cttatccatcttctac[C/T]attaacccataagtgt	C	T	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // --- // ---	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1
SNP_A-2307767	gcttcctcttgaacac[A/G]gtcctcaatgctcctc	A	G	Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 9 (CYP2C9), mRNA. /// ENST00000260682 // CDS // 0 // --- // --- // --- // ---	CYP2C9	CYP2C9, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 9 (CYP2C9), q23.33
SNP_A-2302938	gctaggatttatggaa[C/T]acttactacgttctaa	C	T	Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-2091660	ggtaaaaactagcaaa[A/T]gtcatcggttctaggt	A	T	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2106286	agccctcaactttctg[G/T]atggaaaaaattcatt	G	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2095484	agacaacatgcagtaa[C/T]aaaaaaatacaagaaa	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2058682	aatcatatcaatcgat[A/T]aacttacatcttttaa	A	T	490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 105296 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-2064352	aattcatcaagacaat[C/G]agcccatggcattttc	C	G	Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// ENST00000332981 // intron // 0 // --- // --- // --- // ---	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-2153645	attaggattatttgta[A/C]gtcagcattcataatg	A	C	Homo sapiens chloride channel 6 (CLCN6), transcript variant CIC-6a, mRNA. /// NM_021735 // intron // 0 // Hs.193043 //	CLCN6	CLCN6, Homo sapiens chloride channel 6 (CLCN6), transcript variant CIC-6a, p36.22
SNP_A-2155871	attcctagcctctgta[A/T]ctgtgagaaataaatt	A	T	53354 // Homo sapiens pantothenate kinase 1 (PANK1), transcript variant beta, mRNA. /// NM_148977 // upstream //	PANK1	PANK1, Homo sapiens pantothenate kinase 1 (PANK1), transcript variant beta, q23.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2118408	agtaagcattcctata[C/T]gagacatggagaactc	C	T	Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2182906	cagattactaatgttc[A/G]aaaaccacataggttt	A	G	// 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream // 139890 //	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-2171420	caatcaatcccagcgc[A/G]caagatgccacctccc	A	G	MGC10911 // 84262 // Homo sapiens hypothetical protein MGC10911 (MGC10911), mRNA. /// ENST00000288607 //	MGC10911	MGC10911, Homo sapiens hypothetical protein MGC10911 (MGC10911), p22.3
SNP_A-2211181	cccgttgcttctcctc[C/T]aggtgccgcttctgct	C	T	Homo sapiens oxysterol binding protein-like 10 (OSBPL10), mRNA. /// ENST00000273142 // CDS // 0 // --- // --- // --- // ---	OSBPL10	OSBPL10, Homo sapiens oxysterol binding protein-like 10 (OSBPL10), p24.1
SNP_A-2226176	ctaacggctgcggaaa[G/T]gagactgaagctttga	G	T	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1704145	cctgtaccatgcttggggctgaagg[A/T]atctcctgcaagtgatgaagggcca	A	T	9436 // natural cytotoxicity triggering receptor 2 /// NM_138457 // upstream // 143617 // Hs.199316 // FOXP4 //	NCR2	NCR2 , rs10485325, natural cytotoxicity triggering receptor 2 ,p21.1
SNP_A-1743349	cctgaccaatagtaaatggttgtta[A/C]gtgtatatgtatatgagtgtgtata	A	C	3908 // laminin, alpha 2 (merosin, congenital muscular dystrophy) /// NM_002844 // upstream // 156642 // Hs.354262	LAMA2	LAMA2 , rs526895, laminin, alpha 2 (merosin, congenital muscular dystrophy) ,q22.33
SNP_A-1739153	aggggagaatccctgcaatagaatg[A/G]atgagtgggcagtgatagaaaaaga	A	G	// 8170 // solute carrier family 14 (urea transporter), member 2 /// NM_015559 // downstream // 155036 // Hs.201369 //	SLC14A2	SLC14A2 , rs10502860, solute carrier family 14 (urea transporter), member 2 ,q12.3
SNP_A-1859458	tcaggacatccaggaa[C/T]gcaacctctgatggtg	C	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1848157	tatcttcatgtcattc[A/T]ctttttttaactcccac	A	T	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1841649	ccacaccattgtgacc[A/G]gaaagagacccaaggc	A	G	// 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-1962500	ggaaaagattcaataa[A/C]ccatttgatatttgta	A	C	sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, mRNA. /// NM_199194 // intron // 0 // Hs.258314 // BRE // 9577 // Homo	BRE	BRE, Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, p23.2
SNP_A-1956935	ttttaaggcaagatac[A/G]aattgtgtgccctgtg	A	G	ENST00000343170 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1949135	tttatgccaggggtgc[A/G]cagctttccaagaaaa	A	G	344658 // Homo sapiens sterile alpha motif domain containing 7 (SAMD7), mRNA. /// NM_003262 // upstream //	SAMD7	SAMD7, Homo sapiens sterile alpha motif domain containing 7 (SAMD7), q26.2
SNP_A-1925203	ttatccatctataaca[C/T]aatccatataaactga	C	T	9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 477896 //	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1925634	ttatgagagacattac[A/G]gagacacactaaacgc	A	G	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 566665 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-1927703	ttcaacttgtgtgcca[A/G]tgattctagtgtattg	A	G	// Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// ENST00000297345 // intron // 0 // --- // --- // --- // ---	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-1909546	tgtatttgggtgctta[C/T]aattgctcatggtatg	C	T	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-1907786	aggcaaggggaactgc[A/G]agccccacatcaggca	A	G	125336 // Homo sapiens lipoxygenase homology domains 1 (LOXHD1), mRNA. /// NM_013305 // downstream // 74586 //	LOXHD1	LOXHD1, Homo sapiens lipoxygenase homology domains 1 (LOXHD1), q21.1
SNP_A-1903402	tgggaagaaattcaaa[A/T]gttacctcttggaaga	A	T	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, p15.31
SNP_A-1902546	tggccttcagaaacac[A/G]ctaaacaaaaattaac	A	G	/// ENST00000356718 // upstream // 55684 // --- // --- // --- // ---	-	q24.21
SNP_A-1885176	tgaattcacatctcaa[C/T]gacagtacaactaaac	C	T	// Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), mRNA. /// NM_016192 // downstream // 23584 // Hs.144513 // TMEFF2	SDPR	SDPR, Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), q32.3
SNP_A-1979651	agtgcaggttgaaagc[A/G]aaggagaagtctccat	A	G	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1976461	ttgttttagctgcatc[C/T]ctgaaatcctcaagaa	C	T	// 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 566140 // Hs.5683 // DHX15 //	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1844064	tagttgcaaagtaaca[A/G]aatgataagaatcctc	A	G	Homo sapiens crystallin, gamma S (CRYGS), mRNA. /// ENST00000307944 // intron // 0 // --- // --- // --- // ---	CRYGS	CRYGS, Homo sapiens crystallin, gamma S (CRYGS), q27.3
SNP_A-1833235	tacactagacgaggga[A/G]tatgcacatcagcttt	A	G	Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /// ENST00000264741 // intron // 0 // --- // --- // --- // ---	ITGA9	ITGA9, Homo sapiens integrin, alpha 9 (ITGA9), p22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872246	tctagaaaacagcata[C/T]actttctcacctcact	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1873074	tctatgtacctttccc[A/C]aactccagaactgtgt	A	C	Homo sapiens zinc finger protein Zip67 (ZIP67), mRNA. /// ENST00000293771 // intron // 0 // --- // --- // --- // ---	ZNF653	ZNF653, Homo sapiens zinc finger protein Zip67 (ZIP67), p13.2
SNP_A-1744319	attttgaaataaaagttcagtcata[C/G]aaaaaaaatggttacatttctagtt	C	G	1350 // cytochrome c oxidase subunit VIIc /// NM_002890 // upstream // 547771 // Hs.758 // RASA1 // 5921 // RAS p21	COX7C	COX7C , rs714267, cytochrome c oxidase subunit VIIc ,q14.3
SNP_A-1810560	gtgcaaagaaaagaga[A/G]cagacaaggatgactc	A	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1464358 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2211706	catctgtttcatgacc[A/G]acattggtgtttgata	A	G	LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 39206 // Hs.307086 //	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-2208428	cccaccccaacccgcc[A/G]aatatgtaacttcatc	A	G	sapiens dystonin (DST), transcript variant 1, mRNA. /// M69225 // intron // 0 // Hs.485616 // DST // 667 // Human	DST	DST, Homo sapiens dystonin (DST), transcript variant 1, p12.1
SNP_A-2176206	caccactgcccttgca[C/T]agagttaactgagttt	C	T	Homo sapiens mRNA for KIAA0456 protein, partial cds. /// ENST00000295713 // intron // 0 // --- // --- // --- // ---	SRGAP2	SRGAP2, Homo sapiens for KIAA0456 protein, partial cds. ,q32.1
SNP_A-2146970	atggaaatactttcaa[C/G]tggaaatatttaaagg	C	G	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA. /// Z26653 // intron // 0 // Hs.200841 // LAMA2 // 3908 // H.sapiens mRNA for laminin	LAMA2	LAMA2, Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), q22.33
SNP_A-2140682	atctctctgttttcac[C/T]ggtgagcttgacaatt	C	T	Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // --- // -	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-2063599	aattacatctgtgaaa[G/T]aaatctctatttgtaa	G	T	4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 //	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2061078	aatgcaaatggaataa[G/T]gaaatggattttcaga	G	T	221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream //	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-2106653	agcctctgtggaatga[A/G]ggcagttgctggaatt	A	G	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA. /// NM_022802 // intron // 0 //	CTBP2	CTBP2, Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, q26.13
SNP_A-2085103	actcagaatctgttct[A/G]aaggcaacctgagatg	A	G	sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), mRNA. /// ENST00000232607 // intron // 0 // --- // ---	UMPS	UMPS, Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), q21.2
SNP_A-2005403	agaggttacaaccagc[C/T]cttcggtcagagactt	C	T	57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitochondrial (GPAM), mRNA. /// NM_058222 // upstream //	GPAM	GPAM, Homo sapiens glycerol-3-phosphate acyltransferase, mitochondrial (GPAM), q25.2
SNP_A-2000920	aataatatttctgaag[A/G]aagagtgttccctaag	A	G	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 543698 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2287820	gattagcatccctata[G/T]gactctttgccttcaa	G	T	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1326212 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2233874	ctcatcttgcactgta[C/G]ctcctgtaattcccac	C	G	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 169294 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2258913	ctttttcctgacttaa[G/T]agtctctcctttgtgt	G	T	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 38036 // --- //	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-2257008	ctttcggatataaacc[C/G]agaagtggaagctgag	C	G	9612 // Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /// NM_005505 // downstream // 21181 //	NCOR2	NCOR2, Homo sapiens nuclear receptor co-repressor 2 (NCOR2), q24.31
SNP_A-2273791	gactggagatttccag[A/G]aagtgaagatgaaaat	A	G	7560 // Human Kox5 mRNA for zinc finger protein, partial. /// ENST00000333201 // downstream // 16955 // --- // --- // --- // ---	ZNF13	ZNF13, Human Kox5 for zinc finger protein, partial. q13.13
SNP_A-2232885	ctcagaactgagtgca[C/T]ctttgcttaagctgtg	C	T	Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- // --- /// ENST00000318007 // intron // 0 // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-2237251	ctctcatggcagttaa[C/G]gttaatttgtgaattt	C	G	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1347803 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2289636	gcaaaaatcttcaatg[A/G]aagttgacttgttcag	A	G	/// ENST00000325796 // downstream // 335608 // --- // --- // ---	-	q22.2
SNP_A-2289762	gcaaaatctgtgttca[G/T]gttgagttaggttatg	G	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2308779	gctttgcacttgtagg[G/T]acatttggatgacaca	G	T	MGC26979 // 91147 // Homo sapiens hypothetical protein MGC26979 (MGC26979), mRNA. /// NM_153704 //	MGC26979	MGC26979, Homo sapiens hypothetical protein MGC26979 (MGC26979), q22.1
SNP_A-1997444	aaatagctaatgaata[C/T]ggtaagatgaaactat	C	T	1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017274	tcacttttaggtccaa[C/T]gtaccttgaattcatt	C	T	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 735739 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2012869	tccttatgattgagac[A/G]gatggaaaggggccat	A	G	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2030678	aaagctgaggaatcaa[C/T]tgggggattttgaatt	C	T	130576 // Homo sapiens hypothetical protein LOC130576 (LOC130576), mRNA. /// ENST00000280115 // intron // 0 // ---	LOC130576	LOC130576, Homo sapiens hypothetical protein LOC130576 (LOC130576), q23.2
SNP_A-2038062	aacacacagagttaca[G/T]ggagtcttaggagagc	G	T	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 465726 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2078900	acccaaggaagatgca[C/G]gttctagtaatttttc	C	G	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 528027 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2096870	agactccacacccggc[A/G]actggatggcagacag	A	G	Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), transcript variant 1, mRNA. /// NM_015558 // intron // 0 // Hs.154429 // SS18L1 // 26039 //	SS18L1	SS18L1, Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), transcript variant 1, q13.33
SNP_A-2094971	agaatgctggagtgaa[A/G]cctctactaatccctg	A	G	6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// AB023173 // upstream // 305840 //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2094919	agaatgatactgagaa[G/T]agcaatataaagtaga	G	T	// 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 131028 //	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-2143563	atgactgcatcagcca[C/G]cttttgaatacattga	C	G	// 1962 // Homo sapiens enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (EHHADH),	EHHADH	EHHADH, Homo sapiens enoyl-Coenzyme A, hydratase q27.2
SNP_A-2145935	atgccctgatcatttg[C/T]aggctctgcccattct	C	T	Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// ENST00000355128 // intron // 0 // --- // --- // --- // ---	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-2131935	ataggaggacagaatc[A/C]actatggcatttaaac	A	C	10888 // Homo sapiens G protein-coupled receptor 83 (GPR83), mRNA. /// NM_005590 // downstream // 3260 //	GPR83	GPR83, Homo sapiens G protein-coupled receptor 83 (GPR83), q21
SNP_A-2169116	caagatcaattataaa[A/G]ctacattcctacttcc	A	G	65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 1011046 // Hs.42650 //	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2192599	catccaggcccatgtc[A/G]ctgccaaactagcccc	A	G	Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // intron // 0 // --- // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-2192932	catccttgaggtgctc[A/G]cttcaatatgtcaaat	A	G	// 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// ENST00000334034 // upstream //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-1814381	gtgtgagaatgtgggc[G/T]ctatttaacttgggcc	G	T	5480 // Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), mRNA. /// AF272898 // upstream // 20804 //	PPIC	PPIC, Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), q23.2
SNP_A-1788647	gggatgaggatgccta[C/T]gatgttctgatgcagt	C	T	// 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 643075 // Hs.478682 // C3orf6 // 152137 //	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-1744147	gaaaccaagattgagcttagtataa[A/T]taacataggtatataaggaaagttg	A	T	NM_153203 // upstream // 356141 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf74	C21orf74 , rs2827003, chromosome 21 open reading frame 74,q21.1
SNP_A-1860927	tcatactcaatccaag[A/G]aagcattttctctaga	A	G	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-1976917	gggaagacagtggaaa[C/G]accctcttagatttca	C	G	7345 // Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA. /// ENST00000284440 // downstream // 51590 // --- // --- // --- // ---	UCHL1	UCHL1, Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), p13
SNP_A-1981054	atcatgcattttatga[C/T]gttgccttgatttac	C	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream //	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1981136	tctcaggtgctggcaa[C/T]gggccctggcctgccc	C	T	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1984869	tatgatgccaaataaa[G/T]ttgactgatgctttcc	G	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 558787 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1976108	ggatattgtgagaaaa[A/T]gaaatagcctaacaaa	A	T	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 278052 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1899836	tggaatttgacccaac[C/T]aagagaaggaagcaac	C	T	Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // intron // 0 // Hs.47288 // TRPM3 // 80036 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1894703	tgccagcagatgctaa[C/T]gtcttctaacctcctt	C	T	Homo sapiens lipoma HMGIC fusion partner-like 2 (LHFPL2), mRNA. /// ENST00000274345 // intron // 0 // --- // --- // --- // ---	LHFPL2	LHFPL2, Homo sapiens lipoma HMGIC fusion partner-like 2 (LHFPL2), q14.1
SNP_A-1895280	tgccctcacctggaac[A/G]cattactgaggccctt	A	G	197320 // Homo sapiens hypothetical protein FLJ31875 (FLJ31875), mRNA. /// ENST00000333222 // upstream //	FLJ31875	FLJ31875, Homo sapiens hypothetical protein FLJ31875 (FLJ31875), q24.3
SNP_A-1893626	tgcaggtgaaagatta[A/C]agcacttgagcgaagc	A	C	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1912800	tgtgctgattagagct[C/T]accaaaggacccaggg	C	T	// Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // --- // --- // --- // ---	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-1922174	ttacttcacttggcac[A/G]gcagtgaacatgaacc	A	G	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 553125 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1925277	ttatccttggaaatca[C/T]tatttttcctgcattc	C	T	118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 554264 // Hs.523446 // COL11A1 // 1301 //	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds. p21.1
SNP_A-1924411	ttataatacagagtga[A/G]tatctttttctatgcc	A	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000273432 // intron // 0 // --- // --- // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1902711	tggctagaaaaaaaca[A/T]atgtagaagtctcagg	A	T	FLJ42393 // 401105 // Homo sapiens FLJ42393 protein (FLJ42393), mRNA. /// NM_005578 // upstream // 75098 //	FLJ42393	FLJ42393, Homo sapiens FLJ42393 protein (FLJ42393), q28
SNP_A-1901680	tggcaataaagtccca[C/T]ccataaaatcatgaga	C	T	NM_000197 // downstream // 45167 // Hs.477 // HSD17B3 // 3293 // Homo sapiens hydroxysteroid (17-beta)	-	q22.32
SNP_A-1973540	gaattgtttcttttgg[A/C]atttaaatgcatccct	A	C	Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // intron // 0 // Hs.123642 // EPHA3 // 2042 //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1963680	tggatgctgcacatac[A/T]gagggttcgcatcaca	A	T	25927 // Homo sapiens chromosome 2 open reading frame 32 (C2orf32), mRNA. /// NM_002664 // upstream // 4433 //	C2orf32	C2orf32, Homo sapiens chromosome 2 open reading frame 32 (C2orf32), p14
SNP_A-1985080	gcgacaggacctaaac[C/T]gaacctctgctttttc	C	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 73812 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1984250	actaaattgaaaacaa[A/T]acacttatgccacgtt	A	T	sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- // --- ///	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1988886	tctgacatcagcttta[A/T]aattcattccgtcaac	A	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1943749	ttgtagacacaccttg[A/C]aagtattccaaatgta	A	C	Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // intron // 0 // --- // -	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1861002	tcatagatgaatgaaa[A/G]ggtttctgccaacact	A	G	// 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 54721 //	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1866718	tcccctgctgcaagat[A/G]accatttgtgaactta	A	G	146857 // Homo sapiens hypothetical protein FLJ31952 (FLJ31952), mRNA. /// ENST00000360502 // upstream //	FLJ31952	FLJ31952, Homo sapiens hypothetical protein FLJ31952 (FLJ31952), q12
SNP_A-1835829	tacggttctgttggac[C/T]acaccacttttcctgtt	C	T	9421 // Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA. /// NM_015315 // upstream //	HAND1	HAND1, Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), q33.2
SNP_A-1844277	tagttttccatctgca[C/G]tgacagcataatgcac	C	G	Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-1821330	gtttgcctctaacaaa[C/T]tgtcatatttacactc	C	T	// 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1781900	ggcaaaaatgaacaca[C/T]ggtactggatgaaatt	C	T	KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 54356 //	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1781661	ggattggatttaaaca[A/G]gttggattcatattat	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 106581 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1791532	gggtcaatccactgta[C/G]ctattattctttccaa	C	G	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-1790006	ggggaaaaaatggtaa[A/T]ctcattgccagcttag	A	T	sapiens KIAA0032 mRNA, partial cds. /// ENST00000264345 // intron // 0 // --- // --- // --- // ---	HERC3	HERC3, Homo sapiens KIAA0032 partial cds. q22.1
SNP_A-2192555	catccaccagcaagaa[C/G]ctctcacatggcatca	C	G	121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2206371	ccatcgagttgttagg[A/G]agtaggtgggtgtcac	A	G	Homo sapiens TBC1 domain family, member 7 (TBC1D7), mRNA. /// ENST00000343141 // intron // 0 // --- // --- // --- // ---	TBC1D7	TBC1D7, Homo sapiens TBC1 domain family, member 7 (TBC1D7), p24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2047943	aagcaaattggaaaga[C/T]acaaaagatggcctct	C	T	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3,	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-2067609	acaaattttgaactac[A/G]aatcgccatctgctca	A	G	53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-2031991	aaagtcttcatccata[A/C]gtctaatgcctgggct	A	C	// 23186 // Homo sapiens REST corepressor 1 (RCOR1), mRNA. /// NM_145726 // upstream // 7109 // Hs.510528 //	RCOR1	RCOR1, Homo sapiens REST corepressor 1 (RCOR1), q32.32
SNP_A-2012866	gaggagtaacacagga[C/T]attcaaaataaaacta	C	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2237674	ctctctgatctcacgt[A/G]aattcaattaggaaag	A	G	153201 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 2 (SLC36A2),	SLC36A2	SLC36A2, Homo sapiens solute carrier family 36 (proton q33.1
SNP_A-2244621	ctggagctccaaacaa[C/T]tgccttagttcagatg	C	T	ENST00000217260 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-2235257	ctccctaaaactactg[A/G]actttagtgctggctt	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2239975	ctgaagaacatggatt[A/G]aaatgagcaaatttat	A	G	Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2264465	gaagaaagtagcatga[C/G]tacacagtaggtatca	C	G	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2269861	gacaataagcctatga[A/G]gtgatcgtagggcgtt	A	G	sapiens adducin 1 (alpha) (ADD1), transcript variant 1, mRNA. /// NM_014190 // intron // 0 // Hs.183706 // ADD1 //	ADD1	ADD1, Homo sapiens adducin 1 (alpha) (ADD1), transcript variant 1, p16.3
SNP_A-2270406	catttattctgtgaaa[C/T]ggcctgaaatagctgg	C	T	84529 // Homo sapiens hypothetical protein HH114 (HH114), mRNA. /// ENST00000267752 // downstream // 3292 // --- // ---	HH114	HH114, Homo sapiens hypothetical protein HH114 (HH114), q14
SNP_A-2290054	gcaaagttctgagatc[A/G]ctcactgtgtaggatc	A	G	sapiens P450 (cytochrome) oxidoreductase (POR), mRNA. /// ENST00000265302 // intron // 0 // --- // --- // --- // ---	POR	POR, Homo sapiens P450 (cytochrome) oxidoreductase (POR), q11.23
SNP_A-1995442	tgtcattatcaagagc[C/T]agaaacatttcagctt	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 73801 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2030486	aaagcctaaagcagaa[C/G]agtgaataagtccagg	C	G	// Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// ENST00000274458 // intron // 0 // --- // --- // --- // ---	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-2023841	aaaagaaataggtagc[A/G]ctgattataataatat	A	G	Homo sapiens vav 2 oncogene (VAV2), mRNA. /// S76992 // intron // 0 // Hs.369921 // VAV2 // 7410 // VAV2=VAV	VAV2	VAV2, Homo sapiens vav 2 oncogene (VAV2), q34.2
SNP_A-2068145	acaagaattcaacttc[C/T]gaaagggagaaagaat	C	T	Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000359764 // intron // 0 // --- // --- // --- // ---	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2050201	aaggactgccaagctt[C/T]aagcaggattttgtgt	C	T	sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- // --- // --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-2106195	agcccccagatcacta[C/T]aagctaaagggaggag	C	T	Homo sapiens galactose-3-O-sulfotransferase 2 (GAL3ST2), mRNA. /// ENST00000192314 // intron // 0 // --- // --- // --- // ---	GAL3ST2	GAL3ST2, Homo sapiens galactose-3-O-sulfotransferase 2 (GAL3ST2), q37.3
SNP_A-2086424	actcttgccagaaaag[A/G]caactcaaatgatctt	A	G	983 // Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 2, mRNA. /// NM_001786 //	CDC2	CDC2, Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 2, q21.2
SNP_A-2090320	acttgctggcatgtga[C/T]aaaatattgcttattg	C	T	Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// ENST00000332896 // intron // 0 // --- // --- // --- // --- /// ENST00000306632 // intron	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-2214274	cctacagccttcatta[A/G]atttggcttcattctt	A	G	// --- /// ENST00000355517 // downstream // 125458 // --- // ---	-	q24.32
SNP_A-2192483	catcatttctagtata[C/T]gctgctgtcattgtaa	C	T	/// ENST00000310012 // upstream // 111877 // --- // --- // --- // ---	-	q12
SNP_A-2192644	catccatggttcagta[A/G]ccgagtctgtggtggg	A	G	// Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// ENST00000360220 // intron // 0 // --- // --- // --- // ---	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2176145	caccaccaaaaacttа[A/G]ggaaagtgacactctt	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2111139	aggagagcttcaatca[C/G]taggaagctggggcag	C	G	ENST00000307717 // intron // 0 // --- // --- // --- // ---	-	q23.31
SNP_A-2146610	gaagagtcacaagtgc[C/T]atgctgggctcagtag	C	T	// 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 1581299 // Hs.391781 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-2160859	atttctctctttgctg[A/C]aattaaacaaagtgga	A	C	221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream //	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-1804473	gtcagacccagtcaca[A/G]tgagggatttcaaaca	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-1807178	gtctctaaagagctta[C/T]actctaattgggacac	C	T	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 // upstream // 60929 // Hs.20805 // TSAP6 // 55240 // Homo	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784801	ggcctgtagagaagga[C/T]gcagatggctttgctg	C	T	4953 // Homo sapiens ornithine decarboxylase 1 (ODC1), mRNA. /// NM_024894 // downstream // 40082 // Hs.222494	ODC1	ODC1, Homo sapiens ornithine decarboxylase 1 (ODC1), p25.1
SNP_A-1841163	tagctttctagaggat[A/G]agagacaatatgaagt	A	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1093932 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1838701	tagacataattctcaa[C/G]cctaatttattccatt	C	G	7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1862620	tcattataacgtgttc[A/G]caaaagagtaactgaa	A	G	// 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 151006 //	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-1948478	tttagtgaaatatgaa[C/T]cctgaacaatgacatt	C	T	388121 // Homo sapiens FLJ41287 protein (FLJ41287), mRNA. /// NM_031226 // downstream // 133435 // Hs.511367	FLJ41287	FLJ41287, Homo sapiens FLJ41287 protein (FLJ41287), q21.2
SNP_A-1961535	ttttttgctcaggca[A/C]accctcacacaggctt	A	C	BPESC1 // 60467 // Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1 (BPESC1), mRNA. /// NM_020191 // upstream // 4058 // Hs.14074 //	BPESC1	BPESC1, Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1 (BPESC1), q23
SNP_A-1925082	ttatcagataactcgc[C/T]agtccttgttctaagt	C	T	Homo sapiens PHD finger protein 10 (PHF10), transcript variant 1, mRNA. /// NM_133325 // intron // 0 // Hs.435933 //	PHF10	PHF10, Homo sapiens PHD finger protein 10 (PHF10), transcript variant 1, q27
SNP_A-1904235	tgggctaacagggtac[G/T]gaatctggtatccact	G	T	ENST00000339762 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1890285	tgatcatggaaaaaaa[A/C]cactaattccactacc	A	C	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 479858 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-1877827	tctggtatcctagtgg[A/G]aacccataattcttct	A	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 622081 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1981624	tcatatatgtgtaatc[C/T]agaatgtttttgtgac	C	T	// 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 30698 //	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-1963278	atggatacatttgcaa[A/G]tacaggttaatatttt	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 880103 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1861591	tcatcggtgatcatga[C/T]aggaagaggaacagag	C	T	// 339967 // Homo sapiens hypothetical protein LOC339967 (LOC339967), mRNA. /// ENST00000334830 // upstream //	LOC339967	LOC339967, Homo sapiens hypothetical protein LOC339967 (LOC339967), q13.2
SNP_A-1868920	tcctgagattgctgaa[A/G]ctgccttaaaatcttt	A	G	/// ENST00000354350 // upstream // 121623 // --- // --- // --- // --- /// ENST00000355158 // upstream // 121623 // --- // --- // ---	-	q22.33
SNP_A-1869765	tccttcatccacctaa[C/T]ctggagtctctgatgc	C	T	Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // --- // --- // --- // --- ///	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-1847733	tatctatgacctggaa[A/G]ctctccttcactccct	A	G	ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // downstream // 465704 // Hs.126838	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.2
SNP_A-1838432	tagaatatatcaaata[C/G]ctcaaagttctagaat	C	G	23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // upstream // 706470 // --- // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-1829261	taagtagccacctaga[C/G]ctcctcccgttcacac	C	G	Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /// ENST00000253688 //	SH3BP5	SH3BP5, Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), p25.1
SNP_A-1823149	aaatatgcatcaggaa[A/C]tctagcgtctcagtaa	A	C	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 348995 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-1814717	gtgtgtaaaacagtcc[C/T]aacagcatacaagatg	C	T	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1704452 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1797742	ggtttggtcttgaaca[A/G]gaaaagacacacctct	A	G	// 10625 // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA. /// NM_031935 // upstream // 202906 // Hs.58877 // FIBL-6 //	IVNS1ABP	IVNS1ABP, Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, q25.3
SNP_A-2162122	attttaataagctgga[A/C]ccaatataatttggaa	A	C	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 475318 // Hs.435730 //	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2148651	atggtatcctcaaata[C/T]cgtcaaaatgcttaac	C	T	transforming growth factor-beta 1 binding protein mRNA, complete cds. /// NM_000627 // intron // 0 // Hs.49787 //	LTBP1	LTBP1, Human transforming growth factor-beta 1 binding protein complete cds. ,p22.3
SNP_A-2148437	atgggtaaggctttca[A/G]catcctagctctacag	A	G	SLC39A12 // 221074 // Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), mRNA. /// NM_201593 // upstream // 15446 // Hs.59093 // CACNB2 //	SLC39A12	SLC39A12, Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), p12.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2139460	atccttcgaagatgta[C/T]ataataacttgtatgc	C	T	Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// ENST00000260021 // CDS // 0 // --- // --- // --- // --- ///	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2109154	agcttgatgtacttta[A/T]cacatattatcttttt	A	T	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000340635 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-2134372	atatggaaaatggtca[A/T]acaagtcaagatctac	A	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1294429 // --- // -	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2176179	caccacgcccagccta[C/T]gttttggttgtcttaa	C	T	201931 // Homo sapiens hypothetical protein FLJ38482 (FLJ38482), mRNA. /// NM_007246 // upstream // 43662 //	FLJ38482	FLJ38482, Homo sapiens hypothetical protein FLJ38482 (FLJ38482), q32.3
SNP_A-2175488	cacatcgtaggtgaca[C/T]catttttggatggag	C	T	Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2182764	cagatgctgctgttaa[C/T]acatggaacacactct	C	T	// 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 512378 // Hs.444075 // STS-1 //	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-2168405	caacttcatgcaagga[A/G]tcctgctgagaaattc	A	G	6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 101991 // Hs.528304 // ADAM28 //	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-2054301	aagttggcactggtaa[C/T]ggtatggagcccccac	C	T	79097 // Homo sapiens tripartite motif-containing 48 (TRIM48), mRNA. /// NM_001005274 // upstream // 63390 // -	TRIM48	TRIM48, Homo sapiens tripartite motif-containing 48 (TRIM48), q11
SNP_A-2025124	aaaatactgacaaaga[A/G]atccatctggattatt	A	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2030229	aaagcactactttgga[A/G]cagtctaacagacact	A	G	ENST00000202677 // intron // 0 // --- // --- // --- // ---	-	p11.23
SNP_A-2027008	aaacagactaatacag[A/G]agctgaagtctaaagc	A	G	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 235163 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2036020	aaattaatctcctaca[A/T]gtgctactataattaa	A	T	92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 578856 // ---	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2045455	aagaatcagagaaaac[C/T]attcatggatgatatt	C	T	-- /// ENST00000331540 // downstream // 587436 // --- // --- //	-	p25.3
SNP_A-1992119	tcattcacaacttaac[C/T]acaactgatcaaaaaa	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 16842 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.1
SNP_A-2005105	ctgaatccatctataa[C/T]ctgtaaacccctgctt	C	T	3768 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 12 (KCNJ12), mRNA. /// ENST00000331718 // downstream // 84321 // --- // --- // --- // --	KCNJ12	KCNJ12, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 12 (KCNJ12), p11.2
SNP_A-2007741	tctagtcaggctagac[A/G]acactgctgtcaacaa	A	G	3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 137530 // Hs.118695 // KCNG1	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2293127	gcagacgtaaaataca[C/G]cctcttgaaaaaatag	C	G	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // ---	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-2301771	gcggaatcccagcgag[C/G]aagagctgagtgcagc	C	G	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-2255414	cttgtcatgccaataa[A/G]gttattgcgactaaat	A	G	5727 // Homo sapiens patched homolog (Drosophila) (PTCH), mRNA. /// ENST00000331920 // upstream // 213017	PTCH	PTCH, Homo sapiens patched homolog (Drosophila) (PTCH), q22.32
SNP_A-2256083	ctttacatgaagagta[A/G]caccatttaaatgcat	A	G	Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000304058 // intron // 0 // --- // --- // --- // ---	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2236179	ctccttcttccgttta[A/G]cttgtccatcaccatc	A	G	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2281896	gagtgcagattaacaa[C/T]gtggggtgttgcctag	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 115307	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2010836	ttggacaaaagggata[C/T]gattgtgtctcttctg	C	T	Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, mRNA. /// NM_182799 // intron // 0 //	FLJ39155	FLJ39155, Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, p13.2
SNP_A-2013648	agattagaaggaaata[C/T]caataaagccaaagtt	C	T	85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 227719 // Hs.377155 // LYRIC //	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-2015182	ggtggtcagaacaacc[C/T]catcctgttggctttg	C	T	LOC375108 // 375108 // Homo sapiens membrane-associated phospholipase A1 beta (LOC375108), mRNA. /// ENST00000332705 // downstream // 70384 // --- // --- // --- // --	LOC375108	LOC375108, Homo sapiens membrane-associated phospholipase A1 beta (LOC375108), q11.2
SNP_A-1990759	tagccaaaaattatca[C/T]gtaaggactgtcaaat	C	T	Homo sapiens opsin 3 (encephalopsin, panopsin) (OPN3), mRNA. /// ENST00000063380 // intron // 0 // --- // --- // --- // ---	OPN3	OPN3, Homo sapiens opsin 3 (encephalopsin, panopsin) (OPN3), q43
SNP_A-2039522	aacatccctatatgta[A/C]actttgatcttctact	A	C	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// NM_024767 // intron // 0 // Hs.134296 //	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2025627	aaaatgacaatttagc[G/T]caaagaaattagtttg	G	T	ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // downstream // 285061 // Hs.126838	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.1
SNP_A-2055061	aataaattgtagttta[C/T]gtatttgcaatcattt	C	T	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1457929 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2069939	acacaggcactgccca[A/G]tacatagccactagct	A	G	// 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// NM_030796 // downstream // 24705 // Hs.488307 //	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2064434	aattccactatccaga[C/G]aatctagattagttta	C	G	Homo sapiens asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase) (ALG1), mRNA. /// ENST00000262374 // intron // 0 // --- // --- // --- // ---	ALG1	ALG1, Homo sapiens asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase) (ALG1), p13.3
SNP_A-2107121	agcggctgctgctcag[A/G]cccagcggaggaccgg	A	G	Homo sapiens synaptojanin 2 (SYNJ2), mRNA. /// ENST00000241842 // intron // 0 // --- // --- // --- // ---	SYNJ2	SYNJ2, Homo sapiens synaptojanin 2 (SYNJ2), q25.3
SNP_A-2172751	caatttcacagatatt[A/G]aaagatcttgttgatg	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 613884 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2217926	cctgcagccgatgttc[A/G]ctactgtccaggggcc	A	G	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 181702 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2128387	ataagttatgacaaca[C/T]atacaaagtgatatcc	C	T	// 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 329831 // Hs.478682 // C3orf6 // 152137 //	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2161177	atttgaccaattgttc[A/G]accccaagaggtcaaa	A	G	// 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000329561 // upstream //	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-1798626	gtaacacagcctccaa[A/C]aacacatcgcaaactt	A	C	ENST00000301765 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-1805250	gtcattgggaatgata[A/G]taagtaggatcattcc	A	G	57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 38795 //	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1678158	cataccatgccctgaactcagttga[A/G]ccattcagataatcgtctcaattca	A	G	2295 // forkhead box F2 /// NM_033260 // downstream // 3730 // Hs.297452 // FOXQ1 // 94234 // forkhead box Q1	FOXF2	FOXF2 , rs951318, forkhead box F2 ,p25.3
SNP_A-1844240	tagtttgctgaccctc[A/G]actaaaggaagctatt	A	G	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1973321	ctgaagcaacctcaca[A/G]tcttcagatttcagcc	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 938171 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1949983	tttcaattaatttaaa[A/C]ctggattctgtctctg	A	C	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 275770 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-1940139	ttgcataacagcaaaa[A/G]ctacttttccactaaa	A	G	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // --- //	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-1909674	tgtcaagatcatcaac[C/T]gcaatttataaaggag	C	T	// Homo sapiens hypothetical protein FLJ31153 (FLJ31153), mRNA. /// ENST00000255759 // intron // 0 // --- // --- // --- // ---	FLJ31153	FLJ31153, Homo sapiens hypothetical protein FLJ31153 (FLJ31153), p13.11
SNP_A-1921918	ttactcctctcatgta[A/G]gaaggtgacctaagat	A	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1875197	tctctctaaataaaac[A/G]gccctcaaccactcac	A	G	11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 312809 //	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1892816	gcttattccagtctct[C/G]aaggggaacacagaca	C	G	Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // --- // --- // --- // ---	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1901373	tggattaatagattaa[G/T]gagttatcaggggagg	G	T	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 70100 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1898807	tgctttgcactaatga[A/G]gggttacatgatgacc	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1174234 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1949561	tttatttagatttcaa[C/G]caatactgatggatgc	C	G	// 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 45832 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-1976573	ttcctctattgatgcc[C/T]acaaatgagagtgata	C	T	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3132110 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1978721	aatgaagtgtgaatga[C/G]aatagcacagagatgt	C	G	4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1834385	tacattgctcctatac[A/G]acatgatttaggttaa	A	G	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q11.23
SNP_A-1864326	tccactatatgcataa[C/T]ctactgttaaagattt	C	T	// 64332 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, /// NM_175056 // upstream // 207677 // Hs.352213 // LOC131	NFKBIZ	NFKBIZ, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, q12.3
SNP_A-1783667	ggcattagcaattgca[C/T]tgaaacacattgccca	C	T	652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // downstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-1801367	gtaggagtcttcagaa[A/G]tgaaaataaacaaatc	A	G	H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosarninyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 26703 // Hs.112930 // FLJ35821 // 1	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1785335	ggctataaatgctaca[A/G]gaaagcaaatcaaagt	A	G	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 282903 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2161104	atttgaaagcaggttc[A/T]atagcaacaaatgctt	A	T	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SMARCA2	SMARCA2, Homo sapiens SWI p24.3
SNP_A-2113775	aggctgcagcccattc[A/G]caggcacccgaaagaa	A	G	Homo sapiens sulfatase 1 (SULF1), mRNA. /// ENST00000260128 // 3UTR // 0 // --- // --- // --- // --- ///	SULF1	SULF1, Homo sapiens sulfatase 1 (SULF1), q13.3
SNP_A-2218165	cctgcgccttgaagga[C/T]ggagaggatgtggacc	C	T	Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000324333 // intron // 0 // --- // --- // --- // --- ///	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2223661	cggatacacccgtcct[C/T]aaacttgggtgcgcag	C	T	54436 // Homo sapiens SH3 domain and tetratricopeptide repeats 1 (SH3TC1), mRNA. /// ENST00000318896 //	SH3TC1	SH3TC1, Homo sapiens SH3 domain and tetratricopeptide repeats 1 (SH3TC1), p16.1
SNP_A-2213132	ccgagttgtggaccta[A/C]aagcaattattttctc	A	C	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 72003 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2174043	cacaccagaactaaca[C/T]agccaattatgcaaat	C	T	5784 // Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// NM_016343 // downstream // 406626 // Hs.497741 // CENPF // 1063 //	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41
SNP_A-2196628	cattaacatcgaaggc[C/T]cagagggtaaattcaa	C	T	Homo sapiens hypothetical protein MGC5395 (MGC5395), mRNA. /// M80902 // intron // 0 // Hs.502756 // AHNAK // 195	MGC5395	MGC5395, Homo sapiens hypothetical protein MGC5395 (MGC5395), q12.3
SNP_A-2099280	agaggcagaggtctga[C/T]acttccgatttggggt	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2033077	aaatacagaggaaaaa[A/T]atagaggaattgggag	A	T	sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 //	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26
SNP_A-2045940	aagaccatgtctttca[A/G]attagctagaaaaata	A	G	8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 733307 // Hs.370359	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2008456	cacctgaaggagatga[C/G]ctcacgttacatccat	C	G	// 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 289818 // Hs.154329 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2237820	ctctgaaatctccccg[G/T]aagccaaaactttctg	G	T	9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 495387 // --- // --- // ---	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds. ,q23
SNP_A-2229871	ctagttccatacctttt[A/C]aaagaaatcactctag	A	C	/// ENST00000354860 // upstream // 1010953 // --- // --- // --- //	-	q32.3
SNP_A-2255250	cttggttctagcttaa[C/G]tctgctcctaactagt	C	G	Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA. /// ENST00000237289 // intron // 0 // --- //	TNFAIP3	TNFAIP3, Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), q23.3
SNP_A-2281429	gagtcagacttaaaat[G/T]aacatagtatgtatta	G	T	Homo sapiens HARL2754 (UNQ2754), mRNA. /// ENST00000334706 // intron // 0 // --- // --- // --- // ---	XRG5a	XRG5a, Homo sapiens HARL2754 (UNQ2754), p23.1
SNP_A-2276584	gagaggtgacctctac[C/T]ggtaacagagtattca	C	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2309137	ggaaaaaactcagttc[C/G]aggcaacaagaacacc	C	G	Homo sapiens chromodomain protein, Y-like 2 (CDYL2), mRNA. /// ENST00000299564 // intron // 0 // --- // --- // --- // ---	CDYL2	CDYL2, Homo sapiens chromodomain protein, Y-like 2 (CDYL2), q23.2
SNP_A-2000133	aaacacagaagagtct[C/T]aataatttgtgagata	C	T	Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA. /// ENST00000260524 // intron // 0 // --- // --- // --- // ---	GIPC2	GIPC2, Homo sapiens PDZ domain protein GIPC2 (GIPC2), p31.1
SNP_A-2046271	aagagaaagaaaagga[C/G]tagcaaaatatacaga	C	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2021596	aaaaaatgcatattag[G/T]aatttctcaagtaatt	G	T	84830 // Homo sapiens chromosome 6 open reading frame 105 (C6orf105), mRNA. /// NM_002114 // upstream // 141846	C6orf105	C6orf105, Homo sapiens chromosome 6 open reading frame 105 (C6orf105), p24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098445	agagcaaggaacttga[A/C]gtgaaagacctgaaga	A	C	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 233183 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2085088	actcagaaaagttaaa[A/C]tgcctctattaaaagt	A	C	cell receptor rearranged alpha-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000339800 // downstream // 90622	-	-, Human T-cell receptor rearranged alpha-chain V-region (V-D-J) complete cds. ,q11.2
SNP_A-2195189	catggagtcctcaaca[A/G]tgtactagaaaacaga	A	G	Homo sapiens myosin VI (MYO6), mRNA. /// ENST00000357181 // intron // 0 // --- // --- // --- // --- ///	MYO6	MYO6, Homo sapiens myosin VI (MYO6), q14.1
SNP_A-2184723	cagctgaagataaagg[C/T]caggtcatttaaaaag	C	T	// 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 47118 // --- // --- // --- // ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2129093	ataattcataagctta[A/G]actgagatgtaattaa	A	G	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 259969 // Hs.437966 // PXMP3 //	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2163818	caaaacaccagctgaa[C/T]gtaagataaagaaaca	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 635232 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1786139	ggctggcctcagagca[A/G]agacagtgttcagaac	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1805458	gtccacgtaaagctga[C/T]gcttgtccaaagttcc	C	T	-- /// ENST00000314058 // upstream // 27916 // --- // --- // --- // ---	-	p13.2
SNP_A-1744039	aacatataggtcttgatcttctcat[C/T]agtaaatctgaggcttatgttctac	C	T	NM_001175 // intron // 0 // Hs.292738 // ARHGDIB // 397 // Rho GDP dissociation inhibitor (GDI) beta	ARHGDIB	ARHGDIB , rs10492146, Rho GDP dissociation inhibitor (GDI) beta,p12.3
SNP_A-1642901	aaaaggtaatttaaaa[A/G]tatgtatcaaaatccc	A	G	// synuclein, alpha (non A4 component of amyloid precursor) /// NM_007308 // upstream // 8449 // Hs.76930 // SNCA //	SNCA	SNCA , rs1372522, synuclein, alpha (non A4 component of amyloid precursor) ,q22.1
SNP_A-1848016	tatctggtactgcttt[A/G]aaaataagtagaattg	A	G	/// ENST00000330770 // downstream // 442866 // --- // --- // ---	-	q31.3
SNP_A-1858765	tcagatgttgtacagt[A/G]aagaacagcgactctt	A	G	114821 // Homo sapiens zinc finger protein 452 (ZNF452), mRNA. /// ENST00000357581 // upstream // 87442 // --- // ---	ZNF452	ZNF452, Homo sapiens zinc finger protein 452 (ZNF452), p22.1
SNP_A-1815400	gtgtttggaaatcaca[C/T]gaacataaaaaaagta	C	T	// 6160 // Homo sapiens ribosomal protein L31 (RPL31), mRNA. /// NM_017546 // upstream // 25363 // Hs.30819 //	RPL31	RPL31, Homo sapiens ribosomal protein L31 (RPL31), q11.2
SNP_A-1816572	gttagtggcttcaaca[C/T]ctgggccccaagccac	C	T	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- ///	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-1986259	aggagagagatgcaag[C/T]agaattacggaagact	C	T	346007 // Homo sapiens EGF-like-domain, multiple 11 (EGFL11), mRNA. /// ENST00000342421 // upstream //	EGFL11	EGFL11, Homo sapiens EGF-like-domain, multiple 11 (EGFL11), q12
SNP_A-1949323	tttattacattgtaaa[A/G]atatcaaagtcttgtc	A	G	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	SMARCB1	SMARCB1, Homo sapiens SWI,q11.23
SNP_A-1961917	acagtactagcactcc[A/G]ctatgaccaaagtttt	A	G	6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 182998 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1936046	ttcttaggaggctcat[G/T]atagtctttagttaca	G	T	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-1902656	tggctaacccttttcta[C/T]ggtcctctgagggtgt	C	T	Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans /// NM_002071 // intron // 0 // Hs.136295 // GNAL // 2774 // Homo sap	GNAL	GNAL, Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans ,p11.21
SNP_A-1894619	tgccactgaacttcac[A/G]cttacaaatggttacg	A	G	sapiens low density lipoprotein receptor-related protein 5 (LRP5), mRNA. /// ENST00000294304 // intron // 0 // --- // ---	LRP5	LRP5, Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), q13.2
SNP_A-1918090	ttaaacattcatatac[C/T]acacgaaaaaatgact	C	T	5203 // Homo sapiens prefoldin 4 (PFDN4), mRNA. /// NM_177959 // upstream // 187580 // Hs.473133 // DOK5 //	PFDN4	PFDN4, Homo sapiens prefoldin 4 (PFDN4), q13.2
SNP_A-1931458	ttcccatttaatgccc[C/G]aactaactcatttctc	C	G	DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 20552 // --- // --- // --- // ---	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-1894715	tgccagccccaaacaa[C/T]cagtggtcaactttct	C	T	Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, mRNA. /// NM_176787 // intron // 0 // Hs.157031 // PIGN // 23556 // Homo sapiens	PIGN	PIGN, Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, q21.33
SNP_A-1951303	tttccctctttgtaaa[C/T]tggaaaataatgtgac	C	T	ENST00000228705 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-1819142	gttgctcaaatgtcca[A/C]tactgctttgtcacaa	A	C	Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // upstream // 86106 // Hs.10862 // AK3L2 //	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826342	taaatttccttctgcc[A/C]agttctttctgtacct	A	C	51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream //	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-1849742	tatgtaaagtggctaa[C/T]gtagtaaagtacatga	C	T	79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream //	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-1865414	tccatctcaaaacaaa[G/T]ccgtcttatgttttat	G	T	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1862487	tcatgttgggttgtca[A/G]taatcctaattctttt	A	G	// --- /// ENST00000354793 // downstream // 85915 // --- // ---	-	p13.3
SNP_A-1740679	ccatatggtacctttgtgtagatta[G/T]aaaaagatgccctgtccactgggtg	G	T	NM_152697 // downstream // 207691 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032 , rs3856036, hypothetical protein MGC34032,p31.1
SNP_A-1758661	tgcagttctagagctatgctttcat[A/G]agaaaatttttaaaaaaatgtttag	A	G	PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_015230 // downstream // 3667134 // Hs.427719 //	PCDH7	PCDH7 , rs733046, BH-protocadherin (brain-heart) ,p15.1
SNP_A-1800095	gtaccacagaaacaaa[C/T]ttaatccatgttgtag	C	T	590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 452499 // --- // --- // --- //	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1799700	gtaattttgctggaaa[A/G]atcaaaacacaaagat	A	G	// 3741 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), mRNA. /// NM_207433 // downstream // 171618 // Hs.525253 // --- // 0 //	KCNA5	KCNA5, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), p13.32
SNP_A-2139856	atctaaggaagtacca[A/C]taatgacctcagatta	A	C	8644 // Homo sapiens aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3), mRNA. /// NM_001818 // upstream // 71299 //	AKR1C3	AKR1C3, Homo sapiens aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3), p15.1
SNP_A-2147014	atggaacggcgaccac[A/C]attcattgctgagtgc	A	C	sapiens bone morphogenetic protein 1 (BMP1), transcript variant BMP1-2, mRNA. /// NM_006130 // intron // 0 // Hs.1274 // BMP1 // 649 // Homo sapiens bone	BMP1	BMP1, Homo sapiens bone morphogenetic protein 1 (BMP1), transcript variant BMP1-2, p21.3
SNP_A-2123974	agttaatgatacatct[A/G]aaaaaacattcattat	A	G	Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // --- //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-2135857	atcaaatttactacac[A/G]agctgcactgacattc	A	G	Homo sapiens MEGF10 protein (MEGF10), mRNA. /// ENST00000274473 // CDS // 0 // --- // --- // --- // ---	MEGF10	MEGF10, Homo sapiens MEGF10 protein (MEGF10), q23.2
SNP_A-2108120	agctctgtgcaaaacc[C/G]aagtcacacctatatg	C	G	2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // upstream // 133751 // Hs.533683 // FGFR2 //	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.13
SNP_A-2109697	aggaaaggaggaaagc[A/G]gaatgagagggaaaaa	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3445319 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2168749	caagacaatgaaatgc[A/C]aaagaaaagatctcca	A	C	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2202439	ccacccatctaaaata[A/G]catttgccctttgcac	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2091152	actttggttgtgagga[A/G]taaaagagatgtctga	A	G	// Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// ENST00000297345 // intron // 0 // --- // --- // --- // ---	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2080346	acctaccagccacaga[A/G]gagcaggacgagccga	A	G	Homo sapiens solute carrier family 18 (vesicular monoamine), member 2 (SLC18A2), mRNA. /// ENST00000298472 // CDS // 0 // --- // --- // --- // ---	SLC18A2	SLC18A2, Homo sapiens solute carrier family 18 (vesicular monoamine), member 2 (SLC18A2), q26.11
SNP_A-2106005	agcccaaagcattcca[A/G]tctaatacagaattta	A	G	56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 282693 // Hs.517155 // TMEPAI //	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2103694	agcacagtcaaataac[C/T]aaaggggacaggctgt	C	T	/// ENST00000355553 // upstream // 301998 // --- // --- // --- // --- /// ENST00000358223 // upstream // 301998 // --- // --- // ---	-	q25.1
SNP_A-2074465	acatagaatcatggca[A/C]aattcttcataatagc	A	C	51704 // Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA. /// NM_001502 // downstream // 29037 // Hs.53985 // GP2 // 2813 // Homo	GPRC5B	GPRC5B, Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), p12.3
SNP_A-2042953	aactgaactaataata[A/C]agtactgctgactgcc	A	C	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2006586	tcacattgaggacacc[A/G]gcagttgtaagatgca	A	G	2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream //	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2311099	ggaagtattttaagaa[A/G]gataaaggcaatccag	A	G	10049 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA. /// NM_005494 // upstream // 74770 // Hs.490745 // DNAJB6 //	DNAJB6	DNAJB6, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, q36.3
SNP_A-2264427	gaagaaacatatttca[A/G]gataataacagccatc	A	G	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1783838 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2261920	gaaataatatcaggga[A/G]aataaaagcctggtcc	A	G	Homo sapiens lysophospholipase I (LYPLA1), mRNA. /// ENST00000316963 // 3UTR // 0 // --- // --- // --- // --- ///	LYPLA1	LYPLA1, Homo sapiens lysophospholipase I (LYPLA1), q11.23
SNP_A-2254868	cttggatatggcccaa[C/T]cacagaagtaaattgt	C	T	Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), mRNA. /// NM_019076 // intron // 0 // Hs.546397 // UGT1A8 // 54576 // Homo sapiens UDP	UGT1A10	UGT1A10, Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), q37.1
SNP_A-2254466	cttgcccttacccaga[A/G]caacctctttccttct	A	G	79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. ///	OBFC1	OBFC1, Homo sapiens oligonucleotide q24.33
SNP_A-2249136	ctgtttgcggattacc[A/G]aagggaataaagcata	A	G	84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /// NM_005068 // downstream // 62505 //	GPR145	GPR145, Homo sapiens G protein-coupled receptor 145 (GPR145), q16.3
SNP_A-2270431	gacagaaagcagcggc[G/T]acatcccactgcgccc	G	T	Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // --- // --- // --- // ---	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-2016015	ggatttttctccaaa[A/C]tttatgatgtcatttg	A	C	/// ENST00000331037 // downstream // 776633 // --- // --- // ---	-	q21.1
SNP_A-1992305	acttcaaagtgtgtac[A/G]gcaaaacaacatctta	A	G	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// NM_024767 // intron // 0 // Hs.134296 //	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-2025385	aaaatcagctatcaca[A/G]aacattcctggagatc	A	G	sapiens chromodomain helicase DNA binding protein 3 (CHD3), transcript variant 2, mRNA. /// NM_001005273 // intron // 0 // Hs.25601 // CHD3 // 1107 // Homo sapiens	CHD3	CHD3, Homo sapiens chromodomain helicase DNA binding protein 3 (CHD3), transcript variant 2, p13.1
SNP_A-2053922	aagtgttttcacaggt[A/G]aatttctgcttcctaa	A	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 431327	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2100518	agataatagcaacatc[C/T]agagctaatgtaacac	C	T	81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// NM_030794 // upstream // 29685 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2096069	agacatagtaacatct[C/G]aagtattttccagctc	C	G	EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 569398 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2203406	ccagaaacttcactca[C/G]aatcagagtcatctag	C	G	958 // Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), transcript variant 2, mRNA. /// NM_001250 // downstream // 40627 // Hs.472860	CD40	CD40, Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), transcript variant 2, q13.12
SNP_A-2184656	cagctcgttctacaga[A/C]ccacagagagaagtca	A	C	4634 // Homo sapiens myosin, light polypeptide 3, alkali; ventricular, skeletal, slow (MYL3), mRNA. /// NM_000316 // upstream // 6518 // Hs.1019 // PTHR1 // 5745 // Homo	MYL3	MYL3, Homo sapiens myosin, light polypeptide 3, alkali; ventricular, skeletal, slow (MYL3), p21.31
SNP_A-2121046	agtctccagttttaaa[C/T]gttgacaggtggagat	C	T	9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 203342 // Hs.335079 // MAP1B // 4131 // Homo sapiens	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-2137160	atcagggttagactga[C/T]gtgtttaactccaaag	C	T	285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 403755 //	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-2167309	caacagccaagtcact[A/G]agggaggccagcagat	A	G	Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, mRNA. /// NM_198390 // intron // 0 //	CMIP	CMIP, Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, q23.2
SNP_A-2157084	attgaaactaagctac[A/G]gtaccagtaattagat	A	G	Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), mRNA. /// ENST00000360391 // 3UTR // 0 // --- //	TP53BP2	TP53BP2, Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), q42.11
SNP_A-1804087	gtcacagatgaaacac[G/T]gaaatgccttactccg	G	T	Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), mRNA. /// ENST00000284509 // intron // 0 // --- // -	ATP8B4	ATP8B4, Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), q21.2
SNP_A-1783015	ggcagcccacatccag[C/T]aactatttgacatagg	C	T	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // --- // --- // --- // ---	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1710425	cttgggtcagctccgtcctaccctg[A/G]attgaggacaaggggtcaatctcca	A	G	AB018299 // intron // 0 // Hs.13349 // NFASC // 23114 // neurofascin	NFASC	NFASC , rs6685118, neurofascin,q32.1
SNP_A-1844595	tataacatcgctaaag[C/T]caacttgagttgtatt	C	T	63877 // Homo sapiens chromosome 10 open reading frame 84 (C10orf84), mRNA. /// NM_004248 // downstream //	C10orf84	C10orf84, Homo sapiens chromosome 10 open reading frame 84 (C10orf84), q26.11
SNP_A-1822419	gtttttacaagtgatc[G/T]cctatgaagtcttagc	G	T	Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // intron // 0 // Hs.487200 // SMOC2 //	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. q27

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1836436	tactcattctcaacag[A/G]agcgtatttatttttct	A	G	153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // intron // 0 // ---	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1831472	taatgttccatgttta[C/T]gtggcatcatgctcca	C	T	Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000304853 // intron // 0 // --- // --- // --- // --- ///	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. ,q26.31
SNP_A-1841105	tagcttcccgactagg[C/G]ccattccgcgtctgag	C	G	Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), mRNA. /// ENST00000299163 // CDS // 0	HIF1AN	HIF1AN, Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), q24.31
SNP_A-1952915	tttcttcaacaaataa[C/T]gtgcaatcaaaaaaat	C	T	ENST00000312793 // intron // 0 // --- // --- // --- // ---	-	p36.22
SNP_A-1933922	ttctcaaaatgcccaa[A/G]tgtccttcaacctcat	A	G	54749 // Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), mRNA. /// NM_032016 // upstream // 208630 //	EPDR1	EPDR1, Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), p14.1
SNP_A-1972900	agattctttttctcca[A/T]agtctgcgtatcagga	A	T	Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1963359	tttaaaaattcactta[C/T]gtacatggaatgtgct	C	T	// 55704 // Homo sapiens KIAA1212 (KIAA1212), mRNA. /// NM_080667 // upstream // 61613 // Hs.264208 // MGC15407	KIAA1212	KIAA1212, Homo sapiens KIAA1212 (KIAA1212), p16.1
SNP_A-1882521	tgaaaatgggtcaaca[C/G]gctttccttaccaacc	C	G	Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// ENST00000341928 // intron // 0 // --- //	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-1886258	tgaccgtgtgctgaca[C/T]tggcataccatctaca	C	T	2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 52976 // Hs.448717	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-1877414	tctggaggtaatgtca[C/T]gtgttacagccactct	C	T	57167 // Homo sapiens sal-like 4 (Drosophila) (SALL4), mRNA. /// NM_022088 // downstream // 295432 // Hs.473082	SALL4	SALL4, Homo sapiens sal-like 4 (Drosophila) (SALL4), q13.2
SNP_A-1880476	tcttgagtacttcagc[C/G]acacaccaaccatccc	C	G	9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 12325 // --- //	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1893059	tgcacttcaaattaca[C/G]gtcacggttagcaggt	C	G	ENST00000327131 // intron // 0 // --- // --- // --- // ---	-	q26.13
SNP_A-1899764	tggaatggcaaactca[C/G]aatagaaagaaaattt	C	G	Homo sapiens MAP/microtubule affinity-regulating kinase 1 (MARK1), mRNA. /// ENST00000294888 // intron // 0 // --- // ---	MARK1	MARK1, Homo sapiens MAP q41
SNP_A-1915368	tgttccagaaaactaa[C/G]agaagctcaaatgaac	C	G	// 55093 // Homo sapiens hypothetical protein FLJ10204 (FLJ10204), mRNA. /// NM_058229 // downstream // 10411 //	FLJ10204	FLJ10204, Homo sapiens hypothetical protein FLJ10204 (FLJ10204), q24.13
SNP_A-1989519	aaggtatgaagataaa[C/G]ctgaggatgctactgt	C	G	55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 63326 //	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. q43
SNP_A-1933611	ttctagcttttagtga[A/G]agagcatcctcagttc	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 485984 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1936309	ttcttcctcactctca[A/G]ataatccctatcctcc	A	G	160418 // Homo sapiens SMILE protein (SMILE), mRNA. /// NM_003994 // downstream // 264299 // Hs.1048 // KITLG //	SMILE	SMILE, Homo sapiens SMILE protein (SMILE), q21.32
SNP_A-1950648	tttcatgcattgataa[G/T]gggactgtaaaatggt	G	T	Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// ENST00000307241 // intron //	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1815144	gtgttctggaaagatc[A/G]cttaattaggagtcac	A	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 92555 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1692722	gaaggggtatctgtgaaggtattgc[C/T]aaggcaccaggcagtgaggaagatg	C	T	4803 // nerve growth factor, beta polypeptide /// NM_005725 // upstream // 69377 // Hs.234863 // TSPAN-2 // 10100 //	NGFB	NGFB , rs1286231, nerve growth factor, beta polypeptide ,p13.1
SNP_A-1650494	aaagagaaagggactgcactcatta[A/G]ggaacattataaggaaattcagaaa	A	G	// 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 457057 // Hs.339831 // PENK // 5179 //	FLJ20421	FLJ20421 , rs1876496, hypothetical protein FLJ20421 ,q12.1
SNP_A-1716693	gataaacttccactctatgaaaaac[A/G]cattaagataatcaaatagcaagac	A	G	MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217) /// NM_021153 // upstream // 684173 //	-	- , rs1598486, MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217) ,q22.1
SNP_A-2166010	caaataagatgagaaa[C/G]gtctttagtgattttt	C	G	/// ENST00000321719 // upstream // 428835 // --- // --- // --- // ---	-	p11.21
SNP_A-2163815	caaaacacattctaaa[C/T]tggtgaaatacttttg	C	T	Homo sapiens transient receptor potential cation channel, subfamily M, member 7 (TRPM7), mRNA. /// ENST00000313478 // intron // 0 // --- // --- // --- // ---	TRPM7	TRPM7, Homo sapiens transient receptor potential cation channel, subfamily M, member 7 (TRPM7), q21.2
SNP_A-2148097	atgggaagatcggcgt[A/G]aaggtcttcttggtga	A	G	Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, mRNA. /// NM_134325 // CDS // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens	SLC26A9	SLC26A9, Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, q32.1
SNP_A-2144814	atgatgtgattcagac[A/T]ctcagaggaattgctt	A	T	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2114744	agggatggcctataat[C/G]aacaaaaggttgagaa	C	G	7804 // Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, mRNA. /// NM_004631 // upstream // 115199 // Hs.444637	LRP8	LRP8, Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, p32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2183856	cagccaaagtgcttta[A/T]gtatggagatagcttc	A	T	2770 // Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), mRNA. /// ENST00000354672 // downstream // 89647 // --- //	GNAI1	GNAI1, Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), q21.11
SNP_A-2190142	cataaggttctgattg[G/T]agcttgactatgtgcc	G	T	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 113551 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2169185	caagatgtccaaaagc[C/T]ataggggatacatatt	C	T	Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA. /// ENST00000182377 // intron // 0 // --- // --- // --- // ---	MLSTD1	MLSTD1, Homo sapiens male sterility domain containing 1 (MLSTD1), p11.22
SNP_A-2170653	caagttaacatagaaa[A/G]ttcaccatcatgccct	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1668480 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2182602	cagatcatttctttcc[A/T]accagtttttacacag	A	T	// 84293 // Homo sapiens chromosome 10 open reading frame 58 (C10orf58), mRNA. /// NM_030927 // upstream //	C10orf58	C10orf58, Homo sapiens chromosome 10 open reading frame 58 (C10orf58), q22.3
SNP_A-2208580	cccactcagtgctaga[C/G]gacagcttcaactccc	C	G	5028 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), mRNA. /// NM_002886 // upstream //	P2RY1	P2RY1, Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), q25.2
SNP_A-2222523	cgaggctttgcacaaa[A/G]tatacaataaatattt	A	G	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 338236 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2225744	ctaaagcccagacaca[A/G]agtgattttccccagg	A	G	Homo sapiens chromosome 6 open reading frame 142 (C6orf142), mRNA. /// ENST00000274897 // intron // 0 // --- //	C6orf142	C6orf142, Homo sapiens chromosome 6 open reading frame 142 (C6orf142), p12.1
SNP_A-2101016	agatcaaattctgtaa[A/T]aatagttgtacatgaa	A	T	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1241898 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2047776	aagattgtattttata[A/G]ccataagcataacact	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2063404	aattaactccctcttg[C/G]agcaataaaccaccct	C	G	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 //	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2069143	acaattatttccaaag[G/T]catagttatttggtta	G	T	80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 252736 //	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-1990329	cctgggaatatagcac[C/G]atttgtagcttacaaa	C	G	10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 210023 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-2272850	gactaataaaagtata[C/T]gcaaacaatcctctgt	C	T	404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 36394 //	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2245934	ctgggttccaagtgtg[C/T]acctctggagtctgct	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2254191	cttgatgaacatgaac[A/G]caaagatactcaacaa	A	G	// Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 235041 // Hs.1428 // FSHR // 2492 // Homo	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-2252938	cttctcaccaaattta[C/G]gacattgtagcctata	C	G	Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000328681 // intron // 0 // --- // ---	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-2239393	caagtgatagatatta[C/G]taagtgaataatgtat	C	G	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-2301398	gcctttgttgtttcca[A/G]gttaatatatatctgt	A	G	Homo sapiens molybdenum cofactor sulfurase (MOCOS), mRNA. /// ENST00000261326 // intron // 0 // --- // --- // --- // ---	MOCOS	MOCOS, Homo sapiens molybdenum cofactor sulfurase (MOCOS), q12.2
SNP_A-2044832	aagaaatgtgtgatta[C/T]gtaagaacaattccta	C	T	5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // downstream // 69389 // --- // --- // --- // --- ///	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1
SNP_A-2038456	aacactgtgcagtcca[A/G]cgggttaatcactagc	A	G	sapiens activin A receptor, type I (ACVR1), mRNA. /// ENST00000263640 // intron // 0 // --- // --- // --- // ---	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-2088444	actgtatagctggaga[G/T]aaatgatatgtatata	G	T	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 204867 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2217596	cctgagattagcaatc[A/G]cacatggtttatttta	A	G	Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2204953	ccaggggaatgagaag[A/C]agttctattggaagta	A	C	2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream //	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2201355	ttgcatgtactataca[A/G]aaggtggagcacatgc	A	G	// 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 340489 // --- // --- // --- //	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12
SNP_A-2168324	caactggtgtgagaat[A/G]acggactaactttatt	A	G	// 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // downstream // 221830 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2185056	cagctttagatagttc[A/C]caaatctttgttgaga	A	C	Homo sapiens ankyrin repeat, SAM and basic leucine zipper domain containing 1 (ASZ1), mRNA. /// ENST00000284629 // intron // 0 // --- // --- // --- // ---	ASZ1	ASZ1, Homo sapiens ankyrin repeat, SAM and basic leucine zipper domain containing 1 (ASZ1), q31.2
SNP_A-2152194	attaaagaagagaaca[A/C]aattaagtcatttaga	A	C	Homo sapiens tubulin-specific chaperone d (TBCD), mRNA. /// ENST00000355528 // intron // 0 // --- // --- // --- // --- ///	TBCD	TBCD, Homo sapiens tubulin-specific chaperone d (TBCD), q25.3
SNP_A-1718935	gaatggataatggtgaatggtggta[C/T]atccaataatagaatattggctcag	C	T	2995 // glycophorin C (Gerbich blood group) /// NM_016815 // upstream // 86865 // Hs.81994 // GYPC // 2995 // glycophorin	GYPC	GYPC , rs2083414, glycophorin C (Gerbich blood group) ,q14.3
SNP_A-1673982	tatgaaaagagttgatattccttcc[A/G]atttttgatttggggatagtaacag	A	G	// 1278 // collagen, type I, alpha 2 /// NM_022900 // upstream // 58346 // Hs.324725 // CAS1 // 64921 // O-acetyltransferase	COL1A2	COL1A2 , rs10487260, collagen, type I, alpha 2 ,q21.3
SNP_A-1793864	ggtcaaactggactac[C/T]attaggtcataaaaac	C	T	– /// ENST00000356117 // downstream // 251345 // --- // --- //	-	q23.31
SNP_A-1843366	tagtgaaaactctcaa[G/T]tatttccaagtggagt	G	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 619558	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1837778	tacttttcagaaacta[A/C]atgaatatctccttcc	A	C	Homo sapiens apoptosis antagonizing transcription factor (AATF), mRNA. /// ENST00000225402 // intron // 0 // --- // ---	AATF	AATF, Homo sapiens apoptosis antagonizing transcription factor (AATF), q12
SNP_A-1837022	tactgggtctacgtcc[A/G]gctctggaattttcct	A	G	Homo sapiens actin filament associated protein (AFAP), transcript variant 1, mRNA. /// NM_198595 // intron // 0 //	AFAP	AFAP, Homo sapiens actin filament associated protein (AFAP), transcript variant 1, p16.1
SNP_A-1868114	tcctatggtggcttta[G/T]aagtatttaatgtgta	G	T	// 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 296139 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1952575	tttctgccatgcacca[C/T]aacaaatacacacaca	C	T	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 163100 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1934889	ttctgaactttctgtc[G/T]ctcacggcaatcatgt	G	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 724783 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1964528	tgtgttagaagctagg[A/G]atatattcatctgcaa	A	G	// 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 //	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-1972912	tcaaaagtggccataa[C/T]cttccactctgattat	C	T	Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1927566	ttcaacactatcacta[C/T]cctgaatgccaggcct	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5 (GALNTL5), mRNA. /// ENST00000323750 // intron // 0 // --- // --- // --- // --- ///	GALNTL5	GALNTL5, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5 (GALNTL5), q36.1
SNP_A-1900455	tggagcacaagggaaa[C/T]ctgtaagagttttgaa	C	T	// 84541 // Homo sapiens T-cell activation kelch repeat protein (TA-KRP), mRNA. /// NM_003848 // downstream //	TA-KRP	TA-KRP, Homo sapiens T-cell activation kelch repeat protein (TA-KRP), p14.1
SNP_A-1889701	tgataaggtagcatga[A/G]cttttctacataaaaa	A	G	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1888099	tgagccactgatgtaa[A/G]aacttttgaactttc	A	G	390067 // Homo sapiens olfactory receptor, family 52, subfamily H, member 1 (OR52H1), mRNA. /// NM_001005162 // upstream // 1684 // --- // OR52B6 // 340980	OR52H1	OR52H1, Homo sapiens olfactory receptor, family 52, subfamily H, member 1 (OR52H1), p15.4
SNP_A-1928601	ttcacttaatcccaaa[A/C]tttacttagcattagg	A	C	Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // intron // 0 // Hs.123642 // EPHA3 // 2042 //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1910629	tgtcctgataattcca[C/T]tgatggccattccccc	C	T	25890 // Homo sapiens target of Nesh-SH3 (TARSH), mRNA. /// NM_016247 // downstream // 111188 // Hs.272380 //	ABI3BP	ABI3BP, Homo sapiens target of Nesh-SH3 (TARSH), q12.2
SNP_A-1982549	gagttggtacaaagtg[A/C]agggacaaaatgtaat	A	C	Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // intron // 0 // Hs.209095 // MCTP1 // 79772	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-1980435	aattgatgcatttaac[C/T]gtaagaaaaatgaact	C	T	ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 100569 // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1980668	cctgtcttcaccagca[C/G]tgcctttcctgtgcac	C	G	// 134147 // Homo sapiens hypothetical protein BC001573 (LOC134147), mRNA. /// NM_005885 // upstream // 43027 //	LOC134147	LOC134147, Homo sapiens hypothetical protein BC001573 (LOC134147), p15.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939525	ttgattattttgagct[C/T]aaggcacttgaaaaac	C	T	// 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-1946532	tttaaataacatttta[A/G]cttctccatgtaaata	A	G	// Homo sapiens vanin 2 (VNN2), transcript variant 1, mRNA. /// NM_078488 // upstream // 8048 // Hs.293130 // VNN2 //	VNN2	VNN2, Homo sapiens vanin 2 (VNN2), transcript variant 1, q23.2
SNP_A-1951119	tttccattacctaaca[G/T]aaggtctagtatatag	G	T	// 3790 // Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA. /// NM_020905 // downstream // 219868 // Hs.288880 // RDH14	KCNS3	KCNS3, Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), p24.2
SNP_A-1957185	ttttacggaactctaa[A/G]ctccatgagggagatg	A	G	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 57487 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1868024	tcctagtttctcatca[C/T]taagtacaatgttagt	C	T	10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 439019 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1850335	tatgttgaagttttgc[A/C]aagcaactagtcaaac	A	C	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 152094 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1837652	tactttatgtgctaaa[C/T]gcctacttcatagtcc	C	T	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1127231 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1837494	tacttgaggttgttgg[A/G]attgttgagatgtatt	A	G	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // --- // --- // --- // ---	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-1843064	tagtattttaggtaca[A/G]tggtcaggaaaagcct	A	G	// Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1815772	gttaagctcaggcaaa[A/C]aacacagtgaaacttt	A	C	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 84338 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1794680	ggtctccacacagtca[C/G]attctttctctctcct	C	G	115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream //	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-1645056	ggcactttctcttttctggatcgag[A/C]cccaaattctctacgtgttgtccct	A	C	NM_173465 // intron // 0 // Hs.413494 // COL23A1 // 91522 // collagen, type XXIII, alpha 1	COL23A1	COL23A1 , rs10516148, collagen, type XXIII, alpha 1,q35.3
SNP_A-1757375	aggattaaaaaatatatacagtaca[A/T]catatagagccagggtaaatactgt	A	T	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	ELOVL2	ELOVL2 , rs4711162, elongation of very long chain fatty acids (FEN1,p24.2
SNP_A-2147637	atggcaaacacactta[C/T]ccttgcaggccttcga	C	T	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 235058 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2160667	atttccttctggttaa[G/T]aaccactgttggggag	G	T	56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 907034 // Hs.519693 //	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-2160246	atttcacccctaaaca[A/C]gctgagaactgagggg	A	C	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 227220 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2196562	cattaaaagttctcta[C/T]aactaccatggtgtaa	C	T	CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 //	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2226755	ctaataaaatgagctg[A/G]aagttccagaaatcac	A	G	Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // intron // 0 // --- // ---	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-2091708	agaaaagcagatttaa[A/G]agtgatggacagggaa	A	G	55247 // Homo sapiens DNA glycosylase hFPG2 (FLJ10858), mRNA. /// NM_000027 // downstream // 56495 //	NEIL3	NEIL3, Homo sapiens DNA glycosylase hFPG2 (FLJ10858), q34.3
SNP_A-2086939	actgagcacactcccc[A/G]ctagaaatgataagag	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 550164 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2095158	agaattagagctcaaa[A/G]gcttaaaccaaattgc	A	G	27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // downstream //	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2036345	aaattcccagcaagga[C/T]tagtagtagagaatga	C	T	83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2301657	gcgccagggctgaaac[A/G]aagagtgcacgcaccg	A	G	201456 // Homo sapiens F-box protein 15 (FBXO15), mRNA. /// NM_152676 // upstream // 114 // Hs.465411 // FBXO15 //	FBXO15	FBXO15, Homo sapiens F-box protein 15 (FBXO15), q22.3
SNP_A-2237094	ctctcaagaataactg[A/T]agcatgtgcaggaaaa	A	T	Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2232948	ctcagactagcattac[A/G]ggctgccaagagctct	A	G	Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2271527	gaccaactcaggctga[A/G]taaaatttcggaatca	A	G	64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 339448 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2266335	gaaggtcattctaatt[A/T]aaaaaagtgaagaaat	A	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2302572	gctacagaaatgccct[A/T]aagaatcttgagtgtg	A	T	5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 330563 // Hs.298863 // FLJ23577	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2033545	aaatatagaaaatcac[A/G]acttatcagggcagaa	A	G	ENST00000354422 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2045587	aagaattctacccacc[A/T]caggttgtactgcatg	A	T	116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 52877 // Hs.491941 // VEST1	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2033051	aaatacaatgtcaaca[A/G]aagagaaagtttgaag	A	G	65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 796739 // Hs.42650 // ZWINT	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1992394	ccacttagagatgaaa[C/G]aaaacagacaaaatgc	C	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 726853 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2050946	aaggctactctactta[C/T]caactatactttcaaa	C	T	Homo sapiens ubiquitin specific protease 46 (USP46), mRNA. /// ENST00000226440 // intron // 0 // --- // --- // --- // ---	USP46	USP46, Homo sapiens ubiquitin specific protease 46 (USP46), q12
SNP_A-2195094	catggaatactgtgaa[A/T]ccataaaaggaaatga	A	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2187432	caggttggcgtgagaa[A/G]tgaggtgacgtcatgc	A	G	Homo sapiens transmembrane channel-like 7 (TMC7), mRNA. /// ENST00000304381 // intron // 0 // --- // --- // --- // ---	TMC7	TMC7, Homo sapiens transmembrane channel-like 7 (TMC7), p12.3
SNP_A-2182035	cagaggagcaaactga[A/C]gcccagaatgggaagc	A	C	PHGDHL1 // 337867 // Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), mRNA. /// NM_005292 //	PHGDHL1	PHGDHL1, Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), q32.3
SNP_A-2149329	atgtacaatgattaca[A/C]agatgtaagcttcaca	A	C	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2117293	aggtggatggagagcc[A/G]agcaatatgaggaggg	A	G	Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// ENST00000229686 // intron // 0 // --- // --- // --- // ---	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-2124541	agttccataattcaga[A/T]acatttggtttaagta	A	T	10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// NM_015323 //	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-1729372	ggagcaattaataaatcatgagtta[C/T]ataatatccacacagtgaaaagcct	C	T	NM_001754 // intron // 0 // Hs.410774 // RUNX1 // 861 // runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	RUNX1	RUNX1 , rs2834681, runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene),q22.12
SNP_A-1800949	gtagataaaaggaggc[A/G]agaaatagcaccaatg	A	G	Homo sapiens human immune associated nucleotide 2 (hIAN2), mRNA. /// ENST00000328902 // intron // 0 // --- // ---	GIMAP6	GIMAP6, Homo sapiens human immune associated nucleotide 2 (hIAN2), q36.1
SNP_A-1801683	gtagtatgtaacatca[C/T]atacaggcaacttaca	C	T	10874 // Homo sapiens neuromedin U (NMU), mRNA. /// NM_178237 // upstream // 17531 // Hs.269665 // SEC3L1 //	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-1818148	gttctctcctaaacac[C/T]gcctctttgccattat	C	T	6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 106911 // Hs.546261 //	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1827523	taactctcaaagagca[A/T]tctcactttccttatt	A	T	// 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 118643	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-1828065	taagacaatgaaaaaa[A/C]caaatattagttgata	A	C	Homo sapiens hypothetical protein FLJ10569 (FLJ10569), mRNA. /// ENST00000300321 // intron // 0 // --- // --- // --- // ---	FLJ10569	FLJ10569, Homo sapiens hypothetical protein FLJ10569 (FLJ10569), p21.3
SNP_A-1843378	tagtgaaagacttttta[A/T]agttcagaacatggtc	A	T	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 655914 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1866983	tccctcagcctgcaga[A/C]acatatgcctatgggg	A	C	// Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// ENST00000324072 // intron // 0 // --- // --- // --- // ---	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11
SNP_A-1862179	tcatggacctgataga[C/T]gctgatgtcccacaga	C	T	// 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-1865753	tccatttcatggtaca[C/T]ctttctccatttcttt	C	T	// Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), mRNA. /// NM_001005167 // upstream // 7359 // Hs.534693 // OR52E6 // 390078 // Homo sapiens	OR52E8	OR52E8, Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), p15.4
SNP_A-1967857	tccctagttatgagta[C/T]aaatatgcaccccaga	C	T	Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA. /// ENST00000271529 // intron // 0 // --- // --- // --- // ---	IRTA2	IRTA2, Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), q23.1
SNP_A-1925872	ttatggctgagtaata[C/T]ataccacactttcttt	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 93018 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1880986	tcttgtgtggttgaat[C/G]actatggtctctactg	C	G	-- /// ENST00000345029 // upstream // 863067 // --- // --- // ---	-	p14
SNP_A-1875916	tctgaaatatcacact[C/T]aaggaaaatttgatct	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1755869 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1895509	tgcctactgcacatca[A/C]gttgtctcataaagct	A	C	90273 // Homo sapiens carcinoembryonic antigen-related cell adhesion molecule (R29124_1), mRNA. /// ENST00000320909 // upstream // 39679 // --- // --- // --- // ---	R29124_1	R29124_1, Homo sapiens carcinoembryonic antigen-related cell adhesion molecule (R29124_1), q13.2
SNP_A-1898485	tgcttctggctatggt[A/G]aagtagactgcaacag	A	G	FLJ20604 // 54995 // Homo sapiens hypothetical protein FLJ20604 (FLJ20604), mRNA. /// NM_052953 // upstream //	FLJ20604	FLJ20604, Homo sapiens hypothetical protein FLJ20604 (FLJ20604), p24.2
SNP_A-1944579	ttgtgaaataagcaca[G/T]ccatttaagacagaaa	G	T	UGT2B28 // 54490 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), mRNA. /// NM_021139 // downstream // 51745 // Hs.285887 // UGT2B4 // 7363 //	UGT2B28	UGT2B28, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), q13.2
SNP_A-1861410	tcatcagtttcttgaa[C/T]gcttgtacacacttat	C	T	Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST00000335473 // 3UTR // 0 // --- // --- // --- // ---	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1853534	tattttgttataggaa[A/C]ttcaaccatgaaccca	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2667763 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1836724	tactgaatgtattcca[A/G]agcactaattttaagg	A	G	// 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 47407 // Hs.282787 // FOXP2 //	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1
SNP_A-1804947	gtcatataggtacaat[C/T]agtgacccaaaagcaa	C	T	Homo sapiens adenylate cyclase 1 (brain) (ADCY1), mRNA. /// ENST00000297323 // intron // 0 // --- // --- // --- // ---	ADCY1	ADCY1, Homo sapiens adenylate cyclase 1 (brain) (ADCY1), p13
SNP_A-1809158	gtgacatttggcccaa[C/T]tgtgactctgcttgcc	C	T	Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // --- // --- // --- // ---	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3
SNP_A-1792592	ggtaaagcagcccaga[C/G]aaggcgaagctaaata	C	G	Homo sapiens cartilage acidic protein 1 (CRTAC1), mRNA. /// ENST00000210816 // intron // 0 // --- // --- // --- // ---	CRTAC1	CRTAC1, Homo sapiens cartilage acidic protein 1 (CRTAC1), q24.2
SNP_A-1751749	aaagcacctaaaataattcctgata[C/T]gtaataagaactaactaaatggtat	C	T	3741 // potassium voltage-gated channel, shaker-related subfamily, member 5 /// NM_002527 // upstream // 392765 // Hs.99171 // NTF3 // 4908 // neurotrophin 3	KCNA5	KCNA5 , rs248879, potassium voltage-gated channel, shaker-related subfamily, member 5 ,p13.32
SNP_A-1782872	ggcagaggagaaggaa[A/G]atatgtgtgggggta	A	G	-- /// ENST00000314071 // upstream // 697624 // --- // --- // ---	-	p13.3
SNP_A-1673050	aaaagagagggaagagtaaaggaaa[A/C]ttcatcttgaaacttaggtaccagc	A	C	5359 // phospholipid scramblase 1 /// NM_032153 // downstream // 378477 // Hs.415766 // ZIC4 // 84107 // Zic	PLSCR1	PLSCR1 , rs2102158, phospholipid scramblase 1 ,q24
SNP_A-1681456	tcatcctgctcccacatggctgtga[A/G]cactctttttttttgtcttacacag	A	G	// 400359 // FLJ35695 protein /// AK096850 // upstream // 146336 // Hs.376109 // FLJ39531 // 400360 // FLJ39531	FLJ35695	FLJ35695 , rs10520118, FLJ35695 protein ,q14
SNP_A-2117637	aggttatgatagcaaa[C/T]agctggtgaagtgacc	C	T	Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// ENST00000358317 // intron // 0 // --- // ---	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2120755	agtcctcttttgata[C/G]gtggttttcaggtgct	C	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2156496	attctctctttttttcc[A/G]cagttatactattggg	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, mRNA. /// NM_030668 // intron // 0 // Hs.160871 // PTPRO // 5800 // Homo sapiens protein	PTPRO	PTPRO, Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, p12.3
SNP_A-2166874	caaatttgcaatgtac[A/G]ccctattttatctgca	A	G	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 169223 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2180168	cagaaacatatactaa[C/G]gtctaggaggtcatgg	C	G	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2168344	caactgtctgacataa[A/G]acccatttgaccctg	A	G	/// ENST00000354860 // upstream // 1008449 // --- // --- // --- //	-	q32.3
SNP_A-2172548	caattctataccccct[A/G]agaatccaaaaatttt	A	G	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2221677	cctttgtatccaccta[C/T]aacctggaagaacccc	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2224060	cgggtaggaacttcta[C/T]aggacacaggtataca	C	T	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA. /// NM_013412 // intron // 0 // Hs.446425 // RABL2A // 11159 // Homo sapiens	RABL2A	RABL2A, Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, q13.33
SNP_A-2204655	ccaggagatagaagac[A/T]agtagttattttcctc	A	T	Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), mRNA. /// ENST00000266427 // intron // 0 // --- // --- // --- // ---	ETV6	ETV6, Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), p13.2
SNP_A-2063594	aattacatataggaca[A/G]tggtaggatatgaagt	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1995878	tttcttcttaaaatga[C/T]gtagcacaaccctct	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2053470 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2017704	gaagaacttccaaata[C/G]tacagttatttaattc	C	G	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, mRNA. /// NM_000830 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate	GRIK1	GRIK1, Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, q21.3
SNP_A-2006820	agaagctaagtgaaca[A/G]cagtatctacccttct	A	G	Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA. /// ENST00000259060 // intron // 0 // --- // ---	SCN7A	SCN7A, Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), q24.3
SNP_A-2024738	aaaagtcacacaggaa[C/T]aggttgtttaatatac	C	T	DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream //	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-2022856	aaaacaaagaaatcac[C/T]ctgtttgactctgtgg	C	T	Homo sapiens topoisomerase (DNA) III alpha (TOP3A), mRNA. /// ENST00000321105 // intron // 0 // --- // --- // --- // ---	TOP3A	TOP3A, Homo sapiens topoisomerase (DNA) III alpha (TOP3A), p11.2
SNP_A-2040283	aaccacctgaatggaa[A/T]gctgaggcttaatatt	A	T	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 166393 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2302220	gctaaataaaaacaca[A/G]gaatatagtgaagaca	A	G	2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000360030 // upstream //	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.2
SNP_A-2314941	ggagttcaggtgcaac[A/G]gcttggaatgcagaga	A	G	25790 // Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA. /// ENST00000338203 //	NESG1	NESG1, Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), q23.2
SNP_A-2276260	tgccacaaacagtgta[C/T]aaaatcaaagcaaatt	C	T	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2280575	gaggtagtcagtgaaa[C/G]caccagaaaatggtac	C	G	64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 289124 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2245413	ctgggaagtcagtagc[A/C]agagaaggctcttttt	A	C	Homo sapiens mRNA for KIAA1042 protein, partial cds. /// ENST00000327628 // intron // 0 // --- // --- // --- // ---	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. ,p22.1
SNP_A-2245898	ctgggtgccagacgca[A/G]gtggtcctgcccagag	A	G	Homo sapiens chromosome 6 open reading frame 106 (C6orf106), transcript variant 2, mRNA. /// NM_024294 // 3UTR // 0 // Hs.485162 // C6orf106 // 64771 // Homo sapiens	C6orf106	C6orf106, Homo sapiens chromosome 6 open reading frame 106 (C6orf106), transcript variant 2, p21.31
SNP_A-2241600	ccctttaagtgaatga[A/G]tataaaactgaatcta	A	G	Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // intron // 0 // --- // -	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2266268	gaagggtccggggtcc[A/G]agtcccattttgaggc	A	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 224234 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2261184	gaaagaggcgactcaa[C/G]ggtggctatttttttc	C	G	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2295082	gcataggacaatgaaa[C/T]aatggagaaagaatgt	C	T	METTL2 // 55798 // Homo sapiens methyltransferase like 2 (METTL2), mRNA. /// NM_181725 // downstream // 206630 //	METTL2	METTL2, Homo sapiens methyltransferase like 2 (METTL2), q32.1
SNP_A-2288877	gatttacatttttaaa[G/T]atcctgtggccgctgt	G	T	9808 // Homo sapiens KIAA0087 mRNA, partial cds. /// ENST00000297021 // downstream // 48493 // --- // --- // --- // --	KIAA0087	KIAA0087, Homo sapiens KIAA0087 partial cds. p15.2
SNP_A-2028185	aaactactgggtgtta[C/T]aagatctaatctctgg	C	T	54872 // Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /// NM_000283 // upstream // 78191 //	GPI7	GPI7, Homo sapiens hypothetical protein FLJ20265 (FLJ20265), p16.3
SNP_A-2012873	ggtcaattgctgacca[C/T]tggatgtggagagatg	C	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2003071	aggtaattgagctgat[C/G]actatttttggaaacac	C	G	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA. /// ENST00000228506 // intron // 0 // --- // --- // --- // ---	KIAA0152	KIAA0152, Homo sapiens KIAA0152 gene product (KIAA0152), q24.31
SNP_A-2073037	acaggaggttcagcca[C/T]caaacctgagtcaggt	C	T	Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA. /// ENST00000292807 // intron // 0	AP2M1	AP2M1, Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), q27.1
SNP_A-2062165	aatggtaaaaattata[C/G]aagaatatgcatgtaa	C	G	5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 331992 // Hs.446083 // PTPRD // 5789 // Homo	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p23
SNP_A-2105339	agcatttgctttgaac[A/G]ctttgcactgggtatt	A	G	4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 1895547 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2220865	ccttgccagtttggta[A/C]ccctccggaacagact	A	C	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 483497 //	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-2220422	ccttctaactttggag[A/G]agaacatctgatgaaa	A	G	2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// NM_173675 // downstream // 7547 //	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213497	ccggtgcccaagacac[A/G]gagatccagtccttca	A	G	864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 226333 //	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2115689	agcagaaaaagaatga[A/G]gacaacggtcccactt	A	G	// 54741 // Homo sapiens leptin receptor gene-related protein (OBRGRP), mRNA. /// NM_001003679 // downstream //	LEPROT	LEPROT, Homo sapiens leptin receptor gene-related protein (OBRGRP), p31.2
SNP_A-2127321	ataaattagtgtaaga[C/T]aatgctatgaaacatc	C	T	132789 // Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), mRNA. /// ENST00000295448 //	GNPDA2	GNPDA2, Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), p13
SNP_A-2131859	ataggaaactctagaa[C/T]gcttggaataaaacag	C	T	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1650894	tcccatctttaggtggataaagaac[C/T]gaaagagaggctccatttctttagg	C	T	NM_004932 // upstream // 1788961 // Hs.32963 // CDH6 // 1004 // cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	CDH6 , rs1303755, cadherin 6, type 2, K-cadherin (fetal kidney),p13.3
SNP_A-1795817	ggtggcagtgatgcta[C/T]cttctactcactggct	C	T	/// ENST00000315208 // upstream // 286054 // --- // --- // --- // ---	-	q24.32
SNP_A-1788533	gggatagttcccagac[C/T]gtcgactttctgtccc	C	T	158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream //	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32
SNP_A-1788347	gggaggggtcatgga[C/T]gttaggttcagggtta	C	T	ENST00000321345 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1806459	gtcgccctttggaaga[A/G]cgctggttttgtcaga	A	G	Homo sapiens hypothetical protein FLJ12584 (FLJ12584), mRNA. /// ENST00000349938 // intron // 0 // --- // --- // --- // ---	FLJ12584	FLJ12584, Homo sapiens hypothetical protein FLJ12584 (FLJ12584), q37.1
SNP_A-1802251	gtatatctgtggaaag[A/G]ccccttaaagaaaatg	A	G	NM_198989 // downstream // 257485 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.3
SNP_A-1817471	gttcatattaatcaac[A/G]ctaaaaagactcagcc	A	G	168620 // Homo sapiens class II bHLH protein MIST1 (MIST1), mRNA. /// NM_015379 // upstream // 52340 //	MIST1	MIST1, Homo sapiens class II bHLH protein MIST1 (MIST1), q21.3
SNP_A-1855075	tcaagacaatttaata[A/C]gcaaactttccaatta	A	C	Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // --- // --- // --- // ---	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-1864129	tccacatcattaagaa[G/T]ccttctagaacatgat	G	T	4017 // Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /// NM_004901 // upstream // 20787 // Hs.444389 // ENTPD4 //	LOXL2	LOXL2, Homo sapiens lysyl oxidase-like 2 (LOXL2), p21.3
SNP_A-1863634	tccaacacactgacaa[C/T]tcttaaaaatgtttat	C	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.2
SNP_A-1972261	cagcttgttggcaaaa[A/G]tggttcccttatcacg	A	G	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1987084	tgattaggtacaaaga[A/G]actggatgatacattc	A	G	// 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1321973 // Hs.98262 // GRIK2	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1874180	tctccaaagttcctcc[A/G]ggagacgacaggcaat	A	G	1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// NM_207426 // upstream // 280110 // Hs.449674 //	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-1883163	tgaaatgctctggaaa[A/G]tctcagtaatagaatt	A	G	4159 // Homo sapiens melanocortin 3 receptor (MC3R), mRNA. /// NM_080821 // upstream // 41527 // Hs.143736 //	MC3R	MC3R, Homo sapiens melanocortin 3 receptor (MC3R), q13.31
SNP_A-1921779	ttactaatgaatgtta[A/T]gtcaccgtacaggcat	A	T	sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// ENST00000360890 // intron // 0 // --- // --- // --- // ---	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-1921354	ttaccaagttgaaaga[A/G]cagtaagtatgcaaga	A	G	OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 //	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-1906034	tggtctcacgcagtaa[C/T]acaatctagaaggaaa	C	T	26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 737419 //	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13
SNP_A-1883558	tgaacctcacattgta[A/C]agaatttccttccatg	A	C	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1880244	tcttcttccaaccccc[A/C]aaaatatgttttcatt	A	C	// Homo sapiens UMP-CMP kinase (UMP-CMPK), mRNA. /// ENST00000294340 // intron // 0 // --- // --- // --- // ---	UMP-CMPK	UMP-CMPK, Homo sapiens UMP-CMP kinase (UMP-CMPK), p33
SNP_A-1880688	tcttggaaaatgctca[C/T]gtttttcggtgttgac	C	T	C9orf103 // 414328 // Homo sapiens chromosome 9 open reading frame 103 (C9orf103), mRNA. /// NM_053067 //	C9orf103	C9orf103, Homo sapiens chromosome 9 open reading frame 103 (C9orf103), q21.32
SNP_A-1878823	tctgttgtttcggcca[C/T]ccaatttttggtattt	C	T	Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // --- // --- // --- // --- ///	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-1986620	ttaaagatttaacaga[C/T]ggagcaagcctgaaag	C	T	ENST00000358773 // intron // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-1939609	ttgatttagcaaaaca[C/T]tcaaatccctcaataa	C	T	5570 // Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), transcript variant 1, mRNA. /// NM_032471 // downstream // 31173 // Hs.486354 // PKIB //	PKIB	PKIB, Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), transcript variant 1, q22.31
SNP_A-1948312	tttaggcaggtgtaca[C/T]gggtcaagagttggct	C	T	Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // --- // --- // --- // ---	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1953207	tttctttgatatttac[C/T]gaacaccctctcaagc	C	T	27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 34410 // Hs.381050 // B3GAT1 // 27087 // Homo sa	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-1846901	tatcacctatcgaagc[C/T]aaaacatttcttaaag	C	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1306564	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1741053	ttcacaatagggacgcattcataca[C/T]tgatatgcaaggaaaaaccaaacc c	C	T	AB028948 // intron // 0 // Hs.435249 // THRAP2 // 23389 // thyroid hormone receptor associated protein 2	THRAP2	THRAP2 , rs10507266, thyroid hormone receptor associated protein 2,q24.21
SNP_A-2135917	atcaaccacttggaaa[A/C]tactgggtatagttgg	A	C	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. ///	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2127178	ataaatccttgcagaa[C/T]aacattaaatatggag	C	T	1811 // Homo sapiens solute carrier family 26, member 3 (SLC26A3), mRNA. /// NM_000108 // upstream // 59473 //	SLC26A3	SLC26A3, Homo sapiens solute carrier family 26, member 3 (SLC26A3), q31.1
SNP_A-2168197	caactctgtgaatata[A/G]tacaagccactgaatt	A	G	7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // upstream // 102213 // Hs.510833 // TJP1 //	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.2
SNP_A-2162638	attttctgagatgtta[C/G]agagtaaaatggggcc	C	G	// 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// NM_000882 // upstream // 39397 //	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2162038	attttaaaataagcct[C/G]actggatattttccat	C	G	Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// ENST00000320658 // intron //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2152268	attaaatcacaaacac[A/G]caatcctgtcacccac	A	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. ,q21.1
SNP_A-2226264	ctaacttaatacaaaa[A/C]ggtgtttcaggagaaa	A	C	FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 119354 //	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23
SNP_A-2227625	ctacatcaaagtggaa[A/G]tgttaggtaactggtt	A	G	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2180485	cagaactatattaaaa[C/T]gcaatgaatactcctc	C	T	26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream //	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2185540	caggagaatctgaaca[C/T]gtcttggagggacaag	C	T	// 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 104495	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-2102411	agattcccaggttcaa[C/T]tatgggcagccttact	C	T	-- /// ENST00000361117 // upstream // 1133928 // --- // --- // ---	-	q33.2
SNP_A-2095146	gtggaatgaattctta[C/T]ggtcaccattacaaag	C	T	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2093750	agaagagatcctagag[A/G]ccacctaatccaaact	A	G	64866 // Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, mRNA. /// NM_022842 //	CDCP1	CDCP1, Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, p21.31
SNP_A-2085886	actcggcatgcatgga[A/C]ctttcccaggcagtgt	A	C	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2069864	acacagcacaccttga[A/G]ccagtccttggaagat	A	G	Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000355755 // intron // 0 // --- //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2006067	accttctcacctccaa[A/T]ctcaacacaaatttct	A	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-2010080	caaattagtctatgcc[A/G]attgctaaatgtttac	A	G	Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // intron // 0	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2024671	aaaagtaagcattggc[A/G]caaggctagcctggat	A	G	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2289373	gattttagtgcattct[A/G]aagtttgagaaactag	A	G	Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // intron // 0 // --- // --- // --- // --- ///	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-2297984	gccataaacttttcca[C/T]tatctccaaaagtgtc	C	T	C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 //	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2262464	gaaatgggacttggca[A/G]ctgagtgactagattt	A	G	Homo sapiens zinc finger protein 509 (ZNF509), mRNA. /// ENST00000355834 // intron // 0 // --- // --- // --- // --- ///	ZNF509	ZNF509, Homo sapiens zinc finger protein 509 (ZNF509), p16.3
SNP_A-2268679	gaatgtgggatattca[A/C]acactgaattagtatt	A	C	// Homo sapiens sodium channel, voltage-gated, type IX, alpha (SCN9A), mRNA. /// NM_002976 // downstream //	SCN9A	SCN9A, Homo sapiens sodium channel, voltage-gated, type IX, alpha (SCN9A), q24.3
SNP_A-2287398	gatgttaaaagccata[C/G]agagttctcattattt	C	G	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1181862 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2248732	ctgttctaatactata[C/T]gctttgttgttcctcc	C	T	580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// NM_015657 // downstream // 354 //	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2247663	ctgtgaaaacctccgc[A/G]aatactgctgaggaaa	A	G	rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// NM_206953 // intron // 0 // Hs.30743 // PRAME	-	-, Human clone rev16,q11.22
SNP_A-2042204	aactataaaatagaaaa[A/G]tagactgccagcctgt	A	G	ENST00000356558 // intron // 0 // --- // --- // --- // ---	-	q32
SNP_A-1994240	aggaaactgagggaag[A/T]atgttttgtaaattta	A	T	SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 485063 // Hs.354013 //	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2057844	aatattagttatgatc[C/T]attgtgcctaaactcc	C	T	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 418673 // Hs.497822 // DUSP10 // 11221 //	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2050678	aaggcacttttagtta[C/T]aagtgatgctcaggag	C	T	// 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 800269 // --- // --- // --- //	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2089583	acttcagaggcttccc[G/T]aattgaatctttgtat	G	T	Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), mRNA. /// ENST00000266427 // intron // 0 // --- // --- // --- // ---	ETV6	ETV6, Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), p13.2
SNP_A-2102199	agatgtttttttatcaa[G/T]ttgaggaacttcccct	G	T	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 273868 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2196564	cattaaaatacccaaa[A/G]aggccggacacagtgg	A	G	9616 // Homo sapiens ring finger protein 7 (RNF7), transcript variant 1, mRNA. /// NM_183237 // downstream // 25994 //	RNF7	RNF7, Homo sapiens ring finger protein 7 (RNF7), transcript variant 1, q23
SNP_A-2199011	catttgggcagagcaa[C/G]agcgcctcagctcatc	C	G	154881 // Homo sapiens potassium channel tetramerisation domain containing 7 (KCTD7), mRNA. /// NM_014504 // upstream // 91896 // Hs.530053 // RABGEF1 // 27342 //	KCTD7	KCTD7, Homo sapiens potassium channel tetramerisation domain containing 7 (KCTD7), q11.21
SNP_A-2225083	cgtgtgcttgaacatc[A/G]atgatggccctgcttt	A	G	Homo sapiens cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA. ///	CDON	CDON, Homo sapiens cell adhesion molecule-related q24.2
SNP_A-1740713	catattgaatgaagaaaataacaac[C/T]gaagataaatgccttgatatcaccc	C	T	// cathepsin O /// NM_016205 // downstream // 777676 // Hs.43080 // PDGFC // 56034 // platelet derived growth factor	CTSO	CTSO , rs6820536, cathepsin O ,q32.1
SNP_A-1787600	gggacaaaacgctgat[C/T]aagcgctagaaaacag	C	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 459890 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1850152	tatgtggccctgagga[C/T]agcagaactcatctaa	C	T	// 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream //	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1822610	gtttttgctccttca[C/T]agcttcagtttgtacg	C	T	FLJ44048 // 401024 // Homo sapiens FLJ44048 protein (FLJ44048), mRNA. /// NM_018471 // upstream // 291711 //	FLJ44048	FLJ44048, Homo sapiens FLJ44048 protein (FLJ44048), q32.1
SNP_A-1834415	tacatttattattctc[C/T]agtgatccaaaagtct	C	T	Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // intron // 0 // Hs.410231 // C14orf118 // 55668 // Homo	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-1831967	taattgcttttggctc[A/G]aatttaacttttataa	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA. /// NM_013987 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, q26
SNP_A-1956718	ttttaaaatatcgtct[A/G]aagcagtttatttttaa	A	G	51084 // Homo sapiens crystallin, lambda 1 (CRYL1), mRNA. /// NM_006531 // upstream // 24044 // Hs.187376 // TTC10 //	CRYL1	CRYL1, Homo sapiens crystallin, lambda 1 (CRYL1), q12.11
SNP_A-1961884	acggccaaggatggga[C/T]gcaacctggctctgcc	C	T	sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1939249	ttgatcatcaacctaa[C/T]acaagacattgtggca	C	T	81696 // Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), mRNA. /// ENST00000230221 //	OR5V1	OR5V1, Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), p22.1
SNP_A-1983196	atttgaaaagaatata[A/G]taagtgaaagcataag	A	G	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1979931	aataataataattgga[A/C]aatatggagtaatagc	A	C	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 2141511 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-1978749	cttatcttactgtgcc[C/T]atgctatgtggcagtt	C	T	Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// ENST00000334383 // intron // 0 // --- // --- // --- // ---	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27
SNP_A-1966042	tcttctgtcacaactc[C/T]cttctgtacttcagga	C	T	sapiens titin (TTN), transcript variant N2-B, mRNA. /// NM_133437 // CDS // 0 // Hs.134602 // TTN // 7273 // Homo	TTN	TTN, Homo sapiens titin (TTN), transcript variant N2-B, q31.2
SNP_A-1965074	ttattaaatgcagtta[A/C]cataacatatattaga	A	C	/// ENST00000355063 // upstream // 634444 // --- // --- // --- //	-	q22.1
SNP_A-1895617	tgcctcatcagactga[C/T]taacttttcaatggcc	C	T	54622 // Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// NM_006308 // upstream //	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909511	tgtatttatgccaaag[A/C]atccttccctttcca	A	C	6461 // Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// NM_000692 // upstream // 79352 // Hs.436219 // ALDH1B1 // 219 // Homo	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-1917462	tgttttgtgtggagga[A/G]aaaggggggagtcagg	A	G	89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // downstream // 23524 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1913498	tgtggttagtcaagtc[C/G]atatctggaactcact	C	G	HSD17B2 // 3294 // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// NM_005792 //	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-1921974	ttactgaaaagagaga[A/G]agcagataataaaccc	A	G	7525 // Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), mRNA. /// NM_005433 // upstream // 82789 // Hs.194148 // YES1 // 7525 // Homo	YES1	YES1, Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), p11.32
SNP_A-1923985	ttagtgccaaagatta[G/T]agagacaagaagtaaa	G	T	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1923470	ttaggcatttatttac[A/G]cattggaactacagaa	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 427215 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1892817	tgcacatattttgaca[C/T]taggaagtgagtgagg	C	T	58155 // Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), mRNA. /// NM_000110 // downstream // 189721 //	PTBP2	PTBP2, Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), p21.3
SNP_A-1978316	ttgctgaatggtgtta[G/T]gtagattgatagtgag	G	T	1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 298230 //	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24
SNP_A-1988749	acagaagccagaaaga[C/T]tcgagagggtcaagag	C	T	// 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 835520 // --- // --- // --- //	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1956931	ttttaaggactcttca[C/T]tctcaccctcatgtcc	C	T	57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 89149 // --- // ---	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-1952583	tttctgcctctagcca[A/G]gatggagtaataggga	A	G	ENST00000333722 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-1824503	taaactggtgaaaata[A/T]ggatgaataaagaggg	A	T	Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // --- // --- // --- // ---	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-1827706	taacttacaagccaca[G/T]tcaagagggctttgga	G	T	80045 // Homo sapiens G protein-coupled receptor 157 (GPR157), mRNA. /// NM_004285 // upstream // 49291 //	GPR157	GPR157, Homo sapiens G protein-coupled receptor 157 (GPR157), p36.22
SNP_A-1852331	tattgttttatttcct[G/T]aagtagctgttctcaa	G	T	// Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1852173	tattgtaaattcctta[C/T]agacttaataccatct	C	T	Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 //	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-1847485	tatcctgagtaacaag[A/G]atgttatgatctcatc	A	G	sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// NM_001465 // intron // 0 // Hs.370503 // FYB // 2533 // Homo	FYB	FYB, Homo sapiens FYN binding protein (FYB-120,p13.1
SNP_A-1845125	tatacagtttctagga[C/T]aggcaaaattatggac	C	T	PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // upstream // 106089 // Hs.499705 //	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.2
SNP_A-1814384	gtgtgagagaagatac[A/G]aggccaaagtgatgag	A	G	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1723848	ttccttcaagaaatattaacaatta[A/G]aacacaagtaatcacataattgttc	A	G	1448 // casein kappa /// NM_033122 // upstream // 67371 // Hs.120316 // NYD-SP26 // 85438 // testis development	CSN3	CSN3 , rs10518070, casein kappa ,q13.3
SNP_A-1717657	agactcaaatgaaatgtatctctaa[C/T]ttaactttccctaaactggatcctt	C	T	NM_173538 // intron // 0 // Hs.246284 // FLJ35802 // 168975 // hypothetical protein FLJ35802	FLJ35802	FLJ35802 , rs982290, hypothetical protein FLJ35802,q21.3
SNP_A-2172616	caattgaggaagcagc[G/T]cttgtctttcccatct	G	T	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 314372 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2096695	agactaacacagcttc[C/T]aaacatactgaacttc	C	T	Homo sapiens zinc finger protein 560 (ZNF560), mRNA. /// ENST00000301480 // intron // 0 // --- // --- // --- // ---	ZNF560	ZNF560, Homo sapiens zinc finger protein 560 (ZNF560), p13.2
SNP_A-2049173	aagctacagagtaaaa[C/T]tgatgaaagtgaaaga	C	T	Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 //	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2
SNP_A-2070785	acactaatacttaata[C/T]ctacactaatactaat	C	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2003981	gtccagtcgtctgtac[C/T]gcgaagccttggccca	C	T	sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000262233 // intron // 0 // --- // ---	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2017361	cactgctttctgtgga[C/T]ggcggcggagctaaaa	C	T	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 254040 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2021214	aaaaaaagggatggag[A/G]ataggatgttgagtct	A	G	3482 // Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA. /// NM_153187 // upstream // 14806 //	IGF2R	IGF2R, Homo sapiens insulin-like growth factor 2 receptor (IGF2R), q25.3
SNP_A-2247738	ctgtgaccagttaaca[A/G]ctccttcatgaactgt	A	G	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2259369	gaaaaataatcgggaa[G/T]tatctcatcattttat	G	T	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2294949	gcataatagctattac[A/G]ctttctaaacaagtat	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 523258 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2293175	gcagagactcaaaaac[A/G]cagatgcccaaagggc	A	G	Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // intron // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-2310583	ggaagactagaggtgc[G/T]aggagacatggctcca	G	T	FLJ12584 // 80210 // Homo sapiens hypothetical protein FLJ12584 (FLJ12584), mRNA. /// NM_145236 // upstream //	FLJ12584	FLJ12584, Homo sapiens hypothetical protein FLJ12584 (FLJ12584), q37.1
SNP_A-2302409	gctaagtgtaaacaat[A/T]aacctgttctacctgg	A	T	// 9465 // Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, mRNA. /// NM_004842 // downstream // 127529 // Hs.486483 // AKAP7 // 9465 //	AKAP7	AKAP7, Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, q23.2
SNP_A-2259933	gaaaagtaacaatatc[A/C]aacgaatactaaacag	A	C	Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// ENST00000342505 // 3UTR // 0 // --- // ---	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-2262162	gaaatcagagatacct[A/C]accttcattttctgta	A	C	// 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 3725327 // --- // -	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2278620	gagctgctggaatgaa[C/T]tgaccagacaggacat	C	T	25865 // Homo sapiens protein kinase D2 (PRKD2), mRNA. /// ENST00000323617 // upstream // 8152 // --- // --- // --- // ---	PRKD2	PRKD2, Homo sapiens protein kinase D2 (PRKD2), q13.32
SNP_A-2274554	gagaaaaagtgtgcaa[A/C]agtagtaccagagcag	A	C	/// ENST00000355561 // upstream // 611267 // --- // --- // --- // -	-	q21.31
SNP_A-2236474	ctcggggaaatacggt[A/C]aattgtcctgtgacac	A	C	114899 // Homo sapiens C1q and tumor necrosis factor related protein 3 (C1QTNF3), mRNA. /// ENST00000231338 // upstream // 12684 // --- // --- // --- // --- ///	C1QTNF3	C1QTNF3, Homo sapiens C1q and tumor necrosis factor related protein 3 (C1QTNF3), p13.3
SNP_A-2104926	agcatcaagaagaaaa[C/T]agccaacacttccata	C	T	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 689575 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2104814	agcataagtttataca[C/T]gtgaaatataattcat	C	T	57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 500130 //	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-2157913	attgctcctgttgcaa[C/T]gtgttgacatctcttg	C	T	3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1007286 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2120697	agtccgctcagacaag[A/G]aaatcatcctgggata	A	G	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1652680	tgagaatttcgtttgttaggttgca[C/G]tgtcctccttggaagcaacttggaa	C	G	clone IMAGE:5277680, partial cds /// NM_030932 // downstream // 990752 // Hs.122164 // DIAPH3 // 81624 //	-	- , rs721697, CDNA clone IMAGE:5277680, partial cds ,q21.1
SNP_A-1687834	ataaaacaatttatttccttttaaa[C/G]tatgaaaatccaagagagatttctt	C	G	NM_001880 // intron // 0 // Hs.80285 // ATF2 // 1386 // activating transcription factor 2	ATF2	ATF2 , rs3755488, activating transcription factor 2,q31.1
SNP_A-1707733	tgttaagcatttagtctcatcacaa[A/T]ttctgttttagaaaaaaacaacaga	A	T	NM_004274 // intron // 0 // Hs.419136 // AKAP6 // 9472 // A kinase (PRKA) anchor protein 6	AKAP6	AKAP6 , rs719851, A kinase (PRKA) anchor protein 6,q12
SNP_A-1808280	atgttagattttggct[C/G]tgttctcaacttcttc	C	G	Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000299345 // intron // 0 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1787027	gggaaaccaaatctca[C/T]tcctgaggtctgcttt	C	T	ENST00000338200 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-1841058	tagcttaatcaggaca[A/G]gcctggttcagaattt	A	G	Homo sapiens DKFZP564M182 protein (DKFZP564M182), mRNA. /// ENST00000355674 // intron // 0 // --- // --- // --- // ---	RSL1D1	RSL1D1, Homo sapiens DKFZP564M182 protein (DKFZP564M182), p13.13
SNP_A-1954059	tttgatgaatttttaa[A/G]taaatagcaggctcag	A	G	/// ENST00000333948 // upstream // 494033 // --- // --- // --- // -	-	q31.2
SNP_A-1979010	gtgttgtgggacagcc[C/T]gaaaaccatcaaacat	C	T	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1879274	tcttagcatctccaca[A/G]tgcaaaggatgtcttc	A	G	Homo sapiens adaptor-related protein complex 3, sigma 2 subunit (AP3S2), mRNA. /// ENST00000336418 // intron // 0	AP3S2	AP3S2, Homo sapiens adaptor-related protein complex 3, sigma 2 subunit (AP3S2), q26.1
SNP_A-1923466	ttaggcatactaatca[C/G]aaagtccctctgtttt	C	G	// 9509 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // upstream // 136403 // Hs.120330 // ADAMTS2	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript q35.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1925625	ttatgagaaaatttcg[A/T]aagttccttctatccc	A	T	// 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 1111873 // --- // -	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1925851	ttatggcaaatgtata[A/G]aattgtataatataaa	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p14
SNP_A-1916657	tgtttattgagctcta[A/T]tacttgattcacagtg	A	T	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1916229	tgttggtgggtgtgta[A/C]attaattcaaccattg	A	C	341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 49447 // Hs.102971 // ALG10 //	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-1907882	tgtaatattaagcaac[C/T]agccattctttaccaa	C	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1910253	tgtccaaagggatgac[C/G]agagaaagtctagctc	C	G	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 236746 // Hs.17441	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-1910014	tgtcagtcaactgaaa[C/T]gtctcttggaagagaa	C	T	Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-1888879	tgaggtctattttcag[C/T]ccaaagagtcggcttc	C	T	8612 // Homo sapiens phosphatidic acid phosphatase type 2C (PPAP2C), transcript variant 3, mRNA. /// NM_177526 // upstream // 98636 // Hs.465506 // PPAP2C // 8612 // Homo	PPAP2C	PPAP2C, Homo sapiens phosphatidic acid phosphatase type 2C (PPAP2C), transcript variant 3, p13.3
SNP_A-1903362	tgggaaattatttaaa[C/T]gagttgatcatcaaac	C	T	27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 1145439 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1949262	tttatgtgctttttgg[A/G]catttggagaaaaaaa	A	G	/// ENST00000244032 // upstream // 3709 // --- // --- // --- // ---	-	q13.32
SNP_A-1943784	ttgtagcacttatgag[A/G]cctgtgagattgctag	A	G	Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA. /// ENST00000355999 //	STK39	STK39, Homo sapiens serine threonine kinase 39 (STE20,q24.3
SNP_A-1829761	taataaaatcttcaca[A/G]tgatttttcaacaaat	A	G	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1457692 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1815446	gtgttttattgggcaa[A/G]ccgtcctttctgcgtc	A	G	// 23779 // Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 3, mRNA. /// NM_017701 // upstream // 71655 // Hs.102336 // ARHGAP8 // 23779 //	ARHGAP8	ARHGAP8, Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 3, q13.31
SNP_A-1821901	gttttatgagagctac[A/G]atcgcagcagcagcag	A	G	sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // --- // --- // --- // --- /// ENST00000301226 // intron //	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-1849198	tatgctctggctattc[A/G]atgaaaaatgagtccc	A	G	Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 //	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-1805606	gtccatccatcctttc[A/T]ctgatctgtagctcag	A	T	55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000237194 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-2115519	aggggtctggttataa[C/G]tggaaggtgtcaaccc	C	G	143098 // Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), mRNA. /// NM_173496 // upstream // 149717 // Hs.499159 // MPP7 //	MPP7	MPP7, Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), p12.1
SNP_A-2108110	agctctgtaatttaaa[C/T]gatgattgtgctttta	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2132038	ataggctttgtataaa[A/T]aagatgtttgcacaac	A	T	DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, mRNA. /// NM_015496 // upstream // 36155 // Hs.202238 //	DKFZP434I116	DKFZP434I116, Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, q22.1
SNP_A-2142906	atgaataaagtttcag[C/G]catgcaagtaggcagg	C	G	ENST00000259793 // intron // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2173222	cacaacccccatgtta[A/G]agagatgttgataagg	A	G	sapiens hypothetical protein ET (ET), mRNA. /// ENST00000262771 // intron // 0 // --- // --- // --- // --- ///	ET	ET, Homo sapiens hypothetical protein ET (ET), q25.1
SNP_A-2194802	catgcctgcgccaaga[A/G]ggaatcctgaagaaag	A	G	5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 //	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.22
SNP_A-2193597	catcttagcaaagaca[C/T]aggaacgatctatgcg	C	T	80045 // Homo sapiens G protein-coupled receptor 157 (GPR157), mRNA. /// NM_004285 // upstream // 26936 //	GPR157	GPR157, Homo sapiens G protein-coupled receptor 157 (GPR157), p36.22
SNP_A-2183514	cagcagcactccctcc[A/G]cgtcacactcagacat	A	G	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2191205	catataacatctggca[A/G]catcctgaaatcacac	A	G	-- /// ENST00000344692 // upstream // 17629 // --- // --- // --- //	-	q22.1
SNP_A-2222772	cgatgtgaacgtcagg[A/T]aaaaatcctttctttt	A	T	91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. /// ENST00000324309 // intron // 0	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), p15.2
SNP_A-2215701	cctcagtttaatttca[C/T]tcatgtctgtggctac	C	T	Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA. /// NM_004904 // intron // 0 // Hs.437075 //	CREB5	CREB5, Homo sapiens cAMP responsive element binding protein 5 (CREB5), p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2205942	ccatataatttcatct[A/C]aaaaatgtatgcacat	A	C	4889 // Homo sapiens neuropeptide Y receptor Y5 (NPY5R), mRNA. /// NM_032136 // downstream // 88752 // Hs.303923	NPY5R	NPY5R, Homo sapiens neuropeptide Y receptor Y5 (NPY5R), q32.2
SNP_A-2208449	cccacccttgtaatga[A/G]gacatcaggctgtgca	A	G	ENST00000360575 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2211217	ccctaaagcaatatta[A/G]cagctctgtatttaga	A	G	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 12991 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2087518	actgcctgatacccca[C/T]atttagtcccagtcct	C	T	6478 // Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA. /// NM_052995 // downstream //	SIAH2	SIAH2, Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), q25.1
SNP_A-2074617	acatataattcacaca[A/G]caaatgaaacctagga	A	G	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2048547	aagcattacaccagaa[A/G]agtaaaccttacactg	A	G	3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 284530 // Hs.112783 // AIG1 // 51390 // Homo	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-2059109	aatccgtgataagata[C/T]ccaattcccagaaaaa	C	T	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, mRNA. /// NM_002816 // intron // 0 // Hs.4295 // PSMD12 //	PSMD12	PSMD12, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, q24.2
SNP_A-2024002	aaaagagaaaagaaaa[C/G]tcattaatgaaatgtt	C	G	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2025219	aaaatagtcattgccc[A/G]agattgccctccattt	A	G	/// ENST00000355232 // downstream // 5976 // --- // --- // --- // --- /// ENST00000358040 // downstream // 7889 // --- // --- // ---	-	q11.21
SNP_A-2012884	cccacccttgctaggc[A/T]aaattttccacttccc	A	T	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2254140	cttgataaccaaatac[A/G]gaattaaattgcttac	A	G	Homo sapiens PHD finger protein 7 (PHF7), transcript variant 2, mRNA. /// NM_016483 // intron // 0 // Hs.372719 // PHF7 //	PHF7	PHF7, Homo sapiens PHD finger protein 7 (PHF7), transcript variant 2, p21.1
SNP_A-2308713	gctttctgttctggca[A/C]ccctatgttctgtttg	A	C	ENST00000284630 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2310357	ggaactatctaggtag[C/T]attttgtccaatctaa	C	T	10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 //	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-2309291	ggaaaagatgccataa[C/T]gtaaaatgcctggggg	C	T	Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA. /// ENST00000307333 // intron // 0 // --- // --- // --- // ---	ANTXR2	ANTXR2, Homo sapiens anthrax toxin receptor 2 (ANTXR2), q21.21
SNP_A-2279640	gaggcactgtgtaaaa[C/T]gtatatggtattcaat	C	T	Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // ---	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-2280483	gagggttgttttggaa[A/G]ttacataagctaagtt	A	G	137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// ENST00000330777 // upstream // 18830 // --- // --- // --- // ---	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-2010189	tattgtctgtaatata[G/T]ctcagtctattttctt	G	T	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 213730 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2022221	aaaaaggtaataacac[C/T]cataatgtttgaaaca	C	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-2030679	aaagctgagggttcct[A/G]aagtacagcactaggt	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 101518 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2064915	aattgacttgaagaaa[A/T]ggtctaaagcagttta	A	T	Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2085530	actccagggacttaag[A/C]acattgatgcttctat	A	C	-- /// ENST00000341636 // upstream // 182086 // --- // --- // ---	-	q11.2
SNP_A-2078371	accatcaacataccaa[C/T]cacagcgcacagacta	C	T	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 1098353	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2103061	agcaaatcacagctgc[A/G]caatgtactacagcac	A	G	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 203078 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2099733	agaggtttaatggaca[C/G]atagttcctcgtggct	C	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 76799 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.3
SNP_A-2223226	cgcctggcacaacgcc[A/G]aatttttaaaactaca	A	G	Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2195780	catgtactatacacac[A/C]ctacacataccgtgga	A	C	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 188872 // --- // --- // --- // ---	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2169074	caagataaagacgaag[A/T]accggaaagaggtaag	A	T	sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // --- // --- // --- // ---	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787906	gggactggtcaggagg[A/G]caatggagccaataca	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1857202	tcacctggcgaagaac[C/T]gggactaaagggctgt	C	T	10971 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation	YWHAQ	YWHAQ, Homo sapiens tyrosine 3-monooxygenase,p25.1
SNP_A-1832995	tacacaatgggaaaca[A/G]ggacttcaaacaacat	A	G	Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA. /// ENST00000244040 // 3UTR // 0 // --- //	RAB22A	RAB22A, Homo sapiens RAB22A, member RAS oncogene family (RAB22A), q13.32
SNP_A-1835197	taccgcttatggcagg[A/C]aagttaaaggaggctt	A	C	51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 65545 // Hs.491997 // EYA1	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3
SNP_A-1958190	ttttcattacttctaa[A/G]ggtaggaatcgcaccc	A	G	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1024762 // Hs.27214 // KCNC2	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1978920	ttcctgctaagatgcc[A/G]cactgagatttgtctg	A	G	-- /// ENST00000357636 // upstream // 1349804 // --- // --- // --- // --- /// ENST00000357643 // upstream // 1350449 // --- // --- //	-	q28.2
SNP_A-1979961	gccagctatttaagag[A/G]ctccattctgcctctt	A	G	10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// NM_012180 // downstream // 212722 // Hs.76917 // FBXO8 //	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-1964288	ttaaactcttctctac[A/G]cctttgtgtcccaaac	A	G	8808 // Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), mRNA. /// NM_016232 // upstream // 50402 // Hs.66 //	IL1RL2	IL1RL2, Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), q11.2
SNP_A-1890504	tgatctgggaatggaa[A/G]tcccacactatcgtga	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA. /// NM_130435 // CDS // 0 // Hs.127022 // PTPRE // 5791 // Homo sapiens protein	PTPRE	PTPRE, Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, q26.2
SNP_A-1876032	tctgaataaaaggtca[C/T]caccatttgtatttta	C	T	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_005228 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-1909711	tgtcaatagcctacaa[C/T]ctgcaataaactatta	C	T	MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-1928954	ttcagcagaaaggaaa[A/G]gagaccacaagattca	A	G	Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // intron // 0 // Hs.268942 // ATP2B2 // 491 //	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-1879098	tcttaattaacttgca[C/T]atccactcaccagtaa	C	T	ENST00000317931 // intron // 0 // --- // --- // --- // ---	-	p11.31
SNP_A-1878665	tctgttacataagaga[G/T]ctgtaagtattgtacc	G	T	Homo sapiens chromogranin B (secretogranin 1) (CHGB), mRNA. /// ENST00000203005 // intron // 0 // --- // --- // --- // ---	CHGB	CHGB, Homo sapiens chromogranin B (secretogranin 1) (CHGB), p12.3
SNP_A-1972578	gaaaaaactaatacaa[C/T]ctaccgacaactttaa	C	T	8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 32696 // Hs.413095	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-1984390	gttttgttaacatagg[C/T]acatcatcacagggtt	C	T	Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-1950538	tttcatatctttttatc[C/T]cacattttctaggaac	C	T	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-1952528	tttctgatcttatact[A/T]acatttcatactcatt	A	T	// 27309 // Homo sapiens zinc finger protein 330 (ZNF330), mRNA. /// NM_000585 // upstream // 367396 // Hs.311958 //	ZNF330	ZNF330, Homo sapiens zinc finger protein 330 (ZNF330), q31.21
SNP_A-1815761	gttaagatgcaggaat[A/G]agaatgtgaggacaca	A	G	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m /// NM_020416 // intron // 0 // Hs.479069 // PPP2R2C // 5522 // Ho	PPP2R2C	PPP2R2C, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m ,p16.1
SNP_A-1853342	tattttattttaatcc[A/T]cttaacttgatatgct	A	T	ENST00000334567 // intron // 0 // --- // --- // --- // ---	-	q26.31
SNP_A-1860294	tcagtgaatacatggg[A/G]aagactcagtatgcca	A	G	143279 // Homo sapiens HECT domain containing 2 (HECTD2), transcript variant 2, mRNA. /// NM_182765 // downstream // 12682 // Hs.66378 // HECTD2 // 143279 //	HECTD2	HECTD2, Homo sapiens HECT domain containing 2 (HECTD2), transcript variant 2, q23.32
SNP_A-2196053	catgtcttctctgagt[C/T]acccaaccaagtatca	C	T	Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // --- // --- // --- // ---	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3), p13.3
SNP_A-2212232	ccctggattttattca[A/C]tatttcacaggtcaaa	A	C	9398 // Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA. /// NM_003594 // upstream // 2904 //	IGSF2	IGSF2, Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), p13.1
SNP_A-2161373	atttgcagaactagga[A/G]atgaggtacacgagag	A	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2126539	ataaaatctaagccaa[C/G]agatatatcacctcat	C	G	55920 // Homo sapiens RCC1-like (TD-60), mRNA. /// ENST00000325766 // upstream // 71385 // --- // --- // --- // ---	TD-60	TD-60, Homo sapiens RCC1-like (TD-60), p36.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2122929	agtggcttaattttca[C/T]gatagccagaacagat	C	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2057655	aatatgcttaggggaa[C/G]tacttgttcaatctct	C	G	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 369998 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2021998	aaaaagaatgggaatc[A/G]aattgacctcagacta	A	G	ENST00000361104 // intron // 0 // --- // --- // --- // ---	-	p36.32
SNP_A-2021804	aaaaaccagaatatct[A/G]aagtagaggtgactga	A	G	ENST00000355802 // upstream // 58895 // --- // --- // --- // --- /// ENST00000358682 // upstream // 58911 // --- // --- // --- // ---	-	q13.3
SNP_A-2037036	aacaaaaaagaccgaa[A/T]taatagacactgacta	A	T	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 169281 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3
SNP_A-2005907	actgttttgagaaata[C/G]cggtcaggcattttgt	C	G	63877 // Homo sapiens chromosome 10 open reading frame 84 (C10orf84), mRNA. /// NM_004248 // downstream //	C10orf84	C10orf84, Homo sapiens chromosome 10 open reading frame 84 (C10orf84), q26.11
SNP_A-1997481	aaatagtcaaatacaa[C/T]gaaatgtgcaaactag	C	T	138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 3102 // --- // OR13C2 //	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-2286292	gatgcctcaccctgat[A/G]actcgatttaacttgg	A	G	54888 // Homo sapiens NOL1/NOP2/Sun domain family 2 (NSUN2), mRNA. /// ENST00000338486 // downstream //	NSUN2	NSUN2, Homo sapiens NOL1,p15.31
SNP_A-2285569	gatgaaatcagttgat[A/G]agagtcttgtataagg	A	G	Homo sapiens neurocalcin delta (NCALD), mRNA. /// ENST00000311028 // intron // 0 // --- // --- // --- // --- ///	NCALD	NCALD, Homo sapiens neurocalcin delta (NCALD), q22.3
SNP_A-2265540	gaagcctacttccaaa[C/T]gccacagctggaacca	C	T	51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 47572 // Hs.491997 // EYA1	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3
SNP_A-2275889	gagactcggggcaagg[C/T]aaatatgtccttcaat	C	T	23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 424552	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2272948	gactactttaattcac[A/T]aacacactgtttaatc	A	T	// Homo sapiens neurogenic differentiation 4 (NEUROD4), mRNA. /// ENST00000242994 // intron // 0 // --- // --- // --- // ---	NEUROD4	NEUROD4, Homo sapiens neurogenic differentiation 4 (NEUROD4), q13.2
SNP_A-2237853	ctctgaagcctcttct[C/G]acttccttgggtatgt	C	G	54209 // Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA. /// NM_024807 //	TREM2	TREM2, Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), p21.1
SNP_A-2308707	gctttctgcttgatca[C/T]ggggtctactgggact	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1996960	aatgttatgtaagaaa[A/G]tgttgcatgtaaaccc	A	G	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1627176 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2022915	aaaacaaggatgcaaa[A/C]aactacaaagtgcaat	A	C	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2070706	aatgaggtgtttatca[C/G]gaatctgttcacctat	C	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 340043 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2105775	agccaggagcccctcc[C/T]agtgtgtcatcatcca	C	T	2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 11033 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-2085002	actcacatgattaaag[A/T]cacatggctgtgagca	A	T	Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // intron // 0 // --- // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-2090670	actttaaggactaaca[C/T]cttctcttgctgttat	C	T	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2117576	aggttaatttctgcca[C/T]caatgtaaatgagttg	C	T	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2000640 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2124686	agttctcagctattga[C/G]atctttcttttacctt	C	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2180539 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2132628	atagttgatgatgata[C/T]accatattcttgaaaa	C	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2166570	caaatggtgactgaca[C/T]agtttttggtattaac	C	T	5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // upstream // 231296 // Hs.498570 //	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-2145423	atgcagccatacataa[A/G]tgatgtaactgatact	A	G	147172 // Homo sapiens hypothetical protein DKFZp667M2411 (DKFZp667M2411), mRNA. /// ENST00000355391 // intron // 0 // --- // --- // --- // ---	DKFZp667M2411	DKFZp667M2411, Homo sapiens hypothetical protein DKFZp667M2411 (DKFZp667M2411), q11.2
SNP_A-2207391	ccattgcagggaaaca[A/C]agggactgccaaattg	A	C	10651 // Homo sapiens metaxin 2 (MTX2), transcript variant 1, mRNA. /// ENST00000249442 // downstream // 118925 // --	MTX2	MTX2, Homo sapiens metaxin 2 (MTX2), transcript variant 1, q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2205668	ccataaaatctatgcg[A/G]aaatggttgttatttt	A	G	// 221823 // Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), mRNA. /// NM_014707 // upstream // 152005 // Hs.196054 // HDAC9 // 9734 // Homo	PRPS1L1	PRPS1L1, Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), p21.1
SNP_A-2196717	cattaattgtcattta[A/T]acacttgtattaactc	A	T	// Homo sapiens hypothetical protein FLJ35880 (FLJ35880), mRNA. /// ENST00000312481 // intron // 0 // --- // --- // --- // ---	FLJ35880	FLJ35880, Homo sapiens hypothetical protein FLJ35880 (FLJ35880), q21.3
SNP_A-2183953	cagccaggcactctta[C/T]atcttcagctcaccct	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2170348	caagtagccaaatata[C/T]gtgtgattgaagtgcc	C	T	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream //	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-1841299	taggaagcaggaagta[C/T]gtgatatcagctctct	C	T	Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, mRNA. /// NM_175605 // intron // 0 //	TTC10	TTC10, Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, q12.11
SNP_A-1793612	ggtatcctgttcagca[C/T]tagcagcagcatagaa	C	T	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 476220 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1798126	gtaaacaaaattcaaa[A/G]catttgtcatatgtga	A	G	Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), transcript variant 2, mRNA. /// NM_001001548 // intron // 0 // Hs.120949 // CD36	CD36	CD36, Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), transcript variant 2, q21.11
SNP_A-1805026	gtcatctattgcccca[G/T]cacttaaaggttttta	G	T	ENST00000334904 // intron // 0 // --- // --- // --- // ---	-	q31.3
SNP_A-1728747	ccactctctctcctgtgcttgctga[C/G]cagccttgggcatgttcctcaattg	C	G	NM_177964 // upstream // 40887 // Hs.357567 // LOC130576 // 130576 // hypothetical protein LOC130576	-	- , rs10497050, - ,q23.1
SNP_A-1756309	tcttctacactggttcagagtatac[A/C]caaaacaattcttaaagactgaaat	A	C	NM_016441 // upstream // 350666 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs10495857, cysteine-rich motor neuron 1,p22.3
SNP_A-1952851	tttcttaattgtcaaa[G/T]gatttttgctctgtgt	G	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1960590	tttttcattgtcagaa[A/G]tctttgtacttttgag	A	G	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// ENST00000264377 // intron // 0 // --- //	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-1984016	tatgtaatatctgagc[A/G]agggactctcctatga	A	G	2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// NM_003118 // downstream //	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-1882082	tctttttaccgcccta[C/T]ctttattgtcagtggt	C	T	655 // Homo sapiens bone morphogenetic protein 7 (osteogenic protein 1) (BMP7), mRNA. ///	BMP7	BMP7, Homo sapiens bone morphogenetic protein 7 (osteogenic protein 1) (BMP7), q13.31
SNP_A-1892390	tgcaagccttagaaac[C/T]ggatgaaattctgact	C	T	// 60487 // Homo sapiens chromosome 6 open reading frame 75 (C6orf75), mRNA. /// NM_032784 // upstream // 916290 //	C6orf75	C6orf75, Homo sapiens chromosome 6 open reading frame 75 (C6orf75), q22.32
SNP_A-1926736	ttattgggaatcccca[A/T]gccacagaaagctatg	A	T	// 11156 // Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, mRNA. /// NM_032611 // downstream // 216008 // Hs.43666 // PTP4A3	PTP4A3	PTP4A3, Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, q24.3
SNP_A-1927417	ttcaaaggacatgaat[C/T]actgggactctgcaaa	C	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1904677	tgggggagaaaaagcc[C/T]ctgggtaccacatgct	C	T	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1755099 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1911646	tgtgaaatgtcaggga[A/C]gggccagatcagggat	A	C	Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 3 (CHRNA3), mRNA. /// ENST00000348639 //	CHRNA3	CHRNA3, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 3 (CHRNA3), q25.1
SNP_A-1895047	tgcccagccatatctc[C/T]ataactttaaggggta	C	T	Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // --- // --- // --- // ---	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-1898877	tgcttttatacttttg[A/T]attgttcacttagtgc	A	T	Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, mRNA. /// NM_012428 // intron // 0 // Hs.187866 // SDFR1 // 27020 // Homo sapiens	SDFR1	SDFR1, Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, q24.1
SNP_A-1984357	ccagtatttaatctga[C/G]acatttgatcttcatt	C	G	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 618156 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1977381	ttagacaaaatgaggg[A/G]atgcagaatgttatta	A	G	/// ENST00000360919 // upstream // 1957797 // --- // --- // --- //	-	q13.1
SNP_A-1965179	gttaactgacataaca[C/T]tgaaatcaaagactcc	C	T	// Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // ---	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.2
SNP_A-1967526	gggaacactcaggtgg[A/G]aaaaattcacatagtg	A	G	Homo sapiens hypothetical protein MGC35023 (MGC35023), mRNA. /// ENST00000318405 // downstream // 4284 // --- // ---	-	-, Homo sapiens hypothetical protein MGC35023 (MGC35023), p12.3
SNP_A-1958385	ttttccctctatacta[C/G]gtgcacttggtaatta	C	G	23520 // Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), mRNA. /// ENST00000330241 // upstream // 292193 // --- // --- // --- // ---	ANP32C	ANP32C, Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), q32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802660	gtatgaattaaaggaa[C/G]agatgaggaaatatgt	C	G	79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA. /// Y15723 // upstream // 217496 //	FLJ21159	FLJ21159, Homo sapiens hypothetical protein FLJ21159 (FLJ21159), q32.1
SNP_A-1814576	gtgtggaaggaaatga[G/T]acatggcagagtcctg	G	T	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-1813707	gtgtactttattttca[A/G]gggtcagatttttct	A	G	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // --- ///	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1789668	gggctaggacaggtaa[C/G]aagtgagcaggagtct	C	G	// 64098 // Homo sapiens parvin, gamma (PARVG), mRNA. /// NM_022141 // downstream // 62625 // Hs.546422 //	PARVG	PARVG, Homo sapiens parvin, gamma (PARVG), q13.31
SNP_A-1855523	tcaagttcccacagga[A/G]aatcacaatggagttt	A	G	// 55693 // Homo sapiens jumonji domain containing 2D (JMJD2D), mRNA. /// AB020637 // upstream // 16301 //	JMJD2D	JMJD2D, Homo sapiens jumonji domain containing 2D (JMJD2D), q21
SNP_A-1848692	tatgaggaactagaca[C/T]tattgggaaatgtaca	C	T	Homo sapiens FCH domain only 1 (FCHO1), mRNA. /// ENST00000252771 // intron // 0 // --- // --- // --- // ---	FCHO1	FCHO1, Homo sapiens FCH domain only 1 (FCHO1), p13.11
SNP_A-1850216	tatgtgtgggtaaaac[C/T]aaaatgattgacatgg	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1241711	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1844530	tataaatgcaacaaca[A/G]taagtatgaacagtca	A	G	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 99444 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1847010	tatcaggcatttaatc[A/T]atccttaactgatgat	A	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2174996	cacaggtgtgattaag[A/T]catgagttacgtgtcc	A	T	// 112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-2176603	cacccatgcccactga[A/G]catctctaaattcatg	A	G	7525 // Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), mRNA. /// NM_005433 // upstream // 28994 // Hs.194148 // YES1 // 7525 // Homo	YES1	YES1, Homo sapiens v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), p11.32
SNP_A-2211239	ccctaactacaaagtc[G/T]ccagttttccaaagaa	G	T	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 314530 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-2121191	agtctgctgggcctta[C/G]ctgggtactctctgtc	C	G	// 26953 // Homo sapiens RAN binding protein 6 (RANBP6), mRNA. /// ENST00000329294 // upstream // 20477 // --- // ---	RANBP6	RANBP6, Homo sapiens RAN binding protein 6 (RANBP6), p24.1
SNP_A-2110876	aggactgggctgaatc[C/T]cagcagcatatgcttt	C	T	sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // --- // --- // --- // ---	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-2095612	agacaatttcatcttg[A/G]aagagactatgttaca	A	G	79782 // Homo sapiens hypothetical protein FLJ23259 (FLJ23259), mRNA. /// NM_182610 // upstream // 2981 //	LRRC31	LRRC31, Homo sapiens hypothetical protein FLJ23259 (FLJ23259), q26.2
SNP_A-2098270	agagatgaaatcatta[C/T]acaggtggagaaaatt	C	T	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2064002	aattatgatggtaaga[A/G]gaacctgacactgttg	A	G	/// ENST00000359604 // upstream // 340936 // --- // --- // --- // --- /// ENST00000344172 // upstream // 251679 // --- // --- // ---	-	q11.2
SNP_A-2066617	acaaaaataatcacat[G/T]agttctacagaggtga	G	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 936091 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2055847	aatacaactgaatggc[C/T]cttatcaatgtgcaat	C	T	89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// NM_005639 // upstream // 453199 // Hs.310545 // SYT1 //	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2053021	aagtcctatcacctcc[A/G]ctggaagctgtatttg	A	G	Homo sapiens cyclin T2 (CCNT2), transcript variant a, mRNA. /// NM_058241 // intron // 0 // Hs.292754 // CCNT2 //	CCNT2	CCNT2, Homo sapiens cyclin T2 (CCNT2), transcript variant a, q21.3
SNP_A-2030865	aaaggaacaatctaca[A/C]aacaaccagaaaataa	A	C	// 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1361606 // Hs.98262 // GRIK2	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2038013	aacacaacagaaatgc[A/G]aataatcacaacatag	A	G	1139 // Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 7 (CHRNA7), mRNA. /// NM_148911 // upstream	CHRNA7	CHRNA7, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 7 (CHRNA7), q13.3
SNP_A-1996751	actgtagaggcccaat[A/G]aatgctggctgatatt	A	G	Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // intron // 0 // Hs.47288 // TRPM3 // 80036 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.11
SNP_A-2006028	attcatggcataagaa[A/G]tagtttataagtccac	A	G	2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // downstream // 53618 // Hs.533683 // FGFR2 /	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2240989	ctgagatgatctatta[C/T]gtttgttatttgtttt	C	T	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2254577	cttgctcacaacctca[C/G]tcttggcaagtattag	C	G	163589 // Homo sapiens tudor domain containing 5 (TDRD5), mRNA. /// AK092142 // downstream // 30202 // Hs.197354 //	TDRD5	TDRD5, Homo sapiens tudor domain containing 5 (TDRD5), q25.2
SNP_A-2283561	gatagaaaatagccta[C/T]agttggcccttagtat	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2286332	gatgcgtggggagatc[A/G]cttcagcttaggagtt	A	G	Homo sapiens myotubularin related protein 4 (MTMR4), mRNA. /// ENST00000323456 // intron // 0 // --- // --- // --- // ---	MTMR4	MTMR4, Homo sapiens myotubularin related protein 4 (MTMR4), q23.2
SNP_A-2275943	gagactggtagcagaa[A/G]gagagagcaaatagca	A	G	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2271274	gacatgtggcatgatg[A/T]acaaccctgtcatttt	A	T	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2229806	ctagtggtcaatgtcc[C/T]aaagaaaataaagtgt	C	T	114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 323871 // Hs.204564 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2314142	ggaggagacacaagca[G/T]tccataatagttggtg	G	T	// 285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 218231 // ---	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-2292074	gcaccaccacacacca[C/G]ctacaatgctacactg	C	G	Homo sapiens FXYD domain containing ion transport regulator 6 (FXYD6), mRNA. /// ENST00000260282 // intron // 0 // --- // --- // --- // --- /// ENST00000355741 // intron // 0 // --- //	FXYD6	FXYD6, Homo sapiens FXYD domain containing ion transport regulator 6 (FXYD6), q23.3
SNP_A-2300014	gcctatttaagataca[C/T]cccatacttcagatgt	C	T	5155 // Homo sapiens platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), transcript /// NM_033016 // upstream // 18783 // Hs.1976 // PDGFB // 5155 /	PDGFB	PDGFB, Homo sapiens platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), transcript ,q13.1
SNP_A-2298181	gccatctttaatattc[C/T]agaccatttgagtaac	C	T	23169 // Homo sapiens solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual	SLC35D1	SLC35D1, Homo sapiens solute carrier family 35 (UDP-glucuronic acid,p31.2
SNP_A-1994192	agttcaagtatccata[A/C]ctctttcccctgagca	A	C	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 913253 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2037092	aacaaaacagagaaac[A/G]gaaaatagtaaataca	A	G	// Homo sapiens glycoprotein hormones, alpha polypeptide (CGA), mRNA. /// AB011102 // upstream // 28908 //	CGA	CGA, Homo sapiens glycoprotein hormones, alpha polypeptide (CGA), q15
SNP_A-2022415	aaaaatagggaggtcca[C/T]actgagttagaagaaa	C	T	// 26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 460344 //	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13
SNP_A-2019356	aaaactccagggaaga[C/T]gccagtgaattagagg	C	T	/// ENST00000333546 // upstream // 73051 // --- // --- // --- // ---	-	q22.2
SNP_A-2096432	agaccctggaacaaga[A/G]aaggacaccaggtaaa	A	G	// 56951 // Homo sapiens chromosome 5 open reading frame 15 (C5orf15), mRNA. /// ENST00000231482 // downstream //	C5orf15	C5orf15, Homo sapiens chromosome 5 open reading frame 15 (C5orf15), q31.1
SNP_A-2085941	actctaagctacttcc[A/G]caagcaacccatcagc	A	G	339669 // Homo sapiens hypothetical protein MGC35206 (MGC35206), mRNA. /// NM_003312 // downstream // 2070 //	MGC35206	MGC35206, Homo sapiens hypothetical protein MGC35206 (MGC35206), q12.3
SNP_A-2136639	atcactcaccaaccac[C/T]gagctacagatagcag	C	T	/// ENST00000242916 // upstream // 702999 // --- // --- // --- // -	-	p14
SNP_A-2129371	atacaagagacagaca[A/G]taaatataagacacaa	A	G	Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA. /// ENST00000353809 // intron // 0 // --- // --- // --- // --- /// ENST00000354638 // intron //	OCA2	OCA2, Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), q13.1
SNP_A-2171226	caatatatacttaata[A/C]actctgccaaataaca	A	C	Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 //	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-2190285	cataatgtgattatag[A/C]ctagcttggacttcac	A	C	Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // intron // 0 // --- // --- // --- // ---	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1866650	tcccctaagtgtccac[A/G]gatggatggaacagag	A	G	60529 // Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // upstream // 222793 // Hs.436055 //	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds. p11.2
SNP_A-1799021	gtaagccatcaagggc[A/G]cttctttgtagcctct	A	G	Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // --- // --- // --- // ---	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3
SNP_A-1800025	gtacatcttcactgat[C/T]agccttcgctcaggtg	C	T	91869 // Homo sapiens putative endoplasmic reticulum multispan transmembrane protein (RFT1), mRNA. /// NM_212539 // upstream // 15469 // Hs.155342 // PRKCD //	RFT1	RFT1, Homo sapiens putative endoplasmic reticulum multispan transmembrane protein (RFT1), p21.1
SNP_A-1784766	ggcctggaagacatta[C/T]gtaaaatgaaattagc	C	T	ENST00000272907 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-1699865	cttccttcccactgagcaaagaaac[A/G]aaataaagttgctagagatataacc	A	G	9314 // Kruppel-like factor 4 (gut) /// NM_006686 // downstream // 878844 // Hs.31323 // IKBKAP // 8518 //	KLF4	KLF4 , rs10521086, Kruppel-like factor 4 (gut) ,q31.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1682700	caggccaatctggaagataaaaaag[C/G]caaggtagattcaaatgtaggaggt	C	G	// 3105 // major histocompatibility complex, class I, A /// NM_002127 // downstream // 225327 // Hs.512152 // HLA-G	HLA-A	HLA-A , rs6917477, major histocompatibility complex, class I, A ,p22.1
SNP_A-1955495	tttggtctatttgtca[C/T]gtgcatcggcatcccc	C	T	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA. /// ENST00000280979 // intron // 0 // --- // --- // --- // ---	AKAP6	AKAP6, Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), q12
SNP_A-1949821	tttcaaattagatgtg[A/G]attcttccacttttttt	A	G	sapiens mRNA; cDNA DKFZp761C2021 (from clone DKFZp761C2021). /// NM_024612 // upstream // 37932 //	-	-, Homo sapiens cDNA DKFZp761C2021 (from clone DKFZp761C2021). ,q23.2
SNP_A-1950097	tttcacccaggaggcc[A/G]ccccaagagtttaaca	A	G	23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 233680 // Hs.166017 //	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. p14.1
SNP_A-1972552	tctaagagtgacaaga[A/G]gctataagggaaatag	A	G	356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 //	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-1977882	attctgggctcaacaa[C/T]agtaagtaggcttgtc	C	T	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1978951	tctataaagacaatac[G/T]agagctaaacaatgac	G	T	-- /// ENST00000357643 // downstream // 37415 // --- // --- // --- // --- /// ENST00000358710 // upstream // 23273 // --- // --- // ---	-	q28.3
SNP_A-1894006	tgcatcatgaacccaa[C/T]ggactctttttttct	C	T	ENST00000328457 // intron // 0 // --- // --- // --- // ---	-	p13.1
SNP_A-1883131	tgaaatgacccataag[A/G]aaagaacaatgcagtt	A	G	Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA. /// ENST00000357759 // intron // 0 // --- // --- // --- // --- ///	HHLA2	HHLA2, Homo sapiens HERV-H LTR-associating 2 (HHLA2), q13.13
SNP_A-1879835	tcttccatctgcaaga[A/C]gaagattgctgactct	A	C	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1221288 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1927731	ttcaagagagtgtata[A/C]aaagaaaggctccata	A	C	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 7 (SLC16A7), mRNA. /// ENST00000261187 // intron // 0 // --- // --- // --- // --- ///	SLC16A7	SLC16A7, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 7 (SLC16A7), q14.1
SNP_A-1929658	ttcatatatttgtctg[A/C]atagagtgctgaggtc	A	C	// 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream // 348891 // Hs.12420 // PHF17 // 79960 // Homo sapiens	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-1921621	ttaccttatttggcca[C/T]ataaaagtttgactgc	C	T	// 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-1892399	ttccatataaattaca[C/T]ctcagaaaagttaatt	C	T	284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// NM_001650 // downstream // 128038 // Hs.315369 // AQP4 // 361 // Homo	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-1893481	tgcagcttttctgccc[C/T]gaatgagttctgagtt	C	T	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1698795 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1890850	tgatgccccttgatgc[A/G]actgtccctccaccag	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. ///	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-1974514	gaaggtcactaggtaa[A/G]gcttgctgactggtga	A	G	8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream //	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-1951944	tttctagaatttttta[G/T]agcttgcatcattcaa	G	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1955815	tttgtatagcgtcaac[C/T]gaagaatactttaaaa	C	T	6101 // Homo sapiens retinitis pigmentosa 1 (autosomal dominant) (RP1), mRNA. /// ENST00000220676 //	RP1	RP1, Homo sapiens retinitis pigmentosa 1 (autosomal dominant) (RP1), q12.1
SNP_A-1757431	aggatattatataatgataaaggga[C/T]acatttcaccaaaagatataaccac	C	T	1016 // cadherin 18, type 2 /// NM_006317 // downstream // 1665203 // Hs.511745 // BASP1 // 10409 // brain abundant,	CDH18	CDH18 , rs4131714, cadherin 18, type 2 ,p14.3
SNP_A-1715011	taattttattataacttcttaaaga[C/T]gactgaagcaataaagcatagtgcc	C	T	NM_001175 // intron // 0 // Hs.292738 // ARHGDIB // 397 // Rho GDP dissociation inhibitor (GDI) beta	ARHGDIB	ARHGDIB , rs10492145, Rho GDP dissociation inhibitor (GDI) beta,p12.3
SNP_A-1813107	gtggtacaagcaggca[C/T]tagtttcatgggggtc	C	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1845577	tatagcacttttaaga[C/T]tatggaatgtagaatg	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2186700	cagggccttaggtgtc[C/T]caggaagagattggtc	C	T	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2195640	catggtgtggaaaaga[C/G]ctttatttttttgagga	C	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2178244	cactcaaccctgtcta[C/T]ctttggttcttgactg	C	T	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2201353	ccaatcatgattgccc[C/T]aaatggctctcactct	C	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2222984	cgcaggccaaaactca[A/T]aactcatatgctgtgt	A	T	3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1007475 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2138397	atccagtctccttaaa[C/T]tagtcagactgcctgt	C	T	// 55704 // Homo sapiens KIAA1212 (KIAA1212), mRNA. /// NM_080667 // upstream // 84317 // Hs.264208 // MGC15407	KIAA1212	KIAA1212, Homo sapiens KIAA1212 (KIAA1212), p16.1
SNP_A-2159225	atttaaagtttactgg[G/T]cattgaacaaagaaag	G	T	// 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 352199 // Hs.399984 //	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-2153758	attagtcatatgttct[A/G]aaaatataccatgtag	A	G	/// ENST00000359050 // upstream // 158395 // --- // --- // --- // --- /// ENST00000339373 // downstream // 301383 // --- // --- //	-	q14.3
SNP_A-2038334	aacacgataataggaa[C/G]aaatctacaaatatca	C	G	23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // upstream // 259511 // --- // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-2010243	cacaacagtttacgcc[A/G]accatctgtgtctgca	A	G	// 166614 // Homo sapiens hypothetical protein MGC45428 (MGC45428), mRNA. /// ENST00000335031 // upstream //	DCAMKL2	DCAMKL2, Homo sapiens hypothetical protein MGC45428 (MGC45428), q31.23
SNP_A-2292504	gcactcagttggctga[C/T]agttttaatatgcctg	C	T	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 213947 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2291494	gcaatttccatcaaaa[A/T]tagcaggtagcggagt	A	T	2053 // Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), mRNA. /// NM_001831 // downstream // 28375 //	EPHX2	EPHX2, Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), p21.1
SNP_A-2228812	ctagagctagaaagca[C/T]aggataatgttataat	C	T	// 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 53328 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2241603	ctgataccaagctatc[A/G]gagaaaaagttaaaca	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2246821	ctgtagctcaacttca[C/T]tagtagagtaagcccc	C	T	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_022788 // intron // 0 // Hs.532933 // P2RY12 // 64805 //	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2238789	ctcttagaaacagcca[C/T]tcttaaatcttaaagc	C	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2269193	gaattgtgatataacc[A/G]ctagagtgactatccc	A	G	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 16430 // --- // --- // --- // ---	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2291612	gcacaaggtactgact[A/G]aaatggcctgaataaa	A	G	Homo sapiens development and differentiation enhancing factor 2 (DDEF2), mRNA. /// ENST00000281419 // intron // 0 // --- // --- // --- // --- /// ENST00000315273 // intron // 0 // --- // ---	DDEF2	DDEF2, Homo sapiens development and differentiation enhancing factor 2 (DDEF2), p25.1
SNP_A-2287744	gattacctcagccaaa[C/G]tgccttctgaaatggt	C	G	3187 // Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA. /// ENST00000356705 // upstream // 1525 // --- // --- // --- // --- ///	HNRPH1	HNRPH1, Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), q35.3
SNP_A-2310467	ggaactttcttatcac[A/G]ctggcgaaaactggcc	A	G	149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// NM_001559 // upstream // 40444 // Hs.479347 //	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2310626	ggaagaggacagtagg[G/T]ccccagaagtgagtca	G	T	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 417314 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2015569	acatctgccaccatcc[C/G]aaataaatattcatac	C	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2001832	tgcatgggaggggata[A/G]accagagagaggttta	A	G	// 22891 // Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, mRNA. /// NM_199451 // downstream //	ZNF365	ZNF365, Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, q21.2
SNP_A-2027203	aaacagtgacaggtta[C/T]agtgataggcactgat	C	T	5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 486649 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-2053411	aagtgatagctgatac[A/C]ggttggggtacaaaag	A	C	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 233527 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2066602	acaaaaagcaagcaac[C/G]gctggaaacacacctg	C	G	KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000241471 //	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-2076763	acatttttgtcagag[G/T]agccatttaaagaag	G	T	sapiens chromosome 14 open reading frame 54 (C14orf54), mRNA. /// ENST00000334061 // intron // 0 // --- // --- // --- // ---	C14orf54	C14orf54, Homo sapiens chromosome 14 open reading frame 54 (C14orf54), q23.3
SNP_A-2138364	atccaggctgaaaatc[A/G]cctccaggacgcagcc	A	G	Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA. /// ENST00000265854 // intron // 0 // --- // -	MAD1L1	MAD1L1, Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), p22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2150319	atgtctggaggtagtg[A/G]caacaccataacctca	A	G	sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // intron // 0 // Hs.166017 // MITF // 4286 // Homo sapiens	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-2150596	atgtgataccaaacaa[A/C]cagtccaatccagcaa	A	C	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 602057 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2130702	atactgtcctctctta[C/T]ctttcacaaggtcttg	C	T	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.2
SNP_A-2121606	agtgaaggcttacaga[C/T]tctacagttgagattt	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 681275 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2215696	cctcagttgcctcagc[A/T]ataaatggatataata	A	T	23498 // Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA. /// NM_006887 // downstream	HAAO	HAAO, Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), p21
SNP_A-2203635	ccagacatttattaaa[C/G]tatcagctcttgtgag	C	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 574230 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2213014	ccgaagtgcttcatac[A/C]cattatgacactcagt	A	C	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2208049	aagagacagaattaga[G/T]acaagaacagaacaaa	G	T	// 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream //	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-1836695	tactgaacaccaggtg[A/C]acttcgaatgctgatt	A	C	8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 14176 //	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1819210	gttgctgtttcagaaa[G/T]gaaccaagagaattta	G	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1827580	taactgatgattctgg[G/T]aatttaaacatgccaa	G	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1805704	gtcccagctactaggg[C/T]agtgatgagttcctcc	C	T	3984 // Homo sapiens LIM domain kinase 1 (LIMK1), transcript variant 1, mRNA. /// NM_016735 // downstream //	LIMK1	LIMK1, Homo sapiens LIM domain kinase 1 (LIMK1), transcript variant 1, q11.23
SNP_A-1786962	gggaaaactggacatc[C/T]agaagcaaaagaatga	C	T	51299 // Homo sapiens neuritin 1 (NRN1), mRNA. /// NM_000129 // downstream // 66115 // Hs.335513 // F13A1 //	NRN1	NRN1, Homo sapiens neuritin 1 (NRN1), p25.1
SNP_A-1782912	ggcagataacaactac[C/T]ctcttctctacatatg	C	T	Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // --- // --- // --- // ---	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3
SNP_A-1673256	catggatgctccccagtcttcttaa[C/T]gtgcctttatttagcatgttcaaac	C	T	AB051520 // intron // 0 // Hs.191979 // RPEL1 // 221692 // RPEL repeat containing 1	RPEL1	RPEL1 , rs6934799, RPEL repeat containing 1,p24.1
SNP_A-1972959	ccttgagaagaaagaa[C/T]catgcagttcatatcc	C	T	ENST00000343837 // intron // 0 // --- // --- // --- // ---	-	p14.2
SNP_A-1970433	accattgggactggcc[A/G]acttaacgaactaagc	A	G	Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-1962447	acacactatgtctaca[A/C]aatgggagaatctctt	A	C	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 2065025 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1979043	gatggataacaggtca[A/G]atagatttaggaaact	A	G	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1894987	tgcccaatttctgctg[G/T]actatctttaaaacatt	G	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1904752	tgggggtggctttatc[A/G]gacattctagtaggag	A	G	Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // --- //	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-1909585	tgtatttttttaaatga[C/T]gaatgatgatgagcat	C	T	256710 // Homo sapiens hypothetical protein MGC26856 (MGC26856), mRNA. /// ENST00000312442 // intron // 0 // ---	MGC26856	MGC26856, Homo sapiens hypothetical protein MGC26856 (MGC26856), q21.1
SNP_A-1919104	aaaaatgcttgttgac[C/T]aatgggtggtgaagaa	C	T	/// ENST00000330674 // upstream // 39183 // --- // --- // --- // ---	-	q21.32
SNP_A-1875223	tctctctcctctctac[C/G]cacttcccagacaatg	C	G	PPP4R2 // 151987 // Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), mRNA. ///	PPP4R2	PPP4R2, Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), p13
SNP_A-1978059	ataatatttgtaacag[A/G]aaaacagtatagtatt	A	G	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1662256	tgatgaatgaaacctgtctaacata[C/T]gacaactatcaaacatgtatgggaa	C	T	// FYN binding protein (FYB-120/130) /// NM_001737 // downstream // 49174 // Hs.1290 // C9 // 735 // complement	FYB	FYB , rs1631837, FYN binding protein (FYB-120,p13.1
SNP_A-1758598	ctttggggaagaattaatttgattc[G/T]agtgaaaaagtgtatagagctgctt	G	T	AF116701 // intron // 0 // - // - // - // Homo sapiens PRO2405 mRNA, complete cds.	-	- , rs7035330, Homo sapiens PRO2405 mRNA, complete cds.,q34.3
SNP_A-1758863	atgataaacaaacttggaattatta[C/T]attcatttacaaacaactttggtta	C	T	DKFZP434F1017 // 84075 // hypothetical protein DKFZp434F1017	DKFZP434F1017	DKFZP434F1017 , rs10484174, hypothetical protein DKFZp434F1017,q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787818	gggacctggggaagac[C/G]acaactgagtaagaaa	C	G	// Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), mRNA. /// NM_004588 // downstream // 6406	SCN4B	SCN4B, Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), q23.3
SNP_A-1841988	tagggacaggagagaa[C/T]gctggctttactgtag	C	T	219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 178739 // --- // --- // --- //	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-1844037	tagttgagattggaag[G/T]ccaaacttggattcgc	G	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1839970	tagcaaatgtagaaaa[A/C]aaatacagcacaccaa	A	C	RASL11A // 387496 // Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA. /// NM_002097 // upstream //	RASL11A	RASL11A, Homo sapiens RAS-like, family 11, member A (RASL11A), q12.2
SNP_A-1853436	tctttgaaccatttca[A/G]caatcctctaaggtgg	A	G	8687 // Homo sapiens keratin, hair, acidic, 8 (KRTHA8), mRNA. /// NM_002278 // downstream // 7045 // Hs.41752 //	KRTHA8	KRTHA8, Homo sapiens keratin, hair, acidic, 8 (KRTHA8), q21.2
SNP_A-1856307	tcacacaacagagaca[G/T]acttgataataatagc	G	T	133 // Homo sapiens adrenomedullin (ADM), mRNA. /// NM_000480 // upstream // 73706 // Hs.501890 // AMPD3 //	ADM	ADM, Homo sapiens adrenomedullin (ADM), p15.4
SNP_A-1864590	tccagagtgctgtctc[A/G]aacaccatgtgggcta	A	G	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, mRNA. /// NM_181334 // intron // 0 // Hs.102336 // ARHGAP8 // 23779 // Homo sapiens Rho	ARHGAP8	ARHGAP8, Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, q13.31
SNP_A-1859754	tcagggagcaccattc[A/G]ctgtttatgctgtgaa	A	G	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 36730 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-1872654	tctagtcaccagaaga[A/C]tatgtctaggaattga	A	C	// 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1388106 // Hs.166109 // ELAVL2	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2211955	ccctgacacctccacc[G/T]gaatagaccctggtat	G	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2203349	ccactttgccacaagt[A/G]acccttcttgccccac	A	G	// 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 128569	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-2220871	ccttgcccaacactca[A/G]taacaattgttctgtt	A	G	8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 130548	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2183598	cagcaggtggattttc[G/T]aggcattgtgcttgga	G	T	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1299776 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2119602	agtatggagagagaag[A/C]accagctgcaatagaa	A	C	8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 162090 //	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2113148	aggccatggaagtaca[C/T]tattaaggacatggaa	C	T	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2128548	ataatactggcttaaa[C/T]atgacaagtttatttg	C	T	2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 //	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-2145310	atgcactaaccttctc[G/T]cttctcaacattaaaa	G	T	Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // --- // --- // --- // --- ///	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-2165819	caaagtcaaataaaca[C/T]gagtatttagagatgc	C	T	// 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1859588 // Hs.24212 // LPHN2	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2084167	actaggagtattcaag[C/G]ctgatttctttccttg	C	G	sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA. /// ENST00000276497 // intron // 0 // --- // --- // --- /// ENST00000359619 // intron // 0 // --- // --- //	LYN	LYN, Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), q12.1
SNP_A-2031730	aaagtagctgaacgaa[C/T]tcctacaatagttcaa	C	T	EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 810764 // --- // --- // --- //	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-2293468	gcagcaataataaaga[C/T]gatgataacaacccgt	C	T	10408 // N-cym=DNA-binding transcriptional activator homolog {oncogene} [human, Kelly neuroblastoma cell line, mRNA, 778 nt]. /// ENST00000311168 // downstream //	MYCNOS	MYCNOS, N-cym=DNA-binding transcriptional activator homolog {oncogene} [human, Kelly neuroblastoma cell line, 778 nt]. ,p24.3
SNP_A-2241310	ctgagggctcaactgc[C/T]acaccccagatagagc	C	T	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 749102 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-2239650	ctgaaacataggaaca[A/G]tggctggagattctgc	A	G	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 226581	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2237471	ctctcctggaatcaga[C/T]agaaaggaacagaatg	C	T	5420 // Homo sapiens podocalyxin-like (PODXL), mRNA. /// ENST00000322985 // upstream // 190399 // --- // --- // --- // ---	PODXL	PODXL, Homo sapiens podocalyxin-like (PODXL), q32.3
SNP_A-2229952	ctataaaaacgtatga[C/G]tactgtgtacccacaa	C	G	// 6318 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA. /// NM_006919 // upstream // 74797 // Hs.227948 //	SERPINB4	SERPINB4, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), q21.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2231386	cttcccactaacgcca[A/G]agcagctggactctga	A	G	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 4245 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2242700	ctgcatcgtaactgct[A/G]aacccaaagctgctcc	A	G	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream //	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-2272452	gaccttcaccacacaa[C/T]ctgaggaaggcaaact	C	T	25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// NM_001752 //	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-2291167	gcaatattggtgagaa[C/T]gggattgtgagttcca	C	T	KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 242790 //	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. ,q25.1
SNP_A-2299635	gccgcggggacgcgaa[C/G]tgcgcagccagaaatc	C	G	sapiens xeroderma pigmentosum, complementation group C (XPC), mRNA. /// ENST00000285021 // CDS // 0 // --- // --- // -	XPC	XPC, Homo sapiens xeroderma pigmentosum, complementation group C (XPC), p25.1
SNP_A-2021716	aaaaacactgacctca[A/G]gagaataatttttcca	A	G	// 11098 // Homo sapiens protease, serine, 23 (PRSS23), mRNA. /// NM_012193 // downstream // 6322 // Hs.19545 //	PRSS23	PRSS23, Homo sapiens protease, serine, 23 (PRSS23), q14.2
SNP_A-2035939	aaattaaaacctgcag[C/G]atgtttcagtgacatc	C	G	// 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000329561 // upstream //	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-2003315	agtaagaggggcaaaa[A/G]agatcactgttaggta	A	G	NM_198989 // downstream // 562292 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.2
SNP_A-1995991	accacctgggactgaa[A/T]agacaaatctcctttt	A	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1989765	aggcttagaaaatgtg[C/G]aaattgtggtgatggt	C	G	ENST00000360042 // 3UTR // 0 // --- // --- // --- // ---	-	p13
SNP_A-2017346	acccagctgaactaca[G/T]aatcaaagacaaatat	G	T	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 334391 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2084592	actatgtaacagacaa[A/G]agtcaacttctatatt	A	G	55835 // Homo sapiens centromere protein J (CENPJ), mRNA. /// NM_030979 // upstream // 72439 // Hs.458280 //	CENPJ	CENPJ, Homo sapiens centromere protein J (CENPJ), q12.13
SNP_A-2076484	acatttagggactggc[A/G]aaattctcaccctcct	A	G	sapiens betaine-homocysteine methyltransferase (BHMT), mRNA. /// ENST00000274353 // intron // 0 // --- // --- // --- // ---	BHMT	BHMT, Homo sapiens betaine-homocysteine methyltransferase (BHMT), q14.1
SNP_A-2069275	acaattttaaagaaac[A/G]aatagtaatgaggatc	A	G	/// ENST00000319719 // upstream // 373568 // --- // --- // --- // -- /// ENST00000308537 // upstream // 149693 // --- // --- // ---	-	p13
SNP_A-2061598	aatgcttctgtccatg[A/C]aatataattctgccat	A	C	79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. ///	OBFC1	OBFC1, Homo sapiens oligonucleotide,q24.33
SNP_A-2144778	atgatggttgtgttca[C/T]actttctttaaaatct	C	T	Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), mRNA. /// AK025510 // intron // 0 // Hs.463702 //	BCAS3	BCAS3, Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), q23.2
SNP_A-2181758	cagagatattagtaaa[C/T]gaaattgctttctgaa	C	T	221322 // Homo sapiens chromosome 6 open reading frame 170 (C6orf170), mRNA. /// NM_000165 // upstream // 74742	C6orf170	C6orf170, Homo sapiens chromosome 6 open reading frame 170 (C6orf170), q22.31
SNP_A-1854412	tcaaatcccttcctag[C/G]acagaaaaatgaaaat	C	G	Homo sapiens parvin, alpha (PARVA), mRNA. /// ENST00000334956 // intron // 0 // --- // --- // --- // ---	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.3
SNP_A-1845405	tatacttttagaaatc[C/T]agtagacagcagtgtt	C	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1841821	taggcctattcaagca[G/T]atttacctttttatcag	G	T	Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), mRNA. /// ENST00000334822 // intron // 0 // ---	ZDHHC17	ZDHHC17, Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), q21.2
SNP_A-1819768	gttgtcttacttcctc[G/T]agatcagtacattcat	G	T	sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) mRNA, complete cds. /// NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and	PSD3	PSD3, Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) complete cds. p22
SNP_A-1785615	ggctccatagatggga[C/T]gtgctttcaatatcaa	C	T	Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// ENST00000046794 // intron // 0 // --- // --- // --- // ---	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-1790106	ggggaaggttagcagg[C/G]agaataagaggagtag	C	G	8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 96332 // Hs.503510 // EED // 8726 // Homo	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1798701	gtaaccatgcacaatg[C/G]aacttttttgaatgcc	C	G	-- /// ENST00000329863 // downstream // 560101 // --- // --- //	-	q23.1
SNP_A-1794414	ggtccctatgaggtca[C/T]gtgctccagttcatgt	C	T	Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // --- //	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1805461	gtccactaattattca[A/T]atcatctctctttcat	A	T	NM_198989 // downstream // 666664 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.2
SNP_A-1805937	gtccgatattaatata[A/G]caactccagctctctt	A	G	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 21921 // Hs.153952 // NT5E //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801250	gtagctgggacttcag[A/G]catacatcaccttgcc	A	G	FLJ35530 // 400798 // Homo sapiens FLJ35530 protein (FLJ35530), mRNA. /// NM_018037 // upstream // 48740 //	FLJ35530	FLJ35530, Homo sapiens FLJ35530 protein (FLJ35530), q25.2
SNP_A-1813850	gtgtatgctcattgga[C/T]agctggcagttttaag	C	T	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-1673624	tggtatgctatttctctgctttgaa[A/G]ttatttatccctctttgatgacagt	A	G	// 23469 // PHD finger protein 3	PHF3	PHF3 , rs975618, PHD finger protein 3,q12
SNP_A-1962901	cttcggtattcagact[A/C]actccttctctttctt	A	C	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-1968203	ctcagtcacttaatga[A/G]acatgaattgaggttg	A	G	79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1951201	tttcccagttagtgca[C/T]ctgtattttgaacaat	C	T	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1909793 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1893232	tgcagagctctgacca[A/G]gaaggcccagcagcca	A	G	Homo sapiens cleft lip and palate associated transmembrane protein 1 (CLPTM1), mRNA. /// ENST00000347493 // intron // 0 // --- // --- // --- // --- /// ENST00000337392 // intron // 0 // --- //	CLPTM1	CLPTM1, Homo sapiens cleft lip and palate associated transmembrane protein 1 (CLPTM1), q13.31
SNP_A-1892758	tgcacagcactacaac[A/G]gtcattaagttctctt	A	G	Homo sapiens FGFR1 oncogene partner (FGFR1OP), transcript variant 2, mRNA. /// NM_007045 // intron // 0 //	FGFR1OP	FGFR1OP, Homo sapiens FGFR1 oncogene partner (FGFR1OP), transcript variant 2, q27
SNP_A-1902383	tggccctaaattccac[C/G]actaaatgtattctca	C	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 159677 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-1911808	tgtgaattatgtcttg[C/T]agtccgactggtagga	C	T	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 57295 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1909799	tgtcacagtttcatgg[A/G]actttaattagtttct	A	G	// 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000357839 // upstream // 86328 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1904654	tggggcttcttactac[C/T]attagaataaagagca	C	T	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-1929061	ttcagcttaaaaagca[A/T]atcatttgataacaat	A	T	ENST00000239264 // intron // 0 // --- // --- // --- // ---	-	p21.2
SNP_A-1906747	tttctctttcacttcc[C/T]caaaacaattatctac	C	T	SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 191589 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1884557	tgaataaacatctcac[A/G]aactgtcgctcctaga	A	G	Homo sapiens WD repeat domain 21 (WDR21), transcript variant 2, mRNA. /// NM_015604 // 3UTR // 0 // Hs.331491 //	WDR21	WDR21, Homo sapiens WD repeat domain 21 (WDR21), transcript variant 2, q24.2
SNP_A-1960162	tttttaaataatgaca[C/G]agatgcccaaaagaaa	C	G	7101 // Homo sapiens nuclear receptor subfamily 2, group E, member 1 (NR2E1), mRNA. /// NM_152828 // downstream //	NR2E1	NR2E1, Homo sapiens nuclear receptor subfamily 2, group E, member 1 (NR2E1), q21
SNP_A-1942671	ttgggaggagtgtcca[C/T]gcctttcctcaagtct	C	T	// 134359 // Homo sapiens hypothetical protein FLJ35779 (FLJ35779), mRNA. /// ENST00000282199 // upstream //	FLJ35779	FLJ35779, Homo sapiens hypothetical protein FLJ35779 (FLJ35779), q13.3
SNP_A-1964238	aggattttgtctgacc[A/G]agagaaatccccaagc	A	G	sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // --- // --- // --- // ---	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1689226	tatgtgtatttttcaattactgaga[A/T]tcctgttaagatcccctactgtgaa	A	T	83417 // immunoglobulin superfamily receptor translocation associated 1 /// NM_052939 // downstream // 48895 // Hs.434881 // FCRH3 // 115352 // Fc receptor-like protein 3	IRTA1	IRTA1 , rs6668838, immunoglobulin superfamily receptor translocation associated 1 ,q23.1
SNP_A-1686698	ttttgccctcaggataataatgagc[C/T]aaaaacttacttaattgcgtctgat	C	T	122183 // FLJ40296 protein /// NM_006418 // downstream // 4007259 // Hs.273321 // GW112 // 10562 // differentially	FLJ40296	FLJ40296 , rs9316901, FLJ40296 protein ,q21.1
SNP_A-1707693	acattagttcagtctaaatttatta[A/G]caagacccagaaaatcttatagcaa	A	G	MGC26598 // 196477 // hypothetical protein MGC26598 /// NM_152768 // downstream // 1128 // Hs.350600 // FLJ25378	MGC26598	MGC26598 , rs2178457, hypothetical protein MGC26598 ,q21.33
SNP_A-1803879	gtcaagtatgccctac[C/T]atgttgtacttgtaga	C	T	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 587678 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q12.3
SNP_A-1790117	ggggaagttttgtgta[A/C]aacagtgaaaacggca	A	C	BCL2/adenovirus E1B 19kDa interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein, mRNA. ///	BNIP3	BNIP3, Homo sapiens BCL2,q26.3
SNP_A-1819823	gttgtgcctccattac[C/T]acaatcaattacagat	C	T	3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 57498	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-1828227	taagaggcagtattag[G/T]atataagggccaaatt	G	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2454439 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1822671	gcctagctaactcaca[C/T]tgatagctgagacttc	C	T	// Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 926702 // Hs.98849 // DNCL2B // 83657 // Homo	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1860771	tcataaggaatgcaca[A/G]cctagttccctcacat	A	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 928290 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2220676	ccttgaatgtaactta[C/T]gcatatacttgcagaa	C	T	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2138142	atccaatctttctaaa[A/G]tgacttaaacagagag	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 326984 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2164198	caaaagtggcggtcaa[A/G]tgaattttggggtgag	A	G	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 292535 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2126514	ataaaatagcaggaaa[C/T]acaaaacataagtaaa	C	T	Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // --- // -	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-2121570	agtgaactggactgac[C/T]gctgtactgggggggcg	C	T	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 699760 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2057982	aatatttaaaaaataa[C/T]gaaactgtgacacaga	C	T	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 313607	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2051299	aagggcagctccacca[C/T]tattggttttaactaa	C	T	Homo sapiens chromosome 12 open reading frame 2 (C12orf2), mRNA. /// ENST00000282884 // intron // 0 // --- // --	C12orf2	C12orf2, Homo sapiens chromosome 12 open reading frame 2 (C12orf2), p12.1
SNP_A-2098889	agagctggatgcaagg[A/C]agtttgatgcacctga	A	C	ENST00000323433 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-2010105	taggtaagcagaaaag[A/G]aatggtgtaaagaaac	A	G	// 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 195197 // Hs.480596 // NDST3 //	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2009133	cctcaaatgtgaggaa[A/G]tacatttctgtctgtg	A	G	Homo sapiens hypothetical protein MGC3040 (MGC3040), mRNA. /// ENST00000321871 // intron // 0 // --- // --- // --- // ---	MGC3040	MGC3040, Homo sapiens hypothetical protein MGC3040 (MGC3040), q22.1
SNP_A-2011855	aggccctgagaaggca[C/T]ccaatttgtatcctgc	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1267811	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2001016	tacattttattatgtg[A/G]tttttcctgcttaaaa	A	G	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2308129	gcttgcaaatactgag[C/G]ctcaaaatttgttagg	C	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2259576	gaaaacccacataaga[C/T]ctgaaaatcaaaacaa	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1725235 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2260322	gaaaattgctgagaca[A/G]tgtatcaccttataag	A	G	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 161301 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-2262968	gaacaaggatttggag[A/G]aagaaagtgccttcaa	A	G	KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 80999 //	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2291955	gcacatcatatcagga[A/G]gtacgtgaagtccacc	A	G	// Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 231281 //	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-2014054	agagaatgtgtgacta[C/T]gtgagtagaagatttc	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1420996 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2039103	aacaggtgatcattct[A/C]acagaagtcagaaaga	A	C	Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, mRNA. /// ENST00000256772 // intron //	CRB1	CRB1, Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, q31.3
SNP_A-2032428	aaagtttcctgtgctc[C/T]gagaaaatagtcaggt	C	T	9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 287785 // Hs.136829 // RFX3 //	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-2081099	acctgagctcagatcc[G/T]aattccaccctgtatg	G	T	Homo sapiens LIM homeobox 4 (LHX4), mRNA. /// ENST00000263726 // intron // 0 // --- // --- // --- // ---	LHX4	LHX4, Homo sapiens LIM homeobox 4 (LHX4), q25.2
SNP_A-2054590	aagtttttccttctca[C/G]agcctccaaccattcc	C	G	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // --- // ---	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2063774	aattagcagaatgaaa[A/G]gaatgaaaagatgctg	A	G	// Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 89889 // Hs.12393 // TGDS //	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-2063144	aatgttgtcctcttaa[A/G]gatatgaacatgtcca	A	G	// 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream //	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2064303	aattcagggcagtaaa[A/T]atccagttttaatggt	A	T	Homo sapiens chromosome 6 open reading frame 10 (C6orf10), mRNA. /// ENST00000305725 // intron // 0 // --- // --	C6orf10	C6orf10, Homo sapiens chromosome 6 open reading frame 10 (C6orf10), p21.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113744	aggctgagaaacctat[A/T]agtcttgattcaaatt	A	T	Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // intron // 0 // --- // --- // --- // ---	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2123876	agttaaccaagactca[C/T]agtttatagcttaagc	C	T	Homo sapiens nucleoporin 214kDa (NUP214), mRNA. /// ENST00000321761 // intron // 0 // --- // --- // --- // --- ///	NUP214	NUP214, Homo sapiens nucleoporin 214kDa (NUP214), q34.13
SNP_A-2132342	atagtatcccggaata[C/G]ctaggactctatatca	C	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2155274	attcagtgctctgaaa[A/G]gaggcattttcttcat	A	G	4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 56231 // --- // ---	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-2159120	attgtttttgggaga[A/T]gatttctaggatataa	A	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2202272	ccaccaaccaggtaaa[A/G]tgcctccaaccagtat	A	G	85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 76992 // Hs.461389 // CNTNAP4 // 85445 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2177780	cacgtgactgattaaa[A/G]gtgaactagaatttaa	A	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2175079	cacagtcggtttctcc[A/G]cctttctgtagtcagt	A	G	Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA. /// ENST00000271529 // intron // 0 // --- // --- // --- // ---	IRTA2	IRTA2, Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), q23.1
SNP_A-1859836	tcagggtataggtatc[G/T]cacatctttgttcaac	G	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-1863011	tcattgtctcctgctc[A/G]cattactttccccatt	A	G	Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // --- // --- // --- // ---	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-1866150	tcccagctttgttgtc[A/G]actgtccttgattccc	A	G	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1854554	tcaaatttctgtatta[C/T]gcagttagaatcaaga	C	T	Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), mRNA. /// ENST00000359133 // intron // 0 // --- // --- // --- // --- ///	ERO1L	ERO1L, Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), q22.1
SNP_A-1853941	tcaaaatagtcaagaa[C/G]tgtacataattcaaat	C	G	8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 565477 // --- // --- // --- //	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.3
SNP_A-1853068	tatttgctaaattcag[C/T]ccaagtattcagctat	C	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1838564	tagaattcatgaggtc[A/G]ccctgttgcttctatc	A	G	Homo sapiens somatostatin (SST), mRNA. /// NM_001004312 // downstream // 3264 // Hs.452766 // RTP2	SST	SST, Homo sapiens somatostatin (SST), q27.3
SNP_A-1836885	tactgcccctgttcta[C/G]accagtacaagattag	C	G	4843 // Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, mRNA. /// NM_153292 // upstream // 10567 // Hs.462525 // NOS2A //	NOS2A	NOS2A, Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, q11.2
SNP_A-1807396	gtctgagagttagtta[C/T]gtattaacacagcaga	C	T	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 873590	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1801261	gtagctgtggtgctga[C/T]ggtagacttctcctag	C	T	64111 // Homo sapiens chromosome 7 open reading frame 9 (C7orf9), mRNA. /// ENST00000222674 // upstream //	C7orf9	C7orf9, Homo sapiens chromosome 7 open reading frame 9 (C7orf9), p15.2
SNP_A-1665282	tctctggcccctggcccttaaatg[C/T]cactatacactgccttctagagatg	C	T	AY324801 // intron // 0 // Hs.435063 // ARHGAP22 // 58504 // Rho GTPase activating protein 22	ARHGAP22	ARHGAP22 , rs1965169, Rho GTPase activating protein 22,q11.22
SNP_A-1652618	aaagagtataatgaaagataagatc[A/G]aaaatgaataaatctaggacattga	A	G	196 // aryl hydrocarbon receptor /// NM_015132 // downstream // 19014 // Hs.269881 // SNX13 // 23161 //	AHR	AHR , rs10488475, aryl hydrocarbon receptor ,p21.1
SNP_A-1744561	cgccctgccaagtataactgtctta[C/T]atatcctattcactgccaaatctcc	C	T	// transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) /// NM_021154 // downstream // 999619 //	TLE4	TLE4 , rs10512087, transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) ,q21.31
SNP_A-1963948	aaagtaatatgcctta[C/T]aatgaaacttaatgat	C	T	5068 // Homo sapiens pancreatitis-associated protein (PAP), transcript variant 1, mRNA. /// NM_138937 // upstream //	REG3A	REG3A, Homo sapiens pancreatitis-associated protein (PAP), transcript variant 1, p12
SNP_A-1978168	catcttctgtgggaac[C/G]cgtagtacagatattt	C	G	8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 1947 //	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1982845	caaattttaaaactgc[C/T]aggtcactgtgtaaga	C	T	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 66261 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1941069	ttgctctatttggtag[A/G]aaggctagaaagagag	A	G	114885 // Homo sapiens oxysterol binding protein-like 11 (OSBPL11), mRNA. /// ENST00000296220 // upstream //	OSBPL11	OSBPL11, Homo sapiens oxysterol binding protein-like 11 (OSBPL11), q21.2
SNP_A-1900707	tggaggtagaggaaca[C/T]tgagagaggcagaggc	C	T	// Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds. /// NM_001358 // upstream // 199213 //	DHX15	DHX15, Homo sapiens for ATP-dependent RNA helicase #46, complete cds. p15.2

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1924061	ttagtgtgcagaatta[C/T]acataatggggaaagg	C	T	10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // upstream // 17569 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1941227	ttgctggccatttata[C/T]tagcctgtgacttgtc	C	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-1940475	ttgcccagcactatca[C/G]caatctgcaaaaagat	C	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1943556	ttgtaacagtatgaag[A/C]cctctcatttgctgta	A	C	1147 // Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), mRNA. /// NM_018294 // downstream // 1340	CHUK	CHUK, Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), q24.31
SNP_A-1944547	ttgtctttgtctgtga[C/T]ctgaatgactgtgaag	C	T	5954 // Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA. /// NM_000378 //	RCN1	RCN1, Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), p13
SNP_A-1947044	tttaataattgagtaa[C/T]gcagactcctatgaac	C	T	116379 // Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, mRNA. /// NM_052962 // upstream // 8576 // Hs.126891 // IL22RA2 // 116379 // Homo	IL22RA2	IL22RA2, Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, q23.3
SNP_A-1936269	ttcttccacttctccc[C/T]gccatataaggactca	C	T	// 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 3163589 // --- // -	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1955868	tttgtatttgaaggga[A/G]atgagtgtttctgatg	A	G	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 442361 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3
SNP_A-1987893	atttttacaaagtgcc[A/G]aaaagctacaggagag	A	G	/// ENST00000343481 // downstream // 986933 // --- // --- // ---	-	q24.1
SNP_A-1986855	tgtgtgtacgtgttcc[A/G]atggagaaaaagcact	A	G	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1597673 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1978022	tcatttgttgctttaa[A/C]aaagaacagcaaagga	A	C	6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // upstream // 18097 // Hs.271771 //	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-1981657	gttcaagctttggcca[G/T]ggaaaacaacagatct	G	T	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 224261 // --- // --- // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-1965272	cttcacaaaggtctca[C/T]agattggaaattcatc	C	T	// Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 1249214 // --- // --- // -	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-1740387	tgtgtaagggagtataattatgcac[C/T]gtctatacaaacccttccctaatga	C	T	2262 // glypican 5 /// NM_005708 // upstream // 217851 // Hs.508411 // GPC6 // 10082 // glypican 6	GPC5	GPC5 , rs10492624, glypican 5 ,q31.3
SNP_A-1693286	gtacatgttctatgcatgtatatga[C/T]atttatttctatgggtttgtagata	C	T	XPNPEP1 // 7511 // X-prolyl aminopeptidase (aminopeptidase P) 1, soluble /// NM_052918 // upstream // 990248 // Hs.348923 // SORCS1 // 114815 // sortilin-related	XPNPEP1	XPNPEP1 , rs10509866, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble ,q25.1
SNP_A-1681258	gtctgaagacccagagtatactaca[C/T]agtaagttctacctatcaaatgata	C	T	NM_024614 // intron // 0 // Hs.29725 // FLJ13197 // 79667 // hypothetical protein FLJ13197	FLJ13197	FLJ13197 , rs1993796, hypothetical protein FLJ13197,p14
SNP_A-1675894	atctagaacacacttacagaataga[A/C]atttatagaattactcattgactga	A	C	CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 1559990 // Hs.499861 //	CTNNA3	CTNNA3 , rs10509221, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1806100	gtcctcctattacata[C/G]cacaaaagccagcccc	C	G	6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 514373 // Hs.355606	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1852045	tattgctgaagtgcgg[G/T]aaagtcacgaaagaga	G	T	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1), mRNA. /// ENST00000233084 // intron // 0 // --- // ---	DDX1	DDX1, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1), p24.3
SNP_A-2182768	cagatgcttagtatca[C/T]gagttcaatttgtatc	C	T	Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // --- // --- // --- // ---	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-2181097	cagacagaaccataca[A/T]tacttgtcatttataa	A	T	ENST00000205064 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-2171585	caatcctgctgtgtca[C/T]gctgcaccagatgttt	C	T	54980 // Homo sapiens hypothetical protein FLJ20558 (FLJ20558), mRNA. /// NM_022173 // downstream // 10012 //	FLJ20558	FLJ20558, Homo sapiens hypothetical protein FLJ20558 (FLJ20558), p13.3
SNP_A-2169211	caagattgcatgattg[C/T]actctagcatgggcga	C	T	5742 // Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 2 /// X64989 // upstream // 58893	PTGS1	PTGS1, Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G,q33.2
SNP_A-2168652	caagaagagttttcac[C/G]aattgtaatgaaagcc	C	G	4852 // Homo sapiens neuropeptide Y (NPY), mRNA. /// NM_016447 // upstream // 101434 // Hs.533355 // MPP6 //	NPY	NPY, Homo sapiens neuropeptide Y (NPY), p15.3
SNP_A-2201453	ccaatgccatgaatgc[C/T]gattgtagctatgcag	C	T	/// ENST00000343998 // downstream // 29495 // --- // --- // ---	-	q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2150434	atgtgaaatgtcaaaa[A/C]tatcataaccatacac	A	C	4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 678110 // Hs.166017 // MITF //	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-2123811	agttaaaacatctgcc[A/G]ggattaacatcagtgc	A	G	4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 1669 // Hs.21388 // ZDHHC21	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2129590	atacagaactgtacta[G/T]gagaaaacattttcat	G	T	51299 // Homo sapiens neuritin 1 (NRN1), mRNA. /// NM_000129 // downstream // 92263 // Hs.335513 // F13A1 //	NRN1	NRN1, Homo sapiens neuritin 1 (NRN1), p25.1
SNP_A-2116541	aggtcaataacagaga[C/T]gaaattttgatttcta	C	T	7035 // Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA. /// ENST00000233156 // upstream // 126550 // --- // --- // --- // ---	TFPI	TFPI, Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), q32.1
SNP_A-2067883	acaacctattatttga[A/C]ccggtcattctcttct	A	C	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), mRNA. /// ENST00000280452 // intron // 0 // --- // --- // --- // ---	PIP5K2A	PIP5K2A, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), p12.2
SNP_A-2048383	aagcaggtcagttcaa[C/T]taacgtcagcctttac	C	T	2615 // Homo sapiens glycoprotein A repetitions predominant (GARP), mRNA. /// NM_015516 // upstream // 43334 //	GARP	GARP, Homo sapiens glycoprotein A repetitions predominant (GARP), q13.5
SNP_A-2106237	agcccctgtacaaatc[A/G]ctaccaatcaagcagc	A	G	MGC32124 // 124936 // Homo sapiens hypothetical protein MGC32124 (MGC32124), mRNA. /// NM_020740 //	MGC32124	MGC32124, Homo sapiens hypothetical protein MGC32124 (MGC32124), p13.2
SNP_A-2027230	aaacataaatgcccac[A/G]gatacagccatttcaa	A	G	Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-2044055	aacttgctcaatgaca[A/G]cagttagtaagtggca	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2016878	attaggctggtgaatg[A/C]aagcccttatatctgt	A	C	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 479213	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2006930	agggcatttaacggca[A/C]cccattatactttagt	A	C	/// ENST00000359634 // upstream // 1206007 // --- // --- // --- /// ENST00000359181 // upstream // 1206007 // --- // --- // -	-	q32.3
SNP_A-2295261	gcatcaactcaagcag[A/G]ccactaaggtgccagc	A	G	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2285019	gatcctcactgaaaaa[C/T]atcatgtttaaaaagg	C	T	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 896761	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2228447	ctacttccgtaaagaa[G/T]gtcaatggtagtttga	G	T	// 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream // 86911	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-2239103	ctcttctttagttcca[C/G]ctctggcagagacctt	C	G	Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// ENST00000265283 // intron // 0 // --- // ---	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin q21.13
SNP_A-2263809	gaacgatgtcaaagga[A/G]agatatccttaccttg	A	G	Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), mRNA. /// ENST00000282146 // intron // 0 // --- // -	KCNK13	KCNK13, Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), q32.11
SNP_A-2000376	atatctttggaatttg[G/T]atgcaatatatcctca	G	T	/// ENST00000318905 // downstream // 25514 // --- // --- // --- // --- /// ENST00000304745 // downstream // 25514 // --- // ---	-	q23.1
SNP_A-2004529	ctatgtgggccagaca[A/G]gtcacgtgagtgagat	A	G	// 55662 // Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), mRNA. /// NM_003987 //	HIF1AN	HIF1AN, Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), q24.31
SNP_A-2125968	agttttcactttatcc[C/T]gaacacaagggcatta	C	T	Homo sapiens IBR domain containing 1 (IBRDC1), mRNA. /// ENST00000359704 // intron // 0 // --- // --- // --- // --- ///	IBRDC1	IBRDC1, Homo sapiens IBR domain containing 1 (IBRDC1), q22.31
SNP_A-2137630	atcatgaaagcaggta[A/T]ctcgggggatgacggt	A	T	Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, mRNA. /// NM_052836 // intron // 0 // Hs.546421 // CDH23 //	CDH23	CDH23, Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, q22.1
SNP_A-2134700	atatgttttgcattca[C/T]atgtgcggtgtgtgtg	C	T	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2146206	atgctaaaaatgtaac[A/G]aagtccgtcagcttag	A	G	FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 464066 //	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2153588	attagcttacagtgaa[A/G]gggctatcaaaactaa	A	G	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2222962	cgcagcagtatgtaaa[C/T]gaatgggtgtgtctat	C	T	ENST00000361034 // intron // 0 // --- // --- // --- // ---	-	q13.31
SNP_A-2169638	caagctttcaataaaa[G/T]tcatgtaaaagagaag	G	T	sapiens kinesin 2 60/70kDa, mRNA (cDNA clone MGC:15245 IMAGE:4301579), complete cds. /// NM_182923	KNS2	KNS2, Homo sapiens kinesin 2 60,q32.33
SNP_A-2174501	cacagacttccagaaa[C/T]gaaaggttgctttacc	C	T	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 84525 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-2182512	cagatataaagatgga[C/T]gagacacagactctac	C	T	Homo sapiens dedicator of cytokinesis 2 (DOCK2), mRNA. /// ENST00000256935 // intron // 0 // --- // --- // --- // ---	DOCK2	DOCK2, Homo sapiens dedicator of cytokinesis 2 (DOCK2), q35.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2177916	cactaaggaacagtga[C/T]tactagtttagtacca	C	T	// 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1355024 // --- // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1793933	ggtcaatgagactcaa[A/C]tctgagacttatatat	A	C	-- /// ENST00000329863 // downstream // 140356 // --- // --- //	-	q23.1
SNP_A-1792567	ggtaaacgttattaac[C/G]aaaatctgtggattag	C	G	// Homo sapiens actinin, alpha 1 (ACTN1), mRNA. /// ENST00000193403 // upstream // 42628 // --- // --- // --- // ---	ACTN1	ACTN1, Homo sapiens actinin, alpha 1 (ACTN1), q24.1
SNP_A-1725304	atttctatccccttttcttgccctaa[A/G]tacaaagtttataaaatcttactta	A	G	5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 703825 // Hs.135892 // NCAM2 // 4685 // neural	PRSS7	PRSS7 , rs2826128, protease, serine, 7 (enterokinase) ,q21.1
SNP_A-1782700	ggcactgttgaaggaa[C/T]tgctctattttcaaca	C	T	Homo sapiens tumor protein p53 binding protein, 1 (TP53BP1), mRNA. /// ENST00000263801 // intron // 0 // --- //	TP53BP1	TP53BP1, Homo sapiens tumor protein p53 binding protein, 1 (TP53BP1), q15.3
SNP_A-1781857	ggattttgcatcaaac[G/T]ggtggtagtttattct	G	T	Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), mRNA. /// ENST00000331762 // intron // 0 // --- // --- // --- // ---	IMMP2L	IMMP2L, Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), q31.1
SNP_A-1783562	ggcatgagatggagtc[C/T]gaaaggggtggttctt	C	T	-- /// ENST00000340631 // upstream // 29922 // --- // --- // --- //	-	p24.3
SNP_A-1949376	tttattcaacaatcaa[C/T]ggaaaatgaaatgaga	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1126860 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1940012	ttgcagatgatataaa[C/T]ttgtatctggaaaagc	C	T	ENST00000355094 // intron // 0 // --- // --- // --- // ---	-	q22.31
SNP_A-1946871	tttaagcaccacccaa[A/G]cagtcatttacatctc	A	G	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1323997 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1904529	tggggatccatatggc[A/G]ctagggatataggaga	A	G	5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// NM_005012 // upstream // 86512 // Hs.436456 //	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-1877395	tctggagcaaggtgac[A/C]ggtggcccttaggatc	A	C	6ST // 51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// NM_000274 // downstream //	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-1880165	tcttctgccagtctga[A/G]ctccttcctggctcct	A	G	Homo sapiens ethanolamine kinase 2 (ETNK2), mRNA. /// ENST00000306755 // intron // 0 // --- // --- // --- // ---	ETNK2	ETNK2, Homo sapiens ethanolamine kinase 2 (ETNK2), q32.1
SNP_A-1893684	tgcagtcaagaagttc[A/G]acatcagactagatca	A	G	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 823478 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-1927627	ttcaaccatagcacta[A/G]aatggactgaattgac	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 294705 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1947956	tttagaagggctcaca[A/G]aacagataaaagggga	A	G	79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // upstream // 627 // Hs.209095 //	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-1691406	tggagtgtctttgctaaaagctctg[G/T]tctcaaagccccaaatataaaattt	G	T	NM_000627 // intron // 0 // Hs.241257 // LTBP1 // 4052 // latent transforming growth factor beta binding protein 1	LTBP1	LTBP1 , rs723043, latent transforming growth factor beta binding protein 1,p22.3
SNP_A-1792006	gggtggcatgtaccta[C/T]agttttagctacccag	C	T	Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 //	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-1788403	gggagtattgctcaga[C/T]gcactgtacaccatgc	C	T	84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 281458 // Hs.7353 // APG4C //	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-1801850	gtagttcagtcttaac[A/G]atttggctttttggt	A	G	// 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000357331 // downstream //	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-1845199	tataccatgcaacata[C/T]agacctgtacatatac	C	T	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 //	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-1867170	tccctgcacttcacag[A/G]ctattacgtgggacat	A	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 32792 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.2
SNP_A-1839995	tagcaacgcctgcggg[A/T]agagcttcctctgggt	A	T	// 23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream //	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-2187807	cagtaggtgcccagtg[A/G]atactgaatatacaag	A	G	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 390144 // --- // --- // --- // -	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2225244	cgttctttgtttcaaa[A/G]tgcaaattgtaacaat	A	G	Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) mRNA, complete cds. /// NM_002977 // downstream // 8503 // Hs.2319 // SCN9A // 6335 // Homo	SCN1A	SCN1A, Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) complete cds. ,q24.3
SNP_A-2204816	ccaggcctgagaagga[C/T]ggagtagccaccagag	C	T	// 85509 // Homo sapiens methyl-CpG binding domain protein 3-like 1 (MBD3L1), mRNA. /// ENST00000305625 //	MBD3L1	MBD3L1, Homo sapiens methyl-CpG binding domain protein 3-like 1 (MBD3L1), p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2157294	attgactctggcacaa[A/C]gtgatgaactagacta	A	C	283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream //	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2164589	caaacaagaagtggaa[A/G]cctttgctgagttcct	A	G	sapiens interleukin 3 (colony-stimulating factor, multiple) (IL3), mRNA. /// ENST00000296870 // intron // 0 // --- // --- // --- // ---	IL3	IL3, Homo sapiens interleukin 3 (colony-stimulating factor, multiple) (IL3), q23.3
SNP_A-2134950	atattcaatcacttca[A/G]aaattttatatgtgaa	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-2012276	aactcagagcccttaa[C/T]tgtcccgggaaatagg	C	T	/// ENST00000332248 // downstream // 39079 // --- // --- // --- // --- /// ENST00000361026 // downstream // 39079 // --- // ---	-	q14.1
SNP_A-2106605	agcctccctagaatga[C/G]gaagtgaacagggaaa	C	G	// Homo sapiens esophageal cancer associated protein (MGC16824), mRNA. /// ENST00000251143 // intron // 0 // ---	MGC16824	MGC16824, Homo sapiens esophageal cancer associated protein (MGC16824), p12.3
SNP_A-2053597	aagtggaaagagaaac[A/G]gagtaataaaatgttt	A	G	// Homo sapiens hypothetical protein FLJ25333 (FLJ25333), mRNA. /// ENST00000283357 // intron // 0 // --- // --- // --- // ---	FLJ25333	FLJ25333, Homo sapiens hypothetical protein FLJ25333 (FLJ25333), q15
SNP_A-2062571	aatgtcacagttacta[A/G]attgactcagtataga	A	G	// 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 71152 // Hs.331555 //	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2259923	gaaaaggtattacata[A/G]aagctctgaccctaca	A	G	sapiens KIAA0029 mRNA, partial cds. /// NM_015361 // intron // 0 // Hs.412462 // R3HDM // 23518 // Homo sapiens R3H	R3HDM	R3HDM, Homo sapiens KIAA0029 partial cds. ,q21.3
SNP_A-2243166	ctgcctatttaatgaa[A/T]gggaaagctcagttca	A	T	// Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314809 // intron // 0 // --- // --- // --- // ---	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2289919	gcaaagactgggaaga[G/T]gctgaagtccccaggg	G	T	// 90627 // Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, mRNA. /// NM_178007 // upstream // 397367 // Hs.507704 // STARD13	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.2
SNP_A-2302961	gctaggcttccttata[A/T]cttggccaaataagag	A	T	4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 162960 // --- // FLJ34047 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-2311305	ggaatacttatgataa[C/T]aacataccacattctg	C	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2314805	ggagtgatgaggctca[A/G]attcagggctcttgag	A	G	Homo sapiens ethanolamine kinase 2 (ETNK2), mRNA. /// ENST00000306755 // intron // 0 // --- // --- // --- // ---	ETNK2	ETNK2, Homo sapiens ethanolamine kinase 2 (ETNK2), q32.1
SNP_A-2303692	gctcacttggtagcaa[A/G]aaaatgacctgatctg	A	G	Homo sapiens hypothetical protein FLJ22662 (FLJ22662), mRNA. /// ENST00000240617 // intron // 0 // --- // --- // --- // ---	FLJ22662	FLJ22662, Homo sapiens hypothetical protein FLJ22662 (FLJ22662), p13.1
SNP_A-2251933	cttcattgtttccaga[A/G]aggagagtggggtacc	A	G	Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // intron	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-2239774	ctcgggctttttaatc[A/C]atgagaagactgttct	A	C	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2237123	ctctcacacactcaca[C/T]attctaattttacatt	C	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2261066	gaaagaatggtggaaa[A/G]tgttctaagagagagg	A	G	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2056383	aatactttgtcattgc[G/T]aagaataatcaggtaa	G	T	ENST00000318905 // downstream // 44021 // --- // --- // --- // --- /// ENST00000304745 // downstream // 44021 // --- // --- // ---	-	q23.1
SNP_A-2096500	agacctcaagaaaaag[C/T]actgtttgcattgaac	C	T	THNSL1 // 79896 // Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), mRNA. /// NM_020752 // upstream //	THNSL1	THNSL1, Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), p12.1
SNP_A-2077215	accaataaaatcttac[C/T]ggagagatgaaattaa	C	T	59340 // Homo sapiens histamine receptor H4 (HRH4), mRNA. /// ENST00000256906 // downstream // 2101 // --- // ---	HRH4	HRH4, Homo sapiens histamine receptor H4 (HRH4), q11.2
SNP_A-2080151	accgtcagaaaggacc[A/G]gaggcaatcaaacagc	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2009345	atttagttgcaagtta[C/G]cactgtgttacaactg	C	G	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-1996985	tttaagtctcagccaa[A/C]aaagcttgttcttcac	A	C	// 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 735073 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2041144	aacctatcgcaaagcg[A/G]aggcaggatacacttt	A	G	Homo sapiens androgen-induced 1 (AIG1), mRNA. /// ENST00000305853 // intron // 0 // --- // --- // --- // --- ///	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-2027897	aaacctcttccacgtc[A/G]ctgttctttccaccca	A	G	Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA. /// ENST00000233813 // 3UTR // 0 // --- // --	IGFBP5	IGFBP5, Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), q35

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2026198	aaaattgaagagaaca[C/T]gcaaagtgtgtatatg	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2149661	atgtatatttcattaa[A/C]tctaagagactaccaa	A	C	4644 // Homo sapiens myosin VA (heavy polypeptide 12, myoxin) (MYO5A), mRNA. /// ENST00000358212 // upstream	MYO5A	MYO5A, Homo sapiens myosin VA (heavy polypeptide 12, myoxin) (MYO5A), q21.2
SNP_A-2201999	ccacagccttacccta[C/T]agcttggcttgtctcg	C	T	--- /// ENST00000354623 // downstream // 326796 // --- // --- // --- // --- /// ENST00000283950 // upstream // 264600 // --- // ---	-	q12
SNP_A-2209969	ccccacataccggtaa[A/C]catttcattcatttct	A	C	Homo sapiens butyrate-induced transcript 1 (HSPC121), mRNA. /// ENST00000261875 // intron // 0 // --- // --- // --- // ---	HSPC121	HSPC121, Homo sapiens butyrate-induced transcript 1 (HSPC121), q22.31
SNP_A-2177003	gtgaaaataaaacctg[A/C]aagtgaccaggaacac	A	C	// 5911 // Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA. /// NM_002271 // upstream // 250969	RAP2A	RAP2A, Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), q32.2
SNP_A-1824697	taaagactaggatctc[C/T]aggaaggaaggatcat	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1827114 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1846988	tatcagcactcttgca[A/T]ctgaacccatatttcc	A	T	ENST00000272427 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-1858434	tcagagaacagaatga[C/G]cagttcaggagttcag	C	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1803790	gtcaacttggttgaag[G/T]atgcaaagtattgatt	G	T	ENST00000218652 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1813427	gtggttcacaattata[C/T]agaaagacctggctgt	C	T	// 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 //	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1808064	gtcttgaaagagggcc[A/G]cagcttggactgcatg	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 102346 // --- // --- // --- // ---	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-1809926	gtgagtgacctcagag[C/T]aggtaggctaagttat	C	T	Homo sapiens ubiquitin specific protease 54 (USP54), mRNA. /// ENST00000319786 // intron // 0 // --- // --- // --- // ---	USP54	USP54, Homo sapiens ubiquitin specific protease 54 (USP54), q22.2
SNP_A-1739541	tttcaaaatcctcagtgggcaaaaa[C/G]ctaccaacacagccacaatttttt	C	G	6546 // solute carrier family 8 (sodium/calcium exchanger), member 1	SLC8A1	SLC8A1 , rs1379023, solute carrier family 8 (sodium,p22.1
SNP_A-1962858	ctttcctgaccagtta[C/T]gctccgcacatgaatt	C	T	// 130733 // Homo sapiens hypothetical protein MGC33926 (MGC33926), mRNA. /// NM_025264 // downstream // 15726	MGC33926	MGC33926, Homo sapiens hypothetical protein MGC33926 (MGC33926), p22.1
SNP_A-1930401	ttcattttgagtataa[A/G]ccagggtaacttttaa	A	G	// 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1904538	tggggatgatttgtta[C/T]gtagtagttgctgatt	C	T	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1910117	tgtcatcgtggggaca[C/G]agtctctggatgacac	C	G	FLJ32370 // 137695 // Homo sapiens hypothetical protein FLJ32370 (FLJ32370), mRNA. /// NM_024831 // upstream //	FLJ32370	FLJ32370, Homo sapiens hypothetical protein FLJ32370 (FLJ32370), q12.1
SNP_A-1912917	tgtggaaacgaagata[C/T]ggagatagagcttccg	C	T	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1895419	tgccggatgactaata[C/G]cttttaattgagtggt	C	G	// 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 704802 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-1874080	tctcatggtgttcaca[A/G]ctgcacatgggaaaca	A	G	Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 28461 // Hs.434435 // ALDH1L1 // 10840 // Homo	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-1909788	ctgacattgtgattca[C/T]ggcaccgcttttgctt	C	T	9388 // Homo sapiens lipase, endothelial (LIPG), mRNA. /// NM_006111 // downstream // 113923 // Hs.200136 // ACAA2	LIPG	LIPG, Homo sapiens lipase, endothelial (LIPG), q21.1
SNP_A-1930829	ttccagataaatgaaa[C/G]tccctgcagagagaga	C	G	6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 68603 // Hs.546261 //	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1925832	ttatggagaaaaaagg[C/T]cataaaaaacattcaa	C	T	Homo sapiens polymerase (RNA) I polypeptide A, 194kDa (POLR1A), mRNA. /// ENST00000263857 // intron // 0 // --- //	POLR1A	POLR1A, Homo sapiens polymerase (RNA) I polypeptide A, 194kDa (POLR1A), p11.2
SNP_A-1919706	ttaagtaggaatagaa[A/G]cagtccaattccagta	A	G	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), transcript variant 2, mRNA. /// NM_006759 // intron // 0 // Hs.516217 // UGP2 // 7360 // Homo sapiens UDP-glucose	UGP2	UGP2, Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), transcript variant 2, p14
SNP_A-1962818	attccttgttaacata[C/T]ctgcacaaaaacccag	C	T	285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// NM_022374 // downstream // 33901	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-1963927	ctatgtcaacactgta[A/G]ccagaagtttaagtaa	A	G	130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// NM_006507 // downstream // 56117 // Hs.4158 // REG1B //	REG3G	REG3G, Homo sapiens LPPM429 (REG-III), p12
SNP_A-1982116	taaaacttgccaaatc[G/T]gaagtaatttaaagac	G	T	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 511203 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1662360	cagacaatgcaacagagaagaaata[A/C]agatggctaaaaaacagggacaaaa	A	C	91419 // Ku70-binding protein 3 /// NM_153377 // downstream // 470654 // Hs.19669 // FLJ90440 // 121227 //	KUB3	KUB3 , rs3916105, Ku70-binding protein 3 ,q14.1
SNP_A-1849353	tatggaatgagaatta[A/G]gcttctttctgacaac	A	G	// 54627 // Homo sapiens mRNA for KIAA1383 protein, partial cds. /// NM_032324 // upstream // 95865 // Hs.16034 //	KIAA1383	KIAA1383, Homo sapiens for KIAA1383 protein, partial cds. ,q42.2
SNP_A-1849859	tatgtatacttcttgc[A/G]acctgcattttagaag	A	G	Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// ENST00000355044 // intron // 0 // --- // --- // --- // --- ///	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-1870045	tccttgctagtcttcc[A/G]cttgtagacgcatcgc	A	G	Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // intron // 0 // --- // --- // --- // ---	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1869155	tcctgcttcagtgaca[C/G]catcaataattaagaa	C	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1861623	tcatctagagtctaaa[G/T]tctcatccacagatta	G	T	26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-2176827	caccctatccatctc[A/C]atgctcagaagtggaa	A	C	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase,	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). ,q12.13
SNP_A-2141529	atcttagaacatatta[C/T]ggtgtcatgacgaaat	C	T	375346 // Homo sapiens Similar to RIKEN cDNA 1810038N08 gene (MGC52022), mRNA. ///	MGC52022	MGC52022, Homo sapiens Similar to RIKEN cDNA 1810038N08 gene (MGC52022), p21.1
SNP_A-2153746	attagtatgattgata[C/T]gctaagagaggagaga	C	T	10133 // Homo sapiens optineurin (OPTN), mRNA. /// NM_021980 // downstream // 8157 // Hs.332706 // OPTN //	OPTN	OPTN, Homo sapiens optineurin (OPTN), p13
SNP_A-2038100	aacacagacgcaggga[C/T]ccaatccccagaggct	C	T	3359 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3A (HTR3A), transcript variant 2, mRNA. /// NM_213621 // downstream // 39180 // Hs.413899 // HTR3A //	HTR3A	HTR3A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3A (HTR3A), transcript variant 2, q23.2
SNP_A-2036234	aaattcaaatgctctc[A/G]gacggggtcattatgt	A	G	2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 409503 // Hs.374243 //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1989919	gacaccttgtggtaga[A/G]acatcacagagttcct	A	G	23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 587507	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2081992	accttggatccagag[A/G]caggcacatgacccaa	A	G	NM_198989 // downstream // 581477 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.2
SNP_A-2058323	aatcaatggttactta[C/T]agtcaacttataatga	C	T	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 346215 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2281441	gagtcagcccagataa[C/G]tgtgaaagctcttcac	C	G	64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 234058 // Hs.7482 // RBM19 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-2238345	ctctggcttcctcttc[A/G]cgcgacattctccctg	A	G	// 54877 // Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), mRNA. /// NM_194449 // upstream //	ZCCHC2	ZCCHC2, Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), q21.33
SNP_A-2301645	gcgcatcacctgggcg[G/T]cacccgcggtactgcg	G	T	ENST00000253720 // CDS // 0 // --- // --- // --- // ---	-	q13.33
SNP_A-2312358	ggacattgagtcaagc[C/T]gatctgagctcaaggg	C	T	Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // 3UTR // 0 // --- // --- // --- // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2295650	gcatgaatgtccagga[C/G]gttgcgccttgcaaaa	C	G	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 592318 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-2311407	ggaatcagagttgatg[A/C]atgaatagcccagctt	A	C	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 1635942 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2251096	cttattgatatgggag[A/G]agggaaaattgataag	A	G	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2254543	cttgctaaacaggtta[C/T]ggctcttctgtccaag	C	T	9978 // Homo sapiens ring-box 1 (RBX1), mRNA. /// ENST00000216225 // downstream // 29113 // --- // --- // --- // ---	RBX1	RBX1, Homo sapiens ring-box 1 (RBX1), q13.2
SNP_A-2277354	gagatttccttgaatc[C/G]atatggtagagccaaa	C	G	CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 103178 //	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2278753	gagcttattcctgttg[C/G]agcacatgtgtacagc	C	G	Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// ENST00000281631 // intron // 0 // --- //	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-2273714	gactgcctgtaggaca[A/G]tgcatctcagaaatcc	A	G	140801 // Homo sapiens ribosomal protein L10-like (RPL10L), mRNA. /// NM_182830 // downstream // 63685 //	RPL10L	RPL10L, Homo sapiens ribosomal protein L10-like (RPL10L), q21.3
SNP_A-2268859	gaattagtgtgactaa[C/T]gttgtatcttactggt	C	T	Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // --- // --- // --- // ---	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2049660	aagcttcttagatccc[G/T]gattaatattctctga	G	T	sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2046247	aagagaaaaaaagtaa[C/T]gaatcatagttgagtt	C	T	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 870014 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-2032652	aaataaatccaagaac[A/G]cgtggtgaacaggtgg	A	G	// 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 237418 // --- // --- // --- // ---	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2153395	attagagacagtcttg[C/T]aaagctcctggcatag	C	T	130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 325671	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-2122174	agtgatttgcaggggc[A/G]ctgtggagtatttggg	A	G	ENST00000336168 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2112419	aggcaaggtgtagaga[C/T]atcttacctcttgaga	C	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2224046	cggggtgtctggtgga[C/T]aaagaagaaatcgggg	C	T	sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 //	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-1843556	tagtgctattttctac[C/T]aacaaaacagtctcat	C	T	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1655397	tttacaaatgtaccaagtttaataa[A/G]agtcatcttgttttaaatgatctga	A	G	NM_006226 // intron // 0 // Hs.153322 // PLCL1 // 5334 // phospholipase C-like 1	PLCL1	PLCL1 , rs3771361, phospholipase C-like 1,q33.1
SNP_A-1676148	taatgatttggcagaatctcccaaa[C/T]gcttttggtctgagcttctcagctt	C	T	glutamate receptor, metabotropic 7 /// NM_181874 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamate receptor,	GRM7	GRM7 , rs3792446, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-1732137	aatgtggtaggcaaaattccagaat[G/T]gttccctaagatattcctaattccg	G	T	7112 // thymopoietin /// NM_152905 // downstream // 410822 // Hs.14456 // NEDD1 // 121441 // neural precursor cell	TMPO	TMPO , rs720336, thymopoietin ,q23.1
SNP_A-1807950	gtcttcatgaataggg[A/G]cataatttaatacatt	A	G	11197 // Homo sapiens WNT inhibitory factor 1 (WIF1), mRNA. /// ENST00000229088 // downstream // 133029 // ---	WIF1	WIF1, Homo sapiens WNT inhibitory factor 1 (WIF1), q14.3
SNP_A-1811910	gtggaaagggcagatg[A/G]actgtcttaccccgta	A	G	Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1804971	gtcatcaaaatggtga[C/G]tagaggagtgaactcc	C	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1804724	tagaaaggtgagttaa[A/G]tgcatccttagagaaa	A	G	Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // --- // --- // --- // ---	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-1788010	gggagacactctgaat[A/G]accagatgacttgtcc	A	G	Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1963498	tgagttggggtggcaa[A/C]gtttccccattcctcc	A	C	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-1945634	ttgttgaaatctgtca[A/G]gtctacctcttaaatg	A	G	// 158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// ENST00000355708 //	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-1942278	ttggcataaatgtagc[A/G]gatagtgagaataggt	A	G	// 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1927949	ttcaatattctgaaaa[A/G]ttccctcacatatctc	A	G	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 406342 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-1927565	ttcaacactaagagta[A/G]aataaatctggcagga	A	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 195382 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1916518	tgtttacaaattagga[A/G]attaatggcaactatc	A	G	// 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 662574 // Hs.504943	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-1898798	tgctttgagagtcaca[A/G]ggggatttaatttgac	A	G	Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), mRNA. /// ENST00000302541 // intron // 0 // --- // ---	MYRIP	MYRIP, Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), p22.1
SNP_A-1901388	tggattataccaacca[G/T]gccagttagaaatctc	G	T	// Homo sapiens tenascin R (restrictin, janusin) (TNR), mRNA. /// ENST00000263525 // upstream // 63245 // --- // ---	TNR	TNR, Homo sapiens tenascin R (restrictin, janusin) (TNR), q25.1
SNP_A-1891686	tgattgtcattttcta[C/T]catctctaccctgtgt	C	T	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 272269 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1875428	tctctgctctaaatca[C/T]tactcaaattatatgt	C	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1947790	tttactggaggaaaga[A/G]taagtacaccctgatg	A	G	// 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 59669 // Hs.405156 // PPAP2B // 8613 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-1969175	tttcgattaacaagaa[A/G]aaccgtgagtactagg	A	G	10950 // Homo sapiens BTG family, member 3 (BTG3), mRNA. /// ENST00000348354 // upstream // 56017 // --- // ---	BTG3	BTG3, Homo sapiens BTG family, member 3 (BTG3), q21.1
SNP_A-1984344	agtggatttcccagca[A/T]ggagattatccatccc	A	T	2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 1227800 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1794705	ggtctcggtctcttca[A/T]gcacgtgatttgtcat	A	T	Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1798900	gtaagaatcgttaaga[C/T]gatgtgcaaaagcaaa	C	T	LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1804174	gtcaccaagtgcccta[C/T]gttcaataataggaaa	C	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 432185 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1811881	gtggaaaaattaacta[C/T]gctcaaacataacctg	C	T	Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA. /// ENST00000344836 // intron // 0 // --- // --- // --- // ---	USP7	USP7, Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), p13.2
SNP_A-1814253	gtgtctgtgttcatga[C/G]aggtagtagcctgtaa	C	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 807736	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1821624	gtttgtgctaggatcc[C/T]gagcagagagaagaag	C	T	// 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// NM_017564 // upstream // 19160 // Hs.408249 //	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.3
SNP_A-2217902	cctgcagaaccataag[A/C]cacatgaatctctttt	A	C	Homo sapiens transmembrane protein 16B (TMEM16B), mRNA. /// ENST00000327087 // intron // 0 // --- // --- // --- // ---	TMEM16B	TMEM16B, Homo sapiens transmembrane protein 16B (TMEM16B), p13.31
SNP_A-2198617	catttcagagcagtca[C/G]tctgaaaagctatgta	C	G	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 818310 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2118549	agtaatcactaggggа[C/T]caatggctcaggcagg	C	T	117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 1603 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2125266	agttgtcataagctat[A/G]agagacaacataggtc	A	G	Homo sapiens hypothetical protein FLJ21069 (FLJ21069), mRNA. /// ENST00000320081 // intron // 0 // --- // --- // --- // ---	RSNL2	RSNL2, Homo sapiens hypothetical protein FLJ21069 (FLJ21069), p23.2
SNP_A-2154291	attatggattactcaa[C/T]gaagacagtgactcaa	C	T	Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// ENST00000325839 // intron // 0 // --- // --- // --- // ---	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-2156754	attctgtgcaatcata[A/C]aagttaagtgattgca	A	C	Homo sapiens rotatin (RTTN), mRNA. /// ENST00000255674 // intron // 0 // --- // --- // --- // ---	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-2166418	caaatgactgaaatta[C/T]ggccaacaaaagaaaa	C	T	Homo sapiens ceramide kinase (CERK), transcript variant 1, mRNA. /// ENST00000216264 // intron // 0 // --- // --- // --- // ---	CERK	CERK, Homo sapiens ceramide kinase (CERK), transcript variant 1, q13.31
SNP_A-2161528	atttgctttaagtaag[C/T]agatttttgacgttgc	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 484028 // Hs.116471 // CDH11	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2045021	aagaactctctttgat[A/G]acggtgagaattttgt	A	G	// 137970 // Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), mRNA. /// ENST00000287272 // downstream //	UNC5D	UNC5D, Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), p12
SNP_A-1995546	gtgatggtgacgtgtc[A/C]ttgtgggttcatcagc	A	C	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium p13
SNP_A-2013833	ttttttctactgaga[A/G]gtgagacacaaacact	A	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2048410	aagcagtgagctaaca[G/T]taatgacctggtaggt	G	T	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2078458	accatctacataccaa[C/T]gatttctatattacta	C	T	-- /// ENST00000354800 // downstream // 604392 // --- // --- //	-	q14.1
SNP_A-2100568	agatacaaagctaaac[A/G]gatacagaaaacagtg	A	G	3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 393790 // Hs.105103 //	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-2258087	ctttgtttgatcaaat[G/T]acaaggacggccaaaa	G	T	Homo sapiens molybdenum cofactor sulfurase (MOCOS), mRNA. /// ENST00000261326 // CDS // 0 // --- // --- // --- // ---	MOCOS	MOCOS, Homo sapiens molybdenum cofactor sulfurase (MOCOS), q12.2
SNP_A-2250598	cttagttaactcagaa[A/G]tgaagctgagggtagc	A	G	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 361449 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2244856	cacacagcaggggaaa[C/T]gtgaatagaagatgag	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2245481	ctgggagactgtatac[C/T]gtactaccgaacgcat	C	T	Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // --- // --- // --- // --- ///	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2268555	gaatggtgcttcaata[C/T]aaatgctcaaagttgg	C	T	55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// NM_001444 // upstream // 172071 // Hs.408061 // FABP5 //	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-2268423	gaatgctttcaccagg[A/C]aaaatgcacatatgtg	A	C	Homo sapiens mRNA for KIAA0919 protein, partial cds. /// ENST00000272427 // intron // 0 // --- // --- // --- // --- ///	SEC15L2	SEC15L2, Homo sapiens for KIAA0919 protein, partial cds. p13.2
SNP_A-2084902	actcaagctagaagag[A/G]aaggagctgctaccca	A	G	9788 // Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// NM_152412 // upstream // 53398 // Hs.175350 //	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2074807	acatattttaacaata[A/T]gcttctaccaaagcag	A	T	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2042387	aactcaagtccggtga[C/T]ctgccagacacaatct	C	T	Homo sapiens eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa (EIF2B3), mRNA. /// ENST00000234553 // intron // 0 // --- // --- // --- // --- ///	EIF2B3	EIF2B3, Homo sapiens eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa (EIF2B3), p34.1
SNP_A-2026252	aaaattgtctcaataa[C/T]tgtcaactggctttct	C	T	/// ENST00000357051 // downstream // 3117202 // --- // --- // --	-	p11.1
SNP_A-2156326	attctcaaaaaaatta[A/C]aggcataactgataca	A	C	sapiens calbindin 1, 28kDa (CALB1), mRNA. /// ENST00000265431 // intron // 0 // --- // --- // --- // ---	CALB1	CALB1, Homo sapiens calbindin 1, 28kDa (CALB1), q21.3
SNP_A-2131831	atagcttccactgaga[A/G]gatctaattagcattt	A	G	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // --	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2131952	ataggatagctaggtt[A/G]aaagtccagggatccc	A	G	94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 10716 // --- // --- // --- // --	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-2116628	aggtcaggacttgaga[A/G]accacggttccaggct	A	G	Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, mRNA. /// ENST00000300417 // intron // 0 // --- // --- // --- // --- ///	LRSAM1	LRSAM1, Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, q33.3
SNP_A-2189235	cagttcagtgattcta[C/T]atccatactgcaagtt	C	T	80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// NM_030664 // upstream // 173890	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-2184771	cagctgcaggagtcct[G/T]aagaactagccaggca	G	T	// 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream //	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-2178175	cactatgaatctgtga[A/G]gtattgtcatttgact	A	G	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 328303 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2205074	ccaggtgactccaggc[C/T]caaagatcagagcagc	C	T	84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream //	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-1815745	gttaagagagaaaatg[A/G]aatcagtaaacaaaat	A	G	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA. /// ENST00000263182 // intron // 0 // --- // --- // --- // ---	BBOX1	BBOX1, Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), p14.2
SNP_A-1841122	tagcttgataacatga[A/C]ggctttatggttcctc	A	C	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 139585 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1840041	tagcaagttactcaac[C/T]caaactttcacactgc	C	T	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q25.1
SNP_A-1838879	tagacttgcaggctac[A/G]aaaatcaacataaaaa	A	G	153579 // Homo sapiens butyrophilin-like 9 (BTNL9), mRNA. /// NM_206880 // upstream // 78575 // --- // OR2V2 // 285659	BTNL9	BTNL9, Homo sapiens butyrophilin-like 9 (BTNL9), q35.3
SNP_A-1838409	tagaatacaaagaaga[A/G]taaagccaacgccata	A	G	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-1866115	tcccagcagtttagga[A/G]acagaggcggaaggat	A	G	5518 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA. /// ENST00000322146 // upstream // 20165 // --- // ---	PPP2R1A	PPP2R1A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), q13.41
SNP_A-1869764	tccttcatcagaatta[C/T]caaggttctggtcagc	C	T	-- /// ENST00000304488 // downstream // 140328 // --- // --- //	-	q24.1
SNP_A-1866810	tcccgcgacagacaaa[G/T]ggttacgcaaactttc	G	T	22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 461 // --- // --- // --- // ---	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1858782	tcagattccaaaaaca[A/G]acaaatgaatctcttg	A	G	// 79901 // Homo sapiens cytochrome b reductase 1 (CYBRD1), mRNA. /// NM_001378 // upstream // 54094 //	CYBRD1	CYBRD1, Homo sapiens cytochrome b reductase 1 (CYBRD1), q31.1
SNP_A-1858379	tcagacccctcctcaa[C/T]gtaaaagcttggcaat	C	T	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1340709 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800638	gtagaaaacagaacct[A/G]aagcaaaacttacatg	A	G	118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 476674 // Hs.523446 // COL11A1 // 1301 //	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds. ,p21.1
SNP_A-1799855	tccccagaggcctcta[C/T]attaacttccagtctt	C	T	1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream //	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-1792710	ggtaactgaagcattg[A/G]aaagcaaaaccatgat	A	G	sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, mRNA. /// NM_206810 // intron // 0 //	MOG	MOG, Homo sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, p22.1
SNP_A-1955826	tttgtatcattcccat[C/T]acagatacggatgctg	C	T	NOMO3 // 408050 // Homo sapiens nodal modulator 3 (NOMO3), mRNA. /// NM_014287 // upstream // 219502 //	NOMO3	NOMO3, Homo sapiens nodal modulator 3 (NOMO3), p12.3
SNP_A-1886617	tgggcaatgggccaaa[C/T]gcctggctcccatcac	C	T	Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000269143 // intron // 0 // --- // --- // --- // ---	AFG3L2	AFG3L2, Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, p11.21
SNP_A-1918870	ttaacatctgaatgcc[A/G]agcctcgtcctgttac	A	G	// 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 212105 // --- // --- // --- //	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1906341	tggtgcaaacacagcc[A/G]cgttgtctcatgtgtt	A	G	Homo sapiens polymerase (DNA directed), epsilon (POLE), mRNA. /// ENST00000320574 // intron // 0 // --- // --- // --- // ---	POLE	POLE, Homo sapiens polymerase (DNA directed), epsilon (POLE), q24.33
SNP_A-1917539	tgtttttgacccatta[C/T]aaacccagacttagaa	C	T	832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// U03271 // upstream //	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-1878540	tctgtgggattctagc[C/T]ccctttctgggcagg	C	T	2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 191219 // Hs.122926 // NR3C1 //	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1878047	tctgtaccagtgacac[A/G]ctctgtgagacgacac	A	G	6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-1960415	tttttatctcacccgg[G/T]aattataaagacacct	G	T	Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 //	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-1978031	aattgtaacatcttgg[A/C]aaaagcttttaaaaaa	A	C	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 150072 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1975393	tctggacatttttgag[C/T]cataaagccatcttac	C	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1806158	gtcctgaagtatttca[G/T]aggtattttcaatgac	G	T	Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), mRNA. /// ENST00000309439 // intron // 0 // ---	ANAPC10	ANAPC10, Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), q31.21
SNP_A-1813998	gtgtcagttccaagat[C/T]accacattgaagactt	C	T	10749 // Homo sapiens kinesin family member 1C (KIF1C), mRNA. /// NM_017986 // upstream // 42480 // Hs.110128 //	KIF1C	KIF1C, Homo sapiens kinesin family member 1C (KIF1C), p13.2
SNP_A-1849403	tatggagattttcaaa[C/T]ttgctattcttgcttt	C	T	// 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 54067 //	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-1860463	gtgcagagcaaacata[C/T]ctgaaggctaaaagtt	C	T	FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 602253 //	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2206719	ccatgatccagagaga[A/G]aggtggacacctcagt	A	G	Homo sapiens myosin, heavy polypeptide 14 (MYH14), mRNA. /// ENST00000262269 // intron // 0 // --- // --- // --- // ---	MYH14	MYH14, Homo sapiens myosin, heavy polypeptide 14 (MYH14), q13.33
SNP_A-2181083	cagacactaactacac[C/T]gaggaagaaatactat	C	T	Homo sapiens integrin, alpha 1 (ITGA1), mRNA. /// ENST00000282588 // intron // 0 // --- // --- // --- // ---	ITGA1	ITGA1, Homo sapiens integrin, alpha 1 (ITGA1), q11.2
SNP_A-2170253	caaggttcccaccaaa[A/G]gaaactgcagatttgc	A	G	Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // --- // -	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-2185019	cagcttggctatgcca[C/T]ctgaggtcttgctccc	C	T	84913 // Homo sapiens atonal homolog 8 (Drosophila) (ATOH8), mRNA. /// NM_003896 // downstream // 24138 //	ATOH8	ATOH8, Homo sapiens atonal homolog 8 (Drosophila) (ATOH8), p11.2
SNP_A-2199513	catttttagtaattc[C/T]agtatctggccatcct	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 634980 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2199641	ccaaaagattggatac[A/C]ctgatctaaagtcttg	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 341979 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2116170	aggtaagtgagggacc[C/T]gaaaagaaaagagtta	C	T	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 382648 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2163920	caaaactaactcatga[G/T]ctcccttccagagcct	G	T	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2150899	atgtggctggcctttta[C/T]gaggaaatctggaaag	C	T	Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// ENST00000324072 // CDS // 0 // --- // --- // --- // ---	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2021926	aaaaacttcagtagct[C/T]aactcctaacttgacc	C	T	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 216279 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2031591	aaagtaaaaatgagta[C/T]attagacaagaggttg	C	T	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 609666 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-2037764	aacaagtctggcagaa[A/G]aagtcacatttaaagg	A	G	Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 //	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-2039066	aacaggggcagggaa[C/T]catctgacataacaac	C	T	5450 // Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRNA. /// NM_017589 // downstream //	POU2AF1	POU2AF1, Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), q23.1
SNP_A-2012756	agagacagaagagtaa[A/G]aagtaaatgatgtgag	A	G	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2010288	aacaaatttaatacaa[A/G]gaaaggcaacttatgt	A	G	59350 // Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), mRNA. /// ENST00000340501 // downstream // 118215 // --- // --- // --- //	LGR7	LGR7, Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), q32.1
SNP_A-2052025	aaggttataaggccag[C/T]atatagaaaagctggg	C	T	// 83697 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 9 (SLC4A9), mRNA. /// NM_017747 // upstream // 5590 // Hs.434219 // ANKHD1 //	SLC4A9	SLC4A9, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 9 (SLC4A9), q31.2
SNP_A-2237524	ctctcgtcagaatgga[C/T]gccagctgctggtgcg	C	T	KIAA1838 // 84498 // Homo sapiens KIAA1838 (KIAA1838), mRNA. /// NM_002793 // downstream // 87764 // Hs.352768	KIAA1838	KIAA1838, Homo sapiens KIAA1838 (KIAA1838), q27
SNP_A-2236839	ctctagaactgcttac[C/T]gaagcacagggtgaga	C	T	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // --- // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2239833	ctgaaatttttccaca[A/G]gtgataaaagaaatgt	A	G	LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 //	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-2266860	gaagttcagggtaaag[G/T]ccactcctgctgtgga	G	T	29094 // Homo sapiens HSPC159 protein (HSPC159), mRNA. /// ENST00000335402 // upstream // 44374 // --- // ---	HSPC159	HSPC159, Homo sapiens HSPC159 protein (HSPC159), p14
SNP_A-2273278	gactccaactctcaga[A/T]tcaagggatcctcgca	A	T	Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // intron // 0 // --- // --- //	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2274715	gagaaagagaagaaaa[A/G]tcggagaaactggcca	A	G	2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2068871	acaatcgccctatgtc[C/T]cattcacaagatgttc	C	T	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-2084783	actattttgaccaagc[A/G]gaattccaaagaagtg	A	G	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2100168	agagttaaacaaaaac[A/T]gtcagggaattatgga	A	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 487856	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2094257	agaaggttagttgaaa[A/G]cttcagactcatgatg	A	G	// 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 104763 //	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-2030242	aaagcacttgcctgct[C/T]agaatttgaggagcag	C	T	ENST00000318905 // downstream // 36707 // --- // --- // --- // --- /// ENST00000304745 // downstream // 36707 // --- // --- // ---	-	q23.1
SNP_A-2149788	atgtattggggactta[C/T]catatgctagacactc	C	T	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 275953 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2114148	agggaaaggagattca[A/C]tcaatagagagactga	A	C	1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 115555 // Hs.183850 // DCTD //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-2198301	cattgttctgaagatg[A/G]caaggaaacctttagg	A	G	282617 // Homo sapiens interleukin 28B (interferon, lambda 3) (IL28B), mRNA. /// ENST00000318438 // upstream //	IL28B	IL28B, Homo sapiens interleukin 28B (interferon, lambda 3) (IL28B), q13.2
SNP_A-1844635	tataactatttcaaaa[C/T]tagtgttccattccca	C	T	Homo sapiens phosphodiesterase 11A (PDE11A), mRNA. /// ENST00000286063 // intron // 0 // --- // --- // --- // --- ///	PDE11A	PDE11A, Homo sapiens phosphodiesterase 11A (PDE11A), q31.2
SNP_A-1856323	tcacacactgaatgcc[G/T]cgagtactcacatttc	G	T	sapiens phosphodiesterase 8A (PDE8A), transcript variant 4, mRNA. /// NM_173457 // intron // 0 // Hs.9333 // PDE8A //	PDE8A	PDE8A, Homo sapiens phosphodiesterase 8A (PDE8A), transcript variant 4, q25.3
SNP_A-1854770	tcaacattagagagac[C/T]gtatggcatgggcatg	C	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1843534	tagtgccctgattttc[C/T]agaattctggttgtgc	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 700949 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802986	agagctctgttttgac[A/T]ctgtctttgcctggga	A	T	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 252807 // Hs.435730 //	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1985651	tctccatatgcttcac[A/G]gaaacatgtaacttct	A	G	3111 // Homo sapiens major histocompatibility complex, class II, DO alpha (HLA-DOA), mRNA. /// NM_033554 // downstream // 48006 // Hs.347270 // HLA-DPA1 // 3113 //	HLA-DOA	HLA-DOA, Homo sapiens major histocompatibility complex, class II, DO alpha (HLA-DOA), p21.32
SNP_A-1961741	ctgaaatttattctta[A/C]cattcttctccccact	A	C	Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), mRNA. /// ENST00000342929 //	NALP13	NALP13, Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), q13.43
SNP_A-1956082	tttgtgagcatgacaa[A/G]tctggtcccagtccag	A	G	// 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1555478 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1897492	tgctgaggcagaacag[A/G]cagggcaccaaggcac	A	G	sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 13 (CLECSF13), mRNA. /// ENST00000272367 // intron // 0 // --- // --- // --- // ---	CLEC4F	CLEC4F, Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 13 (CLECSF13), p13.3
SNP_A-1901074	tggatcaggaatcaga[A/T]gtcatatggatctgcc	A	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// NM_006113 // downstream // 48346 // Hs.267659 //	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p13.3
SNP_A-1911423	tgtcttctctgctgat[A/G]aactcactgctggttc	A	G	85019 // Homo sapiens hypothetical protein MGC11386 (MGC11386), mRNA. /// NM_003831 // upstream // 6221 //	C18orf45	C18orf45, Homo sapiens hypothetical protein MGC11386 (MGC11386), q11.2
SNP_A-1934491	ttctctaattacgaaa[A/G]taagcttatgacaact	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1962017	agttggggatgcacac[A/G]agaatttgcatcttca	A	G	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 798886 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1679142	tgggaactgctcagtgaatgggaaa[C/T]ggaattaaatatatctattagtttg	C	T	AK092189 // intron // 0 // Hs.61172 // FLJ34870 // 401013 // FLJ34870 protein	FLJ34870	FLJ34870 , rs4953864, FLJ34870 protein,q21.2
SNP_A-1837086	tactgtcaaaatgaga[C/T]aaatgaaagtacaatt	C	T	Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // --- // --- // --- // ---	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1834641	taccacagatcagaca[C/T]cccaaatattgaaatt	C	T	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 717078 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-1819441	gttggggaaatagtgg[C/T]atggaggtttgctaca	C	T	sapiens hypothetical gene supported by AY129010 (LOC399851), mRNA. /// ENST00000331756 // intron // 0 // ---	-	-, Homo sapiens hypothetical gene supported by AY129010 (LOC399851), p15.5
SNP_A-1823089	taaaacaaagctagaa[A/G]gaagagccattattaa	A	G	Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa (CRSP6), mRNA. /// ENST00000251871 // intron // 0 // --- // --- // --- // ---	CRSP6	CRSP6, Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa (CRSP6), q21
SNP_A-2197846	cattgagcatttacta[C/T]gtgtatgtcatcctgc	C	T	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 245399 // --- // --- // --- // ---	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2194559	catgcacgttgcaggc[A/G]cgttgaatgtgaaggt	A	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 /// Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2181062	cagacacataactgaa[A/C]ctgtctggatctgttt	A	C	7132 // Homo sapiens tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A), mRNA. /// NM_001038 // downstream // 4425 // Hs.130989 // SCNN1A	TNFRSF1A	TNFRSF1A, Homo sapiens tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A), p13.31
SNP_A-2177832	cacgttgttgagttta[C/G]acttgattttatagaa	C	G	// Homo sapiens type I transmembrane C-type lectin receptor DCL-1 (DCL-1), mRNA. /// NM_002349 // downstream // 4173	CD302	CD302, Homo sapiens type I transmembrane C-type lectin receptor DCL-1 (DCL-1), q24.2
SNP_A-2209746	cccattctcccgctgg[A/G]cattcaggtaactgga	A	G	Homo sapiens orosomucoid 1 (ORM1), mRNA. /// NM_000608 // CDS // 0 // Hs.522356 // ORM2 // 5005 //	ORM1	ORM1, Homo sapiens orosomucoid 1 (ORM1), q32
SNP_A-2128888	ataatgctaatgatga[C/T]ggctatttactgggag	C	T	Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // --- // --- // --- // ---	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-2128164	ataaggagataaatgc[A/G]cagaatttagcagaga	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1803254 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2029216	aaagaagacgggacca[C/T]attcacatgtatgacc	C	T	9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000335078 // upstream // 135214 // --- // --- // --- // --- ///	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2036440	aaattctgattttgac[C/T]caacgtttggatttta	C	T	// 25917 // Homo sapiens THUMP domain containing 3 (THUMPD3), mRNA. /// ENST00000345094 // downstream //	THUMPD3	THUMPD3, Homo sapiens THUMP domain containing 3 (THUMPD3), p25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2008870	atagacattggtagaa[A/G]ttagttccacccttaa	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2442856 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-2003049	aacccagcttaagcaa[C/T]gtcatttcctctgcct	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2003651	tttctattgctacagc[C/T]ccatatggtaacccta	C	T	Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000331968 // intron // 0 // --- // --- // --- // ---	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2087355	actgcagcagttgtaa[A/G]atgttgagtgatcctc	A	G	MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-2063981	aattatcttcctcaaa[A/G]taaatataaacatgtc	A	G	51352 // Homo sapiens Wilms tumor associated protein (WIT-1), mRNA. /// NM_006360 // upstream // 12804 // Hs.502244	WIT-1	WIT-1, Homo sapiens Wilms tumor associated protein (WIT-1), p13
SNP_A-2231223	ctattattataattca[A/G]ctcaacttcattagcg	A	G	FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 //	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2244477	ctggacctaattcaaa[A/G]taaaaacaagaggagg	A	G	/// ENST00000360919 // upstream // 287749 // --- // --- // --- // ---	-	q13.1
SNP_A-2304097	gctccatgttcttcca[C/T]gccacactatccagcc	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 338794 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2288919	gatttaggtagaaaca[C/G]tgttcttcatttaaaa	C	G	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 980985 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2292175	gcaccccagcaaagtg[A/T]aacatatttccctggc	A	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2291286	gcaatgagctaattat[A/G]aggtaaaagattatta	A	G	/// ENST00000355063 // upstream // 575404 // --- // --- // --- // ---	-	q22.1
SNP_A-2290751	gcaagcagaaaggcac[A/C]attgacagcccagggt	A	C	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2309346	ggaaaagtgggcagga[C/T]atctgactgtcaggtg	C	T	// Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 // upstream //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2240564	ctgacccctggcaacc[A/G]ctgttataactttctg	A	G	79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream //	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-2054316	aagttgggggatgata[C/T]ggtagagataggcata	C	T	// Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1137272 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2090259	acttgccacaagtcca[A/G]tcattttacatagagt	A	G	6457 // Homo sapiens EEN-B2-L4 mRNA, complete cds. /// NM_003027 // downstream // 33938 // Hs.270055 // SH3GL3	SH3GL3	SH3GL3, Homo sapiens EEN-B2-L4 complete cds. .q25.2
SNP_A-2090401	acttggcacaagatgc[A/G]aagtcagaatgcagaa	A	G	Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// ENST00000265522 // intron // 0 // --- // ---	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p13
SNP_A-2091989	agaaacatgactgaaa[A/G]gactgggagagcccac	A	G	Homo sapiens ER to nucleus signalling 1 (ERN1), transcript variant 1, mRNA. /// ENST00000225768 // intron // 0 // --- // ---	ERN1	ERN1, Homo sapiens ER to nucleus signalling 1 (ERN1), transcript variant 1, q23.3
SNP_A-2102819	agattttgtatcagac[A/T]atggcataattagaga	A	T	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2004759	cctatgtggcaacata[C/T]aatgtgaaagttataa	C	T	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 277588 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1991415	ttggtgttatactact[C/G]aaaaaacaggattgta	C	G	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 527546 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2025471	aaaatccttgccttca[C/T]gatgattccattccac	C	T	Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // --- // ---	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-2204702	ccaggatacagactca[C/T]gtagactggctctaaa	C	T	163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 123084 // Hs.221375 //	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-2222748	cgatggacagggcata[A/C]acatctgctttctcta	A	C	Homo sapiens HEEE9341 (UNQ9341), mRNA. /// ENST00000355819 // intron // 0 // --- // --- // --- // ---	CLEC9A	CLEC9A, Homo sapiens HEEE9341 (UNQ9341), p13.2
SNP_A-1822766	taaaaaatgtaatgca[A/G]cttcttagtcttttc	A	G	FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 579711 //	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-1821362	gtttgctgtaactgcc[C/T]cttcctttcacaaaag	C	T	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1147045 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1862924	ctttgcaggattcagc[C/T]catctggaagtgtctt	C	T	58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 119994 //	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864176	tccaccaacgctgtgc[A/G]agccataaatgtggca	A	G	ENST00000355787 // intron // 0 // --- // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-1872850	tctatatggcagggac[A/G]atctggcagtacttat	A	G	Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // --- // ---	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-1871231	tctaaaataatgataa[C/T]tcttcatctgagattg	C	T	29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 278497 // Hs.98367 //	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-1701963	aaacttaatacagtatccttaaccc[A/G]aaaaacatatattttagcaccagta	A	G	SMC2L1 // 10592 // SMC2 structural maintenance of chromosomes 2-like 1 (yeast) /// NM_015469 // upstream // 353591 // Hs.24608 // NIPSNAP3A // 25934 // nipsnap	SMC2L1	SMC2L1 , rs10521070, SMC2 structural maintenance of chromosomes 2-like 1 (yeast) ,q31.1
SNP_A-1808917	gtgaatgaaagtatca[C/T]gaggcttctaaagtac	C	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 608658	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1787169	gggaaatgtagtttac[A/G]gattgtatgcctctga	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3035279 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1789823	gggctgctgcccatac[A/T]atgtttcctgacattc	A	T	159296 // Homo sapiens NK2 transcription factor related, locus 3 (Drosophila) (NKX2-3), mRNA. /// NM_031212 //	NKX2-3	NKX2-3, Homo sapiens NK2 transcription factor related, locus 3 (Drosophila) (NKX2-3), q24.2
SNP_A-1985725	cgagcctttgtggcca[C/T]gaaatgaactaagata	C	T	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1980393	cagaattggatgagat[C/T]agaatccatttggaag	C	T	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 237666 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1935031	ttctgagtgtatgaga[C/T]gaataatgaatgtggt	C	T	5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 69452 // Hs.42146 // PAX3 //	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-1945471	ttgttcactcacatca[C/T]tgacaaacataattct	C	T	// 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 206548 // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q14.3
SNP_A-1955922	tttgtcatcgtatgaa[A/C]aacatagtgtacttag	A	C	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 81246 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1961263	ttttttccactttaag[A/G]agaggctgactgagtt	A	G	// 287015 // Homo sapiens tripartite motif-containing 42 (TRIM42), mRNA. /// NM_018155 // upstream // 94558 //	TRIM42	TRIM42, Homo sapiens tripartite motif-containing 42 (TRIM42), q23
SNP_A-1950087	tttcaccagcaagatc[G/T]gagcatttttctgctc	G	T	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 242749 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1912499	tgtgcatactcacaaa[A/G]aagcctggagccgctc	A	G	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 590210	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-1919503	ttaagctggcctgtaa[G/T]gttcttcaaattgtga	G	T	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 526698 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1897151	tgctcgtccttcatgg[C/T]cacgtgtgatgagatc	C	T	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // downstream // 95779 // Hs.22543 // UBE3A //	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q11.2
SNP_A-1878670	tctgttaccttaaaaa[C/T]ttctcagacactaaaa	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1599825 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1895701	tgcctctgcctcttat[C/T]agcctgaaactgacat	C	T	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1913942	tgtgtgacttaagcta[A/C]acctgtgtttttattg	A	C	9699 // Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // downstream //	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1906503	tggtggcttccttccc[G/T]gatagacagagctgga	G	T	KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 163362 //	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-1943230	ttggtgactaattata[A/T]gtttggtgtaatcaag	A	T	// 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// NM_080818 //	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-1935348	ttctggaaaaggtaca[A/T]ctatggagaaaataaa	A	T	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 592346 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1789159	gggcaggtttgttcta[A/G]cctcttgacattagct	A	G	7053 // Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3), mRNA. /// NM_198994 // upstream // 22743 // Hs.452039 //	TGM3	TGM3, Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3), p13
SNP_A-1790008	ggggaaaaatggttaa[A/C]aatcccagatgatttc	A	C	Homo sapiens kelch-like ECT2 interacting protein (KLEIP), mRNA. /// ENST00000209884 // intron // 0 // --- // --- // --- // ---	KLHL20	KLHL20, Homo sapiens kelch-like ECT2 interacting protein (KLEIP), q25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801618	gtagtaagaggtgtga[C/T]gaggttattagattct	C	T	// 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000327792 // downstream // 248063 // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p13.11
SNP_A-1731711	gaattaagttgtgggtgtctcttaa[C/T]gtatacttagcttgaaggaaaacaa	C	T	5618 // prolactin receptor /// NM_144722 // upstream // 352824 // Hs.137422 // FLJ23577 // 79925 // KPL2 protein	PRLR	PRLR , rs10512632, prolactin receptor ,p13.2
SNP_A-1744593	attaacttttatacatagtcattaa[C/T]ctagcattttatagtcctaaaatct	C	T	7260 // tumor suppressing subtransferable candidate 1 /// NM_018436 // downstream // 1089342 // Hs.97899 // ALLC //	TSSC1	TSSC1 , rs10495509, tumor suppressing subtransferable candidate 1 ,p25.2
SNP_A-1862875	tcattgaaatgagacc[A/G]gaaggcccatcttgtg	A	G	Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1850974	tattatcccaactaga[C/T]gatcagttcccaatga	C	T	// 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 525865 // Hs.444075 // STS-1 //	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-1834353	tacattcctaccaaca[C/T]tgtgcaagcgttccct	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5 (GALNTL5), mRNA. /// ENST00000323750 // intron // 0 // --- // --- // --- // --- ///	GALNTL5	GALNTL5, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5 (GALNTL5), q36.1
SNP_A-1831409	taatgtcttctaggaa[C/T]ccctatatggcctgcc	C	T	ENST00000339047 // intron // 0 // --- // --- // --- // ---	-	q15
SNP_A-2225971	ctaaattgcttaagaa[C/T]tgtcttactcctttag	C	T	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2206272	ccatcccagctctatg[A/G]aatagtttattatgtg	A	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 175077 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2212009	ccctgagtagctctaa[G/T]tggtatttggcaaagc	G	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2760659 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2178719	cactgaaaaacaatta[C/T]gtcttctggaatgtgc	C	T	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2131894	ataggaatacagcaaa[C/G]taaaatgccacaaaag	C	G	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 989205 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2004616	tagatgagaaaggata[A/G]taacttggaccaggct	A	G	283846 // Homo sapiens mRNA for KIAA0220 gene, partial cds. /// NM_006043 // upstream // 9497 // Hs.115830 //	KIAA0220	KIAA0220, Homo sapiens for KIAA0220 gene, partial cds. ,p12.1
SNP_A-2018903	tcaagacggtgtgtaa[C/T]tgatgtaaccactgag	C	T	23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 214190 //	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-2054007	aagttactctttgaga[A/G]gcactgactcaaagca	A	G	1371 // Homo sapiens coproporphyrinogen oxidase (CPOX), mRNA. /// ENST00000264193 // upstream // 30466 // --- // ---	CPOX	CPOX, Homo sapiens coproporphyrinogen oxidase (CPOX), q12.1
SNP_A-2048772	aagccattgtcttctc[C/G]atcctcaggacaattt	C	G	sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), mRNA. /// ENST00000329185 // intron // 0 // --- // --- // --- // ---	KCNB2	KCNB2, Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), q13.3
SNP_A-2071428	acagaaaaggggtttc[A/C]aacgatacttgaaata	A	C	Homo sapiens dynein, cytoplasmic, light intermediate polypeptide 1 (DNCLI1), mRNA. /// ENST00000273130 //	DNCLI1	DNCLI1, Homo sapiens dynein, cytoplasmic, light intermediate polypeptide 1 (DNCLI1), p23
SNP_A-2071816	acagactcctgcttct[C/T]aaacccctcccccaa	C	T	// Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 1044998 // Hs.232819 // PCDH15 // 65217 //	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2260492	gaaacagacccaaacc[C/T]atagctaattacgtga	C	T	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), mRNA. /// ENST00000338458 // intron // 0 // --- // --- // --- // --- /// ENST00000296315 // intron // 0 // ---	ARHGEF3	ARHGEF3, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), p14.3
SNP_A-2261836	gaaataaacactgacc[G/T]atcattccgatgaaac	G	T	Homo sapiens plexin A2 (PLXNA2), mRNA. /// ENST00000264296 // intron // 0 // --- // --- // --- // ---	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2261797	gaaagtttaagacaca[C/T]tacgatatctcgcaaa	C	T	Homo sapiens ankyrin repeat domain 12 (ANKRD12), mRNA. /// ENST00000262126 // intron // 0 // --- // --- // --- // ---	ANKRD12	ANKRD12, Homo sapiens ankyrin repeat domain 12 (ANKRD12), p11.22
SNP_A-2266832	gaagttacttgccttc[A/G]actacaccatagtgag	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2240647	ctgactaaagacttga[C/T]actactaaacattaat	C	T	// 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // downstream // 19164 // Hs.498570	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1
SNP_A-2244687	ctggagtatgcccaat[A/G]atcacatatattctca	A	G	3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 160034	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2246378	ctggttcctctgcttc[A/G]aatacccgcattcatg	A	G	Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // intron // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-2255809	cttgttttataactaa[C/T]tgaaagctgctggtcc	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2076451	acatttaagttaatgg[A/C]aaaaatgtaacgcttt	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1339189 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2058622	aatcagtcctgttatc[A/G]cccttaaagaaattct	A	G	170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-2106172	agccccaggaagtgac[A/G]aaatcaggaacaccct	A	G	3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000357097 //	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135 q12.3
SNP_A-2018922	caggagtaagatgctg[C/T]cacacaccctggatca	C	T	NM_000411 // intron // 0 // Hs.371350 // HLCS // 3141 // Homo sapiens holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase) (HLCS), mRNA. /// ENST00000336648 // intron // 0 // --- // --- // --- // ---	HLCS	HLCS, Homo sapiens holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase) (HLCS), q22.13
SNP_A-1994725	ctattatctctaattc[A/G]acactgtattatctct	A	G	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-1995086	ctaggcttctcatcag[A/G]atgaagtgaccagtca	A	G	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2039550	aacatctagaactcaa[C/G]aacccagtctgattac	C	G	Homo sapiens RAS guanyl releasing protein 3 (calcium and DAG-regulated) (RASGRP3), mRNA. /// ENST00000337416 // intron // 0 // --- // --- // --- // ---	RASGRP3	RASGRP3, Homo sapiens RAS guanyl releasing protein 3 (calcium and DAG-regulated) (RASGRP3), p22.3
SNP_A-2042622	aactcccccaaacaca[C/T]ataaagggcttagcac	C	T	4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// NM_032829 // upstream // 13661	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11
SNP_A-2040880	aaccctaaaacagcaa[A/C]gttctgcccttccccc	A	C	// 57118 // Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 //	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-2137620	atcatctttcttgcca[C/T]gatttttggtgatcct	C	T	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 886824 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-2110339	aggaatgaacatgaaa[C/G]aatatggatgaaacca	C	G	Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), mRNA. /// ENST00000274695 // intron // 0 // --- // --- // --- // ---	CDKAL1	CDKAL1, Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), p22.3
SNP_A-2110432	aggaatttatcataga[C/T]gtaggcttttcatttc	C	T	// 5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000335192 // downstream // 627324 // ---	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2122537	agtgctgccattaatc[A/G]aagtcgttataaagct	A	G	CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 5256 // Hs.445899 //	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1
SNP_A-2119684	agtattactaaattca[C/T]gttggttcctccccac	C	T	65055 // Homo sapiens chromosome 2 open reading frame 23 (C2orf23), mRNA. /// NM_018433 // upstream // 73362 //	C2orf23	C2orf23, Homo sapiens chromosome 2 open reading frame 23 (C2orf23), p11.2
SNP_A-2143207	atgacaactagactgg[C/T]cagtgattaacatttt	C	T	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 898920	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2142302	atgaaacagccctaaa[A/C]agagcagagaatctgt	A	C	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2159519	tttgttcctttaggta[C/T]gggagatttagtaaat	C	T	Homo sapiens LIM domain 7 (LMO7), mRNA. /// AF330045 // intron // 0 // Hs.207631 // LMO7 // 4008 // Homo sapiens LIM	LMO7	LMO7, Homo sapiens LIM domain 7 (LMO7), q22.2
SNP_A-1830425	taatattgttttcaac[C/T]gtggagagaccccaat	C	T	Homo sapiens MOB1, Mps One Binder kinase activator-like 1B (yeast) (MOBK1B), mRNA. /// ENST00000264089 // intron // 0 // --- // --- // --- // ---	MOBK1B	MOBK1B, Homo sapiens MOB1, Mps One Binder kinase activator-like 1B (yeast) (MOBK1B), p13.1
SNP_A-1821150	gtttgaaatctggttc[A/G]ctttgtaagttctggc	A	G	Homo sapiens keratin, hair, basic, 4 (KRTHB4), mRNA. /// ENST00000257951 // intron // 0 // --- // --- // --- // ---	KRTHB4	KRTHB4, Homo sapiens keratin, hair, basic, 4 (KRTHB4), q13.13
SNP_A-1819127	gttgctagaagaaaac[A/G]cggaataatttttgg	A	G	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1035708 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1828350	taagatgctcacacaa[C/T]cacataaaaatctttg	C	T	/// ENST00000332119 // downstream // 104760 // --- // --- // ---	-	q11.2
SNP_A-1851174	tattcaatgatgttca[A/C]atttttacagcctta	A	C	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1870417	tccttttgatttttta[C/G]catgtttttagaatta	C	G	Homo sapiens hypothetical protein FLJ30596 (FLJ30596), mRNA. /// ENST00000282512 // intron // 0 // --- // --- // --- // ---	FLJ30596	FLJ30596, Homo sapiens hypothetical protein FLJ30596 (FLJ30596), p13.2
SNP_A-1669501	tatttgggagggaactgtaattatg[A/C]aattgggtaagatggtgggaggctt	A	C	5885 // RAD21 homolog (S. pombe) /// NM_173851 // upstream // 228054 // Hs.179082 // SLC30A8 // 169026 //	RAD21	RAD21 , rs2921752, RAD21 homolog (S. pombe) ,q24.11
SNP_A-1801358	gtaggaggaataataa[C/T]aattttggtcagagaa	C	T	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), transcript variant 1, mRNA. /// ENST00000272000 // intron //	LYST	LYST, Homo sapiens Chediak-Higashi syndrome 1 (CHS1), transcript variant 1, q42.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1958184	ttttcattaaaaggaa[C/T]ttcaagtcacaactgc	C	T	sapiens peptidyl-prolyl isomerase G (cyclophilin G) (PPIG), mRNA. /// ENST00000260970 // intron // 0 // --- // --- // --- // ---	PPIG	PPIG, Homo sapiens peptidyl-prolyl isomerase G (cyclophilin G) (PPIG), q31.1
SNP_A-1967324	cctctattaaataagc[A/G]cctgcgactggctggt	A	G	Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (KCNN3),	KCNN3	KCNN3, Homo sapiens potassium intermediate,q22
SNP_A-1905402	tggtaagctagttaga[C/G]gtcctactgagacatt	C	G	Homo sapiens GLIS family zinc finger 1 (GLIS1), mRNA. /// ENST00000312233 // intron // 0 // --- // --- // --- // ---	GLIS1	GLIS1, Homo sapiens GLIS family zinc finger 1 (GLIS1), p32.3
SNP_A-1901324	tggatgtccaactgta[C/T]gacagctttagtgttt	C	T	Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// ENST00000359660 // intron // 0 // --- // ---	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1898825	tgctttggaaagtaga[A/C]aagtttagtgttggca	A	C	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 311264 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1899505	tggaagcagtaggtcc[A/T]catttctgaaggaggg	A	T	Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, mRNA. /// NM_182799 // intron // 0 //	FLJ39155	FLJ39155, Homo sapiens hypothetical protein FLJ39155 (FLJ39155), transcript variant 2, p13.2
SNP_A-1923505	ttaggctgttgtagaa[A/T]agactatttgcaaggc	A	T	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1929358	ttcagtcttttcattc[A/G]agggtgatttacatca	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1975703	aagtggttaagtggca[C/G]cttgtgaaagcctgtt	C	G	Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 //	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-1972956	ggataatcactattca[A/G]gctatgataggctcca	A	G	132204 // Homo sapiens synaptoporin (SYNPR), mRNA. /// ENST00000295894 // downstream // 34829 // --- // --- // --- // ---	SYNPR	SYNPR, Homo sapiens synaptoporin (SYNPR), p14.2
SNP_A-1976717	gtaactggcaatcctg[C/T]aaccatacactccaaa	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1979214	ctaggccttcattcca[C/T]aatattgggcctctat	C	T	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-1986659	ggagaacttggactgc[A/C]atcacctgggtcacag	A	C	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 140487 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-1933316	ttctaaggtagcaata[A/G]gcaaataaccataaca	A	G	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 633387 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1803255	gtattgagccttgcca[C/T]gttggctattcttatt	C	T	Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // intron // 0 // --- //	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2
SNP_A-1813083	gtggtaaaaagtgcaa[A/G]ttaaaaatgtctcgta	A	G	ENST00000283060 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-1787912	gggactgtgccgactc[C/T]agcaagtatgcccca	C	T	7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 329859 //	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-1799468	gtaatgatatcttgaa[C/T]cttaatggacatggag	C	T	/// ENST00000359165 // upstream // 282230 // --- // --- // --- // -	-	p21.3
SNP_A-1646424	tcctgcagagatagaactgtatcaa[G/T]aattcaggattccgactaatgccct	G	T	NM_001729 // intron // 0 // Hs.73105 // BTC // 685 // betacellulin	BTC	BTC , rs10518128, betacellulin,q13.3
SNP_A-1718835	tctcttcccctaggaatgacagaat[C/T]gggtatgtgagacttcctcagaact	C	T	NM_021255 // upstream // 34783 // Hs.44038 // PELI2 // 57161 // pellino homolog 2 (Drosophila)	-	- , rs241557, - ,q22.3
SNP_A-1860823	tcataatgccctgcca[A/G]tctctagctcaggttg	A	G	1) L-type voltage-dependent calcium channel a1 subunit (hHT) mRNA, complete cds. /// NM_000719 // intron // 0 // Hs.335817 // CACNA1C // 775 // Homo sapiens calcium	-	-, Homo sapiens (clone hHT-1) L-type voltage-dependent calcium channel a1 subunit (hHT) complete cds. ,p13.33
SNP_A-1853139	tatttggttctcttaa[A/G]taatcaagaacattaa	A	G	UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 //	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1817523	gttcattaccagagga[A/G]gtagcagaattggtct	A	G	// 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), mRNA. /// NM_173508 // upstream //	KCNK1	KCNK1, Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), q42.2
SNP_A-1831399	taatgtctaaaaatct[A/G]aaatactggcttctat	A	G	57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream //	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-1838106	tagaacactaaactca[A/G]caaccacagaatatac	A	G	55802 // Homo sapiens transcription factor SMIF (HSA275986), mRNA. /// NM_000720 // upstream // 19760 //	DCP1A	DCP1A, Homo sapiens transcription factor SMIF (HSA275986), p21.1
SNP_A-1841529	taggagtaagtaatca[A/C]gcaagggaaagagtat	A	C	140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// NM_019888 // upstream // 4782 // Hs.248018 //	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-1842265	taggtaacatgtttac[C/T]gctcaatgaataggac	C	T	84931 // Homo sapiens hypothetical protein FLJ14816 (FLJ14816), mRNA. /// NM_030381 // upstream // 293392 //	FLJ14816	FLJ14816, Homo sapiens hypothetical protein FLJ14816 (FLJ14816), q14.2
SNP_A-2146501	atgctgaatacagaag[C/T]cagacaaaggaatgca	C	T	/// ENST00000295749 // downstream // 11051 // --- // --- // ---	-	q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2119036	agtagagaagccacca[C/T]gttaagccaaagaatg	C	T	1233 // Homo sapiens chemokine (C-C motif) receptor 4 (CCR4), mRNA. /// ENST00000332361 // downstream //	CCR4	CCR4, Homo sapiens chemokine (C-C motif) receptor 4 (CCR4), p23
SNP_A-2107819	agctcatgactgacag[C/G]caacatggaaacaggg	C	G	Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2123509	agtgtgcaagtgaaaa[C/G]aagagttgcaggtctc	C	G	80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 249103 //	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-2181704	cagagagcccatgacc[A/G]gagtgagaacttcctc	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2174256	cacactgcacccagtc[C/G]atgctacccttttttat	C	G	54852 // Homo sapiens membrane progestin receptor gamma (MPRG), mRNA. /// NM_004856 // upstream // 6873	MPRG	MPRG, Homo sapiens membrane progestin receptor gamma (MPRG), q23
SNP_A-2210862	ccccttcctcatgggc[A/G]catctaaattccaaag	A	G	Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000273382 // intron // 0 // --- // ---	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-2213554	ccgtattcttctggaa[C/T]tgtatttttttaattgt	C	T	ENST00000343505 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2035349	aaatggatttttaaaaa[A/T]tacttgtcctatgaag	A	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2023566	aaaactcgctattaaa[A/T]gctatcttgtgtaacg	A	T	56943 // Homo sapiens e(y)2 protein (e(y)2), mRNA. /// NM_004215 // upstream // 96924 // Hs.409368 // EBAG9 //	e(y)2	e(y)2, Homo sapiens e(y)2 protein (e(y)2), q23.1
SNP_A-2029805	aaagagtcacgaatcc[A/G]agacatttttaaaaca	A	G	Homo sapiens zinc finger protein 323 (ZNF323), mRNA. /// NM_145909 // intron // 0 // Hs.509410 // ZNF323 // 64288 //	ZNF323	ZNF323, Homo sapiens zinc finger protein 323 (ZNF323), p22.1
SNP_A-1994162	atgcttggttccacac[A/T]cacttgccagtgcttt	A	T	Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // intron // 0 // Hs.546267 // MMP16 // 4325 //	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2000947	tattgtgaaaaactca[C/T]gaagctgttctgcttt	C	T	Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 //	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-2007989	atcagggtaaaaggga[A/C]aatggaaatggtcatt	A	C	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 200444	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2009102	aatttcatatccaagc[A/C]aactaattgtgagggc	A	C	ENST00000344062 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-2085466	actccacagatgggat[A/G]agcacaaaagccctat	A	G	// 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 597870 // Hs.478682 // C3orf6 // 152137 //	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2255576	ctlgtgctttgcccca[A/G]atagcctgacatgagg	A	G	Homo sapiens down-regulated in gastric cancer GDDR (GDDR), mRNA. /// ENST00000328895 // intron // 0 // --- // ---	GDDR	GDDR, Homo sapiens down-regulated in gastric cancer GDDR (GDDR), p13.3
SNP_A-2245701	ctgggcttcctttgtc[A/C]cacctggtcaaagctg	A	C	6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA. /// NM_145248 // upstream // 177978 //	SOX1	SOX1, Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), q34
SNP_A-2231020	ctatgtatgtgccagg[C/T]atcttgctggggatag	C	T	79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream //	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-2231344	ctattctgtctactga[A/G]tatgtgaaactttaat	A	G	23543 // Homo sapiens RNA binding motif protein 9 (RBM9), mRNA. /// AF229058 // upstream // 297511 // Hs.282998 //	RBM9	RBM9, Homo sapiens RNA binding motif protein 9 (RBM9), q12.3
SNP_A-2263403	gaacatgctgctgaaa[A/G]tcatgaagcctgtgtg	A	G	55591 // Homo sapiens clone A34.1 transmembrane protein vezatin mRNA, complete cds. /// NM_017599 // downstream // 105459 // Hs.24135 // VEZATIN // 55591 // Homo sapiens	VEZATIN	VEZATIN, Homo sapiens clone A34.1 transmembrane protein vezatin complete cds. ,q22
SNP_A-2308533	gttcaggtgtccacta[C/G]agctatttgggcttag	C	G	// 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1497090 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2287975	gattatgttaaaatta[A/G]atggcaaaaataaata	A	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 718901 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2289730	gcaaaagttaatacaa[C/T]acatgatacagtccca	C	T	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // --- // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2304423	gctctaatcctagcaa[G/T]gaggaaacaatagaca	G	T	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA. /// ENST00000343348 // intron // 0 // --- // --- // --- // ---	SEMA6A	SEMA6A, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), q23.1
SNP_A-2276284	gagagatgctgaaaat[C/G]agaaagagctgtgggc	C	G	Homo sapiens dynamin 2 (DNM2), mRNA. /// ENST00000359692 // intron // 0 // --- // --- // --- // --- ///	DNM2	DNM2, Homo sapiens dynamin 2 (DNM2), p13.2
SNP_A-2231194	ctattagttgtgatca[C/T]ggcattgtgactatat	C	T	56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 46769 // --- // --- // --- // ---	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2229355	ctaggatgaatcacta[A/G]aggaacttgagggtta	A	G	Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // --- // --- // --- // --- ///	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2236949	ctctagtttgtctgtc[C/T]agagccttgtgggaac	C	T	29967 // Homo sapiens low density lipoprotein-related protein 12 (LRP12), mRNA. /// ENST00000276654 // upstream //	LRP12	LRP12, Homo sapiens low density lipoprotein-related protein 12 (LRP12), q22.3
SNP_A-2079385	accccatacataataa[A/G]caagagctacaaaaag	A	G	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2106228	agcccctgcctccgca[A/G]attcacaaattccatc	A	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_022788 // intron // 0 // Hs.532933 // P2RY12 // 64805 //	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2059607	aatctcggggcttcca[C/T]caggattgtggtaggc	C	T	57553 // Homo sapiens mRNA for KIAA1364 protein, partial cds. /// ENST00000207726 // upstream // 14036 // --- // --- // ---	MICAL3	MICAL3, Homo sapiens for KIAA1364 protein, partial cds. ,q11.21
SNP_A-2071900	acagagaggataagac[A/G]gaaatgttgggtctca	A	G	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3,	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-2012719	cattgcatcctcgcac[A/G]acctgttctgtgtgtg	A	G	1021 // Homo sapiens cyclin-dependent kinase 6 (CDK6), mRNA. /// NM_152703 // downstream // 154217 // Hs.489118	CDK6	CDK6, Homo sapiens cyclin-dependent kinase 6 (CDK6), q21.2
SNP_A-1994267	tgtgattactctagca[A/G]gttctattagaaatat	A	G	-- /// ENST00000344692 // upstream // 46683 // --- // --- // --- //	-	q22.1
SNP_A-2222590	cgagtctggagatata[C/T]atacagctaacattcc	C	T	79782 // Homo sapiens hypothetical protein FLJ23259 (FLJ23259), mRNA. /// NM_182610 // upstream // 11480 //	LRRC31	LRRC31, Homo sapiens hypothetical protein FLJ23259 (FLJ23259), q26.2
SNP_A-2182406	cagataaagaatgaga[C/T]tccaagaagtgaagta	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2178423	cactccaggaacttac[C/T]ccaagccctggtgaga	C	T	491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 114187 // Hs.268942 //	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2190064	cataagaaccctggca[C/T]aggaaacgtcagctgt	C	T	sapiens oxytocin receptor (OXTR), mRNA. /// ENST00000316793 // intron // 0 // --- // --- // --- // ---	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-2121802	agtgagaacctttctc[C/T]aaaaatcaggctgggc	C	T	115024 // Homo sapiens hypothetical protein MGC20781 (MGC20781), mRNA. /// ENST00000269534 // intron // 0 // ---	MGC20781	MGC20781, Homo sapiens hypothetical protein MGC20781 (MGC20781), q21.2
SNP_A-2140537	atctcctcatgagctc[A/C]agaacagccgtttcat	A	C	sapiens KIAA0029 mRNA, partial cds. /// NM_015361 // intron // 0 // Hs.412462 // R3HDM // 23518 // Homo sapiens R3H	R3HDM	R3HDM, Homo sapiens KIAA0029 partial cds. q21.3
SNP_A-2153646	attaggattctctttg[C/T]aaattagctgcctcag	C	T	// 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1354011 // --- // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1833312	tacacttggaccctga[C/T]gggcattgtggtggcc	C	T	/// ENST00000333610 // downstream // 13154 // --- // --- // ---	-	p24.1
SNP_A-1833500	tacagatgagcttaac[A/G]cttcttttaaggctta	A	G	81788 // Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK), mRNA. /// NM_018203 //	SNARK	SNARK, Homo sapiens likely ortholog of rat SNF1,q32.1
SNP_A-1827426	taactagtttttctca[C/T]gtgaaagactggcaag	C	T	129831 // Homo sapiens developmentally regulated RNA-binding protein 1 (DRB1), mRNA. /// NM_032523 // upstream	DRB1	DRB1, Homo sapiens developmentally regulated RNA-binding protein 1 (DRB1), q31.2
SNP_A-1755422	tgtaagtgatacaaatggcctttca[C/G]tctacagtcatctggtatcaaataa	C	G	// solute carrier family 26, member 7 /// NM_134266 // intron // 0 // Hs.354013 // SLC26A7 // 115111 // solute carrier family	SLC26A7	SLC26A7 , rs10504903, solute carrier family 26, member 7 ,q21.3
SNP_A-1681452	atatttgcaaaaaagaaaaatccaa[C/T]taaatgattgtcataaggtttaaat	C	T	NM_021828 // intron // 0 // Hs.302018 // HPSE2 // 60495 // heparanase 2	HPSE2	HPSE2 , rs1109233, heparanase 2,q24.2
SNP_A-1689861	ctgagacacaaaaataaatcaatga[A/G]aacttgaatctgcagtttttcctcc	A	G	NM_015153 // downstream // 2702232 // Hs.348921 // PHF3 // 23469 // PHD finger protein 3	PHF3	PHF3 , rs10484414, PHD finger protein 3,q12
SNP_A-1793751	ggtattatggatgtca[A/G]tagttatttcaaagct	A	G	C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 //	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-1813102	gtggtaatatttgtga[A/G]ctactgtgcaagtcac	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1110856 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1814149	gtgtctaattgtagaa[G/T]acagaactgttttgtt	G	T	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1805895	gtccctgtctccaaca[C/T]gtacctcatgatgcag	C	T	8646 // Homo sapiens chordin (CHRD), transcript variant 2, mRNA. /// NM_177979 // downstream // 166092 // Hs.166186	CHRD	CHRD, Homo sapiens chordin (CHRD), transcript variant 2, q27.1
SNP_A-1934812	ttctctttcctaccac[A/G]cttttaggaaattaca	A	G	Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, mRNA. /// NM_016100 // intron // 0 // Hs.368783 // NAT5 // 51126 //	NAT5	NAT5, Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), transcript variant 3, p11.23
SNP_A-1938764	ttgagcctttgaaatc[C/T]actttaaatgctgctg	C	T	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960753	tttttctgccattgca[C/T]atccttgaacttgcca	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1951454	tttcctcagtgtcaag[G/T]agtcaataacatcatc	G	T	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 529260 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1953181	gcgacagatttctata[C/T]gttttgtagagtagat	C	T	Homo sapiens cyclin E1 (CCNE1), transcript variant 1, mRNA. /// NM_057182 // intron // 0 // Hs.244723 // CCNE1 //	CCNE1	CCNE1, Homo sapiens cyclin E1 (CCNE1), transcript variant 1, q12
SNP_A-1985498	agattcagcaaagggc[C/T]caatgaagaaaacagc	C	T	-- /// ENST00000244644 // upstream // 15532 // --- // --- // --- //	-	p22.2
SNP_A-1921427	ttaccatattcatcaa[G/T]ccatctacataaaaca	G	T	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // upstream // 189918 // Hs.5025 //	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1918064	ttaaacagactaaagc[C/G]agcatttggggatatg	C	G	57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 284369 //	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-1887322	tgagaagtcccaagct[C/G]agaggggagacctgcc	C	G	Homo sapiens chromosome 19 open reading frame 21 (C19orf21), mRNA. /// ENST00000339938 // intron // 0 // --- //	C19orf21	C19orf21, Homo sapiens chromosome 19 open reading frame 21 (C19orf21), p13.3
SNP_A-1883606	tgaacgtcaaatgagg[C/T]aataatatctgtgaag	C	T	// Homo sapiens klotho beta like (LOC152831), mRNA. /// ENST00000257408 // intron // 0 // --- // --- // --- // ---	LOC152831	LOC152831, Homo sapiens klotho beta like (LOC152831), p14
SNP_A-1895979	tgccttcctggcagcc[A/G]agcaggctattcagta	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1919383	ttaagatggagcaaca[C/T]acataggaaaagagga	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1950441	tttcagtgagccagca[C/T]agatagcgccactgca	C	T	sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, mRNA. /// NM_020987 // intron // 0 //	ANK3	ANK3, Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, q21.2
SNP_A-1958515	ttttcgacagcaaaaa[G/T]aattgagctgccacat	G	T	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 266596 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-1959339	ttttgcaaatcctagc[C/T]cagttgctaccaagaa	C	T	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // --- // ---	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-1677654	accagcaccatttctgatgagtaga[A/C]ccacagcataagctagtaaactgta	A	C	1316 // core promoter element binding protein /// NM_031436 // upstream // 456190 // Hs.250469 // AKR1CL2 // 83592 //	COPEB	COPEB , rs10508281, core promoter element binding protein ,p15.1
SNP_A-1642723	gccactaagggcttccaggatgtta[C/T]gactacaaccataggtgcagagatg	C	T	NM_182511 // downstream // 1229635 // Hs.131596 // CBLN2 // 147381 // cerebellin 2 precursor	-	- , rs9319816, - ,q22.3
SNP_A-1829052	taaggggatttttaaa[A/T]tattgtctggtgagta	A	T	131566 // Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// NM_020351 // upstream //	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1
SNP_A-1826575	taacaattttagaata[C/T]caaatgagtgtcaatt	C	T	/// ENST00000360991 // downstream // 882418 // --- // --- // ---	-	q12.1
SNP_A-1826845	taacataaattaagga[A/C]cactactatcagttta	A	C	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1853508	tattttgggcagaaac[A/C]acccagaaactacccc	A	C	Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // intron // 0 // ---	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-2157491	attgatcattgccatc[A/G]caatatgtccattaat	A	G	51059 // Homo sapiens hypothetical protein LOC51059 (LOC51059), mRNA. /// ENST00000160713 // upstream //	LOC51059	LOC51059, Homo sapiens hypothetical protein LOC51059 (LOC51059), q24.23
SNP_A-2151437	atgttccacccgcaga[A/G]aaggcccctactgagt	A	G	// 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1397562 //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-2121756	agtgactaagcaggaa[A/G]ctaaggccaccatgca	A	G	79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// NM_014945 // upstream // 19379 // Hs.49688 //	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-2120661	gaagaggcggaaaaaa[A/T]ctggtggattaaagaa	A	T	// 10208 // Homo sapiens chromosome 13 open reading frame 22 (C13orf22), mRNA. /// NM_001629 // upstream //	C13orf22	C13orf22, Homo sapiens chromosome 13 open reading frame 22 (C13orf22), q12.3
SNP_A-2192135	catcactttgctgacc[A/G]cttgcagggccgttta	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2176016	caccaagaaatgtgta[A/C]agcgatgtattttgat	A	C	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-2214006	cctaagactgatttttt[A/T]aaaaagcaacatcaac	A	T	MGC14595 // 84294 // Homo sapiens hypothetical protein MGC14595 (MGC14595), mRNA. /// NM_006265 //	MGC14595	MGC14595, Homo sapiens hypothetical protein MGC14595 (MGC14595), q24.11
SNP_A-2214492	cctacttttccttggg[A/T]actgaaacttggtgcc	A	T	6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 214061 // Hs.175905 // AUH	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2216230	agaaacatgaggtaga[C/T]gaagtgtgtacgcatt	C	T	Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA. /// ENST00000356218 // intron // 0 // --- //	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-2210286	ccccattagctgaaaa[A/G]tcagtccacagtgatg	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1750958 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207205	ccattattctctgaaa[C/T]cccgggcaagaaactt	C	T	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 130659 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2206165	ccatcagatgtcaccc[A/G]attctgttctcttttt	A	G	// 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1955619 // Hs.32452 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-2205333	ccagtctaggtttcca[C/G]taggattcttactggg	C	G	83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 68084 // Hs.432458 // PRG4 //	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2201484	ccaatgggctttaaat[G/T]aataatgttcatcatt	G	T	9728 // Homo sapiens KIAA0256 gene product (KIAA0256), mRNA. /// NM_004236 // downstream // 59922 // Hs.369614	KIAA0256	KIAA0256, Homo sapiens KIAA0256 gene product (KIAA0256), q21.1
SNP_A-1995976	tcattgtattggtata[C/T]cgatgcttatctatta	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2030107	aaagcaaaatgataga[A/G]attacttcactaggtt	A	G	ENST00000251041 // intron // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-2070692	acacggaaatgtcagc[A/G]gcaactctctgggtga	A	G	5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 91634 //	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2062586	aatgtcagagctgtgt[C/T]aatgggcaaagattgt	C	T	284716 // Homo sapiens hypothetical protein MGC47816 (MGC47816), mRNA. /// ENST00000324149 // intron // 0 // ---	MGC47816	MGC47816, Homo sapiens hypothetical protein MGC47816 (MGC47816), p34.2
SNP_A-2053064	aagtcgtccttgatga[G/T]cttactggtcaaagat	G	T	83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 68164 // Hs.432458 // PRG4 //	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2078607	accatgtcatcgaaaa[G/T]tttatttttttgcatg	G	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1813158 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2083359	actaacagtatatctc[C/T]aatgcctttctgtcac	C	T	27178 // Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, mRNA. /// NM_014439 //	IL1F7	IL1F7, Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, q13
SNP_A-2086050	actctcagtctcccca[A/G]agggcaaaggctttcc	A	G	Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA. /// ENST00000265022 // intron // 0 // --- // --- // --- // ---	DGKG	DGKG, Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), q27.2
SNP_A-2236304	ctcgaacccaatcaga[A/G]tcaatatttctctcct	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2230959	ctatgggctaaagtag[A/G]aaaatcacatgactat	A	G	4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream // 7911	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2232155	tgatagccattctatg[A/G]aggaaaagattatgtt	A	G	Homo sapiens ectonucleoside triphosphate diphosphohydrolase 5 (ENTPD5), mRNA. /// ENST00000334696 // intron // 0 // --- // --- // --- // ---	ENTPD5	ENTPD5, Homo sapiens ectonucleoside triphosphate diphosphohydrolase 5 (ENTPD5), q24.3
SNP_A-2232518	ctcaccactctcctga[A/C]cttctttgcacagtat	A	C	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2256264	ctttaggatattctgg[A/G]aactttgctgtgctgt	A	G	PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 1139675 // Hs.405156 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.3
SNP_A-2250151	cttactcttgagcaaa[A/G]aaggatgttaccttaa	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2260158	gaaaatctgcttaaaa[C/T]gctatgtgacactaat	C	T	Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // --- // ---	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2
SNP_A-2272082	gaccctgtcccaaaag[A/G]aaaggctcaggagaga	A	G	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2243310	ctgccttcctatttta[C/G]ctcaagtttgtttggc	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1518943 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2233711	ctcatattctcacgta[G/T]gtttttctcatatatc	G	T	4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream //	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-2235877	ctcctgacacctccac[C/T]actccccagagctgca	C	T	FLJ35725 // 152992 // Homo sapiens hypothetical protein FLJ35725 (FLJ35725), mRNA. /// NM_080819 // upstream //	FLJ35725	FLJ35725, Homo sapiens hypothetical protein FLJ35725 (FLJ35725), p16.1
SNP_A-2239973	ctgaagaaatgcctta[C/T]ctaatggctaaatgcc	C	T	Homo sapiens glutathione transferase zeta 1 (maleylacetoacetate isomerase) (GSTZ1), transcript variant 2, mRNA. /// NM_001513 // intron // 0 // Hs.26403 // GSTZ1 //	GSTZ1	GSTZ1, Homo sapiens glutathione transferase zeta 1 (maleylacetoacetate isomerase) (GSTZ1), transcript variant 2, q24.3
SNP_A-2291136	gcaatataaagttagc[A/G]acatcccattgattta	A	G	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // intron // 0 // Hs.511504 // TCF12 // 6938 //	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-2086116	actctcttcctgggac[A/G]aaactggggaaggcgg	A	G	2615 // Homo sapiens glycoprotein A repetitions predominant (GARP), mRNA. /// NM_015516 // upstream // 34868 //	GARP	GARP, Homo sapiens glycoprotein A repetitions predominant (GARP), q13.5

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100310	agagtttgggagaaaa[G/T]gtatgaggaggaagta	G	T	1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 //	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q22.1
SNP_A-2051070	aaggctttatgattgg[C/T]aatatttactgagtgt	C	T	ENST00000309493 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-2059051	aatccccagttttcca[G/T]aatctcaagttattct	G	T	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 2140592 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2060573	aatgacttagtaatta[C/T]cacttctaggtaacat	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2058476	cctttctttgctccca[C/T]agaacagtactttgta	C	T	sapiens activating transcription factor 1 (ATF1), mRNA. /// ENST00000262053 // intron // 0 // --- // --- // --- // ---	ATF1	ATF1, Homo sapiens activating transcription factor 1 (ATF1), q13.12
SNP_A-2070065	acacatagcgcgtaag[C/T]accagggacacatggg	C	T	23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 96039 // Hs.166017 // MITF	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. ,p14.1
SNP_A-2038337	aacacgcagattacaa[C/T]cagagccaggaaagca	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2041758	aacgtggaatgaagca[C/T]atcaataggtgaagct	C	T	Homo sapiens glycoprotein M6A (GPM6A), transcript variant 1, mRNA. /// NM_201591 // intron // 0 // Hs.75819 // GPM6A //	GPM6A	GPM6A, Homo sapiens glycoprotein M6A (GPM6A), transcript variant 1, q34.2
SNP_A-1995842	atattcaggactgaaa[C/T]gttatgtaactttaag	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 922832 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1993692	gacaagaagtgtgtct[C/T]actcatttttaaacc	C	T	// 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 215500 // Hs.491941	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2207005	ccatgtggctttgcag[A/G]aatgcccctctgaaga	A	G	SLC39A12 // 221074 // Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), mRNA. /// NM_201593 // upstream // 18360 // Hs.59093 // CACNB2 //	SLC39A12	SLC39A12, Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), p12.33
SNP_A-2226377	ctaagactcagcacaa[C/T]tagccgtgcccatcag	C	T	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 727916 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2181642	cagagacatcagcaca[A/G]attgacgaaaatgcaa	A	G	Homo sapiens plasticity related gene 3 (PRG-3), transcript variant 1, mRNA. /// NM_017753 // intron // 0 // Hs.382683 //	PRG-3	PRG-3, Homo sapiens plasticity related gene 3 (PRG-3), transcript variant 1, q31.1
SNP_A-2174020	cacacatttttgccac[C/T]gaacttcctttgggaa	C	T	57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 337414 // --- // ---	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-2183167	cagcaacgttcaggta[C/T]gatgaatcacttcagt	C	T	SLC20A1 // 6574 // Homo sapiens solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA. /// NM_152515 // downstream // 17846 // Hs.469719 //	SLC20A1	SLC20A1, Homo sapiens solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), q13
SNP_A-2124784	agttctgttctaaccc[A/G]cggtggtacagtgaga	A	G	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2157141	attgaagaggcattta[C/T]atacccacgttcatag	C	T	// Homo sapiens hypothetical protein FLJ30707 (FLJ30707), mRNA. /// ENST00000322475 // intron // 0 // --- // --- // --- // ---	FLJ30707	FLJ30707, Homo sapiens hypothetical protein FLJ30707 (FLJ30707), q14.3
SNP_A-1849312	tatggaaaatagacac[A/C]gtacaaactcttcctc	A	C	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 107900 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-1869066	tcctgccaacactcca[C/T]acttcctgattgccct	C	T	FLJ32685 // 152110 // Homo sapiens hypothetical protein FLJ32685 (FLJ32685), mRNA. /// ENST00000358592 //	FLJ32685	FLJ32685, Homo sapiens hypothetical protein FLJ32685 (FLJ32685), p24.2
SNP_A-1822835	taaaaacttcagggaa[A/C]ggaaagatttcttaaa	A	C	Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), mRNA. /// ENST00000284548 // intron // 0 // --- // --- // --- // ---	OBSCN	OBSCN, Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), q42.13
SNP_A-1758660	ccggatactggatgctgtcttttag[A/G]aacctaactctattaccagaaactt	A	G	214 // activated leukocyte cell adhesion molecule /// NM_175056 // downstream // 1018212 // Hs.352213 //	ALCAM	ALCAM , rs10511213, activated leukocyte cell adhesion molecule ,q13.11
SNP_A-1716975	aaaattggaccaatatgtcatttta[G/T]aagaaactttgtaatccacagatac	G	T	CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 1550917 // Hs.499861 //	CTNNA3	CTNNA3 , rs1504476, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1814687	gtgtggtgagtcagca[A/G]agacttgagtcaccat	A	G	5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000217725 // upstream	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1794919	ggtcttgtcgggaaga[A/G]cattgacttttcctgt	A	G	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 466397 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1799540	gtaatgttaagtaaaa[G/T]aagtcacacaaaaaca	G	T	Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // --- // ---	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-1934445	ttctcctttgtaaaat[C/G]aaaatatgagattaag	C	G	Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000299322 // intron // 0 // --- // --- // --- // ---	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1940144	ttgcataatattcagc[C/T]cttagttggtgctgcc	C	T	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1984301	gcatccttaccaagag[A/G]cctccttcttcttttt	A	G	// 10744 // Homo sapiens pituitary tumor-transforming 2 (PTTG2), mRNA. /// NM_004219 // downstream // 119693 //	PTTG2	PTTG2, Homo sapiens pituitary tumor-transforming 2 (PTTG2), q34
SNP_A-1980805	agtgcattcccgaaac[C/T]ggcaacttcaaatgca	C	T	sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA. /// ENST00000344204 // intron // 0 // --- // --- // --- // ---	TRIO	TRIO, Homo sapiens triple functional domain (PTPRF interacting) (TRIO), p15.2
SNP_A-1915592	tgttctcatcttaggc[C/T]acttggaaagcaatga	C	T	/// ENST00000321719 // upstream // 491168 // --- // --- // --- // -	-	p11.21
SNP_A-1912147	tgtgagtgatgctgac[A/G]ggcaaaggacagagac	A	G	9276 // Homo sapiens coatomer protein complex, subunit beta 2 (beta prime) (COPB2), mRNA. /// NM_004164 // downstream // 8187 // Hs.182313 // RBP2 // 5948 // Homo	COPB2	COPB2, Homo sapiens coatomer protein complex, subunit beta 2 (beta prime) (COPB2), q23
SNP_A-1904645	tggggctgtacctcaa[A/G]gcacaggatagcagaa	A	G	Homo sapiens myosin, heavy polypeptide 10, non-muscle (MYH10), mRNA. /// ENST00000269243 // intron // 0 // --- // ---	MYH10	MYH10, Homo sapiens myosin, heavy polypeptide 10, non-muscle (MYH10), p13.1
SNP_A-1894909	tgccattaatgccaaa[A/G]agagttaggcagggat	A	G	MGC34923 // 152028 // Homo sapiens hypothetical protein MGC34923 (MGC34923), mRNA. /// NM_004189 // upstream	MGC34923	MGC34923, Homo sapiens hypothetical protein MGC34923 (MGC34923), q22.3
SNP_A-1882067	tctttgttatgttaa[C/T]gtagagccttagatat	C	T	1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream //	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1887298	tgagaagctggaggaa[C/T]ggattctccctgtgag	C	T	5740 // Homo sapiens prostaglandin I2 (prostacyclin) synthase (PTGIS), mRNA. /// NM_004776 // downstream //	PTGIS	PTGIS, Homo sapiens prostaglandin I2 (prostacyclin) synthase (PTGIS), q13.13
SNP_A-1877812	tctggtagccatcatt[C/G]aactcttgagatcaat	C	G	337976 // Homo sapiens keratin associated protein 20-2 (KRTAP20-2), mRNA. /// NM_181617 // downstream // 33601	KRTAP20-2	KRTAP20-2, Homo sapiens keratin associated protein 20-2 (KRTAP20-2), q22.11
SNP_A-1925175	ttatccacaatgaatc[A/G]atcaaggcttggcttc	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1927491	ttcaaatctgcaaaga[A/G]ctctacatttctgaca	A	G	Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // --- // --- // --- // ---	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1986052	cgtatattttccaaaa[A/C]actagttgcatgttgg	A	C	5314 // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // upstream // 69450 // Hs.446118 //	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-1961113	tttttgttgaactgaa[A/G]taaatccatcctaagt	A	G	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-1954374	tttgcagtttttagcc[A/G]agtgttcctagattca	A	G	22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 //	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1809568	gtgagagttgttaaaa[C/T]agctaacatcaacatg	C	T	154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1467153 //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1823133	taaaacacctgttcag[C/T]acatatcaaataaaat	C	T	/// ENST00000356128 // upstream // 193553 // --- // --- // --- // -	-	q24
SNP_A-1828112	taagacctcctggcag[C/T]atctttcattagatgt	C	T	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 158773 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1820869	gtttccttcttcccac[C/T]gaacacgctttcttaa	C	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1841744	taggcatagaaggaag[C/G]actaattactgagaac	C	G	133418 // Homo sapiens similar to embigin (MGC71745), mRNA. /// NM_024615 // upstream // 183351 // Hs.369581 //	EMB	EMB, Homo sapiens similar to embigin (MGC71745), q11.1
SNP_A-1840160	aacaggacttactcaa[C/T]gcttcatttcttccca	C	T	60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 229148 // Hs.462270	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-2111633	aggagtctgtaaataa[A/G]gactgaaaacaataga	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2181666	cagagactctggacaa[C/T]tgagacatttaggata	C	T	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 419936 // --- // --- // --- // -	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1996673	gttgcacctgattcta[C/T]acttctcaccattctt	C	T	80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// NM_030664 // upstream // 124267	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-2015530	attcaatgtccattca[C/T]gatgtaattgaatagg	C	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2011177	ttatagatatgctaca[A/C]cttctgtaattgtccc	A	C	COMMD10 // 51397 // Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// NM_020796 //	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-2006838	taactgaaatttagca[A/G]tctctttattatgaat	A	G	FLJ13096 // 80067 // Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 //	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-2041131	aacctagtagtcttca[A/C]gaagagagcagtactc	A	C	sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, mRNA. /// NM_182945 // intron // 0 // Hs.310429 //	NIN	NIN, Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, q22.1
SNP_A-2035560	aaatgtaatatattta[G/T]gtcacccaataaaaaa	G	T	// Homo sapiens riboflavin kinase (RFK), mRNA. /// NM_001490 // upstream // 27029 // Hs.521568 // GCNT1 //	RFK	RFK, Homo sapiens riboflavin kinase (RFK), q21.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2021010	aaaaaaaaaacccaca[C/T]attgaatgacaccatt	C	T	SLC15A4 // 121260 // Homo sapiens solute carrier family 15, member 4 (SLC15A4), mRNA. /// ENST00000315208 //	SLC15A4	SLC15A4, Homo sapiens solute carrier family 15, member 4 (SLC15A4), q24.32
SNP_A-2100418	agataacaaggaggag[A/G]agatgtaacattttca	A	G	204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// ENST00000294639 // intron // 0 // ---	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2087546	actgcgcacctataaa[A/G]caggtgataaccccac	A	G	// Homo sapiens olfactomedin-like 2A (OLFML2A), mRNA. /// ENST00000342100 // intron // 0 // --- // --- // --- // --- ///	OLFML2A	OLFML2A, Homo sapiens olfactomedin-like 2A (OLFML2A), q33.3
SNP_A-2089241	acttactgtgtatgta[C/T]atggcttcacagccag	C	T	114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // upstream // 10422 // Hs.413525 // PKD1L2 // 114780 // Homo	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-2236734	ctctacaacctagagc[A/G]cctccttaaccttcag	A	G	// Homo sapiens hypothetical protein LOC136306 (LOC136306), mRNA. /// ENST00000288513 // intron // 0 // ---	LOC136306	LOC136306, Homo sapiens hypothetical protein LOC136306 (LOC136306), q34
SNP_A-2252787	cttctaattagcagaa[A/G]ttaggaatgaaattgg	A	G	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2270274	gacacggaaagaccaa[A/G]tagttgggttgggcca	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2265516	gaagccctgctgacta[C/T]agagttaactcaaagt	C	T	Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // --- // --- // --- // ---	STK32B	STK32B, Homo sapiens serine p16.2
SNP_A-2278320	gagcggttctggagga[A/T]catacttctgctcccc	A	T	Homo sapiens CARD only protein (COP), mRNA. /// NM_033293 // intron // 0 // Hs.2490 // CASP1 // 834 // Homo	COPI	COPI, Homo sapiens CARD only protein (COP), q22.3
SNP_A-2266686	gaagtgacatcttaaa[C/T]tgatcccacaaagatg	C	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 603373	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-2259018	ctttttagatgaaac[A/T]agctttgaatctattg	A	T	Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 // intron // 0 // --- // --- // --- // ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2233005	ctcagaggggtggaaa[G/T]gaaagagagcggccag	G	T	// 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 //	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-2230711	ctatgaagtctgagta[G/T]cccagggtctcacagt	G	T	9227 // Homo sapiens lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase) (LRAT), mRNA. /// NM_004744 // downstream // 2955 // Hs.481028 //	LRAT	LRAT, Homo sapiens lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase) (LRAT), q32.1
SNP_A-2229588	ctaggtggaggccaac[A/G]gattagggccagtaat	A	G	lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // --- // --- // --- // --- ///	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. ,q13.1
SNP_A-2296061	gcattaggtctttgaa[A/G]gttggctagaatccaa	A	G	Homo sapiens kynureninase (L-kynurenine hydrolase) (KYNU), mRNA. /// ENST00000264170 // intron // 0 // --- // ---	KYNU	KYNU, Homo sapiens kynureninase (L-kynurenine hydrolase) (KYNU), q22.2
SNP_A-2311095	ggaagtatttacatca[C/T]ggaaatgagaaaacag	C	T	sapiens complement component 3 (C3), mRNA. /// ENST00000245907 // intron // 0 // --- // --- // --- // ---	C3	C3, Homo sapiens complement component 3 (C3), p13.3
SNP_A-2066431	aattttgtgtaacaca[C/T]agagatattaacctta	C	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2388926 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2048543	aagcattaaaacagaa[C/T]ataatctcaggccttt	C	T	9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // upstream // 17573 // Hs.507755 //	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds. q13.3
SNP_A-1997756	tataattaccttcata[C/T]ctaaaagcaagctct	C	T	sapiens tenascin C (hexabrachion) (TNC), mRNA. /// ENST00000350763 // intron // 0 // --- // --- // --- // --- ///	TNC	TNC, Homo sapiens tenascin C (hexabrachion) (TNC), q33.1
SNP_A-2200858	ccaagattcagtagaa[A/G]aaatacagactgtaga	A	G	/// ENST00000326756 // downstream // 78 // --- // --- // --- // ---	-	p16.1
SNP_A-2200495	ccaactaatttcttga[A/G]agatgcaatctaggct	A	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 281007 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.2
SNP_A-2161613	atttggccctgcaatg[C/G]catctcatctgaccca	C	G	404744 // Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // upstream // 171423 //	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.2
SNP_A-2164570	caaacaaatactaaga[C/G]tcagggtacaaaagga	C	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1839497	tagataggtgagtagt[C/T]acataaaaaactttaa	C	T	Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 11336 // Hs.365706 // MGP //	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-1837757	tacttttaaagtaaac[A/G]cagtgcatcataacat	A	G	// 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 1650665 // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1834383	tacattgcaaccgacc[A/G]caactatgggatgcga	A	G	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 229470 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1813811	gtgtatagtcatttca[G/T]ggcaaataaagaagca	G	T	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // --- // ---	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1805702	gtcccagcagaagtaa[C/T]tgtgaaaactattggc	C	T	ENST00000272427 // intron // 0 // --- // --- // --- // ---	-	p13.2

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802852	gtatggttgtgctcta[A/T]aaggctgtctctcaac	A	T	146 // Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), mRNA. /// NM_000311 // upstream // 212056 //	ADRA1D	ADRA1D, Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), p13
SNP_A-1800594	gtacttggtgactcat[C/T]actgacaaagcggact	C	T	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), mRNA. /// ENST00000330569 // intron // 0 // --- // --- // --- // ---	KCNQ3	KCNQ3, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), q24.22
SNP_A-1757969	acctgctgaccgagcatcggaacaa[C/T]ggttcatagaggaagacatcccagc	C	T	NM_001175 // intron // 0 // Hs.292738 // ARHGDIB // 397 // Rho GDP dissociation inhibitor (GDI) beta	ARHGDIB	ARHGDIB , rs10492147, Rho GDP dissociation inhibitor (GDI) beta,p12.3
SNP_A-1948754	tttatatacctcctga[C/T]ggaaataccaacaata	C	T	ENST00000354890 // upstream // 41028 // --- // --- // --- // ---	-	p15.3
SNP_A-1946737	tttaacgcggacttcc[G/T]gagttatttctcttcg	G	T	118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// ENST00000356858 // intron	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-1980070	gtttagagtaccacta[A/C]gggtggctggagagga	A	C	Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), transcript variant 1b, mRNA. ///	PKP1	PKP1, Homo sapiens plakophilin 1 (ectodermal dysplasia,q32.1
SNP_A-1972774	acgagtttaaataagg[A/C]atcctaaatctgacac	A	C	// 84614 // Homo sapiens zinc finger and BTB domain containing 37 (ZBTB37), mRNA. /// NM_000488 //	ZBTB37	ZBTB37, Homo sapiens zinc finger and BTB domain containing 37 (ZBTB37), q25.1
SNP_A-1968502	tttgggcattggaaga[C/T]aaggacttaggtgttt	C	T	Homo sapiens cadherin-like 22 (CDH22), mRNA. /// ENST00000279063 // intron // 0 // --- // --- // --- // ---	CDH22	CDH22, Homo sapiens cadherin-like 22 (CDH22), q13.12
SNP_A-1926539	ttattctacatagaaa[A/G]caaatacgatgtgatt	A	G	57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 278126 //	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1919713	ttaagtagttaagtga[C/T]ctcatcagatttacac	C	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1909492	tgtattgtggtgtttc[C/G]aagaatttgcaaacac	C	G	// Homo sapiens hypothetical protein MGC14161 (MGC14161), mRNA. /// ENST00000351529 // intron // 0 // ---	MGC14161	MGC14161, Homo sapiens hypothetical protein MGC14161 (MGC14161), q15.3
SNP_A-1885387	tgacaaaatgcctcta[C/T]gacagggcaggactgt	C	T	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-1892903	tgcacctagttataag[A/G]aagcaataagggaggc	A	G	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 18096	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1909576	tgtattttgttttcta[C/G]gaccagttggtgtttt	C	G	Homo sapiens corin, serine protease (CORIN), mRNA. /// ENST00000273857 // intron // 0 // --- // --- // --- // ---	CORIN	CORIN, Homo sapiens corin, serine protease (CORIN), p12
SNP_A-1918898	ttaacattgtgatgga[C/T]gttctgctagttcttc	C	T	58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 65813 //	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2
SNP_A-1924575	ttatactgtgttttgg[A/T]caagtttctttaaact	A	T	// 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 171709 // Hs.201058 // STMN4 //	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-1966852	attaagtgcttcaaga[A/G]tatcatctatagcctg	A	G	// Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 52334 // Hs.203717 //	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-1969636	atgtttttttcaaagc[A/G]cctgtggagttctgct	A	G	sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // intron // 0 // Hs.434980 // APP // 351 // Homo	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3
SNP_A-1980993	tacgatcatcaactca[C/G]ctttgggcatttaagt	C	G	Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000264463 // intron // 0 // --- // --- // --- // ---	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-1953963	tttgataaaccacatg[A/C]attagactaccaacct	A	C	ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // upstream // 218674 // Hs.188746 // ADAM	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip ,q23.1
SNP_A-1952305	tttctctatgagaaca[C/T]attcagtcatgtgttc	C	T	Homo sapiens spermatogenesis associated 6 (SPATA6), mRNA. /// ENST00000254448 // intron // 0 // --- // --- // --- // ---	SPATA6	SPATA6, Homo sapiens spermatogenesis associated 6 (SPATA6), p33
SNP_A-1960545	tttttcaggatttttg[A/G]agatcagatgattgta	A	G	ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 1190661	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-1956258	tttgtgtctgttttga[A/G]cctttaagtttgtgct	A	G	// 3776 // Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), mRNA. /// NM_016121 // upstream //	KCNK2	KCNK2, Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), q41
SNP_A-1722694	accatgaactgctctgttaggatta[C/T]agattataccagccccagggtgaag	C	T	NM_007252 // intron // 0 // Hs.131638 // POU6F2 // 11281 // POU domain, class 6, transcription factor 2	POU6F2	POU6F2 , rs740511, POU domain, class 6, transcription factor 2,p14.1
SNP_A-1662102	atgaaagaggaaaagggctgactga[C/T]atttttattttaaatttaaaatact	C	T	// 2263 // fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, /// NM_018117 // downstream // 209369 // Hs.16677 // WDR11	FGFR2	FGFR2 , rs2250939, fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, ,q26.12
SNP_A-1705183	caatcacaaaatcatttctaatagc[C/T]cttgtattttatttatatatgtgac	C	T	// 3624 // inhibin, beta A (activin A, activin AB alpha polypeptide) /// NM_024728 // downstream // 113038 //	INHBA	INHBA , rs10486700, inhibin, beta A (activin A, activin AB alpha polypeptide) ,p14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802571	gtatctgaaatctaca[A/G]gtgagggaagccccaa	A	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 149814 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-1812938	gtggggccacagatac[A/G]gatggataggaatgta	A	G	PRO1085 mRNA, complete cds. /// ENST00000340003 // intron // 0 // --- // --- // --- // --- /// ENST00000244064 // intron //	-	-, Homo sapiens PRO1085 complete cds. q13.32
SNP_A-1787211	gggaacaccatatgaa[G/T]acacaaagacaaagag	G	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2678329 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1819283	gttggacaaagaagaa[A/G]acagagctaacaaccc	A	G	Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // --- // --- // --- // ---	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1818002	gttctaggaaataaac[A/G]cagatgaattataact	A	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1238939	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1866709	tcccctgattctcaga[C/T]aagtgaatttctgct	C	T	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 87313 // Hs.328883 // C1D //	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1862698	tcattcaccaaagcaa[C/T]atttctttgcagtctg	C	T	PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// NM_000633 // downstream	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-2167967	caacggtaatcacttc[A/G]ctcatatatatcacaa	A	G	lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // --- // --- // --- // --- ///	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. ,q13.1
SNP_A-2140253	atctattttcattaac[C/T]gtaactctattttcaa	C	T	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 348773 // --- // --- // --- // -	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2134407	atatggaggctatcta[A/G]ggatagtattgagtga	A	G	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 275914 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3
SNP_A-2225167	cgttatcgaggttgta[A/G]aagaccttccaagatg	A	G	// Homo sapiens B-cell CLL/lymphoma 9 (BCL9), mRNA. /// ENST00000310023 // downstream // 192586 // --- // --- // --- //	BCL9	BCL9, Homo sapiens B-cell CLL q21.1
SNP_A-2185432	caggaccagtgaaaaa[A/C]caggatcccacatgat	A	C	sapiens BCL2/adenovirus E1B 19kDa interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein,	BNIP3	BNIP3, Homo sapiens BCL2,q26.3
SNP_A-2191158	catagttattaaaatc[C/G]caacaaatgataacag	C	G	ENST00000260323 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-2007643	agaggcaagtatctca[C/G]tatttgcccaagcggg	C	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2058133	aatcaaaagcagctta[A/C]cagtttaacaattaaa	A	C	202151 // Homo sapiens hypothetical protein FLJ25422 (FLJ25422), mRNA. /// NM_004172 // upstream // 253718 //	FLJ25422	FLJ25422, Homo sapiens hypothetical protein FLJ25422 (FLJ25422), p13.2
SNP_A-2055534	aataatatatatcacc[A/G]aaagagaattttaaag	A	G	COPS7B // 64708 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis) (COPS7B), mRNA. /// NM_024409 // downstream // 16160 //	COPS7B	COPS7B, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis) (COPS7B), q37.1
SNP_A-2066068	aatttggcaatgtgta[G/T]caagagtctcaggtgt	G	T	Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000356773 // intron // 0 // --- // --- // --- // --- ///	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2085486	actccagaacaatgaa[C/G]aggacaaagggtttat	C	G	sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // --- // --- // --- // --- ///	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. q43
SNP_A-2104527	agcagggactgagtga[G/T]attcaaagaaagttcc	G	T	LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 //	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-2266564	gaagtcacagcccttc[C/T]ctttgcagacagcctc	C	T	79017 // Homo sapiens chromosome 7 open reading frame 24 (C7orf24), mRNA. /// ENST00000005374 // upstream //	C7orf24	C7orf24, Homo sapiens chromosome 7 open reading frame 24 (C7orf24), p14.3
SNP_A-2277632	gagcactgtgttctgc[A/G]ccttaacatttcttgt	A	G	Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2274605	gagaaaataaaaaata[A/C]gtgttcgtgctgctgc	A	C	Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000323418 // intron // 0 // --- // --- //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-2285746	gatgacatcagacacg[C/T]aattgaggagatttct	C	T	Homo sapiens RAS p21 protein activator 3 (RASA3), mRNA. /// ENST00000357860 // intron // 0 // --- // --- // --- // --- ///	RASA3	RASA3, Homo sapiens RAS p21 protein activator 3 (RASA3), q34
SNP_A-2265566	gaagccttaaccttca[A/G]tatgactgtatttgca	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2255643	cttgttaaataggaaa[C/T]gttgctgtatttatcc	C	T	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. ///	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255116	cttgggggaaggataa[C/G]acagggaaaaattgaa	C	G	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45), mRNA. /// ENST00000269973 // intron // 0 // --- // --- // --- // ---	ZNF45	ZNF45, Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45), q13.31
SNP_A-2312838	ggactgctgtgcccac[A/G]ggatgaaaagcctatc	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 75476 // --- // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2101922	agatgggagcaagtga[C/G]atcagcacagtgttga	C	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2091833	agaaaatctttgtagc[C/T]gagccgacctgacttt	C	T	SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream //	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-2078026	accagcttcataaata[C/G]acccctcgaatattga	C	G	114789 // Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 (SLC25A25), mRNA. /// NM_198939 // downstream // 4031 //	SLC25A25	SLC25A25, Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 (SLC25A25), q34.11
SNP_A-2071760	acagacatctatagaa[A/C]cctcccccaacaacag	A	C	Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA. /// ENST00000271002 //	ITGB3BP	ITGB3BP, Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), p31.3
SNP_A-2057184	aatataccaaacagcc[A/G]ccaaaacaaagaatta	A	G	Homo sapiens oxysterol binding protein (OSBP), mRNA. /// ENST00000263847 // intron // 0 // --- // --- // --- // ---	OSBP	OSBP, Homo sapiens oxysterol binding protein (OSBP), q12.1
SNP_A-2005469	ctgcggaacctaatcc[A/G]gaacataaggtccttt	A	G	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2178961	cactgcagccttaaca[C/T]gcaaaccacattttca	C	T	ENST00000332168 // intron // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2175469	cacatcctccctttttc[C/G]cagtacctatagcatg	C	G	Homo sapiens 5'-nucleotidase, cytosolic III (NT5C3), mRNA. /// ENST00000329714 // intron // 0 // --- // --- // --- // --- ///	NT5C3	NT5C3, Homo sapiens 5'-nucleotidase, cytosolic III (NT5C3), p14.3
SNP_A-2217940	cctgcaggggctcgtc[C/T]atcagaggatcatgtg	C	T	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA. /// ENST00000245620 // intron // 0 // --- // --- // --- // --- /// ENST000003	LILRB3	LILRB3, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), q13.42
SNP_A-2113779	aggctgcatcgcaatt[C/G]aatatggccctcaatt	C	G	// 5265 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran /// NM_001002236 // upstream // 51215 // Hs.525557 // SERPI	SERPINA1	SERPINA1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran q32.13
SNP_A-1853720	tctcagagcaaagtca[A/T]cactcaaatgacaagg	A	T	// Homo sapiens FLJ31222 protein (FLJ31222), mRNA. /// ENST00000301683 // intron // 0 // --- // --- // --- // ---	FLJ31222	FLJ31222, Homo sapiens FLJ31222 protein (FLJ31222), q21.31
SNP_A-1818326	gttctgtctctttaaa[C/T]ttggatccctttgggt	C	T	ENST00000327887 // intron // 0 // --- // --- // --- // ---	-	q31.3
SNP_A-1800105	gtaccactgcaacctg[A/T]aatagtttacgtaact	A	T	Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1646110	gaggaaagatagcatttccaaatag[C/T]tgaactgtaaaccacctagtttcca	C	T	// 2982 // guanylate cyclase 1, soluble, alpha 3 /// NM_024826 // upstream // 117073 // Hs.512735 // FLJ21159 // 79884 //	GUCY1A3	GUCY1A3 , rs717694, guanylate cyclase 1, soluble, alpha 3 ,q32.1
SNP_A-1753037	taaaggcagtgttaataaatcttga[C/T]gaaaactttctaatgattttgcaga	C	T	3696 // integrin, beta 8 /// NM_178559 // upstream // 84399 // Hs.310735 // ABCB5 // 340273 // ATP-binding cassette, sub-	ITGB8	ITGB8 , rs722188, integrin, beta 8 ,p21.1
SNP_A-1955936	tttgtccaggtatcca[C/T]gcggcataggcttcca	C	T	SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 314519 // Hs.511265 // SEM	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN ,q21.1
SNP_A-1957607	ttttatccggctccac[C/T]gcttaccagcatagtg	C	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1862406 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1940586	ttgcctagaatgtgaa[A/G]gtaagggctggggctg	A	G	// 79050 // Homo sapiens hypothetical protein MGC3162 (MGC3162), mRNA. /// NM_021808 // downstream // 22509 //	MGC3162	MGC3162, Homo sapiens hypothetical protein MGC3162 (MGC3162), q24.33
SNP_A-1979267	tttctctgtatcctac[A/G]agtaaaatcgtacaaa	A	G	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1973392	agcatggcttaatgta[A/T]catcaaacttggaaga	A	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 983097 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1967116	gatgtaaatgtggtta[A/G]gtgataccatattaaa	A	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // --- // --- // --- // ---	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1966110	agcatggatcagaaca[A/G]taagagctagcaagat	A	G	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1893914	tgcataggccaagtcc[A/T]cgctgattcaggatat	A	T	Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // ---	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1885991	tgacatttatttttaa[C/G]gactgaccagtggcaa	C	G	51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream //	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-1885088	tgaatgtggaagagac[A/G]ctgaagtctgaaatgt	A	G	5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 102545 // Hs.132225 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1877500	tctggcactgtctcac[C/T]gtatagcttcctgggg	C	T	Homo sapiens hypothetical protein FLJ10597 (FLJ10597), mRNA. /// ENST00000335497 // intron // 0 // --- // --- // --- // ---	FLJ10597	FLJ10597, Homo sapiens hypothetical protein FLJ10597 (FLJ10597), p34.1
SNP_A-1875342	tctctgactgttgcaa[C/T]aacacagttaaatcct	C	T	154064 // Homo sapiens retinoic acid early transcript 1L (RAET1L), mRNA. /// NM_024518 // downstream // 31720 //	RAET1L	RAET1L, Homo sapiens retinoic acid early transcript 1L (RAET1L), q25.1
SNP_A-1918199	ttaaagaaaatatcac[A/G]caatttaaaggtttta	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 317957 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-1913292	tgtgggcaaggccaat[C/G]atggtgaattatttct	C	G	5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1975463	ttttctatcatgttta[C/G]gtcttaattacatgtc	C	G	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1678190	gtgggtgtagagctggtgccgttcc[C/T]atcgacagcagccatgctgtcactg	C	T	595 // cyclin D1 (PRAD1: parathyroid adenomatosis 1) /// NM_138768 // downstream // 209923 // Hs.436000 // MYEOV	CCND1	CCND1 , rs1938684, cyclin D1 (PRAD1: parathyroid adenomatosis 1) ,q13.3
SNP_A-1790069	ggggaactccttctcc[A/G]gcaattaaaggatctt	A	G	Homo sapiens GTF2I repeat domain containing 1 (GTF2IRD1), transcript variant 1, mRNA. /// NM_005685 // intron // 0 // Hs.156302 // GTF2IRD1 // 9569 // Homo sapiens	GTF2IRD1	GTF2IRD1, Homo sapiens GTF2I repeat domain containing 1 (GTF2IRD1), transcript variant 1, q11.23
SNP_A-1796074	ggtgtaaatcgataac[C/T]ctttcatgctgataga	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-1829852	taataactatggcaca[A/G]atgttcaggagtgtat	A	G	Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // 3UTR // 0 // Hs.465213 //	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1841440	taggagaatagccgtc[A/C]acatcaaacaactaag	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 931189 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1854561	tcaaatttgtgacata[C/T]acagtaagcaatgaac	C	T	2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 113895 // Hs.33446 // NR5A2 //	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-1870964	tcggttaaaggagttt[C/G]aaacgaacactgagtc	C	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1871111	tcgtgtgtgaccccgt[A/G]aactctgcaaacagat	A	G	Homo sapiens checkpoint with forkhead and ring finger domains (CHFR), mRNA. /// BC012072 // intron // 0 //	CHFR	CHFR, Homo sapiens checkpoint with forkhead and ring finger domains (CHFR), q24.33
SNP_A-2115528	aggggtgagcgtgact[A/C]aagtacatttttacac	A	C	84159 // Homo sapiens mRNA; cDNA DKFZp686G23148 (from clone DKFZp686G23148). /// NM_145307 // downstream // 62002 // Hs.58559 // PLEKHK1 // 219790 //	ARID5B	ARID5B, Homo sapiens cDNA DKFZp686G23148 (from clone DKFZp686G23148). ,q21.2
SNP_A-2122163	agtgattgtggaaaca[C/T]tggtccattgtctttt	C	T	CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 //	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2116558	aggtcacaatctttta[C/T]aaactgatcttggaag	C	T	sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2148003	atggctgtcttgtaga[A/G]taggtgtgtatccccc	A	G	// 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 60860 // Hs.523852 //	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-2201777	ccacacaacaaacttg[A/G]caagcagatattatcc	A	G	-- /// ENST00000299455 // upstream // 12564 // --- // --- // --- //	-	p12.1
SNP_A-2206161	ccatcagagcttcaga[A/G]gtcttacgaggtgtaa	A	G	65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 130529 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2172710	caatttaaaactgctg[A/G]aagtctttccattttg	A	G	// 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 356017 // Hs.478682 // C3orf6 // 152137 //	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2184034	cagcccaaggtagtcc[C/T]ggaaagaaaggtgttg	C	T	Homo sapiens chromosome 18 open reading frame 11 (C18orf11), mRNA. /// ENST00000269209 // intron // 0 // --- //	C18orf11	C18orf11, Homo sapiens chromosome 18 open reading frame 11 (C18orf11), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2198158	cattgtaagaacaagt[A/G]acactcttttgtgaac	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 215272 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2199292	cattttcctgatggga[G/T]atttgtggcccagagg	G	T	2737 // Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// NM_024054 // downstream // 565502 // Hs.214247 // C7orf25	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-2197473	cattcctagtattcca[C/T]aagagaaagttttgat	C	T	// Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 216512 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2008382	tatcctaattcagaaa[C/T]gcaaaggagcccaagc	C	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1990347	ctaccatataactgaa[C/T]tgaagacgtgataaac	C	T	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2029338	taaatacagtagagaa[C/T]ggaacaggccctttga	C	T	sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2069421	acacaacttccaaata[C/T]gatactacagaatata	C	T	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2289854	gcaaacctcacaaaga[A/T]cttcaatcagagaagc	A	T	ENST00000263665 // intron // 0 // --- // --- // --- // ---	-	p12.3
SNP_A-2257685	ctttgcttgtggattg[A/G]acctgatgcctgctct	A	G	9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// NM_173827 // downstream // 424447 // Hs.356697 // FLJ38991 //	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-2286893	gatgggggttgtttca[C/T]agtccactttagttac	C	T	Homo sapiens hypothetical protein FLJ23834 (FLJ23834), mRNA. /// ENST00000343407 // intron // 0 // --- // --- // --- // ---	FLJ23834	FLJ23834, Homo sapiens hypothetical protein FLJ23834 (FLJ23834), q22.3
SNP_A-2309556	ggaaactaccaagaaa[A/C]ctcaaagatttttagg	A	C	ENST00000290568 // intron // 0 // --- // --- // --- // ---	-	p36.13
SNP_A-2071959	acagagccctctctaa[C/T]tgacagtagccatctg	C	T	170850 // Homo sapiens potassium voltage-gated channel, subfamily G, member 3 (KCNG3), transcript variant 1, mRNA. /// NM_172344 // upstream // 47786 // Hs.352633 // KCNG3 //	KCNG3	KCNG3, Homo sapiens potassium voltage-gated channel, subfamily G, member 3 (KCNG3), transcript variant 1, p21
SNP_A-2083155	acgtttgtggttgata[C/T]gttaggcctaccggat	C	T	sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA. /// ENST00000264178 //	MTR	MTR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), q43
SNP_A-2028183	aaactactgagtttca[A/G]aggtctattttccacc	A	G	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 286710 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2027420	aaacattgacatatag[A/G]aatagagtcgattatc	A	G	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 804801 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2046130	aagactgacaaacata[C/G]cctgagtcatatgtac	C	G	// 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 36624 // Hs.505007	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2003496	aggcttgggttgctca[C/T]accttggatattccca	C	T	Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), mRNA. /// ENST00000261293 // intron // 0 // --- // --- // --- // ---	UGCGL2	UGCGL2, Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), q32.1
SNP_A-2184203	cagcctcctgcctaac[A/G]ccatcttccacagtga	A	G	Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // --- // --- // --- // --- ///	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2173551	cacaatggttgagtaa[C/T]gtgcccaacacctagt	C	T	Homo sapiens chromosome 20 open reading frame 142, mRNA (cDNA clone IMAGE:4933017), with apparent retained intron. /// NM_178491 // upstream // 2000 // Hs.386735 // R3HDML // 140902 // Homo sa	C20orf142	C20orf142, Homo sapiens chromosome 20 open reading frame 142, (cDNA clone IMAGE:4933017), with apparent retained intron. ,q13.12
SNP_A-2218247	cctgctcctgtgtacc[A/G]aaacagccctccctgt	A	G	6821 // Homo sapiens sulfite oxidase (SUOX), nuclear gene encoding mitochondrial protein, mRNA. /// NM_000456 // downstream // 3362 // Hs.534353 // SUOX // 6821 // Homo	SUOX	SUOX, Homo sapiens sulfite oxidase (SUOX), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-2222142	cgaatgctctcaaagc[C/T]attcctacagagccag	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2149586	atgtagtccattatac[A/G]gccagatatactacat	A	G	// Homo sapiens aryl hydrocarbon receptor nuclear translocator-like (ARNTL), mRNA. /// ENST00000340761 // downstream // 192677 // --- // --- // --- // --- ///	ARNTL	ARNTL, Homo sapiens aryl hydrocarbon receptor nuclear translocator-like (ARNTL), p15.2
SNP_A-2144211	atgagtacagaagtta[A/G]ggatattgaaaaataa	A	G	MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 //	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2121969	agtgagtgaatgctca[C/T]aagatatggttgttta	C	T	Homo sapiens zinc finger CCCH type domain containing 8 (ZC3HDC8), mRNA. /// ENST00000272570 // intron // 0 // ---	ZC3HDC8	ZC3HDC8, Homo sapiens zinc finger CCCH type domain containing 8 (ZC3HDC8), q13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869362	tcctgtacccatgaaa[C/T]tcttgcttaattactg	C	T	2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 67510 // Hs.448717	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-1854265	tcaaaggatcatataa[A/G]ttaatgtaacctttct	A	G	Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), transcript variant 2, mRNA. /// NM_173216 // intron // 0 // Hs.207459 // ST6GAL1 // 6480 //	ST6GAL1	ST6GAL1, Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), transcript variant 2, q27.3
SNP_A-1842720	tagtaagctgtaccac[C/T]gacataccatatgtct	C	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1829692	taagtttatattctca[G/T]tatcttggtaacccag	G	T	ARHGAP15 // 55843 // Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// NM_024659 //	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.3
SNP_A-1830837	taatctggcacaggaa[A/T]ctcctaaattaaccag	A	T	Homo sapiens zinc finger protein 318 (ZNF318), mRNA. /// ENST00000318149 // intron // 0 // --- // --- // --- // --- ///	ZNF318	ZNF318, Homo sapiens zinc finger protein 318 (ZNF318), p21.1
SNP_A-1820452	gtttatcctatagata[C/T]attacctgcacataac	C	T	// 29937 // Homo sapiens secreted protein of unknown function (SPUF), mRNA. /// NM_001674 // upstream //	SCIRP10	SCIRP10, Homo sapiens secreted protein of unknown function (SPUF), q32.3
SNP_A-1822385	ctatatgcttttctga[A/T]gactgaaagaaaggga	A	T	51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 71399 // Hs.461453 // WWOX //	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1648374	acctaataaataacattttctctta[A/T]aggtttgtgtaattagatcaaccac	A	T	DKFZP434F1017 // 84075 // hypothetical protein DKFZp434F1017 /// NM_152447 // downstream // 1424712 //	DKFZP434F1017	DKFZP434F1017 , rs10498383, hypothetical protein DKFZp434F1017 ,q21.2
SNP_A-1657069	gcaaatgtttcaactcttagctaat[C/T]aaattaaggatgcaagctggagaaa	C	T	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs2089352, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-1973818	tagctccctatcctgc[A/G]acagatcccagtgtgt	A	G	Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// ENST00000325839 // intron // 0 // --- // --- // --- // ---	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1971820	cctgtctgctctcaca[A/G]gaaactgagagcagcg	A	G	sapiens xeroderma pigmentosum, complementation group C (XPC), mRNA. /// ENST00000285021 // intron // 0 // --- // --- //	XPC	XPC, Homo sapiens xeroderma pigmentosum, complementation group C (XPC), p25.1
SNP_A-1980192	caacctggcgggggaa[A/G]ttactgccaatcattg	A	G	1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 118005 // Hs.183850 // DCTD //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1941404	ttgcttctatgtatcc[A/G]agtactttagatttta	A	G	22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 9725 //	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-1945039	ttgtgtaacccaaacc[C/G]ctatcaaggtacaggc	C	G	5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1935508	ttctggggaagacttg[A/G]aagatatcctggattt	A	G	// 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), mRNA. /// NM_003108 // upstream // 272396 // Hs.432638	MTCBP-1	MTCBP-1, Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), p25.2
SNP_A-1937643	ttgaagagtttctgta[A/C]agctgaacaggcagtg	A	C	// Homo sapiens hypothetical protein FLJ31166 (FLJ31166), mRNA. /// ENST00000298530 // intron // 0 // --- // --- // --- // ---	FLJ31166	FLJ31166, Homo sapiens hypothetical protein FLJ31166 (FLJ31166), p13.2
SNP_A-1960941	tttttgcatctcagca[C/T]tacactcccattttcg	C	T	6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 712270 //	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-1954332	tttgcagatgagacac[A/G]gaggaccagagaggtt	A	G	Homo sapiens guanine nucleotide binding protein (G protein), alpha 15 (Gq class) (GNA15), mRNA. /// ENST00000262958 // intron // 0 // --- // --- // --- // ---	GNA15	GNA15, Homo sapiens guanine nucleotide binding protein (G protein), alpha 15 (Gq class) (GNA15), p13.3
SNP_A-1950274	tttcagacttttatga[C/T]gaaatttacatacaca	C	T	9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 344832 //	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-1892172	tgcaaatatgtcttcc[A/G]ctcaaagaacatatgc	A	G	-- /// ENST00000338636 // upstream // 128196 // --- // --- // --- // --- /// ENST00000334344 // upstream // 216186 // --- // --- // -	-	q12
SNP_A-1882186	tctttttttttctatt[C/T]aacactgtcagtctgc	C	T	9637 // Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), mRNA. /// NM_003162 //	FEZ2	FEZ2, Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), p22.2
SNP_A-1881555	taaaatgtttgatggc[A/G]cagatgtaacacaaga	A	G	/// ENST00000262227 // upstream // 241854 // --- // --- // --- // -- /// ENST00000314319 // upstream // 290333 // --- // --- // ---	-	p11.31
SNP_A-1915396	tgttccatttggataa[G/T]tactagtgctttatct	G	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2553254 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1915200	tgttcacagacaatga[C/T]atacaaatacctccta	C	T	2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 //	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1905935	tggtcccaacagccca[C/T]tgaataggtccacacg	C	T	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R), mRNA. /// ENST00000296474 // CDS // 0 // --- // --- // --- // --- ///	MST1R	MST1R, Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R), p21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1929906	ttcatctttttagac[A/G]actacatgataaatct	A	G	222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 1035569 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1981087	aatcagtaacactgca[A/G]tcaccagctgcatctc	A	G	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1978028	tctagaatttatcacc[A/T]atttctttagacattt	A	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 100337 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1988276	aagcaattttcacaaa[C/T]ggtgttcacgaatctg	C	T	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 129770 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1661496	agctggtcagaaaactcggactgaa[A/G]acagagtcagaagagtggagctgga	A	G	NM_004441 // intron // 0 // Hs.272311 // EPHB1 // 2047 // EphB1	EPHB1	EPHB1 , rs2400445, EphB1,q22.2
SNP_A-1676538	tatcactttaatcgaatggagaaaa[G/T]gactgtattgagaagaaaagttaca	G	T	NM_020185 // upstream // 64345 // Hs.29106 // DUSP22 // 56940 // dual specificity phosphatase 22	DUSP22	DUSP22 , rs742767, dual specificity phosphatase 22,p25.3
SNP_A-1756915	actgccttgctgacttcatcacatc[G/T]ccaaagcagaattcatggatgagga	G	T	NM_003560 // intron // 0 // Hs.309169 // PLA2G6 // 8398 // phospholipase A2, group VI (cytosolic, calcium-independent)	PLA2G6	PLA2G6 , rs10483197, phospholipase A2, group VI (cytosolic, calcium-independent),q13.1
SNP_A-1804453	gtcagaatgagtcagc[C/G]aaaacgaggttgttct	C	G	54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 222599 // Hs.435381 // C9orf39 //	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1811160	gtgcccttgcatgatc[A/T]ctatccgcccactcct	A	T	1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream //	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1818872	gttgataaatgcttgg[C/T]aactgtgactttaagc	C	T	/// ENST00000358087 // upstream // 184232 // --- // --- // --- // -- /// ENST00000344409 // upstream // 183913 // --- // --- // ---	-	p11.21
SNP_A-1831471	taatgttcatgctccc[C/T]aatttgtgtgtgtga	C	T	Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), transcript variant 1, mRNA. /// NM_201437 // intron // 0 // Hs.491745 // TCEA1 // 6917 // Homo sapiens	TCEA1	TCEA1, Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), transcript variant 1, q11.23
SNP_A-1872642	tctagtagaacataga[C/G]gtaggagaggtgagcg	C	G	Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000356773 // intron // 0 // --- // --- // --- // --- ///	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2109843	aggaacacgctgatga[A/G]ctgagcaaaggaaagg	A	G	Homo sapiens G elongation factor, mitochondrial 2 (GFM2), nuclear gene encoding mitochondrial protein, transcript variant 2, mRN /// NM_032380 // intron // 0 // Hs.277154 // GFM2 // 84340 // Homo s	GFM2	GFM2, Homo sapiens G elongation factor, mitochondrial 2 (GFM2), nuclear gene encoding mitochondrial protein, transcript variant 2, mRN q13.3
SNP_A-2134448	atatgggacacatcca[C/T]tatagggtttgggccc	C	T	// Homo sapiens nitric oxide synthase trafficker (NOSTRIN), mRNA. /// ENST00000343642 // intron // 0 // --- // --- // --- // ---	NOSTRIN	NOSTRIN, Homo sapiens nitric oxide synthase trafficker (NOSTRIN), q24.3
SNP_A-2138373	atccaggtagaaatgc[C/T]cagcaagtccttggag	C	T	KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 124358 // Hs.486470	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1
SNP_A-2163678	caaaaatatagggggg[C/T]atatctactgctttac	C	T	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2216706	cctctcgtaaagtcta[C/G]agacactgatcaggtc	C	G	// 57537 // Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// NM_020777 //	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2204469	ccagctgcacctttgc[A/G]agtttcttggtctttg	A	G	201158 // Homo sapiens similar to CGI-148 protein (LOC201158), mRNA. /// ENST00000225576 // intron // 0 // ---	LOC201158	LOC201158, Homo sapiens similar to CGI-148 protein (LOC201158), p12
SNP_A-2211952	ccctgaattatgagac[C/T]atggaaaattcaggct	C	T	Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA. /// NM_015881 // intron // 0 // Hs.292156 // DKK3 //	DKK3	DKK3, Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), p15.3
SNP_A-2179778	cacttggacccggaag[C/G]ctgtagggattggaag	C	G	80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 41934 //	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1
SNP_A-2180196	cagaaactatgacata[A/C]ggtgacataggatatg	A	C	Homo sapiens family with sequence similarity 3, member D (FAM3D), mRNA. /// ENST00000358781 // intron // 0 // --- // ---	FAM3D	FAM3D, Homo sapiens family with sequence similarity 3, member D (FAM3D), p14.2
SNP_A-2005067	ccctggctagcacagt[A/G]aaactctgtctctact	A	G	// 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000342036 // upstream // 267168 // --- // ---	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-1997293	taagacatgggtccca[A/G]cttcagaatgcttcac	A	G	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 3, mRNA. /// NM_003671 // intron // 0 // --- // CDC14B // 8555 // Homo	CDC14B	CDC14B, Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 3, q22.33
SNP_A-2008133	gatgttctggaaaaga[C/T]acacaacccagcaggg	C	T	ENST00000339657 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-2016654	caaaatggtctttact[A/T]actaaaatatgtgcaa	A	T	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 497241 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2047025	aagagtggtgtagaga[A/T]aatagaaataatggtc	A	T	54112 // Homo sapiens G-protein coupled receptor 88 (GPR88), mRNA. /// NM_080682 // upstream // 150268 //	GPR88	GPR88, Homo sapiens G-protein coupled receptor 88 (GPR88), p21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043803	aacttcaagtacttgc[C/T]gattcctaatgtccca	C	T	9497 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA. /// NM_005442 // downstream // 60385 // Hs.147279 // EOMES	SLC4A7	SLC4A7, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), p24.1
SNP_A-2039058	aacagggcaggcctga[A/G]accagcattcttagga	A	G	sapiens zinc finger protein 8 (clone HF.18) (ZNF8), mRNA. /// ENST00000355486 // intron // 0 // --- // --- // --- // --- ///	ZNF8	ZNF8, Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), q13.43
SNP_A-2038807	aacagcacagctctaa[A/G]ccaaggcagaggtcct	A	G	ENST00000273146 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2025172	aaaatagataatgtca[A/G]ctgtccaacatcaggg	A	G	Homo sapiens TU12B1-TY protein (TU12B1-TY), mRNA. /// ENST00000339146 // intron // 0 // --- // --- // --- // ---	TU12B1-TY	TU12B1-TY, Homo sapiens TU12B1-TY protein (TU12B1-TY), q23.3
SNP_A-2077798	accagaagatgactgg[A/C]aggagcaaaatggata	A	C	sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) mRNA, complete cds. /// NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and	PSD3	PSD3, Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) complete cds. ,p22
SNP_A-2308327	gcttgtagactgtcac[C/G]aagtccctcaaatctg	C	G	Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA. /// ENST00000353809 // intron // 0 // --- // --- // --- // --- /// ENST00000354638 // intron //	OCA2	OCA2, Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), q12
SNP_A-2305701	gctgccatagaaccca[A/T]attctctcttgttagc	A	T	1293 // Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 2, mRNA. /// NM_057167 // upstream //	COL6A3	COL6A3, Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 2, q37.3
SNP_A-2294923	gcataagattgcatga[C/T]ggcaaacatcgttgct	C	T	// 11010 // Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), mRNA. /// NM_007043 // upstream //	GLIPR1	GLIPR1, Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), q21.2
SNP_A-2300414	gcctcttaaaccgtac[G/T]aaacagccagactgac	G	T	// Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, mRNA. /// NM_134325 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo	SLC26A9	SLC26A9, Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, q32.1
SNP_A-2275838	gagacgtagagtcagc[G/T]cctggtgtctacccca	G	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2242064	ctgatttacactggat[C/G]aatatctgtctctccc	C	G	// Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), mRNA. /// NM_004588 // downstream // 6118	SCN4B	SCN4B, Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), q23.3
SNP_A-2244840	cctactcattcatcca[G/T]actaacctcagatgtc	G	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2244183	ctgcttttggagaaca[C/T]aaactatgacaatgtg	C	T	receptor rearranged beta-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000361005 // intron // 0 // --- // --- // -	-	-, Human T-cell receptor rearranged beta-chain V-region (V-D-J) complete cds. q34
SNP_A-2247034	ctgtattgtagctgta[C/T]agtattcaatatgtga	C	T	22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 149477 //	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2280352	ctgtagtttatgtgcc[C/T]ggaatttaaactttta	C	T	Homo sapiens secretogranin III (SCG3), mRNA. /// ENST00000220478 // intron // 0 // --- // --- // --- // ---	SCG3	SCG3, Homo sapiens secretogranin III (SCG3), q21.2
SNP_A-2269131	gaattgctggatctta[C/T]ggtgagtctgtgaggt	C	T	27295 // Homo sapiens PDZ and LIM domain 3 (PDLIM3), mRNA. /// ENST00000284771 // upstream // 10850 // --- // ---	PDLIM3	PDLIM3, Homo sapiens PDZ and LIM domain 3 (PDLIM3), q35.1
SNP_A-2296569	gcattttgcaataccc[A/G]ctcagcagccatttac	A	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 822628	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2305738	attcacaaaaacttac[A/G]gagagtgtcctaagta	A	G	FLJ32831 // 145858 // Homo sapiens hypothetical protein FLJ32831 (FLJ32831), mRNA. /// NM_207446 // downstream	FLJ32831	FLJ32831, Homo sapiens hypothetical protein FLJ32831 (FLJ32831), q26.1
SNP_A-2096419	agaccctctatcctac[C/T]agactatattcttgag	C	T	83643 // Homo sapiens coiled-coil domain containing 3 (CCDC3), mRNA. /// NM_021980 // upstream // 84189 //	CCDC3	CCDC3, Homo sapiens coiled-coil domain containing 3 (CCDC3), p13
SNP_A-2098717	agagcctcatcatttc[C/T]cactggacactgcacc	C	T	22990 // Homo sapiens pecanex homolog (Drosophila) (PCNX), mRNA. /// ENST00000304743 // downstream //	PCNX	PCNX, Homo sapiens pecanex homolog (Drosophila) (PCNX), q24.2
SNP_A-2075575	acatgcctggcttata[C/T]gctgcatccacataac	C	T	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9), transcript varian /// NM_148954 // CDS // 0 // Hs.381081 // PSMB9 // 5698 // Homo sapiens	PSMB9	PSMB9, Homo sapiens proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9), transcript varian ,p21.32
SNP_A-2075975	acattagccatattca[A/C]atcatagtattgtact	A	C	/// ENST00000359165 // upstream // 246291 // --- // --- // --- // -	-	p21.3
SNP_A-2062085	aatgggcttcagttcc[A/G]aatgtggactgtgata	A	G	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA. /// ENST00000360555 // intron // 0 // --- // --- // --- // --- ///	AAK1	AAK1, Homo sapiens AP2 associated kinase 1 (AAK1), p13.3
SNP_A-2020577	acagcgtggggatgat[A/C]aaaaggaatcttttga	A	C	Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRABA2b, mRNA. /// NM_015834 // 3UTR // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosine de	ADARB1	ADARB1, Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRABA2b, q22.3
SNP_A-2006499	ttagaactgttttata[A/G]caatgcagcaaggctt	A	G	// 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2004962	gagaaactcatttaat[A/G]acctgtgtgagaacca	A	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2173792	ctgaagtcttaatgta[A/G]acaagcctgagagata	A	G	2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 46310 // Hs.444329 // GPC6 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2189754	tttctttctaatgcaa[C/T]gatcaaaacttagcag	C	T	ENST00000359749 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2207182	ccattatcctgggtaa[A/G]tgagtatggggaactc	A	G	/// ENST00000338912 // downstream // 2820 // --- // --- // --- //	-	q11.2
SNP_A-2207341	ccattctgtgtacaag[C/T]agaacctaaccttgat	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2206830	ccatgctcataagcac[C/T]acattgtccaaaccat	C	T	// 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 773085 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2221793	ccttttcgcctggtaa[C/T]agaagctccatcttgg	C	T	// 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // downstream //	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2226689	ctaagtgcaagcttca[C/T]atttagtcctattaaa	C	T	// Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // --- // --- // --- // ---	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1
SNP_A-2161626	atttggctgcttttcc[A/G]gagtgattaaaaactt	A	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2156166	attctaagatatttta[C/T]agcagtattttggcat	C	T	374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2151569	atgttgaatgaagaga[C/T]agaaatcttggcagag	C	T	Homo sapiens numb homolog (Drosophila) (NUMB), transcript variant 3, mRNA. /// AF171938 // intron // 0 //	NUMB	NUMB, Homo sapiens numb homolog (Drosophila) (NUMB), transcript variant 3, q24.2
SNP_A-2148049	atggctttaggtctta[C/T]gtataactctttaatc	C	T	Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000223864 // intron // 0 // --- // ---	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1868179	tcctcaaagtacccag[A/G]ccaggcaagcatagag	A	G	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-1857648	tcactgaaaaggtcca[A/G]atgcatggctgtccct	A	G	Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1842326	taggtaggttgaaatg[A/G]aaagaatggaaagaga	A	G	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 184238 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-1809936	gtgagtgattgtgtaa[A/C]cccacccaagaaacca	A	C	392390 // Homo sapiens olfactory receptor, family 1, subfamily L, member 6 (OR1L6), mRNA. ///	OR1L6	OR1L6, Homo sapiens olfactory receptor, family 1, subfamily L, member 6 (OR1L6), q33.2
SNP_A-1809868	gtgagtaaacgccatc[A/G]acttgcagatatctca	A	G	Homo sapiens scavenger receptor class B, member 1 (SCARB1), mRNA. /// ENST00000261693 // intron // 0 // --- // ---	SCARB1	SCARB1, Homo sapiens scavenger receptor class B, member 1 (SCARB1), q24.31
SNP_A-1780310	ggataaccaagagaaa[A/T]gttgaatatgatgtac	A	T	Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // --- // --- // --- // --- /// ENST00000349908 // intron //	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-1724296	atctgtcattatatctccagccaaa[C/G]tgcctgaagtatctccacacagtgc	C	G	1758 // dentin matrix acidic phosphoprotein /// NM_004967 // upstream // 11433 // Hs.49215 // IBSP // 3381 // integrin-	DMP1	DMP1 , rs958848, dentin matrix acidic phosphoprotein ,q22.1
SNP_A-1738459	cctaacacagaagtcagaaagaaag[A/T]aataggaggtttggaacatctctta	A	T	NM_173508 // intron // 0 // Hs.158748 // SLC35F3 // 148641 // solute carrier family 35, member F3	SLC35F3	SLC35F3 , rs10495344, solute carrier family 35, member F3,q42.2
SNP_A-1644666	gttggaagaaacaaagaaaagaacc[C/T]agatactctggaggaaatgtaatgc	C	T	NM_016192 // upstream // 1269504 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs764142, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1985589	aaaactagaacctaca[A/G]tcgtctcagaacacaa	A	G	ENST00000354576 // intron // 0 // --- // --- // --- // ---	-	p21.33
SNP_A-1930345	ttcatttctcccatca[C/T]aagtaatgttaagcat	C	T	ANXA10 // 11199 // Homo sapiens annexin A10 (ANXA10), mRNA. /// NM_007193 // downstream // 91553 // Hs.188401	ANXA10	ANXA10, Homo sapiens annexin A10 (ANXA10), q32.3
SNP_A-1911313	tgtctgtgggaactta[A/G]agggcacagccatctc	A	G	1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // upstream // 77256 // Hs.292549	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1881501	tctttctctggtatca[G/T]tattctctgtgcttgt	G	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1874003	tctcatcctccttatc[C/T]aaatagacacaagccc	C	T	1410 // Homo sapiens crystallin, alpha B (CRYAB), mRNA. /// ENST00000317197 // upstream // 13116 // --- // --- // --- // ---	CRYAB	CRYAB, Homo sapiens crystallin, alpha B (CRYAB), q23.1
SNP_A-1880240	tcttcttcagaatgac[C/G]ccagaagtttccatct	C	G	ENST00000358349 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-1891965	tgatttttatttgacc[C/T]atggatttttagaag	C	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 1098189 // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893093	tgcagaaaagcttcat[A/T]aatagtacaaaggatt	A	T	430 // Homo sapiens achaete-scute complex-like 2 (Drosophila) (ASCL2), mRNA. /// AB029488 // downstream //	ASCL2	ASCL2, Homo sapiens achaete-scute complex-like 2 (Drosophila) (ASCL2), p15.5
SNP_A-1899446	tggaagaatttgagga[A/C]acccccctggagtgacc	A	C	Homo sapiens zinc finger CCCH type domain containing 3 (ZC3HDC3), mRNA. /// ENST00000262577 // CDS // 0 // --- //	ZC3HDC3	ZC3HDC3, Homo sapiens zinc finger CCCH type domain containing 3 (ZC3HDC3), q24.3
SNP_A-1919324	ttaagagaattactga[A/T]acgtaacacagagaca	A	T	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1926177	aaagacatatgctaaa[G/T]aaacatcattacagtt	G	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 960752	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1984630	acctgctcccttcagc[C/G]gacacatgcctggaag	C	G	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 538517 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1977884	atcctcatgtagaaca[A/C]cttcagctcagaatca	A	C	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1675025	tccagatcggttcttggcaataaaa[C/T]ttagagcaggagaaagaagataag t	C	T	27152 // PDZ domain containing 6 /// NM_024582 // downstream // 397563 // Hs.25201 // FATJ // 79633 // fat-like	PDZK6	PDZK6 , rs10518477, PDZ domain containing 6 ,q28.1
SNP_A-1734718	caggtgacagagagggagaggaaaa[A/G]gagatgtatttaaagaaatggc agg	A	G	NM_015192 // intron // 0 // Hs.429643 // PLCB1 // 23236 // phospholipase C, beta 1 (phosphoinositide-specific)	PLCB1	PLCB1 , rs761562, phospholipase C, beta 1 (phosphoinositide-specific),p12.3
SNP_A-1809778	gtgaggcagattactc[A/G]agtggagacacctccg	A	G	55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 129066 // --- // --- //	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. ,q36.2
SNP_A-1786098	ggctggagcatcagtc[A/G]cctctttctatccctt	A	G	10397 // Homo sapiens N-myc downstream regulated gene 1 (NDRG1), mRNA. /// NM_003033 // downstream // 21315 //	NDRG1	NDRG1, Homo sapiens N-myc downstream regulated gene 1 (NDRG1), q24.22
SNP_A-1864945	tccaggtctcccaata[A/T]gaatcttttgaagagc	A	T	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 656303 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2145174	atgcaatacaagtctc[A/G]gaatttgttggtgaga	A	G	Homo sapiens thyroid adenoma associated (THADA), mRNA. /// NM_022065 // intron // 0 // Hs.369592 // THADA //	THADA	THADA, Homo sapiens thyroid adenoma associated (THADA), p21
SNP_A-2132507	atagtgcttggtatca[C/T]tgagacagaagcaatt	C	T	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-2133271	atatatagcatcaaaa[A/C]tattcactcaatgtgg	A	C	ENST00000339567 // intron // 0 // --- // --- // --- // --- /// ENST00000343332 // intron // 0 // --- // --- // --- // --- ///	-	p12
SNP_A-2130306	atacggggtcatacag[A/G]aacagcttacttatat	A	G	NM_198989 // downstream // 377564 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7	-	q14.3
SNP_A-2122517	agtgctctttacccaa[C/T]caaagatcattaagag	C	T	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2217430	aatatcatttggacca[C/T]tacatagatttcatag	C	T	Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // intron // 0 // --- // DDHD1 // 80821 // Homo	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2010864	gaactttgctgcttta[C/G]gaaagaatgcaggact	C	G	23530 // Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA. /// NM_182977 //	NNT	NNT, Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), p12
SNP_A-2010511	acagcagaggaggggga[A/G]accactgatgctaagg	A	G	55805 // Homo sapiens hypothetical protein DKFZp761O0113 (DKFZp761O0113), mRNA. /// ENST00000328559 // intron // 0 // --- // --- // --- // --- ///	DKFZp761O0113	DKFZp761O0113, Homo sapiens hypothetical protein DKFZp761O0113 (DKFZp761O0113), q35.1
SNP_A-2021777	aaaaacatatttagta[A/T]atgagtcaattgtgta	A	T	Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// ENST00000313237 // intron // 0 // --- // --- // --- // ---	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-2045098	aagaagaacatttgca[C/T]tgaattagaattggag	C	T	// 5209 // Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA. ///	PFKFB3	PFKFB3, Homo sapiens 6-phosphofructo-2-kinase p15.1
SNP_A-2053321	aagtgacagataagag[A/G]agagcagtcaccgtgg	A	G	9388 // Homo sapiens lipase, endothelial (LIPG), mRNA. /// ENST00000344851 // upstream // 19303 // --- // --- // --- // ---	LIPG	LIPG, Homo sapiens lipase, endothelial (LIPG), q21.1
SNP_A-2076893	gcaagccatgccaaaa[C/G]ttgctggattcaaacc	C	G	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 743874 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2291053	gcaataaacatgacaa[A/G]gtaacaaagctaataa	A	G	51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 167124 //	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-2272137	gaccgtatgtagctta[C/T]agatttgtcttattgt	C	T	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-2247746	ctgtgacctgttttga[C/G]agaatcagagaaggtt	C	G	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 408147 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2244717	ctggagttcagtatca[C/T]gttcttggctcactgc	C	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1401203 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2236766	ctctaccctaaagaca[A/C]cgagatctccacagta	A	C	ENST00000304952 // intron // 0 // --- // --- // --- // ---	-	p11.21
SNP_A-2240492	ctgacatctctcctac[C/T]atagatctgtttttta	C	T	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 902558 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2283213	gataatgttccagata[C/T]acatgccccaaataat	C	T	9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 115278 //	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2285821	gatgagaatgaaagaa[A/G]gaatgcttaagaatta	A	G	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 585744	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2301813	gcggccaggcactcgg[C/T]ccaggtacgcgggggc	C	T	22835 // Homo sapiens mRNA for KIAA0961 protein, partial cds. /// NM_152605 // downstream // 11630 // Hs.531560 //	KIAA0961	KIAA0961, Homo sapiens for KIAA0961 protein, partial cds. ,q13.12
SNP_A-2102318	agattatatggttaaa[C/G]tgcatacatttgtagt	C	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2096740 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2222464	cgagctgctgccgtct[A/G]aaacgcagggctgcta	A	G	Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// NM_001147 // 5UTR // 0 // Hs.490892 //	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2223472	cgcttctaatagagca[A/G]gagagtaaaagtgaac	A	G	22913 // Homo sapiens RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) (RALY), transcript variant 2, mRNA. /// NM_016732 // upstream // 41023 //	RALY	RALY, Homo sapiens RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) (RALY), transcript variant 2, q11.22
SNP_A-2205392	ccagtgaggaggctaa[C/T]gttggcttatgtgcac	C	T	2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream //	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-2202303	ccaccaccacaaccac[C/G]attacaactactaaca	C	G	Homo sapiens EphA7 (EPHA7), mRNA. /// ENST00000257785 // intron // 0 // --- // --- // --- // ---	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2209062	cccaggacaccctgag[A/C]aaaagagaaatttccc	A	C	4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 64738 // --- // --- // --- // ---	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2185164	caggaaatacacaaaa[A/G]gtttgttaccagttat	A	G	64866 // Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, mRNA. /// NM_022842 // upstream // 106536 // Hs.476093 // CDCP1 // 64866 // Homo	CDCP1	CDCP1, Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, p21.31
SNP_A-2181187	cagacatctttttctg[C/T]atttggagtgatttcc	C	T	51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 43654 // --- // ---	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-2176605	cacccatggttaccac[A/G]ggacagtcttgtgggg	A	G	60559 // Homo sapiens hypothetical protein FLJ22649 similar to signal peptidase SPC22/23 (FLJ22649), mRNA. /// NM_005429 // downstream // 216818 // Hs.435215 // VEGFC	SPCS3	SPCS3, Homo sapiens hypothetical protein FLJ22649 similar to signal peptidase SPC22 q34.2
SNP_A-2166410	caaatgacagagccca[C/T]tcttgataaatgttta	C	T	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 55475 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1863531	tccaaagcatttgaca[A/G]acacaaattctcccaa	A	G	2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 142670 // --- // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-1819338	gttggattcccagtca[C/T]gtgaaccaagaaatgg	C	T	Homo sapiens deubiquitinating enzyme DUB4 (DUB4), mRNA. /// NM_201402 // downstream // 201230 // Hs.531448	-	-, Homo sapiens deubiquitinating enzyme DUB4 (DUB4), p23.1
SNP_A-1822818	taaaaactaactcaaa[A/C]ggaatcaaaagacatt	A	C	9388 // Homo sapiens lipase, endothelial (LIPG), mRNA. /// NM_006111 // downstream // 134205 // Hs.200136 // ACAA2	LIPG	LIPG, Homo sapiens lipase, endothelial (LIPG), q21.1
SNP_A-1748707	caagagtttgttttttaaagagta[A/G]tgttctcatctttcccattcttcac	A	G	AB011118 // intron // 0 // Hs.435048 // MGC23401 // 196441 // hypothetical protein MGC23401	MGC23401	MGC23401 , rs724211, hypothetical protein MGC23401,q21.1
SNP_A-1717739	cctaatttctctaggccccagttta[C/T]gcactaatatagtaaaggaatctta	C	T	// transition protein 1 (during histone to protamine replacement) /// NM_022648 // downstream // 188244 //	TNP1	TNP1 , rs1529563, transition protein 1 (during histone to protamine replacement) ,q35
SNP_A-1755402	agacatttttggtagaagcttaact[C/T]aaaaggatttcagaaggaagtttta	C	T	NM_018349 // intron // 0 // Hs.33368 // FLJ11175 // 55784 // hypothetical protein FLJ11175	FLJ11175	FLJ11175 , rs4984391, hypothetical protein FLJ11175,q26.2
SNP_A-1752937	tattcacagggcttcagaaaactac[C/T]ggcaggtccctcacagtaaggaagc	C	T	2706 // gap junction protein, beta 2, 26kDa (connexin 26) /// NM_006783 // downstream // 12502 // Hs.48956 // GJB6 //	GJB2	GJB2 , rs7981959, gap junction protein, beta 2, 26kDa (connexin 26) ,q12.11
SNP_A-1647408	ctaccttatagaagcaatgcttaga[A/G]gaactccttaatgcttgcaaatgct	A	G	NM_004481 // upstream // 76933 // Hs.307582 // GALNT2 // 2590 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) /// NM_014777 // downstream // 403943 // - // - // - // -	GALNT2	GALNT2 , rs10495292, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) ,q42.13
SNP_A-1964259	ttttgagtttctgtga[C/T]gaaatccagtcattta	C	T	Homo sapiens ring finger protein 149 (RNF149), mRNA. /// ENST00000295317 // intron // 0 // --- // --- // --- // ---	RNF149	RNF149, Homo sapiens ring finger protein 149 (RNF149), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1951477	tttcctccagtgctaa[C/T]atcttacaacacaatc	C	T	sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // --- // --- // --- // ---	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1958956	tcaatcctttctatac[A/G]cttggtcattaaaagt	A	G	163126 // Homo sapiens CREBBP/EP300 inhibitor 2 (CRI2), mRNA. /// NM_013268 // upstream // 6562 // Hs.23671 //	CRI2	CRI2, Homo sapiens CREBBP,q13.2
SNP_A-1943215	ttggtgaaatcttgca[A/C]ctgtaagagggtgatg	A	C	Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // --- //	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1917243	tgttttatatctggcc[G/T]actttgctttgaatta	G	T	8892 // Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), mRNA. /// NM_014381 // downstream // 3904 // Hs.279843 // MLH3 // 27030 // Homo	EIF2B2	EIF2B2, Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), q24.3
SNP_A-1887029	tgacttgtttttctcc[A/G]gagctgtgtgaaccaa	A	G	ENST00000294717 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-1911238	tgtctggccctcaaga[C/T]gctatattaacaccag	C	T	/// ENST00000359604 // upstream // 199477 // --- // --- // --- // --- /// ENST00000344172 // upstream // 110220 // --- // --- // ---	-	q11.2
SNP_A-1943619	ttgtaatatcatttct[C/T]acctttggttcatatt	C	T	56955 // Homo sapiens matrix, extracellular phosphoglycoprotein with ASARM motif (bone) (MEPE), mRNA. /// NM_020203 // downstream // 24679 // Hs.189587	MEPE	MEPE, Homo sapiens matrix, extracellular phosphoglycoprotein with ASARM motif (bone) (MEPE), q22.1
SNP_A-1948480	tttagtgaacttaata[C/T]ctgacatgcattattt	C	T	10410 // Homo sapiens interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA. /// NM_178537 // upstream	IFITM3	IFITM3, Homo sapiens interferon induced transmembrane protein 3 (1-8U) (IFITM3), p15.5
SNP_A-1970625	accctgggttttcaga[A/G]atccctgctatgttaa	A	G	6573 // Homo sapiens solute carrier family 19 (folate transporter), member 1 (SLC19A1), transcript variant 1, mRNA. /// NM_194255 // upstream // 47173 // Hs.84190 //	SLC19A1	SLC19A1, Homo sapiens solute carrier family 19 (folate transporter), member 1 (SLC19A1), transcript variant 1, q22.3
SNP_A-1984063	aagatcaggtgtctga[A/G]taagtggttcttcata	A	G	Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1649428	tctagaccagcctcatcactgctca[C/T]tcaacagaagtctgatgaggaaaac	C	T	54834 // ganglioside induced differentiation associated protein 2 /// NM_017709 // downstream // 162464 //	GDAP2	GDAP2 , rs1775752, ganglioside induced differentiation associated protein 2 ,p12
SNP_A-1660109	tttttaaactccaaattcctttatc[A/G]aagcagctatctgctaatattactg	A	G	MUSP1 (MUSP1) mRNA, complete cds. /// NM_002163 // downstream // 148 // Hs.14453 // ICSBP1 // 3394 // interferon	-	- , rs10514611, Homo sapiens MUSP1 (MUSP1) mRNA, complete cds. ,q24.1
SNP_A-1780401	ggatacacttattatc[C/T]agaaaatctggggact	C	T	26664 // Homo sapiens olfactory receptor, family 7, subfamily C, member 1 (OR7C1), mRNA. /// NM_017506 // downstream // 3203 // Hs.137573 // OR7A5 // 26659 // Homo sapiens	OR7C1	OR7C1, Homo sapiens olfactory receptor, family 7, subfamily C, member 1 (OR7C1), p13.12
SNP_A-1780614	ggatattgcttggcac[A/G]gtacacaactctgttc	A	G	// 25950 // Homo sapiens RWD domain containing 3 (RWDD3), mRNA. /// ENST00000354428 // downstream //	RWDD3	RWDD3, Homo sapiens RWD domain containing 3 (RWDD3), p21.3
SNP_A-1742099	ttaggaggcctcacaaagtgctatg[A/G]actcgtgtgactccctaccttgtag	A	G	132789 // glucosamine-6-phosphate deaminase 2 /// NM_173536 // downstream // 1130886 // Hs.375051 //	GNPDA2	GNPDA2 , rs7681587, glucosamine-6-phosphate deaminase 2 ,p13
SNP_A-1811153	gtgccctggtggctac[A/G]ctcctcgaggaaggac	A	G	Homo sapiens mRNA for KIAA0545 protein, partial cds. /// ENST00000222345 // intron // 0 // --- // --- // --- // ---	SIPA1L3	SIPA1L3, Homo sapiens for KIAA0545 protein, partial cds. q13.13
SNP_A-1802351	gtatcaacggaaatga[C/T]acaactccttcaatct	C	T	PRO1085 mRNA, complete cds. /// ENST00000340003 // intron // 0 // --- // --- // --- // --- /// ENST00000244064 // intron //	-	-, Homo sapiens PRO1085 complete cds. q13.32
SNP_A-1832980	tacacaacttctgcta[C/T]gcaacagaatttttat	C	T	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2165053	caaactggtcactgcc[A/G]ggcaggagaagctggt	A	G	sapiens kaptin (actin binding protein) (KPTN), mRNA. /// ENST00000356009 // CDS // 0 // --- // --- // --- // --- ///	KPTN	KPTN, Homo sapiens kaptin (actin binding protein) (KPTN), q13.32
SNP_A-2163972	caaaacttagaaacaa[C/G]caagatagatgtatgg	C	G	/// ENST00000354860 // upstream // 517400 // --- // --- // --- // ---	-	q32.3
SNP_A-2153599	attagctttgcccttа[A/G]taagactccattaggc	A	G	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2111781	aggatacctttaaga[A/C]agagaaaagagaacaa	A	C	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 593978 // Hs.411433	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-2123465	agtgtctttagtatg[A/C]caatgagttgattgat	A	C	// 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // downstream //	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-2137108	atcaggataagaacca[C/G]tgatgtgcgatcatga	C	G	sapiens chromosome 15 open reading frame 26 (C15orf26), mRNA. /// ENST00000286732 // intron // 0 // --- // --- // --- // ---	C15orf26	C15orf26, Homo sapiens chromosome 15 open reading frame 26 (C15orf26), q25.1
SNP_A-2179670	cacttctccttaaaaa[A/T]attctccatctacaag	A	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1226809 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2184776	cagctgcatggaaagg[A/G]caacaagcaagtagca	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2192479	catcatttattgtata[A/G]ggagtccttaccccat	A	G	endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 872579 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env ,q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2194530	catgcacacaattatg[A/G]actggaaatataaatt	A	G	sapiens tec protein tyrosine kinase (TEC), mRNA. /// ENST00000258070 // intron // 0 // --- // --- // --- // ---	TEC	TEC, Homo sapiens tec protein tyrosine kinase (TEC), p12
SNP_A-2216949	cctctgggctgttcca[C/T]gctcctggctcacttc	C	T	SDCCAG33 // 10194 // Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), mRNA. /// ENST00000322038 // downstream // 21466 // --- // --- // --- // --	SDCCAG33	SDCCAG33, Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), q22.3
SNP_A-2086740	actgaatttgcgagca[A/C]aaatgtcaccacttgt	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 652398 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2071706	acagacaaaagctctc[C/T]ccctcaccgtgtgtgc	C	T	Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// ENST00000262976 // intron // 0 // --- // --- // --- // ---	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-2070727	acacgtcaccaagcct[A/G]actatttatttgtttt	A	G	// 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// NM_178552 // downstream // 19871 // Hs.124502	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-2063488	actgactggaaagcaa[C/T]gaggatgtagcgaagc	C	T	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 464415 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2044463	aagaaaactgagaaga[C/T]cgtgtctaattttgaa	C	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2021468	aaaaaagtaaatctaa[C/T]attcagcgttcttacc	C	T	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1095675 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2003749	atgaactctatataac[A/T]aaacgacggtaaaata	A	T	Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // CDS // 0 // --- // DDHD1 // 80821 // Homo	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-1997930	cctgcaaattatcaac[A/C]gtaatctcccagttct	A	C	Homo sapiens chromosome 9 open reading frame 20 (C9orf20), mRNA. /// ENST00000321582 // intron // 0 // --- // --	C9orf20	C9orf20, Homo sapiens chromosome 9 open reading frame 20 (C9orf20), q33.2
SNP_A-1993109	taaatgggataataaa[A/T]ggaaagaatttagagc	A	T	// 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 265618 //	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-2311614	ggaatggtggccctat[A/G]acgtcagctttttctt	A	G	Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA. /// NM_201280 // intron // 0 // Hs.150837 // MUTED // 63915 // Homo sapiens muted	TXNDC5	TXNDC5, Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, p24.3
SNP_A-2292522	gcactccctggaggac[C/G]atgttagtccccagtt	C	G	Homo sapiens spectrin, beta, non-erythrocytic 5 (SPTBN5), mRNA. /// ENST00000320955 // intron // 0 // --- // --- // --- // ---	SPTBN5	SPTBN5, Homo sapiens spectrin, beta, non-erythrocytic 5 (SPTBN5), q15.1
SNP_A-2301539	gcgagcagcatcgcgt[A/G]accgggactggcccgg	A	G	7140 // Homo sapiens troponin T3, skeletal, fast (TNNT3), mRNA. /// NM_021134 // downstream // 7084 // Hs.3254 //	TNNT3	TNNT3, Homo sapiens troponin T3, skeletal, fast (TNNT3), p15.5
SNP_A-2309456	ggaaacaatgaaaaga[A/T]agcacaggccaacatg	A	T	// Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), mRNA. /// ENST00000355700 // intron // 0 // ---	PHGDHL1	PHGDHL1, Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), q32.3
SNP_A-2280766	gaggtgcaactggagc[A/G]aagcacatacttttat	A	G	138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 2148 // --- // OR13C2 //	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-2279735	gaggcattaagggtga[A/G]gaaaagactaattctc	A	G	970 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7), mRNA. /// NM_003807 //	TNFSF7	TNFSF7, Homo sapiens tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7), p13.3
SNP_A-2267477	gaatatcaaggacaaa[C/T]gcattgggggaagcct	C	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2261221	gaaagataaatgagaa[C/T]tcttcagcagcttaca	C	T	9241 // Homo sapiens noggin (NOG), mRNA. /// NM_003647 // upstream // 214962 // Hs.546318 // DGKE // 8526 // Homo	NOG	NOG, Homo sapiens noggin (NOG), q23.2
SNP_A-2243787	ctgctgcatgaagtac[A/G]aaaagttcccccaaaa	A	G	Homo sapiens a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme) (ADAM17), transcrip /// NM_003183 // intron // 0 // Hs.404914 // ADAM17 // 6868 // Homo	ADAM17	ADAM17, Homo sapiens a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme) (ADAM17), transcrip ,p25.1
SNP_A-2011490	ccattcgaatccccct[G/T]agagattgatgggcta	G	T	// 9509 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // upstream // 136641 // Hs.120330 // ADAMTS2	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript ,q35.3
SNP_A-2070481	acacccttcctctaca[A/G]tattttctggattctc	A	G	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2070555	acacctctcgagagca[A/G]cctcaaggtggaagac	A	G	ENST00000359398 // intron // 0 // --- // --- // --- // ---	-	q32.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074025	acagttgtgaggctga[A/C]attgtagtggagagag	A	C	Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2093628	agaagaagtcattata[G/T]atgtcaaggagatgga	G	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1812789 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2218157	cctgcctttgtaccac[C/T]gactgttttagcagat	C	T	79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-2215918	cctccaatatcgctaa[C/T]taaaacatcccacttt	C	T	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2222610	cgagtgggtacttaac[A/G]cttggcagaatgctaa	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2338724 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2194666	catgcattattgctaa[A/G]tgaagagtggagagaa	A	G	1811 // Homo sapiens solute carrier family 26, member 3 (SLC26A3), mRNA. /// NM_000108 // upstream // 60508 //	SLC26A3	SLC26A3, Homo sapiens solute carrier family 26, member 3 (SLC26A3), q31.1
SNP_A-2177882	cactaaattagatgca[C/G]agggatgatttaatat	C	G	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2174254	cacactgacttgaaca[C/T]tggctgtctagaaact	C	T	80832 // Homo sapiens apolipoprotein L, 4 (APOL4), transcript variant b, mRNA. /// NM_030643 // upstream //	APOL4	APOL4, Homo sapiens apolipoprotein L, 4 (APOL4), transcript variant b, q12.3
SNP_A-2110302	aggaatattgtgttct[C/G]acgagtttcgttttct	C	G	Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // intron // 0 // Hs.373857 //	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2110222	aggaagtgatgctcca[A/T]cttggttgaggagttg	A	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2123323	agtgtatgtcgttgat[G/T]aacatggaacactccc	G	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2157732	attgcattgtaaaaaa[A/G]cgtcccctacatcctc	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1830404	taatattcacaggtac[C/T]ccattctaaattatag	C	T	// 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 169535 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1827097	taaccatgttaaaaca[C/T]tcatatttcaagaaaa	C	T	9765 // Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), mRNA. /// ENST00000313424 // upstream //	ZFYVE16	ZFYVE16, Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), q14.1
SNP_A-1817951	gttctaagttgttgat[A/G]agttgaaaatgctctg	A	G	10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// NM_001922 // downstream // 26269 // Hs.301865 // DCT //	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q32.1
SNP_A-1807124	ccaagtgtccttccaa[C/T]ctctgaacatttcagt	C	T	// 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 961237 // --- // --- // --- //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1798778	gtaactcatttgttaa[A/G]attatcaatatctaat	A	G	sapiens interferon, gamma (IFNG), mRNA. /// ENST00000229135 // 3UTR // 0 // --- // --- // --- // ---	IFNG	IFNG, Homo sapiens interferon, gamma (IFNG), q15
SNP_A-1758201	accacaaacatattttctgtaaaca[A/G]gataattctccctcaaaggaaactg	A	G	POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 2692736	POLR2B	POLR2B , rs2880170, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-1975145	ctaaatactccaacag[A/G]ctctatattatatcag	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1953139	tttctttagattcttg[C/T]aagcttttatgagcat	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 295157 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1943197	ttggtctgacatctaa[C/T]gtgtcattgccaaact	C	T	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 753539 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.1
SNP_A-1942440	ttggctcaaaggagga[C/T]tcagcaagggtttgtt	C	T	Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// ENST00000333591 // intron // 0 // --- // --- // --- // ---	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1
SNP_A-1917001	tgtttgattctctact[A/G]aactgatcatatcact	A	G	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-1916045	tgttgcccaaataata[C/T]ctaattgttagccatt	C	T	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), mRNA. /// NM_002213 // downstream // 18139 //	UMPS	UMPS, Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), q21.2
SNP_A-1927494	ttcaaatgacacatcg[G/T]atgcccttctcatgct	G	T	3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 47322 //	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932006	ttcctacttcccctga[C/G]cgtaactcatgacttg	C	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1887108	tgagaaaactgaaaca[A/G]aaagatcttaataact	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-1875016	tctctatcactggacc[A/G]atgtgtctgttctctc	A	G	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 505182	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1924139	ttagttgaaacaatac[A/T]catggcaaagaaatct	A	T	FLJ32685 // 152110 // Homo sapiens hypothetical protein FLJ32685 (FLJ32685), mRNA. /// ENST00000358592 //	FLJ32685	FLJ32685, Homo sapiens hypothetical protein FLJ32685 (FLJ32685), p24.2
SNP_A-1925063	ttatcactatctgatc[G/T]gacatttacttccttt	G	T	ENST00000332912 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1943929	ttgtatctcatcaaaa[A/G]tcctagcgatggctat	A	G	Homo sapiens src family associated phosphoprotein 1 (SCAP1), mRNA. /// ENST00000336915 // intron // 0 // --- // ---	SCAP1	SCAP1, Homo sapiens src family associated phosphoprotein 1 (SCAP1), q21.32
SNP_A-1937064	ttcttttctgtttcac[C/T]gatctatttatgtatt	C	T	388325 // Homo sapiens DTFT5783 (UNQ5783), mRNA. /// NM_004703 // upstream // 28233 // Hs.536036 // RABEP1 //	UNQ5783	UNQ5783, Homo sapiens DTFT5783 (UNQ5783), p13.2
SNP_A-1984617	gccaaaggcatggaac[C/T]gattctagccccatca	C	T	91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream //	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-1747843	taccttgtctcaaacaatgaagaaa[A/G]ctctacaaaagtcaacacataggga	A	G	6235 // ribosomal protein S29 /// NM_080746 // upstream // 2769570 // Hs.308332 // RPL10L // 140801 // ribosomal	RPS29	RPS29 , rs10483555, ribosomal protein S29 ,q21.3
SNP_A-1668642	gaaaaggcaactgttttccaacaga[G/T]ggctttcaaaccattatgaaattta	G	T	// 84899 // hypothetical protein FLJ14624 /// NM_052867 // downstream // 129082 // Hs.391323 // VGCNL1 // 259232 //	FLJ14624	FLJ14624 , rs3886516, hypothetical protein FLJ14624 ,q32.3
SNP_A-1815121	gtgttctatttactca[A/G]tattgtacctccagat	A	G	// 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 // upstream //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1827344	taacgttttgctaaaa[A/C]tgggtaactctcactg	A	C	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1837271	tacttagctattgtag[C/T]acttgaaagctgttta	C	T	79596 // Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA. /// NM_022118 // downstream // 581109	C13orf7	C13orf7, Homo sapiens chromosome 13 open reading frame 7 (C13orf7), q31.1
SNP_A-1862761	tcattccattccgaaa[C/G]aaaatctgtacctatt	C	G	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1872474	tctagcctatcactta[C/T]gttgccatgtgatttt	C	T	sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-2156229	attctactctagaaag[A/C]aacttgagatagtatt	A	C	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2165443	caaagcaccactaata[A/C]aaataaataggcatcg	A	C	ENST00000355094 // intron // 0 // --- // --- // --- // ---	-	q22.31
SNP_A-2144712	atgatgattgggtcta[C/T]gtacctatgactagaa	C	T	// 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2139232	atcctctttgtactga[G/T]attgtaagtgatacga	G	T	// Homo sapiens activin A receptor, type I (ACVR1), mRNA. /// NM_173355 // upstream // 222311 // Hs.128427 // UPP2 //	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-2119881	agtcaactcatttctc[C/T]agttaaaagacacaga	C	T	5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase q22.1
SNP_A-2171356	caatattgttcaaaat[A/G]agcaaatgttacaagt	A	G	ENST00000302763 // intron // 0 // --- // --- // --- // ---	-	q31.2
SNP_A-2178914	cactgatttcttttag[G/T]caccaattcttgtaag	G	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2193726	catcttgttaaattga[A/G]gagaaataaatcagaa	A	G	MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 //	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-2209812	cccattttgatgctga[A/C]caatccagagttcact	A	C	// 1432 // Homo sapiens mitogen-activated protein kinase 14 (MAPK14), transcript variant 4, mRNA. /// NM_139013 // downstream // 42933 // Hs.485233 // MAPK14 // 1432 //	MAPK14	MAPK14, Homo sapiens mitogen-activated protein kinase 14 (MAPK14), transcript variant 4, p21.31
SNP_A-2093802	agaagagtagcacaca[A/G]cagaaacattcttcag	A	G	ENST00000358350 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-2094136	agaaggcaggactaga[C/T]gacctctaagatctca	C	T	// 10602 // Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA. /// NM_144713 // upstream // 268219 // Hs.532901 // FLJ32954 // 151393 //	CDC42EP3	CDC42EP3, Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), p22.2
SNP_A-2060289	aatgaagggcctgaaa[A/G]agaattaactaaaaag	A	G	3360 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, mRNA. /// NM_000870 // upstream // 93926 // Hs.483773 // HTR4 //	HTR4	HTR4, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, q32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015413	ccttgttttatctgaa[A/G]ttcaaatgtattcaag	A	G	29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 262043 // Hs.473370 // USP25 // 29761 // Homo sapiens	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds. q21.1
SNP_A-2000987	atttaacaattggagc[A/G]ctaagaactattacta	A	G	4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 303 // Hs.232819 // PCDH15 // 65217 // Homo	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2027362	aaacatggcagaagca[C/G]ggtgttataagattta	C	G	143187 // Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// NM_030756 // upstream // 179693 // Hs.501080 // TCF7L2 //	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2038894	aacagcctttgttcaa[C/T]ggactgtcctaaacag	C	T	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2036722	aaattgtttcttaaca[C/T]gcagaactccttttg	C	T	sapiens CGI-05 protein mRNA, complete cds. /// NM_016408 // intron // 0 // Hs.435952 // CDK5RAP1 // 51654 // Homo	CDK5RAP1	CDK5RAP1, Homo sapiens CGI-05 protein complete cds. ,q11.21
SNP_A-2249639	cttaaggtttgcttgg[A/C]atcttttacattagcc	A	C	Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 // 3UTR // 0 // --- // --- // --- // ---	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-2257963	ctttgtccttacatta[C/T]gtggatggcatatttg	C	T	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 263503 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-2281138	gagtaccagcactcta[C/T]gctcagcttttggat	C	T	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 447713 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2295584	gcatcttctataaacc[C/G]atgccccagaaaaata	C	G	sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 //	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2292393	gcacgtggaacttctc[A/G]aaggtctgtggccagt	A	G	sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // CDS // 0 // --- // --- // --- // --- /// ENST00000301226 // CDS // 0	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2291729	gcacactcaccagcaa[C/T]gtcctgagaataaata	C	T	// 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream //	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2288260	gattcctgactcagga[A/T]ggttcgaccgacaatt	A	T	Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // intron // 0 // Hs.337696 // SLC8A3 // 6547 //	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-2267118	gaataagggaaataaa[C/G]ctgtctgaaatactgt	C	G	/// ENST00000330777 // downstream // 51633 // --- // --- // ---	-	p23.1
SNP_A-2271733	gaccaggcttgaaaaa[A/G]gagtagtgttaaagaa	A	G	Homo sapiens plasticity related gene 1 (LPPR4), mRNA. /// ENST00000294644 // intron // 0 // --- // --- // --- // --- ///	LPPR4	LPPR4, Homo sapiens plasticity related gene 1 (LPPR4), p21.3
SNP_A-2255774	cttgtttcacttccca[C/T]tccttctgcacagttt	C	T	3108 // Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA), mRNA. /// NM_005104 // upstream // 13978 // Hs.75243 // BRD2 // 6046 // Homo sapiens	HLA-DMA	HLA-DMA, Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA), p21.32
SNP_A-2243386	ctgcgccgattgccag[A/G]ctcaagtttattttgg	A	G	1259 // Homo sapiens cyclic nucleotide gated channel alpha 1 (CNGA1), mRNA. /// NM_207330 // upstream // 502 //	CNGA1	CNGA1, Homo sapiens cyclic nucleotide gated channel alpha 1 (CNGA1), p12
SNP_A-2046722	aagagctggtcagata[C/T]aggggtgtttaggatc	C	T	ENST00000357789 // intron // 0 // --- // --- // --- // ---	-	q21.31
SNP_A-2042255	aactatccctgagtct[A/C]aattaaaagtcctggt	A	C	FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// NM_001819 // upstream //	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3
SNP_A-2029232	aaagaagcaataaaat[A/G]aggtctcactaggctg	A	G	ENST00000306670 // intron // 0 // --- // --- // --- // ---	-	p11.2
SNP_A-2025377	aaaatcagaatgaaca[C/T]ggtaaaaaaggaaaga	C	T	// 112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-2007396	tcccgatctcccatac[C/T]acgtctgcatttctct	C	T	55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// NM_017714 // upstream // 11452 //	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-2055890	gtgtccaagtgactca[C/T]agtatgttcctaattt	C	T	/// ENST00000338636 // upstream // 229119 // --- // --- // --- // --- /// ENST00000334344 // upstream // 317109 // --- // --- // ---	-	q12
SNP_A-2075786	acatgtaaagtgtctg[C/G]aacagcgtctggccca	C	G	// 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-2096285	agaccagatatgcaca[C/T]tgagcaacagagatta	C	T	Homo sapiens signaling lymphocytic activation molecule family member 1 (SLAMF1), mRNA. /// ENST00000343520 // intron // 0 // --- // --- // --- // --- /// ENST00000302035 // intron //	SLAMF1	SLAMF1, Homo sapiens signaling lymphocytic activation molecule family member 1 (SLAMF1), q23.3
SNP_A-2105320	agcatttccttttggc[C/T]ctctttgactttgatt	C	T	sapiens alpha-2-macroglobulin (A2M), mRNA. /// ENST00000318602 // intron // 0 // --- // --- // --- // ---	A2M	A2M, Homo sapiens alpha-2-macroglobulin (A2M), p13.31
SNP_A-2084170	actaggatccaatcaa[G/T]attcttggattgcaac	G	T	10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream //	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13
SNP_A-2213598	ccgtctcaatccggtg[C/T]agccgtttgcgggatg	C	T	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000360355 // CDS // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2184501	cagctagagaatggtg[A/G]aacaaggtctagatcc	A	G	11240 // Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA. /// NM_013358 // upstream // 45707 //	PADI2	PADI2, Homo sapiens peptidyl arginine deiminase, type II (PADI2), p36.13
SNP_A-2176106	caccacacccagccgc[A/G]aacgctttgaatagtg	A	G	10229 // Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), mRNA. /// NM_016524 // upstream // 67482	COQ7	COQ7, Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), p12.3
SNP_A-2172635	caattgcccttaggtc[C/G]catccatttcagagga	C	G	864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 195226 //	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2173219	cacaaccatgctcttc[C/G]caaagtaccactgcct	C	G	// 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 50742 // Hs.118183 // FLJ22833 //	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-2142479	atgaaatgggagactg[A/G]aaaattgttgccagca	A	G	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 799644 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2149552	atgtaggcagtacgaa[A/G]catttcttaaggaccc	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1226745 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2162730	attttgaagtaagata[C/T]cacactcatcctttat	C	T	// Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2); mRNA. /// ENST00000285393 // intron // 0 // --- // --- // --- // ---	ATP6V0D2	ATP6V0D2, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), q21.3
SNP_A-2161811	atttgtcagacgacca[C/T]gctcggatgtcacagg	C	T	ENST00000336769 // intron // 0 // --- // --- // --- // ---	-	q13.32
SNP_A-1861225	tcatattgaacactca[C/T]caagcatcccagtggc	C	T	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 439885 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1832122	taatttattttcctta[C/T]gggctcatagtgtaat	C	T	83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 32235 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1815513	gttaaaaatcttgttg[A/C]actgtaaaaatatatc	A	C	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 421445 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1642173	gtggcctctgaaatcatgtagaagc[C/T]aatacaaaagggtgtggacacagag	C	T	GTPase regulator associated with focal adhesion kinase pp125(FAK)	GRAF	GRAF , rs37192, GTPase regulator associated with focal adhesion kinase pp125(FAK),q31.3
SNP_A-1643301	aatgagggaagcccttgggcaaaga[A/T]catgtcccgggcacaagagtctggt	A	T	FLJ37402 fis, clone BRAMY2028072 /// NM_007190 // downstream // 179380 // Hs.300208 // SEC23IP // 11196 //	-	- , rs10510062, CDNA FLJ37402 fis, clone BRAMY2028072 ,q26.12
SNP_A-1696414	ttttaagtaagaaatagaaaattaa[A/C]tatggaagaaaaactgaaatcagaa	A	C	// 122183 // FLJ40296 protein /// NM_006418 // downstream // 3068809 // Hs.273321 // GW112 // 10562 // differentially	FLJ40296	FLJ40296 , rs280405, FLJ40296 protein ,q21.1
SNP_A-1742147	gtatgtgttaaacatacattatgaa[A/C]cacaggcttctaatgaaaatcagca	A	C	387694 // FLJ41984 protein /// NM_030927 // downstream // 65413 // Hs.509050 // DC-TM4F2 // 81619 // tetraspanin	FLJ41984	FLJ41984 , rs1913758, FLJ41984 protein ,q22.3
SNP_A-1714741	gccctgacattcttaagctggaaaa[C/T]tagccaaccctcgaaccaaccgtgc	C	T	7247 // translin /// NM_130773 // upstream // 2038004 // Hs.437463 // caspr5 // 129684 // caspr5 protein ///	TSN	TSN , rs1219906, translin ,q14.3
SNP_A-1792441	gggtttgagtagtcta[C/T]gcagagggaaggataa	C	T	81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000240780 // downstream //	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-1793479	ggtagtgtctgattga[A/G]agtcctggaggcagtt	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-1792936	ggtacaatactcagca[A/G]attacatgagctagtc	A	G	// 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 36895 // Hs.19872 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1789008	gggcaccaagtgcaat[G/T]agattcttttcccact	G	T	57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream //	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-1986243	cctatagctctgtctc[G/T]gaacctgtgattgctg	G	T	/// ENST00000310012 // upstream // 182917 // --- // --- // --- // -	-	q12
SNP_A-1962098	ctcataaacatgaaaa[A/T]aactcgagcatatata	A	T	Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. /// ENST00000345985 // intron // 0 // --- // --- // --- // ---	FLJ14075	FLJ14075, Homo sapiens hypothetical protein FLJ14075 (FLJ14075), p25.1
SNP_A-1886198	tgacccatctagtgtc[A/G]ccttctcccttacaca	A	G	// Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, mRNA. /// NM_174886 // upstream // 8452 // Hs.373550 // TGIF // 7050	TGIF	TGIF, Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, p11.31
SNP_A-1881434	tctttcctcctacctc[A/G]ataactgtgttagtcc	A	G	55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// NM_017714 // upstream // 54145 //	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-1886808	tgactggaacaaaaca[A/G]cagccatacttacctt	A	G	Homo sapiens SEC10-like 1 (S. cerevisiae) (SEC10L1), mRNA. /// ENST00000340918 // 3UTR // 0 // --- // --- // --- // ---	SEC10L1	SEC10L1, Homo sapiens SEC10-like 1 (S. cerevisiae) (SEC10L1), q22.3
SNP_A-1897727	tgctgcttcatagcca[A/G]gtagaaaagtggaagg	A	G	80267 // Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA. /// NM_022083 // downstream // 9545 //	C1orf22	C1orf22, Homo sapiens chromosome 1 open reading frame 22 (C1orf22), q25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893347	tgcagcacaggtgcct[A/G]acaaaactttggattc	A	G	7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // downstream // 5436 // --- // --- // --- // ---	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-1920675	ttacaaaccatatcca[A/G]tcagagtcattctctt	A	G	ENST00000308461 // intron // 0 // --- // --- // --- // ---	-	p21.32
SNP_A-1912881	tgtgctttaaaatcccc[A/G]aatattattctcatta	A	G	Homo sapiens phospholipase C-like 2 (PLCL2), mRNA. /// ENST00000285094 // 3UTR // 0 // --- // --- // --- // ---	PLCL2	PLCL2, Homo sapiens phospholipase C-like 2 (PLCL2), p24.3
SNP_A-1904544	tggggatggatttccc[A/G]cgggtgctagtctcgt	A	G	10069 // Homo sapiens chromosome 21 open reading frame 6 (C21orf6), mRNA. /// ENST00000309809 // upstream //	C21orf6	C21orf6, Homo sapiens chromosome 21 open reading frame 6 (C21orf6), q21.3
SNP_A-1966706	tgaatcagaagaatgc[C/T]gcatagctgaaaagaa	C	T	ENST00000272845 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1989490	tcatgggcaaactatc[A/G]ctgttgcctaactgac	A	G	// 168667 // Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), mRNA. /// NM_207288 // downstream // 109366 // Hs.487951 // AAA1 // 404744 //	BMPER	BMPER, Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), p14.3
SNP_A-1977679	ccctgatcgtttctca[A/T]ctctcctattgaatcc	A	T	Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1954392	tttgcatataagatca[A/G]gtcaagattcatttta	A	G	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1954184	tttgatttgtggctgc[C/G]agggaaagcagaacca	C	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1959755	ttttggtgtcatagcc[A/G]aatcattgccaaatcc	A	G	55269 // Homo sapiens paraspeckle component 1 (PSPC1), mRNA. /// AJ133355 // downstream // 37977 // Hs.530988 //	PSPC1	PSPC1, Homo sapiens paraspeckle component 1 (PSPC1), q12.11
SNP_A-1805116	gtcatgtaccatagta[C/T]taaagctgaagtagct	C	T	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 263059 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1754936	tagctagaacttggggatatataga[A/C]aaaggctgattaatttaaactttcc	A	C	NM_000865 // upstream // 185163 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E , rs539620, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1816133	gttacccaatgtctgc[A/C]ctttcatacctcctgc	A	C	RNASE9 // 390443 // Homo sapiens ribonuclease-like protein 9 (h461), mRNA. /// ENST00000328444 // downstream //	RNASE9	RNASE9, Homo sapiens ribonuclease-like protein 9 (h461), q11.2
SNP_A-1836429	tactcattagaaataa[A/G]tcagtaagtccaacac	A	G	8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// NM_024560 // upstream // 46615 // Hs.259559 //	LIN7A	LIN7A, Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), q21.31
SNP_A-1859462	tcaggaccctacccag[C/G]ctgcattatccaagtc	C	G	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2151769	atgtttagattgaaac[C/T]atcaactcttccagga	C	T	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2121500	agtgaaaattgtatta[A/G]ggctctgaaacaagag	A	G	Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST00000261206 // intron // 0 // --- // --- // --- // ---	FLJ21963	FLJ21963, Homo sapiens FLJ21963 protein (FLJ21963), q21.31
SNP_A-2121998	agtgataaaagaaaaa[G/T]tcaccatcagactact	G	T	Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// ENST00000265522 // intron // 0 // --- // ---	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p13
SNP_A-2107758	agctcagcagcagcca[C/T]tcaacgcttggtacat	C	T	// Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, mRNA. /// NM_182715 // upstream // 59468 //	SYPL	SYPL, Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, q22.3
SNP_A-2108535	agctggaggtctaaaa[A/T]accattccatgcctgg	A	T	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 108315 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2135929	atcaacctggatctca[A/G]atgtgcttggcataat	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 546888 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2134880	atattatcaataatag[C/G]aaggaatttactagat	C	G	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3), mRNA. ///	ENPP3	ENPP3, Homo sapiens ectonucleotide pyrophosphatase,q23.2
SNP_A-2074513	acatagccatgcttga[C/G]agcaaaaatgaatata	C	G	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 450456 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2073357	acaggtaattgaaaaa[A/T]ggtgtagcttaaacac	A	T	1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream //	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1996758	tttccctggaaaatac[C/T]cagaggctttctgtat	C	T	ENST00000354500 // intron // 0 // --- // --- // --- // ---	-	q21.11
SNP_A-2033212	aaatactccttgaaac[C/T]accaacaaattctttt	C	T	23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// NM_012137	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-2033483	aaatagtgtgggggta[G/T]acttgttgaagtgtga	G	T	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2245237	ctggctcacacctgaa[G/T]agcgtttcctagacct	G	T	Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA. /// ENST00000311083 // intron // 0 // --- // --- // --- // ---	CSRP2	CSRP2, Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2237248	ctctcatgcctttaca[G/T]gaagaggaatgagctc	G	T	135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2233846	ctcatctgcaggataa[C/T]cttgggtggagggtgg	C	T	Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// ENST00000260324 // intron // 0 // --- // ---	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2266503	gaagtaggagaaagaa[A/G]tgggcaataaaaaata	A	G	57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream //	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2261814	gaaagttttgcaatca[A/G]tctgaatattcacaat	A	G	8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 539184 // Hs.127013 // CADPS // 8618 // Homo	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2276536	gagagggcaatgggta[A/T]ctggatcatatcaaag	A	T	GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 36202 // --- // --- // --- // ---	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-2292779	gcacttgtgaaagtta[A/G]agatttagcatgaaca	A	G	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2298561	gcccacatagccttct[C/T]actccttctctgctga	C	T	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // --- // --- // --- // ---	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-2273088	gactatggcttcatta[C/T]acgcagaagctcttat	C	T	Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000306107 // intron // 0 // --- // ---	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2238154	ctctgcctccgtcttc[A/G]catggctctcttccct	A	G	150677 // Homo sapiens otospiralin (OTOS), mRNA. /// NM_002081 // upstream // 254371 // Hs.328232 // GPC1 //	OTOS	OTOS, Homo sapiens otospiralin (OTOS), q37.3
SNP_A-2256147	ctttactgaaagccac[C/T]gtacatactattggaa	C	T	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, mRNA. /// NM_003471 // intron // 0 // Hs.157818 // KCNAB1 // 7881 // Homo sapi	KCNAB1	KCNAB1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, q25.31
SNP_A-2249393	cttaaaggcctcactc[A/G]catcacattggccagt	A	G	221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 15742 // --- // --- // --- // ---	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-2029433	aaagacagaatgaaca[C/T]gtaagaaaacagtatg	C	T	57182 // Homo sapiens mRNA for KIAA1223 protein, partial cds. /// ENST00000281131 // upstream // 225348 // --- // --- //	KIAA1223	KIAA1223, Homo sapiens for KIAA1223 protein, partial cds. ,q28.1
SNP_A-2023937	aaaagacaaaaaccgc[A/C]attagttttgcaccaa	A	C	TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// NM_020346 // upstream	TMEM16E	TMEM16E, Homo sapiens transmembrane protein 16E (TMEM16E), p14.3
SNP_A-2034061	aaatcaggggagaaa[A/G]tacagcattaatgtac	A	G	ENST00000294926 // intron // 0 // --- // --- // --- // ---	-	q44
SNP_A-2001158	tgcatatactcatcca[C/T]aaactactctatcact	C	T	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1997526	tttaactttgggaaga[A/C]aaatgatgaattaatc	A	C	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2014473	ttacaattgtattgta[G/T]gataaaggtctaactc	G	T	4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// ENST00000302728 // upstream //	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2075663	acatggatatgatcta[C/T]gccagttagattcctg	C	T	51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // downstream //	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-2063333	aattaaagttactgta[C/G]gaaaatgaaatatcta	C	G	7350 // Homo sapiens uncoupling protein 1 (mitochondrial, proton carrier) (UCP1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000262999 // upstream // 11299 //	UCP1	UCP1, Homo sapiens uncoupling protein 1 (mitochondrial, proton carrier) (UCP1), nuclear gene encoding mitochondrial protein, q31.21
SNP_A-2063671	aattactctaccaggg[A/T]caaaaagatttacttc	A	T	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2068075	acaagaaactgacaac[A/G]gtagtggcctttgagg	A	G	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2083824	actacctacacccacc[C/T]ggacagttccaaggat	C	T	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 50160 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2082196	acgactgtgaagagtc[A/T]atgagagtgtgtgtgt	A	T	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 279366 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2085731	actcctcagggacgtc[G/T]ccaacccagtgatgct	G	T	25830 // Homo sapiens sulfotransferase family 4A, member 1 (SULT4A1), transcript variant 2, mRNA. /// NM_014351 // upstream // 15716 // Hs.189810 // SULT4A1 // 25830 // Homo	SULT4A1	SULT4A1, Homo sapiens sulfotransferase family 4A, member 1 (SULT4A1), transcript variant 2, q13.2
SNP_A-2093900	agaagcagaaacacaa[A/C]tgaggtctgatggttg	A	C	/// ENST00000262227 // upstream // 229102 // --- // --- // --- // --- /// ENST00000314319 // upstream // 277581 // --- // --- // ---	-	p11.31
SNP_A-2132725	atataaaccttatgaa[C/T]ttcacttttgccattg	C	T	Homo sapiens protease, serine, 35 (PRSS35), mRNA. /// ENST00000275040 // intron // 0 // --- // --- // --- // ---	PRSS35	PRSS35, Homo sapiens protease, serine, 35 (PRSS35), q14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2108307	agctgagggactctta[C/T]gtgactcacccctca	C	T	57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// NM_152749 // upstream // 59529 // Hs.489603 //	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. ,q22.3
SNP_A-2153056	attaccactgaggaaa[C/T]tctcaaataaaatttg	C	T	ENST00000345029 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-1862223	tcatggcctatttaaa[A/G]tctgtgggagaagaat	A	G	Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_016300 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1872796	tctatagaaagggtac[A/C]agactccaatttgaaa	A	C	6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 94352 // Hs.175905 // AUH //	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-1873513	tctcaattaattccaa[A/G]caaggacagtaaagag	A	G	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2862454 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1817228	gttcacagtctgttca[A/G]gggaactcaagacatt	A	G	23303 // Homo sapiens kinesin family member 13B (KIF13B), mRNA. /// NM_015254 // upstream // 22700 // Hs.444767 //	KIF13B	KIF13B, Homo sapiens kinesin family member 13B (KIF13B), p12
SNP_A-1751745	aagtaaaaataaatctgatgtatta[C/T]caagccaaaaatttatttacttact	C	T	BC042047 // intron // 0 // Hs.435365 // FLJ20637 // 55008 // hypothetical protein FLJ20637	FLJ20637	FLJ20637 , rs10516807, hypothetical protein FLJ20637,q22.1
SNP_A-1803163	gtattccactttagac[A/G]attgctatctcttcca	A	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1968954	attagagctatggtac[C/T]gcaacacattagatct	C	T	// 317754 // Homo sapiens ankyrin repeat domain 21 (ANKRD21), mRNA. /// ENST00000309142 // upstream //	ANKRD21	ANKRD21, Homo sapiens ankyrin repeat domain 21 (ANKRD21), q11.2
SNP_A-1921359	ttaccaatgaccaaaa[A/G]cacataccaacgtaaa	A	G	Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // --- // ---	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-1931864	ttccggatctactgac[A/G]agagttggcattggcg	A	G	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1930896	ttccagcttctgacaa[C/T]cagcattccactttct	C	T	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 467688 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1927372	ttcaaactgtagcaga[C/T]cctttgcaaccaattc	C	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 13474 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1928951	ttcagcactttaaaaa[C/T]gtctttatgccgtctt	C	T	/// ENST00000360991 // downstream // 815374 // --- // --- // ---	-	q12.1
SNP_A-1964327	tttgagcagctgtgac[A/G]gaaaccatataaccag	A	G	/// ENST00000360991 // downstream // 784958 // --- // --- // ---	-	q12.1
SNP_A-1981833	atgtacttcagtgaac[G/T]gcaaacaaacagatca	G	T	57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 6467 // --- // FLJ37543 //	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. q12.1
SNP_A-1951678	tttccttgaagttaag[A/G]caaccctgccagggcg	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1952274	tttctccttggcagac[G/T]ctgaactccaattttt	G	T	Homo sapiens cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA. ///	CDON	CDON, Homo sapiens cell adhesion molecule-related q24.2
SNP_A-1952914	tttcttcaaacgtcac[C/T]gctcagagcccagcat	C	T	9228 // Homo sapiens discs, large (Drosophila) homolog-associated protein 2 (DLGAP2), mRNA. /// NM_018941 // upstream // 262545 // Hs.127675 // CLN8 // 2055 // Homo	DLGAP2	DLGAP2, Homo sapiens discs, large (Drosophila) homolog-associated protein 2 (DLGAP2), p23.3
SNP_A-1952587	tttctgcctgcttttc[A/G]ctgctctttaatgttt	A	G	// 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// NM_152616 // upstream // 57342 // Hs.343487 // TRIM42 //	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1943298	ttggtggttccatcca[A/G]gttcagtgatggatgg	A	G	84867 // Homo sapiens cDNA FLJ33604 fis, clone BRAMY2015251, highly similar to PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.4 /// NM_032781 // upstream // 54728 // Hs.79092 // PTPN5 //	PTPN5	PTPN5, Homo sapiens cDNA FLJ33604 fis, clone BRAMY2015251, highly similar to PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.4 ,p15.1
SNP_A-1780892	ggatgaagaaaaagtg[A/G]atctacaactagggac	A	G	9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// NM_019599 // downstream // 120227 // Hs.533930 // TAS2R1	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-1742881	aacagagtcccacaaattcatatgg[A/C]aaaagtcagctacatatccaaacaa	A	C	NM_006727 // intron // 0 // Hs.92489 // CDH10 // 1008 // cadherin 10, type 2 (T2-cadherin)	CDH10	CDH10 , rs7735817, cadherin 10, type 2 (T2-cadherin),p14.2
SNP_A-1731621	cctgccactttcaatgtttatccag[G/T]catttctatatagggtatattatcc	G	T	NM_138458 // intron // 0 // Hs.493450 // LOC116143 // 116143 // hypothetical protein BC014022	LOC116143	LOC116143 , rs7595076, hypothetical protein BC014022,p14
SNP_A-1657347	tttgtgtccctagtggccaagccca[A/G]taggaagctggagggcaaaatgtct	A	G	55734 // zinc finger protein 64 homolog (mouse) /// NM_022088 // upstream // 484832 // Hs.504892 // ZFP64 //	ZFP64	ZFP64 , rs6022041, zinc finger protein 64 homolog (mouse) ,q13.2
SNP_A-1840479	gctgaaattgtccaga[C/T]ttggctaaagaaaaga	C	T	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// ENST00000284110 // intron // 0 // --- // --- // --- // ---	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1866304	tcccatgagatactaa[G/T]ggaactaagaggacat	G	T	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 489150 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2142609	atgaactattttgttc[A/G]aaagagacctaatttc	A	G	ENST00000325276 // intron // 0 // --- // --- // --- // ---	-	q22
SNP_A-2137586	atcatctcaaacttta[C/T]gtgtctacattcagat	C	T	// 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream //	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2180295	cagaaataaatgggac[A/G]gaactgatagcccgtg	A	G	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2182963	cagattcttgagctct[A/G]aaatacactgttattt	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 302433 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2185505	caggacttccactcca[A/G]ctagaaactctagttt	A	G	ENST00000275820 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-2188456	cagtgaatgttcttag[C/T]attcttgtcaaaaata	C	T	// Homo sapiens FLJ46354 protein (FLJ46354), mRNA. /// ENST00000339553 // intron // 0 // --- // --- // --- // --- ///	FLJ46354	FLJ46354, Homo sapiens FLJ46354 protein (FLJ46354), p32.3
SNP_A-2227229	ctaatttttcctggca[A/G]gttatttacactttct	A	G	// 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 632091 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-2203725	ccagagaagctttgtg[C/G]aggggatttgaagaga	C	G	Homo sapiens KIAA1618 (KIAA1618), mRNA. /// ENST00000319921 // intron // 0 // --- // --- // --- // --- ///	KIAA1618	KIAA1618, Homo sapiens KIAA1618 (KIAA1618), q25.3
SNP_A-2088428	actgtagtatagataa[C/T]atggtaccaaatctct	C	T	sapiens dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), mRNA. /// ENST00000357936 // intron // 0 // --- // --- // --- // --- /// ENST00000340197 // intron ///	DDC	DDC, Homo sapiens dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), p12.2
SNP_A-2088978	acttaaaattgtatta[C/T]ctgaatagtctccatg	C	T	23431 // Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA. /// NM_207381 //	AP4E1	AP4E1, Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), q21.2
SNP_A-2068954	acaatgagaaactccc[C/G]ccgtccatcagagtgg	C	G	Homo sapiens mRNA; cDNA DKFZp667H0525 (from clone DKFZp667H0525). /// ENST00000357056 // intron // 0 // --- // -	TTC7B	TTC7B, Homo sapiens cDNA DKFZp667H0525 (from clone DKFZp667H0525). ,q32.12
SNP_A-2065378	aattgtctagggaagt[A/T]aacgtatatatatata	A	T	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 179329 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2049420	aagctgcaagccctgc[A/T]aagattatggtgtccc	A	T	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2010632	ttgatttacatttccc[C/T]gataattagtaatgtt	C	T	11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 477983 //	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-2046307	aagagaacagaagaaa[A/G]aatcagtgaactagaa	A	G	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2025146	aaaatagaaagaatga[A/G]taagatcaggtgtttg	A	G	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-2233837	ctcatctctgcctctg[C/T]agcacgaaagcaatta	C	T	Homo sapiens polymeric immunoglobulin receptor (PIGR), mRNA. /// ENST00000356495 // intron // 0 // --- // --- // --- // ---	PIGR	PIGR, Homo sapiens polymeric immunoglobulin receptor (PIGR), q32.1
SNP_A-2307106	gctgtttttgataaca[C/T]agctgaatctggagga	C	T	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2290781	gcaagcccagaggaac[A/G]cagcctttccgaagag	A	G	1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 170524 // --- // --- // --- // ---	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2
SNP_A-2263897	gaactaaggcttacct[G/T]acattgaccaggggca	G	T	10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 222328 // Hs.489615 // PBEF1 // 10135 // Homo	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-2271455	gacatttgttaaaata[A/T]ggacaacagactgagg	A	T	84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // downstream // 70319 // --- // --- // --- // --	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-2027233	aaacataagcaactca[C/T]tatttttcaaaaaaga	C	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 724135 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2034629	aaatgaaaagcagaaa[G/T]aaaaaactctgcatct	G	T	Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2035611	aaatgtagtcatcttc[A/G]agaaatgaaatagttc	A	G	5359 // Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /// NM_032153 // downstream // 44924 // Hs.415766	PLSCR1	PLSCR1, Homo sapiens phospholipid scramblase 1 (PLSCR1), q24
SNP_A-2008758	aaggaagactgatata[C/G]gtgggtagctggccag	C	G	ENST00000343837 // intron // 0 // --- // --- // --- // ---	-	p14.2
SNP_A-2013165	gtggggccttcattac[A/G]ggattagggcctgtct	A	G	// 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 14073 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017939	aggcggagaggcatat[C/G]acaggcagaagaatgg	C	G	1 // 337880 // Homo sapiens keratin associated protein 11-1 (KRTAP11-1), mRNA. /// NM_003253 // downstream // 4504	KRTAP11-1	KRTAP11-1, Homo sapiens keratin associated protein 11-1 (KRTAP11-1), q22.11
SNP_A-1992070	aaggaccttccattgg[C/G]acaaatacagggcata	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 770746 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2051598	aaggtaaccaggtgac[G/T]aaattatgtcagggtt	G	T	26119 // Homo sapiens LDL receptor adaptor protein (ARH), mRNA. /// NM_020379 // upstream // 7709 // Hs.197043 //	ARH	ARH, Homo sapiens LDL receptor adaptor protein (ARH), p36.11
SNP_A-2062289	aatggttatttggtca[A/G]caattctcaaagtatg	A	G	79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 191009 //	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2097283	agagaaaaaagaagtc[A/C]catggcccctgagagg	A	C	Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, mRNA. /// NM_000337 // intron // 0 // Hs.387207 // SGCD // 6444 //	SGCD	SGCD, Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, q33.3
SNP_A-2106071	agcccagagagaaata[C/G]gtttagaagatccaca	C	G	3486 // Homo sapiens insulin-like growth factor binding protein 3 (IGFBP3), mRNA. /// ENST00000275521 //	IGFBP3	IGFBP3, Homo sapiens insulin-like growth factor binding protein 3 (IGFBP3), p13
SNP_A-2202373	ccaccatagacacctc[A/G]caggtaaatcttagtg	A	G	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 521696 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2212112	ccctgcctaagggcct[C/G]acctagaatggggctt	C	G	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// ENST00000342389 // intron // 0 // --- // --- // --- // ---	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-2214220	cctacaagagttaaca[A/G]tggcacttaaataagt	A	G	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 523887 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2176851	caccgaatccaagatc[A/G]atgccagtgaggcatc	A	G	Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // intron // 0 //	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-2170223	caaggtggcatggtca[C/G]agtcctcagaagcata	C	G	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 882761	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2137715	atcatggatacagtaa[C/T]tctaaaactattcatt	C	T	Homo sapiens osteocrin (OSTN), mRNA. /// ENST00000339051 // intron // 0 // --- // --- // --- // ---	OSTN	OSTN, Homo sapiens osteocrin (OSTN), q28
SNP_A-2131867	ataggaaagttacaac[C/T]atttcatctcacagaa	C	T	GALNT4 // 8693 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), mRNA. /// NM_024642 // downstream // 106627 // Hs.47099	GALNT4	GALNT4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), q22.33
SNP_A-2109602	aggaaaccaaagccta[A/G]aatggtaaactgactt	A	G	MAP2K4 // 6416 // Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /// ENST00000353533 //	MAP2K4	MAP2K4, Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), p12
SNP_A-2119093	agtagattcaacctca[A/G]cattggcaaagacaag	A	G	26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// NM_015224 // downstream // 88712 //	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2161756	atttgtagaaaaggaa[A/C]cagacaaaatgaatgt	A	C	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2163883	caaaaccatgaggaga[G/T]gccattaacatctaat	G	T	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 188714 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1844511	tataaatattgcccaa[C/G]tagtatgatagatcca	C	G	Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-1834974	tacccacctcaatgaa[C/T]tgctttgatgattaaa	C	T	/// ENST00000318905 // downstream // 34639 // --- // --- // --- // --- /// ENST00000304745 // downstream // 34639 // --- // ---	-	q23.1
SNP_A-1832517	tacaaagtcaatatcc[C/T]gaagttcagcattaca	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 498978 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1697166	gtttttccttgtagctttttttgtg[C/T]gagcctctgagatttttttccttg	C	T	NM_022743 // intron // 0 // Hs.8109 // SMYD3 // 64754 // SET and MYND domain containing 3	SMYD3	SMYD3 , rs2787952, SET and MYND domain containing 3,q44
SNP_A-1691290	tcacaggtgatgtgctttaggtatc[A/C]ctgtgagatgaaagggaaattaaga	A	C	AB020672 // intron // 0 // Hs.175411 // MYR8 // 23026 // myosin heavy chain Myr 8	MYR8	MYR8 , rs10492421, myosin heavy chain Myr 8,q33.3
SNP_A-1806660	gtctacaaaataaaca[A/G]tgacttagtgcatttt	A	G	2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream //	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1798850	gtaacttttcaatctg[C/T]agaaccaaaagaccca	C	T	ENST00000331194 // upstream // 30123 // --- // --- // --- // --- /// ENST00000334448 // upstream // 32168 // --- // --- // --- // ---	-	q32.12
SNP_A-1937182	ttgaaaaattttgcca[A/T]atccactttctgttta	A	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1957502	ggctgagtcttagaaa[A/G]cttcaatctttaggga	A	G	ENST00000357615 // intron // 0 // --- // --- // --- // ---	-	q13.12
SNP_A-1925658	ttatgatacaagaaaa[A/T]ctcattgctatgaatc	A	T	OR8A1 // 390275 // Homo sapiens olfactory receptor, family 8, subfamily A, member 1 (OR8A1), mRNA. /// NM_052959 //	OR8A1	OR8A1, Homo sapiens olfactory receptor, family 8, subfamily A, member 1 (OR8A1), q24.2
SNP_A-1897564	tgctgattggcaagga[C/T]gttttggatggacact	C	T	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1900045	tggaccttcgtctcca[A/G]tcaaatctcatgttca	A	G	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 436005 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1895854	tgcctggggactaaca[A/C]tagaaggcactgacgc	A	C	Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // intron // 0 // --- // --- //	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1924327	ttataaatctataaaa[C/T]gtacttccgtcagcat	C	T	MGC33530 // 222008 // Homo sapiens hypothetical protein MGC33530 (MGC33530), mRNA. /// NM_014302 //	MGC33530	MGC33530, Homo sapiens hypothetical protein MGC33530 (MGC33530), p11.2
SNP_A-1926170	aaaagggtcattgata[C/T]gcatggtatttgcctt	C	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 963391	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1943716	ttgtactgggttcaag[A/C]ctaattgctagggttg	A	C	// 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 114658 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1838786	tagacgattacagatg[C/G]attttactatcttatc	C	G	Homo sapiens sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 (SOAT1), transcript variant 688113, mRNA. /// ENST00000320522 // intron // 0 // --- // ---	SOAT1	SOAT1, Homo sapiens sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 (SOAT1), transcript variant 688113, q25.2
SNP_A-1823042	taaaaatgttttaaaa[A/G]gagaactctgccagaa	A	G	4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000299766 // upstream // 25901 // --- // ---	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1872025	tctaccctctgaaacc[C/T]atatgtattaggctgt	C	T	ENST00000356409 // intron // 0 // --- // --- // --- // ---	-	q24.13
SNP_A-2151618	atgttgcatgaaacac[A/G]aggaagagaaatgtgt	A	G	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2195338	catggctagtcactaa[A/T]agtccactaatatttt	A	T	Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // --- // --- // --- // ---	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-2198478	catttagtccaccaaa[C/T]agtgatgtgcggtggg	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2224637	cgtccccacccacaaa[C/G]aatttgaagacaaaaa	C	G	mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 //	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. ,p26.1
SNP_A-2201018	ccaaggctggtgacca[C/T]gtccttcccgggctgc	C	T	50651 // Homo sapiens DNb-5 mRNA, partial cds. /// ENST00000341781 // upstream // 224752 // --- // --- // --- // ---	DNB5	DNB5, Homo sapiens DNb-5 partial cds. p36.23
SNP_A-2095879	agacagatggattact[C/T]actgcttttaactctt	C	T	ENST00000354500 // intron // 0 // --- // --- // --- // ---	-	q21.12
SNP_A-2092226	agaaagaatggcggca[A/G]aagtacagtcaataag	A	G	Homo sapiens hypothetical protein FLJ40089 (FLJ40089), mRNA. /// ENST00000344280 // CDS // 0 // --- // --- // --- // ---	FLJ40089	FLJ40089, Homo sapiens hypothetical protein FLJ40089 (FLJ40089), q23.1
SNP_A-2077784	accagaaagttgcaac[A/G]gcattagactgagtga	A	G	2069 // Homo sapiens epiregulin (EREG), mRNA. /// NM_001657 // upstream // 18087 // Hs.270833 // AREG //	EREG	EREG, Homo sapiens epiregulin (EREG), q13.3
SNP_A-2059089	aatcccttagatgtac[A/G]aggtcttcaagactca	A	G	283310 // Homo sapiens hypothetical protein FLJ90579 (FLJ90579), mRNA. /// ENST00000298820 // downstream //	FLJ90579	FLJ90579, Homo sapiens hypothetical protein FLJ90579 (FLJ90579), q21.31
SNP_A-2075500	acatgatctccttcca[C/T]agcacagaggatatga	C	T	Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA. /// NM_002603 // intron // 0 // Hs.527119 //	PDE7A	PDE7A, Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, q23.3
SNP_A-2017984	ataataattgtcactg[C/T]attaatgggtaatgga	C	T	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2025848	aaaatgggaatgaatt[A/C]aatagcaagaggattt	A	C	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, mRNA. /// NM_199451 // intron // 0 // Hs.22653 //	ZNF365	ZNF365, Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, q21.2
SNP_A-2270460	gacagaaggaagtgga[C/T]ggccaggaaatttagg	C	T	// 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000327792 // downstream // 542140 // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2284797	gatcattccgataaac[C/T]gctgcaccttagaggt	C	T	Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA. /// ENST00000292807 // intron // 0	AP2M1	AP2M1, Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), q27.1
SNP_A-2235104	ctcccatcctacttgc[C/T]gaagtgagtacagtgt	C	T	11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2291253	tgaaagcagcagaaac[C/T]gactggggctataact	C	T	8925 // Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA. /// NM_014326 // downstream // 23030 // Hs.237886 // DAPK2 // 2	HERC1	HERC1, Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), q22.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2307772	gcttcctgaattttaa[C/T]caaactttcatgaga	C	T	Homo sapiens sodium channel, voltage-gated, type IV, alpha (SCN4A), mRNA. /// ENST00000006839 // 3UTR // 0 // --- // ---	SCN4A	SCN4A, Homo sapiens sodium channel, voltage-gated, type IV, alpha (SCN4A), q23.3
SNP_A-2301845	gcggcttggttcttga[C/T]gttagtgagaccaaga	C	T	200523 // Homo sapiens hypothetical protein FLJ25369 (FLJ25369), mRNA. /// ENST00000303271 // upstream //	FLJ25369	FLJ25369, Homo sapiens hypothetical protein FLJ25369 (FLJ25369), p11.2
SNP_A-2234751	ctccaggtttccctca[A/G]cataaaacagtcaaat	A	G	// 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 207190 // Hs.480596 // NDST3 //	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2233715	ctcatattgtgctcca[A/G]taaatgctgtcagttc	A	G	Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // --- // --- // --- // ---	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-2243888	ctgctgtaattacaca[C/T]aaatgtttagtgtggt	C	T	222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 1093713 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2243479	ctgctaatatctgaca[A/C]ctgcaaattgacatct	A	C	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 93421 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2275212	gagaaggaggttggaa[A/G]taagggttgaagaaat	A	G	22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 192888 // Hs.306831 //	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-2274706	gagaaagacacatcaa[A/C]agtcaaagtaagctga	A	C	Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 631473 // Hs.48297 // RCHY1 // 25898 //	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-2276974	gagatctcttaacaag[A/G]cctgcccaagcaagta	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2279794 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2026020	aaaattaaacacatta[A/G]acagagctgtagttgt	A	G	Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), mRNA. /// ENST00000264101 // intron // 0 // --- // ---	KCNK2	KCNK2, Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), q41
SNP_A-2026537	aaacaaatttccaaac[C/T]aaagagcagaacaaga	C	T	Homo sapiens ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) (ARIH1), mRNA. /// ENST00000299305 // intron // 0 // --- // --- // --- // ---	ARIH1	ARIH1, Homo sapiens ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) (ARIH1), q24.1
SNP_A-2029633	aaagagacttgtccaa[C/G]atcaccttctggagcc	C	G	349565 // Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// NM_178177 //	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-2032305	aaagttatcattgaca[C/T]gagatgagcacaagtg	C	T	// 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 48266 // Hs.194766 // SEZ6L //	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2030491	aaagcctaatgaacct[A/G]aaggaaagatcatact	A	G	// Homo sapiens lipase, gastric (LIPF), mRNA. /// NM_004190 // upstream // 56326 // Hs.523130 // LIPF // 8513 // Homo	LIPF	LIPF, Homo sapiens lipase, gastric (LIPF), q23.31
SNP_A-2044839	aagaaattatggctga[A/C]aatgtaaccaaatttc	A	C	/// ENST00000356128 // upstream // 55628 // --- // --- // --- // ---	-	q24
SNP_A-2006412	tctcaattaagccaca[C/T]tgagcattaggatttc	C	T	9783 // Homo sapiens regulating synaptic membrane exocytosis 3 (RIMS3), mRNA. /// NM_014223 // upstream //	RIMS3	RIMS3, Homo sapiens regulating synaptic membrane exocytosis 3 (RIMS3), p34.2
SNP_A-1996285	agaactgttggaaaat[A/G]atggaaatctatggac	A	G	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 523799 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2058597	aatcaggggaaaggga[C/T]gcaactgaaagcatgc	C	T	54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 136941 // ---	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2051742	aaggtcacatttcaag[A/G]attttatgcagactat	A	G	140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 539077 // ---	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-2048199	aagcactccgcgtacc[C/T]atggggcagcccttgt	C	T	6530 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // downstream //	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-2078706	accattgaacacataa[C/T]tgtagagatatagact	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2214756	cctagtcaccccaaag[C/T]caggtcagagaactag	C	T	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2183756	cagcatctttggagcc[A/G]ccctgaagaggtaata	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2176448	caccatgtgccttctc[A/G]ctctcaacaggggaa	A	G	Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), mRNA. /// ENST00000199448 // intron // 0 // --- // ---	EPDR1	EPDR1, Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), p14.1
SNP_A-2180791	cagaatagtgagaaat[A/G]aatcattgtctttgtt	A	G	1618 // Homo sapiens deleted in azoospermia-like (DAZL), mRNA. /// ENST00000250863 // upstream // 136427 // --- // ---	DAZL	DAZL, Homo sapiens deleted in azoospermia-like (DAZL), p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2120955	agtctagtgtggatac[A/G]accattaaatatccac	A	G	LYCAT // 253558 // Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, mRNA. /// NM_182551 // downstream // 21196 // Hs.468048 // LYCAT //	LYCAT	LYCAT, Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, p23.1
SNP_A-2113625	aggctcaaaaaggtca[A/G]gttatcccggcaccag	A	G	80176 // Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), mRNA. /// NM_025106 // downstream	SSB1	SSB1, Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), p36.22
SNP_A-2135320	atatttaccattatct[C/T]aatttctacatcttct	C	T	// 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 442965 // --- // --- // --- //	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1869140	tcctgctgcaggtgaa[C/T]gtgtcaggaaatgagc	C	T	Homo sapiens TRAF and TNF receptor associated protein (TTRAP), mRNA. /// ENST00000341060 // CDS // 0 // --- // ---	TTRAP	TTRAP, Homo sapiens TRAF and TNF receptor associated protein (TTRAP), p22.2
SNP_A-1848871	tatgattgctaagaca[C/T]aggaaaaagcagttgc	C	T	TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 104688 // --- // --- // --- //	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-1793520	ggtataaagagactaa[A/G]gtaaccagaggtcaac	A	G	5796 // Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), mRNA. /// ENST00000309493 // upstream	PTPRK	PTPRK, Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), q22.33
SNP_A-1787170	gggaaatgtattggaa[C/T]ggaaaaccatttttcc	C	T	283576 // Homo sapiens zinc finger, DHHC domain containing 22 (ZDHHC22), mRNA. /// ENST00000319374 //	ZDHHC22	ZDHHC22, Homo sapiens zinc finger, DHHC domain containing 22 (ZDHHC22), q24.3
SNP_A-1645224	tctttagtcatgatttgatgaaaga[C/T]gggctttttttctactcttgtattca	C	T	// 6885 // mitogen-activated protein kinase kinase kinase 7 /// NM_004440 // downstream // 1060474 // Hs.73962 // EPHA7	MAP3K7	MAP3K7 , rs1373376, mitogen-activated protein kinase kinase kinase 7 ,q15
SNP_A-1952293	tttctctacctaatag[A/T]actcataagtgaatgg	A	T	KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 56708 //	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1980597	agaagtttgttgtatc[C/T]agctaaatatgaccta	C	T	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1967777	gttctcacaggaacta[A/G]cagagcaagaactcac	A	G	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 209018 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. ,q23.1
SNP_A-1926531	ttattcgagacaaatc[C/G]ccaacttaaggatttt	C	G	/// ENST00000323868 // upstream // 106024 // --- // --- // --- //	-	q11.23
SNP_A-1902953	tggctgcagagatcaa[A/G]atttctggaataccat	A	G	// 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000340000 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1883183	tgaaatgggttagaag[C/G]ctgtctgaaaaaattt	C	G	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-1880928	tcttgtccttcagacc[A/G]cttatctcagtctgta	A	G	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 95717 // Hs.183817 // USP31 // 57478 //	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-1880941	tcttgtcttgttttgc[C/T]cttaataggaatctct	C	T	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 324011 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1900053	tggacgagcaaaagag[G/T]aagtcaaaagcatgtg	G	T	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 191962 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1911320	tgtctgtgtctcttgc[A/G]gaaggctcccacaagt	A	G	POTE8 // 340441 // Homo sapiens protein expressed in prostate, ovary, testis, and placenta 8 (POTE8), mRNA. /// ENST00000354247 // downstream // 3829407 // --- // --- // ---	POTE8	POTE8, Homo sapiens protein expressed in prostate, ovary, testis, and placenta 8 (POTE8), q11.1
SNP_A-1968922	gcattcctgcactaac[A/G]gcaactctacggtaag	A	G	Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), mRNA. /// ENST00000217159 // CDS // 0 // --- // --- // --- // --- /// ENST00000342674 // CDS // 0	SLCO4A1	SLCO4A1, Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), q13.33
SNP_A-1974529	ggtgatgtttatccat[G/T]ataagccagttgtaca	G	T	22808 // Homo sapiens muscle RAS oncogene homolog (MRAS), mRNA. /// NM_012219 // downstream // 31234 // Hs.527021 // MRAS // 22808 // Homo sapiens muscle RAS	MRAS	MRAS, Homo sapiens muscle RAS oncogene homolog (MRAS), q22.3
SNP_A-1960615	aagtagccaaaggaaa[C/T]aggttcgctgatcagg	C	T	5672 // Homo sapiens pregnancy specific beta-1-glycoprotein 4 (PSG4), transcript variant 2, mRNA. /// NM_002783 // upstream // 21224 // Hs.512647 // PSG7 // 5676 // Homo	PSG4	PSG4, Homo sapiens pregnancy specific beta-1-glycoprotein 4 (PSG4), transcript variant 2, q13.31
SNP_A-1961599	ttttttttgacgatac[C/T]attttccacagcagct	C	T	10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_016588 // downstream //	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-1727763	cttaaaggtagacaggataggaccc[G/T]gaaaaatatatttgaaaaaaatac a	G	T	// 122183 // FLJ40296 protein /// NM_014459 // upstream // 388075 // Hs.106511 // PCDH17 // 27253 // protocadherin 17	FLJ40296	FLJ40296 , rs10492706, FLJ40296 protein ,q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1811437	gtgctatctcttgagc[A/G]aattcctgggaactat	A	G	// Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // upstream //	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2
SNP_A-1809319	gtgactgagagtgtga[C/T]gaaggcaagccttgaa	C	T	// 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 240590 // Hs.480596 // NDST3 //	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1857220	tcacctgtggttgctt[A/T]aaaaagtggatctcag	A	T	285671 // Homo sapiens hypothetical protein LOC285671 (LOC285671), mRNA. /// ENST00000296615 // downstream	RNF180	RNF180, Homo sapiens hypothetical protein LOC285671 (LOC285671), q12.3
SNP_A-1868418	tcctccatctctagaa[C/T]ggtaagtttgacagat	C	T	/// ENST00000355888 // upstream // 99245 // --- // --- // --- // ---	-	q24
SNP_A-1821940	gttttatttttttaag[G/T]atgactcagtaattta	G	T	sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000263145 // intron // 0 // --- // --- // --- // ---	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.2
SNP_A-2112871	aggcatatatatgata[C/T]ggtgatgaccaattct	C	T	760 // Homo sapiens carbonic anhydrase II (CA2), mRNA. /// ENST00000285379 // downstream // 119693 // --- // --- // --- //	CA2	CA2, Homo sapiens carbonic anhydrase II (CA2), q21.2
SNP_A-2114393	agggacctaagtacca[A/T]ctgaatgaatgaaagg	A	T	// 9550 // Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), mRNA. /// ENST00000277323 // upstream // 5316 // --- // --- // --- // --- ///	ATP6V1G1	ATP6V1G1, Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), q32
SNP_A-2140047	atctagcagcttgcca[C/T]agaccacatccttctt	C	T	375567 // Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000324993 // downstream // 489708 // --- // --- // --- //	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-2140452	atctccacattgccta[A/T]aatttcctattaaagt	A	T	5257 // Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. /// NM_145188 // downstream // 117944 // Hs.410111	PHKB	PHKB, Homo sapiens phosphorylase kinase, beta (PHKB), q12.1
SNP_A-2155673	attccagttaagacca[A/G]agatgcagtttgcagg	A	G	8514 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNAB2), transcript variant 2, mRNA. /// NM_003636 // upstream // 119719 // Hs.440497 // KCNAB2 // 851	KCNAB2	KCNAB2, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNAB2), transcript variant 2, p36.31
SNP_A-2224635	cgtccattggcaggaa[C/G]tgggttgtctgtctat	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2502012 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2223624	cggagcactgtgactc[G/T]acaagcggtagatgat	G	T	Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // --- // --- // --- // ---	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-2087316	actgcacctacaagac[C/T]gcagaatggaaacaag	C	T	ENST00000338910 // CDS // 0 // --- // --- // --- // --- /// ENST00000341503 // CDS // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2105441	agccaacagaaaaaaa[A/G]ttctgggacaagagtg	A	G	23086 // Homo sapiens SLAC2-B (SLAC2-B), mRNA. /// NM_015065 // upstream // 11355 // Hs.269591 // SLAC2-B //	SLAC2-B	SLAC2-B, Homo sapiens SLAC2-B (SLAC2-B), q22.3
SNP_A-2058841	aatccaaacttaaaca[A/C]cttgagcatccttttt	A	C	LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 //	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2069479	acacaatattctacac[A/G]aactgcctttatgtga	A	G	1462 // Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA. /// NM_001884 // downstream //	CSPG2	CSPG2, Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), q14.3
SNP_A-2014381	tttggctattatggac[A/T]atgttactctgaacat	A	T	// 56959 // Homo sapiens chromosome 9 open reading frame 102 (C9orf102), mRNA. /// NM_138497 // upstream // 36530	C9orf102	C9orf102, Homo sapiens chromosome 9 open reading frame 102 (C9orf102), q22.32
SNP_A-2036336	aaattccaggattaca[G/T]aagtttgcaagctact	G	T	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 346158 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2034022	aaatcagagaaatagg[A/C]agttacagtttgttat	A	C	219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 596947 // --- // --- // --- //	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2033789	aaatattctttgagtc[A/G]gacaaaacacatctca	A	G	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA. /// ENST00000358362 // intron // 0 // --- // --- // --- // --- ///	SLC2A10	SLC2A10, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), q13.12
SNP_A-2040204	aaccaatgactttata[A/G]gccctcattttggcta	A	G	2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 376455 // Hs.479853 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2
SNP_A-2030717	aaagctgtataaagca[C/G]attgatggggatataa	C	G	118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 506431 // Hs.523446 // COL11A1 // 1301 //	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds. p21.1
SNP_A-2025055	aaaatacaaaaaacta[A/G]taaagtgtggtggtag	A	G	91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream //	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-2022608	aaaaatgatggaaaag[A/T]ccttgtactgtcttct	A	T	Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // intron // 0 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2273501	gactcttctttaaaag[G/T]ctgtatgtgtttgtaa	G	T	80216 // Homo sapiens lymphocyte alpha-kinase (LAK), mRNA. /// ENST00000273997 // upstream // 4435 // --- // --- //	ALPK1	ALPK1, Homo sapiens lymphocyte alpha-kinase (LAK), q25

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2285139	gatctactgaacatca[A/C]atctcatttctttcta	A	C	Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), mRNA. /// ENST00000266427 // intron // 0 // --- // --- // --- // ---	ETV6	ETV6, Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), p13.2
SNP_A-2261577	gaaaggggctaggga[A/G]gcattgcaagcaaagg	A	G	Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // --- // --- // --- // ---	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2233702	ctcatattacaaaaag[G/T]cattgaggatgagaag	G	T	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 405254 // Hs.435730 //	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2233606	ctcataacctgtgaga[C/G]aatatagaaatcagtg	C	G	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 596554 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2295129	gcatataactgccaga[A/C]agcaacgagtttagtg	A	C	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 598319 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2295335	gcatcatataaattaa[A/C]ggtgtcattggtaata	A	C	mRNA for KIAA0227 gene, partial cds. /// ENST00000256367 // 3UTR // 0 // --- // --- // --- // ---	TTC9	TTC9, Human for KIAA0227 gene, partial cds. q24.2
SNP_A-2299617	tccacactcttggtca[A/G]atttcttcacctctca	A	G	Homo sapiens KIAA1199 (KIAA1199), mRNA. /// D42039 // 3UTR // 0 // Hs.513070 // MESDC2 // 23184 // Homo sapiens	KIAA1199	KIAA1199, Homo sapiens KIAA1199 (KIAA1199), q25.1
SNP_A-2299686	gccgggcagccgagga[A/G]agcctgcggagcttgg	A	G	Homo sapiens formin homology 2 domain containing 1 (FHOD1), mRNA. /// ENST00000258201 // CDS // 0 // --- // ---	FHOD1	FHOD1, Homo sapiens formin homology 2 domain containing 1 (FHOD1), q22.1
SNP_A-2290189	gcaaatgtggcttaaa[C/T]aaacttttggaacaat	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2308205	gcttggaacagagttg[A/G]aactttacaccaagct	A	G	Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// ENST00000287097 // intron // 0 // --- // ---	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2271085	gacataggcaagtgta[C/T]gaatagaattgttctt	C	T	Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // --- // --- // --- // ---	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-2020223	atccaggctctgaagc[G/T]gattagacaggaaagc	G	T	Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 15, mRNA. /// NM_001001579 // intron // 0 //	PDE9A	PDE9A, Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 15, q22.3
SNP_A-2043774	aacttattgatgctaa[C/T]aatagctaaagcttat	C	T	56171 // Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), mRNA. /// NM_004226 // downstream // 24625 //	DNAH7	DNAH7, Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), q32.3
SNP_A-2040635	aaccatttctgtagca[A/G]gagtttattattacat	A	G	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// NM_044472 // intron // 0 // Hs.467637 // CDC42 // 998 // Homo sapiens	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2041153	aacctatgtaaattac[A/G]gcagaatttttgaca	A	G	26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2015540	tgatactcaataaaca[A/G]tgatgtaatcagctgg	A	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2009738	gttgcttcgactcagc[A/G]cacaagttaatttaat	A	G	ENST00000313860 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-1990048	tgagaaaaaacaaagg[C/T]aatgactgtaattaaa	C	T	Homo sapiens calcitonin gene-related peptide-receptor component protein (RCP9), mRNA. /// ENST00000338592 // intron // 0 // --- // --- // --- // --- /// ENST00000360415 // intron //	RCP9	RCP9, Homo sapiens calcitonin gene-related peptide-receptor component protein (RCP9), q11.21
SNP_A-2073381	acaggtatgaacaaca[A/G]gggactcagagcccaa	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 756053 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2072017	acagagggacttgcaa[A/G]attcaacagcttcttg	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2089336	acttagtaaaactgaa[C/T]agctgcagcgaggcgc	C	T	Homo sapiens adenylate cyclase 1 (brain) (ADCY1), mRNA. /// ENST00000297323 // intron // 0 // --- // --- // --- // ---	ADCY1	ADCY1, Homo sapiens adenylate cyclase 1 (brain) (ADCY1), p13
SNP_A-2206021	ccatatgtaaagctga[A/T]aggagaaatggaaaca	A	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2153513	attagcatacttgaca[G/T]gatagaatgctaagac	G	T	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 45306 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2161591	atttggatgccctcaa[A/G]tagtgctttaattaac	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 480468 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2166034	caaataatgatcatgg[G/T]attggggagatggagc	G	T	Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // intron // 0 // --- // --- // --- // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2107808	agctcatcgaccgaac[A/G]gactctacttcccagc	A	G	SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 511108 // Hs.354013 //	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2131881	ataggaagattatccc[A/G]gactttcaaggtggac	A	G	/// ENST00000360292 // downstream // 70900 // --- // --- // ---	-	p12.3
SNP_A-1843162	tagtcagtttaagcag[A/G]agagcaaggtcgtgca	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1852429	tatttaattatttacc[A/C]agacctgttgataatc	A	C	9575 // Homo sapiens clock homolog (mouse) (CLOCK), mRNA. /// NM_152401 // downstream // 7734 // Hs.223712 //	CLOCK	CLOCK, Homo sapiens clock homolog (mouse) (CLOCK), q12
SNP_A-1787734	gggacattcaagactg[A/T]agtgggagtggctgtc	A	T	Homo sapiens calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 2, mRNA. /// ENST00000327479 // intron // 0 // --- // --- // --- // --- ///	CACNB4	CACNB4, Homo sapiens calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 2, q23.3
SNP_A-1789144	gggcagggagggagga[A/C]cgaattgtaatttgca	A	C	DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, mRNA. /// NM_015496 // upstream // 38981 // Hs.202238 //	DKFZP434I116	DKFZP434I116, Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, q22.1
SNP_A-1784770	ggcctggagcaggaaa[C/T]gtgtaagatgaacctg	C	T	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1652134	agaaaaatctttatgtcattaaaac[G/T]acgtagatcaatggaaatagaaccc	G	T	NM_006322 // intron // 0 // Hs.9884 // TUBGCP3 // 10426 // tubulin, gamma complex associated protein 3	TUBGCP3	TUBGCP3 , rs9324307, tubulin, gamma complex associated protein 3,q34
SNP_A-1667712	tagaactctaagcctattaagatca[C/T]attaactctaaattaaatgaaatca	C	T	NM_002203 // intron // 0 // Hs.387725 // ITGA2 // 3673 // integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	ITGA2	ITGA2 , rs3212692, integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor),q11.2
SNP_A-1953595	tttgacaagtctgaga[G/T]gaacaggaaaacggcc	G	T	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 582925 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1941896	ttggagagatttacta[G/T]attcactaggtttact	G	T	// Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 580690 // Hs.1428 // FSHR // 2492 // Homo	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1981107	tagagtcctgctatta[A/C]cctaatttatgatgtt	A	C	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1911296	tgtctgtctccccaaa[C/G]agaatattttctccat	C	G	Homo sapiens EF-hand domain (C-terminal) containing 1 (EFHC1), mRNA. /// ENST00000263044 // intron // 0 // --- // ---	EFHC1	EFHC1, Homo sapiens EF-hand domain (C-terminal) containing 1 (EFHC1), p12.2
SNP_A-1915255	tgttcagctctgcaaa[A/C]aagctgatgctagagt	A	C	LOC283537 // 283537 // Homo sapiens hypothetical protein LOC283537 (LOC283537), mRNA. /// ENST00000266943 //	LOC283537	LOC283537, Homo sapiens hypothetical protein LOC283537 (LOC283537), q12.3
SNP_A-1923682	ttaggttaactcatgg[C/T]attctgcgaccagtgt	C	T	283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream //	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1923058	ttagcatcatgccttc[A/G]atgttcatccacgtag	A	G	80854 // Homo sapiens SET domain-containing protein 7 (SET7), mRNA. /// NM_002413 // upstream // 64814 //	SET7	SET7, Homo sapiens SET domain-containing protein 7 (SET7), q31.1
SNP_A-1922931	ttagatttgtaccta[A/C]gaacccaatgtagatt	A	C	sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-1899490	tggaagcaaaacacta[C/T]ggtaaatgaaatcctt	C	T	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 12575 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1902040	tggcatcagttctgca[G/T]gtttcaggcatatagt	G	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2185435 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1879689	tcttcagtgccctaat[G/T]atagaggaaagaagaa	G	T	9406 // Homo sapiens mRNA; cDNA DKFZp586O012 (from clone DKFZp586O012). /// NM_203350 // upstream // 112607	ZNF265	ZNF265, Homo sapiens cDNA DKFZp586O012 (from clone DKFZp586O012). ,p31.1
SNP_A-1886531	tgactagcaataaaaa[A/G]tgtagttaaattgtgt	A	G	CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 //	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1919882	ttaataaaatttgtaa[C/G]aactctgaatcaaccg	C	G	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1711818	gtgtattcttccttctagctctcca[A/G]tcatgctctcttgagtcatttcaca	A	G	51250 // chromosome 6 open reading frame 203 /// NM_018292 // downstream // 25966 // Hs.406917 // QRSL1 //	C6orf203	C6orf203 , rs9320187, chromosome 6 open reading frame 203 ,q21
SNP_A-1721003	tgttctgttatgcatagccctaacc[G/T]atcactacatgttttacattaatac	G	T	NM_152989 // intron // 0 // Hs.87224 // SOX5 // 6660 // SRY (sex determining region Y)-box 5	SOX5	SOX5 , rs10505932, SRY (sex determining region Y)-box 5,p12.1
SNP_A-1785939	ggctgatttatgtaac[A/G]gtctatcccaaggcac	A	G	54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 //	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-2126136	gctcactatcagagcc[A/G]ccttttgaacaagata	A	G	Homo sapiens hypothetical protein FLJ20449 (FLJ20449), mRNA. /// ENST00000218554 // intron // 0 // --- // --- // --- // ---	FLJ20449	FLJ20449, Homo sapiens hypothetical protein FLJ20449 (FLJ20449), q13.3
SNP_A-2128160	ataaggagaaaggcca[A/G]tatctttccgaggggc	A	G	/// ENST00000324915 // downstream // 88228 // --- // --- // ---	-	q22.1
SNP_A-2114040	aggcttgttgtactac[A/G]cgaattaaaatatgtc	A	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_022788 // intron // 0 // Hs.532933 // P2RY12 // 64805 //	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140636	atctctatgttcaaag[G/T]atattgaccctcttct	G	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, mRNA. /// NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, q11.2
SNP_A-2147876	atggcctggaaatgcc[A/G]actctcacactgtgtc	A	G	// 57085 // Homo sapiens angiotensin II receptor-associated protein (AGTRAP), mRNA. /// NM_005957 // downstream //	AGTRAP	AGTRAP, Homo sapiens angiotensin II receptor-associated protein (AGTRAP), p36.22
SNP_A-2202747	ccacggcaggtcaaga[A/C]gctctcttgagcagct	A	C	23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2215159	cctatttgtccttcag[G/T]attcagtttataaatc	G	T	// --- /// ENST00000359634 // upstream // 15975 // --- // --- // --- // --- /// ENST00000359181 // upstream // 15975 // --- // --- // ---	-	q32.3
SNP_A-2063525	aattaatgtgacatag[C/G]ctactgtaaaacataa	C	G	MGC42415 // 168417 // Homo sapiens hypothetical protein MGC42415 (MGC42415), mRNA. /// NM_178558 //	MGC42415	MGC42415, Homo sapiens hypothetical protein MGC42415 (MGC42415), q11.21
SNP_A-2019259	gtactctctgacagtc[A/G]caaggaagactgtcaa	A	G	2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // upstream // 27148 // Hs.473819 // ERG // 2078	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-2025220	aaaatagtgcctggaa[A/G]gatgttcttcattaac	A	G	11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 554338 //	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-2232343	ctcacaacctcttata[A/G]atgatgtgcctttaga	A	G	/// ENST00000335402 // downstream // 52566 // --- // --- // ---	-	p14
SNP_A-2237356	ctctccattttagtcc[C/T]catttaatctttggag	C	T	// Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), mRNA. /// ENST00000318116 // intron // 0 // ---	ARHGAP24	ARHGAP24, Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), q21.23
SNP_A-2252898	cttctattgcagcaaa[A/T]gacccacctagtaact	A	T	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // --- // --- // --- // ---	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-2253519	cttcttcctttgtaaa[C/T]gtgtgagtctggattt	C	T	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 492094 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2293560	gcagcagtggcaacaa[A/T]gctgtgtctagtggag	A	T	Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // intron // 0 // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. ,q14.2
SNP_A-2294867	gcataaaattccagga[C/T]gggaaagagagccacg	C	T	1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream //	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-2263094	tttacaggttgtaata[C/T]aatagcaagaatagca	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2030158	aaagcaaggggaaact[A/G]aaatggagtcatcaca	A	G	Homo sapiens prostate antigen PARIS-1 mRNA, complete cds. /// ENST00000210447 // intron // 0 // --- // --- // --- // --- ///	TBC1D2	TBC1D2, Homo sapiens prostate antigen PARIS-1 complete cds. ,q22.33
SNP_A-2029302	aaagaatcacagaaga[A/G]ccataagctataacaa	A	G	Homo sapiens tubulin-specific chaperone d (TBCD), mRNA. /// ENST00000355528 // intron // 0 // --- // --- // --- // --- ///	TBCD	TBCD, Homo sapiens tubulin-specific chaperone d (TBCD), q25.3
SNP_A-2028162	aaactacaggtagttc[A/G]actagggctgaagctg	A	G	// Homo sapiens mRNA for KIAA0551 protein, partial cds. /// AB011123 // upstream // 30535 // Hs.34024 // TNIK // 23043	TNIK	TNIK, Homo sapiens for KIAA0551 protein, partial cds. q26.2
SNP_A-1993177	tgattaatccataaaa[A/G]acaataacagagtgga	A	G	-- /// ENST00000342478 // downstream // 527447 // --- // --- //	-	q11.21
SNP_A-2006986	ctgctgaaaaatatga[C/T]gtgaaattagtggtat	C	T	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // --- // --- // --- // --- /// ENST00000260943 // intron //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2064151	aattcaaatgataaac[A/G]gttcaaaacaagcaaa	A	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1272907 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2065028	aattgcaaactcttta[C/T]gtctaaagcgcactat	C	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 450381	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2060991	aatgattcaaatgtag[C/T]cccttgaacagtgata	C	T	1462 // Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA. /// NM_001884 // downstream //	CSPG2	CSPG2, Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), q14.3
SNP_A-2050482	aaggatcctccataac[A/G]gccacgcaagtctgtg	A	G	// Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 288783 // Hs.381715	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2091622	agaaaacctaacacca[C/G]gtgtcctcactcttaa	C	G	// Homo sapiens major histocompatibility complex, class I, B (HLA-B), mRNA. /// NM_000247 // upstream // 42516 //	HLA-B	HLA-B, Homo sapiens major histocompatibility complex, class I, B (HLA-B), p21.33
SNP_A-2215511	cctcagaaagatacta[A/G]ggacaaggcagacaat	A	G	sapiens regulator of G-protein signalling 5 (RGS5), mRNA. /// ENST00000313961 // intron // 0 // --- // --- // --- // ---	RGS5	RGS5, Homo sapiens regulator of G-protein signalling 5 (RGS5), q23.3
SNP_A-2200194	ccaaattaatttagaa[A/G]gggtgagcatgaactc	A	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 274642 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2211618	ccctcataagaacaaa[A/G]aaggctcccatgaacc	A	G	// 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 //	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175569	cacatgacggtagaca[A/G]aagaagagagcttggg	A	G	sapiens palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) (PPT1), mRNA. /// ENST00000253546 // intron // 0 // --- // --- // --- // ---	PPT1	PPT1, Homo sapiens palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) (PPT1), p34.2
SNP_A-2169871	caaggcactcccaaca[C/T]agagctggcattcagg	C	T	Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /// ENST00000176763 // intron // 0 // --- // --- // --- // ---	STK10	STK10, Homo sapiens serine,q35.1
SNP_A-2152489	attaagaatttgaaca[A/C]ctcctaaacagcctgt	A	C	H.sapiens rab28 mRNA. /// NM_004249 // intron // 0 // Hs.306899 // RAB28 // 9364 // Homo sapiens RAB28,	RAB28	RAB28, H.sapiens rab28 p15.33
SNP_A-1791233	gggtaaaagacaagtg[A/G]agaacaatatttgctg	A	G	4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 205426 // --- // ---	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1671532	ggccatcagagacccaagaaccaga[C/T]ggtggaaaaaggagaagcagaagta	C	T	NM_007252 // intron // 0 // Hs.131638 // POU6F2 // 11281 // POU domain, class 6, transcription factor 2	POU6F2	POU6F2 , rs10499612, POU domain, class 6, transcription factor 2,p14.1
SNP_A-1841951	tagggaaaccttccaa[A/T]ggcagaagatacagat	A	T	// Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), mRNA. /// ENST00000298215 // intron // 0 // --- // --- // --- // ---	SLC16A9	SLC16A9, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), q21.2
SNP_A-1827929	taagaacaagaacaag[G/T]ctgcggaagcttgagg	G	T	ENST00000356542 // intron // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-1923112	ttagccgatccaaaaa[A/G]acagtcggggcattta	A	G	Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // --- // --- // --- // --- ///	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1926476	ttattcattccttcat[C/T]agtttatggacacttc	C	T	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-1880163	tcttctgcataattag[A/C]cagaatctttctatgc	A	C	// --- /// ENST00000355517 // downstream // 125706 // --- // ---	-	q24.32
SNP_A-1891697	tgattgtgatttctga[G/T]gtgaatgaaaatattt	G	T	/// ENST00000330649 // upstream // 1002509 // --- // --- // --- //	-	q11.2
SNP_A-1973395	tgtaaagatcgttgac[A/G]ctatgaacaaactgca	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1121586 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1964036	tgtatgtgactccagc[A/G]cctttgtgggcaaccc	A	G	Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), mRNA. /// ENST00000359885 // intron // 0 // --- // --- // --- // ---	GDAP2	GDAP2, Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), p12
SNP_A-1963078	ttctgcaagtgatatc[C/T]aacacactgcatttca	C	T	Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), mRNA. /// ENST00000233146 // intron // 0 // --- // --- // --- // ---	MSH2	MSH2, Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), p21
SNP_A-1941062	aagactgggctgtaaa[C/T]ccccacactatcaaat	C	T	148066 // Homo sapiens zinc and ring finger 4 (ZNRF4), mRNA. /// NM_153375 // downstream // 88353 // Hs.515575	ZNRF4	ZNRF4, Homo sapiens zinc and ring finger 4 (ZNRF4), p13.3
SNP_A-1936708	ttcttgtttggtgtca[C/T]agggtaattggttttt	C	T	Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-1958670	ttttctccctctctga[C/T]attcttgaagctcaac	C	T	Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // --- // --- // --- // ---	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-1961600	ttttttttgagtcacc[A/G]ctgctattaggtgctt	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1934902	ttctgaataaacacaa[C/T]gttagtttcctttaag	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 696175 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1933687	ttctagtggttaggcc[C/T]agtgtgcttctccttc	C	T	Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 8970 // Hs.365706 // MGP //	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-1986934	ttaatggcttgtggta[G/T]caagtgacatttgaaa	G	T	// 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 112874 //	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1884414	tgaagtcacaataaca[C/G]gtatatgaaactgagg	C	G	// Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // --- // --- // --- // ---	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1
SNP_A-1928872	ttcagataaagcaaaa[A/G]gacactttcatttaga	A	G	sapiens growth hormone receptor (GHR), mRNA. /// ENST00000230882 // intron // 0 // --- // --- // --- // --- ///	GHR	GHR, Homo sapiens growth hormone receptor (GHR), p12
SNP_A-1912407	tgtgcaacttgttctc[A/T]cctctgttttcttaga	A	T	Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // intron // 0 //	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-1910105	tgtcatccctcaaccc[C/T]gacatggctcatgccc	C	T	219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 41794 // --- // --- // --- // ---	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-1858367	tcagacattaaaaaaa[A/G]ttagctaagctgcaaa	A	G	MRPS30 // 10884 // Homo sapiens mitochondrial ribosomal protein S30 (MRPS30), nuclear gene encoding mitochondrial protein, mRNA. /// NM_021072 // downstream // 33137 //	MRPS30	MRPS30, Homo sapiens mitochondrial ribosomal protein S30 (MRPS30), nuclear gene encoding mitochondrial protein, p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1865879	tcccaagatttagcca[A/G]tcacacattcagggaa	A	G	55288 // Homo sapiens ras homolog gene family, member T1 (RHOT1), mRNA. /// NM_018307 // downstream // 35462 //	RHOT1	RHOT1, Homo sapiens ras homolog gene family, member T1 (RHOT1), q11.2
SNP_A-1696466	ctgtattaaagggtttgggtaaaac[A/G]gaattgcagctggaaaatggaagat	A	G	MGC71806 // 374378 // similar to Hypothetical protein LOC233733 /// NM_021211 // upstream // 363023 //	MGC71806	MGC71806 , rs7927154, similar to Hypothetical protein LOC233733 ,p15.4
SNP_A-1739249	aagtacaagaacaaaaagtttcctc[A/T]ctgggaagtggaagaatggaggaag	A	T	NM_152403 // intron // 0 // Hs.20103 // FLJ39155 // 133584 // hypothetical protein FLJ39155	FLJ39155	FLJ39155 , rs2366979, hypothetical protein FLJ39155,p13.2
SNP_A-1749743	aaaaggaggggcaaaaatatactga[C/T]cataaggtttatacaattactgtc	C	T	NM_016598 // intron // 0 // Hs.61430 // ZDHHC3 // 51304 // zinc finger, DHHC domain containing 3	ZDHHC3	ZDHHC3 , rs10514711, zinc finger, DHHC domain containing 3,p21.31
SNP_A-2130983	atagaactaaagattg[C/T]aatttgttggagttaa	C	T	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 169842 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-2173152	cacaaattgtagcaaa[C/T]agtgtgaaagaatgac	C	T	79012 // Homo sapiens hypothetical protein MGC8407 (MGC8407), mRNA. /// NM_002447 // downstream // 16 //	MGC8407	MGC8407, Homo sapiens hypothetical protein MGC8407 (MGC8407), p21.31
SNP_A-2180172	cagaaaccaatgaaga[A/G]ggtgtcaggcacattt	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// ENST00000328843 // intron // 0 // --- //	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-2222985	gagagatggtttaaaa[C/T]agtgagggtcttggat	C	T	Homo sapiens chromosome 14 open reading frame 149 (C14orf149), mRNA. /// ENST00000247194 // intron // 0 // ---	C14orf149	C14orf149, Homo sapiens chromosome 14 open reading frame 149 (C14orf149), q23.1
SNP_A-2054796	aataaacatggtataa[C/T]gcatggaacaatgctc	C	T	/// ENST00000355063 // upstream // 631603 // --- // --- // --- //	-	q22.1
SNP_A-2003773	ggccctgaaaactcat[C/T]aagaaagccagcctgg	C	T	sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), mRNA. /// ENST00000327153 // intron // 0 // --- // --- // --- // --- /// ENST00000336233 // intron //	LIPA	LIPA, Homo sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), q23.31
SNP_A-2025826	aaaatggatgccagac[C/T]acggcagtgaacaaac	C	T	Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST00000262360 // intron // 0 // --- // --	C9orf39	C9orf39, Homo sapiens chromosome 9 open reading frame 39 (C9orf39), p22.2
SNP_A-2041684	aacggccggctttgga[A/G]gctgaaagacaattcc	A	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // --- // --- // --- // ---	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2039656	aacatgcaaaaactag[A/G]aagtgatccatttgta	A	G	/// ENST00000318847 // downstream // 94985 // --- // --- // ---	-	q23.31
SNP_A-2038224	ctagtttaatcattca[A/G]ggaattttcaggctat	A	G	// 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 754829 // Hs.504943	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-2229404	ctaggcagaagcaaga[C/T]aagaggagttccggag	C	T	83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 59800 // Hs.432458 // PRG4 //	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2228993	ctagcaatggtagtaa[C/G]agttgaattagcccca	C	G	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2299502	aaatcatggaaatgaa[A/C]aagcatcttcctttgc	A	C	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2260035	gaaaataatcatctca[A/G]gttaatcataaattta	A	G	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 516554 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1992486	catgcagttagttaca[C/G]atgggatcatttgtcc	C	G	9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 154737 //	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2050446	aaggatacgaaaaaaa[A/C]cttccattatcaccac	A	C	ENST00000320930 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2057321	aatatatgagcattga[A/C]attatatccactactg	A	C	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2101977	agatggtgaatcagaa[A/G]ctcttactaaaaattt	A	G	10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// NM_005252 // upstream // 97582 //	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2095159	caaagtaggatagata[C/T]gtactttcataaaaga	C	T	27022 // Homo sapiens forkhead box D3 (FOXD3), mRNA. /// NM_013339 // upstream // 14905 // Hs.80042 // ALG6 //	FOXD3	FOXD3, Homo sapiens forkhead box D3 (FOXD3), p31.3
SNP_A-2109188	agcttggcaaaccaca[A/G]tgaaaacttctaagcc	A	G	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2152508	attaagataaacaaaa[A/G]gatccattatcataaa	A	G	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1782383	ggcaattgtgcaatta[G/T]aagaggtttatttaca	G	T	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-1786342	ggctgttcagtgtcac[A/C]acttactatgactgat	A	C	Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1865519	tccatgattttcaaaa[A/T]tatctgatacaattca	A	T	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 567367 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1867191	tccctgctcttaactt[C/T]aaaccacaccatctct	C	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1844477	tataaagtactgagaa[A/G]aggactgctccatagc	A	G	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 375449 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1847166	tatcattatattctca[G/T]tagaccattaaagagg	G	T	sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-1847427	tatccgcagtgcctaa[C/T]gctaagtactcactaa	C	T	Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), mRNA. /// ENST00000261245 // intron // 0 // --- // ---	MNAT1	MNAT1, Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), q23.1
SNP_A-1824826	taaagattttgtttga[A/T]cagaggattctctggt	A	T	1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1835430	tacctcttcatagtca[C/G]gcccattcctacctct	C	G	Homo sapiens coatomer protein complex, subunit gamma 2 (COPG2), mRNA. /// NM_016128 // intron // 0 // Hs.518250 //	COPG2	COPG2, Homo sapiens coatomer protein complex, subunit gamma 2 (COPG2), q21.3
SNP_A-1983071	tggtgctctagctctg[A/C]aagttataagattaat	A	C	// Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// ENST00000274458 // intron // 0 // --- // --- // --- // ---	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-1977002	aaatgccaatggaaca[C/T]agtgattcaaataaga	C	T	132789 // Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), mRNA. /// ENST00000295448 //	GNPDA2	GNPDA2, Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), p13
SNP_A-1935780	ttctgtgtgggataac[C/T]gtgggcaagaagggtt	C	T	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q11.23
SNP_A-1949557	tttatttaccaaaata[C/G]cgtatttccatgtttg	C	G	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1956934	ttttaaggatctgcgc[C/T]cagggaaggggaagcg	C	T	// Homo sapiens KIAA0087 mRNA, partial cds. /// NM_003930 // downstream // 49000 // Hs.200770 // SCAP2 //	KIAA0087	KIAA0087, Homo sapiens KIAA0087 partial cds. p15.2
SNP_A-1933900	ttctatttgacccaac[A/G]actcacggaggaaaga	A	G	284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// NM_145301 // downstream // 592 //	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-1941198	ttgctgcccttggata[G/T]caatctgcttctttgt	G	T	/// ENST00000355561 // upstream // 832535 // --- // --- // --- // ---	-	q21.31
SNP_A-1947423	tttacagatagaaaaa[A/G]aataaagcagtaaggt	A	G	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1356598 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1983169	aagggtgtcaacagggg[A/C]atttgaaaatgatcaa	A	C	// 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1968306	gaaggggtgatcggta[C/T]gaacttcctccttcac	C	T	Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // intron // 0 // Hs.472716 // C20orf129 // 81610 //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. ,q11.23
SNP_A-1881412	tctttcccgtcacctc[A/G]catttccacatgcttg	A	G	// Homo sapiens KIT ligand (KITLG), transcript variant a, mRNA. /// NM_000899 // upstream // 86322 // Hs.1048 //	KITLG	KITLG, Homo sapiens KIT ligand (KITLG), transcript variant a, q21.33
SNP_A-1888443	tgaggaagtgaggaca[C/T]gccgagtgacaagaga	C	T	Homo sapiens ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (ATP1A2), mRNA. /// ENST00000251207 //	ATP1A2	ATP1A2, Homo sapiens ATPase, Na+,q23.2
SNP_A-1838726	tagacatttttagaga[A/T]gacttaagtgcttgta	A	T	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1818266	gttctggaatgtgaac[C/T]gtgactgagttgaaat	C	T	FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000344027 // upstream //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1865820	tcccaaagcatattcc[C/T]atagaaactctggggt	C	T	// 6992 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), transcript variant 2, mRNA. /// NM_021959 // downstream // 27925 // Hs.82887 //	PPP1R11	PPP1R11, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), transcript variant 2, p21.33
SNP_A-1799133	gtaaggttgagaaaaa[C/G]ttgagtaacactttag	C	G	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-1809523	gtgagagagatttcca[C/T]agaaagtgtttctgtg	C	T	6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// NM_032900 // downstream // 15057 // Hs.80305 //	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-1814192	gtgtctccggttgcaa[C/G]aaggggaggaggttag	C	G	Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // --- // --- // --- // --- ///	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-1783323	ggcagtgtttctcgcc[A/G]gcagctgcacagccag	A	G	Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // --- // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-1783936	ggccacatttttgca[C/T]ggttcatcatcatctg	C	T	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000360355 // CDS // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-2222458	cgagctctatcagcaa[A/C]ggcacaattaagtgga	A	C	22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 3668 //	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213225	ccgccagaatttctca[A/T]cactcttatgaatcct	A	T	60481 // Homo sapiens ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (ELOVL5), mRNA. /// NM_001498 // downstream // 70563 //	ELOVL5	ELOVL5, Homo sapiens ELOVL family member 5, elongation of long chain fatty acids (FEN1,p12.1
SNP_A-2207674	ccattttagttgggaa[C/G]tgactgtatgaattct	C	G	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 707879 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2169417	caagccaaattttgaa[C/T]taggggctgtaggact	C	T	Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // upstream // 7795 // Hs.11713 // ELF5 // 2001 // Homo	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13
SNP_A-2093531	agaacttttgcaattc[A/G]ccagtaaatagataaa	A	G	79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 46332 //	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2099798	agagtaagtgagatcc[A/G]cagctcacaccatacc	A	G	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-2049006	aagcctgtttctgcaa[G/T]gctttggttgaaaaga	G	T	sapiens CD9 antigen (p24) (CD9), mRNA. /// ENST00000009180 // intron // 0 // --- // --- // --- // ---	CD9	CD9, Homo sapiens CD9 antigen (p24) (CD9), p13.31
SNP_A-2052364	aagtacaggacaggta[C/T]gcccagtgggtgaaga	C	T	401263 // Homo sapiens FLJ41841 protein (FLJ41841), mRNA. /// ENST00000339488 // upstream // 59708 // --- // ---	FLJ41841	FLJ41841, Homo sapiens FLJ41841 protein (FLJ41841), p12.3
SNP_A-2034443	aaatctcccctaaaag[C/G]ctccttcagtgtttta	C	G	51012 // Homo sapiens chromosome 20 open reading frame 45, mRNA (cDNA clone MGC:3361 IMAGE:3631601), complete cds. /// NM_016045 // upstream // 76192 // Hs.3945	C20orf45	C20orf45, Homo sapiens chromosome 20 open reading frame 45, (cDNA clone MGC:3361 IMAGE:3631601), complete cds. ,q13.32
SNP_A-2035651	aaatgtcactctggac[C/T]gggagctgtacaactc	C	T	374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 297779 // Hs.34198 // FLJ44796 // 401209 //	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-2022420	aaaaataggtgcaata[G/T]cttggaatatcatcca	G	T	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2032741	aaataacggccaactg[A/C]aaataaagccaattag	A	C	Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-2269530	gacaaactgtttctaa[A/G]atttatatcagaatgt	A	G	60559 // Homo sapiens hypothetical protein FLJ22649 similar to signal peptidase SPC22/23 (FLJ22649), mRNA. /// NM_005429 // downstream // 195601 // Hs.435215 // VEGFC	SPCS3	SPCS3, Homo sapiens hypothetical protein FLJ22649 similar to signal peptidase SPC22,q34.2
SNP_A-2284573	gatcactcttacgaaa[C/T]tggaagaaaaggtaaa	C	T	// --- /// ENST00000354793 // downstream // 118932 // --- // ---	-	p13.3
SNP_A-2283614	gatagaccccggcggc[G/T]aacagacttggcgcac	G	T	/// ENST00000311164 // upstream // 14191 // --- // --- // --- // ---	-	q24.1
SNP_A-2293242	gcagagctggttcacg[A/C]cactcctgtggtcttc	A	C	Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 3 (PSCD3), mRNA. /// ENST00000350796 // intron	PSCD3	PSCD3, Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 3 (PSCD3), p22.1
SNP_A-2294305	gcagggtgtgggacgc[C/T]gagtgtagcactctca	C	T	201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// ENST00000284400 // intron // 0 // ---	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-2288656	gattggaggaaatgta[C/G]ctcagcaattgtagtg	C	G	25914 // Homo sapiens rotatin (RTTN), mRNA. /// NM_004232 // upstream // 32296 // Hs.44439 // SOCS6 //	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-2237830	ctctgaacaacgtaaa[C/G]agaccactggggttag	C	G	Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000323713 // intron // 0 // --- // --- // --- // ---	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2032407	aaagtttaatatacac[C/T]atgcatcacaggcaaa	C	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 856363 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.3
SNP_A-2030691	aaagctgctctacagc[A/G]aaaccaagagaaagtt	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-2030519	ggtgctaattgtggaa[G/T]tgggtctactctaaga	G	T	// Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // --- // ---	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31
SNP_A-2031574	aaaggtttacagaaag[A/G]atcaaggagaaatgct	A	G	Homo sapiens limkain b1 (LKAP), transcript variant 2, mRNA. /// NM_014647 // intron // 0 // Hs.173524 // LKAP // 9665 //	LKAP	LKAP, Homo sapiens limkain b1 (LKAP), transcript variant 2, p13.11
SNP_A-2041490	aaccttgtgaatatac[A/G]aaaacccactgaacta	A	G	Homo sapiens KIAA0417 mRNA, complete cds. /// ENST00000298777 // intron // 0 // --- // --- // --- // ---	HSPA12A	HSPA12A, Homo sapiens KIAA0417 complete cds. q25.3
SNP_A-2001410	actactctcaatcaca[C/G]tgtacctgcaggtggt	C	G	7019 // Homo sapiens transcription factor A, mitochondrial (TFAM), mRNA. /// NM_012251 // downstream // 261360 //	TFAM	TFAM, Homo sapiens transcription factor A, mitochondrial (TFAM), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2000926	acccttttatttttggga[A/G]tcacccaggatccttt	A	G	1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 72024 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste ,p15.1
SNP_A-2007146	ccttaggctgtagaat[C/T]atgccagatgttagtc	C	T	10920 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, mRNA. /// NM_006710 // downstream // 79827 // Hs.531713 // COPS8 // 10920 //	COPS8	COPS8, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, q37.3
SNP_A-2006617	agcaaattaacctgaa[A/T]tgactacatagctttc	A	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2050275	aaggagagcaattgga[C/T]gctactaatgtatctg	C	T	4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream //	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2211882	ccctcttcttgtatac[C/T]agggctcgctcttgtt	C	T	// Homo sapiens signal recognition particle 54kDa (SRP54), mRNA. /// ENST00000330704 // downstream // 41869 // --- //	SRP54	SRP54, Homo sapiens signal recognition particle 54kDa (SRP54), q13.2
SNP_A-2204327	ccagcctaaccaccat[A/G]atgaaagcccacatct	A	G	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 1 (MAP4K1), mRNA. /// ENST00000221409 // intron // 0 // --- // --- // --- // ---	MAP4K1	MAP4K1, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 1 (MAP4K1), q13.2
SNP_A-2223987	cgggcttagcatagca[C/T]ctgaaacatcttaaga	C	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2223864	tcacttcccagagcct[C/T]aaatataggataatgt	C	T	Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// ENST00000332981 // intron // 0 // --- // --- // --- // ---	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-2141630	atcttcaggatcagaa[A/G]gattcctagttaggaa	A	G	sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000260947 // intron // 0 // --- // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2156747	attctgtgaaaaatgg[A/C]attagtaatttaatat	A	C	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1143630 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1784742	ggcctgcaccagaagc[A/G]gaatcctgccagaccc	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1707481	tgtacaactgaaaacagtatagtcc[A/G]ataaaataacattctggaactcaaa	A	G	// 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 4205985 // Hs.146858 // PCDH10 // 57575 //	SLC7A11	SLC7A11 , rs10519422, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 ,q28.3
SNP_A-1803801	gtcaagaataagacaa[C/T]tgattaagggtgataa	C	T	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. ///	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-1873172	tctattccttaaactc[C/T]agccgctcatgtcccc	C	T	8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // downstream //	FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-1849640	tatggtcaccctactc[A/G]cgagtacttggttgca	A	G	Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // --- //	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-1859200	tcagctaaaaagacag[A/T]cgcattacaaccagca	A	T	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 49208 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1856308	aaaactcttctgctca[C/T]ataatggttattcatt	C	T	Homo sapiens cell division cycle 27 (CDC27), mRNA. /// ENST00000066544 // intron // 0 // --- // --- // --- // ---	CDC27	CDC27, Homo sapiens cell division cycle 27 (CDC27), q21.32
SNP_A-1829069	taagggtgtttgaagg[C/G]atttttctgggtaatt	C	G	83746 // Homo sapiens l(3)mbt-like 2 (Drosophila) (L3MBTL2), transcript variant 2, mRNA. /// NM_031488 // intron // 0 // Hs.517641 // L3MBTL2 // 83746 // Homo sapiens	L3MBTL2	L3MBTL2, Homo sapiens l(3)mbt-like 2 (Drosophila) (L3MBTL2), transcript variant 2, q13.2
SNP_A-1828596	taagccatttcttaag[G/T]cattctgaagataagc	G	T	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 466858 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1839869	tagattgtgtgttatg[A/G]ataaattaaataaata	A	G	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 851085	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1898745	tgctttcagaatagaa[A/G]tgtctctctataaagc	A	G	// 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream //	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-1883748	tgaacttgtgtaataa[C/T]cattatgctattaggt	C	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2563941 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1948911	tttatcattttcactg[A/C]atatcatgtgtgtata	A	C	// 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 544499 // Hs.353022 // ETAA16 //	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1826633	taacacatttttagaa[A/G]gtcttgaatccttggt	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1823686	taaaatatcaagagta[A/G]acaagtccttttaaat	A	G	5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// NM_173062 // upstream //	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin q15
SNP_A-1818013	gttctaggtcaatgta[A/G]agttatttgatgctca	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 251055 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1820504	gtttattaaactctcc[A/G]atcctaaagatgctgg	A	G	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, mRNA. /// NM_003471 // intron // 0 // Hs.157818 // KCNAB1 // 7881 // Homo sapi	KCNAB1	KCNAB1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, q25.31
SNP_A-1857230	gaaaaagcagtcatca[C/T]ctcccatctacccgga	C	T	Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1), mRNA. /// ENST00000290341 // intron // 0 // --- // --- // --- // ---	IMP-1	IMP-1, Homo sapiens IGF-II binding protein 1 (IMP-1), q21.32
SNP_A-1850566	tattaaggctggaacg[G/T]agctcttagtgactta	G	T	10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// NM_015323 //	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-1804506	gtcagagctgcagtgc[C/T]gagcctgaggccaccg	C	T	ENST00000295150 // 3UTR // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-1800335	gtactaagtttcccca[C/T]gcctcagtaggtataa	C	T	8869 // Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), mRNA. /// NM_015425 // downstream //	ST3GAL5	ST3GAL5, Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), p11.2
SNP_A-1707419	tcaaaggtgctgagatttctctata[C/G]taaatgtagtagtacactatcagtt	C	G	NM_182511 // downstream // 817144 // Hs.131596 // CBLN2 // 147381 // cerebellin 2 precursor	-	- , rs10514020, - ,q22.3
SNP_A-1712569	ccgaaggaagagtgaaaatgcgtaa[C/G]acctgggatcccgtctagtacagct	C	G	// agouti signaling protein, nonagouti homolog (mouse) /// NM_003908 // upstream // 85158 // Hs.429180 // EIF2S2 //	ASIP	ASIP , rs6119471, agouti signaling protein, nonagouti homolog (mouse) ,q11.22
SNP_A-1711040	aatttatataataggagcttaggga[C/T]ttagaatgctttagctttaaacaat	C	T	CENPC1 // 1060 // centromere protein C 1 /// NM_004439 // upstream // 152916 // Hs.201920 // EPHA5 // 2044 // EphA5	CENPC1	CENPC1 , rs2882314, centromere protein C 1 ,q13.2
SNP_A-1682760	gaaaatttgtaagtgtggaattttg[A/C]agtatgttaaattctagattctcct	A	C	AK023791 // intron // 0 // Hs.44175 // SEC15L2 // 23233 // SEC15-like 2 (S. cerevisiae)	SEC15L2	SEC15L2 , rs10496184, SEC15-like 2 (S. cerevisiae),p13.2
SNP_A-1670610	tgtatttcttcagagacaatctgga[A/G]catatctttttgtcaaatgtgaga	A	G	NM_013244 // intron // 0 // Hs.422827 // HGNT-IV-H // 25834 // UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog	HGNT-IV-H	HGNT-IV-H , rs1502800, UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog,q21.31
SNP_A-2168119	caactcacccacttcc[C/T]agtttcagccccaact	C	T	Homo sapiens hypothetical protein MGC35023 (MGC35023), mRNA. /// ENST00000318405 // downstream // 40357 // --- //	-	-, Homo sapiens hypothetical protein MGC35023 (MGC35023), p12.3
SNP_A-2109079	agcttcggagtactta[C/T]agaaggaagtctttta	C	T	// 390061 // Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), mRNA. /// ENST00000332043 // downstream // 17449 // --- // --- // --- // --	OR51Q1	OR51Q1, Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), p15.4
SNP_A-2225884	ctaaatctcattcgtc[A/G]ctctggaaccatcttc	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2192706	catcccatcagtgagc[A/C]cttgggttgcatccaa	A	C	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2054146	aagttccttcctggaa[A/G]gttctctattcaggta	A	G	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // intron // 0 // --- // -	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2071899	acagagaggacctagc[A/G]gctaaggagtccagag	A	G	27178 // Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, mRNA. /// NM_014439 //	IL1F7	IL1F7, Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, q13
SNP_A-2079083	acccagagtaggagaa[C/G]agagaggaagaggagt	C	G	ENST00000338067 // 3UTR // 0 // --- // --- // --- // ---	-	p36.13
SNP_A-2013871	tgggggggacaagtca[A/G]tccttctgatcctcag	A	G	sapiens thyroglobulin (TG), mRNA. /// ENST00000220616 // intron // 0 // --- // --- // --- // ---	TG	TG, Homo sapiens thyroglobulin (TG), q24.22
SNP_A-1994866	atcctgatttatattc[A/G]atgagagttataaaag	A	G	114569 // Homo sapiens mal, T-cell differentiation protein 2 (MAL2), mRNA. /// NM_002514 // upstream // 54228 //	MAL2	MAL2, Homo sapiens mal, T-cell differentiation protein 2 (MAL2), q24.12
SNP_A-2043869	aacttcccacatttca[A/G]ccagagcagagggtcc	A	G	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// ENST00000337517 // intron // 0 // --- // --- // --- // ---	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2035568	aaatgtacacaaatta[C/T]gtcaaaactattatgt	C	T	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream //	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.2
SNP_A-2238856	ctcttatttataagga[C/T]gttttattctcgagtg	C	T	Homo sapiens complement component 6 (C6), mRNA. /// NM_000065 // upstream // 4324 // Hs.481992 // C6 // 729 //	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-2250643	cttataaatgagaata[C/T]gtagcattttgttttc	C	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247733	ctgtgacatatttggc[G/T]ccctcaccttcaatca	G	T	5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 77393 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2275352	gagaatcaaaagctgc[A/G]gaaggtggttcatttc	A	G	5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 62100 // Hs.248136 // HTR1F //	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.1
SNP_A-2292626	gcactggaatagcata[C/T]atggttgaagaaatgt	C	T	83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2310573	ggaagaccaaaagttc[A/C]aggttgcacattgggt	A	C	5648 // Homo sapiens mannan-binding lectin serine protease 1 (C4/C2 activating component of Ra-reactive factor)	MASP1	MASP1, Homo sapiens mannan-binding lectin serine protease 1 (C4,q27.3
SNP_A-2301956	gcgtcacataaagact[A/T]aatcaatacaagttca	A	T	// Homo sapiens 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (BDH), nuclear gene encoding mitochondrial protein, transcri /// NM_203314 // upstream // 36967 // Hs.274539 // BDH // 622 //	BDH	BDH, Homo sapiens 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (BDH), nuclear gene encoding mitochondrial protein, transcri ,q29
SNP_A-2289484	gattttggtgttctaa[C/T]cagaagttcataggca	C	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2280465	gtgaatggttgttcaa[C/T]gggcaactatagtgtc	C	T	Homo sapiens tropomodulin 3 (ubiquitous) (TMOD3), mRNA. /// ENST00000308580 // intron // 0 // --- // --- // --- // ---	TMOD3	TMOD3, Homo sapiens tropomodulin 3 (ubiquitous) (TMOD3), q21.2
SNP_A-2280087	gagggaatggtacata[C/T]caaattcagaatagag	C	T	// 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2248343	ctgtgtctgacatcca[A/G]atatttctagtactga	A	G	Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// ENST00000313129 // intron // 0 // --- // --- // --- // ---	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-2253051	cttctctatggctgga[C/T]aattttaagacctctc	C	T	sapiens catalase (CAT), mRNA. /// ENST00000241052 //	CAT	CAT, Homo sapiens catalase (CAT), p13
SNP_A-2255115	cttggggcttggaata[A/C]ggtttttcaagtggca	A	C	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2229156	ctagctatattccaaa[A/T]gacatatggaccagtt	A	T	946 // Homo sapiens sialic acid binding Ig-like lectin 6 (SIGLEC6), transcript variant 1, mRNA. /// NM_198846 // upstream // 23590 // Hs.397255 // SIGLEC6 // 946 // Homo	SIGLEC6	SIGLEC6, Homo sapiens sialic acid binding Ig-like lectin 6 (SIGLEC6), transcript variant 1, q13.41
SNP_A-2042232	atgtatgtaaagtaac[C/T]gtaaatagcaggttct	C	T	160492 // Homo sapiens hypothetical protein FLJ36004 (FLJ36004), mRNA. /// NM_007211 // upstream // 313219 //	FLJ36004	FLJ36004, Homo sapiens hypothetical protein FLJ36004 (FLJ36004), p12.1
SNP_A-2025952	aaaatgtggataatga[C/T]tatacttacttcatag	C	T	805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // downstream //	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q32.12
SNP_A-2006219	agccaccgttgctaca[C/G]ataatttctcattggc	C	G	64744 // Homo sapiens hypothetical protein AL133206 (LOC64744), mRNA. /// ENST00000309004 // upstream //	LOC64744	LOC64744, Homo sapiens hypothetical protein AL133206 (LOC64744), p34.2
SNP_A-2009389	cagagactgtatgaga[A/T]aataaatgttagttgc	A	T	1962 // Homo sapiens enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (EHHADH),	EHHADH	EHHADH, Homo sapiens enoyl-Coenzyme A, hydratase q27.2
SNP_A-2062492	aatgtataggtatctc[A/T]catatatcaaaaataa	A	T	1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // upstream // 305979 // --- // --- // --- // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2051544	aagggtgtagacaaca[A/G]tgtaagaggcttaaag	A	G	// 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 46338 // Hs.98367 //	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-2183117	cagcaaagcttaatta[A/T]ctgcatgaatggggac	A	T	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2176996	cacctagttatagaca[A/T]acagtgatgtttataa	A	T	Homo sapiens hemicentin (FIBL-6), mRNA. /// ENST00000271588 // intron // 0 // --- // --- // --- // ---	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2207227	ccattcactgcttgaa[A/T]gtttagccccagatgg	A	T	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2110518	aggacacagtggagac[C/T]ctggtgatagcccttc	C	T	136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 678685 // Hs.43297 // MTPN //	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2167562	caacatttgtaagaac[C/T]cttatacagtcagccc	C	T	// 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-1783931	ggccacatctagagaa[C/T]cacatttagaactcag	C	T	Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), mRNA. /// ENST00000356336 // intron // 0 // --- // -	SRGAP3	SRGAP3, Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), p25.3
SNP_A-1782992	ggcagcatcgaaatca[C/T]tgaatgggaaaatgaa	C	T	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 418072 //	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801638	gtagtacattatgtta[C/T]agatagtaggagagtg	C	T	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1864145	tccacatgctgtgtac[A/G]aagtgtactgctaggc	A	G	/// ENST00000359805 // upstream // 33247 // --- // --- // --- // ---	-	q23.2
SNP_A-1837858	tagaaaaatctctgaa[C/G]tcttctctggattcca	C	G	27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 1088065 //	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-1831762	taattcatcaaagagc[A/G]gattcttattcaagat	A	G	FLJ44048 // 401024 // Homo sapiens FLJ44048 protein (FLJ44048), mRNA. /// NM_018471 // upstream // 295824 //	FLJ44048	FLJ44048, Homo sapiens FLJ44048 protein (FLJ44048), q32.1
SNP_A-1949360	tttattatgattgcta[A/T]gtattcttgttatatt	A	T	FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1940851	ttgctaatgaggtttc[C/T]attgatttgtctccct	C	T	23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 84034 //	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-1970036	tctccatccactccaa[C/T]gtaccatttgtcacac	C	T	30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 //	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-1988027	aagagaaggcagtcac[C/T]gaggatgaaaggggag	C	T	// 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream //	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-1982275	acctggttggattgta[C/G]actagagagtgatgag	C	G	Homo sapiens mutS homolog 3 (E. coli) (MSH3), mRNA. /// ENST00000265081 // intron // 0 // --- // --- // --- // ---	MSH3	MSH3, Homo sapiens mutS homolog 3 (E. coli) (MSH3), q14.1
SNP_A-1877100	tctgctctctcttgta[C/T]gtacttaatatgggac	C	T	Homo sapiens cDNA: FLJ23024 fis, clone LNG01684. /// ENST00000358166 // intron // 0 // --- // --- // --- // --- ///	ZCCHC4	ZCCHC4, Homo sapiens cDNA: FLJ23024 fis, clone LNG01684. ,p15.2
SNP_A-1901937	tggcagggattagagc[A/G]atgccaccgcaggcca	A	G	55544 // Homo sapiens RNA-binding region (RNP1, RRM) containing 1 (RNPC1), transcript variant 2, mRNA. /// NM_017495 // downstream // 45127 // Hs.236361 // RNPC1 //	RNPC1	RNPC1, Homo sapiens RNA-binding region (RNP1, RRM) containing 1 (RNPC1), transcript variant 2, q13.32
SNP_A-1911531	tgtctttgctattcaa[C/T]ggatgctggagagaac	C	T	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // --- // ---	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-1927815	ttcaaggcagtgttgg[A/G]catcaggttttgggct	A	G	64106 // Homo sapiens G protein-coupled receptor 147 (GPR147), mRNA. /// NM_207119 // downstream // 25431 //	GPR147	GPR147, Homo sapiens G protein-coupled receptor 147 (GPR147), q22.1
SNP_A-1897605	tgctgcagtagaagga[A/C]ccagatccctttccac	A	C	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000330684 // intron // 0 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1879485	tcttattcctgcagac[C/G]aggccattccactatg	C	G	79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// NM_003012 // downstream // 354840	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-1943998	ttgtattcatctcagc[A/G]actataagatgtcaaa	A	G	/// ENST00000343867 // upstream // 75150 // --- // --- // --- // ---	-	q11.21
SNP_A-1944071	ttgtcaacggtaacac[C/T]acagaagataactact	C	T	Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// ENST00000340214 // intron // 0 // --- //	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11
SNP_A-1949860	tttcaactctatagcc[A/G]aatttattatgcccaa	A	G	5015 // Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), transcript variant 2, mRNA. /// NM_021728 //	OTX2	OTX2, Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), transcript variant 2, q22.3
SNP_A-1952948	tttcttcatttatata[G/T]gcttggaatttttaa	G	T	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 127214 // Hs.129701 //	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1838500	tagaatgagcccttga[G/T]gtctgcaccacataat	G	T	1105 // Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /// ENST00000284049 // upstream	CHD1	CHD1, Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), q21.1
SNP_A-1859881	tcaggtaagataataa[A/G]agagtttgtaagacac	A	G	Homo sapiens TGF-beta induced apotosis protein 2 (TAIP-2), mRNA. /// ENST00000342316 // intron // 0 // --- // --- // --- // ---	TAIP-2	TAIP-2, Homo sapiens TGF-beta induced apotosis protein 2 (TAIP-2), q24.3
SNP_A-1855814	tcaatcttcaaatacc[A/G]cctagggctgtggtgc	A	G	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 77047 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1812546	gtggcctctgcctgca[C/T]gtgaaagtcagactgg	C	T	5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, mRNA. /// NM_012486 //	PSEN2	PSEN2, Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, q42.13
SNP_A-1781350	ggatgtgtcatgatct[A/C]acagttgtccgctttt	A	C	Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-1669775	atttgaaagcagtgaactatagaag[A/G]agaaaataggattaaaaagccgtca	A	G	3958 // lectin, galactoside-binding, soluble, 3 (galectin 3) /// NM_014750 // downstream // 2368 // Hs.77695 // DLG7 //	LGALS3	LGALS3 , rs10498475, lectin, galactoside-binding, soluble, 3 (galectin 3) ,q22.3
SNP_A-2111130	aggagagcagaagggc[C/G]gactcctcctggagga	C	G	10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 205068 // Hs.369907 //	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-2214201	cctaattttattgtca[C/T]gaggcagaaatgaaat	C	T	// --- /// ENST00000328955 // upstream // 488152 // --- // --- // ---	-	q24.23
SNP_A-2216792	cctctgaacatagaca[A/G]tcctattaatcatttc	A	G	/// ENST00000360919 // upstream // 152766 // --- // --- // --- // ---	-	q13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2182366	cagagttctgaaaaca[C/T]aaactccacaaatttc	C	T	Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // intron // 0 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC rela	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. ,q27
SNP_A-2186265	caggctatgtgtataa[A/G]gcatacgtgaatttca	A	G	Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, mRNA. /// NM_133266 // intron // 0 // Hs.268726 // SHANK2 // 22941 // Homo sapiens	SHANK2	SHANK2, Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, q13.4
SNP_A-2198954	catttgcctgaaaaac[A/C]cataggcactcagcac	A	C	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2438167 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2051410	aaggggatgtattcca[C/T]agtatcagatgatgca	C	T	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-2065124	aattgctgagagtaga[C/T]tataattgttctcacc	C	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2071167	acactggtttcctagc[C/T]atcctctgaaaacagt	C	T	Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// ENST00000259030 // 3UTR // 0 // --- // --- // --- // ---	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2082894	acgtccttgaaaatct[C/G]aaattaagaagaaggt	C	G	79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 342620 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2017853	acaaatgcgaaacttc[A/T]atagtacaataaacac	A	T	337882 // Homo sapiens keratin associated protein 19-1 (KRTAP19-1), mRNA. /// NM_181608 // downstream // 4466	KRTAP19-1	KRTAP19-1, Homo sapiens keratin associated protein 19-1 (KRTAP19-1), q22.11
SNP_A-2002309	ttatttgaggatgcca[G/T]gagaaaatgccatgca	G	T	Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000278723 // intron // 0 // --- // ---	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2030598	aaagctaggagtgtcc[C/T]cgaaatgtgggtggta	C	T	Homo sapiens hypothetical protein FLJ12750 (FLJ12750), mRNA. /// ENST00000267202 // intron // 0 // --- // --- // --- // ---	FLJ12750	FLJ12750, Homo sapiens hypothetical protein FLJ12750 (FLJ12750), q24.31
SNP_A-2030320	tataactggattacac[C/T]gtatcaccaacaaccc	C	T	// 25977 // Homo sapiens DKFZP566B183 protein (DKFZP566B183), mRNA. /// NM_016184 // upstream // 2461	NECAP1	NECAP1, Homo sapiens DKFZP566B183 protein (DKFZP566B183), p13.31
SNP_A-2255691	cttgttcatctggaag[C/T]ctcgccttctcctgga	C	T	5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// ENST00000331583 // upstream // 22873	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q32.3
SNP_A-2253185	cttctgagcccaggaa[A/G]gagaatataatggctg	A	G	60481 // Homo sapiens ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (ELOVL5), mRNA. /// NM_001498 // downstream // 31783 //	ELOVL5	ELOVL5, Homo sapiens ELOVL family member 5, elongation of long chain fatty acids (FEN1 p12.1
SNP_A-2246328	ctggtgtttaatccca[C/T]gctacccctcgctggc	C	T	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2244223	ctggaaaatttccaaa[A/G]tagatgaaagacatca	A	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2266834	gaagttagaatctata[C/T]ccacatctgggctgga	C	T	DKFZp434G0625 // 91584 // Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), mRNA. /// NM_173682 // upstream // 41278 // --- // FLJ40288 // 286023	DKFZp434G0625	DKFZp434G0625, Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), q32.3
SNP_A-2298887	ggggaggtgatgatga[A/G]gaaaagaaagcctgtt	A	G	// 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 295566 // Hs.459049 //	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. ,q25.1
SNP_A-2297301	gccacctgctgaccga[G/T]ccagtgaaggaccaca	G	T	Homo sapiens tripartite motif-containing 16 (TRIM16), mRNA. /// ENST00000336708 // CDS // 0 // --- // --- // --- // ---	TRIM16	TRIM16, Homo sapiens tripartite motif-containing 16 (TRIM16), p12
SNP_A-2303569	gctcaatgcttatcta[C/T]actggccagtacgtgc	C	T	Homo sapiens C-terminal binding protein 1 (CTBP1), mRNA. /// ENST00000290921 // intron // 0 // --- // --- // --- // ---	CTBP1	CTBP1, Homo sapiens C-terminal binding protein 1 (CTBP1), p16.3
SNP_A-2304467	gctctaggtagaaaga[C/G]atgtggacacaagttc	C	G	Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA. /// NM_016657 // intron // 0 // Hs.534392 //	KDELR3	KDELR3, Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, q13.1
SNP_A-2311902	ggacaaatagttgtgg[A/G]atgtattagaaaagtg	A	G	// Homo sapiens macrophage antigen h (UNQ5782), mRNA. /// ENST00000348658 // intron // 0 // --- // --- // --- // --- ///	UNQ5782	UNQ5782, Homo sapiens macrophage antigen h (UNQ5782), p13.31
SNP_A-2253345	cttctggtttacaaat[C/G]agtggactctggataa	C	G	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 313307 // Hs.153952 // NT5E //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-2230333	ctatatgattaataca[A/G]agataggtggtcttaa	A	G	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 296764 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238255	ctctggaaaggctaca[A/C]ctagacaagctgatga	A	C	27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 94513 // Hs.381050 // B3GAT1 // 27087 // Homo sa	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-2026277	aaaatttactttaaaa[C/T]tgctgtcacttatatg	C	T	Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // --- // --- // --- // --- ///	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2023103	aaaacagcatttgtaa[A/G]gaaaacgtcattctac	A	G	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2075724	acatggggactattgt[A/T]aatgtattgcatactt	A	T	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 148792 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2196629	cattaaccaatagtca[C/T]acatatttccatgcat	C	T	Homo sapiens G protein-coupled receptor 68 (GPR68), mRNA. /// ENST00000238699 // intron // 0 // --- // --- // --- // ---	GPR68	GPR68, Homo sapiens G protein-coupled receptor 68 (GPR68), q32.12
SNP_A-2188947	cagtgtcctttagagc[C/T]gatacttaaagtcagt	C	T	Homo sapiens creatine kinase, mitochondrial 2 (sarcomeric) (CKMT2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000254035 // intron // 0 // --- // --- // --- // ---	CKMT2	CKMT2, Homo sapiens creatine kinase, mitochondrial 2 (sarcomeric) (CKMT2), nuclear gene encoding mitochondrial protein, q14.1
SNP_A-2221975	cgaaagggttctgcca[A/G]tgcataatagtgttat	A	G	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 755234 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2138754	atccccactcctctaa[C/T]actaatgactgtccaa	C	T	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 56659 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-1675369	agaggggatgtctctatcatcttg[C/G]acagctatagcaaactattatagcc	C	G	// 9364 // RAB28, member RAS oncogene family /// NM_005114 // upstream // 1680193 // Hs.40968 // HS3ST1 //	RAB28	RAB28 , rs472040, RAB28, member RAS oncogene family ,p15.33
SNP_A-1806717	gtctactttgaggtac[C/T]atcttattctccctgg	C	T	// 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 246018 // --- // --- //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1785696	ggctctaaaagaagtc[C/T]gaagctttgcgccggg	C	T	Homo sapiens DiGeorge syndrome critical region gene 14 (DGCR14), mRNA. /// ENST00000252137 // CDS // 0 // --- // -	DGCR14	DGCR14, Homo sapiens DiGeorge syndrome critical region gene 14 (DGCR14), q11.21
SNP_A-1790978	ggggtatacattaaac[C/T]agaaaagccatgagtc	C	T	// 142679 // Homo sapiens dual specificity phosphatase 19 (DUSP19), mRNA. /// NM_138285 // upstream // 7951 //	DUSP19	DUSP19, Homo sapiens dual specificity phosphatase 19 (DUSP19), q32.1
SNP_A-1847938	tatctgaggggtaaa[A/G]cacggatgaaatgacc	A	G	GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// NM_000275 // downstream // 64753 // Hs.130937 // OCA2 //	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-1948676	tttatacctgggtgaa[C/T]ggggcacacctccact	C	T	Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, mRNA. /// NM_172059 // intron // 0 //	EYA1	EYA1, Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, q13.3
SNP_A-1877656	tctgggagaggattcc[A/G]gattctaaaacagcag	A	G	ENST00000302763 // intron // 0 // --- // --- // --- // ---	-	q31.2
SNP_A-1874213	tctccaagtgaagtac[A/G]aagataatgcagttga	A	G	// 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 50526 //	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-1889483	tgagttgcactgggaa[A/C]cttagaactacaagaa	A	C	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 1049145 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1930914	ttccaggactgccctg[C/T]agaggaaggcacatcc	C	T	// 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1932357	ttcctgaatctggctg[C/T]agatagattttggtag	C	T	Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA. /// ENST00000261842 // intron // 0	AP4E1	AP4E1, Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), q21.2
SNP_A-1927725	ttcaagacttgtggca[C/T]cttcaaagataggaat	C	T	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 246553 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1920200	ttaatcttcaaaacaa[C/G]actgagaggttggtac	C	G	2315 // Homo sapiens melan-A (MLANA), mRNA. /// ENST00000251879 // downstream // 98358 // --- // --- // --- // --	MLANA	MLANA, Homo sapiens melan-A (MLANA), p24.1
SNP_A-1907513	tgtaaatcagattgaa[C/T]taagataagcaataca	C	T	SLC17A6 // 57084 // Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), mRNA. /// NM_022725 // downstream	SLC17A6	SLC17A6, Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), p14.3
SNP_A-1883320	tgaacaactagaagaa[A/T]catacaagggcaagga	A	T	6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 381366 // Hs.546261 //	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1881356	tctttcatagcaccta[A/C]gttattcatcttggat	A	C	/// ENST00000356117 // downstream // 658316 // --- // --- // ---	-	q23.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897751	tgctggaaagagaagt[G/T]aaataacatgaggatt	G	T	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 148437 // Hs.32942 // PIK3CG // 5294 // Homo	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-1891549	tgattctggtgtactg[C/T]ataaaatctagatacc	C	T	// 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 64713	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24
SNP_A-1976706	taagacacatccagga[C/T]tagaggatcttaaaca	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1988106	gaaattttgggctaaa[A/G]gtcatgtgtgataata	A	G	Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// ENST00000357180 // intron // 0 // --- // --- // --- // ---	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2
SNP_A-1966824	aaatattgctgcctta[C/T]ccttcttctggaagct	C	T	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1963544	atgttacttccataga[C/G]aggctttctatgaccc	C	G	Homo sapiens EH domain binding protein 1 (EHBP1), mRNA. /// ENST00000263991 // intron // 0 // --- // --- // --- // ---	EHBP1	EHBP1, Homo sapiens EH domain binding protein 1 (EHBP1), p15
SNP_A-1842470	taggtgccagatcttg[C/G]aaagccttgtcggtgg	C	G	91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1833401	tacagacaagggaata[G/T]tattcaacactaaaaa	G	T	// Homo sapiens adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-c, mRNA. /// NM_001111 // upstream // 34251 // Hs.12341 // ADAR // 103 // Homo	ADAR	ADAR, Homo sapiens adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-c, q22
SNP_A-1816833	gttatgcttcttgatc[A/G]ctggattatttttttt	A	G	Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // --- // -	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1816210	gttactccttttcatc[A/G]gacatgacacctcaaa	A	G	54714 // Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), mRNA. /// NM_173538 // upstream // 73090 // ---	CNGB3	CNGB3, Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), q21.3
SNP_A-2161781	atttgtatgcattata[A/T]ctcttatttagttctc	A	T	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 270111 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2161837	atttgtctaataacta[C/G]gagtatcacaggacac	C	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2160608	atttcctatgtgtgag[A/C]aacactgttaagacat	A	C	ENST00000265274 // intron // 0 // --- // --- // --- // --- /// ENST00000360069 // intron // 0 // --- // --- // --- // --- ///	-	q25.2
SNP_A-2127106	ataaatataatttgca[A/G]agaggggtaagagaac	A	G	// 170825 // Homo sapiens homeobox protein GSH-2 (GSH-2), mRNA. /// NM_006206 // upstream // 21529 // Hs.74615 //	GSH-2	GSH-2, Homo sapiens homeobox protein GSH-2 (GSH-2), q12
SNP_A-2136183	atcaatctgataagac[C/T]gatataacggaaaata	C	T	5445 // Homo sapiens paraoxonase 2 (PON2), mRNA. /// AF001601 // upstream // 34896 // Hs.530077 // PON2 // 5445	PON2	PON2, Homo sapiens paraoxonase 2 (PON2), q21.3
SNP_A-2214379	cctacctgggctcaga[A/G]ctttccctggcatctt	A	G	// 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 87176 // Hs.132344	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2201524	ccaattaaattccatg[C/T]agaaaaatcatattgt	C	T	/// ENST00000357331 // upstream // 154128 // --- // --- // --- // -	-	p21.3
SNP_A-2198247	cattgtgaccgtagca[G/T]gatcttctggagagcc	G	T	Homo sapiens tubulin-specific chaperone d (TBCD), mRNA. /// ENST00000355528 // intron // 0 // --- // --- // --- // --- ///	TBCD	TBCD, Homo sapiens tubulin-specific chaperone d (TBCD), q25.3
SNP_A-2192633	catccatgaacattac[G/T]aagctccttgtacctc	G	T	Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // --- // ---	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-2059252	aatccttcattataga[A/C]agagaaattcacccag	A	C	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1982871 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2094135	agaaggcagaatgcac[A/T]gagagaatcttcagat	A	T	// Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), mRNA. /// ENST00000249601 // intron // 0 // ---	ARHGAP22	ARHGAP22, Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), q11.22
SNP_A-2045887	aagacatttatgtggc[C/T]gacaaatatattaaaa	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2034905	aaatgagggctcttaa[A/C]ctttcttgaggtgtca	A	C	sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), mRNA. /// ENST00000329185 // intron // 0 // --- // --- // ---	KCNB2	KCNB2, Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), q13.3
SNP_A-2004142	tgatcttgggtcggaa[A/G]aaagtctcaaaaacta	A	G	SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 345402 // Hs.511265 // SEM	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN q21.1
SNP_A-2312641	ggactaaaatcaggaa[A/G]aaaacaaagtacacca	A	G	ENST00000259793 // CDS // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2302156	gctaaaagtgtcacaa[C/G]gctttggttactagag	C	G	FLJ20604 // 54995 // Homo sapiens hypothetical protein FLJ20604 (FLJ20604), mRNA. /// NM_052953 // upstream //	FLJ20604	FLJ20604, Homo sapiens hypothetical protein FLJ20604 (FLJ20604), p24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2280763	gaggtgattgtgagaa[A/G]gtctgttcccagaaaa	A	G	133 // Homo sapiens adrenomedullin (ADM), mRNA. /// NM_000480 // upstream // 100547 // Hs.501890 // AMPD3 //	ADM	ADM, Homo sapiens adrenomedullin (ADM), p15.4
SNP_A-2282422	agaaaaacctgaccag[A/G]agaattgtagcgaaaa	A	G	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-2274224	gacttcttattttgga[G/T]gtactatgaaagtaga	G	T	– /// ENST00000329885 // downstream // 170835 // --- // --- //	-	q14.3
SNP_A-2004678	gctgtgcagctacaga[A/T]gagcagatcctgaatt	A	T	5257 // Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. /// NM_145188 // downstream // 34149 // Hs.410111	PHKB	PHKB, Homo sapiens phosphorylase kinase, beta (PHKB), q12.1
SNP_A-2026249	aaaattgtcacgaaag[C/G]agtgatttttttttca	C	G	Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. /// ENST00000345985 // intron // 0 // --- // --- // --- // ---	FLJ14075	FLJ14075, Homo sapiens hypothetical protein FLJ14075 (FLJ14075), p25.1
SNP_A-2094733	agaatcacacatctac[A/G]aagaattagcaacatc	A	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 163359 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2065827	aatttccagccattga[A/C]cataggaatgtgtggg	A	C	ENST00000355787 // intron // 0 // --- // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2131283	atagagtagaagatga[C/T]gtagtttattgaaaaa	C	T	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2128213	ataagggaacttttttc[A/G]cttcaccactatgcct	A	G	93408 // Homo sapiens myosin light chain 2, precursor lymphocyte-specific (MYLC2PL), mRNA. /// NM_181552 //	MYLC2PL	MYLC2PL, Homo sapiens myosin light chain 2, precursor lymphocyte-specific (MYLC2PL), q22.1
SNP_A-2115990	agggttggaatttgaa[C/T]gcaggggtctggttct	C	T	8554 // Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), mRNA. /// ENST00000341418 // downstream //	PIAS1	PIAS1, Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), q23
SNP_A-2155471	attcattattttatac[A/G]atgctaggcacatagt	A	G	// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// ENST00000285928 // intron // 0 // --- // --- // --- // ---	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2150339	atgtctgttgtcataa[A/T]caaatataaagatagt	A	T	Homo sapiens beta-carotene dioxygenase 2 (BCDO2), mRNA. /// ENST00000358264 // intron // 0 // --- // --- // --- // ---	BCDO2	BCDO2, Homo sapiens beta-carotene dioxygenase 2 (BCDO2), q23.1
SNP_A-1844689	tataagacataagcaa[C/T]ctaaccaatgaaagaa	C	T	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 282704 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1799943	gtacaggtttgagcaa[A/G]tctactgccttttctg	A	G	3925 // Homo sapiens stathmin 1/oncoprotein 18 (STMN1), transcript variant 1, mRNA. /// NM_005563 // upstream //	STMN1	STMN1, Homo sapiens stathmin 1,p36.11
SNP_A-1814008	gtgtcatcatctcaaa[A/G]aggaaagcctctgcac	A	G	Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // --- //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1807538	gtctggaacattccga[A/G]ggaaaataaaacaatt	A	G	Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, mRNA. /// NM_022114 // intron // 0 //	PRDM16	PRDM16, Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, p36.32
SNP_A-1666244	aacctggcttgcaaatagaatctcc[C/T]gaagttcaagaaaaatgatagccta	C	T	1005 // cadherin 7, type 2 /// NM_021153 // downstream // 329906 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2	CDH7	CDH7 , rs4075384, cadherin 7, type 2 ,q22.1
SNP_A-1649830	tgcaaccaatcaaatattttctttg[C/T]attacttttgagtttgtcctataaa	C	T	NM_182761 // downstream // 111439 // Hs.434682 // LOC340069 // 340069 // hypothetical protein LOC340069	LOC340069	LOC340069 , rs162307, hypothetical protein LOC340069,q23.1
SNP_A-1683126	gtctcagggtatcagaaggcaggta[C/G]aaattctgctgattgggatgcccaa	C	G	NM_003291 // downstream // 1892 // Hs.432424 // TPP2 // 7174 // tripeptidyl peptidase II	TPP2	TPP2 , rs10508094, tripeptidyl peptidase II,q33.1
SNP_A-1733644	gataagcaatacaaatctcaaataa[A/G]ttaagtttataacttaaggctccct	A	G	Similar to dJ153G14.3 (novel C2H2 type Zinc Finger protein) (LOC346157), mRNA /// NM_032030 // downstream // 5163 // Hs.326753 // FKSG83 // 83954 // FKSG83	-	- , rs721600, Similar to dJ153G14.3 (novel C2H2 type Zinc Finger protein) (LOC346157), mRNA ,p22.1
SNP_A-1975554	aacaatattctcaaca[C/T]ggcaatgatttttaat	C	T	ENST00000287546 // intron // 0 // --- // --- // --- // ---	KIAA0804	KIAA0804, --- q27.2
SNP_A-1953685	tttgactaaagagtaa[C/T]gaactgtgaaagttca	C	T	Homo sapiens SMILE protein (SMILE), mRNA. /// ENST00000266712 // intron // 0 // --- // --- // --- // ---	SMILE	SMILE, Homo sapiens SMILE protein (SMILE), q21.32
SNP_A-1951698	tttcctttatgacatt[C/G]aaaatatgactctgtc	C	G	// 9886 // Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, mRNA. /// NM_014836 // upstream // 342577 // Hs.148670 // RHOBTB1 // 9886 //	RHOBTB1	RHOBTB1, Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, q21.2
SNP_A-1960489	tttttcaaatcttatg[A/G]aggagataggagagag	A	G	// 54741 // Homo sapiens leptin receptor gene-related protein (OBRGRP), mRNA. /// NM_001003679 // downstream //	LEPROT	LEPROT, Homo sapiens leptin receptor gene-related protein (OBRGRP), p31.2
SNP_A-1946942	tttaaggttgaatatc[C/G]agagagtagcctgagt	C	G	Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// ENST00000264326 // intron // 0 // --- // --- // --- // ---	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1893536	tgcaggatggttagga[A/G]gatcagaaaaaaaatt	A	G	3459 // Homo sapiens interferon gamma receptor 1 (IFNGR1), mRNA. /// NM_175747 // downstream // 155421 //	IFNGR1	IFNGR1, Homo sapiens interferon gamma receptor 1 (IFNGR1), q23.3
SNP_A-1874518	tctccctgtgatcagc[A/G]caacctgaaatggagg	A	G	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 116386 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1875799	tctctttgattttgaa[G/T]gactatcttgcttcgg	G	T	-- /// ENST00000341636 // upstream // 313917 // --- // --- // ---	-	q11.2
SNP_A-1884280	tgaaggctttgtcata[C/T]gctttgggtctatcta	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 941914 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1901777	tggcaccttcaccacc[A/G]aaccaatgccagcaac	A	G	// 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// NM_173557 // downstream // 81059 // Hs.465316	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.33
SNP_A-1905859	tggtcagtttcgttcc[C/T]gctaacacggtagagt	C	T	23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 81460 // Hs.488293 //	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-1912715	tgtgctacataaagca[C/G]attagattaactaagc	C	G	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 193390 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1914162	tgtgtgtgtatttgta[C/T]aatctcacatcatcct	C	T	6943 // Homo sapiens transcription factor 21 (TCF21), transcript variant 1, mRNA. /// NM_003206 // upstream //	TCF21	TCF21, Homo sapiens transcription factor 21 (TCF21), transcript variant 1, q23.2
SNP_A-1928186	ttcacagaattccttc[C/T]atgtaacccaaattta	C	T	56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 336274 //	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1973430	tttgtaagggtttcag[A/G]ttaaacattttgtttt	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2242064 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.2
SNP_A-1974300	gcctctgcattctcac[A/G]ggacagccagtgcact	A	G	29927 // Homo sapiens Sec61 alpha 1 subunit (S. cerevisiae) (SEC61A1), mRNA. /// NM_003707 // downstream // 9027 //	SEC61A1	SEC61A1, Homo sapiens Sec61 alpha 1 subunit (S. cerevisiae) (SEC61A1), q21.3
SNP_A-1789287	gggccaaatgaattaa[A/G]taccttgtttacagtc	A	G	// 80195 // Homo sapiens chromosome 10 open reading frame 57 (C10orf57), mRNA. /// ENST00000256052 //	C10orf57	C10orf57, Homo sapiens chromosome 10 open reading frame 57 (C10orf57), q22.3
SNP_A-1849795	tatgtacatttccttc[A/G]aaggccatttatcagt	A	G	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, p15.31
SNP_A-1856500	tcacagatacttgtta[A/C]agagtctacttgggtc	A	C	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1306344 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1864291	tccacggatttggctg[C/T]agatccagagagatgg	C	T	11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1870678	tcgccagcacatgtaa[A/G]ccagatcctacagcca	A	G	9372 // Homo sapiens zinc finger, FYVE domain containing 9 (ZFYVE9), transcript variant 2, mRNA. /// NM_007324 // upstream // 39044 // Hs.532345 // ZFYVE9 // 9372 // Homo	ZFYVE9	ZFYVE9, Homo sapiens zinc finger, FYVE domain containing 9 (ZFYVE9), transcript variant 2, p32.3
SNP_A-1837365	tacttcatatgcatca[C/T]cttcttgaaatctcac	C	T	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 894524 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2138667	atcccagcagcgggaa[A/G]tggaccaggacgatga	A	G	sapiens serine/threonine kinase 4 (STK4), mRNA. /// ENST00000262978 // CDS // 0 // --- // --- // --- // ---	STK4	STK4, Homo sapiens serine,q13.12
SNP_A-2165911	caaagtgtgactttaa[C/T]tgatacgatgaataat	C	T	sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-2113737	aggctgaccaacaaga[G/T]agagctggcttcttag	G	T	// 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 170367 //	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2131712	atagccttattgacaa[A/C]tgataactcatataca	A	C	Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// ENST00000264330 // intron // 0 // --- // ---	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-2188292	cagtctctctctttta[C/T]accattaaccgtgctg	C	T	// 28978 // Homo sapiens transmembrane protein 14A (TMEM14A), mRNA. /// NM_000846 // downstream // 21357 //	TMEM14A	TMEM14A, Homo sapiens transmembrane protein 14A (TMEM14A), p12.2
SNP_A-2072960	acaggaatttgagaga[A/C]gttgaggggttcaagg	A	C	Homo sapiens WD repeat domain 37 (WDR37), mRNA. /// ENST00000357007 // intron // 0 // --- // --- // --- // --- ///	WDR37	WDR37, Homo sapiens WD repeat domain 37 (WDR37), p15.3
SNP_A-2084952	actcaattggacactg[A/C]aaagtaaagggagaaa	A	C	Homo sapiens inhibitor of growth family, member 5 (ING5), mRNA. /// ENST00000313552 // intron // 0 // --- // --- // --- // ---	ING5	ING5, Homo sapiens inhibitor of growth family, member 5 (ING5), q37.3
SNP_A-2023766	aaaactttttttgccc[A/T]cacctcatcatttatt	A	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2033880	aaatcaaaaccataac[A/G]agatataccatctcac	A	G	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2282672	gagtttgtgaaattcg[A/G]agtaaaatatgtgcaa	A	G	Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, mRNA. /// NM_022785 // intron // 0 // Hs.368507 // FLJ23588 // 64800 //	FLJ23588	FLJ23588, Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2280997	gagtaaaccttctaaa[A/T]tcaaagcatgtggcta	A	T	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa (TAF1A), transcript variant 2, mRNA. /// NM_005681 // intron // 0 // Hs.153088 //	TAF1A	TAF1A, Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa (TAF1A), transcript variant 2, q41
SNP_A-2263845	gaacggttttacgaac[C/T]agatgggagaagcaac	C	T	/// ENST00000331815 // downstream // 578188 // --- // --- // ---	-	q13.13
SNP_A-2228166	ctactatgcaccattc[A/G]cagacataggcacagt	A	G	SLC2A10 // 81031 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA. /// NM_005244 // upstream // 45804 // Hs.472877 //	SLC2A10	SLC2A10, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), q13.12
SNP_A-2256046	ctttaattttagatga[C/T]ctcatgcctagaaatg	C	T	Homo sapiens gap junction protein, beta 7 (GJB7), mRNA. /// ENST00000296882 // intron // 0 // --- // --- // --- // ---	GJB7	GJB7, Homo sapiens gap junction protein, beta 7 (GJB7), q15
SNP_A-2244219	ctggaaaatgcagtgc[C/T]gaggactatcaactgt	C	T	Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // --- // ---	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-2299907	gcctagcacacagtag[A/G]agctcatcaggggagg	A	G	Homo sapiens hypothetical protein MGC35023 (MGC35023), mRNA. /// ENST00000318405 // downstream // 74711 // --- // -	-	-, Homo sapiens hypothetical protein MGC35023 (MGC35023), p12.3
SNP_A-2288532	gattgagtggtcatta[C/T]agtaatctacacatat	C	T	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-2299595	gccgatcagctgacaa[A/C]tggctaaacaaaatgt	A	C	657 // Homo sapiens bone morphogenetic protein receptor, type IA (BMPR1A), mRNA. /// ENST00000310944 //	BMPR1A	BMPR1A, Homo sapiens bone morphogenetic protein receptor, type IA (BMPR1A), q23.2
SNP_A-2297738	gccaggacaagaatac[A/G]aggagagaaatagaga	A	G	/// ENST00000295830 // downstream // 205695 // --- // --- // ---	-	q26.2
SNP_A-2306966	gctgttactactggac[A/G]ctttttagccgtgtta	A	G	669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 //	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-2251338	cttcaaggccccatga[C/G]taaatacagccacaat	C	G	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2262409	gaaatgctacataaat[C/T]acatgtcctcaaccac	C	T	/// ENST00000357217 // downstream // 62934 // --- // --- // ---	-	q11.2
SNP_A-2286262	gatgcccagcagtcta[C/G]gggtgtcctgcccaat	C	G	3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 18170 //	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-2275156	gagaagcaggggtaga[A/G]acagctcttatggggg	A	G	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 775523 // Hs.146100	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-2276360	gagagcccatttgtag[A/G]aaatctacctgttggt	A	G	60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 222875 // Hs.462270	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-2043820	aacttcactacatgga[G/T]gttaaatggggatctc	G	T	// 9653 // Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), mRNA. /// NM_207357 // downstream // 180879	HS2ST1	HS2ST1, Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), p22.3
SNP_A-2031672	aaagtaatttggctaa[A/G]tatgtaagacactttg	A	G	ENST00000343093 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2000846	gaatgcttccaagtaa[A/G]tgcattctggacaaaa	A	G	// Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // intron // 0 // --- // --- // --- // ---	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1993619	aagcatattgtaccat[G/T]agcctctggtggtcag	G	T	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 304434 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-1991192	tagtaagtgcttaata[A/C]tactcagtttgacaca	A	C	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-2007949	tgcccagccgatgtta[C/T]attttaatgttgattt	C	T	Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-2080890	acctctccaaaaagaa[A/G]agctgtttgaggcatg	A	G	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2105778	agccaggatctgcaaa[C/G]tctccagacccacaat	C	G	LOC400696 // 400696 // Homo sapiens eosinophil lysophospholipase-like (LOC400696), mRNA. /// NM_020129	LOC400696	LOC400696, Homo sapiens eosinophil lysophospholipase-like (LOC400696), q13.2
SNP_A-2050564	aaggattcattattaa[A/G]tagctgcgtgtcaaag	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2048821	aagcccattggtgtac[A/G]gagaatgatgtatgct	A	G	4792 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA. /// NM_032594 // upstream // 118207 //	NFKBIA	NFKBIA, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), q13.2
SNP_A-2193176	catctatttaacattc[C/T]ctctttgaacagcttt	C	T	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // --- // --- // --- // ---	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2191863	catcaaaggatgatgc[A/G]aaagttaaaggtatga	A	G	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 884689 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2181363	cagactaaatgacata[C/T]gacactttcctcagaa	C	T	ENST00000355158 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-2169596	caagctggcctcagag[A/C]caagcctggggagcgt	A	C	Homo sapiens hypothetical protein MGC4266 (MGC4266), mRNA. /// ENST00000333750 // intron // 0 // --- // --- // --- // ---	MGC4266	MGC4266, Homo sapiens hypothetical protein MGC4266 (MGC4266), p13.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2133802	atatccttttactgct[C/T]accaaatccatgtaca	C	T	/// ENST00000355063 // upstream // 589281 // --- // --- // --- //	-	q22.1
SNP_A-2130409	atactagaggaaaata[A/G]ggggaatatttgtgtt	A	G	2730 // Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), mRNA. /// ENST00000263891 // upstream //	GCLM	GCLM, Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), p22.1
SNP_A-2156846	attcttatgatggtga[C/T]atggtttttctatgtc	C	T	8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 77031 //	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2156588	attctgagagaaataa[C/T]ggcacaacaaactcga	C	T	BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 //	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.2
SNP_A-1829372	taagtccatcagtcaa[C/T]agcagatatcctaacc	C	T	Homo sapiens ADP-ribosylation factor GTPase activating protein 3 (ARFGAP3), mRNA. /// ENST00000263245 // intron // 0 // --- // --- // --- // ---	ARFGAP3	ARFGAP3, Homo sapiens ADP-ribosylation factor GTPase activating protein 3 (ARFGAP3), q13.2
SNP_A-1826214	taaattcatacagtca[A/G]aaaatgtaaaccacag	A	G	Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-1870793	tcggaaaacctggccc[A/G]gcttagtgtttattac	A	G	DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 12603 // --- // --- // --- // ---	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-1797850	ggttttctatcagtta[C/T]cattattctctaacaa	C	T	Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST00000262360 // intron // 0 // --- // ---	C9orf39	C9orf39, Homo sapiens chromosome 9 open reading frame 39 (C9orf39), p22.2
SNP_A-1792332	gggttgcagagttaaa[C/T]aaaccggctctcattt	C	T	Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // intron // 0 // --- // --- // --- // --- ///	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1794049	ggtcagaagagacaaa[C/G]tgtgccaagtgcccag	C	G	Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 //	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-1684898	atcatctgttaaatgatggatagga[A/G]taaatgttctcttagctttctgatc	A	G	// 7957 // epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) /// NM_007124 // downstream // 417517 // Hs.250607 // UTRN // 7402 // utrophin (homologous to	EPM2A	EPM2A , rs2038473, epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) ,q24.3
SNP_A-1656151	cagttactcagagttaattaatata[G/T]agcatcaccccctagcacccaccacc	G	T	NM_000956 // downstream // 2481 // Hs.2090 // PTGER2 // 5732 // prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	PTGER2 , rs708503, prostaglandin E receptor 2 (subtype EP2), 53kDa,q22.1
SNP_A-1671852	cttcagacacttacacaattgtcct[C/G]accaatctggagaaggggaaaaaat	C	G	// 5376 // peripheral myelin protein 22 /// NM_006041 // downstream // 117446 // Hs.48384 // HS3ST3B1 // 9953 //	PMP22	PMP22 , rs4791580, peripheral myelin protein 22 ,p12
SNP_A-1941157	ttgctgagatacttgc[C/G]aaaattgataaaacgc	C	G	/// ENST00000336930 // upstream // 1001843 // --- // --- // --- //	-	p14.3
SNP_A-1928696	ttcagaaagcccttca[C/T]ggccaaatcctttcct	C	T	9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 135257 // --- // ---	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-1922006	ttactgatgaaacata[A/C]aaggaaattaagctat	A	C	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1914447	tgtgtttgatttccct[C/T]aattccttgaaagctc	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1824982 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1912340	tgtgattctgatgtga[C/T]tataacttcactcaca	C	T	10186 // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /// ENST00000344021 // downstream // 99758 // --- //	LHFP	LHFP, Homo sapiens lipoma HMGIC fusion partner (LHFP), q13.3
SNP_A-1919193	ttaacttgcccacaat[C/T]aactggtgtgatcagg	C	T	Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1917951	ttaaaatgaaaaaaaa[A/C]atgtgtcttggaatca	A	C	221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream //	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-1889427	tgagttatttataacc[C/T]atcaggcactgcgcca	C	T	79913 // Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5), mRNA. /// NM_015568 // upstream // 13610	ACTR5	ACTR5, Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5), q11.23
SNP_A-1876106	tctgacacaaagaaaa[C/T]gtgttcaatacatgca	C	T	FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 //	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1876573	tctgattccactttca[C/T]gtttgtcttgctgtct	C	T	221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 44034	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1878810	tctgttgtggcactta[C/T]taaactatgtgtgctt	C	T	sapiens etoposide induced 2.4 mRNA (EI24), mRNA. /// ENST00000278903 // intron // 0 // --- // --- // --- // ---	EI24	EI24, Homo sapiens etoposide induced 2.4 (EI24), q24.2
SNP_A-1883680	tgaactgagtactgaa[A/G]ggaatgagagatcatc	A	G	22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 192184 // Hs.306831 //	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-1913852	tgtgtctaagtccaac[A/G]aatgcttttgggtgat	A	G	25890 // Homo sapiens target of Nesh-SH3 (TARSH), mRNA. /// NM_016247 // downstream // 180716 // Hs.272380 //	ABI3BP	ABI3BP, Homo sapiens target of Nesh-SH3 (TARSH), q12.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1907915	tgtaatgaaatctgcg[A/C]catgtgctaaaaccaa	A	C	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 813209 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-1922755	ttagaggctgagttaa[A/C]agcagactacttctaa	A	C	// Homo sapiens hypothetical protein MGC14161 (MGC14161), mRNA. /// ENST00000351529 // intron // 0 // ---	MGC14161	MGC14161, Homo sapiens hypothetical protein MGC14161 (MGC14161), q15.3
SNP_A-1983439	gagcgaggtgttatct[A/G]acagaaacctggaaaa	A	G	51015 // Homo sapiens CGI-111 protein (CGI-111), mRNA. /// NM_133638 // upstream // 321760 // Hs.23751 //	ISOC1	ISOC1, Homo sapiens CGI-111 protein (CGI-111), q23.3
SNP_A-1710551	ccatcaagtatgcaaaatagtgagc[A/G]acttgattcactgttttgcacccag	A	G	polycystic kidney and hepatic disease 1 (autosomal recessive) /// NM_170724 // intron // 0 // Hs.143943 // PKHD1	PKHD1	PKHD1 , rs1535279, polycystic kidney and hepatic disease 1 (autosomal recessive) ,p12.2
SNP_A-1781711	ggatttaaaatgaaga[A/G]atccgttggttgctat	A	G	SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 116192 // --- // --- // --- //	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31
SNP_A-1797259	ggttggcacttgctac[A/G]gaaatgccattctttc	A	G	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 335758 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1799207	gtaagtgtctggtatc[C/G]agtattacctgaaaat	C	G	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1852031	tattgctattttgtgc[A/G]gaagtttggatggtgt	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1847009	tatcaggatcatacag[A/G]aaaacgtgatctcact	A	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1830437	taatatttgacctgca[A/G]gattctgagagtacaa	A	G	166824 // Homo sapiens Ras association (RalGDS/AF-6) domain family 6 (RASSF6), transcript variant 1, mRNA. ///	RASSF6	RASSF6, Homo sapiens Ras association (RalGDS,q13.3
SNP_A-2158862	attgtgcttactgcta[C/T]gaagaaaaaataaaga	C	T	Homo sapiens ribosomal protein L26 (RPL26), mRNA. /// NM_016093 // intron // 0 // Hs.546390 // RPL26L1 // 51121 //	RPL26	RPL26, Homo sapiens ribosomal protein L26 (RPL26), q35.1
SNP_A-2142230	atgaaaactctataaa[A/G]cagctttcatgaagca	A	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 454912 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2109858	aggaacagctttgggc[A/G]agtgggcgacactctc	A	G	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 549011 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2190335	catacaaaaattcaaa[A/T]tcactctgaatgtgtt	A	T	H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1131789 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2202833	ccactacaagtattta[C/T]gcagaaggctttgttt	C	T	9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1425468 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2223767	cggcccccagagctac[C/G]actgtggctgacaccg	C	G	1117 // Homo sapiens chitinase 3-like 2 (CHI3L2), mRNA. /// NM_021797 // upstream // 24547 // Hs.128814 // CHIA //	CHI3L2	CHI3L2, Homo sapiens chitinase 3-like 2 (CHI3L2), p13.2
SNP_A-2226401	ctaagagctcggtgcc[A/G]gctgaacaaaccacat	A	G	10318 // Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), mRNA. /// NM_006058 // upstream // 17643 //	TNIP1	TNIP1, Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), q33.1
SNP_A-2107330	agctaatacacacaaa[A/G]tctgattcatctttgt	A	G	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000309604 // intron // 0 // --- // --- // --- // --- ///	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.3
SNP_A-2099428	agaggctttatgaagt[A/C]aaactgatctgatact	A	C	// Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// ENST00000297345 // intron // 0 // --- // --- // --- // ---	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2007466	cttgcccacggccaca[C/T]gacttgtagtggccaa	C	T	Homo sapiens zinc finger protein 339 (ZNF339), mRNA. /// ENST00000246049 // intron // 0 // --- // --- // --- // --- ///	ZNF339	ZNF339, Homo sapiens zinc finger protein 339 (ZNF339), p11.23
SNP_A-2009430	tgcatttgtatagtaa[A/C]cttagtcccctaagag	A	C	FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 2694 //	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-2013576	actgtgaagaccataa[G/T]ctaactttcttctatg	G	T	-- /// ENST00000329885 // downstream // 10787 // --- // --- // ---	-	q14.3
SNP_A-1990433	tttgtcactcaggtac[C/T]aagcctaatatccaac	C	T	/// ENST00000354196 // upstream // 296903 // --- // --- // --- // -- /// ENST00000355224 // upstream // 296903 // --- // --- // ---	-	q21.11
SNP_A-2032565	aaataaaatttgtgta[C/T]cttgaatcattagaaa	C	T	Homo sapiens FK506 binding protein 5 (FKBP5), mRNA. /// ENST00000337746 // intron // 0 // --- // --- // --- // --- ///	FKBP5	FKBP5, Homo sapiens FK506 binding protein 5 (FKBP5), p21.31
SNP_A-2279118	gaggaattcaaagacc[A/G]ggaataaactcattga	A	G	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2274476	gacttttaagcacaga[C/T]gtttggctcttactca	C	T	6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 116646 // Hs.435458 // SETBP1 //	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251675	cttcaggtctttccca[A/G]gaaattgcttattcct	A	G	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 399573 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2231724	ctcaaaaccacactgc[C/G]acagtgacggatagag	C	G	Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, mRNA. /// NM_198182 // intron // 0 //	TFCP2L2	TFCP2L2, Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, p25.1
SNP_A-2313040	ggagaaaagcaatgtc[G/T]ctttagctttttaggg	G	T	// 8807 // Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA. /// ENST00000264260 //	IL18RAP	IL18RAP, Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), q11.2
SNP_A-2311083	ggaagtaggaggtcag[A/G]atgaggctccttagtg	A	G	// 5209 // Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA. ///	PFKFB3	PFKFB3, Homo sapiens 6-phosphofructo-2-kinase p15.1
SNP_A-2300467	gcctgaaataaaagag[G/T]cactaaatggaatcat	G	T	sapiens cyclin-dependent kinase 2 (CDK2), transcript variant 2, mRNA. /// NM_001798 // intron // 0 // Hs.19192 // CDK2 //	CDK2	CDK2, Homo sapiens cyclin-dependent kinase 2 (CDK2), transcript variant 2, q13.2
SNP_A-2300141	gcctcatttcttttaa[A/G]cctcacatttatagct	A	G	// 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream //	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2255346	cttgtagggctccttc[A/G]caccatccccactgct	A	G	Homo sapiens cancer/testis antigen 3 (CTAG3), transcript variant 2, mRNA. /// NM_175745 // intron // 0 // Hs.367936 //	CAGE1	CAGE1, Homo sapiens cancer,p24.3
SNP_A-2244162	ctgctttgtgaagaca[C/G]agcaacaatgccacat	C	G	84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 164453 // Hs.7353 // APG4C //	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2244700	aagtagttttaacacc[A/G]ctatctggtttatgta	A	G	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2284342	gatatttctaacacta[C/T]agggttttctggattt	C	T	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2258286	cttttatggtgcaaga[A/G]acattgatatattcag	A	G	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream //	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2266365	gaaggtgagacatgct[C/G]aaggcaatactgctct	C	G	Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // intron // 0 // --- // --- // --- // --- ///	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-2269506	gacaaacaaaatttca[G/T]aatcaatgagacaaat	G	T	// Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // --- // --- // --- // --- ///	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2032044	aaagtgactatcaaga[C/G]agtaaacagacaaact	C	G	// 56979 // Homo sapiens PR domain containing 9 (PRDM9), mRNA. /// AF274347 // downstream // 326780 // Hs.406695 //	PRDM9	PRDM9, Homo sapiens PR domain containing 9 (PRDM9), p14.2
SNP_A-2022050	aaaaagagttaactga[A/G]cggactgaactaatag	A	G	56171 // Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), mRNA. /// NM_004226 // downstream // 10954 //	DNAH7	DNAH7, Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), q32.3
SNP_A-2047474	aagatgatgggtctgg[A/T]atcaccttaaacccat	A	T	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 67460 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2045576	aagaattatgtgctta[C/T]gaagttttctcaggaa	C	T	// Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// ENST00000274458 // intron // 0 // --- // --- // --- // ---	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-2038932	aacagctgatatgaaa[G/T]atttgtcctggaatca	G	T	63979 // Homo sapiens fidgetin-like 1 (FIGNL1), mRNA. /// NM_022116 // upstream // 6158 // Hs.137516 // FIGNL1 //	FIGNL1	FIGNL1, Homo sapiens fidgetin-like 1 (FIGNL1), p12.2
SNP_A-1989884	atgtcacggaagagaa[A/G]aattcaggaatcaaat	A	G	10320 // Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA. /// NM_006060 // upstream //	ZNFN1A1	ZNFN1A1, Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), p12.2
SNP_A-2015463	tttttcaccacattct[C/G]aaagccataagagaca	C	G	29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // downstream // 69245 // Hs.473370 // USP25 // 29761 // Homo sapiens	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds. q21.1
SNP_A-2018012	tgcttgctgctggaat[A/C]atctgtgatcatcttg	A	C	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2093356	agaactagctcagaag[C/T]cagtaaatgacaaaat	C	T	// Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 37983 // Hs.12393 // TGDS //	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-2095998	agacagtgagagtgac[G/T]ggcacttttttaatac	G	T	FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// NM_001819 // upstream //	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3
SNP_A-2071869	acagagacaaagccaa[A/T]tccagaggacttacta	A	T	Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// ENST00000250457 // intron // 0 // --- // --- // --- // ---	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2214297	cctacatcatgacccg[C/T]agatgtctggatgatc	C	T	773 // Homo sapiens calcium channel, voltage-dependent, P/Q type, alpha 1A subunit (CACNA1A), transcript variant 2,	CACNA1A	CACNA1A, Homo sapiens calcium channel, voltage dependent, P,p13.13
SNP_A-2211925	ccctgaaattgctcta[C/T]agcttttgcacacttt	C	T	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), mRNA. /// ENST00000263239 // intron // 0 // --- // ---	DDX18	DDX18, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), q14.1
SNP_A-2114146	agggaaagctatgcgg[A/G]aaccaccaccaacacc	A	G	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 151491 //	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134940	atattcaacttggaga[A/G]gaaaatgttcactggg	A	G	604 // Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), transcript variant 1, mRNA. ///	BCL6	BCL6, Homo sapiens B-cell CLL,q27.3
SNP_A-2157222	attgaattttctggtg[A/T]atgaccaaagtcaatc	A	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1649863 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2165237	caaagacaacttccaa[C/T]tcagtaccacattaag	C	T	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 806579 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1821004	gtttctgatttatgaa[C/G]tctgtagtgggaccac	C	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 430209 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1856118	tcacaaaacataagaa[C/T]tctaactagacacaca	C	T	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 999549 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1811658	gtgctgggaacaacac[C/T]gccttaggaatttctg	C	T	Homo sapiens fibulin 5 (FBLN5), mRNA. /// ENST00000342058 // intron // 0 // --- // --- // --- // --- ///	FBLN5	FBLN5, Homo sapiens fibulin 5 (FBLN5), q32.12
SNP_A-1753529	tggtttcaatcttcataaaaaggaa[C/G]agagttggtagagtaatgattagtt	C	G	// alcohol dehydrogenase 1C (class I), gamma polypeptide /// NM_000673 // downstream // 30329 // Hs.389 // ADH7 // 131	ADH1C	ADH1C , rs10516439, alcohol dehydrogenase 1C (class I), gamma polypeptide ,q23
SNP_A-1696682	aaagaagatttttgtcaataaaata[A/G]ctctatttgtgtaatggatgtctta	A	G	8805 // transcriptional intermediary factor 1 /// NM_005989 // downstream // 63310 // Hs.201667 // AKR1D1 // 6718 // aldo-	TIF1	TIF1 , rs2589998, transcriptional intermediary factor 1 ,q33
SNP_A-1665274	cttgcttgccttgtcaggtgatcca[A/G]tgaatgttgggaccatcttcatgaa	A	G	26064 // retinoic acid induced 14 /// NM_030945 // upstream // 596533 // Hs.171929 // C1QTNF3 // 114899 // C1q and	RAI14	RAI14 , rs10521015, retinoic acid induced 14 ,p13.2
SNP_A-1978751	aaaatttctgacacca[C/T]agtagcagagtatctc	C	T	84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// NM_001154 // downstream // 280689 //	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27
SNP_A-1968866	cctacaaaaacgtaag[A/G]cagcaatgaggaaaga	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 993119 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1948681	tttatactacccaaaa[C/T]gatttagatgcaatgc	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1066501	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1929522	ttcataagacttttcc[A/G]cagagttactgccaga	A	G	117178 // Homo sapiens synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP), mRNA. /// NM_012152 //	SSX2IP	SSX2IP, Homo sapiens synovial sarcoma, X breakpoint 2 interacting protein (SSX2IP), p22.3
SNP_A-1883742	tgaacttggagtcctg[C/T]aagacactactttca	C	T	116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 4944 // Hs.491941 // VEST1	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-1883293	tgaacaaaaatagcaa[G/T]gtacaggacagcctta	G	T	9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 174040 // --- // ---	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-1885686	tgacagaatatagtga[C/T]tatttacacagagttg	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-1876212	tctgacttagacatga[C/T]ggcaggggaaagagag	C	T	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1), mRNA. ///	ABCB1	ABCB1, Homo sapiens ATP-binding cassette, sub-family B (MDR,q21.12
SNP_A-1885152	tgaattagtaattgca[A/G]aacttaccatgaagaa	A	G	84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000315948 // upstream // 37897 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1900004	tggaccagaactcaca[A/G]tacagaaaatagtaga	A	G	// Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 216186	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-1930003	ttcatgggaccgcatc[A/G]ctgacaatgatgaaag	A	G	// Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // --- // --- // --- // ---	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1911695	tgtgaagactgtggcc[A/G]gaatgaagggtctgtg	A	G	/// ENST00000357074 // downstream // 252797 // --- // --- // --- // --- /// ENST00000358765 // downstream // 252797 // --- // ---	-	p14
SNP_A-1948983	tttatctcaaatgtct[A/C]actgaagaaattgttt	A	C	3248 // Homo sapiens hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD), mRNA. /// NM_006529 // downstream //	HPGD	HPGD, Homo sapiens hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD), q34.1
SNP_A-1672508	cagtgggaaatggtctcataaattg[C/G]aacagtttagtgaaaggaatgaaag	C	G	// 6885 // mitogen-activated protein kinase kinase kinase 7 /// NM_004440 // downstream // 1056636 // Hs.73962 // EPHA7	MAP3K7	MAP3K7 , rs10498976, mitogen-activated protein kinase kinase kinase 7 ,q15
SNP_A-1784085	ggccagggaggctaac[C/T]gaatttcctgcaatgc	C	T	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine,q12.3
SNP_A-1806251	gtcctgtctttgacag[A/G]agagcctcagcagttt	A	G	// 80777 // Homo sapiens cytochrome b5 outer mitochondrial membrane precursor (CYB5-M), mRNA. /// NM_006599 // upstream // 64309 // Hs.371987 // NFAT5 // 10725 // Homo	CYB5-M	CYB5-M, Homo sapiens cytochrome b5 outer mitochondrial membrane precursor (CYB5-M), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1792594	ggtaaaggagatttac[C/G]gagctggagagaggag	C	G	4087 // Homo sapiens SMAD, mothers against DPP homolog 2 (Drosophila) (SMAD2), transcript variant 1, mRNA. /// NM_001003652 // upstream // 49113 // Hs.465061 // SMAD2	SMAD2	SMAD2, Homo sapiens SMAD, mothers against DPP homolog 2 (Drosophila) (SMAD2), transcript variant 1, q21.1
SNP_A-1846493	tatattcaatccattc[A/T]aatttaacaaatatta	A	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1868180	tcctcaaagtcctcaa[G/T]tctccattcggaacta	G	T	-- /// ENST00000344692 // upstream // 30170 // --- // --- // --- //	-	q22.1
SNP_A-1861420	tcatcatcaggacttc[C/G]ctggcttagttccact	C	G	6670 // Homo sapiens Sp3 transcription factor (SP3), mRNA. /// ENST00000357595 // upstream // 163974 // --- // --- // --- //	SP3	SP3, Homo sapiens Sp3 transcription factor (SP3), q31.1
SNP_A-1825930	taaatgcatttgcagc[C/T]aattcattttcaacaa	C	T	54982 // Homo sapiens ceroid-lipofuscinosis, neuronal 6, late infantile, variant (CLN6), mRNA. /// NM_015322 // upstream //	CLN6	CLN6, Homo sapiens ceroid-lipofuscinosis, neuronal 6, late infantile, variant (CLN6), q23
SNP_A-2187390	caggttcacactgtac[A/G]actccagaaggtgcca	A	G	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2069729	ttatcagcttcttgga[C/G]cacaagggccatgcta	C	G	// 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// NM_003583 // upstream // 279204 // Hs.173135 //	TIP120A	TIP120A, Homo sapiens TBP-interacting protein (TIP120A), q14.3
SNP_A-2068266	acaagcaataggaaaa[A/T]gacttcaatagtcttc	A	T	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 392137 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2068342	acaagctgcagagcca[C/G]tggcaaaggaagcatg	C	G	ENST00000340419 // CDS // 0 // --- // --- // --- // ---	-	q22.32
SNP_A-2047877	aagcaaaatactagta[A/T]gtcagatggcaacaag	A	T	81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 179218 //	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-2016427	aaaacaaaaagaaata[C/T]aaatgtgcaacagaga	C	T	// 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-2016830	ttaatctagctaggaa[A/G]acatataaatctcctt	A	G	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 692211	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2011604	aggccctcattctaca[A/G]acaggggatccaagag	A	G	Homo sapiens H-rev107-like protein 5 (HRLP5), mRNA. /// ENST00000356525 // intron // 0 // --- // --- // --- // --- ///	HRLP5	HRLP5, Homo sapiens H-rev107-like protein 5 (HRLP5), q12.3
SNP_A-1997002	cattacttaagtggag[A/T]catacagttaggataa	A	T	// 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 482309 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2001360	aaaggccttgttggta[C/G]gtcctgcttctgggta	C	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1789610 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2041136	aacctatacaatggta[G/T]catggccataaatctt	G	T	Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000350110 // intron // 0 // --- // --- // --- // --- ///	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2282879	gataaatagttgtaaa[C/T]gctgactggtgaaaag	C	T	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 712258 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2275890	gagactctacctttca[C/T]gaaatcccttagatac	C	T	9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 153823 //	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2276556	gagaggggggaaagga[A/T]tatcttctaagctgta	A	T	23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2233032	ctcagatatactaaaa[C/T]agacgatgggacctgt	C	T	9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 81780 // Hs.248117 //	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-2293632	gcagccatgctgatat[C/T]acaggataccctctgc	C	T	10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 117542 // Hs.334587 // RBPMS //	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-2308636	gctttccacttagggg[A/T]ccaagattaaagatga	A	T	-- /// ENST00000356117 // downstream // 572236 // --- // --- //	-	q23.31
SNP_A-2312892	ggactgtgctctgtca[C/T]gcaaaacaaaggacaa	C	T	2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 148790 // Hs.374243 //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2281883	gagtgcaatgctcata[C/T]agggatggaataagta	C	T	/// ENST00000355063 // upstream // 641828 // --- // --- // --- //	-	q22.1
SNP_A-2000782	gcagccaccactgctc[C/G]ctatgaatccatatgc	C	G	Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // intron // 0 // --- //	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2
SNP_A-1997113	gctgaggtaaggagga[C/T]gggaagttagtcagca	C	T	2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 80509 // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2004325	ccatggaatcttagag[A/G]acttaacgtctagttc	A	G	FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2058896	aatccaccccagtgag[A/G]ctaaaactcatgatta	A	G	SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 66063 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2062286	aatggttataatgatg[C/T]cagaaaggggggcaag	C	T	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2075198	acatctctggtaagaa[C/T]caaaggcaaaattgaa	C	T	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 514214 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2094843	agaatctgatgagtgc[C/T]acctaatctacctccc	C	T	8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 18319 // Hs.413095	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-2102441	agattctatagtgagc[A/C]aaacacagtctctgcc	A	C	Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 //	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds. q13.3
SNP_A-2105828	agccagtagcaggaac[C/T]accgagacgcagggag	C	T	// 10049 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA. /// NM_005494 // downstream // 16002 // Hs.490745 // DNAJB6	DNAJB6	DNAJB6, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, q36.3
SNP_A-2177336	caccttagatttacaa[A/G]taagcacagcatgagt	A	G	Homo sapiens ring finger protein 38 (RNF38), transcript variant 4, mRNA. /// NM_194330 // intron // 0 // Hs.333503 //	RNF38	RNF38, Homo sapiens ring finger protein 38 (RNF38), transcript variant 4, p13.2
SNP_A-2177206	cacctgcgtaacaggc[A/G]caggtgccctcacaag	A	G	10004 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase-like 1 (NAALADL1), mRNA. /// NM_080668 // downstream // 14260 // Hs.434886 // CDCA5 // 113130 //	NAALADL1	NAALADL1, Homo sapiens N-acetylated alpha-linked acidic dipeptidase-like 1 (NAALADL1), q13.1
SNP_A-2176446	caccatgtgaagtctc[A/G]cctctagactgatgct	A	G	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33
SNP_A-2214209	cctacaaactaacctc[C/T]cctgatgaaaattagg	C	T	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 6635 // Hs.328883 // C1D //	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-2160896	atttctgattctttgg[A/T]cacacagggactttct	A	T	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 146573 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2151228	atgttaataggcaaca[C/T]ataatggcagccaaca	C	T	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3294872 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1829519	taagtgctgtagagta[C/T]ctggccatttctagct	C	T	Homo sapiens BCL2-related protein A1 (BCL2A1), mRNA. /// ENST00000267953 // intron // 0 // --- // --- // --- // --- ///	BCL2A1	BCL2A1, Homo sapiens BCL2-related protein A1 (BCL2A1), q25.1
SNP_A-1838960	tagagacagaaacctc[A/G]caaattcagatgccaa	A	G	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 215530 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-1863594	tccaaatctcccgaag[A/G]cagtttcacatttatt	A	G	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q25.1
SNP_A-1783460	ggcatcacctattata[C/T]gcttctttctgaagtg	C	T	Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), mRNA. /// NM_152369 // upstream // 87702 //	F3	F3, Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), p21.3
SNP_A-1660227	gggatatttaaaaacagatgtatac[A/G]aaagataagtagatctgttgctatt	A	G	2741 // glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) /// NM_020167 //	GLRA1	GLRA1 , rs2348424, glycine receptor, alpha 1 (startle disease,q33.1
SNP_A-1651468	aacccccaccgtaaacactcatca[C/G]ggtcagaagtattttcagatagttt	C	G	NM_138453 // intron // 0 // Hs.184691 // RAB3C // 115827 // RAB3C, member RAS oncogene family	RAB3C	RAB3C , rs10514876, RAB3C, member RAS oncogene family,q11.2
SNP_A-1942414	ttggctaatccaacca[C/T]aagttcatcacccaga	C	T	Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // --- // --- // --- // ---	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1976471	ggaaaatgtagaacta[C/T]gctttattcctcctga	C	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 464560	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1988754	gggtcagcggttcaaa[A/T]tgccatattacttgta	A	T	// 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), mRNA. /// NM_173508 // upstream //	KCNK1	KCNK1, Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), q42.2
SNP_A-1920503	ttaattctgttttaga[C/T]cccatatgaagcccct	C	T	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-1920202	ttaatcttcaccagac[C/T]gctatcattcccaatt	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1923290	ttaggaaatgccagaa[C/T]atcatctaaaattccc	C	T	2919 // Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA. /// NM_002619 // downstream // 1140 // Hs.81564 //	CXCL1	CXCL1, Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), q13.3
SNP_A-1932467	ttcctgctgtctttgc[A/G]ccctatgccacagaat	A	G	Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // --- // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932008	ttcctacttggcctcc[C/T]actggcgcagcaacag	C	T	sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an /// NM_001135 // CDS // 0 // Hs.2159 // AGC1 // 176 // Homo sapiens aggreca	AGC1	AGC1, Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an ,q26.1
SNP_A-1928447	ttcacgtatttagtca[C/G]aacatcattgctttga	C	G	/// ENST00000326756 // downstream // 169794 // --- // --- // ---	-	p16.1
SNP_A-1950541	tttcatatgtcaaata[C/G]aactttccatagtggg	C	G	Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// ENST00000282749 // intron // 0 // --- // --- // --- // ---	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1958878	ttttcttaggataagg[C/T]ccaaacataccataaa	C	T	// 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1859205 // Hs.24212 // LPHN2	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1957971	ttttcaatgcgtgtta[C/G]aactttattcaaatct	C	G	-- /// ENST00000356117 // downstream // 603313 // --- // --- // -	-	q23.31
SNP_A-1797432	ggtttacatacactga[A/T]tagcacatacactgca	A	T	Homo sapiens hypothetical protein FLJ20331 (FLJ20331), mRNA. /// ENST00000183657 // intron // 0 // --- // --- // --- // ---	FLJ20331	FLJ20331, Homo sapiens hypothetical protein FLJ20331 (FLJ20331), p31.1
SNP_A-1809826	gtgagggtaaaatgaa[A/G]atattcagtgggatag	A	G	Homo sapiens spermine oxidase (SMOX), transcript variant 3, mRNA. /// NM_175842 // intron // 0 // Hs.433337 // SMOX //	SMOX	SMOX, Homo sapiens spermine oxidase (SMOX), transcript variant 3, p13
SNP_A-1869163	tcctgcttggatctcc[A/G]aaaatgctagaattcc	A	G	151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 //	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-1845135	tatacatagactaaaa[A/T]taggctggaaaaagat	A	T	/// ENST00000354860 // upstream // 267689 // --- // --- // --- // -	-	q32.3
SNP_A-1822950	taaaaatagaagtgaa[A/G]gctaagaaaattgctc	A	G	ENST00000354422 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-1824465	taaactcttctgtttc[A/T]ccatcacgttgttggt	A	T	ENST00000357615 // intron // 0 // --- // --- // --- // ---	-	q13.12
SNP_A-1821707	gtttgttttctgatga[C/T]agaggtagttcaaaga	C	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 956867 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1815790	gttaaggctgattcca[C/T]gctttagtaaataaga	C	T	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2140385	atctcataattttgcg[A/C]ccaaaagggaattatc	A	C	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-2162002	atttgtttctccatga[A/G]caatggcctcagccac	A	G	10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream //	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-2127498	ataacagctcttaaac[A/G]ccataaagagttaaga	A	G	ENST00000328457 // intron // 0 // --- // --- // --- // ---	-	p13.1
SNP_A-2126905	ataaagcttatgtaga[C/G]aactttaaataaaatt	C	G	8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 754411 // Hs.370359	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2220283	ccttccccatatagcc[C/T]acctagcatgagtctg	C	T	8309 // Homo sapiens acyl-Coenzyme A oxidase 2, branched chain (ACOX2), mRNA. /// NM_007177 // downstream // 200	ACOX2	ACOX2, Homo sapiens acyl-Coenzyme A oxidase 2, branched chain (ACOX2), p14.2
SNP_A-2224943	cgtggaggagaacagc[A/G]cccagtaagagaaggg	A	G	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2187889	cagtatcctaaaagac[C/T]ctgatagaaaataaag	C	T	/// ENST00000328673 // upstream // 15932 // --- // --- // --- // ---	-	q11
SNP_A-2186695	aaggtacatctaaatc[C/T]caatctctctctatta	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 107716 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2060877	aatgatcaaaaggaca[C/T]agaaggatattaccta	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2052264	aagtaaggaaagtata[A/G]actcaggtcatccaac	A	G	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 749172 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2052559	aagtagtggataagga[C/T]ggtcagttctgagctt	C	T	114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // upstream // 642 // Hs.413525 // PKD1L2 // 114780 // Homo	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-2052959	aagtccactcatcgaa[C/T]ctgatagacatggacc	C	T	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 33353 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1994352	gcagtgagcacattta[A/T]gcccattgaattcatc	A	T	PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream //	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-1992985	tcttgcactgtgataa[C/G]tggctcatttaactta	C	G	// 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000339085 //	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12
SNP_A-2007595	gaaataaataaacgta[A/G]gtgcaaattagtaaga	A	G	10904 // Homo sapiens bladder cancer associated protein (BLCAP), mRNA. /// NM_181689 // downstream // 150957 //	BLCAP	BLCAP, Homo sapiens bladder cancer associated protein (BLCAP), q11.23
SNP_A-2044132	aacttgtctttatacg[A/T]cacagaaagagcagga	A	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2033503	aaatataaaacatgga[A/G]gatagagtaataagct	A	G	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1306322 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2031055	aaaggagttatttcaa[A/G]agacaggataatgggc	A	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2285522	gatgaaaaatacaccc[A/G]atccaatcaaaatgaa	A	G	-- /// ENST00000314058 // upstream // 204356 // --- // --- // ---	-	p13.2
SNP_A-2274020	gacttaagcaaaacaa[C/T]agagaatgccccaaac	C	T	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-2245381	ctgggaaacaaataca[C/G]cttacttgttatccac	C	G	2957 // Homo sapiens general transcription factor IIA, 1, 19/37kDa (GTF2A1), transcript variant 1, mRNA. ///	GTF2A1	GTF2A1, Homo sapiens general transcription factor IIA, 1, 19,q31.1
SNP_A-2237064	ctctattttcttattc[A/C]atctatacaatgactt	A	C	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2280265	gagggctcatagaggc[C/T]atggattgaatttcaa	C	T	ENST00000335595 // intron // 0 // --- // --- // --- // ---	-	p21.2
SNP_A-2268858	gaattagtggaagatg[C/T]ataaacattttaaatt	C	T	/// ENST00000330816 // downstream // 116721 // --- // --- // ---	-	q12
SNP_A-2259819	gaaaagcattgtgctg[C/T]aaaaaattaacagttc	C	T	220441 // Homo sapiens ring finger protein 152 (RNF152), mRNA. /// NM_012327 // downstream // 15611 // Hs.157031	RNF152	RNF152, Homo sapiens ring finger protein 152 (RNF152), q21.33
SNP_A-2033413	aaataggcactgaata[G/T]aaagtaagtttcaggt	G	T	Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 //	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-2021123	aatgtccaggttcagc[A/G]ctagaccatggactgt	A	G	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 165248 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-2043424	aactgggtaatgggca[C/G]atacctccagagtttg	C	G	/// ENST00000319799 // upstream // 3393 // --- // --- // --- // ---	-	p11.2
SNP_A-2006093	gggcatcgccaataag[A/G]ccaagtcctgtgccca	A	G	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-2004473	ttctgcacatgtgtca[G/T]cttgattagccccaag	G	T	2805 // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA. /// NM_145285 // upstream // 29582 // Hs.243272 // NKX2-3 //	GOT1	GOT1, Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), q24.2
SNP_A-2051331	aagggccctcggatga[C/T]gatggtgctcgtgttt	C	T	C20orf179 // 140836 // Homo sapiens chromosome 20 open reading frame 179 (C20orf179), mRNA. /// NM_178477 //	C20orf179	C20orf179, Homo sapiens chromosome 20 open reading frame 179 (C20orf179), p12.1
SNP_A-2059503	aatctcaataaaacaa[A/T]cagttcaacaagtaat	A	T	6121 // Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000294604 // upstream // 139943 // --- // --- // --- // --- /// ENST00000262340	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-2107187	agcgtctgtcccaata[C/T]caacaaaggcagcatg	C	T	Homo sapiens SKB1 homolog (S. pombe) (SKB1), mRNA. /// ENST00000324366 // intron // 0 // --- // --- // --- // --- ///	SKB1	SKB1, Homo sapiens SKB1 homolog (S. pombe) (SKB1), q11.2
SNP_A-2093254	agaacctatgtaaagc[G/T]ccacaaaagagtcccc	G	T	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 208620 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2170433	caagtcagtgtttctc[A/T]cagggataggagttta	A	T	ENST00000358691 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2224508	cgtatctattgtgtac[A/C]gctttatgatgaatgg	A	C	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2109208	agcttggtgaatcaaa[C/T]agattaagtatgaaaa	C	T	Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // intron // 0 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2108276	agctgagaacttcaaa[C/G]taattcagttttgcca	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2608292 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2120316	agtcatatctaccttа[C/T]aggatacagagagaat	C	T	-- /// ENST00000354623 // downstream // 340612 // --- // --- // -- // --- /// ENST00000283950 // upstream // 250784 // --- // ---	-	q12
SNP_A-2164793	caaaccaagtccatta[C/T]cctaatgagaagcccc	C	T	Homo sapiens nuclear protein localization 4 (NPL4), mRNA. /// ENST00000331134 // intron // 0 // --- // --- // --- // ---	NPL4	NPL4, Homo sapiens nuclear protein localization 4 (NPL4), q25.3
SNP_A-2143360	atgacattgtgaagag[C/T]catctttgatattgta	C	T	UNQ9438 // 387990 // Homo sapiens TIMM9 (UNQ9438), mRNA. /// NM_012460 // upstream // 156558 // Hs.440525 //	UNQ9438	UNQ9438, Homo sapiens TIMM9 (UNQ9438), q23.1
SNP_A-1826164	taaattactttgacca[C/T]gcattgcttagggctg	C	T	54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// NM_175722 // upstream // 38292 // Hs.467554 //	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-1828016	taagaatattgagaac[A/G]agtttatgatcggctt	A	G	Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // intron // 0 // --- // --- // --- // ---	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1830888	taatctttctgtaaaa[A/C]ctcccatagaatcctc	A	C	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 319516 // Hs.131489 // PARD3	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1853108	tatttggctgatttaa[C/T]ggcctcaattacctta	C	T	Homo sapiens mitochondrial ribosomal protein S22 (MRPS22), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000310776 // intron // 0 // --- // --- // --- // ---	MRPS22	MRPS22, Homo sapiens mitochondrial ribosomal protein S22 (MRPS22), nuclear gene encoding mitochondrial protein, q23
SNP_A-1873432	tctcaagaagctctca[A/G]cagccaaggtataaga	A	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1862171	tcatggaatgtactta[A/C]acaaactgagatggta	A	C	Homo sapiens tetratricopeptide repeat domain 4 (TTC4), mRNA. /// ENST00000294374 // intron // 0 // --- // --- // --- // ---	TTC4	TTC4, Homo sapiens tetratricopeptide repeat domain 4 (TTC4), p32.3
SNP_A-1863205	tcatttctaacactat[C/G]aaagggagagagaatc	C	G	sapiens KIAA1043 protein (KIAA1043), mRNA. /// ENST00000266082 // intron // 0 // --- // --- // --- // ---	-	-, Homo sapiens KIAA1043 protein (KIAA1043), q12.1
SNP_A-1738875	tacaggaaaagaaaatttgggcata[A/G]ctttagaaactttagaagttcagat	A	G	// 57554 // densin-180 /// NM_017779 // upstream // 890015 // Hs.445098 // DEPDC1 // 55635 // DEP domain containing 1	KIAA1365	KIAA1365 , rs10493455, densin-180 ,p31.1
SNP_A-1747845	ttagaagtatttatgctttccttga[A/G]cgtgtttatattgtgcaacaaaaat	A	G	11249 // neurexophilin 2 /// NM_018557 // downstream // 924556 // Hs.417952 // LRP1B // 53353 // low density	NXPH2	NXPH2 , rs1439079, neurexophilin 2 ,q22.1
SNP_A-1721514	aaccccaccaatactacatcccaga[A/G]aagaggctccacacaagggcctggc	A	G	// 5455 // POU domain, class 3, transcription factor 3 /// NM_144632 // downstream // 824169 // Hs.436203 //	POU3F3	POU3F3 , rs264968, POU domain, class 3, transcription factor 3 ,q12.1
SNP_A-1976595	agtcaaaggacttagc[G/T]ccaatcctctctgtaa	G	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2384924 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1900076	tggactagaacaaaac[A/G]aactggcttttgagga	A	G	Homo sapiens myosin IIIA (MYO3A), mRNA. /// ENST00000265944 // intron // 0 // --- // --- // --- // ---	MYO3A	MYO3A, Homo sapiens myosin IIIA (MYO3A), p12.1
SNP_A-1897559	tgctgattcagaaaaa[A/G]ggcactcacgagtttc	A	G	27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // downstream //	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1898589	tgcttggaatagtgag[A/G]aacacctgtgggcagt	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1925413	ttatctgctagacaca[C/T]tgaaacaactggggaa	C	T	Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), mRNA. /// ENST00000261293 // intron // 0 // --- // --- // --- // ---	UGCGL2	UGCGL2, Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), q32.1
SNP_A-1921741	ttactaaaatgaaaaa[C/T]gtatgaggggttcaa	C	T	ENST00000339727 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1913509	tgtggttcctactctc[C/T]agtgtgttccttgagg	C	T	Homo sapiens Wolf-Hirschhorn syndrome candidate 1 (WHSC1), transcript variant 3, mRNA. /// NM_133336 // intron // 0 // Hs.113876 // WHSC1 // 7468 // Homo sapiens Wolf-	WHSC1	WHSC1, Homo sapiens Wolf-Hirschhorn syndrome candidate 1 (WHSC1), transcript variant 3, p16.3
SNP_A-1976914	tgctctctggtactaa[C/T]agaagagtaagatctc	C	T	Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA. /// ENST00000284440 // intron // 0 // --- // --- // --- // ---	UCHL1	UCHL1, Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), p13
SNP_A-1986708	tgtagtgacaggtgac[A/G]gaactctcagatgctc	A	G	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 458695 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1971706	tctttaagtgacctgg[A/G]ataacagagaggtcaa	A	G	Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), mRNA. /// ENST00000356336 // intron // 0 // --- //	SRGAP3	SRGAP3, Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), p25.3
SNP_A-1933935	ttctcaaatgaatcac[C/T]ctgctttctgctttat	C	T	Homo sapiens chromosome 10 open reading frame 69 (C10orf69), mRNA. /// ENST00000266059 // intron // 0 // --- //	SPFH1	SPFH1, Homo sapiens chromosome 10 open reading frame 69 (C10orf69), q24.31
SNP_A-1939279	ttgatccttaaatgta[C/T]gcacatgctatcatca	C	T	// 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA. /// NM_032813 // upstream // 245662 //	FLJ14624	FLJ14624, Homo sapiens hypothetical protein FLJ14624 (FLJ14624), q32.3
SNP_A-1746883	gctaaattgtattaatatgatacaa[C/G]agataagatgaaattctaaaataaa	C	G	// 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 //	SLC10A2	SLC10A2 , rs9300945, solute carrier family 10 (sodium,q33.2
SNP_A-1697438	tgacagtgtcttagattcgaagaag[A/T]actattcatagctgttaaaatcttg	A	T	// 80731 // KIAA1679 protein /// NM_006895 // upstream // 87293 // Hs.42151 // HNMT // 3176 // histamine N-	KIAA1679	KIAA1679 , rs10496792, KIAA1679 protein ,q22.1
SNP_A-1837814	tacttttctcttaca[A/C]ccttcacagttctgca	A	C	// 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 684023 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.2
SNP_A-1838353	tagaagtaacataaca[G/T]agctgtgaatcccaga	G	T	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2161921	atttgtgtggtgaata[C/T]aattctctccttctta	C	T	// 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// NM_000827 // downstream //	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2097815	agagactatcactctc[A/G]ctctagtaacccaaac	A	G	4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 696994 // Hs.232819 // PCDH15 // 65217 //	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2089789	acttcctgtgaaagac[A/G]gcaccttatctcagtc	A	G	// Homo sapiens interleukin 7 (IL7), mRNA. /// NM_007029 // upstream // 485677 // Hs.521651 // STMN2 // 11075 // Homo	IL7	IL7, Homo sapiens interleukin 7 (IL7), q21.12
SNP_A-2055065	aataaatttctgttga[A/G]catcttgtatttctga	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, mRNA. /// NM_172362 // intron // 0 // Hs.527656 // KCNH1 //	KCNH1	KCNH1, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, q32.2
SNP_A-2074593	acatagtggttcctga[C/T]aaagggaatcaaattt	C	T	MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 52022 //	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2064216	aattcaatttagacaa[A/C]acaaattcctcaattt	A	C	-- /// ENST00000263635 // upstream // 117709 // --- // --- // ---	-	q24.2
SNP_A-1994317	agaggaataataggaa[A/G]cttaatacaatgcagt	A	G	LOC157657 // 157657 // Homo sapiens hypothetical protein LOC157657 (LOC157657), mRNA. /// ENST00000286688 //	LOC157657	LOC157657, Homo sapiens hypothetical protein LOC157657 (LOC157657), q22.1
SNP_A-2034428	aaatctcagagagaaa[A/G]aaaacacagactctgt	A	G	// 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 90671 // Hs.444992 //	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-2036495	aaattgaagaacaaca[A/G]tggacagatatcaaca	A	G	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B,	ABCC9	ABCC9, Homo sapiens ATP-binding cassette, sub-family C (CFTR p12.1
SNP_A-2263648	gaaccctggttacac[A/G]gtcagagctaaaatgt	A	G	// Homo sapiens hypothetical protein similar to preferentially expressed antigen of melanoma (LOC65121), mRNA. /// AL049680 // intron // 0 // Hs.451982 // LOC343068 // 343068	LOC65121	LOC65121, Homo sapiens hypothetical protein similar to preferentially expressed antigen of melanoma (LOC65121), p36.21
SNP_A-2271287	gacattaagaaaggcc[C/T]agaggaagatctacac	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 228447 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2034287	aaatcctaagaggaaa[A/C]aaagcagaggtaggga	A	C	Homo sapiens platelet-activating factor acetylhydrolase 2, 40kDa (PAFAH2), mRNA. /// ENST00000340529 // intron // 0 // --- // --- // --- // ---	PAFAH2	PAFAH2, Homo sapiens platelet-activating factor acetylhydrolase 2, 40kDa (PAFAH2), p36.11
SNP_A-2019990	ggaggagacgagaaag[A/G]aggaaggttgccctag	A	G	4599 // Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA. /// NM_005656 // upstream // 96039 // Hs.439309 // TMPRSS2 //	MX1	MX1, Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), q22.3
SNP_A-2012184	tgaaactggttttaac[A/G]ctaagtaggatatagg	A	G	80177 // Homo sapiens myc target 1 (MYCT1), mRNA. /// NM_194435 // upstream // 5635 // Hs.53973 // VIP // 7432 //	MYCT1	MYCT1, Homo sapiens myc target 1 (MYCT1), q25.2
SNP_A-2048594	aagcatttttctgtta[C/T]ccatctatcgaagcat	C	T	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2077180	accaagggtgaggtag[A/G]agcaaaagtttaacaa	A	G	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 763959 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2168187	caactctgcttgttga[A/G]gaaactgatgaataaa	A	G	83982 // Homo sapiens family with sequence similarity 14, member A (FAM14A), mRNA. /// NM_020958 // upstream //	FAM14A	FAM14A, Homo sapiens family with sequence similarity 14, member A (FAM14A), q32.13
SNP_A-2167883	caacctgttcacgttc[A/G]ccaccttaaggatgtg	A	G	8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream //	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-2155650	attccaggcaagagaa[A/G]ggcattgagtaaacat	A	G	// 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 139925 // Hs.463466 // CA10 //	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33
SNP_A-2145131	atgcaagacactctcc[C/T]aagaagtgtgatgtca	C	T	7071 // Homo sapiens TGFB inducible early growth response (TIEG), mRNA. /// NM_207505 // upstream // 121438 //	KLF10	KLF10, Homo sapiens TGFB inducible early growth response (TIEG), q22.3
SNP_A-2126637	ataaacaattgactaa[C/G]cttcaagaatgaaatt	C	G	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-2123795	agtgttttctttcacc[C/G]atcaaagctttgagct	C	G	375318 // Homo sapiens aquaporin 12 (AQP12), mRNA. /// NM_004321 // downstream // 6061 // Hs.516802 // KIF1A //	AQP12	AQP12, Homo sapiens aquaporin 12 (AQP12), q37.3
SNP_A-2204029	ccagatttatttatca[C/T]agtgctgattgtagat	C	T	Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // intron // 0 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2182848	cagatgtgataacaga[C/T]gtagtactacagatgt	C	T	65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 26162 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2193952	catgaagatgtttcta[C/T]acaaactcaagcatga	C	T	575 // Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), mRNA. /// NM_015193 // downstream // 49634 //	BAI1	BAI1, Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), q24.3
SNP_A-1818388	gttcttatcacatcac[A/G]ggatctgttaccccat	A	G	3015 // Homo sapiens H2A histone family, member Z (H2AFZ), mRNA. /// NM_016242 // downstream // 37875 //	H2AFZ	H2AFZ, Homo sapiens H2A histone family, member Z (H2AFZ), q24
SNP_A-1862274	tcatggtaattttcaa[C/T]ttagaacaactcaagt	C	T	Homo sapiens dedicator of cytokinesis 9 (DOCK9), mRNA. /// ENST00000357329 // intron // 0 // --- // --- // --- // --- ///	DOCK9	DOCK9, Homo sapiens dedicator of cytokinesis 9 (DOCK9), q32.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864279	tccacgatgaaagatc[A/G]gaatgtggcacaagtt	A	G	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1703045	cccagtccagactgaaagcctccaa[A/G]gaggaagttctaccggcttctccat	A	G	BC006271 // intron // 0 // Hs.43141 // LOC284058 // 284058 // hypothetical protein LOC284058	LOC284058	LOC284058 , rs1056116, hypothetical protein LOC284058,q21.32
SNP_A-1693815	ctatttttctgttcaccttactcac[A/G]ctatgattttagagatctagccggg	A	G	neurexin 3	NRXN3	NRXN3 , rs10483895, neurexin 3,q24.3
SNP_A-1669179	ataactgtctaccacaacgcttaca[A/G]tcccagaagaggagagattctttct	A	G	// 10625 // influenza virus NS1A binding protein /// NM_031935 // upstream // 231651 // Hs.334485 // FIBL-6 //	IVNS1ABP	IVNS1ABP , rs6696736, influenza virus NS1A binding protein ,q25.3
SNP_A-1796823	ggttcagatactttac[A/G]agagaaggcaataagg	A	G	Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000304853 // intron // 0 // --- // --- // --- // --- ///	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. q26.31
SNP_A-1958674	ttttctcgaaatttga[A/G]acaagataggagatga	A	G	// Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // upstream //	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2
SNP_A-1922603	ttagaccataaatctc[C/T]atttagccaaaattag	C	T	// --- /// ENST00000328955 // upstream // 611398 // --- // --- //	-	q24.23
SNP_A-1893431	tgcagctaatgagcca[A/C]acctttcattccactg	A	C	Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // --- //	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-1886928	tgacttattggactcc[A/G]attcctggctcttgtt	A	G	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// NM_013235 // downstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1918867	ttaacatccatttata[C/T]gtgtgtaaggcacaaa	C	T	// Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// ENST00000333190 // intron // 0 // --- // --- // --- // ---	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-1960887	tttttgacttcagtga[C/T]ggtaccgtttgctaga	C	T	FLJ32063 // 150538 // Homo sapiens hypothetical protein FLJ32063 (FLJ32063), mRNA. /// NM_153689 // upstream //	FLJ32063	FLJ32063, Homo sapiens hypothetical protein FLJ32063 (FLJ32063), q33.1
SNP_A-1956023	tttgtctggtacagta[C/G]actcctattccatagt	C	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 362992 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1969621	aaattattgtgttgtg[C/T]accaagttgatgtttt	C	T	54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42), mRNA. /// NM_080794 // downstream //	C21orf42	C21orf42, Homo sapiens chromosome 21 open reading frame 42 (C21orf42), q21.2
SNP_A-1969548	ttaagtgggaaatgta[A/G]gattcaatcaatatct	A	G	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 763593 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1985184	agaggatgcacatcgt[A/G]aatatgtatcgtcttg	A	G	Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // --- // ---	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-1791407	gggtaggggccaggac[C/T]atattcaaacatacat	C	T	Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, mRNA. /// NM_004105 // intron // 0 // Hs.76224 // EFEMP1 // 2202 //	EFEMP1	EFEMP1, Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, p16.1
SNP_A-1787854	gggactagatagagca[C/T]gtcgagggtcttttca	C	T	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33
SNP_A-1805904	gtcccttattagttgc[A/G]gaaggagtcgggggga	A	G	Homo sapiens thioesterase superfamily member 2 (THEM2), mRNA. /// ENST00000230048 // intron // 0 // --- // --- // --- // ---	THEM2	THEM2, Homo sapiens thioesterase superfamily member 2 (THEM2), p22.2
SNP_A-1802727	gtatgcacattccttc[A/G]cctcttttctctggct	A	G	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // --- // ---	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-1870473	tcgaagggaataatac[C/T]gctttaaaataggtat	C	T	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), mRNA. /// ENST00000265382 //	PIP5K1B	PIP5K1B, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), q13
SNP_A-1869889	tccttctcctgtacaa[G/T]ggatcccatcttgtct	G	T	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1855645	tcaataccatagccac[C/T]agtgaaatgtagttat	C	T	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 136191 // Hs.114412 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1849412	tatggagcttattagg[A/C]caattttataaataag	A	C	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1124147 // Hs.27214 // KCNC2	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1817016	gttatttcactttgga[G/T]tacattataatcacct	G	T	Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // --- // --- // --- // --- ///	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-2208278	cccacactaggctttа[C/T]ctcttcaactctcagt	C	T	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 423998 // Hs.497822 // DUSP10 // 11221 //	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2214031	cctaaggaaacaagac[C/T]gggaagatgaggggag	C	T	Homo sapiens fibrillarin (FBL), mRNA. /// NM_003890 // downstream // 8053 // Hs.111732 // FCGBP // 8857 // Homo	FBL	FBL, Homo sapiens fibrillarin (FBL), q13.2
SNP_A-2127337	ataaattcctcttgaa[C/T]gattagaactcactta	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1229260	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113436	catttagaagcataca[A/G]gtttttttaaaggcat	A	G	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1064818 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2165923	ataaagctaagcaaga[A/T]ggcaaatctaccaaag	A	T	/// ENST00000357497 // downstream // 52907 // --- // --- // --- // --- /// ENST00000359402 // downstream // 52960 // --- // ---	-	q31.1
SNP_A-2083245	actaaaccagtgtgta[C/T]gagtcataggatcccc	C	T	56245 // Homo sapiens chromosome 21 open reading frame 62 (C21orf62), mRNA. /// NM_005806 // upstream // 158127	C21orf62	C21orf62, Homo sapiens chromosome 21 open reading frame 62 (C21orf62), q22.11
SNP_A-1990022	aaggagttttcttaga[C/G]actgctttgtgatctg	C	G	// --- /// ENST00000355326 // downstream // 467210 // --- // --- // --- // --- /// ENST00000332323 // downstream // 671154 // ---	-	q11.21
SNP_A-2039363	aacatacgaaagaaag[C/T]ccaacttaattcataa	C	T	ENST00000360383 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2043214	aactgcccagggtgta[G/T]agttagcaaaataggg	G	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2269967	gacaattcatattcaa[A/G]taaataacagcttcca	A	G	306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 151652 // Hs.146551 // BMP2K //	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-2259624	gaaaactagtgtctaa[A/G]ggatgccaagcccagg	A	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-2235491	ctccggtatttcctta[A/T]agcaacgtgagaaggg	A	T	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2234053	ctcattactactccca[A/T]ctttgttctgagaacc	A	T	Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA. /// NM_201280 // intron // 0 // Hs.150837 // MUTED // 63915 // Homo sapiens muted	TXNDC5	TXNDC5, Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, p24.3
SNP_A-2246457	ctggtttctttctgtc[C/G]acttacaacgttcaca	C	G	sapiens Bardet-Biedl syndrome 2 (BBS2), mRNA. /// ENST00000245157 // intron // 0 // --- // --- // --- // ---	BBS2	BBS2, Homo sapiens Bardet-Biedl syndrome 2 (BBS2), q12.2
SNP_A-2313666	ggagattagaaactag[A/G]aaacattcagaacgca	A	G	Homo sapiens diacylglycerol kinase, delta 130kDa (DGKD), transcript variant 1, mRNA. /// NM_152879 // intron // 0 //	DGKD	DGKD, Homo sapiens diacylglycerol kinase, delta 130kDa (DGKD), transcript variant 1, q37.1
SNP_A-2307040	gctgttgggtttcaga[A/G]taggaagaggttttca	A	G	Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // intron // 0 // Hs.527984 //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2303820	gctcagtcacaaaata[C/T]agtctatcctgcaaag	C	T	57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 12599 // --- // --- // --- // ---	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2303012	gctagtcttggagtcc[A/G]gagtccaaaagccttg	A	G	MGC16028 // 112752 // Homo sapiens MGC16028 similar to RIKEN cDNA 1700019E19 gene (MGC16028), mRNA. /// NM_017972 // upstream // 24569 // Hs.410231 // C14orf118 //	MGC16028	MGC16028, Homo sapiens MGC16028 similar to RIKEN cDNA 1700019E19 gene (MGC16028), q24.3
SNP_A-2296703	gccaaataaaccaaca[A/G]tctgaagcgggggaag	A	G	/// ENST00000358837 // downstream // 39232 // --- // --- // ---	-	q21.3
SNP_A-2294831	gcagtttgagcagatg[C/T]agttctagggagttca	C	T	Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-2295895	gcatggtatagaggaa[G/T]taggactgggtaactt	G	T	// Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // --- // --- // --- // --- ///	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2291553	gcacaaagccactcca[A/G]tctgaaaggcccagag	A	G	Homo sapiens keratin protein K6irs (K6IRS2), mRNA. /// ENST00000293745 // intron // 0 // --- // --- // --- // ---	K6IRS2	K6IRS2, Homo sapiens keratin protein K6irs (K6IRS2), q13.13
SNP_A-2302930	gctaggacttaggaaa[A/G]gaggtgatttgctttt	A	G	2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 32765 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2238446	ctctggttaataatga[C/T]gacaacaatgaagtta	C	T	64065 // Homo sapiens PERP, TP53 apoptosis effector (PERP), mRNA. /// NM_020340 // upstream // 15175 //	PERP	PERP, Homo sapiens PERP, TP53 apoptosis effector (PERP), q23.3
SNP_A-2262088	gaaatatgcaacacac[C/G]aggaaaaaattagaga	C	G	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 463972 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-2045157	aagaagaggcatagaa[C/T]agattgactctgagag	C	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2020322	accacttagcagatga[A/G]gttcctcgaggagata	A	G	Homo sapiens SNF1-like kinase (SNF1LK), mRNA. /// ENST00000270162 // intron // 0 // --- // --- // --- // ---	SNF1LK	SNF1LK, Homo sapiens SNF1-like kinase (SNF1LK), q22.3
SNP_A-2003231	aagctgagaggtcttg[A/C]ggatatctagaaaact	A	C	84967 // Homo sapiens LSM10, U7 small nuclear RNA associated (LSM10), mRNA. /// NM_145047 // downstream //	LSM10	LSM10, Homo sapiens LSM10, U7 small nuclear RNA associated (LSM10), p34.3
SNP_A-2084854	actcaaatgttcctaa[A/T]acataatcattaatga	A	T	120103 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 4 (SLC36A4),	SLC36A4	SLC36A4, Homo sapiens solute carrier family 36 (proton q21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2051779	aaggtccaagaactga[A/G]ctttgggacactccaa	A	G	Homo sapiens neurobeachin (NBEA), mRNA. /// ENST00000310336 // intron // 0 // --- // --- // --- // ---	NBEA	NBEA, Homo sapiens neurobeachin (NBEA), q13.3
SNP_A-2075674	acatggcatagtctaa[C/T]agagaagatttactga	C	T	79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 32005 //	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2072786	acagctctatagagtc[A/G]gaatctttgacctttg	A	G	10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 //	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-2141034	atctgccagcggataa[A/G]tgaatggctttgaggt	A	G	168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 444539	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2138042	atccaaatataagcaa[C/T]acttcacaaagccata	C	T	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2151628	atgttgctaagcggat[A/C]acaagcaaaatctcag	A	C	ENST00000228705 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-2111195	aggagatgctcaaata[A/G]caaaacaaaggatata	A	G	1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 23135 // Hs.406191 //	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-2118645	agtaatttactacccc[C/T]gctaaacacctgactt	C	T	6938 // Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // upstream // 4156 // Hs.511504 //	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-2126211	ataaaaacataaacat[A/C]atcactgctaatatca	A	C	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2136640	atcactcaccatctcc[A/G]acctgcagaatcctca	A	G	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-2226698	ctaagtgctgggtaca[C/T]ggtagtcagtcagtaa	C	T	5169 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3), mRNA. ///	ENPP3	ENPP3, Homo sapiens ectonucleotide pyrophosphatase,q23.2
SNP_A-2201549	ccaattcaaatgctaa[A/C]ctttttcagaagcatt	A	C	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 88616 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2194503	catgcaagtaggaaaa[A/C]tatcactaaattattt	A	C	/// ENST00000355561 // upstream // 332555 // --- // --- // --- // ---	-	q21.31
SNP_A-2185321	caggaatcatcctaga[A/C]cactctcccctctctt	A	C	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 872313 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q32.1
SNP_A-2170928	caataagctcctcaat[A/T]aaaaaaactctccctt	A	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-1824998	taaaggaaaaaactaa[C/T]atgttgaagcatttat	C	T	157983 // Homo sapiens chromosome 9 open reading frame 66 (C9orf66), mRNA. /// NM_203447 // upstream // 27342 //	C9orf66	C9orf66, Homo sapiens chromosome 9 open reading frame 66 (C9orf66), p24.3
SNP_A-1853928	tcaaaataaatgcaaa[C/T]ggactaaacttctaga	C	T	117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 4157 //	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1869965	tccttgaaagtttaag[A/G]catgatctagagattt	A	G	5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 711924 // Hs.248136 // HTR1F //	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.2
SNP_A-1787728	gggacatggctgcccc[A/C]aaatggattcttttta	A	C	FLJ40869 // 348654 // Homo sapiens hypothetical protein FLJ40869 (FLJ40869), mRNA. /// ENST00000317402 //	FLJ40869	FLJ40869, Homo sapiens hypothetical protein FLJ40869 (FLJ40869), p24.2
SNP_A-1791627	gggtccaggccatgaa[A/G]cgatgtgttcacccag	A	G	Homo sapiens ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 1 (Renal tubular acidosis	ATP6V1B1	ATP6V1B1, Homo sapiens ATPase, H+ transporting, lysosomal 56,p13.3
SNP_A-1792731	ggtaagaaggtgcagg[A/G]acaggatcacacttga	A	G	805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // downstream //	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q32.12
SNP_A-1989165	ggccaagttaagcctg[C/T]aggagctcagaactta	C	T	// Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /// ENST00000222607 // upstream // 108738 // --- // ---	IL6	IL6, Homo sapiens interleukin 6 (interferon, beta 2) (IL6), p15.3
SNP_A-1982402	gagcagaattccagaa[A/G]aactgaagttggtggt	A	G	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 724724 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1979982	aacacttagcaaatta[C/T]gcacctgaaatcttac	C	T	3248 // Homo sapiens hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD), mRNA. /// NM_006529 // downstream //	HPGD	HPGD, Homo sapiens hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD), q34.1
SNP_A-1972224	aggacaaaatgaaaga[C/T]gattttgattgtgtgt	C	T	// Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1954984	tttggaatatggaaaa[A/G]tcaccagactcacttg	A	G	10513 // Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA. /// NM_003620 // upstream // 42670 // Hs.286073 // PPM1D //	APPBP2	APPBP2, Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), q23.2
SNP_A-1919920	ttaataaggtgaagga[C/T]tatggagtagaaggta	C	T	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 286225 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1923154	ttagcggaggcattta[G/T]ctcacacagccttagt	G	T	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 518279 // ---	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-1931366	ttcccagaggataagg[A/G]aagagatgccagtggg	A	G	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1933005	ttcgcaccaacatttg[A/G]aatagtcagtgatttt	A	G	253018 // Homo sapiens HLA complex group 27 (HCG27), mRNA. /// NM_002117 // downstream // 37819 // Hs.534125	HCG27	HCG27, Homo sapiens HLA complex group 27 (HCG27), p21.33
SNP_A-1888093	tgagccaccatgcagg[C/T]caagtcattcttaaac	C	T	// 146395 // Homo sapiens hypothetical protein MGC18079 (MGC18079), mRNA. /// NM_015171 // downstream // 7415 //	MGC18079	MGC18079, Homo sapiens hypothetical protein MGC18079 (MGC18079), p11.2
SNP_A-1884907	tgaatgaaggagatgg[A/G]actcaggcctgctgtg	A	G	// 3487 // Homo sapiens insulin-like growth factor binding protein 4 (IGFBP4), mRNA. /// NM_032865 // downstream //	IGFBP4	IGFBP4, Homo sapiens insulin-like growth factor binding protein 4 (IGFBP4), q21.2
SNP_A-1880311	tcttctttgaaccatc[C/T]ccaattgctccatact	C	T	1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // upstream // 292327 // Hs.129452 // DACH1 // 1602 // Homo	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-1879692	tcttcagtgtccttca[A/G]agtcttccatgttctg	A	G	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // intron // 0 // Hs.414110 // KCND3 //	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1903243	tggctttaaccactgc[C/T]cttacagggttgggag	C	T	79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. ///	OBFC1	OBFC1, Homo sapiens oligonucleotide,q24.33
SNP_A-1904032	tgggcacctgaaaaac[A/G]accaaactggacatct	A	G	// 6340 // Homo sapiens sodium channel, nonvoltage-gated 1, gamma (SCNN1G), mRNA. /// NM_000336 // upstream //	SCNN1G	SCNN1G, Homo sapiens sodium channel, nonvoltage-gated 1, gamma (SCNN1G), p12.1
SNP_A-1903524	tgggacaaagagccgc[A/G]aggtggtgctattgtc	A	G	ENST00000336168 // upstream // 75712 // --- // --- // --- // ---	---	q11.23
SNP_A-1900574	tggaggaacttactaa[G/T]gcctgtttttcagat	G	T	55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 702012 // Hs.479658 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-1880084	tcttctcataaacccc[A/G]atgaggcaaatactac	A	G	221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 17514 // --- // --- // --- // ---	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-1881164	tctttagaagtgtcag[A/G]aaaattgagaaatgtc	A	G	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1876610	tctgatttgtgtttta[C/T]gtaggtccttggtata	C	T	Homo sapiens KIAA1007 protein (KIAA1007), transcript variant 1, mRNA. /// NM_206999 // intron // 0 // Hs.460923 //	CNOT1	CNOT1, Homo sapiens KIAA1007 protein (KIAA1007), transcript variant 1, q21
SNP_A-1931322	ttcccaattttggcag[C/T]ctctcccgcactctgt	C	T	// 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// NM_004225 // downstream // 53749 // Hs.379414 // MFHAS1	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-1908938	tgtataaggagacaga[A/C]tactatgcagaaatta	A	C	132625 // Homo sapiens zinc finger protein 42 (ZFP42), mRNA. /// NM_173553 // downstream // 39233 // Hs.276429	ZFP42	ZFP42, Homo sapiens zinc finger protein 42 (ZFP42), q35.2
SNP_A-1958068	ttttcagcaataatca[A/G]gttatgtttagatata	A	G	TNFSF11 // 8600 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, mRNA. /// NM_033012 // downstream // 87057 //	TNFSF11	TNFSF11, Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, q14.11
SNP_A-1948037	tttagagacttagaga[C/G]cttcattgttaatgac	C	G	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 307526 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-1984270	ccttggtcagttttac[A/G]gaggcccaccataaag	A	G	NM_002187 // intron // 0 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// ENST00000231228 // intron // 0 // --- // --- // --- // ---	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1717035	caagaaattgaaaatgacctaaagg[A/G]acatcaataatggaatggaaaaata	A	G	BC037341 // upstream // 97414 // Hs.398039 // MGC71806 // 374378 // similar to Hypothetical protein LOC233733	MGC71806	MGC71806 , rs1471013, similar to Hypothetical protein LOC233733,p15.3
SNP_A-1847205	tatcatttttttggca[C/T]tatgctagaataattt	C	T	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 149402 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814792	gtgtgtgagggcgaat[G/T]aggggtcctcagccag	G	T	Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), /// NM_177423 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo	PPFIA1	PPFIA1, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), q13.3
SNP_A-2170966	caataatctgtgataa[A/G]tgaggctttctgaccc	A	G	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1825756 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2178074	cactagctctgatttg[C/G]aaaacctttaactttt	C	G	COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000316225 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2200711	ccaagacacacctctc[G/T]ctgctttcagacggag	G	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2204370	ccagcctttatcaact[A/G]aagaacaattgctgaa	A	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2207816	cccaaactttcaacta[C/T]gctcatcaattactct	C	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2136256	atcaatttgtttccta[G/T]acctgggcagaaagct	G	T	391190 // Homo sapiens olfactory receptor, family 2, subfamily L, member 8 (OR2L8), mRNA. /// NM_001004491	OR2L8	OR2L8, Homo sapiens olfactory receptor, family 2, subfamily L, member 8 (OR2L8), q44
SNP_A-2133929	atatctgccaggcaaa[C/T]ccaagtatagatgagg	C	T	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-2152245	attaaagtgcctgata[G/T]ggttttcagtaatcta	G	T	ENST00000280020 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2164419	caaaatgctgtatcac[C/T]acaactggatctaatc	C	T	ENST00000355802 // upstream // 56886 // --- // --- // --- // --- /// ENST00000358682 // upstream // 56902 // --- // --- // --- // ---	-	q13.3
SNP_A-2054843	aataaagatgatcaaa[C/T]agaagagtgtgatata	C	T	55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 101941	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-1990969	aacaataatttagatc[C/T]aattggctgagtgcag	C	T	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 890600 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-1994630	aattgctgagaagaaa[A/G]ggttgtagaggttaga	A	G	KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 71639 // Hs.99439 //	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-1996390	cttcaaaaggacatgc[C/T]attttatctgagcctc	C	T	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 272268 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2261171	gaaagaggaatgaggc[A/G]aggtttccggtctttt	A	G	388325 // Homo sapiens DTFT5783 (UNQ5783), mRNA. /// NM_004703 // upstream // 49117 // Hs.536036 // RABEP1 //	UNQ5783	UNQ5783, Homo sapiens DTFT5783 (UNQ5783), p13.2
SNP_A-2263949	gaactagttcaataaa[A/G]catggaacatccaact	A	G	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 78928 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2283762	gataggaggagggaga[C/T]gatcgggaaaaataac	C	T	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 455866 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-2278389	gagctagatctgttga[A/G]caaacaaagtgagccc	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 97259 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2235512	ctccgtctgtgccaca[G/T]taggcaatgggaggtg	G	T	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.31
SNP_A-2295231	gcatatttgcatgtgt[A/G]aaagcttagtaatttg	A	G	5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 215195 // Hs.390428 // MAP3K4 //	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-2305808	cccagaaaggttcaat[A/C]aactgcccatatcaga	A	C	// Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), mRNA. /// ENST00000327355 // intron // 0 // --- // --- // --- // ---	LOC400451	LOC400451, Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), q26.1
SNP_A-2234417	ctccaatccctgtcat[C/G]agtgtgcccattcaga	C	G	2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// NM_024997 // upstream // 187726 // Hs.513343 // ATF7IP2 // 80063 //	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2231567	ctatttctaacattga[G/T]ggtgacaaaatatttc	G	T	// 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 289691 //	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-2251304	cttcaacttaattgca[C/G]aagttaaatcagccca	C	G	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2273231	gactcaggtgactatc[A/G]ctggaggagaggcgag	A	G	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 503027 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2266238	gaaggggcctgtacaa[C/G]cactattcaaattcac	C	G	143 // Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA. /// NM_001676 // upstream //	PARP4	PARP4, Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), q12.12
SNP_A-1995718	agcccagtgatttctg[C/T]atttggagcagcattt	C	T	// 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // downstream //	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-1994120	tacattcagtaaggca[C/T]tcccattttaggcaaa	C	T	Homo sapiens copine III (CPNE3), mRNA. /// ENST00000198765 // intron // 0 // --- // --- // --- // ---	CPNE3	CPNE3, Homo sapiens copine III (CPNE3), q21.3
SNP_A-2008916	gttctgaaatgcaggg[A/G]atagaaaaaggctatc	A	G	// 9868 // Homo sapiens translocase of outer mitochondrial membrane 70 homolog A (yeast) (TOMM70A), nuclear gene encoding mitochondrial pro /// NM_018004 // upstream // 23980 // Hs.126598 // TMEM45A /	TOMM70A	TOMM70A, Homo sapiens translocase of outer mitochondrial membrane 70 homolog A (yeast) (TOMM70A), nuclear gene encoding mitochondrial pro ,q12.2
SNP_A-2045565	aagaattagaggttca[C/T]attagaaagcataatt	C	T	ENST00000338956 // intron // 0 // --- // --- // --- // ---	-	p15.2
SNP_A-2041677	aacggcaataatcaaa[C/T]aatgagtctatccaat	C	T	Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2037702	aacaaggaggcactta[A/G]cactgtcttgggcaat	A	G	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // --- // --- // --- // --- /// ENST00000260943 // intron //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2037306	aacaaaggttgaccta[C/T]gtgcagttttatatac	C	T	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 //	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-2050768	aaggcatccagtcttc[C/T]atcattgagcatgtta	C	T	Homo sapiens polymerase (RNA) I polypeptide A, 194kDa (POLR1A), mRNA. /// ENST00000263857 // intron // 0 // --- //	POLR1A	POLR1A, Homo sapiens polymerase (RNA) I polypeptide A, 194kDa (POLR1A), p11.2
SNP_A-2061103	aatgcaagtccctgaa[A/G]cccagactaggatttt	A	G	2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 1450 //	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2098493	agagcagaaactgccc[C/T]gagtgtttaccattag	C	T	Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 //	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-2155258	attcagtctttccaga[A/T]aatgaaattgttgcta	A	T	Homo sapiens KIAA1043 protein (KIAA1043), mRNA. /// ENST00000266082 // upstream // 250727 // --- // --- // --- // ---	-	-, Homo sapiens KIAA1043 protein (KIAA1043), q12.1
SNP_A-2158338	attgggtgagaaacaa[C/T]gtactgaggcagaact	C	T	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2139843	atctaacttgtgccca[A/C]aatgtccctccttcct	A	C	152641 // Homo sapiens hypothetical protein FLJ30277 (FLJ30277), mRNA. /// NM_024949 // upstream // 38548 //	FLJ30277	FLJ30277, Homo sapiens hypothetical protein FLJ30277 (FLJ30277), q35.1
SNP_A-2131770	atagctcaagttctaa[A/G]agaaggtctaaaagac	A	G	/// ENST00000336930 // upstream // 354129 // --- // --- // --- //	-	p14.3
SNP_A-2117288	aggtggagtgaatgga[C/G]ggctgtcatggagaag	C	G	Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), mRNA. /// ENST00000320005 // intron // 0 // --- // ---	CNGB3	CNGB3, Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), q21.3
SNP_A-2114428	agggacttcttccttc[A/G]ccactggggagcaaag	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2208821	cccagaggacaattac[A/G]atgccctttttgaact	A	G	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2472592 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2223513	cggaaacacaaacaaa[C/T]gggcacaagcaccaga	C	T	// 220004 // Homo sapiens IIIG9 protein (FLJ32771), mRNA. /// NM_004200 // downstream // 23035 // Hs.502730 // SYT7	FLJ32771	FLJ32771, Homo sapiens IIIG9 protein (FLJ32771), q12.2
SNP_A-2174987	cacaggtgaaacatta[C/T]ccaaactgttgagaac	C	T	5997 // Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA. /// NM_015984 // downstream //	RGS2	RGS2, Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), q31.2
SNP_A-2190252	cataatgaagacgcca[A/G]agggcatagcagggaa	A	G	ENST00000356513 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-1825126	taaaggtagcaacata[C/G]aggaatttttctgagg	C	G	GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126), mRNA. /// NM_198569 //	GPR126	GPR126, Homo sapiens G protein-coupled receptor 126 (GPR126), q24.2
SNP_A-1826060	taaatgtctcactcga[C/T]cccaaatctcatgaat	C	T	Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // --- // ---	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-1826463	taacaaatgtttctta[C/T]gtgtgttgatgtacgt	C	T	Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // --- //	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-1844257	tagttttaaaatacta[C/T]catctggatgtacata	C	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 680987	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1736411	aaacgttgccttaccacaactacca[C/T]tccttttgcccacggattggggaat	C	T	NM_145117 // intron // 0 // Hs.407934 // NAV2 // 89797 // neuron navigator 2	NAV2	NAV2 , rs2019258, neuron navigator 2,p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1686756	gggttgtctagaatgtaaattcctg[A/G]atggtggcagtgaggaaagcgtctg	A	G	AF520801 // intron // 0 // Hs.484608 // OFCC1 // 266553 // orofacial cleft 1 candidate 1	OFCC1	OFCC1 , rs4712419, orofacial cleft 1 candidate 1,p24.3
SNP_A-1710966	tcctgtagattaggcaggtggttag[A/C]aaattctgcaagaggtatggcatct	A	C	// 6456 // SH3-domain GRB2-like 2 /// NM_052866 // upstream // 39547 // Hs.148564 // ADAMTSL1 // 92949 //	SH3GL2	SH3GL2 , rs10511654, SH3-domain GRB2-like 2 ,p22.2
SNP_A-1795041	ggtgaataatcattag[A/G]aatagaccatcctgat	A	G	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 159971	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1799417	gtaatcgcatttgtta[C/T]gtctttaaatcactta	C	T	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 809353 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1985395	aggccttctgataaca[C/T]taattaccagcagagt	C	T	Homo sapiens prolactin (PRL), mRNA. /// NM_138574 // upstream // 24987 // Hs.97124 // PWWP1 // 154150 // Homo	PRL	PRL, Homo sapiens prolactin (PRL), p22.3
SNP_A-1974848	acttggaatgctgatc[A/T]cctcagttataacagc	A	T	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1962406	ccaggggagccatcaa[A/G]tccatgttcgggtgac	A	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 245092 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1956779	ttttaaataccgaaca[A/C]attttatagaggcaca	A	C	sapiens carboxypeptidase M (CPM), transcript variant 2, mRNA. /// NM_001874 // intron // 0 // Hs.334873 // CPM //	CPM	CPM, Homo sapiens carboxypeptidase M (CPM), transcript variant 2, q15
SNP_A-1939311	ttgatctgttgtttac[A/T]aattcgacagtaagaa	A	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1913915	tgtgtgaaaggtgggc[G/T]aaggtgcctgttcgac	G	T	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1919710	ttaagtagtaatcaat[C/T]agtcgaaaatattttg	C	T	// Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // --- // --- // --- // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.2
SNP_A-1877173	tctgctgtggcatgaa[A/G]gatttcagttagatca	A	G	Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // --- // --- // --- // ---	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-1900022	tggaccctagcaggga[A/C]acatccaaatgccagc	A	C	10184 // Homo sapiens lipoma HMGIC fusion partner-like 2 (LHFPL2), mRNA. /// NM_000046 // downstream // 111356 //	LHFPL2	LHFPL2, Homo sapiens lipoma HMGIC fusion partner-like 2 (LHFPL2), q14.1
SNP_A-1893388	tgcagccagaaatccg[A/G]attatttgctttaatt	A	G	Homo sapiens popeye domain containing 2 (POPDC2), mRNA. /// ENST00000341124 // intron // 0 // --- // --- // --- // ---	POPDC2	POPDC2, Homo sapiens popeye domain containing 2 (POPDC2), q13.33
SNP_A-1874076	tctcatggtagcagta[A/G]atgctggacagcaaaa	A	G	// Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000338242 // intron // 0 // --- // --- // --- // ---	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1878957	tcttaaagaaaccaca[A/G]tcaatcaaatgatttt	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1930350	ttcatttctggcatca[G/T]gttttataatgtttat	G	T	Homo sapiens CDW92 antigen (CDW92), mRNA. /// NM_080546 // intron // 0 // Hs.494700 // CDW92 // 23446 //	CDW92	CDW92, Homo sapiens CDW92 antigen (CDW92), q31.1
SNP_A-1912828	tgtgctgtcctggcat[A/T]aattcaatgacgtgac	A	T	Homo sapiens glycosyltransferase-like 1 (GTDC1), mRNA. /// ENST00000344850 // intron // 0 // --- // --- // --- // --- ///	GTDC1	GTDC1, Homo sapiens glycosyltransferase-like 1 (GTDC1), q22.3
SNP_A-1954773	tttgctgctgactgag[C/T]atcttctctacgcact	C	T	Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // --- // --- // --- // ---	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1964838	ttgttttctgaaggac[A/C]atctattatttcttta	A	C	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q14.3
SNP_A-1965575	caaattgttaggatta[C/T]atgtgtgagccaccac	C	T	29994 // Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA. /// NM_022826 // upstream //	BAZ2B	BAZ2B, Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), q24.2
SNP_A-1985976	agaaaagagtatatag[C/T]acaatgcctgtgcaaa	C	T	/// ENST00000332660 // downstream // 95968 // --- // --- // ---	-	p12.3
SNP_A-1983688	attaaagaggtcaaca[A/G]tgtacacaatatagga	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1987012	acactgtcactatcca[C/T]agctctaccaggaaga	C	T	PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 110767 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1795706	ggtggacaataatata[C/T]gacacacattctacat	C	T	ENST00000343837 // intron // 0 // --- // --- // --- // ---	-	p14.2
SNP_A-1806010	gtcctactccattaca[C/T]tctccctcattttctt	C	T	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2306726 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814379	gtgtgagaagcaacaa[C/G]tgccctggagacccag	C	G	// 63974 // Homo sapiens neurogenic differentiation 6 (NEUROD6), mRNA. /// NM_194300 // upstream // 41302 //	NEUROD6	NEUROD6, Homo sapiens neurogenic differentiation 6 (NEUROD6), p14.3
SNP_A-1703479	gatggtgggcaagtaaacactccca[A/G]taggcagaattgaggcagtgtatct	A	G	// 6595 // SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ///	SMARCA2	SMARCA2 , rs7859562, SWI,p24.3
SNP_A-1699325	gctaagtatacaccttattcttcca[C/T]aaaatattttcacataactaccttа	C	T	NM_153343 // intron // 0 // Hs.297814 // ENPP6 // 133121 // ectonucleotide pyrophosphatase/phosphodiesterase 6	ENPP6	ENPP6 , rs6825330, ectonucleotide pyrophosphatase,q35.1
SNP_A-1842976	tagtatctaacctcta[A/G]ggctactgtgaaaatt	A	G	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1832376	tacaaaaattagctga[A/G]aaagtcattagatttt	A	G	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // intron // 0 // --- // ---	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-1815750	gttaagaggccacctc[A/G]acacgactcacccatg	A	G	22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 375017 // Hs.513902 // NALP1 //	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-1821488	gtttgggtatttacaa[C/T]aaaaaggcatgtgttt	C	T	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 635079 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1849740	tatgtaaagtacctga[C/T]atagttctatgtatag	C	T	6541 // Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// NM_007106 // downstream // 162994 // Hs.145575 // UBL3 //	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-1865490	tccatgaagtctggca[C/T]ggtgataaagtcccag	C	T	10738 // Homo sapiens ret finger protein-like 3 (RFPL3), mRNA. /// NM_014306 // downstream // 1982 // Hs.474643 //	RFPL3	RFPL3, Homo sapiens ret finger protein-like 3 (RFPL3), q12.3
SNP_A-2169546	caagctcaagttcccc[C/G]acttcctctgccacac	C	G	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 (MLLT2),	MLLT2	MLLT2, Homo sapiens myeloid q21.3
SNP_A-2182803	cagatgggggggaaaaa[A/G]atgcccacttccatag	A	G	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 343636 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2204345	ccagcctcggtgacag[G/T]ctaagcaagagagagg	G	T	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2206995	ccatgtggaaagtgaa[C/G]caagggctggatattt	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2109432	agcttttgaggcaatg[A/G]agataattaaaggaac	A	G	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2118969	agtagaacattaaaaa[A/G]acatcagccgtattct	A	G	// Homo sapiens hypothetical protein FLJ23754 (FLJ23754), mRNA. /// ENST00000324808 // intron // 0 // --- // --- // --- // ---	FLJ23754	FLJ23754, Homo sapiens hypothetical protein FLJ23754 (FLJ23754), q25.3
SNP_A-2124974	agttgatggcagggtc[A/T]acctctggggcctgac	A	T	LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 //	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-2144701	atgatgatgaaaggaa[A/T]tgtttctaggagacat	A	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST00000359144 // downstream //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2157421	attgagtcactgaaga[A/T]attaaggaagaaataa	A	T	30061 // Homo sapiens solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1), mRNA. /// NM_019048 // upstream // 38904 // Hs.101364 // NS3TP1 //	SLC40A1	SLC40A1, Homo sapiens solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1), q32.2
SNP_A-2164789	aaatattaaatgatga[C/T]agtccaacattttatt	C	T	1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 391017 // Hs.19904 // CTH // 1491 // Homo	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-2093299	agaacgcccactccaa[C/T]gcctgtgcttcacgca	C	T	23589 // Homo sapiens calcium regulated heat stable protein 1, 24kDa (CARHSP1), mRNA. /// NM_003470 // downstream	CARHSP1	CARHSP1, Homo sapiens calcium regulated heat stable protein 1, 24kDa (CARHSP1), p13.2
SNP_A-2094706	agaatattcagacaat[C/G]acagacacaatggcct	C	G	79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 342550	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2091675	agaaaagactttagaa[A/T]ctaccattcccatacc	A	T	// 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 539615 //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2073832	acagtgctgtgggcca[A/G]acaaccagaagttctg	A	G	5253 // Homo sapiens PHD finger protein 2 (PHF2), transcript variant 2, mRNA. /// NM_005392 // downstream // 192986 //	PHF2	PHF2, Homo sapiens PHD finger protein 2 (PHF2), transcript variant 2, q22.32
SNP_A-2029115	aaagaaatgggactaa[C/G]cattttcaatacccag	C	G	Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, mRNA. /// NM_145321 // intron // 0 // Hs.520259 // OSBPL3 // 26031 // Homo sapiens oxysterol	OSBPL3	OSBPL3, Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, p15.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2009275	agggtcagaatttgaa[C/G]aaaggcaatctgactt	C	G	3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 158281 // Hs.36975 // FSHB //	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-2012187	tcccacggggaggaga[A/G]tacatttgggtttaaa	A	G	4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 860191 // Hs.146100	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-2271744	gaccaggtgcttagta[C/G]ataatgaatgagtgaa	C	G	60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 251176 // Hs.528665 // PROK2 //	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2258526	cttttctgcaaattta[C/T]ctgaaagaaatcatcc	C	T	Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA. /// ENST00000356956 // intron // 0 // --- // --- // --- // ---	IGF2R	IGF2R, Homo sapiens insulin-like growth factor 2 receptor (IGF2R), q25.3
SNP_A-2308505	gctttaggactcatag[A/G]aagggcacctaacaca	A	G	163732 // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 (CITED4),	CITED4	CITED4, Homo sapiens Cbp p34.2
SNP_A-2305297	gctgaggaccagctaa[C/G]ctatgcataaatgtga	C	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 87915 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2290907	gcaaggtcatacctac[A/C]cttaagttacctgaag	A	C	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2292757	gcacttgaaggacacc[A/G]ctgtgctaaagacata	A	G	// Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// ENST00000260021 // intron // 0 // --- // --- // --- // --- ///	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2314521	ggaggtatacaagttg[A/G]atgggacatggagaac	A	G	// Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 165914 // Hs.546432 // SRD5A2L // 79644 //	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-2256365	ctttatatcagaggag[A/T]aaaggaatgtttctct	A	T	81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// NM_183380 // downstream // 127520	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-2264354	gaactttcatgagccc[C/T]aaggacaaatatgaac	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2272749	gacgtgtgttagaaaa[A/G]atattctaaaagacaa	A	G	2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 //	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2280259	gagggctagaacccac[A/C]aagttgcggatcaatt	A	C	Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // --- // ---	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2
SNP_A-2250545	cttagtcacggtagca[A/G]aaaaaatgaaagcgct	A	G	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA. /// ENST00000290541 // 5UTR	PSMB4	PSMB4, Homo sapiens proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), q21.3
SNP_A-2241805	ctgatgaaagtttcac[A/G]agcagagagagcaacc	A	G	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), mRNA. /// ENST00000353125 // intron // 0 // --- // --- // --- /// ENST00000360359 // intron // 0 // ---	ANKS1	ANKS1, Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), p21.31
SNP_A-2008361	catgttagctggttca[C/T]gaaacaaaccaagtag	C	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2014243	ataaagcacgaatatt[C/T]aaactttgtgaggcta	C	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1641682 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2025570	aaaatcttgcagtgaa[A/G]aaaccagcgttaagtt	A	G	// 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// NM_006507 // downstream // 44388 // Hs.4158 // REG1B //	REG3G	REG3G, Homo sapiens LPPM429 (REG-III), p12
SNP_A-2033690	aaatatgaggaccaaa[A/G]tctttagggcttaaga	A	G	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2043867	aacttccatctcaaca[A/C]gtccatgaatgtaata	A	C	/// ENST00000358087 // upstream // 191187 // --- // --- // --- // --- /// ENST00000344409 // upstream // 190868 // --- // --- // ---	-	p11.21
SNP_A-2056184	aatacgaattatagag[A/G]aacggggaagaaggga	A	G	--- /// ENST00000333554 // downstream // 39948 // --- // --- // ---	-	p13.1
SNP_A-2057420	aatatcatctgctaca[A/T]aattttgcctgaaaca	A	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1972650 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2099620	agaggtatgggaaaag[C/G]cagtaccagccctgcc	C	G	5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // downstream // 37436 // --- // --- // --- // --- ///	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1
SNP_A-2159549	atttacctcatctgga[C/T]gttacttttcctaaaa	C	T	84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 61272 //	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-2121620	agtgaataaagatcca[C/G]tgaagttttacagtag	C	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2204979	ccagggtagctgccaa[C/T]ggagggaccagctgtg	C	T	sapiens Friend leukemia virus integration 1 (FLI1), mRNA. /// ENST00000344954 // intron // 0 // --- // --- // --- // ---	FLI1	FLI1, Homo sapiens Friend leukemia virus integration 1 (FLI1), q24.3
SNP_A-2202505	ccacccttggacatca[A/C]agaaatctcactgcag	A	C	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 //	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-2216147	cagtttcctgtctaca[A/G]taatgaatttgggcag	A	G	Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA. /// ENST00000356218 // intron // 0 // --- //	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-2182021	cagaggaccacgtcaa[A/T]caactgtttaatgaat	A	T	Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // --- //	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-2172908	cacaaaaaactcaaag[C/T]ctactgaaggagagca	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 750971 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1851905	tattgatagacaaata[G/T]gtttctaatctcttgc	G	T	// Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 198331 // Hs.158932 // APC //	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1851071	tattattgacttaaga[A/C]caacaggaagatataa	A	C	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 320778 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1847289	tatccagctagtcact[C/G]agatcccagcaagtca	C	G	Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// ENST00000248248 // intron // 0 // --- // --- // --- // ---	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-1817135	caacattcttttatga[C/G]agtatcctgataaaag	C	G	Homo sapiens golgi apparatus protein 1 (GLG1), mRNA. /// ENST00000205061 // intron // 0 // --- // --- // --- // ---	GLG1	GLG1, Homo sapiens golgi apparatus protein 1 (GLG1), q22.3
SNP_A-1834129	tacatctagaaaacca[A/T]acaattctggtgaata	A	T	Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// ENST00000277632 // intron // 0 // --- //	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-1698861	agtacaacgacctgatttggaaaag[G/T]cagtgatagcttacttaagatcatt	G	T	apoptosis related protein APR-4 mRNA, partial cds. /// NM_002312 // downstream // 231849 // Hs.166091 // LIG4 //	-	- , rs10492670, Homo sapiens apoptosis related protein APR-4 mRNA, partial cds. ,q33.3
SNP_A-1784514	ggccgccagggacacc[A/G]ctgagtagggccacag	A	G	ENST00000339765 // intron // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-1758910	gtgtccatttttagatgtaatcaaa[C/T]cttatctacctgtttttctattctt	C	T	CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 1552166 // Hs.499861 //	CTNNA3	CTNNA3 , rs2394132, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1786105	ggctggaggttttcac[A/G]cctggtagtctcatgt	A	G	1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 333343 //	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-1985706	cgatagctgggtttac[C/G]agggtagctaattcct	C	G	// 266727 // Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), mRNA. /// ENST00000358069 // upstream // 83626 // --- // --- // --- // ---	MDGA1	MDGA1, Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), p21.2
SNP_A-1968894	aaaaaaagttatagcc[C/T]cctatgaccaagaata	C	T	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 334070 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1966284	tttcaagtttctttca[C/G]ctcaaactgacagctt	C	G	sapiens glutaminase (GLS), mRNA. /// ENST00000320717 // intron // 0 // --- // --- // --- // --- /// ENST00000338435 // intron //	GLS	GLS, Homo sapiens glutaminase (GLS), q32.2
SNP_A-1970979	cccagggtccccaaga[C/T]caagctatggcaccat	C	T	ENST00000282232 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1960138	tttttaaaccacataa[A/C]cattcaaatatttctt	A	C	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1935255	ttctgcctttaagata[C/T]ggtgaaaaaacatatg	C	T	H.sapiens mRNA for C-reactive protein. /// NM_000567 // upstream // 12583 // Hs.76452 // CRP // 1401 // Homo	CRP	CRP, H.sapiens for C-reactive protein. ,q23.2
SNP_A-1940240	ttgcattatagagacc[A/G]ggaatggaaaaccaaa	A	G	1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // upstream // 109542 //	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1946830	tttaagagcagttaca[C/T]accccagaaagtgttg	C	T	Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // intron // 0 // --- // --- // --- // --- ///	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-1947215	tttaatgttttcctta[A/T]gtttcctctgagcaga	A	T	C6orf75 // 60487 // Homo sapiens chromosome 6 open reading frame 75 (C6orf75), mRNA. /// NM_032784 //	C6orf75	C6orf75, Homo sapiens chromosome 6 open reading frame 75 (C6orf75), q22.33
SNP_A-1928961	ttcagcaggatgcata[A/G]gtcataagtccttccc	A	G	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 85257 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1885053	tgaatggtagcagaaa[A/C]caggaaaagagatttt	A	C	Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // intron // 0 // --- // --- // --- // ---	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-1889532	tgagtttcagacagga[A/C]tatcatgcaaatgtgg	A	C	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1017297 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1887176	tgagaaataacacaac[A/G]catttgaggaatggca	A	G	8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1895049	tgcccagccggcactg[A/C]aagctaaggcaaatca	A	C	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1927174	ttattttgtgatctaa[A/T]tacattgtatcttgtt	A	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1932952	ttcgaagacacatgta[A/T]ggaaattattgtcctg	A	T	// 23704 // Homo sapiens potassium voltage-gated channel, Isk-related family, member 4 (KCNE4), mRNA. /// NM_003469 // downstream // 18738 // Hs.516726 // SCG2 //	KCNE4	KCNE4, Homo sapiens potassium voltage-gated channel, Isk-related family, member 4 (KCNE4), q36.1
SNP_A-1908443	tgtagaatccctgaga[A/C]ctgggaaagcctgtaa	A	C	5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // downstream // 82505 //	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-1943886	ttgtatagtcttttta[C/G]ataattggggttgttc	C	G	89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // downstream // 28803 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1943902	ttgtatatttttctac[A/G]gctggccataaattag	A	G	8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-1939043	ttgagttatatcacac[A/G]ctctgaagcaccacaa	A	G	// Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 907587 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1959978	ttttgtgtgtatggca[A/G]atatacgtaacatgaa	A	G	Homo sapiens Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA. /// ENST00000261535 // intron //	ROCK1	ROCK1, Homo sapiens Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), q11.1
SNP_A-1960582	gaagagaagttttggg[A/T]atattttctttcactg	A	T	Homo sapiens pregnancy specific beta-1-glycoprotein 5 (PSG5), mRNA. /// ENST00000342951 // intron // 0 // --- // ---	PSG5	PSG5, Homo sapiens pregnancy specific beta-1-glycoprotein 5 (PSG5), q13.31
SNP_A-1732786	tcaccagtgtacctgacatataata[A/G]gtgattaataaattcagacactaca	A	G	9096 // T-box 18 /// NM_014895 // upstream // 98971 // - // - // // -	TBX18	TBX18 , rs2206984, T-box 18 ,q14.3
SNP_A-1730951	cagacagaggagacagccttgagct[A/T]acaagatgatgggtttatattgggg	A	T	NM_182758 // upstream // 180244 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	FLJ38736	FLJ38736 , rs1841936, hypothetical protein FLJ38736,q21.3
SNP_A-1844518	tataaatcagtcacct[C/T]agatgactttgccttc	C	T	Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// ENST00000244003 // intron // 0 // --- // ---	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-2173087	cacaaagttcaaggta[A/G]gaagaaatggtaagaa	A	G	// 6604 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member	SMARCD3	SMARCD3, Homo sapiens SWI q36.1
SNP_A-2172244	caatgtggtaagacat[C/T]agtcatgtaaacctca	C	T	// Homo sapiens ADAM-like, decysin 1 (ADAMDEC1), mRNA. /// ENST00000256412 // intron // 0 // --- // --- // --- // ---	ADAMDEC1	ADAMDEC1, Homo sapiens ADAM-like, decysin 1 (ADAMDEC1), p21.2
SNP_A-2201757	ccacaatgaattggta[C/G]aaagagaggaggaaga	C	G	200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream //	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2114471	agggagacttggagct[A/C]aaaacgcattgacttc	A	C	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium p13
SNP_A-2115152	agggctggtcaccttа[A/C]gtcctttgacctccac	A	C	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2133311	atatatatgcctctaa[A/T]tgatgatatatatata	A	T	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2165608	caaaggaagctagaga[A/C]aagggccaaattaccc	A	C	122740 // Homo sapiens olfactory receptor, family 4, subfamily K, member 14 (OR4K14), mRNA. /// ENST00000305051 // downstream // 10583 // --- // --- // --- // ---	OR4K14	OR4K14, Homo sapiens olfactory receptor, family 4, subfamily K, member 14 (OR4K14), q11.2
SNP_A-2094186	agaagggatcatatta[G/T]ctcaacaaaaaccctg	G	T	4953 // Homo sapiens ornithine decarboxylase 1 (ODC1), mRNA. /// NM_024894 // downstream // 38861 // Hs.222494	ODC1	ODC1, Homo sapiens ornithine decarboxylase 1 (ODC1), p25.1
SNP_A-2048827	aagccccacaattcaa[C/T]agcttaatgtgtacaa	C	T	Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA. /// ENST00000259060 // intron // 0 // --- // ---	SCN7A	SCN7A, Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), q24.3
SNP_A-2076410	acattgtgaggagcgc[A/G]gaagtttctaggtgtc	A	G	ENST00000355183 // intron // 0 // --- // --- // --- // ---	-	p24.1
SNP_A-2024777	aaaagtctcagtggga[C/T]aggacttaaggaagaa	C	T	// Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 342918 // Hs.528304 // ADAM28 //	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-2015651	taaagtagcatcaaca[G/T]cccattctggtttttc	G	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// NM_006806 // downstream //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2007855	ccacaacaaaaactta[C/T]agatctgactgatctt	C	T	// Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_080672 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.33
SNP_A-1993370	aacacaccaaattgag[G/T]actggaggtgttatgt	G	T	5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 59335 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2246839	ctgtaggatcactgc[A/G]cccagcagctcaagat	A	G	/// ENST00000330554 // upstream // 28012 // --- // --- // --- // ---	-	q12.2
SNP_A-2251040	cttattaggtgacaaa[G/T]gtataaatggcaaata	G	T	2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 49937	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2273577	aagtttaagtgaatga[C/T]gctaaagggtaatttc	C	T	Homo sapiens RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae) (RAD51), transcript variant 1, mRNA. /// NM_133487 // intron // 0 // Hs.446554 // RAD51 // 5888 //	RAD51	RAD51, Homo sapiens RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae) (RAD51), transcript variant 1, q15.1
SNP_A-2279649	gaggcagaagcaatga[C/T]agaggaaagaaagaca	C	T	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2296339	gcattgttccagaaac[C/T]ggatttatgtgctgat	C	T	29091 // Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), mRNA. /// NM_014178 // upstream // 92881 //	STXBP6	STXBP6, Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), q12
SNP_A-2297788	gccaggcattgcgata[A/G]gaacccaagaaccaac	A	G	285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// D26070 // upstream // 10960 //	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-2290814	gcaagcttctaattcc[A/G]gatggctgtaaaaggt	A	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2288021	gattattttcctatac[C/T]gcctgatgtccagtgt	C	T	Homo sapiens UPF2 regulator of nonsense transcripts homolog (yeast) (UPF2), transcript variant 2, mRNA. /// NM_080599 // intron // 0 // Hs.370689 // UPF2 // 26019 //	UPF2	UPF2, Homo sapiens UPF2 regulator of nonsense transcripts homolog (yeast) (UPF2), transcript variant 2, p14
SNP_A-2313124	ggagaacgaagaatga[A/G]aggcaataaaattttt	A	G	/// ENST00000334919 // upstream // 954393 // --- // --- // --- // -- /// ENST00000322194 // downstream // 814756 // --- // --- //	-	q12.2
SNP_A-2311662	ggaatgttgcaaaagg[C/T]aaacttccagattgcc	C	T	3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream //	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-2275188	gagaaggaaaagagaa[C/T]aaataggagtgcaggg	C	T	MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 //	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-2282765	gataaaagcgccatcc[C/T]gatggtggatcttaca	C	T	5865 // Homo sapiens RAB3B, member RAS oncogene family (RAB3B), mRNA. /// NM_015913 // downstream //	RAB3B	RAB3B, Homo sapiens RAB3B, member RAS oncogene family (RAB3B), p32.3
SNP_A-2286582	gatggacctagtatgc[C/G]actataccacttgtgt	C	G	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-2002389	ggtgtgtagcctcgca[A/G]tgaccacccttcccag	A	G	8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// NM_138788 // upstream // 335474 // Hs.504301 //	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2021055	aaaaaaaaagtgaggc[A/G]agagagaccgtctcta	A	G	9978 // Homo sapiens ring-box 1 (RBX1), mRNA. /// ENST00000216225 // downstream // 48184 // --- // --- // --- // --	RBX1	RBX1, Homo sapiens ring-box 1 (RBX1), q13.2
SNP_A-2031741	aaagtagggaaatgcc[A/G]caatttatagatattt	A	G	22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 139179 // Hs.513902 // NALP1 //	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-2041088	aacctaaggttttaca[C/T]tgactttgacttttttc	C	T	sapiens xeroderma pigmentosum, complementation group A (XPA), mRNA. /// ENST00000259463 // intron // 0 // --- // --- //	XPA	XPA, Homo sapiens xeroderma pigmentosum, complementation group A (XPA), q22.33
SNP_A-2064076	aattattctggccaag[G/T]atacaaaaattatctt	G	T	9989 // Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA. /// NM_006868 // upstream //	PPP4R1	PPP4R1, Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), p11.22
SNP_A-2091092	actttgccctactgga[A/G]aggatctgatgccaga	A	G	// 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 223022 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2086578	actgaaatttttaatc[A/G]actttaggcgtctttg	A	G	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2167924	caacgaccataaaata[C/T]gtgtgagcatgtaata	C	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2161131	atttgaacttagtctg[A/T]attctctgctatgaga	A	T	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 916299 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2138859	atccctctccacacta[C/T]ctttaaaactactgcc	C	T	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-2141430	atctgtttcctgtaaa[G/T]aagcagaagggagaag	G	T	// Homo sapiens motilin (MLN), mRNA. /// NM_000841 // downstream // 84860 // Hs.429018 // GRM4 // 2914 // Homo	MLN	MLN, Homo sapiens motilin (MLN), p21.31
SNP_A-2146511	atgctgactggtccca[C/G]aatcactcacaactgt	C	G	Homo sapiens sorting nexin 13 (SNX13), mRNA. /// ENST00000340108 // intron // 0 // --- // --- // --- // --- ///	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-2128036	tatgttttacttttg[C/T]aggctaatgcccagaa	C	T	51569 // Homo sapiens ubiquitin-fold modifier 1 (Ufm1), mRNA. /// ENST00000239878 // downstream // 65787 // --- //	Ufm1	Ufm1, Homo sapiens ubiquitin-fold modifier 1 (Ufm1), q13.3
SNP_A-2217636	cctgaggacagatgga[G/T]gcagcagttggcagct	G	T	92369 // Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), mRNA. /// NM_152282 // upstream //	SSB4	SSB4, Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), q23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2197631	cattctctgtgggata[A/G]gcagaagtctttgatg	A	G	// 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream // 126804 //	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-1866871	tccctaagcaagatag[A/C]aattctaaaaacctag	A	C	55512 // Homo sapiens sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II) (SMPD3), mRNA. /// AB075834 // upstream // 24765 // Hs.461074 //	SMPD3	SMPD3, Homo sapiens sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II) (SMPD3), q22.1
SNP_A-1820032	gttgtttgtctcttta[A/G]cctccatgccatcctc	A	G	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 1047256 // Hs.465407 // NETO1 // 81832 //	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1780320	ggataacttccagaca[C/T]tgtcatggcctttgta	C	T	6262 // Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000294916 // upstream // 237421 // --- // ---	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-1680572	aagcaggcaatcctatcaggtctga[A/G]tagggcaaggcattgtgtttcttac	A	G	mitogen-activated protein kinase 9 /// NM_139068 // 3UTR // 0 // Hs.348446 // MAPK9 // 5601 // mitogen-activated protein	MAPK9	MAPK9 , rs9605, mitogen-activated protein kinase 9 ,q35.3
SNP_A-1653392	agagtgaatcaggagagcacaatat[A/T]actacacacattagagacaagatag	A	T	NM_033050 // downstream // 78010 // Hs.279575 // GPR91 // 56670 // G protein-coupled receptor 91	-	- , rs989920, - ,q25.1
SNP_A-1645270	aaaagcattttggaaatagtggaca[A/C]ctaaggtttctcttaacgattacat	A	C	NM_000255 // downstream // 1003925 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs2078415, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-1953359	tttgaaaggtcacata[A/G]aaaagaaacattaaca	A	G	4070 // Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), mRNA. /// ENST00000330286 //	TACSTD2	TACSTD2, Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), p32.1
SNP_A-1945667	ttgttgagctaatgag[A/G]caaggacagcagctat	A	G	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1964047	ctcccatccttgtcaa[C/T]gttcaccacgtgttac	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1987009	aaaatctggctgtgat[C/T]aggttaacatcaaaaa	C	T	PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 172208 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1982200	agattcctgagcctaa[C/T]taatagattttagagt	C	T	ENST00000329238 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1912568	tgtgccactggacctc[A/G]caagataagtttaagc	A	G	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1891409	tgattatttcactcat[C/G]atgaccatgtttcaac	C	G	117608 // Homo sapiens zinc finger protein 354B (ZNF354B), mRNA. /// ENST00000331699 // upstream // 3533 // --- // --- //	ZNF354B	ZNF354B, Homo sapiens zinc finger protein 354B (ZNF354B), q35.3
SNP_A-1897505	tgctgagtgaacccca[A/G]agagaataaatggagc	A	G	// 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1903189	tggcttctcaggctgt[A/G]aacttagagttcttca	A	G	80176 // Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), mRNA. /// NM_025106 // downstream	SSB1	SSB1, Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), p36.22
SNP_A-1889387	tgagttaaatgaacaa[A/G]cttcaagaagagataa	A	G	Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /// ENST00000261488 // intron // 0 // --- // --- // --- // ---	FLJ10094	FLJ10094, Homo sapiens hypothetical protein FLJ10094 (FLJ10094), q14.11
SNP_A-1885153	tgaattagtagcaaga[C/T]cttatcagtcaatgtt	C	T	55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000320172 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-1971852	atctcgcccatagtta[C/T]atctccagggccagga	C	T	85403 // Homo sapiens ELL associated factor 1 (EAF1), mRNA. /// NM_012260 // downstream // 33379 // Hs.63290 //	EAF1	EAF1, Homo sapiens ELL associated factor 1 (EAF1), p25.1
SNP_A-1974379	cacggtaagcagttaa[G/T]agacaaactttttttt	G	T	sapiens acid phosphatase, prostate (ACPP), mRNA. /// ENST00000336375 // intron // 0 // --- // --- // --- // --- ///	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-1972957	gcactttctgtaaaaa[C/T]gagaggttgtatcagc	C	T	132204 // Homo sapiens synaptoporin (SYNPR), mRNA. /// ENST00000295894 // downstream // 34963 // --- // --- // --- // ---	SYNPR	SYNPR, Homo sapiens synaptoporin (SYNPR), p14.2
SNP_A-1973012	aaaatattatttagca[C/T]cttctctgtcaggcac	C	T	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 265988 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-1944252	ttgtccactacacgaa[A/G]aactatccaaggggc	A	G	4916 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), mRNA. /// U05012 // upstream // 85663 //	NTRK3	NTRK3, Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), q25.3
SNP_A-1951406	tttcctacatttgcac[C/T]ggacatgggaataaat	C	T	Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1960333	tttttagcacttagca[C/G]aaagttttgtatccaa	C	G	PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 357631 // Hs.405156 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-1956928	ttttaaggacaaatga[C/T]gaggattacaaaatta	C	T	Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /// ENST00000360110 // intron // 0 // --- // --- // --- // ---	TFRC	TFRC, Homo sapiens transferrin receptor (p90, CD71) (TFRC), q29

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1649718	ttgtccctaggagaacaagaaatac[C/G]agaaacatttttattgcagtccttt	C	G	BC029120 // intron // 0 // Hs.436140 // FLJ22789 // 84190 // hypothetical protein FLJ22789	FLJ22789	FLJ22789 , rs4143187, hypothetical protein FLJ22789,q21.31
SNP_A-1682656	tgcatggaagccaagggaacaagta[A/G]agagggatgagttgagctcacacgg	A	G	2255 // fibroblast growth factor 10 /// NM_016640 // upstream // 330285 // Hs.124165 // MRPS30 // 10884 // mitochondrial	FGF10	FGF10 , rs1482684, fibroblast growth factor 10 ,p12
SNP_A-1731781	ttttgatgtttataatacatgaaaa[A/G]gtttttagttataacaaccttcgtg	A	G	COL12A1 // 1303 // collagen, type XII, alpha 1 /// NM_080645 // downstream // 519565 // Hs.101302 // COL12A1 // 1303 //	COL12A1	COL12A1 , rs10498897, collagen, type XII, alpha 1 ,q13
SNP_A-1749737	acccgttcatactcaaaactaaaga[G/T]actgggaaaacgccatgactcctac	G	T	53981 // cleavage and polyadenylation specific factor 2, 100kDa /// NM_153646 // upstream // 83712 // Hs.177386 // SLC24A4 // 123041 // solute carrier family 24	CPSF2	CPSF2 , rs10484036, cleavage and polyadenylation specific factor 2, 100kDa ,q32.12
SNP_A-1795774	ggtggatccttcttac[G/T]ccacgttgaatgaaag	G	T	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 1149065 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1794595	ggtctaacttaatgac[A/G]cacaaagagtcatctt	A	G	Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), mRNA. /// ENST00000355866 // intron //	ITGBL1	ITGBL1, Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), q33.1
SNP_A-1836850	tactgcagacaaggca[C/G]gctgactctgaacccc	C	G	Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // intron // 0 // --- // --- // --- // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1840220	tagcagcttcttcgag[G/T]ccctcaagggcaggat	G	T	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 //	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q21.1
SNP_A-1855417	tcaagtaatatacttc[A/G]atttgtcttgacttttt	A	G	-- /// ENST00000244644 // upstream // 3501 // --- // --- // --- // -	-	p22.2
SNP_A-2177078	cacctccggtctgtcc[A/G]cttctctccatactta	A	G	ENST00000357241 // intron // 0 // --- // --- // --- // --- /// ENST00000358068 // intron // 0 // --- // --- // --- // ---	-	q35.1
SNP_A-2214169	cctaattatgtaggca[C/T]ccaatataggagcacc	C	T	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2141082	atctgctgaatgaaaa[C/G]agaggtttaactctgt	C	G	// 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), mRNA. /// ENST00000266483 // downstream // 2587638 // ---	ALG10	ALG10, Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), q12
SNP_A-2166018	caaataaggagtctta[A/C]atatatgcatgaacaa	A	C	ENST00000296554 // intron // 0 // --- // --- // --- // --- /// ENST00000344565 // intron // 0 // --- // --- // --- // ---	-	q31.3
SNP_A-2158223	attggcgtggtgtttc[G/T]ctagcattgtcttttt	G	T	Homo sapiens KIAA1033 protein (KIAA1033), mRNA. /// ENST00000311317 // intron // 0 // --- // --- // --- // --- ///	KIAA1033	KIAA1033, Homo sapiens KIAA1033 protein (KIAA1033), q23.3
SNP_A-2095145	agaattacactgataa[A/C]ctttgaagcatcaagt	A	C	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 415996 // --- // --- // --- //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2071342	acactttaattctaag[A/T]aagattctgagagtca	A	T	// Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2051363	aagggctgcagtctcc[A/G]aagtcttcagctgtcc	A	G	219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 686130 // --- // --- // --- //	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2044815	aagaaatgctaaaaag[A/G]aagaacataatctagt	A	G	sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE), mRNA. /// ENST00000337907 // intron // 0 // --- // ---	RERE	RERE, Homo sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE), p36.23
SNP_A-2044695	aagaaagctggttgta[C/T]aataaatataggcata	C	T	56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 42673 // --- // --- // --- // ---	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1
SNP_A-2035024	aaatgcaaaatctaaa[A/C]ctataataccctggaa	A	C	// Homo sapiens hypothetical protein LOC91942 (LOC91942), mRNA. /// ENST00000296597 // intron // 0 // ---	LOC91942	LOC91942, Homo sapiens hypothetical protein LOC91942 (LOC91942), q12.1
SNP_A-2314356	ggaggctggcaggaac[A/G]ggaacgagaactcacc	A	G	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2300476	gcctgaaccttatcta[A/C]gaattatggtcccaag	A	C	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, mRNA. /// NM_181334 // intron // 0 // Hs.102336 // ARHGAP8 // 23779 // Homo sapiens Rho	ARHGAP8	ARHGAP8, Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, q13.31
SNP_A-2295439	gcatcctctgtctgta[C/T]gccctaagtcagtttt	C	T	sapiens caspase 6, apoptosis-related cysteine protease (CASP6), transcript variant beta, mRNA. /// NM_001226 // intron // 0 // Hs.3280 // CASP6 // 839 // Homo sapiens	CASP6	CASP6, Homo sapiens caspase 6, apoptosis-related cysteine protease (CASP6), transcript variant beta, q25
SNP_A-2293267	gcagaggcatacttgg[A/T]agaaacagataataag	A	T	/// ENST00000359165 // upstream // 197918 // --- // --- // --- // -	-	p21.3
SNP_A-2293798	gcagctccatacatca[C/G]agtgttaccatacttg	C	G	9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA. /// NM_004904 // downstream //	CREB5	CREB5, Homo sapiens cAMP responsive element binding protein 5 (CREB5), p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2292008	gcacattcctgagtcc[A/G]cttgcaatactggatt	A	G	79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream //	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.13
SNP_A-2305629	gctgcatagataagca[C/G]ggtttccattgtggtg	C	G	SP26 // 85438 // Homo sapiens testis development protein NYD-SP26 (NYD-SP26), mRNA. /// NM_012390 // upstream	NYD-SP26	NYD-SP26, Homo sapiens testis development protein NYD-SP26 (NYD-SP26), q13.3
SNP_A-2268556	gaatggtgctttatca[A/T]gagggtgattataaac	A	T	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 261285 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2256137	ctttactagcctgtaa[C/T]aggtgttaaaagctta	C	T	Homo sapiens pericentriolar material 1 (PCM1), mRNA. /// ENST00000325083 // intron // 0 // --- // --- // --- // --- ///	PCM1	PCM1, Homo sapiens pericentriolar material 1 (PCM1), p22
SNP_A-2245927	ctgggttagaaatacа[A/C]atcagggaacacaggc	A	C	7222 // Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), mRNA. /// ENST00000264811 // upstream // 101192 // --- // --- // --- // ---	TRPC3	TRPC3, Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), q27
SNP_A-2232827	ctcacttcctcattgc[A/C]caagtgggtcacccac	A	C	Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // intron // 0 // --- // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2237398	ctctccctctagcaaa[C/T]gagattctgggtcctt	C	T	FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream //	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-2040618	aaccattccagaacca[C/G]cttaagagccaggctt	C	G	Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// ENST00000281894 // intron // 0 // --- // --- // --- // ---	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41
SNP_A-2002454	ctgatgtggagccgaa[C/G]cagggtttctaattat	C	G	ENST00000360397 // intron // 0 // --- // --- // --- // ---	-	q25
SNP_A-2019092	aaataagtgtgtggta[C/T]atttaattagtcatga	C	T	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2062092	aatggggaaatgttta[C/T]cttatgccaaatcctc	C	T	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1336397 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2090348	acttggaaactgggaa[A/G]atggcgacaaagcttt	A	G	Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-2157802	attgcctacctcagaa[A/G]tgttaattcaatgaga	A	G	// 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 204372 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2163413	atttttttgttttaca[C/T]atttcgacgctttatg	C	T	ENST00000329842 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2144888	atgattcaactcagac[A/G]agtctattcagattac	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2142898	atgaataaaagacaga[A/C]gatccaactgaaagga	A	C	SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2222363	cgagactggggttaaa[C/T]caatcaatctaaaatg	C	T	121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// ENST00000283547 // intron // 0 // ---	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-1863893	tccaatctgttacata[C/T]gtgttctcacgttaaa	C	T	27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // downstream //	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1840213	tagcagcctttcttat[C/T]agcaagaagccctgtg	C	T	59067 // Homo sapiens interleukin 21 (IL21), mRNA. /// NM_152618 // upstream // 43745 // Hs.400698 // FLJ35630 //	IL21	IL21, Homo sapiens interleukin 21 (IL21), q27
SNP_A-1782866	ggcagaggaaacagca[C/T]atagaaagactcagat	C	T	Homo sapiens chloride channel, calcium activated, family member 2 (CLCA2), mRNA. /// ENST00000260541 // intron // 0 // --- // --- // --- // ---	CLCA2	CLCA2, Homo sapiens chloride channel, calcium activated, family member 2 (CLCA2), p22.3
SNP_A-1782827	ggcagagaaaggacaa[A/G]ttgccattgaagtcta	A	G	126231 // Homo sapiens zinc finger protein 573 (ZNF573), mRNA. /// X52336 // upstream // 9357 // Hs.381285 // ZNF13	ZNF573	ZNF573, Homo sapiens zinc finger protein 573 (ZNF573), q13.12
SNP_A-1672056	tctagagtcttgaagaaacctgcta[C/T]gtttttggatccaagcaagtattc	C	T	NM_017515 // intron // 0 // Hs.9711 // SLC35F2 // 54733 // solute carrier family 35, member F2	SLC35F2	SLC35F2 , rs10502098, solute carrier family 35, member F2,q22.3
SNP_A-1939255	ttgatcatttgacact[C/G]agacagaggggagctt	C	G	Homo sapiens SEC13-like 1 (S. cerevisiae) (SEC13L1), transcript variant 1, mRNA. /// NM_183352 // intron // 0 // Hs.166924 // SEC13L1 // 6396 // Homo sapiens SEC13-like 1	SEC13L1	SEC13L1, Homo sapiens SEC13-like 1 (S. cerevisiae) (SEC13L1), transcript variant 1, p25.3
SNP_A-1934196	ttctcattggacacca[C/T]tgaaaaaaatgcagag	C	T	Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // --- // --- // --- // --- /// ENST00000310362 // intron // 0 // --- //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1963641	agatatgagccctttc[C/T]ggtaaaaagcaagtgg	C	T	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 538666 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1967643	taaagaaatgcgttca[A/G]taagcatcaggtactt	A	G	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-1977160	gctcacgtcttccatc[C/T]gaaataaaggagtttc	C	T	Homo sapiens clock homolog (mouse) (CLOCK), mRNA. /// ENST00000309964 // intron // 0 // --- // --- // --- // ---	CLOCK	CLOCK, Homo sapiens clock homolog (mouse) (CLOCK), q12
SNP_A-1894484	tgccaaggctgcacgg[C/T]atctctcctgtctgag	C	T	4155 // Homo sapiens myelin basic protein (MBP), mRNA. /// BC008749 // upstream // 137620 // Hs.501262 // MBP // 4155	MBP	MBP, Homo sapiens myelin basic protein (MBP), q23
SNP_A-1915238	tgttcagaattactga[C/T]agctctggccttccta	C	T	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 443281 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-1930141	ttcattataaattctc[A/G]actcattcagattatt	A	G	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // --- // --- // --- // ---	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-1928573	ttcactgctttgagga[A/C]tagaactgcctgtact	A	C	Homo sapiens phosphodiesterase 6C, cGMP-specific, cone, alpha prime (PDE6C), mRNA. /// ENST00000347778 // intron // 0 // --- // --- // --- // --- /// ENST00000322470 // intron // 0 // ---	PDE6C	PDE6C, Homo sapiens phosphodiesterase 6C, cGMP-specific, cone, alpha prime (PDE6C), q23.33
SNP_A-1905162	tgggtgtcccatcgaa[A/C]agagctaaggcattaa	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2981053 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1889784	tgatacagatggagaa[A/C]aatgaaggagtgtaat	A	C	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1899090	tggaaactggacgaat[A/G]agtgtctgattcacca	A	G	2555 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA. /// NM_000807 //	GABRA2	GABRA2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), p12
SNP_A-1875899	tctgaaagcacactag[A/G]aagattcgaattgaat	A	G	Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1982024	cctaggacagttctca[A/C]aacacacgaggtattt	A	C	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 385401 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1989011	ggattcaaatccaatc[C/G]aaaagctgaacattga	C	G	155465 // Homo sapiens breast cancer membrane protein 11 (BCMP11), mRNA. /// NM_001621 // upstream // 140378 //	BCMP11	BCMP11, Homo sapiens breast cancer membrane protein 11 (BCMP11), p21.1
SNP_A-1947170	tttaatgatccagtca[C/T]gggttcagcttttcct	C	T	/// ENST00000315208 // upstream // 365963 // --- // --- // --- // -	-	q24.32
SNP_A-1941038	cagcttctgtgacatc[A/G]ccctgctacattctgt	A	G	5802 // Homo sapiens protein tyrosine phosphatase, receptor type, S (PTPRS), transcript variant 4, mRNA. /// NM_130853 // upstream // 168987 // Hs.408456 // PTPRS // 5802 // Homo	PTPRS	PTPRS, Homo sapiens protein tyrosine phosphatase, receptor type, S (PTPRS), transcript variant 4, p13.3
SNP_A-1951848	tttctaagcaatgaag[A/G]cagaacaaatttgagt	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1674309	gcaaagaacaaatactaagaaacag[A/G]acatagtgcattctaggggccagat	A	G	NM_058222 // intron // 0 // Hs.348615 // TECTB // 6975 // tectorin beta	TECTB	TECTB , rs10509957, tectorin beta,q25.2
SNP_A-1692460	tacaccatcttttccaaacatgaac[A/G]ggaaaaattattctatttgctactc	A	G	KCNA4 // 3739 // potassium voltage-gated channel, shaker-related subfamily, member 4 /// NM_152636 // downstream // 482491 // Hs.366407 // FLJ33979 // 196074 // hypothetical	KCNA4	KCNA4 , rs10501103, potassium voltage-gated channel, shaker-related subfamily, member 4 ,p14.1
SNP_A-1796058	ggtggttgtgaggcac[A/G]agggggaaaagggaat	A	G	57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // upstream //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1844162	tagtttagtttctttc[G/T]aaagatctacaaagac	G	T	Homo sapiens Abelson helper integration site (AHI1), mRNA. /// ENST00000265602 // intron // 0 // --- // --- // --- // ---	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3
SNP_A-1816960	gttattgctgcctact[A/G]aacaattttctattct	A	G	26953 // Homo sapiens RAN binding protein 6 (RANBP6), mRNA. /// NM_033439 // upstream // 80883 // Hs.348390 //	RANBP6	RANBP6, Homo sapiens RAN binding protein 6 (RANBP6), p24.1
SNP_A-1828979	taaggccttcctggaa[G/T]tagcagggcacggtta	G	T	Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // --- // --- //	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine q23.1
SNP_A-2213274	cttctgtttagaatga[A/G]gatggttgctaggtac	A	G	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2203976	gatgacctggagaata[G/T]acagcatactccgtag	G	T	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187324	caggtgtctatgcaaa[A/G]tagtaaaagcacattt	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 762131 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2158267	attgggaagcatccac[A/G]gaacagatgatctgga	A	G	Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000359764 // intron // 0 // --- // --- // --- // ---	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2135766	atcaaagcaaaagaaa[A/G]tgccaagcaagaaatc	A	G	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 451575 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2112425	aggcaagtccccaagc[C/T]gagtctgcagaggaag	C	T	1397 // Homo sapiens cysteine-rich protein 2 (CRIP2), mRNA. /// ENST00000329146 // downstream // 3620 // --- // ---	CRIP2	CRIP2, Homo sapiens cysteine-rich protein 2 (CRIP2), q32.33
SNP_A-2085166	actcagctgaaatacc[A/T]aaggtcttggtagcac	A	T	Homo sapiens chromosome 9 open reading frame 138 (C9orf138), mRNA. /// ENST00000286333 // intron // 0 // --- //	C9orf138	C9orf138, Homo sapiens chromosome 9 open reading frame 138 (C9orf138), p22.1
SNP_A-2078017	accagctgtggaaccc[A/G]gaagtagctgattgct	A	G	148808 // Homo sapiens hypothetical protein DKFZp761N1114 (DKFZp761N1114), mRNA. /// ENST00000312213 // intron // 0 // --- // --- // --- // ---	DKFZp761N1114	DKFZp761N1114, Homo sapiens hypothetical protein DKFZp761N1114 (DKFZp761N1114), q32.1
SNP_A-2099927	agagtcagctcaccta[C/T]agtttgaatatttcca	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 955788 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2051665	aaggtagcctgcgagc[C/T]aggatgaaggagctat	C	T	64431 // Homo sapiens ARP6 actin-related protein 6 homolog (yeast) (ACTR6), mRNA. /// NM_152317 // downstream //	ACTR6	ACTR6, Homo sapiens ARP6 actin-related protein 6 homolog (yeast) (ACTR6), q23.1
SNP_A-2053981	aagttacaaagaacag[C/G]caaatgctaagaaatg	C	G	Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // --- // --- // --- // --- /// ENST00000349908 // intron //	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-2049192	aagctagaaaacacca[C/T]gctggacattgaactt	C	T	// Homo sapiens hypothetical protein FLJ25421 (FLJ25421), mRNA. /// ENST00000325157 // intron // 0 // --- // --- // --- // ---	FLJ25421	FLJ25421, Homo sapiens hypothetical protein FLJ25421 (FLJ25421), q13.1
SNP_A-2077038	accaacgaagacctaa[A/G]cagaaagtgtggccac	A	G	2882 // Homo sapiens glutathione peroxidase 7 (GPX7), mRNA. /// ENST00000262661 // downstream // 20080 // --- //	GPX7	GPX7, Homo sapiens glutathione peroxidase 7 (GPX7), p32.3
SNP_A-2008505	tgcattgcaaaactct[A/G]aagaacagcattctta	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 266938 // --- // --- // --- //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1997792	ctctaaggctgtttcc[A/G]ctccttgttttctgtg	A	G	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2228906	ctagatcttcttcacc[A/G]aagtcttaaaattttg	A	G	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2264842	gaagagacttccccta[C/T]gtaaaagagagatgaa	C	T	Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, mRNA. /// NM_022842 // intron // 0 // Hs.476093 // CDCP1 // 64866 // Homo sapiens CUB domain-	CDCP1	CDCP1, Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, p21.31
SNP_A-2281894	gagtgcagagtatttg[C/T]atttaatctaattttc	C	T	Homo sapiens component of oligomeric golgi complex 5 (COG5), transcript variant 2, mRNA. /// NM_006348 // intron // 0 // Hs.239631 // COG5 // 10466 // Homo sapiens component	COG5	COG5, Homo sapiens component of oligomeric golgi complex 5 (COG5), transcript variant 2, q22.3
SNP_A-2293101	gcagaccatgttttcc[A/G]cagcctaggccacacc	A	G	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 915746 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2288665	gattggatgcctgatc[A/G]acatctcacacaaaaa	A	G	-- /// ENST00000345111 // upstream // 514192 // --- // --- // ---	-	q24.31
SNP_A-2311297	ggaatacccaggtaga[C/T]ggtaaagcattgatta	C	T	sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), mRNA. /// ENST00000357898 // intron // 0 // --- // ---	SSB1	SSB1, Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), p36.22
SNP_A-2279601	gaggcaatgcttagaa[C/T]tgtgtaaagtgatgga	C	T	sapiens interferon regulatory factor 4 (IRF4), mRNA. /// ENST00000259797 // intron // 0 // --- // --- // --- // --- ///	IRF4	IRF4, Homo sapiens interferon regulatory factor 4 (IRF4), p25.3
SNP_A-2228322	ctactgcattacaaga[G/T]ctgctcatttcagtat	G	T	/// ENST00000354196 // upstream // 838938 // --- // --- // --- // -- /// ENST00000355224 // upstream // 838938 // --- // --- // ---	-	q21.11
SNP_A-2002124	atataaagagcagagc[A/G]aagaaaataatcacac	A	G	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2016253	tgtgatttaatttgcc[C/T]gaaggaagaagaaagg	C	T	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2060323	aatgaatacctacggc[A/G]gaggaagtcatcccag	A	G	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 262693 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2107436	agctacgagttctcca[C/T]gtgaggctcaccaggt	C	T	MGC16664 // 148753 // Homo sapiens hypothetical protein MGC16664 (MGC16664), mRNA. /// NM_145034 //	MGC16664	MGC16664, Homo sapiens hypothetical protein MGC16664 (MGC16664), q25.2
SNP_A-2103581	agcacaacacttgaca[A/G]tcatctcccagtgtca	A	G	Homo sapiens hypothetical protein FLJ10871 (FLJ10871), mRNA. /// ENST00000265614 // intron // 0 // --- // --- // --- // ---	FLJ10871	FLJ10871, Homo sapiens hypothetical protein FLJ10871 (FLJ10871), p21.1
SNP_A-2096949	agactgaaagagggaa[A/C]ccgcaagtcagaattc	A	C	Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 //	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2131114	atagacatcaattcaa[C/G]atgaagcctcaaattt	C	G	// 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2124616	agttccttcttgctca[A/G]tcagtctttgttctat	A	G	// 90865 // Homo sapiens chromosome 9 open reading frame 26 (NF-HEV) (C9orf26), mRNA. /// NM_001001875 //	C9orf26	C9orf26, Homo sapiens chromosome 9 open reading frame 26 (NF-HEV) (C9orf26), p24.1
SNP_A-2153465	attagatgtatgagaa[C/T]gtcccaacaatccttt	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 692147 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2138296	atccagacagtcctct[C/T]aagtacctgaattcct	C	T	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // --- ///	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-2189533	cagtttatatataaga[A/G]aacaagatcggagtaa	A	G	2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 387450 // Hs.374243 //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1826839	taacagttttatctac[A/G]gcctgcccttatctga	A	G	// 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, mRNA. /// NM_201559 // downstream //	FOXO3A	FOXO3A, Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, q21
SNP_A-1815579	gttaaagaacctgcct[A/G]aaatcttaccactagc	A	G	sapiens flavin containing monooxygenase 1 (FMO1), mRNA. /// ENST00000314690 // intron // 0 // --- // --- // --- // --- ///	FMO1	FMO1, Homo sapiens flavin containing monooxygenase 1 (FMO1), q24.3
SNP_A-1861986	tcatgagggcttatag[A/G]aaatatttgtaatgag	A	G	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 820599 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-1857224	gaagaccctggagtta[C/T]gctgtgcctctctatt	C	T	Homo sapiens gastric inhibitory polypeptide (GIP), mRNA. /// NM_006546 // upstream // 27241 // Hs.144936 // IMP-1 //	GIP	GIP, Homo sapiens gastric inhibitory polypeptide (GIP), q21.32
SNP_A-1845225	tatacctctgagtgtc[A/G]gaaagattttgatttt	A	G	Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // --- // ---	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-1847889	tatctcttaagtggca[G/T]agtttgtaagtcattc	G	T	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-1793731	ggtattaaggctaaga[A/G]gtgggggacagggccc	A	G	Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 5 (DNAJB5), mRNA. /// ENST00000312316 // 3UTR // 0 // --- // --- // --- // --- /// ENST00000335998 // 3UTR // 0 // --- // --- // -	DNAJB5	DNAJB5, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 5 (DNAJB5), p13.3
SNP_A-1807664	gtctgtaatatcagac[G/T]gcattaaacagataag	G	T	Homo sapiens proline rich 5 (salivary) (PROL5), mRNA. /// ENST00000226460 // intron // 0 // --- // --- // --- // ---	SMR3A	SMR3A, Homo sapiens proline rich 5 (salivary) (PROL5), q13.3
SNP_A-1807083	gtctcccagacactca[C/T]gtacctgacaaggtga	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-1800509	gtactgtacttatgtg[A/G]aaggtaaaaaagatct	A	G	Homo sapiens ankyrin repeat domain 10 (ANKRD10), mRNA. /// ENST00000267339 // intron // 0 // --- // --- // --- // ---	ANKRD10	ANKRD10, Homo sapiens ankyrin repeat domain 10 (ANKRD10), q34
SNP_A-1692512	agctggcttcacacactagccttcc[C/T]gaagaatgtttaaaccaagaattcc	C	T	NM_024621 // intron // 0 // Hs.126485 // FLJ12604 // 79674 // hypothetical protein FLJ12604	FLJ12604	FLJ12604 , rs10513509, hypothetical protein FLJ12604,q25.31
SNP_A-1718773	tctcatatagacctgtagcctcaca[C/T]ctaagcttaagactgacgagtttac	C	T	// 6456 // SH3-domain GRB2-like 2 /// NM_052866 // upstream // 404093 // Hs.148564 // ADAMTSL1 // 92949 //	SH3GL2	SH3GL2 , rs6475197, SH3-domain GRB2-like 2 ,p22.2
SNP_A-1941909	ttggagatgacttggc[A/G]catagaggaaagtaat	A	G	LOC128153 // 128153 // Homo sapiens hypothetical protein BC014608 (LOC128153), mRNA. /// NM_016052 // upstream	LOC128153	LOC128153, Homo sapiens hypothetical protein BC014608 (LOC128153), q41
SNP_A-1935302	ttctgctgagatttta[C/T]aggaaagtctgtttct	C	T	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 29695 //	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1937451	ttgaacaaataaacac[A/G]aagtttctcataagtg	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1987076	aggcagtctgctggcc[G/T]aattctctcttcttcc	G	T	2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 542898 // Hs.98262 // GRIK2 // 2898 // Homo	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1972580	tggaaaaattaactta[C/T]gccaccttataggtag	C	T	8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 513 // Hs.413095 //	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-1896842	tgctcaatgtctccta[C/T]accttggcctgaagct	C	T	Homo sapiens membrane associated transporter (MATP), mRNA. /// ENST00000296589 // intron // 0 // --- // --- // --- // ---	MATP	MATP, Homo sapiens membrane associated transporter (MATP), p13.3
SNP_A-1910207	tgtcattgacgtttaa[C/T]atttttgacaaaaatt	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1429771 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1931013	ttccagtgtcaagtcc[A/G]aagtcttaagtcttat	A	G	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 //	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. ,q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1931538	ttccccctctcaaac[C/T]cttactactcttccca	C	T	414918 // Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692), mRNA. /// NM_152678 // intron // 0 //	MGC33692	MGC33692, Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692), p14.3
SNP_A-1920855	ttacacacctgagcat[C/G]aggaaccaaaagtcca	C	G	sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), mRNA. /// ENST00000308696 // intron // 0 // --- // --- // --- // ---	PSMD1	PSMD1, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 (PSMD1), q37.1
SNP_A-1878315	tctgtctagaattaaa[A/C]tacaaagtgatgaaag	A	C	// 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 63966 //	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-1965062	cctgctctatgtcagg[A/G]acacatcatttagcat	A	G	11249 // Homo sapiens neurexophilin 2 (NXPH2), mRNA. /// ENST00000272641 // upstream // 186698 // --- // --- // --- // ---	NXPH2	NXPH2, Homo sapiens neurexophilin 2 (NXPH2), q22.1
SNP_A-1937399	ttgaaatctaatgtta[A/T]cttgtgcacagattgg	A	T	/// ENST00000330649 // upstream // 1197738 // --- // --- // --- //	-	q11.2
SNP_A-1957564	ttttatattatgttgc[A/G]attttccgaactatca	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 967716 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1726598	ttggctataagaaaagtaggcagaa[A/G]cagttactaagaaacatgagccatt	A	G	5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 1173397 // Hs.135892 // NCAM2 // 4685 // neural	PRSS7	PRSS7 , rs10482903, protease, serine, 7 (enterokinase) ,q21.1
SNP_A-1748737	aactcttgtacactgctggtagtca[C/T]gtaaattagtacaacagttttggaa	C	T	11249 // neurexophilin 2 /// NM_018557 // downstream // 1043548 // Hs.417952 // LRP1B // 53353 // low density	NXPH2	NXPH2 , rs1595314, neurexophilin 2 ,q22.1
SNP_A-1782363	ggcaattaaaaagaag[C/T]ccatgtagcaaagctc	C	T	25914 // Homo sapiens rotatin (RTTN), mRNA. /// NM_004232 // upstream // 14797 // Hs.44439 // SOCS6 //	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-1808915	gtgaatcttttctaca[A/G]gttgcctttatggttt	A	G	1997 // Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1), mRNA. /// NM_007187 //	ELF1	ELF1, Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1), q14.11
SNP_A-1810804	gtgcagccatgtttga[A/G]ggccatgaatttatac	A	G	// Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 8295 // Hs.12393 // TGDS //	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-1791207	ggggtttcatatcaag[C/G]caatggaggcattctt	C	G	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 231879 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1872757	tctataagtatagata[C/T]gtacacaagaataagg	C	T	ENST00000355326 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-1826975	taacatttagataaaa[A/T]caaaagccaattcaga	A	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2005248 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1824002	taaaattttgataaac[A/G]cagttatagcgaatat	A	G	221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 //	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-2189892	cataaatacgttaaaa[C/T]gaccgggcacggtggg	C	T	Homo sapiens chromosome 9 open reading frame 65 (C9orf65), mRNA. /// ENST00000286521 // intron // 0 // --- // ---	C9orf65	C9orf65, Homo sapiens chromosome 9 open reading frame 65 (C9orf65), q21.2
SNP_A-2193954	catgaagcaaacaggg[A/G]aacagacgatgaaaaa	A	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-2174629	cacagcaaaaccatca[C/G]atcctacgtctgagaa	C	G	-- /// ENST00000359349 // upstream // 206981 // --- // --- // ---	-	p13.2
SNP_A-2219714	ccttaaggacttcaaa[C/G]tgacacagaagcctca	C	G	CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// NM_145304 // upstream	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-2157243	attgacagagaatgcc[C/T]cccttccacgctctgt	C	T	Homo sapiens myosin X (MYO10), mRNA. /// ENST00000274203 // 3UTR // 0 // --- // --- // --- // ---	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-2124744	agttctgctgtgctga[G/T]gtgaaaaagattaata	G	T	PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 256434 // Hs.405156 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-2128487	ataataacttttgta[C/G]caattactgttaagta	C	G	83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 586668 // Hs.546489 // C18orf16 // 147429 //	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q12.1
SNP_A-2108529	agctggagaggtaaga[C/G]agaaaacaggaaaatg	C	G	121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 22935 // --- // --- // --- // ---	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2093519	agaactttctagaaaa[C/T]gggcagtaacttcctg	C	T	// 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // downstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2104883	agcatataatggataa[A/G]tgttcagatttaattt	A	G	// Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// ENST00000345127 // intron // 0 // --- // --- // --- // ---	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2049409	aagctgaggtctagaa[A/G]ggttaagtaacttgcc	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 562128 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2008041	tggagcaagtaattca[C/T]gatcacttgactagca	C	T	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2011345	taaacaaagaaaacta[A/G]gcatagataggttggg	A	G	Homo sapiens oxysterol binding protein (OSBP), mRNA. /// ENST00000263847 // intron // 0 // --- // --- // --- // ---	OSBP	OSBP, Homo sapiens oxysterol binding protein (OSBP), q12.1
SNP_A-1994365	ttttttaccataataa[C/T]gctcctaatggttcac	C	T	10404 // Homo sapiens plasma glutamate carboxypeptidase (PGCP), mRNA. /// NM_033512 // downstream // 24625 //	PGCP	PGCP, Homo sapiens plasma glutamate carboxypeptidase (PGCP), q22.1
SNP_A-2039284	aacataaaactttgca[C/G]taaaggcctatttatc	C	G	22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), mRNA. /// NM_000055 // downstream // 350746	SLITRK3	SLITRK3, Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), q26.1
SNP_A-2235327	ctccctctgccagaag[C/G]atgaagagattatact	C	G	9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// NM_000015 //	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-2246482	ctggtttttagttgct[A/T]aacatgataggctaaa	A	T	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2261274	gaaagattaatagtaa[C/T]gatgccaatagctatg	C	T	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 173822 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2312200	ggacagcttcagctac[A/G]gctttatatcagttat	A	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 43742 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3
SNP_A-2314085	ggaggaagatgcctct[C/T]accgcgaggatgagcg	C	T	374946 // Homo sapiens hypothetical gene supported by AK075558; BC021286 (LOC374946), mRNA. /// ENST00000338580 // intron // 0 // --- // --- // --- // ---	LOC374946	LOC374946, Homo sapiens hypothetical gene supported by AK075558; BC021286 (LOC374946), p36.22
SNP_A-2291590	gcacaactgtacatga[C/T]ggtcctgccagcagag	C	T	988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-2296204	gcattcttacagatga[A/G]ctcccttatgtgctta	A	G	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2296882	gccaagccacacttgg[C/T]atttgcaagctcatca	C	T	DSCR1L2 // 11123 // Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), mRNA. ///	DSCR1L2	DSCR1L2, Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), p36.11
SNP_A-2298274	gccatgtaaaccagta[C/T]atcaaccagtgagtca	C	T	171425 // Homo sapiens citrate lyase beta like (CLYBL), transcript variant 1, mRNA. /// NM_206808 // downstream //	CLYBL	CLYBL, Homo sapiens citrate lyase beta like (CLYBL), transcript variant 1, q32.3
SNP_A-2294604	gcagtgaccacaggat[G/T]aagtcagaacactcaa	G	T	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2305633	gctgcatcccccagaa[A/G]agttgaatgctgtacc	A	G	Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // --- // ---	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2
SNP_A-2303074	gctataataacccaac[A/G]attcctacaaactact	A	G	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2302363	gctaagctcactgtcc[A/C]agcaggcctcaccctc	A	C	sapiens otoferlin (OTOF), transcript variant 1, mRNA. /// NM_194322 // intron // 0 // Hs.91608 // OTOF // 9381 // Homo	OTOF	OTOF, Homo sapiens otoferlin (OTOF), transcript variant 1, p23.3
SNP_A-2270674	gacagcatgtctctga[A/G]caaatgcattttattt	A	G	ENST00000281741 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2270051	gacacacagtggagaa[C/T]aatacacactggggcc	C	T	Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // --- // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2274582	gagaaaagagagcaca[A/G]aagagagccagacacc	A	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2281714	gagtctttttcccgaa[C/T]agggcatactgagtaa	C	T	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-2283476	gatactatgaaaatca[A/G]tccaaaacatcgtgat	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1791850 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2284911	gatccatactcaccaa[C/T]atataatacaaatgag	C	T	1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 1129998 // Hs.199248 // PTGER4	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-2254443	cttgccatttcttaca[A/G]ggatgccagtcatact	A	G	84057 // Homo sapiens GAJ protein (GAJ), mRNA. /// ENST00000240488 // downstream // 90336 // --- // --- // --- // --	GAJ	GAJ, Homo sapiens GAJ protein (GAJ), q31.3
SNP_A-2238485	ctctgtaattcctacc[G/T]ctgggctttttatgta	G	T	3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 27920 //	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q42.12
SNP_A-2037336	aacaaatacacgaatc[A/G]ctttaatttgatgccc	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 256628 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-2027918	aaacctgatccagtta[A/T]caggttcatcaggcct	A	T	8942 // Homo sapiens kynureninase (L-kynurenine hydrolase) (KYNU), mRNA. /// NM_018460 // upstream // 526	KYNU	KYNU, Homo sapiens kynureninase (L-kynurenine hydrolase) (KYNU), q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2022416	aaaaataggagtagta[C/G]gagttgcagtaagagc	C	G	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // --- // --- // --- // ---	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2001424	tgcttatgaatattca[C/T]tattagtgccaggatc	C	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2009107	gctagcacattcctga[C/T]gggcttgttagagatg	C	T	132243 // Homo sapiens H1 histone family, member O, oocyte-specific (H1FOO), mRNA. /// NM_015103 //	H1FOO	H1FOO, Homo sapiens H1 histone family, member O, oocyte-specific (H1FOO), q21.3
SNP_A-2099542	caatctgtctcatatc[C/T]actcccaaaagaaatc	C	T	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 94189 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2090079	acttgaacacaactca[C/T]atcctataagcatcta	C	T	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2112109	aggatgtgagcacaca[A/C]gaacagtacctgctgc	A	C	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2127280	ataaatgtaaaacacc[A/G]cggtccgggaaggcat	A	G	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 367333 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2214574	cctagagactcccttа[A/G]atattcttgattcaat	A	G	OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 //	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-2222836	cgatttgccatatgac[C/T]gcaactgtttaaagac	C	T	84888 // Homo sapiens putative intramembrane cleaving protease (SPPL2A), mRNA. /// NM_007347 // upstream // 47001 // Hs.413366 // AP4E1 // 23431 // Homo sapiens	SPPL2A	SPPL2A, Homo sapiens putative intramembrane cleaving protease (SPPL2A), q21.2
SNP_A-2192377	catcatctaaaacaaa[A/G]cctcaatgcaactaca	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1831212	taatgcttgagttata[A/T]gagttaaacaagtaaa	A	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 681084 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1873369	tctcaaagtatctctg[A/G]agaatgtctattgcag	A	G	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 68346 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-1871622	tctaagtccaagcttg[C/T]attcttcccacacacc	C	T	Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000340699 // intron // 0 // --- // ---	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-1859856	tcagggtgcagccata[G/T]ctttccttagagttga	G	T	Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 //	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds. q13.3
SNP_A-1863859	tccaatatttacatga[A/C]gatgatgccttgctgt	A	C	8516 // Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000324851 // upstream // 68134 // --- // --- // --- // ---	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-1864285	tccacgctccttttta[C/T]agccacactgctccac	C	T	923 // Homo sapiens CD6 antigen (CD6), mRNA. /// NM_014207 // upstream // 44753 // Hs.58685 // CD5 // 921 //	CD6	CD6, Homo sapiens CD6 antigen (CD6), q12.2
SNP_A-1848155	tatcttcatggctcca[A/G]tgaaatggcctctcta	A	G	Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA. /// ENST00000264211 // intron //	EIF4G3	EIF4G3, Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), p36.12
SNP_A-1845377	tatacttcctcataaa[A/T]attacatgtagagaaa	A	T	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 393060 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1857796	tcactgtacttgggtg[A/G]atgtggaatgtcttct	A	G	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 444865 // Hs.411433	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-1855249	tcaagctaagagtttc[A/G]aatatgtaatacataa	A	G	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 424280 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1791416	gggtagtgccaagaca[A/T]ggtgctaaggctgtct	A	T	/// ENST00000310543 // downstream // 101689 // --- // --- // ---	-	q33.3
SNP_A-1784506	ggccgagttcatgagc[C/T]gcaacacgatgtaagt	C	T	sapiens matrix metalloproteinase 1 (interstitial collagenase) (MMP1), mRNA. /// ENST00000315274 // CDS // 0 // --- // ---	MMP1	MMP1, Homo sapiens matrix metalloproteinase 1 (interstitial collagenase) (MMP1), q22.2
SNP_A-1960896	tttttgagattgtgca[A/T]agacagattttctttt	A	T	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 311209 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-1939087	ttgataactgtagtca[C/T]gcaggcccaacatgaa	C	T	// Homo sapiens alpha-1-microglobulin/bikunin precursor (AMBP), mRNA. /// NM_138424 // downstream // 10788 //	AMBP	AMBP, Homo sapiens alpha-1-microglobulin,q32
SNP_A-1962909	tgtgtcactggttaaa[C/T]acctgggcaggcaata	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-1968504	ctttctatgtgaaatc[C/T]aaccttgtcgtgcatc	C	T	284747 // Homo sapiens hypothetical protein DKFZp547G0215 (DKFZp547G0215), mRNA. /// ENST00000317836 // 3UTR // 0 // --- // --- // --- // ---	DKFZp547G0215	DKFZp547G0215, Homo sapiens hypothetical protein DKFZp547G0215 (DKFZp547G0215), q13.12
SNP_A-1976112	gtatttcaacacctaa[A/G]cctgataattcttatc	A	G	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 229816 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977791	aaatttcagtgttaga[C/T]tatctgtggctacatt	C	T	Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// ENST00000264399 // intron // 0 // --- // ---	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1977467	ttgggcaatgcaatgc[A/G]attaccaaatagtaat	A	G	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-1879216	tcttactggccttgaa[C/G]aagcaagctatcatga	C	G	Homo sapiens tripeptidyl peptidase II (TPP2), mRNA. /// ENST00000257342 // intron // 0 // --- // --- // --- // ---	TPP2	TPP2, Homo sapiens tripeptidyl peptidase II (TPP2), q33.1
SNP_A-1880777	tcttggctgcagaaaa[G/T]gtggcatctttcataa	G	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 958999 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1883559	tgaacctcagacctcc[A/G]aaatgtttcaagtata	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), mRNA. /// ENST00000282833 // intron // 0 // --- // ---	PTPRK	PTPRK, Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), q22.33
SNP_A-1921079	ttacagtaactcaagc[A/G]aatattgaagtcagag	A	G	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 65113 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1925264	ttatcctgtatcctcc[A/G]caattccctgaacaac	A	G	23585 // Homo sapiens small membrane protein 1 (SMP1), mRNA. /// NM_138616 // upstream // 13557 // Hs.449968 //	SMP1	SMP1, Homo sapiens small membrane protein 1 (SMP1), p36.11
SNP_A-1905737	tggtattctgagttca[A/T]gtgtcagtcttggagg	A	T	ENST00000359247 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-1907311	tggtttttgagtgtca[A/G]atattgcttggcaggt	A	G	ENST00000327475 // intron // 0 // --- // --- // --- // ---	-	p21.2
SNP_A-1912069	tgtgagctaggataaa[C/G]tcactgcatttcagtg	C	G	10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// NM_005252 // upstream // 25758 //	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-1917609	ttaaaaaaaggaagac[G/T]ctaagagcgggagcaa	G	T	Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // --- // ---	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-1889534	aacttgtaaaatagag[A/G]aagtcacacatacaaa	A	G	57534 // Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), mRNA. /// NM_005257 // upstream // 25767 //	MIB1	MIB1, Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), q11.2
SNP_A-1978078	tcaaagctaaggacaa[A/G]aggtgagaaaattgag	A	G	Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-1974480	atctgagtgcacaaag[G/T]ccaaatatcccaaaat	G	T	// 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// NM_002718 // upstream // 368389 // Hs.518155 // PPP2R3A	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.2
SNP_A-1942448	ttggctcaggccttgt[C/G]aatattctcctctcca	C	G	KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 163647 //	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-1692232	tagtctctttcataagtgctgaaat[C/T]attatagtaacagaatggccaacgg	C	T	57713 // Scm-like with four mbt domains 2 /// AK093639 // upstream // 593140 // - // - // - // Homo sapiens cDNA	SFMBT2	SFMBT2 , rs755648, Scm-like with four mbt domains 2 ,p14
SNP_A-1654021	ttatggaaggcataatgaatttaaa[A/G]gttaaaagcatgatagcctcttaac	A	G	NM_152534 // intron // 0 // Hs.174379 // FLJ32685 // 152110 // hypothetical protein FLJ32685	FLJ32685	FLJ32685 , rs10510591, hypothetical protein FLJ32685,p24.1
SNP_A-1788058	gggagagagaggagga[C/G]gaatgacttgtcagtg	C	G	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1806399	gtcctttgcagcaaaa[G/T]aggtgtagcttgaggc	G	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1857478	tcactattagatctga[A/G]tactgggaagtaaaac	A	G	50834 // Homo sapiens taste receptor, type 2, member 1 (TAS2R1), mRNA. /// NM_199133 // downstream // 205810 //	TAS2R1	TAS2R1, Homo sapiens taste receptor, type 2, member 1 (TAS2R1), p15.2
SNP_A-1870287	tcctttgactcgtgta[A/T]aaaagtttgtaatctc	A	T	TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 88969 // --- // --- // --- // ---	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-2187993	cagtcaagacacagaa[C/T]agttcccatatcacag	C	T	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1357296 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2174355	cacacttttggggagg[A/C]accaagctatggggta	A	C	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2179438	cactgtttgagtttga[A/G]atgaaattgaagcctt	A	G	// Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // --- // --- // --- // ---	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2224823	cgtgagagatacatgg[A/G]cactatctgtcacccc	A	G	/// ENST00000251675 // downstream // 72843 // --- // --- // --- // --- /// ENST00000360855 // downstream // 72873 // --- // ---	-	q32.3
SNP_A-2218125	cctgcctgaattcagt[C/G]accaaaagctcgaatt	C	G	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 548922 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2126740	ataaactagctctgtg[A/G]aaagtaagaccattgc	A	G	ENST00000332432 // intron // 0 // --- // --- // --- // ---	-	p15.1
SNP_A-2080728	acctccacatctgcta[A/G]agaatgaatgctgatt	A	G	sapiens lymphocyte antigen 75 (LY75), mRNA. /// ENST00000263636 // CDS // 0 // --- // --- // --- // ---	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2
SNP_A-2082867	acgtcaccactaaaga[A/T]ctggaagtcatgaaaa	A	T	79854 // Homo sapiens hypothetical protein FLJ22639 (FLJ22639), mRNA. /// ENST00000326725 // upstream //	FLJ22639	FLJ22639, Homo sapiens hypothetical protein FLJ22639 (FLJ22639), p36.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2049884	aaggaaattgaagcac[A/G]gaaaatcaaagatcat	A	G	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 7 (ENPP7), mRNA. ///	ENPP7	ENPP7, Homo sapiens ectonucleotide pyrophosphatase,q25.3
SNP_A-2013908	gtagatagacaaggca[A/C]aagactataaattatt	A	C	143689 // Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// NM_130847 // upstream // 87798 // Hs.503594 //	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-1991714	cagttacctgggcaag[A/T]aacaacccgctctgcc	A	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // --- // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. ///	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-2029014	aaagaaaatgtcatta[A/G]gaaaatcataaggaag	A	G	ENST00000356964 // downstream // 408034 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2040431	aaccaggaaagagatc[G/T]gacggactgtgaggca	G	T	/// ENST00000333948 // upstream // 485733 // --- // --- // --- //	-	q31.2
SNP_A-2042035	aactacctcactttaca[C/T]tgcctctgtctctcag	C	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 705179 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2228535	ctactttctcctaca[C/T]acataaatgacatgaa	C	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2269361	gaatttgtgatctaaa[A/G]tgagctttttccatac	A	G	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 320467 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2268535	gaatgggtgagttgaa[C/T]tggcaaagagcaaccc	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2305758	gctgcctctaaatgca[A/G]caacctttttatatgg	A	G	55967 // Homo sapiens 13kDa differentiation-associated protein (DAP13), mRNA. /// ENST00000341598 //	DAP13	DAP13, Homo sapiens 13kDa differentiation-associated protein (DAP13), q22
SNP_A-2314258	ggaggcagcttgttag[A/T]aatttagtgtgtaggg	A	T	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2304507	gctctcaagtgtgctc[A/G]ataaaatgacatcctc	A	G	55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2299918	gcctaggaatgaagaa[A/C]gatctgactgtatctt	A	C	// --- /// ENST00000355517 // downstream // 83314 // --- // ---	-	q24.32
SNP_A-2286653	gatggataatgactca[A/G]aaaggagctgaggtgg	A	G	- /// ENST00000355517 // downstream // 409229 // --- // --- //	-	q24.32
SNP_A-2235146	ctccccacctcttagc[C/T]caggaatgaaggcatg	C	T	// 121273 // Homo sapiens hypothetical protein MGC35033 (MGC35033), mRNA. /// NM_001005203 // upstream // 26827	MGC35033	MGC35033, Homo sapiens hypothetical protein MGC35033 (MGC35033), q13.11
SNP_A-2043465	aactgtaaaagatgta[C/T]gccactgaacagcgtt	C	T	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2041282	aacctgaatacgcccat[C/G]attatgcaacagctgt	C	G	119391 // Homo sapiens glutathione S-transferase omega 2 (GSTO2), mRNA. /// NM_033397 // downstream // 6163 // 283310 // Homo sapiens hypothetical protein FLJ90579	GSTO2	GSTO2, Homo sapiens glutathione S-transferase omega 2 (GSTO2), q25.1
SNP_A-2046192	aagacttcaagtcagc[C/T]gctctttaggccttat	C	T	(FLJ90579), mRNA. /// ENST00000298820 // downstream //	FLJ90579	FLJ90579, Homo sapiens hypothetical protein FLJ90579 (FLJ90579), q21.31
SNP_A-2024294	aaaagccacaccaata[C/T]gctcccatgtctg	C	T	/// ENST00000246872 // downstream // 85092 // --- // --- // ---	-	q11.21
SNP_A-2002017	ttagcacaattgttga[C/T]aaagttgggcttatgt	C	T	MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882, p34.3
SNP_A-2067058	acaaactccaaagtag[A/G]agcagtagaagtttc	A	G	Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // --- //	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-2067276	acaaaggttcaaacta[C/T]gcaggtccatttatat	C	T	3622 // Homo sapiens inhibitor of growth family, member 1-like (ING1L), mRNA. /// NM_152682 // downstream // 102129	ING2	ING2, Homo sapiens inhibitor of growth family, member 1-like (ING1L), q35.1
SNP_A-2085964	actctactgtacaccc[A/G]ggagaaaatgagcata	A	G	3313 // Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA. /// NM_001903 // upstream // 33535 // Hs.445981 // 4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. ///	HSPA9B	HSPA9B, Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, q31.2
SNP_A-2102465	agattctgcttctaac[C/T]aactagacattgggaa	C	T	NM_181523 // upstream // 89671 // Hs.132225 // PIK3R1 // Homo sapiens N-terminal asparagine amidase (NTAN1),	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2136158	atcaatcaagtatcac[A/C]gctacagcagaagcccc	A	C	mRNA. /// ENST00000325845 // intron // 0 // --- // --- // ---	NTAN1	NTAN1, Homo sapiens N-terminal asparagine amidase (NTAN1), p13.11
SNP_A-2110566	gccgtggctacctttc[C/T]ctaaatggacctgtgg	C	T	ENST00000343130 // intron // 0 // --- // --- // --- // ---	-	q12.11
SNP_A-2110188	aggaagtaacatttac[G/T]ggcacactttcaggt	G	T	ENST00000338506 // intron // 0 // --- // --- // --- // --- /// ENST00000331815 // downstream // 416961 // --- // --- // ---	-	q13.13
SNP_A-2139236	atcctgaaaatccaag[C/T]ccaggttgacctttgg	C	T	23170 // Homo sapiens KIAA0153 protein (KIAA0153), mRNA. /// ENST00000357017 // upstream // 2773 // --- // --- //	KIAA0153	KIAA0153, Homo sapiens KIAA0153 protein (KIAA0153), q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2152477	attaagaaagctgtaa[C/T]tcaccaaaattagttc	C	T	Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // --- // --- // --- // ---	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-2225493	ctaaaacttcaactca[A/G]taccctaggagacttc	A	G	9202 // Homo sapiens zinc finger protein 262 (ZNF262), mRNA. /// NM_024874 // downstream // 10945 // Hs.456507	ZNF262	ZNF262, Homo sapiens zinc finger protein 262 (ZNF262), p34.3
SNP_A-2177638	cacggcatcaagagaa[A/C]gtacccattctcatca	A	C	ENST00000303635 // intron // 0 // --- // --- // --- // ---	-	p36.23
SNP_A-2199025	catttggtatcctcag[C/T]ccataatgctctatgc	C	T	/// ENST00000236495 // upstream // 7512 // --- // --- // --- // ---	-	p33
SNP_A-1867538	tccggaaacaggtaag[C/G]aatcagttcaaaagaa	C	G	Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// ENST00000307241 // intron //	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1847657	tatctacaagttttca[A/G]atagctatagattctc	A	G	-- /// ENST00000345029 // upstream // 316772 // --- // --- // ---	-	p14
SNP_A-1832640	tacaacccatgcctca[A/G]aataatgagacttgaa	A	G	sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA. /// NM_198709 // intron // 0 // Hs.149103 // ARSB // 411 //	ARSB	ARSB, Homo sapiens arylsulfatase B (ARSB), transcript variant 1, q14.1
SNP_A-1802113	gtatactggtagttat[C/T]accatacagcagtgct	C	T	// Homo sapiens ATPase, Ca++ transporting, type 2C, member 1 (ATP2C1), transcript variant 4, mRNA. /// NM_014382 // intron // 0 // Hs.546361 // ATP2C1 // 27032 //	ATP2C1	ATP2C1, Homo sapiens ATPase, Ca++ transporting, type 2C, member 1 (ATP2C1), transcript variant 4, q21.3
SNP_A-1808601	gtgaacacagccaacc[A/G]aggtccaagaaagctt	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1783965	ggccacgtggtacaac[A/G]gacagagccccagttg	A	G	SDCCAG10 // 10283 // Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA. /// NM_197941 // downstream // 75763 // Hs.482291 //	SDCCAG10	SDCCAG10, Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), q12.3
SNP_A-1960598	tttttcatttttttca[C/T]cagtgtcacttgccaa	C	T	Homo sapiens zinc finger protein 79 (pT7) (ZNF79), mRNA. /// ENST00000357834 // intron // 0 // --- // --- // --- // ---	ZNF79	ZNF79, Homo sapiens zinc finger protein 79 (pT7) (ZNF79), q33.3
SNP_A-1961397	ttttttggaaataaag[A/G]cagctttaaaaattat	A	G	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 191820 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-1967735	ctgaatagaggtaata[C/T]gccttttctccaaga	C	T	ENST00000334534 // intron // 0 // --- // --- // --- // ---	-	p12.2
SNP_A-1885884	tgacatatgatctgga[A/G]catcttttaatatgct	A	G	// 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 427234 // ---	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1904202	tgggcctggcatcctc[C/T]agtctgctgaaagcca	C	T	// Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), mRNA. /// ENST00000359309 // intron // 0 // -- // --- // --- // --- /// ENST00000360822 // intron // 0 // --- // --- //	CDK5RAP2	CDK5RAP2, Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), q33.2
SNP_A-1907349	tgtaaaacatattcaa[A/G]gttatacagaattcta	A	G	8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream //	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1907979	tgtaattatctgttca[A/G]taactgccttctcacc	A	G	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1909226	tgtatgatgtgtatta[C/T]atttgtttataagaga	C	T	ENST00000283297 // intron // 0 // --- // --- // ---	-	p12.3
SNP_A-1921976	ttactgaaagaggcca[C/T]gatcataaaagacatg	C	T	80829 // Homo sapiens zinc finger protein 91 homolog (mouse) (ZFP91), transcript variant 1, mRNA. /// NM_170768 // downstream // 72969 // Hs.524920 // ZFP91 // 80829 //	ZFP91	ZFP91, Homo sapiens zinc finger protein 91 homolog (mouse) (ZFP91), transcript variant 1, q12.1
SNP_A-1927197	ttatttttctctaatc[A/G]aatgcaccataaaaag	A	G	51050 // Homo sapiens protease inhibitor 15 (PI15), mRNA. /// NM_031461 // upstream // 93321 // Hs.436542 // LCRISP1	PI15	PI15, Homo sapiens protease inhibitor 15 (PI15), q21.11
SNP_A-1928245	ttcacagtgtgtaaaa[C/T]ctagctttggtgtcta	C	T	7718 // Homo sapiens zinc finger protein 165 (ZNF165), mRNA. /// NM_025231 // upstream // 15501 // Hs.288539 //	ZNF165	ZNF165, Homo sapiens zinc finger protein 165 (ZNF165), p22.1
SNP_A-1925195	ttatccagggagaaaa[C/T]taataaagaaacaatg	C	T	6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 285723 // Hs.522891 // CXCL12 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1890896	tgatgctgctaactca[A/C]aaatgatcagggctga	A	C	ENST00000338882 // intron // 0 // --- // --- // --- // ---	-	q21
SNP_A-1879801	tcttccactcatgctg[C/T]acaaacagttttagca	C	T	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1967225	gccaacatccctcttg[C/G]atcactgaatcataag	C	G	sapiens insulin receptor substrate 1 (IRS1), mRNA. /// ENST00000358349 // intron // 0 // --- // --- // --- // --- ///	IRS1	IRS1, Homo sapiens insulin receptor substrate 1 (IRS1), q36.3
SNP_A-1955765	tttgtagaagccttca[C/T]gctcttatttgtcagt	C	T	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1953222	tttctttgctgcttta[A/G]cttaatccaaatgtag	A	G	Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1950010	tttcacaaacctagaa[G/T]tctaatatttgaacac	G	T	Homo sapiens protein kinase D2 (PRKD2), mRNA. /// ENST00000291281 // intron // 0 // --- // --- // --- // ---	PRKD2	PRKD2, Homo sapiens protein kinase D2 (PRKD2), q13.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1807543	gtctggagaaaagata[A/G]gtgtagtttgtacatc	A	G	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1785892	ggctgagcagtgagac[A/G]gatgctttggaacaat	A	G	11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 610037 //	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1791169	ggggttcagagcagaa[C/T]tgaggaatgtgacagt	C	T	Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), mRNA. /// ENST00000283148 // intron // 0 // --- // --- // --- // ---	UXS1	UXS1, Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), q12.2
SNP_A-1790920	gggggtgtgaaactca[A/G]aagaaaggagatgaaa	A	G	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 208821 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1799056	gtaagctgttaacatc[C/T]cacaagtacagaaata	C	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q22.1
SNP_A-1843046	tagtattctttgtgaa[G/T]gtactacagtttattc	G	T	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, mRNA. /// ENST00000329257 // intron //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, q23.1
SNP_A-1816589	gttagttgtgttgaaa[C/T]gaattgtgccatcgct	C	T	// 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), mRNA. /// NM_003108 // upstream // 209752 // Hs.432638	MTCBP-1	MTCBP-1, Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), p25.2
SNP_A-1847896	tatctcttcttgtgcc[G/T]ctcatgtttaagtatc	G	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1854547	tcaaatttacattccc[C/T]caacagcgtgtgagat	C	T	Homo sapiens synaptotagmin XII (SYT12), mRNA. /// ENST00000308930 // intron // 0 // --- // --- // --- // --- ///	SYT12	SYT12, Homo sapiens synaptotagmin XII (SYT12), q13.2
SNP_A-2199211	cattttaggcataaac[C/T]gttctgctagaatcca	C	T	6659 // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA. /// NM_000948 // downstream // 370828 //	SOX4	SOX4, Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), p22.3
SNP_A-2199453	catttttatgcatagc[G/T]ctgggtgttttacaaa	G	T	Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 3 (SLC37A3), transcript variant 1, mRNA. /// NM_032295 // intron // 0 // Hs.446021 // SLC37A3	SLC37A3	SLC37A3, Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 3 (SLC37A3), transcript variant 1, q34
SNP_A-2204320	tacctgcccatgaaac[A/G]aatacagggtaagtca	A	G	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2140131	atctatacagttaaca[C/T]attcatatcctttctc	C	T	3777 // Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), mRNA. /// NM_017877 // upstream //	KCNK3	KCNK3, Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), p23.3
SNP_A-2163043	atttttacagatgaaa[A/C]atgaaaggggtcatgg	A	C	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 91455 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2068634	acaataaataaatgca[A/G]tacagtgagtagagat	A	G	/// ENST00000358773 // upstream // 70606 // --- // --- // --- // --- /// ENST00000357286 // upstream // 209228 // --- // --- // --- // -	-	q14.1
SNP_A-2054521	aagtttggtgaagttc[C/T]atacccaatgccctac	C	T	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2055791	aataatttttaccaac[A/G]ctctttgagggtgaat	A	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 580041 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2016738	atactgaatccaggca[C/T]tagctacaaaaggaaa	C	T	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 812912 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2009239	caagtcctgccatcac[A/T]ggtctctacttctatt	A	T	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 364550 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2029787	aaagagtaataataca[C/T]gttcctgcttccattt	C	T	oncogene mRNA, complete cds. /// ENST00000348841 // intron // 0 // --- // --- // --- // --- /// ENST00000352462 // intron //	-	-, Human P47 LBC oncogene complete cds. ,q25.3
SNP_A-2045899	aagaccaaaagggaag[A/G]aagtcaacatggacta	A	G	154386 // Homo sapiens chromosome 6 open reading frame 195 (C6orf195), mRNA. /// ENST00000296847 // upstream //	C6orf195	C6orf195, Homo sapiens chromosome 6 open reading frame 195 (C6orf195), p25.2
SNP_A-2250346	cttagatccactgatg[A/C]atcaacgtcaacagtt	A	C	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // --- // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2282087	tgcttgttacatttta[A/C]gagtgacaagcaggtt	A	C	// Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000338242 // intron // 0 // --- // --- // --- // ---	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2288841	gatttaaacttccaaa[C/T]aatcccatctaactgt	C	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2294409	gcaggttctgtaacat[C/G]aacttgagcagctagt	C	G	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2296831	gccaacttgcttgagt[A/G]acactgatgaaaaaag	A	G	Homo sapiens general transcription factor IIIC, polypeptide 4, 90kDa (GTF3C4), mRNA. /// ENST00000245590 // intron // 0 // --- // --- // --- // ---	GTF3C4	GTF3C4, Homo sapiens general transcription factor IIIC, polypeptide 4, 90kDa (GTF3C4), q34.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259464	gaaaaattcttcatgc[A/T]aattaaacaatcaaac	A	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 814766 // --- // --- // --- //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2237017	ctctatgtgcaagaca[A/C]tgcagagtatgaatat	A	C	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2239821	ctgaaattgcagcctc[A/G]ctctgaccatctgggt	A	G	Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-2229890	ctagttcttccaaaag[C/T]acaaaccacagagact	C	T	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2036779	aaatttatgaatgaca[C/G]gtattaggttgagcca	C	G	2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream //	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-2028517	aaactgacttcaaaac[C/T]gataacttactgtatc	C	T	/// ENST00000330649 // upstream // 952790 // --- // --- // --- // ---	-	q11.2
SNP_A-2004768	tgaccagttctggtga[C/T]ccagttataagaggac	C	T	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1992144	cttcccagccccacgg[A/C]aaattctgcttttgtc	A	C	Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// NM_001147 // intron // 0 // Hs.490892 //	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2052958	aagtccactacctcca[C/T]gtcaactggttttgaa	C	T	sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2064646	aattctcagcagtaag[A/G]aagaacaaactactca	A	G	Homo sapiens pecanex homolog (Drosophila) (PCNX), mRNA. /// ENST00000304743 // intron // 0 // --- // --- // --- // ---	PCNX	PCNX, Homo sapiens pecanex homolog (Drosophila) (PCNX), q24.2
SNP_A-2094076	agaaggaatgaataga[A/C]aaagagattctcattt	A	C	Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, mRNA. /// NM_176787 // intron // 0 // Hs.157031 // PIGN // 23556 // Homo sapiens	PIGN	PIGN, Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, q21.33
SNP_A-2084562	actatggaaaaataca[C/G]agctattgaaaatgac	C	G	Homo sapiens chromosome 9 open reading frame 68 (C9orf68), mRNA. /// ENST00000320685 // intron // 0 // --- // ---	C9orf68	C9orf68, Homo sapiens chromosome 9 open reading frame 68 (C9orf68), p24.1
SNP_A-2129585	atacactttaaataca[A/G]catcttccagctctgg	A	G	// 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 489405 //	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-2214091	cctaatagatggaaaa[G/T]atggcaggatgtcttg	G	T	Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2195158	catggagatctggcta[C/T]ggaacagtgagttcta	C	T	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2185034	cagcttgtatggagaa[C/T]ggaaatggagcagatg	C	T	51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 384176 //	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1870646	attatttatccatcca[C/T]gctaaaagaattttcc	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 527508 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1864800	tccagctttctctagc[A/G]ccccaggaagaatcct	A	G	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-1821771	gttttaatctcaccca[C/T]gttcaacttcacagct	C	T	58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 144282 //	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2
SNP_A-1825405	attgtaatgaggcaaa[C/T]gtgacttcatgcagct	C	T	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1822366	gttttgttaaaatgca[C/G]actgtttaggaagact	C	G	2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 316300 // Hs.203717	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-1842735	tagtaagttctggagc[C/T]aggagtcaaacttcag	C	T	23543 // Homo sapiens RNA binding motif protein 9 (RBM9), mRNA. /// AF229058 // upstream // 278838 // Hs.282998 //	RBM9	RBM9, Homo sapiens RNA binding motif protein 9 (RBM9), q12.3
SNP_A-1829722	taagttttctccagga[A/G]gccaaagcatccaagt	A	G	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 208293 // Hs.17441	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-1793408	ggtaggtaggcagtga[A/G]cttgatttaagacttg	A	G	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1790776	gggggagactcctttc[A/G]aacttctgttggccac	A	G	91584 // Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), mRNA. /// ENST00000251676 // intron // 0 // --- // --- // --- // ---	DKFZp434G0625	DKFZp434G0625, Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), q32.3
SNP_A-1788328	gggagggaggagtgaa[C/T]tggtagagcacagagg	C	T	115290 // Homo sapiens F-box protein 17 (FBXO17), transcript variant 2, mRNA. /// NM_148169 // upstream //	FBXO17	FBXO17, Homo sapiens F-box protein 17 (FBXO17), transcript variant 2, q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1812323	gtggattagtagaaca[A/G]tggcatcaaagtgttg	A	G	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 208548 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1803401	gtatttcccactctta[C/G]ctcttattgctcttat	C	G	29068 // Homo sapiens HSPC063 protein (HSPC063), mRNA. /// NM_014155 // upstream // 49830 // Hs.178499 //	HSPC063	HSPC063, Homo sapiens HSPC063 protein (HSPC063), q24.3
SNP_A-1783254	ggcagtacatctttgc[A/G]ctttaaagttgaaact	A	G	254778 // Homo sapiens hypothetical protein MGC33510 (MGC33510), mRNA. /// ENST00000305454 // intron // 0 // ---	MGC33510	MGC33510, Homo sapiens hypothetical protein MGC33510 (MGC33510), q13.1
SNP_A-1732267	ttccctcttatatttcagttggaag[G/T]cccaggcactagattgggcagcatc	G	T	// 2863 // G protein-coupled receptor 39 /// NM_144586 // upstream // 104343 // Hs.372651 // MGC29643 // 116372 //	GPR39	GPR39 , rs7603615, G protein-coupled receptor 39 ,q21.2
SNP_A-1971644	aaaacaaagataaatc[A/G]aagttagttaatcact	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 342413 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971566	tccttcccattcatca[C/T]cagttcagtaatgggc	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 81216 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1986822	gtctgagacagattaa[C/T]gttagaggaaagggaa	C	T	6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 17033 // Hs.485968 // MAP3K7 //	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q15
SNP_A-1989399	aagtgagggataggtc[C/T]cgtagtgactcagaag	C	T	ENST00000342263 // intron // 0 // --- // --- // --- // ---	-	p15.1
SNP_A-1886345	tgacctggaagtaaac[C/G]catagtatctttgggt	C	G	221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1885027	tgaatggatactatcc[C/T]gaccttgaactacatg	C	T	Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, mRNA. /// NM_134431 // intron // 0 // Hs.46440 // SLCO1A2 // 6579 //	SLCO1A2	SLCO1A2, Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, p12.1
SNP_A-1882414	tgaaaagcctgtttga[A/G]caccttgtgcacttta	A	G	// 5209 // Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA. ///	PFKFB3	PFKFB3, Homo sapiens 6-phosphofructo-2-kinase,p15.1
SNP_A-1893760	tgcagtgttccattta[C/T]aggcattggttggtgg	C	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1904225	tgggcggtccaatacc[A/G]ctttattagtcagaga	A	G	LOC113828 // 113828 // Homo sapiens hypothetical protein BC011204 (LOC113828), mRNA. /// NM_138435 //	LOC113828	LOC113828, Homo sapiens hypothetical protein BC011204 (LOC113828), q13.1
SNP_A-1926341	ttattatatggagata[C/T]gtggctacaaaagtat	C	T	Homo sapiens NOL1/NOP2/Sun domain family 6 (NSUN6), mRNA. /// ENST00000302150 // intron // 0 // --- // --- // --- // ---	NSUN6	NSUN6, Homo sapiens NOL1 p12.31
SNP_A-1966393	tattagatgggttttc[A/G]aaaattgcataggttg	A	G	ENST00000260983 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1950424	tttcagtatgcttctc[A/G]cagactctatttgagg	A	G	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 587247 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1942835	ttggggagcagacccc[C/G]acgtctgacagcatac	C	G	/// ENST00000354745 // upstream // 101381 // --- // --- // --- // --- /// ENST00000306392 // upstream // 18498 // --- // --- // --- //	-	q13.32
SNP_A-1938970	ttgagtatctgaggaa[A/T]cacattcttagaaaca	A	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1591397 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1725926	gttagataacatctcaaacataaga[C/T]acgggttataacatctaaagtaaag	C	T	// phosducin-like /// NM_018835 // downstream // 10368 // Hs.112227 // MNAB // 54542 // membrane-associated nucleic	PDCL	PDCL , rs10513414, phosducin-like ,q33.2
SNP_A-1802945	gtatgtgtgtgatgca[A/G]tattacttaaaatcaa	A	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 845020 // --- // ---	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1809536	gtgagagctccagggc[A/G]gagtgggaatcttact	A	G	Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000285689 // intron // 0 // --- // --- // --- // ---	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1820870	gtttccttcttgatac[C/G]actcaatagggataat	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 916502 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1866175	tcccagggactgcaga[C/T]cttaccctgaacagca	C	T	/// ENST00000325796 // downstream // 235691 // --- // --- // ---	-	q22.2
SNP_A-1873883	tctcagtagaaaacca[C/T]gagttagacaggtctc	C	T	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1856937	tcaccagaattagacc[A/G]gactagtcaacctcct	A	G	COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 90632 //	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-1844461	tataaaggaagacgac[C/T]gcaaacgtgtgacatg	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 90878 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227914	ctacctcatgcaaaca[C/T]acacaaatacaaatat	C	T	// 26033 // Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// NM_145793 // downstream // 85686 // Hs.109425 // GFRA1 //	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2200496	ccaactacaagaaagc[A/C]attgggcctcagaaac	A	C	// 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1654266 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2199758	ccaaacaaccagtgca[A/G]aatcctcattctcctc	A	G	ENST00000313159 // downstream // 27689 // --- // --- // --- // ---	-	p23.1
SNP_A-2212335	ccctggttactggaaa[C/T]ggcactttcttactta	C	T	// Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 14D (PPP1R14D), mRNA. /// ENST00000299174 // intron // 0 // --- // --- // --- // ---	PPP1R14D	PPP1R14D, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 14D (PPP1R14D), q15.1
SNP_A-2103991	agcacttcttcttcta[C/T]gcacttcttagtgcac	C	T	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2072611	acagcccctcagaaaa[A/G]aatcgtgtgccatcgg	A	G	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2051502	aagggtccagtattca[C/T]ggtctcttcggggtcc	C	T	ENST00000321345 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1996674	catgttgaacgaatca[A/G]tgagttggtttgtgtc	A	G	80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// NM_030664 // upstream // 95040 //	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-2007005	gccaagatgtgtaaga[A/G]gggagaagcaactcgt	A	G	2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 376121 // Hs.203717	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-2017477	gagaactggaggccaa[A/G]taagattttgtatcat	A	G	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2019387	catcacaacagtagaa[G/T]gaatgacaaaaaccat	G	T	8624 // Homo sapiens Down syndrome critical region gene 2 (DSCR2), transcript variant 2, mRNA. /// NM_003720 // downstream // 7604 // Hs.473838 // DSCR2 // 8624 // Homo	DSCR2	DSCR2, Homo sapiens Down syndrome critical region gene 2 (DSCR2), transcript variant 2, q22.2
SNP_A-2243764	ctgctgatccgataac[C/G]aacatgagatttagta	C	G	4172 // Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA. /// NM_133367 // upstream // 56746 // Hs.239388 // C6orf33 // 85315 // Homo	MCM3	MCM3, Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), p12.2
SNP_A-2274769	gagaaagggaattcag[A/C]atcacactcagttgaa	A	C	// Homo sapiens putative G protein coupled receptor (GPR), mRNA. /// ENST00000299092 // upstream // 11895 // --- // ---	GPR	GPR, Homo sapiens putative G protein coupled receptor (GPR), q15.1
SNP_A-2297740	gccaggacagttaaac[A/G]aaaccatcatcacctc	A	G	C20orf178 // 128866 // Homo sapiens chromosome 20 open reading frame 178 (C20orf178), mRNA. ///	C20orf178	C20orf178, Homo sapiens chromosome 20 open reading frame 178 (C20orf178), q11.22
SNP_A-2303408	gctatttaaagcaaac[A/G]cacattgaatttgata	A	G	27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 299971 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2287390	gatgtgttgatgatta[C/T]cattttctaaaaagtg	C	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1279122 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2260376	gaaacaaatagagcaa[A/G]acaagggaatcacctc	A	G	Homo sapiens ubiquitin specific protease 20 (USP20), mRNA. /// ENST00000315480 // intron // 0 // --- // --- // --- // ---	USP20	USP20, Homo sapiens ubiquitin specific protease 20 (USP20), q34.11
SNP_A-2233039	ctcagatattctgtta[C/G]agaagcataaaacaga	C	G	2519 // Homo sapiens fucosidase, alpha-L- 2, plasma (FUCA2), mRNA. /// ENST00000002165 // upstream //	FUCA2	FUCA2, Homo sapiens fucosidase, alpha-L- 2, plasma (FUCA2), q24.2
SNP_A-2042691	aactccttttgtacta[C/T]gaaaagatgaaacgat	C	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 445388	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2011543	agttgctaggcagtaa[A/G]aacgtagtaaaggcag	A	G	404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 3155 //	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2066815	acaaaataaggtgata[A/G]gtcttaaggaagatag	A	G	Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // --- // --- // --- // ---	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2094495	agaataaaaagttggc[C/T]gaatcttgaagggagc	C	T	SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2084922	actcaagtttcttcta[C/T]ccgagacttagtttta	C	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2226818	ctaatacctgtacaa[A/C]acagggaatctggaag	A	C	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// NM_024767 // intron // 0 // Hs.134296 //	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-2184864	cagctgtacgtagtaa[G/T]agtaccacccatcttt	G	T	SP17 // 84692 // Homo sapiens testes development-related NYD-SP17 (NYD-SP17), mRNA. /// NM_020235 // upstream	NYD-SP17	NYD-SP17, Homo sapiens testes development-related NYD-SP17 (NYD-SP17), q13.12
SNP_A-2187598	cagtaagctcacttca[A/G]atacttgggttttaga	A	G	Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// ENST00000265283 // intron // 0 // --- // ---	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin,q21.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2173346	cacaagcactatatga[C/T]tattaaacatggcttt	C	T	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2128986	ataatgttacctagga[A/G]aagacgcttgaacaag	A	G	// Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1A, mRNA. /// NM_080597 // intron // 0 // Hs.370725 // OSBPL1A // 114876	OSBPL1A	OSBPL1A, Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1A, q11.2
SNP_A-2110740	aggacctgaagatgtt[A/G]aaaagaatgccttgcc	A	G	PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 29830 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-2113068	aggccactggaaagaa[A/G]aagctggagcatggca	A	G	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2114053	aggctttcagacctaa[C/T]gcaataaaagaagagt	C	T	// Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // --- // --- // --- // ---	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2148979	atggttcctgtaatta[C/T]cgtactcagccacgta	C	T	10561 // Homo sapiens interferon-induced protein 44 (IFI44), mRNA. /// AY358360 // downstream // 118146 // Hs.132314 //	IFI44	IFI44, Homo sapiens interferon-induced protein 44 (IFI44), p31.1
SNP_A-1856181	tcacaacagcctcgac[A/C]gaagtagatgtttaag	A	C	11023 // Homo sapiens ventral anterior homeobox 1 (VAX1), mRNA. /// NM_181840 // upstream // 30157 // Hs.449650 //	VAX1	VAX1, Homo sapiens ventral anterior homeobox 1 (VAX1), q26.11
SNP_A-1839052	tagagatcagagaaca[G/T]atggtaagacaacaaa	G	T	ENST00000318116 // intron // 0 // --- // --- // --- // ---	-	q21.23
SNP_A-1788382	gggaggtgtgcaagaa[C/T]ggcagcaggagcctca	C	T	ENST00000343998 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-1671302	acaagggctttaactgtttacacta[C/T]ggcatatggttttgcatcctttctt	C	T	NM_014682 // intron // 0 // Hs.151449 // ST18 // 9705 // suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ST18	ST18 , rs10504138, suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein),q11.23
SNP_A-1937515	ttgaacccaggagaaa[C/T]tgggatatgagggtag	C	T	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 326133 // Hs.131489 // PARD3	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1935706	ttctgtgaacaaaacc[A/C]agcaaattccaacata	A	C	Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1950854	tttccaacctcatgaa[C/T]taggacaggcctagta	C	T	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1963693	ctagaagctaaactaa[A/G]tgactgaaaaaatggc	A	G	27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// NM_182536 // downstream // 60370 //	BMP10	BMP10, Homo sapiens bone morphogenetic protein 10 (BMP10), p13.3
SNP_A-1981237	gaccaatggaaccaac[A/G]ataacttcaggaaagg	A	G	5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 222744 // Hs.298863 // FLJ23577	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1927353	ttcaaaccactgatgg[C/G]aagcagtccaggctct	C	G	4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 // upstream	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.32
SNP_A-1889559	tgagtttgggaataaa[A/G]caggtgattatgatgg	A	G	10887 // Homo sapiens G protein-coupled receptor 73 (GPR73), mRNA. /// D29642 // upstream // 54889 //	GPR73	GPR73, Homo sapiens G protein-coupled receptor 73 (GPR73), p13.3
SNP_A-1875643	tctcttccatttgtgc[A/G]cttactcaccttacga	A	G	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 121061 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-1934712	ttctctgtcaattatt[C/G]aaattatttagcatct	C	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1940576	ttgcctaagtgaaagg[C/T]aattcccagggcagga	C	T	121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 165484 // Hs.31664 //	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1786496	ggcttcaactttgcag[C/G]aagtggtctggctcca	C	G	11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1796910	ggttcccagggcactc[A/G]aaaactgacaaccgac	A	G	LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 //	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-1810604	gtgcaacttgaccccct[A/C]aatgaaacacttaaaa	A	C	Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000306329 // intron // 0 // --- // --- // --- // --- ///	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1829563	taagtgtataccccctg[A/T]aactatcatcacaatc	A	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 468180 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2145523	atgcagttattttaga[A/G]gattgtgtgccaagag	A	G	Homo sapiens protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PPP2CB), mRNA. /// ENST00000221138 // intron // 0 // --- // --- // --- // ---	PPP2CB	PPP2CB, Homo sapiens protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PPP2CB), p12
SNP_A-2156709	attctggttcattcac[A/G]aatcagttttttatttt	A	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 90658	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2113058	aggccactactgcatc[A/G]cataggtagtcctcaa	A	G	AFTIPHILIN // 54812 // Homo sapiens aftiphilin protein (AFTIPHILIN), transcript variant 1, mRNA. /// NM_001002243	AFTIPHILIN	AFTIPHILIN, Homo sapiens aftiphilin protein (AFTIPHILIN), transcript variant 1, p14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172732	caatttataaacacta[C/G]ctgtaaacttctgaac	C	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2190702	catactttaaaagtga[A/G]gacgttagatgttgat	A	G	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2212060	ccctgcacatccacac[A/G]ggccccagcattggac	A	G	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, mRNA. /// NM_080810 // intron // 0 //	COL13A1	COL13A1, Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, q22.1
SNP_A-2206280	ccatccccagctggcc[A/G]gaggggtttgtccaat	A	G	Homo sapiens zinc finger protein 395 (ZNF395), mRNA. /// ENST00000290163 // intron // 0 // --- // --- // --- // ---	ZNF395	ZNF395, Homo sapiens zinc finger protein 395 (ZNF395), p21.1
SNP_A-2089341	acttagtatagtttca[C/T]gtttttgagatacata	C	T	10631 // Homo sapiens periostin, osteoblast specific factor (POSTN), mRNA. /// NM_016179 // downstream // 6188 //	POSTN	POSTN, Homo sapiens periostin, osteoblast specific factor (POSTN), q13.3
SNP_A-2095358	tatgatataacaccaa[C/G]tcttcttcaactgtat	C	G	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2095498	agacaacttacttcta[A/C]ctttctcattttcaag	A	C	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 109259 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3
SNP_A-2074855	acatcaatgtcccaca[G/T]gaggattctgcccatt	G	T	/// ENST00000359604 // upstream // 186094 // --- // --- // --- // -- /// ENST00000344172 // upstream // 96837 // --- // --- // --- //	-	q11.2
SNP_A-2061917	aatggcagttaatgac[C/T]gggcagactgggggat	C	T	29967 // Homo sapiens low density lipoprotein-related protein 12 (LRP12), mRNA. /// ENST00000276654 // upstream //	LRP12	LRP12, Homo sapiens low density lipoprotein-related protein 12 (LRP12), q22.3
SNP_A-2012074	agtgaacatgttagaa[C/T]gctgtgtgttagtttg	C	T	// Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // intron // 0 // ---	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-1994629	atttagattttctgca[G/T]agttttcccacagaat	G	T	KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 158095 // Hs.99439	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-2240979	ctgagatatggtataa[A/T]cttttgttaagtcaat	A	T	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 535253 // Hs.435730 //	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2273211	gactcagattccttaa[C/T]gcttgatacttggctt	C	T	2001 // Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // upstream // 106154 // Hs.11713 // ELF5 //	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13
SNP_A-2303818	gctcagtatgattgca[G/T]agagcccagttttggg	G	T	// 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream //	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-2311337	ggaatagttaaacact[A/T]aatgccttagccatct	A	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 294094 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2301261	gccttgtaatacacaa[C/T]aagaaaagtcacatag	C	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2229008	ctagcacctgcactaa[C/T]gcttcccagtgtgaac	C	T	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2197465 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2002929	accctgattttcttca[A/T]gatctgactgcttcgg	A	T	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 733745 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2018389	taggaccaccatcata[C/T]acgtcgtccattgttc	C	T	539 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP /// NM_172201 // upstream // 255992 // Hs.512862 // KCNE2 // 9	ATP5O	ATP5O, Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP q22.11
SNP_A-2017270	gttcttatcattcctc[A/G]gaaggtatatcataat	A	G	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 748714 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2034339	aaatcctttcaaatgc[A/G]aaagtttttccaaacc	A	G	3613 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2076683	acattttccaagcaca[C/T]ctggtacctagccagg	C	T	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 193956 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2103946	agcactggtatcaata[C/T]gaaaatcaatgtcttt	C	T	FLJ12985 // 79986 // Homo sapiens hypothetical protein FLJ12985 (FLJ12985), mRNA. /// ENST00000313956 //	FLJ12985	FLJ12985, Homo sapiens hypothetical protein FLJ12985 (FLJ12985), q13.41
SNP_A-2115088	agggctatggacccaa[A/G]cattactctctcctgg	A	G	/// ENST00000340135 // upstream // 12917 // --- // --- // --- // --	-	p15.1
SNP_A-2128524	ataatacagtttccaa[C/T]gtaagtgggtcaaaca	C	T	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 225790 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2157712	attgcatagtcactta[A/G]gtgtttccggccctga	A	G	Homo sapiens FLJ10378 protein (FLJ10378), transcript variant 1, mRNA. /// NM_032239 // intron // 0 // Hs.480712 //	FLJ10378	FLJ10378, Homo sapiens FLJ10378 protein (FLJ10378), transcript variant 1, q28.2
SNP_A-2152195	attaaagaagcaaaaa[A/C]agacagttaactggtt	A	C	Homo sapiens ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) (UBE2D2), transcript variant 2, mRNA. ///	UBE2D2	UBE2D2, Homo sapiens ubiquitin-conjugating enzyme E2D 2 (UBC4 q31.2
SNP_A-2141110	atctggaaggttctca[A/G]tgacagttccagaatg	A	G	Homo sapiens hypothetical protein MGC29643 (MGC29643), mRNA. /// ENST00000345008 // intron // 0 // --- // --- // --- // ---	LYPDC1	LYPDC1, Homo sapiens hypothetical protein MGC29643 (MGC29643), q21.2
SNP_A-2141907	atcttgtgaccacaca[C/T]ggacaaatcttcaata	C	T	10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 9473 // Hs.489615 // PBEF1 // 10135 // Homo	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-1832708	tacaagacagtaataa[G/T]ggttagagaccatgtt	G	T	Homo sapiens macrophage receptor with collagenous structure (MARCO), mRNA. /// ENST00000327097 // intron //	MARCO	MARCO, Homo sapiens macrophage receptor with collagenous structure (MARCO), q14.2
SNP_A-1841153	tagctttatggctcca[A/G]agagtatggaagactc	A	G	// 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream //	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-1819004	gttgcagaccagaggc[A/G]cagccaggctgagagg	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-1858194	tcagaacattgataga[A/C]ctcctaattaatttgc	A	C	ENST00000312504 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1873493	tctcaatattcacaaa[A/G]gatagttacaacaatc	A	G	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 944539 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1805697	gtcccagagaaaacca[C/T]gacaaggagcaaagcc	C	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-1792203	gggttaggaggaggag[A/C]atatgtggtgtgattg	A	C	ENST00000333722 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-1647820	tcagtggctggcaattagtcgatac[C/T]aaatagatacgtattaagagatagc	C	T	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // solute carrier family 22 (extraneuronal monoamine transporter), member 3	SLC22A3	SLC22A3 , rs2063345, solute carrier family 22 (extraneuronal monoamine transporter), member 3,q25.3
SNP_A-1701429	tgactgaaggtgtataattaataac[A/G]acttgggactagctataatgtgtaa	A	G	26235 // F-box and leucine-rich repeat protein 4 /// NM_032511 // downstream // 143880 // Hs.16491 // C6orf168	FBXL4	FBXL4 , rs728758, F-box and leucine-rich repeat protein 4 ,q16.2
SNP_A-1934946	ttctgacctattgcca[A/G]cttcattacacacaac	A	G	51124 // Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), mRNA. /// ENST00000256433 // upstream // 644388 // --- // --- // --- // ---	IER3IP1	IER3IP1, Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), q21.1
SNP_A-1977200	aaatgattaagcaaat[G/T]aaattacatgtacata	G	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 231841 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1976293	caaaatcagcagcatt[C/G]aaaactagaccaagac	C	G	ENST00000265018 // intron // 0 // --- // --- // --- // ---	-	p15.32
SNP_A-1985624	tctactctcaaaagtg[A/C]aaatgacattaataac	A	C	56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream //	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1971619	taggatacgcaagcac[C/T]gtgaggagatcagcta	C	T	// Homo sapiens selectin E (endothelial adhesion molecule 1) (SELE), mRNA. /// NM_033418 // downstream // 17028 //	SELE	SELE, Homo sapiens selectin E (endothelial adhesion molecule 1) (SELE), q24.2
SNP_A-1969274	agattagctgttgtca[A/G]cccttaaaaaatctgg	A	G	/// ENST00000331037 // downstream // 893774 // --- // --- // ---	-	q21.1
SNP_A-1909628	tgtcaaatgatagtaa[A/G]gagttcttaaaactca	A	G	ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. ///	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-1905687	tggtatctttttcaca[C/T]tcccaacctaaagatg	C	T	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 545592 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1886813	tgactggaggtgctaa[C/T]tggggaagaattggtg	C	T	ENST00000334591 // CDS // 0 // --- // --- // --- // ---	-	q13.11
SNP_A-1972237	catttttaaatatgta[C/T]cactgtaactgacttt	C	T	// Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, mRNA. /// NM_201994 // upstream // 4371 // Hs.6651 // VAMP4 // 8674 // Homo	VAMP4	VAMP4, Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, q24.3
SNP_A-1973677	atttgaatagtggaaa[C/T]gggagttaatggagta	C	T	Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), mRNA. /// ENST00000193391 // intron // 0 // --- // ---	IMPG2	IMPG2, Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), q12.3
SNP_A-1962643	actccttttgccaca[A/G]tgtcttagacctggga	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1940400	ttgccaggcctgtgtc[A/G]cttgcccactcctgta	A	G	// 84986 // Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), mRNA. /// NM_005479 // upstream // 11733 //	ARHGAP19	ARHGAP19, Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), q24.1
SNP_A-1956049	tttgtgaaagagaccc[A/G]ccttgtccaaggacat	A	G	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 122384	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1956584	tttgtttgaatgcaaa[C/G]gaaactacagcccagg	C	G	1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 67838 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-1711270	aaattaatttgagagg[G/T]atcacaaacttagacg	G	T	203238 // chromosome 9 open reading frame 93 /// NM_173550 // upstream // 12141 // Hs.170652 // C9orf93 //	C9orf93	C9orf93 , rs1396705, chromosome 9 open reading frame 93 ,p22.3
SNP_A-1660161	taaatcgtaggcctttcgcctgtaa[C/T]acctgatccaaatcaatcccaaatg	C	T	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	ELOVL2	ELOVL2 , rs3798709, elongation of very long chain fatty acids (FEN1,p24.2
SNP_A-1742915	gctgtttcatatttttatgatctg[A/T]gtattcactggagaatcacttttaa	A	T	LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_004432 // upstream // 760129	LOC389708	LOC389708 , rs1162609, hypothetical gene supported by BC017510; BC046919 ,p21.3
SNP_A-1807874	gtcttagttgccctgg[A/T]acatgtaaaggaagga	A	T	Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1872142	tctactctctggtctc[A/G]gaacatcaacactggc	A	G	sapiens rap2 interacting protein x (RIPX), mRNA. /// ENST00000226328 // intron // 0 // --- // --- // --- // ---	RIPX	RIPX, Homo sapiens rap2 interacting protein x (RIPX), q13.3
SNP_A-1823812	taaaatgaggtcatac[C/G]ggagtaaggtgagttt	C	G	// 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1832641	tacaacccctccatta[C/T]cttaactccagctgat	C	T	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2152443	attaactgacagctca[C/T]ggaattatttgggcac	C	T	sapiens Fukuyama type congenital muscular dystrophy (fukutin) (FCMD), mRNA. /// NM_207647 // intron // 0 // Hs.132230 // MGC45564 // 405752 // Homo sapiens similar	FCMD	FCMD, Homo sapiens Fukuyama type congenital muscular dystrophy (fukutin) (FCMD), q31.2
SNP_A-2153975	attatataactaaaat[A/T]agtgctcaaaatacca	A	T	159296 // Homo sapiens NK2 transcription factor related, locus 3 (Drosophila) (NKX2-3), mRNA. /// NM_031212 //	NKX2-3	NKX2-3, Homo sapiens NK2 transcription factor related, locus 3 (Drosophila) (NKX2-3), q24.2
SNP_A-2127992	ataagatagcgcacgg[A/G]attgctaggcgcattc	A	G	3192 // Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA. /// NM_004501 // upstream //	HNRPU	HNRPU, Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, q44
SNP_A-2203531	ccagaagtccatgaac[A/C]acattggagaaccatt	A	C	Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 //	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-2212559	cccttatgaaaaagga[C/G]agaaatcactcagcca	C	G	// 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 5521 // --- // --- // --- // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2227443	ctacactgcaaggcca[C/G]gattgaaatccacaat	C	G	2315 // Homo sapiens melan-A (MLANA), mRNA. /// ENST00000251879 // downstream // 80534 // --- // --- // --- // --	MLANA	MLANA, Homo sapiens melan-A (MLANA), p24.1
SNP_A-2179475	cacttacaacatttag[A/G]attggtgtgattctta	A	G	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 //	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). q12.13
SNP_A-2179046	cactgctccatcactg[C/T]cacccactgtgtgcac	C	T	// 79947 // Homo sapiens dehydrodolichyl diphosphate synthase (DHDDS), transcript variant 1, mRNA. /// NM_205861 // downstream // 50839 // Hs.369385 // DHDDS	DHDDS	DHDDS, Homo sapiens dehydrodolichyl diphosphate synthase (DHDDS), transcript variant 1, p36.11
SNP_A-2095192	agaattcaaatagccc[A/C]acagattgtttctctt	A	C	Homo sapiens carboxypeptidase, vitellogenic-like (CPVL), transcript variant 2, mRNA. /// NM_031311 // intron // 0 // Hs.233389 // CPVL // 54504 // Homo sapiens	CPVL	CPVL, Homo sapiens carboxypeptidase, vitellogenic-like (CPVL), transcript variant 2, p15.1
SNP_A-2077212	accaagttgcactata[A/G]aacttaattcacctaa	A	G	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-2068457	acaagggtgacctcca[C/T]gtttaagccttctagc	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// ENST00000332068 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2030878	aaaggaactattcttc[A/G]ctacacgagcactaaa	A	G	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2000370	aagctgacagagaacc[A/G]atatgtcacacggcta	A	G	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 176903 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-1997217	aatgagctttgtcaag[C/G]agagagagtaagaaag	C	G	sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuclear gene encoding mitochondrial	AUH	AUH, Homo sapiens AU RNA binding protein,q22.31
SNP_A-1993530	aggatagacattagcc[A/T]ctcatcacatggtagg	A	T	// Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, mRNA. /// NM_032467 // upstream //	ASPH	ASPH, Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, q12.3
SNP_A-1993719	ttcaaaccatatcaca[C/T]cctgagccatcgctct	C	T	/// ENST00000357074 // downstream // 186012 // --- // --- // --- // --- /// ENST00000358765 // downstream // 186012 // --- // ---	-	p14
SNP_A-2276203	gagagagatacatcga[A/G]gaaaaatttgttgaac	A	G	Homo sapiens fibrous sheath interacting protein 2 (FSIP2), mRNA. /// ENST00000332540 // upstream // 142457 // --- // ---	FSIP2	FSIP2, Homo sapiens fibrous sheath interacting protein 2 (FSIP2), q32.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2283302	gatacaataagactga[C/T]agctagcttcacaaga	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1833455 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2288629	tctttagcatttgttg[A/G]atttttcttgaaaact	A	G	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2288323	gattctaggagctgaa[C/G]tcttgcagggatccag	C	G	54361 // Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), mRNA. /// ENST00000290167 // upstream // 169710 // --- // --- // --- // --- /// ENST00000354898	WNT4	WNT4, Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), p36.12
SNP_A-2307817	gcttcgtggtaatctc[A/G]ctgatgagtatttcaa	A	G	sapiens tumor protein p73 (TP73), mRNA. /// ENST00000160698 // intron // 0 // --- // --- // --- // --- ///	TP73	TP73, Homo sapiens tumor protein p73 (TP73), p36.32
SNP_A-2307728	gcttccctcggacatc[A/G]aactgtagtcccagat	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 369644 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2313813	ggagcatccatataac[C/T]ctaaggaaaggcatta	C	T	CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 //	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2267012	gaataaacatgagtta[C/T]ccagatgaaaatgcag	C	T	// 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// NM_002202 //	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-2233924	ctcatgatgggacata[A/G]aaacagaagaaattta	A	G	Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // --- // --- // --- // --- ///	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2247691	ctgtgaactacagaac[C/T]gaaacatcaatgtatg	C	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1997676	aatattttgctttaac[G/T]ctggaaacaagatttt	G	T	158399 // Homo sapiens mRNA for KIAA1962 protein. /// ENST00000259335 // upstream // 47289 // --- // --- // --- // ---	ZNF483	ZNF483, Homo sapiens for KIAA1962 protein. ,q31.3
SNP_A-2017935	tttgtttggtatccca[A/G]aggttcttcctctaag	A	G	1 // 337880 // Homo sapiens keratin associated protein 11-1 (KRTAP11-1), mRNA. /// NM_003253 // downstream // 7281	KRTAP11-1	KRTAP11-1, Homo sapiens keratin associated protein 11-1 (KRTAP11-1), q22.11
SNP_A-2010037	tgcaactagccagaga[C/T]gacacaagccatggaa	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1247941 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2044870	aagaacaaaaagaaag[C/T]cagcatgctcctaact	C	T	9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 135321 // --- // ---	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-2072001	acagaggatctgtgga[A/G]tagtgggtgcagggag	A	G	Homo sapiens protein kinase, DNA-activated, catalytic polypeptide (PRKDC), mRNA. /// ENST00000314191 // intron	PRKDC	PRKDC, Homo sapiens protein kinase, DNA-activated, catalytic polypeptide (PRKDC), q11.21
SNP_A-2081469	acctgtcagggttact[C/T]agctacctgacatttg	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2102605	agattgtcagccttca[C/T]atagccagcccaagtt	C	T	Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2174121	cacacctggctgtata[A/C]tagtttaaaataatgt	A	C	ENST00000274030 // intron // 0 // --- // --- // --- // ---	-	q26
SNP_A-2123979	agttaatgtatgtgaa[A/G]ctatttattagaacag	A	G	// 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 134995 // Hs.156832 // NPAS2	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-2131277	atagaggttaggactg[C/T]attaggggagaaagat	C	T	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 605571 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1838373	tagaagtggtgaccat[A/G]aagaaaagtttcttgg	A	G	Homo sapiens axonemal dynein light chain (hp28) mRNA, complete cds. /// NM_003462 // downstream // 34132 //	DNALI1	DNALI1, Homo sapiens axonemal dynein light chain (hp28) complete cds. ,p34.3
SNP_A-1822450	gtttttatttctcaga[A/T]aaatgatacaatttag	A	T	// Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), mRNA. /// ENST00000331299 // intron // 0 // --- // --- // --- // ---	SLC25A21	SLC25A21, Homo sapiens solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (SLC25A21), q13.3
SNP_A-1863847	tccaataggaacaaga[C/G]atgaaaggaaagtcca	C	G	Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-1811898	gtggaaacattaagag[C/T]ctccatttctgcatta	C	T	SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 156441 // --- // --- // --- // ---	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31
SNP_A-1791730	gggtctggagtgcact[G/T]agaggaggaaggtggg	G	T	Homo sapiens SKB1 homolog (S. pombe) (SKB1), mRNA. /// ENST00000324366 // intron // 0 // --- // --- // --- // --- ///	SKB1	SKB1, Homo sapiens SKB1 homolog (S. pombe) (SKB1), q11.2
SNP_A-1789240	gggcatgatgctttac[A/C]caactttcaaagtaga	A	C	23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 187199 // Hs.160574	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1961549	ttttttgtctgatta[C/T]gtcatttcaaaaagtt	C	T	153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 639932 // Hs.424156 // IRX1 //	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-1949198	tttatgggtattacca[C/T]gatttattttccatta	C	T	sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA. /// ENST00000223336 // intron // 0 // --- // --- // --- // ---	FLJ10803	FLJ10803, Homo sapiens hypothetical protein FLJ10803 (FLJ10803), p13
SNP_A-1882263	tgaaaaatattatgta[A/G]ctggaatcaaactgtc	A	G	ENST00000354796 // intron // 0 // --- // --- // --- // ---	-	q21.13
SNP_A-1884406	tgaagtcaaaggacta[A/G]aggacctcttctttct	A	G	9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 114748 //	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1892867	tgcaccatgaccctcc[A/G]ctgacctttgacctga	A	G	Homo sapiens T, brachyury homolog (mouse) (T), mRNA. /// NM_175922 // downstream // 49025 // Hs.119062 //	T	T, Homo sapiens T, brachyury homolog (mouse) (T), q27
SNP_A-1894306	tgcattgttagaaata[C/T]gcactgaagccaaggc	C	T	// 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1895083	tgcccagtgatgagaa[G/T]tgaggaccagaacctg	G	T	// 8802 // Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA. /// ENST00000331369 //	SUCLG1	SUCLG1, Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), p11.2
SNP_A-1904933	tgggtagatcttatcc[G/T]atcagtttgtatcctg	G	T	// 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 3024737 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1911256	tgtctggtataaataa[A/C]tactgggctgagaggg	A	C	Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-1920337	ttaatgtaaccaagaa[A/G]ttaaatcaatctatgc	A	G	1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream //	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-1929670	ttcatatctccatgca[G/T]tgatttttttttctc	G	T	3176 // Homo sapiens histamine N-methyltransferase (HNMT), mRNA. /// ENST00000272643 // downstream //	HNMT	HNMT, Homo sapiens histamine N-methyltransferase (HNMT), q22.1
SNP_A-1905158	ctttgtcattagtaac[A/G]actttgtctaacaca	A	G	// Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1170509 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1906524	tggtgggatagcttac[A/T]aactgggccccttcct	A	T	LOC346673 // 346673 // Homo sapiens STRA8 (LOC346673), mRNA. /// NM_013316 // downstream // 51557	LOC346673	LOC346673, Homo sapiens STRA8 (LOC346673), q33
SNP_A-1881358	tctttcatattcacca[C/T]gactctgaaggtgtga	C	T	Homo sapiens PX domain containing serine/threonine kinase (PXK), mRNA. /// ENST00000302779 // intron // 0 // --- // --- //	PXK	PXK, Homo sapiens PX domain containing serine p14.3
SNP_A-1956116	tttgtgcataaagaag[C/T]atagaagtagagtgtg	C	T	// Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1255683 // Hs.435458 // SETBP1	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1943732	ttgtagaaaatgacaa[A/G]aaatgagagttgaatt	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 594365 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1946974	tttaagtgagagagaa[C/T]tgaactggttttaatg	C	T	Homo sapiens sorting nexin 25 (SNX25), mRNA. /// ENST00000264694 // intron // 0 // --- // --- // --- // --- ///	SNX25	SNX25, Homo sapiens sorting nexin 25 (SNX25), q35.1
SNP_A-1945050	ttgtgtacttacatta[C/T]ctttcaggaaaaagaa	C	T	Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 34708 // Hs.434435 // ALDH1L1 // 10840 // Homo	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-1936438	ttcttcttgcaggatt[G/T]aacttttttaaatgt	G	T	Homo sapiens TRAF interacting protein (TRIP), mRNA. /// ENST00000331456 // intron // 0 // --- // --- // --- // ---	TRIP	TRIP, Homo sapiens TRAF interacting protein (TRIP), p21.31
SNP_A-1938074	ttgacaagacaaaggc[A/G]agtggctctatcttta	A	G	55636 // Homo sapiens mRNA for KIAA1416 protein, partial cds. /// ENST00000307121 // downstream // 61167 // --- // ---	CHD7	CHD7, Homo sapiens for KIAA1416 protein, partial cds. q12.2
SNP_A-1968896	taaaaagtgcaacata[A/G]aagttacggactaaac	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 333664 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1969390	aaatacagttaaatac[A/C]agcaataagttctaat	A	C	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-1866271	tcccatccaactgtaa[C/T]aaaatgtggttgatga	C	T	Homo sapiens transforming growth factor, alpha (TGFA), mRNA. /// ENST00000295400 // intron // 0 // --- // --- // --- // ---	TGFA	TGFA, Homo sapiens transforming growth factor, alpha (TGFA), p13.3
SNP_A-1822077	gttttcgacactggac[C/T]ggaagaacaagtctat	C	T	sapiens hypothetical protein FLJ37587 (FLJ37587), mRNA. /// ENST00000310903 // 3UTR // 0 // --- // --- // --- // ---	FLJ37587	FLJ37587, Homo sapiens hypothetical protein FLJ37587 (FLJ37587), q24.11
SNP_A-1836667	ctcagacaagaagtac[A/G]ggaaacactcctcaca	A	G	ENST00000311434 // intron // 0 // --- // --- // --- // ---	-	p13.1
SNP_A-2126933	ataaaggcagtcatct[C/T]aacgacttttttaaga	C	T	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 50339 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2129393	atacaaggaatgtgga[A/G]gttttgtgaaagctgc	A	G	// 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 198840 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2118037	agtaaaaaggagccca[A/T]tgctaattactaagac	A	T	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2159199	atttaaacttgttaga[C/T]gaacactatatgtaat	C	T	// 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1540970 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2164711	caaacagtagaggtga[C/T]ggatcaattaaaatta	C	T	// 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 638209 // --- // --- // --- //	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2164314	caaaatcacaaaataa[A/G]aaaagctctgggagtt	A	G	Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA. /// ENST00000344836 // intron // 0 // --- // --- // --- // ---	USP7	USP7, Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), p13.2
SNP_A-2147726	atggcagcttgcctcc[A/G]cctgcacctgaatggg	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2174511	cacagagaagaatgaa[C/T]gaaaggagcagaatat	C	T	10133 // Homo sapiens optineurin (OPTN), mRNA. /// NM_021980 // downstream // 7596 // Hs.332706 // OPTN //	OPTN	OPTN, Homo sapiens optineurin (OPTN), p13
SNP_A-2224038	cggggtgaggcagagc[A/G]aaaagcaaggagacac	A	G	ENST00000358245 // intron // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-2213876	cctaaatacttttgac[C/T]cttgaacaatctgaac	C	T	sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // --- // --- // --- // ---	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-2217913	cctgcagagaacgaag[A/G]acaggaaacttgcccc	A	G	646 // Homo sapiens basonuclin 1 (BNC1), mRNA. /// AF036272 // upstream // 50754 // Hs.458285 // SH3GL3 //	BNC1	BNC1, Homo sapiens basonuclin 1 (BNC1), q25.2
SNP_A-2066464	aatttttatcactcta[A/T]taagtgtctactgcta	A	T	ENST00000341845 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2062420	aatgtacccccttact[C/G]aaacagatagtagtaa	C	G	Homo sapiens PTPRF interacting protein, binding protein 2 (liprin beta 2), mRNA (cDNA clone MGC:26737 IMAGE:4826610), complete c /// ENST00000299492 // intron // 0 // --- // --- // --- // ---	PPFIBP2	PPFIBP2, Homo sapiens PTPRF interacting protein, binding protein 2 (liprin beta 2), (cDNA clone MGC:26737 IMAGE:4826610), complete c ,p15.4
SNP_A-2060254	aatgaagacacaaact[C/T]acttttcctcagttta	C	T	196410 // Homo sapiens hypothetical protein MGC17301 (MGC17301), mRNA. /// AF032108 // downstream // 38975 //	MGC17301	MGC17301, Homo sapiens hypothetical protein MGC17301 (MGC17301), q13.2
SNP_A-2054417	aagtttaggaggaacg[C/T]atctgtaccatgtggg	C	T	4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // upstream	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-2048148	aagcaccaaatactac[C/T]actaaaagactgcaag	C	T	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2022618	aaaaatgcaataccaa[C/T]atgtcctgatactcag	C	T	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 488693 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2021485	aaaaaagtggtagaaa[C/G]agctagacagggaatc	C	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2011520	agctctggcagtctca[G/T]agcaggagccagctca	G	T	Homo sapiens chromosome 6 open reading frame 145 (C6orf145), mRNA. /// ENST00000306328 // intron // 0 // --- // ---	C6orf145	C6orf145, Homo sapiens chromosome 6 open reading frame 145 (C6orf145), p25.2
SNP_A-2018169	atgaaagttattcttc[C/T]ataaagaggcacagat	C	T	// 59271 // Homo sapiens chromosome 21 open reading frame 63 (C21orf63), mRNA. /// NM_018277 // downstream //	C21orf63	C21orf63, Homo sapiens chromosome 21 open reading frame 63 (C21orf63), q22.11
SNP_A-1995838	caagctttctatacca[C/G]tgacattgatttgata	C	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 882624 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1992053	gacatcacctggtgcc[A/G]gaagttttctgtgtcc	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 937313 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1991437	ttttccatcatccaaa[A/G]tctttaataagaggat	A	G	// 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2270579	gacagaggtaagtcac[C/T]ggactctgtaaaatcc	C	T	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1368837 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2310051	ggaaattattccaaca[A/T]cttatgtcctctatcc	A	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2304666	gctctgagttcctggg[C/T]catcgttctccctgga	C	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2288316	gattctacccagagaa[A/C]tagtgacagctgtctc	A	C	ENST00000360245 // downstream // 5635 // --- // --- // --- // ---	-	q11
SNP_A-2294390	gcaggtgtctccacat[A/T]agaagcatcctatgta	A	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2291259	gcaatgaaaaataacc[A/G]caaaaactcagaagac	A	G	/// ENST00000358396 // downstream // 718095 // --- // --- // ---	-	p12.2
SNP_A-2249249	cttaaaaaacaacaac[A/G]acaaaatgatccccca	A	G	ENST00000303153 // intron // 0 // --- // --- // --- // --- /// ENST00000321078 // intron // 0 // --- // --- // --- // --- ///	-	p11.2
SNP_A-2252983	cttctccacctggctg[A/C]atggtccacaaatgga	A	C	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2000001	ttttccagcaagccaa[C/G]accagattacaaaaga	C	G	83931 // Homo sapiens Ser/Thr-like kinase (MGC4796), mRNA. /// NM_032881 // downstream // 2412 // Hs.3496 //	MGC4796	MGC4796, Homo sapiens Ser p34.3
SNP_A-2044310	aactttgttgagaaaa[C/T]tgtaaagtaataaaag	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2045835	aagacataaagtcatc[A/G]atatctagggaaatct	A	G	ENST00000343093 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2046259	aagagaaaagtaggta[A/G]attggtcagtatgaat	A	G	Homo sapiens hypothetical protein MGC11332 (MGC11332), mRNA. /// ENST00000258436 // intron // 0 // --- // --- // --- // ---	MGC11332	MGC11332, Homo sapiens hypothetical protein MGC11332 (MGC11332), q12.1
SNP_A-2047292	aagatatttcaccctc[A/T]aggaggcagaggacaa	A	T	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2106583	agcctcattgtggtgg[A/G]ataaatcctggaaatc	A	G	// 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA. /// NM_032813 // upstream // 267460 //	FLJ14624	FLJ14624, Homo sapiens hypothetical protein FLJ14624 (FLJ14624), q32.3
SNP_A-2089779	acttcctgattctcct[C/G]aactcatttctggtct	C	G	LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// NM_138551 // upstream	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-2088589	actgtcttcattagta[A/C]gtacatcaatatcact	A	C	sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-2091872	agaaaatgtttggaaa[A/G]tgtaagataccacatt	A	G	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA.	CAMK2D	CAMK2D, Homo sapiens calcium,q26
SNP_A-2219048	cctgtaaatagactca[A/G]tctcccaattgtgtgg	A	G	SLC16A10 // 117247 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), mRNA. /// NM_153369 // upstream // 21584 // Hs.400572 //	SLC16A10	SLC16A10, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), q21
SNP_A-2214797	cctagttaataaatag[C/G]agtcataggaccatta	C	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 843652 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2170729	caagttgagcttaaaa[A/G]tacatcttggaggccg	A	G	Homo sapiens importin 11 (IPO11), mRNA. /// ENST00000325324 // intron // 0 // --- // --- // --- // ---	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1
SNP_A-2179293	cactgtccagatgaaa[C/G]ggtgtacaaaaaggag	C	G	7010 // Homo sapiens TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) (TEK), mRNA. /// ENST00000354568 // downstream // 30251	TEK	TEK, Homo sapiens TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) (TEK), p21.2
SNP_A-2176877	caccgcttcctccatc[A/G]aaggcacccaactgct	A	G	Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, mRNA. /// NM_022114 // intron // 0 //	PRDM16	PRDM16, Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, p36.32
SNP_A-2142976	atgaatcaggaaccaa[C/T]gaatggaaatgagagt	C	T	// 28965 // Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), mRNA. /// NM_014031 // downstream // 13716 // Hs.49765 // SLC27A6 // 28965 //	SLC27A6	SLC27A6, Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), q23.3
SNP_A-1829904	taataagtgattgttc[A/G]cagataacagtgacta	A	G	// 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1554952 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1843467	tagtgagtggcagatc[C/T]cttaaattctgtacaa	C	T	NM_001503 // intron // 0 // Hs.512001 // GPLD1 // 2822 // Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, mRNA. /// ENST00000230036 // intron // 0 // --- // --- // --- // ---	GPLD1	GPLD1, Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, p22.2
SNP_A-1821801	gttttaccactgccta[C/T]gggcaaagaattgaat	C	T	256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 54062 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1822667	taaaaaaaggtgcaga[A/G]taccatggaagttttt	A	G	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 150968 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1825326	taaagttgcaagatac[A/G]aagtcaaaatacaaaa	A	G	// 80195 // Homo sapiens chromosome 10 open reading frame 57 (C10orf57), mRNA. /// ENST00000256052 //	C10orf57	C10orf57, Homo sapiens chromosome 10 open reading frame 57 (C10orf57), q22.3
SNP_A-1856369	tcacaccagtccaaac[A/G]gctattactaaataaa	A	G	64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 63986 // Hs.391781 // PCDH20	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1935601	ttctgtaatatgaaaa[A/G]tagattgactaataaa	A	G	219899 // Homo sapiens hypothetical protein MGC10233 (MGC10233), mRNA. /// ENST00000284259 // intron // 0 // ---	MGC10233	MGC10233, Homo sapiens hypothetical protein MGC10233 (MGC10233), q23.3
SNP_A-1947627	tttaccttcgaatacc[A/G]aggattgtgctataaa	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1940096	ttgcagtcctagaaag[C/T]ataggtcctgataaat	C	T	// 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 187169 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1957528	ttttatagcttaaaaa[C/T]acgaaattcctcttag	C	T	902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 565079 // Hs.379972 //	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1953435	tttgaactgtcactca[A/G]ctacaaaaaatattca	A	G	Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // --- // --- // --- // ---	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-1880977	tcttgtggtcaaggag[A/C]attcaaaagagcagga	A	C	// 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// NM_207503 // downstream //	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-1886375	tgaccttcagggtgct[A/G]acaaaattggaaagca	A	G	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 132552 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1896774	tgctatttatacctca[A/G]taatgtcacagataag	A	G	84250 // Homo sapiens ankyrin repeat domain 32 (ANKRD32), mRNA. /// ENST00000265140 // downstream //	ANKRD32	ANKRD32, Homo sapiens ankyrin repeat domain 32 (ANKRD32), q15
SNP_A-1922211	ttacttcttatctcac[C/G]cctttcctaaaatccc	C	G	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), mRNA. /// ENST00000355685 // intron // 0 // --- //	GALNT13	GALNT13, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), q23.3
SNP_A-1905657	tggtatataaataagt[G/T]aatgtgcagctgaaca	G	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q35.1
SNP_A-1893025	tgcactgccagttgca[C/T]aaaagtatagcacata	C	T	133 // Homo sapiens adrenomedullin (ADM), mRNA. /// NM_000480 // upstream // 46714 // Hs.501890 // AMPD3 //	ADM	ADM, Homo sapiens adrenomedullin (ADM), p15.4
SNP_A-1904156	tgggccatctgcctag[A/T]atcccaatgctttgag	A	T	// Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // intron // 0 // --- // --- // --- // ---	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1881208	tctttataatgcacaa[C/T]tgattgtgtgtgtgag	C	T	2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream //	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1948400	tttagtaaagagtaga[A/G]gttggaagaaaaatgc	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 285148 // --- // --- // --- //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1950147	tttcactctcaccata[C/T]agtaaaataggcaggt	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2243772 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1955376	tttggggtacactgaa[A/G]taagaagcagaccctt	A	G	// Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 299241 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1960010	ttttgttattttggta[C/T]aatttgaggagtccca	C	T	27178 // Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, mRNA. /// NM_014439 //	IL1F7	IL1F7, Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, q13
SNP_A-1973507	aggttttctttccaag[C/T]atatggggctgggaca	C	T	IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p11.2
SNP_A-1981165	agaatgtgtccaaaaa[A/C]tgaatgctaagcattc	A	C	Homo sapiens natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) (NPR3),	NPR3	NPR3, Homo sapiens natriuretic peptide receptor C p13.3
SNP_A-1846061	gtaaactgttatttgc[A/G]aggaaatgctctattt	A	G	57532 // Homo sapiens 82-kD FMRP Interacting Protein (182-FIP), mRNA. /// NM_020791 // upstream // 70116 //	182-FIP	182-FIP, Homo sapiens 82-kD FMRP Interacting Protein (182-FIP), q11.2
SNP_A-1851603	tattctctgaaaatca[A/G]acatctaatattcagc	A	G	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // ---	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1866248	tcccatagctgacaac[C/G]aaggggaaacacaggc	C	G	// 5265 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran /// NM_001002236 // upstream // 23336 // Hs.525557 // SERPI	SERPINA1	SERPINA1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran q32.13
SNP_A-1864101	tccacagtgaggtcca[C/T]taagcacactgcaaat	C	T	4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream //	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-1815950	gttaattcttcaccta[C/T]gcatattggctcgggc	C	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 633195	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1829382	taagtcctgccccta[C/T]gctctccatgtctgtc	C	T	// Homo sapiens poly (ADP-ribose) polymerase family, member 3 (PARP3), transcript variant 1, mRNA. /// NM_001003935 // intron // 0 // Hs.271742 // PARP3 // 10039	PARP3	PARP3, Homo sapiens poly (ADP-ribose) polymerase family, member 3 (PARP3), transcript variant 1, p21.2
SNP_A-1811940	gtggaaccccagtata[C/T]acaggtcagaggcatg	C	T	219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA. /// NM_181698 // downstream //	C10orf9	C10orf9, Homo sapiens chromosome 10 open reading frame 9 (C10orf9), p11.21
SNP_A-1810207	gtgatgaaaatattgc[A/G]gaatgagatagtagtc	A	G	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 608447 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800484	gtactgctgctctcat[C/T]actatctttcctcta	C	T	51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 185320 // Hs.271977	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-1785193	ggctaatatgaatgac[A/G]cctacttctttctcat	A	G	Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// ENST00000282902 // intron // 0 // --- // --- // --- // ---	VMP	VMP, Homo sapiens vesicular membrane protein p24 (VMP), p22.2
SNP_A-1660525	cctctattttgaaatggtataatag[A/G]agtgccaataaagatatatactgtc	A	G	NM_014895 // intron // 0 // - // - // - // -	-	- , rs10498937, -,q14.2
SNP_A-2141945	atctttaactctctta[C/T]gggtgaaaagaaggtt	C	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 3126670 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2164544	caaacaaaaaaaacaa[C/T]gcttgcagtaagccag	C	T	Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // --- // ---	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-2133052	atatactgccatttaa[A/G]caagatttctgctgta	A	G	344901 // Homo sapiens osteocrin (OSTN), mRNA. /// NM_198152 // downstream // 5976 // Hs.518492 // URP //	OSTN	OSTN, Homo sapiens osteocrin (OSTN), q28
SNP_A-2213964	cctaacctgcaatttc[C/G]ctgggttaactcctac	C	G	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2089305	acttagccttctgtta[C/T]gattctaagtttcctg	C	T	// 7558 // Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), mRNA. /// ENST00000331170 // downstream //	ZNF11B	ZNF11B, Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), q11.21
SNP_A-2054776	aataaacaatttcagc[A/G]aagtctcagggatata	A	G	endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 809122 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-2053225	aagtcttgggtgacca[A/G]aaagtcccttcagaaa	A	G	138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 5310 // --- // OR13C2 //	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-2057016	aatagtggtgctcaga[G/T]actcccatcgaaaaaa	G	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-2067203	acaaagccttgaactc[A/G]aagacagctgtgggaa	A	G	// 166614 // Homo sapiens hypothetical protein MGC45428 (MGC45428), mRNA. /// NM_006726 // downstream // 3398 //	DCAMKL2	DCAMKL2, Homo sapiens hypothetical protein MGC45428 (MGC45428), q31.23
SNP_A-2065205	aattggatgagtaaca[A/T]attgtcagttttcaat	A	T	Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // intron // 0 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-2001618	catataaggaaagcaa[C/G]gctgtagaattaagaa	C	G	3632 // Homo sapiens inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA. /// ENST00000320970 // upstream	INPP5A	INPP5A, Homo sapiens inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), q26.3
SNP_A-2252872	cttctatcatacgaca[A/G]tccacaccaccctacc	A	G	Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // --- // ---	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-2231709	ctcaaaaagtagaccc[A/G]atagtgaatacaaaga	A	G	Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// ENST00000287647 // intron // 0 // --- //	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-2262233	gaaatctaaggcaata[C/T]ggtaagcttttctaat	C	T	130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // ---	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-2287489	gatgttggctgaaaca[C/T]tggatcattgtcttac	C	T	MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000315302 //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2289848	gcaaaccaggacacag[A/G]accaatttcaccagtt	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2296898	gccaaggaaagggaga[A/C]aacttatgattccctg	A	C	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2290195	gcaaattaaaatacac[A/G]cacagaaagcaaaatt	A	G	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2307534	gcttcaatgcccagca[G/T]gatctaacccctgcct	G	T	9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 38713 // Hs.458423	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-2284967	gatccctagacctcca[C/T]agacttttgaatttgc	C	T	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 988487 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2262097	gaaatatgtatgtcac[A/G]aatcttagcttaaatt	A	G	Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // --- // --- // --- // ---	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-2252361	cttcccttgctacgaa[C/T]agtaactcattgttaa	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 492517 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1990502	ctcttttgggaataga[C/T]taaaagtgagatgtac	C	T	// Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// ENST00000333190 // intron // 0 // --- // --- // --- // ---	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-1994350	acatttgtcagtcagc[A/G]acaggctttgcagaaa	A	G	PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream //	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-2034894	aaatgaggaagaagcg[A/C]acgtgagaacccctgg	A	C	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2038073	aacacacatttcagag[C/G]agttacttgttccata	C	G	1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 3149227 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2060469	aatgacagggttggaa[C/T]agaattctctggttcc	C	T	55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// NM_013349 // upstream // 16723 //	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-2103191	agcaacggtcctccaa[C/T]aagggctaagagtaaa	C	T	Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA. /// ENST00000265022 // intron // 0 // --- // --- // --- // ---	DGKG	DGKG, Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), q27.2
SNP_A-2094063	agaaggaaatttaaaa[A/C]ttcaggcagcaagggg	A	C	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 7577 //	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2187144	caggtcctctgaaaag[C/T]aggtgcccagacataa	C	T	// Homo sapiens hypothetical protein FLJ10116 (FLJ10116), mRNA. /// NM_018441 // downstream // 1578 // Hs.281680 //	DSU	DSU, Homo sapiens hypothetical protein FLJ10116 (FLJ10116), q35
SNP_A-2188432	cagtgaagaggcataa[A/G]tggccaattactctta	A	G	// 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-2185239	caggaagagccataga[A/G]agaaaagagagaaaca	A	G	Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // --- // --- // --- // --- ///	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2122705	agtggagaaaagcaac[C/G]agacagcgagaaagtc	C	G	Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// ENST00000334383 // intron // 0 // --- // --- // --- // ---	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27
SNP_A-2112508	aggcacagacacaagc[G/T]cccagtcctgtcctac	G	T	/// ENST00000332560 // upstream // 179536 // --- // --- // --- // ---	-	q21.1
SNP_A-2144305	atgagtgttttcagga[C/T]agggctactgtagctt	C	T	3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 221965 // Hs.118695 // KCNG1	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2143548	atgactgaactgtaca[A/G]agtagagaattcttgg	A	G	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2141212 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2149062	atggtttggatgcacc[A/G]ctccacaaaggcaggg	A	G	Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, mRNA. /// NM_024494 // intron // 0 // Hs.258575 // WNT2B // 7482 //	WNT2B	WNT2B, Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, p13.2
SNP_A-2146738	atgcttattggataga[C/T]gcagtttcccttccag	C	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1751411	ctttctagacttaattctgtttcat[C/T]aatctactgtttatccatgtgctaa	C	T	6469 // sonic hedgehog homolog (Drosophila) /// NM_032625 // downstream // 698735 // Hs.124854 // C7orf13 // 129790 //	SHH	SHH , rs963933, sonic hedgehog homolog (Drosophila) ,q36.3
SNP_A-1727637	tacaaaggagctttcttagaaaagg[A/C]tttgtgatctgtgcattcgtctcac	A	C	AF277624 // upstream // 4516030 // Hs.336957 // ZNF479 // 90827 // zinc finger protein 479	ZNF479	ZNF479 , rs2382591, zinc finger protein 479,q11.21
SNP_A-1805620	gtccatgaatgaatgg[A/C]atttggtaaaaaagag	A	C	sapiens carboxypeptidase E (CPE), mRNA. /// ENST00000261510 // intron // 0 // --- // --- // --- // --- ///	CPE	CPE, Homo sapiens carboxypeptidase E (CPE), q32.3
SNP_A-1806148	gtcctctttctcaaaa[A/T]tagcaaagaactatcc	A	T	// 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 877471 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1812538	gtggcctatttctagc[C/T]ctccactgtgctgaat	C	T	2866 // Homo sapiens G protein-coupled receptor 42 (GPR42), mRNA. /// NM_005306 // upstream // 53488 //	GPR42	GPR42, Homo sapiens G protein-coupled receptor 42 (GPR42), q13.12
SNP_A-1792509	ggtaaaaaataataga[A/G]actatgactgcatttg	A	G	60370 // Homo sapiens arginine vasopressin-induced 1 (AVPI1), mRNA. /// NM_031484 // upstream // 12462 //	AVPI1	AVPI1, Homo sapiens arginine vasopressin-induced 1 (AVPI1), q24.2
SNP_A-1792893	ggtaattaggaaatca[A/G]aaccttgaggaattat	A	G	/// ENST00000330649 // upstream // 892157 // --- // --- // --- // ---	-	q11.2
SNP_A-1832946	tacaatttctacaaac[A/G]ataataatctgctgat	A	G	// 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 325828 //	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1840543	tagcccacagtgaaaa[C/G]ctcaagaaagaaaaaa	C	G	// Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, mRNA. /// NM_003894 // upstream //	PER2	PER2, Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, q37.3
SNP_A-1973760	ctttagattggactac[C/T]aacctttagaagtctt	C	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1963656	ggaggtggtcacagaa[C/T]aaatgatggtatcaaa	C	T	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 244750 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1950794	tttcattttgcaacaa[A/G]agaatccattcaaaaa	A	G	5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// NM_017935 // upstream // 227109 //	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1944600	ttgtgaacttatttgg[C/T]atccccagcaacctta	C	T	Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA. /// ENST00000328939 // intron // 0 // --- // --- // --- // ---	KCNIP1	KCNIP1, Homo sapiens Kv channel interacting protein 1 (KCNIP1), q35.1
SNP_A-1880414	tcttgacccagtttca[C/T]gaatttttcgacactg	C	T	Homo sapiens steroid sensitive gene 1 (URB), transcript variant 2, mRNA. /// NM_199511 // intron // 0 // Hs.477128 //	URB	URB, Homo sapiens steroid sensitive gene 1 (URB), transcript variant 2, q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1917320	tgttttcctaagttaa[A/T]agcgttgaaattccaa	A	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 373462 // --- // --- // --- //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1919989	ttaatagaaatcggac[C/G]actgcagccttctct	C	G	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-1930271	ttcattggcattagta[A/G]gtgaccatagaaaatg	A	G	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 148019 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-1921045	ttacaggatttcagcc[C/T]atgatatattacacta	C	T	Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1914745	tgttacatggagccca[A/G]tacattttattaagtg	A	G	// 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	MLLT3	MLLT3, Homo sapiens myeloid,p21.3
SNP_A-1906041	tggtctcatccatcca[G/T]agatgtcattgtgcag	G	T	590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 116256 // --- // --- // --- //	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1907765	tgtaaggacccccaaa[C/T]ctgtagcccattgctc	C	T	2199 // Homo sapiens fibulin 2 (FBLN2), transcript variant 2, mRNA. /// NM_001004019 // downstream // 1483 //	FBLN2	FBLN2, Homo sapiens fibulin 2 (FBLN2), transcript variant 2, p25.1
SNP_A-1878355	tctgtctgtacaagta[A/C]gaatttgtatactagg	A	C	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1885892	tgacatcaaatctttc[A/G]atacatctcactggtt	A	G	163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 13344 // Hs.221375 //	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-1898405	tgcttcccagattttg[C/T]agcaaccctatgtcaa	C	T	25963 // Homo sapiens DKFZP564G2022 protein (DKFZP564G2022), mRNA. /// ENST00000249651 // intron // 0 // --- // --- // --- // ---	DKFZP564G2022	DKFZP564G2022, Homo sapiens DKFZP564G2022 protein (DKFZP564G2022), q15.1
SNP_A-1945665	ttgttgagcaatctta[G/T]gataacaagcaaaatt	G	T	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-1937416	gggcttgtaggatgaa[C/T]tgcacggcccaatata	C	T	GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 95509 // Hs.514980 //	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-1959765	ttttggttcaactcaa[C/T]ttctgatcaagggcaa	C	T	Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron //	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-1961602	ttttttttgcacatac[A/G]atctcactctgttgcc	A	G	54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 230779 // ---	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-1961883	cccagagacttcatgc[C/T]gagcttagatagtcct	C	T	sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1982018	ttgcaatagaggtgtg[C/T]atacagagaacttttt	C	T	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 348282 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1829447	taagtgacacatttca[C/T]gagacaaccagatgtc	C	T	PDZRN4 // 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 //	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12
SNP_A-1817142	gttcaacttgctagaa[A/G]ctttgtcttacttctc	A	G	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 130895	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1851346	tattcatttaacctct[A/T]aaccagcagtgttcaa	A	T	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-1849611	gtgtcacctagttcca[C/G]aaaatagaggcaatgg	C	G	LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 //	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-1794878	ggtcttcagtgtttcc[C/T]gaagcgaagatgaaga	C	T	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 767510 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1796675	ggttataaaattgtca[C/T]aaggacatgggacatg	C	T	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 397891 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-1789216	gggcatcaaactgaag[C/T]agtcgaggatggtctt	C	T	ENST00000359247 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-1789944	gggcttgcataacaaa[C/G]tactacagactgggca	C	G	55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 //	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-1809513	gtgagagaagcgagca[A/G]agtctggattctaacc	A	G	Homo sapiens thyroid hormone receptor associated protein 3 (THRAP3), mRNA. /// ENST00000264293 // intron // 0 // --- // ---	THRAP3	THRAP3, Homo sapiens thyroid hormone receptor associated protein 3 (THRAP3), p34.3
SNP_A-1806447	gtcgattcctaacttc[C/T]ctcggtgatccttta	C	T	/// ENST00000356718 // upstream // 157536 // --- // --- // --- // ---	-	q24.21
SNP_A-1666052	caaatatgaattatcaaaatttcaa[A/G]atattgcctttcattcatatttttt	A	G	PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A , rs6657576, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1699073	gtaccccactcctactcccagaaaa[A/G]aaacggatggaaactgagtagtgtt	A	G	NM_130782 // upstream // 1821258 // Hs.440890 // RGS18 // 64407 // regulator of G-protein signalling 18	RGS18	RGS18 , rs1171381, regulator of G-protein signalling 18,q31.1
SNP_A-2158345	attgggttataagaac[A/T]gcaaactcatacctcc	A	T	55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream //	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-2158495	attgtaatacctaata[C/T]gtttttatgccattaa	C	T	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2198562	catttattgcctatgc[C/T]catttttccttttcta	C	T	3667 // Homo sapiens insulin receptor substrate 1 (IRS1), mRNA. /// NM_032276 // upstream // 965546 // Hs.471514 //	IRS1	IRS1, Homo sapiens insulin receptor substrate 1 (IRS1), q36.3
SNP_A-2173356	cacaagcattgaaaag[A/G]attccaaaaaggaggt	A	G	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1350689 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2218103	acttggtgagaagaat[A/G]actacacattttctaa	A	G	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2227190	ctaatttatttgttgc[A/G]cactgagaaggtaaca	A	G	288 // Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, mRNA. /// NM_020987 //	ANK3	ANK3, Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, q21.2
SNP_A-2102472	agattcttaaaaactt[C/G]aagtactcttaactca	C	G	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2087488	actgcccccatgtttg[A/C]attacctctcaccggg	A	C	-- /// ENST00000314071 // upstream // 616104 // --- // --- // ---	-	p13.3
SNP_A-2053366	aagtgagagcacagga[A/T]acatattttctagaca	A	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, mRNA. /// NM_080422 // intron // 0 // Hs.123352 // PTPN2 // 5771 // Homo sapiens	PTPN2	PTPN2, Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, p11.21
SNP_A-2067451	acaaatcgtaaaagaa[A/G]gcatggataaataagc	A	G	Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // --- //	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-2072372	acagcaatggcagaag[C/G]agtctaattgggcaga	C	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2232084	ctcaagcagtttgaac[C/T]ggtgagccacaccct	C	T	1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 6264 // Hs.498513 // AKR1C2 // 16	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste ,p15.1
SNP_A-2272046	gaccctcttaaagaag[C/T]attttggccaagttta	C	T	5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 457488 // Hs.282787 // FOXP2 //	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1
SNP_A-2282048	ctttggtctcacgtca[C/T]atctgtctgcatctct	C	T	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-2284174	gatatggcatttgtta[A/G]gatatataatgagata	A	G	H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1646051 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2276768	gagataacctctaaaa[A/C]tcctctccacaaaatc	A	C	Homo sapiens dachsous 1 (Drosophila) (DCHS1), mRNA. /// ENST00000299441 // intron // 0 // --- // --- // --- // ---	DCHS1	DCHS1, Homo sapiens dachsous 1 (Drosophila) (DCHS1), p15.4
SNP_A-2275777	gagaccgctctttaca[C/G]aagtctaggtgattta	C	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1149926 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2236625	ctctaaattcacaaac[C/T]aaatgaaggattgtac	C	T	ENST00000324607 // downstream // 54238 // --- // --- // --- // --- /// ENST00000357722 // downstream // 66413 // --- // --- // ---	-	p22.3
SNP_A-2252282	cttcccctacataata[C/T]gtccttttctctgac	C	T	2248 // Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream //	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-2306613	gctgtagaggactgga[C/T]gaaaacagtacatgat	C	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2294251	gcagggcctgagccct[C/G]aagaccgcatggagag	C	G	// 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream //	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2106834	agcctgtttgccagta[A/G]agacaagagcagagta	A	G	Homo sapiens myelin transcription factor 1 (MYT1), mRNA. /// NM_018257 // intron // 0 // Hs.473317 // C20orf36 // 55251 //	MYT1	MYT1, Homo sapiens myelin transcription factor 1 (MYT1), q13.33
SNP_A-2104205	agcagagtccctttaa[G/T]gcaaaacaatggttag	G	T	Homo sapiens interferon, gamma (IFNG), mRNA. /// NM_018402 // downstream // 849 // Hs.272350 // IL26 //	IFNG	IFNG, Homo sapiens interferon, gamma (IFNG), q15
SNP_A-2038304	aacacctgaggggata[C/G]atggcatggcaggaca	C	G	Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000340699 // intron // 0 // --- // ---	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044357	aacttttaggcagta[A/C]ggaatataactatcta	A	C	Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // --- // ---	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-2041044	aaccgtaactgtacat[C/G]agacagaactgcccaa	C	G	26118 // Homo sapiens WD repeat and SOCS box-containing 1 (WSB1), transcript variant 2, mRNA. /// NM_015626 // upstream // 225415 // Hs.446017 // WSB1 // 26118 // Homo	WSB1	WSB1, Homo sapiens WD repeat and SOCS box-containing 1 (WSB1), transcript variant 2, q11.1
SNP_A-2024142	aaaagatgaagggtga[A/C]ccttggtaactgcata	A	C	5001 // Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, mRNA. /// NM_002553 // upstream // 29762 // Hs.432948 // ORC5L //	ORC5L	ORC5L, Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, q22.2
SNP_A-2010064	tagttttagaattcaa[C/T]gggttctctttcacag	C	T	Homo sapiens glutamyl aminopeptidase (aminopeptidase A) (ENPEP), mRNA. /// ENST00000265162 // intron // 0 // --- // --- // --- // ---	ENPEP	ENPEP, Homo sapiens glutamyl aminopeptidase (aminopeptidase A) (ENPEP), q25
SNP_A-2009582	tgtggttttctaaagc[C/T]attactgttagatact	C	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2224837	cgtgagtttagtggcc[A/G]aaaggggaggtagagg	A	G	PCDHB15 // 56121 // Homo sapiens protocadherin beta 15 (PCDHB15), mRNA. /// NM_031947 // downstream // 29269 //	PCDHB15	PCDHB15, Homo sapiens protocadherin beta 15 (PCDHB15), q31.3
SNP_A-2217213	cctcttttctttagaa[C/T]tgccaccttgtcttct	C	T	// 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 445698 // ---	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-2205954	ccatatataatgataa[C/T]ggcttccccttgaaaa	C	T	sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA. /// NM_198709 // intron // 0 // Hs.149103 // ARSB // 411 //	ARSB	ARSB, Homo sapiens arylsulfatase B (ARSB), transcript variant 1, q14.1
SNP_A-2175313	cacatagtactgcttc[C/T]actacccttaatctta	C	T	57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2163134	atttttcagttaatga[C/T]ggtggcatttgctaag	C	T	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2138797	atcccctcagctaggc[A/G]ccttcttttgagtgtg	A	G	197320 // Homo sapiens hypothetical protein FLJ31875 (FLJ31875), mRNA. /// ENST00000333222 // upstream //	FLJ31875	FLJ31875, Homo sapiens hypothetical protein FLJ31875 (FLJ31875), q24.3
SNP_A-2137720	atcatggattcagaga[A/G]ccagcgcattcagcta	A	G	// 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 1620176 // Hs.391781 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-1746434	attgtaggatgaattaatggatgaa[A/C]agtgaatggaactgtccttagggag	A	C	NM_138803 // intron // 0 // Hs.503880 // LOC130940 // 130940 // hypothetical protein BC015395	LOC130940	LOC130940 , rs2030487, hypothetical protein BC015395,q24.1
SNP_A-1756044	ccaacagagaagagccagttcatgc[A/G]gacaggagatacagcgggaagtcag	A	G	// 2263 // fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, /// NM_018117 // downstream // 90855 // Hs.16677 // WDR11 /	FGFR2	FGFR2 , rs2260801, fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, ,q26.12
SNP_A-1794114	ggtcaggatggctcaa[A/G]tggatgccaggggagg	A	G	/// ENST00000356642 // downstream // 458990 // --- // --- // ---	-	q31.1
SNP_A-1792313	gggttgagatttgtta[A/C]aattggaagccattca	A	C	23022 // Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000284630 // upstream // 22489 // --- // --- // --- // ---	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3
SNP_A-1865807	tcccaaacaactacat[A/C]acaaaatccttgaata	A	C	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 329791 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1863448	tccaaaagtactttcg[G/T]attcctggcctgtaca	G	T	9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 297570 // Hs.300834 // GALNT2	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13
SNP_A-1868209	tcctcaatcctgagca[C/T]gtcctgctagattttc	C	T	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-1822538	gtttttgcaaaaacac[A/G]aagcatttttttcatag	A	G	ENST00000261588 // intron // 0 // --- // --- // --- // ---	-	p11.2
SNP_A-1828174	taagagagaattgtga[A/G]agaaatgaaaataact	A	G	Homo sapiens homeodomain-only protein (HOP), transcript variant 3, mRNA. /// NM_032495 // intron // 0 // Hs.121443 //	HOP	HOP, Homo sapiens homeodomain-only protein (HOP), transcript variant 3, q12
SNP_A-1840677	tagccttggctctaat[A/G]agaaattatagtactt	A	G	sapiens complement component 6 (C6), mRNA. /// ENST00000263413 // intron // 0 // --- // --- // --- // ---	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-1958675	ttttctcgagtgtgaa[A/C]attttgagaaccttcc	A	C	// 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 356136	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-1943582	ttgtaagatacattga[C/T]ggattgtgatattcag	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 882485 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1898990	tggaaaagaaagaccc[A/T]ctctcgatgtgggtga	A	T	5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase,q22.1
SNP_A-1901495	tggatttcctttgggc[A/G]aggactagttttactt	A	G	Homo sapiens hypothetical protein FLJ13391 (FLJ13391), mRNA. /// ENST00000233712 // intron // 0 // --- // --- // --- // ---	FLJ13391	FLJ13391, Homo sapiens hypothetical protein FLJ13391 (FLJ13391), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897061	tgctcccaagtcacta[A/G]gtgtaaaaatggacat	A	G	94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 177351 // --- // --- // --- //	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1895432	tgccgtaacaaggcac[C/T]gagactgggcgactta	C	T	// 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1910039	tgtcagttatcccgta[A/C]gtcttttataaactcc	A	C	Homo sapiens heme binding protein 1 (HEBP1), mRNA. /// ENST00000014930 // intron // 0 // --- // --- // --- // ---	HEBP1	HEBP1, Homo sapiens heme binding protein 1 (HEBP1), p13.1
SNP_A-1924925	ttatattccatagctt[C/G]aaaaaactcatcatac	C	G	387836 // Homo sapiens INPE5792 (UNQ5792), mRNA. /// NM_207434 // downstream // 14197 // Hs.446273 //	CLEC2A	CLEC2A, Homo sapiens INPE5792 (UNQ5792), p13.31
SNP_A-1922601	ttagaccagcgggtag[A/C]aagtgaggtcagtgtg	A	C	Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // --- // --- // --- // ---	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. ,q22.1
SNP_A-1909420	tgtattcatcaactca[C/G]aagtttcctgcatccc	C	G	// 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 219645 // Hs.494312 //	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-1893312	tgcagattcattgaac[C/T]agatgaatgtttaagt	C	T	/// ENST00000266432 // upstream // 114830 // --- // --- // --- //	-	p13.31
SNP_A-1941095	ttgctctgccacctaa[C/T]caaaactgaaaaaata	C	T	Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, mRNA. /// NM_005968 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens	HNRPM	HNRPM, Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, p13.2
SNP_A-1985037	acaatgtatttaacca[C/T]agaaagtattgtgctt	C	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 164753 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1969593	ttaagaccaaatctta[C/T]ctcatggggtcaaaat	C	T	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 534909	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1971492	atggctgagattaaca[A/G]caggctcacaaatttc	A	G	// 9695 // Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), mRNA. /// ENST00000295399 // upstream // 138819 // --- // --- // --- // ---	EDEM1	EDEM1, Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), p26.1
SNP_A-1833857	tacagtgtcatgatta[C/T]ctctggctctgagttc	C	T	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 2319797	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1827198	taacctcaatgtaaaa[A/T]tgccatttgcacaata	A	T	4638 // Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, mRNA. /// NM_053028 //	MYLK	MYLK, Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, q21.1
SNP_A-1824931	taaagccattttagta[C/G]gtagcatacataacaa	C	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1228803 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1822074	gttttccttttaggcc[A/G]aaaacaagaacaacat	A	G	LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 //	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-1867083	tccctctctttctggc[A/G]actggagccttgccat	A	G	5862 // Homo sapiens RAB2, member RAS oncogene family (RAB2), mRNA. /// ENST00000262646 // downstream //	RAB2	RAB2, Homo sapiens RAB2, member RAS oncogene family (RAB2), q12.2
SNP_A-1870349	tccttttaaaggacac[A/C]aagccaccagcagtgt	A	C	Homo sapiens DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), transcript variant 3, mRNA. /// NM_175848 // intron // 0 // Hs.251673 // DNMT3B // 1789 // Homo sapiens	DNMT3B	DNMT3B, Homo sapiens DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), transcript variant 3, q11.21
SNP_A-1782212	ggcaaggatatggaga[A/G]attagaacccttgtac	A	G	Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // --- //	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-1741335	cacctggaaaacaaaaatgcaaata[C/T]tatcatcgtaaattataagatttca	C	T	NM_003640 // intron // 0 // Hs.31323 // IKBKAP // 8518 // inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	IKBKAP	IKBKAP , rs838824, inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein,q31.3
SNP_A-2136552	atcacctcttggcaga[A/C]ctatgtgtaatcgcct	A	C	// Homo sapiens tyrosine aminotransferase (TAT), nuclear gene encoding mitochondrial protein, mRNA. /// NM_052858 // upstream // 26484 // Hs.546464 // MARVELD3 // 91862 //	TAT	TAT, Homo sapiens tyrosine aminotransferase (TAT), nuclear gene encoding mitochondrial protein, q22.2
SNP_A-2135611	atatttttagttttga[C/T]gtctttcacagttttg	C	T	29777 // Homo sapiens activator of basal transcription 1 (ABT1), mRNA. /// NM_024639 // downstream // 13785 //	ABT1	ABT1, Homo sapiens activator of basal transcription 1 (ABT1), p22.1
SNP_A-2112346	aggcaaatacagagaa[C/T]gacaactgaccagagc	C	T	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1143154 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-2110777	aggacgtgaactgata[C/T]acactcacataaacct	C	T	// 8732 // Homo sapiens RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA. /// ENST00000333801 // downstream // 136171 // --- // --- // --- // --- ///	RNGTT	RNGTT, Homo sapiens RNA guanylyltransferase and 5'-phosphatase (RNGTT), q15
SNP_A-2139082	atcctatgaggtatag[C/T]agcaacttaatattta	C	T	157869 // Homo sapiens RPE-spondin (RPESP), mRNA. /// NM_000971 // downstream // 106165 // Hs.421257 // RPL7 //	RPESP	RPESP, Homo sapiens RPE-spondin (RPESP), q21.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2143796	atgagagacttcacaa[C/T]gcagagggaagtagat	C	T	SLC17A6 // 57084 // Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), mRNA. /// NM_022725 // downstream	SLC17A6	SLC17A6, Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), p14.3
SNP_A-2146822	atgctttaaaagaaat[A/G]atgatggcaacatctt	A	G	Homo sapiens LIM domain 7 (LMO7), mRNA. /// AF330045 // intron // 0 // Hs.207631 // LMO7 // 4008 // Homo sapiens LIM	LMO7	LMO7, Homo sapiens LIM domain 7 (LMO7), q22.2
SNP_A-2151714	atgttgttcactgcag[A/G]aagccatatgttcctc	A	G	// 157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA. /// ENST00000262109 // upstream //	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3
SNP_A-2166432	caaatgagcaggcttg[C/G]aaaaatctctgcctgg	C	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2179263	cactgtaccaagaaac[A/T]gagaagatgtgagagt	A	T	Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // --- // --- // --- // ---	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-2194634	catgcatacacagaga[A/G]gtctatttctagcccg	A	G	// 402135 // Homo sapiens olfactory receptor, family 5, subfamily K, member 2 (OR5K2), mRNA. /// NM_001004736	OR5K2	OR5K2, Homo sapiens olfactory receptor, family 5, subfamily K, member 2 (OR5K2), q12.1
SNP_A-2186943	cagggttcctttgagc[A/G]cagggctgatcccatg	A	G	// 51586 // Homo sapiens PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-associated protein	PCQAP	PCQAP, Homo sapiens PC2 (positive cofactor 2, multiprotein complex) glutamine,q11.21
SNP_A-2218662	cctggcctagactcca[C/T]attcttattaaaattt	C	T	Homo sapiens leucine aminopeptidase 3 (LAP3), mRNA. /// ENST00000226299 // intron // 0 // --- // --- // --- // ---	LAP3	LAP3, Homo sapiens leucine aminopeptidase 3 (LAP3), p15.32
SNP_A-2041773	aacgtgtcttgcttta[C/T]ggtaattcattttatg	C	T	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1349859 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2045661	aagacaaatgatgaag[C/T]atagttaatgaaaagc	C	T	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA. /// ENST00000351718 // intron // 0 // --- // --- // --- // ---	NRCAM	NRCAM, Homo sapiens neuronal cell adhesion molecule (NRCAM), q31.1
SNP_A-2096268	agaccacgctgtctcc[A/G]gatgacccaacgtgcc	A	G	Homo sapiens tubulin-specific chaperone d (TBCD), mRNA. /// ENST00000355528 // intron // 0 // --- // --- // --- // ---	TBCD	TBCD, Homo sapiens tubulin-specific chaperone d (TBCD), q25.3
SNP_A-2087872	actggagtacaggcac[G/T]cgtggactcaaaacat	G	T	// Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000303045 // intron // 0 // --- // --- // --- // ---	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2073436	acaggtgcctgggaga[A/G]aagctaatgcaaagat	A	G	ENST00000334037 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2291513	gcaatttgtttcaaaa[A/T]ggaactgtataatgtc	A	T	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 24538 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2275199	gagaaggaattggcac[A/T]ctagaattaatattat	A	T	PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-2285759	gatgaccatgaaatta[C/G]caattagagcagcaaa	C	G	Homo sapiens dynein, axonemal, heavy polypeptide 3 (DNAH3), mRNA. /// ENST00000261383 // intron // 0 // --- // ---	DNAH3	DNAH3, Homo sapiens dynein, axonemal, heavy polypeptide 3 (DNAH3), p12.3
SNP_A-2267758	gaatcatggaagcaaa[C/T]tgcaggaattcttaat	C	T	// 64098 // Homo sapiens parvin, gamma (PARVG), mRNA. /// NM_022141 // downstream // 38018 // Hs.546422 //	PARVG	PARVG, Homo sapiens parvin, gamma (PARVG), q13.31
SNP_A-2285903	gatgagggaagggaat[G/T]aggttcatgagcacac	G	T	ENST00000294926 // intron // 0 // --- // --- // --- // ---	-	q44
SNP_A-2278256	gagccttcttactcgt[C/G]aacatttaaattggac	C	G	// Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00000324559 // intron // 0 // --- // --- // --- // ---	TMEM16E	TMEM16E, Homo sapiens transmembrane protein 16E (TMEM16E), p14.3
SNP_A-2243356	ctgcctttactcatc[A/G]gagcagactcctaggg	A	G	// Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // intron // 0 // --- // --- // --- // ---	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2235294	ctccctcacttctcca[A/G]taatctggatgctatg	A	G	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000277647 // upstream // 79680 // --- // --- // --- // ---	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2229242	ctaggaacacagtaaa[C/G]tccaaaacaagctttg	C	G	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 615574 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q12.3
SNP_A-2289905	gcaaagaaaggaaaaa[C/T]tgacatttgagaggat	C	T	sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// ENST00000330276 // intron // 0 // --- // --- // --- // ---	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2296429	gcatttcccaggcatg[A/G]ataagccctagtcctc	A	G	sapiens interleukin 4 receptor (IL4R), mRNA. /// ENST00000170630 // 3UTR // 0 // --- // --- // --- // ---	IL4R	IL4R, Homo sapiens interleukin 4 receptor (IL4R), p12.1
SNP_A-2086811	actgacctgtgtattg[A/C]aagaattaaggggctc	A	C	ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 927029 //	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-2091122	actttggatctacaaa[A/T]tgctttgggaattatg	A	T	163126 // Homo sapiens CREBBP/EP300 inhibitor 2 (CRI2), mRNA. /// NM_013268 // upstream // 29939 // Hs.23671 //	CRI2	CRI2, Homo sapiens CREBBP,q13.2
SNP_A-2080701	acctcattagggctca[C/G]ctcttttcctgtaaca	C	G	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 177427 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2094760	agaatcagtctgacca[C/T]gatctgtaacagtagc	C	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2101521	agatgacaatggaata[A/G]gtgtggaaggctgctg	A	G	/// ENST00000271263 // downstream // 34934 // --- // --- // ---	-	p12
SNP_A-2033912	aaatcaacagtgctcc[C/T]atacatcagcaaaaat	C	T	116512 // Homo sapiens MAS-related GPR, member D (MRGPRD), mRNA. /// NM_145015 // downstream // 16754 // Hs.118513 // MRGPRF // 219928 // Homo sapiens MAS-	MRGPRD	MRGPRD, Homo sapiens MAS-related GPR, member D (MRGPRD), q13.3
SNP_A-2031893	aaagtcaggaaccatc[A/G]gaactgcttacaaagg	A	G	23429 // Homo sapiens RING1 and YY1 binding protein (RYBP), mRNA. /// NM_018130 // downstream // 104425 //	RYBP	RYBP, Homo sapiens RING1 and YY1 binding protein (RYBP), p13
SNP_A-2029647	aaagagagatggagaa[A/G]tcaataaagtttattt	A	G	Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, mRNA. /// NM_024494 // intron // 0 // Hs.258575 // WNT2B // 7482 //	WNT2B	WNT2B, Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, p13.2
SNP_A-2221906	ccttttgaccatata[G/T]ctcttacttcagatct	G	T	Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-2202730	ccacgcctggcctaat[G/T]atagttcttatgatgt	G	T	ENST00000343170 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2172734	caatttatccctgaga[C/T]gatttttatcctgtgt	C	T	Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 4 (ATP6V0A4), transcript variant 1, mRNA. /// NM_130840 // CDS // 0 // Hs.98967 // ATP6V0A4 // 50617	ATP6V0A4	ATP6V0A4, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 4 (ATP6V0A4), transcript variant 1, q34
SNP_A-2149416	atgtactcaacctcct[A/T]aaccaccaagtctagc	A	T	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // --- // --- // --- // ---	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2148331	atggggaaaacagtca[A/T]aactaagaatgatatt	A	T	Homo sapiens G protein-coupled receptor 156 (GPR156), mRNA. /// ENST00000315843 // intron // 0 // --- // --- // --- // ---	GPR156	GPR156, Homo sapiens G protein-coupled receptor 156 (GPR156), q13.33
SNP_A-2109409	agcttttagaacatca[C/G]tccgtaactccaactc	C	G	// 79723 // Homo sapiens suppressor of variegation 3-9 homolog 2 (Drosophila) (SUV39H2), mRNA. /// NM_024670 // downstream // 61539 // Hs.85567 // SUV39H2 // 79723 //	SUV39H2	SUV39H2, Homo sapiens suppressor of variegation 3-9 homolog 2 (Drosophila) (SUV39H2), p13
SNP_A-2129286	atacaaaattctaacc[A/T]aaatattagcaaactg	A	T	Homo sapiens attractin (ATRN), transcript variant 3, mRNA. /// NM_139322 // intron // 0 // Hs.276252 // ATRN // 8455 //	ATRN	ATRN, Homo sapiens attractin (ATRN), transcript variant 3, p13
SNP_A-1718207	taaaaataattccattatttcacta[A/G]ggatttgacatttgaaagccccccac	A	G	2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_002941 // upstream // 931774 // Hs.301198 // ROBO1 // 6091 // r	GBE1	GBE1 , rs925730, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-1676794	taaaataaaagtgtatgctgtttga[A/G]aggcataaattgagaattaatctgt	A	G	FLJ20793 // 54495 // FLJ20793 protein /// NM_032160 // upstream // 889558 // Hs.124673 // NCAG1 // 92126 //	FLJ20793	FLJ20793 , rs10513949, FLJ20793 protein ,q22.1
SNP_A-1672526	atggttttcctctccagcacccatt[G/T]cctccttactcaagcaatggccctg	G	T	// 58516 // chromosome 12 open reading frame 14 /// NM_024799 // upstream // 104356 // - // - // - // - ///	C12orf14	C12orf14 , rs724417, chromosome 12 open reading frame 14 ,p11.21
SNP_A-1645596	acagctgtgatggcttagcatttat[A/G]aggaacatgttctgctacttgagan	A	G	10477 // ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	UBE2E3	UBE2E3 , rs2672662, ubiquitin-conjugating enzyme E2E 3 (UBC4,q31.3
SNP_A-1795134	ggtgactggcgccagg[C/T]caagttctaggtgggc	C	T	Homo sapiens interleukin 2 receptor, alpha (IL2RA), mRNA. /// ENST00000281359 // intron // 0 // --- // --- // --- // ---	IL2RA	IL2RA, Homo sapiens interleukin 2 receptor, alpha (IL2RA), p15.1
SNP_A-1816171	gttacgcttctctttg[C/T]atcagatgaccagatc	C	T	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 835868 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1830252	taatagtttggacaaa[C/T]gagtcctggtcccttt	C	T	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 425360 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1962554	cagctcagacagctga[A/G]gatgatttttatatt	A	G	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 //	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone ,p23.1
SNP_A-1980202	ttctaaccttagagaa[A/C]caccggcaaacgactc	A	C	/// ENST00000357279 // upstream // 23811 // --- // --- // --- // ---	-	q35.1
SNP_A-1945385	ttgttatagtgtctcc[A/G]atgtaaaggctcaatc	A	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1954817	tttgctgtttaattta[C/T]agtatcttagtgggct	C	T	/// ENST00000334919 // upstream // 159721 // --- // --- // --- // -- /// ENST00000322194 // downstream // 1609428 // --- // ---	-	q12.2
SNP_A-1951286	tttccctatcagttaa[C/T]gccttttgatttgca	C	T	3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), mRNA. /// ENST00000326913 // downstream // 198060 // --- // --- // --- //	ID4	ID4, Homo sapiens inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), p22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893898	tgcatagacttctaag[A/C]aactcattacacttac	A	C	// Homo sapiens deoxycytidine kinase (DCK), mRNA. /// NM_003759 // upstream // 260707 // Hs.5462 // SLC4A4 //	DCK	DCK, Homo sapiens deoxycytidine kinase (DCK), q13.3
SNP_A-1903901	tgggatggccgaccta[C/T]aggaaggactccttgg	C	T	160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// ENST00000321196 // intron // 0 // --- // --- // --- // ---	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1902323	taacctactattctca[C/G]catccaatgttttaaa	C	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1900159	tggacttccaccttca[A/G]atccacttcctaggac	A	G	29851 // Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// NM_205863 // upstream // 292678 // Hs.271903 //	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.3
SNP_A-1898061	tgctgtgagtactgaa[A/T]tagtgaatgtcgaacc	A	T	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 486284 // --- // --- // --- //	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-1882831	tgaaagccactcagaa[A/G]aaaacatgattcaata	A	G	51194 // Homo sapiens importin 11 (IPO11), mRNA. /// NM_001826 // upstream // 221517 // Hs.374378 // CKS1B //	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1
SNP_A-1908395	tgtactttgatgatta[C/T]gtttcaggactggaat	C	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 508400 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-1923794	ttagtagaattgcaga[A/G]tacaaaatgaacatag	A	G	Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // --- // --- // --- // --- ///	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-1930921	ttccaggagtgattta[C/T]gatagagagtcagaac	C	T	ENST00000343093 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1904737	tgggggtaatttttca[C/T]gtaggatgtctgggaa	C	T	10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 123772 // Hs.334587 // RBPMS //	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-1915581	tgttctcacagatcag[A/C]ccttttgctcctttct	A	C	151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1899606	tggaagtctggggaac[A/G]caggacaagagccact	A	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 969270 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1936518	ttcttgatcaaacata[A/T]caccaatttgtcagaa	A	T	2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 176883 // Hs.98262 // GRIK2 // 2898 // Homo	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1984711	agaaatccacaacctc[A/G]gaagaagtgtttcgag	A	G	64324 // Homo sapiens nuclear receptor binding SET domain protein 1 (NSD1), transcript variant 1, mRNA. /// NM_022455 // downstream // 3874 // Hs.208961 // NSD1 // 64324 // Homo	NSD1	NSD1, Homo sapiens nuclear receptor binding SET domain protein 1 (NSD1), transcript variant 1, q35.3
SNP_A-1835851	tacgtagtttgaatta[C/G]agattttcaaatattg	C	G	Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // --- // --- // --- // ---	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-1856103	tcaattttgaatacaa[C/G]aatgccaattgaagtt	C	G	Homo sapiens mRNA for KIAA1384 protein, partial cds. /// ENST00000359358 // intron // 0 // --- // --- // --- // --- ///	KLHL14	KLHL14, Homo sapiens for KIAA1384 protein, partial cds. q12.1
SNP_A-1670756	tctatgtatcacaatagcatcatta[C/T]gtagtaacaacacagtatttctcgc	C	T	84457 // phytanoyl-CoA hydroxylase interacting protein-like /// NM_025044 // downstream // 81445 // Hs.287696 // BICC1 //	PHYHIPL	PHYHIPL , rs190749, phytanoyl-CoA hydroxylase interacting protein-like ,q21.1
SNP_A-1730595	ctgaagcttatggtctatttgagaa[C/T]gatgaggtattcaccgcctgccaat	C	T	NM_014840 // downstream // 11273 // - // - // - // -	-	- , rs4275717, -,q23.3
SNP_A-2126994	ataaagtgtttaaaac[C/T]agtcaccttttctctct	C	T	/// ENST00000359165 // upstream // 238517 // --- // --- // --- // -	-	p21.3
SNP_A-2126132	agtttttcttgttgaa[C/T]agttaacatccagtct	C	T	// 10049 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA. /// NM_005494 // downstream // 17947 // Hs.490745 // DNAJB6	DNAJB6	DNAJB6, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, q36.3
SNP_A-2123837	agttaaataactggcc[C/G]gacactacacagttag	C	G	Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // intron // 0 // --- // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2121435	agtctttgggagtgga[C/T]gtgagagctctttcag	C	T	/// ENST00000288466 // upstream // 85486 // --- // --- // --- // --- /// ENST00000307730 // upstream // 237058 // --- // --- // --- //	-	q32
SNP_A-2184131	cagccgcaacatccac[A/G]cattagaaacaaaccg	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2188418	cagtgaaattgctacc[C/T]aaatctaactcatttg	C	T	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 294527 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2200176	ccaaatggtggcccca[C/T]gttcatgcaggtatgt	C	T	// 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 97270 // Hs.132344	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2208623	cccactgctacccaca[A/G]tgatgcttgcaaaggg	A	G	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2209817	cccatttttcacatta[C/T]cctaatctgtttggtc	C	T	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 270525 // --- // --- // --- //	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2021130	aaaaaaaatcctctcc[A/T]cggcattttaatataa	A	T	Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // ---	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-2042714	aactctaacctgaaaa[A/G]gacacgataaccaatg	A	G	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 91047 //	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2080205	acctaaacaactgtgc[A/G]actttcttttgcagtg	A	G	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2087532	actgcctgttttcaaa[A/T]gactaaagtgtttcaa	A	T	166815 // Homo sapiens tigger transposable element derived 2 (TIGD2), mRNA. /// NM_198281 // downstream // 51459 //	TIGD2	TIGD2, Homo sapiens tigger transposable element derived 2 (TIGD2), q22.1
SNP_A-2060867	aatgatatgtacagta[C/T]gattccgttttgtttt	C	T	ATP6V0A2 // 23545 // Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), mRNA. /// NM_207437 // upstream // 15833 // Hs.534768 //	ATP6V0A2	ATP6V0A2, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), q24.31
SNP_A-2057912	aatattctggtaacta[C/T]taggtctttggttcta	C	T	// 23136 // Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// NM_173464 // downstream // 312603 // Hs.128279 // L3MBTL4 // 91133 //	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-2230964	ctatgggtatgctagc[C/T]ctaattcttgctcact	C	T	407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 446761 // Hs.24115 // C13orf25 //	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2283415	gatacccatgaactat[A/G]agagtgtaattcattg	A	G	KIAA0635 // 9662 // Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000264222 // downstream // 240854 // ---	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-2274110	gacttcaaaccataaa[A/C]ctactacaagaaaaca	A	C	255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 335136 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2264666	gaagacaagtgtcatt[C/T]aaatatttctgcataa	C	T	2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 91227 //	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-2263333	gaacatagcatattca[A/G]gtttgtactgctaaag	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2234022	ctcatgtgtgatctga[G/T]atgagagccagctggg	G	T	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 615412 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q12.3
SNP_A-2298440	gcccaaagaaatacca[C/T]aggagtcattaatttt	C	T	6854 // Homo sapiens synapsin II (SYN2), transcript variant IIb, mRNA. /// NM_133625 // downstream // 40736 //	SYN2	SYN2, Homo sapiens synapsin II (SYN2), transcript variant IIb, p25.2
SNP_A-2309804	ggaaagtgccatgtta[C/T]caatttttttctttt	C	T	Homo sapiens HLA-B associated transcript 4 (BAT4), mRNA. /// ENST00000211377 // 3UTR // 0 // --- // --- // --- // ---	BAT4	BAT4, Homo sapiens HLA-B associated transcript 4 (BAT4), p21.33
SNP_A-2072102	acagataatcaaatga[A/C]ggctgtgagacaaaaa	A	C	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2081875	accttggtaacactgc[C/T]catgtgactatagata	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2033612	aaatatcagacttctg[A/T]aatcaatttccaagac	A	T	Homo sapiens chromosome 6 open reading frame 97 (C6orf97), mRNA. /// ENST00000239374 // intron // 0 // --- // --	C6orf97	C6orf97, Homo sapiens chromosome 6 open reading frame 97 (C6orf97), q25.1
SNP_A-2021266	aaaaaaatgatatcac[A/T]aaaaagttcaagaata	A	T	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 149423 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2012729	aggaaatacacaatac[A/C]agtagcatattaaatc	A	C	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2004974	acacattaagggtagc[C/T]aggatgagaattacca	C	T	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2221378	cctttcatctgttcca[C/T]gttgtgcagcctacag	C	T	1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // upstream //	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-2220120	ccttcacttgggaatc[A/G]aggttcatactgcaat	A	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 190138 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2122094	agtgatggaaatgtga[A/G]catggcctggtcttga	A	G	10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream //	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2117801	aggttgcgttttccag[A/G]aataatataaatggag	A	G	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1036544 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2125390	agtttaataaggtcac[C/G]caactaaaattctgga	C	G	22931 // Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA. /// ENST00000329227 // upstream //	RAB18	RAB18, Homo sapiens RAB18, member RAS oncogene family (RAB18), p12.1
SNP_A-2145605	atgcatctaaggtcag[A/C]aactgagcttattaat	A	C	ENST00000261241 // intron // 0 // --- // --- // --- // ---	-	q21.2
SNP_A-1736209	tgaatatttatgagcatgatgacaa[A/G]ttaacacctaaaactggttttccgt	A	G	6240 // ribonucleotide reductase M1 polypeptide /// NM_003141 // downstream // 173500 // Hs.1042 // SSA1 //	RRM1	RRM1 , rs1822285, ribonucleotide reductase M1 polypeptide ,p15.4
SNP_A-1798213	gtaaactgaactgaca[C/T]tcctcatttgtaacca	C	T	65268 // Homo sapiens mRNA for KIAA1760 protein, partial cds. /// NM_006648 // downstream // 24376 // Hs.522291 //	WNK2	WNK2, Homo sapiens for KIAA1760 protein, partial cds. q22.31
SNP_A-1789973	gggctttagagaggaa[A/T]caaagatagtagtgaa	A	T	NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1262158 // ---	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1861508	tcatccatcatggctg[A/G]aatcacttttcttccaa	A	G	Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // ---	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1816998	gttatttacgtgagca[C/T]gtgaaggctttccaga	C	T	// Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 607933 // Hs.451286 // C15orf2 //	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-1978812	ggaacattgaattaac[C/T]atgtttttcctcaaaa	C	T	// 57182 // Homo sapiens mRNA for KIAA1223 protein, partial cds. /// ENST00000329821 // upstream // 184409 // --- // --- //	KIAA1223	KIAA1223, Homo sapiens for KIAA1223 protein, partial cds. ,q28.1
SNP_A-1978204	ttctgagacctatcaa[A/C]aactaagatgcttcta	A	C	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 301046 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1936207	ttcttcagcaagtgaa[A/G]tgaaaggtaattctcc	A	G	Homo sapiens WINS1 protein with Drosophila Lines (Lin) homologous domain (WINS1), transcript variant 3, mRNA. /// NM_018148 // CDS // 0 // Hs.105633 // WINS1 // 55180 //	WINS1	WINS1, Homo sapiens WINS1 protein with Drosophila Lines (Lin) homologous domain (WINS1), transcript variant 3, q26.3
SNP_A-1952032	tttctatgaaattgcc[A/G]cagggattaaatgaga	A	G	// 266727 // Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), mRNA. /// ENST00000358069 // upstream // 76920 // --- // --- // --- // ---	MDGA1	MDGA1, Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), p21.2
SNP_A-1950175	tttcactgttgatcag[A/G]caacgtgttcagtaat	A	G	8900 // Homo sapiens cyclin A1 (CCNA1), mRNA. /// ENST00000239854 // downstream // 54179 // --- // --- // --- // --	CCNA1	CCNA1, Homo sapiens cyclin A1 (CCNA1), q13.3
SNP_A-1905860	tggtcataaaaatgtg[C/G]agttagcattaaaatc	C	G	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-1923458	ttaggcaggttctaca[C/T]cagagaggaatggcaa	C	T	Homo sapiens cyclin D2 (CCND2), mRNA. /// ENST00000261254 // intron // 0 // --- // --- // --- // ---	CCND2	CCND2, Homo sapiens cyclin D2 (CCND2), p13.32
SNP_A-1931818	ttccctttcttccaaa[A/T]cctcattaacatctgt	A	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1856862 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1909425	tgtattccacagaaac[C/T]atattgctgcataaca	C	T	// 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA. /// NM_024781 // upstream // 12532 // Hs.280781 //	TXNDC10	TXNDC10, Homo sapiens FLJ20793 protein (FLJ20793), q22.1
SNP_A-1882329	tgaaaacattgaattc[A/G]ctaagttgtatatgta	A	G	93649 // Homo sapiens myocardin (MYOCD), mRNA. /// NM_014859 // upstream // 20218 // Hs.499758 // KIAA0672 //	MYOCD	MYOCD, Homo sapiens myocardin (MYOCD), p12
SNP_A-1956804	ttttaaatgtctgaaa[C/T]tggtgattatagccca	C	T	LOC152485 // 152485 // Homo sapiens hypothetical protein LOC152485 (LOC152485), mRNA. /// NM_007080 //	LOC152485	LOC152485, Homo sapiens hypothetical protein LOC152485 (LOC152485), q31.22
SNP_A-1943042	ttggtactaaaaatga[C/T]gtcaggttacttattc	C	T	// 219970 // Homo sapiens BXMAS2-10 (BXMAS2-10), mRNA. /// NM_080661 // upstream // 39917 // Hs.38085 //	BXMAS2-10	BXMAS2-10, Homo sapiens BXMAS2-10 (BXMAS2-10), q12.1
SNP_A-1978559	cttttaaagtagagaa[C/G]tatgttgtgaagatta	C	G	sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 //	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26
SNP_A-1976948	ttatacttcatttaga[C/T]ctgatgggtatatata	C	T	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 150188 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1987256	gatacataatttttaaa[A/T]catgaaatttgccatc	A	T	/// ENST00000309379 // upstream // 1257904 // --- // --- // --- //	-	q21
SNP_A-1828917	taaggattgcaaatac[A/G]aaaattataaaatcat	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 894011 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1842191	tagggtaatacttaga[A/G]aaggaaggagaggtct	A	G	8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// NM_207492 // upstream // 292496 // --- // --- // 0 // --- /// ENST00000262992 //	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-1862757	tcattccaggagagtc[C/T]gaagatctggccagcc	C	T	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2), mRNA. /// ENST00000347929 // CDS // 0 // --- // -	GOLGA2	GOLGA2, Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2), q34.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798431	gtaaatcagcagagac[A/C]atcataaaaagacatt	A	C	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1809849	gtgaggtccagtgtgc[C/T]ctggcttagcttcgtg	C	T	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-1748325	ggaaatcctcaccagcttgtgagta[C/T]aaataaaatcacagagacacgatt g	C	T	NM_013244 // intron // 0 // Hs.422827 // HGNT-IV-H // 25834 // UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog	HGNT-IV-H	HGNT-IV-H , rs952851, UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog,q21.31
SNP_A-2150701	aatactggcctaggtc[A/T]cgcatgatcctatgtg	A	T	Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2152403	attaacctctacttac[C/T]agcctaactcatgtac	C	T	26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream //	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2162801	attttgcaagtttaaa[C/T]tgaatgtagaaatatc	C	T	10063 // Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, /// NM_033364 // upstream // 8775 // Hs.341906 // C3orf15 // 8	COX17	COX17, Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, q13.33
SNP_A-2125358	agttgtttaattttca[C/G]caaaatccagttttgg	C	G	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 846663 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2122790	agtggattttagcagg[A/G]aaaagaaataggggaa	A	G	203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream // 417767	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2114246	agggaagagttgaaag[A/G]aggagactgaattgga	A	G	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-2199943	ccaaagattatcctca[C/T]agaacagctgtgggga	C	T	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // intron // 0 // Hs.365690 // KCNK10 // 54207 // Homo sapiens	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-2202378	ccaccatcaacctaac[A/C]ctggaaggatccctgg	A	C	Homo sapiens keratin, hair, basic, 4 (KRTHB4), mRNA. /// ENST00000257951 // intron // 0 // --- // --- // --- // ---	KRTHB4	KRTHB4, Homo sapiens keratin, hair, basic, 4 (KRTHB4), q13.13
SNP_A-2205001	ccagggttataaaaat[A/T]agactgaactgttaat	A	T	Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // intron // 0 // --- // --- // --- // ---	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-2174651	cacagcacattccaac[A/G]caaatcccggagccca	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 580449 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2016474	tatcttgtgtatgctg[A/G]aggtagtataaatttg	A	G	// 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 759472 // --- // --- // --- // --- ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. ,q21.2
SNP_A-2005527	actcttttctctacac[A/C]caaattttaacatgga	A	C	Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // --- // --- // --- // ---	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-2029928	aaagatcagacagtta[G/T]aagtgtgcggtcttat	G	T	56475 // Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), mRNA. /// NM_052917 // upstream // 186001 // Hs.470277 // GALNT13 // 114805 //	RPRM	RPRM, Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), q23.3
SNP_A-2097428	agagaaatgcaaacaa[C/T]gtaaatgcccattgac	C	T	Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), mRNA. /// ENST00000193391 // intron // 0 // --- // ---	IMPG2	IMPG2, Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), q12.3
SNP_A-2063148	cagacaataactgtga[C/G]caataataaatcaatt	C	G	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 51414 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-2060204	aatgaacataccaaaa[A/G]tttaagaagccatgta	A	G	79605 // Homo sapiens piggyBac transposable element derived 5 (PGBD5), mRNA. /// NM_007357 // upstream //	PGBD5	PGBD5, Homo sapiens piggyBac transposable element derived 5 (PGBD5), q42.13
SNP_A-2054418	aagtttaggcaggaaa[C/T]tgatacttatatacta	C	T	Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // --- // --- // --- // ---	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2313971	ggagctcctagccttc[A/G]cctaagcctcaggtca	A	G	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2303369	gctattccgctcaaga[A/G]tatttatttccacctc	A	G	121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 165695 // Hs.31664 //	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2233830	ctcatctcagtgttgg[G/T]acctaaagattgtatt	G	T	FLJ35740 // 253650 // Homo sapiens FLJ35740 protein (FLJ35740), mRNA. /// AB095935 // downstream // 49308 //	FLJ35740	FLJ35740, Homo sapiens FLJ35740 protein (FLJ35740), p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2250924	cttatgccaaaacatc[C/T]atggattagttaagaa	C	T	1910 // Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, mRNA. /// NM_003991 // upstream //	EDNRB	EDNRB, Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, q22.3
SNP_A-2283750	gataggaatataacaa[G/T]ctctacctctttctc	G	T	/// ENST00000309379 // upstream // 200961 // --- // --- // --- // -	-	q21
SNP_A-2256384	ctttatcataaatgga[A/G]gtcacccattctttca	A	G	// 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 36448 // Hs.505007	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2257393	ctttgaaggtcttggc[C/T]gattttatgggcagaa	C	T	Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, mRNA /// ENST00000216862 // CDS // 0 // --- // --- // --- // ---	CYP24A1	CYP24A1, Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-2246465	ctggtttggattctga[C/T]gtttctgggcctcccc	C	T	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 651254 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-2241129	ctgagctccaaattga[A/G]tatacttctcaactcc	A	G	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 394024 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-2237925	ctctgagaagaagaaa[C/T]gaacacaatctccttc	C	T	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA. /// ENST00000331728 // intron // 0 // --- // -	LIMK2	LIMK2, Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, q12.2
SNP_A-2239219	ctcttggctatcacac[A/G]gtattgctcaggaggc	A	G	9241 // Homo sapiens noggin (NOG), mRNA. /// NM_003647 // upstream // 94053 // Hs.546318 // DGKE // 8526 // Homo	NOG	NOG, Homo sapiens noggin (NOG), q23.2
SNP_A-2304779	gctctgtcatccccaa[C/T]gggaagctgcaatacc	C	T	55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 487360 // --- // ---	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-2314874	ggagtgtaaaacagaa[C/G]tgcatccccaacagaa	C	G	Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// ENST00000281437 // intron // 0 // --- // --- // --- // ---	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2299178	gccctaagttttggtc[A/G]cattctcacttaagtg	A	G	7088 // Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), mRNA. /// ENST00000355495 // upstream // 218906 // --- // --- // --- // ---	TLE1	TLE1, Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), q21.32
SNP_A-2301042	gccttataataattaa[G/T]gttctcacaggaattt	G	T	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 493340 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2297098	gccacacataaaatac[A/G]ctaatactaatgatag	A	G	5743 // Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA. /// NM_024420 // upstream // 23314 //	PTGS2	PTGS2, Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G,q31.1
SNP_A-2294275	gcaggggccttaccta[C/T]ggtctggagctctgta	C	T	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2061144	aatgcactcttaggga[A/C]ggtacaacctctaaat	A	C	Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // intron // 0 // Hs.47288 // TRPM3 // 80036 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.11
SNP_A-2055050	aataaattcagctacc[C/G]accaggattgtcatta	C	G	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2097655	agagaattatccaaca[C/T]agtaattggtgcctaa	C	T	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2040043	aaccaaaaacaatgca[A/C]cttaatgataatatta	A	C	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 499696	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2011401	ctcccaccgaattcca[C/G]gtggtctcattttgat	C	G	2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 1196240 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1989710	tgccttgtaaagtcca[C/T]caatcaaagaccaaag	C	T	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2185302	caggaataactgagat[G/T]aggaattactgcttta	G	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1358349 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2193722	catcttgtggcaccta[A/G]aaccaactaataagcc	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1425157 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2193592	catcttagaacctaac[C/T]ctgtcacctcttcatc	C	T	C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 //	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-2220132	ccttcagaatccaaac[A/G]gcattgatgggagtga	A	G	129563 // Homo sapiens hypothetical protein MGC42174 (MGC42174), mRNA. /// ENST00000273009 // intron // 0 // ---	MGC42174	MGC42174, Homo sapiens hypothetical protein MGC42174 (MGC42174), q37.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225005	cgtggtaggggatgaa[A/T]gtatgtctcttggtta	A	T	Homo sapiens PAS domain containing serine/threonine kinase (PASK), mRNA. /// ENST00000234040 // intron // 0 // -	PASK	PASK, Homo sapiens PAS domain containing serine q37.3
SNP_A-2129635	atacagatctattcta[C/T]ctttgttccaaccaga	C	T	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2140733 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2137085	atcaggaatgctaaag[A/C]agccacacctcactca	A	C	Homo sapiens caspase recruitment domain family, member 4 (CARD4), mRNA. /// ENST00000222823 // intron // 0 // --- // ---	CARD4	CARD4, Homo sapiens caspase recruitment domain family, member 4 (CARD4), p15.1
SNP_A-2133284	atatatataaatatac[A/G]caaagccatacaaata	A	G	// 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2165261	caaagacctatcttga[C/T]gtaacaacataacatt	C	T	ENST00000330778 // upstream // 8976 // --- // --- // --- // ---	-	q24.1
SNP_A-2139504	atccttgtaatttcag[A/G]ccctttataggaatg	A	G	Homo sapiens calcium and integrin binding family member 2 (CIB2), mRNA. /// ENST00000258930 // intron // 0 // --- // --- //	CIB2	CIB2, Homo sapiens calcium and integrin binding family member 2 (CIB2), q25.1
SNP_A-1686860	gaagaaaaatcacccgagaagaaat[A/G]agtatctaccttaaatggtatctac	A	G	1602 // dachshund homolog 1 (Drosophila) /// NM_020866 // upstream // 862479 // Hs.106808 // KLHL1 // 57626 // kelch-	DACH1	DACH1 , rs2202560, dachshund homolog 1 (Drosophila) ,q21.33
SNP_A-1810466	gtgattggaaagctca[C/T]agtaaggtttttagtt	C	T	// 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 117026 //	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1791588	gggtcagtgacgtaaa[G/T]ctggcttggtttcaat	G	T	Homo sapiens lipidosin (BG1), mRNA. /// ENST00000258873 // intron // 0 // --- // --- // --- // ---	BG1	BG1, Homo sapiens lipidosin (BG1), q25.1
SNP_A-1868958	tcctgagttcatatga[A/T]atagttcaaccacaca	A	T	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 55300 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1838582	tagaattgtgtgtagc[A/G]ctaaatctatgggaac	A	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1036847	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1825464	taaataatgcttttgt[A/G]aatttgaatggaaaac	A	G	9532 // Homo sapiens BCL2-associated athanogene 2 (BAG2), mRNA. /// NM_016277 // downstream // 1655 //	BAG2	BAG2, Homo sapiens BCL2-associated athanogene 2 (BAG2), p12.1
SNP_A-1818485	gttcttgtttttcttc[C/T]atgagccaaataaatg	C	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2648931 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1819332	gttggatggcattcac[A/G]aatatgtattagtaaa	A	G	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 681877 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.2
SNP_A-1959462	ttttgcctctccggaa[C/T]gccccacttcccagct	C	T	Homo sapiens B-cell novel protein 1 (BCNP1), mRNA. /// ENST00000332386 // intron // 0 // --- // --- // --- // --- ///	BCNP1	BCNP1, Homo sapiens B-cell novel protein 1 (BCNP1), p13.11
SNP_A-1952911	tttcttattgtgcacc[C/T]ggcatggagttaaaca	C	T	Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // intron // 0 // --- // --- // --- // ---	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-1874847	tctcgtaaagctggta[C/G]ctgtttatataatcattg	C	G	ENST00000309493 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-1897741	tgctgctttgagggag[C/T]attaggttatgttatt	C	T	325 // Homo sapiens amyloid P component, serum (APCS), mRNA. /// ENST00000255040 // downstream // 2656 // --- // ---	APCS	APCS, Homo sapiens amyloid P component, serum (APCS), q23.2
SNP_A-1917062	tgtttgctttattttc[A/C]aaagtgcattatgcct	A	C	Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00000355094 // intron // 0 // --- //	TCBA1	TCBA1, Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), q22.31
SNP_A-1912894	tgtgctttggcccaaa[C/T]gtttctcaccttacac	C	T	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000360355 // intron // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-1932153	ttcctcatattttcaa[C/G]ctcactcttccatttc	C	G	ENST00000325747 // CDS // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-1931102	ttccatcatcttccga[C/T]tccctccctgatgaag	C	T	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 107085 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-1930850	ttccagcaagaatttc[A/G]caaagccaaatgcttt	A	G	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // --- // --- // --- // ---	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-1874105	tctcattcctacatag[C/T]agcccctagagttaaa	C	T	/// ENST00000355043 // downstream // 11772 // --- // --- // ---	-	p23.1
SNP_A-1879723	tcttcatcagatcagc[A/G]caatgcgtaacttact	A	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1953640	tttgaccaacggaaaa[A/G]gaatctttggaagtat	A	G	Homo sapiens mitogen-activated protein kinase kinase kinase 14 (MAP3K14), mRNA. /// ENST00000344686 // intron // 0 // --- // --- // --- // ---	MAP3K14	MAP3K14, Homo sapiens mitogen-activated protein kinase kinase kinase 14 (MAP3K14), q21.31
SNP_A-1936099	ttcttatcatccttca[C/T]ggagtcacccaacagg	C	T	Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p22.1
SNP_A-1986591	aggggaatacatttta[A/G]ggatacggtgatgtct	A	G	7272 // Homo sapiens TTK protein kinase (TTK), mRNA. /// NM_183050 // upstream // 2284 // Hs.436387 // BCKDHB //	TTK	TTK, Homo sapiens TTK protein kinase (TTK), q14.1
SNP_A-1966116	tattctggagtacaca[C/T]ggtgggaaacttttag	C	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1821167	gtttgaagttatcaca[A/G]taagtactcaaatatg	A	G	Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, mRNA. /// NM_024806 // intron // 0 //	FLJ23554	FLJ23554, Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, q24.1
SNP_A-1825933	taaatgccaagtgata[A/C]taaaaaatatctgtgc	A	C	5028 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), mRNA. /// NM_002886 // upstream //	P2RY1	P2RY1, Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), q25.2
SNP_A-1873888	tctcagtcaaacaaaa[A/T]gtgatgccagaagtca	A	T	TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 //	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1852144	tattggtatgtttaca[A/G]tcattgggtggtttgt	A	G	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 35767 //	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1799613	gtaattctgtgagatg[C/G]aacagttaatatcccc	C	G	/// ENST00000330649 // upstream // 1200792 // --- // --- // --- //	-	q11.2
SNP_A-1795655	ggtgctttatgtgcaa[C/T]aaccaaaaatgaggga	C	T	63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 170362	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-1792850	ggtaatcactcacttc[A/G]cttctggaagcaacag	A	G	Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// NM_015199 // CDS // 0 // Hs.335239	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-1814010	gtgtcatccaggaact[A/G]aggcctggaacggagg	A	G	Homo sapiens chromosome 10 open reading frame 68 (C10orf68), mRNA. /// ENST00000302316 // intron // 0 // --- //	C10orf68	C10orf68, Homo sapiens chromosome 10 open reading frame 68 (C10orf68), p11.22
SNP_A-1804068	gtcacaccatctgctg[A/G]agtgcacagagctgcc	A	G	sapiens GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA. /// ENST00000254299 // intron // 0 // --- // ---	GCH1	GCH1, Homo sapiens GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), q22.2
SNP_A-1703053	tgtctgtggagtggttgaagaaatc[C/T]gaagaaaagagggaagtctgatggt	C	T	2309 // forkhead box O3A /// NM_032131 // upstream // 150019 // Hs.408216 // ARMC2 // 84071 // armadillo repeat	FOXO3A	FOXO3A , rs531111, forkhead box O3A ,q21
SNP_A-1782795	ggcagacagcccaaag[A/G]atggaaagatgatttc	A	G	Homo sapiens phosphorylase, glycogen; brain (PYGB), mRNA. /// ENST00000216962 // intron // 0 // --- // --- // --- // ---	PYGB	PYGB, Homo sapiens phosphorylase, glycogen; brain (PYGB), p11.21
SNP_A-2141280	atctgtatgaccatag[A/G]agttcctttatgatct	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1830020 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2144055	atgaggaagatgaagc[C/T]cggggtggttaaggga	C	T	Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // --- //	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-2148614	atggtagatgcaatat[A/G]aacttttctctgcct	A	G	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 256742 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2166441	caaatgagttaaagca[G/T]cagaagtcacccaaat	G	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 643195	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2159947	atttatctgtgcaaga[A/C]aatattatccagcaat	A	C	150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 593873	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-2124035	agttacattacaacca[A/G]tcaatggctttccatc	A	G	// 79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream //	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-2115062	agggcggagacctgga[C/T]gagtattcacaagcct	C	T	Homo sapiens catenin, beta like 1 (CTNNBL1), mRNA. /// ENST00000347721 // intron // 0 // --- // --- // --- // --- ///	CTNNBL1	CTNNBL1, Homo sapiens catenin, beta like 1 (CTNNBL1), q11.23
SNP_A-2202296	ccaccacagaccacac[C/G]aaacagcagcctcttt	C	G	145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 233566 // Hs.87889 // DICER1	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2191737	catattgtagtcttca[A/G]acattgtaattttatg	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 955859 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2193187	catctcaaactgaaaa[G/T]gtaaaacatagatctc	G	T	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2183561	cagcagcttctttcaa[A/C]ccactggagtactcct	A	C	sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2003790	ctggaattgttgatac[A/G]gagctgatatttaaag	A	G	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2003695	aagatctaaattctca[A/T]ctctgcctaaccttgt	A	T	Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // --- //	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-2016255	gattcatggaacataa[C/T]agagtccagaaataga	C	T	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2016024	tgagttctttctccat[C/T]agttcctgcgaaagct	C	T	/// ENST00000331037 // downstream // 720802 // --- // --- // ---	-	q21.1
SNP_A-2042541	aactcatgctgcacag[A/G]attttaagtgtaaaat	A	G	5458 // Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA. /// NM_031956 // downstream //	POU4F2	POU4F2, Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), q31.22
SNP_A-2041276	aacctgaacccactta[C/T]gtggaaaactgatgtc	C	T	Homo sapiens CD84 antigen (leukocyte antigen) (CD84), mRNA. /// ENST00000360056 // intron // 0 // --- // --- // --- // ---	CD84	CD84, Homo sapiens CD84 antigen (leukocyte antigen) (CD84), q23.3
SNP_A-2030915	aaaggaatatgattga[C/T]gtattataaagacaca	C	T	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082594	acggagcagtttccaa[A/G]gataagttctgcggta	A	G	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2053503	aagtgcattaacaaag[A/G]cgatgtggagccctga	A	G	92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// NM_006506 // upstream // 130964 // Hs.15999 //	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-2054046	aagttataagtcttga[A/G]aaagatacaagaagct	A	G	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-2311829	ggaatttgaaccctca[C/T]agtttgtttgtgaaaa	C	T	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 127772 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2235490	ctccggtacctgttcc[G/T]cacctgagctcaaggg	G	T	254042 // Homo sapiens methionine aminopeptidase 1D (MAP1D), mRNA. /// ENST00000315796 // downstream //	MAP1D	MAP1D, Homo sapiens methionine aminopeptidase 1D (MAP1D), q31.1
SNP_A-2229896	ctagttgatatggcta[A/C]aaaaaaaagcgtagga	A	C	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q14.3
SNP_A-2244836	ctggatgtgtatttct[C/T]aagctcagcataccat	C	T	// Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000338242 // intron // 0 // --- // --- // --- // ---	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2259898	gaaaaggcccctccca[A/T]tatggtgccttggagc	A	T	143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// NM_199461 // upstream //	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11
SNP_A-2055332	aataagcctgacactt[A/G]aaaaacttaaaaatcc	A	G	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2071699	acagaattctgaacat[C/T]agtataattcctctcc	C	T	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2082010	accttgttggcttcc[A/T]aagaaagtgacccatc	A	T	LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA. /// ENST00000295213 // downstream	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-2087544	tggcgcgagtttgtca[C/T]gagtatggaactgtag	C	T	Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // intron // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-2099908	agagtcacacaagata[C/T]gtttatgtatggatgt	C	T	Homo sapiens chromosome 14 open reading frame 50 (C14orf50), mRNA. /// ENST00000298705 // intron // 0 // --- //	C14orf50	C14orf50, Homo sapiens chromosome 14 open reading frame 50 (C14orf50), q23.3
SNP_A-2023911	aaaagaatccacggta[C/T]aacttgtagagttagg	C	T	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Hom	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript ,q35.3
SNP_A-2036736	aaatttaatgcaagga[C/G]aggcttaaaagtgcct	C	G	Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // intron // 0 // Hs.145384 // GLYAT //	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-2036185	aaattatggctaacaa[A/T]ctctcttttggcttcc	A	T	ENST00000358682 // intron // 0 // --- // --- // --- // ---	-	q14
SNP_A-2001194	gtaactctcaaagaca[C/T]acaaattacttttaca	C	T	// 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 85849 // Hs.42650 //	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2224781	cgtgaagactgatgaa[C/T]gatggacggctgcact	C	T	Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), mRNA. /// ENST00000317467 // intron // 0 // --- // --- // --- // ---	EPHX2	EPHX2, Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), p21.1
SNP_A-2219604	cctgtttgttagataa[A/G]attaggaaacttgaaa	A	G	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2114297	agggaatatggcaatt[G/T]aaaaccagatgcttag	G	T	// Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2121611	agtgaaggtgacttta[G/T]caattagggttgtcac	G	T	// Homo sapiens hypothetical protein FLJ35843 (FLJ35843), mRNA. /// ENST00000308208 // intron // 0 // --- // --- // --- // ---	FLJ35843	FLJ35843, Homo sapiens hypothetical protein FLJ35843 (FLJ35843), q24.11
SNP_A-2115695	agggtcaggaaaataa[C/T]ctgcttcactaatgtt	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2338677 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2164348	tcactatttcaataga[C/T]acacaaactccaattc	C	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1657518	tggagcccgccagcactgggagatc[A/G]atgtgaactggaattttcaacacat	A	G	84569 // similar to lysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17) /// NM_173577 // downstream // 398454 // Hs.375078 // C10orf126 // 283080 // chromosome 10 open	MGC33408	MGC33408 , rs10490900, similar to lysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17) ,p12.1
SNP_A-1809828	gtgagggtcattgctc[A/G]ctcagtaaaactccca	A	G	– /// ENST00000361117 // upstream // 651964 // --- // --- // ---	-	q33.2
SNP_A-1797881	ggttttggaatggaaa[C/T]gatcctgggtggagac	C	T	ENST00000341689 // intron // 0 // --- // --- // --- // ---	-	q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1846438	tatatgttcttacaca[C/G]agttatgactatcaac	C	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1860441	tcagtgtgtgaaaaac[C/T]atatggtaacatatgg	C	T	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 573350 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1838980	tagagacttcttggtc[A/G]atagtccagaaatgct	A	G	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 606023 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1967009	taagattgtgtcacat[C/T]agtgatataggtaggc	C	T	// 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 1178727 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q36.1
SNP_A-1971731	tcctaccaaaatcctt[C/T]aagataattgatgagt	C	T	Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), mRNA. /// ENST00000256458 // intron // 0 // --- // ---	IRAK2	IRAK2, Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), p25.3
SNP_A-1973234	taggagaagactatac[A/C]cactcagctaatgaat	A	C	60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 266466 // Hs.528665 // PROK2 //	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-1983784	tagcagctcttcttcc[A/G]cctccaggagtttatt	A	G	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1978650	tgactggcttatttta[C/T]atggacttggccaaag	C	T	// 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 232367 // Hs.480596 // NDST3 //	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1982589	atcatctggtcaaaac[C/T]atgagttcctggagga	C	T	Homo sapiens type 1 tumor necrosis factor receptor shedding aminopeptidase regulator (ARTS-1), mRNA. /// ENST00000296754 // intron // 0 // --- // --- // --- // ---	ARTS-1	ARTS-1, Homo sapiens type 1 tumor necrosis factor receptor shedding aminopeptidase regulator (ARTS-1), q15
SNP_A-1951118	tttccattaccatgaa[A/T]aaaagacatgtacgta	A	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1957009	ttttaatcagaagcca[A/G]ggtaacactccagggt	A	G	Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /// ENST00000264741 // intron // 0 // --- // --- // --- // ---	ITGA9	ITGA9, Homo sapiens integrin, alpha 9 (ITGA9), p22.3
SNP_A-1899191	tggaaatatctgatga[C/T]gtgactatgtcttagt	C	T	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA), mRNA. /// ENST00000305087 // intron // 0 // --- // --- // --- // --- /// ENST00000341486 // intron // 0 // --- // ---	HLA-DMA	HLA-DMA, Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA), p21.32
SNP_A-1919667	ttaaggttaagctaga[A/C]taggcatgaagtagcc	A	C	390437 // Homo sapiens olfactory receptor, family 4, subfamily N, member 5 (OR4N5), mRNA. ///	OR4N5	OR4N5, Homo sapiens olfactory receptor, family 4, subfamily N, member 5 (OR4N5), q11.2
SNP_A-1921100	ttacagtggatttaaa[A/G]tacagaaagtaatagt	A	G	Homo sapiens androgen-induced 1 (AIG1), mRNA. /// ENST00000305853 // intron // 0 // --- // --- // --- // --- ///	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-1930531	ttccaactgcctcaaa[A/T]gaaatttattagtgtg	A	T	// Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// ENST00000265631 // intron // 0 // ---	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-1928095	ttcacaaaccataaga[C/T]tcactcattttaaata	C	T	// Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 52278 // Hs.12393 // TGDS //	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-1916520	tgtttacaattcatga[G/T]caaatattttggtatt	G	T	ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 2022600	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-1911177	tgtctgcataattcag[A/C]cctatattctttctct	A	C	6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 452936 // Hs.355606	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1898166	tgctgtttgtctgtaa[C/T]catgtccttaaagaaa	C	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-1903361	tgggaaattattatga[A/C]actttgaaaggcaggt	A	C	// 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 568984 // Hs.89426 // FRK // 2444 // Homo	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1884838	tgaatcgacaggggcg[C/T]atgaagtgaggatggg	C	T	/// ENST00000326395 // upstream // 7542 // --- // --- // --- // ---	-	q24.1
SNP_A-1957845	ttttatttcatccata[G/T]cagcttatgagatttt	G	T	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000340635 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q12.1
SNP_A-1944915	ttgtggattttggaaa[A/G]aggactaactaagctt	A	G	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1987245	aacccatttcacaggc[A/G]ctgaagattcgggatt	A	G	Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), mRNA. /// ENST00000284548 // intron // 0 // --- // --- // --- // ---	OBSCN	OBSCN, Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), q42.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1963083	gaaaatgggttttgcc[C/T]ggagccttaagattgg	C	T	10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 91108 // Hs.2561 // NGFB //	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-1829395	taagtctacattctcc[A/G]cagagtccatctggtc	A	G	// 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream // 235787 // Hs.12420 // PHF17 // 79960 // Homo sapiens	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-1822344	gttttgtgaagattcc[A/C]attcctagtttaccac	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 639621 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1821345	gtttgctaagaataat[A/G]accgccaactcctttt	A	G	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1818348	gttctgttagtccagc[A/G]ctctatcctctaacat	A	G	10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 132333 // Hs.489615 // PBEF1 // 10135 // Homo	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-1865235	tccatagcagttgcac[A/G]agtctgcgtctgtgta	A	G	Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), mRNA. /// ENST00000229922 // intron // 0 // -	CAP2	CAP2, Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), p22.3
SNP_A-1870404	tcttttttactgaaat[A/G]atgacaataataatca	A	G	// 317749 // Homo sapiens dehydrogenase/reductase (SDR family) member 4 like 2 (DHRS4L2), mRNA. ///	DHRS4L2	DHRS4L2, Homo sapiens dehydrogenase,q11.2
SNP_A-1858796	tcagattgaagtcagg[C/G]aatgtgctgtatgcat	C	G	Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // intron // 0 // --- // --- // --- // --- ///	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-1758893	aacattcactgactctacactatat[A/G]taccagactctgtgctaaaggccct	A	G	caspr5 protein /// NM_138996 // intron // 0 // Hs.437463 // caspr5 // 129684 // caspr5 protein	caspr5	caspr5 , rs1030531, caspr5 protein ,q14.3
SNP_A-2157841	attgcggtgaaactac[C/T]atagcatagtgggtgg	C	T	7850 // Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA. /// NM_173343 // downstream //	IL1R2	IL1R2, Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, q11.2
SNP_A-2139736	atcgttctcaatctgc[A/G]agattcagtcacacaa	A	G	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2120894	agtctaacaatctgat[A/G]ataaatgctatttcta	A	G	ENST00000258884 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2128583	ataataggtgtgagta[C/T]gtttcactattctctt	C	T	// 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 68996 // Hs.353022 // ETAA16 //	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2131276	cacctactcatttctc[C/T]agttgcagaaaggcag	C	T	Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// ENST00000294602 // intron // 0 // --- // --- // --- // ---	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2219283	cctgtctgtgaatgat[C/T]ataaaattttggattg	C	T	219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 177655 // --- // --- // --- //	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2202969	ccactctccaaataca[A/G]cattctctcttactct	A	G	25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // --- // --- // --- // --- ///	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2205351	ccagtctgctgactac[A/G]aaaggattacagatga	A	G	Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-2210038	ccccagaaagatactc[A/T]gaaaataaacaaaatc	A	T	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// ENST00000341681 // intron // 0 // --- // --- // --- // --- /// ENST00000263881 // intron //	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-2171457	caatcagcatatcaaa[A/G]tgttttttcccaaag	A	G	151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream //	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2001011	tcaaatgaaaactgcc[C/T]aactgagctcaatgaa	C	T	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, mRNA. /// NM_201572 // intron // 0 // Hs.59093 // CACNB2 // 783 //	CACNB2	CACNB2, Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, p12.32
SNP_A-2003922	ggagctagaggtagaa[A/G]aggaaaacctggagag	A	G	9252 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA. /// NM_182398 // upstream // 4037 // Hs.510225 // RPS6KA5 //	RPS6KA5	RPS6KA5, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, q32.12
SNP_A-2024610	aaaaggtaaataaaag[A/C]ataaactgactactag	A	C	427 // Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA. /// NM_004315 // upstream // 42828 // Hs.527412 // ASAH1 //	ASAH1	ASAH1, Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, p22
SNP_A-2020694	ggccatgtgccaatta[C/G]gaaaccaccctcctaa	C	G	Homo sapiens poly(rC) binding protein 3 (PCBP3), mRNA. /// ENST00000327929 // intron // 0 // --- // --- // --- // --- ///	PCBP3	PCBP3, Homo sapiens poly(rC) binding protein 3 (PCBP3), q22.3
SNP_A-2022249	tctttttctcatgta[C/T]agaggagactcagggc	C	T	ENST00000279968 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2029373	aaagacaaaggaccac[A/G]gaaagagtgttcttgg	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 267198 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098376	agagatttaaggaaaa[A/C]gaaactgacagtgcaa	A	C	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2086376	actcttccactgctgc[A/G]ctgaccacattcctcc	A	G	Homo sapiens hypothetical protein FLJ10374 (FLJ10374), mRNA. /// ENST00000262962 // intron // 0 // --- // --- // --- // ---	FLJ10374	FLJ10374, Homo sapiens hypothetical protein FLJ10374 (FLJ10374), p13.3
SNP_A-2067935	acaactaaacttaata[C/G]caaacttcagtgaaat	C	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 484265 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2048490	aagcatctctttgcct[A/G]aaacaatcaaagtaac	A	G	// Homo sapiens riboflavin kinase (RFK), mRNA. /// NM_001490 // upstream // 5519 // Hs.521568 // GCNT1 //	RFK	RFK, Homo sapiens riboflavin kinase (RFK), q21.13
SNP_A-2270181	gacacatgcacttata[C/T]gttcattaccgtggta	C	T	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3098880 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2286701	gatggattttaaaagg[A/G]agatgatggataattt	A	G	/// ENST00000333948 // upstream // 516085 // --- // --- // --- // ---	-	q31.2
SNP_A-2248164	ctgtgggcattcatta[C/G]gactgtggccagttgt	C	G	84141 // Homo sapiens hypothetical protein FLJ13391 (FLJ13391), mRNA. /// NM_014763 // upstream // 40722 //	FLJ13391	FLJ13391, Homo sapiens hypothetical protein FLJ13391 (FLJ13391), p12
SNP_A-2250307	cttagacgcggagaag[A/G]agcatttcacagctgg	A	G	9759 // Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /// NM_207483 // upstream // 78609 // Hs.516794 //	HDAC4	HDAC4, Homo sapiens histone deacetylase 4 (HDAC4), q37.3
SNP_A-2253366	cttctgtatgtttcta[A/C]agctgcagataaaggt	A	C	Homo sapiens leptin receptor (LEPR), transcript variant 2, mRNA. /// NM_002303 // intron // 0 // Hs.23581 // LEPR //	LEPR	LEPR, Homo sapiens leptin receptor (LEPR), transcript variant 2, p31.2
SNP_A-2231559	ctatttcctaccaata[C/T]gttggacacagaatga	C	T	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 10441 //	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2235473	ctccgctgacctgttc[A/G]cttgcccagtatcatc	A	G	92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 1106511 // ---	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2244699	gctttcattcgagatg[A/C]agtacacctgccctca	A	C	123016 // Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, mRNA. /// NM_198309 //	TTC8	TTC8, Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, q32.11
SNP_A-2285846	gatgagatatcagaac[A/G]actgtattttcaagag	A	G	Homo sapiens Alstrom syndrome 1 (ALMS1), mRNA. /// ENST00000264448 // intron // 0 // --- // --- // --- // ---	ALMS1	ALMS1, Homo sapiens Alstrom syndrome 1 (ALMS1), p13.1
SNP_A-2273134	gactcaaaaaaatatg[G/T]agaataagaccatcaa	G	T	Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2308081	gcttgacttcagagaa[A/G]agtcccgccggagacc	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1469469 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2293245	gcagagctgtttacag[A/G]catctattggcctccc	A	G	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA. /// ENST00000311458 // intron // 0 // --- // --- // --- // ---	ITPK1	ITPK1, Homo sapiens inositol 1,3,4-triphosphate 5 q32.13
SNP_A-2289928	gcaaagaggctgttca[C/T]atcgtgtcttcattgt	C	T	94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 165492 // --- // --- // --- //	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-2287969	gattatgtggaatttc[C/G]aaatttttacagtga	C	G	4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 649726 // Hs.166017 // MITF //	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-2084948	actcaattcagaacaa[C/T]tcaccttctatatata	C	T	// Homo sapiens hypothetical protein FLJ32440 (FLJ32440), mRNA. /// ENST00000287437 // intron // 0 // --- // --- // --- // ---	FLJ32440	FLJ32440, Homo sapiens hypothetical protein FLJ32440 (FLJ32440), q24.13
SNP_A-2037038	aacaaaaaatacaccc[A/T]aatatggaaaaacagg	A	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2040747	aacccagatcacgtca[G/T]gtagaaagtcaaacag	G	T	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2003253	ggatgaaagcaaaaaa[C/G]agttcatggatagatc	C	G	ENST00000332738 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1997262	tctaaagtcagctgaa[A/T]ttatttttgctttcatg	A	T	Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA. /// ENST00000311678 // intron // 0 // --- // --- // ---	C9orf3	C9orf3, Homo sapiens chromosome 9 open reading frame 3 (C9orf3), q22.32
SNP_A-2012389	tttgatatgtctttta[C/G]cggttcctaaaaatag	C	G	ENST00000353474 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-2014080	agcatcaataatagga[C/G]atactttcactatttg	C	G	84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 138657 //	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-2015863	tcctctctatctcttc[A/G]agcttacttacccttg	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 115475 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2011450	aattggaacattctta[C/T]agtttgtgtaaaaagc	C	T	2568 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA. /// NM_021025 // upstream //	GABRP	GABRP, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), q35.1
SNP_A-2169698	caaggaagcagaaata[C/T]agccagagatttatac	C	T	sapiens Bardet-Biedl syndrome 2 (BBS2), mRNA. /// ENST00000245157 // intron // 0 // --- // --- // --- // ---	BBS2	BBS2, Homo sapiens Bardet-Biedl syndrome 2 (BBS2), q12.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175170	cacagttagcagatga[A/C]caaagagactaattca	A	C	9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1822770 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2186499	cagggaattgaaactc[A/G]agagcttagcttcaaa	A	G	22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 41846 // Hs.306831 //	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-2188987	cagtgtggaaagagaa[C/G]aggataatggtaagga	C	G	8898 // Homo sapiens myotubularin related protein 2 (MTMR2), transcript variant 1, mRNA. /// NM_201278 //	MTMR2	MTMR2, Homo sapiens myotubularin related protein 2 (MTMR2), transcript variant 1, q21
SNP_A-2218915	cctgggttctctgcga[C/T]gtgcttcactgacctt	C	T	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2215487	cctcactgcttcatta[A/G]gttttgatcctggcta	A	G	Homo sapiens cortactin binding protein 2 (CTTNBP2), mRNA. /// ENST00000160373 // intron // 0 // --- // --- // --- // ---	CTTNBP2	CTTNBP2, Homo sapiens cortactin binding protein 2 (CTTNBP2), q31.2
SNP_A-2129722	atacagtacatataca[A/G]gaagactgtctaggca	A	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 546997 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2115667	agggtattgggaatca[C/T]agccagatgtaatggc	C	T	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2113923	aggcttactctcttaa[C/T]aggggtgtatgtaatg	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2115285	aggggacgtggttcac[C/T]gaactgctgtttccct	C	T	Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST00000335473 // intron // 0 // --- // --- // --- // ---	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2146904	atggaaaaatacaggc[C/T]ctagtatagataaaat	C	T	MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2165838	caaagtcagtgctact[A/G]aataccacattacagg	A	G	5912 // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA. /// ENST00000323534 //	RAP2B	RAP2B, Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), q25.2
SNP_A-2164126	caaaaggagctctgaa[A/G]ggacacacaggaaacg	A	G	// 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 43998 // Hs.132344	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2161032	atttcttggaataagc[C/T]agttttaaaaatcaac	C	T	// Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4), mRNA. /// NM_004411 // upstream // 153200 //	PDK4	PDK4, Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4), q21.3
SNP_A-1788676	gggatgcctctctgta[G/T]ggaaggccaagcttct	G	T	ENST00000331749 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1859321	tcagcttaagtgctca[A/G]gatagattcttctcac	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1849004	tatgcagttatggaaa[C/T]tgacacagaattcaga	C	T	ENST00000358765 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-1870270	tcctttcttcttccta[C/T]agattcctaaactatg	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1864663	tccagcagaagtctaa[C/T]tggcgtcccttcccca	C	T	2326 // Homo sapiens flavin containing monooxygenase 1 (FMO1), mRNA. /// NM_002021 // downstream // 3015 //	FMO1	FMO1, Homo sapiens flavin containing monooxygenase 1 (FMO1), q24.3
SNP_A-1817958	gttctacaactgcaag[A/G]atcaaaattctgtcat	A	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1821361	gtttgctgggtgctcc[A/G]cataaaccatttcata	A	G	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), mRNA. /// ENST00000330569 // intron // 0 // --- // --- // --- // ---	KCNQ3	KCNQ3, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), q24.22
SNP_A-1819388	gttggctactttattc[C/T]aaatcattcaattcat	C	T	996 // Homo sapiens cell division cycle 27 (CDC27), mRNA. /// ENST00000309965 // downstream // 59619 // --- // --- // ---	CDC27	CDC27, Homo sapiens cell division cycle 27 (CDC27), q21.32
SNP_A-1825339	taaagtttagttttca[A/G]gatcctctgtgattca	A	G	5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 135372 // ---	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1832847	tacaatcataagagta[G/T]agaaaatggttctttt	G	T	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1974987	gctaacatcttaaagc[A/T]ccatgtcttattaatt	A	T	389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// ENST00000356539 // intron // 0 // --- // --- // --- // ---	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-1983864	tgtttttggactaga[C/T]aaacttttctgttaca	C	T	3776 // Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), mRNA. /// NM_016121 // upstream //	KCNK2	KCNK2, Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), q41
SNP_A-1982394	gttagcaagtatgtgg[A/T]aaactctgaattcagt	A	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 316090 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1946835	tttaagaggagattag[A/G]ccattagagtttcttc	A	G	// 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1933119	ttcgtgattgccataa[A/C]cattgtggtaaactga	A	C	722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 101308 // Hs.527653 // DAF // 1604 // Homo sapiens decay	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950906	tttccacaatgttaaa[C/T]gattttccttatttca	C	T	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 3 (EMR3), transcript variant 2, mRNA. /// NM_032571 // intron // 0 // Hs.295626 // EMR3 // 84658 //	EMR3	EMR3, Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 3 (EMR3), transcript variant 2, p13.12
SNP_A-1950895	tttccaattgcctccc[A/G]cagggtgtagtactat	A	G	ENST00000242315 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-1901143	tggatcttcagcataa[A/G]ctatttttattcatta	A	G	6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 266502 // Hs.522891 // CXCL12 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1928647	ttcactttaaaacaga[A/T]gaagggcaaggtgcaa	A	T	Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // --- // --- // --- // --- ///	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1929352	ttcagtcttctgtaaa[C/T]gtagattgaggagaag	C	T	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1919903	ttaataaatggtgcta[C/G]acaaagtggatagaca	C	G	10106 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2), mRNA. /// ENST00000310189 // upstream //	CTDSP2	CTDSP2, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (CTDSP2), q14.1
SNP_A-1955434	tttggtaaactttgaa[A/G]cactactttatctact	A	G	Homo sapiens MAWD binding protein (MAWBP), mRNA. /// ENST00000358769 // intron // 0 // --- // --- // --- // --- ///	MAWBP	MAWBP, Homo sapiens MAWD binding protein (MAWBP), q21.3
SNP_A-1956529	tttgtttaatatctaa[C/G]tagccctaaggttaat	C	G	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2054771 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1939802	ttgcaagattctgtta[C/T]cttcatggacaatatt	C	T	/// ENST00000281516 // upstream // 39237 // --- // --- // --- // ---	-	q14.11
SNP_A-1833058	tacacagatatcaagc[C/G]ctttataatctagaca	C	G	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // --- // --- // --- // --- /// ENST00000260943 // intron //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1810794	gtgcagatggcccaga[A/G]gagtagctgtccccac	A	G	11172 // Homo sapiens insulin-like 6 (INSL6), mRNA. /// NM_002195 // upstream // 9194 // Hs.418506 // INSL4 // 3641	INSL6	INSL6, Homo sapiens insulin-like 6 (INSL6), p24.1
SNP_A-1808093	gtcttgcaggactgtc[A/G]caggaattaagtgaca	A	G	TNFSF11 // 8600 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, mRNA. /// NM_033012 // downstream // 92998 //	TNFSF11	TNFSF11, Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, q14.11
SNP_A-2128368	ataagtgtacttgacc[A/G]cagagctttttcagtc	A	G	Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), mRNA. /// ENST00000305531 // intron // 0 // --- //	FRMPD2	FRMPD2, Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), q11.22
SNP_A-2208032	cccaagaaagcccaaa[G/T]gttacatccaggactt	G	T	2919 // Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA. /// NM_002619 // downstream // 37196 // Hs.81564 //	CXCL1	CXCL1, Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), q13.3
SNP_A-2180782	cagaatagaaaactga[A/G]cttactgtagaatcct	A	G	ENST00000335259 // intron // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-2013294	attaaagcaccaccca[A/G]gtagaggtctattcta	A	G	ENST00000335595 // intron // 0 // --- // --- // --- // ---	-	p21.2
SNP_A-1991584	ttctagaatgagaaaa[A/G]agaagacttgctctgc	A	G	// 127623 // Homo sapiens olfactory receptor, family 2, subfamily B, member 11 (OR2B11), mRNA. /// NM_198074 // downstream // 70138 // Hs.332905 // OR2C3 // 81472 //	OR2B11	OR2B11, Homo sapiens olfactory receptor, family 2, subfamily B, member 11 (OR2B11), q44
SNP_A-2037954	aacaattattctagcc[G/T]agttattttccatatt	G	T	Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-2088758	actgtgtgaacttgca[C/T]gggagcacaaaagccc	C	T	mRNA for KIAA0257 gene, partial cds. /// ENST00000186436 // intron // 0 // --- // --- // --- // ---	RW1	RW1, Human for KIAA0257 gene, partial cds. q11.2
SNP_A-2083130	acgtttaacgagaaaa[A/G]agaagacgtaacattt	A	G	FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// NM_198278 // upstream //	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-2097179	agacttccttatcctg[A/G]agacttttgttaaaca	A	G	1493 // Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA. /// NM_012092 // upstream //	CTLA4	CTLA4, Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), q33.2
SNP_A-2103335	agcaaggcaggtagaa[A/G]agacaaaatcagaagg	A	G	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2292222	gcaccgtatggtgcta[C/T]agttttttgaggcag	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2312618	ggacggattccccaca[A/G]tgaaagtttcagttca	A	G	/// ENST00000357663 // downstream // 290483 // --- // --- // ---	-	q22.2
SNP_A-2311474	ggaatctggctacatc[C/T]atactgctaaacctca	C	T	10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// ENST00000334578 // downstream // 127488 // ---	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2280496	gaggtaaaataaagga[A/G]gcataactataatacc	A	G	Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // --- // -	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-2243325	ctgccttgcagttata[C/T]ctctttctctgctgca	C	T	METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream //	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2237446	ctctcctcctcacgca[A/G]gttcgaccttagctca	A	G	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2239297	ctctttaatatatcaa[C/T]gttttggaacttctga	C	T	ENST00000319688 // intron // 0 // --- // --- // --- // ---	-	p25.1
SNP_A-2285796	gatgacttgccatcca[A/G]tcctttctgtttgtgt	A	G	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 235028 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2267631	gaatcaaggaaattca[A/G]taattaccgtgattta	A	G	50834 // Homo sapiens taste receptor, type 2, member 1 (TAS2R1), mRNA. /// NM_199133 // downstream // 64569 //	TAS2R1	TAS2R1, Homo sapiens taste receptor, type 2, member 1 (TAS2R1), p15.2
SNP_A-2262130	gaaatcaacatgacta[C/T]gatccagttttaagtt	C	T	// 5274 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// NM_014498 // downstream // 174519 // Hs.143600	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2308785	gctttgcatttaggta[A/G]gttaactcattttagg	A	G	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1948390 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2289902	gcaaagaaaagaaaaa[C/T]gaagccaatgtgaaca	C	T	// Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 37525 // --- // --- // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2057683	aatatgggaagcctta[A/G]gaagagttctaatggt	A	G	// 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 635827 // --- // --- // --- // ---	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2065248	aattgggataaaccta[C/T]acttaatacatatata	C	T	64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 169566 //	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-2073130	acaggcagtgtggtga[A/G]aagtgcgaggagccca	A	G	8738 // Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// NM_003805 // downstream // 41066 // Hs.38533 // CRADD // 8738 //	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-2030092	aaagattttctgaagc[C/T]aacttgctttctgaaa	C	T	Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), mRNA. /// ENST00000311042 // intron // 0 //	MOBP	MOBP, Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), p22.2
SNP_A-1992246	tcttagtctctattaa[G/T]gttaccagtggagaat	G	T	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2016504	gtttttgcattgtttc[A/G]aattttcttttttcatt	A	G	// 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.2
SNP_A-2018855	tggaatcaaacagaga[A/C]gttgaaaaacaaggat	A	C	Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // intron // 0 // Hs.505146 // CLDN14 //	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-2186969	caggtaaatttctctc[C/G]attggcttccctccca	C	G	80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 3356 //	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-2195285	catggccaagtactga[C/G]gatagagcagagaaca	C	G	54970 // Homo sapiens tetratricopeptide repeat domain 12, mRNA (cDNA clone MGC:40285 IMAGE:5219117), complete cds. /// NM_017868 // downstream // 5709 // Hs.288772 //	TTC12	TTC12, Homo sapiens tetratricopeptide repeat domain 12, (cDNA clone MGC:40285 IMAGE:5219117), complete cds. ,q23.2
SNP_A-2196299	catgtgtttgtcttgc[A/T]agtgtgtcggaaggag	A	T	// 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 990802 // Hs.192039 // PTPRC	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q32.1
SNP_A-2202690	ccaccttggaaataga[G/T]gatccaaccccactca	G	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2215943	cctccactcctgggca[C/T]aagtgtcctctcacct	C	T	// Homo sapiens argininosuccinate lyase (ASL), mRNA. /// NM_014478 // upstream // 21667 // Hs.300684 // RCP9 //	ASL	ASL, Homo sapiens argininosuccinate lyase (ASL), q11.21
SNP_A-2226778	ctaataagacaaagaa[A/G]ctcactgtatagtcca	A	G	// 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 103177 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2128526	ataatacattagctaa[A/G]gtgtgttagaaatatg	A	G	/// ENST00000343481 // downstream // 403344 // --- // --- // ---	-	q24.1
SNP_A-1787419	gggaagtaccattcca[C/T]gctcttcagactggtg	C	T	sapiens spleen tyrosine kinase (SYK), mRNA. /// ENST00000340029 // intron // 0 // --- // --- // --- // --- ///	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-1793723	ggtatgtttttaaaag[C/G]ccaggtctggagtctg	C	G	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1654605	tcctgaggtagaccagcatagtttc[A/G]aatagaccctggaatggatttgaac	A	G	NM_148976 // intron // 0 // Hs.82159 // PSMA1 // 5682 // proteasome (prosome, macropain) subunit, alpha type, 1	PSMA1	PSMA1 , rs10500803, proteasome (prosome, macropain) subunit, alpha type, 1,p15.2
SNP_A-1831012	taatgagctaacctag[A/G]attctaagtcccagcc	A	G	ENST00000304372 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1862469	tcatgttcccaaatcc[C/T]cctcacagctctgtga	C	T	140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 54921 // Hs.31845 // ASB7 //	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1851692	tattcttccctgcacc[A/G]caatccagaatgtgcc	A	G	ITGA11 // 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, mRNA. /// NM_012211 //	ITGA11	ITGA11, Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, q23
SNP_A-1855294	tcaaggaaggcacttg[G/T]agatagatgaggatat	G	T	Homo sapiens protein kinase C binding protein 1 (PRKCBP1), transcript variant 2, mRNA. /// NM_183048 // intron // 0 // Hs.446240 // PRKCBP1 // 23613 // Homo	PRKCBP1	PRKCBP1, Homo sapiens protein kinase C binding protein 1 (PRKCBP1), transcript variant 2, q13.12
SNP_A-1961819	aacaaactcatttaga[C/T]tagagacactgtgatt	C	T	sapiens CD53 antigen (CD53), mRNA. /// ENST00000271324 // intron // 0 // --- // --- // --- // ---	CD53	CD53, Homo sapiens CD53 antigen (CD53), p13.3
SNP_A-1961642	gaaagaaaaacagcaa[A/G]atgccacagtggagcc	A	G	Homo sapiens CD3-epsilon-associated protein; antisense to ERCC-1 (ASE-1), mRNA. /// ENST00000309424 // CDS // 0 //	ASE-1	ASE-1, Homo sapiens CD3-epsilon-associated protein; antisense to ERCC-1 (ASE-1), q13.32
SNP_A-1986976	tcaatgtgaggaatta[G/T]gctaggtttcatggag	G	T	253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 630016	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-1969234	tgccctgatataaacc[A/G]cctgggaatctaaggg	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1962204	tagaactgctctgaca[C/G]taggatgaatagagac	C	G	// 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 263474 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1969118	caggatattttaaaag[C/G]acttccatttaggtat	C	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1930165	ttcattcacagtgtta[G/T]gtaaccactatttctg	G	T	8638 // Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, mRNA. /// NM_003733 // upstream // 74506 // Hs.118633 // OASL // 8638 // Homo	OASL	OASL, Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, q24.31
SNP_A-1904853	tggggtttactaccac[C/T]gtgaatgtccaatcca	C	T	// Homo sapiens male germ cell-associated kinase (MAK), mRNA. /// NM_005906 // upstream // 19542 // Hs.446125 //	MAK	MAK, Homo sapiens male germ cell-associated kinase (MAK), p24.2
SNP_A-1904162	tgggcccagaactata[A/G]ctacaggagtagaagg	A	G	55149 // Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA. /// ENST00000298635 // upstream //	PAPD1	PAPD1, Homo sapiens PAP associated domain containing 1 (PAPD1), p11.23
SNP_A-1882065	tcttttgttaattgta[G/T]gtgttgcagatatctt	G	T	DKFZP564B1023 // 83479 // Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA. /// NM_203459 // upstream // 67805 // Hs.23585 // KIAA1078 //	DKFZP564B1023	DKFZP564B1023, Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), q32.1
SNP_A-1918350	ttaaagtagacctaaa[C/G]agcgagataatagtaa	C	G	5359 // Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /// NM_032153 // downstream // 62052 // Hs.415766	PLSCR1	PLSCR1, Homo sapiens phospholipid scramblase 1 (PLSCR1), q24
SNP_A-1931836	ttccgacactaaaaaa[C/T]gagcattggcgcatta	C	T	4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1921103	ttacagtgggaccaca[A/G]agataaaggacctgcc	A	G	84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// NM_032808 // upstream // 158777 //	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-1920569	ttaatttattcatgca[A/G]gaaatgtttattgtac	A	G	5912 // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA. /// ENST00000323534 //	RAP2B	RAP2B, Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), q25.2
SNP_A-1983597	tccactttattataca[C/T]gaactgcagcaaatct	C	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// ENST00000281894 // intron // 0 // --- // --- // --- // ---	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41
SNP_A-1961112	tttttgttctgtagtc[A/C]agatagcctcgaatgc	A	C	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 82027 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1957961	ttttcaataaaattta[C/T]gaaaaaatgcagcctt	C	T	57119 // Homo sapiens serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin) (SPINLW1), transcript variant 2, mRNA. /// NM_020398 // upstream // 2111 //	SPINLW1	SPINLW1, Homo sapiens serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin) (SPINLW1), transcript variant 2, q13.12
SNP_A-1949942	tttcaataatgaatga[C/T]gctgtgaatacagctg	C	T	/// ENST00000321719 // upstream // 677654 // --- // --- // --- // ---	-	p11.21
SNP_A-1942880	ttgggggtggtttaa[A/G]gatttgatgcaaagca	A	G	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 558330	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-1824581	taaagaaaatgtcttc[A/C]aatagattcatttata	A	C	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 128101 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-1823020	taaaaatgctgaattg[A/G]aagacatgaaagtagg	A	G	5325 // Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA. /// NM_002656 // upstream // 52126 // Hs.444975 // PLAGL1 // 5325 // Homo	PLAGL1	PLAGL1, Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, q24.2
SNP_A-1818963	gttgcaaaacctgttg[C/T]acagatccgtggaaac	C	T	Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters), member 2	SLC12A2	SLC12A2, Homo sapiens solute carrier family 12 (sodium,q23.2
SNP_A-1820275	gtttacttagcccaca[A/G]tgctcaatccctcgtg	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 52452 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1821312	gtttgcattttgagac[A/G]cttgactgagaggctt	A	G	81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// NM_030794 // upstream // 59069 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1693823	cttaacatccctgtaatatatccta[C/T]ggctcaggtctgcgacacggtcccg	C	T	AB046800 // intron // 0 // Hs.135736 // NGL-1 // 57689 // netrin-G1 ligand	NGL-1	NGL-1 , rs10501226, netrin-G1 ligand,p12
SNP_A-1783286	ggcagtgaatgcacaa[A/C]tcaccagctaggtatg	A	C	-- /// ENST00000308105 // upstream // 36020 // --- // --- // --- //	-	q44
SNP_A-1783944	ggccacccaagtcagc[C/T]gcggaaacccacttgg	C	T	1021 // Homo sapiens cyclin-dependent kinase 6 (CDK6), mRNA. /// NM_152703 // downstream // 107029 // Hs.489118	CDK6	CDK6, Homo sapiens cyclin-dependent kinase 6 (CDK6), q21.2
SNP_A-1796937	ggttcctggcacaacc[A/T]cactaagcaagtagat	A	T	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 334565 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2107928	agctccctttttttaa[C/T]tgtgcaaaatacacat	C	T	MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2119625	agtatggttcagcaca[A/G]cgttattactgatcct	A	G	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 31290 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2138547	atccattcatttcata[C/T]ggtcgggaatccccac	C	T	Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 //	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2143723	atgagaagttaaacca[A/G]tggagccttatgggaa	A	G	Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // --- //	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-2143378	atgaccactaggatgc[A/G]acatgaaggcaatatg	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 // upstream // 62708 // Hs.20805 // TSAP6 // 55240 // Homo	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2223307	cgctaatgaacgaaat[C/T]agtgcccttataagaa	C	T	// Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 578684 // ---	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2213985	cctaactgctgtctcc[A/G]aaggtaatcactcttg	A	G	// Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), mRNA. /// ENST00000261486 // intron // 0 // --- // --- // --- // ---	EPB41L4A	EPB41L4A, Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), q22.2
SNP_A-2207572	tattgggaggtcaaaa[G/T]catagcacagcaacaa	G	T	// 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 15530 //	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2190014	cataacctttaacagc[G/T]aatagtcttgaaactg	G	T	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 26389 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-2175814	cacattgtaaataaac[C/T]atagtgcaacccaaga	C	T	6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2009483	actcaatttaaaaaaa[A/G]tctctgagtgctggaa	A	G	Homo sapiens hypothetical protein FLJ35155 (FLJ35155), mRNA. /// ENST00000310380 // intron // 0 // --- // --- // --- // ---	C3orf21	C3orf21, Homo sapiens hypothetical protein FLJ35155 (FLJ35155), q29
SNP_A-1997264	atgttggcaatagaac[A/G]cttctgaaaccagtgg	A	G	Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA. /// ENST00000311678 // intron // 0 // --- // ---	C9orf3	C9orf3, Homo sapiens chromosome 9 open reading frame 3 (C9orf3), q22.32
SNP_A-1997996	atatgtgtgaaaacag[C/G]agctgagacattcttg	C	G	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 17053 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-2002854	agagttttctgtatac[C/T]ggagacctggaggcat	C	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 338732 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2004004	tttcccagagaaaagg[C/G]cataatttgaggggtt	C	G	3087 // Homo sapiens hematopoietically expressed homeobox (HHEX), mRNA. /// NM_019053 // upstream //	HHEX	HHEX, Homo sapiens hematopoietically expressed homeobox (HHEX), q23.33
SNP_A-2029205	aaagaagaaagtgtac[C/T]gaaaatagtaaatcag	C	T	Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // intron // 0 // --- // --- // --- // --- ///	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-2031593	aaagtaaaagtaaatc[A/T]ataggaatgcctcttt	A	T	219409 // Homo sapiens GS homeobox 1 (GSH1), mRNA. /// NM_000209 // upstream // 42048 // Hs.32938 // IPF1 // 3651	GSH1	GSH1, Homo sapiens GS homeobox 1 (GSH1), q12.2
SNP_A-2025958	aaaatgtggtccagaa[G/T]agctgtcatgtcagaa	G	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 453646 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2040217	aaccaattgtattttg[A/G]acatgatttaacatct	A	G	COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 301316 //	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-2064996	aattgatgcccactca[A/G]gttgttcctggttttt	A	G	163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 26477 // Hs.221375 //	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2080000	acccttttgcaataa[C/T]tagcacaccctagatg	C	T	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2266250	gaaggggtggtgtttg[C/T]aaatggcaccgatacg	C	T	Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// ENST00000258416 // intron // 0 // --- // -	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-2272040	gaccctcctggcaaaa[A/C]aattattaacaacaac	A	C	ENST00000314331 // intron // 0 // --- // --- // --- // ---	-	q26.11
SNP_A-2239906	ctgaacctgatagaga[C/T]aaatagaaagagaata	C	T	10060 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B,	ABCC9	ABCC9, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p12.1
SNP_A-2228876	ctagatagatggaatc[A/G]cccaagccaaggcaca	A	G	SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 158087 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2247557	ctgtctgggcttaaac[G/T]actcattatcctcagc	G	T	9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // downstream //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-2254459	cttgccccctattttg[A/T]agtaattgatctaaga	A	T	FLJ46831 // 399823 // Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 58342 //	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-2232357	ctcacaaggctgtgga[A/T]aggatcgaactgagag	A	T	Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /// ENST00000328788 // intron // 0 // --- // --- // --- // --- ///	FRMD3	FRMD3, Homo sapiens FERM domain containing 3 (FRMD3), q21.32
SNP_A-2234348	ctccaaccacccaaac[C/T]aaatcagaacctccaa	C	T	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // --- // --- // --- // ---	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2260980	agaaaatcattgcaag[C/T]catgtagctaattaag	C	T	// Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 598778 // Hs.451286 // C15orf2 //	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-2264050	gaactcgcgttctccc[A/G]caaaattcatctgaaa	A	G	sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA. /// ENST00000309446 // intron // 0 // --- // --- // --- // --- ///	KLF7	KLF7, Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), q33.3
SNP_A-2297768	gccaggatggacgtac[A/C]acttgtgtgaattcag	A	C	3195 // Homo sapiens T-cell leukemia, homeobox 1 (TLX1), mRNA. /// NM_006562 // downstream // 31836 // Hs.37128 //	TLX1	TLX1, Homo sapiens T-cell leukemia, homeobox 1 (TLX1), q24.32
SNP_A-2301231	gccttgccttttgaga[A/G]ctttggaggaaatttg	A	G	// 80067 // Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 // downstream //	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-2300127	gcctcatggtagtaaa[C/T]ataggtaagtgttgga	C	T	4776 // Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 (NFATC4), mRNA. /// NM_004554 // downstream // 12082 // Hs.77810 // NFATC4 //	NFATC4	NFATC4, Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 (NFATC4), q11.2
SNP_A-2299046	gcccctctgaagtgtc[A/G]cacacatcttgctgta	A	G	4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // downstream // 181781 // Hs.307734 // MME //	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN q25.31
SNP_A-2305737	gctgccgcagtcaggc[C/T]ctttccttttaaaaat	C	T	6154 // Homo sapiens ribosomal protein L26 (RPL26), mRNA. /// NM_016093 // downstream // 10950 // Hs.546390	RPL26	RPL26, Homo sapiens ribosomal protein L26 (RPL26), q35.1
SNP_A-2304642	gctctgaagagttaca[G/T]aaaacatcccgggtca	G	T	// 4726 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA. /// NM_016358 // downstream // 15843 // Hs.196927 // IRX4 // 50805 // Homo sa	NDUFS6	NDUFS6, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), p15.33
SNP_A-2105559	cccaattaaaagtatc[C/T]ttgcagttttccttaa	C	T	ENST00000299308 // intron // 0 // --- // --- // --- // ---	-	q24.31
SNP_A-2094282	agaagtaatcaccagt[A/C]acactgagcagttgtt	A	C	Homo sapiens calcium channel, voltage-dependent, P/Q type, alpha 1A subunit (CACNA1A), transcript variant 2,	CACNA1A	CACNA1A, Homo sapiens calcium channel, voltage dependent, P,p13.13
SNP_A-2072075	acagagttactatcac[A/G]ctttggaaggatgtct	A	G	23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// NM_001351 // downstream // 55163 // Hs.73078 //	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-2058994	aatccattatattcag[A/T]caattatctcccctcc	A	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 710805 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2040338	aaccactgtcctaaaa[C/T]tgaatttatttcatcc	C	T	Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // --- // --- // --- // ---	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2036247	aaattcaaggactgta[C/T]agaactgtaggccatt	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2017160 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2034082	aaatcagttggattga[C/T]gaaagctatgagaaga	C	T	ENST00000356494 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2032564	aaataaaatttagaag[G/T]cctgataataacatta	G	T	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// NM_024767 // intron // 0 // Hs.134296 //	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-2177022	cacctattcttagggt[A/C]acattttggatattgc	A	C	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1729000 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2185773	caggatatacagagag[A/T]caggggacaatggaga	A	T	81544 // Homo sapiens hypothetical protein PP1665 (PP1665), mRNA. /// NM_001235 // upstream // 19093 //	PP1665	PP1665, Homo sapiens hypothetical protein PP1665 (PP1665), q13.5
SNP_A-2184356	cagcgagctatgtgac[C/T]ggtgggagtgtcataa	C	T	6478 // Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA. /// NM_052995 // downstream //	SIAH2	SIAH2, Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), q25.1
SNP_A-2196741	cattacacactacaat[C/G]actgcaatcaactcag	C	G	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2210483	ccccctccatgtcata[A/T]ctatttcaaaattgtg	A	T	/// ENST00000321014 // upstream // 521967 // --- // --- // --- // -	-	p12.3
SNP_A-2223267	cgcgccgactgtgtcc[A/G]cttcttcccctccgcg	A	G	9150 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), transcript variant /// NM_048368 // downstream // 29897 // Hs.465490 // CTDP1 //	CTDP1	CTDP1, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), transcript variant ,q23
SNP_A-2145085	atgcaaatattataaa[A/T]tcaggttatgggatgt	A	T	// 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 391589 // Hs.369438 // ETS1 //	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.2
SNP_A-2151939	atgttttatctattac[A/G]cttatgcaacagaggt	A	G	4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 151342 // --- // --- // --- // ---	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2162544	attttccctgagtaaa[C/T]catctgaagcggagct	C	T	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA. /// ENST00000337195 // intron //	CTBP2	CTBP2, Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, q26.13
SNP_A-2165430	caaagcaattcctaaa[C/G]aggcactggacttcaa	C	G	ENST00000299563 // intron // 0 // --- // --- // --- // ---	-	q13.4
SNP_A-2157550	attgattacaattctg[A/G]caatatttttccatca	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 436271 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.1
SNP_A-2156539	attctcttttcaacca[C/T]gttcattttggagata	C	T	401263 // Homo sapiens FLJ41841 protein (FLJ41841), mRNA. /// ENST00000339488 // upstream // 59506 // --- // ---	FLJ41841	FLJ41841, Homo sapiens FLJ41841 protein (FLJ41841), p12.3
SNP_A-2155323	aataattatttgctca[A/G]tgaccacaaacattac	A	G	Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // intron // 0 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-2122234	agtgcacctcagtgaa[A/G]cctcatgtgttaccca	A	G	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 47324 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2113658	aggctcatggctggaa[C/T]ctgtgttctcactctt	C	T	// 7278 // Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, mRNA. /// NM_006001 // downstream // 433484 //	TUBA2	TUBA2, Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, q11
SNP_A-2131825	atagcttacatttatt[A/G]aactctcaccaggtgt	A	G	64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 309719 //	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2133200	atatagtcttgtccaa[C/T]ccttcatggtcgacat	C	T	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 114537 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2133767	atatcctagagtttta[G/T]gtggaagaaatacttg	G	T	126402 // Homo sapiens hypothetical protein FLJ40365 (FLJ40365), mRNA. /// NM_012114 // upstream // 20635 //	FLJ40365	FLJ40365, Homo sapiens hypothetical protein FLJ40365 (FLJ40365), p13.12
SNP_A-2135245	atattgtacttatgca[A/G]ctataagccaaagaac	A	G	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1793644	ggtatgaatgacagca[C/T]ctgaagacatctgata	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1215978 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1713934	taactagttgaaacttgattgctac[A/C]aaattagaaatggaggaaattatag	A	C	// 3556 // interleukin 1 receptor accessory protein /// NM_134470 // downstream // 578069 // Hs.143527 // IL1RAP	IL1RAP	IL1RAP , rs9290978, interleukin 1 receptor accessory protein ,q28
SNP_A-1842383	taggtcactttaatac[C/T]ctgcttgaaagttact	C	T	Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// ENST00000286545 // intron // 0 // --- // --- // --- // ---	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-1863153	tcatttattgttagtt[C/G]aacatttttaaaattt	C	G	// Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, mRNA. /// NM_016083 // upstream //	CNR1	CNR1, Homo sapiens cannabinoid receptor 1 (brain) (CNR1), transcript variant 2, q15
SNP_A-1984978	aagaaacatccacatc[C/T]ctgtctatgaaatctg	C	T	Homo sapiens chromosome 6 open reading frame 151 (C6orf151), mRNA. /// ENST00000342415 // intron // 0 // --- //	C6orf151	C6orf151, Homo sapiens chromosome 6 open reading frame 151 (C6orf151), p24.3
SNP_A-1975395	tctaaccatattctga[C/T]gttgtagagacaatag	C	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1922121	ttacttaagctcttgt[C/T]aacatcggctcatcca	C	T	266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), mRNA. /// NM_003220 // downstream // 186375 //	OFCC1	OFCC1, Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1926335	ttattatagccattac[A/G]gaaaaaactatggagg	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2275843 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.2
SNP_A-1907556	tgtaaattatacctca[A/G]taaatgtgacatatat	A	G	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1908800	tgggatctaaaaatca[A/G]aatgattgaactcttg	A	G	276 // Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /// ENST00000332554 // downstream // 64097 // --- //	AMY1A	AMY1A, Homo sapiens amylase, alpha 1A; salivary (AMY1A), p21.1
SNP_A-1901975	tggcagtgaacaagag[A/G]atggttaggggtccca	A	G	Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), mRNA. /// ENST00000361062 // intron // 0 // --- // --- // --- // ---	TNIP1	TNIP1, Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), q33.1
SNP_A-1892476	tgcaagtttatacata[C/G]acataagcaacaaata	C	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2484457 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1901311	tggatgtataactgaa[A/G]aatatttgagttggtt	A	G	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1898172	tgctgttttgcagaaa[C/T]ggttgttccttctctc	C	T	FLJ46321 // 389763 // Homo sapiens FLJ46321 protein (FLJ46321), mRNA. /// NM_152573 // downstream // 141365	FLJ46321	FLJ46321, Homo sapiens FLJ46321 protein (FLJ46321), q21.32
SNP_A-1886765	tgactgatattcactc[C/T]ctccctcctctaacgt	C	T	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 404596 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-1906557	tggtggtctgtgccaa[G/T]gtcaacagagtaactt	G	T	Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1930415	ttcatttttctggaaa[C/T]gtttagagactgctag	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, mRNA. /// NM_021912 // intron // 0 // Hs.302352 // GABRB3 // 2562 // Homo sapiens	GABRB3	GABRB3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, q12
SNP_A-1984954	cttggcatatgtttgc[C/T]gaaataaaacccaact	C	T	// 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 75298 //	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-1981867	ttttgtggtcactata[A/T]cttttccttgatggct	A	T	HTR1A // 3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. ///	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.1
SNP_A-1947528	tttaccaaggtaagga[C/G]atggacaaatagccta	C	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 425133 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1960554	tttttcagttttcctc[A/G]cgttattgacttctag	A	G	// 474 // Homo sapiens atonal homolog 1 (Drosophila) (ATOH1), mRNA. /// NM_020159 // upstream // 255817 //	ATOH1	ATOH1, Homo sapiens atonal homolog 1 (Drosophila) (ATOH1), q22.3
SNP_A-1864070	tgagttgccagaaaac[C/T]aaaggaatgaaaagtg	C	T	Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 //	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-1857099	tcacccttgaacagca[A/C]ctcctgctcactaaag	A	C	GABARAPL1 // 23710 // Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), mRNA. ///	GABARAPL1	GABARAPL1, Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), p13.2
SNP_A-1843805	tagttaagctcagcag[G/T]aatcatgaaatctaac	G	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 396599 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1826490	taacaacggagaccac[A/G]gaactacaaataatta	A	G	GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream //	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-1742611	agcatttcacaaacatgtggtagac[C/T]ggagaattggactaagaactgtgtg	C	T	NM_021080 // intron // 0 // Hs.333942 // DAB1 // 1600 // disabled homolog 1 (Drosophila)	DAB1	DAB1 , rs10493222, disabled homolog 1 (Drosophila),p32.2
SNP_A-1655541	aataggattcttttgagaatcacaa[A/G]taggaaagccatgagctcacaaaaa	A	G	NM_001219 // intron // 0 // Hs.7753 // CALU // 813 // calumenin	CALU	CALU , rs2060717, calumenin,q32.1
SNP_A-1786826	ggctttgaaggcttcc[G/T]ccccgaagggactctc	G	T	ENST00000355038 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-1785980	ggctgcatgaggtcct[C/G]actgaagttgtaccta	C	G	Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// ENST00000328500 // CDS // 0 // --- // ---	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2135595	atattttgtcctttta[A/G]cgtttctgaattcaga	A	G	ENST00000338458 // intron // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-2157186	attgaataggaagaaa[C/T]gtacagataaacaacc	C	T	// 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 // upstream //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2165113	caaactttatacagca[C/T]tgaaacctacataaat	C	T	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 49105 // --- //	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2166921	caacaaaagaagtgga[G/T]agaggaaagagtaaat	G	T	1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 1151903 //	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.2
SNP_A-2151409	atgttcagagagatat[G/T]actgggctcaataaga	G	T	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 972597 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2144757	atgatggctccttttta[A/T]aacaagagttgacaat	A	T	// Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_080672 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.33
SNP_A-2144078	atgaggacttcatcaa[C/T]agtactgggaatgaaa	C	T	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2215738	cctcatcaaatcagtc[A/G]aaggcccaaatagatt	A	G	ENST00000358765 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-2216563	cctctacttgactaca[C/T]atctagttgcataatt	C	T	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // --- // --- // --- // ---	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2210444	ccccccagtcagaagc[C/T]agatggtctttctact	C	T	// 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream //	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2211590	ccctcagctaaggaag[C/G]ctgctgaagataggaa	C	G	ST3GAL4 // 6484 // Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), mRNA. /// X74570 // downstream // 515980 // Hs.504251 // ST3GAL4 //	ST3GAL4	ST3GAL4, Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), q24.2
SNP_A-2198157	cattgtaagaaaaagc[C/T]gaactgcctgatacat	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-2188548	cagtgaggtagaacaa[C/T]tgacctcccaaattaa	C	T	Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBR1), mRNA. /// ENST00000262458 // 3UTR // 0 // --- // --- // --- // ---	TGFBR1	TGFBR1, Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBR1), q22.33
SNP_A-2168864	caagactggtttaata[A/C]gatagaggtcacaaag	A	C	79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// NM_004530 // upstream // 781 // Hs.513617 //	IRX6	IRX6, Homo sapiens iroquois homeobox protein 6 (IRX6), q12.2
SNP_A-2037019	aaatttttgttatca[A/G]agactacggagtgagg	A	G	// 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 734378 // --- // --- //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-2042354	aactatttttctgtca[A/G]actcccacatcaaaat	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1628473 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2002346	cctttgccacattaca[C/T]tgaacactggatgcat	C	T	Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 1, mRNA. /// NM_018205 // intron // 0 // Hs.7778 // LRRC20 // 55222 // Homo sapiens leucine rich	LRRC20	LRRC20, Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 1, q22.1
SNP_A-2017561	ttgtcctgctgacaca[A/G]ctcccagacttggata	A	G	C21orf100 // 118421 // Homo sapiens chromosome 21 open reading frame 100 (C21orf100), mRNA. /// NM_182749 //	C21orf100	C21orf100, Homo sapiens chromosome 21 open reading frame 100 (C21orf100), q21.3
SNP_A-2075536	acatgcacccataaca[A/C]ctggtttctttgcttc	A	C	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 670507 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-2064433	aattccactacactca[C/T]gaaaaaacaaaggtct	C	T	Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // intron // 0 // --- // DDHD1 // 80821 // Homo	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2092579	agaaatactgacaata[C/T]gtccgagatctggtag	C	T	23438 // Homo sapiens histidyl-tRNA synthetase-like (HARSL), mRNA. /// NM_012208 // downstream // 16300 //	HARSL	HARSL, Homo sapiens histidyl-tRNA synthetase-like (HARSL), q31.3
SNP_A-2106706	agcctgagtctcccta[C/T]agaaaaggtgtatgag	C	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 44036 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3
SNP_A-2103111	agcaaatttggacgga[C/T]gtcatttgagagagag	C	T	55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2100587	agatacagcctaatga[A/G]atcctaaagtggaagg	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // --- //	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2088666	actgtgcccggcctca[C/T]gcaaaactttctaact	C	T	// 132989 // Homo sapiens hypothetical protein MGC26744 (MGC26744), mRNA. /// NM_005935 // upstream // 24230 //	MGC26744	MGC26744, Homo sapiens hypothetical protein MGC26744 (MGC26744), q21.3
SNP_A-2300900	gcctgtccctctggtc[A/G]cttcttacccaatgta	A	G	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2
SNP_A-2292497	gcactcacctctgaac[A/C]cttaagaaaaagactc	A	C	ENST00000355158 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-2228710	ctagacatagatttaa[A/G]ggactgatgagactaa	A	G	ENST00000262144 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-2230847	ctatgcattcttatta[C/T]acctctttctgtctac	C	T	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2255419	cttgtccaagttcaac[A/T]aatggctagaaaaatg	A	T	58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251266	cttcaaatatgaaaaa[A/G]ttacatgaaagatgaa	A	G	29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// NM_015931 // downstream // 46110 //	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-2244381	ctggaatgcatgtcca[C/G]ctagaacttcagaatg	C	G	5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 343040 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2229528	ctagggtttaaggctg[A/G]aaggatatttacggag	A	G	Homo sapiens interleukin 13 (IL13), mRNA. /// NM_172348 // upstream // 10960 // Hs.73917 // IL4 // 3565 // Homo sapiens	IL13	IL13, Homo sapiens interleukin 13 (IL13), q23.3
SNP_A-2269900	gacaatcactggtcta[C/T]ggggaaagatagatat	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 985079 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2287510	gatgtttaataccaca[A/G]tgactatatttttact	A	G	5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// NM_006203 // upstream // 933332 //	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q12.1
SNP_A-2300595	gcctgcaaaatgctta[A/T]accattgaaataagtg	A	T	/// ENST00000307948 // downstream // 245420 // --- // --- // ---	-	p12
SNP_A-2295589	gcatcttggtgaggca[A/C]gccccatcctgagtgt	A	C	PRO1085 mRNA, complete cds. /// NM_020673 // intron // 0 /// Hs.529044 // RAB22A // 57403 // Homo sapiens RAB22A,	-	-, Homo sapiens PRO1085 complete cds. q13.32
SNP_A-2308066	gcttgacacagtacaa[C/T]agaaaaacaacagcaa	C	T	/// ENST00000277685 // downstream // 17754 // --- // --- // ---	-	p12.1
SNP_A-2090238	acttgcagagtgaaca[A/G]gcatgataggttcagg	A	G	ENST00000327381 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2088250	actggtgcctaaggta[G/T]actgagctccatgtca	G	T	Homo sapiens hypothetical protein FLJ11383 (FLJ11383), transcript variant 1, mRNA. /// NM_024938 // intron // 0 //	PCNXL2	PCNXL2, Homo sapiens hypothetical protein FLJ11383 (FLJ11383), transcript variant 1, q42.2
SNP_A-2061359	aatgccccaattaata[C/T]agtacccagtagaaga	C	T	160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// ENST00000321196 // intron // 0 // --- // --- // --- // ---	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2016729	ttattgaacttctagg[A/C]attttgtgtccttatt	A	C	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 761700 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2011636	attttatttcagttta[A/C]atgtatctgtattaat	A	C	// 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1154611 //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-2045679	aagacaagatataaga[C/T]gtttacttaccaatca	C	T	Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // intron // 0 // Hs.481551 // MTRR //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2047183	aagatacctgctcaca[C/G]ccctcacctgattctt	C	G	// 23136 // Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// NM_173464 //	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-2182577	cagatcagaaaataaa[C/T]catattgtgtgtaaga	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2187826	cagtagtcttgaatta[C/T]aaggttgagatgtatg	C	T	3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream //	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-2212965	ccctttttgcttttaa[A/G]gtcatcaaacatttga	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 475796 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2225788	ctaaagtaatggaagc[A/G]ctctgtactttgaatg	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 273319 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2139436	atccttcaaacatcta[C/T]ctaccacctcaggggc	C	T	ENST00000316156 // intron // 0 // --- // --- // --- // ---	-	p34.3
SNP_A-2160118	atttatttgtaataca[C/T]ctagattttcttgttg	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 58384 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2126064	agttttggatttccta[C/T]aatagagtttggatta	C	T	FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1794094	ggtcagctctggcaga[C/G]attagccatagacacc	C	G	Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 2, mRNA. /// NM_007051 // intron // 0 // Hs.530402 // FAF1 // 11124 // Homo sapiens Fas (TNFRSF6)	FAF1	FAF1, Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 2, p32.3
SNP_A-1804306	gtcactcaagtggaaa[A/G]tcctgcaatttttgta	A	G	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1804876	gtcataaaaggactaa[A/G]tcaagattcaaagatt	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1744435	gagttatattcagcaaaattaagtg[A/G]aagagatggaataaaaaagtcaaga	A	G	NM_024532 // intron // 0 // Hs.6783 // PF20 // 79582 // PF20	PF20	PF20 , rs2098979, PF20,q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1728645	tactgtactatagagatattgccag[A/G]atactttattgttatacttacttaa	A	G	CDW92 antigen /// NM_080546 // intron // 0 // Hs.414728 // CDW92 // 23446 // CDW92 antigen	CDW92	CDW92 , rs9299385, CDW92 antigen ,q31.1
SNP_A-1782364	ggcaattacctccaca[C/G]atttccatttctctct	C	G	// 285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// NM_021159 // upstream // 57912 //	MGC46496	MGC46496, Homo sapiens hypothetical protein MGC46496 (MGC46496), q23
SNP_A-1845752	tatagtaactgctcaa[C/T]tgaaaaaagtattaat	C	T	Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, mRNA. /// NM_145321 // intron // 0 // Hs.520259 // OSBPL3 // 26031 // Homo sapiens oxysterol	OSBPL3	OSBPL3, Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, p15.3
SNP_A-1845171	tatacattttctcatc[C/T]gagcttcacagcagct	C	T	Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), mRNA. /// ENST00000356336 // intron // 0 // --- //	SRGAP3	SRGAP3, Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), p25.3
SNP_A-1862395	tcatgtctaacatata[C/G]aagactttcaataaat	C	G	// 219738 // Homo sapiens chromosome 10 open reading frame 35 (C10orf35), mRNA. /// NM_080806 // upstream //	C10orf35	C10orf35, Homo sapiens chromosome 10 open reading frame 35 (C10orf35), q22.1
SNP_A-1869457	tcctgtggacggtttg[C/T]agccagcttggcaatg	C	T	// 29937 // Homo sapiens secreted protein of unknown function (SPUF), mRNA. /// NM_001674 // upstream //	SCIRP10	SCIRP10, Homo sapiens secreted protein of unknown function (SPUF), q32.3
SNP_A-1951639	tttccttagatgtgca[A/G]taaatcaaatttgtta	A	G	Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // intron // 0 // Hs.401954 // ARG99 // 83857 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1944125	ttgtcactgtatatga[A/G]cagttctgctgtgttc	A	G	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1942167	ttggcaaaaccaatca[A/G]agtagcattccaactc	A	G	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-1982343	atctcagaaaactctg[C/G]aataattttgatacat	C	G	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, mRNA. /// NM_003401 // intron // 0 // Hs.171190 // XRCC4 // 7518 // Homo sapiens X	XRCC4	XRCC4, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, q14.2
SNP_A-1987560	gatatcatttctaagc[C/T]gaatagtacctctttt	C	T	Homo sapiens thrombospondin, type I, domain containing 2 (THSD2), mRNA. /// ENST00000356698 // intron // 0 // --- // ---	THSD2	THSD2, Homo sapiens thrombospondin, type I, domain containing 2 (THSD2), q22.33
SNP_A-1918363	ttaaagtctaaaaaga[C/T]agcttcgtcaggtggg	C	T	RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // downstream // 537843 //	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1917196	tgttttaatctacaga[G/T]gtatgactcaagatgt	G	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 558135 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1914454	tgtgtttggaatttca[A/G]atggaagggatgtcgg	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-1913210	tgtggctccttataga[A/C]gcactcagtttagatt	A	C	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 254449 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1881947	tcttttcctcaataaa[C/T]ctcaagtctgtcacct	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1879944	tcttcctcttctgaaa[C/T]gattgattctctgtga	C	T	Homo sapiens GLIS family zinc finger 1 (GLIS1), mRNA. /// ENST00000312233 // intron // 0 // --- // --- // --- // ---	GLIS1	GLIS1, Homo sapiens GLIS family zinc finger 1 (GLIS1), p32.3
SNP_A-1890014	tgatatacagcaagca[G/T]agctctctggctacca	G	T	ENST00000317357 // intron // 0 // --- // --- // --- // ---	-	q21
SNP_A-1878261	tctgtccaaagattca[C/T]agcaaactgtagtgtt	C	T	1999 // Homo sapiens E74-like factor 3 (ets domain transcription factor, epithelial-specific) (ELF3), mRNA. /// NM_004767 // upstream // 96603 // Hs.132049 // GPR37L1 //	ELF3	ELF3, Homo sapiens E74-like factor 3 (ets domain transcription factor, epithelial-specific) (ELF3), q32.1
SNP_A-1917766	ttaaaacatccaatca[A/T]gtcatcttctcaaatt	A	T	Homo sapiens ring finger protein 111 (RNF111), mRNA. /// ENST00000348370 // intron // 0 // --- // --- // --- // ---	RNF111	RNF111, Homo sapiens ring finger protein 111 (RNF111), q22.1
SNP_A-1982467	atttttctaaaataca[A/G]agctgttgatcctgcc	A	G	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 856480 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1974416	atgataaccatgaaga[C/T]aaaagtggatatattt	C	T	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 539212	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-1947596	tttacctaggaattat[A/T]aacgcatattaaaata	A	T	EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 1146647 // --- // --- // --- //	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1871372	tctaaatcccaaccga[A/G]cttcttccaacctcca	A	G	sapiens myoglobin (MB), transcript variant 2, mRNA. /// NM_005368 // 3UTR // 0 // Hs.517586 // MB // 4151 // Homo	MB	MB, Homo sapiens myoglobin (MB), transcript variant 2, q12.3
SNP_A-1848514	tatgaattaaagtaaa[C/T]ttggctcttgagcttt	C	T	ENST00000286031 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1821032	gtttctggtgtttaga[C/G]atggatttctgatgta	C	G	ENST00000355266 // upstream // 12651 // --- // --- // --- // ---	-	q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784343	ggccccagagattatc[A/G]cagtacattgggtgag	A	G	902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 255646 // Hs.379972 //	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1646252	tattcaaaatcagaggctttcaacc[A/C]atgtttcagagagcttaagtaggag	A	C	2993 // glycophorin A (includes MN blood group) /// NM_002100 // upstream // 359938 // Hs.438658 // GYPB //	GYPA	GYPA , rs4469023, glycophorin A (includes MN blood group) ,q31.21
SNP_A-1661175	tcccctgaaacccaccgtgagttca[A/G]aatggagacaaggaggtggttgcag	A	G	NM_032884 // intron // 0 // Hs.194610 // MGC15882 // 84970 // hypothetical protein MGC15882	MGC15882	MGC15882 , rs1771363, hypothetical protein MGC15882,p35.1
SNP_A-1709585	ctaactggtggacaattctacttca[C/G]tcatgtttgggggatgccctacttc	C	G	137868 // sarcoglycan zeta /// NM_152567 // downstream //	SGCZ	SGCZ , rs10503463, sarcoglycan zeta ,p22
SNP_A-1789851	gggctggtaagcgacc[A/G]agggccattatataca	A	G	-- /// ENST00000340000 // upstream // 377223 // --- // --- // ---	-	p12.1
SNP_A-2135384	atatttcatccattca[A/T]tctgttcagtcagttc	A	T	Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // --- // --- // --- // ---	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-2135984	atcaagacacagaaac[A/G]aggagctatatagtat	A	G	FLJ42957 // 400077 // Homo sapiens FLJ42957 protein (FLJ42957), mRNA. /// ENST00000358150 // downstream //	FLJ42957	FLJ42957, Homo sapiens FLJ42957 protein (FLJ42957), q24.22
SNP_A-2122805	agtggcaataagtaaa[C/T]agataactgatgaaca	C	T	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2149171	atgtaacaatcagtag[A/G]acttgacaactgaaag	A	G	// Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 //	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15
SNP_A-2226844	ctaatagtatagaaaa[A/C]attgtcagaaggctga	A	C	Homo sapiens likely ortholog of mouse ubiquitin-conjugating enzyme E2-230K (E2-230K), mRNA. /// ENST00000319380 // intron // 0 // --- // --- // --- // ---	E2-230K	E2-230K, Homo sapiens likely ortholog of mouse ubiquitin-conjugating enzyme E2-230K (E2-230K), q25.1
SNP_A-2202397	ccaccatgcgcggccc[A/G]atttctttcttttttc	A	G	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA. /// ENST00000289890 // intron // 0 // --- // --- // --- // --- /// ENST00000356138 // intron	MACF1	MACF1, Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, p34.3
SNP_A-2206939	ccatgtatccctttac[A/G]cacatatacgcacacc	A	G	5413 // Homo sapiens peanut-like 1 (Drosophila) (PNUTL1), mRNA. /// NM_080647 // upstream // 8223 // Hs.173984 //	SEPT5	SEPT5, Homo sapiens peanut-like 1 (Drosophila) (PNUTL1), q11.21
SNP_A-2035815	aaatgttaatacttaa[C/T]agtaatcagcagcatg	C	T	127733 // Homo sapiens UBX domain containing 3 (UBXD3), mRNA. /// NM_144623 // upstream // 134248 // Hs.205178 //	UBXD3	UBXD3, Homo sapiens UBX domain containing 3 (UBXD3), p36.12
SNP_A-2023957	aaaagacacactctac[C/G]attccactgaaatgaa	C	G	27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 1189284 //	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-2005713	aactgacttttgaaaa[C/T]gaaaactatcccacgc	C	T	Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// ENST00000355044 // intron // 0 // --- // --- // --- // --- // --- ///	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2050882	aaggcctcatgtcaac[C/T]caatttaaatctggtt	C	T	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2053141	aagtctgaacactttа[G/T]gtaatcaacctcatct	G	T	sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // --- // --- // --- // --- ///	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-2066953	acaaacacattgtata[C/T]actttcacactgacag	C	T	Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), mRNA. /// AK025510 // intron // 0 // Hs.463702 //	BCAS3	BCAS3, Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), q23.2
SNP_A-2076798	accaaaagaagctcag[G/T]aattgggcaccccagg	G	T	Homo sapiens microsomal glutathione S-transferase 2 (MGST2), mRNA. /// ENST00000265498 // intron // 0 // --- // ---	MGST2	MGST2, Homo sapiens microsomal glutathione S-transferase 2 (MGST2), q31.1
SNP_A-2102011	agatgtaaggcccaga[C/T]gttattcatataaatt	C	T	2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-2097528	agagaagatgttaaga[C/T]tcatttccctaaacta	C	T	Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // --- // --- // --- // --- // --- ///	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2299802	gcctaagattccagac[A/G]ggtatcactctgtgga	A	G	Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2289864	gcaaactaccataaag[C/G]ccagcgtagtgaaaat	C	G	sapiens ELYS transcription factor-like protein TMBS62 (ELYS), mRNA. /// ENST00000283201 // intron // 0 // --- // ---	-	-, Homo sapiens ELYS transcription factor-like protein TMBS62 (ELYS), q44
SNP_A-2278419	gagctatgacaaggaa[A/G]aaggttagagaataaa	A	G	4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 725381 //	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-2257294	ctttcttgcagggtta[C/T]atgagccaggggcttg	C	T	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 654937 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2241683	ctgatatgcagtttca[C/T]cccagacccattaact	C	T	Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /// ENST00000281806 // intron // 0 // --- // --- // --- // ---	GPR145	GPR145, Homo sapiens G protein-coupled receptor 145 (GPR145), q16.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2254359	cttgcagggaaaccct[A/G]acatgggccagtcatc	A	G	Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA. /// ENST00000271401 // intron // 0 // --- // --- // --- // ---	XCL1	XCL1, Homo sapiens chemokine (C motif) ligand 1 (XCL1), q24.2
SNP_A-2261027	gaaagaagagcaaaaa[G/T]gggaaagaataaagaa	G	T	Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, mRNA. /// NM_004370 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen,	COL12A1	COL12A1, Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, q14.1
SNP_A-2273172	gactcacagttaagac[C/T]gcacagacttatgtcc	C	T	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-2286638	gatggagtcatatctc[A/G]catagagtatagtctt	A	G	ENST00000325192 // upstream // 30174 // --- // --- // --- // ---	-	q21.2
SNP_A-2298269	gccatggtgaaggtaa[A/G]gctgctaatgccaccc	A	G	988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-2294685	gcagtgggtgccaata[C/T]ggcttaagaggctcct	C	T	MGC29898 // 133015 // Homo sapiens hypothetical protein MGC29898 (MGC29898), mRNA. /// NM_147183 // upstream	MGC29898	MGC29898, Homo sapiens hypothetical protein MGC29898 (MGC29898), p15.31
SNP_A-2309501	ggaaacatacatttca[A/G]gtgtgatacattaaat	A	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2304189	gctcccttctagctgc[A/G]acttctgttttaccat	A	G	Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11), mRNA. /// ENST00000215743 // intron // 0 // --- // --- // --- // ---	MMP11	MMP11, Homo sapiens matrix metalloproteinase 11 (stromelysin 3) (MMP11), q11.23
SNP_A-2309837	ggaaataacaaagcca[C/G]gtatgtaaatgtaaac	C	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2313151	ggagaagagtctttaa[C/T]gatatccacccagaca	C	T	DKFZP564F0522 // 25940 // Homo sapiens DKFZP564F0522 protein (DKFZP564F0522), mRNA. /// NM_207329 // downstream // 5056 // Hs.528847 // MYADML	DKFZP564F0522	DKFZP564F0522, Homo sapiens DKFZP564F0522 protein (DKFZP564F0522), p22.3
SNP_A-2092772	agaaatggtgatccaa[C/T]taatgccgctgaacct	C	T	-- /// ENST00000340000 // upstream // 98439 // --- // --- // --- //	-	p12.1
SNP_A-2094047	agaaggaaaacgacga[C/T]gatgggcgtgtcctaa	C	T	Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-2066433	aattttgtgtagccta[C/T]atttaacattttccat	C	T	10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 87945 // Hs.269775 //	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2005972	tgcttctaaaaagtag[C/T]ccatctttaccatttg	C	T	7560 // Human Kox5 mRNA for zinc finger protein, partial. /// ENST00000333201 // downstream // 78810 // --- // --- // --- // --	ZNF13	ZNF13, Human Kox5 for zinc finger protein, partial. ,q13.13
SNP_A-2004357	ccctttgttgggggta[C/T]gcatgtatgaacacac	C	T	ENST00000328153 // 3UTR // 0 // --- // --- // --- // ---	-	q26.1
SNP_A-1996890	cttagcaaattgttca[A/G]aatcctcttagcaata	A	G	5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream //	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin,q21.13
SNP_A-2026675	aaacaataatgactga[C/G]aatttttcccccaaatt	C	G	148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// NM_033020 // downstream // 121394 // Hs.26837 // TRIM33	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2205311	ccagtccgtgccctcc[G/T]ctgaaaaggccttctt	G	T	// 7760 // Homo sapiens zinc finger protein 213 (ZNF213), mRNA. /// NM_012360 // upstream // 23359 // Hs.278464 //	ZNF213	ZNF213, Homo sapiens zinc finger protein 213 (ZNF213), p13.3
SNP_A-2209580	cccatgaatttaaaaa[C/T]gatctctatgctgatg	C	T	10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2227820	ctaccatttgtggcac[C/T]ggaaaaatggcagctg	C	T	Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA. /// ENST00000294507 // intron // 0 // --- // --- // --- // ---	LAPTM5	LAPTM5, Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), p35.2
SNP_A-2148327	atgggcttctgccaaa[A/G]gttgagctactgtctt	A	G	// Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 203439 // Hs.158932 // APC //	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-2141382	atctgtgtgtcttaca[C/T]tgatagccgaggttgt	C	T	Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // intron // 0 // Hs.510989 // MEIS2 // 4212 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2159192	atttaaacattgtctt[A/G]aaagtagctgacctaa	A	G	Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron //	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2156338	attctcaattctgtga[C/T]ggtgaggaaaatgtct	C	T	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26 (DDX26), mRNA. /// NM_182540 // intron // 0 //	DDX26	DDX26, Homo sapiens DEAD,q14.3
SNP_A-2154480	attattccgttcagaa[A/G]aaagacagaaaatatt	A	G	SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 78071 // --- //	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2163453	caaaaaaacacaaaaa[A/G]tctgtagtataagagg	A	G	Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), mRNA. /// ENST00000224892 // intron // 0 // --- // --- // --- // ---	LHPP	LHPP, Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), q26.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123886	agttaactgctctcat[A/T]agtaggcaacaagatg	A	T	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1812695	gtggctttgatctaaa[C/T]tgaatctcttgtagct	C	T	ENST00000360397 // intron // 0 // --- // --- // --- // ---	-	q25
SNP_A-1652230	gttcataaccaatatgaaatttagc[A/G]gaagtaacttgacctcatggaattt	A	G	479 // ATPase, H+/K+ transporting, nongastric, alpha polypeptide /// NM_006437 // upstream // 154776 //	ATP12A	ATP12A , rs3803221, ATPase, H+,q12.12
SNP_A-1825044	taaaggatgcacttca[C/G]tacaaagaaaactgga	C	G	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 293020 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-1944990	ttgtggtaggaataac[C/T]atgaaggcactcaaag	C	T	79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream //	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.13
SNP_A-1940940	ttgctatgaggtcaaa[C/G]caatactagtgaacaa	C	G	NM_001001966 // downstream // 2545 // --- // OR5AT1 // 284532 // Homo sapiens olfactory receptor, family 5,	-	q44
SNP_A-1957075	ttttacaaaattttaa[C/T]tgtcactgctggagaa	C	T	// 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1988764	aataatacattaattc[A/G]ctaatctagctgatga	A	G	// 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 258413 // --- // --- //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1915903	tgttgagtagaaacgc[C/T]ctgtgtgtggtgtgtg	C	T	149699 // Homo sapiens chromosome 20 open reading frame 65 (C20orf65), mRNA. /// NM_032883 // upstream //	C20orf65	C20orf65, Homo sapiens chromosome 20 open reading frame 65 (C20orf65), q13.12
SNP_A-1875487	tctctggggtctggaa[A/T]gttccttatcttggtg	A	T	sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- // --- /// ENST00000357947 // intron //	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-1887483	tgagacctgagtaatg[C/G]cactctgaaggttacc	C	G	407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 125943 // Hs.24115 // C13orf25 //	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1897633	tgctgccattagaaaa[A/T]ttattgtgtatttttt	A	T	26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1896671	tgctatacaaatttca[G/T]taatggattcatcaga	G	T	// Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// ENST00000342303 // intron // 0 // --- // --- // --- // ---	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1875096	tctctcagctaagtga[C/G]agtcaatcaggctaaa	C	G	2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// NM_024997 // upstream // 168766 // Hs.513343 // ATF7IP2 // 80063 //	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1879945	tcttcctctttgctaa[A/G]gatggctttgggtggt	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-1907787	tgtaaggtaaaactga[C/T]gatgcaaattagttca	C	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. ,q21.1
SNP_A-1919726	ttaagtattgcagaaa[A/G]tgtgctctcttgacaa	A	G	FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream //	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-1989067	tgcgtagttagtgcaa[A/G]ttatctgagacactaa	A	G	// 9734 // Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, mRNA. /// NM_058177 // downstream //	HDAC9	HDAC9, Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, p21.1
SNP_A-1974843	aaaatcatcttcatac[C/G]atctacaaaagttcaa	C	G	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1971563	ttagcttgatttaata[A/T]taccaatgctgaatat	A	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 85354 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1965904	tgctggggactggtac[C/T]gatctgtggcgtgtga	C	T	Homo sapiens hypothetical protein PTD004 (PTD004), mRNA. /// ENST00000344357 // intron // 0 // --- // --- // --- // ---	PTD004	PTD004, Homo sapiens hypothetical protein PTD004 (PTD004), q31.1
SNP_A-1934600	ttctctctctaaacag[C/T]cattgaaagagaaaaa	C	T	Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // intron // 0 // Hs.123642 // EPHA3 // 2042 //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1821042	gtttctgtctttttga[A/G]tattgatttttgacta	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1833046	tacacagacagtaagc[A/G]cctaaagagacacaca	A	G	51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 65663 // Hs.491997 // EYA1	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3
SNP_A-1833656	tacaggcaccaaccaa[C/T]acatctggctaatttt	C	T	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 4,	ABCC1	ABCC1, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p13.11
SNP_A-1846499	tatattcagacgccta[A/C]caaattatatgtaatt	A	C	Homo sapiens chromosome 6 open reading frame 32 (C6orf32), mRNA. /// ENST00000259698 // intron // 0 // --- // --	C6orf32	C6orf32, Homo sapiens chromosome 6 open reading frame 32 (C6orf32), p22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1782613	ggcacgctccatcaaa[A/G]catactgtccaatttg	A	G	216 // Homo sapiens aldehyde dehydrogenase 1 family, member A1 (ALDH1A1), mRNA. /// NM_000700 // upstream // 71104 // Hs.494173 // ANXA1 // 301 // Homo sapiens	ALDH1A1	ALDH1A1, Homo sapiens aldehyde dehydrogenase 1 family, member A1 (ALDH1A1), q21.13
SNP_A-1757299	tgactacttttgaacaaaagggtt[A/G]aacacatttgaagaaaatcaatatt	A	G	7128 // tumor necrosis factor, alpha-induced protein 3 /// NM_175747 // upstream // 187106 // Hs.511888 // OLIG3 //	TNFAIP3	TNFAIP3 , rs10499194, tumor necrosis factor, alpha-induced protein 3 ,q23.3
SNP_A-1803577	gtcaaaaagtggtgaa[A/C]tctgtagtaaaatgaa	A	C	28965 // Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), mRNA. /// NM_014031 // downstream // 7472 // Hs.49765 // SLC27A6 // 28965 //	SLC27A6	SLC27A6, Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), q23.3
SNP_A-1785644	ggctccgcagtgttca[C/G]catttccagtcgagca	C	G	130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 364109	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-1795638	ggtgcttccacctagc[A/G]atgggcaagcaaaaat	A	G	Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// ENST00000323829 // intron // 0 // --- // --- // --- // ---	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-2129882	atacatgagaacccca[G/T]aaggtcatccagtaaa	G	T	5450 // Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRNA. /// NM_017589 // downstream //	POU2AF1	POU2AF1, Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), q23.1
SNP_A-2131170	atagacttcttggcaa[A/T]gtattttgaaaatatt	A	T	YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 548490 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.3
SNP_A-2162563	attttccttgctcaac[A/G]atctttaaaattcttt	A	G	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 492713 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2140689	atctctgaattatgaa[G/T]atttgacttatgatct	G	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 321065 // --- // --- // --- //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2213780	cctaaaacataattca[C/T]gtgtaggaaaaagaat	C	T	Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2199711	ccaaaatctgtagata[C/T]attgtctaaaatgacc	C	T	Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 //	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2177705	ctgtgcattgcttaaa[G/T]aatgtgttttctgggt	G	T	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 128268 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2172790	caatttgaacttaagg[C/T]atggacaataaggaaa	C	T	// 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2022152	aaaaagctgaatttta[C/T]atgcatttgacaacca	C	T	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2030138	aaagcaaccaccggga[C/T]tcccagatagtattaa	C	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 604757 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2004344	gtacatccgactgtgc[C/T]gatctcacagatgagc	C	T	84171 // Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA. /// NM_032709 // downstream // 67710 // Hs.238303 //	LOXL4	LOXL4, Homo sapiens lysyl oxidase-like 4 (LOXL4), q24.2
SNP_A-2065676	aatttatagtgctcca[A/G]gtaggtcattaaataa	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2076334	acattgcacatataaa[A/G]taacccaattctccag	A	G	6461 // Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// NM_000692 // upstream // 98800 // Hs.436219 // ALDH1B1 // 219 // Homo	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-2071622	acagaagtggaaggag[G/T]cgtttcacagtaaacg	G	T	Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // intron // 0 // Hs.527984 //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2057384	aatatcacagcattcg[C/T]cctgaaggccaaagtc	C	T	sapiens Ellis van Creveld syndrome (EVC), transcript variant 1, mRNA. /// NM_153717 // CDS // 0 // Hs.28051 // EVC //	EVC	EVC, Homo sapiens Ellis van Creveld syndrome (EVC), transcript variant 1, p16.2
SNP_A-2093844	agaagatgcaccaaga[A/G]cctcaaagtcagaagt	A	G	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // intron // 0 // Hs.494312 //	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-2298538	ctccattctgacagga[A/G]gagatctgtgtgtgct	A	G	Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 //	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-2291113	gcaatagaggattcag[A/G]aaagttgggagaaaag	A	G	NM_174952 // downstream // 242937 // Hs.212840 // MGC46496 // 285555 // Homo sapiens hypothetical protein	-	q22.3
SNP_A-2233670	ctcatagtgcctctga[A/G]tactttagagccaggc	A	G	/// ENST00000327728 // downstream // 70724 // --- // --- // ---	-	q23.2
SNP_A-2256220	ctttagatgggctcaa[C/G]ctttaattttcatgtc	C	G	ENST00000339567 // intron // 0 // --- // --- // --- // --- /// ENST00000343332 // intron // 0 // --- // --- // --- // --- ///	-	p12
SNP_A-2248346	ctgtgtctggtcttca[A/G]tccaggtcattagaaa	A	G	79887 // Homo sapiens hypothetical protein FLJ22662 (FLJ22662), mRNA. /// NM_004963 // downstream // 28104 //	FLJ22662	FLJ22662, Homo sapiens hypothetical protein FLJ22662 (FLJ22662), p13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2292863	taactactggctctgc[C/T]caagactcctggagca	C	T	Homo sapiens hypothetical protein FLJ12476 (FLJ12476), mRNA. /// ENST00000335894 // intron // 0 // --- // --- // --- // ---	FLJ12476	FLJ12476, Homo sapiens hypothetical protein FLJ12476 (FLJ12476), q23
SNP_A-2307769	gcttcctgaaaggagc[C/T]gagagctgtaaaacac	C	T	// 25805 // Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI), mRNA. /// ENST00000224324 // downstream // 163909 // --- // --- // --- //	BAMBI	BAMBI, Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI), p12.1
SNP_A-2104833	agcatacacttttcta[G/T]gccgttttacaagggtg	G	T	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 220494 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2088733	actgtgtaaccatcta[C/T]cgtatgtattcatgat	C	T	Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // --- // --- // --- // ---	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-2064875	aattgaatatgcgccc[A/G]ctttaccagaactaga	A	G	150677 // Homo sapiens otospiralin (OTOS), mRNA. /// NM_002081 // upstream // 242260 // Hs.328232 // GPC1 //	OTOS	OTOS, Homo sapiens otospiralin (OTOS), q37.3
SNP_A-2005275	aaacaaaacagtttca[C/T]acctcaaactcactat	C	T	27250 // Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA. /// NM_014456 // upstream // 140752 // Hs.232543 //	PDCD4	PDCD4, Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, q25.2
SNP_A-2001311	tacttcaaacgcttca[C/T]ctttatatccctttg	C	T	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1177396 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1989960	cattgatagactaaaa[A/T]tgattttcctgcaaac	A	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 943532 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2176323	caccaggttggaaata[A/T]gctttaggcagaatca	A	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1367811 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2181288	cagacctagaagtgta[C/T]taactggctgtctttt	C	T	7849 // Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, mRNA. /// NM_013952 // upstream // 45802 //	PAX8	PAX8, Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, q13
SNP_A-2215171	cctattttcttcctga[C/T]gaatgtgtcctcttca	C	T	57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 242043 // Hs.424711 //	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2207109	ccattaacttcagtac[C/G]aaaggatctaatatca	C	G	Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- // --- /// ENST00000318007 // intron // 0 // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-2203505	ccagaagattgcatga[C/T]agataaaatgcacctt	C	T	151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 //	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-2144973	atgatttagcagttcc[A/T]ctcctaggaatattat	A	T	Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // intron // 0 // --- // --- // --- // --- ///	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2166836	caaatttagattctcc[A/G]cagagggccagttctg	A	G	Homo sapiens histamine receptor H4 (HRH4), mRNA. /// ENST00000256906 // intron // 0 // --- // --- // --- // ---	HRH4	HRH4, Homo sapiens histamine receptor H4 (HRH4), q11.2
SNP_A-2154881	attcaatgatgtagag[A/T]agggagcgctgtgggt	A	T	ENST00000355599 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-2127217	ataaatgaccttacca[A/G]gaactcaggcttcttt	A	G	AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 18489 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-2118204	agtaaataagtgaatc[A/G]aacaatcccaaagggg	A	G	/// ENST00000310012 // upstream // 105075 // --- // --- // --- // -	-	q12
SNP_A-2110567	aggacagcaagttgcc[A/G]gccatattctctagtc	A	G	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA. /// ENST00000263182 // intron // 0 // --- // --- // --- // ---	BBOX1	BBOX1, Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), p14.2
SNP_A-1797445	ggtttagaaaactttc[A/G]atgaaccagtgtgtgt	A	G	Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 //	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds. ,q13.3
SNP_A-1787980	gggagaagatactgtc[A/G]attcttttatagctgt	A	G	SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 154725 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1806520	gtcgtaaagtgtaaag[C/T]atatcttatgagctct	C	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1156109 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1752131	cgtggccatctgtctgggactttcc[A/G]aggcttccattgtctgtctcagcag	A	G	4338 // molybdenum cofactor synthesis 2 /// NM_006350 // upstream // 136895 // Hs.9914 // FST // 10468 // follistatin ///	MOCS2	MOCS2 , rs10491443, molybdenum cofactor synthesis 2 ,q11.2
SNP_A-1784832	ggccttaagatcagac[A/G]gacttttatcctaacg	A	G	Homo sapiens signal peptide peptidase 3 (SPPL3), mRNA. /// ENST00000353487 // intron // 0 // --- // --- // --- // ---	SPPL3	SPPL3, Homo sapiens signal peptide peptidase 3 (SPPL3), q24.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1651658	tctgtggccttgggtggatgaatca[A/G]acctcctagggttattctcctcaca	A	G	NM_153002 // intron // 0 // Hs.308230 // GPR156 // 165829 // G protein-coupled receptor 156	GPR156	GPR156 , rs2319540, G protein-coupled receptor 156,q13.33
SNP_A-1647220	tcttgtagcagccatggaagcatca[C/T]taagggatcttattgttaatgttat	C	T	23414 // zinc finger protein, multitype 2 /// NM_013437 // upstream // 388902 // Hs.301974 // ST7 // 29967 //	ZFPM2	ZFPM2 , rs10505070, zinc finger protein, multitype 2 ,q22.3
SNP_A-1858820	tcagatttctattata[G/T]gaatgtccactcaaag	G	T	116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 57890 // Hs.491941 // VEST1	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-1853011	tatttgatcctaatac[A/G]aagaaataacaaatgt	A	G	// 117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000332754 // downstream // 1902 // --- // --- // --- // --	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-1870176	tcctttaggtgccatc[A/G]agctttcagcagttgt	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1820652	gtttcactgtttttca[A/G]gtctgaatagcttgca	A	G	Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- /// ENST00000318007 // intron // 0 // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1935551	ttctggtctacagtac[A/G]aggagttaaggctttg	A	G	/// ENST00000360895 // upstream // 7448 // --- // --- // --- // ---	-	p12.1
SNP_A-1940062	ttgcaggatcgggcaa[C/T]ccaagtttcacagcca	C	T	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1979712	gctttattgtctatca[C/T]ctgagaaacttcataa	C	T	// 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// NM_012403 // downstream //	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.3
SNP_A-1923950	ttagtgactacaatta[A/G]cctcccttcaccactg	A	G	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2877995 // --- // -	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p13.3
SNP_A-1930174	ttcattcagcaaggag[A/G]ccagggtgaatgaagc	A	G	83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 893844 // Hs.546489 // C18orf16 // 147429 //	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q12.1
SNP_A-1927433	ttcaaaggtgcccgaa[C/T]tcctattggtctgcga	C	T	2977 // Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// NM_152434 // downstream // 284314	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-1906101	tggtctggcatgaaga[G/T]aattgtagagagcacc	G	T	OR4N4 // 283694 // Homo sapiens olfactory receptor, family 4, subfamily N, member 4 (OR4N4), mRNA. ///	OR4N4	OR4N4, Homo sapiens olfactory receptor, family 4, subfamily N, member 4 (OR4N4), q11.2
SNP_A-1875233	tctctctctgtctctc[A/G]cacaggctgaacatat	A	G	23072 // Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// ENST00000322220 // downstream //	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p14.1
SNP_A-1874599	tctcctatcccataat[A/G]acactcactttattgg	A	G	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 228124 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1896188	tgcggagttactggaa[A/G]gttggtggcttgtttc	A	G	ENST00000256013 // intron // 0 // --- // --- // --- // ---	-	q21.32
SNP_A-1890911	tgatgcttgttaccac[A/G]ctaatgaataatggtg	A	G	// Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// NM_015199 // intron // 0 //	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-1893482	tgcaggaaaactcttc[C/T]ctatggaattccagca	C	T	57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 339855 // --- // ---	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-1879318	tcttaggctcagagga[A/T]ataacgtaggtgaaag	A	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 825242 // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1887839	tgagatgtagtgagaa[C/G]tctaaagtctggtgag	C	G	9926 // Homo sapiens mRNA for KIAA0205 gene, partial cds. /// NM_015434 // downstream // 3730 // Hs.369285 //	LPGAT1	LPGAT1, Homo sapiens for KIAA0205 gene, partial cds. ,q32.3
SNP_A-1886238	tgacccttgctaactc[A/G]cacactgaccctctct	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1909853	tgtcactataaaactg[A/G]acaattcaaggataca	A	G	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2763875 // --- // -	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p13.3
SNP_A-1914990	tgttatataaatagac[A/G]ccaagctctagcacta	A	G	Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-1922649	ttagacttgattttga[C/T]ggaggacaatcaattt	C	T	253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 // upstream //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1967275	ttatgtatccttctac[C/G]agaaagacttcctgaa	C	G	Homo sapiens HS1 binding protein (HAX1), mRNA. /// ENST00000271886 // intron // 0 // --- // --- // --- // ---	HAX1	HAX1, Homo sapiens HS1 binding protein (HAX1), q21.3
SNP_A-1974314	tgttgttctttgatta[C/T]actgagtttcagcctg	C	T	Homo sapiens KIAA0779 protein (KIAA0779), mRNA. /// ENST00000329333 // intron // 0 // --- // --- // --- // ---	TMCC1	TMCC1, Homo sapiens KIAA0779 protein (KIAA0779), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1947294	tttaatttttgctcac[A/G]cctttatcacctcttc	A	G	Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- // --- ///	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-1938738	ttgagcatttgagatg[C/T]agctagtgaaacccag	C	T	388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 628721 // --- // ---	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-1821157	gtttgaacagcaaaaa[A/C]taggaattaagacacc	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1328721 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1836554	tactctcaagcttata[C/T]gtaagtgtcagaaaag	C	T	HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 233943 // Hs.48384	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-1832590	tacaaatttactgtat[G/T]aatctgttttcacact	G	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 1130039 // Hs.465407 // NETO1 // 81832 //	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1840816	tagctattaattttca[A/G]tacccaaagacctctg	A	G	// Homo sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), mRNA. /// NM_002421 // downstream // 4333 // Hs.83169 // MMP1 // 4312 // Homo sapiens matrix	MMP10	MMP10, Homo sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), q22.2
SNP_A-1789852	gggctggtcaccttga[A/G]catccaggagtgtctg	A	G	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // --- // --- ///	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-2118057	agtaaaacataaaaac[C/T]ctgtctaatgtatgta	C	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2132109	cacctgctatgcataa[C/T]aacctatctctagacc	C	T	Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /// ENST00000261488 // intron // 0 // --- // --- // --- // ---	FLJ10094	FLJ10094, Homo sapiens hypothetical protein FLJ10094 (FLJ10094), q14.11
SNP_A-2167120	caacacaacttcctta[C/G]agaggcctcattccac	C	G	1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream //	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2161794	atttgtatttataaga[C/G]caatcagttgtaaatc	C	G	Homo sapiens hypothetical protein FLJ22555 (FLJ22555), mRNA. /// ENST00000295079 // intron // 0 // --- // --- // --- // ---	FLJ22555	FLJ22555, Homo sapiens hypothetical protein FLJ22555 (FLJ22555), q33.1
SNP_A-2147866	atggcctccacaataa[C/T]catgcgttctttcacc	C	T	ENST00000310543 // CDS // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-2146924	atggaaaatgcagtca[C/G]ctaatttcaggaaaca	C	G	Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 1 (SLC5A1), mRNA. ///	SLC5A1	SLC5A1, Homo sapiens solute carrier family 5 (sodium,q12.3
SNP_A-2151520	atatttacctgtctca[C/T]aatgatgaaagtacaa	C	T	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 511102 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2149317	atgtaattttgcctaa[C/T]gatataaacatggaag	C	T	10123 // Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA. /// NM_014521 // upstream // 57132 // Hs.516777 //	ARL7	ARL7, Homo sapiens ADP-ribosylation factor-like 7 (ARL7), q37.2
SNP_A-2211737	ccctcctgtcacctca[C/G]aacctcaagtcccact	C	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.2
SNP_A-2220065	ccttcaagccaaccac[A/G]ggctttgtgtattagt	A	G	ENST00000358277 // intron // 0 // --- // --- // --- // ---	-	q12
SNP_A-2181503	cagacttgatgtatga[A/G]gaaggtcccagcagct	A	G	Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-2179266	cactgtagaattttga[G/T]agtttaatacacttca	G	T	56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 115458 // --- // --- // --- // ---	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1
SNP_A-2177642	cacggccaagtctagg[G/T]aaggcaatcagactga	G	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 610946 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2196858	aacaatgtgtttgcaa[C/G]ctaaaggagtgaatag	C	G	// 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 940028 // Hs.211225 // NOVA1 // 4857 //	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2196210	catgtggtgattaata[C/T]taccttgtgcttttgg	C	T	Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B), mRNA. /// ENST00000255417 // intron // 0 // --- // --- // --- // ---	PIK3C2B	PIK3C2B, Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B), q32.1
SNP_A-2000946	gagcacagccacaggc[A/C]atatgcaaagaaatgg	A	C	Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 //	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-2017986	gcaacccaaggaagta[C/T]ctctgaaaccacacaa	C	T	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2015841	ttatactgaaagccca[A/G]gtttcaccagtatgca	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 246196 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2020416	tgacgctgtcggagcc[A/G]atggccttgagactgg	A	G	23308 // Homo sapiens inducible T-cell co-stimulator ligand (ICOSL), mRNA. /// ENST00000327663 // upstream // 23581	ICOSLG	ICOSLG, Homo sapiens inducible T-cell co-stimulator ligand (ICOSL), q22.3
SNP_A-2044233	aactttctcaagccag[A/G]cccaaaggatggggtt	A	G	Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // intron // 0 // --- // -	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2067228	acaaaggataaactaa[C/T]tgcaaaaggagaaaaa	C	T	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2073171	acaggcctgcaaaggg[A/T]atttttttcttgactc	A	T	79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 647724 //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2074147	acataaagacatcacc[A/G]gattttaaaaggggag	A	G	Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA. /// ENST00000302118 // intron // 0 // --- // ---	PCSK9	PCSK9, Homo sapiens proprotein convertase subtilisin p32.3
SNP_A-2074861	acatcacactgtgacc[C/T]gaggcaaggatgctag	C	T	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 685344 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2054056	aagttatcactattac[A/G]atccttgtgggttccc	A	G	FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2048538	aagcatgtctcttacc[C/T]gcttcacagactttat	C	T	Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), mRNA. /// ENST00000317467 // CDS // 0 // --- // --- // --- // ---	EPHX2	EPHX2, Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), p21.1
SNP_A-2089292	acttagcaatttttgg[G/T]agttagtagagcaata	G	T	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-2077131	accaagcagaaaaaag[A/T]atatgtgattttgaag	A	T	// 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2294450 // Hs.485968 // MAP3K7	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2107128	agcgggaagaaaccat[A/G]aagatgcgctgaaggg	A	G	ENST00000314630 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2310454	ggaacttgctctgtag[C/G]agtttaacagatggtg	C	G	2322 // Homo sapiens fms-related tyrosine kinase 3 (FLT3), mRNA. /// ENST00000332715 // upstream // 5688 // --- // --- //	FLT3	FLT3, Homo sapiens fms-related tyrosine kinase 3 (FLT3), q12.2
SNP_A-2288138	gattcaggtggcccca[A/G]gtctctgaagatatta	A	G	Homo sapiens Notch homolog 2 (Drosophila) (NOTCH2), mRNA. /// ENST00000344859 // intron // 0 // --- // --- // --- // ---	NOTCH2	NOTCH2, Homo sapiens Notch homolog 2 (Drosophila) (NOTCH2), p12
SNP_A-2299526	gccctttgactgttga[A/T]gaaagaaagcatgtgc	A	T	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), transcript variant 1, mRNA. /// NM_145687 // intron // 0 // Hs.431550 // MAP4K4 // 9448 //	MAP4K4	MAP4K4, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), transcript variant 1, q11.2
SNP_A-2244885	agtcctgactctagga[C/T]gagttgtatgtgtcac	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2233472	ctcagtgaaagttctc[A/G]aacaaatgggtagaag	A	G	Homo sapiens KIAA1036 (KIAA1036), mRNA. /// ENST00000167106 // intron // 0 // --- // --- // --- // ---	KIAA1036	KIAA1036, Homo sapiens KIAA1036 (KIAA1036), q24.3
SNP_A-2233188	ctcagctagcttttgc[A/C]atgtgccaactgtgtc	A	C	491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 17659 // Hs.268942 // ATP2B2	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2281271	gagtatacttaacacc[C/T]aaattttggtttctaa	C	T	1902 // Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 1, mRNA /// NM_057159 // upstream // 208352 // Hs.126667 // EDG2 // 19	EDG2	EDG2, Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 1, q31.3
SNP_A-2281792	gagtgactttaattgc[G/T]ctatgcttcagtcatc	G	T	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, mRNA. /// AB017133 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, p36.22
SNP_A-2264670	gaagacaatcttaaga[A/G]gtcacatactgtatga	A	G	79634 // Homo sapiens secernin 3 (SCRN3), mRNA. /// NM_152529 // downstream // 4882 // Hs.516604 // GPR155 //	SCRN3	SCRN3, Homo sapiens secernin 3 (SCRN3), q31.1
SNP_A-2262841	gaacaaaagaaacaga[A/G]tcaatatataaaattc	A	G	Homo sapiens prostaglandin F receptor (FP) (PTGFR), mRNA. /// ENST00000241946 // 3UTR // 0 // --- // --- // --- // ---	PTGFR	PTGFR, Homo sapiens prostaglandin F receptor (FP) (PTGFR), p31.1
SNP_A-2229269	ctaggaatatccatgc[A/C]agacaaaagtgtgctg	A	C	221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 94150	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2242744	ctgcatggtgcaggcc[C/T]agaaaatgaccgcctg	C	T	Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // --- // --- // --- // ---	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2255815	cttgttttcagataag[G/T]cggagtcacaagaaag	G	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1316838 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2301401	gccttttaagcaaatg[A/C]atacccaaagaaacag	A	C	// 64895 // Homo sapiens poly(A) polymerase gamma (PAPOLG), mRNA. /// NM_002908 // upstream // 42972 //	PAPOLG	PAPOLG, Homo sapiens poly(A) polymerase gamma (PAPOLG), p16.1
SNP_A-2290865	gcaaggccaggggagg[A/G]ccagtgaaactgagaa	A	G	// 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 281117 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2306809	gctgtgatagactcgc[A/G]acagttcctcctatgc	A	G	ENST00000262227 // intron // 0 // --- // --- // --- // ---	-	p11.31
SNP_A-2104666	agcagtccctatgcca[C/T]ataggaaccaatagtg	C	T	// 50674 // Homo sapiens neurogenin 3 (NEUROG3), mRNA. /// NM_145306 // upstream // 9694 // Hs.522992 // C10orf35 //	NEUROG3	NEUROG3, Homo sapiens neurogenin 3 (NEUROG3), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2094868	agaatctttatgctta[C/T]ctcttagcttgaggaa	C	T	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1906298 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-2084279	actagtggcagtatgc[A/G]aactgttcgttactgg	A	G	// 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 151812 // Hs.353022 // ETAA16 //	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2085889	ggatacctgaaggatc[A/G]cttggttcacaatcaa	A	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 635611 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2058912	aatccagacagaatca[A/T]ataattccattacctt	A	T	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // upstream // 197106 // Hs.411433 //	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-2027751	aaacccatgttgtaag[A/G]aactcagggtaacctc	A	G	7745 // Homo sapiens zinc finger protein 192 (ZNF192), mRNA. /// ENST00000259717 // downstream // 31518 // --- //	ZNF192	ZNF192, Homo sapiens zinc finger protein 192 (ZNF192), p22.1
SNP_A-1998592	tgactttaccacttac[C/T]gctctaacttgtactt	C	T	Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000323059 // intron // 0 // --- // --- // --- // ---	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.1
SNP_A-2186025	caggcagggtgtaaga[A/G]gtaagttggagaaaaa	A	G	Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron //	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2217217	cctctttgcttctta[C/T]gagctattcttaaacc	C	T	Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// ENST00000310430 // intron // 0 // --- // --- // --- // ---	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2203466	ccagaacctggtaaaa[A/G]gtgcagctgaggttca	A	G	Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// ENST00000355128 // intron // 0 // --- // --- // --- // ---	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-2142328	atgaaactgaagaaaa[C/T]gccacaatcctgaagc	C	T	Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), mRNA. /// ENST00000331762 // intron // 0 // --- // --- // --- // ---	IMMP2L	IMMP2L, Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), q31.1
SNP_A-2140367	atctcagtaagtgttc[C/T]atgtactcttaaagaa	C	T	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 291977 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2131756	atagctataaccagtg[C/T]actcttctcttcctaa	C	T	Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), mRNA. /// ENST00000359912 // intron // 0 // --- // ---	BCAR3	BCAR3, Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), p22.1
SNP_A-2124205	agttataaaaactaaa[G/T]tatctgtctcaagtat	G	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2112011	aggatgatagtattag[A/G]cctcattggggttgtc	A	G	9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 241676 //	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-1796848	ggttcagtgcagggat[C/G]aataaagggctagaca	C	G	Homo sapiens RNA polymerase I associated factor 53 (PAF53), mRNA. /// ENST00000259583 // intron // 0 // --- // ---	PAF53	PAF53, Homo sapiens RNA polymerase I associated factor 53 (PAF53), p13.2
SNP_A-1805363	gtccaactttgtgtca[A/G]tagaactgggatgtaa	A	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 816525 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1803139	gtattcagaggaagca[C/T]ggctgtgtcaacacct	C	T	ENST00000330336 // intron // 0 // --- // --- // --- // ---	-	q35.1
SNP_A-1643545	gagcccttaaccatggtggaaaaca[G/T]taccaaattatttctctggtaacat	G	T	2115 // ets variant gene 1 /// NM_005738 // downstream // 213126 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation	ETV1	ETV1 , rs10488241, ets variant gene 1 ,p21.3
SNP_A-1651088	gattatatgcactaatgttataaaa[G/T]tctggtgagtcaggtggtgtactct	G	T	387357 // chromosome 6 open reading frame 190 /// NM_014702 // upstream // 247100 // - // - // - // -	C6orf190	C6orf190 , rs643912, chromosome 6 open reading frame 190 ,q22.33
SNP_A-1712973	atctctaaatcacagatcaaagaac[A/C]actgaatggaatcatgtatgttgtt	A	C	tumor necrosis factor receptor superfamily, member 6 /// NM_152871 // intron // 0 // Hs.82359 // TNFRSF6 // 355 //	TNFRSF6	TNFRSF6 , rs1977389, tumor necrosis factor receptor superfamily, member 6 ,q23.31
SNP_A-1832373	tacaaaaattaaaaga[G/T]tacgcaggtgtggtaa	G	T	Homo sapiens ninjurin 2 (NINJ2), mRNA. /// ENST00000305108 // intron // 0 // --- // --- // --- // ---	NINJ2	NINJ2, Homo sapiens ninjurin 2 (NINJ2), p13.33
SNP_A-1870278	tcctttgaaaaatctc[C/T]caatatggatgttact	C	T	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_023914 // 3UTR // 0 // Hs.546396 // P2RY13 // 53829 //	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1846119	tatatatgttatggta[A/T]ctgtaatcagaaaatt	A	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1939978	ttgcagaatgaggtca[C/T]agtcgttgagtcccac	C	T	Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // 3UTR // 0 // --- // --- // --- // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1946272	tttaaaacttacgtgg[A/G]acataactgtgtgaaa	A	G	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // --- ///	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1942829	ttggggacttcgagag[G/T]atgaatgcagcctctg	G	T	ENST00000344342 // intron // 0 // --- // --- // --- // ---	-	p11.31
SNP_A-1978540	gatcaaacctattaga[C/T]gcgataaacaatataa	C	T	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1983824	ttaatctcttcttttc[C/T]acagagctcaataact	C	T	ENST00000327887 // intron // 0 // --- // --- // --- // ---	-	q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1922814	ttagatacaagtggaa[C/T]accacgtagacctggc	C	T	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2), mRNA. /// ENST00000271965 // intron // 0 // --- // --- // --- // ---	GALNT2	GALNT2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2), q42.13
SNP_A-1906461	tggtggagcacaggca[C/T]tgacatttttaaaag	C	T	// 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000342036 // upstream // 105600 // --- // ---	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-1896160	tgcgcctcagcttcag[A/G]aaaaagcctatcacgg	A	G	// 9655 // Homo sapiens suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, mRNA. /// NM_014011 //	SOCS5	SOCS5, Homo sapiens suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, p21
SNP_A-1875917	tctgaaatatctcatc[A/G]cacattctaccaaaac	A	G	// --- /// ENST00000355326 // downstream // 162278 // --- // --- // --- // --- /// ENST00000332323 // downstream // 366222 // ---	-	q11.21
SNP_A-1973543	tctacatgactaaaac[A/G]ggtggactaacagctg	A	G	Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // intron // 0 // Hs.123642 // EPHA3 // 2042 //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1967737	tatgatcttagttcaa[C/T]ctcatacgccatatgg	C	T	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 289108 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-1942818	ttggggaagcaactga[A/G]gtaggtcatccctcct	A	G	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA. /// ENST00000298171 // intron // 0 // --- // --- // --- // ---	TSHR	TSHR, Homo sapiens thyroid stimulating hormone receptor (TSHR), q31.1
SNP_A-1953511	tttgaatacacccata[C/T]atttttttccacagtcc	C	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 832867 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1870339	tcctttgtgatcctca[C/T]ccccgtctctgaccac	C	T	// 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // downstream // 9201 //	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-1869797	tccttccattaataac[A/G]attccctaaggtcctg	A	G	// 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 //	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.33
SNP_A-1832711	tacaagacgagtaaag[A/G]aagcttgactacctat	A	G	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 181074 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-1828102	taagaccagcagttaa[A/G]gttgtggcttagaact	A	G	Homo sapiens myosin VI (MYO6), mRNA. /// ENST00000357181 // intron // 0 // --- // --- // --- // --- ///	MYO6	MYO6, Homo sapiens myosin VI (MYO6), q14.1
SNP_A-1644622	agcaaacatacggttaagtagttaa[A/G]gtagccggtacactatgaacagcca	A	G	148281 // synaptotagmin VI /// NM_015906 // downstream // 103222 // Hs.293044 // TRIM33 // 51592 // tripartite motif-	SYT6	SYT6 , rs10489667, synaptotagmin VI ,p13.2
SNP_A-1813959	gtgtcactgggttgca[A/G]tcaaggtgttggcagg	A	G	/// ENST00000325796 // downstream // 227767 // --- // --- // ---	-	q22.2
SNP_A-2131657	atagccataatcattg[A/G]caatccaggcacaaaa	A	G	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2140953	atctgatgaaaggcca[G/T]attcagggaaggtatt	G	T	168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 468694	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2142172	atctttttttctgtca[C/T]gtattttatctgcatc	C	T	22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 1312 //	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2146230	atgctaactttgctta[C/T]aaattgccatgggaca	C	T	51384 // Homo sapiens wingless-type MMTV integration site family, member 16 (WNT16), transcript variant 1, mRNA. /// NM_014888 // downstream // 1557 // Hs.434053 // FAM3C //	WNT16	WNT16, Homo sapiens wingless-type MMTV integration site family, member 16 (WNT16), transcript variant 1, q31.31
SNP_A-2145303	atgcacggtaaacgtc[A/G]ccagattatacacata	A	G	ENST00000356562 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2205180	ccagtaatttttttca[G/T]gaagatatgcacttag	G	T	CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 116049 //	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2206508	ccatctgttgtttgga[C/G]ctaaagtgaaagcaat	C	G	Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // --- // --- // --- // --- /// ENST00000349908 // intron //	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-2216599	cctctatcgaaaaatc[A/C]aaaactcaagtaaaaa	A	C	Homo sapiens zinc finger protein 613 (ZNF613), mRNA. /// ENST00000342582 // intron // 0 // --- // --- // --- // --- ///	ZNF613	ZNF613, Homo sapiens zinc finger protein 613 (ZNF613), q13.41
SNP_A-2213357	ccggatgatggcataa[C/G]aatccctctaaacctc	C	G	Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA. /// ENST00000358336 // intron // 0 // --- // --- // --- // --- /// ENST00000320152 // intron // 0 // --- // --- // ---	PRTFDC1	PRTFDC1, Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), p12.1
SNP_A-2189757	cataaaaattctcaaa[C/G]tcctgtctgtttttac	C	G	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2176871	caccgcctccaaatgc[C/T]aacttgtccttttgta	C	T	Homo sapiens tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B), mRNA. /// ENST00000349152 // 3UTR // 0 // --- // --- // --- // --- /// ENST00000029717 // 3UTR //	TNFRSF1B	TNFRSF1B, Homo sapiens tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B), p36.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169984	caaggcttttaaggac[A/G]gaatgactcctgttag	A	G	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2004884	cctgcgagatgaaatc[A/C]aattgttttataatga	A	C	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2003604	ggaaaggctcatgcca[C/T]gttgctcccacaatgg	C	T	404785 // Homo sapiens protein expressed in prostate, ovary, testis, and placenta 14 (POTE14), transcript variant POTE-14B, mRNA. /// NM_001004053 // upstream // 114054	POTE14	POTE14, Homo sapiens protein expressed in prostate, ovary, testis, and placenta 14 (POTE14), transcript variant POTE-14B, q11.2
SNP_A-2013128	cagtgaaagcactttg[C/T]atcatttagcactttg	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1133359 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2013375	gaaaattgatattaaa[A/G]ctgcataaattgctta	A	G	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2029885	aaagataggatttttcc[A/G]agtgctttaaagaaaa	A	G	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 300890 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2023634	aaaactggcactgaga[A/G]aggctaagttacctgc	A	G	// 11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// ENST00000339492 //	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-2034085	aaatcataaatcacaa[A/C]taaaagccaattacat	A	C	ENST00000356802 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2062043	aatgggagaggttata[C/G]aacaagacagatctag	C	G	// Homo sapiens lactate dehydrogenase A-like 6A (LDHAL6A), mRNA. /// ENST00000280706 // intron // 0 // --- //	LDHAL6A	LDHAL6A, Homo sapiens lactate dehydrogenase A-like 6A (LDHAL6A), p15.1
SNP_A-2072938	acaggaaggagaagta[A/C]aaatgccaataaataa	A	C	1105 // Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /// ENST00000284049 // upstream	CHD1	CHD1, Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), q21.1
SNP_A-2091326	acttttcttctccaaa[A/T]ccattcttttcatttt	A	T	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 841810 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type ,p12.1
SNP_A-2080877	acctctatttagtcac[A/G]aatttctgcaatatca	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2093003	agaacacccgaaatgg[A/T]aaatacatggctgaat	A	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1801006 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2100271	agagtttactggaaga[C/T]gaataatgaagggaaa	C	T	6601 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member	SMARCC2	SMARCC2, Homo sapiens SWI q13.2
SNP_A-2290286	aagcacacatgggtta[A/G]gcggagaaatcagtgc	A	G	// 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 143875 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2241544	ctgagtttacaaagga[C/T]aatatgatgaggtgga	C	T	55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// NM_001444 // upstream // 62929 // Hs.408061 // FABP5 //	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-2228802	ctagagccatgtatta[A/G]aattctttgaatatgt	A	G	/// ENST00000335028 // upstream // 115503 // --- // --- // --- // ---	-	q21.31
SNP_A-2267687	gaatcagaatttcacc[A/G]ctttctggttagtgac	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2279489	gaggatgcaaaatatg[C/T]attttctgtagactgg	C	T	// 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 99866 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2275918	gagactgatatttaaa[A/C]agtggaaaaatgaatg	A	C	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2663403 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2268195	gaatgacatgtaatgg[A/C]agctttcaaagtgatt	A	C	/// ENST00000310012 // upstream // 16426 // --- // --- // --- // ---	-	q12
SNP_A-2269377	gaattttacttgctta[C/T]gaaaaactttggaaaa	C	T	// 202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 356731 // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.2
SNP_A-2258691	cttttgccagtttgca[C/T]aggaagacagaagtca	C	T	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 728837	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2229478	ctagggacttctcagc[C/G]cttgtcctgggatcta	C	G	8658 // Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// NM_012331 // upstream // 105006 // Hs.490981 // MSRA //	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2307312	gcttagaagtcagcac[A/G]ctacagaccttcggca	A	G	// 160418 // Homo sapiens SMILE protein (SMILE), mRNA. /// NM_003994 // downstream // 178006 // Hs.1048 // KITLG //	SMILE	SMILE, Homo sapiens SMILE protein (SMILE), q21.32
SNP_A-2304721	gctctggacacctatc[A/G]agtcctcaccagcagg	A	G	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), mRNA. /// NM_032447 // intron // 0 // Hs.370362 // FBN3 // 84467 //	ELAVL1	ELAVL1, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2302266	gctaaatttcaaaaag[A/G]ctattcacatctactt	A	G	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	MLLT10	MLLT10, Homo sapiens myeloid,p12.31
SNP_A-2102417	agattcctagataggg[G/T]attactgaatcaatca	G	T	Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), mRNA. /// ENST00000361062 // intron // 0 // --- // --- // --- // ---	TNIP1	TNIP1, Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), q33.1
SNP_A-2095286	agaattgtgggagctc[A/G]aagaataatggtagct	A	G	Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), mRNA. /// ENST00000193391 // intron // 0 // --- // ---	IMPG2	IMPG2, Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), q12.3
SNP_A-2098202	agagatacatacagaa[C/T]tgtgcctgtactatgt	C	T	58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 373334 // Hs.501911 //	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2079608	acccgtggccattgga[A/C]aataccttcccacct	A	C	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2052912	aagtcatggctatgaa[A/T]ctcttgaggttcagtt	A	T	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2024508	aaaaggagtattttaa[C/G]agaggttcaggaagaa	C	G	374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2019743	tccttctcttatcgaa[C/T]ggtatgttctagcatt	C	T	Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2176898	caccgtctgagatgag[A/T]actttattccttcctc	A	T	Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA. /// ENST00000265946 // intron // 0 // --- // ---	RAB18	RAB18, Homo sapiens RAB18, member RAS oncogene family (RAB18), p12.1
SNP_A-2197900	cattgattaaattgat[A/G]agacagtgtttcagtt	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 727327 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2203756	ccagagagcaaaggtc[A/G]ctttcaaatgaacaat	A	G	Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), mRNA. /// ENST00000338008 // intron // 0 // --- //	ZFYVE16	ZFYVE16, Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), q14.1
SNP_A-2130987	atagaactgcctttaa[A/G]tccttagagactgtgt	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 501459 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-2126774	ataaacttgatgtgaa[C/T]gttctttgataccaat	C	T	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1804622	gtcagctgcccggaaa[C/G]agctaagcatgagtta	C	G	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 73767 //	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1715497	ggtcattattgaatatccgtgtccc[A/G]gactcagctaaaagccccaagagag	A	G	11213 // interleukin-1 receptor-associated kinase 3 /// NM_033647 // upstream // 30814 // Hs.192323 // HELB //	IRAK3	IRAK3 , rs9325181, interleukin-1 receptor-associated kinase 3 ,q14.3
SNP_A-1746563	agtttgtcagtataaaaacaactga[A/G]agtctaagattgggttataacattt	A	G	2246 // fibroblast growth factor 1 (acidic) /// NM_015071 // upstream // 16186 // Hs.132942 // GRAF // 23092 // GTPase	FGF1	FGF1 , rs1347133, fibroblast growth factor 1 (acidic) ,q31.3
SNP_A-1844177	tagtttcagcagacaa[A/C]cccccatttttggagat	A	C	Homo sapiens PHD finger protein 15 (PHF15), mRNA. /// ENST00000282605 // intron // 0 // --- // --- // --- // --- ///	PHF15	PHF15, Homo sapiens PHD finger protein 15 (PHF15), q31.1
SNP_A-1839181	tagagctttgcatagg[A/T]atgtatgtccaaatac	A	T	23418 // Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, mRNA. /// NM_019049 //	CRB1	CRB1, Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, q31.3
SNP_A-1840192	tagcagatagataaga[A/T]cattcaaacaataaga	A	T	/// ENST00000354196 // upstream // 633160 // --- // --- // --- // --- /// ENST00000355224 // upstream // 633160 // --- // --- // ---	-	q21.11
SNP_A-1847559	tatccttttaacctgc[A/G]ctttaataaatgttaa	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 668299 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1959746	ttttggtgctctttcc[C/G]atttctcacttaacac	C	G	26054 // Homo sapiens SUMO1/sentrin specific protease 6 (SENP6), mRNA. /// NM_015571 // downstream // 29867 //	SENP6	SENP6, Homo sapiens SUMO1,q14.1
SNP_A-1946548	tttaaataggtgaaaa[C/T]ttgaagagatactaca	C	T	5885 // Homo sapiens RAD21 homolog (S. pombe) (RAD21), mRNA. /// NM_173851 // upstream // 35377 // Hs.532270 //	RAD21	RAD21, Homo sapiens RAD21 homolog (S. pombe) (RAD21), q24.11
SNP_A-1935336	ttctgcttgtttttaa[C/T]ctgtttttctcaggat	C	T	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 365380 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-1935212	ttctgccaccagcttc[C/T]cagccacttggtttgt	C	T	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 //	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-1966395	acctggtgacttctga[A/G]agccgctccagcttaa	A	G	ENST00000260983 // CDS // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1880064	tcttctattatcttga[C/T]cagaggtttttccttg	C	T	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000339824 // intron // 0 // --- // --- // --- // ---	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1888609	tgaggcaggagaacca[C/G]tcgagcctgggaggcc	C	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1889130	tgagtcagacataccc[A/G]cactgcccctgctgtc	A	G	Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1895942	tgccttagagaccgac[C/T]gacaccaagtagcaat	C	T	// 84435 // Homo sapiens G protein-coupled receptor 123 (GPR123), mRNA. /// NM_033404 // upstream // 17239 //	GPR123	GPR123, Homo sapiens G protein-coupled receptor 123 (GPR123), q26.3
SNP_A-1905742	tggtattgctcattca[A/G]tagctccctgctatgc	A	G	/// ENST00000315208 // upstream // 129003 // --- // --- // --- // -	-	q24.32
SNP_A-1922048	ttactggaatcaaaga[A/G]gtttccccaattaagc	A	G	Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// ENST00000355044 // intron // 0 // --- // --- // --- // --- ///	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-1930868	ttccagccagctaaaa[C/T]gtcatgacccaagcca	C	T	23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 21633 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1910485	tgtccctgagtggcag[C/T]atagggagctgtaggg	C	T	// --- /// ENST00000359634 // upstream // 139110 // --- // --- // -- // --- /// ENST00000359181 // upstream // 139110 // --- // ---	-	q32.3
SNP_A-1912854	tgtgcttcagtcgtac[A/G]attaaaaaatttaata	A	G	// Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00000324559 // intron // 0 // --- // --- // --- // ---	TMEM16E	TMEM16E, Homo sapiens transmembrane protein 16E (TMEM16E), p14.3
SNP_A-1900954	tggatacaaaaagtaa[C/T]gctcttgccatcagca	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 58575 // --- // --- // --- // ---	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1880216	tcttcttaaaactatc[A/G]ctttttcaatgtcacc	A	G	79931 // Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), mRNA. /// NM_198179 // downstream // 65719 //	TNIP3	TNIP3, Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), q27
SNP_A-1878713	tctgttcagtgttctc[C/T]gagaaagcaagaaagt	C	T	133522 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, beta (PPARGC1B), mRNA. /// ENST00000309241 // intron // 0 // --- // --- // --- // --- ///	PPARGC1B	PPARGC1B, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, beta (PPARGC1B), q32
SNP_A-1966449	tgatttgcatatagcc[C/T]acagcgatcttttcca	C	T	Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000260926 // intron // 0 // --- // --- // --- // ---	SATB2	SATB2, Homo sapiens SATB family member 2 (SATB2), q33.1
SNP_A-1973871	tagaagagattggtca[A/G]cagtctgaaaatcaga	A	G	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1969831	ttgcaatgaatgatag[A/G]acaaaagttattaagt	A	G	C21orf100 // 118421 // Homo sapiens chromosome 21 open reading frame 100 (C21orf100), mRNA. /// NM_182749 //	C21orf100	C21orf100, Homo sapiens chromosome 21 open reading frame 100 (C21orf100), q21.3
SNP_A-1985715	tccaatttttacatta[C/G]caaggttgcccaaatc	C	G	Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // --- // --- // --- // ---	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-1989344	tatatggaataaaaca[A/G]tcaatcttagatggtt	A	G	9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA. /// NM_004904 // downstream //	CREB5	CREB5, Homo sapiens cAMP responsive element binding protein 5 (CREB5), p15.1
SNP_A-1989311	aggtttatcaaggtga[A/G]tatgtggaaaagagcc	A	G	Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// ENST00000265395 // intron // 0 // --- // -	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-1986402	cagaacttgtttggaa[C/T]gtctttgtggagggta	C	T	79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 118772	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-1978517	gcctcttccttcatca[C/T]atttctccttgtcgtc	C	T	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 421937 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1941169	ttgctgataaaaagaa[A/T]acaagagccaagagct	A	T	// 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1951155	tttcccaaacgctgca[C/T]gtaaaaaggcaagaac	C	T	222 // Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), mRNA. /// ENST00000349015 // upstream // 22751 // --- // --- // --- // --- /// ENST00000339095	ALDH3B2	ALDH3B2, Homo sapiens aldehyde dehydrogenase 3 family, member B2 (ALDH3B2), q13.2
SNP_A-1948271	tttaggaatcacatga[C/G]gtattgtatgaaaagg	C	G	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // intron // 0 // --- // ---	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-1846722	tatcaaagtctcttca[A/G]gatagatagaaagtat	A	G	3488 // Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA. /// NM_003284 // downstream //	IGFBP5	IGFBP5, Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), q35
SNP_A-1852410	tatttaagtgtatcta[C/G]agtgactttccttttc	C	G	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1127047	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1854696	tcaacaggaactctaa[C/G]atcacacatttaatct	C	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1827954	taagaacctgaaaaaa[G/T]gcaagtaccatagcag	G	T	// 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_016588 // downstream //	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1825756	taaatccttagctcta[C/T]ggatgctggtgtattc	C	T	Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), mRNA. /// ENST00000282111 // intron	TCF7L1	TCF7L1, Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), p11.2
SNP_A-1716819	agagcaatgtttcctgtagggtcca[C/T]tgcatcgaggctacggcagagctca	C	T	NM_052851 // intron // 0 // Hs.369912 // STARD13 // 90627 // START domain containing 13	STARD13	STARD13 , rs2764617, START domain containing 13,q13.1
SNP_A-1645482	gagaaagaagtggactaaggctgaa[C/G]gtagaagatatggccagtgaggacc	C	G	NM_005711 // upstream // 954164 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3 , rs389382, EGF-like repeats and discoidin I-like domains 3,q14.3
SNP_A-1801871	gtagttggagaggacc[A/G]catcaagaagaacgaa	A	G	Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, mRNA. /// NM_020328 // intron // 0 //	ACVR1B	ACVR1B, Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, q13.13
SNP_A-1811485	gtgctcagttggaaag[A/C]atgacctcaagtggca	A	C	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2111952	aggatcttaaaatgcc[A/G]aaagaaaaaagattat	A	G	9734 // Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, mRNA. /// NM_058177 // downstream //	HDAC9	HDAC9, Homo sapiens histone deacetylase 9 (HDAC9), transcript variant 3, p21.1
SNP_A-2115512	aggggtccagtttcaa[C/T]cttatacatagtacta	C	T	NM_021148 // upstream // 6643 // Hs.386264 // ZNF273 // 10793 // Homo sapiens zinc finger protein 273 (ZNF273),	-	q11.21
SNP_A-2219028	cctggttcttgtgtaa[C/T]ctcgctgtgggagaac	C	T	// Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// NM_153825 // downstream // 24309 //	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-2187520	cagtaaaggaggcaat[A/G]aggattatctctcagc	A	G	81930 // Homo sapiens kinesin family member 18A (KIF18A), mRNA. /// ENST00000314102 // upstream // 96392 // --- // ---	KIF18A	KIF18A, Homo sapiens kinesin family member 18A (KIF18A), p14.1
SNP_A-2175501	cacatctccagataaa[C/T]cagacttctacttttt	C	T	// 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 //	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2181514	cagactttagtatcac[A/G]catacctaagttttaa	A	G	81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 71223 //	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-2020602	acgacacatgtttaaa[C/T]ggcattctgtgagccc	C	T	246704 // Homo sapiens chromosome 21 open reading frame 93 (C21orf93), mRNA. /// ENST00000328338 //	C21orf93	C21orf93, Homo sapiens chromosome 21 open reading frame 93 (C21orf93), q22.3
SNP_A-2033096	aaatacaggtcaatgc[A/C]acttgtagaaaattag	A	C	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2033721	aaatatggttatcaga[C/T]gtttatcttgtttaaa	C	T	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 955660 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2039152	aacagtagagaggaaa[A/G]agtcaaagataaaggg	A	G	// 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2047497	aagatgcataactcta[C/G]agtaaaggttattgag	C	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2042102	aactagagaatccaga[C/T]aaatatactcagtaca	C	T	Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), mRNA. /// ENST00000263723 // intron // 0 // --- // --- // --- // ---	CLCA4	CLCA4, Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), p22.3
SNP_A-2041911	acaaagcgcacaagtg[A/C]atttttactcaaagta	A	C	4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /// NM_006152 // downstream // 217231 //	LRMP	LRMP, Homo sapiens lymphoid-restricted membrane protein (LRMP), p12.1
SNP_A-2013261	aaaagagcaagcagta[C/G]aaaggagggtctcact	C	G	Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), mRNA. ///	ChGn	ChGn, Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), p21.3
SNP_A-2016593	tcattagaaatgttaa[A/G]cttaggtcaagatata	A	G	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 182863 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2012154	actttcactaaccaga[C/T]ccaggcagccttctgg	C	T	23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// NM_005715 // upstream // 99080 //	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-2004649	catttttattagtaaa[A/G]gcactaaatgtaagca	A	G	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2047982	aagcaacttgattgca[C/T]attactgcctttcctt	C	T	Homo sapiens hypothetical protein FLJ10637 (FLJ10637), mRNA. /// ENST00000335745 // intron // 0 // --- // --- // --- // ---	C12orf11	C12orf11, Homo sapiens hypothetical protein FLJ10637 (FLJ10637), p11.23
SNP_A-2076678	acattttcacccgtaa[C/T]accttgtcacccgtac	C	T	// 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 315283 // --- // --- // --- // ---	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-2066983	acaaacatacacgcac[C/T]atccccacagaaacac	C	T	ENST00000330102 // intron // 0 // --- // --- // --- // ---	-	q24.13
SNP_A-2068124	acaagaagtcagtata[C/T]gtataacctttcaaaa	C	T	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 569509 // --- // --- // --- // ---	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2069668	acacacattatacata[C/T]agaggtttagccatat	C	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2069432	acacaagatttgagac[C/T]actgcttcaagggag	C	T	152641 // Homo sapiens hypothetical protein FLJ30277 (FLJ30277), mRNA. /// NM_024949 // upstream // 53147 //	FLJ30277	FLJ30277, Homo sapiens hypothetical protein FLJ30277 (FLJ30277), q35.1
SNP_A-2077276	accaatgagtcaaagg[A/G]actggccatgcctcta	A	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 146783 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2082885	acgtccagcctaaacaa[A/C]gtaagttacaaataaa	A	C	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3368665 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2238018	ctctgatgtgaatgaa[C/T]aagaagtgctctgagc	C	T	Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000299322 // intron // 0 // --- // --- // ---	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2252826	cttctagaacagtggaa[A/G]agaagaaaggttaatg	A	G	ENST00000334344 // intron // 0 // --- // --- // ---	-	q12
SNP_A-2273855	gactgggggtataggaaa[A/G]tagaaacaaccagtagg	A	G	Homo sapiens cholecystokinin A receptor (CCKAR), mRNA. /// NM_018317 // upstream // 74696 // Hs.479403 // TBC1D19	CCKAR	CCKAR, Homo sapiens cholecystokinin A receptor (CCKAR), p15.2
SNP_A-2278818	aaaactaaatcggcaa[A/G]ctgataccatgtagt	A	G	Homo sapiens rai-like protein (RaLP), mRNA. /// ENST00000332408 // intron // 0 // --- // --- // --- // ---	RaLP	RaLP, Homo sapiens rai-like protein (RaLP), q21.1
SNP_A-2277958	gagccactgctgcatc[A/G]ctcatttgactactcac	A	G	4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // upstream // 306716 // Hs.307734 // MME // 4311	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN q25.2
SNP_A-2258920	cttttcgaacaaaaa[A/T]aactgagcctgattaa	A	T	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6Gall), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6Gall), q12.3
SNP_A-2255098	ctgggggacagtaacc[C/T]gcttcattaaaacagc	C	T	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 773871 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2238636	ctctgtgtctttcac[A/G]ggttttcatcacatc	A	G	// Homo sapiens sodium channel, voltage-gated, type IX, alpha (SCN9A), mRNA. /// NM_002976 // downstream //	SCN9A	SCN9A, Homo sapiens sodium channel, voltage-gated, type IX, alpha (SCN9A), q24.3
SNP_A-2236137	ctccttcatcataaaa[C/T]acagcagtgatttggc	C	T	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 4,	ABCC1	ABCC1, Homo sapiens ATP-binding cassette, sub-family C (CFTR p13.11
SNP_A-2308673	gctttccttttagata[C/T]agatgtgtcctaccta	C	T	Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, mRNA. /// NM_001372 // intron // 0 // Hs.526552 // DNAH9 // 1770 // Homo sapiens dynein,	DNAH9	DNAH9, Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, p12
SNP_A-2104245	agcagatggtgatgcc[A/G]cgtgcagccagtgagg	A	G	FLJ38377 // 205147 // Homo sapiens hypothetical protein FLJ38377 (FLJ38377), mRNA. /// NM_015320 // upstream //	FLJ38377	FLJ38377, Homo sapiens hypothetical protein FLJ38377 (FLJ38377), q21.1
SNP_A-2064622	aatctatcaccactac[C/T]cacctggtccagata	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 993776 // Hs.435771 // APl5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2075542	acatgcagacaggccc[A/G]aagaggccaagcggat	A	G	Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // intron // 0 // Hs.268942 // ATP2B2 // 491 //	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2049857	aaggaaataatgtcag[A/G]ctagctaaaggaagta	A	G	ENST00000342193 // intron // 0 // --- // --- // ---	-	q24.3
SNP_A-2009303	cagaagttctcagctc[C/T]gaccacatatgagcat	C	T	Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), mRNA. /// ENST00000351298 // intron // 0 // --- // ---	PLD1	PLD1, Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), q26.31
SNP_A-2022559	aaaaatgaaaatgaaa[A/C]ctgaatgtcaactcct	A	C	DKFZp434O0213 // 91355 // Homo sapiens hypothetical protein DKFZp434O0213 (DKFZp434O0213), mRNA. /// NM_005160 // upstream // 153942 // Hs.517493 // ADRBK2 //	DKFZp434O0213	DKFZp434O0213, Homo sapiens hypothetical protein DKFZp434O0213 (DKFZp434O0213), q11.23
SNP_A-2175145	cacagtggtcactaaa[A/G]ggatataacttaat	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2188846	cagtggtatgtgctaa[G/T]gaggagatgaaataaa	G	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2195957	catgtcccgcctgagc[A/G]ataggacactatgtac	A	G	Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // intron // 0 // --- // --- // --- // ---	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2195376	catggctctattaac[C/T]gctttcagtaaagtcc	C	T	2048 // Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // downstream // 91068 // Hs.523329	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-2213844	cctaaagattgagtta[C/T]gcttagttagaatcac	C	T	Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA. /// ENST00000330610 // intron // 0 // --- // --- // ---	KIRREL	KIRREL, Homo sapiens kin of IRRE like (Drosophila) (KIRREL), q23.1
SNP_A-2216536	cctctaatggaagaaat[C/T]agagcgggtcccacag	C	T	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225712	ctaaagactcttctaa[C/T]gctctgagtcaataat	C	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 54064 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2131213	atagagatagacacaa[A/T]tcttagaaggccaaga	A	T	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1135320 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2161545	atttggaaatgaaccc[A/G]caaaaggcctctgggt	A	G	1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 98737 // --- //	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2
SNP_A-2163396	atttttttatagagtg[A/G]aacatacacgtatcat	A	G	// 350383 // Homo sapiens G protein-coupled receptor 142 (GPR142), mRNA. /// NM_018653 // upstream // 30968 //	GPR142	GPR142, Homo sapiens G protein-coupled receptor 142 (GPR142), q25.1
SNP_A-1791447	gggtatatgcatccta[C/T]ggcagccttaggtcat	C	T	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1786528	ggcttcatctttgtga[C/G]aggatgtccttgtggc	C	G	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc q31.1
SNP_A-1728369	tctgcaccaacctgatagattctca[A/G]tgaaagtcaaatacatagatgaaat	A	G	5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 897108 // Hs.285782 // LRRTM4 // 80059 // leucine-rich	REG1B	REG1B , rs908439, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-1729380	caacctgctttgatcaccaaatgag[A/T]cagggagaagaacatggatggaaat	A	T	sapiens cDNA FLJ39824 fis, clone SPLEN2011981. /// NM_006079 // upstream // 292572 // Hs.82071 // CITED2 //	-	- , rs10499211, Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981. ,q24.1
SNP_A-1825032	taaaggagctgagaac[A/G]cttacaacatgagtgc	A	G	55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// NM_001444 // upstream // 184311 // Hs.408061 // FABP5 //	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-1819832	gttgtggaagaaaaaa[A/G]gggcaatactgcagca	A	G	ENST00000327351 // CDS // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-1843242	tagtcctgaaatttcc[A/G]agtggcatactggaag	A	G	Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // --- // --- // --- // ---	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-1833101	tacacatcactgaaga[C/T]attcttgttatgttat	C	T	FLJ20272 // 55622 // Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA. /// M34057 // upstream //	FLJ20272	FLJ20272, Homo sapiens hypothetical protein FLJ20272 (FLJ20272), p22.3
SNP_A-1831919	taattgataagatgag[G/T]aaagaaagtgaatgga	G	T	Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), mRNA. /// ENST00000283148 // intron // 0 // --- // --- // --- // ---	UXS1	UXS1, Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), q12.2
SNP_A-1847360	tatcccagaaccaaaa[A/G]tatttcctgagactta	A	G	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 992731 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1845249	tatacggagagcatag[G/T]agacataatgaccatg	G	T	55128 // Homo sapiens ring finger protein 137 (RNF137), mRNA. /// NM_001004751 // upstream // 13251 // --- //	TRIM68	TRIM68, Homo sapiens ring finger protein 137 (RNF137), p15.4
SNP_A-1863407	tcatttttttgttcaga[G/T]agctggacagcattcc	G	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2549744 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1866344	tcccattcccgcctaa[A/G]ccctggctgttcctgg	A	G	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1922421 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1957888	ttttcaaaataaaaac[C/T]cattagcagatctttt	C	T	4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 //	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-1956039	tttgtctttactccta[A/C]gtatgactctggaaat	A	C	-- /// ENST00000361117 // upstream // 685655 // --- // --- // ---	-	q33.2
SNP_A-1947083	tttaatatctggaaag[C/T]ctaacaagaaggatgt	C	T	Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // intron // 0 // Hs.282871 // CYP2C8 // 1558 //	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-1944188	ttgtcatcagtgggac[A/G]cttcttgttcaagtaa	A	G	343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2146629 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1879782	tcttccaagcccttca[A/G]attgtttgtttcagcc	A	G	SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 309451 // Hs.354013 //	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-1901737	tggcacagcaagcaac[A/G]aaaacattgcttcatt	A	G	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), mRNA. /// ENST00000262367 //	CREBBP	CREBBP, Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), p13.3
SNP_A-1917570	tgtttttaaagcaag[C/T]atcatgatcctatcat	C	T	7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000355985 // upstream // 215357 // --- // ---	ZNF217	ZNF217, Homo sapiens zinc finger protein 217 (ZNF217), q13.2
SNP_A-1931267	ttccatttttgcttta[C/T]ctctacacatattcac	C	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1929000	gagacttgcagtgtga[A/T]agtagtaatttactct	A	T	25914 // Homo sapiens rotatin (RTTN), mRNA. /// NM_004232 // upstream // 2235 // Hs.44439 // SOCS6 //	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-1928624	ttcacttccttggtga[A/G]ctcaaccttcagcctc	A	G	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 173619 // --- // --- // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-1918049	ttaaacaattgaagat[A/C]atcctgagcaaaacat	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 227535 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1905526	tggtactgcaaagaaa[A/G]ccaatgtaggaaccaa	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 96942 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1876115	tctgacactcctataa[A/G]aaagtcccatagagct	A	G	ENST00000309493 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-1946356	tttaaaatgtgtgcaa[C/T]gatgttactttttttt	C	T	Homo sapiens dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP4), mRNA. /// ENST00000360534 // intron // 0 // --- // --- // --- // ---	DPP4	DPP4, Homo sapiens dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP4), q24.2
SNP_A-1943205	ttggtcttcttcacta[C/T]aatcttttattccgta	C	T	PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 649087 // Hs.405156 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-1953489	tttgaagtcccaatga[C/T]gatcacaatttactct	C	T	8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 93203 // --- // --- // --- // ---	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-1979607	aaaactacagagatag[A/G]aaacaaattgttgcca	A	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1616983 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1862467	tcatgttcacagacca[A/G]gttgttttgcactctg	A	G	// Homo sapiens solute carrier family 26, member 8 (SLC26A8), transcript variant 1, mRNA. /// NM_138718 // intron // 0 // Hs.435836 // SLC26A8 // 116369 // Homo	SLC26A8	SLC26A8, Homo sapiens solute carrier family 26, member 8 (SLC26A8), transcript variant 1, p21.31
SNP_A-1859868	tcagggttggggccct[C/T]agaatttgcacttcta	C	T	Homo sapiens BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_138578 // intron // 0 // Hs.516966 // BCL2L1 // 598 //	BCL2L1	BCL2L1, Homo sapiens BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 2, q11.21
SNP_A-1833456	tacagagctaaaaaaa[G/T]cttgcctaatgtcaca	G	T	FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000344027 // upstream //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1686016	catgttgaacagggtaaacatgaaa[C/G]tcatacagaaaggtaacaaacgg ta	C	G	NM_002031 // intron // 0 // Hs.89426 // FRK // 2444 // fyn-related kinase	FRK	FRK , rs7762044, fyn-related kinase,q22.1
SNP_A-1792821	ggtaataaggggttca[C/T]gagtcctaattttaca	C	T	131890 // Homo sapiens G protein-coupled receptor kinase 7 (GRK7), mRNA. /// ENST00000264952 // downstream //	GRK7	GRK7, Homo sapiens G protein-coupled receptor kinase 7 (GRK7), q23
SNP_A-1812847	gtgggcagtgtcaagg[A/G]atatatttgtgttctg	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 664048 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1810965	gtgcattgggcaggga[A/G]cacattgattgcatag	A	G	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), mRNA. /// ENST00000351593 // intron // 0 // --- // --- // --- // ---	ELAVL1	ELAVL1, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), p13.2
SNP_A-1803526	gtattttggaaggggga[C/T]atctaagttccaggca	C	T	1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream //	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-2159599	atttactgaatcctta[C/T]catgttctagaacaat	C	T	140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// NM_019888 // upstream // 74197 // Hs.248018 //	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-2145692	atgcatttgttcagac[A/G]cataggtaaatgcctg	A	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2144596	atgatctacctattcc[A/G]cctcactttaggtgga	A	G	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 217293 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2125169	agttgggatcgcacaa[C/T]aggtagccattttaga	C	T	Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// ENST00000356204 // intron // 0 // --- // --- // --- // ---	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2115502	aggggtattttctagc[C/T]cagagatgacatatcc	C	T	219899 // Homo sapiens hypothetical protein MGC10233 (MGC10233), mRNA. /// ENST00000284259 // intron // 0 // ---	MGC10233	MGC10233, Homo sapiens hypothetical protein MGC10233 (MGC10233), q23.3
SNP_A-2114538	agggagctaatctgta[A/T]aatttattcctgtgca	A	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2110875	aggactgggcatcatt[C/G]aaaaagcagtggactc	C	G	4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 387220 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2111410	aggaggactttcatca[C/T]gtttctctccagtgtc	C	T	Homo sapiens esophagus cancer-related gene-2 (ECG2), mRNA. /// ENST00000274565 // intron // 0 // --- // --- // --- // ---	ECG2	ECG2, Homo sapiens esophagus cancer-related gene-2 (ECG2), q32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2121154	agtctgatgtctgtta[C/G]agtgaaatatccttgtc	C	G	10878 // Homo sapiens complement factor H-related 3 (CFHL3), mRNA. /// NM_002113 // upstream // 11170 //	CFHL3	CFHL3, Homo sapiens complement factor H-related 3 (CFHL3), q31.3
SNP_A-2220218	ccttccaaccctctaa[C/G]agcaacttggcacagc	C	G	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2217018	gaccgcagtccttgac[A/G]ccaccagtctactttc	A	G	ENST00000281741 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2210482	ccccctccaggaggta[C/G]agtttaacgcaccctc	C	G	/// ENST00000357331 // upstream // 122485 // --- // --- // --- // -	-	p21.3
SNP_A-2169526	caagctaattccctcc[C/T]gcagtcttgatggaag	C	T	sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 //	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-2042123	aactagcacatctatc[A/G]cctcaaacacttgtca	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 299606 // --- // --- // --- //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2039932	aacatttagctgaaga[C/T]gacttctattgtctta	C	T	Homo sapiens chromosome 6 open reading frame 60 (C6orf60), mRNA. /// ENST00000338891 // intron // 0 // --- // --	C6orf60	C6orf60, Homo sapiens chromosome 6 open reading frame 60 (C6orf60), q22.31
SNP_A-1991913	tgggtggtacgtagac[C/G]aaaatagtcctgtgac	C	G	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1996971	taaaaggtacaagcca[C/T]aaatcttggcagcatc	C	T	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1089172 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1994902	aacaagcacagaccac[G/T]ctaacatgttcaagtc	G	T	6641 // Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), mRNA. /// NM_021021 // upstream // 157948 // Hs.371902 //	SNTB1	SNTB1, Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), q24.12
SNP_A-2051550	aagggttaacataggc[A/T]attctgtctacttgat	A	T	10651 // Homo sapiens metaxin 2 (MTX2), transcript variant 1, mRNA. /// ENST00000249442 // downstream // 167600 // -	MTX2	MTX2, Homo sapiens metaxin 2 (MTX2), transcript variant 1, q31.1
SNP_A-2054846	aataaagatgtaggaa[A/G]ggaaaatgccattagt	A	G	Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 //	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-2096386	agacccatgacaaatt[C/G]aagtgtatcacttaac	C	G	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-2093801	agaagagtagaaacca[C/T]atcatgaagattttca	C	T	FLJ23834 // 222256 // Homo sapiens hypothetical protein FLJ23834 (FLJ23834), mRNA. /// NM_006754 // downstream	FLJ23834	FLJ23834, Homo sapiens hypothetical protein FLJ23834 (FLJ23834), q22.3
SNP_A-2091499	agaaaaacaggggaag[A/G]aagaccatgcttgata	A	G	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 4930 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2086383	actcttcccccaaaaa[A/G]cccagtgcctgttctg	A	G	ENST00000361026 // intron // 0 // --- // --- // --- // --- /// ENST00000278445 // intron // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-2087551	actgcgctctcctcca[A/G]taaaatctcctaataa	A	G	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2310839	ggaagctgagaggttt[A/G]aaaacaggctggcaat	A	G	257218 // Homo sapiens SNF2 histone linker PHD RING helicase (SHPRH), mRNA. /// NM_000838 // upstream //	SHPRH	SHPRH, Homo sapiens SNF2 histone linker PHD RING helicase (SHPRH), q24.3
SNP_A-2292241	gcacctagaggagcaa[C/G]agtttgggtaaaggca	C	G	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2297718	gccagctttgactcca[A/G]gtacagcaggattctg	A	G	51125 // Homo sapiens golgi autoantigen, golgin subfamily a, 7 (GOLGA7), transcript variant 1, mRNA. /// NM_001002296 // downstream // 1291 // Hs.7953 // GOLGA7 // 51125 //	GOLGA7	GOLGA7, Homo sapiens golgi autoantigen, golgin subfamily a, 7 (GOLGA7), transcript variant 1, p11.21
SNP_A-2235550	ctcctaatcataatca[C/T]attagagtgagtccag	C	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2234192	ctcatttaatcatcac[C/T]actgtaaagttggtgt	C	T	Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// ENST00000246032 // intron // 0 // --- // --- // --- // ---	STK35	STK35, Homo sapiens serine,p13
SNP_A-2252396	cttcctaatcaatgaa[A/C]taatgcacaaggggca	A	C	4843 // Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, mRNA. /// NM_153292 // upstream // 70214 // Hs.462525 // NOS2A //	NOS2A	NOS2A, Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, q11.2
SNP_A-2251659	cttcaggcttctcata[C/T]gttggttttgaattgt	C	T	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // --- // --- // --- // ---	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. ,p24.1
SNP_A-2249607	cttaagcatgatttca[C/T]acacttccaggttcca	C	T	// 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // upstream // 125404 // Hs.437444 // CACNA1E // 777 // Homo sapiens	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2249018	ctgtttactattatta[C/T]gattacatggtgataa	C	T	/// ENST00000288466 // upstream // 103303 // --- // --- // --- // -- /// ENST00000307730 // upstream // 254875 // --- // --- // ---	-	q32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246592	ctgtaacttcttatca[C/T]gggtatagtgatttta	C	T	Homo sapiens chromosome 20 open reading frame 100 (C20orf100), mRNA. /// AK055135 // intron // 0 // Hs.26608 //	C20orf100	C20orf100, Homo sapiens chromosome 20 open reading frame 100 (C20orf100), q13.12
SNP_A-2235144	ctccccacaggtatag[A/T]caaccacatactcaac	A	T	ENST00000358349 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-2280382	gaggggtggagaaaaa[C/G]tcattgaaatatggtt	C	G	Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), mRNA. /// ENST00000324695 // intron // 0 // --- // --- // --- // --- // ---	TRPM8	TRPM8, Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), q37.1
SNP_A-2306369	gctggggaaacaaaac[C/T]caatgactccatcctc	C	T	ENST00000219301 // intron // 0 // --- // --- // --- // ---	-	q21
SNP_A-2303387	gctattgccttgttta[A/G]agtaagcaggagacat	A	G	134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream //	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-2088791	actgttaagaatagcc[C/T]gaagcctgcctgattc	C	T	MAP2K4 // 6416 // Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /// ENST00000353533 //	MAP2K4	MAP2K4, Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), p12
SNP_A-2081967	acctttctctagtcta[A/G]gccatgtaattctctt	A	G	Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-2050758	aaggcatatctgagac[A/G]gtaatttatatggaaa	A	G	KHDRBS3 // 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// ENST00000355849 // downstream // 178954 // ---	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.23
SNP_A-1996759	gacacaggctataaat[G/T]aatcaaagctcatggt	G	T	ENST00000354500 // intron // 0 // --- // --- // --- // ---	-	q21.12
SNP_A-1995539	gcaagggctgtgaaca[C/T]gggcatttgttcctag	C	T	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2038235	aacaccaaatgtctca[C/T]ctgactataactttcc	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 1620269 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2028876	aaactttatgctccta[C/T]gatcaactcctcctcc	C	T	// 399980 // Homo sapiens FLJ45436 protein (FLJ45436), mRNA. /// NM_016522 // upstream // 5077 // Hs.504352 //	FLJ45436	FLJ45436, Homo sapiens FLJ45436 protein (FLJ45436), q25
SNP_A-2026931	aaacactggagtttga[A/G]agaagaacatcacaca	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2178918	cactgattttagtgtg[C/G]aatttaaaatggaagg	C	G	/// ENST00000329863 // downstream // 1006120 // --- // --- // ---	-	q23.1
SNP_A-2184693	cagctcttaaaacgag[A/T]aaggcagttgtatatg	A	T	ENST00000345030 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-2211677	ccctccagccttcaga[C/T]gcaggaacgggaatct	C	T	1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 87509 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2211113	cccggtcaggctcttc[A/G]ctcttccacggcgacc	A	G	6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 3084 // Hs.522891 // CXCL12 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2119951	agtcaatgttagatca[C/G]tctgtacaagcagtag	C	G	Homo sapiens hypothetical protein FLJ21934 (FLJ21934), mRNA. /// ENST00000251566 // intron // 0 // --- // --- // --- // ---	FLJ21934	FLJ21934, Homo sapiens hypothetical protein FLJ21934 (FLJ21934), q13.2
SNP_A-1808798	gtgaaggggtcgtga[A/T]attccacattaacttc	A	T	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 551131 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1694711	cctaaaggggctttatgcagagga[C/T]gacaatacactgtgatagacactgt	C	T	// 10602 // CDC42 effector protein (Rho GTPase binding) 3 /// NM_144713 // upstream // 228446 // Hs.9905 // FLJ32954 //	CDC42EP3	CDC42EP3 , rs1035025, CDC42 effector protein (Rho GTPase binding) 3 ,p22.2
SNP_A-1664974	tgatcatttgccttttggctttaga[A/G]gtgggcttatctgagacaaagagaa	A	G	PCDH20 // 64881 // protocadherin 20 /// NM_030794 // downstream // 311633 // Hs.112707 // TDRD3 // 81550 //	PCDH20	PCDH20 , rs1504418, protocadherin 20 ,q21.2
SNP_A-1758296	cagttggttgggggaattaagata[A/C]gtggagtggtggtgattgaaggctc	A	C	NM_080672 // intron // 0 // Hs.288513 // SCAPIN1 // 116154 // scapinin	SCAPIN1	SCAPIN1 , rs1182524, scapinin,q13.33
SNP_A-1820957	gtttctcattagttcc[C/T]agattttaccaaatta	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-1820789	gtttcccaggtatgca[C/G]aaatcaaccagaacgt	C	G	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 327796 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1824841	taaagcaagccaatga[G/T]gtatccagtcttcacc	G	T	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA. /// ENST00000357431 // intron // 0 // --- // --- // --- // ---	FLJ10826	FLJ10826, Homo sapiens hypothetical protein FLJ10826 (FLJ10826), q12.2
SNP_A-1848653	tatgagattgctatca[C/G]gtaactcccatacatt	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2142230 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1859718	tcagggaaattactca[G/T]ggaaaggatgaaaacc	G	T	Homo sapiens F-box protein 40 (FBXO40), mRNA. /// ENST00000338040 // intron // 0 // --- // --- // --- // ---	FBXO40	FBXO40, Homo sapiens F-box protein 40 (FBXO40), q13.33
SNP_A-1968656	tctaaatacttaaaaa[C/T]tgcacgtgctctttaa	C	T	// 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream //	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889114	tgagtcaagtgaaaaa[C/T]tacagaaaccagaaag	C	T	Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), mRNA. /// ENST00000259146 // intron // 0 // --- // --- // --- // ---	EPRS	EPRS, Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), q41
SNP_A-1897619	tgctgcattttataga[C/T]gggaaaactaaagcat	C	T	9258 // Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), mRNA. /// NM_153332 // upstream // 88952 // Hs.20000 // 3'HEXO // 90459 // Homo	MFHAS1	MFHAS1, Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), p23.1
SNP_A-1896147	tgcgcacctcagctta[C/T]agtgtcaacatacttg	C	T	sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-1918730	ttaacaacatttcaca[C/T]tgataaagccaaaagt	C	T	EBNA1BP2 // 10969 // Homo sapiens EBNA1 binding protein 2 (EBNA1BP2), mRNA. /// ENST00000335282 // downstream	EBNA1BP2	EBNA1BP2, Homo sapiens EBNA1 binding protein 2 (EBNA1BP2), p34.2
SNP_A-1920517	taaagcacaccttatc[A/G]attactttattactaa	A	G	28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 399732 // --- // --- // --- // -	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.32
SNP_A-1932093	ttcctatttcagaacc[C/T]aacttcctagactaaa	C	T	// 125958 // Homo sapiens olfactory receptor, family 7, subfamily D, member 4 (OR7D4), mRNA. ///	OR7D4	OR7D4, Homo sapiens olfactory receptor, family 7, subfamily D, member 4 (OR7D4), p13.2
SNP_A-1895319	tgccctgctacgaact[G/T]aactttgccccctcaa	G	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2805617 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1964101	gttttaaaccattgct[C/T]acttgaaaacaccagc	C	T	// 8802 // Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA. /// ENST00000331369 //	SUCLG1	SUCLG1, Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), p11.2
SNP_A-1969882	tgaaaacatgacatta[A/G]caaacacgggaaaaag	A	G	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, mRNA. /// ENST00000327783 // intron // 0 // --- // --- // --- // ---	GRIK1	GRIK1, Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, q21.3
SNP_A-1981668	gaatgtagggcagaca[A/G]tcacttggcaggggtg	A	G	Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000264777 // intron // 0 // --- // --- // --- // ---	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-1950172	tttcactgttaactat[C/G]ataggtgagatcataa	C	G	sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // --- // --- // --- // ---	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-1848742	tatgataaaagcttca[C/T]atgataactcttgaat	C	T	8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 105647 // Hs.127013 // CADPS // 8618 // Homo	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1828072	taagacactatgctca[C/G]gttttgataaattata	C	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2984339 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1817493	gttcatctaaaactaa[C/T]gcccaacttgttctta	C	T	23635 // Homo sapiens single-stranded DNA binding protein 2 (SSBP2), mRNA. /// NM_031482 // upstream // 64728 //	SSBP2	SSBP2, Homo sapiens single-stranded DNA binding protein 2 (SSBP2), q14.1
SNP_A-1757844	ttctccaattccctgatgccaagaa[C/G]gtgtccaacaattcaattaaattct	C	G	NM_007249 // intron // 0 // Hs.164467 // KLF12 // 11278 // Kruppel-like factor 12	KLF12	KLF12 , rs1590380, Kruppel-like factor 12,q22.1
SNP_A-1785648	ggctcctagtcattaa[A/C]gacctagcatgagtaa	A	C	// Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // upstream // 44203 // Hs.436055 // ALX4 //	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds. ,p11.2
SNP_A-1785368	ggctatctgaaagaga[A/G]gacagaccagttagct	A	G	-- /// ENST00000314058 // upstream // 205457 // --- // --- // ---	-	p13.2
SNP_A-2108786	agctgtggtgttcgtc[A/G]agggaagcaggcagcc	A	G	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-2142917	atgaatacaaaacata[C/G]gaaacagatgtttagt	C	G	FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-2152775	attaattagggtgaaa[A/G]tagagttctttgcatg	A	G	ENST00000284717 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2226510	ctaagcctgagtttaa[A/G]attgtctctgcactca	A	G	ENST00000322410 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2224193	cggtgacaagacagaa[C/T]gaaggtgtcatccgca	C	T	Homo sapiens solute carrier family 26, member 11 (SLC26A11), mRNA. /// ENST00000323768 // intron // 0 // ---	SLC26A11	SLC26A11, Homo sapiens solute carrier family 26, member 11 (SLC26A11), q25.3
SNP_A-2186879	cagggtcagaagtgcc[A/G]agggtcacctgcatcc	A	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2191971	catcaattatgaaaac[A/G]attacaacatcaggaa	A	G	OSBPL8 // 114882 // Homo sapiens oxysterol binding protein-like 8 (OSBPL8), transcript variant 2, mRNA. /// NM_001003712 // upstream // 187850 // Hs.430849 //	OSBPL8	OSBPL8, Homo sapiens oxysterol binding protein-like 8 (OSBPL8), transcript variant 2, q21.2
SNP_A-2174590	cacagataaggggggga[C/T]taactactgtactctc	C	T	Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // --- // --- // --- // ---	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-2026008	aaaatgttttgggccc[C/T]aggatggtgtatatat	C	T	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, mRNA. /// NM_172362 // intron // 0 // Hs.527656 // KCNH1 //	KCNH1	KCNH1, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044863	aagaaatttgcagtac[A/G]ggaaaagcggtagttg	A	G	Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// ENST00000302103 //	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-2004656	tctggcagacggtacc[C/T]agagtgggacaacatc	C	T	HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 315807 // Hs.120831 // TNT //	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2003860	tttatcctcatggtta[C/T]aacacatcaagaaaga	C	T	-- /// ENST00000356117 // downstream // 483184 // --- // --- //	-	q23.31
SNP_A-2054480	aagtttctccaagtag[C/T]caaatcttttcttgct	C	T	1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // upstream // 74875 // Hs.282871 // CYP2C8	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-2061830	aatggatcaacttctc[C/T]cccaagttatactgtc	C	T	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 235774	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2055988	aatacagggaagagac[A/T]gtagctaataaagggt	A	T	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2068880	acaatctagagggaaa[A/G]tgaatgatgcagaaaa	A	G	5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2096800	agactattatttttta[A/G]gttgctgttcacattc	A	G	sapiens interleukin 7 receptor (IL7R), mRNA. /// ENST00000303115 // intron // 0 // --- // --- // --- // --- ///	IL7R	IL7R, Homo sapiens interleukin 7 receptor (IL7R), p13.2
SNP_A-2296648	gccaaaccaatcttca[A/T]aagtgagagagaaata	A	T	KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 222442 //	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. ,q25.1
SNP_A-2298903	gccccagaaatgcttc[G/T]cttctatgactttgtt	G	T	7560 // Human Kox5 mRNA for zinc finger protein, partial. /// ENST00000333201 // downstream // 15992 // --- // --- // --- // --	ZNF13	ZNF13, Human Kox5 for zinc finger protein, partial. ,q13.13
SNP_A-2292856	gcagaaagaatatgca[A/G]atggaggctgcaaggg	A	G	79595 // Homo sapiens mSin3A-associated protein 130 (SAP130), mRNA. /// NM_020120 // upstream // 7915 //	SAP130	SAP130, Homo sapiens mSin3A-associated protein 130 (SAP130), q14.3
SNP_A-2280888	gaggttcattaactgc[A/G]gatggctttgaagaag	A	G	Homo sapiens junction-mediating and regulatory protein (JMY), mRNA. /// ENST00000282259 // intron // 0 // --- // --- //	JMY	JMY, Homo sapiens junction-mediating and regulatory protein (JMY), q14.1
SNP_A-2286102	gatgattttccatacg[A/G]acccaatgacctcagt	A	G	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2275888	gagactcgggagaaca[C/T]atctcgaagttgtcct	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2269213	gaatttaaagtagtga[C/T]agtcaactctggagaa	C	T	Homo sapiens mitochondrial ribosomal protein L3 (MRPL3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000264995 // intron // 0 // --- // --- // --- // ---	MRPL3	MRPL3, Homo sapiens mitochondrial ribosomal protein L3 (MRPL3), nuclear gene encoding mitochondrial protein, q21.3
SNP_A-2234644	ctccagagtatattag[A/G]agtagttagagtggaa	A	G	79596 // Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA. /// NM_022118 // downstream // 23021 //	C13orf7	C13orf7, Homo sapiens chromosome 13 open reading frame 7 (C13orf7), q31.1
SNP_A-2245578	ctgggcaaggggtcta[C/G]acttcacctttagaga	C	G	11262 // Homo sapiens SP140 nuclear body protein (SP140), transcript variant 1, mRNA. /// NM_001005176 // downstream	SP140	SP140, Homo sapiens SP140 nuclear body protein (SP140), transcript variant 1, q37.1
SNP_A-2255855	ctttaaaacatatcca[C/T]aatgtgactgctttca	C	T	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000360355 // intron // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-2249185	ctgttttcccatgtga[C/T]aaagcgtcaagtcttc	C	T	ENST00000281516 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-2248333	ctgtgtctagagctag[A/G]acaagacaccagcaac	A	G	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 760991 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2230680	ctatcttttctttcaa[G/T]cttttaacttctcatt	G	T	92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 264808	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2260718	gaaaccttaaacacaa[C/T]gtgaatacaaataaag	C	T	SLC17A6 // 57084 // Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), mRNA. /// NM_022725 // downstream	SLC17A6	SLC17A6, Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), p14.3
SNP_A-2257168	ctttctgacctcatca[C/T]agtttttaaatccaaa	C	T	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000265154 // intron // 0 // --- // --- // --- // ---	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24
SNP_A-2263453	gaaccaaataacccaa[C/G]tgggccatcatttccc	C	G	Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // intron // 0 // Hs.523329 // EPHB2 // 2048 //	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-2314661	ggagtataacatttac[C/T]ggatactctggaagat	C	T	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2091346	acttttgcataagata[C/G]gtaaatttcacttagg	C	G	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 247203	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2054081	aagttcaaacgttgac[A/G]cttcagcttaatccag	A	G	Homo sapiens syntaxin 8 (STX8), mRNA. /// ENST00000306357 // intron // 0 // --- // --- // --- // ---	STX8	STX8, Homo sapiens syntaxin 8 (STX8), p13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2047794	aagatttaagatcaga[A/G]tattgtggcttgagtt	A	G	GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 506686 // --- // --- // --- // ---	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-2004805	agcattttatggatac[A/C]aggccctggaaagata	A	C	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2009229	acaagtttattaatca[C/T]atgggaactctcctag	C	T	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2040990	aacccttcacatagta[A/G]aaaacattttctggtt	A	G	// 10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 532827 // --- // --- // --- // ---	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3
SNP_A-2034844	aaatgagaaatgattc[A/G]aaaatcgacatttgca	A	G	HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 102262 // --- // --- // ---	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2155070	attcacttgagagaga[C/G]caaattaggctctgaa	C	G	sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, mRNA. /// NM_004516 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin	ILF3	ILF3, Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, p13.2
SNP_A-2164852	caaaccctcctttacc[C/G]agtgaaatgcaaccag	C	G	sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- // --- /// ENST00000357947 // intron //	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2142783	gctttttccctcac[A/G]aagtccacacatccat	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2111365	aggagctttctgaaat[C/G]aagtatctcccttgcc	C	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- // --- // --- ///	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2116220	aggtacacattgaaac[A/G]atctaaaattacctac	A	G	Homo sapiens zinc finger protein 415 (ZNF415), mRNA. /// ENST00000243643 // intron // 0 // --- // --- // --- // ---	ZNF415	ZNF415, Homo sapiens zinc finger protein 415 (ZNF415), q13.42
SNP_A-2133971	atatcttaccaacagc[A/G]aagtttatcccaggct	A	G	338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 310652 // Hs.193268 // MTAP //	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2135149	atattgagtaagtaaa[A/C]catgttgtaaacaaat	A	C	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000317394 // downstream //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-1789930	gggcttctctgacacc[G/T]gagtcacgcggcactg	G	T	Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000287878 // intron // 0 // --- // --- // --- // ---	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-1792957	ggtacacttaaaaaaa[A/T]cttcatgcttcaactc	A	T	/// ENST00000359064 // upstream // 30692 // --- // --- // --- // --- /// ENST00000332041 // downstream // 480882 // --- // --- // ---	-	q22.1
SNP_A-1810562	gtgcaaagacactagg[A/T]agaaggctgtgtgatg	A	T	// 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 244165 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1811136	gtgcccctgttcaact[C/G]aagtccgggagctatc	C	G	ENST00000298635 // intron // 0 // --- // --- // --- // ---	-	p11.23
SNP_A-1800336	gtactaataaataata[A/T]gatgtcgtactaaaca	A	T	Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000294697 // intron // 0 // --- // --- // --- // ---	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1806348	gtccttgacgcatggc[C/T]agactcaacaatgggc	C	T	152006 // Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, mRNA. /// NM_194328 // downstream //	RNF38	RNF38, Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, p13.2
SNP_A-1688828	aagcaaagtaggattaatattctca[C/T]acagaggtggatggttgtctctact	C	T	NM_174941 // intron // 0 // Hs.49636 // M160 // 283316 // scavenger receptor cysteine-rich type 1 protein M160	M160	M160 , rs4075106, scavenger receptor cysteine-rich type 1 protein M160,p13.31
SNP_A-1825090	taaagggatcagctac[G/T]agaatgtttcaaacag	G	T	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 381872 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1839747	tagatgtcatatccca[A/G]tctggcctgtttggga	A	G	ENST00000359407 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-1866509	tccccagttcctgcaa[C/T]aaaatacagagcaaaa	C	T	2822 // Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, mRNA. /// NM_177483 // upstream // 4080 // Hs.512001 // GPLD1 // 2822 // Homo sapiens glycosy	GPLD1	GPLD1, Homo sapiens glycosylphosphatidylinositol specific phospholipase D1 (GPLD1), transcript variant 1, p22.2
SNP_A-1957234	ttttactgtcttctaa[A/G]gtcattaatggcaga	A	G	6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // upstream // 13424 // Hs.271771 //	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-1947676	tttactaattaaggtc[A/C]caatcaggaaatagtt	A	C	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1980296	tcacacagtgctccta[A/C]ctgacagggttgttct	A	C	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12B (PPP1R12B), transcript variant 2, mRNA. /// NM_002481 // intron // 0 // Hs.444403 // PPP1R12B // 4660 //	PPP1R12B	PPP1R12B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12B (PPP1R12B), transcript variant 2, q32.1
SNP_A-1977538	aacaatcagaaaatta[C/T]gttgagagaaactatt	C	T	// Homo sapiens deoxycytidine kinase (DCK), mRNA. /// NM_003759 // upstream // 256513 // Hs.5462 // SLC4A4 //	DCK	DCK, Homo sapiens deoxycytidine kinase (DCK), q13.3
SNP_A-1973488	ataaagttatggcca[C/T]atctcacaaagtaaa	C	T	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1965654	gggacaattaagtaga[C/T]gtcgaaatcaatccta	C	T	Homo sapiens fidgetin (FIGN), mRNA. /// ENST00000333129 // intron // 0 // --- // --- // ---	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1922759	ttagagggttctcta[C/T]ggttcactctctacat	C	T	1240 // Homo sapiens chemokine-like receptor 1 (CMKLR1), mRNA. /// ENST00000312143 // upstream // 39810 // --- // ---	CMKLR1	CMKLR1, Homo sapiens chemokine-like receptor 1 (CMKLR1), q23.3
SNP_A-1906272	tggtgagtctttgatc[C/T]agtctgtgagaaagct	C	T	6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA. /// NM_145248 // upstream // 189865 //	SOX1	SOX1, Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), q34
SNP_A-1899124	tggaaagagtaaagaa[C/T]ggcccccatctgaaacc	C	T	-- /// ENST00000304488 // downstream // 8103 // --- // --- // ---	-	q24.1
SNP_A-1882038	tctttggatacagagg[G/T]aacttctgaacagtg	G	T	/// ENST00000328558 // upstream // 199331 // --- // --- // ---	-	q22.3
SNP_A-1879672	tcttcaggaaaacagcc[C/G]gatttgcgagctactg	C	G	Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000327152 // intron // 0 // --- // --- // --- ///	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1969468	aagctgtggttccagat[A/G]tatgatcaaataattg	A	G	C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.2
SNP_A-1971822	gaacaagcaccataac[A/C]aacaacattgaactca	A	C	sapiens xeroderma pigmentosum, complementation group C (XPC), mRNA. /// ENST00000285021 // intron // 0 // --- // --- //	XPC	XPC, Homo sapiens xeroderma pigmentosum, complementation group C (XPC), p25.1
SNP_A-1941089	ttgctctctttgatcc[C/T]gaagacatcaaggagg	C	T	Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 //	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1955182	tttggccaaggaaacca[A/G]gatgtgtaaaggcatc	A	G	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 547178 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1959076	ttttgaaatgggaaga[C/T]taaaatttgaaaatc	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 993598 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1953647	ttgaccagcacacca[C/T]gatgcgacgtacatc	C	T	Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, mRNA. /// ENST00000305299 // intron // 0 // --- // --- // --- // ---	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, p12.3
SNP_A-1848471	tatgaataatctgca[A/G]tgaatgcaggtgtaca	A	G	Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA. /// ENST00000317931 // intron // 0 // --- // --- // --- ///	L3MBTL4	L3MBTL4, Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), p11.31
SNP_A-1855702	tcaatatggctatcag[C/T]aaattcataagcagaa	C	T	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1837672	tacttcagtgtaccc[A/C]aacggattctaatata	A	C	Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), mRNA. /// ENST00000243218 // intron // 0 // --- // --- // --- /// ENST00000229595 // intron // 0 // ---	ASF1A	ASF1A, Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), q22.31
SNP_A-1662208	atgccactcatgctttttggttaca[C/T]tgcattcttgctgctaatttttgcaa	C	T	83416 // immunoglobulin superfamily receptor translocation associated 2 /// NM_031282 // downstream // 9533 // Hs.120260 // IRTA1 // 83417 // immunoglobulin superfamily	IRTA2	IRTA2, rs10489670, immunoglobulin superfamily receptor translocation associated 2, q23.1
SNP_A-2142138	atcttttcttagagta[C/G]cattcagccctttgat	C	G	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // --- // --- // --- // ---	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2153595	attagcttgggcaaca[A/G]tggagtagactgaggg	A	G	366 // Homo sapiens aquaporin 9 (AQP9), mRNA. /// NM_000236 // upstream // 22410 // Hs.188630 // LIPC // 3990	AQP9	AQP9, Homo sapiens aquaporin 9 (AQP9), q21.3
SNP_A-2159124	atttaaaaaaaaaatc[A/G]gacagcagctaaag	A	G	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 650609 // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2218072	cctgccccttcccagc[C/T]agtgaggaccatgacg	C	T	ENST00000355609 // intron // 0 // --- // --- // ---	-	p36.13
SNP_A-2043589	aactgtgtgaatacag[C/G]cacctaggatctccc	C	G	-- /// ENST00000278194 // downstream // 233218 // --- // --- //	-	p14.3
SNP_A-2027493	aaaccaacctgaggaa[A/G]ctcaacagaggaaaac	A	G	- /// ENST00000354800 // downstream // 467559 // --- // --- //	-	q14.1
SNP_A-2086595	actgaacccagacttc[A/G]caaatgataacttact	A	G	PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 12851 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-2082361	acgcaacacataaaaa[C/G]aatcaagcataccac	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1100876 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2078691	accattcccaagacac[A/G]cagtcatcaggttctc	A	G	Homo sapiens sialic acid binding Ig-like lectin 6 (SIGLEC6), transcript variant 1, mRNA. /// NM_198846 // intron // 0 // Hs.397255 // SIGLEC6 // 946 // Homo sapiens sialic acid	SIGLEC6	SIGLEC6, Homo sapiens sialic acid binding Ig-like lectin 6 (SIGLEC6), transcript variant 1, q13.41

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098451	agagcaagtaatcagal[G/T]agttagaacttgaac	G	T	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 210633 // Hs.463978 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2104036	agcagaaagaaaactcal[A/G]agaggcagcagatgga	A	G		KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-2299214	gccctataatccaaac[A/C]gcaatacttgtagtg	A	C	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 389964 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2296402	gcatttcaaatatgag[C/T]aaggtttaagcaagag	C	T	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000268845 // intron // 0 // --- // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-2232946	ctcagacgtagatgggl[A/G]acgcagatgtgagtac	A	G	Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, mRNA. /// NM_002149 // intron // 0 // Hs.467696 //	HPCAL1	HPCAL1, Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, p25.1
SNP_A-2250252	cttagaaagaaccaac[A/G]cttaagaatgaactgg	A	G	Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), mRNA. /// ENST00000310546 // intron // 0 // -	SSB4	SSB4, Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), q23
SNP_A-2246802	ctgtagcaagcagaac[C/T]ctaacgccttctagga	C	T	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2243199	ctgcctctataaaac[A/T]aaagcaagtatatgaa	A	T	6234 // Homo sapiens ribosomal protein S28 (RPS28). mRNA. /// ENST00000355278 // downstream // 975020 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2235249	ctcccggtaccagcat[C/T]atcaagatcacctggg	C	T	4990 // Homo sapiens sine oculis homeobox homolog 6 (Drosophila) (SIX6), mRNA. /// NM_005982 // downstream //	SIX6	SIX6, Homo sapiens sine oculis homeobox homolog 6 (Drosophila) (SIX6), q23.1
SNP_A-2261601	gaaaggtattgttgtga[C/G]agtagcctacaacttt	C	G	sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // intron // 0 // --- // --- // --- ///	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2259293	gaaaaagagatgagta[C/T]ggaagctcttcactgt	C	T	Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), transcript variant 1, mRNA. /// NM_152942 // intron // 0 // Hs.1314 // TNFRSF8 // 943 //	TNFRSF8	TNFRSF8, Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), transcript variant 1, p36.22
SNP_A-2287499	gatgttgtgatgctca[C/T]aggactccctctctctt	C	T	Homo sapiens phospholipase C, epsilon 1 (PLCE1), mRNA. /// ENST00000347778 // intron // 0 // --- // --- // --- ///	PLCE1	PLCE1, Homo sapiens phospholipase C, epsilon 1 (PLCE1), q23.33
SNP_A-2297232	gccaccagcactataa[A/C]cagtttgcgtgggtt	A	C	Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // 3UTR // 0 // --- // --- // --- ///	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2104596	agcaggtggtcaataa[A/C]tgtttatgtattcaga	A	C	Homo sapiens similar to Protein MGC35450/QtsA-16602 (MGC78665), mRNA. /// ENST00000358241 // intron // 0 // ---	RTP2	RTP2, Homo sapiens similar to Protein MGC35450,q27.3
SNP_A-2106774	agcctggatgaagca[A/G]agtagctagtcagag	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2097810	agagactagaagtagal[A/G]catattatgtgattgg	A	G	// 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// NM_006982 // upstream //	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-2096433	agccacgacatagaca[C/T]ggctatatttgctgg	C	T	// 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2090916	acttttccttggtgtc[A/G]ctgaggagcacatgaa	A	G	9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 395425 // Hs.269059 // JARID2 //	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2050481	aaggatccctgaaaga[A/G]cccaaccatttctgtg	A	G	FLJ30046 // 122060 // Homo sapiens hypothetical protein FLJ30046 (FLJ30046), mRNA. /// NM_000115 // downstream	FLJ30046	FLJ30046, Homo sapiens hypothetical protein FLJ30046 (FLJ30046), q22.3
SNP_A-2070034	acacatataaagataaca[A/T]ggagaactgttgccag	A	T	59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 337219 // Hs.32966 // GUCA2B // 2981 // Homo	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-2021165	aaaaaaacgaatagccd[A/G]aaacaatactgagtaa	A	G	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 45342 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2035086	aaatgcagtcatgggg[C/T]agacacgggtgtttct	C	T	sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // --- // ---	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2016312	ctaacaactggaggca[C/T]ctgctcaaaaaaccag	C	T	// 4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000338221 // upstream //	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2018512	ggcaggctgtttctca[A/G]tctggctttggggaca	A	G	Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2005181	gggatggagccttgtc[C/T]ctcactatgacacact	C	T	10241 // Homo sapiens nuclear domain 10 protein (NDP52), mRNA. /// NM_001002027 // upstream // 22713 // Hs.80986 //	NDP52	NDP52, Homo sapiens nuclear domain 10 protein (NDP52), q21.32
SNP_A-2226328	ctaagaactgaagtaa[C/T]ggtcatgcttgttata	C	T	83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2208283	cccacactttatctaa[C/T]ccctttccaaactagag	C	T	392636 // Homo sapiens FLJ16237 protein (FLJ16237), mRNA. /// ENST00000342526 // intron // 0 // --- // --- // --- // ---	FLJ16237	FLJ16237, Homo sapiens FLJ16237 protein (FLJ16237), p21.1
SNP_A-2175495	cacatctatgcacagc[C/G]aggattcagaagccct	C	G	// Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// ENST00000274458 // intron // 0 // --- // --- // --- // ---	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-2192884	catcctgggggcctta[C/T]gattacgggctcatct	C	T	7434 // Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), mRNA. /// ENST00000262178 // upstream //	VIPR2	VIPR2, Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), q36.3
SNP_A-2195748	catgtacaacactcca[A/G]ggactgagcagagggc	A	G	ENST00000338994 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2185237	caggaagagaaggaga[C/G]aatttctagaggcatg	C	G	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 619231 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2190537	catacccatcacttcc[A/G]agagtttcctgctact	A	G	Homo sapiens replication protein A3, 14kDa (RPA3), mRNA. /// ENST00000223129 // intron // 0 // --- // --- // --- // ---	RPA3	RPA3, Homo sapiens replication protein A3, 14kDa (RPA3), p21.3
SNP_A-2139952	atctaccatagcccta[A/G]gctttcatctcaggcc	A	G	84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// NM_032226 // upstream // 65524 //	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-1658350	tttctgtttcttaaggtgaaagtta[A/G]ataattgaattaagatctttcttct	A	G	// 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 344263 // Hs.339831 // PENK // 5179 //	FLJ20421	FLJ20421 , rs353738, hypothetical protein FLJ20421 ,q12.1
SNP_A-1781255	ggatggttgtctgcaa[C/G]tcaggaaaagaggcct	C	G	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1727196	tcctaatatatcagcaggggaaca[A/G]tatggtaaccatagatcacagatta	A	G	NM_004986 // intron // 0 // - // - // - // -	-	- , rs1951887, -,q22.3
SNP_A-1806256	gtcctgtgcgtcggct[C/T]aacagcgggaaggcag	C	T	Homo sapiens serine/threonine kinase with Dbl- and pleckstrin homology domains (TRAD), mRNA. ///	TRAD	TRAD, Homo sapiens serine q21.2
SNP_A-1822925	taaaaataaaaacata[C/T]cttctggcctggtgag	C	T	126069 // Homo sapiens zinc finger protein 491 (ZNF491), mRNA. /// NM_152357 // upstream // 13346 // Hs.418192 //	ZNF491	ZNF491, Homo sapiens zinc finger protein 491 (ZNF491), p13.2
SNP_A-1816381	gttagataaacaattc[C/T]aggttgaaaatcaatt	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1863520	tccaaagactgggtcc[A/G]aaatcaaggcaatcac	A	G	// 9045 // Homo sapiens ribosomal protein L14 (RPL14), mRNA. /// NM_000706 // downstream // 11507 // Hs.2131 //	RPL14	RPL14, Homo sapiens ribosomal protein L14 (RPL14), q14.2
SNP_A-1935767	ttctgtgtagccagtg[C/T]aactctaaaaacaacc	C	T	ENST00000329238 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1964873	gctagcaggattatag[C/T]agtcctaacttagttc	C	T	/// ENST00000334612 // upstream // 19421 // --- // --- // --- // ---	-	q21.2
SNP_A-1916607	tgtttatacacaaaga[A/T]gttaatcacagtaatt	A	T	144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 459529 // Hs.306322 //	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-1914747	tgttacatttcatgag[A/G]aaaaaaaacaattcag	A	G	Homo sapiens vacuolar protein sorting 39 (yeast) (VPS39), mRNA. /// AB018313 // intron // 0 // Hs.88025 // VPS39 //	VPS39	VPS39, Homo sapiens vacuolar protein sorting 39 (yeast) (VPS39), q15.1
SNP_A-1926548	ttattctcaaggctca[A/G]tatttaatgttgctta	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1283553 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1922734	ttagagctttaagagc[A/G]acactaatctctgcca	A	G	// 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 298912 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1979286	cagtaggaagacatgt[A/G]aacagttttgtactta	A	G	Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), mRNA. /// ENST00000309439 // intron // 0 // ---	ANAPC10	ANAPC10, Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), q31.21
SNP_A-1985675	ttgtgaaaatttgagc[A/C]ctttttctagtagaac	A	C	Homo sapiens chromosome 6 open reading frame 107 (C6orf107), mRNA. /// ENST00000266004 // intron // 0 // --- //	C6orf107	C6orf107, Homo sapiens chromosome 6 open reading frame 107 (C6orf107), p21.31
SNP_A-1985021	gtttgatattcttcac[A/T]ctttttagttggctaa	A	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1379654	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1983687	ttagccaggaaggctg[A/G]atggaaatcaggaaag	A	G	3313 // Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA. /// NM_001903 // upstream // 33342 // Hs.445981 //	HSPA9B	HSPA9B, Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, q31.2
SNP_A-1982905	cagtgggctctaagga[C/T]gagtggaggtaaaaac	C	T	Homo sapiens thymic stromal lymphopoietin (TSLP), transcript variant 2, mRNA. /// NM_033035 // 3UTR // 0 //	TSLP	TSLP, Homo sapiens thymic stromal lymphopoietin (TSLP), transcript variant 2, q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936377	ttcttctccatattcc[C/T]gagattgttttacata	C	T	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-1939109	ttgataatcagcatag[C/T]atggttccttgattta	C	T	Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1862321	tcatgtaactaaccac[A/C]gaaagattaggggtag	A	C	23036 // Homo sapiens mRNA for KIAA0530 protein, partial cds. /// NM_198568 // downstream // 1590 // Hs.146727 //	ZNF292	ZNF292, Homo sapiens for KIAA0530 protein, partial cds. q15
SNP_A-1869103	tcctgccttagccaaa[C/G]cctgagtgctatagag	C	G	35 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain (ACADS), nuclear gene encoding mitochondrial protein, mRNA. /// NM_139015 // downstream // 14487 // Hs.507087 // SPPL3 // 121	ACADS	ACADS, Homo sapiens acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain (ACADS), nuclear gene encoding mitochondrial protein, q24.31
SNP_A-1803603	gtcaaaaggatattga[G/T]atacctgtccaatcag	G	T	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-1789727	gggctccatgcttcaa[A/G]aaagaaaggtaagatg	A	G	54704 // Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein /// AF155661 // downstream // 176642 // Hs.22265 // PPM2C /	PPM2C	PPM2C, Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein q22.1
SNP_A-1719519	cttgtgaagaatacacattaaaatc[A/C]cttcattgtgtttagcagtctaaaa	A	C	gamma-heregulin mRNA, complete cds. /// NM_175885 // downstream // 2426738 // Hs.448218 // MGC33846 // 220382	-	- , rs7481346, Homo sapiens gamma-heregulin mRNA, complete cds. ,q14.1
SNP_A-2161417	atttgccaaataaaat[G/T]aaagcatatagctgga	G	T	23426 // Homo sapiens mRNA for GRIP1 protein. /// NM_018448 // upstream // 421878 // Hs.546407 // TIP120A //	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. ,q14.3
SNP_A-2136008	atcaagcaataattta[G/T]gacaaagccttatctt	G	T	/// ENST00000310012 // upstream // 250364 // --- // --- // --- // -	-	q12
SNP_A-2113288	aggcctagtcaggaag[A/G]aagtttgatagagcct	A	G	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-2209091	cccaggataggctatg[C/T]atttcctcaacttata	C	T	Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), mRNA. /// ENST00000242850 // intron // 0 // ---	GUCY1B2	GUCY1B2, Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), q14.3
SNP_A-2225878	ctaaatcgtgcccca[C/G]tgcttaaaactacaaa	C	G	Homo sapiens hypothetical protein HSPC117 (HSPC117), mRNA. /// ENST00000216038 // intron // 0 // --- // --- // --- // ---	HSPC117	HSPC117, Homo sapiens hypothetical protein HSPC117 (HSPC117), q12.3
SNP_A-2011792	atattatgtatgctat[A/T]aagtacaaaaaatatt	A	T	ENST00000274901 // intron // 0 // --- // --- // --- // ---	-	p12.1
SNP_A-2036777	aaatttatcttctcac[C/T]gatgaattttaaatgc	C	T	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 701793 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2029465	aaagacatctggtaaa[C/G]agcatttacagaaagt	C	G	ENST00000262227 // intron // 0 // --- // --- // --- // ---	-	p11.31
SNP_A-2031362	aaaggggacagtcaca[C/T]gaggaagtgaagactt	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2074365	acatacattcaggtgc[C/T]atacaaggtcattcta	C	T	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-2059535	aatctcagggaggata[C/T]tactccattaggtaca	C	T	55907 // Homo sapiens cytidine monophosphate N-acetylneuraminic acid synthetase (CMAS), mRNA. /// NM_003034 // downstream // 114876 // Hs.408614 //	CMAS	CMAS, Homo sapiens cytidine monophosphate N-acetylneuraminic acid synthetase (CMAS), p12.1
SNP_A-2088558	gagtggccagggttga[A/G]actattgcattaagag	A	G	59277 // Homo sapiens netrin 4 (NTN4), mRNA. /// NM_003095 // upstream // 37260 // Hs.105465 // SNRPF //	NTN4	NTN4, Homo sapiens netrin 4 (NTN4), q23.1
SNP_A-2096460	agaccggcattttaga[C/T]agaggaaataacaagc	C	T	sapiens internexin neuronal intermediate filament protein, alpha (INA), mRNA. /// ENST00000278020 // intron // 0 // --- // --- // --- // ---	INA	INA, Homo sapiens internexin neuronal intermediate filament protein, alpha (INA), q24.33
SNP_A-2230153	ctatacctagcgtaaa[G/T]gtgagttactcagccc	G	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1588714 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2244175	ctgcttttccagatat[G/T]aagtctaacaggaaca	G	T	Homo sapiens chromosome 18 open reading frame 17 (C18orf17), mRNA. /// ENST00000304621 // intron // 0 // --- // -	C18orf17	C18orf17, Homo sapiens chromosome 18 open reading frame 17 (C18orf17), q11.2
SNP_A-2247989	ctgtgcgctctgagac[A/G]gcgactgcaggcgaac	A	G	Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-2249589	cttaagagtagtttca[A/G]acatgttaacatcagt	A	G	Homo sapiens chromosome 10 open reading frame 47 (C10orf47), mRNA. /// ENST00000277570 // intron // 0 // --- //	C10orf47	C10orf47, Homo sapiens chromosome 10 open reading frame 47 (C10orf47), p14
SNP_A-2252756	cttctaaatgctttta[A/G]gtgtcattaccctcaa	A	G	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 78760 //	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2279708	gaggcataagcacaga[A/G]tataggatacttgtgt	A	G	ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 85048 // --- // --- //	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2267639	gaatcaatgtattcca[A/G]ctcaaactttcagaat	A	G	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 391179 // --- // --- // --- //	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2311415	ggaatcagttatcata[C/T]agtcaattattactga	C	T	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2100000	agagtctgacatgtag[A/G]aggtacttaggttata	A	G	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-2085223	actcagtatcttagct[C/T]aagacgacatatccac	C	T	3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 11719 // Hs.36975 // FSHB // 2488	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-2067283	acaaagtaagtgctca[A/G]taaggatttctcctcc	A	G	58515 // Homo sapiens selenoprotein K (SELK), mRNA. /// NM_018398 // upstream // 120088 // Hs.369421 //	SELK	SELK, Homo sapiens selenoprotein K (SELK), p21.1
SNP_A-2028981	aaagaaaagcaaacta[C/T]acaactcagagttata	C	T	Homo sapiens TATA box binding protein like 2 (TBPL2), mRNA. /// ENST00000247219 // intron // 0 // --- // --- // --- // ---	TBPL2	TBPL2, Homo sapiens TATA box binding protein like 2 (TBPL2), q22.3
SNP_A-2021635	aaaaaattgaaaatcc[C/G]caagcttcagaagaca	C	G	Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-1990781	caaatctccatctgaa[C/G]gtctgtaaggaacatg	C	G	// 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// NM_018682 // upstream // 50029 //	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.3
SNP_A-2210166	ccccagtacctcagaa[C/T]gtttattgcatttgga	C	T	// Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// NM_002865 // upstream // 105467 // Hs.369017 // RAB2 //	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2121741	agtgacctgagaaaga[C/T]gagtaaaaggataaga	C	T	// 1278 // Homo sapiens collagen, type I, alpha 2 (COL1A2), mRNA. /// NM_022900 // upstream // 2782 // Hs.260041 //	COL1A2	COL1A2, Homo sapiens collagen, type I, alpha 2 (COL1A2), q21.3
SNP_A-2133258	atatatacgtgagtag[C/T]actgtccagaatgaac	C	T	ENST00000338458 // intron // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-2132511	atagtggaatggcaga[G/T]atcaatgaaggacaga	G	T	ENST00000330778 // CDS // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2132497	atagtgcatttgttga[A/C]aacattaaatgatggt	A	C	/// ENST00000330649 // upstream // 810227 // --- // --- // --- // ---	-	q11.2
SNP_A-1752711	atccgattcttaggtcaaatatgta[C/T]gataattatccttgatagagtctgt	C	T	// follicle stimulating hormone, beta polypeptide /// NM_002233 // upstream // 202544 // Hs.458267 // KCNA4 //	FSHB	FSHB , rs590833, follicle stimulating hormone, beta polypeptide ,p14.1
SNP_A-1806938	gtctcaccataaaaca[C/G]cttgatagatactttt	C	G	157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA. /// ENST00000262109 // intron // 0 // ---	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3
SNP_A-1808872	gtgaatagcgtggtaa[C/T]gaacatatgagtgcgt	C	T	sapiens tachykinin receptor 3 (TACR3), mRNA. /// ENST00000304883 // intron // 0 // --- // --- // --- // ---	TACR3	TACR3, Homo sapiens tachykinin receptor 3 (TACR3), q24
SNP_A-1863734	tccaagaggatgaaac[C/T]gaggtgaaaggcaagt	C	T	9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 105922 //	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-1840670	tagccttctctagggc[A/G]ccttccttgactctcc	A	G	9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 15875 // Hs.335079 // MAP1B // 4131 // Homo sapiens	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-1831569	taattaattgccctca[A/G]acattcattgagcact	A	G	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-1956295	tttgtgttcatgaaaa[A/G]tatatgagaagttctg	A	G	/// ENST00000332119 // downstream // 155463 // --- // --- // ---	-	q11.2
SNP_A-1971726	acatagtatactctca[A/T]ctaagtaaaggaaaat	A	T	Homo sapiens hypothetical protein FLJ22405 (FLJ22405), mRNA. /// ENST00000296003 // intron // 0 // --- // --- // --- // ---	FLJ22405	FLJ22405, Homo sapiens hypothetical protein FLJ22405 (FLJ22405), p25.3
SNP_A-1929655	ttcatatattctgatc[C/T]caagaaatttctttca	C	T	Homo sapiens hypothetical protein FLJ21062 (FLJ21062), mRNA. /// ENST00000333944 // intron // 0 // --- // --- // --- // ---	FLJ21062	FLJ21062, Homo sapiens hypothetical protein FLJ21062 (FLJ21062), q21.13
SNP_A-1913021	tgtggagatgcaggaa[C/T]actgggtcccaggaac	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1905442	tggtaatgttccattc[A/G]aagaagatagtgggga	A	G	ENST00000338458 // intron // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-1910567	tgtcctattcagtttc[A/G]atcactctatctcggg	A	G	6421 // Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ),	SFPQ	SFPQ, Homo sapiens splicing factor proline,p34.3
SNP_A-1910415	tgtcccaaagtagata[C/T]cctataagctctcaga	C	T	55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 68701	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-1906882	tggttcattccacccc[A/G]caatggccaccagaaa	A	G	Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// ENST00000325064 // intron // 0 // --- // --- // --- // --- ///	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1916145	tgttggagctaaataa[C/T]ccacagataaaaccca	C	T	ENST00000341548 // CDS // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-1930235	ttcattcttggccaca[A/T]ccctggtactgacaaa	A	T	Homo sapiens IQ motif containing with AAA domain (IQCA), mRNA. /// ENST00000254653 // intron // 0 // --- // --- // --- // ---	IQCA	IQCA, Homo sapiens IQ motif containing with AAA domain (IQCA), q37.3
SNP_A-1881955	tcttttcggcccagga[A/G]cttctgttcatctgtc	A	G	Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, mRNA. /// NM_153050 // intron // 0 //	MTMR3	MTMR3, Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, q12.2
SNP_A-1888215	tgagcgtaggaggaga[C/T]gaaagacaaactcttg	C	T	ST6GALNAC2 // 10610 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// NM_006456 // upstream // 14473 // Hs.288215 // ST6GA	ST6GALNAC2	ST6GALNAC2, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,q25.1
SNP_A-1975688	gagaattttgctctta[A/C]ctaatgatgcattcca	A	C	Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // --- // --- // --- // ---	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-1961807	gtttggggaaagatga[A/G]ggtcctatttgagttt	A	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-1950432	tttcagtcctgtgtta[G/T]caaagtttacaagcag	G	T	/// ENST00000354860 // upstream // 1064131 // --- // --- // --- //	-	q32.3
SNP_A-1948433	tttagtatatccttgc[C/T]gaaaaaagaagacatg	C	T	25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // --- // --- // --- // --- ///	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-1937712	ttgaaggaggttttca[C/T]attaacatagtcataa	C	T	Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), mRNA. /// ENST00000310546 // intron // 0 // --	SSB4	SSB4, Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), q23
SNP_A-1829151	taaggtggaattctaa[A/T]gctgagagacaagtta	A	T	374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 268962 // Hs.34198 // FLJ44796 // 401209 //	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-1850615	tattaatgtacctaaa[C/T]ttgaccaatagcatta	C	T	// 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 2587 // --- // --- // --- // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1803371	gtatttatgatcaaca[A/G]tgggagcagagatcac	A	G	// Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA. /// NM_015946 // upstream // 395725	ISL1	ISL1, Homo sapiens ISL1 transcription factor, LIM q11.2
SNP_A-1786860	ggctttgggtgactta[A/G]aactgagtctgaatcc	A	G	Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // --- // --- // --- // ---	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2215176	cctatttttgctggtc[A/C]agttttgtcactggaa	A	C	Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000335298 // intron // 0 // --- // --- // --- // --- ///	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2189795	cataaaatgtacaaaa[C/T]gtgttagtttactaac	C	T	Homo sapiens interleukin 8 (IL8), mRNA. /// NM_002993 // upstream // 56697 // Hs.164021 // CXCL6 // 6372 // Homo	IL8	IL8, Homo sapiens interleukin 8 (IL8), q13.3
SNP_A-2190072	cataagagactgaaga[A/G]gttttttacatcacat	A	G	ENST00000322285 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2010891	gagaggagacaggcta[G/T]aattgtagctgggaac	G	T	112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-2034031	aaatcagataaaccaa[G/T]tactctccaaagattt	G	T	Homo sapiens chromosome 8 open reading frame 1 (C8orf1), mRNA. /// ENST00000297438 // intron // 0 // --- // ---	C8orf1	C8orf1, Homo sapiens chromosome 8 open reading frame 1 (C8orf1), q21.3
SNP_A-2067022	acaaacctataaccac[A/G]aggacaagacataata	A	G	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 962499 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2073929	acagtgttgtgactta[C/T]ctgatgttacaatatc	C	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, mRNA. /// NM_080422 // intron // 0 // Hs.123352 // PTPN2 // 5771 // Homo sapiens	PTPN2	PTPN2, Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, p11.21
SNP_A-2059082	aatccctggccttcaa[C/T]gtttcagctctctcat	C	T	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2087564	actgctaaaatcatga[A/G]gaaatgcaacctatag	A	G	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 842739 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2299222	gccctatcttctagtc[A/G]gaacaagtctccagct	A	G	22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// NM_014965 // downstream // 33676 // Hs.535711 //	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. ,p22.1
SNP_A-2289959	gcaaagcgaggttccc[A/G]aaggagaaataatata	A	G	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2276443	gagaggagaccaggaa[A/G]gatcaggaaatagggg	A	G	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), mRNA. /// ENST00000359321 // intron // 0 // --- // --- // --- // ---	XRCC2	XRCC2, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), q36.1
SNP_A-2287281	gatgtgatttgggaaa[C/G]tgctaatactagggac	C	G	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1658624 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2274953	gagaacattctgaccc[A/G]cactttctggcttcta	A	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2272941	gactactgagccccac[A/G]ccagagtctctgagca	A	G	Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// ENST00000284538 // intron // 0 // --- // --- // --- // ---	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1
SNP_A-2243151	ctgcctagccaccttc[A/G]ccacctatttctctca	A	G	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1877102 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2230628	ctatctgctttgattc[A/G]agttagacgaagggga	A	G	Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000331366 // intron // 0 // --- // --- // --- // --- ///	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2231060	gacaagggagagagac[A/G]aaaaccattaggagca	A	G	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2290664	gcaagactggatgcca[C/T]gccaagctctcccagg	C	T	CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 410066 // Hs.437444 // CACNA1E // 777 //	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2301097	gccttcatagctggga[C/T]gagctcttaaaaaata	C	T	2615 // Homo sapiens glycoprotein A repetitions predominant (GARP), mRNA. /// NM_015516 // upstream // 43464 //	GARP	GARP, Homo sapiens glycoprotein A repetitions predominant (GARP), q13.5
SNP_A-2310189	ggaacaggaataggga[A/G]atataatagtagacag	A	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 955479 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-2091719	agaaaagcttcagatg[A/G]aaatatcctaggaagg	A	G	// 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 80356 // Hs.156832 // NPAS2 //	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-2056550	aatagagtgaagtgct[C/T]agaaagataactgatg	C	T	Homo sapiens chromosome 10 open reading frame 32 (C10orf32), mRNA. /// NM_020682 // intron // 0 // Hs.123461	C10orf32	C10orf32, Homo sapiens chromosome 10 open reading frame 32 (C10orf32), q24.32
SNP_A-2055643	aataatgatagtaata[A/G]gttgtaactcgtggaa	A	G	// 55704 // Homo sapiens KIAA1212 (KIAA1212), mRNA. /// NM_080667 // upstream // 70587 // Hs.264208 // MGC15407	KIAA1212	KIAA1212, Homo sapiens KIAA1212 (KIAA1212), p16.1
SNP_A-2054200	aagttcttatgagaac[A/G]gaattacaaagtttcc	A	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2016863	ctaagtatcaaataac[A/C]gtagatggaatatggg	A	C	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 552519	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2189383	cagttgactctgttca[A/G]gttctccactgtaaat	A	G	79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // upstream // 3450 // Hs.468058	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-2108399	agctgcatatgctaaa[C/T]caaagcagagatttga	C	T	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2158839	attgtgcactttcaga[A/G]aactttccctgaaata	A	G	// 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-1785955	ggctgcactcttatcc[C/T]ggaaggctgtgggtca	C	T	ENST00000360575 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1789792	gggctgaggcgggaga[C/T]aaattcaggggtacct	C	T	10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // downstream // 15599 // Hs.501252 // TACC2 //	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-1797551	ggtttccagcttcata[C/G]aggtccctacaaagga	C	G	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 371891 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-1782881	ggcagaggcaggaccc[A/G]aaaccaagatgattcc	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-gamma, mRNA. /// NM_013957 // intron // 0 // Hs.453951 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-gamma, p12
SNP_A-1667758	tgcacaagcattgtctataacttca[A/T]ctgaacacttgctctaccttacaca	A	T	NM_006867 // intron // 0 // Hs.195825 // RBPMS // 11030 // RNA binding protein with multiple splicing	RBPMS	RBPMS , rs2979498, RNA binding protein with multiple splicing,p12
SNP_A-1656569	aagcaaatgatccttctaatactga[C/T]acattaaactgatacttaaaagata	C	T	// 667 // bullous pemphigoid antigen 1, 230/240kDa /// NM_015548 // downstream // 5991 // Hs.443518 // BPAG1 //	BPAG1	BPAG1 , rs10484788, bullous pemphigoid antigen 1, 230,p12.1
SNP_A-1707639	gcgtttgtggtggtcttctttttgaa[A/T]ggaacagtaatttgtgtggatattg	A	T	NM_018422 // 3UTR // 0 // - // - // - // -	-	- , rs3087875, -,p22
SNP_A-1851687	tattcttcagccttca[A/G]aactcatgctgtttta	A	G	// 346547 // Homo sapiens FLJ42291 protein (FLJ42291), mRNA. /// NM_130797 // upstream // 180776 // Hs.490684 //	FLJ42291	FLJ42291, Homo sapiens FLJ42291 protein (FLJ42291), q36.2
SNP_A-1848620	tatgagaatctgaaaa[A/G]caaggactcagtcact	A	G	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 494915 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1849239	tatgctgtagtcttta[C/T]gttcattaaaggcaga	C	T	115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// NM_002353 // downstream // 5471 //	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.1
SNP_A-1866823	tcccgggggcctcca[A/G]cactcatgatgcctag	A	G	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1819243	gttgctttggaagcta[A/G]aaatggtacctccctt	A	G	Homo sapiens inversin (INVS), transcript variant 2, mRNA. /// NM_014425 // intron // 0 // Hs.270443 // INVS // 27130 //	INVS	INVS, Homo sapiens inversin (INVS), transcript variant 2, q31.1
SNP_A-1972001	ttcatgaagcattcac[C/T]gccacaaccaaaagac	C	T	Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // intron // 0 // --- // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1968895	taaaacattgcacaaa[A/G]ttatgttacgatatgt	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 334011 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1979533	tggactttaagcaatc[A/T]caatatgaacagtgaa	A	T	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 163668 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1931101	ttccatcagtggttca[A/G]aaaaccttctcttggg	A	G	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1931264	ttccattttgctctga[C/T]gggctccaattctggc	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 109113 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1926026	ttatgtgactgtttta[C/T]gggagcatgaaaagcc	C	T	112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-1876844	tctgccaaaggtaact[A/C]aattttatccagaact	A	C	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 990390 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1899197	taacatccatgaaaaa[C/T]gtacatggctgcttat	C	T	Homo sapiens zinc finger protein 396 (ZNF396), mRNA. /// ENST00000306346 // intron // 0 // --- // --- // --- // ---	ZNF396	ZNF396, Homo sapiens zinc finger protein 396 (ZNF396), q12.2
SNP_A-1893672	tgcagtatatttggta[C/T]ggctaacaatcctata	C	T	80036 // Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // upstream // 684997 // Hs.47288 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.13
SNP_A-1942131	ttggattgggcaatga[A/G]gaggttggggttgaac	A	G	78986 // Homo sapiens hypothetical protein MGC1136 (MGC1136), mRNA. /// ENST00000256261 // upstream //	MGC1136	MGC1136, Homo sapiens hypothetical protein MGC1136 (MGC1136), p12
SNP_A-1950207	tttcacttgtctatca[A/G]agtttttcctctttg	A	G	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B,	ABCC9	ABCC9, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p12.1
SNP_A-1860476	tcagttaaggatacaa[C/T]ttcccgttttcagtta	C	T	10651 // Homo sapiens metaxin 2 (MTX2), transcript variant 1, mRNA. /// ENST00000249442 // downstream // 240917 // -	MTX2	MTX2, Homo sapiens metaxin 2 (MTX2), transcript variant 1, q31.1
SNP_A-1848101	tatcttaactgctcta[A/T]ggaattcagtctcttg	A	T	57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 196831 //	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1668694	agaccccatttctataaacataagt[A/G]aagttaagctaaaaaatgcctggca	A	G	694 // B-cell translocation gene 1, anti-proliferative /// NM_001920 // upstream // 918922 // Hs.156316 // DCN //	BTG1	BTG1 , rs10507011, B-cell translocation gene 1, anti-proliferative ,q21.33
SNP_A-1745021	ttcccatttgcttttgggcacaaat[A/C]ccacatattacacttcttttctcaa	A	C	// 7957 // epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) /// NM_007124 // downstream // 383132 // Hs.250607 // UTRN // 7402 // utrophin (homologous to	EPM2A	EPM2A , rs492947, epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) ,q24.3
SNP_A-1732632	ctgctcacatctgcattaacttttc[C/T]ctatagacaatggggcagggacaga	C	T	NM_014178 // intron // 0 // Hs.99291 // STXBP6 // 29091 // syntaxin binding protein 6 (amisyn)	STXBP6	STXBP6 , rs1241598, syntaxin binding protein 6 (amisyn),q12
SNP_A-1786313	ggctgtgggacagtta[C/T]gagttttgggggatgt	C	T	Homo sapiens chromosome 9 open reading frame 20 (C9orf20), mRNA. /// ENST00000321582 // intron // 0 // --- // -	C9orf20	C9orf20, Homo sapiens chromosome 9 open reading frame 20 (C9orf20), q33.2
SNP_A-1812130	gtggagagggagaatc[C/T]attaaaggtattatgc	C	T	// 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream //	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-2162371	attttattgaggaagc[C/T]gaagttgagagagggg	C	T	773 // Homo sapiens calcium channel, voltage-dependent, P/Q type, alpha 1A subunit (CACNA1A), transcript variant 2,	CACNA1A	CACNA1A, Homo sapiens calcium channel, voltage dependent, P,p13.13
SNP_A-2108008	agctctacggtaaggg[C/G]aatagcaagggaggtc	C	G	81788 // Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK), mRNA. /// NM_018203 //	SNARK	SNARK, Homo sapiens likely ortholog of rat SNF1,q32.1
SNP_A-2135040	atattccttaaaacta[A/G]aatgtggcatggctta	A	G	1462 // Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA. /// NM_001884 // downstream //	CSPG2	CSPG2, Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), q14.3
SNP_A-2178437	cactccatgtctggct[C/T]acttgtggtgggcatg	C	T	// Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 //	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15
SNP_A-2171429	caatcacagaaagtag[A/G]acatcactgtgaaggc	A	G	// 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 234768 //	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2224528	cgtatgtgagtgtgaa[C/T]gtaagtaccaagcagg	C	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 691470 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2226891	ctaatcaatgtgtgaa[A/T]aatgggtaatgctcac	A	T	Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // --- // ---	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-2208010	cccaactgcctgcaga[A/G]agattaaggtcaaatt	A	G	/// ENST00000321014 // upstream // 477570 // --- // --- // --- // -	-	p12.3
SNP_A-2037869	aacaatccttcagaga[C/T]gacagttgccggaatc	C	T	/// ENST00000309493 // downstream // 5679 // --- // --- // --- //	-	q22.33
SNP_A-2023517	aaaactagttctgata[C/T]ggaaacaatctcaact	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2059113	aatcctaacagttacc[C/T]cttccctcatatgaga	C	T	Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // intron // 0 //	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-2060482	aatgacatcaacaccc[C/T]acttataaatgttgca	C	T	1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 84403 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste ,p15.1
SNP_A-2070971	acactctccctgaatg[A/C]aaacgtgtgccacttc	A	C	ENST00000321736 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-2098982	agagctttgacaccaa[C/T]gataagagtaaaagaa	C	T	7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 23948 //	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-2272832	gactaagcctcatgca[A/G]agactcagggttcatg	A	G	Homo sapiens BCL2-like 14 (apoptosis facilitator) (BCL2L14), transcript variant 1, mRNA. /// NM_138723 // intron // 0 // Hs.504794 // BCL2L14 // 79370 // Homo sapiens BCL2-like	BCL2L14	BCL2L14, Homo sapiens BCL2-like 14 (apoptosis facilitator) (BCL2L14), transcript variant 1, p13.2
SNP_A-2279360	gaggaggcttaatgga[A/C]gtgtgtctggcgggca	A	C	7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream //	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-2300756	gcctggcagctttatg[C/T]aacccttcagctgagg	C	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 45271 // Hs.335933 // MGC33530	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-2295289	gcatcactaagcctta[A/T]gaaatgagggctagag	A	T	/// ENST00000236495 // upstream // 14659 // --- // --- // --- // ---	-	p33
SNP_A-2088992	acttaaaggcgactga[A/G]gcctctcaaaatcctt	A	G	/// ENST00000329376 // downstream // 1737 // --- // --- // --- //	-	p11.12
SNP_A-2078770	accatttcttcttaca[C/G]ctgaccccaaatttta	C	G	LOC131368 // 131368 // Homo sapiens hypothetical protein LOC131368 (LOC131368), mRNA. /// ENST00000306176 //	LOC131368	LOC131368, Homo sapiens hypothetical protein LOC131368 (LOC131368), q12.3
SNP_A-2067575	acaaattctaatgtaa[C/T]gctctcttgtaaacag	C	T	Homo sapiens centrosome protein cep290 (Cep290), mRNA. /// ENST00000309041 // intron // 0 // --- // --- // --- // ---	Cep290	Cep290, Homo sapiens centrosome protein cep290 (Cep290), q21.32
SNP_A-2049096	aagcggctgcccacca[C/G]agcttactttctagca	C	G	ENST00000355038 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-2007612	accaaaaaaaaggtca[A/G]ctcaatcagctattta	A	G	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2226648	ctaagtatgtctatac[A/C]aattatgcattctggc	A	C	8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// NM_014167 // downstream // 588527 // Hs.90527 // HSPC128	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-2213482	ccggtatcagtccaca[C/T]atgaaatattagagaa	C	T	55075 // Homo sapiens uveal autoantigen with coiled-coil domains and ankyrin repeats (UACA), mRNA. /// ENST00000322954 // upstream // 19960 // --- // --- // --- // ---	UACA	UACA, Homo sapiens uveal autoantigen with coiled-coil domains and ankyrin repeats (UACA), q23
SNP_A-2219663	ccttaaatataagttc[G/T]aatttcagatcacctc	G	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1898270 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2176899	caccgtctgcctacta[C/T]gtaacaaaattccaga	C	T	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // --- // --- // --- // ---	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2194589	catgcagattttcctc[C/T]gacatgcccattactc	C	T	Homo sapiens zinc finger protein 415 (ZNF415), mRNA. /// ENST00000243643 // intron // 0 // --- // --- // --- // ---	ZNF415	ZNF415, Homo sapiens zinc finger protein 415 (ZNF415), q13.42
SNP_A-2108959	agcttatgagaaataa[A/G]gtgaggttaaggcaca	A	G	// 283160 // Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), mRNA. ///	OR8D2	OR8D2, Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), q24.1
SNP_A-2114142	agggaaagcaatctac[A/T]cttcagactgctgcaa	A	T	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // intron // 0 // --- // -	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2163355	atttttttccactaagc[G/T]ctacgttcttaacatt	G	T	Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), mRNA. /// ENST00000273179 // intron // 0 // --- // -	CTDSPL	CTDSPL, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), p22.3
SNP_A-2163759	caaaaattgagtcaca[C/T]ggaagaatctgaataa	C	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 195628 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2165544	caaagctatcatcttc[C/T]cctcaaactaaatcta	C	T	170825 // Homo sapiens homeobox protein GSH-2 (GSH-2), mRNA. /// NM_006206 // upstream // 38558 // Hs.74615 //	GSH-2	GSH-2, Homo sapiens homeobox protein GSH-2 (GSH-2), q12
SNP_A-1804072	gtcacacctctcctaa[A/T]tggtggaaccaggctt	A	T	// Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 79616 // Hs.100057 // STK35 //	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13
SNP_A-1745634	cagtactctgaaactcagtggagca[A/G]atgataaatctgtcacaattttcca	A	G	// 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 508821 // Hs.450919 // GPC5 //	SLITRK5	SLITRK5 , rs10507987, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1654193	aagatagatttggatgaaaacatta[C/G]actctatggatgagggcagaggcag	C	G	// 55816 // docking protein 5 /// NM_080617 // downstream // 42121 // Hs.126141 // CBLNL1 // 140689 // cerebellin	DOK5	DOK5 , rs10485801, docking protein 5 ,q13.31
SNP_A-1854259	tcaaaggagaatgtta[C/T]agtcaagggtacattt	C	T	checkpoint suppressor 1 mRNA, complete cds. /// NM_005197 // intron // 0 // Hs.434286 // CHES1 // 1112 //	CHES1	CHES1, Human checkpoint suppressor 1 complete cds. ,q32.11
SNP_A-1859809	tcaggggaaagccgag[C/T]agaaaagaatggatgc	C	T	283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-1818197	gttctgaagaatcaaa[C/G]aggaggagcaatccca	C	G	Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // --- // --- // --- // ---	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-1827925	taagaaattaagacaa[A/C]attcagcaaatgtcac	A	C	Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-1832451	tacaaaccttggaaaa[C/T]cacctaattgattgcc	C	T	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 319405 // --- // --- // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-1935941	ttcttaatcacaaaag[C/G]cagaaatctggaagtc	C	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1643589 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1983052	gggagaagcacaagaa[A/G]aagcaccaaatgtttt	A	G	56929 // Homo sapiens fem-1 homolog c (C.elegans) (FEM1C), mRNA. /// ENST00000317782 // upstream //	FEM1C	FEM1C, Homo sapiens fem-1 homolog c (C.elegans) (FEM1C), q22.3
SNP_A-1983812	aaactaattggaagaa[C/T]ggtaaagacgctataa	C	T	57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 172512 //	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1984440	cctttcttagcctgaa[A/T]gtcatgtgaaacaaac	A	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2567902 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1963214	agtagaataatcacaa[A/G]tatatcaacagggaat	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2676901 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1897774	tgctggacaggtatcc[A/G]catcataagaaaccac	A	G	// 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 280493 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1900579	tggaggaagctgtcca[C/G]ggcagaatgaggaagg	C	G	2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 99387	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-1886947	tgacttcatgactaat[C/G]ataaagggaaaagact	C	G	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000247655 // downstream // 21506 // --- // -	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1909254	tgtatgcttattctaa[C/T]gtttgtgttacctgtg	C	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// ENST00000360955 // upstream // 35025 // --- // --- // --- // ---	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1908014	tgtaatttgggattga[C/T]gggaactgactcacat	C	T	// 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 150219 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1901150	tggatctttgatatta[G/T]aaactggatgtcataa	G	T	25936 // Homo sapiens DKFZP566O1646 protein (DC8), mRNA. /// ENST00000261462 // upstream // 4872 // --- // --- //	C1orf48	C1orf48, Homo sapiens DKFZP566O1646 protein (DC8), q32.3
SNP_A-1900383	tggagagtgggaggtc[C/T]aagatcatggttccag	C	T	// Homo sapiens ADAMTS-like 3 (ADAMTSL3), mRNA. /// ENST00000286744 // intron // 0 // --- // --- // --- // ---	ADAMTSL3	ADAMTSL3, Homo sapiens ADAMTS-like 3 (ADAMTSL3), q25.2
SNP_A-1891557	tgattcttaatatagc[C/T]cacccatcgctaagtc	C	T	8444 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 (DYRK3), transcript variant 1, mRNA. /// NM_001004023 // downstream // 5626 //	DYRK3	DYRK3, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 (DYRK3), transcript variant 1, q32.1
SNP_A-1890168	tgatcaaaaaatgaac[A/G]ggcataccaagacaaa	A	G	Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, mRNA. /// NM_032379 // intron // 0 // Hs.369520 //	SYTL2	SYTL2, Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, q14.1
SNP_A-1967126	cgtcaaccagggctgc[G/T]ctaattagattgcttc	G	T	ENST00000338720 // intron // 0 // --- // --- // --- // ---	-	q36.2
SNP_A-1977796	gaaatctaaactctgc[A/G]gaatcaggattaaaga	A	G	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 174054	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1940152	ttgcataccaaagaca[A/G]agtataagcaccccgg	A	G	Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// ENST00000237161 // intron // 0 // --- // ---	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1951059	tttccataacatggaa[C/T]gtgggtaaggttccta	C	T	// 54805 // Homo sapiens cyclin M2 (CNNM2), transcript variant 3, mRNA. /// NM_199076 // downstream // 7940 //	CNNM2	CNNM2, Homo sapiens cyclin M2 (CNNM2), transcript variant 3, q24.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1955353	tttggggattgaagaa[C/T]tgatgtatttaaagag	C	T	1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // upstream // 1173903 // --- // --- // --- //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1834906	taccattgatcaaacc[A/G]atgaatgtgatcacag	A	G	ENST00000263936 // intron // 0 // --- // --- // --- // ---	-	p36.22
SNP_A-1864068	tccacagccctggaac[A/T]gtggagaaggaggcaa	A	T	Homo sapiens hypothetical protein FLJ12448 (FLJ12448), mRNA. /// ENST00000288757 // CDS // 0 // --- // --- // --- // ---	FLJ12448	FLJ12448, Homo sapiens hypothetical protein FLJ12448 (FLJ12448), q24.31
SNP_A-1867487	tccgagcaggaggcgc[A/G]agggagtccatctctg	A	G	8788 // Homo sapiens delta-like 1 homolog (Drosophila) (DLK1), mRNA. /// ENST00000360899 // downstream // 1596	DLK1	DLK1, Homo sapiens delta-like 1 homolog (Drosophila) (DLK1), q32.2
SNP_A-1857806	tcactgtcacacattc[A/G]aaccacacagaagtat	A	G	ENST00000338458 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-1849696	tatggttcagaagact[C/T]agacatataaataaag	C	T	Homo sapiens 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1), mRNA. /// ENST00000354807 // intron // 0 // --- // ---	BPNT1	BPNT1, Homo sapiens 3'(2'), 5'-bisphosphate nucleotidase 1 (BPNT1), q41
SNP_A-1707451	tcctggcttaattcacttaacataa[C/T]gtgctccaattctatccgcattact	C	T	LOC286016 // 286016 // hypothetical protein LOC286016 /// NM_178562 // upstream // 25639 // Hs.27267 // MGC50844 //	LOC286016	LOC286016 , rs1594423, hypothetical protein LOC286016 ,q32.1
SNP_A-1727729	ttccttctgtctgagtaagaggtca[A/G]tcatgtaccccattctctgaaaatc	A	G	AK091196 // intron // 0 // Hs.442801 // ARHGAP24 // 83478 // Rho GTPase activating protein 24	ARHGAP24	ARHGAP24 , rs10516757, Rho GTPase activating protein 24,q21.23
SNP_A-1785476	ggctcacagtgtcaca[A/G]attccaaaaacaacaa	A	G	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000308488 // intron // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-2164954	caaactaggttgctgg[G/T]aacagtgaagttgtat	G	T	53343 // Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), transcript variant 1, mRNA. /// NM_198039 // downstream // 13260 // Hs.149500 //	NUDT9	NUDT9, Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), transcript variant 1, q22.1
SNP_A-2153878	attataaggtatcatc[A/C]atttggtagccttctg	A	C	ENST00000332853 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2140555	atctcctgggtcccca[A/G]ataactcaccactggt	A	G	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2145093	atgcaaatgactacca[A/G]aagtatgcaggagtag	A	G	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 158416	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2213499	ccggtggctcctgcta[C/T]agctgacttttcacta	C	T	1106 // Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2), mRNA. /// ENST00000330136 //	CHD2	CHD2, Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2), q26.1
SNP_A-2215937	cctccacgtgaggaca[C/T]ggcatttactccctct	C	T	6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 416387 //	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-2223994	cggggaagaaaagccc[A/G]ccatacctgaaatgat	A	G	4255 // Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), mRNA. /// ENST00000248179 //	MGMT	MGMT, Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), q26.3
SNP_A-1996204	gggaaattcctctgaa[A/G]tgtgtgcattatgtct	A	G	338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 282714 // Hs.193268 // MTAP //	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1997058	tcctccgaagacatga[C/T]ccaacctacacattac	C	T	Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// ENST00000356204 // intron // 0 // --- // --- // --- // ---	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2001271	gcttctggggataccg[A/T]cagtattttatttttt	A	T	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 //	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2025243	aaaatataggcaaaaa[C/T]ttaagacaactagtga	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 372454 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2033012	caaggagcccgcttca[C/T]cagtcttaaggagtgc	C	T	Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), mRNA. /// ENST00000266427 // intron // 0 // --- // --- // --- // ---	ETV6	ETV6, Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), p13.2
SNP_A-2061841	aatggatcttgggaaa[G/T]actatgtaacagttgc	G	T	Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_001843 // intron // 0 // Hs.143434 // CNTN1 //	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2075875	acattaaaatctgtga[C/T]cagttatttgtgggaa	C	T	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-2099730	agaggttgctgtctac[C/T]ctctctccatatattt	C	T	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-2294849	gcagtttttaaaaagc[C/T]gattatatctcaataa	C	T	ENST00000329227 // downstream // 18037 // --- // --- // --- // ---	-	p12.1
SNP_A-2274745	gagaaagccaatgttg[G/T]atccacccctgcctga	G	T	56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 96010 // Hs.517155 // TMEPAI //	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2241621	ctgatactgcccacaa[C/G]gataccagtactgagt	C	G	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// ENST00000321536 // downstream	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253864	cttgaatatgagcaga[A/G]gatctacaagaatgct	A	G	Homo sapiens KIAA1754 (KIAA1754), mRNA. /// ENST00000337478 // 3UTR // 0 // --- // --- // --- // --- ///	KIAA1754	KIAA1754, Homo sapiens KIAA1754 (KIAA1754), q25.1
SNP_A-2234510	ctccaccccagttata[C/T]aaatgtgcaagtatca	C	T	// Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2235293	ctccctcacttacaag[C/T]atcgtggtgattaatt	C	T	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q11.23
SNP_A-2298240	ccttggacattaagtc[A/G]cccttccaccaatgag	A	G	Homo sapiens testis development protein NYD-SP29 (NYD-SP29), mRNA. /// ENST00000355948 // CDS // 0 // --- // --- // -	NYD-SP29	NYD-SP29, Homo sapiens testis development protein NYD-SP29 (NYD-SP29), p22.3
SNP_A-2289022	gatttcagttcaggaa[A/G]cgactttctattggcc	A	G	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 573363 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2069458	acacaagtaggaaaga[A/C]aagtggtatcatcccc	A	C	Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // --- // --- // --- // --- /// ENST00000287878 // intron //	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-2035921	aaatgttttctgctga[A/G]tatccatgcttggctc	A	G	153241 // Homo sapiens hypothetical protein FLJ36090 (FLJ36090), mRNA. /// ENST00000306481 // upstream //	FLJ36090	FLJ36090, Homo sapiens hypothetical protein FLJ36090 (FLJ36090), q23.2
SNP_A-1993117	tgttcaatgtcccaga[C/T]acagcaaggactcact	C	T	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // --- // --- // --- // ---	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-2008246	agaatcaaggtgtgag[C/T]agcgccatgctccctc	C	T	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 199402 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2016714	taacatagtcacttaa[C/T]aattgtcttcatattc	C	T	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 689248 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2182172	cagaggtaacatttac[A/G]ctcaaacttggagaga	A	G	ENST00000172853 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2108876	agcttaagataaccca[A/G]aattgtaagaacaaaa	A	G	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1287235 // Hs.27214 // KCNC2	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2134046	atatgaaagttacaaa[A/G]gtagtgcagatgttat	A	G	81696 // Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), mRNA. /// ENST00000230221 //	OR5V1	OR5V1, Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), p22.1
SNP_A-2129199	ataatttcctcatttg[A/T]aaattgaaagtatcct	A	T	21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 326276 // Hs.475902	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1752371	tcacagacaggtgtgttcaactttg[A/G]caaaataaactttctggattaactg	A	G	FLJ32790 fis, clone TESTI2002361 /// NM_018340 // downstream // 48256 // Hs.200481 // FLJ11151 // 55313 //	-	- , rs2115105, CDNA FLJ32790 fis, clone TESTI2002361 ,p13.12
SNP_A-1679024	cgctgggtgggagcagtttgatcac[A/G]gaggaaggcgaatagttaatccttc	A	G	NM_007118 // intron // 0 // Hs.367689 // TRIO // 7204 // triple functional domain (PTPRF interacting)	TRIO	TRIO , rs773702, triple functional domain (PTPRF interacting),p15.2
SNP_A-1651160	gctcccaagcaatgttatccaagta[G/T]gtatgcctgatgatgtggcttgatc	G	T	5308 // paired-like homeodomain transcription factor 2 /// NM_152400 // upstream // 213561 // Hs.23439 // FLJ39370 //	PITX2	PITX2 , rs2057818, paired-like homeodomain transcription factor 2 ,q25
SNP_A-1848957	tatgcaccacttcaaa[A/C]tcctctgtcctcacct	A	C	SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1872557	tctaggattaactaat[A/G]aaaccatcaacccatt	A	G	// 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // downstream // 282948 //	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-1865403	tccatctaggttagta[C/T]atttgtctctagaaaa	C	T	-- /// ENST00000308105 // upstream // 34943 // --- // --- // --- //	-	q44
SNP_A-1833661	tacaggcatatgtcca[A/G]gatattttgggttcgg	A	G	81930 // Homo sapiens kinesin family member 18A (KIF18A), mRNA. /// ENST00000314102 // upstream // 105235 // --- // ---	KIF18A	KIF18A, Homo sapiens kinesin family member 18A (KIF18A), p14.1
SNP_A-1842601	taggttgttagacata[C/T]ggtccagtccttttct	C	T	/// ENST00000355063 // upstream // 707998 // --- // --- // --- // -	-	q22.1
SNP_A-1815274	gtgttgtcaggtgtaa[C/T]ggggacagaggagaag	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1952331	tttctctctgcaggaa[A/C]gtgcctcttcagatct	A	C	Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA. /// ENST00000330610 // intron // 0 // --- // --- // --- // ---	KIRREL	KIRREL, Homo sapiens kin of IRRE like (Drosophila) (KIRREL), q23.1
SNP_A-1946476	tttaaagcctcactga[A/G]aatccacaggattatc	A	G	1834 // Homo sapiens dentin sialophosphoprotein (DSPP), mRNA. /// NM_004407 // upstream // 30784 // Hs.128556 //	DSPP	DSPP, Homo sapiens dentin sialophosphoprotein (DSPP), q22.1
SNP_A-1981000	tagcccttatgtcatc[A/G]cttttgtgttaaagac	A	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1930366 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1981829	tgttactcgtcagtca[C/T]tcatttttgctaaatt	C	T	57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 46518 // --- // FLJ37543 //	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. ,q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1892796	tgcacagtgggttttg[A/G]aaacaccatcaaagtt	A	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1001231 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1894461	tgccaactaaatgcca[C/T]cagaggtcttgttcag	C	T	// 90627 // Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, mRNA. /// NM_178007 // upstream // 408238 // Hs.507704 // STARD13	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.2
SNP_A-1895401	tgccgatgttgagaag[A/G]aacttcatatgcaacc	A	G	sapiens KiSS-1 metastasis-suppressor (KISS1), mRNA. /// ENST00000306118 // intron // 0 // --- // --- // --- // ---	KISS1	KISS1, Homo sapiens KiSS-1 metastasis-suppressor (KISS1), q32.1
SNP_A-1902776	tggctcaaatccttga[C/T]gtcaacattgccttct	C	T	/// ENST00000259567 // downstream // 227529 // --- // --- // --- // --- /// ENST00000360460 // downstream // 229371 // --- // ---	-	p24.1
SNP_A-1874915	catgccttgccgtgaa[C/G]gtgacagggtaatcaa	C	G	Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1) (PSCD1), transcript variant 1, mRNA. /// NM_017456 // intron // 0 // Hs.191215 // PSCD1 // 9267 //	PSCD1	PSCD1, Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1) (PSCD1), transcript variant 1, q25.3
SNP_A-1920323	ttaatgggccttagta[C/T]gtaagacaagaataag	C	T	Homo sapiens mRNA for KIAA0530 protein, partial cds. /// ENST00000339907 // intron // 0 // --- // --- // --- // ---	ZNF292	ZNF292, Homo sapiens for KIAA0530 protein, partial cds. q15
SNP_A-1927091	ttattttacaaaatga[A/G]agaaattggagcttag	A	G	10855 // Homo sapiens heparanase (HPSE), mRNA. /// NM_133636 // downstream // 39890 // Hs.480101 // HEL308	HPSE	HPSE, Homo sapiens heparanase (HPSE), q21.23
SNP_A-1910698	tgtccttccaaaatca[A/T]cttcttttatgtcagt	A	T	// 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// NM_006507 // downstream // 45691 // Hs.4158 // REG1B //	REG3G	REG3G, Homo sapiens LPPM429 (REG-III), p12
SNP_A-1891143	tgatgtctggattcaa[C/T]tcagcttagaagagaa	C	T	51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 55341 //	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1863801	tccaaggtttagcgtg[A/G]caaagcctatcagaaa	A	G	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 738850 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-1861475	tcatccaacagagggg[A/C]atttatagagtgtcta	A	C	4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 197436 // Hs.232819 // PCDH15 // 65217 //	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1872697	tctagtgttggaacaa[A/G]ttgcagtttctccatc	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 3 (DNAH3), mRNA. /// ENST00000261383 // intron // 0 // --- // ---	DNAH3	DNAH3, Homo sapiens dynein, axonemal, heavy polypeptide 3 (DNAH3), p12.3
SNP_A-1847997	tatctggacagcaccc[C/T]atgcaccccatggctt	C	T	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1856519	tcacagcagtcccttа[C/T]gatttctgaccaaaca	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1853076	tatttgctgataaaga[A/G]gagattaccttatgtt	A	G	10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // upstream // 426184 // --- // --- // --- // --- //	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-1642077	caccttttcccatggtatatattta[A/G]gagcagaaaaatatctgtgaaattt	A	G	AB051490 // intron // 0 // Hs.465430 // ZNF407 // 55628 // zinc finger protein 407	ZNF407	ZNF407 , rs10514150, zinc finger protein 407,q22.3
SNP_A-1689428	ttcttcatatgtctaatttaacaac[A/C]agtagacaaggcatggtcctaattt	A	C	401099 // LOC401099 (LOC401099), mRNA /// NM_145035 // upstream // 1150915 // Hs.369104 // ADMP // 165679 //	-	- , rs10513584, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-1728345	ccagtctaattccattgcagttccc[C/T]gtaaatagggtgactgtatgtccta	C	T	MAP2K6 // 5608 // mitogen-activated protein kinase kinase 6 /// NM_018658 // upstream // 194780 // Hs.414021 // KCNJ16	MAP2K6	MAP2K6 , rs1858964, mitogen-activated protein kinase kinase 6 ,q24.3
SNP_A-1743625	gtgtcgactcactattgattcctga[C/T]gcaatgagtcccctagctctctcct	C	T	5125 // proprotein convertase subtilisin/kexin type 5 /// NM_012383 // downstream // 303445 // Hs.47011 // OSTF1 //	PCSK5	PCSK5 , rs10512041, proprotein convertase subtilisin,q21.13
SNP_A-1741129	agatcaggtccatgaggagtaaaga[C/T]attatacaaaacaatgttgagtggt	C	T	NM_024740 // CDS // 0 // Hs.120824 // DIBD1 // 79796 // disrupted in bipolar affective disorder 1	DIBD1	DIBD1 , rs10502151, disrupted in bipolar affective disorder 1,q23.1
SNP_A-1794277	ggtcatttttgttga[A/G]ccacagaactgggaaa	A	G	// 84541 // Homo sapiens T-cell activation kelch repeat protein (TA-KRP), mRNA. /// NM_003848 // downstream //	TA-KRP	TA-KRP, Homo sapiens T-cell activation kelch repeat protein (TA-KRP), p14.1
SNP_A-2117310	aggtggcaggcagatt[A/G]aaagcattttatttat	A	G	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 565323	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2145904	atgcccatcaatgatc[A/G]atgttagactggataa	A	G	5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 121730 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2150896	atgtggctgcagtctc[C/G]accaatggcgctctct	C	G	ENST00000267116 // 5UTR // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2164417	caaaatgctagaagta[C/T]aaacactattatttgc	C	T	// 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 1581 // --- // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169837	caaggatgtggtacaa[C/T]gggccttgcaataaat	C	T	// Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), mRNA. /// ENST00000244563 //	OR2W1	OR2W1, Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), p22.1
SNP_A-2192677	catcccaatgatgaga[C/T]ggaagactggagaagc	C	T	// 29121 // Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, mRNA. /// NM_001004420 // downstream	CLEC2D	CLEC2D, Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, p13.31
SNP_A-2196843	cattagaagtaaccaa[C/T]gaacataattatatta	C	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2223269	cgcgcctggctgataa[C/T]ggacactctgtagcag	C	T	79705 // Homo sapiens leucine-rich repeat kinase 1 (LRRK1), mRNA. /// NM_014918 // downstream // 89801 // Hs.110488	LRRK1	LRRK1, Homo sapiens leucine-rich repeat kinase 1 (LRRK1), q26.3
SNP_A-2223345	cgctcattaattctga[A/T]atgtcacaaacagaag	A	T	// 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2036702	aaattgtgtgcagaaa[A/G]gactcaaggaaagaca	A	G	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // --- // --- // --- // --- /// ENST00000260943 // intron //	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2029102	aaagaaatccagctag[A/C]acgccgcatacaagga	A	C	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2019267	agggccataaaactga[C/T]ggtgcaagctgaaact	C	T	2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // upstream // 86312 // Hs.473819 // ERG // 2078	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-2077919	accagcacggctccag[A/G]ataacaatagtggatt	A	G	3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. /// NM_178532 // upstream //	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.3
SNP_A-2085548	actccataatatgaaa[A/G]ttgaggatatagctcc	A	G	3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 158238	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2297874	gccagtaagaggagca[C/T]tgcctatgtgaaggta	C	T	64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 493095 // Hs.546282 // RBBP8	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-2313747	ggagcaccagtctcaa[A/C]gggcttaacaatatcc	A	C	Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), mRNA. /// ENST00000244563 //	OR2W1	OR2W1, Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), p22.1
SNP_A-2304840	gctcttatcagacagt[G/T]aaagctcaacgataaa	G	T	Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5), mRNA. /// ENST00000243903 // intron // 0 // --- // ---	ACTR5	ACTR5, Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5), q11.23
SNP_A-2241276	ctgaggctcagaggtc[A/G]ccagtaaggaagtggc	A	G	sapiens TU3A protein (TU3A), mRNA. /// ENST00000360997 // intron // 0 // --- // --- // --- // ---	TU3A	TU3A, Homo sapiens TU3A protein (TU3A), p14.2
SNP_A-2230007	ctataaatacctgaca[A/G]ggacatgaaataaaaa	A	G	SLC30A10 // 55532 // Homo sapiens solute carrier family 30 (zinc transporter), member 10 (SLC30A10), transcript variant 1, mRNA. /// ENST00000359296 // upstream // 35067 // --- // -	SLC30A10	SLC30A10, Homo sapiens solute carrier family 30 (zinc transporter), member 10 (SLC30A10), transcript variant 1, q41
SNP_A-2279085	gaggaatatatgagga[A/G]agatggtagtttatgg	A	G	/// ENST00000355802 // upstream // 49408 // --- // --- // --- // --- /// ENST00000358682 // upstream // 49424 // --- // --- // --- // ---	-	q13.3
SNP_A-2279023	gaggaagagctcttca[A/G]atggtgaaagagctgt	A	G	MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream //	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-2268754	gaattaacactggaag[A/G]atataagcttggcata	A	G	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 127970 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2261714	gaaagtgacagagcaa[C/T]aacattaatgaaagcc	C	T	ENST00000355787 // intron // 0 // --- // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2267303	gaatagaacatatcag[A/T]agctacaaatattaag	A	T	83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000356343 // upstream //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-2287523	gatgtttcggaaacgc[C/T]acctagatttcacagg	C	T	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-2232105	ctcaaggaagaaataa[C/T]ggcttttgcttcctgg	C	T	// Homo sapiens interferon regulatory factor 1 (IRF1), mRNA. /// NM_000879 // downstream // 41741 // Hs.2247 // IL5 //	IRF1	IRF1, Homo sapiens interferon regulatory factor 1 (IRF1), q23.3
SNP_A-2253040	cttctctactctccca[A/G]cagcaaacctgccatc	A	G	Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 3 (CHRNA3), mRNA. /// ENST00000348639 //	CHRNA3	CHRNA3, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 3 (CHRNA3), q25.1
SNP_A-2085821	actccttcaacgccta[A/C]gatcaccagctcaggt	A	C	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000328405 // intron // 0 // --- // --- // --- // ---	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2077882	accagatagggcttca[A/G]aacaaggttcctcact	A	G	// 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 205578 // Hs.505007	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2099783	agagtaactaactgca[G/T]ggttacaaagtatgtt	G	T	Homo sapiens YME1-like 1 (S. cerevisiae) (YME1L1), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA. /// NM_139313 // intron // 0 // Hs.499145 // YME1L1 //	YME1L1	YME1L1, Homo sapiens YME1-like 1 (S. cerevisiae) (YME1L1), nuclear gene encoding mitochondrial protein, transcript variant 3, p12.1
SNP_A-2067017	acaaaccctggaataa[G/T]gccgtgaaagcaggga	G	T	83548 // Homo sapiens component of oligomeric golgi complex 3 (COG3), mRNA. /// ENST00000310862 //	COG3	COG3, Homo sapiens component of oligomeric golgi complex 3 (COG3), q14.13
SNP_A-2076576	acatttcttcaggtga[C/G]agataatttcttatac	C	G	81930 // Homo sapiens kinesin family member 18A (KIF18A), mRNA. /// ENST00000314102 // upstream // 87293 // --- // ---	KIF18A	KIF18A, Homo sapiens kinesin family member 18A (KIF18A), p14.1
SNP_A-2058811	aatcatttatgctgaa[C/T]ctgttggtggctttgt	C	T	-- /// ENST00000356117 // downstream // 586189 // --- // --- //	-	q23.31
SNP_A-2055578	aataatccacatacgc[A/C]cttagaatataataag	A	C	CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 125067 //	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2031229	aaaggctactgacata[C/T]gacaccaggatgggag	C	T	9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // downstream //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-2017611	ttggaatcacacacag[A/G]aaaggctgggtatttg	A	G	Homo sapiens chromosome 21 open reading frame 7 (C21orf7), mRNA. /// ENST00000286791 // intron // 0 // --- // --	C21orf7	C21orf7, Homo sapiens chromosome 21 open reading frame 7 (C21orf7), q21.3
SNP_A-2009309	tttgtaaaatgaatcc[C/T]caccaagaatcacttt	C	T	Homo sapiens FAD104 (FAD104), mRNA. /// ENST00000264609 // intron // 0 // --- // --- // --- // --- ///	FNDC3B	FNDC3B, Homo sapiens FAD104 (FAD104), q26.31
SNP_A-2005208	gagctattccaggggg[C/T]attcaacacagaattc	C	T	221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 // upstream // 91378 // Hs.463483 // MMD // 23531 // Homo	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-2004350	cacacccagctgtttc[C/T]acctctgcagctttag	C	T	Homo sapiens Rhesus blood group, C glycoprotein (RHCG), mRNA. /// ENST00000268122 // intron // 0 // --- // --- // --- // ---	RHCG	RHCG, Homo sapiens Rhesus blood group, C glycoprotein (RHCG), q26.1
SNP_A-2210869	ccccttctctaggacc[A/G]aggaaaactggtttaa	A	G	sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA. /// ENST00000344204 // intron // 0 // --- // --- // --- // ---	TRIO	TRIO, Homo sapiens triple functional domain (PTPRF interacting) (TRIO), p15.2
SNP_A-2162329	attttatgggccaagc[A/G]agatttttcctgaacc	A	G	ENST00000339906 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2107784	agctcaggtttagggg[G/T]acctactgcttcttgg	G	T	9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 853817 // --- // --- // ---	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds. q23
SNP_A-2129517	atacaccatgaaatat[C/T]acgtagcccctaaaaca	C	T	/// ENST00000360991 // downstream // 695897 // --- // --- // ---	-	q12.1
SNP_A-1791574	gggtcagctttcccca[C/T]atgatatgatgtcata	C	T	Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// ENST00000286355 // intron // 0 // --- // --- // --- // ---	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1806307	gtccttatcagaaggg[A/G]aaatttgcatacagag	A	G	RPS6KC1 // 26750 // Homo sapiens ribosomal protein S6 kinase, 52kDa, polypeptide 1 (RPS6KC1), mRNA. ///	RPS6KC1	RPS6KC1, Homo sapiens ribosomal protein S6 kinase, 52kDa, polypeptide 1 (RPS6KC1), q32.3
SNP_A-1812703	gtgggaaaagtgtcac[C/T]gagaactagcagctca	C	T	sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// ENST00000360890 // intron // 0 // --- // --- // --- // ---	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-1782732	ggcagaaaacaaacaa[A/G]ttctggatttaaattg	A	G	23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-1712057	aagacatagagaagttattcaaaaa[A/T]gatattacttcctatattattccat	A	T	MAP3K7 // 6885 // mitogen-activated protein kinase kinase kinase 7 /// NM_021813 // upstream // 36104 // Hs.88414 //	MAP3K7	MAP3K7 , rs6940932, mitogen-activated protein kinase kinase kinase 7 ,q15
SNP_A-1858243	tcagaagatttaaaga[A/G]aaagccagatctcatc	A	G	23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // upstream // 7760 // Hs.487648 // SNX13 //	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-1852274	tattgttaatccattg[G/T]aaaagtttattaatgc	G	T	/// ENST00000321014 // upstream // 686192 // --- // --- // --- // -	-	p12.3
SNP_A-1867042	tccctcctggtttgta[C/T]cttaaacttgcttggc	C	T	// Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// NM_002865 // upstream // 9845 // Hs.369017 // RAB2 // 5862	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1864867	tccaggcataagtgct[C/T]aaccagctgaactgat	C	T	Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_001843 // intron // 0 // Hs.143434 // CNTN1 //	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-1841541	taggagttcatcctac[A/G]gatttattcacacaca	A	G	// 1051 // Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA. /// NM_002827 // upstream //	CEBPB	CEBPB, Homo sapiens CCAAT,q13.13
SNP_A-1840462	tagccagcaggggtaa[A/T]acaggatgaagtgcaa	A	T	4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 //	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1877106	tctgctctgctatcac[C/T]atggcttgcactgtat	C	T	57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 208331 // --- // ---	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-1986104	tacaaatggcatgaaa[A/G]aaaccataaatagtat	A	G	// 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream //	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1988120	caagtggactggaaga[A/C]gaccttagtttggacc	A	C	54583 // Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// NM_005999 // upstream // 30359 //	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939628	ttgatttccttttgtg[C/T]caattcacaggggtg	C	T	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // intron // 0 // Hs.414110 // KCND3 //	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1942318	ttggccacctcccaaa[G/T]atatcattctaatgtt	G	T	138803 // Homo sapiens olfactory receptor, family 13, subfamily C, member 3 (OR13C3), mRNA. /// ENST00000277216 // upstream // 7847 // --- // --- // --- // --- ///	OR13C3	OR13C3, Homo sapiens olfactory receptor, family 13, subfamily C, member 3 (OR13C3), q31.1
SNP_A-1948915	tttatccactcactga[A/G]gttatttatccacaat	A	G	ENST00000360988 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1976799	tcagattttgaagaga[C/T]agtatttgcaccccta	C	T	-- /// ENST00000345029 // upstream // 354945 // --- // --- // ---	-	p14
SNP_A-1971127	attcaatgatacagca[A/G]ctcttgatacttgaga	A	G	Homo sapiens protein kinase C and casein kinase substrate in neurons 2 (PACSIN2), mRNA. /// ENST00000263246 // intron // 0 // --- // --- // --- // --- /// ENST00000337959 // intron //	PACSIN2	PACSIN2, Homo sapiens protein kinase C and casein kinase substrate in neurons 2 (PACSIN2), q13.2
SNP_A-1876443	tctgatactatatacc[C/T]ggagttagcatcagat	C	T	4729 // Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), mRNA. /// ENST00000333526 // downstream // 7745 // --- // --- // --- // ---	NDUFV2	NDUFV2, Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), p11.22
SNP_A-1887085	tgacttttaggggca[G/T]attatatttgaggtat	G	T	55227 // Homo sapiens leucine rich repeat containing 1 (LRRC1), mRNA. /// NM_025168 // downstream // 14044 //	LRRC1	LRRC1, Homo sapiens leucine rich repeat containing 1 (LRRC1), p12.1
SNP_A-1888951	tgaggttgaagatcag[C/G]aagttagaccaggttt	C	G	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant c, mRNA. /// NM_003644 // intron // 0 // Hs.462214 //	GAS7	GAS7, Homo sapiens growth arrest-specific 7 (GAS7), transcript variant c, p13.1
SNP_A-1896151	tgcgccaacctagtag[A/G]aactattctaagtccc	A	G	// 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1894239	tgcattatgttccact[A/G]aatgcaatctatttta	A	G	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 480955 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-1899066	gttcccacacacaatg[A/G]aagtgtcaagagcagc	A	G	Homo sapiens microtubule-associated protein, RP/EB family, member 2 (MAPRE2), mRNA. /// ENST00000300249 // 3UTR	MAPRE2	MAPRE2, Homo sapiens microtubule-associated protein, RP,q12.1
SNP_A-1907860	tgtaatactgacctca[A/T]atctaatatttatact	A	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1918291	ttaaagctcacatata[C/T]attgcagtatgccttt	C	T	Homo sapiens F-box protein 8 (FBXO8), mRNA. /// ENST00000296517 // intron // 0 // --- // --- // --- // --- ///	FBXO8	FBXO8, Homo sapiens F-box protein 8 (FBXO8), q34.1
SNP_A-1912961	tgtggaatgatgattc[A/G]agctttgattgctgat	A	G	1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // upstream //	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-1925194	ttatccaggaagaggt[A/G]aaggtagcttagacta	A	G	8491 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// NM_152390 // upstream // 138909 // Hs.40808 // MGC33926 // 130733 //	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-1837621	tactttaacagataat[A/T]aactaactccttcctt	A	T	// Homo sapiens chemokine-like factor super family 8 (CKLFSF8), mRNA. /// ENST00000307526 // intron // 0 // --- //	CKLFSF8	CKLFSF8, Homo sapiens chemokine-like factor super family 8 (CKLFSF8), p23
SNP_A-1840947	tagctgagaagtctgc[A/G]atgttataataagaaa	A	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1862135	tcatgctgaagtctta[A/G]ggtttataagcaggca	A	G	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 372898	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1868591	tcctctccagtgttct[C/T]actctggctgaagccc	C	T	ENST00000329683 // intron // 0 // --- // --- // --- // ---	-	p21.33
SNP_A-1869538	tcctgtttctgttcca[C/T]agagtagactttaact	C	T	ENST00000339727 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1694993	taaacactttagaaatgccttttac[C/T]aggaaactgaattacagcaatcaat	C	T	AB058701 // intron // 0 // Hs.103483 // L3MBTL3 // 84456 // l(3)mbt-like 3 (Drosophila)	L3MBTL3	L3MBTL3 , rs9321206, l(3)mbt-like 3 (Drosophila),q23.1
SNP_A-1652884	aaaaaaaaaaaagaaaagtcgacca[C/T]attattacttttctagtcacattttt	C	T	8440 // NCK adaptor protein 2 /// NM_032411 // upstream // 40310 // Hs.43125 // ECRG4 // 84417 // esophageal cancer	NCK2	NCK2 , rs1647686, NCK adaptor protein 2 ,q12.2
SNP_A-1727022	tttatgtcttaagaaatcatatcca[C/T]ctctgagaccatacaggtaaaaaat	C	T	TMEFF1 // 8577 // transmembrane protein with EGF-like and two follistatin-like domains 1 /// NM_017753 // upstream // 344116 // Hs.382683 // PRG-3 // 54886 // plasticity related	TMEFF1	TMEFF1 , rs10512274, transmembrane protein with EGF-like and two follistatin-like domains 1 ,q31.1
SNP_A-1810031	gtgatacaagagagaa[C/T]attttcaaagtcacag	C	T	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3	SMARCA3	SMARCA3, Homo sapiens SWI q24
SNP_A-1800892	gtagaggaaatacttg[A/C]agatgtggtaaaaagg	A	C	/// ENST00000360919 // upstream // 352937 // --- // --- // --- //	-	q13.1
SNP_A-1794384	ggtcccataccaaacg[A/T]aagtgcaaacatggcc	A	T	7328 // Homo sapiens ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) (UBE2H), transcript variant 1, mRNA. /// NM_182697 // upstream // 39292 // Hs.344165 // UBE2H //	UBE2H	UBE2H, Homo sapiens ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) (UBE2H), transcript variant 1, q32.2
SNP_A-1792620	ggtaaatcaatggaaa[C/T]ttgacaatgtgtacct	C	T	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796016	ggtggtgatgctgaaa[C/T]ggagcaggatgaggtg	C	T	Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// ENST00000337225 // intron // 0 // --- // --- // --- // ---	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2134209	atatgatccaaagaga[A/C]atggaaattacttttg	A	C	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 178100 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2114987	agggccagtgaaagag[C/G]caacaagaagcttcaa	C	G	219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 41726 // --- // --- // --- // --	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2151315	atgttagttgtgtgta[C/T]gatattgagcctagaa	C	T	PPP2R1A // 5518 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA. /// ENST00000322088 // downstream //	PPP2R1A	PPP2R1A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), q13.41
SNP_A-2142475	atgaaatggatcataa[C/G]aatagtagcaaatatt	C	G	6513 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /// ENST00000270929 // upstream // 179214 // --- // --- // --- // ---	SLC2A1	SLC2A1, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), p34.2
SNP_A-2212394	ccctgtctaaccaaac[A/C]aacccactatatttct	A	C	Homo sapiens stromal interaction molecule 1 (STIM1), mRNA. /// ENST00000300737 // intron // 0 // --- // --- // --- // ---	STIM1	STIM1, Homo sapiens stromal interaction molecule 1 (STIM1), p15.4
SNP_A-2186211	caggcctttctaggt[C/G]aaagcaggatggtttt	C	G	Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // intron // 0 // Hs.282787 // FOXP2 //	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2180273	cagaaagtaactgtaa[C/T]ggacttttggtggcc	C	T	// Homo sapiens hypothetical protein LOC221711 (LOC221711), mRNA. /// ENST00000341041 // intron // 0 // --	LOC221711	LOC221711, Homo sapiens hypothetical protein LOC221711 (LOC221711), p24.2
SNP_A-2000753	agctgagtactggtga[C/T]gttagaataaccatgt	C	T	// 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1992746	gtaagttctagtttaa[A/G]tacaaaatgcattgcc	A	G	Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// ENST00000256409 // intron // 0 // --- // --- // --- // ---	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2011658	cagaagatagaagtga[A/G]caaaactttctagctg	A	G	11119 // Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, mRNA. /// NM_194441 // downstream // 8057 // Hs.191510 // BTN3A1 // 11119 //	BTN3A1	BTN3A1, Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, p22.1
SNP_A-2016035	agtcttgagaagtcta[C/T]gcctcttataaggcaa	C	T	/// ENST00000331037 // downstream // 619410 // --- // --- // ---	-	q21.1
SNP_A-2019562	ccatcataaaacgtac[A/G]aaacagcttggaaata	A	G	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 87127	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2040947	aaccctgagtaaccag[A/G]aatagaaggatctaaa	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3228174 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2095827	agacagactgggaaag[G/T]atctgcaagtagtgta	G	T	Homo sapiens myosin ID (MYO1D), mRNA. /// ENST00000318217 // intron // 0 // --- // --- // --- // ---	MYO1D	MYO1D, Homo sapiens myosin ID (MYO1D), q11.2
SNP_A-2083508	actaagttacaggtcc[A/G]aaaatgatgatgatta	A	G	Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000304058 // intron // 0 // --- // --- // --- // ---	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2089947	gggttaggaataaata[A/G]caatgacatctctatt	A	G	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 579935 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2251979	cttccaaagacgtgaa[C/T]cgtattgcttctccca	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 29051 // --- // --- // --- // --	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2235976	ctcctggaaaattggc[A/G]agagaagaaaaacaga	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1089937 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2236600	ctctaaactattctcc[C/T]acactatttcctttag	C	T	Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // --- // --- // --- // --- ///	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3), p13.3
SNP_A-2281134	tgaacattctcgtata[C/T]gtctcctggtacatat	C	T	FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2256787	ctttccaaatcatctt[C/T]aaacctctttaaacac	C	T	// Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), mRNA. /// NM_022918 // upstream // 45046 // Hs.188591 //	FZD4	FZD4, Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), q14.2
SNP_A-2258783	cttttgtgaaagctat[A/G]aagtgagatatccatc	A	G	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2303788	gctcagggaaaagtag[C/G]aatgttgatcctgttc	C	G	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2306640	gctgtatatttttaac[A/G]gagataacactggatt	A	G	/// ENST00000305273 // downstream // 24917 // --- // --- // ---	-	q21.3
SNP_A-2290742	gcaagcaactgtaaag[G/T]cgaagagtagggaaaa	G	T	Homo sapiens mitogen-activated protein kinase kinase 5 (MAP2K5), transcript variant B, mRNA. /// NM_145161 // intron // 0 // Hs.114198 // MAP2K5 // 5607 // Homo sapiens	MAP2K5	MAP2K5, Homo sapiens mitogen-activated protein kinase kinase 5 (MAP2K5), transcript variant B, q23
SNP_A-2297366	gccactcatctcaaaa[C/G]gctatttttagaatta	C	G	-- /// ENST00000314071 // upstream // 78371 // --- // --- // --- //	-	p13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2302376	gctaaggccatcttca[C/T]gttgtgcttttatttt	C	T	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2314293	ggaggccatgaaagaa[C/T]ggggaagactggctct	C	T	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2265951	gaaggaggaggtcata[A/T]ggtggacatgaatggg	A	T	Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA. /// ENST00000249700 // intron // 0 // --- // --- // --- // ---	TMOD2	TMOD2, Homo sapiens tropomodulin 2 (neuronal) (TMOD2), q21.2
SNP_A-2269281	gaatttcgatactgaa[A/G]ggctaaatgtacactt	A	G	9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 547795 // --- // --- // ---	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds. ,q23
SNP_A-2271588	gaccaatttagaaaat[C/G]aagctaaaagaggtca	C	G	Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // intron // 0 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-2278552	gagctgaattcataag[C/T]accaaaaacagaaagg	C	T	2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream //	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1
SNP_A-2275223	gagaaggcatctcagc[G/T]ctaccacagctgaatg	G	T	// 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 7298 // Hs.523852 //	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-2232055	ctcaagagcagatcca[C/G]tctaccaagtgatgac	C	G	Homo sapiens collagen, type IX, alpha 1 (COL9A1), transcript variant 2, mRNA. /// NM_001851 // intron // 0 // Hs.149809 //	COL9A1	COL9A1, Homo sapiens collagen, type IX, alpha 1 (COL9A1), transcript variant 2, q13
SNP_A-2253278	cttctggaaaccaggc[A/G]attaggtgaaaatcga	A	G	ENST00000358295 // intron // 0 // --- // --- // --- // ---	-	q13.32
SNP_A-2246195	ctggtgactcagtcca[C/T]gcatctatcttcttaa	C	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2098108	agagagggttctgtta[C/T]aagcagccaaacggaa	C	T	Homo sapiens KIAA0998 (KIAA0998), mRNA. /// ENST00000298832 // intron // 0 // --- // --- // --- // --- ///	KIAA0998	KIAA0998, Homo sapiens KIAA0998 (KIAA0998), q24.3
SNP_A-2070228	acacattggcgtaaaa[C/T]agcacgtattgacaat	C	T	-- /// ENST00000331540 // downstream // 388756 // --- // --- //	-	p25.3
SNP_A-2066186	aatttgttttaaggta[C/T]atatcacaactctatt	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 639611 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2046392	aagagacatagtttca[C/T]tctattgcctaggcta	C	T	22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 391033 //	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2027622	aaaccagtgatttttta[A/G]cttagcaaagtgagct	A	G	27346 // Homo sapiens hypothetical protein MAC30 (MAC30), mRNA. /// NM_014573 // upstream // 15638 //	MAC30	MAC30, Homo sapiens hypothetical protein MAC30 (MAC30), q11.2
SNP_A-2173755	cacacacacatacatg[A/C]acatagaatcactact	A	C	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 645281 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2139499	atccttgggaaattct[C/G]agaaaggaagagggat	C	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-2160436	atttcattagtgatta[A/T]caaaataagaaattga	A	T	Homo sapiens RNA polymerase II associated protein 1 (RPAP1), mRNA. /// ENST00000357417 // intron // 0 // --- // ---	RPAP1	RPAP1, Homo sapiens RNA polymerase II associated protein 1 (RPAP1), q15.1
SNP_A-2114584	agggaggctttttcac[C/G]cagagcagcctttaat	C	G	Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// ENST00000229686 // intron // 0 // --- // --- // --- // ---	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-2119560	aggtgcttgctactcc[A/C]agtgaccctgagagct	A	C	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// ENST00000343323 // intron // 0 // --- // --- // --- // ---	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-2122458	agtgctaagactctga[C/T]agaaagaaaagcaaga	C	T	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-2125904	agttttaaacagctcc[A/G]cagtgttccatgtcat	A	G	ENST00000242737 // intron // 0 // --- // --- // --- // ---	-	p11.23
SNP_A-1802654	gtatgaatattgaaaa[C/T]catgagttatggaaat	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 113673 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1732530	actgtagaagtagaaagtgtgagta[C/T]aaaacaaagttcagaaagatggaag	C	T	// downstream // 62795 // Hs.367765 // GPR73 // 10887 // G protein-coupled receptor 73	-	- , rs1107629, - ,p13.3
SNP_A-1741515	aagtctgttgaaacaccaggaaata[A/G]gtaattatatataaatgtgttttaa	A	G	BC004474 // intron // 0 // Hs.370422 // VLDLR // 7436 // very low density lipoprotein receptor	VLDLR	VLDLR , rs502309, very low density lipoprotein receptor,p24.2
SNP_A-1783025	ggcagccgacggactc[A/G]gactggagcttcagca	A	G	285492 // Homo sapiens hypothetical protein FLJ35424 (FLJ35424), mRNA. /// ENST00000316915 // downstream //	FLJ35424	FLJ35424, Homo sapiens hypothetical protein FLJ35424 (FLJ35424), p16.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1655823	ctgctgtaacaaaatagcatagacc[A/G]gatagcttaaacaatacatatttgt	A	G	NM_014787 // intron // 0 // - // - // - // -	-	- , rs1886777, -,p31.2
SNP_A-1840234	tagcaggcactagaaa[G/T]tcactgttttaaaacc	G	T	sapiens glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (GNE), mRNA. ///	GNE	GNE, Homo sapiens glucosamine (UDP-N-acetyl)-2-epimerase p13.2
SNP_A-1819406	gttggcttctaatgca[A/G]caacaatttttattgt	A	G	55101 // Homo sapiens hypothetical protein FLJ10241 (FLJ10241), mRNA. /// ENST00000221943 // upstream //	FLJ10241	FLJ10241, Homo sapiens hypothetical protein FLJ10241 (FLJ10241), q13.2
SNP_A-1916655	tgtttattcttgccta[A/G]taaaaatgtatggatt	A	G	Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // --- // -	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-1890539	tgatcttcaaactcca[A/G]actccaatctccaaag	A	G	5359 // Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /// NM_032153 // downstream // 49386 // Hs.415766	PLSCR1	PLSCR1, Homo sapiens phospholipid scramblase 1 (PLSCR1), q24
SNP_A-1889249	tgagtgactggttgaa[A/T]cacaaaaccagggatc	A	T	4635 // Homo sapiens myosin, light polypeptide 4, alkali; atrial, embryonic (MYL4), transcript variant 2, mRNA. /// NM_001002841 // downstream // 1642 // Hs.463300 // MYL4	MYL4	MYL4, Homo sapiens myosin, light polypeptide 4, alkali; atrial, embryonic (MYL4), transcript variant 2, q21.32
SNP_A-1979029	aatgttgtggttttca[A/G]ataccctgctgctccc	A	G	Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_144977 // intron // 0 // Hs.497279 // FAM31B //	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-1936533	ttcttgattgtgataa[A/C]cttgacaattgtggaa	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1563446 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1933983	tccattaaatttcaga[A/G]ggtcaagccatttagt	A	G	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // ---	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1947628	tttaccttgcctaaca[C/T]ggcactggtttaaatt	C	T	Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-1889193	tgagtctgaaatgtcc[A/C]agattggttcctcaaa	A	C	6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 387815 //	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1899131	tggaaagatctggcaa[C/T]gtcaggccacctctct	C	T	Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- // --- // --- ///	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-1902103	tggcattacatcgatc[G/T]attcaaatggctcatt	G	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 973754 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1925586	ttatgaattataaaag[A/G]accagatgtcacagtt	A	G	23520 // Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), mRNA. /// ENST00000330241 // upstream // 131550 // --- // --- // --- // ---	ANP32C	ANP32C, Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), q32.3
SNP_A-1930315	ttcatttatctgaata[C/T]gtactgttactccgca	C	T	Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // --- // ---	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-1817075	gttcaaaagcagctct[A/T]acattgtttctggact	A	T	/// ENST00000334919 // upstream // 883477 // --- // --- // --- // --- /// ENST00000322194 // downstream // 885672 // --- // --- // -	-	q12.2
SNP_A-1859756	tcagggagccagcaga[C/T]gtatcaaaacaaagtc	C	T	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 972800 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1702123	gaaatgcaaaatgattagaagggtc[A/G]ataaacactttgaaaaagaacaaaa	A	G	NM_006259 // intron // 0 // Hs.41749 // PRKG2 // 5593 // protein kinase, cGMP-dependent, type II	PRKG2	PRKG2 , rs980720, protein kinase, cGMP-dependent, type II,q21.21
SNP_A-1678968	ttgaagctcttacattcaattcatt[A/T]aaaaaaaggcgtggagtgctgggtc	A	T	8886 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 /// NM_020868 // downstream // 695597 // Hs.91625 // DPP10 //	DDX18	DDX18 , rs2421608, DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 ,q14.1
SNP_A-1782336	taaaacttgaaaaaaa[A/G]gtcctcagcttattct	A	G	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1808645	gtgaacccatccagtg[A/G]caagcataaaaatgag	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1645693 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1814462	gtgtgcaaagcctcta[C/T]ggtttgtttttccta	C	T	3777 // Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), mRNA. /// NM_017877 // upstream //	KCNK3	KCNK3, Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), p23.3
SNP_A-1797401	ggtttaaaataactta[C/T]gatgaaagggtcactt	C	T	// Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// ENST00000260021 // intron // 0 // --- // --- // --- // --- ///	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1789446	gggccctgcgcctgat[A/G]agctgccatgaaagtg	A	G	Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000254508 // 3UTR // 0 // --- // --- // --- // ---	NUP210	NUP210, Homo sapiens nucleoporin 210 (NUP210), p25.2
SNP_A-2156929	attcttgccttgaaaa[A/G]tattcatgagtttaag	A	G	55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 784895 // Hs.479658 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-2174619	cacagatgtttcaaac[C/T]acttaacagataattt	C	T	10720 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), mRNA. /// NM_001074 // downstream // 135901 // Hs.10319 // UGT2B7 // 7364 //	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2186330	caggctgcagtgcata[A/G]cttactgtggcctcga	A	G	Homo sapiens copine III (CPNE3), mRNA. /// ENST00000198765 // intron // 0 // --- // --- // --- // ---	CPNE3	CPNE3, Homo sapiens copine III (CPNE3), q21.3
SNP_A-2185534	caggagaactgtgtaa[A/T]taacctgggtcgggga	A	T	UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-2189636	cagtttggtgattgtc[A/G]agaaaaagaagcattc	A	G	-- /// ENST00000355156 // upstream // 259538 // --- // --- // ---	-	q24.3
SNP_A-2190487	catacattaacctata[C/T]acatctctctcattat	C	T	388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 527434 // --- // ---	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-2197474	cattcctatggcttca[A/G]gagtctttatttcagg	A	G	Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // --- // ---	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2197998	cattgcgtcctttccc[A/G]aagagtctgttcccat	A	G	sapiens CECR2 protein (CECR2) mRNA, complete cds. /// ENST00000262608 // intron // 0 // --- // --- // --- // ---	CECR2	CECR2, Homo sapiens CECR2 protein (CECR2) complete cds. ,q11.21
SNP_A-2208178	cccaatctttccaaaa[C/T]tctcaaatctaaaaag	C	T	64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 194160 // Hs.146339 //	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2208904	cccagcacactctccc[C/G]caacattttatgattc	C	G	3308 // Homo sapiens heat shock 70kDa protein 4 (HSPA4), transcript variant 2, mRNA. /// NM_002154 // downstream //	HSPA4	HSPA4, Homo sapiens heat shock 70kDa protein 4 (HSPA4), transcript variant 2, q31.1
SNP_A-2215296	cctcaagcttttattg[C/T]atgtataacttttctt	C	T	56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 2928 // Hs.476604 // ADAMTS9 //	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-2219419	cctgtgtatttcatca[C/G]gtaagtactggagtct	C	G	HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream //	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2026923	aaacactgaaaaggca[A/T]tgatctaagtaagcac	A	T	ENST00000338956 // intron // 0 // --- // --- // --- // ---	-	p15.2
SNP_A-2029729	aaagaggaatctccaa[C/T]actgagcttccccctg	C	T	// 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1551805 // Hs.27214 // KCNC2 // 3747 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2030639	aaagctcatgctgttc[G/T]aactggaattacaatt	G	T	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2037351	aacaaatatttaccaa[A/G]tacttactttgagcaa	A	G	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA. /// ENST00000263750 // intron // 0 // --- // --- // --- // ---	GNB1	GNB1, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), p36.33
SNP_A-2011044	tggctatgatttatta[C/T]ggcaaagaatacaaaa	C	T	Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-2009285	tcatgaagctggctta[C/T]gatttagcctagctaa	C	T	Homo sapiens hypothetical protein FLJ23049 (FLJ23049), mRNA. /// ENST00000324629 // intron // 0 // --- // --- // --- // ---	FLJ23049	FLJ23049, Homo sapiens hypothetical protein FLJ23049 (FLJ23049), q26.1
SNP_A-2007783	tgcagaaaagtccacc[G/T]gctgcaatccagacaa	G	T	55031 // Homo sapiens ubiquitin specific protease 47 (USP47), mRNA. /// ENST00000250515 // upstream // 67444	USP47	USP47, Homo sapiens ubiquitin specific protease 47 (USP47), p15.3
SNP_A-2006858	tcacctgcaataaata[G/T]ccaatcatattatagc	G	T	220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. ///	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1993281	aagctcaaggcacacc[A/G]caaaattcatcagcat	A	G	// Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// NM_207413 // downstream // 122206 // Hs.527111 //	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2056984	aatagtgaagccagaa[A/T]cttagctgtgatcttc	A	T	11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 115923 // Hs.526879 // PTPRT //	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-2057930	aatattgaagttaaca[A/T]aggaagttagaaaaga	A	T	Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // intron // 0 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-2049707	aagctttcagtaacta[A/C]agttatatgccatgtg	A	C	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-2096245	agaccaatgccagcca[C/T]gttactggaagccaga	C	T	5980 // Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA. /// NM_147686 // downstream // 32546 // Hs.486228 // C6orf4 // 10758 // Homo	REV3L	REV3L, Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), q21
SNP_A-2088591	actgtcttcctgggca[A/G]atctggtgtttcctta	A	G	Homo sapiens RAB3D, member RAS oncogene family (RAB3D), mRNA. /// ENST00000222120 // intron // 0 // --- // ---	RAB3D	RAB3D, Homo sapiens RAB3D, member RAS oncogene family (RAB3D), p13.2
SNP_A-2302882	gctagcaataagaaaa[C/G]ggtcacgttccaggct	C	G	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 248067 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2244749	ctggatagggttctaa[A/G]agagccagtggaagcc	A	G	SP25 // 89882 // Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, mRNA. /// NM_033516 //	NYD-SP25	NYD-SP25, Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, p24.1
SNP_A-2233500	ctcagtgctggtatcc[C/T]agatcctgcccagaag	C	T	ENST00000312793 // intron // 0 // --- // --- // --- // ---	-	p36.22
SNP_A-2283256	gataatttgctagtac[C/T]gaattgcacttgagtt	C	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 460706	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2270535	gacagagaatattagc[A/C]cttccttgctgtatct	A	C	Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // intron // 0 // --- // -	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1
SNP_A-2098389	agagatttgatttaca[C/T]tgctcattaggctacc	C	T	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 509571 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2008229	caaaccaaaaaaagtc[A/G]agaataatatgtacaa	A	G	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 359495 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2011331	gggtaaatcaaagatg[A/G]atgaggatgaccttcc	A	G	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, mRNA. /// NM_000870 // intron // 0 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-	HTR4	HTR4, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, q32
SNP_A-2014187	atcacagaatatgacc[C/T]gcttgtagcacctctc	C	T	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 592120 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2040246	aaccacaggaaaacaa[A/T]ttacatcagttaaggc	A	T	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 409458 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2045309	aagaaggtttgtagta[A/G]gatataaggctgtcaa	A	G	Homo sapiens solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), mRNA. /// ENST00000236137 // intron // 0 // --- // --- // --- // --- /// ENST00000302778 // intron //	SLC19A2	SLC19A2, Homo sapiens solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), q24.2
SNP_A-2032601	aaataaagaagctaga[G/T]caaaatacgaaatgat	G	T	2209 // Homo sapiens Fc fragment of IgG, high affinity Ia, receptor for (CD64) (FCGR1A), mRNA. /// ENST00000271699 // downstream // 314967 // --- // --- // --- //	FCGR1A	FCGR1A, Homo sapiens Fc fragment of IgG, high affinity Ia, receptor for (CD64) (FCGR1A), q21.1
SNP_A-2032112	taagatcaagtgtttc[C/T]agttgtttattttatc	C	T	Homo sapiens killer cell lectin-like receptor subfamily K, member 1 (KLRK1), mRNA. /// ENST00000240618 // intron //	KLRK1	KLRK1, Homo sapiens killer cell lectin-like receptor subfamily K, member 1 (KLRK1), p13.2
SNP_A-2201798	ccacacacgtatacac[A/G]catgtctacacatcta	A	G	ENST00000338359 // intron // 0 // --- // --- // --- // ---	-	q24.31
SNP_A-2201970	ccacagcaagcctcta[C/T]atgttaatttttaaa	C	T	ENST00000334534 // intron // 0 // --- // --- // --- // ---	-	p12.2
SNP_A-2197476	cattcctcaattatag[A/G]attccaggagatagtg	A	G	25865 // Homo sapiens protein kinase D2 (PRKD2), mRNA. /// ENST00000323617 // upstream // 11207 // --- // --- // --- // ---	PRKD2	PRKD2, Homo sapiens protein kinase D2 (PRKD2), q13.32
SNP_A-2174010	cacacattgagatcca[C/G]taatctacagatttgt	C	G	Homo sapiens TATA box binding protein like 2 (TBPL2), mRNA. /// ENST00000247219 // intron // 0 // --- // --- // --- // ---	TBPL2	TBPL2, Homo sapiens TATA box binding protein like 2 (TBPL2), q22.3
SNP_A-2181943	cagagctctccatatg[A/T]actctgggcaagaccc	A	T	Homo sapiens hypothetical protein FLJ14904 (FLJ14904), mRNA. /// ENST00000271416 // intron // 0 // --- // --- // --- // ---	FLJ14904	FLJ14904, Homo sapiens hypothetical protein FLJ14904 (FLJ14904), q24.1
SNP_A-2175527	cacatcttaattctat[C/T]acactcacctttctc	C	T	Homo sapiens RNA polymerase I associated factor 53 (PAF53), mRNA. /// ENST00000259583 // intron // 0 // --- // ---	PAF53	PAF53, Homo sapiens RNA polymerase I associated factor 53 (PAF53), p13.2
SNP_A-2176707	cacccgaccaagggaa[C/T]tgaaaatttgatttct	C	T	// 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 107716 // Hs.98367 //	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-2154990	attcacctactactta[A/T]acctctttcaagtact	A	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2160328	atttcagcccacaaaa[C/G]actctggtttgatcac	C	G	Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // --- // --- // --- // ---	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2123337	agtgtattttcaggta[A/G]aatgagatgtaaaagt	A	G	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 105266 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1753095	agtaaagttggcctaagggcaatca[A/G]agcatccccaagaatgacaagga ag	A	G	// 23682 // RAB38, member RAS oncogene family /// NM_022918 // downstream // 488613 // Hs.183887 //	RAB38	RAB38 , rs10501648, RAB38, member RAS oncogene family ,q14.2
SNP_A-1671248	gaaagaagagaattgcaacaaatta[C/T]ggtctctgaaacaaattataacta a	C	T	// 1946 // ephrin-A5 /// NM_031438 // upstream // 20348 // Hs.434289 // NUDT12 // 83594 // nudix (nucleoside	EFNA5	EFNA5 , rs861085, ephrin-A5 ,q21.2
SNP_A-1869703	tccttattttaactta[C/T]catgttttggaatacc	C	T	// 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 21199 // Hs.511265 // SEMA6	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN q21.1
SNP_A-1855337	tcaaggcagaggaaga[C/T]gagaaacagacacagc	C	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932636	ttccttaccttcttca[C/T]gctctatttgttggat	C	T	Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1917393	tgttttgagatattta[C/T]aacattcaaactttca	C	T	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-1918576	ttaaatggaagacaac[C/T]gtatcctgatgtcttt	C	T	Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// ENST00000281894 // intron // 0 // --- // --- // --- // ---	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41
SNP_A-1906323	tggtgattcagtgatg[A/G]aaagatagaaaaagaa	A	G	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 561937 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-1879148	tcttacattcaagttc[A/G]cgctgatgcaagaggt	A	G	EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 811544 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-1981055	agttctgatagaaaaa[C/G]caatagtacacatatt	C	G	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream //	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1984234	gaagaaatgtttgagt[A/G]aaagtttgtcttgagg	A	G	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 408151 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1973208	taatctatttatcaaa[C/G]tttgactcttccttct	C	G	Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // --- // --- // --- // --- ///	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-1970982	aatgcttggccatcca[C/T]gctgtctcgtccttct	C	T	Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1972654	agacaccataggtaag[A/G]acatttcacctgactt	A	G	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-1967688	ctggcattaaaaggcc[A/G]cagaatcccaaggtgg	A	G	Homo sapiens chromosome 20 open reading frame 103 (C20orf103), mRNA. /// ENST00000246070 // intron // 0 // ---	C20orf103	C20orf103, Homo sapiens chromosome 20 open reading frame 103 (C20orf103), p12.2
SNP_A-1944458	ttgtctgagtccttga[A/C]acgttactcagctaac	A	C	Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 //	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-1933306	ttctaaggaagaaaac[C/T]caaaagacatcttaaa	C	T	Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// ENST00000333987 // intron // 0 // --- // --- // --- // ---	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-1934204	ttctcattgtttttta[A/C]ggacaacttgtacatc	A	C	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 634779 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1954050	tttgatctttcttgtc[A/T]catcagtcactggagt	A	T	// 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 191731 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-1874773	tctccttgtttatgga[G/T]gctaaaatttgaattt	G	T	56975 // Homo sapiens family with sequence similarity 20, member C (FAM20C), mRNA. /// ENST00000313766 //	FAM20C	FAM20C, Homo sapiens family with sequence similarity 20, member C (FAM20C), p22.3
SNP_A-1907582	tgtaacaagaataggg[A/T]aactttactcccattt	A	T	// 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 402180 //	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1905096	tgggtgataggagcca[C/T]aggacataggtgcaaa	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-1912712	tgtgctacaattttac[A/C]aaaatgattttgaggt	A	C	ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 1194747	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-1931956	ttcctaattaaactta[C/T]gaggctaattgtattt	C	T	// 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1929311	ttcagtcaatgttcac[A/G]ctactgacttgctggc	A	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1924189	ttagtttatttttctcc[C/G]cacatagagtgatata	C	G	Homo sapiens transient receptor potential cation channel, subfamily C, member 4 associated protein (TRPC4AP), transcript variant /// NM_015638 // intron // 0 // Hs.168073 // TRPC4AP // 26133 //	TRPC4AP	TRPC4AP, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 associated protein (TRPC4AP), transcript variant ,q11.22
SNP_A-1919948	ttaatacaaacaatgc[C/T]atagtgaatgtcctag	C	T	sapiens calmegin (CLGN), mRNA. /// ENST00000325617 // intron // 0 // --- // --- // --- // ---	CLGN	CLGN, Homo sapiens calmegin (CLGN), q31.1
SNP_A-1848430	tatgaagaaactggaa[C/T]tctggtgtattgttgg	C	T	8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 31194 // Hs.413095	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1663174	gcggactcgccaccgataatattct[C/G]actacaaaagtgttactgaaaagat	C	G	// bactericidal/permeability-increasing protein /// NM_004139 // upstream // 3304 // Hs.154078 // LBP // 3929 //	BPI	BPI , rs6123609, bactericidal,q11.23
SNP_A-1653914	ctttggctctctgagtatataacag[A/G]ctataactgtgtgggtcctggtgtt	A	G	KIAA1344	KIAA1344	KIAA1344 , rs781382, KIAA1344,q22.1
SNP_A-1710519	agagatccataactggacaaaggga[A/G]ataaagtaatcatgtaatgcaagaa	A	G	clone IMAGE:6103129, partial cds /// NM_013283 // downstream // 167697 // Hs.54642 // MAT2B // 27430 //	-	- , rs10515867, CDNA clone IMAGE:6103129, partial cds ,q34
SNP_A-1785817	ggctgaaagaatctaa[A/T]gctgattgcttctgct	A	T	LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 //	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1787545	gggaatggagattggg[A/G]atttgagttttggggg	A	G	sapiens glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS), mRNA. /// ENST00000258145 // intron //	GNS	GNS, Homo sapiens glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS), q14.3
SNP_A-1811417	gtgctagagggcctca[C/T]attggtaagcacatat	C	T	// 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 326798 // --- // --- // --- //	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12
SNP_A-2121549	agtgaacaaaaaatag[C/G]ctatgaaattctgata	C	G	// Homo sapiens growth differentiation factor 8 (GDF8), mRNA. /// ENST00000260950 // upstream // 89874 // --- // ---	GDF8	GDF8, Homo sapiens growth differentiation factor 8 (GDF8), q32.2
SNP_A-2116984	aggtgaattctgtaaa[C/G]caaaagtacctgaggt	C	G	Homo sapiens destrin (actin depolymerizing factor) (DSTN), mRNA. /// ENST00000340601 // intron // 0 // --- // --- // --- // ---	DSTN	DSTN, Homo sapiens destrin (actin depolymerizing factor) (DSTN), p12.1
SNP_A-2114206	agggaaccaggaaaca[C/T]gaagttgctgaggaca	C	T	/// ENST00000343761 // upstream // 56012 // --- // --- // --- // ---	-	q24.1
SNP_A-2133920	atatctgagcataagg[A/G]aatatattgaagcaga	A	G	9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 81756 // Hs.248117 //	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-2140246	atctatttatggggta[A/C]aatgcgatggtttgat	A	C	Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // --- // --- // --- // ---	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2150142	atgtcctggaagctcc[C/T]ccttcaatgttctaga	C	T	Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), mRNA. /// ENST00000331762 // intron // 0 // --- // --- // --- // --- /// ENST00000332943 // intron	IMMP2L	IMMP2L, Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), q31.1
SNP_A-2184789	cagctgctcttagcca[C/T]attacatacttttgtgt	C	T	FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2220088	ccttcacaactcagtc[A/G]cctcacctacctctgt	A	G	Homo sapiens cytochrome c oxidase subunit IV isoform 2 (lung) (COX4I2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000253368 // intron // 0 // --- // --- //	COX4I2	COX4I2, Homo sapiens cytochrome c oxidase subunit IV isoform 2 (lung) (COX4I2), nuclear gene encoding mitochondrial protein, q11.21
SNP_A-2223578	atgcgaagtcatagga[G/T]aattttgaacagaagt	G	T	Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), mRNA. /// ENST00000261245 // intron // 0 // --- // ---	MNAT1	MNAT1, Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), q23.1
SNP_A-2037259	aacaaagaaaattcta[A/T]attagagagcaagagg	A	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2006419 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2008634	caagagtgatattgct[A/G]aaagaacacgaagtca	A	G	Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), mRNA. /// ENST00000302541 // intron // 0 // --- // ---	MYRIP	MYRIP, Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), p22.1
SNP_A-1993297	actttataattacaca[A/C]gctaataggattcatt	A	C	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-2092633	agaaatcaccattcca[A/C]atatgataaagtgatt	A	C	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2064844	aattgaaataataaag[A/G]cttacaaacacaaagg	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 24471 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2063483	aattaatataagggat[A/C]aggttcgtcctaaaag	A	C	Homo sapiens calmin (calponin-like, transmembrane) (CLMN), mRNA. /// ENST00000298912 // intron // 0 // --- // ---	CLMN	CLMN, Homo sapiens calmin (calponin-like, transmembrane) (CLMN), q32.13
SNP_A-2283337	gatacagagtctaagg[A/G]aatcccaaattgaaca	A	G	114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream //	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-2280000	gaggcttattacagta[G/T]cgtattggtattattt	G	T	Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-2272771	gactaaaaaggaagca[A/G]aggacacaattctgaa	A	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2231969	ctcaaccgacattttc[C/T]agcatgggaacatttt	C	T	26205 // Homo sapiens glucocorticoid modulatory element binding protein 2 (GMEB2), mRNA. /// NM_015894 // downstream // 17240 // Hs.348326 // STMN3 // 50861 //	GMEB2	GMEB2, Homo sapiens glucocorticoid modulatory element binding protein 2 (GMEB2), q13.33
SNP_A-2250547	cttagtcatccgatgc[C/T]atacgtgggctcgcag	C	T	Homo sapiens p66 alpha (p66alpha), mRNA. /// NM_015329 // intron // 0 // Hs.112751 // KIAA0892 // 23383 // Homo	p66alpha	p66alpha, Homo sapiens p66 alpha (p66alpha), p13.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2314920	ggagttactttacttc[C/T]ctgtgtctcggcttcc	C	T	Homo sapiens transglutaminase 6 (TGM6), mRNA. /// ENST00000202625 // intron // 0 // --- // --- // --- // ---	TGM6	TGM6, Homo sapiens transglutaminase 6 (TGM6), p13
SNP_A-2297519	gccagaatccaagaca[C/T]atcactaaggcgccag	C	T	112744 // Homo sapiens interleukin 17F (IL17F), transcript variant 1, mRNA. /// NM_172343 // upstream // 15246 //	IL17F	IL17F, Homo sapiens interleukin 17F (IL17F), transcript variant 1, p12.2
SNP_A-2300116	gcctcatcctaggcta[C/T]ctgatccatcgaatag	C	T	9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2250662	cttataatttggaaag[A/G]ccattattaagtgcca	A	G	// 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2249844	cttacaaaacttagtc[A/C]aattcagcacttccca	A	C	25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 167376 // Hs.369574 // CDC42EP3 // 10602 //	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-2279831	gaggcctcccagagac[A/G]cgaaggggcatatctg	A	G	// 6559 // Homo sapiens solute carrier family 12 (sodium/chloride transporters), member 3 (SLC12A3),	SLC12A3	SLC12A3, Homo sapiens solute carrier family 12 (sodium,q13
SNP_A-2269365	gaatttgttggtcaaa[C/T]tgcagaataattactg	C	T	8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // downstream //	FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-2268461	gaatggattccctcaa[C/G]tgggaccagcctatct	C	G	55937 // Homo sapiens apolipoprotein M (APOM), mRNA. /// NM_033177 // downstream // 1557 // Hs.247478 // BAT4 //	APOM	APOM, Homo sapiens apolipoprotein M (APOM), p21.33
SNP_A-2081333	acctggcctaagaaga[G/T]accaattttgagaagt	G	T	Homo sapiens casein beta (CSN2), mRNA. /// NM_003154 // upstream // 27078 // Hs.37048 // STATH // 6779 // Homo	CSN2	CSN2, Homo sapiens casein beta (CSN2), q13.3
SNP_A-2001076	aacaagaatctccaca[A/G]gataataataaatgag	A	G	// 55149 // Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA. /// ENST00000298635 // upstream //	PAPD1	PAPD1, Homo sapiens PAP associated domain containing 1 (PAPD1), p11.23
SNP_A-2002053	gctgtgtgtgctacaa[C/T]atttaaattgctattg	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2002072	aagtatttagctaccc[A/G]atacctcagtttcccc	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 852066 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2014120	cacaatgaagccagca[C/T]aataaccagcaaagac	C	T	// 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	MLLT3	MLLT3, Homo sapiens myeloid,p21.3
SNP_A-2203384	ccagaaaagaaaaatg[C/T]actgaaaacagcaggt	C	T	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2211682	ccctccagtcctgcac[A/G]gagatagcaataaggc	A	G	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 254180 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2183821	cagcattgcaaatccc[C/G]gaatcctggtctagtc	C	G	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2171428	caatcacacgcacaga[A/G]aagagccttctggctg	A	G	Homo sapiens transient receptor potential cation channel, subfamily V, member 3 (TRPV3), mRNA. /// ENST00000301365 // intron // 0 // --- // --- // --- // ---	TRPV3	TRPV3, Homo sapiens transient receptor potential cation channel, subfamily V, member 3 (TRPV3), p13.2
SNP_A-2141425	atctgtttcaaaatgt[A/G]aagttgtacatgacaa	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 685761 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1812831	gtgggcaagaaacaca[C/G]tcaaggttgggggtcc	C	G	Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // intron // 0 // --- // --- // --- // ---	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-1803198	gtattctaccaattac[C/T]agggtgtgatcttggg	C	T	/// ENST00000318847 // downstream // 32272 // --- // --- // ---	-	q23.31
SNP_A-1806278	gtcctgttttattcca[C/T]gctttggtgcccactg	C	T	sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an /// NM_001135 // intron // 0 // Hs.2159 // AGC1 // 176 // Homo sapiens a	AGC1	AGC1, Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an ,q26.1
SNP_A-1790485	ggggcaggggagtaaa[C/G]gatgccaatgggtaca	C	G	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 56772 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1790788	gggggaggcgttacac[A/G]ctattaaaataaccag	A	G	Homo sapiens hypothetical protein FLJ22761 (FLJ22761), mRNA. /// ENST00000298648 // intron // 0 // --- // --- // --- // ---	FLJ22761	FLJ22761, Homo sapiens hypothetical protein FLJ22761 (FLJ22761), q22.1
SNP_A-1668000	gttgcccaaaatcatgtttgtgaga[A/G]atcctaaagcacattcatgaatgca	A	G	203228 // chromosome 9 open reading frame 72 /// NM_152570 // downstream // 251193 // Hs.446325 //	C9orf72	C9orf72 , rs10511812, chromosome 9 open reading frame 72 ,p21.2
SNP_A-1782166	ggcaagagttttcata[C/T]tacaatgattcaaaaa	C	T	10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 309633 // --- // ---	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-1854884	tcaacgttaattggga[A/G]agaaaatgatggagag	A	G	/// ENST00000356642 // downstream // 370477 // --- // --- // ---	-	q31.1
SNP_A-1859273	tcagctctgttctaaa[G/T]actaaattttcaagga	G	T	9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 64753 //	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1856040	tcaattgtaaagacta[C/T]gtagcaaaatttttga	C	T	// 57542 // Homo sapiens mRNA for KIAA1340 protein, partial cds. /// NM_198964 // downstream // 16346 // Hs.89626 //	KLHDC5	KLHDC5, Homo sapiens for KIAA1340 protein, partial cds. p11.22
SNP_A-1872096	tctactacaaaccctc[A/G]cctagaatttgactgg	A	G	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1871397	tctaaattcagtcaaa[C/T]tgacatctaaaagtaa	C	T	// 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // downstream // 127490 // Hs.479853	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1815766	gttaagcaatatgaag[C/G]agaaatcatttctagc	C	G	Homo sapiens kinesin family member 13A (KIF13A), mRNA. /// ENST00000358380 // intron // 0 // --- // --- // --- // --- ///	KIF13A	KIF13A, Homo sapiens kinesin family member 13A (KIF13A), p22.3
SNP_A-1821175	gtttgaatgatgtcaa[C/G]tagaacttgctgtagc	C	G	338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 145952 // Hs.193268 // MTAP //	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1827417	taactagggctcatca[A/G]gcatctgaggacagcc	A	G	Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (CHST8), mRNA. /// ENST00000262622 // intron // 0 // --- // --- // --- // ---	CHST8	CHST8, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (CHST8), q13.11
SNP_A-1830341	taatatcttctatttc[A/G]cttatgcttgtctggg	A	G	Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// ENST00000335238 // intron // 0 // --- // --- // --- // ---	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12
SNP_A-1914347	tgtgttctttataaat[C/G]agggacagcaacctta	C	G	221749 // Homo sapiens chromosome 6 open reading frame 145 (C6orf145), mRNA. /// NM_012135 // upstream // 63069	C6orf145	C6orf145, Homo sapiens chromosome 6 open reading frame 145 (C6orf145), p25.2
SNP_A-1915628	tgttctctgaatttcc[A/T]gactctgtggtttaaa	A	T	sapiens xanthine dehydrogenase (XDH), mRNA. /// ENST00000289041 // intron // 0 // --- // --- // --- // ---	XDH	XDH, Homo sapiens xanthine dehydrogenase (XDH), p23.1
SNP_A-1905332	tggtaaactgcagcca[A/G]gttcctgtctagtaac	A	G	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 263191 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-1879940	tcttcctctgcaataa[A/G]aaagaatttagaaaaa	A	G	ENST00000356562 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1900983	tggatactgtggaagc[A/C]aaattgatatttcacc	A	C	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // --	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1899173	tggaaagtttccacaa[C/T]agactagaacaagtag	C	T	HNRNPG-T // 27288 // Homo sapiens testes-specific heterogenous nuclear ribonucleoprotein G-T (HNRNPG-T), mRNA. /// NM_175733 // upstream // 141641 // Hs.177193 //	HNRNPG-T	HNRNPG-T, Homo sapiens testes-specific heterogenous nuclear ribonucleoprotein G-T (HNRNPG-T), p15.4
SNP_A-1896243	tgcgtattgagatgac[A/G]cctgcaagaaggagat	A	G	283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream //	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1879916	tcttcctatcaaaact[C/T]accttccatttggcta	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1882100	tctttttcacaaaaga[G/T]gtattggatctacaaa	G	T	Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 //	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-1924415	ttataatactaccatc[A/G]ctacaggtagctttag	A	G	Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), mRNA. /// ENST00000259259 // intron // 0 // --- // --- // --- // ---	STAM	STAM, Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 (STAM), p12.33
SNP_A-1952183	tttctcattcccgaaa[C/G]tatttcctgcatcttg	C	G	5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000217725 // upstream	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.31
SNP_A-1955854	tttgtattaggtatga[A/G]gtttgggtcgtttata	A	G	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-1938658	ttgagatgactcaaga[C/T]aattgcaatagggtca	C	T	1473 // Homo sapiens cystatin D (CST5), mRNA. /// NM_080920 // downstream // 57943 // Hs.355394 // GGTLA4	CST5	CST5, Homo sapiens cystatin D (CST5), p11.21
SNP_A-1946046	ttgttttagatagtcc[A/G]ctgggatcagttttct	A	G	Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000306107 // CDS // 0 // --- // ---	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1965673	gatagaaaattgctta[C/T]agatcatgcggcttgc	C	T	55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 250118 // Hs.411881 // GRB14	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1975315	tttggctccatttaac[A/G]gctcgtaaaataattt	A	G	Homo sapiens FAD104 (FAD104), mRNA. /// ENST00000264609 // intron // 0 // --- // --- // --- // --- ///	FNDC3B	FNDC3B, Homo sapiens FAD104 (FAD104), q26.31
SNP_A-1831949	taattgccctgatttc[A/G]acacgtgctcttacgg	A	G	Homo sapiens chromosome 6 open reading frame 97 (C6orf97), mRNA. /// ENST00000239374 // intron // 0 // --- // --	C6orf97	C6orf97, Homo sapiens chromosome 6 open reading frame 97 (C6orf97), q25.1
SNP_A-1719709	tatatgtgaaaatattcaacagtat[A/T]aaaaggtatgattctagaattgtaa	A	T	7424 // vascular endothelial growth factor C /// NM_021928 // downstream // 116690 // Hs.42194 // FLJ22649 // 60559 //	VEGFC	VEGFC , rs9312601, vascular endothelial growth factor C ,q34.2
SNP_A-1708560	ggttccaaccttagaattttgaaga[C/G]acacaggcattcaaaccgtagccca	C	G	NM_147182 // intron // 0 // Hs.437632 // KCNIP4 // 80333 // Kv channel interacting protein 4	KCNIP4	KCNIP4 , rs1587120, Kv channel interacting protein 4,p15.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787559	gggaatgtttatccaa[C/T]tcctgtaccaccatag	C	T	2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 221908 // Hs.444329 // GPC6 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1785375	ggctatgaccatctta[A/G]catgtactcctccacc	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 287543 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2148896	atggtgtacttacaga[C/T]gctatgtgtggtaaag	C	T	/// ENST00000334919 // upstream // 1491431 // --- // --- // --- // --- /// ENST00000322194 // downstream // 277718 // --- // --- //	-	q12.2
SNP_A-2156617	attctgcaataatggc[A/G]atgttctgtttctata	A	G	ENST00000332811 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2161460	atttgcggttcggtag[A/T]aggaatcttcagtaag	A	T	sapiens chromosome 20 open reading frame 86 (C20orf86), mRNA. /// ENST00000244062 // CDS // 0 // --- // --- // --- // ---	C20orf86	C20orf86, Homo sapiens chromosome 20 open reading frame 86 (C20orf86), q13.32
SNP_A-2166235	caaatcagcctatcca[C/G]aattatgaatagtaag	C	G	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA. /// ENST00000280979 // intron // 0 // --- // --- // --- // ---	AKAP6	AKAP6, Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), q12
SNP_A-2135021	atattcccaaaatgga[A/C]gtgtctctaacctcag	A	C	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2175005	cacaggttcattgtgc[C/G]aggctgagtgttttct	C	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 640976 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2171683	caatctgctttactaa[A/G]tctacccacttaaatg	A	G	83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 63980 // Hs.432458 // PRG4 //	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2196228	catgtgtagtgtgagc[A/G]aaagagattcaaaatt	A	G	93979 // Homo sapiens carboxypeptidase A5 (CPA5), mRNA. /// NM_080385 // downstream // 9216 // Hs.144699 //	CPA5	CPA5, Homo sapiens carboxypeptidase A5 (CPA5), q32.2
SNP_A-2199449	catttttatagctgca[A/G]tcatctttttcaggtc	A	G	Homo sapiens calcitonin receptor (CALCR), mRNA. /// L00587 // intron // 0 // Hs.489127 // CALCR // 799 // Human	CALCR	CALCR, Homo sapiens calcitonin receptor (CALCR), q21.3
SNP_A-2193390	catctgaagtggtgct[A/G]aacttagttcctcagg	A	G	6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 148071 // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2222713	cgatctgaatttttcc[A/G]ctgaagtttgctaagt	A	G	135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2015842	tctccaggcacataaa[A/G]caaaaaattgaaggca	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 237540 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-1995403	agcaatttttgctcca[A/G]ccattttgctgttttt	A	G	ENST00000316225 // intron // 0 // --- // --- // --- // ---	-	q24.23
SNP_A-2020739	actttccgttttgtga[C/T]gagcagtttagttgct	C	T	Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (MCM3AP), mRNA. /// ENST00000291688 // intron // 0 // --- // --- // --- // ---	MCM3AP	MCM3AP, Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (MCM3AP), q22.3
SNP_A-2090911	actttccctctgccac[A/G]gtcctagagtgatcgt	A	G	9962 // Homo sapiens solute carrier family 23 (nucleobase transporters), member 2 (SLC23A2), transcript variant 1, mRNA. /// NM_203327 // upstream // 77124 // Hs.516866 //	SLC23A2	SLC23A2, Homo sapiens solute carrier family 23 (nucleobase transporters), member 2 (SLC23A2), transcript variant 1, p12.3
SNP_A-2105081	agcatgacagaagaga[A/G]gaaggaattgaggcct	A	G	sapiens ketohexokinase (fructokinase) (KHK), transcript variant b, mRNA. /// NM_000221 // intron // 0 // Hs.159525 //	KHK	KHK, Homo sapiens ketohexokinase (fructokinase) (KHK), transcript variant b, p23.3
SNP_A-2058527	aatcagagtctgcacc[A/G]acacagtgtctcataa	A	G	3754 // Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1), mRNA. /// NM_182586 // downstream // 94736 // Hs.329841 // FLJ33534 // 285150 //	KCNF1	KCNF1, Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1), p25.1
SNP_A-2256989	ctttcctttggctcca[C/T]tccttcatctctctcg	C	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2280514	gaggtaagcagcgaat[A/G]agtaagtgaagcttca	A	G	Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, mRNA. /// NM_001004420 // intron // 0 //	CLEC2D	CLEC2D, Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, p13.31
SNP_A-2255353	cttgtatactaaaaac[A/C]agtgaaaagacacatc	A	C	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2295676	gcatgactgtacatta[G/T]cattatcaactatagt	G	T	// 25945 // Homo sapiens poliovirus receptor-related 3 (PVRL3), mRNA. /// NM_005816 // upstream // 107369 //	PVRL3	PVRL3, Homo sapiens poliovirus receptor-related 3 (PVRL3), q13.13
SNP_A-2314738	caaataaaaaaactca[C/G]ggaatatctcagttct	C	G	/// ENST00000314100 // upstream // 24257 // --- // --- // --- // ---	-	p13.3
SNP_A-2314978	ggagttgccaggtgaa[A/G]gcctgctcagttgagt	A	G	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2311958	ggacaagctttgttca[C/T]ggcatggaagaatggc	C	T	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2300771	gcctggcctatgctta[G/T]ctttttaataggggttt	G	T	375323 // Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), mRNA. /// ENST00000287585 //	LOC375323	LOC375323, Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), p25.3
SNP_A-2230228	ctatagatttaaaaac[A/G]gattgtgacccaaaaa	A	G	// 494115 // Homo sapiens kynurenine aminotransferase III (KAT3), mRNA. /// NM_018284 // downstream // 11204 //	LOC494115	LOC494115, Homo sapiens kynurenine aminotransferase III (KAT3), p22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235947	ctcctgccgcagaaca[C/G]atagtatggctgcgca	C	G	Homo sapiens EF hand calcium binding protein 2 (EFCBP2), mRNA. /// ENST00000305202 // intron // 0 // --- // --- // --- // ---	EFCBP2	EFCBP2, Homo sapiens EF hand calcium binding protein 2 (EFCBP2), q23.3
SNP_A-2282819	gataaagaaattgaac[C/T]gtggagagaataaatt	C	T	LOC131368 // 131368 // Homo sapiens hypothetical protein LOC131368 (LOC131368), mRNA. /// ENST00000306176 //	LOC131368	LOC131368, Homo sapiens hypothetical protein LOC131368 (LOC131368), q12.3
SNP_A-2258755	cttttggttcactggc[C/T]gatcgtcctgagggtt	C	T	Homo sapiens mRNA for KIAA1760 protein, partial cds. /// NM_006648 // intron // 0 // Hs.522291 // WNK2 // 65268 //	WNK2	WNK2, Homo sapiens for KIAA1760 protein, partial cds. q22.31
SNP_A-2266761	gaagtgggagttgaga[A/G]tcaaaatgagatgttc	A	G	sapiens B7 gene (B7), transcript variant 2, mRNA. /// NM_201650 // intron // 0 // Hs.155586 // B7 // 10233 // Homo	B7	B7, Homo sapiens B7 gene (B7), transcript variant 2, p13.31
SNP_A-2057684	aatatgggaattcaca[A/G]taactaaatgaagtct	A	G	// 5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000335192 // downstream // 645273 // ---	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2044354	aacttttgttagacta[C/G]aactcatgcttttcta	C	G	Homo sapiens hypothetical protein FLJ10979 (FLJ10979), mRNA. /// ENST00000321906 // intron // 0 // --- // --- // --- // ---	FLJ10979	FLJ10979, Homo sapiens hypothetical protein FLJ10979 (FLJ10979), p13.3
SNP_A-2005277	aaagatttaggagttg[C/G]accaagtttgagtcct	C	G	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 306328 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2016567	aaaaactaatttctag[G/T]caacattcctgcaggc	G	T	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream //	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2225165	cgttatcaactgaaac[A/T]ggtaattatggtcatt	A	T	10202 // Homo sapiens dehydrogenase/reductase (SDR family) member 2 (DHRS2), transcript variant 2, mRNA. ///	DHRS2	DHRS2, Homo sapiens dehydrogenase q11.2
SNP_A-2225807	ctaaagtgcttaatga[A/T]ggtgctggattctccc	A	T	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 160446 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2204973	ccagggtaatattgac[C/T]ctatacaccaggttag	C	T	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2153228	attactgatgaataaa[C/T]agtaaaggaagaaata	C	T	5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 216038 //	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-2148730	atggtcctgaaaataa[C/T]tgtaaggttcaagtaa	C	T	Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-2146617	atgctgggccagaatg[A/G]cagtgaagtttttggg	A	G	// 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 147793 // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q14.3
SNP_A-1711568	cttcccaatctaggatttagatttc[C/T]ataagctgtaaaaattgttccccaa	C	T	// 6558 // solute carrier family 12 (sodium/potassium/chloride transporters), member 2 /// NM_130809 // downstream //	SLC12A2	SLC12A2 , rs9327458, solute carrier family 12 (sodium,q23.2
SNP_A-1836078	tactacgattaaaagt[C/G]acatttctggtgatat	C	G	Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), mRNA. /// ENST00000357257 // intron // 0 // --- // --- // --- // ---	COL27A1	COL27A1, Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), q32
SNP_A-1856963	tcaccagtatggggaa[A/G]tgagtgaataaggtgg	A	G	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1936512	ttcttgagtcagttca[A/G]taagtgtttgctttttt	A	G	7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA. /// NM_178234 //	TUSC3	TUSC3, Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, p22
SNP_A-1955095	tttggatgatcttgcc[A/G]cacaaaattagtctct	A	G	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 845028 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-1951309	tttccctgagggatga[C/T]gagcagcagatggaga	C	T	Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// ENST00000327590 // intron // 0 // --- // --- // --- // ---	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.3
SNP_A-1953494	tttgaagtgtacttag[A/C]aatccagttctattct	A	C	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-1909989	tgtcaggctacagccc[A/G]gatggttggctgagca	A	G	Homo sapiens MLL septin-like fusion (MSF), mRNA. /// ENST00000329047 // intron // 0 // --- // --- // --- // --- ///	SEPT9	SEPT9, Homo sapiens MLL septin-like fusion (MSF), q25.2
SNP_A-1917147	tgtttgttgattgaaa[C/T]gattgcctcaaagaac	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-1889209	tgagtcttagagaaat[C/T]agatggtttgctcaag	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-1951913	tttctacctctccatc[C/T]gaactgcgtgtgggag	C	T	54511 // Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HMGCLL1), mRNA. /// NM_021073 // downstream // 161996 // Hs.296648 // BMP5 // 653 // Homo	HMGCLL1	HMGCLL1, Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HMGCLL1), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1957860	ttttatttgcttttca[C/T]ccaaatctgctagatt	C	T	Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // --- //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1958835	ttttctgtgcagggaa[C/T]ggatttgagaacttcc	C	T	Homo sapiens NFAT activation molecule 1 (NFAM1), mRNA. /// ENST00000329021 // intron // 0 // --- // --- // ---	NFAM1	NFAM1, Homo sapiens NFAT activation molecule 1 (NFAM1), q13.2
SNP_A-1936232	ttcttcatagtgaaca[C/G]tgtaagatttatcaac	C	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 945686 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1944337	ttgtccttccgtttcc[A/G]acattctagatttttg	A	G	5501 // Homo sapiens protein phosphatase 1, catalytic subunit, gamma isoform (PPP1CC), mRNA. /// NM_152591 // upstream // 38171 // Hs.437141 // FLJ35843 // 160762 //	PPP1CC	PPP1CC, Homo sapiens protein phosphatase 1, catalytic subunit, gamma isoform (PPP1CC), q24.11
SNP_A-1983755	gccagagtctttaaaa[C/T]ggccttatgaagctcg	C	T	81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 179541 //	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-1987015	agcacagttgtgcaaa[C/T]aatatacgtttccagg	C	T	PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 14518 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1856060	gctcagtcctgctgca[C/T]gtgatactgacaggaa	C	T	ENST00000341671 // intron // 0 // --- // --- // --- // ---	-	q21.32
SNP_A-1854361	tcaaatagaacaatcc[A/G]gattcacaaatatgtc	A	G	sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020546 // intron // 0 // Hs.481545 // ADCY2 // 108 //	ADCY2	ADCY2, Homo sapiens for KIAA1060 protein, partial cds. ,p15.31
SNP_A-1869236	tcctggcccctataag[C/G]atttgagtttgctcac	C	G	ENST00000278064 // intron // 0 // --- // --- // ---	-	q25.1
SNP_A-1824099	taaacaccaataatca[A/G]taattttcattgctgt	A	G	// 117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000332754 // downstream // 44651 // --- // --- // --- // -	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-1814950	gtgttacaatatctga[A/G]acaaatatgcctgtga	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1675241	gcaatctgatccagaatatatccaa[A/C]tctgaacatccttttccaaaaagta	A	C	7247 // translin /// NM_130773 // upstream // 1429337 // Hs.437463 // caspr5 // 129684 // caspr5 protein ///	TSN	TSN , rs10496589, translin ,q14.3
SNP_A-1754584	aggtgctccctttaaggctaaatca[C/T]gaaatatcctaaatgctggaaatgt	C	T	27152 // PDZ domain containing 6 /// NM_024582 // downstream // 583158 // Hs.25201 // FATJ // 79633 // fat-like	PDZK6	PDZK6 , rs10518484, PDZ domain containing 6 ,q28.1
SNP_A-1811346	gtgcggttgatggcca[C/T]ggtttatagaggggag	C	T	ENST00000228705 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-2141735	atcttctgaatttcaa[C/G]agtactaaaaatattt	C	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2144890	atgattcaatagaaaa[C/T]gagtgaaagatattga	C	T	Homo sapiens hypothetical protein FLJ14904 (FLJ14904), mRNA. /// ENST00000271416 // intron // 0 // --- // --- // --- // ---	FLJ14904	FLJ14904, Homo sapiens hypothetical protein FLJ14904 (FLJ14904), q24.1
SNP_A-2165990	caaataaatgtggtaa[C/T]ggaaatcaggggaatg	C	T	Homo sapiens inversin (INVS), transcript variant 2, mRNA. /// NM_014425 // intron // 0 // Hs.270443 // INVS // 27130 //	INVS	INVS, Homo sapiens inversin (INVS), transcript variant 2, q31.1
SNP_A-2163324	atttttacaagaata[C/T]caagaccattcaatga	C	T	2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 20578 // Hs.122926 // NR3C1 //	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-2133594	atatcacgtcgggtca[C/T]ctcctctgggcctccc	C	T	FLJ46831 // 399823 // Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 106875	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-2109275	agctttagagtgagtc[A/G]agttggggtcctagac	A	G	162417 // Homo sapiens N-acetylglutamate synthase (NAGS), mRNA. /// NM_032376 // downstream // 2379 //	NAGS	NAGS, Homo sapiens N-acetylglutamate synthase (NAGS), q21.31
SNP_A-2202150	ccacatcctagataga[A/C]agggtcaggctcgggg	A	C	Homo sapiens retinoic acid induced 17 (RAI17), mRNA. /// ENST00000334512 // intron // 0 // --- // --- // --- // ---	RAI17	RAI17, Homo sapiens retinoic acid induced 17 (RAI17), q22.3
SNP_A-2211829	ccctctgcactgggac[A/G]ggaccacagggctaag	A	G	mRNA for KIAA0134 gene, partial cds. /// NM_014681 // 3UTR // 0 // Hs.151706 // DHX34 // 9704 // Homo sapiens	DHX34	DHX34, Homo sapiens for KIAA0134 gene, partial cds. q13.32
SNP_A-2214722	cctagggtgaacttaa[A/G]caacagcaacctctga	A	G	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1846613 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2184329	cagcctttgctacatc[A/G]catttcacataacaag	A	G	Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// ENST00000286545 // intron // 0 // --- // --- // --- // ---	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-2179031	cactgctacatcctca[C/G]agttaaggaaaatatt	C	G	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2001923	taattccatctttta[C/T]gactttcatgacttag	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2010293 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1992187	agacacagcagcccac[C/T]gaggcgataggtgatt	C	T	// 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// NM_004225 // downstream // 2273 // Hs.379414 // MFHAS1	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041697	aacgggtttgggatca[A/C]cacttttgcaaatcct	A	C	// 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// NM_144665 // downstream // 11170 // Hs.120633 //	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds. q21
SNP_A-2071438	acagaaaattgaacaa[A/G]tagtgcagagttcctt	A	G	Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-2093114	agaacatagcttgtaa[C/G]aaatcctgttgctcat	C	G	Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // --- // --- // --- // ---	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-2089177	acttacatttattgaa[C/G]atattttgtgtggcag	C	G	5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 226472 //	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-2083415	actaagaaaactgaga[G/T]gtaatcataatataca	G	T	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2237195	ctctcaggagacttta[C/T]ataaacacatttttct	C	T	9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000342288 // upstream // 359448 // --- // ---	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-2289608	gcaaaaacctgaatga[C/T]aaactttccacagtgt	C	T	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 157993 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-2310645	ggaagaggtaatcatc[A/G]aggatggcagctaggg	A	G	// 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2970413 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2313466	ggagagcttcctagag[C/G]aggtgttttgggctaa	C	G	sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA. /// ENST00000261883 // intron // 0 // --- // --- // --- // ---	CILP	CILP, Homo sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), q22.31
SNP_A-2230608	ctatctctctcttcaa[C/T]agcttacttgctgata	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 595225 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2258336	cttttcaagagtctcc[C/G]gaagttttaacttatt	C	G	25948 // Homo sapiens kelch repeat and BTB (POZ) domain containing 2 (KBTBD2), mRNA. /// NM_182827 //	KBTBD2	KBTBD2, Homo sapiens kelch repeat and BTB (POZ) domain containing 2 (KBTBD2), p14.3
SNP_A-2273147	gactcaacagtttgaa[C/T]ccactctatagcttag	C	T	57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 138466 // Hs.424711 //	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2275147	gagaagcacaaaaatg[A/G]atctaagaaaaccaaa	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1806295 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2086433	actcttggtgcatata[A/T]aaagaaccctacaata	A	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2088065	actgggaacaccttga[A/G]tatcttatgcctttgt	A	G	Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// ENST00000286545 // intron // 0 // --- // --- // --- // ---	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-2086527	actgaaaattaaatca[C/T]aacagcctgtgcccta	C	T	51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 23434 // Hs.271977	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-2072727	acagctaagaagatgc[A/G]atctgggtgccggaaa	A	G	/// ENST00000360895 // upstream // 24151 // --- // --- // --- // ---	-	p12.1
SNP_A-2057964	aatattggtttttaca[C/T]ggtattcttagaacta	C	T	ENST00000331169 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2055003	aataaatgaaacatgc[C/T]cttttgtgctttggtg	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 889058 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2171754	caatgaaacgtgaata[A/T]agaggaatcgccgcag	A	T	Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-2199605	ccaaaacccaagtcca[A/G]gttcctgtaatgcctg	A	G	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 225621 // --- // --- // ---	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. ,q11.2
SNP_A-2209680	cccatgtttttggtca[A/T]gtgtggttgaattttt	A	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2201328	ccaatcaaaagtgtgt[A/G]aagtgatatcacaatg	A	G	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2206551	ccatctttaaaaaaaa[A/G]tgctcccttgattaca	A	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 254573 // Hs.33368 // MCTP2 // 55784 // Homo	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2111525	aggagggtctgttacc[A/C]attgcttaaaagaaaa	A	C	FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream //	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2110221	aggaagtgatagtaaa[C/T]gttcttctgggtctct	C	T	Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // intron // 0 // Hs.268942 // ATP2B2 // 491 //	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2124860	agttgaacactggaaa[C/T]tatcagcatacctctg	C	T	Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), mRNA. /// ENST00000256830 // intron // 0 // --- // --- // --- // --- ///	NEDD4L	NEDD4L, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), q21.31
SNP_A-2164975	caaactcactgtaaca[A/G]gcccccgttctgtttc	A	G	5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2166855	ttaaatctggcatgat[C/T]aaacacttacatttac	C	T	Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, mRNA. /// NM_198717 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens	PTGER3	PTGER3, Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, p31.1
SNP_A-2153429	attagagtatacgagc[C/T]agaaaaataaattata	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1810886	gtgcagtttagatgaa[A/G]agggaggtccagtgga	A	G	3732 // Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocl /// NM_130783 // upstream // 105544 // Hs.385634 // LOC90139	KAI1	KAI1, Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocl p11.2
SNP_A-1782517	ggcacatgacagattc[C/T]caataactgtttgcta	C	T	Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // --- // --- // --- // --- ///	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-1783450	ggcatcaagaacactc[A/G]ctaagttcccaaaggg	A	G	81552 // Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA. /// ENST00000285279 // intron // 0 // --- // --- // --- // ---	DKFZP564K0822	DKFZP564K0822, Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), p11.2
SNP_A-1660403	cccgacggtattaccacagtaccaa[C/T]ttgcctctggctaaataaacaaaca	C	T	// 50613 // ubiquilin 3 /// NM_033180 // upstream // 160507 // - // - // - // -	UBQLN3	UBQLN3 , rs10500643, ubiquilin 3 ,p15.4
SNP_A-1651282	tccctaaacaaaagctaaatagtta[C/T]agttaatggtaactggcaagggatt	C	T	NM_014608 // 3UTR // 0 // Hs.26704 // CYFIP1 // 23191 // cytoplasmic FMR1 interacting protein 1	CYFIP1	CYFIP1 , rs1050137, cytoplasmic FMR1 interacting protein 1,q11.2
SNP_A-1652246	aatgtaatcacaaggttcttagaaa[A/C]aaagcaagagggaagcaagaga agc	A	C	// 51000 // solute carrier family 35, member B3 /// NM_153003 // downstream // 917249 // Hs.382068 // OFCC1	SLC35B3	SLC35B3 , rs380319, solute carrier family 35, member B3 ,p24.3
SNP_A-1704569	cgacatacacatgcatatatatgca[A/T]gatttattatttagttatcacagaa	A	T	4552 // 5-methyltetrahydrofolate-homocysteine methyltransferase reductase /// NM_003966 // downstream // 859689 // Hs.528707 // SEMA5A // 9037 // sema domain,	MTRR	MTRR , rs901890, 5-methyltetrahydrofolate-homocysteine methyltransferase reductase ,p15.31
SNP_A-1820479	gtttatgcatgataaa[C/G]agaggaaatggagggg	C	G	HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 349022 // Hs.48384	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-1820541	gtttattgtacaaaat[A/T]atcaaaaggtgttgca	A	T	SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream //	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1842713	tagtaagagtgcttta[C/G]actttaggaaaatctt	C	G	9252 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA. /// NM_182398 // upstream // 20143 // Hs.510225 // RPS6KA5 //	RPS6KA5	RPS6KA5, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, q32.12
SNP_A-1870579	tcgatatttaatccct[C/T]acaaaagctgtttatg	C	T	11023 // Homo sapiens ventral anterior homeobox 1 (VAX1), mRNA. /// NM_181840 // upstream // 48950 // Hs.449650 //	VAX1	VAX1, Homo sapiens ventral anterior homeobox 1 (VAX1), q26.11
SNP_A-1863441	tccaaaactgatgaag[C/G]catcaatcccacaaag	C	G	// Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 78752 // Hs.375684 // RAD18 //	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-1851619	tattctgactccaaac[A/T]caaacatcagagccac	A	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1845889	tatataaagagagaga[A/G]ggttaagtgagataat	A	G	79870 // Homo sapiens brain and acute leukemia, cytoplasmic (BAALC), mRNA. /// NM_003506 // upstream //	BAALC	BAALC, Homo sapiens brain and acute leukemia, cytoplasmic (BAALC), q22.3
SNP_A-1967739	tttacctgcagtcacc[C/T]gggagtttgcaagacc	C	T	sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA. /// ENST00000254958 // CDS // 0 // --- // --- // --- // ---	JAG1	JAG1, Homo sapiens jagged 1 (Alagille syndrome) (JAG1), p12.2
SNP_A-1943174	ttggtcctgcaaaaca[C/T]actacagagaggcact	C	T	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1940232	ttgcattaacacatca[A/G]ctttgaaccagaaaat	A	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000273432 // intron // 0 // --- // --- // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1952642	tttctggatttccaat[C/G]atgggaatttgcctct	C	G	3820 // Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), mRNA. /// NM_013269 // upstream // 6304 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin	KLRB1	KLRB1, Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), p13.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1890132	tgatattgattgaaag[A/G]aaatgatagtgccagt	A	G	Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // intron // 0 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-1915843	tgttgaattactcaaa[A/G]ttgcctgaggcttatg	A	G	10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// NM_001922 // downstream // 11888 // Hs.301865 // DCT //	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q32.1
SNP_A-1923590	ttagggtgcttgaaga[C/T]gaggagagaaagtttg	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 593131 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1926116	ttatgtttctcattaa[A/T]tgtttttggtatcttg	A	T	55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 2520 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1905710	tggtatggttgcaaaa[C/G]atatctccttgcttta	C	G	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 680268 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-1897764	tgctggaataaacata[C/T]ccgtgcaagggtcttt	C	T	ENST00000356372 // intron // 0 // --- // --- // --- // ---	-	p15.5
SNP_A-1956858	ttttaaccctaagacc[G/T]atgcagttttctgatc	G	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1945934	ttgtttcccttaatgc[A/C]ccaaggaaagcagtac	A	C	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 389640 // --- // --- // --- // ---	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-1939079	ttgataaacctcggtg[A/C]aaaatttgtgttgaaa	A	C	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-1966407	gcaacatagagtgaaa[C/G]accaacactgtagtga	C	G	Homo sapiens ankyrin repeat domain 28 (ANKRD28), mRNA. /// ENST00000337207 // intron // 0 // --- // --- // --- // ---	ANKRD28	ANKRD28, Homo sapiens ankyrin repeat domain 28 (ANKRD28), q33.1
SNP_A-1969192	atacacctttaggaca[C/T]tgaagcttataatcta	C	T	54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 275035	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-1984561	gcagtgcaagtcctca[A/C]catggtcctctagcat	A	C	3937 // Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// NM_004137 // downstream // 68429 // Hs.484099	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-1852077	tattggaatactcaaa[A/G]gaagaacctatttctg	A	G	// Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 97911 // Hs.160562	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-1822647	taaaaaaaaattccca[A/G]tggagtgtgagcttct	A	G	8900 // Homo sapiens cyclin A1 (CCNA1), mRNA. /// NM_203451 // upstream // 177629 // Hs.422375 //	CCNA1	CCNA1, Homo sapiens cyclin A1 (CCNA1), q13.3
SNP_A-1713504	atgagtgctgcattatgggagctca[C/T]tatctgctcagtgggttcctgcaga	C	T	AB046863 // intron // 0 // Hs.292056 // ZFYVE28 // 57732 // zinc finger, FYVE domain containing 28	ZFYVE28	ZFYVE28 , rs3135095, zinc finger, FYVE domain containing 28,p16.3
SNP_A-1728655	gtttaaaaggtaagtttgatatata[A/G]gtcaagagatcaaaggggagatctg	A	G	NM_023927 // upstream // 241995 // Hs.281147 // NS3TP2 // 65983 // HCV NS3-transactivated protein 2	NS3TP2	NS3TP2 , rs2408612, HCV NS3-transactivated protein 2,q23.2
SNP_A-1789161	gggcagtaccccagga[C/T]ctatccagagccagcc	C	T	Homo sapiens prostaglandin E synthase (PTGES), transcript variant 2, mRNA. /// NM_004878 // intron // 0 // Hs.146688 //	PTGES	PTGES, Homo sapiens prostaglandin E synthase (PTGES), transcript variant 2, q34.11
SNP_A-2156903	attcttctgggacaaa[G/T]tattggtcagcgctga	G	T	Homo sapiens Ras association (RalGDS/AF-6) domain family 1 (RASSF1), transcript variant C, mRNA. /// NM_170712 //	RASSF1	RASSF1, Homo sapiens Ras association (RalGDS,p21.31
SNP_A-2125876	agtttgtggttccctg[A/C]agaaacatcaggttgc	A	C	// Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // --- // --- // --- // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2126390	ataaaagaacggcagg[C/T]aagcctgagcatcagt	C	T	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2204103	ccagcacagtgtcaag[A/C]aagcacttttcgcagg	A	C	ENST00000328398 // intron // 0 // --- // --- // --- // ---	-	q26.3
SNP_A-2173532	cacaatgatctgtatg[C/T]aggccgtgtgtcaacc	C	T	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2057123	aatataactgtatttg[A/G]atatatggcatctaca	A	G	/// ENST00000328244 // downstream // 15534 // --- // --- // ---	-	q13.41
SNP_A-2073739	acagtctggtgagcag[G/T]attggacaatttaaat	G	T	5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 510931 // Hs.248136 // HTR1F //	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.2
SNP_A-2069110	acaattaaccaacaca[A/G]tgcccagaatatagta	A	G	Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // intron // 0 // --- // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2100693	agatagaaatgccatc[C/T]agccaggagagaaaaa	C	T	// Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), mRNA. /// ENST00000296046 // downstream // 38011 // --- // ---	CPA3	CPA3, Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), q24
SNP_A-2043258	aactgctctgagtaca[A/T]gcatttcaaaaaagga	A	T	Homo sapiens transducer of regulated cAMP response element-binding protein (CREB) 3 (TORC3), mRNA. /// ENST00000268184 // intron // 0 // --- // --- // --- // ---	TORC3	TORC3, Homo sapiens transducer of regulated cAMP response element-binding protein (CREB) 3 (TORC3), q26.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027813	aaaccgatttcggtca[C/T]ctcctctgtgaagtcc	C	T	RAB11FIP4 // 84440 // Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), mRNA. /// NM_018405 // downstream // 176940 // Hs.462729 //	RAB11FIP4	RAB11FIP4, Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), q11.2
SNP_A-2015706	gtctaattgttcatca[C/T]ctcctttagagtttag	C	T	54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 326891	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-2008254	aaagctagaataccaa[C/T]gggatgtggggaggat	C	T	// Homo sapiens eukaryotic translation initiation factor 4E nuclear import factor 1 (EIF4ENIF1), mRNA. /// ENST00000344710 // intron // 0 // --- // --- // --- // --- ///	EIF4ENIF1	EIF4ENIF1, Homo sapiens eukaryotic translation initiation factor 4E nuclear import factor 1 (EIF4ENIF1), q12.2
SNP_A-2008368	agcatctctgaaatcc[A/G]aaactaacacagagga	A	G	Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000350110 // intron // 0 // --- // --- // --- // --- ///	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2282079	gagtggtcttcaaata[C/T]ctgaaaagctgtcacg	C	T	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // --- // --- // --- // ---	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2262878	gaacaaaggaagacca[C/T]tgatgagaataaggaa	C	T	2260 // Homo sapiens fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1), transcript variant /// NM_015850 // upstream // 15500 //	FGFR1	FGFR1, Homo sapiens fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1), transcript variant ,p12
SNP_A-2230595	ctatctcatccagtac[C/T]accaaggaaacaaggt	C	T	Homo sapiens chromosome 14 open reading frame 58 (C14orf58), mRNA. /// ENST00000238667 // intron // 0 // --- //	C14orf58	C14orf58, Homo sapiens chromosome 14 open reading frame 58 (C14orf58), q24.3
SNP_A-2239280	ctcttgttggcagttg[C/T]agtaaaccatctgaaa	C	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 282758 // Hs.13640 //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2242781	ctgcattgtactacat[A/G]agactacatcgagtag	A	G	Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // --- // ---	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2301499	gcgaattatttctaca[C/T]gcataacaaaccaggc	C	T	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2296682	gccaaagccatggaca[A/T]tcctaaagattagatt	A	T	79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 202413 //	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2291825	gcacagctaagccaca[C/T]ggaaaccagaagttgt	C	T	Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // --- // --- // --- // ---	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2256296	ctttagtagcccgtca[A/T]gtgaatatgcttgggt	A	T	153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 10373 // Hs.424156 // IRX1 //	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-2228941	ctagattacttcatat[C/T]atatagctcatctata	C	T	// 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_019049 // upstream // 123151 //	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-2027419	aaacattgaatttcct[C/G]aaaaaccaactttagt	C	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2023744	aaaactttgcacagtc[A/T]atggacaaacaaatct	A	T	sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2047299	aagatcaaagtacagg[C/G]atagcatcatgttgtg	C	G	89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2104776	agcagttttctgaaaa[A/G]gcattaatatgtcatt	A	G	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 1115943 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2198758	catttctatgcaccaa[C/T]aatgatctagttgaaa	C	T	MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// NM_183049 // upstream //	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2197811	cattgaatgggagctc[C/T]agtcttccgggaaaat	C	T	sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), mRNA. /// ENST00000218867 // intron // 0 // --- // --- // --- // ---	SGCG	SGCG, Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), q12.12
SNP_A-2204299	ccagccccttaagca[A/G]acagtatcattatcac	A	G	Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// ENST00000157600 // intron // 0 // --- // --- // --- // ---	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-2209379	cccataagttaaagca[A/G]gcagttcccaaccagg	A	G	/// ENST00000332660 // downstream // 501801 // --- // --- // ---	-	p12.3
SNP_A-2226231	ctaactctgacaaaga[A/C]ggtgcagtgagggctc	A	C	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 //	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-2220839	ccttgcagctaggggga[A/C]ggtcaagctctggtcc	A	C	Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA. /// ENST00000354276 // intron // 0 // --- // --- // --- // --- ///	PLA2G4C	PLA2G4C, Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), q13.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2110113	aggaagcttagggtta[C/T]agtgtcagaatactgg	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1835357 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1812526	gtggccgtccctgcag[A/C]agcatggccctgagga	A	C	119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 27637 // Hs.117530 // LYZL1 //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-1783655	ggcattaaaaagtggc[G/T]caaatctcttcttctg	G	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1449040 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1752835	catgaatctttactcatgatcccta[C/T]ggataactaaggattgatgctatta	C	T	NM_014895 // intron // 0 // - // - // - // -	-	- , rs10498938, -,q14.2
SNP_A-1823135	taaaacaccttgtaaa[C/T]gaaggaggtttatgct	C	T	57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 420146 //	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-1820459	gtttatctgtgcatac[A/G]attaacgtttattgaa	A	G	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 2485274	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1836823	tactgattccacttag[A/T]ccctcatgtcattcaa	A	T	Homo sapiens mannan-binding lectin serine protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1),	MASP1	MASP1, Homo sapiens mannan-binding lectin serine protease 1 (C4,q27.3
SNP_A-1847711	tatctagtacactcag[C/G]acgtcacacaattctt	C	G	UNQ1912 // 345757 // Homo sapiens HGS_RE408 (UNQ1912), mRNA. /// NM_175052 // downstream // 10327 //	UNQ1912	UNQ1912, Homo sapiens HGS_RE408 (UNQ1912), q21.1
SNP_A-1859238	tcagctcagaaggtac[A/G]gggcagtaattgattt	A	G	ENST00000358412 // intron // 0 // --- // --- // --- // ---	-	p15.2
SNP_A-1870929	tcgggttagattacca[A/G]tgcccaccaaataaca	A	G	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1872134	tctactccttcaaaaa[C/G]aagactccagtggcta	C	G	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 342605 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-1873426	tctcaactggtgctcc[A/G]aataaagacttctttt	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 969218 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1944305	ttgtcctccttggttc[A/G]accctctggtctttat	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 754673 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1941351	ttgcttagttttatga[A/C]ctcgaatttttccaag	A	C	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 91949 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1943152	ttggtcattttaagac[A/G]cttttagtaagatggt	A	G	Homo sapiens fructosamine-3-kinase-related protein (FN3KRP), mRNA. /// ENST00000269373 // 3UTR // 0 // --- //	FN3KRP	FN3KRP, Homo sapiens fructosamine-3-kinase-related protein (FN3KRP), q25.3
SNP_A-1880018	ccccaatgaataccac[C/T]attgcccattacacgt	C	T	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 603736 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1905558	tggtagaatttgaggc[A/C]catgatagaaaaaaac	A	C	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 67966 //	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-1921855	ttactattatccacca[C/T]gctgatctgaacgtcc	C	T	Homo sapiens mucin 4, tracheobronchial (MUC4), transcript variant 2, mRNA. /// NM_138297 // intron // 0 // Hs.369646 // MUC4 // 4585 // Homo sapiens mucin 4, tracheobronchial	MUC4	MUC4, Homo sapiens mucin 4, tracheobronchial (MUC4), transcript variant 2, q29
SNP_A-1927726	ttcaagactttcttta[A/G]acaattcacttcactc	A	G	84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// NM_152744 // upstream //	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-1931715	ttccctgaccagtaac[A/G]cattgcttgtgggttt	A	G	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 266168 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1910135	tgtcatcttttgttaa[C/T]gttttgctctaaaacc	C	T	Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000299322 // intron // 0 // --- // --- // --- // ---	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1874661	tctcctcttcgaaaca[A/G]gtaaggggatgctgtc	A	G	Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // --- // --- // --- // --- ///	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-1892580	tgcaatgctggcaaaa[A/T]gtcatacaggtggcca	A	T	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 21016 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1934861	ttctgaaagagacaca[C/T]gaaacttatgttaaag	C	T	Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA. /// ENST00000289175 // intron // 0 // ---	LRRFIP1	LRRFIP1, Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), q37.3
SNP_A-1845640	tatagctctccacctc[C/T]gaggctgcatctcctc	C	T	1577 // Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide 5 (CYP3A5), mRNA. /// NM_000765 // upstream // 92035 // Hs.111944 // CYP3A7 // 1551 // Homo	CYP3A5	CYP3A5, Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide 5 (CYP3A5), q22.1
SNP_A-1821133	gtttgaaaaagtatac[G/T]catatttgcataacaa	G	T	254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 //	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1758884	catagggttcttctgaacctgaacc[A/G]caacaattctaggaggtctgcttgg	A	G	// 667 // bullous pemphigoid antigen 1, 230/240kDa /// NM_015548 // downstream // 202316 // Hs.443518 // BPAG1	BPAG1	BPAG1 , rs724677, bullous pemphigoid antigen 1, 230,p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2129620	atacagaggaaaataa[C/T]tgaagtttggcaacct	C	T	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2134794	atattacagatttgaa[C/G]agaaatagaaaacttt	C	G	79799 // Homo sapiens hypothetical protein FLJ21934 (FLJ21934), mRNA. /// NM_001073 // downstream // 33163 //	FLJ21934	FLJ21934, Homo sapiens hypothetical protein FLJ21934 (FLJ21934), q13.2
SNP_A-2212483	ccctgtttgggaatca[A/T]ggtgaagccacctccc	A	T	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2192573	catccagaaagtcaac[A/G]gatgcaacttactcac	A	G	ENST00000308105 // intron // 0 // --- // --- // --- // ---	-	q44
SNP_A-2190822	catagaggatattcaa[A/T]cattttctcactttcc	A	T	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2175651	cacatggtaagcaatc[A/G]gagtcacctgccatca	A	G	Homo sapiens chromosome 9 open reading frame 20 (C9orf20), mRNA. /// ENST00000321582 // intron // 0 // --- // --	C9orf20	C9orf20, Homo sapiens chromosome 9 open reading frame 20 (C9orf20), q33.2
SNP_A-2067298	acaaagtatccagagc[C/G]ataaccacaactatac	C	G	163223 // Homo sapiens similar to Zinc finger protein 208 (LOC163223), mRNA. /// NM_178523 // intron // 0 //	LOC163223	LOC163223, Homo sapiens similar to Zinc finger protein 208 (LOC163223), p12
SNP_A-2045627	aagaatttgaagagat[C/G]agccagtattctgatg	C	G	285704 // Homo sapiens RGM domain family, member B (RGMB), mRNA. /// ENST00000308338 // downstream //	RGMB	RGMB, Homo sapiens RGM domain family, member B (RGMB), q21.1
SNP_A-2042698	aactcgataagatcga[G/T]tccaagttacagagcc	G	T	// 5314 // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // downstream // 147983 //	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2021496	aaaaaagtttcataga[C/T]gtagagtgcctttgta	C	T	// Homo sapiens fls485 (LOC51066), mRNA. /// ENST00000341795 // intron // 0 // --- // --- // --- // --- ///	LOC51066	LOC51066, Homo sapiens fls485 (LOC51066), p25.3
SNP_A-2026984	aaacagaactgtgacc[A/G]atgttttgcaatttcc	A	G	60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 263718 // Hs.528665 // PROK2 //	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2006439	ctcccacgtccttgac[A/C]gagcagattttaaatc	A	C	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 497710 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-2018892	cgttgctgtgattaac[A/G]aaatagttggatgcat	A	G	23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 158196 //	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-1989611	gtcactgaaggccaga[A/C]ataaatgtaaaagcac	A	C	sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-2000580	atttcacttcctacca[C/T]gaactaaaagaattgt	C	T	Homo sapiens microseminoprotein, beta- (MSMB), transcript variant PSP57, mRNA. /// NM_002443 // intron // 0 //	MSMB	MSMB, Homo sapiens microseminoprotein, beta-(MSMB), transcript variant PSP57, q11.23
SNP_A-2273953	gactgtctgggtgtta[C/T]agaaacaaacatccct	C	T	Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // --- // --- // --- // --- ///	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2312290	ggacatcactgaacaa[A/C]actgggcaactctggg	A	C	-- /// ENST00000304488 // downstream // 20806 // --- // --- // --	-	q24.1
SNP_A-2306335	tcatgatatgattata[A/T]gtccagaaccactcga	A	T	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 181470 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2307695	gcttccagtgagaaat[A/G]atgttgaaacaatgtt	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 // upstream // 19413 // Hs.20805 // TSAP6 // 55240 // Homo	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2300732	gcctggagcactacaa[C/G]aggaggttagcgggcg	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2298002	gccataatgggcaagt[A/C]actgccttctctgctt	A	C	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2277325	gagattgtataagaaa[C/T]agtgaagaacaataaa	C	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2034780	aaatgacacagccatc[C/G]atagcactagagaagg	C	G	6670 // Homo sapiens Sp3 transcription factor (SP3), mRNA. /// ENST00000357595 // upstream // 38275 // --- // --- // --- // --	SP3	SP3, Homo sapiens Sp3 transcription factor (SP3), q31.1
SNP_A-2069430	acacaagatgatttgg[A/G]aggattttcagggtca	A	G	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate q22.3
SNP_A-2075255	acatctgtttacaaca[C/T]ggttcactgaatattt	C	T	// 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000353474 // downstream //	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-2099472	agagggagattcgatg[A/G]cacacgatggaggaaa	A	G	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 712416 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2095360	agaatttggagcaaag[A/G]aagtttcccagctcca	A	G	133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 881376 // Hs.480596 // NDST3 // 9348 // Homo	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086514	actgaaaactgcccac[G/T]ggctacccatagcaga	G	T	84891 // Homo sapiens zinc finger protein 206 (ZNF206), mRNA. /// ENST00000252463 // upstream // 8035 // --- // --- //	ZNF206	ZNF206, Homo sapiens zinc finger protein 206 (ZNF206), p13.3
SNP_A-2087516	actgcctgagcaaagg[A/C]cctaggttgggagcat	A	C	// 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 377005 // --- // --- // --- //	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q16.3
SNP_A-2175074	cacagtcctggtttac[A/G]gagtaagagtaagcgc	A	G	Homo sapiens pleckstrin homology domain containing, family A member 2 (PLEKHA7), mRNA. /// ENST00000355661 // intron // 0 // --- // --- // --- // ---	PLEKHA7	PLEKHA7, Homo sapiens pleckstrin homology domain containing, family A member 2 (PLEKHA7), p15.1
SNP_A-2176886	caccgggaccgcttca[A/T]ggagcagtttacaaag	A	T	sapiens huntingtin interacting protein 1 (HIP1), mRNA. /// ENST00000336926 // CDS // 0 // --- // --- // --- // ---	HIP1	HIP1, Homo sapiens huntingtin interacting protein 1 (HIP1), q11.23
SNP_A-2199833	ccaaacgagtaagata[C/T]attgatcttgtggtaa	C	T	// 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// NM_181354 // upstream // 435707 //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2221721	cctttgttgaagtaac[C/G]atacccccagggcaatg	C	G	51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 606749 //	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-2119009	agtagacacattgaag[A/G]ataaaatttaaagctg	A	G	1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 274463 //	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2145102	atgcaacaagaagaaa[A/C]tgagcaacccaattaa	A	C	// 79888 // Homo sapiens hypothetical protein FLJ12443 (FLJ12443), mRNA. /// NM_032479 // downstream // 59412 //	FLJ12443	FLJ12443, Homo sapiens hypothetical protein FLJ12443 (FLJ12443), p15.33
SNP_A-2147052	atggaagattttgtcc[A/G]acagaatacaatttaa	A	G	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1726326	cacacagcaaggagcaaagcgataa[C/T]gagaacccaagctccccagcgtccc	C	T	// annexin A6 /// NM_004033 // upstream // 9752 // Hs.412117 // ANXA6 // 309 // annexin A6 /// NM_015621 // downstream //	ANXA6	ANXA6 , rs366307, annexin A6 ,q33.1
SNP_A-1733762	aagccaatctcctccaggattcaaa[A/G]ccttcataagcaccgtactttacac	A	G	NM_002372 // intron // 0 // Hs.439599 // MAN2A1 // 4124 // mannosidase, alpha, class 2A, member 1	MAN2A1	MAN2A1 , rs2249413, mannosidase, alpha, class 2A, member 1,q21.3
SNP_A-1805495	gtccagagctgctgca[A/C]gactctaactggctct	A	C	NM_000197 // downstream // 46341 // Hs.477 // HSD17B3 // 3293 // Homo sapiens hydroxysteroid (17-beta)	-	q22.32
SNP_A-1806475	gtcgcttctaatgaga[A/G]ataatgatgtcaaggt	A	G	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 176917 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-1792881	ggtaatgggatcctgc[A/G]ccttctgttccccttc	A	G	// 219738 // Homo sapiens chromosome 10 open reading frame 35 (C10orf35), mRNA. /// NM_080806 // upstream //	C10orf35	C10orf35, Homo sapiens chromosome 10 open reading frame 35 (C10orf35), q22.1
SNP_A-1818389	gttcttatccttacta[C/G]cattgtcttatcttac	C	G	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 169897 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-1840933	tagctgaaatttccaa[C/T]aaaacgcagtcagagc	C	T	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // --- // --- // --- // ---	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-1909389	tgtattataaacgtta[C/T]gcagttaatgataatt	C	T	// 3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. /// ENST00000315260 //	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.1
SNP_A-1919121	ttaactgcatttctca[C/T]gaagaataaatacttc	C	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-1905364	tggtaacaggagaaga[C/T]gcaaaaatagtaaaat	C	T	57569 // Homo sapiens Rho GTPase activating protein 20 (ARHGAP20), mRNA. /// ENST00000260283 // upstream //	ARHGAP20	ARHGAP20, Homo sapiens Rho GTPase activating protein 20 (ARHGAP20), q23.1
SNP_A-1927241	ttcaaaaaatgtgctc[A/G]ccaaaagacaatatac	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 374283 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1922141	ttacttactcaatgaa[C/G]tgcaatgccaagtcaa	C	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1890266	tgatcatactgcttgg[A/G]catctcttgtttgggg	A	G	57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// NM_152749 // upstream // 33179 // Hs.489603 //	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. q22.3
SNP_A-1874457	tctccccagccaaaaa[G/T]gaagtccaggtttctt	G	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-1873893	tctcagtccaaactct[C/T]acccaccatattgtat	C	T	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-1879765	tcttcattctttatta[C/T]caaactctccctgact	C	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 992361 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1952738	tttctgtcgcatttta[C/T]gttgtaatggaaaaga	C	T	Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// ENST00000230859 // intron // 0 // --- // --- // --- // ---	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1989308	aattgggaaataaaac[C/T]aggctggtggccaaga	C	T	11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// ENST00000339492 // upstream //	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1970568	ttgcaataatactgac[A/G]aaggtgttgcctgaga	A	G	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA. /// ENST00000291560 // intron // 0 // --- // --- // --- // ---	HSF2BP	HSF2BP, Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), q22.3
SNP_A-1817737	gttccctttggctcca[C/G]gtaagatctaccaggg	C	G	// 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 849741 // Hs.120831 // TNT // 162083 // Homo	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-1825780	taaatctcagtttacc[C/T]atatctacgctttctg	C	T	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 573627 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-1866665	tcccctatctctttaa[C/T]cagtttaatcaacgtt	C	T	/// ENST00000281516 // upstream // 94159 // --- // --- // --- // ---	-	q14.11
SNP_A-1795808	ggtggcagagacataa[A/T]cttgatgacatgattg	A	T	Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST00000335473 // intron // 0 // --- // --- // --- // ---	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1707870	aatgtaaatgtgtgtcatactatac[A/G]catttttgtaggcttgcttttgtct	A	G	25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 804693 // Hs.317659 // DPPA4 // 55211 //	PVRL3	PVRL3 , rs4131413, poliovirus receptor-related 3 ,q13.13
SNP_A-1701311	atcaatcactaaagattgctatgtc[C/G]aaagaaataccttttatttcctttga	C	G	NM_080745 // intron // 0 // Hs.169810 // RNF36 // 140691 // ring finger protein 36	RNF36	RNF36 , rs2123149, ring finger protein 36,q21.1
SNP_A-2164305	caaaatattccgtggc[C/T]agtgttgcaaaagttt	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2117173	aggtgccaggtagaga[A/C]agctcagaaatggcat	A	C	3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 287834 // Hs.105103 //	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-2129781	atacatacacaaggta[A/G]gcctaggcacccattt	A	G	-- /// ENST00000359634 // upstream // 836777 // --- // --- // --- // --- /// ENST00000359181 // upstream // 836777 // --- // --- // -	-	q32.3
SNP_A-2206872	ccatggatccatggaa[A/C]ttcactttcaaaatgc	A	C	ENST00000359247 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2205777	ccatacaaacatagcc[A/G]aaaaaatagagtaaca	A	G	Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // --- // --- // --- // --- ///	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3), p13.3
SNP_A-2168528	caagaaaagtctctca[A/T]ggtcattactatactt	A	T	Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// ENST00000310454 //	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-2197507	cattcctggtttttcc[A/G]ctaaccagctctgcct	A	G	2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// NM_152715 // upstream // 5280 //	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2082958	acgtgcactgagtgcc[A/G]gctgtgtgtaagatac	A	G	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2072521	acagcatttgaaggta[A/G]ccatgtctgctttgtg	A	G	// 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 71862 // Hs.436996 //	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-2060316	aatgaataacccagaa[C/T]tgtagttagctaactg	C	T	2048 // Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // downstream // 53589 // Hs.523329	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-2047941	aagcaaattcatcttg[G/T]aataggaaaaaaatcc	G	T	ENST00000256925 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-2034321	aaatcctgcgtgctta[A/C]gatgggaaatcggcct	A	C	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2043121	aactgatgcgtataca[C/T]ccacatatgaacccag	C	T	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, mRNA. /// NM_201572 // intron // 0 // Hs.59093 // CACNB2 // 783 //	CACNB2	CACNB2, Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, p12.33
SNP_A-2019396	gtaaatccaacaatca[A/G]gactgtaattttacca	A	G	Homo sapiens chromosome 21 open reading frame 107 (C21orf107), transcript variant 1, mRNA. /// NM_033656 // intron // 0 // Hs.314338 // WDR9 // 54014 // Homo sapiens	WDR9	WDR9, Homo sapiens chromosome 21 open reading frame 107 (C21orf107), transcript variant 1, q22.2
SNP_A-1997127	caggaaaatctgatca[A/T]ccctttagtcttcagt	A	T	// Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 27663 // --- // --- // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1994516	gaatttatgagggatc[A/G]aaaataaagagcaata	A	G	23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2250656	cttataagcttttggg[A/C]aataactaacctatac	A	C	/// ENST00000357663 // downstream // 93366 // --- // --- // ---	-	q22.2
SNP_A-2300688	gcctgctgattttcta[A/C]attgtcccatatatac	A	C	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2294428	gcagtaaagtgctaag[C/T]ctgaggagataccagc	C	T	FLJ32028 // 201799 // Homo sapiens hypothetical protein FLJ32028 (FLJ32028), mRNA. /// ENST00000304389 //	FLJ32028	FLJ32028, Homo sapiens hypothetical protein FLJ32028 (FLJ32028), q31.3
SNP_A-2312245	ggacagtctcctggac[A/G]aggagtttccagctgc	A	G	Homo sapiens synaptonemal complex protein SC65 (SC65), mRNA. /// ENST00000269532 // 3UTR // 0 // --- // --- // --- // ---	SC65	SC65, Homo sapiens synaptonemal complex protein SC65 (SC65), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255834	ctttaaaaaacagcag[A/G]cagaaaaattctaaac	A	G	SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 40996 // --- // --- // --- // ---	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31
SNP_A-2238037	aacagtttgattatgc[A/T]atgcttttgttattgt	A	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-2284856	gatccaatcaacatca[A/G]ggagactcacagagtg	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2257460 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1991070	gtgaaacacaaaaaca[C/G]tgagaatggagtaaaa	C	G	10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream //	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.32
SNP_A-1991888	atctgaggacatttaa[A/C]aatatgcactttatcg	A	C	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA. /// ENST00000339765 // intron // 0 // --- // --- // --- // --- /// ENST00000349830 // intron //	ARHGEF10	ARHGEF10, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), p23.3
SNP_A-2040886	aaccctaaggatatgc[C/T]acagaggctgctaaca	C	T	11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // upstream //	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2064581	aattctaaccaaagga[A/G]tcaagagtcagtagcc	A	G	84333 // Homo sapiens ring finger protein (C3HC4 type) 159 (RNF159), mRNA. /// NM_032373 // downstream // 19723 //	PCGF5	PCGF5, Homo sapiens ring finger protein (C3HC4 type) 159 (RNF159), q23.32
SNP_A-2095835	agacagagaagtttca[G/T]cctggggagaggtatt	G	T	// Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// NM_015199 // intron // 0 //	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-2106468	agcctacagaacccgg[A/C]agccgtaggggaattc	A	C	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 156321 // Hs.17441	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-2203691	ccagactgggaaaaaa[C/T]gtttgaaatgcaaagg	C	T	338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 100961 // Hs.193268 // MTAP //	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2114204	agggaacatttggatg[A/C]agtaagacaccttagc	A	C	HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream //	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2154800	attcaagacatgttgg[A/G]cacctgatcaactcta	A	G	sapiens S-phase kinase-associated protein 2 (p45) (SKP2), transcript variant 1, mRNA. /// NM_032637 // intron // 0 // Hs.23348 // SKP2 // 6502 // Homo sapiens S-phase kinase-	SKP2	SKP2, Homo sapiens S-phase kinase-associated protein 2 (p45) (SKP2), transcript variant 1, p13.2
SNP_A-1667050	gcagacacacaggtaccagatcgac[A/G]gcagagcaggccagttagtgcctgg	A	G	4023 // lipoprotein lipase /// NM_003053 // downstream // 14669 // Hs.158322 // SLC18A1 // 6570 // solute carrier family	LPL	LPL , rs10503672, lipoprotein lipase ,p21.3
SNP_A-1731553	tttgaatagatttctcgtgtgttca[C/G]attagtcttttcccagttagtttgt	C	G	NM_022065 // intron // 0 // Hs.16063 // THADA // 63892 // thyroid adenoma associated	THADA	THADA , rs10495898, thyroid adenoma associated,p21
SNP_A-1750001	attgtagcttctctttgccattgtc[A/G]ctctttatctgtatctttatatctc	A	G	5912 // RAP2B, member of RAS oncogene family /// NM_015595 // upstream // 271753 // Hs.240845 //	RAP2B	RAP2B , rs10513451, RAP2B, member of RAS oncogene family ,q25.2
SNP_A-1752115	ggtcctcattccagaaatgccctat[A/G]aactcgtgattctctagtagacatc	A	G	NM_022748 // downstream // 168929 // Hs.12210 // TENS1 // 64759 // tensin-like SH2 domain containing 1	-	- , rs10499653, - ,p13
SNP_A-1795917	ggtggggaaacaatag[C/T]attagtagttggaaga	C	T	9844 // Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 2, mRNA. /// NM_014800 // upstream // 121907 // Hs.304578 // ELMO1	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 2, p14.1
SNP_A-1790603	ggggcggcatcagtaa[C/T]gttacatattgcttag	C	T	ENST00000265274 // intron // 0 // --- // --- // --- // --- /// ENST00000360069 // intron // 0 // --- // --- // --- // --- ///	-	q25.2
SNP_A-1813989	gtgtcagtcaaaatag[G/T]ctagattatgctgcag	G	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 597651 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1807835	gtcttacacaaactaa[C/T]catgtaactcaaggag	C	T	6251 // Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, mRNA. /// NM_012425 // downstream //	RSU1	RSU1, Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, p13
SNP_A-1872522	tctaggaacaatgctc[A/G]ccttttgtaacttttt	A	G	Homo sapiens zinc finger protein 533 (ZNF533), mRNA. /// ENST00000360320 // intron // 0 // --- // --- // --- // --- ///	ZNF533	ZNF533, Homo sapiens zinc finger protein 533 (ZNF533), q31.2
SNP_A-1872623	tctaggttcacatata[C/T]taggagttaaaacact	C	T	83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-1863196	tcatttcctgtagata[C/T]ataaggtacccagaag	C	T	// 83755 // Homo sapiens keratin associated protein 4-12 (KRTAP4-12), mRNA. /// NM_033188 // upstream // 1656 //	KRTAP4-12	KRTAP4-12, Homo sapiens keratin associated protein 4-12 (KRTAP4-12), q21.2
SNP_A-1846660	tatattttcaagttta[A/G]aagtgatcagtctaca	A	G	Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, mRNA. /// NM_172059 // intron // 0 //	EYA1	EYA1, Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, q13.3
SNP_A-1970697	tctgctctcatgaggc[G/T]cctgtctagcttgtta	G	T	sapiens HIR histone cell cycle regulation defective homolog A (S. cerevisiae) (HIRA), mRNA. /// ENST00000340170 // intron // 0 // --- // --- // --- // --- /// ENST00000263208 // intron // 0 //	HIRA	HIRA, Homo sapiens HIR histone cell cycle regulation defective homolog A (S. cerevisiae) (HIRA), q11.21
SNP_A-1985815	actgggttgactctga[A/G]aggtttatatcttatt	A	G	29964 // Homo sapiens chromosome 6 open reading frame 49 (C6orf49), mRNA. /// NM_018561 // downstream // 6801 //	C6orf49	C6orf49, Homo sapiens chromosome 6 open reading frame 49 (C6orf49), p21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982813	aactctgctaacgcca[G/T]aatttttaagtcact	G	T	Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000333274 // intron // 0 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1957329	ttttagatttccaaaa[A/C]cttcccttctccacct	A	C	/// ENST00000318905 // downstream // 25805 // --- // --- // --- // --- /// ENST00000304745 // downstream // 25805 // --- // ---	-	q23.1
SNP_A-1883077	tgaaatcatccttggc[A/G]aaaacgtcgataccac	A	G	-- /// ENST00000342900 // downstream // 256738 // --- // --- // -- // --- /// ENST00000321814 // upstream // 28885 // --- // --- //	-	q11.22
SNP_A-1910608	tgtcctctgttcttca[A/C]agtggtaccttaaaga	A	C	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1909474	tgtattggagagcaca[C/T]cgttggatgcttccat	C	T	sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // --- // --- // --- // ---	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-1918254	ttaaagatggctgcaa[A/G]tatctgtatcactccc	A	G	ENST00000284920 // intron // 0 // --- // --- // --- // ---	-	p14.3
SNP_A-1922619	ttagacctgttagacc[G/T]gctgctaaatcttgct	G	T	283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA. /// NM_000999 // upstream // 365822 //	FLJ40319	FLJ40319, Homo sapiens hypothetical protein FLJ40319 (FLJ40319), q25.1
SNP_A-1923971	ttagtgattaaaccag[A/G]actcccaaatcctgtt	A	G	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-1900450	tggagcaagagagcta[A/C]gtaggagggacaagaa	A	C	Homo sapiens hypothetical protein FLJ12118 (FLJ12118), mRNA. /// ENST00000257347 // intron // 0 // --- // --- // --- // ---	FLJ12118	FLJ12118, Homo sapiens hypothetical protein FLJ12118 (FLJ12118), q34
SNP_A-1958048	ttttcagaccaatgga[A/T]cttatctcttaagctc	A	T	CSRP2BP // 57325 // Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, mRNA. /// NM_177926 //	CSRP2BP	CSRP2BP, Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, p11.23
SNP_A-1936555	ttcttgccgtcgtccc[A/G]gagatgcctttggaaa	A	G	// Homo sapiens likely ortholog of mouse gene trap locus 3 (GTL3), mRNA. /// NM_001896 // downstream // 28340 //	GTL3	GTL3, Homo sapiens likely ortholog of mouse gene trap locus 3 (GTL3), q21
SNP_A-1940436	ttgccatgtaagaaaa[C/G]atatacagattttagg	C	G	9205 // Homo sapiens mRNA for ZNF237 protein, minor splice variant (a). /// NM_014242 // upstream // 11193 //	ZNF237	ZNF237, Homo sapiens for ZNF237 protein, minor splice variant (a). ,q12.11
SNP_A-1978428	taaattctcagccttc[C/T]ctaaaaattgcccttа	C	T	51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 303567 //	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1987963	ttacaactattacaaa[C/T]ttcaattcctttcagt	C	T	Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// ENST00000282749 // intron // 0 // --- // --- // --- // ---	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1850571	tattaaggtgagatta[C/T]attgtgcttttattta	C	T	10804 // Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), mRNA. /// NM_006783 // upstream // 75347 //	GJB6	GJB6, Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), q12.11
SNP_A-1821894	gttttatctccaatca[A/G]tctttgccaccttagc	A	G	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 325225 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1837732	tactttggaattatag[A/G]agacttggtgagtcac	A	G	/// ENST00000251675 // downstream // 354665 // --- // --- // --- // --- /// ENST00000360855 // downstream // 354695 // --- // ---	-	q32.3
SNP_A-1810107	gtgatattgcagaaaa[A/C]taatccatgatgtatc	A	C	57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 906431 //	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.31
SNP_A-1801572	gtaggtggtgtttgct[C/T]aatgaagaagggaaaa	C	T	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1731115	tatgtacttttctatgttcttaatc[C/T]gagtagatgatggcctgccacgacg	C	T	FLJ11175 // 55784 // hypothetical protein FLJ11175 /// NM_021005 // upstream // 1611407 // Hs.347991 // NR2F2 //	FLJ11175	FLJ11175 , rs10520762, hypothetical protein FLJ11175 ,q26.2
SNP_A-1715235	aggcagatttcagccgaacataaat[A/G]actgacaggagctcttcatggtcca	A	G	NM_015071 // intron // 0 // Hs.132942 // GRAF // 23092 // GTPase regulator associated with focal adhesion kinase pp125(FAK)	GRAF	GRAF , rs728465, GTPase regulator associated with focal adhesion kinase pp125(FAK),q31.3
SNP_A-1664712	gaggctgggaaatgtagtctctacc[C/T]tgaccatgtgccttgttttaaaact	C	T	like module containing, mucin-like, hormone receptor-like 3 /// NM_152939 // intron // 0 // Hs.438468 // EMR3 // 84658 // egf-	EMR3	EMR3 , rs726788, egf-like module containing, mucin-like, hormone receptor-like 3 ,p13.12
SNP_A-2157010	attcttttaatttcac[A/G]cagatgtttcttctga	A	G	81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 154836 //	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-2165665	caaaggcagtcaccac[A/G]aagttctcaggggcac	A	G	Homo sapiens NDRG family member 4 (NDRG4), mRNA. /// NM_020465 // 3UTR // 0 // Hs.322430 // NDRG4 // 65009 //	NDRG4	NDRG4, Homo sapiens NDRG family member 4 (NDRG4), q21
SNP_A-2149946	atgtcaggttgtgata[C/T]gtgctaagaagataaa	C	T	63971 // Homo sapiens kinesin family member 13A (KIF13A), mRNA. /// NM_198586 // downstream // 41399 // Hs.348351	KIF13A	KIF13A, Homo sapiens kinesin family member 13A (KIF13A), p22.3
SNP_A-2140660	atctctcctcttaatc[C/T]cctaattcttgcatac	C	T	Homo sapiens WW domain containing E3 ubiquitin protein ligase 1 (WWP1), mRNA. /// ENST00000265428 // intron // 0	WWP1	WWP1, Homo sapiens WW domain containing E3 ubiquitin protein ligase 1 (WWP1), q21.3
SNP_A-2128651	ataatattccattgga[G/T]acatatagtaagtgcc	G	T	Homo sapiens regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1), mRNA. /// ENST00000258646 // intron // 0 // --- // --- // ---	RCBTB1	RCBTB1, Homo sapiens regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1), q14.2

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123758	agtgtttccattagaa[A/G]tatcttcaggacatag	A	G	// 26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 437519 //	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13
SNP_A-2136304	atcacaagtaatgcta[A/G]ctatttgacatgatgg	A	G	ENST00000281496 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-2203041	ccactgagaggacaga[A/G]ccaagtgattggagga	A	G	Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA), member 11 (SLC6A11), mRNA. /// ENST00000254488 // intron // 0 // --- // --- // --- // --- ///	SLC6A11	SLC6A11, Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA), member 11 (SLC6A11), p25.3
SNP_A-2211612	ccctcagttagcggat[A/G]ataaatgctgtcagga	A	G	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-2219956	gaacctagaagacaaa[C/G]aggtcactagctgtcc	C	G	Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// ENST00000267460 // intron // 0 // --- // --- // --- // ---	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2196152	catgtgctcatgagaa[C/T]gaaatcaacaaataac	C	T	// --- /// ENST00000345111 // upstream // 9256 // --- // --- // ---	-	q24.32
SNP_A-2171954	caatgccagagtgaac[A/G]acctctaatgttctct	A	G	SLC24A2 // 25769 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	SLC24A2	SLC24A2, Homo sapiens solute carrier family 24 (sodium p22.1
SNP_A-2101707	agatgcagcaatttac[G/T]cagattcacgaagacc	G	T	Homo sapiens RAB8B, member RAS oncogene family (RAB8B), mRNA. /// ENST00000321437 // intron // 0 // --- // ---	RAB8B	RAB8B, Homo sapiens RAB8B, member RAS oncogene family (RAB8B), q22.2
SNP_A-2083469	actaaggacatgccca[A/G]atatcctgaagttggg	A	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 200528 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2066140	aatttgtgcagtgaag[C/T]actagaggagagcttt	C	T	327657 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 (SERPINA9), mRNA /// NM_173850 // downstream // 9509 // Hs.99476 // SERPINA	SERPINA9	SERPINA9, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 (SERPINA9), q32.13
SNP_A-2062854	aatgtggatgcaacta[A/G]aggaccttatgtgaag	A	G	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 64454 // --- //	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2072031	acagagtaaaatacta[A/C]ggagtaaagagacata	A	C	138805 // Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), mRNA. /// ENST00000334726 // downstream // 16205 // --- // --- // --- // --	OR13F1	OR13F1, Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), q31.1
SNP_A-2057757	aatatgtgtatttta[A/G]aagtaccagttgctac	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1294478 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2034600	aaatctttaacaggaa[A/G]acaaaagggccacttc	A	G	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 430726 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2269641	gacaacaaattgacag[A/G]agctaatgaaagcggt	A	G	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-2227957	ctacctggctggggaa[C/T]gggaggcttatcttct	C	T	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 233681 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2230720	ctatgaatctggttca[G/T]tcactctaatcaatac	G	T	54872 // Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /// NM_000283 // upstream // 66511 //	GPI7	GPI7, Homo sapiens hypothetical protein FLJ20265 (FLJ20265), p16.3
SNP_A-2292792	gcactttcacttttca[C/T]gatttaatgccctctc	C	T	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2288803	gattgttagtccccca[C/T]gggttaagtggcaatg	C	T	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 311007 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-2289849	gcaaaccatttaacca[C/T]tctaagtctcagaata	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 367684 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2300154	gcctccactcctttga[G/T]gtcttcttcaactgca	G	T	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-2299612	tatttgctgtggaaga[C/G]aatgtgcttgacccag	C	G	Homo sapiens KIAA1199 (KIAA1199), mRNA. /// ENST00000220244 // intron // 0 // --- // --- // --- // --- ///	KIAA1199	KIAA1199, Homo sapiens KIAA1199 (KIAA1199), q25.1
SNP_A-2228738	ctagactctaataaaa[A/C]gtatgctgtaattctt	A	C	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1767869 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2229054	ctagcatgatacctca[C/T]acatagaaacctctca	C	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 517493	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2244258	ctggaaatgcaggaaa[C/G]cactcaactcctttga	C	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3000672 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2261410	gaaagctccacatcaa[C/T]tggattcccacttctt	C	T	11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2285145	gatctagaaactgtta[A/G]aggccaaataaacttg	A	G	3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 //	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2031448	aaaggtaggctaaaaa[C/T]gaatgaaaggaaaacg	C	T	57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 347810 // --- // ---	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-1992245	aaaatttttgcacctg[C/T]attgataaccaatgtt	C	T	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1996740	gtttctctggttttcc[A/G]gaaacatgatgattag	A	G	Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // --- // ---	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-2003242	gacccagcctcattca[C/T]tcatctgtttgcttct	C	T	ENST00000332738 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-2069834	acacagagggccttaa[A/G]tcgttcattcacctct	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 423187 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2174410	cacagaagagatctga[A/G]aggtaaagtcttggca	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2122576	agtgcttatccgatct[C/T]acaggtaaactgatgc	C	T	Homo sapiens rhomboid, veinlet-like 7 (Drosophila) (RHBDL7), mRNA. /// ENST00000006777 // intron // 0 // --- // -	RHBDL7	RHBDL7, Homo sapiens rhomboid, veinlet-like 7 (Drosophila) (RHBDL7), q11.23
SNP_A-2150796	atgtggaaagatccca[A/C]cttttggagctaccaa	A	C	// 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 183798 // Hs.369438 // ETS1 //	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.3
SNP_A-2161497	atttgctgagttacta[G/T]gcaaatttcacaatta	G	T	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 784030 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2155141	attcagatgatttgta[A/G]ggtctgttgctctgat	A	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1663786	atcagcctgtcagattgtttactgc[C/T]gaaatcctagcctaacattcatcta	C	T	6925 // transcription factor 4 /// NM_025214 // upstream // 16962 // Hs.30315 // SE57-1 // 80323 // CTCL tumor antigen	TCF4	TCF4 , rs10502992, transcription factor 4 ,q21.2
SNP_A-1680634	aactgtgtagtactaatagcccccа[C/T]atttgagcactccaaatacgtgata	C	T	27022 // forkhead box D3 /// NM_013339 // upstream // 34577 // Hs.80042 // ALG6 // 29929 // asparagine-linked	FOXD3	FOXD3 , rs10489494, forkhead box D3 ,p31.3
SNP_A-1744837	acaacttgtttcatactgcctctta[C/T]aggaataacaccaaggacaacccca	C	T	// 55816 // docking protein 5 /// NM_080617 // downstream // 41603 // Hs.126141 // CBLNL1 // 140689 // cerebellin	DOK5	DOK5 , rs10485802, docking protein 5 ,q13.31
SNP_A-1753455	tttcccgtgtccaatatttcattcc[A/G]cttggttgtgggacaaggacccaga	A	G	clone IMAGE:5277680, partial cds /// NM_030932 // downstream // 837969 // Hs.122164 // DIAPH3 // 81624 //	-	- , rs1417315, CDNA clone IMAGE:5277680, partial cds ,q21.2
SNP_A-1790809	gggggattaaaacaaa[G/T]ttatacagcatagggc	G	T	6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 10389 // --- // ---	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-1785697	ggctctaaagtggaaa[A/T]ttcaccaagttctttt	A	T	Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1845669	tataggactgaggtag[A/G]cagtggaatgttacag	A	G	55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// NM_013349 // upstream // 2867 //	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-1845624	tatagctaaggaaaat[G/T]aaggccgtgaaataat	G	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2540543 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1871696	tctaatcacaaaggaa[A/G]atatcactgaacaatg	A	G	4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 //	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-1869542	tcctgtttgctcccac[A/G]ctgtctcatctagtac	A	G	81696 // Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), mRNA. /// ENST00000230221 //	OR5V1	OR5V1, Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), p22.1
SNP_A-1870008	tccttgatgagctgag[A/T]cacgaggcccagcaag	A	T	200407 // Homo sapiens cellular repressor of E1A-stimulated genes 2 (CREG2), mRNA. /// NM_207403 // downstream //	CREG2	CREG2, Homo sapiens cellular repressor of E1A-stimulated genes 2 (CREG2), q11.2
SNP_A-1988051	agatcgttcttaacac[A/G]catttcacagactgct	A	G	128061 // Homo sapiens hypothetical protein DKFZp547B1713 (DKFZp547B1713), mRNA. /// ENST00000318906 // 3UTR // 0 // --- // --- // --- // ---	DKFZp547B1713	DKFZp547B1713, Homo sapiens hypothetical protein DKFZp547B1713 (DKFZp547B1713), q42.2
SNP_A-1986688	gcctaatagacctaca[A/G]ctgggcaggttacact	A	G	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 139608 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1985613	atgggtggtaatcaaa[C/T]acaagacaaattaatc	C	T	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 767534 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-1978300	cacaaactacacctaa[A/G]cacagtgcctcagaca	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 674457 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1944611	ttgtgaatagacccat[C/T]acaagacgagattaaa	C	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1044051 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1951834	tttctaacagaagtta[C/T]gttaaagccaggcatc	C	T	Homo sapiens pleckstrin homology domain interacting protein (PHIP), mRNA. /// ENST00000275034 // intron // 0 // --- // --- //	PHIP	PHIP, Homo sapiens pleckstrin homology domain interacting protein (PHIP), q14.1
SNP_A-1948282	tttaggaggaaactga[A/G]atatttttacaatcc	A	G	Homo sapiens annexin A10 (ANXA10), mRNA. /// ENST00000359299 // intron // 0 // --- // --- // --- // ---	ANXA10	ANXA10, Homo sapiens annexin A10 (ANXA10), q32.3
SNP_A-1902258	tggccagctacgttca[A/G]agttcctggctccctt	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1900131	tggactggagtttgaa[C/T]gaggtaacgatcaaga	C	T	4209 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D) (MEF2D), mRNA. /// NM_178229 // downstream // 14874 //	MEF2D	MEF2D, Homo sapiens MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D) (MEF2D), q22
SNP_A-1889841	tgatactccacagcaa[A/G]cagagaagagctattg	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 500442 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1889621	tgataaagctagttaa[A/G]cactatgcatccaata	A	G	22932 // Homo sapiens POM (POM121 homolog, rat) and ZP3 fusion (POMZP3), transcript variant 2, mRNA. /// NM_152992 // upstream // 185146 // Hs.488877 // POMZP3 //	POMZP3	POMZP3, Homo sapiens POM (POM121 homolog, rat) and ZP3 fusion (POMZP3), transcript variant 2, q11.23
SNP_A-1900124	tggactgcagctatca[C/T]tgacctgaaactggag	C	T	57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 271958 // Hs.160373 // KIAA1383 // 54627 //	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1925825	ttatggacacagacaa[A/G]cctgacaaaattgcat	A	G	Homo sapiens chromosome 20 open reading frame 100 (C20orf100), mRNA. /// AK055135 // intron // 0 // Hs.26608 //	C20orf100	C20orf100, Homo sapiens chromosome 20 open reading frame 100 (C20orf100), q13.12
SNP_A-1969254	atctaaaagcatctta[C/T]gaatggaaagaatatg	C	T	5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 //	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, q21.1
SNP_A-1963662	tacttccagcttagaa[C/T]gtttatttcagccttg	C	T	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 192854 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1857560	tcactcccagcctctc[G/T]ctgtcctcactttgca	G	T	Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// ENST00000344450 // intron // 0 // --- // --- // --- // ---	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3
SNP_A-1841311	taggaaggaggcagaa[A/G]ttatcgctgggattga	A	G	Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 //	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-1835416	tacctctgcccctcga[C/T]ggcaacaacaattctg	C	T	Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // --- // --- // --- // --- /// ENST00000287878 // intron //	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-1818672	gttgaatgaacagcca[A/G]agcaaaatccttttat	A	G	128338 // Homo sapiens hypothetical protein MGC54289 (MGC54289), mRNA. /// ENST00000286692 // intron // 0 // ---	MGC54289	MGC54289, Homo sapiens hypothetical protein MGC54289 (MGC54289), p13.3
SNP_A-1792025	gggtgggagatgaaga[A/C]ataaagagtggatgca	A	C	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 254696 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-1796706	ggttatcctgataacc[A/G]aagacttggaaagaca	A	G	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1690485	tgcaacacgcagaagcagaataata[C/T]ggagttggctgggtctgtctgagga	C	T	NM_018629 // upstream // 668920 // - // - // - // -	-	- , rs345006, -,q24
SNP_A-1664522	tttctaaaacatattttgacaccgt[A/G]aatacactgggtttatattaatgag	A	G	8787 // regulator of G-protein signalling 9 /// NM_004655 // downstream // 128047 // Hs.127337 // AXIN2 // 8313 // axin 2	RGS9	RGS9 , rs10491187, regulator of G-protein signalling 9 ,q24.1
SNP_A-2114700	agggatccctgtgata[A/G]aaataatctgtatatt	A	G	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2109505	aggaaaactgttaaaa[A/G]tgctcaaacaatcagg	A	G	3002 // Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA. /// NM_014178 // downstream // 35586 // Hs.508958 // STXBP6	GZMB	GZMB, Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), q12
SNP_A-2172228	caatgtgagaacagat[A/G]atacaagtacacattt	A	G	51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 465113 //	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-2188875	cagtggttataatatg[A/C]aaatgtctcctaagca	A	C	OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 //	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-2223309	cgctacacaatttttta[C/G]aagtaaatacaggaga	C	G	Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 3 (PSCD3), mRNA. /// ENST00000350796 // intron	PSCD3	PSCD3, Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 3 (PSCD3), p22.1
SNP_A-2072401	ttaaaaacggcattga[A/C]gtctttattacagtca	A	C	// 27345 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 4 (KCNMB4), mRNA. /// NM_002837 // downstream // 87185 //	KCNMB4	KCNMB4, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 4 (KCNMB4), q15
SNP_A-2053547	aagtgctagggtagcc[C/T]gaagacattttcagaa	C	T	// 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// NM_002127 // downstream //	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101183	agatcattggcaaaag[C/T]atggccggaatttctt	C	T	sapiens phosphoglucomutase 1 (PGM1), mRNA. /// ENST00000006941 // CDS // 0 // --- // --- // --- // --- ///	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2106860	agccttaggagcaaaa[G/T]gtaatgtattgctttt	G	T	// Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // intron // 0 // Hs.354013 // SLC26A7 // 115111 // Homo	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-1990171	ctataattccagatga[C/G]caggggcgatgtatc	C	G	sapiens huntingtin interacting protein 1 (HIP1), mRNA. /// ENST00000336926 // intron // 0 // --- // --- // --- // ---	HIP1	HIP1, Homo sapiens huntingtin interacting protein 1 (HIP1), q11.23
SNP_A-2017157	gttaagtactcgataa[C/T]aggaagataattttgg	C	T	116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// NM_006988 // downstream // 80402 //	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2012892	ccacttgctcgatcac[A/C]ggaatgaaaggctggc	A	C	93979 // Homo sapiens carboxypeptidase A5 (CPA5), mRNA. /// NM_080385 // downstream // 11345 // Hs.144699	CPA5	CPA5, Homo sapiens carboxypeptidase A5 (CPA5), q32.2
SNP_A-2025773	aaaatgctgctgttta[C/T]agactgaatttctttt	C	T	114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream //	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-2036387	aaattctaatcatacc[G/T]aagggagtctaccagg	G	T	8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 108466 // --- // --- // --- // ---	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2041074	aacctaacaaaagcga[A/T]tagagaaactggcaaa	A	T	121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. ///	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2276995	gagatcttctaatata[C/T]ggagtttatattgtag	C	T	// 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 382887 //	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-2278636	gagctggaagtgctag[C/T]cattcattcattaagt	C	T	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2296232	gcattgacttaaatag[C/G]aactactatagtggga	C	G	79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 648129 //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2313522	ggagagtgacagaaaa[A/G]catatctctattctga	A	G	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 986505 // Hs.116471 // CDH11	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2307635	gcttcatcttacgcca[C/T]gctccctcagtagatt	C	T	ENST00000298453 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-2040790	aacccatgaagtcaaa[C/T]tcaagtggcgtcaggg	C	T	9788 // Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// NM_152412 // upstream // 125403 // Hs.175350 //	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2032233	aaagtgtggttcccca[A/G]actagcagcaacggca	A	G	Homo sapiens chromodomain protein, Y-like (CDYL), transcript variant 3, mRNA. /// NM_004824 // intron // 0 //	CDYL	CDYL, Homo sapiens chromodomain protein, Y-like (CDYL), transcript variant 3, p25.1
SNP_A-2013042	aaaggaacccgctatg[A/G]atacatgaacagcttg	A	G	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2018060	ctagtctactttcaag[A/G]ccttaaattggaagtt	A	G	Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// ENST00000270112 // intron // 0 // -	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2012077	ttagaaatccatgcaa[A/G]tctcactaggctaaaa	A	G	// 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // upstream //	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-2010179	gtgattgtaaaattca[A/G]ctgactgtaaaatgca	A	G	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2001579	tgagtaaatcagccaa[C/G]aatctctgccttagac	C	G	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2097647	agagaatgtcagtcac[C/T]ggtaactattataacc	C	T	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2091054	actttgaggggttact[C/T]aataggcataattgta	C	T	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 5885 // Hs.89404 // MSX2 // 4488	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-2051716	aaggtcaaaactaacc[A/G]aatggccatatcaatc	A	G	OR2W3 // 343171 // Homo sapiens olfactory receptor, family 2, subfamily W, member 3 (OR2W3), mRNA. ///	OR2W3	OR2W3, Homo sapiens olfactory receptor, family 2, subfamily W, member 3 (OR2W3), q44
SNP_A-2050773	aaggcatgagagaaca[C/T]atggctgccacaccta	C	T	55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 93812 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2064465	aattccatgaagacaa[C/T]gtataatgttttcaac	C	T	Homo sapiens hypothetical protein FLJ20203 (FLJ20203), mRNA. /// ENST00000361040 // intron // 0 // --- // --- // --- // ---	FLJ20203	FLJ20203, Homo sapiens hypothetical protein FLJ20203 (FLJ20203), q22
SNP_A-2221112	ccttgtcttttcaccc[A/C]acttgctcgttcagtc	A	C	22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 64382 //	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2219676	ccttaacaggagctgc[A/G]aaggataaagagttag	A	G	/// ENST00000356431 // downstream // 90276 // --- // --- // --- // --- /// ENST00000331425 // downstream // 90267 // --- // ---	-	p11.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189493	cagttgtttagaccaa[A/G]atccttagaattatct	A	G	80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2196376	catgttcatccatcta[A/G]agctctttccattagc	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 489878 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2194758	catgcccgaagttaga[C/T]aggcttagatgaccca	C	T	57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// NM_006420 // upstream // 78651 // Hs.62578 // ARFGEF2	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-2110749	aggacctgttgttatc[A/G]caaggcaactggggag	A	G	Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000265641 // intron // 0 // --- // --- // --- // ---	CPT1A	CPT1A, Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A), nuclear gene encoding mitochondrial protein, q13.3
SNP_A-1801383	gtaggatctataaagc[A/T]ctcattgctaatcagt	A	T	// 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 354796 // Hs.464442 // C18orf2 // 56651 //	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-1873048	tctatggataatggag[A/T]acacgctcagctcttc	A	T	Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000350110 // intron // 0 // --- // --- // --- // --- ///	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1860788	tcataagtggtataag[G/T]caagtgatttattatg	G	T	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 330789 // --- // --- // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-1965082	gattgttctgcttgac[C/T]aaaatctcctctgtgg	C	T	/// ENST00000355063 // upstream // 501564 // --- // --- // --- // -	-	q22.1
SNP_A-1970262	aaaccaaaatcaaaac[A/G]aagaagcaggaaaaaa	A	G	NM_000411 // intron // 0 // Hs.371350 // HLCS // 3141 // Homo sapiens holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase) (HLCS), mRNA. /// ENST00000336648 // intron // 0 // --- // --- // --- // ---	HLCS	HLCS, Homo sapiens holocarboxylase synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase) (HLCS), q22.13
SNP_A-1979007	ccatagaacaaccaaa[A/C]aaaacgcagaggctga	A	C	Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// ENST00000235453 // intron // 0 // --- // --- // --- // ---	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-1977883	cattttgcaatcctaa[C/T]agcaacaagcaatagt	C	T	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1985124	gaataacacttaagaa[C/G]tagaatattgccagta	C	G	6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 124988 // Hs.436996 //	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-1931118	ttccatctaatctaac[C/T]agaggtccgtccaaac	C	T	// Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 //	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.2
SNP_A-1913629	tgtgtacgtctacaca[A/G]aattatacatatttta	A	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1905260	tgggttgggagaaagt[A/G]aagttatatggaaaca	A	G	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1890473	tgatctctctccatga[C/T]ctttctttggagctcc	C	T	sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000262340 // intron // 0 // --- // --- // --- // ---	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-1900096	tggactcattataaaa[A/C]agccaggttttccatg	A	C	51167 // Homo sapiens NADPH cytochrome B5 oxidoreductase (NCB5OR), mRNA. /// NM_138409 //	NCB5OR	NCB5OR, Homo sapiens NADPH cytochrome B5 oxidoreductase (NCB5OR), q14.3
SNP_A-1903547	tgggacagcttttgta[C/T]gtgtatgttccatcat	C	T	390792 // Homo sapiens type I hair keratin KA35 (KA35), mRNA. /// NM_033185 // downstream // 23391 // Hs.307025	KA35	KA35, Homo sapiens type I hair keratin KA35 (KA35), q21.2
SNP_A-1918003	ttaaaattcacaaaca[A/C]aagctttcttgttccc	A	C	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1963882	tactgtaagctcagga[A/G]actctgttgatatcaa	A	G	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1941241	ttgctgggcctgacac[G/T]ccaaacagcaaggcag	G	T	// Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 19562 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1864580	tccagagtacaaacaa[A/G]tgaaacagtgtcgcaa	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// ENST00000328843 // CDS // 0 // --- // --	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-1853203	tatttgttagtaatga[C/T]aataatgtccctgctg	C	T	FLJ20156 // 54839 // Homo sapiens hypothetical protein FLJ20156 (FLJ20156), mRNA. /// ENST00000260382 //	FLJ20156	FLJ20156, Homo sapiens hypothetical protein FLJ20156 (FLJ20156), q23
SNP_A-1787138	gggaaatagacaacac[C/T]cctctgctccttgaaa	C	T	// 29789 // Homo sapiens hypothetical protein PTD004 (PTD004), mRNA. /// NM_013341 // downstream // 43063 //	PTD004	PTD004, Homo sapiens hypothetical protein PTD004 (PTD004), q31.1
SNP_A-1708042	tgcatacaataaacgtaaaataaca[A/T]ggttcaagaatgggtggaaaaaaat	A	T	NM_170662 // intron // 0 // Hs.436986 // CBLB // 868 // Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	CBLB , rs10490830, Cas-Br-M (murine) ecotropic retroviral transforming sequence b,q13.11
SNP_A-1780291	ggataaatgaatgcag[A/G]aatatttgaatgctgg	A	G	ENST00000333145 // intron // 0 // --- // --- // --- // ---	-	q13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116992	aggtgacacagagaaa[A/G]gatgtaatttgattga	A	G	1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 228410 // Hs.19904 // CTH // 1491 // Homo	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-2125061	agttgctcttctactc[C/G]aattttcactctctcc	C	G	// 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 66341 //	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2154813	attcaagccaacagta[A/G]gtctcagcctaaatac	A	G	157376 // Homo sapiens hypothetical protein FLJ32770 (FLJ32770), mRNA. /// ENST00000308614 // upstream //	FLJ32770	FLJ32770, Homo sapiens hypothetical protein FLJ32770 (FLJ32770), q24.13
SNP_A-2160989	atttcttattccactg[A/G]attcctggaaaggggac	A	G	/// ENST00000237253 // downstream // 172860 // --- // --- // ---	-	q12
SNP_A-2152068	attaaaaattcagatg[C/G]cagctgggcgaggtgg	C	G	3172 // Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 3, mRNA. /// NM_000457 // upstream // 14816 // Hs.116462 // HNF4A /// 3172 // Homo	HNF4A	HNF4A, Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 3, q13.12
SNP_A-2138937	atccctttaataggta[C/T]ccagtaacacaatgaa	C	T	SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2217604	cctgagcaacagagcc[A/G]ctgggttgtatctagg	A	G	2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 173893 //	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2222087	cgaagggaaaggggaa[C/G]tgaccagtgggatgct	C	G	10892 // Homo sapiens mucosa associated lymphoid tissue lymphoma translocation gene 1 (MALT1), transcript variant 2, mRNA. /// NM_006785 // downstream // 22402 // Hs.180566	MALT1	MALT1, Homo sapiens mucosa associated lymphoid tissue lymphoma translocation gene 1 (MALT1), transcript variant 2, q21.31
SNP_A-2203540	ccagaagtgtcccaga[A/G]aggcctgcagacaatg	A	G	// 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream //	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2063954	aattatccaatcttgg[A/G]cagttctttacagcag	A	G	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2059591	aatctcccggtgaata[C/G]actgtgaagctagaaa	C	G	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-2106500	agcctaggggacata[C/G]aacagtatcagtggtg	C	G	339145 // Homo sapiens FLJ44299 protein (FLJ44299), mRNA. /// NM_153238 // upstream // 96876 // Hs.375058 //	FLJ44299	FLJ44299, Homo sapiens FLJ44299 protein (FLJ44299), q24.1
SNP_A-2004300	tttatttacttggtga[A/C]ctacgtaggccgagtg	A	C	23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 88456 //	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-2042060	aactactgagtttgcc[A/G]ctctatattttcaggc	A	G	// 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream //	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2034291	aaatcctacactctct[C/T]aacaatccgttccaag	C	T	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 311716 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2295892	gcatggtagatcttac[C/T]gcatacttttacgttg	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2290995	gcaagtgacttttcaa[A/C]ataacaaatcaatttg	A	C	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2288666	gattggattagcagaa[G/T]atcagacattacagaa	G	T	1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream //	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2293373	gcagatctgttccgac[A/G]ccttcacaccctggat	A	G	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1), transcript variant 4, mRNA. /// NM_006162 // intron // 0 // Hs.534074 //	NFATC1	NFATC1, Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1), transcript variant 4, q23
SNP_A-2269956	gacaatgtgtcatggt[A/G]aaagctgttactttga	A	G	148 // Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), transcript variant 2, mRNA. /// NM_033302 //	ADRA1A	ADRA1A, Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), transcript variant 2, p21.2
SNP_A-2231854	ctcaaagtggttaaga[C/T]gagtaaggggatgtga	C	T	23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 216019 // Hs.434255 // PSD3 //	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2241206	ctgaggaccgtgaaga[C/T]agcttgaaatagataa	C	T	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2235307	ctccctcctggtcaaa[C/G]aaaacgaccacatttc	C	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 386460 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2235022	cttctcttcttcctgc[C/T]attcatccctaaatct	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// ENST00000332068 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2270407	gacactttgttaaccc[C/T]ggaaagcattgctact	C	T	// Homo sapiens hypothetical protein FLJ36980 (FLJ36980), mRNA. /// ENST00000317438 // intron // 0 // --- // --- // --- // ---	FLJ36980	FLJ36980, Homo sapiens hypothetical protein FLJ36980 (FLJ36980), p22
SNP_A-2261501	gaaaggaggagtatga[C/T]agatgagactgtattg	C	T	Homo sapiens hypothetical protein FLJ20581 (FLJ20581), mRNA. /// ENST00000331849 // intron // 0 // --- // --- // --- // ---	FLJ20581	FLJ20581, Homo sapiens hypothetical protein FLJ20581 (FLJ20581), p12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2279330	gaggagctttaaaaaa[C/T]atgtatacctagttcc	C	T	Homo sapiens glucose-fructose oxidoreductase domain containing 1 (GFOD1), mRNA. /// ENST00000274688 // intron // 0 // --- // --- // --- // ---	GFOD1	GFOD1, Homo sapiens glucose-fructose oxidoreductase domain containing 1 (GFOD1), p23
SNP_A-2274716	gagaaagagaagctta[C/T]gagttagactaacgtg	C	T	Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // --- // --- // --- // ---	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-2307965	gcttctgttgtccaaa[A/G]tatttcttattcatac	A	G	// Homo sapiens retinoid X receptor, gamma (RXRG), mRNA. /// NM_001005214 // upstream // 96993 // Hs.120487 //	RXRG	RXRG, Homo sapiens retinoid X receptor, gamma (RXRG), q23.3
SNP_A-2037683	aacaagcctcttggac[A/G]ctactattcattgcac	A	G	157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 526463 //	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2047701	aagattattgattgtc[A/G]agtacatcaaggctgc	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 772119 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2019785	aacctcttcatctgga[C/G]aaggctttatttcatc	C	G	Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2003459	ctctgttcactttcca[A/G]ctgcttgcatgtttgc	A	G	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 317628 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-1996659	tccagctgagctacaa[C/T]acgaattcaagactcc	C	T	6461 // Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// NM_000692 // upstream // 79323 // Hs.436219 // ALDH1B1 // 219 // Homo	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-2061505	aatgctctgaaagaac[A/G]gaacaattcaattcag	A	G	Homo sapiens hypothetical protein FLJ20171 (FLJ20171), mRNA. /// ENST00000358397 // intron // 0 // --- // --- // --- // ---	FLJ20171	FLJ20171, Homo sapiens hypothetical protein FLJ20171 (FLJ20171), q22.1
SNP_A-2052648	aagtatggaaatgaga[A/G]ataaagcaacagaaag	A	G	Homo sapiens FLJ44874 protein (FLJ44874), mRNA. /// NM_002527 // upstream // 77696 // Hs.99171 // NTF3 // 4908	-	-, Homo sapiens FLJ44874 protein (FLJ44874), p13.31
SNP_A-2054112	aagttcataatgaaac[A/G]cttaaatgataggtgt	A	G	FLJ35530 // 400798 // Homo sapiens FLJ35530 protein (FLJ35530), mRNA. /// NM_018037 // upstream // 41928 //	FLJ35530	FLJ35530, Homo sapiens FLJ35530 protein (FLJ35530), q25.2
SNP_A-2064129	aattcaaaagagtggc[A/G]aaaggaagccccagac	A	G	// Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // --- // --- // --- // ---	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2207817	cccaaacttttttgta[A/G]agccttctggagctag	A	G	10873 // Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006680 // upstream //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-2226635	ctaagtaaggtctgtg[A/C]atattttatatcagta	A	C	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 511561 //	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2194728	catgccatttcaccag[C/T]atgtagggatttttaa	C	T	23450 // Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA. /// NM_152456 // upstream // 2683 //	SF3B3	SF3B3, Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), q22.1
SNP_A-2195217	catggatcttatggaa[C/T]gtgaattatacctcaa	C	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.12
SNP_A-2172606	caattgaagattgaaa[A/G]tggcctgtttggtaaa	A	G	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// NM_044472 // intron // 0 // Hs.467637 // CDC42 // 998 // Homo sapiens	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2177904	cactaacttgcagaaa[G/T]gtggagaatgtacaaa	G	T	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 225547 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-2149505	atgtagatgtaaaaga[A/G]aagaaataatcacatc	A	G	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-2145857	atgccattaaaagtga[A/G]agaaatgctatattta	A	G	7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-2125883	agtttgttactcagca[A/C]taatgaaaagcatgtc	A	C	// 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA. /// NM_182562 // downstream // 92642 //	ARRDC4	ARRDC4, Homo sapiens arrestin domain containing 4 (ARRDC4), q26.3
SNP_A-2132454	atagtgaagggaatac[C/T]gatttcgtatgtctgc	C	T	// Homo sapiens Rho GTPase activating protein 12 (ARHGAP12), mRNA. /// ENST00000311380 // intron // 0 // ---	ARHGAP12	ARHGAP12, Homo sapiens Rho GTPase activating protein 12 (ARHGAP12), p11.22
SNP_A-2107986	agctcgaccgtacaca[A/C]ctttcacgtgcaaagc	A	C	CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 641507 // Hs.522891 //	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1710900	tgagaatcttctggaactcaggtga[A/C]ctaacattgatttgggcaccttgga	A	C	NM_017700 // intron // 0 // Hs.272787 // FLJ20184 // 54848 // hypothetical protein FLJ20184	FLJ20184	FLJ20184 , rs1374531, hypothetical protein FLJ20184,q24
SNP_A-1690467	ttttcagaattcactttctttaatg[C/G]acttttattctgtaactactccaca	C	G	1539 // cylicin, basic protein of sperm head cytoskeleton 2 /// NM_133445 // upstream // 829354 // Hs.283852 // PPP3R2 //	CYLC2	CYLC2 , rs10521061, cylicin, basic protein of sperm head cytoskeleton 2 ,q31.1
SNP_A-1791246	gggtaaagataggtca[C/G]atgaagtaatctccgc	C	G	// 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// NM_006982 // upstream //	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-1803438	tatgatggatagaggc[A/G]agagggccagtaggct	A	G	10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 44593 // Hs.369907 //	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1809314	gtgactctgtctatag[A/G]aacaattcctagaaat	A	G	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1862351	tcatgtaggtgggatc[A/G]caatatttgccctttt	A	G	// 56886 // Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), mRNA. /// NM_004807 // downstream // 60487 // Hs.512841 // HS6ST1 // 9394 //	UGCGL1	UGCGL1, Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), q14.3
SNP_A-1827005	taaccaaagctcagga[A/G]gtgaacgaggtcactc	A	G	ENST00000277470 // intron // 0 // --- // --- // --- // ---	-	q34.11
SNP_A-1941604	ttggaaataacacaaa[C/T]ggctaccacaataact	C	T	/// ENST00000359064 // upstream // 40573 // --- // --- // --- // --- /// ENST00000332041 // downstream // 471001 // --- // --- // ---	-	q22.1
SNP_A-1950680	tttcatgtagttccat[A/C]agctcagattctaggg	A	C	Homo sapiens centrosomal protein 2 (CEP2), mRNA. /// ENST00000359226 // intron // 0 // --- // --- // --- // --- ///	CEP2	CEP2, Homo sapiens centrosomal protein 2 (CEP2), q11.22
SNP_A-1952811	tttctgtttattctca[C/T]gttagctttgcataaa	C	T	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 237628 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1957082	ttttacaaccttgccc[C/T]ataaaagcagcaatat	C	T	5539 // Homo sapiens pancreatic polypeptide (PPY), mRNA. /// ENST00000340609 // upstream // 10127 // --- // --- // --- // ---	PPY	PPY, Homo sapiens pancreatic polypeptide (PPY), q21.31
SNP_A-1963691	aagttaacaacctgaa[A/G]cactccaagcatatat	A	G	27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// NM_182536 // downstream // 61241 //	BMP10	BMP10, Homo sapiens bone morphogenetic protein 10 (BMP10), p13.3
SNP_A-1976915	gatttctataaaagac[A/G]tagatcacctagaaca	A	G	Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA. /// ENST00000284440 // intron // 0 // --- // --- // --- // ---	UCHL1	UCHL1, Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), p13
SNP_A-1979390	aggctgaaactgtgtc[A/T]ccacttgtgaggtaaa	A	T	4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // upstream // 721004 // --- // --- // --- // --- /// ENST00000355292	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1931424	ttcccatatgtcacac[C/T]caacactctcatctct	C	T	// 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// NM_003012 // downstream // 68224 //	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-1928173	ttcacactactcttac[G/T]acacaaagctccacag	G	T	/// ENST00000259567 // downstream // 284319 // --- // --- // --- // --- /// ENST00000360460 // downstream // 286161 // --- // ---	-	p24.1
SNP_A-1903073	tggctgtggtacccaa[C/T]agtgcaggtgggacaa	C	T	Homo sapiens hypothetical protein FLJ12975 (FLJ12975), mRNA. /// ENST00000303372 // intron // 0 // --- // --- // --- // ---	FLJ12975	FLJ12975, Homo sapiens hypothetical protein FLJ12975 (FLJ12975), q24.31
SNP_A-1899940	tggacagtcatctcca[A/G]gggatccctaggaaga	A	G	8940 // Homo sapiens topoisomerase (DNA) III beta (TOP3B), mRNA. /// NM_003935 // upstream // 5867 //	TOP3B	TOP3B, Homo sapiens topoisomerase (DNA) III beta (TOP3B), q11.22
SNP_A-1894447	tgccaacacatgggta[C/T]ggaatccaaatgaaca	C	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1905671	tggtatccgagaaaga[C/G]ctctccattcacatcc	C	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1907418	tgtaaacattactaga[A/C]ctcttattttgcatat	A	C	sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), mRNA. /// ENST00000263808 // intron // 0 //	ROS1	ROS1, Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), q22.1
SNP_A-1978110	tttcttcaaaaatgcc[A/G]ataaactgacttaact	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 42886 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1984068	atgggagggaaagtgg[C/T]atatgctgaagctgga	C	T	56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 370283 // Hs.519693 //	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-1959469	ttttgccttatcaaaa[A/C]tgtgatagcaaaaatg	A	C	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 233151 // --- // --- // ---	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. q11.2
SNP_A-1959619	ttttggatgcagttga[A/G]cattgttttatgcttc	A	G	// 390061 // Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), mRNA. /// ENST00000332043 // downstream // 16846 // --- // --- // --- // ---	OR51Q1	OR51Q1, Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), p15.4

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950076	tttcacatttcttgtg[A/C]aggatagaggtatcat	A	C	374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 285573 // Hs.34198 // FLJ44796 // 401209 //	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-1826508	taacaagacttaaact[A/G]actaaaactgcaattt	A	G	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1825561	taaatagtacccagca[C/T]tgagagttagaagtgg	C	T	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // --- // --- // --- // ---	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-1851882	tattgagtatacataa[A/T]tcactctaccataaag	A	T	Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // --- //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1791744	gggtctgtgaaagaaa[A/G]cctgaatcaacatggt	A	G	Homo sapiens RAS p21 protein activator 3 (RASA3), mRNA. /// ENST00000357860 // intron // 0 // --- // --- // --- ///	RASA3	RASA3, Homo sapiens RAS p21 protein activator 3 (RASA3), q34
SNP_A-1796921	ggttccctgtgtctga[A/G]gcttggactgagcgag	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2068705 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1797149	ggttgaggtactatga[A/G]ctcacatttaggattt	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3405080 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1734042	gatcttttgagcacaggatgcttta[C/T]gcttcagcttattctcactctgcat	C	T	POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 4065546	POLR2B	POLR2B , rs6848993, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-2115453	agggggcgcccctctc[C/T]gaagtgccaatcctgc	C	T	5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 //	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, p13
SNP_A-2142218	atgaaaaccacaacca[C/T]gtgagtagttgcagag	C	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q22.1
SNP_A-2165868	caaagtgaagatcccc[C/G]caacaatcgtcttgta	C	G	9612 // Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /// NM_005505 // downstream // 173968 //	NCOR2	NCOR2, Homo sapiens nuclear receptor co-repressor 2 (NCOR2), q24.31
SNP_A-2155756	attcccagcctgttta[C/G]atggaagatctcatgt	C	G	Homo sapiens cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA. ///	CDON	CDON, Homo sapiens cell adhesion molecule-related,q24.2
SNP_A-2173460	cacaataaaaagagtg[C/G]atcaatgttttcggt	C	G	7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // downstream // 77004 // Hs.510833 // TJP1 //	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.1
SNP_A-2190149	cataagtcacaagaat[A/T]aataagaatttctgag	A	T	// 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1358867 // Hs.166109 // ELAVL2	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2224639	cgtccccaggcagccc[C/T]aagtctccaaaaaaga	C	T	2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 454642 // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2218105	actaaaaaaacagaca[A/G]tgctggagctcaggaa	A	G	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2220598	ccttcttgttaagtga[A/T]gtaagaagtcctgctg	A	T	SLC28A1 // 9154 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (SLC28A1), mRNA. /// NM_004213 // downstream // 22952 //	SLC28A1	SLC28A1, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (SLC28A1), q25.3
SNP_A-2074529	acataggaaaaaattc[G/T]caacagcactaattat	G	T	DRA // 3122 // Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA. /// ENST00000354615 // downstream // 12664 // --- // --- // --- // --	HLA-DRA	HLA-DRA, Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), p21.32
SNP_A-2103436	agcaatatacgtaatg[C/T]atgggcaacttgtcac	C	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 213792	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2094875	agaatgaaaacgaacc[C/G]ccatgtaactacaatt	C	G	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-2090271	acttgcctatcatagc[A/C]ataaggaactatgtag	A	C	Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // intron // 0 // Hs.47288 // TRPM3 // 80036 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.11
SNP_A-1997998	tcattggtagagagaa[C/T]tggtatctttccacat	C	T	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 16465 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-2040499	aaccagttcattgtca[A/G]attaaaaccctagcaa	A	G	9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 13176 // Hs.448520	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2040295	aaccacggtgcaaacc[A/G]cattgtagggggagat	A	G	Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 (CDS2), mRNA. /// ENST00000217268 // intron // 0 // --- // --- // --- // ---	CDS2	CDS2, Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 (CDS2), p12.3
SNP_A-2039095	aacaggtgaaagcaac[A/G]atctaacatctctgag	A	G	Homo sapiens inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3), mRNA. /// ENST00000235971 // upstream // 42478 // --- // --- // --- // --- /// ENST00000358793	ID3	ID3, Homo sapiens inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3), p36.12
SNP_A-2301253	gccttgggttgcacta[C/T]gaaacttacacaactg	C	T	6869 // Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // upstream //	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-2279365	gaggagggaatgtaaa[A/G]ccagtcaggtaggcta	A	G	// 85413 // Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), mRNA. /// NM_015076 // downstream // 21681 // Hs.193251 // CDC2L6	SLC22A16	SLC22A16, Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), q21
SNP_A-2266204	gaagggcaggaaataa[A/G]ccataaatctgagaaa	A	G	/// ENST00000321719 // upstream // 512977 // --- // --- // --- // -	-	p11.21
SNP_A-2228140	ctactagaagcagcta[C/T]ggtgcgtggttttcat	C	T	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3146324 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2241796	ctgatctttaagctga[G/T]cattattgatgtctat	G	T	// 54741 // Homo sapiens leptin receptor gene-related protein (OBRGRP), mRNA. /// NM_001003679 // downstream //	LEPROT	LEPROT, Homo sapiens leptin receptor gene-related protein (OBRGRP), p31.2
SNP_A-2255605	cttgtggttttcacca[C/T]accttacaccacaaac	C	T	// 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream //	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2271690	gaccagagaaagtgga[C/T]actctttgttttaatc	C	T	Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // --- // --- // --- // ---	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2261730	gaaagtgcaagagcta[C/T]gcaggtggcagctgtg	C	T	// 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000235799 // downstream // 43122 // --- // -	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2262016	gaaatagccattacaa[A/G]tacgtccagagaacta	A	G	91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-2284334	gatatttcaatcgccc[A/G]aaatggagagaggatt	A	G	HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 202458 // --- // --- // ---	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2280063	gagggaagacaatgaa[A/C]caaatctgtgctagga	A	C	Homo sapiens FGF receptor activating protein 1 (FRAG1), mRNA. /// ENST00000350451 // intron // 0 // --- // --- // --- // ---	FRAG1	FRAG1, Homo sapiens FGF receptor activating protein 1 (FRAG1), p15.4
SNP_A-2295942	gcatgtgaacatatcc[A/G]gcgttcgtattcatag	A	G	// Homo sapiens motilin (MLN), mRNA. /// NM_000841 // downstream // 41005 // Hs.429018 // GRM4 // 2914 // Homo	MLN	MLN, Homo sapiens motilin (MLN), p21.31
SNP_A-2295310	gcatcagctgaagtcc[A/T]ataaagaggatgaaaa	A	T	// 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream //	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-2292996	gcagaagtagaaatag[A/C]aacagcatgatctagt	A	C	Homo sapiens myosin, light polypeptide 1, alkali; skeletal, fast (MYL1), transcript variant 1f, mRNA. /// ENST00000352451 // intron // 0 // --- // --- // --- // ---	MYL1	MYL1, Homo sapiens myosin, light polypeptide 1, alkali; skeletal, fast (MYL1), transcript variant 1f, q34
SNP_A-2290703	gaggttaggcaaacac[A/C]accaccttaatccagc	A	C	// 5567 // Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PRKACB), transcript variant 3, mRNA. /// NM_002731 // downstream // 91104 // Hs.487325 // PRKACB	PRKACB	PRKACB, Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PRKACB), transcript variant 3, p31.1
SNP_A-2038488	aacacttgactcaata[C/T]ggactcatagaggcac	C	T	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, mRNA. /// AB017133 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, p36.22
SNP_A-2036175	aaattatgagtcctca[A/G]tatagagatttcaaaa	A	G	5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000331968 // upstream // 88062 // --- // ---	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2015866	catataaaaatcccca[A/G]acttagccaggctcaa	A	G	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 107593 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2082284	acgagttttgtattac[A/G]accagaatactgacat	A	G	4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2095636	agacacacaaccaaat[A/G]atatcaggcacgaatc	A	G	AASDHPPT // 60496 // Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), mRNA. /// NM_000855 // downstream // 125282 // Hs.503756 // GUCY1A2 // 2977 //	AASDHPPT	AASDHPPT, Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), q22.3
SNP_A-2055446	ccatcttaggaaacaa[A/G]atgtactctattgatg	A	G	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2179178	cactggctggggtaaa[A/G]ttgtgtcagtatgaat	A	G	Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-2167391	caacagtctatgtaca[C/T]tgaaagcatatttaca	C	T	- /// ENST00000344692 // upstream // 25070 // --- // --- // --- //	-	q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141045	atctgccctccagcat[C/T]aagtagtcacacttgc	C	T	ENST00000360752 // intron // 0 // --- // --- // --- // ---	-	p33
SNP_A-2146824	atgctttaagggaaga[C/T]aattaagccactagtc	C	T	/// ENST00000360991 // downstream // 443082 // --- // --- // ---	-	q12.1
SNP_A-1727621	caggcacctcttccattcaaggtta[C/T]attcttctctaattagatgtcccaa	C	T	METTL4 // 64863 // methyltransferase like 4 /// NM_031416 // upstream // 1002993 // Hs.326788 // C18orf2 // 56651 //	METTL4	METTL4 , rs620504, methyltransferase like 4 ,p11.32
SNP_A-1706575	ttcagagtcacaagttaccagtttc[C/T]aaaccagaggtaccaggtggttgtt	C	T	// 6419 // SET domain and mariner transposase fusion gene /// NM_182760 // downstream // 37503 // Hs.350475 //	SETMAR	SETMAR , rs711674, SET domain and mariner transposase fusion gene ,p26.1
SNP_A-1797697	ggtttgctgtattaaa[C/T]gaagacagaccagaag	C	T	170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // --- // --- // --- // ---	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-1812671	gtggcttcctctcgct[A/G]acatttgatctaaaac	A	G	// 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-1805524	gtccaggaaaagccta[A/T]cttagaggtaacactt	A	T	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), mRNA. /// ENST00000305206 // intron // 0 // --- // --- // --- // ---	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2
SNP_A-1851632	tattctgccatgacta[A/T]tacaatgtctattctc	A	T	ENST00000275358 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-1857523	tcactcagcattgaac[A/G]gagacctaaaggtggt	A	G	130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 369597	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-1856969	tcaccagtgtggaaac[A/G]gccacatgctcctatg	A	G	sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA. /// ENST00000261883 // intron // 0 // --- // --- // --- // ---	CILP	CILP, Homo sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), q22.31
SNP_A-1833365	tacagaactgtttcca[C/G]cttttagatctaatgg	C	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 595735 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-1953909	tttgagtaactaagaa[A/C]actgtacaataagcag	A	C	CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 62017	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1958851	ttttctgttcctgtta[C/T]acctgagttctttaac	C	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-1956347	tttgttactcactatg[G/T]aatcctgggaaagaca	G	T	Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1939178	ttgatagtggccagag[A/C]agtggctcttgttggt	A	C	26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B), mRNA. /// ENST00000274639 //	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2
SNP_A-1989253	aaacatgagaatagaa[A/C]gtaatggatatacaag	A	C	64111 // Homo sapiens chromosome 7 open reading frame 9 (C7orf9), mRNA. /// ENST00000222674 // upstream //	C7orf9	C7orf9, Homo sapiens chromosome 7 open reading frame 9 (C7orf9), p15.3
SNP_A-1976141	gtagggatccactggg[C/G]atttcatgtcagattc	C	G	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1918578	ttaaatggacattggc[C/T]gcaggaagagtgtgtt	C	T	56940 // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// ENST00000307499 // upstream //	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3
SNP_A-1913146	tgtggcatgatagatg[C/G]agcactatccgaaatt	C	G	-- /// ENST00000356117 // downstream // 521579 // --- // --- //	-	q23.31
SNP_A-1894278	tgcattgagaatatac[A/G]ctacagaaattcagta	A	G	Homo sapiens phosducin-like 2 (PDCL2), mRNA. /// ENST00000295645 // intron // 0 // --- // --- // --- // ---	PDCL2	PDCL2, Homo sapiens phosducin-like 2 (PDCL2), q12
SNP_A-1874689	tctcctgcctcttggc[A/G]atggctgcgcctccga	A	G	3195 // Homo sapiens T-cell leukemia, homeobox 1 (TLX1), mRNA. /// NM_006562 // downstream // 31439 // Hs.37128 //	TLX1	TLX1, Homo sapiens T-cell leukemia, homeobox 1 (TLX1), q24.32
SNP_A-1877302	tctggaagaagaatgg[A/G]cattgttacctcaata	A	G	Homo sapiens growth factor independent 1B (potential regulator of CDKN1A, translocated in CML) (GFI1B), mRNA. /// ENST00000339463 // intron // 0 // --- // --- // --- // ---	GFI1B	GFI1B, Homo sapiens growth factor independent 1B (potential regulator of CDKN1A, translocated in CML) (GFI1B), q34.13
SNP_A-1895510	tgcctactgcttgccc[A/G]aaatgtcaaacaccct	A	G	Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000264463 // intron // 0 // --- // --- // --- // ---	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-1898700	tgctttagaaagtttc[C/T]atttgaaaggcagtaa	C	T	7932 // Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA. /// NM_030883 // upstream //	OR2H2	OR2H2, Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), p22.1
SNP_A-1927408	ttcaaagctaacaaca[A/G]gcatctgagcaatctg	A	G	2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 9629 // --- // --- // --- // --- ///	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-1932501	ttcctggatacctccc[C/T]gcatctgtccttcaac	C	T	84258 // Homo sapiens synaptotagmin III (SYT3), mRNA. /// NM_016148 // downstream // 135482 // Hs.274255 //	SYT3	SYT3, Homo sapiens synaptotagmin III (SYT3), q13.33
SNP_A-1975709	aaatcagaacataaga[C/T]accatccagaaaaagt	C	T	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // intron // 0 // Hs.478673 // IL1RAP // 3556 // Homo sapiens	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1976696	cataaagctcatacta[C/G]aaatgaggttaaaaac	C	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1938166	ttgacatcagaagaga[A/C]tcaatagaaggactat	A	C	2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 219620 // Hs.122926 // NR3C1 //	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1953563	tttgaattctttgaaa[A/G]cattcttctctttata	A	G	444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, mRNA. /// NM_032467 // upstream //	ASPH	ASPH, Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, q12.3
SNP_A-1809028	gtgacaacaatgtcaa[A/C]tactctaaagaagtca	A	C	// Homo sapiens suppressor of hairy wing homolog 4 (Drosophila) (SUHW4), transcript variant 2, mRNA. /// NM_017661 // intron // 0 // Hs.511477 // SUHW4 // 54816 //	SUHW4	SUHW4, Homo sapiens suppressor of hairy wing homolog 4 (Drosophila) (SUHW4), transcript variant 2, q21.3
SNP_A-1793904	ggtcaagaaatattca[C/T]ggaggacccaatatgt	C	T	rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // --- // --- // --- //	-	-, Human clone rev16,q11.22
SNP_A-1684816	taacatttgtcttacataagtcaca[A/G]agagtatatagaaccaaacaaatat	A	G	NM_000255 // downstream // 898380 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs2996268, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-1720253	aagaattcttagaattacattggtg[A/C]actcggataacttagaatgatctct	A	C	5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 3162337 // Hs.435976 // BRUNOL4 // 56853 //	PIK3C3	PIK3C3 , rs325379, phosphoinositide-3-kinase, class 3 ,q12.3
SNP_A-1780363	ggataatccagcaaga[A/T]aatgtttttgtgatct	A	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2148987	atggttctatttgaaa[C/G]agtacacaggcagccc	C	G	Homo sapiens ankyrin repeat and SOCS box-containing 2 (ASB2), mRNA. /// ENST00000315988 // intron // 0 // --- // ---	ASB2	ASB2, Homo sapiens ankyrin repeat and SOCS box-containing 2 (ASB2), q32.13
SNP_A-2149888	atgtcacatggcgaat[A/G]aaccaccacatgccca	A	G	3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream //	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2160389	atttcataattcacta[A/C]aaatgatgtgacttca	A	C	10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// NM_022091 // upstream // 395823 // Hs.486031 // DJ467N11.1 // 63921 //	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-2159441	attttgtagactcaat[C/T]agcaaggcacatcttc	C	T	Homo sapiens ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3), mRNA. /// ENST00000237800 // intron // 0 // --- // --- // --- // ---	UCHL3	UCHL3, Homo sapiens ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3), q22.2
SNP_A-2108950	agcttatcaattatta[C/T]taaaaagcgtgctaaa	C	T	64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 //	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-2109747	aggaaatatttgagga[A/G]gtttgaatatagccct	A	G	168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 476629	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2180625	cagaagcctctctgcc[A/G]ggacttagacacaatc	A	G	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 12999 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2168248	caactgatcataggtc[A/T]ctccctctgaggccat	A	T	694 // Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), mRNA. /// NM_001004330 // upstream //	BTG1	BTG1, Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), q22
SNP_A-2187952	cagtatttacttctca[G/T]agcaggaaaatagaaa	G	T	SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2196164	catgtgctttggtgaa[G/T]agcagtaacagtcaaa	G	T	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-2220222	ccttccaagctcagag[A/G]aaagctcagcctctgg	A	G	220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. ///	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2218027	cctgccactcacacaa[G/T]gctacctcatcccttg	G	T	23108 // Homo sapiens GTPase activating Rap/RanGAP domain-like 4 (GARNL4), mRNA. /// ENST00000322335 //	GARNL4	GARNL4, Homo sapiens GTPase activating Rap,p13.3
SNP_A-2056792	aataggaataagttaa[A/G]catcgtgttatataaa	A	G	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2059372	aatctaacactgaaga[A/G]actggaaaataaatgt	A	G	ENST00000358195 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2052433	aagtacttggaaacca[C/T]aatcacttcaagagac	C	T	6035 // Homo sapiens ribonuclease, RNase A family, 1 (pancreatic) (RNASE1), transcript variant 3, mRNA. /// NM_198235 // upstream // 35530 // Hs.78224 // RNASE1 //	RNASE1	RNASE1, Homo sapiens ribonuclease, RNase A family, 1 (pancreatic) (RNASE1), transcript variant 3, q11.2
SNP_A-2048920	aagcctactctgaatt[A/G]aaatgaggtagaaaaa	A	G	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 225785 // --- // --- //	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. ,q11.2
SNP_A-2096477	agacctaccaacagca[A/G]aacaattacaactcac	A	G	116143 // Homo sapiens hypothetical protein BC014022 (LOC116143), mRNA. /// NM_000945 // intron // 0 //	LOC116143	LOC116143, Homo sapiens hypothetical protein BC014022 (LOC116143), p14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2093673	agaagacagccaagag[C/T]attgtaggaaagtaag	C	T	Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), mRNA. /// ENST00000261367 // intron // 0 // --- // ---	SNCAIP	SNCAIP, Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), q23.2
SNP_A-2101338	agatctctatagacca[A/G]ctttcttttaacccac	A	G	9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 440766 // Hs.269542 // ARMC1 // 55156 //	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-2104251	agcagattcagaacca[C/T]gccttctaaaactctg	C	T	FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream //	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2088213	actggtagtgaacatc[C/T]agtaataacaataaca	C	T	2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 313083 // Hs.444329 // GPC6 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2017435	tggctttcatttttcc[G/T]ataatccatggtgtcc	G	T	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2303086	gctatacaaaacatac[C/G]cgttctgaaaaaattt	C	G	// Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 //	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15
SNP_A-2281485	gagtcatgctggaaag[A/G]aaccctataaatgtga	A	G	/// ENST00000342224 // downstream // 31265 // --- // --- // ---	-	p11.21
SNP_A-2267986	gaatctctctttgggg[A/G]acgctcatcacagaga	A	G	-- /// ENST00000314071 // upstream // 66359 // --- // --- // --- //	-	p13.2
SNP_A-2248242	ctgtggttctccaaga[C/G]gcatgttaatctttt	C	G	// Homo sapiens hypothetical protein BC004921 (LOC93349), mRNA. /// ENST00000243810 // intron // 0 // --- // --- // --- // ---	LOC93349	LOC93349, Homo sapiens hypothetical protein BC004921 (LOC93349), q37.1
SNP_A-2238942	ctcttccatcttctaa[A/G]ccagtaacatcacatc	A	G	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-2250035	cttacccttcaagaca[A/G]atcaaagttaccacct	A	G	54843 // Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, mRNA. /// NM_032379 // upstream //	SYTL2	SYTL2, Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, q14.1
SNP_A-2266146	gaagggaacaaattga[A/G]gccatgaatgtaattg	A	G	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2265239	gaagcaaagagaaaca[A/G]gtcttctccatgatgg	A	G	9655 // Homo sapiens suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, mRNA. /// NM_014011 //	SOCS5	SOCS5, Homo sapiens suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, p21
SNP_A-2269251	gaatttatgacaatgc[C/T]ctctttcctctctttg	C	T	348158 // Homo sapiens xenobiotic/medium-chain fatty acid:CoA ligase (HXMA), nuclear gene encoding	HXMA	HXMA, Homo sapiens xenobiotic,p12.3
SNP_A-2291755	gcacagaacctgactt[A/T]aagccacacactttgg	A	T	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 238117 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2016555	gtgatcactttacaca[C/G]cggatttcctttaatc	C	G	FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream //	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2015306	tgattttcaacctaca[A/G]tcccatacctagccaa	A	G	64092 // Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), mRNA. /// NM_003489 // downstream // 39169 // Hs.155017 // NRIP1 //	SAMSN1	SAMSN1, Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), q11.2
SNP_A-2001735	gtttggctccagttaa[C/T]tactttctcctgaggg	C	T	// 55742 // Homo sapiens parvin, alpha (PARVA), mRNA. /// NM_021961 // upstream // 102047 // Hs.546308 // TEAD1 //	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.2
SNP_A-2005178	attttcaggtctccta[C/T]gccacttctgtaccca	C	T	// Homo sapiens Sp6 transcription factor (SP6), mRNA. /// ENST00000342234 // upstream // 2832 // --- // --- // --- // --- ///	SP6	SP6, Homo sapiens Sp6 transcription factor (SP6), q21.32
SNP_A-2037759	aacaagtcagtgagta[C/T]ctaaatagacaaggat	C	T	ENST00000334896 // intron // 0 // --- // --- // --- // ---	-	q32.2
SNP_A-2041788	aacgttgcattaagaa[A/G]aaaggaaaagaataat	A	G	sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), mRNA. /// ENST00000356913 // intron // 0 // --- // --- // --- // --- /// ENST00000357115 // intron //	LRBA	LRBA, Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), q31.3
SNP_A-2044160	aacttgtttgtgttta[C/T]ccttttgaatctgaca	C	T	27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. ///	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2049642	aagcttccttccacag[A/G]ctgaccttgttttgtg	A	G	5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 60055 // Hs.390428 // MAP3K4 //	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-2059459	aatctatacatggcac[A/T]gaatttattcactcat	A	T	121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// AF425596 // upstream // 80516 // Hs.528316 // FOXN4 //	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2056944	aatagtattatgatga[G/T]ctctcgttacttagta	G	T	// 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream //	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-2073385	acaggtcaacaagcca[C/G]taagccctaatgatgg	C	G	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// ENST00000276297 // intron // 0 // --- // ---	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-2199060	catttgtcagttctgt[A/G]aacccttcccccaaat	A	G	// 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 849846 // --- // --- // --- //	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2174525	cacagagatacacgaa[A/T]tgacgttctgattaat	A	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 932437 // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2119063	agtagagtaacaaaga[C/T]aataaacacaaacatt	C	T	4143 // Homo sapiens methionine adenosyltransferase I, alpha (MAT1A), mRNA. /// NM_138812 // downstream //	MAT1A	MAT1A, Homo sapiens methionine adenosyltransferase I, alpha (MAT1A), q22.3
SNP_A-2135485	atatttgtaacagtta[A/C]agatgtgccactgtat	A	C	Homo sapiens junctophilin 1 (JPH1), mRNA. /// ENST00000342232 // intron // 0 // --- // --- // --- // --- ///	JPH1	JPH1, Homo sapiens junctophilin 1 (JPH1), q21.11
SNP_A-1722062	gaatctagaatctttctcctaatac[A/G]gaatgccacagtaggtttaaaaact	A	G	Hypothetical gene supported by AK093158 (LOC400145), mRNA /// NM_014832 // downstream // 326802 // - // - // -	-	- , rs10492516, Hypothetical gene supported by AK093158 (LOC400145), mRNA ,q22.2
SNP_A-1714991	gaatccttctctattcagtgctcta[A/G]gtagcttataaattgcaatctaacc	A	G	AB046788 // intron // 0 // Hs.13305 // ROBO2 // 6092 // roundabout, axon guidance receptor, homolog 2 (Drosophila)	ROBO2	ROBO2 , rs1470203, roundabout, axon guidance receptor, homolog 2 (Drosophila),p12.3
SNP_A-1741365	tcagtgctaagcatcttgaaatatt[C/T]aaacatatggcatttgaaaggagag	C	T	NM_016489 // intron // 0 // Hs.415641 // NT5C3 // 51251 // 5'-nucleotidase, cytosolic III	NT5C3	NT5C3 , rs7776847, 5'-nucleotidase, cytosolic III,p14.3
SNP_A-1689657	cagagatactcatcatcttaaagac[A/G]actgacagttataggcataagccta	A	G	5001 // origin recognition complex, subunit 5-like (yeast) /// NM_005045 // upstream // 120256 // Hs.431010 // RELN //	ORC5L	ORC5L , rs194825, origin recognition complex, subunit 5-like (yeast) ,q22.1
SNP_A-1788810	gggattgcaaactcca[A/G]gtctttagagtcaaga	A	G	Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- // --- ///	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-1809346	gtgactgtatctgatc[A/G]actcttccaggagcac	A	G	sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, mRNA. /// NM_017488 // intron // 0 // Hs.188528 // ADD2 //	ADD2	ADD2, Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, p13.3
SNP_A-1813586	gtgtaagacacaatgc[C/T]ctgttaatttttttt	C	T	// Homo sapiens choline kinase alpha (CHKA), transcript variant 1, mRNA. /// NM_212469 // upstream // 2553 //	CHKA	CHKA, Homo sapiens choline kinase alpha (CHKA), transcript variant 1, q13.2
SNP_A-1802420	gtatcatgatgtgtaa[C/T]cctgacactcttttga	C	T	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2050977 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1853302	tattttagtagatata[G/T]gtctggactggaatct	G	T	6147 // Homo sapiens ribosomal protein L23a (RPL23A), mRNA. /// ENST00000250979 // upstream // 50406 // --- // ---	RPL23A	RPL23A, Homo sapiens ribosomal protein L23a (RPL23A), q26.1
SNP_A-1864903	tccagggagtatctac[A/T]ctgtcagcaagcttct	A	T	145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// ENST00000344738 // downstream //	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1945331	ttgttacggatactga[A/C]ctgtgagccactgaga	A	C	Homo sapiens integrin-linked kinase-associated serine/threonine phosphatase 2C (ILKAP), transcript variant	ILKAP	ILKAP, Homo sapiens integrin-linked kinase-associated serine q37.3
SNP_A-1962430	ctcttccgtaccatct[A/C]acagtcttctgattaa	A	C	10630 // Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, mRNA. /// NM_006474 // downstream // 3773 // Hs.468675 // T1A-2 //	T1A-2	T1A-2, Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, p36.21
SNP_A-1893846	tgcataataagcagtg[A/G]aaaataaattctaagg	A	G	4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 609005 // Hs.166017 // MITF //	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-1895148	tgccccacggtagagt[A/C]aaaaaatcacaagttg	A	C	6511 // Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6),	SLC1A6	SLC1A6, Homo sapiens solute carrier family 1 (high affinity aspartate p13.12
SNP_A-1878730	tctgttcctggaatcc[C/G]aagttgatttgttatt	C	G	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-1913547	tgtgtaaaatacccaa[C/T]ttaatgacggacacat	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-1915862	gagcacataagtaaag[C/T]aggagttaagcagtgt	C	T	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 840356 // Hs.114412 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1963391	catgtcctgggtcaca[A/C]tacccacactccattt	A	C	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 1652517 //	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-1967843	catttctaagaactga[A/G]gtaattatctgggatg	A	G	Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// ENST00000337743 // intron // 0 // --- //	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-1982961	tttcctccagcctgca[A/G]tatgcccagagacagc	A	G	51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 //	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-1944118	ttgtcactcataactg[C/T]accatctccatgcact	C	T	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-1854624	tcaacaatccctcctc[A/T]ctaagctcagtcattt	A	T	114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream //	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-1843486	tagtgatgacctcaga[A/G]aatcaggttattcttc	A	G	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-1677394	tgccaggaacagacaacacaaccaa[C/T]gcagtcaaatataaccctaaatatg	C	T	IMAGE:4825217, mRNA, partial cds /// NM_000891 // downstream // 1712352 // Hs.1547 // KCNJ2 // 3759 //	-	- , rs9302942, Clone IMAGE:4825217, mRNA, partial cds ,q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1695691	acacactcacaatcctaagagaaca[A/G]gaagattctgtaatgcagatcacc a	A	G	KCTD12 // 115207 // potassium channel tetramerisation domain containing 12	KCTD12	KCTD12 , rs10507852, potassium channel tetramerisation domain containing 12,q22.2
SNP_A-1730581	gtcagactccaaaagaacactaaaa[A/G]tcattttcccaaataagttttcttt	A	G	4085 // MAD2 mitotic arrest deficient-like 1 (yeast) /// NM_018699 // downstream // 78991 // Hs.192867 // PRDM5	MAD2L1	MAD2L1 , rs10518365, MAD2 mitotic arrest deficient-like 1 (yeast) ,q27
SNP_A-1784051	ggccagcctaccagaa[A/C]tgccggcagcctgact	A	C	92211 // Homo sapiens protocadherin 21 (PCDH21), mRNA. /// NM_015613 // downstream // 7090 // Hs.226000 //	PCDH21	PCDH21, Homo sapiens protocadherin 21 (PCDH21), q23.1
SNP_A-2111707	ataactcgagatgtca[C/G]aaaataaggaacgaaa	C	G	Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, mRNA. /// NM_175605 // intron // 0 //	TTC10	TTC10, Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, q12.11
SNP_A-2155677	attccagtttttgcac[A/G]ctggctttgtctggga	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2163420	atttttttcagcaag[C/G]agtcattctgccagaa	C	G	83861 // Homo sapiens radial spokehead-like 2 (RSHL2), mRNA. /// NM_152133 // downstream // 239 // Hs.529984 //	RSHL2	RSHL2, Homo sapiens radial spokehead-like 2 (RSHL2), q25.3
SNP_A-2193067	catctaattaccaagc[C/T]caaagacataggaagg	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2188365	cagtcttctattaagg[A/G]aaatgataagccttat	A	G	Homo sapiens regulator of G-protein signalling 17 (RGS17), mRNA. /// ENST00000206262 // intron // 0 // --- // --- // --- // ---	RGS17	RGS17, Homo sapiens regulator of G-protein signalling 17 (RGS17), q25.2
SNP_A-2208965	cccagcctcagagcca[C/G]tctttaagtaccacaa	C	G	Homo sapiens tumor protein p53 inducible nuclear protein 1 (TP53INP1), mRNA. /// ENST00000342697 // intron // 0 // ---	TP53INP1	TP53INP1, Homo sapiens tumor protein p53 inducible nuclear protein 1 (TP53INP1), q22.1
SNP_A-2206607	ccatgaagacatggac[A/C]aaagaattaagcatcc	A	C	3736 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), mRNA. /// ENST00000228858 // downstream // 111571 // --- // --- //	KCNA1	KCNA1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), p13.32
SNP_A-2201237	ccaataaaccagttag[A/G]caaaatgcttactaca	A	G	Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// ENST00000347596 // intron // 0 // ---	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2063153	aatgtgtcaaaggaga[A/G]gaatcagagaatcctg	A	G	endogenous retrovirus env mRNA. /// ENST00000300145 // downstream // 51861 // --- // --- // --- // --- ///	-	-, Human endogenous retrovirus env q14.1
SNP_A-2087688	actgctgttgctgata[C/T]ccccttccttttgctc	C	T	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2086892	actgagacatattgca[C/G]aaaagatgtttccata	C	G	Homo sapiens dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP4), mRNA. /// ENST00000360534 // intron // 0 // --- // --- // --- // ---	DPP4	DPP4, Homo sapiens dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP4), q24.2
SNP_A-2090781	actttatctagagaaa[C/T]atgagtcagtctttgt	C	T	Homo sapiens putative binding protein 7a5 (7A5), mRNA. /// ENST00000332878 // intron // 0 // --- // --- // --- // ---	7A5	7A5, Homo sapiens putative binding protein 7a5 (7A5), p21.1
SNP_A-2106033	agcccaatgctgccac[A/G]actacattgtcaccct	A	G	sapiens thymidine kinase 2, mitochondrial (TK2), mRNA. /// ENST00000299697 // intron // 0 // --- // --- // --- // ---	TK2	TK2, Homo sapiens thymidine kinase 2, mitochondrial (TK2), q22.1
SNP_A-2009851	agtgtccaacacataa[C/T]caattttcaaaatatcg	C	T	DKFZP586H2123 // 25891 // Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, mRNA. /// NM_001001991 // upstream // 117848 //	DKFZP586H2123	DKFZP586H2123, Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, p13
SNP_A-2006309	tcatcacacgactgta[C/T]atttttatgggctcc	C	T	// 130733 // Homo sapiens hypothetical protein MGC33926 (MGC33926), mRNA. /// NM_025264 // downstream // 15500	MGC33926	MGC33926, Homo sapiens hypothetical protein MGC33926 (MGC33926), p22.1
SNP_A-2006831	caagccaatggcagac[A/G]aatgatttatattgaa	A	G	4036 // Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA. /// NM_152384 // upstream // 90686 //	LRP2	LRP2, Homo sapiens low density lipoprotein-related protein 2 (LRP2), q31.1
SNP_A-2291716	gcacacctgtctcgca[A/T]cacataaaatgcagcg	A	T	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-2295975	gcatgttcagttgcta[C/G]gaatgtggaaaatata	C	G	Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), mRNA. /// U05012 // intron // 0 // Hs.410969 //	NTRK3	NTRK3, Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), q25.3
SNP_A-2310668	ggaagataaagatcca[A/G]atgaactgcaatcata	A	G	SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 131810 // --- // --- // --- // ---	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2272310	gacctcttaagtgcca[C/T]cgtagttcagttaaat	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 114489 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2279468	gaggatcgtaaaaata[A/C]ctatcaagtactatgc	A	C	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 1130569 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2276883	gagatattaacattta[G/T]gctttggcttacctga	G	T	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream //	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251898	cttcattaaatcataa[G/T]gtctaaacaggagttt	G	T	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), mRNA. /// ENST00000353125 // intron // 0 // --- // --- // --- // --- /// ENST00000360359 // intron // 0 // ---	ANKS1	ANKS1, Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), p21.31
SNP_A-2251943	cttcatttccagtcaa[A/G]gcatgcgacattttag	A	G	11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // downstream // 51936 // --- // --- // --- // ---	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22
SNP_A-2255284	cttgtaagagaggcat[G/T]agagagcttgttcacc	G	T	8019 // Homo sapiens bromodomain containing 3 (BRD3), mRNA. /// NM_017588 // upstream // 39861 // Hs.397638 //	BRD3	BRD3, Homo sapiens bromodomain containing 3 (BRD3), q34.2
SNP_A-2233718	ctcatatttctctgca[C/T]gacctttttcaatctgc	C	T	/// ENST00000319719 // upstream // 374782 // --- // --- // --- // --- /// ENST00000308537 // upstream // 150907 // --- // --- // ---	-	p13
SNP_A-2252048	cttccacatttcctaa[C/G]gtctctgaggatttag	C	G	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000353474 // intron // 0 // --- // --- // --- // ---	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-2296726	gccaaatctttgaggc[C/T]atggtggtaacaggaa	C	T	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA. /// ENST00000268124 // intron // 0 // --- // --- // --- // ---	POLG	POLG, Homo sapiens polymerase (DNA directed), gamma (POLG), q26.1
SNP_A-2007705	aattctgcctacaaca[C/T]tggctctcaatacatt	C	T	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 76587 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1992054	ccacaggttttaatcc[C/T]aaaagcaatcctaatc	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 937107 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2036578	aaattgcatcccaaac[A/C]aagagtcgctgcactt	A	C	7094 // Homo sapiens talin 1 (TLN1), mRNA. /// NM_000366 // upstream // 163299 // Hs.133892 // TPM1 // 7168 // Homo	TLN1	TLN1, Homo sapiens talin 1 (TLN1), q22.2
SNP_A-2024743	aaaagtcaggacataa[C/G]agatgctggagaggat	C	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1501499 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2105910	agccatcaggacaaac[C/T]ccttatcctcggggac	C	T	491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 180132 // Hs.268942 //	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2101557	agatgactttacgctc[A/G]gaaactcaaatacata	A	G	// Homo sapiens NY-REN-58 antigen (NY-REN-58), mRNA. /// ENST00000339839 // intron // 0 // --- // --- // --- // ---	NY-REN-58	NY-REN-58, Homo sapiens NY-REN-58 antigen (NY-REN-58), q22
SNP_A-2098958	agagcttctttgtagc[A/G]agacctgtcagtgtct	A	G	ENST00000334363 // intron // 0 // --- // --- // --- // --- /// ENST00000359851 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-2076564	acatttctgagactgg[A/G]aagtaaacagtcttgg	A	G	// Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream // 5659	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-2061214	aatgcagttagggagc[A/G]aagtaaagacaataga	A	G	7844 // Homo sapiens ring finger protein 103 (RNF103), mRNA. /// NM_022780 // upstream // 89504 // Hs.75277 //	RNF103	RNF103, Homo sapiens ring finger protein 103 (RNF103), p11.2
SNP_A-2216035	cctccatgttttttag[A/T]cctttgccaatctgat	A	T	FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2169805	caaggagttcttcaaa[A/G]ggaaggatagagtgat	A	G	MGC15730 // 84966 // Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000355895 //	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-2161245	atttgagtaagaaagc[A/G]ctggggtcttttctct	A	G	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 //	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). q12.13
SNP_A-2110995	aggagaactaataaga[C/T]gaaatggaggggaata	C	T	Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2132943	atatacaatcttgtga[A/G]ccaggggacttaaat	A	G	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // --- // --- // --- // ---	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-1712735	catgaaaatgcaaattttgctatcc[C/T]aaattaaatgaataatgctggtctt	C	T	27445 // piccolo (presynaptic cytomatrix protein) /// NM_000722 // upstream // 313320 // Hs.147871 //	PCLO	PCLO , rs6979945, piccolo (presynaptic cytomatrix protein) ,q21.11
SNP_A-1668564	cagtcaacagctcagtattttgtca[G/T]aggaacacttgctaaaggaaaaacc	G	T	9376 // solute carrier family 22 (organic anion transporter), member 8 /// NM_173586 // downstream // 84849 //	SLC22A8	SLC22A8 , rs4127470, solute carrier family 22 (organic anion transporter), member 8 ,q12.3
SNP_A-1651388	tatttagactttactagtgaaatac[C/T]ggtaccttcattcacagcatatttc	C	T	NM_018557 // intron // 0 // Hs.417952 // LRP1B // 53353 // low density lipoprotein-related protein 1B (deleted in tumors)	LRP1B	LRP1B , rs10496873, low density lipoprotein-related protein 1B (deleted in tumors),q22.1
SNP_A-1654423	ctattgctggtgtatatccgtctcc[C/T]acgctatttctttgccatctggaac	C	T	// 7088 // transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) /// NM_007005 // downstream // 168594 //	TLE1	TLE1 , rs267998, transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) ,q21.31
SNP_A-1833384	tacagaataccacagg[A/G]caaaaggtgaacttta	A	G	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA. /// ENST00000264047 // intron // 0 // — // --- // --- // ---	SLC5A7	SLC5A7, Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), q12.3
SNP_A-1818004	gttctaggagagtaag[G/T]ctctttgttttattca	G	T	// 26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B), mRNA. /// ENST00000274639 //	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1853316	tattttatcaataaaa[C/T]ctgtccaatgatctag	C	T	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1850562	tattaagcttgtcata[C/G]taaacttctttttgt	C	G	Homo sapiens serine active site containing 1 (SERAC1), mRNA. /// ENST00000265129 // intron // 0 // --- // --- // --- // ---	SERAC1	SERAC1, Homo sapiens serine active site containing 1 (SERAC1), q25.3
SNP_A-1845918	tatataactcactacc[C/T]aatatgtgcttttcac	C	T	6003 // Homo sapiens regulator of G-protein signalling 13 (RGS13), transcript variant 2, mRNA. /// NM_002927 //	RGS13	RGS13, Homo sapiens regulator of G-protein signalling 13 (RGS13), transcript variant 2, q31.2
SNP_A-1867003	tccctccacagccaca[C/T]gttgcttttagcttgc	C	T	Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA. /// ENST00000265854 // intron // 0 // --- // -	MAD1L1	MAD1L1, Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), p22.3
SNP_A-1961663	ttttttttttttgcc[C/T]agctgtccataaaaat	C	T	sapiens insulin receptor (INSR), mRNA. /// ENST00000302850 // intron // 0 // --- // --- // --- // --- ///	INSR	INSR, Homo sapiens insulin receptor (INSR), p13.2
SNP_A-1987282	ccacttttagatggg[A/G]acactgagacctggag	A	G	/// ENST00000309379 // upstream // 207297 // --- // --- // --- // -	-	q21
SNP_A-1977182	gaactaaagcctttgg[G/T]acgttcagttgtgttt	G	T	KIAA0635 // 9662 // Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000264222 // downstream // 284568 // ---	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-1964527	taattctctggaaata[C/T]accaagtgaaaaagca	C	T	10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 // upstream //	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-1974989	attacagtctttattc[C/T]atttcatgtgaacatt	C	T	389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// ENST00000356539 // intron // 0 // --- // --- // --- // ---	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-1974552	aaccatgctcccaaca[C/G]tactcactctgaaatc	C	G	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1920977	ttacagagcctggaac[G/T]caatatatttttagta	G	T	51400 // Homo sapiens protein phosphatase methylesterase-1 (PME-1), mRNA. /// NM_182904 // upstream // 9566 //	PME-1	PME-1, Homo sapiens protein phosphatase methylesterase-1 (PME-1), q13.4
SNP_A-1893642	tgcaggtttgctgata[A/G]gtaaattgatgtcttg	A	G	22869 // Homo sapiens mRNA for KIAA0972 protein, partial cds. /// NM_001001662 // downstream // 28219 // Hs.494569	ZNF510	ZNF510, Homo sapiens for KIAA0972 protein, partial cds. ,q22.33
SNP_A-1893144	tgcagaagggtttcaa[A/G]gattctagtgcatagt	A	G	392390 // Homo sapiens olfactory receptor, family 1, subfamily L, member 6 (OR1L6), mRNA. ///	OR1L6	OR1L6, Homo sapiens olfactory receptor, family 1, subfamily L, member 6 (OR1L6), q33.2
SNP_A-1897780	tgctggactcttagta[C/G]ctcaggaagtgggagt	C	G	Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // --- // --- // --- // ---	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-1925479	ttatcttgagcatcta[A/G]agttttgcaagttcta	A	G	KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 632771 // --- // --- // --- //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-1913163	tgtggccagacaggaa[A/C]cttgggagaaatcagc	A	C	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 1108845	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1970273	cagtcaaactgacacg[C/T]aaactcacccaggaca	C	T	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-1983205	accctccactcttttc[A/T]atcacttgtcacattt	A	T	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1952256	tttctcctgagttaca[A/C]aatggcagttgttaat	A	C	// 5781 // Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) (PTPN11), mRNA. /// NM_014954 // upstream // 265672 // Hs.21239 // RPH3A //	PTPN11	PTPN11, Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) (PTPN11), q24.13
SNP_A-1935476	ttctgggaacaagaga[A/G]gtgattcgagatgggc	A	G	346689 // Homo sapiens FLJ44186 protein (FLJ44186), mRNA. /// ENST00000340940 // upstream // 43919 // --- // ---	FLJ44186	FLJ44186, Homo sapiens FLJ44186 protein (FLJ44186), q34
SNP_A-1756128	tcagacagtctggacatgtactgta[C/T]cacttaccagatatacaaagagcag	C	T	AB037812 // upstream // 260724 // Hs.6136 // ARHGAP20 // 57569 // Rho GTPase activating protein 20	ARHGAP20	ARHGAP20 , rs4643108, Rho GTPase activating protein 20,q23.1
SNP_A-2132502	atagtgcctgtgagga[A/G]gaaaatgagactcact	A	G	6121 // Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000294604 // upstream // 138510 // --- // --- // --- // --- /// ENST00000262340	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-2137064	atcaggaaaaataaga[C/T]cgtatgttggtactaa	C	T	Homo sapiens exostoses (multiple) 2 (EXT2), transcript variant 2, mRNA. /// NM_000401 // intron // 0 // Hs.368404 //	EXT2	EXT2, Homo sapiens exostoses (multiple) 2 (EXT2), transcript variant 2, p11.2
SNP_A-2123878	agttaacgtcagattc[A/T]ccctcaattcctccat	A	T	Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // --- //	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-2119348	agtataaaagccctca[A/C]gtgtgttttgcaagca	A	C	10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // upstream // 57040 // --- // --- // --- // ---	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2117906	aggtttcccaatctaa[C/T]agaaaatcattggtaa	C	T	Homo sapiens likely ortholog of mouse monocyte macrophage 19 (MMRP19), mRNA. /// ENST00000278359 // intron // 0 // --- // --- // --- // ---	MMRP19	MMRP19, Homo sapiens likely ortholog of mouse monocyte macrophage 19 (MMRP19), p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2117163	aggtgcatgtgaccaa[C/T]caggctaatttttaaa	C	T	Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000064571 // intron // 0 // --- // --- // ---	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-2148285	atgggccactgtcgca[A/G]acactatttttatttt	A	G	// 10391 // Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA. /// NM_006305 // downstream // 15999 //	CORO2B	CORO2B, Homo sapiens coronin, actin binding protein, 2B (CORO2B), q23
SNP_A-2217843	cctgcaagggaataca[A/G]ataattcattcttaa	A	G	sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), transcript variant 5, mRNA. /// NM_198837 // intron // 0 // Hs.160556 // ACACA // 31 // Homo sapiens acetyl-Coenzyme	ACACA	ACACA, Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), transcript variant 5, q12
SNP_A-2069278	acaatttactgctac[G/T]cactctctaacctaat	G	T	ENST00000337495 // intron // 0 // --- // --- // --- // --- ENST00000360598 // intron // 0 // --- // --- // ---	-	p34.2
SNP_A-2024541	aaaaggcacagctaac[C/T]agaagaggggcccag	G	T	64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 428621 // Hs.546282 // RBBP8	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-2047668	aagattaattaataaa[C/T]tgctgcacttttaaag	C	T	Homo sapiens membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4) (MPP4), mRNA. /// ENST00000315506 // 3UTR // 0 // --- // --- // --- // ---	MPP4	MPP4, Homo sapiens membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4) (MPP4), q33.1
SNP_A-2011590	atcagaggttctacc[A/G]aggatcttcaatatac	A	G	8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 287056 // --- ENST00000356525 // intron // 0 // --- // --- // --- // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2002157	atctaatcacattgga[C/T]actttcaatatttggc	C	T	FLJ33979 // 196074 // Homo sapiens hypothetical protein	FLJ33979	FLJ33979, Homo sapiens hypothetical protein
SNP_A-2009200	gtttgcacataatgaa[C/T]gatgtctcagagacag	C	T	FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream	FLJ33979	FLJ33979 (FLJ33979), p14.1
SNP_A-2011590	atcagaggttctacc[A/G]aggatcttcaatatac	A	G	ENST00000332793 // intron // 0 // --- // --- // --- // --- ENST00000356525 // intron // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-2016367	actgagcccttccttg[A/G]aattatacctcactca	A	G	// 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2255895	acaaatctgaaactca[G/T]ggatataagatagaca	G	T	ENST00000311549 // intron // 0 // --- // --- // ---	-	q32.32
SNP_A-2244625	ctggagctgctgtaac[G/T]aatgaccagggcctа	G	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2281705	gagtcttgtcctggct[A/G]aaagctggaaagtcca	A	G	Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // --- // --- // --- // ---	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2282447	gagtctttagaacaa[C/T]tcaccaggctttcaga	C	T	Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-2279405	gaggagtgattcttta[C/G]ctgcactcttggaaa	C	G	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 437701 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2272495	gaccttggcgagctcc[A/G]cagttccttaatcac	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2269585	gacaaagttttatca[A/G]taaggagttctcagta	A	G	Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // --- // --- // --- // ---	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2263562	gaaccatacaataatc[C/T]aatttctccccttctg	C	T	// Homo sapiens 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (BDH), nuclear gene encoding mitochondrial protein, transcri /// NM_203314 // upstream // 31277 // Hs.274539 // BDH // 622 //	BDH	BDH, Homo sapiens 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (BDH), nuclear gene encoding mitochondrial protein, transcri, q29
SNP_A-2250522	ctagggtttcaaagc[C/T]gcctatttagttaaat	C	T	ENST00000284717 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2019060	gataatatgagattgat[A/G]agacatgacaacaaag	A	G	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2007619	tttccaaagatagccaa[A/T]tatgctgacttacagc	A	T	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2034020	aaatcagaatgggtaa[A/G]aatcaaatatgaaaga	A	G	10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// NM_022091 // upstream // 270595 // Hs.486031 // DJ467N11.1 // 63921 //	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-2068544	acaagtctcagggacc[C/T]aggaacatggtgctct	C	T	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2065458	aattgttcttcagga[C/T]caattgctatggccag	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 139734 // Hs.116471 // CDH11	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2071505	acagaaatgagcaaat[A/G]atacagatcaaaatctt	A	G	Homo sapiens ARG99 protein (ARG99), mRNA. /// ENST00000256062 // intron // 0 // --- // --- // ---	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2071638	acagaataagtactaa[C/T]tgctagaatgaacctg	C	T	sapiens mRNA for KIAA0834 protein, partial cds. /// NM_012395 // intron // 0 // Hs.430742 // PFTK1 // 5218 //	PFTK1	PFTK1, Homo sapiens for KIAA0834 protein, partial cds. q21.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2057348	aatatattgccagata[C/T]catttgaggaaaaagg	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2057391	aatatcacttggctaa[C/T]gtttttctagacctgc	C	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2053857	aagtgtgtaattaagc[A/G]gcagtaagtacagtaa	A	G	rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // --- // --- // --- //	-	-, Human clone rev16 q11.22
SNP_A-2172808	caatttggaactatgg[A/C]aggtagaaattaagag	A	C	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 511263 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2176177	ttctttctcgtgaccc[C/T]gagttcatttaacttc	C	T	Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // --- // -	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-2192432	catcatgtacttctta[C/T]gcatgggacttcctca	C	T	10296 // Homo sapiens macrophage erythroblast attacher (MAEA), mRNA. /// NM_175918 // upstream // 113468 //	MAEA	MAEA, Homo sapiens macrophage erythroblast attacher (MAEA), p16.3
SNP_A-2158542	attgtactgaattatc[A/G]ccttgaggaatcaaag	A	G	// 26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 440815 //	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13
SNP_A-2118912	agtacttagcacatta[C/T]gaatgcagtgttaaat	C	T	5912 // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA. /// ENST00000323534 //	RAP2B	RAP2B, Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), q25.2
SNP_A-2124667	agttctagtttctcca[C/T]attcttgcaaacagtt	C	T	152518 // Homo sapiens ovarian zinc finger protein (HOZFP), mRNA. /// NM_000087 // downstream // 10277 // Hs.1323 //	HOZFP	HOZFP, Homo sapiens ovarian zinc finger protein (HOZFP), p12
SNP_A-2136164	atcaatcagtagaaaa[A/G]tcattcttggcctatt	A	G	MGC26979 // 91147 // Homo sapiens hypothetical protein MGC26979 (MGC26979), mRNA. /// NM_153704 //	MGC26979	MGC26979, Homo sapiens hypothetical protein MGC26979 (MGC26979), q22.1
SNP_A-2136041	atcaaggacgacgcta[A/G]ggtttttagtctaaat	A	G	84667 // Homo sapiens hairy and enhancer of split 7 (Drosophila) (HES7), mRNA. /// NM_002616 // downstream //	HES7	HES7, Homo sapiens hairy and enhancer of split 7 (Drosophila) (HES7), p13.1
SNP_A-1782230	ggcaagggttggtcca[A/G]tggaaatctccaacag	A	G	81793 // Homo sapiens toll-like receptor 10 (TLR10), mRNA. /// NM_006068 // downstream // 8128 // Hs.366986 // TLR6 //	TLR10	TLR10, Homo sapiens toll-like receptor 10 (TLR10), p14
SNP_A-1747719	aatgcaatttttactgaatttttgt[C/T]aaatataggaaatacagatttattt	C	T	10186 // lipoma HMGIC fusion partner /// NM_025138 // upstream // 90569 // Hs.318526 // C13orf23 // 80209 //	LHFP	LHFP , rs1413042, lipoma HMGIC fusion partner ,q13.3
SNP_A-1703373	aatactcactacgagaatacaatag[A/C]attagacatgtcaggaattttataa	A	C	3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 379868 // Hs.127011 // TINAG // 27283 //	HCRTR2	HCRTR2 , rs965009, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1688988	caatctatttttctatttagaatga[A/G]ggccattaggagcaaagacatttct	A	G	1006 // cadherin 8, type 2 /// NM_001797 // downstream // 6331 // Hs.443435 // CDH11 // 1009 // cadherin 11, type 2,	CDH8	CDH8 , rs35168, cadherin 8, type 2 ,q21
SNP_A-1801252	acagtcataacagtca[C/T]aataagggaactctaa	C	T	HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 756789 // --- // --- // ---	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-1812124	ttcagaccccagacaa[C/T]cctgaagtgtcagagg	C	T	// Homo sapiens chemokine-like factor super family 4 (CKLFSF4), transcript variant 1, mRNA. /// NM_181521 // intron // 0 // Hs.325825 // CKLFSF4 // 146223 // Homo	CKLFSF4	CKLFSF4, Homo sapiens chemokine-like factor super family 4 (CKLFSF4), transcript variant 1, q22.1
SNP_A-1867555	tccggattcacttaga[C/T]cactcaacacttctaa	C	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1937060	ttcttttctgtactga[C/T]tcaaaaaaacagaact	C	T	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1955553	tttggtgtggcatcca[C/G]tatagtctgtttaatg	C	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1855026 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1986806	tttcacactggaatta[C/T]aagaagccagcttgtt	C	T	Homo sapiens Ras-related GTP binding D (RRAGD), mRNA. /// ENST00000359203 // intron // 0 // --- // --- // --- // --- ///	RRAGD	RRAGD, Homo sapiens Ras-related GTP binding D (RRAGD), q15
SNP_A-1930224	ttcattctctactcac[G/T]cagtgtatttggagaa	G	T	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1876719	tctgcagaattaaaga[C/T]gtgatgtgacaaaaga	C	T	/// ENST00000359165 // upstream // 193468 // --- // --- // --- // -	-	p21.3
SNP_A-1897390	tgctgaagctaagaaa[A/C]ctataagacacagcaa	A	C	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // --- // ---	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1925335	ttatctatctatctag[C/T]ctaacatctatctatc	C	T	// Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 811954 //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1923230	ttagctgcaatatggc[A/C]ctaataaagagaatag	A	C	// 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1970812	aagtacccaaaatgca[A/C]gctgaatttccatttg	A	C	// 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 66915 // Hs.194766 // SEZ6L //	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1940473	ttgcccagaggaagaa[A/G]ctacacttattatctt	A	G	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1846357	tatatggaatcctgaa[A/G]actatttgatcagttc	A	G	80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// NM_030664 // upstream // 47246 //	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-1859485	tcaggagaaagaataa[C/G]actctgcatttaagca	C	G	Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // intron // 0 // --- // --- // --- // ---	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. p14.1
SNP_A-1817192	gttcaatttaactcag[A/G]aaatatttgttgagca	A	G	Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1786423	ggcttagaaaatcaaa[C/T]ggtttacagtcacgca	C	T	Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // --- // --- // --- // ---	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1794005	ggtcaccttgcacaa[A/G]ttagcatcaacaatct	A	G	23619 // Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /// NM_006210 // downstream // 93940 // Hs.201776	ZIM2	ZIM2, Homo sapiens zinc finger, imprinted 2 (ZIM2), q13.43
SNP_A-1795996	ggtggtccagggctca[A/G]gagaaatcatgccctg	A	G	Homo sapiens MGC4170 protein (MGC4170), mRNA. /// ENST00000299314 // intron // 0 // --- // --- // --- // ---	MGC4170	MGC4170, Homo sapiens MGC4170 protein (MGC4170), q23.2
SNP_A-2126603	ataaaatttaatcacc[A/G]catcatgctaaaatta	A	G	// 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream //	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-2117949	aggtttgtaaaaatca[A/G]taatattgcaaggttg	A	G	/// ENST00000341450 // upstream // 67965 // --- // --- // --- // ---	-	q12.1
SNP_A-2107841	agctcatttagttcat[A/G]agcggtcgagtgaaga	A	G	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), transcript variant 2, mRNA. /// NM_006994 // intron // 0 // Hs.167741 // BTN3A3 // 10384 // Homo sapiens	BTN3A3	BTN3A3, Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), transcript variant 2, p22.1
SNP_A-2152035	attaaaaaatgtcaac[A/G]atgttttcaagggaaa	A	G	4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-2197980	cattgcccaggtagcc[A/G]aacattaaagggatgt	A	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2190686	catacttccttcccag[C/T]catagtgttgcattca	C	T	// Homo sapiens tetraspanin similiar to uroplakin 1 (LOC90139), mRNA. /// ENST00000340160 // intron // 0 // ---	LOC90139	LOC90139, Homo sapiens tetraspanin similiar to uroplakin 1 (LOC90139), p11.2
SNP_A-2202809	ccactaaaccatcaac[A/C]agtatagatactccag	A	C	ENST00000260983 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2207931	cccaaattctgttcca[C/T]gttgaatacttcatgg	C	T	FLJ20604 // 54995 // Homo sapiens hypothetical protein FLJ20604 (FLJ20604), mRNA. /// NM_052953 // upstream //	FLJ20604	FLJ20604, Homo sapiens hypothetical protein FLJ20604 (FLJ20604), p24.2
SNP_A-2094891	agaatgacagatgcca[A/G]aaaagatcattctacc	A	G	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 655699 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2103163	agcaacatgattcaaa[A/C]aaaatgggcaagactt	A	C	1434 // Homo sapiens CSE1 chromosome segregation 1-like (yeast) (CSE1L), transcript variant 2, mRNA. /// NM_001316 // downstream // 12086 // Hs.90073 // CSE1L // 1434 // Homo	CSE1L	CSE1L, Homo sapiens CSE1 chromosome segregation 1-like (yeast) (CSE1L), transcript variant 2, q13.13
SNP_A-2088403	actgtagactagcaca[A/C]ccgattttattcgcag	A	C	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2088317	agtcccaggtaccagc[C/G]agtggccttagaaggg	C	G	Homo sapiens ubiquitin specific protease 44 (USP44), mRNA. /// ENST00000258499 // intron // 0 // --- // --- // --- // ---	USP44	USP44, Homo sapiens ubiquitin specific protease 44 (USP44), q22
SNP_A-2036785	aaatttattcttaata[A/G]cctgggaatctaaact	A	G	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 664631 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-2036211	aaattattggtcttcc[A/G]ccaagtgatgctcttc	A	G	/// ENST00000355063 // upstream // 218758 // --- // --- // --- // ---	-	q22.1
SNP_A-2037662	aacaagcaaaaacaac[C/G]gcaaaattatataagt	C	G	/// ENST00000360991 // downstream // 871163 // --- // --- // ---	-	q12.1
SNP_A-2037928	aacaatgtgcgttaag[C/T]cagccgggaataggaa	C	T	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2009721	acacaataaatgggca[A/T]ataaagctatgggatt	A	T	81793 // Homo sapiens toll-like receptor 10 (TLR10), mRNA. /// NM_006068 // downstream // 21515 // Hs.366986 // TLR6	TLR10	TLR10, Homo sapiens toll-like receptor 10 (TLR10), p14
SNP_A-2016262	ttactgagttaatgaa[A/T]gcttgaatgaagtcaa	A	T	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-1992341	actccagtcttttctc[A/G]actcaaaccatatttt	A	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 302698 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2253087	cttctctcttggacaa[C/T]ggtatttatatcagta	C	T	Homo sapiens TRAF and TNF receptor associated protein (TTRAP), mRNA. /// ENST00000341060 // intron // 0 // --- // ---	TTRAP	TTRAP, Homo sapiens TRAF and TNF receptor associated protein (TTRAP), p22.2
SNP_A-2231486	ctatttaaatagccta[C/T]gaaaagactggccctt	C	T	2326 // Homo sapiens flavin containing monooxygenase 1 (FMO1), mRNA. /// NM_002021 // downstream // 12812 //	FMO1	FMO1, Homo sapiens flavin containing monooxygenase 1 (FMO1), q24.3

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2240873	ctgagaatgcattaaa[A/C]tacagtaacacaatca	A	C	Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), mRNA. /// ENST00000309439 // intron // 0 // ---	ANAPC10	ANAPC10, Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), q31.21
SNP_A-2281224	gagtaggaattaagcc[A/G]aaattgaggaagctaa	A	G	– /// ENST00000355156 // upstream // 298273 // --- // --- // ---	-	q24.3
SNP_A-2307711	gcttccatttttctcc[G/T]gcttcagtccatcttc	G	T	869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// NM_207449 // upstream // 45932 // Hs.514338 //	CBLN1	CBLN1, Homo sapiens cerebellin 1 precursor (CBLN1), q12.1
SNP_A-2301904	gcggtggttcagaaac[A/G]ctttcatctgttttca	A	G	Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // --- // ---	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-2292150	gcacccagaattaatg[C/T]caggggtcagtgactt	C	T	// 79888 // Homo sapiens hypothetical protein FLJ12443 (FLJ12443), mRNA. /// NM_032479 // downstream // 53668 //	FLJ12443	FLJ12443, Homo sapiens hypothetical protein FLJ12443 (FLJ12443), p15.33
SNP_A-2292800	gcactttgaaatgtta[G/T]gttgctgtatgatatg	G	T	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA. /// ENST00000296261 // intron // 0	HEYL	HEYL, Homo sapiens hairy,p34.3
SNP_A-2294013	gcaggagactctaaca[G/T]ctcgtggtccaattcc	G	T	sapiens antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (MFI2), transcript variant 1, /// NM_033316 // intron // 0 // Hs.184727 // MFI2 //	MFI2	MFI2, Homo sapiens antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (MFI2), transcript variant 1, q29
SNP_A-2263423	gaacattcagtaatgc[C/T]gcaagagacaaaaatc	C	T	Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000308488 // intron // 0 // --- // ---	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-2261504	gaaaggaggtgaacca[A/G]cgtggccttgttagta	A	G	// 83896 // Homo sapiens keratin associated protein 3-1 (KRTAP3-1), mRNA. /// ENST00000360088 // upstream //	KRTAP3-1	KRTAP3-1, Homo sapiens keratin associated protein 3-1 (KRTAP3-1), q21.2
SNP_A-2230025	ctataaattatgtgac[C/T]atcctactaattcatc	C	T	64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 231960 // Hs.146339 //	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-1992259	cacagaatcatggggt[A/G]aatgcctaagcggtgt	A	G	/// ENST00000313159 // downstream // 22480 // --- // --- // ---	-	p23.1
SNP_A-2015354	aggagatgcagacttc[A/C]agaagagtgaagctgg	A	C	29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 540083 // Hs.473370 // USP25 // 29761 // Homo sapiens	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds. ,q21.1
SNP_A-2008506	atcttttctgaggcac[C/G]attgtcccttattacc	C	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 267464 // --- // --- // --- //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2034460	aaatctctgaccaaac[A/C]gctcaattaggttaag	A	C	KIAA0802 // 23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000306329 // downstream // 35680 // --- //	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-2024317	aaaagccccaagtcca[A/C]gaagtttgcagtctca	A	C	1123 // Homo sapiens chimerin (chimaerin) 1 (CHN1), mRNA. /// X15875 // downstream // 32836 // Hs.425104 //	CHN1	CHN1, Homo sapiens chimerin (chimaerin) 1 (CHN1), q31.1
SNP_A-2104803	agcataactggaaaaa[C/G]acctgctcccaaaact	C	G	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2093464	agaacttaaaagttgt[C/G]aaccatataattaaat	C	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2053934	aagttaaaattgcaaa[C/G]ggatcagaaaaccagg	C	G	7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 234188 //	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-2069657	acacacatagacatac[A/G]aagacacaggtacaca	A	G	56975 // Homo sapiens family with sequence similarity 20, member C (FAM20C), mRNA. /// ENST00000313766 //	FAM20C	FAM20C, Homo sapiens family with sequence similarity 20, member C (FAM20C), p22.3
SNP_A-2200326	ccaacagcccgactga[C/G]aaatgaacaaaggaaa	C	G	400110 // Homo sapiens FLJ46358 protein (FLJ46358), mRNA. /// NM_153023 // upstream // 171937 // Hs.131017 //	FLJ46358	FLJ46358, Homo sapiens FLJ46358 protein (FLJ46358), q12.12
SNP_A-2184410	cagcgtgctttgaaag[A/G]agtctccctccggctc	A	G	ENST00000261657 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2177145	cacctgaaaaccctgc[A/G]ctggcctggaaatctc	A	G	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 246464 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2182909	cagattagattaccca[C/G]tatattgagttaatac	C	G	9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 239529 // Hs.252451 //	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. ,q21.11
SNP_A-2147159	atggaatttcagacaa[C/G]aattttatttttattta	C	G	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 745796 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2107904	ggctgtggcaaggact[G/T]aaaataagacaacaat	G	T	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-2115474	agggggtcagatggcc[A/C]ggagcctaacaagagt	A	C	51421 // Homo sapiens angiomotin like 2 (AMOTL2), mRNA. /// NM_015391 // downstream // 74679 // Hs.106909 //	AMOTL2	AMOTL2, Homo sapiens angiomotin like 2 (AMOTL2), q22.1
SNP_A-2131060	atagaattcggtcacc[G/T]atttttttccaacttaa	G	T	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1792855	ggtaatccagaaacaa[A/G]tactaaatgttgtatg	A	G	/// ENST00000294926 // upstream // 123910 // --- // --- // --- // -	-	q44

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1689751	atgtgtatacttttttagatttat[C/G]agtcccatgtccaaatccgaagaat	C	G	partial mRNA for steerin3 protein (STEERIN3 gene), alternative exon 1b. /// NM_014903 // upstream // 164401 // Hs.306322 // NAV3 // 89795 // neuron navigator 3	-	- , rs696467, Homo sapiens partial mRNA for steerin3 protein (STEERIN3 gene), alternative exon 1b. ,q21.2
SNP_A-1661081	ggattctgaatgcaaagaaaatact[C/G]agatagctttactagtttatagtgg	C	G	progesterone receptor /// NM_004621 // downstream // 258667 // Hs.159003 // TRPC6 // 7225 // transient receptor	PGR	PGR , rs1942839, progesterone receptor ,q22.1
SNP_A-1738723	tgcagagctaatcatataaaataac[A/T]ggtaaaaaatgtttaaaatattttt	A	T	NM_006727 // intron // 0 // Hs.92489 // CDH10 // 1008 // cadherin 10, type 2 (T2-cadherin)	CDH10	CDH10 , rs1910964, cadherin 10, type 2 (T2-cadherin),p14.1
SNP_A-1756307	ttacattacttaaagtcactgaatc[A/G]cataagcaatatataaatgtgttt	A	G	25950 // RWD domain containing 3 /// NM_152487 // downstream // 24639 // Hs.84522 // FLJ31842 // 148534 //	RWDD3	RWDD3 , rs987111, RWD domain containing 3 ,p21.3
SNP_A-1815625	gttaaatgagtaccaa[C/T]gattaaagaaaatcaa	C	T	Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// ENST00000256007 // intron // 0 // --- // ---	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-1837080	tactgtatagcaaata[C/T]gtttgaatattggaca	C	T	22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 171038 // Hs.513902 // NALP1 //	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-1939016	ttgagtgcaatgctca[C/T]gccaactacctggggt	C	T	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Hom	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript q35.3
SNP_A-1975687	ttcattctgaatatgg[A/C]aaaatgggaaaccaaa	A	C	Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // --- // --- // --- // ---	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-1986489	caatagagaactaata[C/T]acctctgttccagttt	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1211090	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1922804	ttagataaaatggaca[A/G]attcctaaagagacat	A	G	ENST00000359749 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1921565	ttacctctacctgtta[C/T]gctgacaagtaccatt	C	T	158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 50400 //	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-1879995	tcttccttttcatcac[C/T]ctttgcttcctagatt	C	T	3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 63944 //	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1882418	tgaaaagctgtagtac[C/T]caaacctgtgtggctg	C	T	// 55196 // Homo sapiens hypothetical protein FLJ10652 (FLJ10652), mRNA. /// ENST00000340398 // upstream //	FLJ10652	FLJ10652, Homo sapiens hypothetical protein FLJ10652 (FLJ10652), p11.21
SNP_A-1873889	tctcagtcactgcata[A/G]agtcactatatttctt	A	G	54329 // Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA. /// NM_002711 // downstream // 652117 //	GPR85	GPR85, Homo sapiens G protein-coupled receptor 85 (GPR85), q31.1
SNP_A-1915337	tgttcattttattgct[C/G]actacactatgtattt	C	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1906071	tggtctctgctgcaga[A/C]gcaaccagaaatcaca	A	C	// Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // --- // --- // --- // ---	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1
SNP_A-1905464	tggtacaactaactca[A/G]tatttctgaattgcct	A	G	// 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-1986012	ccgactgatctatcaa[C/T]tcatgagctagatata	C	T	/// ENST00000320956 // downstream // 199599 // --- // --- // ---	-	p12.3
SNP_A-1973432	agaaaatgtgattgga[C/T]catagcactattgaga	C	T	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2062998 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1954189	tttgattttccattcc[C/T]gacttaattcactgag	C	T	// 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 20597 //	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1835333	tacctcaaactaaaag[G/T]cttctgcacagaaaag	G	T	Homo sapiens pygopus 1 (PYGO1), mRNA. /// ENST00000302000 // intron // 0 // --- // --- // --- // ---	PYGO1	PYGO1, Homo sapiens pygopus 1 (PYGO1), q21.3
SNP_A-1817020	gttatttcctctttga[A/C]ccccttcagtcaaaa	A	C	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc q31.1
SNP_A-1823093	taaaacaaatgctttc[A/G]caaagtagaggtaaat	A	G	27241 // Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // downstream // 62147 // Hs.372360 // B1 // 27241 // Homo	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-1860816	tcataatgaagttata[A/G]taaggcatacagatga	A	G	401474 // Homo sapiens sterile alpha motif domain containing 12 (SAMD12), mRNA. /// NM_002546 //	SAMD12	SAMD12, Homo sapiens sterile alpha motif domain containing 12 (SAMD12), q24.12
SNP_A-1859935	atttggataaaattga[A/G]cagttaggcctgcttc	A	G	1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// NM_001001688 // downstream // 37546 //	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1792279	gggttctctggtcaaa[G/T]gagatgacattattca	G	T	NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 //	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-2112952	atgaagtctagattgg[C/G]cacttcaggacttttc	C	G	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 512024 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2117189	aggtgccttctgagga[C/T]ggtggcatcgatttcc	C	T	ENST00000272907 // intron // 0 // --- // --- // --- // ---	-	q36.3
SNP_A-2147707	atggcagattagagcc[A/G]ctgtaaacttactgcc	A	G	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 315107 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2162504	attttccaaaaataat[A/G]aatgcatgcatgaaac	A	G	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1452377 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2177527	cacgagtgcttcttat[C/T]aatgatctgttagaaa	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2173196	cacaacataataatta[A/G]aagactgataagcaat	A	G	// Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // upstream // 20788 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2174569	cacagagtaataaaat[A/G]aacagtaaattggctt	A	G	Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // intron // 0 //	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds. ,p23.1
SNP_A-2200517	ccaactcaagtgacaa[C/T]agctccatttgacccc	C	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2208239	cccacaagactgcccc[C/T]gacttccgatgccaat	C	T	Homo sapiens cDNA clone MGC:72138 IMAGE:4068137, complete cds. /// NM_024044 // downstream // 275617 //	-	-, Homo sapiens cDNA clone MGC:72138 IMAGE:4068137, complete cds. ,p11.2
SNP_A-2066203	aattttaacactgaaa[C/T]catctgaatgagtttt	C	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2072282	acagatttgaagagaa[A/T]taggatcattcatact	A	T	283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream //	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2100225	agagttgaaacagaaa[A/G]taattgataaggtgtc	A	G	914 // Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), mRNA. /// NM_020440 // upstream // 109683	CD2	CD2, Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), p13.1
SNP_A-2035725	aaatgtgaggcgctta[C/T]ggaagtgctttgaaaa	C	T	85414 // Homo sapiens prostein protein (Prostein), mRNA. /// NM_022731 // downstream // 25048 // Hs.213061 // NUCKS	PCANAP6	PCANAP6, Homo sapiens prostein protein (Prostein), q32.1
SNP_A-2042121	aactagcaataattca[C/T]gtgtatttaaagccaa	C	T	151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream //	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2010743	ccaacaaccacaagag[C/G]aagcttggaggtagag	C	G	Homo sapiens synaptotagmin XIII (SYT13), mRNA. /// ENST00000020926 // intron // 0 // --- // --- // --- // ---	SYT13	SYT13, Homo sapiens synaptotagmin XIII (SYT13), p11.2
SNP_A-2263679	gaacccttggcttcac[A/G]gaggctcaccatacac	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, mRNA. /// NM_001372 // intron	DNAH9	DNAH9, Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, p12
SNP_A-2265288	gaagcacatcagagcc[A/G]gcaaaggggagagcag	A	G	// 132001 // Homo sapiens hypothetical protein BC015088 (MGC16471), mRNA. /// NM_003178 // upstream // 79494 //	MGC16471	MGC16471, Homo sapiens hypothetical protein BC015088 (MGC16471), p25.2
SNP_A-2292201	gcaccctggttaacaa[A/G]actatgcagggtgtgg	A	G	2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 133666 // --- // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-2296168	gcattcggaagagagg[A/C]aaatgcaacatgaaca	A	C	FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 //	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-2309401	ggaaaatgaattccga[C/T]gtgctagtttctttag	C	T	Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// ENST00000281221 // intron // 0 // --- // --- // --- // ---	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2310704	ggaagatgtaattcag[C/G]cagtattggcagcctg	C	G	54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream //	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2310511	ggaagaacagttttga[C/T]cacattgtgtggcgga	C	T	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2311059	ggaagtaaggacgtga[A/G]ggaagaaaagaaatgg	A	G	Homo sapiens Jun dimerization protein p21SNFT (SNFT), mRNA. /// ENST00000243440 // intron // 0 // --- // --- // --- // ---	SNFT	SNFT, Homo sapiens Jun dimerization protein p21SNFT (SNFT), q32.3
SNP_A-2312270	ggacataaatatggca[A/G]tgattgacactgggga	A	G	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-2307375	gcttagtagattgtca[A/G]ccaaaattcacccaat	A	G	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 58460 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2304054	gctccagcgacgtctc[A/G]atggggataaggtaag	A	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 53957 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2295067	gcatagcatggatata[C/T]gagtgaatatccaatg	C	T	56300 // Homo sapiens interleukin 1 family, member 9 (IL1F9), mRNA. /// NM_014440 // upstream // 12161 //	IL1F9	IL1F9, Homo sapiens interleukin 1 family, member 9 (IL1F9), q13
SNP_A-2288460	gattctttttgcaaca[A/G]tctcttaccaagtagt	A	G	1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// NM_001001688 // downstream // 39820 //	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2262947	gaacaagagtgtgagc[A/G]actgaatctgcatttt	A	G	KIAA0635 // 9662 // Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000264222 // downstream // 298085 // ---	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-2261169	gaaagaggaaacagtg[C/T]aattataaaacatgac	C	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 683637 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2283834	gatagtagagtagaag[G/T]cttcaaaggatcaaac	G	T	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // --- // --- // --- // ---	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2285342	gatctggaaacatggc[A/G]cagcatagcctgctga	A	G	/// ENST00000360575 // upstream // 51727 // --- // --- // --- // --- /// ENST00000231482 // upstream // 58403 // --- // --- // --- // ---	-	q31.1
SNP_A-2279465	gaggatccatgagctc[A/G]cctctgtttgcttaga	A	G	65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 120639 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2272664	gacggcagaagggttc[A/C]aggaagtgcccagaca	A	C	84146 // Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, mRNA. /// NM_032186 // upstream // 133008 // Hs.173001 // ZNF644 // 84146 //	ZNF644	ZNF644, Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, p22.2
SNP_A-2232892	ctcagaagattctgaa[C/T]gaaaccttggtgggca	C	T	Homo sapiens DNA glycosylase hFPG2 (FLJ10858), mRNA. /// ENST00000264596 // intron // 0 // --- // --- // --- // ---	NEIL3	NEIL3, Homo sapiens DNA glycosylase hFPG2 (FLJ10858), q34.3
SNP_A-2249306	cttaaaatagggcaca[C/G]gtataggatccctctt	C	G	55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 1201685 // Hs.479658 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-2015259	tcttctactagctcta[G/T]gaattaggcaaagcat	G	T	ENST00000285670 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2041135	aacctataatgattta[A/G]aggatttgaatggcat	A	G	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2045397	aagaataataacacaa[C/G]ttgtgcctataaaatg	C	G	UNQ9391 // 203074 // Homo sapiens tryptophan/serine protease (UNQ9391), mRNA. /// ENST00000328655 //	UNQ9391	UNQ9391, Homo sapiens tryptophan p23.1
SNP_A-2035410	aaatgggactaaagag[G/T]atggttttattttgtc	G	T	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1030619 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2031200	aaaggccagaggtaaa[C/T]atttgtcatgatgtcc	C	T	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2082962	acgtgcagtgtttcga[C/T]agaagattttccttat	C	T	Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, mRNA. /// NM_134431 // intron // 0 // Hs.46440 // SLCO1A2 // 6579 //	SLCO1A2	SLCO1A2, Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, p12.1
SNP_A-2060214	aatgaaccctaatgct[A/T]acactgggctttgggt	A	T	3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 35358 //	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2210990	cccgatagccagagtc[C/G]aggtgaattcagatgc	C	G	445 // Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, mRNA. /// NM_054012 // downstream //	ASS	ASS, Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, q34.11
SNP_A-2224603	cgtcagtttaaaacag[C/T]acctagtcccacaaac	C	T	84524 // Homo sapiens zinc finger CCCH type domain containing 8 (ZC3HDC8), mRNA. /// AB111887 // upstream //	ZC3HDC8	ZC3HDC8, Homo sapiens zinc finger CCCH type domain containing 8 (ZC3HDC8), q13
SNP_A-2172030	caatggaccacatata[C/T]atcacaccacataata	C	T	Homo sapiens abl-interactor 1 (ABI1), mRNA. /// ENST00000346832 // intron // 0 // --- // --- // --- // --- ///	ABI1	ABI1, Homo sapiens abl-interactor 1 (ABI1), p12.1
SNP_A-2169085	caagataatgtaggag[A/G]agatttacatgtagct	A	G	221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2125134	agttggattactgttg[C/G]atttcaaaagtagagc	C	G	// 10208 // Homo sapiens chromosome 13 open reading frame 22 (C13orf22), mRNA. /// NM_001629 // upstream //	C13orf22	C13orf22, Homo sapiens chromosome 13 open reading frame 22 (C13orf22), q12.3
SNP_A-1783949	ggccacctactaatag[C/G]cagcatcaattcttta	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1730429	ttgatttgccctatgtagtcactaa[C/T]gtcttagagtttggtagaaagttga	C	T	2820 // glycerol-3-phosphate dehydrogenase 2 (mitochondrial) /// NM_014568 // upstream // 238494 //	GPD2	GPD2 , rs10497155, glycerol-3-phosphate dehydrogenase 2 (mitochondrial) ,q24.1
SNP_A-1648944	gtgtctcagggttatatacatttca[A/C]attttcttggtgtcccaggaccaga	A	C	NM_006661 // intron // 0 // Hs.416467 // PDE10A // 10846 // phosphodiesterase 10A	PDE10A	PDE10A , rs10485103, phosphodiesterase 10A,q27
SNP_A-1857839	tcactgttcaattcct[A/G]aagaccctagacaagc	A	G	9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream //	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1819562	gttggttcctcaccaa[A/G]agggagtcagccttcc	A	G	51124 // Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), mRNA. /// ENST00000256433 // upstream // 412710 // --- // --- // --- // ---	IER3IP1	IER3IP1, Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), q21.1
SNP_A-1836753	tactgactggatgtac[C/T]atcatatatttattgc	C	T	sapiens aquaporin 9 (AQP9), mRNA. /// ENST00000219919 // intron // 0 // --- // --- // --- // ---	AQP9	AQP9, Homo sapiens aquaporin 9 (AQP9), q21.3
SNP_A-1833620	tacaggaagcatggcg[A/G]catctgtttggcttcc	A	G	57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 82769 // Hs.129452	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1949261	tttatgtgatttatta[C/T]gctctatagcagagct	C	T	Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000327152 // intron // 0 // --- // --- // --- // --- ///	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1937366	ttgaaagttaggtaca[G/T]aataggcagtacaccg	G	T	FLJ11193 // 55322 // Homo sapiens hypothetical protein FLJ11193 (FLJ11193), mRNA. /// NM_015022 // upstream //	FLJ11193	FLJ11193, Homo sapiens hypothetical protein FLJ11193 (FLJ11193), p13.3
SNP_A-1975970	cacatgaggagtgtta[C/T]aaaagttatagctctt	C	T	/// ENST00000326756 // downstream // 129807 // --- // --- // ---	-	p16.1
SNP_A-1963225	tcattacaataaacta[C/T]gttgaacacagcacaa	C	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2406409 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1980809	ccccatagcttcaacc[A/G]ctgtcactattatcca	A	G	Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // --- // --- // --- // ---	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-1911926	tgtgacgcgatgccga[C/T]gcagagagcctggatg	C	T	ENST00000332811 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-1878361	tctgtcttaaaagaga[A/T]cattgaactaagaatg	A	T	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1889432	tgagttcaacaccata[A/T]taaaaagtatcccagt	A	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 81841 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1887904	tgagattttaaacaag[A/G]ctctagggatggttca	A	G	ALOX5AP // 241 // Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA. /// NM_032849 // upstream // 77497 // Hs.62905 // FLJ14834 //	ALOX5AP	ALOX5AP, Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), q12.3
SNP_A-1888605	tgaggcagcactctag[A/T]aaggatttttaactgc	A	T	// 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 136377 //	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1894163	tgcatggcaataaaaa[G/T]ttagcatagtctttac	G	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // --- ///	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1904657	tggggcttgtgtgtaa[A/G]gggactctctcagcac	A	G	Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // intron // 0 // Hs.47288 // TRPM3 // 80036 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.11
SNP_A-1906651	tggtgtgcatgacaaa[A/C]aaagggtgatagagtc	A	C	51582 // Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, mRNA. /// NM_148174 // upstream // 7466 // Hs.459106 // OAZIN // 51582 // Homo	OAZIN	OAZIN, Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, q22.3
SNP_A-1982989	ttcagcctgcataagc[A/G]atagattagaagttct	A	G	// 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 674947 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-1949791	tttcaaaggctttgaa[C/T]gaagcttggtggagtt	C	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1955558	tttggtgttttccaaa[A/G]ttccttctgttattga	A	G	FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 78187 //	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-1824133	taaacagaaaacctga[C/G]cagcagaaaatattta	C	G	4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // downstream // 1303 // Hs.307734 // MME // 4311	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN q25.2
SNP_A-1861033	tcatagctcctttagc[A/G]ctttttcagtacttc	A	G	404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 8804 //	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-1674106	ggaaaaccaagaagaactctaagta[C/T]ataaattcaacaacataaatttggt	C	T	286343 // chromosome 9 open reading frame 150 /// NM_000550 // downstream // 42082 // Hs.75219 // TYRP1 //	C9orf150	C9orf150 , rs1074789, chromosome 9 open reading frame 150 ,p23
SNP_A-1705371	gagtgggttcttgcaactctaaaca[A/G]gaggacaaacatgtatcctttgtga	A	G	NM_002012 // intron // 0 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene	FHIT	FHIT , rs6762641, fragile histidine triad gene,p14.2
SNP_A-1740019	atcccaggagaaataattaaagtca[C/T]gctgattcgggtaacatatgggaca	C	T	betacellulin /// NM_015393 // upstream // 91905 // Hs.105460 // DKFZP564O0823 // 25849 // DKFZP564O0823 protein ///	BTC	BTC , rs6841078, betacellulin ,q13.3
SNP_A-1758418	attgaaacaagttgcctgttaatca[A/G]gttcatctcaaaatctattcaaggt	A	G	22920 // kinesin-associated protein 3 /// NM_152281 // upstream // 120790 // Hs.183702 // FLJ11752 // 92344 //	KIFAP3	KIFAP3 , rs6427247, kinesin-associated protein 3 ,q24.2
SNP_A-1812877	gtgggctccacaaccc[A/G]atgagtagtcggtgcg	A	G	153579 // Homo sapiens butyrophilin-like 9 (BTNL9), mRNA. /// NM_206880 // upstream // 24605 // --- // OR2V2 // 285659	BTNL9	BTNL9, Homo sapiens butyrophilin-like 9 (BTNL9), q35.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2126627	ataaacaagctgttcc[A/G]actttt gaacaaatcc	A	G	168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 468554	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2115722	agggtcctagaactga[A/G]aagtattgacgaatgt	A	G	// 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 253163 // --- // --- //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-2123161	agtggtgttactctga[A/C]cagtgcatttttattt	A	C	55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 133330 // --- // --- //	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. ,q36.2
SNP_A-2108945	agcttataatataacc[A/G]gcaagacaatttaaac	A	G	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 177017 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2163606	caaaaagaccagtctg[C/T]aagggaatgaaagggg	C	T	// Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 218598 //	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-2174238	cacactctctgacaag[A/G]attattcttcacaata	A	G	sapiens thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor) (TH /// NM_199228 // intron // 0 // Hs.1166 // THPO // 7066 // Homo sapiens	THPO	THPO, Homo sapiens thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor) (TH ,q27.1
SNP_A-2173545	cacaatggccagtgaa[A/G]cccgaatacagagtag	A	G	sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-2224596	cgtcagcccctgcaca[C/T]tgcggatcacatcacg	C	T	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.31
SNP_A-2215384	cctcacagcaacagta[A/G]caggagtaactgctcc	A	G	Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // intron // 0 // --- // --- // --- // ---	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2057308	aatatatctatatcaa[A/T]gttccttgacttacaa	A	T	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1255650 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2065267	aattgggttgtcaagg[A/T]ccaaaatactcaggct	A	T	23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // upstream // 31647 // Hs.487648 // SNX13 //	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-2099842	agagtagagtccagaa[A/G]aatataatgaacacat	A	G	Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), mRNA. /// ENST00000229922 // intron // 0 // -	CAP2	CAP2, Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), p22.3
SNP_A-2020214	gaatgaaccacggata[C/T]aggcgacaacccggat	C	T	Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 15, mRNA. /// NM_001001579 // intron // 0 //	PDE9A	PDE9A, Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 15, q22.3
SNP_A-1993655	acttggatcttaaaca[G/T]cgaagaagaccttacc	G	T	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 179499 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2003738	ggccaccctattcaaa[A/G]ttgcagctctttgcta	A	G	ENST00000282673 // intron // 0 // --- // --- // --- // ---	-	q23.31
SNP_A-1998057	tcattcctgaaacaaa[C/T]gaaccttcctcatggc	C	T	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA. /// NM_022779 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD	DDX31	DDX31, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, q34.13
SNP_A-2238645	ctctgttacttgggta[C/T]gggcacgtggatgtgg	C	T	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 228798 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2283223	gataattatccagtta[C/T]gcaaatagtatattct	C	T	ENST00000333644 // intron // 0 // --- // --- // --- // ---	-	q35.2
SNP_A-2291684	gcacacagtgctttga[C/T]ggtccataagtggacc	C	T	11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 680100 // Hs.497822 // DUSP10 // 11221 //	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2298213	gccatgagtacatctc[A/G]cagcaagtgttaaatt	A	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2310153	ggaacactgaatctca[C/T]agtgctctcagcaaac	C	T	sapiens FLJ40008 protein (FLJ40008), mRNA. /// ENST00000330148 // intron // 0 // --- // --- // --- // ---	-	-, Homo sapiens FLJ40008 protein (FLJ40008), p23.3
SNP_A-2274312	gacttgggagagggga[C/T]ctattcatgggagctc	C	T	283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 141963	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-2275784	gagacctagaatgtca[A/G]aaacttgccaggggggc	A	G	// 8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// NM_138788 // upstream // 148454 // Hs.504301 //	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2239875	ctgaacattaattgag[C/T]atatgtttgcttccca	C	T	Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000265071 // intron // 0 // --- // ---	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-2240127	ctgaagtcttggatga[A/G]gctatgacatcaagag	A	G	Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA. /// ENST00000355470 // intron // 0 // --- // --- // --- // ---	NCOA7	NCOA7, Homo sapiens nuclear receptor coactivator 7 (NCOA7), q22.32
SNP_A-2255705	cttgttctatatgctg[A/G]aaactgttgcagggat	A	G	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000320501 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017000	ttcagctcgttcagcc[A/G]catgatttcataggct	A	G	sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // intron // 0 // Hs.434980 // APP // 351 // Homo	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3
SNP_A-2027993	aaacgaatcaaattta[C/T]attgacaaagtatcta	C	T	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 741725 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2094938	agaatgcaatgacaac[C/T]gagagtggccatctcc	C	T	ENST00000245649 // intron // 0 // --- // --- // --- // ---	-	q13.33
SNP_A-2094534	agaataagacctctcc[A/T]aatgcattaagaccaa	A	T	10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 449619 // --- // ---	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2099011	agaggaaatgaacaga[C/T]atttgattcttataac	C	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2098657	agagccattaaaaaaa[C/T]ctctcaaagtagatat	C	T	Homo sapiens BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA. /// ENST00000323180 // intron // 0 // --- // --- // --- // ---	PHF21A	PHF21A, Homo sapiens BRAF35 p11.2
SNP_A-2120333	agtcatcaggtatttg[C/T]atcagtcaaattaagc	C	T	4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 161960 // Hs.21388 //	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-1801818	gtagtgtccatcacaa[C/G]ttactcaaataatgtg	C	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 548848 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1800679	gtagaacaaattacta[C/T]ggagctcagtggctta	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), /// NM_177423 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo	PPFIA1	PPFIA1, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), q13.3
SNP_A-1752503	ttgaattgtgtcctttcagaattca[C/T]aggctgaagtcctaacctgtatcca	C	T	C9orf121 // 158046 // chromosome 9 open reading frame 121 /// NM_182599 // upstream // 68838 // - // - // - // -	C9orf121	C9orf121 , rs4358869, chromosome 9 open reading frame 121 ,q22.1
SNP_A-1727691	gaaaccaaaatctctagcttcccaa[C/T]ttggcttaataccaattatagcaaa	C	T	10396 // ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 /// NM_182592 // downstream // 1757481 // Hs.200347 // FLJ39576 // 285525 // hypothetical	ATP8A1	ATP8A1 , rs10517058, ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 ,p13
SNP_A-1690659	gagaaaaagaatgaaatgtaatata[C/T]ggcactgagaacacactatgggaga	C	T	NM_024740 // intron // 0 // Hs.120824 // DIBD1 // 79796 // disrupted in bipolar affective disorder 1	DIBD1	DIBD1 , rs10502149, disrupted in bipolar affective disorder 1,q23.1
SNP_A-1667090	taaaatacatgacaagaaaagccac[A/C]gacttacattactactgctctggcc	A	C	2138 // eyes absent homolog 1 (Drosophila) /// NM_016027 // upstream // 455512 // Hs.118554 // LACTB2 // 51110 //	EYA1	EYA1 , rs10504499, eyes absent homolog 1 (Drosophila) ,q13.3
SNP_A-1663720	agagagaagacattcttgacccaac[A/G]gtagtgaaagttctccaccattatg	A	G	NM_024740 // intron // 0 // Hs.120824 // DIBD1 // 79796 // disrupted in bipolar affective disorder 1	DIBD1	DIBD1 , rs10502150, disrupted in bipolar affective disorder 1,q23.1
SNP_A-1664182	aagggccatattgattgaagcctta[A/G]aaaatatacagaaatttcaaggtat	A	G	NM_006457 // intron // 0 // Hs.154103 // LIM // 10611 // LIM protein (similar to rat protein kinase C-binding enigma)	LIM	LIM , rs10516951, LIM protein (similar to rat protein kinase C-binding enigma),q22.3
SNP_A-1871441	tctaacatatatttaa[C/T]tggcatttcagaggag	C	T	LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 //	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-1825686	taaatcactgggtaac[A/G]accataaaaaggatcg	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1830257	ggcttgactgaagtca[C/G]gggtctcatcattcct	C	G	2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 9079 // --- // --- // --- // --- ///	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-1955488	tttggtcgatgacaga[C/T]tacatattgggcaatg	C	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000247655 // downstream // 48111 // --- // -	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1987595	ggagctgttcctattc[C/G]aattatactggtttct	C	G	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA. /// Z26653 // intron // 0 // Hs.200841 // LAMA2 // 3908 // H.sapiens mRNA for laminin	LAMA2	LAMA2, Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), q22.33
SNP_A-1971567	cctaaataagaaagga[C/G]tcataatcattgcaat	C	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 79844 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1932242	ttcctccttttctcca[A/T]ggcattcgcacagtgc	A	T	Homo sapiens KIAA1573 protein (KIAA1573), mRNA. /// ENST00000335761 // intron // 0 // --- // --- // --- // ---	KIAA1573	KIAA1573, Homo sapiens KIAA1573 protein (KIAA1573), p31.3
SNP_A-1928062	ttcaattctgaattca[C/T]ggggccttggatggtg	C	T	Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1931967	ttcctacagaaattga[A/C]ctcatttgttgagaaa	A	C	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1919648	ggtcattccctgatga[C/T]gccaccagaagtgaac	C	T	4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000299766 // upstream // 39556 // --- // ---	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1899220	tggaaatgagcaaata[C/T]agaccatgcagagttc	C	T	221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1878183	tctgtattgcttacaa[C/T]tgaagaaagtgaggtt	C	T	146861 // Homo sapiens transmembrane protein 21A (TMEM21A), mRNA. /// NM_144975 // upstream // 23158 //	AMAC1	AMAC1, Homo sapiens transmembrane protein 21A (TMEM21A), q12
SNP_A-1967512	ttgattagaaaacaca[A/C]atggccactctttagg	A	C	149830 // Homo sapiens M8 protein (LOC149830), mRNA. /// ENST00000326539 // intron // 0 // --- // --- // --- // ---	LOC149830	LOC149830, Homo sapiens M8 protein (LOC149830), p13
SNP_A-1984324	tggcagtcaagcagca[A/G]tctctaattacctttc	A	G	Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-1980419	aatgtgtaagcagatt[A/G]tcatcatcagaatgaa	A	G	170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // --- // --- // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1829554	taagtggtatggtagc[C/T]attagagaaatgagaa	C	T	Homo sapiens chromosome 6 open reading frame 142 (C6orf142), mRNA. /// ENST00000358276 // intron // 0 // --- //	C6orf142	C6orf142, Homo sapiens chromosome 6 open reading frame 142 (C6orf142), p12.1
SNP_A-1841742	taggcataataataaa[G/T]gttgcagaaatgtgta	G	T	Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), mRNA. /// ENST00000005260 // intron // 0 // ---	BAIAP2L1	BAIAP2L1, Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), q22.1
SNP_A-1826155	taaattacaagtaagg[C/T]catttgctttttcttt	C	T	4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream //	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1827430	taactatacagaaata[C/T]ggcctaatttggggaa	C	T	Homo sapiens F-box protein 8 (FBXO8), mRNA. /// ENST00000296517 // intron // 0 // --- // --- // --- // --- ///	FBXO8	FBXO8, Homo sapiens F-box protein 8 (FBXO8), q34.1
SNP_A-1868862	tcctgacacaaatgca[C/G]taagacttctctgtct	C	G	ENST00000281244 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1863172	tcatttcacagttacc[A/G]agtctctaccagagat	A	G	1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// NM_001001688 // downstream // 22662 //	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1804675	gtcaggatggattgtt[C/T]aaagtgatgcctcttg	C	T	Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // intron // 0 // --- //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-1813302	gtggtgattggattac[A/G]atggtagatatgtaaa	A	G	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 330977 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1793436	ggtagtaatcaaaaaa[C/G]agcagcaatattatgg	C	G	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 753813 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2120476	agtccaagatccagtc[A/G]aacaatcataaagtcc	A	G	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA. /// NM_021721 // intron // 0 // Hs.256398 // ADAM22 // 53616 // Homo sapiens	ADAM22	ADAM22, Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, q21.12
SNP_A-2129817	atacatatatatttaa[C/G]gtatgcactatgatga	C	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2130901	gctacaaacttcattc[A/G]cccaattatttctcct	A	G	// 8600 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, mRNA. /// NM_033012 // upstream // 168356 // Hs.333791 //	TNFSF11	TNFSF11, Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, q14.11
SNP_A-2151801	atgtttatttttcaac[C/T]gatgtcatgtttttca	C	T	58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 376953 // Hs.501911 //	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2223124	ttcagagaataccata[A/G]agaaagtgaaagcaca	A	G	Homo sapiens reticulon 1 (RTN1), transcript variant 2, mRNA. /// NM_021136 // intron // 0 // Hs.368626 // RTN1 //	RTN1	RTN1, Homo sapiens reticulon 1 (RTN1), transcript variant 2, q23.1
SNP_A-2201317	ccaatatgctacccgg[A/G]aaaacattcactggct	A	G	Homo sapiens pleckstrin 2 (PLEK2), mRNA. /// ENST00000216446 // intron // 0 // --- // --- // ---	PLEK2	PLEK2, Homo sapiens pleckstrin 2 (PLEK2), q23.3
SNP_A-2203410	ccagaaagacatgttc[C/T]ctgtaggtaaccagaa	C	T	Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2203874	ccagagtgactggttc[A/G]atcacaacactgctgg	A	G	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 118728 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2188751	cagtggagaggactct[A/G]acctgggaggaaggaa	A	G	sapiens clone HQ0628 PRO0628 mRNA, complete cds. /// ENST00000313009 // upstream // 316990 // --- // --- // --- // ---	-	-, Homo sapiens clone HQ0628 PRO0628 complete cds. ,q12
SNP_A-2188712	cagtgctgtgcggcat[C/T]actgaacactgacctc	C	T	// 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 //	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098934	agagcttatgaaaaac[C/T]gaatacccactctaac	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2092962	ttctaggaaccgagga[C/G]gcaggtttgaatgtaa	C	G	3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream //	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-2101876	agatggcacagcggcc[C/T]attttggggagagaat	C	T	10871 // Homo sapiens CMRF35 leukocyte immunoglobulin-like receptor (CMRF35), mRNA. /// NM_152460 // upstream //	CD300C	CD300C, Homo sapiens CMRF35 leukocyte immunoglobulin-like receptor (CMRF35), q25.1
SNP_A-2077053	accaactctaatcagc[A/G]catttaaattacatgg	A	G	Homo sapiens mRNA for KIAA0830 protein, partial cds. /// ENST00000278505 // intron // 0 // --- // --- // --- // ---	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds. q21
SNP_A-2079405	accccatgaatatgta[A/C]gatcggtcaattttaa	A	C	Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), mRNA. /// ENST00000320580 // intron // 0 // --- // ---	PACS1	PACS1, Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), q13.2
SNP_A-2080108	accggatgctttttcc[C/T]caataatctttaggag	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 112569 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2085535	actccaggttgggtga[C/T]agagtaagatcctgtc	C	T	Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 //	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1
SNP_A-2090202	acttgatgttgatagc[A/G]acaggagacaggcaaa	A	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1543060 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2252497	cttcctctgtaaggcc[A/G]aatagtaaaagtttca	A	G	27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 948895 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2244120	ctgctttagtagacta[C/T]ctctattagaactaag	C	T	Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // --- // --- // --- // ---	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-2231538	ctatttatttggttca[C/T]agtctgttgaccccta	C	T	1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 183961 // Hs.417962 // DUSP4 // 1846 // Homo	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-2284887	gatccagattacaagc[A/G]actcaagaaactagtt	A	G	sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- // --- ///	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2270690	gacagccttaatttag[A/G]agtgaggaggaacacc	A	G	221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 //	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2309332	ggaaaaggtagtatac[A/G]ggacaagccattagat	A	G	ENST00000356458 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-2267672	gaatcactggtataga[C/T]agagcagtactgttac	C	T	5330 // Homo sapiens phospholipase C, beta 2 (PLCB2), mRNA. /// NM_207380 // downstream // 11854 // Hs.32433 //	PLCB2	PLCB2, Homo sapiens phospholipase C, beta 2 (PLCB2), q15.1
SNP_A-2279483	gaggatgaagaaaagg[A/G]aaacaaatcagagaga	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 275515 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2231932	ctcaacacagtttgaa[C/T]tccttcctcattgcaa	C	T	// 25805 // Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI), mRNA. /// ENST00000224324 // downstream // 154223 // --- // --- // --- //	BAMBI	BAMBI, Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI), p12.1
SNP_A-2235393	ctccctgtttatgtaa[C/T]gcctgaactttgcaca	C	T	4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// NM_032829 // upstream // 7258 //	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11
SNP_A-2079780	accctgactctgaaaa[A/C]agccctgaaagacaca	A	C	Homo sapiens scavenger receptor class B, member 1 (SCARB1), mRNA. /// ENST00000261693 // intron // 0 // --- //	SCARB1	SCARB1, Homo sapiens scavenger receptor class B, member 1 (SCARB1), q24.31
SNP_A-2026962	aaacagaaaacagctt[A/T]aaaaatatgtgtacta	A	T	sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // intron // 0 // Hs.487561 //	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-2017011	atgtttcataaccacc[C/G]aattccagttcagttt	C	G	163747 // Homo sapiens hypothetical protein FLJ40201 (FLJ40201), mRNA. /// NM_014762 // downstream // 6699 //	FLJ40201	FLJ40201, Homo sapiens hypothetical protein FLJ40201 (FLJ40201), p32.3
SNP_A-2003278	acacagaagcagacaa[A/C]agaggaggaggccatg	A	C	/// ENST00000281516 // upstream // 167818 // --- // --- // --- //	-	q14.11
SNP_A-1995953	aataatgagaaagaga[C/T]gtggatggagcctaga	C	T	Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319198 // intron // 0 // --- // --- // --- // --- ///	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2177241	cacctggccccaaacc[C/G]gactccgctagcatgt	C	G	Homo sapiens KIAA0090 protein (KIAA0090), mRNA. /// ENST00000264214 // intron // 0 // --- // --- // --- // ---	KIAA0090	KIAA0090, Homo sapiens KIAA0090 protein (KIAA0090), p36.13
SNP_A-2212346	ccctggtttctgagtc[A/G]ccacaatggcaatcat	A	G	/// ENST00000330649 // upstream // 887397 // --- // --- // --- //	-	q11.2
SNP_A-2209075	cccaggagatcaaagc[A/G]caagtaatgggtcttt	A	G	Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000278723 // intron // 0 // --- // ---	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2214301	cctacatctctaccttt[C/T]aaatggctgttaattc	C	T	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2220219	ccttccaacttcctga[C/T]caacagtcctgtctgt	C	T	LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 33834 // Hs.307086 //	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2152721	attaatgacatactaa[A/G]cttactgtgtcttaag	A	G	81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA. /// NM_152330 // upstream // 149903 //	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-2145831	atgccatatgtaccca[A/G]cgaattatctagttaa	A	G	Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 //	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.2
SNP_A-2159766	atttagtaaatgctaa[A/G]atgtagatctcaaggc	A	G	4026 // Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), mRNA. /// ENST00000312675 // downstream // 78778 // --- // --- // --- // ---	LPP	LPP, Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), q28
SNP_A-2116906	aggtcttgcattgaaa[C/T]gttttatccatcttgg	C	T	/// ENST00000330649 // upstream // 910984 // --- // --- // --- // ---	-	q11.2
SNP_A-2115353	aggggcaagtgacaga[A/G]caagtgatgaaataat	A	G	// 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 163335 // Hs.446083 // PTPRD	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1787314	gggaagagccagtgga[G/T]aagtgtttccaagtca	G	T	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1741777	acatgccttatccaagaaagtttaa[A/G]tgattagccaatcgggactagttta	A	G	1131 // cholinergic receptor, muscarinic 3 /// NM_021186 // upstream // 874546 // Hs.136241 // ZP4 // 57829 // zona	CHRM3	CHRM3 , rs1357520, cholinergic receptor, muscarinic 3 ,q43
SNP_A-1754822	aactgtgacccattcagaagttcta[C/T]ctcctaagactttcccaaaggtgac	C	T	NM_004438 // intron // 0 // Hs.244624 // EPHA4 // 2043 // EphA4	EPHA4	EPHA4 , rs2288627, EphA4,q36.1
SNP_A-1860851	tcataatttatagtga[C/G]attttcaagagccaat	C	G	91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream //	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-1848987	tatgcagcataaacccc[C/T]gcccattttaagcgta	C	T	FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// NM_018022 // downstream	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-1827380	taactaatggatacta[C/T]acttaatgcctgggtt	C	T	162083 // Homo sapiens TNT protein (TNT), mRNA. /// NM_024773 // upstream // 133906 // Hs.145717 // FLJ13798	TNT	TNT, Homo sapiens TNT protein (TNT), p12.1
SNP_A-1824840	taaagcaagagcaaaa[G/T]atgtttttgactgagg	G	T	8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-1820683	gtttcaggttgtaagc[C/T]ctagagacctgttata	C	T	Homo sapiens PX domain containing serine/threonine kinase (PXK), mRNA. /// ENST00000302779 // intron // 0 // --- // --- // ---	PXK	PXK, Homo sapiens PX domain containing serine p14.3
SNP_A-1838621	tagacaactttcacaa[A/C]cagcttagaaaaatcc	A	C	// 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 383670 // --- // --- // --- // ---	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-1970300	gcattgtaaagtgatc[A/G]agagttgttaaatctt	A	G	Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000340699 // intron // 0 // --- // ---	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-1975873	acgtgaatgaacgaat[C/G]atgatggccaacaggt	C	G	Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // --- // --- // --- // ---	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-1973572	ctgaagataaatatgc[A/G]agaacgtatttttctt	A	G	/// ENST00000330649 // upstream // 913153 // --- // --- // --- // ---	-	q11.2
SNP_A-1958638	ttttctcacttgaacg[A/G]atgttatattaagctg	A	G	6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // upstream // 456733 // Hs.505007 // SOX5 // 6660 // Homo	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-1899469	tggaagagctgttgtg[A/C]atcttctagtaattaa	A	C	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-1889973	tgatagtaaagataca[A/G]caattaagctcatcta	A	G	ENST00000329238 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1923643	ttaggtccaggtttct[C/T]aacagcagtgctactg	C	T	ENST00000355094 // intron // 0 // --- // --- // --- // ---	-	q22.31
SNP_A-1909578	tgtatttttaatccca[A/G]aagtgttgaatgagtc	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 317554 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-1910713	tgtccttgctccattg[C/T]atcacctttgctcctt	C	T	55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 21218 //	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-1880315	tcttctttgtttaagg[C/T]agctccctgcatcttc	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 176657 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1953327	tttgaaacattcaacc[C/T]gccaaaatatccaatg	C	T	ENST00000354860 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-1934886	ttctgaactgccatcc[C/T]atcttcccacttttgc	C	T	8477 // Homo sapiens G protein-coupled receptor 65 (GPR65), mRNA. /// NM_138317 // downstream // 149401 //	GPR65	GPR65, Homo sapiens G protein-coupled receptor 65 (GPR65), q31.3
SNP_A-1946891	tttaagctcccctcaa[C/G]tgtaataaatcatggg	C	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 422844 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1967708	tttctccttgtaatta[C/T]gccaatgagattgata	C	T	57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-1968969	cactaatatgtactga[C/T]agcctccagcctgagg	C	T	375108 // Homo sapiens membrane-associated phospholipase A1 beta (LOC375108), mRNA. /// ENST00000344577 // intron // 0 // --- // --- // --- // ---	LOC375108	LOC375108, Homo sapiens membrane-associated phospholipase A1 beta (LOC375108), q11.2
SNP_A-1978129	gatgggtgagtgcaca[A/G]aaagagttgggtgccg	A	G	10611 // Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// NM_001203 // upstream // 86751 // Hs.480321 // BMPR1B // 658 // Homo	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1988380	tgcaaaggatggcaag[C/T]catggtacaatttaaa	C	T	Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// ENST00000262861 // intron // 0 // --- // --- // --- // --- /// ENST00000308942 // intron // 0 // --- // --- //	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1831561	taattaatattttctc[A/C]gaatgactcagtgttg	A	C	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3456930 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1832922	tacaattagaatacca[C/T]cacttttaatatctca	C	T	223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // upstream // 25816 // Hs.2533 // ALDH9A1 // 223 // Human gamma-	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-1828080	taagacagcagaggcc[A/G]agtctacattagagcc	A	G	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 444067 // Hs.369675 // ANGPT1 // 284 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1717407	ggacatggaaagacagtctcataca[C/T]gcaattgtgtgaagaacaagttcaa	C	T	// 4697 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa /// NM_152745 // downstream // 1888073 // Hs.343660 // NXPH1 // 30010 // neurexophilin 1	NDUFA4	NDUFA4 , rs766653, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa ,p21.3
SNP_A-1797344	ggttgtgagggctcac[A/G]aagacatactcattat	A	G	Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// ENST00000274335 // intron // 0 // --- // --- // --- // ---	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1804109	gtcacaggtaaggaac[A/G]gatggcttcaaatatg	A	G	Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // --- // --- // --- // --- ///	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3), p13.3
SNP_A-1803591	gtcaaaacacaaccaa[C/T]agataatgttaacatg	C	T	84911 // Homo sapiens zinc finger protein 382 (ZNF382), mRNA. /// NM_153257 // downstream // 1480 // Hs.157203 //	ZNF382	ZNF382, Homo sapiens zinc finger protein 382 (ZNF382), q13.12
SNP_A-2115455	agggggctgccagctg[A/C]aagagaaagtgttcgc	A	C	ENST00000299064 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2118672	agtacaaagtcctgaa[A/G]gtaggaatgagcttgc	A	G	Homo sapiens erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) (EPB41), transcript variant 3, mRNA. /// NM_203342 // intron // 0 // Hs.175437 // EPB41 //	EPB41	EPB41, Homo sapiens erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) (EPB41), transcript variant 3, p35.3
SNP_A-2120914	agtctacaaagagatc[A/G]ctgtcattttcaataa	A	G	Homo sapiens chromosome 6 open reading frame 151 (C6orf151), mRNA. /// ENST00000342415 // CDS // 0 // --- // --	C6orf151	C6orf151, Homo sapiens chromosome 6 open reading frame 151 (C6orf151), p24.3
SNP_A-2166033	caaataatctttaagc[C/T]gcattgaaaaaataaa	C	T	// 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA. /// NM_032813 // upstream // 266594 //	FLJ14624	FLJ14624, Homo sapiens hypothetical protein FLJ14624 (FLJ14624), q32.3
SNP_A-2216083	cctcccaccctgctaa[C/T]tgaaggcttgcctcgg	C	T	7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 748027 // --- // --- // --- //	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-2227237	ctacaaaaaagcctta[C/T]gcttgaactggaggtg	C	T	9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 3509 // --- // --	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2205325	ccagtccttggatcta[C/G]acctgccaatctccat	C	G	sapiens glucokinase (hexokinase 4) regulator (GCKR), mRNA. /// ENST00000264717 // intron // 0 // --- // --- // --- // ---	GCKR	GCKR, Homo sapiens glucokinase (hexokinase 4) regulator (GCKR), p23.3
SNP_A-2183512	cagcagcaatggatga[C/G]gtcagggcattagagc	C	G	-- /// ENST00000314071 // upstream // 600699 // --- // --- // ---	-	p13.3
SNP_A-1989908	gctcatagcaataaaa[A/G]aacctggtgaaatatg	A	G	// 2887 // Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // upstream // 164779 // Hs.164060 // GRB10 // 2887 // Homo	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.1
SNP_A-2012728	tcagagttcaagcaaa[C/T]aacctctgagttttga	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2032555	aaataaaatgctcata[G/T]gttgggttaaagctaa	G	T	// 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1842107 // Hs.166109 // ELAVL2	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.2
SNP_A-2022449	aaaaatatgaagaaaa[C/T]ggattgtagtaataga	C	T	// 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2034950	aaatgatcaaatctca[C/T]ctcatttcaaataaat	C	T	// 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2980839 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2081216	aactgcaggatttta[C/G]gttttgaatttatatc	C	G	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1364350 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2107565	agctatacttttcaga[G/T]ccattccaatattctt	G	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 240371 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2094834	agaatctcgccttgtc[C/T]aaagagaggactccag	C	T	57553 // Homo sapiens mRNA for KIAA1364 protein, partial cds. /// ENST00000252134 // upstream // 1698 // --- // --- // ---	MICAL3	MICAL3, Homo sapiens for KIAA1364 protein, partial cds. ,q11.21
SNP_A-2055388	aataagtaaaatgaaa[A/C]ttggaattggaccaca	A	C	/// ENST00000358396 // downstream // 718608 // --- // --- // ---	-	p12.2
SNP_A-2245432	ctgggacaaaacttac[C/T]gctctgataaagaatt	C	T	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-2253885	cttgaatttcctttca[A/T]ctcacacttcccaaag	A	T	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA. /// ENST00000289890 // intron // 0 // --- // --- // --- // --- /// ENST00000356138 // intron	MACF1	MACF1, Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, p34.3
SNP_A-2276772	gagataagaaagcaca[A/G]tgcagttagcaagctg	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 878628 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2274079	gacttatatcttttag[A/C]cctggaaaatttctct	A	C	144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000331366 // upstream // 310210 // --- // --- // --- // ---	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2281008	gagtaaagtttaaagg[C/T]ccaacaaaggcttatt	C	T	10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 //	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2261837	gaaataaacataaaca[C/T]gggattctgccagtaa	C	T	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2297608	gccagattccagggca[C/T]tgatttggcatttctt	C	T	/// ENST00000310149 // downstream // 17688 // --- // --- // ---	-	q23.3
SNP_A-2289763	gcaaaatcttcagtca[A/G]taggttctaggtatga	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2358256 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2292980	gcagaaggccatttaa[C/T]gtgaaaaaaagcacct	C	T	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2303991	gctccaagatcatgac[A/T]cattctttttctctc	A	T	26689 // Homo sapiens olfactory receptor, family 4, subfamily D, member 1 (OR4D1), mRNA. /// NM_001004707 //	OR4D1	OR4D1, Homo sapiens olfactory receptor, family 4, subfamily D, member 1 (OR4D1), q23.2
SNP_A-2266071	gaaggccacagtctac[A/G]acattttggttagagg	A	G	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3), mRNA. /// ENST00000279027 // intron // 0 // --- // --- // --- // --- ///	SLC13A3	SLC13A3, Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3), q13.12
SNP_A-2249032	ctgtttagtgcccatc[A/G]ctccatggcttcactg	A	G	Homo sapiens phosphatidylinositol transfer protein, cytoplasmic 1 (PITPNC1), transcript variant 2, mRNA. /// NM_012417 // intron // 0 // Hs.231295 // PITPNC1 // 26207 //	PITPNC1	PITPNC1, Homo sapiens phosphatidylinositol transfer protein, cytoplasmic 1 (PITPNC1), transcript variant 2, q24.2
SNP_A-2059341	cttcctgtgtactgac[A/C]agaagactgaaaaatt	A	C	Homo sapiens keratin, hair, basic, 4 (KRTHB4), mRNA. /// ENST00000257951 // intron // 0 // --- // --- // --- // ---	KRTHB4	KRTHB4, Homo sapiens keratin, hair, basic, 4 (KRTHB4), q13.13
SNP_A-2073939	acagttaataaaaata[A/G]cacaatgtcacactta	A	G	Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 //	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2092557	agaaataatattcaaa[C/G]ttaaaccatactctga	C	G	Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 //	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2103147	agcaacaggtgtaggt[A/C]aatttgatgatcaagt	A	C	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2461918 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2088924	actgtttggcctgtcc[G/T]cgtcgctgctatctct	G	T	Homo sapiens kallikrein 12 (KLK12), transcript variant 1, mRNA. /// NM_145895 // 5UTR // 0 // Hs.411572 // KLK12 //	KLK12	KLK12, Homo sapiens kallikrein 12 (KLK12), transcript variant 1, q13.41
SNP_A-2014269	gaccacgctcttttaa[A/G]tagcaaagctgtagat	A	G	7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 36299 //	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-1989954	cactgccatgtcagca[G/T]tatgtcttcaaatata	G	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1395729 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1991953	tctaaagtgaggtttt[C/G]aaaaattgtctgtatt	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2557205 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2001447	caacctgctcacacac[C/G]aagcacattgctacta	C	G	sapiens caspase 7, apoptosis-related cysteine protease (CASP7), transcript variant alpha, mRNA. /// NM_033339 // intron // 0 // Hs.9216 // CASP7 // 840 // Homo sapiens	CASP7	CASP7, Homo sapiens caspase 7, apoptosis-related cysteine protease (CASP7), transcript variant alpha, q25.3
SNP_A-2171146	caataggaacataaaa[A/G]ctcaagtaactttaga	A	G	8809 // Homo sapiens interleukin 18 receptor 1 (IL18R1), mRNA. /// NM_003853 // upstream // 505 // Hs.158315 //	IL18R1	IL18R1, Homo sapiens interleukin 18 receptor 1 (IL18R1), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2226194	ctaactactcaaccac[A/G]gagagatggctgagca	A	G	// Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- ///	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q25.1
SNP_A-2220630	ccttgaaaacacacta[A/G]gtgcaagaagttggta	A	G	SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// NM_178540 //	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2152389	attaaccatcacacca[C/T]atttttccgcctttga	C	T	ENST00000354285 // intron // 0 // --- // --- // --- // ---	-	p11.21
SNP_A-2141167	atctggctgcccaaaa[A/T]tgattccttcctctta	A	T	4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 //	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22
SNP_A-2130100	atacccaagagatttg[A/G]aaatatgtcagtacaa	A	G	// Homo sapiens mesenchyme homeo box 1 (MEOX1), transcript variant 2, mRNA. /// NM_004527 // upstream //	MEOX1	MEOX1, Homo sapiens mesenchyme homeo box 1 (MEOX1), transcript variant 2, q21.31
SNP_A-2126564	ataaaatgcttccaca[C/T]gtattctgaaatctag	C	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 1091565 //	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1800456	gtactgagaaaatctg[A/G]caacatacttattcct	A	G	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 271383 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-1798428	gtaaatcactggtgcc[A/G]gaagatttttagagt	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 754235 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1792762	ggtaagctaggagaag[A/G]cagtctggcacacagg	A	G	9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 153741 // Hs.335079 // MAP1B // 4131 // Homo sapiens	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-1691228	tgccaggacacgcatgtacacaaac[A/G]ctcactgacccgacgacaggcc cag	A	G	NM_013279 // intron // 0 // Hs.184640 // C11orf9 // 745 // chromosome 11 open reading frame 9	C11orf9	C11orf9 , rs198475, chromosome 11 open reading frame 9,q12.2
SNP_A-1710143	tgccccaccaaaatgaacacataaa[C/T]aagaaatgcaagatccaagaaa cag	C	T	// 6653 // sortilin-related receptor, L(DLR class) A repeats-containing	SORL1	SORL1 , rs1219391, sortilin-related receptor, L(DLR class) A repeats-containing,q24.1
SNP_A-1700255	atattgcattctggagagaacagga[A/G]caaataagattcagcttcataaacc	A	G	NM_000721 // intron // 0 // Hs.437444 // CACNA1E // 777 // calcium channel, voltage-dependent, alpha 1E subunit	CACNA1E	CACNA1E , rs10489641, calcium channel, voltage-dependent, alpha 1E subunit,q25.3
SNP_A-1815972	gttaattttccagata[C/G]ctgaaggttaagttcc	C	G	285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// NM_022374 // downstream // 52723	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-1843248	tagtccttcttatcca[C/T]tatattgacttgtaat	C	T	Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-1853418	tattttctcctattcc[A/G]caggttgcaaacttac	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 161861 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1854628	tcaacaattgcttaca[G/T]atttttcctcagtgag	G	T	FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ11017), mRNA. /// NM_018302 // downstream	FLJ11017	FLJ11017, Homo sapiens hypothetical protein FLJ11017 (FLJ11017), p14
SNP_A-1989195	ttctgggacatgagcc[C/G]gaattgaggattgtag	C	G	56164 // Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA. /// NM_032944 // downstream //	STK31	STK31, Homo sapiens serine,p15.3
SNP_A-1981659	aaatagtgtagtgcaa[C/T]ggaaaaagtacagaaa	C	T	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 224760 // --- // --- // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. ,q11.2
SNP_A-1963674	gctaggcaatttacac[G/T]cctatcatctgtattt	G	T	Homo sapiens chromosome 2 open reading frame 32 (C2orf32), mRNA. /// ENST00000263655 // intron // 0 // --- // --	C2orf32	C2orf32, Homo sapiens chromosome 2 open reading frame 32 (C2orf32), p14
SNP_A-1965398	tttagctgtcaagctc[A/G]ctggtcatctttccct	A	G	Homo sapiens calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 2, mRNA. /// ENST00000327479 // intron // 0 // --- // --- // --- // --- ///	CACNB4	CACNB4, Homo sapiens calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 2, q23.3
SNP_A-1946389	tttaaacaggtacata[C/T]aaaggtagatggaggg	C	T	Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, mRNA. /// NM_000635 // intron // 0 // Hs.465709 // RFX2 // 5990 //	RFX2	RFX2, Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 2, p13.3
SNP_A-1884880	tgaatcttctgatgga[A/G]agcacacatagaacaa	A	G	6332 // Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA. /// NM_002976 // upstream //	SCN7A	SCN7A, Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), q24.3
SNP_A-1885809	tgacagtatttcaaag[A/C]catgctcctgaggctt	A	C	55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// NM_014143 // upstream // 4569 //	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1959737	ttttggtgaagccatc[A/G]cacagcctgcacagcc	A	G	25914 // Homo sapiens rotatin (RTTN), mRNA. /// NM_004232 // upstream // 31806 // Hs.44439 // SOCS6 //	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-1966911	ccccaaatgctcctaa[C/T]atccagacattgtggc	C	T	199834 // Homo sapiens late cornified envelope 4A (LCE4A), mRNA. /// NM_178354 // upstream // 54655 // --- // LCE1F //	LCE4A	LCE4A, Homo sapiens late cornified envelope 4A (LCE4A), q21.3
SNP_A-1973869	atcactgctttctgta[A/G]aatttttgtcttttgt	A	G	Homo sapiens RAS protein activator like 2 (RASAL2), transcript variant 1, mRNA. /// NM_170692 // intron // 0 //	RASAL2	RASAL2, Homo sapiens RAS protein activator like 2 (RASAL2), transcript variant 1, q25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1856713	tcacatcatcaggtta[C/T]gcatttaacaggttat	C	T	/// ENST00000358396 // downstream // 733106 // --- // --- // ---	-	p12.2
SNP_A-1845665	tataggaatctggtca[A/G]aaatcaagtcattgtg	A	G	2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 262059 // Hs.122926 // NR3C1 //	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1863394	tcatttttgaaaaaac[C/T]gtatctcatggatgtt	C	T	Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// ENST00000287097 // intron // 0 // --- // ---	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1866573	tcccccagcactgaaa[C/T]aattctcttcatcctt	C	T	3221 // Homo sapiens homeo box C4 (HOXC4), transcript variant 1, mRNA. /// NM_153633 // downstream // 29736 //	HOXC4	HOXC4, Homo sapiens homeo box C4 (HOXC4), transcript variant 1, q13.13
SNP_A-1837231	tacttaatattaccca[C/T]ccaaaaggagaaaact	C	T	10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 //	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-1680310	tcataatgccaaactcctaatcaaa[C/G]aatcaattgccttttagaatctttc	C	G	NM_000255 // downstream // 794028 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs2996255, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-1680072	tttatgaaatcttgtttttgaaagg[C/T]caggtaaattacagctaatacagtt	C	T	NM_004061 // intron // 0 // Hs.333997 // CDH12 // 1010 // cadherin 12, type 2 (N-cadherin 2)	CDH12	CDH12 , rs7714938, cadherin 12, type 2 (N-cadherin 2),p14.3
SNP_A-1799670	gtaatttcactactta[C/T]gtagtcagaggtggga	C	T	55791 // Homo sapiens receptor-interacting factor 1 (RIF1), mRNA. /// NM_178454 // downstream // 30730 // Hs.485606	RIF1	RIF1, Homo sapiens receptor-interacting factor 1 (RIF1), p13.3
SNP_A-1812523	gtggccgctgtagaac[A/C]catctaaaaggggctg	A	C	Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA. /// ENST00000263734 // intron // 0 // --- // --- // --- // ---	EPAS1	EPAS1, Homo sapiens endothelial PAS domain protein 1 (EPAS1), p21
SNP_A-2116860	aggtctgagaaatgcg[C/G]actgattaatagagtt	C	G	ENST00000332168 // intron // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2150421	atgtgaaactgctcca[C/T]gaaccccaaagaatta	C	T	1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 87820 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2165574	caaagcttacaggaaa[C/T]atcccttgcaacccac	C	T	11213 // Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), mRNA. /// NM_033647 // upstream //	IRAK3	IRAK3, Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), q14.3
SNP_A-2168426	caacttctgggatcag[A/G]caactagaagaccttg	A	G	// 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2171609	caatctaaaggccaca[A/G]aaagaaaagaacatct	A	G	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2184463	ttcgggaagtctggta[A/T]gattgttcactaaaat	A	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 894841 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2185999	caggcagatcgagaaa[A/G]atcaggacacaccaga	A	G	3737 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 2 (KCNA2), mRNA. /// NM_002232 // downstream // 29375 // Hs.169948 // KCNA3 //	KCNA2	KCNA2, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 2 (KCNA2), p13.3
SNP_A-2198877	catttgaattgacagg[A/G]agaactgcacggagtg	A	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2197167	cattcaagcaggaaaa[C/G]atttttctctagaaaa	C	G	sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000262233 // intron // 0 // --- // ---	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2005082	ggacaagtatccaaac[C/T]atattataggcctcct	C	T	// 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 //	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2019004	agaagaaatacaaaaa[C/T]actcggcacccgacaa	C	T	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, mRNA. /// NM_101395 // intron // 0 // Hs.368240 // DYRK1A // 1859 //	DYRK1A	DYRK1A, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, q22.13
SNP_A-2028883	aaactttcaaaagtca[A/G]tcctaaggaatacaaa	A	G	// Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // --- // --- // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2082599	acggaggatggctcac[A/G]gtgaagaaaagtccag	A	G	2251 // Homo sapiens fibroblast growth factor 6 (FGF6), mRNA. /// NM_020374 // downstream // 4570 // Hs.302977 //	FGF6	FGF6, Homo sapiens fibroblast growth factor 6 (FGF6), p13.32
SNP_A-2096780	agactataaaatgccc[C/T]gaaggcaaagcctggg	C	T	Homo sapiens POU domain, class 2, transcription factor 3 (POU2F3), mRNA. /// ENST00000260264 // intron // 0 // --- // -	POU2F3	POU2F3, Homo sapiens POU domain, class 2, transcription factor 3 (POU2F3), q23.3
SNP_A-2059646	aatctctgtggctggc[A/G]aataccaggaagtagc	A	G	23077 // Homo sapiens MYC binding protein 2 (MYCBP2), mRNA. /// NM_003843 // upstream // 7189 // Hs.115166 //	MYCBP2	MYCBP2, Homo sapiens MYC binding protein 2 (MYCBP2), q22.3
SNP_A-2059642	aatctctgtcctgcga[A/T]tcctctgctttaaaat	A	T	// 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 284064 // Hs.533964 //	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2055833	aatacaaatgaatgtc[A/G]caagagtaacactagg	A	G	Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2058570	aatcagctatgaataa[A/G]tacaatgaggccgtac	A	G	8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 181413	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2050892	aaggcctgcctggacc[A/G]actgcacagaggagca	A	G	7539 // Homo sapiens zinc finger protein 37 homolog (mouse) (ZFP37), mRNA. /// NM_001860 // upstream //	ZFP37	ZFP37, Homo sapiens zinc finger protein 37 homolog (mouse) (ZFP37), q32
SNP_A-2237485	ctctccttcaataaca[A/C]caactcctgcggcaac	A	C	ATP1A1 // 476 // Homo sapiens ATPase, Na+/K+ transporting, alpha 1 polypeptide (ATP1A1), transcript variant	ATP1A1	ATP1A1, Homo sapiens ATPase, Na+,p13.1
SNP_A-2240314	ctgaattcctggactc[A/G]cactatccacagcctc	A	G	ENST00000331807 // intron // 0 // --- // --- // --- // ---	-	q33.1
SNP_A-2229193	ctagctgggtcactaa[G/T]gccaaatcacccctcc	G	T	11240 // Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA. /// NM_013358 // upstream // 45681 //	PADI2	PADI2, Homo sapiens peptidyl arginine deiminase, type II (PADI2), p36.13
SNP_A-2260022	gaaaataagaaataca[A/G]atagaggctctgtgtc	A	G	// 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 652462 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-2284553	gatcacctacaaagac[A/G]actacaatgcatcagc	A	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2309255	ggaaaactgggctttc[A/T]aactcagaggattacc	A	T	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 4 (RAPGEF4), mRNA. /// ENST00000264111 // intron // 0 // --- // --- // --- // --- /// ENST00000354762 // intron // 0 // ---	RAPGEF4	RAPGEF4, Homo sapiens Rap guanine nucleotide exchange factor (GEF) 4 (RAPGEF4), q31.1
SNP_A-2308514	gctttagtgagagact[C/G]aaagtttatctcttgg	C	G	// 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 187937 // Hs.494312 //	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2306716	gctgtcctctactcta[C/T]accaacattcttgctg	C	T	Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA. /// ENST00000311083 // intron // 0 // --- // --- // --- // ---	CSRP2	CSRP2, Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), q21.2
SNP_A-2293499	gcagcactagcatatg[A/G]caataaccagcaaaga	A	G	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2244211	ctggaaaagcagcaaa[C/T]gatgttgttttgttgt	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2255625	cttgtgtgagtctcac[A/G]gaatccgaggccctgg	A	G	// Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), /// ENST00000305579 // downstream // 80083 // --- // --- // ---	IL12A	IL12A, Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), q25.33
SNP_A-2050538	aaggatggtccaaaga[G/T]tatgccactagccata	G	T	10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream //	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-2076942	accaaatctatttctg[C/T]acatatccagactgtc	C	T	// 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1939138 // Hs.27214 // KCNC2 // 3747 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2095783	agacacttgagcttct[A/G]aagggtctgatacttc	A	G	57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 38984 //	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2028830	aaacttgcatatttca[G/T]ggaatttttgtttata	G	T	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000277647 // upstream // 80260 // --- // --- // --- // ---	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2030989	aaaggagaagaagtga[A/G]gaaccaatgtctattc	A	G	60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 92472 // Hs.462270	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-2044885	aagaacaacaaaaaaa[G/T]aacctgtatctaggcc	G	T	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 //	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-2012199	aagggccataaataga[C/T]caataatgacagtata	C	T	ENST00000360752 // intron // 0 // --- // --- // --- // ---	-	p33
SNP_A-2176617	gctccacttgagacca[C/G]gtatcaggatgttcag	C	G	ENST00000326161 // 5UTR // 0 // --- // --- // --- // ---	-	q32.1
SNP_A-2227478	ctacagactccagcca[C/G]gcaagcttttctgctc	C	G	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 361577 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2206681	ccatgagcacttataa[C/G]acaggaagtatgatat	C	G	// 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 704013 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-2207780	cccaaacatttcagaa[C/T]gcgctttgttttcaag	C	T	// 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// ENST00000319884 // upstream	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2122479	agtgctagtaggtaga[A/T]actttaggtggcactg	A	T	6375 // Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA. /// NM_001937 // downstream // 108406 // Hs.80552	XCL1	XCL1, Homo sapiens chemokine (C motif) ligand 1 (XCL1), q24.2
SNP_A-2121660	agtgaatgtggagtac[A/T]aattttctgagaagta	A	T	// 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1066010 // Hs.98262 // GRIK2	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2115065	agggcgttgtcatcaa[A/G]gagactaaactgctgc	A	G	// Homo sapiens hypothetical protein MGC26710 (MGC26710), mRNA. /// ENST00000336726 // intron // 0 // ---	HORMAD2	HORMAD2, Homo sapiens hypothetical protein MGC26710 (MGC26710), q12.2
SNP_A-2111331	aggagctcgagaggtc[A/C]aaaagaagcgtgtaat	A	C	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// ENST00000264377 // intron // 0 // --- //	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-1799498	gtaatggaattgacta[C/T]cctttcataaaatgaa	C	T	// Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 206865 //	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-1797441	ggtttactggagccac[C/T]gtatttctccatgcac	C	T	7879 // Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA. /// NM_014049 // upstream // 28052 //	RAB7	RAB7, Homo sapiens RAB7, member RAS oncogene family (RAB7), q21.3
SNP_A-1840749	tagctacaatattaca[A/G]tctctgtctctgtcta	A	G	10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1,	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1816417	gttagcaggactgtca[C/G]gaagccctctcaaagg	C	G	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000330684 // intron // 0 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1849939	tatgtcagaacttaaa[C/T]tgtgtagttgaaatat	C	T	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 881169 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-1983689	gaaacatgatcatgga[C/G]acaatggtttacatta	C	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1934989	ttctgagatttttcaa[C/T]attaggcacaatggta	C	T	Homo sapiens fucosidase, alpha-L- 2, plasma (FUCA2), mRNA. /// ENST00000002165 // intron // 0 // --- // --- // --- // ---	FUCA2	FUCA2, Homo sapiens fucosidase, alpha-L- 2, plasma (FUCA2), q24.2
SNP_A-1907895	tgtaatccagacagca[C/G]tataggaacatagtgc	C	G	Homo sapiens tektin 1 (TEKT1), mRNA. /// ENST00000338694 // intron // 0 // --- // --- // --- // ---	TEKT1	TEKT1, Homo sapiens tektin 1 (TEKT1), p13.1
SNP_A-1913649	tgtgtagatagattga[C/T]caaggggcatttgtgg	C	T	SMARCAL1 // 50485 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	SMARCAL1	SMARCAL1, Homo sapiens SWI q35
SNP_A-1916539	tgtttaccattgcaag[A/C]ctggaaaatcagttgt	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1750583 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1878409	tctgtgaagtaattta[C/T]gatacctccaaagtga	C	T	ENST00000286031 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1889746	tgataatggaagataa[C/T]gtctggggtgcccact	C	T	10930 // Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2 (APOBEC2), mRNA. /// ENST00000229949 // downstream // 2344 // --- // --- // --- // ---	APOBEC2	APOBEC2, Homo sapiens apolipoprotein B editing enzyme, catalytic polypeptide-like 2 (APOBEC2), p21.1
SNP_A-1895601	tgcctcagaacacccc[A/G]caatgctgtcatctca	A	G	ENST00000341671 // intron // 0 // --- // --- // --- // ---	-	q21.32
SNP_A-1986014	cacccagatcttcacc[G/T]gactggcttcctcttt	G	T	/// ENST00000320956 // downstream // 144392 // --- // --- // ---	-	p12.3
SNP_A-1974976	agcaattctgtgagaa[A/C]ggaaggtgaatatagc	A	C	6747 // Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA. /// NM_015508 // upstream // 28562 // Hs.12813 // TIPARP //	SSR3	SSR3, Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), q25.31
SNP_A-1963914	gttttctacttattca[C/T]ctttcccatagtctga	C	T	// 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1865019	tccagtcactcgtccc[A/G]atccccaaatcccagg	A	G	Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // CDS // 0 // --- // --- // --- // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1868440	tcctcccctgtctcaa[A/G]tcgaggaatgcagaca	A	G	5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 248223 // Hs.519029	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-1871167	tcgttgtcctgtgtca[G/T]tcggtgttcgtgtggg	G	T	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 2 (CACNA2D2), transcript variant 2, mRNA. ///	CACNA2D2	CACNA2D2, Homo sapiens calcium channel, voltage-dependent, alpha 2 p21.31
SNP_A-1838551	tagaattacttttcaa[C/T]tagaatcatagttttg	C	T	SERTAD4 // 56256 // Homo sapiens SERTA domain containing 4 (SERTAD4), mRNA. /// NM_018194 // upstream	SERTAD4	SERTAD4, Homo sapiens SERTA domain containing 4 (SERTAD4), q32.2
SNP_A-1831174	taatgctaataaatcc[A/G]ggaaagaaccactcat	A	G	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-1832321	taattttgttgcttaa[A/C]tcgtcccagctttggc	A	C	3839 // Homo sapiens karyopherin alpha 3 (importin alpha 4) (KPNA3), mRNA. /// ENST00000261667 // upstream // 77214	KPNA3	KPNA3, Homo sapiens karyopherin alpha 3 (importin alpha 4) (KPNA3), q14.2
SNP_A-1791681	gggtctaacgtaatca[A/G]cttaccaacaagtgac	A	G	/// ENST00000355561 // upstream // 44879 // --- // --- // --- // ---	-	q21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1646674	acctcgaaagcattatattgagtta[A/T]agaagttagataagaaagccacata	A	T	4774 // nuclear factor I/A /// NM_152377 // upstream // 753267 // Hs.47385 // MGC34837 // 127795 // hypothetical	NFIA	NFIA , rs602295, nuclear factor I,p31.3
SNP_A-1752481	tgttattgaaaaatagctaaactta[A/G]agtcattcagaaagacaaataaaaa	A	G	NM_005711 // upstream // 295847 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3 , rs9293381, EGF-like repeats and discoidin I-like domains 3,q14.3
SNP_A-2118275	agtaacaaggtaaaaa[A/G]ttttgctccaagatcg	A	G	// Homo sapiens klotho beta like (LOC152831), mRNA. /// ENST00000257408 // intron // 0 // --- // --- // --- // ---	LOC152831	LOC152831, Homo sapiens klotho beta like (LOC152831), p14
SNP_A-2149344	atgtacacgttgcaaa[C/T]aggatgctaaaatact	C	T	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // intron // 0 // --- // ---	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2149829	atgtcaaaagattcca[A/G]gatggaaagttggcta	A	G	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-2207822	cccaaagactcagcac[A/G]aagccagaccaccatg	A	G	9525 // Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA. /// NM_080474 // upstream // 90814 //	VPS4B	VPS4B, Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), q21.33
SNP_A-2171248	caatatcaggagcaaa[C/T]ttagagaaaagatgtc	C	T	167465 // Homo sapiens zinc finger protein 366 (ZNF366), mRNA. /// NM_002270 // upstream // 100674 // Hs.482497 //	ZNF366	ZNF366, Homo sapiens zinc finger protein 366 (ZNF366), q13.2
SNP_A-2184256	cagcctgggagacaga[C/G]actccatttcaaaaaa	C	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1368847 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2184801	cagctggaaaaagcag[A/C]ctcctggatgcatcag	A	C	4753 // Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// NM_001004329 // downstream // 5301 // Hs.302764 //	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2191053	cataggtgatcctaga[C/G]aaaggcatatgatgct	C	G	// 80118 // Homo sapiens hypothetical protein FLJ22684 (FLJ22684), mRNA. /// NM_014452 // downstream // 48297 //	FLJ22684	FLJ22684, Homo sapiens hypothetical protein FLJ22684 (FLJ22684), p12.3
SNP_A-2011994	ccagaaggcccaatga[A/G]aaggggcacatggta	A	G	Homo sapiens pleckstrin homology domain containing, family B (evectins) member 1 (PLEKHB1), mRNA. /// ENST00000354190 // intron // 0 // --- // --- // --- // --- ///	PLEKHB1	PLEKHB1, Homo sapiens pleckstrin homology domain containing, family B (evectins) member 1 (PLEKHB1), q13.4
SNP_A-2015096	ggaaataataagtcaa[A/G]aagatgaacactctga	A	G	Homo sapiens transmembrane phosphatase with tensin homology (TPTE), transcript variant 4, mRNA. /// NM_199260 // intron // 0 // Hs.122986 // TPTE // 7179 // Homo sapiens	TPTE	TPTE, Homo sapiens transmembrane phosphatase with tensin homology (TPTE), transcript variant 4, p11.2
SNP_A-2012793	tttctatggctaactc[A/G]catttattcctgtatt	A	G	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2090578	acttgtggaatagaaa[C/T]gcaacagagctcagag	C	T	54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 231460 // ---	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2091528	agaaaaagcaaattaa[A/G]aggagtctgaaaaaat	A	G	Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2076350	acattgctattgccct[C/G]aagaattttacttaaa	C	G	Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // intron // 0 // --- // --- // --- // ---	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2051504	aagggtcccaatctag[A/G]cacaaaagtgagatta	A	G	LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2253541	cttcttcttcattaaa[C/G]ctttatcagaatatag	C	G	// Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 //	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15
SNP_A-2238700	ctctgtttctttattc[A/G]cagagttttgactgt	A	G	Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // intron // 0 //	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-2258922	ctttttcgtgggagca[C/T]tccttcaacaaatcac	C	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 932885 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2264462	gaagaaagggcagtca[C/T]aatacttacttctaac	C	T	132949 // Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), mRNA. /// ENST00000264229 //	AASDH	AASDH, Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), q12
SNP_A-2290715	gcaagatgaaaagcta[C/T]ggactgataaaaaaat	C	T	ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 96223 // Hs.464442 // C18orf2	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-2296989	gccaatctaagcaaag[A/C]cctaatcttaaggtcc	A	C	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2294983	gcatacaatccggtga[C/T]gccagagagtgagagg	C	T	128989 // Homo sapiens hypothetical protein DKFZp761P1121 (DKFZp761P1121), mRNA. /// ENST00000327374 // intron // 0 // --- // --- // --- // --- ///	DKFZp761P1121	DKFZp761P1121, Homo sapiens hypothetical protein DKFZp761P1121 (DKFZp761P1121), q11.21
SNP_A-2298951	gccccatctttatcac[A/G]cccggaaatgaaaggt	A	G	ENST00000358295 // intron // 0 // --- // --- // --- // ---	-	q13.32
SNP_A-2301393	gcctttgtcccctata[A/C]ggctgttgctgtcctt	A	C	// 162681 // Homo sapiens hypothetical protein MGC33382 (MGC33382), mRNA. /// NM_173629 // upstream // 205019 //	C18orf54	C18orf54, Homo sapiens hypothetical protein MGC33382 (MGC33382), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289856	gcaaacctgctgccca[A/C]ccataaatccaaaaga	A	C	7913 // Homo sapiens DEK oncogene (DNA binding) (DEK), mRNA. /// NM_182757 // upstream // 15647 // Hs.148741 //	DEK	DEK, Homo sapiens DEK oncogene (DNA binding) (DEK), p22.3
SNP_A-2306131	gctggagctgagcaca[C/T]ggatggatagcacttg	C	T	27020 // Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, mRNA. /// NM_012428 // upstream // 168970 // Hs.187866 // SDFR1 // 27020 // Homo	SDFR1	SDFR1, Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, q24.1
SNP_A-2310024	ggaaatgtagtttacg[A/T]aagcacaatttacaga	A	T	Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // --- // --- // --- // ---	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2314587	ggaggttaggctccta[C/T]cctctcacagtcactg	C	T	/// ENST00000324915 // downstream // 77120 // --- // --- // ---	-	q22.1
SNP_A-2262945	gaacaagagtctagcc[A/C]caaaagctggggagag	A	C	Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // intron // 0 // --- // --- // --- // ---	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2278383	gagctagagatgagaa[A/C]gagtttcatatttaac	A	C	5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 453969 // Hs.282787 // FOXP2 //	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1
SNP_A-2238545	ctctgtcctactggca[A/T]ccactacgctgttctt	A	T	7053 // Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3), mRNA. /// NM_198994 // upstream // 16440 // Hs.452039 //	TGM3	TGM3, Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3), p13
SNP_A-2237712	ctctctggtgcattta[A/C]aaatcatccttgcagg	A	C	Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// ENST00000262406 // intron // 0 // --- // --- // --- // ---	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2251704	cttcagtgatggctgc[A/C]aagatgcacggggctc	A	C	Homo sapiens myelin transcription factor 1 (MYT1), mRNA. /// ENST00000360149 // intron // 0 // --- // --- // --- // --- ///	MYT1	MYT1, Homo sapiens myelin transcription factor 1 (MYT1), q13.33
SNP_A-2056000	aatacagtagtgaacc[A/G]ggcacttaggcttgta	A	G	-- /// ENST00000242916 // upstream // 118376 // --- // --- // ---	-	p14
SNP_A-2087460	actgccaggagtgcac[A/C]gtaattgggttgtcag	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1074245 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2102235	agattaataaaaatga[A/G]cccaagtttgaagctg	A	G	// 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2002147	tttaagctagctagaa[C/T]gatttttgttttctac	C	T	10888 // Homo sapiens G protein-coupled receptor 83 (GPR83), mRNA. /// ENST00000328458 // downstream //	GPR83	GPR83, Homo sapiens G protein-coupled receptor 83 (GPR83), q21
SNP_A-2047759	aagattgcgatcatgt[G/T]aagtaaatagccgtcc	G	T	Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// ENST00000262406 // intron // 0 // --- // --- // --- // ---	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2042597	aactccatctcaagaa[A/G]tatgtacctatatgta	A	G	Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), mRNA. /// ENST00000320580 // intron // 0 // --- // ---	PACS1	PACS1, Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), q13.2
SNP_A-2036202	aaattattcagaatcc[C/T]ggagctgtccccagaa	C	T	56888 // Homo sapiens potassium channel modulatory factor 1 (KCMF1), mRNA. /// NM_031283 // upstream // 18900 //	KCMF1	KCMF1, Homo sapiens potassium channel modulatory factor 1 (KCMF1), p11.2
SNP_A-2019516	acacttctatagttcc[A/G]aagtaattattgttaa	A	G	ENST00000328060 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-2170810	caataaaaccccaagc[A/G]gatgctaaaaatgtgt	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 209186 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2211692	ccctcccaactatatc[A/C]atgtttaaccaacaaa	A	C	285704 // Homo sapiens RGM domain family, member B (RGMB), mRNA. /// ENST00000308338 // downstream //	RGMB	RGMB, Homo sapiens RGM domain family, member B (RGMB), q21.1
SNP_A-2209980	ccccaccagaaaaaga[C/T]ggacaatccctgagca	C	T	Homo sapiens adaptor-related protein complex 1, gamma 1 subunit (AP1G1), mRNA. /// ENST00000299980 // intron // 0	AP1G1	AP1G1, Homo sapiens adaptor-related protein complex 1, gamma 1 subunit (AP1G1), q22.2
SNP_A-2226025	ctaacacattcatcac[A/G]ggtccaacctcatgac	A	G	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 215902 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-2222164	cgaattggtacattgc[A/G]gagttccatgctgcta	A	G	// 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-2221728	cctttgtttgttttaa[C/G]agttgctaacatcttc	C	G	Homo sapiens hypothetical protein FLJ20581 (FLJ20581), mRNA. /// ENST00000331849 // intron // 0 // --- // --- // --- // ---	FLJ20581	FLJ20581, Homo sapiens hypothetical protein FLJ20581 (FLJ20581), p12.3
SNP_A-2150145	atgtcctgtgattatg[C/T]atgataccttactttc	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2574540 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2160237	atttcacatttataac[A/C]ctcttcatccaacctc	A	C	4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 392286 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2157673	attgcagatactacct[C/G]aaggttaaagagcata	C	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1740053	cattttgaaatgattcagtgcacaa[C/T]aaccttgtctgggttgggttaaggg	C	T	NM_016441 // upstream // 1635150 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs10495826, cysteine-rich motor neuron 1,p22.3
SNP_A-1645540	attgaagtattgatagcaggtacaa[C/T]agttatttgaggcagtacgttactt	C	T	NM_178123 // intron // 0 // Hs.151414 // SESTD1 // 91404 // SEC14 and spectrin domains 1	SESTD1	SESTD1 , rs10497533, SEC14 and spectrin domains 1,q31.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1683204	tggggtacctcttcttgccaggaat[C/G]agcttaaaatgctcacttataatga	C	G	PPARGC1A // 10891 // peroxisome proliferative activated receptor, gamma, coactivator 1, alpha /// NM_020973 // downstream // 451006 // Hs.146182 // GBA3 // 57733 //	PPARGC1A	PPARGC1A , rs10517008, peroxisome proliferative activated receptor, gamma, coactivator 1, alpha ,p15.2
SNP_A-1709883	attggactgtttatttggggctgca[C/T]ctaacttctgccaaccctttccccg	C	T	// 51000 // solute carrier family 35, member B3 /// NM_153003 // downstream // 409268 // Hs.382068 // OFCC1	SLC35B3	SLC35B3 , rs1003063, solute carrier family 35, member B3 ,p24.3
SNP_A-1791527	gggtcaagacactgga[C/T]gtggtaccctagtaaa	C	T	Homo sapiens DNA glycosylase hFPG2 (FLJ10858), mRNA. /// ENST00000264596 // intron // 0 // --- // --- // --- // ---	NEIL3	NEIL3, Homo sapiens DNA glycosylase hFPG2 (FLJ10858), q34.3
SNP_A-1787246	gggaacgagttgatga[C/T]cttaaaaaggggaatg	C	T	// 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 644610 // Hs.504943	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-1796976	ggttctagtcataaag[A/G]aggcttttattattag	A	G	Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // --- // --- // --- // ---	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1792912	ggtaatttgaatgatc[A/T]attgtctttaggcttg	A	T	3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream //	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-1795970	ggtggtactgtttgga[A/G]aggctatgaagggatt	A	G	Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 1 (KCNC1), mRNA. /// ENST00000265969 // intron // 0 // --- // --- // --- // ---	KCNC1	KCNC1, Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 1 (KCNC1), p15.1
SNP_A-1812082	gtggactgcacgttca[C/G]cataataaacattact	C	G	163590 // Homo sapiens AF464140 (LOC163590), mRNA. /// ENST00000305248 // intron // 0 // --- // --- // --- // ---	LOC163590	LOC163590, Homo sapiens AF464140 (LOC163590), q25.2
SNP_A-1808425	gtgaaaattgcactaa[C/G]aaatcatagagttgag	C	G	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 (ADAMTS19), mRNA. /// ENST00000274487 // intron // 0 // --- // --- // --- // ---	ADAMTS19	ADAMTS19, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 (ADAMTS19), q23.3
SNP_A-1862075	tcatgcattataaacc[A/G]aacccctctatcattg	A	G	// Homo sapiens olfactory receptor, family 10, subfamily T, member 2 (OR10T2), mRNA. /// ENST00000334438 // upstream // 9353 // --- // --- // --- // --- /// ENST00000314902 //	OR10T2	OR10T2, Homo sapiens olfactory receptor, family 10, subfamily T, member 2 (OR10T2), q23.1
SNP_A-1845106	tatacagctcgactca[A/G]tcatttccatttttt	A	G	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 247090 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1859285	tcagctgagtccacac[A/G]atttcaacatgattgt	A	G	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1951774	tttcgtatgctcatac[A/G]ggttttggaaacacca	A	G	1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 255892 //	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-1903898	tgggatggaattgaca[C/T]ggtgggtggccatctt	C	T	ENST00000341671 // intron // 0 // --- // --- // --- // ---	-	q21.32
SNP_A-1901283	attgaatgttgaagga[A/C]gcatcagtaaaacaag	A	C	/// ENST00000334919 // upstream // 883678 // --- // --- // --- // --- /// ENST00000322194 // downstream // 885471 // --- // --- // ---	-	q12.2
SNP_A-1874000	tctcatccgattttca[A/G]gaagtctcctgaggca	A	G	9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // downstream // 356043 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1912397	tgtgcaaccaagctga[C/G]aacaagagttcaagac	C	G	8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 314052	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-1922711	ttagagcacctcatta[A/G]cctgaataactgagac	A	G	220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. ///	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1925532	ttatgaaagacgtaag[C/G]caattttaaccattct	C	G	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-1905020	tgggtccctgcatgac[A/G]gaaagttaccttagcc	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1902616	tggcgggcagacgata[C/T]gtggggagcctctgat	C	T	Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // --- // --- // --- // --- ///	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-1896894	tgctcagaagctagac[A/G]atccgataaattaaaa	A	G	Homo sapiens polymerase (DNA directed), theta (POLQ), transcript variant 2, mRNA. /// NM_006596 // intron // 0 // Hs.241517 // POLQ // 10721 // Homo sapiens polymerase	POLQ	POLQ, Homo sapiens polymerase (DNA directed), theta (POLQ), transcript variant 2, q13.33
SNP_A-1892892	ttgttctcagcttaaa[C/T]ctggagtcatccttta	C	T	Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // --- // --- // --- // ---	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1954981	tttggaataaatccaa[C/G]tcatcttgtgaaggac	C	G	CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 51539	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1975197	atagtttcttctcacc[C/T]aaagtaactggaacaa	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1975227	acctccttcaacaaaa[C/G]gcaaatacctacattg	C	G	Homo sapiens programmed cell death 10 (PDCD10), transcript variant 3, mRNA. /// NM_007217 // intron // 0 //	PDCD10	PDCD10, Homo sapiens programmed cell death 10 (PDCD10), transcript variant 3, q26.1
SNP_A-1865392	tccatcgagccaaatc[A/G]agaaaaagattttcaa	A	G	// 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 114745 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1828827	taaggacaaaccacaa[A/C]tgaatgctcttgagtc	A	C	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // --- // --- // --- // --- ///	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-1794158	ggtcagtgctaattca[C/T]ggttttggaggtttgc	C	T	Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// ENST00000341928 // intron // 0 // --- //	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-1655189	atgttacacaaaataaaaatgaaga[A/G]catctgataaacttgtatacaaaca	A	G	FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 2162624 // Hs.352656 // GHITM // 27069 //	FLJ41984	FLJ41984 , rs10509440, FLJ41984 protein ,q23.1
SNP_A-2159107	attgttttcagtgcta[C/G]gccaattagcattatt	C	G	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 475589 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2127233	ataaatgcaaacactt[A/T]aaacacttctgtgatc	A	T	ENST00000331807 // intron // 0 // --- // --- // --- // ---	-	q33.1
SNP_A-2179504	cacttagaaaattaca[A/G]ctttgccatccaagcc	A	G	23012 // Homo sapiens serine/threonine kinase 38 like (STK38L), mRNA. /// ENST00000330397 // upstream //	STK38L	STK38L, Homo sapiens serine,p11.23
SNP_A-2197257	cattcagattttctcc[G/T]cttcttgaacttttca	G	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 718788 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2024444	aaaaggaaataattta[A/C]gtatgcatgaaaaggg	A	C	29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 729462 //	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-2003171	acttttatgaacagtc[C/T]caaacttgaaatttca	C	T	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1991718	tatattgcaactgtag[C/T]aagtactagttatgtg	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-1990824	tatttgggtcaacaac[C/T]gttagtattcatttgt	C	T	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 105976 // Hs.32942 // PIK3CG // 5294 // Homo	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-2018556	gtatctcattattggc[A/G]agtaggacgagtttct	A	G	Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2093890	agaagcaattatttag[A/G]atgaacgttttcaccc	A	G	// Homo sapiens membrane targeting (tandem) C2 domain containing 1 (MTAC2D1), mRNA. /// ENST00000340892 // intron // 0 // --- // --- // --- // ---	MTAC2D1	MTAC2D1, Homo sapiens membrane targeting (tandem) C2 domain containing 1 (MTAC2D1), q32.12
SNP_A-2092044	agaaacctgcagggac[G/T]ccatgctgccagcctt	G	T	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201284 // 3UTR // 0 // Hs.488293 // EGFR // 1956 // Homo sapiens	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2078482	accatctcttgactac[C/T]atttgtcttcagcaat	C	T	Homo sapiens cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA. ///	CDON	CDON, Homo sapiens cell adhesion molecule-related,q24.2
SNP_A-2072946	acaggaagtgttgaca[C/T]atatttgcagaacttc	C	T	FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ11017), mRNA. /// NM_018302 // downstream	FLJ11017	FLJ11017, Homo sapiens hypothetical protein FLJ11017 (FLJ11017), p14
SNP_A-2066499	aatttttgcttcaata[A/T]aaagagagtatgcaag	A	T	PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 //	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2246971	ctgtatgcaaatcaaa[A/G]gcttacaaataataat	A	G	-- /// ENST00000340153 // upstream // 100665 // --- // --- // --- // --- /// ENST00000308120 // upstream // 104880 // --- // --- // -	-	q34.1
SNP_A-2292335	gcacgactctgaagtg[A/G]aactctgcacctgctc	A	G	27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 580457 // ---	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2307577	gcttcagaaaacgcca[C/T]gagtgtatgatcatga	C	T	4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 3065 // --- // --- // ---	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds. ,q11.2
SNP_A-2229311	ctaggagcttatttcc[C/T]acattaggtcaaaagc	C	T	// 130507 // Homo sapiens similar to F10G7.10.p (KIAA2024), mRNA. /// NM_138995 // upstream // 1175 // Hs.534101 //	ZNF650	ZNF650, Homo sapiens similar to F10G7.10.p (KIAA2024), q31.1
SNP_A-2264534	gaagaactttggcaaa[C/T]ggctttgtgttgtatg	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2236851 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2261928	gaaataatgaatagac[C/T]actgaggccaagtgct	C	T	Homo sapiens dedicator of cytokinesis 2 (DOCK2), mRNA. /// ENST00000256935 // intron // 0 // --- // --- // --- // --- ///	DOCK2	DOCK2, Homo sapiens dedicator of cytokinesis 2 (DOCK2), q35.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2066260	aattttatcgaatcga[A/G]actgaagctgttaggt	A	G	EDARADD // 128178 // Homo sapiens EDAR-associated death domain (EDARADD), transcript variant B, mRNA. /// NM_145861 // downstream // 27293 // Hs.352224 //	EDARADD	EDARADD, Homo sapiens EDAR-associated death domain (EDARADD), transcript variant B, q43
SNP_A-2078041	accaggaacactaaaa[C/G]ttgcttctaatgggga	C	G	3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 44995 //	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-2081344	acctggctccacacta[C/T]catctaagttccttaa	C	T	192670 // Homo sapiens eukaryotic translation initiation factor 2C, 4 (EIF2C4), mRNA. /// NM_012199 // upstream // 3012 //	EIF2C4	EIF2C4, Homo sapiens eukaryotic translation initiation factor 2C, 4 (EIF2C4), p34.3
SNP_A-2098138	agagagtaggctataa[A/G]gaatgattaaatatta	A	G	sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// ENST00000330276 // intron // 0 // --- // --- // --- // ---	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2099937	agagtcatagaacaag[A/G]cacatgggagtatggt	A	G	Homo sapiens transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA. /// ENST00000320763 //	TAP1	TAP1, Homo sapiens transporter 1, ATP-binding cassette, sub-family B (MDR p21.32
SNP_A-2001418	ggatctaagagttagg[A/G]agttgcaccatgtgag	A	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2025674	aaaatgagtgataaaa[C/T]tcccgtgtgttgaaag	C	T	// 8091 // Homo sapiens high mobility group AT-hook 2 (HMGA2), mRNA. /// NM_003483 // downstream // 11567 //	HMGA2	HMGA2, Homo sapiens high mobility group AT-hook 2 (HMGA2), q14.3
SNP_A-2031461	aaaggtattccctttc[A/G]aacgctctttccaaac	A	G	-- /// ENST00000303758 // downstream // 40478 // --- // --- // --	-	q21.31
SNP_A-2028832	aaacttgcatgacaga[A/G]acgaatcttgtacatt	A	G	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, mRNA. /// NM_201268 // intron // 0 // Hs.75890 // MBTPS1 // 8720 //	MBTPS1	MBTPS1, Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, q23.3
SNP_A-2028803	aaacttctggaggcca[C/G]agactctctaatgttg	C	G	6539 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	SLC6A12	SLC6A12, Homo sapiens solute carrier family 6 (neurotransmitter transporter, betaine p13.33
SNP_A-2040046	aaccaaaaagagcagg[C/G]atgataatatctacag	C	G	54504 // Homo sapiens carboxypeptidase, vitellogenic-like (CPVL), transcript variant 2, mRNA. /// NM_031311 // upstream // 40432 // Hs.233389 // CPVL // 54504 // Homo	CPVL	CPVL, Homo sapiens carboxypeptidase, vitellogenic like (CPVL), transcript variant 2, p15.1
SNP_A-2196779	cattacctcttctaca[A/C]ggcaagtgaaacaaaa	A	C	Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000355794 // intron // 0 // --- // --- // --- // ---	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-2179824	cacttgttaactgggc[A/G]ctaaacactgagtaca	A	G	Homo sapiens CGI-90 protein (CGI-90), mRNA. /// NM_003909 // intron // 0 // Hs.191219 // CPNE3 // 8895 //	CGI-90	CGI-90, Homo sapiens CGI-90 protein (CGI-90), q21.3
SNP_A-2217528	cctgactgcccttccc[C/T]ggacaggttctgtttg	C	T	// Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // upstream // 4081 // --- // --- // --- // --- ///	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-2214836	cctataatttgtggca[A/G]gaaaatttatgacaca	A	G	2805 // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA. /// NM_145285 // upstream // 40545 // Hs.243272 // NKX2-3 //	GOT1	GOT1, Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), q24.2
SNP_A-2207258	ccattccacagttcta[C/T]aagatgacaggcagga	C	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1714748 // Hs.529735 // AADAT // 51166 //	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2205792	ccatacaggtgtacca[A/G]cttttggaaaatccca	A	G	Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, mRNA. /// NM_002149 // intron // 0 // Hs.467696 //	HPCAL1	HPCAL1, Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, p25.1
SNP_A-2203866	ccagagtcaagcttga[A/G]gtctgatgttcactta	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // --	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2201196	ccaagttcacatagtc[A/G]actcagagctgggatt	A	G	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2117709	aggttcctgccttgaa[A/T]tgttctccttcatggt	A	T	6694 // Homo sapiens secreted phosphoprotein 2, 24kDa (SPP2), mRNA. /// NM_005737 // downstream // 98453 //	SPP2	SPP2, Homo sapiens secreted phosphoprotein 2, 24kDa (SPP2), q37.1
SNP_A-2108652	agctggttaaggttta[C/T]ctgcagctgatgttgc	C	T	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2114476	agggagagaaggggac[A/G]gagaataattcagatg	A	G	Homo sapiens kinesin family member 17 (KIF17), mRNA. /// ENST00000247986 // intron // 0 // --- // --- // --- // --- ///	KIF17	KIF17, Homo sapiens kinesin family member 17 (KIF17), p36.12
SNP_A-2158761	attgtctgttcctttta[C/G]agaagagattgaccga	C	G	/// ENST00000318060 // upstream // 55998 // --- // --- // --- // -- /// ENST00000316929 // upstream // 85737 // --- // --- // --- // --	-	q26.3
SNP_A-2164538	caaaatttggatggaa[A/G]tcagtcttcagtctgc	A	G	/// ENST00000328167 // upstream // 33320 // --- // --- // --- // --	-	p15.1
SNP_A-2162855	attttgcttccaggag[C/T]catttgaatataaatac	C	T	4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /// NM_006152 // downstream // 233744 //	LRMP	LRMP, Homo sapiens lymphoid-restricted membrane protein (LRMP), p12.1
SNP_A-2161220	atttgagatctataaa[C/T]atatgtgaactagcct	C	T	Homo sapiens dedicator of cytokinesis 3 (DOCK3), mRNA. /// ENST00000266037 // intron // 0 // --- // --- // --- // ---	DOCK3	DOCK3, Homo sapiens dedicator of cytokinesis 3 (DOCK3), p21.31
SNP_A-2161061	atttctttgagaaaac[A/G]actgaataaaacatag	A	G	// Homo sapiens actin, beta (ACTB), mRNA. /// NM_001614 // upstream // 27561 // Hs.514581 // ACTG1 // 71 // Homo	ACTB	ACTB, Homo sapiens actin, beta (ACTB), p22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2146377	atgctcaactttagaa[G/T]taaaatgtctctcctt	G	T	25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 65779 // Hs.369574 // CDC42EP3 // 10602 //	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-2140899	atctgagaagatttga[A/G]gctcactatatgcctc	A	G	151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 //	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-1651004	cctggcttttcagtctttgtaatga[C/T]ggttagtaaataatctgaacaagga	C	T	4547 // microsomal triglyceride transfer protein (large polypeptide, 88kDa) /// NM_014395 // upstream // 111441 //	MTP	MTP , rs10516451, microsomal triglyceride transfer protein (large polypeptide, 88kDa) ,q23
SNP_A-1664908	agcagcatctcacagctaaaataga[C/T]gcacacagtcaagagggtgtctgga	C	T	NM_002044 // intron // 0 // Hs.129228 // GALK2 // 2585 // galactokinase 2	GALK2	GALK2 , rs8040075, galactokinase 2,q21.1
SNP_A-1675009	ctagtagattcaatcttgtgtgtta[C/T]ataatattttctgatttttaacttg	C	T	NM_013244 // intron // 0 // Hs.422827 // HGNT-IV-H // 25834 // UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog	HGNT-IV-H	HGNT-IV-H , rs839177, UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog,q21.31
SNP_A-1716345	aagagggaaacagatgaaaaataga[A/C]gtaaagtactggtaatggaagccgg	A	C	NM_018434 // intron // 0 // Hs.155718 // RNF130 // 55819 // ring finger protein 130	RNF130	RNF130 , rs248257, ring finger protein 130,q35.3
SNP_A-1722648	caagccagccaaatcaaataattcc[G/T]actgtcctcaggtttatttcatgcc	G	T	NM_016195 // downstream // 320975 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs1329165, M-phase phosphoprotein 1,q23.31
SNP_A-1826008	taaatggtcatgtcac[C/T]cttgttggaaatcatt	C	T	1410 // Homo sapiens crystallin, alpha B (CRYAB), mRNA. /// ENST00000317197 // upstream // 1050 // --- // --- // --- // --- ///	CRYAB	CRYAB, Homo sapiens crystallin, alpha B (CRYAB), q23.1
SNP_A-1834184	tacatgaatacacata[A/C]aatagaataccactca	A	C	ENST00000307138 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-1841929	taggcttgagttaaaa[A/T]cacctggcaacaacaa	A	T	// 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // downstream // 70852 // Hs.167317 // SNAP25 // 6616 //	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-1863924	tccaatggtacgggtc[A/G]cagaaagtttatttcc	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1860135	tcagtattccttggta[C/T]ataatcctcattcctg	C	T	// 10885 // Homo sapiens WD repeat domain 3 (WDR3), mRNA. /// NM_206996 // upstream // 341663 // Hs.528821 //	WDR3	WDR3, Homo sapiens WD repeat domain 3 (WDR3), p12
SNP_A-1851128	tattcaaactgaaaag[C/T]cttacaattctggaat	C	T	Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), mRNA. /// ENST00000264424 // intron // 0 // ---	GUCY1B3	GUCY1B3, Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), q32.1
SNP_A-1964279	tactcccgcttgtatt[G/T]aaaactcacttaggtt	G	T	7850 // Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA. /// NM_173343 // downstream //	IL1R2	IL1R2, Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, q11.2
SNP_A-1966931	agactagtcaggaaga[C/T]ggggtgatgcctgatg	C	T	199834 // Homo sapiens late cornified envelope 4A (LCE4A), mRNA. /// NM_178354 // upstream // 9622 // --- // LCE1F //	LCE4A	LCE4A, Homo sapiens late cornified envelope 4A (LCE4A), q21.3
SNP_A-1987699	agtttctgcaaatctg[C/T]cacttccctactttgt	C	T	83551 // Homo sapiens trace amine receptor 5 (TRAR5), mRNA. /// NM_175067 // upstream // 10813 // Hs.434196 //	TRAR5	TRAR5, Homo sapiens trace amine receptor 5 (TRAR5), q23.2
SNP_A-1979557	gttctaaggagctgta[A/C]gatgtgaggttgtagt	A	C	2743 // Homo sapiens glycine receptor, beta (GLRB), mRNA. /// NM_000826 // upstream // 38063 // Hs.32763 // GRIA2 //	GLRB	GLRB, Homo sapiens glycine receptor, beta (GLRB), q32.1
SNP_A-1950366	tttcaggagagtgaag[A/G]ctcaacaggatctact	A	G	390195 // Homo sapiens olfactory receptor, family 5, subfamily AN, member 1 (OR5AN1), mRNA. /// ENST00000361050 // upstream // 78838 // --- // --- // --- // ---	OR5AN1	OR5AN1, Homo sapiens olfactory receptor, family 5, subfamily AN, member 1 (OR5AN1), q12.1
SNP_A-1947841	tttacttcagtttcta[A/C]taacctgcacagaatg	A	C	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 182116 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1942141	ttggatttctgacctc[C/G]agagctgtaagataat	C	G	30814 // Homo sapiens phospholipase A2, group IIE (PLA2G2E), mRNA. /// NM_000300 // downstream // 17234 //	PLA2G2E	PLA2G2E, Homo sapiens phospholipase A2, group IIE (PLA2G2E), p36.13
SNP_A-1889903	tgatagatcccaggca[C/T]gtaagggaacagaaat	C	T	4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 574517 // Hs.467769 //	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-1896815	tgctcaacctctaagc[A/G]gcgagttcggtaacac	A	G	Homo sapiens ELMO domain containing 1 (ELMOD1), mRNA. /// ENST00000265840 // intron // 0 // --- // --- // --- // ---	ELMOD1	ELMOD1, Homo sapiens ELMO domain containing 1 (ELMOD1), q22.3
SNP_A-1878466	tctgtgattcaacagg[C/G]catttcagaagcaggt	C	G	1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 38645 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste p15.1
SNP_A-1881620	tctttgactcgaggtg[A/C]aactatctcagacaca	A	C	7424 // Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA. /// NM_018248 // upstream // 211880 //	VEGFC	VEGFC, Homo sapiens vascular endothelial growth factor C (VEGFC), q34.3
SNP_A-1913966	tgtgtgatcaagtaaa[C/T]gcaagatggtagaaaa	C	T	// 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// NM_006506 // upstream // 68216 // Hs.15999 //	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1914332	tgtgttctagaaggca[C/T]atgacaagtgagagag	C	T	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1919113	ttaactgagtgtaaca[C/T]agtaggtgctcaataa	C	T	Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1907356	tgtaaaagagaagcat[A/G]aaaggtgagtattcag	A	G	ENST00000275246 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1971916	gattttattactctaa[A/G]gtttgtgttggctatt	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 3974 // --- // --- // --- // ---	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1853266	tattttacaatcagag[A/G]ctagaaataggtccag	A	G	/// ENST00000314100 // upstream // 33798 // --- // --- // --- // ---	-	p13.3
SNP_A-1864087	tccacaggcacccaga[A/G]gttgatgctgacaggc	A	G	Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), mRNA. /// ENST00000268296 // CDS // 0 // --- // --- // --- // --- /// ENST00000309201 // CDS // 0	ITGAX	ITGAX, Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), p11.2
SNP_A-1840380	tagcatttaatagata[C/T]ggttgttttagcttct	C	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1834030	tacatatcacaggaag[G/T]cactgccaggtcttag	G	T	Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- // --- // --- ///	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-1829178	taaggtttctttacaa[C/G]agaaggtgggtttgac	C	G	Homo sapiens signal peptide peptidase 3 (SPPL3), mRNA. /// ENST00000353487 // intron // 0 // --- // --- // --- // ---	SPPL3	SPPL3, Homo sapiens signal peptide peptidase 3 (SPPL3), q24.31
SNP_A-1817175	gttcaatatatagttc[A/G]acatcccagactttat	A	G	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 2382785	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1661063	ctctgaatgaggtagacaagtgtaa[C/T]cttcaaagtttctgacaattacaga	C	T	NM_024582 // upstream // 248245 // Hs.25201 // FATJ // 79633 // fat-like cadherin FATJ	FATJ	FATJ , rs10518460, fat-like cadherin FATJ,q28.1
SNP_A-1659702	aaacaaaaaactaggttcctaagta[A/G]gttgcacacttgcctggaaaaaga a	A	G	NM_133445 // intron // 0 // Hs.283852 // PPP3R2 // 5535 // protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II)	PPP3R2	PPP3R2 , rs10512288, protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II),q31.1
SNP_A-1650870	ttaaaaacggacatcgattgaaacc[A/G]cctcctccatttgcttgttgtatga	A	G	KIAA1604 // 57703 // KIAA1604 protein /// NM_152520 // upstream // 98138 // Hs.6295 // ZNF533 // 151126 // zinc	KIAA1604	KIAA1604 , rs1480706, KIAA1604 protein ,q31.3
SNP_A-1796133	ggtgtatttaaatcac[C/T]gactcaagcaaaagag	C	T	Homo sapiens F-box protein 40 (FBXO40), mRNA. /// ENST00000338040 // intron // 0 // --- // --- // --- // ---	FBXO40	FBXO40, Homo sapiens F-box protein 40 (FBXO40), q13.33
SNP_A-1789832	gggctggaccatacaa[C/T]gtgtgttagccaacag	C	T	// 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2204569	ccaggaactgcaagaa[C/T]taaatagcactgatga	C	T	Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 //	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2225366	cgtttgttcttatacc[A/G]gaatgatttgttggga	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2458036 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2224648	cgtccggtcccttctg[A/G]aactggggatcatcct	A	G	Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 //	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2184408	cagcgtcttgcacaga[C/T]acttgtacaccatgtt	C	T	Homo sapiens mRNA for KIAA1130 protein, partial cds. /// ENST00000360173 // intron // 0 // --- // --- // --- // --- ///	GALNTL1	GALNTL1, Homo sapiens for KIAA1130 protein, partial cds. ,q24.1
SNP_A-2029770	aaagaggtccccaggt[A/T]aagagaatgactttct	A	T	2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 385653 // Hs.479853 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2
SNP_A-2024718	aaaagtatatctctac[C/T]gcaataagtatacaaa	C	T	// 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000340000 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2011253	ccatcagaaaaaatgc[A/G]gagcaagagagcccag	A	G	/// ENST00000360575 // upstream // 53269 // --- // --- // --- // --- /// ENST00000231482 // upstream // 56861 // --- // --- // --- // ---	-	q31.1
SNP_A-2093045	agaacagactaataca[A/G]cttctacctattcaat	A	G	7745 // Homo sapiens zinc finger protein 192 (ZNF192), mRNA. /// ENST00000259717 // downstream // 43127 // --- //	ZNF192	ZNF192, Homo sapiens zinc finger protein 192 (ZNF192), p22.1
SNP_A-2071635	acagaataacttcacc[A/G]ggaccattaaagtacc	A	G	Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000258643 // intron // 0 // --- // --- // --- // --- ///	LRCH1	LRCH1, Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.13
SNP_A-2270159	gacacatagaggtatg[G/T]cagtaatgttgaatga	G	T	Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// ENST00000247829 // intron // 0 // --- // ---	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-2278183	gagcctccataatcca[A/G]gtgctgcctgactttc	A	G	11213 // Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), mRNA. /// NM_033647 // upstream //	IRAK3	IRAK3, Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), q14.3
SNP_A-2239039	ctcttctatttggaaa[C/T]acaattctgctcaatt	C	T	Homo sapiens PDZ domain containing 8 (PDZK8), mRNA. /// ENST00000298474 // intron // 0 // --- // --- // --- // --- ///	PDZK8	PDZK8, Homo sapiens PDZ domain containing 8 (PDZK8), q26.11

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2239828	ctgaaatttgaggacc[A/T]cttcagtagatacttc	A	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2301787	gcggaggttctgaacc[C/T]agacctgcccagcgtc	C	T	7559 // Homo sapiens zinc finger protein 12 (KOX 3) (ZNF12), mRNA. /// NM_021163 // upstream // 32723 //	ZNF12	ZNF12, Homo sapiens zinc finger protein 12 (KOX 3) (ZNF12), p22.1
SNP_A-2310519	ggaagaagaagaggaa[A/G]ggttggtttttctgtc	A	G	ENST00000338994 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2287809	gattagatactatcat[C/T]actcctcttacgaatg	C	T	/// ENST00000356209 // upstream // 83623 // --- // --- // --- // --- /// ENST00000330461 // upstream // 95201 // --- // --- // --- // ---	-	q21.3
SNP_A-2307185	gcttaagatgtttgaa[A/T]ggtttcttattgcact	A	T	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 385193 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2238785	ctcttacttatccaac[A/G]gtcttaggtactttct	A	G	Homo sapiens ubiquitin specific protease 12 (USP12), mRNA. /// ENST00000282344 // intron // 0 // --- // --- // --- // ---	USP12	USP12, Homo sapiens ubiquitin specific protease 12 (USP12), q12.13
SNP_A-2238502	ctctgtagtgatgaaa[C/T]aggctggtgctttccc	C	T	sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // --- // --- // --- // --- ///	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. q43
SNP_A-2229493	ctagggcctaaacatc[A/G]gaggcatccagggcat	A	G	-- /// ENST00000332560 // upstream // 116808 // --- // --- // ---	-	q21.1
SNP_A-2243935	ctgctgttcacaataa[A/T]gataagaaatgggctg	A	T	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 236259 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2277125	gagatggatcattgga[A/G]gacatggcctgggtct	A	G	57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream //	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2272914	gactacattttcaaca[A/G]tgattatcagcattag	A	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 505694 // --- // --- // --- //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2281904	gagtgcatactatgtg[C/T]caaattattgtctagg	C	T	56986 // Homo sapiens x 009 protein (MDS009), mRNA. /// ENST00000329873 // downstream // 19880 // --- // --- // --- // ---	MDS009	MDS009, Homo sapiens x 009 protein (MDS009), q21.2
SNP_A-2265222	gaagattttgttaagg[A/C]aaagaaagatggtgaa	A	C	Homo sapiens chromosome 9 open reading frame 5 (C9orf5), mRNA. /// ENST00000223608 // intron // 0 // --- // ---	C9orf5	C9orf5, Homo sapiens chromosome 9 open reading frame 5 (C9orf5), q31.3
SNP_A-2069988	acacagtcagccacac[A/G]aggtgaagccaggatt	A	G	// 84966 // Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000355895 // upstream //	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-2051044	aaggcttcctggaaga[C/G]gtgggacttaagctag	C	G	8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 85871 // Hs.503510 // EED // 8726 // Homo	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2008665	aatgctgacagctgta[A/T]ctcttctcagcctggc	A	T	sapiens parathyroid hormone receptor 1 (PTHR1), mRNA. /// ENST00000313049 // intron // 0 // --- // --- // --- // --- ///	PTHR1	PTHR1, Homo sapiens parathyroid hormone receptor 1 (PTHR1), p21.31
SNP_A-1996133	ccttgttcatctagtc[G/T]caagctttcttgactc	G	T	ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 //	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-2038247	aacaccacaggtagga[C/T]aggtttagcagaaaga	C	T	151963 // Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), mRNA. /// ENST00000315470 // intron // 0 // --- // --- // --- // ---	LOC151963	LOC151963, Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), q29
SNP_A-2034719	aaatgaagctttgagc[A/G]gaaataaatatgaaag	A	G	4436 // Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), mRNA. /// NM_022055 // downstream // 27516 // Hs.243991 // KCNK12 // 56660 //	MSH2	MSH2, Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), p21
SNP_A-2179689	cacttctgcttattta[C/T]ccaaaagaactgaagt	C	T	201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// ENST00000284400 // intron // 0 // ---	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-2149583	atgtagtatctactag[C/T]cagttttggttagaga	C	T	84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 109629 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-2132877	atataatatgggtaag[A/G]aaggaatgatggtagc	A	G	ENST00000358773 // intron // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-1658256	atccagtctgtggctcaatagaaac[C/T]gtgaagaatcatcttctagaatagg	C	T	374462 // protein tyrosine phosphatase, receptor type, Q /// NM_002469 // upstream // 1732 // Hs.35937 // MYF6 // 4618	PTPRQ	PTPRQ , rs2247780, protein tyrosine phosphatase, receptor type, Q ,q21.31
SNP_A-1825814	taaatcttactttaca[C/T]acccatatctttccta	C	T	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-1863053	tcatttaacccaaaac[A/G]acaggccttgatcccc	A	G	55 // Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /// NM_015268 // upstream // 83836 // --- // --- // 0 // ---	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-1867958	gttgtttgtagccaaa[A/G]acatcctcactgctac	A	G	8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 113133 //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982604	tatatatgctttagaa[A/G]atgttactgtctcgta	A	G	Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // intron // 0 // --- // --- // --- // ---	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-1945681	ttgttgattacattta[C/T]actgcgaattgttatt	C	T	Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), mRNA. /// ENST00000321955 // intron // 0 // ---	NAALAD2	NAALAD2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), q14.3
SNP_A-1925907	ttatggtagaacataa[A/G]ctatctcgggtctttc	A	G	8729 // Homo sapiens golgi-specific brefeldin A resistance factor 1 (GBF1), mRNA. /// NM_002502 // upstream // 1545 //	GBF1	GBF1, Homo sapiens golgi-specific brefeldin A resistance factor 1 (GBF1), q24.32
SNP_A-1920845	ttacacaattaaggca[A/G]gaaagaataagttaaa	A	G	85021 // Homo sapiens RALBP1 associated Eps domain containing 1 (REPS1), mRNA. /// AF116682 // upstream //	REPS1	REPS1, Homo sapiens RALBP1 associated Eps domain containing 1 (REPS1), q24.1
SNP_A-1932605	ttcctgttcttgatcc[C/T]acaacttggggctttt	C	T	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 39401 //	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1886119	tgaccagtcactatga[A/G]gcttcgggcaacagac	A	G	Homo sapiens microtubule-associated protein 7 (MAP7), mRNA. /// ENST00000354570 // intron // 0 // --- // --- // --- // ---	MAP7	MAP7, Homo sapiens microtubule-associated protein 7 (MAP7), q23.3
SNP_A-1890819	tgatgcagactgaaaa[C/G]tacaataagaataaaa	C	G	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 222706 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1936399	ttcttctggccaactg[C/T]atcacaatatggtaac	C	T	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1190284 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1936293	ttcttccctgaaaata[A/C]gcagcagagtcatagt	A	C	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1954134	tttgattcaaaatccc[A/G]cactctctttttttgt	A	G	ENST00000265463 // intron // 0 // --- // --- // --- // ---	-	q13.1
SNP_A-1960616	cattggtggtaagaaa[A/G]tgccttttattttaaa	A	G	5672 // Homo sapiens pregnancy specific beta-1-glycoprotein 4 (PSG4), transcript variant 2, mRNA. /// NM_002783 // upstream // 21365 // Hs.512647 // PSG7 // 5676 // Homo	PSG4	PSG4, Homo sapiens pregnancy specific beta-1-glycoprotein 4 (PSG4), transcript variant 2, q13.31
SNP_A-1840863	tagctcatctccctca[A/G]aggacttagggtgccg	A	G	TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. ///	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-1659668	ccatattatcccagtatcctcttag[A/C]catgatggacatgcttgagtagtgc	A	C	sparc/osteonectin, cwcv and kazal-like domains proteoglycan	SPOCK3	SPOCK3 , rs10517927, sparc,q32.3
SNP_A-1668881	gatgttttattgagctgaaatgagg[C/T]aatctgtctgcatcatgggtaggat	C	T	NM_006457 // intron // 0 // Hs.154103 // LIM // 10611 // LIM protein (similar to rat protein kinase C-binding enigma)	LIM	LIM , rs2280002, LIM protein (similar to rat protein kinase C-binding enigma),q22.3
SNP_A-1712681	ttaagttatgctggtagtttaacat[G/T]cacgtattttgctgcaatgtgcaaa	G	T	3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 379168 // Hs.127011 // TINAG // 27283 //	HCRTR2	HCRTR2 , rs1566753, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1718215	gtaattcaatggcttttaatacagt[C/T]acagatctgtacaaattttaccaca	C	T	2917 // glutamate receptor, metabotropic 7 /// NM_014674 // downstream // 900576 // - // - // - /// NM_181874 //	GRM7	GRM7 , rs1504037, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-1738935	tctttagctttttttgaaaaaacaaa[A/T]tctcatatttagtcaaaacttctag	A	T	NM_178827 // intron // 0 // Hs.159650 // FLJ35834 // 154865 // hypothetical protein FLJ35834	FLJ35834	FLJ35834 , rs1525628, hypothetical protein FLJ35834,q31.32
SNP_A-1743735	ttatgtctttaactgtctataaaat[C/G]atattaatgactatagaatgttgta	C	G	FLJ30656 // 124801 // hypothetical protein FLJ30656 /// NM_024025 // upstream // 85488 // Hs.8719 // MGC1136 //	FLJ30656	FLJ30656 , rs4733164, hypothetical protein FLJ30656 ,p12
SNP_A-1786721	ggcttgttactggcaa[A/C]tactactttttttttt	A	C	Homo sapiens damage-specific DNA binding protein 2, 48kDa (DDB2), mRNA. /// ENST00000256996 // intron // 0 // -	DDB2	DDB2, Homo sapiens damage-specific DNA binding protein 2, 48kDa (DDB2), p11.2
SNP_A-1793526	tgcagtgactgcacac[A/T]atagatactctgtaaa	A	T	HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 623477 // Hs.120831 // TNT //	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2136774	atcactttccttggca[A/G]tagttgaagaatgcat	A	G	Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA. /// NM_199185 // intron // 0 // Hs.519452 // NPM1 // 4869 // Homo sapiens nucleophosmin	NPM1	NPM1, Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), q35.1
SNP_A-2127805	ataacttgagttttca[G/T]caacctgtcggaatga	G	T	// 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 381 // Hs.129701 //	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2129147	ataattggacttaaat[G/T]agatcacatgatagca	G	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 721476 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2115529	aggggtgagtaaaata[A/G]gcatacagtgagccat	A	G	// Homo sapiens interferon, omega 1 (IFNW1), mRNA. /// NM_002175 // downstream // 16079 // Hs.113211 // IFNA21 //	IFNW1	IFNW1, Homo sapiens interferon, omega 1 (IFNW1), p21.3
SNP_A-2165897	caaagtggttctcaaa[C/G]tttcaggaacaaacta	C	G	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 707969 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2167758	caaccctatcttgtta[C/T]ccttgatttctctttt	C	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2156422	attctccatattacta[A/C]ggcaactgaaatcaga	A	C	// Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), mRNA. /// ENST00000233242 // upstream // 33825	APOB	APOB, Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), p24.1
SNP_A-2199632	ccaaaagactcttggc[G/T]agaacttgagttttag	G	T	sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mR /// ENST00000282397 // intron // 0 // --- // --- // --- // ---	FLT1	FLT1, Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor,q12.2
SNP_A-2225062	cgtgtctgcattccag[A/C]aagaaagacaggaaag	A	C	// Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // --- // --- // --- // ---	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2225665	ctaaactagaatgatt[A/C]aacacattaagaggca	A	C	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 249098 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2212546	cccttaggcctctagc[A/G]gaatttgtggaaaatg	A	G	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2046321	aagagaagagacaaaa[C/T]tccctcaatgctttgc	C	T	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 756341 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.12
SNP_A-2045067	aagaacttgtttata[A/G]aaccatgtcctctact	A	G	590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 159158 // --- // --- // --- //	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-2027199	aaacagtctgcactca[C/T]aagatggcatcacatc	C	T	220963 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), mRNA. /// NM_005436 // downstream // 1581 // Hs.327068 //	SLC16A9	SLC16A9, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), q21.2
SNP_A-1990069	tgggtcttcatttta[A/G]gtgatcactctggctg	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2048391	aagcaggttgtggaaa[C/T]agtgtgacaagggtgg	C	T	6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// ENST00000354821 // downstream // 11660 // --- // --- // --- // --	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2053267	aagtgaaatgtaaaaa[C/T]atgagcaaagctaatt	C	T	NM_001003792 // upstream // 128008 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single	-	p24.1
SNP_A-2054458	aagtttcatcttccac[C/T]cgaactctagaaccca	C	T	sapiens phosphoglucomutase 1 (PGM1), mRNA. /// ENST00000006941 // intron // 0 // --- // --- // --- // ---	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2061297	aatgccaaggacaatc[A/T]atagacagaggttgcc	A	T	ENST00000344027 // intron // 0 // --- // --- // --- // ---	-	q21.2
SNP_A-2068496	acaagtaaacaaacga[C/T]acatcttaatacattg	C	T	// 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 479253 // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2092456	agaaagtagtatataa[G/T]tgctagttaccaacaa	G	T	-- /// ENST00000340000 // upstream // 430582 // --- // --- // ---	-	p12.1
SNP_A-2077473	accacatccttttacc[C/G]gactcctttgtaatct	C	G	-- /// ENST00000314058 // upstream // 203995 // --- // --- // ---	-	p13.2
SNP_A-2266289	gaaggtaaggaaatgg[A/T]aagccgccctggctga	A	T	10775 // Homo sapiens processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae) (POP4), mRNA.	POP4	POP4, Homo sapiens processing of precursor 4, ribonuclease P q12
SNP_A-2258583	cttttctttccccgcc[C/T]gagagagtcaaacgct	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3577804 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2282440	gagttctgttaaacga[C/T]agattcatttacatgt	C	T	Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// ENST00000217067 // intron // 0 // --- // ---	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-2241207	ctgaggacgctgctac[C/T]gaaaagaaacctcgta	C	T	Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // ---	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-2309699	ggaaagctaatggaac[A/G]agattacaagactgtg	A	G	54851 // Homo sapiens fetal globin-inducing factor (FGIF), mRNA. /// NM_002033 // upstream // 21868 // Hs.390420 //	FGIF	FGIF, Homo sapiens fetal globin-inducing factor (FGIF), q21
SNP_A-2314563	ggaggtgctctcagta[C/T]gcctctttctgtacct	C	T	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream // 67515	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.1
SNP_A-2294065	gcaggatctactttta[A/G]atagtttaagtcaaga	A	G	Homo sapiens zinc finger protein 258 (ZNF258), mRNA. /// NM_145310 // 3UTR // 0 // Hs.533986 // ZNF258 // 9204 //	ZNF258	ZNF258, Homo sapiens zinc finger protein 258 (ZNF258), p34.3
SNP_A-2294517	gcagtcagaactagac[A/G]cacatgcaaggctaac	A	G	Homo sapiens caspase 9, apoptosis-related cysteine protease (CASP9), transcript variant beta, mRNA. /// NM_001229 // intron // 0 // Hs.329502 // CASP9 // 842 //	CASP9	CASP9, Homo sapiens caspase 9, apoptosis-related cysteine protease (CASP9), transcript variant beta, p36.21
SNP_A-2242771	ctgcattcctgacaag[C/T]ctctaggtaatgctga	C	T	153201 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 2 (SLC36A2),	SLC36A2	SLC36A2, Homo sapiens solute carrier family 36 (proton q33.1
SNP_A-2084214	actagggtagttctta[G/T]gttaaatgggctaaat	G	T	ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1032620 // --- // --- // --	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2064064	aattattcacaagaca[C/G]tggtgcagacggcttt	C	G	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 230316 // Hs.17441	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072542	acagccaatgttagtc[C/T]attattagtttgcaca	C	T	22918 // Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), mRNA. /// NM_013248 // upstream // 70034 // Hs.516933 // NXT1 // 29107 // Homo	C1QR1	C1QR1, Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), p11.21
SNP_A-1989811	tagataccaccatata[A/C]aggagtgaatggtagc	A	C	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream //	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-2000592	tatctatagctttaaa[A/G]cagaatattattgcac	A	G	2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 116647 // Hs.33446 // NR5A2 //	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-2028587	aaactgctagtttcaa[G/T]aattcttttgtaaaac	G	T	Homo sapiens RNA terminal phosphate cyclase domain 1 (RTCD1), mRNA. /// ENST00000350363 // intron // 0 // --- // ---	RTCD1	RTCD1, Homo sapiens RNA terminal phosphate cyclase domain 1 (RTCD1), p21.2
SNP_A-2207043	ccatgttcccttcact[C/G]agactcgcccgttcag	C	G	Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // intron // 0 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC rela	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. ,q27
SNP_A-2208877	cccagattcagctcca[C/G]agttttggatgagaag	C	G	163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 134413 // Hs.546355 // TA-LRRP	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2199586	ccaaaaatgttctgaa[C/G]aaagacagcattagct	C	G	// 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p21
SNP_A-2195387	catggctttgtggttg[A/C]actttccctgccagta	A	C	11240 // Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA. /// NM_013358 // upstream // 45968 //	PADI2	PADI2, Homo sapiens peptidyl arginine deiminase, type II (PADI2), p36.13
SNP_A-2156120	attcgtggaagcacac[C/T]ggcttacccaagtacc	C	T	// 55608 // Homo sapiens ankyrin repeat domain 10 (ANKRD10), mRNA. /// NM_145735 // upstream // 83620 //	ANKRD10	ANKRD10, Homo sapiens ankyrin repeat domain 10 (ANKRD10), q34
SNP_A-2164847	caaaccccatgcatca[A/G]gccggtacacaggatc	A	G	ENST00000326677 // intron // 0 // --- // --- // --- // ---	-	q13.13
SNP_A-2147177	atggacactgaggcaa[A/G]gcatttgtactttatt	A	G	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// ENST00000321536 // downstream	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-2143690	atgagaacaagcacta[C/T]ggaaaacagtgtggag	C	T	/// ENST00000355561 // upstream // 665891 // --- // --- // --- // -	-	q21.31
SNP_A-2115844	agggtggaggaagcgc[A/G]cagtgtgaaaacctcc	A	G	23504 // Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// NM_015347 // upstream // 147514 // Hs.225014 //	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-2118263	agtaacaaaagcataa[C/T]ggttgagaagaaccag	C	T	Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, mRNA. /// NM_024852 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens	EIF2C3	EIF2C3, Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, p34.3
SNP_A-1729192	ttgaaatttttttagttctgcctta[C/T]gaaaaagccttttatacccctgata	C	T	clone IMAGE:5277680, partial cds /// NM_030932 // downstream // 761561 // Hs.122164 // DIAPH3 // 81624 //	-	- , rs9317039, CDNA clone IMAGE:5277680, partial cds ,q21.2
SNP_A-1784949	ggcgaccctgggatca[A/G]cccatcactcaacatc	A	G	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 4,	ABCC1	ABCC1, Homo sapiens ATP-binding cassette, sub-family C (CFTR p13.11
SNP_A-1711644	aaaagtgtgtgtcatttttgtgaaa[A/C]gcagtatagcagaatggttaagaga	A	C	NM_001510 // intron // 0 // Hs.248130 // GRID2 // 2895 // glutamate receptor, ionotropic, delta 2	GRID2	GRID2 , rs10516928, glutamate receptor, ionotropic, delta 2,q22.3
SNP_A-1661386	ttgttcatatatatttaaaatatgg[C/T]caaatctacctgaaaagtagcactg	C	T	// 81542 // thioredoxin domain containing /// NM_152330 // upstream // 85493 // Hs.439190 // C14orf31 // 122786 //	TXNDC	TXNDC , rs10484087, thioredoxin domain containing ,q22.1
SNP_A-1653564	aactcggatacccatcatcaataac[A/G]ccttgttccatggcggggagctgcc	A	G	10539 // thioredoxin-like 2 /// NM_174937 // downstream // 697479 // Hs.7621 // TCERG1L // 256536 // transcription	TXNL2	TXNL2 , rs396186, thioredoxin-like 2 ,q26.3
SNP_A-1855233	tcaagccctgtttcac[C/G]accgactgttcttatc	C	G	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-1857617	tcactctgacccttca[A/G]taaaagcacttgccca	A	G	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1848891	gtgtaagacaataaca[C/T]tctcatgatttctccc	C	T	6356 // Homo sapiens chemokine (C-C motif) ligand 11 (CCL11), mRNA. /// NM_005623 // upstream // 17719 //	CCL11	CCL11, Homo sapiens chemokine (C-C motif) ligand 11 (CCL11), q12
SNP_A-1949616	tttatttgaatcctca[C/T]gtgaatttcatcttta	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2128098 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1976618	gaccatctccttttga[A/G]aatcctgaatcagtac	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1418287 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1983768	agcaaacacagaggaa[A/G]gatgagctgagagatg	A	G	2246 // Homo sapiens fibroblast growth factor 1 (acidic) (FGF1), transcript variant 3, mRNA. /// NM_033136 //	FGF1	FGF1, Homo sapiens fibroblast growth factor 1 (acidic) (FGF1), transcript variant 3, q31.3
SNP_A-1984361	agaattttacttttcaa[A/T]gtgccttcaatagact	A	T	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 531935 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1891845	tgatttgagtcttgaa[C/T]ctttgtaggaaaggta	C	T	Homo sapiens transmembrane 4 superfamily member 12 (TM4SF12), mRNA. /// ENST00000222747 // intron // 0 // --- //	TM4SF12	TM4SF12, Homo sapiens transmembrane 4 superfamily member 12 (TM4SF12), q31.31
SNP_A-1930647	ttccacaatgactaaa[A/G]taatatacactcccac	A	G	5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 333403 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-1917960	ttaaaatgcacttgta[A/G]attctgtctgattgat	A	G	Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// ENST00000306821 // intron // 0 // --- // --- // --- ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1911488	tgtctttaaaaggaca[A/G]tgataacgcaagtgaa	A	G	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-1927549	ttcaacaaatctgtaa[A/G]cttgtttggggaaaga	A	G	27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 121577 // Hs.381050 // B3GAT1 // 27087 // Homo	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-1896971	tgctcatgattgacta[C/G]ggattatgacatcttt	C	G	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1950294	tttcagagtagtgaga[C/T]actttagcattcctgt	C	T	// 339512 // Homo sapiens hypothetical protein MGC48998 (MGC48998), mRNA. /// NM_005613 // upstream // 186391 //	MGC48998	MGC48998, Homo sapiens hypothetical protein MGC48998 (MGC48998), q23.3
SNP_A-1824759	taaagagtactggtca[C/T]gtgtattgcaggatgt	C	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1966849 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1821262	gtttgatgagaaacta[A/C]gtgatttactagtaag	A	C	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-1728845	aattagagaggtaatctgttaataa[C/T]ggaggattgccatttgacagctggt	C	T	// glycerol kinase 2 /// NM_058168 // upstream // 251117 // Hs.104215 // GDEP // 118425 // gene differentially expressed	GK2	GK2 , rs2903640, glycerol kinase 2 ,q21.21
SNP_A-1801154	gtagccgttaagctcc[A/G]caaatcacatttaatc	A	G	Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // --- // --- // --- // --- ///	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3), p13.3
SNP_A-2121561	agtgaacatgggacaa[C/T]gagttagggaccacgt	C	T	// 283431 // Homo sapiens growth arrest-specific 2 like 3 (GAS2L3), mRNA. /// NM_178826 // upstream // 48102 //	GAS2L3	GAS2L3, Homo sapiens growth arrest-specific 2 like 3 (GAS2L3), q23.1
SNP_A-2107791	agctcagtgtgaccca[C/T]gttagagtctggactc	C	T	90850 // Homo sapiens zinc finger protein 598 (ZNF598), mRNA. /// AB084276 // upstream // 7676 // Hs.233533 //	ZNF598	ZNF598, Homo sapiens zinc finger protein 598 (ZNF598), p13.3
SNP_A-2143364	atgacatttagctgga[C/G]agatgccataatatag	C	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2166065	caaataccagtgacca[A/G]aaggagttgcgctgtg	A	G	1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 638257 // Hs.199248 // PTGER4 //	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-2155079	attcagaaaattcaca[A/G]atggggcagactattt	A	G	54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 //	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-2202625	ccacctctgttcatca[C/T]tctatgggctctgtgt	C	T	151011 // Homo sapiens septin 10 (SEPT10), transcript variant 1, mRNA. /// NM_178584 // upstream // 53353 //	SEPT10	SEPT10, Homo sapiens septin 10 (SEPT10), transcript variant 1, q13
SNP_A-2027167	aaacaggtgtgtttga[C/G]aacagcaggcaggtac	C	G	// 6638 // Homo sapiens small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 1, mRNA. /// NM_022807 // downstream // 106573 // Hs.525700 // SNRPN	SNRPN	SNRPN, Homo sapiens small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 1, q11.2
SNP_A-2032285	aaagttacaggactca[A/G]aaacctcacaggtctc	A	G	1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1011308 //	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2026301	aaaatttcatatgata[C/T]taaccattgtgtttgg	C	T	-- /// ENST00000354800 // downstream // 87098 // --- // --- // ---	-	q14.1
SNP_A-1995692	tagtatgtgatgggta[A/C]aaatgaggtttgtttt	A	C	Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // --- // --- // --- // ---	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2010154	atttcaaggcagccta[C/T]gtggagtcaagaggat	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2295327 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2016116	agagcccctgttggga[A/G]tacggcaaagaggtcg	A	G	/// ENST00000331037 // downstream // 28159 // --- // --- // ---	-	q21.1
SNP_A-2055390	aataagtaaagggaga[A/G]aacaaatgctacagaa	A	G	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, mRNA. /// NM_138711 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens	PPARG	PPARG, Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, p25.2
SNP_A-2248638	ctgttattttcagcaa[C/T]gtattaacaacatact	C	T	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // intron // 0 // Hs.165195 // VAPA //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235025	ctcccacaagtttcca[C/T]aggcttaggaattttc	C	T	80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 46295 //	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1
SNP_A-2228731	ctagaccttcagagga[C/T]acaaacagatgtaaaa	C	T	ENST00000360397 // intron // 0 // --- // --- // --- // ---	-	q25
SNP_A-2314649	ggagtaggaaagtcaa[C/T]gctttaggaaaatgta	C	T	// Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // intron // 0 // --- // --- // --- // ---	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2314366	ggaggcttcagaggaa[A/T]tactgaacaattagaa	A	T	2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000360030 // upstream // 5217 //	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.1
SNP_A-2288598	gattgcctgtagtcac[A/C]gccaataagtattaga	A	C	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2284115	gatatgaaaaaagcca[C/T]gtgggtcagagtctca	C	T	// 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 487489 // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-2274297	gacttggaaacagtac[A/G]gctttctgaaagattt	A	G	Homo sapiens mRNA for KIAA0611 protein, partial cds. /// ENST00000311637 // intron // 0 // --- // --- // --- // --- ///	ATP9A	ATP9A, Homo sapiens for KIAA0611 protein, partial cds. ,q13.2
SNP_A-2261358	gaaagccagacactgt[A/T]aacccatttttacaag	A	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. ,q21.1
SNP_A-2263097	gaacaccatgataaat[C/T]atctttttttcctgtc	C	T	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-2048413	aagcagtgcctagaaa[A/C]aggtatcactcaggag	A	C	Homo sapiens centaurin, gamma 2 (CENTG2), mRNA. /// ENST00000336665 // intron // 0 // --- // --- // --- // ---	CENTG2	CENTG2, Homo sapiens centaurin, gamma 2 (CENTG2), q37.2
SNP_A-2062472	aatgtagtagcagtcc[A/C]agtttgagagttctac	A	C	ENST00000331305 // intron // 0 // --- // --- // --- // --- /// ENST00000330861 // intron // 0 // --- // --- // --- // --- ///	-	q21.32
SNP_A-2091914	agaaacaacggcagaa[A/G]ctgaacaccggagtgg	A	G	-- /// ENST00000341636 // upstream // 149130 // --- // --- // ---	-	q11.2
SNP_A-2009658	ttgatgaggaagaaga[A/C]aattggataagatggg	A	C	sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// ENST00000282970 // 3UTR // 0 // --- // --- // --- // ---	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-1995843	gagaaactagagatta[A/G]ctcaggatacttcaag	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 934664 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1994427	aatttacagcaaggac[A/C]gggaattgttgtaaag	A	C	// 51123 // Homo sapiens HSPC038 protein (LOC51123), mRNA. /// NM_024915 // upstream // 129719 // Hs.161160 //	LOC51123	LOC51123, Homo sapiens HSPC038 protein (LOC51123), q22.3
SNP_A-2003792	cctcacaggaagtcgc[A/G]cctgaggaaatcatca	A	G	122876 // Homo sapiens glycoprotein hormone beta 5 (GPHB5), mRNA. /// NM_006246 // downstream // 12736 //	GPHB5	GPHB5, Homo sapiens glycoprotein hormone beta 5 (GPHB5), q23.2
SNP_A-2025222	aaaatagtggttgtta[C/G]cggtggcaacagtcca	C	G	// Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 949877	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2047567	aagatgggattaataa[A/C]atagtactgacattca	A	C	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 101122 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2212358	ccctgtactcttccgg[A/G]aagtcaatattacaaa	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-2214187	cctaattgtgatacca[A/G]ggaagtatttaagatt	A	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2169409	caagcatttctcagag[G/T]ctacactttacatgag	G	T	// Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // 3UTR // 0 // --- // --- // --- // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2171782	caatgaagcccgaatg[A/G]cagtatatctctttac	A	G	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2158770	attgtcttgcaacaaa[G/T]aatttctatggtgtcg	G	T	ENST00000301831 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2157824	attgcctggtgcatga[G/T]aaggactcaataaact	G	T	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. ,q12
SNP_A-2162534	attttcccacagtttc[C/G]attattacctgttaat	C	G	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 271668 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2143416	atgaccctgagaacca[A/C]tcagatattgggtcat	A	C	285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 18830 // --- //	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-2144574	atgatccatttttgtc[A/G]atttcaggtatgtttg	A	G	sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // --- // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2140503	atctcccccatcttga[A/C]cttcagaaagctggca	A	C	5076 // Homo sapiens paired box gene 2 (PAX2), transcript variant a, mRNA. /// NM_000278 // downstream // 12429 //	PAX2	PAX2, Homo sapiens paired box gene 2 (PAX2), transcript variant a, q24.31
SNP_A-2147372	atggagctctaggtaa[C/T]gtgtttttttgtttgt	C	T	80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 3473 //	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2146749	atgcttcatctcttca[C/T]aggattctggaggagc	C	T	5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 //	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-1798856	gtaagaaaacagagca[A/G]ctcacggcaacagatc	A	G	// Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// NM_015199 // intron // 0 //	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-1714941	gcttggttctccagtagatacttaa[C/T]agtcaaagctgcaggaagagagcct	C	T	55733 // melanoma antigen recognized by T cells 2 /// NM_019605 // downstream // 42423 // Hs.445835 //	MART2	MART2 , rs10489391, melanoma antigen recognized by T cells 2 ,q32.2
SNP_A-1662144	gggggaacgctgtattttctcacac[A/C]agactctgtaacctggcattcacaa	A	C	betacellulin /// NM_015393 // upstream // 92146 // Hs.105460 // DKFZP564O0823 // 25849 // DKFZP564O0823 protein ///	BTC	BTC , rs10518132, betacellulin ,q13.3
SNP_A-1667500	taaggttttaagattttgtgtacga[C/T]attgtatttcagccagcaattattg	C	T	5139 // phosphodiesterase 3A, cGMP-inhibited /// NM_153207 // downstream // 663607 // Hs.528315 // AEBP2	PDE3A	PDE3A , rs10505864, phosphodiesterase 3A, cGMP-inhibited ,p12.2
SNP_A-1682302	aaaaattgttatttttgaatgtcac[C/T]atttgattatcatcatcattattat	C	T	-		, rs1998574, ,q22.1
SNP_A-1814963	gtgttacctggaaaaa[A/T]ttaaagcagccattac	A	T	-- /// ENST00000360285 // downstream // 527155 // --- // --- // -- // --- /// ENST00000339882 // downstream // 527155 // --- //	-	q12
SNP_A-1843370	tagtgaaaatgtttcc[G/T]aagagagccaagtaaa	G	T	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1847275	tatccagaatgtataa[A/G]tgacttgtaacccagt	A	G	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 1099237 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1854006	tcaaaattgcagttcc[A/G]ccttcaacaacggtta	A	G	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // CDS // 0 // --- // ---	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1954207	tttgcaaaatggaaac[A/G]gcttacctacttcaca	A	G	283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743), mRNA. /// NM_000875 // upstream // 135847 //	FLJ39743	FLJ39743, Homo sapiens hypothetical protein FLJ39743 (FLJ39743), q26.3
SNP_A-1956767	ttttaaagccttcaca[C/T]gatgtcttgagccttt	C	T	FLJ33768 // 283673 // Homo sapiens hypothetical protein FLJ33768 (FLJ33768), mRNA. /// NM_015554 // upstream //	FLJ33768	FLJ33768, Homo sapiens hypothetical protein FLJ33768 (FLJ33768), q23
SNP_A-1965024	gtatttatgaaaagaa[A/G]tcccagtgaaaattgt	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1896973	tagaaggcatttaaca[A/G]gctactatcacttcag	A	G	Homo sapiens chromosome 18 open reading frame 11 (C18orf11), mRNA. /// ENST00000269209 // intron // 0 // --- //	C18orf11	C18orf11, Homo sapiens chromosome 18 open reading frame 11 (C18orf11), q12.1
SNP_A-1881715	tctttggataattaga[G/T]gtcaagtatttgttat	G	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1878807	tctgttgtgaaaaata[C/T]agaaactaactggcag	C	T	Homo sapiens prolyl endopeptidase (PREP), mRNA. /// ENST00000229430 // intron // 0 // --- // --- // --- // ---	PREP	PREP, Homo sapiens prolyl endopeptidase (PREP), q21
SNP_A-1881064	tctttaaagacagaaa[A/G]cctgttagatttattg	A	G	// Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /// ENST00000297435 // upstream // 30504 // --- // ---	DEFA4	DEFA4, Homo sapiens defensin, alpha 4, corticostatin (DEFA4), p23.1
SNP_A-1914876	tgttagcagtagtagc[A/G]gaaggacagtctggac	A	G	/// ENST00000294915 // upstream // 40906 // --- // --- // --- // ---	-	q43
SNP_A-1917642	ttaaaaacaatttatg[A/C]atggtggtgagggtgc	A	C	64399 // Homo sapiens hedgehog interacting protein (HHIP), mRNA. /// NM_014885 // downstream // 94301 // Hs.480876	HHIP	HHIP, Homo sapiens hedgehog interacting protein (HHIP), q31.21
SNP_A-1911599	tgtgaaaattggtaga[C/T]gcatagagcacagcac	C	T	6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// ENST00000325017 // upstream // 53768 // --- // --- // --- // ---	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-1905563	tggtagacttgagtag[A/G]cattgttctgggggag	A	G	10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream //	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-1909118	tgtatccatcactaaa[A/G]tatcatacagaatagt	A	G	// Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 134791 // Hs.98008 // GK2 // 2712	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1925564	ttatgaagtatattaa[C/G]taaacaaatgcagatc	C	G	Homo sapiens neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA. /// ENST00000360051 // intron // 0 // --- // --- // --- // --- ///	SEPT2	SEPT2, Homo sapiens neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), q37.3
SNP_A-1882913	tgaaaggttcgcaaaa[C/G]tagctctgaagaagtg	C	G	56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 78926 // --- // --- // --- // ---	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1
SNP_A-1962401	agattcaaagacttaa[A/G]ctttcagaataaggca	A	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 230516 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1984360	ctcccaatctaaaata[A/G]ctgtaaccatactctc	A	G	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 564618 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1977003	ggaacattcacaacta[C/T]gaaagaactgtaaaag	C	T	132789 // Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), mRNA. /// ENST00000295448 //	GNPDA2	GNPDA2, Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), p13
SNP_A-1946751	tttaactcaatctaaa[A/T]ctactaaaccaatggt	A	T	Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // --- // --- // --- // --- ///	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839976	tagcaacaaatgctaa[A/C]cctaatttacaactct	A	C	Homo sapiens mRNA for KIAA0603 protein, partial cds. /// ENST00000258610 // intron // 0 // --- // --- // --- // ---	TBC1D4	TBC1D4, Homo sapiens for KIAA0603 protein, partial cds. ,q22.2
SNP_A-1823069	attgtgttctcagatc[A/G]cattcggaaaggcaaa	A	G	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 411045 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-1668298	ctctgtatccgacaaaatggcgcat[A/G]atcatctgtgaaaattggaggtaag	A	G	2444 // fyn-related kinase /// NM_153612 // upstream // 765169 // Hs.510015 // HS3ST5 // 222537 // heparan sulfate	FRK	FRK , rs4128355, fyn-related kinase ,q22.1
SNP_A-1806197	gtcctgcctttcccca[A/G]agaaaaagcacgcact	A	G	Homo sapiens fetuin B (FETUB), mRNA. /// ENST00000265029 // CDS // 0 // --- // --- // --- // ---	FETUB	FETUB, Homo sapiens fetuin B (FETUB), q27.3
SNP_A-1812201	gtggagggtcacttgg[A/G]atctgagagtgattgt	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 3 (DNAH3), mRNA. /// ENST00000261383 // intron // 0 // --- // ---	DNAH3	DNAH3, Homo sapiens dynein, axonemal, heavy polypeptide 3 (DNAH3), p12.3
SNP_A-2165611	caaaggaatctgggtc[C/T]acctatgggaggttga	C	T	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2157208	attgaatgtgttaaag[G/T]aagttgtgaagaaaag	G	T	/// ENST00000357497 // downstream // 532633 // --- // --- // --- // --- /// ENST00000359402 // downstream // 532686 // --- // ---	-	q31.1
SNP_A-2117086	aggtgataggaagaca[A/G]agaagacacagagtag	A	G	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 426294 // ---	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-2127526	ataacatcagtgttta[G/T]gagtttacattcagaa	G	T	5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// NM_017935 // upstream // 309681 //	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-2126990	ataaagtggtaaatgc[C/T]gaacagagaggggcca	C	T	Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000265109 // intron // 0 // --- // --- // --- // ---	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-2132558	atagtgttatttgcta[C/T]ccagatgagtcaatat	C	T	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 928053 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2021381	aaaaaagaacatttca[A/G]attaagggatggggca	A	G	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 344029 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2016247	aaaaattgttatgaca[G/T]catttgacttctagtt	G	T	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2081689	accttcacttctttcg[C/T]agtaaaaacccatttt	C	T	Homo sapiens chromosome 6 open reading frame 133 (C6orf133), mRNA. /// ENST00000229488 // intron // 0 // --- //	UBR2	UBR2, Homo sapiens chromosome 6 open reading frame 133 (C6orf133), p21.1
SNP_A-2057344	aatatattcaaaccac[A/G]atttgtccttgtcata	A	G	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase q35.1
SNP_A-2231671	ctattttggtgggtaa[C/G]agcaggaatcaagcca	C	G	// 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 360105 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2251628	cttcagcttctgctcc[A/G]aaatcaactttatctt	A	G	4638 // Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, mRNA. /// NM_053028 //	MYLK	MYLK, Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, q21.1
SNP_A-2251306	cttcaacttttacacg[A/G]cctgtaattcagtcat	A	G	sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 1, mRNA. /// NM_153048 // intron // 0 //	FYN	FYN, Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 1, q21
SNP_A-2253302	cttctggcagcaggag[A/G]ataaaaggaaccaact	A	G	130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // ---	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-2293170	gcagagaatgtttcgc[C/G]ccccttacgaacatg	C	G	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 //	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. q21.1
SNP_A-2307100	gctgttttgcttgtta[C/T]agtttcaatctctttt	C	T	ENST00000263154 // intron // 0 // --- // --- // --- // ---	-	p15.3
SNP_A-2297987	tttctgaataccaaaa[G/T]tctcccctctaagacc	G	T	3419 // Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, mRNA. /// NM_015162 // upstream // 758 // Hs.250616 // BG1 // 23205 // Homo sapien	IDH3A	IDH3A, Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, q25.1
SNP_A-2249383	cttaaagatgctgata[C/T]agccattagtctgaca	C	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2284033	gatatcaaagccacta[A/G]aagaacagaaaattac	A	G	9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1370390 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2103106	agcaaattgcaagaca[A/G]ctaatgagttttaatg	A	G	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 78150 //	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2016191	aggagcagaaaaggaa[G/T]tgttcactttcaggtt	G	T	4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000331037 // upstream //	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-2011731	tgatagaccatactta[A/G]caatggcttttcttac	A	G	ENST00000343352 // intron // 0 // --- // --- // --- // ---	-	p21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2003207	tattgattgtaaccaa[C/T]gtacccaccaaagtaa	C	T	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// ENST00000343323 // intron // 0 // --- // --- // --- // ---	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-2027046	aaacagatctgtatac[A/G]atgaaggccccagagc	A	G	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2036017	aaattaatccattgca[A/G]attgagtaactctggg	A	G	5784 // Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// NM_016343 // downstream // 82971 // Hs.497741 // CENPF // 1063 // Homo	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41
SNP_A-2124648	agttctaatcaatgaa[A/T]atccaatatttgcctg	A	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2845563 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2120127	agtcagaataaaaaca[A/G]atgaagagtcatctca	A	G	Homo sapiens plakophilin 4 (PKP4), transcript variant 1, mRNA. /// ENST00000354977 // intron // 0 // --- // --- // --- // ---	PKP4	PKP4, Homo sapiens plakophilin 4 (PKP4), transcript variant 1, q24.1
SNP_A-2144070	atgaggacatagtgga[C/T]gacgtcggggattgct	C	T	Homo sapiens FXYD domain containing ion transport regulator 3 (FXYD3), transcript variant 2, mRNA. /// NM_005971 // intron // 0 // Hs.301350 // FXYD3 // 5349 //	FXYD3	FXYD3, Homo sapiens FXYD domain containing ion transport regulator 3 (FXYD3), transcript variant 2, q13.12
SNP_A-2199128	catttgttttctatta[C/T]gtgtcaagtgtaatgc	C	T	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 354364 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-2187140	cagctacctaggaaat[A/G]aattgggatggtatca	A	G	ENST00000251041 // intron // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-1813385	gtggtgtgcttgtaca[A/G]caaatgatggtaaaga	A	G	Homo sapiens TUWD12 (TUWD12), mRNA. /// ENST00000313546 // intron // 0 // --- // --- // ---	WDR51B	WDR51B, Homo sapiens TUWD12 (TUWD12), q21.33
SNP_A-1797547	ggtttccagaattgca[A/C]gggtgctacggaggat	A	C	Homo sapiens synaptotagmin II (SYT2), mRNA. /// ENST00000317518 // intron // 0 // --- // --- // --- // ---	SYT2	SYT2, Homo sapiens synaptotagmin II (SYT2), q32.1
SNP_A-1678920	ctggcacacccttgtttcaatatga[C/G]ccatacaaattcatatactattcct	C	G	2776 // guanine nucleotide binding protein (G protein), q polypeptide	GNAQ	GNAQ , rs1556501, guanine nucleotide binding protein (G protein), q polypeptide,q21.2
SNP_A-1826542	taacaatacacgcttg[A/T]aagggacccaggtttt	A	T	10799 // Homo sapiens ribonuclease P 40kDa subunit (RPP40), mRNA. /// NM_020408 // downstream // 44296 //	RPP40	RPP40, Homo sapiens ribonuclease P 40kDa subunit (RPP40), p25.1
SNP_A-1955322	tttgggccacaaattc[A/G]atataatacaaatcta	A	G	Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // --- // --- // --- // ---	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1948593	tttataaagccagaga[A/G]gacagtgttgctgctt	A	G	Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, mRNA. /// NM_000337 // intron // 0 // Hs.387207 // SGCD // 6444 //	SGCD	SGCD, Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, q33.3
SNP_A-1978354	tagtgctgaagacaga[A/G]gttaagataagggcca	A	G	Homo sapiens hypothetical protein FLJ20032 (FLJ20032), mRNA. /// ENST00000305737 // intron // 0 // --- // --- // --- // ---	FLJ20032	FLJ20032, Homo sapiens hypothetical protein FLJ20032 (FLJ20032), q24
SNP_A-1887996	tgagcagataaagttg[A/G]ataactaggcaggagc	A	G	MGC88374 // 440184 // Homo sapiens similar to CG32662-PA (MGC88374), mRNA. /// ENST00000310149 // upstream	MGC88374	MGC88374, Homo sapiens similar to CG32662-PA (MGC88374), q23.3
SNP_A-1919418	ttaagcaatcatatta[C/T]ggtaaaaaagaacaat	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1885858	tgacataatcttaata[C/G]aagtgaggtactagaa	C	G	Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, mRNA. /// NM_024806 // intron // 0 //	FLJ23554	FLJ23554, Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, q24.1
SNP_A-1883974	tgaagatcattagttc[A/G]gaaagatatgaatatt	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1899487	tggaagattgaatcat[C/G]acatggtgtactaaag	C	G	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1977865	tatattccaaaacaga[C/T]tccgaataaaataaca	C	T	Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// ENST00000357940 // intron // 0 // --- // --- // --- // ---	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1984386	tgctatctctatggta[C/T]gggtcctgtctaggat	C	T	Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-1964618	ttgaaatggactcccc[A/G]cttctgccaataaaat	A	G	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), mRNA. /// ENST00000263239 // intron // 0 // --- // ---	DDX18	DDX18, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), q14.1
SNP_A-1961872	tttgtctattattaga[A/C]atcaagtataccaagt	A	C	7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1959792	ttttgtaacatttgaa[A/G]catgattaaccaatta	A	G	CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p15.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946026	ttgtttgttgtctacc[A/G]gaggaagtgagttaag	A	G	54472 // Homo sapiens toll interacting protein (TOLLIP), mRNA. /// NM_003957 // upstream // 22295 // Hs.170819 //	TOLLIP	TOLLIP, Homo sapiens toll interacting protein (TOLLIP), p15.5
SNP_A-1937693	ttgaagctcaaggtta[C/T]gaaccaagagtcattc	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 1637879 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1827256	taacctgtgtaagaag[A/T]aagaaatagctggtaa	A	T	// 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 728755 //	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-1823827	taaaatgcaagtaaga[A/G]cattaataacaataga	A	G	// 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 243805 // Hs.504943	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.3
SNP_A-1842693	tagtaaattgatgaga[A/T]ggaacaatattttgt	A	T	// 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // downstream // 342031 // Hs.123642	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1832910	tacaatgtcaatatct[C/T]acttgtacttagcagt	C	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1691744 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1854429	tcaaatctggtgacta[C/T]agcatccctgatggtc	C	T	sapiens mRNA for KIAA0254 gene, partial cds. /// ENST00000265909 // intron // 0 // --- // --- // --- // ---	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds. ,q24.3
SNP_A-1873414	tctcaaccctaatcc[A/T]cctgtcagagaagaaa	A	T	/// ENST00000328955 // upstream // 1549510 // --- // --- // --- // ---	-	q24.23
SNP_A-1701787	tcaacattggactctacgaatataa[C/T]ggcttgagatccaaggaagaagtcc	C	T	NM_003749 // downstream // 543540 // Hs.143648 // IRS2 // 8660 // insulin receptor substrate 2	IRS2	IRS2 , rs2011035, insulin receptor substrate 2,q33.3
SNP_A-1666420	tctgtagtaaatagaaagagcatgt[C/T]aggaaaatgaaaaactttggaccta	C	T	NM_021238 // intron // 0 // Hs.356223 // C12orf14 // 58516 // chromosome 12 open reading frame 14	C12orf14	C12orf14 , rs1844986, chromosome 12 open reading frame 14,p11.21
SNP_A-1723712	tgaaaatcaattaatgtaattcacc[A/G]actgacgcggaatggtctgtctact	A	G	50805 // iroquois homeobox protein 4 /// NM_178569 // upstream // 147576 // Hs.148486 // CEI // 153571 // CEI	IRX4	IRX4 , rs323685, iroquois homeobox protein 4 ,p15.33
SNP_A-1780867	ggatgaaaatcttaag[C/T]cattctaactctaaaa	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 607085 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1786302	ggctgtgctctaacac[C/T]attgtgatgacatggg	C	T	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-1790594	ggggccttccttgtcc[C/T]gctgatttagagacac	C	T	84258 // Homo sapiens synaptotagmin III (SYT3), mRNA. /// NM_016148 // downstream // 81489 // Hs.274255 // SHANK1	SYT3	SYT3, Homo sapiens synaptotagmin III (SYT3), q13.33
SNP_A-2172213	caatgtctgagcacaa[A/G]agaaaatgggtgtcag	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1526539 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2168926	caagagataatacttg[C/T]caagctcacaaatcaa	C	T	Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // --- // --- // --- // ---	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2178951	cactgcacctggttag[A/G]aactatttgtgtacag	A	G	8565 // Homo sapiens tyrosyl-tRNA synthetase (YARS), mRNA. /// NM_022753 // downstream // 1697 // Hs.440880 //	YARS	YARS, Homo sapiens tyrosyl-tRNA synthetase (YARS), p35.1
SNP_A-2227634	ctacatcatccaggtc[A/G]agaaattcatccagca	A	G	9861 // Homo sapiens proteasome regulatory particle subunit p44S10 (p44S10), mRNA. /// ENST00000295901 // upstream	p44S10	p44S10, Homo sapiens proteasome regulatory particle subunit p44S10 (p44S10), p14.1
SNP_A-2209401	cccatactctgcttct[A/G]acctggatgggggccc	A	G	23765 // Homo sapiens interleukin 17 receptor (IL17R), mRNA. /// ENST00000266136 // upstream // 20227 // --- // ---	IL17R	IL17R, Homo sapiens interleukin 17 receptor (IL17R), q11.1
SNP_A-2144787	atgatgtaggaaaaaa[C/T]gaagcagaaaattgag	C	T	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 178094 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2114366	agggacagcatccgta[C/T]actactctaagtggtg	C	T	Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- // --- ///	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-2129755	atacagttcacctgag[A/T]aatttgcccttgcctc	A	T	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-2035371	aaatggcattagttta[C/T]gtttttcaaggaatta	C	T	// 221223 // Homo sapiens hypothetical protein FLJ31547 (FLJ31547), mRNA. /// NM_138736 // upstream // 156777 //	FLJ31547	FLJ31547, Homo sapiens hypothetical protein FLJ31547 (FLJ31547), q12.2
SNP_A-2040893	aaccctaatggaaagg[A/G]aaacaacatccttcgg	A	G	Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 195027 // Hs.133397 // ITGA6 // 3655 //	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-2028309	aaactcaagtttctcc[A/G]ctacaaagcccatcct	A	G	Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// ENST00000359195 // intron // 0 // --- // --- // --- // --- /// ENST00000222569 // intron // 0 // ---	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-2032033	aaagtgaatgagaaca[A/G]tactgataataatagc	A	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 558654 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2030771	aaagcttgaataatgc[A/G]cggtactttataaaat	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1995376	aaactgtgcaccccca[C/T]ggttttatgtaaagca	C	T	// --- /// ENST00000328955 // upstream // 326737 // --- // --- // ---	-	q24.23
SNP_A-1990988	aagaaattgtgacttc[A/G]actgaaagctgagttt	A	G	sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA. /// ENST00000318493 // intron // 0 //	MET	MET, Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), q31.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2105847	agccagtgtctggaaa[C/T]ccacaccccacctggc	C	T	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2073255	acagggattcataaaa[G/T]aattcaccatataaaa	G	T	51582 // Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, mRNA. /// NM_148174 // upstream // 98059 // Hs.459106 // OAZIN // 51582 // Homo	OAZIN	OAZIN, Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, q22.3
SNP_A-2284185	gatatgggtgttaacc[A/T]aaagcaatgcacatct	A	T	8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 //	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-2276085	gagagaatattttaaa[C/T]tgacgttgcggagaga	C	T	ENST00000322896 // intron // 0 // --- // --- // --- // ---	-	q14.13
SNP_A-2264076	gaactctgaccaggat[G/T]agttttcagagcactt	G	T	/// ENST00000358118 // downstream // 319016 // --- // --- // ---	-	q12
SNP_A-2263933	gaactagagaatctca[A/G]ataacccttagctct	A	G	91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream //	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-2248135	ctgtggctagtttggc[A/C]aattgggaggcaccag	A	C	Homo sapiens neurocalcin delta (NCALD), mRNA. /// ENST00000311028 // intron // 0 // --- // --- // --- // --- ///	NCALD	NCALD, Homo sapiens neurocalcin delta (NCALD), q22.3
SNP_A-2243603	ctgctcagtaggaaga[A/C]ctcttgagatatgcaa	A	C	// Homo sapiens esophageal cancer associated protein (MGC16824), mRNA. /// ENST00000251143 // intron // 0 // ---	MGC16824	MGC16824, Homo sapiens esophageal cancer associated protein (MGC16824), p12.3
SNP_A-2294627	gcagtgatctctcaaa[C/T]ctaaatttccataggg	C	T	// 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 174066 //	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-2310011	ggaaatggcctctcca[A/C]gatccataccgtttta	A	C	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 96906 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2313112	ggagaacagcacagag[A/G]aagtcatagggagggc	A	G	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-2298853	gccccaaatgccacca[C/T]gcatgcgtcagctctt	C	T	// 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 41649 // Hs.132344	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2251639	cttcaggactgctaca[A/C]aacccttagccttcc	A	C	Homo sapiens tubulin tyrosine ligase-like family, member 4 (TTLL4), mRNA. /// ENST00000258398 // intron // 0 // --- // ---	TTLL4	TTLL4, Homo sapiens tubulin tyrosine ligase-like family, member 4 (TTLL4), q35
SNP_A-2263280	gaacagtagatcttac[A/T]cattctttgtaattat	A	T	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2279693	gaggcagtaaatggtg[C/T]aagtatgaaagagttg	C	T	10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 68709 // Hs.2561 // NGFB //	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-2067910	acaaccttgggaggta[A/G]aaacagcaaatgagac	A	G	FLJ38716 // 126868 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 //	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-2060641	aatgagagccttaaga[C/T]acaggcagtgaatttc	C	T	9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 253471 //	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-2084253	actagtcaggagttga[A/G]ctggtttgagcttcaa	A	G	ENST00000359553 // intron // 0 // --- // --- // --- // ---	-	p13.1
SNP_A-2078036	accaggaaaaggaacc[C/T]ggactcggtgaatgtt	C	T	Homo sapiens beaded filament structural protein 1, filensin (BFSP1), mRNA. /// ENST00000246064 // intron // 0 // --- // ---	BFSP1	BFSP1, Homo sapiens beaded filament structural protein 1, filensin (BFSP1), p12.1
SNP_A-1997863	tgattaggaaatgtca[A/T]ggatacgtctgtaaaa	A	T	Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2008888	cattttcatttgtggc[C/T]cagtaaagcatggctc	C	T	ENST00000262917 // intron // 0 // --- // --- // --- // ---	-	p34.1
SNP_A-2006965	gaaggcccatatagca[C/T]agtgcttacaaatcat	C	T	// 151194 // Homo sapiens similar to hepatocellular carcinoma-associated antigen HCA557b (LOC151194), mRNA. /// NM_152523 // upstream // 2943 // Hs.471234 //	LOC151194	LOC151194, Homo sapiens similar to hepatocellular carcinoma-associated antigen HCA557b (LOC151194), q33.3
SNP_A-2136602	atcacgttaattacag[G/T]caggcatttcattagg	G	T	// 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// NM_012403 // downstream //	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.3
SNP_A-2122828	agtggcagagccagag[A/G]agcagacagctggccc	A	G	Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA. /// ENST00000265854 // intron // 0 // --- // -	MAD1L1	MAD1L1, Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), p22.3
SNP_A-2117380	aggtggtggaaggtgc[C/T]acaagccgtgggtctg	C	T	Homo sapiens zinc finger protein 509 (ZNF509), mRNA. /// ENST00000355834 // intron // 0 // --- // --- // --- // --- ///	ZNF509	ZNF509, Homo sapiens zinc finger protein 509 (ZNF509), p16.3
SNP_A-2143601	atgactgtgtttaaaa[G/T]tcaaatacttggagat	G	T	APBB1IP // 54518 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), mRNA. /// NM_014317 // upstream //	APBB1IP	APBB1IP, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), p12.1
SNP_A-2182376	cagagttgggtacaaa[A/G]ttctaaatctagagtc	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3911333 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2176590	cacccatatgtcagaa[G/T]aattgtttacactaca	G	T	// 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 1273616 //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170602	caagtggtaggaaacc[A/G]agcagatggaagacga	A	G	DKFZp434G0625 // 91584 // Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), mRNA. /// NM_173682 // upstream // 67603 // --- // FLJ40288 // 286023	DKFZp434G0625	DKFZp434G0625, Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), q32.3
SNP_A-2195339	catggctagtttctac[A/G]actgacacttctgtaa	A	G	ENST00000281496 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-1787266	gggaactggactgaaa[C/T]caacatataaccgttt	C	T	// 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 9184 // Hs.369438 // ETS1 //	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.3
SNP_A-1758814	gttgttataaaagattaaccacaga[A/C]aaaatgaataaagttgtaagaaaac	A	C	NM_002849 // intron // 0 // Hs.198288 // PTPRR // 5801 // protein tyrosine phosphatase, receptor type, R	PTPRR	PTPRR , rs10506606, protein tyrosine phosphatase, receptor type, R,q15
SNP_A-1850073	tatgtgagagttcaga[C/T]gtaccctcaggctcac	C	T	LOC116123 // 116123 // Homo sapiens hypothetical protein BC014341 (LOC116123), mRNA. /// NM_017542 //	LOC116123	LOC116123, Homo sapiens hypothetical protein BC014341 (LOC116123), q24.1
SNP_A-1833679	tacaggctctggcttc[A/G]ctgggaaactcaggaa	A	G	130560 // Homo sapiens cDNA FLJ36066 fis, clone TESTI2019257. /// NM_139073 // downstream // 9069 //	SPATA3	SPATA3, Homo sapiens cDNA FLJ36066 fis, clone TESTI2019257. ,q37.1
SNP_A-1832566	tacaaatggaaaaagc[A/G]cagatgattgttactt	A	G	157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-1844143	tagtttaattccacta[A/T]atctgccttcaacagt	A	T	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 370353 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1938170	ttgacatctaagaaac[A/G]gaattcatatactgaa	A	G	// 9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 54804 // Hs.136829 // RFX3 //	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-1942697	ttgggataggatcaaa[C/T]tgggtttatgttagga	C	T	Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// NM_173472 // intron // 0 // Hs.190413	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-1957479	ttttataaatttgaaa[A/G]tcagacttttccttgc	A	G	LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 353900 // Hs.307086 //	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-1950046	tttcacagaggaagcc[A/G]aagtccagccaggaga	A	G	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // --- // ---	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-1977769	acacattttcaaggtg[A/G]aaccaatgtgttgaga	A	G	// Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 241039 // Hs.98008 // GK2 // 2712	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1980254	ctattgcagtctctcc[G/T]gagaattacttctgca	G	T	4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 362431 // Hs.481371 //	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1926901	ttatttcaataagaaa[A/G]gagcagctgttttagt	A	G	sapiens mRNA; cDNA DKFZp761C2021 (from clone DKFZp761C2021). /// NM_024612 // upstream // 101259 //	-	-, Homo sapiens cDNA DKFZp761C2021 (from clone DKFZp761C2021). q23.2
SNP_A-1913307	tgtgggccaaacaaaa[C/T]gccacttcagttgagt	C	T	2018 // Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), mRNA. /// NM_014904 // downstream //	EMX2	EMX2, Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), q26.11
SNP_A-1892406	tgcaaggaagtggaga[C/T]ctgggaaactgttctt	C	T	// 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 15946 // --- // --- // --- // --	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-1884430	tgaagtcctcagacca[A/G]tgaccttgaatgtgct	A	G	Homo sapiens polymerase (RNA) I polypeptide A, 194kDa (POLR1A), mRNA. /// ENST00000263857 // intron // 0 // --- //	POLR1A	POLR1A, Homo sapiens polymerase (RNA) I polypeptide A, 194kDa (POLR1A), p11.2
SNP_A-1884652	tgaatactttggatg[A/G]atgggtgcatggacga	A	G	84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream //	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-1888264	tgagctcagctccaaa[C/T]gcaggaaagatggcag	C	T	145173 // Homo sapiens beta 3-glycosyltransferase-like (B3GTL), mRNA. /// NM_130806 // upstream // 215188 //	B3GTL	B3GTL, Homo sapiens beta 3-glycosyltransferase-like (B3GTL), q12.3
SNP_A-1874921	tctctacattttgata[C/T]gtgattattcaattat	C	T	Homo sapiens chromosome 6 open reading frame 106 (C6orf106), transcript variant 2, mRNA. /// NM_024294 // intron // 0 // Hs.485162 // C6orf106 // 64771 // Homo sapiens	C6orf106	C6orf106, Homo sapiens chromosome 6 open reading frame 106 (C6orf106), transcript variant 2, p21.31
SNP_A-1876800	tctgcatcgcataatt[A/T]aaaaaaaatggcaaca	A	T	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-1988498	aagggacagagtgtta[C/T]gagcattatcattcca	C	T	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1974809	tatagcattgaaggca[C/T]atattggaaaagaaga	C	T	/// ENST00000355553 // upstream // 254663 // --- // --- // --- // -- /// ENST00000358223 // upstream // 254663 // --- // --- // ---	-	q25.1
SNP_A-1961149	ttttttaaagatgcac[A/G]ggatattaaatgactg	A	G	Homo sapiens ubiquitin associated protein 1 (UBAP1), mRNA. /// ENST00000356235 // intron // 0 // --- // --- // --- // ---	UBAP1	UBAP1, Homo sapiens ubiquitin associated protein 1 (UBAP1), p13.3
SNP_A-1933606	ttctagctgggcctca[C/T]tcaaattctgcaggtg	C	T	Homo sapiens transient receptor potential cation channel, subfamily M, member 1 (TRPM1), mRNA. /// ENST00000220192 // intron // 0 // --- // --- // --- // --- ///	TRPM1	TRPM1, Homo sapiens transient receptor potential cation channel, subfamily M, member 1 (TRPM1), q13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1832050	taattgttatcaatgg[C/G]aacatttttaaaatct	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1466302 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1827615	taactgctgagttaaa[A/T]ttctcacctttttcg	A	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1295042 // --- // -	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1821641	gtttgtgtatgaattg[A/C]caacttttttagtacc	A	C	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 305716 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1846195	tatatccacatcaaac[A/G]aattatgtggattcat	A	G	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 816346 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1715149	ctgtgtcctagctaaccctagctaa[A/G]agcaaggaatattcactgaccaccc	A	G	6335 // sodium channel, voltage-gated, type IX, alpha /// NM_006920 // upstream // 86009 // Hs.22654 // SCN1A //	SCN9A	SCN9A , rs4667879, sodium channel, voltage-gated, type IX, alpha ,q24.3
SNP_A-1731659	ccctgaactcaaaatgtcttatcat[A/G]tcttactctcccatctaaaatgtat	A	G	8886 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 /// NM_020868 // downstream // 309780 // Hs.91625 // DPP10 //	DDX18	DDX18 , rs1993998, DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 ,q14.1
SNP_A-1788667	gggatgcagtaagaac[C/G]agctattgatggatta	C	G	2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream //	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1
SNP_A-2171806	caatgacacatgttat[C/T]agtggaataaaaatgt	C	T	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 //	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. ,q21.1
SNP_A-2182786	cagatggcattcttaa[A/C]aacttgggtgtctaat	A	C	407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 121662 // Hs.24115 // C13orf25 //	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2182600	cagatcatgttcactc[A/T]aagtaaagactgggca	A	T	8074 // Homo sapiens fibroblast growth factor 23 (FGF23), mRNA. /// NM_020996 // downstream // 49915 // Hs.166015	FGF23	FGF23, Homo sapiens fibroblast growth factor 23 (FGF23), p13.32
SNP_A-2179385	cactgtgtctgtgccc[A/G]agtcttcctccaagtg	A	G	Homo sapiens hypothetical protein FLJ10305 (FLJ10305), mRNA. /// ENST00000261776 // intron // 0 // --- // --- // --- // ---	VAC14	VAC14, Homo sapiens hypothetical protein FLJ10305 (FLJ10305), q22.1
SNP_A-2208006	cccaactgaacataac[A/C]caatccaataaagaaa	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1858412 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2212596	cccttcagagtttcgc[A/C]ctggctgttctgagga	A	C	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2202816	ccactaacaagtcaac[G/T]gctttaatgatttagt	G	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2154416	attattaggatacaga[C/G]agcctagtttagccta	C	G	221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 30651 // --- // --- // --- // --	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-2120124	agtcagaagctgtaaa[C/T]gtggctagtggagaac	C	T	9858 // Homo sapiens KIAA0649 (KIAA0649), mRNA. /// ENST00000320778 // downstream // 135462 // --- // --- // --- // -	KIAA0649	KIAA0649, Homo sapiens KIAA0649 (KIAA0649), q34.3
SNP_A-2109490	aggaaaaatcatacaa[A/T]tatagctctgaaatct	A	T	Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), mRNA. /// ENST00000295798 // intron // 0 // --- // ---	SPTA1	SPTA1, Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), q23.1
SNP_A-2128503	ataataatacttccaa[A/C]agctgtcgcagcgctg	A	C	// 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA. /// NM_000999 // upstream // 751 //	FLJ40319	FLJ40319, Homo sapiens hypothetical protein FLJ40319 (FLJ40319), q25.1
SNP_A-2012870	agggatacaattagtt[G/T]aaattcttcaaatcaa	G	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2032686	aaataaatgtttgtag[C/T]aagtaatcttagtcat	C	T	Homo sapiens chromosome 20 open reading frame 31 (C20orf31), mRNA. /// ENST00000262875 // intron // 0 // --- //	C20orf31	C20orf31, Homo sapiens chromosome 20 open reading frame 31 (C20orf31), q11.22
SNP_A-2019996	catgggggtacgccta[C/T]gtggaaggttgcagaa	C	T	4599 // Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA. /// NM_005656 // upstream // 121598 // Hs.439309 // TMPRSS2	MX1	MX1, Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), q22.3
SNP_A-2036642	aaattggcctaatgaa[C/T]tgactggtatgcacca	C	T	/// ENST00000344163 // upstream // 209450 // --- // --- // --- // -- /// ENST00000249307 // upstream // 234003 // --- // --- // ---	-	q31.33
SNP_A-2086236	actctgggaagaccaa[A/C]ccgtcctctccagggt	A	C	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 228717 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2069466	acacaagtgaggattc[C/T]attccatcaggaatgg	C	T	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2070075	acacatatagaccaaa[C/T]tgtaattctgagcaat	C	T	51059 // Homo sapiens hypothetical protein LOC51059 (LOC51059), mRNA. /// ENST00000160713 // upstream //	LOC51059	LOC51059, Homo sapiens hypothetical protein LOC51059 (LOC51059), q24.23
SNP_A-2282539	gagttgtctttaaaag[A/C]atcacaaatcctcaca	A	C	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, mRNA. /// NM_172362 // intron // 0 // Hs.527656 // KCNH1 //	KCNH1	KCNH1, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, q32.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282168	gagtgtggagcctggc[A/G]aacagaggcagggaac	A	G	28984 // Homo sapiens response gene to complement 32 (RGC32), mRNA. /// ENST00000341475 // downstream //	RGC32	RGC32, Homo sapiens response gene to complement 32 (RGC32), q14.11
SNP_A-2271458	gacattttaaatgcca[C/T]ctgaaacatcacttgt	C	T	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 625684 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2254302	cttgcaatagcattaa[A/G]aaggttgaatcctcaa	A	G	9989 // Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA. /// NM_006868 // upstream //	PPP4R1	PPP4R1, Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), p11.22
SNP_A-2229707	ctagtcaggtgctgga[C/T]ctataggaggacaaga	C	T	60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 189488 // Hs.528665 // PROK2 //	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2235268	ctccctacaccaacca[C/T]ctgattccatacctgg	C	T	Homo sapiens signal peptide, CUB domain, EGF-like 2 (SCUBE2), mRNA. /// ENST00000309263 // intron // 0 // --- //	SCUBE2	SCUBE2, Homo sapiens signal peptide, CUB domain, EGF-like 2 (SCUBE2), p15.4
SNP_A-2292286	gcacctggaacttgtc[A/G]ctacggcatcctgtcg	A	G	/// ENST00000331540 // downstream // 725736 // --- // --- // ---	-	p25.3
SNP_A-2300066	gcctcactaggatcta[C/T]cattgggatcccaacc	C	T	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 //	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2271180	gacatctgtgcgctgc[A/G]gagctaagatttccta	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 121491 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2269933	gacaatgcgcaggaac[C/G]aagaactgttctggtg	C	G	Homo sapiens endothelial cell adhesion molecule (ESAM), mRNA. /// ENST00000278927 // intron // 0 // --- // --- // --- // ---	ESAM	ESAM, Homo sapiens endothelial cell adhesion molecule (ESAM), q24.2
SNP_A-2283350	gatacaggaaatccaa[A/C]cactgggcagtagttt	A	C	Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// ENST00000300105 // intron // 0 // --- // --- // --- // ---	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3
SNP_A-2276318	gagagcaaaggaacaa[C/T]ttgagaaaaactggag	C	T	// 10346 // Homo sapiens tripartite motif-containing 22 (TRIM22), mRNA. /// BC035582 // downstream // 21905 //	TRIM22	TRIM22, Homo sapiens tripartite motif-containing 22 (TRIM22), p15.4
SNP_A-2050033	aaggaatcaataaaaa[A/G]tgaatgggaagacatt	A	G	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 823995 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2087604	actgctcacaaaatca[C/T]acagcgtcccacatga	C	T	// 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 16445 // Hs.132344	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2093465	agaacttaaaatttaa[A/G]gcacaaacacacacag	A	G	Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// ENST00000161863 // intron // 0 // --- // --- // --- // --- ///	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-2047207	aagatagaggatagac[A/C]aagtgtatagattttg	A	C	26953 // Homo sapiens RAN binding protein 6 (RANBP6), mRNA. /// NM_033439 // upstream // 130731 // Hs.348390 //	RANBP6	RANBP6, Homo sapiens RAN binding protein 6 (RANBP6), p24.1
SNP_A-2020494	cccctcggtgttgaac[A/G]atctgggtaaccagct	A	G	Homo sapiens chromosome 21 open reading frame 29 (C21orf29), mRNA. /// ENST00000323084 // intron // 0 // --- //	C21orf29	C21orf29, Homo sapiens chromosome 21 open reading frame 29 (C21orf29), q22.3
SNP_A-2027672	aaaccatgagttaggc[A/G]ctagttttgctggtgt	A	G	Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // --- // --- // --- // --- ///	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-2109244	agcttgttgggtatca[A/G]taaacatgcagggcct	A	G	4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 790139 // Hs.166017 // MITF //	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-2109635	aggaaacttaaatgtg[A/G]caaaccaaacacatgc	A	G	// Homo sapiens RYK receptor-like tyrosine kinase (RYK), transcript variant 2, mRNA. /// ENST00000296084 //	RYK	RYK, Homo sapiens RYK receptor-like tyrosine kinase (RYK), transcript variant 2, q22.1
SNP_A-2114890	agggcagcagaagaca[A/G]cacgatggttcgaagg	A	G	10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 176362 //	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2121294	agtcttagccaaagcc[A/G]aatagcagctgaacag	A	G	Homo sapiens prostein protein (Prostein), mRNA. /// ENST00000289710 // intron // 0 // --- // --- // --- // ---	PCANAP6	PCANAP6, Homo sapiens prostein protein (Prostein), q32.1
SNP_A-2159334	atttaagtaaacaaag[C/G]cttctcatttagaaaa	C	G	ENST00000354422 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2210462	cccccgagtgggcacc[A/G]acgaaccgctcttccc	A	G	4255 // Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), mRNA. /// ENST00000248179 //	MGMT	MGMT, Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), q26.3
SNP_A-2210830	ccccttaatggactga[A/G]cactcacttcccatcc	A	G	23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// NM_207436 // upstream //	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-2172867	caattttcctcaaaga[C/T]ggtgggtgacatggaa	C	T	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 281004 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2197283	cattcagtaggtgaag[C/T]agctagtccagctgct	C	T	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// ENST00000319397 // intron // 0 // --- // --- // --- // --- /// ENST00000345075 // intron //	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2191242	catatacatcatatga[C/T]tcaaatttgtcacagc	C	T	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2186036	caggcagtcatgaaag[A/G]agaactgctgttagag	A	G	sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 //	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-1793377	ggtaggcggggaacac[G/T]cagcaagaacagctct	G	T	Homo sapiens hypothetical protein FLJ38993 (FLJ38993), mRNA. /// ENST00000272133 // intron // 0 // --- // --- // --- // ---	CNIH3	CNIH3, Homo sapiens hypothetical protein FLJ38993 (FLJ38993), q42.12
SNP_A-1712991	gctctgaataaggctaaccatcaaa[A/G]taccaaaaacactgaataaaacct a	A	G	NM_001260 // intron // 0 // Hs.397734 // CDK8 // 1024 // cyclin-dependent kinase 8	CDK8	CDK8 , rs9319288, cyclin-dependent kinase 8,q12.13
SNP_A-1758854	gattaggaaaatgaagttatcggaa[A/C]aaatggtctcttcagacaaacaatt	A	C	// 116 // adenylate cyclase activating polypeptide 1 (pituitary) /// NM_031416 // downstream // 325521 // Hs.326788 //	ADCYAP1	ADCYAP1 , rs10502292, adenylate cyclase activating polypeptide 1 (pituitary) ,p11.32
SNP_A-1642669	tattggccttggaaacttttctcgc[G/T]cagctcatcaatattgttagtgact	G	T	8577 // transmembrane protein with EGF-like and two follistatin-like domains 1 /// NM_017746 // upstream // 13180 // Hs.180236 // TEX10 // 54881 // testis expressed gene 10 ///	TMEFF1	TMEFF1 , rs1961367, transmembrane protein with EGF-like and two follistatin-like domains 1 ,q31.1
SNP_A-1689530	gcactcagcctcctttctgatatta[C/T]gtaaaaaccaggttcttttccaata	C	T	somatostatin /// NM_001706 // downstream // 47667 // Hs.155024 // BCL6 // 604 // B-cell CLL/lymphoma 6 (zinc	SST	SST , rs10513819, somatostatin ,q27.3
SNP_A-1870561	tcgagtccctaaaaaa[C/T]gttcttgtggtgagga	C	T	2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 123328 //	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-1827970	taagaagagagtgaaa[A/G]tatggaggaactggaa	A	G	// 54860 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), mRNA. /// NM_174939 // upstream // 21359 // Hs.372650 // MGC39681 // 283197 //	MS4A12	MS4A12, Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), q12.2
SNP_A-1832820	tacaatacccacttta[G/T]ctatttttgacaagaa	G	T	51022 // Homo sapiens glutaredoxin 2 (GLRX2), transcript variant 2, mRNA. /// NM_016066 // upstream // 8257 //	GLRX2	GLRX2, Homo sapiens glutaredoxin 2 (GLRX2), transcript variant 2, q31.2
SNP_A-1943890	ttgtatataccattta[A/C]gtttaatgtcatattt	A	C	Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB //	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-1959276	ttttgatccaacagta[C/T]cgtttcagctgtttta	C	T	Homo sapiens diacylglycerol kinase, delta 130kDa (DGKD), transcript variant 1, mRNA. /// NM_152879 // intron // 0 //	DGKD	DGKD, Homo sapiens diacylglycerol kinase, delta 130kDa (DGKD), transcript variant 1, q37.1
SNP_A-1957364	ttttagctcttcatta[C/T]agtgtctgtctttaat	C	T	8531 // Homo sapiens cold shock domain protein A (CSDA), mRNA. /// NM_023919 // downstream // 41102 // Hs.533754	CSDA	CSDA, Homo sapiens cold shock domain protein A (CSDA), p13.2
SNP_A-1987141	tcatgggttgtgcaag[A/G]ccctgtagttcacatt	A	G	9474 // Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA. /// U83115 // upstream // 108904 //	APG5L	APG5L, Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), q21
SNP_A-1981344	aagtagctagaactaa[C/T]gtactcctgaataaca	C	T	sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// ENST00000263405 // intron // 0 // --- // --- // --- // ---	FYB	FYB, Homo sapiens FYN binding protein (FYB-120 p13.1
SNP_A-1875624	tctcttatttgaacaa[G/T]gagttcatcacttgtc	G	T	BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. ///	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-1887402	tgagaattttggccca[A/G]gatggataaacctggg	A	G	27063 // Homo sapiens ankyrin repeat domain 1 (cardiac muscle) (ANKRD1), mRNA. /// ENST00000277871 //	ANKRD1	ANKRD1, Homo sapiens ankyrin repeat domain 1 (cardiac muscle) (ANKRD1), q23.31
SNP_A-1893893	tgcatagaacattgta[A/G]agtactggatgttagt	A	G	// 257415 // Homo sapiens hypothetical protein MGC40405 (MGC40405), mRNA. /// ENST00000314437 // upstream //	MGC40405	MGC40405, Homo sapiens hypothetical protein MGC40405 (MGC40405), q12.1
SNP_A-1913612	tgtgtacagtgcccac[A/G]gacctacagagacaga	A	G	Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 //	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-1911703	tgtgaagagttcatga[A/T]catttttaatccacca	A	T	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1912991	tgtggactaggaagac[A/G]gaataattcagtgtcc	A	G	Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // --- // --- // --- // --- ///	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-1925669	ttatgatcccataata[C/T]gatgtttgctgtctta	C	T	259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1927386	ttcaaagaacttacaa[A/G]ctttttgatatgagag	A	G	Homo sapiens CGI-77 protein (CGI-77), mRNA. /// ENST00000285420 // intron // 0 // --- // --- // --- // ---	CGI-77	CGI-77, Homo sapiens CGI-77 protein (CGI-77), q21.3
SNP_A-1900370	tggagaggctgcccca[C/T]ggaaaagaaagatatt	C	T	// Homo sapiens tryptophan/serine protease (UNQ9391), mRNA. /// ENST00000328655 // intron // 0 // --- // --- // --- // ---	UNQ9391	UNQ9391, Homo sapiens tryptophan p23.1
SNP_A-1898754	tgctttccagaccact[C/G]actgaagcaacccctta	C	G	/// ENST00000354793 // downstream // 1555544 // --- // --- // ---	-	p14.1
SNP_A-1882173	tctttttgtcactat[A/C]aagtcatcatgatgta	A	C	NM_181841 // upstream // 49686 // --- // --- // 0 // --- /// NM_032246 // downstream // 617945 // Hs.104744 // RKHD3	-	q25.2
SNP_A-1979346	aagcaaacagaatcca[A/G]tgaagaagacctttgc	A	G	// 1909 // Homo sapiens endothelin receptor type A (EDNRA), mRNA. /// NM_018241 // upstream // 55328 // Hs.203896 //	EDNRA	EDNRA, Homo sapiens endothelin receptor type A (EDNRA), q31.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1983482	tgggcgaatatacagg[G/T]aatagccttattccat	G	T	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-1968501	tcatgattttaacaac[A/C]agtacaactgtaccag	A	C	Homo sapiens cadherin-like 22 (CDH22), mRNA. /// ENST00000279063 // intron // 0 // --- // --- // --- // ---	CDH22	CDH22, Homo sapiens cadherin-like 22 (CDH22), q13.12
SNP_A-1957715	ttttatgtatagttca[C/T]gtctgggaggaaatgt	C	T	4808 // Homo sapiens nescient helix loop helix 2 (NHLH2), mRNA. /// NM_018420 // upstream // 49684 // Hs.125482 //	NHLH2	NHLH2, Homo sapiens nescient helix loop helix 2 (NHLH2), p13.1
SNP_A-1960421	tttttatcttattggc[C/T]catctcggttttggtt	C	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 581233 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1960919	tttttgattaagtggc[G/T]gcaaatcctttattga	G	T	sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// ENST00000332193 // intron // 0 // --- // --- // --- // ---	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds. ,q11.23
SNP_A-1945854	ttgtttaccccatatc[A/G]attcacccttccttcc	A	G	Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000319540 // intron // 0 // --- // --- // --- // --- ///	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-1937972	ttgaattaatgcttgg[C/T]atctttgactgaaaat	C	T	/// ENST00000358087 // upstream // 191137 // --- // --- // --- // --- /// ENST00000344409 // upstream // 190818 // --- // --- // ---	-	p11.21
SNP_A-1827945	ttgttatggtcactca[C/G]agcgtcttgtatgttt	C	G	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA. /// ENST00000262429 // intron // 0 // --- // --- // --- // ---	KIAA0703	KIAA0703, Homo sapiens KIAA0703 gene product (KIAA0703), q24.1
SNP_A-1864004	tccacaatgatttata[C/T]ataggatgctgattgg	C	T	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST00000359144 // downstream //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.32
SNP_A-1848539	tatgacactggtttgt[A/G]aattataaagctctat	A	G	ENST00000339727 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1855062	tcaagaatatcaatgg[C/G]catacattagagacac	C	G	NR4A2 // 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 1029563 // Hs.165258 //	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1799981	gtacataaatccatca[C/T]cccattcagactctcc	C	T	64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 136947 // Hs.7482 // RBM19 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-2178821	cactgagaagctgtga[A/G]tatttggaaattgact	A	G	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 374438 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2178872	cactgatacatttcta[A/G]ggacctactgagacat	A	G	// 9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// NM_173827 // downstream // 288758 // Hs.356697 // FLJ38991 //	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-2182440	cagataatctccaaga[C/G]cccctctctgatgttc	C	G	/// ENST00000356718 // upstream // 100943 // --- // --- // --- // ---	-	q24.21
SNP_A-2199967	ccaaagcagttattca[A/G]ctcagcataccaaact	A	G	// 2569 // Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 1 (GABRR1), mRNA. /// ENST00000275072 //	GABRR1	GABRR1, Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 1 (GABRR1), q15
SNP_A-2205576	ccagttctctgtaagg[C/G]caggttcttctttact	C	G	Homo sapiens defensin, alpha 6, Paneth cell-specific (DEFA6), mRNA. /// NM_001925 // downstream // 7125 //	DEFA6	DEFA6, Homo sapiens defensin, alpha 6, Paneth cell-specific (DEFA6), p23.1
SNP_A-2167939	caacgcagtctttgcc[A/G]gcttctctacaaaggg	A	G	Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 //	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2045278	aagaagggaatgagaa[A/G]gttgcacacaggtaat	A	G	// Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 254051 // Hs.1428 // FSHR // 2492 // Homo	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-2043478	aactgtacaccttaaa[A/G]tgatcacaataatacc	A	G	-- /// ENST00000344692 // upstream // 28915 // --- // --- // --- ///	-	q22.1
SNP_A-1995876	agaggattgcttgcag[A/G]aatcagataacaaagc	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2051023 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2082109	acgaagattttgagta[G/T]agcagggtttctctct	G	T	23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 58963 // Hs.160574	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-2072545	acagccacaaaacata[C/T]ccgtaaaagaacacaa	C	T	ENST00000220192 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2287384	gatgtgttagctaaat[A/G]aacacctccatgaaat	A	G	Homo sapiens forkhead box N4 (FOXN4), mRNA. /// ENST00000355216 // intron // 0 // --- // --- // --- // ---	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2244643	ctggaggagccaacca[A/G]tcacaggcaacgtgca	A	G	1977 // Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /// ENST00000309260 // downstream //	EIF4E	EIF4E, Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), q23
SNP_A-2292715	gcacttagagaaagca[C/T]tcaacttccagaacct	C	T	140947 // Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// NM_006161 // downstream // 2328 //	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1
SNP_A-2308824	gctttggagtgagaaa[C/T]gggctaagtgacaaaa	C	T	2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 471346 // Hs.444225 // ESRRG // 2104 // Homo	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2304826	gctcttacaagcagaa[C/T]gtcagactaatgatga	C	T	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 175587 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2309739	ggaaaggcatattgaa[A/G]agagaagttgccccgt	A	G	Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST00000335681 // intron // 0 // --- // --- // --- // ---	NPAS2	NPAS2, Homo sapiens neuronal PAS domain protein 2 (NPAS2), q11.2
SNP_A-2298565	gcccacatgcagcatc[A/G]caaacatgagagctgc	A	G	Homo sapiens fibulin 1 (FBLN1), transcript variant A, mRNA. /// NM_006486 // intron // 0 // Hs.24601 // FBLN1 // 2192 //	FBLN1	FBLN1, Homo sapiens fibulin 1 (FBLN1), transcript variant A, q13.31
SNP_A-2254845	cttggagcttggatga[A/G]gagtatgtggagtgaa	A	G	1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 279153 // Hs.143434	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2237691	ctctctgcctgactaa[C/T]ggctgcttagcacttt	C	T	5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 //	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-2240533	ctgaccaggagctgcc[A/G]ggacacaaagctttga	A	G	Homo sapiens hypothetical protein FLJ31300 (FLJ31300), mRNA. /// ENST00000290868 // intron // 0 // --- // --- // --- // ---	UROC1	UROC1, Homo sapiens hypothetical protein FLJ31300 (FLJ31300), q21.2
SNP_A-2231449	ctattgtccaagacca[C/T]gtatttcaaaagaaaa	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2865863 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2233387	ctcaggttacaagtac[A/G]caaacaagaggccggg	A	G	Homo sapiens zinc finger protein 564 (ZNF564), mRNA. /// ENST00000339282 // intron // 0 // --- // --- // --- // ---	ZNF564	ZNF564, Homo sapiens zinc finger protein 564 (ZNF564), p13.2
SNP_A-2285381	gatctgtatggccaca[C/G]aaccaaaagtagaaat	C	G	/// ENST00000331332 // downstream // 280120 // --- // --- // ---	-	p11.1
SNP_A-2278070	gagcccaggcaagtca[A/G]taaggaagactttgat	A	G	3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 39409 //	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2049290	aagctcatggccaaaa[C/T]tgtgatccatctctag	C	T	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // --- ///	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-2078984	acccaccctctaagca[A/G]aaacgttgcctggaat	A	G	ENST00000341842 // intron // 0 // --- // --- // --- // ---	-	q42.13
SNP_A-2103725	agcacatctatttcca[C/T]ggaatgtgcatctgat	C	T	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1255878 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1997474	ctgcttcagcaggtca[A/G]aactgtttttggtca	A	G	SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 106480 // --- //	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2006544	gccagccacttggata[C/T]gctaggtcttggtttc	C	T	C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 //	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-2032753	aaataactgaatacca[C/T]caccaatcaacaatgt	C	T	SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 104377 // --- //	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2032501	aaataaaaatcttacc[C/T]agtctaattcagtgct	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2031258	aaaggctgttctgaga[C/G]acactaatgaactaag	C	G	GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// NM_017433 // upstream //	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-2025617	aaaatgaatcaatcag[C/T]agtgaacaaatttatg	C	T	Homo sapiens high-mobility group box 1 (HMGB1), mRNA. /// ENST00000341423 // intron // 0 // --- // --- // --- // ---	HMGB1	HMGB1, Homo sapiens high-mobility group box 1 (HMGB1), q12.3
SNP_A-2162184	attttaccagagagta[A/C]agcaagccactaaata	A	C	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc q31.1
SNP_A-2156786	attctgtttcacatca[A/C]ctaattttattttgtt	A	C	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1973056 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2110669	aggaccaacagtgtga[A/C]ctctatgaccaactta	A	C	ENST00000333254 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2108594	agctgggataagttga[C/T]gtggaacaggggttgg	C	T	9355 // Homo sapiens LIM homeobox 2 (LHX2), mRNA. /// NM_014397 // upstream // 163487 // Hs.197071 // NEK6 //	LHX2	LHX2, Homo sapiens LIM homeobox 2 (LHX2), q33.3
SNP_A-2206859	ccatggaaattaataa[A/G]cctgaagagtgcaaag	A	G	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2841810 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2199955	ccaaagcaatcctgat[A/T]aaaaaaaacaacaaag	A	T	FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2208105	cccaaggtgtttaaca[C/T]ggagcaggagtgacaa	C	T	203062 // Homo sapiens hypothetical protein FLJ31164 (FLJ31164), mRNA. /// NM_001702 // upstream // 56136 //	FLJ31164	FLJ31164, Homo sapiens hypothetical protein FLJ31164 (FLJ31164), q24.3
SNP_A-2221084	ccttgtcataagtcca[A/G]atctttaaattgacat	A	G	ENST00000340052 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-2194238	catgaggacagtacca[C/T]gagggaaatctgcccc	C	T	51633 // Homo sapiens CGI-77 protein (CGI-77), mRNA. /// ENST00000285420 // downstream // 10605 // --- // --- // --- // --	CGI-77	CGI-77, Homo sapiens CGI-77 protein (CGI-77), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1810646	gtgcaatgtgacagaa[C/T]gtgccctttcttatgc	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2309679 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1689096	tcaacttaaattccagagaaaacac[A/G]aacattcaaaccataccaaggggt a	A	G	6619 // small nuclear RNA activating complex, polypeptide 3, 50kDa /// NM_021144 // downstream // 644028 // Hs.351305	SNAPC3	SNAPC3 , rs2818939, small nuclear RNA activating complex, polypeptide 3, 50kDa ,p22.3
SNP_A-1689266	tctttgaaccaatattgtcatcagt[C/T]acttggaggacaaattgagcccatc	C	T	carboxypeptidase E	CPE	CPE , rs1370687, carboxypeptidase E,q32.3
SNP_A-1646422	ggatgtgacctggggttgctgactg[A/C]atgttgagttgttctgatttgtagt	A	C	CDNA FLJ37718 fis, clone BRHIP2019007 /// AY070137 // upstream // 18746 // Hs.154295 // SP3 // 6670 // Sp3	-	- , rs10497423, CDNA FLJ37718 fis, clone BRHIP2019007 ,q31.1
SNP_A-1755936	tatacgtatgatatgtgcacttttc[A/C]ataagcaggctactcttccgcaggc	A	C	8128 // sialyltransferase 8B (alpha-2, 8-sialyltransferase) /// NM_013272 // downstream // 29536 // Hs.113657 //	SIAT8B	SIAT8B , rs10520706, sialyltransferase 8B (alpha-2, 8-sialyltransferase) ,q26.1
SNP_A-1784313	ggcccatgaacagcag[G/T]acctagcctcccttct	G	T	9355 // Homo sapiens LIM homeobox 2 (LHX2), mRNA. /// NM_014397 // upstream // 157408 // Hs.197071 // NEK6 //	LHX2	LHX2, Homo sapiens LIM homeobox 2 (LHX2), q33.3
SNP_A-1859019	tcagcattaggtgtga[C/T]gtgttcagcaagaatc	C	T	2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// NM_144586 // downstream // 242681 //	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-1845173	tatacattttggactc[A/G]cattcttaccaggggt	A	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1865522	tccatgcaaccttgca[A/G]tacaagacttttgtgc	A	G	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- // --- // --- ///	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1819583	gttgtaaagaggaata[C/T]gcgagttaaatatttg	C	T	Homo sapiens myosin VI (MYO6), mRNA. /// ENST00000357181 // intron // 0 // --- // --- // --- // --- ///	MYO6	MYO6, Homo sapiens myosin VI (MYO6), q14.1
SNP_A-1837573	tacttggtgaaataga[C/T]gtgcagggagcttctt	C	T	// 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 344145 // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1938283	ttgaccttgacctcac[A/G]catgggcaataaatga	A	G	// 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 522559 // Hs.111 //	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1955530	tttggtgccaacagaa[A/C]gtgtaaatacatgctg	A	C	Homo sapiens crystallin, gamma A (CRYGA), mRNA. /// ENST00000304502 // intron // 0 // --- // --- // --- // ---	CRYGA	CRYGA, Homo sapiens crystallin, gamma A (CRYGA), q33.3
SNP_A-1968813	aatgatgatgaaacca[A/T]gtcctgtagtagcgcc	A	T	56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 222591 // Hs.517155 // TMEPAI //	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1966601	attggggccagtgtga[A/G]aaaatgtaacctagta	A	G	2825 // Homo sapiens G protein-coupled receptor 1 (GPR1), mRNA. /// NM_005279 // upstream // 87096 // Hs.184907 //	GPR1	GPR1, Homo sapiens G protein-coupled receptor 1 (GPR1), q33.3
SNP_A-1971530	agttgtgaaccaactc[A/G]atgtatttgacacgtg	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 621048 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1980005	aacacagagtaagaga[A/G]aggcaggaagatcaca	A	G	Homo sapiens WD repeat domain 17 (WDR17), transcript variant 1, mRNA. /// NM_181265 // intron // 0 // Hs.532056 //	WDR17	WDR17, Homo sapiens WD repeat domain 17 (WDR17), transcript variant 1, q34.2
SNP_A-1884348	tgaaggttacaaagca[C/G]tgaatcttttcctttc	C	G	55 // Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /// NM_015268 // upstream // 58849 // --- // --- // 0 // ---	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-1894673	tgccagagatggtcag[G/T]aacaacagctatcata	G	T	56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 280083 // Hs.517155 // TMEPAI //	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1964722	gtctacgtatgcacac[A/G]ggtgcttttcttagca	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1279347 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1957802	ttttattgcaactttg[C/T]atcttggagcattttc	C	T	/// ENST00000332660 // downstream // 724365 // --- // --- // ---	-	p12.3
SNP_A-1960036	ttttgttctgttcttg[A/C]ataaaaatcaatgaca	A	C	DKFZP564B1023 // 83479 // Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA. /// NM_203459 // upstream // 13539 // Hs.23585 // KIAA1078 //	DKFZP564B1023	DKFZP564B1023, Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), q32.1
SNP_A-1951424	tttcctaggcttctcc[A/G]caggagttgaggaatg	A	G	UGT2B28 // 54490 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), mRNA. /// NM_021139 // downstream // 47467 // Hs.285887 // UGT2B4 // 7363 //	UGT2B28	UGT2B28, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), q13.2
SNP_A-1937398	ttgaaatctaactaga[A/C]aaattccattatgttt	A	C	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1940460	ttgcccaaatcatatg[C/T]agaaacgcaaagattt	C	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 583812 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1821779	gttttaattatttgga[C/G]agaagtatattgaata	C	G	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 111613 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1823687	taaaatatcaggagaa[A/T]gcaataaatttctttt	A	T	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-1850589	tattaataaatggcaa[C/T]gtttattgtcctgtgg	C	T	ENST00000359190 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-1783829	ggccaactctatgtca[C/T]gcctactggttgctct	C	T	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 168622 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-1781263	ggatgtactttaaaaa[A/T]tttgcagttgtaaatt	A	T	Homo sapiens EGF-like-domain, multiple 11 (EGFL11), mRNA. /// ENST00000342421 // intron // 0 // --- // --- // --- // ---	EGFL11	EGFL11, Homo sapiens EGF-like-domain, multiple 11 (EGFL11), q12
SNP_A-1780568	ggatatgaaagaagag[C/T]atttgcattttactta	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1716428 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1651998	aattattcacaggcttattcttata[A/G]acattacattcttatcaatagccca	A	G	4208 // MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) /// NM_004365 // downstream // 908013 // Hs.528302 // CETN3 // 1070 //	MEF2C	MEF2C , rs1852730, MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) ,q14.3
SNP_A-1685130	ccccaagttagactagtgacttttta[A/C]aatagaaagcaacgactgtttcgtt	A	C	// 259282 // hypothetical protein FLJ33215 /// NM_182485 // upstream // 1250511 // Hs.44833 // CPEB2 // 132864 //	FLJ33215	FLJ33215 , rs2270279, hypothetical protein FLJ33215 ,p15.33
SNP_A-1675784	cacccactttctaatgtaaatgtca[A/G]aaatactatcacatcctttcaattt	A	G	NM_018211 // intron // 0 // - // - // - // -	-	- , rs10493372, -,p31.3
SNP_A-1787394	gggaagggaaatgaag[C/G]ctagaggatgtgtagc	C	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 44526 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1786565	ggcttcctccattacc[A/G]ataccaattcgcttga	A	G	// Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 254849 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-2187795	cagtaggcctagtata[A/G]gtataagtacatgata	A	G	1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // upstream // 90621 // Hs.282871 // CYP2C8	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-2214341	cctaccattctgagga[A/T]attacacaggaaataa	A	T	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2167765	caaccctgtgaggtaa[C/G]tgtattatctccattt	C	G	Homo sapiens hypothetical protein MGC4093 (MGC4093), mRNA. /// ENST00000356385 // intron // 0 // --- // --- // --- // ---	MGC4093	MGC4093, Homo sapiens hypothetical protein MGC4093 (MGC4093), q13.2
SNP_A-2013085	cagttcagaaccctca[C/T]taggcaagaaccctgt	C	T	9228 // Homo sapiens discs, large (Drosophila) homolog-associated protein 2 (DLGAP2), mRNA. /// NM_018941 // upstream // 266067 // Hs.127675 // CLN8 // 2055 // Homo	DLGAP2	DLGAP2, Homo sapiens discs, large (Drosophila) homolog-associated protein 2 (DLGAP2), p23.3
SNP_A-2094230	agaaggtctagaacac[A/G]gctttctgataccaca	A	G	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 930138 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2099178	agaggaggagcaggaa[C/T]agcaagcttgtgcgga	C	T	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), transcript variant 10, mRNA. /// NM_198384 // intron // 0 // Hs.194746 // CACNA1G // 8913 //	CACNA1G	CACNA1G, Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), transcript variant 10, q21.33
SNP_A-2063508	catcctgacctgaagt[A/G]aactttgggtacacag	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 457850 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2250762	cttatcacattctacc[G/T]aatccggaatttctca	G	T	399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 287258 // Hs.299419 //	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds. q25
SNP_A-2243127	ctgcctaaaagactta[C/T]agtacaggtatgatgg	C	T	// Homo sapiens chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA. /// ENST00000307209 // intron // 0 // --- // --- // --- //	GALNACT-2	GALNACT-2, Homo sapiens chondroitin sulfate GalNAcT-2 (GALNACT-2), q11.21
SNP_A-2290345	gcaacagtggactaca[C/T]gacaccaccttccaca	C	T	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2313896	ggagcctgaatgtttc[C/T]cttgtgactagatttt	C	T	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-2307847	gcttctaggctgagaa[G/T]tcaggcacacaggggg	G	T	1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 21906 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste ,p15.1
SNP_A-2234402	ctccaagtatattttc[A/G]ctgatcctggcaatgc	A	G	Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2239002	ctcttcgagtagaccc[A/G]ctgtgctatccaatac	A	G	// Homo sapiens promethin (LOC57146), mRNA. /// ENST00000261388 // intron // 0 // --- // --- // --- // ---	LOC57146	LOC57146, Homo sapiens promethin (LOC57146), p12.3
SNP_A-2265301	gaagcacgaggaccac[A/G]atcatccatagaaaaa	A	G	Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA. /// ENST00000311678 // intron // 0 // --- // ---	C9orf3	C9orf3, Homo sapiens chromosome 9 open reading frame 3 (C9orf3), q22.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2265392	gaagcatccttctaag[A/C]cactctggttcttcct	A	C	55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 149818	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-2076285	acattgaagtacactg[G/T]aaagcctctataatta	G	T	MGC39681 // 283197 // Homo sapiens hypothetical protein MGC39681 (MGC39681), mRNA. /// NM_031457 // upstream	MGC39681	MGC39681, Homo sapiens hypothetical protein MGC39681 (MGC39681), q12.2
SNP_A-2074830	acatcaactctaggtc[A/G]caagtgatgcatttttt	A	G	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2050266	aaggagagacccaaac[C/T]gcaacgtttctggtgt	C	T	5740 // Homo sapiens prostaglandin I2 (prostacyclin) synthase (PTGIS), mRNA. /// NM_004776 // downstream //	PTGIS	PTGIS, Homo sapiens prostaglandin I2 (prostacyclin) synthase (PTGIS), q13.13
SNP_A-2097884	agagagaaaggcagag[A/C]aatgactgcaattccc	A	C	25903 // Homo sapiens olfactomedin-like 2B (OLFML2B), mRNA. /// ENST00000294794 // upstream // 6660 // --- // --- //	OLFML2B	OLFML2B, Homo sapiens olfactomedin-like 2B (OLFML2B), q23.3
SNP_A-2105860	agccagtttccgtgaa[A/G]aagcattagtatcacc	A	G	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 144324 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2016603	atttttgaaatagaac[A/G]actaaagcaattgctt	A	G	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 253942 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2006113	cctgagtcccgctcca[C/T]aactcctgatttagaa	C	T	Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-1991158	ttgcttgtggccaaaa[C/T]aatataataatcacat	C	T	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 616454 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-2029275	aaagaagtgagctata[G/T]aattaggaatgtattg	G	T	3762 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), mRNA. /// NM_145013 // upstream // 23062 // Hs.351133 // MGC35558 // 219833 //	KCNJ5	KCNJ5, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), q24.3
SNP_A-2045989	aagacctgtactataa[C/G]aagaagcagcttgtta	C	G	136259 // Homo sapiens Kruppel-like factor 14 (KLF14), mRNA. /// ENST00000310992 // upstream // 241968 // --- // ---	KLF14	KLF14, Homo sapiens Kruppel-like factor 14 (KLF14), q32.3
SNP_A-2153441	attagataagctctaa[A/G]atccttccagctgcaa	A	G	Homo sapiens chromosome 20 open reading frame 31 (C20orf31), mRNA. /// ENST00000262875 // intron // 0 // --- //	C20orf31	C20orf31, Homo sapiens chromosome 20 open reading frame 31 (C20orf31), q11.22
SNP_A-2148308	atgggctccataagta[C/T]catccttttgttggt	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2110430	aggaatttaggtgaga[C/T]catccaaatttagaga	C	T	27332 // Homo sapiens zinc finger protein 638 (ZNF638), mRNA. /// ENST00000244221 // upstream // 35234 // --- // ---	ZNF638	ZNF638, Homo sapiens zinc finger protein 638 (ZNF638), p13.2
SNP_A-2202950	ccactcgctaaacttg[A/C]agatgcaacaggagtc	A	C	Homo sapiens hypothetical protein FLJ38993 (FLJ38993), mRNA. /// ENST00000272133 // intron // 0 // --- // --- // --- // ---	CNIH3	CNIH3, Homo sapiens hypothetical protein FLJ38993 (FLJ38993), q42.12
SNP_A-2202557	ccacctagaataatga[C/T]gttctggtgttaaaag	C	T	// 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 30985 // Hs.42650 //	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2205483	ccagtgtacacaatca[C/T]cattttccaatttaac	C	T	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 100071 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2187358	caggttaagatgaaga[A/C]aactcaggggcccta	A	C	Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // --- // --- // --- // --- ///	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-2192758	catccctgtatatgga[A/G]cttttgaactcaaaat	A	G	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 235185 // Hs.17441	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-2198147	cattggtttgaaaaaa[A/C]tctctgtaatctagaa	A	C	64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 125128 // Hs.146339 //	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-1809162	gtgaccaaagaaccca[A/C]ctagagattaagatac	A	C	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1697503	gtacatttttctttaaccatactta[C/T]gttttcagttttctcaaattatctt	C	T	NM_018629 // upstream // 608570 // - // - // - // -	-	-, rs345013, -,q24
SNP_A-1697615	aaaaggatttttgagcctaatgtgt[C/G]aacttcagatattcacatgattgtg	C	G	// CD53 antigen /// NM_002232 // upstream // 170557 // Hs.169948 // KCNA3 // 3738 // potassium voltage-gated	CD53	CD53 , rs10494121, CD53 antigen ,p13.3
SNP_A-1706883	aaggagcctgagaaggacagctagt[G/T]aagtaggaagagaatgaagagcatg	G	T	AB002376 // intron // 0 // Hs.476384 // CAST // 26059 // CAZ-associated structural protein	CAST	CAST , rs1376983, CAZ-associated structural protein,p14.3
SNP_A-1854937	tcaactctgcagcaaa[C/T]acttcaatgctactgt	C	T	Homo sapiens dCMP deaminase (DCTD), mRNA. /// ENST00000312820 // 3UTR // 0 // --- // --- // --- // --- ///	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1828361	taagatggttgggtta[C/G]ctttattcctgaagtc	C	G	7702 // Homo sapiens zinc finger protein 143 (clone pHZ-1) (ZNF143), mRNA. /// ENST00000299596 // upstream //	ZNF143	ZNF143, Homo sapiens zinc finger protein 143 (clone pHZ-1) (ZNF143), p15.4

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939725	ttgcaaagaaaacagt[C/G]aaaactcggcttaagt	C	G	Homo sapiens RAB GTPase activating protein 1 (RABGAP1), mRNA. /// ENST00000317419 // intron // 0 // ---	RABGAP1	RABGAP1, Homo sapiens RAB GTPase activating protein 1 (RABGAP1), q33.2
SNP_A-1964811	aattaagtgcccctta[C/T]gcgtttagtccaaagt	C	T	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1663814 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1967633	tctagggaataaggca[G/T]agaagatatgattgct	G	T	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-1898959	tggaaaaaaggaagaa[A/G]cagaaggaatatttga	A	G	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 865780 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1887336	tgagaatacagctcta[C/T]ggattttgtcaagtgt	C	T	Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // intron // 0 // Hs.113253 // PAX7 //	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-1877411	tctggagggcataaaa[C/T]ccaacccataatgggc	C	T	Homo sapiens tyrosine hydroxylase (TH), transcript variant 3, mRNA. /// NM_199292 // upstream // 90434 // Hs.435609 //	TH	TH, Homo sapiens tyrosine hydroxylase (TH), transcript variant 3, p15.5
SNP_A-1874263	tctccactatttacaa[A/C]taaactcggggctcct	A	C	// 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// ENST00000355855 // upstream // 88907 // --- // --- // --- // ---	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-1931178	ttccatgttggatacc[A/G]atgtaatgtctttctc	A	G	Homo sapiens establishment factor-like protein (EFO1), mRNA. /// ENST00000269214 // intron // 0 // --- // --- // --- // ---	ESCO1	ESCO1, Homo sapiens establishment factor-like protein (EFO1), q11.2
SNP_A-1890934	tgatggaattatttac[A/G]ccttaaaaacaggcaa	A	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1238531	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1967842	ctaagagaaatcttta[C/T]catactatttgttttg	C	T	Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// ENST00000337743 // intron // 0 // --- //	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-1982462	atataaatgcaataga[C/T]aagctatcctaaatct	C	T	255928 // Homo sapiens synaptotagmin XIV (SYT14), mRNA. /// NM_019605 // upstream // 21181 // Hs.445835 //	SYT14	SYT14, Homo sapiens synaptotagmin XIV (SYT14), q32.2
SNP_A-1944477	ttgtctggccttttcc[G/T]ccttaagcttaaattc	G	T	MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 31428 // Hs.194766 //	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1955175	tttggcattcattttc[G/T]cttagtctgttcaggc	G	T	-- /// ENST00000359634 // upstream // 299873 // --- // --- // --- // --- /// ENST00000359181 // upstream // 299873 // --- // --- // -	-	q32.3
SNP_A-1835007	tacccaggtgggagca[A/G]ctgattcaccaagaaa	A	G	ENST00000288168 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-1857008	tcaccattttgctata[G/T]ctcagacaactctctc	G	T	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1845338	tatactgctacttctc[A/G]acttttcaggtttgag	A	G	// 144501 // Homo sapiens hypothetical protein LOC144501 (LOC144501), mRNA. /// NM_005556 // upstream // 8128 //	LOC144501	LOC144501, Homo sapiens hypothetical protein LOC144501 (LOC144501), q13.13
SNP_A-1864842	tccaggagtgagtcta[C/T]gaaaaattttgaaaga	C	T	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // --- // --- // --- // ---	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1652712	aaaggcaacagaatcttgggactta[C/T]aggaggcagcaagaacacttggaaa	C	T	NM_004455 // intron // 0 // Hs.150956 // EXTL1 // 2134 // exostoses (multiple)-like 1	EXTL1	EXTL1 , rs1938404, exostoses (multiple)-like 1,p36.11
SNP_A-1732752	gtaactatctaagtccaacagggaa[A/C]aactctgaaggactgttctagttcc	A	C	2045 // EphA7 /// NM_024641 // upstream // 1102242 // Hs.46903 // MANEA // 79694 // mannosidase, endo-alpha	EPHA7	EPHA7 , rs725751, EphA7 ,q16.1
SNP_A-1807483	gtctgccacggctttg[C/T]agggccgagctcagcc	C	T	Homo sapiens mucoepidermoid carcinoma translocated 1 (MECT1), mRNA. /// NM_015321 // intron // 0 // Hs.371096 //	MECT1	MECT1, Homo sapiens mucoepidermoid carcinoma translocated 1 (MECT1), p13.11
SNP_A-1803810	gtcaagagagaataga[G/T]ccagtaaaaggagact	G	T	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 66263 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1786768	ggctttcaacaaaaga[G/T]aggtataacaaaaagc	G	T	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 159047 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-1798993	gtaagatttcttgcta[A/G]gatttaaagctaagtc	A	G	51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 579925 // Hs.89404 // MSX2 //	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-2174048	cacaccagtaataaga[C/T]acgtggctctgtttaa	C	T	sapiens astrotactin (ASTN), transcript variant 1, mRNA. /// ENST00000281881 // intron // 0 // --- // --- // --- // ---	ASTN	ASTN, Homo sapiens astrotactin (ASTN), transcript variant 1, q25.2
SNP_A-2202120	ccacatacatacacaa[A/C]aaaatattttcatctc	A	C	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2222917	cgcacctggccagcaa[C/T]ttctttaccaacacaa	C	T	// Homo sapiens neuropeptide Y (NPY), mRNA. /// NM_016447 // upstream // 255106 // Hs.533355 // MPP6 //	NPY	NPY, Homo sapiens neuropeptide Y (NPY), p15.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2126713	ataaacccttctttta[C/T]ggatgagaagcagagg	C	T	// 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2531380 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2146279	atgctactagtgccaa[A/T]acatgctgtttaaaat	A	T	// 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 2086606 // Hs.307086 // C14orf155 // 84075	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2142364	atgaaagcaaagctca[C/T]gagactctgccagaag	C	T	8674 // Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, mRNA. /// NM_201994 // upstream // 12277 // Hs.6651 // VAMP4 // 8674 // Homo	VAMP4	VAMP4, Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, q24.3
SNP_A-2159142	atttaaaaattatgtg[A/T]agcccctagaggattt	A	T	2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// NM_000408 //	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-2163817	caaaacacattgtatc[C/T]atgccatcacagaaga	C	T	Homo sapiens cDNA FLJ30640 fis, clone CTONG2002816, highly similar to Homo sapiens cadherin-like protein VR20 mRNA. /// NM_177980 // intron // 0 // Hs.54973 // CDH26 //	CDH26	CDH26, Homo sapiens cDNA FLJ30640 fis, clone CTONG2002816, highly similar to Homo sapiens cadherin-like protein VR20 ,q13.33
SNP_A-2044945	aagaacatatggacca[A/T]catatcaattctcttg	A	T	Homo sapiens cytochrome c oxidase subunit VIIb2 (COX7B2), mRNA. /// ENST00000302930 // intron // 0 // --- // ---	COX7B2	COX7B2, Homo sapiens cytochrome c oxidase subunit VIIb2 (COX7B2), p12
SNP_A-2039873	aacattcttgtgtagg[C/T]ccagaaaacggattta	C	T	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 355398 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2020290	gctttacagaaaacag[C/T]cctgggtacctgattc	C	T	1409 // Homo sapiens crystallin, alpha A (CRYAA), mRNA. /// NM_173354 // downstream // 178656 // Hs.282113 //	CRYAA	CRYAA, Homo sapiens crystallin, alpha A (CRYAA), q22.3
SNP_A-1997174	atgcagaggagggtga[C/T]aatgtaaggatcaaaa	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2001416	agaaacaggttgaaat[C/G]agtatctacttttttaa	C	G	7019 // Homo sapiens transcription factor A, mitochondrial (TFAM), mRNA. /// NM_012251 // downstream // 353504 //	TFAM	TFAM, Homo sapiens transcription factor A, mitochondrial (TFAM), q21.1
SNP_A-2007847	ggacttcctctagcac[A/T]gtactcattggaggag	A	T	1908 // Homo sapiens endothelin 3 (EDN3), transcript variant 1, mRNA. /// NM_207034 // downstream // 69033 // Hs.1408	EDN3	EDN3, Homo sapiens endothelin 3 (EDN3), transcript variant 1, q13.32
SNP_A-2094166	agaaggctgcaaatat[C/G]agaagctttttttgatt	C	G	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 646152 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2080004	accgaaataatttgaa[C/T]ctaattgcaatggttt	C	T	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // intron // 0 // Hs.478673 // IL1RAP // 3556 // Homo sapiens	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-2080691	acctcatgaggatgga[C/T]gagcttctcaggaagg	C	T	// 10018 // Homo sapiens BCL2-like 11 (apoptosis facilitator) (BCL2L11), transcript variant 9, mRNA. /// NM_138625 // downstream // 57429 // Hs.469658 // BCL2L11 // 10018 //	BCL2L11	BCL2L11, Homo sapiens BCL2-like 11 (apoptosis facilitator) (BCL2L11), transcript variant 9, q13
SNP_A-2089830	acttctaaaagaaagc[C/T]gcaccaccgcggtctg	C	T	388335 // Homo sapiens similar to RIKEN cDNA A730055C05 gene (LOC388335), mRNA. ///	LOC388335	LOC388335, Homo sapiens similar to RIKEN cDNA A730055C05 gene (LOC388335), p13.1
SNP_A-2051670	aaggtaggtaagctaa[C/T]tgaaagactccaatca	C	T	sapiens pellino homolog 1 (Drosophila) (PELI1), mRNA. /// ENST00000358912 // intron // 0 // --- // --- // --- // ---	PELI1	PELI1, Homo sapiens pellino homolog 1 (Drosophila) (PELI1), p14
SNP_A-2072466	acagcagtctccacca[A/C]agaaataataaccctt	A	C	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 419848 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2266352	gaaggtctgtgaagaa[A/G]tgattgcacaattgtg	A	G	6288 // Homo sapiens serum amyloid A1 (SAA1), transcript variant 1, mRNA. /// NM_199161 // downstream // 8080 //	SAA1	SAA1, Homo sapiens serum amyloid A1 (SAA1), transcript variant 1, p15.1
SNP_A-2264170	gaactggagccaggta[A/G]cagaattcatcatctt	A	G	sapiens olfactory receptor, family 6, subfamily N, member 1 (OR6N1), mRNA. /// ENST00000335094 // CDS // 0 // --- // ---	OR6N1	OR6N1, Homo sapiens olfactory receptor, family 6, subfamily N, member 1 (OR6N1), q23.1
SNP_A-2278013	gagccataaaacattg[C/T]aaaagccataggcttc	C	T	sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase) (DBH), mRNA. /// ENST00000344942 // intron // 0 // --- // --- // --- // --- /// ENST00000263611 // intron //	DBH	DBH, Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase) (DBH), q34.2
SNP_A-2275451	gagaattactaagaaa[A/G]gagtgatggccaaaga	A	G	// 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 387846 // Hs.369438 // ETS1 //	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.2
SNP_A-2231644	ctatttttcaacatcta[A/G]aaatcaattccataat	A	G	COL11A2 // 1302 // Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA. ///	COL11A2	COL11A2, Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, p21.32
SNP_A-2243030	ctgccccatctggctc[C/T]gaaagtggctcccagg	C	T	60678 // Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// NM_153330 // downstream //	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-2251616	cttcagctaacacaaa[A/G]gcttgtggcataacta	A	G	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1655960 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2288901	gatttagaagttgata[C/T]gtactgatcagtagaa	C	T	Homo sapiens pantothenate kinase 2 (Hallervorden-Spatz syndrome) (PANK2), transcript variant 4, mRNA. /// NM_153637 // intron // 0 // Hs.516859 // PANK2 // 80025 //	PANK2	PANK2, Homo sapiens pantothenate kinase 2 (Hallervorden-Spatz syndrome) (PANK2), transcript variant 4, p13
SNP_A-2305718	gctgcccatgtacaaa[A/G]tgaactcatacagata	A	G	Homo sapiens chloride channel, calcium activated, family member 1 (CLCA1), mRNA. /// ENST00000234701 // CDS // 0 // --- // --- // --- // --- /// ENST00000353619 // CDS // 0 // --- //	CLCA1	CLCA1, Homo sapiens chloride channel, calcium activated, family member 1 (CLCA1), p22.3
SNP_A-2314452	ggagggcttgttacag[C/G]agagatgacaggccca	C	G	// Homo sapiens hypothetical protein FLJ31875 (FLJ31875), mRNA. /// ENST00000306502 // intron // 0 // --- // --- // --- // ---	FLJ31875	FLJ31875, Homo sapiens hypothetical protein FLJ31875 (FLJ31875), q24.3
SNP_A-2311523	ggaatgacctgtagcc[A/G]attcccagagcaaggt	A	G	ENST00000360575 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2246841	ctgtaggattttcaca[A/G]tctcggttgatatctg	A	G	Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /// ENST00000261488 // intron // 0 // --- // --- // --- // ---	FLJ10094	FLJ10094, Homo sapiens hypothetical protein FLJ10094 (FLJ10094), q14.11
SNP_A-2267040	gaataaataacagcaa[A/G]tgcaagagtaaattca	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 761263 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2076757	acatttttgtaagaca[C/T]gactttacgtgctcac	C	T	sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-2064497	aattcccgcagtccca[A/G]tgaaggaaccctgcct	A	G	6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// ENST00000325017 // upstream // 48273 // --- // --- // --- // ---	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-2049405	aagctgaggaaattca[C/T]cactaccggaactgct	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, mRNA. /// NM_030668 // intron // 0 // Hs.160871 // PTPRO // 5800 // Homo sapiens protein	PTPRO	PTPRO, Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, p12.3
SNP_A-2087560	actgcgtggaggtctg[A/G]aagagcaacacagcag	A	G	9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 81626 // Hs.248117 //	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-2005774	gtggcttggactactg[A/T]ataaattctcagtctg	A	T	C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 //	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2016199	tcccctcatatcttac[A/G]gcattttctctttgtc	A	G	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2022438	aaaaatatatttcaag[A/G]caaactttggcaatac	A	G	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2028040	aaacggagataaattg[A/G]caaagtgacttgacaa	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2028603	aaactggaaaaggaag[C/G]cttaatcagagttccc	C	G	Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 1 (SLC5A1), mRNA. ///	SLC5A1	SLC5A1, Homo sapiens solute carrier family 5 (sodium,q12.3
SNP_A-2039393	aacataggacatcgaa[C/G]ggtcaattcattgtct	C	G	8638 // Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, mRNA. /// NM_003733 // upstream // 59164 // Hs.118633 // OASL // 8638 // Homo	OASL	OASL, Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 2, q24.31
SNP_A-2045498	aagaatgacgtataca[C/T]ggctcagtatgcatct	C	T	sapiens rTS beta protein (HSRTSBETA), transcript variant 1, mRNA. /// NM_017512 // intron // 0 // Hs.475848 // ENOSF1 //	-	-, Homo sapiens rTS beta protein (HSRTSBETA), transcript variant 1, p11.32
SNP_A-2134739	atattaacctttaaga[A/G]actgtcactcattact	A	G	4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 714109 //	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2109610	aggaaacccaagtata[A/G]gtacaagaaaaacatt	A	G	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2337045 // --- // -	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p21.1
SNP_A-2226072	ctaacagtgaagtgta[A/T]gctaacaagttacagc	A	T	// 134359 // Homo sapiens hypothetical protein FLJ35779 (FLJ35779), mRNA. /// ENST00000282199 // upstream //	FLJ35779	FLJ35779, Homo sapiens hypothetical protein FLJ35779 (FLJ35779), q13.3
SNP_A-2171499	caatcattcctgagaa[C/G]agatgaagtgaacttc	C	G	Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000265371 // intron // 0 // --- // --- // --- // --- ///	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1834786	taccaggagaattctg[A/C]atctacattttcattg	A	C	59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 281844 // Hs.32966 // GUCA2B // 2981 // Homo	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-1826770	taacaggaaaagaaaa[C/T]ggaacaacgaagcctt	C	T	Homo sapiens mutL homolog 3 (E. coli) (MLH3), mRNA. /// AF195657 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo	MLH3	MLH3, Homo sapiens mutL homolog 3 (E. coli) (MLH3), q24.3
SNP_A-1822860	taaaaagattatggaa[A/G]gccaaggaagccaatg	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// ENST00000341317 // intron // 0 // --- // --- // --- // --- /// ENST00000302763 // intron // 0 // --- //	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1818616	gttgaacttacactta[C/T]agggacaacacaggtc	C	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1981860	caatttgaaactagaa[A/T]gaagacattttcgcac	A	T	Homo sapiens importin 11 (IPO11), mRNA. /// ENST00000325324 // intron // 0 // --- // --- // --- // ---	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1898212	tgcttaagctacccac[C/T]gtatggtactttgcta	C	T	1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000284293 // upstream //	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1892055	tgcaaacaatgattct[A/G]acatcagtaaagagcc	A	G	127281 // Homo sapiens hypothetical protein MGC26818 (MGC26818), mRNA. /// ENST00000325716 // 3UTR // 0 // ---	MGC26818	MGC26818, Homo sapiens hypothetical protein MGC26818 (MGC26818), p36.32
SNP_A-1881136	tctttaccatatacaa[C/G]gcaagtaatattgctt	C	G	23759 // Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 1, mRNA. /// NM_148175 // downstream // 61488 // Hs.438587 // PPIL2 // 23759 // Homo	PPIL2	PPIL2, Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 1, q11.21
SNP_A-1882654	tgaaacccagcagtaa[A/G]gtcattaaatctcaaa	A	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 709834 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1911390	tgtcttatttttgtgc[A/C]gattccccgcagcccg	A	C	65078 // Homo sapiens reticulon 4 receptor (RTN4R), mRNA. /// ENST00000328165 // downstream // 3532 // --- // --- // --- //	RTN4R	RTN4R, Homo sapiens reticulon 4 receptor (RTN4R), q11.21
SNP_A-1971779	cagaatcaaaatttgg[A/C]attatgtaattgttca	A	C	// 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1959330	ttttgcaaaatgttga[A/C]catgtcatggttttcc	A	C	8038 // Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // upstream // 8500 // Hs.386283 //	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-1953809	tttgagatggactttc[A/G]cctcaccataacctct	A	G	FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA. /// NM_152655 // downstream	FLJ32191	FLJ32191, Homo sapiens hypothetical protein FLJ32191 (FLJ32191), q13.12
SNP_A-1948972	tttatctagtttccaa[A/G]aaagtaagacatttct	A	G	64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 265007 // Hs.546282 // RBBP8	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-1940048	ttgcagctctgcggac[A/G]gcacaaaccaccgttg	A	G	79066 // Homo sapiens hypothetical protein MGC3329 (MGC3329), mRNA. /// NM_000430 // upstream // 50912 //	MGC3329	MGC3329, Homo sapiens hypothetical protein MGC3329 (MGC3329), p13.3
SNP_A-1937377	ttgaaataatatcaga[A/C]cactttggtgcctttc	A	C	2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 390164 // Hs.479853 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2
SNP_A-1826777	taacaggagtgttaga[C/T]agtaaggagacccaga	C	T	Homo sapiens syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), transcript variant 1, mRNA /// NM_130845 // intron // 0 // Hs.461117 // SNTB2 // 6645 // Homo s	SNTB2	SNTB2, Homo sapiens syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), transcript variant 1, q22.1
SNP_A-1866829	tcccggtgagctctca[C/T]gtaagagtaatgaagt	C	T	26574 // Homo sapiens apoptosis antagonizing transcription factor (AATF), mRNA. /// NM_198838 // downstream // 16333	AATF	AATF, Homo sapiens apoptosis antagonizing transcription factor (AATF), q12
SNP_A-1848612	tatgagaaataaggat[C/G]atattctgatttccat	C	G	// Homo sapiens hypothetical protein FLJ39630 (FLJ39630), mRNA. /// ENST00000328472 // intron // 0 // --- // --- // --- // ---	FLJ39630	FLJ39630, Homo sapiens hypothetical protein FLJ39630 (FLJ39630), q12.3
SNP_A-1853269	tattttacagccatta[A/C]taataataccagctgg	A	C	284716 // Homo sapiens hypothetical protein MGC47816 (MGC47816), mRNA. /// ENST00000324149 // intron // 0 // ---	MGC47816	MGC47816, Homo sapiens hypothetical protein MGC47816 (MGC47816), p34.2
SNP_A-1795118	ggtgactatcacggac[A/G]gtattgtattttatat	A	G	ENST00000332738 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1786592	ggcttctcactgaata[G/T]ctctacttggaggtct	G	T	// 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 371605 // Hs.371823 // PRDM2 // 7799 //	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1790476	ggggcagcatttcata[A/G]cattacaaataaatgc	A	G	// 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream //	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-1790152	ggggacaagggcttat[C/T]acaggtgcagcccct	C	T	Homo sapiens mitochondrial ribosomal protein L55 (MRPL55), nuclear gene encoding mitochondrial protein, transcript variant 8, mR /// NM_181456 // intron // 0 // Hs.63236 // MRPL55 // 128308 // Ho	MRPL55	MRPL55, Homo sapiens mitochondrial ribosomal protein L55 (MRPL55), nuclear gene encoding mitochondrial protein, transcript variant 8, mR ,q42.13
SNP_A-2179202	cactgggctaaaatca[C/T]ggcctgtgttctttct	C	T	// 51218 // Homo sapiens chromosome 14 open reading frame 87 (C14orf87), mRNA. /// NM_020553 // upstream //	C14orf87	C14orf87, Homo sapiens chromosome 14 open reading frame 87 (C14orf87), q32.13
SNP_A-2176403	caccatctcttctcaa[A/C]gccacctgaaacacag	A	C	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 189628 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2196077	catgtgaatagaggga[G/T]agagtcacaaacatac	G	T	9169 // Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA. /// NM_004719 //	SFRS2IP	SFRS2IP, Homo sapiens splicing factor, arginine q13.11
SNP_A-2221903	ccttttttctgatacca[C/T]tctctcctttgaaata	C	T	8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 24200 // Hs.413095	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-2120902	agtctaataaccaaaa[G/T]ctacctcactttactt	G	T	Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 //	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2122128	agtgattaatacatta[C/T]ggtgtcatcagtgaaa	C	T	// 26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 254389 //	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2133125	atatagatccatgtac[A/C]catttggaaatataac	A	C	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2133265	atatatactgtaaaca[A/C]ctaccgagagacactt	A	C	9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 56718 //	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-2167822	caacctcaggcttctc[C/T]cacttcggcttcctga	C	T	sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA. /// ENST00000264178 //	MTR	MTR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), q43
SNP_A-2141755	atcttcttactgagta[A/G]acatcgagaactcagt	A	G	221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 28091 // --- // --- // --- // ---	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-2139305	atcctgcagtctcccc[A/G]cagggatcatttcaat	A	G	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2044952	aagaacatgacccaaa[A/T]taccagccataactac	A	T	UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 //	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-2031248	aaaggctgataggcaa[C/G]acagcaaggaagaaga	C	G	Homo sapiens sterile alpha motif domain containing 6 (SAMD6), mRNA. /// ENST00000353234 // intron // 0 // --- // ---	SAMD6	SAMD6, Homo sapiens sterile alpha motif domain containing 6 (SAMD6), q22.33
SNP_A-2022007	aaaaagacaaggcagc[C/T]aaaccgaaaaaagcac	C	T	Homo sapiens F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 1, mRNA. /// NM_033535 // intron // 0 // Hs.479208 // FBXL5 // 26234 // Homo sapiens F-box	FBXL5	FBXL5, Homo sapiens F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 1, p15.33
SNP_A-2021764	aaaaacagtgtcttgt[A/G]aagtataaattcagta	A	G	27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000356814 // downstream // 225780 // --- // --- // --- // ---	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2009693	atttcctgtaagagta[A/G]gagtgaaggtgggga	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2079915	acccttatgttatgga[G/T]gaagaaactaaagccc	G	T	sapiens KIAA1043 protein (KIAA1043), mRNA. /// ENST00000266082 // intron // 0 // --- // --- // --- // ---	-	-, Homo sapiens KIAA1043 protein (KIAA1043), q12.1
SNP_A-2051219	aagggataatgaatcc[A/G]gaggtatagtattatt	A	G	sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // CDS // 0 // --- // --- // --- // ---	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2274284	gacttgccctttcgca[C/G]acttacgcagttcatt	C	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2245121	ctggcccagtcctgca[C/T]gtcatatccagcgaaa	C	T	135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2237371	ctctcccagttggtta[C/T]ggtcactctcctaatt	C	T	2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 85294 //	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-2312413	ggaccaccacccttca[C/T]cgtgctgcccatgact	C	T	ENST00000277918 // intron // 0 // --- // --- // --- // ---	-	q25.2
SNP_A-2290179	gctgtttgctgacacc[A/G]gagccatccttcccta	A	G	// 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 222869 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2308191	gcttgcttccctttcg[C/T]attctgccataattgt	C	T	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 299719 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-2305949	gctgcttaaacgcatc[A/G]caggactcacaggtgg	A	G	130916 // Homo sapiens hypothetical protein MGC61716 (MGC61716), mRNA. /// ENST00000310397 // 3UTR // 0 // ---	MGC61716	MGC61716, Homo sapiens hypothetical protein MGC61716 (MGC61716), q37.3
SNP_A-2283868	gatagtgggagtggaa[A/G]tagggaaaaaagtaca	A	G	8491 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// NM_152390 // upstream // 138943 // Hs.40808 // MGC33926 // 130733 //	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-2073592	acagtagtgagcaaca[A/G]ataaagtttagtagaa	A	G	FLJ10986 // 55277 // Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// NM_015888 // upstream //	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-2073181	tctgatctcaggagaa[A/G]gtccaaaatcccaaaa	A	G	7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// NM_003667 // upstream //	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-2087056	actgagttaaaatagc[A/C]gagccccagtgattaa	A	C	// 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 433092 // --- // --- // --- // ---	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2092416	agaaaggctttagctg[C/T]atccagattgttttac	C	T	ENST00000334816 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-2001569	aacagtgatactcagg[C/T]actacatcagggtctt	C	T	// 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// NM_207426 // upstream // 17693 // Hs.449674 //	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-2004760	aaggttattatggcca[A/G]tagctcaaaataactc	A	G	2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 464994 // --- // ---	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2019268	accttagcggaatagc[A/G]cctctccatccagttc	A	G	2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // upstream // 90691 // Hs.473819 // ERG // 2078	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-2029470	aaagacatggcagtat[A/C]aaatcaagccccaagc	A	C	84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream //	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1
SNP_A-2044570	aagaaacatgaagaaa[C/T]gctccctggccttta	C	T	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1292639 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2150449	atgtgaactgggctgc[A/G]catacactcagggctc	A	G	// 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 125499 // Hs.328883 // C1D	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-2133270	atatatagatgggaac[C/T]gtaataattactgggt	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2136405	atcacagtacaagtga[C/T]gaacttattattaaat	C	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 480022 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2137213	atcagtaggcacatca[C/G]tatcccaaaccctagc	C	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 404872 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2202700	ccacctttggtaaaga[C/T]gaatcctgtcttcttt	C	T	55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 42222	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2200943	ccaagctcctcaatag[C/T]atttttaagcattcat	C	T	Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // intron // 0 // ---	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-2209129	cccaggctccttgcta[C/G]aaaaattgccaggtca	C	G	3687 // Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), mRNA. /// U37028 // upstream // 4696 // Hs.513528 // ITGAD // 3681 // Human	ITGAX	ITGAX, Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), p11.2
SNP_A-2188668	cagtgcctgggttatc[A/G]atcatgaaaacgttca	A	G	ENST00000332738 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1813094	gtggtaaccattggaa[A/C]gaaaacactgacataa	A	C	57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 172083 //	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1733134	taagccttaaaaaactattcataaa[A/G]gttgtcatcataatggattaaaaag	A	G	286343 // chromosome 9 open reading frame 150 /// NM_000550 // downstream // 41483 // Hs.75219 // TYRP1 //	C9orf150	C9orf150 , rs1543587, chromosome 9 open reading frame 150 ,p23
SNP_A-1656967	tcctgagtgaatgagtttacattaa[C/T]acagttgcagatttgctatggagaa	C	T	NM_152989 // intron // 0 // Hs.87224 // SOX5 // 6660 // SRY (sex determining region Y)-box 5	SOX5	SOX5 , rs10505927, SRY (sex determining region Y)-box 5,p12.1
SNP_A-1654235	ctataaaaaatttctatcctgatta[C/T]aacattgaatgatcaggaattatgt	C	T	PRO1038 mRNA, complete cds. /// NM_018571 // downstream // 5559 // Hs.259230 // ALS2CR2 // 55437 //	-	- , rs2714480, Homo sapiens PRO1038 mRNA, complete cds. ,q33.1
SNP_A-1855018	tcaagaaacatataag[G/T]atcatgcctgaaactg	G	T	5169 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3), mRNA. ///	ENPP3	ENPP3, Homo sapiens ectonucleotide pyrophosphatase q23.2
SNP_A-1860778	tcataagtaacaataa[C/T]agtgcagtgctagcga	C	T	// 10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 67079 // Hs.334587 // RBPMS //	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-1843133	tagtcagaagaagggg[A/G]atttcctgactattca	A	G	8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 470463 // Hs.131489 // PARD3	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1945585	ttgttctctatcatcc[A/G]aatttgacaattactg	A	G	// 154810 // Homo sapiens angiomotin like 1 (AMOTL1), mRNA. /// NM_016403 // downstream // 28327 // Hs.503597	AMOTL1	AMOTL1, Homo sapiens angiomotin like 1 (AMOTL1), q21
SNP_A-1972116	tttttgtttttaagc[A/T]cacgacaagtaggaaa	A	T	7155 // Homo sapiens topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA. /// NM_018297 // downstream // 15402 //	TOP2B	TOP2B, Homo sapiens topoisomerase (DNA) II beta 180kDa (TOP2B), p24.2
SNP_A-1973159	accacaatttgtctaa[A/G]aagtactcaagcccgt	A	G	23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 267745 // Hs.166017 //	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds. ,p14.1
SNP_A-1966340	aaggccaatgggggac[A/G]ctaaagcttttgctca	A	G	-- /// ENST00000359634 // upstream // 855617 // --- // --- // --- // --- /// ENST00000359181 // upstream // 855617 // --- // --- // -	-	q32.3
SNP_A-1987484	cctttcaacagattcc[A/G]cttcatcttaagttaa	A	G	10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 963073 // Hs.269722 // TCBA1 //	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-1986194	agatagcaacataaaa[C/T]gagaacttggaatgtg	C	T	// Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // --- // --- // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-1988983	aagtaaatatgtttag[A/G]aggaaaatccgtacaa	A	G	ENST00000335259 // intron // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-1914687	tgttaattgggtatac[G/T]gagaagccacctacag	G	T	// 147339 // Homo sapiens chromosome 18 open reading frame 25 (C18orf25), mRNA. /// ENST00000321319 //	C18orf25	C18orf25, Homo sapiens chromosome 18 open reading frame 25 (C18orf25), q21.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1923706	ttaggttgtgctggaa[A/G]tgaaacaggcctgcct	A	G	4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 63833 // Hs.467769 // FAM49A	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-1919540	ttaaggaatgaggcaa[A/C]caccaccaggagaaag	A	C	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant c, mRNA. /// NM_003644 // intron // 0 // Hs.462214 //	GAS7	GAS7, Homo sapiens growth arrest-specific 7 (GAS7), transcript variant c, p13.1
SNP_A-1927412	tctggaagctaattga[A/C]agctagaaatttggaa	A	C	// 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA. /// NM_024781 // upstream // 20390 // Hs.280781 //	TXNDC10	TXNDC10, Homo sapiens FLJ20793 protein (FLJ20793), q22.1
SNP_A-1927338	ttcaaacagataggac[A/G]gcggttactaagtcct	A	G	Homo sapiens hect domain and RLD 2 (HERC2), mRNA. /// ENST00000261609 // intron // 0 // --- // --- // --- // ---	HERC2	HERC2, Homo sapiens hect domain and RLD 2 (HERC2), q13.1
SNP_A-1914559	tgttaaatttttcagg[A/G]acaagtgatattttgg	A	G	2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 619210 // ---	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1906793	tggttagtctgggaaa[A/G]cattttaagagacaaa	A	G	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1492880 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1893265	tgcagataagagaaac[A/G]catccttttggtgtt	A	G	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-1988411	tttaatggcatggaaa[C/G]acaccacatgacaaaa	C	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1978107	aatcacatttttaaca[C/T]tcaaaacactcattct	C	T	Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-1957789	ttttattctttagtcc[A/C]aagtacttagcattat	A	C	// 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream //	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1831738	taattcactgccaggc[C/T]agcaaattttcagcga	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2564127 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1823051	taaaaattcagtcaac[C/G]ctcaaggctaccatgg	C	G	29094 // Homo sapiens HSPC159 protein (HSPC159), mRNA. /// ENST00000335402 // upstream // 15573 // --- // ---	HSPC159	HSPC159, Homo sapiens HSPC159 protein (HSPC159), p14
SNP_A-1858531	tcagaggaagccaaga[A/T]gaagagaaagtttttg	A	T	/// ENST00000347726 // upstream // 126428 // --- // --- // --- // -- /// ENST00000335231 // upstream // 126428 // --- // --- // ---	-	p16.1
SNP_A-1809600	gtgagattaatgaaga[C/T]gaaaattttgaatgaa	C	T	Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA. /// NM_080631 // intron // 0 //	VPS41	VPS41, Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, p14.1
SNP_A-1804352	gtcactggaaggtgta[C/T]ataggcttttgccata	C	T	-- /// ENST00000338636 // upstream // 40841 // --- // --- // --- // --- /// ENST00000334344 // upstream // 128831 // --- // --- // ---	-	q12
SNP_A-1798128	gtaaacaaatacagaa[A/G]gttcagatagagacag	A	G	5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 //	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-2177707	cacgtaaacaacttag[G/T]agactgaaaacagact	G	T	Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // intron // 0 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-2174905	cacaggctgcttattc[A/G]aagccaccacatcaat	A	G	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 1109033 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2136228	atcaattatcatctta[C/T]gtattttgagcaattt	C	T	SLC17A6 // 57084 // Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), mRNA. /// NM_022725 // downstream	SLC17A6	SLC17A6, Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), p14.3
SNP_A-2122114	agtgatgtcaaggtga[A/G]gatatttttttagctg	A	G	135112 // Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA. /// NM_138571 // upstream // 22324 //	NCOA7	NCOA7, Homo sapiens nuclear receptor coactivator 7 (NCOA7), q22.32
SNP_A-2116397	aggtagttccaaccaa[A/G]tgtaaactaagttgat	A	G	90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 169974 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.3
SNP_A-2109806	aggaaattgagaaaag[C/T]ctgaagaaaagtctga	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3920286 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2092233	aaatcatggttttata[A/G]gcatcaaagtgtgaag	A	G	Homo sapiens myosin binding protein C, slow type (MYBPC1), transcript variant 4, mRNA. /// NM_206820 // intron // 0 // Hs.506502 // MYBPC1 // 4604 // Homo sapiens	MYBPC1	MYBPC1, Homo sapiens myosin binding protein C, slow type (MYBPC1), transcript variant 4, q23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2093381	agaactcaggaagata[G/T]gtttaccagtttatta	G	T	Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// ENST00000310430 // intron // 0 // --- // --- // --- // ---	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2080821	acctcgacctctgtaa[G/T]tgttcaggggttttgg	G	T	// Homo sapiens B/K protein (LOC51760), mRNA. /// ENST00000261375 // intron // 0 // --- // --- // --- // --- ///	LOC51760	LOC51760, Homo sapiens B,p12.3
SNP_A-2084448	actatcataaccttaa[G/T]atggcttttgcctaaa	G	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2239636	ctgaaacacatccccc[C/T]actcattatgttgtgg	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1368912 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2229763	ctagtgagatgaatac[A/G]gagctcaatggctggg	A	G	// 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000339085 //	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12
SNP_A-2251421	cttcacagcgccttttc[A/G]ctcattcccaccctgg	A	G	3015 // Homo sapiens H2A histone family, member Z (H2AFZ), mRNA. /// NM_016242 // downstream // 200371 //	H2AFZ	H2AFZ, Homo sapiens H2A histone family, member Z (H2AFZ), q24
SNP_A-2312433	ggaccagcgccgtgta[C/T]ctattctgtgcatcct	C	T	6715 // Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA /// NM_006999 // upstream // 8869 // Hs.481542 // POLS // 1104	SRD5A1	SRD5A1, Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), p15.31
SNP_A-2293618	gcagccagccagtgaa[A/T]ctgtcctttcagtcag	A	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 418046 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2300596	gcctgcaaacctcaga[A/T]cggctcctttaaaagt	A	T	RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_002271 // downstream // 116360 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding	RANBP5	RANBP5, Homo sapiens RAN binding protein 5 (RANBP5), q32.2
SNP_A-2301268	gccttgtcataattgc[C/T]ctgtatgtcataccca	C	T	54865 // Homo sapiens hypothetical protein FLJ20249 (FLJ20249), transcript variant 1, mRNA. /// NM_182679 //	GPATC4	GPATC4, Homo sapiens hypothetical protein FLJ20249 (FLJ20249), transcript variant 1, q22
SNP_A-2291818	gcacagcccacatgca[A/C]gagttagcaccacccg	A	C	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// NM_032286 // downstream // 35643 //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2313369	ggagactttctgggca[A/G]ggctttaccagattgc	A	G	28984 // Homo sapiens response gene to complement 32 (RGC32), mRNA. /// ENST00000341475 // downstream //	RGC32	RGC32, Homo sapiens response gene to complement 32 (RGC32), q14.11
SNP_A-2309123	gctttttgggggggtc[A/G]actgctctaaggtata	A	G	580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream //	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2302012	gcgtgaggtcatgtaa[A/G]tggtgatatctggaag	A	G	Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // --- // --- // --- // ---	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-2244660	ctggaggctattatac[C/T]cagtgaaataactcag	C	T	2831 // Homo sapiens G protein-coupled receptor 7 (GPR7), mRNA. /// ENST00000331251 // downstream // 23333 // --- //	GPR7	GPR7, Homo sapiens G protein-coupled receptor 7 (GPR7), q11.23
SNP_A-2245812	ctggggtctgaagaac[A/G]cagctaaatgaaggaa	A	G	// Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 163421 // Hs.546432 // SRD5A2L // 79644 //	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-2233991	ctcatgtaaaatgcaa[G/T]aaggctttgatagtat	G	T	ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1120043 // --- // --- // ---	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2286754	caagagtccacaatga[C/T]aggtttcaaagatgaa	C	T	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2276503	gagaggctcctggtga[G/T]ggggtggctgaaagac	G	T	FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 573998 //	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2090139	acttggaatgaataag[C/T]ctagcaacctaatgca	C	T	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 790090 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2101546	agatgactcagtggtc[A/G]aaagataactgtcttc	A	G	// 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 //	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-2070814	acactagaatcactta[C/T]gaaacttttaaaacac	C	T	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 182658 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2057942	aatattgcaagtaata[A/C]acggtggtcattctca	A	C	26278 // Homo sapiens spastic ataxia of Charlevoix-Saguenay (sacsin) (SACS), mRNA. /// NM_148957 //	SACS	SACS, Homo sapiens spastic ataxia of Charlevoix-Saguenay (sacsin) (SACS), q12.12
SNP_A-2044445	aagaaaacaagatcaa[C/T]aaacaatgagaggtag	C	T	// 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000355465 // upstream //	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-2039207	aacagtgagcctgtta[C/T]caagaaccaactcaac	C	T	RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream //	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2030834	aaaggaaagaagctca[G/T]gtttccggagtgcctg	G	T	sapiens eosinophil peroxidase (EPX), mRNA. /// ENST00000225371 // intron // 0 // --- // --- // --- // ---	EPX	EPX, Homo sapiens eosinophil peroxidase (EPX), q23.2
SNP_A-2002214	atgaacagctttctaa[C/T]gatgaccaggccttgt	C	T	ENST00000358844 // CDS // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2001313	agttactctgacacac[A/G]ctaaactttgagaatc	A	G	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 697715 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-1999735	aatagtcccatcttac[A/G]cttttggtctccctca	A	G	6840 // Homo sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // upstream // 221550 // Hs.499209 //	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-2011901	cattgtgggtcatcca[A/G]gaagcctgggggtggg	A	G	// 8732 // Homo sapiens RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA. /// ENST00000333801 // downstream // 12889 // --- // --- // --- // --- ///	RNGTT	RNGTT, Homo sapiens RNA guanylyltransferase and 5'-phosphatase (RNGTT), q15
SNP_A-2019014	tgtaaaaaatcatgaa[A/G]gattcagtaattatgt	A	G	1859 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, mRNA. /// NM_101395 // downstream // 709 //	DYRK1A	DYRK1A, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, q22.13
SNP_A-2115372	aggggcagtctcatga[C/T]cacacgagtcaaatca	C	T	ENST00000357678 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-2121066	ccagatccgtcatcta[C/G]aaggtggtttctaaaa	C	G	MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 //	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2132765	atataaatcgaacaga[C/T]gagcatttttaaaaac	C	T	220107 // Homo sapiens deleted in lymphocytic leukemia 7 (DLEU7), mRNA. /// ENST00000335465 // upstream // 43938	DLEU7	DLEU7, Homo sapiens deleted in lymphocytic leukemia 7 (DLEU7), q14.3
SNP_A-2129852	atacatcatttcttca[C/T]ctataatccttataca	C	T	137902 // Homo sapiens hypothetical protein FLJ25471 (FLJ25471), mRNA. /// NM_052937 // downstream // 343712	FLJ25471	FLJ25471, Homo sapiens hypothetical protein FLJ25471 (FLJ25471), q11.22
SNP_A-2138537	atccattacatgaatg[A/G]atttgcttacgatgag	A	G	Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // --- // --- // --- // ---	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2158058	attggaacactgtgcc[A/G]aacaacagaataatac	A	G	Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // intron	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-2199152	cattttaagatgctcc[A/G]agaaaaaaaccctgaa	A	G	Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // --- // --- // --- // --- ///	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-2199912	ccaaagactcactgtg[C/T]agctaacgccaattac	C	T	10128 // Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) mRNA, complete cds. /// NM_133259 // upstream // 31518 // Hs.368084 // LRPPRC // 10128 // Homo	LRPPRC	LRPPRC, Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) complete cds. ,p21
SNP_A-2215322	cctcaataactcagaa[A/G]atttggggacttgaac	A	G	Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2218438	cctggaagtgaaatca[C/T]cattttgttggatatt	C	T	9620 // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA. /// ENST00000262738 // upstream // 65076 // --- // ---	CELSR1	CELSR1, Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), q13.31
SNP_A-2219350	cctgtgcatgagacat[G/T]atctaatccctcaagg	G	T	// Homo sapiens succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (SDHB), mRNA. /// NM_007365 // downstream // 4689 // Hs.33455 // PADI2 // 11240 // Homo	SDHB	SDHB, Homo sapiens succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (SDHB), p36.13
SNP_A-1791934	gggtgcgtctgccata[C/T]gaggttgttctcagag	C	T	// 157657 // Homo sapiens hypothetical protein LOC157657 (LOC157657), mRNA. /// ENST00000286688 // upstream //	LOC157657	LOC157657, Homo sapiens hypothetical protein LOC157657 (LOC157657), q22.1
SNP_A-1804399	gtcactttgggtccac[C/T]ggtgaaagtaggggct	C	T	MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC61571), mRNA. /// NM_022461 // upstream	MGC61571	MGC61571, Homo sapiens hypothetical protein MGC61571 (MGC61571), p24.1
SNP_A-1803933	gtcaatagagcttgaa[A/G]atatgtcaatagcaac	A	G	8383 // Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), mRNA. /// NM_002550 // downstream	OR1A1	OR1A1, Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), p13.3
SNP_A-1801169	gtagccttgctcactg[A/G]aagttgaaataattag	A	G	// 79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream //	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-1814134	gtgtcgattagatata[A/C]atgaagtaaagcttct	A	C	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1706817	cctgctggagcatgagaggctcatg[A/T]agaactcagttgccctggctgcctg	A	T	serum/glucocorticoid regulated kinase 2 /// NM_170693 // intron // 0 // Hs.62863 // SGK2 // 10110 //	SGK2	SGK2 , rs2105942, serum,q13.12
SNP_A-1738789	ctgtccaggacatcttaagccaatc[C/T]actggcaccttctcacctgacattg	C	T	NM_004946 // intron // 0 // Hs.17211 // DOCK2 // 1794 // dedicator of cytokinesis 2	DOCK2	DOCK2 , rs764146, dedicator of cytokinesis 2,q35.1
SNP_A-1872616	tctaggtgcagtgcac[A/G]cttagggcaacattca	A	G	23336 // Homo sapiens desmuslin (DMN), transcript variant B, mRNA. /// NM_145728 // upstream // 56949 // Hs.207106 //	DMN	DMN, Homo sapiens desmuslin (DMN), transcript variant B, q26.3
SNP_A-1828328	taagatcccacagtca[C/T]taggagcagaatcaat	C	T	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 682773 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1961844	gttccctcatgtgcaa[C/T]gcaagtgacctcccag	C	T	/// ENST00000331540 // downstream // 679617 // --- // --- // ---	-	p25.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1882858	tgaaagcttataattc[A/G]ctgtgctgctgtttaa	A	G	Homo sapiens mRNA for KIAA1218 protein, partial cds. /// ENST00000297416 // intron // 0 // --- // --- // --- // ---	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. q22.3
SNP_A-1905269	tgggttggttccaata[C/T]ggtgaccctgagaaat	C	T	sapiens mRNA for KIAA0121 protein, partial cds. /// NM_014667 // intron // 0 // Hs.373959 // VGLL4 // 9686 //	VGLL4	VGLL4, Homo sapiens for KIAA0121 protein, partial cds. ,p25.3
SNP_A-1926535	ttattctaaggcctgt[A/G]aagccatactcgcatt	A	G	// 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 63343 // Hs.42650 //	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1925968	ttatgtactatttcag[C/T]catgttgaaaggaagg	C	T	// Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // --- // --- // --- // ---	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-1906473	tggtggcactagagaa[C/T]agaactgagcattcca	C	T	Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// ENST00000355719 // intron // 0 // --- // ---	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-1877050	tctgctagaagacata[A/G]caaggctcagcctaac	A	G	Homo sapiens chromosome 6 open reading frame 157 (C6orf157), mRNA. /// ENST00000237186 // intron // 0 // --- //	C6orf157	C6orf157, Homo sapiens chromosome 6 open reading frame 157 (C6orf157), q14.1
SNP_A-1934264	ttctccagctaggtaa[C/T]cccatagcatcccagt	C	T	24145 // Homo sapiens pannexin 1 (PANX1), mRNA. /// ENST00000227638 // downstream // 37405 // --- // --- // --- // ---	PANX1	PANX1, Homo sapiens pannexin 1 (PANX1), q21
SNP_A-1935001	ttctgagctccttgat[G/T]accatttttttcagttt	G	T	Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// ENST00000248306 // intron // 0 // --- // --- // --- // ---	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-1935090	ttctgatgtacaagaa[A/G]atgtggttagtgtttt	A	G	79577 // Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), mRNA. /// NM_003783 // upstream //	HRPT2	HRPT2, Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), q31.2
SNP_A-1984774	tagtaatggaaagtaa[A/T]tgattataacatctca	A	T	LOC128153 // 128153 // Homo sapiens hypothetical protein BC014608 (LOC128153), mRNA. /// NM_016052 // upstream	LOC128153	LOC128153, Homo sapiens hypothetical protein BC014608 (LOC128153), q41
SNP_A-1984819	attttgtgaacacaac[A/C]atttcaaactaaaatg	A	C	4835 // Homo sapiens NAD(P)H dehydrogenase, quinone 2 (NQO2), mRNA. /// NM_000904 // downstream // 21852 //	NQO2	NQO2, Homo sapiens NAD(P)H dehydrogenase, quinone 2 (NQO2), p25.2
SNP_A-1965981	acttcagagcaaggca[A/G]tctctggcaatgacaa	A	G	220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. ///	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1968205	tatgtttttaattgga[C/T]aaatcagacctttttat	C	T	79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1822864	aggcaggggaatgacc[G/T]ccttgctacattctac	G	T	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 598209 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-1825036	taaaggaggcctggga[C/T]ctattgcctcactttc	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1820655	gtttcacttgtctgct[A/T]agagttttggcaccac	A	T	/// ENST00000324607 // downstream // 34966 // --- // --- // --- // --- /// ENST00000357722 // downstream // 47141 // --- // ---	-	p22.3
SNP_A-1842676	tagtaaagaatagtta[C/G]aatatgcttcattgag	C	G	686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 27832 // --- // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-1844585	tataacagaacatcta[C/T]atgcctctgttgtatc	C	T	// Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// ENST00000282272 // intron // 0 // ---	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-1734144	aagctccctttgtcctggaggcatc[C/G]gaaatcggttcagatctgtttgcag	C	G	tectorin beta	TECTB	TECTB, rs726009, tectorin beta,q25.2
SNP_A-1743605	gcaaggaaatgtgaaccacatagga[C/T]gaattctgcatatgagaggaggtgg	C	T	NM_021255 // upstream // 58098 // Hs.44038 // PELI2 // 57161 // pellino homolog 2 (Drosophila)	-	- , rs409492, - ,q22.3
SNP_A-1744543	accgatctcctaccattcagtctta[C/T]ctactgccaatcctttaaattctaa	C	T	NM_022085 // intron // 0 // Hs.430169 // TXNDC5 // 81567 // thioredoxin domain containing 5	TXNDC5	TXNDC5 , rs155504, thioredoxin domain containing 5,p24.3
SNP_A-1783591	ggcatgctataaactg[A/G]aactctgaaaagacat	A	G	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1782355	ggcaatgtccataagg[A/G]aacccttttctgaatat	A	G	114885 // Homo sapiens oxysterol binding protein-like 11 (OSBPL11), mRNA. /// ENST00000296220 // upstream //	OSBPL11	OSBPL11, Homo sapiens oxysterol binding protein-like 11 (OSBPL11), q21.2
SNP_A-1699673	attaaaacaataagctaaatttcac[A/G]gactgttaacctctgaacaactgct	A	G	fibroblast growth factor 12 /// NM_021032 // intron // 0 // Hs.343809 // FGF12 // 2257 // fibroblast growth factor 12	FGF12	FGF12 , rs1403037, fibroblast growth factor 12 ,q28
SNP_A-2216299	cctcctctcagatgga[A/G]ctaactagccacatgg	A	G	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 710626 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2200983	ccaaggacaaggacta[C/T]gtctttattcaccagt	C	T	2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 60360 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-2185078	cagctttgaaaacata[C/T]ggaattagaacagcag	C	T	84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000261628 // upstream //	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175427	cacatcataagcattc[A/G]atttcaggggcgattt	A	G	2321 // Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mR /// NM_015932 // upstream // 91924 //	FLT1	FLT1, Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor,q12.3
SNP_A-2163864	caaaaccaaagactcc[A/G]aaaagagacaataata	A	G	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // --	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2148417	atggggtctgaaagca[C/T]gttgctgggtgtggtc	C	T	57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream //	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2133019	atatacctgcaataag[C/T]cttaaaaatgtctgta	C	T	84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream //	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-2108519	agctggacagagattc[A/G]aacattagtgaatctg	A	G	// Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// ENST00000270828 // intron // 0 // ---	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2018300	tgcatattaaaaagtc[A/G]cctaagaacatactaa	A	G	Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA. /// ENST00000270139 // intron // 0 // --- // --	IFNAR1	IFNAR1, Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), q22.11
SNP_A-2022662	aaaaatggttaatagg[G/T]agtgggattatgcata	G	T	54797 // Homo sapiens TRAP/mediator complex subunit p28b (FLJ20045), mRNA. /// NM_001269 // upstream //	MED18	MED18, Homo sapiens TRAP p35.3
SNP_A-2037168	aacaaaattatgtaca[A/C]tatgatcccattttgt	A	C	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2054807	aataaacgcaccacgt[G/T]aagtgcttaaagccac	G	T	Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// ENST00000266517 // intron // 0 // --- // --- // --- // ---	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2063236	ctgatgatggggtaaa[A/G]tagaagaaaccacaca	A	G	Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // --- // --- // --- // ---	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-2068962	acaatgagatattatc[A/G]aatgccaatcagaatg	A	G	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 727447 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-2079185	acccagtcttggcttg[C/T]agattagaaaacttta	C	T	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2282147	gagtgtctgtcttgaa[C/T]tggactgggatggcca	C	T	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 264836 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q21
SNP_A-2232003	ctcaactcttccagga[C/G]agtccaagaaagtcca	C	G	// 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream //	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2232312	ctcaattggaaaaata[A/G]cactccatcttacact	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2238425	ctctggtctcccacaa[A/T]cctgagctgcctccag	A	T	3613 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2244646	ctggaggatgggacaa[C/G]gcagttacctctggga	C	G	Homo sapiens copine VII (CPNE7), transcript variant 1, mRNA. /// NM_014427 // intron // 0 // Hs.461775 // CPNE7 //	CPNE7	CPNE7, Homo sapiens copine VII (CPNE7), transcript variant 1, q24.3
SNP_A-2242716	ctgcatgaaaacataa[C/T]tgtgttctctcataag	C	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 502861	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2300528	gcctgagagttcctgg[C/T]ccagagtgcatagaac	C	T	// 51586 // Homo sapiens PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-associated protein	PCQAP	PCQAP, Homo sapiens PC2 (positive cofactor 2, multiprotein complex) glutamine q11.21
SNP_A-2289611	gcaaaaagaaacacac[A/G]ggaccatagctggggt	A	G	sapiens Ellis van Creveld syndrome (EVC), transcript variant 1, mRNA. /// NM_153717 // intron // 0 // Hs.28051 // EVC //	EVC	EVC, Homo sapiens Ellis van Creveld syndrome (EVC), transcript variant 1, p16.2
SNP_A-2306451	gctggtatagtttgtc[C/T]cttccccactgtatgg	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// NM_006113 // downstream // 108167 // Hs.267659 //	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p13.3
SNP_A-2256076	ctttacagctgtttga[G/T]cttaagttacatagcc	G	T	// 55196 // Homo sapiens hypothetical protein FLJ10652 (FLJ10652), mRNA. /// ENST00000340398 // upstream //	FLJ10652	FLJ10652, Homo sapiens hypothetical protein FLJ10652 (FLJ10652), p11.21
SNP_A-2232130	ctcaagtaagagcacc[C/T]atttagccaacactgg	C	T	LOC283537 // 283537 // Homo sapiens hypothetical protein LOC283537 (LOC283537), mRNA. /// ENST00000266943 //	LOC283537	LOC283537, Homo sapiens hypothetical protein LOC283537 (LOC283537), q12.3
SNP_A-2229259	ctaggaagccataaaa[A/C]acaataatattacgta	A	C	114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2280904	gaggttcttggggtca[A/G]agtccacccgtctgag	A	G	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2083685	actacacaacatagat[C/G]aattttcctttcattt	C	G	// 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 522954 //	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2089390	acttatattctcagta[G/T]ctcttctgctcagttc	G	T	FLJ20641 // 55010 // Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA. /// NM_002674 // upstream //	FLJ20641	FLJ20641, Homo sapiens hypothetical protein FLJ20641 (FLJ20641), q23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2092343	agaaagctagggtaaa[A/G]ggagttcttacatttc	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2060855	aatgatagaaagccaa[A/G]taacagtggttggagc	A	G	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 222392	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-2012991	ggtgaatacagtttta[A/G]gatttaaatgattacg	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2011047	aatccacagcaaccca[A/G]tatgggaagaatgatc	A	G	84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // downstream // 64073 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-2117478	aggtgtggcctcaatc[A/G]atcttcacaaccatgc	A	G	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- // --- ///	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2118405	agtaagcagttaatga[C/G]tacatagacaaataca	C	G	Homo sapiens ribosomal protein L26 (RPL26), mRNA. /// NM_016093 // intron // 0 // Hs.546390 // RPL26L1 // 51121 //	RPL26	RPL26, Homo sapiens ribosomal protein L26 (RPL26), q35.1
SNP_A-2152964	attgctttaaaagttg[G/T]actgagtggtcaatat	G	T	5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 2100851 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2154051	attatcaaagttttcc[C/T]agatttgtcaggcttt	C	T	3612 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA. /// NM_024699 //	IMPA1	IMPA1, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), q21.13
SNP_A-2174969	cacaggtaatgcacta[C/T]cgaccctatgattccg	C	T	Homo sapiens hypothetical protein FLJ10204 (FLJ10204), mRNA. /// ENST00000287387 // intron // 0 // --- // --- // --- // ---	FLJ10204	FLJ10204, Homo sapiens hypothetical protein FLJ10204 (FLJ10204), q24.13
SNP_A-2171048	caataccgaacttatg[C/T]caggcactatttctca	C	T	1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 87991 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2185653	caggaggagctgatga[A/G]caaaggctgcagaggg	A	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 576738 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-2227345	ctacaagtcccacgtc[C/G]atgcagcgcaatctgt	C	G	56897 // Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, mRNA. /// NM_020135 // upstream // 61096 // Hs.236828 // WRNIP1 // 56897 // Homo	WRNIP1	WRNIP1, Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, p25.2
SNP_A-1807867	gtcttagggtaaatgg[C/G]accttgccaagtgaca	C	G	MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-1786202	ggctggtaggtgaata[C/T]ggtgtttcattacaat	C	T	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1855182	tcaagatgtgttgaac[C/G]caggcgaaaggaaaga	C	G	83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 899914 // Hs.546489 // C18orf16 // 147429 //	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q12.1
SNP_A-1873571	tctcacagtgaggatg[A/G]aaacaatcaccccaaa	A	G	Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, mRNA. /// NM_004100 // intron // 0 //	EYA4	EYA4, Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, q23.2
SNP_A-1830733	taatccttttgttttc[A/G]ccagtttcttctattt	A	G	55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1973459	aaagtgttattaatcc[A/G]agcctatattccacat	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 398756 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1980810	tccagagctatcagcc[A/G]ctgggattctttcctt	A	G	Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // --- // --- // --- // ---	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-1949674	tttattttgcacataa[A/G]tgattttcctcagtaa	A	G	54927 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA. /// NM_021807 //	CHCHD3	CHCHD3, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), q33
SNP_A-1900828	tggagtgatcctggta[A/T]ctcttccaagttttct	A	T	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	SLC24A2	SLC24A2, Homo sapiens solute carrier family 24 (sodium p22.1
SNP_A-1901064	tgtgattaaattcatg[C/G]aacaattcaggtacca	C	G	/// ENST00000334919 // upstream // 726616 // --- // --- // --- // --- /// ENST00000322194 // downstream // 1042533 // --- // ---	-	q12.2
SNP_A-1894371	tgcattttagggctaa[A/C]caagaagtctcctaaa	A	C	Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST00000264731 // intron // 0 // --- // --- // --- // --- ///	TP73L	TP73L, Homo sapiens tumor protein p73-like (TP73L), q28

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1877358	tctggacctttggtgc[C/G]atttctgactggtgta	C	G	83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // upstream // 215530 // --- // --- // --- // ---	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-1874738	tctccttcaccttcct[C/T]actaccatgaactcag	C	T	2488 // Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), mRNA. /// NM_152316 // upstream //	FSHB	FSHB, Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), p14.1
SNP_A-1905032	tgggtccttcaataca[G/T]agcttgaaaaaacaat	G	T	ENST00000311242 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1924306	ttataaagtcaattta[C/T]gcagccacagatttga	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1981964	tgacactgaaattggt[A/G]aagatacattaatact	A	G	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine q12.3
SNP_A-1834121	tacatccttggtttta[C/T]gtagagattttgagca	C	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1843504	tagtgatttggttacc[A/G]gactctgctgcactgt	A	G	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1819679	gttgtattatggcatg[A/G]caggaaatgaggctga	A	G	/// ENST00000332660 // downstream // 787415 // --- // --- // ---	-	p12.3
SNP_A-1817299	gttcactgtgttgata[A/G]ctgcaaaattcactgt	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1865649	tccattatcttcttcc[A/G]cccagctgctaggggc	A	G	-- /// ENST00000356117 // downstream // 167366 // --- // --- //	-	q23.31
SNP_A-1797714	ggtttggaggtgaaca[C/T]gtgacccaatcaaatg	C	T	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 418251 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1808754	gtgaagccactgtgga[A/G]cgaacgagaaccacaa	A	G	Homo sapiens HECT domain containing 1 (HECTD1), mRNA. /// ENST00000261312 // CDS // 0 // --- // --- // --- // ---	HECTD1	HECTD1, Homo sapiens HECT domain containing 1 (HECTD1), q12
SNP_A-2206563	ccatctttcctgaaat[C/T]atccactacccttct	C	T	FLJ38717 // 401261 // Homo sapiens FLJ38717 protein (FLJ38717), mRNA. /// ENST00000356304 // downstream //	FLJ38717	FLJ38717, Homo sapiens FLJ38717 protein (FLJ38717), p21.1
SNP_A-2185927	caggcaaggctgtaac[G/T]ccctgaaccaggtgat	G	T	sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2183983	cagccatcaaccttta[C/T]ggtggaattagctcca	C	T	/// ENST00000335028 // upstream // 87850 // --- // --- // --- // ---	-	q21.31
SNP_A-2189450	cagttggcttcacgtc[C/T]cttgtctccccttgac	C	T	ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 //	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2180080	cagaaaaccaacaaag[A/C]agcattggacttaatc	A	C	151827 // Homo sapiens hypothetical protein MGC27085 (MGC27085), mRNA. /// ENST00000303740 // upstream //	MGC27085	MGC27085, Homo sapiens hypothetical protein MGC27085 (MGC27085), q26.2
SNP_A-2143550	atgactgaatttagcc[A/G]acacagacaaggctgg	A	G	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // --- // --- // --- // ---	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-2129823	atacatatatttttac[A/G]aagagtagttcacttc	A	G	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 633034 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2008860	tgaaaacattcagacc[A/G]aaaacttagtccacag	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 134875 // Hs.13640 //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-2008847	atctccagaaaaatta[C/T]actttcttcgacattg	C	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 176089 // --- // --- //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2038552	aacagaaaggaagaga[C/T]gcattgtttcatgaaa	C	T	Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// ENST00000299001 // intron // 0 // --- // --- // --- // ---	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-2030408	aaagccagacgcccta[A/G]aggaaaagatttacag	A	G	// Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// NM_022109 // upstream //	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-2057605	aatatgatgagggtca[A/G]gaatatcccttcagtt	A	G	170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-2056340	aatacttagaaactta[A/G]gatgattagcttggaa	A	G	3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 260446 // Hs.112783 // AIG1 // 51390 // Homo	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-2050558	aaggattatcatcata[C/T]gtactttctatagtta	C	T	Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// ENST00000359930 // intron // 0 // --- // --- // --- // ---	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2066842	acaaaatcaaacaaag[A/C]ccgaaaactgtctagt	A	C	6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 146183 // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2098020	agagagattttgcctc[A/G]ctcatcagtgtgactt	A	G	80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 57142 //	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-2099638	agaggtcctcatgata[A/C]cctactctgggctctg	A	C	Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), mRNA. /// NM_000149 //	FUT6	FUT6, Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), p13.3
SNP_A-2088620	actgtgacactagcca[C/T]acttgtctttcatgtc	C	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2287397	gatgtgtttttgataa[C/T]agagtaggcaaaaaac	C	T	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // --- // ---	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-2276311	gagagattgtgtgata[C/G]gcaatttccattttca	C	G	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 220406 //	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2273158	gactcaataaagagac[A/G]gagaactgaccgcctc	A	G	Homo sapiens solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 (SLC6A12), mRNA.	SLC6A12	SLC6A12, Homo sapiens solute carrier family 6 (neurotransmitter transporter, betaine,p13.33
SNP_A-2268919	gaattcaaggaagttc[C/G]aagtatttctcttccc	C	G	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 98733 // Hs.183817 // USP31 // 57478 //	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2263257	gaacagggagttaggc[A/T]aagcaaaaggaaggag	A	T	Homo sapiens mutS homolog 5 (E. coli) (MSH5), transcript variant 3, mRNA. /// NM_025259 // intron // 0 // Hs.371225 //	MSH5	MSH5, Homo sapiens mutS homolog 5 (E. coli) (MSH5), transcript variant 3, p21.33
SNP_A-2228758	ctagacttttctgcca[C/T]gtaaactaagactgat	C	T	Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// ENST00000284308 // intron // 0 // --- // --- // --- // ---	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-2228759	ctagacttttttgcaa[C/G]aatgtcgtaggaagaa	C	G	Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), mRNA. /// ENST00000305296 // intron // 0 // --- // --- // --- // ---	GNG12	GNG12, Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), p31.2
SNP_A-2239984	ctgaagacaactctag[A/G]cctttatcagcccaga	A	G	// 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 281412 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-2247306	ctgtcccacagggtaa[C/T]tgtcttagtctgtctg	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2305067	gctgaaggatctatta[C/T]gtgtggatcagttagt	C	T	79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 331110 //	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2299535	gccctttattaaaaac[C/T]gtggagtcatcaactc	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 966582 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2248542	ctgttacaataagcca[C/T]tcgttggcttgcttca	C	T	-- /// ENST00000329863 // downstream // 226498 // --- // --- // ---	-	q23.1
SNP_A-2239536	ctcttttcctcctga[C/T]atggaatccagcaggc	C	T	64400 // Homo sapiens fused toes homolog (mouse) (FTS), mRNA. /// ENST00000300245 // upstream // 67026 // --- // ---	FTS	FTS, Homo sapiens fused toes homolog (mouse) (FTS), q12.2
SNP_A-2237590	ctctctcatatttcta[A/T]gactaaaacacaaaac	A	T	BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 //	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.2
SNP_A-2282979	gataactcttgtatct[C/T]aaaactcaacctactc	C	T	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2106405	agccgctgcagtggaa[C/T]ggccaccaggaccagg	C	T	80045 // Homo sapiens G protein-coupled receptor 157 (GPR157), mRNA. /// NM_004285 // upstream // 97402 //	GPR157	GPR157, Homo sapiens G protein-coupled receptor 157 (GPR157), p36.22
SNP_A-2094208	agaagggtaaattgag[A/G]cataaagaggctaaga	A	G	25927 // Homo sapiens chromosome 2 open reading frame 32 (C2orf32), mRNA. /// NM_002664 // upstream // 24727 //	C2orf32	C2orf32, Homo sapiens chromosome 2 open reading frame 32 (C2orf32), p14
SNP_A-2064468	aattccatgggtcaca[A/G]tccatctactaccata	A	G	84991 // Homo sapiens RNA binding motif protein 17 (RBM17), mRNA. /// NM_004566 // upstream // 63906 //	RBM17	RBM17, Homo sapiens RNA binding motif protein 17 (RBM17), p15.1
SNP_A-2065713	aatttattacctcacc[C/T]agcaaaatgttcagat	C	T	151525 // Homo sapiens WD repeat and SAM domain containing 1 (WDSAM1), mRNA. /// NM_013450 //	WDSAM1	WDSAM1, Homo sapiens WD repeat and SAM domain containing 1 (WDSAM1), q24.2
SNP_A-2054488	aagtttcttgaatgaa[A/T]gctgataggtctaaaa	A	T	Homo sapiens leucine zipper protein FKSG14 (FKSG14), mRNA. /// ENST00000242872 // intron // 0 // --- // --- // --- // ---	FKSG14	FKSG14, Homo sapiens leucine zipper protein FKSG14 (FKSG14), q12.3
SNP_A-2060474	aatgacagttccacac[A/C]atcttgtttactacag	A	C	MDS009 // 56986 // Homo sapiens x 009 protein (MDS009), mRNA. /// ENST00000329873 // downstream // 127272 // ---	MDS009	MDS009, Homo sapiens x 009 protein (MDS009), q21.2
SNP_A-1989595	aagtgtccatattagc[C/T]atctagtcagttcata	C	T	Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), mRNA. /// ENST00000199448 // 3UTR // 0 // --- // ---	EPDR1	EPDR1, Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), p14.1
SNP_A-1992427	attcgaagttgtaaaa[C/G]tgttcagtgcatttta	C	G	4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 //	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134102	atatgaatcttttct[C/G]actttctgattatttc	C	G	1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream //	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2117403	aggtgtaataactttc[C/T]caagatcacatgggta	C	T	Homo sapiens hypothetical protein FLJ10815 (FLJ10815), mRNA. /// ENST00000219320 // intron // 0 // --- // --- // --- // ---	FLJ10815	FLJ10815, Homo sapiens hypothetical protein FLJ10815 (FLJ10815), q21
SNP_A-2145657	atgcattactgcttgc[A/G]aaactcatagatacat	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3399939 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2181470	cagactgtgctgggaa[C/G]tacgagttggtaatga	C	G	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 283301 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2176472	caccatttatgaagta[C/G]aagtgaaaactcactt	C	G	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 498079 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2200753	ccaagagagaacttac[C/T]gcaatccccagccact	C	T	5744 // Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3, mRNA. /// NM_002820 // upstream // 242125 // Hs.89626 // PTHLH // 5744 // Homo	PTHLH	PTHLH, Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3, p11.22
SNP_A-1807571	gtctggcacaaactga[C/T]gtataagattttacac	C	T	55753 // Homo sapiens oxoglutarate dehydrogenase-like (OGDHL), mRNA. /// ENST00000355036 // upstream //	OGDHL	OGDHL, Homo sapiens oxoglutarate dehydrogenase-like (OGDHL), q11.23
SNP_A-1782110	ggcaacctccttgctc[A/G]gaaacctgcagcctgt	A	G	5047 // Homo sapiens progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin /// NM_001001676 // upstream // 73539 // Hs.532679 // LCN9 //	PAEP	PAEP, Homo sapiens progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin ,q34.3
SNP_A-1817148	gttcaagaccaaactg[C/G]acaaagtggggaaact	C	G	1105 // Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /// ENST00000284049 // upstream	CHD1	CHD1, Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), q21.1
SNP_A-1816108	gttaccaaatttagca[C/T]tactcagtaagtggtt	C	T	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 824003 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1844291	tagttttggctttgta[C/G]gtagagagtctctgtt	C	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2235921 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1838854	tagactggccccagac[A/G]ccacccagcaactgtg	A	G	199704 // Homo sapiens zinc finger protein 585A (ZNF585A), transcript variant 1, mRNA. /// NM_199126 // upstream //	ZNF585A	ZNF585A, Homo sapiens zinc finger protein 585A (ZNF585A), transcript variant 1, q13.12
SNP_A-1966987	acctttggcagatgga[A/G]tagtatttgaatacac	A	G	EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 568571 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-1949906	tttcaagcacatggac[A/G]caagtgtttcaatctc	A	G	-- /// ENST00000308105 // upstream // 36250 // --- // --- // --- //	-	q44
SNP_A-1937625	ttgaagactgggaaac[A/G]aaggctttgagagata	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 979053 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1946192	tttaaaaaatacctgg[A/G]atttgcacccaacaag	A	G	// 158471 // Homo sapiens chromosome 9 open reading frame 65 (C9orf65), mRNA. /// ENST00000223609 //	C9orf65	C9orf65, Homo sapiens chromosome 9 open reading frame 65 (C9orf65), q21.2
SNP_A-1920741	ttacaactaacagaca[C/T]tggactcagttttgca	C	T	ENST00000299308 // intron // 0 // --- // --- // --- // ---	-	q24.31
SNP_A-1911194	tgtctgcctaggaaag[A/G]aagtgttttggaatgt	A	G	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 305591 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-1912373	tgtgattttcatggaa[A/G]aataaaatgcaaatgc	A	G	ENST00000294717 // 3UTR // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-1874432	tctcccaggattcaca[C/T]agaagaaagttacatt	C	T	MGC13125 // 84811 // Homo sapiens hypothetical protein MGC13125 (MGC13125), mRNA. /// ENST00000357928 //	MGC13125	MGC13125, Homo sapiens hypothetical protein MGC13125 (MGC13125), q23.3
SNP_A-1876224	tctgacttttcttcca[C/T]tcttctatccataca	C	T	/// ENST00000307948 // downstream // 33163 // --- // --- // ---	-	p12
SNP_A-1879250	tcttagacgttaaagc[A/G]cagaggaatcttgcta	A	G	ENST00000288861 // intron // 0 // --- // --- // --- // ---	-	p23.3
SNP_A-1881573	tctttctttgtcacca[A/G]cttcattgtatatgta	A	G	3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 79301	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-1887196	tgagaaatgttcaata[A/G]tagtttctattccaaa	A	G	// Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000305775 // downstream // 52718 // --- //	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-1901285	tggatggctgagtggg[A/G]cattagcggtggcctc	A	G	Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// ENST00000356408 // intron // 0 // ---	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-1902593	tggcgcacagtgtata[C/T]gcaattcatgattgtg	C	T	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 517377 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1909181	tgtatcttagtgtgaa[C/T]gtatatacaagcatat	C	T	1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 228600 // --- // --- // --- // ---	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1931376	aatttagaatttttaca[C/T]gacaattttatgctag	C	T	147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 1372092 // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1931716	atgactataagtgtaa[C/T]atgactgtgcttaac	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 39589 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1933048	ttcggaccgtgagaagj[A/C]cacaggtgccccggag	A	C	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1934697	ttctctggtcaaaatc[C/T]atccttctaaaaactg	C	T	90288 // Homo sapiens hypothetical protein LOC90288 (LOC90288), mRNA. /// NM_003925 // downstream // 772 //	LOC90288	LOC90288, Homo sapiens hypothetical protein LOC90288, q21.3
SNP_A-1972612	aggctcagcgtgactа[C/T]actagcagctccaggc	C	T	sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // --- // --- // --- // ---	BSN	LOC90288 (LOC90288), q21.3 BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-1842183	tagggtgcccctgtag[A/G]acagtaagaagagaat	A	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 214912 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1821891	gttttatcggaaaccaa[A/G]atatgtagatgagctc	A	G	160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// ENST00000321196 // intron // 0 // --- // --- // ---	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1871864	tctacacacatcgtca[C/T]caccttaccatgatt	C	T	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 48965 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1869423	tccgtgttattcaaa[A/G]gaaaacatttctccca	A	G	sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// ENST00000319712 // intron // 0 // --- // --- // ---	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-1850929	tattatacttctaata[C/T]gctatgctaaatgtct	C	T	Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // ---	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1720983	caaagaacattttgaaacaattaa[C/G]aattatagatatgtacaaactgttc	C	G	29099 // COMM domain containing 9 /// NM_024841 // upstream // 53895 // Hs.183506 // FLJ14213 // 79899 //	COMMD9	COMM domain containing 9, rs7127214, COMM domain containing 9 ,p13
SNP_A-1693507	agttttgtgtaaattactgaaggaa[C/T]ggaatttgatcaggattagtggcaa	C	T	NM_130902 // intron // 0 // Hs.98701 // COX7B2 // 170712 // cytochrome c oxidase subunit VIIb2	COX7B2	COX7B2 , rs953380, cytochrome c oxidase subunit VIIb2,p12
SNP_A-1811484	gtgctcagtgttagcc[A/G]cattgttctgactaaa	A	G	// 10125 // Homo sapiens RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), mRNA. /// NM_207444 // upstream // 90623 // Hs.448785 // FLJ35695 //	RASGRP1	RASGRP1, Homo sapiens RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), q14
SNP_A-1793859	ggtcaaacatctcatc[A/G]gaatagaatatggcct	A	G	ENST00000261588 // CDS // 0 // --- // --- // ---	-	p11.2
SNP_A-1786932	ggcttttgatgctac[A/G]gcaatatgatcttggt	A	G	55521 // Homo sapiens tripartite motif-containing 36 (TRIM36), mRNA. /// NM_005023 // downstream // 25356 //	TRIM36	TRIM36, Homo sapiens tripartite motif-containing 36 (TRIM36), q22.3
SNP_A-2222452	cgaggctaggcaggga[A/C]gattccaagcacaacg	A	C	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2220208	ccttcatttgtccaac[A/T]aaaccagatgggtctt	A	T	DKFZp761B107 // 91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. ///	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), p15.2
SNP_A-2185076	cagctttcttcatacti[C/T]accttcagtgggtccc	C	T	59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 391073 // Hs.32966 // GUCA2B // 2981 // Homo	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-2152079	attaaaacatacccagt[A/G]aatccatcatggtttt	A	G	55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 //	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-2154961	attcacatagccttca[C/T]agtgactagtgccctc	C	T	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 212100 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2156745	attctgtcttgtcacc[A/G]ccaggtaagaagtgcc	A	G	55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // upstream // 1907 // Homo sapiens endothelin 2 (EDN2), mRNA. ///	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-2156848	attcttatgcccaaat[G/T]acccaggatcagagtc	G	T	ENST00000326197 // upstream // 229974 // --- // --- // ---	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2
SNP_A-2116079	aggtaaagactaaaag[A/G]attcattgaagcagca	A	G	ENST00000251030 // intron // 0 // --- // --- // ---	-	q14.11
SNP_A-2017452	agtatatttgagtcta[A/G]gcctcaggacatttc	A	G	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2031774	aaagtataacagtagt[A/G]atggacagaaaataaa	A	G	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2036188	aaattatgtaatttgc[A/C]acaatatgaatgtagc	A	C	122742 // Homo sapiens olfactory receptor, family 4, subfamily L, member 1 (OR4L1), mRNA. /// NM_001004715	OR4L1	OR4L1, Homo sapiens olfactory receptor, family 4, subfamily L, member 1 (OR4L1), q11.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2093060	agaacagcaaataccg[A/G]ccaggccagaagtgca	A	G	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2104610	agcagtaaaacaaata[C/G]catatgttctcactta	C	G	84466 // Homo sapiens MEGF10 protein (MEGF10), mRNA. /// ENST00000327728 // upstream // 9692 // --- // --- // --- // ---	MEGF10	MEGF10, Homo sapiens MEGF10 protein (MEGF10), q23.2
SNP_A-2079038	acccactttgtgaagg[A/T]aagtaaaataactgat	A	T	55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2274651	gagaaacaggtagatc[C/T]gagaataatcaatgcc	C	T	/// ENST00000309493 // downstream // 38401 // --- // --- // ---	-	q22.33
SNP_A-2277799	gagcatatagtacagg[A/G]aaatgataggattcaa	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3804493 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2272353	gacctgcaacttatac[A/G]cctttattgttcacct	A	G	ENST00000308497 // intron // 0 // --- // --- // --- // ---	-	q35.1
SNP_A-2246824	ctgtagctgtaggtat[C/G]agtatagttggctaag	C	G	Homo sapiens KIAA1363 protein (KIAA1363), mRNA. /// ENST00000273512 // 3UTR // 0 // --- // --- // --- // ---	KIAA1363	KIAA1363, Homo sapiens KIAA1363 protein (KIAA1363), q26.31
SNP_A-2246301	ctggtgtcatattgga[A/G]aagattttagagtcaa	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// NM_203403 // upstream // 16131 // Hs.445356 //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2234465	ctccacactattacca[C/T]aagactggtgacagca	C	T	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), mRNA. /// ENST00000265174 // intron	PAPSS1	PAPSS1, Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), q25
SNP_A-2275578	gagacacgctgcccta[A/T]agtggtcctcggtata	A	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2305369	gctgataactgatgaa[A/G]tagacctgagaaatat	A	G	UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 266724 // ---	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2078762	accatttcatagagag[C/T]cagaacttgatgccca	C	T	// Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// ENST00000297345 // intron // 0 // --- // --- // --- // ---	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2088584	actgtctgtctgacac[C/G]aggtaaggagagttga	C	G	// 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream // 613694 //	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2084917	actcaagtgactacga[A/G]caaacagctcccccac	A	G	/// ENST00000326756 // downstream // 323539 // --- // --- // ---	-	p16.1
SNP_A-2053739	aagtggtccacagaca[C/T]ggatgatcagtcaaat	C	T	2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 147343 //	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-2075574	acatgcctccatccac[C/T]gaaggcagccctgcat	C	T	// 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 85925 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2046758	aagaggaagagtagac[C/T]aatcttgtcactgttc	C	T	// 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream //	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-2018170	acatggagcacgatca[C/T]gtttggagtcaccctg	C	T	// 59271 // Homo sapiens chromosome 21 open reading frame 63 (C21orf63), mRNA. /// NM_018277 // downstream //	C21orf63	C21orf63, Homo sapiens chromosome 21 open reading frame 63 (C21orf63), q22.11
SNP_A-2011090	cgtcactcatgataag[A/T]ccacatttctctcctc	A	T	7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 417562 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2000135	cctttcttctttcagc[A/G]aaaagaggttttggag	A	G	ENST00000358040 // CDS // 0 // --- // --- // --- // --- /// ENST00000345581 // CDS // 0 // --- // --- // --- // --- ///	-	q11.21
SNP_A-2115775	agggtgaaggccccaa[C/T]gtatctgggagcttat	C	T	// 340441 // Homo sapiens protein expressed in prostate, ovary, testis, and placenta 8 (POTE8), mRNA. /// ENST00000297798 // downstream // 18621 // --- // --- // --- // ---	POTE8	POTE8, Homo sapiens protein expressed in prostate, ovary, testis, and placenta 8 (POTE8), p11.21
SNP_A-2119265	agtagtaagtccatta[C/T]gagtgaggtccagaaa	C	T	// Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// ENST00000341547 // upstream // 179110 // --- // ---	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2121938	agtgaggttcttaaag[G/T]cttcctagatgctcta	G	T	// 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2132994	atatacattttagaat[C/G]aagttgctagtaccta	C	G	// Homo sapiens constitutive photomorphogenic protein (COP1), transcript variant 2, mRNA. /// NM_022457 // intron // 0 // Hs.523744 // RFWD2 // 64326 // Homo sapiens	RFWD2	RFWD2, Homo sapiens constitutive photomorphogenic protein (COP1), transcript variant 2, q25.1
SNP_A-2160854	atttctctccctctct[A/G]aaaaggctgatgtcac	A	G	7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 523523 // --- // --- // --- // ---	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-2170275	caaggtttgattcata[A/T]gagaggaagagagatt	A	T	1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream //	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2217439	cctgacaatcaaaggc[C/T]gacactgtgctggatt	C	T	2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// NM_173675 // downstream // 45403 //	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215465	cctcactaaatgagca[C/T]ggaaaaggtaggaatg	C	T	// Homo sapiens FLJ46082 protein (FLJ46082), mRNA. /// ENST00000343036 // intron // 0 // --- // --- // --- // ---	FLJ46082	FLJ46082, Homo sapiens FLJ46082 protein (FLJ46082), q34.13
SNP_A-2222664	cgatataagcgataaa[C/G]gattccacccaaaaat	C	G	51816 // Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, mRNA. /// NM_017424 // upstream // 221360 // Hs.170310 // CECR1 //	CECR1	CECR1, Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, q11.1
SNP_A-2223695	cggcaagaatcagaag[A/G]ccgggaagccattcac	A	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2206285	ccatcccgtctaacac[C/G]gtgaaagcctgtctgt	C	G	ENST00000357747 // intron // 0 // --- // --- // --- // ---	-	q42.13
SNP_A-2208765	cccagaccagtgtgaa[C/T]tgagttataaaaatat	C	T	5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 634730 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-1717019	aacaattgagattatagatggtctc[C/T]aatttatgaaggttcaacttagatt	C	T	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) /// NM_020203 // downstream // 68008 // Hs.283095 // MEPE // 56955 // matrix,	SPP1	SPP1 , rs1381948, secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) ,q22.1
SNP_A-1737607	actggtagattttgtaacagtctaa[C/T]gattactactttactattaattact	C	T	BC040876 // intron // 0 // Hs.20495 // DKFZP434F011 // 25947 // ion transporter protein	DKFZP434F011	DKFZP434F011 , rs9328169, ion transporter protein,p25.2
SNP_A-1869644	tccttagccaagagaa[A/G]tgaaatacaactacct	A	G	10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 //	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-1865580	tccatgtagatgctgc[A/G]aacttttcttctcat	A	G	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-1861185	tcatatgctgcatcag[A/G]aagcaagtcttggcac	A	G	6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// NM_000143 // downstream // 114152 //	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-1816016	gttacaattaatgaac[A/C]actacccatacattaa	A	C	2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream //	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1827590	taactgcaatgactct[C/T]aagtctcttttctttt	C	T	80775 // Homo sapiens hypothetical protein MGC10993 (MGC10993), mRNA. /// ENST00000295220 // downstream //	MGC10993	MGC10993, Homo sapiens hypothetical protein MGC10993 (MGC10993), q14.2
SNP_A-1837664	tactttcaatctaccg[C/T]ccaaataatcaatatc	C	T	AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 13040 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd p15.1
SNP_A-1969383	actttggctataggca[C/T]gttaatgtatgagtgt	C	T	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 100447 // --- // --- // --- // --- ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. ,q21.1
SNP_A-1975104	gagaataagcctgcta[A/C]ctcctgtctgaggtgg	A	C	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1923833	ttagtatgctgtacaa[C/T]gggtaatataggatga	C	T	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), mRNA. /// ENST00000265174 // intron	PAPSS1	PAPSS1, Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), q25
SNP_A-1894038	tgcatcctgtcccccа[C/T]tactcctagccaggga	C	T	// 80224 // Homo sapiens chromosome 14 open reading frame 127 (C14orf127), mRNA. /// ENST00000356390 //	NUBPL	NUBPL, Homo sapiens chromosome 14 open reading frame 127 (C14orf127), q12
SNP_A-1896324	tgctaaatctgttggt[C/G]aatttttaatcctcat	C	G	Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), mRNA. /// BC003044 // intron // 0 // Hs.495138 // MAPKAP1 // 79109 // Homo sapiens mitogen-	MAPKAP1	MAPKAP1, Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), q33.3
SNP_A-1880652	tcttgctcttctatca[C/T]tccaaggcttaggcat	C	T	// Homo sapiens claudin 3 (CLDN3), mRNA. /// NM_001305 // upstream // 54423 // Hs.520942 // CLDN4 // 1364 // Homo	CLDN3	CLDN3, Homo sapiens claudin 3 (CLDN3), q11.23
SNP_A-1923529	ttagggacctgatgac[C/T]aatggtttaaaagcat	C	T	Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1910034	tgtcagtggtgctgag[A/G]atttgaaagggatgct	A	G	// 25950 // Homo sapiens RWD domain containing 3 (RWDD3), mRNA. /// ENST00000354428 // downstream //	RWDD3	RWDD3, Homo sapiens RWD domain containing 3 (RWDD3), p21.3
SNP_A-1975426	gttgacttaagagaca[C/G]tgtcagatactccagg	C	G	// 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream //	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1973389	aacaattagtaaatcc[A/G]aattttcatgaatcat	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 921464 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1982236	agtgttacatgatagc[A/G]cctatattctaaaggc	A	G	sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA. /// NM_198709 // intron // 0 // Hs.149103 // ARSB // 411 //	ARSB	ARSB, Homo sapiens arylsulfatase B (ARSB), transcript variant 1, q14.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1978479	acttggaatacaacac[A/G]gtcactgcagagttat	A	G	Homo sapiens FLJ44691 protein (FLJ44691), mRNA. /// ENST00000327908 // CDS // 0 // --- // --- // --- // ---	FLJ44691	FLJ44691, Homo sapiens FLJ44691 protein (FLJ44691), q25
SNP_A-1986452	aatcctaataaacaca[C/G]tatcgtcaatacccac	C	G	Homo sapiens hypothetical protein FLJ38993 (FLJ38993), mRNA. /// ENST00000272133 // intron // 0 // --- // --- // --- // ---	CNIH3	CNIH3, Homo sapiens hypothetical protein FLJ38993 (FLJ38993), q42.12
SNP_A-1819261	gttggaaatcttgaca[C/T]gacatcctgttaaaaa	C	T	Homo sapiens calpain 13 (CAPN13), mRNA. /// ENST00000295055 // CDS // 0 // --- // --- // --- // --- ///	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1
SNP_A-1864264	tccaccttcattgtcc[C/T]attttagggatatgta	C	T	sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), mRNA. /// ENST00000327153 // intron // 0 // --- // --- // --- // ---	LIPA	LIPA, Homo sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), q23.31
SNP_A-1873785	tctcagcatggttaca[A/G]tattaatgctgggtac	A	G	147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// NM_138966 // downstream // 190625 // Hs.465407	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1854652	tcaacaccgatagcta[A/G]ggactgccacaaaatg	A	G	2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 387282 // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1853469	tattttgatgtgggta[A/G]aaatacatgaaagatt	A	G	Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // intron // 0 // --- // --- // --- // ---	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3
SNP_A-1679550	aggagatagcggatgggagatgcaa[C/T]ggtagaagagggccgagggctgtgc	C	T	// GRB2-associated binding protein 1 /// NM_032557 // downstream // 50714 // Hs.332841 // USP38 // 84640 //	GAB1	GAB1 , rs10519679, GRB2-associated binding protein 1 ,q31.21
SNP_A-1703999	cctctccaaaatgcacttgagtgaa[C/T]ggaaaaacaacaccttgactgtttg	C	T	Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 1888036 // Hs.201920 // EPHA5 // 2044 //	-	- , rs1156251, Clone IMAGE:4429392, mRNA, partial cds ,q13.1
SNP_A-1787156	gggaaatgaaagaacc[A/G]agtaaacaataggtca	A	G	390168 // Homo sapiens olfactory receptor, family 5, subfamily M, member 1 (OR5M1), mRNA. /// NM_001004741	OR5M1	OR5M1, Homo sapiens olfactory receptor, family 5, subfamily M, member 1 (OR5M1), q11
SNP_A-1803868	gtcaagggcactaaac[G/T]gtatgtttctaaggaa	G	T	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1330217 // --- // -	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2208812	cccagagcgggtagta[C/T]gacttcagtgagaaat	C	T	SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 276461 //	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2225414	ctaaaaaaatcaacac[A/T]gataatactaatgcaa	A	T	153328 // Homo sapiens similar to CG4995 gene product (LOC153328), mRNA. /// ENST00000274513 // intron // 0 // ---	LOC153328	LOC153328, Homo sapiens similar to CG4995 gene product (LOC153328), q31.1
SNP_A-2217905	cctgcagaagttccta[C/T]catgatgcctagatct	C	T	1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 158612 // Hs.488293 // EGFR /	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-2171032	caataccaagctagaa[A/G]tattcctaagattcat	A	G	// 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 299180 //	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-2177222	cacctggaacactcaa[A/T]gggaacgtccttctgt	A	T	/// ENST00000329678 // downstream // 100314 // --- // --- // ---	-	p15.5
SNP_A-2156135	attctaaaaataaaga[A/G]actgtacctcagagga	A	G	sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, mRNA. /// NM_182945 // intron // 0 // Hs.310429 //	NIN	NIN, Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, q22.1
SNP_A-2164303	caaaatattatctttc[A/G]ccatgcccagaggaag	A	G	160418 // Homo sapiens SMILE protein (SMILE), mRNA. /// NM_003994 // downstream // 239386 // Hs.1048 // KITLG //	SMILE	SMILE, Homo sapiens SMILE protein (SMILE), q21.32
SNP_A-2166166	caaatatgaaccatta[A/G]gagtccaaagaaagtc	A	G	// 57045 // Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), mRNA. /// NM_006788 // upstream //	TWSG1	TWSG1, Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), p11.22
SNP_A-2138637	atcccacgcttttagg[C/T]caaaaccaatgtgtaa	C	T	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15
SNP_A-2137957	atcatttgcctttgcc[C/T]ggagtatctgcatcct	C	T	Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA. /// ENST00000207451 // intron // 0 // --- // ---	EIF2C1	EIF2C1, Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), p34.3
SNP_A-2137645	atcatgacaaaattca[C/T]agagtgaccttgatag	C	T	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1), mRNA. /// ENST00000316623 // intron // 0 // --- // --- // --- // ---	FBN1	FBN1, Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1), q21.1
SNP_A-2124831	agttctttgtgcaaat[C/G]agatgaaagtgccaat	C	G	22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 7916 //	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2002102	tttaagtagattaata[A/G]catgcttccagtcaca	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2003128	gtgtcccgggttccca[C/T]gctggagaagtccctc	C	T	1296 // Homo sapiens collagen, type VIII, alpha 2 (COL8A2), mRNA. /// NM_014408 // downstream // 20197 // Hs.523131	COL8A2	COL8A2, Homo sapiens collagen, type VIII, alpha 2 (COL8A2), p34.3
SNP_A-1995567	tccagagcaggaagaa[C/T]gggatttaggtagaca	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-2008828	tgatgattaaaccaaa[G/T]tagttggctaactgct	G	T	PPP4R2 // 151987 // Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), mRNA. ///	PPP4R2	PPP4R2, Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2042056	aactactcccattact[C/G]aattgcaaagctgctt	C	G	SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2022481	aaaaatcacaatatca[C/T]gacaggtgtgtttaac	C	T	Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-2060670	aatgagatgtacagag[A/C]aaatgcagtctccata	A	C	CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. ///	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2101547	agatgactccacttca[C/T]aggatttgcataaatt	C	T	167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 103210 //	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3
SNP_A-2293050	gcagacaaccttcgta[A/G]agcctgtgagagtgcc	A	G	283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743), mRNA. /// NM_000875 // upstream // 76898 //	FLJ39743	FLJ39743, Homo sapiens hypothetical protein FLJ39743 (FLJ39743), q26.3
SNP_A-2278743	gagcttagaatgacca[C/T]gaataaagatctcttt	C	T	22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 //	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-2271911	gacccaggctagatac[A/G]ggtaaatgcagatttc	A	G	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2270193	gacacattgttgatac[A/G]ggtgtcaaggggaag	A	G	// 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. ///	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2259899	gaaaaggctcagaaaa[C/T]gcaaagacctatctgg	C	T	1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 135227 // Hs.148162 // PDGFC	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2239358	ctctttcattggcaga[C/T]aatttttgcttctacc	C	T	Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2242969	ctgccattaggatatg[C/G]acaacgaccagtcttt	C	G	8087 // Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA. /// ENST00000331490 // upstream // 39187 // --- // --- // --- // --- /// ENST00000357559	FXR1	FXR1, Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), q26.33
SNP_A-2255021	cttggcttgtgacaaa[A/G]tgggaacattctctct	A	G	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2276035	gagagaaattgtatga[A/G]ctgaggccaatgatag	A	G	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 754278 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-2304603	gctctctctcttacta[A/G]cttatttccaagccgt	A	G	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), transcript variant E, mRNA. /// NM_001228 // intron // 0 // Hs.369736 // CASP8 // 841 //	CASP8	CASP8, Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), transcript variant E, q33.1
SNP_A-2303899	gctcatccacgtccca[A/C]aactgcttaaaatccg	A	C	Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// ENST00000217067 // intron // 0 // --- // ---	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-2306821	gctgtgcacagactcc[A/T]caaaggacggattgtc	A	T	Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 //	ARGBP2	ARGBP2, Homo sapiens Arg q35.1
SNP_A-2309447	ggaaacaaatgcattg[A/G]aagaatggtagtgaaa	A	G	// Homo sapiens DEK oncogene (DNA binding) (DEK), mRNA. /// NM_182757 // upstream // 102878 // Hs.148741 //	DEK	DEK, Homo sapiens DEK oncogene (DNA binding) (DEK), p22.3
SNP_A-2092548	agaaaataagaacatga[A/G]ctgttactctggactc	A	G	// 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 635787 // --- // --- // --- //	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2085172	actcaggaaatgccaa[A/G]cgttttcgaagccctg	A	G	5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // upstream // 233912 // Hs.498570 //	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-2059369	aatctaaattcagcca[A/T]aacattttaaggaagt	A	T	-- /// ENST00000329885 // downstream // 621186 // --- // --- //	-	q14.3
SNP_A-2052461	aagtagactttccaaa[C/T]agagctacaatatcaa	C	T	23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 250167 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2074225	acataagccacacata[C/T]taagttgtagtttctt	C	T	Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // --	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2074741	acatatgtcaacacaa[G/T]gtttgtggatctcctt	G	T	ATP6V1E2 // 90423 // Homo sapiens ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 2 (ATP6V1E2), mRNA. /// ENST00000343465 // downstream //	ATP6V1E2	ATP6V1E2, Homo sapiens ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 2 (ATP6V1E2), p21
SNP_A-2026385	aaacaaaaactctctt[A/G]aacgtgatactgtatt	A	G	84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000320501 // upstream //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2023383	aaaacctcacaatcca[A/G]ctcaaagagacgctgt	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-2044454	aagaaaaccaagacaa[C/T]cggcaaagctttgaag	C	T	Homo sapiens mRNA for KIAA0562 protein, partial cds. /// ENST00000263739 // intron // 0 // --- // --- // --- // --- ///	KIAA0562	KIAA0562, Homo sapiens for KIAA0562 protein, partial cds. ,p36.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2127026	ataaataaagggagtc[C/T]gaaaatagcaaagatt	C	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1273298 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2132556	atagtgttaagaacaa[A/C]ggaagcgtcgagaagg	A	C	// 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 132403 // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q14.3
SNP_A-2115155	agggctgtatctccgc[A/G]attactggtactggtg	A	G	23746 // Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA. /// ENST00000317744 //	AIPL1	AIPL1, Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), p13.2
SNP_A-2148734	atggtctaatctgaac[G/T]cttaaatgttgacttt	G	T	/// ENST00000359349 // upstream // 393061 // --- // --- // --- //	-	p13.2
SNP_A-2162846	attttgctgattgtta[C/T]aattttagcaattttg	C	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2153208	attactcttatgggta[A/G]gtctaagaacagcagt	A	G	253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream //	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-2159283	atttaacgatggagaa[A/G]gaaaaaggagacaata	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2196891	cattagcgtaatagaa[A/G]tgacagagaggtcatc	A	G	RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 280887 //	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.2
SNP_A-2225810	ctaaagtggtcccatg[A/C]actggctgtatctggt	A	C	79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA. /// Y15723 // upstream // 179205 //	FLJ21159	FLJ21159, Homo sapiens hypothetical protein FLJ21159 (FLJ21159), q32.1
SNP_A-2202821	ccactaagacttggaa[C/T]ggtttgctgggtagca	C	T	ENST00000353285 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-1804389	gtcacttggcagaatc[A/C]gaaaacagtcttgaaa	A	C	10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 362399 //	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-1808561	gtgaaatgggggctaa[C/T]accatctttcatgtat	C	T	// 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 //	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.33
SNP_A-1685612	ctcacgttcccctctctgcatgtga[C/T]acaactaccagagaactgaatttat	C	T	DKFZp547I048 // 127254 // hypothetical protein DKFZp547I048 /// NM_001889 // downstream // 97135 //	DKFZp547I048	DKFZp547I048 , rs699848, hypothetical protein DKFZp547I048 ,p31.1
SNP_A-1858072	tcacttttgtactcca[C/T]agccactccagcaaag	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 496131 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1830880	taatcttgtgtattta[C/G]aaaggctaaagaaaaa	C	G	Homo sapiens mitochondrial ribosomal protein S27 (MRPS27), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000261413 // intron // 0 // --- // --- // --- // ---	MRPS27	MRPS27, Homo sapiens mitochondrial ribosomal protein S27 (MRPS27), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-1979568	aaattaaaaatacagg[A/G]cagtttcacttaggga	A	G	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 296322 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-1966609	ccaaaaatgacaaagc[A/T]atcatatgtttctctc	A	T	ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. ///	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-1966401	gcaacccatgctgtcc[A/G]cttctctgtgcatttc	A	G	80055 // Homo sapiens GPI deacylase (PGAP1), mRNA. /// NM_153697 // downstream // 30599 // Hs.432706 //	PGAP1	PGAP1, Homo sapiens GPI deacylase (PGAP1), q33.1
SNP_A-1966058	ggagatctcaggagca[A/G]ataggaaaattaccac	A	G	91404 // Homo sapiens SEC14 and spectrin domains 1 (SESTD1), mRNA. /// NM_152520 // downstream // 19564 //	SESTD1	SESTD1, Homo sapiens SEC14 and spectrin domains 1 (SESTD1), q31.2
SNP_A-1950066	tttcacatatataagc[A/G]actgagactggatggt	A	G	80205 // Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), mRNA. /// AF150735 // downstream //	CHD9	CHD9, Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), q12.2
SNP_A-1961313	ttttttctatgaaaac[A/C]atttctgcgtttgaaa	A	C	Homo sapiens mesoderm induction early response 1 (MI-ER1), mRNA. /// ENST00000355977 // intron // 0 // --- // --- // -	MI-ER1	MI-ER1, Homo sapiens mesoderm induction early response 1 (MI-ER1), p31.2
SNP_A-1960028	ttttgttcctttcacc[A/G]caggtttattactcac	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 113140 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1910364	tgtccataatcacata[A/G]caaggcaggaataagc	A	G	3779 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 1 (KCNMB1), mRNA. /// NM_014592 // upstream // 68930 // Hs.484111 //	KCNMB1	KCNMB1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 1 (KCNMB1), q35.1
SNP_A-1905104	tgggtgcaattagaaa[C/T]atctggagcatttatt	C	T	8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 123656 // ---	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-1907411	tgtaaacagattttcc[A/G]gcaaagaaaaaaaata	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 466889 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1877419	tctggaggttctgtct[A/G]aacttaaaatctcagc	A	G	Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), mRNA. /// ENST00000318222 // intron // 0 // --- // --- // --- // ---	PKD2L1	PKD2L1, Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), q24.31
SNP_A-1886382	tgaccttctacaattc[A/G]cttcccttctctgagc	A	G	// Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// ENST00000270828 // intron // 0 // ---	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884823	tgaatcccagtcagaa[A/G]tcacatgcatcactgc	A	G	MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 //	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-1882667	tgaaaccgtatctacc[A/G]cttattagctgtctga	A	G	Homo sapiens proline-serine-threonine phosphatase interacting protein 2, mRNA (cDNA clone MGC:34175 IMAGE:4524856), complete cds /// NM_024430 // intron // 0 // Hs.368623 // PSTPIP2 // 9050 // Hom	PSTPIP2	PSTPIP2, Homo sapiens proline-serine-threonine phosphatase interacting protein 2, (cDNA clone MGC:34175 IMAGE:4524856), complete cds ,q21.1
SNP_A-1879921	tcttcctatttttcag[A/T]atcaggctggttgtct	A	T	1021 // Homo sapiens cyclin-dependent kinase 6 (CDK6), mRNA. /// NM_152703 // downstream // 200020 // Hs.489118	CDK6	CDK6, Homo sapiens cyclin-dependent kinase 6 (CDK6), q21.2
SNP_A-1955291	tttgggagaaaacact[A/G]agagttgacagagagg	A	G	160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// ENST00000321196 // intron // 0 // --- // --- // --- // ---	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1934660	ttctctgcataaaaca[C/T]tagcatttaccaaggt	C	T	5602 // Homo sapiens mitogen-activated protein kinase 10 (MAPK10), transcript variant 4, mRNA. /// NM_002753 // upstream // 68889 // Hs.25209 // MAPK10 // 5602 // Homo	MAPK10	MAPK10, Homo sapiens mitogen-activated protein kinase 10 (MAPK10), transcript variant 4, q21.3
SNP_A-1938487	ttgagaaaaggatcta[C/T]gacaaaattactagtg	C	T	// 55149 // Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA. /// ENST00000298635 // upstream //	PAPD1	PAPD1, Homo sapiens PAP associated domain containing 1 (PAPD1), p11.23
SNP_A-1939349	ttgatgaattaatgta[C/G]acaaagtgcttagaga	C	G	6608 // Homo sapiens smoothened homolog (Drosophila) (SMO), mRNA. /// NM_015328 // upstream // 7692 //	SMO	SMO, Homo sapiens smoothened homolog (Drosophila) (SMO), q32.1
SNP_A-1945545	ttgttcctagaagtta[A/G]gtcagaagatagaagt	A	G	/// ENST00000357074 // downstream // 231394 // --- // --- // --- // --- /// ENST00000358765 // downstream // 231394 // --- // ---	-	p14
SNP_A-1943908	ttgtatcagagaacaa[C/G]tgcatggaataaactt	C	G	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1979127	gtgataaaaacaagaa[A/G]agctgattccaaacag	A	G	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 401945 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-1986702	tttacttggcttgtta[A/G]aatagtcttccaactt	A	G	9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 389231 // --- // --- // --- // ---	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1842490	taggtggcctaaaacc[A/C]gatattgtagattttg	A	C	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 206461 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1853367	tattttcagcaacaaa[C/G]agtatctggtaccaaa	C	G	Homo sapiens RNA binding motif protein 6 (RBM6), mRNA. /// ENST00000266022 // intron // 0 // --- // --- // --- // ---	RBM6	RBM6, Homo sapiens RNA binding motif protein 6 (RBM6), p21.31
SNP_A-1851604	tattctctgaagttag[A/C]aaatcaagtgaaataa	A	C	4048 // Homo sapiens leukotriene A4 hydrolase (LTA4H), mRNA. /// NM_005230 // upstream // 134811 // Hs.46523 //	LTA4H	LTA4H, Homo sapiens leukotriene A4 hydrolase (LTA4H), q23.1
SNP_A-1869344	tcctggttctcctcca[A/G]ctctctgaggacttct	A	G	// 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), mRNA. /// NM_003108 // upstream // 336836 // Hs.432638	MTCBP-1	MTCBP-1, Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), p25.2
SNP_A-1704837	atccaaactatttttcttcaatacc[A/G]atgaataattattaaaacataatta	A	G	145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs1376835, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1643768	tgtggacacatctcaaaggtaaaca[A/C]aaagtagcacatcttcttcatgttg	A	C	NM_145036 // intron // 0 // Hs.500501 // MGC33887 // 201134 // hypothetical protein MGC33887	MGC33887	MGC33887 , rs9303490, hypothetical protein MGC33887,q24.1
SNP_A-1661169	atgtttctctataattattgtcaca[A/C]agttataccatacaggtaattccag	A	C	5896 // recombination activating gene 1 /// NM_000536 // upstream // 1853596 // Hs.159376 // RAG2 // 5897 //	RAG1	RAG1 , rs10501199, recombination activating gene 1 ,p12
SNP_A-1658262	caggtatccagagacattgctaaaa[A/G]atgtcaataccaaatctaatcacag	A	G	BC037495 // intron // 0 // Hs.77546 // ANKRD15 // 23189 // ankyrin repeat domain 15	ANKRD15	ANKRD15 , rs2282038, ankyrin repeat domain 15,p24.3
SNP_A-1737896	tggactggaaccagctccttaatca[C/T]tatggatattgtgtctaagaggaag	C	T	NM_016953 // intron // 0 // Hs.408261 // PDE11A // 50940 // phosphodiesterase 11A	PDE11A	PDE11A , rs10497477, phosphodiesterase 11A,q31.2
SNP_A-1800066	gtacatttactctgag[A/T]cctatcactataaatg	A	T	FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2225280	cgttggtaattaacaa[A/C]agatcaagaatacctt	A	C	// Homo sapiens protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, mRNA. /// NM_032009 // intron // 0 // Hs.368160 // PCDHGA2 // 56113 // Homo	PCDHGA2	PCDHGA2, Homo sapiens protocadherin gamma subfamily A, 2 (PCDHGA2), transcript variant 1, q31.3
SNP_A-2183531	cagcagccccctacaa[C/G]tgcttcttatcactcc	C	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2148013	atggcttaagggtaag[A/G]cattttcagattcatg	A	G	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1349738 // Hs.335933 //	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138328	atccagcatatgtgaa[A/G]ggagaagttagaaagg	A	G	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2112115	aggatgtgctttaaaa[A/C]aatggtgcagtgtgtg	A	C	22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 110468 //	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2110533	aggacactgagtttta[C/T]agcacaattccaaaca	C	T	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 355527 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2010510	attgtatggcccatta[G/T]caaacagaacgcattc	G	T	Homo sapiens sorting nexin 25 (SNX25), mRNA. /// ENST00000264694 // intron // 0 // --- // --- // --- // --- ///	SNX25	SNX25, Homo sapiens sorting nexin 25 (SNX25), q35.1
SNP_A-1992870	gattgtctgctgggta[A/G]cttgatgaaagagggc	A	G	1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 250852 // Hs.417962 // DUSP4 // 1846 // Homo	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-2068881	acaatctataacaata[A/T]catcatactgctttga	A	T	// 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 121208 // Hs.546345 //	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-2055473	aataatataaaaatc[C/T]caaatcaagcctttga	C	T	Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// ENST00000282749 // intron // 0 // --- // --- // --- // ---	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2088960	acttaaaacagctctg[A/G]agaacaaaaatggtgc	A	G	// 10208 // Homo sapiens chromosome 13 open reading frame 22 (C13orf22), mRNA. /// NM_001629 // upstream //	C13orf22	C13orf22, Homo sapiens chromosome 13 open reading frame 22 (C13orf22), q12.3
SNP_A-2091804	agaaaatattacttag[C/G]attgcacatggtattg	C	G	Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1
SNP_A-2091183	actttgtgaattgtta[C/T]gtgtaggctgttgtat	C	T	51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 64812 // Hs.491997 // EYA1	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3
SNP_A-2260817	gaaactccctgacaca[C/T]catcatcttgcatcag	C	T	NM_181841 // upstream // 28475 // --- // --- // 0 // --- /// NM_032246 // downstream // 639156 // Hs.104744 // RKHD3	-	q25.1
SNP_A-2235003	ctcccaagatgcttcc[A/G]gaaatcaagcacgctg	A	G	MGC50104 // 341032 // Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), mRNA. ///	MGC50104	MGC50104, Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), q23.1
SNP_A-2235601	ctcctagaggatgttg[A/C]aatctttacttaggtc	A	C	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 90898	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2230996	ctatgtaaactcctgt[A/G]aaaactctcactgaag	A	G	ENST00000343352 // intron // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-2248533	ctgttaagttgtataa[C/T]gctgcatacgtgtaac	C	T	UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-2260556	gaaacataagctgaga[A/G]acttggaagacaaagg	A	G	ENST00000283141 // CDS // 0 // --- // --- // --- // ---	-	p24.2
SNP_A-2261415	gaaagctctggaacta[C/T]cacctgaagcttcaac	C	T	Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // --- // -	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-2260921	gaaacttcaaattacc[A/G]atgggcagaaactaat	A	G	10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 238152 // Hs.126575 //	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2272085	gaccctgtctccacac[A/G]caaagacagcaggcag	A	G	LOC90557 // 90557 // Homo sapiens hypothetical protein BC016861 (LOC90557), mRNA. /// ENST00000295171 //	LOC90557	LOC90557, Homo sapiens hypothetical protein BC016861 (LOC90557), q21.1
SNP_A-2276539	gagagggcagctatag[C/G]aattcttgtccaggag	C	G	ENST00000307248 // downstream // 97367 // --- // --- // --- // ---	-	q34
SNP_A-2277621	gagcactctgcctgca[C/T]gaactggggagaccta	C	T	/// ENST00000341422 // downstream // 245496 // --- // --- // ---	-	p33
SNP_A-2284525	gatcacagtaatctac[A/G]cacagctatcacacat	A	G	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 549308 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2292571	gcactgacctttacaa[A/G]tactgttctttagggt	A	G	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2290640	gcaagacaattccata[C/T]atttaggagtggaaag	C	T	// 202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 164734 // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2088608	actgtgaaccacagaa[A/G]tatagcccactcaact	A	G	8404 // Homo sapiens SPARC-like 1 (mast9, hevin) (SPARCL1), mRNA. /// NM_014208 // upstream // 40345 //	SPARCL1	SPARCL1, Homo sapiens SPARC-like 1 (mast9, hevin) (SPARCL1), q22.1
SNP_A-2080256	acctaagatagagaaa[C/T]attggtagtatgtgtg	C	T	1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream //	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2092241	agaaagactactatag[A/G]cactttgaagtcttca	A	G	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), mRNA. /// ENST00000279593 // intron // 0 // --- // --- // --- // ---	GRIN2B	GRIN2B, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), p13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2061538	tcttcccttcagggca[C/T]aagtgagcttctgaag	C	T	117159 // Homo sapiens dermcidin (DCD), mRNA. /// NM_058173 // upstream // 34627 // Hs.348419 // LOC118430	DCD	DCD, Homo sapiens dermcidin (DCD), q13.2
SNP_A-2074486	acatagagttgctgga[A/G]aaacagctcaggcaaa	A	G	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 592071 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2005217	atcctagcccttagtc[A/G]cagttcactggagctg	A	G	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2026582	aaacaacgtccaaaaa[A/G]gtattgtttcaacatt	A	G	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 689454 // --- // --- // --- //	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2031355	aaagggcttctgggaa[A/T]aaaagtgcagattaca	A	T	283078 // Homo sapiens chromosome 10 open reading frame 48 (C10orf48), mRNA. /// NM_018076 // downstream //	C10orf48	C10orf48, Homo sapiens chromosome 10 open reading frame 48 (C10orf48), p12.1
SNP_A-2108320	agctgagtgcaatttа[C/G]agcttgggctaactgg	C	G	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2135497	atatttgtgactggaa[C/T]gctagaaagagagatg	C	T	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1235117	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2124106	agttactttgaattga[C/T]gaaattaaattttctg	C	T	9984 // Homo sapiens THO complex 1 (THOC1), mRNA. /// NM_030781 // downstream // 15217 // Hs.464422 //	THOC1	THOC1, Homo sapiens THO complex 1 (THOC1), p11.32
SNP_A-2129533	atacacctgacagaaa[C/T]gggtgccacttttgac	C	T	Homo sapiens PRKC, apoptosis, WT1, regulator (PAWR), mRNA. /// ENST00000328827 // intron // 0 // --- // --- // --- // ---	PAWR	PAWR, Homo sapiens PRKC, apoptosis, WT1, regulator (PAWR), q21.2
SNP_A-2144321	atgagttcaattttcc[G/T]aagtctgcttgcaaaa	G	T	SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), mRNA. /// ENST00000318445 // downstream // 108175 // --- // --- // --- //	SLCO3A1	SLCO3A1, Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), q26.1
SNP_A-2146812	atgcttgtataaaata[C/T]gtgacaacaaatggag	C	T	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), mRNA. /// NM_001074 // intron // 0 // Hs.10319 // UGT2B7 // 7364 // Homo sapiens UDP	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2
SNP_A-2150568	atgtgaggattatcca[C/G]gtgaaactgcccttac	C	G	84665 // Homo sapiens myopalladin (FLJ14437), mRNA. /// NM_032578 // downstream // 3908 // Hs.55205 // MYPN //	MYPN	MYPN, Homo sapiens myopalladin (FLJ14437), q21.3
SNP_A-2161499	atttgctgccaggatc[A/G]ccagacaagtgactta	A	G	PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.2
SNP_A-2164948	caaactagagcgtggc[A/G]agattagcgtttcaga	A	G	// 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 245737	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-2188062	cagtcaggcaataggg[A/C]actcgactccctcaca	A	C	117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000332754 // downstream // 248790 // --- // --- // --- //	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-2195739	catgtaatttcactga[A/G]gaatcatggactcaca	A	G	/// ENST00000341956 // downstream // 39061 // --- // --- // ---	-	q26.33
SNP_A-2180973	cagaattttccagcac[A/T]gaatgttgtgatcagg	A	T	127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream //	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2168699	caagaatacttagtga[C/G]caattaaactacagca	C	G	Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // --- //	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-2225507	ctaaaagacttttaa[C/T]gtaaggcatatcagtt	C	T	126069 // Homo sapiens zinc finger protein 491 (ZNF491), mRNA. /// NM_152357 // upstream // 18036 // Hs.418192 //	ZNF491	ZNF491, Homo sapiens zinc finger protein 491 (ZNF491), p13.2
SNP_A-2225087	cgtgtggcctacaccc[A/G]gaagcagactcaatga	A	G	3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 4624 // Hs.36975 // FSHB // 2488	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-2213442	ccgggcttttcatttc[A/G]aggactgagtaggaag	A	G	130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 128765	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-2211281	ccctaatctcctaatc[C/T]agcatgacttcggtac	C	T	604 // Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), transcript variant 1, mRNA. ///	BCL6	BCL6, Homo sapiens B-cell CLL q27.3
SNP_A-2212184	ggcgtaagatgcacat[A/G]ttgtagcttgggaact	A	G	ENST00000267433 // intron // 0 // --- // --- // --- // ---	-	q21.2
SNP_A-1787851	gggactacggatcaga[C/T]gcatgccactatgcca	C	T	1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 300078 // --- // --- // --- // ---	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2
SNP_A-1853420	tattttctctcaaaaa[C/G]tttaataattcagctt	C	G	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // --- // --- // --- // ---	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1844169	tagtttattgatttac[C/G]aaagaaccagcagcca	C	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1831613	taattactttcacaaa[G/T]gtacatataaatgtac	G	T	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 4 (CACNA2D4), transcript variant 1, mRNA. ///	CACNA2D4	CACNA2D4, Homo sapiens calcium channel, voltage-dependent, alpha 2 p13.33
SNP_A-1828745	taagcttatctcagct[A/G]actcctcggaggtact	A	G	bridging integrator 2 (BIN2), mRNA. /// NM_016293 // CDS // 0 // Hs.14770 // BIN2 // 51411 // Homo sapiens bridging	-	-, Homo sapiens bridging integrator 2 (BIN2), q13.13
SNP_A-1972528	atgaaagtctacccaa[A/G]tctgaggtttgctata	A	G	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 55201 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1947086	tttaatatgaaaaaac[C/T]ctatgatctacaaatc	C	T	Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001001924 // intron // 0 // Hs.7946 //	MTUS1	MTUS1, Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, p22
SNP_A-1939621	ttgatttcagtctcac[A/G]agaacttggacagaga	A	G	Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // intron // 0 // Hs.337696 // SLC8A3 // 6547 //	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-1935731	ttctgtgagtacaaga[C/T]ggtctttgcaggtggc	C	T	/// ENST00000294916 // downstream // 21569 // --- // --- // ---	-	q43
SNP_A-1876006	tctgaagggtcagtcc[C/T]atttcaaaacaaactg	C	T	Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1902620	tggcgggggcacatat[A/G]atatactgagacacca	A	G	/// ENST00000359776 // upstream // 3662 // --- // --- // --- // ---	-	q12.1
SNP_A-1903023	tggctggtagagcgcc[A/C]aggccttctctttatg	A	C	C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 //	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-1921069	ttacaggtgagaatca[C/T]agataacagtcaatgg	C	T	129563 // Homo sapiens hypothetical protein MGC42174 (MGC42174), mRNA. /// ENST00000273009 // intron // 0 // ---	MGC42174	MGC42174, Homo sapiens hypothetical protein MGC42174 (MGC42174), q37.1
SNP_A-1919279	ttaagaagtgcaagcc[G/T]aagaagccagagtcag	G	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1899330	tggaacatttatcata[A/G]taacgccaatgtctac	A	G	Homo sapiens testis nuclear RNA-binding protein (Tenr), mRNA. /// ENST00000296513 // intron // 0 // --- // --- // --- // ---	Tenr	Tenr, Homo sapiens testis nuclear RNA-binding protein (Tenr), q27
SNP_A-1972837	attcctaaactgcaaa[C/T]atatgaagagaccaat	C	T	2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // upstream // 102406 // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1984155	caggggagtaggagaa[C/G]gcaaaggcctcagtca	C	G	-- /// ENST00000361117 // upstream // 768937 // --- // --- // ---	-	q33.2
SNP_A-1978383	agggttatttgccagg[C/T]atcctgagagccatca	C	T	LOC255743 // 255743 // Homo sapiens hypothetical protein LOC255743 (LOC255743), mRNA. /// NM_033115 //	LOC255743	LOC255743, Homo sapiens hypothetical protein LOC255743 (LOC255743), q24
SNP_A-1828701	taagctcctgcctttа[A/G]atgctgatgcttcctg	A	G	23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 438478	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1826657	taacactaaggaagaa[G/T]gtctaggaggtacaaa	G	T	Homo sapiens WW domain containing E3 ubiquitin protein ligase 1 (WWP1), mRNA. /// ENST00000265428 // intron // 0	WWP1	WWP1, Homo sapiens WW domain containing E3 ubiquitin protein ligase 1 (WWP1), q21.3
SNP_A-1839018	tagagaggcctgagaa[G/T]gaattctgactgtagg	G	T	transforming growth factor-beta 1 binding protein mRNA, complete cds. /// NM_000627 // intron // 0 // Hs.49787 //	LTBP1	LTBP1, Human transforming growth factor-beta 1 binding protein complete cds. p22.3
SNP_A-1808456	gtgaaactgttggcct[C/G]aaatggtcctcccact	C	G	Homo sapiens HBxAg transactivated protein 2 (XTP2), mRNA. /// ENST00000338920 // intron // 0 // --- // --- // --- // ---	BAT2D1	BAT2D1, Homo sapiens HBxAg transactivated protein 2 (XTP2), q24.3
SNP_A-1720497	gtcatttggattcttactgaaggta[C/T]acaattagcctacggatgatgaccc	C	T	// 6885 // mitogen-activated protein kinase kinase kinase 7 /// NM_004440 // downstream // 1620652 // Hs.73962 // EPHA7	MAP3K7	MAP3K7 , rs369910, mitogen-activated protein kinase kinase kinase 7 ,q15
SNP_A-1784255	ggcccacggtgcactg[A/C]aggaagcacaattgta	A	C	COMMD10 // 51397 // Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// NM_020796 //	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-1784631	ggcctcataggaagac[A/G]cttggtcattctatga	A	G	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.31
SNP_A-2207093	ccattaaacattttca[A/G]agccaaagaaagtcag	A	G	1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream //	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-2181924	cagagctactttgata[A/C]ccagttcagaaagcag	A	C	// 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// NM_181354 // upstream // 163950 //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2188916	cagtgtatgcggttca[A/G]gagggtaaccaatcac	A	G	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- //--- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2190764	catagaatcctactta[C/T]gattccaagttatttc	C	T	7184 // Homo sapiens tumor rejection antigen (gp96) 1 (TRA1), mRNA. /// ENST00000344460 // upstream // 45181 //	TRA1	TRA1, Homo sapiens tumor rejection antigen (gp96) 1 (TRA1), q23.3
SNP_A-2163565	caaaaacataaaaatt[A/T]aaaaaatgctgacagg	A	T	10513 // Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA. /// NM_003620 // upstream // 15991 // Hs.286073 // PPM1D //	APPBP2	APPBP2, Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), q23.2
SNP_A-2151593	atgttgataattgtca[A/G]gaagcaaaatgaaata	A	G	/// ENST00000316807 // downstream // 1651 // --- // --- // --- //	-	q13.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2129644	atacagattttaattc[A/G]aagtacatttcaagga	A	G	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // intron // 0 // --- // --- // --- // ---	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-2124457	agttcagcacaaggga[C/T]gaaacaagggggtaga	C	T	94033 // Homo sapiens ferritin mitochondrial (FTMT), mRNA. /// NM_152546 // upstream // 85502 // Hs.107622 //	FTMT	FTMT, Homo sapiens ferritin mitochondrial (FTMT), q23.1
SNP_A-2036539	aaattgagttggatca[A/T]gaggcacttacaatgg	A	T	9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 9390 // Hs.458423 //	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-2034023	aaatcagagaagaaca[A/G]agggctttgcaaggca	A	G	6310 // Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // upstream // 274341 // --- // --- // --- // ---	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3
SNP_A-2069343	acacaaacttaactga[C/G]ccattgaggaacagtt	C	G	// 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2083849	actacggactgaatta[G/T]gtccctgcccaaatcc	G	T	Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2084802	actcaaaaatgttacc[C/G]gaagtgcatttttttaa	C	G	MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 523097 // Hs.463978 //	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2087002	actgaggcttaaaaaa[A/G]taataattggccagtc	A	G	59345 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA. /// NM_004301 // upstream // 88887 // Hs.435326 // ACTL6A // 86 // Homo	GNB4	GNB4, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), q26.32
SNP_A-2297680	gccagctagaagccga[C/T]ggtcagtactcgttta	C	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 941654 // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p21.1
SNP_A-2285338	gatctgcttggaagca[C/T]agagaaaaggaccatg	C	T	Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // --- // --- //	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine q23.1
SNP_A-2285101	agagtcatataagagc[A/G]ctatctttaaatgact	A	G	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // intron // 0 // Hs.511504 // TCF12 // 6938 //	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-2243844	ctgctggaatggacaa[A/G]aatgctttaaaacaaa	A	G	54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 37724 // --- //	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2229677	ctagtagtaatgctta[A/G]caacaataaaaattac	A	G	Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // intron // 0 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2239228	attgactggtgccaaa[C/G]gggaaacttttggaaa	C	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2246760	ctgtacttcactctta[C/G]aaagtctttgttttttt	C	G	9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA. /// NM_004904 // downstream //	CREB5	CREB5, Homo sapiens cAMP responsive element binding protein 5 (CREB5), p15.1
SNP_A-2260955	gaaagaaaaattaagg[A/T]aagtgaggagagtggg	A	T	/// ENST00000341422 // downstream // 1425 // --- // --- // --- //	-	p33
SNP_A-2299674	ctgagatcatactggt[A/T]acaactgtcacaaaat	A	T	161502 // Homo sapiens chromosome 15 open reading frame 26 (C15orf26), mRNA. /// NM_172217 // upstream //	C15orf26	C15orf26, Homo sapiens chromosome 15 open reading frame 26 (C15orf26), q25.1
SNP_A-2305410	gctgatcttgccaaga[C/T]gcaaaattgtaggccc	C	T	11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2069497	acacaatgctggaggt[A/T]aaggtaataaatattt	A	T	8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 341814	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2076811	accaaaagtgtgaaat[A/G]aatcaacgaatttgtt	A	G	10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 133068 // Hs.489615 // PBEF1 // 10135 // Homo	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-2076383	acattggtttgaagaa[A/G]ggatttcatgagattc	A	G	/// ENST00000334919 // upstream // 1195632 // --- // --- // --- // --- /// ENST00000322194 // downstream // 573517 // --- // --- //	-	q12.2
SNP_A-2031752	tttaatgtggagttca[C/T]gtaactttgaagatag	C	T	Homo sapiens myeloid inhibitory C-type lectin-like receptor (MICL), transcript variant 2, mRNA. /// NM_138337 // CDS // 0 // Hs.190519 // CLEC12A // 160364 // Homo sapiens myeloid	CLEC12A	CLEC12A, Homo sapiens myeloid inhibitory C-type lectin-like receptor (MICL), transcript variant 2, p13.31
SNP_A-1992957	acttaggtggcaaata[C/T]gaaaattattataagt	C	T	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1994856	atgttcaacatatgat[C/G]aatcaagacctgggtt	C	G	// 4982 // Homo sapiens tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA. /// NM_006438 // upstream // 69185 // Hs.176615 //	TNFRSF11B	TNFRSF11B, Homo sapiens tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), q24.12
SNP_A-2007251	aatgcctattgttaca[C/T]atgattgctagcgata	C	T	Homo sapiens hypothetical protein MGC35023 (MGC35023), mRNA. /// ENST00000318405 // downstream // 40567 // --- //	-	-, Homo sapiens hypothetical protein MGC35023 (MGC35023), p12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017347	ttgaactagccttcca[C/T]acctgaaataaatcat	C	T	11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 327973 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT ,q21.3
SNP_A-2132584	atagttagctttaaaa[G/T]ttgtaggcaaaagtcc	G	T	Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // --- // --- // --- // ---	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-2139522	atcctttcaatctgca[A/G]gacttttacttctctt	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1182175 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2196648	cattaagaaaaatagc[A/G]cttaagtcagtggtgt	A	G	Homo sapiens dedicator of cytokinesis 8 (DOCK8), mRNA. /// ENST00000287364 // intron // 0 // --- // --- // --- // ---	DOCK8	DOCK8, Homo sapiens dedicator of cytokinesis 8 (DOCK8), p24.3
SNP_A-2194511	catgcaatcatttaac[A/T]aatattcactaatcat	A	T	Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000358603 // intron // 0 // --- // --- // --- // ---	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-2177680	cacgggttggcattga[C/T]gggtatggcttttcca	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2209486	cccatcattcttccta[A/G]acaagagactattgaa	A	G	Homo sapiens hypothetical protein FLJ30834 (FLJ30834), mRNA. /// ENST00000337677 // 5UTR // 0 // --- // --- // --- // ---	FLJ30834	FLJ30834, Homo sapiens hypothetical protein FLJ30834 (FLJ30834), q27
SNP_A-2212644	cccttcctctcctata[C/T]gcacgtgtggtcccta	C	T	ENST00000339762 // intron // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-2212577	cccttcaacggcttat[A/G]aagtatagtaacatcc	A	G	ALS2CR7 // 65061 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7 (ALS2CR7), mRNA. /// NM_003507 // upstream // 31788 //	ALS2CR7	ALS2CR7, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7 (ALS2CR7), q33.1
SNP_A-2214360	cctacctataatgtca[C/G]gctccaccttgccagc	C	G	// 387700 // Homo sapiens similar monocarboxylate transporter (LOC387700), mRNA. /// NM_148978 // downstream // 34964 // Hs.465933 // PANK1 // 53354 //	LOC387700	LOC387700, Homo sapiens similar monocarboxylate transporter (LOC387700), q23.31
SNP_A-1681966	aagtgacactggccctaatcagtgc[A/C]ttctaataggaggtacataatgtca	A	C	// 51000 // solute carrier family 35, member B3 /// NM_153003 // downstream // 916305 // Hs.382068 // OFCC1	SLC35B3	SLC35B3 , rs446710, solute carrier family 35, member B3 ,p24.3
SNP_A-1803452	gtatttggaaagaata[C/T]aatgctattggtttta	C	T	Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // ---	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-1798271	gtaaagatctggctag[A/G]ctaccagtttaagatg	A	G	HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 89700 // Hs.48384 //	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-1837473	tacttgaaatgtgtgc[C/T]aatgtccacagtcttt	C	T	ENST00000259335 // intron // 0 // --- // --- // ---	-	q31.3
SNP_A-1873738	tctcagaccagtggga[G/T]agaccagcagggttag	G	T	10578 // Homo sapiens granulysin (GNLY), transcript variant NKG5, mRNA. /// NM_012483 // downstream // 262 //	GNLY	GNLY, Homo sapiens granulysin (GNLY), transcript variant NKG5, p11.2
SNP_A-1873230	tctatttatagccaaa[A/G]gatggctgctttccat	A	G	5019 // Homo sapiens 3-oxoacid CoA transferase 1 (OXCT1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000321394 // upstream // 53041 // --- // --- // --- // ---	OXCT1	OXCT1, Homo sapiens 3-oxoacid CoA transferase 1 (OXCT1), nuclear gene encoding mitochondrial protein, p13.1
SNP_A-1972117	taaaaatccagcaggc[A/G]attggtttgcttccaa	A	G	7155 // Homo sapiens topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA. /// NM_018297 // downstream // 14522 //	TOP2B	TOP2B, Homo sapiens topoisomerase (DNA) II beta 180kDa (TOP2B), p24.2
SNP_A-1955691	tttgtaatatgtctac[A/G]aagtttggttctccag	A	G	Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // --- // --- // --- // ---	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1895723	tgcctcttgttggcta[C/T]aggatagaagctgtag	C	T	ENST00000340052 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-1901633	tggcaagaaacctcta[C/T]agaccaggcacttgga	C	T	Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1909697	tgtcaagttcagaggc[A/G]agaaggtggaggagat	A	G	124857 // Homo sapiens WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	WFIKKN2	WFIKKN2, Homo sapiens WAP, follistatin,q21.33
SNP_A-1955908	tttgtcagggcttaac[A/G]gtcatccactgaatga	A	G	133522 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, beta (PPARGC1B), mRNA. /// ENST00000309241 // intron // 0 // --- // --- // --- // --- ///	PPARGC1B	PPARGC1B, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, beta (PPARGC1B), q32
SNP_A-1942012	tcctgaattttagatg[A/G]agtcagatgtgagttc	A	G	Homo sapiens inactive EMR4 mRNA, complete sequence. /// ENST00000335052 // intron // 0 // --- // --- // --- // --- ///	EMR4	EMR4, Homo sapiens inactive EMR4 complete sequence. p13.2
SNP_A-1968102	gcacagggtaggagaa[C/G]taagggcccttgagga	C	G	sapiens CD1B antigen, b polypeptide (CD1B), mRNA. /// ENST00000289434 // intron // 0 // --- // --- // --- // ---	CD1B	CD1B, Homo sapiens CD1B antigen, b polypeptide (CD1B), q23.1
SNP_A-1989294	agcacaatgcaagttc[A/G]ataatcactggaaata	A	G	Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // --- // ---	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864746	tccagctacactcaac[A/G]catttcaccccacccc	A	G	Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), mRNA. /// ENST00000316427 // intron // 0 // --- // --- // --- // ---	NOTCH4	NOTCH4, Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), p21.32
SNP_A-1864913	tccagggctccacaga[A/C]aaataatctaaaatga	A	C	Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-1852567	tatttagtcttttgta[A/G]aacacttcaagaagaa	A	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1847305	tatccagtctaccacc[A/G]atcagcacttaagttg	A	G	// 84692 // Homo sapiens testes development-related NYD-SP17 (NYD-SP17), mRNA. /// ENST00000355304 //	NYD-SP17	NYD-SP17, Homo sapiens testes development-related NYD-SP17 (NYD-SP17), q13.12
SNP_A-1840233	tagcaggagcaaatca[G/T]gaaatccaattgaaaa	G	T	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 573634 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1842427	taggtcttcctggaac[C/T]gtgccaaaaagagaaa	C	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1827280	taaccttgtactggac[A/C]accttactggcacttg	A	C	UQCRFS1 // 7386 // Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), mRNA. /// ENST00000327999 // upstream // 809 // --- // --- // -	UQCRFS1	UQCRFS1, Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), q12
SNP_A-1819787	gttgtgaaggtgatga[A/G]agggccagcgttgact	A	G	Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /// ENST00000261488 // intron // 0 // --- // --- // --- // ---	FLJ10094	FLJ10094, Homo sapiens hypothetical protein FLJ10094 (FLJ10094), q14.11
SNP_A-1796549	ggttacagacaaactc[A/G]gacatgttcagccctc	A	G	sapiens ubiquitin specific protease 4 (proto-oncogene) (USP4), transcript variant 2, mRNA. /// NM_003363 // CDS // 0 // Hs.77500 // USP4 // 7375 // Homo sapiens ubiquitin	USP4	USP4, Homo sapiens ubiquitin specific protease 4 (proto-oncogene) (USP4), transcript variant 2, p21.31
SNP_A-1797088	ggttgaaaatgaggtc[A/G]aatatctgttaaaacc	A	G	Homo sapiens NADPH oxidase 4 (NOX4), mRNA. /// ENST00000343727 // intron // 0 // --- // --- // --- // --- ///	NOX4	NOX4, Homo sapiens NADPH oxidase 4 (NOX4), q14.3
SNP_A-1802060	gtatacagttaaaatc[A/C]aattgaactaaatagc	A	C	Homo sapiens matrilin 2 (MATN2), transcript variant 1, mRNA. /// NM_030583 // intron // 0 // Hs.189445 // MATN2 //	MATN2	MATN2, Homo sapiens matrilin 2 (MATN2), transcript variant 1, q22.1
SNP_A-1813682	gtgtacctgagctgta[A/G]agatgtttagtcttag	A	G	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3,	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-1708759	aaaggtttctgtagctaatactcta[C/T]ggactgaaacacaataaaattcaac	C	T	NM_145016 // 5UTR // 0 // Hs.254271 // BXMAS2-10 // 219970 // BXMAS2-10	BXMAS2-10	BXMAS2-10 , rs1943282, BXMAS2-10,q12.1
SNP_A-1701225	atctttcttctaattcatcatcgga[A/C]aatatccaggagccaggctagaaaa	A	C	50508 // NADPH oxidase 3 /// NM_020732 // upstream // 684545 // Hs.436008 // ARID1B // 57492 // AT rich interactive	NOX3	NOX3 , rs921298, NADPH oxidase 3 ,q25.3
SNP_A-2214556	cctagacatcaggcaa[G/T]ttgcccaccaagaaag	G	T	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2227058	ctaatgtctttataca[C/T]tggaagcagcagaaaa	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1831172 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2207441	ccattgtaatgtttca[C/T]agttaacttggagtat	C	T	Homo sapiens RNA binding motif protein 6 (RBM6), mRNA. /// ENST00000266022 // intron // 0 // --- // --- // ---	RBM6	RBM6, Homo sapiens RNA binding motif protein 6 (RBM6), p21.31
SNP_A-2205117	ccaggttataaccaga[A/T]cttccctggcagggcg	A	T	Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // --- // --- // --- // ---	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-2179503	cacttactttctctac[C/T]ctgcgtcaaggattgt	C	T	ENST00000330888 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2194434	catgattgtagaacca[A/G]gtgttagctgggaaag	A	G	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2149347	atgtacacttaaatta[C/G]gcatattttatgtact	C	G	// 63973 // Homo sapiens neurogenin 2 (NEUROG2), mRNA. /// NM_138698 // downstream // 8463 // Hs.444338 //	NEUROG2	NEUROG2, Homo sapiens neurogenin 2 (NEUROG2), q25
SNP_A-2119105	agtagcaagaagaaac[C/T]ggtaagaagccttggg	C	T	sapiens astrotactin (ASTN), transcript variant 1, mRNA. /// ENST00000281881 // intron // 0 // --- // --- // --- // ---	ASTN	ASTN, Homo sapiens astrotactin (ASTN), transcript variant 1, q25.2
SNP_A-2116786	aggtcggtggtagaac[C/T]aggaaggcccatgtca	C	T	388 // Homo sapiens ras homolog gene family, member B (RHOB), mRNA. /// NM_022460 // downstream // 20407 //	RHOB	RHOB, Homo sapiens ras homolog gene family, member B (RHOB), p24.1
SNP_A-2117093	aggtgatattcaaagg[A/G]agggaatccagacctc	A	G	FLJ22789 // 84190 // Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// NM_152588 // upstream //	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-2058538	aatcagatagtgttag[C/T]ccttcaagtttattat	C	T	Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // intron // 0 // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. q14.2
SNP_A-2054121	aagttcatgcttccac[A/G]cggaaaggtttttcct	A	G	1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 58016 // --- //	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2078089	accaggcagcctaaga[C/T]gatagaagatggaaga	C	T	Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.33
SNP_A-2308239	gcttggccagtcacta[C/G]aatgggtggatattaa	C	G	Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2313239	ggagacaaaaccacac[A/G]aactccagaggccggg	A	G	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA. /// NM_022802 // intron // 0 //	CTBP2	CTBP2, Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, q26.13
SNP_A-2281556	gagtcccctccagcaa[C/G]aaggccctcattagat	C	G	490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 131787 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-2276936	gagatccagaaaccaa[A/G]tataaaagagctgcag	A	G	// 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 //	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-2274580	gagaaaagaaattgta[C/T]agattgcctccaaagg	C	T	/// ENST00000324709 // upstream // 66390 // --- // --- // --- // --- /// ENST00000359360 // downstream // 75576 // --- // --- // ---	-	q12.2
SNP_A-2274806	gagaaatagggataga[A/G]aacaacccaggcagag	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 569671 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2286110	gatgcaaacttgacag[G/T]ctccctgggtaatcaa	G	T	143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // ---	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-2245240	ctggctcaggagctga[A/G]ggtcactcaaacctga	A	G	// 147495 // Homo sapiens adenomatosis polyposis coli down-regulated 1 (APCDD1), mRNA. /// NM_153000 // downstream // 5149 // Hs.293274 // APCDD1 // 147495 // Homo sapiens	APCDD1	APCDD1, Homo sapiens adenomatosis polyposis coli down-regulated 1 (APCDD1), p11.22
SNP_A-2239355	ctctttcatcttacaa[C/G]tagcaatgttctatgc	C	G	ALDH8A1 // 64577 // Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 209664 //	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2
SNP_A-2232182	ctcaataaatgttcac[C/T]cttccctcacctattt	C	T	// 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 //	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-2231357	ctattcttgtcgactc[A/G]aaaaccagacaaatga	A	G	Homo sapiens chromosome 5 open reading frame 11 (C5orf11), mRNA. /// ENST00000274382 // intron // 0 // --- // ---	LIX1	LIX1, Homo sapiens chromosome 5 open reading frame 11 (C5orf11), q15
SNP_A-2081639	accttagtgtcctatc[C/T]accttcttgggtcaat	C	T	– /// ENST00000356117 // downstream // 567138 // --- // --- //	-	q23.31
SNP_A-2056922	aatagtactttagaga[C/T]aatcaaatcccacccc	C	T	// Homo sapiens olfactory receptor, family 6, subfamily T, member 1 (OR6T1), mRNA. /// NM_001004474 //	OR6T1	OR6T1, Homo sapiens olfactory receptor, family 6, subfamily T, member 1 (OR6T1), q24.1
SNP_A-2072815	acagctgccagatggt[A/G]aaacttctgtgcctaa	A	G	Homo sapiens EMI domain containing 2 (EMID2), mRNA. /// ENST00000313669 // intron // 0 // --- // --- // --- // ---	EMID2	EMID2, Homo sapiens EMI domain containing 2 (EMID2), q22.1
SNP_A-2016725	acaaaaatgtacaaaa[C/T]ctcatcttccatcgaa	C	T	// 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 733047 // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2006258	gtgtgcagacacttga[A/G]ggaacagggctcagac	A	G	// Homo sapiens xanthine dehydrogenase (XDH), mRNA. /// ENST00000272274 // downstream // 24810 // --- // --- // --- // ---	XDH	XDH, Homo sapiens xanthine dehydrogenase (XDH), p23.1
SNP_A-2030151	aaagcaagcagcagaa[A/G]aagattacggttgaat	A	G	23670 // Homo sapiens transmembrane protein 2 (TMEM2), mRNA. /// ENST00000325310 // upstream // 71579 // --- // ---	TMEM2	TMEM2, Homo sapiens transmembrane protein 2 (TMEM2), q21.13
SNP_A-2023916	aaaagaatgagaaata[C/T]gtaagcaaaaatgaga	C	T	// 137970 // Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), mRNA. /// ENST00000287272 // downstream //	UNC5D	UNC5D, Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), p12
SNP_A-2040105	aaccaaatctatgttg[C/T]attcaaactctcaagt	C	T	// 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2142249	atgaaaaggatgcaga[A/G]cgagtggaagccatga	A	G	FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 //	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2143283	atgacagattaatctc[A/G]ccattaaaaattaaag	A	G	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 214696 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2164084	caaaagccagcaacga[C/T]accagcttaaatattc	C	T	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2192178	catcagattgtgttga[A/G]agcaatgaagaaatta	A	G	ENST00000357709 // intron // 0 // --- // --- // ---	-	q21.3
SNP_A-2176037	caccaagtccagttct[C/T]aactgaatgacagcag	C	T	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 84666 // Hs.33368 // MCTP2 // 55784 // Homo	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2202291	ccaccacaactggcaa[C/T]gtttttatttttttgt	C	T	// 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 250769 // Hs.268515	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1675555	agttcttgagtaaaaatatttcaac[A/G]agataaatgaggccatatctatctg	A	G	NM_032151 // intron // 0 // Hs.5038 // DCOHM // 84105 // dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle	DCOHM	DCOHM , rs10515466, dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle,q31.1
SNP_A-1737403	acttctccaaaatgataaagcacca[A/C]ctaaatttcattaaaagaactgata	A	C	79627 // opioid growth factor receptor-like 1 /// NM_024882 // downstream // 107847 // Hs.368337 // C6orf155 // 79940 //	OGFRL1	OGFRL1 , rs9294899, opioid growth factor receptor-like 1 ,q13
SNP_A-1742767	aaagatggtgaagttgaagaaatat[G/T]aagcctaagtatttgctgcagcttt	G	T	// 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 922105 // Hs.234790 // CNTN5 // 53942 //	JRKL	JRKL , rs652531, jerky homolog-like (mouse) ,q22.1
SNP_A-1821494	gtttgggtctcacatc[C/T]ccccttatatccatat	C	T	sapiens olfactory receptor, family 52, subfamily A, member 1 (OR52A1), mRNA. /// NM_001005222 // CDS // 0 // --- // OR52A4 // 390053 // Homo sapiens olfactory receptor, family	OR52A1	OR52A1, Homo sapiens olfactory receptor, family 52, subfamily A, member 1 (OR52A1), p15.4
SNP_A-1830232	taatagtagcttccta[A/T]aaatcccactagactt	A	T	sapiens cardiomyopathy associated 5 (CMYA5), mRNA. /// ENST00000238522 // intron // 0 // --- // --- // --- // ---	-	-, Homo sapiens cardiomyopathy associated 5 (CMYA5), q14.1
SNP_A-1986939	agaacacttatgggaa[C/T]gtcaactgatccaggg	C	T	// 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 54495 //	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1962286	aggtcataatatagaa[C/T]agtgagcttggaacaa	C	T	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1973414	aaaaatggcataaaat[G/T]agtttcctgattattc	G	T	Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// ENST00000264326 // intron // 0 // --- // --- // --- // ---	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1925975	ttatgtagccaaactg[A/G]attcaaatccgggggc	A	G	Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-1886994	tgacttgatcacatca[C/T]ctaacctatctctaag	C	T	Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1904390	tgggcttttctcaaaa[C/G]gatggctgacagccgt	C	G	2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream //	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1897807	tgctggagttagggca[C/T]gaatccaggcagttgg	C	T	Homo sapiens hypothetical protein FLJ10305 (FLJ10305), mRNA. /// ENST00000261776 // intron // 0 // --- // --- // --- // ---	VAC14	VAC14, Homo sapiens hypothetical protein FLJ10305 (FLJ10305), q22.1
SNP_A-1924242	ttagtttttctacaaa[C/T]tcacaaaagtattgag	C	T	Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// ENST00000322953 // intron // 0 // --- // ---	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1963632	aaacagatccgatggg[C/T]atatcgcctggataaa	C	T	// 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 75168 // Hs.353022 // ETAA16 //	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1984746	ctaacttgaagtctga[C/T]cctttataccagaact	C	T	4245 // Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA. /// ENST00000307832 // upstream // 46820 // --- // --- // --- // ---	MGAT1	MGAT1, Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), q35.3
SNP_A-1985932	tctccctaaatttcga[A/T]ctttgaattctctcca	A	T	// 80118 // Homo sapiens hypothetical protein FLJ22684 (FLJ22684), mRNA. /// NM_014452 // downstream // 4820 //	FLJ22684	FLJ22684, Homo sapiens hypothetical protein FLJ22684 (FLJ22684), p12.3
SNP_A-1947832	tttacttaggactttg[G/T]aaagatagcaaaacaa	G	T	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 340456 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-1944738	ttgtgattctgaataa[C/T]atttttttccaacatta	C	T	1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 77612 // Hs.72901 // CDKN2B //	CDKN2B	CDKN2B, Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3
SNP_A-1944499	ttgtcttaataaagac[A/T]gaaaatgcttcagcgt	A	T	sapiens leptin (obesity homolog, mouse) (LEP), mRNA. /// ENST00000308868 // intron // 0 // --- // --- // --- // ---	LEP	LEP, Homo sapiens leptin (obesity homolog, mouse) (LEP), q32.1
SNP_A-1818075	gttctcacttttgaa[A/G]tcatgtataggaaggc	A	G	163223 // Homo sapiens similar to Zinc finger protein 208 (LOC163223), mRNA. /// NM_178523 // intron // 0 //	LOC163223	LOC163223, Homo sapiens similar to Zinc finger protein 208 (LOC163223), p12
SNP_A-1824742	taaagagcaatggtga[C/G]ctagaaaagacagatc	C	G	Homo sapiens Cbl-interacting protein Sts-1 (STS-1), mRNA. /// ENST00000284273 // intron // 0 // --- // --- // --- // ---	STS-1	STS-1, Homo sapiens Cbl-interacting protein Sts-1 (STS-1), q24.1
SNP_A-1848481	tatgaatatacacaca[A/C]ctatactgggaattct	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 3001390 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1852937	tatttctttatgatac[A/G]acgatttatatttctt	A	G	143162 // Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), mRNA. /// NM_139046 // upstream // 135752 //	FRMPD2	FRMPD2, Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), q11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1862883	tcattgaataatgcaa[A/G]ctagaattatatgaaa	A	G	Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // intron // 0 // Hs.47288 // TRPM3 // 80036 //	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.11
SNP_A-1718593	gagcgagatgccaatttctttgaca[C/T]gctatctttcagactgggccattgc	C	T	NM_002465 // intron // 0 // Hs.169849 // MYBPC1 // 4604 // myosin binding protein C, slow type	MYBPC1	MYBPC1 , rs7308665, myosin binding protein C, slow type,q23.2
SNP_A-1714018	gtgtttggaaggtgctgcacgagac[A/C]aattttgtttttaagaggtgaggac	A	C	8848 // transforming growth factor beta 1 induced transcript 4 /// NM_012345 // downstream // 233918 // Hs.120247 //	TGFB1I4	TGFB1I4 , rs10507531, transforming growth factor beta 1 induced transcript 4 ,q14.12
SNP_A-1706253	tgggacacaatccaagtatagggcc[A/G]ttgaaaaacacacgtaaaaaatcac	A	G	4045 // limbic system-associated membrane protein /// NM_152538 // downstream // 15532 // Hs.6658 // IGSF11 //	LSAMP	LSAMP , rs1464413, limbic system-associated membrane protein ,q13.32
SNP_A-2201536	ccaattagacaataag[C/G]ctggcatcttactgag	C	G	/// ENST00000311164 // upstream // 21201 // --- // --- // --- // ---	-	q24.1
SNP_A-2207330	ccattctgattttgcc[C/G]aaatgaaaaagtggtg	C	G	// Homo sapiens son of sevenless homolog 2 (Drosophila) (SOS2), mRNA. /// NM_024884 // downstream // 13565 //	SOS2	SOS2, Homo sapiens son of sevenless homolog 2 (Drosophila) (SOS2), q21.3
SNP_A-2226856	ctaatatatttgagta[A/G]atgaaccttaaaatac	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2222633	cgagtttctattttca[A/T]ccttctgaaacctcct	A	T	// Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 99170 // Hs.451286 // C15orf2 //	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-2173988	cacacatggagacaag[C/G]aagggaacaacagaca	C	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2192723	gattcagggacctcca[C/T]ataatgcactgcacac	C	T	OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 //	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-2189074	cagttaaatgagacta[C/T]gtgtgtaattatcagt	C	T	Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-2152021	atgttttttatcacac[C/T]catgaaaagcagaatc	C	T	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2034628	aaatgaaaactttgca[A/T]cggaagaaaaacgagc	A	T	122742 // Homo sapiens olfactory receptor, family 4, subfamily L, member 1 (OR4L1), mRNA. /// NM_001004715	OR4L1	OR4L1, Homo sapiens olfactory receptor, family 4, subfamily L, member 1 (OR4L1), q11.2
SNP_A-2005800	tttcatttttggagcc[A/G]gagcaccctctttttc	A	G	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 480328 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2012103	taaacccttgacctg[A/C]agagtcttatcattct	A	C	Homo sapiens Abelson helper integration site (AHI1), mRNA. /// ENST00000265602 // intron // 0 // --- // --- // --- // ---	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3
SNP_A-1991109	agatgacacctggata[A/C]aaatttctgctctact	A	C	6561 // Homo sapiens solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1), mRNA. /// NM_178827 //	SLC13A1	SLC13A1, Homo sapiens solute carrier family 13 (sodium,q31.32
SNP_A-2002944	gcacaatggatgctca[A/G]tagatgctaattacca	A	G	8738 // Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// NM_003805 // downstream // 68617 // Hs.38533 // CRADD // 8738 //	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-2073034	acaggaggtcagcaag[A/T]ctggtatcacaagtta	A	T	// 26509 // Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // downstream // 31745 // Hs.500572 // FER1L3 // 26509 //	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-2073070	acaggatcaatcaatc[C/T]gaaacctcatcatcat	C	T	Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // intron // 0 // Hs.268707 // CNTN5 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2075148	acatctagtctaactc[C/T]caatttgtgaaagagt	C	T	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2063647	aattacggattactca[C/G]aaaagggccaatattt	C	G	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2079895	accctgtgttcacaaa[G/T]gcagagagtcagaccc	G	T	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-delta9-10-11b, mRNA. /// NM_007295 // 3UTR // 0 // Hs.194143 // BRCA1 // 672 //	BRCA1	BRCA1, Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-delta9-10-11b, q21.31
SNP_A-2099944	agagtcattaaaatta[A/G]cacatctagatccgag	A	G	// 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 536105 // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-2101587	agatgagcccactgga[C/T]tcaaagataagtggaa	C	T	Homo sapiens dedicator of cytokinesis 2 (DOCK2), mRNA. /// ENST00000256935 // intron // 0 // --- // --- // --- // ---	DOCK2	DOCK2, Homo sapiens dedicator of cytokinesis 2 (DOCK2), q35.1
SNP_A-2107373	agctacacagcttttta[C/T]atggcagagccagggc	C	T	ENST00000303635 // intron // 0 // --- // --- // --- // ---	-	p36.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238744	ctcttaatagcaacta[C/T]gtataggagttccctc	C	T	// 64332 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, /// NM_175056 // upstream // 514195 // Hs.352213 // LOC1313	NFKBIZ	NFKBIZ, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, q12.3
SNP_A-2240493	ctgacatctgactgca[A/G]ctgtgtaggagatcca	A	G	54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 45650 // Hs.464079	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-2242355	ctgcacccagaagata[A/T]aatttttcagcacatg	A	T	51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// ENST00000346248 // intron //	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-2251388	cttcacaaaatgtgcc[A/G]agacctatatgaagtc	A	G	57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 177148 // Hs.130356 //	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-2287645	gattaagtcctgttga[C/T]agtatgtactgtgata	C	T	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 344418 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. ,q23.1
SNP_A-2274528	gagaaaaaagcttgga[A/C]atcatccaagttctcc	A	C	FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2276490	gagaggcctcgggaga[A/C]accaacgtggccgaca	A	C	80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// NM_003357 // upstream // 25199 // Hs.523732 //	ASRGL1	ASRGL1, Homo sapiens asparaginase like 1 (ASRGL1), q12.3
SNP_A-2262849	gaacaaaatatactac[C/T]acatgatactacattc	C	T	// Homo sapiens hypothetical protein FLJ39599 (FLJ39599), mRNA. /// ENST00000287594 // intron // 0 // --- // --- // --- // ---	FLJ39599	FLJ39599, Homo sapiens hypothetical protein FLJ39599 (FLJ39599), p13.11
SNP_A-2298641	gcccagaatggagggg[G/T]atcctggaatacaaga	G	T	83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 61609 // Hs.432458 // PRG4 //	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2301530	gcgagaggtcatttgc[A/G]atggcagtaatgggtt	A	G	7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// NM_016617 // upstream // 361673 // Hs.524969 // Ufm1 //	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2300983	gcctgttttccacatg[C/G]atttctgccctttgtg	C	G	ENST00000314630 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2296132	gcattcatggccccca[A/T]aatacagtggcggtgg	A	T	Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA. /// ENST00000303236 // intron // 0 // --- // --- // --- // ---	EIF2AK3	EIF2AK3, Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), p11.2
SNP_A-2272246	gacctcaggagccttc[A/G]cctcggtctcctcctc	A	G	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 372406 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2285977	gatgatacatttggta[C/T]ggagagaaaaactatg	C	T	ENST00000272427 // intron // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-2235071	ctcccagcgcaaacтt[A/C]aagagacagggctttg	A	C	ENST00000359057 // CDS // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-2234764	ctccagtcccaaagat[C/G]atacaaaatatttatt	C	G	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2679719 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2073264	acagggcagatatatg[C/G]aatgctttttggaata	C	G	// 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// NM_001001317 //	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2055734	aataattctgatctac[C/T]ctgagctaagaaactt	C	T	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2060945	aatgatgctttcttca[A/G]tattcctgtgacagtc	A	G	54970 // Homo sapiens tetratricopeptide repeat domain 12, mRNA (cDNA clone MGC:40285 IMAGE:5219117), complete cds. /// NM_017868 // downstream // 12492 // Hs.288772 //	TTC12	TTC12, Homo sapiens tetratricopeptide repeat domain 12, (cDNA clone MGC:40285 IMAGE:5219117), complete cds. ,q23.2
SNP_A-2054473	aagtttccttcagtta[A/G]atgctaaccttcttgg	A	G	7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 368125 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-2051850	aaggtctttggcagaa[A/G]gatcacacatcattat	A	G	ENST00000354581 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2011135	taactctgttgagtaa[A/G]taaactcatggaaaac	A	G	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-2034645	aaatgaaacatcatct[A/G]aagaaagagaaacacc	A	G	Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA. /// ENST00000358336 // intron // 0 // --- // --- // --- /// ENST00000320152 // intron // 0 // --- // --- // ---	PRTFDC1	PRTFDC1, Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), p12.1
SNP_A-2033868	aaatattttctttcta[C/T]gtaatttgccacagaa	C	T	Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // --- // ---	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2
SNP_A-2025303	aaaatattcagctcca[C/T]gctacccttggagtta	C	T	// 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 1144103 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2193637	catcttccataggcac[A/T]gaatatttctaaaata	A	T	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 222364	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2181197	cagacatgctataagg[C/T]ccccagcccagtcact	C	T	Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000274462 // intron // 0 // --- // --- // --- // --- ///	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2220522	ccttctgatgtgtgga[G/T]ccctgagggcagtgtt	G	T	79897 // Homo sapiens ribonuclease P 21kDa subunit (RPP21), mRNA. /// ENST00000259862 // downstream //	RPP21	RPP21, Homo sapiens ribonuclease P 21kDa subunit (RPP21), p21.33
SNP_A-2209086	cccaggagttattcaa[A/G]ggtgagccctttactt	A	G	Homo sapiens kallikrein 2, prostatic (KLK2), transcript variant 1, mRNA. /// NM_001002232 // 3UTR // 0 // Hs.515560 //	KLK2	KLK2, Homo sapiens kallikrein 2, prostatic (KLK2), transcript variant 1, q13.41
SNP_A-2210808	cccctgtatggagcaa[A/G]gaggaaaagggaaaag	A	G	2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 563389 // Hs.98262 // GRIK2 // 2898 // Homo	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2205852	ccatagagcttccata[C/G]ggcagaattagaatcc	C	G	HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// NM_001303 // upstream // 353019 // Hs.462278 //	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12
SNP_A-1807594	gtctggcttagtgccc[A/G]aacttccaccaggcac	A	G	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.23
SNP_A-1801587	gtaggttagttcaaga[C/T]atgattattggtagtt	C	T	// 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 514020 // Hs.478673 // IL1RAP // 3556 //	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1805154	gtcattaacctaccca[C/T]gtgtgtccgtgtcctt	C	T	-- /// ENST00000242916 // upstream // 349462 // --- // --- // ---	-	p14
SNP_A-1787233	gggaacatgtcacaaa[C/G]agccaatgcgctgggc	C	G	ALOX5AP // 241 // Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA. /// NM_032849 // upstream // 70763 // Hs.62905 // FLJ14834 //	ALOX5AP	ALOX5AP, Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), q12.3
SNP_A-1791003	ggggtcaaaggaaata[C/G]gatatggatcaagcaa	C	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1022996 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1856260	tcacaatattctggaa[C/T]tggaaaaaatcttcaa	C	T	23036 // Homo sapiens mRNA for KIAA0530 protein, partial cds. /// NM_198568 // downstream // 5152 // Hs.146727 //	ZNF292	ZNF292, Homo sapiens for KIAA0530 protein, partial cds. q15
SNP_A-1849118	tatgcctgcaattcca[C/T]gttggttgtgaatact	C	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream //	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-1816982	gttattgttaattcca[A/G]gtcatacaatagtcat	A	G	Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA. /// ENST00000350459 // intron // 0 // --- // --- // --- // ---	FLJ10375	FLJ10375, Homo sapiens hypothetical protein FLJ10375 (FLJ10375), p22.1
SNP_A-1840726	tagctaacagcctgaa[A/C]tgaatgtaaactttga	A	C	Homo sapiens adaptor-related protein complex 3, beta 1 subunit (AP3B1), mRNA. /// ENST00000255194 // intron // 0	AP3B1	AP3B1, Homo sapiens adaptor-related protein complex 3, beta 1 subunit (AP3B1), q14.1
SNP_A-1967920	tatgtagttcaaatat[C/T]agcttcagtgttatgt	C	T	-- /// ENST00000340000 // upstream // 104186 // --- // --- // ---	-	p12.1
SNP_A-1970435	tgaaatggattgttac[A/G]aaactgatcaattccg	A	G	Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-1923019	ttagcagaagcattta[C/T]gtgctaataagttctg	C	T	64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 319627 // Hs.546282 // RBBP8	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-1926028	ttatgtgagcatccaa[A/C]agtctgttttctcttc	A	C	SEC23IP // 11196 // Homo sapiens SEC23 interacting protein (SEC23IP), mRNA. /// NM_000982 // downstream // 180099 //	SEC23IP	SEC23IP, Homo sapiens SEC23 interacting protein (SEC23IP), q26.12
SNP_A-1919601	ttaaggccccacagga[C/T]gatggcagactgccag	C	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1901176	tggatgaatgccaaga[A/G]caatgtgcttatacag	A	G	// Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 887565 // Hs.451286 // C15orf2 //	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-1879133	tcttacagcaagatgg[C/T]caaaagtgcaggtaaa	C	T	Homo sapiens zinc finger protein 462 (ZNF462), mRNA. /// ENST00000277225 // intron // 0 // --- // --- // --- // ---	ZNF462	ZNF462, Homo sapiens zinc finger protein 462 (ZNF462), q31.2
SNP_A-1887004	tgacttgcctatccaa[A/T]gagaatacacttgaaa	A	T	Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // --- // -	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1
SNP_A-1884846	tgaatctatacattaa[A/G]tgcaaccccaatcaaa	A	G	FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 //	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-1897617	tgctgcattaactcca[C/T]ctgtagcaacggacat	C	T	9699 // Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // downstream //	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1895594	tgcctcacagttgccc[A/G]aacagcgctgcctcct	A	G	Homo sapiens p21(CDKN1A)-activated kinase 4 (PAK4), mRNA. /// ENST00000358301 // intron // 0 // --- // --- // --- // ---	PAK4	PAK4, Homo sapiens p21(CDKN1A)-activated kinase 4 (PAK4), q13.2
SNP_A-1893639	tgcaggttgtatcaca[C/T]tatcaacggattatta	C	T	Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// ENST00000359660 // intron // 0 // --- // --	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1982884	aaaatcaactttatgc[A/T]cattctaaatctctca	A	T	MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-1933888	ttctatttatcttcac[A/T]cataattaacactgaa	A	T	sapiens glycoprotein hormones, alpha polypeptide (CGA), mRNA. /// ENST00000257800 // intron // 0 // --- // --- // --- // ---	CGA	CGA, Homo sapiens glycoprotein hormones, alpha polypeptide (CGA), q15

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950309	tttcagatataacaag[A/C]caaggatgtttattat	A	C	sapiens mRNA for KIAA0618 protein, partial cds. /// ENST00000257665 // intron // 0 // --- // --- // --- // ---	POM121	POM121, Homo sapiens for KIAA0618 protein, partial cds. q11.23
SNP_A-1816467	gttaggaactcaaaat[A/G]atggcagtaaaacgca	A	G	167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 239047 //	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3
SNP_A-1863238	tcatttctttggtctc[C/T]atcaaacgaggaccct	C	T	Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron //	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-1862367	tcatgtcaaagcaggc[A/G]gaagtgagtaaaaact	A	G	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1871391	tctaaatgtgtggaga[A/G]caaaggctttccagta	A	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 816056 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1789086	gggcagagatgagcaa[A/G]ggatttctctgtattc	A	G	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.1
SNP_A-1806838	gtctatgatatgagcc[C/T]gaataaaaactctgga	C	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 559528 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1809179	gtgaccaggctcatca[G/T]agacattcataactat	G	T	340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. /// NM_005454 //	ZDHHC21	ZDHHC21, Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), p22.3
SNP_A-1690315	ccaagacattcatgagagaagacac[A/G]ctctttggatagtatgcttctaatt	A	G	NM_016304 // downstream // 520410 // Hs.274772 // C15orf15 // 51187 // chromosome 15 open reading frame 15	C15orf15	C15orf15 , rs2078426, chromosome 15 open reading frame 15,q21.3
SNP_A-2212250	ccctggcctgctgcct[A/T]actatgagtaggtgtg	A	T	80118 // Homo sapiens hypothetical protein FLJ22684 (FLJ22684), mRNA. /// NM_014452 // downstream // 173558	FLJ22684	FLJ22684, Homo sapiens hypothetical protein FLJ22684 (FLJ22684), p12.3
SNP_A-2215240	cctcaacacatggcaa[C/T]agaatccttggcaacc	C	T	Homo sapiens THUMP domain containing 3 (THUMPD3), mRNA. /// ENST00000345094 // intron // 0 // --- // --- // --- // ---	THUMPD3	THUMPD3, Homo sapiens THUMP domain containing 3 (THUMPD3), p25.3
SNP_A-2172900	caatttttcacacga[C/T]ctcattcctcctggac	C	T	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 898313 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2171612	caatctacaaccaatc[A/T]attttaccaatgagga	A	T	57459 // Homo sapiens transcription repressor p66 beta component of the MeCP1 complex (P66beta), mRNA. /// ENST00000306140 // downstream // 112 // --- // --- // --- // ---	P66beta	P66beta, Homo sapiens transcription repressor p66 beta component of the MeCP1 complex (P66beta), q21.3
SNP_A-2193767	catctttgcctcaaca[A/G]cacagcagttctcaaa	A	G	GALNT4 // 8693 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), mRNA. /// NM_024642 // downstream // 118747 // Hs.47099	GALNT4	GALNT4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), q22.33
SNP_A-2192156	tcattttacagacagc[A/G]gaaactgtatcttgct	A	G	ENST00000327351 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-2196468	catgtttagctgtata[C/T]gattttctaatgttta	C	T	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 282984 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2191017	cataggctgctgtaca[A/G]taagtggtaaatcacc	A	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2120097	agtcacttcccagaag[C/T]ctcctcctaataccat	C	T	146 // Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), mRNA. /// NM_000311 // upstream // 242469 //	ADRA1D	ADRA1D, Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), p13
SNP_A-2031611	aaagtaaatgccttag[A/G]actgccaggtagcaca	A	G	sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, mRNA. /// NM_017488 // intron // 0 // Hs.188528 // ADD2 //	ADD2	ADD2, Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, p13.3
SNP_A-1997277	tggaagatatttcata[G/T]gtggcagctaaattta	G	T	ENST00000288985 // intron // 0 // --- // --- // --- // ---	-	q22.32
SNP_A-1993213	acaaagagcagagaac[A/G]gctgaaagtttccttt	A	G	54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 610412 // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2072687	aggaaagatttatagt[A/G]aaggcgaagtagagac	A	G	ENST00000334414 // intron // 0 // --- // --- // --- // ---	-	q15
SNP_A-2074125	acataaaagctttgta[C/G]gttctgtttatatgct	C	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 827948 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2069691	acacacctaggttcta[C/T]gggatagcctattgct	C	T	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 186187 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2105274	agcattgaactcaacc[A/G]cctgtttatttctgca	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 44143 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2093597	agaagaactattcaga[A/C]ccatgcggaatgaaac	A	C	55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// NM_001444 // upstream // 46186 // Hs.408061 // FABP5 //	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-2098904	agagctgtacccgtgt[C/T]aagggatggagggagc	C	T	ENST00000312371 // intron // 0 // --- // --- // --- // ---	-	p22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2081850	accttgctcttagcag[C/T]atagaaggactactga	C	T	84888 // Homo sapiens putative intramembrane cleaving protease (SPPL2A), mRNA. /// NM_007347 // upstream // 24110 // Hs.413366 // AP4E1 // 23431 // Homo sapiens	SPPL2A	SPPL2A, Homo sapiens putative intramembrane cleaving protease (SPPL2A), q21.2
SNP_A-2088966	acttaaaagtcagaaa[C/G]cacattctggaccagg	C	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 15616 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2292689	gcactgttcattagca[G/T]aaaggagggatcttaa	G	T	// Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2311966	ggacaagttgggactg[A/G]aacaaagaaagccaca	A	G	ENST00000309950 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2314278	ggaggccaagagaccc[C/T]caatgtcccccagtgt	C	T	5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-2255539	cttgtgagttttgcca[C/T]agatcccaattccaac	C	T	oncogene mRNA, complete cds. /// ENST00000348841 // intron // 0 // --- // --- // --- // --- /// ENST00000352462 // intron //	-	-, Human P47 LBC oncogene complete cds. ,q25.3
SNP_A-2267249	gaatacgagcttgaaa[G/T]gctttatccagttgac	G	T	Homo sapiens hypothetical protein FLJ14007 (FLJ14007), mRNA. /// ENST00000220669 // intron // 0 // --- // --- // --- // ---	FLJ14007	FLJ14007, Homo sapiens hypothetical protein FLJ14007 (FLJ14007), q21.13
SNP_A-2265798	gaaggaaatcaatggc[C/T]cccgactaaaaaccgg	C	T	153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 57795 // Hs.424156 // IRX1 //	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-2078738	accattgtgttctctg[A/G]atggcctaatggaacc	A	G	// 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2059187	aatcctgagggcaaag[A/G]agaatacacgtgattt	A	G	// 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream //	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-1994195	atgaaaatgacctaca[G/T]aagtgagttgacagta	G	T	8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA. /// ENST00000326299 // upstream	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-2010044	aatgtagaaggaatag[C/T]atttttgacagactc	C	T	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 36476 //	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-2029656	aaagagagggaaatga[C/T]gcttactacaagttaa	C	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2045106	aagaagaagcaatgag[A/C]aatggaggccagacac	A	C	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 323664 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2122401	agtgcctccaggaaaa[C/G]catttgtgtaactgag	C	G	54768 // Homo sapiens hydrocephalus inducing (HYDIN), mRNA. /// NM_018348 // downstream // 4741 // Hs.72782 //	HYDIN	HYDIN, Homo sapiens hydrocephalus inducing (HYDIN), q22.2
SNP_A-2144935	atgattgcttatactc[A/C]gagctccatctcatag	A	C	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 146452 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2138305	atccagagctcttcca[A/G]aggcatttccaaacac	A	G	Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// ENST00000328500 // intron // 0 // --- // -	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2141227	atctggtttatatcta[C/T]ctctaaagttgctttt	C	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2204225	ccagcatggatcatga[C/G]ggttgctagaagagtg	C	G	Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000323059 // intron // 0 // --- // --- // --- // --- ///	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.1
SNP_A-2199821	ccaaacctacactcaa[A/G]gagacagtcaagtatc	A	G	NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. ///	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-2202340	ccaccagcagtcaccc[A/G]cgttcatcacctgccc	A	G	8720 // Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, mRNA. /// NM_201268 // downstream // 548 // Hs.75890 // MBTPS1 //	MBTPS1	MBTPS1, Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, q23.3
SNP_A-1680018	ccaagaaggtttttccactgtgaa[A/G]gccttgggcacacataaacattgtc	A	G	NM_147189 // upstream // 3341 // Hs.34054 // MGC39325 // 90362 // hypothetical protein MGC39325	-	- , rs10504244, - ,q12.1
SNP_A-1700249	actatagactagagtgctacatata[A/G]gtcaatctgaaaaggtggaagaga a	A	G	1602 // dachshund homolog 1 (Drosophila) /// NM_020866 // upstream // 849350 // Hs.106808 // KLHL1 // 57626 // kelch-	DACH1	DACH1 , rs950942, dachshund homolog 1 (Drosophila) ,q21.33
SNP_A-1781149	ggatggaagcacatca[A/G]gtatgaaccagacaaa	A	G	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// ENST00000261192 // intron // 0 // --- // ---	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-1753413	attatgtccttaacactgtgtttaa[C/T]tactaaaggggacaagacagtttta	C	T	NM_002849 // intron // 0 // Hs.198288 // PTPRR // 5801 // protein tyrosine phosphatase, receptor type, R	PTPRR	PTPRR , rs907752, protein tyrosine phosphatase, receptor type, R,q15
SNP_A-1870505	tcgacgacccatggga[A/T]tatgtcatcatatgga	A	T	Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // intron // 0 // --- // --- // --- // --- ///	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1868123	tcctatgtttcatcac[C/T]cttaacacagggaatt	C	T	// 285676 // Homo sapiens zinc finger protein 454 (ZNF454), mRNA. /// NM_000843 // upstream // 8055 // Hs.248131 //	ZNF454	ZNF454, Homo sapiens zinc finger protein 454 (ZNF454), q35.3
SNP_A-1853515	tattttggtaggagaa[A/T]gattaacaatgacttg	A	T	/// ENST00000336930 // upstream // 399345 // --- // --- // --- // -	-	p14.3
SNP_A-1824595	taaagaaatactggag[G/T]aacaaattctggcttt	G	T	// 64757 // Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA. /// NM_021958 // upstream // 56456 //	FLJ22390	FLJ22390, Homo sapiens hypothetical protein FLJ22390 (FLJ22390), q41
SNP_A-1822705	taaaaaactttccacc[A/G]gaaaatcatccaataa	A	G	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1826159	taaattacattagcaa[A/G]ccatacatacattttc	A	G	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-1839565	ccaatgccacaacatg[A/G]ctggaatgctcagaca	A	G	ENST00000313495 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-1948872	tttatcagaaaagtca[C/T]gctgagccctttggta	C	T	4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 64823 // --- // --- // --- // ---	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1956864	ttttaacgagcctatc[A/G]atgaatttcattcttt	A	G	Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1960409	tttttatcattcaggg[C/T]ccaatcaggaaaacag	C	T	490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 157951 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1982897	atattggtttccccag[C/G]cagtcattttcttagg	C	G	91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1970494	ctcacctgtgtagtac[C/T]gcagtgtcgctggcat	C	T	Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant b, mRNA. /// NM_138991 // intron // 0 //	BACE2	BACE2, Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant b, q22.3
SNP_A-1965832	ctgcgggccacatata[C/T]ctcctgaaaacagata	C	T	Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 // intron // 0 // --- // --- // --- // ---	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-1883010	tgaaatactgtacccc[A/G]agtagctaagtggtgg	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 542071 // Hs.13640 //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-1924737	ttatagttatagggga[C/G]aatgaagacagattgt	C	G	Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // intron // 0 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-1927944	ttcaatatcttgtcta[A/C]aagtgaggttaacatg	A	C	203074 // Homo sapiens tryptophan/serine protease (UNQ9391), mRNA. /// ENST00000357748 // upstream //	UNQ9391	UNQ9391, Homo sapiens tryptophan p23.1
SNP_A-1920532	ttaattggccatggac[G/T]cctttcccacattggc	G	T	// Human mRNA for KIAA0257 gene, partial cds. /// NM_144992 // upstream // 80956 // Hs.269977 // MGC26733	RW1	RW1, Human for KIAA0257 gene, partial cds. q11.2
SNP_A-1905790	tggtcaagtctttaac[A/G]caggtgtgcaccacgg	A	G	sapiens otoferlin (OTOF), transcript variant 1, mRNA. /// NM_194322 // intron // 0 // Hs.91608 // OTOF // 9381 // Homo	OTOF	OTOF, Homo sapiens otoferlin (OTOF), transcript variant 1, p23.3
SNP_A-1879974	tcttccttaagcggac[C/T]cttacatattgctttg	C	T	ENST00000359550 // intron // 0 // --- // --- // --- // ---	-	q21.2
SNP_A-1891203	tgatgtgtcctttctg[C/T]agttgcaggcccccgg	C	T	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 172764 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1967359	ctttctaaatattcca[C/G]aactatttccctgaac	C	G	55355 // Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA. /// ENST00000243201 // CDS // 0 // --- // --- // --- // ---	DKFZp762E1312	DKFZp762E1312, Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), q37.1
SNP_A-1962997	gacagctgcgaaggag[A/G]aagaaagtgaaaattt	A	G	6496 // Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA. /// NM_016932 // downstream //	SIX3	SIX3, Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), p21
SNP_A-1843209	tagtccatttttccta[A/G]catcatcactgataaa	A	G	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1816763	gttatctcctcaacca[G/T]aatatcaagaatattg	G	T	Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // intron // 0 // Hs.436387 // BCKDHB // 594 // Homo s	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-1847853	tatctctatagcctaa[A/C]tcttttgtgaagataa	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2769407 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1751221	atataaacctcctgcaaatcaaaga[C/G]gagaaatttattaaaatagagctat	C	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs10503211, CUB and Sushi multiple domains 1,p23.2
SNP_A-1726352	aggtttggtgcactgcggttcacca[A/C]cagagactggacaatgcacctgctg	A	C	NM_007353 // intron // 0 // Hs.182874 // GNA12 // 2768 // guanine nucleotide binding protein (G protein) alpha 12	GNA12	GNA12 , rs798525, guanine nucleotide binding protein (G protein) alpha 12,p22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1709467	tacctctggccacccagaaaagcat[C/T]agatctgggaaaagggagaaacaat	C	T	caspr5 protein /// NM_138996 // intron // 0 // Hs.437463 // caspr5 // 129684 // caspr5 protein	caspr5	caspr5 , rs2421084, caspr5 protein ,q14.3
SNP_A-1711424	tggggatccaatcaaaatgtaaaca[A/G]aggcactgtagagaagacagagact	A	G	NM_152570 // intron // 0 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs7853840, hypothetical protein FLJ31810,p21.2
SNP_A-1798625	gtaacacagatttaaa[A/T]gagagcaagtttctct	A	T	4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // upstream // 9666 // Hs.357630 // LMX1A //	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-1794662	ggtctcagaaaggaaa[C/T]taacctcagcaaactt	C	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-2200708	ccaagacaagaaacta[C/T]ataactgagagagagg	C	T	Homo sapiens cyclin D2 (CCND2), mRNA. /// ENST00000261254 // 3UTR // 0 // --- // --- // --- // ---	CCND2	CCND2, Homo sapiens cyclin D2 (CCND2), p13.32
SNP_A-2216872	cctctgccccttgtta[C/T]ggtcctgactctgatg	C	T	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 4,	ABCC1	ABCC1, Homo sapiens ATP-binding cassette, sub-family C (CFTR p13.11
SNP_A-2227541	ctacaggcatgcccta[C/T]taagctcaaaaaaatt	C	T	// 51015 // Homo sapiens CGI-111 protein (CGI-111), mRNA. /// NM_133638 // upstream // 179747 // Hs.23751 //	ISOC1	ISOC1, Homo sapiens CGI-111 protein (CGI-111), q23.3
SNP_A-2190599	catactaaatggcaaa[A/G]tggagtcgcagtcctg	A	G	Homo sapiens programmed cell death 10 (PDCD10), transcript variant 3, mRNA. /// NM_007217 // intron // 0 //	PDCD10	PDCD10, Homo sapiens programmed cell death 10 (PDCD10), transcript variant 3, q26.1
SNP_A-2192601	catccagggaaccaca[C/T]gcctagaaagacccca	C	T	ENST00000328627 // intron // 0 // --- // --- // --- // ---	-	q37.3
SNP_A-2195022	catgcttggttaccca[A/G]tgaggatacccactgg	A	G	SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 171861 // --- //	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2139872	atctaatagtcactca[A/G]taagtatgttttgaat	A	G	GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 //	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2119351	agtataaaattactaa[A/C]ccttcgatagtttgaa	A	C	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2124988	agttgatttttttata[A/C]ggtgagaaatgaggat	A	C	Homo sapiens FLJ20160 protein (FLJ20160), mRNA. /// ENST00000281416 // intron // 0 // --- // --- // --- // ---	FLJ20160	FLJ20160, Homo sapiens FLJ20160 protein (FLJ20160), q32.2
SNP_A-2126916	ataaaggaagagttga[C/G]taagtatgcataaatc	C	G	Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// ENST00000206249 // intron // 0 // --- // --- // --- // --- ///	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.1
SNP_A-2040454	aaccaggctttgaacc[A/G]ggaagtctgagtttga	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 13096 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2031208	aaaggcccagttatta[A/T]ggagtggatggaatct	A	T	Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- ///	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1993286	tcaactattgactcat[G/T]atctaccaggggaagg	G	T	9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 121930 // Hs.248117 //	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-1989879	gcagattttcttagtc[C/T]gaagcaatgacatgac	C	T	// 10320 // Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA. /// NM_006060 // upstream //	ZNFN1A1	ZNFN1A1, Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), p12.2
SNP_A-2004381	gacagcaaattgctcc[A/G]caccccagtagcacag	A	G	56963 // Homo sapiens RGM domain family, member A (RGMA), mRNA. /// NM_207447 // upstream // 114362 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens	RGMA	RGMA, Homo sapiens RGM domain family, member A (RGMA), q26.1
SNP_A-2060466	aatgacagcttcacag[A/G]aagaggttggcttgta	A	G	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 15 (NUDT15), mRNA. /// ENST00000258662 // intron // 0 // --- // --- // --- // ---	NUDT15	NUDT15, Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 15 (NUDT15), q14.2
SNP_A-2070599	acacctgtttcaagac[C/T]aagttaagtttcttta	C	T	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2093296	agaacgcaaactaatc[C/G]acagccgcagaaagca	C	G	// 1051 // Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA. /// NM_002827 // upstream //	CEBPB	CEBPB, Homo sapiens CCAAT,q13.13
SNP_A-2094191	agaagggcagactcat[A/G]agagacactcttctcc	A	G	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1513313 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2276533	gagagggattctagag[A/G]atgagcaatattacgt	A	G	/// ENST00000360991 // downstream // 411760 // --- // --- // ---	-	q12.1
SNP_A-2313759	ggagcagaaataatac[C/T]acttcctggggcatac	C	T	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), mRNA. /// ENST00000263239 // intron // 0 // --- // ---	DDX18	DDX18, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 (DDX18), q14.1
SNP_A-2295640	gcatgaatacagaacc[C/G]aaaggaaccatgggga	C	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284813	gatcattgtcagttta[C/T]gtctcacccagtattg	C	T	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 366439 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2237755	ctctcttccttctatc[A/G]ccataatggctgaatg	A	G	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 448819 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2238787	ctcttactttgtttac[G/T]atggtgaagaaggttg	G	T	Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2229501	ctagggctgctatacg[A/G]aagtaccacaaggcag	A	G	// 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// NM_182666	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4,p24.3
SNP_A-2094426	agaagtgtcaaacaaa[C/T]acgggaaaagcccctt	C	T	ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 96626 // --- // --- //	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2103665	agcacagatgaatgag[C/G]caaagtgacccctcag	C	G	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // intron // 0 // Hs.494312 //	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-2100245	agagttggatgaaaag[A/G]acacaggagataaaat	A	G	// Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), mRNA. /// ENST00000244563 //	OR2W1	OR2W1, Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), p22.1
SNP_A-2081289	acctggagaagctaaa[A/T]gagtgccccaggacac	A	T	// Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA. /// NM_173343 // upstream //	IL1R2	IL1R2, Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, q11.2
SNP_A-2084686	actattcgccacttga[A/G]gcacagtttaggcatc	A	G	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2083945	actacttgtaaccctg[A/C]atctatggaaataata	A	C	ENST00000309493 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-2085101	actcagaataaaatag[A/T]cattaaaaccacactg	A	T	Homo sapiens nuclear protein localization 4 (NPL4), mRNA. /// ENST00000331134 // intron // 0 // --- // --- // --- // ---	NPL4	NPL4, Homo sapiens nuclear protein localization 4 (NPL4), q25.3
SNP_A-2011532	gatctatttaatttga[A/G]gtggtttggtttatgg	A	G	// 4246 // Homo sapiens secretoglobin, family 2A, member 1 (SCGB2A1), mRNA. /// NM_006551 // upstream // 13082 //	SCGB2A1	SCGB2A1, Homo sapiens secretoglobin, family 2A, member 1 (SCGB2A1), q12.3
SNP_A-2018627	tattatgatttatcca[C/T]tcaaccaacatgtctg	C	T	RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 271330 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2020451	tttcaacacaatgtga[A/G]aaatgttggcaaaaca	A	G	Homo sapiens chromosome 21 open reading frame 29 (C21orf29), mRNA. /// ENST00000323084 // intron // 0 // --- //	C21orf29	C21orf29, Homo sapiens chromosome 21 open reading frame 29 (C21orf29), q22.3
SNP_A-2109987	aggaagaatcccggaa[C/G]gaaatgttatcagggc	C	G	ENST00000355094 // intron // 0 // --- // --- // --- // ---	-	q22.31
SNP_A-2141080	atctgctcttggctac[C/T]ggatgatggggctcta	C	T	// 51123 // Homo sapiens HSPC038 protein (LOC51123), mRNA. /// NM_024915 // upstream // 39029 // Hs.161160 //	LOC51123	LOC51123, Homo sapiens HSPC038 protein (LOC51123), q22.3
SNP_A-2147031	atggaacttccttaaa[A/C]tcccagtggtttgctt	A	C	83992 // Homo sapiens cortactin binding protein 2 (CTTNBP2), mRNA. /// ENST00000160373 // upstream //	CTTNBP2	CTTNBP2, Homo sapiens cortactin binding protein 2 (CTTNBP2), q31.31
SNP_A-2148629	atggtagtaccctgaa[A/G]gtaggttttttgtttg	A	G	53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1084440 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2148650	atggtatcccagtaaa[A/G]ttcatatgttaaagat	A	G	8754 // Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), transcript variant 1, mRNA. /// ENST00000302458 // downstream // 51934 // --- //	ADAM9	ADAM9, Homo sapiens a disintegrin and metalloproteinase domain 9 (meltrin gamma) (ADAM9), transcript variant 1, p11.23
SNP_A-2158325	attggggtctcactcc[A/C]ggactcttactctttc	A	C	// 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// NM_206892 // downstream	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2153283	attacttcaaaaaaaa[A/C]cagacataggaatctt	A	C	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1509848 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2192128	catcacttctcagaaa[C/T]ccagacagtggatgaa	C	T	55081 // Homo sapiens estrogen-related receptor beta like 1 (ESRRBL1), mRNA. /// NM_007072 // upstream // 26797 //	ESRRBL1	ESRRBL1, Homo sapiens estrogen-related receptor beta like 1 (ESRRBL1), q13.13
SNP_A-2171037	caataccagttgaagg[C/G]agagccaggattagca	C	G	SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2170335	caagtagaacactgta[C/T]gtttagtatcttgaaa	C	T	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 391579 // --- // --- // --- //	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2177632	agtagcagtggatcta[C/T]agctctttttttgagaa	C	T	Homo sapiens serine/threonine kinase 24 (STE20 homolog, yeast) (STK24), mRNA. /// ENST00000261573 // intron // 0 //	STK24	STK24, Homo sapiens serine q32.2
SNP_A-2203843	ccagaggtagtgaagc[A/G]gagagtaatgcatagg	A	G	120 // Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /// NM_016824 // downstream // 61415 //	ADD3	ADD3, Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, q25.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2204511	ccagcttattcccaga[A/G]gattttgtatctacca	A	G	202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 42428 // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2207892	cccaaatcatgggaga[A/C]cccgacaaattcagag	A	C	Homo sapiens retinoid X receptor, beta (RXRB), mRNA. /// ENST00000230234 // 3UTR // 0 // --- // --- // --- // ---	RXRB	RXRB, Homo sapiens retinoid X receptor, beta (RXRB), p21.32
SNP_A-1703543	agataggcaggtagaacaaatgcag[C/T]gaaatgttaattgttgaatttaggt	C	T	6156 // ribosomal protein L30 /// NM_173549 // upstream // 8460 // Hs.171455 // FLJ39553 // 203111 // hypothetical	RPL30	RPL30 , rs2010014, ribosomal protein L30 ,q22.2
SNP_A-1690229	ttccttcttaccattgaatcacata[A/G]caaataattataggctctcaaatgt	A	G	NM_153041 // intron // 0 // Hs.123533 // FLJ32955 // 150596 // hypothetical protein FLJ32955	FLJ32955	FLJ32955 , rs10490078, hypothetical protein FLJ32955,q23.3
SNP_A-1684740	cagcacaacacaaaggtcttgcatt[G/T]ctccctccaaaaggtgagacatgct	G	T	Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human) /// NM_005065 // upstream // 3915307 // Hs.181300 // SEL1L // 6400 // sel-1 suppressor of	-	- , rs1885315, Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human) ,q31.3
SNP_A-1648830	aagctatgtccaccccagccaatag[A/G]gatcaatctagctatattaaatcac	A	G	like module containing, mucin-like, hormone receptor-like 3 /// NM_152939 // intron // 0 // Hs.438468 // EMR3 // 84658 // egf-	EMR3	EMR3 , rs726789, egf-like module containing, mucin-like, hormone receptor-like 3 ,p13.12
SNP_A-1730923	gatgtctatgtacagccaagattga[A/G]actttctcacgttaagtcttaggat	A	G	4289 // muskelin 1, intracellular mediator containing kelch motifs	MKLN1	MKLN1 , rs7781339, muskelin 1, intracellular mediator containing kelch motifs,q32.3
SNP_A-1816356	gttagagagacagaca[A/T]aaccttgtttactgtc	A	T	199834 // Homo sapiens late cornified envelope 4A (LCE4A), mRNA. /// NM_178354 // upstream // 12268 // --- // LCE1F //	LCE4A	LCE4A, Homo sapiens late cornified envelope 4A (LCE4A), q21.3
SNP_A-1835967	tactaacttattcata[C/T]gggaaacaggtttgca	C	T	51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 594305 // Hs.529735 // AADAT // 51166 // Homo	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1964400	gatcttataaaacaag[C/G]aaacacaagatagtga	C	G	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-1971657	atacctacatttctac[C/T]acctgggattaaattc	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 456414 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1978539	ttaggagtcaatccaa[A/C]ggttaacccaataaat	A	C	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1960900	tttttgagggaattgc[A/G]cttttgaataggtttc	A	G	-- /// ENST00000360296 // downstream // 63079 // --- // --- // --	-	p21.1
SNP_A-1933354	ttctaatgaggcaaag[A/T]ctgaaatatgaagatg	A	T	/// ENST00000309379 // upstream // 385005 // --- // --- // --- // -	-	q21
SNP_A-1940280	ttgcattttagcttct[A/G]aatgatagtccaggag	A	G	Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// ENST00000282902 // intron // 0 // --- // --- // --- // ---	VMP	VMP, Homo sapiens vesicular membrane protein p24 (VMP), p22.2
SNP_A-1892012	tgcaaaactctgaact[A/G]aagtttgacattaagt	A	G	201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// ENST00000284400 // intron // 0 // ---	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-1908853	tgtagtgtcattcttc[A/C]aagtcaggggatcagg	A	C	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3), mRNA. /// ENST00000340101 // intron // 0 // --- // --- // --- // --- ///	PSMD3	PSMD3, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3), q21.1
SNP_A-1929356	ttcagtctttctaaac[A/C]aaagcttcctagtgat	A	C	// 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// NM_000623 // upstream //	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-1927173	ttattttgtctcacca[A/G]tcctactttcctcgtc	A	G	// 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// NM_144665 // downstream // 19501 // Hs.120633 //	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds. ,q21
SNP_A-1906313	tggtgatggtattaga[C/T]caagacaggagaattg	C	T	83876 // Homo sapiens maestro (MRO), mRNA. /// NM_031939 // upstream // 21885 // Hs.131072 // MRO //	MRO	MRO, Homo sapiens maestro (MRO), q21.1
SNP_A-1906294	tggtgatctttttgga[C/G]aaaggatgggtttgtc	C	G	Homo sapiens Tandem PH Domain Containing Protein-2 mRNA, partial cds. /// ENST00000302511 // intron // 0 // --- // -	PLEKHA2	PLEKHA2, Homo sapiens Tandem PH Domain Containing Protein-2 partial cds. ,p11.23
SNP_A-1894046	tgcatctactctgcta[C/G]aataccaaccaattag	C	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2446405 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1902119	tggcattgaggataga[C/T]gggtaaattatatgtg	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // -	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1939206	ttgatattgatattag[A/G]agaggttattccatgt	A	G	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 953911 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1978844	gatgtcatgaataaca[A/G]caccattgaggaatgt	A	G	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 692437 // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1974372	acatatgtcaaggaat[A/G]aatatctgaatgtgaa	A	G	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 139138 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1975121	caagtaggccttactg[G/T]aggaattgttaacttt	G	T	ENST00000167825 // intron // 0 // --- // --- // --- // ---	-	p36.13
SNP_A-1835119	taccctcctgccttac[A/T]aatttttgtgtagta	A	T	Homo sapiens mRNA for KIAA0715 protein, partial cds. /// ENST00000327245 // intron // 0 // --- // --- // --- // ---	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. ,q34
SNP_A-1816123	gttaccatatagggaa[G/T]aaggtctaaatatgaa	G	T	Homo sapiens FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12B, mRNA. /// NM_054014 // intron // 0 //	FKBP1A	FKBP1A, Homo sapiens FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12B, p13
SNP_A-1854844	tcaaccgacatgtgca[C/T]caaaaaacatacgcaa	C	T	/// ENST00000343481 // downstream // 384760 // --- // --- // ---	-	q24.1
SNP_A-1855332	tcaaggcaaaagcagg[A/C]aatacttaagttctcc	A	C	Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1862031	tcatgattaaacttga[A/G]ggaataggagctgctt	A	G	// 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 1319113 // Hs.308628 //	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1860516	tcagttcaacagtcag[A/G]cagatagaaaaaaggg	A	G	/// ENST00000331815 // downstream // 668880 // --- // --- // ---	-	q13.13
SNP_A-1747275	tattcaacccctcctgactactgaa[C/G]tgggaaacattttaggtttcctgac	C	G	NM_014802 // intron // 0 // Hs.30656 // KIAA0528 // 9847 // KIAA0528 gene product	KIAA0528	KIAA0528 , rs10505881, KIAA0528 gene product,p12.1
SNP_A-1731739	ctacaaacacattaagctactcctc[C/T]gagcaaaagccttcatcttagcatg	C	T	6445 // sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) /// NM_002010 // downstream // 1427393 // Hs.111 // FGF9 // 2254 // fibroblast growth factor 9 (glia-	SGCG	SGCG , rs9317500, sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) ,q12.12
SNP_A-1758149	gcagagcttgcctttcaatgagaac[A/T]ggccctttatataaatactctatc	A	T	NM_022776 // upstream // 83816 // Hs.61260 // OSBPL11 // 114885 // oxysterol binding protein-like 11	OSBPL11	OSBPL11 , rs10512658, oxysterol binding protein-like 11,q21.2
SNP_A-1792514	ggtaaaaagggaattg[C/G]attcaaggtatttggc	C	G	sapiens glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (GNE), mRNA. ///	GNE	GNE, Homo sapiens glucosamine (UDP-N-acetyl)-2-epimerase p13.2
SNP_A-1791935	gggtgctaaatgaaga[A/T]gctatataaacggcat	A	T	80759 // Homo sapiens chromosome 6 open reading frame 148 (C6orf148), mRNA. /// ENST00000257765 // upstream //	C6orf148	C6orf148, Homo sapiens chromosome 6 open reading frame 148 (C6orf148), q13
SNP_A-1807996	gtcttcctctaccccc[A/C]accagtgatctgatct	A	C	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33
SNP_A-1813229	gtggtcccttgcatca[A/G]gtggtatttgaggtag	A	G	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 282407 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2210546	ccccgctcactctcaa[A/C]tgaggctcctgtgatg	A	C	Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA. /// ENST00000350459 // 3UTR // 0 // --- // --- // --- // ---	FLJ10375	FLJ10375, Homo sapiens hypothetical protein FLJ10375 (FLJ10375), p22.1
SNP_A-2199792	ccaaacagtaaacatc[G/T]cctattgcttactgct	G	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2176906	caccgtgggatacaca[C/G]cttggctatttgtgga	C	G	23235 // Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000322479 // upstream // 28057	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine q23.1
SNP_A-2194217	tcagagagtcttgaag[C/G]ccttgtcactttgggt	C	G	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), transcript variant 1, mRNA /// NM_182728 // intron // 0 // Hs.22891 //	SLC7A8	SLC7A8, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), transcript variant 1, q11.2
SNP_A-2196398	catgttctcgcatgcc[A/G]ctctcccttgcagagc	A	G	sapiens ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET), tr /// NM_020975 // intron // 0 // Hs.350321 // RET // 5979 // Homo sapie	RET	RET, Homo sapiens ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET), tr ,q11.21
SNP_A-2159552	atttacctgaataatc[A/C]gaacagttgctccagt	A	C	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 653199 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2164258	caaaatacaatctca[C/G]tcttaaaaaataatag	C	G	Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), mRNA. /// ENST00000261367 // intron // 0 // --- // -	SNCAIP	SNCAIP, Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), q23.2
SNP_A-2113229	aggccctattatgggc[A/G]aggcactgttcaagac	A	G	// 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 53778 //	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2121181	agtctgccttgaacac[A/G]gaagagatcttgttct	A	G	Homo sapiens granulysin (GNLY), transcript variant NKG5, mRNA. /// NM_012483 // CDS // 0 // Hs.105806 // GNLY //	GNLY	GNLY, Homo sapiens granulysin (GNLY), transcript variant NKG5, p11.2
SNP_A-2135912	atcaaccaaatccaca[A/T]tgagagacagtctact	A	T	Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), mRNA. /// ENST00000324695 // intron // 0 // --- // --- // --- // --- ///	TRPM8	TRPM8, Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), q37.1
SNP_A-2020547	acctagaaagtcaagg[C/T]acacccgcagtctcgc	C	T	// 85395 // Homo sapiens chromosome 21 open reading frame 70 (C21orf70), mRNA. /// BC004343 // downstream //	C21orf70	C21orf70, Homo sapiens chromosome 21 open reading frame 70 (C21orf70), q22.3
SNP_A-2033881	aaatcaaaactacaac[A/G]aggcaccacctaacag	A	G	Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-1996077	actcttgtgtccactg[A/T]acgtactacttaccta	A	T	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// ENST00000315856 // intron // 0 // --- // --- // --- // ---	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084500	actatcttccttaaaa[C/G]aagtcttcagcaaaat	C	G	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2077163	accaagctggttagca[A/G]caaaaacaaatagctt	A	G	ENST00000259793 // intron // 0 // --- // --- // --- // ---	-	p22.2
SNP_A-2079669	accctagctacaggcc[A/G]aattcccaacactgtt	A	G	PAPOLA // 10914 // Homo sapiens poly(A) polymerase alpha (PAPOLA), mRNA. /// NM_020144 // downstream // 185484 //	PAPOLA	PAPOLA, Homo sapiens poly(A) polymerase alpha (PAPOLA), q32.2
SNP_A-2093917	agaagcaggacataca[C/G]agatacatacagaagc	C	G	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 157985 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2071731	acagacagacatggag[A/G]aaatgcatcaggtcgg	A	G	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 //	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2073561	acagtacttcattata[A/G]caactcaatggattac	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2059807	aatctgtaactaggat[C/G]agcataatagaatgtc	C	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1238423	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2231326	ctattctcagagcaag[A/G]aaagtcactgattgta	A	G	3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1242266	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2236337	tttgtactgttttcaa[A/T]ccttaaagcctctgtt	A	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // downstream // 54068 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2241722	ctgatcagagtatcca[A/G]tccagtggcaatcccc	A	G	Homo sapiens DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), transcript variant 3, mRNA. /// NM_175848 // intron // 0 // Hs.251673 // DNMT3B // 1789 // Homo sapiens	DNMT3B	DNMT3B, Homo sapiens DNA (cytosine-5-)-methyltransferase 3 beta (DNMT3B), transcript variant 3, q11.21
SNP_A-2287655	gattaagttttatcac[A/G]aacggataccagagtg	A	G	Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// NM_173472 // intron // 0 // Hs.190413	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-2287044	gatgtaaagttctcca[A/C]tgaatgttctataaat	A	C	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2120609 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2264703	gaagacagggaaaaat[C/T]actgaaaaataagtga	C	T	// 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 356838 // Hs.436944	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2267199	gaatacacctcacgta[C/T]cgaacgtcacagctca	C	T	Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST00000295624 // intron // 0 // --- // --- // --- // --- ///	NAV1	NAV1, Homo sapiens neuron navigator 1 (NAV1), q32.1
SNP_A-2300993	gccttaaacttcttcc[A/G]gatcccccaaagccaa	A	G	sapiens nuclear factor I/A (NFIA), mRNA. /// ENST00000357977 // intron // 0 // --- // --- // --- // ---	NFIA	NFIA, Homo sapiens nuclear factor I,p31.3
SNP_A-2311358	ggaatatcccagtaca[A/G]gaaggtgaaagaacac	A	G	21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 331012 // Hs.475902	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2266908	gaagttggatttatta[C/T]aactatacaagactca	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 118076 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2287126	gatgtattgtctttaa[C/T]cattaaaaatctgaga	C	T	5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 251734 // Hs.298863 // FLJ23577	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2285985	gatgatagccagctag[G/T]caatgaagatgttagt	G	T	// 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 29203 // Hs.353022 // ETAA16 //	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2274154	gacttccaaaccaagt[A/T]acacaggacaaactgg	A	T	253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 598145	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2250396	cttagccaatcatgta[C/T]gttcaccctggatcct	C	T	283358 // Homo sapiens beta 1,4-N-acetylgalactosaminyltransferase-transferase-III (B4GalNac-T3), mRNA. /// ENST00000266383 // intron // 0 // --- // --- // ---	B4GalNac-T3	B4GalNac-T3, Homo sapiens beta 1,4-N-acetylgalactosaminyltransferase-transferase-III (B4GalNac-T3), p13.33
SNP_A-2238761	ctcttacattgttgaa[C/T]ggagggcttgagcaca	C	T	6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// ENST00000354821 // downstream // 2554 // --- // --- // --- // ---	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2228981	ctagcaacagaagaaa[C/G]aagaacaacttccagt	C	G	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1481106 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2057316	aatatatgaagctgtc[A/G]gaaaagagccaccctg	A	G	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2051956	aaggtggctgagatgc[A/G]gagtagccttcccccc	A	G	Homo sapiens cardiotrophin 1 (CTF1), mRNA. /// ENST00000279804 // 3UTR // 0 // --- // --- // --- // ---	CTF1	CTF1, Homo sapiens cardiotrophin 1 (CTF1), p11.2
SNP_A-2070941	acactccctcgggcta[C/T]ccctttgtagtcccat	C	T	sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, mRNA. /// NM_013993 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain	DDR1	DDR1, Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, p21.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2069292	acaatttttcacata[G/T]aagtgtgccttaaaat	G	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2085960	actctactatccaaca[C/T]tgaatttattccttcc	C	T	312 // Homo sapiens annexin A13 (ANXA13), transcript variant 2, mRNA. /// NM_004306 // upstream // 22424 //	ANXA13	ANXA13, Homo sapiens annexin A13 (ANXA13), transcript variant 2, q24.13
SNP_A-2090429	acttggctttgtgttg[C/T]aaactatggttcatct	C	T	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1990356	aatgaggcccaagcta[C/T]atatgaatttcaaaga	C	T	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2013791	cctgactgctgggata[A/C]agccagagacttttcc	A	C	// 157378 // Homo sapiens hypothetical protein BC017881 (LOC157378), mRNA. /// NM_017956 // upstream // 55961 //	LOC157378	LOC157378, Homo sapiens hypothetical protein BC017881 (LOC157378), q24.13
SNP_A-2045847	aagacatactcttcaa[A/C]cttattcaccactatg	A	C	Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // --- // --- // --- // --- ///	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-2023817	aaaagaaacatctgac[G/T]agttagtgctcagctg	G	T	Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /// ENST00000222607 // upstream // 161363 // --- // --- // --- //	IL6	IL6, Homo sapiens interleukin 6 (interferon, beta 2) (IL6), p15.3
SNP_A-2134944	atattcaagattgata[C/T]tactattgcttattag	C	T	Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// ENST00000303854 // 3UTR // 0 // --- // --- // --- // ---	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2133892	atatctccaagtagaa[C/T]aggtggctatgtggct	C	T	23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 122491 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2162062	attttaaataaactgg[C/G]caagaaagaccttcct	C	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 26046 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2168112	caactcacacagaccc[A/G]actggaagcccagcct	A	G	// 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 29680 // Hs.502116 //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2141909	atcttgtgatgaaaac[C/T]gtgattcattcattca	C	T	4179 // Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, mRNA. /// NM_172357 // downstream // 70844 // Hs.510402 // MCP // 417	MCP	MCP, Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, q32.2
SNP_A-2188588	cagtgatgctgcccac[A/G]caaatgaggctcttgc	A	G	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // --- // ---	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-2175724	cacattatcattgagg[A/G]aaaaaaggatctaaat	A	G	-- /// ENST00000276737 // downstream // 232779 // --- // --- //	-	q24.23
SNP_A-2181675	cagagactttcttagc[A/G]aaataatctctccttt	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 835374 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2171565	caatccgggcaaaaga[A/G]gatatctaactccagg	A	G	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA. /// ENST00000324684 // 3UTR // 0 // --- // --- // --- // --- ///	PRPSAP1	PRPSAP1, Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), q25.1
SNP_A-2173410	cacaaggtatcttaac[A/G]ctgatggaatgttatt	A	G	Homo sapiens NOL1/NOP2/Sun domain family 2 (NSUN2), mRNA. /// ENST00000356741 // intron // 0 // --- // --- // --- // ---	NSUN2	NSUN2, Homo sapiens NOL1,p15.31
SNP_A-2207422	ccattggaattcagtg[A/G]atcatctatctatgca	A	G	81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 90062 //	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-1809342	gtgactgggaacttcc[A/T]gagtatgacttcaggg	A	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2406740 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1793370	ggtaggcaacattttc[A/G]catcggtagccctgga	A	G	/// ENST00000321719 // upstream // 673082 // --- // --- // --- //	-	p11.21
SNP_A-1796316	ggtgtgttacattgaa[A/T]ttatgtaaatcagtac	A	T	/// ENST00000321719 // upstream // 492057 // --- // --- // --- //	-	p11.21
SNP_A-1725610	gttgcagctgtctgtttttgagcga[C/T]gtctgtatgccttgcagaaccatct	C	T	2045 // EphA7 /// NM_024641 // upstream // 1273455 // Hs.46903 // MANEA // 79694 // mannosidase, endo-alpha	EPHA7	EPHA7 , rs574793, EphA7 ,q16.1
SNP_A-1703827	cagaccacacagctcctaaataaga[A/G]gctaagccagcattcagacctgtct	A	G	NM_001094 // intron // 0 // Hs.6517 // ACCN1 // 40 // amiloride-sensitive cation channel 1, neuronal (degenerin)	ACCN1	ACCN1 , rs63953, amiloride-sensitive cation channel 1, neuronal (degenerin),q11.2
SNP_A-1704327	aaacatttatttttcgtatgacttt[C/T]ggttcttttttatctcataaattgt	C	T	plexin A4	PLXNA4	PLXNA4 , rs1450885, plexin A4,q32.3
SNP_A-1861421	tcatcatcataaccaa[C/T]tgacttcatagtttgt	C	T	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 556640 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1862098	tcatgccccatggtac[A/G]atggcctcgcatttca	A	G	Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 //	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912). q12.13
SNP_A-1854007	tcaaaattgctactta[C/T]ggcatttcctacaatg	C	T	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA. /// ENST00000268182 // intron // 0 // ---	IQGAP1	IQGAP1, Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), q26.1
SNP_A-1856904	tcaccacactgtgggc[A/C]aagaggagagaagagc	A	C	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1845461	tatagaatcttttccc[C/T]ggagccactggaagca	C	T	Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // --- // --- // --- // ---	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. ,p24.1
SNP_A-1844271	tagttttatgtgtcaa[C/G]ttagaggatgttttgg	C	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 110860 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1839771	tagatgttcagttgat[A/G]aaaatgctgtcaccag	A	G	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 799280 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1837351	tacttcagagaaaaga[A/G]gaacacaaatgcttct	A	G	79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 266639	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-1983349	tcacggaatatttgac[C/T]acctgcttggtatggg	C	T	50809 // Homo sapiens HP1-BP74 (HP1-BP74), mRNA. /// NM_016287 // upstream // 19343 // Hs.142442 // HP1-BP74 //	HP1-BP74	HP1-BP74, Homo sapiens HP1-BP74 (HP1-BP74), p36.12
SNP_A-1987715	aaaggaatcaggtgaa[C/T]aggaaaagtcatttta	C	T	// 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 5072 // Hs.102408 //	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1933558	ttctagacctgcttgg[C/T]cataatttgtgacact	C	T	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 198543 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1933960	ttctcaaggtggcacc[C/T]cagagtggcctccaag	C	T	Homo sapiens tripartite motif-containing 40 (TRIM40), mRNA. /// ENST00000307859 // intron // 0 // --- // --- // --- // ---	TRIM40	TRIM40, Homo sapiens tripartite motif-containing 40 (TRIM40), p21.33
SNP_A-1951020	tttccaggctttttag[A/C]atggtggcagtcaaga	A	C	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// ENST00000357652 // upstream // 127276 // --- // ---	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1899214	tggaaatctgaacaca[C/G]actgggtatttaacag	C	G	7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 448484 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v ,q12
SNP_A-1877849	tctggtcccggtttcc[G/T]agacaggtaagaatgg	G	T	Homo sapiens prion protein 2 (dublet) (PRND), mRNA. /// ENST00000305817 // intron // 0 // --- // --- // --- // ---	PRND	PRND, Homo sapiens prion protein 2 (dublet) (PRND), p13
SNP_A-1887994	tgagcagagccctaag[A/G]atgtgctgaaagtcaa	A	G	23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 577372	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1889989	tgatagtgcagtggat[C/G]aagtttggccacagat	C	G	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1916386	tgttgttcagttctag[G/T]acctattatttttaag	G	T	// 54877 // Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), mRNA. /// NM_194449 // upstream //	ZCCHC2	ZCCHC2, Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), q21.33
SNP_A-1925706	ttatgcaatgctacac[A/G]gctcaagaaatgtttt	A	G	// 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 71003 //	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-1934034	ttctcactctgccacc[A/G]ctgtaatttatcactc	A	G	/// ENST00000336930 // upstream // 1097675 // --- // --- // --- //	-	p14.3
SNP_A-1827296	taacgacaagcatgat[A/G]aatactccaagtggga	A	G	57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 21945 // --- // FLJ37543 //	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. q12.1
SNP_A-1846664	tatattttcctaacca[A/T]ctgatagagccaggtg	A	T	// 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-1857845	tcactgttgttcaata[A/C]ctagtaaaagctcaat	A	C	Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1853779	tcaaaaagtggggaaa[C/G]gtagccttattgtagg	C	G	Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// ENST00000262095 // intron // 0 // ---	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-1854512	tcaaattatacttaca[G/T]aagactgcgcttcagt	G	T	Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// ENST00000287097 // intron // 0 // --- // ---	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1866357	tcccattgttgacttc[A/C]cgctgttccagccatg	A	C	// Homo sapiens prohibitin (PHB), mRNA. /// NM_002507 // upstream // 6069 // Hs.415768 // NGFR // 4804 // Homo	PHB	PHB, Homo sapiens prohibitin (PHB), q21.33
SNP_A-1867399	tcccttgtgtcagaaa[C/G]catatctcagatttgt	C	G	// 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 69000 //	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-1702161	cttaactcctaaaatgtaagctcgg[A/G]atagctcagatgttcttacagaaat	A	G	NM_003728 // intron // 0 // Hs.125605 // UNC5C // 8633 // unc 5 homolog C (C. elegans)	UNC5C	UNC5C , rs10516971, unc-5 homolog C (C. elegans),q22.3
SNP_A-1782344	ggcaatggcagaggta[C/G]aagaggacacacacag	C	G	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 84537 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1792412	gggtttcagagataat[A/G]agtgaaggtgcttggt	A	G	Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 //	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1808322	gtcttttcctatccac[G/T]aaacaacgttatctgc	G	T	Homo sapiens endosulfine alpha (ENSA), transcript variant 1, mRNA. /// NM_207043 // intron // 0 // Hs.511916 // ENSA //	ENSA	ENSA, Homo sapiens endosulfine alpha (ENSA), transcript variant 1, q21.2
SNP_A-1807864	gtcttaggaaagcaga[C/T]gtgaattttcttcagc	C	T	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 154045 // --- // --- // --- //	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2207254	ccattccaagtgataa[C/G]atagtctgatacctttt	C	G	// 84541 // Homo sapiens T-cell activation kelch repeat protein (TA-KRP), mRNA. /// NM_003848 // downstream //	TA-KRP	TA-KRP, Homo sapiens T-cell activation kelch repeat protein (TA-KRP), p14.1
SNP_A-2214469	cctactgtcattataa[A/C]ctgtgaccaaaaagca	A	C	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2170066	caagggctgctgctca[C/G]attattttgaaccatg	C	G	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2140390	atctcatcaaatgtta[C/T]gaaatgctttaaaaga	C	T	FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-2150233	atgtctcacctcaaag[C/T]caagatagcaagcatt	C	T	Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA. /// ENST00000330610 // intron // 0 // --- // --- // --- // ---	KIRREL	KIRREL, Homo sapiens kin of IRRE like (Drosophila) (KIRREL), q23.1
SNP_A-2125631	agtttcgttgctaaaa[G/T]tttggttgcttaaagt	G	T	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 122065 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2124854	agttgaacaaaatgca[C/G]aaacaaagcagcaaaa	C	G	KIAA0117 // 23029 // Homo sapiens KIAA0117 protein (KIAA0117), mRNA. /// ENST00000323183 // upstream //	KIAA0117	KIAA0117, Homo sapiens KIAA0117 protein (KIAA0117), q42.3
SNP_A-2129072	ataattattactcttc[A/G]atgtggcccaaggacg	A	G	Homo sapiens plakophilin 4 (PKP4), transcript variant 1, mRNA. /// ENST00000354977 // intron // 0 // --- // --- // --- // ---	PKP4	PKP4, Homo sapiens plakophilin 4 (PKP4), transcript variant 1, q24.1
SNP_A-2081776	accttctgccaaaatc[C/T]attctctacaagggag	C	T	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2067736	acaacagagtttgtaa[C/T]catatatatatatata	C	T	1454 // Homo sapiens casein kinase 1, epsilon (CSNK1E), transcript variant 1, mRNA. /// NM_001894 // upstream //	CSNK1E	CSNK1E, Homo sapiens casein kinase 1, epsilon (CSNK1E), transcript variant 1, q13.1
SNP_A-2059592	aatctccctgtctcaa[A/G]agccttagcttaatca	A	G	// Homo sapiens fibrillarin (FBL), mRNA. /// NM_003890 // downstream // 6936 // Hs.111732 // FCGBP // 8857 // Homo	FBL	FBL, Homo sapiens fibrillarin (FBL), q13.2
SNP_A-2253571	cttcttggacttggga[C/T]aagtgacagatggggt	C	T	Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 //	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2274301	gacttggacaagtcgc[C/T]gaattctctgggactc	C	T	Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // intron // 0 // Hs.513902 // NALP1 // 22861 //	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-2284035	gatatcaagatcatcc[A/G]acaactcgtccctttt	A	G	Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// ENST00000332896 // intron // 0 // --- // --- // --- // --- /// ENST00000306632 // intron	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-2269770	gacaagatttaaagac[A/C]ggattccaggtaaatt	A	C	// Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // intron // 0 // --- // --- // --- // ---	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-2265455	gaagccactggttgac[C/G]ccatcttgaataacag	C	G	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2255908	ctttaaatatcgtgac[A/C]cttaaaatatcaaatt	A	C	Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 2 (GABRR2), mRNA. /// ENST00000229606 // intron // 0	GABRR2	GABRR2, Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 2 (GABRR2), q15
SNP_A-2246090	ctggtcagtgtccaat[C/G]atctagccaaatgcca	C	G	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3247835 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2231771	ctcaaacaaaacaaaa[A/G]ctgacagcatgcaact	A	G	Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// ENST00000359660 // intron // 0 // --- // ---	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-2293622	gcagccaggtggtact[A/G]aaaagacaatgaaaaa	A	G	sapiens interferon regulatory factor 6 (IRF6), mRNA. /// ENST00000236254 // intron // 0 // --- // --- // --- // ---	IRF6	IRF6, Homo sapiens interferon regulatory factor 6 (IRF6), q32.2
SNP_A-2054166	cagcacatgtgtcctg[A/C]agaaatgacgaccagt	A	C	// 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 616479	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2075578	acatgcgattctacaa[A/G]aaagatgatattgtag	A	G	sapiens MAX interactor 1 (MXI1), transcript variant 2, mRNA. /// L07648 // intron // 0 // --- // --- // 0 // Human MXI1 mRNA,	MXI1	MXI1, Homo sapiens MAX interactor 1 (MXI1), transcript variant 2, q25.2
SNP_A-2090322	acttgctgtaactacc[C/T]gctgagagggacaaat	C	T	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2099557	agagggtcaccagaaa[C/T]ggcttgatctttgtga	C	T	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2023560	aaaactccagcccaaa[A/T]gaagcaaaatttcctt	A	T	ENST00000320930 // intron // 0 // --- // --- // --- // --- /// ENST00000329131 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-2040791	aacccatgagaagccc[A/G]atatgtgatatctttg	A	G	// 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// NM_002127 // downstream //	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2034964	aaatgatgaaagaaga[C/T]ggggaattacattgct	C	T	// 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1707146 // Hs.27214 // KCNC2 // 3747 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2119467	agtatcaaatgtgtca[C/T]agtcttttgatctgaa	C	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2149976	atgtcatcaagactta[C/T]cttagaaattagtaaa	C	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2144975	atgatttatcttgaaa[C/T]gtgacagactcatgac	C	T	148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// NM_033020 // downstream // 106398 // Hs.26837 // TRIM33	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2166544	caaatggccaacatcg[C/G]aaaaattgttcagcat	C	G	/// ENST00000329798 // downstream // 131489 // --- // --- // ---	-	q31.21
SNP_A-2164432	caaaatggatcccata[A/G]aggtaattcaaaggac	A	G	164684 // Homo sapiens hypothetical protein MGC26816 (MGC26816), mRNA. /// ENST00000354469 // intron // 0 // ---	MGC26816	MGC26816, Homo sapiens hypothetical protein MGC26816 (MGC26816), q13.2
SNP_A-2166159	caaatatctcagaagt[C/T]acaggttgtacacatg	C	T	3156 // Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA. /// ENST00000274361 // upstream // 98559 // --- // --- // --- // --- /// ENST00000343975	HMGCR	HMGCR, Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), q13.3
SNP_A-2205522	ccagttaaaagggcca[A/G]gagtgaaagccgagct	A	G	Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 //	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2206192	ccatcataatgttcta[C/T]aatgaaggcttctatt	C	T	// Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA. /// NM_001761 // upstream //	ABCA3	ABCA3, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), p13.3
SNP_A-1796720	ggttatgctcagactc[A/G]cccttcatcacctcct	A	G	sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA. /// ENST00000254958 // intron // 0 // --- // --- // --- // ---	JAG1	JAG1, Homo sapiens jagged 1 (Alagille syndrome) (JAG1), p12.2
SNP_A-1682888	ctcgcaaagtaccatttctccattt[C/T]attctagttgctgggtcattccagc	C	T	carboxypeptidase E	CPE	CPE , rs1837171, carboxypeptidase E,q32.3
SNP_A-1870314	tcctttggcctaagat[C/T]aagtggaggtccccct	C	T	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 4 (CACNA2D4), transcript variant 1, mRNA. ///	CACNA2D4	CACNA2D4, Homo sapiens calcium channel, voltage-dependent, alpha 2 p13.33
SNP_A-1827959	taagaactgaagccca[C/G]taagttgggagtgggg	C	G	Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), mRNA. /// ENST00000331079 // intron // 0 // --- // --- // --- // --- /// ENST00000330796 // intron //	HRMT1L3	HRMT1L3, Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), p15.1
SNP_A-1820690	gtttcagttacttaat[C/T]agtgcagggtttctta	C	T	55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 677065 // Hs.473082 // ZFP64 // 55734 // Homo	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1820750	gtttccacatctctaa[C/T]ggtaatagcacattga	C	T	Homo sapiens FLJ40536 protein (FLJ40536), mRNA. /// ENST00000316750 // upstream // 42789 // --- // --- // --- // ---	-	-, Homo sapiens FLJ40536 protein (FLJ40536), q26.13
SNP_A-1954295	tttgcacctagcaata[A/C]tagcaattggccaata	A	C	9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // downstream //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-1952430	tttctgaaatcgacac[A/G]gaggttcccaaacccc	A	G	25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// ENST00000343505 // upstream //	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q23.3
SNP_A-1960252	tttttaatttcaggta[A/G]aagtattccacctcat	A	G	// 389400 // Homo sapiens IVFI9356 (UNQ9356), mRNA. /// NM_019036 // downstream // 80121 // Hs.147054 //	UNQ9356	UNQ9356, Homo sapiens IVFI9356 (UNQ9356), p12.1
SNP_A-1979274	tataacctttcccaga[A/C]tcaaggaaactaacat	A	C	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 178167	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1914326	tgtgttcgaattttaa[A/G]caggtaatgctacatt	A	G	Homo sapiens butyryl Coenzyme A synthetase 1 (BUCS1), mRNA. /// ENST00000307493 // intron // 0 // --- // --- // --- // ---	BUCS1	BUCS1, Homo sapiens butyryl Coenzyme A synthetase 1 (BUCS1), p12.3
SNP_A-1904061	tgggcagccactaaac[A/G]gaacacagcagatgtg	A	G	Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-1889359	tgagtgtgatatcacc[A/G]catcaattggaaatgg	A	G	50834 // Homo sapiens taste receptor, type 2, member 1 (TAS2R1), mRNA. /// NM_199133 // downstream // 79322 //	TAS2R1	TAS2R1, Homo sapiens taste receptor, type 2, member 1 (TAS2R1), p15.2
SNP_A-1882803	tgaaagattgagccaa[C/G]attgaagagaaagttt	C	G	Homo sapiens chromosome 6 open reading frame 162 (C6orf162), mRNA. /// ENST00000229570 // intron // 0 // --- //	C6orf162	C6orf162, Homo sapiens chromosome 6 open reading frame 162 (C6orf162), q15
SNP_A-1878988	tcttaaatgaaaacca[A/G]gccaaataatagacat	A	G	// Homo sapiens retinoid X receptor, gamma (RXRG), mRNA. /// NM_001005214 // upstream // 90939 // Hs.120487 //	RXRG	RXRG, Homo sapiens retinoid X receptor, gamma (RXRG), q23.3
SNP_A-1880010	tcttcgtgcagtagaa[A/G]taataggtaaatttag	A	G	Homo sapiens SWAP-70 protein (SWAP70), mRNA. /// ENST00000355139 // intron // 0 // --- // --- // --- // --- ///	SWAP70	SWAP70, Homo sapiens SWAP-70 protein (SWAP70), p15.4
SNP_A-1880014	tcttctaaaaacaaga[C/T]gagaagaacaaagcac	C	T	Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // --- // --- // --- // ---	HNT	HNT, Homo sapiens neurotrimin (HNT), q25

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903942	tgggattgcattacac[A/G]gattatggggtctcta	A	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // intron // 0 // Hs.453951 // NRG1 //	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1908441	tgtagaatcatgtaaa[C/T]atctttggaccaacca	C	T	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1923572	ttaggggtcgagaaga[C/T]gtggtgagactccgtg	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-1976440	atgctaacgtgaatca[A/C]aaatcatattcagact	A	C	57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 548446 //	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-1981634	catgacccttaactta[A/T]cgtggtctagccaaat	A	T	// 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 145327 //	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-1962725	atttgaactactggaa[A/G]ccatgtatatttgtcc	A	G	Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // --- // --- // --- // ---	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1961556	ttttttttaagcctgc[C/T]ctgaagattttgtttt	C	T	FLJ32833 // 148545 // Homo sapiens hypothetical protein FLJ32833 (FLJ32833), mRNA. /// ENST00000334476 //	FLJ32833	FLJ32833, Homo sapiens hypothetical protein FLJ32833 (FLJ32833), p13.3
SNP_A-1955264	tttggctttagatgtc[C/T]aggtaactaaggcaag	C	T	// 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA (cDNA clone IMAGE:4791744), partial cds. /// NM_017799 // downstream // 74189 // Hs.497253 //	C14orf101	C14orf101, Homo sapiens chromosome 14 open reading frame 101, (cDNA clone IMAGE:4791744), partial cds. q22.3
SNP_A-1817873	gttcctttgctgaggc[C/T]actgctattttctaaa	C	T	// 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 241750 // Hs.499705 // FAM13C1 // 220965	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1823139	taaaacactctgacca[C/T]gcccctctttgccctt	C	T	1003 // Homo sapiens cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA. /// ENST00000341529	CDH5	CDH5, Homo sapiens cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), q22.1
SNP_A-1824421	taaactagaatggggc[A/G]agaccataatcagaga	A	G	Homo sapiens syntaxin 12 (STX12), mRNA. /// ENST00000236419 // intron // 0 // --- // --- // --- // ---	STX12	STX12, Homo sapiens syntaxin 12 (STX12), p35.3
SNP_A-1830308	taatatattggtgcaa[A/G]ctttgagaggtatcta	A	G	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1868462	tcctcctacaagtgac[C/T]gatctcatacattaaa	C	T	165679 // Homo sapiens ADMP (ADMP), mRNA. /// NM_000984 // downstream // 37695 // Hs.419463 // RPL23A	ADMP	ADMP, Homo sapiens ADMP (ADMP), q26.1
SNP_A-1852411	tatttaataagcaacc[A/G]aggcaagtttgctggg	A	G	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1856120	tcacaaaactgcccaa[A/G]gtaattatgataatca	A	G	Homo sapiens integrin, beta 8 (ITGB8), mRNA. /// ENST00000222573 // intron // 0 // --- // --- // --- // ---	ITGB8	ITGB8, Homo sapiens integrin, beta 8 (ITGB8), p21.1
SNP_A-1676590	ggaacagagtatactggttaattga[A/G]cttctgattaagtatgggttaatga	A	G	7479 // wingless-type MMTV integration site family, member 8B /// NM_005063 // downstream // 65815 // Hs.119597 //	WNT8B	WNT8B , rs10509743, wingless-type MMTV integration site family, member 8B ,q24.31
SNP_A-1641749	gaaaacaccccagtggaaactgcat[A/G]aatgattgataagagctgagagctg	A	G	RPS24 // 6229 // ribosomal protein S24 /// NM_020338 // upstream // 47901 // Hs.438767 // RAI17 // 57178 // retinoic	RPS24	RPS24 , -, ribosomal protein S24 ,q22.3
SNP_A-1783264	ggcagtataaatgagg[A/C]cattgtagagttattc	A	C	7932 // Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA. /// NM_030883 // upstream //	OR2H2	OR2H2, Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), p22.1
SNP_A-1788996	gggcacagttctcact[C/G]agtaggttggggacgt	C	G	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-1788997	gggcacatccaactgc[A/G]caagaagttttccagc	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1296098 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1787694	gggacaggagatcatc[A/G]gacattttgcctacta	A	G	SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium,p11.23
SNP_A-2208333	cccacataagttcaag[A/C]aacaatgaattgaacc	A	C	114907 // Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, mRNA. /// NM_148177 // upstream //	FBXO32	FBXO32, Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, q24.13
SNP_A-2211922	ccctgaaatgaatatc[C/T]aaaccagcaccaaaaa	C	T	Homo sapiens gasdermin-like (GSDML), mRNA. /// ENST00000360317 // intron // 0 // --- // --- // --- // --- ///	GSDML	GSDML, Homo sapiens gasdermin-like (GSDML), q21.1
SNP_A-2198407	catttacacactaaaa[C/T]acaccctcacactcaa	C	T	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2164918	caaacggtaacaggcc[A/G]atttatcagcttctaa	A	G	29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 268872 // Hs.98367 //	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2159315	atttaagatgctccaa[C/T]gaaagtgccttaagat	C	T	202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 46566 // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2158916	attgtgtctacactaa[C/T]gttgtgtccaaaattc	C	T	EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 546889 // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2144304	atgagtgttggaagc[C/G]aactagggtgggactg	C	G	2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 //	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2141440	atcttaaaaactcaca[A/G]gcggctttggaatatt	A	G	Homo sapiens galactokinase 2 (GALK2), transcript variant 1, mRNA. /// NM_001001556 // intron // 0 // Hs.117532 // GALK2	GALK2	GALK2, Homo sapiens galactokinase 2 (GALK2), transcript variant 1, q21.1
SNP_A-2146440	atgctccctggccaca[C/G]cattactattggctgt	C	G	57665 // Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA. /// NM_001002006 // upstream //	RDH14	RDH14, Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), p24.1
SNP_A-2121039	agtctccaagtcatat[C/T]acaatcaaagtttaag	C	T	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2120143	agtcagagaaaagtac[C/T]ggtttgagtagatgaa	C	T	ENST00000360575 // intron // 0 // --- // --- // ---	-	q31.1
SNP_A-2121788	agtgacttctgtctac[A/G]ctacagatgaactgaa	A	G	Homo sapiens chromosome 7 open reading frame 6 (C7orf6), mRNA. /// ENST00000318238 // intron // 0 // --- // ---	C7orf6	C7orf6, Homo sapiens chromosome 7 open reading frame 6 (C7orf6), q21.3
SNP_A-2113399	aggccttttcttcctc[G/T]agagacagcccccagtc	G	T	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33
SNP_A-2125373	agtttaaataaagacc[A/G]agttgtattcagactc	A	G	Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. /// ENST00000224950 // intron	OBFC1	OBFC1, Homo sapiens oligonucleotide,q24.33
SNP_A-2134032	atatgaaaagaggctc[A/G]ccatattcaatcatca	A	G	ENST00000318973 // intron // 0 // --- // --- // ---	-	q14.3
SNP_A-2012491	agttttttggctgaag[G/T]aaccagggagaaatcc	G	T	ENST00000284920 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-2008613	gggagggtaatccaa[A/C]caatgaggttcgctat	A	C	ENST00000301807 // intron // 0 // --- // --- // ---	-	p22.3
SNP_A-2003208	caccaaagtaagatac[A/G]cgttcctaatgggaaa	A	G	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// ENST00000343323 // intron // 0 // --- // --- // ---	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-2001224	aggtcagcaagttgta[A/G]ctaagatataaacaat	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 267101 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2086405	actcttcgttaggta[C/G]accttttgttctttttg	C	G	27043 // Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), mRNA. /// NM_199004 // upstream // 1913	PELP1	PELP1, Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), p13.2
SNP_A-2083861	actactaatttcttgaat[A/G]gacatttttggtgtg	A	G	7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream //	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2077566	accacccaggctctca[A/G]ctaactctccaagtg	A	G	8654 // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, mRNA. /// NM_033437 //	PDE5A	PDE5A, Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, q26
SNP_A-2293276	gcagaggctcttccaa[C/T]gttcagtcattctgc	C	T	23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000322896 // upstream // 44074 // --- // --- // ---	LRCH1	LRCH1, Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.13
SNP_A-2251711	cttcagtgggtcagc[A/G]gattctggttatggt	A	G	Homo sapiens keratin 5b (K5B), mRNA. /// ENST00000304620 // CDS // 0 // --- // --- // --- ///	K5B	K5B, Homo sapiens keratin 5b (K5B), q13.13
SNP_A-2267578	gaatatttattaaaac[A/T]caggcaagctggagag	A	T	Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// ENST00000282272 // intron // 0 // ---	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-2260353	gaaacaaaagaatccaa[A/G]aagaattgatgttttc	A	G	84727 // Homo sapiens likely ortholog of mouse gene rich cluster, C9 gene (GRCC9), mRNA. /// NM_006992 // upstream // 19609 // Hs.155586 // B7 // 10233 // Homo	GRCC9	GRCC9, Homo sapiens likely ortholog of mouse gene rich cluster, C9 gene (GRCC9), p13.31
SNP_A-2280437	gagggtctggttgaaa[C/T]gagccgttccctgtgg	C	T	Homo sapiens chromosome 20 open reading frame 36 (C20orf36), mRNA. /// ENST00000356590 // intron // 0 // --- // ---	C20orf36	C20orf36, Homo sapiens chromosome 20 open reading frame 36 (C20orf36), q13.33
SNP_A-2274741	gagaaagcaatgctcc[A/T]aacactgttttctac	A	T	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 239697 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2251215	cttcaaaactctttca[A/G]tccaggagctgggcat	A	G	FLJ13150 // 79871 // Homo sapiens hypothetical protein FLJ13150 (FLJ13150), mRNA. /// NM_005263 // downstream // 92344 // Homo sapiens NTKL-binding protein 1	FLJ13150	FLJ13150, Homo sapiens hypothetical protein FLJ13150 (FLJ13150), p22.1
SNP_A-2234114	ctcattctatctctg[G/T]aatataagatcttcat	G	T	(FLJ11752), mRNA. /// ENST00000286050 // upstream //	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2238126	ctctgccatgctaaat[A/G]actgacctgaagccat	A	G	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // --- // --- // ---	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2291865	gcacaggttaggagaa[C/T]gcacacctcctggta	C	T	sapiens Charcot-Leyden crystal protein (CLC), mRNA. /// ENST00000221804 // intron // 0 // --- // --- // ---	CLC	CLC, Homo sapiens Charcot-Leyden crystal protein (CLC), q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289103	gatttctcgcatccca[A/G]tactttaaaactttgc	A	G	ENST00000360575 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2297789	gccaggccaagcggac[A/G]gaacaagtccagagaa	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1146834 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2308569	gctttcaaagcaatta[C/G]gtccatatgtaggggc	C	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1198483 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2304067	gctccagggtacagaa[A/G]tcggggtaagagtatt	A	G	sapiens renin (REN), mRNA. /// ENST00000272190 // intron	REN	REN, Homo sapiens renin (REN), q32.1
SNP_A-2085083	actcactttctgagta[C/T]ggtttccagcaggaag	C	T	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 35558 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2090757	actttaggtagtctca[C/T]agaaaaattaagagtc	C	T	ENST00000326018 // intron // 0 // --- // --- // --- // --- /// ENST00000358624 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2101595	agatgaggaggtgaaa[A/G]acttgatgagtcatgc	A	G	FLJ44112 // 374467 // Homo sapiens FLJ44112 protein (FLJ44112), mRNA. /// ENST00000342887 // downstream //	FLJ44112	FLJ44112, Homo sapiens FLJ44112 protein (FLJ44112), q23.1
SNP_A-2101755	agatgcctggaattgc[A/C]gacagatccctggttc	A	C	// 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2098786	agagctaaggatggtg[G/T]aaagacagtcaggctg	G	T	// 112616 // Homo sapiens chemokine-like factor super family 7 (CKLFSF7), transcript variant 2, mRNA. /// NM_138410 // downstream // 1241 // Hs.440494 // CKLFSF7 // 112616 //	CKLFSF7	CKLFSF7, Homo sapiens chemokine-like factor super family 7 (CKLFSF7), transcript variant 2, p23
SNP_A-2074479	acatagagagcttaga[C/T]atttctgtctggaaca	C	T	2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 102381 // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-2050591	aaggattttatgagaa[A/C]tggtattagctcccac	A	C	DKFZP564F0522 // 25940 // Homo sapiens DKFZP564F0522 protein (DKFZP564F0522), mRNA. /// NM_207329 // downstream // 4841 // Hs.528847 // MYADML	DKFZP564F0522	DKFZP564F0522, Homo sapiens DKFZP564F0522 protein (DKFZP564F0522), p22.3
SNP_A-2055779	aataatttggtaatac[C/T]gaagtctccaacagaa	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 723525 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2002154	ctagctgttaactgaa[C/G]tatgcacagaaaactg	C	G	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2008101	aaaaagataggtaata[A/G]tatactgctcacgcca	A	G	ENST00000288344 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-2014256	ggaaatgtaagatgga[C/T]acagagatatactgca	C	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1843875 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2039387	aacatagctaactgca[A/G]attagttacgaaaggg	A	G	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2041414	aaccttaagaggaagc[C/T]gctattgttatctctc	C	T	10920 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, mRNA. /// NM_006710 // downstream // 49212 // Hs.531713 // COPS8 // 10920 //	COPS8	COPS8, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, q37.3
SNP_A-2042882	aactcttcttggtcct[A/G]agcccagtgtcagcct	A	G	Homo sapiens bone morphogenetic protein 8a (BMP8A), mRNA. /// ENST00000331593 // intron // 0 // --- // --- // --- // ---	BMP8A	BMP8A, Homo sapiens bone morphogenetic protein 8a (BMP8A), p34.3
SNP_A-2122176	agtgatttgcttttga[C/T]aatcctgtgaggcagg	C	T	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 429307 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2150216	atgtctatatctgctg[C/T]atgtattttataattg	C	T	sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // --- // --- // --- // ---	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-2140125	atctataatctttcta[C/T]gacctgaggaaccttg	C	T	// 81621 // Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), mRNA. /// ENST00000224809 //	KAZALD1	KAZALD1, Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), q24.31
SNP_A-2189218	cagttcaattgtaatc[C/G]atgttcataggaatgt	C	G	6659 // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA. /// NM_000948 // downstream // 63259 //	SOX4	SOX4, Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), p22.3
SNP_A-2169726	caaggaatttgggggga[A/G]taagagacaaagtcta	A	G	// 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream //	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2179501	cacttacttattttga[A/G]gaaaaaagcaaattgt	A	G	Homo sapiens topoisomerase (DNA) III beta (TOP3B), mRNA. /// ENST00000215840 // intron // 0 // --- // --- // --- // ---	TOP3B	TOP3B, Homo sapiens topoisomerase (DNA) III beta (TOP3B), q11.22
SNP_A-2208355	cccacatgaaattaat[C/T]agaggacttcagggct	C	T	// 400451 // Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), mRNA. /// NM_004965 // upstream // 38581 // Hs.356285 // HMGN1 // 3150 // Homo	LOC400451	LOC400451, Homo sapiens hypothetical gene supported by AK075564; BC060873 (LOC400451), q26.1
SNP_A-2204916	ccagggatgaatcaga[C/T]agaatgtttatgtaga	C	T	ENST00000309493 // intron // 0 // --- // --- // --- // ---	-	q22.33
SNP_A-2202597	ccacctcctttaagcc[C/T]ccagaatatctcatat	C	T	1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 67517 //	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2214015	cctaagatccaagatc[A/G]cagaaagcatgagaac	A	G	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2213974	cctaactcacagtcct[A/G]aagtatcttcgagata	A	G	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 // 53947 // Homo sapiens alpha 1,4-galactosyltransferase (A4GALT), mRNA. /// ENST00000249005 // upstream //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-2216354	cctcctggctgaagc[G/T]atctgccatctcaac	G	T		A4GALT	A4GALT, Homo sapiens alpha 1,4-galactosyltransferase (A4GALT), q13.2
SNP_A-2219867	ccttagccagcatgcc[A/G]aaagagagatctggaa	A	G	Homo sapiens zinc finger protein 423 (ZNF423), mRNA. /// ENST00000262383 // intron // 0 // --- // --- // ---	ZNF423	ZNF423, Homo sapiens zinc finger protein 423 (ZNF423), q12.1
SNP_A-2227117	ctaattatcactgac[A/G]aatacataagctgttt	A	G	// Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // --- // --- // ---	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2225203	cgttcatggacgcaga[C/G]gctcagtggtgggct	C	G	Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-1788896	gggcaaatgagattag[A/G]actgagaattactga	A	G	Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), mRNA. /// ENST00000262750 // intron // 0 // --- // --- // ---	ATPAF1	ATPAF1, Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), p33
SNP_A-1791629	gggtccagggagtgcc[C/T]aaagtgtctagaaggc	C	T	9620 // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA. /// ENST00000262738 // upstream // 45708 // --- // ---	CELSR1	CELSR1, Homo sapiens cadherin, EGF LAG seven pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), q13.31
SNP_A-1790807	gggggatggtttaaa[A/G]aggatggaactgacta	A	G	/// ENST00000304952 // downstream // 33785 // --- // --- // ---	-	p11.21
SNP_A-1797634	ggtttctctactgaa[C/T]gtatccaaatctggg	C	T	/// ENST00000360919 // upstream // 282964 // --- // --- // ---	-	q13.1
SNP_A-1794766	ggtctgatctaattac[A/G]cgagtctttttttt	A	G	1 // 337880 // Homo sapiens keratin associated protein 11-1 (KRTAP11-1), mRNA. /// NM_003253 // downstream // 87678	KRTAP11-1	KRTAP11-1, Homo sapiens keratin associated protein 11-1 (KRTAP11-1), q22.11
SNP_A-1809572	gtgagatagcaaagaa[A/T]gtcgggcagaggctct	A	T	Homo sapiens annexin A4 (ANXA4), mRNA. /// ENST00000355054 // intron // 0 // --- // --- // ---	ANXA4	ANXA4, Homo sapiens annexin A4 (ANXA4), p13.3
SNP_A-1812416	gtggcagcctgcctca[C/T]ggccaaaatgtgatct	C	T	7441 // Homo sapiens pre-B lymphocyte gene 1 (VPREB1), mRNA. /// ENST00000333289 // downstream // 9630 // --- // ---	VPREB1	VPREB1, Homo sapiens pre-B lymphocyte gene 1 (VPREB1), q11.22
SNP_A-1804732	gtcagggtgtgaagta[C/T]aggaaaatgcttcttc	C	T	Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA. /// ENST00000350459 // intron // 0 // --- // --- // ---	FLJ10375	FLJ10375, Homo sapiens hypothetical protein FLJ10375 (FLJ10375), p22.1
SNP_A-1752591	caagtgaactacagtaagatcccaa[A/G]agaactgaaaaggctacctttata	A	G	2012 // epithelial membrane protein 1 /// NM_182558 // downstream // 10521 // Hs.448717 // FLJ33810 // 283422 //	EMP1	EMP1 , rs1993511, epithelial membrane protein 1 p13.1
SNP_A-1744979	aaaaggcgacttgtagtgtatgtta[C/G]gcaaaaagaggtgggtggaglg	C	G	// 319089 // chromosome 14 open reading frame 25 /// NM_001049 // upstream // 124352 // Hs.248160 // SSTR1 //	C14orf25	C14orf25, rs10498336, chromosome 14 open reading frame 25 ,q21.1
SNP_A-1657748	aaatagactcccccaaatcaaacaa[A/G]tacctatgtcctaacaggcttaga	A	G	51696 // headcase homolog (Drosophila) /// NM_153235 // downstream // 47572 // - // - // - // -	HECA	HECA , rs9436653, headcase homolog (Drosophila) q24.1
SNP_A-1825555	taaataggccaaaaa[C/T]ctgagggagatggtt	C	T	91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. /// ENST00000324309 // intron // 0	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), p15.2
SNP_A-1827647	taactggtgataataa[C/T]gtactgtgacatatcc	C	T	2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream //	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1819029	gttgcatattgcaaca[C/T]gataatacctgaag	C	T	// 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 // upstream //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-1982492	ttttatcaatggtaaa[C/T]aattgttgatttaact	C	T	84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000315948 // upstream // 76466 // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1925653	ttatgagtgagcatca[A/G]aggaaatcaagagtgt	A	G	2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 20516	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1922435	ttagaacacatagaag[A/G]aaaagttactctaacc	A	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // /// ENST00000259567 // downstream // 12228 // --- // --- // ---	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-1926139	ttattaaacaggaca[A/G]aaatcaaatctgacat	A	G	// --- /// ENST00000360460 // downstream // 14070 // --- // ---	-	p24.1
SNP_A-1909712	tgtcaatagcgctgca[A/G]taaatacggaggtgtg	A	G	129685 // Homo sapiens taube nuss homolog (mouse) (TBN), mRNA. /// ENST00000356905 // downstream // 14070	TBN	TBN, Homo sapiens taube nuss homolog (mouse) (TBN), p21.1
SNP_A-1878586	tctgtgctagaataa[C/T]tgattgcccatgtta	C	T	Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1874281	tctccagaagtttac[A/G]cttgagtgcacccaga	A	G	Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // 253827 // Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// NM_003483 // upstream // 301863 //	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1881714	tcttggagtttgaa[A/G]tctctcctagcttat	A	G		MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1888746	tgagggattttgagga[C/T]taatgatgggtacagg	C	T	sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- // --- // --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-1887989	tgagcagacacaaaga[C/T]atttctgagctctctc	C	T	Homo sapiens mRNA for KIAA0456 protein, partial cds. /// ENST00000295713 // intron // 0 // --- // --- // --- // ---	SRGAP2	SRGAP2, Homo sapiens for KIAA0456 protein, partial cds. ,q32.1
SNP_A-1881920	tcttttcatctgtcta[A/G]atctactaatcttatt	A	G	152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 //	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1875151	tctctcccagctccaa[A/T]caatctctgacagatt	A	T	64111 // Homo sapiens chromosome 7 open reading frame 9 (C7orf9), mRNA. /// ENST00000222674 // upstream //	C7orf9	C7orf9, Homo sapiens chromosome 7 open reading frame 9 (C7orf9), p15.2
SNP_A-1902330	tggcccaagaagagaa[C/T]gtatactgatctctca	C	T	// 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 101962 // Hs.100431 // CXCL13 //	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1899778	tggaatgtgatttttta[C/T]gtagccattatactat	C	T	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1894145	tgcatggaaagagaaa[C/T]ggccagatatgcaatt	C	T	5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase,q22.1
SNP_A-1906309	tggtgatggagggaag[A/G]atgcacaagctctgtg	A	G	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2), transcript variant 1, mRNA. /// ENST00000355896 // intron // 0 // --- // --- // --- // ---	CBFA2T2	CBFA2T2, Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2), transcript variant 1, q11.22
SNP_A-1917100	tgtttggtggttttaa[A/G]acatgacctcaaattc	A	G	Homo sapiens LETM1 domain containing 1 (LETMD1), mRNA. /// ENST00000262055 // intron // 0 // --- // --- // --- // ---	LETMD1	LETMD1, Homo sapiens LETM1 domain containing 1 (LETMD1), q13.12
SNP_A-1973652	ttgaatccctggctcc[A/G]attattcccattcctc	A	G	Homo sapiens hypothetical protein MGC4308 (MGC4308), mRNA. /// NM_182909 // intron // 0 // Hs.104672 // DOC1 //	MGC4308	MGC4308, Homo sapiens hypothetical protein MGC4308 (MGC4308), q12.1
SNP_A-1959799	ttttgtaagtaataaa[A/T]cctctgcataaattca	A	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1933395	ttctaattttgatacc[A/G]caatgattaattctgt	A	G	51378 // Homo sapiens angiopoietin 4 (ANGPT4), mRNA. /// ENST00000262924 // upstream // 29435 // --- // --- // --- // ---	ANGPT4	ANGPT4, Homo sapiens angiopoietin 4 (ANGPT4), p13
SNP_A-1943452	ttggttttagacttcc[A/C]atcaacatcacttgat	A	C	CAPZA3 // 93661 // Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA. /// NM_019012 // upstream // 183836 // Hs.188614 // PLEKHA5	CAPZA3	CAPZA3, Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), p12.3
SNP_A-1944333	ttgtccttattctacc[G/T]caatcacttttattaa	G	T	Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1832903	tacaatggtggaccca[C/G]aagactataatagagc	C	G	Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // --- // --- // --- // --- ///	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-1842995	tagtatgaggtatgag[C/T]aatgagaggatagcat	C	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-1842538	taggttaatggataaa[C/T]gcagaaattgaccttt	C	T	sapiens mRNA for KIAA0121 protein, partial cds. /// NM_014667 // intron // 0 // Hs.373959 // VGLL4 // 9686 //	VGLL4	VGLL4, Homo sapiens for KIAA0121 protein, partial cds. ,p25.3
SNP_A-1853960	tcaaaatccaccttaa[C/T]gtaggtcctgatcttg	C	T	80759 // Homo sapiens chromosome 6 open reading frame 148 (C6orf148), mRNA. /// ENST00000257765 // upstream //	C6orf148	C6orf148, Homo sapiens chromosome 6 open reading frame 148 (C6orf148), q13
SNP_A-1847394	tatccctatcaagaga[A/G]aaaatcaagcttcaca	A	G	55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000237194 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-1870764	tcgctgcctttgagga[A/G]tatacagattaagcca	A	G	Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // intron // 0 // --- // --- // --- // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-1866480	tccccagccaggtggc[A/G]cggagaccatgacagc	A	G	Homo sapiens hypothetical protein FLJ14966 (FLJ14966), mRNA. /// ENST00000256186 // intron // 0 // --- // --- // --- // ---	FLJ14966	FLJ14966, Homo sapiens hypothetical protein FLJ14966 (FLJ14966), p15.3
SNP_A-1864111	tccacagttggtttaa[C/T]gcgatgtggaactcac	C	T	sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) mRNA, complete cds. /// NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and	PSD3	PSD3, Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) complete cds. p22
SNP_A-1692376	atgtaagaatgttcaattttaatca[C/T]aataactctaaactggaaacagccc	C	T	// 7048 // transforming growth factor, beta receptor II (70/80kDa) /// NM_178862 // upstream // 386193 //	TGFBR2	TGFBR2 , rs839594, transforming growth factor, beta receptor II (70,p24.1
SNP_A-1703091	taatatctgtctattttatgtaaga[C/G]tatatataatccagtaatttttgag	C	G	// 26040 // SET binding protein 1 /// NM_020783 // upstream // 4014 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs816753, SET binding protein 1 ,q12.3
SNP_A-1732972	ttttgtcctgatctcaagtttaagg[A/G]ccatctttatgggtgatgcgtcact	A	G	50508 // NADPH oxidase 3 /// NM_020732 // upstream // 1132499 // Hs.436008 // ARID1B // 57492 // AT rich	NOX3	NOX3 , rs10499302, NADPH oxidase 3 ,q25.3
SNP_A-1740429	gaaatagttatgttaaaggaagaga[A/C]cattttcccatgaagcaattggtta	A	C	NM_020675 // intron // 0 // Hs.421956 // Spc25 // 57405 // kinetochore protein Spc25	Spc25	Spc25 , rs560494, kinetochore protein Spc25,q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1758175	tttagttactaacttacaatttaaa[C/G]tatgataaagtaattgctgcataat	C	G	54674 // leucine rich repeat neuronal 3 /// NM_032549 // downstream // 531375 // Hs.89576 // IMMP2L // 83943 //	LRRN3	LRRN3 , rs1525499, leucine rich repeat neuronal 3 ,q31.1
SNP_A-1805073	gtcatgataggaatgc[A/G]cctaccccactttaat	A	G	/// ENST00000354196 // upstream // 1178983 // --- // --- // --- // --- /// ENST00000355224 // upstream // 1178983 // --- // --- // ---	-	q21.11
SNP_A-2220371	ccttcctgtcttcctc[A/T]ccagattgtgagatat	A	T	115019 // Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, mRNA. /// NM_134325 // upstream // 3075 // Hs.164073 // SLC26A9 // 115019 // Homo	SLC26A9	SLC26A9, Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, q32.1
SNP_A-2210302	ccccattggtgtgtag[C/T]cccgcgcagtcgccgg	C	T	// Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// ENST00000341909 // upstream // 85544	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2211665	ccctccacgaggtcaa[C/T]tgtagttcagtgattt	C	T	1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 272695 //	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2173438	cacaagtccacaccag[G/T]aataaaggaagtcaaa	G	T	1400 // Homo sapiens collapsin response mediator protein 1 (CRMP1), mRNA. /// NM_207405 // downstream // 3520 //	CRMP1	CRMP1, Homo sapiens collapsin response mediator protein 1 (CRMP1), p16.1
SNP_A-2198333	catttaaaatgctttc[C/G]aggtattcatgaaaat	C	G	Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// ENST00000354440 // intron // 0 // --- //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2196511	catgtttgtggaatca[A/G]gagttccaatttttct	A	G	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 331035 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2139680	atcggggttcaaattc[G/T]caaatggcatgaactg	G	T	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2144538	atgatcaatcctttaa[A/C]aaccaagtatgtatta	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 58280 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2038622	aacagaatttaaaagg[A/G]ccattctaattatagt	A	G	sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA. /// ENST00000267163 // intron // 0 // --- // --- // --- // ---	RB1	RB1, Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), q14.2
SNP_A-2029404	ccgcagctcctggcac[C/G]gccgacaggagttgaa	C	G	sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2028978	aaagaaaagaaaatga[C/G]gagcacactagttggt	C	G	143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// NM_199461 // upstream //	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11
SNP_A-2106888	agccttccatttcaga[A/G]agggcccacgccatcc	A	G	// 56951 // Homo sapiens chromosome 5 open reading frame 15 (C5orf15), mRNA. /// ENST00000231482 // downstream //	C5orf15	C5orf15, Homo sapiens chromosome 5 open reading frame 15 (C5orf15), q31.1
SNP_A-2299103	gcccgacctcagtccc[A/G]ctgtccaagccatctt	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-2233970	ctcatggcctgtcaca[A/G]tggtccctgaagtatg	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 888912 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2231738	ctcaaaagatacaaaa[A/C]tattcattgctttgtt	A	C	// 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 681978 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2252474	cttcctcccagggcta[C/T]gcaattctgtgagtct	C	T	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2), mRNA. /// ENST00000271965 // intron // 0 // --- // --- // --- // ---	GALNT2	GALNT2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2), q42.13
SNP_A-2253350	cttctgtaactcatat[C/G]acatcaaataattcac	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2233128	ctcagccagcaagtaa[C/G]aaagtgggaaaggagt	C	G	4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 152243 // Hs.21388 //	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2230567	ctatctaaaaccacaa[A/T]gacccaaatactactt	A	T	Homo sapiens leptin receptor (LEPR), transcript variant 2, mRNA. /// NM_002303 // intron // 0 // Hs.23581 // LEPR //	LEPR	LEPR, Homo sapiens leptin receptor (LEPR), transcript variant 2, p31.2
SNP_A-2282609	gagtttcaatcttgga[C/T]gatgaaaaaagttctg	C	T	/// ENST00000343280 // upstream // 48024 // --- // --- // --- // --- /// ENST00000340130 // upstream // 47853 // --- // --- // --- // ---	-	q11.2
SNP_A-2258842	ctttttaatgacgttg[A/C]agtttgcttctcagaa	A	C	51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 2837 // --- // --- //	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-2261481	gaaaggacatgaaaac[A/T]gaataatttaatggtg	A	T	Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // --- // --- // --- // ---	PCAF	PCAF, Homo sapiens p300 p24.3
SNP_A-2267128	gaataagtgttttaca[A/G]cttgaagaaaaatgat	A	G	Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2288008	gattattgtcaggaac[A/G]attttctgtagacatc	A	G	131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// NM_144715 // downstream // 306688 // Hs.257224 // EFHB //	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2314442	ggagggctacaggagt[A/G]acaggcttaagcactg	A	G	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2054953	aataaatagcaataga[G/T]agcaaatatacctagt	G	T	57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 79528 // Hs.424711 //	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2070569	acacctgcacttaacc[A/G]cacgttcctctccagc	A	G	151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 //	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-2000460	ttttttaatctgaaaa[C/T]gagccaggcatttctg	C	T	sapiens dermatopontin (DPT), mRNA. /// ENST00000271418 // intron // 0 // --- // --- // --- // ---	DPT	DPT, Homo sapiens dermatopontin (DPT), q24.2
SNP_A-2150789	atgtgcttggctcaca[C/T]tagtggttcagatcct	C	T	SH3BGRL2 // 83699 // Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA. /// NM_022726 // downstream // 149216 // Hs.101915 //	SH3BGRL2	SH3BGRL2, Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), q14.1
SNP_A-2113367	aggccttcccctaaca[C/T]tgaaaacaagacaagg	C	T	Homo sapiens TBC1 domain family, member 14 (TBC1D14), mRNA. /// ENST00000340816 // intron // 0 // --- // --- // --- // ---	TBC1D14	TBC1D14, Homo sapiens TBC1 domain family, member 14 (TBC1D14), p16.1
SNP_A-2208931	cccagcatggagtaaa[C/T]gcttaaactgtgctta	C	T	349565 // Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// NM_178177 //	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-2209827	ccccaaaatcacatga[A/G]tcaattccttagaata	A	G	137695 // Homo sapiens hypothetical protein FLJ32370 (FLJ32370), mRNA. /// NM_024831 // downstream // 44957 //	FLJ32370	FLJ32370, Homo sapiens hypothetical protein FLJ32370 (FLJ32370), q12.1
SNP_A-2203451	ccagaaattgtttaca[C/G]gaggaaaattaatcta	C	G	// 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 // upstream //	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2221356	cctttcagactgcaag[A/G]ctgtaccaacagagat	A	G	// 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1789435	gggcccgactgcacac[G/T]catgtgaacacacaca	G	T	10158 // Homo sapiens membrane-associated protein 17 (MAP17), mRNA. /// NM_003189 // downstream // 24823 //	MAP17	MAP17, Homo sapiens membrane-associated protein 17 (MAP17), p33
SNP_A-1755026	tttcatagaagaaaccttaatgatg[A/C]aatagaagagtagaagttgtcaaaa	A	C	NM_138484 // upstream // 1032735 // Hs.105153 // SGOL1 // 151648 // shugoshin-like 1 (S. pombe)	SGOL1	SGOL1 , rs718896, shugoshin-like 1 (S. pombe),p24.3
SNP_A-1653510	aaatgcagaaccaaaggtgagtaat[A/G]agtgaaaggaccttctaactctaaa	A	G	90871 // chromosome 9 open reading frame 123 /// NM_002839 // downstream // 137943 // Hs.323079 // PTPRD	C9orf123	C9orf123 , rs4130580, chromosome 9 open reading frame 123 ,p24.1
SNP_A-1648666	gcttttattaatattatcacctcta[C/T]gaaaatctacatattcacctctggc	C	T	claudin 10	CLDN10	CLDN10 , rs9302076, claudin 10,q32.1
SNP_A-1872907	tctatcattgcaagta[G/T]ccatcatgttatcatt	G	T	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 446559 // --- // --- // --- // -	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1868864	tcctgacaccctctcc[A/G]ctcattctaagctgca	A	G	B3GALT1 // 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// NM_013233 // downstream // 69536 // Hs.276271	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-1858158	tcagaaatctggacaa[C/T]aacaactttcagggt	C	T	// Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4), mRNA. /// NM_004411 // upstream // 110126 //	PDK4	PDK4, Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4), q21.3
SNP_A-1858522	tcagagctgcaggtca[A/T]tcagactaaatcttag	A	T	Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF237782 // intron // 0 // Hs.407755 // LNX // 84708 // Homo	LNX	LNX, Homo sapiens ligand of numb-protein X (LNX), q12
SNP_A-1831343	taatgtaccatacata[A/C]ccatgtaacatgacca	A	C	1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream //	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1815224	gtgttgctcttaggaa[A/G]gttcagcccatctcta	A	G	// 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 194916 // Hs.462859	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-1980324	attcactgagttgtca[C/T]gcaaatgccgtcatca	C	T	50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 14394 // Hs.282089	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-1895752	tgcctgacattgtgaa[C/T]atctgaaacaaaataa	C	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 589200 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1896099	tgcgaacttgtagaga[C/T]aacatcaaataaagga	C	T	// 7531 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation	YWHAE	YWHAE, Homo sapiens tyrosine 3-monooxygenase p13.3
SNP_A-1896352	tgctaactcctcagaa[C/T]gagtggatgccggaga	C	T	KIAA0117 // 23029 // Homo sapiens KIAA0117 protein (KIAA0117), mRNA. /// ENST00000323183 // upstream //	KIAA0117	KIAA0117, Homo sapiens KIAA0117 protein (KIAA0117), q42.3
SNP_A-1891110	tgatgtattcttcagc[A/C]acagtggaattaaact	A	C	Homo sapiens glyoxalase I (GLO1), mRNA. /// ENST00000244746 // intron // 0 // --- // --- // --- // ---	GLO1	GLO1, Homo sapiens glyoxalase I (GLO1), p21.2
SNP_A-1879982	tcttccttgaaaagaa[C/T]ggtcagaggcagaaac	C	T	4258 // Homo sapiens microsomal glutathione S-transferase 2 (MGST2), mRNA. /// ENST00000265498 // downstream //	MGST2	MGST2, Homo sapiens microsomal glutathione S-transferase 2 (MGST2), q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1887922	tgagcaaagatcacaa[A/G]gaaaaaaagaagtaaa	A	G	51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream //	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-1878377	tctgtcttggagaacc[A/G]actgttctagaatttt	A	G	219409 // Homo sapiens GS homeobox 1 (GSH1), mRNA. /// NM_000209 // upstream // 91351 // Hs.32938 // IPF1 // 3651	GSH1	GSH1, Homo sapiens GS homeobox 1 (GSH1), q12.2
SNP_A-1912058	tgtgagccactacacc[A/C]agctttattaaatctt	A	C	Homo sapiens putative homeodomain transcription factor 2 (PHTF2), mRNA. /// ENST00000307305 // intron // 0 // --- // ---	PHTF2	PHTF2, Homo sapiens putative homeodomain transcription factor 2 (PHTF2), q11.23
SNP_A-1988274	ataccttcaaccttat[C/G]aaagagatatccttat	C	G	50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 223181 // Hs.291587 // ARID1B //	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1967050	acgagcctcctctgta[C/T]cataactttgagttct	C	T	/// ENST00000358997 // upstream // 281402 // --- // --- // --- //	-	q36.1
SNP_A-1936666	ttcttgtcaatgtcta[C/T]ggattaaaccagagca	C	T	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// ENST00000199936 // intron // 0 // --- //	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-1821874	gttttataaaacccac[A/G]aacacgggagtatcaa	A	G	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 536138 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-1843991	tagttctatatcatta[A/G]gccatttgcccttagc	A	G	Homo sapiens RAB21, member RAS oncogene family (RAB21), mRNA. /// ENST00000261263 // intron // 0 // --- // ---	RAB21	RAB21, Homo sapiens RAB21, member RAS oncogene family (RAB21), q21.1
SNP_A-1848389	tatgaaatttccaatg[A/T]atacctttaagcacac	A	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 692390 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1873397	tctcaaatttagctaa[C/T]ggcctgaggattcttg	C	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-1734140	tttccaatgttacttgaacacaata[C/T]aagtaatataagttttaaaaatgaa	C	T	NM_017419 // intron // 0 // Hs.381349 // ACCN5 // 51802 // amiloride-sensitive cation channel 5, intestinal	ACCN5	ACCN5 , rs1399044, amiloride-sensitive cation channel 5, intestinal,q32.1
SNP_A-1785732	ggctctcgcctcagaa[C/T]cagagcaaatacttca	C	T	7932 // Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA. /// NM_030883 // downstream	OR2H2	OR2H2, Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), p22.1
SNP_A-1798859	gtaagaaaatccttct[A/G]aaaatcagtcacaccc	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1813145	gtggtagttcttggag[C/T]aaaattcatgatgtgg	C	T	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 132546 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1809854	gtgaggtgaaatgata[A/G]atccaagatgggcatt	A	G	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 234263 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2227616	ctacataggagaaaaa[A/G]gttgcaaatggctgtt	A	G	// 54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// NM_144651 // downstream // 11599 // Hs.444882	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2207427	ccattggcatagactc[G/T]cagacccttcttggat	G	T	GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream //	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2184944	cagcttatctggactc[G/T]agaaaggtaataacca	G	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2173198	cacaacatcacaaaaa[A/T]ttaagaccaacagagc	A	T	// 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 568957 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2108035	agctctcagaagcata[A/G]gtgaaaagtctgtctg	A	G	9638 // Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA. /// NM_022549 // upstream // 17019 // Hs.224008 // FEZ1 //	FEZ1	FEZ1, Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, q24.2
SNP_A-2120554	agactctacagttata[G/T]cagtcctttatgaaac	G	T	Homo sapiens high-mobility group box 1 (HMGB1), mRNA. /// ENST00000341423 // intron // 0 // --- // --- // --- // ---	HMGB1	HMGB1, Homo sapiens high-mobility group box 1 (HMGB1), q12.3
SNP_A-2124221	agttatacatgcctga[A/C]gctagattttctggga	A	C	9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream //	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-2157436	attgagttcccaagcc[A/G]atttctgtcccagagg	A	G	Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // --- // ---	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-2167451	caacataggctaagta[A/G]agaccagtgaacagag	A	G	9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 353349 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-1991779	cagtctaatcttgcac[A/T]ggagtaaaaccaagct	A	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1994440	atggctctcttctaac[C/T]atcttattctcaagtt	C	T	Homo sapiens neurocalcin delta (NCALD), mRNA. /// ENST00000311028 // intron // 0 // --- // --- // --- // --- ///	NCALD	NCALD, Homo sapiens neurocalcin delta (NCALD), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006917	tttttgcttttgctca[A/G]aatgatgaaataatct	A	G	// 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 134393 // Hs.118183 // FLJ22833	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-2107405	agctaccatcttaaac[A/G]aagtgtactttcttat	A	G	Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // --- // ---	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-2095210	tcaatcatggagttac[A/G]aagatggaccaagata	A	G	LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream //	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2093608	agaagaagaagaagaa[C/G]aattgcaatcctccct	C	G	sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, mRNA. /// NM_206810 // intron // 0 //	MOG	MOG, Homo sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, p22.1
SNP_A-2257996	ctttgtgcaagatgat[C/T]agtctagagtttacca	C	T	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 222824	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-2260495	gaaacagactggaacg[A/G]caaagctgaatagaga	A	G	10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 520683	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-2273248	gactcatcgtacattg[C/T]agcattccttataata	C	T	7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 758475 //	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-2281458	gagtcagtggctgcta[A/G]ggttaacaacacaaag	A	G	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2230866	ctatgctaagagaaaa[A/G]gtgaggaaaagtgctg	A	G	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // intron // 0 // --- // ---	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2231581	ctatttctgtgtacaa[A/C]tacttaccccaaatgt	A	C	// 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2918510 // --- // --- // --- // ---	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2245764	ctggggcttagtggtg[G/T]aaatactttgcctgcc	G	T	// 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream //	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-2241773	ctgatctcaatatgac[C/T]aagagttgacatgaaa	C	T	Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, mRNA. /// ENST00000256772 // intron //	CRB1	CRB1, Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, q31.3
SNP_A-2094390	agaagtgataatgata[C/T]gttacttatttggtag	C	T	Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 //	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2070545	acacctccttgcatta[A/T]cctgatttgagagtat	A	T	// 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 462192 // --- // --- // --- //	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q21
SNP_A-2070350	ggctcacaagaactaa[C/T]gatggccctagagttc	C	T	// Homo sapiens interferon, gamma (IFNG), mRNA. /// ENST00000327938 // downstream // 56464 // --- // --- // --- // ---	IFNG	IFNG, Homo sapiens interferon, gamma (IFNG), q15
SNP_A-2067054	acaaactcacgaaggg[G/T]agaaagaatcaacgag	G	T	SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q23.1
SNP_A-2062137	aatgggtctaaatttg[A/C]agtgtctttgctctca	A	C	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- ///	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-2017454	gatagatcctattta[A/T]gcatcgaagtttagtc	A	T	C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 //	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2026502	aaacaaataatcaaga[C/T]ctaaactttgtgaggt	C	T	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2019442	aaccacatggagttac[C/T]ctgtgactcaataata	C	T	// 6450 // Homo sapiens SH3 domain binding glutamic acid-rich protein (SH3BGR), transcript variant 1, mRNA. /// NM_001001713 // downstream // 33818 // Hs.473847 //	SH3BGR	SH3BGR, Homo sapiens SH3 domain binding glutamic acid-rich protein (SH3BGR), transcript variant 1, q22.2
SNP_A-2147395	cctttctactgcagga[A/G]cactgtataacttctg	A	G	// 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 2195160 // Hs.391781 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-2124417	agttcacatgcataca[A/G]ctttttgtgcaggttg	A	G	// Homo sapiens FLJ46481 protein (FLJ46481), mRNA. /// ENST00000324058 // intron // 0 // --- // --- // --- // ---	FLJ46481	FLJ46481, Homo sapiens FLJ46481 protein (FLJ46481), p16.1
SNP_A-2128777	ataatctctactaaaa[C/T]tcttctacctggtggt	C	T	2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream //	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2137609	atcatcttagctcttg[A/G]actatcatgtatcagt	A	G	94033 // Homo sapiens ferritin mitochondrial (FTMT), mRNA. /// NM_152546 // upstream // 87441 // Hs.107622 //	FTMT	FTMT, Homo sapiens ferritin mitochondrial (FTMT), q23.1
SNP_A-2133598	atatcactaagcctag[C/T]acttaatgatgtgact	C	T	90827 // Homo sapiens KRAB zinc finger protein (KR19) mRNA, complete cds. /// ENST00000331162 // upstream //	ZNF479	ZNF479, Homo sapiens KRAB zinc finger protein (KR19) complete cds. ,p11.1
SNP_A-2179755	cacttgcatttttccc[A/G]ctgtaatatgttaaaa	A	G	Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// ENST00000276297 // intron // 0 // --- // ---	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2182078	cagaggcatcatatta[C/T]ctggcttaaaactaca	C	T	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 768781 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2186851	cagggtaaagggactg[A/T]actcctttctgtaagg	A	T	4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 155866 // Hs.491737	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2207598	ccatttcttaccctaa[C/T]ctcgaaacctaaatta	C	T	Homo sapiens INPE5792 (UNQ5792), mRNA. /// ENST00000339766 // intron // 0 // --- // --- // --- // ---	CLEC2A	CLEC2A, Homo sapiens INPE5792 (UNQ5792), p13.31
SNP_A-2201314	ccaatatctttttta[C/T]gtgagctgtcatcaag	C	T	7037 // Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /// NM_003234 // upstream // 68662 //	TFRC	TFRC, Homo sapiens transferrin receptor (p90, CD71) (TFRC), q29
SNP_A-2220909	ccttgctctccctgaa[C/T]ccaacatatcaagcag	C	T	Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. ///	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-1791804	gggtgaattttgctcc[A/G]agtctgacggccttgc	A	G	ENST00000328627 // intron // 0 // --- // --- // --- // ---	-	q37.3
SNP_A-1715065	ttgccttgatagcatgtttaggttg[C/T]gctaaaatttacattattttcttga	C	T	1005 // cadherin 7, type 2 /// NM_021153 // downstream // 29154 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2 ///	CDH7	CDH7 , rs725901, cadherin 7, type 2 ,q22.1
SNP_A-1780418	ggatacattacccaaa[C/T]ggtcacaggtcaaagg	C	T	91937 // Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), mRNA. /// NM_012206 //	TIMD4	TIMD4, Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), q33.3
SNP_A-1657063	ggagggcacgcagtgatggacatac[C/T]ggctctagagtactggttgtcaaat	C	T	148281 // synaptotagmin VI /// NM_015906 // downstream // 218282 // Hs.293044 // TRIM33 // 51592 // tripartite motif-	SYT6	SYT6 , rs172355, synaptotagmin VI ,p13.2
SNP_A-1683354	ttgatattagagctaagtctatgcg[G/T]aaggtcttggttcacacaaaggtac	G	T	// 23389 // thyroid hormone receptor associated protein 2 /// NM_005996 // upstream // 737774 // Hs.129895 // TBX3 //	THRAP2	THRAP2 , rs2891563, thyroid hormone receptor associated protein 2 ,q24.21
SNP_A-1855346	tcaaggcctagagaaa[C/T]gctagtgtcactttgg	C	T	// 3454 // Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA. /// NM_005534 // upstream //	IFNAR1	IFNAR1, Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), q22.11
SNP_A-1843348	tagtcttgcattcatg[A/T]aatttaattatttccg	A	T	Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // --- // --- // --- // --- /// ENST00000349908 // intron //	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-1841835	taggccttctagtaaa[C/T]aagccatgatacccta	C	T	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // --- // --- // --- // ---	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-1816122	gttaccataaaacttc[A/G]catcttggattttata	A	G	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 155094 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1936244	ttcttcatgcagcaca[A/T]tcctcagtgtctagca	A	T	Homo sapiens PBX/knotted 1 homeobox 2 (PKNOX2), mRNA. /// ENST00000298282 // intron // 0 // --- // --- // --- // ---	PKNOX2	PKNOX2, Homo sapiens PBX q24.2
SNP_A-1975843	attctgagtccaatta[C/T]aggatgtttttaactt	C	T	Homo sapiens syntaxin 18 (STX18), mRNA. /// ENST00000306200 // intron // 0 // --- // --- // --- // ---	STX18	STX18, Homo sapiens syntaxin 18 (STX18), p16.2
SNP_A-1969319	taacaaattctagttg[A/G]acaagaacattctcga	A	G	/// ENST00000331037 // downstream // 20219 // --- // --- // ---	-	q21.1
SNP_A-1987188	tgtaacagccggcacc[A/C]aatttgctttatatgg	A	C	// 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, mRNA. /// NM_201559 // downstream //	FOXO3A	FOXO3A, Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, q21
SNP_A-1890328	tgatccaggaaataaa[A/G]tactagaaataacaca	A	G	Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), mRNA. /// ENST00000282146 // intron // 0 // --- // -	KCNK13	KCNK13, Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), q32.11
SNP_A-1882405	tgaaaagcaagtgctg[A/C]atgttgataatctata	A	C	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 3 (HSD17B3), mRNA. /// ENST00000253260 // intron // 0 // --- //	HSD17B3	HSD17B3, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 3 (HSD17B3), q22.32
SNP_A-1921468	ttacccatctgaacaa[C/T]ccagagaaagcaggct	C	T	9150 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), transcript variant /// NM_048368 // downstream // 19117 // Hs.465490 // CTDP1 //	CTDP1	CTDP1, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), transcript variant ,q23
SNP_A-1921965	ttactcttctctatttt[A/T]aaaaaatcacgtatta	A	T	55749 // Homo sapiens cell division cycle and apoptosis regulator 1 (CCAR1), mRNA. /// ENST00000265872 //	CCAR1	CCAR1, Homo sapiens cell division cycle and apoptosis regulator 1 (CCAR1), q21.3
SNP_A-1979289	caagaggcctacctgc[A/G]cttcagaaataaagcc	A	G	54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 //	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-1965742	caagggtcttcgggca[C/T]tatttcagaaggcgtc	C	T	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1935831	ttctgttctgttgtga[C/G]aacatacgacatgggg	C	G	Homo sapiens plasminogen activator, tissue (PLAT), transcript variant 2, mRNA. /// NM_033011 // intron // 0 //	PLAT	PLAT, Homo sapiens plasminogen activator, tissue (PLAT), transcript variant 2, p11.21
SNP_A-1938021	ttgaatttcaatacaa[C/T]tataacgcagaagtca	C	T	// 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 733770 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1944439	aatgcttgaaatttcc[A/T]gataagagcaaggtgg	A	T	FLJ46419 // 388507 // Homo sapiens FLJ46419 protein (FLJ46419), mRNA. /// AL080125 // downstream // 74 //	FLJ46419	FLJ46419, Homo sapiens FLJ46419 protein (FLJ46419), p13.2
SNP_A-1954004	tttgatatatctgttg[C/G]agctaacttttttgaa	C	G	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1820958	gtttctccaatcaaac[A/G]aaaggcatccttccaa	A	G	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-1833896	ccttccatcatcgtcc[G/T]gccttgttgatggtaa	G	T	Homo sapiens integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) (ITGAE), mRNA. /// ENST00000263087 // intron // 0 // --- // --- // --- // ---	ITGAE	ITGAE, Homo sapiens integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide) (ITGAE), p13.2
SNP_A-1835756	tacgcaagtagaaaat[C/T]atctagagtgttatac	C	T	Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-1854927	tcaactccccaacaac[A/G]actttcattgctcctc	A	G	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 401957 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-1851932	tattgattacatcaac[A/T]gaagctgaagctgtaa	A	T	// 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1693497	caacaggacacttagtgttggctac[C/T]atgcaaaggtaagtgtagatgacac	C	T	// 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 1283604 // Hs.450919 // GPC5 //	SLITRK5	SLITRK5 , rs1388193, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1695055	ggtatttagaaaaaattgaacagtc[A/G]aaggtgcgtgtaccatctacctacc	A	G	TERF2IP // 54386 // telomeric repeat binding factor 2, interacting protein /// NM_033401 // upstream // 152400 //	TERF2IP	TERF2IP , rs918689, telomeric repeat binding factor 2, interacting protein ,q23.1
SNP_A-1712235	cttaaaagggttaaaatgttttaaa[A/G]ttagctagtgagaatggtagcatac	A	G	NM_016441 // upstream // 1479008 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs280734, cysteine-rich motor neuron 1,p22.3
SNP_A-1753809	gtaagcatgtagtattgcttttaaa[G/T]tctcctagtagagcaatagatgaga	G	T	RAB28 // 9364 // RAB28, member RAS oncogene family /// NM_005114 // upstream // 419416 // Hs.40968 // HS3ST1 //	RAB28	RAB28 , rs10516232, RAB28, member RAS oncogene family ,p15.33
SNP_A-1790165	ggggacactgagtcac[A/G]gagcagaagaggcttg	A	G	ENST00000304519 // intron // 0 // --- // --- // --- // ---	-	p23.1
SNP_A-1793290	ggtagcagggagacca[C/T]cattaagcagcccaag	C	T	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine,q12.3
SNP_A-1802371	aatgtctgactcatca[C/T]ggaggttttcgttaaa	C	T	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// ENST00000357652 // upstream // 6092 // --- // --- //	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2200081	ccaaatagtggatgcc[C/T]agaatgcaggatggcc	C	T	255061 // Homo sapiens tachykinin 4 (hemokinin) (TAC4), mRNA. /// NM_001934 // upstream // 15162 // Hs.172648 //	TAC4	TAC4, Homo sapiens tachykinin 4 (hemokinin) (TAC4), q21.33
SNP_A-2184684	cagctctgggccttca[A/G]tcatgtgttgcatgaa	A	G	// Homo sapiens thioredoxin (TXN), mRNA. /// ENST00000259332 // upstream // 82178 // --- // --- // --- // ---	TXN	TXN, Homo sapiens thioredoxin (TXN), q31.3
SNP_A-2191961	catcaatctgaaacag[G/T]aaagttccctgatgcc	G	T	// 90441 // Homo sapiens zinc finger protein 622 (ZNF622), mRNA. /// ENST00000332432 // upstream // 101245 // --- // ---	ZNF622	ZNF622, Homo sapiens zinc finger protein 622 (ZNF622), p15.1
SNP_A-2182412	cagataaagtgtaagg[A/G]aagttataggtgtggt	A	G	Homo sapiens chromosome 6 open reading frame 105 (C6orf105), mRNA. /// ENST00000229583 // intron // 0 // --- //	C6orf105	C6orf105, Homo sapiens chromosome 6 open reading frame 105 (C6orf105), p24.1
SNP_A-2172509	caattccataggataa[A/G]tgccttcagagatata	A	G	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 435629 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-2173762	cacacacacctcacac[A/C]atgtatatagcttgca	A	C	SLC39A12 // 221074 // Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), mRNA. /// NM_201593 // upstream // 19054 // Hs.59093 // CACNB2 //	SLC39A12	SLC39A12, Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), p12.33
SNP_A-2136657	atcactccagaaaaac[A/G]caaggtgaaattatgt	A	G	92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 978361 // ---	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2124067	agttactacaaacgta[C/T]aagcacaaacacaagt	C	T	Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // --- // --- // --- // ---	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2113081	aggccagacttaggaa[C/T]tggtctcttatcacag	C	T	Homo sapiens LAG1 longevity assurance homolog 6 (S. cerevisiae) (LASS6), mRNA. /// ENST00000305747 // intron // 0 // --- // --- // --- // ---	LASS6	LASS6, Homo sapiens LAG1 longevity assurance homolog 6 (S. cerevisiae) (LASS6), q24.3
SNP_A-2151497	atgttctcactcataa[A/G]tcagagctgaacaatg	A	G	Homo sapiens hypothetical protein FLJ14627 (FLJ14627), mRNA. /// ENST00000319176 // intron // 0 // --- // --- // --- // ---	FLJ14627	FLJ14627, Homo sapiens hypothetical protein FLJ14627 (FLJ14627), q24.22
SNP_A-2142451	atgaaatccatgtaag[C/G]ctggacgtggtggctc	C	G	Homo sapiens suppressor of Ty 5 homolog (S. cerevisiae) (SUPT5H), mRNA. /// ENST00000359191 // intron // 0 // --- // -	SUPT5H	SUPT5H, Homo sapiens suppressor of Ty 5 homolog (S. cerevisiae) (SUPT5H), q13.2
SNP_A-2156371	attctcaggaatagaa[C/T]ggggcttgatcctcac	C	T	// 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// NM_006552 // upstream //	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-2039391	aacatagctttcttta[C/T]gtttgttgctaaatag	C	T	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2040503	aaccagttgcacccgg[A/G]aagcaaatcagcaagt	A	G	Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // intron // 0 // --- //	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2047035	aagagtgtgtgtagcc[A/G]agcgtgatgtcacatg	A	G	3817 // Homo sapiens kallikrein 2, prostatic (KLK2), transcript variant 1, mRNA. /// NM_001002232 // downstream // 16222	KLK2	KLK2, Homo sapiens kallikrein 2, prostatic (KLK2), transcript variant 1, q13.41
SNP_A-2060486	aatgacatcatgctat[C/T]aggtggaatgagcaag	C	T	54734 // Homo sapiens RAB39, member RAS oncogene family (RAB39), mRNA. /// NM_003478 // upstream // 20943	RAB39	RAB39, Homo sapiens RAB39, member RAS oncogene family (RAB39), q22.3
SNP_A-2055302	aataagatttttgca[C/G]ctatcagtccaattta	C	G	Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2048817	aagcccatctaccttа[C/T]ggagtctaagacagac	C	T	FLJ16641 // 389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// NM_020307 // downstream // 93642 //	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-2070097	acacatatttgggtca[C/T]accatagcttattcag	C	T	Homo sapiens hypothetical protein FLJ20265 (FLJ20265), mRNA. /// NM_000283 // upstream // 85974 // Hs.59872 //	GPI7	GPI7, Homo sapiens hypothetical protein FLJ20265 (FLJ20265), p16.3
SNP_A-2102053	agatgtcagggtgatc[A/G]attcaaagcatttatt	A	G	// 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream //	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2102551	agattgctcttattta[C/T]cttactcctaactgat	C	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2241925	ctgatgtcatgaccca[A/C]agtttgaacagcactt	A	C	sapiens peptidase D (PEPD), mRNA. /// ENST00000244137 // intron // 0 // --- // --- // --- // ---	PEPD	PEPD, Homo sapiens peptidase D (PEPD), q13.11
SNP_A-2244690	tgtttgtttttgttaa[C/T]aggactctagtgtgga	C	T	123016 // Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, mRNA. /// NM_198309 //	TTC8	TTC8, Homo sapiens tetratricopeptide repeat domain 8 (TTC8), transcript variant 3, q32.11
SNP_A-2228689	ctagacaactatggcc[G/T]agtgactgggatacat	G	T	5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // downstream // 88316 // --- // --- // --- // --- ///	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1
SNP_A-2238933	ctcttccagactcaga[A/T]taagcagctctgttgg	A	T	6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 409731 //	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-2234578	ctccactgtgcttcac[A/G]atggaaatggcagaca	A	G	6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 282411 // Hs.175905 // AUH	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2285087	agacaaagttaaagca[C/T]ggtgtgattatccata	C	T	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // intron // 0 // Hs.511504 // TCF12 // 6938 //	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-2274863	gagaaattacttttta[A/T]ctctcaatcctcagtt	A	T	Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // --- // --- // --- // ---	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2277430	gagcaaataaagcttc[A/G]cgtgtcacctgccttc	A	G	Homo sapiens mitochondrial solute carrier protein (MSCP), mRNA. /// NM_016612 // intron // 0 // Hs.122514 // MSCP //	MSCP	MSCP, Homo sapiens mitochondrial solute carrier protein (MSCP), p21.2
SNP_A-2284132	gatatgaggctgtcca[A/G]aatttccaattgatct	A	G	Homo sapiens chromosome 1 open reading frame 41 (C1orf41), mRNA. /// ENST00000194214 // intron // 0 // --- // --	C1orf41	C1orf41, Homo sapiens chromosome 1 open reading frame 41 (C1orf41), p32.3
SNP_A-2237363	ctctcccacaaaaaac[A/G]accgtgaaggccaggc	A	G	55836 // Homo sapiens chromosome 6 open reading frame 35 (C6orf35), mRNA. /// NM_024630 // upstream // 26707 //	C6orf35	C6orf35, Homo sapiens chromosome 6 open reading frame 35 (C6orf35), q25.3
SNP_A-2237134	ctctcacatttcataa[A/T]gtttgtttggtgaaca	A	T	138803 // Homo sapiens olfactory receptor, family 13, subfamily C, member 3 (OR13C3), mRNA. /// ENST00000277216 // upstream // 4275 // --- // --- // --- // --- ///	OR13C3	OR13C3, Homo sapiens olfactory receptor, family 13, subfamily C, member 3 (OR13C3), q31.1
SNP_A-2249842	cttacaaaaaggaata[A/T]ctgattttctctgaac	A	T	Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// ENST00000339837 // intron // 0 // --- //	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-2312243	ggacagtcccaaaaat[A/G]acaagcgatgattgtg	A	G	Homo sapiens recombination protein REC14 (REC14), mRNA. /// ENST00000267973 // intron // 0 // --- // --- // --- // ---	REC14	REC14, Homo sapiens recombination protein REC14 (REC14), q25.1
SNP_A-2095731	agacacgatggaggaa[A/G]taacttagtctgttaa	A	G	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2091987	agaaacatctattaga[A/T]tcacttcacctacttt	A	T	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, mRNA. /// NM_138711 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens	PPARG	PPARG, Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, p25.2
SNP_A-2078922	acccaatgactaccca[A/G]taagagacccttaata	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3362282 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2082782	acggttccaacacaaa[C/T]ataacatgaggtgact	C	T	Homo sapiens ubiquitin domain containing 1 (UBTD1), mRNA. /// ENST00000298807 // intron // 0 // --- // --- // --- // ---	UBTD1	UBTD1, Homo sapiens ubiquitin domain containing 1 (UBTD1), q24.2
SNP_A-2065730	aatttatttcaacaca[C/G]tctttcactttgaata	C	G	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, mRNA. /// NM_003401 // intron // 0 // Hs.171190 // XRCC4 // 7518 // Homo sapiens X	XRCC4	XRCC4, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, q14.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2050133	aaggacatcatcctaa[A/G]tgatttaacacaggaa	A	G	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 311763 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2055816	aatacaaactaagcta[C/T]gctgataaattatttt	C	T	767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 443706 // --- // --- // ---	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2057280	aatatatagtatagtc[A/T]atgctttacaaagtct	A	T	84078 // Homo sapiens kelch repeat and BTB (POZ) domain containing 7 (KBTBD7), mRNA. /// NM_004294 //	KBTBD7	KBTBD7, Homo sapiens kelch repeat and BTB (POZ) domain containing 7 (KBTBD7), q14.11
SNP_A-2062264	aatggtgtctgtttca[G/T]ctttcaccatgttact	G	T	// 54838 // Homo sapiens chromosome 10 open reading frame 26 (C10orf26), mRNA. /// NM_000102 // downstream //	C10orf26	C10orf26, Homo sapiens chromosome 10 open reading frame 26 (C10orf26), q24.32
SNP_A-2041204	aacctcatcattcctc[A/G]cacatccattagttcc	A	G	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2034947	aaatgatatgagtaaa[A/C]cagggtgagattttct	A	C	Homo sapiens interleukin 18 receptor 1 (IL18R1), mRNA. /// ENST00000233957 // intron // 0 // --- // --- // --- // ---	IL18R1	IL18R1, Homo sapiens interleukin 18 receptor 1 (IL18R1), q11.2
SNP_A-2035283	aaatggaataggatag[A/G]aacttctagttacccc	A	G	// 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2007364	tcctgtaacttaaata[C/T]agtgatgtagagttgg	C	T	-- /// ENST00000358396 // downstream // 136544 // --- // --- // ---	-	p12.2
SNP_A-1989667	tctcccagcttttcaa[C/T]ggccccaagttgccag	C	T	Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2159427	atttaattggcctaca[A/G]atttaataatgcttgg	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 555174 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2167619	caaccacatacttgac[C/T]ctctctccagggcaca	C	T	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 68502 //	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2164283	caaaatagtcatgata[C/T]aatggtagatgatata	C	T	// 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// NM_012403 // downstream //	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.3
SNP_A-2143066	atgaatgcctggcaaa[C/T]tgaagttgactgtgta	C	T	6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2173530	cacaatgagatttcga[C/T]acacagatgattgaaa	C	T	Homo sapiens lymphocyte alpha-kinase (LAK), mRNA. /// ENST00000177648 // intron // 0 // --- // --- // --- // --- ///	ALPK1	ALPK1, Homo sapiens lymphocyte alpha-kinase (LAK), q25
SNP_A-2193018	catcgtcattttgtac[A/G]gcaaatggtaattccc	A	G	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	SMARCD3	SMARCD3, Homo sapiens SWI,q36.1
SNP_A-2194522	catgcaattcaactaa[A/G]tcctgattacaatgtg	A	G	2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 457742 // Hs.98262 // GRIK2 // 2898 // Homo	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2200179	ccaaatgtcaagaaat[A/C]agtgcttacaggccaa	A	C	ENST00000262996 // intron // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-2208266	cccacaccagtaagat[A/C]actttcaaataaaaca	A	C	Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1810431	gtgattccaataggtc[A/G]catgttctgggaggcc	A	G	6869 // Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // upstream //	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-1667894	atttctgaactgagctgtgtttgca[G/T]attggagccaccataggccaaagac	G	T	CXCL12 // 6387 // chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) /// NM_005758 // upstream // 239258 // - // - // - // -	CXCL12	CXCL12 , rs10508880, chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) ,q11.21
SNP_A-1858140	tcagaaaggtctgttc[A/G]atgtcttctcactctt	A	G	// Homo sapiens hypothetical protein MGC39827 (MGC39827), mRNA. /// ENST00000327554 // intron // 0 // ---	MGC39827	MGC39827, Homo sapiens hypothetical protein MGC39827 (MGC39827), q24.23
SNP_A-1863779	tccaagctttctgagc[C/T]atcctatccttctaga	C	T	/// ENST00000251675 // downstream // 360873 // --- // --- // --- // --- /// ENST00000360855 // downstream // 360903 // --- // ---	-	q32.3
SNP_A-1829625	taagttattgaaaaaa[C/G]tagggctcaaatcaat	C	G	ENST00000251041 // intron // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-1961038	tttttggttcccttaa[A/G]gaatatgcagtaacaa	A	G	7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 501990 // Hs.411433	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-1945345	ttgttagaaataataa[G/T]gctcatgtttattcag	G	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1988711	ctaaattttgaaacaa[A/T]gcctcttaagaacaat	A	T	3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream //	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-1983668	tttcagttaatgataa[A/G]tgttgtgaaggaaata	A	G	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. ///	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1985728	gctgattcctgtataa[A/G]ggtattaaaatgtcta	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1922159	ttacttatatgcaaat[A/C]atgctgccattcctgc	A	C	// 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 186790 // Hs.523852 //	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-1918834	ttaacagggtctataa[A/G]aatcctcatatcacca	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2361448 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1881468	tctttctaatacctga[C/G]gctcaataaggtctta	C	G	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 489028 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1886149	tgaccatgacaacatc[A/C]acagtggtaagtcatg	A	C	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1888053	tgagcatcttttcaca[C/T]ggctgttggccactca	C	T	5015 // Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), transcript variant 2, mRNA. /// NM_021728 //	OTX2	OTX2, Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), transcript variant 2, q22.3
SNP_A-1916133	tgttggactgcggcac[G/T]gccctaacatgtgggc	G	T	Homo sapiens transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase) (TGM1), mRNA. /// ENST00000206765 // intron // 0 // --- // ---	TGM1	TGM1, Homo sapiens transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase) (TGM1), q11.2
SNP_A-1913342	tgtggggtatctctga[A/G]aacatgtttgccctgc	A	G	2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 //	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1909646	tgtcaacccatgtgtc[C/T]ctaaccccaatgtccg	C	T	DJ971N18.2 // 56255 // Homo sapiens hypothetical protein DJ971N18.2 (DJ971N18.2), mRNA. /// NM_182734 //	DJ971N18.2	DJ971N18.2, Homo sapiens hypothetical protein DJ971N18.2 (DJ971N18.2), p12.3
SNP_A-1908930	tgtataactgaaataa[C/T]gtgaatttgtctccag	C	T	Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), mRNA. /// ENST00000357444 // intron // 0 // ---	RABGAP1L	RABGAP1L, Homo sapiens RAB GTPase activating protein 1-like (RABGAP1L), q25.1
SNP_A-1923772	ttagtacagacggagc[A/G]gagaaatcccagggcc	A	G	3929 // Homo sapiens lipopolysaccharide binding protein (LBP), mRNA. /// ENST00000217407 // downstream // 12178	LBP	LBP, Homo sapiens lipopolysaccharide binding protein (LBP), q11.23
SNP_A-1926351	ttattatctgtttgtc[C/T]aaacccataatgtgta	C	T	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // --- // --- // --- // ---	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-1928239	ttcacagtgaagtaga[C/T]agcttgtagagaaaaa	C	T	// 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 207273 // --- // --- // --- //	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1976635	cctgctggaaatgtca[A/G]ggtcactaagtatacc	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 971363 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1980434	aaagtgatttgaagcc[A/G]gagagtaaacatgttg	A	G	ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 100112 // --- // ---	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1941403	ttgcttctagaatgga[C/T]caatttgtgaacaaat	C	T	10886 // Homo sapiens G protein-coupled receptor 74 (GPR74), mRNA. /// NM_004885 // downstream // 95518 //	GPR74	GPR74, Homo sapiens G protein-coupled receptor 74 (GPR74), q13.3
SNP_A-1958332	ttttccattatgctgg[A/T]atcttatagaaaatag	A	T	// 8732 // Homo sapiens RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA. /// ENST00000333801 // downstream // 161866 // --- // --- // --- // --- ///	RNGTT	RNGTT, Homo sapiens RNA guanylyltransferase and 5'-phosphatase (RNGTT), q15
SNP_A-1829817	taataaattcaaggca[C/T]aatgcaaactttcact	C	T	// Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), mRNA. /// NM_021955 // upstream // 10031 // Hs.546258 //	TFPI2	TFPI2, Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), q21.3
SNP_A-1819460	gttggggtggctacca[C/T]gttaagaccacgtttc	C	T	3394 // Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /// ENST00000268638 //	IRF8	IRF8, Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), q24.1
SNP_A-1660359	agaccgtgcacaaagcccttcctca[C/G]gttttccttgctagcaaagtcctga	C	G	5501 // protein phosphatase 1, catalytic subunit, gamma isoform /// NM_152591 // upstream // 4207 // Hs.437141 //	PPP1CC	PPP1CC , rs2238147, protein phosphatase 1, catalytic subunit, gamma isoform ,q24.11
SNP_A-1781980	ggcaaagacatacaga[C/T]gctaggttttgaaagt	C	T	407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// NM_182522 // downstream // 132996 // Hs.187873 //	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-1749019	agaagaaggagaagtagaggtggtc[C/T]atccaagaagagaaaggggtg agtt	C	T	NM_173667 // downstream // 20290 // Hs.376312 // FLJ37543 // 285668 // hypothetical protein FLJ37543	FLJ37543	FLJ37543 , rs1466011, hypothetical protein FLJ37543,q12.1
SNP_A-2212178	ccctgcttctacagaa[A/G]ggagtagcatccattt	A	G	7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000355985 // upstream // 213134 // --- // ---	ZNF217	ZNF217, Homo sapiens zinc finger protein 217 (ZNF217), q13.2
SNP_A-2225811	ctaaagttatacccta[C/T]gaaagaagttgcagga	C	T	Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // --- // --- // --- // ---	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2184127	cagccctttatgaga[C/T]cccacaaggccaggtg	C	T	Homo sapiens interferon stimulated gene 20kDa (ISG20), mRNA. /// ENST00000306072 // intron // 0 // --- // --- // --- // ---	ISG20	ISG20, Homo sapiens interferon stimulated gene 20kDa (ISG20), q26.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2139333	atcctggaattatgaa[C/T]gcaggtagaccactgt	C	T	Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// ENST00000316386 // 3UTR // 0 // --- // --- // --- // ---	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.2
SNP_A-2163377	atttttgctaatatc[A/T]accttttttctatct	A	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1933056 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2153567	attagctatttatccc[A/G]atgctatctctcttcc	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2529936 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1993720	tccctcacaaagatct[A/G]aatgtgtaagcagatg	A	G	// 81796 // Homo sapiens solute carrier organic anion transporter family, member 5A1 (SLCO5A1), mRNA. /// NM_024504 // downstream // 98441 // Hs.287532 // PRDM14	SLCO5A1	SLCO5A1, Homo sapiens solute carrier organic anion transporter family, member 5A1 (SLCO5A1), q13.3
SNP_A-2034716	aaatgaagaggacaga[A/C]atttaacaaaagcaac	A	C	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 279716 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2074828	acatcaacatctagta[C/G]cacctcctctgtgccc	C	G	Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 5 (CHCHD5), mRNA. /// ENST00000324913 // intron // 0 // --- // --- // --- // ---	CHCHD5	CHCHD5, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 5 (CHCHD5), q13
SNP_A-2083501	actaagtctactctcc[A/G]gagcaatgtttctgta	A	G	5648 // Homo sapiens mannan-binding lectin serine protease 1 (C4/C2 activating component of Ra-reactive factor)	MASP1	MASP1, Homo sapiens mannan-binding lectin serine protease 1 (C4,q27.3
SNP_A-2095349	agaatttgaagactta[C/T]gttaaaatcaccacag	C	T	CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 117504 //	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2313056	ggagaaaccttgaaaa[C/T]gccatgtgaagtgaaa	C	T	Homo sapiens KIAA0417 mRNA, complete cds. /// ENST00000298777 // intron // 0 // --- // --- // --- // ---	HSPA12A	HSPA12A, Homo sapiens KIAA0417 complete cds. q25.3
SNP_A-2304159	gctcccgtcatccctg[A/G]attttctctctctgtg	A	G	29968 // Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // upstream // 5113 // Hs.494261 // PSAT1 // 29968 // Homo	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.2
SNP_A-2288302	gattctaaagtgtagc[C/T]gatttgagaactactg	C	T	ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 226135 // Hs.464442 // C18orf2	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-2259000	ctttttgtgtgctagc[C/G]cttcctctccaaaata	C	G	// 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 //	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-2262886	gaacaaagtactcata[G/T]acacaatgtgggtgaa	G	T	23498 // Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA. /// NM_006887 // downstream	HAAO	HAAO, Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), p21
SNP_A-2285957	gatgataaaacaaaca[C/T]gataaggacagacaga	C	T	Homo sapiens abhydrolase domain containing 2 (ABHD2), transcript variant 1, mRNA. /// NM_152924 // intron // 0 //	ABHD2	ABHD2, Homo sapiens abhydrolase domain containing 2 (ABHD2), transcript variant 1, q26.1
SNP_A-2286055	gatgatgtgtccacgg[G/T]aagcttgttttgcctt	G	T	3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 76739 //	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2249676	cttaataaaactttca[C/T]ggccatctacagtgtg	C	T	165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. ///	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2243621	ctgctccaagcttgaa[C/T]tcccagacgaaaaaca	C	T	7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 35654 //	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-2089807	acttcctttgtacctc[C/T]ccttgtagctgtagga	C	T	// Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 670193 // Hs.153952 // NT5E //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. .q14.3
SNP_A-2085387	actcattgataaaact[C/T]acttgtaactgtgcta	C	T	253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream //	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-2043761	aacttatctctttcta[C/T]agctctagcccattgg	C	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 74526 // Hs.335933 // MGC33530	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-2005080	ttctgtccccaagcaa[A/T]gtggaatgtagtctag	A	T	HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 233873 // Hs.48384	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-2009278	cccattcccagtctca[C/T]ctttttgttgactagt	C	T	SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 //	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2157551	attgattacacccaca[C/G]tgattcgaacctgctg	C	G	Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // intron // 0 // --- // --- // --- // ---	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2150493	atgtgacacctttcca[A/G]gaagtgcggattccct	A	G	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2108137	agctcttaaggtagca[C/T]gtctgaagttattcgt	C	T	9972 // Homo sapiens nucleoporin 153kDa (NUP153), mRNA. /// NM_022113 // downstream // 19195 // Hs.189915	NUP153	NUP153, Homo sapiens nucleoporin 153kDa (NUP153), p22.3
SNP_A-2117433	aggtgtcccaaaagaa[C/T]gactaatggaagttat	C	T	121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 186975 // Hs.31664 //	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2127718	ataactcattgtagat[G/T]aacaactgagaaaatg	G	T	Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// ENST00000286355 // intron // 0 // --- // --- // --- // ---	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2135702	atcaaaatggtttcca[C/T]ataaagaacactttgg	C	T	Homo sapiens KIAA0999 protein (KIAA0999), mRNA. /// ENST00000292055 // intron // 0 // --- // --- // --- // ---	KIAA0999	KIAA0999, Homo sapiens KIAA0999 protein (KIAA0999), q23.3
SNP_A-2183138	cagcaaattaaagaaa[C/G]ttcagagaattcacca	C	G	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // --- // ---	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2209786	cccatttctaatatga[C/T]gaactcagaaatgcag	C	T	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 961072 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2205326	ccagtcggatttatat[C/G]acacatcaacaatcaa	C	G	Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // ---	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-1739149	cctgttttatacttaaatagacata[C/G]agttttcatctgtgtagcacactct	C	G	7088 // transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) /// NM_007005 // downstream // 1033815 //	TLE1	TLE1 , rs10491935, transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) ,q21.31
SNP_A-1658344	ataaatattgaagtgctatcgctta[C/T]aggagaaaatgcaaatgcctcagtc	C	T	NM_015049 // intron // 0 // Hs.154248 // ALS2CR3 // 66008 // amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3	ALS2CR3	ALS2CR3 , rs4507084, amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3,q33.1
SNP_A-1683724	gcacatctgccatctttggtcagca[A/G]ccctccaggactgccttcttcacac	A	G	NM_006255 // intron // 0 // Hs.315366 // PRKCH // 5583 // protein kinase C, eta	PRKCH	PRKCH , rs10483732, protein kinase C, eta,q23.1
SNP_A-1802031	gtataattgatgtaag[A/G]aaagttttggaagctg	A	G	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 868131 // Hs.13640 //	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1800129	gtaccatgacagatcc[A/G]ggaggaaaaacggtgg	A	G	902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 50517 // Hs.379972 //	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1793450	ggtagtctcttgattc[A/G]attatcaaaagggcca	A	G	490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 143823 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1797644	ggtttctttccaccaa[C/T]gagttcttttgatagt	C	T	LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 //	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-1838814	tagactataccaagaa[C/T]aggtgaaagataataa	C	T	sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-1858108	tcagaaaattaacaga[A/G]ggtcagatattacatc	A	G	PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 552355 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1856614	tcacagtgcaaggtcc[A/G]gaaaactgggctatgt	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1293527 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1957804	ttttattgccatttgg[G/T]attgattcacttctct	G	T	rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // --- // --- // --- //	-	-, Human clone rev16 q11.22
SNP_A-1951417	tttcctagaaccaaaa[A/C]gtacgagtgacctgat	A	C	ENST00000320865 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1940291	ttgcatttttggtcac[A/C]gagctacaagggtgag	A	C	142940 // Homo sapiens TruB pseudouridine (psi) synthase homolog 1 (E. coli) (TRUB1), mRNA. /// NM_207303 // upstream // 24300 // Hs.501127 // ATRNL1 // 26033 // Homo	TRUB1	TRUB1, Homo sapiens TruB pseudouridine (psi) synthase homolog 1 (E. coli) (TRUB1), q25.3
SNP_A-1945662	ttgttgagaccccagc[A/C]aactaactgcctgcct	A	C	Homo sapiens staufen, RNA binding protein, homolog 2 (Drosophila) (STAU2), mRNA. /// ENST00000343268 // intron // 0 // --- // --- // --- // --- /// ENST00000355780 // intron // 0 // ---	STAU2	STAU2, Homo sapiens staufen, RNA binding protein, homolog 2 (Drosophila) (STAU2), q21.11
SNP_A-1977803	agtcatggtaatatga[C/T]agataaatgctgtgat	C	T	5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 50323 //	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1977868	cccccaggctggagcg[C/T]aatcctggctcactgc	C	T	MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 //	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1930320	ttcatttattaattca[C/G]agcatataccacaagg	C	G	Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// ENST00000262078 // intron // 0 // --- // --- // --- // ---	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-1919412	ttaagcaactacaaaa[C/T]gcaggcactggaaagg	C	T	/// ENST00000357595 // downstream // 40888 // --- // --- // ---	-	q31.1
SNP_A-1922250	ttacttgtcgttaaaa[A/C]gttggcaatttacttc	A	C	ZNF429 // 353088 // Homo sapiens zinc finger protein 429 (ZNF429), mRNA. /// NM_173531 // downstream // 71172 //	ZNF429	ZNF429, Homo sapiens zinc finger protein 429 (ZNF429), p12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1894221	tgcattagcaaaataa[A/G]aagtgtaccaggatcc	A	G	FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 129613 //	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-1968270	cagatgataaggtagc[G/T]atccagtgccatgaca	G	T	ENST00000325632 // CDS // 0 // --- // --- // --- // ---	-	q23.1
SNP_A-1973372	taataaagttaaagag[A/C]agatttccagacatta	A	C	Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, mRNA. /// ENST00000305299 // intron // 0 // --- // --- // --- // ---	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, p12.3
SNP_A-1945106	ttgtgtctgataatta[C/G]aacatctgaagagtct	C	G	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-1939180	ttgatatacatagcca[C/T]tgctcaataaatatgt	C	T	Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// ENST00000157600 // intron // 0 // --- // --- // --- // ---	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-1949043	tttatgaaagaagtaa[C/T]accaatcttagacaac	C	T	/// ENST00000321014 // upstream // 473467 // --- // --- // --- // ---	-	p12.3
SNP_A-1873543	tctcacacactcctaa[A/T]gtcagtgaatgctgtt	A	T	51704 // Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA. /// NM_001502 // downstream // 112831 // Hs.53985 // GP2 // 2813 // Homo	GPRC5B	GPRC5B, Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), p12.3
SNP_A-1790520	ggggcattggaggtca[C/T]gattatgtcttgatca	C	T	79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// NM_004530 // upstream // 1566 // Hs.513617 //	IRX6	IRX6, Homo sapiens iroquois homeobox protein 6 (IRX6), q12.2
SNP_A-1802147	gtatagcctatgttaa[A/G]acttgtcctaatagac	A	G	FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 //	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-1804553	gtcagcaaactcagcc[A/C]acacgctctatctgac	A	C	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1119275 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1813918	gtgtcaaattgagtca[A/G]gattgtggctttctca	A	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1689248	ctattcagaaataaaaaagacccaa[C/T]taccaacacacacagccacaggggc	C	T	// 6229 // ribosomal protein S24 /// NM_020338 // upstream // 126448 // Hs.438767 // RAI17 // 57178 // retinoic acid induced	RPS24	RPS24 , rs3910579, ribosomal protein S24 ,q22.3
SNP_A-1644752	tgcgggaccatttggacagtttcaa[A/G]gaactctggatccattccaccatca	A	G	// 10129 // hypothetical protein CG003 /// NM_145293 // downstream // 33068 // Hs.352186 // LOC196549 // 196549 //	13CDNA73	13CDNA73 , rs457936, hypothetical protein CG003 ,q13.1
SNP_A-1741915	tattagtacttctttccctatgata[A/C]tataaggtattcttgggagctgcta	A	C	25890 // target of Nesh-SH3 /// NM_016247 // downstream // 173540 // Hs.272380 // IMPG2 // 50939 // interphotoreceptor	TARSH	TARSH , rs1449319, target of Nesh-SH3 ,q12.2
SNP_A-1751427	ataatatataaaaagagagaaacaa[C/T]cttcatggatatattttgctttcct	C	T	390575 // Similar to casein kinase 1, alpha 1 (LOC390575), mRNA /// NM_032499 // upstream // 664748 // Hs.48348 //	-	- , rs789785, Similar to casein kinase 1, alpha 1 (LOC390575), mRNA ,q14
SNP_A-2225096	cgtgtgtctcagttcc[C/T]cttcccatggaataga	C	T	Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 3 (SLC37A3), transcript variant 1, mRNA. /// NM_032295 // intron // 0 // Hs.446021 // SLC37A3	SLC37A3	SLC37A3, Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 3 (SLC37A3), transcript variant 1, q34
SNP_A-2170715	caagttctctccttta[C/T]gtgttctccagaaatc	C	T	7849 // Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, mRNA. /// NM_013952 // upstream // 158462	PAX8	PAX8, Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, q13
SNP_A-2130540	atactctaagggcttc[C/T]ccatattgttacagct	C	T	138805 // Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), mRNA. /// ENST00000334726 // downstream // 16623 // --- // --- // --- // ---	OR13F1	OR13F1, Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), q31.1
SNP_A-2113477	aggcggtggttaatga[A/G]gacagatggagggttc	A	G	sapiens B lymphoid tyrosine kinase (BLK), mRNA. /// ENST00000259089 // intron // 0 // --- // --- // --- // ---	BLK	BLK, Homo sapiens B lymphoid tyrosine kinase (BLK), p23.1
SNP_A-2139576	atcgaacaatgcacac[A/C]ctgtgttaactcacag	A	C	Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000354673 // intron // 0 // --- // ---	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-2140506	atctcccctaggcaca[A/G]taaaagtattcatgca	A	G	1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 639426 // Hs.156316 //	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2143661	atgacttttactcaa[C/T]tgaaaacactatcttt	C	T	79003 // Homo sapiens MIS12 homolog (yeast) (MIS12), mRNA. /// NM_014922 // downstream // 23870 // Hs.513902	MIS12	MIS12, Homo sapiens MIS12 homolog (yeast) (MIS12), p13.2
SNP_A-2012850	ggaggaagagagggag[G/T]caaagaaggaggaaag	G	T	Homo sapiens hypothetical protein FLJ21986 (FLJ21986), mRNA. /// ENST00000310396 // intron // 0 // --- // --- // --- // ---	FLJ21986	FLJ21986, Homo sapiens hypothetical protein FLJ21986 (FLJ21986), q31.31
SNP_A-2024483	aaaaggactttggttg[A/G]aattatccaaattatg	A	G	Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, mRNA. /// NM_024806 // intron // 0 //	FLJ23554	FLJ23554, Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, q24.1
SNP_A-2089202	acttacctgttgaatt[A/C]aagaggattatataaa	A	C	Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // CDS // 0 // --- // --- // --- // ---	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-2064560	aattcgccaggtcctc[A/G]attcattgggtaaaat	A	G	988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235742	ctcctcccttggtaag[A/G]aaaaccagcatcctcc	A	G	7049 // Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFBR3), mRNA. /// NM_001726 // upstream // 29801 // Hs.482520 // BRDT // 676	TGFBR3	TGFBR3, Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFBR3), p22.1
SNP_A-2229918	ctagtttctgatccca[C/T]tatgactgaaaatttt	C	T	Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA. /// ENST00000336047 // intron // 0 // --- // ---	NEK1	NEK1, Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), q33
SNP_A-2231661	ctattttctttgcaac[C/T]ctccttagcaactagt	C	T	84614 // Homo sapiens zinc finger and BTB domain containing 37 (ZBTB37), mRNA. /// NM_000488 //	ZBTB37	ZBTB37, Homo sapiens zinc finger and BTB domain containing 37 (ZBTB37), q25.1
SNP_A-2275793	gagacctcaagtgtca[C/T]gcagagctccagccct	C	T	ENST00000357747 // intron // 0 // --- // --- // --- // ---	-	q42.13
SNP_A-2273678	gactgcaccgttgtac[C/T]ccaaaatgggcgacag	C	T	/// ENST00000333071 // downstream // 23287 // --- // --- // ---	-	q11.21
SNP_A-2259153	gaaaaaacctttcacc[A/G]acaaagattcccactt	A	G	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // --- // -	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2287770	gattactgtcaatccc[C/T]acttgttttcttttct	C	T	79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 178586	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2305564	gctgcacctcccagag[A/G]cctacagtttactctc	A	G	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2308961	gcttttataaaggatc[A/G]gacagtaccatgcctg	A	G	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// ENST00000245519 // intron // 0 // --- // --- // --- // --- ///	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-2311131	ggaagtctctaaagac[A/C]aaaaatgagaacatat	A	C	// Homo sapiens hypothetical protein FLJ33069 (FLJ33069), mRNA. /// ENST00000356838 // intron // 0 // --- // --- // --- // ---	FLJ33069	FLJ33069, Homo sapiens hypothetical protein FLJ33069 (FLJ33069), q24.22
SNP_A-2309725	ggaaaggagacggaaa[G/T]tggaaggctgtggccc	G	T	// 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // downstream // 59353 // Hs.167317 // SNAP25 // 6616 //	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-2269545	gacaaagattcggcac[A/G]agaattccggcaccat	A	G	// 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 147075 //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2229933	ctagttttatttttaa[C/T]gtggtcagagaaaaca	C	T	// 54749 // Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), mRNA. /// NM_032016 // upstream // 41553	EPDR1	EPDR1, Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), p14.1
SNP_A-2240782	ctgacttgtctttgaa[C/T]acaactggggctttga	C	T	-- /// ENST00000360285 // downstream // 440380 // --- // --- // -- // --- /// ENST00000339882 // downstream // 440380 // --- // -	-	q12
SNP_A-2252684	cttcgagacaaagaga[C/T]agccgctgagctgagg	C	T	389376 // Homo sapiens GSGL541 (UNQ541), mRNA. /// NM_080870 // upstream // 10901 // Hs.485071 // DPCR1 //	UNQ541	UNQ541, Homo sapiens GSGL541 (UNQ541), p21.33
SNP_A-2256259	ctttaggagacaccca[A/G]tgaggtcttgaaggaa	A	G	Homo sapiens golgi SNAP receptor complex member 2 (GOSR2), transcript variant A, mRNA. /// NM_054022 // intron // 0 // Hs.463278 // GOSR2 // 9570 // Homo sapiens golgi	GOSR2	GOSR2, Homo sapiens golgi SNAP receptor complex member 2 (GOSR2), transcript variant A, q21.32
SNP_A-2254985	cttggctacatgagga[C/T]actacatctgaccaga	C	T	Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, mRNA. /// NM_001372 // intron	DNAH9	DNAH9, Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, p12
SNP_A-2070258	acaccaaaagtgaacc[C/T]ggagaaaactgtggat	C	T	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2050252	aaggagacaaacccaa[C/T]ggcttagaaccaagac	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// ENST00000333447 // intron // 0 // --- // --- // --- // --	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-2090932	actttccttatcttga[C/T]caaatatccacaaggc	C	T	// 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 307902 //	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2083799	actaccattacaccac[C/T]gtactacattgatgtg	C	T	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2080182	accgtgtctaaaggggg[G/T]cagtccctactctttc	G	T	/// ENST00000330554 // upstream // 90261 // --- // --- // --- // ---	-	q12.1
SNP_A-2097051	agactggcttttgaga[A/C]cctgagtctagggcgt	A	C	23327 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), mRNA. /// ENST00000303758 // upstream // 6154 // --- // --- // --- // --- ///	NEDD4L	NEDD4L, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), q21.31
SNP_A-2102792	agattttcaaatgtaa[C/T]cattatctggaatgtt	C	T	54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA. /// NM_024781 // upstream // 72780 // Hs.280781 //	TXNDC10	TXNDC10, Homo sapiens FLJ20793 protein (FLJ20793), q22.1
SNP_A-2101038	agatcaaggtcccaaa[C/T]tgcctattgctggagg	C	T	Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2028801	aaacttctgacccacc[A/G]aaatcaaatctatgta	A	G	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 144975 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2047194	aagatacttttgcaga[C/T]gaatgagaaaatgaag	C	T	Homo sapiens cell division cycle and apoptosis regulator 1 (CCAR1), mRNA. /// ENST00000265872 // intron // 0 // --- // ---	CCAR1	CCAR1, Homo sapiens cell division cycle and apoptosis regulator 1 (CCAR1), q21.3
SNP_A-2007805	ttaagcactcttcccc[A/G]gcttcttgcagacact	A	G	4159 // Homo sapiens melanocortin 3 receptor (MC3R), mRNA. /// NM_080821 // upstream // 1596 // Hs.143736 //	MC3R	MC3R, Homo sapiens melanocortin 3 receptor (MC3R), q13.31
SNP_A-2004154	gaattattctggcaaa[C/T]gctaggtcaatacagt	C	T	23312 // Homo sapiens rabconnectin-3 (RC3), mRNA. /// NM_013243 // upstream // 31095 // Hs.232618 // SCG3 //	DMXL2	DMXL2, Homo sapiens rabconnectin-3 (RC3), q21.2
SNP_A-2159130	atttaaaaagagtaag[C/G]cctaaaagtctcaact	C	G	22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), mRNA. /// NM_000055 // downstream // 172917	SLITRK3	SLITRK3, Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), q26.1
SNP_A-2136007	atcaagcaagtttgat[G/T]acaccgacttagttct	G	T	221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream //	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-2171095	caatagaagggagtaa[C/T]atataaagccccagca	C	T	ENST00000354796 // intron // 0 // --- // --- // --- // ---	-	q21.13
SNP_A-2224233	cggtgggatatctgtc[A/G]acggtaaatggcttta	A	G	/// ENST00000315185 // downstream // 5595 // --- // --- // --- // ---	-	q24.31
SNP_A-1758849	atagaaaaaaaagaggaccctaagaa[A/T]ctggagtcaaaatttcctctctcat	A	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs4875767, CUB and Sushi multiple domains 1,p23.2
SNP_A-1784358	ggcccccaccagatac[A/C]ctttaatctgccaggc	A	C	ENST00000358529 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-1739505	aatttctggtctggtatctaaaaga[A/G]agaggaagttccagtgtaaacctct	A	G	23273 // KIAA0367 /// NM_138818 // downstream // 86917 // Hs.352153 // C9orf65 // 158471 // chromosome 9 open	KIAA0367	KIAA0367 , rs10521473, KIAA0367 ,q21.2
SNP_A-1652468	atctagcaagcatcacttgccatta[C/T]ggtgtttcaactctactggcacca	C	T	autophagy Apg3p/Aut1p-like	APG3	APG3 , rs2638017, autophagy Apg3p,q13.2
SNP_A-1696208	aatttatgatgcaggataatgtcaa[A/G]cactaaagattcattttatttcaaa	A	G	3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 380290 // Hs.127011 // TINAG // 27283 //	HCRTR2	HCRTR2 , rs2397170, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1806110	gtcctccttttctcaa[C/T]ggcttctcagttggct	C	T	4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 714899 // Hs.232819 // PCDH15 // 65217 //	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1798861	ttgctcgatatggaaa[C/T]agcttgggaagcagag	C	T	9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 34590 // Hs.458423	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-1872910	tctatcatttttacta[C/T]gtacttccatctagtt	C	T	4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream //	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-1872509	tctagctttaatatac[C/T]gctttccactttattg	C	T	Homo sapiens fibroblast growth factor 10 (FGF10), mRNA. /// ENST00000264664 // intron // 0 // --- // --- // --- // ---	FGF10	FGF10, Homo sapiens fibroblast growth factor 10 (FGF10), p12
SNP_A-1869654	tccttagggaagaaag[C/T]ctcatcatggttagca	C	T	7434 // Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), mRNA. /// ENST00000262178 // upstream //	VIPR2	VIPR2, Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), q36.3
SNP_A-1869834	tccttcctgtagcgga[C/G]aaggcccaccagcgtg	C	G	// 51372 // Homo sapiens hypothetical protein HSPC016 (HSPC016), mRNA. /// NM_022873 // downstream // 14660 //	HSPC016	HSPC016, Homo sapiens hypothetical protein HSPC016 (HSPC016), p36.11
SNP_A-1860486	tcagttacagtgttgg[C/T]cagatttcgggagcag	C	T	Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// ENST00000286353 // intron // 0 // --- // --- // --- // ---	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-1859819	tcaggggatgcttgga[A/G]cgtgattcacacagga	A	G	FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ11017), mRNA. /// NM_018302 // downstream	FLJ11017	FLJ11017, Homo sapiens hypothetical protein FLJ11017 (FLJ11017), p14
SNP_A-1849983	tatgtccttctctagc[A/G]cctgagttccttgact	A	G	6049 // Homo sapiens ring finger protein (C3H2C3 type) 6 (RNF6), transcript variant 2, mRNA. /// NM_183043 // downstream // 93758 // Hs.136885 // RNF6 // 6049 // Homo	RNF6	RNF6, Homo sapiens ring finger protein (C3H2C3 type) 6 (RNF6), transcript variant 2, q12.13
SNP_A-1842860	tagtagagtgaggaac[A/G]gaactacatgattatc	A	G	Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, mRNA. /// NM_022785 // intron // 0 // Hs.368507 // FLJ23588 // 64800 //	FLJ23588	FLJ23588, Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, q13.2
SNP_A-1836508	tactcctctttgtcca[C/T]gtatcagttcactcta	C	T	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- ///	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-1950610	tttcatcttcagccaa[C/G]tgaaaaaacattggtg	C	G	Homo sapiens mRNA for KIAA0611 protein, partial cds. /// ENST00000311637 // intron // 0 // --- // --- // --- // --- ///	ATP9A	ATP9A, Homo sapiens for KIAA0611 protein, partial cds. ,q13.2
SNP_A-1957235	ttttactgtgtacatc[A/T]ccattattttacttta	A	T	ENST00000309963 // intron // 0 // --- // --- // --- // ---	-	q14.13
SNP_A-1956556	tttgtttcataagtaa[C/T]atagtttgtgagtatt	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- // ---	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1939215	ttgatatttttggaca[C/T]ggtattttaatgagaa	C	T	C20orf79 // 140856 // Homo sapiens chromosome 20 open reading frame 79 (C20orf79), mRNA. /// NM_020689 //	C20orf79	C20orf79, Homo sapiens chromosome 20 open reading frame 79 (C20orf79), p11.23
SNP_A-1939634	ttgatttctgttctaa[A/G]taagcaactctgccct	A	G	57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 424286 // --- // ---	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-1975363	tcacaagtcttggaaa[A/G]ctgaatagattatctg	A	G	Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000304853 // intron // 0 // --- // --- // --- // --- ///	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. q26.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1972130	tgtttcctaccactac[A/G]gatacttaatgccttc	A	G	2329 // Homo sapiens flavin containing monooxygenase 4 (FMO4), mRNA. /// NM_015172 // upstream // 127400 //	FMO4	FMO4, Homo sapiens flavin containing monooxygenase 4 (FMO4), q24.3
SNP_A-1966690	cttatctttccaaatc[C/T]ctccttattgggtgct	C	T	// 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 230714 //	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1962483	aggagattaataagga[C/T]agaaggaagtcaggtg	C	T	Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, mRNA. /// ENST00000256640 // intron // 0 // --- // --- // --- // ---	WNT2B	WNT2B, Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, p13.2
SNP_A-1889220	tgagtcttttggccta[C/T]ggaagttggtcaggtg	C	T	Homo sapiens apoptosis, caspase activation inhibitor (AVEN), mRNA. /// ENST00000306730 // intron // 0 // --- // ---	AVEN	AVEN, Homo sapiens apoptosis, caspase activation inhibitor (AVEN), q14
SNP_A-1880560	tcttgcacttccacca[A/G]tcatctatgagaattg	A	G	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-1930291	ttcatttaaaaatacc[C/T]cagctgatgccagcac	C	T	54888 // Homo sapiens NOL1/NOP2/Sun domain family 2 (NSUN2), mRNA. /// ENST00000338486 // downstream //	NSUN2	NSUN2, Homo sapiens NOL1,p15.31
SNP_A-1917397	tgttttgataaatgca[C/T]aaatgagtgaatgaac	C	T	56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream //	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.2
SNP_A-1907635	tgtaaccaggctgtta[C/T]gtaggctattatttgg	C	T	// Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 79505 // Hs.314543 // CTNND2	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1904750	tgggggtgccatgacc[C/T]gcttactttggctcat	C	T	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-1940821	gagcccacttggaccc[A/G]gcagtgtgagcgccat	A	G	Homo sapiens jumonji domain containing 2B (JMJD2B), mRNA. /// ENST00000159111 // intron // 0 // --- // --- // --- // ---	JMJD2B	JMJD2B, Homo sapiens jumonji domain containing 2B (JMJD2B), p13.3
SNP_A-1961436	ttttttgtttttgcca[A/G]tatatgttagtcaggc	A	G	// 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1352046 // --- // ---	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1855972	tcaattaccccaacac[C/T]cagaagtggaattact	C	T	Homo sapiens translocation associated membrane protein 2 (TRAM2), mRNA. /// ENST00000182527 // intron // 0 // --- // ---	TRAM2	TRAM2, Homo sapiens translocation associated membrane protein 2 (TRAM2), p12.2
SNP_A-1852705	tatttcaatgattttc[C/T]attgtggttttcttca	C	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2063388 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1867552	tccggagtttcttgaa[G/T]tctcacaagtgttttc	G	T	Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000265071 // intron // 0 // --- // ---	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1787153	gggaaatctatcttga[C/T]gggcaggattttagat	C	T	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA. /// ENST00000303015 // intron // 0 // --- // ---	KCNK9	KCNK9, Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), q24.3
SNP_A-1786306	ggctgtggaaagtgta[C/T]ctacatttcgtgcttt	C	T	1608 // Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA. /// NM_017541 // downstream // 28102 //	DGKG	DGKG, Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), q27.3
SNP_A-1806274	gtcctgtttagcctga[G/T]gaagatgaaatggaag	G	T	Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, mRNA. /// NM_201443 // intron // 0 //	TEAD4	TEAD4, Homo sapiens TEA domain family member 4 (TEAD4), transcript variant 2, p13.33
SNP_A-1694723	gacagaggtgtgagatttagttcat[C/T]acagccaggggtaggagagagggtg	C	T	AB032953 // intron // 0 // Hs.173560 // ODZ2 // 57451 // odd Oz/ten-m homolog 2	ODZ2	ODZ2 , rs1013017, odd Oz,q34
SNP_A-1689564	ttgatcctgtggggccttgacaaag[C/T]attgattgttccttcaaccttcaga	C	T	bullous pemphigoid antigen 1, 230/240kDa /// NM_015548 // intron // 0 // Hs.443518 // BPAG1 // 667 // bullous pemphigoid	BPAG1	BPAG1 , rs6941626, bullous pemphigoid antigen 1, 230,p12.1
SNP_A-1651454	gcagaatgaaaagctacatattaga[A/G]catcatagaataacttgaaattcac	A	G	// glycerol kinase 2 /// NM_058168 // upstream // 210506 // Hs.104215 // GDEP // 118425 // gene differentially expressed	GK2	GK2 , rs4550960, glycerol kinase 2 ,q21.21
SNP_A-1647656	agtgggcttatgagatgtttgccca[C/T]tgccataggttctgggctatggatt	C	T	NM_002585 // intron // 0 // Hs.408222 // PBX1 // 5087 // pre-B-cell leukemia transcription factor 1	PBX1	PBX1 , rs10494425, pre-B-cell leukemia transcription factor 1,q23.3
SNP_A-1668450	aagggctgaaattcatgattgaaag[A/C]ctggaaatatttttgtgctttccaa	A	C	// glycerol kinase 2 /// NM_058168 // upstream // 239616 // Hs.104215 // GDEP // 118425 // gene differentially expressed	GK2	GK2 , rs2709847, glycerol kinase 2 ,q21.21
SNP_A-1725366	atatatctatgtaccaattgaataa[A/C]ataagtcaagtaaaaaagccatcat	A	C	IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 170755 // Hs.201920 // EPHA5 // 2044 //	-	- , rs441785, Clone IMAGE:4429392, mRNA, partial cds ,q13.1
SNP_A-2220826	ccttgcaccagttgtg[A/G]aattaacctgcttgga	A	G	/// ENST00000326756 // downstream // 97314 // --- // --- // ---	-	p16.1
SNP_A-2191625	catatgtgttctataa[C/T]gtatttgaaagatttc	C	T	57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 83236 //	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2136745	atcacttctatttgga[A/T]caaaattcccaaggat	A	T	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 168696 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2128240	ataaggtcttagcttc[C/T]aaccactctatggaac	C	T	// 137392 // Homo sapiens similar to CG6405 gene product (LOC137392), mRNA. /// ENST00000344692 // downstream	LOC137392	LOC137392, Homo sapiens similar to CG6405 gene product (LOC137392), q22.1
SNP_A-2124887	agttgaattacttttc[C/T]catctctctataactc	C	T	29094 // Homo sapiens HSPC159 protein (HSPC159), mRNA. /// ENST00000335402 // upstream // 85484 // --- // ---	HSPC159	HSPC159, Homo sapiens HSPC159 protein (HSPC159), p14

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2144835	atgatgttgacagcga[C/T]gaggttttattggtta	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2011148	aacagacgccacctca[A/T]gtcaggaggtccaaga	A	T	sapiens mutated in colorectal cancers (MCC), mRNA. /// ENST00000359932 // intron // 0 // --- // --- // --- // --- ///	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-2014490	tcttttggcatatcga[C/G]ccatatagttaagttg	C	G	Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // intron // 0 // Hs.268707 // CNTN5 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2032888	aaataataaatgccaa[A/T]ttcagaataatagcta	A	T	sapiens alcohol dehydrogenase 4 (class II), pi polypeptide (ADH4), mRNA. /// ENST00000265512 // intron // 0 // --- // ---	ADH4	ADH4, Homo sapiens alcohol dehydrogenase 4 (class II), pi polypeptide (ADH4), q23
SNP_A-2106521	agcctattatttcaga[A/T]agccttgaggaagctg	A	T	339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// NM_130782 // upstream // 1271813 // Hs.440890 // RGS18	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.2
SNP_A-2104538	agcagggcagggatac[A/G]aaggcatgttgaattt	A	G	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-2090874	actttcatgaactcaa[C/T]gagatactgcaagagg	C	T	9436 // Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), mRNA. /// NM_138457 // upstream // 163343 //	NCR2	NCR2, Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), p21.1
SNP_A-2239926	ctgaactagagctaac[G/T]atgacagccaacattc	G	T	51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 16043 // --- // ---	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-2231904	ctcaaattcagtctct[C/T]acgattaaactaaagg	C	T	Homo sapiens hypothetical protein FLJ10305 (FLJ10305), mRNA. /// ENST00000261776 // intron // 0 // --- // --- // --- // ---	VAC14	VAC14, Homo sapiens hypothetical protein FLJ10305 (FLJ10305), q22.1
SNP_A-2233019	ctcagagtccaagctc[A/T]cttgtcttgaagcaat	A	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2270164	gacacatatataaccc[A/G]acattttcttgcacac	A	G	64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 702257 //	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2264893	gaagagccagaaaacg[G/T]atatcacagaaaaagg	G	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2310349	ggaactaattcacaaa[A/T]ctaggaatgttcttaa	A	T	23406 // Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), mRNA. /// NM_024731 // upstream // 13521 //	COTL1	COTL1, Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), q24.1
SNP_A-2287725	gattacattcctaaaa[C/T]ctcacctgacttcatt	C	T	Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001001924 // intron // 0 // Hs.7946 //	MTUS1	MTUS1, Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, p22
SNP_A-2267060	gaataacaacctgtaa[C/T]gtagtattgtataatg	C	T	ENST00000264158 // intron // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-2282367	gagttcagtttctgaa[C/T]caacaaaagaaaggca	C	T	Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 //	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2235423	ctcccttggcagacac[A/G]gaaattctaaacaaat	A	G	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // downstream //	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2250489	cttagggaccatcttc[A/C]attgatatgcttattt	A	C	6252 // Homo sapiens reticulon 1 (RTN1), transcript variant 3, mRNA. /// NM_206857 // upstream // 23596 // Hs.368626 //	RTN1	RTN1, Homo sapiens reticulon 1 (RTN1), transcript variant 3, q23.1
SNP_A-2248443	ctgtgttacacagata[A/T]gatagaagagaaaatt	A	T	sapiens fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94) (FER), mRNA. /// ENST00000281092 // intron // 0 // -	FER	FER, Homo sapiens fer (fps q21.3
SNP_A-2092825	agaaattcacacctta[C/T]gcaaatgacataccta	C	T	64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 215965 //	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-2053176	aagtctggcttttgtg[C/T]atcagccctggatttc	C	T	// 222546 // Homo sapiens regulatory factor X domain containing 1 (RFXDC1), mRNA. /// NM_153453 // upstream //	RFXDC1	RFXDC1, Homo sapiens regulatory factor X domain containing 1 (RFXDC1), q22.1
SNP_A-2070817	acactagacgtgttaa[A/G]tgagcaagactttaga	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 342000 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2005164	gggctctgaagagatc[A/G]actgttctcccagcac	A	G	// 83900 // Homo sapiens keratin associated protein 9-3 (KRTAP9-3), mRNA. /// NM_031961 // upstream // 15713 //	KRTAP9-3	KRTAP9-3, Homo sapiens keratin associated protein 9-3 (KRTAP9-3), q21.2
SNP_A-1993170	gcacaactttactgac[A/G]caaaaaagtgaaaaga	A	G	/// ENST00000342478 // downstream // 627903 // --- // --- // ---	-	q11.21
SNP_A-1995345	ttcagcataaatacac[C/T]ggacaaagggctgatt	C	T	-- /// ENST00000328955 // upstream // 1140690 // --- // --- // ---	-	q24.23
SNP_A-2148134	atgggacaaatgatac[C/T]ggctgtaataaactat	C	T	114884 // Homo sapiens oxysterol binding protein-like 10 (OSBPL10), mRNA. /// ENST00000273142 // upstream //	OSBPL10	OSBPL10, Homo sapiens oxysterol binding protein-like 10 (OSBPL10), p24.1
SNP_A-2188337	cagtctgtctgtacac[C/T]atgtctaccattcaac	C	T	PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream //	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-2192985	catcgccgcgactctc[C/T]agccccaggttcttag	C	T	2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 111652 //	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2182740	cagatgccacaggaaa[A/G]catttttcttctcttca	A	G	DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 266653 //	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2219440	cctgtgtgattttacg[A/G]aacttgtcctgacccg	A	G	sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), mRNA. /// ENST00000357898 // intron // 0 // --- // ---	SSB1	SSB1, Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), p36.22
SNP_A-2209332	cccagttccttctcca[A/C]cttactatcagtgtga	A	C	58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 157950 //	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2
SNP_A-1689182	ttggtttttaaatatggcaaaatta[C/T]atatgagcttcccattttacaggtt	C	T	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs1387381, cadherin 13, H-cadherin (heart),q23.3
SNP_A-1686532	agacagggccttgatgttctccaaa[C/T]tctttcatccccaacaatcccatga	C	T	// 2625 // GATA binding protein 3 /// NM_006561 // upstream // 2759280 // Hs.211610 // CUGBP2 // 10659 // CUG triplet	GATA3	GATA3 , rs7092384, GATA binding protein 3 ,p14
SNP_A-1686920	tgtaggatttgaattggagctatca[A/G]taagtgggagatcatgatctgatac	A	G	4651 // myosin X /// NM_019000 // upstream // 118824 // Hs.82273 // FLJ20152 // 54463 // hypothetical protein	MYO10	MYO10 , rs6861112, myosin X ,p15.1
SNP_A-1787672	gggacagaagtaatgc[C/T]acctccagtggaaaaa	C	T	Homo sapiens flotillin 2 (FLOT2), mRNA. /// ENST00000335362 // intron // 0 // --- // --- // --- // ---	FLOT2	FLOT2, Homo sapiens flotillin 2 (FLOT2), q11.2
SNP_A-1790081	ggggaagaacaggggga[C/G]aatccttacagcagca	C	G	ENST00000298738 // intron // 0 // --- // --- // --- // ---	-	q14.13
SNP_A-1859844	tcagggtctctagtca[C/T]ggattccctgggaacc	C	T	Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, mRNA. /// NM_022785 // intron // 0 // Hs.368507 // FLJ23588 // 64800 //	FLJ23588	FLJ23588, Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, q13.2
SNP_A-1861704	tcatctgaaatctaca[A/G]tattagtcattttcta	A	G	/// ENST00000242916 // upstream // 699330 // --- // --- // --- // -	-	p14
SNP_A-1845706	tatagggaatagagga[C/T]attaagaatacagctt	C	T	sapiens selectin P (granule membrane protein 140kDa, antigen CD62) (SELP), mRNA. /// ENST00000263686 // intron // 0 // --- // --- // --- // ---	SELP	SELP, Homo sapiens selectin P (granule membrane protein 140kDa, antigen CD62) (SELP), q24.2
SNP_A-1840658	tagcctgtgtttgcaa[C/T]tgagtcatttctcagc	C	T	// 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 180441 // Hs.523852 //	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-1815813	gttaagtccttttatc[C/T]ctatgatcttatctct	C	T	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 156092 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1957854	ttttatttgaagtgta[G/T]ataaagccatctatgt	G	T	7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 180355 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1954343	tttgcagcttacatta[C/T]aaattgacaagataga	C	T	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1938599	ttgagagaagctttta[G/T]cagatacaaagtctgc	G	T	// 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 1043852 // --- // --- // -	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1983837	tgaagatccatatggt[A/G]acatacatgaaatgta	A	G	MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 814149 // Hs.314261 //	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q31.3
SNP_A-1919123	ttaactgccctactta[C/T]ctcagatgattgttat	C	T	ENST00000312493 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1898187	tgcttaaaatggatag[A/G]actttgcttccacatt	A	G	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-1903788	tgggagttgttcatgt[C/G]aaacttcccataaatg	C	G	// 490 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 // upstream // 1217076 // Hs.506276 //	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1901327	tggatgtccccattgt[A/G]aatcactaagctagga	A	G	366 // Homo sapiens aquaporin 9 (AQP9), mRNA. /// NM_000236 // upstream // 122371 // Hs.188630 // LIPC //	AQP9	AQP9, Homo sapiens aquaporin 9 (AQP9), q21.3
SNP_A-1879391	tcttataggattgctg[C/T]acaatttaaatgagac	C	T	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1912260	tgtgatgagaatctca[A/G]gacagtgaggtttagt	A	G	56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream //	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1927515	ttcaaatgtgccttca[G/T]gatatacttcatagta	G	T	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 143120 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1988461	tcaaatgttctgcttt[C/T]ctcttgacctgcataa	C	T	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1075137 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1955579	tttggttgcatgtacc[A/G]gaatactgactacaga	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1815653	gttaacaactgtagca[C/T]ctaaagtcaatttcct	C	T	Homo sapiens coiled-coil domain containing 3 (CCDC3), mRNA. /// ENST00000281144 // intron // 0 // --- // --- // --- // ---	CCDC3	CCDC3, Homo sapiens coiled-coil domain containing 3 (CCDC3), p13
SNP_A-1859909	tcaggtcaacaccttа[C/T]actggtttatgtatca	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2625149 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1788015	gggagacagagtttgc[C/G]ataagccgggattgtg	C	G	Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000355794 // intron // 0 // --- // --- // --- // ---	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-1793902	ggtcaactgtatttta[C/T]aatttcattccatttt	C	T	// Homo sapiens hypothetical protein FLJ25351 (FLJ25351), mRNA. /// ENST00000286195 // intron // 0 // --- // --- // --- // ---	ALS2CR11	ALS2CR11, Homo sapiens hypothetical protein FLJ25351 (FLJ25351), q33.1
SNP_A-1805197	gtcattcaaccattcc[A/G]aatcttacaaagcctg	A	G	4676 // Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA. /// NM_139207 // upstream // 288301 //	NAP1L4	NAP1L4, Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), q21.2
SNP_A-1814188	gtgtctccactacccc[C/T]gattcaaatgctcaaa	C	T	/// ENST00000359349 // upstream // 346797 // --- // --- // --- // ---	-	p13.2
SNP_A-1808876	gtgaatagtaaagtaa[C/T]gcggggctggtatcta	C	T	6894 // Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), mRNA. /// NM_182972 // downstream // 71511 //	TARBP1	TARBP1, Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), q42.2
SNP_A-1660743	gaggataaattattttaatagaatg[C/T]cataaccacaagggtaaatactagc	C	T	NM_022445 // intron // 0 // Hs.127548 // TPK1 // 27010 // thiamin pyrophosphokinase 1	TPK1	TPK1 , rs7455032, thiamin pyrophosphokinase 1,q35
SNP_A-1785156	ggctaaatgaatcact[A/G]acacacaaagcaggta	A	G	284176 // Homo sapiens hypothetical protein FLJ40457 (FLJ40457), mRNA. /// ENST00000300671 // upstream //	FLJ40457	FLJ40457, Homo sapiens hypothetical protein FLJ40457 (FLJ40457), q25.3
SNP_A-1750745	tccaagggaccaaaagaagccatag[A/T]atgtgtgggcaggtgtaggcgtgag	A	T	NM_002020 // intron // 0 // Hs.415048 // FLT4 // 2324 // fms-related tyrosine kinase 4	FLT4	FLT4 , rs307810, fms-related tyrosine kinase 4,q35.3
SNP_A-1752091	aaaaatgtaacatcccaagagccca[C/T]cataatgacatcacaaatgaaaggа	C	T	NM_005246 // intron // 0 // Hs.121558 // FER // 2241 // fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94)	FER	FER , rs3797819, fer (fps,q21.3
SNP_A-2216375	cctcctgtggctgcca[C/G]cttttcgccattcaga	C	G	Homo sapiens chromosome 6 open reading frame 10 (C6orf10), mRNA. /// ENST00000305725 // intron // 0 // --- // ---	C6orf10	C6orf10, Homo sapiens chromosome 6 open reading frame 10 (C6orf10), p21.32
SNP_A-2182677	cagatgaaccaataaa[C/T]accatgtggtccatct	C	T	10908 // Homo sapiens neuropathy target esterase (NTE), mRNA. /// ENST00000221249 // downstream // 994 // --- // ---	NTE	NTE, Homo sapiens neuropathy target esterase (NTE), p13.2
SNP_A-2174062	cacacccaccagcatc[A/G]ctagtgcttttcatcc	A	G	414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 425962 // Hs.369438 // ETS1 //	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.2
SNP_A-2172090	caatggcttgttgcac[A/T]gcatggagaagttgat	A	T	Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// ENST00000305375 // intron // 0 // --- // --- // --- // ---	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2198524	catttatggactgata[C/T]ggtcttttcaagtgat	C	T	sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), mRNA. /// ENST00000218867 // intron // 0 // --- // --- // --- // ---	SGCG	SGCG, Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), q12.12
SNP_A-2145944	atgcccttcagacaca[C/G]aacaaagcttagcaga	C	G	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2129049	ataattagtgctaaga[A/T]ctgctaagaaatttta	A	T	257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1517711 //	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2107943	agctcctcaggcaaaa[A/G]cgacagaaggaaacta	A	G	// 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2109686	aggaaagctgcctaaa[C/T]ccaagttgcctaaaat	C	T	sapiens complement component 5 (C5), mRNA. /// ENST00000223642 // intron // 0 // --- // --- // --- // ---	C5	C5, Homo sapiens complement component 5 (C5), q33.2
SNP_A-2119508	agtatccctatatcaa[A/G]ttaaccttcttctaga	A	G	Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// ENST00000005198 // intron //	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2120658	tcaacggctgtagtcc[A/C]aaagactgtagtcaga	A	C	// 10208 // Homo sapiens chromosome 13 open reading frame 22 (C13orf22), mRNA. /// NM_001629 // upstream //	C13orf22	C13orf22, Homo sapiens chromosome 13 open reading frame 22 (C13orf22), q12.3
SNP_A-1994454	ttcttccccctgtgtc[C/T]caagaatactcttatc	C	T	51582 // Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, mRNA. /// NM_148174 // upstream // 135161 // Hs.459106 // OAZIN // 51582 // Homo	OAZIN	OAZIN, Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, q22.3
SNP_A-2013230	gccatagggcacaatc[A/G]cctttaatactaaga	A	G	84950 // Homo sapiens hypothetical protein FLJ14936 (FLJ14936), mRNA. /// NM_032864 // downstream // 832 //	FLJ14936	FLJ14936, Homo sapiens hypothetical protein FLJ14936 (FLJ14936), p32.3
SNP_A-2067103	acaaagaaattcaagc[A/G]gattttccatgaggga	A	G	8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 55642 // Hs.425091 // FAM44B	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2092029	agaaaccctgatttac[A/C]acattaatatctttca	A	C	399967 // Homo sapiens LVLF3112 (UNQ3112), mRNA. /// NM_145014 // upstream // 6040 // Hs.98133 // FLJ32915 //	UNQ3112	UNQ3112, Homo sapiens LVLF3112 (UNQ3112), q24.2
SNP_A-2086385	actcttccttgtgatg[A/G]aaccataatctaggta	A	G	sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082266	acgaggttcagggcaa[C/G]tgacttctttagactt	C	G	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 478519 // --- // --- // --- // -	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2252510	cttcctgaaagtgtaa[G/T]tgaagttgacaggttc	G	T	50840 // Homo sapiens taste receptor, type 2, member 14 (TAS2R14), mRNA. /// NM_176890 // downstream // 3859 // --	TAS2R14	TAS2R14, Homo sapiens taste receptor, type 2, member 14 (TAS2R14), p13.2
SNP_A-2253454	cttcttagactaccaa[A/G]cgtcttatatttggat	A	G	ENST00000263154 // intron // 0 // --- // --- // --- // ---	-	p15.3
SNP_A-2287547	gatgtttttgcttgca[C/G]attacagaaaatcaac	C	G	/// ENST00000328167 // upstream // 95108 // --- // --- // --- // --	-	p15.1
SNP_A-2257134	ctttctctctcaccca[A/G]cgtccaatctgtcaac	A	G	90198 // Homo sapiens HBV pre-s2 binding protein 1 (SBP1), mRNA. /// NM_032488 // downstream // 3687 // Hs.148590 //	SBP1	SBP1, Homo sapiens HBV pre-s2 binding protein 1 (SBP1), q13.2
SNP_A-2292499	gcactcagaaatggca[A/G]tctctctctctccttc	A	G	-- /// ENST00000329863 // downstream // 397921 // --- // --- //	-	q23.1
SNP_A-2291154	gcaatatgagatgata[C/T]gcctttgtaacctaat	C	T	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 118644 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2286823	ctgtaaatattcagtc[C/T]attgatgaagagctct	C	T	sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // --- // --- // --- // ---	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2274296	gacttggaaaagacaa[C/T]gtctgtagtattccca	C	T	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-2277842	gagcatgatttgaaaa[C/T]tactttcctaggttaa	C	T	Homo sapiens putative prolyl oligopeptidase (KIAA0436), mRNA. /// ENST00000260648 // 3UTR // 0 // --- // --- // --- // ---	KIAA0436	KIAA0436, Homo sapiens putative prolyl oligopeptidase (KIAA0436), p21
SNP_A-2066925	acaaacaaacaaaaaa[C/G]gatttctcctctgtct	C	G	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 3, mRNA. /// NM_017701 // intron // 0 // Hs.102336 // ARHGAP8 // 23779 // Homo sapiens Rho	ARHGAP8	ARHGAP8, Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 3, q13.31
SNP_A-2069717	acacactagaggaaga[C/G]aatactaatttggaga	C	G	Homo sapiens hypothetical protein FLJ32915 (FLJ32915), mRNA. /// NM_031307 // CDS // 0 // Hs.98682 // PUS3 //	FLJ32915	FLJ32915, Homo sapiens hypothetical protein FLJ32915 (FLJ32915), q24.2
SNP_A-2061520	aatgctgaggggaata[G/T]cacgtaaaaaggtaga	G	T	ENST00000338644 // intron // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-2060593	aatgagaaaagtacca[A/T]caatttcatatatatt	A	T	Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), mRNA. /// ENST00000235547 // intron // 0 // --- // --- // --- // ---	HSD3B1	HSD3B1, Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), p12
SNP_A-2004291	cggtattgttgatgca[A/G]tcttttgtgtaggtac	A	G	Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), mRNA. /// ENST00000355366 // intron // 0 // ---	ARHGAP19	ARHGAP19, Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), q24.1
SNP_A-2024950	aaaataaataaataaa[C/G]gtcatttgcaaagggc	C	G	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// ENST00000199936 // intron // 0 // --- //	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-2021103	aaaaaaaagagctcac[A/G]aatgtccctgctgttt	A	G	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2123382	agtgtccagagggtgc[C/T]gagtaaccagggaatg	C	T	Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // --- // ---	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2160141	atttcaaaatccgaag[C/T]agtttggcttgcatcc	C	T	10736 // Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA. /// NM_018079 // downstream //	SIX2	SIX2, Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), p21
SNP_A-2161735	atttgtaagtagaata[A/C]agggtccgtgggaata	A	C	sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000264382 // intron // 0 // --- // --- // --- // ---	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2194334	catgataggtgcttca[A/G]aggaaaatatttctga	A	G	PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 1151796 // Hs.405156 //	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.3
SNP_A-2222318	cgacttgacaccttca[C/T]gcgaagattctaataa	C	T	Homo sapiens junctophilin 1 (JPH1), mRNA. /// ENST00000342232 // intron // 0 // --- // --- // --- // --- ///	JPH1	JPH1, Homo sapiens junctophilin 1 (JPH1), q21.11
SNP_A-2224687	cgtctattgaaatgct[A/C]aatctgaaaagtatct	A	C	SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2213075	ccgagactaagagtac[A/G]aaattatgaggatcat	A	G	ENST00000319540 // intron // 0 // --- // --- // --- // ---	-	q21.22
SNP_A-2210405	cccccagtcaagcaga[C/T]gagagacctaaccctc	C	T	Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA. /// NM_199185 // intron // 0 // Hs.519452 // NPM1 // 4869 // Homo sapiens nucleophosmin	NPM1	NPM1, Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), q35.1
SNP_A-1813351	gtggtgggctggaaca[A/G]aaaatgcaatatttca	A	G	5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 310939 // Hs.470412 // RBMS1 //	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-1801947	acaaaaaatcacaatg[A/T]aaacagtagaaccaga	A	T	// 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 //	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1793394	ggtaggggtgacatcc[A/C]aacaggagcctcaggg	A	C	Homo sapiens centaurin, delta 2 (CENTD2), transcript variant 1, mRNA. /// NM_015242 // intron // 0 // Hs.503165 //	CENTD2	CENTD2, Homo sapiens centaurin, delta 2 (CENTD2), transcript variant 1, q13.4
SNP_A-1791957	gggtgcttacccagga[A/G]ctcggtctagacctct	A	G	sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. /// ENST00000344573 // intron // 0 // --- // --- // --- // ---	ALPL	ALPL, Homo sapiens alkaline phosphatase, liver,p36.12
SNP_A-1863923	tccaatgggtgatcct[A/T]aaactgaaatgcaggc	A	T	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA. /// NM_013987 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, q26
SNP_A-1870679	tcatttgtgtgtaaaa[A/G]ctgtgatgttatatac	A	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 561237 // --- // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1852191	tattgtagcaataaga[A/G]tagtaatcagaatcca	A	G	79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// ENST00000357652 // upstream // 113093 // --- // ---	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1853319	tattttatctgtaaac[A/T]ctgagctgatggcttt	A	T	LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 407126 // Hs.307086 //	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-1837167	tactgttgagtaccaa[A/G]ttcttatttaaaaagc	A	G	// 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 537639 // Hs.516617	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1835124	taccctctgaagaata[C/T]gtagagtaagtgcccc	C	T	9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 189126 //	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-1833053	tacacagagaaatgac[A/C]aaactattttcttaac	A	C	25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// NM_001752 //	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-1944356	ttgtcgaagctgggcc[A/G]aggccttcacaggtgt	A	G	// 58158 // Homo sapiens neurogenic differentiation 4 (NEUROD4), mRNA. /// ENST00000257883 // upstream //	NEUROD4	NEUROD4, Homo sapiens neurogenic differentiation 4 (NEUROD4), q13.2
SNP_A-1989440	ggtttacctttttccac[A/G]gaggtatggcagcact	A	G	5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 //	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1964933	tagtatgtgcttcata[C/G]agaggttgtaagaata	C	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 363568 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1876251	tctgagacaagtgcca[A/G]tcaatttagaagctta	A	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 586701	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1876762	tctgcagtctcatcgc[A/G]ctttgcttgtgtgcat	A	G	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1903066	ctactgttcccactac[C/T]ctactcaattcctccc	C	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1898543	tgcttgaggtgagccc[C/T]gaccaaatgcaagcct	C	T	ENST00000265018 // intron // 0 // --- // --- // --- // ---	-	p15.32
SNP_A-1932288	ttcctctgacctttca[C/G]caaggctcttagcttc	C	G	3099 // Homo sapiens hexokinase 2 (HK2), mRNA. /// NM_019896 // upstream // 9672 // Hs.469060 // POLE4 //	HK2	HK2, Homo sapiens hexokinase 2 (HK2), p12
SNP_A-1916199	tgttgggctccacaaa[A/G]ctggctgagatccagt	A	G	25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream //	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2
SNP_A-1916255	tgttgtaatgttagaa[A/G]agtagaacagcttgtg	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1972358	gtgggtgtttagagaa[G/T]catgatgatgcatcaa	G	T	Homo sapiens dynamin 3 (DNM3), mRNA. /// ENST00000358155 // intron // 0 // --- // --- // --- // --- ///	DNM3	DNM3, Homo sapiens dynamin 3 (DNM3), q24.3
SNP_A-1838532	tagaatgtaggaattc[A/T]aaactttgtgctttga	A	T	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// NM_044472 // intron // 0 // Hs.467637 // CDC42 // 998 // Homo sapiens	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-1801966	gtataaatgtctgttg[C/T]ataacccagtgcttgt	C	T	Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // --- // --- // --- // ---	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1808782	gtgaaggcacaaaatc[A/G]cttctcaagttgggcc	A	G	1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream //	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1713780	agtgtaactaccatactcttttcca[C/T]agaatctgttccattctgtgttcct	C	T	// 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 2095253 // Hs.450919 // GPC5 //	SLITRK5	SLITRK5 , rs2184270, SLIT and NTRK-like family, member 5 ,q31.2
SNP_A-1675938	acataacctctcttttgtgatctct[C/G]acatcaatgatactaacaaaagcag	C	G	NM_018723 // intron // 0 // Hs.57937 // A2BP1 // 54715 // ataxin 2-binding protein 1	A2BP1	A2BP1 , rs970426, ataxin 2-binding protein 1,p13.2
SNP_A-2174176	cacacgttgtcaagat[C/T]agcaagggatgtcagc	C	T	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // --- // ---	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2160692	atttcgactttacaca[C/G]aggtgcccctacttac	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2158713	attgtccttcgtctcc[C/G]atatcaaatctgtgct	C	G	Homo sapiens zinc finger protein 215 (ZNF215), mRNA. /// ENST00000278319 // intron // 0 // --- // --- // --- // --- ///	ZNF215	ZNF215, Homo sapiens zinc finger protein 215 (ZNF215), p15.4
SNP_A-2153387	attagacttcaaaaga[A/T]ccttagtctccacaat	A	T	// 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 203143 //	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-2149077	atggttttctatggca[A/G]ctgttcttcaaaaatg	A	G	27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 981761 // Hs.352656 // GHITM // 27069 // Homo	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2142211	atgaaaacaagaagag[A/G]aagcaaggattgtaca	A	G	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000357362 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2139791	atctaaataatgtctg[C/T]aatgcactagtatgaa	C	T	Homo sapiens Alstrom syndrome 1 (ALMS1), mRNA. /// ENST00000264448 // intron // 0 // --- // --- // --- // ---	ALMS1	ALMS1, Homo sapiens Alstrom syndrome 1 (ALMS1), p13.1
SNP_A-2109906	aggaactaattgacac[G/T]cctataaaatgggttg	G	T	Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-2108340	agctgatccgtggcca[A/G]tgccaggctttctatt	A	G	Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2028524	aaactgagatggcaaa[C/T]cccaaaccaaggtgct	C	T	Homo sapiens lipin 2 (LPIN2), mRNA. /// ENST00000261596 // intron // 0 // --- // --- // --- // ---	LPIN2	LPIN2, Homo sapiens lipin 2 (LPIN2), p11.31
SNP_A-2043454	aactggtgttcttaga[A/C]ggctcaggactaaact	A	C	3744 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10), mRNA. /// NM_004974 // downstream // 73645 // Hs.248139 // KCNA2 //	KCNA10	KCNA10, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10), p13.3
SNP_A-2034399	aaatctaggtattgcc[A/G]ccaaagaggcagtgaa	A	G	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 51666 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2018306	gatttggtgggacttc[A/C]atgcgtatacacataa	A	C	// 3454 // Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA. /// NM_005534 // upstream //	IFNAR1	IFNAR1, Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), q22.11
SNP_A-2069003	acaatgcattgggga[A/G]aaaacacttagccttt	A	G	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 595141 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-2081313	acctggattgtgtacc[A/G]cagtgactcattaatc	A	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1280726 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2097837	agagactgcgtcttaa[C/T]agcattatttgagtcc	C	T	KIAA0582 // 23177 // Homo sapiens KIAA0582 (KIAA0582), mRNA. /// NM_004161 // upstream // 93219 // Hs.310645 //	KIAA0582	KIAA0582, Homo sapiens KIAA0582 (KIAA0582), p14
SNP_A-2102348	agattcaaacttaatg[C/G]aagaaactgaggctca	C	G	// 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 215468 // Hs.407755 //	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-2247925	ctgtgcattatgaaaa[G/T]caaacggcatgctttt	G	T	// 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 950454 // Hs.79101 // CCNG1 //	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2236792	ctctacgttctttttc[A/T]actatggaaatgtatg	A	T	SEC61A2 // 55176 // Homo sapiens Sec61 alpha 2 subunit (S. cerevisiae) (SEC61A2), mRNA. /// NM_014142 //	SEC61A2	SEC61A2, Homo sapiens Sec61 alpha 2 subunit (S. cerevisiae) (SEC61A2), p13
SNP_A-2298461	gcccaacaaaatgcca[A/C]gtaatcttgtaagtaa	A	C	sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2301089	gccttcagcccgacca[C/G]gtctacgcactgcaaa	C	G	Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), mRNA. /// ENST00000272117 // intron // 0 // --- // ---	ITPKB	ITPKB, Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), q42.12
SNP_A-2300611	gcctgcaccagaggaa[A/G]aagagatgagggcagg	A	G	ENST00000330898 // intron // 0 // --- // --- // --- // ---	-	p12.1
SNP_A-2306884	gctgtgggatgctcta[C/T]ctttgaaaatatgatc	C	T	9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 91457 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2313543	ggagagttgacacaca[G/T]cattgacacaacttac	G	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 159478 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2299171	gccctaagaaggaatc[A/G]agtcattttcagcctt	A	G	9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 452895 // Hs.510324 // QKI //	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-2296042	gcattagaattctccc[A/G]ctttgaaattctgttt	A	G	// 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream //	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-2294221	gcagggagccagggtc[A/G]aagaactaagtgttgg	A	G	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-2238830	ctcttatagagaagac[A/G]aatatgaactgagcat	A	G	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2248380	ctgtgtgccagtccaa[A/G]atcatttatttattta	A	G	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 881187 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2258750	ctttggtccttgtca[C/T]ggcaaacatcaactcc	C	T	57097 // Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), mRNA. /// NM_001759 // upstream // 163573 // Hs.376071 // CCND2 // 894 // Homo sapiens cyclin	PARP11	PARP11, Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), p13.32
SNP_A-2100944	agatattaccattggg[A/G]aaatttgattaaagtg	A	G	5149 // Homo sapiens phosphodiesterase 6H, cGMP-specific, cone, gamma (PDE6H), mRNA. /// NM_032918 //	PDE6H	PDE6H, Homo sapiens phosphodiesterase 6H, cGMP-specific, cone, gamma (PDE6H), p12.3
SNP_A-2104445	agcaggagatctttta[A/T]attacaaagccctttg	A	T	80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // downstream // 27604 // ---	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2098191	agagataaaaccatac[A/G]actcttacaagaaaac	A	G	4792 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA. /// NM_032594 // upstream // 44980 //	NFKBIA	NFKBIA, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), q13.2
SNP_A-2079838	accctggaatgtaaac[A/C]gatctctgggcagggg	A	C	Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// ENST00000262244 // intron // 0 // --- // --- // --- // ---	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-2011681	tatttccatttaaaaa[A/G]gacccactttatgcaa	A	G	3133 // Homo sapiens major histocompatibility complex, class I, E (HLA-E), mRNA. /// ENST00000259907 // downstream //	HLA-E	HLA-E, Homo sapiens major histocompatibility complex, class I, E (HLA-E), p21.33
SNP_A-2010498	gtcagagaccagaaca[C/G]cagggaagcagggctg	C	G	sapiens interferon regulatory factor 2 (IRF2), mRNA. /// ENST00000303389 // intron // 0 // --- // --- // --- // ---	IRF2	IRF2, Homo sapiens interferon regulatory factor 2 (IRF2), q35.1
SNP_A-2005950	ggatgcttataaggag[A/G]aagtgttagaatgttg	A	G	Homo sapiens eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa (EIF3S10), mRNA. ///	EIF3S10	EIF3S10, Homo sapiens eukaryotic translation initiation factor 3, subunit 10 theta, 150,q26.11
SNP_A-2039143	aacagtacaattcggc[A/G]aaataggaaatctaaa	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2038600	aacagaatagataata[C/G]agatggagacataaat	C	G	/// ENST00000336930 // upstream // 587666 // --- // --- // --- // -	-	p14.3
SNP_A-2021386	aaaaaagaagaggaag[C/G]aaccgtgaggccagta	C	G	80725 // Homo sapiens SNAP25-interacting protein (SNIP), mRNA. /// AK126665 // downstream // 21668 // Hs.448872 //	SNIP	SNIP, Homo sapiens SNAP25-interacting protein (SNIP), q12
SNP_A-2025424	aaaatcattgagcttg[A/C]aaataagtcaagaaat	A	C	// --- /// ENST00000355517 // downstream // 70701 // --- // ---	-	q24.32
SNP_A-2134983	atattcagtccatagc[A/G]ctccacatagagtagg	A	G	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2237311 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2133484	atatatttggaaaaaa[A/T]ttcacattatgtattt	A	T	Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 //	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2142714	atgaagatgtcgtcaa[A/G]cgatctgaactctgat	A	G	2700 // Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), mRNA. /// NM_004004 // downstream	GJA3	GJA3, Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), q12.11
SNP_A-2169647	caagcttttggctttc[A/G]acaatcctcagttgaa	A	G	860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream //	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-2195078	catggaagacagagaa[C/T]gattgagtactaacga	C	T	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2195251	catggcaaccatagta[C/G]agtggtctgcaagggt	C	G	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1684598	tagagtggctgcgttgccaggttta[C/G]agatcctgaaggccaaggctgactc	C	G	NM_017512 // intron // 0 // Hs.475848 // HSRTSBETA // 55556 // rTS beta protein	HSRTSBETA	HSRTSBETA , rs2298581, rTS beta protein,p11.32
SNP_A-1781920	ggcaaaatagaatcaa[C/T]atcttcatcttcaaaa	C	T	10249 // Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // upstream // 100763 //	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-1801428	gtaggccagtggaata[C/T]gcagaaagtccagaaa	C	T	// Homo sapiens chromosome 10 open reading frame 107 (C10orf107), mRNA. /// ENST00000330194 // intron // 0 // ---	C10orf107	C10orf107, Homo sapiens chromosome 10 open reading frame 107 (C10orf107), q21.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787973	gggagaacggcctgga[C/T]gagctttgggtatatt	C	T	Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), mRNA. /// ENST00000291440 // intron // 0 // --- // --- // --- // ---	CPAMD8	CPAMD8, Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), p13.11
SNP_A-1787705	gggacagtaagaagta[A/G]ataaggagtaggtctt	A	G	// Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // ---	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.2
SNP_A-1797474	ggtttatagtttgagg[C/T]actttgttgcatttttt	C	T	/// ENST00000288466 // upstream // 139602 // --- // --- // --- // --- /// ENST00000307730 // upstream // 291174 // --- // --- // ---	-	q32
SNP_A-1837926	tagaaaattaccaaac[C/T]gatgaactcaccggcc	C	T	// 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1834779	taccagctgggtaaga[C/T]acagataacaactatg	C	T	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1872207	tctacttctcaaatta[C/T]ctcttctcccaagctt	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2356303 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1868969	tcctgatccccttgca[A/G]taagaagcgttacaca	A	G	79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1976288	acccggcaaattccac[A/G]ggagcaagagttagca	A	G	ENST00000265018 // intron // 0 // --- // --- // --- // ---	-	p15.32
SNP_A-1974292	attaacaagccaccaa[C/T]tccacctttgaaaact	C	T	131601 // Homo sapiens seven transmembrane domain orphan receptor (TPRA40), mRNA. /// NM_016372 // downstream // 363986 // Hs.6418 // GPR175 // 131601 //	GPR175	GPR175, Homo sapiens seven transmembrane domain orphan receptor (TPRA40), q21.3
SNP_A-1968476	tagctctcgtaatcat[C/G]agtttcttaagtcatt	C	G	325 // Homo sapiens amyloid P component, serum (APCS), mRNA. /// ENST00000255040 // downstream // 5385 // --- // ---	APCS	APCS, Homo sapiens amyloid P component, serum (APCS), q23.2
SNP_A-1967758	ccaaacctctcactta[C/T]atagttttccaaacca	C	T	Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 249386 // Hs.415950 // IRTA2 //	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-1947022	tttaataaataattaa[A/G]tgattgctgtattcca	A	G	FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1923889	ttagtccatttttgc[A/G]ctactgataaagacat	A	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1923473	ttaggccaattttcac[A/G]aaaagtattaagaacc	A	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 880110	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1925981	ttatgtatatcctcta[A/T]gccttttttcttttag	A	T	Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA. /// ENST00000256689 // intron // 0 // --- //	SLC38A2	SLC38A2, Homo sapiens solute carrier family 38, member 2 (SLC38A2), q13.11
SNP_A-1899861	tggacaacccagtcca[C/G]gtagtacaggatctgc	C	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1899199	tggaaatcacaaaaaa[A/C]ttcttcattgtaatgc	A	C	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-1889927	tgatagcctcctcaaa[C/G]atcgcctgcagcggtt	C	G	// 255104 // Homo sapiens hypothetical protein LOC255104 (LOC255104), mRNA. /// NM_019062 // downstream // 11966	LOC255104	LOC255104, Homo sapiens hypothetical protein LOC255104 (LOC255104), p36.13
SNP_A-1890688	tgatgacttcctaaaa[C/T]ggctagttaggaggta	C	T	C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 //	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-1876980	tctgcctgagaagcga[C/G]caagagcagagacaga	C	G	sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA. /// ENST00000344204 // intron // 0 // --- // --- // --- // ---	TRIO	TRIO, Homo sapiens triple functional domain (PTPRF interacting) (TRIO), p15.2
SNP_A-1876199	tctgactgctagctaa[G/T]gtctctgcccgggaac	G	T	2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // upstream // 138451 // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1886132	tgaccatacggcagaa[A/T]ttcaacatccctcctt	A	T	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1885964	tgacattcacaaaaat[G/T]aacatgtagttgtaca	G	T	79744 // Homo sapiens hypothetical protein FLJ23233 (FLJ23233), mRNA. /// NM_198542 // upstream // 5947 //	ZNF419	ZNF419, Homo sapiens hypothetical protein FLJ23233 (FLJ23233), q13.43
SNP_A-1882543	tgaaaattattattta[C/T]ctgagcctcatcctat	C	T	TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 29536 // Hs.27214 // KCNC2 //	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1890425	tgatctacctggcaga[A/G]catttttttttcattg	A	G	23530 // Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), mRNA. /// NM_182977 //	NNT	NNT, Homo sapiens nicotinamide nucleotide transhydrogenase (NNT), p12
SNP_A-1925490	ttatctttactttcca[A/C]catgatcttacttggt	A	C	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 398347 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-1923080	ttagccaagtactcaa[C/T]agtcagatgtagccag	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 733933 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1928807	ttcagagaactaatgc[A/G]agagatcaccttgatt	A	G	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// ENST00000332068 // intron // 0 // --- // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-1928822	ttcagagcaagatacg[A/G]aaaaggtaacttggag	A	G	Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// ENST00000284538 // intron // 0 // --- // --- // --- // ---	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1
SNP_A-1945425	ttgttattggtctatc[G/T]agtctttatatgtctt	G	T	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 608891 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1953113	tttcttgttcttgatt[C/G]aataaagatgaagaca	C	G	// Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 264620 // Hs.1428 // FSHR // 2492 // Homo	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1951380	tttcctaaaatcttcc[A/G]gaaagtcattcagctt	A	G	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 570560	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1981077	cattataacaaatgca[C/G]tatacttgtcctaaag	C	G	-- /// ENST00000354793 // downstream // 827322 // --- // --- //	-	p13.3
SNP_A-1860535	tcagttctataaaatc[A/G]cagctaatatcacaca	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1853894	tcaaaaggagacatga[A/G]caaagctgcccaagct	A	G	91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream //	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1841554	taggataagagtcaca[A/G]acctgtcaccagaaaa	A	G	Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 189713 // Hs.448520 //	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. ,p22
SNP_A-1790116	ggggaagtttgtatga[C/T]ggttttgcacataccc	C	T	Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), mRNA. /// ENST00000256194 // intron // 0 // --- // --	MICAL2	MICAL2, Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), p15.3
SNP_A-1812806	gtgggatccatttaag[A/G]actgaattatgaaatg	A	G	Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // --- // ---	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1742775	agcaaaatacaagaggggagtgaca[A/G]tcttatccagccctccctcttctgg	A	G	// 1413 // crystallin, beta A4 /// NM_002430 // downstream // 762429 // Hs.268515 // MN1 // 4330 // meningioma (disrupted	CRYBA4	CRYBA4 , rs4345013, crystallin, beta A4 ,q12.1
SNP_A-1656625	aaggctttccagaacgtagtctatg[C/T]tggacacttccttctgcctctctgc	C	T	presenilin 2 (Alzheimer disease 4) /// NM_012486 // intron // 0 // Hs.25363 // PSEN2 // 5664 // presenilin 2 (Alzheimer	PSEN2	PSEN2 , rs2073489, presenilin 2 (Alzheimer disease 4) ,q42.13
SNP_A-2199297	cattttcctttgatta[C/T]catgttctagtcaatc	C	T	Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// NM_002865 // upstream // 167906 // Hs.369017 // RAB2 //	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2181586	cagagaaggccaaata[C/T]gctcccgtaaccgatc	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium p13
SNP_A-2180442	cagaacattgcagtag[C/T]aaagtgaaagctctgt	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2220802	ccttgatgttgtctgg[C/G]caatgaacaggaatta	C	G	ENST00000264141 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-2141719	atcttctcactatgaa[A/G]taagacaagaattgga	A	G	401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 680473 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2146667	atgctgtgtagaaaaa[C/T]ggaattaagtatgaaa	C	T	Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // --- // --- // --- // ---	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-2160635	atttcctgatcaccaa[C/G]cttcaccaagagattg	C	G	84057 // Homo sapiens GAJ protein (GAJ), mRNA. /// ENST00000240488 // downstream // 32719 // --- // --- // --- // --	GAJ	GAJ, Homo sapiens GAJ protein (GAJ), q31.3
SNP_A-2111259	aggagcaggatggtga[C/T]gcttagagagtagcag	C	T	Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT), nuclear gene encoding mitochondrial protein, transcript varian /// NM_148173 // CDS // 0 // Hs.287717 // PEMT // 10400 // Homo sapiens	PEMT	PEMT, Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT), nuclear gene encoding mitochondrial protein, transcript varian p11.2
SNP_A-2121716	agtgacataaagtaaa[A/C]agacaggatgttgtga	A	C	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15
SNP_A-2116954	aggtgaacaccttaga[A/G]accactgtccaggtca	A	G	// 81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA. /// NM_152330 // upstream // 129408 //	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-2029441	aaagacaggatttaac[C/T]gcagtctggtaattct	C	T	51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 393524 //	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-2034276	aaatccgaaaaagcta[C/T]atacttcctcccaaaa	C	T	Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// ENST00000341928 // intron // 0 // --- //	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-2016486	agaatgctgtgggaga[A/G]taagtgtgatgagaag	A	G	// 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.2
SNP_A-2013437	gggaatattggctaga[A/C]ggagtgtgaggaagcc	A	C	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1994686	cttagttcctcatcaa[C/T]aggacacagaggaaac	C	T	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.3
SNP_A-2081503	acctgtgatactggga[A/G]aagagaacgaatttgt	A	G	Homo sapiens family with sequence similarity 3, member D (FAM3D), mRNA. /// ENST00000358781 // intron // 0 // --- // ---	FAM3D	FAM3D, Homo sapiens family with sequence similarity 3, member D (FAM3D), p14.2
SNP_A-2083143	acgtttcttggtattg[C/T]aaagtctgttaggtta	C	T	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, mRNA. /// NM_006710 // intron // 0 // Hs.531713 // COPS8 // 10920 // Homo sapiens COP	COPS8	COPS8, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, q37.3
SNP_A-2061406	aatgcctgtcccttac[A/G]ctattattcagctact	A	G	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-2258961	ctttttgaggaaataa[C/T]tgcatcttatgaaacc	C	T	Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2312953	ggacttctgaactgcg[A/G]aattcaacaactgtgc	A	G	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2311100	ggaagtattttacccc[A/G]attctctcagcagttg	A	G	26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 215867 //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2304046	gctccagatgacgaca[A/G]ggtgagattctcactt	A	G	ENST00000319945 // CDS // 0 // --- // --- // --- // --- /// ENST00000301610 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2258603	cttttgaacacttgta[C/T]acttaatgaatgtatt	C	T	767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 43432 // --- // --- // ---	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2261290	gaaagcaaaaccttga[A/C]gaggggagactactgt	A	C	ENST00000354581 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2275830	gagacggagtccaaag[A/G]cgaagaccaatgtccc	A	G	8662 // Homo sapiens eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa (EIF3S9), transcript variant 1, mRNA. /// NM_182712 // downstream // 36424 // Hs.371001 //	EIF3S9	EIF3S9, Homo sapiens eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa (EIF3S9), transcript variant 1, p22.3
SNP_A-2286241	gatgccatcgtgtata[A/C]accaaacaagaaccag	A	C	2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 903339 // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-2282538	gagttgtcttcttcaa[G/T]gaacttaattctgaga	G	T	// Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // --- // --- // --- // ---	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2246873	ctgtagtacttttac[A/G]attggatctacagtta	A	G	ENST00000319549 // intron // 0 // --- // --- // --- // ---	-	p24.3
SNP_A-2246397	ctggttctgtctatac[A/G]atttccaacactactt	A	G	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1808956 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2251864	cttcatgcagttaaaa[A/G]tgcaggaccatcgaga	A	G	// 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 55231 //	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-2097189	agacttctgggattca[C/T]cagagaggagatggga	C	T	Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /// ENST00000304195 // intron // 0 // --- // --- // --- // ---	FRMD3	FRMD3, Homo sapiens FERM domain containing 3 (FRMD3), q21.32
SNP_A-2000419	ctcataagttcctgta[C/T]ctacctcagctacata	C	T	// 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 665970 // Hs.234545 // CDCA1 // 83540 //	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1999886	gggcactccacctctc[C/T]gacgtcatctcctacc	C	T	10630 // Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, mRNA. /// NM_006474 // downstream // 3067 // Hs.468675 // T1A-2 //	T1A-2	T1A-2, Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, p36.21
SNP_A-2012249	gagttgaacaagggac[G/T]cttgcccaaagttaca	G	T	Homo sapiens GRB2-associated binding protein 2 (GAB2), transcript variant 2, mRNA. /// NM_080491 // intron // 0 //	GAB2	GAB2, Homo sapiens GRB2-associated binding protein 2 (GAB2), transcript variant 2, q14.1
SNP_A-2033569	aaatatagttctacaa[A/G]tatacacataacatat	A	G	83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 449661 // Hs.546345 //	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-2046901	aagaggtccgtagcag[A/T]ctgcctcccaatcata	A	T	9958 // Homo sapiens deubiquitinating enzyme (UNPH4) mRNA, complete cds. /// NM_006313 // downstream // 20066	USP15	USP15, Homo sapiens deubiquitinating enzyme (UNPH4) complete cds. q14.1
SNP_A-2044259	aactttctttcaaaac[A/G]acatggggcaactcct	A	G	54888 // Homo sapiens NOL1/NOP2/Sun domain family 2 (NSUN2), mRNA. /// ENST00000338486 // downstream //	NSUN2	NSUN2, Homo sapiens NOL1,p15.31
SNP_A-2135175	atattgcaggtttaga[G/T]gcagactattgcaata	G	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2137101	atcaggagggaggata[A/G]taagtaatcatttcat	A	G	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 //	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2221828	cctttgaactgatta[C/T]gctgttattaaacttt	C	T	Homo sapiens armadillo repeat containing 3 (ARMC3), mRNA. /// ENST00000298032 // intron // 0 // --- // --- // --- // ---	ARMC3	ARMC3, Homo sapiens armadillo repeat containing 3 (ARMC3), p12.2
SNP_A-2226327	ctaagaactagacaag[A/G]caatccaacagctgta	A	G	3742 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 6 (KCNA6), mRNA. /// NM_000217 // upstream // 27933 // Hs.60843 // KCNA1 //	KCNA6	KCNA6, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 6 (KCNA6), p13.32
SNP_A-2214400	cctactaaactcctca[A/G]aacggttgcaaatcct	A	G	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), transcript variant 4, mRNA. /// NM_178587 // intron // 0 // Hs.368264 // PPP2R5C	PPP2R5C	PPP2R5C, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), transcript variant 4, q32.31
SNP_A-2203436	ccagaaatcaccaggt[A/C]aaatcagatggaataa	A	C	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-2187853	cagtataagggccttc[A/G]cagacggagaaagagg	A	G	5678 // Homo sapiens pregnancy specific beta-1-glycoprotein 9 (PSG9), mRNA. /// NM_031451 // upstream // 123057 //	PSG9	PSG9, Homo sapiens pregnancy specific beta-1-glycoprotein 9 (PSG9), q13.31
SNP_A-2190432	catacagctttgaatg[C/G]atacattatggggtct	C	G	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2184470	cagctacaagcaacaa[C/T]gtaagtgacccaggaa	C	T	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // --	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-1650598	atcaaacaaatcatgaaagagatag[C/T]ggatatggcaaaaatgatgtgttgg	C	T	AF486622 // intron // 0 // Hs.102754 // - // 388815 // LOC388815 (LOC388815), mRNA	-	- , rs4092003, LOC388815 (LOC388815), mRNA,q21.1
SNP_A-1687328	cttcccttggtatgacaatgaagac[A/C]gatagcaaacatagtattctattaa	A	C	NM_003467 // upstream // 633306 // Hs.421986 // CXCR4 // 7852 // chemokine (C-X-C motif) receptor 4	CXCR4	CXCR4 , rs10496753, chemokine (C-X-C motif) receptor 4,q21.3
SNP_A-1781426	ggattaataccaggcc[A/G]cgagggactcagtgta	A	G	sapiens tensin (TNS), mRNA. /// ENST00000355713 // intron // 0 // --- // --- // --- // --- /// ENST00000171887 // intron // 0 // ---	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-1783470	ggcatcagggacaaag[A/G]agattagagaaaagac	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3941343 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1810336	gtgatggtgatactta[A/C]ctatttcttgtattct	A	C	Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1802124	gtatagacgtacaaca[C/T]tatattgcactttgct	C	T	8715 // Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// NM_001390 // upstream // 39289 // Hs.58919 // DTNA // 1837	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-1806138	gtcctctgtaatcttc[C/T]ctctccttcccctaag	C	T	27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// NM_182536 // downstream // 44438 //	BMP10	BMP10, Homo sapiens bone morphogenetic protein 10 (BMP10), p13.3
SNP_A-1798992	gtaagatttcccaacc[A/C]aacattttcaagagaa	A	C	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1835857	tacgtcaatacgcata[C/T]tacaatggttgggcac	C	T	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.3
SNP_A-1827185	taacctagacatccaa[G/T]ctcccttcataccctg	G	T	// 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 12186 // Hs.78948 // RABGGTB // 5	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN ,p31.1
SNP_A-1857611	tcactctctagaacca[A/G]aatccaaaaattagag	A	G	MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-1863430	tccaaaaatctggatc[C/T]aatagtcttcacctct	C	T	Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000273432 // intron // 0 // --- // --- // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1873719	gggtcctctctcgcta[A/G]gttcaatcatggccac	A	G	ENST00000319945 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-1986746	gcattataaaagggag[A/G]cattataaaaagaggg	A	G	// 10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 428893 // --- // --- // --- // ---	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3
SNP_A-1983335	tgccaaggttgctgaa[C/T]gttgctgggaaaaaga	C	T	65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream //	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1965492	tttgtctgttgcctta[C/T]gtaaaaacaaaatcat	C	T	// 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 746861 // Hs.165258 // NR4A2	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1956266	tttgtgtgatgattac[C/T]ggtaacattctcattt	C	T	// Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream //	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-1929372	ttcagtgagcctgcca[A/G]ctgaaatttcagaaca	A	G	Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1926123	ttatgtttggctttac[A/T]aaggccagatttttta	A	T	131566 // Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// NM_020351 // upstream //	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1
SNP_A-1906766	tggttactaaggtgcc[A/G]attctcccaatactgc	A	G	ENST00000360388 // intron // 0 // --- // --- // --- // ---	-	q22.31
SNP_A-1909930	tgtcagattgcagtaa[C/T]agaagtctaaagttta	C	T	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1893629	tgcaggtgagaccacc[A/G]gaagtgcagtacttag	A	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1902178	tggccaaccctggaga[A/G]ccgacatccagatttc	A	G	29094 // Homo sapiens HSPC159 protein (HSPC159), mRNA. /// ENST00000335402 // upstream // 90462 // --- // ---	HSPC159	HSPC159, Homo sapiens HSPC159 protein (HSPC159), p14
SNP_A-1890763	tgatgatgaaggacaa[C/G]tctaacaaatagaaaa	C	G	CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-1906756	tggttacagggccaaa[A/G]tgatattcacacaact	A	G	sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-1928889	ttcagatcacagaaca[A/G]cagaccaattagtaat	A	G	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. ///	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-1961480	ttttttcatagcctg[A/G]cagaaattggcaataa	A	G	HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream //	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-1952156	tttctcagtgcaaaaa[C/T]gagagcaattggtcac	C	T	3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1952827	tttcttaaaaattcaa[A/C]aataacaagcattacc	A	C	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 874523 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-1979313	atgcatatatgtaaac[C/T]gtattcaagatactga	C	T	// 127124 // Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 3 (ATP6V1G3), transcript variant 1, mRNA. /// NM_133326 // upstream //	ATP6V1G3	ATP6V1G3, Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 3 (ATP6V1G3), transcript variant 1, q31.3
SNP_A-1873280	tctattttgcatgaaa[A/G]aaaaagagtcgtagtt	A	G	7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 600714 //	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1870271	agaaatgttcaagaag[C/T]ctcgatcaccattgac	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 118881 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1863458	tccaaaatcggaaaaa[A/G]tctgaagtctgaaaca	A	G	Homo sapiens hypothetical protein FLJ10871 (FLJ10871), mRNA. /// ENST00000265614 // intron // 0 // --- // --- // --- // ---	FLJ10871	FLJ10871, Homo sapiens hypothetical protein FLJ10871 (FLJ10871), p21.1
SNP_A-1855739	tcaatcactatcctga[A/G]gacaccacaaagccat	A	G	Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // --- //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1815658	gttaacaatctacata[A/G]agcaactgggattaaa	A	G	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-1810805	gtgcagccgtggacac[C/T]aactccttccttctgc	C	T	148066 // Homo sapiens zinc and ring finger 4 (ZNRF4), mRNA. /// NM_153375 // downstream // 88545 // Hs.515575	ZNRF4	ZNRF4, Homo sapiens zinc and ring finger 4 (ZNRF4), p13.3
SNP_A-1732271	ccacatctaggcctcatctttaaaa[G/T]gttctgacttctgctctttccttca	G	T	NM_014840 // downstream // 3606 // - // - // - // -	-	- , rs1808691, -,q23.3
SNP_A-1691864	aaattcacatttaatggaagtacat[A/G]agtataatttcctttgtaaagaaaa	A	G	// 6677 // sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding) /// NM_005302 // downstream // 345195 // Hs.406094 // GPR37 // 2861 // G protein-coupled	SPAM1	SPAM1 , rs7790511, sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding) ,q31.33
SNP_A-1646616	aaataacttctgggtctaataacaa[A/G]tatcagctgagggaagccatgaacc	A	G	CDNA FLJ37718 fis, clone BRHIP2019007 /// AY070137 // upstream // 11160 // Hs.154295 // SP3 // 6670 // Sp3	-	- , rs10497424, CDNA FLJ37718 fis, clone BRHIP2019007 ,q31.1
SNP_A-2188086	cagtcatccagggtgc[G/T]ctgagtccgcgtgggc	G	T	Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2175494	cacatctagtttgcaa[C/T]cccacatttttgtata	C	T	Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2170544	caagtgatcagtgaag[A/G]ccttttaaagccgccc	A	G	4923 // Homo sapiens neurotensin receptor 1 (high affinity) (NTSR1), mRNA. /// NM_018270 // upstream // 15339 //	NTSR1	NTSR1, Homo sapiens neurotensin receptor 1 (high affinity) (NTSR1), q13.33
SNP_A-2174419	cacagaagtaagccca[C/G]tgactgaaacagaatg	C	G	-- /// ENST00000345029 // upstream // 908551 // --- // --- // ---	-	p14
SNP_A-2209426	cccatagtgtctccac[G/T]gagaaaaagatgagac	G	T	10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 //	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2044568	aagaaacatcatggga[A/G]cctctaaccgcttgta	A	G	55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 675334 // Hs.473082 // ZFP64 // 55734 // Homo	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043434	aactggtaaaagagaa[A/C]cttagatttcatgatt	A	C	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2582590 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2036341	aaattcccacaacgaa[C/T]gccataaaaaaatgaa	C	T	Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-2038222	aacacatttcaagagc[A/G]agcaataatccaaaac	A	G	80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2011649	cgtacaaggacgaaac[C/T]gcctaatgacgcatttt	C	T	7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // downstream // 678 // Hs.371723 // ALDH5A1 //	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding ,p22.2
SNP_A-2078093	accaggccatttgcaa[C/T]gaggtgactgactttg	C	T	// Homo sapiens hypothetical protein FLJ40089 (FLJ40089), mRNA. /// ENST00000344280 // intron // 0 // --- // --- // --- // ---	FLJ40089	FLJ40089, Homo sapiens hypothetical protein FLJ40089 (FLJ40089), q23.1
SNP_A-2070173	acacatggcaactatg[G/T]aaggtatatgttaatt	G	T	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 //	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-2236634	ctctaacagagctaaa[C/T]cataaaaggtggcact	C	T	10267 // Homo sapiens receptor (calcitonin) activity modifying protein 1 (RAMP1), mRNA. /// NM_080678 // upstream //	RAMP1	RAMP1, Homo sapiens receptor (calcitonin) activity modifying protein 1 (RAMP1), q37.3
SNP_A-2231287	ctattccactctaaca[A/G]caagcaggcagtaata	A	G	6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 390532 // Hs.221127	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-2305285	gctgagctgaacttta[C/T]ggtttaaaatgtgtat	C	T	// 137970 // Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), mRNA. /// ENST00000287272 // downstream //	UNC5D	UNC5D, Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), p12
SNP_A-2313693	ggagcaaaatttcaga[A/G]gcaaaataactaaaac	A	G	Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // --- // --- // --- // ---	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2313333	ggagacggagcttccc[A/G]gccctcgtgactcagt	A	G	Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 30583 // Hs.434435 // ALDH1L1 // 10840 // Homo	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2313851	ggagccaggcttcaga[C/T]ggacatgaggaaatgg	C	T	Homo sapiens hypothetical protein FLJ10597 (FLJ10597), mRNA. /// ENST00000335497 // intron // 0 // --- // --- // --- // ---	FLJ10597	FLJ10597, Homo sapiens hypothetical protein FLJ10597 (FLJ10597), p34.1
SNP_A-2296332	gcattgtgtcatctgg[C/T]actcaggagccagtgc	C	T	FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000355115 //	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2285769	gatgacgacagtccca[C/T]gtgatcctcaacgtca	C	T	Homo sapiens unc-84 homolog A (C. elegans) (UNC84A), mRNA. /// ENST00000359946 // intron // 0 // --- // --- // --- // ---	UNC84A	UNC84A, Homo sapiens unc-84 homolog A (C. elegans) (UNC84A), p22.3
SNP_A-2062095	aatggggaatcgttta[A/G]ctcattttatgaggca	A	G	1889 // Homo sapiens endothelin converting enzyme 1 (ECE1), mRNA. /// ENST00000357071 // upstream // 82648 //	ECE1	ECE1, Homo sapiens endothelin converting enzyme 1 (ECE1), p36.12
SNP_A-2054929	aataaataaatcaaag[C/T]ataatcaatgcctaag	C	T	Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // intron // 0 //	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-2051249	aagggatggtgaagaa[A/T]tgactgcagaagggat	A	T	Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // --- // --- // --- // --- // --- ///	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2054142	aagttcctgctctgga[C/G]tcaattgtgtctacaa	C	G	4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream //	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-2012102	aatgataacaaaggca[C/T]tcagccgtactctagt	C	T	Homo sapiens Abelson helper integration site (AHI1), mRNA. /// ENST00000265602 // intron // 0 // --- // --- // --- // ---	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3
SNP_A-2007048	tcatttcgcattcctg[A/C]agaggtgttccaagct	A	C	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // --- // --- // --- // ---	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2008138	tcgacactatttctaa[C/T]ctttgtcatataaaca	C	T	Homo sapiens mRNA for AIE-75, complete cds. /// NM_153676 // intron // 0 // Hs.502072 // USH1C // 10083 //	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-1997714	tgatgtgttgttctaa[C/T]tcatgactcagtggaa	C	T	ENST00000238256 // intron // 0 // --- // --- // --- // ---	-	q32
SNP_A-1994915	aaagattgtgttcaat[A/G]ataaagctgtcaaggt	A	G	6641 // Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), mRNA. /// NM_021021 // upstream // 699655 // Hs.371902 //	SNTB1	SNTB1, Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), q24.13
SNP_A-1996963	tgttatcattacacca[A/G]gtcattataagcccgt	A	G	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1438785 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207168	ccattagtttttagca[C/T]attcttgcaccacaaa	C	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2149242 // Hs.116471 //	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2221656	aagaaagggatgctta[C/T]ctcatatttaatgctt	C	T	sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 //	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2189183	cagttatgcggaagaa[C/T]gacctagttattgggc	C	T	// 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1738447 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2112392	aggcaagacccttcca[A/G]atgcactgtgaatgag	A	G	ENST00000228705 // intron // 0 // --- // --- // --- // ---	-	q14.2
SNP_A-2152668	attaatatcagtatgc[A/G]aactttagattctaca	A	G	Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2141589	atcttattttgcctaa[A/C]tgacaggtggggtaca	A	C	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-1650756	ttaattggtattccaaattcattga[A/G]cagggtgctaaaaacaacccaaatg	A	G	AK095523 // 3UTR // 0 // Hs.91559 // LOC91801 // 91801 // hypothetical protein BC015183	LOC91801	LOC91801 , rs10502092, hypothetical protein BC015183,q22.3
SNP_A-1709163	tgtccaatccctaaaggaactagta[C/T]gtaaataatgggagtcatatgggtt	C	T	NM_147182 // intron // 0 // Hs.437632 // KCNIP4 // 80333 // Kv channel interacting protein 4	KCNIP4	KCNIP4 , rs10516395, Kv channel interacting protein 4,p15.31
SNP_A-1793860	ggtcaaaccactgtgc[A/G]ctatgatttaagttgt	A	G	2794 // Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA. /// L25665 // upstream // 347272 //	GNL1	GNL1, Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), p21.33
SNP_A-1829367	taagtccaataagaaa[C/G]agtttacaacctgctg	C	G	-- /// ENST00000342478 // downstream // 122065 // --- // --- //	-	q11.21
SNP_A-1831120	taatgcagcctttaca[A/G]aagatgctaatttttt	A	G	10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream //	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.32
SNP_A-1832015	taattgtaacacctac[A/G]ccataaagtagctgtg	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1852782	tatttccaagcttatg[A/G]agaaaaaaatatcatt	A	G	Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // 5UTR // 0 // --- // --- // --- // --- ///	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1854264	tcaaaggagtagggta[C/G]gctatgcatggtgatg	C	G	2202 // Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, mRNA. /// NM_004105 // upstream // 182305 // Hs.76224 // EFEMP1 //	EFEMP1	EFEMP1, Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, p16.1
SNP_A-1965710	agggtgtgttataata[C/G]ctgcactctgatatat	C	G	6332 // Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA. /// NM_002976 // upstream //	SCN7A	SCN7A, Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), q24.3
SNP_A-1935300	ttctgctgagacgaaa[C/G]tgaattcaaaaatgga	C	G	Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// NM_020847 // intron // 0 // Hs.407740 // TNRC6A //	TNRC6A	TNRC6A, Homo sapiens trinucleotide repeat containing 6 (TNRC6), p12.1
SNP_A-1917149	tgtttgttgtctaggc[A/G]atctggtcactaactg	A	G	/// ENST00000332660 // downstream // 698985 // --- // --- // ---	-	p12.3
SNP_A-1901971	tggcagtcatggcagc[A/G]agcatatggatagcag	A	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1897340	tgctctttcttcatcc[A/G]aatctaactccctgct	A	G	Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // --- // --- // --- // --- ///	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-1888446	tgaggaatatgtcctg[C/T]agttcccacactagcc	C	T	5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 24188 //	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-1919292	ttaagaatgagccaaa[A/C]aacaaacgggaaactg	A	C	// 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 3416 //	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1913438	tgtggtccaagttata[A/T]gtagatgagtgggtgt	A	T	28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1145852 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1906486	tggtggcccttctctc[A/G]ctttagattccaagtt	A	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1905827	tggtcactgaacgtta[A/G]cattgaaagcccacaa	A	G	sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1908530	tgtagatgcataacca[C/T]tgccattctaggccct	C	T	Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), mRNA. /// ENST00000233146 // intron // 0 // --- // --- // --- // ---	MSH2	MSH2, Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), p21
SNP_A-1932705	ttccttccgttggcac[A/T]ctataaaaatcaacca	A	T	sapiens mRNA for KIAA1938 protein, partial cds. /// NM_152735 // downstream // 34102 // Hs.528028 // ZBTB9 //	-	-, Homo sapiens for KIAA1938 protein, partial cds. p21.32
SNP_A-1938928	ttgaggttatagaaaa[A/G]gcctgagaattgtgat	A	G	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1953441	tttgaagaaacaggaa[C/G]agctttaacatgaggt	C	G	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 (B4GALT6), mRNA. /// ENST00000306851 // intron // 0 // --- // --- // --- // --- ///	B4GALT6	B4GALT6, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6 (B4GALT6), q12.1
SNP_A-1958568	ttttctacatcaaaca[A/T]tacctaaacaaaacta	A	T	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 2146833 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1968597	agttaagaagaattga[C/T]atcagaaggaaagaaa	C	T	3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 314068 // Hs.118695 // KCNG1	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-1856018	tcaattcttccatcac[G/T]gtgagaaaaccagtag	G	T	/// ENST00000326474 // upstream // 120962 // --- // --- // --- // -	-	q25.33
SNP_A-1870500	tcgaccctgaggacac[G/T]gactctctcttcttcc	G	T	ENST00000303635 // intron // 0 // --- // --- // --- // ---	-	p36.23
SNP_A-1813636	gtgtaattatcacttc[C/T]atctagatccaaaatt	C	T	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), mRNA. /// ENST00000305206 // intron // 0 // --- // --- // --- // ---	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2
SNP_A-1806563	gtcgttgtgcttgcta[C/G]gttggtggccagatag	C	G	6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 217650 // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-1648978	tttatttagacataatgcaatctca[C/T]acttactagactatactatagtgca	C	T	BX161411 // intron // 0 // Hs.269452 // - // - // Human full-length cDNA clone CS0DI028YM15 of Placenta of Homo sapiens (human)	-	- , rs1955639, Human full-length cDNA clone CS0DI028YM15 of Placenta of Homo sapiens (human),q23.1
SNP_A-1746675	atcttaaatgccacaa[C/T]aagaatgattagtgat	C	T	// 7048 // transforming growth factor, beta receptor II (70/80kDa) /// NM_178862 // upstream // 722929 //	TGFBR2	TGFBR2 , rs1393749, transforming growth factor, beta receptor II (70,p24.1
SNP_A-1719253	aatcctaatacgagactgtgttgaa[A/C]gtaatgaaaaggcctggggtgggg a	A	C	AL832454 // intron // 0 // - // - // - // Homo sapiens mRNA; cDNA DKFZp451G231 (from clone DKFZp451G231).	-	- , rs881985, Homo sapiens mRNA; cDNA DKFZp451G231 (from clone DKFZp451G231).,p24.3
SNP_A-1752339	aggttgttatgaagctggtaacctg[A/G]acagatgaggtaatgtctctccctg	A	G	64764 // cAMP responsive element binding protein 3-like 2 /// NM_004717 // upstream // 47288 // Hs.242947 // DGKI //	CREB3L2	CREB3L2 , rs1364401, cAMP responsive element binding protein 3-like 2 ,q33
SNP_A-2151251	atgttacagccagaag[A/G]aacgatacgctcccag	A	G	FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 1159072 //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2150915	atgtgggcaaagtaaa[C/T]ggaaagtcttctggaa	C	T	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-2147045	atggaagatcttggga[C/T]ggatcttttggtaaga	C	T	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), mRNA. /// ENST00000265382 //	PIP5K1B	PIP5K1B, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), q13
SNP_A-2112451	aggcaatgactcatac[A/G]gtaatagttgatagag	A	G	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 179565 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2192742	catccctcactcatag[C/T]caagcctgagccaacc	C	T	sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2182580	cagatcagccctatca[C/T]ggaggcttggtccaga	C	T	// 5518 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA. /// ENST00000322088 // downstream // 4286 // --- // ---	PPP2R1A	PPP2R1A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), q13.41
SNP_A-2219408	cctgtggttgcattgc[C/G]agagactgtctcagaa	C	G	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2205146	ccagtaaactttgcta[C/T]aattacacaaactcta	C	T	/// ENST00000354800 // downstream // 682287 // --- // --- // ---	-	q14.1
SNP_A-1991540	gactcaccttcaggta[A/C]aactggctggtgctac	A	C	ENST00000361005 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1992943	ctccctttttcttagat[C/G]aattaaatcagaattt	C	G	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // --- // --- // --- // ---	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2005376	gaggtttgtggctgta[C/T]gaagggcaaacatggg	C	T	ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream //	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2040946	aaccctgagccagaac[C/T]gtctaggccaagatgc	C	T	// 58516 // Homo sapiens chromosome 12 open reading frame 14 (C12orf14), mRNA. /// ENST00000354978 //	C12orf14	C12orf14, Homo sapiens chromosome 12 open reading frame 14 (C12orf14), p11.21
SNP_A-2076457	acatttaatggtacac[A/G]ctgctgcaagtataaa	A	G	Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1860164 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2077875	accagataaaagagca[A/G]aaagtgacgtgcaggg	A	G	Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // --- // --- // --- // ---	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2081051	acctgaattttcacat[C/G]aagggctaaaaaaacc	C	G	/// ENST00000320956 // downstream // 102410 // --- // --- // ---	-	p12.3
SNP_A-2106581	agcctcattatttctc[C/T]ccaggagtagctcaga	C	T	PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 493347	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2263799	gaacgaccatttctaa[A/C]tcttaatgtgtcctcc	A	C	85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 83692 // Hs.461389 // CNTNAP4 // 85445 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2258854	ctttttaggtatctca[C/T]gtggtggtcatttcct	C	T	217 // Homo sapiens aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), nuclear gene encoding mitochondrial protein, mRNA. /// NM_016534 // downstream // 12773 // Hs.333120 // FLJ39616 // 5127	ALDH2	ALDH2, Homo sapiens aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), nuclear gene encoding mitochondrial protein, q24.12
SNP_A-2256525	ctttatttctggtctg[C/T]agtagctgtctttatt	C	T	Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-2260108	gaaaatatttgcaaaa[A/C]agtccaagctggaagc	A	C	// Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 (SERPINA9), mRNA /// ENST00000298845 // intron // 0 // --- // --- // --- // ---	SERPINA9	SERPINA9, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 (SERPINA9), q32.13
SNP_A-2230541	ctatcctgctccccac[A/G]ctgttaatccattccc	A	G	ENST00000358195 // intron // 0 // --- // --- // --- // ---	-	q11.23
SNP_A-2230031	ctataacagaagacct[A/G]aagctgggaaatccat	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2236900	ctctaggaaggattaa[C/T]gatttttgtttttggc	C	T	// 9585 // Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA. /// ENST00000260753 // downstream	MPHOSPH1	MPHOSPH1, Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), q23.31
SNP_A-2236945	ctctagttagtggaaa[G/T]attttttagtgtctcc	G	T	-- /// ENST00000345029 // upstream // 627470 // --- // --- // ---	-	p14
SNP_A-2241530	ctgagttgagtaaatg[A/G]atcttaaaaatggatc	A	G	sapiens olfactory receptor, family 4, subfamily L, member 1 (OR4L1), mRNA. /// ENST00000315683 // CDS // 0 // --- // ---	OR4L1	OR4L1, Homo sapiens olfactory receptor, family 4, subfamily L, member 1 (OR4L1), q11.2
SNP_A-2243994	ctgcttattctaccca[C/G]aactcttattctaccc	C	G	sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA. /// ENST00000288602 // intron // 0 // --- // ---	BRAF	BRAF, Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), q34
SNP_A-2309108	gctttttgatcaaata[A/G]actgtaaggatagaag	A	G	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2299853	gcctacccaaaatcca[A/G]tgagagtgtttaaaat	A	G	Homo sapiens DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57 (DHX57), transcript variant 3, mRNA. /// NM_198963 //	DHX57	DHX57, Homo sapiens DEAH (Asp-Glu-Ala-Asp,p22.1
SNP_A-2253765	cttgaacaagacctca[A/T]taatctactccctaac	A	T	/// ENST00000360991 // downstream // 967916 // --- // --- // ---	-	q12.1
SNP_A-2258334	cttttcaagaccatca[A/G]tctctgcactctgaat	A	G	Homo sapiens kinesin family member 13B (KIF13B), mRNA. /// ENST00000355514 // intron // 0 // --- // --- // --- // --- ///	KIF13B	KIF13B, Homo sapiens kinesin family member 13B (KIF13B), p12
SNP_A-2264078	gaactctgaggttttg[C/T]aatggatgtcattaga	C	T	283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream //	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-2262375	gaaatgatttcacaaa[C/T]ggtacaaaaacatcat	C	T	Homo sapiens crystallin, lambda 1 (CRYL1), mRNA. /// ENST00000340808 // intron // 0 // --- // --- // --- // --- ///	CRYL1	CRYL1, Homo sapiens crystallin, lambda 1 (CRYL1), q12.11
SNP_A-2273814	gactggcaagagatag[G/T]aggacggctcatacta	G	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2747131 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2272868	gactaatgatcaaata[A/C]gaaaggcaaaatggac	A	C	2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 650910 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-2106908	agccttctgacacttg[A/G]atgaatgagtttagaa	A	G	Homo sapiens nuclear antigen Sp100 (SP100), mRNA. /// ENST00000264052 // intron // 0 // --- // --- // --- // --- ///	SP100	SP100, Homo sapiens nuclear antigen Sp100 (SP100), q37.1
SNP_A-2106992	agcgaagaatttaaaa[A/C]ctagacacagatggcc	A	C	4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 534089 // Hs.132225 // PIK3R1 //	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2086623	actgaagaagctacaa[A/G]gaaactacaccactaa	A	G	80224 // Homo sapiens chromosome 14 open reading frame 127 (C14orf127), mRNA. /// ENST00000356390 //	NUBPL	NUBPL, Homo sapiens chromosome 14 open reading frame 127 (C14orf127), q12
SNP_A-2052950	aagtccaattccagaa[A/G]gacagtatttgggata	A	G	// Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 305417 // Hs.381715	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2050015	aaggaataaaaaataa[A/G]ggagatgtgttactaa	A	G	/// ENST00000265121 // upstream // 24833 // --- // --- // --- // ---	-	q35.1
SNP_A-2049959	aaggaagataggagaa[C/T]agtggtagaggaatat	C	T	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1
SNP_A-2046624	aagagcagtggctcca[C/T]gcacaagtcagcaagc	C	T	Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000355755 // intron // 0 // --- //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2004701	catttgaaggaaaatg[G/T]agtgaattctatgaat	G	T	/// ENST00000330554 // upstream // 29869 // --- // --- // --- // ---	-	q12.2
SNP_A-1989743	ttttataaatgtcata[C/T]atcacagtaccatttg	C	T	ENST00000322220 // intron // 0 // --- // --- // --- // ---	-	p14.1
SNP_A-2206303	ccatcctaaccatacc[C/T]atctcttttaggatta	C	T	84532 // Homo sapiens acetyl-Coenzyme A synthetase 2 (AMP forming)-like (ACAS2L), nuclear gene encoding mitochondrial protein, mRNA. /// NM_014588 // downstream // 14565 // Hs.274264 // VSX1 // 30813	ACAS2L	ACAS2L, Homo sapiens acetyl-Coenzyme A synthetase 2 (AMP forming)-like (ACAS2L), nuclear gene encoding mitochondrial protein, p11.21

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2168762	caagacagaattagac[A/G]agcttaatttatgggg	A	G	130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // ---	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-2112889	aggcatcatcttgaaa[C/T]ggaaagagcactagac	C	T	Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// ENST00000258416 // intron // 0 // --- // -	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-2119674	agtattaagcttctca[A/G]ccagcttgccctgaag	A	G	Homo sapiens solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (SLC6A6), mRNA. /// ENST00000360861 // intron // 0 // --- // --- // --- // --- ///	SLC6A6	SLC6A6, Homo sapiens solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (SLC6A6), p25.1
SNP_A-2136017	gttatctcttgaagta[C/T]catcgtttcaggcatt	C	T	Homo sapiens regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1), mRNA. /// ENST00000258646 // intron // 0 // --- // --- // --- // ---	RCBTB1	RCBTB1, Homo sapiens regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1), q14.2
SNP_A-2133422	atatatgttactggaa[A/T]ggtagggtttgaacag	A	T	1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 810533 // Hs.116471 // CDH11	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2148556	atggtaaccacagaaa[A/G]tacactgcagttttta	A	G	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2149856	atgtcaactagtcaag[A/G]aagacttactccaata	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2160949	atttctgtctaaaact[C/G]aaaataccaactgagg	C	G	Homo sapiens karyopherin alpha 5 (importin alpha 6) (KPNA5), mRNA. /// ENST00000359264 // intron // 0 // --- // ---	KPNA5	KPNA5, Homo sapiens karyopherin alpha 5 (importin alpha 6) (KPNA5), q22.1
SNP_A-1729043	aacaacatgtacttcaagggttcca[A/G]tgagattttctgagctaatgtgcca	A	G	2040 // stomatin /// NM_032552 // upstream // 106823 // Hs.238465 // DAB2IP // 153090 // DAB2 interacting protein	STOM	STOM , rs10513376, stomatin ,q33.2
SNP_A-1727817	aaaactttagaatctgttagaaaaa[C/T]ctgtaattcaagatggatgtttttt	C	T	1231 // chemokine (C-C motif) receptor 2 /// NM_000648 // upstream // 49369 // Hs.511794 // CCR2 // 1231 // chemokine	CCR2	CCR2 , rs7372094, chemokine (C-C motif) receptor 2 ,p21.31
SNP_A-1870375	tccttttcccattctg[C/T]cactcattgtgtgacc	C	T	54865 // Homo sapiens hypothetical protein FLJ20249 (FLJ20249), transcript variant 1, mRNA. /// NM_182679 //	GPATC4	GPATC4, Homo sapiens hypothetical protein FLJ20249 (FLJ20249), transcript variant 1, q22
SNP_A-1871176	tcgtttcaggcaatca[A/G]tacttttttcctcccc	A	G	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1843701	tagtgtatgctcatta[C/T]ccaagaaacttccttc	C	T	6017 // Homo sapiens retinaldehyde binding protein 1 (RLBP1), mRNA. /// ENST00000355100 // downstream //	RLBP1	RLBP1, Homo sapiens retinaldehyde binding protein 1 (RLBP1), q26.1
SNP_A-1971440	tctaaccagtaaagag[A/G]accacctgtaattatg	A	G	57633 // Homo sapiens leucine rich repeat neuronal 1 (LRRN1), mRNA. /// ENST00000319331 // downstream //	LRRN1	LRRN1, Homo sapiens leucine rich repeat neuronal 1 (LRRN1), p26.2
SNP_A-1959741	ttttggtgagttggta[C/T]taatattttcaatagg	C	T	Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // --- // -	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1933335	ttctaataaatctgac[G/T]ggcctttgacttctca	G	T	Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // --- // ---	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-1934054	ttctcagaacctagaa[C/T]gtggctatgtgactca	C	T	// 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), mRNA. /// ENST00000266483 // downstream // 165197 // ---	ALG10	ALG10, Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), p11.1
SNP_A-1924334	ttataaatgggattaa[A/G]cgctcaaactagattc	A	G	Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA. /// ENST00000261842 // intron // 0	AP4E1	AP4E1, Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), q21.2
SNP_A-1919571	ttaaggataaggcaca[C/T]atataattgatacagg	C	T	10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 623676 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1884211	tgaaggagaaggatgg[A/C]aactaggaagatgcct	A	C	2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 71191 // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1899777	tggaatgtgataagca[C/T]gaagtcattggagatt	C	T	23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 635494	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1892307	tgcaactcaaagttta[A/G]ccgtctatgtattatt	A	G	/// ENST00000278194 // downstream // 495755 // --- // --- // ---	-	p14.3
SNP_A-1888994	tgagtaacggattttg[A/G]agagagagctctgtct	A	G	/// ENST00000359457 // downstream // 193372 // --- // --- // ---	-	q14.3
SNP_A-1919006	ttaaccttggttcaga[A/G]gatcacttcaaaatga	A	G	ENST00000281129 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1940141	ttgcataagaggatga[C/T]gtgtttttagaaggtc	C	T	sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA. /// ENST00000344204 // intron // 0 // --- // --- // --- // ---	TRIO	TRIO, Homo sapiens triple functional domain (PTPRF interacting) (TRIO), p15.2
SNP_A-1941467	ttgctttaaacaataa[A/C]tctctgcgctggggaa	A	C	Homo sapiens jun D proto-oncogene (JUND), mRNA. /// NM_012321 // downstream // 19383 // Hs.515255 // LSM4 //	JUND	JUND, Homo sapiens jun D proto-oncogene (JUND), p13.11
SNP_A-1943885	ttgtatagtagcataa[C/G]agttttggataaagta	C	G	Homo sapiens hypothetical protein FLJ21069 (FLJ21069), mRNA. /// ENST00000320081 // intron // 0 // --- // --- // --- // ---	RSNL2	RSNL2, Homo sapiens hypothetical protein FLJ21069 (FLJ21069), p23.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960707	tttttctatggtggaa[A/C]aaaaatagaataattg	A	C	/// ENST00000329504 // upstream // 130125 // --- // --- // --- // -	-	q44
SNP_A-1841100	tagcttccagattgca[A/G]taagcatcgtgtaaag	A	G	1105 // Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /// ENST00000284049 // upstream	CHD1	CHD1, Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), q21.1
SNP_A-1838591	tagaatttgaatatga[C/T]ccaagctgagtattat	C	T	Homo sapiens rabconnectin-3 (RC3), mRNA. /// ENST00000251076 // 3UTR // 0 // --- // --- // --- // ---	DMXL2	DMXL2, Homo sapiens rabconnectin-3 (RC3), q21.2
SNP_A-1817913	gttcgtcgtctgtcac[A/G]cgggccttcatttgac	A	G	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), mRNA. /// ENST00000353125 // intron // 0 // --- // --- // --- // --- /// ENST00000360359 // intron // 0 // ---	ANKS1	ANKS1, Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), p21.31
SNP_A-1822143	gttttcttagtgccta[G/T]aatagagaaaatatat	G	T	80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1827101	taaccattattgtgaa[C/T]tctatccctacagata	C	T	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1873401	tctcaacaaggaagta[C/T]ccagtctcatcttctg	C	T	// Homo sapiens chemokine-like factor super family 8 (CKLFSF8), mRNA. /// ENST00000307526 // intron // 0 // --- //	CKLFSF8	CKLFSF8, Homo sapiens chemokine-like factor super family 8 (CKLFSF8), p23
SNP_A-1860156	tcagtcaatcagcagt[A/G]aacaagatttctacaa	A	G	ENST00000343352 // intron // 0 // --- // --- // --- // ---	-	p21.1
SNP_A-1848739	tatgagtttgggaagt[A/G]aagcaaaaactgaaat	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1856716 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1750241	ctgcaaacaatacagctccatggaa[C/T]tgaagcgacttgaaccaggtccaaa	C	T	NM_002998 // intron // 0 // Hs.1501 // SDC2 // 6383 // syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	SDC2	SDC2 , rs2253255, syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan),q22.1
SNP_A-1737355	aattgatgacaaaatgttagaaata[C/T]taagcttgagaaaaaactgatttaa	C	T	NM_004768 // intron // 0 // Hs.443458 // SFRS11 // 9295 // splicing factor, arginine/serine-rich 11	SFRS11	SFRS11 , rs3767206, splicing factor, arginine,p31.1
SNP_A-1659524	tacatgagaatcaaacagccttcta[A/G]ggaattgaatatgtaggagactatt	A	G	AB067505 // intron // 0 // Hs.13485 // GALNT13 // 114805 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	GALNT13	GALNT13 , rs10490526, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13),q24.1
SNP_A-1810291	gtgatgctggacatta[C/T]ggtcattttctttact	C	T	Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// ENST00000354496 // intron // 0 // --- // --- // --- // --- /// ENST00000351738 // intron // 0 // --- //	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.22
SNP_A-1791698	gggtctcaggtagaag[G/T]aagaagttcttgtgtg	G	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 3002454 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1787081	gggaaagagagtaaga[A/G]aaatcaaaggtgatga	A	G	Homo sapiens GRINL1A complex upstream protein (Gup1), mRNA. /// ENST00000267853 // intron // 0 // --- // --- // --- // ---	Gup1	Gup1, Homo sapiens GRINL1A complex upstream protein (Gup1), q21.3
SNP_A-2120294	agtcataagtcctgta[G/T]gcgtattatatttcct	G	T	Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// ENST00000272902 // intron // 0 // --- // --- // --- // ---	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-2170864	caataaagttcgaata[A/C]atcactacaatagtaa	A	C	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1876814 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2181250	cagaccagaggttata[C/T]gaaggaaacaggtggt	C	T	ENST00000339803 // intron // 0 // --- // --- // ---	-	p13.11
SNP_A-2199368	cattttgcctgtttta[A/G]ctccactaatcctcac	A	G	Homo sapiens signal-regulatory protein beta 1 (SIRPB1), mRNA. /// ENST00000342311 // intron // 0 // --- // --- // --- // ---	SIRPB1	SIRPB1, Homo sapiens signal-regulatory protein beta 1 (SIRPB1), p13
SNP_A-2187154	caggtctaacacaggg[C/G]agagtggtcatttggc	C	G	23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 222339 // Hs.488293 //	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-2183829	cagcatttagtgcaca[C/T]gacagtggccaagaca	C	T	Homo sapiens fibroblast growth factor receptor 4 (FGFR4), transcript variant 3, mRNA. /// NM_002011 // intron // 0 //	FGFR4	FGFR4, Homo sapiens fibroblast growth factor receptor 4 (FGFR4), transcript variant 3, q35.2
SNP_A-2210244	ttcttggatcatttgg[A/C]aatgtgaaagatctac	A	C	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 1104377 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2218616	cctggcagtgttctgg[A/G]cacatacgcacattaa	A	G	1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 343907 // Hs.116471 // CDH11 //	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2008129	cctaccctcagagaga[C/T]gcttcctcactcccca	C	T	// Homo sapiens chromosome 21 open reading frame 121 (C21orf121), mRNA. /// ENST00000339657 // intron // 0 // ---	C21orf121	C21orf121, Homo sapiens chromosome 21 open reading frame 121 (C21orf121), q22.3
SNP_A-2009254	ttccccagctcactcc[A/G]cttgtggctttggaca	A	G	79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 201862 //	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2046569	gaacagacaagctaac[A/G]gcaacctacattctat	A	G	83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 560120 // Hs.401954 // ARG99 //	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2038491	aacacttgcgctgcac[C/T]gggcaataaacactaa	C	T	Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- // --- ///	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2048940	aagcctcagtccaaga[A/G]tcaaaaaagtcaagtt	A	G	// Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRNA. /// NM_024940 // upstream // 224846 //	NEFL	NEFL, Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), p21.2
SNP_A-2049289	aagctcatcccaacaa[C/G]gcttcccagctttctt	C	G	sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2053434	aagtgatgtaatgagc[A/G]aggaggacgtgtaaga	A	G	Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /// ENST00000354214 // intron // 0 // --- // --- // --- // ---	PDIR	PDIR, Homo sapiens for protein disulfide isomerase related (PDIR), q21.1
SNP_A-2055460	aataataaatatacaa[A/T]gttggttctttcatag	A	T	2999 // Homo sapiens granzyme H (cathepsin G-like 2, protein h-CCPX) (GZMH), mRNA. /// NM_004131 //	GZMH	GZMH, Homo sapiens granzyme H (cathepsin G-like 2, protein h-CCPX) (GZMH), q11.2
SNP_A-2075032	acatccatattcatta[A/T]ccatgacctgtctgca	A	T	Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2100665	agatactggaatatac[A/G]gatacctgattttgg	A	G	// 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 124251 // Hs.491941	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2264281	gaacttccgggcaaat[G/T]atcaaacttcagcaag	G	T	132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2269046	gaattcttacaggtcc[C/T]gaaatatctttattct	C	T	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 567468	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2253312	cttctggctccctccc[A/C]actttacgtctcactg	A	C	FLJ44048 // 401024 // Homo sapiens FLJ44048 protein (FLJ44048), mRNA. /// NM_018471 // upstream // 265552 //	FLJ44048	FLJ44048, Homo sapiens FLJ44048 protein (FLJ44048), q32.1
SNP_A-2250379	cttagcagaggattac[A/G]aacagtgcccgagatc	A	G	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 507961 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2249518	cttaacctatatcccc[A/G]cagatcaaaagaagct	A	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2234801	ctccataaaacactaa[C/T]aaccctgtagccttag	C	T	4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// NM_032028 // downstream // 43798 // Hs.519507	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-2295282	gcatcacagcagctac[C/T]ggcaattaggagcatc	C	T	NM_174952 // downstream // 352878 // Hs.212840 // MGC46496 // 285555 // Homo sapiens hypothetical protein	-	q22.3
SNP_A-2312541	ggacctccaattatac[C/T]ggtcatgggtttctgg	C	T	284944 // Homo sapiens hypothetical protein FLJ37357 (FLJ37357), mRNA. /// ENST00000314395 // downstream //	FLJ37357	FLJ37357, Homo sapiens hypothetical protein FLJ37357 (FLJ37357), p11.2
SNP_A-2311668	ggaatgttttctcata[C/G]cagcaaagtggcgttt	C	G	// 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1433288 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2249682	cttaataaatgtggaa[C/T]tggaatcgcaccgtcc	C	T	Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// ENST00000157600 // intron // 0 // --- // --- // --- // ---	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-2246939	ctgtatcaagccacta[C/T]cccttgatctctccaa	C	T	Homo sapiens general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), mRNA. /// ENST00000264720 // intron // 0 // --- // --- // --- // ---	GTF3C2	GTF3C2, Homo sapiens general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), p23.3
SNP_A-2260852	gaaactgaggcacagg[A/G]agctataacttactct	A	G	152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 //	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-2275711	gagaccaacaggaaaa[C/G]actcatttgtgtctgg	C	G	ENST00000356159 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-2096654	agacgtcaaaacataa[A/G]gtgatgaatgtcagaa	A	G	// Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// ENST00000355875 // intron // 0 // ---	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44
SNP_A-2098319	agagatgtataaagca[C/G]atgaggtccctttct	C	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 734066 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2050330	aaggagctcctcagac[C/T]ggaaaagagtccagag	C	T	253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 942842	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-2032703	aaataacaaacagaaa[C/T]ggagactctaactaca	C	T	PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 //	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2032450	aaagtttgcaggacaa[A/C]aaacaccatattaaaa	A	C	FLJ38968 // 120534 // Homo sapiens hypothetical protein FLJ38968 (FLJ38968), mRNA. /// NM_001585 // downstream	FLJ38968	FLJ38968, Homo sapiens hypothetical protein FLJ38968 (FLJ38968), p14.1
SNP_A-1989570	agttagcatttcatca[C/T]cttttcagtgcagttt	C	T	Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 //	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.2
SNP_A-1996702	ttacattcctattcaa[A/G]atgtcatataaatact	A	G	Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // --- // ---	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2004558	acatccatgagggcaa[A/G]tagcccaggccgagct	A	G	10660 // Homo sapiens transcription factor similar to D. melanogaster homeodomain protein lady bird late (LBX1), mRNA. /// NM_003939 // upstream // 63254 // Hs.500812 //	LBX1	LBX1, Homo sapiens transcription factor similar to D. melanogaster homeodomain protein lady bird late (LBX1), q24.32
SNP_A-2214619	cctagatggctaaaca[A/T]ggatttcaccttcaaa	A	T	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2209609	cccatgcatctgatac[C/T]gggactgccagactta	C	T	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 265631 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-2203767	ccagagatttgctagg[A/G]aaccaaaagtgcttga	A	G	ENST00000356808 // 3UTR // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-2201803	ccacacagcctccgta[A/G]cataggttccagctcc	A	G	56944 // Homo sapiens olfactomedin-like 3 (OLFML3), mRNA. /// NM_205848 // downstream // 102909 // Hs.370963	OLFML3	OLFML3, Homo sapiens olfactomedin-like 3 (OLFML3), p13.2
SNP_A-2187552	cagtaacaccagaagc[A/G]ctcatcatgggagagg	A	G	406 // Homo sapiens aryl hydrocarbon receptor nuclear translocator-like (ARNTL), mRNA. /// ENST00000340761 // downstream // 155330 // --- // --- // --- // --- ///	ARNTL	ARNTL, Homo sapiens aryl hydrocarbon receptor nuclear translocator-like (ARNTL), p15.2
SNP_A-2198736	catttctaataagcag[A/G]aagtcaactgtaacat	A	G	Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA. /// ENST00000285124 // intron // 0 // --- // -	PPP4R1	PPP4R1, Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), p11.22
SNP_A-2117663	aggttcacttcaattc[A/G]attaagagttctacat	A	G	57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 212043 //	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-2131524	atagcaccaccggcaa[C/G]gattaaatgacagaac	C	G	// Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// ENST00000355875 // intron // 0 // ---	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44
SNP_A-2125815	agtttggatccttgaa[A/C]aaatgactatagtcca	A	C	1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 374306 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2156239	attctagaattatcta[C/T]gttctgaaatgttacc	C	T	Homo sapiens MRS2-like, magnesium homeostasis factor (S. cerevisiae) (MRS2L), mRNA. /// ENST00000244487 // intron // 0 // --- // --- // --- // --- /// ENST00000274747 // intron // 0 // ---	MRS2L	MRS2L, Homo sapiens MRS2-like, magnesium homeostasis factor (S. cerevisiae) (MRS2L), p22.2
SNP_A-1656281	ttgttgattgagaataaagcataaa[C/G]gaaactaaaaccatcgtgcatttat	C	G	7260 // tumor suppressing subtransferable candidate 1 /// NM_018436 // downstream // 1405294 // Hs.97899 // ALLC //	TSSC1	TSSC1 , rs7559913, tumor suppressing subtransferable candidate 1 ,p25.2
SNP_A-1655085	ttgcaaatcaatggctttggtctag[C/T]gtcctatagagcttggtgttcctgt	C	T	NM_014660 // downstream // 204237 // - // - // - // -	-	- , rs2189344, -,p21.3
SNP_A-1653240	agttatagactagaaatgagcccag[C/T]tgaacactctatatgaaaaagacaa	C	T	NM_052896 // intron // 0 // Hs.160962 // CSMD2 // 114784 // CUB and Sushi multiple domains 2	CSMD2	CSMD2 , rs1036756, CUB and Sushi multiple domains 2,p35.1
SNP_A-1748975	aagaagaaatatcaaagtgctttac[A/G]aaaaaatatcataatcatgaaatct	A	G	CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 1559923 // Hs.499861 //	CTNNA3	CTNNA3 , rs10509222, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1718761	tgaatgcgtagttatgcaaaattaa[A/G]aagcaatgatactgtctattgagaa	A	G	// 27255 // contactin 6 /// NM_175607 // upstream // 473759 // Hs.121115 // CNTN4 // 152330 // contactin 4 /// NM_175612	CNTN6	CNTN6 , rs10510212, contactin 6 ,p26.3
SNP_A-1848248	tatctttagttaccta[C/G]tacatgggatctaatt	C	G	Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 45994 // Hs.486109	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-1957379	ttttagcttttcatgg[A/G]catacagtcatgtata	A	G	56963 // Homo sapiens RGM domain family, member A (RGMA), mRNA. /// NM_207447 // upstream // 17991 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens	RGMA	RGMA, Homo sapiens RGM domain family, member A (RGMA), q26.1
SNP_A-1968327	tacttgaactctttga[A/G]gtgggcattattctgt	A	G	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1983554	cctgatttactgatcc[A/G]aatgcagaaacacaga	A	G	// 91368 // Homo sapiens similar to RIKEN cDNA A430101B06 gene (MGC13017), mRNA. /// NM_015288 //	MGC13017	MGC13017, Homo sapiens similar to RIKEN cDNA A430101B06 gene (MGC13017), q31.1
SNP_A-1918882	ttaacatggtgcttga[C/T]caacattatggattca	C	T	UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3),	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1908039	tgtacaaatacacaaa[G/T]aagcaaaaggaataaa	G	T	DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1645032 // Hs.44424 //	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1883677	tgaactgagaacacct[C/T]aagggcaggtcttgtt	C	T	sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // intron // 0 // Hs.10862 // AK3L2 // 387851 //	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-1883322	tgaacaactccatgga[A/T]gtaattaatgccattg	A	T	// 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1876562	tctgattatgcaaata[C/T]cttaaactacaaatat	C	T	7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	YWHAZ	YWHAZ, Homo sapiens tyrosine 3-monooxygenase,q22.3
SNP_A-1896267	tgcgtggcaaaagaac[A/G]gatgtctatgacatta	A	G	Homo sapiens tuftelin 1 (TUFT1), mRNA. /// ENST00000342552 // intron // 0 // --- // --- // --- // --- ///	TUFT1	TUFT1, Homo sapiens tuftelin 1 (TUFT1), q21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1908924	tgtataaatttttca[C/T]catcattcttgacaga	C	T	55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1917666	ccctgatttgtctgaa[G/T]taggccaaacaaggat	G	T	Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA. /// ENST00000357493 // intron // 0 // --- // -	ATP8B1	ATP8B1, Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), q21.31
SNP_A-1918154	ttaaactgacaactta[C/T]agctaattacttttaa	C	T	Homo sapiens heat shock 22kDa protein 8 (HSPB8), mRNA. /// ENST00000281938 // intron // 0 // --- // --- // --- // ---	HSPB8	HSPB8, Homo sapiens heat shock 22kDa protein 8 (HSPB8), q24.23
SNP_A-1923653	ttaggtctatttacca[C/G]atgaatgtacctggga	C	G	Homo sapiens sodium channel, voltage-gated, type X, alpha (SCN10A), mRNA. /// ENST00000333091 // intron // 0 // --- // -	SCN10A	SCN10A, Homo sapiens sodium channel, voltage-gated, type X, alpha (SCN10A), p22.2
SNP_A-1930830	ttccagataagtctga[C/T]gcaggctaaagtttga	C	T	ENST00000312504 // intron // 0 // --- // --- // --- // ---	-	q35
SNP_A-1929368	ttcagtgacttatata[C/G]attcctattgttatgc	C	G	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 445996 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-1926446	ttattcaggtaatgca[A/C]ctaataaacaggaggt	A	C	Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-1978810	cttgggttcaaataag[A/G]atacaatacttgctag	A	G	KIAA1223 // 57182 // Homo sapiens mRNA for KIAA1223 protein, partial cds. /// ENST00000329821 // upstream //	KIAA1223	KIAA1223, Homo sapiens for KIAA1223 protein, partial cds. q28.1
SNP_A-1972838	atatgaagagaccaat[A/T]aactaagcaaaaatca	A	T	2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // upstream // 102423 // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1948631	tttataataaagcttg[A/G]agtaagtggaacacag	A	G	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1939492	ttgattaaatttcacc[A/G]aacatctctgggcagc	A	G	143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 213975 // Hs.288304 //	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1850065	tatgtgacaggctgaa[C/T]aagctcccatcaaaat	C	T	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2357634 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1829338	taagtcagaaaaactc[A/G]gaaaactactgaaaat	A	G	26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 330648 // Hs.240845 // SGEF //	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1652926	tttagcttaattccctaatctttac[A/G]ccatgcataccattcagaaatga	A	G	80730 // KIAA1680 protein /// NM_007351 // downstream // 152039 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680 , rs10516864, KIAA1680 protein ,q22.1
SNP_A-1659852	gttttaaaataacacaaaattatgt[A/G]tagttcctgacttctgttatttcct	A	G	NM_138784 // upstream // 22652 // Hs.348539 // LOC116123 // 116123 // hypothetical protein BC014341	LOC116123	LOC116123 , rs1372685, hypothetical protein BC014341,q24.1
SNP_A-1673132	gtctttttatactcttagaaagtta[C/T]gtgtttctcatgaaaaaatgttcac	C	T	serine/threonine kinase 3 (STE20 homolog, yeast)	STK3	STK3 , rs10504986, serine,q22.2
SNP_A-1793666	ggtatgctggtacaac[A/C]gaaattagcaaatgct	A	C	ENST00000361005 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1798573	gtaacaaagcaaagga[C/T]acaatatttttaaat	C	T	GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream //	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-1811864	gtgctttgtcatagaa[C/T]attccagtctatgtgt	C	T	5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 174658 // --- // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2153933	attatagaatacatac[G/T]cagagcaccagtgaat	G	T	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 948735 // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-2147971	atggctgagccttcgc[C/T]aaaccaccaatatctc	C	T	9833 // Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA. /// NM_016734 // downstream //	MELK	MELK, Homo sapiens maternal embryonic leucine zipper kinase (MELK), p13.2
SNP_A-2142991	atgaatcctgattgca[A/T]aaaactgtcactctta	A	T	8436 // Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), mRNA. /// ENST00000354253 // downstream // 38039 // --- // --- // --- // --	SDPR	SDPR, Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), q32.3
SNP_A-2125667	agtttctgatttagta[A/G]gttgagatgcagccta	A	G	Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 //	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2128965	ataatgtcgatataaa[A/C]aaagagacaactcaat	A	C	sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) p21.2
SNP_A-2122432	agtgccttcctcttca[C/T]gcctcgtccaccctac	C	T	8050 // Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), mRNA. /// NM_001001392 // upstream	PDHX	PDHX, Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), p13
SNP_A-2195180	catggagggttgtcgc[A/G]gaaatcaaagagggtg	A	G	7071 // Homo sapiens TGFB inducible early growth response (TIEG), mRNA. /// NM_207505 // upstream // 92056 //	KLF10	KLF10, Homo sapiens TGFB inducible early growth response (TIEG), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175874	cacatttgccttcaag[A/G]ctgggtacctctggct	A	G	8387 // Homo sapiens olfactory receptor, family 1, subfamily E, member 1 (OR1E1), mRNA. /// ENST00000323164 //	OR1E1	OR1E1, Homo sapiens olfactory receptor, family 1, subfamily E, member 1 (OR1E1), p13.2
SNP_A-2200114	ccaaatccaaatgaga[C/G]gctgattccatcgcgc	C	G	MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// NM_015069 //	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-2210766	cccctgctttcttagg[A/G]acctgagtcagtagaa	A	G	Homo sapiens hypothetical protein FLJ30834 (FLJ30834), mRNA. /// ENST00000337677 // intron // 0 // --- // --- // --- // ---	FLJ30834	FLJ30834, Homo sapiens hypothetical protein FLJ30834 (FLJ30834), q27
SNP_A-2222168	cgaatttcttggaaca[A/G]tcctgctttgagcact	A	G	222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 118247 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-2031950	aaagtcgtgaagaagc[A/G]acatataatttggaaa	A	G	– /// ENST00000354800 // downstream // 80576 // --- // --- // --	-	q14.1
SNP_A-2021599	aaaaaatgccctgtaa[C/T]gggtgccatgctatat	C	T	1114 // Homo sapiens chromogranin B (secretogranin 1) (CHGB), mRNA. /// NM_015939 // downstream // 1774 //	CHGB	CHGB, Homo sapiens chromogranin B (secretogranin 1) (CHGB), p12.3
SNP_A-2053222	aagtcttgccatgata[C/T]acgttcatttaccgct	C	T	Homo sapiens GRINL1A complex upstream protein (Gup1), mRNA. /// ENST00000267853 // intron // 0 // --- // --- // --- // ---	Gup1	Gup1, Homo sapiens GRINL1A complex upstream protein (Gup1), q21.3
SNP_A-2054966	aataaatatatcccaa[A/C]tctaaagtagcctaat	A	C	Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // --- // --- // --- // ---	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2073429	acaggtgcacttaacc[C/T]catcttggagtacctg	C	T	131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 141362 // Hs.199877 // CPNE4 //	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2071457	acagaaagactgattt[A/C]aaatacctctgcccat	A	C	10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 116987 // Hs.369907 //	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-2064241	aattcaccagggaagc[A/C]aagcaaaaaagcaagc	A	C	ENST00000260983 // intron // 0 // --- // --- // --- // ---	-	q32.3
SNP_A-2103912	agcactgaagacctga[C/G]gatagttcctagttac	C	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2274658	gagaaaccaaggccca[A/G]acaaatcaggtggact	A	G	6530 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // downstream //	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-2285841	gatgagagttgactac[A/G]aaggttcagcatgaga	A	G	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 2172506 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-2262429	gaaatggaaagtcaaa[C/T]agaggctcctaagggg	C	T	// 10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 48285 // Hs.334587 // RBPMS //	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-2261176	gaaagaggagtgcgga[G/T]aaaaggtttgctccct	G	T	LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2265364	gaagcagtcaggtacg[C/G]atttgtctcagttgag	C	G	79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-2250601	cttagttatccaaacc[A/T]gcacaaatgtgtcaaa	A	T	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2240134	ctgaagtggttctgag[A/G]cacatattagtaggta	A	G	// 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 129412 // --- // --- // --- //	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2300268	gcctcgtattcaccaa[C/T]gtgcagctttttgtca	C	T	168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 83859 //	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2290557	gcaacttcctacaatc[C/T]cccttgtgagtcctct	C	T	// 84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 30229 // Hs.153504 //	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2236013	ctcctgggctagtgac[C/T]gaagcaacactctggc	C	T	ENST00000298815 // CDS // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2231953	ctcaacatctattcca[C/T]tctcctagcgcacctt	C	T	339345 // Homo sapiens nanos homolog 2 (Drosophila), mRNA (cDNA clone IMAGE:5270224), partial cds. /// NM_002516 // downstream // 11745 // Hs.375439 // NOVA2 //	NANOS2	NANOS2, Homo sapiens nanos homolog 2 (Drosophila), (cDNA clone IMAGE:5270224), partial cds. q13.32
SNP_A-2250503	cttaggtactatgtta[C/T]actgcctcctagaaga	C	T	ENST00000333616 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2251956	cttcattttccccaac[C/T]gtacaatgcccacctt	C	T	// Homo sapiens chromosome 20 open reading frame 185 (C20orf185), mRNA. /// ENST00000342109 // intron // 0 // ---	C20orf185	C20orf185, Homo sapiens chromosome 20 open reading frame 185 (C20orf185), q11.21
SNP_A-2246363	ctggttcaatagttga[C/T]gctagaagtgagtgtg	C	T	ENST00000331986 // CDS // 0 // --- // --- // --- // ---	-	p13.2
SNP_A-2090608	acttgttagtcccata[A/G]gagcagagcacagcct	A	G	1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 26660 // Hs.406191 //	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-2075633	acatggaataaaatga[A/G]tattgcagaaaactcc	A	G	// Homo sapiens hypothetical protein FLJ90013 (FLJ90013), mRNA. /// ENST00000304584 // intron // 0 // --- // --- // --- // ---	FLJ90013	FLJ90013, Homo sapiens hypothetical protein FLJ90013 (FLJ90013), p15.32

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2058857	aatccaactataattg[A/C]caacattttccacttc	A	C	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA. /// ENST00000343348 // intron // 0 // --- // --- // --- // ---	SEMA6A	SEMA6A, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), q23.1
SNP_A-2048054	aagcaatatgaaaaag[C/G]aagacaaagtgagaga	C	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 817593 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2022358	aaaaataagtgtgtga[A/G]gtgatggatatgttaa	A	G	// 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 109701 //	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-2000112	caaacaccatttgctc[C/T]agtcacatagaatgac	C	T	1647 // Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA. /// ENST00000271011 // upstream // 237005 // --- // --- // --- // --- ///	GADD45A	GADD45A, Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), p31.2
SNP_A-2001077	gaacaaactgtaaatt[C/G]aaaataccaaatggaa	C	G	Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // --- // --- // --- // ---	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2192221	catcagcttctcatac[G/T]agttaacagcgtatgt	G	T	Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA. /// NM_004315 // intron // 0 // Hs.527412 // ASAH1 // 427 //	ASAH1	ASAH1, Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, p22
SNP_A-2187895	cagtatcgctcataat[C/T]agagaaaggcaaagca	C	T	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 474449 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2184852	cagctggtaggccata[C/T]tatcataataaccaac	C	T	DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 //	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2136844	atcagaatgcttgaaa[C/T]ttgtaatgagagctgg	C	T	284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// NM_001650 // downstream // 130329 // Hs.315369 // AQP4 // 361 // Homo	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-1808746	gtgaagcacttacctg[A/G]agcaggaggatgaact	A	G	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA. /// ENST00000339765 // intron // 0 // --- // --- // --- // --- /// ENST00000349830 // CDS //	ARHGEF10	ARHGEF10, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), p23.3
SNP_A-1664844	aaatttgccaagatgcatgatcaac[C/G]actcctgggaaatgaaaatgttcat	C	G	11107 // PR domain containing 5 /// NM_024574 // downstream // 3349 // Hs.16026 // FLJ23191 // 79625 //	PRDM5	PRDM5 , rs4604073, PR domain containing 5 ,q27
SNP_A-1642407	atcaagactgcctcagggaactaca[A/G]tgtactatgctcagatgaaaattag	A	G	NM_153355 // intron // 0 // Hs.94181 // TCBA1 // 154215 // T-cell lymphoma breakpoint associated target 1	TCBA1	TCBA1 , rs715942, T-cell lymphoma breakpoint associated target 1,q22.31
SNP_A-1692794	cataatggactgtcaactcaaagaa[C/G]tggctccaagataggaactgcatgg	C	G	2863 // G protein-coupled receptor 39 /// NM_144586 // upstream // 19039 // Hs.372651 // MGC29643 // 116372 //	GPR39	GPR39 , rs10496690, G protein-coupled receptor 39 ,q21.2
SNP_A-1682374	ctcacagggttgttgcaagacatga[C/T]ggtaagagtgacattctgtaaccga	C	T	BX537436 // 3UTR // 0 // Hs.13768 // CACNA2D4 // 93589 // calcium channel, voltage-dependent, alpha 2/delta subunit 4	CACNA2D4	CACNA2D4 , rs2041139, calcium channel, voltage-dependent, alpha 2,p13.33
SNP_A-1747419	tatgaggaataagagataatattca[C/T]gtttttgacttaagcaagtgtcatt	C	T	5592 // protein kinase, cGMP-dependent, type I /// NM_014576 // upstream // 66146 // Hs.8349 // ACF // 29974	PRKG1	PRKG1 , rs10490966, protein kinase, cGMP-dependent, type I ,q11.23
SNP_A-1750993	agatgaagaaagtcatgtaagaagg[A/G]ccatgaaagagtatgggcagcattg	A	G	5099 // BH-protocadherin (brain-heart) /// NM_020860 // downstream // 557734 // Hs.278894 // STIM2 // 57620 //	PCDH7	PCDH7 , rs10517122, BH-protocadherin (brain-heart) ,p15.2
SNP_A-1783608	ggcatggccaagtcca[C/T]gaggttgtgcctccag	C	T	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 1, mRNA. /// NM_007098 // CDS // 0 // Hs.368266 // CLTCL1 // 8218 // Homo sapiens clathrin, heavy	CLTCL1	CLTCL1, Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 1, q11.21
SNP_A-1832423	tacaaaattacttaat[A/G]agcacctagtgtgtgc	A	G	1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 365075 // Hs.25674	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1834203	tacatgatcttactta[C/T]gtgcagaatcttaaaa	C	T	CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 68323 // Hs.461389 //	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1824044	taaacaagacagataa[A/G]gtccttgtcctcacga	A	G	Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA. /// ENST00000354276 // intron // 0 // --- // --- // --- // --- ///	PLA2G4C	PLA2G4C, Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), q13.32
SNP_A-1820963	gtttctcctagatgag[G/T]agggtatttagactta	G	T	162394 // Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA. /// ENST00000299977 // intron // 0 // ---	MGC19764	MGC19764, Homo sapiens hypothetical protein MGC19764 (MGC19764), q12
SNP_A-1815257	gtgttggtgaatccta[C/T]gaattaagtggaggtt	C	T	158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 30973 //	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-1933262	ttctaaccaggttcaa[A/C]atttaatgtccttatt	A	C	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1109679 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1948904	tttatcattaagactc[C/T]atgcatttcctagtta	C	T	Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000294649 // intron // 0 // --- // --- // --- // ---	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p13.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950717	tttcattatcctcttc[A/G]ccaagtcagaaatcca	A	G	137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// ENST00000330777 // upstream // 261144 // --- // --- // --- // ---	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-1951833	tttctaacacgtgacc[A/G]cattataatctttgca	A	G	552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 339431 //	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-1957072	ttttaatttgtgttta[C/T]gtaatgattagtgatg	C	T	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1982036	ggttacacatacacaa[C/G]gggaaaatgccatgtg	C	G	Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA. /// ENST00000358731 // intron // 0 // --- // --- // --- // ---	BDP1	BDP1, Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), q13.2
SNP_A-1923492	ttaggctgaagtaccc[A/G]caaaaaagtctttctt	A	G	-- /// ENST00000357810 // downstream // 133836 // --- // --- //	-	q21.2
SNP_A-1920390	ttaatgttaggacata[A/T]ctgttagcacaagggt	A	T	170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip ,q23.1
SNP_A-1918284	aaagggttcaaatcta[C/G]ctctgtctatggcctg	C	G	Homo sapiens zinc finger protein 532 (ZNF532), mRNA. /// ENST00000336078 // intron // 0 // --- // --- // --- // --- ///	ZNF532	ZNF532, Homo sapiens zinc finger protein 532 (ZNF532), q21.32
SNP_A-1917413	tgttttgctgatccag[C/T]aggctatcaggagtag	C	T	Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, mRNA. /// NM_019894 // intron // 0 // Hs.161985 // TMPRSS4 // 56649 // Homo	TMPRSS4	TMPRSS4, Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, q23.3
SNP_A-1917156	tgtttgtttcttgcaa[C/T]aaattagttatcctgg	C	T	Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // --- //	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-1916677	tgtttcaaagacctag[G/T]acttcactgtcataaa	G	T	Homo sapiens corin, serine protease (CORIN), mRNA. /// ENST00000273857 // intron // 0 // --- // --- // --- // ---	CORIN	CORIN, Homo sapiens corin, serine protease (CORIN), p12
SNP_A-1891257	tgatgtttccagccaa[A/T]ggtctgtgatagtcac	A	T	// 79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream //	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-1874845	tctcggtgtaaaaccc[A/G]actgcacattctattt	A	G	CACNA1B // 774 // Homo sapiens calcium channel, voltage-dependent, L type, alpha 1B subunit (CACNA1B), mRNA. /// ENST00000277549 // downstream // 11308 // --- // --- // --- // --	CACNA1B	CACNA1B, Homo sapiens calcium channel, voltage-dependent, L type, alpha 1B subunit (CACNA1B), q34.3
SNP_A-1877676	tctgggcacccaggac[G/T]actctggtggaaaggc	G	T	/// ENST00000326756 // downstream // 120416 // --- // --- // ---	-	p16.1
SNP_A-1888363	tgagcttgagtacatg[A/G]aaagtataatgtattc	A	G	/// ENST00000310012 // upstream // 105226 // --- // --- // --- // -	-	q12
SNP_A-1900023	tggaccctctcttctc[C/T]accaagcctctcacct	C	T	440044 // Homo sapiens FLJ16331 protein (FLJ16331), mRNA. /// NM_004561 // intron // 0 // Hs.134434 // OVOL1 //	FLJ16331	FLJ16331, Homo sapiens FLJ16331 protein (FLJ16331), q13.1
SNP_A-1921087	ttacagtagtgagaga[A/C]ggggtgagacagaaag	A	C	Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // --- // --	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2
SNP_A-1924964	ttatatttgtgttcta[G/T]atctgcaacaaaagta	G	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1198025	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1983416	gttcacaatataaaga[C/T]gtggaaacagcctaaa	C	T	Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 //	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-1965680	ttcatgttttgcaaaa[G/T]gtacttaagtttgagt	G	T	ENST00000342193 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1965420	tcaatgcattcctctg[A/C]aatgaaggtactctgc	A	C	Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 //	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1940056	ttgcaggaaaacctgc[G/T]caatgatctcactgat	G	T	79596 // Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA. /// NM_022118 // downstream // 167351	C13orf7	C13orf7, Homo sapiens chromosome 13 open reading frame 7 (C13orf7), q31.1
SNP_A-1939734	ttgcaaagcctacaaa[A/G]atctgagccatgagcg	A	G	Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA. /// NM_153746 // intron // 0 // Hs.187459	ZDHHC14	ZDHHC14, Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), q25.3
SNP_A-1944848	ttgtgcttaagggaca[C/G]catcaaacaagtgaaa	C	G	202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 46855 // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-1835175	taccgaacctctctgg[G/T]agccctgtaaatttag	G	T	Homo sapiens RNA binding protein with multiple splicing (RBPMS), mRNA. /// ENST00000339877 // intron // 0 // --- // --	RBPMS	RBPMS, Homo sapiens RNA binding protein with multiple splicing (RBPMS), p12
SNP_A-1832536	tacaaatagatacaca[A/G]ataatgacacatacat	A	G	23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 142427 // Hs.480763 //	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-1841910	taggctgttagataaa[C/T]tttaaccagaaatgga	C	T	Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // intron // 0 // --- // --- // --- // ---	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1856956	tcaccaggtgcgagaa[C/T]cttgggacctctcatt	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA. /// ENST00000282356 // intron // 0 // ---	CAMK4	CAMK4, Homo sapiens calcium q22.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869256	tcctggctgagagtcc[C/T]gatcaaaggaggatat	C	T	Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA. /// ENST00000350459 // intron // 0 // --- // --- // --- // ---	FLJ10375	FLJ10375, Homo sapiens hypothetical protein FLJ10375 (FLJ10375), p21.33
SNP_A-1866899	tccctactctccttaa[C/T]agcagaatcatatcat	C	T	sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1758409	tagctgtgccttttataagagttga[A/C]catattagtgattttcctgccacat	A	C	// 319089 // chromosome 14 open reading frame 25 /// NM_001049 // upstream // 119802 // Hs.248160 // SSTR1 //	C14orf25	C14orf25 , rs1959675, chromosome 14 open reading frame 25 ,q21.1
SNP_A-1659989	agtctagaaacaagtaatctaatcg[C/T]caaggggaccaatcgccaggcaaac	C	T	// 64919 // B-cell CLL/lymphoma 11B (zinc finger protein) /// NM_138576 // downstream // 317650 // Hs.57987 // BCL11B	BCL11B	BCL11B , rs10484061, B-cell CLL,q32.2
SNP_A-1675183	ttctagaaactggaagatgttttgc[C/T]agatgctccttttcgtcaggatgtt	C	T	NM_007353 // intron // 0 // Hs.182874 // GNA12 // 2768 // guanine nucleotide binding protein (G protein) alpha 12	GNA12	GNA12 , rs208358, guanine nucleotide binding protein (G protein) alpha 12,p22.3
SNP_A-1812039	gtggacagctataacc[A/G]cagtctatattccatg	A	G	64866 // Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, mRNA. /// NM_022842 //	CDCP1	CDCP1, Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, p21.31
SNP_A-1800126	gtaccatagtgcttga[A/C]gtttcactctcggaaa	A	C	Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // --- //	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1786897	ggcttttcccctggaa[C/T]tgtctactgtttgcag	C	T	// 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /// NM_000222 // upstream // 226938 // Hs.479754 // KIT // 3815	PDGFRA	PDGFRA, Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), q12
SNP_A-2151929	atgttttaaaatcaaa[A/G]tagtggacaggattta	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 410820 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2159243	atttaaatggacagaa[A/G]agtttcaagaagagca	A	G	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 393267 // --- // --- // --- //	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2160023	atttatgttgtaaaat[A/T]agcaaatcatggacat	A	T	Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 //	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2160054	atttattcaattctaa[A/G]aaggcagagagaggta	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 788987 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2186041	caggcagttcatttta[C/T]ggaaacttaatggagt	C	T	22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// NM_207015 // upstream // 497652 // Hs.416922 //	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds. q26.31
SNP_A-2196409	catgttgaaactgaca[C/T]taattgctgtgggaag	C	T	Homo sapiens laminin, beta 1 (LAMB1), mRNA. /// ENST00000222399 // intron // 0 // --- // --- // --- // ---	LAMB1	LAMB1, Homo sapiens laminin, beta 1 (LAMB1), q31.1
SNP_A-2168589	caagaaatttcactaa[A/G]gtggtagattccttag	A	G	6513 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /// ENST00000270929 // upstream // 115837 // --- // --- // --- // ---	SLC2A1	SLC2A1, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), p34.2
SNP_A-2169627	caagcttgaaatttca[C/G]agtcatttttgaaaca	C	G	// 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream //	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1992864	tggggaagtaaatctc[A/G]ctgagctagaaaagga	A	G	1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 561415 //	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1992052	gatgcatcacattctg[A/G]aagctacagaagccat	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 937404 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2026436	aaacaaaatttcatga[C/G]caaagttcctttatcc	C	G	Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // intron // 0 // Hs.478682 // C3orf6 // 152137 // Homo sapiens	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2036690	aaattgtgagtaaata[C/G]aaacgtgggtggctgt	C	G	Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA. /// ENST00000342228 // intron // 0 // --- // --- // --- // ---	SLC20A2	SLC20A2, Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), p11.21
SNP_A-2048678	aagccactatccataa[C/T]cctattgtgtcacctg	C	T	Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2061544	aatgctggaattaaga[C/T]tcagatccaggtctac	C	T	MGC26690 // 145773 // Homo sapiens hypothetical protein MGC26690 (MGC26690), mRNA. /// NM_004751 // upstream	MGC26690	MGC26690, Homo sapiens hypothetical protein MGC26690 (MGC26690), q22.2
SNP_A-2094440	agaagttacaggagaa[C/T]attaaatgcagtaaaa	C	T	/// ENST00000354860 // upstream // 1009119 // --- // --- // --- //	-	q32.3
SNP_A-2228105	ctactaatggcaatgg[A/G]catatggaacatggta	A	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2238295	ctctggagtaactaaa[C/T]agaaaaatgctgtaat	C	T	Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // --- // --- // --- // --- ///	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2285542	gatgaaaccttaatac[A/C]agttaagatcaaatta	A	C	9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 141737 //	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289102	gatttctcctaaggta[C/G]ctgaaagcaaacataa	C	G	1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// NM_007118 // upstream // 74613 //	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-2294493	gcagtatggttcatac[A/G]catggaaacactagat	A	G	151258 // Homo sapiens hypothetical protein FLJ39822 (FLJ39822), mRNA. /// ENST00000303735 // upstream //	FLJ39822	FLJ39822, Homo sapiens hypothetical protein FLJ39822 (FLJ39822), q24.3
SNP_A-2310688	ggaagatcctaagttc[C/T]atctgaaacattctga	C	T	57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 106391 //	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2307510	gcttcaaagcctaaga[G/T]aaggcaaggcgctgac	G	T	117159 // Homo sapiens dermcidin (DCD), mRNA. /// NM_058173 // upstream // 15 // Hs.348419 // LOC118430 //	DCD	DCD, Homo sapiens dermcidin (DCD), q13.2
SNP_A-2305614	cctgcttgcattacta[C/T]catcacaatttgaatg	C	T	FLJ32831 // 145858 // Homo sapiens hypothetical protein FLJ32831 (FLJ32831), mRNA. /// NM_207446 // downstream	FLJ32831	FLJ32831, Homo sapiens hypothetical protein FLJ32831 (FLJ32831), q26.1
SNP_A-2314650	ggagtaggatgcagcc[A/G]aatgctctcatcttaa	A	G	10874 // Homo sapiens neuromedin U (NMU), mRNA. /// NM_178237 // upstream // 136240 // Hs.269665 // SEC3L1 //	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-2300080	gcctcagaagtgtgtg[C/T]acctttgctgtgtgat	C	T	// 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1397038 // Hs.166109 // ELAVL2	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2270558	gacagagcagcagtag[C/T]attttcagaaaaatca	C	T	22862 // Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// NM_014923 // upstream // 323076 //	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-2092891	agaacaaaagtctcct[A/T]aacttaagcaagatga	A	T	6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ENST00000313571 // upstream // 621840	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2103439	agcaatatgaaactta[C/T]actgtaggttactgag	C	T	Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // --- // ---	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-2067969	acaactccactgtagc[C/T]gatgagaggagtcagg	C	T	Homo sapiens prolyl endopeptidase (PREP), mRNA. /// ENST00000229430 // intron // 0 // --- // --- // --- // ---	PREP	PREP, Homo sapiens prolyl endopeptidase (PREP), q21
SNP_A-2038903	aacagctaataacaaa[A/G]cactgtggatattaca	A	G	CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1551481 // Hs.21975 //	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2040158	aaccaagcacttggct[A/G]aattaaaagaataaaa	A	G	1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 333195 // --- // --- // --- //	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2039854	aacattctaagtacca[C/T]gtgaaaagtatcactc	C	T	// 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// NM_002718 // upstream // 480033 // Hs.518155 // PPP2R3A	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.2
SNP_A-2030209	aaagcacagttatcca[A/G]aatgtctaggcttaca	A	G	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), mRNA. /// ENST00000353125 // intron // 0 // --- // --- // --- // --- /// ENST00000360359 // intron // 0 // ---	ANKS1	ANKS1, Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), p21.31
SNP_A-2000853	aagctgagggagatac[C/T]gaggtgccaccttccc	C	T	// 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream //	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1998023	tttatgatggcctcga[C/G]gagtaagctggtagtt	C	G	9536 // Homo sapiens prostaglandin E synthase (PTGES), transcript variant 2, mRNA. /// NM_004878 // upstream //	PTGES	PTGES, Homo sapiens prostaglandin E synthase (PTGES), transcript variant 2, q34.11
SNP_A-2008615	aagcagaagtgttgtg[A/G]aaacagataccacacc	A	G	/// ENST00000336930 // upstream // 1052152 // --- // --- // --- //	-	p14.3
SNP_A-2169469	caagcccttcaggaaa[C/T]agtctctactttgagt	C	T	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 459163 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-2186044	caggcagtttagggaa[A/G]gacactcagttctgcc	A	G	Homo sapiens thyroid adenoma associated (THADA), mRNA. /// NM_022065 // intron // 0 // Hs.369592 // THADA //	THADA	THADA, Homo sapiens thyroid adenoma associated (THADA), p21
SNP_A-2208055	tggaacccagcttacc[A/G]gatacaagtctatgaa	A	G	// 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream //	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2205420	ccagtgccaggaggaa[C/G]aaaatttgcttagaaa	C	G	/// ENST00000329678 // downstream // 91259 // --- // --- // ---	-	p15.5
SNP_A-2153005	attacatatctggaag[C/T]agtgttaaagactgat	C	T	ENST00000328983 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2164099	caaaagctatgcatga[A/C]gtgcaaaggtaaagac	A	C	// 30814 // Homo sapiens phospholipase A2, group IIE (PLA2G2E), mRNA. /// ENST00000304491 // downstream //	PLA2G2E	PLA2G2E, Homo sapiens phospholipase A2, group IIE (PLA2G2E), p36.13
SNP_A-2120018	agtcaccaaataaaag[C/G]cttctctaagtgatct	C	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2116156	aggtaaggagaaacaa[C/T]gaaaggcaggaagaca	C	T	// 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 763971 // Hs.306899 // RAB28 // 9364 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2114839	agggcaattgaaactc[A/G]ctccattcttttcaaa	A	G	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 573924 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1798501	gtaaatgtacacaaaa[C/G]agtgacaaaatatgaa	C	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-1795348	ggtgatggtcccagga[A/G]agaatggtgagcagca	A	G	Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // intron // 0 // --- //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-1751281	ttacttacatatgtctcctagaatg[C/T]atttttaaaactgatttaaaaaatt	C	T	7991 // tumor suppressor candidate 3 /// NM_139167 // upstream // 361235 // Hs.348641 // SGCZ // 137868 //	TUSC3	TUSC3 , rs10503522, tumor suppressor candidate 3 ,p22
SNP_A-1783720	aatctctttgcttgga[A/G]cttcttacataatact	A	G	// 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1782033	ggcaaatctatccata[C/T]cctcatctaatccttt	C	T	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), mRNA. /// ENST00000295454 // intron // 0	GABRB1	GABRB1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), p12
SNP_A-1868167	tcctattttgctacct[C/T]agaccttcatgtgata	C	T	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-1872330	tctagactggcagatt[C/T]aaaccagcccagtctg	C	T	ENST00000278064 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-1871872	tctacacattttgacc[G/T]cctctccctcttcccg	G	T	Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA. /// ENST00000359357 // intron // 0 // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1863341	tcattttcctatctca[C/G]gttaaaggagagttta	C	G	10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 117122 // Hs.5025	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1832291	taattttctacatggc[C/T]aaaaactatcaaataa	C	T	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 173216 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1942371	ttggcctagactagac[C/T]ctcgatatttcattga	C	T	/// ENST00000330649 // upstream // 863005 // --- // --- // --- // ---	-	q11.2
SNP_A-1961575	ttttttttcaggtcaa[A/C]gattaggtgcattagc	A	C	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 498347 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1966028	atttcttcatatgtaa[A/G]atgggataatagaacc	A	G	Homo sapiens oxysterol binding protein-like 6 (OSBPL6), transcript variant 1, mRNA. /// ENST00000357080 // intron // 0 // --- // --- // --- // --- /// ENST00000190611 // intron // 0 // --- //	OSBPL6	OSBPL6, Homo sapiens oxysterol binding protein-like 6 (OSBPL6), transcript variant 1, q31.2
SNP_A-1916934	tgtttgaaaggagata[A/G]gaaaaagagtgagacg	A	G	10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 //	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-1918370	ttaaagtgaatttcat[C/T]agaagacacatttctt	C	T	Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // --- // --- // --- // ---	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-1915325	tgttcattcattcaac[A/G]gacttttttttaagag	A	G	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 623580	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1894873	tgccatcttccctaaa[C/T]agcacccccctatcagc	C	T	57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 218769 //	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-1893804	tgcagtttctacctac[C/T]gctttgtgagtgcgca	C	T	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 312685 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1875046	tctctattgatttcca[C/T]gtgtagctgacatcaa	C	T	// --- /// ENST00000361117 // upstream // 130703 // --- // --- // ---	-	q33.2
SNP_A-1910503	tgtcccttgagggtta[A/G]gaagacccagaattag	A	G	Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // --- //	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-1905115	tgggtgcctctgcaaa[C/T]gcccaagccatggctg	C	T	55 // Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /// NM_015268 // upstream // 80119 // --- // --- // 0 // ---	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-1907121	tggtttactttgttca[A/T]gttagtggtaggaaac	A	T	Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// ENST00000316386 // 3UTR // 0 // --- // --- // --- // ---	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.2
SNP_A-1907589	tgtaacacaggtatga[C/T]aattttggacacagct	C	T	// 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 102229 // Hs.183817 // USP31 // 57478 //	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-1922385	acatactggataccta[C/T]gttgcaagtaacttct	C	T	// 6318 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA. /// NM_006919 // upstream // 55853 // Hs.227948 //	SERPINB4	SERPINB4, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), q21.33
SNP_A-1821289	gtttgcaggaaaaata[A/G]gtttccagtgtgatgc	A	G	1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 89387 //	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1828417	taagattttctggctg[C/T]caccgtattgccagat	C	T	63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// NM_018371 // downstream // 6397 //	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-1849478	taactacacacaatgt[A/G]acagtgcaacaagaat	A	G	LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 //	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803980	gtcaatgtcattcaac[C/T]gagacttattgagtgt	C	T	10736 // Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA. /// NM_018079 // downstream //	SIX2	SIX2, Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), p21
SNP_A-2111282	aggagccacggcagcc[A/G]gatgtcatgtggtgtc	A	G	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2161536	atttggaaaatatctc[A/C]gaaattgccaccgtag	A	C	// 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 413140 // ---	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2167544	caacattggaaatgaa[G/T]agtaggcaatggagaa	G	T	ENST00000251041 // intron // 0 // --- // --- // --- // ---	-	q33.3
SNP_A-2142162	atctttttatttctca[A/T]gattatcccagtgttt	A	T	Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // --- // -	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2212593	cccttcacttctggaa[C/T]atgcctcagggtcttt	C	T	Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 //	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2222312	cgacttccctgaaagc[A/C]gctctgaactaattac	A	C	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // --- // --- // --- // ---	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2223342	cgctcatacgaaatga[A/G]acctgcctatgccttg	A	G	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream //	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-2182965	cagattgaactaaact[C/T]aaggacttggtcgggg	C	T	389792 // Homo sapiens immediate early response 5-like (IER5L), mRNA. /// ENST00000339671 // upstream // 82457	IER5L	IER5L, Homo sapiens immediate early response 5-like (IER5L), q34.11
SNP_A-2012504	tctctctgcaactcca[C/T]acttttcgtttcagtt	C	T	6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1802623 // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2015845	aataacagaaagctaa[C/T]gtcctacaaaattatt	C	T	5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 232618 //	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2019036	gcttgtttgcaaacaa[C/T]agatagagaccctgac	C	T	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // --- // --- // --- // ---	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2001445	tcagaagcagaattac[C/T]aagttaaaccagatgg	C	T	// 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-1991093	ttacaagttggttcca[A/G]atctactccacctgtc	A	G	93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // upstream // 16379 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32
SNP_A-2024567	aaaaggctcttgcaga[C/T]aaactcagctctgaac	C	T	PPP4R2 // 151987 // Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), mRNA. ///	PPP4R2	PPP4R2, Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), p13
SNP_A-2019550	tcataaatttgaatag[A/T]catattacctctgttt	A	T	// Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 89958	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2020348	tagacatgtgaaatat[C/T]agtaagttttgaaatg	C	T	Homo sapiens KIAA0179 mRNA, complete cds. /// ENST00000340648 // intron // 0 // --- // --- // --- // ---	KIAA0179	KIAA0179, Homo sapiens KIAA0179 complete cds. ,q22.3
SNP_A-2044803	aagaaatgacatagag[A/G]cgatactacttcatcc	A	G	23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 1078080 // Hs.24212 // LPHN2 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2061418	ctgactcttttcacca[C/T]ggaacaccaaagagac	C	T	117159 // Homo sapiens dermcidin (DCD), mRNA. /// NM_058173 // upstream // 201912 // Hs.348419 //	DCD	DCD, Homo sapiens dermcidin (DCD), q13.2
SNP_A-2059855	aatctgttgcatggga[A/C]acagaacattcggttt	A	C	Homo sapiens dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA. /// ENST00000340296 // intron // 0 // --- // -	DNCI2	DNCI2, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), q31.1
SNP_A-2057461	aatatcgagtatttaa[C/T]gatctgtagatagagg	C	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-2103562	agcaattttcttattc[A/G]agtccaaaatgggtca	A	G	8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 166152 //	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2102876	agcaaaaccgtgaata[C/T]gggaggaccactatat	C	T	8089 // Homo sapiens YEATS domain containing 4 (YEATS4), mRNA. /// NM_006654 // upstream // 64538 //	YEATS4	YEATS4, Homo sapiens YEATS domain containing 4 (YEATS4), q15
SNP_A-2094808	agaatcctgtaggtta[C/T]ggaatgttagaactaa	C	T	3313 // Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA. /// NM_001903 // upstream // 140502 // Hs.445981 //	HSPA9B	HSPA9B, Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, q31.2
SNP_A-2097282	agagaaaaaaacctga[A/G]aataatcagcagcttc	A	G	84146 // Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, mRNA. /// NM_032186 // upstream // 139295 // Hs.173001 // ZNF644 // 84146 //	ZNF644	ZNF644, Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, p22.2
SNP_A-2090347	acttggaaacaactca[A/G]acgttcatctatggta	A	G	// Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 656020 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2271388	gacattggtctagaaa[A/G]cctcatccagccggct	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 877048 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2266334	gaaggtcattatagtc[C/T]attggaataaatgaat	C	T	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 104018 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2260834	gaaactgaactaaacc[A/G]actcattctcacattt	A	G	PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream //	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-2257720	ctttggactcccaacc[C/T]ctcagtctaacagagt	C	T	Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 //	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2276222	gagagaggaccttcca[A/T]ccatgctacagacttt	A	T	// 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 132663 // ---	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-2296856	gccaagagagaaagag[A/C]agatggggtgaaatgt	A	C	2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 92694 //	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2291218	gcaatcccaaagcacc[C/G]agacatcatgctcagg	C	G	130367 // Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA. /// ENST00000343903 //	SGPP2	SGPP2, Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), q36.1
SNP_A-2291635	gcacaatccaggctga[C/T]gagtctactgatgttg	C	T	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 804134 // Hs.437966 // PXMP3 //	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-2289320	gatttgttgtatcact[A/G]agcttttctcttttc	A	G	// 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// NM_003583 // upstream // 255984 // Hs.173135 //	TIP120A	TIP120A, Homo sapiens TBP-interacting protein (TIP120A), q14.3
SNP_A-2276869	gagatatatagctaaa[C/T]tggtaggtggttgggg	C	T	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 661827 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2279100	gaggaatctagttgtc[A/G]aaagcattacatgaga	A	G	-- /// ENST00000361117 // upstream // 689244 // --- // --- // ---	-	q33.2
SNP_A-2267811	gaatccagctttccca[C/T]gatttggttccccgtg	C	T	6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 //	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2237723	ctctctgtctctctga[A/G]ccacagtttgctcatt	A	G	6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 //	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2255461	cttgtctaatggatgc[C/T]cccctctaacaaagaa	C	T	Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // intron // 0 // --- // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2096572	agaccttcattaacca[C/T]agtatccacaggtcca	C	T	ANAPC4 // 29945 // Homo sapiens anaphase promoting complex subunit 4 (ANAPC4), mRNA. /// ENST00000315368	ANAPC4	ANAPC4, Homo sapiens anaphase promoting complex subunit 4 (ANAPC4), p15.2
SNP_A-2054863	aataaagctgtcgcta[C/T]gtgcaaatgacataat	C	T	// Homo sapiens hypothetical protein FLJ40089 (FLJ40089), mRNA. /// ENST00000344280 // intron // 0 // --- // --- // --- // ---	FLJ40089	FLJ40089, Homo sapiens hypothetical protein FLJ40089 (FLJ40089), q23.1
SNP_A-2054162	ccattaagaagcccca[C/T]tgaaatacctcctcac	C	T	// 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 617388	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2054496	aagtttgagaatcaaa[G/T]gctgagtttttctctc	G	T	64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 243710 // Hs.7482 // RBM19 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-2033622	aaatatccaaaccata[A/G]caattggattaagggc	A	G	5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 343148 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI q36.1
SNP_A-2025598	aaaatgaaatgaatgc[A/G]aaattccaaatgttat	A	G	// 90627 // Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, mRNA. /// NM_178007 // upstream // 404970 // Hs.507704 // STARD13	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.2
SNP_A-2006124	gacctggaactgatcc[A/C]cctgtgtcattgttgg	A	C	Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), mRNA. /// ENST00000305997 // intron // 0 // --- // --- // --- // --- /// ENST00000354442 // intron // 0 // ---	OACT2	OACT2, Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), p25.1
SNP_A-2186224	caggcgtgaaccacca[C/T]gatcagttacttttct	C	T	Homo sapiens RAB10, member RAS oncogene family (RAB10), mRNA. /// ENST00000264710 // intron // 0 // --- // ---	RAB10	RAB10, Homo sapiens RAB10, member RAS oncogene family (RAB10), p23.3
SNP_A-2214494	cctacttttgctaggc[C/G]atgtgcctgatccccc	C	G	Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // --- // --- // --- // ---	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2202766	ccacgtaacattctac[A/G]acggacccggtctaca	A	G	Homo sapiens rabconnectin-3 (RC3), mRNA. /// ENST00000251076 // intron // 0 // --- // --- // --- // ---	DMXL2	DMXL2, Homo sapiens rabconnectin-3 (RC3), q21.2
SNP_A-2166966	caacaaatatctataa[A/G]aacatactccttgtcc	A	G	// 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 921052 //	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2114353	agggacacaggacact[C/T]agaaaattcaattgtg	C	T	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 417389 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134862	atattagttggtgtga[A/C]aagctccaaaatgcat	A	C	Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // --- // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2127047	ataaataagaaaaatg[C/G]caacagtagataaata	C	G	// 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1052428 // Hs.98262 // GRIK2	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1807308	gtctcttctctcaaaa[A/T]ctatagatcttagtta	A	T	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-1810812	gtgcagctgcaatgga[A/C]aacactatagcagatc	A	C	55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 307548 //	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1792861	ggtaatctcaagtgta[A/T]gagctaaggctttaat	A	T	Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 //	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-1797709	ggtttggaatggtcca[A/G]gagcacataaaggctg	A	G	2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1905957 // Hs.533323 // MANEA //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1785738	ggctctctgctatgca[A/G]atttagtggtggcggt	A	G	// 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// NM_002127 // downstream //	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1755224	tcttctattctttactgacatttaa[G/T]atgtgaaatttatgagaaaattttg	G	T	NM_016441 // intron // 0 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs1179500, cysteine-rich motor neuron 1,p22.2
SNP_A-1756126	agtagagtgagcccttaatctaata[C/T]aacatggatctttataagaaaagga	C	T	for OK/SW-CL.36, complete cds. /// NM_006168 // downstream // 559483 // Hs.347185 // NKX6-1 // 4825 // NK6	-	- , rs1827814, MRNA for OK,q21.23
SNP_A-1750243	ttcactctgagccttattatactac[C/T]ggcctcagggtctgagtgataggag	C	T	23024 // PDZ domain containing RING finger 3 /// AB040929 // downstream // 245708 // Hs.512593 // CNTN3 // 5067 //	PDZRN3	PDZRN3 , rs1405396, PDZ domain containing RING finger 3 ,p13
SNP_A-1737868	tgatcactcacacaaaatagattaa[C/T]gaatcagctaacaaaagaaaactta	C	T	D31886 // intron // 0 // Hs.306327 // RAB3GAP // 22930 // RAB3 GTPase-ACTIVATING PROTEIN	RAB3GAP	RAB3GAP , rs1869829, RAB3 GTPase-ACTIVATING PROTEIN,q21.3
SNP_A-1670518	aaagtctcagtcaacagtcccaaaa[G/T]aaatgttgcctgttgctgggaaagt	G	T	TMEM16F // 196527 // transmembrane protein 16F /// BC018661 // upstream // 162063 // Hs.317304 // ARID2 //	TMEM16F	TMEM16F , rs726603, transmembrane protein 16F ,q12
SNP_A-1857684	tcactgagaacttcaa[C/G]atagctctcctatggg	C	G	339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1832098	taatttataacaaaaa[A/G]tatctgcaataacact	A	G	/// ENST00000344163 // upstream // 333768 // --- // --- // --- // --- /// ENST00000249307 // upstream // 109685 // --- // --- // ---	-	q31.33
SNP_A-1842813	tagtacctgacctttc[C/T]caagaaaccattcact	C	T	Homo sapiens GTP binding protein 4 (GTPBP4), mRNA. /// ENST00000360059 // intron // 0 // --- // --- // --- // --- ///	GTPBP4	GTPBP4, Homo sapiens GTP binding protein 4 (GTPBP4), p15.3
SNP_A-1907282	tggttttctgatgaca[A/G]gttagccattaatctt	A	G	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), mRNA. /// ENST00000261461 // intron // 0 // --- // --- // --- // ---	PPP2R5A	PPP2R5A, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), q32.3
SNP_A-1890232	tgatcagacacactca[C/T]ggtttggaaaatcaag	C	T	283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream //	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1975601	ttcctgttcctgtcac[G/T]gctagggccttcagca	G	T	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // --- // ---	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-1954264	tttgcaatggcattat[C/G]agttgaaattggggaa	C	G	/// ENST00000354565 // upstream // 67 // --- // --- // --- // ---	-	q12.1
SNP_A-1949537	tttattgttaatggga[A/G]ggagcttcatagaggg	A	G	Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, mRNA. /// NM_019894 // intron // 0 // Hs.161985 // TMPRSS4 // 56649 // Homo	TMPRSS4	TMPRSS4, Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, q23.3
SNP_A-1940677	ttgcctgggttaatag[C/T]agtctttagggctgca	C	T	Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA. /// ENST00000284440 // intron // 0 // --- // --- // --- // ---	UCHL1	UCHL1, Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), p13
SNP_A-1933654	ttctaggtggagttag[A/C]atccatgtcttctcat	A	C	Homo sapiens N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2 (ASAH2), mRNA. /// ENST00000341534 // intron // 0 // --- // --- // --- // ---	ASAH2	ASAH2, Homo sapiens N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2 (ASAH2), q11.23
SNP_A-1969289	tttgtgttgtagttaa[C/T]ggtattttatcaatgc	C	T	/// ENST00000331037 // downstream // 676126 // --- // --- // ---	-	q21.1
SNP_A-1971187	aagggaagtcttttaa[C/T]gttgcaccattgactt	C	T	// Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // intron // 0 // --- // ---	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-1983208	tacaagaaaattgagt[C/T]tgaattaatttctgcc	C	T	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1898720	tgctttatggtaaaca[G/T]catggagacaacttcc	G	T	132949 // Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), mRNA. /// NM_002703 //	AASDH	AASDH, Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), q12
SNP_A-1881825	tctttgtttctataac[A/T]caccatgtggtcatag	A	T	KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 364579 // Hs.486470	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1906231	tggtgactgttttccc[C/T]gcgccagtaggatttg	C	T	1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 116122	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1915437	tgttccgttttcacaa[C/G]taagaatgggtgtccc	C	G	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA. /// ENST00000324684 // intron // 0 // --- // --- // --- // --- ///	PRPSAP1	PRPSAP1, Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), q25.1
SNP_A-1924777	ttatatacatctgtta[A/G]ggtgacacacattcag	A	G	Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // intron // 0 //	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1933111	ttcgtcttacccagcc[A/G]gataacgcccaagaat	A	G	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1830783	taatctcagatcatta[A/G]ctattgcttggatgaa	A	G	3776 // Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), mRNA. /// NM_016121 // upstream //	KCNK2	KCNK2, Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), q41
SNP_A-1827894	taagaaagaataatta[C/T]gagatacagttctaaa	C	T	Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. /// ENST00000345985 // intron // 0 // --- // --- // --- // ---	FLJ14075	FLJ14075, Homo sapiens hypothetical protein FLJ14075 (FLJ14075), p25.1
SNP_A-1851233	tattcagaactgccag[A/G]agaaaccttcatgact	A	G	// Homo sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), mRNA. /// NM_002421 // downstream // 5594 // Hs.83169 // MMP1 // 4312 // Homo sapiens matrix	MMP10	MMP10, Homo sapiens matrix metalloproteinase 10 (stromelysin 2) (MMP10), q22.2
SNP_A-1847613	tatcgtttgaccaaca[C/T]ctgactctttttttca	C	T	260425 // Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // upstream // 19827 // Hs.486189 // MAGI-3 // 260425 // Homo	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-1703609	aaaatagtttgtatccctgctctta[C/T]gattctaggattgtcatctttaaat	C	T	NM_002012 // intron // 0 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene	FHIT	FHIT , rs967318, fragile histidine triad gene,p14.2
SNP_A-1695633	accactggccctacctggtatttta[C/T]gattcaggtgtcctcagtgaggttt	C	T	NM_000865 // upstream // 186745 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E , rs485963, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1757295	tttcccttggaagaaaggcacgtta[C/T]ggttctaaggtggcaaacattaaat	C	T	1734 // deiodinase, iodothyronine, type II /// NM_013989 // upstream // 245915 // Hs.436020 // DIO2 // 1734 //	DIO2	DIO2 , rs10483951, deiodinase, iodothyronine, type II ,q31.1
SNP_A-1785457	aaacagtgccatcatc[C/T]gagcaatgacctgaat	C	T	ENST00000261657 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-1810947	gtgcatgtctacattc[A/C]agctactgagactgag	A	C	Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-1807751	gtctgtgtctctgaaa[C/T]gtgccctgctgggaag	C	T	Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // intron // 0 //	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-1805241	gtcattgccccctcac[C/T]ctttgaacaactcagg	C	T	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2132085	ataggggagcagatac[C/T]gagttctaaaccttct	C	T	// 4010 // Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), mRNA. /// AF057135 // downstream // 108365	LMX1B	LMX1B, Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), q33.3
SNP_A-2133060	atatactgtagactta[C/T]aataaaatgagctaga	C	T	Homo sapiens Arylsulfatase G (KIAA1001), mRNA. /// ENST00000355179 // intron // 0 // --- // --- // --- // --- ///	KIAA1001	KIAA1001, Homo sapiens Arylsulfatase G (KIAA1001), q24.2
SNP_A-2120965	agtctatcctctgtaa[C/T]ctcacatgaaattcca	C	T	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // --- // --- // --- // ---	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2121793	agtgagaaaacatata[A/G]aagccttctggaaatg	A	G	Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA. /// ENST00000262601 // intron // 0 // --- // ---	C20orf9	C20orf9, Homo sapiens chromosome 20 open reading frame 9 (C20orf9), q13.12
SNP_A-2162970	attttgtgtttctcta[C/T]attgattccaaaaagt	C	T	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 292300 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-2154850	attcaatagaatggga[A/G]agattacattaggagt	A	G	LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2220645	ccttgaaatggctcag[A/C]attgtaaacacctgta	A	C	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 121882 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2007373	tgtcccatcagtgtac[A/G]ggatcacccacacaac	A	G	// 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 //	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-2009521	gtgtggaggagccacc[A/G]aaggacagggtgaagc	A	G	Homo sapiens zinc finger protein 509 (ZNF509), mRNA. /// ENST00000355834 // intron // 0 // --- // --- // --- // --- ///	ZNF509	ZNF509, Homo sapiens zinc finger protein 509 (ZNF509), p16.3
SNP_A-2011363	tgaaagagactttgga[C/G]attatatagctcatcc	C	G	9421 // Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA. /// NM_015315 // upstream //	HAND1	HAND1, Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), q33.2
SNP_A-1993522	gagggctattcatgga[A/G]ctgatatcctgggttg	A	G	MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// NM_020164 //	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2032324	aaagttcatgcttcaa[A/G]gaacataacacagtac	A	G	27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 156828 // Hs.165830	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-2042815	aactctgctatcataa[C/T]ccttctgtaaatctaa	C	T	3248 // Homo sapiens hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD), mRNA. /// NM_006529 // downstream //	HPGD	HPGD, Homo sapiens hydroxyprostaglandin dehydrogenase 15-(NAD) (HPGD), q34.1
SNP_A-2051690	aaggtatgaaaaggta[A/G]taaaggctgattgtaa	A	G	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1591678 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2055392	aagcaatcaagcacaa[C/T]gattcaaaattgaaac	C	T	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2056313	aatactggcaacatta[C/G]agttcacccaagtagc	C	G	Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // ---	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2064690	aattctgaagagtatg[G/T]caggctgattctcttg	G	T	Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// ENST00000261180 // intron // 0 // --- // --- // --- // ---	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2229674	ctagtaggtgaacaca[A/T]tggaagtgacataggc	A	T	Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000352877 // intron // 0 // --- // --- // --- // --- ///	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-2231098	ctatgttgctaattcc[A/T]aagtaactgctttgac	A	T	Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // --- // --- // --- // --- /// ENST00000356360 // intron // 0 // --- // --	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2266537	gaagtatgcatagtaa[C/T]taataggagttctctg	C	T	114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2269016	gaattctatgtattaa[A/C]accgcagaaaaacaca	A	C	149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// NM_001559 // upstream // 25632 // Hs.479347 //	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2258089	ctttgttttaatctcg[A/C]atatctatatagtacc	A	C	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2258132	cttttaactcaacctc[C/G]ctgctccctgggtgtc	C	G	// Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB //	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-2259215	gaaaaacagaggaggc[A/G]acatcacagcatggag	A	G	// Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	SLC24A4	SLC24A4, Homo sapiens solute carrier family 24 (sodium,q32.12
SNP_A-2288480	gattgaagatgtgaag[A/C]aaaactatgctttaaa	A	C	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 284945 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2295681	gcatgagaacagacca[A/T]tacagatgctcttaca	A	T	/// ENST00000355063 // upstream // 96716 // --- // --- // --- // --	-	q22.1
SNP_A-2290484	gcaactacttactcca[A/T]ctcttttagttccagg	A	T	// Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 327257 //	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2303797	gctcaggggctaacca[A/C]agtgattccaggcaga	A	C	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 131172 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2307633	gcttcatctagtctca[A/T]atccttccattaatgc	A	T	-- /// ENST00000356117 // downstream // 553644 // --- // --- //	-	q23.31
SNP_A-2262889	gaacaaagtcacttcc[C/G]aaaagtttttgcatca	C	G	// 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 //	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2274106	gacttattttgcatta[C/T]gtaatctgctattgat	C	T	132864 // Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, mRNA. /// NM_182485 // downstream // 10264 // Hs.374216	CPEB2	CPEB2, Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, p15.33
SNP_A-2232261	ctcaatgctatcctgc[A/G]aaggcacccaggaggg	A	G	81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-2252530	cttcctgccttttcca[A/G]cttccagatgctgccc	A	G	143279 // Homo sapiens HECT domain containing 2 (HECTD2), transcript variant 2, mRNA. /// NM_182765 // downstream // 12324 // Hs.66378 // HECTD2 // 143279 //	HECTD2	HECTD2, Homo sapiens HECT domain containing 2 (HECTD2), transcript variant 2, q23.32
SNP_A-2066855	acaaaatcttaaatga[A/G]gactgctgaagtagat	A	G	9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 84601 // Hs.248117 //	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-2072211	acagatggctataaaa[C/T]gagatgctcagtgcca	C	T	// 2887 // Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // upstream // 12234 // Hs.164060 // GRB10 // 2887 // Homo	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2048478	aagcatcattatagaa[C/T]catcgaaaatagaaat	C	T	Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // --- // --- // --- // ---	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-2048473	aagcatcaacacaatc[A/C]aacagaggaatttgct	A	C	6375 // Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA. /// NM_001937 // downstream // 108591 // Hs.80552	XCL1	XCL1, Homo sapiens chemokine (C motif) ligand 1 (XCL1), q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2094388	agaagtgaggtaactg[C/T]atgacataatggccat	C	T	27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2841631 // --- // --- // --- //	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2101933	agatgggctcattcac[A/G]gagacaccgaggcact	A	G	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-2080996	acctcttttccttcca[C/T]agaatgtgaggactaa	C	T	Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// ENST00000331217 // intron // 0 // --- // --- // --- // ---	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-2078122	accagggctcatccaa[A/G]cctctgtaatttttaa	A	G	22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2869729 // --- // -	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p13.3
SNP_A-2037370	aacaaatgaagaaaga[A/G]ctgttattttggattc	A	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4368318 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2011689	tgcagagaataggtga[C/T]cctttgaggtgagct	C	T	56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream //	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-2219766	ccttacaacaatagta[G/T]gccatttagagggatc	G	T	// 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 12009 // --- // --- // ---	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2214161	cctaatgtttgatgtg[C/T]actaccctataagatc	C	T	// 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream //	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-2210230	tgcacaattgagcaaa[C/T]atatcctaatgcagaa	C	T	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 1057319 // --- // --- // --- // --	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2181443	cagactgccttgatca[C/G]taaaggattttcagtt	C	G	// 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-2175772	cacattctgcaaactg[A/G]aagtgggagctgtcaa	A	G	Homo sapiens T, brachyury homolog (mouse) (T), mRNA. /// NM_175922 // downstream // 16020 // Hs.119062 //	T	T, Homo sapiens T, brachyury homolog (mouse) (T), q27
SNP_A-2163085	atttttatccttggaa[A/G]ccatgctgcaaagcct	A	G	Homo sapiens pre T-cell antigen receptor alpha (PTCRA), mRNA. /// ENST00000304672 // intron // 0 // --- // --- // --- // ---	PTCRA	PTCRA, Homo sapiens pre T-cell antigen receptor alpha (PTCRA), p21.1
SNP_A-2161395	atttgcatataagcgc[A/G]aatgccccctgaaaac	A	G	63930 // Homo sapiens chromosome 20 open reading frame 51 (C20orf51), mRNA. /// NM_017798 // downstream // 72736	C20orf51	C20orf51, Homo sapiens chromosome 20 open reading frame 51 (C20orf51), q13.33
SNP_A-2123021	agtgggggaggcagac[A/G]agtaaattatgatgta	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-2123736	agtgttggtatcacac[A/C]ggatatcgataggata	A	C	ENST00000343268 // intron // 0 // --- // --- // --- // ---	-	q21.11
SNP_A-2129351	atacaacattagtgag[A/T]acttcaggattctggg	A	T	84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 218313 //	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-1805849	gtccctcgctgatgcc[A/G]aatgaaagcttcagag	A	G	// 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 68169 // --- // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1800630	gtagaaaaaacggacc[A/G]aagtgcctgcctaagg	A	G	// 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1032 // --- // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1750267	cattggtgttagtccagtgaaaata[G/T]taactatgctctccttgagtcatct	G	T	NM_002581 // intron // 0 // Hs.440769 // PAPPA // 5069 // pregnancy-associated plasma protein A	PAPPA	PAPPA , rs10513276, pregnancy-associated plasma protein A,q33.1
SNP_A-1783302	ggcagtgcttcattaa[C/T]aatcgatttacagaat	C	T	221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream //	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-1746723	agcaggtacttactcaaatcgtaa[A/G]catccaatttatatcaaatacacca	A	G	NM_014390 // intron // 0 // Hs.511400 // SND1 // 27044 // staphylococcal nuclease domain containing 1	SND1	SND1 , rs7785596, staphylococcal nuclease domain containing 1,q32.1
SNP_A-1746478	gtagccagccagcaaccttgggaga[C/T]gtctttaaatcgtgtaaattggcaa	C	T	NM_002298 // intron // 0 // Hs.381099 // LCP1 // 3936 // lymphocyte cytosolic protein 1 (L-plastin)	LCP1	LCP1 , rs1886039, lymphocyte cytosolic protein 1 (L-plastin),q14.13
SNP_A-1720061	aatatcatgggtgctaactatgatg[G/T]acattattaatcttgttaaaaatga	G	T	NM_001438 // intron // 0 // Hs.151017 // ESRRG // 2104 // estrogen-related receptor gamma	ESRRG	ESRRG , rs2818758, estrogen-related receptor gamma,q41
SNP_A-1656107	ataatgtcagattattattctaaaa[C/T]gaagccaacttgcaattatttggaa	C	T	2115 // ets variant gene 1 /// NM_005738 // downstream // 212864 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation	ETV1	ETV1 , rs10269685, ets variant gene 1 ,p21.3
SNP_A-1829174	taaggttgtgttttcc[C/G]cattgtgaagatactg	C	G	64425 // Homo sapiens RNA polymerase I associated factor 53 (PAF53), mRNA. /// AF176705 // downstream // 24799 //	PAF53	PAF53, Homo sapiens RNA polymerase I associated factor 53 (PAF53), p13.2
SNP_A-1840852	tagctcagctgtaaac[A/G]aaaggatacgaccttg	A	G	7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // upstream // 95594 // Hs.510833 // TJP1 //	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1840279	tagcagttgtgttgaa[C/G]tggagggtataaaagg	C	G	Homo sapiens MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (MCM6), mRNA. /// ENST00000264156 // intron // 0 // --- // ---	MCM6	MCM6, Homo sapiens MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (MCM6), q21.3
SNP_A-1924574	ttatactgtagttgga[C/T]agcaaatttgttcata	C	T	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1915935	tgttgatcctccgata[G/T]gctcagcagaccaatg	G	T	580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream //	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-1913357	tgtgggtatatactta[C/G]gatcatgtgattttac	C	G	Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /// ENST00000256397 // intron // 0 // --- // --- // --- // --- ///	LOXL2	LOXL2, Homo sapiens lysyl oxidase-like 2 (LOXL2), p21.3
SNP_A-1878610	tctgtgtgtgtaaatg[A/G]aggccttttcccttgt	A	G	151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream //	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1985095	tcacagaatgttgtgg[A/G]aaaggtctttaaagaa	A	G	4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 346192 // Hs.37982 // NEDD9 //	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-1980190	gcataataaggacagt[A/G]aatctggaatgacagt	A	G	1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 113080 // Hs.183850 // DCTD //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1963924	tctcaggtgaggttaa[A/G]cttggacaatggtcag	A	G	// 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1936304	ttcttcctataatcaa[A/G]tgggagtccctggaat	A	G	64168 // Homo sapiens EF hand calcium binding protein 1 (EFCBP1), mRNA. /// ENST00000324979 // upstream // 9056	EFCBP1	EFCBP1, Homo sapiens EF hand calcium binding protein 1 (EFCBP1), q21.3
SNP_A-1938709	ttgagcacgtactgca[C/T]gccaggccatgttata	C	T	7335 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA. /// NM_021988 // upstream // 47424 // Hs.420529 // UBE2V1 //	UBE2V1	UBE2V1, Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, q13.13
SNP_A-1946831	tttaagagcctttgca[C/T]ggttccacagttgcat	C	T	ENST00000277891 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1971946	tcatggaatgtggtgc[A/G]gattaacttgaatagc	A	G	151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 3836	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1973685	agatattatagttgtc[A/G]cctcacaaattacaca	A	G	// 54931 // Homo sapiens RNA (guanine-9-) methyltransferase domain containing 1 (RG9MTD1), mRNA. /// NM_020357 // upstream // 3451 // Hs.275865 // PCNP //	RG9MTD1	RG9MTD1, Homo sapiens RNA (guanine-9-) methyltransferase domain containing 1 (RG9MTD1), q12.3
SNP_A-1981725	gcattagaattttaag[A/T]ctatctctgtgttgtc	A	T	10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// NM_152687 // upstream // 9198 //	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1879195	tcttactcctgtaaca[A/G]tggccgttatcaaaaa	A	G	// Homo sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// NM_053036 // upstream // 216019 //	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-1879701	tcttcataagggcagc[A/G]atcaccctcatggcct	A	G	Homo sapiens rabphilin 3A-like (without C2 domains) (RPH3AL), mRNA. /// ENST00000323434 // intron // 0 // --- // -	RPH3AL	RPH3AL, Homo sapiens rabphilin 3A-like (without C2 domains) (RPH3AL), p13.3
SNP_A-1884115	tgaagcggctattact[C/T]aggattctccctactg	C	T	ENST00000261657 // intron // 0 // --- // --- // --- // ---	-	p13.13
SNP_A-1885726	tgacagatggaaacac[A/C]cccactcctgttggag	A	C	64094 // Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // downstream // 48714 // Hs.487200 // SMOC2 // 64094 //	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. ,q27
SNP_A-1890787	tgatgattgtcatcat[C/T]atccccgtttttcaaa	C	T	8216 // Homo sapiens leucine-zipper-like transcriptional regulator 1 (LZTR1), mRNA. /// NM_030573 // downstream //	LZTR1	LZTR1, Homo sapiens leucine-zipper-like transcriptional regulator 1 (LZTR1), q11.21
SNP_A-1916334	tgttgtgatggtaacc[C/T]cataagcagccattta	C	T	Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// ENST00000332896 // intron // 0 // --- // --- // --- // --- /// ENST00000306632 // intron	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-1917011	tgtttgcaagacattc[G/T]aacctactgatatgag	G	T	FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream //	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-1831733	taattcacctgcgttg[A/C]atccataccttccctt	A	C	51050 // Homo sapiens protease inhibitor 15 (PI15), mRNA. /// NM_031461 // upstream // 16206 // Hs.436542 // LCRISP1	PI15	PI15, Homo sapiens protease inhibitor 15 (PI15), q21.11
SNP_A-1834305	tacattagaagttaaa[A/G]taaccatgttttttgt	A	G	-- /// ENST00000354793 // downstream // 1151512 // --- // ---	-	p13.3
SNP_A-1848096	tatctgttttgaagaa[C/T]ctttccttcatctgag	C	T	// 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 91669 // Hs.370267 // TNKS // 8658 // Homo	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-1856485	tcacagagcaaaagac[A/T]catttgtgtagaaac	A	T	56956 // Homo sapiens partial mRNA for LIM-homeobox 9 (LHX9 gene). /// NM_020204 // downstream // 246967 //	LHX9	LHX9, Homo sapiens partial for LIM-homeobox 9 (LHX9 gene). q31.3
SNP_A-1864499	tccagaagtgcaagaa[A/C]gtataatgcttgtagg	A	C	Homo sapiens KIAA1772 (KIAA1772), mRNA. /// ENST00000269218 // intron // 0 // --- // --- // --- // ---	KIAA1772	KIAA1772, Homo sapiens KIAA1772 (KIAA1772), q11.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1670357	aatgcatattatatagatgaaagtat[A/C]aatgtaaacaaatgaaaagcaatat	A	C	3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 379014 // Hs.127011 // TINAG // 27283 //	HCRTR2	HCRTR2 , rs3929470, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1670193	atagagtatgacattagggaacttc[A/G]gaaggtagtgttgagagatccaggc	A	G	3458 // interferon, gamma /// NM_003583 // downstream // 114187 // Hs.173135 // DYRK2 // 8445 // dual-specificity	IFNG	IFNG , rs10492206, interferon, gamma ,q15
SNP_A-1665056	cctccctcctttttgtcctgtgtaaa[C/T]tcttacatatgcttctagactcaac	C	T	2262 // glypican 5 /// NM_005708 // upstream // 303375 // Hs.508411 // GPC6 // 10082 // glypican 6	GPC5	GPC5 , rs7328931, glypican 5 ,q31.3
SNP_A-1682790	cttttttaaatgcaccttttgttata[C/T]atccaagcagggaactattatggaa	C	T	NM_005853 // upstream // 185614 // Hs.25351 // IRX5 // 10265 // iroquois homeobox protein 5	IRX5	IRX5 , rs7499390, iroquois homeobox protein 5,q12.2
SNP_A-1742991	tgtgaagcctaagtatagaaagct[C/G]agaagctgtatcttctactgagtt	C	G	1948 // ephrin-B2 /// NM_172368 // upstream // 327373 // Hs.406746 // G30 // 282706 // putative protein LG30 ///	EFNB2	EFNB2 , rs10508166, ephrin-B2 ,q33.2
SNP_A-2154981	attcaccacctgcac[G/T]gacctcagaaccgtcg	G	T	Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // --- // ---	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2147270	atggagaaagaacaaaa[A/G]tcaccaaaaaggaggg	A	G	79596 // Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA. /// NM_022118 // downstream // 198279	C13orf7	C13orf7, Homo sapiens chromosome 13 open reading frame 7 (C13orf7), q31.1
SNP_A-2171841	caatgagaggagagtg[A/C]agaaacttacttgtta	A	C	Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), mRNA. /// ENST00000341815 // intron // 0 // --- // ---	SCML4	SCML4, Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), q21
SNP_A-2198894	cattgagtagaccaa[C/T]attaagcaattttc	C	T	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1460540 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2211289	ccctaatggaaacttg[A/G]actgagtctctagag	A	G	Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, mRNA. /// NM_201268 // intron // 0 // Hs.75890 // MBTPS1 // 8720 //	MBTPS1	MBTPS1, Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1 , q23.3
SNP_A-2207762	cccaaaagtggtacac[C/T]ctgctctgctcacatc	C	T	203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 186062 // Hs.493639 // C9orf72 // 203228 //	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2205956	ccatatattcacactg[A/G]agatgaaaagggcact	A	G	Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, mRNA. /// NM_134431 // intron // 0 // Hs.46440 // SLCO1A2 // 6579 //	SLCO1A2	SLCO1A2, Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, p12.1
SNP_A-2206224	ccatcatttttgggacal[C/T]ctcttctaactccat	C	T	339221 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 7 (ENPP7), mRNA. ///	ENPP7	ENPP7, Homo sapiens ectonucleotide pyrophosphatase,q25.3
SNP_A-1993014	acctgagtgtgagttat[C/G]catttcttattccta	C	G	FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 //	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2033501	aaatagtttctttctc[A/G]ccaacaattgttcccat	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 507452 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2106487	agcctagaagttcacc[G/T]gatttatgggcagtaa	G	T	// 23215 // Homo sapiens HBxAg transactivated protein 2 (XTP2), mRNA. /// NM_000261 // downstream // 29787 //	BAT2D1	BAT2D1, Homo sapiens HBxAg transactivated protein 2 (XTP2), q24.3
SNP_A-2076163	acattccctcaccttc[C/G]atactgccattcccct	C	G	// 58504 // Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), mRNA. /// NM_173524 // upstream // 31689 // -	ARHGAP22	ARHGAP22, Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), q11.23
SNP_A-2062711	aatgtctgttagcag[A/G]aaagctctggctctta	A	G	7341 // Homo sapiens SMT3 suppressor of mif two 3 homolog 1 (yeast) (SUMO1), transcript variant 1, mRNA. /// NM_015934 // upstream // 15530 // Hs.471104 //	SUMO1	SUMO1, Homo sapiens SMT3 suppressor of mif two 3 homolog 1 (yeast) (SUMO1), transcript variant 1, q33.1
SNP_A-2252717	cttcgggccttctac[A/G]ctgaggtttaacatat	A	G	// Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // --- // --- // ---	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1
SNP_A-2251112	cttattggtctgacc[A/G]attctgatgtgattac	A	G	9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // upstream //	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-2248324	ctgtgtcctggaata[C/T]gatttcatctggactg	C	T	// Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // --- // --- // --- // ---	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-2242407	ctgcactgctgagtaa[C/T]gggtcctcttgtct	C	T	// Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // --- // --- // ---	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1
SNP_A-2280578	gaggtagttactgtta[C/T]gctcatttacagtta	C	T	Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// ENST00000278198 // intron // 0 // --- // --- // ---	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2262311	gaaatgacaagtatatt[C/G]aaaccctgaaaatatg	C	G	Homo sapiens alanine-glyoxylate aminotransferase 2 (AGXT2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000231420 // intron // 0 // --- // --- // ---	AGXT2	AGXT2, Homo sapiens alanine-glyoxylate aminotransferase 2 (AGXT2), nuclear gene encoding mitochondrial protein, p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2272048	gaccctcttcaagtcc[C/T]agactgaacatggcac	C	T	Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // --- // -	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-2283905	gatataaaaggaggcc[A/G]gatgccactggaacag	A	G	sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-2287619	gattaactgattgcct[A/G]aagttatgtaatgcat	A	G	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2244230	ctggaaaccaacatga[C/T]gatgaaagagacacat	C	T	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1364803 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2240457	ctgacaggatactcat[A/G]aaaacccggtgggacc	A	G	57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 133964 // --- // FLJ37543 //	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. ,q12.1
SNP_A-2314673	ggagtattgatcctga[A/G]agttagttcttcaggc	A	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2311734	ggaattcctgggagca[A/T]ctgatagacagaattt	A	T	Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2312620	ggacggccatgtgacc[C/T]gaaggttggccaccat	C	T	sapiens developmentally regulated GTP binding protein 2 (DRG2), mRNA. /// ENST00000225729 // intron // 0 // --- // ---	DRG2	DRG2, Homo sapiens developmentally regulated GTP binding protein 2 (DRG2), p11.2
SNP_A-2300110	gcctcataaatgaagg[A/G]aaggtagtcttttaca	A	G	// 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // downstream // 293338 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2069357	acacaaagctgcttta[A/T]ctttctgctccaaccc	A	T	Homo sapiens src family associated phosphoprotein 1 (SCAP1), mRNA. /// ENST00000336915 // intron // 0 // --- // ---	SCAP1	SCAP1, Homo sapiens src family associated phosphoprotein 1 (SCAP1), q21.32
SNP_A-2058195	aatcaacaatgtacaa[C/T]gcacagtgagtttgtc	C	T	23312 // Homo sapiens rabconnectin-3 (RC3), mRNA. /// NM_013243 // upstream // 2228 // Hs.232618 // SCG3 //	DMXL2	DMXL2, Homo sapiens rabconnectin-3 (RC3), q21.2
SNP_A-2059856	aatctgttggcaaaca[G/T]gaataataatgtcttt	G	T	Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // --- // --- // ---	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2105230	agcattcaaagtcaag[A/T]agcgccatttatcttc	A	T	Homo sapiens microsomal glutathione S-transferase 2 (MGST2), mRNA. /// ENST00000265498 // 5UTR // 0 // --- // -	MGST2	MGST2, Homo sapiens microsomal glutathione S-transferase 2 (MGST2), q31.1
SNP_A-2104668	agcagtcggcctcttc[C/T]atgcagtgtacaccct	C	T	// 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 304424	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-2096628	agacgctgtacatcta[C/G]gactttgggggaacat	C	G	Homo sapiens nuclear protein in testis (NUT), mRNA. /// ENST00000357224 // intron // 0 // --- // --- // --- // --- ///	NUT	NUT, Homo sapiens nuclear protein in testis (NUT), q14
SNP_A-2079699	accctcacagatgaca[A/G]cctccaatgtcactca	A	G	Homo sapiens prolactin (PRL), mRNA. /// NM_138574 // upstream // 68079 // Hs.97124 // PWWP1 // 154150 // Homo	PRL	PRL, Homo sapiens prolactin (PRL), p22.3
SNP_A-2035286	aaatggaatccagagg[G/T]agtcaaatgatgtgtt	G	T	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2039704	aacatgggaaagaggc[A/G]aagagatcttccagta	A	G	Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // --- // --- // --- // ---	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1990628	gggtagttattacagc[A/G]attacttgtttataaa	A	G	64388 // Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), mRNA. /// NM_002924 // downstream // 129266 // Hs.130171 // RGS7 //	GREM2	GREM2, Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), q43
SNP_A-1994315	ttccagccttctgaca[C/T]cttccctgtacttaaa	C	T	LOC157657 // 157657 // Homo sapiens hypothetical protein LOC157657 (LOC157657), mRNA. /// ENST00000286688 //	LOC157657	LOC157657, Homo sapiens hypothetical protein LOC157657 (LOC157657), q22.1
SNP_A-2217266	cctgaaagcctccacc[A/G]agttcagtcaaatcct	A	G	65055 // Homo sapiens chromosome 2 open reading frame 23 (C2orf23), mRNA. /// NM_018433 // upstream // 71267 //	C2orf23	C2orf23, Homo sapiens chromosome 2 open reading frame 23 (C2orf23), p11.2
SNP_A-2227949	ctacctgcagaataac[A/G]acacaagcgaagtcca	A	G	Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA. /// NM_002603 // intron // 0 // Hs.527119 //	PDE7A	PDE7A, Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, q23.3
SNP_A-2195710	tccgtccatgcaggta[C/G]gtacacgagttgttgc	C	G	3002 // Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA. /// NM_014178 // downstream // 43931 // Hs.508958 // STXBP6	GZMB	GZMB, Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), q12
SNP_A-2176973	cacctagaaagcactc[A/G]gaaatggcagcttatt	A	G	// 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1089726 // Hs.19718 // PTPRU	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-2132935	atatacaaatgaataa[A/T]cattcaaggtccaaaa	A	T	4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 //	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22
SNP_A-2131190	atagagaccgtattaa[C/T]gatgtgatctggaaga	C	T	// 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 13780 // Hs.378893 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123398	agtgtcctacctctca[C/T]aattaactactttaaa	C	T	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 266202 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-1713133	tctaataatcttattggtgttcggc[A/C]acataatagttaataatgacaaact	A	C	// 8707 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 /// NM_024529 // downstream // 876026 // Hs.259502 // HRPT2 // 79577 //	B3GALT2	B3GALT2 , rs10494698, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 ,q31.3
SNP_A-1751817	taacaggtactcaatgagtaaatga[C/T]gcactgtcctcagctatcattttgt	C	T	NM_001461 // intron // 0 // Hs.396595 // FMO5 // 2330 // flavin containing monooxygenase 5	FMO5	FMO5 , rs10494243, flavin containing monooxygenase 5,q21.1
SNP_A-1678782	ctggctttaatttggtcaccgcaag[A/G]agtaaggtctgaggaaagcaggacc	A	G	NM_018967 // intron // 0 // Hs.388360 // SNTG1 // 54212 // syntrophin, gamma 1	SNTG1	SNTG1 , -, syntrophin, gamma 1,q11.21
SNP_A-1654387	gtgttgatccctcagctgaaccttc[A/G]aaaatttgttccaaatccaagaggc	A	G	387357 // chromosome 6 open reading frame 190 /// NM_014702 // upstream // 254625 // - // - // - // -	C6orf190	C6orf190 , rs668527, chromosome 6 open reading frame 190 ,q22.33
SNP_A-1857078	tcaccctcacaggcaa[C/T]ggggagttctagagca	C	T	Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // --- // --- // --- // --- ///	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1853308	tattttataacacaca[A/G]ggaatgatttcgtttt	A	G	Homo sapiens PDZ and LIM domain 1 (elfin) (PDLIM1), mRNA. /// ENST00000265995 // intron // 0 // --- // --- // --- // ---	PDLIM1	PDLIM1, Homo sapiens PDZ and LIM domain 1 (elfin) (PDLIM1), q24.1
SNP_A-1819619	gttgtacgagtttgga[A/T]ccaatatagaccaaga	A	T	6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 559897 // --- // --- // -	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1817489	gttcatcctgttccta[C/T]gctcggtcaatttttg	C	T	/// ENST00000314058 // upstream // 297219 // --- // --- // --- // -	-	p13.2
SNP_A-1817085	gttcaaactctctgca[A/G]catctgttcaccagct	A	G	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, mRNA. /// NM_003471 // intron // 0 // Hs.157818 // KCNAB1 // 7881 // Homo sapi	KCNAB1	KCNAB1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, q25.31
SNP_A-1910060	tgtcataattgaatgg[A/G]cactaagcagagaatg	A	G	3577 // Homo sapiens interleukin 8 receptor, alpha (IL8RA), mRNA. /// NM_005731 // upstream // 22053 // Hs.529303 //	IL8RA	IL8RA, Homo sapiens interleukin 8 receptor, alpha (IL8RA), q35
SNP_A-1893422	tgcagcgatgcattca[C/T]gtcagagagctaccaa	C	T	93107 // Homo sapiens potassium voltage-gated channel, subfamily G, member 4 (KCNG4), transcript variant 2, mRNA. /// NM_172347 // upstream // 21730 // Hs.335877 // KCNG4 //	KCNG4	KCNG4, Homo sapiens potassium voltage-gated channel, subfamily G, member 4 (KCNG4), transcript variant 2, q24.1
SNP_A-1900648	tggaggctagctccta[C/T]gaacagtgacaccatc	C	T	Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // --- // --- // --- // ---	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-1938812	ttgaggaatgagtgtc[A/G]atcaagaggtagagac	A	G	ENST00000357678 // intron // 0 // --- // --- // --- // ---	-	p13
SNP_A-1936690	ttcttgtgtgtgaaga[C/T]agacaatgagcaaaat	C	T	Homo sapiens synaptotagmin IX (SYT9), mRNA. /// ENST00000318881 // intron // 0 // --- // --- // --- // --- ///	SYT9	SYT9, Homo sapiens synaptotagmin IX (SYT9), p15.4
SNP_A-1934281	ttctccatgagccccc[C/G]actgctgcagcaaact	C	G	// 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 1205673 // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1959672	ttttgggaattgacca[C/T]gtttgtaacatctcag	C	T	SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1975990	cacatttgccgtcttc[A/G]ctctaggaacattcgg	A	G	116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream //	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1897133	tgctcctttgagaatc[A/G]atgccgctactgattg	A	G	55051 // Homo sapiens chromosome 14 open reading frame 102 (C14orf102), transcript variant 2, mRNA. /// NM_017970 // upstream // 23199 // Hs.528131 // C14orf102 // 55051 //	C14orf102	C14orf102, Homo sapiens chromosome 14 open reading frame 102 (C14orf102), transcript variant 2, q32.11
SNP_A-1895704	tgcctctggttcacag[A/G]atagagccgccccctc	A	G	// Homo sapiens TCR gamma alternate reading frame protein (TARP), nuclear gene encoding mitochondrial protein, transcript variant 2 /// ENST00000358695 // intron // 0 // --- // - - // --- // ---	TARP	TARP, Homo sapiens TCR gamma alternate reading frame protein (TARP), nuclear gene encoding mitochondrial protein, transcript variant 2 ,p14.1
SNP_A-1884143	tgaagctgcaagtctg[A/G]aggctgactgtatgtt	A	G	ENST00000321345 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1909752	tgtcacaaagagtacc[A/G]aaaacttcgaggtaca	A	G	// Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// NM_025212 // downstream // 693646 // Hs.12248 // CXXC4 //	TACR3	TACR3, Homo sapiens tachykinin receptor 3 (TACR3), q24
SNP_A-1919012	ttaacgaattacacag[A/G]aagtatgtgtttttac	A	G	375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine,q12.3
SNP_A-1920757	ttacaagaacttccta[A/C]aaattgtttcttcatt	A	C	Homo sapiens periostin, osteoblast specific factor (POSTN), mRNA. /// ENST00000350926 // intron // 0 // --- // --- // --- // ---	POSTN	POSTN, Homo sapiens periostin, osteoblast specific factor (POSTN), q13.3
SNP_A-1815162	gtgttcttggagaccc[C/T]gaaacctgttgcaaaa	C	T	Homo sapiens ras responsive element binding protein 1 (RREB1), transcript variant 2, mRNA. /// NM_001003699 // intron // 0 // Hs.298248 // RREB1 // 6239 // Homo sapiens ras	RREB1	RREB1, Homo sapiens ras responsive element binding protein 1 (RREB1), transcript variant 2, p24.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1815571	gttaaactccttgcca[A/C]taaaaaatgaaatgca	A	C	// 83896 // Homo sapiens keratin associated protein 3-1 (KRTAP3-1), mRNA. /// ENST00000360088 // upstream //	KRTAP3-1	KRTAP3-1, Homo sapiens keratin associated protein 3-1 (KRTAP3-1), q21.2
SNP_A-1820471	gtttatgaatgacaaa[A/C]gggtcaatgaagaaat	A	C	PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 568089 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1838180	tagaactcatcatcca[A/G]tatgggattccagctt	A	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1660257	atcagtgagtttccaaaagaaaatg[C/G]cttcagtaccacaaaattaacaaaa	C	G	10186 // lipoma HMGIC fusion partner /// NM_025138 // upstream // 90812 // Hs.318526 // C13orf23 // 80209 //	LHFP	LHFP , rs726051, lipoma HMGIC fusion partner ,q13.3
SNP_A-1677794	gctctgggaatcctgggcaaggtca[A/G]agtggtctaggaacaagtctgtgga	A	G	NM_032309 // intron // 0 // Hs.375707 // CHCHD5 // 84269 // coiled-coil-helix-coiled-coil-helix domain containing 5	CHCHD5	CHCHD5 , rs719667, coiled-coil-helix-coiled-coil-helix domain containing 5,q13
SNP_A-1699523	ggagggagtagaagctttaaagaaa[C/T]ggaagaaatcttctagaaggaagaa	C	T	4306 // nuclear receptor subfamily 3, group C, member 2 /// NM_152619 // upstream // 1409560 // Hs.45057 //	NR3C2	NR3C2 , rs2358469, nuclear receptor subfamily 3, group C, member 2 ,q31.23
SNP_A-1783769	ggcattttggaggcta[C/T]gatgattaacttcatg	C	T	ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 79028 // --- // --- //	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1731799	cttgaaaatgtttggttttacagat[C/T]aacagccagacacttcataaatatc	C	T	histone deacetylase 9 /// NM_058176 // intron // 0 // Hs.487662 // HDAC9 // 9734 // histone deacetylase 9 ///	HDAC9	HDAC9 , rs10486293, histone deacetylase 9 ,p21.1
SNP_A-1785918	ggctgagtttctagat[A/T]aagatttaattagtaa	A	T	MGC35033 // 121273 // Homo sapiens hypothetical protein MGC35033 (MGC35033), mRNA. /// NM_001005203 //	MGC35033	MGC35033, Homo sapiens hypothetical protein MGC35033 (MGC35033), q13.11
SNP_A-2164714	caaacagtccataaaa[A/C]cctgccttaaaataat	A	C	// 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2181932	cagagctattaaagca[A/C]tgatttttttactcag	A	C	27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 158882 // Hs.165830	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-2169320	caagcacttgatatga[C/T]cacaggcctgtgctct	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 465336 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2226986	ctaatgagagaggcaa[C/G]ctaggaagctggaaac	C	G	// 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 157870 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2214749	cctagtactccatacc[C/T]gaggccaaagaaatcc	C	T	Homo sapiens hypothetical protein FLJ23514 (FLJ23514), mRNA. /// ENST00000278487 // intron // 0 // --- // --- // --- // ---	FLJ23514	FLJ23514, Homo sapiens hypothetical protein FLJ23514 (FLJ23514), q14.2
SNP_A-1994652	cattcaatgaaagagt[A/T]aaccagagtaagaatg	A	T	27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream //	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-2009032	attgtttgatgactgc[C/T]cttttcagtagaagg	C	T	ENST00000273666 // intron // 0 // --- // --- // --- // ---	-	q13.33
SNP_A-2013554	agcacacttcttgcag[A/C]ccttatgtaaaaagag	A	C	-- /// ENST00000329885 // downstream // 160862 // --- // --- //	-	q14.3
SNP_A-2041648	aacgcttcaaaaaaga[C/T]gtaaattgttaaccag	C	T	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2046812	aagaggatgctctccc[A/G]cactgaccggaatgac	A	G	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant alpha, mRNA. /// NM_032940 // intron // 0 // Hs.79402 // POLR2C //	POLR2C	POLR2C, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant alpha, q13
SNP_A-2099202	agaggataaagttaga[A/C]agttctgtagtcagaa	A	C	Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // --- // --- // --- // ---	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2104795	agcataaattctaaaa[C/T]gatggctactgtacta	C	T	285704 // Homo sapiens RGM domain family, member B (RGMB), mRNA. /// ENST00000308338 // downstream //	RGMB	RGMB, Homo sapiens RGM domain family, member B (RGMB), q21.1
SNP_A-2063067	aatgttcagctcaata[C/G]gtttaaaaagtcactt	C	G	Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // --- // ---	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2063384	aattaacattattcag[C/G]acttagaagtatagtt	C	G	LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 //	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2250494	cttagggccctttccg[A/C]agcctggcttgtaagt	A	C	ENST00000343364 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-2285461	gatcttgagttaaaag[A/G]atgccaggccgggcga	A	G	80854 // Homo sapiens SET domain-containing protein 7 (SET7), mRNA. /// NM_002413 // upstream // 81290 //	SET7	SET7, Homo sapiens SET domain-containing protein 7 (SET7), q31.1
SNP_A-2281171	gagtagaaatgtttaa[C/G]atggtagaaaataaag	C	G	4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 10674 // Hs.467769 // FAM49A	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2281050	gagtaagctacaaaaa[A/C]ctgtgaattaatagca	A	C	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2275963	gagacttaacatgagg[C/T]atatggaagatgaggc	C	T	ENST00000313860 // 3UTR // 0 // --- // --- // --- // ---	-	p13
SNP_A-2270178	gacacatgaacgcagg[C/T]aggggtacaccacaca	C	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1050760 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2259216	gaaaaacagcctcctc[A/T]atgaacgaaccctgcc	A	T	// 57584 // Homo sapiens Rho GTPase activating protein 21 (ARHGAP21), mRNA. /// NM_020200 // downstream // 48504	ARHGAP21	ARHGAP21, Homo sapiens Rho GTPase activating protein 21 (ARHGAP21), p12.1
SNP_A-2250903	cttatgatccaatata[C/G]aagtatgaggaatgtc	C	G	// 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 328343 // --- // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2236046	ctcctgtatccaaaag[A/G]cagaataaggaggaac	A	G	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2300046	gcctcaataaactgca[A/G]ctgtaccaatgggcat	A	G	// 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // downstream // 1630 // Hs.493272 // ANKRD15 // 23189 //	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2312949	ggacttctattcagga[G/T]taaaagaaaataagtc	G	T	C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream //	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2308978	gcttttcaattcgtaa[A/G]tccccacttggcaaat	A	G	Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // intron // 0 // Hs.436387 // BCKDHB // 594 // Homo s	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco .q14.1
SNP_A-2050486	aaggatctagccatgc[A/G]gacatttgtgctaggt	A	G	Homo sapiens general transcription factor IIIA (GTF3A), mRNA. /// ENST00000241462 // intron // 0 // --- // --- // --- // ---	GTF3A	GTF3A, Homo sapiens general transcription factor IIIA (GTF3A), q12.2
SNP_A-2107546	agctagttcctgacca[A/G]taataaagtatgtgtt	A	G	CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 //	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-2013952	ctaagatctcaataaa[C/T]ggttttcatgctgatg	C	T	Homo sapiens mRNA for KIAA0830 protein, partial cds. /// ENST00000278505 // intron // 0 // --- // --- // --- // ---	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds. q21
SNP_A-2010680	tggacgataatacata[A/G]atgagtggatatggcg	A	G	1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// NM_007118 // upstream // 83664 //	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-2005995	ctttgctgttatggaa[A/C]cttggttctctcatgg	A	C	SEC23IP // 11196 // Homo sapiens SEC23 interacting protein (SEC23IP), mRNA. /// NM_000982 // downstream // 234651 //	SEC23IP	SEC23IP, Homo sapiens SEC23 interacting protein (SEC23IP), q26.12
SNP_A-2217814	cctgcaaaactaggca[C/T]atattacttgaagcaa	C	T	81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // intron // 0 // --- // --- // --- // --- /// ENST00000281924 // intron // 0 // --- // ---	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-2208157	cccaatatctgttccc[C/T]gcttcctccttagtag	C	T	Homo sapiens chromosome 20 open reading frame 31 (C20orf31), mRNA. /// ENST00000262875 // intron // 0 // --- //	C20orf31	C20orf31, Homo sapiens chromosome 20 open reading frame 31 (C20orf31), q11.22
SNP_A-2210285	ccccattagacttgtc[A/T]ccatcttccctttaga	A	T	ENST00000313063 // intron // 0 // --- // --- // --- // ---	-	p21.31
SNP_A-2167003	caacaacataatccac[A/G]cgggactactaatgac	A	G	7292 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF /// NM_004905 // upstream // 138311 // Hs.120 // PRDX6 // 95	TNFSF4	TNFSF4, Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF q25.1
SNP_A-2160410	atttcatccatttaac[A/G]gggaatttgcacccag	A	G	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 333630 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2142090	atctttgtatcctcta[C/T]agctagaaaaagaaca	C	T	Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2141260	atctgtaccaggacac[A/G]caataatttaaaccac	A	G	7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 215519 // Hs.148609	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2133091	atatagaactttgtgc[C/T]aaaaaataaaagcact	C	T	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA.	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-1807806	gtctgtttttatgcca[C/T]tactatactgtcttgt	C	T	57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // upstream // 159748 // --- // ---	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-1753105	attgttgcggaaatgtttggtgtat[C/T]tctccgttgtgaagttactttтcct	C	T	3910 // laminin, alpha 4 /// NM_002356 // upstream // 662742 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich	LAMA4	LAMA4 , rs774568, laminin, alpha 4 ,q21
SNP_A-1706519	gtcatcttgaccatattccaggata[A/G]caattaattttactctagttccctc	A	G	// 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 2117679 // Hs.450919 // GPC5 //	SLITRK5	SLITRK5 , rs9301548, SLIT and NTRK-like family, member 5 ,q31.2
SNP_A-1678634	aggagtctcttttgaagtcaatagc[C/T]ctatagccaggggttaacggacgag	C	T	2042 // EphA3 /// NM_173824 // downstream // 555516 // Hs.406060 // MGC26717 // 285237 // hypothetical protein	EPHA3	EPHA3 , rs1603312, EphA3 ,p11.1
SNP_A-1667190	atgacccaagatgacctttctctca[A/C]gttactctccttatcatcccaggac	A	C	10135 // pre-B-cell colony enhancing factor 1 /// NM_175884 // downstream // 85458 // Hs.29692 // FLJ36031 // 168455 //	PBEF1	PBEF1 , rs10486016, pre-B-cell colony enhancing factor 1 ,q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1850293	tatgttcaagatgaca[G/T]aggatataaggaatac	G	T	LOC124411 // 124411 // Homo sapiens hypothetical protein LOC124411 (LOC124411), mRNA. /// NM_003414 //	LOC124411	LOC124411, Homo sapiens hypothetical protein LOC124411 (LOC124411), p11.2
SNP_A-1864804	tccagcttttagaaca[C/T]agtgagagctggatca	C	T	NM_003240 // intron // 0 // Hs.520187 // LEFTY2 // 7044 // Homo sapiens endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfa /// ENST00000272113 // intron // 0 // --- // --- // --- // ---	LEFTY2	LEFTY2, Homo sapiens endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfa q42.12
SNP_A-1865081	tccagtgcttactcaa[C/T]gggtttctggtcatcc	C	T	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // --- // --- // --- // --- ///	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-1860715	tcataacaagttctgg[A/G]aaagagctaaacaaac	A	G	sapiens B lymphoid tyrosine kinase (BLK), mRNA. /// ENST00000259089 // intron // 0 // --- // --- // --- // ---	BLK	BLK, Homo sapiens B lymphoid tyrosine kinase (BLK), p23.1
SNP_A-1867951	tcctagcacaagtcta[C/T]gcatttaaccttatag	C	T	84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-1929786	ttcatcatttggtagc[A/T]gataacaattccagcc	A	T	MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1926631	ttattgaatatttaga[A/G]gttcccagcaccatga	A	G	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 969063 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1913877	tgtgtctgcaagcaca[C/T]gcgatctggtgctagt	C	T	Homo sapiens glioma tumor suppressor candidate region gene 1 (GLTSCR1), mRNA. /// ENST00000263282 // intron // 0 // --- // --- // --- // ---	GLTSCR1	GLTSCR1, Homo sapiens glioma tumor suppressor candidate region gene 1 (GLTSCR1), q13.32
SNP_A-1899153	tggaaagtaaattttc[A/G]ccaagagccctagggt	A	G	/// ENST00000332660 // downstream // 859132 // --- // --- // ---	-	p12.3
SNP_A-1969137	cgtccattatattcta[A/G]gcaccataatctcagt	A	G	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1977830	tgatgattaaaccaca[C/T]catgaccagtaaagtg	C	T	RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. ///	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1961024	tttttgggtctggtta[C/G]agatagagatccagtt	C	G	/// ENST00000343867 // upstream // 63369 // --- // --- // --- // ---	-	q11.21
SNP_A-1933778	ttctatctataaagcc[A/T]agggaaactcagatgc	A	T	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1943595	ttgtaaggaacaagga[C/T]tcacattgctgccctt	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-1943180	ttggtcgccaaccaaa[A/G]agaaagcttccgaatc	A	G	ENST00000342631 // intron // 0 // --- // --- // --- // ---	-	q37.3
SNP_A-1952573	tttctgccactaacaa[A/T]ctcaaaactcacttct	A	T	// 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 437120 // Hs.522019 //	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1978426	ccataaataggtctta[C/T]ggaaaagctccattaa	C	T	51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 341363 //	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1984961	ttatctctaatgctta[C/T]agcaacccttccagat	C	T	// 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 342451	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-1893052	tgcacttaataaatca[G/T]ggtgatcttaataagt	G	T	10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// ENST00000321536 // downstream	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-1912957	tgtggaatcttgccag[C/G]ctctttttaaaaaatt	C	G	ENST00000331807 // intron // 0 // --- // --- // --- // ---	-	q33.1
SNP_A-1907778	tgtaagggactagccc[A/G]catgttctagctggga	A	G	163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 116695 // Hs.221375 //	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-1923055	ttagcatattagcaca[C/G]gtttctttattggatt	C	G	// 63899 // Homo sapiens NOL1/NOP2/Sun domain family 3 (NSUN3), mRNA. /// ENST00000314622 // downstream //	NSUN3	NSUN3, Homo sapiens NOL1 q11.2
SNP_A-1866690	tcccctctctgattca[A/C]cacattattcatcacc	A	C	114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // upstream // 560 // Hs.413525 // PKD1L2 // 114780 // Homo	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-1863057	tcatttaactagtttg[A/G]atatgtgcctactata	A	G	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1194062 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1837425	tacttctatgtggtca[G/T]acctctggggtttact	G	T	55802 // Homo sapiens transcription factor SMIF (HSA275986), mRNA. /// NM_000720 // upstream // 93350 //	DCP1A	DCP1A, Homo sapiens transcription factor SMIF (HSA275986), p21.1
SNP_A-1815315	gtgtttaggtcaagaa[A/G]gttgtctccaaaaaat	A	G	80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream //	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1816414	gttagcagacagcgga[A/G]ctatgaattagacttg	A	G	// 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 93473 //	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1670824	acacgatgacaacaaatcatttggg[A/G]actagaacctgtagcattaccttaa	A	G	2262 // glypican 5 /// NM_005708 // upstream // 199912 // Hs.508411 // GPC6 // 10082 // glypican 6	GPC5	GPC5 , rs10492622, glypican 5 ,q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1653306	gtattcacaattccgtctaataata[A/G]ctatatacatctcatttaacagttt	A	G	NM_022445 // intron // 0 // Hs.127548 // TPK1 // 27010 // thiamin pyrophosphokinase 1	TPK1	TPK1 , rs1406720, thiamin pyrophosphokinase 1,q35
SNP_A-1682268	cttgtgaactatgtttctgccgtta[C/G]cagtgttggacccgccttcctcttt	C	G	// 57539 // WD repeat domain 35 /// NM_145260 // upstream // 543460 // Hs.123933 // ODD // 130497 // odd-skipped	WDR35	WDR35 , rs2278528, WD repeat domain 35 ,p24.1
SNP_A-1702617	ttcatacaactccttggattttata[C/T]actcttggaagctcttctctgagtt	C	T	// 23389 // thyroid hormone receptor associated protein 2 /// NM_005996 // upstream // 333050 // Hs.129895 // TBX3 //	THRAP2	THRAP2 , rs10492259, thyroid hormone receptor associated protein 2 ,q24.21
SNP_A-1746344	gtctgaaatagtttggaaatggata[A/G]atgctgaaggcaaggagacacaacc	A	G	5629 // prospero-related homeobox 1 /// NM_012424 // downstream // 611924 // Hs.30352 // RPS6KC1 // 26750 //	PROX1	PROX1 , rs765087, prospero-related homeobox 1 ,q32.3
SNP_A-1791012	ggggtcacttgtccca[C/T]aaagatatctactata	C	T	253769 // Homo sapiens hypothetical protein MGC43690 (MGC43690), mRNA. /// ENST00000354562 // intron // 0 // ---	MGC43690	MGC43690, Homo sapiens hypothetical protein MGC43690 (MGC43690), q27
SNP_A-2131516	atagcacactgtacac[C/T]gaaaatgttgacatct	C	T	134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream //	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-2158636	attgtattaaacttta[C/T]gttgccagcacctacc	C	T	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // --- // ---	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-2202729	ccacgcctggagtagc[A/G]agggtttagacttcct	A	G	7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 259278 // Hs.108049 // UACA // 55075 //	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2169535	caagctagaccgataa[A/G]agcttcatatttgggt	A	G	// 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 724181	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2182405	cagataaagaacatac[C/G]atttaaagaccacaca	C	G	-- /// ENST00000314058 // upstream // 82073 // --- // --- // --- //	-	p13.2
SNP_A-2001215	taatattcacagccca[A/G]actctacaggtggatt	A	G	11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 244368 //	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2039965	aacatttcctgaggct[C/T]aactgtatgctagcca	C	T	// 5019 // Homo sapiens 3-oxoacid CoA transferase 1 (OXCT1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000321394 // upstream // 38138 // --- // ---	OXCT1	OXCT1, Homo sapiens 3-oxoacid CoA transferase 1 (OXCT1), nuclear gene encoding mitochondrial protein, p13.1
SNP_A-2037716	aacaagggaactcaga[A/C]atgcagagggatgaaa	A	C	130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 381115	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-2107164	agcgtatagagaccaa[G/T]gaatatctacagcaaa	G	T	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 531366	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2089720	acttccattttcatcc[C/T]atatctttttcatctt	C	T	// 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 //	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2068938	acaatgacaaacaaca[A/C]actgggaaactattta	A	C	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2241719	ctgatcactagtcctt[C/T]aagcactgcaggaagt	C	T	Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2241720	ctgatcactttaccac[A/G]atttgccccagcccaa	A	G	ENST00000327669 // downstream // 16734 // --- // --- // --- // ---	-	p25.3
SNP_A-2258684	cttttgcatcttctgg[A/G]aaaaagtcccacgtac	A	G	Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, mRNA. /// NM_022114 // intron // 0 //	PRDM16	PRDM16, Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, p36.32
SNP_A-2271916	gacccaggtgcagaga[A/C]gttatgcttcgtggcc	A	C	10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream //	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13
SNP_A-2271808	gaccatcttgggctca[C/T]gtcttcaggacttcct	C	T	// Homo sapiens deleted in azoospermia-like (DAZL), mRNA. /// ENST00000250863 // upstream // 65482 // --- // --- // --- // ---	DAZL	DAZL, Homo sapiens deleted in azoospermia-like (DAZL), p24.3
SNP_A-2283152	gataatcaaagcagag[A/T]aatcaatggaccctgg	A	T	HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 139912 // Hs.120831 // TNT //	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2266968	gaagttttgattttaa[C/T]gaagtctgacttaacc	C	T	Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // --- // --- // --- // ---	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2232136	ctcaagtagatgctaa[C/T]gtattttgttttcttc	C	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2312763	ggactctagtgatttc[A/T]atgttgaataggatgg	A	T	Homo sapiens WD repeat domain 20 (WDR20), transcript variant 3, mRNA. /// NM_144574 // intron // 0 // Hs.36859 //	WDR20	WDR20, Homo sapiens WD repeat domain 20 (WDR20), transcript variant 3, q32.32
SNP_A-2313726	ggagcaatgaggtcct[C/T]aatgtttatggccccg	C	T	1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 28303 // --- //	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2
SNP_A-2311318	ggaatagcccaacaaa[A/C]tgccccaggatgtttc	A	C	Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (KCNN3),	KCNN3	KCNN3, Homo sapiens potassium intermediate q22
SNP_A-2066626	acaaaaatatttcaag[C/T]ctgagtgccaccactt	C	T	Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), mRNA. /// ENST00000266054 // intron // 0 // --- // ---	CHUK	CHUK, Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), q24.31

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2071226	acacttaactaaaaca[C/T]tgaaccctatggacat	C	T	50834 // Homo sapiens taste receptor, type 2, member 1 (TAS2R1), mRNA. /// NM_199133 // downstream // 235752 //	TAS2R1	TAS2R1, Homo sapiens taste receptor, type 2, member 1 (TAS2R1), p15.2
SNP_A-2053028	aagtcctcgattttac[A/C]caataccagttgaggg	A	C	4010 // Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), mRNA. /// AF057135 // downstream // 47492 //	LMX1B	LMX1B, Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), q33.3
SNP_A-2057466	aatatcgttaataaaa[A/T]tttctctgtataagag	A	T	7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// NM_016617 // upstream // 431040 // Hs.524969 // Ufm1 //	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2055284	aataagataaaagaga[A/G]gcaaggaattaataag	A	G	// 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 183297 //	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2037899	aacaatgatcatgaac[A/G]aggcaatttagtgcct	A	G	22862 // Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// NM_014923 // upstream // 300748 //	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-2046313	aagagaactgagtgca[A/C]aaaggaaggagcagat	A	C	23426 // Homo sapiens mRNA for GRIP1 protein. /// NM_018448 // upstream // 389150 // Hs.546407 // TIP120A //	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. q14.3
SNP_A-2041167	aacctcaaactaccag[A/C]ctaaagcgatcctgtt	A	C	5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 393452 // Hs.437966 // PXMP3 //	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2020337	tgtgatagacatagcc[C/G]gaaggtaattttatat	C	G	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA. /// ENST00000291560 // intron // 0 // --- // --- // --- // ---	HSF2BP	HSF2BP, Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), q22.3
SNP_A-2020180	tgtgggtcaaacccag[C/T]cgttccgaatcatcaa	C	T	Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 1 (SLC37A1), mRNA. /// ENST00000339657 // intron // 0 // --- // --- // --- // --- ///	SLC37A1	SLC37A1, Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 1 (SLC37A1), q22.3
SNP_A-2005647	ctcatttttaggcaaa[A/G]gcccatgaaggttttc	A	G	9388 // Homo sapiens lipase, endothelial (LIPG), mRNA. /// NM_006111 // downstream // 28676 // Hs.200136 // ACAA2 //	LIPG	LIPG, Homo sapiens lipase, endothelial (LIPG), q21.1
SNP_A-2007942	agagatccctcctaga[A/G]tccgtggcaacatgaa	A	G	Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-2178206	ctgagtgtggacagca[A/G]atggattcgtttgtgc	A	G	// Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), mRNA. /// ENST00000355700 // intron // 0 // ---	PHGDHL1	PHGDHL1, Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), q32.3
SNP_A-2185552	caggagacccaggaga[C/T]gtgatagcaagcctgg	C	T	10928 // Homo sapiens ralA binding protein 1 (RALBP1), mRNA. /// NM_005134 // downstream // 8231 // Hs.464595 //	RALBP1	RALBP1, Homo sapiens ralA binding protein 1 (RALBP1), p11.22
SNP_A-2188672	cagtgccttctggaac[A/G]cttcccaaaggatctg	A	G	RASL11A // 387496 // Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA. /// NM_002097 // upstream //	RASL11A	RASL11A, Homo sapiens RAS-like, family 11, member A (RASL11A), q12.2
SNP_A-2203399	ccagaaacagaaatca[C/T]attctactctgcaaac	C	T	// Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // --- // --- // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2211554	ccctcaccctcttgaa[C/T]ctactgcagtggtcac	C	T	// 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 651060 //	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2217571	tgataatgtagcacaa[C/T]gaaggaaagggcttca	C	T	80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // upstream // 192064 // --- //	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2144951	atgattgtcactaacc[C/T]gatgcttcaccatcac	C	T	64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 313893 // --- // ---	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2131735	atagctaaaacacact[A/G]agtacttaccatattt	A	G	Homo sapiens transcriptional adaptor 2 (ADA2 homolog, yeast)-like (TADA2L), transcript variant 2, mRNA. /// NM_001488 // intron // 0 // Hs.500066 // TADA2L // 6871 //	TADA2L	TADA2L, Homo sapiens transcriptional adaptor 2 (ADA2 homolog, yeast)-like (TADA2L), transcript variant 2, q12
SNP_A-2130373	atactaatcctataac[C/T]ggggtagaataaatat	C	T	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 499401 // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2124071	agttactcaaactgtc[A/T]ctggtgatgacacagg	A	T	353376 // Homo sapiens toll-like receptor adaptor molecule 2 (TICAM2), mRNA. /// NM_181836 // upstream // 31635 //	TICAM2	TICAM2, Homo sapiens toll-like receptor adaptor molecule 2 (TICAM2), q22.3
SNP_A-2115004	agggcccccaacacag[A/G]atgacgaagcacgtgg	A	G	284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 222446 //	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1797254	ggttggatgtggtgcc[A/G]gagaatcatgacttct	A	G	221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 45166	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1798782	gtaactcctcaaatta[C/T]acactaaaaagggcaa	C	T	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1700610	gtctggttcaactgttacctcaaga[C/G]aagagggtcaatctcccctcaactt	C	G	AF225426 // intron // 0 // Hs.24889 // FMN2 // 56776 // formin 2	FMN2	FMN2 , rs10495467, formin 2,q43
SNP_A-1704895	caccacatatcagctctgtcggtaa[C/T]tacaaaatgttctacttatcaaaat	C	T	11130 // ZW10 interactor /// NM_032997 // downstream // 73794 // Hs.42650 // ZWINT // 11130 // ZW10 interactor ///	ZWINT	ZWINT , rs7093020, ZW10 interactor ,q21.1
SNP_A-1817435	gttcagttggagaaga[A/G]ggagcatcctgatagg	A	G	// 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 52220 // Hs.196981	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-1851074	tattattggtgcacta[C/T]acatgattgaagctga	C	T	868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 420942 // --- // --- // --- // ---	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1849836	tatgtaggaacacaga[C/T]ggtgtgagtccacttg	C	T	10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 913414 // Hs.19718 // PTPRU //	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1922301	ttactttggagcaaca[G/T]attagcattcttactt	G	T	// Homo sapiens constitutive photomorphogenic protein (COP1), transcript variant 2, mRNA. /// NM_022457 // intron // 0 // Hs.523744 // RFWD2 // 64326 // Homo sapiens	RFWD2	RFWD2, Homo sapiens constitutive photomorphogenic protein (COP1), transcript variant 2, q25.1
SNP_A-1914686	tgttaattgctcaatc[G/T]aaattagtcagatatt	G	T	// 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 203853 // --- // --- // --- //	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1916041	ttatccttgaaatcaa[C/G]tctccatttcttcaac	C	G	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 641228 // Hs.114412 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1881202	tctttataaacagggc[A/G]ataattgaggacacta	A	G	SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 67721 // --- //	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-1950858	tttccaactcacagaa[A/G]gtttctcacaaagatc	A	G	79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 1277692 // Hs.387861 //	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-1955985	tttgtctagacttaca[A/G]ggtctttttcaggaac	A	G	Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // --- // --- // --- // ---	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-1938098	ttgacacatcacacaa[C/G]gtaatactgccaaaga	C	G	Homo sapiens serine/threonine kinase with Dbl- and pleckstrin homology domains (TRAD), mRNA. ///	TRAD	TRAD, Homo sapiens serine,q21.2
SNP_A-1959326	ttttgcaaaaatatac[A/G]gcctgtagcactatag	A	G	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1987642	gtcctctttgtacagg[C/G]ccgtgggagaaattaa	C	G	KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 169019 // Hs.486470	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1
SNP_A-1989145	caagaattgagatata[A/G]gtaaaaactatgcatt	A	G	Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// ENST00000328843 // intron // 0 // --- //	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-1980598	ctggcaaccttcctac[A/G]acctggaccatctcgc	A	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1964629	atcccagggttctgta[A/G]agcaactttgggagag	A	G	Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// ENST00000340599 // intron // 0 // --- // --- // --- // --- ///	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.1
SNP_A-1975553	tttgtctaaaggagac[A/G]ccaaaggctgggagag	A	G	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // --- // --	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-1891418	tgattcaagctaccca[A/T]gatggaataaagttaa	A	T	Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // --- // --- // --- // ---	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1890630	tgatgaaggcatcccc[A/C]gctttagctcactatg	A	C	Homo sapiens sorting nexin 13 (SNX13), mRNA. /// ENST00000340108 // CDS // 0 // --- // --- // --- // --- // --- ///	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-1898759	tgctttccctagaaga[A/T]gcctgaattcttttt	A	T	4292 // Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1), mRNA. /// ENST00000301807 // upstream // 76552 // --- // --- // --- // ---	MLH1	MLH1, Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1), p22.3
SNP_A-1915596	tgttctccaactaaga[C/T]gaccagctctttgtct	C	T	4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// NM_001263 // upstream	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1827432	gtcagagaaagataaa[A/C]ggagcaactgcaacat	A	C	Homo sapiens steroid dehydrogenase-like (LOC83693), mRNA. /// ENST00000219439 // intron // 0 // --- // --- // --- // ---	HSDL1	HSDL1, Homo sapiens steroid dehydrogenase-like (LOC83693), q24.1
SNP_A-1674565	gaactactgctccacagatctactc[A/G]aacaagaaagccctttttatggcaa	A	G	NM_033045 // intron // 0 // Hs.272336 // KRTHB4 // 3890 // keratin, hair, basic, 4	KRTHB4	KRTHB4 , rs1791661, keratin, hair, basic, 4,q13.13

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1673474	tgtaaaaaggatgctaagaagaaga[A/G]acaaacacacagggtctttgtac cc	A	G	// 2263 // fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, /// NM_018117 // downstream // 209245 // Hs.16677 // WDR11	FGFR2	FGFR2 , rs2250942, fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, ,q26.12
SNP_A-1752879	gttcacacttgaaaacataaataca[A/T]taaaacatttcaaactgcatttata	A	T	NM_005711 // upstream // 1610637 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3 , rs4131578, EGF-like repeats and discoidin I-like domains 3,q14.3
SNP_A-1782375	ggcaattcctagatga[A/G]gatattggaataacta	A	G	4808 // Homo sapiens nescient helix loop helix 2 (NHLH2), mRNA. /// NM_018420 // upstream // 27798 // Hs.125482 //	NHLH2	NHLH2, Homo sapiens nescient helix loop helix 2 (NHLH2), p13.1
SNP_A-2126824	ataaagacttttggtg[C/G]acttaaagctatgcta	C	G	TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. ///	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-2128654	ataatattcttgcttt[A/T]aaaatgtagctctggc	A	T	23591 // Homo sapiens apoptosis related protein APR-2 mRNA, complete cds. /// ENST00000315714 // downstream	APR-2	APR-2, Homo sapiens apoptosis related protein APR-2 complete cds. ,q21.31
SNP_A-2133081	atatagaaaaatagct[A/T]aaaaagacatctggag	A	T	/// ENST00000334919 // upstream // 1146160 // --- // --- // --- // --- /// ENST00000322194 // downstream // 622989 // --- // --- //	-	q12.2
SNP_A-2206492	ccatctggttgactct[G/T]acttgtgaagccttca	G	T	KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 225112 // Hs.486470	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1
SNP_A-2008058	tacagctactcagtta[C/T]acttaaactcaagaca	C	T	Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2018563	cctatttaccccacaa[C/T]agcccatctcgaacat	C	T	RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 11959 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-1995247	tctgttgtagcagaaa[G/T]aatccaaggctatggg	G	T	6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 31588 // Hs.374257 //	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2024496	aaaaggagagtagtaa[C/T]ctgtaggaagtattta	C	T	Homo sapiens component of oligomeric golgi complex 3 (COG3), mRNA. /// ENST00000357794 // intron // 0 // --- // ---	COG3	COG3, Homo sapiens component of oligomeric golgi complex 3 (COG3), q14.13
SNP_A-2031641	aaagtaagtctctaac[A/C]attagtaatagatcca	A	C	Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// NM_000965 // intron // 0 // Hs.436538 //	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-2029975	aaagatgagtgaatca[A/G]tctagctgaagggata	A	G	ACTL7B // 10880 // Homo sapiens actin-like 7B (ACTL7B), mRNA. /// ENST00000333948 // downstream // 47872 // --- //	ACTL7B	ACTL7B, Homo sapiens actin-like 7B (ACTL7B), q31.3
SNP_A-2028790	aaacttcgcattccca[A/G]tatgaagaagtgataa	A	G	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 989038 // --- // --- // --- //	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2039945	aacatttattgagcat[G/T]aataagcactggggct	G	T	5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // upstream // 105946 // Hs.498570 //	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-2040090	aaccaaaggaatgaga[C/T]ggtagatcacaatcat	C	T	57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3280985 //	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2050605	aaggcaaactatttta[C/T]agtgacagattggtga	C	T	ENST00000312468 // intron // 0 // --- // --- // --- // ---	-	p11.1
SNP_A-2065942	tttcaggtgagtaatc[C/T]gaggttcatggaattt	C	T	FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2104153	agcagagagagagtaa[C/T]agatttgaattcagag	C	T	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA. /// ENST00000356386 // intron // 0 // --- // -	BTN3A2	BTN3A2, Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), p22.1
SNP_A-2099383	agaggctgaagcttga[G/T]aatcacttgagcctgg	G	T	6691 // Homo sapiens serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), mRNA. /// NM_005612 // upstream // 30105 // Hs.401145 // REST // 5978 // Homo	SPINK2	SPINK2, Homo sapiens serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), q12
SNP_A-2297544	gccagacgctcttcca[A/G]taagaaggtgtcaaga	A	G	158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 67181 //	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-2290088	gcaaatactgtgaaaa[C/T]aatttgctaggaattg	C	T	386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000331273 // upstream // 125204 // --- // --- // --- // --- ///	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2291833	gcacagcttaatggaa[A/G]cgtaacatgcagtttg	A	G	SLC15A4 // 121260 // Homo sapiens solute carrier family 15, member 4 (SLC15A4), mRNA. /// ENST00000315208 //	SLC15A4	SLC15A4, Homo sapiens solute carrier family 15, member 4 (SLC15A4), q24.32
SNP_A-2228743	ctagactggagcatta[C/T]gggacacagtcaactc	C	T	SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 96606 // Hs.509872 // RGS6 //	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2261059	gaaagaatctgatgtc[A/C]caggttgggtcagatg	A	C	// 55704 // Homo sapiens KIAA1212 (KIAA1212), mRNA. /// NM_080667 // upstream // 77969 // Hs.264208 // MGC15407	KIAA1212	KIAA1212, Homo sapiens KIAA1212 (KIAA1212), p16.1
SNP_A-2286652	gatggataagatggaa[A/G]ggacggtaggtgagga	A	G	5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 1313540 // Hs.199068 // CAMK1G	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2285913	gatgaggggtggataa[G/T]gttgatatgttaggca	G	T	10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream //	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2274138	gacttcagttatatcc[C/T]ggaactggcaaattgt	C	T	2880 // Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA. /// NM_001509 // upstream // 78217 // Hs.248129 //	GPX5	GPX5, Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, p22.1
SNP_A-2288993	ccagaaaagattgcat[C/G]agggcctggagatggt	C	G	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 //	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2297543	gccagacgcgaaaggt[C/T]acatattatacgattc	C	T	ADAMTS15 // 170689 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 (ADAMTS15), mRNA. /// NM_173580 // upstream // 44718 // --- // FLJ39058 // 2	ADAMTS15	ADAMTS15, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 (ADAMTS15), q24.3
SNP_A-2301417	gccttttcagttcctc[A/G]gaatatttttactatt	A	G	// Homo sapiens hypothetical protein FLJ36980 (FLJ36980), mRNA. /// ENST00000317438 // intron // 0 // --- // --- // --- // ---	FLJ36980	FLJ36980, Homo sapiens hypothetical protein FLJ36980 (FLJ36980), p22
SNP_A-2080775	ccattgtcctcagtag[G/T]aacttttatcgcagtt	G	T	FLJ22789 // 84190 // Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// NM_152588 // upstream //	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-2081299	acctggagtatgagac[A/G]gaataaggaaggcacc	A	G	7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-2081307	acctggatcctctctt[C/G]aaagctgtttctctcc	C	G	// Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), mRNA. /// ENST00000359309 // CDS // 0 // --- // --- // --- /// ENST00000360822 // CDS // 0 // --- // --- // ---	CDK5RAP2	CDK5RAP2, Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), q33.2
SNP_A-2063008	aatgttaagttcagac[A/G]gaggtgactctataaa	A	G	ENST00000281496 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-2049499	aagctggggctgttat[G/T]aaggtaccaacacata	G	T	ENST00000311061 // intron // 0 // --- // --- // --- // ---	-	q14
SNP_A-2053069	aagtcgtgggtccttc[C/G]ccttgagcttgggacc	C	G	Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 //	CAMK1D	CAMK1D, Homo sapiens calcium p13
SNP_A-2025306	aaaatattccgaacaa[A/T]tgggttcagcataaaa	A	T	1998 // Homo sapiens E74-like factor 2 (ets domain transcription factor) (ELF2), transcript variant 2, mRNA. /// NM_201999 // upstream // 108253 // Hs.260903 // ELF2 //	ELF2	ELF2, Homo sapiens E74-like factor 2 (ets domain transcription factor) (ELF2), transcript variant 2, q31.1
SNP_A-2018550	agcttacactagaacc[C/T]gggaactttgatcctg	C	T	Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2013609	ttctttttttcaaaccc[A/G]agcaaggaaaatcaga	A	G	MGC26979 // 91147 // Homo sapiens hypothetical protein MGC26979 (MGC26979), mRNA. /// NM_153704 //	MGC26979	MGC26979, Homo sapiens hypothetical protein MGC26979 (MGC26979), q22.1
SNP_A-2007093	gaaagtcacgtggata[A/G]gactatgctccctgaa	A	G	// 143496 // Homo sapiens olfactory receptor, family 52, subfamily B, member 4 (OR52B4), mRNA. /// NM_003141 // downstream // 9942 // Hs.532357 // TRIM21 // 6737 // Homo	OR52B4	OR52B4, Homo sapiens olfactory receptor, family 52, subfamily B, member 4 (OR52B4), p15.4
SNP_A-2213034	ccgacaagggaaacga[C/T]gcacgtcagcaccgtg	C	T	Homo sapiens G protein-coupled receptor MRGX1 (MRGX1), mRNA. /// ENST00000302797 // CDS // 0 // --- // --- // --- // ---	MRGX1	MRGX1, Homo sapiens G protein-coupled receptor MRGX1 (MRGX1), p15.1
SNP_A-2215670	tattcagtaagcaccc[A/G]ataaaagctggttgaa	A	G	Homo sapiens spastic paraplegia 3A (autosomal dominant) (SPG3A), mRNA. /// NM_181598 // intron // 0 // Hs.241503 //	SPG3A	SPG3A, Homo sapiens spastic paraplegia 3A (autosomal dominant) (SPG3A), q22.1
SNP_A-2214004	cctaagacatatttac[A/T]atacattcatccaatg	A	T	// 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000329561 // upstream //	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-2188178	cagtcctaaagaaaga[C/T]acaggctggacacagt	C	T	Homo sapiens hypothetical protein MGC2744 (MGC2744), mRNA. /// ENST00000338100 // intron // 0 // --- // --- // --- // ---	MGC2744	MGC2744, Homo sapiens hypothetical protein MGC2744 (MGC2744), q21.31
SNP_A-2190145	cataagtagagaaaca[A/C]aaattgaactcaaaat	A	C	7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-2191598	catatgtagggtaata[C/T]tagtttggtgatgtta	C	T	Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000260926 // intron // 0 // --- // --- // --- // ---	SATB2	SATB2, Homo sapiens SATB family member 2 (SATB2), q33.1
SNP_A-2185941	caggcacacagaaaat[A/G]aagttgctttctacaa	A	G	-- /// ENST00000356397 // upstream // 1123773 // --- // --- // ---	-	q24
SNP_A-2172664	caattggctgcagaca[A/G]ataggctttttattt	A	G	MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 //	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-2128365	ataagtgtaagtcaaa[A/G]atgaaagtacaactct	A	G	// Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// ENST00000310105 // 3UTR // 0 // --- // --- // --- // ---	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2111312	aggagcctgggggtg[C/T]atgaagccatgtcccc	C	T	Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // --- // --- // --- // --- /// ENST00000287878 // intron //	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-2122504	agtgctcctagtttca[C/T]caatcaggataacctt	C	T	134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream //	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-2121345	agtcttctattccgta[G/T]gtagcaaggagctgac	G	T	ENST00000308497 // intron // 0 // --- // --- // --- // ---	-	q35.1
SNP_A-2145767	atgccactgaaatgta[C/T]actcaacaatggctaa	C	T	// Homo sapiens FLJ42280 protein (FLJ42280), mRNA. /// ENST00000356686 // intron // 0 // --- // --- // --- // ---	FLJ42280	FLJ42280, Homo sapiens FLJ42280 protein (FLJ42280), q21.3
SNP_A-2149631	atgtatactataaatc[A/G]accaatgaacaagcca	A	G	9601 // Homo sapiens protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (ERP70), mRNA. /// NM_152411 // downstream // 28728 // Hs.201648	ERP70	ERP70, Homo sapiens protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (ERP70), q36.1
SNP_A-2167073	caacaatagaatggac[A/C]aaacaattaactgtga	A	C	Homo sapiens wingless-type MMTV integration site family, member 5B (WNT5B), transcript variant 2, mRNA. /// NM_032642 // intron // 0 // Hs.306051 // WNT5B // 81029 //	WNT5B	WNT5B, Homo sapiens wingless-type MMTV integration site family, member 5B (WNT5B), transcript variant 2, p13.33
SNP_A-2162388	attttatttttaaagaa[C/T]gttcatgtgatgataa	C	T	// Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 580800 // Hs.446075 // ACO1 // 48	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-1642859	attattgatctgtctcatttgagca[C/T]acatttccatgttactcttattctt	C	T	AB067505 // intron // 0 // Hs.13485 // GALNT13 // 114805 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	GALNT13	GALNT13 , rs6709870, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13),q24.1
SNP_A-1797600	ggtttctctctcttcc[G/T]ctggactttaacaagc	G	T	64091 // Homo sapiens popeye domain containing 2 (POPDC2), mRNA. /// NM_005694 // downstream // 3232 //	POPDC2	POPDC2, Homo sapiens popeye domain containing 2 (POPDC2), q13.33
SNP_A-1809950	gtgagtgtgtttgcac[A/G]agcaatcccgaattcc	A	G	9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 168461 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-1819139	gttgctattagaatga[C/T]ggctttttattagcct	C	T	// Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 306448 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1834242	tacatggccactcaga[C/T]ctccaagaacaagtgt	C	T	RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_002271 // downstream // 113644 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding	RANBP5	RANBP5, Homo sapiens RAN binding protein 5 (RANBP5), q32.2
SNP_A-1845701	tataggcttccttccc[C/G]atttctccttttctcc	C	G	23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// NM_024827 // upstream // 55707 // Hs.404802 // HDAC11	NUP210	NUP210, Homo sapiens nucleoporin 210 (NUP210), p25.1
SNP_A-1865402	tccatctaggccagta[G/T]agaagtataaggaaga	G	T	// 6711 // Homo sapiens spectrin, beta, non-erythrocytic 1 (SPTBN1), transcript variant 1, mRNA. /// NM_003128 // downstream // 67017 // Hs.503178 // SPTBN1 // 6711 //	SPTBN1	SPTBN1, Homo sapiens spectrin, beta, non-erythrocytic 1 (SPTBN1), transcript variant 1, p16.2
SNP_A-1908661	tgtaggacactggaaa[C/T]ggatccagagttcaca	C	T	DKFZp761N1114 // 148808 // Homo sapiens hypothetical protein DKFZp761N1114 (DKFZp761N1114), mRNA. /// NM_001973 // upstream // 7132 // Hs.497520 // ELK4 // 2005	DKFZp761N1114	DKFZp761N1114, Homo sapiens hypothetical protein DKFZp761N1114 (DKFZp761N1114), q32.1
SNP_A-1921917	ttactcctatttagca[C/G]ctccctaagaaatgaa	C	G	Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// ENST00000281437 // intron // 0 // --- // --- // ---	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-1889319	tgagtggctgccaacc[A/G]catgaaactggggtat	A	G	5795 // Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 //	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2
SNP_A-1964326	gtgtgaccgtaatgtc[A/G]ataagcttcatttgca	A	G	/// ENST00000360991 // downstream // 978680 // --- // --- // ---	-	q12.1
SNP_A-1949907	tttcaagccaaatgat[A/G]actcccaacagagaag	A	G	FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream //	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-1951200	tttcccagtggctgac[A/G]cttcatccaagccgca	A	G	sapiens CECR2 protein (CECR2) mRNA, complete cds. /// ENST00000262608 // intron // 0 // --- // --- // --- // --- ///	CECR2	CECR2, Homo sapiens CECR2 protein (CECR2) complete cds. q11.21
SNP_A-1937495	ttgaacatcatttgta[A/G]acagattgccttctta	A	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1946581	tttaaatgcaaccagg[A/G]aaataagtaccatttt	A	G	FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-1944201	ttgtcatgggaatata[G/T]cgtatgtttggttcag	G	T	/// ENST00000359604 // upstream // 429493 // --- // --- // --- // --- /// ENST00000344172 // upstream // 340236 // --- // --- // ---	-	q11.2

1504

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1879815	tcttccaggcttcacc[C/T]atatcagttacagatg	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4462060 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1918498	ttaaatcataaaaagc[C/T]gctctatatacagttt	C	T	Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 //	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1865359	tccatccattcactca[C/T]tcttgtgttgctgctg	C	T	// 2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 142758 // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-1864614	tcaatccaatccgaca[A/G]gagagacaagagctct	A	G	6426 // Homo sapiens splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA.	SFRS1	SFRS1, Homo sapiens splicing factor, arginine,q23.2
SNP_A-1845243	tatacgacttgcatca[C/T]tgaaagtaaggagtca	C	T	55214 // Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// NM_021101 // downstream // 174244 // Hs.439060 //	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-1831841	taattctcagggaaga[C/T]cttatgagactataaa	C	T	10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream //	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1800176	gtaccctgcggacatc[C/G]agcgacccttttatttt	C	G	10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 172849 // Hs.2561 // NGFB //	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-1789478	gggcctatgggccaaa[A/G]ttagtcacacagatgc	A	G	sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, mRNA. /// NM_017488 // intron // 0 // Hs.188528 // ADD2 //	ADD2	ADD2, Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, p13.3
SNP_A-2158143	attggatcagaccgta[G/T]gtattgaaaaggacct	G	T	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2142926	atgaatacatttttcc[A/G]gaatttttctagccgt	A	G	9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // downstream //	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-2196102	catgtgagggcacagt[A/G]accagggaaccatctg	A	G	FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream //	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2196638	cattaactcactcata[C/G]tatacttgctctttta	C	G	23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 431416 // Hs.434255 // PSD3 //	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p21.3
SNP_A-2191851	catcaaagaaaaaaga[A/C]caacactaagcacaat	A	C	Homo sapiens axotrophin (AXOT), mRNA. /// ENST00000259050 // intron // 0 // --- // --- // --- // ---	MARCH7	MARCH7, Homo sapiens axotrophin (AXOT), q24.2
SNP_A-2214794	cctagtgttacaaaga[A/G]gaaaagctggagcatc	A	G	Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), mRNA. /// ENST00000263160 // intron // 0 // --- // --- // --- // ---	SLC17A6	SLC17A6, Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), p14.3
SNP_A-2211310	ccctacagagtttgta[A/G]ctgacattataaacag	A	G	FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream //	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-2005799	tggtagggacaatacc[C/T]ataaatcactggggac	C	T	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 421807 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1996717	aagggctgaacccgga[C/T]gtctatctaggacaca	C	T	sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // --- // --- // --- // ---	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2036429	aaattctctgggcaaa[A/T]gttacctcttgttcct	A	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2064329	gaaagatccacaggtc[G/T]aaagccatctgcaaag	G	T	121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. ///	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2306601	gctgtactgtttggta[A/G]cattcccttgtaaagc	A	G	FLJ44313 // 400658 // Homo sapiens FLJ44313 protein (FLJ44313), mRNA. /// NM_207461 // upstream // 135950 //	FLJ44313	FLJ44313, Homo sapiens FLJ44313 protein (FLJ44313), q23
SNP_A-2273765	gactggaagaaacaat[A/G]agcaatatgcacctcg	A	G	SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 //	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2276202	gagagagatacaggac[A/G]ggaaggccctttcttt	A	G	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // --- // --- // --- // ---	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2266599	gaagtccaaaagggaa[A/T]ctacttcaaatgacca	A	T	Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // intron // 0 // --- // --- // --- // ---	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2252347	cttccctgtcactctc[C/T]ccacttctaggtcgcc	C	T	MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. ///	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2254040	cttgagctatgacaag[A/G]acaagtctggcaaaga	A	G	CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3),	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2244971	ctggcactgaagcact[A/G]actatcttgaattctg	A	G	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 432660 // Hs.253736 // LRIG3 // 121227 //	-	-, Human endogenous retrovirus env q14.1
SNP_A-2266180	gaagggagataccacc[A/G]ccaagaaggtcccgat	A	G	988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream //	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-2283197	gataatgcgtaagttc[A/G]catgaggtctaatggt	A	G	90827 // Homo sapiens KRAB zinc finger protein (KR19) mRNA, complete cds. /// ENST00000331162 // upstream //	ZNF479	ZNF479, Homo sapiens KRAB zinc finger protein (KR19) complete cds. p11.1
SNP_A-2310069	ggaaattgggatttga[A/T]aataaataatgctacc	A	T	Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_001843 // intron // 0 // Hs.143434 // CNTN1 //	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2301356	gcctttcttcacactg[C/G]agtagaggccgatatg	C	G	// 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// NM_178552 // downstream // 60 // Hs.124502 //	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-2050207	aaggacttaagcgcag[C/G]aaagccaatttctctt	C	G	ENST00000354500 // intron // 0 // --- // --- // --- // ---	-	q21.13
SNP_A-2048632	aagccaagttctcaac[A/G]acataaaataaaacga	A	G	DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2060480	aatgacatatgtcaaa[A/T]tgaaaacacatacaag	A	T	PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 //	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2090099	acttgaatactgttga[A/T]gaggatgtaaattagt	A	T	Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // --- //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2106353	agcccttaaatattga[C/T]gattttgttaagcttc	C	T	Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // --- // --- // --- // ---	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-2105914	agccatccaagtctta[C/T]gtgtgtggagaggcag	C	T	Homo sapiens junctophilin 2 (JPH2), transcript variant 1, mRNA. /// ENST00000278973 // intron // 0 // --- // --- // --- // ---	JPH2	JPH2, Homo sapiens junctophilin 2 (JPH2), transcript variant 1, q13.12
SNP_A-2098510	agagcagatgactcac[C/T]ggatggttttgtgctg	C	T	PTPN11 // 5781 // Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) (PTPN11), mRNA. /// NM_014954 // upstream // 53241 //	PTPN11	PTPN11, Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) (PTPN11), q24.13
SNP_A-2037077	gagctgtatccttaaa[A/G]ttatcagccttttatt	A	G	Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // --- // --- // --- // ---	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-2044675	aagaaagagtgtttcc[A/G]aaagtgaaagggaaga	A	G	Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // ---	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2025447	aaaatcccactagaaa[A/C]cagacctcttagacac	A	C	MGC33692 // 414918 // Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692), mRNA. ///	MGC33692	MGC33692, Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692), p14.3
SNP_A-2025866	aaaatggtacaaacaa[C/T]actacaacaaatcttt	C	T	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 373496 // --- // --- // --- //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2026918	aaacactctctttgaa[A/G]tcgttgctgtcactag	A	G	79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 397503 // ---	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2005436	acatcggatttgtagc[C/T]aagctaggtaatggga	C	T	Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// ENST00000281221 // intron // 0 // --- // --- // --- // ---	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2010948	ccctcatgactaaagc[C/T]gccagtcacatttatc	C	T	Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA. /// ENST00000358731 // intron // 0 // --- // --- // --- // ---	BDP1	BDP1, Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), q13.2
SNP_A-2184294	cagccttccatcatag[A/T]caggggatgctgtttt	A	T	22862 // Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// NM_014923 // upstream // 300231 //	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-2179964	cactttggaaatgcaa[A/G]aagtagaaggcaaaga	A	G	169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 3416 // Hs.444915 //	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2140527	atctcctaatggcttc[C/T]agatgtttgataggtg	C	T	ENST00000354349 // intron // 0 // --- // --- // --- // ---	-	p13.3
SNP_A-2162244	attttagcctctggat[A/C]aaatgaggtacccatt	A	C	ENST00000251030 // intron // 0 // --- // --- // --- // ---	-	q14.11
SNP_A-2107911	agctcccagcttctca[C/T]tgaaatagtgctcctg	C	T	TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2109280	tttgagggtagcattg[C/T]agttatgttggaagtt	C	T	Homo sapiens hypothetical protein FLJ10770 (KIAA1579), mRNA. /// ENST00000294428 // intron // 0 // --- // --- // --- // ---	KIAA1579	KIAA1579, Homo sapiens hypothetical protein FLJ10770 (KIAA1579), p31.3
SNP_A-1812956	gtgggggaaaggagta[A/G]ggacttgtttatggga	A	G	Homo sapiens myofibrillogenesis regulator 1 (MR-1), mRNA. /// NM_022152 // intron // 0 // Hs.98475 // PP1201 // 64114 //	MR-1	MR-1, Homo sapiens myofibrillogenesis regulator 1 (MR-1), q35

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783359	ggcataaccacctata[C/T]gctaggtttaccactt	C	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 958047 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1830517	taatcacccaggtaaa[A/G]aagttcaagaataagt	A	G	Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1839476	tagatactgttcatca[A/C]gtcttgctatgtgcca	A	C	3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 177508 // Hs.414110	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1817551	gttcatttatgaccttt[A/G]aaaaaaatcgtttaca	A	G	51352 // Homo sapiens Wilms tumor associated protein (WIT-1), mRNA. /// NM_006360 // upstream // 129875 // Hs.502244	WIT-1	WIT-1, Homo sapiens Wilms tumor associated protein (WIT-1), p13
SNP_A-1846586	tatatttacttaaatc[A/G]cctgccatagaaattc	A	G	51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 56859 // Hs.491997 // EYA1	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3
SNP_A-1854888	tcaactaagttggtaa[A/T]gaccttgatctaaatt	A	T	Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), mRNA. /// NM_016653 // intron // 0 // Hs.444451 // ZAK // 51776 // Homo sapiens sterile	ZAK	ZAK, Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), q31.1
SNP_A-1904701	tgggggccactgttcc[A/G]cctatcacaccaaaca	A	G	sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // --- // --- // --- // --- ///	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-1929521	ttcataagacttgtac[C/T]gagtggctactgtgtg	C	T	// Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 342934 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc q31.1
SNP_A-1875085	tctctcactcttcata[A/G]caatactggaaggtaa	A	G	112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-1883932	tgaagaggaggaagga[A/C]cttctgctgtagaggc	A	C	// Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // ---	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1896214	tgcgggtataaaaggc[A/C]gcatgaggggtcctta	A	C	2706 // Homo sapiens gap junction protein, beta 2, 26kDa (connexin 26) (GJB2), mRNA. /// NM_006783 // downstream	GJB2	GJB2, Homo sapiens gap junction protein, beta 2, 26kDa (connexin 26) (GJB2), q12.11
SNP_A-1947662	tttactaaatgatttc[C/T]ctgacactttcagtg	C	T	Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // --- // --- // --- // --- ///	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-1938810	ttgaggaaggaaccac[A/T]gaaataaggcaacaac	A	T	// 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 379461	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-1963692	ttcctcattcgctttta[C/G]cttagacctagtttaa	C	G	27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// NM_182536 // downstream // 60920 //	BMP10	BMP10, Homo sapiens bone morphogenetic protein 10 (BMP10), p13.3
SNP_A-1969303	tcacatttttttctcca[C/T]agatcttatcaagaag	C	T	/// ENST00000331037 // downstream // 446718 // --- // --- // ---	-	q21.1
SNP_A-1972525	gcagcaaagtgaaaac[A/C]gtgaatcagctagaat	A	C	84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 55846 //	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1979790	ctgttgctgtgcctta[C/T]attttgattttagaat	C	T	7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 469319 // Hs.481133 // SPOCK3	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1987409	catggagaattaccta[C/T]acttttgcatccttga	C	T	4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1961075	tttttgtcagcacata[C/T]aatcccaagtaactaa	C	T	ENST00000311061 // intron // 0 // --- // --- // --- // ---	-	q14
SNP_A-1893630	tgcaggtgcacaggct[A/G]aacatcagagccagac	A	G	3625 // Homo sapiens inhibin, beta B (activin AB beta polypeptide) (INHBB), mRNA. /// NM_032845 // downstream	INHBB	INHBB, Homo sapiens inhibin, beta B (activin AB beta polypeptide) (INHBB), q14.2
SNP_A-1928178	ttcacactgcatcaaa[A/G]cctccagaacgtcctt	A	G	94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 493 // --- // --- // --- // ---	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1868461	tcctcctaagatttct[C/G]aaaagatcatgacact	C	G	sapiens RNA binding motif protein 19 (RBM19), mRNA. /// ENST00000261741 // intron // 0 // --- // --- // --- // ---	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-1871879	tctacactgctgatgg[C/G]aatgaaactagtacag	C	G	// 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 //	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-1820456	gtttatctaaaataaa[A/T]cacaccgcattgaatg	A	T	FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 214688 //	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1823616	taaaataagagcttga[C/T]aactttgactagatta	C	T	PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream //	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-1840470	tagccaggctagtagc[G/T]aagaccattggcacta	G	T	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, mRNA. /// NM_001001290 // intron // 0 // Hs.444612 //	SLC2A9	SLC2A9, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, p16.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1843403	tagtgaatcatactcc[C/G]gcatctcttgaagtga	C	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 771530 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1834521	taccaaatgacttctc[A/G]ctaggacagatgccaa	A	G	// Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. ///	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-1836281	tactattgtcctttga[G/T]gcaaaaaaactgagaa	G	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1753349	taacactgcgctagaatcatactga[A/T]cttttcattatggataaaaatgctt	A	T	NM_022354 // intron // 0 // Hs.312720 // SPATA1 // 64173 // spermatogenesis associated 1	SPATA1	SPATA1 , rs1246253, spermatogenesis associated 1,p22.3
SNP_A-1745754	agtggtctctggacagcagaatgca[C/T]gtggatgttggagttgccagatcta	C	T	NM_020211 // upstream // 288559 // Hs.271277 // RGMA // 56963 // RGM domain family, member A	RGMA	RGMA , rs10520726, RGM domain family, member A,q26.1
SNP_A-1737331	cctattctgcaaatttgttctaatg[A/C]aataagttgtgtatgcagaaaaggt	A	C	51299 // neuritin 1	NRN1	NRN1 , rs1323198, neuritin 1,p25.1
SNP_A-1723934	aaaatattgcgttaattaaaatgca[A/C]acaggttataaacaatttttgttt	A	C	protein tyrosine phosphatase, receptor type, T /// NM_133170 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine	PTPRT	PTPRT , rs6030208, protein tyrosine phosphatase, receptor type, T ,q12
SNP_A-1672826	agtacctttcagagcaagtttcaac[A/G]gtaaggagcaggtagatttttcatc	A	G	401099 // LOC401099 (LOC401099), mRNA /// NM_145035 // upstream // 1027719 // Hs.369104 // ADMP // 165679 //	-	- , rs2405755, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-1694639	tcccgccttttgtgttatatcctgt[A/C]aatccttgaaggggcaaactatccc	A	C	10003 // N-acetylated alpha-linked acidic dipeptidase 2 /// NM_020358 // upstream // 309946 // Hs.283103 // RNF18 //	NAALAD2	NAALAD2 , rs10501709, N-acetylated alpha-linked acidic dipeptidase 2 ,q14.3
SNP_A-1698269	ccacgttctgcacatgtacaaaaaa[G/T]aattagggagagatactttctcaga	G	T	// 319089 // chromosome 14 open reading frame 25 /// NM_001049 // upstream // 112822 // Hs.248160 // SSTR1 //	C14orf25	C14orf25 , rs1959694, chromosome 14 open reading frame 25 ,q21.1
SNP_A-1698377	tcactagtctgaatgtcagagatag[C/T]agtaccttgcatcaactctgaataa	C	T	7444 // vaccinia related kinase 2 /// NM_018014 // downstream // 1823728 // Hs.314623 // BCL11A // 53335 // B-	VRK2	VRK2 , rs2041813, vaccinia related kinase 2 ,p16.1
SNP_A-1693405	caataggttcatgtgttgattagaa[A/G]atctcagtaaatgatgcaggtcaaa	A	G	// 1006 // cadherin 8, type 2 /// NM_002080 // upstream // 231947 // Hs.314658 // GOT2 // 2806 // glutamic-oxaloacetic	CDH8	CDH8 , rs10500409, cadherin 8, type 2 ,q21
SNP_A-1692106	ttgtatgactgtttctagcttaaat[C/G]agtactttattagtattttgcttc	C	G	KIAA1221 // 84146 // KIAA1221 protein /// NM_032186 // downstream // 436804 // Hs.173001 // KIAA1221 // 84146 //	KIAA1221	KIAA1221 , rs699532, KIAA1221 protein ,p22.2
SNP_A-1687784	aaaaaagcaaaagcttctcactcac[C/T]aatagcttagaaaagtttcacatct	C	T	NM_002349 // intron // 0 // Hs.153563 // LY75 // 4065 // lymphocyte antigen 75	LY75	LY75 , rs2271383, lymphocyte antigen 75,q24.2
SNP_A-1688088	ttagtgaatgcagaatgaagagaaa[A/G]ttggtggaaaatagataagaaagta	A	G	NM_016192 // upstream // 2832748 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs10497746, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1814404	gtgtgagtacaaatga[C/G]aggaacaatggacatc	C	G	Homo sapiens similar to F10G7.10.p (KIAA2024), mRNA. /// ENST00000272793 // intron // 0 // --- // --- // --- // ---	ZNF650	ZNF650, Homo sapiens similar to F10G7.10.p (KIAA2024), q31.1
SNP_A-1791967	gggtggaaacacccca[A/G]atgtctaacagtgcgt	A	G	ENST00000329238 // intron // 0 // --- // --- // --- // ---	-	q13.3
SNP_A-1785352	ggctatataggatacc[A/G]caacaactctctggtt	A	G	27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 1118825 // Hs.298705 // CNTN4 //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2131198	atagagagaaatgcaa[G/T]aagtaaaatcattaag	G	T	Homo sapiens lipin 2 (LPIN2), mRNA. /// ENST00000261596 // intron // 0 // --- // --- // --- // ---	LPIN2	LPIN2, Homo sapiens lipin 2 (LPIN2), p11.31
SNP_A-2156970	attctttataaatcaa[C/T]tggagttggtccatga	C	T	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 621691 // Hs.269560	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2144752	atgatggcagagaaaa[A/G]tagtcatataaagata	A	G	Homo sapiens RAS guanyl releasing protein 3 (calcium and DAG-regulated) (RASGRP3), mRNA. /// ENST00000337416 // intron // 0 // --- // --- // --- // ---	RASGRP3	RASGRP3, Homo sapiens RAS guanyl releasing protein 3 (calcium and DAG-regulated) (RASGRP3), p22.3
SNP_A-2145108	atgcaacattttctca[A/G]taaagatgattttcct	A	G	Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), mRNA. /// ENST00000302541 // intron // 0 // --- // ---	MYRIP	MYRIP, Homo sapiens myosin VIIA and Rab interacting protein (MYRIP), p22.1
SNP_A-2198705	catttcctattagcac[C/T]atggccaattgttttc	C	T	64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 523820 //	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2220483	ccccctgtctctgttg[A/T]aatcagtgatctctgt	A	T	// 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA (cDNA clone IMAGE:4791744), partial cds. /// NM_017799 // downstream // 15785 // Hs.497253 //	C14orf101	C14orf101, Homo sapiens chromosome 14 open reading frame 101, (cDNA clone IMAGE:4791744), partial cds. q22.3
SNP_A-2000152	tgttgtaagacattcc[A/G]gaactatagaagtgca	A	G	79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 59154 //	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2046886	aagaggtaagtagtag[C/T]caaccttgtacctacc	C	T	Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2038814	aacagcactaaggaag[A/C]aaaccatgctaaatgc	A	C	ENST00000344698 // intron // 0 // --- // --- // --- // ---	-	q42.2
SNP_A-2098353	agagattccataacta[A/C]aagtctgcttcaatat	A	C	9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 81736 // Hs.248117 //	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2097920	agagagacaaagacca[A/G]agactgagcgttggct	A	G	Homo sapiens formyltetrahydrofolate synthetase domain containing 1 (FTHFSDC1), mRNA. /// ENST00000265365 // intron // 0 // --- // --- // --- // ---	MTHFD1L	MTHFD1L, Homo sapiens formyltetrahydrofolate synthetase domain containing 1 (FTHFSDC1), q25.1
SNP_A-2090456	acttgggtaccactga[C/T]gacaatatccagagca	C	T	9252 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA. /// NM_182398 // upstream // 4181 // Hs.510225 // RPS6KA5 //	RPS6KA5	RPS6KA5, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, q32.12
SNP_A-2057062	aatagtttagtgaaaa[A/G]cttttgagatgacctc	A	G	55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 440966 //	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2067479	acaaatgagttatcaa[G/T]atttgaaaagtcatgg	G	T	// 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 780856 //	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2073640	acagtcaagagcttca[A/G]taacagatgagaccaa	A	G	C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 //	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-2270858	gacaggtggacaaaag[A/G]cgtagtaccgttctgc	A	G	/// ENST00000330777 // downstream // 10262 // --- // --- // ---	-	p23.1
SNP_A-2270764	gacaggagattgaaaa[C/T]gcaaactgcttgagaa	C	T	118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA. /// NM_020226 // upstream // 106676 // Hs.373642 //	ANTXR2	ANTXR2, Homo sapiens anthrax toxin receptor 2 (ANTXR2), q21.21
SNP_A-2265602	gaagctaaatggacta[A/C]actgagcaatcctcgc	A	C	// 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 114110	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2263777	gaaccttccacaaggc[A/G]aacttagagaaaccct	A	G	79595 // Homo sapiens mSin3A-associated protein 130 (SAP130), mRNA. /// NM_020120 // upstream // 30375 //	SAP130	SAP130, Homo sapiens mSin3A-associated protein 130 (SAP130), q14.3
SNP_A-2260625	gaaaccagaagactac[A/G]gagaagacggcaaaaa	A	G	Homo sapiens KIAA0652 gene product (KIAA0652), mRNA. /// BC002378 // intron // 0 // Hs.410092 // KIAA0652 // 9776 //	KIAA0652	KIAA0652, Homo sapiens KIAA0652 gene product (KIAA0652), p11.2
SNP_A-2284152	gtggaactattttaga[C/G]agtaatttggcaatat	C	G	4734 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 4 (NEDD4), mRNA. /// NM_006154 // downstream // 113399 // Hs.1565 // NEDD4 //	NEDD4	NEDD4, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4 (NEDD4), q21.3
SNP_A-2244140	ctgctttcgtaaaata[A/T]gttcagatataaccaa	A	T	5046 // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 //	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-2241229	ctgaggagttggtttc[C/T]aacacgtgatctgacc	C	T	Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 2 (PLCXD2), mRNA. /// ENST00000312791 // intron // 0 // --- // --- // --- // ---	PLCXD2	PLCXD2, Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 2 (PLCXD2), q13.2
SNP_A-2299126	gcccggacaactagct[A/G]acactaactggccaca	A	G	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2298392	gccatttaaagccaca[A/G]ctgtttttaatgccaa	A	G	722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 24572 // Hs.527653 // DAF // 1604 // Homo sapiens decay	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2
SNP_A-2297031	gccaattagtagctac[A/G]ctgcttgatcctgagc	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2296051	gcattagcataataaa[A/G]ataacatatgggaaaa	A	G	27248 // Homo sapiens chromosome 2 open reading frame 30 (C2orf30), mRNA. /// NM_006794 // downstream // 27030	C2orf30	C2orf30, Homo sapiens chromosome 2 open reading frame 30 (C2orf30), p16.2
SNP_A-2308148	gcttgcatcatagcac[A/C]atttttaacttgcttt	A	C	IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. ///	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2065607	aatttagaaatatatc[C/G]agccttacatggccaa	C	G	221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 589108 //	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2051496	aagggtcagaattaga[G/T]gtagaggattattgat	G	T	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2092488	agaaagtggaagagaa[G/T]ccagcatgcgcaaaga	G	T	23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1997573	gaaagcattatactaa[A/G]tgtcctcaatggaagg	A	G	/// ENST00000333948 // upstream // 466285 // --- // --- // --- // -	-	q31.2
SNP_A-1991244	acattacaaaccacct[C/T]aattgatattgataga	C	T	-- /// ENST00000308105 // upstream // 23026 // --- // --- // --- //	-	q44
SNP_A-1993071	tagtatatccagggca[C/T]gagtgacacgtcagtc	C	T	// 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream //	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2220476	ccttctcatatcagga[C/T]gcaataaacatttgtt	C	T	/// ENST00000319719 // upstream // 282021 // --- // --- // --- // - -- /// ENST00000308537 // upstream // 58146 // --- // --- // --- //	-	p13
SNP_A-2143788	atgagacttcctaaca[C/T]tgattttagataactg	C	T	386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000331273 // upstream // 127977 // --- // --- // --- // --- ///	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13

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Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140381	atctcagtttttggaa[G/T]tatttttggaagcagg	G	T	HTR1A // 3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. ///	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.1
SNP_A-2151654	atgttggataatctag[A/C]aaaagtaagacaatta	A	C	// 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// AF106069 // upstream // 53181 // Hs.434951 // USP15 //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2154546	attattggtaactata[C/T]cacattcctgtgaatc	C	T	27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 563734 //	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2164498	caaaattccctagaag[C/G]cctaactttgttttgc	C	G	5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2270	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.2
SNP_A-2132359	atagtattgtaaatac[C/G]aggcaataggaatttt	C	G	FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream //	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2134220	atatgatgggaaatta[A/G]atgtcagctatactca	A	G	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2124095	agttacttatttctta[C/T]caatcctccctagctc	C	T	LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 //	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-1812277	gtggatctcccatgta[C/T]gtcacaggaaagagcc	C	T	200728 // Homo sapiens transmembrane protein 17 (TMEM17), mRNA. /// NM_015252 // upstream // 74079 //	TMEM17	TMEM17, Homo sapiens transmembrane protein 17 (TMEM17), p15
SNP_A-1800580	gtacttcttcccatga[A/G]attgctaagagaaatg	A	G	OR1L3 // 26735 // Homo sapiens olfactory receptor, family 1, subfamily L, member 3 (OR1L3), mRNA. /// NM_001005235	OR1L3	OR1L3, Homo sapiens olfactory receptor, family 1, subfamily L, member 3 (OR1L3), q33.2
SNP_A-1824316	taaacctaagaactga[C/T]gtttctgagcccattg	C	T	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1358059 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1820326	gtttagcacttttgtg[C/T]caaaataagtctgtgg	C	T	4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 2058237 // Hs.211225 // NOVA1 // 4857 // Homo	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1864439	tccacttgacaggcca[C/T]cttctctagagtttgg	C	T	// 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 332186 // Hs.115903 //	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1863678	tccaacgtatttcccc[A/G]cgctagattcacttag	A	G	LOC220929 // 220929 // Homo sapiens hypothetical protein LOC220929 (LOC220929), mRNA. /// NM_030751 //	LOC220929	LOC220929, Homo sapiens hypothetical protein LOC220929 (LOC220929), p11.22
SNP_A-1846005	tatatagctcattatc[C/T]gaccagtacaatttttt	C	T	// Homo sapiens alcohol dehydrogenase 1C (class I), gamma polypeptide (ADH1C), mRNA. /// NM_000668 // upstream //	ADH1C	ADH1C, Homo sapiens alcohol dehydrogenase 1C (class I), gamma polypeptide (ADH1C), q23
SNP_A-1852141	tattggtatcatcata[C/T]acatatcaaccttata	C	T	84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 224290 //	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-1909001	tgtatagtaactttca[C/T]gttgaggacaagtctc	C	T	Homo sapiens RNA polymerase I associated factor 53 (PAF53), mRNA. /// ENST00000259583 // intron // 0 // --- // ---	PAF53	PAF53, Homo sapiens RNA polymerase I associated factor 53 (PAF53), p13.2
SNP_A-1918588	ttaaatggcttgtgaa[A/T]tgtttttccacacca	A	T	Homo sapiens T, brachyury homolog (mouse) (T), mRNA. /// NM_175922 // downstream // 135065 // Hs.119062 //	T	T, Homo sapiens T, brachyury homolog (mouse) (T), q27
SNP_A-1914141	tgtgtgtgatcaacca[C/T]attggatatataaaag	C	T	50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 442830 // Hs.106015 // DDEF1 // 50807 // Homo	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-1897786	tgctggagaatcttca[A/G]gtaaatcacaagcagt	A	G	ENST00000319540 // intron // 0 // --- // --- // --- // ---	-	q21.22
SNP_A-1944396	ttgtctatgccgcatc[A/G]gaagggtagaaaagaa	A	G	7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1945527	ttgttccactatctta[A/G]cttattcttagacata	A	G	Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // --- // --- // --- // ---	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1988622	tgccttagcaagacac[A/T]atgtaaatgtattgaa	A	T	Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// ENST00000272005 // intron // 0 // --- // --- // --- // ---	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1987766	ctaaaacacgctgaac[A/C]gaaagctgaggggagt	A	C	sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA. /// ENST00000339290 // intron // 0 // ---	MYB	MYB, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), q23.3
SNP_A-1970330	ttgactcagaggtaaa[A/C]gctcccttgctcccaa	A	C	sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 2, mRNA. /// ENST00000357391 // intron // 0 // --- // --- // --- // --- ///	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 2, q22.2
SNP_A-1967289	aacatattgtccacac[A/G]gtaaagaagagagcat	A	G	Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // --- // --- // --- // ---	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1978675	gatgcagcctgaacca[C/T]ctaatcttcaggattt	C	T	171024 // Homo sapiens mRNA; cDNA DKFZp451G189 (from clone DKFZp451G189). /// NM_016599 // upstream // 13958 // Hs.381047 // MYOZ2 // 51778 // Homo sapiens	SYNPO2	SYNPO2, Homo sapiens cDNA DKFZp451G189 (from clone DKFZp451G189). q26
SNP_A-1937278	ttgaaaccgggttaag[C/G]ctccaacagcaccacc	C	G	Homo sapiens CGI-51 protein (CGI-51), mRNA. /// ENST00000350028 // intron // 0 // --- // --- // --- // ---	CGI-51	CGI-51, Homo sapiens CGI-51 protein (CGI-51), q13.31
SNP_A-1938275	ttgacctgagggcatc[A/G]caacttccttgttttc	A	G	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1949364	tttattattatactaa[A/G]acaactcttctctttt	A	G	// Homo sapiens spermatogenesis associated 5-like 1 (SPATA5L1), mRNA. /// ENST00000305560 // intron // 0 // ---	SPATA5L1	SPATA5L1, Homo sapiens spermatogenesis associated 5-like 1 (SPATA5L1), q21.1
SNP_A-1888218	tgagcgtggatttctc[A/C]atttattctgttagga	A	C	// Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 90636 // Hs.100057 // STK35 //	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13
SNP_A-1847686	tatctactggtttctg[C/G]aaatcacttaaggaag	C	G	/// ENST00000354196 // upstream // 260643 // --- // --- // --- // --- /// ENST00000355224 // upstream // 260643 // --- // --- // ---	-	q21.11
SNP_A-1852537	tatttagccatgaaac[C/T]ctcttgcaagaaatgt	C	T	84966 // Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000355895 // upstream //	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-1859178	tcagcgaatggaaaaa[A/T]caaagttatgttagct	A	T	Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // --- // --- // --- // --- /// ENST00000349908 // intron //	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-1796011	ggtggtgaaatatagc[A/G]gagactttggtgtctt	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1127519 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1660133	taaagcccactgtgggttatttatc[A/G]ctagaaacagagcagggtgcagaaa	A	G	3293 // hydroxysteroid (17-beta) dehydrogenase 3 /// NM_138497 // downstream // 127110 // Hs.336414 //	HSD17B3	HSD17B3 , rs2031321, hydroxysteroid (17-beta) dehydrogenase 3 ,q22.32
SNP_A-1642787	tgctttactaaaagagggatataca[C/T]tgtagctaaagtgttgccctttct	C	T	apolipoprotein H (beta-2-glycoprotein I) /// NM_002737 // upstream // 59201 // Hs.349611 // PRKCA // 5578 // protein	APOH	APOH , rs735866, apolipoprotein H (beta-2-glycoprotein I) ,q24.2
SNP_A-1751015	tgcctttccattacacacaataaaa[A/T]cctaagtctactgtggcccataatg	A	T	2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 16702 // Hs.279943 // LMCD1 // 29995 // LIM and	GRM7	GRM7 , rs9312021, glutamate receptor, metabotropic 7 ,p25.3
SNP_A-1782765	ggcagaagccatattg[A/C]atctctagtctgacat	A	C	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), mRNA. /// ENST00000330569 // intron // 0 // --- // --- // --- // ---	KCNQ3	KCNQ3, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), q24.22
SNP_A-2110813	aggactatcttacccc[C/T]ggaacttgtaggagtt	C	T	8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// NM_207492 // upstream // 248354 // --- // --- // 0 // --- /// ENST00000262992 //	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2122907	agtggctccttagaac[C/G]ccctctgggacaggtg	C	G	LOC283537 // 283537 // Homo sapiens hypothetical protein LOC283537 (LOC283537), mRNA. /// ENST00000266943 //	LOC283537	LOC283537, Homo sapiens hypothetical protein LOC283537 (LOC283537), q12.3
SNP_A-2167911	caaccttaaatctca[G/T]ctgtgcctcagtttta	G	T	7088 // Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), mRNA. /// ENST00000355495 // upstream // 157722 // --- // --- // --- // ---	TLE1	TLE1, Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), q21.32
SNP_A-2163399	ctgcagaaaggaccag[C/G]ctacgaagaccttatt	C	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2156270	atctagtgaacaaaa[A/T]ctgcctactggagatt	A	T	27020 // Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, mRNA. /// NM_012428 // upstream // 134384 // Hs.187866 // SDFR1 // 27020 // Homo	SDFR1	SDFR1, Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, q24.1
SNP_A-2159818	atttagttttcctcca[A/G]cgtgggcacttcagca	A	G	Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 //	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31
SNP_A-1997063	tccatctcacaggtca[C/T]gtacaaggtgaaatga	C	T	// 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 51432 // Hs.494312 //	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2034640	aaatgaaaattctcct[C/T]aaattgatccatagat	C	T	1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 //	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2028989	aaagaaaagggtacta[C/T]agctgcatgaatagaa	C	T	SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2024626	aaaaggtctgaaaggc[C/T]ataaacccagtgttga	C	T	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA. /// ENST00000332624 // intron // 0 // --- // --- // --- // ---	ALS2CR3	ALS2CR3, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), q33.1
SNP_A-2089998	acttctgttttggtaa[C/G]tggattacagttgatt	C	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086536	actgaaactaaatgaa[A/C]tcatctattggcaaca	A	C	6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 951375 // Hs.13640 //	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2086046	actctcaggaaagcaa[C/G]gttaaagcaagcaaaa	C	G	// Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, mRNA. /// NM_201994 // upstream // 2594 // Hs.6651 // VAMP4 // 8674 // Homo	VAMP4	VAMP4, Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, q24.3
SNP_A-2300344	gcctctctgaattgca[C/T]agatgtactcggatgc	C	T	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2290811	gcaagcttagggagac[C/G]gggaggacagatcctt	C	G	/// ENST00000288466 // upstream // 143998 // --- // --- // --- // --- /// ENST00000307730 // upstream // 295570 // --- // --- // ---	-	q32
SNP_A-2291566	gcacaaatatcagaac[A/G]acaaaattatcaagac	A	G	Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// ENST00000359025 // intron // 0 // --- //	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-2237638	ctctctctctctgtta[C/T]ctccttttttaaaaaca	C	T	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 //	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-2233202	ctcagctctggcttta[C/T]gcttttaacacaagtc	C	T	57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 865886 // Hs.435771 // API5 //	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2257955	ctttgtccacccatcc[C/T]gaaggtcattgaaagg	C	T	4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.3
SNP_A-2239911	ctgaacctttcctgct[C/T]acagtgtgtgggaaga	C	T	Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), mRNA. /// NM_014608 // intron // 0 // Hs.26704 //	CYFIP2	CYFIP2, Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), q11.2
SNP_A-2245428	ctgggaatgttataaa[C/G]ttgtgtccttataact	C	G	ENST00000302830 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2092418	agaaagggaaactgcc[A/G]aaaactgtacctccca	A	G	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2066787	acaaaaggttgagtga[C/T]gagttaatgtcacagt	C	T	Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 777336 // ---	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2076794	accaaaagaaaaggaa[A/G]tcatgaacgtatacat	A	G	1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream //	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2028580	aaactgcctagcataa[C/G]agttgaaaccacctct	C	G	6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. ///	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2001623	ggtattgactccagag[C/G]cagtcttttgttgttg	C	G	Homo sapiens deformed epidermal autoregulatory factor 1 (Drosophila) (DEAF1), mRNA. /// ENST00000317330 // intron // 0 // --- // --- // --- // -- /// ENST00000338675 // intron // 0 // ---	DEAF1	DEAF1, Homo sapiens deformed epidermal autoregulatory factor 1 (Drosophila) (DEAF1), p15.5
SNP_A-2003098	taaactgtattctgga[C/T]cataaacaaatcttaa	C	T	-- /// ENST00000355517 // downstream // 638579 // --- // --- //	-	q24.32
SNP_A-1990655	atagttctttctcata[A/G]acactgttagtttgtt	A	G	Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // --- // -	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-2012973	ctgagcctgagggaga[C/T]aaatgagggtcagcct	C	T	Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000323418 // intron // 0 // --- // --- //	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-2164512	caaaattgcaaattac[A/G]acaacagaagataaca	A	G	-- /// ENST00000354800 // downstream // 210601 // --- // --- //	-	q14.1
SNP_A-2148968	atggttattagttctc[A/C]agctagtccacactga	A	C	1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 186930 // --- // ---	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2138180	atccacagaagacagc[A/G]cctccaaccccagtca	A	G	ENST00000334919 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2116827	aggtctcatggaggta[A/G]ccagatattttccatt	A	G	EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 639027 // --- // --- // --- // ---	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2219105	cctgtagctttaagca[C/T]catatccccaaccttg	C	T	27136 // Homo sapiens microrchidia homolog (mouse) (MORC), mRNA. /// NM_138815 // downstream // 38949 //	MORC	MORC, Homo sapiens microrchidia homolog (mouse) (MORC), q13.13
SNP_A-2217009	cctctgttcgctcttc[G/T]cagataggtaattgtg	G	T	CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. ///	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2210358	cccccacagttcaaaa[C/G]tcgtcttctttctatc	C	G	Homo sapiens deubiquitinating enzyme DUB4 (DUB4), mRNA. /// NM_201402 // downstream // 98342 // Hs.531448	-	-, Homo sapiens deubiquitinating enzyme DUB4 (DUB4), p23.1
SNP_A-2209727	cccattcccaagattc[G/T]catcctttcccctgcc	G	T	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2197509	cattcctgtcttctac[A/G]ccatctgtaaattcct	A	G	199834 // Homo sapiens late cornified envelope 4A (LCE4A), mRNA. /// NM_178354 // upstream // 24032 // --- // LCE1F //	LCE4A	LCE4A, Homo sapiens late cornified envelope 4A (LCE4A), q21.3
SNP_A-2196150	catgtgctatgtaaca[A/G]gtgctatgaaaaatac	A	G	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 637958 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1675109	gttattatgtggcattattattaaa[C/T]gtgtgtgtattcatatatgtattaa	C	T	HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 142680 // Hs.129882 // IMPG1 //	HTR1B	HTR1B , rs1976106, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-1792041	gggtgggggtgattgg[A/C]agcccactggaacgat	A	C	27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 303684 // Hs.511605 //	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-1873764	tctcagatggttcaca[G/T]ggttctatgggaaaac	G	T	endogenous retrovirus env mRNA. /// NM_153377 // downstream // 4237 // Hs.253736 // LRIG3 // 121227 // Homo	-	-, Human endogenous retrovirus env q14.1
SNP_A-1831870	taattcttagaagaca[C/T]agcattggtttaagtc	C	T	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 603945 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1874371	tctccatcctagagac[A/G]gcagaaggacaaacat	A	G	ENST00000328043 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-1890718	tgatgaggacatattc[A/C]ctggtgtacactgtgc	A	C	Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 //	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1915425	tgttcccttattgttg[C/G]aaaatatgatgaacac	C	G	// 54839 // Homo sapiens hypothetical protein FLJ20156 (FLJ20156), mRNA. /// ENST00000260382 // downstream //	FLJ20156	FLJ20156, Homo sapiens hypothetical protein FLJ20156 (FLJ20156), q23
SNP_A-1915199	tgttcacactgtgtat[C/T]aagtctttttgcctaa	C	T	LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 //	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1960128	tttttaaaatgaacag[C/T]agaagctattcccata	C	T	// Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // --- // --- // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-1982240	tagaactgtggtggaa[A/T]ggatgtaaattaatag	A	T	Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000255189 // intron // 0 // --- // --- // --- // ---	DMGDH	DMGDH, Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, q14.1
SNP_A-1971655	tgctagccttccctcc[A/G]ataatctcagttgact	A	G	2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 455685 // Hs.475336 // GRM7 // 2917 // Homo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1982451	ttcagtgatggtcaaa[C/G]agaagtatttgacagt	C	G	MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 //	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-1989314	tctggctgaagataat[A/G]aagagtccacactaaa	A	G	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA. /// ENST00000265393 // intron // 0 // --- // --- // --- // ---	TAX1BP1	TAX1BP1, Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), p15.2
SNP_A-1950219	tttcagaaaaaattaa[A/G]tcacaccatggaagga	A	G	Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1936092	ttcttatcactaaaca[G/T]cattcaattttatgca	G	T	/// ENST00000360919 // upstream // 268650 // --- // --- // --- //	-	q13.1
SNP_A-1926186	ttattaagctccaaca[G/T]ctataggaaaaatata	G	T	// 9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// NM_173827 // downstream // 288851 // Hs.356697 // FLJ38991 //	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-1929925	ttcatgagaaaactca[A/G]tgaagagaaatgtgac	A	G	57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1356066 //	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-1875991	tctgaagcctacatca[C/G]acattgaagctatcgt	C	G	54558 // Homo sapiens spermatogenesis associated 6 (SPATA6), mRNA. /// NM_032785 // downstream // 2645 //	SPATA6	SPATA6, Homo sapiens spermatogenesis associated 6 (SPATA6), p33
SNP_A-1889538	ttacaaaaagattata[A/T]ccatttaagcccactt	A	T	57534 // Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), mRNA. /// NM_005257 // upstream // 25477 //	MIB1	MIB1, Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), q11.2
SNP_A-1884909	tgaatgaagtcaacac[A/G]gagcgaagcagagctg	A	G	-- /// ENST00000331540 // downstream // 513983 // --- // --- //	-	p25.3
SNP_A-1843470	tagtgataaaaagcta[A/G]ccctgattttcctagg	A	G	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1842957	tagtatatttgaatta[C/G]gatctaagtaagctcc	C	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // --- // --- // --- // ---	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1821305	gtttgcatctccagca[A/T]tacgtttcccaaggta	A	T	sapiens selectin E (endothelial adhesion molecule 1) (SELE), mRNA. /// ENST00000333360 // intron // 0 // --- // --- // --- // ---	SELE	SELE, Homo sapiens selectin E (endothelial adhesion molecule 1) (SELE), q24.2
SNP_A-1828466	taagcaattctctcaa[C/T]taccctgtaaagtcca	C	T	// Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 587347 // Hs.153952 // NT5E //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1867894	tcctactctattctta[C/G]cacccacgcagtgcat	C	G	952 // Homo sapiens CD38 antigen (p45) (CD38), mRNA. /// NM_005130 // downstream // 4978 // Hs.1690 // FGFBP1 //	CD38	CD38, Homo sapiens CD38 antigen (p45) (CD38), p15.32
SNP_A-1846712	tatcaaagatattgca[C/G]tcatgataactttgcc	C	G	// 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. ///	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1848537	tatgacacctgctggc[A/T]aggtaatattattccc	A	T	Homo sapiens monocyte to macrophage differentiation-associated 2, mRNA (cDNA clone IMAGE:5274201), partial cds. /// ENST00000258798 // intron // 0 // --- // --- // --- // ---	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2, (cDNA clone IMAGE:5274201), partial cds. p22.1
SNP_A-1795877	ggtgggaaattccaaa[A/G]tccaatcatcaaaaac	A	G	// 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 973801 // --- // --- // --- //	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1802642	gtatgaaagatatacc[C/T]aagcaccgaaaagaga	C	T	ENST00000356808 // intron // 0 // --- // --- // --- // ---	-	q12.1
SNP_A-1660499	ccctagttgcttcagtaatgtcctt[C/T]atagtgaaaagatccagttacgaac	C	T	26018 // leucine-rich repeats and immunoglobulin-like domains 1 /// NM_032505 // upstream // 38364 // Hs.116665	LRIG1	LRIG1 , rs726083, leucine-rich repeats and immunoglobulin-like domains 1 ,p14.1
SNP_A-1648334	ccactgtagattagttttgcctatc[C/T]aggaatttttaatgaatgaacagca	C	T	XPNPEP1 // 7511 // X-prolyl aminopeptidase (aminopeptidase P) 1, soluble /// NM_052918 // upstream // 2647219 // Hs.348923 // SORCS1 // 114815 // sortilin-related	XPNPEP1	XPNPEP1 , rs1931233, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble ,q25.1
SNP_A-1681868	aaccactgaaaagtatgtcctttaa[C/T]aaaagaagtctctaacttatgagaa	C	T	5000 // origin recognition complex, subunit 4-like (yeast) /// NM_018328 // upstream // 25294 // Hs.458312 // MBD5 //	ORC4L	ORC4L , rs1446553, origin recognition complex, subunit 4-like (yeast) ,q23.1
SNP_A-2183082	cagcaaaatacttgag[G/T]cctacccaggtgtgaa	G	T	ENST00000267067 // CDS // 0 // --- // --- // --- // ---	-	q13.1
SNP_A-2174253	cacactgacgaaggca[A/T]aataggagtaccagat	A	T	2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream //	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2209981	ccccaccagaaatgaa[A/T]gaaaatggccattgct	A	T	// 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 530997 // Hs.42650	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2200001	ccaaaggtgtggactt[A/T]aagcatttcaaggacc	A	T	sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE), mRNA. /// ENST00000337907 // intron // 0 // --- // ---	RERE	RERE, Homo sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE), p36.23
SNP_A-2118099	agtaaaatgcccttaa[C/T]gctctggccaaaccca	C	T	Homo sapiens netrin 1 (NTN1), mRNA. /// ENST00000173229 // intron // 0 // --- // --- // --- // ---	NTN1	NTN1, Homo sapiens netrin 1 (NTN1), p13.1
SNP_A-2123149	agtggtggtgaataga[A/G]ggatgtccatatttgt	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3398936 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2114579	agggaggccatagggc[A/G]ctctgaagttgcttgt	A	G	// 5567 // Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PRKACB), transcript variant 3, mRNA. /// NM_002731 // downstream // 28465 // Hs.487325 // PRKACB	PRKACB	PRKACB, Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PRKACB), transcript variant 3, p31.1
SNP_A-2138786	atccccctgtacctca[A/C]tctagctctctaaaat	A	C	79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream //	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.12
SNP_A-2016317	tcttaccatttaccca[A/G]attatctgaggatgtt	A	G	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 16144 // --- // --- // --- // --- ///	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. ,q21.1
SNP_A-2016990	aatgtggaagggagga[C/T]taggcttgctctgtgt	C	T	sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // intron // 0 // Hs.434980 // APP // 351 // Homo	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3
SNP_A-2003547	catgccttttaagac[C/T]acttttgtaagattat	C	T	// 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. ///	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1
SNP_A-2001010	ttcattcgagaggaga[C/T]acaatttttttccgag	C	T	// Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), mRNA. /// ENST00000277633 // intron // 0 // --- // --- // --- // ---	SLC39A12	SLC39A12, Homo sapiens solute carrier family 39 (zinc transporter), member 12 (SLC39A12), p12.33
SNP_A-2075665	acatggatcccgtcaa[A/C]atggttaattttatgt	A	C	/// ENST00000358493 // upstream // 232109 // --- // --- // --- // --- /// ENST00000329590 // downstream // 184848 // --- // --- // ---	-	p23.3
SNP_A-2066785	acaaaaggtgctggaa[C/T]aatcgattaaccttat	C	T	23492 // Homo sapiens chromobox homolog 7 (CBX7), mRNA. /// ENST00000216133 // upstream // 12128 // --- // ---	CBX7	CBX7, Homo sapiens chromobox homolog 7 (CBX7), q13.1
SNP_A-2062936	aatgtgtctcccttaa[C/T]ggtctccactggccac	C	T	23619 // Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /// NM_006210 // upstream // 238974 // Hs.201776 //	ZIM2	ZIM2, Homo sapiens zinc finger, imprinted 2 (ZIM2), q13.43

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2063648	aattacggtgaagaca[A/G]gaaaaatgggaaagag	A	G	145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 1065147 // --- // --- // --- // ---	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2049161	aagctaatctgtaagc[A/T]gagagttaaatttgtt	A	T	Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// ENST00000333447 // intron // 0 // --- // --- // --- // ---	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-2093063	agaacagcacttcacc[C/T]ctacttctcctactgt	C	T	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 49252 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2250285	cttagaatcaatccaa[C/T]ttgaaaatccatcccc	C	T	11059 // Homo sapiens WW domain containing E3 ubiquitin protein ligase 1 (WWP1), mRNA. /// NM_016033 //	WWP1	WWP1, Homo sapiens WW domain containing E3 ubiquitin protein ligase 1 (WWP1), q21.3
SNP_A-2268703	gaatgttattcctgga[A/G]caatacagtctcccct	A	G	// Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 182859 // Hs.98008 // GK2 // 2712	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-2272608	gacgcacaggctgtca[C/T]ggaaaaggtgccttcc	C	T	// Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 37229 // --- // --- // --- // ---	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2281945	gagtgcgtgttcttta[C/G]aatactgctgtaagag	C	G	4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 //	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22
SNP_A-2274334	gacttgtatatctcca[A/C]ctatgttatttgttaa	A	C	1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 338111 // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2298737	gcccagtactttcccc[C/T]ggactcctccatcaga	C	T	SDCCAG8 // 10806 // Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// NM_181690	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44
SNP_A-2295344	gcatcatccagaaata[C/G]cagctgttgtcatcgg	C	G	Homo sapiens KIAA0690 (KIAA0690), mRNA. /// ENST00000315563 // intron // 0 // --- // --- // --- // --- ///	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-2291593	gcacaacttgtgaaca[A/T]attgaaaccactgaat	A	T	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA. /// ENST00000262429 // intron // 0 // --- // --- // --- // ---	KIAA0703	KIAA0703, Homo sapiens KIAA0703 gene product (KIAA0703), q24.1
SNP_A-2294162	gcaggctccggagtta[C/T]atggcctaagttcaaa	C	T	3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15
SNP_A-2304420	gctctaaggagtaaga[C/T]agacaatgcctaccac	C	T	Homo sapiens uridine-cytidine kinase 2 (UCK2), mRNA. /// ENST00000271395 // intron // 0 // --- // --- // --- // ---	UCK2	UCK2, Homo sapiens uridine-cytidine kinase 2 (UCK2), q24.1
SNP_A-2273689	gactgcaggataataa[A/G]gcttatacactgtttc	A	G	Homo sapiens myosin IB (MYO1B), mRNA. /// ENST00000339514 // intron // 0 // --- // --- // --- // --- ///	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-2282328	gagttatttgctctga[C/T]cctaagtcatcaaaaa	C	T	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // --- ///	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2262458	gaaatgggaacacaat[G/T]atataaactacagtcc	G	T	// 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1655848 // ---	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2254977	cttggcggtcttccaa[A/G]ccttcatttattcata	A	G	/// ENST00000321014 // upstream // 29086 // --- // --- // --- // ---	-	p12.3
SNP_A-2227990	ctaccttgtgagatga[A/G]caatattatccccatg	A	G	Homo sapiens cartilage acidic protein 1 (CRTAC1), mRNA. /// ENST00000210816 // intron // 0 // --- // --- // --- // --- ///	CRTAC1	CRTAC1, Homo sapiens cartilage acidic protein 1 (CRTAC1), q24.2
SNP_A-2093773	agaagaggaaggtcat[A/C]atataaaatcataagc	A	C	142940 // Homo sapiens TruB pseudouridine (psi) synthase homolog 1 (E. coli) (TRUB1), mRNA. /// ENST00000281244 // downstream // 3438 // --- // --- // --- // --- ///	TRUB1	TRUB1, Homo sapiens TruB pseudouridine (psi) synthase homolog 1 (E. coli) (TRUB1), q25.3
SNP_A-2094789	agaatccagcaactag[A/G]aacttagtggcagttc	A	G	4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // upstream	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-2096516	agacctcctccaaagc[C/T]gatttgcagactaagc	C	T	sapiens THO complex 1 (THOC1), mRNA. /// ENST00000261600 // intron // 0 // --- // --- // --- // ---	THOC1	THOC1, Homo sapiens THO complex 1 (THOC1), p11.32
SNP_A-2100120	agagtggtactctata[C/T]ggctaggacatctgga	C	T	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 117648 //	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2087406	actgcatccttattaa[C/G]tatcctatcaagtaag	C	G	50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-2078266	accataaagtggagac[C/T]gaagccatcatatttg	C	T	283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream //	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-2078715	accattgagtttagca[A/G]acaaaacgccaacatt	A	G	// 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1345099 // Hs.514980 // SALL3	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2059424	aatctagaaaggcaac[A/C]aatatatcatagcata	A	C	Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // --- // --- // --- // ---	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2013083	agtgagaaaatgataa[C/T]gtcttcccatccaaga	C	T	ENST00000359770 // intron // 0 // --- // --- // --- // ---	-	p23.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2046485	aagagaggcagtagag[G/T]aacctttgtatgacca	G	T	9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2670106 //	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2041085	aacctaagcatttaga[A/G]gttttccttccagatt	A	G	3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 268075 //	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-2113958	aggcttcagtaggggа[A/G]aagtgtgacctggagc	A	G	// Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // --- // --- // --- // ---	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2221202	cctttaacacttcacc[C/T]ggtgaacttttccact	C	T	// 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream //	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2184730	actaagaaataatgaa[A/C]aagaaccacgtaggaa	A	C	267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 628142 //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2196257	catgtgtgatattcac[C/T]gaggcatgtccctgga	C	T	84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 85957 //	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-1700694	ataaaaatacaaataaaatatgaca[A/T]caatttccattgtgtaggtatcata	A	T	NM_017905 // intron // 0 // Hs.27337 // C13orf11 // 55002 // chromosome 13 open reading frame 11	C13orf11	C13orf11 , rs2490955, chromosome 13 open reading frame 11,q34
SNP_A-1657117	ctttttttattaatctggagagcaa[A/C]atgtcaggaggtaaagttttcagag	A	C	MAP2K4 // 6416 // mitogen-activated protein kinase kinase 4 /// NM_182567 // upstream // 91226 // Hs.376614 //	MAP2K4	MAP2K4 , rs237315, mitogen-activated protein kinase kinase 4 ,p12
SNP_A-1750413	aacactaatgggtaaaagtttatca[A/G]gaacagtacatttacatagttccaa	A	G	for OK/SW-CL.36, complete cds. /// NM_006168 // downstream // 34840 // Hs.347185 // NKX6-1 // 4825 // NK6	-	- , rs977463, MRNA for OK,q21.23
SNP_A-1717879	caccaggatataaaaccctttagac[C/T]aagaatcatgtatatatctttgcat	C	T	AB023177 // intron // 0 // Hs.23799 // KIAA0960 // 23249 // KIAA0960 protein	KIAA0960	KIAA0960 , rs10486144, KIAA0960 protein,p21.3
SNP_A-1801982	gtataaccaacataaa[G/T]atgccacgatttgaat	G	T	5550 // Homo sapiens prolyl endopeptidase (PREP), mRNA. /// NM_182907 // upstream // 141308 // Hs.436023 // PRDM1	PREP	PREP, Homo sapiens prolyl endopeptidase (PREP), q21
SNP_A-1851527	tattctacccgtaaga[A/C]gtccaggtcgttaatg	A	C	sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // --- // --- // --- // ---	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1853905	tcaaaaggcttatgta[A/T]aggagattctacggct	A	T	/// ENST00000310149 // downstream // 72408 // --- // --- // ---	-	q23.3
SNP_A-1864444	tccacttggcaatgaa[G/T]ggtgatgctgaaaata	G	T	sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // --- // --- // --- // ---	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.1
SNP_A-1885759	tgacagctgggtctga[C/T]gactcctctgttacac	C	T	// 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, mRNA. /// NM_012211 // upstream //	ITGA11	ITGA11, Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, q23
SNP_A-1895321	aggacaaactgactct[A/G]aagattccatcaaata	A	G	1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream //	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1911641	tgtgaaatctcctgaa[A/T]tgaattaaaatacaca	A	T	Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// ENST00000262113 // intron // 0 // --- // --- // --- // ---	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.3
SNP_A-1938050	ttgacaaaaggagtga[C/T]gggcagaattgcctgg	C	T	404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 16082 //	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-1943253	ttggtgccctttttata[A/G]gtgagaggcagtgtac	A	G	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1959070	ttttgaaagtgacgac[A/G]gaacaatgagtaggtg	A	G	7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1826573 // ---	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1960776	tttttctgtgtttcca[C/T]tatgtttcttcaaagc	C	T	/// ENST00000331195 // upstream // 11661 // --- // --- // --- // ---	-	q11.22
SNP_A-1977298	tctgccactgtgaacc[C/T]ccttctcacctcactc	C	T	POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2821871 // Hs.479808 // IGFBP7 //	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1969407	atcatatactgagaac[A/G]agcctgtaagcttcac	A	G	54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-1973056	taagaagaccgttgga[C/G]tatcacaagctaaaca	C	G	Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- // --- ///	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-1948641	tttataatagccactc[C/T]aactgggctgaaataa	C	T	56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 70857 // Hs.315186 // PCSK2 //	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-1952941	tttcttcatccataaa[A/G]tgggtataataacagt	A	G	Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), mRNA. /// ENST00000256194 // intron // 0 // --- // --	MICAL2	MICAL2, Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), p15.3
SNP_A-1930469	ttccaaagcaaagtta[C/T]gccagtgtgttcaaaa	C	T	79664 // Homo sapiens NMDA receptor-regulated gene 2 (NARG2), mRNA. /// NM_134261 // downstream // 4502 //	NARG2	NARG2, Homo sapiens NMDA receptor-regulated gene 2 (NARG2), q22.2
SNP_A-1902495	tggcctgaccatttca[C/T]accctctccctgttca	C	T	ENST00000354225 // intron // 0 // --- // --- // --- // ---	-	q26.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1881551	tctttcttcacactat[C/G]aagttaggcaaaataa	C	G	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4484962 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1863558	tccaaagtgcattctg[C/T]atatatgatactcctt	C	T	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // intron // 0 // Hs.478673 // IL1RAP // 3556 // Homo sapiens	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-1857155	tcacctcaaaaatata[A/T]ctttgtcagtttatgg	A	T	7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 146767 //	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-1788686	gggatgcttcagttaa[A/T]ccacattgttctacca	A	T	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1696882	gtttaagcagctctgctttttagga[C/G]aactcaatgtggctaggcttaaggg	C	G	B3GALT5 // 10317 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 /// NM_006198 // upstream // 69295 // Hs.80296 // PCP4 // 5121 // Purkinje cell	B3GALT5	B3GALT5 , rs462555, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 ,q22.2
SNP_A-1677404	tgttttgtgtttaaaacagtggaga[A/T]attgtagattcagaaagggagagct	A	T	3820 // killer cell lectin-like receptor subfamily B, member 1 /// U33834 // upstream // 157523 // Hs.447869 // - // 387832 //	KLRB1	KLRB1 , rs2058427, killer cell lectin-like receptor subfamily B, member 1 ,p13.31
SNP_A-2194679	catgcatttcaaaata[C/G]ccattgtatggcaaag	C	G	sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA. /// ENST00000276497 // intron // 0 // --- // --- // --- /// ENST00000359619 // intron // 0 // --- // --- // ---	LYN	LYN, Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), q12.1
SNP_A-2194361	catgatccaactgttc[A/G]cacaaaagggaggttg	A	G	57405 // Homo sapiens kinetochore protein Spc25 (Spc25), mRNA. /// NM_021176 // upstream // 280 // Hs.283963 //	Spc25	Spc25, Homo sapiens kinetochore protein Spc25 (Spc25), q24.3
SNP_A-2212287	ccctgggccacaggac[A/T]ctagcctttagctcgt	A	T	5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// NM_177399 // downstream // 56584 //	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-2113234	aggccctccttcatac[C/T]atacttgaaatataga	C	T	// 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4484580 // Hs.54642 // MAT2B // 27430 //	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2120392	agtcatgtcatgtaac[A/G]gtccctagagaaagcc	A	G	3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 142350 // Hs.377090 //	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2128374	ataagtgtttacagga[C/G]atgacccttggagtta	C	G	4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// NM_032028 // downstream // 40317 // Hs.519507	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-2142979	atgaatcatagctacc[A/G]aaattccctgtgtgat	A	G	23426 // Homo sapiens mRNA for GRIP1 protein. /// NM_018448 // upstream // 299381 // Hs.546407 // TIP120A //	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. q14.3
SNP_A-2150506	atgtgaccaagatcat[A/G]aagctctgattgacaa	A	G	TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 113909 // --- // --- // --- //	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-2161817	atttgtcatgtacata[C/T]agcacattgaccagaa	C	T	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA. /// ENST00000351718 // intron // 0 // --- // --- // --- // ---	NRCAM	NRCAM, Homo sapiens neuronal cell adhesion molecule (NRCAM), q31.1
SNP_A-2023419	ctttgctctgctgaga[A/C]ctgcccagaggggtta	A	C	sapiens Friend leukemia virus integration 1 (FLI1), mRNA. /// ENST00000344954 // intron // 0 // --- // --- // --- // ---	FLI1	FLI1, Homo sapiens Friend leukemia virus integration 1 (FLI1), q24.3
SNP_A-2002871	cacgatggcctaagtg[C/T]aactgtgaaggtttgg	C	T	9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream //	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1992566	ccaggctttagtaaaa[A/G]taatcagagcgttctg	A	G	23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 213818 // Hs.434255 // PSD3 //	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2052262	aagtaagcttagcaca[C/G]tcttacattaaatatg	C	G	137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 843217 // Hs.426324 // TUSC3 //	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2078496	accatcttcaccagta[G/T]aggtatttccccttga	G	T	7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 647124 // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2079660	accctagaccacagta[C/T]ccaagcttaggcagag	C	T	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2089681	acttccactctcaaaa[C/T]aaaagcaatctgttag	C	T	2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 131403 //	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-2229068	ctagccaagagctcca[C/T]gttcttaacgggaaag	C	T	10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// NM_005252 // upstream // 34028 //	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2235499	ctccgtaattagctca[A/C]gattttcccttctcct	A	C	175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2727471 // --- // --- // --- //	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2245086	gcagttagtctgttac[A/T]caattattcacaaagg	A	T	64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2305228	gctgagacacacaaaa[A/G]ctccatttgaactgca	A	G	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // --- ///	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2312022	ggacacactctcatga[C/T]gcaatctactgtaggt	C	T	64419 // Homo sapiens hypothetical protein FLJ22405 (FLJ22405), mRNA. /// NM_153635 // upstream // 618 //	FLJ22405	FLJ22405, Homo sapiens hypothetical protein FLJ22405 (FLJ22405), p25.3
SNP_A-2312116	ggacagaaaattctgg[A/G]atatccatgtaatatt	A	G	5912 // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA. /// ENST00000323534 //	RAP2B	RAP2B, Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), q25.2
SNP_A-2297823	gccaggggcacatcac[A/G]caatgagacacagcgg	A	G	ENST00000306140 // CDS // 0 // --- // --- // --- // ---	-	q21.3
SNP_A-2300117	gcctcatctattcccc[A/G]ctcaccagccttttct	A	G	120 // Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /// NM_016824 // downstream // 68817 //	ADD3	ADD3, Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, q25.2
SNP_A-2302172	gctaaacaaatgtcag[G/T]cattgttaagaatctc	G	T	// 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, mRNA. /// NM_012211 // upstream //	ITGA11	ITGA11, Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, q23
SNP_A-2307524	tcattgtaaatttttc[A/G]cttggctatgttgaac	A	G	55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 390892 // Hs.33368 // MCTP2 // 55784 //	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2244958	ctggcacatagcaggc[G/T]ctcaatatttcttgaa	G	T	Homo sapiens adenosine monophosphate deaminase (isoform E) (AMPD3), mRNA. /// D12775 // intron // 0 // Hs.501890 // AMPD3 // 272 // Homo sapiens ampd-3 mRNA	AMPD3	AMPD3, Homo sapiens adenosine monophosphate deaminase (isoform E) (AMPD3), p15.4
SNP_A-2244293	ctggaactctgcctga[A/G]acctagcaagcattgt	A	G	Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // --- // --- // --- // ---	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2252172	cttccatgtcaaatca[A/C]acttacttcctagagg	A	C	// 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 307321 // Hs.407755 //	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-2237098	ctctcaagctctctca[A/G]taagaacataaattga	A	G	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA. /// ENST00000234392 // intron // 0 // --- // --- // --- // ---	VAX2	VAX2, Homo sapiens ventral anterior homeobox 2 (VAX2), p13.3
SNP_A-2264056	gaactctaagctcagg[A/G]aacctagcggggtca	A	G	256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), mRNA. /// NM_007214 // downstream	SCML4	SCML4, Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), q21
SNP_A-2078589	accatggctaccctta[A/G]acccctcgtgaagccc	A	G	/// ENST00000355553 // upstream // 257784 // --- // --- // --- // --- /// ENST00000358223 // upstream // 257784 // --- // --- // ---	-	q25.1
SNP_A-2081770	accttctcccttcgag[A/G]aatgtgtcatccaaac	A	G	4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream //	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-2050567	aaggattgaggtaaca[G/T]gttggacagatagata	G	T	51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 63622 // Hs.491997 // EYA1	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3
SNP_A-1996451	caatgctcagtgggga[C/G]attttcagtggatttg	C	G	// 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1994354	ccaccttcgcaccaac[A/G]ctgtccactgggctat	A	G	sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), mRNA. /// ENST00000302190 // intron // 0 // --- // --- // --- // ---	SDC2	SDC2, Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), q22.1
SNP_A-2010400	ttaattgttggattca[A/T]atatgtccatatggcc	A	T	10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// NM_012180 // downstream // 501243 // Hs.76917 // FBXO8 //	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-2025809	aaaatggactcgtaca[C/G]caggcattattacttt	C	G	/// ENST00000358431 // upstream // 91746 // --- // --- // --- // ---	-	q11.23
SNP_A-2162903	attttggtagccagaa[C/T]aagttacactgccaag	C	T	Homo sapiens zinc finger protein 285 (ZNF285), mRNA. /// ENST00000330997 // intron // 0 // --- // --- // --- // ---	ZNF285	ZNF285, Homo sapiens zinc finger protein 285 (ZNF285), q13.31
SNP_A-2157929	attgctgacgcaataa[A/G]tgagtggaaggataag	A	G	28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 259348 // --- // --- // --- // ---	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2146286	atgctacttttcccga[C/T]gtgtaggttcatggga	C	T	NM_005530 // intron // 0 // Hs.546262 // IDH3A // 3419 // Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299518 // intron // 0 // --- // --- // --- // ---	IDH3A	IDH3A, Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, q25.1
SNP_A-2133682	atatcatttccatctc[A/T]cacatgaaacatgttg	A	T	399 // Homo sapiens ras homolog gene family, member H (RHOH), mRNA. /// NM_017581 // upstream // 31706 //	RHOH	RHOH, Homo sapiens ras homolog gene family, member H (RHOH), p14
SNP_A-2200818	ccaagatagtcctgga[C/T]aataccacttggattc	C	T	83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 68610 //	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2203075	ccactgcactttagcc[A/G]ccctactgcactccag	A	G	11074 // Homo sapiens tripartite motif-containing 31 (TRIM31), transcript variant 1, mRNA. /// NM_052816 // upstream // 3695 // Hs.493275 // TRIM31 // 11074 // Homo	TRIM31	TRIM31, Homo sapiens tripartite motif-containing 31 (TRIM31), transcript variant 1, p21.33
SNP_A-2201715	ccacaagaaattgttg[C/T]aataaaatgcttcatg	C	T	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 841102 // --- // ---	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2197152	cattcaacaaaaccaa[C/T]cgacacaagcacaatc	C	T	// 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1644230	ctgcatgcatgattaattgagacaa[A/T]cattccatttaactaatatttgagg	A	T	NM_152996 // intron // 0 // Hs.85618 // SIAT7C // 256435 // sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C	SIAT7C	SIAT7C , rs1486932, sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C,p31.1
SNP_A-1801269	gtagcttatagatccc[C/T]caggctctgaccagcc	C	T	3925 // Homo sapiens stathmin 1/oncoprotein 18 (STMN1), transcript variant 1, mRNA. /// NM_005563 // upstream //	STMN1	STMN1, Homo sapiens stathmin 1,p36.11
SNP_A-1808010	gtcttccttgttccaa[C/T]tgaagatataaattgc	C	T	// 79577 // Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), mRNA. /// NM_003783 // upstream //	HRPT2	HRPT2, Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), q31.2
SNP_A-1848840	tatgatgtgtccatca[A/G]agagctcttgcagttc	A	G	54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 77243 // Hs.365690 // KCNK10 //	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-1826030	taaatgtacatcaaca[A/G]tcagacagcttccaga	A	G	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 633508 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1825520	taaatactttagaaga[C/T]gcaagttgttatttgg	C	T	ENST00000207157 // intron // 0 // --- // --- // --- // ---	-	p12
SNP_A-1876969	tctgcctctctcttcc[A/G]aactcaagcttcctct	A	G	6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 670265 // Hs.114412 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1889574	tgagttttgatctgga[C/T]gttttgttctgcgatg	C	T	10920 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, mRNA. /// NM_006710 // downstream // 83667 // Hs.531713 // COPS8 // 10920 //	COPS8	COPS8, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, q37.3
SNP_A-1946188	tttaaaaaacatccca[C/T]tgactacaaatggatg	C	T	// 7518 // Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, mRNA. /// NM_003401 // downstream // 113000 // Hs.171190 // XRCC4 // 7518	XRCC4	XRCC4, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, q14.2
SNP_A-1963925	acacggcatcagtaaa[A/G]tcctccagtggttccc	A	G	// 10905 // Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA. /// NM_017709 // upstream //	MAN1A2	MAN1A2, Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN1A2), p12
SNP_A-1983142	gcagagggaacacaac[C/T]gaactcagatctgctg	C	T	-- /// ENST00000329863 // downstream // 108544 // --- // --- // ---	-	q23.1
SNP_A-1937485	ttgaacaggttgctaa[A/G]gctctatgagtctcaa	A	G	FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1937337	ttgaaaggaatttgta[C/G]gccattagtttagccc	C	G	Homo sapiens fidgetin (FIGN), mRNA. /// ENST00000333129 // intron // 0 // --- // --- // --- // ---	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1954348	tttgcaggattctaca[C/G]cttattttatcaaaat	C	G	7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1532138 // Hs.197320 // TLE1 // 7088 //	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1949151	tttatgctgtaaatca[C/T]tcatcttgtcttttg	C	T	7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-1956379	tttgttagtgcctaca[A/G]ctcttagatagtggaa	A	G	3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N,	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-1955486	tttggtccattagaaa[C/G]aaaataacccatccat	C	G	FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1826264	taaattgagcacttta[C/T]atacattttctcttct	C	T	55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 975327 // Hs.473082 // ZFP64 // 55734 // Homo	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1830707	taatcctccataatgg[A/G]aataaaccacaaagct	A	G	// Homo sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// NM_053036 // upstream // 216277 //	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-1859158	tcagccttataatcaa[C/T]gttcagtagttatttt	C	T	// 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 353596 // --- // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1855619	tcaataatgattgaaa[A/G]aggattgtttgtagtt	A	G	57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 210490 // --- // ---	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-1809965	gtgagttcctacacaa[A/G]atagaaccacaagagg	A	G	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // intron // 0 //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.2
SNP_A-1791806	gggtgacaacaatcac[C/T]ggtgtggagagggaaa	C	T	54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream //	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1791917	ggggtgcagggttaaat[A/G]agaactcacatttctg	A	G	10047 // Homo sapiens cystatin 8 (cystatin-related epididymal specific) (CST8), mRNA. /// NM_080610 // downstream //	CST8	CST8, Homo sapiens cystatin 8 (cystatin-related epididymal specific) (CST8), p11.21
SNP_A-1790433	ggggcaagcgtaaaga[C/G]ctgagacaaaaaagtt	C	G	SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. ///	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1728459	ttttatttttcccctcagtaagact[G/T]taccattcatcattacaggaaaaga	G	T	NM_022063 // intron // 0 // Hs.11859 // C10orf84 // 63877 // chromosome 10 open reading frame 84	C10orf84	C10orf84 , rs722525, chromosome 10 open reading frame 84,q26.11
SNP_A-1756737	aactgagacttacttaatacagtcc[A/G]gcaaagcagaactggataaaagcct	A	G	// cAMP responsive element binding protein 5 /// NM_175061 // upstream // 60280 // Hs.368944 // JAZF1 // 221895 //	CREB5	CREB5 , rs10486580, cAMP responsive element binding protein 5 ,p15.1
SNP_A-1780661	ggatcactgaaaaaaa[C/T]taaatgtgtggcttgc	C	T	80854 // Homo sapiens SET domain-containing protein 7 (SET7), mRNA. /// NM_002413 // upstream // 44495 //	SET7	SET7, Homo sapiens SET domain-containing protein 7 (SET7), q31.1
SNP_A-2198967	catttgctctccccac[C/T]gaacaaagggattgca	C	T	/// ENST00000306733 // upstream // 38612 // --- // --- // --- // ---	-	q13.3
SNP_A-2174955	cacagggtgaaaggaa[C/T]gtgcctgctaagggtg	C	T	Homo sapiens chromosome 5 open reading frame 12 (C5orf12), mRNA. /// ENST00000329637 // intron // 0 // --- // ---	C5orf12	C5orf12, Homo sapiens chromosome 5 open reading frame 12 (C5orf12), q14.1
SNP_A-2178644	cactctgccatccaga[C/T]gctagtgtcgcagggg	C	T	Homo sapiens regulator of G-protein signalling 3 (RGS3), transcript variant 2, mRNA. /// NM_134427 // intron // 0 //	RGS3	RGS3, Homo sapiens regulator of G-protein signalling 3 (RGS3), transcript variant 2, q32
SNP_A-2203254	ccacttcatgaaagcc[A/G]ctgcagctcaagaagg	A	G	Homo sapiens mRNA for KIAA0293 gene, partial cds. /// ENST00000261726 // intron // 0 // --- // --- // --- // ---	CUTL2	CUTL2, Homo sapiens for KIAA0293 gene, partial cds. ,q24.12
SNP_A-2211894	ccctctttatacaagt[A/G]acggtcttatcatcaa	A	G	Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA. /// ENST00000327680 // intron // 0 // --- // --- // --- // ---	FLJ20641	FLJ20641, Homo sapiens hypothetical protein FLJ20641 (FLJ20641), q23.2
SNP_A-2224432	cgtagatggccacata[A/C]atttacaatatgatac	A	C	2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 235575	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2227654	ctacatgagcccaaaa[C/G]actgtgcatttaatgc	C	G	Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// ENST00000281221 // intron // 0 // --- // --- // --- // ---	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2111919	aggatctaaccacgca[C/T]tcactatgcattcaac	C	T	Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00000340079 // intron // 0 // --- // --- // --- // ---	COL4A1	COL4A1, Homo sapiens collagen, type IV, alpha 1 (COL4A1), q34
SNP_A-2108864	agcttaaagtctatca[G/T]aacataagacattcca	G	T	Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// ENST00000281437 // intron // 0 // --- // --- // --- // ---	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2142761	agctctcaacatgtga[A/G]gggacctgaagcaggt	A	G	// 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2024960	aaaataaatgtaaaac[C/T]gatctcaaaaagctgt	C	T	2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA.	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease,q33.1
SNP_A-2030144	aaagcaacttcttaga[A/G]attatcaaacacagag	A	G	3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 229667 // Hs.118695 // KCNG1	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2045128	aagaagacagtaatta[C/T]ccaacagcataacaca	C	T	401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // ---	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2065647	aatttagtaaacttga[A/G]aatccttctagaattg	A	G	// Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), mRNA. /// NM_022918 // upstream // 44969 // Hs.188591 //	FZD4	FZD4, Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), q14.2
SNP_A-2101743	agatgcccaaatgaat[A/G]atcaggtgaacacact	A	G	// Homo sapiens solute carrier family 13 (sodium-dependent citrate transporter), member 5 (SLC13A5), mRNA. /// ENST00000293800 // intron // 0 // --- // --- // --- // ---	SLC13A5	SLC13A5, Homo sapiens solute carrier family 13 (sodium-dependent citrate transporter), member 5 (SLC13A5), p13.1
SNP_A-2102912	agcaaaataaatcagg[A/T]ccagaaagataaatac	A	T	10739 // Homo sapiens ret finger protein-like 2 (RFPL2), mRNA. /// NM_014227 // downstream // 22345 // Hs.130101	RFPL2	RFPL2, Homo sapiens ret finger protein-like 2 (RFPL2), q12.3
SNP_A-2271700	gaccagcatatccaca[C/T]acctgctacacccctg	C	T	Homo sapiens F-box protein 21 (FBXO21), transcript variant 2, mRNA. /// NM_033624 // intron // 0 // Hs.159699 // FBXO21	FBXO21	FBXO21, Homo sapiens F-box protein 21 (FBXO21), transcript variant 2, q24.22
SNP_A-2270614	gacagatgataagtcc[A/G]agatgtcacgtctcat	A	G	81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 421711 // Hs.465407 // NETO1 // 81832 // Homo	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2267213	gaatacagtcatcaca[A/G]gcggtagacaggcaat	A	G	// 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 280414 // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.32
SNP_A-2279788	gaggccatggttgcta[C/G]gcagctggttcagaac	C	G	ALS2CR7 // 65061 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7 (ALS2CR7), mRNA. /// NM_003507 // upstream // 25209 //	ALS2CR7	ALS2CR7, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7 (ALS2CR7), q33.1
SNP_A-2241362	catcaggtatgttcaa[A/G]atggtgacaagaagga	A	G	6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream //	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238554	ctctgtctacacaaac[A/G]gatcagaggattcagg	A	G	Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// ENST00000320658 // intron //	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2252886	cttctatgtcaccaga[A/C]gttaactatggcatct	A	C	ENST00000339713 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-2256188	ctttagaagtttgaac[C/T]catcattgtacaagtg	C	T	/// ENST00000314100 // upstream // 23501 // --- // --- // --- // ---	-	p13.3
SNP_A-2253986	cttgacttttgctcca[C/T]cactcccctgaaatag	C	T	11269 // Homo sapiens DEAD (Asp-Glu-Ala-As) box polypeptide 19 (DDX19), mRNA. /// NM_018332 // upstream	DDX19	DDX19, Homo sapiens DEAD (Asp-Glu-Ala-As) box polypeptide 19 (DDX19), q22.1
SNP_A-2254071	cttgaggcaaatccaa[C/T]tgagttccttcattcc	C	T	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2290226	gcaaatttgaataatc[C/T]aggctaaactaatctc	C	T	10666 // Homo sapiens CD226 antigen (CD226), mRNA. /// NM_173630 // downstream // 34981 // Hs.31931 // RTTN //	CD226	CD226, Homo sapiens CD226 antigen (CD226), q22.2
SNP_A-2307620	gcttcataaccctgga[C/T]gtattcactaactccc	C	T	Homo sapiens misshapen/NIK-related kinase (MINK), transcript variant 2, mRNA. /// NM_015716 // intron // 0 //	MINK1	MINK1, Homo sapiens misshapen,p13.2
SNP_A-2230376	ctatattggtcctctc[C/T]ccatgctgttttacac	C	T	// 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 306246	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-2273725	gactgctaatcgtaca[A/G]tatttcttcttgaagt	A	G	131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream //	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2100969	agatattgaattttca[C/G]ctgggtcatacctgct	C	G	10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream //	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2106801	agcctgtcatactagg[C/G]acttttatctcacaca	C	G	5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-2105533	agccaattatttctca[A/G]tctcataaccattatt	A	G	63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 816661	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2046757	aagaggaagaggacta[C/T]taaaattaccaagaag	C	T	Homo sapiens golgi-specific brefeldin A resistance factor 1 (GBF1), mRNA. /// ENST00000286983 // intron // 0 // --- // ---	GBF1	GBF1, Homo sapiens golgi-specific brefeldin A resistance factor 1 (GBF1), q24.32
SNP_A-2046695	aagagctcatgggcca[C/T]gttaaggcgctcagat	C	T	// Homo sapiens Lutheran blood group (Auberger b antigen included) (LU), mRNA. /// NM_002856 // upstream // 22817 //	LU	LU, Homo sapiens Lutheran blood group (Auberger b antigen included) (LU), q13.31
SNP_A-2028533	aaactgataaaagggc[A/T]cacatcaggagaacgt	A	T	1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 335514 // Hs.166109 // ELAVL2 //	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2030430	aaagccatcagtgata[C/T]gatgtgggttcttcat	C	T	// Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// ENST00000342303 // intron // 0 // --- // --- // --- // ---	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1991153	tctattttgcatgtgg[A/C]aggcttactgggatca	A	C	25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 444878 // Hs.31968 // POT1 // 25913 // Homo	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-2160248	atttcacctctctttc[C/T]agttctatgtttttcta	C	T	/// ENST00000360991 // downstream // 808664 // --- // --- // ---	-	q12.1
SNP_A-2156086	attcgctatagatgcc[A/C]aaatctgcttagcctg	A	C	Homo sapiens importin 11 (IPO11), mRNA. /// ENST00000325324 // intron // 0 // --- // --- // --- // ---	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1
SNP_A-2161427	atttgccattggtgtg[G/T]acttagaatgtttcca	G	T	CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2131460	atagatttccagatac[C/T]gcgaggttattcctgt	C	T	lectomedin-3 (LEC3) mRNA, complete cds. /// NM_015236 // intron // 0 // Hs.411097 // LPHN3 // 23284 // Homo sapiens	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-2216164	cctccctcattctcaa[G/T]gactttggaaatttaa	G	T	Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// ENST00000260197 // intron // 0 // --- // --- // --- // ---	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q23.3
SNP_A-2199432	catttttaaattgctc[C/T]cttattgtgtagtcca	C	T	DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 69136 // Hs.335933 // MGC33530	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-2192139	catcagaaaatctaaa[C/T]aagctcagaatccaaa	C	T	// 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream //	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1750451	caatcagttcagtttgaatggatca[C/T]ggaattctgagtcaattcttgattt	C	T	NM_017868 // intron // 0 // Hs.288772 // TTC12 // 54970 // tetratricopeptide repeat domain 12	TTC12	TTC12 , rs10502172, tetratricopeptide repeat domain 12,q23.1
SNP_A-1749161	aaccccagcaggtgactctaatgca[A/C]atgatctataaatcacactttgaga	A	C	NM_004540 // downstream // 64982 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	NCAM2	NCAM2 , rs2739352, neural cell adhesion molecule 2,q21.1
SNP_A-1680560	ataactttcacttgactttcatttc[C/T]atgccaataagttcattctagtaat	C	T	NM_004540 // downstream // 63853 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	NCAM2	NCAM2 , rs236063, neural cell adhesion molecule 2,q21.1
SNP_A-1809701	gtgagctagaaattta[C/G]aattatacagaattga	C	G	4908 // Homo sapiens neurotrophin 3 (NTF3), mRNA. /// NM_020373 // downstream // 45494 // Hs.148970 //	NTF3	NTF3, Homo sapiens neurotrophin 3 (NTF3), p13.31

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1810815	gtgcagctttgtatat[A/T]aagtgatttctctgtg	A	T	220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. ///	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1814557	gtgtgcttgactaaga[A/G]actgaaatgtcagcat	A	G	3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream //	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-1806462	gtcgccttccactcca[A/G]gagaaccacaacccca	A	G	Homo sapiens cat eye syndrome chromosome region, candidate 5 (CECR5), transcript variant 1, mRNA. /// NM_033070 // intron // 0 // Hs.26890 // CECR5 // 27440 //	CECR5	CECR5, Homo sapiens cat eye syndrome chromosome region, candidate 5 (CECR5), transcript variant 1, q11.1
SNP_A-1870218	tcctttcattttccat[A/G]aacacgtggtgagacc	A	G	27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000356814 // downstream // 125898 // --- // --- // --- //	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1832330	taatttttcaaggagg[C/T]caactattttgcaaca	C	T	sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // --- // --- // --- // ---	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-1842141	taggggaacctgttgg[A/G]acccatagcttttgtc	A	G	MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1960376	tttttagtttttgag[A/G]atcttctacagagttt	A	G	// 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1394424 // Hs.504908 // LMO3 // 55885 // Homo	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1948704	tttatagataagacca[A/T]agccagtagctgtaaa	A	T	28957 // Homo sapiens mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, mRNA. /// NM_005079 // downstream // 5498 // Hs.368433 //	MRPS28	MRPS28, Homo sapiens mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, q21.13
SNP_A-1950801	tttcatttttatcaca[A/G]tgctagatgctacctg	A	G	Homo sapiens C-type lectin-like receptor-1 (CLEC1), mRNA. /// ENST00000315330 // intron // 0 // --- // --- // --- // ---	CLEC1A	CLEC1A, Homo sapiens C-type lectin-like receptor-1 (CLEC1), p13.2
SNP_A-1940642	ttgcctgacacagaga[C/G]gtaacaggttgagtga	C	G	// 6559 // Homo sapiens solute carrier family 12 (sodium/chloride transporters), member 3 (SLC12A3),	SLC12A3	SLC12A3, Homo sapiens solute carrier family 12 (sodium,q13
SNP_A-1966317	aattaattgagcaaaa[C/G]attatcagtggatgct	C	G	23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // upstream // 287728 // --- // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-1875867	tctgaaaataagcaaa[C/T]gagaaaagacaatagg	C	T	137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 //	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1878772	tctgttgcagccttta[C/T]gctaaacagagctaag	C	T	C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 //	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1922928	ttagatttctagtaca[A/C]cttgctaattggatta	A	C	Homo sapiens UBX domain containing 2 (UBXD2), mRNA. /// ENST00000272638 // intron // 0 // --- // --- // --- // ---	UBXD2	UBXD2, Homo sapiens UBX domain containing 2 (UBXD2), q21.3
SNP_A-1921768	ttactaagttagggga[C/T]agataaggcaaacatt	C	T	ENST00000296328 // intron // 0 // --- // --- // --- // ---	-	q29
SNP_A-1877394	tctggagcaaatgaaa[C/G]agtcaaccaaactgta	C	G	// 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 111241 // Hs.98367 //	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-1884464	tgaagtgatggtatca[A/G]cagactgtggtaaatt	A	G	MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// NM_031415 //	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1893390	tgcagccagcatttaa[A/T]atagtgtgtttttctc	A	T	/// ENST00000356128 // upstream // 256680 // --- // --- // --- // -	-	q24
SNP_A-1987866	aaaaaggacctattaa[C/T]gattaagcaattgtat	C	T	Homo sapiens RALBP1 associated Eps domain containing 1 (REPS1), mRNA. /// ENST00000258062 // intron // 0 // --- // ---	REPS1	REPS1, Homo sapiens RALBP1 associated Eps domain containing 1 (REPS1), q24.1
SNP_A-1938347	ttgactatagcatgga[C/T]taaaatgggatgcaat	C	T	ATP6V0D2 // 245972 // Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), mRNA. /// NM_138817 // downstream // 31877	ATP6V0D2	ATP6V0D2, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), q21.3
SNP_A-1843780	tagtgtttgtagatca[C/G]agattttattttcttt	C	G	375096 // Homo sapiens FLJ44670 protein (FLJ44670), mRNA. /// NM_152257 // upstream // 77693 // Hs.460807 //	FLJ44670	FLJ44670, Homo sapiens FLJ44670 protein (FLJ44670), q11.23
SNP_A-1837586	tacttgtattatccta[C/T]atttgaccacagatag	C	T	9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 392656 // --- // --- // --- // -	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-1827166	taaccgaaaaagcata[C/T]gtaatcctctctgtca	C	T	55031 // Homo sapiens ubiquitin specific protease 47 (USP47), mRNA. /// ENST00000250515 // upstream // 33350	USP47	USP47, Homo sapiens ubiquitin specific protease 47 (USP47), p15.3
SNP_A-1815374	gtgtttcttaaatctc[C/T]gagagcaacatattca	C	T	Homo sapiens stonin 2 (STN2), mRNA. /// ENST00000267540 // intron // 0 // --- // --- // --- // ---	STN2	STN2, Homo sapiens stonin 2 (STN2), q31.1
SNP_A-1847887	tatctctgtggtacgt[G/T]aagattttcaagaagt	G	T	Homo sapiens transient receptor potential cation channel, subfamily M, member 7 (TRPM7), mRNA. /// ENST00000313478 // intron // 0 // --- // --- // --- // ---	TRPM7	TRPM7, Homo sapiens transient receptor potential cation channel, subfamily M, member 7 (TRPM7), q21.2
SNP_A-1809216	gtgacctcagtagaca[A/C]tgattttagccactgt	A	C	Homo sapiens hypothetical protein FLJ38993 (FLJ38993), mRNA. /// ENST00000272133 // intron // 0 // --- // --- // --- // ---	CNIH3	CNIH3, Homo sapiens hypothetical protein FLJ38993 (FLJ38993), q42.12

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1742973	caggcttcgaagccccttcattaca[C/G]attgacacgagtgctcccagaattg	C	G	NM_153697 // intron // 0 // Hs.11571 // LOC91526 // 91526 // hypothetical protein DKFZp434D2328	LOC91526	LOC91526 , rs10497803, hypothetical protein DKFZp434D2328,q33.1
SNP_A-1782592	ggcacctggaacccac[A/G]caaccttgctctgggg	A	G	LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 //	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-1782024	ggcaaataggtataaa[C/G]tgcacgacaggcaagc	C	G	/// ENST00000336930 // upstream // 1497164 // --- // --- // --- //	-	p14.3
SNP_A-2191956	catcaatatttacttc[A/G]aagagtgatttttccaa	A	G	64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // upstream // 336800 // --- // --- // --- //	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2175137	cacagtggatgcagac[C/T]aagctggatcccgaga	C	T	Homo sapiens mRNA for AIE-75, complete cds. /// ENST00000344020 // intron // 0 // --- // --- // --- //	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-2133896	atatctctaacaatta[C/T]cgaaatcagtaaaaca	C	T	Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA. /// ENST00000302271 // intron // 0 // --- // --- //	HNRPR	HNRPR, Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), p36.12
SNP_A-2136500	atcaccatcctagagc[A/G]aaaaatttcacattag	A	G	// 9585 // Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA. /// ENST00000260753 // downstream	MPHOSPH1	MPHOSPH1, Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), q23.31
SNP_A-2130433	atactatagattggtc[C/T]cgtggctagtataaaa	C	T	3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1232354 // --- // --- // ---	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2111609	aggagtatgtaatgta[C/G]ggagaatgctctgaag	C	G	LOC283537 // 283537 // Homo sapiens hypothetical protein LOC283537 (LOC283537), mRNA. /// ENST00000266943 //	LOC283537	LOC283537, Homo sapiens hypothetical protein LOC283537 (LOC283537), q12.3
SNP_A-2122894	agtggcgtgacttcca[C/T]gttgactacatttag	C	T	// 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1177018	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2159706	atttaggcaaccacgc[A/G]atctcacattctgtct	A	G	Homo sapiens NIMA (never in mitosis gene a)-related kinase 6 (NEK6), mRNA. /// ENST00000238356 // intron // 0 // --- // ---	NEK6	NEK6, Homo sapiens NIMA (never in mitosis gene a)-related kinase 6 (NEK6), q33.3
SNP_A-2149235	atgtaagctggtggcgg[A/G]cagccagagaaatagc	A	G	// Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB //	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-2149517	atgtagcactgggccd[A/G]gacaaggttgatggtg	A	G	Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /// NM_018070 // intron // 0 // Hs.175551 //	SSBP3	SSBP3, Homo sapiens single stranded DNA binding protein 3 (SSBP3), p32.3
SNP_A-1992433	gctgcaaacagaaaga[C/T]gatgaaagttatccca	C	T	4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 //	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22
SNP_A-1994188	ctctggcttcactaac[C/T]agttctttgatccttt	C	T	4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 862389 // Hs.546267 // MMP16	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-1999065	tcctcaattgtttcag[C/T]acgatttggtagcat	C	T	// 54518 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), mRNA. /// NM_014317 // upstream // 44081 // Hs.546357 //	APBB1IP	APBB1IP, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), p12.1
SNP_A-2009046	atggatccattcaaac[A/G]cacaaatgtggaaagt	A	G	54554 // Homo sapiens WD repeat domain 5B (WDR5B). mRNA. /// NM_002264 // downstream // 4482 // Hs.161008 //	WDR5B	WDR5B, Homo sapiens WD repeat domain 5B (WDR5B), q21.1
SNP_A-2037516	aacaaccccatcaaaaa[A/C]gtcagtgaaggatatg	A	C	1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream //	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2106246	agccccttctggaaa[C/T]taggctctctggatag	C	T	// Homo sapiens T-cell leukemia/lymphoma 1A (TCL1A), mRNA. /// ENST00000216612 // upstream // 1134 // --- // --- //	TCL1A	TCL1A, Homo sapiens T-cell leukemia,q32.13
SNP_A-2078934	acccaatgtttagatg[C/T]cactcatttttaaaa	C	T	ENST00000355698 // intron // 0 // --- // --- // --- /// ENST00000354349 // intron // 0 // --- // --- // ---	-	p13.3
SNP_A-2068179	acaagacttatgcacc[A/G]aaaactacaacacact	A	G	4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 798113 // Hs.98849 // DNCL2B //	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-2069927	acacaggacgtataaa[A/G]caaaaacacaaittta	A	G	TMEM45A // 55076 // Homo sapiens hypothetical protein FLJ10134 (FLJ10134), mRNA. /// NM_032787 // upstream //	TMEM45A	TMEM45A, Homo sapiens hypothetical protein FLJ10134 (FLJ10134), q12.2
SNP_A-2074823	acatcaaagtattaaa[C/G]tgcttcactgaattgt	C	G	5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 3454807 //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2070597	acacctgttcaatttta[C/T]ggtaatgatttgtaga	C	T	6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2051782	aaggtccaggtaacca[G/T]gtcccaagattgtatc	G	T	Homo sapiens emopamil binding protein-like (EBPL), mRNA. /// ENST00000242827 // intron // 0 // --- // --- // ---	EBPL	EBPL, Homo sapiens emopamil binding protein-like (EBPL), q14.2
SNP_A-2277042	gagatgacttgatac[C/T]gatatgtgatttgatt	C	T	MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 1078094 // Hs.314261 //	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q31.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282195	gagtgttctgagcaga[A/G]gagggacttgatccag	A	G	Homo sapiens calcium channel, voltage-dependent, P/Q type, alpha 1A subunit (CACNA1A), transcript variant 2,	CACNA1A	CACNA1A, Homo sapiens calcium channel, voltage dependent, P,p13.13
SNP_A-2270523	gacagactctacttga[A/G]ctttgcaaatacaaaa	A	G	23312 // Homo sapiens rabconnectin-3 (RC3), mRNA. /// NM_013243 // upstream // 2017 // Hs.232618 // SCG3 //	DMXL2	DMXL2, Homo sapiens rabconnectin-3 (RC3), q21.2
SNP_A-2251944	cttcatttcttttaaa[A/G]attggggatcaggaag	A	G	C14orf118 // 55668 // Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // downstream // 106812 // Hs.410231 //	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-2312214	ggacaggagtcttttc[C/G]attgtgcagggaagta	C	G	341405 // Homo sapiens hypothetical protein DKFZp686O1689 (DKFZp686O1689), mRNA. ///	ANKRD33	ANKRD33, Homo sapiens hypothetical protein DKFZp686O1689 (DKFZp686O1689), q13.13
SNP_A-2310881	ccagtaatggtgatcc[C/T]ctcaaacaggcaaaaa	C	T	140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 82747 // Hs.31845 // ASB7 //	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3
SNP_A-2290053	gcaaagttctaatgaa[A/C]gatttgagaagagaaaa	A	C	-- /// ENST00000355517 // downstream // 612574 // --- // --- //	-	q24.32
SNP_A-2300907	gcctgtctagggaaca[A/G]tagccagggctcaagt	A	G	1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream //	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-2291849	gcacaggcttatataa[C/T]ggtaaaagagaaataa	C	T	PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 395630 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2312259	ggacagtgtttgatga[C/T]attaaaaaggtaggct	C	T	sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-2304847	gctcttatggggctca[C/T]attacagtaagccaat	C	T	2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// NM_173675 // downstream // 167559 //	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1
SNP_A-2305707	gctgccatgactctcc[A/G]ccattgctcatgctat	A	G	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 //	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone ,p23.1
SNP_A-2256282	ctttagggtatgaatg[C/T]aactttgctgtatgac	C	T	8321 // Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), mRNA. /// NM_006980 // downstream // 205536 //	FZD1	FZD1, Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), q21.2
SNP_A-2244320	ctggaagatgaggaaa[A/G]ctagtagtgtaattca	A	G	C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2265223	gaagatttttaccttc[A/T]acaaactaagtatgaa	A	T	1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // upstream //	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2265113	gaagatgaatgtaacc[A/G]agtatctgccttcaaa	A	G	ENST00000284717 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2260954	gaaagaaaaagacata[A/G]aaggctaccaaataga	A	G	1910 // Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, mRNA. /// NM_003991 // upstream //	EDNRB	EDNRB, Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, q22.3
SNP_A-2281096	gagtaatgttctatac[A/C]ctaagccatgcaattt	A	C	Homo sapiens non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (NME7), transcript variant 1, mRNA. /// NM_197972 // intron // 0 // Hs.274479 // NME7 //	NME7	NME7, Homo sapiens non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (NME7), transcript variant 1, q24.2
SNP_A-2062331	aatgtaaacagggtta[C/T]gtgcactgtgcatgtc	C	T	// Homo sapiens deleted in azoospermia-like (DAZL), mRNA. /// ENST00000250863 // upstream // 17503 // --- // --- // --- // ---	DAZL	DAZL, Homo sapiens deleted in azoospermia-like (DAZL), p24.3
SNP_A-2079905	acccttactctgggct[A/G]aaactatcattcaatt	A	G	624 // Homo sapiens bradykinin receptor B2 (BDKRB2), mRNA. /// NM_000710 // upstream // 12817 // Hs.525572 //	BDKRB2	BDKRB2, Homo sapiens bradykinin receptor B2 (BDKRB2), q32.2
SNP_A-2093205	agaaccaggctccagt[C/T]aatacagaatcttatt	C	T	3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 13980 // Hs.36975 // FSHB // 2488	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-2092774	agaaatgtaaatccac[A/G]ggtaatatgaaagaat	A	G	5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002736 // upstream // 126714 // Hs.433068 // PRKAR2B // 5577 //	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-2047648	aagatgtttaccaagc[C/T]aacttgtcaattttaa	C	T	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2030249	aaagcagaaagcccaa[A/G]tcagacagtgaatcag	A	G	Homo sapiens SLAC2-B (SLAC2-B), mRNA. /// ENST00000265843 // 3UTR // 0 // --- // --- // --- // --- ///	SLAC2-B	SLAC2-B, Homo sapiens SLAC2-B (SLAC2-B), q22.3
SNP_A-2000215	atgtcttgtgtagagg[A/G]aacagctgctttcagt	A	G	1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// NM_001001688 // downstream // 30297 //	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2005412	tataacagtttcaaaa[A/G]ccaaataaacaagatg	A	G	DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 1356612 //	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2149810	atgtatttgtcaggag[A/G]aatcacattggctgtt	A	G	// 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // downstream // 305148 //	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2152320	attaaattgtgttagg[A/C]aatggaaaggaagagg	A	C	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2148852	atggtggaaagctaga[A/C]agatgatgtagaacat	A	C	23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // upstream // 275919 // --- // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-2148675	atggtatttttccttc[A/G]aggctcaacccaaaca	A	G	220032 // Homo sapiens GDPD domain containing protein (LOC220032), mRNA. /// ENST00000315938 // intron // 0 // ---	LOC220032	LOC220032, Homo sapiens GDPD domain containing protein (LOC220032), q13.5
SNP_A-2160506	atttccagacctgtgg[A/G]acgtaaaaggtgaagg	A	G	58491 // Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), mRNA. /// ENST00000328070 // downstream //	ZNF71	ZNF71, Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), q13.43
SNP_A-2161674	atttgggttgagacac[A/G]gagccaaatgatatca	A	G	160418 // Homo sapiens SMILE protein (SMILE), mRNA. /// NM_003994 // downstream // 260939 // Hs.1048 // KITLG //	SMILE	SMILE, Homo sapiens SMILE protein (SMILE), q21.32
SNP_A-2128091	ataagccagaatgtaa[C/T]agtagcttaaaataat	C	T	650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 396315 // Hs.193640	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2181047	cagacacaagcacata[A/C]taggtggttccattta	A	C	4869 // Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA. /// NM_199185 // downstream // 5790 // Hs.519452 // NPM1 //	NPM1	NPM1, Homo sapiens nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), q35.1
SNP_A-2219327	cctgtgagctgcatga[C/G]tagggaaagctctctg	C	G	Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- // --- ///	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2212841	ccctttcatttctcaa[C/T]gctttctccacaattt	C	T	LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 //	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2200769	ccaagagcacatctgc[A/C]agaagtcatgtcaatg	A	C	84465 // Homo sapiens MEGF11 protein (MEGF11), mRNA. /// NM_133375 // upstream // 4261 // Hs.446251 // MGC4562	MEGF11	MEGF11, Homo sapiens MEGF11 protein (MEGF11), q22.31
SNP_A-1783003	ggcagccaaatcaact[C/G]aacccctgtcctcaca	C	G	Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // intron // 0 // --- // --- // --- // ---	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1724638	tagactagcattttgatctttctcc[A/G]cagtgagttgacaattattcaaaga	A	G	COMMD9 // 29099 // COMM domain containing 9 /// NM_174902 // downstream // 5444 // Hs.205865 //	COMMD9	COMMD9 , rs10501147, COMM domain containing 9 ,p13
SNP_A-1646410	tttaaagacagcatgttacatttac[A/G]acaagtttgaggacacataacatct	A	G	NM_002214 // intron // 0 // Hs.355722 // ITGB8 // 3696 // integrin, beta 8	ITGB8	ITGB8 , rs10486392, integrin, beta 8,p21.1
SNP_A-1794097	ggtcagctgccaggtc[A/G]gacacctctccctcca	A	G	Homo sapiens FLJ43486 protein (FLJ43486), mRNA. /// ENST00000339192 // CDS // 0 // --- // --- // --- // ---	FLJ43486	FLJ43486, Homo sapiens FLJ43486 protein (FLJ43486), q24.31
SNP_A-1855560	tcaagttttagtaaaa[C/T]gatgcttgatgactta	C	T	Homo sapiens non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (NME7), transcript variant 1, mRNA. /// NM_197972 // intron // 0 // Hs.274479 // NME7 //	NME7	NME7, Homo sapiens non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (NME7), transcript variant 1, q24.2
SNP_A-1861030	atggaatctaaaggaa[C/T]tgtaaagtcattaaaa	C	T	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 966793 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-1861641	ttgacataagacaata[C/T]gcgtccaaccacaaga	C	T	84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 210450 // Hs.153504 // TOM1L1	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-1823363	taaaagactgatgaca[C/G]tgaagattggtaagga	C	G	9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 874339 // --- // ---	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1951048	tttccagttctgtgaa[G/T]tatctaaatgatagtt	G	T	285671 // Homo sapiens hypothetical protein LOC285671 (LOC285671), mRNA. /// ENST00000296615 // downstream	RNF180	RNF180, Homo sapiens hypothetical protein LOC285671 (LOC285671), q12.3
SNP_A-1978527	atacagcagtataaac[A/C]accatatctgcacaac	A	C	5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 714606 // Hs.92282 // PITX2 // 5308 // Homo	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1901858	tggcagagtccaaaga[A/C]ctgttttcagcctaga	A	C	/// ENST00000354800 // downstream // 671572 // --- // --- // ---	-	q14.1
SNP_A-1884242	tgaaggatgtatttttg[A/C]aggtagtgattcctgt	A	C	sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-1932514	ttcctggcgttgggct[C/T]acctggagacttttttc	C	T	Homo sapiens topoisomerase (DNA) III beta (TOP3B), mRNA. /// ENST00000215840 // intron // 0 // --- // --- // --- // ---	TOP3B	TOP3B, Homo sapiens topoisomerase (DNA) III beta (TOP3B), q11.22

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1926944	ttatttcctcattctc[A/G]cttctattggaaaaat	A	G	214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1927250	ttcaaaaagtattgca[A/G]gaactcagaaggtaga	A	G	55338 // Homo sapiens hypothetical protein FLJ11292 (FLJ11292), mRNA. /// NM_002890 // upstream // 22323 //	FLJ11292	FLJ11292, Homo sapiens hypothetical protein FLJ11292 (FLJ11292), q14.3
SNP_A-1908432	tgtagaagccctgagc[A/G]gcaaatagaagctttc	A	G	57864 // Homo sapiens thymic stromal co-transporter (TSCOT), mRNA. /// NM_003408 // downstream // 90185 //	TSCOT	TSCOT, Homo sapiens thymic stromal co-transporter (TSCOT), q32
SNP_A-1918481	ttaaatatgctaattc[A/G]ccactacaatttaaaa	A	G	5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1965324	tactattgataataaa[G/T]cctcatttgtatcagt	G	T	130576 // Homo sapiens hypothetical protein LOC130576 (LOC130576), mRNA. /// ENST00000280115 // intron // 0 // ---	LOC130576	LOC130576, Homo sapiens hypothetical protein LOC130576 (LOC130576), q23.2
SNP_A-1944746	ttgtgatttggaacaa[C/T]atgaatgaacctggag	C	T	ENST00000318973 // intron // 0 // --- // --- // --- // ---	-	q14.3
SNP_A-1821672	gtttgttgcaaaattg[C/T]acaatgtaacctccac	C	T	Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 2725703 // --- // -	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1838623	tagacaagaggcttca[C/T]cacagatttttcctgg	C	T	1373 // Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), mRNA. /// NM_005235 // downstream	CPS1	CPS1, Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), q34
SNP_A-1834846	taccatatctcagaga[A/G]ggaagcagtcagggaa	A	G	7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 26586 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1786674	ggcttggaataagttg[G/T]aaacttctgatggaaa	G	T	// 160777 // Homo sapiens hypothetical protein MGC39827 (MGC39827), mRNA. /// ENST00000326763 // downstream //	MGC39827	MGC39827, Homo sapiens hypothetical protein MGC39827 (MGC39827), q24.23
SNP_A-1786252	ggctgtatgaggaaaa[C/T]ttaaaaactataatga	C	T	// 5265 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran /// NM_001002236 // upstream // 42231 // Hs.525557 // SERPI	SERPINA1	SERPINA1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran q32.13
SNP_A-1659344	gtagcttcattctctctaagcttaa[A/T]cttgaaactcaccatccaaagtatt	A	T	RAB28 // 9364 // RAB28, member RAS oncogene family /// NM_005114 // upstream // 290348 // Hs.40968 // HS3ST1 //	RAB28	RAB28 , rs4361405, RAB28, member RAS oncogene family ,p15.33
SNP_A-1666790	ctatatattttgaacaatataaaac[A/G]attcaaaaatgtatgtgtgagatgc	A	G	NM_018374 // upstream // 294948 // Hs.396358 // FLJ11273 // 54664 // hypothetical protein FLJ11273	FLJ11273	FLJ11273 , rs6946775, hypothetical protein FLJ11273,p21.3
SNP_A-1661968	aagtttcatctagaaacaagcataa[A/T]gaccaagtaacatgaccagtgggca	A	T	POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 4065975	POLR2B	POLR2B , rs6827711, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-1683170	ttaattcagtttcctcctttgattc[A/G]agaacatctgaaacattgttttcta	A	G	RAB28 // 9364 // RAB28, member RAS oncogene family /// NM_005114 // upstream // 286382 // Hs.40968 // HS3ST1 //	RAB28	RAB28 , rs10488986, RAB28, member RAS oncogene family ,p15.33
SNP_A-1689600	tacattctgactattagctccatca[C/T]gatattgaaattgctctcttgaatg	C	T	NM_016230 // upstream // 48885 // Hs.5741 // NCB5OR // 51167 // NADPH cytochrome B5 oxidoreductase	-	- , rs1570843, - ,q14.2
SNP_A-1699281	atctttcacatcttagttgaatcaa[C/T]gtcctcagtaatagaaaactgtctt	C	T	54875 // chromosome 9 open reading frame 39 /// NM_152576 // upstream // 465518 // - // - // - // -	C9orf39	C9orf39 , rs1856558, chromosome 9 open reading frame 39 ,p22.2
SNP_A-1706491	agttagctattgtcttcatcaccta[C/T]agctccgtggagctattcattgtat	C	T	4604 // myosin binding protein C, slow type /// NM_152323 // downstream // 48239 // Hs.511791 // SPIC // 121599 // Spi-C	MYBPC1	MYBPC1 , rs950792, myosin binding protein C, slow type ,q23.2
SNP_A-1730731	tctctggagcagtgattcatgtaac[A/T]ccagtataagaatcacctttagaca	A	T	NM_003467 // upstream // 519561 // Hs.421986 // CXCR4 // 7852 // chemokine (C-X-C motif) receptor 4	CXCR4	CXCR4 , rs10496751, chemokine (C-X-C motif) receptor 4,q21.3
SNP_A-2203318	ccacttgtgacctgat[A/G]agaagagtcaattctg	A	G	7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 717831 // Hs.21975 // CNTNAP5 // 129684 //	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2118978	agtagaagataatgaa[A/G]tcaataaacgaagcag	A	G	ENST00000354422 // intron // 0 // --- // --- // --- // ---	-	q24.1
SNP_A-2162349	attttattatagcagg[C/G]caagtggactaagata	C	G	552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 343222 //	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2163953	caaaactgcaaactta[A/G]taaattagggatagaa	A	G	60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// NM_020348 // upstream // 52141 // Hs.274579 // CNNM1 //	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2000554	agcctagttgtgaata[C/G]ctgttacacctttctc	C	G	PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1408169 // --- // --- // ---	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2013199	tttctataaagagtgg[A/C]aatctttcttctgtgg	A	C	Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// ENST00000284538 // intron // 0 // --- // --- // --- // ---	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1
SNP_A-2012976	atcttggcagacaact[A/T]actgtaaaattccaac	A	T	Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // ---	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2014856	aagaatgtccccatag[A/C]acttcgagccatattt	A	C	// 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 //	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2041894	aactaactatcctaat[A/C]aaaaaggaagagcttt	A	C	Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33

Table 1

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2042826	aactctggtcatttaa[A/G]aacaaatacatttcaa	A	G	Homo sapiens cyclin T2 (CCNT2), transcript variant a, mRNA. /// NM_058241 // intron // 0 // Hs.292754 // CCNT2 // 0 // --- // --- // ---	CCNT2	CCNT2, Homo sapiens cyclin T2 (CCNT2), transcript variant a, q21.3
SNP_A-2084099	actagccaggagaaaa[C/G]ctgtgactgaagaaac	C	G	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// ENST00000342389 // intron // 0 // --- // --- // ---	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-2090554	acttgtctggctatcc[G/T]cacacaatagtttgat	G	T	6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 350933 // Hs.221127	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-2059254	aatccttcctaacaga[A/G]cctgtatacgtgttat	A	G	27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 416208 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. ///	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-2051619	aaggtaatcacttata[A/C]attgttctgacatg	A	C		BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2262783	gaaatttctatacctc[A/G]aatggtacaatgaatg	A	G	Homo sapiens leukotriene A4 hydrolase (LTA4H), mRNA. /// ENST00000228740 // intron // 0 // --- // --- // ---	LTA4H	LTA4H, Homo sapiens leukotriene A4 hydrolase (LTA4H), q23.1
SNP_A-2249101	ctgtttctcaaaacat[A/G]aatgtcatagactagt	A	G	56897 // Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, mRNA. /// NM_020135 // upstream // 52893 // Hs.236828 // WRNIP1 // 56897 // Homo // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 320977 // Hs.89576 // IMMP2L // 83943 // Homo sapiens	WRNIP1	WRNIP1, Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, p25.2
SNP_A-2254663	cttgctgtttggaaac[C/T]cttctgacctctactt	C	T		DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2081399	C	C	192	182	234	166	4.008	0.0453	rs3737628	1	1755094	p36.33
SNP_A-1919019	G	G	388	14	341	29	6.948	8.40E-03	rs9786963	1	1791188	p36.33
SNP_A-2278444	C	C	393	1	382	10	7.515	6.10E-03	rs6603797	1	1797745	p36.33
SNP_A-2223642	C	C	405	15	390	28	4.209	0.0402	rs7511905	1	1825948	p36.33
SNP_A-1856955	G	A	213	205	237	181	4.916	2.66E-02	rs6603803	1	1844850	p36.33
SNP_A-1642581	C	C	383	21	377	37	4.34	3.72E-02	rs10492941	1	2910120	p36.32
SNP_A-1978484	C	C	323	47	319	71	4.383	3.63E-02	rs10489588	1	2974991	p36.32
SNP_A-1858853	C	C	390	18	375	37	6.838	8.90E-03	rs4308918	1	3142886	p36.32
SNP_A-2098079	C	C	269	151	305	113	7.723	5.50E-03	rs6687835	1	3260331	p36.32
SNP_A-2049610	C	C	338	72	365	51	4.579	3.24E-02	rs2821041	1	3427384	p36.32
SNP_A-1953724	G	G	254	160	207	185	6.007	1.42E-02	rs6703035	1	3755939	p36.32
SNP_A-1997922	A	A	254	118	282	94	4.158	4.14E-02	rs17404435	1	3789443	p36.32
SNP_A-2288864	T	T	409	7	419	1	4.602	3.19E-02	rs10915495	1	3940106	p36.32
SNP_A-2176838	T	T	314	36	300	60	6.18	0.0129	rs4400585	1	4093158	p36.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2202358	G	G	218	174	248	148	4.011	4.52E-02	rs4654492	1	4112188	p36.32
SNP_A-2254182	T	T	202	176	234	144	5.549	1.85E-02	rs9426494	1	4116661	p36.32
SNP_A-2211019	T	C	203	177	206	174	4.427	3.54E-02	rs4654426	1	4242156	p36.32
SNP_A-1784353	C	C	329	33	326	52	3.917	4.78E-02	rs7418164	1	4290891	p36.32
SNP_A-1924023	C	C	302	94	335	71	4.792	0.0286	rs496925	1	4306925	p36.32
SNP_A-2035185	C	C	374	10	409	3	4.354	3.69E-02	rs12043606	1	4370635	p36.32
SNP_A-2299722	A	A	282	82	310	58	5.417	1.99E-02	rs664520	1	4433730	p36.32
SNP_A-2004332	C	C	337	17	338	34	5.225	0.0223	rs350165	1	4475057	p36.32
SNP_A-2303721	C	C	328	34	321	57	5.545	1.85E-02	rs17348734	1	4489101	p36.32
SNP_A-2072682	C	C	177	175	192	134	5.06	2.45E-02	rs241238	1	4497892	p36.32
SNP_A-2149899	C	C	368	30	401	15	6.021	0.0141	rs10915551	1	4497968	p36.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2104217	C	C	347	13	322	24	3.928	4.75E-02	rs12403290	1	4592905	p36.32
SNP_A-1999854	G	G	294	126	266	154	4.2	4.04E-02	rs2101195	1	4607673	p36.32
SNP_A-2297571	G	G	305	81	270	112	7.089	7.80E-03	rs7533451	1	4616304	p36.32
SNP_A-2120497	G	G	301	93	327	61	7.68	5.60E-03	rs3947662	1	4628924	p36.32
SNP_A-1873908	T	T	404	12	396	26	5.195	2.26E-02	rs4448488	1	4703027	p36.32
SNP_A-1822227	A	A	403	11	403	3	4.494	3.40E-02	rs1886110	1	4896679	p36.32
SNP_A-1910067	C	C	340	70	368	50	4.364	3.67E-02	rs2411956	1	4896843	p36.32
SNP_A-1809821	A	A	233	167	205	195	3.956	4.67E-02	rs12049256	1	4905399	p36.32
SNP_A-1871192	G	G	372	42	354	64	4.993	2.54E-02	rs7541612	1	4958997	p36.32
SNP_A-1667950	A	A	378	26	398	14	4.037	4.45E-02	rs4475768	1	4982363	p36.32
SNP_A-2281828	C	C	293	103	323	75	5.861	0.0155	rs10915336	1	5048039	p36.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282669	T	T	279	39	262	66	7.324	6.80E-03	rs6681359	1	5111105	p36.32
SNP_A-2078896	A	A	308	38	303	19	5.519	1.88E-02	rs10915375	1	5160870	p36.32
SNP_A-1827498	C	C	299	69	285	97	4.799	2.85E-02	rs7418357	1	5405783	p36.31
SNP_A-2050915	A	A	288	62	235	79	5.485	1.92E-02	rs7515958	1	5538116	p36.31
SNP_A-2271384	C	C	404	16	390	30	4.508	3.37E-02	rs1695621	1	5615494	p36.31
SNP_A-2088032	T	T	242	164	266	134	4.11	4.26E-02	rs1295101	1	5990434	p36.31
SNP_A-1755914	G	G	369	27	389	15	3.877	4.90E-02	rs10489536	1	6089833	p36.31
SNP_A-1676650	A	A	298	94	268	130	7.331	6.80E-03	rs1396904	1	6605831	p36.31
SNP_A-1836468	G	G	241	163	275	135	4.827	2.80E-02	rs277686	1	6682163	p36.31
SNP_A-2096412	G	G	333	27	320	46	5.155	2.32E-02	rs11122129	1	6742943	p36.31
SNP_A-1899466	T	T	376	14	355	29	5.79	0.0161	rs1542899	1	6787621	p36.31
SNP_A-2231290	G	G	239	155	276	112	9.538	0.002	rs6657847	1	6861789	p36.31
SNP_A-2200438	C	C	353	27	333	43	4.219	4.00E-02	rs6655933	1	6873794	p36.31
SNP_A-1884194	C	C	337	23	310	38	4.613	3.17E-02	rs10399866	1	6879796	p36.31
SNP_A-2146553	A	A	391	5	414	0	5.26	0.0218	rs11120837	1	7076079	p36.31
SNP_A-1922613	A	A	254	106	285	79	5.702	1.69E-02	rs4908612	1	7256426	p36.23
SNP_A-1915177	C	C	281	61	254	84	4.988	2.55E-02	rs1149332	1	7463112	p36.23
SNP_A-2298623	T	T	374	16	375	33	5.496	1.91E-02	rs4908473	1	7665996	p36.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1806560	G	A	218	138	186	180	10.603	1.10E-03	rs3011926	1	7672065	p36.23
SNP_A-1794435	C	C	331	57	355	33	7.24	7.10E-03	rs697680	1	7775815	p36.23
SNP_A-1691698	T	T	237	165	270	138	4.51	3.37E-02	rs4350217	1	8082082	p36.23
SNP_A-2171736	A	A	294	70	276	104	6.871	8.80E-03	rs6683603	1	8207443	p36.23
SNP_A-1780483	C	C	220	166	251	139	4.41	3.57E-02	rs6577499	1	8546370	p36.23
SNP_A-1892754	G	G	283	83	311	63	3.974	4.62E-02	rs809972	1	9168629	p36.22
SNP_A-1912444	A	A	317	63	310	94	5.47	1.94E-02	rs9660890	1	9432379	p36.22
SNP_A-2286423	C	C	331	27	309	9	7.415	6.50E-03	rs4073710	1	9590061	p36.22
SNP_A-1750171	C	C	362	6	382	26	11.005	9.00E-04	rs10492968	1	9509709	p36.22
SNP_A-2270634	G	G	385	3	368	10	4.023	4.49E-02	rs17034615	1	10246143	p36.22
SNP_A-1948295	G	G	283	129	315	95	6.868	8.80E-03	rs3748578	1	10355184	p36.22
SNP_A-1717751	G	A	222	180	215	199	4.182	4.08E-02	rs67969	1	10458743	p36.22
SNP_A-2298739	G	G	378	8	367	27	10.396	1.30E-03	rs2480782	1	10527562	p36.22
SNP_A-2021932	T	T	237	105	180	140	12.074	5.00E-04	rs12045923	1	10578095	p36.22
SNP_A-2281771	A	A	310	58	305	83	3.947	0.047	rs1292657	1	10827347	p36.22
SNP_A-2176916	C	C	285	91	325	67	5.938	1.48E-02	rs12085319	1	10963744	p36.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2291726	T	T	363	7	379	1	4.713	2.99E-02	rs3765897	1	11008848	p36.22
SNP_A-2261658	T	T	407	7	409	1	4.486	3.42E-02	rs17036421	1	11150262	p36.22
SNP_A-1911729	T	G	190	148	164	150	4.649	3.11E-02	rs10159458	1	11468319	p36.22
SNP_A-2309196	G	G	273	133	293	105	3.922	4.77E-02	rs1534989	1	11695769	p36.22
SNP_A-1781313	A	A	269	125	310	98	5.93	0.0149	rs6667720	1	11765881	p36.22
SNP_A-1852165	G	G	189	157	219	115	8.482	3.60E-03	rs4845882	1	11777433	p36.22
SNP_A-1827473	A	A	312	58	289	81	4.686	0.0304	rs9651118	1	11796480	p36.22
SNP_A-2153521	A	A	413	7	420	0	7.059	7.90E-03	rs7517758	1	12126519	p36.22
SNP_A-2270127	C	C	401	7	420	0	7.267	7.00E-03	rs7551317	1	12126572	p36.22
SNP_A-1735683	C	C	319	43	379	31	4.135	4.20E-02	rs1419299	1	12421997	p36.21
SNP_A-2141957	T	T	384	30	403	17	4.011	4.52E-02	rs12059239	1	12755341	p36.21
SNP_A-2260132	G	G	317	7	320	18	4.56	0.0327	rs12118479	1	12858228	p36.21
SNP_A-1787780	C	C	278	60	300	42	3.99	0.0458	rs2999865	1	13586601	p36.21
SNP_A-1712855	T	T	342	26	354	52	7.025	8.00E-03	rs725398	1	13666453	p36.21
SNP_A-2287018	G	G	391	27	373	43	4.076	4.35E-02	rs12409667	1	13700458	p36.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802292	T	T	289	91	257	121	6.116	0.0134	rs4077841	1	13765711	p36.21
SNP_A-1999887	T	T	222	150	243	119	4.385	3.62E-02	rs2359756	1	13841726	p36.21
SNP_A-1942378	T	T	294	112	273	143	4.425	3.54E-02	rs6429800	1	13973383	p36.21
SNP_A-2073931	G	G	354	26	353	53	8.378	0.0038	rs6678410	1	14059886	p36.21
SNP_A-1719635	T	T	243	159	282	132	5.227	2.22E-02	rs6678924	1	14114173	p36.21
SNP_A-2241164	T	T	241	161	211	191	4.548	3.30E-02	rs916430	1	14191099	p36.21
SNP_A-2050726	A	G	202	154	185	181	3.848	4.98E-02	rs1934656	1	14213863	p36.21
SNP_A-2041897	C	C	359	31	335	49	4.834	2.79E-02	rs16853948	1	14394277	p36.21
SNP_A-1964807	T	T	204	200	246	166	7.001	8.10E-03	rs4573512	1	14489278	p36.21
SNP_A-1791731	T	T	211	201	254	158	9.127	2.50E-03	rs2183102	1	14505940	p36.21
SNP_A-2104528	G	G	195	165	232	136	5.913	1.50E-02	rs6680164	1	14506978	p36.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1958749	C	A	208	162	202	186	5.2	2.26E-02	rs6659078	1	14522038	p36.21
SNP_A-2059550	A	A	255	165	282	136	4.147	4.17E-02	rs6668363	1	14523712	p36.21
SNP_A-1964848	T	G	214	174	208	190	4.325	3.75E-02	rs6690681	1	14527895	p36.21
SNP_A-2191464	G	A	203	153	184	172	5.414	0.02	rs12567471	1	14528264	p36.21
SNP_A-1808759	T	C	206	168	205	175	6.145	0.0132	rs7530275	1	14528962	p36.21
SNP_A-1964852	C	A	212	148	181	171	7.61	5.80E-03	rs2486769	1	14531615	p36.21
SNP_A-1965048	C	C	264	74	298	56	4.182	4.09E-02	rs2103694	1	14653379	p36.21
SNP_A-1686366	A	A	345	59	323	83	4.776	2.89E-02	rs10489453	1	14852514	p36.21
SNP_A-1678816	A	A	345	59	326	88	6.138	0.0132	rs10489452	1	14852581	p36.21
SNP_A-1862219	C	C	396	20	373	35	4.702	3.01E-02	rs2103117	1	14902042	p36.21
SNP_A-2292495	G	G	235	145	272	124	4.011	4.52E-02	rs10803320	1	14933325	p36.21
SNP_A-2075051	G	G	318	94	347	67	5.788	0.0161	rs3765379	1	14935725	p36.21
SNP_A-2187234	-	G	193	193	229	163	5.553	0.0184	rs2049374	1	14954188	p36.21
SNP_A-1855573	G	G	263	157	298	122	6.574	0.0103	rs6693394	1	15010710	p36.21
SNP_A-1896658	A	A	305	111	332	84	4.883	2.71E-02	rs2175773	1	15044978	p36.21
SNP_A-1806163	T	T	375	23	399	9	6.746	9.40E-03	rs4661579	1	15210793	p36.21
SNP_A-2171049	G	G	350	30	361	15	5.149	2.33E-02	rs10754883	1	15216479	p36.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1867154	C	C	298	16	315	5	6.177	0.0129	rs4661581	1	15227360	p36.21
SNP_A-2059674	C	C	362	36	390	16	8.656	0.0033	rs7539166	1	15241211	p36.21
SNP_A-1814246	C	C	330	82	357	61	4.102	4.28E-02	rs16851358	1	15245638	p36.21
SNP_A-2106377	T	T	278	98	321	61	11.65	6.00E-04	rs10754886	1	15247787	p36.21
SNP_A-1935880	G	G	275	91	337	67	8.071	4.50E-03	rs10754887	1	15247845	p36.21
SNP_A-2269239	T	T	249	107	265	73	6.458	1.10E-02	rs12883758	1	15248957	p36.21
SNP_A-1967181	T	T	271	115	284	82	5.304	2.13E-02	rs12883426	1	15471422	p36.21
SNP_A-1857548	A	A	286	130	320	100	5.802	0.016	rs2092324	1	15478700	p36.21
SNP_A-1856143	G	G	298	80	276	110	5.497	1.91E-02	rs11583306	1	15606109	p36.13
SNP_A-2158614	T	T	285	85	252	120	7.998	4.70E-03	rs16851819	1	15664045	p36.13
SNP_A-1957325	G	G	311	95	265	139	11.942	5.00E-04	rs6669417	1	15667677	p36.13
SNP_A-2138694	A	A	283	87	238	116	7.68	5.60E-03	rs12385690	1	15678238	p36.13
SNP_A-1871939	C	C	312	100	276	142	9.45	2.10E-03	rs6696286	1	15714076	p36.13
SNP_A-1817181	A	A	341	73	300	104	7.931	4.90E-03	rs941686	1	15728607	p36.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1967671	A	A	305	93	258	132	10.603	1.10E-03	rs17448778	1	15730612	p36.13
SNP_A-2276046	G	G	311	71	282	108	8.984	2.70E-03	rs12082523	1	15751098	p36.13
SNP_A-2247260	G	G	286	80	239	113	9.581	0.002	rs7516683	1	15765808	p36.13
SNP_A-2093789	G	G	270	44	264	72	6.068	1.36E-02	---	1	15794591	p36.13
SNP_A-2113504	G	G	305	75	271	123	13.394	3.00E-04	rs6668919	1	15795199	p36.13
SNP_A-2125523	T	T	343	67	362	46	4.41	3.57E-02	—	1	16042001	p36.13
SNP_A-2174387	G	G	378	34	393	17	5.954	0.0147	rs1763612	1	16077877	p36.13
SNP_A-2173463	C	C	334	12	347	25	3.879	4.89E-02	rs1056207	1	16090133	p36.13
SNP_A-2030323	A	A	307	103	355	67	10.933	9.00E-04	rs11203277	1	17045033	p36.13
SNP_A-2082647	G	G	290	96	318	72	4.698	3.02E-02	rs2501810	1	17236138	p36.13
SNP_A-2296337	A	A	278	50	315	35	4.246	3.93E-02	rs17458091	1	17341231	p36.13
SNP_A-2023584	A	A	289	95	321	75	3.848	4.98E-02	rs1204890	1	17440007	p36.13
SNP_A-1814818	G	G	251	85	273	55	7.257	7.10E-03	rs2428740	1	17531042	p36.13
SNP_A-2270517	A	A	390	24	380	40	4.087	4.32E-02	rs2248697	1	17617416	p36.13
SNP_A-2198998	G	G	371	25	383	13	3.98	4.60E-02	rs2256787	1	17638122	p36.13
SNP_A-1941268	T	T	364	40	342	58	3.972	4.63E-02	rs12063085	1	17776839	p36.13
SNP_A-2170025	C	C	334	44	318	72	6.965	8.30E-03	rs4920630	1	17819648	p36.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027433	A	A	230	124	204	154	4.773	2.89E-02	rs7547331	1	17836235	p36.13
SNP_A-2302259	C	C	292	128	262	158	4.771	2.89E-02	rs685987	1	17904801	p36.13
SNP_A-2273080	T	T	288	128	258	160	5.199	2.26E-02	rs683259	1	17905439	p36.13
SNP_A-2115903	T	T	401	5	412	0	5.105	2.39E-02	rs697758	1	17924643	p36.13
SNP_A-2188844	G	A	216	172	215	191	5.908	1.51E-02	rs622689	1	17950138	p36.13
SNP_A-2073690	C	C	330	70	353	47	5.296	2.14E-02	rs638425	1	17955334	p36.13
SNP_A-2254666	G	A	219	191	226	192	4.635	3.13E-02	rs9286085	1	18139230	p36.13
SNP_A-2115313	C	C	352	46	382	30	3.887	0.0487	rs909949	1	18570148	p36.13
SNP_A-2074620	G	G	395	11	378	24	5.183	2.28E-02	rs2076020	1	18763711	p36.13
SNP_A-1951081	T	T	351	9	355	25	7.017	8.10E-03	rs2236826	1	18765286	p36.13
SNP_A-2075652	C	C	397	11	386	28	7.521	6.10E-03	rs2282708	1	18766904	p36.13
SNP_A-1951298	C	C	307	7	322	20	5.432	1.98E-02	rs2282704	1	18769152	p36.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1952590	C	C	411	9	399	21	4.978	2.57E-02	rs17352302	1	18780508	p36.13
SNP_A-2049994	G	G	254	156	204	192	8.942	0.0028	rs3748761	1	19145997	p36.13
SNP_A-1786206	C	C	229	189	264	158	5.235	2.21E-02	rs2146866	1	19150543	p36.13
SNP_A-2208638	T	T	223	157	252	130	4.305	3.80E-02	rs4912048	1	19180738	p36.13
SNP_A-2254743	T	T	206	152	244	130	4.578	3.24E-02	rs4911974	1	19187814	p36.13
SNP_A-2164834	C	C	248	156	208	200	8.927	0.0028	rs6691238	1	19226135	p36.13
SNP_A-1942629	C	C	373	5	360	14	4.473	0.0344	rs1738025	1	19354560	p36.13
SNP_A-2123870	A	A	252	124	299	95	7.433	6.40E-03	rs6426790	1	19392071	p36.13
SNP_A-2079529	C	C	290	124	261	153	4.562	0.0327	rs10753558	1	19443221	p36.13
SNP_A-2257983	T	T	291	121	262	148	4.226	3.98E-02	rs10753559	1	19443332	p36.13
SNP_A-1842478	C	C	282	118	251	153	6.304	0.012	rs10917434	1	19452608	p36.13
SNP_A-2137126	C	C	207	141	237	117	4.209	0.0402	rs4912085	1	19474393	p36.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2237517	C	C	351	69	381	39	9.563	0.002	rs11583187	1	19499153	p36.13
SNP_A-1897118	A	A	334	54	363	31	7.385	0.0066	rs11585820	1	19505141	p36.13
SNP_A-2192315	T	T	288	132	262	160	3.909	4.80E-02	rs12045440	1	19510824	p36.13
SNP_A-2282993	C	C	200	182	220	150	3.846	0.0499	rs4911997	1	19510975	p36.13
SNP_A-2154725	C	C	277	115	246	146	5.519	1.88E-02	rs6669496	1	19554691	p36.13
SNP_A-1857001	C	C	290	126	263	153	3.931	4.74E-02	rs7415949	1	19618096	p36.13
SNP_A-2184139	C	C	408	8	407	1	5.369	2.05E-02	rs10916669	1	19979564	p36.13
SNP_A-1788390	A	A	370	38	382	22	4.439	3.51E-02	rs12080654	1	20368937	p36.12
SNP_A-1892008	G	G	345	3	325	11	4.959	2.59E-02	rs4654849	1	20377713	p36.12
SNP_A-1921149	G	G	363	29	338	48	5.534	1.87E-02	rs17412284	1	20575433	p36.12
SNP_A-2266514	G	G	373	27	397	13	5.525	1.87E-02	rs1253890	1	20635455	p36.12
SNP_A-2114132	C	C	361	25	378	10	6.815	9.00E-03	rs678980	1	20656710	p36.12
SNP_A-1817070	G	G	210	188	233	157	3.899	4.83E-02	rs651085	1	20843089	p36.12
SNP_A-2063476	A	A	233	61	240	108	8.694	3.20E-03	rs785195	1	21441742	p36.12
SNP_A-1842330	T	T	342	68	312	100	7.467	0.0063	rs10916972	1	21457037	p36.12
SNP_A-2049557	A	A	356	40	351	61	4.086	4.32E-02	rs12116570	1	21588562	p36.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102609	A	A	366	16	358	6	4.202	4.04E-02	rs3767134	1	21765634	p36.12
SNP_A-1785992	C	C	347	39	341	65	6.051	1.39E-02	rs17459139	1	21905417	p36.12
SNP_A-2297900	A	A	257	139	286	110	4.926	2.65E-02	rs2501257	1	21974142	p36.12
SNP_A-1795087	A	A	290	76	323	55	4.951	2.61E-02	rs8179387	1	22035462	p36.12
SNP_A-2146741	G	G	362	50	388	30	5.858	0.0155	rs7529773	1	22065821	p36.12
SNP_A-2151483	C	T	212	178	202	176	4.67	3.07E-02	rs2473277	1	22107151	p36.12
SNP_A-2285252	A	A	236	162	260	132	3.953	4.68E-02	rs16826658	1	22231177	p36.12
SNP_A-1818844	C	C	309	93	344	66	6.383	0.0115	rs7543680	1	22476575	p36.12
SNP_A-2070502	G	G	349	61	369	33	8.82	3.00E-03	rs4409621	1	22478055	p36.12
SNP_A-2296730	G	G	275	115	287	77	6.889	8.70E-03	rs1890775	1	22519572	p36.12
SNP_A-2175725	T	T	283	115	321	89	5.527	1.87E-02	rs10917234	1	22527908	p36.12
SNP_A-1986940	T	T	289	121	327	91	6.513	1.07E-02	rs4655067	1	22559595	p36.12
SNP_A-1792137	G	G	295	119	325	91	5.18	2.28E-02	rs4655068	1	22559660	p36.12
SNP_A-2077347	G	G	263	95	305	71	6.138	0.0132	rs4655071	1	22573237	p36.12
SNP_A-1811651	G	G	370	20	350	34	4.139	0.0419	rs10917263	1	22661977	p36.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308314	G	G	349	61	315	85	5.564	0.0183	rs6692586	1	23045212	p36.12
SNP_A-1854058	T	T	355	65	320	86	4.499	0.0339	rs10429877	1	23053860	p36.12
SNP_A-2306194	T	T	349	63	333	87	4.139	0.0419	rs4655141	1	23057331	p36.12
SNP_A-1913373	T	T	344	56	332	84	5.501	0.019	rs522802	1	23084290	p36.12
SNP_A-2163486	T	-	239	173	193	193	5.149	2.33E-02	rs2806561	1	23250101	p36.12
SNP_A-1850643	C	C	300	66	268	86	4.236	3.96E-02	rs10917360	1	23284316	p36.12
SNP_A-1786361	G	G	373	17	363	37	7.418	6.50E-03	rs667311	1	23335957	p36.12
SNP_A-1898138	T	T	378	14	377	27	3.943	4.71E-02	rs1535179	1	23384315	p36.12
SNP_A-2205892	C	C	302	78	264	98	4.39	3.62E-02	rs10753555	1	23448424	p36.12
SNP_A-2166572	T	T	381	19	365	33	4.107	4.27E-02	rs651542	1	23452707	p36.12
SNP_A-2285512	T	T	352	14	344	28	4.71	3.00E-02	rs2092933	1	23456682	p36.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170912	T	T	367	51	341	77	6.236	1.25E-02	rs649458	1	23457834	p36.12
SNP_A-1906192	C	C	353	29	376	16	3.984	4.59E-02	rs4648858	1	24351865	p36.11
SNP_A-2112044	A	A	203	169	238	138	5.887	1.53E-02	rs12121909	1	24355890	p36.11
SNP_A-2150341	C	G	209	205	236	180	4.336	0.0373	rs11249081	1	24377596	p36.11
SNP_A-1990582	T	T	286	106	319	81	5.062	2.45E-02	rs10489439	1	24459702	p36.11
SNP_A-2304689	C	C	300	116	329	91	4.337	0.0373	rs12125143	1	24491511	p36.11
SNP_A-2136325	T	T	268	90	300	70	4.106	4.27E-02	rs2235550	1	24494135	p36.11
SNP_A-1990698	G	G	289	107	315	75	6.7	9.60E-03	rs10489443	1	24495012	p36.11
SNP_A-2233813	G	G	298	120	325	91	5.151	2.32E-02	rs7542174	1	24510060	p36.11
SNP_A-2200554	T	T	297	119	323	89	5.398	2.02E-02	rs7534396	1	24510221	p36.11
SNP_A-1991336	A	A	263	157	299	121	6.968	8.30E-03	rs2361150	1	24939605	p36.11
SNP_A-2131563	T	T	211	153	185	183	4.384	3.67E-02	rs4649033	1	24952935	p36.11
SNP_A-2184348	C	C	358	22	362	46	7.507	6.10E-03	rs4478762	1	25026321	p36.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169223	G	G	382	2	370	12	7.329	6.80E-03	rs452227	1	25108818	p36.11
SNP_A-2189659	T	G	180	164	193	157	3.874	4.90E-02	rs11248972	1	25122472	p36.11
SNP_A-1991848	C	C	209	199	237	155	6.91	0.0086	rs178135	1	25153739	p36.11
SNP_A-2170063	T	T	408	4	414	0	4.039	4.45E-02	rs7543018	1	25187030	p36.11
SNP_A-2115093	A	A	415	5	420	0	5.03	2.49E-02	rs12068771	1	25623720	p36.11
SNP_A-2219947	A	A	409	5	418	0	5.079	2.42E-02	rs11247912	1	25648891	p36.11
SNP_A-1956086	C	C	411	5	420	0	5.078	2.42E-02	rs3767911	1	25651657	p36.11
SNP_A-1854732	A	A	404	6	416	0	6.132	1.33E-02	rs11802540	1	25682014	p36.11
SNP_A-2226539	C	C	286	118	311	87	5.69	1.71E-02	rs4659382	1	25819072	p36.11
SNP_A-1839188	G	G	408	4	406	0	3.961	4.66E-02	rs4659403	1	26047743	p36.11
SNP_A-2212290	A	A	322	52	336	28	7.364	6.70E-03	rs4908343	1	27615840	p36.11
SNP_A-1786559	C	C	405	13	414	4	4.864	2.74E-02	rs530599	1	27648917	p36.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2050545	G	G	278	108	301	77	6.025	0.0141	rs6682922	1	28374313	p35.3
SNP_A-2253994	G	G	366	8	315	23	9.281	0.0023	rs4078312	1	29636261	p35.3
SNP_A-2061355	T	T	189	163	212	128	5.322	2.11E-02	rs502545	1	29778575	p35.3
SNP_A-2093991	G	G	414	0	408	6	6.044	0.014	rs441380	1	30201683	p35.2
SNP_A-2080968	A	A	352	50	338	76	5.474	1.93E-02	rs4949566	1	30404745	p35.2
SNP_A-1781382	G	G	418	2	411	11	6.285	1.22E-02	rs16833842	1	30669171	p35.2
SNP_A-1842387	G	G	410	6	393	15	4.14	0.0419	rs12043086	1	30711009	p35.2
SNP_A-1803060	A	A	382	6	382	16	4.419	3.55E-02	rs12045420	1	30711066	p35.2
SNP_A-1999832	C	C	406	6	388	16	4.876	2.72E-02	rs10915161	1	30712718	p35.2
SNP_A-2037183	G	G	310	96	341	57	11.339	8.00E-04	rs10914167	1	30782235	p35.2
SNP_A-1999915	C	C	316	102	352	70	7.875	5.00E-03	rs1882027	1	30782325	p35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1930995	G	G	368	48	391	29	5.366	2.05E-02	rs16865763	1	30959240	p35.2
SNP_A-2218066	G	G	335	63	354	42	4.719	0.0298	rs12408228	1	31006510	p35.2
SNP_A-1786660	G	G	337	69	314	96	5.211	0.0224	rs6425717	1	31363196	p35.2
SNP_A-2041225	G	G	331	63	301	99	9.379	2.20E-03	rs6699372	1	31373426	p35.2
SNP_A-2165958	G	G	287	51	322	34	4.948	2.61E-02	rs924930	1	31399179	p35.2
SNP_A-2232455	T	T	336	44	299	75	10.184	0.0014	—	1	31443596	p35.2
SNP_A-1929512	G	G	362	56	326	82	6.662	9.80E-03	rs3795432	1	31498966	p35.2
SNP_A-2000252	C	C	344	48	294	74	8.71	3.20E-03	rs4949391	1	31502799	p35.2
SNP_A-2311560	G	G	375	45	347	75	8.581	3.40E-03	rs17495262	1	31506725	p35.2
SNP_A-2000268	T	T	325	55	282	82	8.027	4.60E-03	rs1995585	1	31524567	p35.2
SNP_A-2086435	A	A	356	54	335	81	5.995	0.0143	rs12122236	1	31527994	p35.2
SNP_A-2043532	C	C	369	47	344	74	6.897	0.0086	rs7534378	1	31532651	p35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2143386	C	C	347	35	321	59	7.134	0.0076	rs7534465	1	31532756	p35.2
SNP_A-2123191	G	G	386	16	391	3	8.847	2.90E-03	rs16834529	1	31645053	p35.2
SNP_A-2186144	G	G	380	0	357	5	5.284	2.15E-02	rs7525091	1	31804428	p35.2
SNP_A-1865075	T	T	343	23	356	8	7.494	6.20E-03	rs12037019	1	31882748	p35.2
SNP_A-1887389	A	A	381	23	403	9	6.665	9.80E-03	rs12037400	1	31884271	p35.2
SNP_A-2279309	A	A	232	160	200	192	5.279	2.16E-02	rs630789	1	31910426	p35.2
SNP_A-1792958	C	C	276	130	313	99	6.477	0.0109	rs552124	1	31935119	p35.2
SNP_A-2273675	G	-	226	160	191	191	5.655	1.74E-02	rs11589992	1	31969223	p35.2
SNP_A-2206650	A	A	286	104	318	80	4.745	2.94E-02	rs7516503	1	31990049	p35.2
SNP_A-2262406	G	G	303	7	334	0	7.625	5.80E-03	rs9803844	1	32562646	p35.1
SNP_A-2064882	G	G	334	42	361	25	5.232	2.22E-02	rs881393	1	32925738	p35.1
SNP_A-2047615	T	T	348	62	360	40	4.826	2.80E-02	rs12760548	1	32949741	p35.1
SNP_A-2171870	G	G	329	67	311	95	5.222	0.0223	rs1746661	1	33004132	p35.1
SNP_A-1851464	C	C	281	73	294	50	4.452	0.0349	rs10798953	1	33606228	p35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2050739	C	C	333	19	290	34	6.064	0.0138	rs1493995	1	33697523	p35.1
SNP_A-2122515	C	A	173	159	196	146	5.995	0.0144	rs1690551	1	33704654	p35.1
SNP_A-2026881	T	T	323	73	296	110	8.535	3.50E-03	rs10798965	1	33708367	p35.1
SNP_A-2084250	T	T	291	117	258	152	6.533	0.0106	rs1389560	1	33711903	p35.1
SNP_A-2171006	T	T	224	188	253	157	4.544	3.30E-02	rs732889	1	33824594	p35.1
SNP_A-2258104	G	G	392	10	411	3	4.043	4.43E-02	rs16835832	1	33891446	p35.1
SNP_A-2001522	G	G	233	159	208	192	4.439	3.51E-02	rs1950895	1	33974322	p35.1
SNP_A-1649902	A	A	335	67	319	93	4.494	3.40E-02	rs10493056	1	34256783	p35.1
SNP_A-1677866	C	C	336	68	319	93	4.245	3.94E-02	rs4653014	1	34257635	p35.1
SNP_A-1938453	G	G	368	30	389	15	5.538	1.86E-02	rs705210	1	34278487	p35.1
SNP_A-2184927	G	G	394	8	391	21	5.717	1.68E-02	rs1318222	1	34325272	p34.3
SNP_A-2279355	G	G	412	0	416	4	3.943	4.71E-02	rs297794	1	34344848	p34.3
SNP_A-1866277	A	A	332	70	297	99	6.879	8.70E-03	rs12043879	1	34355223	p34.3
SNP_A-1949339	A	G	189	183	217	159	5.455	0.0195	rs10914894	1	34403159	p34.3
SNP_A-2145851	C	C	335	59	320	84	4.59	3.22E-02	rs10914896	1	34405031	p34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215480	T	G	211	199	236	174	6.703	9.60E-03	rs10799035	1	34407791	p34.3
SNP_A-2002016	G	G	269	117	240	154	6.623	0.0101	rs2359233	1	34439197	p34.3
SNP_A-2002028	T	T	271	137	235	167	5.478	1.93E-02	rs6425887	1	34452643	p34.3
SNP_A-1957986	C	C	251	101	222	140	7.951	4.80E-03	rs7548252	1	34462867	p34.3
SNP_A-2186646	G	G	210	116	187	155	6.566	0.0104	rs10914912	1	34462923	p34.3
SNP_A-2045040	C	C	303	49	320	30	5.028	2.49E-02	rs705206	1	34507126	p34.3
SNP_A-1796833	A	T	212	182	219	191	4.192	4.06E-02	rs10914991	1	34743953	p34.3
SNP_A-2279588	C	C	338	14	351	3	7.357	6.70E-03	rs17502414	1	34792159	p34.3
SNP_A-2202697	A	A	354	38	362	18	7.047	7.90E-03	rs16836900	1	34829005	p34.3
SNP_A-2233851	A	A	381	7	341	21	8.325	3.90E-03	rs12078977	1	35056408	p34.3
SNP_A-2227129	C	C	393	15	411	5	5.326	2.10E-02	rs12407202	1	35131580	p34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2165460	A	A	389	17	414	6	5.804	0.016	rs12401429	1	35153111	p34.3
SNP_A-2268897	G	G	389	25	372	42	4.693	3.03E-02	rs2791961	1	36040512	p34.3
SNP_A-1957769	T	T	382	24	367	41	4.742	2.94E-02	rs12031138	1	36076899	p34.3
SNP_A-1848235	T	T	384	0	396	4	3.86	4.95E-02	rs716924	1	36093431	p34.3
SNP_A-2003050	T	T	304	18	277	33	5.441	1.97E-02	rs683622	1	36112662	p34.3
SNP_A-2297919	A	A	243	161	281	133	5.301	2.13E-02	rs17498436	1	36672366	p34.3
SNP_A-2310967	G	G	328	10	365	3	4.478	3.43E-02	rs17484348	1	36734294	p34.3
SNP_A-2119090	T	T	364	20	367	9	4.101	4.29E-02	rs12410895	1	36857373	p34.3
SNP_A-2193705	C	C	363	27	381	11	7.167	7.40E-03	---	1	37067270	p34.3
SNP_A-1841294	G	C	191	177	234	152	11.917	6.00E-04	rs501832	1	37091051	p34.3
SNP_A-1813646	A	A	354	18	355	33	4.078	4.34E-02	rs218394	1	37218732	p34.3
SNP_A-2309338	C	C	347	43	369	25	5.42	1.99E-02	rs4653247	1	37265853	p34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2234555	T	-	229	173	194	194	3.851	4.97E-02	rs4653254	1	37313830	p34.3
SNP_A-1899449	G	G	236	124	198	150	5.593	1.80E-02	rs1501540	1	37392171	p34.3
SNP_A-2304796	G	G	400	0	385	5	5.161	2.31E-02	rs11264025	1	37449455	p34.3
SNP_A-2203638	C	C	313	39	312	60	3.907	4.81E-02	rs4653278	1	37471964	p34.3
SNP_A-2004296	C	C	333	75	357	53	4.611	3.18E-02	rs215208	1	37622069	p34.3
SNP_A-1890380	G	G	330	74	369	45	9.122	2.50E-03	rs2174769	1	37675452	p34.3
SNP_A-1825425	G	G	326	72	363	45	8.095	4.40E-03	rs6426024	1	37718645	p34.3
SNP_A-1859496	G	G	369	23	361	41	5.025	2.50E-02	rs7547921	1	38271166	p34.3
SNP_A-2264596	A	A	220	184	251	151	5.286	2.15E-02	rs12142825	1	38559713	p34.3
SNP_A-2050289	A	A	393	7	394	18	4.665	3.08E-02	rs17556209	1	38832165	p34.3
SNP_A-2311272	G	G	393	15	412	2	10.346	1.30E-03	rs16825658	1	39064976	p34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138978	G	G	345	27	337	45	4.462	3.47E-02	rs6696013	1	39120950	p34.3
SNP_A-2049858	G	G	371	35	347	55	5.227	2.22E-02	rs1539435	1	39637917	p34.3
SNP_A-1929197	C	C	354	2	342	12	7.344	6.70E-03	rs10888885	1	39754188	p34.3
SNP_A-2201440	C	C	354	22	340	38	4.544	3.30E-02	rs546422	1	39827921	p34.2
SNP_A-1916197	C	C	365	11	356	2	5.905	1.51E-02	rs16826583	1	39960285	p34.2
SNP_A-2210431	T	C	207	203	234	180	4.063	4.38E-02	rs3103778	1	40102864	p34.2
SNP_A-1870760	A	A	222	180	254	138	7.574	5.90E-03	rs209583	1	40516584	p34.2
SNP_A-1929756	C	C	320	16	321	35	6.507	1.07E-02	rs4660408	1	40533389	p34.2
SNP_A-2037728	G	G	381	27	394	10	8.009	4.70E-03	rs16827281	1	40545377	p34.2
SNP_A-1857269	C	C	379	37	356	56	4.582	3.23E-02	rs209606	1	40550134	p34.2
SNP_A-2140644	C	C	290	100	257	123	4.234	3.96E-02	rs10789262	1	41106510	p34.2
SNP_A-2197768	G	G	328	80	310	110	5.072	2.43E-02	rs3819842	1	41232179	p34.2
SNP_A-2164648	C	C	406	10	418	2	5.489	1.91E-02	rs17358725	1	41584976	p34.2
SNP_A-2192816	A	A	172	154	203	117	7.559	6.00E-03	rs2483692	1	41594143	p34.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209886	G	G	396	16	369	31	5.564	0.0183	rs6700172	1	41811482	p34.2
SNP_A-1835253	A	A	364	52	346	74	4.279	3.86E-02	rs972352	1	41966697	p34.2
SNP_A-2065192	G	G	343	53	350	34	4.036	4.45E-02	rs16829473	1	42554616	p34.2
SNP_A-2007652	G	G	349	59	354	38	4.264	3.89E-02	rs4660634	1	42570266	p34.2
SNP_A-2108928	C	C	317	103	342	78	4.401	3.59E-02	rs7540604	1	42968928	p34.2
SNP_A-1854723	G	G	375	35	393	19	5.158	2.31E-02	rs579001	1	43200624	p34.2
SNP_A-2266041	C	C	365	43	379	25	5.009	0.0252	rs583116	1	43217350	p34.2
SNP_A-2008128	C	C	368	42	386	26	4.19	0.0407	rs610200	1	43285846	p34.2
SNP_A-1801495	A	A	263	55	312	40	4.831	2.80E-02	rs2764420	1	43342738	p34.2
SNP_A-2151912	A	A	342	46	368	30	4.194	4.06E-02	rs1760672	1	43347770	p34.2
SNP_A-2171157	A	A	265	105	251	143	5.454	0.0195	rs2782641	1	43682448	p34.2
SNP_A-1926718	T	T	288	112	255	145	6.243	1.25E-02	rs12401813	1	43932508	p34.1
SNP_A-1657251	C	C	228	132	199	167	6.017	1.42E-02	rs10493116	1	43943648	p34.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784431	G	G	349	71	372	48	5.179	0.0229	rs16831558	1	44171256	p34.1
SNP_A-2129525	C	C	279	109	289	79	4.437	3.52E-02	rs2485993	1	44172133	p34.1
SNP_A-2279694	A	A	299	85	284	112	3.903	0.0482	rs17413167	1	44176866	p34.1
SNP_A-1757999	C	C	273	89	256	130	7.46	0.0063	rs1890948	1	44343159	p34.1
SNP_A-2184496	G	G	348	0	310	4	4.46	3.47E-02	rs6671158	1	44693459	p34.1
SNP_A-1744333	C	C	404	0	410	4	3.923	4.76E-02	rs631840	1	46487861	p33
SNP_A-1825836	G	G	406	4	399	13	4.821	0.0281	rs7542528	1	46632107	p33
SNP_A-2290627	C	C	300	28	288	48	5.412	0.02	rs2025384	1	46679910	p33
SNP_A-2299183	C	C	420	0	416	4	4.019	4.50E-02	rs1258065	1	46815637	p33
SNP_A-2056167	C	C	420	0	418	4	4	4.55E-02	rs736188	1	46820848	p33
SNP_A-2126509	G	G	400	0	408	4	3.903	0.0482	rs631368	1	46833522	p33
SNP_A-1933319	T	T	418	0	410	4	4.058	4.40E-02	rs597221	1	46843339	p33
SNP_A-2105026	A	A	409	1	409	11	8.214	4.20E-03	rs11211378	1	47023555	p33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2035385	C	C	277	87	263	119	4.902	2.68E-02	rs1502909	1	47197844	p33
SNP_A-1960295	T	T	358	38	383	23	4.408	3.58E-02	rs2292059	1	47216737	p33
SNP_A-2000041	A	A	272	118	294	92	4.054	0.0441	rs2250495	1	47405397	p33
SNP_A-2131024	C	C	327	11	304	26	6.825	9.00E-03	rs517384	1	47664683	p33
SNP_A-1883913	G	G	362	22	354	46	8.237	4.10E-03	rs4926559	1	47683666	p33
SNP_A-1956299	A	A	352	22	333	45	8.401	3.70E-03	rs1572547	1	47684169	p33
SNP_A-2206282	C	C	410	4	414	0	4.019	4.50E-02	rs11211555	1	47741059	p33
SNP_A-1901293	T	C	198	188	208	164	3.946	0.047	rs931937	1	47814141	p33
SNP_A-2313927	C	C	230	132	257	107	4.107	4.27E-02	rs3850885	1	47959097	p33
SNP_A-1947261	A	A	410	6	406	16	4.522	3.35E-02	rs11581081	1	48006140	p33
SNP_A-1645024	C	C	305	89	335	63	5.834	1.57E-02	rs20637l2	1	48173522	p33
SNP_A-1903859	A	C	180	158	205	165	5.302	2.13E-02	rs10888596	1	48280692	p33
SNP_A-2300632	G	G	261	159	280	132	4.027	0.0448	rs10788882	1	48342458	p33
SNP_A-1951535	T	T	268	134	297	103	5.538	1.86E-02	rs7541597	1	48367234	p33
SNP_A-1905163	G	G	277	115	310	92	4.285	3.84E-02	rs12140934	1	48380668	p33
SNP_A-2098482	G	G	273	141	306	114	4.697	3.02E-02	rs12128169	1	48382435	p33
SNP_A-2150456	G	G	280	94	273	63	4.188	0.0407	rs743065	1	48446386	p33
SNP_A-2311204	G	G	323	77	347	53	5.29	2.14E-02	rs1114192	1	48509352	p33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2146794	A	A	278	142	243	173	5.383	2.03E-02	rs2803270	1	48743258	p33
SNP_A-2209549	A	A	398	18	378	32	4.392	0.0361	rs11205517	1	48804059	p33
SNP_A-1664052	T	T	387	17	403	7	4.447	3.50E-02	rs1343426	1	48835932	p33
SNP_A-2210487	A	A	366	12	349	3	4.884	2.71E-02	rs4926763	1	49004700	p33
SNP_A-1865067	C	C	373	37	349	57	5.034	2.49E-02	rs11578524	1	49067660	p33
SNP_A-1831020	C	C	212	136	198	172	4.016	4.51E-02	rs3121512	1	49159105	p33
SNP_A-2111518	G	G	235	111	197	129	4.101	4.29E-02	rs7534689	1	51738405	p32.3
SNP_A-2306420	C	C	243	145	266	110	5.656	1.74E-02	rs269324	1	52838176	p32.3
SNP_A-2267982	A	C	201	141	172	140	12.633	4.00E-04	rs6698595	1	53523963	p32.3
SNP_A-2042516	G	G	381	29	364	52	6.876	8.70E-03	rs12033075	1	53609538	p32.3
SNP_A-2081035	G	G	301	91	325	69	3.94	4.71E-02	rs11206191	1	53870123	p32.3
SNP_A-2298673	C	C	287	47	301	29	4.573	3.25E-02	rs4927031	1	53895212	p32.3
SNP_A-1657532	T	T	334	70	367	43	7.961	4.80E-03	rs10489565	1	54196105	p32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2264592	C	C	398	4	416	0	4.16	4.14E-02	rs2236512	1	54231128	p32.3
SNP_A-2131109	A	A	297	103	270	128	3.986	4.59E-02	rs623888	1	54466869	p32.3
SNP_A-2084201	G	G	222	168	253	139	4.757	0.0292	rs7553843	1	54546549	p32.3
SNP_A-1879387	C	C	203	195	237	165	5.107	2.38E-02	rs6690450	1	54566100	p32.3
SNP_A-2301367	G	G	251	129	292	110	3.99	0.0458	rs213500	1	54576029	p32.3
SNP_A-2219558	C	C	384	4	375	13	4.871	2.73E-02	rs17110749	1	54760211	p32.3
SNP_A-2015679	C	C	399	17	389	31	4.191	4.06E-02	rs10489663	1	54898707	p32.3
SNP_A-2293217	A	A	383	11	356	26	6.884	8.70E-03	rs6698255	1	54924740	p32.3
SNP_A-1788580	G	G	288	54	316	36	4.755	0.0292	rs10430114	1	54946732	p32.3
SNP_A-2198430	G	G	341	79	362	54	5.308	0.0212	rs6681687	1	55015460	p32.3
SNP_A-2080137	C	C	367	29	384	16	4.12	0.0424	rs4927168	1	55038366	p32.3
SNP_A-2217534	C	C	184	180	207	149	4.186	4.08E-02	rs618101	1	55099549	p32.3
SNP_A-2087376	G	G	340	66	318	90	4.423	3.55E-02	rs2495516	1	55161639	p32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1668518	A	A	328	36	318	60	5.893	0.0152	rs4497258	1	55687752	p32.2
SNP_A-2134473	G	G	412	4	414	0	4	4.55E-02	rs17113538	1	56414788	p32.2
SNP_A-2066349	A	A	310	52	278	70	4.123	4.23E-02	rs2793685	1	56474464	p32.2
SNP_A-2205970	G	G	380	0	386	4	3.918	4.78E-02	rs2051038	1	56779443	p32.2
SNP_A-2029049	T	T	350	38	362	18	7.263	7.00E-03	rs1156845	1	56921716	p32.2
SNP_A-2037225	G	G	352	68	374	48	4.11	4.26E-02	rs6696458	1	56928397	p32.2
SNP_A-1828709	A	G	172	164	208	156	4.873	2.73E-02	rs1738403	1	56958580	p32.2
SNP_A-2199658	G	G	324	28	295	11	5.58	1.82E-02	rs3768184	1	57259724	p32.2
SNP_A-1945613	G	G	304	32	276	54	6.926	8.50E-03	rs1202833	1	58071917	p32.2
SNP_A-1945127	G	G	273	53	225	81	9.854	1.70E-03	rs1022636	1	58072586	p32.2
SNP_A-2169961	G	G	351	39	369	21	5.85	1.56E-02	rs17116802	1	58242321	p32.2
SNP_A-2251853	A	A	364	56	382	38	3.881	4.88E-02	rs7527995	1	58243275	p32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2131649	T	T	320	16	313	3	8.367	0.0038	rs849480	1	58576481	p32.2
SNP_A-1813979	C	C	205	183	231	139	7.139	7.50E-03	rs706430	1	58615359	p32.2
SNP_A-2091695	A	A	350	36	355	21	3.852	4.97E-02	rs644319	1	58638736	p32.2
SNP_A-1945511	C	C	311	47	288	72	6.13	1.33E-02	rs11207233	1	58645479	p32.2
SNP_A-2049646	C	C	349	63	324	88	5.068	2.44E-02	rs12139475	1	58717208	p32.1
SNP_A-1790615	C	C	244	140	274	108	5.861	0.0155	rs11207281	1	58825906	p32.1
SNP_A-1790716	G	G	291	41	298	18	8.66	0.0033	rs11583201	1	58898798	p32.1
SNP_A-1787022	C	C	302	14	328	4	6.237	1.25E-02	rs1886745	1	59083267	p32.1
SNP_A-1862763	G	G	412	4	420	0	4.058	4.40E-02	rs2716161	1	59119011	p32.1
SNP_A-2074696	T	T	304	82	348	62	5.028	2.49E-02	rs12133535	1	59602430	p32.1
SNP_A-1835571	G	G	363	47	391	29	5.183	2.28E-02	rs11207488	1	59781317	p32.1
SNP_A-1744711	A	A	233	163	277	133	6.595	1.02E-02	rs169872	1	60156163	p32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829950	C	C	377	37	394	22	4.184	4.08E-02	rs17120013	1	60206128	p31.3
SNP_A-2228473	C	C	407	3	397	11	4.691	3.03E-02	rs3909438	1	60369234	p31.3
SNP_A-1655453	A	A	282	122	255	159	6.108	0.0135	rs10493290	1	60412782	p32.1
SNP_A-1751045	C	C	282	122	257	157	5.429	1.98E-02	rs508507	1	60488234	p32.1
SNP_A-1664280	A	A	284	106	255	143	6.978	8.30E-03	rs554692	1	60489267	p32.1
SNP_A-2068187	G	G	245	115	214	148	6.229	0.0126	rs7546563	1	60532625	p31.3
SNP_A-1694803	G	G	320	82	356	58	5.856	0.0155	rs4915575	1	60538781	p32.1
SNP_A-1944102	C	C	218	168	256	140	5.465	1.94E-02	rs298141	1	60545657	p31.3
SNP_A-2161686	G	G	231	183	265	155	4.607	3.18E-02	rs1414314	1	60548075	p31.3
SNP_A-2068500	C	C	216	188	245	149	6.213	1.27E-02	rs11207597	1	60573802	p31.3
SNP_A-1659997	C	C	298	72	293	109	6.29	0.0121	rs310186	1	60621302	p31.3
SNP_A-2069201	C	C	227	179	259	151	4.463	3.46E-02	rs1461356	1	60749036	p31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1919344	G	G	268	148	218	200	12.909	3.00E-04	rs10749720	1	60844806	p31.3
SNP_A-1662148	C	C	204	200	242	170	5.592	1.80E-02	rs1779866	1	60852316	p31.3
SNP_A-2070146	C	C	246	154	199	197	10.212	0.0014	rs484335	1	60858191	p31.3
SNP_A-2070452	T	T	378	32	405	15	8.96	8.30E-03	rs12038037	1	60882323	p31.3
SNP_A-2035716	G	G	376	2	369	11	6.291	0.0121	rs333145	1	61393876	p31.3
SNP_A-2249832	A	A	346	8	360	24	7.07	7.80E-03	rs332832	1	61415987	p31.3
SNP_A-1835166	G	G	308	34	310	58	5.322	2.11E-02	rs11207751	1	61680864	p31.3
SNP_A-2034477	T	T	324	0	322	4	4	4.55E-02	rs9783018	1	61847377	p31.3
SNP_A-2284365	A	A	286	90	307	65	4.755	0.0292	rs11207882	1	62159098	p31.3
SNP_A-2278365	C	C	400	6	404	0	6.015	1.42E-02	rs17123527	1	62532547	p31.3
SNP_A-1683822	T	T	240	160	218	194	4.146	4.17E-02	rs6683832	1	62646821	p31.3
SNP_A-1753671	G	G	242	162	218	194	4.051	4.42E-02	rs2886770	1	62672703	p31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1751609	C	C	291	107	317	83	4.138	0.0419	rs10493339	1	62960871	p31.3
SNP_A-2054037	A	A	249	165	221	197	4.478	3.43E-02	rs10889383	1	63008782	p31.3
SNP_A-2084306	T	T	244	164	213	191	4.137	4.20E-02	rs2050248	1	63050139	p31.3
SNP_A-1878152	C	C	237	109	257	73	7.556	6.00E-03	rs7544711	1	63126791	p31.3
SNP_A-1947985	C	C	318	90	270	116	6.595	1.02E-02	rs1498934	1	63273834	p31.3
SNP_A-2314016	G	G	310	92	278	136	10.058	0.0015	rs6690203	1	63276031	p31.3
SNP_A-2074096	C	C	314	74	275	111	9.977	1.60E-03	rs1498940	1	63284157	p31.3
SNP_A-2152004	G	G	227	193	269	149	9.213	2.40E-03	rs1498936	1	63287276	p31.3
SNP_A-2093533	A	G	214	182	215	191	3.925	4.76E-02	rs11208137	1	63310016	p31.3
SNP_A-2285397	C	C	295	121	265	153	5.34	2.08E-02	rs9436678	1	63663611	p31.3
SNP_A-1953782	G	G	292	118	261	149	5.337	2.09E-02	rs6588044	1	63670325	p31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2096297	C	C	356	32	329	57	8.082	4.50E-03	rs217452	1	63714877	p31.3
SNP_A-1790843	A	A	263	99	241	127	4.38	3.64E-02	rs855318	1	63780407	p31.3
SNP_A-2132027	C	T	214	170	197	165	7.679	5.60E-03	rs2284997	1	63817796	p31.3
SNP_A-2211354	G	G	279	49	259	73	5.441	1.97E-02	rs3790857	1	63823887	p31.3
SNP_A-1875088	C	C	323	75	298	98	4.059	4.39E-02	rs2269238	1	63829558	p31.3
SNP_A-2221908	C	C	393	1	392	12	9.185	2.40E-03	rs6663111	1	63873239	p31.3
SNP_A-2098023	A	A	362	52	345	73	3.918	4.78E-02	rs10493350	1	63877566	p31.3
SNP_A-2098115	T	T	377	11	361	3	4.157	4.15E-02	rs1506399	1	63885505	p31.3
SNP_A-2098147	C	C	401	11	417	3	4.808	2.83E-02	rs10493351	1	63886164	p31.3
SNP_A-1732107	T	T	295	109	332	82	5.879	1.53E-02	rs10493360	1	64421040	p31.3
SNP_A-2066875	C	C	342	34	337	17	5.045	0.0247	rs6659298	1	64599795	p31.3
SNP_A-2061835	T	T	304	22	283	37	4.509	3.37E-02	rs1992098	1	64695825	p31.3
SNP_A-2169450	G	G	327	19	315	33	3.988	0.0458	rs9326061	1	64698820	p31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2109056	C	C	254	102	284	74	6.122	0.0134	rs1926310	1	64900519	p31.3
SNP_A-1920931	G	G	297	41	307	17	9.805	1.70E-03	rs12023363	1	64999622	p31.3
SNP_A-2268370	A	A	283	109	307	83	4.492	3.41E-02	rs310241	1	65015359	p31.3
SNP_A-1886144	A	A	258	148	284	120	4.168	4.12E-02	rs310207	1	65059062	p31.3
SNP_A-2266533	A	A	347	35	345	59	5.522	1.88E-02	rs7539178	1	65095023	p31.3
SNP_A-2286009	G	G	364	50	342	74	5.326	2.10E-02	rs10889504	1	65102524	p31.3
SNP_A-1813078	A	A	352	46	342	68	4.212	4.01E-02	rs7553101	1	65132211	p31.3
SNP_A-2231431	A	A	407	5	400	16	5.803	0.016	rs553002	1	65206459	p31.3
SNP_A-2111607	T	T	362	8	340	26	10.197	0.0014	rs478665	1	65227554	p31.3
SNP_A-2049393	C	C	195	181	233	161	4.125	4.23E-02	rs10465850	1	65411224	p31.3
SNP_A-2286058	G	G	290	92	246	110	4.305	3.80E-02	rs1889928	1	65422823	p31.3
SNP_A-2248595	A	A	307	107	272	140	6.52	1.07E-02	rs10889531	1	65426139	p31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2223020	G	G	289	73	268	100	4.957	2.60E-02	rs12037114	1	65428893	p31.3
SNP_A-2084149	T	T	369	37	386	16	8.684	3.20E-03	rs7541003	1	65544373	p31.2
SNP_A-2160984	C	C	296	8	328	2	4.182	4.09E-02	rs11579567	1	65669162	p31.2
SNP_A-2000104	C	C	387	13	398	4	4.914	2.66E-02	rs2455012	1	66233019	p31.2
SNP_A-2212297	G	G	310	50	315	27	6.453	0.0111	rs1392815	1	66256978	p31.2
SNP_A-1934901	A	A	367	49	387	31	4.576	3.24E-02	rs4655595	1	66270780	p31.2
SNP_A-1735947	T	T	318	70	367	43	9.357	2.20E-03	rs1572930	1	66273034	p31.2
SNP_A-1921172	G	G	414	0	406	4	4.059	4.39E-02	rs17128467	1	66332865	p31.2
SNP_A-2166229	A	A	209	171	249	141	6.249	0.0124	rs699262	1	66642664	p31.2
SNP_A-1936692	G	G	327	61	309	83	3.85	4.97E-02	rs7551967	1	66652099	p31.2
SNP_A-1802975	T	T	305	77	325	49	6.773	9.30E-03	rs7543244	1	66671565	p31.2
SNP_A-1871513	G	G	321	91	342	62	6.084	1.36E-02	rs4336823	1	66680590	p31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2124281	T	T	340	56	320	82	5.46	0.0195	rs17472890	1	66703513	p31.2
SNP_A-2130393	G	G	298	62	306	40	4.575	3.24E-02	rs6667872	1	67268199	p31.2
SNP_A-1804219	C	C	203	193	230	156	5.479	1.92E-02	rs7539795	1	67321467	p31.2
SNP_A-2181569	C	C	308	92	278	118	4.735	2.96E-02	rs11805303	1	67387537	p31.2
SNP_A-2131610	C	T	170	152	200	156	5.455	0.0195	rs10489629	1	67400370	p31.2
SNP_A-2045577	A	A	254	142	289	113	5.509	0.0189	—	1	67401629	p31.2
SNP_A-1946676	G	G	362	30	349	13	5.774	1.63E-02	rs11209026	1	67417979	p31.2
SNP_A-1916487	G	G	349	19	377	7	6.281	1.22E-02	—	1	67434940	p31.2
SNP_A-1924276	A	G	191	177	206	160	4.928	0.0264	rs6660226	1	67456622	p31.2
SNP_A-2087317	A	A	235	81	223	109	4.048	4.42E-02	rs11209034	1	67456705	p31.2
SNP_A-2135666	G	G	332	76	345	51	4.993	2.55E-02	rs675327	1	67869617	p31.2
SNP_A-1946937	G	G	385	15	375	29	4.566	3.26E-02	rs663612	1	67876519	p31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796596	T	T	383	29	372	48	4.772	2.89E-02	rs17130314	1	67993272	p31.2
SNP_A-2149843	G	G	384	4	406	0	4.207	4.03E-02	rs4433365	1	68212904	p31.2
SNP_A-1900417	A	A	388	24	397	11	4.912	2.67E-02	rs2820477	1	68420655	p31.2
SNP_A-1923262	G	G	311	25	342	8	9.948	1.60E-03	rs3001033	1	68420829	p31.2
SNP_A-2033274	G	G	190	132	238	102	8.746	3.10E-03	rs3125929	1	68577466	p31.2
SNP_A-1909061	C	C	246	114	266	86	4.612	3.18E-02	rs9436398	1	68586040	p31.2
SNP_A-2088457	G	G	222	182	252	156	3.879	4.89E-02	rs3125695	1	68613756	p31.2
SNP_A-1894643	C	C	388	16	406	4	7.564	6.00E-03	rs3762282	1	68656813	p31.2
SNP_A-2143957	A	A	385	15	397	5	5.179	0.0229	rs10493447	1	68662415	p31.2
SNP_A-2144702	T	T	366	30	385	17	4.032	4.47E-02	rs10518303	1	68762493	p31.2
SNP_A-1891630	C	C	378	24	396	12	4.374	3.65E-02	rs11209332	1	68800683	p31.2
SNP_A-2285185	A	A	312	18	306	6	5.558	0.0184	rs11209336	1	68838149	p31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2146427	G	G	327	43	315	63	3.913	4.79E-02	rs854276	1	68948401	p31.2
SNP_A-1916842	A	A	337	3	315	11	5.022	2.50E-02	rs7417717	1	69010507	p31.2
SNP_A-2128635	A	A	242	112	244	70	7.332	6.80E-03	rs288923	1	69545744	p31.1
SNP_A-2101649	T	T	254	88	248	52	6.609	0.0101	rs1304513	1	69611862	p31.1
SNP_A-1715931	C	C	380	12	373	27	5.754	1.65E-02	rs12045965	1	69793578	p31.1
SNP_A-1679464	A	A	382	12	370	28	6.571	0.0104	rs1015819	1	69815001	p31.1
SNP_A-1756683	G	G	373	25	368	44	5.025	2.50E-02	rs10489927	1	70075231	p31.1
SNP_A-2141532	C	C	400	16	381	33	6.355	0.0117	rs12040177	1	70152583	p31.1
SNP_A-2038794	C	C	397	13	378	26	4.755	0.0292	rs12047627	1	70165026	p31.1
SNP_A-1940343	T	T	391	5	369	17	7.056	7.90E-03	rs12023122	1	70170933	p31.1
SNP_A-1949730	G	G	383	3	365	11	4.874	2.73E-02	rs12035355	1	70172259	p31.1
SNP_A-1817963	C	C	306	8	328	2	3.968	4.64E-02	rs4650029	1	70313047	p31.1
SNP_A-2298820	T	T	228	156	246	124	4.082	4.33E-02	rs535112	1	70601497	p31.1
SNP_A-2284752	G	G	298	114	275	145	4.557	3.28E-02	rs4311837	1	70736159	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2088393	A	A	223	157	204	192	4.027	0.0448	rs4612577	1	70736289	p31.1
SNP_A-1810166	C	C	312	82	294	108	4.013	4.52E-02	rs4650065	1	70737017	p31.1
SNP_A-2262452	G	G	175	169	207	147	4.07	4.37E-02	rs2820551	1	70875929	p31.1
SNP_A-2183155	T	T	247	139	222	172	4.753	0.0293	rs10443262	1	71047528	p31.1
SNP_A-1955471	G	G	275	137	246	172	5.536	1.86E-02	rs2421805	1	71051769	p31.1
SNP_A-2168255	C	C	341	35	365	21	4.185	4.08E-02	rs17090681	1	71107043	p31.1
SNP_A-1718783	A	A	348	48	337	71	4.444	3.50E-02	rs1385919	1	71976334	p31.1
SNP_A-1791900	C	C	338	52	309	81	7.623	5.80E-03	rs6424464	1	72558481	p31.1
SNP_A-1868266	C	C	364	52	333	79	6.924	8.50E-03	rs782245	1	72627865	p31.1
SNP_A-1938917	C	C	337	43	313	71	7.743	5.40E-03	rs2764508	1	72948035	p31.1
SNP_A-2263905	T	T	396	8	411	1	5.645	1.75E-02	rs17093667	1	73106114	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2055269	A	A	332	58	369	41	4.375	3.65E-02	rs9661557	1	73732584	p31.1
SNP_A-1846754	A	A	322	44	325	25	4.891	0.027	rs1576429	1	73804516	p31.1
SNP_A-1806099	C	T	205	181	213	157	8.629	0.0033	rs2132999	1	73948678	p31.1
SNP_A-2137058	T	T	380	24	402	10	6.306	0.012	rs6685128	1	74044408	p31.1
SNP_A-2228080	C	C	384	20	403	9	4.553	3.29E-02	rs17094539	1	74056935	p31.1
SNP_A-1717337	G	G	337	63	370	42	5.564	0.0183	rs696699	1	74437995	p31.1
SNP_A-2238862	G	G	400	4	416	0	4.139	0.0419	rs274576	1	74607669	p31.1
SNP_A-2194787	A	A	376	4	396	0	4.19	0.0407	rs6701139	1	74685693	p31.1
SNP_A-1744127	A	A	341	51	373	33	5.047	0.0247	rs277362	1	74710537	p31.1
SNP_A-2079811	C	C	339	73	358	48	5.64	1.76E-02	rs3911348	1	74731063	p31.1
SNP_A-2160576	C	C	331	53	369	35	5.24	2.21E-02	rs696694	1	74772334	p31.1
SNP_A-1667262	G	G	312	86	346	66	4.148	4.17E-02	rs10493550	1	74882926	p31.1
SNP_A-1690777	T	T	302	98	336	74	5.038	2.48E-02	rs7529122	1	74908350	p31.1
SNP_A-1734400	G	G	311	89	347	63	6.294	0.0121	rs10493553	1	75033004	p31.1
SNP_A-1723982	C	C	295	87	281	121	5.391	2.02E-02	rs1852349	1	75033155	p31.1
SNP_A-2102329	C	C	321	81	296	108	4.865	2.74E-02	rs1327098	1	75074014	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2033146	A	A	307	107	333	75	6.639	0.01	rs11162190	1	75089501	p31.1
SNP_A-1735406	G	G	356	34	339	69	11.909	6.00E-04	rs4949821	1	75093550	p31.1
SNP_A-1744709	C	C	361	39	339	69	8.946	0.0028	rs10493561	1	75097735	p31.1
SNP_A-1914997	G	G	288	78	260	116	8.741	3.10E-03	rs11162286	1	75139418	p31.1
SNP_A-2239445	A	A	303	89	270	122	7.062	7.90E-03	rs6693646	1	75178431	p31.1
SNP_A-1647200	A	A	334	44	322	66	4.49	3.41E-02	rs10493569	1	75196566	p31.1
SNP_A-1709059	C	C	356	30	335	47	4.371	3.66E-02	rs10493570	1	75202621	p31.1
SNP_A-2250512	G	G	285	95	301	67	5.085	0.0241	rs279713	1	75212280	p31.1
SNP_A-2313303	G	G	307	97	342	68	6.941	8.40E-03	rs1818970	1	75214135	p31.1
SNP_A-1941670	T	T	314	78	275	97	4.124	4.23E-02	rs11162482	1	75259291	p31.1
SNP_A-2000126	A	A	314	64	261	77	3.861	4.94E-02	rs7541725	1	75261827	p31.1
SNP_A-2108372	T	T	307	85	270	112	5.945	1.48E-02	rs12729173	1	75275643	p31.1
SNP_A-1786886	T	T	277	83	244	118	8.179	4.20E-03	rs12138223	1	75327047	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170600	C	C	249	87	260	62	4.136	4.20E-02	rs1343519	1	75577836	p31.1
SNP_A-2282142	G	G	411	5	420	0	5.078	2.42E-02	rs17097978	1	75591361	p31.1
SNP_A-1689897	C	C	266	130	228	178	10.281	1.30E-03	rs1250880	1	75619195	p31.1
SNP_A-1680208	G	G	225	175	275	137	9.453	2.10E-03	rs1146635	1	75674928	p31.1
SNP_A-2206350	G	G	222	136	241	81	12.85	3.00E-04	rs11163860	1	75806255	p31.1
SNP_A-1894544	G	G	181	163	201	129	4.717	2.99E-02	rs211719	1	75817778	p31.1
SNP_A-2069645	C	C	235	135	279	99	9.22	2.40E-03	rs12732722	1	75819909	p31.1
SNP_A-2191689	A	A	243	121	295	95	7.268	7.00E-03	rs12745456	1	75820076	p31.1
SNP_A-1838639	C	C	187	141	238	120	6.51	1.07E-02	rs211713	1	75820179	p31.1
SNP_A-2206660	C	C	205	153	234	104	10.692	1.10E-03	rs814875	1	75821594	p31.1
SNP_A-2129254	A	A	208	176	239	135	7.424	6.40E-03	rs399160	1	75826685	p31.1
SNP_A-2103311	G	G	242	124	286	100	5.71	1.69E-02	rs2347540	1	75831489	p31.1
SNP_A-1936931	A	A	223	187	260	150	6.897	0.0086	rs440826	1	75832321	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207550	G	G	220	108	269	81	8.062	4.50E-03	rs6695055	1	75886170	p31.1
SNP_A-2221597	T	T	217	123	253	91	7.519	6.10E-03	rs11161465	1	75903765	p31.1
SNP_A-2207767	G	G	272	126	234	172	9.876	1.70E-03	rs1250876	1	75905253	p31.1
SNP_A-1729868	A	A	266	130	317	95	9.593	0.002	rs10493578	1	75912827	p31.1
SNP_A-1842968	C	C	281	133	237	181	11.056	9.00E-04	rs7516477	1	75916523	p31.1
SNP_A-1700963	A	A	200	182	220	150	3.846	0.0499	rs4083965	1	75925859	p31.1
SNP_A-1680550	C	C	281	119	323	89	7.072	7.80E-03	rs10493580	1	75927505	p31.1
SNP_A-1813054	C	C	213	165	253	139	5.404	0.0201	rs7552289	1	75950462	p31.1
SNP_A-2043557	A	A	195	139	231	101	9.053	2.60E-03	rs1146607	1	75952789	p31.1
SNP_A-2042338	A	A	217	179	261	143	7.996	4.70E-03	rs1146610	1	75953344	p31.1
SNP_A-2208385	C	C	212	204	262	150	13.493	2.00E-04	rs1146632	1	75963767	p31.1
SNP_A-2208399	C	T	174	156	210	144	9.968	1.60E-03	rs1146634	1	75964032	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2216699	C	C	305	83	255	121	11.357	8.00E-04	rs1498311	1	75966747	p31.1
SNP_A-2197338	G	G	188	176	242	136	11.65	6.00E-04	rs1146644	1	75976809	p31.1
SNP_A-2174178	T	T	319	43	325	25	4.62	3.16E-02	rs1251272	1	76001025	p31.1
SNP_A-2160339	A	A	383	19	385	5	7.992	4.70E-03	rs5745391	1	76018681	p31.1
SNP_A-2232014	A	A	242	60	230	106	11.272	8.00E-04	rs1001160	1	76070612	p31.1
SNP_A-2205106	T	T	241	107	195	149	11.721	6.00E-04	rs1303870	1	76071556	p31.1
SNP_A-2208450	G	G	299	77	246	112	11.201	8.00E-04	rs946163	1	76095070	p31.1
SNP_A-1845735	G	A	219	197	243	177	9.245	2.40E-03	rs12043473	1	76101807	p31.1
SNP_A-1879299	T	T	255	155	289	115	8.007	4.70E-03	rs12410373	1	76110270	p31.1
SNP_A-2209521	T	T	299	93	264	142	12.151	5.00E-04	rs1251584	1	76136461	p31.1
SNP_A-2210387	C	C	283	107	323	87	4.205	4.03E-02	rs12035171	1	76202109	p31.1
SNP_A-2211024	G	G	236	84	218	116	5.536	1.86E-02	rs1251465	1	76250417	p31.1
SNP_A-1855364	C	C	282	132	255	159	3.863	4.94E-02	rs1144345	1	76261996	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2117714	C	C	354	50	343	73	4.92	2.66E-02	rs6673424	1	76296835	p31.1
SNP_A-2295408	C	C	357	45	346	68	4.678	3.05E-02	rs2631779	1	76302018	p31.1
SNP_A-2213596	C	C	340	50	376	30	6.491	1.08E-02	rs752819	1	76515543	p31.1
SNP_A-2160408	G	G	319	45	357	25	7.42	6.40E-03	rs7539896	1	76518295	p31.1
SNP_A-2084821	G	G	399	3	407	11	4.34	3.72E-02	rs4364924	1	76545222	p31.1
SNP_A-2024464	G	G	300	108	330	86	3.846	0.0499	rs17098942	1	76590177	p31.1
SNP_A-1804005	C	C	230	152	271	127	5.269	2.17E-02	rs4949718	1	76611485	p31.1
SNP_A-1827601	A	A	307	45	331	25	6.595	1.02E-02	rs9437150	1	76617373	p31.1
SNP_A-2293268	T	T	306	106	279	133	4.296	3.82E-02	rs12756608	1	76617864	p31.1
SNP_A-2214618	C	C	316	82	342	60	4.416	0.0356	rs1436085	1	76677639	p31.1
SNP_A-2214643	T	T	390	0	379	7	7.137	0.0076	rs315095	1	76683949	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2313027	G	G	337	33	338	18	4.145	4.18E-02	rs1002451	1	76691999	p31.1
SNP_A-2076029	G	G	316	48	336	26	7.149	7.50E-03	rs315080	1	76712120	p31.1
SNP_A-2195527	C	C	408	0	408	6	5.957	0.0147	rs12120882	1	76902486	p31.1
SNP_A-1749763	C	C	378	22	401	11	4.169	4.12E-02	rs10493537	1	77160975	p31.1
SNP_A-2272145	A	A	356	8	375	1	5.745	1.65E-02	rs17099802	1	77173109	p31.1
SNP_A-2176940	C	C	253	145	198	156	4.55	3.29E-02	rs7517698	1	77461384	p31.1
SNP_A-1903255	G	G	255	43	333	25	9.705	0.0018	rs12079185	1	77473196	p31.1
SNP_A-2265224	C	C	349	25	368	8	9.256	0.0023	rs2602953	1	77487725	p31.1
SNP_A-2222756	G	G	372	42	388	24	5.241	2.21E-02	rs17098286	1	77579845	p31.1
SNP_A-1843966	C	C	286	54	297	25	10.371	1.30E-03	rs7551211	1	77715106	p31.1
SNP_A-2265689	G	G	277	111	301	87	3.906	4.81E-02	rs631045	1	78269535	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2037348	A	A	238	154	203	195	7.549	6.00E-03	rs12406019	1	78390151	p31.1
SNP_A-1941548	C	C	354	60	366	40	4.122	4.23E-02	rs11162463	1	78493944	p31.1
SNP_A-2229606	T	T	233	145	180	160	5.544	1.85E-02	rs6669498	1	78843826	p31.1
SNP_A-1664318	G	G	246	146	288	106	9.648	0.0019	rs953403	1	78951103	p31.1
SNP_A-2233661	T	T	253	145	296	122	4.862	0.0275	rs1386594	1	79258538	p31.1
SNP_A-2233778	A	A	261	131	294	102	5.551	1.85E-02	rs12760876	1	79262299	p31.1
SNP_A-1911870	T	T	253	99	220	138	8.67	3.20E-03	rs12120643	1	80223971	p31.1
SNP_A-2244906	G	G	277	133	242	166	5.998	0.0143	rs6699329	1	80226794	p31.1
SNP_A-2244932	A	A	265	125	235	159	5.85	1.56E-02	rs12123981	1	80227262	p31.1
SNP_A-2141961	G	G	285	85	240	118	9.026	2.70E-03	rs4306087	1	80277468	p31.1
SNP_A-2052245	T	T	259	121	239	159	5.547	1.85E-02	rs11162928	1	80300385	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253559	G	G	259	125	229	149	3.899	4.83E-02	rs12119851	1	80301979	p31.1
SNP_A-2000144	C	C	366	6	364	0	5.919	1.50E-02	rs7529438	1	80447117	p31.1
SNP_A-2233367	G	G	400	4	416	0	4.139	0.0419	rs2997198	1	80472887	p31.1
SNP_A-1832179	G	G	309	21	318	10	4.026	0.0448	rs6684037	1	81144962	p31.1
SNP_A-1904387	C	C	376	12	395	3	5.742	0.0166	rs6424730	1	81154571	p31.1
SNP_A-1914602	C	C	330	26	334	50	6.553	1.05E-02	rs1346245	1	81259706	p31.1
SNP_A-2140491	G	C	198	182	197	159	4.076	4.35E-02	rs677675	1	81288345	p31.1
SNP_A-2279983	T	T	343	9	322	2	3.965	0.0465	rs10874241	1	81600626	p31.1
SNP_A-2066489	T	T	305	69	322	46	5.013	0.0252	rs11163289	1	81604528	p31.1
SNP_A-2060413	A	A	301	59	313	25	13.316	3.00E-04	rs7536003	1	81799303	p31.1
SNP_A-2198559	C	C	337	39	304	56	4.395	3.60E-02	rs17423764	1	81858123	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801146	T	T	350	6	381	1	3.975	4.62E-02	rs17107063	1	81918099	p31.1
SNP_A-2030292	A	A	410	4	418	0	4.058	4.40E-02	rs17107225	1	81997040	p31.1
SNP_A-2155998	G	G	314	4	322	0	4.076	4.35E-02	rs17107348	1	82028363	p31.1
SNP_A-2063796	C	C	405	5	420	0	5.153	2.32E-02	rs386783	1	82114811	p31.1
SNP_A-2265055	G	G	241	165	258	132	3.926	4.76E-02	rs1144283	1	82538486	p31.1
SNP_A-1898645	G	G	344	40	304	60	5.939	1.48E-02	rs2767656	1	82567259	p31.1
SNP_A-1878564	A	A	351	25	331	43	5.346	2.08E-02	rs17491079	1	82569867	p31.1
SNP_A-1942757	A	A	261	115	236	142	4.089	4.32E-02	rs7537152	1	82677010	p31.1
SNP_A-1914025	T	T	330	14	344	4	5.823	1.58E-02	rs17108486	1	82686917	p31.1
SNP_A-2156118	T	T	246	162	223	195	4.058	4.40E-02	rs1998927	1	83030116	p31.1
SNP_A-2264264	A	A	412	4	418	0	4.039	4.45E-02	rs11163592	1	83051003	p31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2165088	C	C	412	4	420	0	4.058	4.40E-02	rs17109363	1	83057186	p31.1
SNP_A-2276792	G	G	335	65	345	43	4.447	3.50E-02	rs2022623	1	83265678	p31.1
SNP_A-2098262	T	T	356	60	379	41	4.275	3.87E-02	rs3904795	1	83552294	p31.1
SNP_A-1742823	C	C	240	128	225	175	6.452	0.0111	rs7552393	1	83677144	p31.1
SNP_A-1883581	C	C	307	27	316	12	5.845	1.56E-02	rs1324487	1	84021884	p31.1
SNP_A-1765625	C	C	303	39	305	13	12.15	5.00E-04	rs2642183	1	84315508	p31.1
SNP_A-1717837	A	A	315	53	303	79	5.095	0.024	rs2297139	1	85460827	p22.3
SNP_A-1806688	T	T	363	51	346	72	3.974	4.62E-02	rs1342323	1	85569595	p22.3
SNP_A-2300533	C	C	343	53	317	79	6.145	0.0132	rs2037584	1	85583639	p22.3
SNP_A-1685536	G	G	260	58	227	109	17.329	3.14E-05	rs952837	1	85595571	p22.3
SNP_A-1898789	C	C	323	79	350	54	5.778	1.62E-02	rs17384381	1	85609591	p22.3
SNP_A-1822518	C	C	315	77	348	50	7.338	6.80E-03	rs12130591	1	85617006	p22.3
SNP_A-2300845	G	G	229	123	256	94	5.373	2.05E-02	rs11161615	1	85618837	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1855100	G	G	307	95	344	70	5.716	1.68E-02	rs11161616	1	85619646	p22.3
SNP_A-1812763	G	G	301	95	275	131	6.784	9.20E-03	rs480414	1	85639484	p22.3
SNP_A-2068094	G	G	314	76	343	51	6.181	0.0129	rs17391800	1	85663243	p22.3
SNP_A-1921745	C	C	281	59	254	88	7.078	7.80E-03	rs9658584	1	85759332	p22.3
SNP_A-2047626	A	A	287	127	331	83	12.352	4.00E-04	rs1980927	1	85782639	p22.3
SNP_A-2268270	A	A	397	19	410	8	4.686	0.0304	rs1360239	1	85804414	p22.3
SNP_A-2304380	A	A	299	47	263	65	4.722	0.0298	rs12563027	1	85959339	p22.3
SNP_A-2028601	G	G	357	43	338	62	3.958	4.67E-02	—	1	85961599	p22.3
SNP_A-1837840	T	T	266	90	222	122	8.594	3.40E-03	rs272504	1	86545674	p22.3
SNP_A-1866267	G	G	179	157	197	119	5.485	1.92E-02	rs1321695	1	86659768	p22.3
SNP_A-1956783	A	A	377	23	394	10	5.476	1.93E-02	rs2231586	1	86741623	p22.3
SNP_A-1876047	G	G	324	50	352	26	8.718	3.20E-03	rs17129945	1	87485524	p22.3
SNP_A-1782087	A	G	183	151	168	146	4.454	3.48E-02	rs1856047	1	87609928	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805515	C	C	302	82	333	57	5.964	0.0146	rs983332	1	87844401	p22.3
SNP_A-2090152	A	A	390	18	398	6	6.062	0.0138	rs17130103	1	87862563	p22.3
SNP_A-2215820	C	C	358	38	379	23	4.242	3.94E-02	rs12726803	1	88009948	p22.3
SNP_A-1785447	C	C	302	32	324	16	6.054	1.39E-02	rs1334334	1	88092488	p22.3
SNP_A-1690423	T	T	369	29	396	14	6.009	1.42E-02	rs10493597	1	88213746	p22.2
SNP_A-1719699	C	C	370	30	397	15	5.774	1.63E-02	rs10489567	1	88270837	p22.2
SNP_A-1659490	T	T	370	30	397	15	5.774	1.63E-02	rs10489568	1	88271115	p22.2
SNP_A-1861363	T	T	225	157	196	184	4.13	4.21E-02	rs10923040	1	88376029	p22.2
SNP_A-1787407	G	G	369	27	353	45	4.85	2.77E-02	rs10493806	1	88405970	p22.2
SNP_A-1901282	C	C	308	92	273	121	6.012	1.42E-02	rs661446	1	88427388	p22.2
SNP_A-2069632	C	C	385	13	356	30	7.674	5.60E-03	rs673212	1	88441020	p22.2
SNP_A-1792253	A	A	378	18	364	40	8.53	3.50E-03	rs1295491	1	88452886	p22.2
SNP_A-2043455	A	A	347	15	307	35	9.886	1.70E-03	rs10923053	1	88455678	p22.2
SNP_A-2092300	G	G	384	18	359	37	7.36	6.70E-03	rs6692873	1	88472441	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1797602	G	G	310	104	279	133	5.175	0.0229	rs608410	1	88482684	p22.2
SNP_A-1788588	A	A	380	30	402	14	6.394	0.0115	rs932486	1	88516573	p22.2
SNP_A-2059888	T	T	317	25	305	7	8.999	2.70E-03	---	1	88529129	p22.2
SNP_A-2195596	G	G	362	0	344	4	4.184	4.08E-02	rs10923083	1	88671940	p22.2
SNP_A-1753563	G	G	273	127	311	101	5.261	0.0218	rs4658149	1	89325103	p22.2
SNP_A-1750825	A	A	347	29	364	14	5.634	1.76E-02	rs4259628	1	89394147	p22.2
SNP_A-1735979	A	G	209	191	227	185	4.386	3.62E-02	rs1380416	1	89416126	p22.2
SNP_A-2243326	G	G	416	0	416	4	3.981	4.60E-02	rs17130801	1	89572289	p22.2
SNP_A-1687562	C	C	280	120	253	159	6.643	0.01	rs6656884	1	89604748	p22.2
SNP_A-1805366	A	A	341	29	369	17	3.898	4.83E-02	rs4326608	1	89639210	p22.2
SNP_A-2085904	G	G	263	69	305	45	7.689	5.60E-03	rs12403074	1	89665437	p22.2
SNP_A-2265277	C	T	209	183	216	180	4.871	2.73E-02	rs10801744	1	89665565	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2190925	C	C	269	139	323	91	14.9	0.0001	rs12409358	1	89704855	p22.2
SNP_A-2080800	C	C	285	115	334	84	8.316	3.90E-03	rs12755723	1	89719716	p22.2
SNP_A-2149684	G	G	271	131	319	85	13.697	2.00E-04	rs17438800	1	89723496	p22.2
SNP_A-2069841	G	G	268	124	313	87	9.894	1.70E-03	rs12730853	1	89775201	p22.2
SNP_A-1957603	A	A	234	122	263	85	8.216	4.20E-03	rs1923766	1	89775867	p22.2
SNP_A-2238455	C	C	319	55	325	35	4.235	3.96E-02	rs12045241	1	89794245	p22.2
SNP_A-2087227	T	C	197	189	215	161	5.163	2.31E-02	rs10922680	1	89813347	p22.2
SNP_A-2260059	G	G	249	87	208	112	6.433	0.0112	rs2390794	1	89837587	p22.2
SNP_A-1925141	C	C	292	120	258	162	8.281	4.00E-03	rs6675409	1	89846413	p22.2
SNP_A-1842541	C	T	191	185	210	154	5.357	0.0206	rs17441836	1	89847454	p22.2
SNP_A-1918994	C	C	267	95	243	123	4.704	3.01E-02	rs4658318	1	89944201	p22.2
SNP_A-2162183	C	C	320	42	305	61	3.843	5.00E-02	rs1744664	1	89993136	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1828248	G	G	358	2	288	12	9.351	2.20E-03	rs2480472	1	90249491	p22.2
SNP_A-1801876	G	G	393	13	399	3	6.276	1.22E-02	rs7539781	1	90568267	p22.2
SNP_A-1803563	C	C	404	12	416	4	4.157	4.15E-02	rs17131081	1	90721862	p22.2
SNP_A-1805847	T	T	348	26	376	10	8.007	4.70E-03	rs1615273	1	90975031	p22.2
SNP_A-1854354	G	G	374	24	398	12	4.569	3.26E-02	rs1188930	1	91021545	p22.2
SNP_A-1926120	A	A	384	30	404	12	8.217	4.10E-03	rs1188928	1	91023933	p22.2
SNP_A-2087173	C	C	327	85	355	61	5.076	2.43E-02	rs613217	1	91332249	p22.2
SNP_A-1926310	A	A	401	9	415	1	6.597	1.02E-02	rs17131472	1	91674988	p22.2
SNP_A-2084608	C	C	395	17	399	5	6.488	0.0109	rs546975	1	91675760	p22.2
SNP_A-2090583	A	A	405	7	420	0	7.196	7.30E-03	rs11164900	1	91711756	p22.1
SNP_A-2284942	C	C	410	6	416	0	6.044	0.014	rs17131547	1	91923041	p22.1
SNP_A-2091586	A	A	371	15	361	3	7.498	6.20E-03	rs2634019	1	92039898	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2298354	T	T	271	129	247	159	4.193	4.06E-02	rs2811600	1	93046159	p22.1
SNP_A-1677858	A	A	259	157	288	130	4.073	0.0436	rs4240956	1	93935790	p22.1
SNP_A-2304399	C	C	242	138	264	110	4.07	0.0436	rs2818164	1	93949216	p22.1
SNP_A-1829059	A	A	257	149	277	119	3.983	4.60E-02	rs2143990	1	93961538	p22.1
SNP_A-1652084	T	T	259	141	299	111	6.316	0.012	rs3789405	1	94003125	p22.1
SNP_A-1647442	C	C	279	119	318	94	5.242	2.21E-02	rs3789407	1	94003407	p22.1
SNP_A-1807012	T	T	225	127	247	99	4.443	3.50E-02	rs12140446	1	94076580	p22.1
SNP_A-1830036	A	A	227	127	183	141	4.134	4.20E-02	—	1	94157814	p22.1
SNP_A-2154478	C	C	291	111	323	85	5.073	2.43E-02	rs4147839	1	94221247	p22.1
SNP_A-2152658	C	C	287	125	327	93	7.227	7.20E-03	rs2275035	1	94257181	p22.1
SNP_A-2242068	C	C	263	79	315	51	9.907	1.60E-03	rs4847196	1	94266474	p22.1
SNP_A-2059540	C	C	210	140	244	114	5.118	2.37E-02	rs4147825	1	94272959	p22.1
SNP_A-1893196	C	C	280	90	260	116	3.974	4.62E-02	rs6697764	1	94450867	p22.1
SNP_A-2237408	G	G	368	16	360	32	5.339	2.08E-02	rs1778214	1	94773376	p21.3
SNP_A-1870807	G	G	378	28	369	45	3.99	0.0458	rs1747649	1	94774053	p21.3
SNP_A-2250409	T	T	385	7	372	20	6.483	0.0109	rs2391383	1	94798430	p21.3
SNP_A-1727112	C	C	370	16	401	7	4.162	4.13E-02	rs592097	1	95184259	p21.3
SNP_A-1921269	T	T	235	135	200	156	4.063	4.38E-02	rs11165383	1	95512574	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247092	A	A	376	16	395	7	3.865	4.93E-02	rs12410939	1	95862226	p21.3
SNP_A-2081493	T	T	301	97	278	124	4.192	4.06E-02	rs1144303	1	96208319	p21.3
SNP_A-1847048	G	G	282	110	293	81	4.193	4.06E-02	rs161110	1	96216097	p21.3
SNP_A-1756162	T	T	352	48	378	32	4.003	4.54E-02	rs10489720	1	96301428	p21.3
SNP_A-2088624	T	T	268	130	308	110	3.957	4.67E-02	rs613614	1	96405899	p21.3
SNP_A-1709077	T	T	328	52	322	76	4.141	0.0419	rs10489798	1	96716847	p21.3
SNP_A-1926824	T	T	267	101	257	137	4.755	0.0292	rs1325756	1	96818982	p21.3
SNP_A-2312167	C	C	344	50	367	31	5.181	2.28E-02	rs635578	1	97016592	p21.3
SNP_A-2181399	C	C	313	77	288	108	6.189	0.0129	rs559734	1	97016889	p21.3
SNP_A-2175840	G	G	311	27	331	11	7.337	6.80E-03	rs9783115	1	97515615	p21.3
SNP_A-2122395	C	C	391	17	403	5	6.727	9.50E-03	rs11165869	1	97599155	p21.3
SNP_A-1731873	G	G	344	56	321	91	8.953	0.0028	rs7527085	1	97716328	p21.3
SNP_A-1724252	A	A	332	46	296	72	7.66	5.60E-03	rs10493894	1	97728590	p21.3
SNP_A-1708050	T	T	333	65	320	92	4.662	3.08E-02	rs10493895	1	97734149	p21.3
SNP_A-2198386	G	G	342	62	311	91	6.963	8.30E-03	rs4246514	1	98009752	p21.3
SNP_A-1851845	C	C	359	9	385	1	6.883	8.70E-03	rs6693444	1	98402235	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2046999	C	C	270	76	276	52	4.088	4.32E-02	rs12084220	1	98627428	p21.3
SNP_A-2086927	T	T	278	100	258	132	4.974	2.57E-02	rs1655577	1	98689096	p21.3
SNP_A-1884836	A	A	274	86	245	121	7.489	6.20E-03	rs1434377	1	98692012	p21.3
SNP_A-2159779	C	C	294	88	255	117	6.741	9.40E-03	rs7527591	1	98780528	p21.3
SNP_A-2133273	G	G	401	11	410	2	6.331	1.19E-02	rs10875167	1	98793706	p21.3
SNP_A-2000219	A	A	272	112	245	139	4.314	0.0378	rs4617427	1	98892128	p21.3
SNP_A-1878314	G	G	318	10	284	24	7.063	7.90E-03	---	1	99142085	p21.3
SNP_A-1702433	C	C	385	11	385	23	4.057	4.40E-02	rs953020	1	99651046	p21.2
SNP_A-2144250	A	A	300	110	272	142	5.415	0.02	rs11166268	1	99720628	p21.2
SNP_A-2082034	C	C	304	112	279	139	3.972	4.63E-02	rs10875236	1	99738459	p21.2
SNP_A-1943945	G	G	319	53	290	74	4.767	2.90E-02	rs11166344	1	99984192	p21.2
SNP_A-1811573	C	C	405	11	418	2	6.417	1.13E-02	rs4908033	1	100031122	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1877368	T	T	216	146	175	173	6.311	0.012	rs12038567	1	100060676	p21.2
SNP_A-2000232	C	C	221	143	201	177	4.298	3.82E-02	rs6577142	1	100063656	p21.2
SNP_A-2199176	C	C	308	96	278	120	4.158	4.14E-02	rs486408	1	100064777	p21.2
SNP_A-1718931	C	C	317	79	352	58	4.808	2.83E-02	rs6687613	1	100380551	p21.2
SNP_A-2130102	T	T	334	68	314	92	4.198	4.05E-02	rs651042	1	100505060	p21.2
SNP_A-1886964	C	C	299	51	323	27	8.311	3.90E-03	rs1545021	1	100585434	p21.2
SNP_A-1843960	G	G	305	49	342	34	4.168	4.12E-02	rs1971779	1	100585729	p21.2
SNP_A-2000237	C	C	317	73	351	51	5.453	0.0195	rs6577171	1	100598991	p21.2
SNP_A-2282813	C	C	367	29	372	12	6.9	0.0086	rs1063302	1	100696460	p21.2
SNP_A-1838327	G	G	298	38	304	22	4.176	4.10E-02	rs17123149	1	100850800	p21.2
SNP_A-2307506	C	C	353	25	376	12	5.164	2.31E-02	rs7524946	1	101316802	p21.2
SNP_A-1887975	G	G	297	117	324	92	4.16	4.14E-02	rs12041851	1	101479295	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1821837	C	C	387	13	359	29	6.965	8.30E-03	rs10874491	1	101610734	p21.2
SNP_A-2280913	C	C	336	16	323	35	7.285	7.00E-03	rs6699556	1	101620418	p21.2
SNP_A-1888890	C	C	341	67	365	47	4.305	3.80E-02	rs10493954	1	101635236	p21.2
SNP_A-2251902	T	T	387	13	365	27	5.463	1.94E-02	rs2201116	1	101636347	p21.2
SNP_A-2100758	G	G	376	22	389	11	3.883	4.88E-02	rs12026998	1	101941800	p21.2
SNP_A-2101919	G	G	309	59	333	33	8.24	4.10E-03	rs10874514	1	101946985	p21.2
SNP_A-2263973	G	G	348	54	376	32	6.667	9.80E-03	rs11164296	1	101948143	p21.2
SNP_A-2174214	A	A	400	4	385	13	5.007	0.0252	rs11164339	1	102117082	p21.1
SNP_A-1643900	G	G	374	22	399	9	6.082	0.0137	rs1341913	1	102297998	p21.1
SNP_A-1693415	C	C	372	20	395	5	9.61	0.0019	rs10874598	1	102298866	p21.1
SNP_A-2251752	C	C	378	32	399	17	5.116	2.37E-02	rs7546407	1	102430956	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2088476	A	A	376	24	394	12	4.376	3.64E-02	rs17126268	1	102438420	p21.1
SNP_A-1899759	A	A	382	30	404	16	4.8	2.85E-02	rs1572999	1	102542456	p21.1
SNP_A-2150310	T	T	379	29	394	16	4.042	4.44E-02	rs1418096	1	102542870	p21.1
SNP_A-2191136	T	T	351	21	356	10	3.89	4.86E-02	rs1340401	1	102549903	p21.1
SNP_A-2127314	A	A	388	22	405	11	3.988	0.0458	rs2376022	1	102552795	p21.1
SNP_A-2176975	T	T	367	23	389	11	4.75	0.0293	rs769340	1	102561809	p21.1
SNP_A-1782250	G	G	394	22	411	9	5.792	0.0161	rs17126603	1	102580079	p21.1
SNP_A-2268942	G	G	369	11	390	2	6.627	0.01	rs11164503	1	102592022	p21.1
SNP_A-1827835	T	T	365	19	374	6	6.849	8.90E-03	rs10782894	1	102605393	p21.1
SNP_A-2157474	C	C	394	18	410	8	4.121	4.23E-02	---	1	104151165	p21.1
SNP_A-2233624	C	C	378	16	401	7	3.958	4.67E-02	rs3849298	1	104195859	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2118147	C	C	387	29	409	9	11.13	8.00E-04	rs7548445	1	104196955	p21.1
SNP_A-2289298	A	A	378	20	402	8	5.704	1.69E-02	rs7516686	1	104196974	p21.1
SNP_A-2157806	C	C	386	24	405	11	5.242	2.21E-02	---	1	104201543	p21.1
SNP_A-2199830	C	A	203	191	221	169	5.272	2.17E-02	rs11185393	1	104464022	p21.1
SNP_A-1896772	G	G	350	36	348	18	5.478	1.93E-02	---	1	104733671	p21.1
SNP_A-1872138	C	C	347	37	338	18	5.63	0.0177	rs7538177	1	105106521	p21.1
SNP_A-1846534	G	G	396	8	409	1	5.61	1.79E-02	rs11184619	1	105828069	p21.1
SNP_A-2234891	T	T	350	12	339	3	5.011	0.0252	rs7537222	1	105848934	p21.1
SNP_A-2061847	C	C	338	64	364	40	6.497	1.08E-02	rs12408810	1	106352985	p21.1
SNP_A-1681976	A	A	396	4	399	13	4.6	3.20E-02	rs10494047	1	106528167	p21.1
SNP_A-1912513	G	G	274	108	295	81	4.585	3.23E-02	rs10881418	1	106824265	p21.1
SNP_A-1938713	C	C	361	23	380	12	3.862	4.94E-02	rs17509160	1	107567055	p13.3
SNP_A-1739415	C	C	295	95	270	136	8.065	4.50E-03	rs10494078	1	107710452	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207697	G	G	250	156	222	186	4.288	3.84E-02	rs4914946	1	107726270	p13.3
SNP_A-1943362	T	C	210	206	236	180	4.344	3.71E-02	rs7543435	1	107914752	p13.3
SNP_A-2081711	A	A	313	25	347	11	6.627	0.01	rs17020104	1	108065712	p13.3
SNP_A-2135185	G	G	310	106	279	139	6.072	0.0137	rs17485868	1	108068042	p13.3
SNP_A-2098632	C	C	307	89	280	112	3.854	4.96E-02	rs6583052	1	108105451	p13.3
SNP_A-1945525	A	A	294	80	276	106	4.119	0.0424	rs10494081	1	108114145	p13.3
SNP_A-1783761	G	G	209	139	243	109	6.164	1.30E-02	rs6677889	1	108118868	p13.3
SNP_A-1915486	G	G	400	10	393	23	5.14	2.34E-02	rs17558834	1	108135067	p13.3
SNP_A-2196540	G	G	314	10	350	2	6.136	0.0132	rs1149168	1	109685429	p13.3
SNP_A-2064877	A	A	407	5	416	0	5.079	2.42E-02	rs17023269	1	109796058	p13.3
SNP_A-2061412	G	G	377	23	392	10	5.409	0.02	rs7535932	1	110363964	p13.3
SNP_A-2289520	T	T	258	82	242	112	4.871	2.73E-02	rs609690	1	110549832	p13.3
SNP_A-1808144	G	G	350	60	330	82	3.992	4.57E-02	rs1857512	1	110705391	p13.3
SNP_A-1868665	G	G	321	43	311	65	4.446	3.50E-02	rs1857513	1	110705499	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1680030	A	A	382	18	375	37	6.452	0.0111	rs1631763	1	110767483	p13.3
SNP_A-1733042	C	C	298	100	281	129	3.994	4.57E-02	rs1418425	1	110767613	p13.3
SNP_A-1696890	A	A	382	18	370	32	4.107	4.27E-02	rs1780569	1	110768490	p13.3
SNP_A-2253411	C	C	391	15	408	6	4.141	0.0419	rs1769203	1	110784000	p13.3
SNP_A-2074179	G	G	245	65	232	90	4.16	4.14E-02	rs12085135	1	110955417	p13.3
SNP_A-1961770	C	C	301	81	334	50	9.046	2.60E-03	rs4839556	1	110974382	p13.3
SNP_A-2000298	C	C	266	74	254	104	4.872	2.73E-02	rs343820	1	111054570	p13.3
SNP_A-1726612	C	C	267	103	254	140	5.209	2.25E-02	rs10489793	1	111302849	p13.2
SNP_A-2039242	A	A	322	36	319	19	4.698	3.02E-02	rs588885	1	111380218	p13.3
SNP_A-2195007	C	C	333	73	318	98	3.88	4.89E-02	rs679407	1	111416965	p13.3
SNP_A-1661348	C	C	272	128	253	159	3.86	4.95E-02	rs155678	1	112012580	p13.2
SNP_A-1916196	T	T	358	20	348	38	5.645	1.75E-02	rs767373	1	112129981	p13.2
SNP_A-1898265	G	G	380	16	361	31	5.254	2.19E-02	rs17028939	1	112137839	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2068814	C	C	376	26	358	44	5.07	2.43E-02	rs6681719	1	112250785	p13.2
SNP_A-2310038	C	C	308	22	268	50	13.449	2.00E-04	rs3017626	1	112270073	p13.2
SNP_A-2284193	G	G	249	127	229	157	3.875	4.90E-02	rs269107	1	112426836	p13.2
SNP_A-1834861	T	T	256	154	289	129	4.13	4.21E-02	rs12071268	1	112429735	p13.2
SNP_A-1962385	A	A	285	131	257	161	4.524	3.34E-02	rs1440167	1	112433142	p13.2
SNP_A-2304824	A	A	270	118	251	151	4.495	3.40E-02	rs1992509	1	112435506	p13.2
SNP_A-1852679	C	C	283	131	255	161	4.535	0.0332	rs4838942	1	112436979	p13.2
SNP_A-2250812	C	C	313	85	292	112	4.385	3.63E-02	rs2788424	1	112443844	p13.2
SNP_A-2273588	G	G	332	66	362	34	11.532	7.00E-04	rs11102457	1	112578639	p13.2
SNP_A-1962432	G	G	348	12	330	30	8.192	4.20E-03	rs1936048	1	112599095	p13.2
SNP_A-1902063	G	G	240	154	257	117	5.116	2.37E-02	rs2483351	1	112685644	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1820594	G	G	198	158	235	139	3.936	4.73E-02	rs2483345	1	112693646	p13.2
SNP_A-2239538	C	C	317	81	345	61	3.922	4.77E-02	rs2273368	1	112775813	p13.2
SNP_A-1841793	C	G	216	146	178	168	8.803	3.00E-03	rs10776755	1	112795016	p13.2
SNP_A-1785545	G	C	135	169	192	144	6.109	0.0134	rs2999156	1	112959169	p13.2
SNP_A-1712863	G	G	192	94	281	81	8.921	0.0028	rs1324893	1	113031872	p13.2
SNP_A-2040888	G	G	252	98	299	71	7.773	0.0053	rs12410629	1	113497845	p13.2
SNP_A-2050449	C	C	247	169	290	128	9.098	2.60E-03	rs773618	1	113503380	p13.2
SNP_A-1962626	A	A	317	33	335	19	4.244	3.94E-02	rs17031460	1	113631935	p13.2
SNP_A-2132888	T	T	361	29	361	13	5.763	1.64E-02	rs4839321	1	113759506	p13.2
SNP_A-1785543	A	A	259	75	252	106	4.578	3.24E-02	rs2774308	1	114382967	p13.2
SNP_A-2172475	C	C	333	79	298	106	5.804	0.016	rs2774307	1	114383011	p13.2
SNP_A-2074621	G	G	310	48	284	70	5.217	0.0224	rs17534892	1	114394070	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2165302	C	C	374	36	386	18	6.146	0.0132	rs7556442	1	114488347	p13.2
SNP_A-2000309	C	C	272	70	296	50	4.324	3.76E-02	rs6695414	1	114547132	p13.2
SNP_A-2159458	G	G	234	128	256	98	4.881	2.71E-02	rs9429539	1	114635678	p13.2
SNP_A-2055806	G	G	247	119	285	99	4.12	0.0424	rs9429542	1	114640785	p13.2
SNP_A-1733370	C	C	283	115	320	88	5.738	0.0166	rs10494171	1	115000636	p13.1
SNP_A-1925362	A	A	323	7	304	16	3.945	0.047	rs11585572	1	115210299	p13.1
SNP_A-1810971	C	C	233	93	275	65	8.144	0.0043	rs7528116	1	115399308	p13.1
SNP_A-2050318	T	T	344	14	347	31	5.896	0.0152	rs1286227	1	115421780	p13.1
SNP_A-1963064	C	C	267	109	303	85	5.056	2.45E-02	rs6691441	1	115434855	p13.1
SNP_A-1963065	C	C	282	120	307	93	4.479	3.43E-02	rs9803637	1	115434959	p13.1
SNP_A-1947161	T	T	283	123	309	95	4.733	2.96E-02	rs195177	1	115467216	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1914703	A	A	314	66	318	42	4.822	0.0281	rs4076018	1	115554852	p13.1
SNP_A-2278642	G	G	258	122	291	97	4.755	0.0292	rs4623701	1	115615773	p13.1
SNP_A-1963173	T	T	372	10	353	23	5.572	1.82E-02	rs17033794	1	115657192	p13.1
SNP_A-1942655	A	A	389	21	408	10	4.279	3.86E-02	rs1942230	1	115825644	p13.1
SNP_A-1854205	G	G	386	18	407	7	5.275	2.16E-02	rs3017158	1	115831957	p13.1
SNP_A-1871433	T	T	346	14	383	5	5.1	2.39E-02	rs7543596	1	115847218	p13.1
SNP_A-2112005	T	T	402	14	413	5	4.407	3.58E-02	rs4839460	1	115866873	p13.1
SNP_A-2234484	T	T	389	25	405	13	4.093	4.31E-02	rs10923133	1	115913106	p13.1
SNP_A-1792207	C	C	371	41	355	63	4.963	2.59E-02	rs4428890	1	115917890	p13.1
SNP_A-2070567	G	G	375	11	393	3	4.866	2.74E-02	rs815118	1	116147949	p13.1
SNP_A-2156402	C	C	383	13	403	5	3.886	0.0487	rs815105	1	116153556	p13.1
SNP_A-2283952	T	T	280	136	254	164	3.874	4.90E-02	rs9887967	1	116517202	p13.1
SNP_A-2095230	T	T	222	146	228	98	7.006	8.10E-03	rs973142	1	116545346	p13.1
SNP_A-1682546	T	T	286	114	261	151	6.133	1.33E-02	rs3767770	1	116963029	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251341	C	C	285	77	245	97	4.753	0.0292	rs797999	1	117005805	p13.1
SNP_A-2306032	G	G	286	48	310	32	4.072	0.0436	rs17587765	1	117283121	p13.1
SNP_A-2235004	A	A	356	40	342	62	4.946	2.61E-02	rs12132610	1	117539328	p12
SNP_A-2148257	A	A	346	30	338	48	4.117	4.25E-02	rs878618	1	117591108	p12
SNP_A-1731267	G	G	395	5	412	0	5.182	2.28E-02	rs2273581	1	117842884	p12
SNP_A-2063902	T	T	366	34	380	20	3.892	4.85E-02	rs17037436	1	117852620	p12
SNP_A-2110371	T	T	369	25	393	7	10.836	0.001	rs1437257	1	117869426	p12
SNP_A-2098300	T	T	380	36	399	21	4.392	0.0361	rs1657818	1	117870995	p12
SNP_A-2233108	A	A	327	5	328	0	4.977	2.57E-02	rs10923364	1	117897860	p12
SNP_A-1786703	C	C	279	133	249	161	4.366	3.67E-02	rs17257575	1	117988577	p12
SNP_A-1963979	T	G	216	166	208	182	7.539	6.00E-03	rs4659339	1	117993864	p12
SNP_A-2253811	C	C	313	79	339	57	4.575	3.24E-02	rs319464	1	118005135	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2038727	G	A	231	181	223	197	6.991	8.20E-03	rs4659059	1	118007967	p12
SNP_A-1963988	C	C	324	90	351	67	4.43	3.53E-02	rs1469919	1	118009013	p12
SNP_A-1954884	G	-	243	171	207	207	6.309	0.012	rs10801987	1	118038946	p12
SNP_A-1963999	T	T	240	162	199	191	6.031	0.0141	rs1946625	1	118048260	p12
SNP_A-2203495	G	C	238	172	204	196	6.665	9.80E-03	rs1418729	1	118070003	p12
SNP_A-1789396	C	C	231	169	202	198	4.234	3.96E-02	rs1578739	1	118071407	p12
SNP_A-2178793	A	G	230	176	213	203	5.082	2.42E-02	rs6680046	1	118079343	p12
SNP_A-2090224	T	T	317	7	332	0	7.25	7.10E-03	rs17037680	1	118101643	p12
SNP_A-1823836	G	G	231	147	194	184	7.357	6.70E-03	rs911250	1	118105004	p12
SNP_A-1947810	A	A	406	4	416	0	4.078	4.34E-02	rs17037690	1	118120317	p12
SNP_A-1964040	T	T	359	53	336	74	4.229	3.97E-02	rs10489592	1	118152037	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903390	A	A	410	4	416	0	4.039	4.45E-02	—	1	118162293	p12
SNP_A-2285834	T	C	220	170	216	184	8.565	3.40E-03	rs10923448	1	118192633	p12
SNP_A-2148762	A	G	210	160	209	187	6.965	8.30E-03	rs6678671	1	118219935	p12
SNP_A-1952805	T	T	411	5	420	0	5.078	2.42E-02	rs17037773	1	118228296	p12
SNP_A-1964071	C	C	218	134	204	172	4.397	3.60E-02	rs6677802	1	118272089	p12
SNP_A-2224565	C	C	311	55	313	35	4	4.55E-02	rs1779413	1	119097591	p12
SNP_A-2314041	T	T	351	19	361	7	5.674	0.0172	rs2798868	1	142445417	q21.1
SNP_A-1851111	C	C	374	6	370	16	4.52	3.35E-02	rs2799312	1	142545761	q21.1
SNP_A-1921193	A	A	398	8	409	1	5.575	1.82E-02	rs2791916	1	143583561	q21.1
SNP_A-2297123	T	T	341	39	360	24	4.066	4.38E-02	rs7539416	1	144106402	q21.1
SNP_A-1966066	G	G	360	0	355	5	5.035	2.48E-02	rs791269	1	144462372	q21.1
SNP_A-2237411	C	C	348	66	375	47	4.127	4.22E-02	rs7512708	1	144594241	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2163812	G	G	310	62	332	40	5.499	0.019	rs1814653	1	144857947	q21.1
SNP_A-1739665	A	A	325	75	357	53	5.16	2.31E-02	rs903784	1	144871176	q21.1
SNP_A-1781144	A	A	312	98	336	72	4.86	0.0275	rs1932366	1	144917189	q21.1
SNP_A-2298873	G	G	319	59	350	40	4.897	0.0269	rs481176	1	144922189	q21.1
SNP_A-2256223	A	A	314	102	340	78	4.229	3.97E-02	rs1805204	1	144929606	q21.1
SNP_A-1928641	T	T	324	62	355	37	7.683	5.60E-03	rs2999617	1	144940574	q21.1
SNP_A-1756597	G	G	371	21	373	39	4.911	2.67E-02	rs10494363	1	147126077	q21.2
SNP_A-1841285	C	C	346	0	340	4	4.047	4.43E-02	rs11803792	1	147821339	q21.2
SNP_A-2045632	A	A	326	0	300	4	4.317	3.77E-02	rs4354539	1	148242156	q21.3
SNP_A-1966528	T	T	222	190	259	163	4.792	0.0286	rs1891593	1	148348989	q21.3
SNP_A-1798452	T	T	279	95	259	125	4.703	3.01E-02	rs12751350	1	148363746	q21.3
SNP_A-2296621	A	A	379	35	386	20	4.077	4.35E-02	rs4845388	1	148667149	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2303782	A	A	341	29	362	14	5.812	1.59E-02	rs1490191	1	148729824	q21.3
SNP_A-2298544	G	G	366	4	384	0	4.173	4.11E-02	rs2104179	1	149166693	q21.3
SNP_A-2302233	A	A	202	118	178	144	4.09	4.31E-02	rs6701376	1	149511828	q21.3
SNP_A-2045259	T	T	328	0	318	4	4.1	4.29E-02	rs16834843	1	149768923	q21.3
SNP_A-1867021	C	C	310	28	347	13	6.885	8.70E-03	rs11205279	1	150171758	q21.3
SNP_A-2257688	C	C	377	37	395	21	4.829	2.80E-02	rs3006412	1	150203615	q21.3
SNP_A-1786440	T	A	214	194	232	188	4.898	0.0269	rs11264249	1	151506254	q22
SNP_A-1967356	G	G	350	0	309	7	7.836	5.10E-03	rs1218563	1	151631426	q22
SNP_A-2243606	G	G	399	17	413	7	4.389	3.62E-02	rs1218586	1	151645395	q22
SNP_A-2146782	T	T	214	158	194	192	4.026	0.0448	rs10908455	1	151880356	q22
SNP_A-2252665	C	C	217	93	193	127	6.502	1.08E-02	rs4971059	1	151961854	q22
SNP_A-1902447	C	C	359	47	339	67	4.082	4.33E-02	rs11545882	1	152838169	q22
SNP_A-2099609	A	G	218	196	229	189	4.61	3.18E-02	rs7542798	1	153037377	q22
SNP_A-2185830	A	A	323	51	285	67	3.881	4.88E-02	rs2287025	1	153043214	q22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2045866	G	G	326	62	311	93	6.233	1.25E-02	---	1	153118235	q22
SNP_A-2055555	T	C	220	192	229	185	6.272	0.0123	rs2274226	1	153127700	q22
SNP_A-1967491	G	G	221	143	185	163	4.142	4.18E-02	rs2842854	1	153156765	q22
SNP_A-2309907	A	A	367	19	349	39	7.344	6.70E-03	rs1171556	1	153244414	q22
SNP_A-1716727	C	C	271	81	297	59	4.625	0.0315	rs2764404	1	153503215	q22
SNP_A-1651558	T	C	208	180	213	183	4.288	3.84E-02	rs2296374	1	153504195	q22
SNP_A-1780685	G	G	370	30	399	17	4.377	3.64E-02	rs943551	1	153668570	q23.1
SNP_A-1857436	G	G	294	66	301	41	5.466	1.94E-02	rs6692812	1	154096944	q23.1
SNP_A-1784853	G	G	315	31	336	14	7.077	7.80E-03	rs1807765	1	154295444	q23.1
SNP_A-2291615	T	T	271	53	276	32	4.832	2.79E-02	rs12135411	1	154295960	q23.1
SNP_A-2252301	C	C	268	134	302	104	5.79	0.0161	rs3843307	1	154297648	q23.1
SNP_A-1967848	C	C	338	58	370	38	5.435	1.97E-02	rs3761961	1	154310336	q23.1
SNP_A-2283470	T	T	319	43	351	25	6.03	0.0141	rs1972239	1	154321874	q23.1
SNP_A-2285620	T	T	214	110	256	90	5.036	2.48E-02	rs2779158	1	154362243	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1894633	C	C	246	130	289	105	5.698	1.70E-02	rs12755544	1	154366090	q23.1
SNP_A-1967879	A	A	215	135	241	97	7.5	6.20E-03	rs2208753	1	154397374	q23.1
SNP_A-1859266	C	C	249	149	297	113	8.99	2.70E-03	rs12134075	1	154399589	q23.1
SNP_A-2027337	C	G	206	162	193	175	5.229	2.22E-02	rs2777982	1	154406947	q23.1
SNP_A-2250932	A	C	220	168	198	192	4.357	3.69E-02	rs12734504	1	154434308	q23.1
SNP_A-1693825	T	T	232	168	269	145	4.183	4.08E-02	rs725377	1	154436881	q23.1
SNP_A-1736105	G	G	241	157	287	125	7.399	6.50E-03	rs2779159	1	154767149	q23.1
SNP_A-1720575	A	A	238	154	287	125	7.095	7.70E-03	rs2777965	1	154767209	q23.1
SNP_A-1722824	G	G	254	146	295	119	5.574	1.82E-02	rs10489674	1	154782811	q23.1
SNP_A-1724392	G	G	240	112	274	82	6.866	8.80E-03	rs2224607	1	154788513	q23.1
SNP_A-2130067	C	C	378	34	392	18	5.173	0.0229	rs4445460	1	154806332	q23.1
SNP_A-2076774	A	A	365	45	352	66	4.132	4.21E-02	rs10908647	1	155107015	q23.1
SNP_A-1968120	T	T	273	137	246	168	4.536	0.0332	rs4656283	1	155193901	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2314952	T	T	278	118	253	145	3.944	0.047	rs12127259	1	155518068	q23.1
SNP_A-1937751	G	G	303	47	269	81	11.052	9.00E-04	rs11265075	1	155600511	q23.1
SNP_A-1874007	C	C	347	53	317	75	5.056	2.45E-02	rs11265081	1	155609618	q23.1
SNP_A-2196970	T	T	309	59	275	91	8.801	3.00E-03	rs11265085	1	155620084	q23.1
SNP_A-1816504	C	C	350	58	320	88	7.508	6.10E-03	rs11805139	1	155629811	q23.1
SNP_A-2000384	G	G	294	104	317	77	4.873	2.73E-02	rs2820153	1	155665593	q23.1
SNP_A-1825368	G	G	330	60	350	38	5.522	1.66E-02	rs1623601	1	155757200	q23.1
SNP_A-2099899	T	T	409	7	421	1	4.631	3.14E-02	rs1615480	1	155757657	q23.1
SNP_A-2128876	C	C	306	22	314	8	6.582	0.0103	rs2494260	1	156059258	q23.2
SNP_A-1966464	A	A	241	111	211	141	5.563	0.0183	rs1584252	1	156336701	q23.2
SNP_A-2139924	T	T	259	105	270	74	5.036	2.48E-02	rs2275674	1	156340553	q23.2
SNP_A-1915603	G	G	343	15	337	3	7.594	5.90E-03	rs16842641	1	156560983	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1968577	C	C	402	12	404	4	3.961	4.66E-02	rs16831210	1	156767862	q23.2
SNP_A-2307565	G	G	332	10	328	24	5.646	1.75E-02	rs1016732	1	156900041	q23.2
SNP_A-2294519	T	T	411	3	409	11	4.533	0.0332	rs12028921	1	157162697	q23.2
SNP_A-2265899	A	A	217	175	257	153	4.449	0.0349	rs4073054	1	158013560	q23.3
SNP_A-1853217	G	G	359	57	383	39	4.109	4.27E-02	rs12746613	1	158280097	q23.3
SNP_A-1937815	A	A	278	138	307	113	3.909	4.80E-02	rs10918214	1	158631119	q23.3
SNP_A-2049064	A	A	257	121	284	90	5.881	1.53E-02	rs4570397	1	158635341	q23.3
SNP_A-1893888	G	G	356	40	381	25	4.186	4.08E-02	rs16839677	1	158719043	q23.3
SNP_A-1652430	C	C	295	75	284	110	6.083	0.0137	rs412965	1	158769138	q23.3
SNP_A-1812997	T	T	294	80	302	56	3.995	4.56E-02	rs4480335	1	158905035	q23.3
SNP_A-1784130	G	G	257	99	293	75	5.469	1.94E-02	rs4657178	1	158942268	q23.3
SNP_A-2280830	T	T	290	108	326	74	8.451	3.60E-03	rs10918963	1	158945525	q23.3
SNP_A-2040339	A	A	335	77	372	48	8.588	3.40E-03	rs10919039	1	158977280	q23.3
SNP_A-1826221	T	T	322	62	356	38	7.338	6.80E-03	rs4370746	1	158982290	q23.3
SNP_A-2244951	G	G	320	66	362	40	8.643	0.0033	rs10800409	1	158992373	q23.3
SNP_A-1800741	C	C	335	57	375	31	9.693	0.0019	rs10800422	1	159000426	q23.3
SNP_A-1969210	C	C	226	156	255	125	5.163	2.31E-02	rs1858233	1	159035657	q23.3
SNP_A-1969223	G	G	213	181	255	145	7.7	5.50E-03	rs347282	1	159044411	q23.3
SNP_A-1809795	G	G	269	107	315	85	5.407	0.0201	rs449908	1	159056103	q23.3
SNP_A-1932810	G	G	309	69	272	90	4.786	0.0287	rs10800533	1	159148287	q23.3
SNP_A-1667278	C	C	298	62	327	43	4.648	3.11E-02	rs10494365	1	159271366	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137000	T	T	291	85	263	107	3.888	4.86E-02	rs6702820	1	159335539	q23.3
SNP_A-1689438	G	G	298	98	274	132	5.909	1.51E-02	rs347311	1	159491284	q23.3
SNP_A-1641893	T	T	342	56	384	24	15.108	0.0001	rs3751286	1	159500762	q23.3
SNP_A-2313452	C	C	307	51	279	75	5.887	1.53E-02	rs2841957	1	159784676	q23.3
SNP_A-2031880	A	A	293	121	270	150	4	4.55E-02	rs2661314	1	159784811	q23.3
SNP_A-2283609	G	G	324	44	271	71	10.122	0.0015	rs17363152	1	160066216	q23.3
SNP_A-1949416	C	C	363	41	343	67	6.782	9.20E-03	rs7522124	1	160066301	q23.3
SNP_A-2201227	T	T	373	9	368	24	6.724	9.50E-03	rs17364621	1	160396616	q23.3
SNP_A-1688216	G	G	358	38	340	60	5.383	2.03E-02	rs4448497	1	160527394	q23.3
SNP_A-2314674	C	C	322	94	350	72	4.04	4.44E-02	rs17366977	1	160637331	q23.3
SNP_A-1650544	C	C	267	131	304	110	3.914	4.79E-02	rs9287057	1	160642224	q23.3
SNP_A-1969946	C	C	361	29	364	14	5.059	2.45E-02	rs12039313	1	160674030	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2032067	C	C	341	43	371	27	4.672	3.07E-02	rs16824651	1	160791088	q23.3
SNP_A-2160235	C	C	281	65	261	95	6.222	0.0126	rs12129943	1	160939514	q23.3
SNP_A-1823445	T	T	378	16	394	6	4.832	2.79E-02	rs1387353	1	161146399	q23.3
SNP_A-1912521	G	G	373	37	392	20	5.537	1.86E-02	rs16833478	1	161339760	q23.3
SNP_A-1970271	A	A	263	131	233	165	5.7	1.70E-02	rs2800780	1	161343347	q23.3
SNP_A-1650146	G	G	361	31	364	50	3.872	4.91E-02	rs7544769	1	161352324	q23.3
SNP_A-1693134	A	A	352	18	350	40	7.83	5.10E-03	rs10494412	1	161399857	q23.3
SNP_A-1892239	G	G	253	127	225	153	4.049	4.42E-02	rs10918068	1	161473246	q23.3
SNP_A-2138036	G	A	207	193	225	167	6.648	9.90E-03	rs1343546	1	161868885	q23.3
SNP_A-2078173	T	T	312	100	284	132	5.71	1.69E-02	rs1891931	1	161892236	q23.3
SNP_A-1947965	C	G	210	196	229	181	4.694	3.03E-02	rs1039588	1	161897335	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1970560	A	A	259	55	266	86	5.682	1.71E-02	rs17403138	1	161908828	q23.3
SNP_A-1833156	A	A	372	28	391	15	4.359	3.68E-02	rs10733043	1	162024257	q23.3
SNP_A-1970593	A	A	337	35	368	22	3.905	4.81E-02	rs2055681	1	162027347	q23.3
SNP_A-2000431	C	C	377	25	391	11	5.7	1.70E-02	rs6702087	1	162041844	q23.3
SNP_A-2291469	T	T	340	68	368	48	4.478	3.43E-02	rs12035029	1	162069289	q23.3
SNP_A-2208562	G	G	312	40	275	55	3.995	4.56E-02	rs466639	1	162126540	q23.3
SNP_A-2194407	C	C	349	65	332	90	4.38	3.64E-02	rs12402931	1	162154945	q23.3
SNP_A-2051071	C	C	351	9	361	1	6.535	0.0106	rs7542419	1	162157598	q23.3
SNP_A-1970656	A	A	305	93	282	126	5.751	1.65E-02	rs369598	1	162263325	q23.3
SNP_A-2302761	G	G	314	92	291	123	5.267	2.17E-02	rs2766081	1	162265638	q23.3
SNP_A-1970658	T	T	229	125	220	168	4.943	2.62E-02	rs1326376	1	162274281	q23.3
SNP_A-1970660	T	T	383	25	375	45	5.626	0.0177	rs16847331	1	162290601	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1861176	C	C	239	159	194	188	6.775	9.20E-03	rs10800114	1	162303808	q24.1
SNP_A-2207326	C	T	187	143	175	143	8.868	2.90E-03	rs1337441	1	162305508	q24.1
SNP_A-2199041	G	G	264	146	303	117	5.761	1.64E-02	rs7551594	1	162357132	q24.1
SNP_A-1715855	A	A	388	12	409	3	5.777	1.62E-02	rs1553512	1	162359190	q23.3
SNP_A-2157367	G	G	204	144	171	167	4.46	3.47E-02	rs12072634	1	162377491	q24.1
SNP_A-1891710	A	A	270	120	245	151	4.714	2.99E-02	rs2882006	1	162382811	q24.1
SNP_A-1745722	G	A	217	183	218	194	4.166	4.13E-02	rs10494436	1	162383777	q23.3
SNP_A-2087458	G	G	258	118	240	148	3.847	4.98E-02	rs6703993	1	162383931	q24.1
SNP_A-1714146	G	G	327	37	318	60	5.317	2.11E-02	rs10494438	1	162386400	q23.3
SNP_A-2023762	A	A	228	148	201	177	4.282	0.0385	rs10753688	1	162398106	q24.1
SNP_A-1663616	T	T	192	148	236	130	4.738	2.95E-02	rs1394438	1	162401539	q23.3
SNP_A-1836094	A	A	371	43	355	63	4.107	4.27E-02	rs6699874	1	162412404	q24.1
SNP_A-1659452	C	C	239	119	220	154	4.926	2.65E-02	rs722259	1	162718290	q24.1
SNP_A-1706033	C	C	292	102	276	138	5.359	0.0206	rs10494449	1	163070680	q24.1
SNP_A-2041828	A	A	358	0	326	4	4.365	3.67E-02	rs4656503	1	163208329	q24.1
SNP_A-1914076	A	G	226	154	193	183	8.883	2.90E-03	rs1389778	1	163222795	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2199679	A	A	348	4	348	0	3.977	4.61E-02	rs1021499	1	163223096	q24.1
SNP_A-1970761	G	G	226	170	264	132	7.728	5.40E-03	rs454751	1	163275200	q24.1
SNP_A-1919674	A	A	279	91	242	112	4.449	0.0349	rs7539202	1	163284381	q24.1
SNP_A-2222153	C	C	219	135	236	104	4.375	3.65E-02	rs571669	1	163316559	q24.1
SNP_A-1970824	A	A	290	74	284	46	4.942	2.62E-02	rs8440506	1	163467100	q24.1
SNP_A-2049924	A	A	353	25	332	40	4.058	4.40E-02	rs858783	1	163476135	q24.1
SNP_A-1901795	G	G	246	106	208	130	5.339	2.08E-02	rs858798	1	163497900	q24.1
SNP_A-2000447	G	G	379	33	366	54	5.219	0.0223	rs2312236	1	163525875	q24.1
SNP_A-2111338	A	A	386	8	385	1	5.364	0.0206	rs2025890	1	163745745	q24.1
SNP_A-1970901	C	C	295	121	326	90	6.102	0.0135	rs1041236	1	163786638	q24.1
SNP_A-1970951	A	T	233	177	211	203	5.024	2.50E-02	rs6427082	1	164027496	q24.2
SNP_A-2301926	A	A	358	54	342	76	4.046	4.43E-02	rs16859595	1	164464642	q24.2
SNP_A-1706843	G	G	343	3	377	15	6.765	9.30E-03	rs10489194	1	164805137	q24.2
SNP_A-2034097	G	G	320	56	305	85	6.071	0.0137	rs12049040	1	165253273	q24.2
SNP_A-1796842	T	T	258	106	222	146	9.028	2.70E-03	rs1015000	1	165358157	q24.2
SNP_A-2038735	T	T	284	92	253	129	7.937	4.80E-03	rs1015001	1	165358365	q24.2
SNP_A-2026151	G	G	352	60	332	84	4.566	3.26E-02	rs2146205	1	165611011	q24.2
SNP_A-1822822	C	C	365	39	340	64	6.954	8.40E-03	rs11586213	1	165618062	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2122469	A	A	199	139	237	117	4.835	2.79E-02	rs1358713	1	165762536	q24.2
SNP_A-1971373	G	G	380	8	402	2	3.897	4.84E-02	rs3753299	1	165908677	q24.2
SNP_A-2023618	C	C	395	13	399	3	6.226	0.0126	rs12091844	1	166164931	q24.2
SNP_A-1931833	G	G	389	15	396	6	3.915	4.79E-02	rs5355	1	166427528	q24.2
SNP_A-2000468	A	A	247	101	178	114	7.143	7.50E-03	rs2750016	1	166640760	q24.2
SNP_A-2055828	A	A	304	100	276	128	4.79	0.0286	rs16862933	1	166717454	q24.2
SNP_A-1790219	A	A	232	124	199	151	5.127	2.36E-02	rs2027020	1	167118792	q24.2
SNP_A-2238031	T	T	250	136	215	159	4.239	0.0395	rs12145296	1	167121173	q24.2
SNP_A-2099979	A	A	231	109	193	143	7.97	4.80E-03	rs1999523	1	167198834	q24.2
SNP_A-2240568	C	C	341	39	379	23	5.52	1.88E-02	rs11801783	1	167257689	q24.2
SNP_A-1882064	C	C	322	70	356	42	8.66	0.0033	rs12071298	1	167261917	q24.2
SNP_A-1928462	G	G	347	15	332	28	4.256	3.91E-02	rs17615321	1	167345964	q24.2
SNP_A-1738807	G	G	249	125	236	160	4.021	4.49E-02	rs1537390	1	167661036	q24.2
SNP_A-2311665	C	C	383	19	401	7	5.908	1.51E-02	rs16864136	1	167865547	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1912445	T	T	324	92	350	70	3.972	4.63E-02	rs11799420	1	168384635	q24.3
SNP_A-2298342	G	G	209	107	246	84	5.478	1.93E-02	rs9943293	1	168386625	q24.3
SNP_A-2112313	A	A	290	76	311	45	8.539	3.50E-03	rs11580415	1	168398489	q24.3
SNP_A-2046797	C	C	292	76	326	50	7.15	7.50E-03	rs11579698	1	168398579	q24.3
SNP_A-1830975	A	A	312	76	334	54	4.472	0.0344	rs10913529	1	168411122	q24.3
SNP_A-1972239	G	G	271	73	296	52	4.607	3.18E-02	rs3753539	1	168447842	q24.3
SNP_A-2234341	C	C	314	98	349	69	6.841	8.90E-03	rs2421950	1	168721826	q24.3
SNP_A-1972371	T	T	397	9	404	2	4.516	3.36E-02	rs16843896	1	168832854	q24.3
SNP_A-1831466	G	G	331	57	347	35	5.592	1.80E-02	rs16844620	1	169195590	q24.3
SNP_A-2185951	C	C	230	156	211	197	4.975	2.57E-02	rs10458360	1	169365632	q24.3
SNP_A-1929570	T	T	299	115	272	146	4.94	2.62E-02	rs859665	1	169396099	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2222598	G	G	312	16	289	33	6.723	9.50E-03	rs12117954	1	169398478	q24.3
SNP_A-1917447	A	A	344	56	323	95	10.343	1.30E-03	rs10798178	1	169408831	q24.3
SNP_A-1934801	A	A	354	52	320	90	11.885	6.00E-04	rs10912276	1	169410511	q24.3
SNP_A-2308528	C	C	217	121	189	157	6.5	1.08E-02	rs4916213	1	170000478	q25.1
SNP_A-2124605	A	A	361	25	351	43	4.824	0.0281	rs16845720	1	170058321	q25.1
SNP_A-1972692	G	G	257	119	264	88	3.95	4.69E-02	rs1547811	1	170061096	q25.1
SNP_A-1839575	C	C	352	54	366	36	3.853	4.96E-02	rs12139941	1	171859273	q25.1
SNP_A-1843707	C	C	391	5	402	0	5.108	2.38E-02	rs4140637	1	171884726	q25.1
SNP_A-1653284	A	A	354	46	388	26	6.875	8.70E-03	rs10489332	1	172190444	q25.1
SNP_A-1973201	A	A	334	6	317	15	4.206	4.03E-02	---	1	172234811	q25.1
SNP_A-2235451	G	G	301	87	277	119	5.886	1.53E-02	rs491132	1	172564563	q25.1
SNP_A-2288052	G	G	305	73	289	99	4.231	3.97E-02	rs505189	1	172575142	q25.1
SNP_A-1679160	T	T	233	165	272	142	4.421	3.55E-02	rs10489315	1	172607175	q25.1
SNP_A-1649914	C	C	234	166	271	141	4.57	3.25E-02	rs859448	1	172607624	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1792899	C	C	222	142	247	111	5.082	2.42E-02	rs2745255	1	173263852	q25.2
SNP_A-1973574	A	A	347	39	336	20	5.091	0.024	rs227519	1	173821561	q25.2
SNP_A-2121459	T	T	407	9	405	1	6.284	1.22E-02	rs12090000	1	173884017	q25.2
SNP_A-1798426	A	A	295	41	285	61	3.948	4.69E-02	rs10913339	1	174125844	q25.2
SNP_A-2244212	T	T	352	0	328	4	4.266	3.89E-02	---	1	174184610	q25.2
SNP_A-2143672	A	A	290	118	321	87	6.261	0.0123	rs1252078	1	174347207	q25.2
SNP_A-2281679	A	A	285	117	324	92	5.25	2.19E-02	rs1252077	1	174347251	q25.2
SNP_A-1792031	A	A	293	119	326	88	6.397	0.0114	rs7529907	1	174370672	q25.2
SNP_A-1845423	G	G	372	4	372	0	3.979	4.61E-02	rs16851816	1	174453628	q25.2
SNP_A-2303310	A	A	339	47	344	28	4.593	3.21E-02	rs6674700	1	174514561	q25.2
SNP_A-1751907	A	A	296	8	388	2	5.4	0.0201	rs12026256	1	174672952	q25.2
SNP_A-2215149	G	G	323	45	315	69	4.815	2.82E-02	rs1336779	1	174699854	q25.2
SNP_A-2157152	A	A	378	12	370	24	4.065	4.38E-02	rs16852325	1	174700896	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829029	C	C	271	127	227	163	8.276	4.00E-03	rs4652286	1	174700972	q25.2
SNP_A-2192987	C	C	319	85	293	117	6.13	1.33E-02	rs12409286	1	174702804	q25.2
SNP_A-2153629	A	A	285	75	263	107	6.374	1.16E-02	rs10913494	1	174708724	q25.2
SNP_A-2297469	C	C	275	123	258	160	4.892	0.027	rs1932847	1	174711465	q25.2
SNP_A-2103814	T	T	310	96	285	133	6.855	8.80E-03	rs7531837	1	174711877	q25.2
SNP_A-2175124	G	G	349	27	336	48	6.043	0.014	rs946819	1	174726129	q25.2
SNP_A-2109339	A	A	378	12	380	28	6.002	0.0143	rs16852397	1	174762256	q25.2
SNP_A-1758838	G	G	369	31	350	60	9.622	0.0019	rs1415083	1	175234986	q25.2
SNP_A-1884325	G	G	321	55	291	79	5.721	1.68E-02	rs2811261	1	175393797	q25.2
SNP_A-2145710	T	T	318	82	294	106	4.005	4.54E-02	rs7543277	1	175410851	q25.2
SNP_A-2218092	A	A	241	175	270	144	4.654	0.031	rs10913619	1	175423023	q25.2
SNP_A-2112656	T	T	366	50	340	80	7.862	5.00E-03	rs965558	1	175514282	q25.2
SNP_A-2223973	T	T	360	44	362	26	4.313	0.0378	rs7512551	1	176218255	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783280	A	A	400	4	404	0	4.02	4.50E-02	rs10913837	1	176322723	q25.2
SNP_A-1974306	G	G	304	54	337	29	9.142	2.50E-03	rs7543669	1	176974316	q25.2
SNP_A-2259500	C	C	390	4	369	15	6.822	9.00E-03	rs2254465	1	176989349	q25.2
SNP_A-1974322	T	T	327	17	277	31	6.254	0.0124	rs6673113	1	177172698	q25.3
SNP_A-1948290	T	T	220	164	254	134	5.438	1.97E-02	rs3845412	1	177624818	q25.3
SNP_A-1801932	A	A	322	86	289	109	4.372	3.65E-02	rs6700566	1	177827209	q25.3
SNP_A-2113159	G	G	311	57	282	86	7.299	6.90E-03	rs4652565	1	177840665	q25.3
SNP_A-1677039	C	C	315	81	296	112	5.392	2.02E-02	rs3856075	1	177841754	q25.3
SNP_A-2058801	A	A	354	4	374	0	4.202	4.04E-02	rs10910947	1	178212966	q25.3
SNP_A-2092745	T	T	271	131	308	102	5.896	0.0152	rs1281323	1	178833397	q25.3
SNP_A-2150834	A	A	406	8	397	19	4.578	3.24E-02	rs1779826	1	178863197	q25.3
SNP_A-1856347	C	C	246	96	275	61	9.364	2.20E-03	rs1779819	1	178910139	q25.3
SNP_A-2083515	T	T	250	156	220	200	7.118	0.0076	rs1857570	1	178913744	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2000533	C	C	214	106	265	87	5.79	0.0161	rs1419326	1	178914308	q25.3
SNP_A-2066407	T	T	251	165	224	194	3.873	4.91E-02	rs10911032	1	178917017	q25.3
SNP_A-2148291	T	T	233	147	213	179	3.852	4.97E-02	rs10911042	1	178937072	q25.3
SNP_A-1807576	A	A	235	153	212	188	4.594	3.21E-02	rs12031309	1	178987605	q25.3
SNP_A-1794854	A	A	245	163	221	197	4.327	3.75E-02	rs12741962	1	178988179	q25.3
SNP_A-2251914	A	A	248	168	223	199	3.903	0.0482	rs7543476	1	178989454	q25.3
SNP_A-2284211	A	C	185	151	184	162	4.63	3.14E-02	rs511918	1	179311259	q25.3
SNP_A-2227823	G	G	240	144	209	179	5.912	1.50E-02	rs12132529	1	179311986	q25.3
SNP_A-2187450	G	G	362	52	385	33	4.936	0.0263	rs528846	1	179323993	q25.3
SNP_A-1693250	G	G	244	154	209	195	7.476	0.0063	rs516567	1	179818416	q25.3
SNP_A-2301183	C	C	345	9	323	21	5.382	2.03E-02	rs12025732	1	180346512	q25.3
SNP_A-1850998	A	A	384	8	335	17	4.442	3.51E-02	rs12033293	1	180372079	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2268124	C	C	269	101	304	78	4.903	2.68E-02	rs7524927	1	180610168	q25.3
SNP_A-1975413	G	G	261	103	295	81	4.516	3.36E-02	rs12562685	1	180616927	q25.3
SNP_A-1975415	A	A	289	89	253	117	6.112	0.0134	rs10911467	1	180617063	q25.3
SNP_A-2315045	A	A	252	94	241	131	6.613	0.0101	rs7530464	1	180673211	q25.3
SNP_A-1756300	T	T	375	7	379	17	3.937	4.72E-02	rs6658064	1	180860556	q25.3
SNP_A-1703803	A	A	279	121	318	96	5.189	2.27E-02	rs10494568	1	181027951	q25.3
SNP_A-2101899	A	A	313	99	290	126	4.098	4.29E-02	rs4399119	1	181053286	q25.3
SNP_A-2124650	A	A	308	40	286	68	8.023	4.60E-03	rs4381150	1	181057271	q25.3
SNP_A-1920203	T	T	351	29	332	52	7.039	8.00E-03	rs7522628	1	181146605	q25.3
SNP_A-1919761	C	C	316	26	309	45	4.957	2.60E-02	rs11805001	1	181150486	q25.3
SNP_A-2303579	G	G	265	61	215	97	13.11	3.00E-04	rs7513091	1	181220620	q25.3
SNP_A-2172846	A	A	365	15	358	4	6.003	0.0143	rs16823344	1	181320367	q25.3
SNP_A-2056136	G	T	197	193	228	158	7.174	7.40E-03	rs861590	1	181470957	q25.3
SNP_A-2036035	A	A	335	55	363	33	6.578	0.0103	rs10752942	1	181478744	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2070562	C	C	192	170	246	162	4.117	4.25E-02	rs861607	1	181482692	q25.3
SNP_A-2180478	G	G	285	51	308	34	4.239	0.0395	rs338564	1	181508736	q25.3
SNP_A-2158177	T	T	293	115	325	93	3.863	4.94E-02	rs4651234	1	181531000	q25.3
SNP_A-1799507	T	C	195	193	236	174	4.902	2.68E-02	rs626576	1	181541010	q25.3
SNP_A-2245984	A	A	201	189	240	170	3.957	4.67E-02	rs677953	1	181557603	q25.3
SNP_A-2095641	A	A	395	7	411	1	4.695	3.02E-02	rs234669	1	181561705	q25.3
SNP_A-1725812	A	A	359	41	349	65	5.336	2.09E-02	rs7415961	1	181602484	q25.3
SNP_A-1666298	A	A	356	40	345	65	5.884	1.53E-02	rs6424950	1	181603218	q25.3
SNP_A-1859123	G	G	213	189	249	149	7.519	6.10E-03	rs4650671	1	181613361	q25.3
SNP_A-1701643	T	T	353	45	343	67	4.288	3.84E-02	rs10489721	1	181661355	q25.3
SNP_A-1678646	C	C	354	46	343	69	4.597	3.20E-02	rs10489722	1	181661934	q25.3
SNP_A-1975754	T	T	358	14	361	29	4.823	0.0281	rs17379801	1	181772115	q25.3
SNP_A-1738367	A	A	379	17	405	7	4.714	2.99E-02	rs2207521	1	181800818	q25.3
SNP_A-1952651	T	T	401	7	413	1	4.633	3.14E-02	rs17519658	1	181995865	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1685544	A	T	202	198	248	166	8.889	2.90E-03	rs689157	1	182046893	q25.3
SNP_A-1975795	G	G	406	10	419	3	3.931	4.74E-02	rs16823947	1	182067021	q25.3
SNP_A-2240769	T	T	268	108	220	124	4.411	3.57E-02	rs10798013	1	182126386	q25.3
SNP_A-2246052	C	C	404	10	413	3	3.864	4.93E-02	rs13375410	1	182220369	q25.3
SNP_A-2127835	A	A	386	30	405	17	4.009	4.52E-02	rs333714	1	182295471	q25.3
SNP_A-2000542	T	T	315	19	392	8	3.856	4.93E-02	rs7416006	1	182322135	q25.3
SNP_A-2065650	C	C	338	0	300	4	4.475	0.0344	rs1322356	1	182602614	q31.1
SNP_A-1790305	G	G	311	55	290	76	4.1	4.29E-02	rs663665	1	182921662	q31.1
SNP_A-2181264	T	T	335	81	311	107	4.483	3.42E-02	rs654335	1	182929403	q31.1
SNP_A-2214380	G	G	322	68	269	85	4.911	2.67E-02	rs655434	1	182932880	q31.1
SNP_A-1903176	A	A	331	75	305	101	4.904	2.68E-02	rs664058	1	182933240	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2139853	G	G	295	51	275	75	5.25	2.19E-02	rs639851	1	182933996	q31.1
SNP_A-1908068	C	C	299	29	278	48	5.447	1.96E-02	rs638391	1	182934327	q31.1
SNP_A-1932610	C	C	322	72	296	94	3.989	0.0458	rs633606	1	182935465	q31.1
SNP_A-1880317	G	G	299	43	266	70	8.326	3.90E-03	rs622480	1	182935677	q31.1
SNP_A-2309548	A	A	335	81	313	109	4.831	2.80E-02	rs611643	1	182935714	q31.1
SNP_A-1940288	G	G	312	56	290	82	5.681	1.71E-02	rs608155	1	182936600	q31.1
SNP_A-1894169	C	C	331	77	309	105	5.02	2.51E-02	rs596457	1	182936826	q31.1
SNP_A-2076428	A	A	326	48	330	30	3.913	4.79E-02	---	1	183173433	q31.1
SNP_A-1834761	C	C	292	112	328	90	4.249	3.93E-02	rs10911877	1	183238269	q31.1
SNP_A-2175747	C	C	335	41	347	23	5.226	0.0223	rs6674145	1	183278990	q31.1
SNP_A-1743907	G	G	321	77	310	104	3.906	4.81E-02	rs586281	1	183438476	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1656691	G	G	310	64	295	89	4.326	3.75E-02	rs585738	1	183438633	q31.1
SNP_A-1709459	C	C	320	68	295	91	4.338	0.0373	rs609400	1	183477024	q31.1
SNP_A-1833335	G	G	388	4	414	0	4.246	3.94E-02	rs16825907	1	183485734	q31.1
SNP_A-1692238	C	C	342	14	324	34	8.814	3.00E-03	rs3818293	1	183531795	q31.1
SNP_A-1904199	C	C	299	73	291	43	5.839	1.57E-02	rs10752979	1	183567652	q31.1
SNP_A-2076741	C	C	199	161	231	127	6.39	0.0115	rs10737277	1	183679386	q31.1
SNP_A-1815866	C	C	300	76	306	48	5.724	0.0167	rs12065385	1	183816380	q31.1
SNP_A-1737501	A	A	384	16	410	4	7.813	5.20E-03	rs10489403	1	183991566	q31.1
SNP_A-1783001	A	A	244	152	278	128	4.148	4.17E-02	rs1892543	1	184166424	q31.1
SNP_A-1880856	G	G	286	122	254	146	3.967	4.64E-02	rs2249494	1	184167566	q31.1
SNP_A-2239583	C	C	252	136	289	115	3.966	4.64E-02	rs2789394	1	184274811	q31.1
SNP_A-2289564	C	C	324	44	362	26	6.209	1.27E-02	rs2789397	1	184279244	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1820248	C	C	318	46	357	31	4.414	0.0356	rs10798122	1	184316356	q31.1
SNP_A-1936969	G	G	387	15	402	6	4.098	4.29E-02	rs2430088	1	184510968	q31.1
SNP_A-1692498	C	C	395	5	400	14	4.055	4.40E-02	rs10494596	1	184739306	q31.1
SNP_A-2257085	G	G	302	66	313	45	4.033	4.46E-02	rs2632538	1	184854104	q31.1
SNP_A-1862436	T	T	314	84	324	58	4.591	3.21E-02	rs17539220	1	184864091	q31.1
SNP_A-2255922	G	G	299	49	333	33	4.5	0.0339	rs4517311	1	184983882	q31.1
SNP_A-2092767	C	C	397	15	415	5	5.323	2.11E-02	rs16828505	1	185002304	q31.1
SNP_A-2151736	C	C	350	66	359	41	5.644	1.75E-02	rs10753046	1	185096182	q31.1
SNP_A-2190160	C	C	307	55	339	39	3.964	0.0465	rs3919967	1	185103259	q31.1
SNP_A-2151396	C	C	330	80	353	59	3.942	4.71E-02	rs10753049	1	185104519	q31.1
SNP_A-2000556	C	C	304	52	338	36	4.268	3.88E-02	rs1565272	1	185114704	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2033410	C	C	267	57	237	79	5.245	2.20E-02	rs4480360	1	185404238	q31.1
SNP_A-1743817	G	G	347	53	381	31	7.174	7.40E-03	rs1489261	1	185671084	q31.1
SNP_A-2287544	A	A	232	136	191	155	4.541	3.31E-02	rs12757118	1	185699357	q31.1
SNP_A-1976835	T	T	240	138	204	168	5.812	1.59E-02	rs2861426	1	185716050	q31.1
SNP_A-1894634	A	G	202	150	176	160	6.578	0.0103	rs10921102	1	185726253	q31.1
SNP_A-2159367	C	C	209	137	171	159	5.059	2.45E-02	rs10921121	1	185734428	q31.1
SNP_A-2171342	A	G	209	151	171	165	5.598	1.80E-02	rs1912923	1	185753645	q31.1
SNP_A-1976870	A	-	212	154	179	179	4.574	3.25E-02	rs2175550	1	185811059	q31.1
SNP_A-1801396	A	A	229	159	195	193	6.011	1.42E-02	rs10801337	1	185966303	q31.1
SNP_A-2067313	T	C	215	169	205	177	7.144	7.50E-03	rs6428256	1	185971623	q31.1
SNP_A-1846992	G	G	237	141	199	173	6.525	0.0106	rs1935660	1	185974783	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2039392	G	G	257	159	223	195	6.065	0.0138	rs12135892	1	186008619	q31.1
SNP_A-2189148	C	C	247	137	208	162	5.175	0.0229	rs1336891	1	186049278	q31.1
SNP_A-2000559	G	A	192	186	217	167	4.079	4.34E-02	rs7417337	1	186116030	q31.1
SNP_A-1976936	T	T	226	132	207	167	4.583	3.23E-02	rs1704589	1	186139184	q31.1
SNP_A-2275018	A	A	236	148	192	176	6.606	1.02E-02	rs269720	1	186223059	q31.1
SNP_A-1909593	A	A	243	149	208	188	7.209	7.30E-03	rs269728	1	186251905	q31.1
SNP_A-1720521	G	G	244	154	220	188	4.498	0.0339	rs6428195	1	186449154	q31.1
SNP_A-1727423	T	T	244	156	221	193	4.821	0.0281	rs10494628	1	186548423	q31.1
SNP_A-1878643	G	G	224	138	254	110	5.039	2.48E-02	rs10753908	1	186716570	q31.1
SNP_A-2071336	G	G	249	159	273	127	4.605	3.19E-02	rs12032930	1	186723724	q31.1
SNP_A-1835102	T	T	233	145	250	110	4.966	0.0258	rs6704228	1	186724313	q31.1
SNP_A-1908761	G	A	209	165	181	171	3.877	4.90E-02	rs10920351	1	186726869	q31.1
SNP_A-1977150	G	A	206	160	187	177	4.291	3.83E-02	rs6657359	1	186729714	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977159	A	A	255	115	225	139	4.094	4.30E-02	rs17374565	1	186741902	q31.1
SNP_A-1977188	A	A	386	22	408	10	4.989	2.55E-02	rs10494630	1	186835972	q31.1
SNP_A-2271788	G	G	297	67	243	83	5.029	2.49E-02	rs6681246	1	186918044	q31.1
SNP_A-1715165	A	C	214	184	222	190	4.742	2.94E-02	rs1529311	1	187313752	q31.1
SNP_A-1681514	A	A	287	113	259	155	7.78	0.0053	rs1935881	1	187354645	q31.1
SNP_A-1734132	C	T	207	163	212	182	7.263	7.00E-03	rs1935880	1	187355001	q31.1
SNP_A-1697036	C	C	374	24	402	10	6.535	0.0106	rs10494631	1	187393188	q31.1
SNP_A-1829362	T	T	347	51	332	76	5.129	0.0235	rs1936992	1	187557193	q31.2
SNP_A-1709253	G	G	256	142	237	177	4.259	0.039	rs500764	1	187593098	q31.1
SNP_A-2035980	T	T	367	39	385	19	7.323	6.80E-03	rs535509	1	188160138	q31.2
SNP_A-1831205	A	A	374	20	353	35	4.652	0.031	rs562619	1	188170182	q31.2
SNP_A-1977519	G	G	262	72	255	41	6.33	1.19E-02	rs669885	1	188181640	q31.2
SNP_A-2062635	A	A	299	61	319	31	10.291	1.30E-03	rs20660086	1	188899194	q31.2
SNP_A-2058375	G	T	206	204	229	171	4.57	3.25E-02	rs1175165	1	188912928	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2028261	T	T	189	183	228	156	5.609	1.79E-02	rs1781256	1	188955848	q31.2
SNP_A-1855248	C	C	310	82	348	48	11.067	9.00E-04	rs17523810	1	188976687	q31.2
SNP_A-2063055	C	C	199	125	228	94	6.352	0.0117	rs7521847	1	188991149	q31.2
SNP_A-1977661	G	G	197	139	228	116	4.242	3.94E-02	rs2369660	1	188995246	q31.2
SNP_A-2282008	T	T	211	193	248	152	7.835	5.10E-03	rs6428094	1	189013077	q31.2
SNP_A-1865058	A	A	201	187	244	148	8.675	3.20E-03	rs1339129	1	189014886	q31.2
SNP_A-2177101	T	A	203	201	242	172	6.236	1.25E-02	rs1936663	1	189079759	q31.2
SNP_A-2059828	T	T	371	19	376	8	4.469	3.45E-02	rs10754006	1	189122290	q31.2
SNP_A-2156127	T	T	326	56	301	81	5.559	0.0184	rs12568515	1	189142937	q31.2
SNP_A-2135099	C	C	300	98	271	141	8.97	2.70E-03	rs1317165	1	189151417	q31.2
SNP_A-1883875	A	A	292	112	262	148	6.565	0.0104	rs4378188	1	189151662	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1818212	A	A	271	87	280	60	4.645	3.11E-02	rs10801121	1	189210531	q31.2
SNP_A-1677772	C	C	296	104	343	71	9.442	2.10E-03	rs1936671	1	189612012	q31.2
SNP_A-2030520	G	G	342	22	307	37	5.14	2.34E-02	rs710140	1	189643765	q31.2
SNP_A-2075620	C	C	392	22	383	37	3.875	4.90E-02	rs842798	1	189654832	q31.2
SNP_A-1829339	G	G	392	22	379	37	4.028	0.0448	rs7512241	1	189678489	q31.2
SNP_A-2288287	T	T	399	7	390	18	4.938	0.0263	rs10801186	1	189875436	q31.2
SNP_A-1709171	G	G	245	23	361	11	9.799	1.70E-03	rs2146609	1	189970930	q31.2
SNP_A-2247645	A	A	390	2	316	8	4.943	2.62E-02	rs7544199	1	190268740	q31.2
SNP_A-2099787	C	C	382	10	393	1	7.515	6.10E-03	rs16835692	1	190399553	q31.2
SNP_A-1799780	C	C	390	4	402	0	4.102	4.28E-02	rs2025761	1	190549500	q31.3
SNP_A-1661914	C	C	388	10	407	3	4.046	4.43E-02	rs10489940	1	190953943	q31.2
SNP_A-1880545	C	C	263	105	236	130	4.115	4.25E-02	rs4570405	1	191113758	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2147914	A	A	255	135	222	164	5.075	2.43E-02	rs6700592	1	191123684	q31.3
SNP_A-2028004	C	C	252	104	200	116	4.271	3.88E-02	rs4381164	1	191148467	q31.3
SNP_A-2154390	T	T	265	127	222	158	6.984	8.20E-03	rs10754108	1	191170045	q31.3
SNP_A-2100788	G	G	283	131	259	161	4.102	4.28E-02	rs10921585	1	191178206	q31.3
SNP_A-2184660	G	G	284	132	259	161	4.002	4.54E-02	rs2494147	1	191199469	q31.3
SNP_A-2076349	C	C	321	23	287	37	4.573	3.25E-02	rs7514907	1	191219447	q31.3
SNP_A-1678226	T	T	349	31	350	50	3.948	4.69E-02	rs7515996	1	191613085	q31.3
SNP_A-1978430	T	T	306	86	337	65	4.29	3.83E-02	---	1	191674561	q31.3
SNP_A-2207757	A	A	254	118	273	89	4.612	3.17E-02	rs10801378	1	191763495	q31.3
SNP_A-1836040	C	C	348	66	373	39	7.805	5.20E-03	rs6695362	1	192175918	q31.3
SNP_A-1937838	C	C	307	61	326	36	6.965	8.30E-03	rs1339559	1	192225195	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1978635	C	C	412	4	416	0	4.019	4.50E-02	rs16838837	1	192418564	q31.3
SNP_A-1863039	G	G	333	57	340	36	4.56	0.0327	rs9427902	1	192622899	q31.3
SNP_A-2044011	A	A	299	85	308	58	4.802	2.84E-02	rs4295871	1	192648544	q31.3
SNP_A-1978722	C	C	329	87	307	113	4.122	4.23E-02	rs10494740	1	192696851	q31.3
SNP_A-2156630	G	G	376	34	397	19	4.772	2.89E-02	rs16839508	1	192831896	q31.3
SNP_A-2100848	C	C	369	11	368	24	4.645	3.12E-02	rs7531491	1	193187022	q31.3
SNP_A-1658014	A	A	344	56	380	34	6.929	8.50E-03	rs4554704	1	193244888	q31.3
SNP_A-2287102	C	C	313	103	286	134	5.253	2.19E-02	rs16840224	1	193301338	q31.3
SNP_A-1647918	G	G	262	124	241	173	7.991	4.70E-03	rs10494743	1	193713392	q31.3
SNP_A-2308026	G	G	338	28	303	43	4.522	3.35E-02	rs12133659	1	194206311	q31.3
SNP_A-1805656	G	G	366	6	384	0	6.243	1.25E-02	rs10922241	1	194208894	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1979006	G	G	353	63	325	95	7.618	5.80E-03	rs4915550	1	194239922	q31.3
SNP_A-2126577	A	A	339	55	318	82	5.947	0.0147	rs1833464	1	194303234	q31.3
SNP_A-2257967	C	C	331	53	306	76	5.077	2.42E-02	rs1775466	1	194486624	q31.3
SNP_A-2141655	T	T	333	63	315	91	5.467	1.94E-02	rs7366451	1	194488729	q31.3
SNP_A-1952893	G	G	295	51	314	32	4.942	2.62E-02	rs4915257	1	194707906	q31.3
SNP_A-2231362	T	T	383	11	382	24	4.651	0.031	rs12135790	1	194811016	q31.3
SNP_A-1720263	A	A	337	63	325	89	4.425	3.54E-02	rs10494756	1	194816408	q31.3
SNP_A-1836193	A	A	300	32	320	16	5.955	0.0147	rs4556393	1	195105052	q31.3
SNP_A-1719405	T	T	395	5	414	0	5.207	2.25E-02	rs1233832	1	195324737	q31.3
SNP_A-2219125	G	A	203	165	180	162	4.311	3.79E-02	rs322912	1	195806048	q31.3
SNP_A-1979468	G	G	339	75	317	99	4.043	4.43E-02	rs12049402	1	195857959	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1713328	A	A	319	75	306	106	5.18	2.28E-02	rs10494786	1	196484149	q32.1
SNP_A-1851704	T	T	298	56	302	32	5.996	0.0143	rs12041297	1	196818081	q32.1
SNP_A-2056827	C	C	239	153	276	122	6.108	0.0135	rs2737631	1	196873834	q32.1
SNP_A-2031188	G	G	238	166	282	130	8.024	4.60E-03	rs2690035	1	196873974	q32.1
SNP_A-2256417	A	A	337	47	347	25	6.68	9.80E-03	rs12042611	1	196892982	q32.1
SNP_A-2080993	G	G	291	115	328	94	4.014	4.51E-02	rs10919835	1	196897541	q32.1
SNP_A-1652378	C	C	342	12	375	27	4.258	3.91E-02	rs962923	1	196935207	q32.1
SNP_A-1932532	A	A	396	6	406	0	6.105	0.0135	rs16846446	1	197016954	q32.1
SNP_A-2300052	C	C	406	6	418	0	6.132	1.33E-02	rs16846454	1	197017710	q32.1
SNP_A-1907909	C	C	406	4	420	0	4.117	0.0424	rs10919897	1	197031694	q32.1
SNP_A-1979852	C	C	408	6	418	0	6.102	0.0135	rs10494816	1	197144130	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1841271	C	C	362	4	390	0	4.285	0.0385	rs10919928	1	197147756	q32.1
SNP_A-1785651	T	T	310	24	324	12	4.303	3.80E-02	rs12021556	1	197166085	q32.1
SNP_A-2277281	C	C	375	5	386	0	5.112	2.38E-02	rs16846791	1	197194474	q32.1
SNP_A-1979871	G	G	388	6	354	14	3.875	4.90E-02	rs6674109	1	197201327	q32.1
SNP_A-2273037	G	G	224	154	191	185	5.454	0.0195	rs2364685	1	197424047	q32.1
SNP_A-1720867	A	A	341	59	372	40	4.818	2.82E-02	rs7556049	1	197427031	q32.1
SNP_A-1904317	T	T	191	127	231	111	4	4.55E-02	rs10449265	1	197435563	q32.1
SNP_A-1979910	T	C	197	191	221	161	5.758	1.64E-02	rs10494819	1	197436411	q32.1
SNP_A-1680784	A	A	390	4	414	0	4.224	3.99E-02	rs10494812	1	197587697	q32.1
SNP_A-2031745	G	G	299	105	325	79	4.757	0.0292	rs296513	1	197638130	q32.1
SNP_A-2264597	C	T	189	151	188	166	5.248	2.20E-02	rs3767499	1	197752508	q32.1
SNP_A-1662940	A	T	206	186	224	174	6.171	1.30E-02	rs10494820	1	197991691	q32.1
SNP_A-1653268	A	A	226	140	268	118	4.918	2.66E-02	rs2047147	1	198036124	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1851643	A	A	210	108	255	91	4.635	3.13E-02	rs7527761	1	198191909	q32.1
SNP_A-2272642	C	C	262	144	287	115	4.366	3.67E-02	rs641581	1	198193692	q32.1
SNP_A-1810390	C	C	238	150	216	186	4.677	3.06E-02	rs680198	1	198195097	q32.1
SNP_A-2260157	C	C	378	30	394	14	6.15	1.31E-02	rs475416	1	198201264	q32.1
SNP_A-1879907	C	C	231	171	274	128	9.845	1.70E-03	rs7552162	1	198227864	q32.1
SNP_A-1784546	A	A	222	158	256	118	8.168	0.0043	rs11587472	1	198229626	q32.1
SNP_A-2090892	G	G	215	175	261	143	7.421	6.40E-03	rs17469306	1	198235012	q32.1
SNP_A-2190809	C	C	233	171	259	143	3.866	4.93E-02	rs11579478	1	198244653	q32.1
SNP_A-2000604	C	C	384	12	404	4	4.329	3.75E-02	rs6701121	1	198453852	q32.1
SNP_A-1980242	A	A	395	13	404	4	4.866	2.74E-02	rs950114	1	198571867	q32.1
SNP_A-2290588	T	T	202	146	175	171	3.9	4.83E-02	rs7368409	1	198727051	q32.1
SNP_A-2128112	C	C	383	33	370	52	4.429	3.53E-02	rs12735966	1	198863721	q32.1
SNP_A-2053081	G	G	357	5	358	0	4.979	2.57E-02	rs11810671	1	199099488	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2088313	T	T	282	116	257	151	5.624	0.0177	rs10920451	1	199372947	q32.1
SNP_A-2197288	T	T	239	89	240	140	7.582	5.90E-03	rs10920452	1	199372997	q32.1
SNP_A-1862712	C	C	289	115	261	147	5.314	0.0212	rs4950866	1	199374664	q32.1
SNP_A-2284806	T	T	194	120	235	91	7.682	5.60E-03	rs11587775	1	199397238	q32.1
SNP_A-2307907	T	T	401	5	401	19	7.932	4.90E-03	rs10920462	1	199423922	q32.1
SNP_A-1980356	T	T	352	4	337	13	5.041	2.48E-02	rs10494838	1	199450632	q32.1
SNP_A-2207695	C	C	206	144	232	110	6.003	0.0143	rs10920573	1	199840165	q32.1
SNP_A-2192255	G	G	380	10	409	3	4.235	3.96E-02	rs3753476	1	199841909	q32.1
SNP_A-2223653	T	T	383	27	403	9	9.504	2.10E-03	rs10920606	1	200004878	q32.1
SNP_A-2309014	C	C	365	29	354	50	5.626	0.0177	rs4971234	1	200005023	q32.1
SNP_A-1790517	G	G	384	28	406	12	6.97	8.30E-03	rs12085417	1	200008710	q32.1
SNP_A-2218545	G	C	197	195	229	169	4.823	0.0281	rs17534202	1	200012832	q32.1
SNP_A-2279546	G	G	329	83	357	55	6.824	9.00E-03	rs16851314	1	200031937	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2222054	T	T	244	66	224	102	8.172	0.0043	rs10800928	1	200104537	q32.1
SNP_A-2269290	C	C	351	15	350	30	4.74	2.95E-02	rs7539189	1	200313988	q32.1
SNP_A-1789516	C	C	397	13	389	25	3.852	4.97E-02	rs7539296	1	200314140	q32.1
SNP_A-1642993	C	C	181	139	237	129	4.813	2.83E-02	rs722915	1	200375914	q32.1
SNP_A-2268291	A	A	334	38	369	23	4.911	2.67E-02	rs6679960	1	200836461	q32.1
SNP_A-2293103	C	C	363	51	386	32	5.037	2.48E-02	rs4951307	1	200840150	q32.1
SNP_A-1675688	T	T	309	53	306	78	4.14	0.0419	rs10494845	1	200869612	q32.1
SNP_A-2175179	G	G	262	140	297	111	5.498	0.019	rs4075219	1	200982551	q32.1
SNP_A-2233984	G	G	288	112	317	89	3.977	4.61E-02	rs10900579	1	201020708	q32.1
SNP_A-2103910	G	G	282	106	313	81	4.912	2.67E-02	rs7549429	1	201021560	q32.1
SNP_A-1891397	G	G	296	120	326	94	4.587	3.22E-02	rs6672429	1	201023477	q32.1
SNP_A-2235610	G	G	295	119	325	95	4.1	4.29E-02	rs4951360	1	201024899	q32.1
SNP_A-2074749	T	T	377	19	397	5	8.639	0.0033	rs4951362	1	201045876	q32.1
SNP_A-2078437	A	A	350	48	363	31	3.875	4.90E-02	rs11240725	1	201048741	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215261	A	A	364	4	370	0	4.044	4.43E-02	rs2999495	1	201145502	q32.1
SNP_A-2025746	A	A	330	48	338	30	4.116	4.25E-02	rs10793715	1	201399799	q32.1
SNP_A-2039703	T	T	380	34	368	52	3.917	4.78E-02	rs11240266	1	201475483	q32.1
SNP_A-2122311	T	T	368	22	347	37	4.384	3.63E-02	rs12039630	1	201500617	q32.1
SNP_A-1732528	A	A	327	71	365	49	5.807	0.016	rs955323	1	201512198	q32.1
SNP_A-2185341	C	C	370	28	363	45	3.902	0.0482	rs7525016	1	201524652	q32.1
SNP_A-2000618	T	T	327	19	328	36	4.803	2.84E-02	rs4951129	1	201528221	q32.1
SNP_A-1709563	C	C	380	16	409	3	9.648	0.0019	rs1877394	1	201584414	q32.1
SNP_A-2081698	G	G	310	92	343	71	4.198	4.05E-02	rs17345997	1	202011269	q32.1
SNP_A-2297089	T	T	286	94	249	127	7.466	0.0063	rs11240414	1	202024077	q32.1
SNP_A-1861493	A	A	273	109	242	150	8.229	4.10E-03	rs13374813	1	202024621	q32.1
SNP_A-1955323	C	C	270	74	239	97	4.888	0.027	rs11240441	1	202039446	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872841	T	T	238	94	264	70	4.853	0.0276	rs1059657	1	202135894	q32.1
SNP_A-2280573	C	C	270	136	305	105	6.099	0.0135	rs6692041	1	202166400	q32.1
SNP_A-1868273	A	A	248	122	288	98	5.267	2.17E-02	rs6693681	1	202169194	q32.1
SNP_A-1878562	C	C	378	16	400	6	4.989	2.55E-02	rs16855729	1	202226581	q32.1
SNP_A-1809586	A	A	268	144	295	115	4.537	0.0332	rs11240521	1	202264739	q32.1
SNP_A-1683500	T	T	265	27	302	56	5.906	1.51E-02	rs1562866	1	202434771	q32.1
SNP_A-1802599	G	G	366	40	347	61	4.868	2.74E-02	rs2224	1	202501208	q32.1
SNP_A-2240342	C	C	184	174	238	150	7.493	6.20E-03	rs823082	1	202518592	q32.1
SNP_A-2263989	C	C	211	201	249	161	7.554	6.00E-03	rs1361754	1	202533529	q32.1
SNP_A-1895300	G	G	382	30	351	59	10.756	0.001	rs7366689	1	202619929	q32.1
SNP_A-1937888	G	G	375	17	338	40	10.95	9.00E-04	rs7366893	1	202625933	q32.1
SNP_A-2048754	A	A	322	28	297	53	8.726	3.10E-03	rs7366204	1	202628132	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1876852	G	G	401	5	420	0	5.204	2.25E-02	rs12072062	1	202983409	q32.1
SNP_A-1895602	G	G	243	151	275	121	5.281	2.16E-02	rs1429907	1	203749406	q32.2
SNP_A-1845949	C	C	226	142	195	187	8.179	4.20E-03	rs2039544	1	203808312	q32.2
SNP_A-1981503	G	G	241	97	268	76	3.929	4.75E-02	rs7545125	1	203813122	q32.2
SNP_A-1798590	A	A	283	133	313	109	3.847	4.98E-02	rs2802233	1	203859619	q32.2
SNP_A-1904398	G	G	256	120	310	106	4.009	0.0453	rs2564978	1	203882811	q32.2
SNP_A-2055661	C	C	397	7	387	17	4.294	3.82E-02	rs1410408	1	204054703	q32.2
SNP_A-2301967	T	T	351	33	357	17	5.04	2.48E-02	—	1	204315548	q32.2
SNP_A-1896003	T	T	391	17	403	5	6.727	9.50E-03	rs14374	1	204356652	q32.2
SNP_A-2070077	C	C	356	32	382	18	4.654	0.031	rs1204673	1	204433764	q32.2
SNP_A-2027021	C	C	287	101	304	74	4.525	3.34E-02	rs1009897	1	204451900	q32.2
SNP_A-1752463	A	A	218	150	209	197	4.701	3.01E-02	rs6540429	1	204630952	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800736	C	C	234	158	203	187	4.632	3.14E-02	rs6671923	1	204714197	q32.2
SNP_A-2047747	G	A	217	179	211	189	4.537	0.0332	rs7525987	1	204761707	q32.2
SNP_A-1749801	T	T	337	29	341	53	6.025	0.0141	rs6667619	1	205160919	q32.2
SNP_A-1982029	G	G	327	81	304	116	6.884	8.70E-03	rs10494906	1	205316493	q32.2
SNP_A-1982030	T	T	332	82	304	116	7.028	8.00E-03	rs10494907	1	205316736	q32.2
SNP_A-2264790	G	G	297	111	267	137	4.302	3.81E-02	rs11585869	1	205326632	q32.2
SNP_A-2287838	G	G	343	73	315	105	6.925	8.50E-03	rs1933566	1	205327065	q32.2
SNP_A-1982031	C	C	357	41	318	58	4.551	3.29E-02	rs17013230	1	205328713	q32.2
SNP_A-2277339	T	T	316	32	305	55	6.074	0.0137	rs6694350	1	205338861	q32.2
SNP_A-1982032	T	T	326	22	309	37	4.263	0.039	rs12079343	1	205339292	q32.2
SNP_A-1982033	C	C	372	40	344	60	5.017	2.51E-02	rs12084143	1	205339560	q32.2
SNP_A-2225918	G	G	391	25	376	44	5.506	0.0189	rs1890340	1	205401370	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982092	G	G	308	58	321	39	3.941	4.71E-02	rs11119189	1	205530237	q32.2
SNP_A-1982103	T	T	336	22	351	9	5.774	1.63E-02	rs10494914	1	205585534	q32.2
SNP_A-2190552	C	C	288	126	259	159	5.339	2.08E-02	rs11580204	1	205640684	q32.2
SNP_A-1813021	C	C	251	153	211	171	3.85	4.97E-02	rs6540507	1	205658022	q32.2
SNP_A-2243399	G	G	273	105	242	144	7.892	5.00E-03	rs1174566	1	205675445	q32.2
SNP_A-2244884	A	A	266	98	230	126	6.025	0.0141	rs7546058	1	205695831	q32.2
SNP_A-1830779	C	C	286	114	322	88	5.355	0.0207	rs6540525	1	205837834	q32.2
SNP_A-2285656	G	G	292	120	311	93	3.943	4.71E-02	rs2843171	1	205844870	q32.2
SNP_A-1982187	A	A	353	57	363	31	7.506	6.10E-03	rs1395753	1	205878922	q32.2
SNP_A-2278977	C	C	350	52	370	28	7.736	5.40E-03	rs17014370	1	205928486	q32.2
SNP_A-2250959	T	T	312	98	348	70	6.554	1.05E-02	rs1857967	1	205949647	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1680544	T	T	232	124	282	96	7.775	0.0053	rs1166903	1	206056296	q32.2
SNP_A-1756182	G	G	378	22	366	46	8.489	3.60E-03	rs10494908	1	206136251	q32.2
SNP_A-2238360	T	T	252	92	226	130	7.715	5.50E-03	rs760832	1	206169143	q32.2
SNP_A-1810371	C	C	336	32	365	15	7.158	7.50E-03	rs4393158	1	206240292	q32.2
SNP_A-2071087	C	C	332	68	365	41	8.206	4.20E-03	rs17015226	1	206358491	q32.2
SNP_A-1691658	C	C	392	6	414	0	6.288	1.22E-02	rs10489336	1	206767571	q32.2
SNP_A-2034690	C	C	297	101	319	77	4.017	4.51E-02	rs11119499	1	206999711	q32.2
SNP_A-1684986	C	C	384	14	407	5	4.691	3.03E-02	rs10489341	1	207011510	q32.2
SNP_A-2046472	A	A	311	33	289	49	3.876	4.90E-02	rs12145163	1	207077179	q32.2
SNP_A-2294611	C	C	276	28	330	16	5.393	2.02E-02	rs4845043	1	207089794	q32.2
SNP_A-2081319	T	T	382	10	399	3	4.014	4.51E-02	rs11119536	1	207101693	q32.2
SNP_A-1814280	C	C	384	8	375	19	4.583	3.23E-02	rs12060387	1	207208243	q32.2
SNP_A-2212912	C	C	402	10	418	2	5.569	0.0183	rs1538755	1	207282270	q32.2
SNP_A-1737669	A	A	332	60	366	42	4.514	3.36E-02	rs645890	1	207539190	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982816	C	C	329	27	327	13	4.541	3.31E-02	rs11582143	1	207905371	q32.3
SNP_A-2213283	C	C	346	40	339	13	12.286	5.00E-04	rs11119748	1	208040580	q32.3
SNP_A-2000674	C	C	376	20	375	35	3.85	4.97E-02	rs7553035	1	208080101	q32.3
SNP_A-2275734	T	T	283	53	328	36	5.45	1.96E-02	rs7524697	1	208092914	q32.3
SNP_A-2115387	C	C	371	15	397	3	8.634	0.0033	rs11119762	1	208093839	q32.3
SNP_A-1683240	G	G	348	34	358	14	8.344	3.90E-03	rs11119765	1	208094212	q32.3
SNP_A-2154363	A	A	389	15	366	28	4.506	3.38E-02	rs17699316	1	208471588	q32.3
SNP_A-2187834	T	T	403	1	402	8	5.402	0.0201	rs17018237	1	208500639	q32.3
SNP_A-2292044	C	C	414	2	410	10	5.334	2.09E-02	rs2358385	1	208518829	q32.3
SNP_A-2168014	C	C	414	2	410	10	5.334	2.09E-02	---	1	208536807	q32.3
SNP_A-1802291	A	A	410	2	405	9	4.48	3.43E-02	rs17018375	1	208598002	q32.3
SNP_A-2244353	C	C	202	196	222	158	4.609	3.18E-02	rs1472224	1	208739714	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2112604	G	G	335	75	306	102	5.426	1.98E-02	rs17719838	1	208742213	q32.3
SNP_A-1982996	T	T	305	53	283	81	6.624	0.0101	rs17018853	1	208819595	q32.3
SNP_A-1982999	A	G	234	166	205	199	6.909	0.0086	rs7527863	1	208819826	q32.3
SNP_A-1895325	C	C	234	156	273	123	6.858	8.80E-03	rs4951588	1	208888828	q32.3
SNP_A-2075534	C	C	302	44	286	76	8.612	0.0033	rs12145484	1	208938926	q32.3
SNP_A-2275636	T	C	239	173	214	200	7.804	5.20E-03	rs1473321	1	208967450	q32.3
SNP_A-1942458	C	C	239	145	199	189	9.429	2.10E-03	rs12239580	1	208972578	q32.3
SNP_A-1947313	T	T	317	59	280	80	5.12	2.36E-02	rs12403586	1	208975131	q32.3
SNP_A-2184906	T	T	327	79	302	104	4.409	3.58E-02	rs11119934	1	208992185	q32.3
SNP_A-1892781	G	G	196	142	213	107	5.138	2.34E-02	rs6540742	1	209059260	q32.3
SNP_A-1690207	G	G	367	33	359	53	4.563	0.0327	rs4132401	1	209085099	q32.3
SNP_A-1959812	C	C	330	24	329	11	4.55	3.29E-02	rs17019780	1	209418209	q32.3
SNP_A-1719241	C	C	254	140	294	120	3.966	4.64E-02	rs351408	1	209497626	q32.3
SNP_A-2173880	T	T	252	136	287	107	5.688	1.71E-02	rs320463	1	209977594	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2038302	T	T	368	2	358	10	5.466	1.94E-02	rs17020933	1	210098202	q32.3
SNP_A-1983384	C	C	392	6	385	23	9.906	1.60E-03	rs12084751	1	210388137	q32.3
SNP_A-2082027	A	A	339	59	327	83	4.095	4.30E-02	rs9651104	1	210392113	q32.3
SNP_A-2058616	A	A	390	6	392	16	4.372	3.65E-02	rs17712208	1	210538840	q41
SNP_A-1894340	C	C	416	0	413	5	5.006	0.0253	rs11120251	1	210627713	q41
SNP_A-1853309	G	G	368	30	393	17	4.24	0.0395	rs11120267	1	210749441	q41
SNP_A-2121564	G	G	370	30	393	17	4.166	4.12E-02	rs17022165	1	210755488	q41
SNP_A-2116411	T	T	386	20	376	36	4.659	0.0309	rs1147677	1	210803874	q41
SNP_A-2208272	C	C	205	169	231	141	4.074	4.35E-02	rs7544984	1	210855327	q41
SNP_A-2171900	C	C	363	21	378	8	6.126	1.33E-02	rs17733739	1	211026203	q41
SNP_A-1712089	G	G	309	45	320	70	3.894	4.84E-02	rs10494967	1	211058092	q32.3
SNP_A-2199532	A	A	370	6	334	14	3.984	0.0465	rs11120444	1	211482109	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1668090	C	C	374	18	375	33	4.095	4.30E-02	rs4465172	1	211665377	q41
SNP_A-2230115	A	A	297	85	316	56	6.422	1.13E-02	rs6694364	1	211814857	q41
SNP_A-1899190	T	T	264	62	241	87	5.236	2.21E-02	rs6694510	1	212303041	q41
SNP_A-1817040	A	A	357	31	354	54	5.737	0.0166	rs6686550	1	212526121	q41
SNP_A-2157980	G	G	361	55	343	77	4.108	4.27E-02	rs12120923	1	212593344	q41
SNP_A-1920098	A	C	192	160	203	161	7.617	5.80E-03	rs301734	1	212680961	q41
SNP_A-1828994	C	C	395	9	403	1	6.48	0.0109	rs17026130	1	212687128	q41
SNP_A-2069268	T	T	295	101	320	64	9.131	2.50E-03	rs17026208	1	212730098	q41
SNP_A-1899570	A	A	280	72	313	53	4.453	3.48E-02	rs415508	1	212759167	q41
SNP_A-1829878	G	G	270	104	295	79	4.521	3.35E-02	rs2669057	1	212788417	q41
SNP_A-1781773	G	G	276	76	304	50	6.711	9.60E-03	rs386654	1	212820357	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141680	C	C	249	117	273	87	5.466	1.94E-02	rs2168924	1	212828500	q41
SNP_A-1984152	C	C	241	163	258	128	4.381	3.63E-02	rs1588656	1	212937477	q41
SNP_A-2075357	G	G	239	149	271	121	4.891	0.027	rs7349114	1	212992848	q41
SNP_A-2125755	T	T	235	151	216	192	5.096	0.024	rs6697616	1	213025345	q41
SNP_A-2270697	G	G	264	138	269	101	4.456	3.48E-02	rs4540735	1	213026045	q41
SNP_A-2221449	C	C	287	91	255	117	5.092	0.024	rs4579828	1	213031765	q41
SNP_A-1872497	G	G	284	114	301	85	4.538	0.0332	rs4240923	1	213045654	q41
SNP_A-1652308	A	A	271	129	252	162	4.193	4.06E-02	rs1811900	1	213352217	q41
SNP_A-1671784	C	C	252	120	238	158	4.849	2.77E-02	rs1811901	1	213352254	q41
SNP_A-1916391	A	A	310	78	274	106	6.397	0.0114	rs2789716	1	213371346	q41
SNP_A-2286869	T	T	267	99	236	132	6.619	0.0101	rs12760372	1	213371429	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2265336	A	A	290	84	236	112	8.619	0.0033	rs1339337	1	213371884	q41
SNP_A-2201964	A	A	323	91	294	122	5.87	0.0154	rs2576235	1	213375362	q41
SNP_A-2246541	T	T	300	76	279	115	8.309	3.90E-03	rs2576234	1	213375400	q41
SNP_A-2232021	A	A	314	40	336	22	5.948	0.0147	rs17044214	1	213416709	q41
SNP_A-2085979	C	C	340	46	369	29	4.857	0.0275	rs11117717	1	213450535	q41
SNP_A-2216963	A	A	265	107	234	138	5.848	1.56E-02	rs2818742	1	213456281	q41
SNP_A-1787227	A	G	208	190	222	176	5.152	2.32E-02	rs946438	1	213573038	q41
SNP_A-1879530	C	C	260	56	292	32	8.302	4.00E-03	rs11572424	1	213588128	q41
SNP_A-1658118	A	A	220	178	261	153	5.07	2.43E-02	rs10495023	1	213689158	q41
SNP_A-1747007	A	A	246	154	299	115	10.571	1.10E-03	rs10495024	1	213689446	q41
SNP_A-1846355	C	C	307	95	272	136	9.349	2.20E-03	rs17696625	1	213740884	q41
SNP_A-2119714	G	G	372	30	397	17	4.233	3.96E-02	rs1553345	1	213756746	q41
SNP_A-2077462	G	G	303	97	278	126	4.827	2.80E-02	rs11117811	1	213786978	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1984811	C	C	294	104	319	81	3.874	4.90E-02	rs2796821	1	214974216	q41
SNP_A-2090841	T	T	226	182	257	151	4.876	2.72E-02	rs2796822	1	214974527	q41
SNP_A-2173601	C	C	169	161	207	141	4.69	3.03E-02	rs623356	1	215035781	q41
SNP_A-2313208	C	T	217	161	186	182	4.738	2.95E-02	rs550238	1	215079343	q41
SNP_A-1798988	C	C	362	16	395	5	6.584	0.0103	rs1481365	1	215171949	q41
SNP_A-2214231	T	T	390	18	376	34	5.174	0.0229	rs10746381	1	215494945	q41
SNP_A-2112503	T	T	230	164	260	132	5.291	2.14E-02	rs638699	1	215514843	q41
SNP_A-2213852	C	C	330	72	368	40	11.168	8.00E-04	rs1546207	1	215515019	q41
SNP_A-1985056	C	C	223	151	260	128	4.475	0.0344	rs7413149	1	215606270	q41
SNP_A-2148413	C	C	327	69	349	31	14.832	0.0001	rs12128850	1	215617211	q41
SNP_A-2185417	T	T	263	149	289	121	4.123	4.23E-02	rs1764844	1	215631214	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255182	C	C	236	106	266	76	6.738	9.40E-03	rs11118204	1	215631752	q41
SNP_A-1912346	G	G	250	86	207	115	7.936	4.80E-03	rs12134260	1	215703211	q41
SNP_A-1985094	T	T	258	112	223	137	4.921	2.65E-02	rs4846532	1	215717752	q41
SNP_A-1947831	G	G	282	128	246	152	4.334	0.0373	rs6660443	1	215721298	q41
SNP_A-1921645	A	G	198	178	213	159	7.372	0.0066	rs11590608	1	215723614	q41
SNP_A-1954086	G	T	182	156	170	136	5.679	0.0172	rs10863439	1	215782475	q41
SNP_A-1734668	G	G	239	161	218	194	3.856	4.96E-02	rs62817	1	215803361	q41
SNP_A-1985112	G	A	211	175	214	174	7.461	0.0063	rs885533	1	215803859	q41
SNP_A-2161669	G	A	207	187	217	171	5.611	1.79E-02	rs10863444	1	215852539	q41
SNP_A-1782797	T	T	243	149	207	201	10.29	1.30E-03	rs4570430	1	215865544	q41
SNP_A-2140696	A	A	292	124	249	167	9.772	0.0018	rs12043736	1	215866548	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189285	G	G	270	146	305	115	5.793	0.0161	rs10157397	1	215872724	q41
SNP_A-2226787	A	G	216	154	205	169	12.962	3.00E-04	rs7355178	1	215874700	q41
SNP_A-1868678	C	C	230	96	276	74	6.185	0.0129	rs1455703	1	215888540	q41
SNP_A-1839069	G	G	345	17	353	7	4.253	3.92E-02	rs1340092	1	215911872	q41
SNP_A-1838467	A	A	279	137	309	107	5.219	0.0223	rs6670103	1	215935445	q41
SNP_A-1955916	G	G	195	125	242	98	7.725	5.40E-03	rs1547502	1	215952752	q41
SNP_A-2234244	A	A	254	116	200	158	12.667	4.00E-04	rs1598472	1	215959914	q41
SNP_A-2233803	G	G	309	57	334	36	5.692	1.70E-02	rs2791563	1	215984883	q41
SNP_A-2154785	T	T	239	151	207	185	5.731	0.0167	rs7523871	1	215985094	q41
SNP_A-2060029	A	A	232	144	213	181	4.605	3.19E-02	rs2168333	1	216004603	q41
SNP_A-2305216	C	G	214	180	221	199	3.91	4.80E-02	rs6541229	1	216035202	q41
SNP_A-1758974	T	T	390	10	411	3	4.08	4.34E-02	rs10495113	1	216145426	q41
SNP_A-1701185	C	C	324	76	364	48	8.473	3.60E-03	rs10495117	1	216191556	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1901913	C	C	414	0	410	4	4.019	4.50E-02	rs6675807	1	216218353	q41
SNP_A-2306191	T	T	303	69	311	47	4.01	4.52E-02	rs2789812	1	216579183	q41
SNP_A-2160081	C	C	293	59	280	26	9.939	1.60E-03	rs1768676	1	216582262	q41
SNP_A-1798494	G	G	238	160	291	111	14.15	2.00E-04	rs2808026	1	216721271	q41
SNP_A-2126666	C	C	365	25	379	11	5.708	1.69E-02	rs11118501	1	216765068	q41
SNP_A-1917116	G	G	392	24	408	12	4.301	3.81E-02	rs10127631	1	216790563	q41
SNP_A-1856534	A	A	250	142	308	98	13.854	2.00E-04	rs7535619	1	216793106	q41
SNP_A-1892747	C	C	378	24	362	40	4.346	3.71E-02	rs17565935	1	216853305	q41
SNP_A-2063743	G	G	377	5	386	18	6.844	8.90E-03	rs1338775	1	217001908	q41
SNP_A-2252705	T	T	256	110	286	84	5.123	2.36E-02	rs11118609	1	217376885	q41
SNP_A-2172389	A	A	395	11	399	1	8.309	3.90E-03	rs1414513	1	217573795	q41
SNP_A-2071016	C	C	266	84	298	48	11.611	7.00E-04	rs3131543	1	217943195	q41
SNP_A-1643393	A	A	288	112	322	88	4.652	0.031	rs903319	1	218042102	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1985780	G	G	309	73	278	100	5.83	1.58E-02	rs11581623	1	218323113	q41
SNP_A-2096481	T	T	184	182	211	155	4.009	0.0453	rs7543041	1	218323187	q41
SNP_A-2108731	G	G	382	34	365	55	5.323	2.10E-02	rs11118860	1	218341953	q41
SNP_A-1819465	G	G	250	76	216	104	6.781	9.20E-03	rs2800853	1	218499401	q41
SNP_A-2146305	T	T	302	104	333	81	4.295	3.82E-02	rs17494423	1	218500793	q41
SNP_A-1670762	G	G	322	76	306	108	5.66	1.74E-02	rs4846704	1	218504613	q41
SNP_A-1928191	C	C	362	10	379	3	4.027	0.0448	rs12022351	1	218669229	q41
SNP_A-2128784	G	G	291	93	258	114	3.925	4.76E-02	rs1537852	1	218748641	q41
SNP_A-1728663	G	G	366	28	361	51	6.332	1.19E-02	rs7531435	1	218815620	q41
SNP_A-1804147	A	A	314	76	268	92	3.966	4.64E-02	rs11591051	1	218983235	q41
SNP_A-2238887	G	G	314	62	288	96	8.356	0.0038	rs11581653	1	218983661	q41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247817	G	G	330	84	308	110	4.224	3.99E-02	rs4436398	1	218983992	q41
SNP_A-2258710	A	A	307	19	323	7	5.921	1.50E-02	rs2936040	1	219152056	q41
SNP_A-1757910	A	A	275	81	344	64	6.174	1.30E-02	rs1108869	1	219634586	q41
SNP_A-1713608	G	G	390	10	411	3	4.08	4.34E-02	rs10495196	1	219806439	q41
SNP_A-2216984	G	A	212	196	240	180	6.88	8.70E-03	rs6690293	1	220035284	q42.11
SNP_A-1669310	G	G	220	154	187	181	4.804	2.84E-02	rs4623692	1	220035607	q42.11
SNP_A-2087735	T	C	188	182	210	150	6.136	0.0132	rs4661273	1	220037247	q42.11
SNP_A-2111471	T	G	216	198	234	184	5.541	1.86E-02	rs10916022	1	220160527	q42.11
SNP_A-2128855	C	C	244	92	296	72	6.004	0.0143	rs4653859	1	220174029	q42.11
SNP_A-1868099	A	A	384	4	398	0	4.124	4.23E-02	rs11804140	1	220654126	q42.12
SNP_A-2299812	T	T	222	158	187	183	4.695	3.02E-02	rs4653402	1	221181035	q42.12
SNP_A-2101194	C	C	282	132	312	108	3.872	4.91E-02	rs1876084	1	222186730	q42.12
SNP_A-2301487	A	A	284	120	312	94	4.469	3.45E-02	rs7554842	1	222202040	q42.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2125384	G	G	264	118	242	150	4.649	3.11E-02	rs12754943	1	222535362	q42.12
SNP_A-2314193	G	G	403	5	420	0	5.178	0.0229	rs6426101	1	222569150	q42.12
SNP_A-1807547	G	A	194	178	209	157	6.335	0.0118	rs10915928	1	222573175	q42.12
SNP_A-2086675	T	T	212	132	236	98	6.166	1.30E-02	rs1355391	1	222591886	q42.12
SNP_A-1835168	T	T	247	163	219	199	5.186	2.28E-02	rs2306121	1	222660256	q42.12
SNP_A-2271124	T	T	305	55	273	73	4.027	0.0448	rs12133895	1	222764770	q42.12
SNP_A-2224431	A	G	220	194	226	192	4.322	3.76E-02	rs10915975	1	222827927	q42.12
SNP_A-1959890	A	A	328	30	322	50	4.789	0.0286	rs12077348	1	223152241	q42.12
SNP_A-2054862	G	G	314	88	344	56	8.474	3.60E-03	rs6660109	1	223313707	q42.13
SNP_A-1893666	C	C	294	78	331	57	5.122	2.36E-02	rs1295652	1	223359536	q42.13
SNP_A-1928465	T	T	300	74	273	117	10.622	1.10E-03	rs6426554	1	223389180	q42.13
SNP_A-1891063	G	G	219	187	247	155	4.657	0.0309	rs11802358	1	223391890	q42.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2273853	A	A	334	76	293	119	12.158	5.00E-04	rs1800672	1	223392197	q42.13
SNP_A-1815300	A	A	306	98	275	135	7.486	6.20E-03	rs6661550	1	223399597	q42.13
SNP_A-1853562	G	G	337	63	296	92	7.901	4.90E-03	rs12145777	1	223428966	q42.13
SNP_A-1865632	C	C	317	21	284	40	7.437	6.40E-03	rs2802277	1	223460968	q42.13
SNP_A-1804995	G	G	350	18	312	30	4.235	3.96E-02	rs4263966	1	223510377	q42.13
SNP_A-1986993	C	C	309	39	236	70	15.983	6.46E-05	rs6681959	1	223548411	q42.13
SNP_A-1898443	C	C	293	35	332	20	5.685	1.71E-02	rs7368083	1	223587376	q42.13
SNP_A-1987070	G	G	354	34	295	61	11.683	6.00E-04	rs7518813	1	223800764	q42.13
SNP_A-1952154	G	G	378	38	347	73	12.343	4.00E-04	rs7539662	1	223818064	q42.13
SNP_A-2193819	C	C	232	146	281	119	6.815	9.00E-03	rs3014272	1	223890175	q42.13
SNP_A-2099685	C	C	305	51	303	75	3.922	4.77E-02	rs7549565	1	223986449	q42.13
SNP_A-1651962	C	C	303	45	325	77	5.304	2.13E-02	rs2297419	1	224157385	q42.13
SNP_A-1746408	C	C	358	40	337	75	11.048	9.00E-04	rs10495272	1	224197998	q42.13
SNP_A-1743091	C	C	358	40	338	76	11.436	7.00E-04	rs10495271	1	224198211	q42.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2104884	A	A	332	6	300	14	3.942	4.71E-02	rs10916199	1	224209207	q42.13
SNP_A-2266341	C	C	303	51	283	71	3.961	4.66E-02	rs12077397	1	224247473	q42.13
SNP_A-2142662	A	A	288	114	267	145	4.383	3.63E-02	rs1582114	1	224323105	q42.13
SNP_A-2209036	G	G	329	39	370	24	5.095	0.024	rs3738681	1	224583870	q42.13
SNP_A-2109032	C	C	211	127	234	102	3.912	4.79E-02	rs1411912	1	224741764	q42.13
SNP_A-1801362	G	G	265	127	288	98	4.648	3.11E-02	rs878388	1	224762882	q42.13
SNP_A-1800963	T	T	253	135	286	112	4.036	4.46E-02	rs564636	1	224790104	q42.13
SNP_A-2058061	T	T	336	4	332	0	3.929	4.75E-02	rs6692047	1	225262982	q42.13
SNP_A-1823765	C	C	412	4	408	12	4	4.55E-02	rs6679643	1	225357645	q42.13
SNP_A-1897385	C	C	319	55	296	80	5.484	1.92E-02	rs2220741	1	225380720	q42.13
SNP_A-1987385	G	G	246	80	286	62	4.576	3.24E-02	rs778373	1	225398310	q42.13
SNP_A-2290844	C	C	246	90	259	63	4.804	2.84E-02	rs603404	1	225411880	q42.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235916	C	A	217	191	229	187	5.589	1.81E-02	rs10916409	1	225462983	q42.13
SNP_A-1769850	A	A	251	135	217	169	6.273	0.0123	rs6426532	1	225512814	q42.13
SNP_A-2000755	T	T	402	0	378	4	4.231	3.97E-02	rs6703901	1	225649674	q42.13
SNP_A-2277350	A	A	261	123	307	95	6.913	0.0086	rs237756	1	225726156	q42.13
SNP_A-2052106	A	A	281	47	247	63	4.012	4.52E-02	rs237826	1	225760358	q42.13
SNP_A-1828092	A	A	273	121	245	153	5.231	2.22E-02	rs4925479	1	225862235	q42.13
SNP_A-2262023	G	G	232	114	176	136	7.886	5.00E-03	rs17704219	1	225865303	q42.13
SNP_A-1859931	T	T	272	134	243	173	6.467	1.10E-02	rs6440333	1	226219835	q42.13
SNP_A-2047831	C	C	241	111	204	136	5.4	0.0201	rs557208	1	226223395	q42.13
SNP_A-2056116	C	C	237	117	213	159	7.229	7.20E-03	rs479531	1	226228662	q42.13
SNP_A-1889664	G	G	267	119	231	147	5.467	1.94E-02	rs2780629	1	226236033	q42.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2288661	A	A	361	37	384	22	4.444	3.50E-02	rs12044467	1	226450382	q42.13
SNP_A-2099361	G	G	229	139	272	120	4.331	3.74E-02	rs200162	1	226920845	q42.13
SNP_A-1908691	A	A	330	48	343	31	3.888	4.86E-02	rs1615876	1	227007413	q42.2
SNP_A-1886668	G	G	317	51	358	36	4.194	4.06E-02	rs200591	1	227013658	q42.2
SNP_A-1792852	T	T	186	172	218	140	5.817	1.59E-02	rs2225146	1	227102376	q42.2
SNP_A-1938818	G	G	343	7	344	22	7.406	6.50E-03	rs11568030	1	227153578	q42.2
SNP_A-1801452	G	G	308	10	318	2	5.487	1.92E-02	rs7542523	1	227295459	q42.2
SNP_A-2000767	G	G	334	32	313	51	5.026	2.50E-02	rs4658871	1	227623914	q42.2
SNP_A-1861485	C	C	402	4	420	0	4.158	4.14E-02	rs12089353	1	227735144	q42.2
SNP_A-2204457	A	A	407	7	420	0	7.162	7.40E-03	rs6657827	1	227740177	q42.2
SNP_A-2070100	C	C	372	20	335	33	4.371	3.65E-02	rs1572794	1	227859230	q42.2
SNP_A-2158575	C	C	377	29	347	47	5.327	2.10E-02	rs2095935	1	227860154	q42.2
SNP_A-2296199	A	A	376	32	352	56	7.337	6.80E-03	rs7544586	1	227866075	q42.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784409	C	C	236	138	247	103	4.543	3.31E-02	rs17802224	1	227990982	q42.2
SNP_A-2101953	C	C	308	72	345	55	3.862	4.94E-02	rs11122348	1	228291252	q42.2
SNP_A-2231810	A	A	383	25	399	11	5.767	1.63E-02	rs11122414	1	228555482	q42.2
SNP_A-1898440	A	A	225	141	202	184	6.401	0.0114	rs867844	1	228573013	q42.2
SNP_A-1895673	A	A	365	33	354	60	7.695	5.50E-03	rs537135	1	228577095	q42.2
SNP_A-2270831	T	T	239	159	199	191	6.498	1.08E-02	rs10864720	1	228577967	q42.2
SNP_A-1752427	C	C	365	33	356	58	6.668	9.80E-03	rs545937	1	228578548	q42.2
SNP_A-1668634	A	A	366	34	355	57	5.805	0.016	rs546774	1	228578627	q42.2
SNP_A-1699203	C	C	367	33	354	54	5.225	0.0223	rs479311	1	228578747	q42.2
SNP_A-1708214	C	C	369	31	355	55	6.846	8.90E-03	rs1890767	1	228596035	q42.2
SNP_A-2290879	A	A	312	76	262	106	8.777	3.00E-03	rs12564542	1	228726354	q42.2
SNP_A-1849565	G	G	270	62	276	92	4.069	4.37E-02	rs10910403	1	228839609	q42.2
SNP_A-2114373	C	C	316	80	352	48	9.92	1.60E-03	rs6424233	1	228969601	q42.2
SNP_A-1889468	T	T	264	44	309	27	6.399	0.0114	rs11589828	1	228976007	q42.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1941810	T	T	294	74	339	55	5.116	2.37E-02	rs6424234	1	228976849	q42.2
SNP_A-2048294	G	G	288	94	266	144	10.401	1.30E-03	rs16857721	1	229033011	q42.2
SNP_A-2314750	C	C	408	4	406	0	3.961	4.66E-02	rs12405218	1	229080915	q42.2
SNP_A-1785520	C	C	319	17	309	31	4.219	4.00E-02	rs9424487	1	229326336	q42.2
SNP_A-2058559	C	C	200	190	248	144	11.473	7.00E-04	rs10910665	1	229602017	q42.2
SNP_A-1988623	A	A	198	164	228	134	5.133	0.0235	rs1294235	1	229825488	q42.2
SNP_A-2152270	C	C	223	189	254	154	5.567	0.0183	rs1294198	1	229832110	q42.2
SNP_A-2230939	C	C	217	187	248	160	4.148	4.17E-02	rs10910153	1	229837267	q42.2
SNP_A-2130517	G	G	265	121	219	155	8.373	0.0038	rs4630074	1	229870226	q42.2
SNP_A-1880783	C	C	280	78	322	60	4.504	3.38E-02	rs10797461	1	229927323	q42.2
SNP_A-2106921	C	C	235	119	200	148	5.915	1.50E-02	rs9645294	1	229930723	q42.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2267142	G	G	282	110	253	151	7.833	5.10E-03	rs10910192	1	229939114	q42.2
SNP_A-2204864	G	G	310	92	333	65	5.446	1.96E-02	rs1557129	1	229949845	q42.2
SNP_A-2303195	C	C	319	73	294	100	5.228	2.22E-02	rs10910204	1	229959759	q42.2
SNP_A-1958109	A	A	298	112	266	140	4.907	2.67E-02	rs780240	1	229987298	q42.2
SNP_A-1873535	C	C	331	85	354	60	5.078	2.42E-02	rs780247	1	230001973	q42.2
SNP_A-2286409	C	C	273	109	309	89	3.92	4.77E-02	rs532657	1	230119807	q42.2
SNP_A-1988750	A	A	349	51	326	72	4.364	3.67E-02	rs7530423	1	230223768	q42.2
SNP_A-1716193	T	T	284	98	273	131	4.36	3.68E-02	rs7550169	1	230379046	q42.2
SNP_A-1901960	T	T	382	4	377	15	6.355	0.0117	rs10910318	1	230406785	q42.2
SNP_A-1853688	C	C	267	57	247	91	8.297	4.00E-03	rs4364940	1	230433251	q42.2
SNP_A-1690791	G	G	312	44	313	77	7.468	0.0063	rs10489692	1	230600799	q42.2
SNP_A-2062039	G	G	328	4	325	15	6.288	1.22E-02	rs12133361	1	230767918	q42.2
SNP_A-2101289	T	T	193	191	214	158	4.014	4.51E-02	rs271751	1	230934694	q42.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2271642	C	C	302	104	330	80	4.351	3.70E-02	rs2602987	1	231356658	q42.3
SNP_A-1958192	G	G	376	30	355	47	4.337	0.0373	rs17543709	1	231890965	q42.3
SNP_A-1812701	G	G	299	101	335	77	5.104	2.39E-02	rs10924301	1	232618556	q42.3
SNP_A-1958883	G	G	375	3	385	11	4.287	3.84E-02	rs3820560	1	232714134	q42.3
SNP_A-2144181	C	C	265	93	303	57	11.177	8.00E-04	rs600988	1	232842710	q42.3
SNP_A-2280658	T	T	334	22	326	8	5.935	1.48E-02	rs10925108	1	232845156	q42.3
SNP_A-2206649	G	G	287	109	313	71	8.966	2.70E-03	rs660351	1	232845223	q42.3
SNP_A-2179988	A	A	260	104	285	73	6.527	0.0106	rs585537	1	232850421	q42.3
SNP_A-2260578	G	G	209	199	244	164	6.079	0.0137	rs2590577	1	232850507	q42.3
SNP_A-1784683	A	A	240	162	273	135	4.533	0.0332	rs4659689	1	233115901	q43
SNP_A-2079595	G	G	274	72	299	51	4.653	0.031	rs819648	1	233125322	q43
SNP_A-2186472	G	G	331	27	353	15	3.999	4.55E-02	rs530876	1	233129612	q43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255926	C	C	346	24	363	3	16.72	4.33E-05	rs475488	1	233147888	q43
SNP_A-1797914	A	A	328	18	324	6	5.649	1.75E-02	rs499666	1	233148228	q43
SNP_A-1989561	C	C	343	61	361	41	4.377	3.64E-02	rs1366990	1	233207744	q43
SNP_A-1989577	G	G	197	189	224	158	4.48	3.43E-02	rs4659466	1	233237792	q43
SNP_A-2203236	C	C	396	20	413	9	4.487	3.42E-02	rs12066406	1	233399433	q43
SNP_A-1758846	A	A	286	64	337	49	4.416	0.0356	rs1110423	1	233419858	q42.3
SNP_A-2303739	C	C	335	39	309	59	5.083	2.42E-02	---	1	233518910	q43
SNP_A-2251403	G	G	369	25	385	13	4.109	4.27E-02	rs2485600	1	233600254	q43
SNP_A-1840379	T	T	194	118	231	95	5.4	0.0201	rs2779400	1	234054908	q43
SNP_A-2144299	T	T	352	24	370	12	4.402	3.59E-02	rs3766865	1	234055081	q43
SNP_A-2084614	G	G	265	111	306	84	6.429	0.0112	rs7513677	1	234069140	q43
SNP_A-2000816	G	G	249	165	216	196	4.999	2.54E-02	rs2499595	1	234435376	q43
SNP_A-1856832	T	T	408	4	420	0	4.097	4.29E-02	rs2255597	1	234575525	q43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798011	A	A	416	0	416	4	3.981	4.60E-02	rs10737822	1	234723812	q43
SNP_A-1725582	A	A	341	59	324	86	5.34	2.08E-02	rs939698	1	234831829	q43
SNP_A-2227004	C	C	385	15	406	4	6.804	9.10E-03	rs11802576	1	234835414	q43
SNP_A-1821315	G	G	297	57	258	74	4.245	3.94E-02	rs12118091	1	234902655	q43
SNP_A-2219796	A	A	314	86	276	116	6.823	9.00E-03	rs7529140	1	234903038	q43
SNP_A-1780931	T	T	316	88	280	120	7.078	7.80E-03	rs7552223	1	234903066	q43
SNP_A-2285362	C	C	280	52	288	24	9.817	1.70E-03	rs2392861	1	234981403	q43
SNP_A-2046064	G	G	288	82	303	51	7.256	7.10E-03	rs6672862	1	235109852	q43
SNP_A-1741903	C	C	240	140	282	122	3.885	0.0487	rs970522	1	235465884	q43
SNP_A-2232512	C	C	340	22	356	10	4.846	2.77E-02	rs12039788	1	235587719	q43
SNP_A-1872655	C	C	293	55	307	27	9.604	0.0019	rs1027897	1	235590032	q43
SNP_A-2163449	G	G	299	99	322	70	5.783	1.62E-02	rs6670952	1	235634657	q43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1666540	C	C	288	58	262	86	6.668	9.80E-03	rs574819	1	235816677	q43
SNP_A-2292446	G	G	275	103	255	135	4.871	2.73E-02	rs12137225	1	235907339	q43
SNP_A-1823452	A	A	392	18	398	8	3.872	4.91E-02	rs1218659	1	236038202	q43
SNP_A-2096116	C	C	269	91	300	58	8.992	2.70E-03	rs7533134	1	236251150	q43
SNP_A-1835556	G	G	319	55	304	84	6.156	1.31E-02	rs7536133	1	236314890	q43
SNP_A-1990436	G	G	278	92	260	130	6.585	0.0103	rs10495451	1	236463852	q43
SNP_A-1740937	A	A	296	80	283	107	3.936	4.73E-02	rs4570412	1	236512421	q43
SNP_A-1943131	T	T	318	76	296	108	6.229	0.0126	rs17669345	1	236634451	q43
SNP_A-2062375	G	G	324	62	301	95	7.656	5.70E-03	rs7542817	1	236665929	q43
SNP_A-2279472	T	T	310	76	269	105	7.362	6.70E-03	rs7530706	1	236671775	q43
SNP_A-2090153	C	C	284	80	245	113	8.468	3.60E-03	rs11589961	1	236672344	q43
SNP_A-1786656	G	G	308	82	276	110	5.816	1.59E-02	rs9970045	1	236675957	q43
SNP_A-2070611	A	A	243	133	270	104	4.964	2.59E-02	rs994276	1	236798586	q43
SNP_A-1845364	T	T	335	53	315	81	6.385	0.0115	rs11582676	1	236945694	q43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897216	A	A	338	60	325	89	5.586	1.81E-02	rs12403072	1	236946219	q43
SNP_A-2287091	A	A	337	9	365	1	6.961	8.30E-03	rs2065833	1	236987678	q43
SNP_A-2241470	G	G	300	98	285	127	3.882	4.86E-02	rs11583177	1	237035137	q43
SNP_A-1885816	C	C	286	98	264	126	4.334	3.74E-02	rs11588607	1	237037961	q43
SNP_A-1990673	T	T	339	63	365	43	4.69	3.03E-02	rs7544372	1	237313795	q43
SNP_A-2256631	T	C	175	173	204	138	6.871	8.80E-03	rs261833	1	237372946	q43
SNP_A-2086524	A	A	337	9	380	2	5.266	2.17E-02	rs1915880	1	237691741	q43
SNP_A-2141806	C	T	233	175	214	198	6.733	9.50E-03	rs9428865	1	237721234	q43
SNP_A-1836417	T	C	219	157	190	188	5.494	1.91E-02	rs4290050	1	237725554	q43
SNP_A-1894569	G	G	198	182	225	155	3.887	0.0487	rs4660080	1	237868834	q43
SNP_A-2272219	G	G	272	142	239	181	6.797	9.10E-03	rs3922506	1	238237542	q43
SNP_A-1878873	T	T	228	156	275	129	6.446	0.0111	rs6669036	1	238237953	q43
SNP_A-1797302	A	A	227	151	252	122	4.364	3.67E-02	rs6429315	1	238280294	q43
SNP_A-1951611	C	C	380	34	366	54	4.765	2.90E-02	rs10926579	1	238290079	q43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2293602	T	T	313	49	339	33	4.023	4.49E-02	rs4658798	1	238301188	q43
SNP_A-2306859	C	C	343	35	323	57	5.856	0.0155	rs3902093	1	238321944	q43
SNP_A-1758395	G	G	311	87	294	116	4.443	3.50E-02	rs4131804	1	238330027	q43
SNP_A-2268618	G	G	245	169	281	137	5.791	0.0161	rs6673338	1	238526925	q43
SNP_A-1990940	T	T	357	51	380	34	4.074	4.35E-02	rs1439524	1	238857660	q43
SNP_A-2284230	G	G	259	157	232	190	4.58	3.23E-02	rs1027697	1	238988549	q43
SNP_A-1669183	T	T	306	30	307	65	11.095	9.00E-04	rs10489350	1	239034980	q43
SNP_A-2224754	C	C	299	115	327	89	4.561	0.0327	rs7523607	1	239093719	q43
SNP_A-1806834	T	T	349	51	350	30	4.936	0.0263	rs2019842	1	239243982	q43
SNP_A-1991004	A	A	317	91	340	66	4.781	2.88E-02	rs2210612	1	239315198	q43
SNP_A-1838203	A	A	277	79	285	55	4.047	4.43E-02	rs6694819	1	239318027	q43
SNP_A-2184339	G	G	359	55	338	80	5.243	2.20E-02	rs11800122	1	239939789	q44

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1734358	C	C	390	6	382	16	4.623	0.0315	rs950125	1	239956113	q43
SNP_A-1884712	C	C	330	46	311	23	5.766	1.63E-02	rs6704286	1	240004430	q44
SNP_A-2187035	A	A	350	44	327	67	5.547	1.85E-02	rs4658413	1	240648428	q44
SNP_A-1867171	C	C	310	98	289	125	3.962	0.0465	rs651292	1	240820269	q44
SNP_A-1781343	C	C	344	48	313	73	6.582	0.0103	rs2806599	1	241126719	q44
SNP_A-2000868	G	G	342	42	304	60	4.88	2.72E-02	rs2806597	1	241140446	q44
SNP_A-1991262	A	A	242	132	191	161	8.218	4.10E-03	rs2050632	1	241485608	q44
SNP_A-2135288	A	A	285	129	260	158	4.058	4.40E-02	rs626070	1	241493372	q44
SNP_A-1940412	G	G	247	99	236	132	4.291	3.83E-02	rs10927369	1	241506001	q44
SNP_A-1799979	A	A	334	16	390	8	3.934	4.73E-02	rs4658446	1	241678348	q44
SNP_A-1821958	G	G	374	28	397	13	6.096	1.36E-02	rs12072874	1	241837892	q44
SNP_A-1991411	G	G	398	4	408	0	4.08	4.34E-02	rs1934578	1	242342518	q44
SNP_A-1666890	C	T	208	182	220	188	4.198	4.05E-02	rs1173844	1	242481669	q44
SNP_A-1850582	C	C	395	5	386	14	4.367	3.66E-02	rs4926450	1	243255224	q44
SNP_A-2299821	C	C	333	83	310	108	4.09	4.31E-02	rs10924866	1	243410912	q44

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2203488	T	T	311	21	272	40	7.913	4.90E-03	rs924085	1	243638516	q44
SNP_A-1792376	C	C	376	18	369	33	4.398	3.60E-02	rs11806327	1	243646909	q44
SNP_A-2299986	A	A	336	12	343	3	5.466	1.94E-02	rs1771928	1	243764562	q44
SNP_A-1876191	G	G	271	31	315	17	5.981	1.45E-02	rs10924984	1	243811973	q44
SNP_A-1884075	G	G	361	9	369	1	6.488	0.0109	rs10157521	1	243931709	q44
SNP_A-1884957	T	T	331	63	296	92	7.334	6.80E-03	rs4634945	1	243962056	q44
SNP_A-1819973	T	T	329	45	313	25	4.304	3.80E-02	rs3862182	1	244045418	q44
SNP_A-1921939	G	G	263	153	229	191	6.528	0.0106	rs3844081	1	244049711	q44
SNP_A-1828510	G	G	268	60	287	41	4.225	3.98E-02	rs7541715	1	244301696	q44
SNP_A-1793996	C	C	374	22	395	11	4.116	4.25E-02	rs10888286	1	244442376	q44
SNP_A-2212385	C	C	316	80	320	54	4.445	3.50E-02	rs7541216	1	244848937	q44
SNP_A-2097006	T	T	303	81	285	113	5.581	1.82E-02	rs6729766	2	814614	p25.3
SNP_A-1909369	G	G	329	73	287	93	4.658	0.0309	rs9973322	2	829556	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2069302	A	A	239	113	221	147	4.797	2.85E-02	rs4854426	2	901098	p25.3
SNP_A-2260450	C	C	291	89	283	49	8.508	3.50E-03	rs7603971	2	1010741	p25.3
SNP_A-2304388	A	A	267	83	299	59	5.776	1.62E-02	rs10192365	2	1213866	p25.3
SNP_A-2192909	A	A	280	120	314	94	5.026	2.50E-02	rs7606172	2	1258021	p25.3
SNP_A-2110760	G	G	380	26	393	11	6.295	0.0121	rs11678486	2	1358502	p25.3
SNP_A-1835765	A	A	387	29	402	16	4.036	4.45E-02	rs11666823	2	1362368	p25.3
SNP_A-2202564	T	T	375	19	402	6	7.456	0.0063	rs11211642	2	1376818	p25.3
SNP_A-1897117	G	G	360	4	364	0	4.022	4.49E-02	rs11690515	2	1435225	p25.3
SNP_A-2113638	C	C	377	21	402	10	4.465	3.46E-02	rs11211654	2	1453138	p25.3
SNP_A-1862951	C	C	226	132	267	93	10.164	0.0014	rs6705087	2	1529316	p25.3
SNP_A-2203168	G	G	263	151	291	119	5.188	2.27E-02	rs7602248	2	1553883	p25.3
SNP_A-2083636	A	A	343	37	330	58	4.81	2.83E-02	rs11676050	2	1590614	p25.3
SNP_A-2236381	T	T	306	44	300	80	9.294	0.0023	rs4853754	2	1846089	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835042	T	T	323	55	308	78	4.251	3.92E-02	rs3934845	2	1849224	p25.3
SNP_A-2076101	G	G	299	53	289	79	4.938	0.0263	rs4853825	2	1849575	p25.3
SNP_A-1881712	T	T	315	65	281	95	7.544	6.00E-03	rs13389573	2	1906410	p25.3
SNP_A-1889635	G	G	284	60	289	91	4.629	3.14E-02	rs10181146	2	1918942	p25.3
SNP_A-2267656	G	G	321	69	309	95	4.105	4.28E-02	rs10185662	2	1935203	p25.3
SNP_A-1722194	T	T	318	76	308	106	4.613	3.17E-02	rs1515746	2	2108194	p25.3
SNP_A-1802265	G	G	218	182	249	153	4.563	0.0327	rs1540379	2	2213160	p25.3
SNP_A-2194248	G	G	335	79	362	56	4.945	2.62E-02	rs10177243	2	2411448	p25.3
SNP_A-2243995	A	A	333	77	367	55	5.146	2.33E-02	rs4853940	2	2418262	p25.3
SNP_A-1961818	C	C	321	79	352	54	6.083	0.0137	rs1858405	2	2425609	p25.3
SNP_A-2294386	A	A	283	109	247	139	6.028	0.0141	rs6548098	2	2500137	p25.3
SNP_A-2224503	G	G	337	17	323	31	4.38	3.64E-02	rs17247006	2	2503281	p25.3
SNP_A-2071071	G	G	210	174	249	147	5.401	0.0201	rs12714360	2	2577279	p25.3
SNP_A-2285222	T	T	213	197	244	168	4.402	3.59E-02	rs7603656	2	2578879	p25.3
SNP_A-2251224	G	G	220	192	256	158	6.021	0.0141	rs7580381	2	2581075	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826514	C	C	224	178	269	143	7.802	5.20E-03	rs4853901	2	2582449	p25.3
SNP_A-2171494	T	T	209	181	238	146	5.581	1.82E-02	rs7584578	2	2584295	p25.3
SNP_A-2104801	C	C	197	155	236	126	6.367	1.16E-02	rs7568648	2	2584471	p25.3
SNP_A-2235738	C	C	197	155	245	125	7.983	4.70E-03	rs1031349	2	2588454	p25.3
SNP_A-1888545	T	T	218	180	262	146	7.456	0.0063	rs1031350	2	2588535	p25.3
SNP_A-2113474	C	C	302	112	343	77	9.045	2.60E-03	rs2122728	2	2712926	p25.3
SNP_A-2145280	G	G	363	45	334	70	6.622	0.0101	rs12466602	2	2713045	p25.3
SNP_A-2242839	C	C	412	4	420	0	4.058	4.40E-02	rs823201	2	2865461	p25.3
SNP_A-2111207	C	C	297	89	313	65	4.077	4.35E-02	rs2385435	2	2984151	p25.3
SNP_A-2253590	G	A	205	167	197	155	8.871	2.90E-03	rs4133261	2	3106213	p25.3
SNP_A-1956304	G	G	322	20	336	38	4.463	3.46E-02	rs12621171	2	3203832	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1928652	G	G	238	142	288	106	9.729	0.0018	rs6738683	2	3235525	p25.3
SNP_A-2063064	G	G	271	93	246	136	8.854	2.90E-03	rs357977	2	3287434	p25.3
SNP_A-1825556	C	C	308	102	263	119	3.869	4.92E-02	rs4849887	2	3307675	p25.3
SNP_A-2006097	C	C	218	196	264	158	8.393	0.0038	rs1563175	2	3332309	p25.3
SNP_A-1794958	C	C	327	81	354	60	4.155	4.15E-02	rs17018072	2	3332500	p25.3
SNP_A-1921271	A	A	357	59	382	38	5.373	2.04E-02	rs17018222	2	3404298	p25.3
SNP_A-2197652	C	C	264	138	291	99	7.551	6.00E-03	rs4340532	2	3417395	p25.3
SNP_A-1656105	G	G	334	64	320	92	5.085	0.0241	rs10495493	2	3460875	p25.3
SNP_A-1846371	G	G	248	160	285	135	4.514	3.36E-02	rs1565806	2	3463930	p25.3
SNP_A-1684984	T	T	341	59	375	39	5.457	0.0195	rs10495494	2	3470252	p25.3
SNP_A-1870455	C	C	343	7	379	1	5.071	2.43E-02	rs10178647	2	3588357	p25.3
SNP_A-2310609	A	A	252	142	218	164	3.857	4.95E-02	rs17388778	2	3643437	p25.3
SNP_A-1889561	C	C	413	1	411	7	4.486	3.42E-02	rs11692873	2	3676726	p25.3
SNP_A-2053304	A	A	297	97	312	68	5.215	0.0224	rs7576476	2	3789586	p25.3
SNP_A-2104140	C	C	343	33	363	19	4.289	3.84E-02	rs7577749	2	3790683	p25.3
SNP_A-1909924	C	C	382	12	363	27	6.234	1.25E-02	rs17562715	2	4077531	p25.2
SNP_A-2040921	T	T	308	72	297	101	4.647	3.11E-02	rs10187813	2	4151796	p25.2
SNP_A-1786649	G	G	304	102	334	80	3.992	4.57E-02	rs2169943	2	4172659	p25.2
SNP_A-1729610	G	G	300	92	331	69	4.728	2.97E-02	rs10495506	2	4236203	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1684824	A	A	343	57	377	37	5.622	0.0177	rs826015	2	4244224	p25.2
SNP_A-2074946	C	C	249	159	219	193	5.188	2.27E-02	rs1446137	2	4316341	p25.2
SNP_A-1946431	G	G	316	82	333	59	4.152	4.16E-02	rs12617403	2	4331304	p25.2
SNP_A-1801191	T	T	363	29	391	15	5.25	2.19E-02	rs11691587	2	4341507	p25.2
SNP_A-1921774	C	C	302	78	308	44	8.476	3.60E-03	rs11692765	2	4341721	p25.2
SNP_A-1889375	T	T	257	147	272	114	4.19	0.0407	rs2620437	2	4452357	p25.2
SNP_A-1785111	G	G	356	28	389	11	8.549	3.50E-03	rs6710928	2	4455860	p25.2
SNP_A-2244455	C	C	357	15	377	5	5.413	0.02	rs2013565	2	4671884	p25.2
SNP_A-2042814	T	T	243	57	244	88	5.022	2.50E-02	rs6750358	2	4699910	p25.2
SNP_A-2122887	T	T	328	22	363	43	4.434	3.52E-02	rs4854133	2	4737909	p25.2
SNP_A-2304397	A	A	380	12	358	26	5.732	0.0167	rs7563563	2	4739700	p25.2
SNP_A-2113249	G	G	174	150	208	126	4.962	2.59E-02	rs6548128	2	4743256	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100004	A	A	378	4	371	13	4.825	0.0281	rs11127389	2	4765391	p25.2
SNP_A-1961882	G	G	396	4	384	14	5.735	0.0166	rs6548142	2	4780962	p25.2
SNP_A-1953174	A	A	354	20	290	40	10.317	1.30E-03	rs10198129	2	4801097	p25.2
SNP_A-2093309	C	C	284	112	258	140	4.353	3.69E-02	rs4641971	2	5020140	p25.2
SNP_A-1839232	C	C	396	6	395	19	6.586	0.0103	rs9678657	2	5035450	p25.2
SNP_A-1961888	C	C	340	60	354	40	4.237	0.0395	rs11696066	2	5246554	p25.2
SNP_A-2126668	T	T	201	183	227	153	4.237	0.0395	rs10174005	2	5295004	p25.2
SNP_A-1729348	T	T	366	32	361	51	4.143	4.18E-02	rs10495520	2	5608616	p25.2
SNP_A-1929967	G	G	325	47	344	30	4.288	3.84E-02	rs10929738	2	5755950	p25.2
SNP_A-2198539	A	A	403	7	417	1	4.662	3.08E-02	rs16864175	2	5861984	p25.2
SNP_A-1836321	G	G	271	105	248	144	6.797	9.10E-03	rs2163030	2	5862170	p25.2
SNP_A-2132168	G	G	402	10	418	2	5.569	0.0183	rs16864179	2	5863087	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1961916	C	C	290	118	257	151	6.039	0.014	rs1346608	2	5877517	p25.2
SNP_A-1961918	G	G	266	86	300	58	8.185	4.20E-03	rs11892486	2	5881818	p25.2
SNP_A-1961919	G	G	276	110	318	86	5.501	0.019	rs10495524	2	5881900	p25.2
SNP_A-2069780	C	C	287	121	322	92	5.916	1.50E-02	rs7425362	2	5882495	p25.2
SNP_A-1961921	G	G	256	74	280	42	9.806	1.70E-03	rs10803749	2	5884443	p25.2
SNP_A-1877639	T	T	302	92	271	117	4.622	3.16E-02	rs4668786	2	5901071	p25.2
SNP_A-2295600	C	C	365	17	311	33	7.465	0.0063	rs1429237	2	5909372	p25.2
SNP_A-1809981	G	A	202	192	224	162	6.776	9.20E-03	rs11683095	2	5919941	p25.2
SNP_A-1961927	A	A	260	92	230	124	6.572	0.0104	rs6730239	2	5923086	p25.2
SNP_A-2095500	C	C	185	169	243	133	11.499	7.00E-04	rs2709448	2	5924128	p25.2
SNP_A-2212616	C	C	372	26	342	58	13.446	2.00E-04	rs1366738	2	5930542	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1961929	G	G	188	148	218	118	5.6	1.80E-02	rs1346612	2	5936521	p25.2
SNP_A-2077673	C	C	235	111	198	136	5.482	1.92E-02	rs7593997	2	5939978	p25.2
SNP_A-2162204	G	G	288	40	280	22	4.273	3.87E-02	rs2609090	2	6082538	p25.2
SNP_A-1878608	A	A	308	100	320	74	3.871	4.91E-02	rs941009	2	6091884	p25.2
SNP_A-2069041	T	T	331	11	319	3	4.194	4.06E-02	rs16865230	2	6580786	p25.2
SNP_A-2088551	C	C	339	13	352	2	8.306	4.00E-03	rs12692318	2	6608846	p25.2
SNP_A-1961965	C	C	340	42	306	60	4.626	0.0315	rs17748352	2	6738609	p25.2
SNP_A-2117694	C	C	297	19	311	9	3.869	4.92E-02	rs17749020	2	6746862	p25.2
SNP_A-1798308	G	G	331	65	295	85	4.409	3.58E-02	rs771302	2	7028629	p25.1
SNP_A-2035645	G	G	226	134	208	172	4.929	0.0264	rs11676629	2	7063713	p25.1
SNP_A-2089027	G	G	198	178	226	148	4.604	3.19E-02	rs4669123	2	7066675	p25.1
SNP_A-2140670	C	C	262	104	233	147	8.806	3.00E-03	rs11691419	2	7083513	p25.1
SNP_A-2242505	C	C	205	181	236	156	3.988	0.0458	rs11685858	2	7092778	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2145958	C	G	208	182	215	175	5.586	1.81E-02	rs309307	2	7110368	p25.1
SNP_A-1847811	A	A	239	127	213	157	4.643	3.12E-02	rs380605	2	7122028	p25.1
SNP_A-1742233	G	G	253	107	236	156	8.374	0.0038	rs389351	2	7159904	p25.1
SNP_A-2186203	C	C	234	164	266	138	4.242	3.94E-02	rs4669133	2	7202807	p25.1
SNP_A-2234688	G	G	346	30	341	49	4.352	3.70E-02	rs16865965	2	7213429	p25.1
SNP_A-1708206	T	T	266	124	244	164	6.102	0.0135	rs309275	2	7221734	p25.1
SNP_A-1694997	G	G	265	121	246	168	7.379	0.0066	rs309274	2	7222587	p25.1
SNP_A-1754986	T	T	244	104	219	141	6.736	9.40E-03	rs309271	2	7224235	p25.1
SNP_A-1671558	C	C	224	102	234	158	6.266	0.0123	rs4669147	2	7353359	p25.1
SNP_A-2228539	C	C	188	186	229	147	8.593	3.40E-03	rs193932	2	8057981	p25.1
SNP_A-2033365	A	A	196	194	241	155	8.947	0.0028	rs193931	2	8058033	p25.1
SNP_A-1891759	-	T	204	204	243	161	8.449	3.70E-03	rs193929	2	8058218	p25.1
SNP_A-2302667	A	A	210	200	243	167	5.371	2.05E-02	rs41007	2	8059641	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2292388	A	G	206	192	225	165	7.062	7.90E-03	rs13430914	2	8065246	p25.1
SNP_A-2209354	A	G	208	186	226	166	8.595	3.40E-03	rs17433703	2	8065898	p25.1
SNP_A-2206525	C	C	280	66	280	42	4.477	0.0344	rs6431919	2	8135347	p25.1
SNP_A-2150090	T	T	326	70	361	51	4.451	0.0349	rs17498121	2	8552426	p25.1
SNP_A-1918630	C	C	200	194	240	164	6.026	0.0141	rs4668573	2	8559881	p25.1
SNP_A-2047730	G	G	330	72	366	52	4.777	2.88E-02	rs17445442	2	8559973	p25.1
SNP_A-2289876	G	G	253	89	227	119	5.712	1.68E-02	rs6709070	2	8560184	p25.1
SNP_A-2195085	C	C	313	83	282	106	4.333	3.74E-02	rs6727210	2	8560237	p25.1
SNP_A-2052087	C	C	335	79	366	56	5.213	0.0224	rs17445491	2	8560884	p25.1
SNP_A-1962043	C	C	367	39	341	59	4.992	2.55E-02	rs2356132	2	8624182	p25.1
SNP_A-2199246	A	A	251	113	306	92	4.981	2.56E-02	rs6737516	2	8668888	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1892134	T	T	279	125	306	92	6.22	0.0126	rs11904418	2	8669028	p25.1
SNP_A-1889496	C	C	261	107	298	80	6.214	1.27E-02	rs10929537	2	8669204	p25.1
SNP_A-2312192	G	G	389	25	377	41	4.048	4.42E-02	rs10432404	2	8721759	p25.1
SNP_A-2216312	C	C	331	65	352	42	5.585	1.81E-02	rs6709598	2	8787615	p25.1
SNP_A-1885296	C	C	394	6	392	20	7.368	0.0066	rs3736459	2	9106345	p25.1
SNP_A-2141641	C	C	357	27	337	13	3.91	4.80E-02	rs6747070	2	9571328	p25.1
SNP_A-2284499	A	A	369	23	381	11	4.427	3.54E-02	rs11688654	2	9574190	p25.1
SNP_A-1737203	T	T	245	91	238	124	4.204	4.03E-02	rs4278906	2	9683328	p25.1
SNP_A-1896128	C	C	402	10	397	23	5.076	2.43E-02	rs7576067	2	9748994	p25.1
SNP_A-1962075	C	C	233	97	264	72	5.578	1.82E-02	rs17526033	2	9784626	p25.1
SNP_A-2253968	G	G	241	175	282	140	7.06	7.90E-03	rs4605345	2	9806335	p25.1
SNP_A-2029177	G	G	283	91	268	122	4.587	3.22E-02	rs4669466	2	9887633	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1706689	G	G	338	28	345	53	6.459	1.10E-02	rs1533388	2	9916757	p25.1
SNP_A-2248993	C	C	357	55	371	35	4.67	3.07E-02	rs3762536	2	10040320	p25.1
SNP_A-2258466	C	C	222	114	183	135	5.035	2.48E-02	rs2303918	2	10045590	p25.1
SNP_A-1829169	C	C	261	61	279	39	5.415	0.02	rs11902236	2	10068466	p25.1
SNP_A-1819368	G	G	291	31	293	15	5.264	0.0218	rs2116017	2	10088807	p25.1
SNP_A-2266692	A	A	216	122	256	102	4.605	3.19E-02	rs11695971	2	10401709	p25.1
SNP_A-1864574	G	G	403	11	414	2	6.374	1.16E-02	rs12477018	2	10470445	p25.1
SNP_A-1696533	C	T	213	185	219	183	5.114	2.37E-02	rs1641143	2	10621623	p25.1
SNP_A-2277845	A	G	225	191	228	192	5.86	0.0155	rs1641145	2	10621782	p25.1
SNP_A-2136942	G	C	213	139	180	176	8.767	3.10E-03	rs736725	2	10640487	p25.1
SNP_A-1812183	C	C	382	8	373	19	4.584	3.23E-02	rs4668690	2	10664530	p25.1
SNP_A-1714128	C	G	224	176	214	200	4.822	0.0281	rs6751075	2	10745285	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1727006	A	G	222	172	205	197	4.3	3.81E-02	rs7600820	2	10761783	p25.1
SNP_A-2006133	C	C	256	64	239	91	5.134	0.0235	rs2357878	2	10957298	p25.1
SNP_A-2280234	T	T	337	49	299	65	3.874	4.90E-02	rs1922717	2	10974956	p25.1
SNP_A-2006134	A	A	347	37	336	56	3.977	4.61E-02	rs4669654	2	11054094	p25.1
SNP_A-2176258	T	T	315	17	334	4	8.551	3.50E-03	rs11682194	2	11097851	p25.1
SNP_A-1938320	A	A	206	194	240	168	4.381	3.64E-02	rs10929722	2	11209522	p25.1
SNP_A-2266753	G	G	311	59	347	41	4.785	0.0287	rs4669727	2	11491087	p25.1
SNP_A-1888162	C	C	283	91	256	128	7.473	0.0063	rs10929740	2	11523504	p25.1
SNP_A-1838342	G	G	301	93	272	128	6.966	8.30E-03	rs12611958	2	11527011	p25.1
SNP_A-2080538	G	G	292	118	253	143	4.944	2.62E-02	rs6432193	2	11534595	p25.1
SNP_A-1814487	A	A	249	145	213	173	5.189	2.27E-02	rs2716620	2	11953283	p25.1
SNP_A-2266918	C	C	288	106	262	132	4.069	4.37E-02	rs2716628	2	11966361	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2212419	G	G	286	86	247	111	5.76	1.64E-02	---	2	12000019	p25.1
SNP_A-1795257	G	G	323	25	304	42	4.883	2.71E-02	rs2380421	2	12295295	p24.3
SNP_A-1962148	G	G	395	13	411	3	6.524	0.0106	rs4669836	2	12384089	p24.3
SNP_A-1962161	T	T	227	89	222	132	6.287	1.22E-02	rs624895	2	12779844	p24.3
SNP_A-2201491	A	A	219	135	192	164	4.581	3.23E-02	rs779339	2	12994482	p24.3
SNP_A-2161383	G	G	200	188	224	158	3.913	4.79E-02	rs779367	2	13016375	p24.3
SNP_A-2032192	C	C	185	173	208	132	6.398	0.0114	rs1402545	2	13059987	p24.3
SNP_A-1884930	C	C	271	137	244	174	5.697	1.70E-02	rs10929862	2	13602607	p24.3
SNP_A-2085250	C	C	268	136	237	173	6.29	0.0121	rs11686208	2	13602693	p24.3
SNP_A-1649264	G	G	342	6	315	17	5.997	0.0143	rs1510823	2	13790156	p24.3
SNP_A-2069224	T	T	389	1	393	7	4.395	0.0361	rs1588477	2	13842690	p24.3
SNP_A-2089975	C	C	412	0	414	4	3.962	0.0465	rs7560320	2	14306319	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1886143	G	G	186	166	226	150	3.907	4.81E-02	rs4145975	2	14522342	p24.3
SNP_A-2027340	A	A	329	9	318	2	4.152	4.16E-02	rs16861856	2	14648006	p24.3
SNP_A-1755752	C	C	389	9	410	2	4.766	2.90E-02	rs1434977	2	14756379	p24.3
SNP_A-2253895	A	A	400	0	380	4	4.188	0.0407	rs13422389	2	14907900	p24.3
SNP_A-2297714	T	T	339	15	341	5	4.915	2.66E-02	rs11895526	2	14935426	p24.3
SNP_A-2035341	C	C	263	67	273	39	7.084	7.80E-03	rs4668431	2	15178028	p24.3
SNP_A-2246887	G	G	269	145	303	117	4.97	0.0258	rs10192667	2	15235344	p24.3
SNP_A-2218867	G	G	213	105	191	133	4.436	3.52E-02	rs12617832	2	15870710	p24.3
SNP_A-2157160	G	G	328	78	361	55	5.437	1.97E-02	rs2245018	2	15965675	p24.3
SNP_A-2299045	G	G	248	134	287	111	4.676	3.06E-02	rs4669011	2	15980325	p24.3
SNP_A-1881083	G	G	232	138	211	173	4.676	3.06E-02	rs10929400	2	16028363	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1888188	A	A	345	35	340	54	3.841	5.00E-02	rs10929404	2	16081516	p24.3
SNP_A-2139008	G	G	347	59	377	41	4.309	3.79E-02	rs6431747	2	16087897	p24.3
SNP_A-2045480	A	A	347	55	377	37	4.589	3.22E-02	rs2114802	2	16088209	p24.3
SNP_A-2190400	T	T	262	100	287	65	8.424	3.70E-03	rs16982292	2	16511239	p24.3
SNP_A-2109529	C	C	382	14	398	4	5.839	1.57E-02	rs16982439	2	16577269	p24.3
SNP_A-1816757	A	A	379	13	411	3	6.951	8.40E-03	rs16982495	2	16594003	p24.3
SNP_A-2312926	A	A	342	74	359	53	3.865	4.93E-02	rs798365	2	16818384	p24.2
SNP_A-1895981	C	C	326	30	339	15	5.249	2.20E-02	rs1012708	2	16976714	p24.2
SNP_A-1890212	C	C	382	20	397	7	6.543	1.05E-02	rs6756921	2	17017530	p24.2
SNP_A-2179223	T	T	375	27	387	13	5.084	0.0241	rs11096710	2	17038587	p24.2
SNP_A-1900717	G	G	346	48	327	71	4.962	2.59E-02	rs1812211	2	17289830	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2228528	A	A	349	31	339	53	5.722	1.68E-02	rs13031329	2	17309828	p24.2
SNP_A-1727178	G	G	377	19	395	9	3.912	4.80E-02	rs1507979	2	17332285	p24.2
SNP_A-1820296	C	C	388	2	387	9	4.41	3.57E-02	rs16983574	2	17557295	p24.2
SNP_A-1663662	G	G	259	61	234	96	8.919	0.0028	rs1991315	2	17824603	p24.2
SNP_A-1880794	A	A	365	25	328	50	10.124	0.0015	rs7574887	2	17870277	p24.2
SNP_A-2044379	A	A	363	25	295	39	6.085	1.36E-02	rs11893763	2	17871910	p24.2
SNP_A-2257612	T	T	355	9	365	1	6.533	0.0106	rs9306660	2	17931757	p24.2
SNP_A-1704279	T	T	356	26	336	52	9.199	2.40E-03	rs750772	2	17952099	p24.2
SNP_A-1785934	T	T	254	134	226	160	3.928	4.75E-02	rs11889711	2	18038864	p24.2
SNP_A-1725574	C	C	348	42	344	64	4.185	4.08E-02	rs1350881	2	18052006	p24.2
SNP_A-1695829	T	T	248	152	287	123	5.779	1.62E-02	rs10495673	2	18125741	p24.2
SNP_A-2212976	A	A	312	74	336	54	3.993	4.57E-02	rs16985332	2	18725454	p24.2
SNP_A-2262442	T	T	321	33	346	20	3.927	4.75E-02	rs4832620	2	18874736	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1685638	T	T	383	7	389	17	3.893	4.85E-02	rs10495692	2	18905857	p24.2
SNP_A-2006183	C	C	349	67	328	90	4.016	4.51E-02	rs4240225	2	18934742	p24.2
SNP_A-2054005	C	C	347	21	348	40	5.394	2.02E-02	rs1574072	2	19193818	p24.2
SNP_A-1962347	T	T	331	25	314	40	3.904	0.0482	rs13012083	2	19550039	p24.1
SNP_A-1879390	A	A	347	35	335	65	8.801	3.00E-03	rs12991182	2	19595502	p24.1
SNP_A-2227433	T	T	164	150	223	141	5.616	0.0178	rs4666348	2	19913337	p24.1
SNP_A-2237201	T	T	391	25	409	9	7.93	4.90E-03	rs16987151	2	19964882	p24.1
SNP_A-2108084	T	T	225	155	265	129	5.394	2.02E-02	rs6729518	2	19994086	p24.1
SNP_A-1699539	C	C	354	44	378	26	5.371	2.05E-02	rs964864	2	20043543	p24.1
SNP_A-1962368	C	A	202	176	211	159	8.203	4.20E-03	rs1595414	2	20089316	p24.1
SNP_A-2094049	C	C	305	55	327	33	6.266	0.0123	rs11096633	2	20125682	p24.1
SNP_A-1736761	A	A	216	180	258	154	5.431	1.98E-02	rs10495700	2	20151477	p24.1
SNP_A-1785954	G	G	406	10	415	3	3.863	4.94E-02	rs16987384	2	20250522	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006197	G	G	270	116	221	157	10.965	9.00E-04	rs6531212	2	20259648	p24.1
SNP_A-2078329	C	C	326	16	322	32	5.153	2.32E-02	rs12619827	2	20677527	p24.1
SNP_A-2282919	G	G	287	41	259	61	5.26	0.0218	rs13013281	2	20718716	p24.1
SNP_A-1826524	A	A	396	18	410	8	4.07	0.0436	rs16982026	2	20916346	p24.1
SNP_A-2208002	G	G	355	11	388	4	3.845	0.0499	rs519025	2	20938021	p24.1
SNP_A-2202577	C	C	258	132	279	99	5.349	0.0207	rs7575840	2	21185142	p24.1
SNP_A-1879709	G	G	410	4	422	0	4.097	4.30E-02	rs17041755	2	21204219	p24.1
SNP_A-1962391	A	A	261	131	301	107	4.949	2.61E-02	rs754523	2	21223343	p24.1
SNP_A-2159042	C	C	380	26	404	14	4.161	4.14E-02	rs6753025	2	21451050	p24.1
SNP_A-1685904	A	A	366	32	394	18	4.711	3.00E-02	rs10490607	2	21493714	p24.1
SNP_A-2054680	G	G	406	4	414	0	4.059	4.39E-02	rs11126835	2	21704624	p24.1
SNP_A-1947047	A	A	378	36	393	19	5.542	1.86E-02	rs6547844	2	21832640	p24.1
SNP_A-1962417	C	C	400	14	403	5	4.231	3.97E-02	rs10495724	2	22132858	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1758439	C	C	336	60	365	37	6.609	0.0101	rs10495726	2	22538050	p24.1
SNP_A-2207856	G	G	382	0	358	4	4.244	3.94E-02	rs17043765	2	22568456	p24.1
SNP_A-1701215	T	C	223	175	209	199	4.252	3.92E-02	rs1858124	2	22586018	p24.1
SNP_A-1712033	A	A	364	34	390	20	4.349	3.70E-02	rs3849399	2	22886263	p24.1
SNP_A-1743873	C	C	364	34	387	19	4.871	2.73E-02	rs4332948	2	22887038	p24.1
SNP_A-2077762	A	A	242	102	204	126	5.476	1.93E-02	rs7586848	2	23067514	p24.1
SNP_A-2145188	G	G	393	17	415	5	7.025	8.00E-03	rs17044552	2	23128825	p24.1
SNP_A-2222012	G	G	390	26	410	10	7.592	5.90E-03	rs13399239	2	23128873	p24.1
SNP_A-1737125	T	T	277	115	262	150	4.545	3.30E-02	rs10495735	2	23129654	p24.1
SNP_A-2290342	T	T	229	109	207	135	3.857	4.95E-02	rs11687055	2	23138097	p24.1
SNP_A-2238276	C	C	240	156	262	124	4.494	3.40E-02	rs13004805	2	23138936	p24.1
SNP_A-1866085	C	C	350	48	355	29	4.475	0.0344	rs13033086	2	23200766	p24.1
SNP_A-2071399	G	G	274	96	241	129	6.955	8.40E-03	rs6755932	2	23334569	p24.1
SNP_A-1962445	A	A	318	98	292	124	4.153	4.16E-02	rs17673828	2	23340113	p24.1
SNP_A-1938382	G	G	320	0	313	7	7.077	7.80E-03	rs17045299	2	23540290	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2103733	A	A	257	99	283	77	3.98	4.61E-02	rs1465677	2	23617328	p24.1
SNP_A-2307536	A	-	231	165	201	201	5.58	1.82E-02	rs7601971	2	23624759	p24.1
SNP_A-1810623	C	C	262	128	220	160	7.087	7.80E-03	rs583168	2	23740797	p24.1
SNP_A-2062129	A	A	332	28	325	47	4.692	3.03E-02	rs6728930	2	24204004	p23.3
SNP_A-1839839	G	G	276	92	294	68	4.119	0.0424	rs17789375	2	24414205	p23.3
SNP_A-1840942	T	T	330	26	319	45	5.183	2.28E-02	rs6545697	2	24870800	p23.3
SNP_A-1827619	A	A	383	21	368	40	6.198	1.28E-02	rs6717100	2	24930412	p23.3
SNP_A-2051120	A	A	279	67	229	89	6.855	8.80E-03	rs12991495	2	25398421	p23.3
SNP_A-2207847	T	T	261	87	291	67	4.087	4.32E-02	rs10180663	2	25544893	p23.3
SNP_A-1935523	G	G	309	105	342	78	5.614	0.0178	rs10189164	2	25545019	p23.3
SNP_A-1962479	A	A	288	48	253	89	14.482	0.0001	rs10495752	2	25567799	p23.3
SNP_A-1902477	C	C	287	77	252	108	7.445	6.40E-03	rs6546199	2	25595098	p23.3
SNP_A-2072826	A	A	247	135	208	160	5.202	2.26E-02	rs4063544	2	25954166	p23.3
SNP_A-1700001	G	G	394	0	400	4	3.921	4.77E-02	rs10495755	2	26238643	p23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2233419	C	C	313	5	297	19	8.58	3.40E-03	rs11126464	2	26539174	p23.3
SNP_A-2262418	C	C	299	81	283	107	3.906	4.81E-02	rs13031842	2	26622787	p23.3
SNP_A-1886222	C	C	305	67	294	96	4.939	0.0263	rs1275538	2	27353048	p23.3
SNP_A-1693829	T	T	262	138	241	171	4.225	3.98E-02	rs780102	2	27634026	p23.3
SNP_A-1816236	G	G	398	16	406	6	4.62	3.16E-02	rs7586131	2	28495865	p23.2
SNP_A-2249649	C	C	256	138	286	106	5.852	1.56E-02	rs13404237	2	28722782	p23.2
SNP_A-2216577	C	C	327	27	306	62	14.195	2.00E-04	rs4666111	2	28750446	p23.2
SNP_A-2253996	C	C	218	138	177	167	6.809	9.10E-03	rs11127181	2	28759457	p23.2
SNP_A-2297231	C	C	258	134	231	163	4.317	3.77E-02	rs6721990	2	28768245	p23.2
SNP_A-2229828	C	C	355	29	367	13	6.274	0.0123	rs13399528	2	28894478	p23.2
SNP_A-1900844	G	G	231	165	199	193	4.551	3.29E-02	rs10166861	2	28972762	p23.2
SNP_A-1799010	T	T	378	28	387	15	4.016	4.51E-02	rs7589735	2	29011403	p23.2
SNP_A-1807500	G	G	372	36	360	56	4.467	3.45E-02	rs6731230	2	29397729	p23.2
SNP_A-2224722	G	G	402	6	408	0	6.044	0.014	rs11679467	2	29397931	p23.2
SNP_A-2259513	G	G	398	8	416	0	8.278	4.00E-03	rs1406236	2	29411093	p23.2
SNP_A-2231369	C	C	408	8	420	0	8.155	0.0043	rs1406237	2	29411276	p23.2
SNP_A-2180363	A	A	307	7	327	1	4.828	2.80E-02	rs2339467	2	29426244	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1780447	T	T	407	9	416	2	4.548	3.30E-02	rs4666194	2	29431736	p23.2
SNP_A-2168357	C	C	408	8	419	1	5.572	0.0183	rs1969528	2	29436720	p23.2
SNP_A-2006243	G	G	230	110	223	149	4.552	3.29E-02	rs3885974	2	29613904	p23.2
SNP_A-1928021	G	G	398	10	413	3	3.969	4.63E-02	rs4575680	2	29682414	p23.2
SNP_A-2283959	C	C	331	39	363	25	4.113	4.26E-02	rs2541183	2	29892059	p23.2
SNP_A-1716349	C	C	395	5	414	0	5.207	2.25E-02	rs4666273	2	29986403	p23.2
SNP_A-2194370	T	T	270	70	298	50	4.621	3.16E-02	rs4280416	2	29999674	p23.1
SNP_A-1839669	G	G	397	9	408	2	4.585	3.22E-02	rs3768669	2	30291988	p23.1
SNP_A-1818946	A	A	250	54	300	40	4.633	3.14E-02	rs1869424	2	30746636	p23.1
SNP_A-1901405	G	G	339	63	292	84	5.638	1.76E-02	rs4952173	2	30799997	p23.1
SNP_A-2030474	A	A	251	111	205	139	7.322	6.80E-03	rs17041364	2	30856283	p23.1
SNP_A-2200885	G	G	359	45	379	27	5.037	2.48E-02	rs17010098	2	30868442	p23.1
SNP_A-2076045	A	A	378	0	298	6	7.527	6.10E-03	rs17010206	2	30896548	p23.1
SNP_A-1873788	A	A	349	65	329	93	5.476	1.93E-02	rs17010322	2	30934164	p23.1
SNP_A-1661372	G	G	324	24	330	42	4.169	4.12E-02	rs499476	2	30960309	p23.1
SNP_A-1870765	G	G	298	100	325	77	4.139	0.0419	rs17393065	2	31030250	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1870519	T	T	305	61	293	85	3.993	4.57E-02	rs11889636	2	31076996	p23.1
SNP_A-1962546	G	G	402	14	413	5	4.407	3.58E-02	rs17010500	2	31081958	p23.1
SNP_A-2193305	G	G	335	5	354	0	5.244	2.20E-02	rs17010574	2	31155615	p23.1
SNP_A-1962549	C	T	180	144	163	145	4.543	3.31E-02	rs2113490	2	31215798	p23.1
SNP_A-1962553	G	C	212	166	199	187	4.467	3.46E-02	rs12712310	2	31227111	p23.1
SNP_A-1962558	G	G	196	184	221	143	6.298	0.0121	rs2194464	2	31240302	p23.1
SNP_A-1962559	T	C	210	206	240	180	4.881	2.72E-02	rs2216829	2	31240324	p23.1
SNP_A-2069801	G	G	226	158	207	195	4.302	3.81E-02	rs6729079	2	31252140	p23.1
SNP_A-2225720	G	G	230	168	247	135	3.873	4.91E-02	rs12621306	2	31254028	p23.1
SNP_A-1663968	A	G	204	196	235	177	5.266	2.17E-02	rs1862976	2	31280808	p23.1
SNP_A-1678374	-	T	196	196	231	167	5.14	2.34E-02	rs10490518	2	31285888	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1691818	-	A	198	198	239	173	5.217	0.0224	rs3919588	2	31286083	p23.1
SNP_A-1676156	G	G	238	158	212	194	5.06	2.45E-02	rs1862975	2	31300967	p23.1
SNP_A-2174009	G	G	258	64	316	50	4.786	0.0287	rs1373217	2	31303553	p23.1
SNP_A-1962569	A	A	356	48	319	97	18.415	1.78E-05	rs644736	2	31408329	p23.1
SNP_A-1962570	G	G	365	47	321	95	19.029	1.29E-05	rs646103	2	31408635	p23.1
SNP_A-1962571	C	C	335	31	282	66	16.738	4.29E-05	rs646200	2	31408698	p23.1
SNP_A-1891720	T	T	306	40	268	74	12.633	4.00E-04	rs674791	2	31409968	p23.1
SNP_A-2278873	A	A	310	78	265	115	10.533	1.20E-03	rs11124256	2	31416672	p23.1
SNP_A-1795278	G	G	243	77	222	100	3.931	4.74E-02	rs207425	2	31461313	p23.1
SNP_A-1676786	C	C	312	84	289	121	7.317	6.80E-03	rs4952078	2	31479240	p23.1
SNP_A-1722988	A	A	342	58	324	90	7.167	7.40E-03	rs207416	2	31514890	p23.1
SNP_A-2058818	A	A	181	149	220	132	4.116	4.25E-02	rs1028600	2	32869838	p22.3
SNP_A-2160002	C	C	324	16	302	34	7.23	7.20E-03	rs11900724	2	32923199	p22.3
SNP_A-1677334	G	G	296	92	314	66	4.727	2.97E-02	rs3769583	2	32942656	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2108596	C	C	373	43	398	24	6.156	1.31E-02	rs7573847	2	33014681	p22.3
SNP_A-1945831	C	C	401	15	414	6	4.045	4.43E-02	rs219056	2	33258258	p22.3
SNP_A-2181407	T	C	194	178	205	165	4.241	0.0395	rs1454379	2	33351696	p22.3
SNP_A-1695345	A	G	204	196	232	180	4.352	3.70E-02	rs4671024	2	33420193	p22.3
SNP_A-1718999	T	T	303	95	336	74	4.136	4.20E-02	rs1993306	2	33420870	p22.3
SNP_A-1731003	G	G	351	9	354	2	4.445	3.50E-02	rs7569074	2	33555489	p22.3
SNP_A-1962614	T	T	337	11	296	22	4.981	2.56E-02	---	2	33557897	p22.3
SNP_A-1735659	T	T	275	119	251	151	4.808	2.83E-02	rs10495791	2	33697719	p22.3
SNP_A-1721277	G	G	359	25	363	47	5.899	1.51E-02	rs1349119	2	33768294	p22.3
SNP_A-1962623	G	G	313	49	320	30	4.446	3.50E-02	rs2367955	2	33851592	p22.3
SNP_A-2172287	C	C	218	162	263	141	4.935	0.0263	rs10221753	2	33904382	p22.3
SNP_A-2282141	C	C	288	100	254	122	4.126	4.22E-02	rs1425025	2	34214394	p22.3
SNP_A-2196610	C	C	314	86	342	62	5.067	2.44E-02	---	2	34479618	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259155	G	G	299	93	329	69	4.943	2.62E-02	—	2	34479694	p22.3
SNP_A-1742567	A	A	307	87	344	68	4.032	4.46E-02	rs10490439	2	34522440	p22.3
SNP_A-1699951	T	T	308	92	344	70	4.736	2.95E-02	rs10495811	2	34538289	p22.3
SNP_A-1822900	G	G	323	49	311	15	15.325	9.05E-05	rs2139476	2	34593145	p22.3
SNP_A-1962666	A	A	296	96	260	116	3.886	0.0487	rs3731951	2	34858769	p22.3
SNP_A-1697635	C	C	296	104	279	133	3.875	4.90E-02	rs10495827	2	34922938	p22.3
SNP_A-2222698	A	A	183	173	224	154	4.579	3.24E-02	rs12712404	2	34931338	p22.3
SNP_A-2309250	C	C	278	76	266	112	6.378	1.16E-02	rs399420	2	34961646	p22.3
SNP_A-1844299	T	C	193	161	189	153	6.659	9.90E-03	rs280709	2	34969176	p22.3
SNP_A-1889595	C	T	193	129	169	161	8.165	0.0043	rs280694	2	34985806	p22.3
SNP_A-1898631	C	C	230	150	202	184	5.229	2.22E-02	rs183975	2	34998314	p22.3
SNP_A-2041942	A	A	283	45	303	29	4.118	0.0424	rs10202622	2	35355984	p22.3
SNP_A-2295199	T	T	385	7	408	0	7.35	6.70E-03	rs4289165	2	35647173	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2078980	A	A	393	5	385	17	6.608	1.02E-02	rs6716534	2	35933453	p22.3
SNP_A-2031563	G	G	414	0	412	4	4	4.55E-02	rs17402488	2	36081118	p22.3
SNP_A-1956601	G	G	276	110	292	70	8.578	3.40E-03	rs833759	2	36099617	p22.3
SNP_A-1962706	A	A	414	0	410	6	6.015	1.42E-02	rs17017987	2	36124374	p22.3
SNP_A-2198472	G	G	330	12	332	26	4.801	2.84E-02	rs2063403	2	36140764	p22.3
SNP_A-2185696	A	A	279	95	319	73	5.136	2.34E-02	rs6759368	2	36148419	p22.3
SNP_A-1962709	A	A	291	119	331	87	7.467	0.0063	rs4670134	2	36151801	p22.3
SNP_A-2162507	T	T	284	96	304	72	4.088	4.32E-02	rs13022609	2	36181076	p22.3
SNP_A-2052048	G	G	395	15	390	28	3.885	0.0487	rs305205	2	36187920	p22.3
SNP_A-2161457	C	C	396	16	379	29	4.109	4.27E-02	rs305203	2	36189620	p22.3
SNP_A-1898201	T	T	398	18	385	35	5.65	1.75E-02	rs17038799	2	36265516	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1748265	T	T	312	88	352	62	6.677	9.80E-03	rs4115339	2	36334740	p22.3
SNP_A-2050608	G	G	338	30	293	45	4.943	2.62E-02	rs11124503	2	36367488	p22.3
SNP_A-1952683	C	C	366	6	361	17	5.248	2.20E-02	rs6544006	2	36456820	p22.3
SNP_A-1962724	A	A	311	59	300	88	5.495	1.91E-02	rs17018690	2	36532708	p22.2
SNP_A-1708526	T	T	286	74	263	99	4.571	3.25E-02	rs717806	2	36550070	p22.2
SNP_A-2307648	G	G	282	116	250	142	4.5	0.0339	rs3770911	2	36550124	p22.2
SNP_A-2290840	C	C	366	42	337	65	6.096	0.0135	rs3821157	2	36581321	p22.2
SNP_A-1924301	G	G	218	102	244	80	4.098	4.29E-02	rs711254	2	36592499	p22.2
SNP_A-1879525	C	C	292	118	322	92	4.666	3.08E-02	rs3770839	2	36629271	p22.2
SNP_A-1916968	G	G	292	116	312	88	4.427	3.54E-02	rs3899034	2	36629470	p22.2
SNP_A-1658656	C	C	274	104	304	82	4.076	4.35E-02	rs848530	2	36705321	p22.2
SNP_A-2246806	C	A	197	183	221	179	3.926	4.76E-02	rs721349	2	36858323	p22.2
SNP_A-2267857	A	A	281	135	304	108	3.885	0.0487	rs1558701	2	36939470	p22.2
SNP_A-2279944	C	C	253	145	258	100	6.215	1.27E-02	rs2372715	2	36960938	p22.2
SNP_A-2275021	G	G	376	12	377	27	5.45	1.96E-02	rs7581702	2	37164503	p22.2
SNP_A-1872788	T	T	276	132	247	163	4.861	0.0275	rs12620426	2	37291520	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284065	A	A	269	127	238	168	7.47	0.0063	rs3856500	2	37298937	p22.2
SNP_A-1865388	C	C	346	44	362	24	6.223	0.0126	rs2714474	2	37371386	p22.2
SNP_A-2037703	A	A	228	122	195	143	4.031	4.47E-02	rs1158219	2	37458471	p22.2
SNP_A-1793786	T	T	284	74	324	50	6.93	8.50E-03	rs10173794	2	37540873	p22.2
SNP_A-2282032	G	G	386	24	404	12	4.367	3.66E-02	rs4131231	2	37550288	p22.2
SNP_A-2109233	T	T	390	20	405	9	4.436	3.52E-02	rs17020696	2	37550552	p22.2
SNP_A-2041952	T	T	312	86	328	62	4.211	0.0402	rs12712534	2	37590096	p22.2
SNP_A-1648540	T	T	319	53	358	36	4.866	2.74E-02	rs10490445	2	37592019	p22.2
SNP_A-2265577	C	C	290	70	323	51	4.495	3.40E-02	rs4670203	2	37592622	p22.2
SNP_A-1920321	C	C	272	74	245	103	6.156	1.31E-02	rs2215605	2	37729887	p22.2
SNP_A-1753153	C	C	266	132	242	168	5.277	2.16E-02	rs4670762	2	37897354	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1899489	A	A	346	66	356	42	5.235	2.21E-02	rs4143265	2	37968602	p22.2
SNP_A-2301457	A	A	339	61	357	39	5.286	2.15E-02	rs934207	2	37976245	p22.2
SNP_A-2062351	T	T	319	55	342	32	6.881	8.70E-03	rs2194381	2	38316446	p22.2
SNP_A-2153826	C	C	329	45	345	23	7.449	0.0063	rs13396572	2	38320611	p22.2
SNP_A-1962812	A	A	229	179	258	150	4.283	0.0385	rs1871163	2	38353634	p22.2
SNP_A-2183382	C	C	204	122	225	97	3.857	4.95E-02	rs4670829	2	38353756	p22.2
SNP_A-2288724	A	A	293	75	319	51	5.671	1.73E-02	rs4101522	2	38382143	p22.2
SNP_A-2258507	C	C	336	36	356	22	3.91	4.80E-02	rs17493370	2	38691925	p22.1
SNP_A-1898671	C	C	381	1	391	7	4.303	3.80E-02	rs7596222	2	39523033	p22.1
SNP_A-2213566	T	T	376	12	401	3	5.884	1.53E-02	rs4670947	2	39731112	p22.1
SNP_A-2116167	T	T	245	167	278	138	4.82	0.0281	rs2056619	2	39766099	p22.1
SNP_A-1861878	C	C	359	21	367	9	4.867	2.74E-02	rs3749056	2	40396596	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2155515	G	G	208	206	238	178	4.055	4.40E-02	rs12611602	2	40488776	p22.1
SNP_A-2289949	G	G	215	171	254	142	5.803	0.016	rs6544324	2	40494709	p22.1
SNP_A-1962890	T	T	377	5	374	0	4.928	0.0264	rs12619139	2	40636437	p22.1
SNP_A-2135087	G	G	374	22	391	9	5.809	1.59E-02	rs1379037	2	40892805	p22.1
SNP_A-2133263	G	G	200	110	178	148	6.479	0.0109	rs17027254	2	41302903	p22.1
SNP_A-1909689	A	A	313	99	293	127	4.053	0.0441	rs7597664	2	41338455	p22.1
SNP_A-2284158	G	G	250	118	218	142	4.316	0.0378	rs7599534	2	41533898	p22.1
SNP_A-1838175	C	C	264	152	233	183	4.802	2.84E-02	rs1508128	2	41573414	p22.1
SNP_A-2129664	C	C	242	138	207	159	3.952	4.68E-02	rs7586603	2	41664493	p22.1
SNP_A-1962936	G	G	215	135	253	111	5.154	2.32E-02	rs1550429	2	42138495	p21
SNP_A-2068675	C	C	334	64	312	86	3.976	4.62E-02	rs12477943	2	42270362	p21
SNP_A-2178628	A	A	241	143	270	118	4.02	4.50E-02	rs12612692	2	43016739	p21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805508	A	A	335	73	362	50	5.327	2.10E-02	rs11124899	2	43043760	p21
SNP_A-2192578	G	G	220	140	255	101	8.868	2.90E-03	rs11124901	2	43044078	p21
SNP_A-2276183	G	G	299	47	281	83	10.078	0.0015	rs13414085	2	43257665	p21
SNP_A-2071772	T	T	238	140	261	107	5.336	2.09E-02	rs12477432	2	43557819	p21
SNP_A-1673892	T	T	235	163	215	197	3.859	4.95E-02	rs4952999	2	43904788	p21
SNP_A-1744637	C	C	235	161	215	197	4.194	4.06E-02	rs4953002	2	43905711	p21
SNP_A-1867683	C	C	282	46	298	18	12.472	4.00E-04	rs17031775	2	44092156	p21
SNP_A-2042965	C	C	331	81	305	109	5.184	2.28E-02	rs1453866	2	44207564	p21
SNP_A-2118235	A	A	333	83	309	109	4.413	3.57E-02	rs4953053	2	44207972	p21
SNP_A-1962976	G	G	319	89	346	64	5.176	0.0229	rs1067344	2	44532461	p21
SNP_A-1781899	C	C	349	49	367	23	9.761	0.0018	rs698822	2	44632403	p21
SNP_A-1928772	G	G	364	6	340	0	5.561	0.0184	rs17581117	2	44636643	p21
SNP_A-1788425	G	G	219	139	198	174	4.705	3.01E-02	rs341577	2	44970897	p21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2154768	G	G	328	50	308	94	13.348	3.00E-04	rs895636	2	45100004	p21
SNP_A-2147776	G	G	247	153	278	126	4.424	3.54E-02	rs6544781	2	45190445	p21
SNP_A-1839690	A	A	376	18	375	33	4.17	4.11E-02	rs11888802	2	45477201	p21
SNP_A-1660695	C	A	184	146	204	168	7.854	5.10E-03	rs2216505	2	45568944	p21
SNP_A-1963010	G	G	274	88	231	113	6.316	0.012	rs3770251	2	45580321	p21
SNP_A-2222071	T	T	281	115	253	153	6.733	9.50E-03	rs11125017	2	45592816	p21
SNP_A-1827977	C	C	193	167	235	123	10.792	0.001	rs17394081	2	45604598	p21
SNP_A-1722354	C	C	295	105	269	139	5.858	0.0155	rs10490348	2	45606987	p21
SNP_A-1963013	T	T	341	75	318	102	4.902	2.68E-02	rs3770278	2	45650048	p21
SNP_A-1927112	A	C	215	197	233	181	5.928	0.0149	rs17322370	2	45650696	p21
SNP_A-2236870	A	G	210	198	238	178	6.232	1.25E-02	rs4425122	2	45661174	p21
SNP_A-2244532	A	G	207	197	224	174	4.545	3.30E-02	rs6708810	2	45685701	p21
SNP_A-2042997	A	C	205	199	222	166	5.035	2.48E-02	rs6710581	2	45690869	p21
SNP_A-2142002	T	T	311	105	336	80	4.344	3.71E-02	rs7576649	2	45728220	p21
SNP_A-2187175	C	C	317	99	347	73	5.267	2.17E-02	rs1517001	2	45769002	p21
SNP_A-1736703	A	A	297	101	332	78	4.726	2.97E-02	rs6544836	2	45790525	p21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1947258	A	A	328	10	345	1	7.701	5.50E-03	rs17033982	2	45817763	p21
SNP_A-1807533	C	C	389	15	395	3	8.001	4.70E-03	rs1463157	2	45978369	p21
SNP_A-2292520	T	T	250	164	289	121	9.29	0.0023	rs1982366	2	46029565	p21
SNP_A-2236378	C	C	201	145	251	127	5.318	2.11E-02	rs4953288	2	46037622	p21
SNP_A-1679796	G	G	242	158	286	126	7.097	7.70E-03	rs872288	2	46089559	p21
SNP_A-2138342	C	T	219	163	165	157	5.159	2.31E-02	rs13430530	2	46204824	p21
SNP_A-2220197	C	C	344	22	381	11	4.669	3.07E-02	rs3768758	2	46231653	p21
SNP_A-2094853	A	A	380	36	401	17	7.371	0.0066	rs7583750	2	46392597	p21
SNP_A-1845186	G	A	172	154	191	153	4.599	3.20E-02	rs7583392	2	46515089	p21
SNP_A-2185039	G	G	255	155	226	182	3.907	4.81E-02	rs7571218	2	46517310	p21
SNP_A-2307381	C	C	157	149	195	129	5.031	2.49E-02	rs1109286	2	46545581	p21
SNP_A-2077998	G	G	381	3	374	14	7.162	7.40E-03	rs17771201	2	46871710	p21
SNP_A-2184001	C	C	192	100	253	87	5.653	1.74E-02	rs4332965	2	47167709	p21
SNP_A-2285049	A	A	335	13	359	5	4.028	0.0448	rs11695805	2	47228527	p21
SNP_A-1784858	G	G	346	2	359	9	4.139	0.0419	rs11674800	2	47694407	p21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2240247	A	A	396	10	410	2	5.533	1.87E-02	rs17036815	2	47816083	p16.3
SNP_A-1819314	C	C	355	5	371	15	4.452	0.0349	rs2098242	2	47668470	p16.3
SNP_A-1861551	A	A	376	4	396	0	4.19	0.0407	rs11895219	2	48384619	p16.3
SNP_A-2104195	T	T	302	62	319	43	3.898	4.83E-02	rs7557600	2	48683853	p16.3
SNP_A-1881768	G	G	299	55	309	29	7.846	5.10E-03	rs17038059	2	49162911	p16.3
SNP_A-2248307	C	C	343	69	369	47	5.103	2.39E-02	rs1504183	2	49285702	p16.3
SNP_A-2310361	T	T	262	98	233	123	4.505	3.38E-02	rs4971697	2	49327365	p16.3
SNP_A-2050103	T	T	239	81	277	61	5.127	2.36E-02	rs1365853	2	49408796	p16.3
SNP_A-1908852	T	T	394	14	386	30	5.823	1.58E-02	rs6708337	2	49572272	p16.3
SNP_A-1709615	A	A	384	12	379	31	8.187	4.20E-03	rs1527894	2	49622559	p16.3
SNP_A-2097465	C	C	391	25	403	11	5.621	0.0177	rs6705020	2	49689587	p16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2297032	C	C	387	21	396	6	8.393	0.0038	rs10188077	2	49693640	p16.3
SNP_A-1840294	C	C	391	21	402	10	4.056	4.40E-02	rs2114656	2	49737519	p16.3
SNP_A-1963152	C	C	351	23	370	12	3.874	4.91E-02	rs17178439	2	49742265	p16.3
SNP_A-2076922	C	C	324	24	336	12	4.218	4.00E-02	rs17039430	2	50051137	p16.3
SNP_A-1817083	C	C	280	58	299	39	4.345	3.71E-02	rs2045003	2	50228936	p16.3
SNP_A-1839613	G	G	325	57	346	36	5.399	0.0201	rs17039940	2	50270921	p16.3
SNP_A-2064139	G	G	332	56	341	35	4.779	2.88E-02	rs12468477	2	50295864	p16.3
SNP_A-1889344	C	C	308	30	309	51	4.757	0.0292	rs1915237	2	50421282	p16.3
SNP_A-1957545	T	T	374	12	382	4	4.085	4.33E-02	rs1915228	2	50436536	p16.3
SNP_A-1686432	A	A	349	51	378	34	4.38	3.64E-02	rs10490231	2	50512000	p16.3
SNP_A-1724654	C	C	349	51	377	33	4.814	2.82E-02	rs10490230	2	50512861	p16.3
SNP_A-1698423	G	G	348	50	378	34	4.047	4.43E-02	rs1814972	2	50515248	p16.3
SNP_A-1963210	C	C	210	186	239	143	7.244	7.10E-03	rs1914722	2	50837179	p16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2151407	G	G	243	111	254	82	4.134	4.20E-02	rs17040972	2	50849784	p16.3
SNP_A-1792640	G	G	352	28	377	13	6.216	1.27E-02	rs17568979	2	50943582	p16.3
SNP_A-1829747	A	A	193	189	223	157	5.118	2.37E-02	rs6545190	2	51194260	p16.3
SNP_A-2075467	T	T	266	56	231	85	8.374	0.0038	rs6713682	2	51231101	p16.3
SNP_A-1690325	C	A	183	171	217	159	6.481	0.0109	rs2287234	2	51233421	p16.3
SNP_A-1963216	T	T	298	52	280	78	5.671	0.0172	rs2069318	2	51235546	p16.3
SNP_A-1839253	C	C	357	59	327	93	8.902	0.0028	rs7559189	2	51247338	p16.3
SNP_A-2179725	G	G	355	11	394	2	7.091	7.70E-03	rs11562945	2	51582831	p16.3
SNP_A-1796311	G	G	346	34	336	14	7.259	7.10E-03	rs9973524	2	51841311	p16.3
SNP_A-1651394	C	C	385	15	407	5	5.435	1.97E-02	rs4108601	2	51850700	p16.3
SNP_A-1923934	C	C	329	51	347	33	4.336	0.0373	rs12468211	2	52464674	p16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884504	C	C	248	94	233	127	4.937	0.0263	rs12615642	2	52635579	p16.3
SNP_A-2101014	G	G	347	29	358	16	3.922	4.77E-02	rs350716	2	52869845	p16.2
SNP_A-1963276	C	C	337	33	365	17	6.047	1.39E-02	rs350722	2	52892153	p16.2
SNP_A-2166041	G	G	348	20	358	8	5.279	2.16E-02	rs350728	2	52894211	p16.2
SNP_A-1952366	T	T	399	5	408	0	5.081	2.42E-02	rs12052333	2	53413380	p16.2
SNP_A-2285044	T	T	265	115	226	154	8.752	3.10E-03	rs11890869	2	53452251	p16.2
SNP_A-1879699	G	G	280	116	284	78	5.959	0.0146	rs1521949	2	53581197	p16.2
SNP_A-2169713	G	G	370	12	382	2	7.329	6.80E-03	rs10187264	2	53638918	p16.2
SNP_A-2143719	A	A	275	117	249	147	4.679	3.05E-02	rs6753258	2	53758198	p16.2
SNP_A-2046744	C	C	366	6	351	15	4.122	4.23E-02	rs7584996	2	53773258	p16.2
SNP_A-1963316	T	T	388	20	403	9	4.437	3.52E-02	rs3755119	2	53868991	p16.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1850869	A	A	332	72	351	43	7.717	5.50E-03	rs12613353	2	53885874	p16.2
SNP_A-1744191	T	T	342	16	368	6	5.15	2.32E-02	rs10490472	2	53974308	p16.2
SNP_A-1734044	C	C	378	22	403	7	8.437	3.70E-03	rs3755113	2	54062558	p16.2
SNP_A-1854506	T	T	288	46	240	60	4.402	3.59E-02	rs805445	2	54087091	p16.2
SNP_A-1963325	G	G	353	31	373	17	4.588	3.22E-02	rs3929001	2	54194538	p16.2
SNP_A-1846523	A	A	260	60	279	41	4.244	3.94E-02	rs11125521	2	54264009	p16.2
SNP_A-1895085	G	G	246	92	276	72	4.018	4.50E-02	rs4606970	2	54484829	p16.2
SNP_A-2276256	C	C	364	0	354	4	4.09	4.31E-02	rs2280717	2	54499029	p16.2
SNP_A-2284407	G	G	363	21	368	10	3.89	4.86E-02	rs6761960	2	54927415	p16.1
SNP_A-1937464	C	C	280	132	326	86	13.198	3.00E-04	rs12713281	2	54993413	p16.1
SNP_A-2268627	C	A	195	183	222	172	4.867	2.74E-02	rs7595552	2	54994554	p16.1
SNP_A-1888634	G	G	281	127	256	162	5.282	2.15E-02	rs2033413	2	54996922	p16.1
SNP_A-1854985	T	T	233	85	214	110	3.957	4.67E-02	rs6727776	2	55003230	p16.1
SNP_A-2264205	C	C	370	46	352	66	4.015	4.51E-02	rs17046424	2	55003444	p16.1
SNP_A-2110202	A	A	250	164	286	134	5.395	2.02E-02	rs17417862	2	55031571	p16.1
SNP_A-1836992	T	T	208	150	250	112	9.341	2.20E-03	rs6545458	2	55059446	p16.1
SNP_A-1913483	T	T	242	172	274	144	4.446	3.50E-02	rs13390825	2	55064238	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1646566	C	C	270	96	251	141	8.355	0.0038	rs1961245	2	55068376	p16.1
SNP_A-2131511	G	G	248	146	279	119	4.554	3.28E-02	rs7590265	2	55077188	p16.1
SNP_A-2313471	C	C	273	143	305	107	6.936	8.40E-03	rs6744548	2	55077745	p16.1
SNP_A-2268664	T	T	308	102	274	134	6.32	1.19E-02	rs7593229	2	55592147	p16.1
SNP_A-2117337	T	T	377	19	391	5	8.422	3.70E-03	rs17736147	2	55630878	p16.1
SNP_A-1727180	G	G	293	91	255	131	9.837	1.70E-03	rs897097	2	55660192	p16.1
SNP_A-1963361	G	G	395	19	381	33	4.022	4.49E-02	rs9309267	2	55761984	p16.1
SNP_A-1963362	A	A	376	14	376	30	5.499	0.019	rs7594497	2	55784189	p16.1
SNP_A-1963366	A	A	238	136	199	157	4.545	3.30E-02	rs4355154	2	55922454	p16.1
SNP_A-1891643	G	G	355	35	357	19	4.492	3.41E-02	rs11680866	2	56020340	p16.1
SNP_A-1853604	A	A	213	203	248	172	5.201	2.26E-02	rs4487120	2	56043927	p16.1
SNP_A-1939668	C	C	352	4	312	12	4.915	2.66E-02	rs13397916	2	56162898	p16.1
SNP_A-1750531	G	G	303	97	282	130	5.375	2.04E-02	rs6545537	2	56192368	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1724864	G	G	278	78	263	117	7.441	6.40E-03	rs6545538	2	56192434	p16.1
SNP_A-1851797	G	G	336	68	367	41	8.036	4.60E-03	rs979504	2	56358325	p16.1
SNP_A-2295740	G	G	272	118	304	94	4.414	0.0356	rs1160647	2	56365351	p16.1
SNP_A-2187544	C	C	304	48	291	69	3.964	0.0465	rs4672103	2	56401106	p16.1
SNP_A-2168798	T	T	314	76	346	46	8.924	0.0028	rs214047	2	56402331	p16.1
SNP_A-2250660	A	A	378	34	363	57	6.04	0.014	rs1549031	2	56419094	p16.1
SNP_A-1963386	T	T	369	41	347	63	5.33	2.10E-02	rs4671278	2	56440024	p16.1
SNP_A-1861948	A	A	310	38	307	67	7.097	7.70E-03	rs10203280	2	56464354	p16.1
SNP_A-1929128	G	G	195	187	217	155	4.037	4.45E-02	rs6728372	2	56811206	p16.1
SNP_A-2091600	T	T	302	18	316	38	5.76	1.64E-02	rs17049423	2	58373554	p16.1
SNP_A-1963450	A	A	408	2	395	9	4.621	3.16E-02	rs10490088	2	58692452	p16.1
SNP_A-1835324	T	T	376	26	392	14	3.914	4.79E-02	rs7559374	2	58821755	p16.1
SNP_A-1963457	T	T	252	140	210	164	5.293	2.14E-02	rs2192692	2	59016175	p16.1
SNP_A-1836255	C	C	321	33	339	17	5.605	1.79E-02	rs10178739	2	59362896	p16.1
SNP_A-1963470	C	C	373	29	389	13	6.431	0.0112	rs10490114	2	59483881	p16.1
SNP_A-2052221	G	G	377	33	391	19	4.024	0.0448	rs17050135	2	59492340	p16.1
SNP_A-1859746	C	C	330	32	327	17	4.149	4.17E-02	rs2540093	2	59673169	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2152944	A	A	288	62	293	41	3.952	4.68E-02	rs10174893	2	59703044	p16.1
SNP_A-2273986	C	C	311	41	314	20	6.776	9.20E-03	rs174845	2	59797062	p16.1
SNP_A-2237321	A	A	271	107	203	121	6.5	1.08E-02	rs4141843	2	60066971	p16.1
SNP_A-1963497	T	T	354	32	388	14	8.28	4.00E-03	rs13005300	2	60166534	p16.1
SNP_A-2286759	G	G	376	40	401	19	8.26	4.10E-03	rs13016030	2	60179911	p16.1
SNP_A-2129899	A	G	169	151	174	140	4.293	3.83E-02	rs994972	2	60191069	p16.1
SNP_A-2096388	C	G	181	147	173	153	4.454	3.48E-02	rs6712720	2	60193259	p16.1
SNP_A-1963521	A	A	242	166	215	195	3.92	4.77E-02	rs12474142	2	60815332	p16.1
SNP_A-1910781	T	T	390	16	391	5	5.639	1.76E-02	rs17010833	2	61714960	p15
SNP_A-2162824	A	A	292	96	273	123	3.886	0.0487	rs17013350	2	61889998	p15
SNP_A-2284233	C	C	374	0	378	6	5.89	0.0152	rs4671412	2	62048487	p15
SNP_A-1963535	G	G	297	25	336	12	5.97	1.45E-02	rs10518958	2	62188624	p15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1745356	C	C	295	105	275	133	3.917	4.78E-02	rs10496096	2	62282313	p15
SNP_A-1865857	C	C	270	116	293	91	3.954	4.68E-02	rs360804	2	62851048	p15
SNP_A-2085218	T	T	287	79	324	58	5.12	2.37E-02	rs12987254	2	63098765	p15
SNP_A-2283403	G	G	392	12	396	4	4.001	4.55E-02	rs6710437	2	64045213	p14
SNP_A-2057412	T	T	376	30	385	13	6.748	9.40E-03	rs7579192	2	64084963	p14
SNP_A-1963553	C	C	252	90	255	59	5.282	2.15E-02	rs329477	2	64168552	p14
SNP_A-1902688	T	T	246	128	267	99	4.479	3.43E-02	rs2555417	2	64431792	p14
SNP_A-2037592	C	C	308	102	353	63	12.239	5.00E-04	rs1426704	2	64473331	p14
SNP_A-2132727	C	C	301	51	328	32	5.419	1.99E-02	rs6546069	2	64507134	p14
SNP_A-1930181	T	T	376	4	388	0	4.106	4.27E-02	rs7574786	2	64916325	p14
SNP_A-1896972	G	G	297	111	271	143	5.178	0.0229	rs9677813	2	65124171	p14
SNP_A-1841073	A	A	288	28	319	15	5.019	2.51E-02	rs3771105	2	65235740	p14
SNP_A-1905675	T	T	348	22	350	38	3.847	4.98E-02	rs6760380	2	65279645	p14
SNP_A-1814884	T	T	369	47	383	29	4.505	3.38E-02	rs6745303	2	65391845	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289773	A	A	326	66	362	48	4.324	3.76E-02	rs6743585	2	65467371	p14
SNP_A-2090962	T	T	351	35	374	16	7.788	0.0053	rs268140	2	65518555	p14
SNP_A-2308520	G	G	310	104	346	74	6.989	8.20E-03	rs840958	2	65637849	p14
SNP_A-1859900	C	C	298	18	310	8	4.077	4.35E-02	rs840962	2	65639218	p14
SNP_A-2079035	C	C	372	20	399	9	4.8	2.85E-02	rs1673441	2	65705765	p14
SNP_A-2152454	C	C	308	8	313	1	5.478	1.93E-02	rs1484484	2	66143730	p14
SNP_A-2099882	G	G	332	36	357	21	4.721	0.0298	rs17031432	2	66205557	p14
SNP_A-2296568	G	G	342	60	366	42	3.946	0.047	rs17031435	2	66209163	p14
SNP_A-2028245	G	G	281	47	308	32	3.871	4.91E-02	rs2932252	2	66335642	p14
SNP_A-2182784	G	G	405	5	403	15	4.928	0.0264	rs6717698	2	66529045	p14
SNP_A-1646416	T	T	394	6	396	16	4.374	3.65E-02	rs952203	2	66618307	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006432	G	G	393	5	418	0	5.284	2.15E-02	rs6546234	2	66638553	p14
SNP_A-2192209	A	A	258	156	291	129	4.499	0.0339	rs2861182	2	66985495	p14
SNP_A-2128969	C	C	310	90	283	133	9.211	2.40E-03	rs4671756	2	67021379	p14
SNP_A-1853014	T	T	268	126	234	152	4.653	0.031	rs12713584	2	67025838	p14
SNP_A-1699279	A	A	347	53	376	34	5.19	2.27E-02	rs10490198	2	67096232	p14
SNP_A-2227987	G	G	357	3	346	12	5.567	0.0183	rs12996858	2	67321763	p14
SNP_A-1963629	C	C	335	43	285	61	5.745	1.65E-02	rs10496144	2	67396679	p14
SNP_A-1963631	A	A	305	35	317	17	6.409	0.0114	rs10496146	2	67440669	p14
SNP_A-1726202	C	C	319	81	354	54	7.142	7.50E-03	rs752165	2	67457138	p14
SNP_A-1842349	A	A	357	35	367	17	6.287	1.22E-02	rs17544516	2	67479743	p14
SNP_A-1815134	T	G	229	173	201	197	4.48	3.43E-02	rs11126123	2	67517977	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140454	C	C	234	182	273	141	8.2	4.20E-03	rs694637	2	67596363	p14
SNP_A-2080620	T	T	201	151	234	114	7.647	5.70E-03	rs686880	2	67596743	p14
SNP_A-1694297	G	A	214	174	215	193	4.905	2.68E-02	rs1385931	2	67648001	p14
SNP_A-1668196	C	C	254	118	214	180	15.699	7.43E-05	rs600524	2	67648314	p14
SNP_A-1707928	C	C	274	126	234	178	11.87	6.00E-04	rs650638	2	67648576	p14
SNP_A-2161578	A	A	327	73	348	50	4.949	2.61E-02	rs7606107	2	67662254	p14
SNP_A-1853710	G	G	273	117	295	91	4.082	4.34E-02	rs1367473	2	67790664	p14
SNP_A-1881110	G	G	244	88	289	67	5.814	1.59E-02	rs1594415	2	67797394	p14
SNP_A-1847196	T	T	319	97	346	74	4.171	4.11E-02	rs4671822	2	67814820	p14
SNP_A-1915323	C	C	261	113	264	80	4.414	0.0356	rs2861713	2	67817423	p14
SNP_A-2287958	C	C	219	157	234	118	5.242	2.20E-02	rs130144491	2	67910693	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2037505	T	T	223	97	266	74	6.274	1.22E-02	rs11687935	2	68080971	p14
SNP_A-1835171	G	G	288	94	260	138	9.451	2.10E-03	rs11686851	2	68112447	p14
SNP_A-1801030	C	C	392	14	411	5	4.592	3.21E-02	rs10176792	2	68433393	p14
SNP_A-2061548	C	C	245	67	280	44	6.875	8.70E-03	rs1155426	2	68533475	p13.3
SNP_A-2301566	T	T	223	159	179	173	4.187	0.0407	rs6742200	2	68534953	p13.3
SNP_A-1947035	T	T	233	181	270	150	5.582	1.81E-02	rs13000568	2	68947074	p13.3
SNP_A-2125986	G	G	342	38	321	63	6.833	9.00E-03	rs11897459	2	68956280	p13.3
SNP_A-1815870	A	A	398	8	371	19	5.11	2.38E-02	rs13401986	2	69003423	p13.3
SNP_A-1672250	G	G	297	71	316	50	4.228	3.98E-02	rs10496167	2	69006129	p13.3
SNP_A-1963689	T	T	206	130	247	107	5.477	1.93E-02	rs2312076	2	69006555	p13.3
SNP_A-2091177	C	C	246	154	270	114	6.763	9.30E-03	rs4567971	2	69022581	p13.3
SNP_A-1865869	A	A	309	69	293	95	4.417	0.0356	rs13419507	2	69267522	p13.3
SNP_A-2140516	T	T	357	51	333	71	4.094	4.30E-02	rs4488695	2	69282627	p13.3
SNP_A-2218551	A	A	375	1	347	7	4.927	0.0264	rs7572381	2	69966693	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2229044	G	G	279	103	245	125	4.138	0.0419	rs13420455	2	70503458	p13.3
SNP_A-2218114	G	A	207	201	234	180	4.344	3.71E-02	rs1523305	2	70610511	p13.3
SNP_A-1780913	A	A	228	174	256	138	5.694	1.70E-02	rs2108482	2	70737116	p13.3
SNP_A-1887842	A	A	325	1	323	7	4.482	3.43E-02	rs740387	2	70807554	p13.3
SNP_A-2065461	A	A	313	89	295	121	5.171	0.023	rs17656087	2	70952007	p13.3
SNP_A-1963746	A	A	213	173	251	149	4.653	0.031	rs741326	2	70970490	p13.3
SNP_A-2184747	C	C	297	95	249	113	4.591	3.21E-02	rs6725822	2	71883798	p13.2
SNP_A-2312249	A	A	321	53	315	85	6.611	0.0101	rs11695965	2	71936990	p13.2
SNP_A-1862427	G	G	190	148	227	117	6.857	8.80E-03	—	2	71974552	p13.2
SNP_A-1880525	C	C	214	188	255	157	6.248	0.0124	rs6737513	2	72008032	p13.2
SNP_A-2124404	T	T	289	121	326	92	6.098	0.0135	rs1159764	2	72376021	p13.2
SNP_A-2283943	A	A	318	54	337	35	4.607	3.18E-02	rs17673916	2	72399019	p13.2
SNP_A-1803687	C	C	335	53	362	30	7.399	6.50E-03	rs6719255	2	72412030	p13.2
SNP_A-2164998	C	C	313	83	356	58	6.8	9.10E-03	rs11126366	2	72465947	p13.2
SNP_A-1691100	T	T	291	71	338	54	4.638	3.13E-02	rs9309464	2	72508501	p13.2
SNP_A-1738761	T	T	331	43	374	28	4.788	0.0287	rs9309465	2	72510016	p13.2
SNP_A-2208042	T	T	286	46	318	28	5.787	0.0161	rs7604296	2	72553533	p13.2
SNP_A-1871359	A	A	351	41	375	17	10.724	1.10E-03	rs6733532	2	72568803	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1736813	T	T	328	66	358	46	4.759	2.91E-02	rs10496185	2	72723154	p13.2
SNP_A-2060671	T	T	333	57	367	41	3.86	4.95E-02	rs11126378	2	72813039	p13.2
SNP_A-2172836	G	G	339	59	349	31	8.445	3.70E-03	rs1562361	2	72817093	p13.2
SNP_A-2285926	C	C	347	65	357	37	7.43	6.40E-03	rs17008371	2	72875452	p13.2
SNP_A-1963773	G	G	303	19	303	37	5.3	2.13E-02	rs10496188	2	73147013	p13.2
SNP_A-2125595	G	G	325	41	328	22	5.389	2.03E-02	rs869927	2	73454340	p13.2
SNP_A-2287233	T	T	330	32	306	54	6.528	0.0106	rs1246096	2	73616743	p13.1
SNP_A-1751809	T	T	343	53	371	35	4.656	0.0309	rs10519327	2	74084559	p13.1
SNP_A-1946554	C	C	331	13	338	4	4.832	2.79E-02	rs3771729	2	74414865	p13.1
SNP_A-2021678	C	C	411	1	399	11	8.506	3.50E-03	rs7569357	2	74690299	p13.1
SNP_A-1818339	C	C	371	1	340	6	3.987	4.59E-02	rs10170219	2	74715172	p13.1
SNP_A-2044244	G	G	344	0	344	6	5.949	0.0147	rs363681	2	74724221	p13.1
SNP_A-1929956	C	C	412	0	410	4	4	4.55E-02	rs363696	2	74757796	p13.1
SNP_A-2289699	T	T	394	0	386	6	6.077	0.0137	rs3025979	2	74759470	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1855262	A	A	358	40	330	58	4.319	3.77E-02	rs363624	2	74842497	p13.1
SNP_A-1963803	T	T	226	164	197	195	4.66	0.0309	rs594220	2	74953945	p13.1
SNP_A-2045246	T	C	226	178	211	199	4.471	3.45E-02	rs619850	2	74970668	p13.1
SNP_A-1847402	G	G	286	92	316	62	7.339	6.70E-03	rs17564182	2	75213961	p12
SNP_A-2300331	G	G	336	46	313	65	4.046	4.43E-02	rs7604227	2	75583369	p12
SNP_A-1828115	A	A	343	45	321	67	5.05	0.0246	rs6547001	2	75583650	p12
SNP_A-1963831	C	C	343	73	318	100	5.155	2.32E-02	rs10515917	2	75681465	p12
SNP_A-2238829	C	C	254	114	215	157	10.045	0.0015	rs11675945	2	75741534	p12
SNP_A-2283039	C	C	280	136	239	179	9.104	2.60E-03	rs11677196	2	75741876	p12
SNP_A-2275434	A	A	300	116	272	146	4.801	2.84E-02	rs3771875	2	75789467	p12
SNP_A-2059146	C	C	205	177	233	147	4.563	0.0327	rs1859707	2	75890930	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1899549	A	A	301	109	278	136	3.87	4.92E-02	rs6760389	2	75942768	p12
SNP_A-1960911	C	C	218	160	233	121	5.13	0.0235	rs6755718	2	76012219	p12
SNP_A-1893700	G	G	376	22	391	7	8.052	4.50E-03	rs11885264	2	76336251	p12
SNP_A-1848932	C	C	278	90	281	61	4.64	3.12E-02	rs10196661	2	76568381	p12
SNP_A-1797554	T	T	370	4	376	0	4.043	4.44E-02	rs17013452	2	77098839	p12
SNP_A-1963872	A	A	248	164	265	131	3.94	4.72E-02	rs1837426	2	77306805	p12
SNP_A-2162914	T	T	350	30	371	17	4.125	4.23E-02	rs3943682	2	77391209	p12
SNP_A-1963878	T	T	349	39	380	24	4.568	3.26E-02	rs17013902	2	77406946	p12
SNP_A-1963879	A	A	386	16	403	5	6.084	1.36E-02	rs13416390	2	77432106	p12
SNP_A-1848160	C	C	260	118	258	80	5.082	2.42E-02	rs13018089	2	77473529	p12
SNP_A-1860591	A	A	373	43	355	65	4.908	2.67E-02	rs4278958	2	77766336	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783420	A	A	359	35	338	58	6.316	0.012	rs12471047	2	77784824	p12
SNP_A-1933093	T	T	292	68	258	86	3.844	0.0499	rs7598757	2	77839969	p12
SNP_A-1679972	C	C	352	30	356	52	5.075	2.43E-02	rs2861264	2	78341614	p12
SNP_A-2221592	T	T	358	58	384	36	6.041	0.014	rs6547193	2	78362599	p12
SNP_A-1687812	A	A	286	114	318	92	3.922	4.77E-02	rs1526386	2	78566746	p12
SNP_A-2063403	T	T	239	85	272	64	4.874	2.73E-02	rs1455385	2	78593183	p12
SNP_A-2069404	A	A	277	83	300	60	4.616	3.17E-02	rs2203582	2	78620367	p12
SNP_A-2105279	C	C	221	137	190	160	4.029	4.47E-02	rs1239103	2	78784087	p12
SNP_A-2025552	A	A	243	111	274	80	6.89	8.70E-03	rs13016535	2	78888702	p12
SNP_A-2147504	C	C	327	89	302	114	4.072	0.0436	rs1156016	2	78960301	p12
SNP_A-1784579	C	C	278	88	333	55	11.935	6.00E-04	rs7608086	2	79034564	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1931865	C	C	305	109	349	71	10.94	9.00E-04	rs2139974	2	79036469	p12
SNP_A-1871174	G	G	362	6	368	16	4.256	3.91E-02	rs17015885	2	79062737	p12
SNP_A-1758999	G	G	282	118	317	91	5.454	0.0195	rs1521970	2	79067995	p12
SNP_A-1817220	G	G	216	150	180	172	4.505	3.38E-02	rs10164874	2	79074456	p12
SNP_A-1963907	T	T	273	57	240	74	3.934	4.73E-02	rs1261236	2	79097663	p12
SNP_A-1963910	C	C	339	25	309	41	4.995	2.54E-02	rs789304	2	79138802	p12
SNP_A-1963911	G	G	308	46	294	72	5.856	0.0155	rs283819	2	79138898	p12
SNP_A-1963920	A	G	203	173	203	173	4.787	0.0287	rs2117728	2	79145666	p12
SNP_A-2051276	G	G	335	39	306	66	8.25	4.10E-03	rs369221	2	79164605	p12
SNP_A-2066147	C	C	351	47	319	65	4.172	4.11E-02	rs1595017	2	79171150	p12
SNP_A-2151821	G	G	205	187	239	159	4.824	0.0281	rs10193163	2	79264192	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2248322	A	A	356	56	382	36	5.221	0.0223	rs17016675	2	79409484	p12
SNP_A-2050653	C	C	349	57	377	35	6.297	0.0121	rs4566392	2	79418298	p12
SNP_A-1832054	T	T	207	193	239	167	4.129	4.21E-02	rs12472740	2	79823489	p12
SNP_A-1871758	A	A	274	82	300	60	4.564	0.0327	rs994984	2	79922030	p12
SNP_A-1781858	A	C	190	138	171	169	4.539	3.31E-02	rs1434117	2	79986434	p12
SNP_A-1893030	T	T	338	76	314	106	5.786	1.62E-02	rs17261195	2	80046570	p12
SNP_A-2050577	A	A	204	142	184	176	4.39	0.0361	rs2974168	2	80056204	p12
SNP_A-1933645	G	G	197	139	170	164	4.043	4.44E-02	rs2974169	2	80056351	p12
SNP_A-1804964	A	G	197	149	192	176	5.932	0.0149	rs6729700	2	80172828	p12
SNP_A-1927024	A	A	373	31	389	13	7.695	5.50E-03	rs17339821	2	80174325	p12
SNP_A-1929978	A	A	316	78	301	113	6.287	1.22E-02	rs1812391	2	80190302	p12
SNP_A-2052721	A	G	204	168	205	181	4.787	0.0287	rs7426225	2	80191720	p12
SNP_A-2258713	T	T	410	0	412	4	3.961	4.66E-02	rs7585787	2	80368602	p12
SNP_A-1739831	G	G	353	47	335	75	6.775	9.20E-03	rs1006154	2	80526004	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1651136	C	C	350	48	334	74	5.792	0.0161	rs1006155	2	80526149	p12
SNP_A-1920304	G	G	356	24	336	42	5.482	1.92E-02	rs7589069	2	80552075	p12
SNP_A-2291019	T	T	408	6	392	16	4.822	0.0281	---	2	80573639	p12
SNP_A-1963990	T	T	274	88	261	117	4.074	4.35E-02	rs1434077	2	80608962	p12
SNP_A-1730799	G	G	360	36	348	62	6.86	8.80E-03	rs2043450	2	80640964	p12
SNP_A-2155301	A	A	375	39	398	22	5.379	2.04E-02	rs7591588	2	80771025	p12
SNP_A-1799387	C	C	316	52	314	30	5.106	2.38E-02	rs10185684	2	81957973	p12
SNP_A-1964045	G	G	268	94	289	63	6.774	9.20E-03	rs934310	2	82307869	p12
SNP_A-1693391	A	A	376	18	398	8	4.292	3.83E-02	rs10496270	2	82812360	p12
SNP_A-2022346	G	G	366	38	376	20	5.642	1.75E-02	rs7559513	2	82853483	p12
SNP_A-1744705	C	C	388	12	406	4	4.285	3.84E-02	rs1582382	2	83099300	p12
SNP_A-2031087	A	A	340	62	297	81	4.693	3.03E-02	rs17023660	2	83648861	p11.2
SNP_A-1806786	G	G	396	0	405	5	4.859	0.0275	rs10190107	2	84112716	p11.2
SNP_A-2111826	T	T	300	52	313	33	4.472	3.45E-02	rs7579223	2	84273920	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2126606	G	G	356	24	387	11	5.709	1.69E-02	rs17024868	2	84448736	p11.2
SNP_A-2099460	G	G	367	11	383	3	4.83	2.80E-02	rs13000280	2	84608654	p11.2
SNP_A-2078528	C	C	376	12	388	4	4.168	4.12E-02	rs7559623	2	84697832	p11.2
SNP_A-1814289	T	T	364	30	385	15	5.544	1.85E-02	rs1811537	2	84726894	p11.2
SNP_A-2100025	T	T	374	38	389	21	5.188	2.27E-02	rs7570369	2	84743425	p11.2
SNP_A-1913756	C	C	373	39	395	23	4.716	2.99E-02	rs11126970	2	84763421	p11.2
SNP_A-2251796	C	C	291	27	317	13	5.792	0.0161	rs11676670	2	84763669	p11.2
SNP_A-2273998	T	T	366	32	379	15	6.356	0.0117	rs6726617	2	84771546	p11.2
SNP_A-2209890	G	G	370	36	389	21	4.403	3.59E-02	rs4313996	2	84774501	p11.2
SNP_A-2176394	C	C	370	34	392	20	4.187	0.0407	rs7572042	2	84778910	p11.2
SNP_A-1883133	T	T	255	81	275	55	5.672	0.0172	rs6547578	2	84823175	p11.2
SNP_A-1964108	T	T	373	41	391	25	4.298	3.82E-02	rs1192266	2	84847858	p11.2
SNP_A-1806680	G	G	292	104	321	81	4.187	0.0407	rs1192343	2	84857337	p11.2
SNP_A-2285779	C	C	384	22	400	8	6.855	8.80E-03	rs1192340	2	84859679	p11.2
SNP_A-2198832	G	G	375	41	393	25	4.296	3.82E-02	rs1192324	2	84873393	p11.2
SNP_A-2265233	T	T	330	10	347	3	4.052	0.0441	rs11692245	2	84945704	p11.2
SNP_A-1811759	A	A	390	20	407	7	6.603	1.02E-02	rs11686936	2	84947598	p11.2
SNP_A-1743713	T	T	376	24	396	12	4.439	3.51E-02	rs10520406	2	85354592	p11.2
SNP_A-1928170	C	C	372	20	362	36	4.662	3.08E-02	rs17713036	2	85393057	p11.2
SNP_A-1964122	T	T	371	17	375	1	14.059	2.00E-04	rs6719271	2	85426375	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215679	C	C	321	75	303	107	5.904	1.51E-02	rs960066	2	85612582	p11.2
SNP_A-2271325	C	C	357	59	376	38	5.034	2.49E-02	rs13426038	2	85715056	p11.2
SNP_A-1790562	G	G	286	54	323	33	6.953	8.40E-03	rs7425090	2	85873801	p11.2
SNP_A-1928725	G	G	326	80	354	58	4.616	3.17E-02	rs4832006	2	85876014	p11.2
SNP_A-1840923	G	G	218	144	197	175	3.94	4.72E-02	rs9309628	2	86083986	p11.2
SNP_A-2294362	G	G	392	20	399	7	6.278	1.22E-02	rs2303339	2	86257838	p11.2
SNP_A-1964145	G	G	332	14	353	5	4.704	3.01E-02	rs3731817	2	86354206	p11.2
SNP_A-1954718	A	A	328	4	356	0	4.314	0.0378	rs3731815	2	86356176	p11.2
SNP_A-1812246	T	T	286	34	267	51	4.047	4.43E-02	rs4832258	2	86376183	p11.2
SNP_A-2155774	C	C	269	129	283	99	3.976	4.62E-02	rs7557796	2	86677811	p11.2
SNP_A-1694131	C	C	314	26	351	13	5.58	1.82E-02	rs894198	2	88304481	p11.2
SNP_A-1736727	C	C	362	38	388	24	3.886	0.0487	rs1530272	2	88317362	p11.2
SNP_A-1821324	G	G	347	3	353	11	4.35	3.70E-02	rs2176053	2	88816255	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259900	C	C	301	37	349	17	9.854	1.70E-03	rs7572174	2	88949523	p11.2
SNP_A-2103502	A	A	349	23	374	12	4.064	4.38E-02	rs331821	2	89973576	p11.2
SNP_A-1919470	C	C	235	85	255	61	4.737	2.95E-02	rs772173	2	96422270	q11.2
SNP_A-1828636	G	G	250	152	271	119	4.684	0.0304	rs2314109	2	96665406	q11.2
SNP_A-2174210	T	T	287	33	263	51	4.848	2.77E-02	rs17636359	2	97082493	q11.2
SNP_A-1907200	G	G	216	146	237	115	4.516	3.36E-02	rs6736735	2	97794951	q11.2
SNP_A-1817937	A	A	263	141	289	107	5.807	0.016	rs6543088	2	97830799	q11.2
SNP_A-2136365	G	G	266	130	303	103	5.411	0.02	rs6760008	2	97836183	q11.2
SNP_A-2189689	G	G	283	71	303	51	3.961	4.66E-02	rs11690482	2	98018682	q11.2
SNP_A-2194552	C	C	387	19	392	8	4.469	3.45E-02	rs6705251	2	98172963	q11.2
SNP_A-1698895	A	A	257	143	233	177	4.665	3.08E-02	rs953320	2	98228170	q11.2
SNP_A-2202778	T	C	190	178	212	168	4.125	4.23E-02	rs17429208	2	98420107	q11.2
SNP_A-2168979	G	G	252	102	295	81	5.132	0.0235	rs937725	2	98452932	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2270024	T	T	339	59	354	36	5.812	1.59E-02	rs7579999	2	99316188	q11.2
SNP_A-2125037	G	G	219	107	191	133	4.723	0.0298	rs901596	2	99346975	q11.2
SNP_A-1901677	C	C	330	28	366	16	4.361	3.68E-02	rs3828162	2	99435082	q11.2
SNP_A-1897682	A	A	372	38	391	23	4.142	4.18E-02	rs7602535	2	99498182	q11.2
SNP_A-1817367	G	G	359	17	379	7	4.578	3.24E-02	rs3811556	2	99719373	q11.2
SNP_A-2028186	C	C	316	32	334	18	4.396	3.60E-02	rs7561009	2	99752342	q11.2
SNP_A-1946373	G	G	280	48	307	31	4.751	0.0293	rs1404176	2	99817169	q11.2
SNP_A-1951575	C	C	320	36	328	16	7.588	5.90E-03	rs6751316	2	99823579	q11.2
SNP_A-2131174	A	A	290	102	322	78	4.793	0.0286	rs940458	2	99836292	q11.2
SNP_A-1959912	G	G	310	106	339	81	4.619	3.16E-02	rs6542893	2	99844189	q11.2
SNP_A-1900373	A	A	245	121	262	90	4.853	0.0276	rs10176509	2	99910151	q11.2
SNP_A-2062284	T	T	361	55	337	75	3.883	4.88E-02	rs7577040	2	100013463	q11.2
SNP_A-2054214	C	C	360	40	336	58	4.089	4.32E-02	rs10198187	2	100040070	q11.2
SNP_A-2144205	C	C	366	48	343	77	7.431	6.40E-03	rs17352801	2	100123203	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1703649	T	T	345	55	334	78	3.979	4.61E-02	rs4129805	2	100207906	q11.2
SNP_A-1741511	T	T	347	43	318	64	5.304	2.13E-02	rs2001722	2	100213815	q11.2
SNP_A-1909823	C	C	260	144	230	172	4.313	0.0378	rs4851266	2	100276997	q11.2
SNP_A-2153003	G	A	197	195	231	175	4.099	4.29E-02	rs9653442	2	100283885	q11.2
SNP_A-2058346	C	C	272	142	239	175	5.566	0.0183	rs13026283	2	100301156	q11.2
SNP_A-2072458	C	C	271	143	306	112	5.873	0.0154	rs6542922	2	100337343	q11.2
SNP_A-2143294	G	G	219	149	191	181	4.994	2.54E-02	rs4622752	2	100350536	q11.2
SNP_A-2299202	C	C	406	0	410	4	3.942	4.71E-02	rs6727379	2	100353789	q11.2
SNP_A-2092987	G	G	219	161	242	132	3.97	4.63E-02	rs2309821	2	100356822	q11.2
SNP_A-2035740	A	A	229	153	268	128	5.034	2.49E-02	rs2309824	2	100360179	q11.2
SNP_A-2049191	C	C	220	126	261	103	5.352	0.0207	rs7582180	2	100370981	q11.2
SNP_A-2081175	A	G	228	156	209	193	10.199	0.0014	rs4850927	2	100427585	q11.2
SNP_A-2262711	A	G	234	182	233	187	11.496	7.00E-04	rs11685401	2	100435203	q11.2
SNP_A-1783665	T	C	203	169	217	169	8.821	3.00E-03	rs6542938	2	100439041	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1810168	T	T	385	5	390	0	5.032	2.49E-02	rs17024136	2	100453901	q11.2
SNP_A-2053672	G	A	230	174	216	186	9.172	2.50E-03	rs10193204	2	100463058	q11.2
SNP_A-1718361	A	A	252	146	288	124	3.952	4.68E-02	rs7597861	2	100474587	q11.2
SNP_A-1644582	G	G	266	134	244	168	4.6	3.20E-02	rs10496346	2	100474667	q11.2
SNP_A-1787665	T	T	405	5	416	0	5.104	2.39E-02	rs7561516	2	100517728	q11.2
SNP_A-1964241	G	G	334	52	323	75	4.167	4.12E-02	rs750563	2	100521882	q11.2
SNP_A-1964243	T	T	350	46	332	72	6.124	1.33E-02	rs13383638	2	100523161	q11.2
SNP_A-1964244	C	C	334	38	325	61	5.21	2.25E-02	rs13398213	2	100523617	q11.2
SNP_A-2272051	G	G	333	41	307	59	4.21	0.0402	rs10204004	2	100523895	q11.2
SNP_A-2118587	A	A	347	5	348	0	4.979	2.57E-02	rs6718243	2	100586068	q11.2
SNP_A-1868640	T	C	181	165	198	160	4.09	4.31E-02	rs12621996	2	100801905	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835259	C	C	200	150	250	130	5.761	1.64E-02	rs11686712	2	100876488	q11.2
SNP_A-1913993	G	G	368	28	399	15	4.786	0.0287	rs7565981	2	100882849	q11.2
SNP_A-1814554	T	T	316	86	293	111	4.036	4.45E-02	rs930309	2	100943052	q11.2
SNP_A-2153358	A	A	387	27	407	11	7.222	7.20E-03	rs1369482	2	100961934	q11.2
SNP_A-1822473	G	G	212	202	242	172	4.389	3.62E-02	rs882272	2	101034717	q11.2
SNP_A-2104622	C	C	309	87	288	118	5.303	2.13E-02	rs3739014	2	101097406	q11.2
SNP_A-1958476	T	T	370	46	350	70	5.502	0.019	rs6727200	2	101156662	q11.2
SNP_A-1859304	A	A	319	43	289	63	5.115	2.37E-02	rs7608232	2	101157581	q11.2
SNP_A-1818317	A	A	269	143	244	174	4.207	4.03E-02	rs17190412	2	101381291	q11.2
SNP_A-1756601	A	A	192	174	221	143	5.062	2.45E-02	rs10496353	2	101538859	q11.2
SNP_A-1823557	A	G	216	170	189	175	4.663	3.08E-02	rs10171484	2	101685366	q11.2
SNP_A-2050162	G	G	380	10	399	3	4.052	0.0441	rs7571274	2	101715283	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2068150	C	C	217	115	172	128	4.292	3.83E-02	rs12472284	2	102032164	q11.2
SNP_A-2108422	A	A	347	27	346	48	5.364	0.0206	rs2072477	2	102095277	q11.2
SNP_A-1958688	A	A	367	49	345	73	5.396	2.02E-02	rs6727859	2	102196682	q11.2
SNP_A-1964281	T	T	367	9	357	1	6.1	0.0135	rs1922300	2	102278112	q11.2
SNP_A-1964282	A	A	266	144	289	115	4.156	4.15E-02	rs2178675	2	102282312	q11.2
SNP_A-2207616	T	T	230	116	252	90	4.263	0.039	rs1922293	2	102298273	q11.2
SNP_A-2081874	T	G	225	181	219	185	7.508	6.10E-03	rs12475055	2	102337409	q11.2
SNP_A-1689540	G	A	168	160	202	148	5.431	1.98E-02	rs3213732	2	102619679	q11.2
SNP_A-1743539	A	A	304	96	285	125	4.296	3.82E-02	rs2075190	2	102739959	q11.2
SNP_A-2167218	A	A	289	87	298	60	4.659	0.0309	rs2540315	2	102812907	q12.1
SNP_A-2177207	T	G	215	161	192	182	5.46	0.0195	rs266069	2	103534938	q12.1
SNP_A-2136068	A	A	372	4	374	0	4	4.55E-02	rs17037249	2	103570733	q12.1
SNP_A-2304321	T	C	220	170	202	190	4.943	2.62E-02	rs7573399	2	103581752	q12.1
SNP_A-1952890	A	T	203	187	212	172	4.083	4.33E-02	rs4851656	2	103620981	q12.1
SNP_A-1874322	A	A	209	177	230	146	3.849	4.98E-02	rs6725608	2	103635603	q12.1
SNP_A-2080999	G	G	248	168	214	200	5.28	2.16E-02	rs11675245	2	103779028	q12.1
SNP_A-2023870	A	A	345	39	353	23	4.137	4.20E-02	rs17029176	2	103893002	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1750175	C	C	228	154	210	194	4.725	2.97E-02	rs264962	2	103929945	q12.1
SNP_A-1654355	C	T	208	184	225	181	5.74	0.0166	rs9308868	2	103982820	q12.1
SNP_A-2184030	C	C	398	10	416	2	5.611	0.0178	rs10165112	2	104753367	q12.1
SNP_A-1800706	A	A	312	98	348	68	7.342	6.70E-03	rs1517861	2	104759045	q12.1
SNP_A-1905999	T	T	402	14	405	5	4.231	3.97E-02	rs1517862	2	104759106	q12.1
SNP_A-1865740	C	C	403	11	417	3	4.768	2.90E-02	rs6727249	2	104762914	q12.1
SNP_A-1869712	C	C	401	15	412	4	6.517	1.07E-02	rs6543265	2	104764823	q12.1
SNP_A-1878219	C	C	236	114	257	89	3.95	4.69E-02	rs17627543	2	104773335	q12.1
SNP_A-2068910	G	G	325	7	365	1	5.175	0.0229	rs2138918	2	104806198	q12.1
SNP_A-2242482	G	G	401	15	417	3	8.294	4.00E-03	rs1474080	2	104819132	q12.1
SNP_A-1783651	A	A	395	11	401	3	4.612	3.18E-02	rs1474081	2	104819243	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1945626	G	G	401	15	416	2	10.212	0.0014	rs3404	2	104821691	q12.1
SNP_A-2197575	A	A	273	79	260	108	4.461	3.47E-02	rs3811547	2	104821785	q12.1
SNP_A-1696136	C	C	308	90	341	67	4.924	2.65E-02	rs2222186	2	104917510	q12.1
SNP_A-2086322	C	C	238	92	215	117	4.152	4.16E-02	rs754481	2	104938716	q12.1
SNP_A-1712773	T	T	384	16	408	2	11.494	7.00E-04	rs2037261	2	104978294	q12.1
SNP_A-1844072	T	T	295	105	269	151	8.982	2.70E-03	rs4266037	2	105189267	q12.1
SNP_A-1893886	T	T	294	100	245	127	7.04	8.00E-03	rs4271787	2	105189393	q12.1
SNP_A-2265206	T	T	226	146	255	121	4.068	4.37E-02	rs4641957	2	105204555	q12.1
SNP_A-2310843	C	C	251	161	286	132	5.108	2.38E-02	rs4377353	2	105204788	q12.1
SNP_A-1927777	A	A	245	93	267	71	3.897	4.84E-02	rs873738	2	105383599	q12.1
SNP_A-2134404	C	C	203	145	243	117	6.378	1.16E-02	rs12712206	2	105470674	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2048401	T	T	214	174	248	144	5.312	0.0212	rs6543294	2	105494975	q12.1
SNP_A-1811751	G	G	285	109	264	142	4.963	2.59E-02	rs6543296	2	105529519	q12.2
SNP_A-2083447	A	A	278	132	254	166	4.842	2.78E-02	rs6543297	2	105529677	q12.2
SNP_A-2266508	A	A	258	84	215	101	4.451	0.0349	rs4851783	2	105584618	q12.2
SNP_A-1886241	G	G	255	101	284	80	3.908	4.80E-02	rs4851813	2	105692133	q12.2
SNP_A-1919321	A	A	339	1	353	7	4.215	4.01E-02	rs11899967	2	105804799	q12.2
SNP_A-1789985	A	A	278	80	299	59	3.937	4.72E-02	rs3769489	2	105965942	q12.2
SNP_A-2181121	A	A	285	121	315	97	4.098	4.29E-02	rs12612803	2	105970583	q12.2
SNP_A-2028823	G	G	226	112	264	88	5.545	1.85E-02	rs6706041	2	106112524	q12.2
SNP_A-2053800	T	T	325	59	352	38	5.577	1.82E-02	rs11679299	2	106118085	q12.2
SNP_A-2099133	C	C	317	53	354	36	4.764	2.91E-02	rs11673993	2	106119092	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2070493	T	T	261	81	238	106	4.397	3.60E-02	rs11893325	2	106120881	q12.2
SNP_A-1912496	A	A	315	85	321	59	4.241	0.0395	rs13386274	2	106137555	q12.2
SNP_A-1848995	T	T	252	122	280	90	6.283	1.22E-02	rs737101	2	106191063	q12.2
SNP_A-1828209	T	T	270	144	300	114	5.067	2.44E-02	rs4676155	2	106346590	q12.2
SNP_A-2271748	G	G	368	44	349	63	3.877	4.89E-02	rs12620430	2	106370428	q12.2
SNP_A-1871093	G	G	294	52	329	37	3.936	4.73E-02	rs4574118	2	106406961	q12.2
SNP_A-2185408	G	G	330	64	289	83	4.543	3.30E-02	rs11124109	2	106536870	q12.2
SNP_A-2153867	G	G	296	86	271	113	4.76	2.91E-02	rs7584087	2	106586064	q12.2
SNP_A-2137321	A	A	347	67	382	36	10.992	9.00E-04	rs6744483	2	106604173	q12.2
SNP_A-2071925	A	A	234	154	200	178	4.269	3.88E-02	rs1606266	2	106783017	q12.2
SNP_A-2066189	G	G	363	33	342	52	4.868	2.74E-02	rs6543436	2	106787545	q12.2
SNP_A-2277051	A	A	366	48	344	72	5.477	1.93E-02	rs13409196	2	106844756	q12.2
SNP_A-1964369	G	G	209	189	219	147	4.151	4.16E-02	rs1006413	2	106859154	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1693387	T	T	357	39	345	63	5.674	0.0172	rs10514794	2	106983971	q12.2
SNP_A-1964385	C	T	206	196	214	154	6.813	9.00E-03	rs979186	2	107037108	q12.3
SNP_A-2187802	A	G	199	187	225	165	6.66	9.90E-03	rs1524297	2	107046863	q12.3
SNP_A-2271126	C	C	261	155	225	189	6.022	0.0141	rs6760504	2	107135887	q12.3
SNP_A-2082036	T	T	238	126	204	154	5.366	2.05E-02	rs2907913	2	107247956	q12.3
SNP_A-1839928	C	C	379	5	406	0	5.32	2.11E-02	rs17034130	2	107400484	q12.3
SNP_A-2150186	A	A	283	105	237	137	8.046	4.60E-03	rs4299335	2	107621202	q12.3
SNP_A-2006597	C	C	276	140	307	111	4.994	2.54E-02	rs328026	2	107839049	q12.3
SNP_A-1921876	A	A	304	24	300	42	4.645	3.11E-02	rs3856400	2	107998827	q12.3
SNP_A-1931148	T	T	325	13	332	4	4.833	2.79E-02	rs2084991	2	108349924	q12.3
SNP_A-1876886	G	G	416	0	416	4	3.981	4.60E-02	rs12712031	2	109433499	q13
SNP_A-1909563	G	A	198	194	230	174	4.425	3.54E-02	rs6745464	2	109487816	q13
SNP_A-2265236	C	C	230	156	251	107	9.005	2.70E-03	rs9330310	2	109622926	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1811631	C	C	358	54	380	36	4.237	3.95E-02	rs13384147	2	109805604	q13
SNP_A-1827100	A	A	263	87	280	62	4.635	3.13E-02	rs17040773	2	112216266	q13
SNP_A-1810195	C	C	200	182	221	141	5.718	1.68E-02	rs7601200	2	112805498	q13
SNP_A-1947213	A	A	295	105	317	77	5.053	0.0246	rs3849317	2	113090181	q13
SNP_A-1690405	T	T	290	110	267	143	5.131	0.0235	rs2254860	2	113090956	q13
SNP_A-1955078	G	G	208	206	238	176	4.374	3.65E-02	rs13023016	2	113095106	q13
SNP_A-2299275	T	T	376	0	362	4	4.132	4.21E-02	rs6708268	2	113350213	q13
SNP_A-2234539	A	A	235	149	212	184	4.679	3.05E-02	rs10188765	2	113431907	q13
SNP_A-2027256	A	A	328	40	318	20	5.557	0.0184	---	2	113703112	q13
SNP_A-2144846	C	C	223	125	198	178	9.687	0.0019	rs7604877	2	113877614	q13
SNP_A-1866033	C	C	307	81	317	57	4.078	4.34E-02	---	2	114235560	q14.1
SNP_A-1780666	A	A	299	61	281	83	3.898	4.84E-02	rs6711542	2	114263352	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2117797	T	T	364	52	336	84	8.63	0.0033	rs10195628	2	114289279	q14.1
SNP_A-2152711	C	C	344	34	308	54	6.19	1.28E-02	rs4295010	2	114296106	q14.1
SNP_A-1800861	C	C	373	23	384	10	5.276	2.16E-02	rs9941605	2	114326118	q14.1
SNP_A-2041690	C	C	263	67	224	86	4.862	2.74E-02	rs6705036	2	114456597	q14.1
SNP_A-1947390	T	T	299	97	306	70	3.931	4.74E-02	rs10189293	2	114629415	q14.1
SNP_A-2285918	C	C	325	89	352	64	5.157	2.32E-02	rs3097609	2	114668047	q14.1
SNP_A-2157772	C	C	303	99	340	70	7.027	8.00E-03	rs1119845	2	114673883	q14.1
SNP_A-1709403	C	C	263	83	262	126	6.467	1.10E-02	rs400960	2	114880542	q14.1
SNP_A-1964540	G	G	342	16	336	30	4.226	3.98E-02	rs17048536	2	115102685	q14.1
SNP_A-1893491	C	C	341	43	298	60	4.794	0.0286	rs13425741	2	115120308	q14.1
SNP_A-1964541	A	A	342	70	317	99	5.906	1.51E-02	rs9308697	2	115123889	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2042540	C	C	237	163	267	137	4.019	4.50E-02	rs2176737	2	115276671	q14.1
SNP_A-1964549	A	A	281	119	325	87	7.99	4.70E-03	rs958457	2	115613964	q14.1
SNP_A-1650864	A	A	396	0	404	4	3.902	0.0482	rs10496472	2	115623115	q14.1
SNP_A-1758900	A	A	400	0	404	4	3.941	4.71E-02	rs10496473	2	115623666	q14.1
SNP_A-1804989	C	C	269	123	291	95	4.415	0.0356	rs2421104	2	115958495	q14.1
SNP_A-1698043	A	A	224	162	198	196	4.749	0.0293	rs10496484	2	116031248	q14.1
SNP_A-1822886	C	C	258	138	217	159	4.509	3.37E-02	rs996581	2	116204064	q14.1
SNP_A-2191620	T	T	359	39	359	19	6.385	0.0115	rs7557870	2	116483253	q14.1
SNP_A-2066627	C	C	274	130	301	105	3.922	4.76E-02	rs12613559	2	116522387	q14.1
SNP_A-2039164	C	C	377	11	393	3	4.823	0.0281	rs6728856	2	116531030	q14.1
SNP_A-1752211	G	G	254	144	229	179	4.963	2.59E-02	rs9308717	2	116590687	q14.1
SNP_A-2057815	A	A	284	82	325	63	4.612	3.18E-02	rs17045562	2	116619940	q14.1
SNP_A-1822062	C	C	216	168	259	117	12.936	3.00E-04	rs12157271	2	116666722	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2156354	A	A	195	181	212	136	6.024	0.0141	rs7593329	2	116737926	q14.1
SNP_A-1827723	A	A	259	107	292	84	4.612	3.17E-02	rs2202506	2	116779161	q14.1
SNP_A-1875810	A	A	210	178	254	140	8.668	3.20E-03	rs4257412	2	116840893	q14.1
SNP_A-1864216	C	C	227	185	265	145	7.779	0.0053	rs11674077	2	116863409	q14.1
SNP_A-2246838	C	C	213	171	245	133	6.939	8.40E-03	rs10864945	2	116871164	q14.1
SNP_A-1884447	A	A	215	177	242	146	4.55	3.29E-02	rs1388407	2	116900083	q14.1
SNP_A-1964572	T	T	220	116	252	90	5.398	2.02E-02	rs12618047	2	116936495	q14.1
SNP_A-2314115	C	C	231	145	252	114	4.49	3.41E-02	rs13029624	2	117033236	q14.1
SNP_A-2053714	C	C	222	164	235	125	4.732	2.96E-02	rs6705249	2	117238085	q14.1
SNP_A-2280089	G	G	340	0	340	4	3.977	4.61E-02	rs334841	2	117802770	q14.1
SNP_A-2127023	G	G	324	36	321	61	5.81	1.59E-02	rs6742148	2	117819235	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889785	G	G	402	8	396	18	3.872	4.91E-02	rs11884677	2	117912617	q14.1
SNP_A-2145135	T	T	396	10	383	21	4.115	4.25E-02	rs7421092	2	117928583	q14.1
SNP_A-1804416	G	G	284	98	253	131	6.54	1.05E-02	rs17047368	2	118233954	q14.1
SNP_A-1808375	A	A	309	47	288	26	4.163	4.13E-02	rs7605250	2	118895107	q14.2
SNP_A-1796205	G	G	280	120	310	90	5.811	1.59E-02	rs972143	2	119291507	q14.2
SNP_A-1844465	C	C	338	52	313	71	3.849	4.98E-02	rs6718150	2	119293695	q14.2
SNP_A-1914501	A	C	193	187	208	160	4.01	4.52E-02	rs12991703	2	119536476	q14.2
SNP_A-2115991	C	A	220	190	226	190	5.267	2.17E-02	rs893769	2	119556314	q14.2
SNP_A-2171051	G	G	229	141	250	108	5.098	0.024	rs13017276	2	119580446	q14.2
SNP_A-2177211	G	G	196	118	169	151	5.989	0.0144	rs1838766	2	119585605	q14.2
SNP_A-2117636	A	A	285	129	248	164	6.745	9.40E-03	rs10182413	2	119596866	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1964663	C	C	321	95	285	135	9.076	2.60E-03	rs745884	2	119625615	q14.2
SNP_A-1964664	G	G	250	142	211	177	7.119	0.0076	rs7583824	2	119648809	q14.2
SNP_A-2187049	C	C	270	124	301	101	3.954	4.68E-02	rs7595954	2	119691751	q14.2
SNP_A-2159026	A	A	393	11	415	1	8.759	3.10E-03	rs2920692	2	119982080	q14.2
SNP_A-2309180	G	G	404	10	418	0	10.219	0.0014	rs2579611	2	119987943	q14.2
SNP_A-1883494	C	C	338	10	367	1	8.004	4.70E-03	rs2579612	2	119988013	q14.2
SNP_A-2187283	A	A	317	55	330	34	5.13	0.0235	rs17049540	2	120063077	q14.2
SNP_A-1897885	G	G	317	69	346	48	4.956	2.60E-02	rs939778	2	120159673	q14.2
SNP_A-2288488	C	C	330	38	343	21	5.128	0.0235	rs734680	2	120197817	q14.2
SNP_A-1964670	A	A	354	18	375	5	7.869	5.00E-03	rs17668924	2	120480782	q14.2
SNP_A-2168443	G	G	384	20	397	9	4.384	3.63E-02	rs17049991	2	120578074	q14.2
SNP_A-2267825	C	C	393	3	392	12	5.322	2.11E-02	rs17050160	2	120939504	q14.2
SNP_A-2188784	G	G	340	24	313	43	6.416	1.13E-02	rs13412688	2	121127660	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2184292	G	G	375	23	395	11	4.676	3.06E-02	rs6720819	2	121165567	q14.2
SNP_A-2280951	G	G	360	22	320	46	10.486	1.20E-03	rs2166898	2	121328889	q14.2
SNP_A-2029564	G	G	386	14	370	26	3.919	4.78E-02	rs2166565	2	121408707	q14.2
SNP_A-1914697	A	A	216	160	266	128	8.326	3.90E-03	rs6724707	2	121626028	q14.2
SNP_A-1889306	A	A	206	144	245	113	7.022	8.10E-03	rs12616919	2	121627437	q14.2
SNP_A-1945243	T	T	350	0	354	4	3.933	4.74E-02	rs750413	2	121714084	q14.2
SNP_A-1845845	G	G	307	81	274	104	4.604	3.19E-02	rs4368337	2	122378337	q14.3
SNP_A-1866496	A	A	274	80	249	103	4.08	4.34E-02	rs4299342	2	122378559	q14.3
SNP_A-2136012	T	T	293	73	267	95	4.066	4.37E-02	rs17007002	2	122422664	q14.3
SNP_A-1964690	G	G	315	89	285	115	4.794	0.0286	rs7587881	2	122425377	q14.3
SNP_A-2006660	C	C	322	94	297	119	3.944	0.047	rs7590810	2	122425639	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1940267	C	C	320	92	297	117	3.843	5.00E-02	rs17007023	2	122426848	q14.3
SNP_A-1859889	G	G	314	92	294	124	5.225	0.0223	rs17007042	2	122429271	q14.3
SNP_A-1964691	C	C	307	79	266	98	4.332	3.74E-02	rs10496575	2	122435184	q14.3
SNP_A-2216327	G	G	320	92	295	125	5.958	0.0146	rs6718435	2	122450438	q14.3
SNP_A-2205297	T	T	268	80	262	112	4.471	3.45E-02	rs1219910	2	122466109	q14.3
SNP_A-2211060	A	A	353	21	353	37	4.081	4.34E-02	rs17007222	2	122584283	q14.3
SNP_A-1964694	C	C	337	19	337	7	5.334	2.09E-02	rs1368108	2	122729655	q14.3
SNP_A-1964717	G	G	389	23	397	11	4.297	3.82E-02	rs10496591	2	123072715	q14.3
SNP_A-1792535	G	G	337	73	361	45	7.45	0.0063	rs10177647	2	123147861	q14.3
SNP_A-2188199	T	T	365	29	371	15	4.422	3.55E-02	rs13014649	2	123148028	q14.3
SNP_A-2179424	A	A	344	66	374	46	4.705	3.01E-02	rs7598320	2	123148151	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798617	T	T	329	27	372	14	5.556	0.0184	rs13014799	2	123161748	q14.3
SNP_A-1964721	T	T	312	32	352	18	5.39	2.03E-02	rs893743	2	123166025	q14.3
SNP_A-2137495	A	A	288	24	310	12	4.653	0.031	rs12619304	2	123188349	q14.3
SNP_A-2199126	G	G	348	20	376	8	5.888	0.0152	rs11122930	2	123205908	q14.3
SNP_A-2065642	A	A	368	36	388	22	3.864	4.93E-02	rs7607585	2	123206523	q14.3
SNP_A-2263573	C	C	357	3	355	13	6.168	1.30E-02	rs13429900	2	123356234	q14.3
SNP_A-2142672	T	T	330	16	306	28	3.968	4.64E-02	rs1850585	2	123379520	q14.3
SNP_A-1845901	C	C	322	56	289	75	4.275	3.87E-02	rs2661018	2	123430634	q14.3
SNP_A-2181685	C	C	290	112	319	81	6.355	0.0117	rs11691993	2	123490200	q14.3
SNP_A-1864049	C	C	283	91	312	68	4.693	3.03E-02	rs17368305	2	123520012	q14.3
SNP_A-1832032	G	G	380	12	379	3	5.273	2.17E-02	rs7569433	2	123611622	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2068167	G	G	263	89	264	60	4.494	3.40E-02	rs12711622	2	123639850	q14.3
SNP_A-2045506	C	C	384	16	400	4	7.507	6.10E-03	rs1519277	2	123735029	q14.3
SNP_A-1933374	C	C	230	140	263	111	5.538	1.86E-02	rs2139300	2	123735126	q14.3
SNP_A-1964738	A	A	262	118	270	80	6.191	1.28E-02	rs1519290	2	123808659	q14.3
SNP_A-1964743	C	C	248	136	280	102	6.791	9.20E-03	rs10496615	2	123995698	q14.3
SNP_A-1917263	G	G	217	167	253	141	4.825	0.0281	rs4359660	2	124060886	q14.3
SNP_A-2265150	C	T	203	181	205	165	5.158	2.31E-02	rs4848885	2	124130353	q14.3
SNP_A-1708993	C	C	286	108	262	138	4.665	3.08E-02	rs10496610	2	124136597	q14.3
SNP_A-2298164	T	T	282	132	252	162	4.747	2.94E-02	rs4848893	2	124138079	q14.3
SNP_A-2262810	G	G	340	46	350	26	5.57	0.0183	rs13035760	2	124347869	q14.3
SNP_A-1818225	C	C	334	16	355	5	6.262	0.0123	rs12711662	2	124376469	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1690503	A	T	220	180	215	197	4.193	4.06E-02	rs4497882	2	124470772	q14.3
SNP_A-1851764	C	C	329	29	348	16	4.239	0.0395	rs17010743	2	124514067	q14.3
SNP_A-2235789	G	G	305	13	312	2	8.121	4.40E-03	rs17010871	2	124590875	q14.3
SNP_A-2264179	C	C	298	80	278	106	4.282	0.0385	rs4848243	2	125004440	q14.3
SNP_A-2299720	C	C	226	190	255	161	4.144	4.18E-02	rs13015323	2	125007264	q14.3
SNP_A-1964778	T	T	279	49	285	75	4.036	4.45E-02	rs13385718	2	125141110	q14.3
SNP_A-2006673	G	G	230	136	202	178	7.172	7.40E-03	rs4848259	2	125227399	q14.3
SNP_A-2055316	T	T	247	151	215	181	4.922	2.65E-02	rs7588987	2	125228134	q14.3
SNP_A-1747695	A	A	334	66	320	90	3.869	4.92E-02	-	2	125539073	q14.3
SNP_A-1694135	G	A	194	188	214	164	4.175	4.10E-02	rs2168024	2	125621651	q14.3
SNP_A-1918263	G	G	336	10	302	2	4.45	0.0349	rs17013262	2	126468917	q14.3
SNP_A-2056721	T	T	254	142	225	177	5.551	1.85E-02	rs6753603	2	126525165	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2220766	T	T	290	114	269	145	4.378	3.64E-02	rs17013435	2	126697279	q14.3
SNP_A-1877762	G	G	333	23	331	39	3.867	4.93E-02	rs2404205	2	126703101	q14.3
SNP_A-2033535	T	T	284	82	251	109	5.803	0.016	rs390949	2	126711196	q14.3
SNP_A-1887442	A	A	310	102	280	128	4.445	3.50E-02	rs360256	2	126725313	q14.3
SNP_A-2234209	A	A	321	91	292	118	4.855	0.0276	rs6748721	2	126879264	q14.3
SNP_A-2176829	A	A	332	74	305	101	5.31	0.0212	rs12992542	2	126899905	q14.3
SNP_A-2242941	G	G	352	14	383	5	4.933	0.0263	rs12053420	2	127158453	q14.3
SNP_A-2219837	G	G	342	74	310	106	7.259	7.10E-03	rs6713073	2	127162052	q14.3
SNP_A-1781692	T	T	276	126	241	159	6.186	0.0129	rs10210850	2	127243330	q14.3
SNP_A-1786661	C	C	264	90	227	111	4.615	3.17E-02	rs13002288	2	127248059	q14.3
SNP_A-1892696	C	C	235	155	210	190	4.829	2.80E-02	rs4608470	2	127257689	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2139375	T	T	230	126	265	99	5.627	0.0177	rs8712879	2	127259998	q14.3
SNP_A-2006677	G	G	233	131	260	100	5.617	0.0178	rs4131510	2	127265778	q14.3
SNP_A-2006679	C	C	237	157	264	120	6.27	0.0123	rs4413104	2	127272648	q14.3
SNP_A-2006680	A	A	239	177	273	145	5.433	1.98E-02	rs4322791	2	127272778	q14.3
SNP_A-2029485	A	A	235	169	264	134	5.684	1.71E-02	rs6745340	2	127274710	q14.3
SNP_A-2095819	A	A	235	129	267	89	9.292	0.0023	rs10181914	2	127294314	q14.3
SNP_A-2252424	A	A	224	182	264	146	7.21	7.20E-03	rs11884665	2	127294785	q14.3
SNP_A-1782773	G	G	359	53	331	79	6.253	0.0124	rs4663097	2	127578136	q14.3
SNP_A-1723668	A	A	337	41	315	61	4.659	0.0309	rs873270	2	127952687	q14.3
SNP_A-2293837	C	C	207	135	220	98	5.406	0.0201	rs10174611	2	128097384	q14.3
SNP_A-1916013	A	A	240	170	212	202	4.468	3.45E-02	rs2244042	2	128121228	q14.3
SNP_A-2172565	G	G	223	111	246	80	6.063	0.0138	rs11692056	2	128347002	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2304061	G	G	347	57	360	38	3.994	4.57E-02	rs2438013	2	128425882	q14.3
SNP_A-1888840	C	C	206	130	234	104	4.665	3.08E-02	rs11542865	2	128663735	q14.3
SNP_A-1796142	C	T	228	188	222	198	4.913	2.67E-02	rs4429419	2	128732357	q14.3
SNP_A-2130151	G	G	208	206	238	176	4.374	3.65E-02	rs6431005	2	128742979	q14.3
SNP_A-2252739	C	C	215	153	221	113	4.461	3.47E-02	rs840879	2	128788004	q14.3
SNP_A-2222537	A	A	352	60	375	39	5.177	0.0229	rs841302	2	129033335	q14.3
SNP_A-2190918	A	A	182	178	221	143	7.569	5.90E-03	rs12996713	2	129199336	q14.3
SNP_A-2155147	A	A	297	37	313	9	17.249	3.28E-05	rs17049003	2	129482567	q14.3
SNP_A-1898927	A	A	216	156	196	190	4.055	4.40E-02	rs6431068	2	129679094	q21.1
SNP_A-1964840	G	C	219	163	196	190	5.069	2.44E-02	rs7575506	2	129680066	q21.1
SNP_A-2302355	A	A	195	135	170	168	5.211	0.0224	rs1441138	2	129683864	q21.1
SNP_A-2087793	A	T	211	155	186	184	4.642	3.12E-02	rs4662904	2	129684257	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2184260	A	A	222	154	188	178	4.42	3.55E-02	rs1155773	2	129686949	q21.1
SNP_A-2294185	C	T	238	176	209	207	4.983	2.56E-02	rs7569776	2	129695820	q21.1
SNP_A-2297770	G	G	284	126	257	153	3.96	4.66E-02	rs4662908	2	129747877	q21.1
SNP_A-1898704	C	C	323	77	298	100	3.99	0.0458	rs17049328	2	129776387	q21.1
SNP_A-1851185	A	A	368	44	343	67	5.64	1.76E-02	rs10169498	2	129803894	q21.1
SNP_A-2262986	A	A	369	35	351	55	4.89	0.027	rs1597908	2	129971340	q21.1
SNP_A-1683854	T	T	268	126	243	167	6.645	9.90E-03	rs837903	2	130114756	q21.1
SNP_A-1734002	T	T	297	101	280	132	4.385	3.63E-02	rs1349734	2	130364473	q21.1
SNP_A-2006702	A	A	354	54	340	76	3.928	4.75E-02	rs4377367	2	131558637	q21.1
SNP_A-1951731	A	A	284	110	312	86	4.234	3.96E-02	rs2313160	2	131670974	q21.1
SNP_A-2034024	C	C	252	120	255	75	7.918	4.90E-03	rs6430791	2	131999940	q21.1
SNP_A-2276680	A	A	376	2	342	10	6.025	0.0141	rs4108018	2	132577051	q21.2
SNP_A-1945057	C	C	261	115	233	147	5.474	1.93E-02	rs7605278	2	133050046	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1808611	C	C	246	104	213	135	6.388	0.0115	rs4508654	2	133050145	q21.2
SNP_A-2212904	C	C	357	59	378	38	5.146	2.33E-02	rs16833598	2	133116982	q21.2
SNP_A-1964877	G	G	344	50	313	77	7.183	7.40E-03	rs9287421	2	133147577	q21.2
SNP_A-1855354	C	C	320	90	289	127	7.844	5.10E-03	rs3109146	2	133155295	q21.2
SNP_A-1929802	G	G	284	116	316	86	6.157	1.31E-02	rs10803535	2	133159369	q21.2
SNP_A-2253076	C	C	413	3	408	12	5.411	0.02	rs4954010	2	133547845	q21.2
SNP_A-1964890	A	A	385	31	370	50	4.736	2.95E-02	rs16845733	2	133616503	q21.2
SNP_A-1856168	A	A	323	93	352	66	5.826	1.58E-02	rs6712415	2	133702529	q21.2
SNP_A-2027334	A	A	297	71	304	42	6.853	8.90E-03	rs16856818	2	133703407	q21.2
SNP_A-1838799	C	C	356	52	334	74	4.543	3.31E-02	rs1529570	2	133885595	q21.2
SNP_A-1781966	C	C	338	54	363	33	5.94	1.48E-02	rs934265	2	133904149	q21.2
SNP_A-1710912	A	A	395	3	400	12	5.191	2.27E-02	rs1005941	2	133926102	q21.2
SNP_A-2308927	A	A	329	73	343	51	4.115	4.25E-02	rs6430423	2	134055130	q21.2
SNP_A-2195173	T	T	270	134	237	159	4.201	4.04E-02	rs2195839	2	134077443	q21.2
SNP_A-2194219	G	G	398	4	404	0	4.04	4.44E-02	rs2278850	2	134149352	q21.2
SNP_A-1869869	T	T	297	61	276	90	6.252	0.0124	rs13421559	2	134160255	q21.2
SNP_A-2065186	T	T	211	147	247	109	8.465	3.60E-03	rs721269	2	134261706	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140985	G	G	371	13	372	28	5.165	0.023	rs16827735	2	134262182	q21.2
SNP_A-2006722	C	C	317	89	347	63	5.783	1.62E-02	rs4954096	2	134562943	q21.2
SNP_A-1859810	C	C	286	118	236	158	10.463	1.20E-03	rs12477481	2	134564791	q21.2
SNP_A-2199594	G	G	249	125	210	158	7.114	0.0076	rs12469200	2	134564857	q21.2
SNP_A-1964937	T	C	201	197	238	158	9.01	2.70E-03	rs10172395	2	134590359	q21.2
SNP_A-1935400	G	G	297	45	309	23	7.208	7.30E-03	rs6414017	2	134609765	q21.2
SNP_A-1900254	G	A	212	160	203	189	5.893	0.0152	rs12151412	2	134625951	q21.2
SNP_A-1900304	A	A	268	134	294	106	4.465	3.46E-02	rs6430487	2	134626263	q21.2
SNP_A-1938867	T	T	232	132	277	107	6.063	0.0138	rs1715008	2	134650748	q21.2
SNP_A-1945177	G	G	296	104	326	82	3.97	4.63E-02	rs4954103	2	134659739	q21.2
SNP_A-1652148	T	G	218	174	215	197	4.89	0.027	rs6740690	2	134988804	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1751917	T	C	213	171	212	194	4.667	3.07E-02	rs6743570	2	134988899	q21.2
SNP_A-1964967	G	G	380	14	356	34	8.024	4.60E-03	rs6730778	2	135172372	q21.3
SNP_A-1861265	A	A	319	95	347	73	4.015	4.51E-02	rs6430527	2	135220313	q21.3
SNP_A-2212853	T	C	181	163	194	156	4.495	3.40E-02	rs10928507	2	135230363	q21.3
SNP_A-1809317	A	A	325	41	339	25	4.169	4.12E-02	rs4346444	2	135320626	q21.3
SNP_A-2195598	C	C	409	1	403	11	8.358	0.0038	rs2156004	2	135332275	q21.3
SNP_A-2072518	G	G	412	4	403	15	6.463	1.10E-02	rs6720061	2	135358010	q21.3
SNP_A-2229014	G	G	190	174	214	138	5.38	2.04E-02	rs6430538	2	135373699	q21.3
SNP_A-2255963	C	C	406	2	400	12	7.168	7.40E-03	rs16831098	2	135412502	q21.3
SNP_A-1957159	C	C	183	171	228	154	4.758	0.0292	rs4953936	2	135415244	q21.3
SNP_A-1890052	A	T	201	159	177	159	5.043	0.0247	rs5430543	2	135436141	q21.3
SNP_A-2223549	C	C	275	129	329	81	15.756	7.21E-05	rs10928521	2	135453917	q21.3
SNP_A-2163386	A	G	224	174	223	189	8.775	3.10E-03	rs7593370	2	135457249	q21.3
SNP_A-2135570	C	A	227	177	218	184	8.75	3.10E-03	rs3814358	2	135457740	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1961121	G	G	282	66	303	47	3.943	4.71E-02	rs13427841	2	135550972	q21.3
SNP_A-2157247	G	G	301	113	325	87	4.295	3.82E-02	rs12463963	2	135552788	q21.3
SNP_A-1892617	C	C	318	54	343	37	4.037	4.45E-02	rs10928525	2	135569870	q21.3
SNP_A-1828766	G	G	312	74	336	52	4.725	2.97E-02	rs16831235	2	135578861	q21.3
SNP_A-2193719	T	T	380	6	406	0	6.359	0.0117	rs3739028	2	135741578	q21.3
SNP_A-1906194	A	A	325	55	336	36	4.065	4.38E-02	rs11891774	2	135834947	q21.3
SNP_A-1782289	C	C	351	59	381	37	6.194	1.28E-02	rs7572152	2	135902622	q21.3
SNP_A-2049118	C	C	356	58	382	36	6.046	1.39E-02	rs6749387	2	135935555	q21.3
SNP_A-1871291	C	C	352	10	363	3	3.917	4.78E-02	rs1898524	2	135985144	q21.3
SNP_A-1815664	T	T	317	61	344	38	6.425	0.0112	rs4954256	2	136020884	q21.3
SNP_A-2278323	C	C	353	51	383	35	3.962	0.0465	rs4953951	2	136021077	q21.3
SNP_A-2194354	T	T	257	149	270	116	3.928	4.75E-02	rs1446584	2	136253693	q21.3
SNP_A-2295479	G	G	368	14	393	5	4.758	0.0292	rs16831992	2	136343192	q21.3
SNP_A-2067262	A	A	286	90	294	60	5.452	0.0195	rs2304371	2	136395289	q21.3
SNP_A-2045698	G	G	378	22	404	10	5.125	2.36E-02	rs11884924	2	136409619	q21.3
SNP_A-1741139	A	A	342	56	386	26	13.397	3.00E-04	rs4954265	2	136534994	q21.3
SNP_A-1745136	A	A	376	18	400	4	9.528	0.002	rs7608702	2	136572329	q21.3
SNP_A-1836051	T	T	250	162	279	129	5.313	0.0212	rs7371606	2	136640506	q21.3
SNP_A-2099998	C	C	347	63	373	45	3.862	4.94E-02	rs9287448	2	136821480	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1875317	A	A	380	34	366	52	4.011	4.52E-02	rs4599171	2	136892165	q21.3
SNP_A-1714186	G	G	393	7	411	1	4.727	2.97E-02	rs10496739	2	136962738	q21.3
SNP_A-1796653	C	C	394	22	409	11	3.928	4.75E-02	rs16834018	2	136989084	q21.3
SNP_A-2292962	A	A	350	58	379	35	6.798	9.10E-03	rs16836162	2	137299354	q21.3
SNP_A-2089532	T	T	353	59	377	39	4.851	0.0276	rs1346369	2	137345010	q21.3
SNP_A-1964994	T	T	333	77	358	50	6.64	0.01	rs2001872	2	137355776	q21.3
SNP_A-1943413	C	C	355	61	331	85	4.785	0.0287	rs16855716	2	137414412	q22.1
SNP_A-1965003	C	T	182	168	209	169	3.869	4.92E-02	rs1835313	2	137501922	q22.1
SNP_A-2154076	A	A	302	108	323	83	3.958	4.66E-02	rs1432220	2	137702472	q22.1
SNP_A-1965009	A	A	307	93	337	67	5.603	1.79E-02	rs4954468	2	137710951	q22.1
SNP_A-1965010	A	A	283	99	306	74	4.506	3.38E-02	rs1550089	2	137711555	q22.1
SNP_A-1929845	C	C	282	126	305	99	4.122	4.23E-02	rs7370327	2	138019021	q22.1
SNP_A-1745670	C	C	335	63	369	43	5.175	0.0229	rs1432216	2	138085385	q22.1
SNP_A-1693863	C	C	272	70	269	105	5.598	1.80E-02	rs2375116	2	138157936	q22.1
SNP_A-1914623	G	G	349	53	371	33	5.318	2.11E-02	rs3113227	2	138540324	q22.1
SNP_A-1881217	C	C	278	72	295	49	4.825	0.0281	rs4954853	2	138813306	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1757775	C	C	281	117	262	148	4.114	4.25E-02	rs10496793	2	138846809	q22.1
SNP_A-2310173	T	T	330	42	352	26	4.427	3.54E-02	rs13388206	2	139166663	q22.1
SNP_A-2114234	A	A	305	91	284	118	4.192	4.06E-02	rs17607405	2	139432334	q22.1
SNP_A-1815953	T	T	325	83	357	57	6.287	1.22E-02	rs17660173	2	139471905	q22.1
SNP_A-1965064	C	C	335	81	350	58	4.057	4.40E-02	rs10496802	2	139478604	q22.1
SNP_A-2116231	C	C	311	45	332	26	5.765	1.64E-02	rs17660836	2	139493688	q22.1
SNP_A-1925941	T	T	384	0	396	4	3.86	4.95E-02	rs1825497	2	139522598	q22.1
SNP_A-1830423	T	T	284	116	260	144	4.054	0.0441	rs13001729	2	139656629	q22.1
SNP_A-2161664	T	T	257	59	227	89	7.941	4.80E-03	rs6708367	2	139688915	q22.1
SNP_A-2146524	G	G	304	48	291	27	4.45	0.0349	rs7567315	2	139690520	q22.1
SNP_A-2024793	C	C	279	105	257	141	5.923	0.0149	rs6752557	2	139714304	q22.1
SNP_A-2053578	G	G	335	73	360	50	5.195	2.26E-02	rs12623964	2	139770547	q22.1
SNP_A-2056564	G	G	325	71	360	50	5.191	2.27E-02	rs13011616	2	139774399	q22.1
SNP_A-2091144	G	G	330	68	349	43	6.117	0.0134	rs13033152	2	139775699	q22.1
SNP_A-1882237	A	A	329	71	351	49	4.745	2.94E-02	rs13027447	2	139777264	q22.1
SNP_A-2154164	C	C	336	72	360	50	4.79	0.0286	rs16841830	2	139781665	q22.1
SNP_A-1726370	T	T	268	106	250	158	9.407	2.20E-03	rs9287506	2	139819878	q22.1
SNP_A-1813645	G	G	377	37	354	62	7.032	8.00E-03	rs13419861	2	139837545	q22.1
SNP_A-1965078	C	C	341	11	304	22	4.799	2.85E-02	rs10189421	2	139871038	q22.1
SNP_A-2242480	C	C	309	67	335	47	4.511	3.37E-02	rs4517921	2	139959861	q22.1
SNP_A-2193199	C	C	305	75	317	39	10.829	0.001	rs6755750	2	139961165	q22.1
SNP_A-1869469	C	C	399	9	391	21	4.862	0.0275	rs7590867	2	140229022	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1709849	C	C	371	19	367	35	4.582	3.23E-02	rs344907	2	140287807	q22.1
SNP_A-1925045	C	C	270	146	237	181	5.869	0.0152	rs1520091	2	140427611	q22.1
SNP_A-1820582	C	C	316	16	332	6	4.887	2.71E-02	rs16844072	2	141065720	q22.1
SNP_A-2068218	C	C	261	123	300	98	5.29	2.14E-02	rs1385766	2	141104518	q22.1
SNP_A-1844723	C	C	219	135	187	161	4.755	0.0292	rs483128	2	141183038	q22.1
SNP_A-2160897	C	C	256	154	287	125	4.779	2.88E-02	rs488610	2	141188476	q22.1
SNP_A-2033121	T	T	215	139	177	161	4.93	0.0264	rs547663	2	141216559	q22.1
SNP_A-1669487	-	A	185	185	213	157	4.262	0.039	rs1385775	2	141489870	q22.1
SNP_A-2033004	G	G	239	163	261	131	4.326	3.75E-02	rs2380920	2	141587886	q22.1
SNP_A-2039169	G	G	393	5	412	0	5.208	2.25E-02	rs7564751	2	141611961	q22.1
SNP_A-1821821	A	A	292	74	267	97	4.206	4.03E-02	rs4422109	2	141999364	q22.1
SNP_A-1881106	C	C	361	15	356	28	3.881	4.88E-02	rs16855058	2	142140911	q22.1
SNP_A-1754152	A	A	273	125	247	155	4.494	3.40E-02	rs9283437	2	142209329	q22.1
SNP_A-1749827	G	G	301	77	300	108	4.057	4.40E-02	rs355577	2	142589564	q22.1
SNP_A-1820579	G	G	323	41	307	71	8.181	4.20E-03	rs10198134	2	142759354	q22.2
SNP_A-2022405	G	G	294	42	334	26	5.491	1.91E-02	rs12478952	2	144060313	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1758460	C	C	259	127	309	101	6.649	9.90E-03	rs827228	2	144120488	q22.2
SNP_A-1875621	C	C	278	132	290	100	4.17	4.11E-02	rs12691689	2	144262018	q22.3
SNP_A-2227328	A	A	343	7	326	20	6.668	9.80E-03	rs1864245	2	144612250	q22.3
SNP_A-1965188	C	C	402	12	394	24	4.061	4.39E-02	rs9287357	2	144632926	q22.3
SNP_A-2179826	G	G	365	13	373	27	4.368	3.66E-02	rs17677434	2	145053420	q22.3
SNP_A-1836284	A	A	348	28	323	13	4.185	4.08E-02	rs17678683	2	145120291	q22.3
SNP_A-1854404	G	G	352	18	377	7	5.439	1.97E-02	rs6718158	2	145264368	q22.3
SNP_A-1707850	C	T	182	178	220	162	4.947	2.61E-02	rs2381575	2	145289728	q22.3
SNP_A-1642899	C	C	273	93	237	115	4.597	3.20E-02	rs706624	2	145794608	q22.3
SNP_A-1803657	G	G	350	2	289	9	5.832	1.57E-02	rs11904231	2	145846926	q22.3
SNP_A-1894237	A	A	333	57	356	38	4.547	3.30E-02	rs16824790	2	145940250	q22.3
SNP_A-1956293	C	C	208	124	173	145	4.555	3.28E-02	rs6430080	2	145953379	q22.3
SNP_A-2110041	A	A	375	15	360	36	8.908	0.0028	rs13426482	2	146355942	q22.3
SNP_A-1756224	G	G	355	35	350	54	3.846	0.0499	rs2381762	2	146660868	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1728605	G	G	379	21	370	42	6.932	8.50E-03	rs10496989	2	146743789	q22.3
SNP_A-1680510	T	T	331	65	311	95	6.124	1.33E-02	rs10496990	2	146759473	q22.3
SNP_A-1703537	A	A	369	21	366	42	6.61	0.0101	rs1228055	2	146782277	q22.3
SNP_A-1675087	T	T	372	28	366	46	4.251	3.92E-02	rs1228054	2	146782866	q22.3
SNP_A-2006765	G	G	216	146	252	108	8.449	3.70E-03	rs4433946	2	147190059	q22.3
SNP_A-2064551	G	G	409	7	396	18	5.045	0.0247	—	2	148129507	q22.3
SNP_A-1848298	G	G	202	194	239	167	5	2.54E-02	rs1550319	2	148137049	q22.3
SNP_A-1957279	A	A	172	146	219	119	7.798	5.20E-03	rs17673675	2	148141511	q22.3
SNP_A-2289760	A	A	402	8	391	19	4.634	3.13E-02	rs13022277	2	148146527	q22.3
SNP_A-2163200	C	A	197	193	229	171	4.782	2.88E-02	rs11675603	2	148157822	q22.3
SNP_A-1792061	A	A	362	8	356	20	5.145	2.33E-02	—	2	148163055	q22.3
SNP_A-1865477	C	C	254	146	228	176	4.178	4.10E-02	rs12478252	2	148214443	q22.3
SNP_A-2006771	T	T	205	147	179	173	3.873	4.91E-02	rs1950047	2	148262345	q22.3
SNP_A-1965322	G	G	312	72	345	51	5.059	2.45E-02	rs10490386	2	149878221	q23.2
SNP_A-1808199	G	G	299	61	343	41	6.169	1.30E-02	rs12613053	2	149879121	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1965319	C	C	317	29	363	15	6.164	1.30E-02	rs9678368	2	149884876	q23.2
SNP_A-2144780	A	A	375	23	406	10	5.957	0.0147	rs6744188	2	150597893	q23.3
SNP_A-2234331	G	G	374	30	387	15	5.217	0.0224	rs12464081	2	150610354	q23.3
SNP_A-1906587	G	G	390	16	375	29	4.045	4.43E-02	rs2674624	2	150697368	q23.3
SNP_A-1645334	A	A	368	24	395	9	7.594	5.90E-03	rs1437965	2	150998083	q23.3
SNP_A-1664342	C	C	372	26	392	12	5.637	1.76E-02	rs10497042	2	151052850	q23.3
SNP_A-1965334	C	C	408	6	404	16	4.522	3.35E-02	rs17434723	2	151058340	q23.3
SNP_A-2215897	G	G	303	99	266	122	4.553	3.29E-02	rs2222760	2	151170621	q23.3
SNP_A-1931830	T	T	245	81	262	56	5.033	2.49E-02	rs1356738	2	151451933	q23.3
SNP_A-1954713	A	A	332	16	315	5	5.044	0.0247	rs7570251	2	151577837	q23.3
SNP_A-1725642	G	G	236	154	216	188	4.019	4.50E-02	rs7603668	2	151699069	q23.3
SNP_A-1688566	G	G	348	14	358	32	6.151	1.31E-02	rs9287861	2	151701828	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1698549	G	G	361	13	358	26	4.215	4.01E-02	rs2341086	2	151702045	q23.3
SNP_A-2102746	C	C	363	35	348	58	5.926	0.0149	rs16829331	2	151721636	q23.3
SNP_A-2080294	T	T	269	135	305	107	5.42	1.99E-02	rs13034178	2	151728109	q23.3
SNP_A-1703907	T	T	291	109	271	139	4.218	4.00E-02	rs10497071	2	151811310	q23.3
SNP_A-1849352	G	G	401	15	416	2	10.212	0.0014	rs16830400	2	152502249	q23.3
SNP_A-1713033	A	A	380	20	406	6	8.223	4.10E-03	rs10497086	2	152895021	q23.3
SNP_A-1912096	C	C	359	51	381	33	4.492	3.41E-02	rs4664103	2	153034221	q23.3
SNP_A-1818372	C	C	393	9	393	23	5.887	1.53E-02	rs16831043	2	153073854	q23.3
SNP_A-2152095	G	G	362	40	391	25	4.34	3.72E-02	rs2345873	2	153073912	q23.3
SNP_A-1895895	A	A	406	10	397	23	5.203	2.25E-02	rs2345875	2	153078953	q23.3
SNP_A-2167563	C	C	348	50	368	28	6.759	9.30E-03	rs6737699	2	153123085	q23.3
SNP_A-1781652	G	G	410	4	418	0	4.058	4.40E-02	rs6710689	2	153273754	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1749429	A	A	336	64	364	46	3.943	4.71E-02	rs4664573	2	153411501	q23.3
SNP_A-1743669	C	C	286	50	259	81	8.65	0.0033	rs727327	2	153667044	q23.3
SNP_A-1965433	A	A	376	40	352	62	5.532	1.87E-02	rs1960289	2	153902363	q23.3
SNP_A-2221742	T	T	361	47	342	68	4.343	3.72E-02	rs11897939	2	153970352	q23.3
SNP_A-2047193	A	A	366	46	348	68	4.68	3.05E-02	rs10196515	2	154065817	q23.3
SNP_A-1806126	C	C	379	13	369	25	3.918	4.78E-02	rs4294953	2	154191123	q23.3
SNP_A-1948440	G	G	356	22	375	11	4.077	4.35E-02	rs4664688	2	154239647	q23.3
SNP_A-2308049	G	G	375	39	388	22	4.94	2.62E-02	rs16833615	2	154239942	q23.3
SNP_A-2086677	A	A	253	41	275	69	4.151	4.16E-02	rs11693958	2	154317021	q23.3
SNP_A-1781053	G	G	272	104	294	78	4.548	3.30E-02	rs6735884	2	154612285	q23.3
SNP_A-1644588	T	T	347	39	347	61	4.234	3.96E-02	rs1940253	2	154645133	q23.3
SNP_A-1807804	G	G	332	74	309	99	4.433	3.52E-02	rs11899646	2	155156502	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044002	C	C	351	27	340	12	5.025	2.50E-02	rs16837822	2	155232133	q24.1
SNP_A-2117987	C	C	394	0	373	7	7.324	6.80E-03	rs16838068	2	155430491	q24.1
SNP_A-2303060	G	G	325	89	350	66	4.334	3.74E-02	rs2591153	2	155480816	q24.1
SNP_A-2282744	G	G	290	94	307	65	5.584	1.81E-02	rs2349755	2	155663550	q24.1
SNP_A-1965484	T	T	298	92	321	59	7.938	4.80E-03	rs1882459	2	155819622	q24.1
SNP_A-2236624	G	G	296	90	329	67	4.985	2.56E-02	rs7570973	2	155845169	q24.1
SNP_A-1965487	C	C	304	104	332	76	5.588	1.81E-02	rs2019463	2	155913117	q24.1
SNP_A-2142560	G	C	188	172	193	147	5.659	1.74E-02	rs2677479	2	156258773	q24.1
SNP_A-1902238	C	C	266	150	292	122	4.089	4.32E-02	rs278881	2	156266436	q24.1
SNP_A-2081107	T	T	267	87	302	62	6.209	1.27E-02	rs843219	2	156275147	q24.1
SNP_A-2313967	T	T	291	119	248	138	4.115	4.25E-02	rs2882511	2	156350897	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1847650	A	A	225	149	244	114	5.08	2.42E-02	rs11885215	2	156536585	q24.1
SNP_A-1936238	C	C	304	102	331	75	5.267	2.17E-02	rs1919159	2	156954263	q24.1
SNP_A-2075173	C	C	410	0	402	4	4.059	4.39E-02	rs298228	2	157127699	q24.1
SNP_A-2120071	G	G	385	1	362	12	9.829	1.70E-03	rs12694629	2	157137655	q24.1
SNP_A-1965508	A	A	260	70	285	45	6.582	0.0103	rs2288760	2	157252830	q24.1
SNP_A-1876401	A	C	210	188	218	184	3.913	4.79E-02	rs6436555	2	157313785	q24.1
SNP_A-2044411	C	C	253	101	258	72	4.073	0.0436	rs7582705	2	157331279	q24.1
SNP_A-2071230	T	T	201	151	218	112	5.769	1.63E-02	rs1543932	2	157390700	q24.1
SNP_A-1965510	T	T	395	17	412	6	5.576	1.82E-02	rs10497160	2	157610912	q24.1
SNP_A-1871586	T	T	384	6	377	19	6.779	9.20E-03	rs16842215	2	158550060	q24.1
SNP_A-2255013	G	G	366	46	338	68	5.316	2.11E-02	rs6745237	2	158627242	q24.1
SNP_A-1965533	A	A	388	14	387	3	6.939	8.40E-03	rs17193070	2	158856956	q24.1
SNP_A-1746727	T	T	258	132	294	96	8.032	4.60E-03	rs10497192	2	158874245	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1782251	G	G	391	19	375	41	8.358	0.0038	rs7570724	2	159054493	q24.1
SNP_A-2279455	A	A	235	157	273	131	5.01	0.0252	rs1111212	2	159138241	q24.1
SNP_A-2207968	C	C	280	130	304	102	4.346	3.71E-02	rs2069100	2	159241028	q24.1
SNP_A-1902202	G	G	230	126	201	157	5.341	2.08E-02	rs17809100	2	159418342	q24.1
SNP_A-1794665	T	T	261	153	236	184	4.066	4.37E-02	rs4664262	2	159418901	q24.1
SNP_A-2074993	G	G	219	105	258	82	5.635	1.76E-02	rs10169705	2	159497251	q24.1
SNP_A-1679952	C	C	345	29	341	47	4.031	4.47E-02	rs6738665	2	159579582	q24.1
SNP_A-1736085	G	G	308	34	311	61	6.439	0.0112	rs719931	2	159645482	q24.1
SNP_A-2110441	T	T	340	34	354	16	6.741	9.40E-03	rs432451	2	159789703	q24.2
SNP_A-2248578	A	A	301	113	330	86	4.991	2.55E-02	rs7595446	2	159791555	q24.2
SNP_A-2196124	A	A	293	105	325	83	4.108	4.27E-02	rs264586	2	159793020	q24.2
SNP_A-2237161	G	G	377	29	402	14	5.914	1.50E-02	rs264592	2	159801792	q24.2
SNP_A-2085133	C	C	379	5	373	17	6.547	1.05E-02	rs2288105	2	159818206	q24.2
SNP_A-1720549	C	C	301	99	279	131	5.164	2.31E-02	rs6722518	2	159858816	q24.1
SNP_A-2046462	G	G	401	13	400	4	4.644	3.12E-02	rs16843861	2	159959302	q24.2
SNP_A-2226835	C	C	384	10	409	1	7.836	5.10E-03	rs12618929	2	159979210	q24.2
SNP_A-1954969	T	T	297	99	273	133	5.87	0.0154	rs17495716	2	160212030	q24.2
SNP_A-1714753	C	C	186	166	222	136	6.106	0.0135	rs4665050	2	160312002	q24.2
SNP_A-2035964	C	C	289	79	306	52	5.914	1.50E-02	rs7566887	2	160489185	q24.2
SNP_A-2094744	A	A	336	80	364	56	5.336	2.09E-02	rs9789367	2	160559521	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2268465	G	G	209	169	235	137	4.821	0.0281	rs6735923	2	160595095	q24.2
SNP_A-2130783	C	C	305	107	340	70	9.629	0.0019	rs6724314	2	160595700	q24.2
SNP_A-2160758	G	G	289	79	328	62	3.88	4.89E-02	rs12692579	2	160666646	q24.2
SNP_A-1805568	G	G	308	106	342	78	5.986	0.0143	rs3792167	2	160671089	q24.2
SNP_A-2266468	T	C	157	151	203	143	6.104	0.0135	rs17830904	2	160717195	q24.2
SNP_A-1831860	C	C	364	4	358	14	5.584	1.81E-02	rs1355421	2	160738725	q24.2
SNP_A-1786508	G	G	356	24	340	40	4.368	3.66E-02	rs4665146	2	160741590	q24.2
SNP_A-2278960	C	C	270	104	282	74	4.876	2.72E-02	rs6432603	2	160825850	q24.2
SNP_A-1701057	C	C	321	73	358	52	5.228	2.22E-02	rs2292388	2	160937552	q24.2
SNP_A-1702663	A	A	278	90	333	67	6.999	8.20E-03	rs1877195	2	160985228	q24.2
SNP_A-1813819	C	C	246	138	279	111	4.956	2.60E-02	rs7557611	2	161265706	q24.2
SNP_A-1947279	A	A	374	28	378	14	4.563	0.0327	rs4508611	2	161285415	q24.2
SNP_A-1965592	A	A	378	26	358	42	4.288	3.84E-02	rs10497216	2	161413986	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893089	C	T	210	150	188	176	7.245	7.10E-03	rs1026236	2	161430933	q24.2
SNP_A-2066859	-	G	190	190	221	161	4.729	2.97E-02	rs7581204	2	161468796	q24.2
SNP_A-2035658	A	C	199	175	214	166	6.846	8.90E-03	rs558692	2	161492634	q24.2
SNP_A-2085300	G	A	207	203	242	168	7.474	0.0063	rs6743276	2	161492707	q24.2
SNP_A-2147536	A	T	206	200	227	171	4.877	2.72E-02	rs6720147	2	161511621	q24.2
SNP_A-2195028	A	G	205	193	216	168	4.715	2.99E-02	rs4664386	2	161570744	q24.2
SNP_A-2304448	C	C	302	64	290	94	5.511	0.0189	rs8179756	2	161571518	q24.2
SNP_A-2311625	G	G	389	15	404	6	4.097	4.30E-02	rs12624207	2	161641858	q24.2
SNP_A-1667816	G	T	190	168	200	160	5.349	0.0207	rs2123034	2	161847716	q24.2
SNP_A-1728927	G	A	209	191	228	182	5.009	0.0252	rs10497221	2	161951764	q24.2
SNP_A-1689703	T	T	310	88	289	121	5.77	1.63E-02	rs997015	2	161982502	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1965611	A	A	308	70	327	43	6.935	8.50E-03	rs2013879	2	162001551	q24.2
SNP_A-2140021	A	A	253	111	279	85	4.72	0.0298	rs3769957	2	162089351	q24.2
SNP_A-2047452	A	A	347	13	345	3	6.054	1.39E-02	rs16846047	2	162387453	q24.2
SNP_A-1965616	G	G	288	116	238	160	11.723	6.00E-04	rs1227921	2	162517707	q24.2
SNP_A-2299333	G	G	234	150	196	190	8.059	4.50E-03	rs6432705	2	162605465	q24.2
SNP_A-1849486	A	A	302	86	321	59	5.524	1.88E-02	rs9808497	2	162655409	q24.2
SNP_A-1677022	A	A	293	107	255	157	11.93	6.00E-04	rs10497224	2	162924917	q24.2
SNP_A-1714851	G	G	292	96	270	134	6.819	9.00E-03	rs1996266	2	162935228	q24.2
SNP_A-1942126	C	C	360	4	378	0	4.176	4.10E-02	rs10930059	2	163262581	q24.2
SNP_A-1849639	A	A	371	15	384	6	4.06	4.39E-02	rs16847045	2	163320225	q24.2
SNP_A-2178663	C	C	266	134	231	163	5.251	2.19E-02	rs4667466	2	163514654	q24.2
SNP_A-1879625	A	-	218	138	167	167	8.821	3.00E-03	rs4667467	2	163514776	q24.2
SNP_A-2087090	A	A	264	142	221	165	5.034	2.49E-02	rs1001911	2	163539107	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043936	G	G	390	14	369	35	9.581	0.002	rs1036697	2	164255840	q24.3
SNP_A-2057856	G	G	359	11	337	23	4.795	2.85E-02	rs10169055	2	164262314	q24.3
SNP_A-2057830	G	G	245	155	276	114	7.968	4.80E-03	rs16848743	2	164321874	q24.3
SNP_A-2049383	T	T	360	16	372	6	4.737	2.95E-02	---	2	164378188	q24.3
SNP_A-1965664	G	G	322	46	307	67	4.212	4.01E-02	rs1446475	2	164802223	q24.3
SNP_A-1965671	T	T	297	45	273	71	6.832	9.00E-03	rs1446466	2	164861394	q24.3
SNP_A-1795184	C	C	336	56	320	78	3.957	4.67E-02	rs1439218	2	164865647	q24.3
SNP_A-2100589	A	A	237	155	209	189	5.073	2.43E-02	rs1121308	2	164867571	q24.3
SNP_A-1965674	T	T	231	139	206	168	4.148	4.17E-02	rs1371183	2	164924840	q24.3
SNP_A-1943874	A	A	384	10	403	3	4.049	4.42E-02	rs16849420	2	164968136	q24.3
SNP_A-1679570	C	C	306	68	287	95	4.997	2.54E-02	rs1371178	2	165334058	q24.3
SNP_A-2218798	T	T	261	55	289	37	4.793	0.0286	rs427059	2	165432461	q24.3
SNP_A-1965681	G	G	339	59	316	82	4.559	0.0327	rs10490693	2	165474684	q24.3
SNP_A-2027137	G	G	310	36	329	17	7.376	0.0066	rs1840329	2	165619984	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141790	T	T	311	23	309	11	3.944	0.047	---	2	165657920	q24.3
SNP_A-1854585	T	T	284	112	254	136	3.95	4.69E-02	rs10192208	2	165943657	q24.3
SNP_A-2197615	G	G	351	57	319	83	6.313	0.012	rs9287856	2	165964056	q24.3
SNP_A-2294507	A	A	410	0	409	5	4.982	2.56E-02	rs3762550	2	166561512	q24.3
SNP_A-1815172	T	T	315	31	307	49	4.011	4.52E-02	rs534798	2	166810563	q24.3
SNP_A-2128376	T	T	302	8	332	2	4.131	4.21E-02	---	2	166823706	q24.3
SNP_A-2127476	A	A	258	158	288	132	3.96	4.66E-02	rs4447616	2	166989170	q24.3
SNP_A-2312109	A	A	236	106	270	84	4.626	0.0315	rs16852700	2	167492230	q24.3
SNP_A-1718961	A	A	281	101	269	133	4.13	4.21E-02	rs1157750	2	167593527	q24.3
SNP_A-1789625	A	A	317	49	337	25	8.374	0.0038	rs11896680	2	167633994	q24.3
SNP_A-1965727	A	A	361	15	339	27	3.986	4.59E-02	rs16853036	2	167826977	q24.3
SNP_A-2184296	C	C	355	13	329	25	4.508	3.37E-02	rs7573953	2	167897754	q24.3
SNP_A-2107646	C	C	402	4	408	0	4.04	4.44E-02	rs16853751	2	168237996	q24.3
SNP_A-2123421	G	G	348	64	323	89	5.016	2.51E-02	rs1835745	2	168268059	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2229164	T	T	258	72	249	101	4.437	3.52E-02	rs6743050	2	168274068	q24.3
SNP_A-2240658	A	A	316	70	307	97	4.087	4.32E-02	rs1147147	2	168320444	q24.3
SNP_A-2116262	G	G	408	0	414	4	3.923	4.76E-02	rs16854676	2	168761838	q24.3
SNP_A-1891664	T	T	382	14	387	3	7.105	7.70E-03	rs16855893	2	169478154	q24.3
SNP_A-1965774	G	G	376	4	384	0	4.063	4.38E-02	rs16856196	2	169596768	q24.3
SNP_A-1707762	G	G	349	47	333	67	3.864	4.93E-02	rs829955	2	169864568	q24.3
SNP_A-2300156	T	T	234	176	260	146	4.144	4.18E-02	rs11887007	2	169975361	q31.1
SNP_A-1710750	A	A	232	162	272	122	8.808	3.00E-03	rs484066	2	169985025	q24.3
SNP_A-2117741	G	G	263	77	248	106	4.755	0.0292	rs3845731	2	170012612	q31.1
SNP_A-1959224	C	C	230	124	197	151	5.15	2.32E-02	rs2673172	2	170030307	q31.1
SNP_A-2026211	A	A	295	87	324	66	4.159	4.14E-02	rs10182522	2	170749628	q31.1
SNP_A-1920377	C	C	399	5	400	0	4.981	2.56E-02	rs11883608	2	170787019	q31.1
SNP_A-2297170	C	C	292	114	258	148	6.514	1.07E-02	rs1035625	2	170917952	q31.1
SNP_A-1906543	T	T	220	188	243	153	4.557	3.28E-02	rs10930422	2	171033749	q31.1

Table 2

	Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
	SNP_A-1965816	A	A	334	60	323	89	5.429	1.98E-02	rs10497370	2	171094385	q31.1
	SNP_A-1965817	A	A	265	145	299	117	4.999	2.54E-02	rs12477031	2	171113184	q31.1
	SNP_A-2140904	G	G	216	180	251	151	5.119	2.37E-02	rs11895735	2	171174258	q31.1
	SNP_A-1785187	A	A	370	4	374	0	4.022	4.49E-02	rs12623840	2	171225782	q31.1
	SNP_A-2059723	T	T	397	3	388	10	3.867	4.92E-02	rs17608242	2	171573872	q31.1
	SNP_A-1847600	A	A	285	113	222	138	8.435	3.70E-03	rs13384194	2	172179294	q31.1
	SNP_A-2023371	G	G	296	94	264	120	4.941	2.62E-02	rs6743679	2	172209935	q31.1
	SNP_A-1840030	T	T	341	59	319	87	6.059	0.0138	rs2111720	2	172248384	q31.1
	SNP_A-2075060	G	G	299	33	296	58	6.184	0.0129	rs6747365	2	172901052	q31.1
	SNP_A-2076256	C	C	296	48	282	72	4.997	2.54E-02	rs7575468	2	172907674	q31.1
	SNP_A-2269905	A	A	356	46	387	31	3.905	4.81E-02	rs7574709	2	172978015	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2178882	T	T	379	35	406	14	9.886	1.70E-03	rs10184567	2	173124503	q31.1
SNP_A-1965848	C	C	336	52	373	31	6.924	8.50E-03	rs9287954	2	173133080	q31.1
SNP_A-1965852	G	G	326	62	357	37	7.675	5.60E-03	rs7584977	2	173158232	q31.1
SNP_A-1921748	C	C	324	60	358	36	7.568	5.90E-03	rs3792254	2	173158336	q31.1
SNP_A-1955388	A	A	353	51	390	26	9.786	0.0018	rs10803874	2	173202891	q31.1
SNP_A-1700612	C	C	358	34	395	13	10.885	0.001	rs10497381	2	173508074	q31.1
SNP_A-1732516	C	C	335	65	377	35	11.303	8.00E-04	rs7596259	2	173508275	q31.1
SNP_A-1706853	G	G	258	136	287	107	5.004	0.0253	rs2272499	2	173534659	q31.1
SNP_A-2071583	G	G	391	25	405	13	4.031	4.47E-02	rs4972538	2	173919104	q31.1
SNP_A-1941060	G	G	297	115	322	90	4.058	4.40E-02	rs2163960	2	174141558	q31.1
SNP_A-2076105	T	T	306	86	347	59	7.359	6.70E-03	rs10930609	2	174308438	q31.1
SNP_A-1885725	C	C	331	5	323	17	6.62	0.0101	rs16862246	2	174676397	q31.1
SNP_A-1670916	C	C	286	114	323	89	5.151	2.32E-02	rs672524	2	174687982	q31.1
SNP_A-1691696	G	G	218	136	196	170	4.748	0.0293	rs10497407	2	174806473	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1684096	C	C	389	9	382	24	6.803	9.10E-03	rs6729538	2	174939131	q31.1
SNP_A-1938139	A	A	304	72	330	50	5.012	0.0252	rs6732758	2	175435466	q31.1
SNP_A-2038571	G	G	400	14	384	28	4.988	2.55E-02	rs10183675	2	175895942	q31.1
SNP_A-1784383	A	A	255	97	273	73	3.951	4.69E-02	rs2461750	2	176143164	q31.1
SNP_A-1733166	A	A	382	16	374	36	7.6	5.80E-03	rs2300582	2	176155625	q31.1
SNP_A-1862285	C	C	266	110	288	82	4.909	2.67E-02	rs6736485	2	176207426	q31.1
SNP_A-1823296	G	G	282	124	309	97	4.532	3.33E-02	rs1522829	2	176224321	q31.1
SNP_A-2298325	C	C	267	103	296	70	7.767	0.0053	rs10207413	2	176224553	q31.1
SNP_A-1680924	A	A	387	13	385	27	4.729	2.97E-02	rs10497435	2	176250212	q31.1
SNP_A-2204882	G	G	328	0	315	7	7.208	7.30E-03	rs12477983	2	176430301	q31.1
SNP_A-1877286	C	C	378	4	372	0	3.916	4.78E-02	rs10208017	2	176490953	q31.1
SNP_A-1884341	G	G	333	39	320	16	8.067	4.50E-03	rs1867879	2	176588833	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1949354	T	T	329	85	305	113	4.849	2.77E-02	rs10183544	2	177289453	q31.1
SNP_A-1789291	C	C	351	27	320	50	8.218	4.10E-03	rs10184742	2	177469409	q31.1
SNP_A-2238691	G	G	334	22	319	37	4.158	4.14E-02	rs3731798	2	177482744	q31.1
SNP_A-2023119	G	G	389	5	387	15	4.925	2.65E-02	rs16864468	2	177500499	q31.1
SNP_A-1965969	C	C	343	15	337	35	7.787	0.0053	rs10497474	2	177567952	q31.1
SNP_A-1965971	T	T	341	25	326	46	6.5	1.08E-02	rs6706678	2	177569711	q31.1
SNP_A-2163186	T	T	372	14	356	28	5.013	0.0252	rs6433620	2	177594348	q31.1
SNP_A-2071469	G	G	356	42	349	63	4.029	4.47E-02	rs3906062	2	177611514	q31.1
SNP_A-2147193	A	A	411	3	400	12	5.544	1.85E-02	rs7593064	2	177675742	q31.1
SNP_A-1965976	A	A	394	16	374	34	6.996	8.20E-03	rs10198127	2	177737710	q31.1
SNP_A-2006859	G	G	367	13	348	26	4.791	0.0286	rs1534682	2	177757744	q31.1
SNP_A-1655905	A	A	396	4	392	14	5.532	1.87E-02	rs10497468	2	178054835	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1651858	C	C	371	27	366	46	4.739	2.95E-02	rs1919631	2	178132332	q31.1
SNP_A-1965992	G	G	302	18	349	7	6.334	0.0118	—	2	178280271	q31.2
SNP_A-2184478	T	T	289	75	266	104	5.603	1.79E-02	rs1405718	2	178325316	q31.2
SNP_A-2077939	C	C	336	8	354	2	3.865	4.93E-02	rs1565287	2	179561452	q31.2
SNP_A-1955771	C	C	340	34	352	18	5.11	2.38E-02	rs17454527	2	179959524	q31.2
SNP_A-1947624	A	A	291	77	250	100	5.648	1.75E-02	rs17363868	2	180097929	q31.2
SNP_A-1691656	T	T	338	62	367	43	4.508	3.37E-02	rs10497532	2	180137699	q31.2
SNP_A-2209289	C	C	277	117	297	89	4.421	3.55E-02	rs262265	2	180702892	q31.3
SNP_A-2271811	T	T	345	25	384	14	4.174	4.11E-02	rs17793860	2	180805419	q31.3
SNP_A-1872918	C	C	356	8	359	1	5.435	1.97E-02	rs4516385	2	180888180	q31.3
SNP_A-1780301	T	T	319	21	287	35	4.704	3.01E-02	rs16867352	2	181375274	q31.3
SNP_A-1966113	T	T	410	4	414	0	4.019	4.50E-02	rs908735	2	181749391	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1966114	A	A	412	4	420	0	4.058	4.40E-02	rs10497575	2	181772986	q31.3
SNP_A-2196174	A	A	264	96	246	124	4.063	4.38E-02	rs13025711	2	181844967	q31.3
SNP_A-2150700	C	C	297	85	273	111	4.454	3.48E-02	rs6734603	2	181864235	q31.3
SNP_A-1834351	G	G	277	81	252	104	4.035	4.46E-02	rs12052256	2	181873145	q31.3
SNP_A-2224136	C	T	202	190	200	158	4.101	4.29E-02	rs7424879	2	181884034	q31.3
SNP_A-2175572	T	C	206	198	250	162	11.219	8.00E-04	rs4666716	2	181887502	q31.3
SNP_A-1791927	A	A	257	105	227	143	7.596	5.90E-03	rs976384	2	182018257	q31.3
SNP_A-1727184	C	C	280	70	280	104	5.08	2.42E-02	rs4077213	2	182067172	q31.3
SNP_A-1679308	G	G	252	100	224	148	10.393	1.30E-03	rs1371617	2	182323673	q31.3
SNP_A-1737683	G	G	252	122	246	158	4.628	0.0315	rs7557202	2	182408623	q31.3
SNP_A-1966165	G	G	309	83	276	108	5.052	0.0246	rs10497618	2	183695652	q32.1
SNP_A-1707275	A	A	335	63	318	94	6.324	1.19E-02	rs2368351	2	184078757	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2070560	C	C	255	81	276	58	4.63	3.14E-02	rs7561599	2	185023962	q32.1
SNP_A-1879869	T	T	326	0	312	4	4.152	4.16E-02	rs6729481	2	185112717	q32.1
SNP_A-2267523	G	G	282	132	304	102	4.594	3.21E-02	rs1583049	2	185618324	q32.1
SNP_A-1693923	T	T	385	11	379	23	4.238	0.0395	rs10497658	2	185848563	q32.1
SNP_A-2028848	T	G	181	163	206	156	6.411	1.13E-02	rs11687947	2	186032881	q32.1
SNP_A-2082812	G	G	243	155	196	190	8.401	0.0038	rs12477917	2	186041943	q32.1
SNP_A-1885687	A	A	307	65	257	79	3.974	4.62E-02	rs16826724	2	186042192	q32.1
SNP_A-2284959	C	C	281	87	295	61	4.71	3.00E-02	rs6434188	2	187275377	q32.1
SNP_A-2023907	T	T	297	57	294	90	6.214	1.27E-02	rs10931275	2	187861453	q32.1
SNP_A-2290076	G	G	334	60	306	88	6.522	1.07E-02	rs3821183	2	188081664	q32.1
SNP_A-1781560	A	A	329	55	308	88	8.125	4.40E-03	rs3821182	2	188093507	q32.1
SNP_A-1966228	C	C	335	53	300	70	3.853	4.96E-02	rs3821181	2	188094437	q32.1
SNP_A-1891370	G	G	408	4	420	0	4.097	4.29E-02	rs8176481	2	188182195	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1736021	T	T	395	3	399	11	4.414	0.0356	rs4666753	2	189134656	q32.1
SNP_A-2042579	C	C	324	28	350	8	12.064	5.00E-04	rs7419288	2	189776377	q32.2
SNP_A-2289546	G	G	317	67	347	43	6.546	1.05E-02	rs10181597	2	189779733	q32.2
SNP_A-2043045	C	C	319	91	340	68	3.991	4.57E-02	rs17270987	2	189898624	q32.2
SNP_A-2155888	C	C	231	139	276	114	5.942	1.48E-02	rs1878085	2	189898872	q32.2
SNP_A-1966254	C	C	258	148	286	122	3.94	4.72E-02	rs4667272	2	189931971	q32.2
SNP_A-1877300	T	T	257	147	276	116	4.151	4.16E-02	rs10931418	2	190090541	q32.2
SNP_A-2089383	T	T	239	135	269	107	5.006	0.0253	rs11695159	2	190108721	q32.2
SNP_A-1966257	G	G	249	139	284	110	5.63	0.0177	rs13032853	2	190134918	q32.2
SNP_A-2183316	C	C	221	115	262	88	6.789	9.20E-03	rs12613876	2	190178272	q32.2
SNP_A-2042177	G	G	360	46	385	23	8.501	3.60E-03	rs6434347	2	190239799	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027694	T	T	354	50	349	29	4.759	0.0292	rs4667287	2	190257381	q32.2
SNP_A-1922621	C	C	362	0	334	4	4.309	3.79E-02	rs10931429	2	190355924	q32.2
SNP_A-2143703	T	T	310	54	318	34	4.447	3.50E-02	rs3791767	2	190465421	q32.2
SNP_A-1712965	C	C	265	133	295	107	4.404	3.59E-02	rs7419276	2	190521731	q32.2
SNP_A-1751461	A	A	238	156	277	127	5.801	0.016	rs10497703	2	190557898	q32.2
SNP_A-2027985	A	A	225	155	189	187	6.104	0.0135	rs9646748	2	191126874	q32.2
SNP_A-2085214	C	C	282	102	302	76	4.436	3.52E-02	rs4853710	2	191150761	q32.2
SNP_A-1918158	C	C	374	14	391	3	7.45	0.0063	rs4853511	2	191156533	q32.2
SNP_A-2120256	A	A	372	14	390	4	5.899	1.51E-02	rs6707244	2	191199281	q32.2
SNP_A-1910612	G	G	189	185	209	129	9.196	2.40E-03	rs10165399	2	191267101	q32.2
SNP_A-2023267	G	G	372	16	393	5	6.212	1.27E-02	rs16832766	2	191294468	q32.2
SNP_A-1880553	A	A	256	96	242	140	7.383	0.0066	rs13004849	2	191331200	q32.2
SNP_A-2036369	C	C	302	80	311	53	5.182	2.28E-02	rs4599150	2	191343704	q32.2
SNP_A-1780774	G	G	328	50	327	29	4.929	0.0264	rs9678841	2	191387266	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1854509	G	G	305	111	276	144	5.699	1.70E-02	rs10183692	2	191452582	q32.2
SNP_A-2242288	T	T	263	101	248	132	4.223	3.99E-02	rs1013895	2	191494345	q32.2
SNP_A-2057635	G	G	285	85	257	107	3.919	4.78E-02	rs6757660	2	191498796	q32.2
SNP_A-1957269	T	T	303	101	330	74	5.317	2.11E-02	rs7596437	2	191508894	q32.2
SNP_A-2084281	G	G	318	24	347	9	7.805	5.20E-03	rs11691127	2	191584274	q32.2
SNP_A-2146003	T	T	214	172	250	144	5.193	2.27E-02	rs17817966	2	191707769	q32.2
SNP_A-1826477	G	G	265	143	300	114	5.397	2.02E-02	rs16833260	2	191797071	q32.2
SNP_A-2181556	T	T	392	0	381	5	5.111	2.38E-02	rs16833677	2	192104562	q32.3
SNP_A-1904358	T	T	305	87	274	114	5.266	2.17E-02	rs4853628	2	192298968	q32.3
SNP_A-1831962	C	C	277	103	248	138	6.638	0.01	rs4383276	2	192302445	q32.3
SNP_A-2312139	G	G	322	94	282	136	10.314	1.30E-03	rs10201292	2	192313782	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1817162	C	C	275	83	248	114	6.25	0.0124	rs13019574	2	192317512	q32.3
SNP_A-2106862	T	T	383	11	315	27	9.736	0.0018	rs2884024	2	192768472	q32.3
SNP_A-1966310	A	A	245	109	209	143	7.436	6.40E-03	rs10497725	2	192818722	q32.3
SNP_A-1858348	A	A	250	126	223	153	4.154	4.15E-02	rs1601324	2	193162601	q32.3
SNP_A-1913651	C	T	180	174	221	139	10.812	0.001	rs16835140	2	193970877	q32.3
SNP_A-1877265	T	C	195	193	246	152	11.602	7.00E-04	rs16835141	2	193973546	q32.3
SNP_A-2034526	T	C	205	203	257	155	13.264	3.00E-04	rs10166062	2	193994835	q32.3
SNP_A-2091341	-	G	187	187	237	149	10.007	1.60E-03	rs1439223	2	194010592	q32.3
SNP_A-1966329	T	T	275	123	247	153	4.758	0.0292	rs1530155	2	194083000	q32.3
SNP_A-1905579	A	A	282	128	254	156	4.223	3.99E-02	rs1371638	2	194131130	q32.3
SNP_A-1679662	C	C	274	126	254	158	4.187	0.0407	rs2247613	2	194459505	q32.3
SNP_A-1663402	C	C	274	126	252	160	4.786	0.0287	rs2251355	2	194473471	q32.3
SNP_A-1648626	T	T	268	120	246	154	4.979	2.57E-02	rs2357647	2	194477748	q32.3
SNP_A-1709637	C	C	270	122	254	156	4.245	3.94E-02	rs726129	2	194506253	q32.3
SNP_A-1757493	C	C	274	126	255	157	3.902	0.0482	rs726130	2	194506343	q32.3
SNP_A-1832400	C	C	351	41	381	23	6.112	0.0134	rs1919641	2	194513251	q32.3
SNP_A-2162695	T	T	337	39	366	16	10.768	0.001	rs16835330	2	194532062	q32.3
SNP_A-2006927	A	A	335	25	365	11	6.385	0.0115	rs6434634	2	194560154	q32.3
SNP_A-1915718	C	C	368	30	383	17	3.89	4.86E-02	rs16835422	2	194639344	q32.3
SNP_A-2308873	G	G	364	26	368	8	9.299	0.0023	rs16835444	2	194644270	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1737726	G	G	350	50	380	32	5.008	0.0252	rs10497745	2	194881743	q32.3
SNP_A-1950459	A	A	366	32	386	14	7.57	5.90E-03	rs4266033	2	194987956	q32.3
SNP_A-1878237	C	C	402	14	393	27	4.205	4.03E-02	rs1406021	2	195191091	q32.3
SNP_A-2059815	A	A	299	69	312	48	3.958	4.66E-02	rs6735841	2	195302933	q32.3
SNP_A-1912392	A	A	335	63	318	96	6.979	8.20E-03	rs12990870	2	195560082	q32.3
SNP_A-2037973	T	T	345	49	319	69	4.362	3.67E-02	rs4850566	2	195611049	q32.3
SNP_A-2165091	G	G	339	49	325	71	4.247	3.93E-02	rs4850568	2	195611270	q32.3
SNP_A-2184670	T	T	325	27	306	48	6.446	0.0111	rs13030671	2	195637240	q32.3
SNP_A-2256238	G	G	347	55	329	87	7.453	0.0063	rs1430697	2	195676597	q32.3
SNP_A-2151487	A	A	278	50	259	73	4.949	2.61E-02	rs13391145	2	195728980	q32.3
SNP_A-1802552	A	A	318	50	270	64	4	4.55E-02	rs11687841	2	195740382	q32.3
SNP_A-1824050	G	G	391	17	402	6	5.413	0.02	rs7424669	2	195871024	q32.3
SNP_A-1659516	T	T	316	24	308	44	5.779	1.62E-02	rs1073982	2	196038462	q32.3
SNP_A-1915828	T	T	388	14	365	29	5.855	0.0155	rs16840328	2	196099617	q32.3
SNP_A-1653278	A	A	384	6	384	18	5.82	1.58E-02	rs1965394	2	196177066	q32.3
SNP_A-1837812	C	C	365	13	374	4	4.874	2.73E-02	rs7589521	2	196534477	q32.3
SNP_A-2142516	C	C	362	28	344	44	4.009	4.52E-02	rs17366980	2	196845234	q32.3
SNP_A-2063608	T	T	358	0	328	4	4.338	0.0373	rs17300883	2	196902413	q32.3
SNP_A-2122834	A	A	386	10	403	3	4.011	4.52E-02	rs11902313	2	197076759	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1817397	A	A	306	20	323	9	4.578	3.24E-02	rs16859861	2	197649402	q33.1
SNP_A-1794283	C	C	357	15	346	30	5.151	2.32E-02	rs7565685	2	197699069	q33.1
SNP_A-2219623	A	G	200	194	220	168	4.37	3.66E-02	rs12471228	2	198977567	q33.1
SNP_A-1745842	T	T	269	129	245	157	3.842	5.00E-02	rs2880366	2	199168038	q33.1
SNP_A-1738206	C	C	270	126	243	155	4.409	3.58E-02	rs3732231	2	199168800	q33.1
SNP_A-1966426	G	G	379	19	366	34	4.467	3.46E-02	rs4241198	2	199170581	q33.1
SNP_A-1785209	C	C	356	60	336	84	4.559	0.0327	rs12624206	2	199190864	q33.1
SNP_A-1950447	T	T	325	71	283	91	4.746	2.94E-02	rs1996464	2	199393766	q33.1
SNP_A-2273809	G	G	283	129	316	98	6.047	1.39E-02	rs4673212	2	199408166	q33.1
SNP_A-1815163	T	T	267	127	288	96	4.976	2.57E-02	rs4673215	2	199408601	q33.1
SNP_A-2060818	G	G	338	78	308	108	6.232	1.25E-02	rs13013140	2	199409163	q33.1
SNP_A-2092833	A	A	300	72	281	99	4.8	2.85E-02	rs1518079	2	199461566	q33.1
SNP_A-1651186	C	C	342	58	318	88	6.993	8.20E-03	rs1014226	2	199615007	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1707303	T	T	270	106	292	80	4.474	0.0344	rs1518099	2	199779668	q33.1
SNP_A-1723486	T	T	300	66	274	110	11.752	6.00E-04	rs1518081	2	199836311	q33.1
SNP_A-1908618	C	C	332	82	352	50	8.168	0.0043	rs13392032	2	200134999	q33.1
SNP_A-1966457	G	G	258	144	217	169	5.213	0.0224	rs11694792	2	200474574	q33.1
SNP_A-1807959	G	G	350	24	383	9	7.885	5.00E-03	rs769951	2	200557496	q33.1
SNP_A-2221995	C	C	297	23	347	11	6.006	0.0143	rs1704189	2	200588730	q33.1
SNP_A-1966466	G	G	325	49	302	68	3.908	4.81E-02	rs16832223	2	200730666	q33.1
SNP_A-1966467	G	G	347	45	328	64	3.847	4.98E-02	rs12473681	2	200771360	q33.1
SNP_A-2116569	G	G	313	37	298	60	5.732	0.0167	rs16832566	2	200843453	q33.1
SNP_A-1862306	A	A	402	0	400	4	4	4.55E-02	rs12467694	2	200873954	q33.1
SNP_A-1748307	A	A	219	175	266	136	9.366	2.20E-03	rs10497841	2	200904331	q33.1
SNP_A-2242330	G	G	408	4	398	0	3.883	4.88E-02	rs17592192	2	200927581	q33.1
SNP_A-2112910	G	G	293	89	326	68	4.384	3.63E-02	rs4673837	2	200956665	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2089006	T	T	303	107	334	82	4.772	2.89E-02	rs10931895	2	200968748	q33.1
SNP_A-1926092	T	T	214	160	247	127	6.157	1.31E-02	rs17447186	2	201038297	q33.1
SNP_A-2253309	T	T	335	67	301	93	5.963	0.0146	rs7575286	2	201039013	q33.1
SNP_A-2034988	A	A	373	33	346	64	10.902	0.001	rs1550293	2	201051754	q33.1
SNP_A-1966477	G	G	363	7	362	20	6.071	0.0137	rs192680	2	201054396	q33.1
SNP_A-1837611	T	T	378	22	374	42	5.96	0.0146	rs296780	2	201064991	q33.1
SNP_A-1966483	C	C	402	8	377	21	6.453	0.0111	rs1217061	2	201097522	q33.1
SNP_A-1869036	G	G	299	95	272	120	4.179	4.09E-02	rs2348121	2	201436090	q33.1
SNP_A-1966497	C	C	181	153	211	127	4.687	0.0304	rs2348126	2	201443456	q33.1
SNP_A-2110387	G	G	252	58	239	89	6.379	0.0115	rs10185328	2	201458494	q33.1
SNP_A-2286448	T	T	262	146	280	114	4.293	3.83E-02	rs2080320	2	202204679	q33.1
SNP_A-1948009	C	C	367	33	364	52	3.947	0.047	rs2302610	2	202471996	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805393	C	C	195	151	244	114	10.434	1.20E-03	rs6435130	2	202848042	q33.1
SNP_A-2079814	G	G	204	170	252	146	6.135	1.33E-02	rs6435143	2	203019762	q33.1
SNP_A-1856798	G	G	176	150	204	122	4.946	2.62E-02	rs7569317	2	203353485	q33.2
SNP_A-2091524	T	T	302	56	294	32	5.167	0.023	rs4675310	2	203706340	q33.2
SNP_A-2049288	G	G	338	68	350	46	4.331	3.74E-02	rs2351524	2	203706498	q33.2
SNP_A-1844482	A	A	186	166	221	143	4.522	3.35E-02	rs6435197	2	204322842	q33.2
SNP_A-1966530	T	T	370	24	393	11	5.397	2.02E-02	rs4673259	2	204408129	q33.2
SNP_A-1920299	C	C	379	35	398	20	4.536	0.0332	rs231747	2	204513938	q33.2
SNP_A-2137381	C	C	226	160	265	139	4.165	4.13E-02	rs11571292	2	204545645	q33.2
SNP_A-1966540	G	G	258	154	289	129	3.922	4.77E-02	rs231726	2	204566372	q33.2
SNP_A-1728449	A	A	376	24	401	11	5.457	0.0195	rs4675360	2	204786999	q33.2
SNP_A-1781825	G	G	238	160	204	198	6.629	0.01	rs726833	2	204971271	q33.3
SNP_A-1833233	C	C	385	31	366	54	6.685	9.70E-03	---	2	205007151	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814575	G	G	201	139	229	113	4.5	0.0339	rs12373801	2	205174230	q33.3
SNP_A-1898829	T	T	322	0	310	4	4.128	4.22E-02	rs16836329	2	205237398	q33.3
SNP_A-1966571	T	T	365	47	347	67	3.959	4.66E-02	rs10490278	2	205653170	q33.3
SNP_A-2205144	T	T	336	34	305	51	4.631	3.14E-02	rs2335704	2	205690338	q33.3
SNP_A-1966575	A	A	351	19	327	33	4.483	3.42E-02	rs6754606	2	205749783	q33.3
SNP_A-1914368	A	A	253	159	225	195	5.225	0.0223	rs4675490	2	205768066	q33.3
SNP_A-2257942	G	G	369	45	344	68	5.553	0.0184	rs11904275	2	205902480	q33.3
SNP_A-1708096	T	T	364	34	352	54	4.667	3.07E-02	rs10497880	2	206083795	q33.3
SNP_A-2032101	G	G	222	150	244	116	5.189	2.27E-02	---	2	206244524	q33.3
SNP_A-2172047	A	A	342	64	319	89	4.88	2.72E-02	rs849565	2	206435557	q33.3
SNP_A-1841101	G	G	304	70	331	51	4.047	4.42E-02	rs13394153	2	206613951	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1966603	A	A	252	72	223	97	5.444	1.96E-02	rs10497882	2	207058621	q33.3
SNP_A-2300290	A	A	284	80	325	57	6.191	1.28E-02	rs2269183	2	207180860	q33.3
SNP_A-2078241	G	G	303	79	345	51	8.504	3.50E-03	rs3821172	2	207290470	q33.3
SNP_A-2121775	T	C	201	161	188	170	4.657	0.0309	rs1991537	2	207298079	q33.3
SNP_A-1966607	A	A	289	59	332	30	12.156	5.00E-04	rs10186957	2	207312395	q33.3
SNP_A-1899298	T	T	319	93	292	122	5.1	2.39E-02	rs10186535	2	207343690	q33.3
SNP_A-2267284	T	T	283	107	308	80	4.951	2.61E-02	rs16838626	2	207395221	q33.3
SNP_A-2310490	T	T	390	26	410	8	10.025	0.0015	rs16838677	2	207407341	q33.3
SNP_A-2278044	A	A	311	69	325	45	5.228	2.22E-02	rs3815686	2	207458508	q33.3
SNP_A-1870081	C	C	309	63	340	42	5.549	1.85E-02	rs7576591	2	207474732	q33.3
SNP_A-2187702	C	C	324	72	349	49	5.296	2.14E-02	rs2287629	2	207475920	q33.3
SNP_A-2282148	G	G	328	58	342	34	6.423	1.13E-02	rs13400622	2	207511410	q33.3
SNP_A-2174029	T	T	315	101	287	129	4.711	3.00E-02	rs4675643	2	207626414	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2252192	A	C	223	161	193	189	5.693	1.70E-02	rs8732962	2	207955424	q33.3
SNP_A-2254599	G	G	252	106	230	134	4.221	3.99E-02	rs12995614	2	207979544	q33.3
SNP_A-1756240	G	G	340	32	336	16	4.808	2.83E-02	rs1990810	2	208100420	q33.3
SNP_A-1791076	C	C	354	46	354	28	3.966	4.64E-02	rs10172070	2	208133267	q33.3
SNP_A-1642081	C	C	280	120	261	151	4.037	4.45E-02	rs3791995	2	208212896	q33.3
SNP_A-2301718	G	G	315	69	344	50	4.182	4.09E-02	rs12475932	2	208955798	q34
SNP_A-2226783	T	T	352	56	385	29	10.011	1.60E-03	rs12991283	2	209053053	q34
SNP_A-1966667	G	G	393	13	409	3	6.526	0.0106	rs13014969	2	209073927	q34
SNP_A-1801890	A	A	348	54	383	29	9.084	2.60E-03	rs11897777	2	209089692	q34
SNP_A-2081326	A	A	319	59	338	40	4.196	4.05E-02	rs4462735	2	209100305	q34
SNP_A-1966668	C	C	248	142	221	181	6.083	1.36E-02	rs10497900	2	209122449	q34
SNP_A-2226345	G	G	368	36	387	15	9.12	2.50E-03	rs1437413	2	209132299	q34
SNP_A-2030429	A	A	302	20	307	9	4.157	4.15E-02	rs16841224	2	209140704	q34
SNP_A-1859999	T	T	238	146	261	117	4.211	0.0402	rs3769517	2	209153210	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1966670	A	A	362	28	372	14	4.782	2.88E-02	rs1259699	2	209164264	q34
SNP_A-1814319	G	G	338	18	358	8	4.283	0.0385	rs1869535	2	209222055	q34
SNP_A-1947228	A	A	360	30	384	16	4.909	2.67E-02	rs7595880	2	209222752	q34
SNP_A-2160700	G	G	360	44	382	28	4.164	4.13E-02	rs13018313	2	209298057	q34
SNP_A-1810858	T	T	287	59	259	93	8.99	2.70E-03	rs1517347	2	209339421	q34
SNP_A-1648284	A	A	336	64	368	44	4.982	2.56E-02	rs10497897	2	209369373	q34
SNP_A-1654685	C	C	356	40	388	24	5.061	2.45E-02	rs7564720	2	209525093	q34
SNP_A-1754800	G	G	387	13	408	4	5.143	2.33E-02	rs10497908	2	209710834	q34
SNP_A-1799295	G	A	201	187	218	176	3.985	4.59E-02	rs17677155	2	209891289	q34
SNP_A-1869272	C	C	230	114	252	88	4.327	3.75E-02	rs2166513	2	209944288	q34
SNP_A-2233577	A	A	330	20	359	3	13.587	2.00E-04	rs2084208	2	209996787	q34
SNP_A-2302987	G	G	363	27	368	12	5.675	0.0172	rs11688922	2	210724538	q34
SNP_A-2261523	G	G	297	47	311	29	4.562	0.0327	rs16844839	2	211406751	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2060333	G	G	295	55	311	35	4.844	2.77E-02	rs16845514	2	211880153	q34
SNP_A-1703227	G	G	299	71	329	47	6.267	0.0123	rs10497940	2	212179870	q34
SNP_A-2197248	A	A	328	46	330	24	6.376	1.16E-02	rs6740215	2	212422893	q34
SNP_A-2179257	G	G	389	7	396	0	7.062	7.90E-03	rs16847491	2	212705977	q34
SNP_A-1720445	C	C	385	15	406	6	4.238	0.0395	rs1402708	2	213034976	q34
SNP_A-1703471	A	A	386	12	394	4	4.082	4.33E-02	rs7579746	2	213219514	q34
SNP_A-2288964	C	C	285	73	274	100	4.083	4.33E-02	rs7599312	2	213238737	q34
SNP_A-1851212	C	C	386	20	365	37	5.638	1.76E-02	rs16848939	2	213307891	q34
SNP_A-2033482	C	C	326	22	268	34	5.004	0.0253	rs6749215	2	213308499	q34
SNP_A-2230181	G	A	231	183	212	196	4.954	2.60E-02	rs900369	2	213601855	q34
SNP_A-2059718	C	C	332	66	364	44	5.748	1.65E-02	rs4672672	2	213772137	q34
SNP_A-1966798	A	A	334	62	348	42	4.088	4.32E-02	rs965000	2	213784261	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2110254	C	C	337	39	362	20	6.966	8.30E-03	rs7579484	2	213803419	q34
SNP_A-1966802	G	G	390	24	403	11	5.042	0.0247	rs17364234	2	213980833	q34
SNP_A-2272155	C	C	224	116	273	89	7.705	5.50E-03	rs10932481	2	214105556	q34
SNP_A-1966807	C	C	234	120	274	94	6.039	0.014	rs10498006	2	214170589	q34
SNP_A-2116323	C	C	226	130	267	97	8.119	4.40E-03	rs7560229	2	214274149	q34
SNP_A-1914688	C	C	243	167	295	125	10.948	9.00E-04	rs6435780	2	214338653	q34
SNP_A-2180792	T	T	200	138	232	96	9.761	0.0018	rs10804215	2	214342475	q34
SNP_A-2098266	G	G	226	136	270	100	9.308	0.0023	rs2013922	2	214357229	q34
SNP_A-2279595	T	T	240	170	288	126	10.885	0.001	rs10176906	2	214401395	q34
SNP_A-2099001	A	A	234	150	266	102	10.855	0.001	rs10165804	2	214401430	q34
SNP_A-2069107	C	C	262	130	237	161	4.51	3.37E-02	rs11893486	2	214497797	q34
SNP_A-2198277	G	G	273	135	242	168	5.455	0.0195	rs4503943	2	214540481	q34
SNP_A-2056068	A	A	198	116	204	168	4.741	2.95E-02	rs10179905	2	214551745	q34
SNP_A-1942809	T	T	247	113	281	93	3.866	4.93E-02	rs12471502	2	214575499	q34
SNP_A-2050296	G	G	254	112	278	88	3.963	0.0465	rs10191167	2	214582006	q34
SNP_A-1966812	A	A	271	141	303	113	4.851	0.0276	rs2042784	2	214589823	q34
SNP_A-1794851	G	G	272	132	299	105	4.353	3.70E-02	rs6718488	2	214595159	q34
SNP_A-2272886	T	T	272	144	304	114	5.261	0.0218	rs4672695	2	214614434	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2025452	A	T	233	163	207	205	6.708	9.60E-03	rs11678221	2	214629199	q34
SNP_A-1703617	G	G	253	147	296	112	8.019	4.60E-03	rs4132244	2	214759069	q34
SNP_A-2297213	C	C	291	77	310	56	3.911	4.80E-02	rs13007666	2	214902886	q34
SNP_A-1966823	A	A	237	109	271	87	4.542	3.31E-02	rs1549116	2	214935096	q34
SNP_A-1949788	C	C	323	65	347	39	7.355	6.70E-03	rs7425848	2	215284139	q35
SNP_A-2006998	A	A	313	81	338	60	4.068	4.37E-02	rs4430957	2	215294500	q35
SNP_A-1966828	C	C	328	76	351	51	5.695	1.70E-02	rs5018475	2	215297456	q35
SNP_A-2175331	C	C	330	78	353	57	4.036	4.45E-02	rs7566300	2	215301873	q35
SNP_A-2187923	T	T	328	74	340	46	6.427	0.0112	rs10932551	2	215302437	q35
SNP_A-1966831	A	A	287	63	301	41	4.895	0.0269	rs13009193	2	215309160	q35
SNP_A-1815330	C	C	305	71	321	47	5.205	2.25E-02	rs5019643	2	215319147	q35
SNP_A-2279710	G	G	326	72	342	44	6.96	8.30E-03	rs7574717	2	215321797	q35
SNP_A-1687698	G	G	248	148	287	117	6.39	0.0115	rs10490503	2	215348307	q34
SNP_A-1966849	C	C	228	134	199	173	6.789	9.20E-03	rs10498027	2	215645519	q35

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1961084	A	A	355	33	366	16	6.019	0.0141	rs10198064	2	215701877	q35
SNP_A-1880269	A	A	346	62	311	87	5.936	1.48E-02	rs1967603	2	215725593	q35
SNP_A-1730747	C	C	365	35	391	21	4.218	4.00E-02	rs952718	2	216091166	q35
SNP_A-1645712	G	G	392	4	410	0	4.162	4.13E-02	rs1464680	2	216110642	q35
SNP_A-2248272	T	T	245	103	253	75	3.945	0.047	rs1250224	2	216150780	q35
SNP_A-2242459	C	C	232	184	268	150	6.048	1.39E-02	rs13384892	2	216188896	q35
SNP_A-1966855	T	T	395	13	380	26	4.619	3.16E-02	rs7597684	2	216208018	q35
SNP_A-2007004	T	T	324	50	334	32	4.017	4.50E-02	rs2037516	2	216465012	q35
SNP_A-2179890	G	G	247	137	276	106	5.558	0.0184	rs10804244	2	216521822	q35
SNP_A-1752331	G	G	383	13	379	29	5.938	1.48E-02	rs7583379	2	216584779	q35
SNP_A-1933868	T	T	327	69	354	50	4.025	0.0448	rs3770542	2	216672657	q35
SNP_A-2031280	A	A	378	26	373	13	3.959	4.66E-02	rs6747159	2	216697036	q35
SNP_A-1966875	T	T	279	91	264	122	4.59	3.22E-02	rs2372682	2	216700079	q35

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1700849	T	T	360	4	408	0	4.507	3.38E-02	-	2	217073034	q35
SNP_A-2151011	T	T	327	41	293	65	7.162	7.40E-03	rs11892361	2	217114461	q35
SNP_A-2063398	G	G	325	35	336	18	5.586	1.81E-02	rs17558615	2	217138344	q35
SNP_A-2309102	A	A	382	4	402	0	4.187	0.0407	rs6753128	2	217267162	q35
SNP_A-1966904	C	C	318	14	324	28	4.141	4.18E-02	rs715051	2	217482869	q35
SNP_A-1885013	A	G	209	141	181	175	7.929	4.90E-03	rs1014680	2	217498330	q35
SNP_A-1892381	A	A	363	23	352	40	4.711	3.00E-02	rs3922271	2	217507153	q35
SNP_A-1966917	A	A	358	16	395	7	4.335	0.0373	rs1882423	2	217675015	q35
SNP_A-2259457	A	A	399	17	411	7	4.34	3.72E-02	rs2141817	2	217680594	q35
SNP_A-2118781	A	A	336	60	361	39	5.331	2.09E-02	rs6435981	2	218083149	q35
SNP_A-1860491	C	C	322	32	355	19	4.376	3.64E-02	rs1478573	2	218085251	q35

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2240203	G	G	334	52	356	34	4.448	0.0349	rs16857490	2	218092766	q35
SNP_A-1755248	G	G	345	47	366	30	4.353	3.69E-02	rs10490759	2	218342677	q35
SNP_A-1873878	C	C	380	18	398	8	4.183	4.08E-02	rs2671222	2	218858108	q35
SNP_A-2265298	G	G	279	81	311	57	5.822	1.58E-02	rs4674297	2	219054652	q35
SNP_A-1788623	G	G	410	6	420	0	6.101	0.0135	rs7576974	2	219073295	q35
SNP_A-2045764	A	A	320	0	307	7	7.213	7.20E-03	rs1465535	2	219387219	q35
SNP_A-2115171	C	C	346	70	372	46	5.902	1.51E-02	rs6754599	2	219557647	q35
SNP_A-2184087	G	G	413	1	411	7	4.486	3.42E-02	rs12477394	2	220225519	q35
SNP_A-1966981	T	T	238	128	198	146	4.175	4.10E-02	rs715347	2	220649298	q35
SNP_A-2181453	A	A	291	125	258	160	6.277	1.22E-02	rs12618287	2	220652110	q35
SNP_A-2007026	T	T	302	114	329	89	4.229	3.97E-02	rs2971628	2	220734984	q35
SNP_A-1844026	G	G	363	21	371	9	4.866	2.74E-02	rs17610391	2	220956003	q35
SNP_A-2258579	A	A	268	102	296	72	6.557	0.0104	rs4362549	2	221138081	q35

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1966998	T	T	306	36	327	21	4.592	3.21E-02	rs10498084	2	221209862	q35
SNP_A-2294590	T	T	374	34	381	19	4.231	3.97E-02	rs11892630	2	221212423	q35
SNP_A-2138735	A	A	378	36	399	21	4.472	3.45E-02	rs10207037	2	221218883	q35
SNP_A-1831421	A	A	341	33	359	17	5.578	1.82E-02	rs13424721	2	221242200	q35
SNP_A-2069764	C	C	379	33	398	18	4.857	0.0275	rs10048783	2	221244278	q35
SNP_A-2030231	G	G	300	50	344	32	6.034	0.014	rs13414015	2	221248210	q35
SNP_A-1900813	C	C	270	64	278	40	5.266	2.17E-02	rs1712236	2	221270723	q35
SNP_A-2160132	T	T	370	44	387	27	4.452	0.0349	rs10932875	2	221308148	q35
SNP_A-1897595	A	A	347	31	355	51	3.974	4.62E-02	rs16861557	2	221316629	q35
SNP_A-2066348	T	T	401	7	409	1	4.574	3.25E-02	rs12694542	2	221432338	q36.1
SNP_A-2250175	G	G	388	2	383	11	6.243	1.25E-02	rs16861747	2	221468745	q36.1
SNP_A-1748705	G	G	317	81	357	53	8.048	4.60E-03	rs1568178	2	221644578	q35
SNP_A-1835692	G	G	302	46	297	25	5.252	2.19E-02	rs11694780	2	221677221	q36.1
SNP_A-2215731	C	C	320	82	346	60	4.404	3.59E-02	rs9808155	2	221753357	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1866446	T	T	304	6	306	26	11.766	6.00E-04	rs3770177	2	222142996	q36.1
SNP_A-1804972	C	C	358	12	337	25	5.115	2.37E-02	rs13030635	2	222349947	q36.1
SNP_A-1954912	C	C	287	111	302	76	6.422	1.13E-02	rs7580262	2	222520851	q36.1
SNP_A-2088722	C	C	385	25	373	41	4.049	4.42E-02	rs4099419	2	222565084	q36.1
SNP_A-1831851	A	A	330	4	323	13	4.834	2.79E-02	rs11902772	2	222720941	q36.1
SNP_A-2265658	T	T	233	175	205	203	3.864	4.93E-02	rs6436291	2	222741922	q36.1
SNP_A-2290506	C	C	369	5	346	14	4.738	2.95E-02	rs16863332	2	222742758	q36.1
SNP_A-1960637	G	G	375	39	355	59	4.63	3.14E-02	rs12989756	2	222812626	q36.1
SNP_A-1967064	G	G	362	40	336	62	5.694	1.70E-02	rs7568291	2	222819166	q36.1
SNP_A-2033547	T	T	375	23	351	43	6.834	8.90E-03	rs7585448	2	222835846	q36.1
SNP_A-2111105	A	A	340	44	290	68	8.21	4.20E-03	rs2395847	2	222861928	q36.1
SNP_A-1967073	G	G	229	175	264	138	6.854	8.80E-03	rs17563513	2	223199761	q36.1
SNP_A-2314109	A	G	186	172	215	167	5.027	2.50E-02	rs6740937	2	223210020	q36.1
SNP_A-2229300	C	C	214	170	267	131	10.646	1.10E-03	rs1436788	2	223236998	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2270243	C	C	224	182	269	139	9.863	1.70E-03	rs5016700	2	223248225	q36.1
SNP_A-2251422	T	T	229	115	204	154	6.821	9.00E-03	rs13388047	2	223260578	q36.1
SNP_A-1801529	G	G	277	125	246	162	6.563	0.0104	rs17564655	2	223261156	q36.1
SNP_A-1836599	A	A	252	164	288	132	5.84	1.57E-02	rs13009608	2	223265446	q36.1
SNP_A-2209814	C	C	249	161	284	128	6.062	0.0138	rs16863916	2	223282698	q36.1
SNP_A-2283199	T	T	251	159	272	118	6.416	1.13E-02	rs874364	2	223300252	q36.1
SNP_A-2027278	C	C	217	135	266	96	11.418	7.00E-04	rs2121566	2	223312727	q36.1
SNP_A-2291377	A	A	294	122	253	157	7.421	6.40E-03	rs12151627	2	223317427	q36.1
SNP_A-1841146	G	G	214	102	271	89	4.74	2.95E-02	rs868392	2	223342764	q36.1
SNP_A-1859479	A	A	177	167	209	139	5.192	2.27E-02	rs6749903	2	223479491	q36.1
SNP_A-2170160	C	A	208	204	243	173	6.599	1.02E-02	rs11686397	2	223481519	q36.1
SNP_A-2039260	C	C	356	22	331	37	4.59	3.22E-02	rs10182865	2	223482925	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2039900	A	A	401	11	401	3	4.493	3.40E-02	rs16864189	2	223498229	q36.1
SNP_A-1821382	C	C	346	26	368	12	5.751	1.65E-02	rs13429507	2	224236767	q36.1
SNP_A-2075038	A	A	374	20	389	9	4.447	3.50E-02	rs627016	2	224557630	q36.1
SNP_A-2104957	C	C	404	8	415	1	5.573	1.82E-02	rs16865284	2	224562619	q36.1
SNP_A-1967107	C	C	398	10	416	2	5.611	0.0178	rs10498155	2	224566905	q36.1
SNP_A-2063013	A	A	305	107	345	75	8.012	4.60E-03	rs10171599	2	224592077	q36.1
SNP_A-2198600	A	A	368	46	395	25	7.124	0.0076	rs860839	2	224600941	q36.1
SNP_A-1824375	G	G	370	46	393	25	6.9	0.0086	rs858694	2	224601269	q36.1
SNP_A-2104470	C	T	236	176	209	207	4.708	3.00E-02	rs6734908	2	224639691	q36.1
SNP_A-2198694	A	G	180	156	186	154	4.632	3.14E-02	rs7597833	2	224667655	q36.1
SNP_A-1967111	C	C	282	48	319	33	4.35	3.70E-02	rs6748795	2	224676228	q36.1
SNP_A-1855338	G	G	323	93	349	67	5.231	2.22E-02	rs12479146	2	224686445	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1912690	G	G	297	69	330	48	5.314	0.0212	rs13392268	2	224689690	q36.1
SNP_A-2046493	C	C	292	50	329	35	4.17	4.11E-02	rs13392374	2	224689761	q36.1
SNP_A-2007047	C	C	372	4	360	0	3.851	4.97E-02	rs4674846	2	224710283	q36.1
SNP_A-2250270	G	G	412	4	420	0	4.058	4.40E-02	rs1866151	2	224715891	q36.1
SNP_A-2232474	C	C	398	4	414	0	4.14	0.0419	rs282272	2	224748195	q36.1
SNP_A-2023995	A	A	406	6	412	0	6.044	0.014	rs282274	2	224751816	q36.1
SNP_A-1967120	A	A	319	33	327	15	6.706	9.60E-03	rs16865548	2	224772758	q36.1
SNP_A-2139215	G	G	293	51	299	77	3.928	4.75E-02	rs2396056	2	224794432	q36.1
SNP_A-1824438	A	A	385	27	391	13	4.868	2.74E-02	rs16865681	2	224910078	q36.1
SNP_A-1726634	G	G	388	12	409	3	5.777	1.62E-02	rs10498156	2	224944181	q36.1
SNP_A-1677994	T	T	355	41	388	24	5.597	1.80E-02	rs717610	2	224997277	q36.1
SNP_A-2259198	A	A	287	59	283	85	4.048	4.42E-02	rs918289	2	225052080	q36.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1799259	G	G	211	117	226	84	5.429	1.98E-02	rs7569781	2	225657091	q36.2
SNP_A-1827984	A	A	266	50	241	73	5.527	1.87E-02	rs1947223	2	225771562	q36.2
SNP_A-1967168	C	C	182	152	206	110	7.725	5.40E-03	rs7608276	2	225848408	q36.2
SNP_A-2027962	G	G	232	144	189	159	4.058	4.40E-02	rs753161	2	225852953	q36.2
SNP_A-1815795	A	A	251	131	211	155	5.137	2.34E-02	rs1443668	2	225857931	q36.2
SNP_A-1839821	T	T	265	113	237	143	5.072	2.43E-02	rs1443667	2	225858060	q36.2
SNP_A-1967169	G	G	277	127	240	150	4.312	0.0378	rs1596395	2	225861458	q36.2
SNP_A-2201109	C	C	211	197	244	162	5.801	0.016	rs12621630	2	225866610	q36.2
SNP_A-2283105	T	T	227	123	182	152	7.639	5.70E-03	rs1470327	2	225877503	q36.2
SNP_A-1810964	C	C	223	183	257	151	5.469	1.94E-02	rs7591717	2	225887923	q36.2
SNP_A-1734468	C	C	287	101	257	133	6.025	0.0141	rs7598761	2	226129961	q36.2
SNP_A-1861073	T	C	211	173	194	164	6.189	0.0129	rs10933097	2	226220685	q36.3
SNP_A-2087902	G	G	414	2	411	9	4.446	3.50E-02	rs6745318	2	226888184	q36.3
SNP_A-2263512	G	G	416	0	411	7	7.025	8.00E-03	rs6436607	2	226976415	q36.3
SNP_A-2123330	C	C	237	161	257	121	5.972	1.45E-02	rs10933137	2	227010136	q36.3
SNP_A-1967219	T	T	330	40	354	24	4.757	0.0292	rs2178701	2	227383000	q36.3
SNP_A-2045224	G	G	357	51	331	75	5.549	1.85E-02	rs4675160	2	227941823	q36.3
SNP_A-1908354	C	C	338	34	312	52	4.721	0.0298	rs6715914	2	227942893	q36.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1958004	C	C	309	21	299	45	8.605	3.40E-03	rs6729294	2	227942971	q36.3
SNP_A-2007068	T	T	375	1	370	8	5.473	1.93E-02	rs6436676	2	227986671	q36.3
SNP_A-2022253	G	G	314	74	274	104	7.648	5.70E-03	rs10208046	2	228428082	q36.3
SNP_A-1864592	G	G	235	161	209	195	4.69	3.03E-02	rs7562781	2	228434616	q36.3
SNP_A-1967243	T	T	256	122	275	89	5.579	1.82E-02	---	2	228517629	q36.3
SNP_A-1949357	C	C	362	44	342	68	5.692	1.70E-02	rs17197476	2	228598651	q36.3
SNP_A-1784598	G	G	252	76	201	105	9.636	0.0019	rs11690643	2	228617986	q36.3
SNP_A-1944985	C	C	370	28	396	14	5.372	2.05E-02	rs16824237	2	228622959	q36.3
SNP_A-2051082	A	A	379	27	384	14	4.076	4.35E-02	rs12619223	2	228653058	q36.3
SNP_A-2155664	A	A	273	117	291	89	4.251	3.92E-02	rs16825347	2	229443689	q36.3
SNP_A-1871348	G	G	252	104	271	77	4.628	0.0315	rs2103259	2	229509017	q36.3
SNP_A-2104191	T	T	180	170	218	152	4.082	4.33E-02	rs13419855	2	229727984	q36.3
SNP_A-1967277	G	G	373	35	376	18	5.222	0.0223	rs17614031	2	229803370	q36.3
SNP_A-2148753	T	T	245	99	251	71	3.962	0.0465	rs2396615	2	229846671	q36.3
SNP_A-2151486	G	A	204	178	196	166	4.234	3.96E-02	rs10933281	2	229919942	q36.3
SNP_A-2123700	C	C	361	53	344	76	4.468	3.45E-02	rs7609541	2	230178335	q36.3
SNP_A-1735092	C	C	306	48	316	74	3.969	4.63E-02	rs6436840	2	230181559	q36.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1837599	A	A	319	13	288	24	4.236	3.96E-02	rs17765502	2	231624658	q37.1
SNP_A-2245940	C	C	228	128	271	109	4.451	0.0349	rs11674265	2	231687206	q37.1
SNP_A-2042821	C	C	411	5	418	0	5.054	0.0246	rs16827933	2	232015972	q37.1
SNP_A-1819182	C	C	219	193	247	155	5.71	1.69E-02	rs10204481	2	232325637	q37.1
SNP_A-1866624	G	G	281	125	312	98	4.87	2.73E-02	rs3098610	2	232543547	q37.1
SNP_A-1943548	A	A	272	44	267	67	4.317	3.77E-02	rs1190442	2	233247710	q37.1
SNP_A-1967339	C	T	194	158	185	159	5.504	0.019	rs1550098	2	233253747	q37.1
SNP_A-2073767	A	A	280	128	246	152	4.131	4.21E-02	rs7585327	2	233266457	q37.1
SNP_A-2049507	G	G	246	154	305	107	14.607	0.0001	rs17296210	2	233272073	q37.1
SNP_A-1808910	G	G	390	18	408	8	4.175	4.10E-02	rs9752615	2	233794948	q37.1
SNP_A-2120724	G	G	339	53	371	35	4.88	2.72E-02	rs4233633	2	234401937	q37.1
SNP_A-1967366	G	G	379	1	359	7	4.781	2.88E-02	rs2108807	2	234589661	q37.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227846	G	G	302	48	287	71	4.738	2.95E-02	rs6711120	2	234627134	q37.1
SNP_A-1967368	G	G	363	29	335	47	5.258	0.0218	rs7577157	2	234630903	q37.1
SNP_A-2268731	C	C	356	40	332	62	5.577	1.82E-02	rs11563201	2	234705954	q37.1
SNP_A-2296498	C	C	366	50	340	78	7.078	7.80E-03	rs11563199	2	234707521	q37.1
SNP_A-2103352	T	T	258	140	292	114	4.684	0.0304	rs7557035	2	234761872	q37.1
SNP_A-1881009	G	G	344	50	322	70	4.055	4.40E-02	rs250959	2	234774833	q37.1
SNP_A-1860902	T	T	369	43	346	72	8.01	4.70E-03	rs7586559	2	235488615	q37.2
SNP_A-2063417	A	A	257	73	241	105	5.891	0.0152	rs10929060	2	235515155	q37.2
SNP_A-1800856	C	C	338	16	330	36	7.59	5.90E-03	rs1863815	2	235561262	q37.2
SNP_A-1738687	C	C	283	53	359	37	6.97	8.30E-03	rs1880746	2	235743434	q37.1
SNP_A-2304974	C	C	306	40	257	61	7.464	0.0063	rs11684611	2	235766919	q37.2
SNP_A-1841494	-	G	171	171	224	158	5.432	1.98E-02	rs4581844	2	235769035	q37.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2007121	C	C	325	69	305	95	4.712	3.00E-02	rs1991704	2	235911029	q37.2
SNP_A-2141825	G	G	270	98	252	126	3.987	0.0458	rs10173166	2	235925651	q37.2
SNP_A-1893867	G	G	318	90	294	122	5.694	1.70E-02	rs9989782	2	235927150	q37.2
SNP_A-2213718	C	C	319	81	274	98	4.019	4.50E-02	rs12692162	2	235927803	q37.2
SNP_A-2166328	G	A	199	169	191	163	4.655	0.031	rs2043194	2	235962672	q37.2
SNP_A-2029631	G	G	351	43	339	63	3.902	0.0482	rs1897331	2	235970582	q37.2
SNP_A-1920911	C	C	398	10	385	27	8.007	4.70E-03	rs6712139	2	236039346	q37.2
SNP_A-1898421	G	G	264	104	223	141	9.018	2.70E-03	rs12692166	2	236040449	q37.2
SNP_A-1942947	T	T	268	136	303	107	5.562	0.0184	rs13428584	2	236047539	q37.2
SNP_A-1792569	C	C	260	106	295	85	4.255	3.91E-02	rs12478435	2	236519133	q37.2
SNP_A-1893427	G	G	370	46	395	25	7.009	8.10E-03	rs3768953	2	236734594	q37.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2071974	G	G	297	11	323	3	5.155	2.32E-02	rs4414633	2	237227129	q37.3
SNP_A-2292905	A	A	319	15	300	28	4.459	3.47E-02	rs13412209	2	237228884	q37.3
SNP_A-1902978	G	A	220	166	192	190	4.063	4.38E-02	rs2720157	2	237394848	q37.3
SNP_A-1967391	G	G	307	37	295	59	5.139	2.34E-02	rs2568569	2	237578392	q37.3
SNP_A-1799618	C	C	189	181	218	140	7.107	7.70E-03	rs12692194	2	237579389	q37.3
SNP_A-2271476	A	C	202	168	197	177	3.932	4.74E-02	rs10192099	2	237585300	q37.3
SNP_A-1942788	T	T	278	116	257	147	4.354	3.69E-02	rs7576705	2	237729288	q37.3
SNP_A-1688398	A	A	278	48	294	90	8.549	3.50E-03	rs1368208	2	238035145	q37.3
SNP_A-1967397	C	C	361	5	355	21	9.763	0.0018	rs2325838	2	238168515	q37.3
SNP_A-1789600	C	C	295	17	298	34	5.066	2.44E-02	rs4144851	2	238832356	q37.3
SNP_A-1642069	T	T	276	8	380	2	5.793	0.0161	rs3754728	2	238885571	q37.3
SNP_A-2132231	A	A	365	11	376	2	6.389	0.0115	rs11891894	2	238908258	q37.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1786588	T	T	384	22	359	43	7.606	5.80E-03	rs4663865	2	238927960	q37.3
SNP_A-1929971	G	G	377	17	366	36	6.894	0.0086	rs2304672	2	238968589	q37.3
SNP_A-2194848	T	T	391	25	401	13	3.911	4.80E-02	rs10205543	2	239025117	q37.3
SNP_A-1781719	T	C	202	186	209	163	5.172	0.023	rs13430969	2	239267732	q37.3
SNP_A-1804439	T	T	261	123	294	94	5.817	1.59E-02	rs2334026	2	239319238	q37.3
SNP_A-2047571	C	-	211	139	168	168	7.335	6.80E-03	rs6431623	2	239456876	q37.3
SNP_A-2294252	G	G	326	28	306	8	9.382	2.20E-03	rs4241228	2	239601719	q37.3
SNP_A-2270560	G	G	190	118	243	93	8.248	4.10E-03	rs10195501	2	239923581	q37.3
SNP_A-2181359	C	C	290	28	320	14	5.753	1.65E-02	rs7568886	2	240188421	q37.3
SNP_A-1967413	C	C	241	113	262	84	5.055	0.0246	rs920247	2	240354864	q37.3
SNP_A-2086976	C	C	253	137	225	165	4.236	3.96E-02	rs2412033	2	240447395	q37.3
SNP_A-1831950	G	G	336	40	375	25	4.863	2.74E-02	rs12712298	2	240468894	q37.3
SNP_A-2270273	G	G	363	25	382	12	5.006	0.0253	rs6761699	2	240473102	q37.3
SNP_A-1746364	T	T	334	66	316	92	4.688	3.02E-02	rs709274	2	240543975	q37.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829287	A	A	284	98	286	64	5.755	1.64E-02	rs3792085	2	240668779	q37.3
SNP_A-2175016	T	T	283	127	249	161	6.187	0.0129	rs10933552	2	240691509	q37.3
SNP_A-2007166	A	A	369	11	355	25	5.715	1.68E-02	rs4853996	2	240829737	q37.3
SNP_A-2218959	C	C	338	62	348	42	3.866	4.93E-02	rs12695014	2	240952744	q37.3
SNP_A-2148399	A	A	372	38	391	23	4.142	4.18E-02	rs7607116	2	240959367	q37.3
SNP_A-2212691	T	C	215	179	215	193	4.233	3.97E-02	rs2975788	2	241291848	q37.3
SNP_A-2236223	C	C	304	24	322	12	4.464	3.46E-02	rs4676399	2	241308038	q37.3
SNP_A-1821519	T	T	264	118	233	155	6.902	0.0086	rs1583259	2	241364924	q37.3
SNP_A-2244434	A	A	236	166	208	198	4.559	0.0327	rs6706171	2	241605191	q37.3
SNP_A-2304225	A	A	294	66	342	38	10.628	1.10E-03	rs2286321	2	241724856	q37.3
SNP_A-1850337	C	C	317	53	335	33	5.143	2.33E-02	rs2240538	2	241755136	q37.3
SNP_A-1967416	C	C	264	110	232	140	5.659	1.74E-02	rs14704l3	2	241797675	q37.3
SNP_A-1791178	C	C	278	96	319	73	5.526	1.87E-02	rs16843440	2	241858055	q37.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2304299	T	T	318	60	306	84	4.044	4.43E-02	rs935262	2	241873661	q37.3
SNP_A-2305408	T	T	320	78	286	98	3.931	4.74E-02	rs895121	2	241911970	q37.3
SNP_A-2301799	G	G	301	111	331	87	4.29	3.83E-02	rs10188318	2	242004635	q37.3
SNP_A-1944557	T	T	282	108	297	81	4.059	4.39E-02	rs11684105	2	242030164	q37.3
SNP_A-1648538	A	A	376	24	367	43	5.374	2.04E-02	rs4129624	2	242124818	q37.3
SNP_A-1916461	A	A	327	85	354	64	3.987	4.59E-02	rs12468297	2	242712226	q37.3
SNP_A-2026779	C	C	313	101	290	128	4.042	4.44E-02	rs13078425	3	192644	p26.3
SNP_A-1855503	A	A	351	15	339	35	8.123	4.40E-03	rs17264626	3	247256	p26.3
SNP_A-2243097	C	C	301	81	308	56	4.211	0.0402	rs6795631	3	287177	p26.3
SNP_A-1826002	T	T	360	22	345	45	8.133	0.0043	rs17017690	3	291189	p26.3
SNP_A-2153864	C	C	375	11	373	25	5.267	2.17E-02	rs9990005	3	301537	p26.3
SNP_A-1864787	A	A	395	11	409	1	8.558	3.40E-03	rs6442824	3	411042	p26.3
SNP_A-2098842	C	C	266	68	240	92	4.93	0.0264	rs12629825	3	970334	p26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1901028	A	A	309	107	286	134	3.895	4.84E-02	rs17050401	3	981429	p26.3
SNP_A-1852601	C	C	377	33	391	19	4.024	0.0448	rs6443261	3	1015539	p26.3
SNP_A-2194978	C	C	244	138	220	176	5.59	1.81E-02	rs6792904	3	1038667	p26.3
SNP_A-1809275	C	C	365	47	350	68	4.106	4.27E-02	rs4684830	3	1235260	p26.3
SNP_A-2177900	T	T	344	32	372	16	6.241	1.25E-02	rs265772	3	1346260	p26.3
SNP_A-1811856	G	G	383	19	363	33	4.261	0.039	rs111128726	3	1532413	p26.3
SNP_A-1905584	T	T	274	62	303	33	10.31	1.30E-03	rs9829889	3	1540113	p26.3
SNP_A-1971348	C	C	392	16	404	6	4.721	0.0298	rs446435	3	1564052	p26.3
SNP_A-1961587	C	C	284	76	304	48	6.914	0.0086	rs17042645	3	1706848	p26.3
SNP_A-1653500	A	A	373	27	397	15	4	4.55E-02	rs4684321	3	1842614	p26.3
SNP_A-2082443	G	G	386	12	395	3	5.504	0.019	—	3	1875711	p26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207998	A	A	381	21	404	8	6.38	0.0115	rs2729328	3	2054975	p26.3
SNP_A-2008378	G	G	400	12	408	4	4.079	4.34E-02	rs4630919	3	2057449	p26.3
SNP_A-1950426	G	C	169	141	175	151	4.271	3.88E-02	rs9827746	3	2199619	p26.3
SNP_A-1753023	C	C	377	19	372	38	6.125	1.33E-02	rs1502565	3	2410721	p26.3
SNP_A-1920474	A	A	381	31	360	60	9.761	0.0018	rs2648690	3	2451543	p26.3
SNP_A-1803194	T	T	224	190	260	160	5.206	2.25E-02	rs749613	3	2527565	p26.3
SNP_A-2309217	C	C	324	88	298	118	5.437	1.97E-02	rs13081043	3	2583506	p26.3
SNP_A-1971381	C	A	173	167	191	141	4.776	2.89E-02	rs2619578	3	2658008	p26.3
SNP_A-2183646	G	G	295	75	331	51	6.452	0.0111	rs2600275	3	2691796	p26.3
SNP_A-1810782	G	G	222	160	250	132	4.346	3.71E-02	rs2600277	3	2693697	p26.3
SNP_A-1930854	G	G	325	15	294	26	3.901	4.83E-02	rs9830446	3	2719503	p26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1879238	C	T	202	176	211	165	6.89	8.70E-03	rs1474020	3	2805601	p26.2
SNP_A-1944581	C	C	315	51	352	36	4	4.55E-02	rs6780611	3	2872822	p26.2
SNP_A-2008388	C	C	246	72	265	51	4.286	3.84E-02	rs7636197	3	2876065	p26.2
SNP_A-2284111	A	G	210	154	185	183	4.668	3.07E-02	rs427502	3	2974019	p26.2
SNP_A-1684994	G	G	374	20	365	35	4.155	4.15E-02	rs10510247	3	3023016	p26.2
SNP_A-1971396	T	T	302	84	308	54	5.817	1.59E-02	rs10510248	3	3023519	p26.2
SNP_A-1892596	G	G	388	18	362	34	5.701	1.70E-02	rs17024684	3	3030247	p26.2
SNP_A-2051011	A	A	389	25	368	48	7.824	5.20E-03	rs1420020	3	3035913	p26.2
SNP_A-1816095	C	C	403	7	420	0	7.232	7.20E-03	rs9861982	3	3207895	p26.2
SNP_A-2217985	C	C	246	108	226	138	4.368	3.66E-02	rs13080820	3	3236438	p26.2
SNP_A-2170145	G	G	254	150	231	181	3.916	4.78E-02	rs3914759	3	3240099	p26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903269	C	C	211	147	179	171	4.347	3.71E-02	rs13068305	3	3246778	p26.2
SNP_A-2157567	G	G	410	4	410	0	3.981	4.60E-02	rs17032106	3	3502974	p26.2
SNP_A-2147784	T	T	319	23	331	9	6.341	0.0118	rs2035661	3	3589282	p26.2
SNP_A-1696500	A	A	367	17	365	7	3.983	4.60E-02	rs10510275	3	3742703	p26.2
SNP_A-1971458	G	G	240	164	216	196	4.03	4.47E-02	rs13087536	3	4276095	p26.1
SNP_A-2246787	C	C	297	87	329	65	4.692	3.03E-02	rs310724	3	4326751	p26.1
SNP_A-1699503	G	G	233	165	267	141	4.071	0.0436	rs711673	3	4340560	p26.1
SNP_A-2290012	C	C	357	31	379	17	4.66	0.0309	rs308739	3	4351030	p26.1
SNP_A-2040287	A	A	303	27	317	13	5.216	0.0224	rs308728	3	4355161	p26.1
SNP_A-1909710	C	C	299	85	310	60	4.251	3.92E-02	rs308717	3	4361594	p26.1
SNP_A-2029498	T	T	320	34	347	15	8.372	0.0038	rs711667	3	4436569	p26.1
SNP_A-2029544	T	T	364	40	381	25	3.845	0.0499	rs17040706	3	4466126	p26.1
SNP_A-2142670	C	C	321	37	354	18	7.911	4.90E-03	rs7634154	3	4466540	p26.1
SNP_A-1940542	C	C	353	31	393	19	4.045	4.43E-02	rs9875154	3	4477165	p26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1791727	G	G	359	27	392	10	8.94	0.0028	rs1825914	3	4488582	p26.1
SNP_A-2122078	C	C	375	35	394	20	4.541	3.31E-02	rs9818866	3	4493662	p26.1
SNP_A-1652666	T	T	359	41	390	20	8.39	0.0038	rs10510293	3	4505992	p26.1
SNP_A-1971469	T	T	281	41	289	21	6.338	0.0118	rs769099	3	4506294	p26.1
SNP_A-1971474	G	G	307	3	311	11	4.371	3.66E-02	rs4685770	3	4603468	p26.1
SNP_A-1900001	G	G	235	143	205	167	3.856	4.96E-02	rs9850086	3	4622352	p26.1
SNP_A-1944801	C	C	235	177	277	143	6.982	8.20E-03	rs12638018	3	4760230	p26.1
SNP_A-1907260	T	T	223	191	255	163	4.338	0.0373	rs4685814	3	4771784	p26.1
SNP_A-2062694	G	G	269	147	297	121	3.903	0.0482	rs3792499	3	4779081	p26.1
SNP_A-1880914	C	C	313	41	334	26	3.99	0.0458	rs17042221	3	5323717	p26.1
SNP_A-2059749	C	C	247	143	268	114	4.046	4.43E-02	rs12491626	3	5394894	p26.1
SNP_A-1737690	T	T	289	111	322	88	4.318	3.77E-02	rs7611998	3	5478187	p26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2087172	G	G	252	114	280	82	6.676	9.80E-03	rs1430011	3	5582681	p26.1
SNP_A-1971498	C	C	306	102	330	74	5.341	2.08E-02	rs1430009	3	5582917	p26.1
SNP_A-1883962	G	G	236	92	270	68	5.736	0.0166	rs9311568	3	5591260	p26.1
SNP_A-2185837	C	C	247	137	273	109	4.482	3.43E-02	rs6762454	3	5599873	p26.1
SNP_A-2084081	G	G	206	150	248	120	7.022	8.10E-03	rs1864428	3	5607123	p26.1
SNP_A-1971502	C	C	170	166	220	152	5.21	2.25E-02	rs11721059	3	5700560	p26.1
SNP_A-1857144	T	T	395	1	389	7	4.546	3.30E-02	rs17043417	3	5760324	p26.1
SNP_A-2202551	T	T	338	2	345	11	5.938	1.48E-02	rs1400669	3	5969108	p26.1
SNP_A-1662234	G	G	371	29	364	48	4.579	3.24E-02	rs10510325	3	6109806	p26.1
SNP_A-1892595	C	C	378	20	355	39	6.82	9.00E-03	rs17234374	3	6173982	p26.1
SNP_A-2045419	A	A	358	20	347	43	8.383	0.0038	rs17234402	3	6179928	p26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1971529	G	G	240	168	208	204	5.75	1.65E-02	rs286588	3	6220005	p26.1
SNP_A-1806302	G	G	272	132	245	159	3.915	4.79E-02	rs4684534	3	6579066	p26.1
SNP_A-1882447	A	A	192	180	222	146	5.698	1.70E-02	rs164729	3	6617817	p26.1
SNP_A-2189245	A	A	290	126	264	156	4.393	0.0361	rs7430827	3	6617993	p26.1
SNP_A-1873120	C	C	257	103	223	131	5.709	1.69E-02	rs6790955	3	6639642	p26.1
SNP_A-1875627	T	T	248	146	204	188	9.56	0.002	rs2323813	3	6654798	p26.1
SNP_A-1897965	G	G	218	132	177	175	10.273	1.30E-03	rs4686074	3	6657834	p26.1
SNP_A-1971554	T	T	226	168	274	136	7.661	5.60E-03	rs352276	3	6660044	p26.1
SNP_A-1971557	G	G	301	33	338	14	9.357	2.20E-03	rs163968	3	6770490	p26.1
SNP_A-1971558	G	G	242	116	259	89	3.992	4.57E-02	rs345224	3	6770637	p26.1
SNP_A-1971565	G	G	269	133	284	100	4.671	3.07E-02	rs467166	3	6796681	p26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1696798	C	C	384	16	381	31	4.623	3.16E-02	rs10510341	3	6808535	p26.1
SNP_A-2307305	A	A	341	7	287	15	4.319	3.77E-02	rs1356268	3	6996095	p26.1
SNP_A-1734076	G	G	342	58	330	82	4.152	4.16E-02	rs9311980	3	7179774	p26.1
SNP_A-2065708	C	C	255	79	251	109	3.85	4.97E-02	rs752300	3	7495084	p26.1
SNP_A-1819085	C	C	361	27	330	12	4.278	3.86E-02	rs10222587	3	7508618	p26.1
SNP_A-2138748	G	G	292	34	289	55	4.49	3.41E-02	rs7614915	3	7595382	p26.1
SNP_A-2199896	T	T	339	45	307	79	10.903	0.001	rs1485167	3	7639334	p26.1
SNP_A-1870785	C	C	365	51	337	81	7.93	4.90E-03	rs17723289	3	7641994	p26.1
SNP_A-1971612	A	A	365	51	337	81	7.93	4.90E-03	rs10510370	3	7642672	p26.1
SNP_A-1740481	C	C	349	51	334	78	5.805	0.016	rs3804867	3	7642909	p26.1
SNP_A-2024809	A	A	327	63	356	38	7.399	6.50E-03	rs3804859	3	7653340	p26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1971613	C	C	322	56	347	35	5.759	1.64E-02	rs1872397	3	7655410	p26.1
SNP_A-2100890	G	G	352	12	329	25	5.206	2.25E-02	rs1352411	3	7774831	p26.1
SNP_A-1971652	A	A	332	50	355	33	4.205	4.03E-02	rs1878175	3	8139718	p26.1
SNP_A-2044718	T	T	356	52	374	34	4.211	0.0402	rs2675248	3	8141787	p26.1
SNP_A-1669963	G	G	334	52	372	40	6.476	0.0109	rs2675257	3	8147893	p26.1
SNP_A-2114587	C	C	263	95	276	68	4.509	3.37E-02	rs2729668	3	8148161	p26.1
SNP_A-1647834	A	A	342	52	375	31	6.654	9.90E-03	rs10510385	3	8148750	p26.1
SNP_A-1667662	T	T	348	52	378	34	4.831	2.80E-02	rs7649994	3	8149097	p26.1
SNP_A-1751819	G	G	347	51	378	32	5.498	0.019	rs7640853	3	8149292	p26.1
SNP_A-1641759	T	T	348	52	378	32	5.879	1.53E-02	rs10510386	3	8149415	p26.1
SNP_A-1971659	A	A	362	42	380	24	5.346	2.08E-02	rs6764798	3	8175271	p26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1971660	A	A	333	55	355	35	5.143	2.33E-02	rs10510387	3	8175749	p26.1
SNP_A-2023055	T	T	210	138	171	163	5.784	1.62E-02	rs10866089	3	8489038	p25.3
SNP_A-1791344	T	C	218	166	196	180	6.031	0.0141	rs6770049	3	8497388	p25.3
SNP_A-2310368	G	G	367	3	361	13	6.278	1.22E-02	rs17049229	3	8528991	p25.3
SNP_A-1838290	G	G	232	100	257	131	6.371	1.16E-02	rs6801316	3	8548095	p25.3
SNP_A-1971680	C	C	299	93	318	68	4.421	3.55E-02	rs1493594	3	8573670	p25.3
SNP_A-2274060	G	G	229	159	251	119	6.34	0.0118	rs4686268	3	8586344	p25.3
SNP_A-2121801	T	T	367	13	358	26	4.424	3.54E-02	rs2014165	3	8626999	p25.3
SNP_A-2262754	G	G	283	53	268	78	5.034	2.49E-02	rs4686281	3	8649677	p25.3
SNP_A-2204039	C	C	270	142	239	179	6.11	0.0134	rs3774209	3	8669057	p25.3
SNP_A-1874974	T	T	342	64	351	41	4.911	2.67E-02	rs237923	3	8794661	p25.3
SNP_A-2110308	G	G	338	66	362	44	5.218	0.0224	rs237924	3	8795828	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282615	A	A	314	102	349	71	7.384	0.0066	rs7427933	3	8823342	p25.3
SNP_A-1910869	A	A	247	77	294	56	6.406	0.0114	rs1643021	3	8823793	p25.3
SNP_A-1916983	G	G	371	5	364	14	4.325	3.76E-02	rs11131152	3	8872402	p25.3
SNP_A-1782940	C	C	329	55	347	33	5.959	0.0146	rs9816708	3	8881295	p25.3
SNP_A-2008442	G	G	406	8	398	20	5.203	2.25E-02	rs658339	3	8907353	p25.3
SNP_A-1974949	C	C	244	106	267	75	6.253	0.0124	rs593483	3	8908048	p25.3
SNP_A-2276866	T	T	233	101	250	74	4.613	3.17E-02	rs11161805	3	8947222	p25.3
SNP_A-1690427	C	C	284	100	322	78	4.777	2.88E-02	rs370526	3	9045495	p25.3
SNP_A-1931545	C	C	251	109	239	143	4.233	3.97E-02	rs2669986	3	9098116	p25.3
SNP_A-1825949	G	G	323	47	334	28	4.911	2.67E-02	rs17050220	3	9325167	p25.3
SNP_A-2209147	C	C	327	53	295	85	9.067	2.60E-03	rs2728945	3	9393510	p25.3
SNP_A-1898647	G	G	273	99	303	73	5.471	1.93E-02	rs12487333	3	9632001	p25.3
SNP_A-2127597	G	G	269	99	292	76	3.966	4.64E-02	rs4686363	3	9637966	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2205343	G	G	331	85	297	123	8.764	3.10E-03	rs3846169	3	9972054	p25.3
SNP_A-1807655	T	T	349	61	317	97	9.721	0.0018	rs17050675	3	10002686	p25.3
SNP_A-1879302	C	C	355	53	323	79	6.587	0.0103	rs17032295	3	10061680	p25.3
SNP_A-1819349	C	C	356	56	315	89	9.938	1.60E-03	rs17032299	3	10062638	p25.3
SNP_A-2046409	G	G	320	52	278	74	6.243	1.25E-02	rs12374115	3	10109766	p25.3
SNP_A-1934228	C	C	349	51	297	73	6.931	8.50E-03	rs17032414	3	10133302	p25.3
SNP_A-2214370	C	C	377	17	387	7	4.298	3.82E-02	rs696322	3	10233192	p25.3
SNP_A-1814398	G	G	401	1	369	11	9.051	2.60E-03	rs11465901	3	10233579	p25.3
SNP_A-2113455	G	G	393	9	396	2	4.446	3.50E-02	rs2289272	3	10388526	p25.3
SNP_A-2237905	T	T	319	85	295	111	4.382	3.63E-02	rs11719939	3	10432572	p25.3
SNP_A-1911388	G	G	397	13	388	26	4.417	0.0356	rs17032876	3	10445911	p25.3
SNP_A-2191545	C	C	241	143	278	108	7.513	6.10E-03	rs17787095	3	10473920	p25.3
SNP_A-1787873	C	C	249	137	234	174	4.261	0.039	rs9873870	3	10514482	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884552	A	A	259	149	226	184	5.919	1.50E-02	rs6442177	3	10548967	p25.3
SNP_A-2058038	A	G	231	175	206	200	4.752	0.0293	rs6795673	3	10568224	p25.3
SNP_A-2102397	A	A	226	140	205	171	3.979	4.61E-02	rs6803992	3	10597941	p25.3
SNP_A-2252490	C	T	210	172	207	167	8.053	4.50E-03	rs2697159	3	10949427	p25.3
SNP_A-1726482	C	C	303	39	308	80	11.313	8.00E-04	rs10514669	3	11050912	p25.3
SNP_A-2260485	T	T	303	31	259	49	6.452	0.0111	rs11716141	3	12083754	p25.2
SNP_A-1811629	G	G	347	7	364	18	4.187	0.0407	rs17035910	3	12158083	p25.2
SNP_A-1955132	A	A	350	36	369	19	5.752	1.65E-02	rs308953	3	12172997	p25.2
SNP_A-2165736	T	T	186	162	229	143	4.844	2.77E-02	rs15620241	3	12260734	p25.2
SNP_A-1655831	T	T	311	89	293	117	4.219	4.00E-02	rs10510410	3	12321738	p25.2
SNP_A-1651698	G	G	311	89	292	120	5.021	2.50E-02	rs10510411	3	12321849	p25.2
SNP_A-1648728	C	C	313	85	294	118	5.719	1.68E-02	rs10510412	3	12321962	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134922	C	C	301	63	265	83	4.672	3.07E-02	rs11715073	3	12327971	p25.2
SNP_A-1946610	G	A	198	192	233	165	6.875	8.70E-03	rs2972162	3	12399793	p25.2
SNP_A-1674385	C	C	350	40	345	63	4.768	2.90E-02	rs105104 19	3	12401936	p25.2
SNP_A-1804355	C	C	340	68	371	41	8.02	4.60E-03	rs17825940	3	12994064	p25.2
SNP_A-2131349	C	C	312	48	315	73	4.137	0.0419	rs361052	3	13045799	p25.2
SNP_A-2168092	G	G	297	55	320	38	3.914	4.79E-02	rs11128630	3	13051226	p25.2
SNP_A-1815109	T	T	244	156	222	192	4.523	3.34E-02	rs360902	3	13063312	p25.2
SNP_A-2237129	G	G	252	160	224	194	4.869	2.73E-02	rs360899	3	13064725	p25.2
SNP_A-2211933	C	C	198	138	228	116	3.925	4.76E-02	rs360898	3	13064779	p25.2
SNP_A-2208263	A	G	224	174	217	179	9.749	0.0018	rs360875	3	13081302	p25.2
SNP_A-1971808	A	A	382	32	398	18	4.243	3.94E-02	rs17037953	3	13259218	p25.2
SNP_A-2170713	C	C	321	29	346	16	4.492	3.41E-02	rs12493865	3	13259483	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1971814	C	T	192	182	198	152	4.534	0.0332	rs59585	3	13476254	p25.1
SNP_A-2170044	G	G	373	13	365	25	3.856	4.96E-02	rs12635063	3	13483455	p25.1
SNP_A-1971823	G	G	353	5	386	0	5.428	1.98E-02	rs3731123	3	14176460	p25.1
SNP_A-2292891	A	A	312	0	311	5	4.976	2.57E-02	rs752137	3	14295279	p25.1
SNP_A-1645766	G	G	399	1	402	10	7.199	7.30E-03	rs10510430	3	14687025	p25.1
SNP_A-2041636	A	A	209	103	191	131	4.004	4.54E-02	rs853334	3	14792658	p25.1
SNP_A-1971843	A	A	381	11	373	23	4.3	3.81E-02	rs10510434	3	14995353	p25.1
SNP_A-2297668	A	A	371	31	396	16	5.48	1.92E-02	rs7636739	3	15308555	p25.1
SNP_A-1959435	G	G	366	36	386	20	5.084	2.42E-02	rs17040969	3	15311217	p25.1
SNP_A-2145780	G	G	244	138	225	179	5.461	1.94E-02	rs12638270	3	15334823	p25.1
SNP_A-1793839	T	T	239	143	278	110	7.2	7.30E-03	rs2605396	3	15515477	p25.1
SNP_A-1920655	A	A	225	139	264	110	6.354	0.0117	rs9821793	3	15516041	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1842256	C	C	312	58	367	29	13.255	3.00E-04	rs2124493	3	15530274	p25.1
SNP_A-2067577	C	C	261	147	296	104	9.488	2.10E-03	rs905648	3	15540326	p25.1
SNP_A-2162263	T	T	317	81	292	116	7.122	0.0076	rs17485390	3	15587217	p25.1
SNP_A-1855759	A	A	318	42	300	64	5.068	2.44E-02	rs9647358	3	15662846	p25.1
SNP_A-2174402	T	T	298	116	324	92	3.851	4.97E-02	rs2455853	3	15665029	p25.1
SNP_A-2209032	C	C	265	59	295	41	4.63	3.14E-02	rs2455807	3	15682449	p25.1
SNP_A-2077599	T	T	218	168	257	143	4.964	2.59E-02	rs2470550	3	15718725	p25.1
SNP_A-2008484	G	G	229	169	259	133	6.09	1.36E-02	rs2455793	3	15718848	p25.1
SNP_A-1804589	G	G	212	128	236	102	4.219	4.00E-02	rs6762442	3	15808907	p25.1
SNP_A-2257337	T	T	220	178	252	144	5.755	1.64E-02	rs11128762	3	15858443	p25.1
SNP_A-2008485	C	C	299	73	257	99	6.755	9.40E-03	rs4684263	3	15914146	p25.1
SNP_A-2086232	A	A	375	41	347	65	6.501	1.08E-02	rs2730363	3	16068327	p25.1
SNP_A-2046024	T	T	259	37	276	68	6.127	1.33E-02	rs2603764	3	16068528	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2107699	A	A	391	11	386	24	4.782	2.88E-02	rs17200327	3	16475054	p24.3
SNP_A-1893505	G	A	208	150	176	160	7.645	5.70E-03	rs17272530	3	16518326	p24.3
SNP_A-1849056	C	C	212	146	179	175	5.383	2.03E-02	rs9854036	3	16522598	p24.3
SNP_A-2008491	G	G	294	122	258	156	6.501	1.08E-02	rs1429163	3	16526291	p24.3
SNP_A-1781558	T	C	227	155	197	191	8.066	4.50E-03	rs2881514	3	16528684	p24.3
SNP_A-1956810	G	A	241	169	207	203	7.093	7.70E-03	rs4685343	3	16528973	p24.3
SNP_A-2056907	G	G	262	148	232	184	5.682	1.71E-02	rs895945	3	16734636	p24.3
SNP_A-1666964	T	T	312	38	309	67	7.102	7.70E-03	rs1823370	3	16744272	p24.3
SNP_A-2199702	C	C	353	27	327	47	6.352	0.0117	rs978302	3	16783307	p24.3
SNP_A-2108034	A	A	386	24	364	42	5.535	1.86E-02	rs6764961	3	16830329	p24.3
SNP_A-2206323	A	A	318	74	331	51	4.364	3.67E-02	rs4383507	3	17048036	p24.3
SNP_A-2299893	C	C	407	1	407	7	4.456	3.48E-02	rs17043486	3	17374010	p24.3
SNP_A-2219793	G	G	403	1	366	8	6.077	0.0137	rs17044053	3	17822886	p24.3
SNP_A-1935026	G	G	411	1	410	10	7.289	6.90E-03	rs11927436	3	17823071	p24.3
SNP_A-1971904	T	T	414	0	412	4	4	4.55E-02	rs17200930	3	17823869	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1971905	T	T	410	0	404	4	4.039	4.45E-02	rs6780341	3	17824951	p24.3
SNP_A-1901045	A	A	382	0	381	5	4.981	2.56E-02	rs6793958	3	17828060	p24.3
SNP_A-1971907	C	C	414	0	413	5	4.982	2.56E-02	rs17044097	3	17864755	p24.3
SNP_A-1971908	C	C	406	0	412	6	5.87	0.0154	rs17044102	3	17864843	p24.3
SNP_A-1751919	T	T	398	0	404	6	5.868	0.0154	rs10510481	3	17865169	p24.3
SNP_A-1876170	A	A	367	23	348	40	5.087	0.0241	rs7648933	3	17906857	p24.3
SNP_A-1714068	A	A	377	21	371	39	5.271	2.17E-02	rs10510482	3	17913733	p24.3
SNP_A-2269145	G	G	393	23	377	41	5.39	2.03E-02	rs1430889	3	17922880	p24.3
SNP_A-2194056	C	C	382	14	370	28	4.853	0.0276	rs12493003	3	17925132	p24.3
SNP_A-2299301	G	G	313	23	302	38	3.862	4.94E-02	rs2102623	3	18181169	p24.3
SNP_A-2008503	T	T	396	4	400	0	4.02	4.50E-02	rs1440968	3	18637481	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1837658	C	C	356	40	371	23	4.892	0.027	rs7643832	3	18812940	p24.3
SNP_A-1949317	T	T	277	107	316	80	6.28	1.22E-02	rs7640928	3	18815937	p24.3
SNP_A-2008507	A	A	212	126	267	97	9.136	2.50E-03	rs6778628	3	18824031	p24.3
SNP_A-1873819	G	A	189	163	208	152	9.384	2.20E-03	rs9881034	3	18852430	p24.3
SNP_A-2098602	T	T	316	94	275	129	8.284	4.00E-03	rs7428879	3	18934960	p24.3
SNP_A-2025265	G	G	359	27	376	14	4.495	3.40E-02	rs12485415	3	19311364	p24.3
SNP_A-1971936	C	C	252	164	282	138	3.905	4.81E-02	rs4241540	3	19957976	p24.3
SNP_A-1881728	C	C	339	17	321	31	4.552	3.29E-02	rs13070718	3	19978232	p24.3
SNP_A-2199677	C	C	395	17	378	30	3.95	4.69E-02	rs2929403	3	20070918	p24.3
SNP_A-1971940	C	C	261	127	233	163	5.975	1.45E-02	rs2686322	3	20088109	p24.3
SNP_A-1865788	G	G	267	139	227	165	5.219	0.0223	rs3021408	3	20088834	p24.3
SNP_A-2121006	G	G	257	125	216	148	5.06	2.45E-02	rs3749180	3	20088993	p24.3
SNP_A-1679572	A	A	239	159	216	194	4.456	3.48E-02	rs2365367	3	20091042	p24.3
SNP_A-1929090	C	C	204	182	228	134	7.863	5.00E-03	rs4241546	3	20122566	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287956	G	G	251	95	285	75	4.234	3.96E-02	rs2686313	3	20149341	p24.3
SNP_A-2067676	C	C	349	13	331	31	7.84	5.10E-03	rs17797581	3	20149400	p24.3
SNP_A-2064830	C	C	402	12	376	26	5.852	1.56E-02	rs2661376	3	20167150	p24.3
SNP_A-1685912	T	T	313	85	292	118	5.917	1.50E-02	rs10514674	3	20193758	p24.3
SNP_A-1912335	A	A	300	84	315	61	3.93	4.74E-02	rs6550401	3	20194698	p24.3
SNP_A-2035167	C	C	326	90	296	120	5.733	0.0167	rs11713727	3	20196245	p24.3
SNP_A-1875690	G	G	315	39	344	24	4.578	3.24E-02	rs610310	3	20490562	p24.3
SNP_A-1906899	C	C	332	64	345	43	4.29	3.83E-02	rs5998845	3	20490749	p24.3
SNP_A-1829308	T	T	324	68	344	46	4.839	2.78E-02	rs1880045	3	20566088	p24.3
SNP_A-2091777	G	G	261	95	296	72	5.169	0.023	rs1395103	3	20590277	p24.3
SNP_A-2179681	A	A	292	92	329	71	4.585	3.22E-02	rs12497305	3	20626949	p24.3
SNP_A-1819361	G	G	354	28	385	15	4.819	0.0281	rs13925567	3	20738641	p24.3
SNP_A-1961262	C	C	329	71	356	48	5.49	1.91E-02	rs1908984	3	21039517	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2091363	G	G	208	140	169	155	3.945	0.047	rs6791138	3	21081387	p24.3
SNP_A-1726650	T	T	261	135	240	168	4.296	3.82E-02	rs1436832	3	21180259	p24.3
SNP_A-1971967	T	T	221	171	243	139	4.218	4.00E-02	rs7627112	3	21239774	p24.3
SNP_A-2129322	T	T	383	9	403	1	6.73	9.50E-03	rs17008367	3	21295065	p24.3
SNP_A-1971992	A	A	209	201	225	163	3.953	4.68E-02	rs1841914	3	21598635	p24.3
SNP_A-2097072	A	A	199	133	210	96	5.223	0.0223	rs2335808	3	21608229	p24.3
SNP_A-1971995	A	A	198	160	236	132	5.875	0.0154	rs10510514	3	21610565	p24.3
SNP_A-1754238	T	C	216	182	213	191	3.924	4.76E-02	rs3860583	3	21645485	p24.3
SNP_A-1851785	T	G	203	201	224	168	4.367	3.66E-02	rs2054942	3	21673398	p24.3
SNP_A-1816934	T	T	317	47	347	31	4.375	3.65E-02	rs2630788	3	21850130	p24.3
SNP_A-2106687	G	G	297	105	305	73	5.126	2.36E-02	rs2620532	3	21885968	p24.3
SNP_A-1972010	G	G	359	7	369	1	4.616	3.17E-02	rs17010082	3	21926911	p24.3
SNP_A-1972014	C	C	224	152	198	182	4.275	3.87E-02	rs2291817	3	21994886	p24.3
SNP_A-2233182	T	T	300	68	321	47	4.545	3.30E-02	rs12497048	3	22247420	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1849941	A	A	404	4	414	0	4.079	4.34E-02	rs937106	3	22306393	p24.3
SNP_A-1882062	T	T	412	4	420	0	4.058	4.40E-02	rs11917426	3	22311763	p24.3
SNP_A-2135617	C	C	302	98	315	71	4.34	3.72E-02	rs6774197	3	22338890	p24.3
SNP_A-1932268	C	C	322	42	332	22	6.265	0.0123	rs2047156	3	22452495	p24.3
SNP_A-1849632	T	T	330	64	362	36	9.3	0.0023	rs13069748	3	22565048	p24.3
SNP_A-1743125	C	C	341	57	373	37	5.512	0.0189	rs296167	3	22796445	p24.3
SNP_A-1649684	A	A	209	145	250	128	3.938	4.72E-02	rs633464	3	23023005	p24.3
SNP_A-1683202	G	A	210	182	206	174	4.674	3.06E-02	rs9310709	3	23068539	p24.3
SNP_A-1804497	C	C	382	4	366	14	5.851	1.56E-02	rs17012829	3	23236338	p24.3
SNP_A-2130288	G	G	377	33	359	55	5.921	1.50E-02	rs7627380	3	23321799	p24.3
SNP_A-1972053	G	G	308	58	321	39	3.941	4.71E-02	rs1692619	3	23435236	p24.3
SNP_A-2277412	A	A	293	95	312	60	8.167	0.0043	rs13323077	3	23495745	p24.3
SNP_A-2228543	T	T	302	80	305	55	3.996	4.56E-02	rs2055307	3	23517258	p24.3
SNP_A-2230203	G	G	359	19	366	38	5.543	1.86E-02	rs7637788	3	23719107	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2108400	A	G	244	172	213	203	8.127	4.40E-03	rs6767406	3	23837467	p24.2
SNP_A-2037748	T	T	375	19	364	8	4.017	4.51E-02	rs2168424	3	23844252	p24.2
SNP_A-2180967	A	A	279	125	307	99	4.351	3.70E-02	rs11922577	3	23965245	p24.2
SNP_A-2266915	G	G	387	3	370	10	4.022	4.49E-02	rs3935253	3	23974760	p24.2
SNP_A-1972058	C	C	292	112	318	88	3.983	4.60E-02	rs1567581	3	24011410	p24.2
SNP_A-2215062	A	A	365	43	394	24	6.376	1.16E-02	rs1397878	3	24069113	p24.2
SNP_A-1888586	G	G	293	95	329	65	7.663	5.60E-03	rs6765461	3	24084752	p24.2
SNP_A-1941987	A	A	187	181	211	151	4.109	4.27E-02	rs7630879	3	24103340	p24.2
SNP_A-1972059	G	G	289	89	324	58	8.515	3.50E-03	rs2360959	3	24118204	p24.2
SNP_A-1757399	A	A	296	104	335	77	6.262	0.0123	rs2360958	3	24118238	p24.2
SNP_A-1698769	A	A	299	101	341	71	7.813	5.20E-03	rs2063480	3	24118462	p24.2
SNP_A-1972063	C	C	406	0	402	4	4.02	4.50E-02	rs17014338	3	24230083	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1972067	C	C	332	46	289	63	4.709	3.00E-02	rs4474983	3	24248409	p24.2
SNP_A-2297259	C	C	212	134	172	160	6.18	0.0129	rs7625900	3	24248465	p24.2
SNP_A-1972070	A	-	240	176	206	206	4.929	0.0264	rs4858594	3	24248858	p24.2
SNP_A-1745834	G	G	314	72	298	102	5.343	2.08E-02	rs10490835	3	24621073	p24.2
SNP_A-2270964	G	G	195	192	236	150	8.856	2.90E-03	rs2362758	3	24644963	p24.2
SNP_A-1972082	A	T	207	181	217	169	7.092	7.70E-03	rs4131483	3	24666496	p24.2
SNP_A-2008534	G	A	216	182	209	179	5.204	2.25E-02	rs1984874	3	24690109	p24.2
SNP_A-2008535	C	A	182	162	177	139	5.245	2.20E-02	rs1984870	3	24690139	p24.2
SNP_A-1948829	T	T	264	50	252	82	7.426	6.40E-03	rs6776123	3	24770623	p24.2
SNP_A-2288234	G	G	291	75	256	94	4.02	4.50E-02	rs7642276	3	24772529	p24.2
SNP_A-2008540	G	G	183	115	232	102	4.528	3.33E-02	rs4241536	3	24773191	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1930947	C	T	220	190	229	181	7.423	6.40E-03	—	3	24930794	p24.2
SNP_A-2300254	C	C	208	200	231	167	4.049	4.42E-02	rs9846880	3	24938071	p24.2
SNP_A-2090409	C	G	184	176	199	153	4.173	4.11E-02	rs9872534	3	24948504	p24.2
SNP_A-1908134	T	C	204	184	223	181	4.79	0.0286	rs9882350	3	24955767	p24.2
SNP_A-2313336	A	T	227	187	219	197	4.64	3.12E-02	rs7648839	3	24956626	p24.2
SNP_A-1972089	C	T	204	184	220	176	5.19	2.27E-02	rs1574375	3	24975269	p24.2
SNP_A-1972090	G	G	334	62	345	37	6.241	1.25E-02	rs17195108	3	24976229	p24.2
SNP_A-1895961	G	G	295	95	271	121	4.142	4.18E-02	rs4858694	3	25072740	p24.2
SNP_A-2300582	C	C	232	92	197	111	4.231	3.97E-02	rs4858697	3	25091586	p24.2
SNP_A-1822258	A	A	316	88	354	64	5.708	1.69E-02	rs17576085	3	25139629	p24.2
SNP_A-2148250	G	G	327	73	334	38	10.108	0.0015	---	3	25139888	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2254763	T	T	287	117	248	162	10.057	0.0015	rs11129181	3	25143644	p24.2
SNP_A-1815171	G	G	341	55	324	78	4.367	3.66E-02	rs9826795	3	25225870	p24.2
SNP_A-1972099	C	C	213	117	224	86	4.39	0.0361	rs958737	3	25240537	p24.2
SNP_A-1650526	T	T	331	55	322	88	7.022	8.10E-03	rs2363594	3	25245029	p24.2
SNP_A-2122555	A	A	384	24	401	11	5.177	0.0229	rs6769438	3	25361700	p24.2
SNP_A-1662594	A	A	372	28	397	15	4.567	3.26E-02	rs10510565	3	25363855	p24.2
SNP_A-1939008	G	G	233	115	189	157	11.067	9.00E-04	rs6784301	3	25406393	p24.2
SNP_A-2200732	A	A	388	18	375	37	6.741	9.40E-03	rs4260361	3	25520472	p24.2
SNP_A-2136180	T	T	335	41	354	26	3.861	4.94E-02	rs1286646	3	25523735	p24.2
SNP_A-2273816	A	A	318	62	278	84	5.566	0.0183	rs12490758	3	26289907	p24.2
SNP_A-1679386	C	C	342	58	330	82	4.152	4.16E-02	rs9310825	3	27003232	p24.1
SNP_A-1691230	T	T	316	76	299	105	4.937	0.0263	rs9310833	3	27038035	p24.1
SNP_A-1650982	T	T	316	84	293	117	6.164	1.30E-02	rs939832	3	27050619	p24.1
SNP_A-1720359	C	C	316	84	295	117	5.964	0.0146	rs939833	3	27050644	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041933	T	T	324	82	304	108	4.151	4.16E-02	rs9810135	3	27077644	p24.2
SNP_A-2132234	C	C	263	117	290	86	6.031	0.0141	rs1402974	3	27102166	p24.1
SNP_A-2114798	G	G	358	2	334	8	3.973	4.62E-02	rs9848011	3	27475664	p24.1
SNP_A-2110602	A	A	367	29	379	13	6.268	0.0123	rs17020249	3	27756407	p24.1
SNP_A-2312097	G	G	325	87	342	56	6.914	0.0086	rs2581178	3	27929182	p24.1
SNP_A-1972165	G	G	400	16	416	4	7.495	6.20E-03	rs10510602	3	27998931	p24.1
SNP_A-1972168	G	G	385	13	413	5	4.05	4.42E-02	rs12054294	3	28015726	p24.1
SNP_A-1972169	G	G	388	16	406	4	7.564	6.00E-03	rs10510604	3	28015776	p24.1
SNP_A-2169376	A	A	293	73	325	53	4.639	3.12E-02	rs9990290	3	28030971	p24.1
SNP_A-2248822	C	C	290	84	313	63	3.872	4.91E-02	rs6803915	3	28512136	p24.1
SNP_A-1879401	G	G	286	64	279	101	7.163	7.40E-03	rs6789363	3	28599223	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100751	A	A	318	98	346	72	5.152	2.32E-02	rs668626	3	29097990	p24.1
SNP_A-1859261	T	T	300	98	312	72	3.962	0.0465	rs603682	3	29109113	p24.1
SNP_A-2085318	T	T	281	41	277	63	4.196	4.05E-02	rs12496180	3	29187939	p24.1
SNP_A-2118713	C	C	271	117	297	93	3.928	4.75E-02	rs2217935	3	29296035	p24.1
SNP_A-1646284	T	T	189	169	237	141	7.399	6.50E-03	rs7622604	3	29425947	p24.1
SNP_A-2119463	A	A	237	137	265	107	5.245	2.20E-02	rs4583597	3	29464270	p24.1
SNP_A-2152652	C	C	404	4	408	0	4.02	4.50E-02	rs9882926	3	29469504	p24.1
SNP_A-1863373	G	G	305	53	326	30	7.067	7.90E-03	rs3773090	3	29584841	p24.1
SNP_A-2297573	T	T	367	21	371	5	9.682	0.0019	rs12633199	3	29593373	p24.1
SNP_A-1929392	A	A	342	40	330	22	4.221	3.99E-02	rs3773101	3	29602575	p24.1
SNP_A-2195987	A	A	342	50	370	32	4.927	0.0264	rs7641657	3	29619813	p24.1
SNP_A-1679680	T	T	314	78	339	55	4.93	0.0264	rs1495589	3	30419986	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189978	C	C	336	0	288	6	6.923	8.50E-03	rs6780266	3	30511945	p24.1
SNP_A-1899443	C	C	390	26	402	12	5.335	2.09E-02	rs11129414	3	30545365	p24.1
SNP_A-2292681	C	C	383	21	401	9	5.169	0.023	rs11129415	3	30556183	p24.1
SNP_A-2084872	G	G	292	44	286	20	7.677	5.60E-03	rs2116138	3	30577634	p24.1
SNP_A-1896730	A	A	223	131	189	155	4.678	3.06E-02	rs11129420	3	30633545	p24.1
SNP_A-2196130	A	A	400	0	390	4	4.081	4.34E-02	rs1461081	3	30682119	p24.1
SNP_A-1928049	T	T	237	101	236	62	6.845	8.90E-03	rs11129433	3	31009534	p24.1
SNP_A-1936203	G	A	170	168	204	144	5.492	1.91E-02	rs1506206	3	31015381	p24.1
SNP_A-1667296	-	C	198	198	238	174	4.903	2.68E-02	rs7642265	3	31024170	p24.1
SNP_A-2273061	C	C	302	44	318	28	3.968	4.64E-02	rs6810010	3	31066442	p24.1
SNP_A-2186019	A	A	262	44	296	30	4.092	4.31E-02	rs4955377	3	31187597	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2149608	G	G	310	60	331	41	4.257	3.91E-02	rs4955385	3	31210572	p24.1
SNP_A-2222703	C	C	392	24	380	40	4.167	4.12E-02	rs6790622	3	31336279	p24.1
SNP_A-1940265	T	T	374	0	382	4	3.896	4.84E-02	rs17027382	3	31357129	p24.1
SNP_A-2301205	T	T	307	65	312	42	4.541	3.31E-02	rs17027389	3	31358632	p24.1
SNP_A-1711570	C	C	329	71	315	97	4.152	4.16E-02	rs4339137	3	31385244	p24.1
SNP_A-2098286	T	T	347	9	358	22	4.846	2.77E-02	rs17027774	3	31497477	p24.1
SNP_A-2040953	G	G	271	97	248	126	4.742	2.94E-02	rs7653447	3	31814139	p24.1
SNP_A-1951741	A	A	329	85	306	110	4.033	4.46E-02	rs4955248	3	32213244	p23
SNP_A-1813031	C	C	335	33	337	15	6.404	0.0114	rs4075566	3	32257690	p23
SNP_A-1972293	G	G	373	5	365	15	5.081	2.42E-02	rs1370718	3	32328135	p23
SNP_A-2105846	A	G	205	139	173	167	7.564	6.00E-03	rs164215	3	32473092	p23
SNP_A-2179214	A	A	252	158	220	192	5.468	1.94E-02	rs164214	3	32473158	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246490	G	G	360	52	331	87	9.987	1.60E-03	rs9681018	3	33504519	p23
SNP_A-2221841	A	A	270	106	317	85	5.209	2.25E-02	rs7649799	3	33825283	p23
SNP_A-1855518	C	C	279	121	314	94	5.378	2.04E-02	rs12495243	3	33841933	p23
SNP_A-2024681	C	C	232	146	278	126	4.76	2.91E-02	rs9311042	3	33948241	p23
SNP_A-2008602	C	C	208	194	237	161	4.938	0.0263	rs1992346	3	34061084	p23
SNP_A-2259866	T	T	283	87	272	116	3.936	4.73E-02	rs987532	3	34089056	p23
SNP_A-2168163	T	T	388	4	418	0	4.286	3.84E-02	rs17031497	3	34288358	p23
SNP_A-1691188	A	A	228	172	262	148	4.036	4.45E-02	rs1114855	3	34448034	p23
SNP_A-2259074	T	T	339	27	351	11	6.924	8.50E-03	rs6794147	3	34555675	p23
SNP_A-2283932	C	C	310	104	333	77	4.831	2.80E-02	rs11920118	3	34575762	p23
SNP_A-2031308	G	G	235	87	265	59	7.164	7.40E-03	rs76510666	3	34628662	p23
SNP_A-2230244	C	C	363	21	381	9	5.189	2.27E-02	rs1520638	3	34683481	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2119685	C	C	212	162	243	137	4.155	4.15E-02	rs6766288	3	34689047	p23
SNP_A-2284826	T	T	322	28	275	45	6.328	1.19E-02	rs2884663	3	35040405	p22.3
SNP_A-2167225	G	G	370	36	340	60	7.223	7.20E-03	rs7620914	3	35060418	p22.3
SNP_A-1829330	A	A	357	39	371	23	4.393	0.0361	rs9878258	3	35277389	p22.3
SNP_A-1972331	C	C	353	33	371	11	11.427	7.00E-04	rs11160578	3	35363148	p22.3
SNP_A-1855077	C	C	412	4	418	0	4.039	4.45E-02	rs17033220	3	35459476	p22.3
SNP_A-1916686	C	C	400	14	415	5	4.496	3.40E-02	rs9865772	3	35769904	p22.3
SNP_A-1928489	G	G	379	11	358	2	5.638	1.76E-02	rs17033755	3	35772852	p22.3
SNP_A-2228315	A	A	304	94	279	125	5.416	0.02	rs17228111	3	35772914	p22.3
SNP_A-1903606	G	G	251	145	222	178	5.13	0.0235	rs735353	3	35817608	p22.3
SNP_A-1972352	G	G	207	149	183	181	4.492	3.41E-02	rs1455489	3	35820857	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1972353	C	C	219	119	190	146	4.801	2.84E-02	rs2884825	3	35821232	p22.3
SNP_A-1834245	C	C	214	128	189	165	6.018	1.42E-02	rs1488095	3	35824399	p22.3
SNP_A-2158424	A	A	223	117	195	141	4.085	4.33E-02	rs4234248	3	35887093	p22.3
SNP_A-1697220	G	G	310	90	289	119	4.681	3.05E-02	rs2167488	3	36092165	p22.3
SNP_A-1700925	T	T	206	190	243	169	3.962	0.0465	rs10510672	3	36092967	p22.3
SNP_A-2232664	C	C	214	200	247	171	4.61	3.18E-02	rs2359966	3	36119916	p22.3
SNP_A-1972361	T	T	183	157	190	118	4.092	4.31E-02	rs13067611	3	36123453	p22.3
SNP_A-1846470	A	A	240	166	266	138	3.91	4.80E-02	rs4678839	3	36131610	p22.3
SNP_A-1862249	A	A	231	139	240	100	5.278	2.16E-02	rs12630703	3	36137024	p22.3
SNP_A-2091124	G	G	312	18	320	8	3.941	4.71E-02	rs7432296	3	36151942	p22.3
SNP_A-1887373	C	C	350	18	352	34	4.502	0.0339	rs1357068	3	36566875	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2127637	T	T	313	63	248	76	4.911	2.67E-02	rs6550430	3	36711927	p22.3
SNP_A-2111085	C	C	389	27	404	12	6.053	1.39E-02	rs17230261	3	37548197	p22.3
SNP_A-1938839	A	A	244	166	215	193	3.858	4.95E-02	rs2555233	3	37586339	p22.3
SNP_A-1972414	C	C	399	5	398	0	4.957	2.60E-02	rs6550508	3	37784406	p22.3
SNP_A-1972415	A	A	334	72	309	97	4.67	3.07E-02	rs9816217	3	37935049	p22.3
SNP_A-2038608	G	G	362	30	338	54	7.68	5.60E-03	rs9878581	3	37944699	p22.3
SNP_A-2183485	C	C	408	0	402	4	4.04	4.44E-02	rs9875265	3	37959452	p22.3
SNP_A-1877570	A	A	404	6	392	20	7.715	5.50E-03	rs17788141	3	38209733	p22.2
SNP_A-1848501	C	C	407	1	409	9	6.285	1.22E-02	rs2844434	3	38365888	p22.2
SNP_A-2307909	C	C	382	10	390	2	5.416	0.02	rs704947	3	38384604	p22.2
SNP_A-2008631	C	C	327	23	326	40	4.233	3.96E-02	rs1913242	3	39240937	p22.2
SNP_A-2122233	C	C	401	7	401	1	4.456	3.48E-02	rs7620499	3	39567646	p22.2
SNP_A-1724870	T	T	390	2	401	9	4.206	4.03E-02	rs10510707	3	40198914	p22.1
SNP_A-2095390	G	G	404	8	411	1	5.505	0.019	rs6599101	3	40422552	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813994	A	A	373	23	385	11	4.425	3.54E-02	rs7616490	3	40688022	p22.1
SNP_A-1714150	T	T	372	28	393	15	4.428	3.54E-02	rs10510715	3	40700304	p22.1
SNP_A-2030053	A	A	288	32	307	17	5.174	0.0229	rs12639177	3	40712313	p22.1
SNP_A-2277280	T	T	343	53	372	34	5.202	2.26E-02	rs6632776	3	40769461	p22.1
SNP_A-1871229	A	A	242	102	282	74	7.304	6.90E-03	rs7624356	3	41545776	p22.1
SNP_A-1721638	G	G	251	147	278	114	5.505	0.019	rs7627367	3	41571820	p22.1
SNP_A-1674761	A	A	387	7	382	20	6.212	1.27E-02	rs6807793	3	41679813	p22.1
SNP_A-2288121	A	A	408	8	399	21	5.909	1.51E-02	rs9864051	3	41700009	p22.1
SNP_A-1972492	A	A	406	8	401	19	4.47	3.45E-02	rs9864465	3	41700261	p22.1
SNP_A-1819483	A	A	404	4	394	14	5.681	0.0172	rs9814399	3	41708337	p22.1
SNP_A-2185328	A	A	374	2	368	10	5.377	2.04E-02	rs9856703	3	41718119	p22.1
SNP_A-1883951	T	T	407	5	395	15	5.175	0.0229	rs17081304	3	41799436	p22.1
SNP_A-2235993	A	A	408	6	400	16	4.62	3.16E-02	rs9830599	3	41896323	p22.1
SNP_A-2216097	C	C	234	90	207	125	7.254	7.10E-03	rs9870002	3	42232712	p22.1
SNP_A-2238475	G	G	253	93	223	115	4.125	4.23E-02	rs3774389	3	42232987	p22.1
SNP_A-1932199	G	G	261	99	235	135	6.766	9.30E-03	rs3774391	3	42240373	p22.1
SNP_A-2162505	A	A	336	74	367	51	5.522	1.88E-02	rs4533619	3	42264816	p22.1
SNP_A-1876396	C	C	331	35	347	21	3.872	4.91E-02	rs342525	3	42560465	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1789927	A	A	264	98	222	118	4.797	2.85E-02	rs2372349	3	43198451	p22.1
SNP_A-1664494	C	C	400	0	407	5	4.884	2.71E-02	rs10510734	3	43241743	p22.1
SNP_A-2306408	G	G	354	60	331	83	4.472	3.45E-02	rs4637262	3	43253301	p22.1
SNP_A-1859838	G	G	375	41	357	61	4.359	3.68E-02	rs1026888	3	43476403	p22.1
SNP_A-1922358	G	G	398	12	408	4	4.119	0.0424	rs17075884	3	43719412	p21.33
SNP_A-2136541	A	A	383	23	368	40	4.882	2.71E-02	rs17076032	3	43797976	p21.33
SNP_A-2219632	A	A	384	0	370	8	8.213	4.20E-03	rs6778205	3	43835866	p21.33
SNP_A-1888642	C	C	336	10	336	22	4.297	3.82E-02	rs6782921	3	43877080	p21.33
SNP_A-1877441	G	G	368	0	354	4	4.135	4.20E-02	rs6766034	3	43931373	p21.33
SNP_A-2223481	C	C	280	134	309	101	6.043	0.014	rs9825080	3	44226274	p21.33
SNP_A-2241450	G	G	225	127	247	97	4.952	2.61E-02	rs4683035	3	45086152	p21.31
SNP_A-2059908	C	C	304	112	280	140	4.078	4.34E-02	rs6795559	3	45319060	p21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2249889	T	T	230	118	203	143	4.073	0.0436	rs6765732	3	45660390	p21.31
SNP_A-1727240	G	G	251	85	237	135	9.961	1.60E-03	rs2118750	3	45671579	p21.31
SNP_A-1911668	G	G	235	157	270	128	5.331	2.09E-02	rs2742398	3	45734040	p21.31
SNP_A-1972579	A	A	228	150	267	127	4.653	0.031	rs1468542	3	45754140	p21.31
SNP_A-1738236	A	A	240	148	289	123	6.131	1.33E-02	rs764177	3	45770041	p21.31
SNP_A-1908319	A	A	354	60	369	39	4.722	0.0298	rs3851346	3	46028585	p21.31
SNP_A-1867667	C	C	288	82	261	105	4.135	4.20E-02	rs6441942	3	46069544	p21.31
SNP_A-1842011	C	C	302	98	277	127	4.797	2.85E-02	rs1546076	3	46125521	p21.31
SNP_A-2116891	G	G	287	73	255	97	5.188	2.27E-02	rs9820016	3	46129845	p21.31
SNP_A-1697685	G	G	336	42	380	20	9.896	1.70E-03	rs10510749	3	46141008	p21.31
SNP_A-2181158	A	A	307	51	304	26	7.004	8.10E-03	rs13075270	3	46228793	p21.31
SNP_A-2180906	A	A	338	38	370	14	12.44	4.00E-04	rs11919943	3	46241730	p21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839056	C	C	359	49	393	15	19.6	9.55E-06	rs13067058	3	46248770	p21.31
SNP_A-1835635	C	C	360	52	397	23	12.946	3.00E-04	rs17217831	3	46280445	p21.31
SNP_A-1972590	T	T	362	52	397	23	12.785	3.00E-04	rs4987053	3	46281704	p21.31
SNP_A-2284181	A	A	363	51	395	23	11.927	6.00E-04	rs13100243	3	46292902	p21.31
SNP_A-2220032	C	C	325	69	299	97	5.801	0.016	rs7649764	3	46305866	p21.31
SNP_A-1841981	A	A	354	46	392	18	14.064	2.00E-04	rs17284138	3	46306856	p21.31
SNP_A-1972591	C	C	245	115	284	90	5.659	1.74E-02	rs6441961	3	46327388	p21.31
SNP_A-1727451	C	C	237	137	274	114	4.531	3.33E-02	rs2888524	3	46329053	p21.31
SNP_A-2181093	C	C	287	33	296	18	4.494	3.40E-02	rs17765307	3	46360165	p21.31
SNP_A-2098504	A	A	320	46	390	22	12.697	4.00E-04	rs3749461	3	46370317	p21.31
SNP_A-2280133	C	C	356	40	394	16	11.971	5.00E-04	rs3092957	3	46378965	p21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1794515	G	G	283	75	341	59	4.99	2.55E-02	rs6441980	3	46435722	p21.31
SNP_A-2286565	G	G	343	55	313	77	4.958	2.60E-02	rs17141113	3	46451352	p21.31
SNP_A-1900517	A	A	348	38	298	60	7.766	0.0053	rs1829538	3	46603730	p21.31
SNP_A-2186048	G	G	376	10	370	24	5.732	0.0167	rs6768627	3	46870380	p21.31
SNP_A-1790706	G	G	344	44	376	22	8.63	0.0033	rs7652849	3	46923530	p21.31
SNP_A-2245648	G	G	313	51	287	75	5.693	1.70E-02	rs9883000	3	49642695	p21.31
SNP_A-2067663	A	A	325	61	300	84	4.643	3.12E-02	rs9824435	3	49649347	p21.31
SNP_A-1896623	T	A	177	161	187	147	4.697	3.02E-02	rs11873626	3	49650146	p21.31
SNP_A-2223565	A	G	218	172	203	191	4.325	3.76E-02	rs2329020	3	49660077	p21.31
SNP_A-1943135	G	G	330	40	307	63	5.966	0.0146	rs1078341	3	49660596	p21.31
SNP_A-2071813	A	A	347	63	321	89	5.459	0.0195	rs7637711	3	49804657	p21.31
SNP_A-1750375	A	A	338	62	380	32	11.857	6.00E-04	rs2624842	3	50155430	p21.31
SNP_A-1781320	G	G	296	112	258	152	8.662	3.20E-03	rs12632110	3	50199229	p21.31
SNP_A-1972619	G	G	276	60	298	36	6.837	8.90E-03	---	3	50500158	p21.31
SNP_A-2237373	G	G	311	63	270	106	13.829	2.00E-04	rs2040397	3	50645082	p21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1910547	T	T	398	16	409	3	9.04	2.60E-03	rs12489219	3	51301491	p21.31
SNP_A-1700307	G	G	384	16	407	5	6.255	0.0124	rs2170177	3	51308935	p21.31
SNP_A-1957533	A	A	273	107	226	124	4.453	3.48E-02	rs11720298	3	51556549	p21.2
SNP_A-2309510	G	G	321	93	292	120	4.79	0.0286	rs11130296	3	51787992	p21.2
SNP_A-2045906	C	C	363	21	306	36	6.396	0.0114	rs3821841	3	52059080	p21.2
SNP_A-2024469	A	A	404	10	406	2	5.295	2.14E-02	rs4532127	3	52702776	p21.1
SNP_A-2172939	C	C	260	142	223	187	8.911	0.0028	rs9861459	3	54134360	p21.1
SNP_A-2072324	G	G	239	109	213	135	4.266	3.89E-02	rs9861843	3	54134398	p21.1
SNP_A-2269474	A	A	267	147	226	192	9.364	2.20E-03	rs9881544	3	54134457	p21.1
SNP_A-2025606	A	G	212	142	185	177	8.715	3.20E-03	rs7621151	3	54135946	p21.1
SNP_A-2160354	A	A	268	140	223	179	8.848	2.90E-03	rs9839987	3	54137628	p21.1
SNP_A-2023302	C	C	271	145	233	187	8.159	0.0043	rs9882539	3	54138244	p21.1
SNP_A-1907176	G	G	291	95	267	133	7.118	0.0076	rs7653648	3	54382242	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2304155	T	T	266	98	241	129	5.418	1.99E-02	rs1473348	3	54364035	p21.1
SNP_A-1903804	A	A	296	92	272	118	4.228	3.98E-02	rs731508	3	54397364	p21.1
SNP_A-2298412	G	G	297	55	275	81	5.794	0.0161	rs1992963	3	54438481	p14.3
SNP_A-1837035	C	C	241	147	197	163	4.204	4.03E-02	rs11747001	3	54486159	p14.3
SNP_A-2038724	C	C	385	23	405	5	12.073	5.00E-04	rs529098	3	54652231	p14.3
SNP_A-2119547	T	T	381	29	394	16	3.974	4.62E-02	rs510605	3	54684202	p14.3
SNP_A-1916606	G	G	363	13	388	4	5.266	2.17E-02	rs608142	3	54717602	p14.3
SNP_A-1797763	T	T	389	1	394	8	5.296	2.14E-02	rs1526591	3	54856323	p14.3
SNP_A-1741181	C	C	354	46	343	69	4.597	3.20E-02	rs1526594	3	54886110	p14.3
SNP_A-2212587	A	A	346	18	320	36	6.927	8.50E-03	rs9868201	3	54904540	p14.3
SNP_A-2174088	T	T	369	33	348	62	9.39	2.20E-03	rs9868221	3	54904586	p14.3
SNP_A-1862114	C	C	372	42	352	68	6.655	9.90E-03	rs9848771	3	54904630	p14.3
SNP_A-2246472	A	A	339	37	317	67	9.308	0.0023	rs6445708	3	54905739	p14.3
SNP_A-2035856	G	G	326	36	295	63	8.889	2.90E-03	rs17054524	3	54905834	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289310	T	T	335	35	301	55	5.994	0.0144	rs2141034	3	54918069	p14.3
SNP_A-2057458	G	G	377	35	347	53	4.749	0.0293	rs6782759	3	54925428	p14.3
SNP_A-2093862	G	G	203	181	241	153	5.472	1.93E-02	rs1526585	3	54926878	p14.3
SNP_A-1802352	G	T	210	206	238	182	4.287	3.84E-02	rs358004	3	55096567	p14.3
SNP_A-1791030	A	C	190	184	226	170	4.789	0.0286	rs358005	3	55096940	p14.3
SNP_A-2159673	A	A	289	125	261	157	5.038	2.48E-02	rs2068709	3	55195726	p14.3
SNP_A-2138986	C	C	253	89	229	115	4.503	3.38E-02	rs12106807	3	55553035	p14.3
SNP_A-2266139	A	A	270	118	252	156	5.392	2.02E-02	rs11711663	3	55577868	p14.3
SNP_A-1747441	T	T	322	66	363	49	4.251	3.92E-02	rs10510779	3	56068371	p14.3
SNP_A-1723756	G	G	330	62	362	44	4.292	3.83E-02	rs10510780	3	56068720	p14.3
SNP_A-1858994	C	C	315	71	325	47	4.781	2.88E-02	rs9865648	3	56087033	p14.3
SNP_A-1675553	C	C	324	68	362	50	4.356	3.69E-02	rs9311594	3	56089998	p14.3
SNP_A-2231542	G	G	340	72	368	52	4.257	3.91E-02	rs17235396	3	56130338	p14.3
SNP_A-2301045	A	A	300	58	344	36	7.506	6.10E-03	rs1545920	3	56261086	p14.3
SNP_A-2204901	C	C	357	27	366	14	4.213	4.01E-02	rs11719707	3	56666433	p14.3
SNP_A-1846186	G	G	353	49	371	27	6.796	9.10E-03	rs17235778	3	56883038	p14.3
SNP_A-1972712	G	G	266	134	238	170	5.74	0.0166	rs950155	3	56895920	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137644	G	G	213	139	252	120	4.115	4.25E-02	rs7612786	3	57483052	p14.3
SNP_A-2080060	A	A	355	55	337	77	4.116	4.25E-02	rs6790418	3	57580337	p14.3
SNP_A-2114709	T	T	384	22	346	46	10.206	0.0014	rs6791589	3	57839689	p14.3
SNP_A-2092471	C	C	356	18	341	33	4.735	2.96E-02	rs1866161	3	57933865	p14.3
SNP_A-1905818	G	G	390	20	372	36	4.992	2.55E-02	rs11708590	3	58311675	p14.3
SNP_A-2304194	A	A	391	21	379	41	6.562	0.0104	rs9864325	3	58311886	p14.3
SNP_A-1846609	C	C	212	146	242	100	10.224	0.0014	rs11712139	3	58359815	p14.3
SNP_A-1739637	A	A	258	140	229	171	4.812	2.83E-02	rs753819	3	58571728	p14.2
SNP_A-1972733	G	G	242	112	212	134	3.859	4.95E-02	rs753821	3	58589460	p14.2
SNP_A-2050187	C	C	227	103	201	145	8.318	3.90E-03	rs4681886	3	58594303	p14.2
SNP_A-2312676	A	G	198	168	209	185	3.874	4.90E-02	rs731608	3	58599810	p14.2
SNP_A-2236649	G	G	245	113	211	147	6.981	8.20E-03	rs13325549	3	59568534	p14.2
SNP_A-1972753	T	T	280	116	252	148	5.333	2.09E-02	rs1504913	3	59573582	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1830829	C	C	290	96	313	67	5.99	0.0144	rs9841870	3	59582258	p14.2
SNP_A-2145194	G	G	341	75	312	106	6.593	1.02E-02	rs3821473	3	59600917	p14.2
SNP_A-2120372	T	T	340	68	313	95	5.589	1.81E-02	rs3732548	3	59601005	p14.2
SNP_A-2070102	A	A	354	16	382	6	5.186	2.28E-02	rs17061096	3	59675643	p14.2
SNP_A-2109846	G	G	337	51	326	78	5.513	0.0189	rs1868190	3	59676470	p14.2
SNP_A-2285006	G	G	342	48	335	71	4.198	4.05E-02	rs2366846	3	59680934	p14.2
SNP_A-1859342	C	C	378	12	370	24	4.065	4.38E-02	rs17061176	3	59730881	p14.2
SNP_A-1972771	C	C	347	57	335	81	4.21	0.0402	rs17295225	3	59732868	p14.2
SNP_A-1972773	A	A	407	7	403	17	4.143	4.18E-02	rs6772278	3	59733714	p14.2
SNP_A-1972778	A	A	398	4	399	17	7.812	5.20E-03	rs17061328	3	59845297	p14.2
SNP_A-1832184	C	C	388	16	362	30	4.982	2.56E-02	rs1038517	3	59924180	p14.2
SNP_A-1941122	G	G	379	11	352	22	4.331	3.74E-02	rs974035	3	59926636	p14.2
SNP_A-2022904	C	C	209	187	252	136	11.983	5.00E-04	rs3772491	3	59944706	p14.2
SNP_A-2046273	G	G	201	165	251	141	6.529	0.0106	rs3772492	3	59944934	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1941427	C	C	356	12	346	24	4.137	4.20E-02	rs2736814	3	59945126	p14.2
SNP_A-1932762	G	G	217	189	265	147	9.987	1.60E-03	rs3821481	3	59946817	p14.2
SNP_A-1680492	G	G	229	167	263	143	4.084	4.33E-02	rs6788821	3	60081915	p14.2
SNP_A-1807454	C	C	360	4	368	0	4.066	4.38E-02	rs213355	3	60238886	p14.2
SNP_A-1972812	G	G	329	63	354	42	5.095	0.024	rs9878437	3	60296311	p14.2
SNP_A-1880774	G	G	332	54	353	35	4.695	3.03E-02	rs6789978	3	60312953	p14.2
SNP_A-1928810	C	C	193	137	215	111	3.888	4.86E-02	rs6782631	3	60325749	p14.2
SNP_A-1831230	C	C	375	31	391	17	4.413	3.57E-02	rs6807877	3	60506282	p14.2
SNP_A-2252467	A	A	283	33	291	57	4.981	2.56E-02	rs17031618	3	60518715	p14.2
SNP_A-1700221	G	G	305	77	299	107	4.224	3.99E-02	rs10510852	3	60574125	p14.2
SNP_A-2137198	T	T	409	7	402	18	4.881	2.71E-02	rs9839778	3	60661812	p14.2
SNP_A-2281736	C	C	409	7	402	18	4.881	2.71E-02	rs9876876	3	60667332	p14.2
SNP_A-1958173	A	A	193	179	231	151	5.65	1.75E-02	rs2044613	3	60883053	p14.2
SNP_A-2243088	A	A	209	195	237	157	5.736	0.0166	rs9827976	3	60898995	p14.2
SNP_A-2008743	C	C	322	80	345	55	5.418	1.99E-02	rs6776499	3	60935204	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1655725	C	C	341	37	324	60	5.841	1.57E-02	rs10510860	3	61059315	p14.2
SNP_A-2049906	G	G	388	26	407	13	4.745	2.94E-02	rs4688324	3	61140583	p14.2
SNP_A-1673018	G	G	336	64	318	92	5.398	2.02E-02	rs815719	3	61209807	p14.2
SNP_A-1972860	A	A	337	35	318	54	4.607	3.18E-02	rs815718	3	61228928	p14.2
SNP_A-2053502	C	C	401	5	416	0	5.155	2.32E-02	rs13085977	3	61656820	p14.2
SNP_A-1972878	C	C	354	30	364	16	4.379	3.64E-02	rs2189693	3	61943483	p14.2
SNP_A-1870564	T	T	408	2	401	9	4.515	3.36E-02	rs17055637	3	61952592	p14.2
SNP_A-2197804	G	G	219	185	253	157	4.698	3.02E-02	rs6774478	3	62012539	p14.2
SNP_A-2228144	G	G	339	21	345	43	6.576	0.0103	rs17066200	3	62108128	p14.2
SNP_A-1859097	A	A	304	52	333	33	5.43	1.98E-02	rs3755827	3	62335411	p14.2
SNP_A-1972898	T	C	209	197	223	171	5.231	2.22E-02	rs7650561	3	62466087	p14.2
SNP_A-2230171	A	A	286	54	269	75	3.916	4.78E-02	rs4447757	3	62519880	p14.2
SNP_A-2241866	T	T	335	19	321	5	7.325	6.80E-03	rs17696120	3	62526070	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2241580	C	C	378	16	392	6	4.78	2.88E-02	rs2048495	3	62535216	p14.2
SNP_A-1643065	T	T	360	40	350	60	4.018	4.50E-02	rs10510884	3	62619283	p14.2
SNP_A-1650918	T	T	289	109	260	150	7.846	5.10E-03	rs1506746	3	62661518	p14.2
SNP_A-1734866	T	T	241	159	216	196	5.048	0.0247	rs2886937	3	62661595	p14.2
SNP_A-1658196	C	C	241	159	216	196	5.048	0.0247	rs1561336	3	62661988	p14.2
SNP_A-2095258	A	A	336	66	311	95	6.17	1.30E-02	rs4688315	3	62663087	p14.2
SNP_A-1851943	G	G	213	131	194	166	4.65	0.031	rs4688320	3	62668392	p14.2
SNP_A-1700384	C	C	323	73	310	100	4.239	0.0395	rs488273	3	62674138	p14.2
SNP_A-1682684	A	A	309	91	288	124	5.628	0.0177	rs543060	3	62675081	p14.2
SNP_A-2164866	C	C	266	100	220	124	6.25	0.0124	rs6776257	3	62678202	p14.2
SNP_A-1942598	C	C	282	66	258	102	8.58	3.40E-03	rs581316	3	62690930	p14.2
SNP_A-2057908	C	C	317	89	277	115	5.763	1.64E-02	rs573009	3	62691342	p14.2
SNP_A-1720441	C	C	312	54	315	85	5.43	1.98E-02	rs10510892	3	62952488	p14.2
SNP_A-2298288	G	G	326	88	296	112	4.283	0.0385	rs13063547	3	63030222	p14.2
SNP_A-1840688	C	C	314	100	341	77	4.083	4.33E-02	rs6763613	3	63127947	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1748865	C	C	337	21	349	41	5.302	2.13E-02	rs2367773	3	63205266	p14.2
SNP_A-1972943	A	A	400	14	415	5	4.496	3.40E-02	rs17068381	3	63329586	p14.2
SNP_A-2281820	C	C	321	37	299	59	5.822	1.58E-02	rs11130939	3	63493103	p14.2
SNP_A-1911649	T	T	352	0	340	4	4.117	4.25E-02	rs4254651	3	63509759	p14.2
SNP_A-2172154	C	C	344	48	322	72	5.522	1.88E-02	rs13082882	3	63616027	p14.2
SNP_A-2143055	C	C	354	48	327	69	4.795	2.85E-02	rs17698642	3	63617707	p14.2
SNP_A-1839843	T	T	350	54	329	75	4.068	4.37E-02	rs11918391	3	63628287	p14.2
SNP_A-2143624	T	T	348	50	327	73	4.949	2.61E-02	rs13066470	3	63628995	p14.2
SNP_A-1958094	T	T	337	1	319	7	4.779	2.88E-02	rs17069314	3	63688285	p14.2
SNP_A-1972969	G	G	412	4	418	0	4.039	4.45E-02	rs161655	3	64062709	p14.1
SNP_A-2269673	A	A	412	4	412	0	3.981	4.60E-02	rs152245	3	64072014	p14.1
SNP_A-2095527	A	A	333	81	302	106	4.812	2.83E-02	rs6972270	3	64105561	p14.1
SNP_A-2263329	C	C	354	54	337	81	5.698	1.70E-02	rs13066611	3	64210467	p14.1
SNP_A-2217075	T	T	312	8	301	21	6.019	1.42E-02	rs3846223	3	64213362	p14.1
SNP_A-1972978	C	C	347	49	363	31	4.406	3.58E-02	rs704407	3	64220305	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2239370	T	T	385	5	408	0	5.264	0.0218	rs17070644	3	64343326	p14.1
SNP_A-1959190	C	C	247	155	275	127	4.282	0.0385	rs4688187	3	64347647	p14.1
SNP_A-1972994	C	A	218	184	212	190	3.901	0.0482	rs2371526	3	64400013	p14.1
SNP_A-2277686	T	T	283	105	247	135	6.149	1.31E-02	rs6768681	3	64458155	p14.1
SNP_A-2265507	A	A	279	75	310	56	4.188	0.0407	rs1036921	3	64518944	p14.1
SNP_A-2183290	A	T	200	184	221	173	5.207	2.25E-02	rs11130973	3	64533160	p14.1
SNP_A-2303772	G	G	240	82	265	51	8.408	3.70E-03	rs9820942	3	64535053	p14.1
SNP_A-2083737	C	C	291	119	307	91	3.984	4.59E-02	rs6780659	3	64570611	p14.1
SNP_A-2091752	G	G	289	113	307	87	3.844	0.0499	rs4607103	3	64686944	p14.1
SNP_A-1898776	G	G	404	4	403	13	4.689	0.0304	rs1862304	3	64687984	p14.1
SNP_A-1817989	A	A	300	44	275	65	5.11	2.38E-02	rs12635138	3	64875274	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1790083	T	T	338	66	309	93	5.88	1.53E-02	rs1442024	3	64880538	p14.1
SNP_A-1973011	C	C	242	164	267	131	4.84	2.78E-02	rs793291	3	64882689	p14.1
SNP_A-2311296	A	A	382	32	366	50	4.289	3.84E-02	rs17071837	3	64896620	p14.1
SNP_A-2058976	T	T	382	34	367	53	4.431	3.53E-02	rs17071854	3	64898934	p14.1
SNP_A-1753165	G	G	385	15	406	6	4.238	0.0395	rs10510917	3	64927639	p14.1
SNP_A-1647214	T	T	382	10	385	27	7.33	6.80E-03	rs10514722	3	64927939	p14.1
SNP_A-1973020	A	A	370	4	378	0	4.064	4.38E-02	rs17072474	3	65128555	p14.1
SNP_A-1973021	C	C	281	135	314	104	5.846	1.56E-02	rs9311935	3	65128739	p14.1
SNP_A-1683556	T	T	321	39	310	60	4.51	3.37E-02	rs781300	3	65199520	p14.1
SNP_A-2072598	C	C	325	78	342	56	3.951	4.69E-02	rs9866792	3	65209107	p14.1
SNP_A-1866671	C	C	396	4	404	0	4.06	4.39E-02	rs9854780	3	65337433	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2096622	C	C	325	65	356	42	6.275	1.22E-02	rs4362751	3	65707714	p14.1
SNP_A-2113893	A	A	263	101	297	79	4.56	0.0327	rs2566349	3	65836434	p14.1
SNP_A-1946208	C	C	378	14	388	4	5.686	1.71E-02	rs1482036	3	66379260	p14.1
SNP_A-1833372	T	T	237	135	287	99	10.054	0.0015	rs332340	3	66401147	p14.1
SNP_A-2150403	C	C	240	112	214	148	6.335	0.0118	rs782751	3	66432984	p14.1
SNP_A-2289923	A	A	240	148	274	114	6.661	9.90E-03	rs7637307	3	66741892	p14.1
SNP_A-2267179	T	T	371	43	352	62	3.937	4.72E-02	rs9875865	3	66989686	p14.1
SNP_A-2238046	C	C	346	10	339	21	3.953	4.68E-02	rs17043972	3	66990560	p14.1
SNP_A-2307085	A	A	309	61	291	91	6.271	0.0123	rs9310249	3	67023104	p14.1
SNP_A-2057601	C	C	280	92	254	118	4.485	3.42E-02	rs2198795	3	67089922	p14.1
SNP_A-2131552	C	C	304	106	279	133	4.117	0.0424	rs9874651	3	67095948	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2032280	A	A	295	75	226	84	4.388	3.62E-02	rs12714803	3	67114828	p14.1
SNP_A-2287944	A	A	199	181	234	158	4.204	4.03E-02	rs4435567	3	67259375	p14.1
SNP_A-2213551	A	A	388	2	363	9	4.864	2.74E-02	rs17046237	3	67463878	p14.1
SNP_A-2313386	C	C	333	7	338	18	4.512	3.37E-02	rs2772473	3	67678797	p14.1
SNP_A-1973112	T	T	344	0	302	4	4.525	3.34E-02	rs1026537	3	67836658	p14.1
SNP_A-1746532	G	G	351	49	336	72	4.621	3.16E-02	rs1597082	3	67916503	p14.1
SNP_A-1749299	A	A	348	34	336	62	8.052	4.50E-03	rs1597083	3	67917898	p14.1
SNP_A-1792914	C	C	305	93	328	62	6.955	8.40E-03	rs1585383	3	67939031	p14.1
SNP_A-2193229	A	A	314	100	352	68	8.221	4.10E-03	rs7627319	3	67945122	p14.1
SNP_A-1931840	G	G	377	23	366	40	4.706	3.01E-02	rs4856909	3	68045430	p14.1
SNP_A-1973118	A	A	340	40	295	59	5.922	1.50E-02	rs1872434	3	68068627	p14.1
SNP_A-1919055	G	G	328	30	318	48	4.221	3.99E-02	rs1905797	3	68097824	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189160	A	A	298	100	278	128	4.054	0.0441	rs17140815	3	68098241	p14.1
SNP_A-1973120	C	C	299	75	267	101	5.602	1.79E-02	rs4145917	3	68099517	p14.1
SNP_A-2165297	G	A	187	141	182	164	6.235	1.25E-02	rs1491744	3	68460500	p14.1
SNP_A-2173570	T	T	247	163	219	193	4.206	4.03E-02	rs12489206	3	68482579	p14.1
SNP_A-2267918	G	G	248	124	216	148	4.238	0.0395	rs262198	3	68508072	p14.1
SNP_A-2154334	A	G	199	183	212	156	7.079	7.80E-03	rs2221759	3	68519515	p14.1
SNP_A-2167259	T	T	211	177	246	152	4.454	3.48E-02	rs6809730	3	68678897	p14.1
SNP_A-2212447	G	G	353	5	285	13	5.36	0.0206	rs17047825	3	68682878	p14.1
SNP_A-2087340	G	G	267	103	235	143	8.459	3.60E-03	rs1504298	3	68850146	p14.1
SNP_A-1876220	G	G	250	124	218	158	6.282	1.22E-02	rs9856483	3	68859507	p14.1
SNP_A-2211826	C	C	229	111	186	144	8.579	3.40E-03	rs1504299	3	68863715	p14.1
SNP_A-2291677	A	A	288	124	259	159	5.823	1.58E-02	rs6795777	3	68872908	p14.1
SNP_A-1879733	C	C	299	99	258	126	6.009	1.42E-02	rs4484195	3	68905626	p14.1
SNP_A-1824824	A	A	281	73	240	104	8.514	3.50E-03	rs4855515	3	68938426	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1973141	C	C	281	81	246	130	13.443	2.00E-04	rs4855516	3	68940970	p14.1
SNP_A-1896139	C	C	323	57	285	81	6.288	1.22E-02	rs7650625	3	69046799	p14.1
SNP_A-2091553	T	T	253	75	234	100	4.259	3.91E-02	rs7642925	3	69046912	p14.1
SNP_A-2147495	C	C	338	70	312	94	4.547	3.30E-02	rs7609906	3	69048242	p14.1
SNP_A-2109401	C	C	400	4	416	0	4.139	0.0419	rs9829895	3	69053524	p14.1
SNP_A-1973148	G	G	375	1	376	8	5.362	0.0206	rs17005366	3	69249046	p14.1
SNP_A-2087557	T	T	358	8	377	1	5.744	1.65E-02	rs937863	3	69253538	p14.1
SNP_A-1904505	T	T	414	2	409	9	4.48	3.43E-02	rs4447768	3	69363593	p14.1
SNP_A-1973153	C	C	392	22	383	37	3.875	4.90E-02	rs900668	3	69508309	p14.1
SNP_A-2008798	C	C	389	19	378	34	4.384	3.63E-02	rs1982747	3	69510320	p14.1
SNP_A-1973161	A	A	333	33	333	55	4.862	0.0275	rs7620140	3	69678826	p14.1
SNP_A-1973162	C	C	375	31	358	48	4.052	0.0441	rs7650789	3	69678898	p14.1
SNP_A-1811698	C	C	306	28	330	14	5.426	1.98E-02	rs9310163	3	69682512	p14.1
SNP_A-2286675	G	G	365	21	354	36	4.095	4.30E-02	rs17435195	3	69702681	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2230213	T	T	230	120	255	95	4.196	4.05E-02	rs7641148	3	69859414	p14.1
SNP_A-2035601	A	A	312	0	337	5	4.597	3.20E-02	rs6769936	3	70156333	p13
SNP_A-1666784	T	T	331	63	305	103	10.46	1.20E-03	rs9310194	3	70563677	p13
SNP_A-1960215	T	T	283	87	317	65	4.921	2.65E-02	rs995051	3	70599874	p13
SNP_A-1973192	A	A	259	101	270	60	9.383	2.20E-03	rs1491607	3	70661075	p13
SNP_A-1751637	A	A	252	142	294	116	5.535	1.86E-02	rs2293171	3	70937618	p13
SNP_A-1940613	C	T	211	153	182	178	5.288	2.15E-02	rs9874207	3	71102440	p13
SNP_A-1914215	A	A	386	8	377	19	4.583	3.23E-02	rs3846029	3	71237809	p13
SNP_A-2044372	A	A	331	35	324	54	3.938	4.72E-02	rs6776058	3	71367067	p13
SNP_A-2283489	C	C	377	39	392	24	3.864	4.93E-02	rs3732733	3	71369457	p13
SNP_A-1868221	C	C	229	171	265	147	4.258	3.91E-02	rs864386	3	71508060	p13
SNP_A-1679554	A	A	250	148	286	126	3.944	4.71E-02	rs830604	3	71510724	p13
SNP_A-2247058	A	A	260	136	289	109	4.502	3.38E-02	rs6773658	3	71694839	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1731295	C	C	284	116	254	156	7.433	6.40E-03	rs1374913	3	71732475	p13
SNP_A-2245634	C	C	380	20	384	8	5.084	2.42E-02	rs9877458	3	71828378	p13
SNP_A-2094158	G	G	190	142	242	118	7.354	6.70E-03	rs9822586	3	71868740	p13
SNP_A-1887037	T	A	160	158	191	123	7.933	4.90E-03	rs2684381	3	71879530	p13
SNP_A-1935169	A	A	174	152	191	117	4.839	2.78E-02	rs2874710	3	72039132	p13
SNP_A-2290083	T	T	218	160	240	130	4.075	4.35E-02	rs6801579	3	72039498	p13
SNP_A-1865523	C	C	175	171	184	116	7.528	6.10E-03	rs9917816	3	72320862	p13
SNP_A-2008822	C	C	246	124	292	94	7.726	5.40E-03	rs4128691	3	72432553	p13
SNP_A-1919711	C	C	227	159	253	131	4.107	4.27E-02	rs11708482	3	72787429	p13
SNP_A-2079723	G	G	362	4	352	0	3.869	4.92E-02	rs1542735	3	72825317	p13
SNP_A-2118592	A	A	312	104	286	132	4.448	0.0349	rs6808341	3	72997537	p13
SNP_A-2223458	A	A	271	133	238	162	4.971	0.0258	rs4274693	3	73032065	p13
SNP_A-2024269	G	G	266	120	234	152	5.813	1.59E-02	rs11925587	3	73034917	p13
SNP_A-2082369	A	A	280	136	243	169	6.169	1.30E-02	rs13063441	3	73035090	p13
SNP_A-2127765	C	C	243	129	277	107	4.084	4.33E-02	rs3821379	3	73099664	p13
SNP_A-2025685	C	C	223	137	242	102	5.541	1.86E-02	rs6793043	3	73103454	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1788953	A	A	285	77	247	107	7.517	6.10E-03	rs7647234	3	73461534	p13
SNP_A-1895412	A	A	325	5	338	0	5.16	2.31E-02	rs9883532	3	73571949	p13
SNP_A-2301370	G	G	294	50	258	72	6.027	0.0141	rs9818674	3	73573872	p13
SNP_A-1738423	T	T	251	149	288	124	4.653	0.031	rs1526723	3	73951809	p13
SNP_A-2008837	T	C	223	175	203	175	7.352	6.70E-03	rs291485	3	73961357	p13
SNP_A-2209411	A	A	361	17	406	8	4.253	3.92E-02	—	3	74136458	p13
SNP_A-1947277	A	A	319	61	333	39	5.056	2.45E-02	rs1440625	3	74242144	p12.3
SNP_A-1938447	T	A	198	174	203	163	5.576	1.82E-02	rs35986	3	74353650	p12.3
SNP_A-1973290	C	A	207	189	219	179	4.232	3.97E-02	rs39693	3	74355365	p12.3
SNP_A-2286490	A	A	296	102	328	62	11.317	8.00E-04	rs862823	3	74439290	p12.3
SNP_A-2025076	G	G	323	77	342	56	3.854	4.96E-02	rs2197742	3	74439371	p12.3
SNP_A-1931074	G	G	392	8	417	1	5.824	1.58E-02	rs1266585	3	74447335	p12.3
SNP_A-1821734	A	A	280	112	302	86	4.225	3.98E-02	rs4676967	3	74545676	p12.3
SNP_A-2302718	C	C	377	33	356	50	4.064	4.38E-02	rs6797762	3	74579764	p12.3
SNP_A-1730010	A	G	214	186	218	180	5.464	1.94E-02	rs4131575	3	74696398	p12.3
SNP_A-2227099	G	G	193	181	224	144	6.469	1.10E-02	rs9874426	3	74805605	p12.3
SNP_A-2135198	C	T	218	186	229	183	7.433	6.40E-03	rs9861122	3	74853137	p12.3
SNP_A-2265057	G	G	197	159	232	134	4.851	0.0276	rs9837543	3	74853182	p12.3
SNP_A-1937695	C	C	213	201	249	169	5.554	0.0184	rs7635818	3	74866166	p12.3
SNP_A-1938020	A	C	225	183	225	187	7.809	5.20E-03	rs6549652	3	74873680	p12.3
SNP_A-1973294	G	A	167	161	180	134	4.373	3.65E-02	rs2049623	3	74904290	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946738	T	C	221	179	211	191	4.805	2.84E-02	rs9827925	3	74916743	p12.3
SNP_A-1911767	G	A	227	187	218	194	4.955	2.60E-02	rs7651319	3	74919064	p12.3
SNP_A-2192435	A	A	333	61	316	86	4.617	3.17E-02	rs11712680	3	75091709	p12.3
SNP_A-1813783	A	A	270	142	300	112	5.122	2.36E-02	rs13083349	3	75332099	p12.3
SNP_A-2025658	C	C	254	110	280	86	4.199	4.04E-02	rs4072316	3	75352178	p12.3
SNP_A-2200097	G	G	408	4	418	0	4.078	4.34E-02	rs12496616	3	75476955	p12.3
SNP_A-1938279	G	G	370	12	379	3	5.508	0.0189	rs2918469	3	75847317	p12.3
SNP_A-1816084	A	A	221	127	195	155	4.399	3.60E-02	rs7610010	3	76177052	p12.3
SNP_A-1955714	C	C	341	33	355	13	8.929	0.0028	rs3884321	3	76970294	p12.3
SNP_A-2049025	C	C	349	33	365	15	7.103	7.70E-03	rs5745841	3	76971147	p12.3
SNP_A-1888115	A	A	330	34	371	17	7.306	6.90E-03	rs4521284	3	77164589	p12.3
SNP_A-1946159	G	G	229	155	198	182	4.393	0.0361	rs7648530	3	77263329	p12.3
SNP_A-1817376	T	T	317	79	354	60	4.239	0.0395	rs9826655	3	77331337	p12.3
SNP_A-1909341	A	A	324	80	341	55	4.985	2.56E-02	rs1523756	3	77679369	p12.3
SNP_A-1869426	A	A	306	60	278	82	4.702	3.01E-02	rs9831754	3	78436281	p12.3
SNP_A-2214067	T	T	324	82	297	111	5.527	1.87E-02	rs9840031	3	78478830	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872629	C	C	291	121	256	144	4.059	4.39E-02	rs4680938	3	78661330	p12.3
SNP_A-2049889	A	A	286	118	257	143	3.924	4.76E-02	rs6808324	3	78661932	p12.3
SNP_A-1973362	A	A	365	31	342	48	4.361	3.68E-02	rs17300673	3	78677401	p12.3
SNP_A-2143403	C	C	396	0	394	10	9.926	1.60E-03	rs4532095	3	79312582	p12.3
SNP_A-2163208	T	T	377	17	377	35	5.832	1.57E-02	rs17395825	3	79440079	p12.3
SNP_A-2263546	C	C	331	53	319	79	5.094	0.024	rs9882958	3	79687184	p12.3
SNP_A-2102956	C	C	366	10	389	3	4.138	0.0419	rs9835692	3	79713308	p12.3
SNP_A-2242647	G	G	346	20	356	8	5.28	2.16E-02	rs1502291	3	79967750	p12.2
SNP_A-1663956	T	C	200	160	211	173	8.2	4.20E-03	rs4856497	3	80053546	p12.2
SNP_A-2181134	T	T	283	75	289	45	6.739	9.40E-03	rs1384762	3	80117768	p12.2
SNP_A-1845979	C	C	280	112	257	153	6.928	8.50E-03	rs6787260	3	80238653	p12.2
SNP_A-1681826	C	C	273	123	315	93	6.989	8.20E-03	rs950318	3	80324087	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1715709	A	A	266	88	258	122	4.712	3.00E-02	rs6764710	3	80374806	p12.2
SNP_A-2078137	G	A	216	184	220	192	4.443	3.50E-02	rs9855082	3	80442545	p12.2
SNP_A-1704763	C	C	252	148	286	124	4.144	4.18E-02	rs1356030	3	80464004	p12.2
SNP_A-2086530	C	C	231	119	195	153	7.287	6.90E-03	rs1606717	3	80493393	p12.2
SNP_A-2126442	A	A	170	152	191	117	5.467	1.94E-02	rs6785111	3	80544332	p12.2
SNP_A-1973385	C	C	219	161	250	132	4.914	2.66E-02	rs4856616	3	80549171	p12.2
SNP_A-2261485	C	C	234	128	260	98	5.329	2.10E-02	rs9883980	3	80553686	p12.2
SNP_A-2224613	A	A	225	181	259	149	5.487	1.92E-02	rs9309860	3	80553990	p12.2
SNP_A-1822421	T	T	248	76	229	111	6.926	8.50E-03	rs4510346	3	80578450	p12.2
SNP_A-1909214	A	A	227	125	258	94	6.37	1.16E-02	rs11918372	3	80627826	p12.2
SNP_A-1973387	C	C	233	125	273	95	7.117	0.0076	rs12635325	3	80630759	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044697	G	G	237	135	286	92	9.552	0.002	rs11719208	3	80634166	p12.2
SNP_A-2302111	C	C	219	101	253	77	5.533	1.87E-02	rs8180054	3	80636308	p12.2
SNP_A-2200042	G	G	207	103	250	86	4.536	0.0332	rs13081960	3	80638182	p12.2
SNP_A-1864610	G	G	241	127	262	100	4.039	4.45E-02	rs6548709	3	80643098	p12.2
SNP_A-1934754	A	A	251	143	277	113	4.776	2.89E-02	rs1399556	3	80647028	p12.2
SNP_A-2053504	C	C	261	153	293	125	4.649	3.11E-02	rs10865586	3	80673887	p12.2
SNP_A-2051721	A	A	240	134	263	107	4.055	4.40E-02	rs1516585	3	80687393	p12.2
SNP_A-1810925	A	A	217	119	242	92	4.811	2.83E-02	rs1437046	3	80748644	p12.2
SNP_A-2271219	A	A	244	142	274	104	7.524	6.10E-03	rs521796	3	80757077	p12.2
SNP_A-2130656	C	C	234	126	268	100	5.207	2.25E-02	rs878245	3	80775368	p12.2
SNP_A-2305795	A	A	229	133	277	117	4.23	3.97E-02	rs641490	3	80776141	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909127	T	T	210	112	258	96	4.649	3.11E-02	rs632116	3	80788767	p12.2
SNP_A-1838643	T	T	219	113	250	90	4.56	0.0327	rs485487	3	80794579	p12.2
SNP_A-1973398	G	G	230	124	250	92	5.369	2.05E-02	rs2139685	3	80869953	p12.2
SNP_A-2130118	A	A	224	108	243	77	5.749	1.65E-02	rs1520590	3	80877946	p12.2
SNP_A-1973402	G	G	215	111	271	91	6.567	0.0104	rs2372735	3	81094894	p12.2
SNP_A-2275244	G	G	245	105	214	132	5.147	2.33E-02	rs6807149	3	81110241	p12.2
SNP_A-1781697	C	C	242	136	268	108	4.533	0.0332	rs2578305	3	81125801	p12.2
SNP_A-1695047	A	A	387	13	379	31	7.325	6.80E-03	rs10511100	3	82065098	p12.2
SNP_A-2169239	C	C	255	141	269	109	4.054	0.0441	rs7635420	3	82620908	p12.2
SNP_A-1908706	G	G	221	187	249	159	3.934	4.73E-02	rs6548831	3	82652949	p12.2
SNP_A-1658444	G	G	233	167	272	140	5.21	2.25E-02	rs1382069	3	82687689	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1742225	T	T	234	166	272	140	4.887	2.71E-02	rs726174	3	82687898	p12.2
SNP_A-1675115	C	C	235	161	271	133	5.148	2.33E-02	rs10511098	3	82700835	p12.2
SNP_A-2162726	C	C	306	104	336	82	3.927	4.75E-02	rs834840	3	82795044	p12.2
SNP_A-2199892	G	G	282	40	318	24	5.563	0.0183	rs1382068	3	82814931	p12.2
SNP_A-2282730	A	A	235	163	264	136	4.119	0.0424	rs1351039	3	82856244	p12.2
SNP_A-1746873	G	G	283	111	255	151	7.386	0.0066	rs9309917	3	82867947	p12.2
SNP_A-2117514	A	A	263	81	231	101	4.059	4.39E-02	rs9837776	3	82965467	p12.2
SNP_A-1973431	A	A	225	129	178	144	4.802	2.84E-02	rs9875881	3	82986544	p12.2
SNP_A-1816514	G	G	287	115	254	140	4.384	3.63E-02	rs13072850	3	83027115	p12.2
SNP_A-1939785	G	G	342	22	363	11	4.157	4.15E-02	rs6548923	3	84022255	p12.1
SNP_A-1807382	A	A	272	138	298	112	3.89	4.86E-02	rs7633979	3	84137907	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2008874	G	G	331	27	315	9	7.72	5.50E-03	rs4390938	3	84261919	p12.1
SNP_A-2270605	A	A	282	78	297	51	5.838	1.57E-02	rs12633731	3	84485807	p12.1
SNP_A-2081587	C	C	268	140	297	103	7.044	8.00E-03	rs9844070	3	84635281	p12.1
SNP_A-2151686	G	G	250	120	286	100	3.899	4.83E-02	rs9837635	3	84639646	p12.1
SNP_A-1973457	C	C	274	140	307	113	4.713	2.99E-02	rs9309944	3	84657181	p12.1
SNP_A-1973460	C	C	351	53	384	32	6.496	1.08E-02	rs2171056	3	84730396	p12.1
SNP_A-1929376	G	G	337	45	348	16	13.537	2.00E-04	rs17021652	3	84760920	p12.1
SNP_A-1706429	A	A	379	21	404	8	6.45	0.0111	rs10490896	3	85022402	p12.1
SNP_A-2187656	G	G	393	13	410	4	5.047	0.0247	—	3	85112415	p12.1
SNP_A-1915625	T	T	373	21	398	8	6.46	1.10E-02	rs11914646	3	85176319	p12.1
SNP_A-1973466	T	T	371	13	377	3	6.277	1.22E-02	rs10490897	3	85184263	p12.1
SNP_A-2257192	G	G	196	148	198	106	4.503	3.38E-02	rs7623714	3	85226226	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044431	C	C	361	11	381	3	4.921	2.65E-02	rs6809486	3	85480803	p12.1
SNP_A-2028447	C	C	336	14	375	5	5.178	0.0229	rs9309974	3	85480882	p12.1
SNP_A-2108361	G	G	388	8	409	1	5.756	1.64E-02	rs9873752	3	85484338	p12.1
SNP_A-1948082	G	G	335	41	354	24	4.965	2.59E-02	rs9824840	3	85513529	p12.1
SNP_A-1937463	A	A	306	26	307	11	5.784	1.62E-02	rs9824071	3	85582283	p12.1
SNP_A-1973484	A	A	409	7	405	1	4.399	3.60E-02	rs2875492	3	86088900	p12.1
SNP_A-1952584	C	C	386	4	400	0	4.123	4.23E-02	rs17024414	3	86170761	p12.1
SNP_A-1795526	G	G	337	79	305	103	4.683	3.05E-02	rs1845768	3	86522285	p12.1
SNP_A-1683594	G	G	291	47	319	27	6.598	1.02E-02	rs979626	3	87035363	p12.1
SNP_A-1848438	C	C	363	15	372	6	3.967	4.64E-02	—	3	87253646	p11.2
SNP_A-2097444	G	G	241	155	210	188	5.301	2.13E-02	rs1844097	3	87283325	p11.2
SNP_A-2180638	C	T	237	169	204	200	6.412	1.13E-02	rs6805890	3	87311162	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2075389	G	G	361	31	383	17	4.654	0.031	rs11127974	3	87352247	p11.2
SNP_A-1973510	C	C	193	125	216	96	5.042	0.0247	rs2646215	3	87433248	p11.2
SNP_A-2041332	G	G	372	44	388	28	3.892	4.85E-02	rs7618952	3	87453387	p11.2
SNP_A-2287110	C	C	392	24	409	11	5.17	0.023	rs11917983	3	87541530	p11.2
SNP_A-1945794	T	T	322	52	338	32	5.128	0.0235	rs11127993	3	87701108	p11.2
SNP_A-2057935	C	C	309	63	317	37	6.42	1.13E-02	rs7650135	3	88395955	p11.1
SNP_A-2299626	G	G	294	80	286	112	4.702	3.01E-02	rs936361	3	88410116	p11.1
SNP_A-1800198	G	G	313	31	340	14	7.397	6.50E-03	---	3	88464836	p11.1
SNP_A-2062229	T	T	286	124	320	96	5.428	1.98E-02	rs11713321	3	88597456	p11.1
SNP_A-1750233	G	G	216	134	200	184	6.917	8.50E-03	rs1603314	3	88683633	p11.1
SNP_A-1873214	T	T	335	31	358	18	4.078	4.34E-02	rs955291	3	88720601	p11.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1859546	C	C	224	124	249	89	6.928	8.50E-03	rs6809708	3	88836082	p11.1
SNP_A-2062339	C	C	229	143	199	177	5.694	1.70E-02	rs13084044	3	88855357	p11.1
SNP_A-2255818	T	T	249	163	215	197	5.702	1.69E-02	rs1384772	3	88866530	p11.1
SNP_A-1883343	C	C	320	86	297	113	4.501	0.0339	rs17026944	3	89603821	p11.1
SNP_A-1973546	G	G	301	45	301	25	5.124	2.36E-02	rs17801309	3	89604354	p11.1
SNP_A-2061599	A	A	371	43	392	24	5.961	0.0146	rs7618160	3	89718321	p11.1
SNP_A-1876730	T	T	351	19	328	32	3.957	4.67E-02	rs7634358	3	89953636	p11.1
SNP_A-1937211	C	C	302	62	304	40	4.19	0.0407	rs9289536	3	95031169	q11.2
SNP_A-1946268	A	A	395	11	383	23	4.42	3.55E-02	rs5548545	3	95540029	q11.2
SNP_A-1933745	C	C	366	16	396	2	11.747	6.00E-04	rs6790126	3	96199074	q11.2
SNP_A-1693395	G	G	369	31	396	16	5.564	0.0183	rs9288884	3	96337618	q11.2
SNP_A-2250565	G	G	364	28	387	13	6.112	0.0134	rs11715081	3	96469139	q11.2
SNP_A-1796197	A	A	376	35	393	19	5.63	0.0177	rs9834958	3	96495196	q11.2
SNP_A-1844699	C	C	374	34	394	20	4.107	4.27E-02	rs9812397	3	96507118	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225324	G	G	370	46	347	71	6.075	0.0137	rs520258	3	96545176	q11.2
SNP_A-1973570	T	T	388	8	375	21	6.049	1.39E-02	rs1581214	3	96612964	q11.2
SNP_A-2063662	C	C	238	144	207	187	7.562	6.00E-03	rs6784642	3	96634157	q11.2
SNP_A-1834207	T	G	204	152	186	184	4.183	4.08E-02	rs5000487	3	96664292	q11.2
SNP_A-1888343	G	G	217	151	184	172	3.883	4.88E-02	rs6437890	3	96703953	q11.2
SNP_A-1833084	C	C	233	153	202	182	4.714	2.99E-02	rs6786347	3	96717021	q11.2
SNP_A-1924710	T	A	188	158	189	153	6.339	0.0118	rs6801582	3	96717069	q11.2
SNP_A-2279899	G	G	253	141	229	173	4.376	3.64E-02	rs6790116	3	96735786	q11.2
SNP_A-2195986	G	G	236	162	205	195	5.225	0.0223	rs4073617	3	96781117	q11.2
SNP_A-2132455	C	C	204	128	169	151	4.961	2.59E-02	rs6437963	3	96817950	q11.2
SNP_A-1857925	G	G	216	146	191	179	4.8	2.85E-02	rs6437968	3	96820158	q11.2
SNP_A-2048449	C	C	352	6	388	0	6.556	1.05E-02	rs7434063	3	97294072	q11.2
SNP_A-2256744	C	C	322	52	323	27	7.125	0.0076	rs1453610	3	97338858	q11.2
SNP_A-2258658	T	T	263	149	235	179	4.313	0.0378	rs13088064	3	97503012	q11.2
SNP_A-2021760	A	A	287	129	259	159	4.556	3.28E-02	rs1514423	3	97544033	q11.2
SNP_A-2121198	C	C	374	2	340	8	4.142	4.18E-02	rs9826636	3	98030546	q11.2
SNP_A-1729822	G	G	205	147	201	195	4.203	4.04E-02	rs1024055	3	99245589	q12.1
SNP_A-2039992	T	T	351	53	374	32	5.913	1.50E-02	rs4241471	3	99465807	q12.1
SNP_A-2226450	G	G	358	30	374	16	4.605	3.19E-02	rs7614425	3	99656948	q12.1
SNP_A-1973606	G	A	183	129	186	178	6.422	1.13E-02	rs1529047	3	99734717	q12.1
SNP_A-1973619	T	T	300	74	329	49	6.397	0.0114	rs10511171	3	100195955	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101984	G	G	347	11	338	26	6.15	1.31E-02	rs7653590	3	100817091	q12.1
SNP_A-1973641	G	G	305	51	293	77	5.254	2.19E-02	rs496664	3	100824533	q12.1
SNP_A-1854364	A	A	376	16	386	6	4.677	3.06E-02	rs7628739	3	100831101	q12.1
SNP_A-1960770	C	C	296	78	278	104	4.195	4.06E-02	rs9815950	3	100848555	q12.1
SNP_A-1913913	G	G	401	15	414	6	4.045	4.43E-02	rs277655	3	101527277	q12.2
SNP_A-1973656	C	C	310	86	290	120	6.037	0.014	rs12591	3	101565547	q12.2
SNP_A-1862402	A	A	276	102	304	80	3.964	0.0465	rs3773921	3	101937829	q12.2
SNP_A-2163612	G	G	261	67	277	45	4.742	2.94E-02	rs1048364	3	101951190	q12.2
SNP_A-2069182	T	T	242	152	217	195	6.291	0.0121	rs7642041	3	101962074	q12.2
SNP_A-1922437	C	C	353	63	361	39	5.425	1.98E-02	rs16843216	3	102279569	q12.2
SNP_A-1790273	C	C	291	43	312	28	3.847	4.98E-02	rs7651740	3	102500308	q12.3
SNP_A-2109984	C	C	386	30	393	15	4.986	2.56E-02	rs6794860	3	102892355	q12.3
SNP_A-2088625	G	G	378	26	402	12	5.775	1.63E-02	rs2625289	3	102987314	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2292995	G	G	328	88	354	66	4.115	4.25E-02	rs9850918	3	103149537	q12.3
SNP_A-2294851	G	G	307	63	338	46	3.883	4.88E-02	rs1707574	3	103154445	q12.3
SNP_A-2137206	T	T	287	43	290	20	7.795	5.20E-03	rs771787	3	103193047	q12.3
SNP_A-1973695	A	A	326	16	327	35	6.517	1.07E-02	rs7635336	3	103286196	q12.3
SNP_A-2154529	A	A	378	30	370	50	4.913	2.67E-02	rs2670132	3	103680144	q12.3
SNP_A-1701721	C	C	268	132	244	168	5.269	2.17E-02	rs1241287	3	103919014	q12.3
SNP_A-1860207	A	A	328	84	307	109	3.914	4.79E-02	rs10470520	3	103938290	q12.3
SNP_A-2283089	A	A	360	48	328	82	10.376	1.30E-03	rs3849511	3	104133713	q12.3
SNP_A-2129937	G	G	343	27	360	12	6.175	1.30E-02	rs17781819	3	104364631	q13.11
SNP_A-1973727	A	A	325	43	347	27	4.329	3.75E-02	rs16846607	3	104886801	q13.11
SNP_A-2249846	T	T	297	37	315	21	4.937	0.0263	rs16846632	3	104908550	q13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2305962	C	C	346	50	357	29	5.627	0.0177	rs9883601	3	105314372	q13.11
SNP_A-1973742	A	A	301	65	324	42	5.79	0.0161	rs747319	3	105328103	q13.11
SNP_A-1945650	C	C	345	41	364	24	4.95	2.61E-02	rs17534353	3	105329613	q13.11
SNP_A-1953416	G	G	247	111	299	87	6.817	9.00E-03	rs1920332	3	105397447	q13.11
SNP_A-2139191	T	T	337	61	299	105	13.889	2.00E-04	rs2178417	3	105398394	q13.11
SNP_A-1973744	A	A	350	66	309	107	12.268	5.00E-04	rs2141621	3	105398479	q13.11
SNP_A-1729548	G	G	400	0	408	4	3.903	0.0482	rs10511224	3	105416910	q13.11
SNP_A-1945495	C	C	259	141	302	102	9.535	0.002	rs7639492	3	105421132	q13.11
SNP_A-1930451	C	C	231	109	268	70	11.235	8.00E-04	rs9881249	3	105435046	q13.11
SNP_A-2274077	C	C	258	142	303	103	9.774	0.0018	rs12497672	3	105435238	q13.11
SNP_A-2150943	G	G	221	113	263	77	10.413	1.30E-03	rs6775741	3	105454300	q13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137226	G	G	252	158	285	125	5.876	1.53E-02	rs11708792	3	105458017	q13.11
SNP_A-2023444	A	A	242	156	288	120	8.565	3.40E-03	rs11710903	3	105480662	q13.11
SNP_A-2302416	T	T	223	145	242	108	5.74	0.0166	rs2398981	3	105481285	q13.11
SNP_A-1929532	G	G	220	140	236	106	4.802	2.84E-02	rs2633702	3	105901394	q13.11
SNP_A-1973780	C	C	216	134	211	89	5.325	2.10E-02	rs9868520	3	106468340	q13.11
SNP_A-1687556	G	G	293	33	286	76	15.206	9.64E-05	rs726444	3	106759439	q13.11
SNP_A-2131135	A	A	366	46	376	28	4.435	3.52E-02	rs894934	3	106820842	q13.11
SNP_A-2079966	G	G	275	69	250	98	6.203	1.27E-02	rs1443108	3	106905095	q13.11
SNP_A-2144394	A	A	283	85	266	116	5.048	0.0247	rs3772513	3	106971262	q13.11
SNP_A-2078211	T	T	402	8	400	20	5.028	2.49E-02	rs2120103	3	107002006	q13.11
SNP_A-1846659	A	A	374	34	360	58	6.408	0.0114	rs12497428	3	107007179	q13.11
SNP_A-1694411	G	G	398	2	403	9	4.309	3.79E-02	rs2127091	3	107050927	q13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2262706	C	C	415	1	412	8	5.436	1.97E-02	rs729067	3	107270190	q13.11
SNP_A-2126040	T	T	358	10	349	23	5.214	0.0224	rs7632189	3	107372793	q13.11
SNP_A-1726970	T	T	347	53	375	35	4.645	3.11E-02	rs7627016	3	107568729	q13.12
SNP_A-2162422	G	G	384	4	381	13	4.731	2.96E-02	rs7634049	3	107838105	q13.12
SNP_A-1908498	G	G	408	4	403	13	4.776	2.89E-02	rs6796767	3	107982786	q13.12
SNP_A-1824021	A	A	298	92	277	119	4.176	4.10E-02	rs4895039	3	108005925	q13.12
SNP_A-1898821	A	A	299	109	272	144	6.042	0.014	rs1520717	3	108011334	q13.12
SNP_A-2196721	A	A	264	152	221	199	10.087	0.0015	rs1709915	3	108096126	q13.12
SNP_A-1730865	C	C	216	162	217	119	4.126	4.22E-02	rs661276	3	108686450	q13.12
SNP_A-2184248	G	G	328	56	300	80	5.463	1.94E-02	rs1282401	3	108769956	q13.12
SNP_A-1890297	C	C	327	67	338	42	5.665	1.73E-02	rs13317948	3	109077156	q13.12
SNP_A-1752045	A	A	315	85	348	62	5.118	2.37E-02	rs10511271	3	109435473	q13.13
SNP_A-2268564	T	T	361	29	341	49	5.698	1.70E-02	rs17830898	3	109519838	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1940404	A	A	272	104	289	73	5.681	1.71E-02	rs936262	3	109546293	q13.13
SNP_A-1780900	C	C	266	88	298	64	5.516	1.88E-02	rs936261	3	109546548	q13.13
SNP_A-2188034	C	C	318	74	350	50	6.098	0.0135	rs7636575	3	109598552	q13.13
SNP_A-2068839	C	C	223	149	244	114	5.336	2.09E-02	rs6782469	3	110225179	q13.13
SNP_A-2306583	G	G	335	17	337	7	4.081	4.34E-02	rs1606828	3	110353612	q13.13
SNP_A-2305609	G	G	353	57	382	38	4.824	0.0281	rs1564703	3	110566139	q13.13
SNP_A-2035368	G	G	406	10	418	2	5.489	1.91E-02	rs16855602	3	110583446	q13.13
SNP_A-2312472	C	C	387	29	406	14	5.669	1.73E-02	rs17805873	3	110583609	q13.13
SNP_A-1847086	G	G	276	90	247	113	4.165	4.13E-02	rs1163589	3	110625859	q13.13
SNP_A-1973868	G	G	294	100	261	133	6.636	0.01	rs769518	3	110638889	q13.13
SNP_A-2290824	G	G	237	121	190	134	4.151	4.16E-02	rs13314017	3	110657227	q13.13
SNP_A-2131627	G	G	292	104	258	134	5.863	0.0155	rs769530	3	110663482	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123521	T	T	408	0	386	4	4.206	4.03E-02	rs11917486	3	110732338	q13.13
SNP_A-1821807	A	A	258	142	285	111	5.121	2.36E-02	rs1729595	3	110782976	q13.13
SNP_A-1849057	G	G	267	133	299	101	6.185	0.0129	rs1729594	3	110783010	q13.13
SNP_A-1788446	T	T	271	137	302	108	5.105	2.39E-02	rs6772950	3	110785471	q13.13
SNP_A-1795347	C	C	196	124	221	93	5.871	0.0154	rs1729622	3	110807269	q13.13
SNP_A-1689610	C	C	379	21	373	37	4.339	0.0373	rs10511278	3	110814016	q13.13
SNP_A-2008970	G	G	263	129	296	102	5.059	2.45E-02	rs1729616	3	110814933	q13.13
SNP_A-2068627	G	G	246	130	286	86	11.949	5.00E-04	rs1529187	3	110987795	q13.13
SNP_A-2216581	A	A	239	135	245	99	4.367	3.66E-02	rs775666	3	111153011	q13.13
SNP_A-1746947	T	T	286	112	267	143	4.244	3.94E-02	rs1903580	3	111214741	q13.13
SNP_A-1735871	A	A	287	111	262	138	4.061	4.39E-02	rs1993754	3	111233940	q13.13
SNP_A-1724722	A	A	352	18	338	38	7.379	0.0066	rs1381365	3	111281135	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1701973	T	T	387	13	386	26	4.158	4.14E-02	rs6795038	3	111394100	q13.13
SNP_A-2231590	A	A	394	4	396	0	4	4.55E-02	rs1462295	3	111931790	q13.13
SNP_A-1973903	A	A	338	24	340	42	4.381	3.64E-02	rs10511289	3	112008263	q13.13
SNP_A-2042678	C	C	245	149	240	100	5.752	1.65E-02	rs1881675	3	112487809	q13.13
SNP_A-1973926	G	A	218	154	208	188	9.531	0.002	rs2173318	3	112751926	q13.13
SNP_A-1802857	T	T	304	108	265	143	7.534	6.10E-03	rs10934114	3	113045495	q13.2
SNP_A-2080384	G	G	311	101	279	125	4.206	4.03E-02	rs4682365	3	113377523	q13.2
SNP_A-2163807	A	A	358	22	371	11	3.893	4.85E-02	rs2633595	3	113585255	q13.2
SNP_A-2008988	C	C	366	14	372	2	9.002	2.70E-03	rs923349	3	113708624	q13.2
SNP_A-1845574	T	T	327	23	293	39	5.522	1.88E-02	rs2638022	3	113748466	q13.2
SNP_A-2142200	G	G	368	12	373	29	6.469	1.10E-02	rs766968	3	113774568	q13.2
SNP_A-2242465	G	G	307	29	318	12	7.189	7.30E-03	rs7628337	3	114036490	q13.2
SNP_A-2111044	T	T	371	29	381	13	6.183	0.0129	—	3	114179120	q13.2
SNP_A-2099058	A	A	290	68	263	103	8.395	0.0038	rs7650483	3	114237316	q13.2
SNP_A-1735598	C	C	376	20	404	8	5.833	1.57E-02	rs10511324	3	114287805	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2293406	A	A	359	45	333	75	8.457	3.60E-03	rs7625411	3	114294118	q13.2
SNP_A-1700129	C	C	276	124	319	93	7.36	6.70E-03	rs712530	3	114336857	q13.2
SNP_A-1973980	T	T	360	22	350	8	5.902	1.51E-02	rs9288980	3	114447682	q13.2
SNP_A-2286960	G	G	362	28	378	14	5.008	0.0252	rs9849714	3	114453312	q13.2
SNP_A-2113300	C	C	390	18	404	8	4.074	0.0436	rs3995908	3	114481220	q13.2
SNP_A-2008992	T	T	384	18	398	6	6.246	0.0124	rs7652801	3	114491296	q13.2
SNP_A-1795893	C	C	275	87	318	68	4.682	3.05E-02	rs2291905	3	114493156	q13.2
SNP_A-2261880	A	A	226	120	254	80	9.425	2.10E-03	rs775214	3	114493640	q13.2
SNP_A-1743445	A	A	279	119	318	92	5.826	1.58E-02	rs6769604	3	114505965	q13.2
SNP_A-2286449	T	T	396	20	412	8	5.441	1.97E-02	rs7625829	3	114586434	q13.2
SNP_A-1668312	C	C	350	42	373	23	6.265	0.0123	rs7620700	3	114591891	q13.2
SNP_A-2095440	G	G	307	79	336	56	5.18	2.28E-02	rs7622740	3	114689461	q13.2
SNP_A-1973983	C	C	320	96	351	69	5.831	1.57E-02	rs6798938	3	114700896	q13.2
SNP_A-1841789	G	G	395	21	410	8	6.102	0.0135	rs4419353	3	114737627	q13.2
SNP_A-2082510	G	G	367	49	388	30	5.149	2.33E-02	rs4508746	3	114737677	q13.2
SNP_A-2033314	C	C	344	36	365	21	4.523	3.34E-02	rs4580515	3	114737833	q13.2
SNP_A-2040482	G	G	320	46	349	27	6.069	0.0138	rs4621301	3	114737862	q13.2
SNP_A-2107850	G	G	289	119	312	84	6.737	9.40E-03	rs2669909	3	114748417	q13.2
SNP_A-1902881	C	C	309	69	317	43	5.702	1.69E-02	rs2614191	3	114751891	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826274	A	A	366	50	393	25	9.289	0.0023	rs7646262	3	114753110	q13.2
SNP_A-2084982	C	C	365	45	377	23	7.189	7.30E-03	rs11922598	3	114753930	q13.2
SNP_A-2054039	G	G	387	5	383	19	8.063	4.50E-03	rs2630351	3	115357749	q13.31
SNP_A-1941167	C	C	280	88	308	46	14.231	2.00E-04	rs1983079	3	115444624	q13.31
SNP_A-2036847	A	A	171	167	184	128	4.599	3.20E-02	rs7646039	3	115558825	q13.31
SNP_A-2108665	C	C	377	31	365	49	4.2	4.04E-02	rs11920398	3	115950349	q13.31
SNP_A-2025458	T	T	335	27	312	44	4.838	2.78E-02	rs2140345	3	115954621	q13.31
SNP_A-2177333	A	A	383	25	369	47	6.906	0.0086	rs2056534	3	115966848	q13.31
SNP_A-1917341	A	A	310	84	323	59	4.453	3.48E-02	rs9848751	3	116467580	q13.31
SNP_A-2263703	C	C	350	40	372	20	7.332	6.80E-03	rs1459519	3	116483503	q13.31
SNP_A-2097339	T	T	282	124	254	156	5.1	2.39E-02	rs9879234	3	116582906	q13.31
SNP_A-1890323	C	C	282	86	253	109	4.236	3.96E-02	rs9873283	3	116622209	q13.31
SNP_A-2112400	C	C	412	2	407	13	8.054	4.50E-03	rs1561380	3	116864492	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974034	A	A	362	54	384	36	4.23	3.97E-02	rs16824224	3	117079479	q13.31
SNP_A-1783560	T	T	379	29	390	16	3.908	4.81E-02	rs16824235	3	117080599	q13.31
SNP_A-2278272	C	C	385	19	367	7	4.82	0.0281	rs16824766	3	117514285	q13.31
SNP_A-2303631	G	G	359	27	376	4	17.412	3.01E-05	rs4831139	3	117611095	q13.31
SNP_A-1974051	T	T	338	18	328	32	4.048	4.42E-02	rs1518326	3	117799431	q13.31
SNP_A-1742239	C	C	341	19	340	40	6.941	8.40E-03	rs871216	3	118056189	q13.31
SNP_A-1974063	G	G	322	58	344	40	4.012	4.52E-02	rs2177331	3	118169072	q13.31
SNP_A-1644302	G	G	348	40	365	25	3.862	4.94E-02	rs1851236	3	118178335	q13.31
SNP_A-2094235	C	C	295	103	325	81	4.003	4.54E-02	rs1518898	3	118211238	q13.31
SNP_A-1693501	A	A	281	119	256	156	5.966	0.0146	rs1462845	3	118263911	q13.31
SNP_A-2291606	T	T	310	50	302	30	3.978	4.61E-02	rs7611371	3	118281770	q13.31
SNP_A-1678750	A	A	337	61	318	94	7.337	6.80E-03	rs7616414	3	118315553	q13.31
SNP_A-1952447	G	G	305	29	348	18	3.951	4.68E-02	rs12635804	3	118324548	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1830153	A	A	289	101	253	139	8.403	3.70E-03	rs1462852	3	118446688	q13.31
SNP_A-1884408	A	A	345	37	307	59	6.917	8.50E-03	rs16826476	3	118455161	q13.31
SNP_A-2144129	A	G	215	199	220	178	4.222	3.99E-02	rs4855941	3	118496755	q13.31
SNP_A-1974074	C	C	361	55	381	31	7.218	7.20E-03	rs1877544	3	118536303	q13.31
SNP_A-2064041	G	G	201	165	237	127	7.899	4.90E-03	rs13074405	3	118543674	q13.31
SNP_A-1958690	C	C	204	188	248	164	5.425	1.98E-02	rs1513157	3	118549336	q13.31
SNP_A-2154108	G	G	325	85	348	52	8.613	0.0033	rs6778230	3	118549634	q13.31
SNP_A-2030007	C	C	295	121	331	85	8.362	0.0038	rs11716267	3	118586537	q13.31
SNP_A-1974075	T	T	392	20	373	35	4.543	3.30E-02	rs4073625	3	118628997	q13.31
SNP_A-1865995	C	C	251	119	274	84	6.846	8.90E-03	rs4632551	3	118631263	q13.31
SNP_A-1960564	A	A	236	162	203	189	4.512	3.37E-02	rs9867372	3	118775668	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1924055	C	C	336	58	370	28	12.083	5.00E-04	rs13320071	3	118829361	q13.31
SNP_A-2035907	A	A	255	155	275	119	5.168	0.023	rs9810976	3	118877663	q13.31
SNP_A-1838100	C	C	240	152	268	114	6.844	8.90E-03	rs3923050	3	118893188	q13.31
SNP_A-2278969	C	C	275	79	314	52	7.949	4.80E-03	rs7650244	3	118909927	q13.32
SNP_A-2167656	C	C	284	112	320	84	6.066	0.0138	rs1486337	3	119331709	q13.32
SNP_A-2077312	G	G	323	37	346	22	4.517	3.36E-02	rs6438441	3	119374423	q13.32
SNP_A-1854556	A	A	358	50	337	71	4.279	3.86E-02	rs6775526	3	119409587	q13.32
SNP_A-2120286	T	T	340	14	355	5	4.537	0.0332	rs16828424	3	119635356	q13.32
SNP_A-1974116	C	C	319	71	298	100	5.552	1.85E-02	rs1401953	3	119666634	q13.32
SNP_A-1952778	T	C	207	155	163	153	5.204	2.25E-02	rs2970106	3	119732163	q13.32
SNP_A-1851916	C	C	379	5	390	0	5.111	2.38E-02	rs17465281	3	120019795	q13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974133	A	A	298	78	273	101	4.045	4.43E-02	rs812824	3	120037336	q13.32
SNP_A-1974137	G	G	341	59	319	83	4.785	0.0287	rs6782002	3	120107321	q13.32
SNP_A-1942231	T	T	284	82	255	105	4.34	3.72E-02	rs7641626	3	120202706	q13.32
SNP_A-1812504	T	T	214	134	242	104	5.495	1.91E-02	rs9832079	3	120374631	q13.32
SNP_A-1974149	A	A	217	107	258	88	4.673	3.06E-02	rs2873688	3	120593647	q13.33
SNP_A-1653654	G	G	196	142	241	115	7.008	8.10E-03	rs2692618	3	120674745	q13.33
SNP_A-1917944	T	T	210	166	239	127	6.931	8.50E-03	rs7633444	3	120858739	q13.33
SNP_A-2146539	A	A	273	89	245	117	5.319	2.11E-02	rs2102627	3	120895490	q13.33
SNP_A-1897022	G	G	272	52	243	73	5.062	2.45E-02	rs9846716	3	120908997	q13.33
SNP_A-2036631	A	A	308	90	313	59	5.618	0.0178	rs4624596	3	121054231	q13.33
SNP_A-1920921	T	T	350	22	301	33	3.854	4.96E-02	rs4688043	3	121073938	q13.33
SNP_A-1864328	G	G	345	15	339	5	4.691	3.03E-02	rs11927974	3	121306727	q13.33
SNP_A-2089414	C	C	376	20	307	31	4.79	0.0286	rs9853082	3	121368120	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1894139	G	G	334	68	361	47	4.84	2.78E-02	rs10934519	3	121405708	q13.33
SNP_A-1974160	C	C	385	23	402	10	5.469	1.94E-02	rs1873652	3	121466775	q13.33
SNP_A-1974166	A	A	343	57	365	39	4.039	4.45E-02	rs1147700	3	121606246	q13.33
SNP_A-1974171	C	C	250	72	229	95	4.082	4.33E-02	rs11713908	3	121703465	q13.33
SNP_A-2314491	G	G	237	135	263	93	8.741	3.10E-03	rs373188	3	121994180	q13.33
SNP_A-1974182	A	A	237	153	268	112	8.118	4.40E-03	rs607953	3	121996174	q13.33
SNP_A-2218008	T	T	277	127	309	101	4.668	3.07E-02	rs603847	3	122058542	q13.33
SNP_A-2045296	C	C	393	23	409	11	4.535	0.0332	rs9812927	3	122070280	q13.33
SNP_A-1855968	G	G	388	12	398	0	12.122	5.00E-04	rs9871427	3	122226670	q13.33
SNP_A-2255110	G	G	362	16	359	5	5.512	0.0189	rs12634158	3	122276606	q13.33
SNP_A-1807140	A	A	346	18	376	6	6.816	9.00E-03	rs9289161	3	122327983	q13.33
SNP_A-1805871	T	C	201	179	203	161	5.586	1.81E-02	rs3934093	3	122329752	q13.33
SNP_A-2280075	G	G	271	93	277	55	8.369	0.0038	rs11191296	3	122406894	q13.33
SNP_A-1654005	C	C	276	108	291	79	4.636	3.13E-02	rs7632907	3	122462619	q13.33
SNP_A-1889901	T	T	393	19	396	8	4.415	0.0356	rs13324223	3	122498247	q13.33
SNP_A-1682740	T	T	377	17	375	31	3.91	4.80E-02	rs501099	3	122574799	q13.33
SNP_A-2090989	T	T	285	77	309	45	9.275	0.0023	rs7627978	3	122613827	q13.33
SNP_A-1909572	C	C	268	92	290	70	3.855	4.96E-02	rs7609781	3	122615507	q13.33
SNP_A-1974190	C	C	281	113	313	89	4.495	3.40E-02	rs6787048	3	122623726	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1926565	A	A	387	15	382	28	3.884	0.0487	rs716688	3	122632246	q13.33
SNP_A-1918793	G	G	235	117	205	159	8.238	4.10E-03	rs11715640	3	122796225	q13.33
SNP_A-1846855	A	A	303	83	326	56	6.065	0.0138	rs6775899	3	122802514	q13.33
SNP_A-1670383	G	G	304	88	273	125	8.048	4.60E-03	rs1129055	3	123159220	q21.1
SNP_A-1928403	C	C	253	143	288	118	4.535	0.0332	rs4308217	3	123275877	q13.33
SNP_A-2046445	A	A	326	78	291	99	4.231	3.97E-02	rs937630	3	123347749	q21.1
SNP_A-2112995	A	A	358	48	335	67	3.883	4.88E-02	rs884095	3	123509184	q21.1
SNP_A-2141783	T	T	347	41	320	58	3.882	4.88E-02	rs9842752	3	123539553	q21.1
SNP_A-1711330	G	G	384	16	380	32	5.178	0.0229	rs10511414	3	123797683	q21.1
SNP_A-1791203	T	T	380	28	391	11	7.523	6.10E-03	rs9833545	3	123809268	q21.1
SNP_A-2043582	G	G	366	22	369	7	7.584	5.90E-03	rs9823535	3	123810640	q21.1
SNP_A-2167361	G	G	278	86	310	60	6.323	1.19E-02	rs13078584	3	123859417	q21.1
SNP_A-1844077	G	G	400	16	388	32	5.497	0.019	rs17270364	3	123889270	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796102	A	A	399	15	387	31	5.729	0.0167	rs17270460	3	123890064	q21.1
SNP_A-2224409	T	T	382	16	384	32	4.943	2.62E-02	---	3	123890289	q21.1
SNP_A-1974211	T	T	338	70	312	92	4.008	0.0453	rs13062151	3	123907303	q21.1
SNP_A-1857223	G	G	310	62	307	89	4.096	4.30E-02	rs2063515	3	123918440	q21.1
SNP_A-2165875	C	C	353	51	378	30	6.28	1.22E-02	rs4677984	3	124152319	q21.1
SNP_A-2135470	G	G	313	29	359	15	6.186	0.0129	rs11707039	3	124152829	q21.1
SNP_A-2237086	C	C	312	50	324	32	4.128	4.22E-02	rs895074	3	124177090	q21.1
SNP_A-2244319	A	A	408	8	397	21	5.973	1.45E-02	rs11709496	3	124292090	q21.1
SNP_A-1954288	T	T	316	52	305	77	4.78	2.88E-02	rs836839	3	124317577	q21.1
SNP_A-2080759	T	T	197	179	228	150	4.812	2.83E-02	rs1969262	3	124345717	q21.1
SNP_A-1676716	C	C	350	22	362	46	7.026	8.00E-03	rs10511420	3	124709015	q21.1
SNP_A-1861733	T	T	412	4	420	0	4.058	4.40E-02	rs865358	3	124901603	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936391	T	T	183	143	198	112	3.959	4.66E-02	rs2332682	3	125137323	q21.1
SNP_A-1888836	C	C	373	11	366	26	6.066	0.0138	rs1373612	3	125409482	q21.2
SNP_A-1974240	T	T	393	7	381	21	7.181	7.40E-03	rs6768010	3	125433103	q21.2
SNP_A-2126558	C	C	398	6	383	17	5.529	1.87E-02	rs9870514	3	125437366	q21.2
SNP_A-2265036	T	T	395	9	384	26	8.369	0.0038	rs7616435	3	125442275	q21.2
SNP_A-2155114	T	T	237	117	196	144	6.396	0.0114	rs7653717	3	125637062	q21.2
SNP_A-1793433	C	C	221	141	192	168	4.39	0.0361	rs686507	3	125837297	q21.2
SNP_A-1929905	G	G	223	135	189	169	6.608	0.0101	rs1440146	3	125854793	q21.2
SNP_A-2194106	G	G	351	53	339	75	3.868	4.92E-02	rs17308266	3	125888788	q21.2
SNP_A-2275271	G	G	262	116	295	93	4.356	3.69E-02	rs3772807	3	125945400	q21.2
SNP_A-2115871	C	C	269	141	308	108	6.966	8.30E-03	rs10934685	3	125949210	q21.2
SNP_A-2092352	A	A	416	0	416	4	3.981	4.60E-02	rs3772819	3	125968969	q21.2
SNP_A-1806659	C	C	243	115	222	150	5.304	2.13E-02	rs614664	3	125969683	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1789222	T	T	406	0	414	4	3.904	0.0482	rs3772823	3	125974207	q21.2
SNP_A-2300814	G	G	245	109	285	75	9.252	2.40E-03	rs702037	3	125983231	q21.2
SNP_A-1809208	G	G	416	0	416	4	3.981	4.60E-02	rs1909587	3	126013884	q21.2
SNP_A-2122779	G	G	330	60	305	91	7.303	6.90E-03	rs3772845	3	126043580	q21.2
SNP_A-2070300	T	T	238	146	271	111	6.901	0.0086	rs10804563	3	126081189	q21.2
SNP_A-2193836	C	C	337	79	368	52	6.909	0.0086	rs568456	3	126354375	q21.2
SNP_A-1892279	C	C	318	74	359	47	8.265	4.00E-03	rs564809	3	126354748	q21.2
SNP_A-2296627	G	G	350	14	363	3	7.349	6.70E-03	rs9832863	3	126412438	q21.2
SNP_A-2133630	T	T	336	0	316	6	6.318	1.19E-02	rs16836826	3	126652282	q21.2
SNP_A-2305724	C	C	309	41	335	21	7.451	0.0063	rs2001665	3	126885942	q21.2
SNP_A-1723704	G	G	317	83	367	45	14.762	0.0001	rs2017409	3	126990628	q21.3
SNP_A-2273653	T	T	287	121	313	91	5.352	0.0207	rs9844318	3	127101223	q21.2
SNP_A-1649388	C	C	249	103	254	148	4.823	0.0281	rs2365001	3	127173380	q21.3
SNP_A-2067848	C	C	277	139	238	168	5.572	0.0183	rs7644324	3	127177945	q21.2
SNP_A-1811448	A	A	251	143	218	168	4.25	3.93E-02	rs10804573	3	127203712	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2263568	C	C	261	147	238	182	4.611	3.18E-02	rs2279819	3	127206746	q21.2
SNP_A-1716739	G	C	189	187	241	161	8.193	4.20E-03	rs2197704	3	127281237	q21.3
SNP_A-1703283	C	C	176	170	219	145	6.213	1.27E-02	rs1447666	3	127282197	q21.3
SNP_A-2275577	C	C	231	131	259	101	5.474	1.93E-02	rs2003334	3	127304701	q21.2
SNP_A-2295994	C	C	244	158	273	131	4.144	4.18E-02	rs4646751	3	127308359	q21.2
SNP_A-2077792	T	T	378	22	402	6	9.803	1.70E-03	rs6766233	3	127354444	q21.2
SNP_A-2237504	T	A	215	187	215	187	3.9	4.83E-02	rs10934756	3	127406083	q21.2
SNP_A-2194615	G	A	204	162	193	177	4.599	3.20E-02	rs4679218	3	127410274	q21.2
SNP_A-1785247	C	T	218	172	206	190	4.934	0.0263	rs10804575	3	127411525	q21.2
SNP_A-1868365	T	C	206	202	239	169	6.755	9.30E-03	rs1562470	3	127427696	q21.2
SNP_A-2296379	G	G	208	202	247	153	9.984	1.60E-03	rs1562471	3	127427767	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2065482	T	C	189	183	220	150	7.878	5.00E-03	rs1868114	3	127428514	q21.2
SNP_A-2279299	-	C	182	182	230	150	8.336	3.90E-03	rs1868115	3	127428652	q21.2
SNP_A-2075795	-	C	208	208	249	171	7.272	7.00E-03	rs9865763	3	127428962	q21.2
SNP_A-1671214	A	A	262	96	238	126	5.157	2.32E-02	rs812368	3	127496310	q21.3
SNP_A-1897598	C	C	338	8	337	21	5.626	0.0177	rs12695485	3	127593802	q21.2
SNP_A-2313538	G	G	365	25	391	11	6.158	1.31E-02	rs17690518	3	127624861	q21.2
SNP_A-1886989	C	C	379	19	404	8	5.039	2.48E-02	rs17691268	3	127672247	q21.2
SNP_A-1788079	A	A	311	89	273	127	9.158	2.50E-03	rs17743103	3	127771107	q21.2
SNP_A-1865037	T	T	304	100	286	128	3.866	4.93E-02	rs1873389	3	127772060	q21.2
SNP_A-2264584	A	A	408	0	405	5	5.006	0.0253	rs782439	3	128899487	q21.3
SNP_A-1896578	G	G	324	70	355	45	6.805	9.10E-03	rs11916152	3	128932259	q21.3
SNP_A-2294815	A	A	405	7	411	1	4.544	3.30E-02	rs693742	3	128976934	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801826	A	A	218	194	239	161	3.856	4.96E-02	rs11716997	3	129034328	q21.3
SNP_A-2247337	A	A	416	0	415	5	4.982	2.56E-02	rs4494948	3	129432035	q21.3
SNP_A-2009094	G	G	352	28	336	44	3.928	4.75E-02	rs2811416	3	129474636	q21.3
SNP_A-1974304	T	T	328	4	358	0	4.338	0.0373	rs16844000	3	129535187	q21.3
SNP_A-2085653	C	C	330	76	292	116	10.65	1.10E-03	rs729847	3	129593468	q21.3
SNP_A-2210337	A	A	336	72	302	100	6.326	1.19E-02	rs760383	3	129602263	q21.3
SNP_A-2213480	T	T	348	66	326	90	4.406	3.58E-02	rs12634139	3	129668230	q21.3
SNP_A-1893464	T	T	303	109	339	81	6.069	0.0138	rs7431368	3	129673639	q21.3
SNP_A-2247309	C	C	330	38	357	23	4.558	3.28E-02	rs2712429	3	129818919	q21.3
SNP_A-1651814	T	T	311	89	342	68	4.158	4.14E-02	rs3772157	3	129854899	q21.3
SNP_A-1942275	A	A	339	25	356	6	12.056	5.00E-04	rs6793907	3	129874324	q21.3
SNP_A-2080402	C	C	319	73	353	45	8.319	3.90E-03	rs9820753	3	129928890	q21.3
SNP_A-1974308	G	G	302	60	339	39	6.247	0.0124	rs6804596	3	129993209	q21.3
SNP_A-1831143	C	C	352	38	380	22	5.157	2.32E-02	rs9862461	3	130055012	q21.3
SNP_A-1840464	C	C	380	4	406	0	4.251	3.92E-02	rs6807994	3	130468279	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2009105	C	C	328	52	288	86	10.927	9.00E-04	rs6439167	3	130533454	q21.3
SNP_A-2009106	C	C	341	63	310	104	11.422	7.00E-04	rs6439168	3	130533641	q21.3
SNP_A-1974316	C	C	353	63	375	43	4.434	3.52E-02	rs13073206	3	131422319	q21.3
SNP_A-2306306	G	G	295	105	321	81	4.189	0.0407	rs2219026	3	131615207	q21.3
SNP_A-2314145	G	G	374	10	385	3	3.908	4.81E-02	rs9883988	3	131645093	q21.3
SNP_A-1745902	A	A	231	45	327	25	13.227	3.00E-04	rs6802634	3	131693385	q22.1
SNP_A-1876607	A	A	266	110	248	140	4.043	4.44E-02	rs4682639	3	131926197	q21.3
SNP_A-2271751	C	C	392	24	408	12	4.301	3.81E-02	rs11920352	3	132439456	q21.3
SNP_A-1974346	T	A	171	159	192	148	4.613	3.17E-02	rs1913290	3	132964138	q22.1
SNP_A-1908664	A	A	218	120	243	93	4.772	2.89E-02	rs6767389	3	132987964	q22.1
SNP_A-1908237	A	A	315	91	298	120	4.283	0.0385	rs11918334	3	132988177	q22.1
SNP_A-1673128	T	T	362	38	385	23	4.318	3.77E-02	rs884432	3	133252891	q22.1
SNP_A-1956175	G	G	357	43	372	26	4.492	3.41E-02	rs10934990	3	133363920	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247251	G	G	325	91	361	57	9.695	0.0018	rs11710455	3	133398970	q22.1
SNP_A-2144689	C	C	289	83	341	53	10.286	1.30E-03	rs1316655	3	133404654	q22.1
SNP_A-1932424	T	T	286	66	320	36	10.709	1.10E-03	rs1827816	3	133406706	q22.1
SNP_A-1929271	G	G	253	65	271	39	7.018	8.10E-03	rs10934991	3	133421406	q22.1
SNP_A-1906715	C	C	319	85	357	59	6.656	9.90E-03	rs10934992	3	133421593	q22.1
SNP_A-1795501	C	C	309	65	358	44	6.644	9.90E-03	rs9878957	3	133430635	q22.1
SNP_A-1929315	G	G	397	9	390	20	4.215	4.01E-02	rs7611943	3	133488992	q22.1
SNP_A-1974380	A	A	280	104	293	77	4.064	4.38E-02	rs2310229	3	133541978	q22.1
SNP_A-1833343	A	A	304	80	335	47	10.074	0.0015	rs11924491	3	133582343	q22.1
SNP_A-2059726	G	G	340	74	368	50	5.733	0.0166	rs11706084	3	133615397	q22.1
SNP_A-2238720	A	A	227	147	208	180	3.904	0.0482	rs4854697	3	134373375	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287021	G	G	273	91	239	111	3.965	0.0465	rs6439388	3	134398172	q22.1
SNP_A-1915537	C	C	332	30	327	15	4.473	0.0344	rs17297332	3	134480782	q22.1
SNP_A-1910946	T	T	318	40	307	73	9.183	2.40E-03	rs10049438	3	134776901	q22.1
SNP_A-1748619	A	A	296	100	328	78	4.236	3.96E-02	rs2715608	3	134871887	q22.1
SNP_A-1974437	A	A	305	107	331	83	4.09	4.31E-02	rs2715609	3	135032636	q22.1
SNP_A-2209880	C	C	344	50	322	70	4.055	4.40E-02	rs1880666	3	135035581	q22.1
SNP_A-2081606	C	C	283	41	320	28	3.867	4.92E-02	rs2692682	3	135077389	q22.1
SNP_A-1787014	T	T	198	118	224	92	4.821	0.0281	rs2692685	3	135112060	q22.1
SNP_A-2094832	A	A	246	164	276	132	5.179	0.0229	rs10935089	3	135140330	q22.1
SNP_A-1692418	A	A	365	35	356	56	4.782	2.88E-02	rs983401	3	135982339	q22.2
SNP_A-1662250	C	C	238	156	209	189	5.018	2.51E-02	rs972234	3	135989668	q22.2
SNP_A-1663672	T	T	222	178	265	145	7.046	7.90E-03	rs36117	3	136019686	q22.2
SNP_A-2120591	C	T	221	169	202	196	4.353	3.69E-02	rs39704	3	136129905	q22.1
SNP_A-2232823	T	G	190	166	199	165	4.656	0.0309	rs40157	3	136130816	q22.1
SNP_A-1865671	A	G	231	185	212	200	4.047	4.43E-02	rs36172	3	136133981	q22.1
SNP_A-1974452	T	T	239	159	216	192	4.142	4.18E-02	rs11707505	3	136150545	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974453	G	G	250	164	216	200	6.036	0.014	rs4955520	3	136152565	q22.1
SNP_A-1809689	G	G	246	164	219	199	4.866	2.74E-02	rs9825380	3	136156092	q22.1
SNP_A-2068553	G	G	237	139	207	175	6.107	0.0135	rs4955524	3	136158499	q22.1
SNP_A-1834162	C	C	247	155	202	174	4.744	2.94E-02	rs936323	3	136165331	q22.1
SNP_A-2045768	C	C	225	139	189	161	4.471	3.45E-02	rs4955461	3	136166320	q22.1
SNP_A-2049992	A	A	231	153	199	179	4.371	3.66E-02	rs4955527	3	136166639	q22.1
SNP_A-2291703	A	A	293	101	320	76	4.715	2.99E-02	rs7644618	3	136239458	q22.1
SNP_A-1974474	G	G	269	63	286	42	4.697	3.02E-02	rs4894283	3	136614244	q22.2
SNP_A-2078318	C	C	294	40	288	64	5.132	0.0235	rs548288	3	137452453	q22.3
SNP_A-1974499	G	G	328	46	334	26	5.345	2.08E-02	---	3	138549415	q22.3
SNP_A-1852010	C	C	178	160	195	125	4.584	3.23E-02	rs9836078	3	138640303	q22.3
SNP_A-2119226	G	T	190	170	204	168	4.247	3.93E-02	rs1442585	3	139002368	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225865	A	A	338	68	366	48	4.484	3.42E-02	rs1001162	3	139016217	q22.3
SNP_A-1931730	T	T	229	117	262	96	4.085	4.33E-02	rs149862	3	139017156	q22.3
SNP_A-1887777	C	A	237	177	208	200	5.585	1.81E-02	rs157276	3	139017808	q22.3
SNP_A-2009148	C	C	363	31	361	11	8.905	0.0028	rs7619950	3	139173656	q22.3
SNP_A-2311758	A	A	286	64	309	45	4.178	4.09E-02	rs2622726	3	139261018	q22.3
SNP_A-1716203	C	C	392	4	400	0	4.061	4.39E-02	rs1679177	3	139477452	q22.3
SNP_A-1912589	A	A	346	56	327	81	5.054	0.0246	rs2347252	3	139578223	q22.3
SNP_A-2009156	A	A	346	60	323	81	3.913	4.79E-02	rs940188	3	140323643	q22.3
SNP_A-2202767	C	C	320	24	284	50	10.236	0.0014	rs661149	3	140326401	q22.3
SNP_A-1663090	T	T	295	103	342	70	9.523	0.002	rs211587	3	140602062	q23
SNP_A-1647966	G	G	248	150	225	187	4.94	2.62E-02	rs211588	3	140602100	q23
SNP_A-2313314	G	G	246	154	222	196	5.878	1.53E-02	rs12635533	3	140813759	q23
SNP_A-2100432	G	G	280	106	314	78	6.161	1.31E-02	rs16849220	3	140831216	q23
SNP_A-1698033	G	G	338	56	319	79	4.448	0.0349	rs10513087	3	140910777	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1706341	T	T	266	106	265	143	3.847	4.98E-02	rs727763	3	140969235	q23
SNP_A-1651610	T	T	247	105	297	91	3.853	4.96E-02	rs2882426	3	141105618	q23
SNP_A-1792807	G	A	236	154	195	189	9.968	1.60E-03	rs7641890	3	141183790	q23
SNP_A-1944884	A	-	241	159	200	200	8.494	3.60E-03	rs13080287	3	141185573	q23
SNP_A-2243749	T	T	284	118	303	91	4.023	4.49E-02	rs11929650	3	141186033	q23
SNP_A-2056338	A	G	218	138	189	187	9.788	0.0018	rs9833439	3	141190300	q23
SNP_A-1974560	A	A	287	127	318	100	4.781	2.88E-02	rs2350487	3	141268087	q23
SNP_A-1938196	C	C	210	178	227	143	4.052	0.0441	rs11708993	3	141514427	q23
SNP_A-1830220	C	C	314	74	299	101	4.351	3.70E-02	rs10212231	3	141658931	q23
SNP_A-2307425	T	T	293	11	326	4	3.966	4.64E-02	rs11706567	3	141777602	q23
SNP_A-1854504	C	C	336	4	388	0	4.59	3.22E-02	rs6439978	3	142280993	q23
SNP_A-1974588	G	G	366	0	351	5	5.176	0.0229	rs10935421	3	142415929	q23
SNP_A-1641973	T	T	239	159	214	196	5.059	2.45E-02	rs6806936	3	142430230	q23
SNP_A-2177999	C	C	269	81	307	61	4.876	2.72E-02	rs6803826	3	142479667	q23
SNP_A-2065093	T	T	386	30	370	48	4.488	3.41E-02	rs16851294	3	142480450	q23
SNP_A-2084259	G	G	272	106	287	77	4.736	2.95E-02	rs1993904	3	142486052	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2254810	C	C	280	122	227	147	6.862	8.80E-03	rs12695732	3	142579434	q23
SNP_A-1798847	G	C	209	155	188	180	5.315	2.11E-02	rs1344672	3	142608403	q23
SNP_A-2303993	C	C	299	115	331	89	4.896	0.0269	rs9831276	3	142995721	q23
SNP_A-2117534	C	C	356	50	355	31	3.956	4.67E-02	rs11569235	3	143173803	q23
SNP_A-2030062	A	A	308	58	330	40	4.043	4.44E-02	rs2862124	3	143252699	q23
SNP_A-1825204	C	C	266	68	286	42	6.816	9.00E-03	rs2707977	3	144129858	q23
SNP_A-2049281	A	A	299	99	324	74	4.616	3.17E-02	rs11708528	3	144278135	q23
SNP_A-2241529	G	G	223	113	215	151	4.342	3.72E-02	rs10935490	3	144572550	q24
SNP_A-1974635	A	A	236	162	269	137	4.168	4.12E-02	rs12488097	3	144683470	q24
SNP_A-1712845	A	A	273	79	273	111	4.006	0.0453	rs1242075	3	144687739	q24
SNP_A-2273954	T	T	312	18	332	6	6.526	0.0106	rs16853772	3	144739111	q24
SNP_A-1847515	T	T	395	11	409	1	8.558	3.40E-03	rs4025523	3	144739652	q24
SNP_A-1974641	G	G	358	40	329	75	11.832	6.00E-04	rs10513209	3	144752356	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974643	A	A	285	119	317	89	6.023	0.0141	rs6763202	3	144775710	q24
SNP_A-2120068	A	A	361	45	314	74	9.937	1.60E-03	rs17582102	3	144794151	q24
SNP_A-1974647	A	A	360	38	378	20	6.025	0.0141	rs10513214	3	144851326	q24
SNP_A-1724764	A	A	368	4	358	0	3.871	4.91E-02	rs10513238	3	145057180	q24
SNP_A-1974656	C	C	249	129	211	149	4.141	4.18E-02	rs17602500	3	145148715	q24
SNP_A-1974659	C	C	410	4	418	0	4.058	4.40E-02	rs16854851	3	145238402	q24
SNP_A-1852033	T	T	345	29	343	13	5.661	1.73E-02	rs7640226	3	145803273	q24
SNP_A-1662356	G	G	357	43	382	28	3.892	4.85E-02	rs10513251	3	145914170	q24
SNP_A-2086488	A	A	370	42	386	26	4.103	4.28E-02	rs7645211	3	146060169	q24
SNP_A-1956463	A	A	274	82	248	110	5.373	2.05E-02	rs9819103	3	146178051	q24
SNP_A-2250280	G	G	330	20	320	36	4.675	3.06E-02	rs344973	3	146647684	q24
SNP_A-2076779	C	C	331	79	356	58	4.109	4.26E-02	rs9815774	3	146774154	q24
SNP_A-2051381	C	C	328	86	346	60	5.033	2.49E-02	rs9815801	3	146774196	q24
SNP_A-1878066	C	C	237	139	260	108	4.87	2.73E-02	rs1881036	3	146774375	q24
SNP_A-2077140	G	G	331	85	308	112	4.509	3.37E-02	rs3863992	3	146940884	q24
SNP_A-1974709	T	T	342	0	298	4	4.558	3.28E-02	rs2055993	3	147042759	q24
SNP_A-2061685	A	A	245	79	261	53	5.472	1.93E-02	rs9828457	3	147082918	q24
SNP_A-2102629	G	G	402	14	415	5	4.451	0.0349	rs16857722	3	147181759	q24
SNP_A-1874975	A	A	401	15	383	35	8.409	3.70E-03	rs12374006	3	147582183	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215119	C	C	389	17	375	33	5.372	2.05E-02	rs6440440	3	147662234	q24
SNP_A-2069920	A	A	393	17	376	32	4.963	2.59E-02	rs10935633	3	147673596	q24
SNP_A-1896181	G	G	325	43	324	70	5.572	1.82E-02	rs342899	3	147761314	q24
SNP_A-1756226	T	T	388	10	390	22	4.264	3.89E-02	rs4131188	3	148021286	q24
SNP_A-2125529	T	T	319	33	337	19	4.241	0.0395	rs11924113	3	148100353	q24
SNP_A-1743915	C	C	240	152	210	190	6.142	0.0132	rs10513321	3	148770976	q24
SNP_A-1852183	G	C	168	146	180	142	5.627	0.0177	rs6808981	3	148833465	q24
SNP_A-2060683	A	A	253	149	226	182	4.768	2.90E-02	rs17511826	3	148907283	q24
SNP_A-1824601	G	G	288	100	275	131	4.054	0.0441	rs6440527	3	149258567	q24
SNP_A-2217520	G	G	224	98	264	78	4.954	2.60E-02	rs6804238	3	149446807	q24
SNP_A-1677330	T	T	283	91	307	63	6.046	1.39E-02	rs4681413	3	149478820	q24
SNP_A-2148973	G	G	224	158	261	123	7.177	7.40E-03	rs9874416	3	149531533	q24
SNP_A-2274673	T	T	310	12	308	4	3.85	4.98E-02	rs6440537	3	149561886	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1833596	T	T	390	12	369	23	3.913	4.79E-02	rs10935734	3	150108504	q24
SNP_A-2089130	T	T	266	134	236	162	4.436	3.52E-02	rs9819699	3	150195354	q24
SNP_A-1923686	C	C	244	142	279	107	7.262	7.00E-03	rs4938	3	150209831	q24
SNP_A-1974787	C	C	239	129	284	94	9.233	2.40E-03	rs10513348	3	150238559	q24
SNP_A-2071011	C	C	240	132	278	92	9.925	1.60E-03	rs12488819	3	150249814	q24
SNP_A-2293211	C	C	222	142	265	111	7.402	6.50E-03	rs7646166	3	150307110	q24
SNP_A-1944681	T	T	245	159	304	112	14.319	2.00E-04	rs6792168	3	150319271	q24
SNP_A-2235058	C	C	303	81	330	58	4.937	0.0263	rs9833887	3	150446093	q25.1
SNP_A-2088806	G	G	314	6	335	17	4.427	3.54E-02	rs16862326	3	151179374	q25.1
SNP_A-2313634	C	C	340	46	347	27	4.828	2.80E-02	rs6785242	3	151317703	q25.1
SNP_A-1923270	G	G	357	25	322	40	4.731	2.96E-02	rs2242018	3	151508581	q25.1
SNP_A-1705247	A	A	281	119	261	151	4.354	3.69E-02	rs6797044	3	151586792	q25.1
SNP_A-1676282	T	T	269	107	256	144	5.039	2.48E-02	rs1522351	3	151617804	q25.1
SNP_A-2124486	G	G	238	84	233	115	3.879	4.89E-02	rs9862757	3	151754324	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1818429	A	A	213	119	179	147	5.842	1.56E-02	rs6780355	3	151900291	q25.1
SNP_A-2180651	C	C	380	16	401	7	3.908	4.81E-02	rs6795396	3	151992925	q25.1
SNP_A-2110746	G	G	365	21	392	8	6.543	1.05E-02	---	3	151998421	q25.1
SNP_A-2190748	A	A	395	3	337	17	11.862	6.00E-04	rs16862934	3	152077977	q25.1
SNP_A-1726900	A	A	382	10	405	3	4.123	4.23E-02	rs10513385	3	152220768	q25.1
SNP_A-1705999	G	G	186	166	240	158	4.237	0.0395	rs10513390	3	152257962	q25.1
SNP_A-2304468	A	A	213	171	248	142	5.298	2.14E-02	rs2048229	3	152295372	q25.1
SNP_A-2284795	C	C	401	7	388	0	6.716	9.60E-03	rs16863149	3	152295514	q25.1
SNP_A-2120573	T	T	200	170	241	149	4.671	3.07E-02	rs891666	3	152309888	q25.1
SNP_A-2133339	C	C	401	9	413	1	6.558	0.0104	rs16863204	3	152372577	q25.1
SNP_A-1878379	G	G	381	7	401	1	4.765	2.90E-02	rs16863208	3	152374975	q25.1
SNP_A-1747773	A	A	193	143	248	134	4.222	3.99E-02	rs2307020	3	152375534	q25.1
SNP_A-1974824	T	T	405	11	419	1	8.552	3.50E-03	rs3732755	3	152394103	q25.1
SNP_A-2048106	G	G	325	85	292	124	8.999	2.70E-03	rs3108727	3	152406514	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2159825	T	T	284	112	255	141	4.884	2.71E-02	rs2870518	3	152427941	q25.1
SNP_A-1974825	G	G	335	43	312	62	4.235	3.96E-02	---	3	152456063	q25.1
SNP_A-1803799	A	A	304	100	323	75	4.103	4.28E-02	rs9864095	3	152489924	q25.1
SNP_A-1974827	A	A	256	82	274	54	6.227	0.0126	rs1873619	3	152501211	q25.1
SNP_A-2023924	A	A	201	137	224	106	5.104	2.39E-02	rs4679958	3	153215076	q25.1
SNP_A-1868002	C	T	168	160	187	133	6.073	0.0137	rs6772317	3	153226104	q25.1
SNP_A-2306820	A	A	310	26	271	45	7.096	7.70E-03	rs942501	3	153252297	q25.1
SNP_A-2135143	T	T	315	11	284	24	5.927	0.0149	rs17283360	3	153269162	q25.1
SNP_A-2101864	T	T	190	150	223	127	4.403	3.59E-02	rs188981	3	153336813	q25.1
SNP_A-2184664	A	A	219	145	227	109	4.132	4.21E-02	rs191758	3	153345645	q25.1
SNP_A-1832961	G	G	335	17	366	8	3.948	4.69E-02	rs17283506	3	153358827	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974853	A	A	231	177	264	152	4.022	4.49E-02	rs325772	3	153369883	q25.1
SNP_A-1787440	C	C	375	7	392	0	7.249	7.10E-03	—	3	153631228	q25.2
SNP_A-2252807	C	C	396	4	400	0	4.02	4.50E-02	rs12638688	3	153849754	q25.2
SNP_A-2122305	C	C	285	121	256	148	4.26	0.039	rs955013	3	154581734	q25.2
SNP_A-1974886	A	A	284	104	251	131	5.091	0.024	rs2862824	3	154650143	q25.2
SNP_A-2281069	T	T	238	126	257	97	4.362	3.67E-02	rs13061256	3	154737123	q25.2
SNP_A-2009237	G	G	319	93	292	118	4.15	4.16E-02	rs4680074	3	154768902	q25.2
SNP_A-2009238	C	C	353	9	383	1	6.98	8.20E-03	rs965573	3	154828919	q25.2
SNP_A-1974894	A	A	253	141	277	113	4.153	4.16E-02	rs952124	3	154891493	q25.2
SNP_A-1745592	T	T	332	68	365	47	5.221	0.0223	rs1879558	3	154975264	q25.2
SNP_A-2232080	C	C	233	127	270	106	4.269	3.88E-02	rs16823180	3	154992187	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974899	T	A	199	165	206	178	5.17	0.023	rs1112514	3	155017098	q25.2
SNP_A-1818057	C	C	275	49	292	28	6.212	1.27E-02	rs4613417	3	155212935	q25.2
SNP_A-2028368	T	C	214	200	234	186	4.581	3.23E-02	rs6766612	3	155233921	q25.2
SNP_A-1872816	T	T	277	89	293	63	4.759	2.91E-02	rs13058971	3	155244798	q25.2
SNP_A-2189510	G	G	311	95	287	125	5.01	0.0252	rs17442808	3	156290579	q25.2
SNP_A-1974932	C	C	241	163	254	128	3.938	4.72E-02	rs10513469	3	156318424	q25.2
SNP_A-1974933	C	C	406	4	408	0	4	4.55E-02	rs3732886	3	156349224	q25.2
SNP_A-2237812	A	A	402	6	412	0	6.103	0.0135	rs6440982	3	156612025	q25.31
SNP_A-2049402	G	G	409	3	408	12	5.325	2.10E-02	rs6766110	3	157525735	q25.31
SNP_A-2163693	T	T	348	0	330	6	6.269	0.0123	rs12107942	3	157765004	q25.31
SNP_A-2087272	A	A	241	87	209	137	12.965	3.00E-04	rs6765828	3	158341002	q25.31
SNP_A-2171598	G	G	192	124	225	97	5.854	0.0155	rs6809003	3	158344452	q25.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1670225	C	C	277	121	319	93	6.383	0.0115	rs10513508	3	158367717	q25.31
SNP_A-1683182	T	T	277	123	317	91	7.4	6.50E-03	rs1500924	3	158368067	q25.31
SNP_A-2009253	A	A	273	115	305	79	8.432	3.70E-03	rs6781682	3	158373804	q25.31
SNP_A-2165318	T	T	237	159	266	126	5.473	1.93E-02	rs1500925	3	158456506	q25.31
SNP_A-2266012	A	A	194	154	234	118	8.48	3.60E-03	rs9289980	3	158457133	q25.31
SNP_A-1783349	T	T	252	98	295	81	4.069	4.37E-02	rs12633429	3	158474094	q25.31
SNP_A-2173931	G	G	279	127	315	97	6.156	1.31E-02	rs2874616	3	158491615	q25.31
SNP_A-1974993	G	G	210	154	169	167	3.848	4.98E-02	rs1403105	3	158492788	q25.31
SNP_A-2280204	T	C	207	167	201	167	7.371	0.0066	rs1546260	3	158498270	q25.31
SNP_A-1889744	G	G	219	109	209	153	5.962	0.0146	rs1546261	3	158498463	q25.31
SNP_A-2120373	C	C	245	71	290	54	4.918	2.66E-02	rs1403108	3	158499511	q25.31
SNP_A-2115968	G	G	257	85	284	62	4.923	2.65E-02	rs6799567	3	158501805	q25.32
SNP_A-2263026	T	G	204	148	198	174	9.061	2.60E-03	rs10936077	3	158503676	q25.32
SNP_A-1974994	T	T	267	119	285	85	5.918	1.50E-02	rs1522392	3	158528552	q25.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1974995	G	G	226	142	177	161	5.885	1.53E-02	rs1581413	3	158532867	q25.32
SNP_A-1846560	G	G	260	120	234	162	7.297	6.90E-03	rs988588	3	158536718	q25.32
SNP_A-2209482	A	A	242	166	204	186	3.97	4.63E-02	rs1392798	3	158538989	q25.32
SNP_A-1783322	T	T	237	121	215	151	4.292	3.83E-02	rs9990136	3	158558536	q25.32
SNP_A-2162068	A	A	279	119	306	94	4.175	4.10E-02	rs12494465	3	158558910	q25.32
SNP_A-2042328	A	A	268	144	242	178	4.839	2.78E-02	rs7617727	3	158588260	q25.32
SNP_A-2302500	A	A	228	150	187	165	3.844	0.0499	rs4679793	3	158605363	q25.32
SNP_A-2070451	G	A	202	168	198	178	3.927	4.75E-02	rs1840680	3	158638731	q25.32
SNP_A-1975023	T	T	262	118	247	157	5.243	2.20E-02	rs1503107	3	160095861	q25.32
SNP_A-2119959	C	C	253	67	274	44	5.596	1.80E-02	rs9290030	3	160155282	q25.32
SNP_A-1975035	C	C	316	96	342	74	3.855	4.96E-02	rs9290036	3	160539461	q25.33
SNP_A-2075737	A	A	182	168	195	119	6.883	8.70E-03	rs9809080	3	160721441	q25.33
SNP_A-1889417	T	T	251	97	248	134	4.37	3.66E-02	rs2169303	3	160980293	q25.33
SNP_A-2278847	T	T	258	138	294	112	4.928	0.0264	rs7648959	3	161045199	q25.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140561	C	C	216	140	190	188	8.037	4.60E-03	rs480350	3	161150993	q25.33
SNP_A-2231216	C	C	190	182	241	169	4.681	3.05E-02	rs6441282	3	161181779	q25.33
SNP_A-1894630	C	C	292	78	282	106	4.01	4.52E-02	rs7638469	3	161237718	q25.33
SNP_A-1829671	A	A	203	135	238	108	5.685	1.71E-02	rs9847915	3	161279892	q25.33
SNP_A-1710033	C	C	391	9	390	22	5.277	2.16E-02	rs1378663	3	161799766	q25.33
SNP_A-1949280	G	G	388	10	383	23	5.075	2.43E-02	rs17826370	3	162001800	q25.33
SNP_A-1949506	A	A	400	8	386	24	8.245	4.10E-03	rs7629154	3	162003257	q25.33
SNP_A-2262822	A	A	405	9	390	22	5.73	0.0167	rs1455870	3	162017028	q25.33
SNP_A-2255152	C	C	401	7	375	17	4.72	0.0298	rs1455871	3	162017113	q25.33
SNP_A-2173534	A	A	366	8	338	28	12.14	5.00E-04	rs16831520	3	162024409	q25.33
SNP_A-1747173	G	G	394	6	412	0	6.226	0.0126	rs6790705	3	162030394	q26.1
SNP_A-1758507	A	A	396	0	390	4	4.041	4.44E-02	rs1588020	3	162641277	q26.1
SNP_A-2300838	G	G	352	48	361	29	4.676	3.06E-02	rs6771433	3	163049441	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1657173	T	T	245	149	279	125	4.184	4.08E-02	rs951475	3	163081462	q26.1
SNP_A-1837975	A	A	218	122	249	99	4.359	3.68E-02	rs907080	3	163223984	q26.1
SNP_A-2235563	G	G	226	136	267	111	5.597	1.80E-02	rs1397241	3	163240738	q26.1
SNP_A-1975124	G	G	231	147	274	114	7.705	5.50E-03	rs1397224	3	163263650	q26.1
SNP_A-1827329	T	T	383	3	358	10	4.185	4.08E-02	rs16850942	3	163381392	q26.1
SNP_A-1884254	A	A	384	4	384	12	3.919	4.77E-02	rs16851775	3	163393022	q26.1
SNP_A-1749179	G	G	222	178	273	137	10.469	1.20E-03	rs7641368	3	163491924	q26.1
SNP_A-1813567	C	C	213	171	242	140	4.933	0.0263	rs6441443	3	163499147	q26.1
SNP_A-1667854	C	C	259	129	228	156	4.511	3.37E-02	rs9283619	3	163561223	q26.1
SNP_A-1887210	A	A	233	151	275	117	7.704	5.50E-03	rs4488852	3	163593416	q26.1
SNP_A-2149276	A	A	226	184	263	131	11.403	7.00E-04	rs6789378	3	163650098	q26.1
SNP_A-2180296	T	T	199	165	214	124	5.406	0.0201	rs7434223	3	163666164	q26.1
SNP_A-2075971	A	G	200	172	207	175	4.767	2.90E-02	rs1382203	3	163701551	q26.1
SNP_A-1975141	A	A	256	134	224	170	6.376	1.16E-02	rs1478149	3	163719656	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1975143	-	C	204	204	248	154	11.223	8.00E-04	rs1031837	3	163720197	q26.1
SNP_A-2197103	G	G	269	143	239	177	5.365	2.05E-02	rs2061739	3	163720722	q26.1
SNP_A-2184232	G	G	324	28	309	49	6.032	0.014	rs13317574	3	163847807	q26.1
SNP_A-1940587	G	G	326	48	288	64	3.974	4.62E-02	rs7624234	3	163873220	q26.1
SNP_A-1861581	G	G	345	45	341	27	3.888	4.86E-02	rs12696205	3	165482093	q26.1
SNP_A-1975192	C	C	208	148	250	128	4.646	3.11E-02	rs2126806	3	165769179	q26.1
SNP_A-2180482	C	C	310	68	318	42	5.812	1.59E-02	rs10106369	3	165881558	q26.1
SNP_A-1941314	C	C	339	77	317	101	3.969	4.63E-02	rs9838256	3	166216975	q26.1
SNP_A-2197156	A	A	392	22	381	39	4.851	0.0276	rs7635751	3	166318761	q26.1
SNP_A-1975199	G	G	371	5	350	16	6.24	1.25E-02	rs2053369	3	166378670	q26.1
SNP_A-2043661	C	C	377	19	358	36	5.741	0.0166	rs17449213	3	166386435	q26.1
SNP_A-1960018	A	A	391	25	373	43	5.189	2.27E-02	rs11922760	3	166388272	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2264894	A	A	369	3	352	12	5.715	1.68E-02	rs829505	3	166927048	q26.1
SNP_A-2022530	A	A	321	43	351	27	4.734	2.96E-02	rs1370899	3	167093853	q26.1
SNP_A-1799379	A	A	353	43	366	24	5.578	1.82E-02	rs7615933	3	167113355	q26.1
SNP_A-2113505	A	A	351	43	330	76	9.621	0.0019	rs4680618	3	167349706	q26.1
SNP_A-1975212	A	A	321	49	293	79	8.303	4.00E-03	rs1440678	3	167350180	q26.1
SNP_A-1939550	C	C	320	78	353	47	9.301	0.0023	rs12374202	3	167362713	q26.1
SNP_A-1975213	A	A	335	79	363	49	8.15	0.0043	rs2024539	3	167367754	q26.1
SNP_A-2098669	T	T	273	45	304	16	15.446	8.49E-05	rs2024537	3	167369736	q26.1
SNP_A-2170958	A	A	292	40	252	54	3.973	4.62E-02	rs12491610	3	168563271	q26.1
SNP_A-1844427	A	A	322	0	316	8	8.05	4.50E-03	—	3	168594025	q26.1
SNP_A-2129547	T	T	392	10	396	2	5.334	2.09E-02	rs2419134	3	168600547	q26.1
SNP_A-1838221	A	A	361	9	325	21	5.891	0.0152	rs12696273	3	168637745	q26.1
SNP_A-1928526	C	C	379	17	369	37	7.418	6.50E-03	rs9863185	3	168650850	q26.1
SNP_A-2131252	T	T	309	99	279	133	6.494	1.08E-02	rs6774632	3	168762352	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215185	A	A	258	92	224	112	4.075	4.35E-02	rs4599308	3	168801575	q26.1
SNP_A-1839695	A	A	387	25	363	43	5.489	1.91E-02	rs13096396	3	168976236	q26.1
SNP_A-2027075	A	A	245	137	191	147	4.368	3.66E-02	rs1492022	3	168985879	q26.1
SNP_A-2216235	G	G	376	24	362	46	7.101	7.70E-03	---	3	168988133	q26.1
SNP_A-2115245	G	G	365	17	353	33	5.3	2.13E-02	rs2229697	3	168993174	q26.1
SNP_A-2186345	G	G	344	10	363	1	7.736	5.40E-03	rs7627581	3	169180786	q26.1
SNP_A-2058821	A	A	331	43	343	27	3.849	4.98E-02	rs6766475	3	169645614	q26.2
SNP_A-2102209	G	G	313	13	342	4	5.458	0.0195	rs329079	3	169716449	q26.2
SNP_A-1975246	C	C	318	98	283	131	6.789	9.20E-03	rs4955625	3	170118918	q26.2
SNP_A-1835737	G	G	414	0	416	4	3.962	0.0465	rs16853626	3	170589425	q26.2
SNP_A-2279761	C	C	290	50	311	27	7.598	5.80E-03	rs12493227	3	170702004	q26.2
SNP_A-1879857	G	G	333	29	328	48	4.462	3.47E-02	rs12490374	3	171109021	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2120093	C	C	390	8	411	1	5.755	1.64E-02	rs16854694	3	171184534	q26.2
SNP_A-2171532	C	C	405	3	378	12	5.928	0.0149	rs7620870	3	171461354	q26.2
SNP_A-2268343	A	A	411	3	402	10	3.864	4.93E-02	rs2291930	3	171473444	q26.2
SNP_A-2290161	G	G	413	3	403	11	4.689	0.0304	rs2292386	3	171482116	q26.2
SNP_A-2187743	G	G	318	58	335	39	4.159	4.14E-02	rs9856511	3	171622867	q26.2
SNP_A-1975277	A	A	286	94	260	146	11.657	6.00E-04	rs16855137	3	171694784	q26.2
SNP_A-2237328	G	G	368	42	349	61	4.008	0.0453	rs9873736	3	171856612	q26.2
SNP_A-2308473	A	A	355	11	373	25	4.557	3.28E-02	rs6789594	3	172434905	q26.2
SNP_A-2036347	A	A	406	0	410	4	3.942	4.71E-02	rs6781809	3	172905227	q26.31
SNP_A-1846775	C	C	322	44	279	21	4.721	0.0298	rs4378993	3	172941882	q26.31
SNP_A-1975319	C	C	313	97	288	122	3.894	4.85E-02	rs953882	3	173580444	q26.31
SNP_A-1823068	T	T	307	11	336	4	3.843	0.0499	rs9868789	3	173625419	q26.31
SNP_A-1929430	C	C	356	10	365	3	3.876	4.90E-02	rs9990128	3	173626080	q26.31
SNP_A-2278418	C	C	273	131	241	171	7.212	7.20E-03	rs437197	3	173819256	q26.31
SNP_A-2091520	G	G	179	177	214	138	7.923	4.90E-03	rs6778941	3	173851403	q26.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2076072	A	A	252	140	216	162	4.119	0.0424	rs9883329	3	173867292	q26.31
SNP_A-2312697	T	T	333	59	304	80	4.411	3.57E-02	rs6765863	3	174045389	q26.31
SNP_A-2097429	G	G	268	92	293	65	5.752	1.65E-02	rs9823588	3	174048260	q26.31
SNP_A-1850819	T	T	302	64	327	41	6.026	0.0141	rs16826691	3	174659455	q26.31
SNP_A-1915159	G	G	316	56	341	39	3.909	4.80E-02	rs17318925	3	174662000	q26.31
SNP_A-1894908	T	T	332	84	349	61	4.029	4.47E-02	rs16827207	3	174692394	q26.31
SNP_A-1847564	A	A	384	28	397	15	4.147	4.17E-02	rs17254553	3	174711498	q26.31
SNP_A-1717461	A	A	294	74	289	107	5.04	2.48E-02	rs1345535	3	175224373	q26.31
SNP_A-2034317	G	G	375	25	365	41	3.969	4.63E-02	rs1356810	3	175543158	q26.31
SNP_A-1708861	T	T	312	88	296	116	4.088	4.32E-02	rs575582	3	175717253	q26.31
SNP_A-1916597	G	G	402	4	408	0	4.04	4.44E-02	rs9826059	3	176186931	q26.31
SNP_A-2060645	C	C	230	146	241	101	6.861	8.80E-03	rs7642577	3	176406720	q26.31
SNP_A-1861257	G	G	363	1	351	11	8.53	3.50E-03	rs4323016	3	176784358	q26.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1836618	G	G	333	55	329	33	4.628	3.14E-02	rs9842255	3	177326888	q26.31
SNP_A-2077705	A	A	343	41	340	24	3.927	4.75E-02	rs2626491	3	177593375	q26.32
SNP_A-1957119	G	G	233	139	267	115	4.448	0.0349	rs9839536	3	177938936	q26.32
SNP_A-2245681	A	A	317	17	349	7	5.008	0.0252	rs936700	3	178155214	q26.32
SNP_A-2053121	G	G	184	132	234	98	10.618	1.10E-03	rs1566412	3	178622159	q26.32
SNP_A-2158483	G	G	259	119	301	95	5.426	1.98E-02	rs6783019	3	178639862	q26.32
SNP_A-2106048	G	G	190	148	240	110	11.205	8.00E-04	rs1909567	3	178641459	q26.32
SNP_A-2169528	A	A	267	147	236	178	4.867	2.74E-02	rs1995242	3	178678783	q26.32
SNP_A-2152563	T	T	305	83	336	62	4.414	0.0356	rs17556594	3	178723976	q26.32
SNP_A-2108793	T	T	290	108	269	137	4.142	4.18E-02	rs4857717	3	178811024	q26.32
SNP_A-2114680	C	C	279	93	254	118	4.135	4.20E-02	rs16828300	3	178820236	q26.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2069358	T	T	293	113	261	139	4.486	3.42E-02	rs1875101	3	178825319	q26.32
SNP_A-2164224	A	A	362	54	386	34	5.296	2.14E-02	rs17633881	3	178829591	q26.32
SNP_A-1801524	G	G	286	120	303	91	4.297	3.82E-02	rs6788878	3	178926670	q26.32
SNP_A-1975445	C	C	346	70	371	49	4.559	3.28E-02	rs13093519	3	179343701	q26.32
SNP_A-2088322	C	C	375	1	316	6	4.458	3.47E-02	rs16829646	3	179707956	q26.32
SNP_A-2103802	G	G	184	162	216	134	5.186	2.28E-02	rs7652997	3	179858961	q26.32
SNP_A-2298012	C	C	280	134	252	162	4.122	4.23E-02	rs7626901	3	179985917	q26.32
SNP_A-1811745	C	C	285	131	258	160	4.228	3.98E-02	rs4398411	3	179995891	q26.32
SNP_A-2235779	G	G	279	41	250	68	8.272	4.00E-03	rs9879637	3	180164670	q26.32
SNP_A-1900356	G	G	323	71	292	94	4.687	0.0304	rs4501160	3	180165683	q26.32
SNP_A-2250608	C	C	296	114	264	144	5.312	0.0212	rs4583702	3	180170436	q26.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2106702	A	A	277	87	244	118	6.773	9.30E-03	rs4955797	3	180182385	q26.32
SNP_A-2176360	C	C	334	82	307	111	5.49	1.91E-02	rs7652946	3	180187651	q26.32
SNP_A-2116527	T	T	308	36	335	17	7.854	5.10E-03	rs11920864	3	180292567	q26.32
SNP_A-2099765	G	G	317	63	267	87	7.209	7.30E-03	rs2699905	3	180367039	q26.32
SNP_A-1683918	T	T	314	86	296	112	3.866	4.93E-02	rs2287310	3	180443831	q26.32
SNP_A-1975465	T	T	406	4	416	0	4.078	4.34E-02	rs16830238	3	180476857	q26.32
SNP_A-2165054	G	G	227	131	193	179	9.92	1.60E-03	rs9822116	3	180557317	q26.32
SNP_A-2185816	G	A	201	181	217	161	7.655	5.70E-03	rs4855084	3	180714886	q26.33
SNP_A-2023979	A	A	268	108	241	137	4.86	0.0275	rs2080516	3	180721780	q26.33
SNP_A-2250182	G	G	346	52	320	76	5.51	0.0189	rs2879588	3	180862304	q26.33
SNP_A-1786068	C	C	235	135	270	112	4.377	3.64E-02	rs3821794	3	181022879	q26.33
SNP_A-1975478	T	T	248	162	285	133	5.343	2.08E-02	rs10513765	3	181027572	q26.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796254	A	A	278	94	313	69	5.776	1.63E-02	---	3	181049330	q26.33
SNP_A-1811441	T	T	255	159	212	198	8.201	4.20E-03	rs2339912	3	181049882	q26.33
SNP_A-2159434	G	G	242	154	212	192	6.076	0.0137	rs2339913	3	181049925	q26.33
SNP_A-2192929	C	C	231	131	204	176	7.84	5.10E-03	rs3774237	3	181053119	q26.33
SNP_A-1922791	C	C	253	151	209	187	7.946	4.80E-03	rs3774238	3	181053343	q26.33
SNP_A-2061248	A	G	182	150	178	144	6.668	9.80E-03	rs6767081	3	181054144	q26.33
SNP_A-2288940	A	A	249	123	275	97	4.363	3.67E-02	rs6804380	3	181154527	q26.33
SNP_A-1839598	G	G	325	91	352	68	4.385	3.63E-02	rs12497997	3	181892099	q26.33
SNP_A-1931417	A	A	274	104	299	81	3.945	0.047	rs1805572	3	182129965	q26.33
SNP_A-1975501	C	C	306	14	328	4	6.1	0.0135	rs1805625	3	182174363	q26.33
SNP_A-2061898	A	A	258	158	278	124	4.607	3.18E-02	rs9810292	3	182197009	q26.33
SNP_A-2103626	A	A	353	55	378	38	3.885	0.0487	rs16832660	3	182978803	q26.33
SNP_A-2104641	C	C	382	34	351	65	11.018	9.00E-04	rs1096897	3	183055244	q26.33
SNP_A-1895347	T	T	210	142	247	119	4.751	0.0293	rs12489180	3	183062411	q26.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284149	T	T	328	10	359	1	8.077	4.50E-03	rs16833022	3	183507467	q26.33
SNP_A-2251529	T	T	340	10	377	3	4.453	3.48E-02	rs1488139	3	183524952	q26.33
SNP_A-2009367	G	G	402	10	412	2	5.451	1.96E-02	rs4638958	3	183551179	q26.33
SNP_A-2009369	C	C	379	33	391	19	3.951	4.68E-02	rs2710934	3	183710980	q26.33
SNP_A-2052663	G	G	375	33	389	19	4.026	0.0448	rs2710937	3	183719381	q26.33
SNP_A-2029045	A	A	320	24	327	9	6.801	9.10E-03	rs10937090	3	183723689	q26.33
SNP_A-2248403	T	T	378	32	402	18	4.539	3.31E-02	rs2710935	3	183729781	q26.33
SNP_A-1939287	G	G	286	48	254	68	5.127	2.36E-02	rs2687788	3	183964892	q26.33
SNP_A-2032401	A	A	310	98	279	123	4.415	0.0356	rs1357451	3	183968785	q26.33
SNP_A-1886535	C	C	264	102	231	125	4.393	0.0361	rs9870317	3	183997338	q26.33
SNP_A-1884833	G	G	370	22	379	7	7.821	5.20E-03	rs7632904	3	184265803	q27.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1845517	A	A	366	0	352	4	4.135	4.20E-02	rs9841950	3	184423190	q27.1
SNP_A-2207192	T	T	310	96	271	123	5.768	1.63E-02	rs1001190	3	184693674	q27.1
SNP_A-2112285	G	G	317	93	289	117	4.017	4.50E-02	rs1979983	3	184693693	q27.1
SNP_A-2251695	C	C	320	96	290	126	5.529	1.87E-02	rs3821514	3	184694389	q27.1
SNP_A-1833435	T	T	239	175	211	205	4.106	4.27E-02	rs1520101	3	184694608	q27.1
SNP_A-1800587	T	T	356	54	331	77	4.943	2.62E-02	rs7614051	3	184714079	q27.1
SNP_A-2024505	G	C	218	178	219	185	6.857	8.80E-03	rs7430671	3	185244366	q27.1
SNP_A-2081346	T	T	295	113	256	152	8.5	3.60E-03	rs844540	3	185346515	q27.1
SNP_A-1932730	T	T	283	109	222	136	8.821	3.00E-03	rs4575925	3	185349545	q27.1
SNP_A-1877549	C	G	209	165	200	186	4.507	3.38E-02	rs843344	3	185389734	q27.1
SNP_A-1882379	C	C	177	159	205	135	3.988	0.0458	rs843336	3	185395041	q27.1
SNP_A-1844820	T	T	301	105	257	145	9.85	1.70E-03	rs7371826	3	185402652	q27.1
SNP_A-1975544	T	T	232	88	263	67	4.634	3.13E-02	rs843348	3	185427939	q27.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1975545	T	T	294	98	330	70	6.663	9.80E-03	rs843350	3	185428976	q27.1
SNP_A-2186143	C	C	300	108	337	59	16.351	5.26E-05	rs1709620	3	185459396	q27.1
SNP_A-1916087	C	C	382	32	392	18	4.03	4.47E-02	rs1709621	3	185459608	q27.1
SNP_A-2254550	G	G	276	42	290	22	6.54	1.05E-02	rs7630982	3	185627348	q27.1
SNP_A-2280423	G	G	195	149	245	121	7.911	4.90E-03	rs4912555	3	185656168	q27.1
SNP_A-1789316	A	A	241	159	299	111	14.642	0.0001	rs1138510	3	185781869	q27.1
SNP_A-1735318	C	C	369	15	398	6	4.449	0.0349	rs727272	3	185788483	q27.1
SNP_A-2009385	G	G	402	14	411	5	4.363	3.67E-02	rs4389455	3	185951470	q27.1
SNP_A-2282321	G	G	356	38	343	57	3.997	4.56E-02	rs2377371	3	186371891	q27.2
SNP_A-2302193	A	A	362	0	338	4	4.258	3.91E-02	rs16859819	3	186412005	q27.2
SNP_A-1921698	C	G	225	171	215	187	8.476	3.60E-03	rs2276738	3	186683575	q27.2
SNP_A-1945011	G	A	226	178	211	193	5.399	2.02E-02	rs1054843	3	186689419	q27.2
SNP_A-1795654	G	G	201	197	237	167	5.387	2.03E-02	rs16860081	3	186700977	q27.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1877013	G	G	339	31	363	15	6.301	0.0121	rs1861877	3	187455413	q27.2
SNP_A-1934176	C	C	296	116	318	90	4.05	4.42E-02	rs1861876	3	187455793	q27.2
SNP_A-2073526	T	A	168	162	191	135	5.952	0.0147	rs12696555	3	187712475	q27.3
SNP_A-2305532	T	T	340	38	362	22	4.909	2.67E-02	rs5030102	3	187928789	q27.3
SNP_A-2026835	G	G	326	4	300	24	15.312	9.11E-05	rs17299991	3	187988632	q27.3
SNP_A-2208306	G	G	321	77	359	55	5.477	1.93E-02	rs6809750	3	188165314	q27.3
SNP_A-1931851	C	C	365	49	379	27	6.554	1.05E-02	rs13322149	3	188177915	q27.3
SNP_A-1975591	C	C	363	53	346	74	3.861	4.94E-02	rs698104	3	188485219	q27.3
SNP_A-1975598	A	A	223	185	268	148	8.158	0.0043	rs2687923	3	188636073	q27.3
SNP_A-1975596	C	C	313	103	355	63	12.275	5.00E-04	rs9852121	3	188643992	q27.3
SNP_A-1905127	A	A	306	110	348	72	10.612	1.10E-03	rs9824824	3	188646004	q27.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798358	C	C	216	118	189	157	7.121	0.0076	rs6771852	3	188703479	q27.3
SNP_A-2074977	A	A	241	121	285	93	7.001	8.10E-03	rs2378269	3	188705928	q27.3
SNP_A-1659430	T	T	347	53	375	35	4.645	3.11E-02	rs1365113	3	188713641	q27.3
SNP_A-2181518	A	A	269	139	238	164	3.914	4.79E-02	rs6444238	3	188776371	q27.3
SNP_A-1797121	C	C	209	87	261	71	5.327	2.10E-02	rs9868558	3	188793054	q27.3
SNP_A-2059555	C	C	351	43	320	62	4.686	0.0304	rs1863391	3	188794275	q27.3
SNP_A-2059450	T	T	307	45	268	74	9.57	0.002	rs1863392	3	188794720	q27.3
SNP_A-2188759	C	C	341	29	344	48	4.07	4.37E-02	rs10937312	3	188802391	q27.3
SNP_A-1858766	G	G	247	149	288	120	6.091	1.36E-02	rs4686897	3	188838177	q27.3
SNP_A-2293966	A	A	231	141	271	115	5.571	0.0183	rs1030373	3	188849947	q27.3
SNP_A-2203048	G	G	339	39	370	22	5.841	1.57E-02	rs3755792	3	188872663	q27.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1975615	C	C	355	57	384	36	5.804	0.016	rs17728902	3	188873846	q27.3
SNP_A-2272355	G	G	323	69	304	96	4.914	2.66E-02	rs10937316	3	188896390	q27.3
SNP_A-1975628	G	G	346	62	330	86	4.193	4.06E-02	rs12330507	3	189196755	q27.3
SNP_A-2145932	T	T	320	56	309	85	5.739	0.0166	rs1007308	3	189372425	q27.3
SNP_A-2096670	C	C	213	137	231	101	5.704	1.69E-02	rs20305 16	3	189584441	q28
SNP_A-2253700	T	T	319	11	312	28	7.34	6.70E-03	rs6444286	3	189608043	q28
SNP_A-2050691	C	C	332	84	309	109	4.059	4.39E-02	rs9867093	3	190027113	q28
SNP_A-1975664	G	G	287	83	292	42	11.681	6.00E-04	rs9290892	3	190689193	q28
SNP_A-1865576	C	C	371	45	394	26	5.757	1.64E-02	rs10937395	3	190819072	q28
SNP_A-2240512	C	C	357	27	386	14	4.929	0.0264	rs16864652	3	190822849	q28
SNP_A-2107247	A	A	328	80	360	58	4.875	2.72E-02	rs9830151	3	190827816	q28

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2185115	C	C	392	8	394	20	4.909	2.67E-02	rs9876702	3	190937042	q28
SNP_A-2133490	G	G	366	4	376	0	4.087	4.32E-02	rs6444397	3	190950949	q28
SNP_A-1828380	A	A	333	11	329	1	8.07	4.50E-03	rs10433488	3	191160566	q28
SNP_A-2118048	G	G	281	85	301	59	5.333	2.09E-02	rs1447947	3	191232940	q28
SNP_A-1975686	G	G	271	71	295	45	6.839	8.90E-03	rs1719615	3	191236409	q28
SNP_A-2091254	C	C	282	40	299	25	3.953	4.68E-02	rs1447935	3	191244886	q28
SNP_A-1975696	T	T	294	82	267	109	5.116	2.37E-02	rs10513848	3	191358900	q28
SNP_A-1837207	A	A	379	29	361	51	6.468	1.10E-02	rs17500920	3	191507595	q28
SNP_A-2136895	G	G	387	27	365	51	8.023	4.60E-03	rs17501010	3	191509356	q28
SNP_A-1825899	C	C	323	59	338	40	3.966	4.64E-02	rs7651888	3	191628097	q28
SNP_A-1658738	T	T	261	133	299	107	5.216	0.0224	rs1015704	3	191659325	q28
SNP_A-2252754	C	C	326	66	337	35	9.18	2.40E-03	rs3773978	3	191769588	q28
SNP_A-2185183	G	G	310	10	328	2	5.689	1.71E-02	rs6791358	3	191988806	q28
SNP_A-2227377	G	G	246	106	229	135	3.898	4.83E-02	rs16886328	3	192403878	q28

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1953764	A	A	374	38	340	58	5.545	1.85E-02	rs10048931	3	192420717	q28
SNP_A-2124898	A	A	339	75	311	107	6.813	9.00E-03	rs10048935	3	192421260	q28
SNP_A-1798531	C	C	307	75	305	47	5.215	0.0224	rs6801942	3	192546445	q28
SNP_A-2123204	C	C	365	31	391	15	6.336	0.0118	rs579405	3	192613277	q28
SNP_A-2221806	T	T	350	32	372	18	4.508	3.37E-02	rs167150	3	192613926	q28
SNP_A-2162788	A	A	376	36	396	22	3.854	4.96E-02	rs293845	3	192614869	q28
SNP_A-2220854	C	C	277	57	311	41	4.109	4.27E-02	rs293822	3	192651997	q28
SNP_A-2140735	C	C	244	86	248	60	3.909	4.80E-02	rs293825	3	192652404	q28
SNP_A-1909319	G	G	276	66	296	38	8.144	0.0043	rs293831	3	192661172	q28
SNP_A-2113196	G	G	296	104	314	72	6.102	0.0135	rs445237	3	192671190	q28
SNP_A-1890568	T	T	364	50	389	27	7.695	5.50E-03	rs9790048	3	192700017	q28
SNP_A-2009442	C	C	238	142	211	177	5.381	2.04E-02	rs779291	3	192924767	q28

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308310	A	A	342	48	366	28	6.056	1.39E-02	rs9850123	3	193524885	q28
SNP_A-2243426	G	G	345	43	366	18	10.846	0.001	rs4438608	3	193526180	q28
SNP_A-1958603	T	T	319	49	278	64	3.86	4.95E-02	rs1574091	3	193564784	q28
SNP_A-1715267	G	G	247	115	302	92	6.723	9.50E-03	rs3897920	3	193623883	q28
SNP_A-1714384	A	A	294	106	275	135	4.001	4.55E-02	rs781424	3	193624596	q28
SNP_A-1664652	T	T	295	105	278	134	3.847	4.98E-02	rs2701595	3	193632133	q28
SNP_A-2259619	A	A	266	84	222	106	5.807	0.016	rs1827546	3	193797157	q28
SNP_A-2056059	A	A	307	87	278	110	4.077	4.35E-02	rs1827545	3	193797228	q28
SNP_A-2224775	G	G	309	105	280	132	4.499	0.0339	rs2708309	3	193797769	q28
SNP_A-1931411	G	C	209	163	189	173	5.178	0.0229	rs2654689	3	193798101	q28
SNP_A-1866842	A	A	200	162	229	133	4.811	2.83E-02	rs2044585	3	194237574	q29
SNP_A-1864773	C	C	269	93	291	69	4.414	0.0356	rs13068101	3	194254997	q29
SNP_A-1893977	A	A	320	94	297	123	4.69	3.03E-02	rs9810201	3	194293991	q29
SNP_A-2172176	C	C	239	157	272	114	8.828	3.00E-03	rs6764121	3	194613086	q29

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2144384	T	T	293	69	272	94	4.593	3.21E-02	rs12696666	3	194665417	q29
SNP_A-2185526	A	A	198	110	193	151	4.531	3.33E-02	rs7620342	3	194782316	q29
SNP_A-1975785	C	C	355	19	358	36	4.75	0.0293	rs724767	3	195205032	q29
SNP_A-1852784	T	T	239	159	245	121	3.898	4.83E-02	rs1873413	3	195279121	q29
SNP_A-1898894	G	G	229	133	248	96	6.28	1.22E-02	rs13090351	3	195907039	q29
SNP_A-1975807	G	G	239	145	268	114	5.364	0.0206	rs1461774	3	195921205	q29
SNP_A-2009475	G	G	351	59	373	39	4.745	2.94E-02	rs4558689	3	196011738	q29
SNP_A-2296324	G	G	317	19	302	34	4.609	3.18E-02	rs9846403	3	196032239	q29
SNP_A-1868989	A	A	357	33	333	51	4.646	3.11E-02	rs2131879	3	196320213	q29
SNP_A-2204969	C	C	394	12	404	4	4.12	0.0424	rs9856486	3	196397428	q29
SNP_A-1934297	A	A	239	73	288	60	3.875	4.90E-02	rs6437471	3	196533192	q29
SNP_A-1941094	C	C	269	85	300	60	5.949	0.0147	rs2029708	3	196602407	q29
SNP_A-1752539	C	C	190	134	251	125	4.915	2.66E-02	rs2284890	3	197114668	q29

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1914097	C	C	273	139	303	113	4.226	3.98E-02	rs4927850	3	197239940	q29
SNP_A-1866540	C	C	263	113	219	135	5.31	0.0212	rs3964310	3	197736861	q29
SNP_A-2230808	A	A	287	87	227	103	5.623	0.0177	rs7628045	3	198400540	q29
SNP_A-1793882	G	G	284	44	264	64	4.434	3.52E-02	rs403274	3	198462764	q29
SNP_A-1855309	C	C	270	146	310	110	7.802	5.20E-03	rs6777317	3	198559269	q29
SNP_A-1960693	C	C	321	41	331	17	9.812	1.70E-03	rs13083034	3	198662338	q29
SNP_A-1866280	A	A	352	28	378	16	3.947	0.047	rs6583217	3	198677873	q29
SNP_A-1922091	T	T	341	43	368	26	5.089	0.0241	rs12107047	3	198935197	q29
SNP_A-1868155	C	C	328	66	308	90	4.301	3.81E-02	rs10084890	4	1043764	p16.3
SNP_A-2243706	T	T	319	53	306	86	7.587	5.90E-03	rs12645644	4	1043989	p16.3
SNP_A-2281541	G	G	336	72	312	96	4.317	3.77E-02	rs7669622	4	1048489	p16.3
SNP_A-2137417	T	T	265	45	248	74	7.405	6.50E-03	rs6599278	4	1048628	p16.3
SNP_A-2313769	C	C	317	59	281	77	4.111	4.26E-02	rs2014318	4	1056608	p16.3
SNP_A-2270212	T	T	305	49	280	80	8.468	3.60E-03	rs1010342	4	1058649	p16.3
SNP_A-1874824	C	C	243	109	229	151	6.136	0.0132	rs11947258	4	1486049	p16.3
SNP_A-1804094	G	G	245	85	235	133	8.734	3.10E-03	rs3128809	4	2339161	p16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1873633	A	A	327	37	293	57	5.848	1.56E-02	rs959770	4	2362528	p16.3
SNP_A-1820953	C	C	392	20	407	5	9.282	0.0023	rs2071674	4	2364315	p16.3
SNP_A-2065046	C	C	192	152	219	121	5.271	2.17E-02	rs2471327	4	3063178	p16.3
SNP_A-2150779	G	G	218	130	236	98	4.92	2.66E-02	rs11731237	4	3188816	p16.3
SNP_A-2106294	C	C	306	14	356	4	7.003	8.10E-03	rs46990018	4	3674395	p16.3
SNP_A-1906438	A	A	353	61	328	90	6.468	1.10E-02	rs2092898	4	3766621	p16.3
SNP_A-2259422	C	C	297	57	294	82	3.852	4.97E-02	rs16835882	4	4669683	p16.2
SNP_A-1915566	T	T	315	59	276	86	7.408	6.50E-03	rs13130037	4	4842748	p16.2
SNP_A-1935175	C	C	370	22	360	38	4.358	3.68E-02	—	4	4904956	p16.2
SNP_A-1895222	C	C	274	68	295	49	3.855	4.96E-02	rs7681595	4	4912886	p16.2
SNP_A-2009526	A	A	316	24	279	41	6.147	0.0132	rs2087868	4	4967191	p16.2
SNP_A-2189753	A	A	237	177	271	147	5.034	2.49E-02	rs4303923	4	5051299	p16.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255172	C	C	396	16	410	6	4.769	2.90E-02	rs6849207	4	5057419	p16.2
SNP_A-1896141	T	T	350	66	323	95	6.302	0.0121	rs7672542	4	5057594	p16.2
SNP_A-2147871	T	T	367	19	363	7	5.224	0.0223	rs16836412	4	5057722	p16.2
SNP_A-2243652	G	G	240	102	272	72	7.167	7.40E-03	rs6831989	4	5059759	p16.2
SNP_A-1919992	C	C	349	65	320	94	6.546	1.05E-02	rs16836433	4	5062171	p16.2
SNP_A-2291481	T	T	348	66	312	96	7.476	0.0063	rs16836437	4	5062540	p16.2
SNP_A-1906866	C	C	341	17	384	8	4.258	3.91E-02	rs4547750	4	5067245	p16.2
SNP_A-1793872	A	A	394	16	407	5	5.968	0.0146	rs11721707	4	5067543	p16.2
SNP_A-2090499	G	G	395	15	403	5	5.075	2.43E-02	rs7681839	4	5068256	p16.2
SNP_A-2246370	A	A	344	62	320	92	6.668	9.80E-03	rs16836497	4	5070749	p16.2
SNP_A-1975853	A	A	335	47	311	83	10.678	1.10E-03	rs16836513	4	5071857	p16.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2162286	T	T	301	65	275	87	4.336	0.0373	rs2968709	4	5072347	p16.2
SNP_A-2262517	G	G	338	74	312	104	6.077	0.0137	rs11939863	4	5089081	p16.2
SNP_A-2216535	G	G	304	26	289	45	5.44	1.97E-02	rs4072934	4	5123290	p16.2
SNP_A-1975857	T	T	246	92	236	122	3.842	5.00E-02	rs1077365	4	5283127	p16.2
SNP_A-2009531	T	T	267	53	253	81	5.931	0.0149	rs1077366	4	5283147	p16.2
SNP_A-1936320	A	A	369	43	395	23	6.902	0.0086	rs1992832	4	5310799	p16.2
SNP_A-1901803	G	G	411	5	405	15	5.025	2.50E-02	rs16837029	4	5451163	p16.2
SNP_A-1858015	C	C	404	6	394	16	4.671	3.07E-02	rs11724992	4	5528395	p16.2
SNP_A-1794830	G	G	398	18	412	8	4.069	4.37E-02	—	4	5594248	p16.2
SNP_A-1780431	G	G	322	22	310	38	4.472	3.45E-02	rs11729670	4	5625590	p16.2
SNP_A-2300516	C	C	357	47	375	23	8.627	0.0033	rs3774867	4	5872187	p16.2
SNP_A-2041048	T	C	224	186	219	195	4.677	3.06E-02	rs11727881	4	6024752	p16.1
SNP_A-2264024	A	A	363	31	388	18	4.102	4.28E-02	rs4993355	4	6114176	p16.1
SNP_A-2180109	C	C	317	63	275	85	5.714	1.68E-02	rs16838298	4	6244621	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1922106	A	A	367	3	386	12	4.865	2.74E-02	rs11929728	4	6263478	p16.1
SNP_A-2082225	C	C	406	0	402	4	4.02	4.50E-02	rs4392572	4	6267970	p16.1
SNP_A-2245559	G	G	409	3	400	12	5.5	0.019	rs4560489	4	6269326	p16.1
SNP_A-1903751	G	G	403	9	396	22	5.47	1.93E-02	rs4689420	4	6482290	p16.1
SNP_A-1905140	G	G	411	3	405	13	6.275	1.22E-02	rs4368678	4	6830534	p16.1
SNP_A-1905305	C	C	311	81	299	109	4.044	4.43E-02	rs9762239	4	7255703	p16.1
SNP_A-2186816	A	A	183	121	164	162	6.22	0.0126	rs9994752	4	7441522	p16.1
SNP_A-1787110	T	T	321	37	355	23	4.437	3.52E-02	rs7654768	4	7599078	p16.1
SNP_A-1810491	G	G	382	30	397	17	3.88	4.89E-02	rs10470724	4	7665561	p16.1
SNP_A-2178318	C	C	396	4	392	12	4.001	4.55E-02	rs16840586	4	7711396	p16.1
SNP_A-1901191	G	G	224	78	209	121	8.587	3.40E-03	rs2359630	4	7822866	p16.1
SNP_A-1907170	C	C	358	20	363	9	4.159	4.14E-02	rs12511919	4	7906929	p16.1
SNP_A-2223065	T	T	317	63	344	38	7.286	7.00E-03	rs16841845	4	8260401	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2171563	G	G	244	126	220	154	4.02	4.50E-02	rs922521	4	8325881	p16.1
SNP_A-2076208	G	G	389	11	385	25	5.342	2.08E-02	rs4270574	4	8433301	p16.1
SNP_A-1834667	A	A	388	0	393	11	10.713	1.10E-03	rs899486	4	8442540	p16.1
SNP_A-2246277	G	G	315	47	304	70	4.522	3.35E-02	rs13136987	4	8508930	p16.1
SNP_A-2116565	C	C	363	19	349	35	5.011	0.0252	rs6850810	4	8652354	p16.1
SNP_A-2106197	T	T	336	26	333	43	3.938	4.72E-02	rs3115401	4	8656078	p16.1
SNP_A-1870862	G	G	375	35	361	57	5.45	1.96E-02	rs3103091	4	8657052	p16.1
SNP_A-1859505	T	T	279	69	263	99	5.556	0.0184	rs939134	4	9544862	p16.1
SNP_A-2113235	G	G	345	13	338	4	4.473	0.0344	rs13101772	4	9673993	p16.1
SNP_A-2181248	A	A	164	160	207	129	8.094	4.40E-03	rs4444830	4	9801088	p16.1
SNP_A-2027540	A	A	332	4	370	0	4.43	3.53E-02	rs2241466	4	9835372	p16.1
SNP_A-2112723	G	G	361	17	371	5	6.677	9.80E-03	rs4697976	4	9886659	p16.1
SNP_A-1954809	T	T	378	0	386	4	3.897	4.84E-02	rs1017123	4	9926866	p16.1
SNP_A-1975955	T	T	250	142	279	117	3.983	4.60E-02	rs12505222	4	9947405	p16.1
SNP_A-2131108	A	A	269	109	312	86	5.383	2.03E-02	rs17407555	4	9951263	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253364	G	G	263	141	296	106	6.903	0.0086	rs6833142	4	9952251	p16.1
SNP_A-1975963	T	T	257	141	294	118	4.286	3.84E-02	rs7435841	4	9954821	p16.1
SNP_A-1975971	C	C	244	172	212	204	4.969	0.0258	rs9291683	4	10000429	p16.1
SNP_A-2117204	C	C	247	69	269	45	5.984	0.0144	rs4541501	4	10164890	p16.1
SNP_A-2310442	C	C	322	64	350	46	3.985	4.59E-02	rs17467252	4	10169883	p16.1
SNP_A-1950155	C	C	295	107	320	78	5.542	1.86E-02	rs5000857	4	10178603	p16.1
SNP_A-1975977	C	C	190	186	220	158	4.469	3.45E-02	rs997219	4	10200940	p16.1
SNP_A-1872439	C	T	213	195	241	175	8.498	3.60E-03	rs4296670	4	10327429	p16.1
SNP_A-1975983	G	A	196	184	233	165	8.008	4.70E-03	rs11725559	4	10330539	p16.1
SNP_A-1819519	C	C	253	139	278	112	4.076	4.35E-02	rs10009156	4	10343155	p16.1
SNP_A-2163861	C	C	174	146	207	113	7.063	7.90E-03	rs11933682	4	10347180	p16.1
SNP_A-1975987	C	G	201	153	194	156	10.494	1.20E-03	rs6820771	4	10358504	p16.1
SNP_A-1975988	C	C	209	125	162	160	10.036	0.0015	rs6821184	4	10358657	p16.1
SNP_A-1975989	C	A	244	170	215	203	9.001	2.70E-03	rs13145414	4	10364353	p16.1
SNP_A-2166922	G	A	244	172	219	201	9.786	0.0018	rs4501215	4	10365613	p16.1
SNP_A-1825535	C	C	304	104	247	161	18.157	2.03E-05	rs17209689	4	10370042	p16.1
SNP_A-1680670	T	C	202	198	239	171	6.301	0.0121	rs10516208	4	10412617	p16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1975992	A	A	309	81	284	108	4.906	2.68E-02	rs9291449	4	10419455	p16.1
SNP_A-1949005	G	G	289	127	321	95	6.291	0.0121	rs224490	4	11094910	p15.33
SNP_A-1821854	G	G	386	26	364	44	5.255	2.19E-02	rs16885832	4	11342915	p15.33
SNP_A-2035460	A	A	368	28	368	50	6.729	9.50E-03	rs16885853	4	11349531	p15.33
SNP_A-1846174	G	G	343	45	351	27	4.462	3.46E-02	rs17326638	4	11700692	p15.33
SNP_A-1976069	G	G	340	52	309	73	4.88	2.72E-02	rs2168202	4	11918559	p15.33
SNP_A-1976070	A	A	313	47	282	70	6.047	1.39E-02	rs1479249	4	11919713	p15.33
SNP_A-2250321	C	C	328	34	321	53	4.03	4.47E-02	rs6448906	4	12153973	p15.33
SNP_A-1901334	G	G	316	72	279	91	4.09	4.31E-02	rs6448910	4	12194066	p15.33
SNP_A-2197315	T	T	305	49	282	80	8.262	4.00E-03	rs6448930	4	12262804	p15.33
SNP_A-1976081	A	A	297	105	274	136	4.836	2.79E-02	rs10516257	4	12320731	p15.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1883328	G	G	261	149	229	185	5.951	0.0147	rs7668124	4	12346659	p15.33
SNP_A-1932627	A	A	261	139	226	174	6.429	0.0112	rs13151462	4	12347237	p15.33
SNP_A-2197801	G	G	312	32	344	16	6.534	0.0106	rs2222309	4	12368109	p15.33
SNP_A-2295976	T	T	234	90	265	69	4.549	3.29E-02	rs10805312	4	12546611	p15.33
SNP_A-2049918	A	A	403	5	404	0	4.982	2.56E-02	rs10029912	4	13166205	p15.33
SNP_A-1835196	A	A	356	50	380	26	8.362	0.0038	rs7695513	4	13166927	p15.33
SNP_A-2224459	T	T	314	82	324	44	10.605	1.10E-03	rs12499127	4	13305990	p15.33
SNP_A-1959490	T	T	365	31	383	15	5.993	0.0144	rs17810216	4	13464835	p15.33
SNP_A-2198396	A	A	223	185	252	154	4.6	3.20E-02	rs543907	4	13674368	p15.33
SNP_A-1665710	G	G	208	178	249	155	4.859	0.0275	rs572468	4	13744348	p15.33
SNP_A-1976142	A	A	258	108	271	79	4.461	3.47E-02	—	4	13828738	p15.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2056965	C	C	219	163	241	113	9.058	2.60E-03	rs2010594	4	14072254	p15.33
SNP_A-2064153	T	T	183	163	225	121	10.535	1.20E-03	rs2001171	4	14083509	p15.33
SNP_A-2229654	T	T	221	177	249	127	9.274	0.0023	rs2001172	4	14083529	p15.33
SNP_A-1976160	C	C	232	184	274	138	10.039	0.0015	rs3857163	4	14085718	p15.33
SNP_A-2227774	A	A	209	203	244	174	4.892	0.027	rs1501173	4	14114571	p15.33
SNP_A-1921259	C	C	185	131	225	111	4.946	2.61E-02	rs1014165	4	14143747	p15.33
SNP_A-1957899	A	A	276	98	287	71	4.181	4.09E-02	rs1909917	4	14148903	p15.33
SNP_A-2269507	A	G	204	160	204	178	6.658	9.90E-03	rs6835379	4	14483463	p15.33
SNP_A-2221871	C	C	225	163	272	128	8.474	3.60E-03	rs13138689	4	14551014	p15.33
SNP_A-2314312	T	A	179	155	176	140	5.606	1.79E-02	rs923985	4	14553331	p15.33
SNP_A-2097000	C	T	179	159	203	149	7.811	5.20E-03	rs6857060	4	14602487	p15.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102315	T	C	207	173	191	165	4.855	0.0276	rs17450892	4	14757678	p15.33
SNP_A-1737043	A	A	339	19	373	9	4.421	3.55E-02	rs2604580	4	14808943	p15.33
SNP_A-1949623	A	A	262	116	273	81	5.664	1.73E-02	rs12651461	4	14829957	p15.33
SNP_A-1643565	C	C	363	37	391	21	5.277	2.16E-02	rs1817186	4	14918431	p15.33
SNP_A-2009602	C	C	394	14	384	32	7.095	7.70E-03	rs6449162	4	15371852	p15.33
SNP_A-2076265	T	T	357	23	357	11	4.044	4.43E-02	rs16892537	4	15562879	p15.32
SNP_A-2250269	T	T	300	28	312	14	4.896	0.0269	rs1400776	4	15697580	p15.32
SNP_A-1942423	T	T	324	26	333	13	4.434	3.52E-02	rs1829271	4	15697807	p15.32
SNP_A-1681708	A	A	305	93	339	73	3.964	0.0465	rs884227	4	15823975	p15.32
SNP_A-1976228	G	G	369	3	345	13	6.791	9.20E-03	—	4	16078931	p15.32
SNP_A-1948052	G	G	334	72	363	43	8.52	3.50E-03	rs6855048	4	16225384	p15.32
SNP_A-2052263	A	A	376	36	394	20	4.987	2.55E-02	rs17502924	4	16644279	p15.32
SNP_A-2201923	T	T	352	28	372	12	6.932	8.50E-03	rs13110653	4	16649280	p15.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1925123	A	G	204	148	167	159	5.736	0.0166	rs12507442	4	16952573	p15.32
SNP_A-1863463	T	T	285	27	309	15	4.173	4.11E-02	rs746213	4	16996307	p15.32
SNP_A-1868695	G	G	345	33	372	18	5.242	2.20E-02	rs2518651	4	17125818	p15.32
SNP_A-2229418	A	A	293	85	277	117	5.189	2.27E-02	rs1031327	4	17164513	p15.32
SNP_A-2193055	G	G	278	74	236	100	6.949	8.40E-03	rs13129002	4	17243782	p15.32
SNP_A-2166417	C	C	255	159	224	194	5.457	0.0195	rs2302212	4	17495154	p15.32
SNP_A-2056403	A	A	404	12	415	3	5.543	1.86E-02	rs16895927	4	17551499	p15.32
SNP_A-2267287	T	T	283	77	244	94	3.887	0.0487	rs17518793	4	17577621	p15.32
SNP_A-2088320	T	T	295	87	272	120	6.066	0.0138	rs2011603	4	17701753	p15.32
SNP_A-1914098	A	A	294	106	269	133	4.155	4.15E-02	rs1553460	4	17872130	p15.32
SNP_A-2297500	G	G	227	151	267	129	4.551	3.29E-02	rs6449368	4	17938425	p15.32
SNP_A-1914965	A	G	234	182	213	207	4.067	4.37E-02	rs2110499	4	18057581	p15.32
SNP_A-2058604	T	G	211	199	235	181	5.239	2.21E-02	rs1395099	4	18058481	p15.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181072	G	G	294	70	255	91	5.057	2.45E-02	rs10009099	4	18349257	p15.32
SNP_A-1879096	C	C	325	41	314	62	4.337	0.0373	rs7664024	4	18620925	p15.31
SNP_A-2087162	G	G	224	188	252	156	4.604	3.19E-02	rs1478052	4	18850729	p15.31
SNP_A-2178804	A	A	320	76	283	103	6.216	1.27E-02	rs12374356	4	18850799	p15.31
SNP_A-1839464	T	T	322	72	295	97	4.875	2.73E-02	rs17496372	4	18863180	p15.31
SNP_A-1824903	G	G	339	77	311	101	4.423	3.55E-02	rs312355	4	18938081	p15.31
SNP_A-2111727	A	A	325	65	296	86	4.192	4.06E-02	rs312354	4	18938382	p15.31
SNP_A-2202329	A	A	320	70	300	96	4.672	3.07E-02	rs312393	4	18953901	p15.31
SNP_A-1976321	A	A	255	119	221	155	7.153	7.50E-03	rs724515	4	18995266	p15.31
SNP_A-1921993	A	A	215	93	193	127	6.214	1.27E-02	rs1490878	4	19027083	p15.31
SNP_A-1976323	A	G	211	179	211	185	4.287	3.84E-02	rs4697634	4	19079466	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213678	G	G	373	37	382	22	3.877	4.90E-02	rs12508229	4	19870147	p15.31
SNP_A-1976335	G	G	358	22	385	11	4.32	3.77E-02	rs10516352	4	19879488	p15.31
SNP_A-1887969	T	T	297	31	291	55	6.283	1.22E-02	rs4280728	4	20014656	p15.31
SNP_A-2082414	G	G	368	46	342	74	7.481	6.20E-03	rs7687359	4	20019114	p15.31
SNP_A-1821296	G	G	295	31	271	49	5.012	0.0252	rs16869591	4	20113287	p15.31
SNP_A-2098238	T	T	372	22	398	6	9.897	1.70E-03	rs17611297	4	20146488	p15.31
SNP_A-1693268	A	A	342	28	358	14	5.027	2.50E-02	rs10516369	4	20641380	p15.31
SNP_A-2009634	G	G	378	0	352	4	4.27	3.88E-02	rs6826348	4	20736490	p15.31
SNP_A-2093410	A	A	358	48	342	70	4.424	3.54E-02	rs7695878	4	20754489	p15.31
SNP_A-2182437	G	A	214	192	213	175	4.593	3.21E-02	rs11942384	4	21191351	p15.31
SNP_A-2164972	C	C	357	43	382	28	3.892	4.85E-02	rs376617	4	21248871	p15.31
SNP_A-2009639	T	C	204	188	210	166	4.788	0.0287	rs6448099	4	21556734	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2314028	G	G	346	34	335	53	4.244	3.94E-02	rs10938885	4	21969487	p15.31
SNP_A-2075300	G	G	262	52	289	25	10.791	0.001	rs10938887	4	22006250	p15.31
SNP_A-2259133	G	G	403	9	408	2	4.481	3.43E-02	rs7687254	4	22200522	p15.31
SNP_A-1976444	C	C	239	173	272	146	4.373	3.65E-02	rs7661870	4	22983581	p15.2
SNP_A-2177173	T	T	316	36	276	50	3.991	0.0458	rs11943464	4	23026368	p15.2
SNP_A-1727795	C	C	371	29	360	46	3.974	4.62E-02	rs10517014	4	23286022	p15.2
SNP_A-2035633	C	C	367	33	383	19	4.106	4.27E-02	rs7694084	4	23391451	p15.2
SNP_A-1976455	T	T	249	139	218	164	4.074	4.35E-02	rs1352802	4	23412617	p15.2
SNP_A-2153678	G	G	323	37	329	15	9.004	2.70E-03	rs4697426	4	23541078	p15.2
SNP_A-1942466	C	C	302	64	320	44	4.219	4.00E-02	rs2946386	4	23569848	p15.2
SNP_A-1924900	G	G	378	34	394	18	5.255	2.19E-02	rs597082	4	23672906	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2281529	C	C	297	71	330	52	4.412	3.57E-02	rs624456	4	23686056	p15.2
SNP_A-2270979	A	A	220	130	255	105	5.099	2.39E-02	rs6448238	4	23691437	p15.2
SNP_A-2116007	T	T	330	30	361	15	6.046	1.39E-02	rs582581	4	23700759	p15.2
SNP_A-1976474	A	A	358	54	376	36	4.041	4.44E-02	rs2052107	4	23744065	p15.2
SNP_A-2226815	C	C	377	39	396	22	5.2	2.26E-02	rs3815419	4	23746821	p15.2
SNP_A-2229258	C	C	308	92	270	120	6.071	0.0137	rs17188642	4	23781878	p15.2
SNP_A-1956389	C	C	293	115	326	88	5.307	0.0212	rs1705089	4	23818881	p15.2
SNP_A-1687490	C	C	363	37	390	22	4.605	3.19E-02	rs2215488	4	23822946	p15.2
SNP_A-1941183	C	C	227	137	197	185	8.849	2.90E-03	rs6448254	4	23932111	p15.2
SNP_A-1976489	T	T	237	163	201	195	5.799	0.016	rs17648006	4	23938260	p15.2
SNP_A-1976490	C	C	248	164	222	196	4.24	0.0395	rs17581643	4	23938358	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1919670	C	C	218	166	258	142	4.907	2.67E-02	rs4697446	4	23945891	p15.2
SNP_A-2199431	A	A	322	4	338	0	4.172	4.11E-02	---	4	24400383	p15.2
SNP_A-1956886	C	C	353	51	380	32	5.266	2.17E-02	rs17594619	4	24573418	p15.2
SNP_A-1802050	T	T	353	51	373	31	5.429	1.98E-02	rs17594723	4	24577251	p15.2
SNP_A-2307600	G	G	359	55	384	34	5.777	1.62E-02	---	4	24600433	p15.2
SNP_A-1976514	T	T	342	44	375	25	6.503	1.08E-02	rs10517059	4	24601851	p15.2
SNP_A-1866703	T	T	407	9	418	2	4.582	3.23E-02	---	4	24756357	p15.2
SNP_A-1841377	C	C	285	123	255	151	4.523	3.34E-02	rs4697544	4	24764126	p15.2
SNP_A-2307081	G	G	322	48	276	66	5.288	2.15E-02	rs17408391	4	24777853	p15.2
SNP_A-1976520	T	T	305	37	324	22	4.364	3.67E-02	rs964228	4	24889077	p15.2
SNP_A-1976521	T	T	349	57	335	85	5.572	0.0183	rs10517063	4	24891357	p15.2
SNP_A-2300058	C	C	355	53	376	34	4.748	0.0293	rs313579	4	24898043	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284389	A	A	331	73	304	110	8.508	3.50E-03	rs1973603	4	24981932	p15.2
SNP_A-2218844	C	C	324	60	286	86	6.809	9.10E-03	rs16876992	4	24986897	p15.2
SNP_A-1859154	C	C	311	49	359	31	6.299	0.0121	rs316777	4	25033527	p15.2
SNP_A-2063842	A	A	348	56	368	36	4.906	2.68E-02	rs13149511	4	25034378	p15.2
SNP_A-1754262	G	G	329	71	305	105	7.354	6.70E-03	rs316800	4	25067769	p15.2
SNP_A-2177771	G	G	317	19	341	7	6.205	1.27E-02	rs7667147	4	25508658	p15.2
SNP_A-2199102	T	T	342	68	318	90	3.931	4.74E-02	rs16877748	4	25609956	p15.2
SNP_A-2183254	A	A	346	50	369	31	5.177	0.0229	rs4692168	4	25611009	p15.2
SNP_A-2087702	A	A	375	33	343	51	5.04	2.48E-02	rs4420968	4	25668449	p15.2
SNP_A-2162764	C	C	284	56	270	90	7.706	5.50E-03	rs4692348	4	25748936	p15.2
SNP_A-2151311	C	C	309	41	293	65	5.77	1.63E-02	rs1386903	4	26938144	p15.2
SNP_A-2309738	C	C	229	159	275	135	5.555	0.0184	rs210773	4	27104722	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1836253	G	G	270	146	302	118	4.741	2.95E-02	rs169778	4	27126390	p15.2
SNP_A-1740315	C	T	206	170	209	171	7.242	7.10E-03	rs2110176	4	27150964	p15.2
SNP_A-1953834	C	C	280	136	309	111	3.939	4.72E-02	rs7683223	4	27199878	p15.2
SNP_A-1865747	C	C	212	156	238	126	4.672	3.07E-02	rs1456088	4	27255308	p15.2
SNP_A-1726762	C	C	209	183	246	146	7.17	7.40E-03	rs6842495	4	27319876	p15.2
SNP_A-2254394	G	G	374	0	330	4	4.504	3.38E-02	rs297291	4	27348072	p15.2
SNP_A-1795969	C	C	334	82	313	107	3.969	4.63E-02	rs7686001	4	27926200	p15.1
SNP_A-1682336	A	A	278	38	266	60	5.049	0.0246	rs3925061	4	27960911	p15.2
SNP_A-1976610	C	C	252	100	277	75	4.753	0.0292	rs1389177	4	28415915	p15.1
SNP_A-2009670	A	A	283	109	310	74	7.842	5.10E-03	rs4515148	4	28466148	p15.1
SNP_A-1931342	C	C	287	115	314	82	6.696	9.70E-03	rs9991479	4	28471141	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2239816	T	T	281	111	302	74	7.826	5.10E-03	rs7375838	4	28481290	p15.1
SNP_A-1682416	T	T	289	111	321	89	3.976	4.62E-02	rs1038905	4	28490761	p15.1
SNP_A-2102455	G	G	331	71	321	97	3.866	4.93E-02	rs4532298	4	28672851	p15.1
SNP_A-2009673	C	C	257	83	290	58	6.331	1.19E-02	rs6845700	4	28701069	p15.1
SNP_A-1843825	C	C	276	120	316	86	8.27	4.00E-03	rs17655022	4	28706430	p15.1
SNP_A-2147910	A	A	261	131	237	163	4.559	0.0327	rs6832398	4	28706557	p15.1
SNP_A-2108942	C	C	388	4	390	0	4	4.55E-02	rs1436074	4	28915580	p15.1
SNP_A-2058289	A	A	340	50	314	72	4.98	2.56E-02	rs6824303	4	28918189	p15.1
SNP_A-1976621	T	T	293	115	265	149	5.74	0.0166	rs6817648	4	29015299	p15.1
SNP_A-1781373	T	T	383	23	360	38	4.321	3.76E-02	rs16881804	4	29100010	p15.1
SNP_A-2265299	G	G	369	35	368	18	5.047	0.0247	rs6841667	4	29100107	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2228873	G	G	340	40	334	22	4.501	0.0339	rs963247	4	29195057	p15.1
SNP_A-2199259	C	C	195	145	226	122	4.171	4.11E-02	rs1441670	4	29266415	p15.1
SNP_A-2140090	A	A	270	72	284	44	6.823	9.00E-03	rs1441683	4	29320304	p15.1
SNP_A-2282231	G	G	317	45	330	24	6.564	0.0104	rs16882193	4	29402634	p15.1
SNP_A-1926729	T	T	355	13	358	4	4.728	2.97E-02	rs7670151	4	29439616	p15.1
SNP_A-1915182	C	C	346	18	343	7	4.58	3.23E-02	rs4362781	4	29735264	p15.1
SNP_A-1826976	T	T	324	34	331	17	5.601	1.80E-02	rs2613179	4	29874013	p15.1
SNP_A-1976645	C	C	359	37	370	18	6.649	9.90E-03	rs2053146	4	29886623	p15.1
SNP_A-2310906	G	G	366	50	386	30	5.532	1.87E-02	rs1369658	4	30008513	p15.1
SNP_A-2088961	C	C	369	11	357	3	4.232	3.97E-02	rs6858756	4	30102081	p15.1
SNP_A-1976647	T	T	340	34	345	17	5.509	0.0189	rs2203140	4	30112757	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2144658	C	C	381	31	397	15	5.894	0.0152	rs6448713	4	30321812	p15.1
SNP_A-2166413	A	A	340	14	343	5	4.225	3.98E-02	rs721760	4	30355036	p15.1
SNP_A-1790246	C	C	315	39	283	17	5.937	1.48E-02	rs4692481	4	30367411	p15.1
SNP_A-1950353	C	C	392	22	415	5	11.317	8.00E-04	rs1447372	4	30511231	p15.1
SNP_A-2293152	G	G	412	4	418	0	4.039	4.45E-02	rs16867994	4	30807118	p15.1
SNP_A-1976673	G	G	289	83	268	116	6.075	0.0137	rs1456754	4	31278962	p15.1
SNP_A-1929064	T	T	266	96	222	126	7.748	5.40E-03	rs1510809	4	31340348	p15.1
SNP_A-2148337	A	A	322	24	328	12	4.003	4.54E-02	rs17080898	4	31985010	p15.1
SNP_A-1911456	T	T	225	173	254	142	4.802	2.84E-02	rs9312611	4	32049599	p15.1
SNP_A-2142706	G	G	331	37	368	22	5.138	2.34E-02	rs10031547	4	32121675	p15.1
SNP_A-2247017	T	T	372	30	393	11	9.376	2.20E-03	rs13124843	4	32124538	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826217	T	T	367	35	387	19	5.252	2.19E-02	rs1454303	4	32124873	p15.1
SNP_A-1789349	G	G	373	29	392	12	7.516	6.10E-03	rs10049615	4	32125285	p15.1
SNP_A-2248847	C	C	370	28	393	13	6.102	0.0135	rs10049661	4	32125522	p15.1
SNP_A-1798686	G	G	205	195	220	156	4.124	4.23E-02	rs6826171	4	32170857	p15.1
SNP_A-2123321	C	C	191	175	226	142	6.368	1.16E-02	rs1037498	4	32207457	p15.1
SNP_A-2056705	C	C	234	182	266	154	4.362	3.67E-02	rs9997593	4	32230770	p15.1
SNP_A-1657770	A	A	262	124	295	101	4.179	4.09E-02	rs10517249	4	32238771	p15.1
SNP_A-2038694	A	A	254	118	260	80	5.937	1.48E-02	rs11723172	4	32293350	p15.1
SNP_A-2229069	C	C	262	82	288	58	5.338	2.09E-02	rs9312619	4	32307799	p15.1
SNP_A-2063638	C	C	352	56	331	77	3.961	4.66E-02	rs10003290	4	32428277	p15.1
SNP_A-1976753	G	G	332	38	344	18	7.269	7.00E-03	rs16990305	4	34578158	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1846788	C	C	264	64	285	45	4.109	4.27E-02	rs6531402	4	35820665	p14
SNP_A-1920198	C	C	380	4	380	0	3.979	4.61E-02	rs11096808	4	36194198	p14
SNP_A-1976781	T	T	313	99	277	137	8.31	3.90E-03	rs4131540	4	36283505	p14
SNP_A-1877809	A	A	286	78	249	113	8.967	2.70E-03	rs6531448	4	36319589	p14
SNP_A-2070137	A	A	368	40	381	23	4.793	0.0286	rs16992534	4	36468884	p14
SNP_A-1793857	G	G	253	65	297	51	3.866	4.93E-02	rs7681348	4	36493312	p14
SNP_A-1815156	A	A	332	82	361	57	5.691	1.71E-02	rs1444313	4	36788798	p14
SNP_A-1710634	G	G	313	65	352	44	5.918	1.50E-02	rs1373475	4	36828604	p14
SNP_A-2070600	A	A	325	89	346	54	8.986	2.70E-03	rs986647	4	36833198	p14
SNP_A-1912867	T	T	329	87	355	65	4.153	4.15E-02	rs6815622	4	36856970	p14
SNP_A-1908189	T	T	302	54	327	37	4.081	4.34E-02	rs7657063	4	36863109	p14
SNP_A-1976814	A	A	376	8	367	19	4.585	3.22E-02	rs16993308	4	37018623	p14
SNP_A-1737569	T	G	213	177	215	193	4.265	3.89E-02	rs724522	4	37053005	p14
SNP_A-1723392	T	C	216	180	213	191	4.227	3.98E-02	rs10484215	4	37053633	p14
SNP_A-1650470	C	T	212	176	209	187	4.314	0.0378	rs10484216	4	37053728	p14
SNP_A-1854449	T	T	404	4	379	15	6.924	8.50E-03	rs4585313	4	37062802	p14
SNP_A-1686840	T	T	380	12	373	25	4.587	3.22E-02	rs7678296	4	37079826	p14
SNP_A-1831943	A	A	352	64	315	103	11.156	8.00E-04	rs3910363	4	37087397	p14
SNP_A-1713906	C	C	381	17	373	39	8.488	3.60E-03	rs1435385	4	37125686	p14
SNP_A-2259655	G	G	330	52	291	93	14.037	2.00E-04	rs17575883	4	37151586	p14
SNP_A-1928004	C	C	351	65	317	103	10.307	1.30E-03	rs17575897	4	37153363	p14
SNP_A-1729830	C	C	377	23	401	9	6.743	9.40E-03	rs10517405	4	37156883	p14
SNP_A-1901959	G	G	237	113	259	79	6.789	9.20E-03	rs11729824	4	37157321	p14
SNP_A-1666894	A	A	326	58	312	94	8.227	4.10E-03	rs1369410	4	37157586	p14
SNP_A-1655151	G	G	292	104	328	82	4.451	0.0349	rs1369409	4	37157623	p14
SNP_A-1842949	G	G	293	123	321	95	4.873	2.73E-02	rs6823583	4	37196612	p14
SNP_A-1731505	T	T	336	62	317	95	7.249	7.10E-03	rs10517407	4	37198510	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2228764	T	T	205	133	237	111	4.155	4.15E-02	rs7659133	4	37374513	p14
SNP_A-2298558	A	A	365	21	338	36	4.796	2.85E-02	rs12640317	4	37432265	p14
SNP_A-2027996	G	G	401	5	400	14	4.187	0.0407	rs17577515	4	37456325	p14
SNP_A-2190439	A	A	383	33	368	52	4.528	3.34E-02	rs17424192	4	37584706	p14
SNP_A-2177094	A	A	254	140	228	176	5.379	2.04E-02	rs4832743	4	37747782	p14
SNP_A-1976844	T	T	191	157	192	106	6.059	0.0138	rs10517456	4	37777298	p14
SNP_A-2063089	T	T	385	25	367	41	4.305	3.80E-02	rs6841833	4	37827532	p14
SNP_A-2251687	C	C	338	40	368	22	6.315	0.012	rs16994165	4	37884829	p14
SNP_A-2267901	C	C	270	62	282	42	4.01	4.52E-02	rs933823	4	37926116	p14
SNP_A-2274776	G	G	374	0	332	8	8.9	2.90E-03	rs17579911	4	37956594	p14
SNP_A-2310284	G	A	186	142	166	154	4.784	0.0287	rs4832749	4	37992226	p14
SNP_A-2041579	C	C	330	82	302	114	6.446	0.0111	rs907311	4	37992623	p14
SNP_A-1906290	G	G	258	86	246	112	4.333	3.74E-02	rs2137036	4	37994362	p14
SNP_A-2204360	C	C	253	111	287	91	3.858	4.95E-02	—	4	38017835	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102422	G	G	355	9	348	2	4.251	3.92E-02	rs16994357	4	38067190	p14
SNP_A-2009714	A	A	167	137	210	114	6.382	0.0115	rs4259067	4	38078308	p14
SNP_A-1843407	C	C	341	29	360	16	4.223	3.99E-02	rs4995512	4	38111253	p14
SNP_A-2175922	A	A	240	172	210	208	5.367	2.05E-02	rs6819003	4	38181883	p14
SNP_A-2192229	A	G	217	163	201	197	4.519	3.35E-02	rs11943642	4	38394832	p14
SNP_A-1651572	T	T	334	60	362	40	5.047	0.0247	rs2163276	4	38909810	p14
SNP_A-2120398	A	A	395	21	410	8	6.102	0.0135	rs10019211	4	39367852	p14
SNP_A-1782665	C	C	308	92	282	128	6.914	0.0086	rs7692279	4	39368017	p14
SNP_A-1813109	A	A	339	29	330	12	6.226	0.0126	rs17510706	4	39379895	p14
SNP_A-1834967	T	T	358	18	369	7	5.006	0.0253	rs16995404	4	39393161	p14
SNP_A-2113469	G	G	360	36	377	19	5.647	1.75E-02	rs4616763	4	40070177	p14
SNP_A-2099947	G	G	330	74	358	50	5.765	1.63E-02	—	4	40080771	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2180245	G	G	258	158	229	191	4.828	2.80E-02	rs9685160	4	40090346	p14
SNP_A-2294271	T	T	263	147	237	177	4.11	4.26E-02	rs6818783	4	40164331	p14
SNP_A-2271376	T	C	184	176	199	153	4.173	4.11E-02	rs4861306	4	40185946	p14
SNP_A-1821029	C	C	377	37	391	17	7.619	5.80E-03	rs17512637	4	40261732	p14
SNP_A-2151446	A	A	267	85	242	108	3.963	0.0465	rs278985	4	40335520	p14
SNP_A-1797849	T	T	279	81	230	106	7.24	7.10E-03	rs16852274	4	40343869	p14
SNP_A-2009732	C	C	354	32	375	15	6.733	9.50E-03	rs4262020	4	40768194	p14
SNP_A-2009734	T	C	196	182	213	167	4.744	2.94E-02	rs4861072	4	40779953	p14
SNP_A-1882987	A	A	350	34	361	19	4.395	0.0361	rs11929986	4	40871236	p14
SNP_A-1889780	G	G	274	78	222	90	3.913	4.79E-02	rs1876493	4	40885866	p14
SNP_A-2044093	A	A	266	80	319	57	7.429	6.40E-03	rs10026868	4	40963726	p14
SNP_A-1921981	G	G	207	145	244	106	9.09	2.60E-03	---	4	40990244	p14
SNP_A-2135856	T	T	195	123	241	107	4.624	0.0315	rs11735595	4	41023993	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1806877	C	C	338	54	338	32	4.997	2.54E-02	rs7681634	4	41405968	p13
SNP_A-2229189	T	T	393	11	387	23	4.237	0.0395	rs16853711	4	41718153	p13
SNP_A-2051822	G	G	349	65	326	92	5.408	0.02	rs936899	4	42227529	p13
SNP_A-1976932	C	C	340	76	310	106	6.33	1.19E-02	rs10517025	4	42294181	p13
SNP_A-2306970	A	A	336	64	310	94	6.723	9.50E-03	rs3935029	4	42325324	p13
SNP_A-1802016	G	G	331	61	288	82	5.44	1.97E-02	rs10034610	4	42345755	p13
SNP_A-2069774	G	G	261	123	203	175	16.278	5.47E-05	rs12502828	4	42415301	p13
SNP_A-1869634	A	A	259	129	284	102	4.302	3.81E-02	rs17447926	4	42450392	p13
SNP_A-2238646	T	T	271	141	299	109	5.452	0.0195	rs11942664	4	42450540	p13
SNP_A-2282712	A	A	272	144	302	116	4.579	3.24E-02	rs11943841	4	42450892	p13
SNP_A-2125948	A	A	363	37	355	57	4.168	4.12E-02	rs10938217	4	42618070	p13
SNP_A-2164980	C	C	416	0	414	6	5.986	0.0144	rs767754	4	42625236	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1976954	C	C	288	82	279	115	4.922	2.65E-02	rs1450906	4	42747028	p13
SNP_A-1850981	A	A	335	59	304	86	6.511	1.07E-02	rs17534403	4	42747670	p13
SNP_A-2073060	A	A	314	56	287	83	6.458	1.10E-02	rs17450034	4	42753502	p13
SNP_A-1976956	T	T	323	69	307	95	4.403	3.59E-02	rs17534598	4	42766950	p13
SNP_A-2133212	C	C	305	93	336	70	4.665	3.08E-02	rs1597565	4	42780965	p13
SNP_A-1807421	A	A	390	22	376	40	5.462	1.94E-02	rs1376317	4	42787110	p13
SNP_A-1952728	C	C	295	83	270	108	4.378	3.64E-02	---	4	42788236	p13
SNP_A-1976960	G	G	285	129	322	92	8.45	3.70E-03	rs10517069	4	42881991	p13
SNP_A-1682126	G	G	184	180	220	160	4.042	4.44E-02	rs1436469	4	42966150	p13
SNP_A-2238313	G	G	314	102	347	73	6.434	0.0112	rs1442860	4	43118053	p13
SNP_A-2085255	C	C	307	89	334	54	9.623	0.0019	rs16855779	4	43149993	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803948	T	T	315	101	349	71	6.955	8.40E-03	rs7687831	4	43154042	p13
SNP_A-2286428	G	G	308	84	339	51	9.547	0.002	rs10938270	4	43167128	p13
SNP_A-1976969	A	A	400	4	404	0	4.02	4.50E-02	rs10517076	4	43208860	p13
SNP_A-1855733	C	C	256	120	273	91	4.339	0.0373	rs7697210	4	43767951	p13
SNP_A-2047468	G	G	221	115	239	89	3.922	4.77E-02	rs6858778	4	43891029	p13
SNP_A-2240631	C	C	328	60	353	41	4.446	3.50E-02	rs7693710	4	43932639	p13
SNP_A-2234582	C	C	293	69	322	50	4.266	3.89E-02	rs7678483	4	43940315	p13
SNP_A-2247981	C	C	262	136	285	107	4.383	3.63E-02	rs6825835	4	44377885	p13
SNP_A-2025987	G	G	205	173	207	129	3.963	0.0465	rs9991261	4	44405958	p13
SNP_A-1976999	A	C	170	158	191	145	5.009	0.0252	rs12500057	4	44713108	p13
SNP_A-1785088	A	A	179	157	207	111	9.438	2.10E-03	rs10000940	4	44835715	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2095841	G	G	310	56	341	33	7.334	6.80E-03	rs1858410	4	45032784	p13
SNP_A-1649946	T	T	384	16	378	34	6.351	0.0117	rs10517126	4	45181982	p13
SNP_A-1824102	G	G	262	88	274	58	5.962	0.0146	rs1492842	4	45689719	p13
SNP_A-1956425	G	G	296	110	332	84	5.427	1.98E-02	rs1353014	4	45692012	p13
SNP_A-2188282	C	C	302	114	334	84	6.151	1.31E-02	rs1353015	4	45692212	p13
SNP_A-1977014	C	C	333	53	364	36	4.378	3.64E-02	rs1394346	4	45765762	p13
SNP_A-1977015	G	G	327	47	352	30	4.59	3.22E-02	rs9291279	4	45771993	p13
SNP_A-1919708	T	T	401	13	411	3	6.373	1.16E-02	rs11936504	4	46004413	p12
SNP_A-1909676	C	C	295	63	277	91	5.521	1.88E-02	rs478179	4	46079665	p12
SNP_A-1948999	A	A	271	123	251	161	5.452	1.96E-02	rs6856130	4	46234088	p12
SNP_A-2267713	T	T	219	137	181	163	5.659	1.74E-02	rs6847731	4	46243080	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2034489	A	A	348	38	350	22	4.015	4.51E-02	rs6847738	4	46695682	p12
SNP_A-2026799	G	G	268	146	240	178	4.685	0.0304	rs6852985	4	46951311	p12
SNP_A-1977046	T	T	220	134	202	170	4.587	3.22E-02	rs4694846	4	47209726	p12
SNP_A-2087996	G	G	239	95	214	124	5.196	2.26E-02	rs13102764	4	47271855	p12
SNP_A-1824974	C	C	256	122	221	153	6.042	0.014	rs4356892	4	47304773	p12
SNP_A-2186974	G	G	218	134	269	111	6.438	0.0112	rs12503999	4	47364667	p12
SNP_A-2009776	A	A	238	130	277	103	5.891	0.0152	rs4296657	4	47382777	p12
SNP_A-2123719	T	T	249	143	289	113	6.365	1.16E-02	rs12651326	4	47383199	p12
SNP_A-2204415	G	G	298	116	326	92	4.007	0.0453	rs6825063	4	47421041	p12
SNP_A-2313257	A	A	383	27	367	43	3.998	4.55E-02	rs4695274	4	47560452	p12
SNP_A-1883233	C	C	350	56	373	37	4.594	3.21E-02	rs10938519	4	47879512	p12
SNP_A-1958424	C	C	359	45	388	28	4.91	2.67E-02	rs10938521	4	47954147	p12
SNP_A-1977059	G	G	342	0	320	4	4.248	3.93E-02	rs16861029	4	47979302	p12
SNP_A-1724044	C	C	265	135	304	104	6.615	0.0101	rs3792623	4	48029569	p12
SNP_A-1977063	C	C	379	11	355	25	6.1	0.0135	rs16861113	4	48036929	p12
SNP_A-1669019	T	T	197	195	240	172	5.178	0.0229	rs10517231	4	48833937	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2080774	G	G	337	61	306	80	3.872	4.91E-02	rs2128191	4	52980563	q11
SNP_A-2210398	A	A	327	61	298	82	4.347	3.71E-02	rs2128188	4	52980785	q11
SNP_A-2251282	A	A	327	35	312	56	5.149	2.33E-02	rs7670041	4	52992103	q11
SNP_A-2221098	T	T	312	28	290	46	5.159	2.31E-02	rs17578260	4	53005449	q11
SNP_A-1826664	G	G	325	53	304	78	5.451	1.96E-02	rs349383	4	53024938	q11
SNP_A-2279512	C	C	347	63	309	89	6.472	1.10E-02	rs4865206	4	53047922	q11
SNP_A-1899325	G	G	346	58	317	81	5.03	2.49E-02	rs6853024	4	53066248	q11
SNP_A-1748897	G	G	335	63	317	93	6.089	1.36E-02	rs1023941	4	53073307	q11
SNP_A-1889617	-	C	184	184	226	168	4.147	4.17E-02	rs11732165	4	53165950	q11
SNP_A-1733316	A	A	324	68	352	48	4.528	3.34E-02	rs10517269	4	53624719	q12
SNP_A-2060342	G	G	254	112	273	85	4.298	3.82E-02	rs6554072	4	53920475	q12
SNP_A-2207307	A	A	347	13	332	26	4.659	0.0309	rs1481822	4	53994742	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2109471	A	A	395	7	386	22	7.818	5.20E-03	rs1481816	4	54059600	q12
SNP_A-1977108	T	T	347	11	286	20	4.446	3.50E-02	rs10014172	4	54092646	q12
SNP_A-1977109	T	T	401	9	385	21	5.106	2.38E-02	---	4	54097378	q12
SNP_A-1977110	A	A	404	12	390	26	5.405	0.0201	---	4	54097568	q12
SNP_A-1829310	T	T	400	12	389	25	4.716	2.99E-02	rs17839071	4	54137309	q12
SNP_A-2121350	G	G	258	86	308	70	4.467	3.46E-02	rs1040084	4	54251152	q12
SNP_A-1751365	G	G	313	87	347	63	5.469	1.94E-02	rs1369353	4	54312503	q12
SNP_A-2139586	C	C	295	107	318	74	6.755	9.40E-03	rs1022187	4	54358503	q12
SNP_A-1828147	T	T	287	115	315	91	4.079	4.34E-02	rs2590810	4	54389254	q12
SNP_A-2048856	A	G	214	192	222	186	4.129	4.22E-02	rs2590791	4	54411205	q12
SNP_A-1787055	C	C	320	82	355	57	6.189	0.0129	rs1382084	4	54439715	q12
SNP_A-1943502	G	G	342	4	344	0	4	4.55E-02	---	4	54478598	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2145578	G	G	366	12	377	25	3.996	4.56E-02	rs17084040	4	54915296	q12
SNP_A-2200815	C	C	230	128	240	90	5.707	1.69E-02	rs4864878	4	55014643	q12
SNP_A-1889771	A	A	325	37	306	56	4.454	3.48E-02	rs2537879	4	55313623	q12
SNP_A-1878086	A	A	373	39	354	60	4.946	2.61E-02	rs2703480	4	55316337	q12
SNP_A-1977152	G	G	411	5	403	15	5.074	2.43E-02	rs17710298	4	55807545	q12
SNP_A-1895118	C	C	329	27	355	15	4.148	4.17E-02	rs7437260	4	55875279	q12
SNP_A-1791126	C	C	371	25	397	11	6.147	0.0132	rs1458833	4	55888264	q12
SNP_A-1977153	G	G	320	36	313	17	5.912	1.50E-02	rs1531293	4	55892910	q12
SNP_A-1887723	A	A	368	22	389	11	4.123	4.23E-02	rs4336284	4	56010978	q12
SNP_A-2209421	A	A	258	124	286	98	4.481	3.43E-02	rs476184	4	56087792	q12
SNP_A-2172232	G	G	275	97	291	69	4.98	2.56E-02	—	4	56129671	q12
SNP_A-1977161	C	C	249	109	222	138	4.947	2.61E-02	rs4580704	4	56167635	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1943277	A	A	251	117	221	143	4.485	3.42E-02	rs9312662	4	56227299	q12
SNP_A-2100732	T	T	270	138	233	159	3.888	4.86E-02	rs6829182	4	56295084	q12
SNP_A-1718923	G	G	242	116	224	146	3.934	4.73E-02	rs2177127	4	56295501	q12
SNP_A-1945443	T	T	317	75	341	55	3.932	4.74E-02	rs17781708	4	56321997	q12
SNP_A-1946178	G	G	340	8	322	26	10.019	0.0015	rs6554306	4	56414115	q12
SNP_A-2009817	C	C	352	28	336	46	4.745	2.94E-02	rs4864562	4	56429777	q12
SNP_A-1671646	T	A	218	178	218	192	5.448	1.96E-02	rs10517356	4	56433835	q12
SNP_A-1726312	A	A	249	151	222	188	5.463	1.94E-02	rs1488939	4	56434686	q12
SNP_A-2009819	A	A	325	51	327	77	4.288	3.84E-02	rs2726736	4	56504982	q12
SNP_A-1862953	A	A	319	89	285	121	6.785	9.20E-03	rs11937308	4	56556744	q12
SNP_A-1670564	G	G	292	96	266	134	7.309	6.90E-03	rs722709	4	56611380	q12
SNP_A-2045210	C	C	333	5	280	12	4.128	4.22E-02	---	4	56836530	q12
SNP_A-1663412	T	T	392	0	402	4	3.882	4.88E-02	rs10517368	4	56863122	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1941164	A	A	394	12	405	3	5.547	1.85E-02	rs17086350	4	56870763	q12
SNP_A-2120346	T	T	282	114	253	139	4.022	4.49E-02	rs7683781	4	57027614	q12
SNP_A-1977184	C	C	283	117	239	153	8.429	3.70E-03	rs4865087	4	57035857	q12
SNP_A-2245954	C	C	258	158	220	200	7.929	4.90E-03	rs7671868	4	57097129	q12
SNP_A-2153361	G	G	229	171	257	143	4.11	4.26E-02	rs1042040	4	57101226	q12
SNP_A-2134716	A	A	288	124	248	160	7.529	6.10E-03	rs9684298	4	57119095	q12
SNP_A-1905110	T	T	256	126	225	161	6.246	1.25E-02	rs9683679	4	57119243	q12
SNP_A-2196691	A	A	346	52	365	33	4.755	0.0292	rs11133443	4	57177237	q12
SNP_A-2206950	A	A	301	75	320	52	4.725	2.97E-02	rs6554358	4	57213504	q12
SNP_A-1866398	C	C	182	176	213	137	7.203	7.30E-03	rs899628	4	57393738	q12
SNP_A-1935827	T	T	325	19	363	9	4.582	3.23E-02	rs2219861	4	57428491	q12
SNP_A-1953506	G	G	333	13	288	26	6.057	1.39E-02	rs1708768	4	57531641	q12
SNP_A-1833309	T	T	260	86	280	64	3.962	0.0465	rs2412761	4	57574427	q12
SNP_A-2292416	G	G	314	46	313	25	5.525	1.87E-02	rs1829982	4	58035991	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977208	A	A	320	0	312	6	6.095	1.36E-02	—	4	58139085	q12
SNP_A-2277718	A	A	373	9	360	22	5.682	1.71E-02	rs10020991	4	58173685	q12
SNP_A-1848992	C	C	373	17	358	30	3.898	4.83E-02	rs6554468	4	58181623	q12
SNP_A-1977210	G	G	324	28	311	49	5.904	1.51E-02	rs2028437	4	58285134	q12
SNP_A-1977217	A	A	364	32	347	51	4.751	0.0293	rs4865258	4	58367671	q12
SNP_A-1977230	A	A	324	66	303	89	4.111	4.26E-02	rs343516	4	58441889	q12
SNP_A-1977233	G	G	315	49	299	73	5.052	0.0246	rs498103	4	58445567	q12
SNP_A-1883815	T	T	328	46	292	62	3.914	4.79E-02	rs343569	4	58482163	q12
SNP_A-1748103	T	T	323	71	309	97	4.155	4.15E-02	rs2048267	4	58517950	q12
SNP_A-1743107	T	T	327	63	318	88	3.945	0.047	rs1509528	4	58571443	q12
SNP_A-1720039	C	C	320	52	304	74	4.204	4.03E-02	rs10517413	4	58573590	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977253	C	C	308	94	279	119	4.347	3.71E-02	rs10517433	4	58800840	q12
SNP_A-1661598	A	A	382	4	402	0	4.187	0.0407	rs1986511	4	59283175	q12
SNP_A-1741995	C	C	299	101	271	129	4.784	0.0287	rs282705	4	59418229	q12
SNP_A-2211205	T	T	224	114	257	91	4.7	3.02E-02	rs2122149	4	59432883	q12
SNP_A-2034355	G	G	295	117	314	86	5.151	2.32E-02	rs2166993	4	59432969	q12
SNP_A-2139940	A	A	325	83	282	114	7.747	5.40E-03	rs7699155	4	59465615	q12
SNP_A-1860800	G	G	203	199	225	161	4.819	0.0281	rs6832361	4	59466351	q12
SNP_A-1977268	C	C	199	181	226	150	4.598	3.20E-02	rs2166997	4	59473811	q12
SNP_A-1939958	G	G	289	121	325	87	7.664	5.60E-03	rs4865372	4	59476896	q12
SNP_A-2184589	A	A	318	96	269	147	14.789	0.0001	rs962145	4	59496230	q12
SNP_A-1698825	A	A	277	123	315	95	5.913	1.50E-02	rs6843409	4	59515064	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1865925	T	T	278	60	310	36	7.649	5.70E-03	rs6819651	4	59543985	q12
SNP_A-1932741	C	C	331	73	343	51	3.992	4.57E-02	rs6551609	4	59648311	q12
SNP_A-1785197	A	A	254	86	200	104	6.135	1.33E-02	rs6849738	4	59718664	q13.1
SNP_A-2133942	G	G	326	34	297	51	4.548	3.30E-02	rs2036098	4	59745440	q13.1
SNP_A-1799680	G	G	236	108	250	78	4.864	2.74E-02	rs7674419	4	59986594	q13.1
SNP_A-2252801	C	C	273	139	297	111	4.127	4.22E-02	rs1013028	4	60013403	q13.1
SNP_A-1944870	G	G	254	118	271	89	4.418	0.0356	rs1013029	4	60013519	q13.1
SNP_A-2160294	C	T	197	181	205	167	3.917	4.78E-02	rs974866	4	60262433	q13.1
SNP_A-1821871	A	A	376	0	331	5	5.635	1.76E-02	rs17089728	4	60359603	q13.1
SNP_A-2093117	A	A	321	57	282	74	4.073	0.0436	rs1032030	4	60367315	q13.1
SNP_A-1833060	A	A	268	84	236	104	3.953	4.68E-02	rs11736631	4	60385035	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2065547	C	C	312	72	332	46	6.303	0.0121	rs11931527	4	60389985	q13.1
SNP_A-2052514	G	G	383	13	368	26	4.628	0.0315	rs2200126	4	60394279	q13.1
SNP_A-2255764	T	T	385	13	382	26	4.222	3.99E-02	rs17827839	4	60401385	q13.1
SNP_A-2040741	T	T	246	126	214	150	4.227	3.98E-02	rs6843734	4	61325830	q13.1
SNP_A-2255413	C	C	357	17	343	37	7.64	5.70E-03	rs1898849	4	61362758	q13.1
SNP_A-1894089	C	C	366	34	345	53	4.765	2.90E-02	rs7670158	4	61373028	q13.1
SNP_A-2253665	A	A	355	37	342	66	8.091	4.40E-03	rs17090278	4	61508700	q13.1
SNP_A-1875576	A	A	362	44	342	68	5.692	1.70E-02	rs17090286	4	61524744	q13.1
SNP_A-2054220	T	T	319	25	300	46	6.789	9.20E-03	rs6856003	4	61596881	q13.1
SNP_A-1977327	C	C	358	16	369	5	5.928	0.0149	rs17238674	4	61603159	q13.1
SNP_A-1669269	T	T	355	45	344	66	4.023	4.49E-02	rs725264	4	61685875	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1879898	C	C	251	129	280	102	4.734	2.96E-02	rs17291801	4	61758512	q13.1
SNP_A-1895982	A	A	244	146	279	107	8.334	3.90E-03	rs1386115	4	61763310	q13.1
SNP_A-2163192	G	G	216	134	242	100	6.325	1.19E-02	rs10017149	4	61777827	q13.1
SNP_A-2143666	T	T	357	19	376	8	4.89	0.027	rs1449624	4	61853403	q13.1
SNP_A-2311821	C	C	390	16	411	7	3.898	4.83E-02	rs1375681	4	61866471	q13.1
SNP_A-1745458	G	G	255	143	292	118	4.72	0.0298	rs2129267	4	61895124	q13.1
SNP_A-2157259	A	A	240	108	216	142	5.747	1.65E-02	rs1394954	4	61915874	q13.1
SNP_A-2212113	C	C	329	73	359	49	5.985	0.0144	—	4	61950277	q13.1
SNP_A-1712487	A	A	246	152	290	118	7.771	0.0053	rs1486506	4	61951234	q13.1
SNP_A-1644932	C	C	249	75	245	107	4.507	3.38E-02	rs1449613	4	62047939	q13.1
SNP_A-1757541	G	G	274	102	269	137	4.027	0.0448	rs4146080	4	62048704	q13.1
SNP_A-1739771	A	A	309	69	336	46	5.709	1.69E-02	rs10517529	4	62133465	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084017	G	G	264	106	282	80	4.141	0.0419	rs17090543	4	62509728	q13.1
SNP_A-2268215	G	G	265	107	283	77	5.287	2.15E-02	rs9942184	4	62521205	q13.1
SNP_A-1827594	G	G	393	23	379	39	4.378	3.64E-02	rs17239198	4	62613687	q13.1
SNP_A-1909373	T	T	385	23	383	9	5.813	1.59E-02	rs995447	4	62647234	q13.1
SNP_A-2277676	G	G	242	114	184	132	6.857	8.80E-03	rs9993397	4	62781005	q13.1
SNP_A-1798865	C	C	262	100	255	63	5.67	1.73E-02	rs11131366	4	63062780	q13.1
SNP_A-1947911	G	G	370	16	349	29	4.286	3.84E-02	rs778938	4	63072182	q13.1
SNP_A-1815759	G	G	377	19	362	34	4.55	3.29E-02	rs778959	4	63083785	q13.1
SNP_A-1843112	G	G	307	67	277	93	5.745	1.65E-02	rs11131405	4	63488244	q13.1
SNP_A-1896345	G	G	334	82	311	107	4.122	4.23E-02	rs11131406	4	63488425	q13.1
SNP_A-2024625	A	A	295	87	306	62	4.136	4.20E-02	rs11940289	4	63753603	q13.1
SNP_A-1977375	G	G	298	74	309	51	4.236	3.96E-02	rs2346595	4	63762424	q13.1
SNP_A-1783257	C	C	223	117	241	91	3.854	4.96E-02	rs7680634	4	63863609	q13.1
SNP_A-2026049	C	C	301	67	313	45	4.419	3.55E-02	rs1599630	4	63974761	q13.1
SNP_A-2133307	C	C	340	34	349	15	7.351	6.70E-03	rs2347409	4	64144141	q13.1
SNP_A-2177176	T	T	355	49	364	30	4.558	3.28E-02	rs1464336	4	64825446	q13.1
SNP_A-1915580	A	A	322	16	294	28	4.16	4.14E-02	rs1425393	4	65220960	q13.1
SNP_A-1883339	C	C	328	80	344	48	8.064	4.50E-03	rs1430504	4	65509956	q13.1
SNP_A-2157087	G	G	342	46	372	26	6.69	9.70E-03	—	4	65548437	q13.1
SNP_A-2066406	G	G	244	112	267	87	4.17	4.11E-02	rs17085463	4	65569153	q13.1
SNP_A-2268543	A	A	226	174	270	132	9.663	0.0019	rs13145935	4	65630697	q13.1
SNP_A-1843768	A	A	266	126	307	87	10.07	0.0015	rs12501731	4	65636214	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829735	C	C	291	125	331	83	11.048	9.00E-04	rs7664968	4	65648272	q13.1
SNP_A-2030715	G	G	224	166	260	124	8.714	3.20E-03	rs10434238	4	65648452	q13.1
SNP_A-2310754	A	A	254	126	281	91	6.923	8.50E-03	rs1440921	4	65659796	q13.1
SNP_A-1977413	T	T	192	164	226	138	4.916	2.66E-02	rs979759	4	65681361	q13.1
SNP_A-1977415	G	G	236	98	269	73	5.718	1.68E-02	rs4143	4	65681895	q13.1
SNP_A-1977417	G	G	287	127	329	89	9.53	0.002	rs6830454	4	65682139	q13.1
SNP_A-1819819	T	T	274	110	322	86	6.083	1.36E-02	rs1036722	4	65683718	q13.1
SNP_A-1655249	G	G	318	78	349	59	3.898	4.84E-02	rs2349110	4	65690876	q13.1
SNP_A-2262299	A	A	267	117	299	85	6.878	8.70E-03	rs7658322	4	65707415	q13.1
SNP_A-2240665	C	C	238	172	272	132	7.486	6.20E-03	rs7687341	4	65707484	q13.1
SNP_A-2048189	G	G	269	121	304	84	8.811	3.00E-03	rs1155608	4	65709041	q13.1
SNP_A-1781631	T	T	223	161	265	123	8.679	3.20E-03	rs12650263	4	65715593	q13.1
SNP_A-1823883	C	C	276	120	317	81	10.397	1.30E-03	rs17085781	4	65722995	q13.1
SNP_A-2151040	A	A	218	146	269	123	6.279	1.22E-02	rs17085784	4	65723061	q13.1
SNP_A-2195351	G	G	286	130	326	92	9.114	2.50E-03	rs1440940	4	65723876	q13.1
SNP_A-2152739	T	T	231	169	266	136	6.03	0.0141	rs2196985	4	65724351	q13.1
SNP_A-1924253	T	T	235	101	271	71	7.741	5.40E-03	rs2196983	4	65724417	q13.1
SNP_A-2126062	T	T	255	153	298	120	7.213	7.20E-03	rs4860651	4	66017061	q13.1
SNP_A-2075025	A	A	354	60	380	36	6.916	8.50E-03	rs4860662	4	66112582	q13.1
SNP_A-2046208	G	G	339	45	372	28	5.166	0.023	rs4860182	4	66120846	q13.1
SNP_A-1685174	T	T	273	79	318	54	7.579	5.90E-03	rs1514269	4	66124656	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939833	A	A	273	103	272	72	4.079	4.34E-02	rs4320185	4	66213001	q13.1
SNP_A-2194032	G	G	373	25	317	41	6.325	1.19E-02	rs12644315	4	66249591	q13.1
SNP_A-2009859	A	-	256	154	208	208	12.978	3.00E-04	rs6834811	4	66281715	q13.1
SNP_A-1847465	C	C	253	109	219	135	5.131	0.0235	rs7667410	4	66315752	q13.1
SNP_A-2147147	T	T	393	23	377	41	5.39	2.03E-02	rs4611975	4	66329014	q13.1
SNP_A-2282851	A	C	245	157	211	199	12.612	4.00E-04	rs4608860	4	66342774	q13.1
SNP_A-2132574	T	T	375	15	362	30	5.224	0.0223	rs7663607	4	66367949	q13.1
SNP_A-1814481	T	T	207	159	241	121	7.716	5.50E-03	rs7688203	4	66397622	q13.1
SNP_A-1910193	G	G	266	118	286	92	3.897	4.84E-02	rs2350070	4	66545238	q13.2
SNP_A-1949169	G	G	220	128	235	93	5.451	1.96E-02	rs1433635	4	66586043	q13.2
SNP_A-1938195	G	G	221	125	248	100	4.326	3.75E-02	rs1433634	4	66586232	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977435	C	C	243	161	264	130	4.048	4.42E-02	rs7669544	4	66586887	q13.2
SNP_A-2060391	G	G	379	15	389	5	5.13	0.0235	rs17086994	4	67012678	q13.2
SNP_A-1977442	A	A	226	108	244	62	11.934	6.00E-04	rs10000219	4	67028790	q13.2
SNP_A-2114876	C	C	376	34	390	18	5.174	0.0229	rs17787026	4	67176948	q13.2
SNP_A-2176511	C	C	400	4	400	0	3.98	4.60E-02	rs6821691	4	67514367	q13.2
SNP_A-2045272	C	C	408	4	418	0	4.078	4.34E-02	rs10032907	4	67514533	q13.2
SNP_A-2088668	T	T	323	5	300	0	4.61	3.18E-02	—	4	67655417	q13.2
SNP_A-2191602	T	T	364	32	382	16	5.763	1.64E-02	rs1364983	4	67756322	q13.2
SNP_A-1714719	G	G	271	79	301	55	5.821	1.58E-02	rs1481253	4	67762634	q13.2
SNP_A-1820387	C	C	382	34	399	17	6.037	0.014	rs11732162	4	67789522	q13.2
SNP_A-2146997	T	T	290	30	315	17	4.409	3.57E-02	rs7690481	4	67799939	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084322	G	G	353	25	365	11	5.64	1.76E-02	rs1541747	4	67814255	q13.2
SNP_A-1977468	A	A	313	41	347	25	5.187	2.28E-02	rs10017714	4	67884789	q13.2
SNP_A-2039712	A	G	208	150	182	180	5.083	2.42E-02	rs9998837	4	68385552	q13.2
SNP_A-1853375	T	C	202	170	198	176	3.913	4.79E-02	rs2630488	4	68424134	q13.2
SNP_A-1723790	C	C	304	86	280	126	8.215	4.20E-03	rs719391	4	68514882	q13.2
SNP_A-1658928	T	T	300	94	279	127	5.51	0.0189	rs1038428	4	68543151	q13.2
SNP_A-1977508	A	A	400	16	404	6	4.522	3.35E-02	rs2017990	4	70043934	q13.2
SNP_A-2201297	T	C	229	175	205	195	5.075	2.43E-02	rs4327554	4	70167168	q13.2
SNP_A-1856825	A	A	293	109	254	146	8.144	0.0043	rs4348160	4	70198291	q13.2
SNP_A-2272872	C	A	198	180	212	168	5.066	2.44E-02	rs9999103	4	70226483	q13.2
SNP_A-2227740	G	G	311	33	290	54	5.803	0.016	rs2088092	4	70479481	q13.2
SNP_A-2208610	G	G	337	41	340	20	6.808	9.10E-03	rs1827559	4	70830609	q13.3
SNP_A-1939134	G	G	240	128	207	153	4.573	3.25E-02	rs812348	4	71015201	q13.3
SNP_A-1752741	C	C	338	16	354	34	5.303	2.13E-02	rs1383436	4	71377387	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1731755	T	T	357	43	345	67	5.265	0.0218	rs10518073	4	71380453	q13.3
SNP_A-1977534	G	G	293	45	308	26	5.435	1.97E-02	rs2029495	4	71504826	q13.3
SNP_A-2279423	C	C	400	8	380	20	5.577	1.82E-02	rs6813178	4	71940274	q13.3
SNP_A-2024667	A	A	398	6	378	16	4.936	0.0263	rs3775730	4	71991607	q13.3
SNP_A-1707151	G	G	375	13	379	29	5.617	0.0178	rs2362330	4	72147697	q13.3
SNP_A-2294811	A	A	379	29	390	14	5.37	2.05E-02	rs10012631	4	72324326	q13.3
SNP_A-1742409	C	C	391	9	390	20	4.051	0.0441	rs10518080	4	72351011	q13.3
SNP_A-1683674	G	G	391	9	392	20	3.997	4.56E-02	rs936868	4	72358386	q13.3
SNP_A-2009879	A	A	361	31	363	15	5.318	2.11E-02	rs4280704	4	72728580	q13.3
SNP_A-2155365	G	G	385	3	370	14	7.395	6.50E-03	rs16846789	4	72880725	q13.3
SNP_A-2091737	G	G	285	129	259	157	3.979	4.61E-02	rs6858790	4	73103714	q13.3
SNP_A-2204981	A	A	307	83	270	102	3.901	4.83E-02	---	4	73132513	q13.3
SNP_A-1676504	T	T	286	114	268	144	3.897	4.84E-02	rs10518093	4	73301283	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2272244	T	T	299	117	258	136	3.85	4.97E-02	rs12508636	4	73565029	q13.3
SNP_A-2129055	A	A	289	119	327	85	7.992	4.70E-03	rs12504695	4	73565160	q13.3
SNP_A-1808324	A	C	200	180	217	177	4.6	3.20E-02	rs10938039	4	73947515	q13.3
SNP_A-1726528	A	A	362	38	352	60	4.903	2.68E-02	rs409336	4	75323909	q13.3
SNP_A-1844379	G	G	303	7	316	18	4.224	3.98E-02	rs551906	4	75400249	q13.3
SNP_A-2107379	A	A	382	10	372	22	4.628	0.0315	rs6840142	4	75749487	q13.3
SNP_A-1729222	T	T	387	11	387	23	4.058	4.40E-02	rs1246396	4	75816054	q13.3
SNP_A-1706997	C	C	386	10	387	23	4.881	2.72E-02	rs1908423	4	75844188	q13.3
SNP_A-2278906	A	A	236	80	221	113	5.641	1.75E-02	rs13133546	4	75881027	q13.3
SNP_A-2283655	A	A	336	32	357	19	3.865	4.93E-02	rs11944347	4	75956850	q13.3
SNP_A-2294869	G	G	260	134	288	102	5.749	1.65E-02	rs10025144	4	75986494	q13.3
SNP_A-1893783	A	A	236	130	203	167	7.069	7.80E-03	rs10856876	4	76012369	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977623	A	A	342	0	334	4	4.071	0.0436	rs1452308	4	76077330	q13.3
SNP_A-2009895	C	C	325	5	328	16	5.487	1.92E-02	rs6832232	4	76120362	q13.3
SNP_A-2040153	T	T	322	26	324	44	4.079	4.34E-02	rs10034825	4	76417308	q13.3
SNP_A-1831845	T	T	227	133	257	107	4.654	0.031	rs1995635	4	76571975	q13.3
SNP_A-1781116	G	G	240	132	275	107	4.862	0.0275	rs10014607	4	76572093	q13.3
SNP_A-1815131	G	G	374	8	358	18	4.149	4.17E-02	rs17000487	4	76633454	q21.1
SNP_A-2201346	A	A	324	80	293	101	3.869	4.92E-02	rs13126597	4	76844531	q21.1
SNP_A-2238055	G	G	381	25	363	41	4.309	3.79E-02	rs13434876	4	77119853	q21.1
SNP_A-2280336	G	G	319	77	312	50	4.301	3.81E-02	rs2271528	4	77246015	q21.1
SNP_A-2235054	T	T	414	0	405	5	5.08	2.42E-02	rs1465923	4	77493390	q21.1
SNP_A-2146121	T	T	226	160	262	132	5.259	0.0218	rs13106227	4	77775860	q21.1
SNP_A-2168703	A	A	353	39	347	59	3.889	4.86E-02	rs6532433	4	77781437	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872664	A	A	362	48	345	69	4.159	4.14E-02	rs13140663	4	77865042	q21.1
SNP_A-1942255	C	C	397	9	378	22	5.873	0.0154	rs11723588	4	77943438	q21.1
SNP_A-2224540	C	C	241	173	211	207	5.014	2.51E-02	rs4276307	4	78021327	q21.1
SNP_A-2081964	A	A	239	169	208	200	4.754	0.0292	rs10002991	4	78023904	q21.1
SNP_A-1790454	A	A	233	125	231	87	4.469	3.45E-02	rs4859712	4	78027826	q21.1
SNP_A-2074627	C	C	335	27	336	14	3.922	4.76E-02	rs12645488	4	78093780	q21.1
SNP_A-1801094	C	C	367	47	351	69	4.486	3.42E-02	rs2703109	4	78251578	q21.1
SNP_A-2009902	A	A	305	27	303	45	4.132	4.21E-02	rs2645670	4	78258435	q21.1
SNP_A-2227423	C	C	245	139	216	192	9.592	0.002	rs6834234	4	78261879	q21.1
SNP_A-2152265	A	A	256	150	232	182	4.187	0.0407	rs2055209	4	78267709	q21.1
SNP_A-1977682	C	C	244	134	215	161	4.298	3.82E-02	rs6836567	4	78273884	q21.1
SNP_A-2146566	C	C	237	141	192	162	5.395	2.02E-02	rs6532761	4	78276444	q21.1
SNP_A-1939171	A	A	357	5	355	17	6.416	1.13E-02	rs2279711	4	78278493	q21.1
SNP_A-1850696	C	C	409	7	403	17	4.192	4.06E-02	rs6824360	4	78306275	q21.1
SNP_A-2272056	T	T	362	6	353	15	3.97	4.63E-02	rs17002334	4	78306457	q21.1
SNP_A-2067268	C	C	400	4	396	12	4	4.55E-02	rs10002443	4	78310837	q21.1
SNP_A-1977684	G	G	342	6	302	20	9.028	2.70E-03	rs17002346	4	78313139	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1646960	T	T	324	44	305	91	15.932	6.57E-05	rs2703137	4	78313374	q21.1
SNP_A-1679814	G	G	349	49	312	90	14.145	2.00E-04	rs2645690	4	78314239	q21.1
SNP_A-2094567	A	A	338	4	338	14	5.413	0.02	rs10006033	4	78325373	q21.1
SNP_A-1701621	G	G	233	107	235	159	6.235	1.25E-02	rs7683005	4	78346962	q21.1
SNP_A-2166637	A	A	274	118	303	89	5.52	1.88E-02	rs12505050	4	78366571	q21.1
SNP_A-2275160	G	G	398	12	388	24	4.122	4.23E-02	rs4150060	4	78438142	q21.1
SNP_A-2271298	G	G	401	11	391	25	5.552	1.85E-02	rs10006360	4	78459865	q21.1
SNP_A-1977698	G	G	355	39	373	21	5.845	1.56E-02	rs736601	4	78538832	q21.1
SNP_A-2268100	A	A	369	31	395	17	4.792	0.0286	rs4460017	4	78548230	q21.1
SNP_A-1977705	A	A	377	39	397	21	5.912	1.50E-02	rs10518170	4	78551092	q21.1
SNP_A-1977707	T	T	339	29	384	18	3.882	4.88E-02	rs10518171	4	78552328	q21.1
SNP_A-2237678	C	C	373	39	398	14	12.603	4.00E-04	rs4859480	4	78555903	q21.1
SNP_A-2097809	A	A	375	41	400	18	9.768	0.0018	rs17002495	4	78558206	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2083756	G	G	371	39	351	61	5.389	2.03E-02	rs17400392	4	78566020	q21.1
SNP_A-2173251	G	G	347	47	329	71	5.316	2.11E-02	rs17396361	4	78567475	q21.1
SNP_A-1977714	T	T	324	42	301	19	6.463	1.10E-02	rs17401246	4	78590030	q21.1
SNP_A-1804263	T	T	363	25	383	7	10.656	1.10E-03	rs4859489	4	78595210	q21.1
SNP_A-1712139	A	A	358	42	345	65	5.062	2.45E-02	rs736600	4	78639798	q21.1
SNP_A-1818833	T	T	304	94	273	127	6.588	0.0103	rs7375603	4	78648352	q21.1
SNP_A-2052204	T	T	290	80	263	109	5.763	1.64E-02	rs7375525	4	78648448	q21.1
SNP_A-1657267	A	A	360	40	393	19	8.745	3.10E-03	rs10518170	4	78652308	q21.1
SNP_A-1977719	T	T	311	91	290	120	4.641	3.12E-02	rs4859827	4	78654481	q21.1
SNP_A-2114961	A	A	267	87	263	119	3.942	4.71E-02	rs4859831	4	78662681	q21.1
SNP_A-1908276	A	A	375	31	362	48	3.868	4.92E-02	rs9307270	4	78663598	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2081083	G	G	314	88	283	121	6.815	9.00E-03	rs11724731	4	78665373	q21.1
SNP_A-1844478	G	G	283	95	265	125	4.496	3.40E-02	rs4859834	4	78667990	q21.1
SNP_A-2251999	G	G	312	98	287	127	4.762	2.91E-02	rs7679224	4	78678701	q21.1
SNP_A-1977721	C	C	297	95	286	128	4.494	3.40E-02	rs10518179	4	78684453	q21.1
SNP_A-1791156	G	G	316	96	289	129	6.002	0.0143	rs6533029	4	78687056	q21.1
SNP_A-1790943	T	T	317	97	286	130	6.386	0.0115	rs6832575	4	78687148	q21.1
SNP_A-1886128	A	A	293	79	270	108	5.389	2.03E-02	rs17002668	4	78687527	q21.1
SNP_A-2202168	C	C	316	96	287	127	5.699	1.70E-02	rs1372786	4	78687612	q21.1
SNP_A-1705443	C	C	353	31	390	16	6.022	0.0141	rs10518175	4	78725316	q21.1
SNP_A-1864352	A	A	272	102	291	75	4.674	3.06E-02	rs355675	4	78832090	q21.1
SNP_A-2283975	C	C	379	31	350	56	8.318	3.90E-03	rs4566676	4	78941159	q21.1
SNP_A-1729194	A	A	283	111	323	87	5.233	2.22E-02	rs355684	4	78962358	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1739225	G	G	293	85	325	63	4.797	2.85E-02	rs355686	4	78963767	q21.1
SNP_A-2063747	C	C	328	4	382	0	4.628	3.14E-02	---	4	79595251	q21.21
SNP_A-1858380	A	A	337	13	324	28	5.738	0.0166	rs10032457	4	79636297	q21.21
SNP_A-2222745	C	C	245	105	210	140	7.692	5.50E-03	rs4466067	4	79859748	q21.21
SNP_A-1944785	G	G	286	100	252	150	11.829	6.00E-04	rs6533804	4	79868152	q21.21
SNP_A-2117570	A	A	320	88	286	126	8.636	0.0033	rs6811335	4	79891636	q21.21
SNP_A-1870032	G	G	280	132	234	184	12.631	4.00E-04	rs11098275	4	79893825	q21.21
SNP_A-1977746	C	C	322	84	284	114	6.849	8.90E-03	rs13138005	4	79898333	q21.21
SNP_A-1906948	A	A	328	78	274	122	14.401	0.0001	rs6854055	4	79908771	q21.21
SNP_A-1930163	G	G	263	143	233	175	5.03	2.49E-02	rs1806906	4	79961099	q21.21
SNP_A-2009921	A	A	268	146	241	179	4.74	2.95E-02	rs6855458	4	79967211	q21.21
SNP_A-1875968	C	C	266	126	215	165	10.45	1.20E-03	rs4560439	4	79969023	q21.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920983	T	T	263	119	211	161	11.874	6.00E-04	rs6533940	4	79978618	q21.21
SNP_A-2079074	G	G	269	143	212	174	8.949	0.0028	rs4472163	4	79983406	q21.21
SNP_A-1647602	T	T	310	84	272	112	6.354	0.0117	rs3927159	4	80001737	q21.21
SNP_A-2214609	A	A	312	36	289	55	4.824	0.0281	rs8854347	4	80206221	q21.21
SNP_A-1878735	T	C	210	192	227	173	6.493	1.08E-02	rs11728698	4	80270642	q21.21
SNP_A-1977755	T	T	279	111	242	148	7.913	4.90E-03	rs985892	4	80293749	q21.21
SNP_A-1912055	G	C	213	193	233	173	7.901	4.90E-03	rs2086429	4	80299703	q21.21
SNP_A-1922721	A	A	320	76	345	47	7.757	5.40E-03	rs1026394	4	80465360	q21.21
SNP_A-2116485	T	T	361	33	376	14	7.966	4.80E-03	rs7676343	4	80483413	q21.21
SNP_A-2307401	G	G	340	24	375	9	8.002	4.70E-03	rs6534213	4	80484887	q21.21
SNP_A-1921658	G	G	316	78	344	56	4.755	0.0292	rs9307489	4	80512063	q21.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1959445	G	G	308	20	289	39	6.723	9.50E-03	rs4376173	4	80578985	q21.21
SNP_A-2289120	G	G	303	45	326	28	4.749	0.0293	rs12509468	4	80716597	q21.21
SNP_A-1882638	G	G	329	87	355	63	4.824	0.0281	rs11098735	4	80815592	q21.21
SNP_A-1915741	T	T	307	83	322	56	5.416	0.02	rs6850999	4	80859117	q21.21
SNP_A-1700364	T	T	316	84	347	63	4.327	3.75E-02	rs1971838	4	80877026	q21.21
SNP_A-1728777	T	T	232	168	210	202	4.043	4.44E-02	rs1808870	4	81001672	q21.21
SNP_A-1643435	T	T	306	94	338	72	4.383	3.63E-02	rs1866835	4	81005648	q21.21
SNP_A-1665202	T	T	232	168	207	203	4.603	3.19E-02	rs7677759	4	81006213	q21.21
SNP_A-1670161	A	A	369	29	359	49	5.142	2.33E-02	rs10518221	4	81028895	q21.21
SNP_A-2240303	A	A	175	155	194	108	8.153	0.0043	rs4632592	4	81084513	q21.21
SNP_A-1847238	A	A	207	193	238	168	3.846	0.0499	rs11931463	4	81088569	q21.21
SNP_A-1804557	A	G	210	204	229	177	4.18	4.09E-02	rs11938096	4	81108915	q21.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2305491	C	C	416	0	416	4	3.981	4.60E-02	rs4463018	4	81136027	q21.21
SNP_A-2211569	A	A	377	23	351	41	5.911	1.50E-02	rs2903651	4	81360700	q21.21
SNP_A-2149602	C	C	362	16	344	34	6.939	8.40E-03	---	4	81411867	q21.21
SNP_A-1977772	G	G	379	21	363	39	5.74	0.0166	rs10518233	4	81414035	q21.21
SNP_A-1925496	A	A	351	17	299	35	8.765	3.10E-03	---	4	81414200	q21.21
SNP_A-2113356	T	T	297	63	309	41	4.752	0.0293	rs6822305	4	81609898	q21.21
SNP_A-2314457	C	C	395	7	400	0	7.027	8.00E-03	rs6855317	4	81643113	q21.21
SNP_A-1869794	C	C	407	7	411	1	4.515	3.36E-02	rs17004962	4	81920518	q21.21
SNP_A-1852476	T	T	323	7	317	1	4.336	0.0373	rs17005013	4	82231822	q21.21
SNP_A-1751647	C	C	362	38	389	23	4.483	3.42E-02	rs1112880	4	82473279	q21.21
SNP_A-2009935	T	T	263	105	289	73	6.929	8.50E-03	rs1712387	4	82499730	q21.21
SNP_A-1977797	T	T	275	141	302	114	4.122	4.23E-02	rs10488936	4	82569349	q21.21
SNP_A-1880617	C	C	289	93	323	73	4.048	4.42E-02	rs17427459	4	82586390	q21.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2146423	T	T	258	130	276	92	6.587	0.0103	—	4	82626807	q21.21
SNP_A-2241318	C	C	267	111	298	84	5.418	1.99E-02	rs11725731	4	82628613	q21.21
SNP_A-2209240	A	A	184	176	205	139	5.119	2.37E-02	rs7677239	4	82629002	q21.21
SNP_A-2240130	T	T	263	135	298	112	4.148	4.17E-02	—	4	82629284	q21.21
SNP_A-1918409	G	G	284	118	304	92	3.854	4.96E-02	rs2109662	4	82629744	q21.21
SNP_A-2135887	C	C	269	141	304	110	5.947	0.0147	rs7696324	4	82634060	q21.21
SNP_A-1780701	T	T	274	136	306	108	4.959	2.60E-02	rs17499843	4	82655931	q21.21
SNP_A-2165934	T	T	224	178	264	148	5.917	1.50E-02	rs17499877	4	82661611	q21.21
SNP_A-1651222	A	A	225	173	266	146	5.469	1.94E-02	rs10488935	4	82675927	q21.21
SNP_A-2115652	C	C	351	19	340	58	18.933	0.000013541	rs1444891	4	82733800	q21.22
SNP_A-1957916	A	A	320	0	318	6	5.982	1.45E-02	—	4	82798833	q21.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100490	G	G	238	100	261	75	4.626	0.0315	rs11099490	4	82914940	q21.22
SNP_A-1787352	C	G	230	178	229	181	12.228	5.00E-04	rs4279197	4	83001103	q21.22
SNP_A-2128693	A	A	331	77	350	56	3.841	5.00E-02	rs1381795	4	83249231	q21.22
SNP_A-1934354	G	G	268	124	287	95	4.362	3.67E-02	rs1443764	4	83284367	q21.22
SNP_A-1801166	C	C	289	111	254	136	4.661	0.0309	rs13119377	4	83360385	q21.22
SNP_A-1852961	C	C	265	83	227	103	4.611	3.18E-02	rs11099543	4	83872698	q21.22
SNP_A-2293436	G	G	249	109	217	133	4.488	3.41E-02	rs6838784	4	83906298	q21.22
SNP_A-2070661	T	T	266	124	229	155	6.164	1.30E-02	rs4693474	4	83921008	q21.22
SNP_A-1889372	C	C	296	114	261	139	4.547	3.30E-02	rs10014168	4	83923296	q21.22
SNP_A-2085282	T	T	294	64	250	90	7.489	6.20E-03	rs7679857	4	83926916	q21.22
SNP_A-2164059	T	T	280	134	241	179	9.346	2.20E-03	rs4693478	4	83930479	q21.22
SNP_A-2048950	G	G	257	89	202	118	9.653	0.0019	rs993380	4	83941675	q21.22
SNP_A-2050170	T	T	365	41	341	71	8.808	3.00E-03	rs10030631	4	83953924	q21.22
SNP_A-2155779	A	A	257	91	237	117	4.009	0.0453	rs7682126	4	83954461	q21.22
SNP_A-2089949	C	C	327	85	302	110	4.199	4.05E-02	rs13106297	4	83970811	q21.22
SNP_A-2305914	C	C	251	139	280	104	6.579	0.0103	rs10014388	4	83976041	q21.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2270490	A	A	342	20	304	32	4.042	4.44E-02	rs4693491	4	83984762	q21.22
SNP_A-2209235	C	T	198	180	199	163	4.002	4.55E-02	rs6535395	4	83999005	q21.22
SNP_A-1667404	A	A	277	117	253	151	5.276	2.16E-02	rs4693470	4	84008265	q21.22
SNP_A-1662228	A	A	277	119	257	153	4.757	0.0292	rs7670515	4	84008808	q21.22
SNP_A-1689951	G	G	275	121	255	151	3.939	4.72E-02	rs7675887	4	84009001	q21.22
SNP_A-1693789	A	A	276	118	254	150	4.61	3.18E-02	rs6840	4	84009402	q21.22
SNP_A-2174142	C	C	278	90	305	69	3.976	4.62E-02	rs7436836	4	84645193	q21.23
SNP_A-1832892	C	C	394	16	382	32	5.5	0.019	rs9997497	4	84672790	q21.23
SNP_A-1977855	G	G	337	19	332	34	4.145	4.18E-02	rs17006788	4	84685160	q21.23
SNP_A-1905382	T	T	333	43	322	74	7.886	5.00E-03	rs1921886	4	85307457	q21.23
SNP_A-2177445	A	A	315	69	313	97	3.882	4.88E-02	rs1950129	4	85307823	q21.23
SNP_A-2269061	G	G	337	69	306	90	4.144	4.18E-02	rs1921877	4	85319832	q21.23
SNP_A-2188079	G	G	312	92	334	66	5.008	0.0252	rs17007921	4	85326283	q21.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977872	C	C	286	62	218	90	11.938	6.00E-04	rs17007935	4	85337476	q21.23
SNP_A-1714627	A	A	381	19	403	9	4.012	4.52E-02	rs1847819	4	85353386	q21.23
SNP_A-2262541	C	C	344	0	340	4	4.023	4.49E-02	rs7681490	4	85368909	q21.23
SNP_A-1757966	A	A	247	141	225	173	4.16	4.14E-02	rs10516711	4	85446809	q21.23
SNP_A-2175477	C	C	346	68	319	95	5.569	0.0183	rs1390088	4	85606666	q21.23
SNP_A-1787374	C	C	342	12	356	26	4.38	3.64E-02	rs6857631	4	85619987	q21.23
SNP_A-2064889	C	C	301	115	276	142	3.915	4.79E-02	rs2278672	4	85773622	q21.23
SNP_A-1744339	C	C	310	90	293	117	3.878	4.89E-02	rs763540	4	85833962	q21.23
SNP_A-2122349	G	G	291	67	292	36	8.035	4.60E-03	rs11730096	4	86524699	q21.23
SNP_A-2090958	A	A	410	2	408	10	5.295	2.14E-02	rs1994069	4	86824964	q21.23
SNP_A-2141357	T	T	313	91	334	66	4.643	3.12E-02	rs13152150	4	86990486	q21.23
SNP_A-1977914	A	A	257	111	275	81	5.099	2.39E-02	rs343849	4	87020234	q21.23
SNP_A-1977917	C	C	253	127	268	98	3.908	4.80E-02	rs10516755	4	87023220	q21.23
SNP_A-1928721	G	A	178	154	196	146	8.054	4.50E-03	rs346515	4	87200683	q21.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1977928	C	C	280	110	243	131	4.114	4.25E-02	rs346502	4	87214582	q21.23
SNP_A-2262623	A	A	262	60	293	43	4.241	3.94E-02	rs11097084	4	87237880	q21.23
SNP_A-2295811	C	C	290	96	311	73	3.859	4.95E-02	rs12503695	4	87282642	q21.23
SNP_A-1952665	T	T	359	17	348	42	10.512	1.20E-03	rs11097119	4	88046712	q21.3
SNP_A-1958156	G	G	354	26	355	47	5.428	1.98E-02	rs12498681	4	88047589	q21.3
SNP_A-2105597	T	T	233	111	244	80	4.69	3.03E-02	rs6855564	4	88832793	q22.1
SNP_A-1643632	G	G	289	111	267	143	4.779	2.88E-02	rs4129319	4	88853780	q22.1
SNP_A-1643461	A	A	333	51	319	81	6.795	9.10E-03	rs4129320	4	88853954	q22.1
SNP_A-2161139	T	A	236	170	199	187	7.455	0.0063	rs6813055	4	88987210	q22.1
SNP_A-1743077	T	T	289	111	324	86	5.048	0.0247	rs1381632	4	89027379	q22.1
SNP_A-2130845	C	C	212	134	233	107	3.964	0.0465	rs6532032	4	89204862	q22.1
SNP_A-2202971	A	G	203	181	209	171	4.727	2.97E-02	rs1440581	4	89583601	q22.1
SNP_A-1943446	C	C	339	27	362	12	6.438	0.0112	rs17014602	4	90088164	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1959063	A	G	183	143	180	166	4.475	0.0344	rs6532123	4	90448725	q22.1
SNP_A-2052457	C	C	354	60	372	40	4.441	3.51E-02	rs17015187	4	90493789	q22.1
SNP_A-2261187	G	G	324	8	318	20	5.146	2.33E-02	rs17015958	4	90915718	q22.1
SNP_A-2245046	C	C	371	5	357	15	5.248	2.20E-02	rs3775439	4	91066919	q22.1
SNP_A-1901147	T	T	318	92	349	67	5.328	2.10E-02	rs2572318	4	91075897	q22.1
SNP_A-2059577	G	G	292	100	314	74	4.663	3.08E-02	rs1837890	4	91093184	q22.1
SNP_A-2257906	C	C	282	32	307	15	7.111	7.70E-03	rs1442144	4	91093291	q22.1
SNP_A-2252416	C	C	316	90	351	69	4.374	3.65E-02	rs1837891	4	91093309	q22.1
SNP_A-1807077	T	T	319	95	350	70	5.181	2.28E-02	rs1811442	4	91104929	q22.1
SNP_A-1928999	G	G	289	45	315	27	5.525	1.87E-02	rs2737002	4	91110358	q22.1
SNP_A-2055955	G	A	224	188	228	186	7.363	6.70E-03	---	4	91127102	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801078	G	G	306	92	346	60	9.112	2.50E-03	rs2736994	4	91141706	q22.1
SNP_A-2125541	G	A	201	199	238	166	6.799	9.10E-03	rs6831847	4	91142519	q22.1
SNP_A-1853741	T	T	238	174	207	203	4.385	3.62E-02	rs1442136	4	91176204	q22.1
SNP_A-2234712	A	G	212	186	227	175	7.588	5.90E-03	rs1442134	4	91176332	q22.1
SNP_A-1978024	A	G	190	180	207	151	6.148	0.0132	rs9307077	4	91190550	q22.1
SNP_A-2190194	G	G	394	20	408	8	5.382	2.03E-02	rs6532206	4	91224469	q22.1
SNP_A-2009979	C	C	213	167	251	133	6.945	8.40E-03	rs3775482	4	91227518	q22.1
SNP_A-1978025	T	T	216	168	269	137	8.336	3.90E-03	rs3775483	4	91227537	q22.1
SNP_A-2195047	A	A	238	176	269	139	6.198	1.28E-02	rs7689553	4	91268152	q22.1
SNP_A-2232037	A	A	250	158	296	116	10.294	1.30E-03	rs12641504	4	91299000	q22.1
SNP_A-1978027	G	-	204	142	175	175	5.632	1.76E-02	rs10516858	4	91309602	q22.1
SNP_A-1883672	T	T	254	156	219	193	6.508	1.07E-02	rs723992	4	91311728	q22.1
SNP_A-2305381	A	A	230	164	251	125	5.762	1.64E-02	rs6842029	4	91314833	q22.1
SNP_A-1755762	G	G	365	7	371	21	6.53	0.0106	rs10516853	4	91325213	q22.1
SNP_A-2279018	A	A	220	152	269	115	9.849	1.70E-03	rs894803	4	91350350	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2034816	A	T	189	177	229	145	12.371	4.00E-04	rs1031125	4	91350520	q22.1
SNP_A-1679748	A	A	367	23	353	43	6.287	1.22E-02	rs10516855	4	91382872	q22.1
SNP_A-1711502	T	T	240	150	212	192	6.648	9.90E-03	rs7661577	4	91402179	q22.1
SNP_A-1651792	A	A	246	154	215	195	6.779	9.20E-03	rs10516857	4	91402764	q22.1
SNP_A-1669593	T	T	244	152	217	195	6.596	1.02E-02	rs10516860	4	91423481	q22.1
SNP_A-1748961	A	A	234	150	288	118	8.801	3.00E-03	rs722937	4	91430139	q22.1
SNP_A-1978032	T	C	212	176	214	168	8.751	3.10E-03	rs6818163	4	91473243	q22.1
SNP_A-1801216	T	A	215	191	231	169	9.258	0.0023	rs1431026	4	91489790	q22.1
SNP_A-2202695	C	T	196	178	213	157	7.42	6.40E-03	rs6532218	4	91505033	q22.1
SNP_A-1890244	T	C	167	139	192	140	9.818	1.70E-03	rs2116123	4	91512958	q22.1
SNP_A-2148903	G	T	173	165	207	153	5.281	2.16E-02	rs2870246	4	91591676	q22.1
SNP_A-1920422	G	G	308	64	270	84	4.758	0.0292	rs2126283	4	91594140	q22.1
SNP_A-1978033	T	C	206	164	208	176	7.303	6.90E-03	rs4694022	4	91599126	q22.1
SNP_A-2135083	C	C	167	165	193	113	10.562	1.20E-03	rs1903579	4	91611134	q22.1
SNP_A-2207553	T	C	197	195	234	170	5.352	0.0207	rs13103126	4	91619162	q22.1
SNP_A-2102508	G	G	271	119	241	147	4.7	3.02E-02	rs11097248	4	91648585	q22.1
SNP_A-1696450	T	T	310	86	287	125	7.781	0.0053	rs1551794	4	91695465	q22.1
SNP_A-1724588	C	A	216	184	233	179	9.048	2.60E-03	rs1551795	4	91695630	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172954	G	G	377	27	398	14	4.613	3.17E-02	rs11097281	4	92228940	q22.1
SNP_A-1907734	T	T	387	29	406	14	5.669	1.73E-02	rs1454334	4	92233669	q22.1
SNP_A-2127264	A	A	342	38	328	62	5.924	0.0149	rs10446698	4	92336272	q22.1
SNP_A-2261091	G	G	368	6	370	16	4.362	3.67E-02	rs9998701	4	92426429	q22.1
SNP_A-2056312	T	T	323	79	345	57	4.283	0.0385	rs1544017	4	92517008	q22.1
SNP_A-1978056	G	G	385	19	392	6	6.779	9.20E-03	rs1406317	4	92610952	q22.1
SNP_A-1733556	T	T	399	1	405	7	4.368	3.66E-02	rs10516889	4	92665937	q22.1
SNP_A-2095257	T	T	285	67	258	96	6.496	1.08E-02	rs1997497	4	92722360	q22.1
SNP_A-1951642	G	G	341	71	316	100	5.85	1.56E-02	rs1997496	4	92722494	q22.1
SNP_A-2247928	G	G	295	119	250	162	10.291	1.30E-03	rs13123986	4	92739861	q22.1
SNP_A-1700378	C	C	338	62	323	89	4.992	2.55E-02	rs1919225	4	92744999	q22.1
SNP_A-2111029	G	G	321	95	289	117	3.841	5.00E-02	rs1997498	4	92779959	q22.1
SNP_A-1716791	C	C	284	90	280	130	5.66	1.74E-02	rs7672281	4	92788749	q22.1
SNP_A-1839859	C	C	350	58	371	39	4.328	3.75E-02	rs17218334	4	92838539	q22.1
SNP_A-1744691	G	G	337	63	315	97	7.792	5.20E-03	rs1922227	4	92860054	q22.1
SNP_A-1978065	A	A	237	137	208	166	4.665	3.08E-02	rs10213431	4	92996052	q22.1
SNP_A-1949768	C	C	355	19	360	6	6.709	9.60E-03	rs1564957	4	93195524	q22.1
SNP_A-1978085	C	C	360	40	372	20	6.783	9.20E-03	rs17019800	4	93979799	q22.3
SNP_A-2201748	C	C	400	10	409	3	3.865	4.93E-02	rs6836612	4	94247276	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1853677	C	C	379	11	401	3	4.947	2.61E-02	rs10011751	4	94342173	q22.3
SNP_A-2093452	C	C	325	91	351	69	4.006	0.0453	rs17021048	4	94991354	q22.3
SNP_A-1898746	C	T	215	151	175	173	5.863	0.0155	rs4493502	4	95119723	q22.3
SNP_A-1814559	G	G	318	98	292	124	4.153	4.16E-02	rs1353044	4	95798488	q22.3
SNP_A-1825392	A	G	202	194	222	170	4.617	3.17E-02	rs7662466	4	95866941	q22.3
SNP_A-2104592	G	G	257	113	234	150	6.025	0.0141	rs17021918	4	95920055	q22.3
SNP_A-1941710	T	T	214	122	202	168	6.019	1.42E-02	rs12500116	4	95936917	q22.3
SNP_A-1978128	G	G	239	141	209	177	6.038	0.014	rs998071	4	95949154	q22.3
SNP_A-2126379	T	T	386	4	390	0	4.021	4.49E-02	rs17022474	4	96169606	q22.3
SNP_A-2230575	A	A	348	30	316	50	6.35	0.0117	rs17023017	4	96382272	q22.3
SNP_A-1978149	C	C	366	14	381	5	4.518	3.35E-02	rs1369087	4	96391156	q22.3
SNP_A-2276058	C	C	293	35	295	17	5.841	1.57E-02	rs3775003	4	96528389	q22.3
SNP_A-2260743	A	A	332	70	356	48	4.934	0.0263	rs17023470	4	96570999	q22.3
SNP_A-1978156	A	A	300	84	329	59	5.687	1.71E-02	rs1843018	4	96613851	q22.3
SNP_A-2061483	G	G	241	167	207	195	4.702	3.01E-02	rs2626035	4	96643971	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944860	C	C	264	80	297	53	7.371	0.0066	rs6532557	4	96735810	q22.3
SNP_A-1929622	G	G	232	106	244	74	5.387	2.03E-02	rs13148787	4	96794940	q22.3
SNP_A-1893275	T	T	269	81	286	58	4.275	3.87E-02	rs1385674	4	96851629	q22.3
SNP_A-1888209	A	A	219	181	241	149	4.029	4.47E-02	rs12644144	4	96919213	q22.3
SNP_A-2149455	C	C	347	61	371	41	4.704	3.01E-02	rs1369994	4	96956262	q22.3
SNP_A-2085076	G	G	345	59	364	38	5.051	0.0246	rs1369993	4	96956292	q22.3
SNP_A-1978166	C	C	334	38	362	18	8.185	4.20E-03	rs1898250	4	96962677	q22.3
SNP_A-1791578	C	C	343	65	376	42	6.338	0.0118	rs4699446	4	96966968	q22.3
SNP_A-2158125	A	A	342	58	365	39	4.45	0.0349	rs13112562	4	96967897	q22.3
SNP_A-1901042	T	T	303	43	319	27	4.069	4.37E-02	rs4699272	4	96971012	q22.3
SNP_A-2075874	T	T	315	49	337	29	5.865	0.0154	rs4699449	4	96971413	q22.3
SNP_A-2222999	C	C	334	68	354	48	4.03	4.47E-02	rs9993596	4	96985251	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141051	C	C	226	182	249	149	4.28	3.86E-02	rs1370004	4	96985831	q22.3
SNP_A-2199310	A	A	330	68	349	45	5.193	2.27E-02	rs1370002	4	96985959	q22.3
SNP_A-2216768	G	G	342	60	367	39	5.316	2.11E-02	rs11729357	4	96991023	q22.3
SNP_A-1674351	T	T	326	66	355	47	4.304	3.80E-02	rs1821742	4	97103088	q22.3
SNP_A-2173005	A	A	270	68	289	47	4.475	0.0344	rs17025392	4	97619794	q22.3
SNP_A-2100833	C	C	363	53	342	74	4.098	4.29E-02	---	4	97816361	q22.3
SNP_A-1802533	A	A	253	109	281	83	4.984	2.56E-02	rs10007764	4	97867929	q22.3
SNP_A-1880333	G	G	254	108	304	84	6.587	0.0103	rs6830552	4	98247219	q22.3
SNP_A-2237533	G	G	320	38	330	16	8.915	0.0028	rs260903	4	99042880	q22.3
SNP_A-1934762	T	T	316	56	302	78	3.844	0.0499	rs13150465	4	99452070	q23
SNP_A-2179909	A	A	228	96	201	121	4.573	3.25E-02	rs11727079	4	100185505	q23
SNP_A-1740385	T	T	324	64	363	39	8.036	4.60E-03	rs2851292	4	100761895	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1657954	C	C	381	19	371	37	5.84	1.57E-02	rs284780	4	100762817	q23
SNP_A-1735613	C	C	381	19	372	36	5.283	2.15E-02	rs284781	4	100763134	q23
SNP_A-1978240	C	C	270	116	234	148	6.43	0.0112	rs10516445	4	100881857	q23
SNP_A-1753767	C	C	380	10	383	1	7.329	6.80E-03	rs7675468	4	100920263	q23
SNP_A-2213549	G	G	372	6	366	16	4.573	3.25E-02	rs17029260	4	100924638	q23
SNP_A-2165926	G	G	307	39	311	65	5.288	2.15E-02	rs6858032	4	100933504	q23
SNP_A-1890478	C	C	407	9	393	27	9.226	2.40E-03	rs7667218	4	100993687	q23
SNP_A-2141375	G	G	285	105	323	83	4.63	3.14E-02	rs3775501	4	101103516	q23
SNP_A-1924650	T	T	367	7	363	1	4.387	3.62E-02	rs3886172	4	101289579	q23
SNP_A-2010011	C	C	225	159	199	187	3.855	4.96E-02	rs4699770	4	101342379	q23
SNP_A-1978253	G	G	358	4	358	12	3.913	4.79E-02	rs17620626	4	101443215	q24
SNP_A-1712253	G	G	293	105	331	77	6.499	1.08E-02	rs10516461	4	101527780	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2261125	G	G	312	10	343	3	4.38	3.64E-02	rs7682797	4	101828691	q24
SNP_A-2238892	C	C	342	56	341	33	5.204	2.25E-02	rs13121097	4	102208314	q24
SNP_A-2255969	C	C	349	11	367	3	4.888	0.027	rs2645368	4	102246308	q24
SNP_A-2030935	C	C	400	10	392	22	4.561	0.0327	rs10026319	4	102332813	q24
SNP_A-2054727	G	G	335	67	352	42	6.075	0.0137	rs2732514	4	102416020	q24
SNP_A-1837329	G	G	223	133	241	105	3.851	4.97E-02	rs2063058	4	102434160	q24
SNP_A-1845503	G	G	282	94	299	69	4.246	3.93E-02	rs713455	4	102504823	q24
SNP_A-2198784	A	A	300	112	317	85	4.047	4.43E-02	rs2583405	4	102530159	q24
SNP_A-1851113	A	A	270	90	292	68	3.925	4.76E-02	rs2850336	4	102535236	q24
SNP_A-2080771	T	T	293	41	336	26	5.18	0.0229	rs1441433	4	102566538	q24
SNP_A-2286062	C	C	326	54	365	35	5.748	1.65E-02	rs2850356	4	102569100	q24
SNP_A-1666486	C	C	367	31	357	53	5.723	0.0167	rs10516469	4	102719647	q24
SNP_A-2194168	C	C	274	134	303	109	4.01	4.52E-02	rs10009721	4	102927627	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2130232	G	G	247	111	264	82	4.72	0.0298	rs7679597	4	102933954	q24
SNP_A-2104512	G	G	358	32	384	18	4.65	0.031	rs4385063	4	103188463	q24
SNP_A-1948031	G	G	277	69	299	45	5.887	1.53E-02	rs238476	4	103401555	q24
SNP_A-2305553	C	C	303	53	324	32	5.892	0.0152	rs151499	4	103423129	q24
SNP_A-1942592	A	A	303	59	319	37	5.403	0.0201	rs236781	4	103441752	q24
SNP_A-2094657	G	G	389	17	393	5	6.487	0.0109	rs7661718	4	103448943	q24
SNP_A-2157548	A	A	313	81	259	95	4.084	4.33E-02	rs6419158	4	103474467	q24
SNP_A-1748831	G	G	323	77	354	58	3.917	4.78E-02	rs173218	4	103481443	q24
SNP_A-1895017	C	A	190	176	206	156	5.675	0.0172	rs151413	4	103495119	q24
SNP_A-1676696	A	G	185	181	235	161	7.505	6.20E-03	rs4606610	4	103612524	q24
SNP_A-2173624	A	A	338	0	344	4	3.908	4.81E-02	rs4648064	4	103873930	q24
SNP_A-2256913	C	C	373	41	384	24	4.562	0.0327	rs6533086	4	104652393	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2090142	C	C	375	29	392	16	4.113	4.26E-02	rs6837313	4	104661122	q24
SNP_A-1952125	C	C	298	26	318	14	4.152	4.16E-02	rs374343	4	104824176	q24
SNP_A-1876501	G	G	255	143	283	107	6.561	0.0104	rs3900348	4	104866771	q24
SNP_A-1863960	T	T	291	123	320	94	5.252	2.19E-02	rs4446310	4	104866835	q24
SNP_A-2285236	C	C	411	5	418	0	5.054	0.0246	---	4	105278083	q24
SNP_A-2165903	T	T	253	115	261	83	4.492	3.40E-02	rs2214397	4	105848456	q24
SNP_A-1978340	G	G	334	76	353	53	4.607	3.18E-02	rs2107006	4	105999689	q24
SNP_A-1978353	A	A	404	10	415	3	3.898	4.83E-02	rs2866774	4	106434330	q24
SNP_A-2062488	G	A	189	153	170	152	4.311	3.79E-02	rs2726502	4	106656500	q24
SNP_A-1853320	G	G	217	159	241	121	6.151	1.31E-02	rs2713827	4	106666161	q24
SNP_A-1978365	G	G	205	139	247	95	12.17	5.00E-04	rs2713834	4	106668124	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869251	T	T	202	164	241	131	7.077	7.80E-03	rs2636732	4	106694459	q24
SNP_A-2088025	C	C	212	200	246	172	4.588	3.22E-02	rs2726516	4	106703810	q24
SNP_A-1837008	A	A	213	201	244	172	4.353	3.69E-02	rs2636739	4	106709709	q24
SNP_A-2143496	A	A	346	34	331	53	4.461	3.47E-02	rs3898404	4	106713999	q24
SNP_A-2118277	C	C	320	62	346	36	7.913	4.90E-03	rs1048518	4	106750311	q24
SNP_A-1691140	C	C	224	162	272	136	6.309	0.012	rs2726526	4	106750941	q24
SNP_A-1677946	G	G	200	160	247	127	8.472	3.60E-03	rs923589	4	106780874	q24
SNP_A-2287214	A	A	329	77	350	42	10.701	1.10E-03	rs3864227	4	106805356	q24
SNP_A-2199628	G	G	313	81	307	51	5.165	2.31E-02	rs6830281	4	106806786	q24
SNP_A-2244967	G	G	371	29	391	15	4.935	0.0263	rs10032241	4	106831682	q24
SNP_A-1978374	G	G	297	87	329	63	5.394	2.02E-02	rs10516519	4	106875603	q24
SNP_A-1844813	G	G	354	30	383	17	4.412	3.57E-02	rs17035917	4	106878346	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2300054	T	T	301	27	297	11	6.141	0.0132	rs17036076	4	106932873	q24
SNP_A-1978378	G	G	370	10	391	1	7.758	0.0053	rs17036129	4	106982133	q24
SNP_A-2081830	C	C	356	18	369	7	5.068	2.44E-02	rs17036139	4	106990261	q24
SNP_A-2198992	C	C	380	26	404	14	4.161	4.14E-02	rs17036156	4	107020838	q24
SNP_A-1832981	T	T	374	20	341	35	5.196	2.26E-02	rs4698951	4	107029802	q24
SNP_A-1870827	A	A	384	28	387	13	5.323	2.10E-02	rs17036225	4	107067696	q24
SNP_A-2190503	A	A	377	19	397	9	3.964	0.0465	rs17036230	4	107072752	q24
SNP_A-2303241	C	C	378	26	397	11	6.527	0.0106	rs17036341	4	107154433	q24
SNP_A-1721199	G	G	373	27	397	15	4	4.55E-02	rs10516528	4	107198413	q24
SNP_A-1728537	C	C	315	41	296	74	9.794	0.0018	rs2553453	4	107266992	q24
SNP_A-1799303	G	T	214	180	219	185	5.795	0.0161	rs13148020	4	107780768	q24
SNP_A-2218672	A	T	225	169	196	186	5.514	0.0189	rs13148463	4	107780972	q24

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829867	G	G	221	139	195	167	4.182	4.09E-02	rs1915918	4	107784029	q24
SNP_A-1922989	A	A	212	150	250	130	4.12	0.0424	rs1522221	4	107784955	q24
SNP_A-1954712	G	G	402	2	392	10	5.454	0.0195	—	4	107812191	q24
SNP_A-1646944	G	A	223	169	202	194	4.932	0.0264	rs10516535	4	107853796	q24
SNP_A-2072846	C	C	303	39	330	24	4.518	3.35E-02	rs1522215	4	107874842	q24
SNP_A-2178454	G	G	212	128	224	96	4.3	3.81E-02	rs2324	4	108184309	q25
SNP_A-1978400	T	T	266	134	287	99	5.807	0.016	rs429941	4	108193915	q25
SNP_A-1831836	C	C	237	135	259	107	4.167	4.12E-02	rs419764	4	108201761	q25
SNP_A-1839697	A	A	311	61	260	78	5.018	2.51E-02	rs17037236	4	108301051	q25
SNP_A-1953094	G	C	181	163	175	123	8.238	4.10E-03	rs1399405	4	108844442	q25
SNP_A-1929116	C	T	187	157	192	162	5.159	2.31E-02	rs2672477	4	108656385	q25
SNP_A-1803534	C	T	179	119	169	163	7.616	5.80E-03	rs2726684	4	108857238	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903471	C	C	356	26	396	12	6.437	0.0112	rs2251908	4	108896121	q25
SNP_A-1681558	C	C	359	29	393	17	4.064	4.38E-02	rs9307311	4	109049099	q25
SNP_A-2125094	T	T	385	1	365	7	4.776	2.89E-02	rs4571411	4	109496590	q25
SNP_A-1803520	C	C	408	0	410	4	3.961	4.66E-02	rs1003169	4	109533765	q25
SNP_A-2064260	C	C	323	25	333	13	3.936	4.73E-02	rs9992383	4	109612717	q25
SNP_A-1923587	C	C	377	37	353	61	6.667	9.80E-03	rs17039065	4	109743007	q25
SNP_A-1868802	A	A	198	158	211	121	4.488	3.41E-02	rs17583662	4	109819589	q25
SNP_A-2038949	C	C	255	125	260	64	15.379	8.80E-05	rs17800095	4	109850857	q25
SNP_A-1978436	A	A	253	89	222	112	4.561	0.0327	rs3796938	4	109868838	q25
SNP_A-1791805	G	G	269	107	232	134	5.624	0.0177	rs11097999	4	109910485	q25
SNP_A-1733108	T	T	265	133	303	105	5.713	1.68E-02	rs4266352	4	109925167	q25
SNP_A-1933118	G	G	282	118	323	93	5.429	1.98E-02	rs17039240	4	109982686	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287766	C	T	203	191	216	168	4.71	3.00E-02	rs2575617	4	109985568	q25
SNP_A-1919409	G	G	268	64	299	37	8.889	2.90E-03	rs1405159	4	110253751	q25
SNP_A-1978449	C	C	341	73	379	39	12.308	5.00E-04	rs1405154	4	110259028	q25
SNP_A-2206860	G	G	337	21	335	37	4.153	4.16E-02	rs3096491	4	110339128	q25
SNP_A-2110592	C	C	364	20	379	9	4.455	3.48E-02	rs7674074	4	110393104	q25
SNP_A-2242962	G	G	405	7	399	21	6.968	8.30E-03	—	4	110497157	q25
SNP_A-2301708	A	A	315	25	281	39	4.4	3.59E-02	rs714586	4	110584010	q25
SNP_A-1679176	C	C	390	8	389	21	5.652	1.74E-02	rs2189705	4	110595663	q25
SNP_A-1702847	T	T	391	9	391	21	4.624	0.0315	rs10488876	4	110596094	q25
SNP_A-2045644	G	G	400	8	416	0	8.237	4.10E-03	rs11929767	4	111051139	q25
SNP_A-1978476	G	G	336	28	334	10	7.974	4.70E-03	rs2347130	4	111146343	q25
SNP_A-1850736	A	A	407	5	418	0	5.104	2.39E-02	rs11569080	4	111272355	q25
SNP_A-1882312	C	C	374	2	379	11	6.01	1.42E-02	rs1060855	4	111329494	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2070329	A	A	272	104	268	70	4.664	3.08E-02	rs1386476	4	111676421	q25
SNP_A-1674689	T	T	379	5	388	14	3.959	4.66E-02	rs10488888	4	111742528	q25
SNP_A-2041244	T	T	378	4	386	0	4.063	4.38E-02	rs17042528	4	112200028	q25
SNP_A-2203280	T	T	332	60	308	84	4.9	0.0269	rs886840	4	112215720	q25
SNP_A-1960869	G	G	410	6	420	0	6.101	0.0135	rs9307360	4	112306938	q25
SNP_A-1663742	A	A	395	5	412	0	5.182	2.28E-02	rs159440	4	112442452	q25
SNP_A-1910094	A	G	223	157	179	175	6.316	0.012	rs7690819	4	112478262	q25
SNP_A-2154313	C	C	304	112	268	148	7.25	7.10E-03	rs7664517	4	112887633	q25
SNP_A-2191220	G	G	266	90	249	117	3.945	0.047	rs13434948	4	113149175	q25
SNP_A-2159758	A	A	274	118	235	163	10.15	0.0014	rs6842731	4	113157234	q25
SNP_A-2274035	G	G	257	107	208	132	6.968	8.30E-03	rs2348650	4	113173024	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1957238	G	G	275	139	303	113	4.034	4.46E-02	rs13107428	4	113232563	q25
SNP_A-2237616	G	G	330	56	299	89	9.033	2.70E-03	rs7654718	4	113262827	q25
SNP_A-1978537	T	T	321	15	315	31	5.476	1.93E-02	rs3850487	4	113287245	q25
SNP_A-1839087	G	G	231	129	262	106	4.113	4.26E-02	rs4834158	4	113321087	q25
SNP_A-1728199	G	G	257	129	277	101	4.074	4.35E-02	rs9307376	4	113328956	q25
SNP_A-2133496	G	G	246	124	282	100	4.836	2.79E-02	rs17594556	4	113331057	q25
SNP_A-1656643	G	G	259	133	288	108	4.111	4.26E-02	rs2016740	4	113339234	q25
SNP_A-1744357	C	C	261	139	293	115	4.037	4.45E-02	rs877936	4	113339688	q25
SNP_A-2124260	C	C	269	135	296	100	6.424	1.13E-02	rs6533594	4	113357313	q25
SNP_A-1800597	A	A	281	121	318	96	4.99	2.55E-02	rs12510412	4	113373330	q25
SNP_A-1905683	C	C	282	120	316	88	6.851	8.90E-03	rs10155491	4	113379394	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893949	A	A	250	158	283	133	4.114	4.25E-02	rs12643407	4	113407242	q25
SNP_A-1978544	T	T	227	115	278	70	16.045	6.18E-05	rs2164446	4	113429438	q25
SNP_A-2057213	A	A	198	170	224	142	4.109	4.26E-02	rs10402 78	4	113436995	q25
SNP_A-1923322	T	T	367	13	348	30	7.221	7.20E-03	rs909034	4	113455310	q25
SNP_A-2153689	G	G	396	18	370	38	7.982	4.70E-03	rs1554467	4	113484186	q25
SNP_A-1834416	A	A	379	9	382	2	4.446	3.50E-02	rs6832157	4	113801021	q25
SNP_A-2083391	G	G	342	26	281	49	10.99	9.00E-04	rs17605622	4	113839750	q25
SNP_A-1803955	A	A	265	95	316	74	5.896	0.0152	rs17615706	4	114133430	q25
SNP_A-1898770	T	T	292	88	334	64	6.194	1.28E-02	rs12503758	4	114206646	q25
SNP_A-2118399	A	A	257	67	308	36	13.347	3.00E-04	rs11930182	4	114267123	q25
SNP_A-1978548	G	G	259	97	292	76	4.328	3.75E-02	rs2352223	4	114268572	q25
SNP_A-1978550	T	T	309	29	287	61	12.047	5.00E-04	rs1532878	4	114285015	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960559	G	G	241	113	191	125	4.251	3.92E-02	rs2055656	4	114288318	q25
SNP_A-1795029	C	C	269	63	310	44	5.577	1.82E-02	rs17660801	4	114295742	q25
SNP_A-1884941	G	G	335	75	315	103	4.943	2.62E-02	rs6849033	4	114301938	q25
SNP_A-1922847	G	G	306	54	285	77	4.779	2.88E-02	rs6826293	4	114302057	q25
SNP_A-2210503	T	T	353	31	322	48	4.824	0.0281	rs7674202	4	114317233	q25
SNP_A-1827105	T	T	344	52	286	78	9.209	2.40E-03	rs11942005	4	114478764	q26
SNP_A-1834078	A	A	367	43	347	65	5.037	2.48E-02	rs29355	4	114567367	q26
SNP_A-2119867	C	C	346	14	377	5	4.944	2.62E-02	rs17531701	4	114869741	q26
SNP_A-2261036	A	A	309	47	333	25	7.614	5.80E-03	rs17593296	4	114977527	q26
SNP_A-1905642	T	T	321	45	321	27	4.049	4.42E-02	rs4141007	4	115037286	q26
SNP_A-1978587	T	T	238	152	195	181	6.542	1.05E-02	rs1112494	4	115433647	q26

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936442	G	G	243	163	216	204	5.933	0.0149	rs2055231	4	115438983	q26
SNP_A-1789375	A	A	251	165	216	204	6.726	9.50E-03	rs17484977	4	115439298	q26
SNP_A-1926648	C	C	230	120	202	150	5.142	2.33E-02	rs7685626	4	115468259	q26
SNP_A-2304419	C	C	228	156	200	194	5.83	1.58E-02	rs10019345	4	115547425	q26
SNP_A-1715143	C	C	257	89	278	64	4.886	2.71E-02	rs10516600	4	115610241	q26
SNP_A-1758819	T	T	230	164	205	197	4.373	3.65E-02	rs9307402	4	115628256	q26
SNP_A-2164325	C	C	202	186	237	143	8.328	3.90E-03	rs7656442	4	115654278	q26
SNP_A-1872115	A	A	265	131	228	160	5.586	1.81E-02	rs17624737	4	117081442	q26
SNP_A-2298432	A	A	327	61	298	84	4.947	2.61E-02	rs7376639	4	117117275	q26
SNP_A-1781032	A	A	253	107	182	120	7.308	6.90E-03	rs1588040	4	117442344	q26
SNP_A-2303754	A	A	290	56	218	68	5.721	1.68E-02	rs11098335	4	117519452	q26

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839392	C	C	401	9	386	20	4.439	3.51E-02	rs10428494	4	117584934	q26
SNP_A-1836439	C	C	302	80	333	51	7.928	4.90E-03	rs10008214	4	117827902	q26
SNP_A-1794753	G	G	317	35	270	48	4.084	4.33E-02	rs7657128	4	117944140	q26
SNP_A-2137759	A	G	204	184	215	165	6.448	0.0111	rs4833523	4	118005466	q26
SNP_A-2026529	A	C	183	173	201	153	4.769	2.90E-02	rs12499273	4	118019140	q26
SNP_A-2145730	A	G	190	172	204	156	6.059	0.0138	rs4834580	4	118031714	q26
SNP_A-1887032	G	C	194	172	210	168	5.455	0.0195	rs885245	4	118031943	q26
SNP_A-2075627	T	T	299	115	269	145	5.046	0.0247	rs4834583	4	118073986	q26
SNP_A-1822297	G	G	301	25	295	11	4.877	2.72E-02	rs1875302	4	118089894	q26
SNP_A-2223447	C	C	276	98	252	142	8.643	0.0033	rs17590084	4	118138105	q26
SNP_A-2152019	A	A	304	108	272	140	5.907	1.51E-02	rs17505748	4	118160277	q26

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2205564	T	T	277	91	314	70	4.717	2.99E-02	rs1371774	4	118219527	q26
SNP_A-1816190	G	G	305	107	275	135	4.787	0.0287	rs17590513	4	118226135	q26
SNP_A-2172096	G	G	286	54	322	38	4.346	3.71E-02	rs6840134	4	118248658	q26
SNP_A-1830138	G	C	195	177	194	148	5.969	0.0146	rs6842113	4	118249346	q26
SNP_A-2196834	A	A	344	30	373	17	4.436	3.52E-02	rs11734096	4	118289050	q26
SNP_A-1844512	T	T	287	115	252	140	4.598	3.20E-02	rs1036693	4	118313618	q26
SNP_A-1677610	C	C	294	100	274	138	6.373	1.16E-02	rs717904	4	118327701	q26
SNP_A-2136044	A	A	271	99	286	74	3.88	4.89E-02	rs9918053	4	118349705	q26
SNP_A-1978639	A	A	348	24	368	10	6.276	1.22E-02	rs11724737	4	118376111	q26
SNP_A-1756230	C	C	279	117	251	147	4.883	2.71E-02	rs10516634	4	118404075	q26
SNP_A-1936344	C	C	336	42	364	26	4.698	3.02E-02	rs1532108	4	118812113	q26

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2077698	C	C	344	70	363	47	5.013	0.0252	rs7677505	4	118966332	q26
SNP_A-1978646	C	C	208	202	246	170	5.89	0.0152	rs1459543	4	119007948	q26
SNP_A-2206310	C	C	209	161	238	128	5.628	0.0177	rs1870481	4	119020623	q26
SNP_A-1829512	T	T	214	178	255	147	6.416	1.13E-02	rs9307442	4	119022325	q26
SNP_A-1816699	G	G	329	33	343	13	8.938	0.0028	rs11562835	4	119025123	q26
SNP_A-2091227	C	C	224	190	264	154	7.027	8.00E-03	rs7695744	4	119028833	q26
SNP_A-1786668	A	A	357	51	373	25	9.123	2.50E-03	rs11562834	4	119034990	q26
SNP_A-1978648	G	G	217	177	246	138	6.518	1.07E-02	rs1023890	4	119059049	q26
SNP_A-2138089	T	T	352	48	378	24	8.921	0.0028	rs11562903	4	119072599	q26
SNP_A-1937289	A	A	296	44	315	27	4.655	0.031	rs11939867	4	119073409	q26
SNP_A-2156392	T	T	344	36	377	23	3.865	4.93E-02	rs7699060	4	119075163	q26

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1923023	G	G	221	189	255	151	6.656	9.90E-03	rs1350617	4	119084225	q26
SNP_A-1713458	C	C	203	197	244	168	5.889	0.0152	rs1459543	4	119109164	q26
SNP_A-1723664	G	G	203	197	242	168	5.599	1.80E-02	rs4269248	4	119109482	q26
SNP_A-1875605	A	A	360	46	382	30	3.977	4.61E-02	rs7670282	4	119120365	q26
SNP_A-2313589	G	G	385	15	398	6	4.053	0.0441	rs10021128	4	119347746	q26
SNP_A-1955541	A	A	395	11	404	2	6.332	1.19E-02	rs17049656	4	119472837	q26
SNP_A-2252891	G	G	412	4	406	14	5.581	1.82E-02	rs17049690	4	119511627	q26
SNP_A-1657536	T	T	333	29	351	13	6.563	0.0104	rs955753	4	120358558	q26
SNP_A-1868990	G	G	397	5	396	14	4.186	4.08E-02	rs6836195	4	121114293	q27
SNP_A-2296074	C	C	266	128	293	103	4.005	4.54E-02	rs13134800	4	121257885	q27
SNP_A-1978716	T	T	221	107	203	135	3.855	4.96E-02	rs10518343	4	121260404	q27
SNP_A-2273959	A	A	312	82	288	110	5.023	2.50E-02	rs6534171	4	121418375	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113422	A	A	219	103	255	85	3.971	4.63E-02	rs7377461	4	121504094	q27
SNP_A-2034670	A	A	195	163	229	133	5.745	1.65E-02	rs2662734	4	121518141	q27
SNP_A-2029565	G	G	229	155	267	123	6.549	1.05E-02	rs2662738	4	121525558	q27
SNP_A-1803978	A	A	279	117	309	93	4.229	3.97E-02	rs2715990	4	121526367	q27
SNP_A-2116228	C	C	354	24	344	46	6.872	8.80E-03	rs6838192	4	121528079	q27
SNP_A-2037257	G	G	250	158	285	129	5.177	0.0229	rs2662709	4	121553993	q27
SNP_A-1867253	A	G	192	174	198	148	6.686	9.70E-03	rs2715997	4	121561197	q27
SNP_A-2108054	C	C	236	94	270	58	10.805	0.001	rs2715996	4	121561914	q27
SNP_A-2093611	G	C	194	192	222	162	5.045	0.0247	rs2662732	4	121571257	q27
SNP_A-1936962	G	G	250	114	288	86	6.47	1.10E-02	rs2715958	4	121584080	q27
SNP_A-1697683	T	T	221	179	268	140	9.207	2.40E-03	rs2715953	4	121697307	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1727481	T	T	257	79	258	116	5.003	0.0253	rs950658	4	121728549	q27
SNP_A-2221723	C	C	247	95	271	63	7.499	6.20E-03	rs7697117	4	121754326	q27
SNP_A-1936401	T	T	266	134	277	89	7.81	5.20E-03	rs11098565	4	121758448	q27
SNP_A-1726962	C	C	324	76	309	103	4.252	3.92E-02	rs4088802	4	121924252	q27
SNP_A-2183234	A	A	216	102	248	76	5.949	0.0147	rs11729301	4	121974890	q27
SNP_A-1889260	A	A	268	96	311	71	6.505	1.08E-02	rs4532258	4	122294684	q27
SNP_A-2218634	C	C	234	144	256	116	3.955	4.67E-02	---	4	122317455	q27
SNP_A-1736249	G	G	370	30	395	17	4.236	3.96E-02	rs10518381	4	122492233	q27
SNP_A-2156573	C	C	218	190	263	151	8.627	0.0033	rs12647085	4	122556376	q27
SNP_A-1688474	G	G	360	10	381	3	4.106	4.27E-02	rs10518384	4	122558341	q27
SNP_A-2259084	G	G	394	0	397	7	6.887	8.70E-03	rs11947978	4	122577075	q27
SNP_A-1870222	T	C	172	168	202	148	4.78	2.88E-02	rs6855615	4	122591575	q27
SNP_A-1782354	G	G	319	97	295	123	4.006	0.0453	rs7688947	4	122655820	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1667904	C	C	274	124	253	155	4.158	4.14E-02	rs10518387	4	122724267	q27
SNP_A-2200710	C	C	385	5	396	0	5.109	2.38E-02	rs7686886	4	122813735	q27
SNP_A-2136889	G	G	351	27	379	13	5.721	1.68E-02	rs17442282	4	122867454	q27
SNP_A-2010122	T	T	292	106	318	82	4.167	4.12E-02	rs4833227	4	122908404	q27
SNP_A-2186517	C	C	374	28	359	45	4.261	0.039	rs10019865	4	122986160	q27
SNP_A-1823548	C	C	219	163	229	125	4.178	4.10E-02	rs4833769	4	123030575	q27
SNP_A-2245353	G	G	323	7	328	18	4.502	0.0339	rs6534324	4	123055488	q27
SNP_A-1916604	T	T	299	115	265	141	4.613	3.17E-02	rs9684454	4	123243089	q27
SNP_A-1978772	A	A	239	155	210	184	4.354	3.69E-02	rs10516617	4	123306302	q27
SNP_A-2073688	C	C	217	149	193	181	4.422	3.55E-02	rs10004294	4	123306657	q27
SNP_A-1739261	A	A	231	169	273	139	6.246	0.0124	rs1405483	4	123473044	q27
SNP_A-1685606	C	C	216	180	254	156	4.545	3.30E-02	rs3108397	4	123476955	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1904559	C	C	360	26	347	11	5.274	2.16E-02	rs2136425	4	124252190	q27
SNP_A-2043979	G	G	347	53	326	74	4.128	4.22E-02	rs7669991	4	124541855	q28.1
SNP_A-1824519	G	G	319	57	338	36	5.286	2.15E-02	rs7665722	4	124559106	q28.1
SNP_A-2171884	G	G	253	81	291	63	4.327	3.75E-02	rs4833891	4	124589059	q28.1
SNP_A-1906585	C	C	313	65	335	41	6.176	1.30E-02	rs12510460	4	124598542	q28.1
SNP_A-1978786	A	G	212	204	238	182	4.881	2.72E-02	rs10518414	4	124663414	q28.1
SNP_A-1922279	G	G	291	113	332	84	6.793	9.20E-03	rs10013957	4	124774267	q28.1
SNP_A-2273615	A	A	201	169	240	150	4.057	4.40E-02	rs10461205	4	124807753	q28.1
SNP_A-1670221	C	C	284	114	326	84	7.261	7.00E-03	rs896678	4	124875972	q28.1
SNP_A-1697847	T	T	235	145	297	113	10.07	0.0015	rs896676	4	124876171	q28.1
SNP_A-1685824	A	A	324	76	308	104	4.584	3.23E-02	rs9307531	4	125085668	q28.1
SNP_A-2170991	A	A	197	123	226	96	5.311	0.0212	rs3097903	4	125123936	q28.1
SNP_A-1747387	G	G	286	82	345	61	6.751	9.40E-03	rs986345	4	125253024	q28.1
SNP_A-1978800	C	C	384	0	398	4	3.84	5.00E-02	rs17007852	4	125444259	q28.1
SNP_A-2264931	G	G	376	6	346	18	6.816	9.00E-03	rs17758987	4	125494522	q28.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1648592	C	C	317	79	304	106	3.971	4.63E-02	rs720900	4	125527090	q28.1
SNP_A-1891754	T	T	273	97	218	110	4.466	3.46E-02	rs7691579	4	125690521	q28.1
SNP_A-1855325	C	C	280	100	266	136	5.236	2.21E-02	rs1567396	4	125923984	q28.1
SNP_A-1816816	T	T	328	50	302	72	5.019	2.51E-02	rs3733471	4	125949292	q28.1
SNP_A-1942118	C	C	374	10	381	1	7.423	6.40E-03	rs4645225	4	126368436	q28.1
SNP_A-1978829	A	A	342	20	343	7	6.06	0.0138	rs7676058	4	126628378	q28.1
SNP_A-2045346	G	G	377	29	398	14	5.758	1.64E-02	rs17009908	4	126796798	q28.1
SNP_A-1914106	G	G	408	6	392	0	5.724	0.0167	rs7682566	4	126814252	q28.1
SNP_A-2033449	T	T	330	62	343	27	13.391	3.00E-04	rs7656934	4	127163994	q28.1
SNP_A-2201119	C	C	336	72	365	53	3.967	4.64E-02	rs11932292	4	127165796	q28.1
SNP_A-1711640	A	A	328	72	355	51	4.608	3.18E-02	rs10518476	4	127270707	q28.1
SNP_A-1670001	G	G	314	42	340	26	4.661	0.0309	rs9307579	4	127271896	q28.1
SNP_A-2028795	C	C	375	23	384	10	5.208	2.25E-02	rs12642816	4	127277008	q28.1
SNP_A-2238810	A	A	304	34	331	17	6.67	9.80E-03	rs11098851	4	127334693	q28.1
SNP_A-2029382	C	C	283	97	255	123	4.525	3.34E-02	rs10013769	4	127433793	q28.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2272986	G	G	376	26	393	13	4.689	3.03E-02	rs11098878	4	127771857	q28.1
SNP_A-1978855	T	T	349	25	363	13	4.059	4.39E-02	rs17197343	4	127813102	q28.1
SNP_A-1694217	C	C	343	57	373	39	4.456	3.48E-02	rs1397676	4	127898830	q28.1
SNP_A-1647110	T	T	301	99	338	72	6.283	1.22E-02	rs1877169	4	127906961	q28.1
SNP_A-2074553	T	T	226	144	239	105	5.532	1.87E-02	rs313063	4	127978456	q28.1
SNP_A-1664902	G	G	261	139	294	116	3.914	4.79E-02	rs1160368	4	128011396	q28.1
SNP_A-2283402	G	G	285	103	230	124	6.272	0.0123	rs11722194	4	128048512	q28.1
SNP_A-2052115	G	G	407	5	416	0	5.079	2.42E-02	rs1822359	4	128617493	q28.1
SNP_A-1915922	G	G	323	55	329	31	6.318	0.012	rs4975235	4	129805562	q28.2
SNP_A-2228185	G	G	406	10	418	2	5.489	1.91E-02	rs17013510	4	129917117	q28.2
SNP_A-2113323	C	C	403	9	418	2	4.652	0.031	rs17013538	4	129939398	q28.2
SNP_A-1918836	C	C	220	168	250	120	9.493	2.10E-03	---	4	130744909	q28.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1876502	G	G	228	156	257	113	8.351	3.90E-03	rs7666727	4	130747970	q28.2
SNP_A-2060934	A	A	349	59	295	95	12.544	4.00E-04	rs587191	4	130771679	q28.2
SNP_A-1850139	T	T	353	63	309	109	15.222	9.56E-05	rs586814	4	130771748	q28.2
SNP_A-2289152	A	A	316	42	265	93	23.743	1.10E-06	rs679878	4	130772722	q28.2
SNP_A-2110019	C	C	321	27	270	54	12.56	4.00E-04	rs604759	4	130772897	q28.2
SNP_A-1951339	G	G	277	97	213	147	18.345	1.84E-05	rs618131	4	130789994	q28.2
SNP_A-2215160	G	G	293	119	237	179	17.979	0.00002234	rs619042	4	130806361	q28.2
SNP_A-2124192	C	T	200	192	228	170	5.473	1.93E-02	rs688455	4	130813873	q28.2
SNP_A-2165369	G	C	205	163	197	175	5.558	0.0184	rs661194	4	130824199	q28.2
SNP_A-1978909	C	C	309	49	350	30	6.47	1.10E-02	rs4864023	4	130832656	q28.2
SNP_A-1878908	C	C	351	31	367	17	4.435	3.52E-02	rs677114	4	130876875	q28.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2301023	A	A	310	98	279	129	5.865	0.0154	rs3106876	4	130892720	q28.2
SNP_A-2124949	T	T	355	37	366	22	3.961	4.66E-02	rs594497	4	130896159	q28.2
SNP_A-1660059	T	A	204	196	239	173	6.624	0.0101	rs642218	4	130911897	q28.2
SNP_A-1809492	A	T	189	151	196	138	13.738	2.00E-04	rs1491150	4	130920480	q28.2
SNP_A-1735765	G	C	215	183	231	181	8.245	4.10E-03	rs2391475	4	131017593	q28.2
SNP_A-1724602	C	C	372	8	404	2	4.064	4.38E-02	rs10518559	4	131388281	q28.2
SNP_A-1808289	A	A	280	58	301	35	6.441	0.0111	rs17050898	4	131485443	q28.2
SNP_A-1949167	G	G	410	4	407	13	4.733	2.96E-02	rs4406035	4	131569389	q28.3
SNP_A-2148926	A	A	261	125	246	158	3.884	4.88E-02	rs7680226	4	131607241	q28.3
SNP_A-1666900	T	T	265	133	245	167	4.397	3.60E-02	rs9307625	4	131701648	q28.3
SNP_A-1812433	G	G	309	77	275	105	6.241	1.25E-02	rs6534808	4	131925835	q28.3
SNP_A-2148161	C	C	312	76	284	102	5.108	2.38E-02	rs17424760	4	131965553	q28.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2262394	A	A	280	78	241	95	3.896	4.84E-02	rs7674705	4	131969288	q28.3
SNP_A-1805787	C	C	410	4	414	0	4.019	4.50E-02	rs1904085	4	132084738	q28.3
SNP_A-1744549	A	A	306	88	285	121	5.778	1.62E-02	rs306388	4	132174300	q28.3
SNP_A-1829393	A	A	391	19	369	41	8.704	3.20E-03	rs4864029	4	132382089	q28.3
SNP_A-2120963	T	T	392	24	377	43	5.662	1.73E-02	rs9884172	4	132412581	q28.3
SNP_A-2031756	C	C	398	12	410	4	4.159	4.14E-02	rs10018289	4	132578752	q28.3
SNP_A-1860478	T	T	387	15	403	5	5.28	2.16E-02	rs12711166	4	132595478	q28.3
SNP_A-1934763	A	A	376	14	387	5	4.417	0.0356	rs1343670	4	132641678	q28.3
SNP_A-2264559	G	G	383	7	399	1	4.702	3.01E-02	rs11945624	4	132688352	q28.3
SNP_A-2074214	C	C	326	56	344	38	3.93	4.74E-02	rs7663583	4	132852930	q28.3
SNP_A-2091038	A	A	346	38	340	58	3.97	4.63E-02	rs989974	4	132913792	q28.3
SNP_A-1698831	T	T	261	125	241	161	5.005	0.0253	rs348085	4	133586473	q28.3
SNP_A-2140473	G	G	237	93	246	66	4.251	3.92E-02	rs1499348	4	133711135	q28.3
SNP_A-1896882	A	A	240	168	277	133	6.713	9.60E-03	rs12508742	4	134871823	q28.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1826279	G	G	231	167	271	131	7.516	6.10E-03	rs6822985	4	134875998	q28.3
SNP_A-1953483	G	G	231	163	271	127	7.636	5.70E-03	---	4	134876145	q28.3
SNP_A-2166999	C	C	209	131	241	79	14.559	0.0001	rs2713294	4	134890696	q28.3
SNP_A-1860721	G	G	243	171	279	139	5.767	1.63E-02	rs2660720	4	134925563	q28.3
SNP_A-1934168	A	A	244	168	282	136	6.071	0.0137	rs2660719	4	134925592	q28.3
SNP_A-1952465	C	C	234	166	279	135	6.901	0.0086	rs2246872	4	134926084	q28.3
SNP_A-1814787	G	G	223	157	266	126	6.992	8.20E-03	rs1567176	4	134936433	q28.3
SNP_A-2126411	T	T	230	170	260	122	9.318	0.0023	rs1567174	4	134936900	q28.3
SNP_A-2088255	T	T	193	153	219	115	6.819	9.00E-03	rs2713265	4	134957382	q28.3
SNP_A-1717433	A	A	232	166	272	140	5.143	2.33E-02	rs925084	4	134989207	q28.3
SNP_A-1716065	C	C	237	163	278	130	6.902	0.0086	rs2660727	4	135013676	q28.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1739469	C	C	230	162	274	136	5.709	1.69E-02	rs2724261	4	135030348	q28.3
SNP_A-1695039	A	A	275	115	312	94	4.122	4.23E-02	rs7671017	4	135078405	q28.3
SNP_A-1688004	C	C	277	115	315	91	4.991	2.55E-02	rs2660693	4	135078432	q28.3
SNP_A-2175969	C	G	215	165	205	173	8.866	2.90E-03	rs4426842	4	135806242	q28.3
SNP_A-1813894	G	T	222	180	223	171	11.127	9.00E-04	rs10021834	4	135806866	q28.3
SNP_A-2010169	A	A	318	62	297	87	4.891	0.027	rs6535027	4	135838715	q28.3
SNP_A-1918642	A	A	246	118	189	135	6.307	0.012	rs6833325	4	135858342	q28.3
SNP_A-2214691	C	C	348	30	319	45	3.998	4.56E-02	rs17573425	4	136125829	q28.3
SNP_A-1918502	A	A	307	69	330	50	3.843	5.00E-02	rs13137701	4	136187041	q28.3
SNP_A-1803685	T	T	297	91	326	70	4.008	0.0453	rs10049821	4	136192778	q28.3
SNP_A-2060799	G	G	274	94	305	69	5.446	1.96E-02	rs4470695	4	136220509	q28.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1692788	A	G	218	178	211	189	4.846	2.77E-02	rs1354757	4	136235653	q28.3
SNP_A-1887154	A	A	325	5	312	0	4.764	2.91E-02	rs4505882	4	136303617	q28.3
SNP_A-2093566	G	G	373	1	315	7	5.535	1.86E-02	rs4342240	4	136306060	q28.3
SNP_A-2125175	T	T	306	106	275	139	6.094	1.36E-02	rs7685386	4	137931184	q28.3
SNP_A-1797092	G	G	293	101	334	74	6.604	1.02E-02	rs994912	4	138192572	q28.3
SNP_A-2140281	T	T	270	90	303	67	5.134	0.0235	rs17049140	4	138203229	q28.3
SNP_A-1979057	C	C	260	144	294	118	4.589	3.22E-02	rs10519404	4	138233054	q28.3
SNP_A-2296713	T	T	285	121	323	93	5.918	1.50E-02	rs17049170	4	138235668	q28.3
SNP_A-1827300	G	G	357	55	365	35	4.357	3.69E-02	rs9685021	4	138772968	q28.3
SNP_A-1817831	C	C	344	4	312	12	4.71	3.00E-02	rs652302	4	139617710	q28.3
SNP_A-1903937	C	C	345	59	361	39	4.424	3.54E-02	rs298468	4	139620752	q28.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2312894	C	C	322	26	312	42	3.871	4.91E-02	rs17246587	4	139759977	q28.3
SNP_A-1955649	T	T	341	33	335	13	7.823	5.20E-03	---	4	139798051	q28.3
SNP_A-2187759	A	A	270	130	245	165	5.243	2.20E-02	rs6828351	4	139921603	q31.1
SNP_A-2071376	G	G	280	136	254	166	4.227	3.98E-02	rs11721545	4	139925126	q31.1
SNP_A-2129429	C	C	279	117	303	91	4.235	3.96E-02	rs4863589	4	139977630	q31.1
SNP_A-2194070	T	T	335	5	344	0	5.096	0.024	rs26049 17	4	141118059	q31.1
SNP_A-1925801	C	C	406	8	399	19	4.523	3.34E-02	rs17005641	4	141510262	q31.1
SNP_A-2117133	G	G	368	14	358	34	8.343	3.90E-03	rs3851422	4	141858000	q31.21
SNP_A-2083488	G	G	181	151	203	105	8.638	0.0033	rs3796700	4	142145574	q31.21
SNP_A-1845529	C	C	305	93	281	125	5.601	1.79E-02	rs982136	4	142156265	q31.21
SNP_A-2189167	A	A	373	33	361	53	4.77	2.90E-02	rs17338203	4	142189785	q31.21
SNP_A-2214943	C	C	191	177	200	122	7.29	6.90E-03	rs13111885	4	142192278	q31.21
SNP_A-2153898	G	G	307	99	337	65	8.427	3.70E-03	rs9991795	4	142322763	q31.21
SNP_A-1979172	A	A	342	54	366	34	5.339	2.09E-02	rs10510579	4	142327116	q31.21
SNP_A-1715521	T	T	250	146	277	119	4.134	4.20E-02	rs10519595	4	142783142	q31.21
SNP_A-2077982	C	C	339	5	357	17	5.768	1.63E-02	rs1389102	4	143036252	q31.21
SNP_A-1908772	C	C	249	119	256	74	8.546	3.50E-03	rs1604243	4	143222524	q31.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2157614	C	C	257	131	266	98	4.149	4.17E-02	rs11100738	4	143241746	q31.21
SNP_A-1979206	G	G	350	16	342	6	4.187	0.0407	rs1846843	4	143277337	q31.21
SNP_A-2301007	C	C	404	2	403	9	4.412	3.57E-02	rs336340	4	143317506	q31.21
SNP_A-2114822	A	A	316	50	279	79	8.733	3.10E-03	rs3775657	4	143409285	q31.21
SNP_A-2300529	T	T	330	32	313	49	4.017	4.50E-02	rs17705389	4	143490256	q31.21
SNP_A-1979227	G	G	328	12	320	24	4.076	4.35E-02	rs10519659	4	143692662	q31.21
SNP_A-1979231	G	G	319	61	328	38	5.208	2.25E-02	rs10519649	4	143812158	q31.21
SNP_A-1710950	A	A	368	32	361	51	4.24	0.0395	rs10519642	4	143820777	q31.21
SNP_A-1979236	G	G	310	34	326	18	5.326	2.10E-02	rs1443190	4	143910638	q31.21
SNP_A-2247541	A	A	334	58	320	82	4.289	3.84E-02	rs11100790	4	144800216	q31.21
SNP_A-2126297	G	A	209	145	178	174	6.564	0.0104	rs7685063	4	144800955	q31.21
SNP_A-1979259	A	A	409	7	419	1	4.602	3.19E-02	rs17017982	4	144908745	q31.21
SNP_A-2094289	T	T	350	6	350	0	5.949	0.0147	rs6537195	4	145115809	q31.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187687	C	C	270	142	242	172	4.393	0.0361	rs4240360	4	145482997	q31.21
SNP_A-2234104	A	A	220	158	200	196	4.615	3.17E-02	rs7689179	4	145553254	q31.21
SNP_A-2255188	A	G	209	175	197	173	4.435	3.52E-02	rs7681225	4	145561136	q31.21
SNP_A-1872019	A	G	216	178	209	185	4.88	2.72E-02	rs7681569	4	145561245	q31.21
SNP_A-2080173	C	C	272	34	263	59	6.468	1.10E-02	rs6537278	4	145615544	q31.21
SNP_A-2221666	C	C	269	115	290	88	4.333	3.74E-02	rs17019340	4	145691368	q31.21
SNP_A-2036195	T	T	340	52	344	30	5.506	0.019	rs11938704	4	145800975	q31.21
SNP_A-1979279	C	T	225	157	193	185	7.584	5.90E-03	rs1512285	4	145808564	q31.21
SNP_A-1939405	T	T	216	156	248	124	5.864	0.0155	rs13147758	4	145817835	q31.21
SNP_A-1900252	A	A	217	167	252	128	7.747	5.40E-03	rs1828591	4	145838385	q31.21
SNP_A-2053930	C	C	237	179	273	147	5.663	1.73E-02	rs1980057	4	145843343	q31.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2222758	A	A	233	177	267	143	5.924	0.0149	rs7655625	4	145843520	q31.21
SNP_A-1704941	A	C	231	167	210	202	6.607	1.02E-02	rs4834986	4	146056404	q31.21
SNP_A-1979284	G	A	207	151	181	173	5.731	0.0167	rs789350	4	146225930	q31.21
SNP_A-2084450	A	A	233	125	201	153	5.157	2.31E-02	rs6537336	4	146537244	q31.21
SNP_A-2055856	T	T	352	40	379	25	4.279	3.86E-02	rs17727691	4	146561555	q31.21
SNP_A-2150141	A	A	289	115	256	140	4.37	3.66E-02	rs11731479	4	146628353	q31.21
SNP_A-1929006	G	G	386	0	352	6	6.522	1.07E-02	rs525600	4	146716030	q31.21
SNP_A-2213433	G	G	366	10	387	3	4.1	4.29E-02	rs4074113	4	147009085	q31.21
SNP_A-2010227	T	T	273	87	234	114	6.425	1.13E-02	rs3815967	4	147460077	q31.22
SNP_A-2292576	G	G	241	79	219	113	6.854	8.80E-03	rs9308199	4	147460467	q31.22
SNP_A-1831327	T	T	267	83	247	113	5.23	2.22E-02	rs17757522	4	147461344	q31.22
SNP_A-1845204	A	A	297	93	261	121	5.904	1.51E-02	rs919483	4	147461868	q31.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944716	A	A	301	87	268	108	3.988	0.0458	rs6824313	4	147473999	q31.22
SNP_A-1979310	T	T	277	67	260	90	3.856	4.96E-02	rs891382	4	147509945	q31.22
SNP_A-2144482	A	A	246	76	248	112	4.799	2.85E-02	rs4835295	4	147606501	q31.22
SNP_A-1874276	T	T	307	91	289	119	4.154	4.15E-02	rs7670877	4	147654172	q31.22
SNP_A-2183458	C	C	288	68	268	96	5.412	0.02	rs11100926	4	147770008	q31.22
SNP_A-2260380	A	A	275	63	267	91	4.638	3.13E-02	rs4835316	4	147791250	q31.22
SNP_A-2176768	C	C	356	28	328	46	5.394	2.02E-02	rs2102251	4	147824663	q31.22
SNP_A-1881026	T	T	352	46	356	28	4.152	4.16E-02	rs9996620	4	147830919	q31.22
SNP_A-1850764	T	T	362	6	395	1	3.989	0.0458	rs17021632	4	147890797	q31.22
SNP_A-2310014	C	C	315	27	339	15	4.104	4.28E-02	rs1979904	4	147906648	q31.22
SNP_A-1911121	G	G	317	61	291	83	4.452	0.0349	rs17021755	4	147938243	q31.22
SNP_A-2113350	T	T	278	96	234	122	6.442	0.0111	rs1816596	4	148222710	q31.22
SNP_A-1931981	T	T	273	113	244	140	4.503	3.38E-02	rs7660168	4	148280771	q31.22
SNP_A-2096106	G	G	373	25	396	8	9.401	2.20E-03	rs6817074	4	148297766	q31.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1785181	C	C	378	6	373	15	3.87	4.92E-02	rs1370300	4	148299085	q31.22
SNP_A-2285575	G	G	363	13	386	2	8.587	3.40E-03	rs17022322	4	148303926	q31.22
SNP_A-2262937	G	G	383	27	405	11	7.308	6.90E-03	rs3747684	4	148305292	q31.22
SNP_A-2292590	A	A	389	25	409	11	5.903	1.51E-02	rs3747686	4	148307417	q31.22
SNP_A-2305061	A	A	338	24	386	10	7.437	6.40E-03	rs3747687	4	148307448	q31.22
SNP_A-2151162	A	A	382	26	404	10	7.684	5.60E-03	rs17022364	4	148317260	q31.22
SNP_A-2250025	G	G	371	25	395	9	8.202	4.20E-03	rs17022369	4	148317310	q31.22
SNP_A-2240553	T	T	334	16	364	4	8.043	4.60E-03	rs11734148	4	148322538	q31.22
SNP_A-2152750	G	G	314	38	325	23	3.855	4.96E-02	rs17022415	4	148332517	q31.22
SNP_A-2240061	G	G	307	21	295	7	6.177	0.0129	rs11737107	4	148617357	q31.22
SNP_A-1979340	C	C	381	11	403	3	4.945	2.62E-02	rs1429138	4	148639947	q31.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2279445	A	A	242	172	280	138	6.476	0.0109	rs10028838	4	146828937	q31.23
SNP_A-2231622	A	A	228	160	262	126	6.401	0.0114	rs11734418	4	148830058	q31.23
SNP_A-2058266	C	C	231	79	272	62	4.503	3.38E-02	rs12647366	4	148834828	q31.23
SNP_A-1832620	T	T	191	181	224	140	7.775	0.0053	rs1914331	4	148857781	q31.23
SNP_A-2089220	A	A	198	126	170	148	3.841	5.00E-02	rs12643170	4	149285977	q31.23
SNP_A-1874779	C	C	328	34	332	14	8	4.70E-03	rs17484259	4	149542639	q31.23
SNP_A-1979369	G	G	302	24	319	45	4.778	2.88E-02	rs10519958	4	149670174	q31.23
SNP_A-1900941	T	T	389	5	379	21	9.932	1.60E-03	rs13142486	4	149743007	q31.23
SNP_A-1979382	T	T	303	39	295	63	5.391	2.02E-02	rs17583738	4	150048269	q31.23
SNP_A-1684618	G	G	323	77	354	56	4.613	3.17E-02	rs549653	4	150270124	q31.23
SNP_A-1683236	T	T	347	53	329	83	6.921	8.50E-03	rs951219	4	150280595	q31.23
SNP_A-1737089	G	G	321	79	355	57	5.093	0.024	rs506729	4	150280769	q31.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2156367	A	T	216	178	209	191	3.974	4.62E-02	rs6851434	4	150306931	q31.23
SNP_A-1708983	A	A	315	79	289	121	9.625	0.0019	rs2520488	4	150487578	q31.23
SNP_A-1824138	T	T	325	89	351	65	4.735	2.95E-02	rs10010177	4	151071471	q31.23
SNP_A-2094799	A	A	334	62	352	42	4.313	0.0378	rs12643201	4	151190556	q31.23
SNP_A-1926034	T	T	346	20	360	8	5.415	0.02	rs1960919	4	151579752	q31.23
SNP_A-2026312	G	G	359	29	358	12	6.626	0.01	rs11099777	4	152132864	q31.3
SNP_A-2273365	G	T	226	166	207	187	8.184	4.20E-03	rs1316858	4	152556336	q31.3
SNP_A-2169288	A	A	199	183	215	147	4.011	4.52E-02	rs11734518	4	152570718	q31.3
SNP_A-1979416	C	C	377	25	366	42	4.432	3.53E-02	rs907238	4	152980890	q31.3
SNP_A-2120517	G	G	301	107	332	80	5.397	2.02E-02	rs361195	4	153120626	q31.3
SNP_A-2028622	C	C	298	108	327	77	6.535	0.0106	rs361197	4	153121161	q31.3
SNP_A-2220555	T	T	352	32	351	17	4.255	3.91E-02	rs17028413	4	153304982	q31.3
SNP_A-1664072	G	G	289	111	328	84	6.028	0.0141	rs361192	4	153339699	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187547	A	A	363	21	349	9	4.169	4.12E-02	rs17028529	4	153345467	q31.3
SNP_A-1732606	A	A	349	9	342	20	4.221	3.99E-02	rs901207	4	153381767	q31.3
SNP_A-2178583	A	A	242	100	294	84	4.648	3.11E-02	rs11736628	4	153411965	q31.3
SNP_A-1661836	G	G	349	43	349	25	4.344	3.71E-02	rs6837953	4	154508590	q31.3
SNP_A-2134839	G	G	253	127	272	92	5.94	1.48E-02	rs1371156	4	154874344	q31.3
SNP_A-2010265	C	C	252	88	293	71	4.089	4.32E-02	rs2606328	4	155011469	q31.3
SNP_A-2036290	C	C	297	107	313	75	5.725	0.0167	rs17298985	4	155021866	q31.3
SNP_A-1874976	C	C	272	98	305	63	9.491	2.10E-03	rs17030437	4	155061830	q31.3
SNP_A-1930330	A	A	209	111	250	88	5.833	1.57E-02	rs872453	4	155084736	q31.3
SNP_A-1961294	C	C	279	119	315	87	7.133	0.0076	rs1020704	4	155094099	q31.3
SNP_A-2268978	C	C	272	106	308	86	3.988	0.0458	rs10376647	4	155095596	q31.3
SNP_A-1794694	C	C	288	122	316	90	6.109	0.0135	rs1456397	4	155102159	q31.3
SNP_A-2058051	T	T	261	121	299	91	6.742	9.40E-03	rs1350189	4	155102556	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1902186	T	T	251	123	272	96	4.124	4.23E-02	rs4434231	4	155103898	q31.3
SNP_A-2094396	C	C	287	119	317	89	5.817	1.59E-02	rs1037652	4	155104170	q31.3
SNP_A-1891201	G	G	287	125	312	98	4.308	3.79E-02	rs4525952	4	155104211	q31.3
SNP_A-1860868	C	C	280	106	313	85	3.963	0.0465	rs897608	4	155112565	q31.3
SNP_A-1850369	T	C	210	164	172	156	5.166	0.023	rs13131753	4	155604173	q31.3
SNP_A-1979478	G	G	300	52	283	29	4.634	3.13E-02	rs10517594	4	155757047	q31.3
SNP_A-2200788	C	C	314	96	341	73	4.224	3.99E-02	rs2227424	4	155850325	q31.3
SNP_A-2209400	G	G	301	97	325	73	4.308	3.79E-02	rs2227426	4	155850776	q31.3
SNP_A-1926211	T	T	262	118	230	148	5.46	0.0195	rs2124660	4	156314606	q32.1
SNP_A-2120984	G	G	244	148	218	176	3.878	4.89E-02	rs10085000	4	156324836	q32.1
SNP_A-1979503	C	C	354	60	379	37	6.301	0.0121	rs17032814	4	156596695	q32.1
SNP_A-2235011	A	G	187	165	201	147	8.309	3.90E-03	rs10002012	4	156694908	q32.1
SNP_A-2225793	A	A	328	80	361	53	7.018	8.10E-03	rs17033050	4	156759298	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2203273	G	G	269	139	284	106	4.448	0.0349	rs908592	4	156810924	q32.1
SNP_A-1979509	A	A	280	64	317	43	6.054	1.39E-02	rs1466515	4	156872484	q32.1
SNP_A-1853971	T	T	334	68	318	92	3.914	4.79E-02	rs10032771	4	157099463	q32.1
SNP_A-1901997	G	G	369	39	342	62	6.243	1.25E-02	rs1841273	4	157101133	q32.1
SNP_A-2248979	G	G	346	26	371	13	5.016	2.51E-02	rs10029718	4	157274095	q32.1
SNP_A-2163651	C	C	402	14	413	5	4.407	3.58E-02	rs4277734	4	157274149	q32.1
SNP_A-1945847	G	G	364	52	394	26	9.835	1.70E-03	rs4579068	4	157364588	q32.1
SNP_A-1979519	C	C	291	71	245	97	7.409	6.50E-03	rs4286588	4	157447310	q32.1
SNP_A-1979520	A	A	309	97	277	137	8.508	3.50E-03	rs4260587	4	157447550	q32.1
SNP_A-2159090	T	T	307	101	276	134	6.278	1.22E-02	rs12511271	4	157462293	q32.1
SNP_A-1667330	C	C	347	53	324	88	9.301	0.0023	rs6852748	4	157471519	q32.1
SNP_A-1752133	G	G	330	66	303	103	9.129	2.50E-03	rs2879979	4	157688383	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1979527	C	C	325	19	336	6	6.937	8.40E-03	rs11734801	4	157699484	q32.1
SNP_A-1979531	T	T	236	152	203	179	4.637	3.13E-02	rs1554472	4	157847511	q32.1
SNP_A-1799905	C	C	195	175	230	144	5.874	0.0154	rs1608012	4	157850191	q32.1
SNP_A-1979532	T	T	185	157	212	132	3.993	4.57E-02	rs1521701	4	157854658	q32.1
SNP_A-1782755	C	C	193	149	232	122	6.064	0.0138	rs13137613	4	157858443	q32.1
SNP_A-2265305	T	T	331	71	353	49	4.741	2.95E-02	rs17035257	4	158072667	q32.1
SNP_A-1979543	A	A	383	27	374	46	4.932	0.0264	rs17035367	4	158143830	q32.1
SNP_A-2205859	C	C	380	36	399	21	4.392	0.0361	rs17035412	4	158172031	q32.1
SNP_A-2135308	A	A	317	79	293	103	4.109	4.27E-02	rs9995432	4	158934920	q32.1
SNP_A-1979572	T	T	229	143	189	167	5.337	2.09E-02	---	4	158997272	q32.1
SNP_A-1736757	C	C	300	30	299	63	10.254	0.0014	rs4314333	4	159226316	q32.1
SNP_A-1937896	C	C	379	7	385	17	3.891	4.86E-02	rs4690903	4	159680886	q32.1
SNP_A-2206727	C	C	332	0	335	5	4.919	2.66E-02	rs17037755	4	160217535	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1928892	A	A	222	128	237	95	4.902	2.68E-02	rs17223094	4	160271837	q32.1
SNP_A-2086581	T	T	209	139	178	168	5.217	0.0224	rs10017696	4	160571639	q32.1
SNP_A-2296355	A	A	249	157	215	185	4.739	2.95E-02	rs6816396	4	160597050	q32.1
SNP_A-1823615	T	T	301	89	316	62	5.006	0.0253	rs3856996	4	160737809	q32.1
SNP_A-1979599	C	C	245	65	277	47	4.548	3.30E-02	rs2699011	4	160740636	q32.1
SNP_A-1979600	C	C	261	101	267	73	3.888	4.86E-02	rs4035044	4	160740654	q32.1
SNP_A-1952349	G	G	286	108	312	84	4.125	4.22E-02	rs12499551	4	160746186	q32.1
SNP_A-2310280	T	T	286	120	312	94	4.289	3.84E-02	rs4260489	4	160748296	q32.1
SNP_A-1892449	G	G	371	7	357	17	4.415	0.0356	rs1986853	4	160831363	q32.1
SNP_A-2240024	T	T	392	0	371	9	9.394	2.20E-03	rs1304931	4	160952221	q32.1
SNP_A-1758426	G	G	221	171	255	141	5.293	2.14E-02	rs1986432	4	161469838	q32.1
SNP_A-1888424	G	G	190	148	217	117	5.394	2.02E-02	rs17039386	4	161517238	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1979619	C	C	257	99	275	73	4.449	0.0349	rs2028323	4	161665972	q32.1
SNP_A-1979620	C	C	210	196	242	166	4.747	2.94E-02	rs6536518	4	161666028	q32.1
SNP_A-2194015	C	C	221	193	253	163	4.684	3.05E-02	rs1371251	4	161739087	q32.1
SNP_A-1937251	A	A	233	163	263	137	4.048	4.42E-02	rs6847416	4	161749255	q32.1
SNP_A-2067376	G	G	241	165	268	132	5.055	0.0246	rs6827941	4	161757139	q32.1
SNP_A-2227662	C	C	241	173	271	147	3.851	4.97E-02	rs6827968	4	161757257	q32.1
SNP_A-2063220	G	A	206	200	239	171	6.695	9.70E-03	rs17334496	4	161776681	q32.1
SNP_A-2171394	G	A	204	202	239	159	8.604	3.40E-03	rs2882364	4	161780370	q32.1
SNP_A-2262341	A	A	242	170	274	144	4.094	4.30E-02	rs7375971	4	161786730	q32.1
SNP_A-1853835	A	A	216	152	246	120	5.707	1.69E-02	rs12509599	4	161786996	q32.1
SNP_A-2043738	A	A	299	95	326	60	8.989	2.70E-03	rs17039649	4	161801331	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2211402	C	C	308	84	347	55	8.248	4.10E-03	rs2083306	4	161819282	q32.1
SNP_A-2151424	G	G	211	155	245	125	5.728	0.0167	rs7697236	4	161842776	q32.1
SNP_A-2268762	T	T	233	167	273	141	5.118	2.37E-02	rs17039884	4	161895895	q32.1
SNP_A-1689847	A	G	201	199	237	171	5.653	1.74E-02	rs10517718	4	161972498	q32.1
SNP_A-2059874	C	C	308	60	320	32	8.4	0.0038	rs1439263	4	162313055	q32.2
SNP_A-2313928	G	G	270	74	247	101	5.166	0.023	rs17375482	4	162370002	q32.2
SNP_A-2261144	A	A	219	139	182	176	7.76	0.0053	rs934932	4	162377768	q32.2
SNP_A-2264858	C	C	250	148	208	176	6.023	0.0141	rs4691732	4	162381057	q32.2
SNP_A-1979644	G	G	285	127	318	100	4.974	2.57E-02	rs10517742	4	162559877	q32.2
SNP_A-1729472	C	C	350	48	342	70	3.953	4.68E-02	rs6825391	4	162584451	q32.2
SNP_A-1731507	A	A	249	151	225	187	4.873	2.73E-02	rs4505772	4	162591676	q32.2
SNP_A-1718795	T	T	249	151	225	187	4.873	2.73E-02	rs4446269	4	162592086	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2203980	C	C	310	104	270	144	9.21	2.40E-03	rs7438099	4	162622377	q32.2
SNP_A-2293793	G	G	282	74	227	93	6.205	1.27E-02	rs7689071	4	162624807	q32.2
SNP_A-1826861	G	G	284	90	257	113	3.932	4.74E-02	rs10028311	4	162872913	q32.2
SNP_A-1920160	G	G	321	69	276	96	7.389	0.0066	rs6814878	4	163109094	q32.2
SNP_A-1961349	A	A	357	59	322	96	10.632	1.10E-03	rs10016003	4	163139887	q32.2
SNP_A-1979658	T	T	224	168	253	131	6.26	0.0124	rs359512	4	163238692	q32.2
SNP_A-2207773	T	T	299	25	268	46	7.751	5.40E-03	rs7674343	4	163261320	q32.2
SNP_A-1803109	C	C	309	39	268	60	6.782	9.20E-03	rs7675218	4	163261599	q32.2
SNP_A-2089999	T	T	328	40	296	62	6.25	0.0124	rs1483549	4	163262544	q32.2
SNP_A-1847155	T	T	308	40	268	62	7.05	7.90E-03	rs10031685	4	163262593	q32.2
SNP_A-1659168	G	G	373	27	364	48	5.814	1.59E-02	rs10517754	4	163358622	q32.2
SNP_A-2250529	G	G	281	77	240	94	4.089	4.32E-02	rs12505723	4	163416935	q32.2
SNP_A-2213297	T	C	219	177	203	187	4.256	3.91E-02	rs4533716	4	163600849	q32.2
SNP_A-1802363	A	A	268	82	270	54	4.776	2.89E-02	rs1993022	4	163628730	q32.2
SNP_A-2214971	C	C	391	15	379	31	5.733	0.0167	rs2597467	4	163660909	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1952603	C	C	301	75	290	48	4.121	0.0424	rs1870600	4	163786514	q32.2
SNP_A-1872054	C	C	332	26	329	13	3.983	4.60E-02	rs11100490	4	164610444	q32.2
SNP_A-1925016	A	A	286	66	330	48	5.065	2.44E-02	rs7442072	4	164662468	q32.2
SNP_A-2034079	A	A	304	84	345	63	5.091	0.0241	rs6852899	4	164695632	q32.2
SNP_A-2141379	C	C	376	16	364	36	7.807	5.20E-03	rs17473073	4	164818250	q32.2
SNP_A-1851651	G	G	400	14	393	27	4.141	0.0419	rs17657444	4	164885188	q32.2
SNP_A-1682272	T	T	303	95	341	69	6.187	0.0129	rs1441716	4	164902691	q32.2
SNP_A-2136471	G	G	353	11	350	24	4.707	3.00E-02	rs12641183	4	164917106	q32.3
SNP_A-2147845	A	A	308	48	302	28	4.343	3.72E-02	rs4507321	4	165301439	q32.3
SNP_A-1841356	G	G	345	57	361	37	4.598	3.20E-02	rs6536779	4	165329767	q32.3
SNP_A-2039952	T	T	368	4	374	0	4.043	4.44E-02	rs10012260	4	165685593	q32.3
SNP_A-1837295	A	A	279	77	315	51	7.326	6.80E-03	rs11724553	4	166080024	q32.3
SNP_A-1828545	A	A	269	93	284	62	6.248	0.0124	rs11939248	4	166080626	q32.3
SNP_A-2220812	T	T	360	34	386	20	4.357	3.69E-02	rs6837162	4	166344151	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289739	C	C	195	159	205	107	7.798	5.20E-03	rs4328874	4	166796256	q32.3
SNP_A-1877859	C	C	409	7	419	1	4.602	3.19E-02	rs17046756	4	166849169	q32.3
SNP_A-1979766	T	T	341	33	350	56	4.756	0.0292	rs17046758	4	166854991	q32.3
SNP_A-2291544	A	A	343	27	328	48	6.167	1.30E-02	rs6536921	4	166859001	q32.3
SNP_A-1844856	A	A	264	82	218	102	5.557	0.0184	rs1870478	4	166962968	q32.3
SNP_A-2264745	-	G	152	152	205	123	10.03	0.0015	rs2322443	4	167155265	q32.3
SNP_A-1979789	A	A	389	5	376	0	4.803	2.84E-02	rs17047389	4	167513330	q32.3
SNP_A-2282983	C	C	372	12	376	2	7.117	0.0076	rs7677325	4	167534706	q32.3
SNP_A-1939413	G	G	351	63	367	39	5.926	0.0149	rs382628	4	167537186	q32.3
SNP_A-1979792	G	G	377	29	393	15	4.782	2.88E-02	rs366220	4	167566064	q32.3
SNP_A-1787583	G	G	376	20	394	8	5.519	1.88E-02	rs423541	4	167579170	q32.3
SNP_A-2072761	C	C	267	71	284	50	4.145	4.17E-02	rs11944903	4	167579682	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1891455	C	C	304	102	337	75	5.774	1.63E-02	rs11100647	4	167706437	q32.3
SNP_A-1664304	G	G	371	27	395	15	4.003	4.54E-02	rs391309	4	167779569	q32.3
SNP_A-1756991	G	G	373	27	397	15	4	4.55E-02	rs453042	4	167782709	q32.3
SNP_A-1659502	G	G	373	27	397	15	4	4.55E-02	rs418488	4	167783233	q32.3
SNP_A-1665644	T	T	368	30	396	16	5.047	0.0247	rs411699	4	167783321	q32.3
SNP_A-2196833	C	C	343	17	338	6	4.936	0.0263	rs17519960	4	168101915	q32.3
SNP_A-1957604	T	T	369	35	330	56	6.615	0.0101	rs2703840	4	168278223	q32.3
SNP_A-1695723	T	T	365	35	351	59	6.279	1.22E-02	rs2703843	4	168612794	q32.3
SNP_A-2245366	G	G	384	32	402	16	5.741	0.0166	rs17647174	4	168635041	q32.3
SNP_A-1841266	G	G	331	71	345	45	5.937	1.48E-02	rs2319250	4	168663058	q32.3
SNP_A-2140029	C	C	235	125	257	99	3.979	4.61E-02	rs13142632	4	168986388	q32.3
SNP_A-2262851	G	G	320	22	294	36	4.267	3.89E-02	rs10021284	4	169003101	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2010359	A	C	173	165	204	136	8.547	3.50E-03	rs4444854	4	169057504	q32.3
SNP_A-2125351	T	C	169	153	197	145	6.77	9.30E-03	rs10016857	4	169058020	q32.3
SNP_A-2150542	C	T	202	192	215	169	4.107	4.27E-02	rs12499605	4	169181116	q32.3
SNP_A-1979833	-	G	206	206	239	177	4.624	0.0315	rs10517962	4	169189455	q32.3
SNP_A-2241368	A	A	319	11	320	2	6.135	1.33E-02	rs13104196	4	169227331	q32.3
SNP_A-2232803	T	T	386	30	403	15	5.362	0.0206	rs17612144	4	169690597	q32.3
SNP_A-2108237	C	C	318	58	304	84	4.888	0.027	rs2451039	4	169735288	q32.3
SNP_A-2010364	T	T	233	145	264	120	4.245	3.94E-02	rs3937839	4	169748124	q32.3
SNP_A-2038797	G	G	357	57	328	80	5.046	0.0247	rs17054309	4	169829047	q32.3
SNP_A-1813640	C	C	281	129	252	160	4.898	0.0269	rs10009813	4	169831837	q32.3
SNP_A-1820023	C	C	362	26	344	48	6.979	8.20E-03	rs17054438	4	169949131	q32.3
SNP_A-2120878	T	T	316	8	351	1	6.132	1.33E-02	rs10010909	4	169981583	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1915891	T	T	352	54	372	34	5.098	0.024	rs11132793	4	170322730	q32.3
SNP_A-1979869	G	G	363	53	386	34	4.837	2.79E-02	rs10518033	4	170322788	q32.3
SNP_A-1886154	T	T	330	24	354	12	4.643	3.12E-02	rs10014681	4	170322870	q32.3
SNP_A-2136381	T	T	264	110	288	84	4.523	3.34E-02	rs752625	4	170346647	q32.3
SNP_A-2312402	C	C	380	10	395	3	3.979	4.61E-02	rs17543916	4	170373636	q32.3
SNP_A-1740395	T	T	290	70	264	106	8.448	3.70E-03	rs4692552	4	170460521	q32.3
SNP_A-2010372	C	C	380	26	369	47	6.082	0.0137	rs4295223	4	170604904	q33
SNP_A-1806219	A	A	381	33	359	55	6.154	1.31E-02	rs6553427	4	170631405	q33
SNP_A-2047332	A	A	253	153	268	120	4.015	4.51E-02	rs13152305	4	170676452	q33
SNP_A-2128327	G	G	346	30	396	16	5.998	0.0143	rs7655924	4	170720623	q33
SNP_A-1887160	C	C	379	35	403	15	8.718	3.20E-03	rs10024935	4	170850963	q33
SNP_A-1819234	T	T	372	26	390	10	7.531	6.10E-03	rs11733111	4	170981562	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1667684	C	C	358	42	388	22	7.334	6.80E-03	rs1578975	4	170992488	q33
SNP_A-1707946	A	A	354	44	385	27	5.13	0.0235	rs1010713	4	171330298	q33
SNP_A-2246262	G	G	242	144	221	177	4.162	4.13E-02	rs1522605	4	171484833	q33
SNP_A-2052007	G	G	391	3	378	10	3.943	4.71E-02	rs1522600	4	171524441	q33
SNP_A-2154458	T	A	201	175	208	170	5.428	1.98E-02	rs13109743	4	171686231	q33
SNP_A-2062366	T	T	381	35	365	53	4.02	4.50E-02	rs7694510	4	171965754	q33
SNP_A-2196685	A	A	387	13	351	25	4.808	2.83E-02	rs17056139	4	172036564	q33
SNP_A-1837690	T	T	405	11	396	24	4.911	2.67E-02	rs1821144	4	172112605	q33
SNP_A-2101541	G	G	414	0	414	4	3.981	4.60E-02	—	4	172122170	q33
SNP_A-1898659	A	A	414	0	406	4	4.059	4.39E-02	rs1017362	4	172136133	q33
SNP_A-1886083	C	C	345	65	329	89	4.043	4.44E-02	rs17056275	4	172149983	q33
SNP_A-2058578	G	G	397	3	384	10	3.941	4.71E-02	—	4	172165262	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1660669	A	A	201	197	237	173	4.338	0.0373	rs2332027	4	172367928	q33
SNP_A-1684036	A	A	338	62	320	92	6.161	1.31E-02	rs1560566	4	172484040	q33
SNP_A-1691464	A	A	314	22	347	43	4.44	3.51E-02	rs1491354	4	172816023	q34.1
SNP_A-2272991	C	C	357	23	382	10	5.782	1.62E-02	rs17211953	4	173001510	q34.1
SNP_A-2132617	A	A	341	57	372	36	5.967	0.0146	rs9993451	4	173008615	q34.1
SNP_A-2278443	T	T	314	24	310	10	5.302	2.13E-02	rs836028	4	173036407	q34.1
SNP_A-1929300	C	C	379	17	404	6	5.818	1.59E-02	rs17057442	4	173084460	q34.1
SNP_A-2087887	A	A	341	5	281	13	5.152	2.32E-02	rs6553687	4	174549419	q34.1
SNP_A-1783670	C	C	365	5	394	0	5.359	0.0206	rs6824278	4	174893151	q34.1
SNP_A-2302074	G	G	340	56	347	33	5.688	1.71E-02	rs4549354	4	175278347	q34.1
SNP_A-1979966	C	C	350	58	366	34	6.54	1.05E-02	rs10520270	4	175421715	q34.1
SNP_A-2161133	A	A	294	70	318	50	4.253	3.92E-02	rs2171139	4	175999044	q34.1
SNP_A-2128681	A	A	301	69	297	39	6.738	9.40E-03	rs2130936	4	176145534	q34.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2112379	C	C	347	19	345	35	4.485	3.42E-02	rs6826366	4	176220840	q34.1
SNP_A-2106382	C	C	352	24	347	11	4.426	3.54E-02	rs1491413	4	176362089	q34.1
SNP_A-2299987	C	C	320	4	314	12	4.051	4.42E-02	rs6842506	4	176707689	q34.2
SNP_A-2271593	C	C	400	4	395	13	4.777	2.88E-02	rs10866376	4	176710051	q34.2
SNP_A-2261665	A	A	388	8	381	19	4.525	3.34E-02	rs11732917	4	176945937	q34.2
SNP_A-1980006	G	A	217	195	232	176	7.464	0.0063	rs4475089	4	177466978	q34.2
SNP_A-2129528	G	G	377	21	387	9	4.926	2.65E-02	rs4690671	4	177540705	q34.2
SNP_A-1658314	C	C	331	15	354	6	4.353	3.69E-02	rs1692787	4	178337356	q34.3
SNP_A-2151803	G	G	321	69	335	43	6.148	0.0132	rs17665388	4	178402103	q34.3
SNP_A-1851068	G	G	376	36	363	55	4.153	4.16E-02	rs6856498	4	178574635	q34.3
SNP_A-1663034	G	G	370	10	376	26	6.546	1.05E-02	rs10520373	4	178867012	q34.3
SNP_A-2086350	G	A	227	175	208	194	5.43	1.98E-02	rs10866222	4	179261157	q34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1949448	G	G	394	6	402	0	6.075	0.0137	rs17065568	4	179377463	q34.3
SNP_A-2072634	T	T	294	100	322	76	4.525	3.34E-02	rs13117571	4	179394845	q34.3
SNP_A-1851933	A	A	289	87	312	62	5.07	2.43E-02	rs898088	4	179408385	q34.3
SNP_A-2134856	T	T	280	96	319	65	8.425	3.70E-03	rs7376754	4	179438345	q34.3
SNP_A-1900806	A	C	216	190	216	186	3.884	0.0487	rs1841096	4	179493167	q34.3
SNP_A-1853993	C	A	213	183	215	189	3.926	4.75E-02	rs2063396	4	179552027	q34.3
SNP_A-2010440	G	G	295	95	322	70	4.964	2.59E-02	rs1355329	4	179624723	q34.3
SNP_A-2084299	T	T	291	103	326	74	6.692	9.70E-03	rs6850841	4	179649740	q34.3
SNP_A-2027927	T	T	307	101	338	74	5.636	1.76E-02	rs6552295	4	179653568	q34.3
SNP_A-2145349	C	C	296	84	340	62	5.745	1.65E-02	rs2706020	4	179655572	q34.3
SNP_A-1793606	G	G	279	73	298	42	8.777	3.10E-03	rs1510627	4	179685438	q34.3
SNP_A-2273140	A	A	225	123	197	155	5.519	1.88E-02	rs9968366	4	180277344	q34.3
SNP_A-2112125	T	A	204	150	187	173	6.561	0.0104	rs1451436	4	180320724	q34.3
SNP_A-1980071	C	C	251	131	214	162	6.177	0.0129	rs9312239	4	180337508	q34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284791	G	G	412	4	420	0	4.058	4.40E-02	rs4862654	4	180385573	q34.3
SNP_A-2010458	C	C	386	26	371	43	4.481	3.43E-02	rs6827730	4	180899669	q34.3
SNP_A-2058866	T	T	392	18	405	7	5.047	0.0247	rs12506343	4	180925024	q34.3
SNP_A-1944768	A	A	368	6	314	14	4.481	3.43E-02	rs1458686	4	181187278	q34.3
SNP_A-1953215	G	G	336	56	347	33	5.936	1.48E-02	---	4	181356025	q34.3
SNP_A-2154916	G	G	303	77	238	100	8.37	0.0038	rs2442020	4	181432389	q34.3
SNP_A-2173999	C	C	384	30	370	48	4.395	0.0361	rs10007350	4	181501647	q34.3
SNP_A-2208545	A	A	379	29	359	45	3.982	4.60E-02	rs11727732	4	181523413	q34.3
SNP_A-1880939	C	C	402	4	412	0	4.079	4.34E-02	rs17069033	4	181537901	q34.3
SNP_A-1901102	G	G	274	142	303	115	4.289	3.84E-02	rs10021323	4	182477755	q34.3
SNP_A-1739379	T	T	379	17	377	33	4.884	2.71E-02	rs1879908	4	182537746	q34.3
SNP_A-1654185	G	G	386	14	381	27	4.076	4.35E-02	rs2309378	4	182571005	q34.3
SNP_A-1980141	G	G	344	52	313	73	4.864	2.74E-02	rs17195902	4	182728698	q34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939042	C	C	313	43	335	27	4.354	3.69E-02	rs17071469	4	182737055	q34.3
SNP_A-2042638	A	A	335	35	340	20	3.992	4.57E-02	---	4	182759042	q34.3
SNP_A-1980148	C	C	320	28	341	15	4.507	3.38E-02	rs17198456	4	182775114	q34.3
SNP_A-1980153	C	C	356	50	378	28	6.865	8.80E-03	rs998326	4	182821312	q34.3
SNP_A-1807067	A	A	278	56	276	88	5.84	1.57E-02	rs4861489	4	182973604	q34.3
SNP_A-1980159	G	G	256	122	289	99	4.262	0.039	rs6839199	4	183089807	q34.3
SNP_A-1827888	C	C	387	21	389	9	4.682	3.05E-02	---	4	183199720	q34.3
SNP_A-1822540	T	T	344	68	319	99	6.654	9.90E-03	rs2048914	4	183200396	q34.3
SNP_A-1851659	T	T	345	43	333	23	4.906	2.68E-02	---	4	183445212	q34.3
SNP_A-2146253	T	T	396	18	411	7	5.1	2.39E-02	rs1588967	4	183566586	q34.3
SNP_A-1937905	C	C	358	0	350	4	4.068	4.37E-02	---	4	183602799	q35.1
SNP_A-2300389	C	C	354	52	357	33	3.94	4.72E-02	rs7685326	4	183680227	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098566	C	C	254	118	296	82	9.64	0.0019	rs7691334	4	184035510	q35.1
SNP_A-1846474	G	G	205	107	242	88	4.413	3.57E-02	rs12645760	4	184037050	q35.1
SNP_A-2301921	G	G	290	108	328	84	5.096	0.024	rs6552604	4	184038756	q35.1
SNP_A-2196548	G	C	214	184	220	194	3.875	4.90E-02	rs6817534	4	184090459	q35.1
SNP_A-2190497	G	G	330	78	309	107	5.159	2.31E-02	rs3866768	4	184192473	q35.1
SNP_A-1739109	C	C	365	31	352	56	7.242	7.10E-03	rs10520536	4	184199501	q35.1
SNP_A-2294630	G	G	221	133	194	164	4.97	0.0258	rs7682268	4	184317208	q35.1
SNP_A-1809245	A	A	232	132	184	146	4.589	3.22E-02	rs7695591	4	184319424	q35.1
SNP_A-1980193	G	G	280	134	253	165	4.563	0.0327	rs2061022	4	184331761	q35.1
SNP_A-1980194	G	G	239	111	211	135	4.061	4.39E-02	rs2061021	4	184333006	q35.1
SNP_A-1980195	C	C	261	117	237	151	5.34	2.08E-02	rs6835002	4	184333832	q35.1
SNP_A-2200631	G	G	259	117	236	156	6.31	0.012	rs6552638	4	184360349	q35.1
SNP_A-1915281	G	G	281	135	222	170	7.145	7.50E-03	rs1912806	4	184548678	q35.1
SNP_A-1870941	C	C	401	3	382	10	4.05	4.42E-02	rs17074536	4	184555533	q35.1
SNP_A-2264286	G	G	175	161	223	129	8.953	0.0028	rs6812460	4	184563553	q35.1
SNP_A-1950256	A	G	220	168	199	193	4.363	3.67E-02	rs4861543	4	184651603	q35.1
SNP_A-2299726	T	T	333	13	335	3	6.163	1.30E-02	rs10050045	4	184838622	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1910326	G	G	359	49	395	25	9.331	0.0023	rs6841248	4	184854594	q35.1
SNP_A-1898802	A	A	302	82	335	59	5.334	2.09E-02	rs4862281	4	185296043	q35.1
SNP_A-1923596	A	A	256	160	285	133	4.038	4.45E-02	rs6552734	4	185328072	q35.1
SNP_A-1834264	T	T	255	131	278	100	5.069	2.44E-02	rs13118056	4	185422666	q35.1
SNP_A-2188644	A	A	264	144	291	115	4.556	3.28E-02	rs4241786	4	185425549	q35.1
SNP_A-1947586	G	G	332	12	336	2	7.115	0.0076	rs7680786	4	185432722	q35.1
SNP_A-2056554	A	A	385	23	374	40	4.703	3.01E-02	rs17075459	4	185498799	q35.1
SNP_A-2161180	C	C	367	31	379	13	7.512	6.10E-03	rs1217944	4	185568572	q35.1
SNP_A-1980221	T	T	263	109	240	136	4.006	0.0453	rs3756098	4	185729576	q35.1
SNP_A-2057323	C	C	307	57	281	81	5.318	2.11E-02	rs13146124	4	185766557	q35.1
SNP_A-1980224	T	T	233	157	199	187	5.272	2.17E-02	rs4862374	4	185811527	q35.1
SNP_A-1783734	C	C	318	48	336	30	4.649	3.11E-02	rs1401358	4	186015206	q35.1
SNP_A-2281715	A	A	302	60	279	87	5.848	1.56E-02	rs10027540	4	186125989	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189676	G	G	343	71	365	47	5.56	0.0184	rs10866272	4	186259355	q35.1
SNP_A-1833553	T	T	306	24	296	40	4.112	4.26E-02	rs4466084	4	186269135	q35.1
SNP_A-1904259	G	G	261	101	240	140	6.759	9.30E-03	rs3112857	4	186558091	q35.1
SNP_A-1934507	-	C	208	208	239	179	4.318	3.77E-02	rs2587163	4	186595184	q35.1
SNP_A-2222135	A	A	389	25	401	13	3.972	4.63E-02	rs12646976	4	186765291	q35.1
SNP_A-2107108	C	C	342	10	351	3	3.88	4.89E-02	rs11938111	4	186770106	q35.1
SNP_A-2134995	T	T	188	182	221	153	5.152	2.32E-02	rs10866277	4	186842117	q35.1
SNP_A-1730443	-	T	178	178	224	162	4.812	2.83E-02	rs1288547	4	186912026	q35.1
SNP_A-1953338	G	G	335	69	365	49	4.554	3.28E-02	rs13435843	4	186917716	q35.1
SNP_A-1807821	A	A	190	154	236	136	4.997	2.54E-02	rs11132340	4	187013804	q35.1
SNP_A-2032924	A	A	308	102	334	76	4.851	0.0276	rs7669883	4	187035225	q35.1
SNP_A-1867976	C	C	335	45	302	62	4.068	4.37E-02	rs1027521	4	187036352	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920580	C	C	280	58	291	37	4.705	3.01E-02	rs1021678	4	187053917	q35.1
SNP_A-1871412	G	G	374	42	353	67	6.322	1.19E-02	rs10028428	4	187074733	q35.1
SNP_A-1980239	G	G	291	105	324	64	11.637	6.00E-04	rs1566354	4	187151895	q35.1
SNP_A-2010521	C	C	224	126	169	157	10.254	0.0014	rs2648111	4	187166673	q35.1
SNP_A-1838839	A	A	262	148	281	115	4.564	0.0327	rs4861686	4	187168904	q35.1
SNP_A-2063019	G	G	274	118	302	94	4.058	4.40E-02	rs12643549	4	187181834	q35.1
SNP_A-1807994	T	T	266	90	295	67	4.819	2.82E-02	rs2310372	4	187190246	q35.1
SNP_A-1780646	A	A	289	115	317	85	5.789	0.0161	rs10031442	4	187191629	q35.1
SNP_A-2172614	T	T	273	139	302	110	4.84	2.78E-02	rs4637445	4	187197290	q35.1
SNP_A-2255746	G	G	279	107	317	79	6.511	1.07E-02	rs1947455	4	187203528	q35.1
SNP_A-2092274	C	C	230	146	267	111	7.516	6.10E-03	rs4862600	4	187228163	q35.1
SNP_A-1896102	C	C	290	46	247	83	14.003	2.00E-04	rs10002339	4	187232537	q35.1
SNP_A-2190434	G	A	227	181	203	189	4.413	3.57E-02	rs12649886	4	187777509	q35.2
SNP_A-1949632	T	T	233	129	210	164	5.181	2.28E-02	rs13105379	4	188130020	q35.2
SNP_A-1787307	C	C	263	127	236	156	4.428	3.54E-02	rs322442	4	188163460	q35.2
SNP_A-2289605	G	G	276	112	250	140	4.391	0.0361	rs433477	4	188190015	q35.2
SNP_A-2141798	C	C	281	89	268	124	5.428	1.98E-02	rs370915	4	188193405	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1694123	G	G	247	121	237	163	5.093	0.024	rs1583219	4	188447044	q35.2
SNP_A-1895950	T	T	224	164	261	141	4.31	3.79E-02	rs7660073	4	188492602	q35.2
SNP_A-1936474	A	A	313	33	325	15	6.924	8.50E-03	rs1038597	4	188503292	q35.2
SNP_A-2154783	A	A	355	53	381	35	4.523	3.34E-02	rs6817449	4	188506541	q35.2
SNP_A-1899513	G	G	294	112	332	80	7.596	5.80E-03	rs7691022	4	188532515	q35.2
SNP_A-2126634	G	G	256	102	271	73	4.955	2.60E-02	rs7695955	4	188532891	q35.2
SNP_A-2105043	A	A	290	114	301	77	6.515	1.07E-02	rs1948112	4	188533076	q35.2
SNP_A-1783267	A	A	340	62	372	38	7.12	0.0076	rs6553048	4	188546838	q35.2
SNP_A-2010543	A	A	311	63	353	31	13.421	2.00E-04	rs4478239	4	188566455	q35.2
SNP_A-2010544	A	A	330	54	359	27	10.215	0.0014	rs4478240	4	188566665	q35.2
SNP_A-2250196	C	C	272	84	303	59	5.992	0.0144	rs76994910	4	188573303	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2010550	G	G	346	54	362	36	3.957	4.67E-02	rs7686928	4	189108978	q35.2
SNP_A-1780417	G	G	271	61	318	44	5.216	0.0224	rs6843362	4	189179335	q35.2
SNP_A-1980266	C	C	375	39	393	21	5.822	1.58E-02	rs902910	4	189395497	q35.2
SNP_A-1826593	G	G	375	11	379	23	3.933	4.73E-02	rs7376789	4	189638866	q35.2
SNP_A-2074562	C	C	340	48	366	32	4.031	4.47E-02	rs1876374	4	189714719	q35.2
SNP_A-2192802	A	A	291	113	329	77	9.145	2.50E-03	rs12715880	4	189740532	q35.2
SNP_A-2138433	G	G	222	184	267	151	7.219	7.20E-03	rs10866310	4	189841530	q35.2
SNP_A-1887007	A	A	230	172	267	131	8.283	4.00E-03	rs4339258	4	189871040	q35.2
SNP_A-1665052	G	G	215	177	256	148	5.977	1.45E-02	rs1606234	4	189991922	q35.2
SNP_A-1651106	C	C	294	64	353	51	4.088	4.32E-02	rs713507	4	190038259	q35.2
SNP_A-1909475	T	T	245	103	222	146	8.006	4.70E-03	rs2377334	4	190048433	q35.2
SNP_A-2117450	C	C	364	8	386	2	3.91	4.80E-02	rs4379101	4	190118273	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2161125	A	T	162	160	204	132	8.086	4.50E-03	rs7664971	4	190343243	q35.2
SNP_A-2235584	T	T	342	64	370	46	3.926	4.76E-02	rs2132668	4	190356476	q35.2
SNP_A-2086032	C	C	307	59	276	84	5.97	0.0146	rs1390884	4	190362179	q35.2
SNP_A-1872916	C	C	320	82	307	109	3.848	4.98E-02	rs7684484	4	190500956	q35.2
SNP_A-1668813	A	A	367	15	358	34	7.351	6.70E-03	rs4429890	5	367256	p15.33
SNP_A-2237907	G	G	325	63	348	38	6.969	8.30E-03	rs27064	5	1412938	p15.33
SNP_A-2098871	G	G	219	189	258	160	5.478	1.93E-02	rs4975741	5	1907650	p15.33
SNP_A-1814089	C	C	332	32	302	50	5.171	0.023	rs2353580	5	1924880	p15.33
SNP_A-1891196	A	A	379	35	362	54	4.441	3.51E-02	rs11960538	5	2193755	p15.33
SNP_A-2141788	A	A	310	12	301	33	9.716	0.0018	rs16903629	5	2249941	p15.33
SNP_A-2206694	C	C	299	77	282	104	4.395	0.0361	rs11954767	5	2304847	p15.33
SNP_A-1882841	A	A	324	72	300	96	4.352	3.70E-02	rs11952611	5	2305084	p15.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2263062	A	A	262	44	320	22	11.148	8.00E-04	rs563704	5	2335193	p15.33
SNP_A-1818222	G	G	387	9	367	19	3.975	4.62E-02	rs875221	5	2752110	p15.33
SNP_A-2087048	G	G	348	66	371	47	3.911	4.80E-02	rs2961787	5	3066033	p15.33
SNP_A-1784273	G	G	347	25	384	14	4.102	4.28E-02	rs1215689	5	3276581	p15.33
SNP_A-1923542	G	G	297	53	274	74	4.393	0.0361	rs1983048	5	3441500	p15.33
SNP_A-2260028	A	A	228	142	250	112	4.469	3.45E-02	rs414134	5	3476000	p15.33
SNP_A-2126446	C	C	386	28	397	15	4.08	4.34E-02	rs17686287	5	3560990	p15.33
SNP_A-2052794	C	C	331	61	309	93	7.281	7.00E-03	rs13436137	5	3818085	p15.33
SNP_A-1980364	T	T	296	48	312	28	5.661	1.73E-02	rs2398648	5	3888686	p15.33
SNP_A-2250837	G	G	340	36	339	15	7.993	4.70E-03	rs11738731	5	3916152	p15.33
SNP_A-1919429	C	C	367	37	376	22	3.878	4.89E-02	rs11740522	5	3917942	p15.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2054392	C	C	344	18	354	6	6.138	0.0132	rs13355619	5	3918209	p15.33
SNP_A-2067009	G	G	315	29	308	48	4.563	0.0327	rs6866903	5	4281049	p15.33
SNP_A-2147310	A	A	355	61	333	87	5.252	2.19E-02	rs458537	5	4319325	p15.33
SNP_A-1980378	C	C	345	57	318	84	6.27	0.0123	rs463803	5	4320126	p15.33
SNP_A-2134937	A	A	348	62	328	86	4.464	3.46E-02	rs456741	5	4330513	p15.33
SNP_A-2188706	G	G	278	64	263	93	5.494	1.91E-02	rs457961	5	4330869	p15.33
SNP_A-1827162	C	C	357	57	324	80	5.339	2.09E-02	rs462922	5	4330958	p15.33
SNP_A-2304174	T	T	342	64	369	45	4.26	0.039	rs418752	5	4701002	p15.32
SNP_A-1817408	G	G	312	20	291	5	7.693	5.50E-03	rs11134064	5	4705364	p15.32
SNP_A-1824926	G	G	386	12	370	24	4.319	3.77E-02	rs3913374	5	4938009	p15.32
SNP_A-1897387	G	G	249	141	214	162	3.847	4.98E-02	rs11746248	5	4938156	p15.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2183747	C	C	226	190	263	153	6.791	9.20E-03	rs610722	5	4965310	p15.32
SNP_A-1935285	C	C	254	148	232	182	4.323	3.76E-02	rs3733787	5	5131313	p15.32
SNP_A-1842811	G	G	324	50	320	78	5.409	0.02	rs2560412	5	5202621	p15.32
SNP_A-1882547	C	C	338	50	346	32	3.915	4.79E-02	rs6874190	5	5203205	p15.32
SNP_A-1980420	G	G	262	142	236	178	5.286	2.15E-02	rs997427	5	5220587	p15.32
SNP_A-2140346	T	T	237	75	233	107	4.466	3.46E-02	rs10038199	5	5236642	p15.32
SNP_A-2238735	A	A	302	96	279	123	4.219	4.00E-02	rs1808529	5	5236700	p15.32
SNP_A-2299449	G	C	218	178	217	195	4.817	2.82E-02	rs13170100	5	5273741	p15.32
SNP_A-2044432	T	T	360	0	334	4	4.285	0.0385	rs16875143	5	5301663	p15.32
SNP_A-1893254	T	T	328	50	325	75	4.395	3.60E-02	rs2964462	5	5403303	p15.32
SNP_A-2309470	A	A	365	37	331	55	4.86	0.0275	rs13174247	5	5419625	p15.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213240	G	G	369	15	384	6	4.11	4.26E-02	rs1863939	5	5440840	p15.32
SNP_A-1745180	G	G	313	87	347	63	5.469	1.94E-02	rs930049	5	5453125	p15.32
SNP_A-2187429	G	G	359	57	338	80	4.489	3.41E-02	rs2964385	5	5457366	p15.32
SNP_A-2300041	A	A	337	53	360	32	5.942	1.48E-02	rs2937813	5	5593609	p15.32
SNP_A-1915968	C	C	402	12	386	32	9.397	2.20E-03	rs17788422	5	5620590	p15.32
SNP_A-2097888	A	A	400	10	377	29	9.918	1.60E-03	rs16875765	5	5628229	p15.32
SNP_A-1902851	C	C	292	12	299	33	8.667	3.20E-03	rs10043593	5	5629881	p15.32
SNP_A-2263592	G	G	238	88	196	110	5.882	1.53E-02	rs12522553	5	5654744	p15.32
SNP_A-1980440	C	C	296	92	328	66	5.874	0.0154	rs34210	5	5718597	p15.32
SNP_A-1841797	G	G	295	101	325	79	4.061	4.39E-02	rs34218	5	5721798	p15.32
SNP_A-1750959	C	T	188	170	201	159	5.008	0.0252	rs2895450	5	5790213	p15.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1980459	G	G	375	15	386	6	4.011	4.52E-02	rs17767636	5	6062018	p15.32
SNP_A-2235966	A	A	279	125	312	100	4.542	3.31E-02	rs173577	5	6087364	p15.32
SNP_A-1680348	G	G	223	121	188	172	11.5	7.00E-04	rs248673	5	6104521	p15.32
SNP_A-1865633	A	A	273	95	245	125	5.599	1.80E-02	rs307197	5	6122369	p15.32
SNP_A-2243267	G	G	291	125	257	153	4.886	2.71E-02	rs729017	5	6130184	p15.32
SNP_A-1980470	A	A	249	81	214	112	7.601	5.80E-03	rs423531	5	6138623	p15.32
SNP_A-1712255	C	C	249	151	225	187	4.873	2.73E-02	rs2398255	5	6173756	p15.32
SNP_A-2216201	G	G	360	18	376	8	4.147	4.17E-02	rs12654440	5	6196023	p15.32
SNP_A-2083064	A	A	240	130	205	169	7.818	5.20E-03	rs17825239	5	6326100	p15.32
SNP_A-1980483	C	C	240	142	267	111	5.215	0.0224	rs3776433	5	6668092	p15.31
SNP_A-1980490	G	G	402	2	372	8	4.032	4.46E-02	rs371869	5	6740557	p15.31
SNP_A-1850078	G	G	299	107	268	134	4.7	3.02E-02	rs416847	5	6792567	p15.31
SNP_A-1697206	G	G	308	90	287	123	5.677	0.0172	rs172080	5	6800677	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1727839	C	C	295	105	274	138	5.08	2.42E-02	rs5001282	5	6810406	p15.31
SNP_A-1913890	T	C	192	190	216	160	4.527	3.34E-02	rs6893958	5	6895842	p15.31
SNP_A-1796308	C	C	374	38	396	20	6.196	1.28E-02	rs2644919	5	6896564	p15.31
SNP_A-1907906	G	G	239	177	271	149	4.394	0.0361	rs275437	5	6932978	p15.31
SNP_A-1946081	T	T	290	48	264	76	7.537	6.00E-03	rs12514493	5	6963110	p15.31
SNP_A-2234834	A	A	336	76	318	102	4.217	4.00E-02	rs11134201	5	7098934	p15.31
SNP_A-2069830	G	G	377	17	389	7	4.35	3.70E-02	rs9313193	5	7571186	p15.31
SNP_A-1882570	A	A	312	54	318	34	4.331	3.74E-02	rs12659288	5	7755167	p15.31
SNP_A-1899270	A	A	412	0	403	5	5.08	2.42E-02	rs16879167	5	7875390	p15.31
SNP_A-1980531	C	C	268	140	294	112	4.309	3.79E-02	rs1993716	5	7885387	p15.31
SNP_A-2063204	C	C	309	49	275	77	8.152	0.0043	rs163116	5	8217750	p15.31
SNP_A-1980552	A	A	317	49	293	73	5.666	1.73E-02	rs16880016	5	8231834	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920704	G	G	358	54	367	33	5.004	0.0253	rs2174977	5	8390324	p15.31
SNP_A-2206423	A	A	315	101	344	74	5.437	1.97E-02	rs16880863	5	8626076	p15.31
SNP_A-1945169	G	G	366	44	342	66	5.209	2.25E-02	rs4701815	5	8679931	p15.31
SNP_A-2078214	G	G	351	29	337	59	10.187	0.0014	rs7381046	5	8686805	p15.31
SNP_A-2174593	G	G	370	46	348	70	5.635	1.76E-02	rs200116	5	8703331	p15.31
SNP_A-2075361	T	T	344	52	263	69	7.63	5.70E-03	rs200012	5	8748751	p15.31
SNP_A-2145326	G	G	376	0	383	7	6.811	9.10E-03	rs2078758	5	8882457	p15.31
SNP_A-2086087	A	A	399	7	396	24	9.099	2.60E-03	rs16881626	5	8954097	p15.31
SNP_A-2105554	A	A	330	72	362	50	5.325	2.10E-02	rs2963335	5	8954944	p15.31
SNP_A-1736413	T	T	390	10	386	24	5.663	1.73E-02	rs10512994	5	8956052	p15.31
SNP_A-2010647	G	G	345	71	367	51	3.954	4.68E-02	rs2963341	5	8961533	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041496	C	C	403	9	394	22	5.534	1.86E-02	rs16881658	5	8962713	p15.31
SNP_A-2119645	C	C	407	9	400	20	4.214	4.01E-02	rs2962729	5	8999324	p15.31
SNP_A-1980596	C	C	359	15	348	2	9.327	0.0023	rs2174442	5	9151608	p15.31
SNP_A-1826277	A	A	242	168	212	200	4.76	2.91E-02	rs2456237	5	9158283	p15.31
SNP_A-1839775	A	A	394	18	409	7	5.101	2.39E-02	rs7731508	5	9160887	p15.31
SNP_A-2276694	T	T	227	117	180	142	7.122	0.0076	rs253651	5	9169125	p15.31
SNP_A-1813841	G	G	310	18	369	9	4.609	3.18E-02	rs983856	5	9193848	p15.31
SNP_A-1864158	T	T	239	149	206	184	6.121	0.0134	rs6863413	5	9197667	p15.31
SNP_A-2036339	G	G	240	164	207	195	5.108	2.38E-02	rs12189232	5	9201278	p15.31
SNP_A-1980602	A	A	322	92	293	115	3.879	4.89E-02	rs899575	5	9208331	p15.31
SNP_A-2254179	C	C	347	55	318	74	3.938	4.72E-02	rs1806090	5	9245833	p15.31
SNP_A-1928079	A	A	328	46	288	68	6.403	0.0114	rs40692	5	9247630	p15.31
SNP_A-1692506	T	T	339	61	323	85	4.253	3.92E-02	rs1806111	5	9253067	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1657782	G	G	339	61	327	85	3.985	4.59E-02	rs1806083	5	9253086	p15.31
SNP_A-1697424	C	C	382	16	405	5	6.257	0.0124	rs1806110	5	9253278	p15.31
SNP_A-1877622	G	A	202	152	183	177	4.468	3.45E-02	rs877191	5	9267028	p15.31
SNP_A-1980614	A	A	219	163	194	192	3.862	4.94E-02	rs1805962	5	9268068	p15.31
SNP_A-1690970	A	A	208	190	244	160	5.394	2.02E-02	rs1805960	5	9268069	p15.31
SNP_A-1665154	C	C	378	20	371	39	6.007	1.42E-02	rs1806004	5	9292165	p15.31
SNP_A-1980628	C	C	354	54	338	76	4.049	4.42E-02	rs386073	5	9446029	p15.31
SNP_A-1674833	A	A	270	124	313	97	6.154	1.31E-02	rs953018	5	9451949	p15.31
SNP_A-1755346	A	A	356	8	340	18	4.164	4.13E-02	rs10513017	5	9476202	p15.31
SNP_A-1908719	G	G	392	10	377	23	5.409	0.02	rs17324408	5	9489878	p15.31
SNP_A-2110105	G	G	318	24	304	44	6.146	0.0132	rs16882871	5	9532622	p15.31
SNP_A-2224941	C	C	351	41	338	62	4.446	3.50E-02	rs160504	5	9646459	p15.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2313182	G	G	335	35	302	50	3.91	4.80E-02	rs12520289	5	10520257	p15.2
SNP_A-2194837	G	G	391	17	370	36	7.386	0.0066	rs2962327	5	10575013	p15.2
SNP_A-1869086	C	C	318	70	293	97	5.383	2.03E-02	rs9791065	5	10638156	p15.2
SNP_A-1944247	C	C	325	87	294	116	5.691	1.71E-02	---	5	10720969	p15.2
SNP_A-1810140	A	A	382	30	397	17	3.88	4.89E-02	rs5745289	5	10736822	p15.2
SNP_A-2282884	G	G	375	7	352	22	8.403	3.70E-03	rs6867140	5	10842989	p15.2
SNP_A-2266992	G	G	331	39	335	23	3.956	4.67E-02	rs1470023	5	10853150	p15.2
SNP_A-2272469	C	C	294	104	253	131	5.927	0.0149	rs6860830	5	10927644	p15.2
SNP_A-2114993	T	T	260	152	212	198	10.922	0.001	rs4361487	5	10930143	p15.2
SNP_A-2028909	G	-	252	162	204	204	9.829	1.70E-03	rs1548703	5	10934013	p15.2
SNP_A-1797364	C	C	283	91	226	120	9.294	0.0023	rs4352573	5	10934181	p15.2
SNP_A-2256039	C	C	285	87	246	112	5.739	0.0166	rs4235599	5	10934326	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2162603	T	C	205	141	184	170	8.866	2.90E-03	rs7729886	5	10935082	p15.2
SNP_A-2266484	G	T	214	156	182	162	8.256	4.10E-03	rs16901086	5	10937865	p15.2
SNP_A-1867320	T	G	236	178	216	196	7.364	6.70E-03	rs4702748	5	10938408	p15.2
SNP_A-1886969	C	C	226	104	186	152	12.79	3.00E-04	rs4702749	5	10938474	p15.2
SNP_A-1789550	A	G	224	168	203	177	8.626	0.0033	rs11948902	5	10942839	p15.2
SNP_A-2266675	G	G	291	125	245	161	8.359	0.0038	rs7705870	5	10942883	p15.2
SNP_A-1853489	A	A	286	122	250	152	5.658	1.74E-02	rs852603	5	10951927	p15.2
SNP_A-2305073	C	C	283	113	309	89	3.988	0.0458	rs852621	5	11065130	p15.2
SNP_A-2207130	A	A	272	100	310	80	4.281	3.86E-02	rs852622	5	11065202	p15.2
SNP_A-2178924	C	C	386	20	377	35	4.153	4.16E-02	rs16901200	5	11070597	p15.2
SNP_A-1758104	T	T	377	21	370	38	4.841	2.78E-02	rs9312751	5	11072416	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1881861	T	T	390	20	391	9	4.051	0.0441	rs2973488	5	11096917	p15.2
SNP_A-1807546	T	T	337	25	335	11	5.091	0.024	rs11133646	5	11171840	p15.2
SNP_A-1950180	G	G	384	10	398	2	5.539	1.86E-02	rs16901383	5	11238728	p15.2
SNP_A-2061623	C	A	184	180	214	160	4.474	0.0344	rs32274	5	11243998	p15.2
SNP_A-1980697	A	A	293	103	272	130	3.864	4.93E-02	rs32269	5	11250322	p15.2
SNP_A-1980700	T	C	221	159	197	187	6.869	8.80E-03	rs27520	5	11271488	p15.2
SNP_A-1980701	C	C	311	77	287	113	7.603	5.80E-03	rs17792743	5	11287452	p15.2
SNP_A-1724584	C	C	306	94	277	125	5.826	1.58E-02	rs443005	5	11328023	p15.2
SNP_A-1711436	G	G	258	112	236	142	4.438	3.51E-02	rs445607	5	11328663	p15.2
SNP_A-2053512	T	T	215	123	172	140	4.844	2.77E-02	rs439893	5	11335453	p15.2
SNP_A-1980705	C	C	247	97	231	127	4.276	3.87E-02	rs194188	5	11347265	p15.2
SNP_A-2280750	T	T	309	93	282	128	6.698	9.70E-03	rs2530217	5	11352244	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2224767	C	C	264	136	228	184	9.659	0.0019	rs40403	5	11352801	p15.2
SNP_A-2143110	C	C	371	35	372	18	5.135	0.0235	rs10075848	5	11488767	p15.2
SNP_A-2308033	G	G	380	28	364	44	3.9	4.83E-02	rs1990267	5	11637285	p15.2
SNP_A-1980720	C	T	183	179	216	132	11.451	7.00E-04	rs4312856	5	11650666	p15.2
SNP_A-1720873	T	T	216	182	256	148	6.848	8.90E-03	rs3852170	5	11661268	p15.2
SNP_A-2090396	T	T	202	164	249	127	9.469	2.10E-03	rs6883334	5	11681467	p15.2
SNP_A-2166121	C	C	204	184	236	126	12.292	5.00E-04	rs6889997	5	11682999	p15.2
SNP_A-1914783	G	G	412	2	411	9	4.413	3.57E-02	—	5	13018585	p15.2
SNP_A-1918497	G	G	410	0	402	10	10.074	0.0015	rs16902347	5	13030507	p15.2
SNP_A-1715093	T	T	314	86	357	55	9.396	2.20E-03	rs4298252	5	13706156	p15.2
SNP_A-1649020	C	C	228	164	207	205	5.075	2.43E-02	rs966430	5	13735922	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1952028	C	C	232	162	207	203	5.713	1.68E-02	rs2896111	5	13744045	p15.2
SNP_A-1842300	A	C	181	159	172	144	3.85	4.97E-02	rs1445693	5	13747598	p15.2
SNP_A-1674947	A	G	219	169	207	201	4.112	4.26E-02	rs10513149	5	13756581	p15.2
SNP_A-1980781	C	C	380	14	367	37	10.475	1.20E-03	rs17275319	5	13927951	p15.2
SNP_A-1844690	A	A	342	12	255	21	5.561	0.0184	rs16902962	5	13996499	p15.2
SNP_A-1670880	G	G	305	75	330	54	4.382	3.63E-02	rs30617	5	14320674	p15.2
SNP_A-1737541	T	T	316	54	308	78	4.129	4.21E-02	rs247141	5	14376964	p15.2
SNP_A-2314914	G	G	244	100	275	77	4.749	0.0293	rs30773	5	14448220	p15.2
SNP_A-1850316	T	T	257	83	214	108	6.713	9.60E-03	rs26178	5	14639413	p15.2
SNP_A-1890450	A	A	379	17	387	7	4.245	3.94E-02	rs153822	5	14680833	p15.2
SNP_A-2037945	T	T	290	92	247	109	3.97	4.63E-02	rs6864641	5	14803251	p15.2
SNP_A-2065069	G	G	355	5	376	16	5.013	0.0252	rs4702052	5	14823753	p15.2
SNP_A-1980822	A	A	406	0	413	5	4.886	2.71E-02	rs10513195	5	15072660	p15.2
SNP_A-1980837	C	C	170	146	200	118	5.396	2.02E-02	rs4702084	5	15613837	p15.1
SNP_A-1888842	A	A	388	22	373	41	6.007	0.0143	rs12652729	5	15686019	p15.1
SNP_A-1980841	T	T	334	36	322	56	4.482	3.42E-02	rs17703976	5	15706765	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2028779	A	A	388	16	390	6	4.471	3.45E-02	rs17647886	5	15773478	p15.1
SNP_A-2269277	C	C	225	129	204	158	3.869	4.92E-02	rs11748700	5	15776346	p15.1
SNP_A-1902523	G	G	284	114	314	84	6.05	1.39E-02	rs7714352	5	15804517	p15.1
SNP_A-1704467	A	A	287	109	319	87	4.035	4.46E-02	rs10520822	5	15806156	p15.1
SNP_A-1958161	C	C	220	196	254	164	5.278	2.16E-02	rs2219770	5	16326280	p15.1
SNP_A-1880105	T	T	378	22	406	6	9.968	1.60E-03	rs1371974	5	16340578	p15.1
SNP_A-1875082	G	G	202	128	231	103	4.624	0.0315	rs6891867	5	16498077	p15.1
SNP_A-1930574	G	G	387	27	398	14	4.271	3.88E-02	rs17650584	5	16633841	p15.1
SNP_A-2150358	C	C	288	124	259	155	4.977	2.57E-02	rs168899	5	16647997	p15.1
SNP_A-1790630	T	T	259	103	226	130	5.324	2.10E-02	rs149447	5	16648199	p15.1
SNP_A-1929133	C	C	276	118	246	154	6.444	0.0111	rs35001	5	16650174	p15.1
SNP_A-2094116	C	C	231	163	276	142	4.735	2.96E-02	rs1964335	5	16662763	p15.1
SNP_A-2148472	A	A	272	106	212	136	9.934	1.60E-03	rs4482904	5	16663555	p15.1
SNP_A-1929944	C	C	309	105	341	75	6.571	0.0104	rs31499	5	16896108	p15.1
SNP_A-1919662	C	C	306	74	350	48	8.08	4.50E-03	rs10213765	5	16901200	p15.1
SNP_A-1698567	C	C	388	12	406	4	4.285	3.84E-02	rs10520845	5	16932671	p15.1
SNP_A-2291933	T	T	227	107	192	130	4.938	0.0263	rs31454	5	16983761	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2226374	C	C	330	82	306	112	5.502	0.019	rs4129967	5	17053364	p15.1
SNP_A-1898579	A	A	359	37	349	65	7.431	6.40E-03	rs11953330	5	17059372	p15.1
SNP_A-1980890	T	T	336	34	367	17	6.776	9.20E-03	rs17542943	5	17123705	p15.1
SNP_A-2085706	A	A	324	38	337	23	3.939	4.72E-02	rs297221	5	17187109	p15.1
SNP_A-1801227	A	A	207	199	241	163	6.156	1.31E-02	rs297180	5	17210291	p15.1
SNP_A-1896086	A	A	213	149	252	126	4.851	0.0276	rs167213	5	17213112	p15.1
SNP_A-1954008	C	C	308	78	273	103	5.431	1.98E-02	rs11952802	5	17253074	p15.1
SNP_A-1938371	T	T	200	168	240	134	7.416	6.50E-03	rs6554996	5	17409166	p15.1
SNP_A-1817710	C	C	287	45	292	80	7.595	5.90E-03	rs690799	5	18038426	p15.1
SNP_A-1958085	A	A	270	76	288	52	5.029	2.49E-02	rs10057043	5	18182664	p15.1
SNP_A-2040211	C	C	373	11	360	24	5.059	2.45E-02	rs17661079	5	18208926	p15.1
SNP_A-2143150	G	G	389	27	374	46	5.221	0.0223	rs11950780	5	18214146	p15.1
SNP_A-1753031	C	C	389	9	390	20	3.996	4.56E-02	rs904747	5	18353014	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1980912	T	T	348	52	334	78	5.311	0.0212	rs6870006	5	18505215	p14.3
SNP_A-2260180	G	G	246	130	279	105	4.65	3.11E-02	rs17549728	5	18812958	p14.3
SNP_A-1863519	G	G	324	26	304	42	4.379	3.64E-02	rs7379061	5	18819377	p14.3
SNP_A-2118012	A	A	315	87	285	111	4.364	3.67E-02	rs2387569	5	18881094	p14.3
SNP_A-1905694	G	G	384	32	366	52	5.189	2.27E-02	rs4469198	5	18955605	p14.3
SNP_A-1724732	C	C	323	17	333	39	7.372	0.0066	rs4131713	5	18994639	p14.3
SNP_A-2055021	T	T	347	57	358	38	3.892	4.85E-02	rs6892698	5	18997535	p14.3
SNP_A-2101758	G	G	289	77	331	53	6.848	8.90E-03	rs10940990	5	19026601	p14.3
SNP_A-1958340	G	G	362	12	374	4	4.174	4.10E-02	rs1911859	5	20052952	p14.3
SNP_A-2044121	C	C	292	68	286	44	3.908	4.81E-02	rs12517972	5	20498266	p14.3
SNP_A-2124710	A	A	363	35	376	20	4.315	0.0378	rs17238896	5	21037368	p14.3
SNP_A-1980956	A	A	383	7	373	17	4.299	3.81E-02	rs16888773	5	21619011	p14.3
SNP_A-2010729	A	A	258	128	283	101	4.334	3.74E-02	rs4701222	5	21636380	p14.3
SNP_A-2010731	T	T	410	0	402	4	4.059	4.39E-02	rs6452011	5	21899075	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2120893	G	G	361	31	348	48	3.876	4.90E-02	rs7727257	5	22604281	p14.3
SNP_A-2306147	G	G	222	162	199	195	4.179	4.09E-02	rs199139	5	22626933	p14.3
SNP_A-1850636	T	T	308	34	281	53	5.293	2.14E-02	rs10941965	5	22627229	p14.3
SNP_A-1980963	T	A	203	195	213	163	4.544	3.30E-02	rs166576	5	22634920	p14.3
SNP_A-2032533	G	G	262	122	226	144	4.217	4.00E-02	rs7723664	5	22761763	p14.3
SNP_A-2046964	T	T	390	18	375	33	4.706	3.01E-02	rs1661975	5	22861878	p14.3
SNP_A-1831722	C	C	392	16	371	29	4.255	3.91E-02	rs1707069	5	22862009	p14.3
SNP_A-1935456	A	A	388	20	368	34	4.115	4.25E-02	rs17294204	5	22869180	p14.3
SNP_A-1790059	A	A	397	15	406	6	3.958	4.66E-02	rs16892274	5	23278048	p14.3
SNP_A-1980979	A	A	381	25	388	12	4.587	3.22E-02	rs1589417	5	23649317	p14.2
SNP_A-1814648	G	G	392	18	370	36	6.616	0.0101	rs16893369	5	24463342	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884487	C	C	395	21	381	39	5.634	1.76E-02	rs331256	5	24487642	p14.2
SNP_A-2218761	T	T	290	110	325	79	7.057	7.90E-03	rs7732575	5	24728161	p14.1
SNP_A-2138383	G	G	297	117	332	86	6.662	9.80E-03	rs1896890	5	24738958	p14.1
SNP_A-1842246	A	A	244	102	259	71	5.627	0.0177	rs6891806	5	24741042	p14.1
SNP_A-2173942	G	G	290	82	300	52	6.338	0.0118	rs7711384	5	24792361	p14.1
SNP_A-1981008	C	C	377	27	380	14	4.009	0.0453	rs4701484	5	25552363	p14.1
SNP_A-1848600	A	A	295	91	325	63	6.537	0.0106	rs6859698	5	25633905	p14.1
SNP_A-2140225	A	A	255	73	241	101	4.61	3.18E-02	rs7733598	5	25679112	p14.1
SNP_A-2165163	G	G	225	169	258	144	4.171	4.11E-02	rs6894836	5	25980703	p14.1
SNP_A-2235044	T	T	402	0	388	4	4.123	4.23E-02	rs7726206	5	26142519	p14.1
SNP_A-2059730	A	A	344	4	360	0	4.161	4.14E-02	rs4048799	5	26143452	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2094225	A	A	195	115	167	157	8.346	3.90E-03	rs10058113	5	26213464	p14.1
SNP_A-2177331	C	C	357	15	365	5	5.083	2.42E-02	rs11952920	5	26491343	p14.1
SNP_A-2179004	A	A	349	25	352	12	4.446	3.50E-02	rs778750	5	26539470	p14.1
SNP_A-1981024	C	C	213	165	250	126	8.178	4.20E-03	rs9293241	5	26606178	p14.1
SNP_A-1981025	T	T	278	132	246	160	4.62	3.16E-02	rs1553235	5	26609985	p14.1
SNP_A-1800612	C	C	219	159	253	127	6.024	0.0141	rs6869421	5	26848658	p14.1
SNP_A-2249099	G	G	225	183	258	150	5.525	1.87E-02	rs6870087	5	26849001	p14.1
SNP_A-2055912	T	T	267	143	212	174	8.631	0.0033	rs257796	5	26882650	p14.1
SNP_A-2187303	A	A	198	192	221	157	4.586	3.22E-02	rs12658938	5	26924217	p14.1
SNP_A-2307471	T	G	229	183	224	192	7.363	6.70E-03	rs3846562	5	27363094	p14.1
SNP_A-2119380	A	A	270	146	234	186	7.372	0.0066	rs12513991	5	27393195	p14.1
SNP_A-1873123	G	A	220	168	215	185	8.612	0.0033	rs161763	5	27404360	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1925131	T	T	224	138	178	172	8.793	3.00E-03	rs844187	5	27433494	p14.1
SNP_A-1898572	G	G	265	135	234	172	6.341	0.0118	rs10039598	5	27484561	p14.1
SNP_A-2144204	G	A	210	156	189	169	7.504	6.20E-03	rs4558955	5	27486752	p14.1
SNP_A-2202887	G	A	241	171	213	201	8.209	4.20E-03	rs6894886	5	27491969	p14.1
SNP_A-2010765	C	C	277	63	232	78	4.198	4.05E-02	rs1989419	5	27512233	p14.1
SNP_A-2114653	C	C	307	63	270	88	6.316	0.012	rs12656583	5	27515731	p14.1
SNP_A-1948572	A	A	211	139	261	97	12.682	4.00E-04	rs12659482	5	27526542	p14.1
SNP_A-2196580	G	G	254	152	295	121	6.461	1.10E-02	rs11952569	5	27534997	p14.1
SNP_A-2146923	G	G	315	89	288	124	6.882	8.70E-03	rs13159709	5	27563236	p14.1
SNP_A-1981048	A	A	311	79	262	106	7.499	6.20E-03	rs2329628	5	27575247	p14.1
SNP_A-1889278	T	T	289	111	257	145	6.386	0.0115	rs10053615	5	27626546	p14.1
SNP_A-1836234	T	T	298	90	271	113	3.866	4.93E-02	rs7712988	5	27631480	p14.1
SNP_A-2145889	C	C	285	99	240	122	5.607	1.79E-02	rs10940680	5	27655227	p14.1
SNP_A-1687902	G	G	343	27	349	47	4.58	3.23E-02	rs6880876	5	28327042	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1853558	A	A	346	40	366	24	4.541	3.31E-02	rs10066522	5	28734513	p14.1
SNP_A-2095148	A	A	312	26	321	13	4.438	3.52E-02	rs17537132	5	28768336	p14.1
SNP_A-2159882	C	C	412	4	418	0	4.039	4.45E-02	rs16898321	5	29011933	p14.1
SNP_A-2148776	A	A	408	4	418	0	4.078	4.34E-02	rs16898525	5	29053182	p14.1
SNP_A-2044125	G	G	315	37	314	20	4.603	3.19E-02	rs638477	5	29083949	p14.1
SNP_A-2131163	G	G	273	109	248	140	5.013	0.0252	rs7717789	5	29285153	p14.1
SNP_A-2283702	T	T	250	142	287	111	6.303	0.0121	rs9784631	5	29361320	p13.3
SNP_A-2280653	G	G	252	134	265	95	6.07	0.0137	rs10069118	5	29375689	p13.3
SNP_A-2079840	C	C	216	200	247	169	4.68	3.05E-02	rs12697213	5	29430811	p13.3
SNP_A-1807071	C	C	374	42	394	26	4.266	3.89E-02	rs1824110	5	29826729	p13.3
SNP_A-1748445	A	A	327	25	310	44	5.68	0.0172	rs1463413	5	29830648	p13.3
SNP_A-1895013	G	G	249	115	221	143	4.707	3.00E-02	rs4446473	5	30262176	p13.3
SNP_A-2131063	A	A	370	20	375	9	4.16	4.14E-02	rs1390631	5	30557762	p13.3
SNP_A-2293796	A	A	314	50	332	32	4.453	3.48E-02	rs10057939	5	30609959	p13.3
SNP_A-1900030	A	A	364	24	374	12	4.13	4.21E-02	---	5	30675417	p13.3
SNP_A-1891974	G	G	376	0	373	5	5.007	0.0252	rs1392425	5	30942805	p13.3
SNP_A-2220532	G	G	416	0	415	5	4.982	2.56E-02	rs1697073	5	30943025	p13.3
SNP_A-1732680	T	T	346	54	366	34	5.107	2.38E-02	rs4867292	5	31020738	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1785401	C	C	363	49	375	31	4.201	4.04E-02	rs1500167	5	31037494	p13.3
SNP_A-1813910	T	T	249	67	296	50	5.174	0.0229	rs3805523	5	31444428	p13.3
SNP_A-2079494	A	A	315	45	360	32	3.84	5.00E-02	---	5	31444470	p13.3
SNP_A-1929946	G	G	345	69	373	45	6.125	1.33E-02	rs16901121	5	31453972	p13.3
SNP_A-1668350	G	G	307	93	346	66	6.738	9.40E-03	rs615344	5	31471289	p13.3
SNP_A-2096860	C	C	392	22	360	38	5.315	2.11E-02	rs16901494	5	31766567	p13.3
SNP_A-1981141	G	A	192	168	201	169	4.28	3.86E-02	rs919337	5	31806490	p13.3
SNP_A-2010790	G	A	209	169	199	185	3.861	4.94E-02	rs6450857	5	31807153	p13.3
SNP_A-2254992	C	T	238	176	215	193	8.545	3.50E-03	rs10940964	5	31811599	p13.3
SNP_A-2300706	T	T	339	45	330	66	3.91	4.80E-02	rs13340334	5	31834660	p13.3
SNP_A-1680004	C	C	337	19	338	34	3.897	4.84E-02	rs10520990	5	31881593	p13.3
SNP_A-2254616	G	G	326	80	358	52	7.417	6.50E-03	rs4867102	5	32054682	p13.3
SNP_A-1981148	G	G	337	79	368	50	7.878	5.00E-03	rs2330882	5	32064081	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2208396	A	A	261	69	282	40	8.431	3.70E-03	rs165958	5	32114826	p13.3
SNP_A-1894041	A	A	265	129	308	68	21.706	3.18E-06	rs157496	5	32123131	p13.3
SNP_A-1805315	T	T	355	41	387	23	6.201	1.28E-02	rs283107	5	32137157	p13.3
SNP_A-2064025	A	A	244	86	267	59	6.039	0.014	rs283115	5	32150127	p13.3
SNP_A-1842797	C	C	237	165	272	130	6.559	0.0104	rs157489	5	32159648	p13.3
SNP_A-2021230	C	C	221	159	241	111	8.34	3.90E-03	rs7705367	5	32197934	p13.3
SNP_A-2062989	T	T	221	163	253	133	5.196	2.26E-02	rs10472812	5	32627931	p13.3
SNP_A-2149039	C	C	246	162	283	127	6.822	9.00E-03	rs2112867	5	32671166	p13.3
SNP_A-1959825	T	T	329	33	361	17	6.261	0.0123	rs16890250	5	32799888	p13.3
SNP_A-1929750	T	T	264	136	228	166	5.569	0.0183	rs1345597	5	32826373	p13.3
SNP_A-2134190	A	A	322	64	282	92	7.487	6.20E-03	rs4867478	5	32853333	p13.3
SNP_A-1904376	G	G	349	47	372	30	4.442	3.51E-02	rs16890437	5	32907837	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2309819	C	C	199	189	222	146	6.251	0.0124	rs13170607	5	33025516	p13.3
SNP_A-1894613	T	T	246	142	288	116	5.603	1.79E-02	rs3860754	5	33185206	p13.3
SNP_A-1951323	A	A	367	49	346	70	4.324	3.76E-02	rs9292484	5	33189004	p13.3
SNP_A-1688164	A	A	253	147	290	118	5.616	0.0178	rs1366267	5	33206249	p13.3
SNP_A-2185324	C	C	366	48	390	28	6.006	0.0143	rs7706830	5	33264668	p13.3
SNP_A-2128527	A	A	356	48	382	30	4.992	2.55E-02	rs972465	5	33291213	p13.3
SNP_A-2127213	A	A	226	160	255	135	3.847	4.98E-02	rs6868223	5	33672351	p13.3
SNP_A-2190992	A	A	218	154	251	123	5.786	1.62E-02	rs4263503	5	33674629	p13.3
SNP_A-2010803	A	A	167	153	192	124	4.752	0.0293	rs4504387	5	33685564	p13.3
SNP_A-1806716	C	C	412	4	405	13	4.82	0.0281	rs10076385	5	33717543	p13.3
SNP_A-1801321	C	C	412	4	404	14	5.629	0.0177	rs10080136	5	33718846	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2179432	C	C	263	145	296	114	5.654	1.74E-02	rs4866399	5	33923176	p13.3
SNP_A-2214645	A	G	199	171	216	174	6.386	0.0115	rs35405	5	33981515	p13.3
SNP_A-1853234	C	C	342	6	367	1	3.897	4.84E-02	rs173781	5	34031547	p13.3
SNP_A-1889429	C	C	197	149	230	128	3.939	4.72E-02	rs384751	5	34661025	p13.2
SNP_A-2128897	G	G	185	129	213	103	4.877	2.72E-02	rs366050	5	34661418	p13.2
SNP_A-1981215	A	A	251	143	221	177	5.499	0.019	rs895357	5	34723003	p13.2
SNP_A-1981216	T	T	281	125	261	159	4.572	3.25E-02	rs2279604	5	34723668	p13.2
SNP_A-1850836	A	A	230	160	204	194	4.742	2.94E-02	rs10036600	5	34742078	p13.2
SNP_A-2211745	C	C	325	45	344	20	10.107	0.0015	rs3857367	5	34896187	p13.2
SNP_A-1706709	C	C	394	4	398	12	3.843	5.00E-02	rs37437	5	35000089	p13.2
SNP_A-2171078	C	C	291	85	252	108	5.197	2.26E-02	rs1039427	5	35201692	p13.2
SNP_A-2137408	G	G	313	97	276	128	6.552	1.05E-02	rs7729932	5	35204127	p13.2
SNP_A-2253431	G	G	280	70	256	100	6.318	0.012	rs13154347	5	35217590	p13.2
SNP_A-1827780	A	A	312	86	279	113	5.461	1.94E-02	rs7713837	5	35219733	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1942853	T	T	302	66	289	97	5.755	1.64E-02	rs1587607	5	35234219	p13.2
SNP_A-1855254	A	A	386	20	381	35	4.002	4.54E-02	rs10038062	5	35256276	p13.2
SNP_A-1849911	G	G	385	13	400	4	5.007	0.0252	rs1604428	5	35263805	p13.2
SNP_A-2127616	C	C	312	32	321	57	5.562	0.0184	rs10080135	5	35267744	p13.2
SNP_A-1741409	C	C	396	4	395	13	4.687	0.0304	rs10512631	5	35312128	p13.2
SNP_A-2267380	G	G	341	19	312	32	4.24	0.0395	rs12523012	5	35341337	p13.2
SNP_A-2194955	C	C	364	38	381	23	4.072	0.0436	rs284756	5	35509366	p13.2
SNP_A-1836728	T	T	393	17	410	6	5.577	1.82E-02	rs1508662	5	35602993	p13.2
SNP_A-2266662	G	G	393	15	414	6	4.231	3.97E-02	rs286441	5	35673325	p13.2
SNP_A-2196111	C	C	234	154	201	183	4.978	2.57E-02	rs6897434	5	35735038	p13.2
SNP_A-2288086	G	G	242	164	214	198	4.869	2.73E-02	rs6451206	5	35736355	p13.2
SNP_A-1802315	G	G	228	148	195	175	4.783	0.0287	rs7733039	5	35743050	p13.2
SNP_A-2266966	G	G	276	88	261	119	4.72	0.0298	rs6895099	5	35834061	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2053918	G	G	372	42	357	63	4.466	3.46E-02	rs1908369	5	35843872	p13.2
SNP_A-2305108	A	A	370	0	351	5	5.233	2.22E-02	rs7731311	5	36395668	p13.2
SNP_A-2254460	C	C	398	6	400	16	4.376	3.65E-02	rs36678	5	36771628	p13.2
SNP_A-2085225	G	G	363	43	340	66	5.606	1.79E-02	rs7731209	5	37852602	p13.2
SNP_A-2107203	C	C	275	47	306	32	4.117	4.25E-02	rs2973116	5	37890495	p13.2
SNP_A-1749455	C	C	330	48	301	81	9.754	0.0018	rs3935014	5	38468492	p13.2
SNP_A-1734316	A	A	350	42	338	66	5.363	0.0206	rs2956597	5	38486102	p13.2
SNP_A-2102177	A	A	393	13	407	3	6.476	0.0109	rs2471157	5	38726292	p13.1
SNP_A-2112436	C	C	305	57	325	39	4.004	4.54E-02	rs357282	5	38904792	p13.1
SNP_A-2133368	G	G	364	14	325	31	7.978	4.70E-03	rs6879555	5	39297270	p13.1
SNP_A-1981356	T	T	374	20	393	9	4.563	0.0327	rs3849766	5	39451617	p13.1
SNP_A-1715019	A	A	375	19	403	9	4.179	4.09E-02	rs3849763	5	39458112	p13.1
SNP_A-1710590	A	A	380	20	403	9	4.672	3.07E-02	rs3849765	5	39458299	p13.1
SNP_A-1714903	A	A	341	23	363	11	4.788	0.0287	rs10491482	5	39547712	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2010842	A	A	203	161	230	132	4.548	3.29E-02	rs2939335	5	39618523	p13.1
SNP_A-2198095	G	G	341	9	360	2	4.769	2.90E-02	rs10805644	5	39635240	p13.1
SNP_A-1881633	G	G	390	16	390	6	4.421	3.55E-02	rs6451436	5	39664592	p13.1
SNP_A-1799857	C	C	367	7	367	1	4.452	0.0349	rs537289	5	39905022	p13.1
SNP_A-1732638	A	A	365	25	382	12	4.934	0.0263	rs924981	5	40145871	p13.1
SNP_A-1882019	G	G	392	18	403	7	4.992	2.55E-02	rs4403223	5	40173826	p13.1
SNP_A-2269403	A	A	253	87	198	98	4.338	0.0373	rs350089	5	40210203	p13.1
SNP_A-1885438	C	C	322	74	334	50	4.681	3.05E-02	rs7718309	5	40564656	p13.1
SNP_A-1696734	T	T	373	27	363	49	6.328	1.19E-02	rs10512745	5	40632972	p13.1
SNP_A-1981395	C	C	374	42	401	19	9.594	0.002	rs16870155	5	40638960	p13.1
SNP_A-1852576	C	C	390	8	410	2	3.859	4.95E-02	rs188933	5	40908044	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1825449	C	C	300	70	330	52	3.894	4.85E-02	rs1645519	5	40913936	p13.1
SNP_A-1891191	G	G	304	78	325	47	8.258	4.10E-03	rs10472342	5	40923808	p13.1
SNP_A-1901441	G	G	307	77	325	53	4.896	0.0269	rs11748194	5	40925681	p13.1
SNP_A-1940162	C	C	293	61	329	43	4.756	0.0292	rs1393155	5	40925894	p13.1
SNP_A-2303799	G	G	302	28	274	48	6.527	0.0106	rs3792633	5	40965153	p13.1
SNP_A-1797846	C	C	310	88	322	58	5.979	1.45E-02	rs2455307	5	40965300	p13.1
SNP_A-2061489	C	C	310	62	271	79	4.001	4.55E-02	rs2455305	5	40965572	p13.1
SNP_A-1677066	G	G	304	94	327	71	4.044	4.43E-02	rs10512750	5	40977315	p13.1
SNP_A-1932286	A	A	317	35	308	14	7.81	5.20E-03	rs6875226	5	40979199	p13.1
SNP_A-1981408	C	C	310	82	290	110	4.67	3.07E-02	rs2167230	5	41005837	p13.1
SNP_A-1981409	A	A	364	48	379	27	6.139	0.0132	rs3792648	5	41011874	p13.1
SNP_A-2153227	G	G	330	34	343	17	5.896	0.0152	rs1450659	5	41051060	p13.1
SNP_A-2125337	G	G	343	53	366	34	4.876	2.72E-02	rs6865420	5	41194329	p13.1
SNP_A-1800622	C	C	342	48	364	28	5.944	1.48E-02	rs10075985	5	41194428	p13.1
SNP_A-2031693	C	C	342	48	365	29	5.416	1.99E-02	rs3805717	5	41197278	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2133566	T	G	174	148	172	146	4.225	3.98E-02	rs4957383	5	41280642	p13.1
SNP_A-1830109	G	G	296	98	303	71	3.877	4.89E-02	rs392077	5	41300085	p13.1
SNP_A-2070196	G	G	277	83	263	115	5.099	2.39E-02	rs2194208	5	41324009	p13.1
SNP_A-1740195	C	C	254	144	228	180	5.279	2.16E-02	rs9292806	5	41462303	p13.1
SNP_A-1718115	G	G	303	53	362	34	7.277	7.00E-03	rs3851442	5	41567911	p13.1
SNP_A-1981435	A	A	367	21	388	10	4.361	3.68E-02	rs17291699	5	41762612	p13.1
SNP_A-1710457	T	T	356	42	345	65	4.939	0.0263	rs10512793	5	41797203	p13.1
SNP_A-2268411	A	A	328	82	350	60	4.122	4.23E-02	rs3764451	5	42434222	p12
SNP_A-2213328	T	G	188	162	187	161	3.874	4.90E-02	rs6866354	5	44662567	p12
SNP_A-1870550	T	T	330	38	362	24	4.214	4.01E-02	rs12655990	5	45265149	p12
SNP_A-1758245	A	A	365	35	397	15	9.168	2.50E-03	rs10512876	5	45295105	p12
SNP_A-1863112	G	G	311	77	318	50	5.293	2.14E-02	rs10473384	5	45379567	p12
SNP_A-2135741	C	C	289	77	306	48	7.016	8.10E-03	—	5	45390556	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2034537	A	A	267	73	292	54	3.908	4.80E-02	rs1483309	5	45450325	p12
SNP_A-2010876	T	T	277	79	318	62	4.097	4.30E-02	rs4532370	5	45542575	p12
SNP_A-1836153	C	C	289	91	323	65	6.14	0.0132	rs1351719	5	45556242	p12
SNP_A-2298296	C	C	299	43	257	57	3.945	0.047	rs1993955	5	50101806	q11.1
SNP_A-1933829	C	C	247	97	229	129	4.934	0.0263	rs26072	5	50139375	q11.1
SNP_A-1840815	T	T	394	20	365	33	3.983	4.60E-02	rs13163470	5	50141459	q11.1
SNP_A-2179531	C	C	267	99	239	123	4.122	4.23E-02	rs27255	5	50157380	q11.1
SNP_A-1881076	G	G	276	54	333	29	11.41	7.00E-04	rs17818181	5	50318857	q11.1
SNP_A-2099108	A	A	188	180	222	150	5.525	1.87E-02	rs2250210	5	50328781	q11.1
SNP_A-1981486	A	A	313	101	355	63	11.427	7.00E-04	rs10512918	5	50329633	q11.1
SNP_A-1981487	A	A	304	100	351	61	12.743	4.00E-04	rs17219934	5	50345549	q11.1
SNP_A-1981489	C	C	307	75	337	37	14.207	2.00E-04	rs10512927	5	50346833	q11.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2276015	C	C	342	20	310	38	6.883	8.70E-03	rs10067693	5	51724287	q11.2
SNP_A-2022136	T	T	328	18	375	7	6.217	1.27E-02	rs7713283	5	51834913	q11.2
SNP_A-2075296	A	A	351	65	378	40	6.948	8.40E-03	rs2432143	5	52167072	q11.2
SNP_A-2199600	G	G	314	34	326	58	4.727	2.97E-02	rs30637	5	52483309	q11.2
SNP_A-1949137	C	C	396	14	373	27	4.687	0.0304	rs38059	5	52593351	q11.2
SNP_A-2226594	G	G	370	36	345	59	6.438	0.0112	rs251529	5	52599397	q11.2
SNP_A-1800764	G	G	375	41	353	67	6.905	0.0086	rs251530	5	52599417	q11.2
SNP_A-1645954	A	A	356	34	337	59	7.196	7.30E-03	rs27313	5	52613835	q11.2
SNP_A-1981541	T	T	203	199	231	163	5.307	0.0212	rs4865763	5	52632147	q11.2
SNP_A-1691178	A	A	327	51	362	36	3.851	4.97E-02	rs445347	5	52991615	q11.2
SNP_A-2010885	T	T	323	27	295	51	8.631	0.0033	rs2221387	5	53109429	q11.2
SNP_A-2105888	C	C	349	35	322	52	4.277	3.86E-02	rs6450167	5	53129319	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2158580	T	C	228	176	202	198	3.881	4.88E-02	rs702604	5	53202393	q11.2
SNP_A-2081743	G	G	327	45	270	70	9.458	2.10E-03	rs4543225	5	53203183	q11.2
SNP_A-2295031	G	G	380	22	368	38	4.439	3.51E-02	rs6898965	5	53270465	q11.2
SNP_A-1708368	A	A	268	130	300	106	4.164	4.13E-02	rs9292042	5	53552883	q11.2
SNP_A-2219297	T	T	210	160	237	113	9.174	2.50E-03	rs1469096	5	53614072	q11.2
SNP_A-2170142	G	G	321	95	349	71	4.621	3.16E-02	rs35930	5	53617481	q11.2
SNP_A-1836360	G	G	300	74	329	53	4.725	2.97E-02	rs35931	5	53617500	q11.2
SNP_A-1681002	C	C	324	70	298	108	9.021	2.70E-03	rs35943	5	53618442	q11.2
SNP_A-2211170	G	G	321	61	274	82	5.888	0.0152	rs35939	5	53642897	q11.2
SNP_A-2233313	G	G	316	22	333	11	4.059	4.39E-02	rs12520084	5	53815968	q11.2
SNP_A-1788062	A	A	354	36	363	19	5.285	2.15E-02	rs13163919	5	53815985	q11.2
SNP_A-1936165	G	G	340	74	364	50	5.463	1.94E-02	rs7734538	5	53935426	q11.2
SNP_A-1870309	G	G	298	64	334	42	6.353	0.0117	rs17626937	5	53950232	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1981606	G	G	357	31	319	45	3.953	4.68E-02	rs334879	5	54555904	q11.2
SNP_A-1822330	G	G	366	2	386	10	4.846	2.77E-02	rs6876554	5	54659023	q11.2
SNP_A-2140873	C	C	359	3	379	11	4.077	4.35E-02	rs6886473	5	54706396	q11.2
SNP_A-1783602	C	C	300	34	278	56	6.215	1.27E-02	rs6859219	5	55474337	q11.2
SNP_A-2258789	A	A	266	122	300	100	4.041	4.44E-02	rs161222	5	55526937	q11.2
SNP_A-1981623	T	T	223	105	263	85	4.81	2.83E-02	rs152345	5	55595454	q11.2
SNP_A-2206704	A	A	257	71	266	44	5.991	0.0144	rs12517669	5	55689902	q11.2
SNP_A-1981633	C	C	218	164	244	130	5.311	0.0212	rs398588	5	55689928	q11.2
SNP_A-2129100	A	A	289	111	323	87	4.675	3.06E-02	rs7732351	5	55707228	q11.2
SNP_A-2203057	C	C	348	26	382	14	4.559	3.28E-02	rs1382906	5	55916217	q11.2
SNP_A-1981650	C	C	295	117	324	92	4.33	3.74E-02	rs9292118	5	55935953	q11.2
SNP_A-1733376	A	A	365	33	395	17	6.064	0.0138	rs9282978	5	56001190	q11.2
SNP_A-1840339	C	C	370	40	391	25	3.998	4.56E-02	rs16886018	5	56013808	q11.2
SNP_A-1981658	G	G	376	26	394	10	7.527	6.10E-03	rs16886056	5	56021933	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1901276	A	A	381	33	395	17	5.368	2.05E-02	rs6878189	5	56022953	q11.2
SNP_A-2087179	C	C	378	30	392	16	4.515	3.36E-02	rs6892240	5	56022987	q11.2
SNP_A-1882316	A	A	244	124	264	94	4.779	2.88E-02	rs6888317	5	56129064	q11.2
SNP_A-1668632	C	C	346	38	348	20	5.254	2.19E-02	rs4700657	5	56320258	q11.2
SNP_A-1937845	T	G	218	188	215	189	3.87	4.91E-02	rs831780	5	56383379	q11.2
SNP_A-1981676	G	G	206	142	175	165	4.153	4.16E-02	rs831790	5	56385455	q11.2
SNP_A-1981677	A	A	234	148	208	178	4.269	3.88E-02	rs831791	5	56385520	q11.2
SNP_A-1981679	T	C	194	170	193	151	6.257	0.0124	rs865553	5	56386202	q11.2
SNP_A-2150947	C	G	231	177	206	200	4.421	3.55E-02	rs831818	5	56393904	q11.2
SNP_A-1731549	C	C	386	10	388	22	4.263	3.89E-02	rs1423142	5	56866126	q11.2
SNP_A-2261733	G	G	267	109	242	136	4.198	4.05E-02	rs4699908	5	56950018	q11.2
SNP_A-2010905	G	G	224	90	202	114	3.953	4.68E-02	rs230877	5	56967784	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2053610	G	G	322	86	294	112	4.682	3.05E-02	rs702697	5	56982898	q11.2
SNP_A-1954624	G	G	404	10	412	2	5.412	0.02	rs12654351	5	57024263	q11.2
SNP_A-1981696	C	C	351	47	363	27	5.526	1.87E-02	rs9292147	5	57313279	q11.2
SNP_A-1922011	C	C	346	36	368	22	3.975	4.62E-02	rs4699919	5	57317763	q11.2
SNP_A-1823692	C	C	333	27	361	15	4.212	4.01E-02	rs1489787	5	57333087	q11.2
SNP_A-1845540	G	G	364	12	379	3	5.656	1.74E-02	—	5	57431444	q11.2
SNP_A-2163729	C	C	348	0	300	4	4.607	3.18E-02	rs6880607	5	57496003	q11.2
SNP_A-1848128	G	G	338	70	343	47	4.154	4.15E-02	rs42964	5	57653662	q11.2
SNP_A-2073641	T	T	363	51	337	71	4.201	4.04E-02	rs6877247	5	58005107	q11.2
SNP_A-1981734	T	T	356	46	334	68	4.947	2.61E-02	rs9283719	5	58009859	q11.2
SNP_A-1981739	G	G	215	149	253	125	4.925	2.65E-02	rs293007	5	58060653	q11.2
SNP_A-1981744	T	T	364	6	384	0	6.277	1.22E-02	rs1423372	5	58121086	q11.2
SNP_A-2125704	A	A	361	53	335	75	4.733	2.96E-02	rs1516435	5	58191112	q11.2
SNP_A-1669985	T	T	308	48	293	79	7.593	5.90E-03	rs9283720	5	58317288	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1684928	T	T	328	68	311	97	5.371	2.05E-02	rs9292189	5	58317315	q11.2
SNP_A-1785381	G	G	342	72	315	97	4.803	2.84E-02	rs9292184	5	58334117	q11.2
SNP_A-1981758	T	T	340	66	307	101	9.014	2.70E-03	rs7727206	5	58337368	q11.2
SNP_A-1981759	T	T	317	57	274	88	9.563	0.002	rs7723432	5	58337541	q11.2
SNP_A-1981765	T	T	279	127	243	155	5.184	2.28E-02	rs2910642	5	58431868	q11.2
SNP_A-2159777	A	A	308	76	284	106	5.872	0.0154	rs13361218	5	58505834	q11.2
SNP_A-1928334	T	C	231	179	207	197	4.688	0.0304	rs6450530	5	59095265	q12.1
SNP_A-2041448	A	A	354	10	381	1	7.926	4.90E-03	rs16877898	5	59642004	q12.1
SNP_A-1843663	T	T	320	50	295	69	4.001	4.55E-02	rs6877757	5	60145279	q12.1
SNP_A-1797442	A	A	248	106	264	74	5.822	1.58E-02	rs7726671	5	60226351	q12.1
SNP_A-1886943	A	A	247	165	277	139	3.922	4.77E-02	rs34638	5	60386244	q12.1
SNP_A-2229643	G	G	340	68	360	46	4.812	2.83E-02	rs12332549	5	60713531	q12.1
SNP_A-2079174	A	A	278	68	316	48	5.426	1.98E-02	rs16892251	5	60863726	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2216136	C	C	232	156	259	127	4.451	0.0349	rs11954764	5	60906914	q12.1
SNP_A-2162546	C	C	311	41	342	22	7.003	8.10E-03	rs696888	5	60933914	q12.1
SNP_A-1981826	A	G	191	167	202	166	4.934	0.0263	rs696891	5	60940318	q12.1
SNP_A-2264422	C	C	400	4	416	0	4.139	0.0419	rs12516216	5	61128382	q12.1
SNP_A-1785306	G	G	369	33	347	51	4.513	3.36E-02	rs17456510	5	61129765	q12.1
SNP_A-1981844	C	C	328	8	350	2	3.944	0.047	—	5	61137308	q12.1
SNP_A-1981852	A	A	261	81	285	57	5.229	2.22E-02	rs7719350	5	61455215	q12.1
SNP_A-1808642	A	A	372	34	394	18	5.511	0.0189	rs13189446	5	61608746	q12.1
SNP_A-2305281	A	A	368	34	382	18	5.179	0.0229	rs153864	5	61756699	q12.1
SNP_A-1652154	T	T	220	98	199	127	4.692	3.03E-02	rs32186	5	61837534	q12.1
SNP_A-2205712	C	C	374	42	392	26	4.183	4.08E-02	rs32170	5	61882830	q12.1
SNP_A-1929262	T	T	279	123	250	154	5.054	0.0246	rs12516160	5	61936540	q12.1
SNP_A-2221876	T	T	244	104	251	75	4.084	4.33E-02	rs6449605	5	62067121	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1824728	T	T	410	4	405	15	6.356	0.0117	rs1357207	5	62215167	q12.1
SNP_A-1878571	C	C	269	87	257	117	4.244	3.94E-02	rs7736115	5	63583267	q12.3
SNP_A-1647162	C	C	266	134	240	172	5.879	1.53E-02	rs1584164	5	63731800	q12.3
SNP_A-2143702	G	G	277	91	305	63	6.438	0.0112	rs1347246	5	64275279	q12.3
SNP_A-2032262	T	T	178	174	197	139	4.507	3.38E-02	rs6896392	5	64276494	q12.3
SNP_A-2285929	G	G	245	133	258	100	4.47	3.45E-02	rs460262	5	64899588	q12.3
SNP_A-1713157	C	C	247	153	282	130	4.008	0.0453	rs37253	5	64937636	q12.3
SNP_A-2261518	G	G	233	157	255	127	4.078	4.34E-02	rs462907	5	64955633	q12.3
SNP_A-1923755	G	G	225	113	260	92	4.395	3.60E-02	rs942961	5	64990651	q12.3
SNP_A-1753871	C	C	293	69	277	103	6.737	9.40E-03	rs2247193	5	65054259	q12.3
SNP_A-2100609	C	C	193	135	159	155	4.36	3.68E-02	rs34982	5	65087412	q12.3
SNP_A-1641865	A	A	250	136	296	108	6.682	9.70E-03	rs2561195	5	65124761	q12.3
SNP_A-2197428	T	T	364	4	390	0	4.262	0.039	rs16875218	5	65127903	q12.3
SNP_A-2041978	A	A	223	183	261	147	6.906	0.0086	rs2250861	5	65150759	q12.3
SNP_A-2115433	C	C	318	44	323	27	3.908	4.80E-02	rs3733657	5	65157124	q12.3
SNP_A-1870006	C	C	246	164	215	201	5.792	0.0161	rs784573	5	65214655	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2280504	C	C	246	168	217	197	4.121	0.0424	rs251316	5	65219038	q12.3
SNP_A-1981943	G	G	212	198	256	162	7.66	5.60E-03	rs251312	5	65221755	q12.3
SNP_A-2251998	T	T	242	148	205	187	7.598	5.80E-03	rs251291	5	65226446	q12.3
SNP_A-2145418	G	G	254	158	218	202	8.047	4.60E-03	rs251288	5	65227632	q12.3
SNP_A-1785546	T	T	190	174	241	147	7.548	6.00E-03	rs706691	5	65230340	q12.3
SNP_A-2255397	T	C	206	202	253	165	10.128	0.0015	rs251298	5	65234468	q12.3
SNP_A-1907828	C	C	216	178	251	149	5.15	2.32E-02	rs2548467	5	65237246	q12.3
SNP_A-2187830	C	C	203	129	233	101	5.467	1.94E-02	rs2432133	5	65239055	q12.3
SNP_A-2034644	T	T	186	182	196	140	4.294	3.82E-02	rs10055584	5	65239180	q12.3
SNP_A-1906605	A	A	372	12	339	25	5.568	0.0183	rs16894640	5	65304630	q12.3
SNP_A-2196014	G	G	317	39	308	22	3.887	4.86E-02	rs6893041	5	65649994	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072771	G	G	246	158	285	125	6.669	9.80E-03	rs4613646	5	65949148	q12.3
SNP_A-2213839	G	G	349	27	335	47	5.645	1.75E-02	rs13157458	5	66098234	q12.3
SNP_A-1982005	G	G	316	86	336	62	4.486	3.42E-02	rs281441	5	67342532	q13.1
SNP_A-2285396	C	C	301	115	329	89	4.553	3.29E-02	rs10940155	5	67482891	q13.1
SNP_A-1982011	A	A	268	80	275	53	4.984	2.56E-02	rs10515070	5	67561331	q13.1
SNP_A-2298315	T	T	282	92	304	66	5.083	2.42E-02	rs16897511	5	67562069	q13.1
SNP_A-1680700	C	C	345	55	373	37	4.491	3.41E-02	rs391974	5	67630777	q13.1
SNP_A-2283645	G	G	286	48	310	28	6.206	1.27E-02	rs411751	5	67641640	q13.1
SNP_A-1982013	A	A	307	95	327	67	5.391	2.02E-02	rs16897699	5	67671813	q13.1
SNP_A-2211147	C	C	320	96	284	134	8.419	3.70E-03	rs12234004	5	67743460	q13.1
SNP_A-2153214	C	C	304	70	271	95	5.596	1.80E-02	rs10075612	5	67748961	q13.1
SNP_A-1948177	G	G	365	27	347	49	6.803	9.10E-03	rs17324835	5	67959214	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982019	A	A	376	18	395	5	7.771	0.0053	rs40309	5	67978636	q13.1
SNP_A-1982025	A	A	224	104	256	84	4.047	4.43E-02	rs246977	5	68042270	q13.1
SNP_A-2181090	T	C	220	196	225	187	4.654	0.031	rs6863228	5	68140404	q13.1
SNP_A-2107969	T	T	201	175	223	139	5.005	0.0253	rs1366108	5	68150692	q13.1
SNP_A-2243396	G	G	193	139	174	172	4.198	4.05E-02	rs7730795	5	68287956	q13.1
SNP_A-2010944	A	A	412	4	416	0	4.019	4.50E-02	rs2972362	5	68591120	q13.2
SNP_A-1863314	A	A	227	119	253	71	12.826	3.00E-04	rs10057258	5	70807449	q13.2
SNP_A-1879532	G	G	240	150	267	119	4.99	2.55E-02	rs3761966	5	70836231	q13.2
SNP_A-1957310	G	G	220	124	250	86	8.698	3.20E-03	rs421128	5	70842829	q13.2
SNP_A-1747513	G	G	242	158	280	130	5.366	2.05E-02	rs277941	5	70942267	q13.2
SNP_A-2251236	T	T	233	165	275	131	7.299	6.90E-03	rs277990	5	70954659	q13.2
SNP_A-1641991	C	C	334	44	327	67	4.51	3.37E-02	rs7731217	5	71108525	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138961	G	G	341	9	306	18	3.896	4.84E-02	rs2644977	5	71275617	q13.2
SNP_A-1846698	A	A	238	94	237	65	3.881	4.88E-02	rs1217770	5	71343136	q13.2
SNP_A-1869077	G	G	343	31	360	16	5.193	2.27E-02	rs1692375	5	71373844	q13.2
SNP_A-1860201	G	G	337	61	357	41	4.498	0.0339	rs10043295	5	71778780	q13.2
SNP_A-2264346	C	C	306	24	295	41	4.594	3.21E-02	rs7722077	5	72040332	q13.2
SNP_A-1982080	G	G	412	4	420	0	4.058	4.40E-02	rs16902903	5	72428422	q13.2
SNP_A-1953163	G	G	213	125	183	153	5.087	0.0241	rs4435846	5	72609843	q13.2
SNP_A-2027594	A	A	366	44	352	64	3.933	4.73E-02	rs4131513	5	72614202	q13.2
SNP_A-1787529	T	T	337	51	357	33	4.428	3.53E-02	rs2973915	5	72676341	q13.2
SNP_A-1865368	T	T	318	80	293	109	5.453	0.0195	rs1220620	5	72813638	q13.2
SNP_A-2036586	T	T	338	78	313	101	3.911	4.80E-02	rs1220627	5	72906819	q13.2
SNP_A-2122391	A	G	211	191	220	178	4.826	2.80E-02	rs7722018	5	73127261	q13.2
SNP_A-2032884	G	G	367	31	341	61	10.718	1.10E-03	rs2927703	5	73268292	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253540	C	C	355	5	364	14	3.939	4.72E-02	rs12153699	5	73309487	q13.3
SNP_A-1791037	A	A	284	102	306	76	4.597	3.20E-02	rs4703622	5	73465917	q13.3
SNP_A-2170403	C	C	246	116	257	81	5.643	1.75E-02	rs10071742	5	73507433	q13.3
SNP_A-1888158	G	G	229	95	212	126	4.71	3.00E-02	rs292210	5	73592420	q13.3
SNP_A-1811532	G	G	389	15	382	30	4.986	2.56E-02	rs472986	5	73608117	q13.3
SNP_A-2297512	C	C	382	30	394	16	4.442	3.51E-02	rs17557368	5	73646115	q13.3
SNP_A-1851363	C	C	322	92	348	68	4.604	3.19E-02	rs294995	5	73708705	q13.3
SNP_A-1982120	G	G	330	72	349	47	5.739	0.0166	rs452853	5	73715141	q13.3
SNP_A-1808674	G	G	302	56	333	37	5.199	2.26E-02	rs6878185	5	73753780	q13.3
SNP_A-2131166	G	G	241	163	199	195	6.745	9.40E-03	rs212925	5	73846234	q13.3
SNP_A-1868972	C	C	273	57	311	27	13.093	3.00E-04	rs11745925	5	73847006	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086809	T	T	282	114	320	92	4.433	3.52E-02	rs11748424	5	73870003	q13.3
SNP_A-1851776	C	C	325	87	289	111	4.844	2.77E-02	rs298390	5	73884546	q13.3
SNP_A-1849188	A	G	200	148	190	184	4.956	2.60E-02	rs12152861	5	73990375	q13.3
SNP_A-2262542	C	C	374	6	363	15	4.016	4.51E-02	rs3761740	5	74667889	q13.3
SNP_A-1982167	G	G	414	0	415	5	4.958	2.60E-02	rs16873303	5	75627265	q13.3
SNP_A-1839936	A	A	261	151	229	181	4.796	2.85E-02	rs2913248	5	75668501	q13.3
SNP_A-1982169	C	C	347	7	312	16	4.396	3.60E-02	rs11954110	5	75669623	q13.3
SNP_A-2023090	A	A	307	87	286	114	4.325	3.75E-02	rs4516825	5	75845999	q13.3
SNP_A-1982177	G	G	395	7	395	1	4.455	3.48E-02	rs2069697	5	75952789	q13.3
SNP_A-1943819	G	G	393	23	409	11	4.535	0.0332	rs12513912	5	75964333	q13.3
SNP_A-2287557	G	G	369	39	385	19	7.217	7.20E-03	rs7721799	5	76286134	q13.3
SNP_A-1686850	T	T	248	104	231	133	3.952	4.68E-02	rs3903346	5	76303469	q13.3
SNP_A-1931386	C	C	219	135	257	111	5.106	2.38E-02	rs6889575	5	76518096	q13.3
SNP_A-1834175	G	G	351	15	350	4	6.172	1.30E-02	rs7715119	5	76711174	q13.3
SNP_A-2115586	G	C	198	152	183	177	3.905	0.0482	rs1678772	5	76774626	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1655329	G	G	193	169	232	144	5.312	0.0212	rs251470	5	76862558	q13.3
SNP_A-1982201	A	A	194	192	209	153	4.201	4.04E-02	rs2279010	5	76964513	q14.1
SNP_A-2168701	C	C	374	34	392	12	10.925	9.00E-04	rs6453340	5	76998030	q14.1
SNP_A-1821849	C	C	400	6	410	0	6.104	0.0135	rs351878	5	77047906	q14.1
SNP_A-2082248	C	C	196	148	223	121	4.45	0.0349	rs1396614	5	77152853	q14.1
SNP_A-1915981	C	C	346	10	365	3	4.079	4.34E-02	rs353967	5	77155814	q14.1
SNP_A-1855862	C	C	347	19	366	8	4.902	2.68E-02	rs354616	5	77157996	q14.1
SNP_A-1827708	A	A	362	14	379	5	4.569	3.25E-02	rs353972	5	77165256	q14.1
SNP_A-2188855	C	C	215	99	255	77	5.657	1.74E-02	rs355422	5	77284286	q14.1
SNP_A-1982221	T	T	366	0	354	4	4.112	4.26E-02	rs6870027	5	77810312	q14.1
SNP_A-1812024	A	A	214	140	239	95	9.423	2.10E-03	rs3114492	5	78206368	q14.1
SNP_A-2292771	C	C	414	2	411	9	4.446	3.50E-02	rs16876106	5	78257943	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2135439	A	G	230	170	199	193	5.435	1.97E-02	rs337887	5	78264792	q14.1
SNP_A-1982237	C	C	279	49	297	25	8.292	4.00E-03	rs1067263	5	78344487	q14.1
SNP_A-2166724	C	C	284	116	266	148	4.228	3.98E-02	rs16876363	5	78363515	q14.1
SNP_A-2137713	A	A	335	61	328	88	4.477	0.0344	rs259129	5	79095173	q14.1
SNP_A-2023855	A	A	277	113	261	145	4.125	4.23E-02	rs259130	5	79095304	q14.1
SNP_A-2010999	A	A	331	29	323	15	3.863	4.94E-02	rs2434310	5	79338377	q14.1
SNP_A-2134693	G	G	238	148	256	116	4.278	3.86E-02	rs4704638	5	79550489	q14.1
SNP_A-2066511	A	A	301	55	304	30	6.673	9.80E-03	rs7703773	5	79665480	q14.1
SNP_A-1838542	G	G	378	10	367	23	5.279	2.16E-02	rs16877757	5	79719119	q14.1
SNP_A-1982267	C	C	377	13	369	25	3.855	4.96E-02	rs1423113	5	79730585	q14.1
SNP_A-1754646	C	C	361	21	364	38	4.403	3.59E-02	rs249039	5	79831364	q14.1
SNP_A-1840584	G	G	383	17	379	31	3.981	4.60E-02	rs10474632	5	79993473	q14.1
SNP_A-1672178	C	C	275	123	255	157	4.643	3.12E-02	rs35000	5	80361309	q14.1
SNP_A-2063709	A	A	216	116	234	84	5.541	1.86E-02	rs34121	5	80474671	q14.1
SNP_A-2105253	G	G	359	29	346	46	4.073	0.0436	rs6872459	5	80718471	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1822665	C	C	372	28	356	44	3.907	4.81E-02	rs6889735	5	81255715	q14.1
SNP_A-1668586	T	T	287	101	324	80	4.356	3.69E-02	rs6888977	5	81617808	q14.2
SNP_A-1982311	G	G	363	23	347	41	5.418	1.99E-02	rs10514237	5	81651106	q14.2
SNP_A-1674967	C	C	265	135	299	109	4.741	2.94E-02	rs226199	5	81656537	q14.2
SNP_A-2044999	C	C	386	16	377	5	5.361	0.0206	rs224825	5	81718984	q14.2
SNP_A-1982327	A	A	292	106	261	137	5.693	1.70E-02	rs2015915	5	81988939	q14.2
SNP_A-1916653	C	C	310	34	329	15	7.932	4.90E-03	rs17283939	5	82024581	q14.2
SNP_A-1694351	T	T	297	103	331	77	5.518	1.88E-02	rs10514242	5	82042399	q14.2
SNP_A-1910602	A	A	273	87	241	113	5.322	2.11E-02	rs1423510	5	82163385	q14.2
SNP_A-1814637	T	T	220	188	238	152	4.115	4.25E-02	rs4533865	5	82213182	q14.2
SNP_A-1874210	C	C	374	10	397	3	4.131	4.21E-02	rs37547	5	82332438	q14.2
SNP_A-2270966	G	G	215	145	188	180	5.491	1.91E-02	rs376689	5	82334829	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2303251	A	A	383	33	404	16	6.439	0.0112	rs378147	5	82344871	q14.2
SNP_A-1982345	A	A	354	56	374	32	7.075	7.80E-03	rs301279	5	82631937	q14.2
SNP_A-1678132	C	C	395	5	396	16	5.587	1.81E-02	rs10514252	5	82642665	q14.2
SNP_A-1703103	G	G	369	19	401	9	4.298	3.82E-02	rs717938	5	82648889	q14.2
SNP_A-1696856	A	A	394	4	391	13	4.732	2.96E-02	rs10514253	5	82674123	q14.2
SNP_A-2086161	G	G	364	28	375	13	5.631	1.76E-02	rs521500	5	83355598	q14.3
SNP_A-2011023	T	T	359	33	358	18	4.082	4.34E-02	rs1858207	5	83827113	q14.3
SNP_A-2063689	A	A	339	13	338	26	4.135	4.20E-02	rs7711571	5	84014830	q14.3
SNP_A-1918143	A	A	343	33	297	57	9.051	2.60E-03	rs9968641	5	84437455	q14.3
SNP_A-2083713	A	A	335	63	352	34	8.909	0.0028	rs12520620	5	84444708	q14.3
SNP_A-1946918	A	A	290	110	250	132	4.551	3.29E-02	rs10942370	5	84444987	q14.3
SNP_A-2097113	T	C	217	161	217	167	14.76	0.0001	rs7443317	5	84455571	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1823782	G	A	210	168	203	165	8.569	3.40E-03	rs6879600	5	84458220	q14.3
SNP_A-2287411	C	C	250	110	189	143	11.667	6.00E-04	rs9293407	5	84466583	q14.3
SNP_A-2045133	T	C	209	183	223	169	8.174	0.0043	rs9293421	5	84472609	q14.3
SNP_A-2060066	C	G	197	139	181	157	10.026	0.0015	rs13157826	5	84480200	q14.3
SNP_A-2071818	A	C	208	190	230	186	4.642	3.12E-02	rs10071739	5	84542611	q14.3
SNP_A-2251517	G	A	208	182	218	166	7.911	4.90E-03	rs10462442	5	84551997	q14.3
SNP_A-1872248	C	C	311	41	302	66	5.62	0.0178	rs2931116	5	84639708	q14.3
SNP_A-1920048	C	C	347	63	317	85	4.547	3.30E-02	rs445600	5	84651901	q14.3
SNP_A-1734474	G	G	331	63	318	88	4.22	3.99E-02	rs173540	5	84708260	q14.3
SNP_A-2266313	A	A	321	45	299	65	4.412	3.57E-02	rs247722	5	84715625	q14.3
SNP_A-1859970	C	C	264	138	239	171	4.688	0.0304	rs247652	5	84740454	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2243763	C	C	336	56	318	82	5.314	0.0212	rs481689	5	84812541	q14.3
SNP_A-2033333	A	A	274	130	241	153	3.859	4.95E-02	rs800837	5	84853165	q14.3
SNP_A-1790883	T	T	274	128	241	161	5.883	1.53E-02	rs479076	5	84862649	q14.3
SNP_A-2097713	A	A	357	49	327	67	3.93	4.74E-02	rs300838	5	84867569	q14.3
SNP_A-2215612	A	A	342	8	364	0	8.414	3.70E-03	rs1827347	5	84896722	q14.3
SNP_A-1908236	G	G	361	45	326	62	4.078	4.34E-02	rs1429049	5	85060187	q14.3
SNP_A-2178112	G	A	208	180	233	157	13.922	2.00E-04	rs13161683	5	85082957	q14.3
SNP_A-1982399	T	T	283	101	312	70	7.028	8.00E-03	rs1346584	5	85085910	q14.3
SNP_A-1948420	C	C	280	134	317	101	6.908	0.0086	rs9293438	5	85088169	q14.3
SNP_A-1982401	T	T	309	79	335	51	7.075	7.80E-03	rs1604089	5	85143956	q14.3
SNP_A-1722522	A	A	298	94	328	70	4.905	2.68E-02	rs1500150	5	85168545	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072465	C	C	217	127	156	138	6.554	1.05E-02	rs6879389	5	85178284	q14.3
SNP_A-1949598	G	G	216	196	257	161	6.942	8.40E-03	rs2974092	5	85218272	q14.3
SNP_A-2132350	A	A	220	182	264	138	10.05	0.0015	rs12521745	5	85230103	q14.3
SNP_A-1982403	G	A	179	175	205	153	4.382	3.63E-02	rs2898535	5	85267392	q14.3
SNP_A-1982404	A	G	197	165	197	169	4.949	2.61E-02	rs893554	5	85267959	q14.3
SNP_A-2219732	C	C	284	92	287	65	3.872	4.91E-02	rs12521073	5	85303222	q14.3
SNP_A-1670918	A	A	296	104	264	140	7.12	0.0076	rs986943	5	85316736	q14.3
SNP_A-1982405	G	G	296	46	311	29	4.218	4.00E-02	rs1363274	5	85388982	q14.3
SNP_A-2168096	C	C	274	118	231	147	6.583	0.0103	rs1862230	5	85480624	q14.3
SNP_A-2065322	T	T	260	124	229	159	6.273	0.0123	rs6452689	5	85480815	q14.3
SNP_A-1688826	A	T	223	165	190	184	5.242	2.20E-02	rs1363278	5	85513188	q14.3
SNP_A-2116253	T	T	342	60	372	40	5.138	2.34E-02	rs7726912	5	85640733	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2310398	G	G	324	44	356	24	7.198	7.30E-03	rs1445702	5	85662044	q14.3
SNP_A-2171405	C	C	325	39	353	23	5.092	0.024	rs7700535	5	85671585	q14.3
SNP_A-1982408	A	A	340	24	361	9	7.399	6.50E-03	rs756451	5	85703846	q14.3
SNP_A-2132795	T	T	319	71	352	48	5.943	1.48E-02	---	5	85738608	q14.3
SNP_A-2111405	G	G	220	156	238	112	7.009	8.10E-03	rs1392473	5	85816409	q14.3
SNP_A-2281062	C	C	223	159	251	125	5.677	0.0172	rs1472527	5	85836471	q14.3
SNP_A-2085631	G	G	372	8	382	20	4.66	0.0309	rs1098507	5	87023209	q14.3
SNP_A-1855046	G	G	404	4	410	0	4.039	4.45E-02	rs16902705	5	87034687	q14.3
SNP_A-2302553	G	G	314	84	307	51	6.046	1.39E-02	rs12110233	5	87128522	q14.3
SNP_A-1929691	C	C	290	122	314	96	4.05	4.42E-02	rs5019341	5	87155425	q14.3
SNP_A-1715401	A	A	254	140	289	117	4.135	4.20E-02	rs1423634	5	87180178	q14.3
SNP_A-1720081	G	G	296	104	329	81	4.479	3.43E-02	rs9293491	5	87244876	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1648808	G	G	282	92	313	53	12.02	5.00E-04	rs10514296	5	87274157	q14.3
SNP_A-2198078	A	A	291	87	317	65	4.275	3.87E-02	rs1108098	5	87275287	q14.3
SNP_A-2063402	A	A	237	101	270	76	5.586	1.81E-02	rs16902899	5	87282748	q14.3
SNP_A-1982444	C	C	280	92	314	70	4.745	2.94E-02	rs13356445	5	87284603	q14.3
SNP_A-1745476	T	T	274	116	311	93	4.626	0.0315	rs9293494	5	87288194	q14.3
SNP_A-2174586	G	G	298	106	327	77	5.941	1.48E-02	rs11948159	5	87304761	q14.3
SNP_A-2057742	G	G	304	112	329	87	4.128	4.22E-02	rs6878137	5	87433419	q14.3
SNP_A-2089262	C	C	296	88	321	59	6.713	9.60E-03	rs10079980	5	87434758	q14.3
SNP_A-2155589	G	G	282	82	315	59	5.441	1.97E-02	rs1816740	5	87469833	q14.3
SNP_A-1721902	T	T	297	101	327	73	5.943	1.48E-02	rs6863354	5	87490989	q14.3
SNP_A-1758886	G	G	276	92	305	61	7.723	5.50E-03	rs1427920	5	87506843	q14.3
SNP_A-2134292	A	A	277	107	310	70	9.569	0.002	rs33708	5	87542893	q14.3
SNP_A-1727685	G	G	267	103	315	75	7.842	5.10E-03	rs33706	5	87589237	q14.3
SNP_A-2173140	T	T	244	82	260	52	6.92	8.50E-03	rs33704	5	87597521	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1886785	G	G	305	109	345	75	8.701	3.20E-03	rs33703	5	87602487	q14.3
SNP_A-2028220	C	C	283	75	340	56	6.071	0.0137	rs2115885	5	87634574	q14.3
SNP_A-2036932	A	A	209	185	245	141	8.712	3.20E-03	rs6452787	5	87748587	q14.3
SNP_A-1881338	C	C	282	118	331	89	7.496	6.20E-03	rs6452788	5	87748669	q14.3
SNP_A-2273045	C	C	211	159	231	115	7.174	7.40E-03	rs4244212	5	87800374	q14.3
SNP_A-1715955	C	C	235	165	288	124	11.013	9.00E-04	rs6860708	5	87884954	q14.3
SNP_A-2044636	G	G	341	41	355	25	4.155	4.15E-02	rs2161228	5	88037554	q14.3
SNP_A-1893005	T	T	184	172	223	155	3.965	0.0465	rs628158	5	88077537	q14.3
SNP_A-1648260	C	C	223	177	256	150	4.458	3.47E-02	rs639725	5	88086042	q14.3
SNP_A-1691740	C	C	221	175	257	151	4.3	3.81E-02	rs40504	5	88095212	q14.3
SNP_A-1659959	C	C	228	172	265	147	4.56	0.0327	rs34321	5	88104392	q14.3
SNP_A-2247163	A	A	366	24	383	11	5.194	2.27E-02	rs1650626	5	88274962	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1643678	G	G	370	30	390	16	4.743	2.94E-02	rs301719	5	88316988	q14.3
SNP_A-2065441	C	C	311	51	356	22	14.217	2.00E-04	rs16903471	5	88475663	q14.3
SNP_A-2187931	C	C	339	71	361	37	11.219	8.00E-04	rs16903479	5	88506721	q14.3
SNP_A-1982463	T	T	334	64	364	40	6.783	9.20E-03	rs702850	5	88593084	q14.3
SNP_A-2244677	T	T	325	73	355	45	7.963	4.80E-03	rs194131	5	88598347	q14.3
SNP_A-1922216	G	G	364	48	388	30	4.877	2.72E-02	rs17500041	5	88599364	q14.3
SNP_A-1813703	T	T	369	23	378	10	5.209	2.25E-02	rs40603	5	88600147	q14.3
SNP_A-1817351	T	T	351	47	377	29	5.113	2.38E-02	rs6872041	5	88629311	q14.3
SNP_A-1982466	A	A	242	158	213	185	3.969	4.64E-02	rs4537088	5	88868246	q14.3
SNP_A-1881077	A	A	265	105	219	133	7.222	7.20E-03	rs12655756	5	88893964	q14.3
SNP_A-1927596	A	G	207	179	204	168	5.431	1.98E-02	rs9293518	5	88911327	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098193	G	G	310	38	334	24	3.915	4.79E-02	rs6452846	5	89040983	q14.3
SNP_A-1982474	A	A	324	78	357	53	6.292	0.0121	rs6888553	5	89275736	q14.3
SNP_A-1677508	A	A	284	110	265	143	4.719	0.0298	rs4569906	5	89866012	q14.3
SNP_A-1911600	C	T	212	146	180	172	7.663	5.60E-03	rs10062714	5	89988287	q14.3
SNP_A-2260020	G	G	221	149	260	122	5.662	1.73E-02	rs4916813	5	89992722	q14.3
SNP_A-1982494	A	A	225	145	239	113	3.945	0.047	rs1028191	5	90004382	q14.3
SNP_A-1684940	C	C	247	145	223	183	5.384	2.03E-02	rs1474119	5	90086958	q14.3
SNP_A-2035529	G	G	219	139	245	109	5.064	2.44E-02	rs2913442	5	91139391	q14.3
SNP_A-1982516	G	G	276	56	307	35	6.348	0.0118	rs825388	5	91276966	q14.3
SNP_A-1982521	T	T	269	91	303	71	4.225	3.98E-02	rs6861029	5	91918851	q15
SNP_A-1947138	A	A	217	153	257	111	10.052	0.0015	rs905217	5	91991717	q15
SNP_A-1714547	A	A	224	162	271	131	7.421	6.40E-03	rs1155697	5	92033729	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2185758	C	C	329	17	328	34	5.309	0.0212	rs1199899	5	92152419	q15
SNP_A-1927459	-	A	164	164	189	135	4.559	0.0327	rs163952	5	92302191	q15
SNP_A-1756260	A	G	194	184	227	171	5.436	1.97E-02	rs2635182	5	92329239	q14.3
SNP_A-2311178	T	T	374	10	368	22	4.502	3.38E-02	rs17082799	5	92344239	q15
SNP_A-1792967	A	A	264	62	243	85	4.462	3.46E-02	rs7701128	5	92621505	q15
SNP_A-2076210	G	G	387	17	401	7	4.396	3.60E-02	rs17368734	5	92724143	q15
SNP_A-1982540	G	G	310	18	280	30	4.021	4.49E-02	rs17083213	5	92912225	q15
SNP_A-1642771	C	C	396	4	412	0	4.14	0.0419	rs10514375	5	93010815	q15
SNP_A-2177709	T	T	316	52	292	90	10.859	0.001	rs10060331	5	93045806	q15
SNP_A-1982542	C	C	334	58	299	79	4.901	2.68E-02	rs9314086	5	93047752	q15
SNP_A-1735378	C	C	334	62	322	90	5.063	2.44E-02	rs7717718	5	93080255	q15
SNP_A-2267880	T	T	363	53	340	78	5.519	1.88E-02	rs13155452	5	93190205	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814023	G	G	312	86	294	112	3.87	4.92E-02	rs17083380	5	93196232	q15
SNP_A-1755052	T	T	325	35	312	62	7.516	6.10E-03	-	5	93235540	q15
SNP_A-2311453	T	T	361	51	337	75	5.397	2.02E-02	rs7715562	5	93247790	q15
SNP_A-2107343	A	A	338	46	312	68	5.265	0.0218	rs17314825	5	93260693	q15
SNP_A-2186884	G	G	330	38	306	60	5.839	1.57E-02	rs12188163	5	93276364	q15
SNP_A-2021288	A	A	349	35	309	51	4.639	3.13E-02	rs9314092	5	93352118	q15
SNP_A-2033299	G	G	332	46	296	66	5.292	2.14E-02	rs12716455	5	93376011	q15
SNP_A-2284868	A	A	268	42	263	71	6.604	1.02E-02	rs2290937	5	93382271	q15
SNP_A-1895530	C	C	342	36	275	49	5.14	2.34E-02	rs12716459	5	93424848	q15
SNP_A-2299624	A	A	352	46	324	70	6.105	0.0135	rs9314100	5	93473150	q15
SNP_A-1718341	C	C	341	39	332	70	8.325	3.90E-03	rs10514380	5	93483443	q15
SNP_A-2097794	C	C	349	11	313	21	4.114	4.25E-02	rs13174700	5	93580400	q15
SNP_A-1883822	T	T	307	49	288	72	4.956	2.60E-02	rs17376456	5	93583458	q15
SNP_A-2295068	T	T	346	36	314	60	7.468	0.0063	rs12188453	5	93586563	q15
SNP_A-1756929	G	G	350	50	338	74	4.678	3.05E-02	rs10514382	5	93640607	q15
SNP_A-2034033	C	C	342	30	363	17	4.137	4.20E-02	rs12655669	5	94035412	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1705059	T	T	309	31	320	54	4.808	2.83E-02	rs430555	5	94082340	q15
SNP_A-1893019	T	T	365	51	386	28	7.279	7.00E-03	—	5	94239098	q15
SNP_A-1931328	T	T	359	37	387	17	8.379	0.0038	—	5	94239150	q15
SNP_A-1982551	G	G	270	94	291	71	3.987	4.59E-02	rs293053	5	94296999	q15
SNP_A-2298649	T	T	375	9	382	2	4.519	3.35E-02	rs293043	5	94315965	q15
SNP_A-2169992	A	A	271	67	290	46	4.54	3.31E-02	rs7715499	5	94357154	q15
SNP_A-1872398	T	T	225	119	270	98	5.32	2.11E-02	rs6556858	5	94449804	q15
SNP_A-2089474	G	G	300	28	295	55	8.12	4.40E-03	rs10079049	5	94584565	q15
SNP_A-2142153	G	G	408	4	416	0	4.058	4.40E-02	rs17085176	5	95217663	q15
SNP_A-1924145	C	C	287	85	267	111	4.123	4.23E-02	rs17085593	5	95656461	q15
SNP_A-2266383	C	C	223	99	258	80	4.178	4.09E-02	rs10045787	5	95693430	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1834029	A	A	237	165	271	139	4.421	3.55E-02	rs1353797	5	95715579	q15
SNP_A-1900509	G	G	249	117	287	91	5.752	1.65E-02	rs11948824	5	95730061	q15
SNP_A-1856562	A	A	293	61	268	96	8.779	3.00E-03	rs7713317	5	95742478	q15
SNP_A-1713386	C	C	244	112	286	88	5.768	1.63E-02	rs1995186	5	95752374	q15
SNP_A-1798950	A	A	266	138	298	112	4.476	0.0344	rs3811942	5	95754196	q15
SNP_A-1952471	G	G	279	137	316	104	6.801	9.10E-03	rs11743265	5	95770500	q15
SNP_A-2213265	T	T	221	163	258	130	6.554	1.05E-02	rs156019	5	95773119	q15
SNP_A-1930408	G	G	229	165	267	135	5.831	1.57E-02	rs155971	5	95776152	q15
SNP_A-2220513	C	C	224	154	265	129	5.317	2.11E-02	rs456709	5	95785179	q15
SNP_A-1668488	A	A	231	169	270	142	5.204	2.25E-02	rs271927	5	95815874	q15
SNP_A-1880669	C	C	364	0	368	4	3.935	4.73E-02	rs261965	5	95874972	q15
SNP_A-1982583	T	T	302	88	268	126	8.756	3.10E-03	rs26503	5	96104065	q15
SNP_A-1715791	G	G	299	89	260	128	9.73	0.0018	rs26504	5	96153100	q15
SNP_A-1724140	C	C	274	64	275	25	14.881	0.0001	rs469736	5	96195142	q15
SNP_A-1720783	T	T	221	105	226	150	4.458	3.47E-02	rs1363974	5	96367889	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1696100	C	C	225	137	221	183	4.359	3.68E-02	rs27294	5	96431333	q15
SNP_A-2313697	C	C	297	51	296	24	8.563	3.40E-03	rs100039917	5	96478101	q15
SNP_A-1982601	C	C	203	137	225	103	5.734	0.0166	rs43497	5	96511656	q15
SNP_A-2198304	T	C	210	176	205	177	5.001	0.0253	rs7349811	5	96513963	q15
SNP_A-1798851	C	G	222	176	216	198	5.14	2.34E-02	rs316214	5	96523394	q15
SNP_A-2126524	C	C	361	25	371	9	7.619	5.80E-03	rs10463199	5	96571231	q15
SNP_A-2176514	G	G	322	82	298	106	3.993	4.57E-02	rs4869168	5	96901670	q15
SNP_A-2198350	A	A	324	20	326	36	4.121	4.23E-02	rs10041715	5	96908125	q15
SNP_A-1931809	G	G	329	25	353	11	6.151	1.31E-02	rs1896947	5	97076449	q15
SNP_A-2192342	C	C	402	12	416	4	4.197	4.05E-02	rs6557020	5	97300956	q21.1
SNP_A-1889155	C	C	315	29	332	16	4.179	4.09E-02	rs2352229	5	97332025	q21.1
SNP_A-1872399	C	C	313	35	327	17	6.514	1.07E-02	rs17166099	5	97931040	q21.1
SNP_A-1682854	C	C	202	144	212	108	4.376	3.64E-02	rs1978419	5	97944087	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982644	G	G	306	62	287	85	4.186	4.08E-02	rs6878136	5	98386091	q21.1
SNP_A-1982665	C	C	296	18	283	45	11.564	7.00E-04	rs17164416	5	99415346	q21.1
SNP_A-2221140	G	G	403	13	416	4	4.952	2.61E-02	rs17777011	5	100107822	q21.1
SNP_A-1982684	G	G	397	7	399	17	3.997	4.56E-02	rs17133261	5	100579903	q21.1
SNP_A-2233681	A	A	290	112	331	75	10.008	1.60E-03	rs1459581	5	100663882	q21.1
SNP_A-2113498	C	C	281	73	327	53	5.741	0.0166	rs2125715	5	100686064	q21.1
SNP_A-1663408	A	A	387	13	408	4	5.143	2.33E-02	rs4415055	5	100693461	q21.1
SNP_A-2077466	C	C	295	57	322	36	5.873	0.0154	rs10074812	5	100702908	q21.1
SNP_A-1890366	G	G	300	102	317	69	6.515	1.07E-02	rs898297	5	100710537	q21.1
SNP_A-1936876	G	G	312	96	330	58	9.385	2.20E-03	rs17135187	5	100733960	q21.1
SNP_A-2159995	G	G	297	87	346	62	7.208	7.30E-03	rs1459570	5	100735024	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213154	C	C	346	10	293	1	5.899	1.51E-02	rs980831	5	100778766	q21.1
SNP_A-1959117	C	C	403	13	416	4	4.952	2.61E-02	---	5	100779590	q21.1
SNP_A-2135408	A	A	400	12	416	4	4.237	0.0395	---	5	100784772	q21.1
SNP_A-2146760	C	C	401	15	410	6	3.957	4.67E-02	rs17135627	5	100786738	q21.1
SNP_A-1810601	T	T	380	12	359	1	8.558	3.40E-03	rs17135652	5	100789674	q21.1
SNP_A-1721275	A	A	301	97	345	67	8.245	4.10E-03	rs1037796	5	100796854	q21.1
SNP_A-2063684	A	A	402	0	403	5	4.957	2.60E-02	rs17137919	5	100992148	q21.1
SNP_A-1889891	C	C	396	14	416	4	5.929	0.0149	rs10036886	5	101232873	q21.1
SNP_A-1708915	A	A	288	92	325	73	4.007	0.0453	rs7731840	5	101286464	q21.1
SNP_A-2288605	C	C	337	61	356	42	4.026	0.0448	rs1453115	5	101289699	q21.1
SNP_A-1741859	G	G	327	69	360	46	6.061	0.0138	rs9285932	5	101310337	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1822029	A	A	354	60	373	39	4.946	2.61E-02	rs6886984	5	101328723	q21.1
SNP_A-1982696	A	A	308	26	337	11	7.101	7.70E-03	rs7708030	5	101391397	q21.1
SNP_A-1982697	T	T	227	189	255	159	4.208	0.0402	rs1381967	5	101466805	q21.1
SNP_A-2185873	A	A	278	132	303	105	4.147	4.17E-02	rs1901519	5	101782372	q21.1
SNP_A-2291749	A	A	328	4	315	13	5.003	0.0253	rs6874903	5	101863842	q21.1
SNP_A-2242763	C	C	257	127	218	150	4.774	2.89E-02	rs1039623	5	102028322	q21.1
SNP_A-2191083	T	T	257	147	230	178	4.434	3.52E-02	rs9327870	5	102031456	q21.1
SNP_A-2177844	A	A	261	149	230	180	4.878	2.72E-02	rs2657439	5	102031706	q21.1
SNP_A-1869978	C	C	263	149	234	184	5.328	2.10E-02	rs2657446	5	102032748	q21.1
SNP_A-2097999	C	C	260	146	234	182	5.199	2.26E-02	rs2545599	5	102042960	q21.1
SNP_A-1870002	A	T	210	168	192	176	4.462	3.47E-02	rs258132	5	102128755	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1817580	G	G	245	129	226	172	6.169	1.30E-02	rs2431322	5	102153646	q21.1
SNP_A-1803935	T	T	233	115	207	153	6.723	9.50E-03	rs456036	5	102181313	q21.1
SNP_A-2177959	A	A	253	109	228	134	3.871	4.91E-02	rs258247	5	102188684	q21.1
SNP_A-1905662	C	C	274	120	244	150	5.071	2.43E-02	rs258242	5	102195607	q21.1
SNP_A-1674443	T	T	275	125	256	156	3.923	4.76E-02	rs468501	5	102242290	q21.1
SNP_A-1659342	C	C	301	99	335	77	4.391	0.0361	rs9327877	5	102457857	q21.1
SNP_A-1810139	A	A	312	86	339	55	7.915	4.90E-03	rs12332762	5	102459173	q21.1
SNP_A-1982747	A	A	308	96	275	119	4.204	4.03E-02	rs10515364	5	103479624	q21.2
SNP_A-1982763	A	A	319	65	297	89	4.521	3.35E-02	rs11242537	5	104142954	q21.2
SNP_A-1982764	C	C	323	31	344	16	5.398	2.02E-02	rs17157107	5	104143012	q21.2
SNP_A-1723354	A	A	283	115	256	152	6.357	0.0117	rs58982	5	104236349	q21.2
SNP_A-2265732	C	C	332	82	305	109	4.961	2.59E-02	rs16659064	5	104249715	q21.2
SNP_A-2295614	G	G	306	66	314	42	5.087	0.0241	rs13157625	5	104395522	q21.2
SNP_A-1953415	A	A	340	66	353	43	4.973	2.57E-02	rs4389663	5	104451583	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1982767	T	T	304	66	301	43	3.927	4.75E-02	rs294149	5	104488059	q21.2
SNP_A-2044582	C	C	321	53	332	28	7.637	5.70E-03	rs10051540	5	104522482	q21.3
SNP_A-1838545	G	G	331	13	347	5	3.842	5.00E-02	rs1393092	5	104651453	q21.3
SNP_A-1982774	T	T	254	114	272	88	3.875	4.90E-02	rs2135048	5	105845478	q21.3
SNP_A-1831300	C	C	287	55	288	34	4.358	3.68E-02	rs296266	5	106227611	q21.3
SNP_A-2277987	T	G	209	155	182	170	5.977	1.45E-02	rs6596717	5	106455508	q21.3
SNP_A-2209622	T	T	235	161	209	203	6.054	1.39E-02	rs2410946	5	106482294	q21.3
SNP_A-2041938	G	G	329	25	323	11	4.922	2.65E-02	rs17159492	5	106485001	q21.3
SNP_A-2149499	A	G	227	163	196	192	5.952	0.0147	rs4957691	5	106528868	q21.3
SNP_A-2172427	A	A	224	190	259	161	4.889	0.027	rs4957534	5	106529101	q21.3
SNP_A-1685270	G	T	232	166	202	196	6.55	1.05E-02	rs4637535	5	106535366	q21.3
SNP_A-1654353	G	G	344	12	335	27	5.839	1.57E-02	rs2410936	5	106549965	q21.3
SNP_A-1982786	A	A	202	188	232	152	5.839	1.57E-02	rs960004	5	106563033	q21.3
SNP_A-1687350	A	A	212	188	252	158	5.927	0.0149	rs10515368	5	106581066	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2162987	C	C	247	165	211	201	6.371	1.16E-02	rs7446610	5	106584145	q21.3
SNP_A-2042018	A	A	221	147	199	191	6.247	0.0124	rs1363311	5	106584749	q21.3
SNP_A-1982787	G	G	234	140	198	180	7.979	4.70E-03	rs6596730	5	106585031	q21.3
SNP_A-2201413	C	C	202	160	233	129	5.534	1.86E-02	rs2898615	5	106589226	q21.3
SNP_A-2113183	A	A	242	94	205	111	3.863	4.94E-02	rs1645618	5	106622153	q21.3
SNP_A-1982799	G	G	309	91	303	59	5.003	0.0253	rs152608	5	106799108	q21.3
SNP_A-1982819	C	C	332	62	293	83	5.057	2.45E-02	rs27550	5	106999467	q21.3
SNP_A-1658284	C	C	371	13	374	30	6.229	0.0126	-	5	107121190	q21.3
SNP_A-2125439	C	A	186	170	170	132	4.77	2.90E-02	rs6875297	5	107716753	q21.3
SNP_A-2254697	T	T	309	27	297	45	4.685	0.0304	rs7728461	5	107909173	q21.3
SNP_A-1982848	T	T	332	82	305	109	4.961	2.59E-02	rs2048212	5	108062154	q21.3
SNP_A-1757277	A	A	317	77	299	107	5.238	2.21E-02	rs2174973	5	108108682	q21.3
SNP_A-1700512	C	C	268	126	243	159	4.964	2.59E-02	rs9326745	5	108111163	q21.3
SNP_A-1859740	G	G	365	27	341	45	5.27	2.17E-02	---	5	108471322	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2046053	A	A	330	74	297	111	9.117	2.50E-03	rs10043540	5	108471425	q21.3
SNP_A-2050223	C	C	215	127	209	171	4.594	3.21E-02	rs6873546	5	108508552	q21.3
SNP_A-1982865	T	T	335	17	324	34	5.8	0.016	rs17481197	5	108993008	q21.3
SNP_A-2141445	G	G	235	65	236	102	5.958	0.0147	rs253242	5	109049076	q21.3
SNP_A-1716315	A	A	386	12	409	3	5.825	1.58E-02	rs2269197	5	109113293	q21.3
SNP_A-1729846	C	C	359	17	353	33	5.04	2.48E-02	rs2218071	5	109163253	q21.3
SNP_A-2243907	A	A	388	20	379	39	6.104	0.0135	rs36820	5	109284704	q21.3
SNP_A-1918949	A	T	176	172	216	152	6.192	1.28E-02	rs2925074	5	109448930	q21.3
SNP_A-1739099	A	A	313	87	291	121	6.183	0.0129	rs10515412	5	109612799	q21.3
SNP_A-2149417	A	A	340	44	355	25	5.535	1.86E-02	rs4957896	5	109664263	q22.1
SNP_A-2116441	C	C	350	50	370	32	4.502	0.0339	rs17131955	5	109694292	q22.1
SNP_A-2166897	C	C	368	20	367	7	6.005	0.0143	rs11955625	5	109736860	q22.1
SNP_A-1908593	C	C	339	47	374	30	5.064	2.44E-02	rs311710	5	109778214	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869681	G	G	322	48	350	22	10.818	0.001	rs1438698	5	109860259	q22.1
SNP_A-1754964	G	G	347	49	378	30	5.717	1.68E-02	rs1488602	5	109876557	q22.1
SNP_A-2124643	C	C	357	47	379	27	6.058	0.0138	rs10051407	5	109878540	q22.1
SNP_A-2011136	C	C	316	98	349	71	5.908	1.51E-02	rs4317370	5	109937966	q22.1
SNP_A-1889596	G	G	305	69	333	37	10.868	0.001	rs1363477	5	110002481	q22.1
SNP_A-1852712	G	G	370	44	392	24	6.513	1.07E-02	rs10478021	5	110049078	q22.1
SNP_A-1873527	C	C	366	48	389	31	4.316	0.0378	rs10038233	5	110052825	q22.1
SNP_A-1982899	G	G	314	84	350	58	6.589	0.0103	rs10061929	5	110089153	q22.1
SNP_A-2089165	C	C	358	22	381	11	4.197	4.05E-02	rs10059343	5	110093410	q22.1
SNP_A-1913500	T	T	363	35	377	19	5.001	0.0253	rs3843243	5	110116146	q22.1
SNP_A-1725404	C	C	304	96	335	75	3.96	4.66E-02	rs2443513	5	110128715	q22.1
SNP_A-2091739	T	T	350	50	372	30	5.665	1.73E-02	rs13357478	5	110318060	q22.1
SNP_A-1960793	C	C	346	38	371	23	4.432	3.53E-02	rs10079816	5	110318922	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1846344	T	T	321	43	313	25	3.908	4.81E-02	rs17132949	5	110570350	q22.1
SNP_A-1866514	T	T	327	23	329	11	4.097	4.30E-02	rs306082	5	110673099	q22.1
SNP_A-1658250	G	G	371	21	394	6	8.945	0.0028	rs3797757	5	110773485	q22.1
SNP_A-1877124	A	A	292	28	349	13	8	4.70E-03	rs432983	5	110948797	q22.1
SNP_A-2157559	C	C	384	26	400	12	5.48	1.92E-02	rs1904155	5	110958973	q22.1
SNP_A-1701875	C	C	373	27	395	15	3.936	4.73E-02	rs1457715	5	111042429	q22.1
SNP_A-2158146	C	C	330	18	341	7	5.02	2.51E-02	rs1197244	5	111407492	q22.1
SNP_A-1693106	A	A	364	36	389	21	4.655	0.031	rs187500	5	111476322	q22.1
SNP_A-2164288	A	A	330	28	326	46	4.136	4.20E-02	rs17252695	5	111485843	q22.1
SNP_A-2116851	C	C	313	13	329	5	3.858	4.95E-02	rs17134238	5	111564809	q22.2
SNP_A-2092149	G	G	319	9	358	0	9.954	1.60E-03	rs17134250	5	111573942	q22.2
SNP_A-1792945	C	C	330	14	321	27	4.223	3.99E-02	rs7732687	5	111599541	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1790247	T	T	256	126	229	167	6.991	8.20E-03	rs1191496	5	111893396	q22.2
SNP_A-2265401	G	G	315	65	288	100	8.551	3.50E-03	rs189296	5	111897574	q22.2
SNP_A-1739833	G	G	293	107	262	150	8.751	3.10E-03	rs462241	5	111912037	q22.2
SNP_A-1731689	T	T	258	116	220	150	7.345	6.70E-03	rs255714	5	111923532	q22.2
SNP_A-1827635	G	G	297	119	266	154	6.175	1.30E-02	rs7381078	5	111937977	q22.2
SNP_A-1902061	T	T	319	97	278	134	8.723	3.10E-03	rs4958066	5	111941663	q22.2
SNP_A-1812432	T	T	284	56	234	76	6.486	0.0109	rs6897239	5	111943779	q22.2
SNP_A-2011142	G	G	177	137	222	106	8.729	3.10E-03	rs7709207	5	112000094	q22.2
SNP_A-1959663	C	C	268	82	283	55	5.522	1.88E-02	rs11956702	5	112010672	q22.2
SNP_A-1725102	G	G	221	167	265	123	10.659	1.10E-03	rs964417	5	112046780	q22.2
SNP_A-2042130	A	A	414	0	408	4	4.039	4.45E-02	rs4458560	5	112490977	q22.2
SNP_A-2011149	C	C	226	108	240	72	6.879	8.70E-03	rs2416306	5	112511831	q22.2
SNP_A-2119088	G	G	350	30	315	47	5.162	2.31E-02	rs7701895	5	112641357	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803416	T	T	362	44	336	68	6.106	0.0135	rs17325307	5	112641991	q22.2
SNP_A-2069589	A	C	202	172	212	170	6.835	8.90E-03	rs11241200	5	112702998	q22.2
SNP_A-2120925	C	G	202	168	217	181	6.375	1.16E-02	rs10067046	5	112703923	q22.2
SNP_A-1916645	T	T	249	117	211	157	8.973	2.70E-03	rs1965429	5	112707272	q22.2
SNP_A-1837453	A	G	177	163	178	132	5.841	1.57E-02	rs10074214	5	112730113	q22.2
SNP_A-2220455	T	T	327	53	303	75	4.69	3.03E-02	rs13181732	5	112752677	q22.2
SNP_A-1731771	C	C	311	67	300	94	4.396	3.60E-02	rs6870401	5	112814580	q22.2
SNP_A-1920955	G	G	284	132	246	156	4.486	3.42E-02	rs348963	5	112846926	q22.2
SNP_A-2136447	C	C	277	121	243	145	4.262	0.039	rs348962	5	112846985	q22.2
SNP_A-2161693	A	A	376	22	391	5	10.992	9.00E-04	rs17330898	5	112872633	q22.2
SNP_A-2194692	C	C	373	21	385	9	4.99	2.55E-02	rs2972658	5	113023021	q22.2
SNP_A-1799016	A	A	279	89	312	60	7.466	0.0063	rs2954377	5	113437164	q22.3
SNP_A-1821462	C	C	307	61	287	85	4.597	3.20E-02	rs4429843	5	113517144	q22.3
SNP_A-1890476	C	C	316	42	304	64	4.661	3.08E-02	rs4476712	5	113609684	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2269656	G	G	360	4	366	0	4.044	4.43E-02	rs7717926	5	113959304	q22.3
SNP_A-1941790	C	C	383	33	400	18	4.776	2.89E-02	rs17365340	5	113989891	q22.3
SNP_A-1781901	C	C	314	32	293	55	6.801	9.10E-03	rs1356826	5	114000638	q22.3
SNP_A-1871896	T	T	247	149	273	121	4.199	4.05E-02	rs992418	5	114010130	q22.3
SNP_A-2120609	G	G	335	29	354	12	7.567	5.90E-03	rs2394	5	114091318	q22.3
SNP_A-1673626	T	T	367	31	390	18	4.024	0.0448	rs10491499	5	114100003	q22.3
SNP_A-1707653	A	A	319	63	347	31	12.05	5.00E-04	rs7728321	5	114127431	q22.3
SNP_A-2122643	C	C	383	31	395	17	4.264	3.89E-02	rs6594842	5	114202964	q22.3
SNP_A-1913268	C	C	363	19	389	9	4.144	4.18E-02	rs6869793	5	114246813	q22.3
SNP_A-1983042	G	G	327	35	334	58	4.576	3.24E-02	rs9326938	5	114321754	q22.3
SNP_A-2210265	A	A	188	158	215	121	6.571	0.0104	rs2303001	5	114594773	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1708572	T	T	378	6	385	19	6.321	1.19E-02	rs10519400	5	114610048	q22.3
SNP_A-1901022	G	G	211	175	231	141	4.306	3.80E-02	rs3805580	5	114622038	q22.3
SNP_A-1983053	G	G	340	54	354	32	5.829	1.58E-02	rs256985	5	114934412	q22.3
SNP_A-2036686	G	G	363	45	383	25	6.25	0.0124	rs2288384	5	114943927	q22.3
SNP_A-2305533	A	A	261	109	296	76	8.08	4.50E-03	rs6881698	5	115278171	q23.1
SNP_A-1912930	A	A	196	148	225	123	4.281	0.0385	rs9326979	5	115313413	q23.1
SNP_A-2024531	G	G	238	126	274	96	6.537	0.0106	rs1428091	5	115315163	q23.1
SNP_A-1859159	T	T	370	0	334	4	4.404	3.59E-02	rs6594913	5	115318692	q23.1
SNP_A-1956676	C	C	238	180	261	149	3.904	0.0482	rs4920897	5	115320744	q23.1
SNP_A-2096819	T	T	253	141	295	113	6.063	0.0138	rs6896619	5	115329965	q23.1
SNP_A-2137787	C	C	337	7	326	18	5.023	2.50E-02	rs949686	5	115363633	q23.1
SNP_A-2104684	T	T	212	114	175	131	4.088	4.32E-02	rs17484600	5	115371045	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1892703	G	G	324	12	323	1	9.094	2.60E-03	rs2560671	5	115410550	q23.1
SNP_A-1803683	C	C	325	51	305	25	6.56	0.0104	rs2136210	5	115412245	q23.1
SNP_A-1942844	A	A	385	11	377	23	4.299	3.81E-02	rs17138841	5	115440705	q23.1
SNP_A-1983093	T	T	336	6	359	1	3.874	4.91E-02	rs12514156	5	115848325	q23.1
SNP_A-2190311	A	A	389	7	385	1	4.394	0.0361	rs4337886	5	116481932	q23.1
SNP_A-1983131	A	A	239	117	254	88	4.28	3.86E-02	rs1389934	5	116622752	q23.1
SNP_A-2193902	A	A	190	144	224	118	5.278	2.16E-02	rs1565892	5	116689662	q23.1
SNP_A-1820182	C	C	284	90	285	53	7.775	0.0053	rs2560633	5	116859987	q23.1
SNP_A-2157495	A	T	210	200	231	175	5.392	2.02E-02	rs265900	5	116916065	q23.1
SNP_A-2075552	G	G	354	52	387	25	10.894	0.001	rs17403069	5	116972569	q23.1
SNP_A-1906718	C	C	261	143	292	118	4.088	4.32E-02	rs397925	5	116998548	q23.1
SNP_A-1856305	A	A	308	104	344	66	10.477	1.20E-03	rs9327047	5	116999827	q23.1
SNP_A-2033991	T	T	247	133	276	104	5.157	2.32E-02	rs434363	5	117000415	q23.1
SNP_A-1802741	T	T	282	94	328	54	14.233	2.00E-04	rs9327048	5	117001096	q23.1
SNP_A-2109266	C	C	245	141	276	112	5.164	2.31E-02	rs371616	5	117001959	q23.1
SNP_A-1903743	T	T	375	3	350	18	11.444	7.00E-04	rs6896671	5	117247429	q23.1
SNP_A-1802357	C	C	337	43	362	24	6.236	1.25E-02	rs494036	5	117333949	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074393	C	C	352	54	379	35	4.976	2.57E-02	rs682926	5	117334225	q23.1
SNP_A-2172541	T	T	351	61	380	40	5.44	1.97E-02	rs6888787	5	117346217	q23.1
SNP_A-1983149	C	C	347	57	362	32	7.216	7.20E-03	rs9327061	5	117355336	q23.1
SNP_A-2140967	A	A	316	94	296	124	4.662	3.08E-02	rs673479	5	118134800	q23.1
SNP_A-1739199	C	C	389	11	387	23	4.118	0.0424	rs10491430	5	118180118	q23.1
SNP_A-1751551	G	G	278	120	257	153	4.636	3.13E-02	rs631514	5	118202962	q23.1
SNP_A-2265744	A	A	301	37	306	20	4.896	0.0269	rs4243445	5	118551008	q23.1
SNP_A-1983173	G	G	292	64	352	48	5.333	2.09E-02	rs1553543	5	118646439	q23.1
SNP_A-1951461	G	G	355	57	385	35	6.401	0.0114	rs2112323	5	118657178	q23.1
SNP_A-1880973	G	G	357	53	380	36	3.922	4.77E-02	rs6879919	5	118673819	q23.1
SNP_A-1868447	A	A	273	91	249	115	3.9	4.83E-02	rs330193	5	119021690	q23.1
SNP_A-1649326	C	C	302	98	282	130	5	0.0253	rs330196	5	119068199	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1700494	A	A	235	165	209	203	5.27	2.17E-02	rs780429	5	119072331	q23.1
SNP_A-2220299	T	T	252	86	252	120	3.993	4.57E-02	rs12521697	5	119155103	q23.1
SNP_A-2238550	C	C	350	52	375	33	5.065	2.44E-02	rs347558	5	119447493	q23.1
SNP_A-1983207	T	T	250	58	293	39	6.236	1.25E-02	rs982358	5	119507933	q23.1
SNP_A-2119022	G	G	282	110	325	79	7.952	4.80E-03	rs17146184	5	119517614	q23.1
SNP_A-2125518	G	G	290	120	327	83	8.963	0.0028	rs982476	5	119530725	q23.1
SNP_A-1680022	A	A	294	92	274	122	4.783	0.0287	rs2112498	5	119602548	q23.1
SNP_A-2131042	G	G	266	144	284	114	3.9	4.83E-02	rs10066018	5	119672571	q23.1
SNP_A-2041692	G	G	319	19	327	37	4.929	0.0264	rs7706727	5	119922742	q23.1
SNP_A-2155732	T	T	290	102	305	73	4.931	0.0264	rs17147484	5	120557020	q23.1
SNP_A-1917240	A	A	363	21	361	9	4.547	3.30E-02	rs11952813	5	121129122	q23.1
SNP_A-2058916	A	A	376	22	391	11	3.94	4.71E-02	rs1431950	5	121154351	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259609	C	C	332	40	293	55	4.006	0.0453	rs4836196	5	122092320	q23.2
SNP_A-2252067	C	C	355	45	376	28	4.542	3.31E-02	rs6595415	5	122234657	q23.2
SNP_A-1983269	G	G	377	21	401	9	5.363	0.0206	---	5	122325666	q23.2
SNP_A-2300631	A	A	328	40	336	20	6.566	0.0104	rs6895561	5	122418042	q23.2
SNP_A-2253950	G	G	378	24	395	11	5.183	2.28E-02	---	5	122542262	q23.2
SNP_A-2081619	C	C	317	15	340	6	4.375	3.65E-02	rs17150658	5	123082616	q23.2
SNP_A-1877102	C	C	384	14	393	3	7.217	7.20E-03	rs4085308	5	123141397	q23.2
SNP_A-2174552	C	C	353	37	379	23	4.009	0.0453	rs6887119	5	123878855	q23.2
SNP_A-2116950	C	C	239	153	192	180	6.796	9.10E-03	rs11739029	5	123896704	q23.2
SNP_A-1808928	A	A	404	12	394	24	4.121	0.0424	rs4458563	5	124304963	q23.2
SNP_A-2229394	A	A	205	189	237	157	5.276	2.16E-02	rs12186483	5	124510345	q23.2
SNP_A-2052409	T	T	225	129	268	102	6.556	1.05E-02	rs769334	5	124844892	q23.2
SNP_A-2164415	G	G	226	112	267	81	8.245	4.10E-03	rs6876182	5	124845919	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1924294	G	G	340	46	297	65	5.39	2.02E-02	rs331695	5	124857012	q23.2
SNP_A-2075362	T	T	197	167	251	133	9.835	1.70E-03	rs4621558	5	124860906	q23.2
SNP_A-2213183	C	C	343	49	283	75	9.681	0.0019	rs331756	5	124873836	q23.2
SNP_A-1834009	A	A	355	5	309	15	6.309	0.012	rs331749	5	124878694	q23.2
SNP_A-1649002	C	C	341	59	312	100	11.685	6.00E-04	rs331693	5	124909438	q23.2
SNP_A-1644494	A	A	330	46	303	91	15.52	8.16E-05	rs179505	5	124910428	q23.2
SNP_A-2221224	C	C	364	46	390	30	4.145	4.18E-02	rs2029549	5	125048696	q23.2
SNP_A-1896374	C	C	366	48	390	32	3.886	0.0487	rs2029550	5	125048883	q23.2
SNP_A-2037972	G	G	242	140	263	109	4.601	3.20E-02	rs3860119	5	125456690	q23.2
SNP_A-1758355	T	T	248	150	284	128	3.936	4.73E-02	rs1383555	5	125516269	q23.2
SNP_A-1674529	C	C	248	150	284	128	3.936	4.73E-02	rs1383556	5	125516395	q23.2
SNP_A-1922415	T	T	339	53	358	32	5.701	1.70E-02	rs13182402	5	125946047	q23.2
SNP_A-2168219	A	A	234	174	207	205	4.169	4.12E-02	rs4836316	5	126555774	q23.2
SNP_A-1936237	C	C	267	139	284	104	5.16	2.31E-02	rs441411	5	126925062	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2229302	G	G	195	173	240	150	5.659	1.74E-02	rs1013375	5	127305116	q23.2
SNP_A-1813353	C	C	309	91	352	64	7.19	7.30E-03	rs4836348	5	127306672	q23.2
SNP_A-1808045	C	C	210	192	239	159	4.956	2.60E-02	rs12523625	5	127322676	q23.2
SNP_A-1892646	C	C	301	83	346	54	8.946	0.0028	rs6869756	5	127332304	q23.2
SNP_A-1656315	G	G	290	108	335	79	7.425	6.40E-03	rs2409037	5	127362406	q23.2
SNP_A-1673022	T	T	286	106	331	79	6.822	9.00E-03	rs9327463	5	127391353	q23.2
SNP_A-1908504	T	T	307	103	329	69	7.305	6.90E-03	rs36701	5	127580428	q23.2
SNP_A-1983409	C	C	381	29	372	46	3.884	0.0487	rs6893195	5	127637008	q23.2
SNP_A-2180483	A	A	348	26	338	44	4.69	3.03E-02	rs15661006	5	127739955	q23.2
SNP_A-2284333	G	G	365	37	354	56	3.972	4.63E-02	rs11949692	5	127938433	q23.3
SNP_A-1938270	G	G	326	22	304	42	7.013	8.10E-03	rs13173831	5	127963281	q23.3
SNP_A-1819167	A	A	350	32	335	53	5.47	1.93E-02	rs6864907	5	127984250	q23.3
SNP_A-2233629	C	C	375	39	361	59	4.305	3.80E-02	rs13165572	5	127986875	q23.3
SNP_A-2264444	A	A	285	61	316	44	4.075	4.35E-02	rs189687	5	128120719	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1697789	T	T	286	84	343	67	5.041	2.48E-02	rs2310809	5	128245456	q23.3
SNP_A-2130411	C	C	316	94	348	68	5.672	0.0172	rs2545018	5	128269807	q23.3
SNP_A-1983432	T	T	317	15	298	28	4.463	3.46E-02	rs2189661	5	128315172	q23.3
SNP_A-1669563	C	C	308	92	346	68	5.569	0.0183	rs2522379	5	128320226	q23.3
SNP_A-1749717	G	G	309	91	346	68	5.178	0.0229	rs2545021	5	128320546	q23.3
SNP_A-1983435	G	G	315	87	344	64	4.735	2.95E-02	rs2577548	5	128389795	q23.3
SNP_A-1917505	G	G	314	94	334	70	4.11	4.26E-02	rs257938	5	128407548	q23.3
SNP_A-2136654	A	A	297	79	322	56	4.923	2.65E-02	rs183760	5	128412448	q23.3
SNP_A-1983440	G	G	403	1	393	11	8.459	3.60E-03	rs17839618	5	128505338	q23.3
SNP_A-2131261	C	C	390	18	366	32	4.559	3.28E-02	rs17768474	5	128769447	q23.3
SNP_A-2290935	A	A	363	31	347	15	4.579	3.24E-02	rs17515089	5	129498398	q23.3
SNP_A-1983464	T	T	361	21	353	37	4.421	3.55E-02	rs110411	5	129752270	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939340	A	A	300	44	274	62	4.141	0.0419	rs6874868	5	129825862	q23.3
SNP_A-2185970	G	G	270	120	210	162	13.338	3.00E-04	rs7731850	5	129913054	q23.3
SNP_A-1692604	C	C	217	127	218	172	3.907	4.81E-02	rs2215258	5	129953261	q23.3
SNP_A-1983468	G	G	392	2	401	9	4.24	0.0395	rs10491339	5	130124583	q23.3
SNP_A-1923561	T	T	314	60	284	84	5.457	0.0195	rs9327603	5	130586662	q23.3
SNP_A-2199854	C	C	248	160	221	193	4.596	3.21E-02	rs3756295	5	130720739	q23.3
SNP_A-2303939	A	A	393	1	393	9	6.32	1.19E-02	rs10063129	5	130868284	q23.3
SNP_A-1799007	C	C	309	61	299	85	3.851	4.97E-02	rs3776007	5	130902984	q23.3
SNP_A-2090005	T	T	390	26	369	47	6.622	0.0101	rs17671387	5	130911895	q23.3
SNP_A-2285411	G	G	311	77	285	103	4.89	0.027	rs8180462	5	130935088	q23.3
SNP_A-2011247	G	G	388	4	386	0	3.959	4.66E-02	rs4425498	5	131247909	q23.3
SNP_A-2200079	G	G	313	77	289	101	4.193	4.06E-02	rs559971	5	131344063	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1856533	A	A	336	80	317	105	3.888	4.86E-02	rs173812	5	131347359	q23.3
SNP_A-1851285	A	A	339	39	320	66	7.408	6.50E-03	rs82125	5	131350140	q23.3
SNP_A-2296858	G	G	338	46	300	64	4.677	3.06E-02	rs253949	5	131350875	q23.3
SNP_A-1863704	C	T	194	180	208	186	4.198	4.05E-02	rs3914026	5	131380958	q23.3
SNP_A-2308316	T	T	332	46	306	84	11.983	5.00E-04	rs17132324	5	131391878	q23.3
SNP_A-2235038	G	G	363	27	340	46	5.677	0.0172	rs181781	5	131423014	q23.3
SNP_A-2096646	C	C	373	37	355	63	7.128	0.0076	rs246841	5	131430085	q23.3
SNP_A-2217595	-	T	191	191	226	170	3.909	4.80E-02	rs39897	5	131464795	q23.3
SNP_A-2099343	G	G	376	26	353	49	7.779	0.0053	rs3792876	5	131665208	q23.3
SNP_A-1788463	C	C	383	31	363	53	6.293	0.0121	rs3792880	5	131672864	q23.3
SNP_A-2303297	G	G	381	31	343	57	9.501	2.10E-03	rs13179900	5	131675489	q23.3
SNP_A-2256665	C	C	343	23	340	42	5.227	2.22E-02	rs3828673	5	131679464	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1954772	G	G	375	27	358	48	6.255	0.0124	rs2304081	5	131695447	q23.3
SNP_A-2139951	G	G	380	28	361	51	7.164	7.40E-03	rs3805676	5	131696366	q23.3
SNP_A-1841657	C	C	379	31	352	54	7.201	7.30E-03	rs2306772	5	131703880	q23.3
SNP_A-1866185	A	A	365	33	356	58	6.668	9.80E-03	rs4705943	5	131782903	q23.3
SNP_A-1691028	C	C	346	42	348	66	4.501	0.0339	rs725580	5	131840319	q23.3
SNP_A-1949019	G	G	224	162	202	198	4.488	3.41E-02	rs4958165	5	132543394	q31.1
SNP_A-1939747	C	C	234	176	209	207	3.877	4.90E-02	rs2162769	5	132568008	q31.1
SNP_A-2273843	C	C	395	21	411	9	5.099	2.39E-02	rs2864680	5	132665665	q31.1
SNP_A-1851005	G	G	272	142	245	175	4.802	2.84E-02	rs246781	5	132889488	q31.1
SNP_A-1885374	T	T	367	23	359	39	4.136	4.20E-02	rs1094789	5	132901665	q31.1
SNP_A-1983523	A	G	224	176	213	165	11.855	6.00E-04	rs187411	5	132913640	q31.1
SNP_A-2065481	C	C	248	110	209	133	5.142	2.34E-02	rs11747858	5	132918155	q31.1
SNP_A-2216657	G	G	244	124	221	155	4.497	3.40E-02	rs2036006	5	132921629	q31.1
SNP_A-1983529	G	G	320	96	351	69	5.831	1.57E-02	rs256259	5	132945005	q31.1
SNP_A-2104499	A	A	381	29	368	48	4.871	2.73E-02	rs415839	5	132960650	q31.1
SNP_A-1711808	C	C	261	139	239	175	4.856	0.0275	rs13633245	5	132963754	q31.1
SNP_A-2280920	T	T	263	139	229	167	4.867	2.74E-02	rs409855	5	132967260	q31.1
SNP_A-1666938	A	A	261	133	241	169	4.772	2.89E-02	rs256333	5	132977113	q31.1
SNP_A-1983530	C	C	263	125	240	166	6.424	1.13E-02	rs430104	5	132981422	q31.1
SNP_A-1849858	A	A	275	133	320	100	7.905	4.90E-03	rs256225	5	133002368	q31.1
SNP_A-2172911	T	T	360	28	339	67	16.242	0.0000557153	rs100555155	5	133010597	q31.1
SNP_A-1896242	C	C	312	88	283	121	6.604	1.02E-02	rs10068192	5	133016328	q31.1
SNP_A-2063418	T	T	285	75	255	109	7.927	4.90E-03	rs10076045	5	133016464	q31.1
SNP_A-2142534	A	A	332	72	353	51	4.229	3.97E-02	rs7726345	5	133024503	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074983	G	G	307	95	333	69	5.178	0.0229	rs4958139	5	133027220	q31.1
SNP_A-1983533	G	G	244	158	261	123	4.522	3.35E-02	rs11739949	5	133029830	q31.1
SNP_A-1825736	A	A	219	143	263	125	4.329	3.75E-02	rs1860207	5	133032681	q31.1
SNP_A-1871370	C	C	301	73	331	49	6.098	0.0135	rs872900	5	133033041	q31.1
SNP_A-2250542	C	C	395	11	407	1	8.508	3.50E-03	rs7713865	5	133050834	q31.1
SNP_A-1691546	G	G	291	35	309	69	7.857	5.10E-03	rs10515461	5	133142529	q31.1
SNP_A-1755628	C	C	359	19	368	36	4.506	3.38E-02	rs9327668	5	133143021	q31.1
SNP_A-1983552	T	T	366	36	376	18	6.055	1.39E-02	rs10491287	5	133726836	q31.1
SNP_A-2048375	A	A	300	58	320	40	3.946	0.047	rs11950943	5	133944618	q31.1
SNP_A-1896115	A	A	310	36	331	21	4.584	3.23E-02	rs11948613	5	133974910	q31.1
SNP_A-1801554	C	C	184	182	222	154	5.756	1.64E-02	rs1346440	5	134600906	q31.1
SNP_A-2095889	C	C	191	159	218	118	7.568	5.90E-03	rs4976281	5	134603999	q31.1
SNP_A-2070953	A	A	397	9	400	2	4.446	3.50E-02	rs17662111	5	134631260	q31.1
SNP_A-1903245	A	A	375	37	400	20	5.8	0.016	rs3756366	5	134724667	q31.1
SNP_A-2112640	G	G	274	126	284	94	4.215	4.01E-02	rs11242249	5	134825478	q31.1
SNP_A-2229922	G	G	341	23	344	40	4.069	4.37E-02	rs251562	5	134826622	q31.1
SNP_A-2206017	C	C	231	149	257	123	3.871	4.91E-02	rs2532030	5	134879300	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1954010	T	T	347	41	363	23	5.418	1.99E-02	rs6863329	5	134880985	q31.1
SNP_A-1870699	A	A	411	1	409	7	4.486	3.42E-02	rs9327725	5	134915332	q31.1
SNP_A-1750477	C	C	250	148	291	123	5.1	2.39E-02	rs3860106	5	134920805	q31.1
SNP_A-2111017	T	T	379	35	396	20	4.459	3.47E-02	rs2109004	5	134949695	q31.1
SNP_A-2307125	G	G	320	32	358	14	8.627	0.0033	rs17168691	5	134951398	q31.1
SNP_A-2105560	C	C	378	38	399	21	5.447	1.96E-02	rs11738804	5	134975616	q31.1
SNP_A-1683132	C	C	365	35	393	19	5.599	1.80E-02	rs2237061	5	134988546	q31.1
SNP_A-2284010	C	C	322	36	352	22	4.367	3.66E-02	rs7710084	5	135037127	q31.1
SNP_A-2053012	G	G	334	52	353	29	7.036	8.00E-03	rs4976316	5	135047354	q31.1
SNP_A-2101691	G	G	320	46	344	22	9.338	2.20E-03	rs4976324	5	135083355	q31.1
SNP_A-2154934	G	G	213	201	256	162	8.113	4.40E-03	rs4496704	5	135111393	q31.1
SNP_A-2047526	C	C	185	145	221	95	13.312	3.00E-04	rs11750461	5	135111721	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2249929	C	C	215	199	256	164	6.901	0.0086	rs11747540	5	135111751	q31.1
SNP_A-1876228	C	T	206	188	217	179	3.965	0.0465	rs2304072	5	135187975	q31.1
SNP_A-1818423	C	T	193	175	209	167	4.803	2.84E-02	rs2304071	5	135188273	q31.1
SNP_A-1728183	G	G	326	70	311	95	4.017	4.50E-02	rs42258	5	135409015	q31.1
SNP_A-2257870	A	A	383	31	361	55	7.343	6.70E-03	rs10069968	5	135645497	q31.1
SNP_A-2152470	C	C	382	32	358	54	6.401	0.0114	rs17695029	5	135650851	q31.1
SNP_A-1887598	C	C	381	29	359	45	4.07	4.37E-02	rs3777147	5	135694388	q31.1
SNP_A-2233270	G	G	282	92	265	123	4.742	2.94E-02	rs2673926	5	135725523	q31.1
SNP_A-1895030	T	T	273	91	251	123	5.574	1.82E-02	rs2649696	5	135734750	q31.1
SNP_A-2202221	G	G	346	36	296	58	7.989	4.70E-03	rs13177840	5	135757076	q31.1
SNP_A-2183619	G	G	362	44	335	77	10.002	1.60E-03	rs11948560	5	135760364	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1868473	G	G	350	36	315	59	7.223	7.20E-03	rs13186797	5	135764137	q31.1
SNP_A-2025120	A	A	351	37	315	63	8.577	3.40E-03	rs1499772	5	135776766	q31.1
SNP_A-2299306	G	G	355	45	326	68	5.871	0.0154	rs13158415	5	135778451	q31.1
SNP_A-1913064	C	C	362	52	338	78	6.018	1.42E-02	rs7705405	5	135780907	q31.1
SNP_A-1818682	C	C	301	83	276	106	3.877	4.90E-02	rs11737955	5	135990446	q31.1
SNP_A-1892622	T	T	288	108	313	79	5.517	1.88E-02	rs7701533	5	136074419	q31.1
SNP_A-1784382	C	C	274	98	294	72	4.632	3.14E-02	rs17712730	5	136217669	q31.1
SNP_A-1806822	A	A	306	108	334	84	4.206	4.03E-02	rs7721942	5	136433496	q31.1
SNP_A-1983644	T	T	261	127	286	100	4.349	3.70E-02	rs4976402	5	136445259	q31.1
SNP_A-1983658	C	C	248	86	240	120	4.775	2.89E-02	rs2060428	5	136633415	q31.1
SNP_A-2269138	A	A	314	30	294	50	5.658	1.74E-02	rs2961634	5	136666679	q31.1
SNP_A-1795576	A	A	384	14	393	5	4.367	3.66E-02	rs10479154	5	136749046	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1705063	G	G	242	146	215	183	5.63	0.0177	rs1229732	5	136760984	q31.1
SNP_A-2121587	A	A	312	66	277	85	4.127	4.22E-02	rs217272	5	137514325	q31.2
SNP_A-2292089	A	A	261	115	276	84	4.903	2.68E-02	rs744675	5	138019751	q31.2
SNP_A-1874912	A	A	265	117	298	84	7.352	6.70E-03	rs744674	5	138019850	q31.2
SNP_A-1787748	C	C	281	81	303	45	10.843	0.001	rs882740	5	138020608	q31.2
SNP_A-2115284	C	C	299	83	330	60	5.145	2.33E-02	rs6878910	5	138309160	q31.2
SNP_A-1882178	T	C	201	173	216	180	5.286	2.15E-02	rs7701338	5	138433893	q31.2
SNP_A-2289981	G	G	402	14	417	5	4.495	3.40E-02	rs17131938	5	138478148	q31.2
SNP_A-2204509	G	G	366	4	398	0	4.325	3.76E-02	rs6596467	5	138579047	q31.2
SNP_A-1789964	A	A	385	29	407	13	6.664	9.80E-03	rs10061228	5	139203329	q31.2
SNP_A-1904719	A	A	325	13	319	29	6.007	0.0143	rs1800954	5	139225270	q31.2
SNP_A-2059272	A	A	279	121	298	94	3.936	4.73E-02	rs13173983	5	139390694	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140353	A	A	258	144	290	118	4.405	3.58E-02	rs7723119	5	139391887	q31.2
SNP_A-1983707	A	A	364	52	347	75	4.529	3.33E-02	rs1835959	5	139900495	q31.3
SNP_A-2271827	G	G	323	93	301	119	3.945	0.047	rs5744441	5	139997031	q31.3
SNP_A-1702631	G	G	236	76	245	117	5.198	2.26E-02	rs56003	5	140327033	q31.3
SNP_A-2210087	C	C	369	29	405	9	11.89	6.00E-04	rs13163241	5	140354072	q31.3
SNP_A-2081928	G	G	346	38	386	12	15.46	8.43E-05	rs246584	5	140416247	q31.3
SNP_A-1983716	A	A	341	29	365	11	8.868	2.90E-03	rs31861	5	140445772	q31.3
SNP_A-1957646	C	C	342	26	376	10	8.296	4.00E-03	rs13171965	5	140478782	q31.3
SNP_A-1821469	A	A	361	43	394	20	9.718	0.0018	rs246725	5	140497615	q31.3
SNP_A-2219555	C	C	387	19	382	34	4.157	4.15E-02	rs6897709	5	141058154	q31.3
SNP_A-1855223	G	G	383	15	383	29	4.214	4.01E-02	rs7713536	5	141060427	q31.3
SNP_A-2041004	A	A	259	85	238	114	5.022	2.50E-02	rs13160849	5	141158153	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187147	G	G	359	31	355	51	4.581	3.23E-02	rs13162099	5	141186515	q31.3
SNP_A-2094333	A	A	309	73	272	94	4.657	0.0309	rs252149	5	141421354	q31.3
SNP_A-1914824	A	C	199	175	209	175	4.419	3.55E-02	rs4554260	5	141631340	q31.3
SNP_A-2113862	C	T	217	171	191	167	6.419	1.13E-02	rs12515244	5	141646477	q31.3
SNP_A-2188596	C	T	217	183	217	195	3.888	4.86E-02	rs4324715	5	141649691	q31.3
SNP_A-1898069	A	T	209	159	187	177	4.897	0.0269	rs6580240	5	141664573	q31.3
SNP_A-2147586	T	C	210	202	243	179	6.129	1.33E-02	rs6897876	5	141667823	q31.3
SNP_A-2103805	A	A	297	73	312	46	6.299	0.0121	rs153423	5	141794129	q31.3
SNP_A-2229857	T	T	343	29	339	15	4.034	4.46E-02	rs17577085	5	141843788	q31.3
SNP_A-2185859	A	A	334	8	357	1	5.847	1.56E-02	rs11749540	5	142140051	q31.3
SNP_A-1983772	T	T	304	94	324	60	7.895	5.00E-03	rs409509	5	142269057	q31.3
SNP_A-1856164	G	G	279	123	312	100	4.093	4.31E-02	rs37185	5	142291083	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2228238	T	T	234	130	260	104	4.257	3.91E-02	rs712176	5	142291626	q31.3
SNP_A-1820292	T	T	263	117	287	87	5.412	0.02	rs252234	5	142309329	q31.3
SNP_A-1886082	G	G	294	98	313	73	4.204	4.03E-02	rs42464	5	142311818	q31.3
SNP_A-1983775	T	T	269	131	285	95	5.688	1.71E-02	rs173750	5	142324494	q31.3
SNP_A-1868662	A	A	313	85	349	65	4.311	3.79E-02	rs3822398	5	142368154	q31.3
SNP_A-2234017	A	A	325	93	345	69	4.133	4.20E-02	rs10875598	5	142371351	q31.3
SNP_A-2262930	C	C	362	18	383	7	5.303	2.13E-02	rs246636	5	142391623	q31.3
SNP_A-1758100	C	C	393	9	413	1	6.721	9.50E-03	rs245815	5	142426451	q31.3
SNP_A-1700065	C	C	265	135	301	113	4.002	4.55E-02	rs6580266	5	142464258	q31.3
SNP_A-1676812	C	C	265	135	301	113	4.002	4.55E-02	rs7734364	5	142464662	q31.3
SNP_A-1933697	G	A	191	159	180	158	4.213	4.01E-02	rs246600	5	142497090	q31.3
SNP_A-2124947	G	A	181	157	195	163	4.473	0.0344	rs17100309	5	142829802	q31.3
SNP_A-2030888	C	C	341	51	326	74	4.489	3.41E-02	rs12187799	5	142883197	q31.3
SNP_A-2155623	T	T	323	79	300	104	4.259	0.039	rs6859024	5	142955947	q31.3
SNP_A-1874683	C	T	239	173	210	206	6.002	0.0143	rs10875603	5	142998132	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1983792	C	C	288	108	311	81	4.72	0.0298	rs6869469	5	143029817	q31.3
SNP_A-1941224	A	A	406	10	417	3	3.897	4.84E-02	rs10062205	5	143249543	q31.3
SNP_A-1983810	A	C	207	171	202	184	3.846	0.0499	rs318404	5	143339832	q31.3
SNP_A-1949955	T	T	317	37	299	17	5.797	0.0161	rs312625	5	143384328	q31.3
SNP_A-2239477	T	T	380	34	398	20	4.027	0.0448	rs6868068	5	143570142	q31.3
SNP_A-1808021	T	T	395	5	402	0	5.057	2.45E-02	rs17101786	5	143682640	q31.3
SNP_A-1983825	T	T	370	8	384	0	8.213	4.20E-03	rs20042972	5	143746198	q31.3
SNP_A-1927269	A	A	232	152	206	192	5.946	1.48E-02	rs2895621	5	144030334	q31.3
SNP_A-1743951	A	A	219	145	196	182	5.199	2.26E-02	rs9324964	5	144081846	q32
SNP_A-2053982	A	A	242	100	195	117	5.021	2.50E-02	rs6894954	5	144294556	q31.3
SNP_A-2213556	C	C	371	19	395	9	4.078	4.35E-02	rs419844	5	144399502	q31.3
SNP_A-2226013	G	C	224	174	216	196	6.15	1.31E-02	rs451977	5	144838730	q32
SNP_A-2045696	A	A	344	22	365	11	4.155	4.15E-02	rs2195938	5	144996311	q32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084551	A	A	409	1	411	7	4.428	3.54E-02	rs10063177	5	145061388	q32
SNP_A-2065237	T	T	385	5	390	0	5.032	2.49E-02	rs17103648	5	145063399	q32
SNP_A-1983872	A	A	208	138	176	160	4.145	4.18E-02	rs11742574	5	145391528	q32
SNP_A-1880577	G	G	367	51	397	25	10.054	0.0015	---	5	145900463	q32
SNP_A-1799441	G	G	290	106	267	137	4.825	0.0281	---	5	145910514	q32
SNP_A-1748775	A	A	357	45	346	66	4.023	4.49E-02	rs10515571	5	145952794	q32
SNP_A-1670790	A	A	397	5	414	0	5.181	2.28E-02	rs322477	5	145993407	q32
SNP_A-2250173	A	A	336	64	355	43	4.639	3.13E-02	rs462706	5	146034170	q32
SNP_A-1983908	G	G	333	7	316	22	8.198	4.20E-03	rs10491404	5	146525649	q32
SNP_A-2270840	C	C	360	10	363	23	4.797	2.85E-02	rs17561784	5	147040038	q32
SNP_A-1938810	C	C	327	59	338	38	4.598	3.20E-02	rs7716258	5	147148685	q32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282437	A	A	313	81	330	52	6.589	0.0103	rs12519829	5	147221663	q32
SNP_A-1688638	T	T	331	71	363	51	4.579	3.24E-02	rs10515594	5	147241484	q32
SNP_A-1913948	C	C	281	29	305	15	5.28	2.16E-02	rs17774641	5	147282558	q32
SNP_A-2046597	G	G	345	17	373	5	7.295	6.90E-03	rs17717956	5	147283934	q32
SNP_A-2050640	A	A	298	10	348	0	11.474	7.00E-04	rs7724336	5	147313980	q32
SNP_A-1709971	G	G	374	28	400	14	5.365	2.05E-02	rs10515599	5	147361487	q33.1
SNP_A-1723856	C	C	232	170	209	205	4.291	3.83E-02	rs6580511	5	147362455	q33.1
SNP_A-1983930	A	A	375	27	392	6	13.721	2.00E-04	rs10491342	5	147392268	q32
SNP_A-1920429	A	A	379	31	409	9	13.166	3.00E-04	rs17107665	5	147399938	q32
SNP_A-2155501	A	A	324	28	372	10	10.628	1.10E-03	rs1363720	5	147400252	q32
SNP_A-2127542	G	G	376	32	391	13	8.296	4.00E-03	rs1363719	5	147400393	q32
SNP_A-2291484	C	C	380	32	407	9	13.81	2.00E-04	rs11958071	5	147412063	q32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1850060	T	T	347	25	390	8	10.4	1.30E-03	rs17718403	5	147414124	q32
SNP_A-2025965	A	A	380	32	410	10	12.587	4.00E-04	rs17718420	5	147414249	q32
SNP_A-1710764	G	G	222	152	262	128	5.03	2.49E-02	rs4705049	5	147415225	q33.1
SNP_A-2151544	C	C	371	25	400	6	12.613	4.00E-04	rs2287774	5	147423553	q32
SNP_A-1746793	G	G	372	30	404	10	11.146	8.00E-04	rs10491341	5	147436600	q33.1
SNP_A-2205867	C	C	224	178	253	149	4.335	0.0373	rs4529181	5	147449164	q32
SNP_A-1881426	C	C	354	54	382	32	6.65	9.90E-03	rs1422987	5	147466552	q32
SNP_A-2109163	A	A	386	26	413	5	15.096	0.0001	rs3777138	5	147475363	q32
SNP_A-2247572	G	G	334	28	355	15	4.483	3.42E-02	rs12517179	5	147588821	q32
SNP_A-1787868	A	A	326	18	343	7	5.221	0.0223	rs1432693	5	147589329	q32
SNP_A-2288804	C	C	376	14	399	5	4.7	3.02E-02	rs1583280	5	147605941	q32
SNP_A-2243944	G	G	387	7	354	20	7.213	7.20E-03	rs1345739	5	147727781	q32
SNP_A-1909150	A	A	353	39	353	21	4.98	2.56E-02	rs17720733	5	147930671	q32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1804811	C	C	319	35	315	63	7.246	7.10E-03	rs1347110	5	148167624	q32
SNP_A-2122414	T	T	306	56	259	73	4.862	2.74E-02	rs877743	5	148177153	q32
SNP_A-2304037	A	A	389	25	412	10	7.013	8.10E-03	rs10036926	5	148262006	q32
SNP_A-2076198	C	C	246	156	224	188	3.884	0.0487	rs1045942	5	148361390	q32
SNP_A-1896144	T	T	394	22	413	9	5.856	0.0155	rs1864950	5	148389958	q32
SNP_A-1983967	T	T	263	57	253	81	4.07	4.37E-02	rs250679	5	148415145	q32
SNP_A-2123839	G	G	310	44	255	63	6.819	9.00E-03	rs36045	5	148421377	q32
SNP_A-2266601	G	G	247	139	214	174	6.271	0.0123	rs12655076	5	148465763	q32
SNP_A-2251251	G	G	354	6	346	0	5.816	1.59E-02	rs17109825	5	148597883	q32
SNP_A-2297691	G	G	307	29	321	57	6.982	8.20E-03	rs353295	5	148782069	q32
SNP_A-2158496	G	A	201	183	208	170	4.142	4.18E-02	rs4705353	5	148945090	q32
SNP_A-1824018	G	G	334	48	329	73	4.696	3.02E-02	rs17711038	5	149074639	q32
SNP_A-2117295	T	T	301	69	282	98	5.523	1.88E-02	rs245081	5	149336268	q32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2136859	T	T	318	54	299	77	4.602	3.19E-02	rs2276883	5	149405159	q32
SNP_A-1953532	A	A	403	11	392	28	7.52	6.10E-03	rs7718213	5	149411371	q32
SNP_A-2115507	G	G	393	1	381	7	4.64	3.12E-02	rs2237089	5	149423463	q32
SNP_A-1789093	G	G	296	58	338	38	6.292	0.0121	rs7727195	5	149468134	q32
SNP_A-1869031	C	C	254	74	239	103	4.917	2.66E-02	rs1290147	5	149899932	q33.1
SNP_A-2314432	G	G	239	107	265	83	4.367	3.66E-02	rs3097830	5	149910235	q33.1
SNP_A-2147562	G	G	243	133	224	170	4.873	2.73E-02	rs10044420	5	149946883	q33.1
SNP_A-1915205	G	G	338	14	317	27	4.704	3.01E-02	rs10071236	5	150120333	q33.1
SNP_A-1832364	A	A	360	4	374	0	4.132	4.21E-02	rs931058	5	150313891	q33.1
SNP_A-2279874	G	G	301	79	273	107	5.581	1.82E-02	rs4958893	5	150467184	q33.1
SNP_A-1984006	C	C	330	24	329	43	4.946	2.61E-02	rs17802052	5	150638453	q33.1
SNP_A-2170752	G	G	330	74	352	50	5.35	0.0207	rs10044636	5	150714711	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1896249	G	G	318	62	335	37	6.671	9.80E-03	rs11167544	5	150757991	q33.1
SNP_A-2306037	G	G	316	70	324	40	7.643	5.70E-03	rs11949709	5	150827380	q33.1
SNP_A-2099040	T	T	384	0	359	5	5.31	0.0212	rs6884262	5	150830243	q33.1
SNP_A-1984015	A	-	237	179	209	209	4.073	0.0436	rs2304054	5	150923278	q33.1
SNP_A-1818200	G	A	217	161	198	194	4.848	2.77E-02	rs9324700	5	150926629	q33.1
SNP_A-1882814	A	A	183	169	207	129	6.477	0.0109	rs7710596	5	150934780	q33.1
SNP_A-2257262	A	A	241	161	205	187	4.723	0.0298	rs7728335	5	150955764	q33.1
SNP_A-2154681	C	C	219	147	197	195	7.017	8.10E-03	rs7729398	5	150956233	q33.1
SNP_A-2087625	A	A	314	104	286	130	4.191	4.06E-02	rs753458	5	150961452	q33.1
SNP_A-1677408	C	C	381	21	377	37	4.259	0.039	rs3846714	5	150963929	q33.1
SNP_A-1984018	G	G	359	5	358	16	5.629	0.0177	rs17741337	5	150980350	q33.1
SNP_A-2244327	A	A	283	101	312	78	4.323	3.76E-02	rs1508767	5	151451753	q33.1
SNP_A-1916789	G	G	299	113	326	88	4.271	3.88E-02	rs485313	5	151454127	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2278047	C	C	324	20	336	8	5.361	0.0206	rs11951018	5	151631303	q33.1
SNP_A-2277171	C	C	364	38	379	23	3.991	4.57E-02	rs10077784	5	151642810	q33.1
SNP_A-2147102	G	G	341	57	343	37	3.847	4.98E-02	rs7721306	5	151920809	q33.1
SNP_A-2011347	C	C	397	7	399	19	5.307	0.0212	rs2974548	5	152030753	q33.1
SNP_A-2146482	C	C	339	41	360	18	9.592	0.002	rs17490390	5	152342899	q33.1
SNP_A-1984065	A	A	322	36	307	59	5.838	1.57E-02	rs17493476	5	152462999	q33.1
SNP_A-1793946	C	C	303	91	281	123	5.489	1.91E-02	rs2910029	5	152515585	q33.1
SNP_A-2301441	C	C	386	4	377	13	4.871	2.73E-02	rs2973138	5	152531056	q33.1
SNP_A-1698947	G	G	306	96	284	128	5.27	2.17E-02	rs294700	5	152548956	q33.2
SNP_A-2313741	A	A	394	10	382	22	4.686	0.0304	rs2546331	5	152554158	q33.1
SNP_A-1878430	G	G	394	18	409	7	5.101	2.39E-02	rs177521	5	152747835	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2304728	A	A	399	3	398	12	5.323	2.10E-02	rs519968	5	152825439	q33.2
SNP_A-1984082	C	C	242	90	267	53	10.584	1.10E-03	rs17114681	5	152867760	q33.2
SNP_A-1984099	G	G	382	8	377	23	7.166	7.40E-03	rs17115017	5	153042789	q33.2
SNP_A-1984100	C	C	398	16	389	31	4.847	2.77E-02	rs17115020	5	153043107	q33.2
SNP_A-2100470	G	G	402	16	388	32	5.577	1.82E-02	rs17115039	5	153045248	q33.2
SNP_A-1789168	T	T	362	32	343	55	6.572	0.0104	rs10035262	5	153045939	q33.2
SNP_A-1876248	T	T	316	42	256	64	8.757	3.10E-03	rs10075495	5	153046281	q33.2
SNP_A-2156003	A	A	381	7	366	18	5.121	2.36E-02	rs6891142	5	153122855	q33.2
SNP_A-2288596	C	C	295	107	272	140	5.22	0.0223	rs2617244	5	153435126	q33.2
SNP_A-1699923	C	C	242	96	243	133	3.969	4.63E-02	rs816037	5	153453591	q33.2
SNP_A-1804433	G	G	385	17	378	36	6.701	9.60E-03	rs17115951	5	153694817	q33.2
SNP_A-1883552	T	T	280	86	267	117	4.614	3.17E-02	rs13166462	5	153931917	q33.2
SNP_A-1984128	G	G	256	142	227	173	4.787	0.0287	rs1824935	5	153966506	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2066729	C	C	354	32	341	51	4.547	3.30E-02	rs2001431	5	153998622	q33.2
SNP_A-1704929	G	G	252	150	229	181	3.925	4.76E-02	rs1824936	5	154014554	q33.2
SNP_A-1717023	G	G	252	150	231	183	4.008	0.0453	rs1824935	5	154014823	q33.2
SNP_A-1896095	C	C	333	79	309	107	5.093	0.024	rs4117784	5	154082068	q33.2
SNP_A-2233712	C	C	341	69	323	95	4.533	0.0332	rs17116710	5	154375651	q33.2
SNP_A-1984143	C	C	363	47	383	23	8.745	3.10E-03	rs1422832	5	154581750	q33.2
SNP_A-1906570	C	C	261	45	309	31	4.845	2.77E-02	rs6580149	5	154598503	q33.2
SNP_A-1851052	G	G	282	120	318	86	7.767	0.0053	rs6881952	5	154612310	q33.2
SNP_A-2296243	G	G	321	23	293	39	5.195	2.27E-02	rs1820797	5	154748064	q33.2
SNP_A-2308153	C	C	361	13	360	4	4.631	3.14E-02	rs12717890	5	154809393	q33.2
SNP_A-2246068	C	C	336	38	320	58	4.536	0.0332	rs267013	5	154834122	q33.2
SNP_A-2268503	C	C	333	41	317	65	5.744	1.65E-02	rs267015	5	154836363	q33.2
SNP_A-1781477	T	T	329	47	321	71	4.649	3.11E-02	rs2432922	5	154847787	q33.2
SNP_A-2041275	T	T	325	51	279	73	6.623	0.0101	rs2312974	5	154922984	q33.2
SNP_A-1984157	G	G	311	51	282	74	5.6	1.80E-02	rs10515709	5	154953129	q33.2
SNP_A-1871673	G	G	338	78	307	109	6.629	0.01	rs2161991	5	154958491	q33.2
SNP_A-2091465	C	C	304	58	299	85	4.494	3.40E-02	rs2552992	5	154990411	q33.2
SNP_A-2128514	C	C	375	43	358	64	4.497	3.40E-02	rs2552991	5	154990461	q33.2
SNP_A-1687874	T	T	313	89	347	65	5.37	2.05E-02	rs3922737	5	155130950	q33.2
SNP_A-1683330	T	T	313	89	350	64	5.975	1.45E-02	rs3922736	5	155131009	q33.2
SNP_A-2209351	A	A	313	19	319	5	8.127	4.40E-03	rs244990	5	155237614	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813070	T	T	245	129	231	163	3.852	4.97E-02	rs1821243	5	155513605	q33.2
SNP_A-1884458	G	G	283	131	257	163	4.692	3.03E-02	rs1821242	5	155513707	q33.2
SNP_A-2044712	A	A	366	8	354	18	4.041	4.44E-02	rs6898902	5	156200560	q33.3
SNP_A-2226518	A	A	360	0	356	6	6.017	1.42E-02	rs6555720	5	156240220	q33.3
SNP_A-2237497	A	A	295	83	309	57	4.961	2.59E-02	rs10070224	5	156278313	q33.3
SNP_A-2076013	T	T	271	83	313	57	7.499	6.20E-03	rs1345618	5	156283925	q33.3
SNP_A-1984200	G	G	313	103	341	77	4.95	2.61E-02	rs7700944	5	156298759	q33.3
SNP_A-2041368	A	A	323	45	335	27	4.67	3.07E-02	rs2434971	5	156510994	q33.3
SNP_A-2164339	A	A	263	151	292	122	4.596	3.20E-02	rs246871	5	156517832	q33.3
SNP_A-2125528	C	C	307	25	291	45	6.119	0.0134	rs25855	5	156556978	q33.3
SNP_A-1921139	G	G	329	19	337	37	4.952	2.61E-02	rs11134736	5	156759091	q33.3
SNP_A-1822879	C	C	355	33	380	18	5.136	2.34E-02	rs17054709	5	156905866	q33.3
SNP_A-2088704	G	G	321	53	310	76	4.104	4.28E-02	rs18616576	5	157235562	q33.3
SNP_A-1984224	A	A	216	102	202	132	3.925	4.76E-02	rs24193387	5	157422346	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2231859	G	G	333	23	325	43	5.961	0.0146	rs4512122	5	157520940	q33.3
SNP_A-1817562	A	A	309	103	282	128	3.934	4.73E-02	rs202816	5	157537986	q33.3
SNP_A-1984229	T	T	297	103	275	131	4.152	4.16E-02	rs202809	5	157552601	q33.3
SNP_A-1984230	A	A	303	107	276	138	5.162	2.31E-02	rs1145631	5	157578858	q33.3
SNP_A-2135084	A	A	321	55	304	78	4.393	0.0361	rs882884	5	157660226	q33.3
SNP_A-1795125	A	A	266	78	281	41	11.201	8.00E-04	rs3934712	5	157860774	q33.3
SNP_A-1984239	T	T	320	92	354	60	8.447	3.70E-03	rs2963451	5	157864576	q33.3
SNP_A-1984240	C	C	306	92	350	62	8.556	3.40E-03	rs2964499	5	157865257	q33.3
SNP_A-2034373	G	G	227	123	268	106	3.867	4.93E-02	rs2963444	5	157871448	q33.3
SNP_A-2220617	G	G	250	122	280	84	8.622	0.0033	rs2963440	5	157875274	q33.3
SNP_A-1984241	G	G	331	57	356	34	6.718	9.50E-03	rs10515764	5	157877758	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2290830	C	C	242	140	259	109	4.176	4.10E-02	rs2914223	5	157925242	q33.3
SNP_A-1807464	T	T	412	4	422	0	4.077	4.35E-02	rs2042875	5	158078484	q33.3
SNP_A-1984249	A	A	341	55	310	74	4.091	4.31E-02	rs1541649	5	158118880	q33.3
SNP_A-2242010	C	C	340	32	324	54	5.966	0.0146	rs10067813	5	158126991	q33.3
SNP_A-2241486	A	A	287	33	265	51	4.709	3.00E-02	rs7720275	5	158179228	q33.3
SNP_A-2283740	C	C	328	82	356	62	3.847	4.98E-02	rs10054046	5	158242261	q33.3
SNP_A-2011384	T	T	334	76	362	56	4.08	4.34E-02	rs6556377	5	158326158	q33.3
SNP_A-1984259	A	A	261	107	270	76	4.731	2.96E-02	rs10515786	5	158408564	q33.3
SNP_A-2259676	G	G	271	83	249	111	4.922	2.65E-02	rs6884239	5	158557147	q33.3
SNP_A-1730807	G	G	344	36	349	57	3.922	4.77E-02	rs10515776	5	158577268	q33.3
SNP_A-1785868	C	C	269	115	318	92	5.801	0.016	rs11957668	5	158961702	q33.3
SNP_A-2100510	A	A	329	65	346	44	4.454	3.48E-02	rs6888132	5	158965014	q33.3
SNP_A-1820518	C	C	304	94	342	70	5.507	0.0189	---	5	158965093	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181719	G	G	272	126	305	101	4.562	0.0327	rs1363656	5	159000823	q33.3
SNP_A-1859915	A	A	273	141	302	116	3.875	4.90E-02	rs10428678	5	159005756	q33.3
SNP_A-2073711	C	C	339	73	367	51	4.971	0.0258	rs6876859	5	159036802	q33.3
SNP_A-2173580	A	A	308	76	317	49	5.533	1.87E-02	rs13360959	5	159040477	q33.3
SNP_A-1678364	T	T	163	119	258	104	12.704	4.00E-04	rs2195926	5	159303818	q33.3
SNP_A-2083240	C	C	319	69	363	51	4.701	3.01E-02	rs2910211	5	159809466	q33.3
SNP_A-2203940	A	A	360	18	382	6	6.523	0.0106	rs17057913	5	159874003	q33.3
SNP_A-2238698	T	T	348	32	371	15	6.838	8.90E-03	rs7709677	5	159928968	q34
SNP_A-2022602	A	A	326	76	304	100	4.036	4.45E-02	rs1990886	5	159833592	q34
SNP_A-1878518	C	C	247	133	284	106	5.499	0.019	rs1421957	5	160032344	q34
SNP_A-1780369	A	A	226	128	259	93	7.783	0.0053	rs6879149	5	160033645	q34
SNP_A-1872670	A	A	333	73	357	45	7.459	0.0063	rs7701824	5	160040911	q34
SNP_A-1857219	C	C	334	84	359	63	3.883	4.88E-02	rs6894908	5	160048357	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1727891	A	A	221	179	255	155	4.03	4.47E-02	rs10515815	5	160124835	q34
SNP_A-1813420	A	A	402	12	408	4	4.04	4.44E-02	rs17502295	5	160315930	q34
SNP_A-1862585	C	C	215	129	237	97	5.455	0.0195	rs395560	5	160469694	q34
SNP_A-2212042	C	C	244	108	274	78	6.576	0.0103	rs861320	5	160470410	q34
SNP_A-1788106	A	A	263	111	298	88	4.654	0.031	rs349763	5	160471139	q34
SNP_A-2149231	A	A	261	117	275	87	4.434	3.52E-02	rs417781	5	160490574	q34
SNP_A-1984332	G	G	339	71	363	49	4.849	2.77E-02	rs10515830	5	160984524	q34
SNP_A-1855502	T	T	340	76	365	55	4.234	3.96E-02	rs4921195	5	161044166	q34
SNP_A-2188989	A	A	275	47	286	30	3.913	4.79E-02	rs7708651	5	161612552	q34
SNP_A-2011406	A	A	368	20	387	9	4.569	3.25E-02	rs4329053	5	161802125	q34
SNP_A-2011409	A	A	292	76	249	95	4.725	2.97E-02	rs6862855	5	162133613	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2228529	G	G	276	104	292	68	7.45	0.0063	rs3097318	5	162138493	q34
SNP_A-1642339	A	A	320	82	304	110	4.318	3.77E-02	rs4921469	5	162175914	q34
SNP_A-2245073	C	C	315	81	333	57	4.628	3.14E-02	rs1458351	5	162346399	q34
SNP_A-2049824	C	C	355	19	330	32	4.032	4.47E-02	rs300200	5	162632244	q34
SNP_A-2044109	C	C	222	144	265	113	7.344	6.70E-03	rs1427997	5	162634837	q34
SNP_A-1850317	A	A	363	21	343	37	4.96	2.59E-02	rs300206	5	162664599	q34
SNP_A-1813644	A	A	332	14	345	5	4.49	3.41E-02	rs2112237	5	162763061	q34
SNP_A-1828542	C	C	310	40	283	19	5.198	2.26E-02	rs6879346	5	162899365	q34
SNP_A-1655967	G	G	368	32	358	52	4.777	2.88E-02	rs10491405	5	162956831	q34
SNP_A-1803934	A	A	390	16	371	37	8.79	3.00E-03	rs573125	5	163015927	q34
SNP_A-2029282	C	C	386	10	363	27	8.472	3.60E-03	rs659919	5	163016166	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1837382	C	C	317	31	283	51	6.52	1.07E-02	rs3961976	5	163103617	q34
SNP_A-2226380	G	G	318	50	292	78	7.228	7.20E-03	rs6888266	5	163103649	q34
SNP_A-1668676	C	C	204	196	252	160	8.518	3.50E-03	rs641436	5	163106589	q34
SNP_A-1671796	A	A	343	59	330	84	4.446	3.50E-02	rs6890173	5	163124880	q34
SNP_A-1933817	G	G	380	2	388	10	5.091	0.0241	rs12153552	5	163225551	q34
SNP_A-2207379	C	C	222	120	248	96	4.099	4.29E-02	rs1895178	5	163283841	q34
SNP_A-2284688	A	A	249	137	216	170	5.889	0.0152	rs4868859	5	163520043	q34
SNP_A-1984400	T	A	233	173	207	199	5.718	1.68E-02	rs4132889	5	163548920	q34
SNP_A-2032723	G	G	226	148	196	176	4.547	3.30E-02	rs4868871	5	163562658	q34
SNP_A-1984403	C	C	277	95	295	71	3.988	0.0458	rs3923169	5	163744136	q34
SNP_A-2126493	G	G	375	27	394	14	4.547	3.30E-02	rs4368753	5	163752900	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2096501	A	A	378	30	395	15	5.369	2.05E-02	rs10058433	5	163753090	q34
SNP_A-2066053	C	C	298	98	275	125	4.172	4.11E-02	rs765272	5	163824066	q34
SNP_A-1811987	A	A	362	32	383	9	13.489	2.00E-04	rs4868935	5	164941974	q34
SNP_A-1945816	C	C	243	157	270	128	4.367	3.66E-02	rs262747	5	164979276	q34
SNP_A-1707764	T	T	289	113	269	145	4.51	3.37E-02	rs262750	5	165030221	q34
SNP_A-2099721	C	C	386	26	402	14	3.906	4.81E-02	rs10045204	5	165234489	q34
SNP_A-1647242	T	T	343	45	343	69	4.337	0.0373	rs1975525	5	165353187	q34
SNP_A-1917450	C	C	303	91	335	69	4.505	3.38E-02	rs11134409	5	165446720	q34
SNP_A-1942595	C	C	283	83	319	53	8.722	3.10E-03	rs2644730	5	165452349	q34
SNP_A-2231640	A	A	309	105	279	131	4.376	3.65E-02	rs1799547	5	165703556	q34
SNP_A-1815084	G	G	304	98	273	123	4.449	0.0349	rs2178081	5	165705761	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2178473	T	T	300	104	279	135	4.661	0.0309	rs1799549	5	165706882	q34
SNP_A-2195820	T	T	309	79	277	107	5.942	1.48E-02	rs1799543	5	165716625	q34
SNP_A-2163205	C	C	190	130	215	99	5.683	1.71E-02	rs1631380	5	165826952	q34
SNP_A-2047561	C	C	282	54	310	38	3.898	4.84E-02	rs441417	5	166058188	q34
SNP_A-1714178	T	T	362	40	349	59	3.84	5.00E-02	rs10516023	5	166134635	q34
SNP_A-1984458	G	G	363	5	383	15	4.368	3.66E-02	rs17067598	5	166166487	q34
SNP_A-1984464	C	C	317	33	314	12	8.974	2.70E-03	rs7728198	5	166425538	q34
SNP_A-2133571	G	G	357	45	380	28	4.632	3.14E-02	rs6555735	5	166430953	q34
SNP_A-2011427	A	-	224	160	189	189	5.329	2.10E-02	rs2910044	5	166457604	q34
SNP_A-1698853	G	G	211	145	206	194	4.597	3.20E-02	rs1432949	5	166469923	q34
SNP_A-1841022	G	G	196	164	235	133	6.678	9.80E-03	rs2915858	5	166475199	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101589	G	G	405	9	420	0	9.23	2.40E-03	rs6555755	5	166846418	q34
SNP_A-2039086	C	C	409	9	420	0	9.141	2.50E-03	rs12652771	5	166851436	q34
SNP_A-2204971	A	A	402	6	418	0	6.192	1.28E-02	rs2112626	5	166898288	q34
SNP_A-1679270	G	G	257	125	270	94	4.277	3.86E-02	rs6881950	5	166991941	q34
SNP_A-1883226	A	A	359	45	344	68	5.553	0.0184	rs2337017	5	167085900	q34
SNP_A-1886807	C	C	406	12	420	2	7.361	6.70E-03	rs1024971	5	167222513	q34
SNP_A-1799166	A	A	266	96	297	69	6.103	0.0135	rs1421980	5	167246839	q34
SNP_A-2089409	A	A	234	120	211	157	5.862	0.0155	rs11951480	5	167269405	q34
SNP_A-2123598	C	C	394	4	380	12	4.208	0.0402	rs17069629	5	167380326	q34
SNP_A-1788750	T	T	284	36	329	17	9.114	2.50E-03	rs17070005	5	167573645	q34
SNP_A-2162686	A	A	294	116	268	150	5.472	1.93E-02	rs1862354	5	167666574	q34
SNP_A-2251037	T	T	286	116	256	150	5.987	0.0144	rs11744297	5	167666805	q34
SNP_A-2150645	C	T	176	146	193	171	4.032	4.46E-02	rs7731635	5	167723587	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2229273	T	T	375	23	351	41	5.811	1.59E-02	rs6555806	5	167731740	q34
SNP_A-2098515	C	C	357	37	325	57	5.573	1.82E-02	rs4976550	5	167779292	q34
SNP_A-1789640	A	A	356	36	340	58	5.471	1.93E-02	rs7722478	5	167797818	q34
SNP_A-2170306	G	G	196	162	240	138	5.821	1.58E-02	rs2085449	5	167818328	q34
SNP_A-1884219	G	G	224	118	194	154	6.866	8.80E-03	rs6555817	5	167897313	q34
SNP_A-2180368	T	T	220	122	191	157	6.385	0.0115	rs1120242	5	168005933	q34
SNP_A-2290798	C	C	367	45	336	80	11.148	8.00E-04	rs11750308	5	168049971	q34
SNP_A-1751137	G	G	334	68	306	92	4.805	2.84E-02	rs10516048	5	168075212	q34
SNP_A-2245434	T	C	237	169	218	196	10.009	1.60E-03	rs7715777	5	168079907	q34
SNP_A-2242475	T	T	362	54	387	35	4.848	2.77E-02	rs891922	5	168141342	q34
SNP_A-2025435	T	T	310	76	268	110	9.184	2.40E-03	rs17070503	5	168160834	q34
SNP_A-1788216	G	A	220	194	231	183	6.618	0.0101	rs3797716	5	168165991	q34
SNP_A-2220348	T	T	332	58	318	86	5.501	0.019	rs10066747	5	168202822	q34
SNP_A-2085599	C	C	272	94	310	72	5.057	2.45E-02	rs7724207	5	168331119	q34
SNP_A-2184726	C	C	383	35	394	20	4.228	3.98E-02	rs17667992	5	168576988	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2176174	C	C	400	0	402	10	9.83	1.70E-03	rs17071195	5	168749079	q35.1
SNP_A-2275247	C	C	247	133	295	109	5.902	1.51E-02	rs3860755	5	169292733	q35.1
SNP_A-2314711	G	G	273	125	312	98	5.692	1.70E-02	rs6895199	5	169294660	q35.1
SNP_A-1706573	T	T	242	150	272	124	4.198	4.05E-02	rs261004	5	169317518	q35.1
SNP_A-2291541	C	C	404	10	395	25	6.487	0.0109	rs17647921	5	169471014	q35.1
SNP_A-1807179	A	A	296	114	335	83	7.212	7.20E-03	rs6880991	5	169478220	q35.1
SNP_A-1944152	G	G	257	151	305	107	11.584	7.00E-04	rs4867936	5	169540264	q35.1
SNP_A-1891804	C	C	231	177	269	139	7.458	0.0063	rs4867588	5	169547131	q35.1
SNP_A-2055574	G	G	246	132	201	175	10.548	1.20E-03	rs2287742	5	169557568	q35.1
SNP_A-2165138	C	A	235	153	198	194	9.667	0.0019	rs10447195	5	169560235	q35.1
SNP_A-2281946	T	A	246	166	215	197	11.722	6.00E-04	rs9313494	5	169560602	q35.1
SNP_A-1952057	C	T	232	184	214	204	4.055	4.40E-02	rs11743438	5	169577814	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170177	G	G	316	102	343	79	4.01	4.52E-02	rs17072346	5	169580109	q35.1
SNP_A-2159067	C	C	403	13	391	25	3.971	4.63E-02	rs17072432	5	169653908	q35.1
SNP_A-2189092	T	T	338	10	330	26	7.117	0.0076	rs13360847	5	169654926	q35.1
SNP_A-1888297	T	T	402	14	392	30	5.901	1.51E-02	rs3761747	5	169659948	q35.1
SNP_A-1984559	A	A	302	68	266	102	9.076	2.60E-03	rs17739586	5	169667902	q35.1
SNP_A-2288264	G	G	306	88	292	118	4.38	3.64E-02	rs4867607	5	169859417	q35.1
SNP_A-2295815	G	G	347	69	359	47	4.255	3.91E-02	rs11957313	5	169882972	q35.1
SNP_A-2034327	T	T	314	66	261	83	5.047	0.0247	rs4867985	5	169947368	q35.1
SNP_A-2128329	C	C	332	70	313	97	4.847	2.77E-02	rs2089192	5	169970500	q35.1
SNP_A-2170464	C	C	304	64	309	93	3.904	0.0482	rs4867625	5	170021180	q35.1
SNP_A-2108878	C	C	287	55	280	34	3.853	4.96E-02	rs1363713	5	170095672	q35.1
SNP_A-1806847	C	T	199	189	216	166	4.737	2.95E-02	rs732157	5	170143829	q35.1
SNP_A-2021772	A	A	212	104	248	86	4.027	0.0448	rs3792811	5	170147972	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2109518	A	A	324	66	310	90	3.875	4.90E-02	rs4620037	5	170807702	q35.1
SNP_A-1866005	G	G	329	75	359	51	5.836	1.57E-02	rs6883796	5	170855757	q35.1
SNP_A-2032978	G	G	328	70	359	51	4.205	4.03E-02	rs9313575	5	171437235	q35.1
SNP_A-2304516	G	G	321	39	338	18	8.153	0.0043	rs6889761	5	171446104	q35.1
SNP_A-1795192	C	C	362	26	347	47	6.313	0.012	rs3103590	5	171464882	q35.1
SNP_A-2270828	C	C	369	33	350	52	4.749	0.0293	rs3111482	5	171465492	q35.1
SNP_A-2189287	T	T	252	130	277	99	5.331	2.10E-02	rs6863095	5	171575142	q35.1
SNP_A-2052765	T	T	232	164	252	132	4.102	4.28E-02	rs9332410	5	171590892	q35.1
SNP_A-2219601	G	G	248	132	290	108	5.265	0.0218	rs12521646	5	171600173	q35.1
SNP_A-2222601	T	T	262	114	234	144	5.064	2.44E-02	rs7736157	5	171620316	q35.1
SNP_A-1809976	C	C	289	127	247	169	9.251	2.40E-03	rs6881831	5	171691086	q35.1
SNP_A-2143816	T	T	384	18	399	7	5.108	2.38E-02	rs17074690	5	171706968	q35.1
SNP_A-1819104	C	C	391	21	400	8	5.911	1.50E-02	rs13436547	5	171773330	q35.1
SNP_A-2298904	G	G	274	108	244	146	7.34	6.70E-03	rs2731685	5	171794068	q35.1
SNP_A-2145643	C	C	369	39	386	24	3.949	4.69E-02	rs4868172	5	171847924	q35.1
SNP_A-2011460	G	G	285	105	291	77	5.518	1.88E-02	rs4867686	5	172083595	q35.1
SNP_A-2154105	A	A	338	2	337	9	4.404	3.59E-02	rs888699	5	172279254	q35.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960070	G	G	292	74	324	56	3.893	4.85E-02	rs11134782	5	172635604	q35.1
SNP_A-1790442	G	G	285	111	312	88	3.859	4.95E-02	rs13162731	5	172641877	q35.1
SNP_A-2154596	A	A	342	60	372	42	4.261	0.039	rs13155020	5	172652854	q35.1
SNP_A-2021541	C	C	393	1	398	12	9.024	2.70E-03	rs17075777	5	172664733	q35.1
SNP_A-1878725	C	C	286	66	327	41	8.232	4.10E-03	rs17075905	5	172772190	q35.2
SNP_A-2180506	C	C	293	109	267	139	4.816	2.82E-02	rs1445787	5	172785484	q35.2
SNP_A-1949083	G	G	397	3	375	11	4.951	2.61E-02	rs17075944	5	172802893	q35.2
SNP_A-2266588	G	G	221	167	260	130	7.766	0.0053	rs12517986	5	172927766	q35.2
SNP_A-1984613	C	C	198	182	232	154	4.975	2.57E-02	rs17738166	5	172930584	q35.2
SNP_A-1888429	A	A	235	175	266	136	6.731	9.50E-03	rs7704555	5	172932608	q35.2
SNP_A-2087377	G	G	278	98	329	57	15.002	0.0001	rs2339962	5	172935830	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209932	A	G	189	165	227	145	15.166	9.85E-05	rs12153774	5	172940197	q35.2
SNP_A-2069415	T	T	255	163	296	126	7.769	0.0053	rs12152984	5	172940442	q35.2
SNP_A-2274161	C	C	391	1	375	7	4.706	3.01E-02	rs6884856	5	172943598	q35.2
SNP_A-2257028	G	G	182	178	227	119	16.4	5.13E-05	rs746214	5	172943721	q35.2
SNP_A-2234893	T	A	211	167	198	170	6.912	0.0086	rs735058	5	172944222	q35.2
SNP_A-1984615	C	T	226	186	224	186	7.401	6.50E-03	rs393952	5	172951457	q35.2
SNP_A-1743383	C	C	221	171	267	145	5.981	1.45E-02	rs889014	5	172965037	q35.2
SNP_A-1876441	A	A	294	116	330	82	7.91	4.90E-03	---	5	172984937	q35.2
SNP_A-1926873	T	T	242	140	222	174	4.293	3.83E-02	rs812619	5	173145177	q35.2
SNP_A-1934641	G	G	322	48	325	29	4.351	3.70E-02	rs6556098	5	173329497	q35.2
SNP_A-1658734	A	A	261	85	305	65	5.289	2.15E-02	rs1036172	5	173564335	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1984632	C	C	310	86	261	117	8.525	3.50E-03	rs17077005	5	173578620	q35.2
SNP_A-1984635	G	G	351	57	378	40	3.859	4.95E-02	rs356078	5	173610570	q35.2
SNP_A-1850577	G	G	338	10	305	21	4.884	2.71E-02	rs17077140	5	173618334	q35.2
SNP_A-1941977	G	G	313	49	282	78	8.232	4.10E-03	rs10463032	5	173619745	q35.2
SNP_A-1945013	C	C	359	59	334	86	5.925	0.0149	rs17077144	5	173620078	q35.2
SNP_A-1984643	G	G	362	32	389	19	4.041	4.44E-02	rs7715861	5	173644143	q35.2
SNP_A-2011471	G	G	410	4	416	0	4.039	4.45E-02	rs1346449	5	173769526	q35.2
SNP_A-1693857	G	G	364	24	369	41	3.877	4.90E-02	rs10516121	5	174395631	q35.2
SNP_A-1984663	C	C	361	23	339	41	5.733	0.0166	rs949637	5	174447933	q35.2
SNP_A-1984665	T	T	375	1	376	10	7.235	7.10E-03	rs10516127	5	174449209	q35.2
SNP_A-2300461	A	A	207	201	246	172	5.492	1.91E-02	rs2248804	5	174491104	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835786	G	G	341	25	336	42	4.158	4.14E-02	rs17808228	5	174539505	q35.2
SNP_A-2011476	A	A	244	162	279	139	3.926	4.76E-02	rs7449443	5	174653499	q35.2
SNP_A-1903499	A	A	377	3	359	11	4.879	2.72E-02	rs2471013	5	174698406	q35.2
SNP_A-1897862	A	A	305	89	327	67	3.868	4.92E-02	rs10476160	5	174907182	q35.2
SNP_A-1857118	G	G	381	35	401	21	3.969	4.64E-02	rs11957214	5	175054206	q35.2
SNP_A-1689130	T	T	386	16	407	7	3.902	0.0482	rs686874	5	175090568	q35.2
SNP_A-1670956	G	G	314	50	309	81	6.487	0.0109	rs7727183	5	175210209	q35.2
SNP_A-2231260	A	A	375	21	359	37	4.763	2.91E-02	rs973356	5	175371041	q35.2
SNP_A-1930511	C	C	375	15	376	2	9.757	0.0018	rs11749216	5	175823705	q35.2
SNP_A-1919369	T	T	329	53	297	81	7.466	0.0063	rs2913900	5	175856973	q35.2
SNP_A-2043987	A	A	284	52	260	74	4.894	0.0269	rs2963673	5	175869979	q35.2
SNP_A-2193493	G	G	260	142	290	106	6.817	9.00E-03	rs4868672	5	175996155	q35.2
SNP_A-2173404	G	G	393	5	396	14	4.097	4.30E-02	rs17229383	5	176070414	q35.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2314369	C	C	293	47	305	29	4.451	0.0349	rs729823	5	176101113	q35.2
SNP_A-1789757	T	T	366	16	371	3	8.845	2.90E-03	rs1000144	5	176217319	q35.2
SNP_A-1675071	A	A	385	15	406	6	4.238	0.0395	rs691268	5	176244473	q35.2
SNP_A-2207454	G	G	224	154	195	179	3.863	4.94E-02	rs6861925	5	176257335	q35.2
SNP_A-1742457	C	C	332	58	373	41	4.591	3.21E-02	rs10516138	5	176343237	q35.2
SNP_A-2112553	G	G	230	148	201	181	5.24	2.21E-02	rs601923	5	176349992	q35.2
SNP_A-2251603	G	G	306	102	317	67	6.722	9.50E-03	rs442656	5	176449898	q35.2
SNP_A-2120778	G	G	309	91	284	118	4.537	0.0332	rs11949767	5	176672850	q35.3
SNP_A-2306995	T	T	285	87	260	128	8.632	0.0033	rs6885410	5	176673602	q35.3
SNP_A-2222913	G	G	402	0	404	4	3.961	4.66E-02	rs6897423	5	177540801	q35.3
SNP_A-1873453	G	G	373	11	388	24	4.144	4.18E-02	rs13172345	5	177736666	q35.3
SNP_A-1809256	C	C	373	45	405	17	13.943	2.00E-04	rs4976769	5	177740794	q35.3
SNP_A-2262903	G	G	212	140	188	180	6.087	1.36E-02	rs17648049	5	177763420	q35.3
SNP_A-1656465	A	A	235	75	332	70	4.962	2.59E-02	rs2913838	5	177819432	q35.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100041	T	T	315	45	334	28	4.51	3.37E-02	rs7713731	5	178170470	q35.3
SNP_A-2274038	A	A	196	150	230	122	5.545	1.85E-02	rs7716645	5	178186927	q35.3
SNP_A-1891606	T	T	195	157	213	123	4.553	3.29E-02	rs2645339	5	178348669	q35.3
SNP_A-2122975	A	A	221	79	276	62	5.894	0.0152	rs17666172	5	178435826	q35.3
SNP_A-1984730	T	T	232	118	251	89	4.666	3.08E-02	rs173072	5	178571166	q35.3
SNP_A-2162085	A	A	301	109	271	147	7.137	7.50E-03	rs6601028	5	178627692	q35.3
SNP_A-2122677	T	T	280	128	246	152	4.131	4.21E-02	rs166031	5	178653574	q35.3
SNP_A-1826522	A	A	327	83	358	62	4.324	3.76E-02	rs4700799	5	178687551	q35.3
SNP_A-2184848	T	T	347	7	354	0	7.07	7.80E-03	rs6870903	5	179373514	q35.3
SNP_A-2054376	T	T	186	154	240	134	6.63	0.01	rs4700858	5	179429855	q35.3
SNP_A-1918569	G	G	233	141	194	160	4.215	4.01E-02	rs4700921	5	179794189	q35.3
SNP_A-1902911	G	G	363	25	351	45	5.835	1.57E-02	rs2453176	5	179908398	q35.3
SNP_A-2198389	G	G	286	96	274	126	3.899	4.83E-02	rs2447736	5	179947747	q35.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2272386	A	A	222	92	263	63	8.67	3.20E-03	rs1601182	5	180072591	q35.3
SNP_A-1799900	T	T	272	126	308	102	4.584	3.23E-02	rs12719876	5	180089797	q35.3
SNP_A-2288309	A	A	285	131	318	102	5.396	2.02E-02	rs10479581	5	180097973	q35.3
SNP_A-2265763	C	C	308	100	329	75	4.244	3.94E-02	rs1843070	5	180113689	q35.3
SNP_A-2080454	T	T	281	107	328	80	7.028	8.00E-03	rs6884018	5	180141456	q35.3
SNP_A-1821921	A	A	291	101	325	73	6.337	0.0118	rs655437	5	180142060	q35.3
SNP_A-2050841	C	C	296	58	286	82	4.016	4.51E-02	rs29654	5	180199735	q35.3
SNP_A-1913817	C	C	386	16	404	6	4.877	2.72E-02	rs10479597	5	180384879	q35.3
SNP_A-2034126	G	G	329	75	352	54	4.19	0.0407	rs17080884	5	180578571	q35.3
SNP_A-1984754	C	C	339	49	365	33	3.956	4.67E-02	rs1418708	6	150610	p25.3
SNP_A-1896999	A	A	248	128	278	96	6.277	1.22E-02	rs7771527	6	158782	p25.3
SNP_A-1861626	A	A	355	11	338	22	4.034	4.46E-02	rs815582	6	231587	p25.3
SNP_A-2275925	G	G	396	18	412	8	4.12	0.0424	rs3866814	6	323703	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869223	G	G	350	4	341	13	4.882	2.71E-02	rs6923764	6	547935	p25.3
SNP_A-2233730	C	C	329	81	300	108	5.189	2.27E-02	rs9379132	6	773403	p25.3
SNP_A-1889530	A	A	319	63	297	89	5.212	0.0224	rs9405352	6	773492	p25.3
SNP_A-2092386	C	C	312	38	271	63	8.702	3.20E-03	rs7770224	6	785475	p25.3
SNP_A-1956451	G	G	370	36	392	22	3.937	4.72E-02	rs17141325	6	865523	p25.3
SNP_A-1675718	C	C	312	76	301	103	3.948	4.69E-02	rs707774	6	945604	p25.3
SNP_A-2184727	G	G	291	115	327	85	6.553	1.05E-02	rs2459602	6	1209403	p25.3
SNP_A-1896011	T	T	271	137	309	107	6.101	0.0135	rs2438077	6	1217236	p25.3
SNP_A-1683128	T	T	264	134	308	104	6.926	8.50E-03	rs2252693	6	1222151	p25.3
SNP_A-1823301	G	G	351	45	379	23	8.147	0.0043	rs12209110	6	1234462	p25.3
SNP_A-1787632	C	C	346	68	322	90	3.921	4.77E-02	rs1437288	6	1234926	p25.3
SNP_A-1806909	A	A	223	135	209	171	4.037	4.45E-02	rs2569866	6	1475051	p25.3
SNP_A-1710157	G	G	228	166	271	139	5.779	1.62E-02	rs2317961	6	1478115	p25.3
SNP_A-2176824	T	T	221	103	213	137	3.967	4.64E-02	rs2816288	6	1482275	p25.3
SNP_A-1881465	G	G	304	62	357	39	8.319	3.90E-03	rs9405141	6	1525837	p25.3
SNP_A-1806503	T	T	213	145	239	119	4.056	4.40E-02	rs2569824	6	1538645	p25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1912364	T	T	308	32	281	51	5.493	1.91E-02	rs6934205	6	1603909	p25.3
SNP_A-1936000	G	G	371	43	389	27	4.079	4.34E-02	rs689035	6	1726380	p25.3
SNP_A-2031506	C	C	416	0	414	4	4	4.55E-02	rs6596857	6	1793387	p25.3
SNP_A-1934425	G	G	269	67	252	90	3.871	4.91E-02	rs7776397	6	1812101	p25.3
SNP_A-2270547	G	G	230	178	263	149	4.761	2.91E-02	rs6596866	6	1940507	p25.3
SNP_A-1679152	T	T	393	3	397	11	4.414	3.57E-02	rs10484948	6	2053584	p25.3
SNP_A-2242202	C	C	348	42	349	25	3.982	4.60E-02	rs3778568	6	2170679	p25.3
SNP_A-1815011	C	C	365	51	387	33	4.482	3.43E-02	rs17134819	6	2189655	p25.3
SNP_A-2011511	T	T	377	15	382	30	4.538	3.31E-02	rs6913700	6	2536710	p25.2
SNP_A-2046066	C	C	399	11	389	25	5.552	1.85E-02	rs13437440	6	2607677	p25.2
SNP_A-1809970	C	C	364	44	396	20	10.271	0.0014	rs4959698	6	2615632	p25.2
SNP_A-2142721	A	A	334	8	325	19	4.599	3.20E-02	rs17135501	6	2649474	p25.2
SNP_A-1787199	G	G	219	193	251	165	4.349	3.70E-02	rs6915338	6	2980522	p25.2
SNP_A-1932306	G	G	366	0	347	5	5.235	2.21E-02	rs2103677	6	3110117	p25.2
SNP_A-1915390	C	C	258	92	277	65	5.226	2.22E-02	rs9378799	6	3398956	p25.2
SNP_A-1848114	T	T	302	104	333	81	4.295	3.82E-02	rs928027	6	3400045	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2075531	C	C	295	107	326	78	6.089	1.36E-02	rs9392499	6	3421102	p25.2
SNP_A-2106968	A	A	294	98	320	76	3.862	4.94E-02	rs913534	6	3426661	p25.2
SNP_A-2114894	G	G	190	168	220	132	6.465	1.10E-02	rs6935818	6	3427569	p25.2
SNP_A-1835327	-	A	191	191	213	151	5.445	1.96E-02	rs1205032	6	3430133	p25.2
SNP_A-2112406	C	C	213	203	245	171	4.974	2.57E-02	rs1205036	6	3430485	p25.2
SNP_A-2255752	G	G	210	188	238	160	4.003	4.54E-02	rs1205038	6	3430963	p25.2
SNP_A-1984837	A	A	206	194	241	171	4.013	4.51E-02	rs6901207	6	3798905	p25.2
SNP_A-1984838	G	T	200	186	232	174	6.369	1.16E-02	rs6905680	6	3799038	p25.2
SNP_A-2011521	G	G	213	201	242	170	4.434	3.52E-02	rs7768021	6	3800205	p25.2
SNP_A-2069584	A	A	338	76	306	106	6.53	0.0106	rs7761276	6	3802886	p25.2
SNP_A-2272800	A	A	305	91	330	68	4.306	3.80E-02	rs7738894	6	3825893	p25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027654	A	A	348	60	370	40	4.669	3.07E-02	rs4266528	6	3975707	p25.2
SNP_A-1901181	C	C	305	61	310	96	5.786	1.62E-02	rs11755877	6	4027176	p25.2
SNP_A-2185938	A	A	351	65	374	44	4.771	2.89E-02	rs9503947	6	4134875	p25.1
SNP_A-2285789	T	T	350	64	375	43	4.964	2.59E-02	rs9503950	6	4137134	p25.1
SNP_A-2145368	G	G	349	9	324	20	4.824	0.0281	rs9392045	6	4352324	p25.1
SNP_A-2107264	C	C	328	86	296	122	7.853	5.10E-03	rs12197303	6	4407200	p25.1
SNP_A-1899685	T	T	326	26	379	13	6.185	0.0129	rs7772028	6	4545609	p25.1
SNP_A-2098415	T	T	259	111	273	83	4.141	0.0419	rs9378928	6	5013524	p25.1
SNP_A-1789198	C	C	357	43	388	22	7.952	4.80E-03	rs666518	6	5020863	p25.1
SNP_A-2300597	A	A	303	103	314	74	4.542	3.31E-02	rs200852	6	5026744	p25.1
SNP_A-1984874	G	G	327	61	301	93	7.68	5.60E-03	rs10484846	6	5048614	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238676	A	A	248	118	229	157	5.76	1.64E-02	rs462749	6	5067993	p25.1
SNP_A-1781209	C	C	377	25	397	13	4.228	3.98E-02	rs388597	6	5069189	p25.1
SNP_A-1984876	T	T	267	143	232	174	5.467	1.94E-02	rs85204	6	5078431	p25.1
SNP_A-1984877	G	G	356	18	371	7	5.128	0.0235	rs424006	6	5079573	p25.1
SNP_A-2060096	T	T	313	61	278	88	6.88	8.70E-03	rs6597115	6	5087841	p25.1
SNP_A-1784527	C	C	227	137	176	160	7.127	0.0076	rs12190412	6	5148951	p25.1
SNP_A-1953708	C	C	276	130	298	100	4.677	3.06E-02	rs17312134	6	5154831	p25.1
SNP_A-1818918	G	G	317	99	291	129	5.04	2.48E-02	rs6597126	6	5251398	p25.1
SNP_A-1984888	A	A	273	83	248	108	4.472	3.45E-02	rs2432789	6	5338304	p25.1
SNP_A-2179150	T	T	307	87	275	111	4.587	3.22E-02	rs2503838	6	5399012	p25.1
SNP_A-2165474	C	C	319	97	287	123	4.719	0.0298	rs2432797	6	5403146	p25.1
SNP_A-2212408	G	G	346	4	366	0	4.206	4.03E-02	rs418040	6	5430182	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1868691	C	C	382	32	366	52	5.085	0.0241	rs6910841	6	5465849	p25.1
SNP_A-2254284	G	G	298	114	327	79	7.649	5.70E-03	rs9504443	6	5547343	p25.1
SNP_A-2245042	C	C	300	116	327	87	5.301	2.13E-02	rs9504449	6	5549112	p25.1
SNP_A-2131838	C	C	411	1	411	7	4.457	3.48E-02	rs9504481	6	5599711	p25.1
SNP_A-2215506	G	G	338	2	327	11	6.407	0.0114	rs3812176	6	5714705	p25.1
SNP_A-2048530	T	T	262	82	245	111	4.723	0.0298	rs9504552	6	5791720	p25.1
SNP_A-2212862	T	T	333	25	339	43	4.044	4.43E-02	rs12527274	6	5829706	p25.1
SNP_A-1866925	G	G	384	26	400	10	7.438	6.40E-03	rs11243046	6	5928362	p25.1
SNP_A-1809696	G	G	330	86	305	113	4.643	3.12E-02	rs12719577	6	6039406	p25.1
SNP_A-1651132	C	C	282	118	325	85	8.288	4.00E-03	rs2274393	6	6127604	p25.1
SNP_A-2036569	C	C	253	129	222	160	5.348	0.0207	rs3024317	6	6264378	p25.1
SNP_A-1746348	G	G	238	126	223	165	4.954	2.60E-02	rs9328354	6	6289006	p25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889936	G	G	334	36	360	16	8.619	0.0033	rs4422662	6	6344782	p25.1
SNP_A-2186715	G	G	222	128	248	100	4.871	2.73E-02	rs10434903	6	6525078	p25.1
SNP_A-1697080	A	A	318	82	347	61	4.27	3.88E-02	rs9328377	6	6539320	p25.1
SNP_A-2218980	G	G	311	33	352	20	4.636	3.13E-02	rs3804480	6	6577294	p25.1
SNP_A-1739279	C	C	271	85	268	126	6.074	0.0137	rs3804484	6	6582809	p25.1
SNP_A-1984952	G	G	297	103	263	125	4.005	4.54E-02	rs3804486	6	6582994	p25.1
SNP_A-1984953	A	A	304	104	257	125	5.013	0.0252	rs2064236	6	6584424	p25.1
SNP_A-1864808	G	G	312	78	324	54	4.404	3.59E-02	rs3748060	6	6846006	p25.1
SNP_A-1905369	C	C	324	52	310	76	4.679	3.05E-02	rs1615495	6	6979458	p25.1
SNP_A-1804937	C	C	277	119	260	150	3.869	4.92E-02	rs9406022	6	7273579	p24.3
SNP_A-1663144	A	A	312	16	289	29	4.482	3.43E-02	rs823695	6	7442109	p24.3
SNP_A-1984979	T	T	330	34	352	20	4.253	3.92E-02	rs6597271	6	7545468	p24.3
SNP_A-1679784	G	G	346	54	380	32	7.044	8.00E-03	rs1044761	6	7557037	p24.3
SNP_A-2047582	C	C	354	58	386	32	8.852	2.90E-03	rs9505240	6	7558341	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2236932	A	A	327	77	300	104	5.19	2.27E-02	rs11243204	6	7717698	p24.3
SNP_A-2149507	C	C	319	77	366	54	6.563	0.0104	rs267179	6	7775047	p24.3
SNP_A-2257015	A	A	305	109	349	71	10.94	9.00E-04	rs267203	6	7802731	p24.3
SNP_A-1857627	T	T	342	28	374	12	7.495	6.20E-03	rs267840	6	7804215	p24.3
SNP_A-2083382	T	T	275	133	308	96	7.827	5.10E-03	rs7769739	6	7919866	p24.3
SNP_A-1878303	T	G	190	186	214	164	3.864	4.93E-02	rs2163455	6	7933820	p24.3
SNP_A-1985004	T	T	257	127	306	90	10.391	1.30E-03	rs7771933	6	8293905	p24.3
SNP_A-1885956	T	T	239	149	288	104	12.54	4.00E-04	rs7741973	6	8294228	p24.3
SNP_A-1649490	T	T	311	59	360	40	6.065	0.0138	rs9328470	6	8341747	p24.3
SNP_A-1985006	G	G	333	73	340	38	10.122	0.0015	rs9392217	6	8343776	p24.3
SNP_A-2132930	A	A	297	21	330	10	4.91	2.67E-02	rs17790009	6	8461542	p24.3
SNP_A-2136683	T	T	306	104	352	60	15.016	0.0001	rs9393036	6	8475655	p24.3
SNP_A-1849667	T	T	357	43	331	69	7.018	8.10E-03	rs230253	6	8485866	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1985016	A	A	308	104	350	64	12.2	5.00E-04	rs330121	6	8495968	p24.3
SNP_A-2166886	C	C	175	157	218	106	14.499	0.0001	rs9378560	6	8496549	p24.3
SNP_A-2122606	G	G	202	194	258	140	15.543	8.06E-05	rs7753991	6	8506427	p24.3
SNP_A-1718891	A	A	235	155	276	128	5.62	0.0178	rs850179	6	8511405	p24.3
SNP_A-1873459	A	A	224	136	250	100	6.778	9.20E-03	rs1100632	6	8515038	p24.3
SNP_A-2198164	G	C	217	169	197	189	4.073	0.0436	rs980083	6	8534915	p24.3
SNP_A-1985019	A	A	303	27	302	48	5.298	2.13E-02	rs1207798	6	8604667	p24.3
SNP_A-2120213	G	G	216	158	183	181	4.155	4.15E-02	rs9393057	6	8613299	p24.3
SNP_A-1704335	A	A	227	167	270	130	8.285	4.00E-03	rs4959496	6	8627165	p24.3
SNP_A-2011554	A	A	403	11	411	3	4.65	3.11E-02	rs6597362	6	8826514	p24.3
SNP_A-2043930	C	C	378	34	340	56	7.075	7.80E-03	rs4145032	6	8841332	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2057526	G	G	291	51	272	72	4.221	3.99E-02	rs4403296	6	8841444	p24.3
SNP_A-2121710	G	G	313	103	284	136	5.946	0.0147	rs438259	6	8975335	p24.3
SNP_A-2175930	G	G	310	4	337	15	5.344	2.08E-02	rs9406237	6	9073799	p24.3
SNP_A-1935444	A	A	308	30	341	17	4.703	3.01E-02	rs4260747	6	9373734	p24.3
SNP_A-1985031	G	G	362	38	386	18	7.893	5.00E-03	rs10484248	6	9375787	p24.3
SNP_A-1731075	G	G	357	43	382	24	6.189	0.0129	rs10484247	6	9406961	p24.3
SNP_A-2023854	T	T	227	103	266	82	4.995	2.54E-02	rs13217597	6	9481736	p24.3
SNP_A-1896585	T	T	280	122	243	171	10.638	1.10E-03	rs2209543	6	9492979	p24.3
SNP_A-2029711	A	A	324	90	296	114	4.069	4.37E-02	rs214440	6	9502146	p24.3
SNP_A-1947358	T	T	218	136	190	176	6.852	8.90E-03	rs2327167	6	9519959	p24.3
SNP_A-2011559	G	G	348	42	347	25	3.892	4.85E-02	rs7761690	6	9777768	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2155997	G	G	290	52	281	75	4.028	0.0448	rs2327200	6	9844962	p24.3
SNP_A-1701743	T	T	351	45	371	27	5.049	0.0246	rs1889211	6	10220283	p24.3
SNP_A-2098919	C	C	163	155	214	144	4.954	2.60E-02	rs9358212	6	10271707	p24.3
SNP_A-2153095	C	C	234	130	203	167	6.76	9.30E-03	rs6926769	6	10292710	p24.3
SNP_A-2082093	T	T	339	75	312	102	5.238	2.21E-02	rs9366301	6	10294561	p24.3
SNP_A-1985060	C	C	252	86	274	58	6.311	0.012	rs611542	6	10582826	p24.3
SNP_A-1955382	G	G	264	98	242	136	6.785	9.20E-03	rs4470837	6	10961526	p24.2
SNP_A-1985069	T	T	270	128	247	157	3.929	4.74E-02	rs2076257	6	10983224	p24.2
SNP_A-1985070	A	A	332	48	307	75	6.9	0.0086	rs4713039	6	11014242	p24.2
SNP_A-1855217	A	A	247	95	207	115	4.831	2.80E-02	rs2788872	6	11055168	p24.2
SNP_A-1800666	G	G	327	53	306	74	4.169	4.12E-02	rs3778166	6	11141150	p24.2
SNP_A-2168061	A	A	239	143	273	115	5.25	2.19E-02	rs6926422	6	11584604	p24.2
SNP_A-2112689	T	T	277	135	313	105	5.904	1.51E-02	rs176075537	6	11589118	p24.2
SNP_A-1670227	C	C	345	29	329	47	4.638	3.13E-02	rs10498678	6	11598190	p24.2
SNP_A-1892665	C	C	242	70	279	49	5.937	1.48E-02	rs628980	6	11605322	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1654415	C	C	354	46	338	74	6.727	9.50E-03	rs821545	6	11607378	p24.2
SNP_A-1742629	T	T	249	115	308	100	4.804	2.84E-02	rs687163	6	11607722	p24.2
SNP_A-2157831	C	C	251	115	302	80	10.648	1.10E-03	rs675565	6	11653568	p24.2
SNP_A-2011573	A	A	283	111	323	75	9.588	0.002	rs586105	6	11668148	p24.2
SNP_A-2303139	G	G	237	95	278	70	6.679	9.80E-03	rs490466	6	11685071	p24.2
SNP_A-2118695	A	A	308	74	291	99	4.013	4.52E-02	rs295065	6	11706917	p24.1
SNP_A-1985096	G	G	393	23	404	10	5.268	2.17E-02	rs821437	6	11742708	p24.1
SNP_A-1693230	G	G	218	182	260	152	6.209	1.27E-02	rs9296117	6	11777627	p24.1
SNP_A-2215227	G	G	225	175	246	142	4.19	0.0407	rs4713821	6	11793047	p24.1
SNP_A-1985097	A	A	223	179	257	149	5.133	0.0235	rs1416451	6	11793949	p24.1
SNP_A-2103992	C	C	195	185	229	153	5.751	1.65E-02	rs10947516	6	11794213	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1845997	G	G	196	170	234	140	6.176	1.30E-02	rs7750635	6	11809959	p24.1
SNP_A-2282362	C	C	315	65	307	39	5.022	2.50E-02	rs9469986	6	11857166	p24.1
SNP_A-1961506	T	T	331	41	364	24	5.679	0.0172	rs9470663	6	12094807	p24.1
SNP_A-1919757	A	A	340	52	318	76	5.231	2.22E-02	rs7741589	6	12237033	p24.1
SNP_A-2070041	C	C	408	6	416	0	6.073	0.0137	rs219962	6	12278816	p24.1
SNP_A-2229953	G	G	245	139	265	109	4.282	0.0385	rs4711607	6	12325772	p24.1
SNP_A-2107622	A	A	321	3	318	14	7.035	8.00E-03	rs2504889	6	12664926	p24.1
SNP_A-2203623	A	A	349	41	327	59	3.935	4.73E-02	rs6928588	6	12712003	p24.1
SNP_A-2309710	C	C	407	9	394	24	7.024	8.00E-03	rs16873173	6	12752926	p24.1
SNP_A-2100855	C	C	263	85	231	105	3.969	4.63E-02	rs2516252	6	12762525	p24.1
SNP_A-2048101	G	G	332	68	296	94	6.111	0.0134	rs539133	6	12845008	p24.1
SNP_A-2084657	G	G	378	22	364	40	5.47	1.93E-02	rs4711856	6	12980463	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1848836	A	A	388	18	382	34	4.849	2.77E-02	rs17617584	6	12990050	p24.1
SNP_A-1852327	A	A	398	0	406	4	3.902	0.0482	rs9463487	6	13275190	p24.1
SNP_A-1985138	A	A	272	110	301	87	4.106	4.27E-02	rs1150595	6	13310194	p24.1
SNP_A-2124295	A	A	256	114	304	92	5.588	1.81E-02	rs12193156	6	13311549	p24.1
SNP_A-2243237	A	A	350	48	385	27	7.307	6.90E-03	rs12194742	6	13342210	p24.1
SNP_A-2094717	C	C	361	53	385	33	5.404	0.0201	rs202064	6	13372005	p24.1
SNP_A-1872209	C	C	355	55	385	33	6.64	0.01	rs1223393	6	13373313	p24.1
SNP_A-2079287	A	A	357	51	386	34	4.359	3.68E-02	rs182148	6	13375526	p24.1
SNP_A-2218160	C	C	356	60	371	41	3.865	4.93E-02	rs202038	6	13396627	p24.1
SNP_A-1736197	C	C	340	60	369	39	5.562	0.0184	rs8541	6	13398217	p24.1
SNP_A-1948955	C	C	254	70	265	41	7.301	6.90E-03	rs500197	6	13503590	p23
SNP_A-2082062	C	C	292	104	270	134	4.563	0.0327	rs6924799	6	13881944	p23
SNP_A-1679224	C	T	202	168	204	176	5.14	2.34E-02	rs280171	6	14062611	p23
SNP_A-2145148	A	G	214	200	229	185	4.068	4.37E-02	rs2092204	6	14201535	p23
SNP_A-2147921	T	T	222	162	191	187	4.071	0.0436	rs10949243	6	14492535	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189449	G	G	354	60	330	84	4.842	2.78E-02	rs1267494	6	14824189	p23
SNP_A-1916680	C	C	336	16	314	28	3.874	4.90E-02	rs9396531	6	14850368	p23
SNP_A-2257626	C	C	360	30	338	48	4.827	2.80E-02	rs2500080	6	14879936	p23
SNP_A-2230160	T	T	396	0	367	5	5.357	0.0206	rs9476658	6	14898954	p23
SNP_A-2249821	G	G	391	21	380	38	5.012	0.0252	rs415133	6	14901440	p23
SNP_A-1820168	C	C	382	12	375	25	4.587	3.22E-02	rs2031298	6	14948029	p23
SNP_A-1673536	G	G	339	61	326	86	4.329	3.75E-02	rs4285324	6	15051825	p23
SNP_A-1871957	C	C	341	53	309	71	3.936	4.73E-02	rs4715938	6	15052836	p23
SNP_A-2011597	A	A	303	57	301	93	7.128	0.0076	rs432442	6	15087116	p23
SNP_A-1875418	C	C	293	113	261	145	5.817	1.59E-02	rs6459385	6	15105685	p23
SNP_A-2113088	C	-	225	163	195	195	4.998	2.54E-02	rs10949271	6	15139830	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238621	C	C	300	68	272	88	3.847	4.98E-02	rs2038288	6	15149922	p23
SNP_A-1911330	A	T	198	160	201	173	5.994	0.0144	rs11757092	6	15481631	p22.3
SNP_A-2280824	G	G	204	162	252	132	7.686	5.60E-03	rs2237156	6	15499187	p22.3
SNP_A-2011605	G	G	228	172	260	146	4.18	4.09E-02	rs2237152	6	15512229	p22.3
SNP_A-1892102	G	G	232	152	263	117	6.475	0.0109	rs4085876	6	15537710	p22.3
SNP_A-2034612	T	T	384	24	404	12	4.43	3.53E-02	rs2056943	6	15632542	p22.3
SNP_A-2251582	G	G	304	60	287	85	4.713	2.99E-02	rs9476904	6	15859309	p22.3
SNP_A-2257892	G	G	199	143	226	104	7.661	5.60E-03	rs373949	6	15925607	p22.3
SNP_A-2194884	G	G	316	66	275	85	4.587	3.22E-02	rs13216265	6	15925857	p22.3
SNP_A-1874729	T	T	384	28	368	44	3.896	4.84E-02	rs2072781	6	16255328	p22.3
SNP_A-2273817	G	G	397	17	378	42	11.016	9.00E-04	rs17641827	6	16265098	p22.3
SNP_A-2074502	G	G	326	10	285	29	11.276	8.00E-04	rs179944	6	16506117	p22.3
SNP_A-2297576	G	G	397	19	384	36	5.452	0.0195	rs3819403	6	16507820	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1985230	A	A	239	113	207	135	4.104	4.28E-02	rs6921608	6	16779315	p22.3
SNP_A-2258050	T	T	362	30	374	14	5.993	0.0144	rs16878738	6	16783170	p22.3
SNP_A-1673746	G	G	358	42	386	26	4.642	3.12E-02	rs10484365	6	16791651	p22.3
SNP_A-1704483	T	T	196	138	187	181	4.371	3.66E-02	rs1150625	6	16821287	p22.3
SNP_A-2088632	T	T	372	32	376	16	5.175	0.0229	rs16879766	6	17619606	p22.3
SNP_A-1894712	T	T	363	21	358	38	4.749	0.0293	rs4716185	6	17892943	p22.3
SNP_A-2188726	C	C	329	85	351	63	3.982	4.60E-02	rs16870039	6	18188344	p22.3
SNP_A-1949316	G	G	369	37	338	56	5.062	2.45E-02	rs17420046	6	18300532	p22.3
SNP_A-2232117	A	A	410	4	416	0	4.039	4.45E-02	rs6902280	6	18312324	p22.3
SNP_A-1950815	G	G	370	36	346	56	5.133	0.0235	---	6	18315241	p22.3
SNP_A-1681126	A	A	371	27	362	48	5.814	1.59E-02	rs2077780	6	18429050	p22.3
SNP_A-1664478	G	G	365	33	356	52	4.236	3.96E-02	rs728471	6	18429104	p22.3
SNP_A-1737301	C	C	358	34	338	58	6.815	9.00E-03	rs7757820	6	18443410	p22.3
SNP_A-2265241	G	G	230	96	220	134	5.357	0.0206	rs1324574	6	18553729	p22.3
SNP_A-2225281	G	G	386	10	381	29	9.049	2.60E-03	rs532347	6	18584639	p22.3
SNP_A-1985272	G	G	402	12	386	26	5.478	1.93E-02	rs536700	6	18594397	p22.3
SNP_A-1722196	T	T	385	11	381	25	5.341	2.08E-02	rs490618	6	18594466	p22.3
SNP_A-2248256	T	T	402	14	390	28	4.844	2.77E-02	rs16880897	6	18642403	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1985278	C	C	327	65	343	45	3.998	4.56E-02	rs1569531	6	18679504	p22.3
SNP_A-1985280	T	T	313	49	270	64	4.043	4.44E-02	rs9477786	6	18686417	p22.3
SNP_A-1758115	A	A	334	18	324	32	4.05	4.42E-02	rs10484371	6	18712183	p22.3
SNP_A-2076737	G	G	297	87	310	62	4.284	0.0385	rs9371087	6	18794949	p22.3
SNP_A-2265293	G	G	342	30	342	14	5.469	1.94E-02	rs16881504	6	19043693	p22.3
SNP_A-2111071	G	G	394	18	385	35	5.48	1.92E-02	rs17715484	6	19082288	p22.3
SNP_A-2280838	C	C	339	7	281	21	9.482	2.10E-03	rs1407497	6	19146275	p22.3
SNP_A-1985305	G	G	303	101	277	129	4.569	3.25E-02	rs16881760	6	19277697	p22.3
SNP_A-1985322	T	C	202	172	199	171	4.52	3.35E-02	rs9295444	6	19719354	p22.3
SNP_A-2028968	A	A	300	106	276	138	5.119	2.37E-02	rs2876555	6	19761978	p22.3
SNP_A-2132309	T	T	271	61	244	90	6.979	8.20E-03	rs9350178	6	19871632	p22.3
SNP_A-1702715	A	A	347	47	329	67	3.983	4.60E-02	rs10484638	6	20228939	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1654191	C	C	319	59	296	86	5.867	0.0154	rs4537124	6	20229621	p22.3
SNP_A-1985336	C	C	320	74	305	101	4.347	3.71E-02	rs949550	6	20232839	p22.3
SNP_A-1686904	G	G	356	44	339	71	6.633	0.01	rs2483766	6	20234635	p22.3
SNP_A-1940830	G	G	368	38	350	62	6.168	1.30E-02	rs16883398	6	20235575	p22.3
SNP_A-2207001	G	G	373	5	370	0	4.927	0.0264	rs16883859	6	20582597	p22.3
SNP_A-1859466	A	A	309	103	331	77	4.492	3.40E-02	rs6938091	6	20630269	p22.3
SNP_A-2041515	T	T	357	9	358	2	4.407	3.58E-02	rs16884319	6	21067986	p22.3
SNP_A-1985362	G	G	367	11	381	3	4.787	0.0287	rs11968036	6	21211436	p22.3
SNP_A-1985373	T	T	387	7	377	19	5.664	1.73E-02	rs16884819	6	21397196	p22.3
SNP_A-2193180	C	C	267	147	236	180	5.236	2.21E-02	rs12213632	6	22030687	p22.3
SNP_A-1940898	A	A	354	8	373	1	5.747	1.65E-02	rs9393229	6	22220623	p22.3
SNP_A-1698575	A	A	373	27	398	14	4.756	0.0292	rs10498708	6	22327631	p22.3
SNP_A-1780901	C	C	374	14	377	5	4.229	3.97E-02	rs9466319	6	22433607	p22.3
SNP_A-2157065	G	G	378	28	370	46	4.343	3.72E-02	rs16886284	6	22601677	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1949651	A	A	314	28	270	42	4.749	0.0293	rs7748467	6	22627328	p22.3
SNP_A-1883480	A	-	226	170	195	195	3.949	4.69E-02	rs2057017	6	22765593	p22.3
SNP_A-1929488	T	T	364	52	344	74	4.401	3.59E-02	rs4712717	6	22937411	p22.3
SNP_A-1835585	A	A	414	2	411	9	4.446	3.50E-02	rs6903116	6	23055173	p22.3
SNP_A-1985411	C	C	324	70	350	46	5.963	0.0146	rs7746463	6	23116094	p22.3
SNP_A-2230370	A	A	356	6	372	0	6.217	1.27E-02	rs9348550	6	23298103	p22.3
SNP_A-1985418	G	G	361	9	356	2	4.293	3.83E-02	rs1925458	6	23486930	p22.3
SNP_A-1935707	C	C	216	194	266	146	11.958	5.00E-04	rs521036	6	23724640	p22.3
SNP_A-1721451	A	A	209	179	248	154	4.959	2.60E-02	rs542063	6	23754854	p22.3
SNP_A-2115506	A	A	395	13	397	3	6.176	0.0129	rs9466963	6	23995567	p22.3
SNP_A-1716787	T	T	275	121	252	150	4.062	4.39E-02	rs4327688	6	23998856	p22.3
SNP_A-2223511	G	G	352	24	296	44	8.934	0.0028	rs16888718	6	24254433	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1822515	A	A	299	113	261	151	8.048	4.60E-03	rs7775073	6	24607530	p22.2
SNP_A-2187877	C	C	230	102	195	131	6.438	0.0112	rs2760117	6	24612168	p22.2
SNP_A-1826493	A	A	350	52	367	31	5.696	1.70E-02	rs2744594	6	24635812	p22.2
SNP_A-1879192	T	T	368	38	394	20	6.396	0.0114	rs2744597	6	24641053	p22.2
SNP_A-2267404	G	G	293	45	275	69	5.571	0.0183	rs2744601	6	24641484	p22.2
SNP_A-1915017	C	C	235	115	196	138	5.249	2.20E-02	rs1091031	6	24647118	p22.2
SNP_A-1843088	G	G	388	4	388	12	3.92	4.77E-02	rs4472344	6	24709219	p22.2
SNP_A-2187613	T	T	275	133	300	106	4.132	4.21E-02	rs2143337	6	24797980	p22.2
SNP_A-1835750	C	C	264	118	288	86	5.979	1.45E-02	rs3822901	6	24799006	p22.2
SNP_A-2011650	T	T	212	152	230	120	4.225	3.98E-02	rs6456630	6	24801054	p22.2
SNP_A-2032911	A	G	198	174	192	154	5.451	1.96E-02	rs9366585	6	24949299	p22.2
SNP_A-1985479	G	G	324	4	348	14	4.749	0.0293	rs618393	6	25062214	p22.2
SNP_A-1876611	T	T	412	4	405	15	6.409	0.0114	rs384411	6	25065082	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2250768	C	C	412	4	406	14	5.581	1.82E-02	rs379206	6	25069230	p22.2
SNP_A-2250582	C	A	194	148	187	153	9.379	2.20E-03	rs2690106	6	25365559	p22.2
SNP_A-1707880	T	T	242	142	221	185	5.999	0.0143	rs1983579	6	25445614	p22.2
SNP_A-1609754	C	C	290	50	261	77	7.261	7.00E-03	rs2328853	6	25456168	p22.2
SNP_A-1903670	G	G	399	15	379	35	8.514	3.50E-03	rs7752195	6	25527073	p22.2
SNP_A-2087785	G	G	383	25	366	44	5.613	0.0178	rs4712969	6	25872171	p22.2
SNP_A-1661151	G	G	345	55	378	34	6.285	1.22E-02	rs3887266	6	25951725	p22.2
SNP_A-1985518	C	C	395	15	404	6	3.959	4.66E-02	rs579996	6	25979023	p22.2
SNP_A-1985524	G	G	341	55	367	37	4.397	3.60E-02	rs10484434	6	26139592	p22.2
SNP_A-2058146	A	A	308	36	293	61	6.676	9.80E-03	rs9379851	6	26462759	p22.1
SNP_A-1895062	G	G	376	38	349	57	4.728	2.97E-02	rs9358932	6	26470684	p22.1
SNP_A-2092012	C	C	252	126	223	177	9.74	0.0018	rs3734536	6	26473325	p22.1
SNP_A-2215001	C	C	374	36	351	55	4.677	3.06E-02	rs9358937	6	26482253	p22.1
SNP_A-2105565	A	A	352	54	340	78	4.398	3.60E-02	rs4712986	6	26504182	p22.1
SNP_A-1985528	A	C	207	201	251	161	11.262	8.00E-04	rs742090	6	26523616	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1790429	G	G	345	69	321	93	4.42	3.55E-02	rs4712993	6	26524378	p22.1
SNP_A-2253180	C	C	333	55	312	78	4.656	0.0309	rs10946824	6	26524633	p22.1
SNP_A-2046272	G	G	289	35	258	54	5.589	1.81E-02	rs12201546	6	26536293	p22.1
SNP_A-1715909	A	A	336	64	319	91	5.022	2.50E-02	rs3846849	6	26557415	p22.1
SNP_A-1985530	A	A	317	59	282	110	17.11	3.53E-05	rs9295690	6	26564048	p22.1
SNP_A-2281320	T	T	345	59	318	80	4.228	3.98E-02	rs9358945	6	26580093	p22.1
SNP_A-1985533	G	G	377	33	356	54	5.671	1.73E-02	rs2893857	6	26582040	p22.1
SNP_A-1906590	G	G	377	39	356	62	5.834	1.57E-02	rs4713001	6	26595289	p22.1
SNP_A-2217720	T	T	180	172	223	125	12.003	5.00E-04	rs9467779	6	26644666	p22.1
SNP_A-1814746	C	C	192	184	250	148	10.898	0.001	rs9467783	6	26650873	p22.1
SNP_A-2267664	G	G	218	168	262	130	8.833	3.00E-03	rs1884947	6	26661252	p22.1
SNP_A-1843049	G	G	187	179	228	130	11.734	6.00E-04	rs6922824	6	26661794	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1658660	T	T	177	175	246	154	9.571	0.002	rs10484442	6	26663858	p22.1
SNP_A-1781673	G	G	199	187	245	135	13.117	3.00E-04	rs9467791	6	26670465	p22.1
SNP_A-2021293	C	C	184	174	235	125	14.232	2.00E-04	rs6924838	6	26679735	p22.1
SNP_A-2204670	T	T	370	36	360	56	4.364	3.67E-02	rs4634439	6	26705983	p22.1
SNP_A-1881021	A	A	337	75	308	98	4.318	3.77E-02	rs3800307	6	27293771	p22.1
SNP_A-1817270	C	C	364	50	381	33	3.87	4.92E-02	rs6917419	6	27351459	p22.1
SNP_A-1985538	G	G	288	54	253	71	4.093	4.31E-02	rs7746199	6	27369303	p22.1
SNP_A-2188850	C	C	269	95	289	51	13.174	3.00E-04	rs9368502	6	27408820	p22.1
SNP_A-2309504	G	G	275	91	305	59	8.373	0.0038	rs9348760	6	27410699	p22.1
SNP_A-2057298	C	C	225	95	238	70	3.925	4.76E-02	rs9461366	6	27418512	p22.1
SNP_A-1985540	G	G	282	36	299	15	9.12	2.50E-03	rs1028311	6	27640929	p22.1
SNP_A-2102296	G	G	381	29	396	16	4.04	4.44E-02	rs16867983	6	27840219	p22.1
SNP_A-2263504	C	C	335	35	310	54	4.976	2.57E-02	rs200991	6	27923473	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787205	A	A	328	12	350	0	12.572	4.00E-04	rs200955	6	27947291	p22.1
SNP_A-2133870	T	T	393	7	384	18	4.939	0.0263	rs16893533	6	28041688	p22.1
SNP_A-2275446	C	C	401	7	382	16	3.859	4.95E-02	rs16893540	6	28066090	p22.1
SNP_A-1941289	A	A	395	5	398	0	5.006	0.0253	rs1233709	6	28281264	p22.1
SNP_A-2201299	C	C	378	38	354	62	6.547	1.05E-02	rs17720293	6	28322677	p22.1
SNP_A-2207283	C	C	396	22	412	10	4.798	2.85E-02	rs6906897	6	29523615	p22.1
SNP_A-1834270	C	C	339	73	317	99	4.649	3.11E-02	rs3129063	6	29753592	p22.1
SNP_A-1952037	T	T	304	66	269	87	4.752	0.0293	rs3117295	6	29761356	p22.1
SNP_A-1721658	A	A	339	53	369	35	4.773	2.89E-02	rs9258170	6	29797547	p22.1
SNP_A-2205105	T	T	333	43	358	26	5.009	0.0252	rs2072898	6	29800708	p22.1
SNP_A-2105603	A	A	330	50	380	30	7.393	6.50E-03	rs7753946	6	29808503	p22.1
SNP_A-1819018	A	A	341	51	359	33	4.32	3.77E-02	rs9258205	6	29811802	p22.1
SNP_A-1807008	T	T	310	48	309	23	7.836	5.10E-03	rs9258215	6	29815286	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2312287	C	C	317	37	308	60	5.314	0.0212	rs1610613	6	29818942	p22.1
SNP_A-1796187	C	T	202	164	191	165	5.646	1.75E-02	rs1633085	6	29823976	p22.1
SNP_A-2092698	G	G	309	59	302	94	7.07	7.80E-03	rs1633063	6	29834025	p22.1
SNP_A-1819319	G	G	377	23	396	12	3.845	0.0499	rs16895757	6	29870157	p22.1
SNP_A-2222525	G	G	390	4	394	12	3.841	5.00E-02	rs2894117	6	29876780	p22.1
SNP_A-2122691	A	A	385	33	401	19	4.09	4.31E-02	rs4084097	6	29919729	p22.1
SNP_A-2025602	C	C	298	24	335	13	4.431	3.53E-02	rs2734973	6	29941927	p22.1
SNP_A-2302210	G	G	347	55	378	38	4.195	4.06E-02	rs2253523	6	29984938	p22.1
SNP_A-2169882	C	C	364	46	384	28	4.908	2.67E-02	rs2571410	6	29989443	p22.1
SNP_A-2294141	C	C	315	27	319	45	3.843	0.0499	rs9259842	6	30003952	p21.33
SNP_A-2272067	A	A	361	23	386	10	5.775	1.63E-02	rs4087726	6	30006876	p21.33
SNP_A-1789797	C	C	339	39	339	61	4.221	3.99E-02	rs1655900	6	30024597	p21.33
SNP_A-2082218	T	T	277	99	208	130	12.025	5.00E-04	rs2517672	6	30045241	p21.33
SNP_A-2306363	T	T	274	68	323	49	5.857	0.0155	rs2523969	6	30046756	p21.33
SNP_A-1929198	C	C	348	42	356	24	4.871	2.73E-02	rs423808	6	30057102	p21.33
SNP_A-2247868	A	A	352	60	376	42	3.925	4.76E-02	rs9261013	6	30072927	p21.33
SNP_A-2186346	A	A	338	20	366	10	4.008	0.0453	rs6922640	6	30074948	p21.33
SNP_A-1805077	C	C	385	5	390	0	5.032	2.49E-02	rs6924054	6	30075597	p21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1780726	A	A	351	57	367	35	5.573	1.82E-02	rs6931776	6	30094406	p21.33
SNP_A-1985586	A	A	319	99	289	131	5.928	0.0149	rs259940	6	30119913	p21.33
SNP_A-2201632	C	C	364	44	388	28	4.244	3.94E-02	rs7770092	6	30136850	p21.33
SNP_A-1908239	A	A	345	45	341	25	4.981	2.56E-02	rs9261282	6	30143436	p21.33
SNP_A-1904181	C	C	356	62	374	42	4.285	3.84E-02	rs20744482	6	30144450	p21.33
SNP_A-1849682	G	G	348	34	329	59	7.207	7.30E-03	rs2844792	6	30188935	p21.33
SNP_A-2011678	T	T	337	33	327	55	5.461	0.0195	rs3132625	6	30455699	p21.33
SNP_A-2126163	G	G	350	62	378	42	4.847	2.77E-02	rs9261799	6	30484466	p21.33
SNP_A-2106299	C	C	341	33	369	17	6.036	0.014	rs9261863	6	30492801	p21.33
SNP_A-2204668	A	A	343	61	363	41	4.488	3.41E-02	rs1548515	6	30495382	p21.33
SNP_A-2306779	T	T	316	62	336	42	4.46	3.47E-02	rs1548513	6	30495666	p21.33
SNP_A-2160421	C	C	346	62	369	35	8.236	4.10E-03	rs9261926	6	30500385	p21.33
SNP_A-2252536	C	C	323	57	363	37	6.079	0.0137	rs9295878	6	30525128	p21.33
SNP_A-2117095	C	C	332	28	364	16	4.207	4.03E-02	rs9295888	6	30530460	p21.33
SNP_A-2270968	T	T	263	53	268	84	5.136	2.34E-02	rs3094127	6	30805426	p21.33
SNP_A-1834011	G	G	272	58	228	82	7.368	0.0066	rs16897888	6	30848494	p21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2260001	T	T	397	5	418	0	5.231	2.22E-02	rs6930444	6	30871611	p21.33
SNP_A-2267163	A	A	337	53	323	79	5.238	2.21E-02	rs12195469	6	30897587	p21.33
SNP_A-2090405	C	C	322	22	350	10	5.306	2.13E-02	rs2844678	6	31058029	p21.33
SNP_A-1810600	C	C	360	58	383	39	4.415	0.0356	rs2844673	6	31069905	p21.33
SNP_A-1811070	T	T	354	52	372	32	5.203	2.25E-02	rs2252926	6	31074283	p21.33
SNP_A-2131300	C	C	340	40	361	19	8.104	4.40E-03	rs2530690	6	31075181	p21.33
SNP_A-1985604	G	G	306	32	306	14	6.556	1.05E-02	rs2508016	6	31077506	p21.33
SNP_A-1790821	C	C	313	41	345	27	3.995	4.56E-02	rs2256514	6	31080450	p21.33
SNP_A-2213548	A	A	324	46	361	27	6.52	1.07E-02	rs2523915	6	31081337	p21.33
SNP_A-1887257	C	C	366	16	366	30	4.01	4.52E-02	rs3873352	6	31130092	p21.33
SNP_A-2097929	C	C	290	56	288	88	5.882	1.53E-02	rs1966	6	31215712	p21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2200407	C	C	325	93	297	123	5.422	1.99E-02	rs6899874	6	31270307	p21.33
SNP_A-2115227	G	G	292	34	310	20	4.144	4.18E-02	rs1793895	6	31300171	p21.33
SNP_A-2140943	C	C	310	32	320	56	5.106	2.38E-02	rs3130532	6	31316432	p21.33
SNP_A-2242624	G	G	351	33	318	52	5.617	0.0178	rs7382297	6	31355046	p21.33
SNP_A-2234603	A	A	288	120	261	155	5.705	1.69E-02	rs16899205	6	31374340	p21.33
SNP_A-1857537	A	A	292	114	263	141	4.369	3.66E-02	rs16899207	6	31374366	p21.33
SNP_A-1944921	C	C	368	36	379	19	5.372	2.05E-02	rs396038	6	31380959	p21.33
SNP_A-2248558	C	C	314	42	316	68	5.1	2.39E-02	rs2077102	6	31719819	p21.33
SNP_A-2188055	G	G	371	43	391	27	4.163	4.13E-02	rs9267673	6	31991658	p21.33
SNP_A-2225939	C	C	306	106	281	137	4.976	2.57E-02	rs644045	6	31991936	p21.33
SNP_A-1869974	G	G	413	3	409	11	4.572	3.25E-02	rs8192590	6	32295761	p21.32
SNP_A-2182330	A	A	349	3	356	12	5.116	2.37E-02	rs9268208	6	32388569	p21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1655875	G	G	280	122	259	155	4.574	3.25E-02	rs2073045	6	32410777	p21.32
SNP_A-1684424	A	A	332	42	319	75	9.053	2.60E-03	rs2050189	6	32410876	p21.32
SNP_A-1701785	T	T	348	54	335	79	4.771	2.89E-02	rs2213580	6	32459755	p21.32
SNP_A-2261465	G	G	353	11	335	1	7.697	5.50E-03	rs17423753	6	32468319	p21.32
SNP_A-1815451	C	C	344	44	326	66	4.863	2.74E-02	rs3129953	6	32469799	p21.32
SNP_A-1650978	T	T	343	55	329	83	5.733	0.0167	rs1041885	6	32483998	p21.32
SNP_A-1985623	G	G	328	36	297	57	6.141	0.0132	rs2001099	6	32491611	p21.32
SNP_A-1826835	G	G	337	49	297	67	4.675	3.06E-02	rs3135378	6	32493077	p21.32
SNP_A-1985626	C	C	315	21	299	35	3.911	4.80E-02	rs2395167	6	32496286	p21.32
SNP_A-1860550	T	T	241	77	215	119	10.096	0.0015	rs3129847	6	32504484	p21.32
SNP_A-2075637	C	C	300	82	263	115	7.939	4.80E-03	rs3135342	6	32504593	p21.32
SNP_A-1888575	G	G	308	104	268	142	8.643	0.0033	rs3135339	6	32507239	p21.32
SNP_A-2238286	G	G	209	183	245	149	6.332	1.19E-02	rs9268645	6	32516505	p21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2220563	C	C	310	104	272	142	8.351	3.90E-03	rs3129877	6	32516575	p21.32
SNP_A-2073634	A	A	359	57	339	79	4.127	4.22E-02	rs3135393	6	32516820	p21.32
SNP_A-2112717	C	C	273	145	234	178	6.328	1.19E-02	rs3135392	6	32517220	p21.32
SNP_A-2261840	C	C	322	76	300	104	5.089	0.0241	rs9268856	6	32537697	p21.32
SNP_A-1944573	G	G	331	83	301	113	6.016	1.42E-02	rs7746922	6	32538953	p21.32
SNP_A-2072098	A	A	252	68	220	96	6.925	8.50E-03	rs7747521	6	32539083	p21.32
SNP_A-1758454	C	C	281	111	315	87	4.723	0.0298	rs719654	6	32799110	p21.32
SNP_A-1933954	A	A	354	44	376	22	7.996	4.70E-03	rs2239800	6	32821245	p21.32
SNP_A-1935018	C	C	217	107	258	78	7.869	5.00E-03	rs2071474	6	32890560	p21.32
SNP_A-2059814	G	G	236	124	255	89	6.126	1.33E-02	rs241427	6	32912392	p21.32
SNP_A-2229836	T	T	220	192	259	155	7.116	0.0076	rs3101942	6	32978035	p21.32
SNP_A-2050102	C	C	396	14	414	4	5.879	1.53E-02	rs3129302	6	33082321	p21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1727489	T	T	249	137	230	180	5.868	0.0154	rs2395360	6	33149423	p21.32
SNP_A-1985655	C	C	388	18	410	6	6.486	0.0109	rs7763822	6	33168406	p21.32
SNP_A-1850392	G	G	393	13	414	2	8.493	3.60E-03	rs7764491	6	33168818	p21.32
SNP_A-2205583	G	G	288	58	335	39	6.188	0.0129	rs9277637	6	33190613	p21.32
SNP_A-2154723	C	C	190	152	232	122	7.26	7.10E-03	rs3117039	6	33193829	p21.32
SNP_A-2150633	G	A	206	188	234	176	7.055	7.90E-03	rs3130233	6	33203154	p21.32
SNP_A-1904499	A	A	271	91	299	63	6.466	1.10E-02	rs3116996	6	33205942	p21.32
SNP_A-2293289	G	G	295	37	258	54	5.035	2.48E-02	rs2855459	6	33262634	p21.32
SNP_A-1715481	G	G	323	19	342	38	4.89	0.027	rs466886	6	33287587	p21.32
SNP_A-1828873	G	G	263	139	302	112	5.421	1.99E-02	rs211455	6	33436496	p21.32
SNP_A-1985660	T	T	241	169	277	143	4.549	3.29E-02	rs211453	6	33438109	p21.32
SNP_A-2039436	A	A	286	102	254	126	4.34	3.72E-02	rs7747216	6	33584696	p21.32
SNP_A-1783972	C	C	373	23	397	7	9.202	2.40E-03	rs435945	6	33604610	p21.31
SNP_A-2038264	A	G	194	180	229	181	4.678	3.06E-02	rs4711336	6	33767024	p21.31
SNP_A-1870092	-	A	206	206	238	180	4.014	4.51E-02	rs9394163	6	33790392	p21.31
SNP_A-2134101	C	T	208	204	230	178	3.87	4.92E-02	rs4713670	6	33807860	p21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116755	G	G	200	186	219	151	4.16	4.14E-02	rs9394169	6	33886942	p21.31
SNP_A-2251657	A	A	389	17	372	6	4.647	3.11E-02	rs13196449	6	34191542	p21.31
SNP_A-2110325	C	C	410	8	396	20	5.381	2.04E-02	rs17703197	6	34950928	p21.31
SNP_A-2137293	A	A	329	69	348	44	6.019	1.42E-02	rs9296139	6	34981980	p21.31
SNP_A-1905315	G	G	340	64	361	45	3.936	4.73E-02	rs16871809	6	35198367	p21.31
SNP_A-2051928	A	A	265	31	332	20	5.09	0.0241	rs6457816	6	35470826	p21.31
SNP_A-1843731	G	G	404	4	414	0	4.079	4.34E-02	rs9658136	6	35487324	p21.31
SNP_A-1873190	C	C	399	7	411	1	4.634	3.13E-02	rs9296154	6	35495356	p21.31
SNP_A-2225530	A	A	373	7	341	1	3.945	0.047	rs16879378	6	35705681	p21.31
SNP_A-1892335	T	T	297	91	267	129	8.079	4.50E-03	rs9462104	6	35782823	p21.31
SNP_A-2280831	C	C	273	91	256	118	3.9	4.83E-02	rs9470162	6	35971864	p21.31
SNP_A-2123085	G	G	268	100	253	131	4.254	3.92E-02	rs236445	6	36831550	p21.2
SNP_A-2281443	C	C	304	62	282	94	7.257	7.10E-03	rs9380597	6	36837545	p21.2
SNP_A-1783843	C	C	355	27	324	48	7.164	7.40E-03	rs236430	6	36839704	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044556	T	-	228	168	203	203	4.628	0.0315	rs9380605	6	36902043	p21.2
SNP_A-1802711	G	A	178	170	205	155	4.653	0.031	rs7743783	6	37066971	p21.2
SNP_A-2216947	G	G	211	181	234	144	5.148	2.33E-02	rs7739340	6	37075595	p21.2
SNP_A-2178377	T	T	235	167	255	135	4.026	0.0448	rs831512	6	37083011	p21.2
SNP_A-1948987	A	A	189	179	206	140	4.826	2.80E-02	rs9394410	6	37206357	p21.2
SNP_A-1985703	C	C	337	21	346	46	7.922	4.90E-03	rs10498738	6	37604945	p21.2
SNP_A-2103937	C	C	304	54	279	83	7.189	7.30E-03	rs804846	6	37655240	p21.2
SNP_A-1691682	G	G	356	46	389	25	7.498	6.20E-03	rs9296240	6	38257374	p21.2
SNP_A-1655589	G	G	354	46	389	25	7.621	5.80E-03	rs9296241	6	38257430	p21.2
SNP_A-1673492	G	G	356	46	387	25	7.383	0.0066	rs9296242	6	38257567	p21.2
SNP_A-1985712	A	A	364	34	382	16	6.914	0.0086	rs16890428	6	38265120	p21.2
SNP_A-2172353	A	A	326	20	350	6	8.25	4.10E-03	rs9349063	6	38322495	p21.2
SNP_A-2138764	A	A	332	4	378	0	4.525	3.34E-02	rs4711531	6	38358758	p21.2
SNP_A-2222249	A	A	281	45	279	27	3.878	4.89E-02	rs4711549	6	38582641	p21.2
SNP_A-1849285	T	T	309	13	315	1	10.288	1.30E-03	rs9296255	6	38724245	p21.2
SNP_A-1707221	G	G	254	148	225	189	6.569	0.0104	rs874808	6	38820148	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1748223	G	G	299	103	278	136	5.145	2.33E-02	rs726108	6	38821276	p21.2
SNP_A-2091697	T	T	237	147	271	115	6.179	0.0129	rs1738247	6	38863631	p21.2
SNP_A-1676472	G	G	247	137	220	180	7.07	7.80E-03	rs4380739	6	38892169	p21.2
SNP_A-1854122	A	A	253	151	226	180	4.058	4.40E-02	rs1678717	6	38901381	p21.2
SNP_A-2132354	T	C	198	146	175	159	6.734	9.50E-03	rs9380791	6	38938388	p21.2
SNP_A-2107091	G	G	259	157	232	186	3.932	4.74E-02	rs9394550	6	38960939	p21.2
SNP_A-1685624	C	C	357	45	348	66	3.912	4.79E-02	rs1332014	6	38995949	p21.2
SNP_A-1750425	G	G	339	59	377	37	6.746	9.40E-03	rs10484849	6	39026363	p21.2
SNP_A-2092051	G	G	332	62	357	39	6.14	0.0132	rs10947766	6	39029032	p21.2
SNP_A-2102996	A	A	331	67	346	42	5.94	1.48E-02	rs10947767	6	39029218	p21.2
SNP_A-1869759	C	C	342	70	369	51	3.932	4.74E-02	rs16891340	6	39029340	p21.2
SNP_A-2269319	A	A	348	28	325	47	5.578	1.82E-02	rs9380817	6	39069726	p21.2
SNP_A-2098434	T	T	301	37	333	23	4.418	0.0356	rs12192920	6	39085444	p21.2
SNP_A-1985729	C	C	335	61	356	36	7.061	7.90E-03	rs10484851	6	39086749	p21.2
SNP_A-1783561	G	G	371	45	350	70	6.027	0.0141	rs7766930	6	39094142	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2179931	T	C	198	178	204	168	4.207	0.0402	rs2815022	6	39347243	p21.2
SNP_A-1802524	T	T	387	15	392	6	3.869	4.92E-02	rs1571362	6	39484930	p21.2
SNP_A-2112883	G	G	365	49	394	26	8.119	4.40E-03	rs10947809	6	39493160	p21.2
SNP_A-1985738	G	G	390	26	410	10	7.592	5.90E-03	rs9296299	6	39550553	p21.2
SNP_A-1930307	T	T	379	21	408	8	6.585	0.0103	rs9367008	6	39558379	p21.2
SNP_A-1809960	A	A	297	63	331	37	8.514	3.50E-03	rs9296300	6	39566128	p21.2
SNP_A-1799754	A	A	387	19	400	8	4.691	3.03E-02	rs9394609	6	39622990	p21.2
SNP_A-2190744	A	A	332	18	350	6	6.425	1.13E-02	rs4711620	6	40360422	p21.2
SNP_A-2138812	T	T	380	0	383	5	4.929	0.0264	rs12207208	6	40409357	p21.2
SNP_A-1870085	G	G	213	179	247	153	4.469	3.45E-02	rs13196792	6	40500347	p21.2
SNP_A-2210914	T	T	244	100	270	78	4.011	4.52E-02	rs7776304	6	40787717	p21.1
SNP_A-1816134	C	C	335	15	357	3	8.56	3.40E-03	rs4714372	6	40818454	p21.1
SNP_A-2307261	G	G	349	15	354	6	3.871	4.91E-02	rs9381009	6	41026079	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138646	C	C	277	103	255	131	4.213	4.01E-02	rs12208451	6	41057844	p21.1
SNP_A-2048864	A	A	265	151	295	125	4.037	4.45E-02	rs9394756	6	41124161	p21.1
SNP_A-1985795	G	G	244	118	265	85	6.03	0.0141	rs2268196	6	41129928	p21.1
SNP_A-1985797	G	G	249	129	278	104	4.257	3.91E-02	rs2294696	6	41144966	p21.1
SNP_A-2247089	A	A	389	25	409	11	5.903	1.51E-02	rs7748513	6	41235950	p21.1
SNP_A-2217566	G	G	390	22	411	9	5.926	0.0149	rs9471490	6	41261015	p21.1
SNP_A-1796201	G	G	328	18	374	8	5.093	0.024	rs9462675	6	41261216	p21.1
SNP_A-2025116	G	G	381	19	408	8	5.094	0.024	rs9471491	6	41261600	p21.1
SNP_A-2277639	G	G	307	65	283	87	4.155	4.15E-02	rs12212557	6	41533388	p21.1
SNP_A-2270063	G	G	387	23	377	39	4.217	4.00E-02	rs2493835	6	42146699	p21.1
SNP_A-1789027	C	C	281	35	266	60	6.836	8.90E-03	rs10456507	6	42192124	p21.1
SNP_A-1652702	G	G	337	65	374	36	10.174	0.0014	rs489743	6	42359855	p21.1
SNP_A-1692174	G	G	338	56	365	29	9.613	0.0019	rs260225	6	42366162	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2029481	A	A	336	68	358	40	7.912	4.90E-03	rs654043	6	42413032	p21.1
SNP_A-2245052	G	G	403	5	418	0	5.154	2.32E-02	rs260275	6	42417051	p21.1
SNP_A-2072803	A	A	351	61	381	39	5.993	0.0144	rs550668	6	42417123	p21.1
SNP_A-2112281	C	C	413	5	422	0	5.078	2.42E-02	rs260276	6	42417178	p21.1
SNP_A-1985819	A	A	403	5	420	0	5.178	0.0229	rs533706	6	42420353	p21.1
SNP_A-2247765	G	G	355	41	389	15	13.547	2.00E-04	rs94776	6	42450893	p21.1
SNP_A-1843223	A	A	290	92	309	65	5.162	2.31E-02	rs12190755	6	43430209	p21.1
SNP_A-2011747	T	T	235	157	211	187	3.862	4.94E-02	rs6905288	6	43866851	p21.1
SNP_A-1823971	A	A	290	118	253	151	6.55	1.05E-02	rs4714737	6	44146800	p21.1
SNP_A-1722400	G	G	327	73	313	99	4.06	4.39E-02	rs950230	6	44360277	p21.1
SNP_A-1919346	A	A	386	28	405	13	5.925	0.0149	rs6909090	6	44553968	p21.1
SNP_A-2298495	C	C	236	136	283	91	13.172	3.00E-04	rs9381333	6	44584274	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1930973	C	C	394	14	368	28	5.376	2.04E-02	rs13196428	6	44633176	p21.1
SNP_A-1822347	A	A	414	4	420	0	4.038	4.45E-02	rs6912544	6	44637801	p21.1
SNP_A-2065095	C	C	395	21	408	10	4.109	4.27E-02	rs2153164	6	44714285	p21.1
SNP_A-1791239	G	G	356	4	325	11	3.855	4.96E-02	rs16873428	6	45540434	p21.1
SNP_A-2242121	A	A	306	76	294	104	4.269	3.88E-02	rs3763191	6	45645653	p21.1
SNP_A-1985869	G	G	362	52	342	76	5.049	0.0246	rs6924440	6	45692846	p21.1
SNP_A-1827650	C	C	366	50	335	79	7.886	5.00E-03	rs16873751	6	45820228	p21.1
SNP_A-2299376	C	C	363	21	377	9	5.06	2.45E-02	rs9395123	6	45887710	p21.1
SNP_A-1939292	A	A	373	43	395	23	6.686	9.70E-03	rs3777582	6	46022006	p21.1
SNP_A-1881885	G	G	312	52	337	31	6.255	0.0124	rs1204334	6	46034940	p21.1
SNP_A-1985884	T	T	205	171	263	131	12.072	5.00E-04	rs1204339	6	46138499	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1985890	G	G	318	76	341	55	4.164	4.13E-02	rs3823240	6	46298256	p21.1
SNP_A-1985892	G	G	318	82	349	61	4.402	3.59E-02	rs2799353	6	46300260	p12.3
SNP_A-1985894	C	C	303	37	321	19	6.305	0.012	rs4711844	6	46342065	p12.3
SNP_A-1709523	G	G	370	32	396	18	4.627	0.0315	rs10498772	6	47091851	p12.3
SNP_A-1915729	C	C	250	106	244	158	7.552	6.00E-03	rs9473045	6	47339700	p12.3
SNP_A-2237070	G	G	392	2	394	10	5.214	0.0224	rs7766125	6	47515275	p12.3
SNP_A-1755638	T	T	266	130	295	105	4.139	0.0419	rs2022335	6	47910482	p12.3
SNP_A-2286950	A	A	260	136	276	104	4.416	0.0356	rs474725	6	47915971	p12.3
SNP_A-1685958	C	C	236	166	272	142	4.246	3.93E-02	rs1536818	6	47925874	p12.3
SNP_A-1662860	C	C	236	166	272	142	4.246	3.93E-02	rs1576277	6	47926190	p12.3
SNP_A-2232320	T	T	235	147	275	115	6.963	8.30E-03	rs514974	6	47933304	p12.3
SNP_A-1806607	C	C	261	155	292	128	4.295	3.82E-02	rs1328974	6	47941446	p12.3
SNP_A-2076274	A	G	192	176	190	150	4.593	3.21E-02	rs988817	6	48254116	p12.3
SNP_A-1865548	G	G	383	1	328	6	4.365	3.67E-02	rs325037	6	48435389	p12.3
SNP_A-1898323	C	C	398	0	373	5	5.299	2.13E-02	rs325040	6	48437069	p12.3
SNP_A-1723038	A	A	221	151	199	197	6.489	0.0109	rs1013401	6	48441770	p12.3
SNP_A-2047370	A	A	224	122	187	147	5.444	1.96E-02	rs9473384	6	48549731	p12.3
SNP_A-1884878	T	C	192	184	198	152	4.239	0.0395	rs4715080	6	48566680	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1928551	T	T	367	35	375	17	6.192	1.28E-02	rs2894754	6	48600721	p12.3
SNP_A-1832976	A	A	199	173	225	133	6.557	0.0104	rs9463425	6	48620994	p12.3
SNP_A-1828646	T	T	385	25	373	41	4.049	4.42E-02	rs2996252	6	48706158	p12.3
SNP_A-1985970	T	T	364	22	362	40	4.908	2.67E-02	rs243125	6	48739467	p12.3
SNP_A-2215590	C	C	366	14	372	4	5.583	1.81E-02	rs16877973	6	48777430	p12.3
SNP_A-2146133	C	C	319	69	332	44	5.603	1.79E-02	rs6934867	6	49707421	p12.3
SNP_A-1706109	G	G	287	37	311	21	5.28	2.16E-02	rs360555	6	49711740	p12.3
SNP_A-1823645	G	G	302	96	317	65	6.007	0.0143	rs9369911	6	49745740	p12.3
SNP_A-1696388	A	A	342	58	373	39	4.889	0.027	rs10498781	6	50116000	p12.3
SNP_A-2064705	C	C	376	16	396	6	4.938	0.0263	rs9395549	6	50172318	p12.3
SNP_A-2086151	G	G	227	117	257	81	8.353	3.90E-03	rs280346	6	50634248	p12.3
SNP_A-1851344	C	C	301	45	326	30	3.855	4.96E-02	rs280322	6	50741340	p12.3
SNP_A-2282701	G	G	269	129	245	157	3.842	5.00E-02	rs2505262	6	51211514	p12.3
SNP_A-1753899	C	C	316	16	369	5	7.39	0.0066	rs1327261	6	51222078	p12.3
SNP_A-2161055	T	T	241	101	218	126	3.9	4.83E-02	rs2505271	6	51225741	p12.3
SNP_A-1986018	A	A	401	15	413	5	5.172	0.023	rs17813135	6	51283334	p12.3
SNP_A-2287869	C	C	359	7	381	1	4.814	2.82E-02	rs4385301	6	51472414	p12.2
SNP_A-1689622	C	C	262	136	235	163	3.905	4.81E-02	rs6921799	6	51839473	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2274875	T	T	265	135	220	160	5.785	1.62E-02	rs1321519	6	51877578	p12.2
SNP_A-1922698	G	G	274	142	243	175	5.289	2.15E-02	rs9370082	6	51903836	p12.2
SNP_A-2174218	G	G	280	126	254	156	4.438	3.51E-02	rs6907923	6	51910628	p12.2
SNP_A-2102541	C	C	336	68	365	43	6.811	9.10E-03	rs9382099	6	52328752	p12.2
SNP_A-2170962	T	T	355	11	387	3	5.195	2.27E-02	rs16882435	6	52353107	p12.2
SNP_A-2048969	G	G	349	25	335	49	7.94	4.80E-03	rs17591255	6	52374293	p12.2
SNP_A-1668943	G	G	319	83	296	114	5.66	1.74E-02	rs2038741	6	52380503	p12.2
SNP_A-2038711	A	A	285	35	307	19	5.503	0.019	rs1266794	6	52413841	p12.2
SNP_A-2149741	T	T	394	10	403	1	7.465	0.0063	rs16883058	6	52861117	p12.2
SNP_A-1986076	A	A	390	4	396	0	4.041	4.44E-02	rs9464004	6	53905622	p12.1
SNP_A-2235000	C	C	271	103	258	64	5.573	1.82E-02	rs4715447	6	54118640	p12.1
SNP_A-1986087	G	G	352	16	370	6	4.909	2.67E-02	rs10155669	6	54168722	p12.1
SNP_A-1734824	A	A	330	72	312	98	4.403	3.59E-02	rs1316576	6	54212153	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909222	A	A	341	15	345	5	4.973	0.0258	rs17755505	6	54352087	p12.1
SNP_A-1712261	T	T	396	0	400	4	3.94	4.71E-02	rs10484980	6	54498462	p12.1
SNP_A-1687486	G	G	355	47	387	27	6.61	0.0101	rs10484981	6	54501030	p12.1
SNP_A-1642655	G	G	354	48	385	29	5.814	1.59E-02	rs10484982	6	54507318	p12.1
SNP_A-1748497	G	G	354	48	385	29	5.814	1.59E-02	rs10484983	6	54507338	p12.1
SNP_A-1986099	A	A	279	67	253	91	4.91	2.67E-02	rs6559446	6	54509248	p12.1
SNP_A-1723116	A	A	359	43	386	26	5.045	0.0247	rs1507109	6	54569417	p12.1
SNP_A-2126472	A	A	329	35	366	20	5.42	1.99E-02	rs16885549	6	54570687	p12.1
SNP_A-1703399	A	A	359	41	385	25	4.665	3.08E-02	rs9296762	6	54608137	p12.1
SNP_A-1986102	C	C	321	71	298	100	5.727	0.0167	rs608873	6	54614797	p12.1
SNP_A-1717981	G	G	359	43	387	25	5.694	1.70E-02	rs10484991	6	54616860	p12.1
SNP_A-1664698	A	A	359	27	396	14	5.216	0.0224	rs10484994	6	54671307	p12.1
SNP_A-2157445	T	T	314	80	278	108	6.278	1.22E-02	rs16869519	6	54702138	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2085561	T	T	322	86	293	117	6.097	0.0135	rs1890239	6	54723794	p12.1
SNP_A-1986108	A	A	367	37	393	19	6.597	1.02E-02	rs17545325	6	54731760	p12.1
SNP_A-1794177	G	G	249	147	218	176	4.656	0.0309	rs6926482	6	54809644	p12.1
SNP_A-2298868	C	C	274	138	244	172	5.447	1.96E-02	rs7750012	6	54810602	p12.1
SNP_A-1959835	A	A	386	24	392	12	4.002	4.54E-02	rs6912059	6	55235885	p12.1
SNP_A-1742599	T	T	338	48	366	30	5.14	2.34E-02	rs10498805	6	55337772	p12.1
SNP_A-2119491	T	T	359	57	381	35	5.915	1.50E-02	rs4346852	6	55365500	p12.1
SNP_A-1676858	A	A	240	124	286	104	4.886	2.71E-02	rs4128949	6	55546544	p12.1
SNP_A-1907918	C	C	252	112	280	88	4.332	3.74E-02	rs6459097	6	55643310	p12.1
SNP_A-2073616	A	A	332	46	346	28	4.646	3.11E-02	rs2145900	6	55715214	p12.1
SNP_A-1872730	C	C	346	52	354	32	4.671	3.07E-02	rs228139	6	55736242	p12.1
SNP_A-1986123	T	C	172	166	201	153	4.081	4.34E-02	rs1447132	6	55854927	p12.1
SNP_A-2139217	C	C	399	15	408	4	6.464	1.10E-02	rs7748142	6	55931145	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1651296	C	C	380	20	374	40	6.476	0.0109	rs10484724	6	55977448	p12.1
SNP_A-1858503	C	C	394	20	379	41	7.478	6.20E-03	rs17817455	6	56036735	p12.1
SNP_A-1718801	T	T	380	20	371	39	6.104	0.0135	rs1925178	6	56062952	p12.1
SNP_A-2159189	G	G	404	4	422	0	4.157	4.15E-02	rs16887565	6	56067979	p12.1
SNP_A-1883082	G	G	386	14	356	26	4.401	3.59E-02	rs2143359	6	56111398	p12.1
SNP_A-2189672	A	A	240	144	193	173	7.327	6.80E-03	rs9475663	6	56287451	p12.1
SNP_A-1729067	T	T	229	155	232	114	4.302	3.81E-02	rs10484858	6	56510848	p12.1
SNP_A-2269496	A	A	400	4	398	16	7.084	7.80E-03	rs7759479	6	56618101	p12.1
SNP_A-1844559	G	G	313	41	325	21	6.587	0.0103	rs17684784	6	56786401	p12.1
SNP_A-1927812	G	G	231	141	186	158	4.735	2.96E-02	rs2064245	6	57225583	p12.1
SNP_A-2297582	C	C	286	76	303	53	4.542	3.31E-02	rs6927914	6	57740670	p11.2
SNP_A-2141183	C	C	346	8	384	2	4.202	4.04E-02	rs7773770	6	57890220	p11.2
SNP_A-2045091	C	C	355	23	376	8	7.815	5.20E-03	rs4527737	6	58254046	p11.2
SNP_A-1838521	C	C	306	52	300	32	3.847	4.98E-02	rs9342639	6	62817818	q11.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2226340	G	G	339	61	355	41	4.27	3.88E-02	rs515188	6	63100848	q11.1
SNP_A-2159866	G	G	324	42	344	22	6.849	8.90E-03	rs2492805	6	63175644	q11.1
SNP_A-2060583	C	C	179	125	218	108	4.309	3.79E-02	rs7757616	6	64712492	q12
SNP_A-1727523	G	G	264	128	294	104	4.05	4.42E-02	rs10494883	6	65203767	q12
SNP_A-2252300	C	C	266	126	304	104	4.319	3.77E-02	rs9351272	6	65243497	q12
SNP_A-2149892	T	T	270	94	240	118	4.432	3.53E-02	rs6924505	6	65913525	q12
SNP_A-1747625	C	C	385	15	367	33	7.181	7.40E-03	rs10498832	6	65997347	q12
SNP_A-2072965	C	C	276	110	305	85	4.632	3.14E-02	rs9342473	6	66161065	q12
SNP_A-1951754	G	G	200	160	236	140	3.96	4.66E-02	rs12662737	6	67331421	q12
SNP_A-1892530	G	G	173	149	209	131	4.063	4.38E-02	rs12525745	6	67696610	q12
SNP_A-2176537	G	G	331	37	298	60	7.049	7.90E-03	rs9360251	6	67702785	q12
SNP_A-1671816	G	G	315	17	348	36	4.702	3.01E-02	rs1901926	6	67847639	q12
SNP_A-1740897	A	A	378	22	401	11	4.169	4.12E-02	rs10498860	6	68890732	q12
SNP_A-2156873	C	C	235	111	249	79	5.318	2.11E-02	rs10455670	6	69347352	q12
SNP_A-1808349	A	A	304	110	328	86	3.85	4.97E-02	rs7761592	6	69348223	q12
SNP_A-2074047	C	C	258	150	287	121	4.646	3.11E-02	rs11963528	6	69584891	q12
SNP_A-1837824	C	C	261	91	248	120	3.964	0.0465	rs523962	6	69635461	q12
SNP_A-1986337	G	G	229	141	248	108	4.862	0.0275	rs2184723	6	69703807	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207627	T	T	201	147	220	106	6.791	9.20E-03	rs13201188	6	69705545	q12
SNP_A-2051035	G	G	281	133	315	103	5.734	0.0166	rs1415031	6	69757118	q12
SNP_A-2231832	A	A	341	7	320	24	9.967	1.60E-03	rs3798995	6	69757481	q12
SNP_A-2027159	G	A	208	182	221	187	4.487	3.42E-02	rs9446083	6	69768622	q12
SNP_A-1986340	C	C	303	25	336	14	4.097	4.30E-02	rs10485430	6	69785173	q12
SNP_A-1814147	G	G	330	52	349	31	5.84	1.57E-02	rs2296975	6	70091703	q13
SNP_A-1672772	T	T	238	152	273	127	4.512	3.37E-02	rs1410692	6	70181567	q13
SNP_A-2253743	C	C	296	98	267	125	4.758	0.0292	rs10806627	6	70424445	q13
SNP_A-1703151	G	G	199	177	255	149	8.318	3.90E-03	rs3799117	6	70446021	q13
SNP_A-2226000	A	A	188	172	229	119	13.485	2.00E-04	rs7741758	6	70469101	q13
SNP_A-1746406	G	G	254	144	225	183	6.284	1.22E-02	rs2345564	6	70478034	q13
SNP_A-2128647	C	C	212	192	258	148	10.191	0.0014	rs9351772	6	70484921	q13
SNP_A-2295865	C	A	198	194	240	152	10.921	0.001	rs7762400	6	70502355	q13
SNP_A-1930953	A	A	213	167	254	124	9.948	1.60E-03	rs7758405	6	70502405	q13
SNP_A-1902838	T	T	215	199	263	157	9.732	0.0018	rs11970363	6	70527237	q13
SNP_A-2203182	C	C	179	171	196	136	4.289	3.84E-02	rs9351776	6	70560842	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2048977	G	G	295	55	262	78	5.789	0.0161	rs2445977	6	70564884	q13
SNP_A-1931167	C	C	205	173	249	145	6.401	0.0114	rs9364063	6	70571471	q13
SNP_A-1645960	C	C	300	94	279	131	6.53	0.0106	rs10498870	6	70581930	q13
SNP_A-1986360	C	C	351	21	337	9	4.149	4.17E-02	rs6415072	6	70662029	q13
SNP_A-1747493	T	T	314	72	335	51	4.265	3.89E-02	rs1207171	6	71832689	q13
SNP_A-1801757	G	G	331	1	321	7	4.629	3.14E-02	rs13437398	6	71859713	q13
SNP_A-1986390	G	G	279	77	313	59	3.985	4.59E-02	rs1935810	6	71890829	q13
SNP_A-2060141	T	T	327	73	345	51	4.365	3.67E-02	rs1857223	6	71892286	q13
SNP_A-1943917	C	C	345	37	352	20	5.009	0.0252	rs6908858	6	72047320	q13
SNP_A-1822304	A	A	372	36	396	20	5.244	2.20E-02	rs9346455	6	72048537	q13
SNP_A-2273613	A	A	329	61	293	83	5.191	2.27E-02	rs2295956	6	72093997	q13
SNP_A-1902206	C	C	324	78	359	55	5.596	1.80E-02	rs1322761	6	72098669	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1986394	T	T	316	94	292	122	4.558	3.28E-02	rs828630	6	72100618	q13
SNP_A-1805684	G	G	343	71	318	96	4.688	0.0304	rs828655	6	72113631	q13
SNP_A-2054004	C	C	370	40	353	65	6.275	1.22E-02	rs7382024	6	72527040	q13
SNP_A-1961402	A	A	320	22	341	11	4.191	4.06E-02	rs17779688	6	72585104	q13
SNP_A-2024257	C	C	330	86	309	111	3.844	0.0499	rs9360509	6	72624267	q13
SNP_A-1807370	T	T	333	83	308	110	4.747	0.0293	rs1147524	6	72638362	q13
SNP_A-2075090	A	A	224	136	182	174	8.981	2.70E-03	rs9358988	6	72730986	q13
SNP_A-2147869	C	C	371	45	355	65	3.97	4.63E-02	rs1482570	6	72738670	q13
SNP_A-1932218	C	C	330	72	290	98	6.311	0.012	rs9446521	6	72738744	q13
SNP_A-1833916	G	G	307	85	261	127	12.026	5.00E-04	rs1482571	6	72738976	q13
SNP_A-1865895	G	G	349	51	332	78	5.953	0.0147	rs12524886	6	72762605	q13
SNP_A-2310268	A	A	349	67	323	95	5.841	1.57E-02	rs11759297	6	72947483	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1685806	A	A	367	33	359	53	4.563	0.0327	rs10485036	6	73111696	q13
SNP_A-1703095	T	T	243	155	221	187	3.914	4.79E-02	rs985564	6	73164775	q13
SNP_A-1751853	C	C	329	33	335	55	4.518	3.35E-02	rs10485213	6	73366708	q13
SNP_A-2163313	A	G	187	141	156	150	4.061	4.39E-02	rs10943076	6	73784462	q13
SNP_A-1783384	A	A	405	5	392	14	4.456	3.48E-02	rs16883236	6	73806595	q13
SNP_A-2158876	T	T	392	10	366	22	5.145	2.33E-02	rs7742112	6	73840369	q13
SNP_A-1810836	G	G	399	3	381	13	6.586	0.0103	rs6921049	6	73842658	q13
SNP_A-2155809	C	C	248	98	273	75	4.252	3.92E-02	rs17812683	6	74149544	q13
SNP_A-2043220	A	A	370	16	373	5	5.691	1.71E-02	rs541178	6	74262352	q13
SNP_A-1986443	A	A	391	13	388	26	4.223	3.99E-02	rs3857464	6	74336861	q13
SNP_A-1930065	G	G	360	28	375	15	4.231	3.97E-02	rs476838	6	74374563	q13
SNP_A-2086425	T	T	374	28	388	14	4.924	2.65E-02	rs473078	6	74374986	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835696	C	C	264	146	294	120	4.135	4.20E-02	rs2033736	6	74548920	q13
SNP_A-2269957	A	A	386	12	376	26	5.269	2.17E-02	rs16884139	6	74573859	q13
SNP_A-2307780	A	A	309	87	335	57	7.28	7.00E-03	rs9341446	6	74837309	q13
SNP_A-2185939	G	G	287	35	313	17	7.26	7.00E-03	rs9360735	6	74855237	q13
SNP_A-1743279	T	T	369	27	397	9	9.9	1.70E-03	rs9293954	6	74876904	q13
SNP_A-1839339	T	T	288	96	306	72	3.927	4.75E-02	rs4469252	6	74909228	q13
SNP_A-1898533	A	A	367	17	405	3	10.953	9.00E-04	rs4708135	6	74934620	q13
SNP_A-1930550	A	A	367	21	398	8	6.679	9.80E-03	rs9360745	6	74936028	q13
SNP_A-2111436	G	G	250	144	255	103	5.144	2.33E-02	rs1931271	6	75010359	q13
SNP_A-1961033	C	C	355	9	354	20	4.039	4.45E-02	rs9352087	6	75044066	q13
SNP_A-2173959	C	C	384	24	394	12	4.124	4.23E-02	rs16884759	6	75129553	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2026693	T	T	408	4	418	0	4.078	4.34E-02	rs9360790	6	75177554	q13
SNP_A-1811478	T	T	377	19	388	8	4.64	3.12E-02	rs6912037	6	75247853	q13
SNP_A-1687604	A	A	338	42	340	66	4.484	3.42E-02	rs756258	6	75485638	q13
SNP_A-1986475	C	C	403	13	415	3	6.421	1.13E-02	rs2015242	6	75870887	q13
SNP_A-2036956	A	A	403	13	416	4	4.952	2.61E-02	rs9343271	6	75894633	q13
SNP_A-2032975	C	C	369	23	360	8	6.618	0.0101	rs3777510	6	75959524	q14.1
SNP_A-2124893	C	C	349	21	328	38	5.528	1.87E-02	rs9350591	6	76298247	q14.1
SNP_A-2238556	G	G	306	24	289	41	4.932	0.0264	rs12208366	6	76474506	q14.1
SNP_A-1836223	T	T	338	2	343	11	5.987	0.0144	rs17195381	6	76840050	q14.1
SNP_A-1647518	T	T	257	73	347	51	11.059	9.00E-04	rs1905974	6	76882093	q14.1
SNP_A-2257930	G	G	355	51	383	33	4.799	2.85E-02	rs4708220	6	76918206	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2070398	G	G	333	45	361	25	6.761	9.30E-03	rs6453855	6	76919249	q14.1
SNP_A-1721191	A	A	329	71	361	51	4.586	3.22E-02	rs1976109	6	76920835	q14.1
SNP_A-2310617	C	C	354	54	364	34	4.561	0.0327	rs9352266	6	76958371	q14.1
SNP_A-1872304	T	T	357	11	383	3	5.058	2.45E-02	rs2314199	6	76961141	q14.1
SNP_A-1685654	G	G	348	50	386	24	10.927	9.00E-04	rs9294012	6	76973900	q14.1
SNP_A-2030794	C	C	338	64	361	43	4.873	2.73E-02	rs9352272	6	76974389	q14.1
SNP_A-2213654	G	G	221	129	259	105	5.197	2.26E-02	rs3943166	6	76986284	q14.1
SNP_A-2250824	G	G	255	153	293	125	5.335	2.09E-02	rs1825653	6	76989490	q14.1
SNP_A-2122911	G	G	226	130	247	103	4.01	4.52E-02	rs1385901	6	76993682	q14.1
SNP_A-1872391	A	A	228	130	257	95	7.128	0.0076	rs9447668	6	77015933	q14.1
SNP_A-1986488	G	G	367	49	392	28	6.532	0.0106	rs1564967	6	77017319	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2094620	T	T	188	128	215	97	6.055	1.39E-02	rs6919801	6	77057497	q14.1
SNP_A-1919407	T	T	224	108	262	84	5.685	1.71E-02	rs9343396	6	77059153	q14.1
SNP_A-2155225	G	G	354	26	389	13	5.367	2.05E-02	rs4481399	6	77078698	q14.1
SNP_A-2271039	A	A	246	146	277	109	7.16	7.50E-03	rs9341562	6	77080517	q14.1
SNP_A-1929304	G	G	338	26	375	9	9.649	0.0019	rs16887433	6	77090814	q14.1
SNP_A-2196083	A	A	258	154	294	124	5.542	1.86E-02	rs2451590	6	77113672	q14.1
SNP_A-1676828	C	C	258	94	308	78	4.348	3.70E-02	rs951993	6	77137597	q14.1
SNP_A-1785144	G	G	235	139	285	115	6.209	1.27E-02	rs2504668	6	77180523	q14.1
SNP_A-2069134	G	G	246	142	268	112	4.402	3.59E-02	rs1490207	6	77191660	q14.1
SNP_A-1961052	A	A	238	142	276	106	8.03	4.60E-03	rs5009482	6	77202293	q14.1
SNP_A-1838900	T	T	272	106	300	72	7.818	5.20E-03	rs1490208	6	77226507	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1831628	T	T	234	104	254	70	7.17	7.40E-03	rs6453904	6	77230588	q14.1
SNP_A-2250650	C	C	265	91	293	63	6.496	1.08E-02	rs7740045	6	77233785	q14.1
SNP_A-1859457	G	G	260	144	294	116	5.058	2.45E-02	rs9447705	6	77249940	q14.1
SNP_A-1939584	T	T	320	38	337	15	10.371	1.30E-03	rs6929491	6	77262956	q14.1
SNP_A-2157434	G	G	212	124	251	107	3.843	5.00E-02	rs6453912	6	77315837	q14.1
SNP_A-1705813	C	C	282	108	307	81	4.913	2.67E-02	rs5012256	6	77603450	q14.1
SNP_A-2097426	G	G	292	114	313	81	6.135	1.33E-02	rs9447905	6	77673247	q14.1
SNP_A-1827460	A	A	292	110	320	84	4.761	2.91E-02	rs7772149	6	77679844	q14.1
SNP_A-2252880	T	T	299	113	324	88	4.113	4.26E-02	rs7772268	6	77679871	q14.1
SNP_A-1986502	A	A	288	106	312	80	4.589	3.22E-02	rs7768254	6	77694652	q14.1
SNP_A-2080432	C	C	326	6	328	16	4.34	3.72E-02	rs2446248	6	78373344	q14.1
SNP_A-1926429	C	C	364	44	338	66	5.343	2.08E-02	rs1483050	6	78528639	q14.1
SNP_A-1986522	C	C	369	47	340	70	5.664	1.73E-02	rs9294087	6	78581437	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172926	A	A	227	137	230	100	4.14	0.0419	rs6919826	6	78638311	q14.1
SNP_A-1916440	G	G	205	131	186	162	3.994	4.57E-02	rs235460	6	79109332	q14.1
SNP_A-1959842	T	G	224	170	185	177	4.797	2.85E-02	rs2493225	6	79137205	q14.1
SNP_A-2259878	C	C	380	26	400	14	4.035	4.46E-02	rs1938554	6	79426313	q14.1
SNP_A-1986557	T	T	264	90	205	105	5.685	1.71E-02	rs1361043	6	79893786	q14.1
SNP_A-2075887	G	G	362	22	383	9	5.962	0.0146	rs17785485	6	79910945	q14.1
SNP_A-1957416	C	C	361	29	383	13	6.7	9.60E-03	rs17723508	6	79911083	q14.1
SNP_A-1930965	A	A	377	15	400	6	4.294	3.83E-02	rs10806163	6	79951373	q14.1
SNP_A-1986561	G	G	388	18	406	8	4.177	4.10E-02	rs4706756	6	79992348	q14.1
SNP_A-2089497	G	A	219	185	225	173	9.256	0.0023	rs1060419	6	80001713	q14.1
SNP_A-1714925	A	A	199	197	246	164	7.74	5.40E-03	rs16760	6	80034777	q14.1
SNP_A-2171184	T	T	386	16	409	7	3.949	4.69E-02	rs4706766	6	80044288	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2231423	C	C	326	54	345	27	9.454	2.10E-03	rs10943632	6	80072480	q14.1
SNP_A-1955124	G	A	210	202	247	169	8.926	0.0028	rs7383447	6	80077256	q14.1
SNP_A-2308014	C	C	293	73	330	42	10.506	1.20E-03	rs4530821	6	80120222	q14.1
SNP_A-1986562	A	A	245	159	286	126	6.909	0.0086	rs7740673	6	80120699	q14.1
SNP_A-2178750	A	A	213	113	283	83	12.199	5.00E-04	rs3846733	6	80143211	q14.1
SNP_A-1934988	A	A	346	46	364	28	4.835	2.79E-02	rs3907327	6	80164301	q14.1
SNP_A-1986565	C	C	361	51	377	33	4.199	4.04E-02	rs10484943	6	80181477	q14.1
SNP_A-1726384	G	G	339	3	367	13	5.375	2.04E-02	rs723981	6	80360871	q14.1
SNP_A-2205300	T	T	392	20	381	37	5.184	2.28E-02	rs6925597	6	80522983	q14.1
SNP_A-1943001	-	A	206	206	235	171	5.113	2.38E-02	rs932492	6	80531291	q14.1
SNP_A-1986584	G	G	346	60	324	84	4.718	2.99E-02	rs1550035	6	80787567	q14.1
SNP_A-1948553	G	G	380	20	343	41	8.8	3.00E-03	rs9352839	6	81208560	q14.1
SNP_A-2231191	G	G	385	23	346	50	11.891	6.00E-04	rs9344005	6	81230090	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2106953	G	G	376	16	335	45	15.968	6.44E-05	rs17810414	6	81244646	q14.1
SNP_A-1871488	T	T	372	26	339	57	13.105	3.00E-04	rs9344006	6	81248684	q14.1
SNP_A-2115673	G	G	377	11	346	34	13.003	3.00E-04	rs7738642	6	81249174	q14.1
SNP_A-2241746	A	A	361	55	330	84	7.436	6.40E-03	rs9443793	6	81282980	q14.1
SNP_A-2065490	G	G	353	43	324	60	3.864	4.93E-02	rs17755364	6	81297112	q14.1
SNP_A-1986606	T	T	351	37	315	61	7.637	5.70E-03	rs10498923	6	81310626	q14.1
SNP_A-2245766	T	T	234	162	256	126	5.238	2.21E-02	rs9449067	6	81322214	q14.1
SNP_A-2285586	G	G	313	35	282	56	6.317	0.012	rs2674883	6	81389596	q14.1
SNP_A-1685090	T	T	357	43	345	67	5.265	0.0218	rs10485284	6	81474826	q14.1
SNP_A-1656637	T	T	363	17	394	8	3.894	4.85E-02	rs1822546	6	81835475	q14.1
SNP_A-2210086	C	C	394	18	407	7	5.046	0.0247	rs9352923	6	81846272	q14.1
SNP_A-1795220	G	G	393	17	410	6	5.577	1.82E-02	rs7750817	6	81900802	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796639	C	C	357	9	340	2	4.06	4.39E-02	rs16893209	6	82309913	q14.1
SNP_A-2029236	T	T	264	110	210	126	5.218	0.0224	rs1341219	6	82398726	q14.1
SNP_A-2055355	T	C	213	203	237	181	5.221	0.0223	rs10943829	6	82456630	q14.1
SNP_A-2243178	A	A	320	90	301	117	4.026	0.0448	rs194905	6	82483196	q14.1
SNP_A-1922547	G	G	347	51	333	73	4.112	4.26E-02	rs194915	6	82489885	q14.1
SNP_A-1946652	T	T	351	23	335	45	7.444	6.40E-03	rs12207462	6	82512770	q14.1
SNP_A-1897571	A	A	255	131	223	155	4.073	0.0436	rs194630	6	82573296	q14.1
SNP_A-1910502	T	T	188	122	168	162	6.138	0.0132	rs2875087	6	82672802	q14.1
SNP_A-2058218	T	T	339	29	315	47	5.095	0.024	rs2104061	6	83274701	q14.1
SNP_A-2181785	G	G	181	161	209	125	6.448	0.0111	rs2989879	6	83428944	q14.1
SNP_A-2035206	A	A	225	161	192	188	4.654	0.031	rs1318150	6	83429044	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1986653	C	C	164	158	188	126	5.142	2.34E-02	rs285972	6	83431989	q14.1
SNP_A-2027836	G	G	253	151	221	179	4.516	3.36E-02	rs392692	6	83443240	q14.1
SNP_A-1808984	A	A	319	73	291	95	4.12	0.0424	rs6902437	6	83965457	q14.2
SNP_A-1986670	A	A	254	92	267	65	4.681	3.05E-02	rs10485147	6	84180069	q14.2
SNP_A-2249867	T	T	305	53	301	33	3.85	4.98E-02	rs4707000	6	84246116	q14.2
SNP_A-2169792	T	T	347	47	378	30	4.836	2.79E-02	rs4707001	6	84246402	q14.2
SNP_A-2161687	C	C	270	114	307	91	4.704	3.01E-02	rs512140	6	84287372	q14.2
SNP_A-2011887	C	C	284	120	305	89	5.222	0.0223	rs798395	6	84326036	q14.2
SNP_A-1894876	G	G	274	108	295	83	4.026	0.0448	rs9341963	6	84343957	q14.2
SNP_A-1835490	A	A	376	20	406	8	5.897	0.0152	rs6940118	6	84422197	q14.2
SNP_A-2277509	G	G	343	69	363	49	3.956	4.67E-02	rs2924667	6	84483165	q14.2
SNP_A-2120208	C	C	334	48	361	31	4.579	3.24E-02	rs586661	6	84484999	q14.2
SNP_A-1947245	G	G	399	7	399	1	4.456	3.48E-02	rs12524136	6	84992160	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2079007	C	C	321	67	342	40	7.432	6.40E-03	rs735641	6	85008568	q14.3
SNP_A-1986689	A	A	265	93	296	70	4.871	2.73E-02	rs9341974	6	85129893	q14.3
SNP_A-2095219	T	T	239	149	196	186	8.291	4.00E-03	rs7760461	6	85140975	q14.3
SNP_A-2181861	A	A	238	120	209	167	9.142	2.50E-03	rs7763662	6	85175003	q14.3
SNP_A-2143908	G	G	259	137	231	163	3.848	4.98E-02	rs2209041	6	85197480	q14.3
SNP_A-1787596	C	C	314	64	347	45	4.706	3.00E-02	rs2324670	6	85416402	q14.3
SNP_A-2221077	A	A	253	149	284	122	4.46	3.47E-02	rs7768657	6	85439915	q14.3
SNP_A-1986712	G	G	254	160	285	131	4.668	3.07E-02	rs7774683	6	85474565	q14.3
SNP_A-1887315	T	T	253	163	289	127	6.86	8.80E-03	rs6905550	6	85476471	q14.3
SNP_A-1819649	A	A	394	20	380	34	3.883	4.88E-02	rs16875178	6	85572819	q14.3
SNP_A-1715923	C	C	356	38	382	24	3.898	4.83E-02	rs2104467	6	85858909	q14.3
SNP_A-2110785	C	C	371	37	384	20	5.274	2.16E-02	rs10944062	6	85888985	q14.3
SNP_A-2157522	C	C	331	81	283	117	10.123	0.0015	rs484746	6	85894007	q14.3
SNP_A-1812252	C	T	195	157	172	150	5.229	2.22E-02	rs1926019	6	85904216	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2288582	G	G	355	37	379	23	3.926	4.75E-02	rs1407165	6	85933239	q14.3
SNP_A-2151169	A	A	376	38	397	23	4.216	4.00E-02	rs11962094	6	86044985	q14.3
SNP_A-1643159	A	A	289	71	287	101	4.197	4.05E-02	rs10498953	6	86060887	q14.3
SNP_A-2172505	A	G	229	183	215	199	4.671	3.07E-02	rs9362180	6	86067798	q14.3
SNP_A-1883256	G	C	224	180	214	196	4.757	0.0292	rs476613	6	86068142	q14.3
SNP_A-1903106	G	A	207	159	204	184	6.295	0.0121	rs9344507	6	86084548	q14.3
SNP_A-2118336	T	C	202	158	191	171	5.691	1.70E-02	rs543073	6	86087375	q14.3
SNP_A-1870220	G	G	275	71	250	92	3.873	4.91E-02	rs970568	6	86113446	q14.3
SNP_A-1843799	C	C	253	87	220	114	5.876	1.53E-02	rs2224595	6	86117342	q14.3
SNP_A-2078687	A	A	244	156	268	128	3.866	4.93E-02	rs12213431	6	86557675	q14.3
SNP_A-2291340	T	T	221	155	244	120	5.399	0.0201	rs2816822	6	86715011	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2073615	T	T	228	140	257	107	6.121	0.0134	rs6933377	6	86761974	q14.3
SNP_A-2069095	A	A	338	18	359	7	5.335	2.09E-02	rs7748330	6	87083846	q14.3
SNP_A-2041156	A	A	266	70	241	95	5.021	2.50E-02	rs9344602	6	87129957	q14.3
SNP_A-2224527	A	A	263	147	230	184	6.326	1.19E-02	---	6	87217709	q14.3
SNP_A-1702001	C	C	208	108	269	85	8.414	3.70E-03	rs2020079	6	87287413	q14.3
SNP_A-1714919	A	A	360	40	350	60	4.018	4.50E-02	rs10485361	6	87345491	q14.3
SNP_A-1673910	T	T	364	32	356	50	3.916	4.78E-02	rs542732	6	87405238	q14.3
SNP_A-1986752	C	C	368	24	348	42	5.463	1.94E-02	rs10485359	6	87409196	q14.3
SNP_A-1756116	G	G	368	32	360	52	4.673	3.06E-02	rs487570	6	87446683	q14.3
SNP_A-1787623	T	T	363	29	309	41	4.032	4.46E-02	rs592728	6	87477371	q14.3
SNP_A-1719305	C	C	366	34	359	53	4.041	4.44E-02	rs494991	6	87479290	q14.3
SNP_A-1986755	G	G	369	33	355	53	4.878	2.72E-02	rs584256	6	87548960	q15
SNP_A-1831437	G	C	214	194	236	178	7.365	6.70E-03	rs4707318	6	87557058	q15
SNP_A-1862732	C	C	236	138	268	114	4.233	3.96E-02	rs1321317	6	87612757	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2091506	T	T	342	26	325	43	4.622	3.16E-02	rs1408447	6	87657032	q15
SNP_A-1840770	T	-	213	157	180	180	4.205	4.03E-02	rs1075068	6	87882028	q15
SNP_A-1948337	A	G	230	178	211	203	4.44	3.51E-02	rs4707345	6	87970195	q15
SNP_A-1853801	T	T	183	119	167	161	5.969	0.0146	rs451465	6	88100091	q15
SNP_A-1918865	C	C	179	175	202	146	3.957	4.67E-02	rs242270	6	88118909	q15
SNP_A-1986775	G	A	224	186	217	197	4.097	4.30E-02	rs107690	6	88126071	q15
SNP_A-2056161	A	C	223	193	228	190	5.542	1.86E-02	rs6454649	6	88560028	q15
SNP_A-1889345	T	T	378	18	385	7	4.884	2.71E-02	rs9450829	6	88681156	q15
SNP_A-1662210	A	A	242	158	219	191	4.145	4.18E-02	rs366676	6	88713362	q15
SNP_A-2086312	G	G	242	150	210	174	3.961	4.66E-02	rs10944335	6	88714066	q15
SNP_A-2026348	G	G	321	59	317	37	4.151	4.16E-02	rs662847	6	88730890	q15
SNP_A-2244288	A	A	297	71	291	43	5.304	2.13E-02	rs7760757	6	88748031	q15
SNP_A-1652150	A	A	377	15	396	6	4.199	4.05E-02	rs2875547	6	88896441	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1986789	C	C	386	20	381	7	5.887	1.53E-02	rs1154586	6	89088796	q15
SNP_A-1950019	G	G	275	97	244	122	4.657	0.0309	rs17577546	6	89302780	q15
SNP_A-1887330	T	T	256	122	293	99	4.634	3.13E-02	rs12527253	6	89350464	q15
SNP_A-1986802	C	C	318	48	332	18	13.587	2.00E-04	rs3777530	6	89966276	q15
SNP_A-2096036	C	C	351	31	363	17	4.28	3.86E-02	rs660543	6	90644201	q15
SNP_A-2282217	C	C	324	92	366	54	12.428	4.00E-04	rs1055403	6	90695684	q15
SNP_A-2072804	C	C	348	68	379	41	7.991	4.70E-03	rs3173197	6	90713028	q15
SNP_A-2283857	G	G	267	77	235	101	5.182	2.28E-02	rs9444725	6	90770775	q15
SNP_A-1811895	C	C	356	20	382	10	3.918	4.78E-02	rs9444729	6	90787159	q15
SNP_A-2169249	A	A	354	14	342	36	9.755	0.0018	rs1451075	6	91195678	q15
SNP_A-1794755	A	A	229	139	197	165	4.578	3.24E-02	rs464339	6	91258916	q15
SNP_A-1938545	T	T	226	118	194	158	8.144	0.0043	rs466479	6	91259242	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2156652	G	G	182	178	223	153	5.694	1.70E-02	rs806272	6	91260936	q15
SNP_A-1824340	T	T	320	44	347	21	9.21	2.40E-03	rs205661	6	91267361	q15
SNP_A-1816125	G	G	405	11	392	28	7.603	5.80E-03	rs1504289	6	91569215	q15
SNP_A-1887947	T	T	349	43	364	26	4.499	0.0339	rs4707672	6	92068252	q15
SNP_A-2191523	A	G	225	185	209	191	4.118	0.0424	rs2655641	6	92208027	q16.1
SNP_A-2119688	C	C	355	27	358	14	4.003	4.54E-02	rs4324752	6	92311910	q16.1
SNP_A-2191876	G	G	345	15	356	6	4.024	4.49E-02	rs17558183	6	92626626	q16.1
SNP_A-2258062	G	G	235	157	201	179	3.906	4.81E-02	rs9362923	6	92695716	q16.1
SNP_A-1896366	C	C	348	52	380	34	4.935	0.0263	rs890560	6	93215870	q16.1
SNP_A-1878626	G	G	232	184	280	140	10.456	1.20E-03	rs1346298	6	93216140	q16.1
SNP_A-2122765	T	T	232	184	276	140	9.786	0.0018	rs12215940	6	93234468	q16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2023587	T	T	286	126	312	96	5.165	0.023	rs6909411	6	93612665	q16.1
SNP_A-1930684	A	A	351	23	377	7	9.332	0.0023	rs6454915	6	93623983	q16.1
SNP_A-2093976	G	G	313	83	331	61	3.844	0.0499	rs488429	6	93784568	q16.1
SNP_A-2053037	A	A	277	103	298	66	8.527	3.50E-03	rs7769656	6	93813789	q16.1
SNP_A-1951803	C	C	370	14	381	5	4.419	3.55E-02	rs373675	6	94018753	q16.1
SNP_A-2098535	A	A	401	11	409	3	4.65	0.031	rs9345405	6	94612191	q16.1
SNP_A-2036174	A	A	410	6	420	0	6.101	0.0135	rs1937367	6	94629506	q16.1
SNP_A-1909297	G	G	410	6	420	0	6.101	0.0135	rs7449883	6	94717168	q16.1
SNP_A-1986905	G	G	408	4	420	0	4.097	4.29E-02	rs1463675	6	94733004	q16.1
SNP_A-1839453	T	T	284	52	280	78	4.536	0.0332	rs220949	6	95017595	q16.1
SNP_A-2226845	C	C	344	36	369	19	6.048	1.39E-02	rs6931706	6	95478595	q16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2223986	T	T	204	174	225	141	4.293	3.83E-02	rs9399724	6	95998631	q16.1
SNP_A-1815281	C	C	336	72	346	50	3.936	4.73E-02	rs6905412	6	96003236	q16.1
SNP_A-2308496	G	G	332	70	347	49	3.992	4.57E-02	rs6910024	6	96003452	q16.1
SNP_A-1826756	A	A	218	194	256	162	5.88	1.53E-02	rs9387352	6	96138824	q16.1
SNP_A-2045353	G	G	212	174	246	144	5.334	2.09E-02	rs9400893	6	96144620	q16.1
SNP_A-2200223	A	A	191	169	206	134	4.042	4.44E-02	rs9387522	6	96161656	q16.1
SNP_A-1819569	T	T	197	179	232	146	6.201	1.28E-02	rs9489578	6	96171771	q16.1
SNP_A-1986931	G	G	344	68	317	89	3.868	4.92E-02	rs1336959	6	96401361	q16.1
SNP_A-1837782	C	C	282	90	248	128	8.784	3.00E-03	rs2799644	6	96464883	q16.1
SNP_A-1650594	C	C	343	17	344	32	4.247	3.93E-02	rs590973	6	96472550	q16.1
SNP_A-1758002	T	T	176	172	218	150	5.426	1.98E-02	rs2147716	6	96549604	q16.1
SNP_A-1717173	C	G	201	199	240	172	5.908	1.51E-02	rs4002794	6	96557543	q16.1
SNP_A-1986941	C	C	203	173	232	148	3.859	4.95E-02	rs1318073	6	96610688	q16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2173834	C	C	198	162	221	117	7.835	5.10E-03	rs9404179	6	96619196	q16.1
SNP_A-2251342	G	G	255	77	287	59	3.984	4.59E-02	rs4598084	6	96636820	q16.1
SNP_A-2259663	G	G	303	39	283	57	4.052	0.0441	rs9390936	6	96702177	q16.1
SNP_A-1724106	C	C	316	44	323	71	4.893	0.027	rs10499000	6	96711757	q16.1
SNP_A-2036512	T	T	266	148	234	184	5.933	0.0149	rs12210219	6	96790516	q16.1
SNP_A-2175432	G	G	388	28	406	14	5.056	2.45E-02	rs17056495	6	96811395	q16.1
SNP_A-1798603	A	C	181	151	186	146	7.381	0.0066	rs211170	6	97176821	q16.1
SNP_A-1986952	C	C	285	127	317	103	4.129	4.22E-02	rs9320281	6	97315150	q16.1
SNP_A-1986956	T	T	278	134	306	108	4.131	4.21E-02	rs9374204	6	97464120	q16.1
SNP_A-1871384	T	T	268	74	246	98	4.285	0.0385	rs7766184	6	97495364	q16.1
SNP_A-2086047	T	T	317	49	295	73	5.507	0.0189	rs6917254	6	97498574	q16.1
SNP_A-1796401	T	T	337	21	326	8	5.184	2.28E-02	rs9374661	6	98131901	q16.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2114263	A	A	329	81	355	55	5.959	0.0146	rs9387585	6	98238635	q16.1
SNP_A-2191082	C	C	310	82	334	60	4.298	3.82E-02	rs9385058	6	98268675	q16.1
SNP_A-2135638	A	A	353	53	332	76	4.74	2.95E-02	rs6922758	6	98424947	q16.1
SNP_A-1926985	C	C	310	94	288	126	5.342	2.08E-02	rs210405	6	99035101	q16.2
SNP_A-1986978	T	C	199	171	202	164	5.929	0.0149	rs2227121	6	99045555	q16.2
SNP_A-1785426	C	C	237	163	261	123	6.427	0.0112	rs158773	6	99056271	q16.2
SNP_A-1861298	C	C	402	10	419	1	7.639	5.70E-03	rs211218	6	99085199	q16.2
SNP_A-2248935	C	C	394	12	411	1	9.623	0.0019	rs9388545	6	99085826	q16.2
SNP_A-2049870	T	T	222	194	265	153	8.636	0.0033	rs17058818	6	99341951	q16.2
SNP_A-2238883	G	G	229	127	166	136	5.965	0.0146	rs1809181	6	99380409	q16.2
SNP_A-2129549	C	C	300	64	295	91	4.103	4.28E-02	rs2092769	6	99578970	q16.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1986994	A	A	337	53	329	77	4.207	4.03E-02	rs726488	6	99645914	q16.2
SNP_A-1909089	A	A	339	55	316	78	4.785	0.0287	rs11154725	6	99725042	q16.2
SNP_A-2310763	T	T	318	98	292	126	4.603	3.19E-02	rs11154726	6	99725086	q16.2
SNP_A-2058297	C	C	290	56	255	73	4.01	4.52E-02	rs6908689	6	99772267	q16.2
SNP_A-1753727	T	T	278	122	258	152	3.908	4.81E-02	rs4839746	6	99839800	q16.2
SNP_A-1851572	G	G	308	34	298	52	3.84	5.00E-02	rs9373106	6	99841500	q16.2
SNP_A-1946589	G	G	265	101	245	135	5.422	1.99E-02	rs9321491	6	99899259	q16.2
SNP_A-2164050	C	A	211	203	237	183	4.574	3.25E-02	rs6923983	6	99983940	q16.2
SNP_A-1987002	A	T	184	160	198	154	6.605	1.02E-02	rs6915401	6	99987560	q16.2
SNP_A-2112549	A	G	188	176	211	155	6.335	0.0118	rs9402794	6	99999245	q16.2
SNP_A-1827231	C	G	208	206	240	178	4.904	2.68E-02	rs6912228	6	100021900	q16.3
SNP_A-2284670	G	G	281	55	319	39	4.437	3.52E-02	rs7775207	6	100066829	q16.3
SNP_A-1913699	C	C	223	187	261	151	6.813	9.00E-03	rs9402863	6	100078150	q16.3
SNP_A-1873603	T	T	392	18	406	8	4.072	0.0436	rs2220793	6	100236827	q16.3
SNP_A-1987008	A	A	257	145	286	116	4.771	2.89E-02	rs2894869	6	100268661	q16.3
SNP_A-2172510	A	A	314	84	300	112	4.078	4.34E-02	rs4240580	6	100308187	q16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2053822	C	C	219	149	246	124	3.852	4.97E-02	rs6570355	6	100335314	q16.3
SNP_A-1910419	C	C	260	118	297	93	5.234	2.22E-02	rs4840087	6	100355665	q16.3
SNP_A-1935152	A	A	271	123	279	89	4.688	0.0304	rs4840097	6	100434919	q16.3
SNP_A-1987014	C	C	270	136	304	110	4.684	0.0304	rs2397673	6	100449710	q16.3
SNP_A-1742677	T	T	295	105	278	134	3.847	4.98E-02	rs718268	6	100904757	q16.3
SNP_A-1830072	A	A	357	59	387	33	8.539	3.50E-03	rs9403683	6	100908789	q16.3
SNP_A-1987025	A	A	337	41	302	58	4.4	3.59E-02	rs17240428	6	100939550	q16.3
SNP_A-1701437	T	T	379	7	377	21	6.823	9.00E-03	rs240165	6	101088824	q16.3
SNP_A-1918240	G	G	403	13	413	3	6.373	1.16E-02	rs12660722	6	101233992	q16.3
SNP_A-1987037	G	G	392	12	406	2	7.369	0.0066	rs6925086	6	101285620	q16.3
SNP_A-1958915	A	A	400	14	415	5	4.496	3.40E-02	rs6902414	6	101329410	q16.3
SNP_A-1931258	T	T	294	30	281	49	4.809	2.83E-02	rs2764271	6	101758338	q16.3
SNP_A-1720675	C	C	311	61	346	42	5.035	2.48E-02	rs2399711	6	101985313	q16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2080141	C	C	193	179	223	155	3.84	5.00E-02	rs1338167	6	102008690	q16.3
SNP_A-1802231	T	T	250	146	213	173	5.115	2.37E-02	rs2749054	6	102076621	q16.3
SNP_A-1987062	G	G	216	126	259	97	7.386	0.0066	rs2749052	6	102077237	q16.3
SNP_A-1918269	A	A	313	25	331	11	5.924	0.0149	rs2852584	6	102183608	q16.3
SNP_A-2025335	A	A	374	0	382	4	3.896	4.84E-02	rs1222959	6	102273967	q16.3
SNP_A-2259035	A	A	315	15	338	4	6.966	8.30E-03	rs9485549	6	102415291	q16.3
SNP_A-2166907	C	C	378	12	380	2	7.066	7.90E-03	rs2248800	6	102519869	q16.3
SNP_A-1658534	G	G	241	129	220	170	6.057	1.39E-02	rs479856	6	102986050	q16.3
SNP_A-1673546	A	A	245	141	221	177	5.129	0.0235	rs9322664	6	103044877	q16.3
SNP_A-2205879	A	A	296	56	295	29	7.431	6.40E-03	rs680011	6	103060721	q16.3
SNP_A-1700482	C	T	215	185	219	191	4.157	4.15E-02	rs1934009	6	103061365	q16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2275458	T	C	213	199	232	174	6.413	1.13E-02	rs9404221	6	103152908	q16.3
SNP_A-1688386	G	G	227	169	203	201	4.028	0.0448	rs10499034	6	103208040	q16.3
SNP_A-1644066	A	A	261	139	236	176	5.427	1.98E-02	rs967405	6	103228208	q16.3
SNP_A-1704413	G	G	256	144	233	179	4.698	3.02E-02	rs1431213	6	103244426	q16.3
SNP_A-2158582	C	C	395	17	382	34	5.865	0.0154	rs13215015	6	103602020	q16.3
SNP_A-2118663	A	A	385	15	378	28	3.95	4.69E-02	rs2157527	6	103625749	q16.3
SNP_A-2167770	G	G	365	3	341	13	6.797	9.10E-03	rs176421	6	103641993	q16.3
SNP_A-1956917	G	G	392	0	374	4	4.17	4.12E-02	rs17772313	6	103648363	q16.3
SNP_A-2238737	T	T	394	6	382	18	6.186	0.0129	rs17772332	6	103649947	q16.3
SNP_A-1821412	A	A	396	18	383	35	5.651	1.74E-02	rs9377437	6	103657459	q16.3
SNP_A-2195844	C	C	396	6	379	15	4.15	4.16E-02	rs7775385	6	103752987	q16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2118454	T	T	366	6	314	20	9.497	2.10E-03	—	6	103841518	q16.3
SNP_A-1959294	G	G	262	130	236	162	4.819	0.0281	rs9322744	6	104114509	q16.3
SNP_A-2021345	A	A	215	109	185	145	7.298	6.90E-03	rs9373707	6	104115769	q16.3
SNP_A-1877242	A	A	242	144	197	167	5.673	0.0172	rs7759394	6	104119230	q16.3
SNP_A-1842698	A	A	283	97	245	119	4.634	3.14E-02	rs11156311	6	104120657	q16.3
SNP_A-2011963	T	T	258	138	216	160	4.831	2.80E-02	rs4555956	6	104124047	q16.3
SNP_A-2043275	C	C	283	133	249	167	6.026	0.0141	rs9391062	6	104130343	q16.3
SNP_A-2153798	A	A	250	106	203	131	6.819	9.00E-03	rs11156316	6	104137512	q16.3
SNP_A-2110633	C	C	392	6	412	0	6.257	0.0124	rs7454808	6	104156623	q16.3
SNP_A-1869985	T	T	276	74	242	98	5.437	1.97E-02	rs9377535	6	104161850	q16.3
SNP_A-1884221	A	A	260	98	239	53	7.672	5.60E-03	rs12192060	6	104320668	q16.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2219912	C	C	319	27	323	11	6.552	1.05E-02	rs9391134	6	104462307	q16.3
SNP_A-1925071	G	G	343	25	351	13	3.86	4.95E-02	rs9485928	6	104628273	q16.3
SNP_A-1816926	T	T	358	6	360	16	4.358	3.68E-02	rs271854	6	105054832	q16.3
SNP_A-2219789	T	T	390	0	388	4	4	4.55E-02	rs7767928	6	105151951	q21
SNP_A-1826131	A	A	285	65	283	33	8.743	3.10E-03	rs9386426	6	105272060	q21
SNP_A-1876903	T	T	288	52	288	30	5.173	0.0229	rs221636	6	105636657	q21
SNP_A-2211778	T	T	334	10	345	3	3.924	4.76E-02	rs1211490	6	105864431	q21
SNP_A-1644142	C	C	366	32	360	52	4.571	3.25E-02	rs2202766	6	106283075	q21
SNP_A-1830032	C	C	409	7	414	0	7.026	8.00E-03	rs9399952	6	106421512	q21
SNP_A-2027212	C	T	204	200	235	175	4.991	2.55E-02	rs1040411	6	106704716	q21
SNP_A-1987135	G	G	354	4	368	0	4.135	4.20E-02	rs17066840	6	106898902	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2267396	C	C	238	144	259	103	7.161	7.50E-03	rs4946748	6	106952368	q21
SNP_A-2107106	C	C	230	146	264	116	5.754	1.64E-02	rs987377	6	106967405	q21
SNP_A-1987142	G	G	244	160	266	120	6.256	0.0124	rs2066199	6	106974406	q21
SNP_A-1987146	C	C	394	10	382	2	5.015	2.51E-02	rs17067219	6	107092513	q21
SNP_A-1650902	T	T	390	10	410	2	5.657	1.74E-02	rs10485221	6	107190951	q21
SNP_A-2275479	A	A	328	24	360	12	4.94	2.62E-02	rs1970594	6	107249814	q21
SNP_A-1858556	A	A	358	0	354	4	4.022	4.49E-02	rs11153025	6	107322606	q21
SNP_A-2089002	C	C	373	33	362	52	4.334	3.74E-02	rs3734677	6	107639958	q21
SNP_A-2031360	G	G	253	123	209	161	9.227	2.40E-03	rs4945779	6	107969771	q21
SNP_A-2049429	G	G	294	30	287	49	4.437	3.52E-02	rs9398133	6	107972837	q21
SNP_A-1929783	G	G	230	130	179	147	5.732	0.0167	rs7762852	6	107973208	q21
SNP_A-1645322	C	C	375	23	406	6	10.957	9.00E-04	rs1028498	6	108020648	q21
SNP_A-1935979	C	C	416	0	410	4	4.039	4.45E-02	rs17068356	6	108027947	q21
SNP_A-2231740	G	G	402	0	407	5	4.909	2.67E-02	rs17068371	6	108031503	q21
SNP_A-1987167	C	C	280	118	303	91	4.375	3.65E-02	rs9373956	6	108035718	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2245622	T	T	379	17	395	5	6.856	8.80E-03	rs846973	6	108059503	q21
SNP_A-1922127	A	A	381	15	403	5	5.439	1.97E-02	rs3800209	6	108077755	q21
SNP_A-2141388	C	C	377	25	392	6	11.918	6.00E-04	rs1728109	6	108082425	q21
SNP_A-2248667	A	A	396	20	404	8	5.204	2.25E-02	rs12665132	6	108088690	q21
SNP_A-1906815	G	G	394	16	414	6	4.921	2.65E-02	rs4945782	6	108089658	q21
SNP_A-2030916	C	C	382	16	371	33	6.014	1.42E-02	rs4083443	6	108135535	q21
SNP_A-2220754	A	A	323	87	288	108	4.024	0.0448	rs1624055	6	108137098	q21
SNP_A-1987176	T	T	325	89	354	64	5.304	2.13E-02	rs9320231	6	108176932	q21
SNP_A-2178524	A	A	248	78	279	57	4.94	2.62E-02	rs9373971	6	108185502	q21
SNP_A-1987177	A	A	293	75	334	56	4.802	2.84E-02	rs12660169	6	108185714	q21
SNP_A-1987178	G	G	326	90	355	65	5.248	2.20E-02	rs12663083	6	108185814	q21
SNP_A-1733760	G	G	359	17	398	6	6.273	0.0123	rs10484905	6	108387765	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181295	A	A	374	8	399	1	5.842	1.57E-02	rs6931135	6	108428014	q21
SNP_A-1895575	G	G	342	74	366	54	3.92	4.77E-02	rs4946889	6	108439070	q21
SNP_A-2209945	C	C	379	23	399	7	9.028	2.70E-03	rs6900313	6	108464848	q21
SNP_A-2124389	T	T	235	171	191	187	4.265	3.89E-02	rs1537862	6	108796849	q21
SNP_A-1987189	T	T	380	36	396	20	4.901	2.68E-02	rs4946938	6	109127327	q21
SNP_A-2086638	A	A	326	68	309	95	4.803	2.84E-02	rs541020	6	109190725	q21
SNP_A-2059510	T	T	269	79	247	113	6.757	9.30E-03	rs472656	6	109222040	q21
SNP_A-2249554	T	T	320	62	357	43	5.049	0.0246	rs7767017	6	109626615	q21
SNP_A-2219942	G	G	390	4	388	0	3.959	4.66E-02	rs9386835	6	110135655	q21
SNP_A-1904470	A	A	280	100	267	67	3.882	4.88E-02	rs11968978	6	110203589	q21
SNP_A-2156198	C	C	355	57	339	79	3.885	0.0487	rs9487321	6	110662094	q21
SNP_A-2125608	A	A	380	4	378	0	3.958	4.66E-02	---	6	110866014	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1987220	C	T	216	162	204	194	5.488	1.91E-02	rs1989634	6	110952941	q21
SNP_A-2163774	G	G	355	15	328	34	8.348	3.90E-03	rs7746477	6	110960661	q21
SNP_A-1894972	T	T	361	19	325	43	10.99	9.00E-04	rs739516	6	110971876	q21
SNP_A-1869241	C	C	386	22	356	44	8.468	3.60E-03	rs17807032	6	111629316	q21
SNP_A-2193743	A	A	335	77	366	52	6.173	1.30E-02	rs17756732	6	111686847	q21
SNP_A-2268014	T	T	339	77	368	52	6.015	1.42E-02	rs12196873	6	111704751	q21
SNP_A-2254158	C	C	318	50	359	25	10.481	1.20E-03	rs12195578	6	111721479	q21
SNP_A-2302568	A	A	313	47	354	32	4.468	3.45E-02	rs12203741	6	111784237	q21
SNP_A-2130194	C	C	328	80	361	53	7.018	8.10E-03	rs12198788	6	111793484	q21
SNP_A-2238073	C	C	336	60	359	39	5.211	0.0224	rs174407	6	112038380	q21
SNP_A-1744387	T	T	382	18	404	8	4.286	3.84E-02	rs1409836	6	112214920	q21
SNP_A-1755228	C	C	371	19	393	9	4.024	4.49E-02	rs910683	6	112228857	q21
SNP_A-1911502	T	T	324	6	301	17	5.887	1.53E-02	rs526479	6	112365613	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1821822	A	A	362	48	379	31	4.048	4.42E-02	rs3752577	6	112586734	q21
SNP_A-2122519	T	T	342	16	354	38	7.644	5.70E-03	rs9487891	6	112756363	q21
SNP_A-2192595	C	C	364	14	398	4	6.34	0.0118	rs9400538	6	112787113	q21
SNP_A-1676568	C	C	344	52	333	79	5.429	1.98E-02	rs10499071	6	113223872	q21
SNP_A-1734610	T	T	344	54	328	76	4.059	4.39E-02	rs10499070	6	113226776	q21
SNP_A-1726428	T	T	357	43	347	65	4.447	3.50E-02	rs9320420	6	113230262	q21
SNP_A-2164004	G	G	322	26	322	12	4.873	2.73E-02	rs2795582	6	113367736	q21
SNP_A-1728497	C	C	223	173	259	151	3.941	4.71E-02	rs2185710	6	113422618	q21
SNP_A-1676346	C	C	219	181	256	154	4.936	0.0263	rs2502397	6	113507949	q21
SNP_A-1932568	A	A	232	78	264	56	5.519	1.88E-02	rs6568760	6	113535478	q21
SNP_A-2245695	G	G	191	163	230	132	6.782	9.20E-03	rs1922941	6	113583484	q21
SNP_A-2202090	C	C	207	135	233	109	4.307	3.80E-02	rs2473965	6	113586818	q21
SNP_A-2193912	C	C	219	167	241	133	4.717	2.99E-02	rs1406832	6	113587620	q21
SNP_A-1987271	T	T	391	13	379	25	3.976	4.61E-02	rs1474789	6	113598076	q21
SNP_A-1731005	G	G	276	118	320	92	6.068	0.0138	rs2637524	6	113637838	q21
SNP_A-2290928	C	C	366	44	385	25	5.713	1.68E-02	rs9488125	6	113694427	q21
SNP_A-1847204	T	T	236	90	283	71	5.355	0.0207	rs7760762	6	113700746	q21
SNP_A-1939646	G	G	287	117	317	85	6.554	1.05E-02	rs9942437	6	113747826	q21
SNP_A-1822183	G	G	284	110	309	73	8.351	3.90E-03	rs1937239	6	113751575	q21
SNP_A-2076857	G	G	373	43	397	21	8.306	4.00E-03	rs6932656	6	113760205	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1799018	C	C	312	60	329	35	6.944	8.40E-03	rs11756338	6	113914635	q21
SNP_A-1879172	C	C	214	122	269	105	5.518	1.88E-02	rs9384878	6	114081811	q21
SNP_A-2154793	T	T	402	14	389	29	5.441	1.97E-02	rs17075386	6	114131902	q21
SNP_A-2261587	A	A	306	38	320	18	7.404	6.50E-03	rs538681	6	114360795	q21
SNP_A-2061118	C	C	241	91	258	64	5.131	0.0235	rs9400760	6	115254086	q22.1
SNP_A-1800015	G	G	363	21	369	7	6.966	8.30E-03	rs4348350	6	115296668	q22.1
SNP_A-2079233	G	G	383	19	397	7	5.785	1.62E-02	rs4245477	6	115320345	q22.1
SNP_A-1876538	T	T	391	25	402	10	6.562	0.0104	rs7747918	6	115382998	q22.1
SNP_A-2276723	G	G	243	129	202	154	5.637	1.76E-02	rs1034437	6	115446747	q22.1
SNP_A-2261430	T	T	291	125	257	159	6.18	0.0129	rs17834507	6	115453039	q22.1
SNP_A-1902243	A	A	277	127	307	101	4.486	3.42E-02	rs371324	6	115454194	q22.1
SNP_A-2064194	A	A	282	128	311	97	5.684	1.71E-02	rs396666	6	115456235	q22.1
SNP_A-2200746	G	G	248	112	180	138	10.948	9.00E-04	rs732060	6	115564109	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1921546	T	T	252	98	207	121	6.12	0.0134	rs2017590	6	115564661	q22.1
SNP_A-2247211	T	T	336	70	354	48	4.552	3.29E-02	rs17164603	6	115569492	q22.1
SNP_A-2094995	C	C	239	159	270	134	3.976	4.61E-02	rs1548305	6	115715535	q22.1
SNP_A-1645592	A	A	274	124	247	161	6.08	0.0137	rs2350791	6	115834371	q22.1
SNP_A-1739229	A	A	306	94	342	70	5.336	2.09E-02	rs10484297	6	115837804	q22.1
SNP_A-1692724	G	G	261	109	248	158	7.671	5.60E-03	rs2001149	6	115851794	q22.1
SNP_A-1754474	T	T	312	88	349	61	6.841	8.90E-03	rs9320535	6	115851883	q22.1
SNP_A-1987312	G	G	265	83	294	54	7.643	5.70E-03	rs10484296	6	115918822	q22.1
SNP_A-2267356	T	T	318	88	341	57	7.351	6.70E-03	rs12216142	6	115939103	q22.1
SNP_A-2261003	C	C	245	65	282	44	6.245	1.25E-02	rs6940372	6	115980726	q22.1
SNP_A-2287095	G	G	372	22	393	11	4.118	0.0424	rs7754247	6	116031725	q22.1
SNP_A-2162957	T	T	371	41	357	21	5.267	2.17E-02	rs6568910	6	116047349	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814558	C	C	254	86	251	55	5.058	2.45E-02	rs4266518	6	116081988	q22.1
SNP_A-2110956	C	C	404	10	415	3	3.898	4.83E-02	rs9488770	6	116188945	q22.1
SNP_A-1859375	G	G	274	96	268	134	5.027	2.50E-02	rs9387369	6	116237379	q22.1
SNP_A-1987323	C	C	266	142	295	117	3.893	4.85E-02	rs3777425	6	116385510	q22.1
SNP_A-2206583	T	T	227	119	260	98	4.065	4.38E-02	rs9387379	6	116397042	q22.1
SNP_A-1850499	T	T	299	85	294	116	3.976	4.61E-02	rs1193609	6	116405172	q22.1
SNP_A-2157055	T	T	371	1	342	6	3.955	4.67E-02	rs6568930	6	116735608	q22.1
SNP_A-1799422	A	A	371	45	348	70	6.166	1.30E-02	rs17078051	6	116973642	q22.1
SNP_A-1749847	G	G	323	71	357	53	3.996	4.56E-02	rs1321364	6	117309777	q22.1
SNP_A-1758637	G	A	215	181	215	193	3.927	4.75E-02	rs9320589	6	117396473	q22.1
SNP_A-2171300	T	C	165	157	180	130	5.496	1.91E-02	rs1321365	6	117408307	q22.1
SNP_A-1691788	G	T	212	188	223	189	4.123	4.23E-02	rs1605598	6	117424375	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1857403	A	A	302	100	329	75	4.722	0.0298	rs17291964	6	117454068	q22.1
SNP_A-1843178	A	A	341	61	368	38	6.352	0.0117	rs498251	6	117745959	q22.1
SNP_A-1918054	C	C	380	36	366	54	3.844	0.0499	rs13204089	6	117828154	q22.1
SNP_A-2129365	C	C	222	96	241	73	3.885	0.0487	rs6930292	6	117890463	q22.1
SNP_A-1919348	A	A	353	55	330	76	4.136	4.20E-02	rs17336166	6	118611443	q22.31
SNP_A-2127786	T	T	411	5	418	0	5.054	0.0246	rs1150119	6	118623191	q22.31
SNP_A-2076028	T	T	372	2	356	10	5.599	1.80E-02	rs12207554	6	118967398	q22.31
SNP_A-2094603	G	G	247	135	204	162	6.215	1.27E-02	rs6569031	6	119298438	q22.31
SNP_A-2097956	G	G	259	119	220	148	6.192	1.28E-02	rs7381535	6	119303974	q22.31
SNP_A-2133603	T	T	330	84	305	113	5.234	2.21E-02	rs954753	6	119405675	q22.31
SNP_A-1645344	C	C	345	35	342	58	5.192	2.27E-02	rs9320678	6	119410802	q22.31
SNP_A-2039050	C	C	298	44	329	29	4.251	3.92E-02	rs3819723	6	119549306	q22.31
SNP_A-1723430	T	C	225	175	208	202	3.959	4.66E-02	rs2357524	6	119866904	q22.31
SNP_A-2245832	G	G	306	98	346	64	9.546	0.002	rs17081398	6	119907626	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1824713	A	A	260	140	293	111	5.3	2.13E-02	rs8180610	6	119909548	q22.31
SNP_A-1910350	G	G	309	101	346	64	10.387	1.30E-03	rs7741053	6	119910529	q22.31
SNP_A-1987408	G	G	307	105	338	70	8.471	3.60E-03	rs17081419	6	119913919	q22.31
SNP_A-2229525	A	A	412	4	416	0	4.019	4.50E-02	rs17081421	6	119914750	q22.31
SNP_A-1987410	C	C	272	140	309	111	5.63	0.0177	rs6905827	6	119927180	q22.31
SNP_A-1669603	A	A	224	140	201	177	5.301	2.13E-02	rs807311	6	119938834	q22.31
SNP_A-1987411	C	C	266	128	296	90	8.144	0.0043	rs12206925	6	119956849	q22.31
SNP_A-1755960	C	C	305	93	338	72	4.189	0.0407	rs1986402	6	120071833	q22.31
SNP_A-2261546	C	C	271	71	293	49	4.891	0.027	rs1417843	6	120079896	q22.31
SNP_A-1735717	T	T	310	90	346	66	5.492	1.91E-02	rs10499093	6	120088136	q22.31
SNP_A-1678784	T	T	251	149	294	118	6.816	9.00E-03	rs7751642	6	120122757	q22.31
SNP_A-2260720	T	T	256	90	286	64	6.027	0.0141	rs10872185	6	120128132	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1807810	T	C	191	143	173	151	7.376	0.0066	rs13199160	6	120135144	q22.31
SNP_A-1842806	C	C	290	66	336	48	5.17	0.023	rs4945648	6	120135566	q22.31
SNP_A-2063913	T	T	271	57	275	35	4.786	0.0287	rs12208543	6	120160147	q22.31
SNP_A-2197640	C	C	241	135	290	108	6.902	0.0086	rs7761829	6	120176413	q22.31
SNP_A-1987413	G	G	254	144	223	181	6.182	0.0129	rs4644102	6	120183405	q22.31
SNP_A-1683586	G	G	275	111	255	157	7.811	5.20E-03	rs10499097	6	120519589	q22.31
SNP_A-2108312	A	A	344	28	369	15	4.617	3.16E-02	rs9489928	6	120648057	q22.31
SNP_A-2159158	C	C	353	25	377	11	6.104	0.0135	rs9489929	6	120648138	q22.31
SNP_A-1987423	C	C	304	90	319	65	4.266	3.89E-02	rs9387742	6	120674797	q22.31
SNP_A-2036698	A	G	217	199	231	187	4.604	3.19E-02	rs3013685	6	120685965	q22.31
SNP_A-1855712	C	C	206	138	180	176	6.146	0.0132	rs3013688	6	120687385	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1868844	A	G	214	196	226	184	4.394	0.0361	rs3013689	6	120687558	q22.31
SNP_A-2023308	G	G	376	20	390	6	7.794	5.20E-03	rs3013705	6	120714956	q22.31
SNP_A-2028950	G	G	267	133	235	157	3.946	0.047	rs12660882	6	120817325	q22.31
SNP_A-2204155	C	C	277	129	241	155	4.758	0.0292	rs1486200	6	120836788	q22.31
SNP_A-1843924	G	G	268	132	244	166	4.881	2.71E-02	rs9387798	6	120844945	q22.31
SNP_A-2086213	G	G	337	13	296	26	5.832	1.57E-02	rs4946518	6	121216502	q22.31
SNP_A-1751737	C	C	364	36	386	22	3.946	0.047	rs7747541	6	121248718	q22.31
SNP_A-1944034	A	A	411	3	396	10	3.97	4.63E-02	rs17083385	6	121660900	q22.31
SNP_A-1867957	T	T	340	2	342	10	5.196	2.26E-02	rs17083420	6	121683273	q22.31
SNP_A-1698251	T	T	291	105	323	81	4.685	0.0304	rs6569212	6	121809990	q22.31
SNP_A-2089171	G	G	366	0	343	5	5.296	2.14E-02	rs6938102	6	122017262	q22.31
SNP_A-1697525	G	G	380	18	403	5	7.901	4.90E-03	rs9388016	6	122200324	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1907385	G	G	279	47	281	27	4.905	2.68E-02	rs7772387	6	122375597	q22.31
SNP_A-2163206	T	T	324	28	337	11	7.643	5.70E-03	rs2684266	6	122403016	q22.31
SNP_A-1789208	G	G	410	0	374	4	4.361	3.68E-02	rs1402541	6	122423901	q22.31
SNP_A-1781680	G	G	394	4	404	0	4.081	4.34E-02	rs9482224	6	122483202	q22.31
SNP_A-2129107	G	G	237	117	275	87	7.144	7.50E-03	rs13197292	6	122568286	q22.31
SNP_A-1753737	C	C	259	141	299	111	6.316	0.012	rs536165	6	122600891	q22.31
SNP_A-2291916	A	A	261	135	295	101	6.977	8.30E-03	rs225086	6	122640068	q22.31
SNP_A-2288619	T	T	270	142	304	108	6.638	0.01	rs2066121	6	122651575	q22.31
SNP_A-1800633	A	A	246	112	282	88	5.138	2.34E-02	rs9375170	6	123082761	q22.31
SNP_A-2252809	T	T	312	82	278	106	4.895	0.0269	rs9490546	6	123120336	q22.31
SNP_A-2012031	G	A	182	138	174	168	3.987	0.0458	rs6569294	6	123224719	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1809566	A	A	251	161	284	134	4.464	3.46E-02	rs9490571	6	123233573	q22.31
SNP_A-2310466	C	C	237	119	209	143	3.934	4.73E-02	rs6569311	6	123309683	q22.31
SNP_A-2195133	A	A	250	162	280	134	4.342	3.72E-02	rs4591879	6	123395622	q22.31
SNP_A-1675748	G	G	306	58	306	88	4.985	2.56E-02	rs9283099	6	123608697	q22.31
SNP_A-1828582	C	C	403	3	402	12	5.324	2.10E-02	rs4289676	6	124041002	q22.31
SNP_A-1745202	C	C	373	25	403	9	8.45	3.70E-03	rs10495162	6	124044081	q22.31
SNP_A-2115481	A	A	342	4	339	13	4.727	2.97E-02	rs9482426	6	124050618	q22.31
SNP_A-1792387	A	A	403	13	392	28	5.621	0.0177	rs7748723	6	124065206	q22.31
SNP_A-1787653	A	A	369	7	364	22	7.663	5.60E-03	rs9490880	6	124066354	q22.31
SNP_A-2157998	C	C	395	19	367	35	5.594	1.80E-02	rs184658	6	124068220	q22.31
SNP_A-1655939	G	G	363	35	394	18	6.482	0.0109	rs9320960	6	124077897	q22.31
SNP_A-1834957	C	C	362	0	329	5	5.458	0.0195	rs342639	6	124086439	q22.31
SNP_A-1987486	G	G	316	8	318	20	4.855	0.0276	---	6	124110141	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2026523	G	G	385	31	406	14	6.961	8.30E-03	rs17085994	6	124140135	q22.31
SNP_A-2277711	G	G	407	7	393	19	5.779	1.62E-02	rs9490937	6	124173325	q22.31
SNP_A-1987496	T	T	347	43	334	66	4.976	2.57E-02	rs6927822	6	124387925	q22.31
SNP_A-1731511	C	C	344	32	347	53	4.463	3.46E-02	rs2552085	6	124755880	q22.31
SNP_A-1687286	T	T	303	91	340	70	4.552	3.29E-02	rs584197	6	124781189	q22.31
SNP_A-1987510	A	A	304	94	322	66	5.291	2.14E-02	rs643630	6	124839601	q22.31
SNP_A-1800133	C	C	272	122	290	88	5.752	1.65E-02	rs628914	6	124847242	q22.31
SNP_A-1871792	T	T	251	89	269	63	4.976	2.57E-02	rs594401	6	124905860	q22.31
SNP_A-2171877	T	C	196	172	195	165	4.016	4.51E-02	rs1415766	6	125102415	q22.31
SNP_A-2235341	G	G	245	81	242	120	5.718	1.68E-02	rs1741748	6	125541811	q22.31
SNP_A-2012054	T	T	307	97	280	122	4.091	4.31E-02	rs3807003	6	125544698	q22.31
SNP_A-2155305	T	T	385	27	407	9	9.592	0.002	rs17053071	6	125713650	q22.31
SNP_A-1987536	C	C	341	75	320	100	4.22	4.00E-02	rs4896986	6	125845658	q22.31
SNP_A-2141074	T	T	377	27	370	44	4.014	4.51E-02	rs6941500	6	125852409	q22.31
SNP_A-1870247	C	C	216	140	228	106	4.326	3.75E-02	rs7758956	6	125918519	q22.31
SNP_A-1691298	T	T	364	36	354	56	4.364	3.67E-02	rs481233	6	126146035	q22.32
SNP_A-1824103	C	C	412	4	420	0	4.058	4.40E-02	rs3813375	6	126160587	q22.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798849	C	C	263	141	289	113	4.306	3.80E-02	rs6569440	6	126219137	q22.32
SNP_A-2263398	C	C	312	28	292	44	4.194	4.06E-02	rs9482716	6	126287337	q22.32
SNP_A-2282339	G	T	189	183	203	151	4.84	2.78E-02	rs4897168	6	126413481	q22.32
SNP_A-2246896	T	T	231	171	278	128	10.504	1.20E-03	rs6569510	6	127962618	q22.33
SNP_A-2314556	C	C	193	171	244	118	15.666	7.56E-05	rs11154421	6	127977700	q22.33
SNP_A-1859959	G	G	243	151	205	177	5.1	2.39E-02	rs583072	6	128056908	q22.33
SNP_A-1698753	A	A	249	133	222	182	8.561	3.40E-03	rs270015	6	128074072	q22.33
SNP_A-1946345	T	T	334	72	361	45	7.28	7.00E-03	rs7744896	6	128103306	q22.33
SNP_A-1742561	G	G	372	26	397	11	6.771	9.30E-03	rs9209992	6	128109950	q22.33
SNP_A-2043850	T	T	387	25	406	10	6.865	8.80E-03	rs12193548	6	128141830	q22.33
SNP_A-1899852	G	G	329	61	359	39	6.068	0.0138	rs7768836	6	128168215	q22.33
SNP_A-1874514	C	C	230	132	204	160	4.237	3.96E-02	rs6921729	6	128190682	q22.33
SNP_A-2066579	A	A	392	4	404	0	4.101	4.28E-02	rs4897235	6	128259998	q22.33
SNP_A-1872786	G	G	371	19	389	9	3.917	4.78E-02	rs809709	6	128306697	q22.33
SNP_A-1868919	G	G	340	68	313	91	4.424	3.54E-02	rs17461290	6	128870929	q22.33
SNP_A-1677734	G	G	396	4	412	0	4.14	0.0419	rs265355	6	129520594	q22.33
SNP_A-1648970	G	G	396	4	412	0	4.14	0.0419	rs265354	6	129520684	q22.33
SNP_A-1681738	C	C	396	4	412	0	4.14	0.0419	rs265353	6	129520718	q22.33
SNP_A-2128122	C	C	363	23	371	11	4.302	3.81E-02	rs3798662	6	129676119	q22.33
SNP_A-2041536	G	G	264	112	242	140	4.02	4.50E-02	rs9375652	6	130023699	q22.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2196801	A	A	354	26	353	13	4.073	0.0436	rs11154491	6	130053359	q22.33
SNP_A-1933997	T	T	379	23	341	37	4.538	3.31E-02	rs1041915	6	130055946	q22.33
SNP_A-2149950	C	C	371	25	362	12	4.053	0.0441	rs2066685	6	130071532	q22.33
SNP_A-2247425	T	T	359	15	365	31	4.99	2.55E-02	rs17470157	6	130108670	q22.33
SNP_A-1797209	T	T	248	112	274	78	7.29	6.90E-03	rs4458716	6	130193989	q22.33
SNP_A-2082628	G	G	249	109	278	84	4.812	2.83E-02	rs2326873	6	130195239	q22.33
SNP_A-1906851	T	T	339	13	369	5	4.164	4.13E-02	rs9321195	6	130217597	q22.33
SNP_A-2259075	G	G	400	6	418	0	6.223	0.0126	rs9388747	6	130235245	q22.33
SNP_A-1824019	T	T	228	156	186	180	5.546	1.85E-02	rs7759872	6	130248767	q22.33
SNP_A-2314684	C	C	272	130	239	153	3.875	4.90E-02	rs17058152	6	130279787	q22.33
SNP_A-1877552	G	A	235	175	206	202	5.009	0.0252	rs6902109	6	130358252	q22.33
SNP_A-1950244	A	A	288	118	259	147	4.711	3.00E-02	rs9375695	6	130400637	q23.1
SNP_A-2292637	A	A	237	97	224	140	6.892	8.70E-03	rs9388769	6	130421647	q23.1
SNP_A-1828144	A	A	414	2	411	9	4.446	3.50E-02	rs6908750	6	130946822	q23.1
SNP_A-1920980	C	C	376	10	398	2	5.711	1.69E-02	rs9402289	6	131190179	q23.1
SNP_A-1686282	C	C	372	24	360	50	9.091	2.60E-03	rs10499182	6	131473979	q23.2
SNP_A-2259055	T	T	374	22	366	40	5.188	2.27E-02	rs17787339	6	131515054	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1733114	A	A	339	19	371	9	4.362	3.68E-02	rs6935095	6	131717181	q23.2
SNP_A-1748367	C	C	367	29	387	11	8.626	0.0033	rs983502	6	131722810	q23.2
SNP_A-1917306	G	G	365	43	380	18	10.425	1.20E-03	rs17060727	6	132131968	q23.2
SNP_A-1916917	C	C	365	41	389	23	5.783	1.62E-02	rs17060759	6	132137998	q23.2
SNP_A-1818867	G	G	322	34	287	55	6.688	9.70E-03	rs1931004	6	132304007	q23.2
SNP_A-1819906	G	G	204	200	241	165	6.428	0.0112	rs12527379	6	132321533	q23.2
SNP_A-2152241	G	G	338	54	313	79	5.659	1.74E-02	rs9375854	6	132343988	q23.2
SNP_A-1987684	A	A	275	131	232	172	9.19	2.40E-03	rs170881	6	132358254	q23.2
SNP_A-2042610	T	T	252	148	212	192	9.123	2.50E-03	rs403374	6	132370642	q23.2
SNP_A-2159068	C	C	240	116	208	164	10.168	0.0014	rs412319	6	132370911	q23.2
SNP_A-1724718	T	T	359	33	353	55	5.233	2.22E-02	rs723071	6	132400420	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308112	G	G	220	172	244	136	5.264	0.0218	rs1206734	6	132404651	q23.2
SNP_A-2249036	A	A	365	33	353	55	5.577	1.82E-02	rs6916800	6	132442819	q23.2
SNP_A-1816686	G	G	331	37	302	56	5.074	2.43E-02	rs1406930	6	132590197	q23.2
SNP_A-2266360	A	A	389	21	381	39	5.363	0.0206	rs17718841	6	132653145	q23.2
SNP_A-2042353	C	C	321	67	305	91	3.973	4.62E-02	rs17637818	6	132700249	q23.2
SNP_A-2012086	A	A	283	39	257	69	9.561	0.002	rs7761051	6	132718658	q23.2
SNP_A-1741807	T	T	367	33	356	56	5.935	1.48E-02	rs2282315	6	132757304	q23.2
SNP_A-2311891	C	C	287	85	290	56	5.045	0.0247	rs9483454	6	132825558	q23.2
SNP_A-1987697	A	A	243	95	288	76	4.969	0.0258	rs9321344	6	132834878	q23.2
SNP_A-1960438	G	G	298	114	328	88	4.765	2.90E-02	rs9483463	6	132846845	q23.2
SNP_A-2307350	A	A	358	28	352	46	4.246	3.93E-02	rs2842892	6	132856076	q23.2
SNP_A-1788711	G	G	217	137	247	109	5.121	2.36E-02	rs2842904	6	132881158	q23.2
SNP_A-1955528	C	C	289	17	316	8	3.934	4.73E-02	rs7744878	6	132943213	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1832441	G	G	254	118	231	149	4.605	3.19E-02	rs9402461	6	133206135	q23.2
SNP_A-2012088	A	A	347	53	377	31	6.926	8.50E-03	rs4895946	6	133278544	q23.2
SNP_A-2237754	A	A	290	58	330	34	8.486	3.60E-03	rs7763318	6	133282476	q23.2
SNP_A-2024710	A	A	352	60	375	33	8.547	3.50E-03	rs7745773	6	133282629	q23.2
SNP_A-1822851	T	T	302	50	354	30	7.745	5.40E-03	rs7383689	6	133284825	q23.2
SNP_A-2040110	G	G	213	149	184	182	5.387	2.03E-02	rs271129	6	133287227	q23.2
SNP_A-2133031	T	T	303	73	351	57	4.193	4.06E-02	rs6912746	6	133298188	q23.2
SNP_A-2030440	T	C	198	160	211	191	4.605	3.19E-02	rs6904471	6	133309096	q23.2
SNP_A-2265365	C	C	341	67	358	42	6.069	0.0138	rs17301249	6	133654607	q23.2
SNP_A-1918818	G	G	243	129	263	101	4.113	4.26E-02	rs1343867	6	133675043	q23.2
SNP_A-1987737	T	T	271	109	242	144	6.435	0.0112	rs1414668	6	134149753	q23.2
SNP_A-2096052	C	C	279	77	239	101	5.96	0.0146	rs6909803	6	134152891	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1657820	G	G	343	53	372	32	6.285	1.22E-02	rs1208261	6	134173413	q23.2
SNP_A-1926992	G	G	311	89	266	116	6.655	9.90E-03	rs7752775	6	134214039	q23.2
SNP_A-2183755	C	C	274	86	232	108	5.414	0.02	rs17062991	6	134235603	q23.2
SNP_A-1941510	A	A	351	53	371	35	4.231	3.97E-02	rs7738638	6	134433066	q23.2
SNP_A-1893151	C	C	212	132	249	107	5.381	2.04E-02	rs374522	6	134690107	q23.2
SNP_A-1663882	C	A	170	142	188	160	4.766	2.90E-02	rs2223995	6	134916334	q23.2
SNP_A-2260941	A	A	284	54	262	28	5.494	1.91E-02	rs9483723	6	134948360	q23.2
SNP_A-2080760	C	C	395	9	390	2	4.306	3.80E-02	rs9321466	6	135021676	q23.2
SNP_A-1878573	C	C	374	24	379	11	4.781	2.88E-02	rs9494087	6	135205436	q23.3
SNP_A-2237319	T	T	278	106	314	84	4.487	3.41E-02	rs1040806	6	135217869	q23.3
SNP_A-2180065	G	G	192	150	216	124	3.873	4.91E-02	rs9402661	6	135239809	q23.3
SNP_A-1744439	A	A	235	163	212	196	4.093	4.31E-02	rs6931735	6	135605381	q23.3
SNP_A-1823877	A	A	330	12	330	2	6.996	8.20E-03	—	6	135772002	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2154460	T	T	388	22	401	11	3.876	4.90E-02	rs6901981	6	135935247	q23.3
SNP_A-2115714	C	C	331	3	333	11	4.431	3.53E-02	rs9376153	6	136182844	q23.3
SNP_A-1955970	T	T	246	124	287	103	4.573	3.25E-02	rs2327671	6	136267519	q23.3
SNP_A-1926184	G	G	238	106	194	142	9.615	0.0019	rs11154829	6	136289621	q23.3
SNP_A-2066687	G	G	222	134	196	162	4.26	0.039	rs4896187	6	136323537	q23.3
SNP_A-1899653	C	C	391	1	386	10	7.376	0.0066	rs7740905	6	137545221	q23.3
SNP_A-1830546	C	C	382	4	376	14	5.583	1.81E-02	rs6570140	6	137545290	q23.3
SNP_A-2095264	A	A	242	120	227	161	5.567	0.0183	rs632535	6	137995375	q23.3
SNP_A-1852707	C	C	291	115	318	88	4.788	0.0287	rs17066662	6	138002706	q23.3
SNP_A-2149841	G	G	277	87	310	68	3.921	4.77E-02	rs13207033	6	138007111	q23.3
SNP_A-1899538	C	C	362	46	370	28	4.342	3.72E-02	rs11961920	6	138162747	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2132242	G	G	354	36	337	59	5.941	1.48E-02	rs17780429	6	138264281	q23.3
SNP_A-2136659	A	A	322	24	326	10	5.644	1.75E-02	rs1509683	6	138561622	q23.3
SNP_A-1959180	C	T	208	200	228	166	6.306	0.012	rs4321841	6	139118463	q24.1
SNP_A-1802172	A	G	210	198	240	164	9.666	0.0019	rs7746731	6	139149842	q24.1
SNP_A-2012120	C	C	313	97	335	61	8.709	3.20E-03	rs7773485	6	139154791	q24.1
SNP_A-1987852	C	C	277	95	303	73	4.025	0.0448	rs1474963	6	139157575	q24.1
SNP_A-2263771	T	T	299	105	333	83	4.229	3.97E-02	rs10457678	6	139163933	q24.1
SNP_A-1987853	T	T	294	94	325	65	6.837	8.90E-03	rs9321674	6	139164034	q24.1
SNP_A-1783021	T	T	255	149	283	115	5.791	0.0161	rs11155010	6	139184093	q24.1
SNP_A-1956819	A	A	258	156	290	130	4.189	0.0407	rs10872493	6	139189114	q24.1
SNP_A-2193263	G	G	306	16	320	4	7.507	6.10E-03	rs17067944	6	139195127	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1825607	A	A	291	87	271	115	4.51	3.37E-02	rs4133172	6	139428403	q24.1
SNP_A-1707285	G	G	274	112	249	139	4.094	4.30E-02	rs2327935	6	139471663	q24.1
SNP_A-1753753	G	G	251	149	225	187	5.542	1.86E-02	rs7745259	6	139480705	q24.1
SNP_A-2068863	T	T	261	143	224	172	5.413	0.02	rs6927118	6	139483775	q24.1
SNP_A-2302263	A	A	326	38	309	61	5.75	1.65E-02	rs2498678	6	139508203	q24.1
SNP_A-2060167	T	T	266	110	221	141	7.724	5.40E-03	rs3777672	6	139535705	q24.1
SNP_A-1838567	T	T	224	132	198	174	7.018	8.10E-03	rs9484242	6	139543901	q24.1
SNP_A-1987873	C	C	293	115	251	145	6.527	0.0106	rs7750538	6	139551903	q24.1
SNP_A-1925011	T	C	205	139	163	145	10.236	0.0014	rs12191514	6	139554294	q24.1
SNP_A-2308658	T	T	316	94	288	122	4.928	0.0264	rs9373237	6	139758634	q24.1
SNP_A-1829104	T	C	188	186	232	144	10.888	0.001	rs12215895	6	139771371	q24.1
SNP_A-1803524	T	T	233	133	207	163	4.555	3.28E-02	rs11155066	6	139773282	q24.1
SNP_A-1951800	C	C	219	193	248	164	4.157	4.15E-02	rs634869	6	139873450	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1654875	G	G	395	5	410	0	5.157	2.32E-02	rs10484811	6	140211652	q24.1
SNP_A-1664928	A	A	319	81	297	113	5.942	1.48E-02	rs590585	6	140212050	q24.1
SNP_A-1649854	T	T	211	183	248	162	3.944	0.047	rs6916580	6	140907038	q24.1
SNP_A-1805933	C	C	242	106	225	135	3.906	4.81E-02	rs9484448	6	141260753	q24.1
SNP_A-2097840	T	T	356	32	313	49	5.437	1.97E-02	rs1563051	6	141499055	q24.1
SNP_A-1726726	T	T	274	112	256	142	3.972	4.63E-02	rs6570450	6	141512970	q24.1
SNP_A-1814199	T	T	313	59	277	79	4.746	2.94E-02	rs9385969	6	141967156	q24.1
SNP_A-1856286	T	T	238	82	251	57	4.614	3.17E-02	rs2064480	6	142176343	q24.1
SNP_A-2109561	C	C	244	48	323	39	4.497	0.0339	rs4407737	6	142419393	q24.1
SNP_A-1696998	T	T	231	163	201	189	3.983	4.59E-02	rs1319584	6	142581133	q24.2
SNP_A-2086829	C	C	319	39	312	70	8.124	4.40E-03	rs702294	6	142927644	q24.2
SNP_A-2192700	G	G	391	25	377	41	4.129	4.21E-02	rs519740	6	143077753	q24.2
SNP_A-1665658	G	G	292	108	328	76	7.636	5.70E-03	rs126343	6	143082233	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082994	T	T	320	4	293	15	7.157	7.50E-03	rs639901	6	143093544	q24.2
SNP_A-1742833	C	C	378	14	370	34	8.24	4.10E-03	rs185588	6	143154568	q24.2
SNP_A-1987927	T	T	251	153	276	124	4.202	4.04E-02	rs550149	6	143160779	q24.2
SNP_A-1917324	C	C	222	192	261	155	7.09	7.80E-03	rs561642	6	143169811	q24.2
SNP_A-2111456	A	A	396	18	366	44	12.065	5.00E-04	rs198664	6	143194187	q24.2
SNP_A-1745450	G	G	345	55	376	36	5.124	2.36E-02	rs3804526	6	143364806	q24.2
SNP_A-1655877	T	T	345	55	374	36	5.014	2.51E-02	rs3804527	6	143364828	q24.2
SNP_A-2163664	A	A	281	75	265	101	4.172	4.11E-02	rs199245	6	143379239	q24.2
SNP_A-2250609	G	A	183	167	204	146	7.851	5.10E-03	rs200153	6	143479138	q24.2
SNP_A-1758423	T	T	385	15	408	4	6.86	8.80E-03	rs742378	6	143698594	q24.2
SNP_A-1830901	G	G	244	132	214	158	4.275	3.87E-02	rs2216917	6	143718999	q24.2
SNP_A-1918013	T	T	244	134	227	173	4.95	2.61E-02	rs7760341	6	143719024	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1921912	A	A	298	14	313	5	4.575	3.24E-02	rs6937122	6	143736536	q24.2
SNP_A-1923704	C	C	395	17	410	4	8.322	3.90E-03	rs7760371	6	143753945	q24.2
SNP_A-1835901	C	C	247	107	227	139	4.808	2.83E-02	rs223586	6	143760971	q24.2
SNP_A-2067875	A	A	339	61	367	33	9.451	2.10E-03	rs223590	6	143766211	q24.2
SNP_A-1705275	C	C	284	104	319	83	4.143	4.18E-02	rs10484803	6	143896247	q24.2
SNP_A-2139775	G	G	294	28	300	14	4.627	0.0315	rs17072766	6	143913383	q24.2
SNP_A-2188723	A	A	363	21	365	9	4.674	3.06E-02	rs2047	6	144194971	q24.2
SNP_A-2012137	G	G	319	71	347	49	5.165	0.023	rs1998017	6	144358817	q24.2
SNP_A-1745826	C	C	227	143	223	189	4.165	4.13E-02	rs681854	6	144581903	q24.2
SNP_A-1750937	C	C	257	113	232	148	5.839	1.57E-02	rs926397	6	144612769	q24.2
SNP_A-1706345	A	A	255	145	229	181	5.249	2.20E-02	rs951573	6	144926400	q24.2
SNP_A-1666026	T	T	349	27	346	48	5.475	1.93E-02	rs10499239	6	145195522	q24.2
SNP_A-1987968	A	A	393	1	372	10	7.756	5.40E-03	rs9484926	6	145306251	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1945032	T	T	390	4	378	14	5.738	0.0166	rs11969952	6	145319333	q24.2
SNP_A-1721708	C	C	299	83	284	116	5.447	1.96E-02	rs993701	6	145527234	q24.3
SNP_A-2130109	C	C	252	94	273	67	5.316	2.11E-02	rs509673	6	145622832	q24.2
SNP_A-1921940	G	G	378	26	359	53	9.64	0.0019	rs482410	6	145647522	q24.2
SNP_A-1920966	A	A	327	1	343	11	7.735	5.40E-03	rs1949031	6	145784030	q24.3
SNP_A-2050057	C	C	406	6	390	20	7.855	5.10E-03	rs9497314	6	145833464	q24.3
SNP_A-1685210	G	G	379	21	402	10	4.404	3.59E-02	rs10484860	6	146605604	q24.3
SNP_A-1987995	G	G	395	21	410	10	4.164	4.13E-02	rs1543349	6	146665031	q24.3
SNP_A-2216740	A	A	395	21	409	9	5.039	2.48E-02	rs7741271	6	146680674	q24.3
SNP_A-2279607	T	T	400	16	402	6	4.473	0.0344	rs844626	6	147940251	q24.3
SNP_A-2282922	G	G	245	155	282	124	5.998	0.0143	rs13195044	6	148506214	q24.3
SNP_A-2193744	G	G	254	152	282	122	4.742	2.94E-02	rs6936603	6	148506866	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1988045	G	G	196	174	229	143	5.589	1.81E-02	rs9322128	6	148517366	q24.3
SNP_A-2274014	G	G	372	38	392	22	4.771	2.89E-02	rs9497980	6	148604610	q24.3
SNP_A-2012152	T	T	314	102	284	132	5.351	0.0207	rs2328901	6	148817988	q24.3
SNP_A-2309569	C	C	306	88	278	120	6.245	1.25E-02	rs11155572	6	148825931	q24.3
SNP_A-1952063	A	G	213	201	236	184	4.879	2.72E-02	rs7743076	6	148829109	q24.3
SNP_A-1887892	G	G	360	4	392	0	4.331	3.74E-02	rs7748095	6	148956442	q24.3
SNP_A-1794488	C	C	356	54	377	35	4.653	0.031	rs9399673	6	149277913	q25.1
SNP_A-1988068	T	T	243	107	190	120	4.825	2.80E-02	rs2500536	6	149371182	q25.1
SNP_A-2012155	G	G	271	89	296	66	4.51	3.37E-02	rs2486419	6	149371464	q25.1
SNP_A-1858344	G	G	352	24	348	46	6.52	1.07E-02	rs9390651	6	149374827	q25.1
SNP_A-1988070	T	T	400	16	389	31	4.922	2.65E-02	rs2486416	6	149377702	q25.1
SNP_A-1988071	T	T	376	30	359	51	5.818	1.59E-02	rs2500548	6	149378047	q25.1
SNP_A-2046355	T	C	202	156	186	172	5.038	2.48E-02	rs653982	6	149573740	q25.1
SNP_A-1806529	C	C	256	108	281	77	6.309	0.012	rs17725371	6	149578616	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100263	C	T	209	197	234	176	5.985	0.0144	rs926408	6	149594280	q25.1
SNP_A-1875414	A	A	263	149	292	122	4.201	4.04E-02	rs7748981	6	149602659	q25.1
SNP_A-2114286	G	G	209	137	233	105	5.442	1.97E-02	rs9498266	6	149607212	q25.1
SNP_A-1868161	A	A	234	166	205	199	4.679	2.72E-02	rs4897103	6	149632132	q25.1
SNP_A-2032105	T	T	288	128	256	160	5.438	1.97E-02	rs597144	6	149667305	q25.1
SNP_A-2125284	G	G	264	134	243	169	4.672	3.07E-02	rs439495	6	149834917	q25.1
SNP_A-1651114	G	G	387	5	388	14	4.139	0.0419	rs952414	6	150192552	q25.1
SNP_A-1930889	C	C	368	2	329	13	9.162	2.50E-03	rs9478945	6	150256304	q25.1
SNP_A-2202346	G	G	289	125	262	154	4.333	3.74E-02	rs880245	6	150259512	q25.1
SNP_A-2078825	C	C	284	102	244	122	4.287	3.84E-02	rs4870054	6	150261652	q25.1
SNP_A-1988082	T	T	341	23	324	44	6.995	8.20E-03	rs9397053	6	150294147	q25.1
SNP_A-1835014	A	A	210	112	262	78	11.332	8.00E-04	rs6557176	6	150344410	q25.1
SNP_A-1821848	A	A	262	150	224	166	7.243	7.10E-03	rs4242288	6	150522514	q25.1
SNP_A-2069425	G	G	303	101	272	124	3.943	4.71E-02	rs6910439	6	150589294	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2048976	A	C	206	170	204	184	4.144	4.18E-02	rs11155719	6	150729591	q25.1
SNP_A-2153579	C	C	381	7	402	0	7.317	6.80E-03	rs1538484	6	150733839	q25.1
SNP_A-1935612	G	G	333	75	353	51	5.135	2.34E-02	rs1416483	6	150820676	q25.1
SNP_A-1880904	G	G	336	38	369	23	4.813	2.82E-02	rs665670	6	150826370	q25.1
SNP_A-2086573	A	A	316	40	302	60	4.267	3.89E-02	rs9480528	6	151093674	q25.1
SNP_A-1794337	C	C	280	56	316	36	6.154	1.31E-02	rs803407	6	151248441	q25.1
SNP_A-1824389	C	G	207	199	230	180	4.104	4.28E-02	rs4870007	6	151673371	q25.1
SNP_A-1642137	T	T	300	90	279	127	6.752	9.40E-03	rs3800274	6	151790183	q25.1
SNP_A-2053985	C	C	348	26	349	45	4.568	3.26E-02	rs7746473	6	151809648	q25.1
SNP_A-2105131	C	C	373	37	394	22	4.345	3.71E-02	rs3757318	6	152006227	q25.1
SNP_A-1900705	C	C	371	1	356	8	5.668	1.73E-02	rs2046211	6	152040398	q25.1
SNP_A-1662916	A	A	270	130	248	162	4.318	3.77E-02	rs1884054	6	152322557	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1988127	C	C	373	41	390	24	4.825	0.0281	rs10484863	6	152555602	q25.1
SNP_A-2081510	A	A	264	132	286	100	5.167	0.023	rs2147378	6	152632582	q25.2
SNP_A-2287886	T	T	264	78	268	112	4.126	4.22E-02	rs6905741	6	152651917	q25.2
SNP_A-2140714	C	C	280	88	289	59	5.309	0.0212	rs1999829	6	152748329	q25.2
SNP_A-2100512	T	T	330	72	349	51	4.112	4.26E-02	rs9479313	6	152836864	q25.2
SNP_A-2090345	A	A	347	65	375	43	5.524	1.88E-02	rs9397105	6	152864608	q25.2
SNP_A-2063462	G	G	295	67	306	44	4.766	2.90E-02	rs9371600	6	152882647	q25.2
SNP_A-1960717	G	G	308	56	352	40	4.569	3.26E-02	rs7751588	6	152889467	q25.2
SNP_A-1932923	C	C	313	57	268	90	10.699	1.10E-03	rs2758791	6	152978440	q25.2
SNP_A-2255961	G	G	334	78	294	116	9.986	1.60E-03	rs2623960	6	152985555	q25.2
SNP_A-2313986	G	G	336	34	303	53	5.586	1.81E-02	rs6557235	6	153031530	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2280164	G	G	298	76	265	115	9.851	1.70E-03	rs2623951	6	153055383	q25.2
SNP_A-2074836	T	T	320	96	275	121	5.794	0.0161	rs2758809	6	153055502	q25.2
SNP_A-2264771	G	G	262	88	206	114	8.722	3.10E-03	rs2800642	6	153107316	q25.2
SNP_A-1729704	T	T	284	116	253	157	7.825	5.20E-03	rs688136	6	153111052	q25.2
SNP_A-2090667	G	G	279	91	243	135	10.965	9.00E-04	rs1282555	6	153118892	q25.2
SNP_A-1905767	T	T	298	68	252	84	4.257	3.91E-02	rs2244217	6	153120017	q25.2
SNP_A-1683060	T	T	363	27	384	14	4.632	3.14E-02	rs7765062	6	153305417	q25.2
SNP_A-1677774	T	T	368	26	389	13	4.836	2.79E-02	rs10484864	6	153306316	q25.2
SNP_A-1940810	C	C	344	56	366	38	4.109	4.27E-02	rs7750861	6	153644378	q25.2
SNP_A-1932163	G	G	236	122	252	94	3.951	4.68E-02	rs9383660	6	153708637	q25.2
SNP_A-1915282	G	G	338	58	362	40	4.084	4.33E-02	rs17083982	6	153796293	q25.2
SNP_A-1703597	T	T	292	78	276	104	4.032	4.46E-02	rs558025	6	154472955	q25.2
SNP_A-1931953	C	C	294	82	327	59	5.375	2.04E-02	rs2010884	6	154550320	q25.2
SNP_A-1988215	T	T	377	1	342	6	4.042	4.44E-02	rs17085106	6	154570787	q25.2
SNP_A-1988222	C	C	283	37	294	22	3.998	4.55E-02	rs9322451	6	154614774	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238419	C	C	216	176	224	128	5.59	1.81E-02	rs790260	6	154630526	q25.2
SNP_A-2249551	G	G	280	112	233	153	10.604	1.10E-03	rs6557344	6	154775694	q25.2
SNP_A-1832586	G	G	319	81	363	53	8.379	0.0038	rs13219291	6	155424428	q25.2
SNP_A-2086734	C	C	332	24	355	11	5.461	1.94E-02	rs3749930	6	155853359	q25.3
SNP_A-2053085	C	C	349	63	380	38	7.463	0.0063	rs4870397	6	156231302	q25.3
SNP_A-2075738	A	A	217	195	248	166	4.391	0.0361	rs12191885	6	156407424	q25.3
SNP_A-2026689	T	T	192	184	210	150	3.921	4.77E-02	rs11156073	6	156412002	q25.3
SNP_A-2275335	G	G	213	165	238	134	4.552	3.29E-02	rs11156103	6	156748070	q25.3
SNP_A-2198975	T	T	346	54	362	32	5.944	1.48E-02	rs2819071	6	156961677	q25.3
SNP_A-1648068	G	G	373	27	402	10	8.721	3.10E-03	rs10499278	6	157053875	q25.3
SNP_A-1670866	A	A	372	26	403	9	9.258	0.0023	rs10499277	6	157053906	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2142622	C	C	388	22	409	7	8.269	4.00E-03	rs6911412	6	157066531	q25.3
SNP_A-2012206	C	C	386	22	409	9	5.997	0.0143	rs6916489	6	157066972	q25.3
SNP_A-2252233	A	A	369	21	350	8	4.97	0.0258	rs6919504	6	157068763	q25.3
SNP_A-2111114	G	G	355	53	335	79	5.657	1.74E-02	rs533589	6	157207904	q25.3
SNP_A-2235996	C	C	298	118	328	92	4.638	3.13E-02	rs287899	6	157258555	q25.3
SNP_A-2073558	G	G	414	0	399	5	5.155	2.32E-02	rs17088007	6	157416604	q25.3
SNP_A-2153491	G	G	288	32	296	18	3.973	4.62E-02	rs9372035	6	157427169	q25.3
SNP_A-2126119	T	T	408	0	398	4	4.08	4.34E-02	rs12663721	6	157477043	q25.3
SNP_A-1687034	A	A	323	69	308	102	6.324	1.19E-02	rs4128492	6	157677867	q25.3
SNP_A-1988288	C	C	287	87	251	113	5.654	1.74E-02	rs4708937	6	157731494	q25.3
SNP_A-1895505	T	T	292	78	282	114	6.049	1.39E-02	rs9365159	6	157995010	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1650706	G	G	264	136	303	107	6.021	0.0141	rs589588	6	157996410	q25.3
SNP_A-2305926	C	C	229	177	269	145	6.316	0.012	rs4708872	6	158013174	q25.3
SNP_A-1954429	G	A	212	192	225	177	5.756	1.64E-02	rs602890	6	158039808	q25.3
SNP_A-1890988	T	T	359	41	335	59	4.025	0.0448	rs9458550	6	158197689	q25.3
SNP_A-2037389	G	G	354	10	343	25	6.581	0.0103	rs9458565	6	158200735	q25.3
SNP_A-1808907	G	G	386	16	358	32	6.207	1.27E-02	rs9365674	6	158381565	q25.3
SNP_A-2173708	C	C	243	145	224	178	3.898	4.84E-02	rs662185	6	158592800	q25.3
SNP_A-1741469	C	C	262	138	297	113	4.559	3.28E-02	rs635995	6	158796144	q25.3
SNP_A-1731735	A	A	261	137	294	112	4.393	0.0361	rs585078	6	158796277	q25.3
SNP_A-1988313	G	G	352	22	337	39	5.059	2.45E-02	rs6920842	6	158840956	q25.3
SNP_A-1988315	T	T	271	141	291	109	4.631	3.14E-02	rs341138	6	158841582	q25.3
SNP_A-1871150	G	G	245	111	263	77	6.422	1.13E-02	rs1754416	6	158848341	q25.3
SNP_A-1988316	C	C	251	129	271	99	4.581	3.23E-02	rs2362576	6	158850042	q25.3
SNP_A-1988317	G	G	250	118	283	97	3.903	0.0482	rs588580	6	158850353	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2203109	A	A	239	107	279	89	4.068	4.37E-02	rs628203	6	158866736	q25.3
SNP_A-1913360	A	A	373	13	358	30	7.024	8.00E-03	rs2033970	6	158936741	q25.3
SNP_A-2220003	A	A	232	160	275	131	6.293	0.0121	rs9457403	6	158950760	q25.3
SNP_A-2177746	G	G	330	44	376	22	9.594	0.002	rs7754383	6	158952610	q25.3
SNP_A-1938740	G	G	228	148	206	180	4.107	4.27E-02	rs9355246	6	158960396	q25.3
SNP_A-1988325	G	G	317	11	292	22	4.39	3.62E-02	rs3123125	6	159192856	q25.3
SNP_A-1699779	G	G	275	73	273	105	4.528	3.33E-02	rs169858	6	159394062	q25.3
SNP_A-1692668	C	C	306	52	295	77	4.78	2.88E-02	rs212390	6	159398853	q25.3
SNP_A-2087552	A	A	362	32	385	19	3.897	4.84E-02	rs365045	6	159602659	q25.3
SNP_A-2115479	G	G	355	13	372	4	5.077	2.42E-02	rs3814448	6	159662816	q25.3
SNP_A-2012218	C	C	349	45	351	25	5.302	2.13E-02	rs687314	6	159686673	q25.3
SNP_A-1807843	T	T	337	71	355	45	6.217	1.27E-02	rs9355713	6	159692959	q25.3
SNP_A-2037579	A	A	384	12	388	4	4.001	4.55E-02	rs9365040	6	159693454	q25.3
SNP_A-2070985	G	G	386	30	403	15	5.362	0.0206	rs12213461	6	159796566	q25.3
SNP_A-2294515	G	G	347	21	359	5	10.029	0.0015	rs9364516	6	159814252	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2037770	T	T	239	143	279	121	4.51	3.37E-02	rs6916581	6	159974114	q25.3
SNP_A-2286326	G	G	189	145	226	118	5.924	0.0149	rs6931787	6	159974182	q25.3
SNP_A-2109851	G	G	253	147	287	111	7.159	7.50E-03	rs9457675	6	159974789	q25.3
SNP_A-1988346	C	C	204	126	237	105	4.166	4.13E-02	rs927450	6	160152507	q25.3
SNP_A-2200035	C	C	280	136	310	110	4.254	3.91E-02	rs9365108	6	160259709	q25.3
SNP_A-1816194	G	G	290	82	325	57	6.357	0.0117	rs2297357	6	160425665	q25.3
SNP_A-2121666	T	T	193	189	209	141	6.232	1.25E-02	rs6909681	6	160439510	q25.3
SNP_A-2172282	G	G	372	22	405	9	6.362	0.0117	rs8191898	6	160469376	q25.3
SNP_A-2081665	G	A	202	166	207	185	4.5	0.0339	rs509707	6	160742221	q25.3
SNP_A-2187171	G	A	220	174	207	195	4.284	0.0385	rs539958	6	160743253	q25.3
SNP_A-2212082	G	A	209	175	199	171	5.082	2.42E-02	rs487060	6	160744870	q25.3
SNP_A-2012229	G	T	218	168	207	197	4.711	3.00E-02	rs487152	6	160744897	q25.3
SNP_A-2012231	C	C	339	67	370	48	4.321	3.77E-02	rs512077	6	160745339	q25.3
SNP_A-1988374	C	C	334	0	320	4	4.149	4.17E-02	rs884743	6	160777129	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803733	G	G	332	82	365	55	6.841	8.90E-03	rs9456538	6	160823804	q25.3
SNP_A-1961463	C	C	253	135	277	93	8.401	0.0038	rs3127599	6	160877545	q25.3
SNP_A-2272818	C	C	360	50	341	79	6.915	8.50E-03	rs6919346	6	160930770	q25.3
SNP_A-1944780	C	C	318	72	350	50	5.374	2.04E-02	rs2465836	6	161157455	q26
SNP_A-2025992	C	C	233	161	199	197	6.291	0.0121	rs1247555	6	161159429	q26
SNP_A-2152857	G	A	240	172	208	206	5.998	0.0143	rs1247557	6	161160081	q26
SNP_A-1839788	C	C	234	160	199	189	5.193	2.27E-02	rs1620921	6	161167498	q26
SNP_A-1895407	G	G	340	16	350	34	5.573	1.82E-02	rs12203960	6	161569817	q26
SNP_A-2149514	T	T	373	21	373	3	13.086	3.00E-04	rs6933493	6	161918064	q26
SNP_A-2137515	C	C	279	119	301	89	5.081	2.42E-02	rs9365300	6	161957461	q26
SNP_A-1885378	G	G	409	7	419	1	4.602	3.19E-02	rs16892989	6	162136172	q26

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1708336	A	A	296	96	285	127	4.023	4.49E-02	rs951196	6	162571278	q26
SNP_A-2127870	T	T	326	88	301	117	5.08	2.42E-02	rs2023068	6	162634775	q26
SNP_A-1920996	T	T	289	121	255	159	7.263	7.00E-03	rs7743065	6	162651499	q26
SNP_A-2274121	T	T	375	41	356	64	5.513	0.0189	rs9364646	6	162680359	q26
SNP_A-2131780	A	A	355	29	370	14	5.543	1.86E-02	rs6904379	6	162915628	q26
SNP_A-2023264	A	A	232	168	252	136	4.013	4.51E-02	rs9347785	6	164140438	q26
SNP_A-2247924	T	T	333	81	356	60	3.891	4.86E-02	rs3799336	6	164269387	q26
SNP_A-2160567	C	C	207	191	242	164	4.703	3.01E-02	rs4709819	6	164433766	q26
SNP_A-1892152	T	T	224	186	256	160	4.044	4.43E-02	rs4709820	6	164433983	q26
SNP_A-2294066	G	G	301	63	269	103	11.349	8.00E-04	rs9347820	6	164534368	q27
SNP_A-2157571	A	A	387	11	384	24	4.717	2.99E-02	rs7759125	6	164612941	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2038385	C	C	271	97	256	132	5.251	2.19E-02	rs9295262	6	164689863	q27
SNP_A-1746144	C	C	317	79	328	56	3.922	4.76E-02	rs2029870	6	164797654	q27
SNP_A-1949406	C	C	328	28	362	12	7.636	5.70E-03	rs9459178	6	165087705	q27
SNP_A-1939940	T	T	296	120	327	93	4.946	2.62E-02	rs4709892	6	165136400	q27
SNP_A-2217982	C	C	324	80	342	58	3.974	4.62E-02	rs9347929	6	165179227	q27
SNP_A-1853427	C	C	288	86	266	112	4.267	3.89E-02	rs6918467	6	165462242	q27
SNP_A-1988472	G	G	293	15	323	31	3.848	4.98E-02	---	6	165582267	q27
SNP_A-1651116	G	G	314	60	337	33	8.63	0.0033	rs1546141	6	166078296	q27
SNP_A-2173622	A	A	230	166	259	137	4.495	3.40E-02	rs9347088	6	166169427	q27
SNP_A-2202884	C	C	290	48	316	32	4.171	4.11E-02	rs1389921	6	166181430	q27
SNP_A-2304458	A	A	208	194	246	168	4.873	2.73E-02	rs10806833	6	166184648	q27
SNP_A-1783033	C	C	292	120	258	158	7.277	7.00E-03	rs10806834	6	166201984	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1788849	T	C	232	170	183	181	4.904	2.68E-02	rs10946105	6	166275168	q27
SNP_A-1854829	C	A	207	147	168	158	6.837	8.90E-03	rs7751048	6	166278995	q27
SNP_A-2114334	C	G	216	142	170	168	7.945	4.80E-03	rs7749915	6	166279022	q27
SNP_A-1873077	C	C	291	49	322	34	3.913	4.79E-02	rs10946106	6	166297553	q27
SNP_A-2266811	G	G	365	45	389	27	5.221	0.0223	rs3778418	6	166899115	q27
SNP_A-1867422	A	A	347	49	371	33	3.845	0.0499	rs3778409	6	166924655	q27
SNP_A-1652330	A	A	337	15	341	35	7.24	7.10E-03	rs3799568	6	166945123	q27
SNP_A-1861879	G	G	308	86	291	117	4.974	2.57E-02	rs3799612	6	166952051	q27
SNP_A-1657496	A	A	314	74	297	111	7.375	0.0066	rs2072641	6	167097780	q27
SNP_A-1782689	C	C	308	50	332	28	7.1	7.70E-03	rs16899333	6	167117494	q27
SNP_A-2193581	C	C	408	0	409	5	4.958	2.60E-02	rs9347155	6	167149540	q27
SNP_A-2180342	T	T	265	129	236	154	3.867	4.92E-02	rs533810	6	167160100	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2157503	T	T	345	47	314	74	7.463	0.0063	rs12182264	6	167160372	q27
SNP_A-1988510	G	G	346	56	325	79	4.571	3.25E-02	rs7357046	6	167166322	q27
SNP_A-2138029	T	T	261	105	223	139	7.699	5.50E-03	rs9457212	6	167171082	q27
SNP_A-1792983	C	C	242	96	222	134	6.678	9.80E-03	rs9366120	6	167620618	q27
SNP_A-1848464	G	G	233	135	271	109	5.444	1.96E-02	rs3010562	6	167735662	q27
SNP_A-2112277	T	T	259	101	250	136	4.427	3.54E-02	rs4708679	6	168391715	q27
SNP_A-2104987	C	C	363	31	378	14	6.721	9.50E-03	rs12193632	6	168425764	q27
SNP_A-1988529	G	G	389	21	391	9	4.682	3.05E-02	rs2749257	6	168729857	q27
SNP_A-2179390	C	C	384	26	402	14	3.969	4.63E-02	rs9364293	6	169016711	q27
SNP_A-1864019	G	G	329	77	355	51	6.27	0.0123	rs9355112	6	169157780	q27
SNP_A-2117974	G	G	281	111	222	122	4.328	3.75E-02	rs7770399	6	169227235	q27
SNP_A-2087937	T	T	365	33	384	18	4.874	2.73E-02	rs9294948	6	169276762	q27
SNP_A-1933994	C	C	303	21	319	39	4.127	4.22E-02	rs6908401	6	169382348	q27

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2210289	T	C	245	171	215	201	9.356	2.20E-03	rs6605524	6	169473752	q27
SNP_A-1886953	T	T	271	141	243	177	5.524	1.88E-02	rs6605523	6	169473880	q27
SNP_A-2248629	T	T	380	2	326	10	6.543	1.05E-02	rs9294981	6	169506213	q27
SNP_A-2058505	T	T	395	11	404	2	6.332	1.19E-02	rs7740096	6	169536264	q27
SNP_A-2222460	C	C	327	85	351	63	4.115	4.25E-02	rs11756073	6	170281212	q27
SNP_A-1812767	C	C	321	5	370	0	5.716	1.68E-02	rs4710868	6	170318920	q27
SNP_A-2169775	C	C	318	40	348	24	5.085	0.0241	rs3012454	6	170362150	q27
SNP_A-2012314	C	C	281	107	246	128	3.945	0.047	rs910424	6	170575588	q27
SNP_A-2059621	G	G	347	5	338	16	5.875	0.0154	rs4281072	7	149266	p22.3
SNP_A-2027752	G	G	307	17	310	6	5.176	0.0229	rs7799786	7	293523	p22.3
SNP_A-2082482	C	C	195	143	221	117	4.225	3.98E-02	rs4495324	7	576482	p22.3
SNP_A-2067331	C	C	214	128	195	167	5.475	1.93E-02	rs7785252	7	675635	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2260671	G	G	403	7	397	17	4.192	4.06E-02	rs17132239	7	1951024	p22.3
SNP_A-1854959	C	C	401	7	400	18	4.721	0.0298	rs6967879	7	1979150	p22.3
SNP_A-1790878	G	G	370	44	350	66	4.951	2.61E-02	rs2286690	7	2468858	p22.3
SNP_A-1909312	A	A	288	118	260	152	5.668	1.73E-02	rs1639046	7	2486924	p22.3
SNP_A-1935839	A	A	288	122	246	150	5.944	1.48E-02	rs1639044	7	2487576	p22.3
SNP_A-2150683	A	A	363	43	336	62	4.402	3.59E-02	rs11769575	7	2526908	p22.3
SNP_A-2099415	C	C	213	107	245	73	8.652	0.0033	rs2258960	7	2600517	p22.3
SNP_A-2214798	C	C	343	39	321	61	5.569	0.0183	rs6957938	7	2692019	p22.3
SNP_A-1788851	G	G	342	40	368	18	9.276	0.0023	rs7787896	7	2716375	p22.2
SNP_A-2257734	T	T	195	193	215	151	5.466	1.94E-02	rs2679258	7	2724587	p22.2
SNP_A-1784957	C	C	307	83	291	113	4.775	2.89E-02	rs7794757	7	2758316	p22.2
SNP_A-1908712	G	G	283	71	255	97	5.475	1.93E-02	rs11772124	7	2891115	p22.2
SNP_A-2070596	C	C	362	54	342	78	4.913	2.67E-02	rs7779245	7	2953232	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2274830	A	A	362	54	338	78	5.186	2.28E-02	rs6970481	7	2955238	p22.2
SNP_A-2245904	G	G	236	166	211	201	4.614	3.17E-02	rs12056190	7	3081163	p22.2
SNP_A-2274205	G	G	331	85	350	60	4.797	2.85E-02	rs1525554	7	3117258	p22.2
SNP_A-1925837	A	A	340	36	327	57	4.912	2.67E-02	rs12234397	7	3129603	p22.2
SNP_A-2214488	A	A	343	29	325	47	4.748	0.0293	rs1882426	7	3317984	p22.2
SNP_A-2096328	A	A	313	37	321	21	4.423	3.55E-02	rs10215340	7	3713988	p22.2
SNP_A-1786631	C	C	342	2	368	10	4.695	3.03E-02	rs17134038	7	3737758	p22.2
SNP_A-2198093	G	G	284	110	317	87	4.373	3.65E-02	rs10230104	7	3738089	p22.2
SNP_A-1988602	C	C	251	107	277	83	4.306	3.80E-02	rs17330921	7	3833672	p22.2
SNP_A-2022832	T	T	281	55	309	39	3.843	5.00E-02	rs10259896	7	3854143	p22.2
SNP_A-2178449	C	C	344	22	359	9	5.766	1.63E-02	rs626138	7	3948193	p22.2
SNP_A-2076063	T	T	313	103	345	67	9.161	2.50E-03	rs620175	7	3977351	p22.2
SNP_A-1896617	C	C	276	102	322	68	10.153	0.0014	rs675119	7	3983495	p22.2
SNP_A-2198637	G	G	324	44	293	63	4.734	2.96E-02	rs10232703	7	4109718	p22.2
SNP_A-2282120	T	T	358	52	381	31	6.024	0.0141	rs17134702	7	4154984	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2184233	T	T	405	9	410	2	4.48	3.43E-02	rs6462867	7	4291393	p22.2
SNP_A-2031519	C	C	306	42	326	24	5.536	1.86E-02	rs6963829	7	4510477	p22.1
SNP_A-2245724	C	C	293	97	308	68	5.217	0.0224	rs10951714	7	4720118	p22.1
SNP_A-1867562	G	G	180	146	222	130	4.325	3.76E-02	rs6951799	7	4724456	p22.1
SNP_A-1914035	G	G	336	54	335	79	3.988	0.0458	rs11768145	7	4741561	p22.1
SNP_A-1936575	C	C	255	69	266	42	6.399	0.0114	rs6463445	7	5188431	p22.1
SNP_A-1929217	G	G	324	72	304	98	4.569	3.26E-02	rs852499	7	5382173	p22.1
SNP_A-2215767	G	G	326	0	337	5	4.802	2.84E-02	rs852451	7	5443713	p22.1
SNP_A-1940105	T	T	406	0	402	4	4.02	4.50E-02	rs852466	7	5457442	p22.1
SNP_A-2269704	A	A	400	0	381	7	7.281	7.00E-03	rs852518	7	5470570	p22.1
SNP_A-2231103	G	G	374	4	375	17	7.797	5.20E-03	rs852516	7	5471169	p22.1
SNP_A-2225597	G	G	398	0	394	6	6.015	1.42E-02	rs852404	7	5490046	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2105931	T	T	227	145	261	117	5.314	0.0212	rs13239194	7	5542730	p22.1
SNP_A-2109538	G	G	412	0	410	6	5.986	0.0144	rs6463508	7	5548370	p22.1
SNP_A-1898831	C	C	366	0	371	7	6.842	8.90E-03	rs4720643	7	5575896	p22.1
SNP_A-1913461	G	G	410	0	394	4	4.141	0.0419	rs2345863	7	5577144	p22.1
SNP_A-2157242	G	G	221	175	254	140	6.176	0.0129	rs4724724	7	5581288	p22.1
SNP_A-1889072	G	G	368	0	363	7	7.029	8.00E-03	rs4724734	7	5601277	p22.1
SNP_A-1858076	G	G	238	78	214	100	3.987	0.0458	rs12537672	7	5641802	p22.1
SNP_A-1815061	C	C	382	28	401	15	4.348	3.71E-02	rs17322413	7	5652245	p22.1
SNP_A-2212493	C	C	210	196	229	159	4.273	3.87E-02	rs2254593	7	6482840	p22.1
SNP_A-1920728	G	G	366	44	346	70	6.448	0.0111	—	7	6490656	p22.1
SNP_A-2090060	T	T	321	35	293	63	9.277	0.0023	rs10250100	7	6493581	p22.1
SNP_A-1949964	T	T	363	41	336	60	4.538	0.0332	rs17199832	7	6495851	p22.1
SNP_A-1819735	C	C	367	37	354	56	4.072	0.0436	rs17789894	7	6516337	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1988644	G	G	322	4	318	0	3.926	4.75E-02	rs1830075	7	6526934	p22.1
SNP_A-2229781	C	C	372	42	395	25	4.96	2.59E-02	rs12539689	7	7075727	p21.3
SNP_A-1988652	T	T	362	40	390	22	6.146	0.0132	rs10487592	7	7080705	p21.3
SNP_A-2118078	C	C	369	39	354	58	4.013	4.51E-02	rs1294622	7	7165954	p21.3
SNP_A-2177762	A	G	217	167	190	182	4.363	3.67E-02	rs3735461	7	7452884	p21.3
SNP_A-1988680	G	G	406	0	390	4	4.143	4.18E-02	rs16871555	7	7573479	p21.3
SNP_A-2196358	C	C	282	74	243	93	4.485	3.42E-02	rs37958	7	7774813	p21.3
SNP_A-2207525	T	T	182	128	160	158	4.461	3.47E-02	rs38018	7	7820409	p21.3
SNP_A-2273069	A	A	332	64	310	86	3.981	4.60E-02	rs7791362	7	7916167	p21.3
SNP_A-2082898	C	C	305	65	283	87	4.007	0.0453	rs10268598	7	7934767	p21.3
SNP_A-1819957	T	T	307	59	317	39	4.104	4.28E-02	rs17147407	7	8137456	p21.3
SNP_A-1901332	A	A	310	28	339	11	8.499	3.60E-03	rs12702723	7	8186422	p21.3
SNP_A-1988705	C	C	336	22	363	11	4.362	3.68E-02	rs10486231	7	8305973	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1988719	T	T	194	182	231	161	4.175	4.10E-02	rs10486247	7	8523002	p21.3
SNP_A-1988720	T	T	217	169	257	143	5.295	2.14E-02	rs1017002	7	8524672	p21.3
SNP_A-2257670	A	A	219	195	247	165	4.178	4.10E-02	rs10228121	7	8595074	p21.3
SNP_A-2129935	T	C	203	193	230	160	8.285	4.00E-03	rs9655529	7	8602067	p21.3
SNP_A-2305563	-	A	191	191	218	146	7.361	6.70E-03	rs7791419	7	8606803	p21.3
SNP_A-2146105	G	G	260	92	276	68	3.986	4.59E-02	rs16874906	7	8772427	p21.3
SNP_A-1885144	G	G	335	61	304	84	5.071	2.43E-02	rs10952130	7	8787013	p21.3
SNP_A-1782115	G	G	287	39	294	20	5.98	1.45E-02	rs13233920	7	8961088	p21.3
SNP_A-1988736	A	A	263	53	297	37	4.414	3.57E-02	rs6950672	7	9006168	p21.3
SNP_A-1883798	C	C	353	41	378	26	4.089	4.32E-02	rs7802428	7	9148401	p21.3
SNP_A-2295875	C	C	348	34	351	19	4.068	4.37E-02	rs4365998	7	9149198	p21.3
SNP_A-1832140	G	G	361	43	338	64	4.873	2.73E-02	rs6968820	7	9304319	p21.3
SNP_A-1836515	T	T	232	178	264	146	5.225	0.0223	rs2709064	7	9315239	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2159848	C	C	191	189	225	157	5.733	0.0166	rs6463919	7	9332834	p21.3
SNP_A-1742827	A	A	223	167	255	131	6.471	1.10E-02	rs2708997	7	9367630	p21.3
SNP_A-2169209	G	G	201	187	228	150	5.632	1.76E-02	rs2915131	7	9699270	p21.3
SNP_A-1750983	A	A	251	149	230	182	4.03	4.47E-02	rs1024538	7	9769653	p21.3
SNP_A-1915917	G	G	316	96	345	69	5.686	1.71E-02	rs6948280	7	9890245	p21.3
SNP_A-1889882	G	G	318	96	342	68	5.634	1.76E-02	rs12702976	7	9894306	p21.3
SNP_A-1810463	C	C	393	7	405	1	4.636	3.13E-02	rs10236575	7	10016934	p21.3
SNP_A-1955642	C	C	288	64	271	99	7.588	5.90E-03	rs12699150	7	10614260	p21.3
SNP_A-1917136	T	T	341	11	316	2	5.471	1.93E-02	rs17163974	7	10946609	p21.3
SNP_A-2274874	C	C	297	81	319	59	4.243	3.94E-02	rs2040798	7	11063526	p21.3
SNP_A-2227356	C	C	352	58	329	85	5.855	0.0155	rs17164640	7	11288105	p21.3
SNP_A-1744587	C	C	382	14	381	27	3.945	0.047	rs10486139	7	11302292	p21.3
SNP_A-2171370	C	C	227	137	188	162	5.483	1.92E-02	rs10950351	7	11305537	p21.3
SNP_A-1819516	T	T	372	10	364	2	5.08	2.42E-02	rs11764106	7	11724266	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1907279	A	A	277	127	242	156	5.287	2.15E-02	rs7790754	7	11788968	p21.3
SNP_A-2268119	C	C	283	125	253	151	4.109	4.27E-02	rs12699294	7	11790075	p21.3
SNP_A-1988844	A	A	303	67	287	93	4.526	3.34E-02	rs1435534	7	11990452	p21.3
SNP_A-1731559	T	T	243	155	219	193	5.156	2.32E-02	rs6460898	7	11997230	p21.3
SNP_A-2038665	A	A	309	101	284	130	4.675	3.06E-02	rs17165701	7	12012514	p21.3
SNP_A-2180355	G	G	207	201	243	173	4.899	0.0269	rs3800845	7	12037391	p21.3
SNP_A-1879104	G	G	203	139	166	156	4.091	4.31E-02	rs4721059	7	12040735	p21.3
SNP_A-2288474	A	A	234	148	177	165	6.639	0.01	rs7792410	7	12040854	p21.3
SNP_A-2182847	A	A	254	162	221	197	5.7	1.70E-02	rs1468804	7	12048748	p21.3
SNP_A-1950405	C	C	390	20	367	37	5.725	0.0167	rs849786	7	12423642	p21.3
SNP_A-1738547	C	C	306	88	289	117	4.409	3.57E-02	rs11180398	7	12433812	p21.3
SNP_A-1659951	A	A	360	40	352	60	3.913	4.79E-02	rs702478	7	12548537	p21.3
SNP_A-2208915	G	G	267	127	284	80	10.024	0.0015	rs6956076	7	12669503	p21.3
SNP_A-1885035	A	A	236	110	259	83	4.823	0.0281	rs6460981	7	12676511	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800358	A	A	204	202	238	168	5.74	0.0166	rs10272911	7	12682060	p21.3
SNP_A-1952570	G	C	212	196	232	184	4.931	0.0264	rs10258007	7	12682555	p21.3
SNP_A-1712695	T	T	371	29	394	16	4.324	3.76E-02	rs10488238	7	12685967	p21.3
SNP_A-2133657	G	G	281	115	316	90	4.977	2.57E-02	rs7795573	7	12693015	p21.3
SNP_A-2083119	A	A	412	4	416	0	4.019	4.50E-02	rs17166492	7	12707442	p21.3
SNP_A-2308601	C	C	385	31	403	17	4.475	0.0344	---	7	12711480	p21.3
SNP_A-1920457	G	G	412	4	420	0	4.058	4.40E-02	---	7	12716499	p21.3
SNP_A-2173843	G	G	366	30	404	16	4.652	0.031	---	7	12716654	p21.3
SNP_A-1781383	G	G	178	158	197	113	7.401	6.50E-03	rs7786098	7	12775787	p21.3
SNP_A-1906222	T	T	289	51	253	73	6.003	0.0143	rs17700347	7	12902322	p21.3
SNP_A-1721506	A	A	332	60	367	35	8.207	4.20E-03	rs2884164	7	13018599	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2256694	C	C	231	127	223	83	5.32	2.11E-02	rs4721192	7	13021952	p21.3
SNP_A-1671222	G	G	258	138	288	112	4.332	3.74E-02	rs2041656	7	13111517	p21.3
SNP_A-1885786	G	G	268	74	245	97	4.125	4.23E-02	rs2466495	7	13322160	p21.2
SNP_A-2021929	C	C	337	61	316	90	6.166	1.30E-02	rs1917724	7	13335991	p21.2
SNP_A-1812660	C	C	333	49	316	84	9.246	2.40E-03	rs2723483	7	13344684	p21.2
SNP_A-2128446	C	G	222	162	189	179	6.35	0.0117	rs12699516	7	13352069	p21.2
SNP_A-1893681	T	C	196	174	199	165	4.289	3.84E-02	rs11773320	7	13394875	p21.2
SNP_A-1922474	C	C	262	106	225	125	3.925	4.76E-02	rs1859689	7	13518846	p21.2
SNP_A-1666652	C	C	271	109	251	155	7.93	4.90E-03	rs13240870	7	13578151	p21.2
SNP_A-2152100	A	A	302	70	353	55	4.118	0.0424	rs7803649	7	13633390	p21.2
SNP_A-1988902	G	A	190	138	162	158	4.764	2.91E-02	rs2067634	7	13641841	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2012397	C	C	322	44	341	27	4.61	3.18E-02	rs7784117	7	13644773	p21.2
SNP_A-2171986	C	C	323	47	341	27	5.888	0.0152	rs9986861	7	13652704	p21.2
SNP_A-1923769	G	G	303	61	323	39	5.474	1.93E-02	rs2357852	7	13917046	p21.2
SNP_A-2122071	G	G	218	148	212	94	6.831	9.00E-03	rs993548	7	13978756	p21.2
SNP_A-2041614	C	C	406	8	405	1	5.368	2.05E-02	rs17167969	7	14027974	p21.2
SNP_A-2120357	T	T	213	193	243	159	5.238	2.21E-02	rs38271	7	14080271	p21.2
SNP_A-1783043	G	G	212	170	230	130	5.419	1.99E-02	rs10267273	7	14826829	p21.2
SNP_A-2107293	A	A	401	15	388	32	6.344	0.0118	rs218080	7	14856301	p21.2
SNP_A-2035386	C	C	358	4	338	14	5.991	0.0144	rs17168935	7	15446197	p21.1
SNP_A-2282118	C	C	317	85	288	110	4.575	3.24E-02	rs12056299	7	15469391	p21.1
SNP_A-2053497	C	C	266	86	233	111	5.264	0.0218	rs10046551	7	15486345	p21.1
SNP_A-1782760	A	A	255	129	198	138	4.295	3.82E-02	rs1050290	7	15499306	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1729146	T	T	374	18	375	35	5.053	0.0246	rs10486777	7	15514481	p21.2
SNP_A-2133396	A	A	370	38	344	62	6.702	9.60E-03	rs17150130	7	15520923	p21.1
SNP_A-1669503	C	C	391	5	370	14	4.659	0.0309	rs10239570	7	15535409	p21.1
SNP_A-2149857	C	C	404	8	390	22	6.78	9.20E-03	rs10239819	7	15535461	p21.1
SNP_A-1826545	G	G	406	10	393	25	6.635	0.01	rs17169023	7	15537713	p21.1
SNP_A-2030347	C	C	371	23	368	44	6.195	1.28E-02	rs37417	7	15557963	p21.1
SNP_A-2061172	G	G	377	25	387	11	5.555	0.0184	rs17169080	7	15606918	p21.1
SNP_A-1890628	T	T	316	80	265	103	6.35	0.0117	rs10262042	7	15609238	p21.1
SNP_A-2030160	C	C	337	23	282	46	11.089	9.00E-04	rs984809	7	16131667	p21.1
SNP_A-2042878	T	T	274	132	241	157	4.198	4.05E-02	rs2526602	7	16156231	p21.1
SNP_A-2134703	T	T	273	129	251	161	4.333	3.74E-02	rs6974766	7	16156409	p21.1
SNP_A-2163604	T	T	276	72	302	52	4.344	3.71E-02	rs818503	7	16495593	p21.1
SNP_A-1947075	A	A	287	55	291	33	5.045	0.0247	rs3807482	7	16500769	p21.1
SNP_A-1650428	C	C	326	72	359	45	7.776	0.0053	rs10499475	7	16567212	p21.1
SNP_A-1721592	T	T	316	76	350	52	6.111	0.0134	rs10499478	7	16617911	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1756947	G	G	317	79	351	59	4.387	3.62E-02	rs847371	7	16722044	p21.1
SNP_A-1945725	C	C	324	70	344	46	5.544	1.85E-02	rs847397	7	16741697	p21.1
SNP_A-1758312	T	T	352	44	339	71	6.342	0.0118	rs10269143	7	17143299	p21.1
SNP_A-2123873	C	C	344	20	337	39	5.998	0.0143	rs2080061	7	17433345	p21.1
SNP_A-2310423	C	C	259	101	281	75	4.715	2.99E-02	rs12670374	7	17473510	p21.1
SNP_A-2268524	T	A	209	187	223	177	5.794	0.0161	rs2691556	7	17589300	p21.1
SNP_A-1989030	A	A	213	151	187	181	4.379	3.64E-02	rs1404414	7	17639627	p21.1
SNP_A-1702941	A	A	271	121	315	95	6.032	0.014	rs1464804	7	17705143	p21.1
SNP_A-1853875	C	C	229	159	196	192	5.665	1.73E-02	rs4544985	7	17757047	p21.1
SNP_A-2193208	G	G	218	146	188	180	5.741	0.0166	rs4470902	7	17781550	p21.1
SNP_A-2147219	A	A	320	46	303	67	4.345	3.71E-02	rs12699933	7	17787668	p21.1
SNP_A-1989037	C	C	302	80	320	56	4.709	3.00E-02	rs10281630	7	18050233	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1724438	G	G	361	37	388	22	4.61	3.18E-02	rs10259495	7	18469999	p21.1
SNP_A-1714296	G	G	385	7	383	21	6.826	9.00E-03	rs2905456	7	18848221	p21.1
SNP_A-1656039	T	T	391	9	383	21	4.863	2.74E-02	rs2521720	7	18848242	p21.1
SNP_A-1881271	G	G	378	4	384	0	4.042	4.44E-02	rs17140924	7	19029343	p21.1
SNP_A-1956474	T	-	226	166	181	181	4.437	3.52E-02	rs12540501	7	19135638	p21.1
SNP_A-1989078	G	G	390	6	402	0	6.137	0.0132	rs11767467	7	19288563	p21.1
SNP_A-1839947	C	C	381	23	401	11	4.669	3.07E-02	rs6461437	7	19293714	p21.1
SNP_A-2232674	G	G	305	49	314	30	4.558	3.28E-02	rs17141622	7	19384056	p21.1
SNP_A-2288509	G	G	369	23	372	8	7.085	7.80E-03	rs17141736	7	19432079	p21.1
SNP_A-1658910	G	G	318	82	353	59	5.401	0.0201	rs2189571	7	19555431	p21.1
SNP_A-1877484	C	C	352	28	394	16	4.505	3.38E-02	rs13231772	7	19877464	p21.1
SNP_A-1797328	G	G	351	23	341	39	4.226	3.98E-02	rs727339	7	20155710	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1915699	A	A	404	12	394	26	5.264	0.0218	rs1968052	7	20254821	p21.1
SNP_A-1842984	T	T	278	38	308	24	4.305	3.80E-02	rs6977158	7	20362357	p21.1
SNP_A-2088262	A	A	280	78	308	58	4.187	0.0407	rs4721922	7	20408549	p21.1
SNP_A-2033180	G	G	406	4	392	0	3.844	0.0499	rs17143304	7	20541194	p21.1
SNP_A-2038543	A	A	350	22	345	39	4.584	3.23E-02	rs6978624	7	20626491	p21.1
SNP_A-1989115	G	G	187	155	224	132	4.895	0.0269	rs7795600	7	20857569	p15.3
SNP_A-1910091	G	G	269	121	298	98	3.853	4.97E-02	rs4995080	7	20873718	p15.3
SNP_A-2280998	C	C	321	45	292	66	5.257	2.19E-02	rs1174991	7	21800306	p15.3
SNP_A-2309735	G	G	251	81	216	108	6.384	0.0115	rs1174956	7	21812237	p15.3
SNP_A-2194022	C	C	227	189	264	150	7.27	7.00E-03	rs1419771	7	21872418	p15.3
SNP_A-1827555	G	G	391	5	383	17	6.608	1.02E-02	rs7805427	7	21876618	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1671004	G	G	377	23	371	41	4.934	0.0263	rs10499552	7	22092177	p15.3
SNP_A-1673378	A	A	374	20	369	39	5.91	1.51E-02	rs10499551	7	22093212	p15.3
SNP_A-2291368	A	A	287	83	265	107	3.903	0.0482	rs7811699	7	22672349	p15.3
SNP_A-2208620	C	C	197	153	232	130	4.524	3.34E-02	rs2037606	7	22688119	p15.3
SNP_A-1848538	C	C	321	55	331	31	6.588	0.0103	rs7782946	7	23601447	p15.3
SNP_A-1887026	C	C	313	89	333	65	4.34	3.72E-02	rs17148778	7	23899558	p15.3
SNP_A-2265906	C	C	246	94	276	74	3.961	4.66E-02	rs156267	7	23942638	p15.3
SNP_A-1715813	T	T	370	20	376	36	4.019	4.50E-02	rs16162	7	24046079	p15.3
SNP_A-1894344	T	T	375	15	362	34	7.551	6.00E-03	rs16172	7	24070565	p15.3
SNP_A-1880981	C	C	374	16	370	32	5.174	0.0229	rs17208939	7	24514967	p15.3
SNP_A-2292514	C	C	387	7	389	23	8.141	0.0043	rs7790129	7	24879172	p15.3
SNP_A-1871275	A	A	271	121	314	92	6.866	8.80E-03	rs7805812	7	25116174	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1648396	A	A	373	23	399	11	4.869	2.73E-02	rs10486417	7	25554340	p15.2
SNP_A-2030192	C	C	395	21	411	9	5.099	2.39E-02	rs1014201	7	25588977	p15.2
SNP_A-1899883	A	A	403	11	415	3	4.728	2.97E-02	rs6461881	7	25610929	p15.2
SNP_A-2103624	G	G	331	39	318	64	6.138	0.0132	---	7	25643680	p15.2
SNP_A-1798806	G	G	265	119	231	153	6.581	0.0103	rs7809764	7	25718892	p15.2
SNP_A-2266901	G	G	281	131	243	165	6.642	0.01	rs7810044	7	25718910	p15.2
SNP_A-2314749	A	A	305	39	299	17	7.528	6.10E-03	rs10951130	7	26159066	p15.2
SNP_A-2199056	G	G	221	141	179	163	5.438	1.97E-02	rs11980563	7	26397368	p15.2
SNP_A-2085951	C	C	235	95	254	72	3.882	4.88E-02	rs17154072	7	26417667	p15.2
SNP_A-1989286	G	G	362	18	332	32	4.875	2.72E-02	rs2078118	7	26422147	p15.2
SNP_A-2107250	C	T	200	188	217	173	4.026	0.0448	rs212851	7	26498629	p15.2
SNP_A-1664894	A	A	242	150	278	126	4.399	3.60E-02	rs10085721	7	26562189	p15.2
SNP_A-2314842	A	A	218	178	248	146	5.087	0.0241	rs1123158	7	26589888	p15.2
SNP_A-2032219	G	G	238	98	256	74	3.951	4.68E-02	rs17315929	7	26637413	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2012467	G	G	333	1	315	9	6.75	9.40E-03	rs6461981	7	26718406	p15.2
SNP_A-1795425	T	T	365	19	374	8	4.586	3.22E-02	rs2023843	7	27016461	p15.2
SNP_A-1849398	A	A	348	58	369	39	4.332	3.74E-02	rs4722680	7	27093054	p15.2
SNP_A-1795608	C	C	334	82	310	106	3.958	4.66E-02	rs11563321	7	27201330	p15.2
SNP_A-1871344	C	C	360	46	337	65	3.992	4.57E-02	rs6977425	7	27222346	p15.2
SNP_A-2192263	C	C	263	133	275	99	4.626	0.0315	rs9639553	7	27351407	p15.2
SNP_A-1989309	A	A	188	160	234	144	4.625	0.0315	rs10951172	7	27387351	p15.2
SNP_A-2065699	A	A	254	78	205	109	9.876	1.70E-03	rs17150563	7	27501089	p15.2
SNP_A-1795079	G	G	325	81	289	117	8.656	0.0033	rs17155702	7	27548868	p15.2
SNP_A-1874163	T	T	249	101	231	153	9.787	0.0018	rs17611937	7	27549134	p15.2
SNP_A-2296951	T	T	308	90	285	127	6.961	8.30E-03	rs7801301	7	27622203	p15.2
SNP_A-2181832	C	C	339	1	361	9	5.834	1.57E-02	rs3823945	7	27646358	p15.2
SNP_A-1661938	C	C	244	148	286	124	5.044	0.0247	rs757397	7	27650813	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1645120	T	T	252	148	216	196	9.292	0.0023	rs735664	7	27651309	p15.2
SNP_A-2113591	A	A	248	150	271	119	4.511	3.37E-02	rs7806169	7	27680833	p15.2
SNP_A-2310811	T	T	231	101	241	73	4.219	4.00E-02	rs4719913	7	27706472	p15.1
SNP_A-2113866	A	A	384	16	400	6	4.828	2.80E-02	rs17623527	7	27811981	p15.1
SNP_A-1883943	A	A	394	0	390	6	6.015	1.42E-02	rs6946007	7	27834570	p15.1
SNP_A-1948121	C	C	412	0	415	5	4.934	0.0263	rs12673479	7	27902853	p15.1
SNP_A-2196998	T	T	373	25	386	12	4.79	0.0286	rs11520706	7	27975988	p15.1
SNP_A-1955949	T	C	206	184	198	166	3.922	4.77E-02	rs177485	7	28093202	p15.1
SNP_A-1796433	A	A	265	125	286	92	5.633	1.76E-02	rs12700862	7	28114850	p15.1
SNP_A-2180426	G	G	284	48	267	71	4.917	2.66E-02	rs17642724	7	28169847	p15.1
SNP_A-1989328	G	A	170	166	195	141	5.034	2.49E-02	rs2191827	7	28174577	p15.1
SNP_A-2120499	T	T	316	74	289	109	7.819	5.20E-03	rs6462079	7	28189067	p15.1
SNP_A-1843339	T	G	214	172	212	186	5.944	1.48E-02	rs6963615	7	28192956	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1666428	C	C	269	119	249	161	6.471	1.10E-02	rs10486584	7	28218785	p15.1
SNP_A-2066960	A	A	236	170	202	194	4.098	4.29E-02	rs177572	7	28267535	p15.1
SNP_A-1685608	A	A	322	74	307	103	4.867	2.74E-02	rs10486588	7	28337194	p15.1
SNP_A-2249778	A	A	301	77	275	103	4.929	0.0264	rs17156863	7	28392278	p15.1
SNP_A-2157910	G	G	253	139	269	101	5.877	1.53E-02	rs3793292	7	29133807	p15.1
SNP_A-2073362	C	C	177	151	190	112	5.18	0.0229	rs2189440	7	29220509	p15.1
SNP_A-1925361	A	A	364	10	364	24	5.509	0.0189	rs10229219	7	29248804	p15.1
SNP_A-1816061	A	A	389	7	383	21	6.967	8.30E-03	rs3828983	7	29255180	p15.1
SNP_A-1658596	A	A	317	79	305	107	4.131	4.21E-02	rs722611	7	29256331	p15.1
SNP_A-2198648	G	G	329	45	347	25	6.188	0.0129	rs3793252	7	29291698	p15.1
SNP_A-1663838	C	C	244	40	268	80	8.06	4.50E-03	rs1362355	7	29347428	p15.1
SNP_A-1919521	A	A	267	69	216	86	5.453	0.0195	rs10951234	7	29367610	p15.1
SNP_A-1959483	T	T	174	156	199	131	3.853	4.96E-02	rs2893359	7	29694652	p15.1
SNP_A-1692496	A	A	386	12	406	4	4.328	3.75E-02	rs10488083	7	29735686	p15.1
SNP_A-2061907	G	G	386	20	372	34	3.888	4.86E-02	rs12701006	7	29920539	p15.1
SNP_A-1850190	T	C	214	192	222	180	5.088	0.0241	rs6973967	7	29950275	p15.1
SNP_A-2048866	T	T	279	113	301	81	5.985	0.0144	rs887884	7	29988451	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2162623	C	C	247	93	234	124	4.319	3.77E-02	rs4722971	7	29994868	p15.1
SNP_A-2304983	G	G	263	125	218	144	4.656	0.0309	rs2192398	7	30003144	p15.1
SNP_A-2012481	C	C	358	14	367	3	7.224	7.20E-03	rs6462197	7	30072885	p15.1
SNP_A-2208290	C	C	378	8	357	1	4.998	2.54E-02	rs6979671	7	30143291	p15.1
SNP_A-1683894	A	A	395	5	412	0	5.182	2.28E-02	rs9639615	7	30170584	p15.1
SNP_A-1841465	C	C	329	33	307	51	4.596	3.20E-02	rs4722988	7	30285270	p15.1
SNP_A-1879084	T	T	245	145	201	163	4.502	0.0339	rs2256023	7	30288231	p15.1
SNP_A-2132152	A	A	338	74	362	54	3.929	4.75E-02	rs38437	7	30332916	p14.3
SNP_A-2068234	T	T	288	54	320	38	4.103	4.28E-02	rs38474	7	30369109	p14.3
SNP_A-1989404	C	C	320	44	359	21	10.039	0.0015	rs38488	7	30390714	p14.3
SNP_A-2031303	T	T	334	72	360	46	6.703	9.60E-03	rs973002	7	30472144	p14.3
SNP_A-1789189	C	C	343	71	372	44	7.511	6.10E-03	rs1003929	7	30492289	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1791820	T	T	298	60	330	36	7.543	6.00E-03	rs11766609	7	30816756	p14.3
SNP_A-2299229	A	A	241	173	208	204	4.97	0.0258	rs7801471	7	31186011	p14.3
SNP_A-2179440	T	C	206	196	234	164	8.106	4.40E-03	rs6966782	7	31197947	p14.3
SNP_A-1882722	G	G	258	88	267	63	3.917	4.78E-02	rs10951291	7	31198139	p14.3
SNP_A-2183394	A	A	285	115	322	86	6.361	0.0117	rs7780365	7	31211850	p14.3
SNP_A-1906104	T	T	362	18	348	6	5.362	0.0206	rs7807145	7	31365569	p14.3
SNP_A-2094188	A	A	270	124	249	155	4.169	4.12E-02	rs2159688	7	31529602	p14.3
SNP_A-2124994	T	T	340	44	314	62	4.006	0.0453	rs17483922	7	31574662	p14.3
SNP_A-2176245	T	T	261	107	285	83	4.087	4.32E-02	---	7	31586001	p14.3
SNP_A-2196703	G	G	280	126	300	98	4.11	4.26E-02	rs6961705	7	31586625	p14.3
SNP_A-2174650	C	C	227	163	253	123	6.749	9.40E-03	rs10247918	7	31627635	p14.3
SNP_A-1665596	C	C	312	88	293	117	4.576	3.24E-02	rs28190	7	31799078	p14.3
SNP_A-1738230	G	G	355	45	342	68	4.801	2.84E-02	rs30568	7	31813417	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1825742	G	G	190	120	245	105	5.55	1.85E-02	rs17336340	7	31821356	p14.3
SNP_A-1679582	T	T	363	37	354	58	4.579	3.24E-02	rs28179	7	31831713	p14.3
SNP_A-1834283	C	C	240	88	215	117	5.452	0.0195	rs30558	7	31832565	p14.3
SNP_A-1800718	C	C	339	37	337	21	3.981	4.60E-02	rs17160893	7	31915497	p14.3
SNP_A-2033066	G	G	360	38	368	22	4.274	3.87E-02	rs11981809	7	32128027	p14.3
SNP_A-1989443	T	T	315	25	325	11	5.577	1.82E-02	rs215720	7	32196639	p14.3
SNP_A-1989444	C	C	315	11	330	2	6.525	0.0106	rs215735	7	32215318	p14.3
SNP_A-1989446	G	G	302	112	277	139	3.979	4.61E-02	rs1376289	7	32260220	p14.3
SNP_A-1852087	A	A	278	68	212	76	4.062	4.39E-02	rs4141788	7	32292504	p14.3
SNP_A-2189022	C	C	266	78	282	54	4.737	2.95E-02	rs17468378	7	32685990	p14.3
SNP_A-1989455	C	C	319	91	289	121	5.726	0.0167	rs7778110	7	32722241	p14.3
SNP_A-2259916	G	G	343	39	323	61	5.435	1.97E-02	rs6973757	7	32951429	p14.3
SNP_A-1702983	G	G	371	21	370	38	4.581	3.23E-02	rs10486523	7	32984213	p14.3
SNP_A-2253449	G	G	330	48	313	79	7.764	0.0053	rs17170203	7	33172356	p14.3
SNP_A-1676350	G	T	205	195	232	180	4.653	0.031	rs6971826	7	33312169	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225830	C	G	204	194	228	172	5.458	0.0195	rs6945776	7	33341807	p14.3
SNP_A-1748881	A	A	266	74	274	110	4.505	3.38E-02	rs2034514	7	33443051	p14.3
SNP_A-2220092	C	C	298	46	299	25	5.619	0.0178	rs1156238	7	33593227	p14.3
SNP_A-2161637	T	T	406	4	418	0	4.098	4.29E-02	rs17170442	7	33616746	p14.3
SNP_A-1989507	T	T	308	102	345	69	8.446	3.70E-03	rs14119794	7	34474245	p14.3
SNP_A-1945539	C	C	351	49	372	30	5.175	0.0229	rs9792042	7	34478100	p14.3
SNP_A-2138315	A	A	302	102	338	78	5.05	0.0246	rs2609218	7	34485549	p14.3
SNP_A-2055805	G	G	345	21	358	6	8.568	3.40E-03	rs323909	7	34510359	p14.3
SNP_A-2183341	A	A	256	122	282	96	4.357	3.68E-02	rs324978	7	34587572	p14.3
SNP_A-1989513	G	G	345	45	375	27	5.569	0.0183	rs17789642	7	34638955	p14.3
SNP_A-2080081	C	C	370	46	399	21	10.403	1.30E-03	rs11768189	7	34661757	p14.3
SNP_A-2225076	G	G	332	68	347	47	4.121	0.0424	rs328906	7	34797155	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253527	G	G	252	144	212	168	4.967	0.0258	rs988270	7	35073801	p14.2
SNP_A-2302035	C	C	389	25	360	48	8.326	3.90E-03	---	7	35185281	p14.2
SNP_A-2124522	A	A	381	27	358	50	7.586	5.90E-03	rs17676520	7	35214750	p14.2
SNP_A-2160301	A	A	363	45	331	65	4.934	0.0263	rs10228514	7	35237035	p14.2
SNP_A-1922403	C	C	383	23	359	41	5.794	0.0161	rs17677393	7	35304650	p14.2
SNP_A-1804825	T	T	407	5	420	0	5.128	0.0235	rs2727852	7	35659843	p14.2
SNP_A-2229940	C	C	392	4	394	0	4	4.55E-02	rs2727851	7	35660988	p14.2
SNP_A-2075205	C	C	409	5	406	0	4.933	0.0263	rs2727855	7	35704055	p14.2
SNP_A-2304239	T	T	304	104	333	81	4.136	4.20E-02	rs12155215	7	35970161	p14.2
SNP_A-2079922	G	G	303	95	329	71	4.535	0.0332	rs12154572	7	35970196	p14.2
SNP_A-1803737	A	A	285	97	312	72	4.914	2.66E-02	rs6973372	7	35973161	p14.2
SNP_A-2031964	T	T	369	37	392	20	5.722	1.68E-02	rs10277506	7	36026252	p14.2
SNP_A-2301378	C	T	187	139	162	158	4.14	0.0419	rs2098368	7	36042524	p14.2
SNP_A-1945390	G	G	302	106	327	79	4.929	0.0264	rs196580	7	36087318	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235247	C	C	384	8	401	1	5.688	1.71E-02	rs2160273	7	36089420	p14.2
SNP_A-2088796	T	T	396	14	401	5	4.275	3.87E-02	rs196649	7	36132627	p14.2
SNP_A-1844619	T	T	279	45	283	69	3.928	4.75E-02	---	7	36297876	p14.2
SNP_A-2252900	G	G	330	42	320	64	4.531	3.33E-02	rs6961245	7	36495605	p14.2
SNP_A-1660861	C	C	216	184	251	159	4.322	3.76E-02	rs1986568	7	37127958	p14.1
SNP_A-2210123	C	C	399	17	410	4	8.192	4.20E-03	rs2717948	7	37151709	p14.1
SNP_A-1785701	T	T	203	189	243	167	4.545	3.30E-02	rs6462758	7	37159512	p14.1
SNP_A-1812669	G	G	214	158	243	133	3.967	4.64E-02	rs2724014	7	37163018	p14.1
SNP_A-2055053	T	T	220	188	262	156	6.516	1.07E-02	rs1882079	7	37164506	p14.1
SNP_A-1744095	A	C	213	175	210	192	4.024	4.49E-02	rs1530822	7	37665517	p14.1
SNP_A-1660307	G	A	220	178	214	198	4.223	3.99E-02	rs1349392	7	37667091	p14.1
SNP_A-1989590	A	G	228	188	218	200	4.044	4.43E-02	rs935765	7	37698678	p14.1
SNP_A-1948890	A	A	236	154	265	123	5.143	2.33E-02	rs1547446	7	37754287	p14.1
SNP_A-2043344	G	G	360	30	377	17	3.968	4.64E-02	rs10262830	7	38084338	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2182538	T	T	344	0	309	5	5.52	1.88E-02	rs6973776	7	38092618	p14.1
SNP_A-1828787	A	A	331	41	365	25	5.117	2.37E-02	rs2267808	7	38241703	p14.1
SNP_A-1817180	T	T	270	104	316	76	7.548	6.00E-03	rs2392577	7	38273593	p14.1
SNP_A-2132068	C	C	251	107	259	75	4.925	2.65E-02	rs1019290	7	38280129	p14.1
SNP_A-2022820	A	A	236	146	197	179	6.816	9.00E-03	rs11767573	7	38290571	p14.1
SNP_A-1820534	A	A	283	59	330	34	9.648	0.0019	rs2043785	7	38302843	p14.1
SNP_A-2044216	A	A	300	50	288	82	7.453	0.0063	rs10263645	7	38410131	p14.1
SNP_A-1989624	A	A	394	10	374	24	6.241	1.25E-02	rs10486680	7	38596814	p14.1
SNP_A-2259639	T	T	319	15	292	32	7.192	7.30E-03	rs713243	7	38644345	p14.1
SNP_A-1911527	A	A	296	118	268	150	5.192	2.27E-02	rs8180755	7	39284416	p14.1
SNP_A-2102662	G	G	298	118	268	146	4.555	3.28E-02	rs6462920	7	39284632	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2297909	T	T	274	114	235	143	6.131	1.33E-02	rs7803420	7	39287346	p14.1
SNP_A-2083805	T	T	271	113	239	139	4.643	3.12E-02	rs7803821	7	39287432	p14.1
SNP_A-2061583	G	G	354	58	365	31	8.046	4.60E-03	rs7789960	7	39658249	p14.1
SNP_A-2101278	T	T	391	25	407	13	4.091	4.31E-02	rs1267269	7	39893375	p14.1
SNP_A-1905379	T	T	332	82	359	57	5.547	1.85E-02	rs11973006	7	40411605	p14.1
SNP_A-1989669	C	C	333	81	359	55	5.947	0.0147	rs10486811	7	40424095	p14.1
SNP_A-2012536	A	A	306	78	320	56	3.841	5.00E-02	rs6948724	7	40429515	p14.1
SNP_A-1855160	G	G	390	26	378	42	3.933	4.73E-02	rs886765	7	40457092	p14.1
SNP_A-2185100	A	A	286	50	268	28	4.275	3.87E-02	rs6952969	7	40489941	p14.1
SNP_A-1989679	A	A	323	19	348	8	5.134	0.0235	rs17171786	7	40688015	p14.1
SNP_A-2254055	G	G	321	57	309	81	4.216	4.00E-02	rs6952070	7	40796001	p14.1
SNP_A-1904342	G	G	375	41	358	62	4.657	0.0309	rs4720396	7	40805315	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2225794	C	C	371	29	355	49	5.461	1.94E-02	rs10240176	7	40812540	p14.1
SNP_A-1900501	A	A	347	27	319	57	11.886	6.00E-04	rs1990136	7	40844815	p14.1
SNP_A-1957422	C	C	372	26	394	14	4.108	4.27E-02	rs17622696	7	40849855	p14.1
SNP_A-1903498	T	T	260	66	233	89	4.867	2.74E-02	rs10216048	7	40895601	p14.1
SNP_A-2032297	T	T	277	79	247	105	5.369	2.05E-02	rs12701862	7	40896692	p14.1
SNP_A-2162908	T	T	213	201	246	162	6.519	1.07E-02	rs7799191	7	40921860	p14.1
SNP_A-2063897	A	A	358	34	358	18	4.592	3.21E-02	rs17623158	7	40922468	p14.1
SNP_A-1796181	A	A	195	147	224	116	5.655	1.74E-02	rs29492	7	40966893	p14.1
SNP_A-2219616	A	A	226	188	252	154	4.717	2.99E-02	rs255013	7	41002471	p14.1
SNP_A-2145240	G	G	333	11	334	30	8.248	4.10E-03	rs6943592	7	41167423	p14.1
SNP_A-1989694	G	G	401	3	390	12	5.548	1.85E-02	rs10486715	7	41251848	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1697583	G	G	278	116	242	160	9.427	2.10E-03	rs713290	7	41523881	p14.1
SNP_A-1750471	T	T	257	143	232	180	5.34	2.08E-02	rs10486721	7	41525640	p14.1
SNP_A-2290216	A	A	236	170	200	194	4.376	3.65E-02	rs4724067	7	41532449	p14.1
SNP_A-1817574	G	G	326	46	292	64	4.467	3.46E-02	rs6463037	7	41533240	p14.1
SNP_A-2311219	A	A	203	131	170	166	7.038	8.00E-03	rs10251553	7	41535257	p14.1
SNP_A-2281594	A	A	350	62	325	85	4.52	3.35E-02	rs11771454	7	41546046	p14.1
SNP_A-1989707	T	C	218	164	197	195	4.169	4.12E-02	rs720816	7	41548988	p14.1
SNP_A-1840323	A	A	347	61	329	87	4.97	0.0258	rs10951655	7	41550117	p14.1
SNP_A-1822444	G	G	265	141	234	174	5.378	2.04E-02	rs10951656	7	41550481	p14.1
SNP_A-1849758	G	G	354	60	334	86	5.169	0.023	rs2190336	7	41574494	p14.1
SNP_A-1989708	A	A	298	104	265	143	8.048	4.60E-03	rs10486722	7	41585148	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1818585	G	C	233	179	212	206	4.403	3.59E-02	rs10441105	7	41595196	p14.1
SNP_A-2238054	T	T	240	118	274	94	4.829	2.80E-02	rs6977695	7	41601554	p14.1
SNP_A-2059041	G	G	281	37	258	54	4.101	4.29E-02	rs10234444	7	41601767	p14.1
SNP_A-1989712	A	A	223	151	182	172	4.97	0.0258	rs2108179	7	41746584	p14.1
SNP_A-2025584	G	G	202	138	161	157	5.125	2.36E-02	rs3801164	7	41875952	p14.1
SNP_A-2199358	G	G	351	61	366	38	5.579	1.82E-02	rs3801165	7	41875979	p14.1
SNP_A-1989721	G	G	343	27	327	43	4.039	4.45E-02	rs3801187	7	41929603	p14.1
SNP_A-1838600	C	C	397	13	376	26	4.825	2.80E-02	rs10085826	7	42277931	p14.1
SNP_A-2164167	G	G	285	79	314	60	3.866	4.93E-02	rs6463159	7	42825165	p14.1
SNP_A-2289399	C	C	382	0	378	4	4.021	4.49E-02	rs7781519	7	42849314	p14.1
SNP_A-1854224	C	C	167	139	208	126	3.903	0.0482	rs17723745	7	43145092	p13
SNP_A-2259939	T	T	256	80	258	120	5.556	0.0184	rs17209297	7	43337382	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1942349	G	G	334	68	312	96	5.486	1.92E-02	rs4377864	7	43382832	p13
SNP_A-2227332	A	A	351	1	353	7	4.416	0.0356	rs3750098	7	44394095	p13
SNP_A-1989767	A	A	323	75	299	109	7.086	7.80E-03	rs3757572	7	44919896	p13
SNP_A-2045798	T	T	251	107	215	135	5.931	0.0149	rs4724413	7	45356016	p13
SNP_A-1960310	A	G	162	148	184	136	6.015	1.42E-02	rs4724414	7	45356098	p13
SNP_A-2141047	G	G	273	111	248	146	5.839	1.57E-02	rs7357339	7	45379238	p13
SNP_A-1732502	A	A	333	27	339	51	6.248	0.0124	-	7	45909295	p13
SNP_A-1732588	C	C	272	20	297	39	4.155	4.15E-02	rs11766636	7	45909328	p13
SNP_A-1681616	G	G	346	28	343	51	6.193	1.28E-02	rs10255992	7	45910625	p13
SNP_A-2201351	T	T	398	16	390	30	4.299	3.81E-02	rs11984179	7	46267286	p13
SNP_A-2056366	G	G	296	84	291	55	4.511	3.37E-02	rs12668566	7	46666528	p13
SNP_A-1666916	C	C	229	171	205	203	3.986	4.59E-02	rs6945120	7	46756182	p13
SNP_A-1989805	T	A	194	148	174	150	7.246	7.10E-03	rs2107789	7	46787032	p13
SNP_A-1905904	T	T	230	150	263	111	7.989	4.70E-03	rs17172811	7	46879166	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1643946	C	C	264	112	312	86	6.794	9.10E-03	rs2728481	7	46932130	p13
SNP_A-1914167	T	T	267	69	304	50	4.965	2.59E-02	rs2118665	7	46937385	p13
SNP_A-1841124	T	T	282	118	314	90	5.468	1.94E-02	rs2053315	7	46941162	p13
SNP_A-2061617	T	T	300	104	330	82	3.953	4.68E-02	rs2053313	7	46962990	p13
SNP_A-1719149	A	A	261	99	240	136	6.361	0.0117	rs2248642	7	47002343	p13
SNP_A-2022745	G	G	360	34	347	55	5.114	2.37E-02	rs1438595	7	47026681	p13
SNP_A-2171982	A	A	293	109	256	156	10.708	1.10E-03	rs1837236	7	47030572	p13
SNP_A-2079626	A	A	293	109	247	147	9.48	2.10E-03	rs2578405	7	47031741	p13
SNP_A-1989814	T	T	220	170	256	146	4.365	3.67E-02	rs2728468	7	47033300	p13
SNP_A-2012565	T	T	335	63	324	92	5.214	0.0224	rs2578414	7	47044621	p13
SNP_A-2067338	A	A	406	2	393	11	6.423	1.13E-02	rs865603	7	47230706	p12.3
SNP_A-2313845	C	C	309	103	340	70	7.771	0.0053	rs4724648	7	47643615	p12.3
SNP_A-2022246	G	G	268	112	243	157	8.244	4.10E-03	rs10280228	7	47659947	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2088193	G	G	269	99	292	74	4.55	3.29E-02	rs6965759	7	47688210	p12.3
SNP_A-2036677	G	G	323	91	345	65	5.039	2.48E-02	rs17131904	7	47694028	p12.3
SNP_A-1955787	A	G	175	135	172	154	5.401	0.0201	rs2348666	7	47852033	p12.3
SNP_A-2073969	G	G	376	26	392	14	3.914	4.79E-02	---	7	48355753	p12.3
SNP_A-1951055	G	G	293	29	321	13	7.155	7.50E-03	rs6959034	7	48726495	p12.3
SNP_A-2198458	A	G	206	188	214	170	5.001	0.0253	---	7	48741011	p12.3
SNP_A-2052540	A	G	200	180	209	169	4.761	2.91E-02	rs4269482	7	48839570	p12.3
SNP_A-1863885	C	T	203	181	200	164	4.56	0.0327	rs4292637	7	48898375	p12.3
SNP_A-2271026	C	C	403	5	414	0	5.105	2.39E-02	rs6583518	7	48942221	p12.3
SNP_A-1942935	A	A	370	44	349	65	4.659	0.0309	rs2067574	7	49063263	p12.3
SNP_A-2056515	C	C	286	120	308	94	3.954	4.68E-02	rs12718224	7	49646828	p12.3
SNP_A-2115451	T	T	325	27	357	13	5.956	0.0147	rs2221656	7	49876665	p12.2
SNP_A-2144374	C	C	301	85	310	54	6.406	0.0114	rs6583429	7	49925196	p12.2
SNP_A-2216344	G	G	257	133	294	106	5.409	0.02	rs6963357	7	50199500	p12.2
SNP_A-2189903	C	C	310	60	271	83	5.967	0.0146	rs6592963	7	50356054	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2243110	C	C	312	100	334	74	4.615	3.17E-02	rs3807552	7	50384951	p12.2
SNP_A-1734526	A	A	313	85	295	115	4.856	0.0276	rs2715094	7	50472201	p12.2
SNP_A-2012588	G	G	305	9	349	1	7.43	6.40E-03	rs2529402	7	50543539	p12.2
SNP_A-1757949	C	C	355	33	348	52	4.135	4.20E-02	rs990358	7	50559121	p12.2
SNP_A-1817645	A	A	327	23	317	41	5.128	0.0235	rs6593140	7	50572342	p12.2
SNP_A-2214527	G	G	347	35	340	58	5.434	1.98E-02	rs6593171	7	50604680	p12.2
SNP_A-1660885	C	C	385	15	404	4	6.747	9.40E-03	rs10486746	7	50725898	p12.2
SNP_A-1846811	G	G	376	16	396	4	7.638	5.70E-03	rs6593324	7	50923806	p12.1
SNP_A-2181045	G	A	209	191	234	174	7.471	0.0063	rs4948203	7	51068288	p12.1
SNP_A-2070634	T	T	227	149	206	184	4.443	3.50E-02	rs695081	7	51198532	p12.1
SNP_A-2127517	G	G	339	29	357	13	6.555	1.05E-02	rs11760754	7	51306241	p12.1
SNP_A-2214355	C	C	331	31	329	53	5.234	2.21E-02	rs2191256	7	51457917	p12.1
SNP_A-1836545	A	A	286	94	320	74	4.037	4.45E-02	rs2329831	7	51466745	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2270016	G	G	220	188	260	150	7.601	5.80E-03	rs10281287	7	51468216	p12.1
SNP_A-1843528	C	C	203	139	251	123	4.631	3.14E-02	rs6977872	7	51572692	p12.1
SNP_A-2079245	C	C	350	40	345	21	5.197	2.26E-02	rs9642434	7	51664680	p12.1
SNP_A-1824352	A	A	271	75	265	49	3.977	4.61E-02	rs11770662	7	51831274	p12.1
SNP_A-2216839	C	C	411	5	420	0	5.078	2.42E-02	rs6944706	7	51894730	p12.1
SNP_A-1919502	A	A	316	46	317	27	4.491	3.41E-02	rs4540364	7	52059435	p12.1
SNP_A-2102851	G	G	396	16	385	35	7.157	7.50E-03	rs1729819	7	52484047	p12.1
SNP_A-1876874	C	C	335	59	340	38	4.254	3.92E-02	rs4947735	7	52494568	p12.1
SNP_A-2153246	C	C	294	56	252	78	6.26	0.0124	rs1442242	7	52495700	p12.1
SNP_A-1989936	G	G	316	50	252	64	5.293	2.14E-02	rs10499703	7	52496376	p12.1
SNP_A-1989950	A	A	303	61	327	35	7.951	4.80E-03	rs17135491	7	52879809	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1853178	G	T	211	165	195	181	4.796	2.85E-02	rs1826529	7	52892118	p12.1
SNP_A-2268958	G	G	263	115	292	92	4.024	4.49E-02	rs10247706	7	52927067	p12.1
SNP_A-2156684	G	G	215	197	245	161	5.533	1.87E-02	rs10228032	7	53035667	p12.1
SNP_A-1927261	A	A	175	173	207	135	7.317	6.80E-03	rs10251336	7	53044073	p12.1
SNP_A-2048793	G	G	344	52	305	69	4.107	4.27E-02	rs6952158	7	53045123	p12.1
SNP_A-2106762	C	C	328	72	350	50	4.681	3.05E-02	rs10276450	7	53082465	p12.1
SNP_A-1875136	C	C	218	130	177	149	4.837	2.79E-02	rs4498492	7	53087878	p12.1
SNP_A-2209619	C	C	270	124	239	159	6.197	1.28E-02	rs4947426	7	53096189	p12.1
SNP_A-1844894	C	C	328	30	354	16	5.056	2.45E-02	rs11771010	7	53103262	p12.1
SNP_A-2071784	A	A	321	63	346	42	5.116	2.37E-02	rs13441815	7	53107527	p12.1
SNP_A-1645030	C	C	366	18	387	5	7.852	5.10E-03	rs10499727	7	53865000	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2184758	C	C	402	12	413	1	9.456	2.10E-03	rs6946553	7	53990229	p11.2
SNP_A-1883061	C	C	400	10	402	2	5.294	2.14E-02	rs17738041	7	54001900	p11.2
SNP_A-2012605	A	A	385	21	399	9	5.045	0.0247	rs2330680	7	54014554	p11.2
SNP_A-2143658	T	T	280	124	310	98	4.551	3.29E-02	rs11771043	7	54309278	p11.2
SNP_A-1849427	C	C	249	139	280	112	4.701	3.02E-02	rs10215617	7	54569479	p11.2
SNP_A-2158027	T	T	256	154	275	121	4.398	3.60E-02	rs10216072	7	54570709	p11.2
SNP_A-2249666	G	G	280	46	302	24	7.746	5.40E-03	rs7780063	7	54574630	p11.2
SNP_A-1951164	G	G	350	14	379	5	4.886	2.71E-02	rs2709297	7	54608583	p11.2
SNP_A-2307420	G	G	383	27	404	14	4.605	3.19E-02	rs2709305	7	54619891	p11.2
SNP_A-1864517	T	C	194	156	189	167	5.125	2.36E-02	rs2709322	7	54631643	p11.2
SNP_A-1929482	G	G	315	19	351	9	4.55	3.29E-02	rs11981543	7	54670157	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235361	A	A	320	48	274	68	6.067	0.0138	rs13236867	7	54670368	p11.2
SNP_A-2249413	G	G	326	38	357	17	9.291	0.0023	rs7807376	7	54706015	p11.2
SNP_A-2137617	T	T	295	113	274	144	4.394	0.0361	rs10899766	7	54724760	p11.2
SNP_A-1702427	A	A	301	95	276	122	4.438	3.52E-02	rs2330915	7	54744381	p11.2
SNP_A-1664696	T	T	294	96	277	127	4.57	3.25E-02	rs2015549	7	54746618	p11.2
SNP_A-1841884	C	C	279	73	259	99	4.623	0.0315	rs4947957	7	54805713	p11.2
SNP_A-2235821	C	C	323	39	352	22	5.79	0.0161	rs6969537	7	54856627	p11.2
SNP_A-2252883	G	G	287	125	255	159	5.955	0.0147	rs12718939	7	54879529	p11.2
SNP_A-2101835	C	C	344	50	362	26	7.992	4.70E-03	rs729969	7	54902416	p11.2
SNP_A-2135346	A	A	358	58	334	84	5.588	1.81E-02	rs17586344	7	54914607	p11.2
SNP_A-2166333	T	T	269	67	318	46	6.884	8.70E-03	rs17172432	7	54915526	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2281385	T	T	262	76	299	53	6.26	0.0124	rs17172438	7	54925746	p11.2
SNP_A-2152543	C	C	207	155	245	131	4.945	2.62E-02	rs7783970	7	55064577	p11.2
SNP_A-2132459	G	G	347	11	315	23	5.212	0.0224	rs1534130	7	55083941	p11.2
SNP_A-1929477	T	T	326	50	291	77	7.64	5.70E-03	rs11982525	7	55087437	p11.2
SNP_A-2240871	C	C	256	160	287	127	5.559	0.0184	rs7805062	7	55149036	p11.2
SNP_A-2243730	A	A	270	78	250	102	3.947	0.047	rs10249105	7	55186614	p11.2
SNP_A-2211301	T	T	221	161	261	133	5.802	0.016	rs6965302	7	55239807	p11.2
SNP_A-2064488	T	T	316	38	302	58	4.434	3.52E-02	rs1722979	7	55240580	p11.2
SNP_A-1934374	C	C	288	90	241	133	12.446	4.00E-04	rs3807359	7	55266107	p11.2
SNP_A-2063645	C	C	370	30	343	49	5.512	0.0189	rs815987	7	55272814	p11.2
SNP_A-2139429	C	C	254	132	286	108	4.215	4.01E-02	rs2293322	7	55272964	p11.2
SNP_A-2206160	G	G	296	108	261	155	10.425	1.20E-03	rs712821	7	55278324	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074833	A	A	289	103	248	146	10.551	1.20E-03	rs10251825	7	55377799	p11.2
SNP_A-2281595	A	A	299	89	253	115	6.623	0.0101	rs11764362	7	55377834	p11.2
SNP_A-2250072	A	A	291	101	244	128	6.793	9.10E-03	rs1880528	7	55395933	p11.2
SNP_A-2202119	A	A	314	64	334	36	8.373	0.0038	rs10245396	7	55479775	p11.2
SNP_A-2120438	A	A	379	13	399	3	6.639	0.01	rs11981883	7	55665975	p11.2
SNP_A-1696540	G	G	270	108	295	85	3.842	5.00E-02	rs2634083	7	56441935	p11.2
SNP_A-1990010	A	A	232	166	280	120	11.894	6.00E-04	rs1543109	7	56506407	p11.2
SNP_A-1802722	G	G	245	169	296	122	12.38	4.00E-04	rs1387072	7	56509337	p11.2
SNP_A-2069639	T	T	228	148	273	109	9.913	1.60E-03	rs2634096	7	56520781	p11.2
SNP_A-2012620	C	C	239	115	275	71	12.84	3.00E-04	rs2671206	7	56528235	p11.2
SNP_A-1804055	A	A	270	132	244	164	4.73	2.96E-02	rs3885714	7	57020354	p11.1
SNP_A-1796524	A	A	277	61	243	95	9.633	0.0019	rs3860829	7	57122651	p11.1
SNP_A-2312162	C	C	250	110	275	85	4.396	3.60E-02	rs11765617	7	57127573	p11.1
SNP_A-1755050	T	T	350	36	343	57	4.565	3.26E-02	rs4095884	7	57526720	p11.2
SNP_A-2107060	G	G	258	130	295	93	8.615	0.0033	rs2382609	7	61431488	q11.21
SNP_A-1656697	C	C	358	38	345	65	7.077	7.80E-03	rs1595989	7	61841131	q11.21
SNP_A-2105961	C	C	268	86	292	54	8.253	4.10E-03	rs17748654	7	61929252	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1670704	T	T	267	131	308	104	5.785	1.62E-02	rs1533823	7	61945255	q11.21
SNP_A-1912675	T	T	342	40	316	62	5.752	1.65E-02	rs2686846	7	61954133	q11.21
SNP_A-1797703	A	A	368	32	348	60	9.002	2.70E-03	rs2582705	7	61961779	q11.21
SNP_A-1956721	G	G	284	92	296	60	6.443	0.0111	rs6956675	7	62021920	q11.21
SNP_A-2047506	C	C	278	60	290	24	14.819	0.0001	rs1608134	7	62097757	q11.21
SNP_A-2246264	C	C	365	31	380	12	8.677	3.20E-03	rs2952514	7	62676013	q11.21
SNP_A-2134968	C	C	411	5	420	0	5.078	2.42E-02	rs2019225	7	62762408	q11.21
SNP_A-2012626	C	C	290	52	289	81	5.232	2.22E-02	rs623142	7	63196433	q11.21
SNP_A-2067241	A	-	195	139	163	163	4.671	3.07E-02	rs10224870	7	63357511	q11.21
SNP_A-2012630	G	G	371	45	393	27	5.114	2.37E-02	rs3110902	7	64819252	q11.21
SNP_A-1791753	T	T	349	35	368	14	9.498	2.10E-03	rs958550	7	65079829	q11.21
SNP_A-1855416	G	G	353	13	382	4	5.381	2.04E-02	rs6958420	7	65195321	q11.21
SNP_A-2065427	G	G	195	135	228	108	5.521	1.88E-02	rs7783779	7	65240776	q11.21
SNP_A-2105378	A	A	202	172	237	151	3.9	4.83E-02	rs10244498	7	65560206	q11.21
SNP_A-2272581	G	G	312	32	339	15	7.127	0.0076	rs1573944	7	65683953	q11.21
SNP_A-1944002	C	C	360	56	340	78	4.179	4.09E-02	rs12532805	7	65821384	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1751691	G	G	354	16	352	38	8.448	3.70E-03	rs3800818	7	65832759	q11.21
SNP_A-2108629	A	A	314	102	354	66	10.091	0.0015	rs4718584	7	66398998	q11.21
SNP_A-1888483	A	A	280	64	333	49	4.597	3.20E-02	rs11980024	7	66407511	q11.21
SNP_A-1888213	A	A	320	84	351	59	5.759	1.64E-02	rs6460356	7	66407883	q11.21
SNP_A-2153924	C	C	259	153	213	197	10.01	1.60E-03	rs1024591	7	66590609	q11.22
SNP_A-2285782	G	G	262	152	219	195	9.173	2.50E-03	rs2530429	7	66604588	q11.22
SNP_A-2115750	A	A	256	156	220	190	6.059	0.0138	rs2530433	7	66607645	q11.22
SNP_A-1912485	G	G	257	157	225	195	6.184	0.0129	rs9654873	7	66607855	q11.22
SNP_A-2264404	C	C	339	35	341	19	4.481	3.43E-02	rs2530435	7	66610981	q11.22
SNP_A-1883612	C	C	365	19	362	36	5.018	2.51E-02	rs12666376	7	66795201	q11.22
SNP_A-1681840	G	G	335	47	329	75	5.869	0.0154	rs727845	7	67018825	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990070	T	A	222	158	190	188	5.757	1.64E-02	rs12534426	7	67272511	q11.22
SNP_A-1790724	C	C	263	83	251	113	4.418	0.0356	rs7810583	7	67285527	q11.22
SNP_A-1815492	G	G	400	10	409	3	3.865	4.93E-02	rs1474284	7	67432534	q11.22
SNP_A-2297317	T	T	348	20	312	32	3.928	4.75E-02	rs7799454	7	67619426	q11.22
SNP_A-2198266	A	A	314	46	311	27	4.27	3.88E-02	rs2428831	7	67699496	q11.22
SNP_A-2259417	G	G	331	49	280	68	5.947	0.0147	rs1718768	7	68177168	q11.22
SNP_A-2107042	T	T	266	104	292	80	4.337	0.0373	rs1699452	7	68196575	q11.22
SNP_A-2195769	C	C	244	166	278	132	6.094	1.36E-02	rs1699451	7	68198208	q11.22
SNP_A-2238140	C	C	284	116	320	94	4.211	0.0402	rs1718610	7	68200897	q11.22
SNP_A-1932609	A	A	265	147	306	110	8.252	4.10E-03	rs2938486	7	68228512	q11.22
SNP_A-1813184	C	C	207	141	236	112	5.223	0.0223	rs2965445	7	68228987	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2223257	T	T	331	55	348	28	9.079	2.60E-03	rs2938496	7	68279843	q11.22
SNP_A-1784412	G	G	204	150	247	129	5.022	2.50E-02	rs4339527	7	68305011	q11.22
SNP_A-2206223	G	G	352	60	328	88	6.125	1.33E-02	rs41867	7	68441685	q11.22
SNP_A-1731973	C	C	319	81	304	108	4.042	4.44E-02	rs7809475	7	69512464	q11.22
SNP_A-1758254	T	T	231	165	268	138	5.026	2.50E-02	rs740166	7	69549598	q11.22
SNP_A-2262037	G	A	214	202	232	182	4.655	0.031	rs4717540	7	69551220	q11.22
SNP_A-2150876	A	T	221	165	212	182	9.553	0.002	rs1079550	7	69589180	q11.22
SNP_A-2046625	T	T	263	121	233	157	6.43	0.0112	rs6946693	7	69597719	q11.22
SNP_A-2308257	C	C	347	59	377	41	4.309	3.79E-02	rs1569079	7	69669394	q11.22
SNP_A-2249118	C	C	301	67	294	42	4.371	3.66E-02	rs12698946	7	69745997	q11.22
SNP_A-2281928	G	G	362	10	328	22	5.51	0.0189	rs1525302	7	69874832	q11.22
SNP_A-2242466	A	A	362	10	390	2	5.856	0.0155	rs4717581	7	70034600	q11.22
SNP_A-1868027	A	A	386	30	370	48	4.488	3.41E-02	rs2158733	7	70086296	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990139	T	T	369	29	351	47	4.713	2.99E-02	rs10272163	7	70087078	q11.22
SNP_A-1814256	T	C	198	174	195	163	4.322	3.76E-02	rs6974582	7	70150105	q11.22
SNP_A-1897903	A	G	209	185	224	184	5.066	2.44E-02	rs1882569	7	70178529	q11.22
SNP_A-1910376	G	A	226	184	211	175	7.615	5.80E-03	rs10950254	7	70181858	q11.22
SNP_A-2268090	C	C	323	85	337	57	5.575	1.82E-02	rs10272997	7	70209167	q11.22
SNP_A-1888248	A	A	360	8	388	2	4.013	4.52E-02	rs11976167	7	70300825	q11.22
SNP_A-1835631	C	C	355	35	388	22	3.933	4.73E-02	rs11975195	7	70573052	q11.22
SNP_A-2094698	G	G	394	18	379	37	6.836	8.90E-03	rs12699086	7	70695362	q11.22
SNP_A-2169582	C	C	295	91	251	109	4.265	3.89E-02	rs6964517	7	70820411	q11.22
SNP_A-2031412	T	T	355	59	336	82	4.255	3.91E-02	rs6961327	7	70841292	q11.22
SNP_A-2126598	C	C	305	67	335	49	4.01	4.52E-02	rs12673109	7	70986852	q11.22
SNP_A-2057322	C	C	324	90	352	68	4.18	4.09E-02	rs10950297	7	71018779	q11.22
SNP_A-2202626	T	T	267	73	314	52	6.381	0.0115	rs9638643	7	71124932	q11.22
SNP_A-2304543	T	T	299	73	340	52	5.639	1.76E-02	rs479035	7	71155926	q11.22
SNP_A-2196497	T	T	347	35	334	18	4.482	3.42E-02	rs1914378	7	71279583	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2066201	G	G	277	125	307	101	4.046	4.43E-02	rs2909985	7	71345426	q11.22
SNP_A-1868526	A	A	354	42	341	63	4.364	3.67E-02	rs7779186	7	71413281	q11.22
SNP_A-1890326	T	T	341	43	368	22	7.767	0.0053	rs4361659	7	71451749	q11.22
SNP_A-2081058	C	C	298	66	283	91	4.233	3.96E-02	rs2286276	7	72432005	q11.23
SNP_A-2299263	C	C	212	154	180	178	4.259	0.039	rs6975355	7	72850106	q11.23
SNP_A-2250981	C	C	354	52	378	34	4.511	3.37E-02	rs4412258	7	73513102	q11.23
SNP_A-1803741	A	A	324	74	353	51	5.43	1.98E-02	rs1167793	7	74816073	q11.23
SNP_A-1838304	G	G	341	23	327	39	4.417	0.0356	rs10277880	7	74905322	q11.23
SNP_A-1863583	A	A	274	120	256	152	4.133	4.21E-02	rs4732416	7	75086413	q11.23
SNP_A-2209732	C	C	277	55	260	82	5.712	1.68E-02	rs757589	7	75140175	q11.23
SNP_A-1671884	G	G	339	61	320	90	5.995	0.0143	rs10488574	7	75536081	q11.23
SNP_A-2073386	T	T	398	4	410	0	4.1	4.29E-02	rs868269	7	75652460	q11.23
SNP_A-2263000	G	G	340	4	352	0	4.117	4.25E-02	rs17155678	7	76464940	q11.23
SNP_A-1799822	C	C	355	9	349	25	7.446	6.40E-03	—	7	76466493	q11.23
SNP_A-2259788	G	G	395	21	413	7	7.382	0.0066	rs10224522	7	76542150	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2067311	G	G	305	99	280	130	5.221	0.0223	rs10953284	7	76814433	q11.23
SNP_A-1990207	C	C	216	108	230	80	4.303	3.81E-02	rs2109923	7	76861797	q11.23
SNP_A-2104908	G	G	191	151	223	129	4.059	4.39E-02	rs9691617	7	76904486	q11.23
SNP_A-2258541	C	T	225	169	201	195	4.905	2.68E-02	rs9986707	7	77026914	q11.23
SNP_A-2183607	C	C	228	142	192	168	5.13	0.0235	rs9986891	7	77026939	q11.23
SNP_A-1935975	C	C	387	11	393	3	4.613	3.17E-02	rs6970749	7	77071274	q11.23
SNP_A-1949990	C	C	383	23	367	41	5.399	0.0201	rs17158527	7	77103976	q11.23
SNP_A-2083838	G	G	367	23	348	42	6.059	0.0138	rs12537648	7	77128426	q11.23
SNP_A-2221100	C	T	231	175	210	208	4.213	4.01E-02	rs848461	7	77226916	q21.11
SNP_A-2245875	C	C	311	99	285	127	4.598	3.20E-02	rs848473	7	77239321	q21.11
SNP_A-2111723	C	C	293	109	272	140	4.518	3.35E-02	rs10238177	7	77514659	q21.11
SNP_A-1686004	C	C	244	144	216	176	4.884	2.71E-02	rs1477033	7	77708530	q21.11
SNP_A-1885907	G	G	363	35	368	14	8.71	3.20E-03	rs17150823	7	77731078	q21.11
SNP_A-2305636	A	A	244	150	215	181	4.731	2.96E-02	rs17372719	7	77834836	q21.11
SNP_A-1756078	A	A	282	94	314	72	4.503	3.38E-02	rs319871	7	77841475	q21.11
SNP_A-2226306	G	G	254	108	227	135	4.516	3.36E-02	rs1390824	7	77987830	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072764	G	G	341	37	373	21	5.519	1.88E-02	rs37884	7	78082005	q21.11
SNP_A-2012680	C	C	303	31	299	15	4.979	2.57E-02	rs6466533	7	78437543	q21.11
SNP_A-1990278	C	C	344	28	351	13	5.472	1.93E-02	rs2886214	7	78691126	q21.11
SNP_A-1673122	G	G	339	61	363	39	5.656	1.74E-02	rs10254386	7	79350567	q21.11
SNP_A-1818077	A	A	335	73	364	52	4.654	0.031	rs17153558	7	79470150	q21.11
SNP_A-1848789	T	T	266	92	299	67	5.771	1.63E-02	rs17245731	7	79477284	q21.11
SNP_A-2299198	G	G	356	28	348	8	10.157	0.0014	rs471775	7	79668575	q21.11
SNP_A-1919384	C	C	380	0	324	4	4.66	0.0309	rs6958853	7	79984343	q21.11
SNP_A-1747683	G	G	393	7	409	1	4.696	3.02E-02	rs2886792	7	79988312	q21.11
SNP_A-2063945	G	G	410	6	420	0	6.101	0.0135	rs1527467	7	80004457	q21.11
SNP_A-2299589	G	G	408	4	420	0	4.097	4.29E-02	rs1949971	7	80018993	q21.11
SNP_A-1862888	A	A	397	5	373	15	5.502	0.019	rs12673722	7	80054195	q21.11
SNP_A-1681622	C	C	296	68	341	45	7.221	7.20E-03	rs853042	7	80253141	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990320	A	A	273	73	287	43	7.734	5.40E-03	rs1636559	7	80333194	q21.11
SNP_A-1925246	A	A	231	143	251	105	6.212	1.27E-02	rs6956639	7	80413351	q21.11
SNP_A-2095389	T	T	355	39	316	58	5.471	1.93E-02	rs6969041	7	80598314	q21.11
SNP_A-1652690	G	G	275	123	315	93	6.756	9.30E-03	rs1023534	7	80640950	q21.11
SNP_A-1990326	A	A	333	43	358	24	6.245	1.25E-02	rs10486822	7	80666613	q21.11
SNP_A-1847535	T	T	208	182	244	152	5.516	1.88E-02	rs2967913	7	80703254	q21.11
SNP_A-1913668	G	G	381	29	391	13	6.181	0.0129	rs2217183	7	80871056	q21.11
SNP_A-1847235	G	G	303	81	330	60	4.233	3.96E-02	rs10954663	7	81391271	q21.11
SNP_A-1734588	A	A	389	11	405	3	4.815	2.82E-02	rs10486949	7	81413420	q21.11
SNP_A-1960563	G	G	252	116	281	81	7.747	5.40E-03	rs1157097	7	81415638	q21.11
SNP_A-1960834	C	C	358	24	343	39	3.892	4.85E-02	rs2367910	7	81430694	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2219919	G	G	294	120	255	145	4.89	0.027	rs42489	7	81599031	q21.11
SNP_A-2040614	G	G	283	109	261	141	4.861	0.0275	rs42342	7	81599269	q21.11
SNP_A-2151209	G	G	415	1	413	7	4.486	3.42E-02	rs17156266	7	81684457	q21.11
SNP_A-1746254	C	C	282	118	259	153	5.322	2.11E-02	rs10486967	7	81765454	q21.11
SNP_A-1671462	C	C	357	33	337	55	6.071	0.0137	rs9791531	7	81809099	q21.11
SNP_A-2022393	T	T	297	115	335	81	8.164	0.0043	rs11972597	7	81813518	q21.11
SNP_A-2271278	C	C	416	0	416	4	3.981	4.60E-02	rs13221663	7	81816159	q21.11
SNP_A-2209616	G	G	414	0	414	4	3.981	4.60E-02	rs12707507	7	81827090	q21.11
SNP_A-1990371	T	T	370	42	389	23	6.029	0.0141	rs7785190	7	81876973	q21.11
SNP_A-1658152	C	C	358	42	385	27	4.066	4.38E-02	rs916853	7	81907480	q21.11
SNP_A-1702521	C	T	228	162	207	205	6.111	0.0134	rs10486985	7	81998133	q21.11
SNP_A-1727599	G	T	173	165	196	150	4.207	4.03E-02	rs2158219	7	82011242	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903941	C	C	254	158	222	192	5.449	1.96E-02	rs6959361	7	82033900	q21.11
SNP_A-1707131	C	C	241	159	216	196	5.048	0.0247	rs2715158	7	82081657	q21.11
SNP_A-1922407	C	C	265	101	226	134	7.683	5.60E-03	rs2522834	7	82105597	q21.11
SNP_A-1958111	G	G	205	119	183	163	7.398	6.50E-03	rs2522843	7	82124373	q21.11
SNP_A-2132324	T	C	169	151	204	150	7.348	6.70E-03	rs2888019	7	82148060	q21.11
SNP_A-2213794	C	C	354	46	381	29	4.722	0.0298	rs12666205	7	82436090	q21.11
SNP_A-1892665	G	T	222	172	204	194	4.588	3.22E-02	rs2189116	7	82501849	q21.11
SNP_A-2228706	G	G	329	79	354	56	4.829	2.80E-02	rs2709920	7	82567349	q21.11
SNP_A-1990398	C	C	393	11	403	3	4.692	3.03E-02	rs17157992	7	82994358	q21.11
SNP_A-1860706	T	T	370	18	384	6	6.255	0.0124	rs6943654	7	82996691	q21.11
SNP_A-2023531	C	C	392	16	391	3	8.654	0.0033	rs6967717	7	82998727	q21.11
SNP_A-1835359	G	G	396	18	406	4	9.015	2.70E-03	rs6968843	7	82998783	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1820795	T	T	391	15	394	4	6.301	0.0121	rs17158091	7	83040168	q21.11
SNP_A-2121599	A	A	287	87	306	58	6.274	1.22E-02	rs7796199	7	83222053	q21.11
SNP_A-1923413	C	C	265	83	289	61	4.395	3.60E-02	rs7802100	7	83232566	q21.11
SNP_A-1946404	G	G	308	84	330	60	4.754	0.0292	rs6963635	7	83238456	q21.11
SNP_A-1943946	C	C	381	35	386	20	4.002	4.54E-02	rs11976275	7	83480084	q21.11
SNP_A-1826537	G	A	190	178	219	171	4.6	3.20E-02	rs594533	7	83581215	q21.11
SNP_A-2128904	A	A	348	2	343	9	4.485	3.42E-02	rs17158998	7	83659552	q21.11
SNP_A-2055405	G	G	318	52	321	29	5.994	0.0144	rs2715038	7	83739748	q21.11
SNP_A-2266102	G	G	384	10	395	3	3.904	0.0482	rs17316553	7	84560079	q21.11
SNP_A-2146730	A	A	410	4	420	0	4.078	4.35E-02	rs17159821	7	84637301	q21.11
SNP_A-1990424	A	A	308	92	277	117	4.588	3.22E-02	rs1403786	7	84659006	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1662556	T	T	269	45	298	76	4.225	3.98E-02	rs3934484	7	84954886	q21.11
SNP_A-2311138	T	T	303	81	271	109	5.89	0.0152	rs10262303	7	85806165	q21.11
SNP_A-1748801	C	C	282	38	287	61	4.221	3.99E-02	rs727989	7	86025626	q21.12
SNP_A-2239694	A	A	342	0	354	4	3.843	0.0499	rs4728658	7	86271970	q21.12
SNP_A-2216900	A	A	325	55	301	79	5.219	0.0223	rs4236504	7	86420763	q21.12
SNP_A-1915495	T	T	384	12	376	24	4.064	4.38E-02	rs2051950	7	86640573	q21.12
SNP_A-2198487	C	C	391	19	330	36	7.946	4.80E-03	rs6977739	7	86706185	q21.12
SNP_A-1921021	G	G	269	47	297	29	5.494	1.91E-02	rs12720067	7	86814007	q21.12
SNP_A-1669879	A	A	376	24	368	44	5.792	0.0161	rs10487009	7	87395195	q21.12
SNP_A-1990470	C	C	349	53	319	83	7.965	4.80E-03	rs10268574	7	87412825	q21.12
SNP_A-1849700	A	A	336	66	312	92	5.162	2.31E-02	rs2058331	7	87611220	q21.12
SNP_A-2028496	C	C	336	68	313	97	5.868	0.0154	rs2058332	7	87611333	q21.12
SNP_A-1990472	T	T	320	70	303	99	5.26	0.0218	rs17260153	7	87626083	q21.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2257079	G	G	256	72	275	47	5.877	1.53E-02	rs1468106	7	87740608	q21.13
SNP_A-1848305	G	G	356	30	345	47	3.88	4.89E-02	rs181062	7	87754044	q21.13
SNP_A-1812729	T	T	332	50	331	29	4.936	0.0263	rs6968172	7	88092772	q21.13
SNP_A-1908057	T	T	339	23	313	43	7.048	7.90E-03	rs2213984	7	88275081	q21.13
SNP_A-2281265	C	C	399	7	413	1	4.664	3.08E-02	rs16868596	7	88308913	q21.13
SNP_A-1990503	C	C	266	62	287	43	4.23	3.97E-02	rs1208854	7	88549428	q21.13
SNP_A-1809974	T	T	360	14	326	26	4.623	3.16E-02	rs12704504	7	89252653	q21.13
SNP_A-2214495	T	T	382	12	359	23	3.986	4.59E-02	rs17620438	7	89331811	q21.13
SNP_A-2174177	T	T	308	52	213	73	12.538	4.00E-04	rs39200	7	89378708	q21.13
SNP_A-2212131	T	G	196	192	211	161	3.992	4.57E-02	rs12704550	7	89871592	q21.13
SNP_A-2195552	A	A	392	6	394	16	4.373	3.65E-02	rs11563828	7	89891834	q21.13
SNP_A-1826967	C	C	399	5	404	0	5.031	2.49E-02	rs17476298	7	90167730	q21.13
SNP_A-1851769	C	C	400	6	399	17	5.141	2.34E-02	rs705345	7	90278692	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990561	G	G	280	72	299	47	5.824	1.58E-02	rs17163799	7	90590566	q21.13
SNP_A-1720451	C	C	366	20	373	9	4.218	4.00E-02	rs7787692	7	90786292	q21.2
SNP_A-1702357	C	C	207	165	230	136	3.956	4.67E-02	rs2110770	7	90806736	q21.2
SNP_A-1862016	A	C	201	153	183	175	4.454	3.48E-02	rs2540569	7	90852350	q21.2
SNP_A-2248434	T	T	265	101	292	76	4.834	2.79E-02	rs42992	7	91050774	q21.2
SNP_A-1652086	G	G	387	13	407	5	3.883	4.88E-02	rs2066743	7	91759403	q21.2
SNP_A-1661432	C	C	268	132	245	167	4.952	2.61E-02	rs10236337	7	92259808	q21.2
SNP_A-1823111	T	T	328	20	311	35	4.537	0.0332	rs3802062	7	92546210	q21.3
SNP_A-2160088	A	A	376	16	384	4	7.264	7.00E-03	—	7	92731803	q21.3
SNP_A-1755358	G	G	389	1	399	7	4.307	3.80E-02	rs10234339	7	92742846	q21.3
SNP_A-2274692	G	G	369	33	383	19	4.03	4.47E-02	rs718048	7	93038160	q21.3
SNP_A-2284225	G	G	326	28	360	14	5.807	0.016	rs10953104	7	93153996	q21.3
SNP_A-1943756	T	T	362	24	355	51	9.289	0.0023	rs4729116	7	93624250	q21.3
SNP_A-1740497	A	A	223	173	264	146	5.495	1.91E-02	rs4729134	7	93684956	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1736623	G	G	359	37	352	58	4.469	3.45E-02	rs10499907	7	93803117	q21.3
SNP_A-1904439	A	A	334	38	297	57	5.527	1.87E-02	rs11983951	7	93851444	q21.3
SNP_A-1715123	G	G	278	110	260	150	6.154	1.31E-02	rs3917498	7	94558284	q21.3
SNP_A-2012726	G	G	363	7	341	1	4.093	4.31E-02	rs3917464	7	94599396	q21.3
SNP_A-1801924	T	C	210	158	188	178	5.235	2.21E-02	rs10953143	7	94636895	q21.3
SNP_A-2191263	T	T	369	37	383	21	4.67	3.07E-02	rs468	7	94642604	q21.3
SNP_A-2078902	G	A	228	184	217	197	4.972	0.0258	rs1053275	7	94646206	q21.3
SNP_A-2228559	T	T	289	93	256	124	6.422	1.13E-02	rs10953149	7	94733760	q21.3
SNP_A-1897120	C	C	279	107	229	141	9.248	2.40E-03	rs6950550	7	94754078	q21.3
SNP_A-1706845	A	A	333	65	320	90	4.114	4.25E-02	rs2158047	7	94763968	q21.3
SNP_A-1953102	T	T	399	17	388	32	4.727	2.97E-02	rs10260514	7	94959341	q21.3
SNP_A-2159202	T	T	305	23	290	46	7.95	4.80E-03	rs2171555	7	95132709	q21.3
SNP_A-2039364	C	C	354	38	362	22	4.274	3.87E-02	rs3847049	7	95149463	q21.3
SNP_A-1722832	G	G	273	127	315	93	8.176	4.20E-03	rs1488516	7	95175420	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1952190	C	C	279	121	310	94	5.002	0.0253	rs319339	7	95234041	q21.3
SNP_A-1823464	A	A	278	116	309	91	4.611	3.18E-02	rs1029393	7	95242264	q21.3
SNP_A-1879691	G	G	284	126	316	102	4.156	4.15E-02	rs9640639	7	95243166	q21.3
SNP_A-2262372	T	T	231	165	256	136	4.057	4.40E-02	rs1029391	7	95461882	q21.3
SNP_A-2080444	A	A	256	152	291	121	5.74	0.0166	rs11763512	7	95555459	q21.3
SNP_A-1960740	G	G	227	119	264	86	8.078	4.50E-03	rs2375057	7	95587782	q21.3
SNP_A-2293401	G	G	232	138	266	112	4.94	2.62E-02	rs12704845	7	95588227	q21.3
SNP_A-1990664	G	G	409	5	402	14	4.319	3.77E-02	rs6964209	7	95665085	q21.3
SNP_A-1942576	A	A	208	110	188	140	4.456	3.48E-02	rs1989968	7	95694149	q21.3
SNP_A-2086187	G	G	358	56	375	37	4.271	3.88E-02	rs9656041	7	96132847	q21.3
SNP_A-1990679	A	A	379	25	403	11	6.06	0.0138	rs10486858	7	96185079	q21.3
SNP_A-1864166	A	A	365	19	391	9	4.141	0.0419	---	7	96192366	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1916453	A	A	322	34	338	20	4.012	4.52E-02	rs4727353	7	96205635	q21.3
SNP_A-1869815	C	C	392	22	408	10	4.801	2.84E-02	rs4729322	7	96206100	q21.3
SNP_A-2075212	C	C	366	50	390	30	5.743	0.0166	rs17252863	7	96829074	q21.3
SNP_A-1892282	C	C	294	22	303	45	6.504	1.08E-02	rs2665452	7	97091734	q21.3
SNP_A-2092914	T	T	293	75	325	47	8.062	4.50E-03	rs12704945	7	97093405	q21.3
SNP_A-2184780	G	G	324	58	346	40	4.008	0.0453	rs7792742	7	97098965	q21.3
SNP_A-1912334	G	G	331	79	351	49	7.495	6.20E-03	rs12668997	7	97110539	q21.3
SNP_A-2192110	A	A	305	55	293	79	4.344	3.71E-02	rs1049674	7	97133220	q21.3
SNP_A-2129307	T	T	376	12	387	3	5.553	0.0184	rs4727384	7	97292082	q21.3
SNP_A-1852383	G	G	319	55	336	30	7.709	5.50E-03	rs2107718	7	97650113	q22.1
SNP_A-1790718	C	C	308	98	332	74	4.249	3.93E-02	rs12539761	7	97658490	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical Position	Cytoband
SNP_A-2270967	G	G	371	1	364	10	7.425	6.40E-03	rs4729465	7	97933845	q22.1
SNP_A-2210571	C	C	406	4	414	0	4.059	4.39E-02	rs41644	7	98212668	q22.1
SNP_A-2023141	A	A	334	12	327	1	8.907	0.0028	rs12721625	7	99020441	q22.1
SNP_A-1789679	C	C	217	131	195	165	4.878	2.72E-02	rs2158738	7	100748945	q22.1
SNP_A-2073506	A	A	322	20	313	41	7.152	7.50E-03	rs11974028	7	101041279	q22.1
SNP_A-2201451	C	C	379	21	371	9	4.375	3.65E-02	rs11560369	7	102445422	q22.1
SNP_A-2033595	T	T	231	107	250	80	4.554	3.28E-02	rs2109697	7	102827160	q22.1
SNP_A-1990750	T	T	300	66	331	39	8.444	3.70E-03	rs2283029	7	102992170	q22.1
SNP_A-1846964	G	G	199	147	217	103	7.519	6.10E-03	rs1705107	7	102997027	q22.1
SNP_A-1960004	A	A	184	134	211	103	5.875	0.0154	rs262339	7	103011829	q22.1
SNP_A-2023037	T	T	297	111	337	83	6.392	0.0115	rs4729931	7	103032793	q22.1
SNP_A-1847665	G	G	365	43	341	67	6.052	1.39E-02	rs13233763	7	103078327	q22.1
SNP_A-1681568	A	A	363	41	338	64	5.925	0.0149	rs10487173	7	103098529	q22.1
SNP_A-2140345	T	T	392	18	375	45	11.829	6.00E-04	rs17321820	7	103105356	q22.1
SNP_A-2273945	C	C	368	44	342	66	5.333	2.09E-02	rs2299394	7	103105894	q22.1
SNP_A-2066020	A	A	361	37	330	54	4.317	3.77E-02	rs2283034	7	103112000	q22.1
SNP_A-1922961	T	T	329	37	319	57	4.276	3.87E-02	rs2237641	7	103113722	q22.1
SNP_A-2303302	T	T	325	27	326	50	6.087	1.36E-02	rs3857819	7	103141086	q22.1
SNP_A-2012759	C	C	382	12	377	25	4.521	3.35E-02	rs4729950	7	103281006	q22.1
SNP_A-1744929	T	T	338	58	372	32	9.06	2.60E-03	rs441027	7	103703166	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2238923	C	C	307	55	352	32	8.512	3.50E-03	rs41038	7	103739832	q22.2
SNP_A-1866034	A	A	244	124	216	158	5.755	1.64E-02	rs28253	7	103748801	q22.2
SNP_A-1723124	C	C	273	125	246	166	6.941	8.40E-03	rs4727605	7	103818268	q22.2
SNP_A-1901174	T	T	221	185	254	154	5.123	2.36E-02	rs995661	7	103881778	q22.2
SNP_A-1681382	A	A	345	55	330	82	5.478	1.93E-02	rs4338031	7	103919757	q22.2
SNP_A-2012760	C	C	341	75	369	51	5.657	1.74E-02	rs4584085	7	103956655	q22.2
SNP_A-2112194	A	A	281	121	247	145	4.23	3.97E-02	rs2470965	7	104025139	q22.2
SNP_A-1906859	A	G	221	165	193	189	4.667	3.08E-02	rs10435352	7	104846669	q22.3
SNP_A-1805526	A	A	340	36	329	17	5.756	1.64E-02	rs505288	7	104955786	q22.3
SNP_A-1930791	C	C	275	67	258	102	7.334	6.80E-03	rs13235564	7	104972579	q22.3
SNP_A-2158491	G	G	295	51	311	33	4.274	3.87E-02	rs17152107	7	105007873	q22.3
SNP_A-1680900	G	G	344	36	332	56	4.478	3.43E-02	rs10487836	7	105048861	q22.3
SNP_A-2152458	G	G	314	86	325	61	4.193	4.06E-02	rs17152480	7	105260081	q22.3
SNP_A-2023639	C	C	327	61	345	37	6.313	0.012	rs6959584	7	105270456	q22.3
SNP_A-2160068	C	C	332	66	360	46	4.625	0.0315	rs17152488	7	105270796	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1875945	A	A	341	1	373	9	5.641	1.75E-02	rs176506	7	105349516	q22.3
SNP_A-1808719	G	G	409	1	402	10	7.419	6.50E-03	rs176510	7	105351860	q22.3
SNP_A-2092080	T	T	297	37	277	57	4.952	2.61E-02	rs17153078	7	105652423	q22.3
SNP_A-1665796	G	G	227	163	277	133	7.506	6.20E-03	rs10486020	7	105707800	q22.3
SNP_A-2280031	G	G	186	184	227	159	5.556	0.0184	rs9886235	7	105750204	q22.3
SNP_A-1757247	G	A	212	186	240	172	10.773	0.001	rs342242	7	105899520	q22.3
SNP_A-1718775	T	C	200	146	200	170	10.067	0.0015	rs10274553	7	105917177	q22.3
SNP_A-1781296	C	G	233	181	222	198	6.971	8.30E-03	rs4727657	7	105918009	q22.3
SNP_A-1725478	C	C	389	11	409	3	4.896	0.0269	rs10487917	7	105920940	q22.3
SNP_A-1847203	C	C	188	184	230	150	7.597	5.80E-03	rs342275	7	105953167	q22.3
SNP_A-1990823	C	G	199	167	199	143	11.167	8.00E-04	rs342293	7	105966170	q22.3
SNP_A-2246987	G	G	299	81	331	59	4.954	2.60E-02	rs12705390	7	106004728	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2111397	C	T	219	189	219	191	4.113	4.25E-02	rs7791727	7	106014801	q22.3
SNP_A-1684666	C	T	209	191	230	182	5.301	2.13E-02	rs717099	7	106301469	q22.3
SNP_A-2237792	T	T	305	67	344	46	5.824	1.58E-02	rs7785892	7	106528126	q22.3
SNP_A-2268166	G	G	331	29	303	47	5.36	0.0206	rs7799849	7	106900372	q31.1
SNP_A-2261826	A	A	229	173	238	134	3.971	4.63E-02	rs11769313	7	106907898	q31.1
SNP_A-1831925	A	G	190	160	165	141	4.399	3.60E-02	rs11977213	7	106927265	q31.1
SNP_A-2104602	G	G	190	186	216	154	4.629	3.14E-02	rs2283044	7	107034504	q31.1
SNP_A-2169579	A	A	210	182	242	150	5.35	0.0207	rs6959729	7	107040131	q31.1
SNP_A-1936669	T	T	166	162	203	143	4.416	0.0356	rs7805114	7	107043984	q31.1
SNP_A-2244085	C	C	376	4	378	0	4	4.55E-02	rs17155022	7	107356377	q31.1
SNP_A-1990850	G	G	298	52	294	76	3.975	4.62E-02	rs439652	7	107423811	q31.1
SNP_A-2209216	G	G	343	23	366	10	5.734	0.0166	rs12112172	7	107978422	q31.1
SNP_A-2012794	C	C	384	12	387	3	5.366	2.05E-02	rs1404697	7	108138412	q31.1
SNP_A-1842142	T	T	347	17	328	32	5.105	2.39E-02	rs10953597	7	108423780	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990870	A	A	241	165	273	139	4.172	4.11E-02	rs1525031	7	108450039	q31.1
SNP_A-1715115	C	C	321	79	354	58	4.656	0.0309	rs10487317	7	109472226	q31.1
SNP_A-2100338	T	T	247	77	280	56	5.166	0.023	rs12671447	7	109505287	q31.1
SNP_A-1665566	G	G	317	83	289	121	8.25	4.10E-03	rs2159700	7	109577501	q31.1
SNP_A-1990891	C	C	306	52	259	73	6.467	1.10E-02	rs1859027	7	109580982	q31.1
SNP_A-1990892	G	G	319	59	294	82	4.766	2.90E-02	rs2159699	7	109610860	q31.1
SNP_A-2282554	A	A	292	56	282	34	4.019	4.50E-02	rs17157642	7	109617312	q31.1
SNP_A-1920487	G	G	319	63	295	105	11.03	9.00E-04	rs12705683	7	109617970	q31.1
SNP_A-1786632	T	T	332	78	298	108	6.654	9.90E-03	rs4140833	7	109621763	q31.1
SNP_A-1990893	G	G	243	129	215	163	5.623	0.0177	rs10487324	7	109630552	q31.1
SNP_A-2091208	T	T	292	92	317	69	4.307	3.80E-02	rs1354991	7	109752197	q31.1
SNP_A-1694563	C	C	281	109	322	90	4.001	4.55E-02	rs10499993	7	109920844	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082191	T	T	253	139	268	104	4.953	2.60E-02	rs7810543	7	110488729	q31.1
SNP_A-1814956	G	G	304	8	307	25	8.159	0.0043	rs11772348	7	110855621	q31.1
SNP_A-2129441	C	T	214	158	178	170	5.438	1.97E-02	rs1544475	7	110879771	q31.1
SNP_A-2046736	G	G	245	79	264	56	4.603	3.19E-02	rs2074119	7	110993928	q31.1
SNP_A-1781916	G	G	392	0	300	6	7.753	5.40E-03	rs2040628	7	111228587	q31.1
SNP_A-1641945	A	A	372	4	402	0	4.289	3.81E-02	rs10487339	7	111283467	q31.1
SNP_A-1990923	G	G	363	49	345	71	4.472	3.45E-02	rs2106913	7	111334604	q31.1
SNP_A-2139720	C	C	333	25	341	13	3.862	4.94E-02	rs10953703	7	111403091	q31.1
SNP_A-2047341	C	C	319	29	354	14	6.499	1.08E-02	rs6971023	7	111423407	q31.1
SNP_A-2056609	T	T	358	26	334	12	4.023	4.49E-02	rs2708588	7	111624446	q31.1
SNP_A-1874555	C	C	341	53	361	29	7.574	5.90E-03	rs4329201	7	112038044	q31.1
SNP_A-1788870	C	C	266	98	282	72	4.305	3.80E-02	rs821785	7	112058792	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1990936	T	T	274	106	300	82	4.236	3.96E-02	rs821783	7	112063729	q31.1
SNP_A-1785328	A	A	288	118	310	90	4.534	0.0332	rs821787	7	112070707	q31.1
SNP_A-1990937	A	A	290	120	320	94	4.615	3.17E-02	rs685259	7	112130691	q31.1
SNP_A-1743199	G	G	306	56	345	41	3.89	4.86E-02	rs10500014	7	112164518	q31.1
SNP_A-1794178	A	A	252	102	227	129	4.455	3.48E-02	rs10953726	7	112442580	q31.1
SNP_A-1990952	T	T	271	135	240	160	3.955	4.67E-02	rs10500030	7	112684977	q31.1
SNP_A-1926768	T	A	196	168	201	165	5.608	1.79E-02	rs6962108	7	112694540	q31.1
SNP_A-2300178	G	T	219	163	188	180	5.333	2.09E-02	rs12705875	7	112694658	q31.1
SNP_A-2254610	C	C	373	33	379	17	5.044	0.0247	rs12705950	7	113363138	q31.1
SNP_A-2289324	A	A	354	16	366	6	4.74	2.95E-02	rs12705958	7	113539446	q31.1
SNP_A-2089872	C	C	368	44	390	28	4.151	4.16E-02	rs17137135	7	113814810	q31.1
SNP_A-2195367	G	G	313	25	334	12	5.156	2.32E-02	rs662217	7	113939451	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1785075	A	A	384	20	404	8	5.573	1.82E-02	rs627579	7	113954902	q31.1
SNP_A-1894687	G	G	371	27	386	12	6.066	0.0138	rs589252	7	113976340	q31.1
SNP_A-2193310	A	A	346	28	333	13	4.655	0.031	rs9649371	7	114022264	q31.1
SNP_A-1790763	G	G	381	35	403	15	8.613	0.0033	rs1448351	7	114041599	q31.1
SNP_A-1908638	A	A	348	32	372	14	7.797	5.20E-03	rs1011449	7	114048288	q31.1
SNP_A-2214348	C	C	373	31	394	14	6.978	8.30E-03	rs289194	7	114048745	q31.1
SNP_A-1813949	G	G	301	39	347	21	7.57	5.90E-03	rs1971627	7	114054271	q31.1
SNP_A-2201052	C	C	309	21	337	7	7.926	4.90E-03	rs289198	7	114057339	q31.1
SNP_A-2174638	G	G	383	29	406	14	5.827	1.58E-02	rs989714	7	114058865	q31.1
SNP_A-1990967	T	T	387	29	405	15	4.845	2.77E-02	rs2007801	7	114067491	q31.1
SNP_A-2167241	A	A	336	24	354	12	4.42	3.55E-02	rs4730650	7	114100216	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1744617	G	G	365	33	395	17	6.064	0.0138	rs4609131	7	114137601	q31.1
SNP_A-1836165	C	C	352	24	392	6	12.335	4.00E-04	rs4595064	7	114173986	q31.1
SNP_A-2012821	C	C	371	33	401	13	9.741	0.0018	rs4551278	7	114177708	q31.1
SNP_A-1953623	G	G	412	4	418	0	4.039	4.45E-02	rs4727818	7	114729171	q31.2
SNP_A-1895489	A	A	329	63	334	42	3.906	4.81E-02	rs1004108	7	115454915	q31.2
SNP_A-1854038	G	G	319	87	297	113	4.146	4.17E-02	rs4808	7	116122191	q31.2
SNP_A-2282454	G	G	382	32	367	53	5.446	1.96E-02	rs17139625	7	116529429	q31.2
SNP_A-2236034	T	T	316	48	278	68	5.426	1.98E-02	rs7790040	7	117136858	q31.31
SNP_A-1709113	A	C	224	176	212	200	4.522	3.35E-02	rs2402460	7	118329604	q31.31
SNP_A-1959439	G	G	196	158	207	111	6.603	1.02E-02	rs12536780	7	118418005	q31.31
SNP_A-1991037	G	A	182	132	168	156	6.165	1.30E-02	rs7456900	7	118419061	q31.31
SNP_A-2065603	A	C	231	185	220	198	5.558	0.0184	rs4130671	7	118871088	q31.31
SNP_A-2061160	G	A	210	170	203	167	7.692	5.50E-03	rs10464520	7	118876968	q31.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259856	G	G	222	134	179	149	4.267	3.89E-02	rs4727899	7	118943150	q31.31
SNP_A-1880544	T	T	362	6	378	0	6.213	1.27E-02	rs17142823	7	119789559	q31.31
SNP_A-2246640	G	G	379	7	361	1	4.172	4.11E-02	rs1997229	7	119833868	q31.31
SNP_A-2216040	G	G	381	13	401	5	3.888	4.86E-02	rs3757557	7	120092317	q31.31
SNP_A-1937088	G	G	309	107	340	80	5.36	0.0206	rs2536163	7	120596861	q31.31
SNP_A-2139022	T	T	300	98	335	73	5.461	1.94E-02	rs2707479	7	120602154	q31.31
SNP_A-1892458	T	T	309	103	335	79	4.21	0.0402	rs1990446	7	120604160	q31.31
SNP_A-2294316	C	C	307	87	265	117	7.312	6.90E-03	rs10270768	7	120668544	q31.31
SNP_A-2105584	T	T	335	79	310	106	4.905	2.68E-02	rs11521035	7	120684404	q31.31
SNP_A-1991076	G	G	309	29	290	46	4.45	0.0349	rs11974324	7	120915076	q31.32
SNP_A-2267172	A	A	414	0	415	5	4.958	2.60E-02	rs10262109	7	121038150	q31.32
SNP_A-2288664	A	A	367	27	344	44	4.769	2.90E-02	rs17144099	7	121349753	q31.32
SNP_A-1808902	T	T	329	7	357	1	4.95	2.61E-02	rs12538802	7	121784831	q31.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical Position	Cytoband
SNP_A-1839409	A	A	341	69	370	50	4.097	4.30E-02	rs17144922	7	122044633	q31.32
SNP_A-2066052	G	G	322	22	345	11	4.255	3.91E-02	rs17144945	7	122049322	q31.32
SNP_A-2160208	C	C	341	65	362	38	7.661	5.60E-03	rs17144949	7	122049433	q31.32
SNP_A-1793027	T	T	303	61	332	44	3.883	4.88E-02	rs13240237	7	122086291	q31.32
SNP_A-2169157	T	T	364	42	391	25	5.158	2.31E-02	---	7	122123341	q31.32
SNP_A-2074072	C	C	375	31	396	18	3.943	4.71E-02	rs4288315	7	122302500	q31.32
SNP_A-1911570	C	C	331	83	356	62	3.932	4.74E-02	rs2470983	7	122368554	q31.32
SNP_A-1919954	A	A	278	56	281	87	5.102	2.39E-02	rs805782	7	122813164	q31.32
SNP_A-1933507	C	C	403	9	416	2	4.618	3.16E-02	rs12706543	7	122880765	q31.32
SNP_A-2062015	G	G	209	149	166	164	4.517	3.36E-02	rs7782625	7	123386665	q31.33
SNP_A-1921747	G	G	216	144	196	194	7.179	7.40E-03	rs17554581	7	123388533	q31.33
SNP_A-2294800	T	T	238	172	211	207	4.779	2.88E-02	rs1860484	7	123395713	q31.33
SNP_A-1948304	G	G	295	61	307	29	11.048	9.00E-04	rs6980348	7	123561657	q31.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227973	G	G	360	32	398	12	10.597	1.10E-03	rs929452	7	123690691	q31.33
SNP_A-2272695	C	C	335	37	376	22	5.306	2.13E-02	rs11761806	7	123711825	q31.33
SNP_A-1890004	G	G	368	38	396	18	8.092	4.40E-03	rs1990255	7	123715517	q31.33
SNP_A-2145496	A	A	370	46	401	19	12.443	4.00E-04	rs6466932	7	123735327	q31.33
SNP_A-1906462	G	G	363	49	382	24	9.003	2.70E-03	rs11983364	7	123740454	q31.33
SNP_A-2148467	G	G	357	45	376	18	11.985	5.00E-04	rs2215155	7	123748402	q31.33
SNP_A-1826084	T	T	289	39	313	19	7.829	5.10E-03	rs12537567	7	123749270	q31.33
SNP_A-2151606	T	T	270	142	310	106	7.965	4.80E-03	rs1524771	7	123827247	q31.33
SNP_A-2076287	T	T	256	118	289	79	9.671	0.0019	rs1404412	7	123861815	q31.33
SNP_A-2278927	C	C	243	105	311	79	9.662	0.0019	rs1917365	7	123878249	q31.33
SNP_A-1926472	C	C	279	137	324	94	11.358	8.00E-04	rs4598199	7	123922126	q31.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991135	C	C	260	132	281	105	3.845	0.0499	rs4639456	7	123984359	q31.33
SNP_A-1991143	A	A	378	6	404	0	6.361	0.0117	rs17147811	7	124254431	q31.33
SNP_A-1911789	C	C	318	86	333	61	4.473	0.0344	rs11766248	7	124624170	q31.33
SNP_A-1743227	G	G	234	150	266	124	4.469	3.45E-02	rs1362047	7	125062636	q31.33
SNP_A-1718903	C	C	267	133	317	93	11.239	8.00E-04	rs10487424	7	125067511	q31.33
SNP_A-2216282	C	C	330	14	380	6	4.319	3.77E-02	rs9656339	7	125104247	q31.33
SNP_A-1991169	C	C	323	83	365	49	11.245	8.00E-04	rs9656340	7	125104300	q31.33
SNP_A-1910240	G	G	345	41	358	16	11.019	9.00E-04	rs4141359	7	125337665	q31.33
SNP_A-2040506	A	A	382	0	354	4	4.291	3.83E-02	rs17149498	7	125470899	q31.33
SNP_A-1991209	A	A	325	37	355	13	12.795	3.00E-04	rs11563302	7	126356195	q32.1
SNP_A-2294924	C	C	381	1	382	10	7.237	7.10E-03	rs10266148	7	126513376	q32.1
SNP_A-2116624	G	G	323	65	340	36	8.576	3.40E-03	rs6943385	7	126902379	q32.1
SNP_A-1695685	G	G	282	118	321	89	6.463	1.10E-02	rs2043981	7	126954954	q32.1
SNP_A-1805899	A	A	293	117	325	93	4.323	3.76E-02	rs6467148	7	127022333	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113499	G	G	320	58	347	39	4.731	2.96E-02	rs6969353	7	127065591	q32.1
SNP_A-2261267	C	C	320	78	282	98	4.257	3.91E-02	rs7809182	7	127115007	q32.1
SNP_A-1935924	A	A	228	136	257	105	5.716	1.68E-02	rs3779526	7	127219587	q32.1
SNP_A-1917355	T	T	245	159	279	129	5.312	0.0212	rs1345509	7	127233365	q32.1
SNP_A-1899627	C	C	252	162	287	131	5.533	1.87E-02	rs6973092	7	127254571	q32.1
SNP_A-1908636	G	G	326	58	365	39	5.419	1.99E-02	rs3757758	7	127289364	q32.1
SNP_A-2243829	A	A	292	120	263	145	3.854	4.96E-02	rs11764840	7	127451999	q32.1
SNP_A-2047088	A	A	377	37	396	18	7.031	8.00E-03	rs791607	7	127466786	q32.1
SNP_A-2187222	C	C	412	0	412	6	5.957	0.0147	rs17151956	7	127518944	q32.1
SNP_A-2301500	C	C	355	57	374	38	4.295	3.82E-02	rs7804472	7	127927709	q32.1
SNP_A-1868108	C	C	341	75	318	100	4.369	3.66E-02	rs4731508	7	127943583	q32.1
SNP_A-1991247	G	G	326	60	295	79	3.956	4.67E-02	rs3807125	7	127948888	q32.1
SNP_A-1834435	C	C	328	10	352	0	10.567	1.20E-03	rs17133193	7	130106861	q32.3
SNP_A-1783621	A	A	245	131	203	169	8.73	3.10E-03	rs6943595	7	130414511	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1825260	T	T	356	56	322	88	8.811	3.00E-03	rs2909683	7	130727989	q32.3
SNP_A-1991285	G	G	343	65	374	42	6.207	1.27E-02	rs1106684	7	130910920	q32.3
SNP_A-2137944	G	G	337	59	368	38	5.786	1.62E-02	rs4535659	7	130911311	q32.3
SNP_A-2247456	A	A	296	14	315	3	7.608	5.80E-03	rs10954327	7	130915261	q32.3
SNP_A-2215321	T	T	335	63	371	41	6.249	0.0124	rs11770938	7	130920045	q32.3
SNP_A-2239608	T	T	290	124	318	100	3.842	5.00E-02	rs10272905	7	130954062	q32.3
SNP_A-2188313	C	C	363	11	334	22	4.432	3.53E-02	rs17165966	7	130982160	q32.3
SNP_A-1991292	C	C	374	22	355	37	4.289	3.84E-02	rs10488340	7	130983050	q32.3
SNP_A-2155834	C	C	357	15	380	6	4.318	3.77E-02	rs10226716	7	131054263	q32.3
SNP_A-1991299	G	G	225	153	266	98	15.217	9.59E-05	rs1514066	7	131186421	q32.3
SNP_A-1991300	T	T	241	153	278	116	7.727	5.40E-03	rs1355884	7	131196128	q32.3
SNP_A-1884063	A	A	376	18	361	35	5.753	1.65E-02	rs2137819	7	131198190	q32.3
SNP_A-2293905	G	G	343	61	317	93	7.63	5.70E-03	rs1028066	7	131205148	q32.3
SNP_A-1794370	T	T	351	57	317	91	9.541	0.002	rs1514057	7	131205495	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1799933	C	C	266	128	295	99	5.204	2.25E-02	rs10954357	7	131235703	q32.3
SNP_A-2237786	C	C	264	138	303	109	5.965	0.0146	rs1996161	7	131235747	q32.3
SNP_A-2104645	A	A	331	35	334	20	3.906	4.81E-02	rs17166207	7	131307236	q32.3
SNP_A-2086242	C	C	370	34	392	18	5.514	0.0189	rs12386585	7	131309367	q32.3
SNP_A-1880937	C	C	318	92	341	67	4.729	2.97E-02	rs1364513	7	131381812	q32.3
SNP_A-1886012	C	C	241	99	262	76	3.894	4.85E-02	rs10954376	7	131595059	q32.3
SNP_A-2084931	A	A	307	103	324	68	7.221	7.20E-03	rs7804370	7	132102477	q33
SNP_A-1817766	G	G	242	150	274	126	3.991	4.57E-02	rs11982160	7	132160026	q33
SNP_A-2185785	A	A	249	147	292	106	10.057	0.0015	rs11562037	7	132534140	q33
SNP_A-1694893	G	G	321	79	300	112	6.236	1.25E-02	rs958408	7	132557131	q33
SNP_A-1859907	A	A	299	63	281	87	4.35	3.70E-02	rs7778778	7	132560844	q33
SNP_A-2101717	G	G	209	143	267	111	10.186	0.0014	rs7783217	7	132561372	q33
SNP_A-1991332	A	A	255	135	287	101	6.783	9.20E-03	rs10488164	7	132563454	q33
SNP_A-1991334	T	T	270	138	301	99	8.022	4.60E-03	rs1345938	7	132595122	q33
SNP_A-1801189	G	G	336	80	308	112	6.532	0.0106	rs17656452	7	132650680	q33
SNP_A-1656009	T	T	321	79	293	113	7.253	7.10E-03	rs10488169	7	132675942	q33
SNP_A-2078222	C	C	352	44	374	28	4.177	4.10E-02	rs9640874	7	132682436	q33
SNP_A-1744531	A	A	223	151	194	192	6.73	9.50E-03	rs2911495	7	132747619	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2156359	C	C	360	52	388	32	5.734	0.0166	rs17167177	7	132767473	q33
SNP_A-2261225	G	G	230	158	199	185	4.345	3.71E-02	rs10235846	7	132765477	q33
SNP_A-2125187	A	G	219	173	208	186	5.899	1.51E-02	rs7776986	7	132802890	q33
SNP_A-1928827	G	A	227	173	208	198	5.15	2.33E-02	rs2430769	7	132806404	q33
SNP_A-1792774	G	A	235	171	202	196	6.026	0.0141	rs1041621	7	132811220	q33
SNP_A-2247825	C	A	210	174	203	179	4.696	3.02E-02	rs10954431	7	132888156	q33
SNP_A-2291838	C	C	203	119	175	157	7.155	7.50E-03	rs9649046	7	132890657	q33
SNP_A-1947360	G	G	270	62	244	82	4.039	4.45E-02	rs7781266	7	132962356	q33
SNP_A-2225061	C	C	279	73	227	101	9.014	2.70E-03	rs11971531	7	132996202	q33
SNP_A-1757595	T	T	232	166	270	142	4.506	3.38E-02	rs6962865	7	133015562	q33
SNP_A-1742987	A	A	233	167	270	142	4.568	3.26E-02	rs6963032	7	133015656	q33
SNP_A-2068176	G	G	235	163	270	140	3.994	4.57E-02	rs7792546	7	133052757	q33
SNP_A-1650442	T	T	238	112	223	165	8.695	3.20E-03	rs2346275	7	133078293	q33
SNP_A-1667674	A	A	265	135	237	175	6.547	1.05E-02	rs2971953	7	133079703	q33
SNP_A-2100925	A	A	256	124	205	141	5.152	2.32E-02	rs10269665	7	133087673	q33
SNP_A-2138753	A	A	317	47	331	29	4.544	3.30E-02	rs2001618	7	133096207	q33
SNP_A-1707145	C	C	335	63	368	44	4.682	3.05E-02	rs10488421	7	133132848	q33
SNP_A-2283991	G	G	346	64	368	36	8.474	3.60E-03	rs17167401	7	133180476	q33
SNP_A-1844683	T	T	268	110	232	130	3.915	4.79E-02	rs7810574	7	133209233	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2106202	A	C	199	145	189	169	7.966	4.80E-03	rs12668057	7	133227862	q33
SNP_A-1938488	G	G	249	159	206	200	8.741	3.10E-03	rs7782175	7	133284712	q33
SNP_A-1824360	A	G	213	163	210	184	7.624	5.80E-03	rs12669960	7	133389037	q33
SNP_A-2263474	C	C	257	93	285	71	4.347	3.71E-02	rs1450890	7	133391452	q33
SNP_A-1815262	T	C	217	175	206	192	4.005	4.54E-02	rs1901214	7	133402363	q33
SNP_A-1730555	T	G	226	174	214	196	6.134	1.33E-02	rs1619682	7	133412830	q33
SNP_A-1670395	G	A	229	171	212	198	6.517	1.07E-02	rs10488428	7	133413687	q33
SNP_A-1941073	C	G	218	162	199	177	8.027	4.60E-03	rs2544201	7	133420816	q33
SNP_A-2255440	A	G	234	174	207	201	5.362	0.0206	rs2241332	7	133426694	q33
SNP_A-1790678	C	T	235	181	216	200	5.902	1.51E-02	rs2241333	7	133428005	q33
SNP_A-2034997	G	C	215	155	197	193	5.675	0.0172	rs1862048	7	133435422	q33
SNP_A-1840181	C	G	231	183	216	200	4.954	2.60E-02	rs2241334	7	133436480	q33
SNP_A-2106564	C	G	197	141	188	182	5.874	0.0154	rs2598291	7	133445568	q33
SNP_A-1725726	G	G	213	187	259	153	7.707	5.50E-03	rs1362985	7	133447945	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991345	T	C	207	173	212	160	9.886	1.70E-03	rs1978504	7	133464188	q33
SNP_A-1937772	C	C	369	21	353	37	4.768	2.90E-02	rs17167747	7	133477765	q33
SNP_A-1894951	A	T	227	181	217	183	7.9	4.90E-03	rs6945485	7	133481770	q33
SNP_A-1915921	G	A	212	186	232	184	6.647	9.90E-03	rs1643051	7	133482627	q33
SNP_A-1865712	G	A	213	167	214	172	10.118	0.0015	rs6951333	7	133482753	q33
SNP_A-2143176	T	G	186	162	202	134	12.639	4.00E-04	rs4352788	7	133483886	q33
SNP_A-1947058	T	C	223	173	221	179	10.644	1.10E-03	rs1424428	7	133485645	q33
SNP_A-1936040	T	C	214	178	225	181	7.995	4.70E-03	rs759856	7	133485835	q33
SNP_A-2165480	C	T	221	165	216	180	10.893	0.001	rs6972323	7	133486536	q33
SNP_A-2183400	C	C	239	131	219	171	5.649	1.75E-02	rs4481531	7	133517421	q33
SNP_A-1741541	C	C	224	102	236	150	4.431	3.53E-02	rs2137608	7	133572177	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2062973	T	T	332	26	369	11	7.385	0.0066	rs12537899	7	133769839	q33
SNP_A-2117033	A	G	229	175	211	191	6.791	9.20E-03	rs6972896	7	133845773	q33
SNP_A-1918349	A	A	281	69	329	53	4.485	3.42E-02	rs10275062	7	133854603	q33
SNP_A-2178698	G	G	313	71	347	51	4.781	2.88E-02	rs10245702	7	133854644	q33
SNP_A-1991365	T	T	281	75	260	110	7.169	7.40E-03	rs10488453	7	133862857	q33
SNP_A-1853353	G	G	313	99	287	131	5.536	1.86E-02	rs17168006	7	133863255	q33
SNP_A-1717349	C	C	322	78	358	54	6.094	1.36E-02	rs2347896	7	133881503	q33
SNP_A-1715439	T	T	320	78	358	54	6.253	0.0124	rs1377296	7	133881726	q33
SNP_A-2054407	C	C	226	150	242	114	4.913	2.67E-02	rs12538586	7	133886665	q33
SNP_A-1818542	T	T	237	139	191	181	10.435	1.20E-03	rs11769810	7	133915665	q33
SNP_A-2145207	T	T	216	116	158	146	11.219	8.00E-04	rs3807337	7	133921077	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2232890	A	A	343	55	357	35	4.679	3.05E-02	rs4732118	7	134469192	q33
SNP_A-2031643	G	G	278	108	254	136	4.275	3.87E-02	rs2348526	7	134500643	q33
SNP_A-1789513	G	G	283	93	296	68	3.98	4.60E-02	rs6467606	7	134912479	q33
SNP_A-2068346	C	C	320	74	308	100	3.871	4.91E-02	rs2129800	7	135188291	q33
SNP_A-1825221	T	T	360	4	380	0	4.198	4.05E-02	rs6958301	7	135201262	q33
SNP_A-1855566	C	C	384	14	399	5	4.506	3.38E-02	rs7797352	7	135202582	q33
SNP_A-1642489	G	G	309	83	342	64	3.884	0.0487	rs2114337	7	135371033	q33
SNP_A-1849523	G	G	195	189	220	156	4.579	3.24E-02	rs10275541	7	135514242	q33
SNP_A-1696656	C	-	220	154	193	193	5.96	0.0146	rs10488619	7	135589640	q33
SNP_A-2135826	G	A	215	179	207	171	6.718	9.50E-03	rs17483846	7	135661271	q33
SNP_A-2069700	C	T	188	172	211	155	7.097	7.70E-03	rs1473220	7	135662991	q33
SNP_A-2262883	G	G	189	187	219	149	6.418	1.13E-02	rs6943470	7	135670283	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1781389	C	C	277	123	308	92	6.113	0.0134	rs10248350	7	135685827	q33
SNP_A-1801009	A	A	281	129	315	97	6.466	1.10E-02	rs2113909	7	135693657	q33
SNP_A-2236669	A	A	275	123	308	92	6.333	1.19E-02	rs4317499	7	135761699	q33
SNP_A-2212453	A	A	273	137	248	166	3.956	4.67E-02	rs6467680	7	135839700	q33
SNP_A-1725114	T	T	225	175	272	140	8.158	0.0043	rs832972	7	136247196	q33
SNP_A-2216241	A	A	312	72	309	41	6.959	8.30E-03	rs16874907	7	136252139	q33
SNP_A-2291732	T	T	206	150	198	94	6.756	9.30E-03	rs1035688	7	136255421	q33
SNP_A-2275049	C	C	238	166	268	124	7.682	5.60E-03	rs1964318	7	136255682	q33
SNP_A-1933780	C	C	243	145	278	120	4.583	3.23E-02	rs1035686	7	136256023	q33
SNP_A-2263372	G	G	218	142	247	89	13.157	3.00E-04	rs10274449	7	136256838	q33
SNP_A-2290426	A	A	196	178	226	134	8.074	4.50E-03	rs1425074	7	136257326	q33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803092	A	A	211	157	257	117	10.313	1.30E-03	rs10254754	7	136267960	q33
SNP_A-2244328	C	C	224	158	260	118	8.454	3.60E-03	rs1425079	7	136271923	q33
SNP_A-2215648	A	A	235	181	278	142	8.294	4.00E-03	rs832966	7	136290381	q33
SNP_A-1674189	A	A	227	163	269	143	4.263	3.89E-02	rs721239	7	136336396	q33
SNP_A-2244634	A	A	213	157	249	135	4.204	4.03E-02	rs322323	7	136397815	q33
SNP_A-2028096	T	T	302	66	319	43	5.27	2.17E-02	rs10435425	7	136398055	q33
SNP_A-1832336	C	C	396	4	406	0	4.08	4.34E-02	rs17169038	7	136428294	q33
SNP_A-2066665	G	G	362	0	359	5	5.007	0.0252	rs10279889	7	136807530	q33
SNP_A-2266701	G	G	369	19	335	39	8.284	4.00E-03	rs3800665	7	136933826	q33
SNP_A-2067410	G	G	364	26	358	44	4.498	0.0339	rs4732276	7	137116156	q34
SNP_A-2150091	G	G	239	151	247	109	5.378	2.04E-02	rs6467736	7	137255502	q34
SNP_A-1687886	T	T	346	20	350	44	8.002	4.70E-03	rs357396	7	137463700	q33
SNP_A-1991469	T	T	289	63	249	81	4.519	3.35E-02	rs357424	7	137490117	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134149	A	A	352	0	368	8	7.573	5.90E-03	rs1982914	7	137554717	q34
SNP_A-1864829	A	A	340	44	356	20	9.285	0.0023	rs6973199	7	137868967	q34
SNP_A-2289901	G	G	378	4	392	0	4.126	4.22E-02	rs7804914	7	138249500	q34
SNP_A-2103150	A	A	307	113	342	80	7.525	6.10E-03	rs12056143	7	138255097	q34
SNP_A-2308767	G	G	279	57	310	28	11.52	7.00E-04	rs2134955	7	138256851	q34
SNP_A-1958532	A	A	304	110	341	79	7.164	7.40E-03	rs17133453	7	138260678	q34
SNP_A-2235193	T	T	216	104	250	80	5.459	0.0195	rs4321936	7	138266532	q34
SNP_A-1991476	A	A	292	114	327	83	6.838	8.90E-03	rs7798474	7	138274495	q34
SNP_A-2118945	C	C	404	4	406	0	4	4.55E-02	rs6948804	7	138487895	q34
SNP_A-2060329	T	T	299	25	272	46	7.433	6.40E-03	rs6943849	7	138748871	q34
SNP_A-2012943	G	G	350	42	334	66	5.627	0.0177	rs7778038	7	138758143	q34
SNP_A-1822043	G	G	376	36	356	54	4.142	4.18E-02	rs10271123	7	138759057	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2196360	A	A	312	26	320	46	4.55	3.29E-02	rs4732392	7	136762283	q34
SNP_A-1888516	G	G	377	41	361	61	4.25	3.93E-02	rs10276928	7	138771071	q34
SNP_A-1747525	G	G	367	17	368	34	5.259	0.0218	rs10487666	7	139090951	q34
SNP_A-1991489	C	C	324	96	295	125	5.164	2.31E-02	rs12539669	7	139227198	q34
SNP_A-2199774	A	A	332	88	357	63	5.046	0.0247	rs10247426	7	139583847	q34
SNP_A-2276008	C	C	344	30	361	17	3.985	4.59E-02	rs6952208	7	139679222	q34
SNP_A-2046620	A	A	370	10	376	26	6.546	1.05E-02	rs7802537	7	139809736	q34
SNP_A-2140536	T	T	372	4	371	19	9.531	0.002	rs17623204	7	139959588	q34
SNP_A-1991500	C	C	406	4	414	0	4.059	4.39E-02	rs16882367	7	140135257	q34
SNP_A-2221815	C	C	271	131	247	163	4.517	3.36E-02	rs17566000	7	140373572	q34
SNP_A-2255475	T	T	199	173	222	142	4.221	3.99E-02	rs6464436	7	140399438	q34
SNP_A-1815002	C	C	232	188	261	159	4.13	4.21E-02	rs9791400	7	140405031	q34
SNP_A-1933703	G	G	347	31	349	55	5.845	1.56E-02	rs6951796	7	140415083	q34
SNP_A-2188098	A	A	231	187	260	158	4.151	4.16E-02	rs4140983	7	140417459	q34
SNP_A-2240057	C	C	228	184	247	149	4.123	4.23E-02	rs10247172	7	140428430	q34
SNP_A-1878871	G	G	358	22	350	42	6.155	1.31E-02	rs13225438	7	140824991	q34
SNP_A-1872412	A	A	339	41	337	63	4.15	4.16E-02	rs1655263	7	141015825	q34
SNP_A-1939791	G	G	342	58	372	38	5.305	2.13E-02	rs1880924	7	141170409	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113840	G	G	264	144	230	176	5.535	1.86E-02	rs4341081	7	141212971	q34
SNP_A-2062848	A	A	239	129	212	182	9.773	0.0018	rs9986802	7	141326058	q34
SNP_A-2100460	C	C	262	142	218	186	9.936	1.60E-03	rs9986873	7	141326076	q34
SNP_A-2310784	C	C	227	109	191	145	8.203	4.20E-03	rs4389847	7	141329303	q34
SNP_A-2154361	C	C	369	37	360	56	3.872	4.91E-02	rs6963035	7	141404973	q34
SNP_A-1865385	A	A	278	88	304	62	5.668	1.73E-02	rs4726506	7	141405048	q34
SNP_A-2065925	A	A	298	110	324	84	4.571	3.25E-02	rs6964443	7	141405811	q34
SNP_A-1932459	A	A	284	92	311	69	4.49	3.41E-02	rs6464482	7	141416167	q34
SNP_A-1991525	A	A	289	73	303	49	4.913	2.67E-02	rs1894319	7	141418604	q34
SNP_A-2100733	G	G	254	84	282	64	4.072	0.0436	rs10273175	7	141448609	q34
SNP_A-2284184	A	A	387	9	382	2	4.303	3.80E-02	rs8175950	7	142178532	q34
SNP_A-2094404	C	C	365	31	363	15	5.155	2.32E-02	rs10246397	7	142267516	q34
SNP_A-1757843	C	C	208	194	250	156	7.958	4.80E-03	rs2103193	7	142503108	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1717309	G	G	189	175	232	140	8.195	4.20E-03	rs10500138	7	142503154	q34
SNP_A-1737457	G	G	214	190	257	157	6.943	8.40E-03	rs2272252	7	142507267	q34
SNP_A-1991555	G	G	385	7	397	1	4.639	3.13E-02	rs3212148	7	142515995	q34
SNP_A-2238872	A	A	308	34	262	66	13.666	2.00E-04	rs2367941	7	142546208	q34
SNP_A-2259281	G	G	211	179	252	150	6.006	0.0143	rs4726606	7	142547734	q34
SNP_A-2101680	C	C	363	29	328	62	13.735	2.00E-04	rs1880650	7	142554956	q34
SNP_A-2212319	T	T	215	197	252	168	5.159	2.31E-02	rs2293365	7	142555742	q34
SNP_A-1820739	T	T	216	190	243	157	4.682	3.05E-02	rs940864	7	142556148	q34
SNP_A-1904794	A	C	198	134	177	169	7.951	4.80E-03	rs4489232	7	142580875	q34
SNP_A-2074080	G	G	292	68	283	97	4.701	3.01E-02	rs4726628	7	142715405	q34
SNP_A-2147090	T	T	240	148	212	176	4.154	4.15E-02	rs1208173	7	143541563	q35
SNP_A-2058411	G	G	380	10	369	21	4.065	4.38E-02	rs6968395	7	143867446	q35
SNP_A-2271452	C	T	233	171	206	202	5.439	1.97E-02	rs2692390	7	144041073	q35
SNP_A-1913042	A	C	178	172	208	158	4.246	3.94E-02	rs2692379	7	144061037	q35

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2176938	C	C	371	11	365	25	5.411	0.02	rs4726747	7	144320836	q35
SNP_A-2073551	T	T	339	37	362	20	5.778	1.62E-02	rs4726774	7	145004180	q35
SNP_A-2115656	T	T	290	84	304	58	4.896	0.0269	rs10277217	7	145314011	q35
SNP_A-1991618	A	A	384	22	405	7	8.274	4.00E-03	rs802524	7	145389290	q35
SNP_A-1991619	G	G	383	19	405	9	4.01	4.52E-02	rs2430327	7	145390594	q35
SNP_A-2033428	A	A	405	15	416	6	4	4.55E-02	rs10241465	7	145455921	q35
SNP_A-1991631	T	T	347	63	330	86	3.934	4.73E-02	rs10487930	7	145713283	q35
SNP_A-1835757	C	C	293	71	309	47	5.218	0.0223	rs1948489	7	145786210	q35
SNP_A-2297464	C	C	314	98	331	69	5.308	0.0212	rs12540802	7	145791267	q35
SNP_A-2076636	G	G	238	80	262	60	3.984	4.59E-02	rs10239703	7	145923749	q35
SNP_A-1722554	T	T	228	138	215	183	5.359	0.0206	rs903900	7	146263654	q35
SNP_A-2302679	T	T	243	149	212	174	4.001	4.55E-02	rs4725704	7	146306259	q35
SNP_A-1991663	T	T	219	147	202	188	4.947	2.61E-02	rs826821	7	146491510	q35
SNP_A-1890414	C	C	260	96	280	72	4.147	4.17E-02	rs6961608	7	146626167	q35
SNP_A-1908803	C	C	270	110	299	85	4.662	3.08E-02	rs2222764	7	146630323	q35
SNP_A-2045103	C	C	260	94	265	59	6.74	9.40E-03	rs12113038	7	146636150	q35
SNP_A-1914046	G	G	420	0	417	5	5.006	0.0253	rs17170714	7	147006467	q35

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2159445	A	G	220	196	225	185	4.979	2.57E-02	rs2538990	7	147017689	q35
SNP_A-2249201	C	T	193	165	192	166	4.073	0.0436	rs2538979	7	147020367	q35
SNP_A-1907989	A	A	233	143	206	170	3.99	0.0458	rs10238572	7	147045233	q35
SNP_A-1827027	T	T	212	114	189	143	4.537	0.0332	rs7798639	7	147046096	q35
SNP_A-1942401	G	G	323	97	292	126	5.329	2.10E-02	rs1922886	7	147081394	q35
SNP_A-1991696	G	G	318	92	289	127	6.936	8.40E-03	rs1922885	7	147081571	q35
SNP_A-2012992	G	G	224	182	242	142	5.025	2.50E-02	rs2141954	7	147087671	q35
SNP_A-1991704	A	A	310	108	337	81	4.984	2.56E-02	rs10485845	7	147192464	q35
SNP_A-2154728	C	C	416	4	410	12	4.039	4.45E-02	rs6960875	7	147210614	q35
SNP_A-1991705	C	C	312	62	342	42	5.091	0.024	rs10485842	7	147226598	q35
SNP_A-2150041	T	T	407	1	395	7	4.635	3.13E-02	rs1990070	7	147230877	q35
SNP_A-1884657	C	C	331	71	358	46	6.395	0.0114	rs17170840	7	147249840	q35
SNP_A-2144391	C	C	301	115	277	143	4.016	4.51E-02	rs2972106	7	147317205	q36.1
SNP_A-2170767	T	T	299	101	278	132	4.766	2.90E-02	rs1859537	7	147317811	q36.1
SNP_A-2238057	T	T	228	154	195	179	4.367	3.66E-02	rs6946212	7	147453605	q36.1
SNP_A-2024588	C	C	256	148	228	180	4.722	0.0298	rs6464877	7	147488156	q36.1
SNP_A-1883524	A	A	313	91	350	68	5.155	2.32E-02	rs17171051	7	147710593	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991722	A	A	363	33	384	16	6.468	1.10E-02	rs3801977	7	147723530	q36.1
SNP_A-2267485	G	G	348	6	385	1	4.063	4.38E-02	rs17171072	7	147786064	q36.1
SNP_A-2067586	T	T	204	150	234	124	4.5	0.0339	rs243536	7	147847589	q36.1
SNP_A-2225335	A	A	203	135	247	119	4.203	4.03E-02	rs933436	7	147924977	q36.1
SNP_A-1835892	G	G	227	165	261	131	6.274	0.0123	rs2007404	7	147925043	q36.1
SNP_A-1816275	C	C	302	110	340	80	6.91	0.0086	rs12534095	7	148158353	q36.1
SNP_A-2194161	G	G	328	54	340	30	6.883	8.70E-03	rs7385573	7	148457360	q36.1
SNP_A-1930750	A	A	279	101	321	71	7.988	4.70E-03	rs354093	7	148779510	q36.1
SNP_A-2142050	T	T	274	98	255	125	3.867	4.93E-02	rs2373489	7	148798615	q36.1
SNP_A-2201002	G	G	252	68	231	101	7.138	7.50E-03	rs2888583	7	148822770	q36.1
SNP_A-2311720	A	A	282	106	280	68	6.15	1.31E-02	rs10271868	7	149880199	q36.1
SNP_A-2201768	G	G	324	96	348	70	4.925	2.65E-02	rs7781814	7	149934085	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi Square	p value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101333	C	C	286	114	259	145	5.028	2.49E-02	rs2608289	7	150346348	q36.1
SNP_A-1864197	A	A	274	130	298	104	3.891	4.85E-02	rs219246	7	150426557	q36.1
SNP_A-2178216	C	G	224	192	224	194	4.61	3.18E-02	rs219247	7	150427015	q36.1
SNP_A-1837627	C	C	222	158	190	186	4.743	2.94E-02	rs219248	7	150428186	q36.1
SNP_A-1812832	A	A	304	106	278	136	4.861	0.0275	rs2727527	7	150785110	q36.1
SNP_A-2191235	G	G	274	46	263	67	3.975	4.62E-02	rs4726084	7	150822151	q36.1
SNP_A-2036134	A	A	336	50	336	78	5.151	2.32E-02	rs6970666	7	150827149	q36.1
SNP_A-1818278	G	G	321	77	285	105	6.366	1.16E-02	rs4530949	7	150944633	q36.1
SNP_A-1991758	C	C	352	30	389	15	6.237	1.25E-02	rs1108845	7	150960363	q36.1
SNP_A-1744383	C	C	300	102	279	129	3.873	4.91E-02	rs1112401	7	151060063	q36.1
SNP_A-1944517	T	T	268	90	214	122	10.193	0.0014	rs11770365	7	151115321	q36.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2163479	C	C	236	90	193	117	7.434	6.40E-03	rs2014611	7	151618335	q36.1
SNP_A-1805509	A	A	202	192	232	166	3.942	4.71E-02	rs10278129	7	151855347	q36.1
SNP_A-2104427	T	T	290	114	260	142	4.694	3.03E-02	rs570378	7	152140548	q36.2
SNP_A-2123319	G	G	298	48	293	29	3.873	4.91E-02	rs760223	7	152190611	q36.2
SNP_A-1892812	C	C	394	10	411	3	4.007	0.0453	rs2311854	7	152292601	q36.2
SNP_A-2040038	T	T	328	72	353	47	6.17	1.30E-02	rs7802831	7	152603366	q36.2
SNP_A-2186181	C	C	248	122	282	100	4.171	4.11E-02	rs2961094	7	152604842	q36.2
SNP_A-2070900	A	A	355	29	373	9	10.966	9.00E-04	rs4726304	7	152708290	q36.2
SNP_A-2045382	T	T	346	24	358	6	10.956	9.00E-04	rs4726305	7	152708316	q36.2
SNP_A-2192508	G	G	269	133	238	158	3.998	4.55E-02	rs7803356	7	152839732	q36.2
SNP_A-2237241	G	G	363	1	291	7	5.905	1.51E-02	rs10259108	7	153366459	q36.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991780	A	A	221	187	252	154	5.22	0.0223	rs7780487	7	153449632	q36.2
SNP_A-1836546	T	T	220	168	253	135	5.896	0.0152	rs4726405	7	153454069	q36.2
SNP_A-1786209	C	C	361	49	343	73	5.138	2.34E-02	rs6959816	7	153464086	q36.2
SNP_A-1834253	G	G	306	92	335	71	3.938	4.72E-02	rs10256276	7	153522306	q36.2
SNP_A-1991786	G	G	336	78	359	57	4.023	4.49E-02	rs286854	7	153549119	q36.2
SNP_A-1991787	G	G	374	40	393	25	3.913	4.79E-02	rs286855	7	153549503	q36.2
SNP_A-2211318	C	C	352	0	306	8	9.077	2.60E-03	rs10280822	7	153845565	q36.2
SNP_A-1868985	T	T	379	3	349	15	8.807	3.00E-03	rs4960616	7	154028798	q36.2
SNP_A-1886323	T	T	369	21	336	36	5.07	2.43E-02	rs4960617	7	154031399	q36.2
SNP_A-2161646	A	A	394	20	379	35	4.382	3.63E-02	rs4960618	7	154031554	q36.2
SNP_A-1927809	A	A	328	40	310	62	5.231	2.22E-02	rs4960552	7	154038806	q36.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138464	T	T	353	53	336	74	3.872	4.91E-02	rs4960620	7	154046705	q36.2
SNP_A-2176729	A	A	347	49	332	74	5.289	2.15E-02	rs7789522	7	154047924	q36.2
SNP_A-1792252	C	C	298	98	315	73	4.045	4.43E-02	rs930436	7	154173598	q36.2
SNP_A-1782333	C	C	349	15	361	5	5.197	2.26E-02	rs7786195	7	154365816	q36.2
SNP_A-1888813	C	C	249	139	269	103	5.793	0.0161	rs4146257	7	154372295	q36.2
SNP_A-2120750	C	C	294	64	313	45	3.907	4.81E-02	rs10267993	7	154374966	q36.2
SNP_A-1922422	T	T	287	87	319	57	7.934	4.90E-03	rs7777949	7	154381897	q36.2
SNP_A-2284918	C	C	297	55	349	37	6.154	1.31E-02	rs6961707	7	154382947	q36.2
SNP_A-2235052	A	A	286	56	299	29	8.577	3.40E-03	rs1529082	7	154384297	q36.2
SNP_A-2093968	G	G	308	106	340	78	5.822	1.58E-02	rs7800026	7	154384719	q36.2
SNP_A-2013051	G	G	198	180	240	156	5.326	2.10E-02	rs4960697	7	154423980	q36.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2095320	A	A	200	176	225	145	4.416	0.0356	rs6597477	7	154427124	q36.2
SNP_A-1781608	T	T	324	8	310	18	4.131	4.21E-02	rs10258075	7	154537155	q36.3
SNP_A-2287061	C	C	376	30	364	50	5.117	2.37E-02	rs7804368	7	155131014	q36.3
SNP_A-1735677	T	T	379	21	405	9	5.423	1.99E-02	rs963932	7	155149315	q36.3
SNP_A-2308118	A	A	338	76	365	51	5.953	0.0147	rs4716930	7	155217717	q36.3
SNP_A-2081105	A	A	345	75	367	51	5.246	2.20E-02	rs2363904	7	155218968	q36.3
SNP_A-2129992	T	T	304	90	255	111	5.465	1.94E-02	rs12698401	7	155619588	q36.3
SNP_A-2195071	A	A	352	50	379	27	7.848	5.10E-03	rs4560686	7	155650020	q36.3
SNP_A-1878480	A	A	392	16	382	30	4.371	3.66E-02	rs12698431	7	155652082	q36.3
SNP_A-1836237	C	C	395	21	382	40	6.093	1.36E-02	rs6967289	7	155754819	q36.3
SNP_A-2174305	T	T	290	110	312	80	5.461	0.0195	rs12697969	7	155795038	q36.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1721860	C	C	320	84	352	60	5.446	1.96E-02	rs10488069	7	155797787	q36.3
SNP_A-2126068	G	G	382	28	402	14	5.134	0.0235	rs12697982	7	155847124	q36.3
SNP_A-1754544	T	C	230	174	209	203	4.804	2.84E-02	rs2365509	7	155880835	q36.3
SNP_A-1667442	G	A	215	189	224	190	4.388	3.62E-02	rs2365511	7	155880966	q36.3
SNP_A-2050258	T	T	387	31	393	17	4.053	0.0441	rs6956930	7	156037106	q36.3
SNP_A-2292766	C	C	242	176	272	140	5.809	1.59E-02	rs2969125	7	156214230	q36.3
SNP_A-2076880	C	C	314	84	295	111	4.252	3.92E-02	rs12668289	7	156247371	q36.3
SNP_A-1852522	G	G	275	75	243	101	5.766	1.63E-02	rs10949615	7	156248035	q36.3
SNP_A-2032646	G	G	238	150	216	188	5.017	2.51E-02	rs10260499	7	156263548	q36.3
SNP_A-2082832	T	T	318	72	300	98	4.42	3.55E-02	rs1558428	7	156280661	q36.3
SNP_A-1818966	C	C	278	118	239	137	3.842	5.00E-02	rs10949620	7	156283203	q36.3
SNP_A-1738945	T	T	160	146	204	126	5.892	0.0152	rs724688	7	156315973	q36.3
SNP_A-1712025	A	A	363	19	296	36	8.607	0.0033	rs1859550	7	156405250	q36.3
SNP_A-1955155	T	T	394	10	417	3	4.112	4.26E-02	rs17837717	7	156416675	q36.3
SNP_A-2129361	C	C	346	14	359	5	4.481	3.43E-02	rs3802090	7	156671270	q36.3
SNP_A-1854769	G	G	220	136	191	165	4.84	2.78E-02	rs2072421	7	156709697	q36.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2312321	T	T	345	17	341	33	5.991	0.0144	rs2366564	7	156760145	q36.3
SNP_A-2222442	C	C	247	129	227	173	6.518	1.07E-02	rs6459804	7	157009671	q36.3
SNP_A-2253841	C	C	267	143	237	175	5.001	0.0253	rs6459806	7	157009959	q36.3
SNP_A-1940008	C	C	352	40	385	25	4.537	0.0332	rs1638756	7	157051843	q36.3
SNP_A-1879478	C	C	348	44	372	26	5.383	2.03E-02	rs6952172	7	157182089	q36.3
SNP_A-2224535	A	A	294	38	302	22	4.277	3.86E-02	rs4716836	7	157248059	q36.3
SNP_A-2082842	G	G	349	55	378	38	4.09	4.31E-02	rs4716837	7	157248255	q36.3
SNP_A-2228918	T	T	357	63	377	43	4.319	3.77E-02	rs4317459	7	157249475	q36.3
SNP_A-1707643	C	C	375	23	363	39	4.304	3.80E-02	rs262144	7	158164369	q36.3
SNP_A-2186481	G	G	391	17	384	34	5.61	1.79E-02	rs2075180	7	158388758	q36.3
SNP_A-2201379	C	C	383	15	361	27	3.953	4.68E-02	rs3793235	7	158410131	q36.3
SNP_A-2098297	T	C	250	164	211	209	9.51	0.002	rs10864416	8	431457	p23.3
SNP_A-1991853	T	T	388	14	373	27	4.413	3.57E-02	rs17738513	8	436359	p23.3
SNP_A-2077423	G	G	258	104	227	135	6.002	0.0143	rs1669681	8	596117	p23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991858	G	T	216	156	187	179	6.219	0.0126	rs925280	8	629681	p23.3
SNP_A-2225294	C	T	234	182	224	196	7.684	5.60E-03	rs9314603	8	629796	p23.3
SNP_A-2023608	C	C	309	61	290	84	4.23	3.97E-02	rs4735907	8	650575	p23.3
SNP_A-2213254	C	C	210	110	187	135	3.877	4.89E-02	rs13257920	8	850907	p23.3
SNP_A-1947715	G	G	411	3	398	16	9.104	2.60E-03	rs17753534	8	1116972	p23.3
SNP_A-1933828	A	A	363	3	367	17	9.395	2.20E-03	rs17815675	8	1117062	p23.3
SNP_A-1787012	G	G	400	2	391	19	13.787	2.00E-04	rs17065750	8	1120564	p23.3
SNP_A-2123618	C	C	387	9	386	20	4.05	4.42E-02	rs17064302	8	1767386	p23.3
SNP_A-1881243	A	A	256	126	238	162	4.744	2.94E-02	rs7842515	8	1811435	p23.3
SNP_A-2139929	T	T	284	20	288	40	5.792	0.0161	rs7386814	8	1859902	p23.3
SNP_A-1945262	G	G	326	26	321	11	5.54	1.86E-02	rs2956890	8	2116686	p23.3
SNP_A-1858481	G	G	226	140	250	112	4.299	3.81E-02	rs1869751	8	2259538	p23.2
SNP_A-2067518	A	A	337	9	338	24	6.461	1.10E-02	rs1244622	8	2275672	p23.2
SNP_A-2182863	T	T	397	19	410	8	4.686	0.0304	rs4242542	8	2291450	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175472	A	A	383	27	369	43	3.913	4.79E-02	rs6558653	8	2298560	p23.2
SNP_A-1780479	C	C	377	37	398	20	5.62	0.0178	rs6995938	8	2475685	p23.2
SNP_A-2067754	G	G	354	60	371	41	3.968	4.64E-02	rs17755291	8	2554590	p23.2
SNP_A-2286525	C	C	354	6	364	0	6.117	0.0134	rs1026377	8	2640862	p23.2
SNP_A-1731223	A	A	312	86	297	113	3.855	4.96E-02	rs1979509	8	2799115	p23.2
SNP_A-1654813	G	G	328	70	365	45	7.234	7.20E-03	rs10503190	8	2940698	p23.2
SNP_A-1752995	A	A	282	78	325	55	6.488	0.0109	rs7827348	8	3020222	p23.2
SNP_A-2301596	A	A	375	35	394	18	5.917	1.50E-02	rs17391662	8	3112519	p23.2
SNP_A-2211691	T	T	331	73	350	48	5.651	1.74E-02	rs4875508	8	3128993	p23.2
SNP_A-1752307	T	T	351	49	340	72	4.371	3.66E-02	rs10503201	8	3158001	p23.2
SNP_A-1791778	C	C	352	8	334	26	10.002	1.60E-03	rs1161531	8	3248890	p23.2
SNP_A-2138215	C	C	335	59	310	84	5.34	2.08E-02	rs270084	8	3265302	p23.2
SNP_A-2229126	C	C	323	53	350	34	5.149	2.33E-02	rs7018325	8	3280551	p23.2
SNP_A-2184132	A	A	334	58	348	32	7.614	5.80E-03	rs10282982	8	3292439	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991931	G	G	397	19	412	8	4.741	2.95E-02	rs17066612	8	3466994	p23.2
SNP_A-1643730	G	G	375	17	402	6	5.881	1.53E-02	rs7015502	8	3468420	p23.2
SNP_A-1732686	C	C	380	18	404	8	4.34	3.72E-02	rs10503212	8	3469977	p23.2
SNP_A-1666042	C	C	381	19	404	8	4.979	2.57E-02	rs10503213	8	3470039	p23.2
SNP_A-1878099	C	C	391	19	403	7	5.72	1.68E-02	rs11778669	8	3475452	p23.2
SNP_A-2063301	G	G	363	19	387	5	8.807	3.00E-03	rs7826250	8	3583994	p23.2
SNP_A-1991945	C	C	381	35	399	19	5.151	2.32E-02	rs7843194	8	3592989	p23.2
SNP_A-2278117	G	G	249	131	269	101	4.519	3.35E-02	rs13250204	8	3609045	p23.2
SNP_A-2048755	T	T	374	32	396	16	5.918	1.50E-02	rs1994054	8	3615131	p23.2
SNP_A-2044534	C	C	357	23	361	11	4.173	4.11E-02	rs1383953	8	3630967	p23.2
SNP_A-1718271	T	T	304	96	283	127	4.938	0.0263	rs2720811	8	3635728	p23.2
SNP_A-2070575	G	G	227	157	241	119	4.882	2.71E-02	rs10102521	8	3650879	p23.2
SNP_A-1902493	G	G	215	169	249	139	5.393	2.02E-02	rs7015612	8	3651379	p23.2

Table 2

Name	Major Allele_1	Major Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1991947	T	T	212	168	250	138	5.984	0.0144	rs11136668	8	3652805	p23.2
SNP_A-1663590	C	C	332	68	308	104	8.259	4.10E-03	rs4477054	8	3653506	p23.2
SNP_A-1720303	C	C	384	16	405	7	3.904	0.0482	rs1871816	8	3653864	p23.2
SNP_A-1729338	G	G	394	6	396	16	4.374	3.65E-02	rs900090	8	3654252	p23.2
SNP_A-1720623	T	T	372	28	400	12	7.24	7.10E-03	rs2720887	8	3656059	p23.2
SNP_A-1678090	A	A	376	22	392	8	6.862	8.80E-03	rs2720888	8	3656344	p23.2
SNP_A-2088225	T	T	330	82	289	125	11.643	6.00E-04	rs10102119	8	3657789	p23.2
SNP_A-2150562	G	G	235	131	290	102	8.49	3.60E-03	rs10866958	8	3665233	p23.2
SNP_A-2247600	T	T	362	6	343	15	4.232	3.97E-02	rs7840128	8	3665395	p23.2
SNP_A-1859162	G	G	252	110	304	88	6.124	1.33E-02	rs11988752	8	3675256	p23.2
SNP_A-2156561	C	C	285	93	272	124	4.316	0.0378	rs10107710	8	3749145	p23.2
SNP_A-2170270	C	C	331	79	312	104	3.933	4.73E-02	rs1523259	8	3750688	p23.2
SNP_A-1825007	T	T	308	80	336	58	4.679	3.05E-02	rs11136687	8	3796912	p23.2
SNP_A-1863022	T	T	366	34	387	19	4.787	0.0287	rs17068542	8	3857017	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1916127	G	G	345	69	374	46	5.727	0.0167	rs2554692	8	3916484	p23.2
SNP_A-2035231	T	T	331	65	352	38	7.678	5.60E-03	rs10091045	8	3946832	p23.2
SNP_A-1890638	T	T	327	85	356	60	5.522	1.88E-02	rs12056743	8	3965575	p23.2
SNP_A-2034958	C	C	318	76	351	49	7.415	6.50E-03	rs9314517	8	3968050	p23.2
SNP_A-2269152	A	A	241	109	262	82	4.642	3.12E-02	rs2407304	8	3981508	p23.2
SNP_A-2193118	G	G	226	146	263	115	6.434	0.0112	rs3849830	8	4014286	p23.2
SNP_A-1672022	C	C	227	141	273	113	6.893	8.70E-03	rs1714757	8	4016921	p23.2
SNP_A-2128679	C	C	363	21	387	9	5.385	2.03E-02	rs10096696	8	4027418	p23.2
SNP_A-2066641	G	G	284	58	249	79	5.227	2.22E-02	rs11136707	8	4030137	p23.2
SNP_A-2034314	A	A	371	21	381	9	4.928	0.0264	rs11785627	8	4055310	p23.2
SNP_A-2288601	C	C	381	13	394	4	4.963	2.59E-02	rs17069762	8	4100452	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2160669	T	T	387	21	372	36	4.244	3.94E-02	rs17069985	8	4192395	p23.2
SNP_A-2286757	C	C	378	4	376	12	3.959	4.66E-02	rs17070157	8	4253682	p23.2
SNP_A-1754404	C	C	366	16	370	30	3.87	4.91E-02	rs1405244	8	4358793	p23.2
SNP_A-2276886	C	C	413	3	408	12	5.411	0.02	rs17070710	8	4436914	p23.2
SNP_A-2253268	C	C	327	87	305	113	4.127	4.22E-02	rs2028237	8	4754112	p23.2
SNP_A-2118079	A	A	251	101	229	129	4.367	3.66E-02	rs4076510	8	4774854	p23.2
SNP_A-1728467	C	C	339	59	368	42	3.874	4.91E-02	rs10503288	8	4880440	p23.2
SNP_A-1758242	G	G	340	60	371	41	4.75	0.0293	rs10503289	8	4880479	p23.2
SNP_A-2013123	T	T	226	138	241	105	4.51	3.37E-02	rs2977707	8	4895740	p23.2
SNP_A-1829657	C	C	275	119	301	87	6.099	0.0135	rs4875138	8	4917841	p23.2
SNP_A-2256013	T	T	351	33	319	49	4.312	0.0378	rs2407744	8	4924179	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1992046	G	G	253	101	258	68	5.349	0.0207	rs1377882	8	4949245	p23.2
SNP_A-1943942	A	A	313	103	339	79	4.197	4.05E-02	rs13279982	8	4962706	p23.2
SNP_A-2161378	T	T	214	166	243	123	7.978	4.70E-03	rs11779265	8	4976549	p23.2
SNP_A-1858228	A	A	253	69	269	49	3.855	4.96E-02	rs17435668	8	4978049	p23.2
SNP_A-1870634	C	C	208	152	243	115	7.838	5.10E-03	rs11774681	8	4981351	p23.2
SNP_A-2160891	G	G	315	89	326	64	4.028	4.47E-02	rs17351138	8	4981420	p23.2
SNP_A-2054679	G	G	390	4	388	14	5.481	1.92E-02	rs7000771	8	4988210	p23.2
SNP_A-2045083	C	C	378	38	388	22	4.354	3.69E-02	rs7013412	8	5103498	p23.2
SNP_A-2081407	G	G	361	21	339	35	4.107	4.27E-02	rs4552921	8	5143724	p23.2
SNP_A-1798555	C	C	221	171	259	149	4.203	4.04E-02	rs6982488	8	5201450	p23.2
SNP_A-2068042	C	C	294	24	292	46	6.317	0.012	rs7003556	8	5213929	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2036269	G	C	226	180	211	201	3.878	4.89E-02	rs971046	8	5326925	p23.2
SNP_A-1737611	C	C	294	66	307	101	4.635	3.13E-02	rs10503310	8	5358347	p23.2
SNP_A-1946053	A	A	334	40	314	62	5.357	0.0206	rs12680380	8	5375967	p23.2
SNP_A-2175745	G	C	185	171	189	149	4.316	3.77E-02	rs2527728	8	5376122	p23.2
SNP_A-2071022	G	G	303	63	331	39	6.862	8.80E-03	rs984673	8	5588817	p23.2
SNP_A-2142549	G	G	253	101	297	75	6.919	8.50E-03	rs12549894	8	5630262	p23.2
SNP_A-1884193	C	C	372	36	392	20	5.076	2.43E-02	rs11136930	8	5672160	p23.2
SNP_A-2090665	G	G	311	47	334	30	4.524	3.34E-02	rs17075075	8	5752789	p23.2
SNP_A-1657524	G	G	280	118	313	91	5.28	2.16E-02	rs2703322	8	5813048	p23.2
SNP_A-1749099	C	C	275	125	311	95	6.258	0.0124	rs2840500	8	5813503	p23.2
SNP_A-1742559	G	G	265	133	300	100	6.837	8.90E-03	rs2816430	8	5813919	p23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308680	G	G	307	105	285	135	4.491	3.41E-02	rs9314587	8	5814453	p23.2
SNP_A-1817077	G	G	252	76	229	101	4.625	0.0315	rs890024	8	5927132	p23.2
SNP_A-1992108	C	T	199	157	173	159	4.413	3.57E-02	rs10503358	8	6003550	p23.2
SNP_A-1899988	C	C	262	124	267	85	5.771	1.63E-02	rs2552279	8	6006187	p23.2
SNP_A-2080790	C	C	396	12	404	4	4.08	4.34E-02	rs4496986	8	6067151	p23.2
SNP_A-1992111	G	G	379	5	387	15	4.674	3.06E-02	rs10503373	8	6155384	p23.2
SNP_A-1992117	T	T	386	4	400	0	4.123	4.23E-02	rs17076773	8	6259546	p23.1
SNP_A-1872272	G	G	377	1	376	8	5.399	0.0201	rs11137028	8	6288954	p23.1
SNP_A-2260245	G	G	263	133	291	103	5.224	0.0223	rs1868555	8	6333439	p23.1
SNP_A-2221590	A	A	259	135	296	110	4.839	2.78E-02	rs2920678	8	6333573	p23.1
SNP_A-2197566	C	T	203	165	189	173	3.972	4.63E-02	rs17623313	8	6383749	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2204171	C	C	399	17	387	31	4.262	0.039	rs3739390	8	6407898	p23.1
SNP_A-1924146	C	C	396	12	375	23	3.906	4.81E-02	rs12546205	8	6408685	p23.1
SNP_A-2212582	T	T	364	44	345	69	5.997	0.0143	rs2515514	8	6414463	p23.1
SNP_A-1814777	T	T	395	15	380	38	10.195	0.0014	rs2922840	8	6414613	p23.1
SNP_A-1785608	A	A	399	17	379	39	9.152	2.50E-03	rs2922841	8	6414804	p23.1
SNP_A-1886957	G	G	298	118	327	89	5.408	0.02	rs7829311	8	6519709	p23.1
SNP_A-2155306	C	C	368	0	355	7	7.185	7.40E-03	rs1014199	8	6527395	p23.1
SNP_A-2073815	T	T	230	158	253	123	5.267	2.17E-02	rs10108451	8	6549500	p23.1
SNP_A-2179938	C	C	245	153	269	119	5.244	2.20E-02	rs2928623	8	6562742	p23.1
SNP_A-1992152	A	C	158	148	196	148	4.819	0.0281	rs1469272	8	6647164	p23.1
SNP_A-2291482	C	G	235	177	217	203	6.322	1.19E-02	rs2978901	8	6677625	p23.1
SNP_A-2308640	T	T	239	113	219	145	4.643	3.12E-02	rs5743404	8	6724531	p23.1
SNP_A-1992163	C	C	321	81	358	50	9.308	0.0023	rs2738079	8	6804222	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1653808	T	T	315	85	352	60	6.187	0.0129	rs2738078	8	6804434	p23.1
SNP_A-1707774	C	C	252	134	226	162	4.058	4.40E-02	rs2978951	8	6810705	p23.1
SNP_A-1713093	C	C	255	145	295	115	6.248	0.0124	rs2702910	8	6811301	p23.1
SNP_A-2195497	T	T	407	1	403	9	6.4	0.0114	rs17078436	8	6814575	p23.1
SNP_A-2280551	T	G	177	143	180	150	6.315	0.012	rs2738113	8	6816495	p23.1
SNP_A-2183882	C	C	393	7	411	1	4.727	2.97E-02	rs6999181	8	6891919	p23.1
SNP_A-2119057	T	T	254	150	278	120	4.371	3.65E-02	rs712255	8	8157126	p23.1
SNP_A-2148466	G	G	390	26	397	13	4.352	3.70E-02	rs2921005	8	8271523	p23.1
SNP_A-2013156	C	C	266	144	297	113	5.446	1.96E-02	rs2921080	8	8338822	p23.1
SNP_A-2038468	A	A	369	19	372	8	4.411	3.57E-02	rs12547034	8	8497521	p23.1
SNP_A-2060944	A	A	339	61	360	42	4.131	4.21E-02	rs17629935	8	8656791	p23.1
SNP_A-1802481	A	A	327	83	363	55	7.483	6.20E-03	rs17154709	8	8657551	p23.1
SNP_A-1992185	G	G	341	55	371	37	4.608	3.18E-02	rs2427	8	8678535	p23.1
SNP_A-1813585	A	A	318	16	343	5	6.423	1.13E-02	rs11995244	8	8727803	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1914493	G	G	201	145	191	187	4.162	4.13E-02	rs7820738	8	8740017	p23.1
SNP_A-2173321	G	G	398	6	408	0	6.105	0.0135	---	8	9155229	p23.1
SNP_A-1847018	A	A	308	44	306	70	5.151	2.32E-02	rs17149709	8	9191804	p23.1
SNP_A-2182290	G	G	257	143	279	115	3.897	4.84E-02	rs13259937	8	9314465	p23.1
SNP_A-2139160	G	G	265	133	230	166	6.112	0.0134	rs1466338	8	9343409	p23.1
SNP_A-1841206	C	C	209	157	250	122	8.005	4.70E-03	rs10100760	8	9407969	p23.1
SNP_A-1992219	A	A	378	34	367	53	4.235	3.96E-02	rs4841171	8	9437099	p23.1
SNP_A-2013166	C	C	296	24	270	54	12.708	4.00E-04	rs7388554	8	9440072	p23.1
SNP_A-2198434	T	T	332	20	300	36	5.823	1.58E-02	rs4535743	8	9529470	p23.1
SNP_A-2189874	T	T	274	112	239	137	4.768	2.90E-02	rs17734290	8	9717633	p23.1
SNP_A-1961531	T	T	350	2	355	9	4.29	3.83E-02	rs580415	8	9860985	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1879792	C	C	356	60	380	38	5.717	1.68E-02	rs1521190	8	9931186	p23.1
SNP_A-2186795	C	C	287	79	310	56	4.805	2.84E-02	rs598523	8	9956896	p23.1
SNP_A-1893389	C	C	306	92	339	71	4.217	4.00E-02	rs1402525	8	9957717	p23.1
SNP_A-1935863	G	G	303	85	332	52	9.253	2.40E-03	rs583167	8	9957980	p23.1
SNP_A-1945368	C	C	293	73	320	52	4.669	3.07E-02	rs814406	8	9965207	p23.1
SNP_A-2077413	G	G	357	55	380	32	6.798	9.10E-03	rs17739113	8	9973359	p23.1
SNP_A-2143572	G	G	364	36	373	15	8.576	3.40E-03	rs17739179	8	9974627	p23.1
SNP_A-2303148	T	T	340	28	325	49	6.017	1.42E-02	rs17151117	8	10012622	p23.1
SNP_A-1992228	G	A	216	182	209	185	4.241	0.0395	rs6983332	8	10015328	p23.1
SNP_A-1755102	C	C	349	51	336	74	4.356	3.69E-02	rs10503403	8	10118354	p23.1
SNP_A-2013184	C	C	280	98	290	64	5.59	1.81E-02	rs4841405	8	10543645	p23.1
SNP_A-1821455	C	C	376	8	397	1	5.766	1.63E-02	rs11250122	8	11130718	p23.1
SNP_A-2187022	G	G	346	44	335	65	4.098	4.29E-02	rs7018402	8	11330445	p23.1
SNP_A-2086162	C	C	345	39	345	65	5.655	1.74E-02	rs12114115	8	11336016	p23.1
SNP_A-2287071	G	G	209	109	240	86	4.754	0.0292	rs2739997	8	12291512	p23.1
SNP_A-1875974	A	A	193	127	215	99	4.599	3.20E-02	rs9969455	8	12661526	p23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864222	C	C	372	44	354	64	4.145	4.18E-02	rs17830061	8	12667407	p23.1
SNP_A-1919602	T	T	193	149	231	123	5.686	1.71E-02	rs6530976	8	12672249	p23.1
SNP_A-1931521	A	A	337	73	307	101	5.898	0.0152	rs6987998	8	12723422	p22
SNP_A-2231168	G	G	163	151	194	130	4.106	4.27E-02	rs4831834	8	12731869	p22
SNP_A-1922449	G	G	287	119	254	154	6.495	1.08E-02	rs6981317	8	12739561	p22
SNP_A-2200136	C	C	289	113	262	146	5.484	1.92E-02	rs12677284	8	12752271	p22
SNP_A-2297560	A	A	327	29	330	14	5.042	0.0247	rs2977170	8	12778270	p22
SNP_A-2013205	A	A	331	7	343	1	4.661	0.0309	rs7817159	8	12841733	p22
SNP_A-2305411	T	T	393	15	379	29	4.708	3.00E-02	rs17786052	8	12922389	p22
SNP_A-1716461	C	C	270	130	241	171	7.055	7.90E-03	rs537330	8	12937573	p22
SNP_A-1725518	C	C	270	128	241	169	7.129	0.0076	rs2584561	8	12937660	p22

Table 2

Name	Major Allele_1	Major Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1992291	T	T	274	138	244	170	5.057	2.45E-02	rs1474139	8	12945100	p22
SNP_A-2111409	C	C	253	141	227	175	4.987	2.55E-02	rs630969	8	12945844	p22
SNP_A-1944723	C	C	302	8	331	1	6.026	0.0141	rs543443	8	12952342	p22
SNP_A-2297842	T	T	256	152	222	180	4.736	2.95E-02	rs607499	8	12961886	p22
SNP_A-1992292	C	C	239	175	202	196	3.979	4.61E-02	rs10503433	8	12971125	p22
SNP_A-2263189	A	A	379	11	378	2	6.103	0.0135	rs7813492	8	13063566	p22
SNP_A-2152877	C	C	344	0	344	4	3.977	4.61E-02	rs7005024	8	13113613	p22
SNP_A-1992304	G	G	383	13	347	27	6.052	1.39E-02	rs17128435	8	13192028	p22
SNP_A-1750343	T	T	293	97	323	61	9.618	0.0019	rs10503457	8	13432096	p22
SNP_A-1992323	A	A	337	71	372	48	6.001	0.0143	—	8	13471164	p22
SNP_A-1992324	G	G	300	62	323	43	4.265	3.89E-02	rs4145815	8	13471203	p22
SNP_A-2094003	C	C	258	158	291	129	4.895	0.0269	rs4379451	8	13478403	p22
SNP_A-2177974	G	G	338	36	343	21	3.849	4.98E-02	rs1982690	8	13499901	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2071178	C	C	274	76	253	103	4.859	0.0275	rs2898376	8	13581301	p22
SNP_A-2206738	G	G	331	37	361	19	6.896	0.0086	rs17238535	8	13584750	p22
SNP_A-1905156	T	T	387	15	363	33	7.473	0.0063	rs10092799	8	13659506	p22
SNP_A-1896956	T	T	241	171	278	140	5.685	1.71E-02	rs7839640	8	13698151	p22
SNP_A-2298680	A	A	253	125	235	161	4.779	2.88E-02	rs2062004	8	13791052	p22
SNP_A-2177792	A	A	389	25	401	13	3.972	4.63E-02	rs7831132	8	13866578	p22
SNP_A-1643886	T	T	255	143	216	172	5.773	1.63E-02	rs10503473	8	13874429	p22
SNP_A-1716285	A	A	250	138	215	171	6.154	1.31E-02	rs1546696	8	13877006	p22
SNP_A-1992346	T	T	265	111	221	145	8.366	0.0038	rs10503470	8	13910499	p22
SNP_A-2304087	A	A	232	118	179	145	8.616	0.0033	rs7010639	8	13911363	p22
SNP_A-2181088	G	C	217	183	211	181	5.166	0.023	rs9325685	8	13962387	p22
SNP_A-1654369	A	A	217	151	192	180	4.047	4.42E-02	rs2035141	8	14306203	p22
SNP_A-2087818	A	A	307	97	287	127	4.57	3.25E-02	rs12547889	8	14367956	p22
SNP_A-2257346	G	G	284	74	259	97	4.239	0.0395	rs7815841	8	14369962	p22
SNP_A-1833551	A	A	231	169	192	188	4.097	4.30E-02	rs12679497	8	14396454	p22
SNP_A-1814261	A	A	275	107	313	79	6.543	1.05E-02	rs17119609	8	14421763	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903365	C	C	306	38	340	24	4.389	3.62E-02	rs825909	8	14456386	p22
SNP_A-1992375	C	C	224	154	186	174	4.305	3.80E-02	rs10503502	8	14473658	p22
SNP_A-2048785	C	C	288	98	301	69	4.986	2.55E-02	rs1397293	8	14549919	p22
SNP_A-2271858	A	A	282	114	315	91	4.281	3.86E-02	---	8	14555058	p22
SNP_A-1846960	T	T	406	2	384	8	3.894	4.85E-02	rs1010895	8	14624602	p22
SNP_A-1992392	G	G	236	166	276	116	11.866	6.00E-04	rs972018	8	14653073	p22
SNP_A-2256375	C	G	203	151	190	184	4.847	2.77E-02	rs2246639	8	14700476	p22
SNP_A-2087580	T	T	407	9	419	1	6.555	1.05E-02	rs7829831	8	14717539	p22
SNP_A-2189505	G	G	319	59	347	37	6.172	1.30E-02	rs17120353	8	14731468	p22
SNP_A-1728263	T	T	251	99	240	134	4.714	2.99E-02	rs4348492	8	14895064	p22
SNP_A-1827606	C	C	295	97	270	122	3.96	4.66E-02	rs6530824	8	14905780	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2055516	T	T	177	161	221	147	4.234	3.96E-02	rs7817295	8	14915797	p22
SNP_A-1819395	T	T	326	78	296	102	4.602	3.19E-02	rs13273444	8	14966783	p22
SNP_A-2283097	G	G	372	44	395	23	7.267	7.00E-03	rs17609019	8	14967266	p22
SNP_A-1826481	G	G	380	28	392	14	4.848	2.77E-02	rs17655425	8	14989328	p22
SNP_A-2224559	A	A	294	36	306	66	6.574	0.0103	rs17120908	8	14995614	p22
SNP_A-1992402	G	G	306	44	284	70	6.728	9.50E-03	rs17471523	8	15018241	p22
SNP_A-2214101	C	C	256	158	213	183	5.378	2.04E-02	rs2054060	8	15020595	p22
SNP_A-1752559	C	C	219	139	206	186	5.665	1.73E-02	rs1587099	8	15337510	p22
SNP_A-1992412	G	G	384	10	391	1	7.422	6.40E-03	rs4087769	8	15569829	p22
SNP_A-1959358	A	A	394	12	396	4	3.961	4.66E-02	rs1017665	8	15749265	p22
SNP_A-1992430	C	C	244	96	209	121	5.436	1.97E-02	—	8	15965771	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1691980	A	A	383	17	405	7	4.605	3.19E-02	rs10503574	8	15994956	p22
SNP_A-1935160	T	T	349	7	355	1	4.551	3.29E-02	rs12677705	8	16932710	p22
SNP_A-1906490	T	T	209	133	241	107	5.04	2.48E-02	rs2959634	8	17071223	p22
SNP_A-1644472	C	C	353	29	386	16	4.722	0.0298	rs2898465	8	17239516	p22
SNP_A-2312831	T	T	351	31	348	12	7.763	0.0053	rs4921542	8	17249948	p22
SNP_A-2013243	T	T	371	33	397	17	5.879	1.53E-02	rs7822451	8	17266781	p22
SNP_A-2218576	G	G	193	181	230	158	4.541	3.31E-02	rs12679696	8	17285087	p22
SNP_A-1992485	G	C	211	199	229	181	4.399	3.60E-02	rs2410528	8	17285880	p22
SNP_A-2302096	T	T	348	4	342	0	3.909	4.80E-02	rs12114309	8	17289983	p22
SNP_A-2085934	A	A	315	33	326	12	9.845	1.70E-03	rs6587041	8	17291194	p22
SNP_A-2090870	T	T	223	105	241	71	6.871	8.80E-03	rs2188021	8	17421621	p22
SNP_A-1849993	C	C	406	10	417	3	3.897	4.84E-02	rs17124783	8	17440174	p22
SNP_A-2110859	T	T	325	77	286	100	5.155	2.32E-02	rs9792165	8	17482758	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1812648	T	T	275	129	239	159	5.602	1.79E-02	rs10104873	8	17484075	p22
SNP_A-2094572	A	A	321	57	298	78	4.116	4.25E-02	rs2720565	8	17486402	p22
SNP_A-2279852	T	T	260	62	232	96	8.855	2.90E-03	rs2705093	8	17486464	p22
SNP_A-2022113	A	A	324	68	309	93	4.112	4.26E-02	rs2517280	8	17486481	p22
SNP_A-2162720	A	A	406	10	397	23	5.203	2.25E-02	rs2588153	8	17493946	p22
SNP_A-1861446	C	C	397	15	385	33	6.891	8.70E-03	rs2588152	8	17493999	p22
SNP_A-2035664	G	G	246	86	303	69	5.528	1.87E-02	rs437548	8	17599309	p22
SNP_A-2085817	C	C	338	44	305	67	6.328	1.19E-02	rs2979790	8	17599702	p22
SNP_A-2162248	A	A	343	59	313	81	4.749	0.0293	rs2937897	8	17608911	p22
SNP_A-1992498	C	C	332	34	300	56	6.861	8.80E-03	rs2937891	8	17617387	p22
SNP_A-1757769	C	T	217	167	213	199	5.369	2.05E-02	rs966118	8	17939677	p22
SNP_A-2151828	T	T	225	147	208	182	3.968	4.64E-02	rs7825389	8	17981644	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1940142	T	T	365	33	374	18	4.476	0.0344	rs916552	8	17998784	p22
SNP_A-2221747	A	A	290	108	306	82	3.861	4.94E-02	rs7837306	8	18119866	p22
SNP_A-2170381	A	A	401	15	414	6	4.045	4.43E-02	rs1389109	8	18165710	p22
SNP_A-1933254	C	C	297	63	309	35	7.878	5.00E-03	rs6993117	8	18258050	p22
SNP_A-2297583	C	C	313	45	352	30	4.514	3.36E-02	rs6997046	8	18258123	p22
SNP_A-1839774	T	T	282	120	263	151	4.033	4.46E-02	rs7013253	8	18287748	p22
SNP_A-2277657	G	G	237	77	272	52	7.097	7.70E-03	rs4646257	8	18306826	p22
SNP_A-1918238	G	G	277	109	317	73	9.794	0.0018	rs1495743	8	18317580	p22
SNP_A-1684734	T	T	326	70	302	100	6.167	1.30E-02	rs9741	8	18395329	p22
SNP_A-1909275	A	A	317	31	304	56	7.255	7.10E-03	rs10090117	8	18425515	p22
SNP_A-2188648	A	A	332	50	312	70	3.954	4.67E-02	rs10087450	8	18425788	p22
SNP_A-1992532	A	A	324	56	312	80	4.276	3.86E-02	rs17595783	8	18428754	p22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2216861	C	C	363	27	384	10	8.381	0.0038	rs3758143	8	18434303	p22
SNP_A-2025184	G	G	282	108	259	141	5.226	0.0223	rs11992396	8	18575527	p22
SNP_A-1992545	A	A	405	9	418	2	4.617	3.17E-02	rs11203992	8	18641945	p22
SNP_A-2290700	A	A	368	4	366	12	3.958	4.67E-02	rs17127274	8	18732203	p22
SNP_A-2106410	T	T	236	142	198	170	5.707	1.69E-02	rs3736273	8	18766809	p22
SNP_A-1992558	C	C	338	64	369	43	5.359	0.0206	rs12155557	8	18823979	p22
SNP_A-1797529	G	G	399	17	411	3	9.973	1.60E-03	rs11984524	8	18994327	p22
SNP_A-1787248	T	T	290	48	320	22	11.109	9.00E-04	rs4921994	8	18999082	p22
SNP_A-2211836	C	C	397	13	417	3	6.622	0.0101	rs10104096	8	19001985	p22
SNP_A-2173491	C	C	290	116	260	146	5.071	2.43E-02	rs17127839	8	19018088	p22
SNP_A-1899643	G	G	388	8	408	0	8.325	3.90E-03	rs6986924	8	19129064	p21.3

Table 2

Name	Major Allele_1	Major Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2045949	G	G	320	18	290	30	3.986	4.59E-02	rs7388399	8	19187769	p21.3
SNP_A-2123316	T	T	377	37	360	60	5.803	0.016	rs17128235	8	19243968	p21.3
SNP_A-2051978	T	T	324	14	296	44	16.776	4.21E-05	rs17478238	8	19244700	p21.3
SNP_A-2086330	G	G	331	23	326	46	7.263	7.00E-03	rs17128247	8	19250530	p21.3
SNP_A-1885985	A	A	377	39	354	66	7.648	5.70E-03	rs17128267	8	19257352	p21.3
SNP_A-2287681	G	G	367	39	334	66	8.452	3.60E-03	rs17128269	8	19257579	p21.3
SNP_A-2198662	C	C	365	27	339	47	6.32	1.19E-02	rs17128272	8	19257994	p21.3
SNP_A-1860485	C	C	300	74	324	44	8.502	3.50E-03	rs2410611	8	19292641	p21.3
SNP_A-1992579	A	A	271	129	293	95	5.837	1.57E-02	rs6586829	8	19326299	p21.3
SNP_A-1992580	T	T	257	81	229	103	4.19	0.0407	rs6586830	8	19329169	p21.3
SNP_A-1787329	C	C	378	38	393	23	3.98	4.60E-02	rs17128418	8	19346742	p21.3
SNP_A-2209120	G	G	346	20	369	9	4.72	0.0298	rs11204087	8	19985307	p21.3
SNP_A-1790940	T	T	295	53	313	33	5.178	0.0229	rs1497023	8	20063494	p21.3
SNP_A-1812477	C	C	365	29	353	47	4.419	3.55E-02	rs4922156	8	20198230	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1824166	G	G	370	42	344	62	4.749	0.0293	rs7817225	8	20228619	p21.3
SNP_A-2030596	G	G	323	59	329	35	5.752	1.65E-02	rs11775998	8	20233679	p21.3
SNP_A-1992618	A	A	403	7	413	1	4.603	3.19E-02	rs17093171	8	20699828	p21.3
SNP_A-2143981	G	G	295	107	314	80	4.411	3.57E-02	rs2616186	8	20768748	p21.3
SNP_A-1780496	C	C	351	13	322	26	5.226	0.0223	rs17495439	8	20870829	p21.3
SNP_A-1790616	T	T	360	46	340	76	7.828	5.10E-03	rs2280488	8	20877074	p21.3
SNP_A-2235585	A	A	369	47	342	76	7.858	5.10E-03	rs17495515	8	20877108	p21.3
SNP_A-1992628	G	G	329	17	286	30	5.254	2.19E-02	rs17496196	8	21078970	p21.3
SNP_A-1935012	G	G	233	181	267	149	5.41	0.02	rs13255049	8	21461146	p21.3
SNP_A-2069245	G	G	262	152	288	122	4.494	3.40E-02	rs12678061	8	21501538	p21.3
SNP_A-1927796	A	A	270	82	283	53	6.166	1.30E-02	rs1979450	8	21525610	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2040406	T	T	213	171	236	140	4.184	4.08E-02	rs17427734	8	21554368	p21.3
SNP_A-2013280	A	A	254	130	284	104	4.541	3.31E-02	rs6587002	8	21625500	p21.3
SNP_A-1868693	G	G	352	0	300	10	11.529	7.00E-04	rs7006417	8	21733781	p21.3
SNP_A-1880729	G	G	373	37	382	22	3.877	4.90E-02	rs11785770	8	21782334	p21.3
SNP_A-1656917	C	C	341	57	374	32	8.467	3.60E-03	-	8	21788040	p21.3
SNP_A-1992653	A	A	401	7	409	1	4.574	3.25E-02	rs10503714	8	21906802	p21.3
SNP_A-2299579	T	T	292	110	268	140	4.584	3.23E-02	rs4872360	8	22084613	p21.3
SNP_A-1697468	C	C	188	104	193	155	5.248	2.20E-02	rs1116084	8	22417247	p21.3
SNP_A-2196663	C	C	356	38	374	16	9.387	2.20E-03	rs17733355	8	22444802	p21.3
SNP_A-2044441	G	G	396	14	406	4	5.68	0.0172	rs10217040	8	22563577	p21.3
SNP_A-2198776	T	T	272	124	287	93	4.503	3.38E-02	rs12676524	8	22759502	p21.3
SNP_A-2099059	G	G	305	83	264	110	6.476	0.0109	rs7007235	8	22768957	p21.3
SNP_A-2136287	A	A	343	59	319	81	4.322	3.76E-02	rs4278155	8	23052724	p21.3

Table 2

Name	Major_Allele 1	Major_Allele 2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1793467	G	G	304	70	330	48	5.147	2.33E-02	rs7824768	8	23305892	p21.3
SNP_A-1735170	A	A	311	75	303	107	5.012	0.0252	rs1355600	8	23472105	p21.2
SNP_A-2259925	A	A	249	163	279	137	3.939	4.72E-02	rs7830129	8	23475814	p21.2
SNP_A-1931978	G	G	315	19	366	10	4.142	4.18E-02	rs6986233	8	23477102	p21.2
SNP_A-1784262	C	C	206	178	239	155	3.908	4.81E-02	rs11986046	8	23534754	p21.2
SNP_A-1671152	T	T	350	0	325	5	5.342	2.08E-02	rs10503737	8	23835118	p21.2
SNP_A-2032333	G	G	350	26	370	10	7.646	5.70E-03	rs4872206	8	23843684	p21.2
SNP_A-2273003	G	G	395	21	406	10	4.054	0.0441	rs6557716	8	23878424	p21.2
SNP_A-2128829	A	A	370	10	389	3	4.059	4.39E-02	rs7827129	8	24086898	p21.2
SNP_A-2129726	A	A	403	11	417	3	4.768	2.90E-02	rs4871910	8	24107616	p21.2
SNP_A-1754294	A	A	358	38	394	16	10.446	1.20E-03	rs1492404	8	24373566	p21.2
SNP_A-1992705	C	C	376	40	398	22	5.832	1.57E-02	rs10503759	8	24426724	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1992707	C	C	322	62	360	38	7.629	5.70E-03	rs4872244	8	24440418	p21.2
SNP_A-1911590	A	A	328	50	354	22	11.875	6.00E-04	rs6557750	8	24443891	p21.2
SNP_A-2112421	G	G	379	35	399	19	5.236	2.21E-02	rs17813759	8	24452013	p21.2
SNP_A-2253538	A	A	347	33	390	20	4.565	3.26E-02	rs11781460	8	24499049	p21.2
SNP_A-2082306	G	G	297	73	302	48	4.655	0.031	rs4871923	8	24606364	p21.2
SNP_A-1992716	T	T	336	56	363	39	3.96	4.66E-02	rs1457265	8	24839743	p21.2
SNP_A-1922868	G	G	303	43	334	24	6.694	9.70E-03	rs2445940	8	24843114	p21.2
SNP_A-2035244	T	T	244	160	274	134	4.017	4.50E-02	rs11135835	8	24875360	p21.2
SNP_A-2191069	A	A	280	100	301	71	5.593	1.80E-02	rs11779795	8	24894579	p21.2
SNP_A-2252357	A	A	250	166	281	139	4.181	4.09E-02	rs4242419	8	24896045	p21.2
SNP_A-1829186	A	A	300	34	269	59	8.356	0.0038	rs1606035	8	25168872	p21.2
SNP_A-2231218	G	G	327	33	330	54	4.313	0.0378	rs868335	8	25215582	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2273256	A	A	351	39	341	59	4.1	4.29E-02	rs11986771	8	25216197	p21.2
SNP_A-2046726	T	T	303	69	273	89	3.959	4.66E-02	rs2666172	8	25238886	p21.2
SNP_A-1893950	A	A	304	82	334	58	5.479	1.92E-02	rs1346092	8	25579053	p21.2
SNP_A-2025522	A	A	274	50	277	77	4.438	3.52E-02	rs9694240	8	25738401	p21.2
SNP_A-1731875	A	A	369	29	364	48	4.482	3.43E-02	rs10503781	8	25901636	p21.2
SNP_A-1750361	T	T	366	26	361	45	4.875	2.73E-02	-	8	25908067	p21.2
SNP_A-1798651	C	C	197	109	172	150	7.782	0.0053	rs1485749	8	25931227	p21.2
SNP_A-2287478	A	A	384	16	378	6	4.268	3.88E-02	rs4872391	8	25970610	p21.2
SNP_A-1861770	C	C	325	91	351	67	4.641	3.12E-02	---	8	26033556	p21.2
SNP_A-2174926	T	T	397	11	408	2	6.376	1.16E-02	rs4871969	8	26064282	p21.2
SNP_A-1992755	T	T	213	163	238	130	5.017	2.51E-02	rs2976340	8	26081577	p21.2
SNP_A-2289656	T	T	352	16	380	6	5.19	2.27E-02	rs17055141	8	26254664	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi Square	p value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2034089	C	C	175	145	215	125	4.983	2.56E-02	rs2046223	8	26266095	p21.2
SNP_A-1909371	C	C	385	25	388	12	4.456	3.48E-02	rs1908650	8	26641530	p21.2
SNP_A-2243433	T	T	378	16	403	7	4.005	4.54E-02	rs4732908	8	26740522	p21.2
SNP_A-1753925	C	C	215	185	251	159	4.623	0.0315	rs10503809	8	26955034	p21.2
SNP_A-2071591	C	G	223	191	232	182	8.125	4.40E-03	rs11135972	8	26957936	p21.2
SNP_A-2048090	C	A	209	175	200	166	6.169	1.30E-02	rs1878447	8	26977511	p21.2
SNP_A-1912689	C	C	301	67	321	43	5.858	0.0155	rs3906912	8	27009573	p21.2
SNP_A-2039261	T	G	220	194	237	183	7.644	5.70E-03	rs10092619	8	27010329	p21.2
SNP_A-1686104	A	A	198	170	248	144	7.007	8.10E-03	rs1584233	8	27013715	p21.2
SNP_A-1677072	T	T	216	184	259	153	6.568	0.0104	rs2322509	8	27018284	p21.2
SNP_A-2055751	C	C	193	163	236	132	7.371	0.0066	rs2322507	8	27037064	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2047348	C	C	209	141	251	123	4.271	3.88E-02	rs10094660	8	27037581	p21.2
SNP_A-1862093	G	A	178	176	207	141	6.75	9.40E-03	rs11775507	8	27057092	p21.2
SNP_A-2289443	G	G	293	111	275	143	4.365	3.67E-02	rs17366040	8	27072243	p21.2
SNP_A-2013308	C	C	346	52	347	31	4.802	2.84E-02	rs3757908	8	27324667	p21.2
SNP_A-1798483	G	G	403	11	413	3	4.689	0.0304	rs17057417	8	27492760	p21.1
SNP_A-1820964	A	A	297	85	279	121	6.443	0.0111	rs6558008	8	27494223	p21.1
SNP_A-2096598	G	G	194	182	217	145	5.21	2.25E-02	rs9797	8	27647768	p21.1
SNP_A-2149781	A	A	357	17	345	35	6.389	0.0115	rs6989156	8	27660469	p21.1
SNP_A-1807463	G	G	239	169	270	142	4.213	4.01E-02	rs17477565	8	27664098	p21.1
SNP_A-1953806	G	G	372	22	367	39	4.593	3.21E-02	rs6989497	8	27668810	p21.1
SNP_A-1956286	C	C	236	164	261	127	5.781	1.62E-02	rs6987535	8	27762207	p21.1
SNP_A-2061978	T	T	222	156	261	133	4.65	3.11E-02	rs2236	8	27766019	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2260938	T	T	223	173	255	145	4.588	3.22E-02	rs4585704	8	27766421	p21.1
SNP_A-2264547	A	A	220	152	253	129	4.053	0.0441	rs7010741	8	27770098	p21.1
SNP_A-1795370	A	A	230	166	258	138	4.186	4.08E-02	rs898467	8	27770841	p21.1
SNP_A-2305834	C	C	233	129	259	95	6.446	0.0111	rs4342548	8	27771492	p21.1
SNP_A-2034467	A	A	236	168	269	141	4.472	3.45E-02	rs7824383	8	27772520	p21.1
SNP_A-1740599	G	G	242	120	235	173	6.967	8.30E-03	rs2685370	8	27783730	p21.1
SNP_A-1992817	T	T	360	0	317	5	5.631	1.76E-02	rs17058050	8	27789216	p21.1
SNP_A-2303982	G	G	328	84	303	115	5.777	1.62E-02	rs4515501	8	27819048	p21.1
SNP_A-2206430	T	T	382	16	390	6	4.623	0.0315	rs4732625	8	28029839	p21.1
SNP_A-1955877	C	C	315	9	325	1	6.55	1.05E-02	rs7839077	8	28377262	p21.1
SNP_A-1890015	A	A	357	17	330	30	4.391	0.0361	rs11997714	8	28516735	p21.1
SNP_A-1919438	G	G	263	145	235	183	5.857	0.0155	rs241174	8	28685079	p21.1
SNP_A-2028818	A	A	289	83	312	62	3.916	4.78E-02	rs241181	8	28698624	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1822218	T	T	349	31	344	50	4.241	0.0395	rs17455458	8	29075907	p12
SNP_A-2087487	C	C	397	9	410	0	9.19	2.40E-03	rs17059722	8	29076877	p12
SNP_A-1780993	G	G	331	19	329	43	8.634	0.0033	rs12542566	8	29213585	p12
SNP_A-1957377	C	C	299	45	301	27	4.128	4.22E-02	rs4732950	8	29362090	p12
SNP_A-2212835	C	C	299	97	330	66	7.424	6.40E-03	rs4236681	8	29409838	p12
SNP_A-1662586	A	C	222	178	214	198	4.501	0.0339	rs4295704	8	29417423	p12
SNP_A-2197798	G	G	298	84	269	135	12.754	4.00E-04	rs13250654	8	29445534	p12
SNP_A-1992868	G	G	314	102	291	129	4.011	4.52E-02	rs17060351	8	29469355	p12
SNP_A-2283286	C	C	344	36	336	56	4.256	3.91E-02	rs6468360	8	29863536	p12
SNP_A-2077301	C	C	308	92	341	69	4.841	2.78E-02	rs10096447	8	29950807	p12
SNP_A-2275396	C	C	394	20	405	9	4.324	3.76E-02	rs7823643	8	30115855	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308624	G	G	362	28	368	14	4.634	3.14E-02	rs4733159	8	30179402	p12
SNP_A-1798186	A	A	273	53	266	78	4.381	3.63E-02	rs17535262	8	30294695	p12
SNP_A-2060119	T	T	375	29	390	16	4.045	4.43E-02	rs2111862	8	30838139	p12
SNP_A-1856993	C	C	378	34	350	64	10.256	0.0014	—	8	31207801	p12
SNP_A-1992913	G	G	333	75	359	49	6.428	0.0112	rs10503686	8	31380038	p12
SNP_A-1666516	T	T	369	29	363	49	4.937	0.0263	rs10489347	8	31462947	p12
SNP_A-1916010	A	G	230	172	205	201	4.82	0.0281	rs6990289	8	31514214	p12
SNP_A-1856239	T	T	237	159	202	184	4.485	3.42E-02	rs4489285	8	31517663	p12
SNP_A-1892841	A	A	257	151	283	117	5.487	1.92E-02	rs9792122	8	31520978	p12
SNP_A-2191788	C	C	238	110	210	140	5.344	2.08E-02	rs10097675	8	31528879	p12
SNP_A-2255315	C	C	248	130	274	104	4.184	4.08E-02	rs12681411	8	31582591	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2054073	G	T	192	184	220	172	3.975	4.62E-02	rs10109424	8	31606330	p12
SNP_A-2239905	C	C	278	70	297	37	10.522	1.20E-03	rs11775125	8	31714461	p12
SNP_A-1824788	C	C	398	2	391	9	4.517	3.36E-02	---	8	32134050	p12
SNP_A-1694989	G	G	296	104	276	132	3.943	4.71E-02	rs970998	8	32258752	p12
SNP_A-2309931	G	G	361	27	361	13	4.644	3.12E-02	rs17631092	8	32276202	p12
SNP_A-1847690	T	T	288	72	263	95	4.296	3.82E-02	rs11778887	8	32276266	p12
SNP_A-1992956	G	G	396	18	387	33	4.472	0.0344	rs16879298	8	32359504	p12
SNP_A-2303707	A	A	217	161	222	112	6.156	1.31E-02	rs12114401	8	32375403	p12
SNP_A-1934607	T	T	269	137	298	112	3.974	4.62E-02	rs9297190	8	32378468	p12
SNP_A-2208625	A	A	269	131	297	105	4.245	3.94E-02	rs17713685	8	32381124	p12
SNP_A-1992959	T	T	322	68	347	49	3.974	4.62E-02	rs4129581	8	32417642	p12
SNP_A-1992963	T	T	205	131	180	164	5.222	0.0223	rs4633020	8	32464690	p12
SNP_A-1992975	C	C	309	37	338	22	4.838	2.78E-02	rs13266765	8	32748740	p12
SNP_A-2137889	G	G	259	147	294	112	6.945	8.40E-03	rs12544147	8	32962597	p12
SNP_A-1919248	T	T	243	149	215	187	5.884	1.53E-02	rs4733142	8	32994669	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2122362	C	C	338	16	339	33	5.457	0.0195	rs6989877	8	33042060	p12
SNP_A-1836854	G	G	362	0	302	4	4.761	2.91E-02	rs16880956	8	33406307	p12
SNP_A-1904330	C	G	208	142	180	178	6.727	9.50E-03	rs1530345	8	33651668	p12
SNP_A-2074965	T	T	342	46	363	29	4.458	3.47E-02	rs12546407	8	34441948	p12
SNP_A-2236674	T	T	349	59	377	37	6.078	0.0137	rs16882556	8	34583402	p12
SNP_A-2281222	G	G	326	2	299	9	4.997	2.54E-02	rs7013553	8	34657077	p12
SNP_A-1993015	G	G	233	119	213	151	4.49	3.41E-02	rs6468274	8	34658236	p12
SNP_A-1881311	A	A	402	0	380	4	4.209	0.0402	rs4549767	8	34659005	p12
SNP_A-1886834	A	A	328	4	309	19	10.325	1.30E-03	rs7836686	8	34809867	p12
SNP_A-1801244	T	T	366	6	339	19	7.528	6.10E-03	rs7842929	8	34812005	p12
SNP_A-1861679	T	T	408	4	401	17	8.065	4.50E-03	rs7000035	8	34834353	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1953997	A	A	407	3	397	17	9.905	1.60E-03	rs10090035	8	34849560	p12
SNP_A-1648476	T	T	345	55	334	78	3.979	4.61E-02	rs1590095	8	35209415	p12
SNP_A-2074840	G	G	408	8	399	19	4.577	3.24E-02	rs10105890	8	35315959	p12
SNP_A-2287535	A	A	313	67	347	39	9.101	2.60E-03	rs1334866	8	36196622	p12
SNP_A-2283544	A	A	329	87	357	63	4.964	2.59E-02	rs1413875	8	36233781	p12
SNP_A-2249051	T	T	321	87	352	62	5.579	1.82E-02	rs7815581	8	36250253	p12
SNP_A-1894456	G	G	346	0	342	4	4.023	4.49E-02	rs7004799	8	36460241	p12
SNP_A-1848131	C	C	213	113	175	149	8.662	3.20E-03	rs557725	8	37167781	p12
SNP_A-2195016	A	A	253	153	221	189	5.93	0.0149	rs472223	8	37192198	p12
SNP_A-2174690	G	G	337	47	374	24	9.128	2.50E-03	rs10282916	8	38677734	p11.23
SNP_A-2035616	T	T	296	48	315	25	7.814	5.20E-03	rs7463038	8	38706200	p11.23
SNP_A-1698435	T	T	305	93	286	126	5.343	2.08E-02	rs726922	8	40102802	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1925152	C	C	254	128	219	169	8.204	4.20E-03	rs10091442	8	40178807	p11.21
SNP_A-2304820	A	A	194	118	176	152	4.76	2.91E-02	rs1869708	8	40181530	p11.21
SNP_A-1993105	T	T	319	75	290	102	5.495	1.91E-02	rs1584991	8	40218904	p11.21
SNP_A-1831458	T	T	333	7	355	1	4.838	2.78E-02	rs16889225	8	40337415	p11.21
SNP_A-1665272	T	T	395	1	397	7	4.425	3.54E-02	rs988197	8	40352529	p11.21
SNP_A-1730727	G	G	340	54	374	34	5.922	1.50E-02	rs2722425	8	40501607	p11.21
SNP_A-2217164	C	C	397	1	395	7	4.485	3.42E-02	rs1429967	8	40509288	p11.21
SNP_A-2197416	T	T	328	40	342	20	6.91	0.0086	rs1429948	8	40520192	p11.21
SNP_A-1915535	G	G	384	32	401	17	4.955	2.60E-02	rs7829042	8	40548187	p11.21
SNP_A-2308820	A	A	252	160	282	130	4.789	0.0286	rs16889787	8	40616135	p11.21
SNP_A-1854933	A	A	335	35	308	52	4.319	3.77E-02	rs907559	8	40850636	p11.21
SNP_A-1861495	G	G	354	42	343	65	4.94	2.62E-02	rs10956864	8	41149582	p11.21
SNP_A-2049024	A	G	230	176	210	202	4.766	2.90E-02	rs968427	8	41284951	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1993125	C	C	302	82	332	62	4.069	4.37E-02	rs10106323	8	41430379	p11.21
SNP_A-2293937	C	C	242	86	250	50	8.428	3.70E-03	rs7005484	8	41494403	p11.21
SNP_A-2245267	A	G	189	171	210	170	4.46	3.47E-02	rs563118	8	41640820	p11.21
SNP_A-1993130	T	T	229	181	260	154	4.122	4.23E-02	rs551580	8	41719805	p11.21
SNP_A-2304316	G	G	284	90	314	66	5.15	2.32E-02	rs2355641	8	41828227	p11.21
SNP_A-2260856	G	G	406	10	398	22	4.561	0.0327	rs4282553	8	42269519	p11.21
SNP_A-2256148	G	G	409	3	407	11	4.533	0.0332	rs16891454	8	42604697	p11.21
SNP_A-1871615	C	C	368	0	346	4	4.229	3.97E-02	rs10108540	8	47793774	q11.1
SNP_A-1741725	T	T	358	30	359	49	4.071	0.0436	rs10504060	8	48331438	q11.21
SNP_A-2246716	C	C	344	56	373	33	7.072	7.80E-03	rs4347021	8	49333697	q11.21
SNP_A-1917861	A	A	345	63	377	41	5.952	0.0147	rs4552931	8	49333780	q11.21
SNP_A-2136070	T	T	359	25	367	11	5.486	1.92E-02	rs16935801	8	49384285	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2197371	G	G	274	140	303	107	5.847	1.56E-02	rs955467	8	49469934	q11.21
SNP_A-1993153	C	C	318	60	347	35	7.823	5.20E-03	rs1123189	8	49520992	q11.21
SNP_A-1800296	C	C	326	86	356	56	7.658	5.70E-03	rs10110839	8	49544829	q11.21
SNP_A-1993154	T	T	305	89	310	62	4.24	0.0395	rs10098707	8	49586813	q11.21
SNP_A-1713532	A	A	336	64	368	42	5.898	0.0152	rs10504066	8	49613996	q11.21
SNP_A-2083022	C	C	290	44	335	25	7.508	6.10E-03	rs1393550	8	49615550	q11.21
SNP_A-2146012	T	T	330	82	360	56	6.184	0.0129	rs16937921	8	49654428	q11.21
SNP_A-1916666	G	G	274	88	320	64	6.709	9.60E-03	rs16938118	8	49677446	q11.21
SNP_A-1802407	A	A	272	78	297	51	6.744	9.40E-03	rs10957175	8	49690718	q11.21
SNP_A-2013377	G	G	262	78	302	54	6.836	8.90E-03	rs6471906	8	49692538	q11.21
SNP_A-1811087	G	G	206	106	269	89	6.711	9.60E-03	rs2279302	8	49699157	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2222783	T	T	338	62	356	42	4.308	3.79E-02	rs10086031	8	49714525	q11.21
SNP_A-2295823	C	C	349	59	372	38	5.275	2.16E-02	rs10098811	8	49714558	q11.21
SNP_A-2299425	G	G	334	66	374	44	6.267	0.0123	rs13275840	8	49717849	q11.21
SNP_A-2066375	A	A	338	58	365	29	10.699	1.10E-03	rs13251674	8	49717935	q11.21
SNP_A-2195398	A	A	343	67	365	43	5.915	1.50E-02	rs10107998	8	49729522	q11.21
SNP_A-2095583	A	A	187	179	243	151	8.649	0.0033	rs2385117	8	50026172	q11.21
SNP_A-2270766	A	G	208	192	247	163	12.227	5.00E-04	rs11774804	8	50043528	q11.21
SNP_A-2166469	G	A	242	158	204	198	10.24	0.0014	rs2203065	8	50044540	q11.21
SNP_A-1791095	T	C	197	151	215	149	17.5	2.87E-05	rs10957317	8	50051423	q11.21
SNP_A-1993161	G	G	339	43	278	66	8.919	0.0028	rs3849805	8	50060059	q11.21
SNP_A-1993164	A	A	343	63	296	96	10.064	0.0015	rs10504069	8	50113363	q11.21
SNP_A-2114221	T	T	219	157	270	122	9.38	2.20E-03	rs2385127	8	50138299	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1993166	C	C	239	151	278	112	8.725	3.10E-03	rs341815	8	50140977	q11.21
SNP_A-2075969	A	C	187	179	229	155	8.695	3.20E-03	rs7011891	8	50146091	q11.21
SNP_A-1993169	A	A	236	168	270	142	4.387	3.62E-02	rs341817	8	50186153	q11.21
SNP_A-1993171	T	T	209	207	248	168	7.384	0.0066	rs10504073	8	50187497	q11.21
SNP_A-1886043	C	C	228	142	238	102	5.514	0.0189	rs11779250	8	50221706	q11.21
SNP_A-1849784	A	A	347	69	369	47	4.848	2.77E-02	rs17721252	8	50362515	q11.21
SNP_A-2074963	G	G	386	18	357	33	5.298	2.13E-02	rs2926090	8	50622669	q11.21
SNP_A-2053268	G	G	383	15	357	27	4.093	4.31E-02	rs10081463	8	50670808	q11.21
SNP_A-1804142	G	G	369	9	349	21	5.272	2.17E-02	rs10081584	8	50673450	q11.21
SNP_A-1809235	G	G	369	21	332	34	4.268	3.88E-02	rs13263794	8	50673797	q11.21
SNP_A-1926140	A	A	366	24	350	44	6.22	0.0126	rs7843358	8	50680907	q11.21
SNP_A-2055569	T	T	374	22	360	40	5.473	1.93E-02	rs11778828	8	50682583	q11.21
SNP_A-2117768	G	G	381	27	366	46	5.227	2.22E-02	rs1390595	8	50769285	q11.21
SNP_A-2049580	G	G	382	26	370	46	5.67	1.73E-02	rs10094841	8	50792516	q11.21
SNP_A-1840615	A	A	296	56	255	87	9.629	0.0019	rs1352113	8	50934820	q11.21
SNP_A-1855935	T	T	368	40	343	61	5.226	0.0223	rs6999728	8	51106589	q11.21
SNP_A-2057710	T	T	276	110	257	139	3.928	4.75E-02	rs4292700	8	51455302	q11.21
SNP_A-2303970	G	G	345	45	333	69	5.084	0.0241	rs13252069	8	51718637	q11.21
SNP_A-1721718	T	T	338	62	321	87	4.554	3.28E-02	rs10504137	8	53200232	q11.23
SNP_A-2247246	A	A	351	53	331	79	5.664	1.73E-02	rs17221900	8	53305498	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2160314	C	C	359	57	339	79	4.127	4.22E-02	rs17313586	8	53319377	q11.23
SNP_A-1878077	A	A	227	113	188	134	4.965	2.59E-02	rs7842486	8	53330935	q11.23
SNP_A-2023863	C	C	356	36	376	20	5.098	0.024	rs16917670	8	53394490	q11.23
SNP_A-2061184	C	C	379	35	398	20	4.536	0.0332	rs6996763	8	53439500	q11.23
SNP_A-1890483	C	C	342	32	337	17	4.082	4.33E-02	rs12674582	8	53440357	q11.23
SNP_A-2299009	G	G	378	36	398	20	5.068	2.44E-02	rs10113051	8	53444353	q11.23
SNP_A-2260364	T	T	373	39	393	19	7.419	6.50E-03	rs11991947	8	53446258	q11.23
SNP_A-1925631	G	G	366	26	392	14	4.248	3.93E-02	rs7388668	8	53456729	q11.23
SNP_A-1884733	T	T	301	49	309	75	3.99	0.0458	rs7465621	8	53496253	q11.23
SNP_A-2277879	C	C	406	8	419	1	5.606	1.79E-02	rs16917837	8	53500806	q11.23
SNP_A-1811919	A	A	271	115	303	93	3.984	4.59E-02	rs2613279	8	53539031	q11.23
SNP_A-1804503	A	A	264	98	290	70	5.881	1.53E-02	rs2582635	8	53539206	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1860980	G	C	179	137	168	156	4.631	3.14E-02	rs17253789	8	53870240	q11.23
SNP_A-1993289	A	A	275	73	302	44	8.446	3.70E-03	rs2884946	8	53908391	q11.23
SNP_A-1993290	A	A	283	107	315	81	5.263	0.0218	rs2884945	8	53908561	q11.23
SNP_A-1993293	A	A	326	8	318	20	5.219	0.0223	rs10504149	8	53972009	q11.23
SNP_A-1853157	A	A	371	3	358	10	3.953	4.68E-02	rs16918595	8	54197442	q11.23
SNP_A-2050022	G	G	410	6	403	15	3.913	4.79E-02	rs16918598	8	54201590	q11.23
SNP_A-2069606	C	C	221	165	245	135	4.189	0.0407	rs1477967	8	54510156	q11.23
SNP_A-2070917	T	T	295	81	262	102	4.171	4.11E-02	rs2086074	8	54646328	q11.23
SNP_A-2021122	T	T	252	120	235	151	3.882	4.88E-02	rs11778957	8	54659415	q11.23
SNP_A-2082768	G	G	306	80	289	107	4.257	3.91E-02	rs7464824	8	54674989	q11.23
SNP_A-2148180	T	T	206	128	161	151	6.672	9.80E-03	rs12549792	8	54677369	q11.23
SNP_A-1828966	G	G	318	74	297	105	5.961	0.0146	rs12680850	8	54683688	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2013408	T	T	325	81	298	104	4.01	4.52E-02	rs6473864	8	54691313	q11.23
SNP_A-2111641	A	A	255	139	228	166	3.899	4.83E-02	rs10958387	8	54703084	q11.23
SNP_A-2013411	T	T	385	11	393	3	4.654	0.031	rs6473901	8	55080561	q11.23
SNP_A-1937129	G	G	406	10	417	3	3.897	4.84E-02	rs6983650	8	55100384	q11.23
SNP_A-2193907	C	C	387	1	398	8	5.193	2.27E-02	rs11984645	8	55231858	q11.23
SNP_A-1874519	A	A	301	69	285	97	4.97	0.0258	rs7834481	8	55240770	q11.23
SNP_A-1909326	T	T	248	160	289	125	7.385	0.0066	rs2666871	8	55251737	q11.23
SNP_A-2270422	T	T	256	154	289	125	4.993	2.54E-02	rs1511147	8	55253780	q11.23
SNP_A-1902075	A	A	258	156	293	123	6.122	0.0134	rs2666874	8	55254114	q11.23
SNP_A-2185764	T	T	251	143	267	107	5.161	2.31E-02	rs1250613	8	55274023	q11.23
SNP_A-2120396	G	G	391	5	412	0	5.234	2.21E-02	rs11991652	8	55504699	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116061	T	T	332	40	344	24	4.192	4.06E-02	rs4737824	8	56082884	q12.1
SNP_A-1889515	C	C	201	127	233	107	3.855	4.96E-02	rs10958442	8	56203745	q12.1
SNP_A-1921685	A	A	329	5	328	0	4.948	2.61E-02	rs16921396	8	56281845	q12.1
SNP_A-1643964	C	C	394	6	412	0	6.226	0.0126	rs10504191	8	56461691	q12.1
SNP_A-1677358	A	A	394	6	412	0	6.226	0.0126	rs10504192	8	56461881	q12.1
SNP_A-1876114	G	G	389	23	407	11	4.599	3.20E-02	rs7831274	8	56496615	q12.1
SNP_A-1820521	T	T	353	23	371	11	4.636	3.13E-02	rs6473986	8	56497796	q12.1
SNP_A-1846689	C	C	399	11	415	3	4.809	2.83E-02	rs13439780	8	56506740	q12.1
SNP_A-2024891	A	A	258	146	277	115	4.177	4.10E-02	rs1876236	8	56565688	q12.1
SNP_A-1913267	G	G	410	6	418	0	6.073	0.0137	rs7839044	8	56568307	q12.1
SNP_A-1993350	T	T	347	7	368	0	7.348	6.70E-03	rs10504193	8	56574727	q12.1
SNP_A-1993351	T	T	373	5	368	0	4.901	2.68E-02	rs10504194	8	56582363	q12.1
SNP_A-1993361	C	C	387	13	410	4	5.189	2.27E-02	rs16922400	8	56990293	q12.1
SNP_A-1675319	A	A	264	84	305	67	4.073	0.0436	rs2670028	8	57473634	q12.1
SNP_A-2258228	C	C	301	97	326	68	6.074	0.0137	rs12545109	8	57476460	q12.1
SNP_A-1789233	G	G	283	105	316	78	4.832	2.79E-02	rs1975284	8	57477217	q12.1
SNP_A-1806329	A	A	294	114	325	85	5.774	1.63E-02	rs2438063	8	57546914	q12.1
SNP_A-1817893	C	C	300	96	331	75	3.978	4.61E-02	rs2016795	8	57552940	q12.1
SNP_A-1801776	A	A	293	105	300	72	5.363	0.0206	rs21118261	8	57555840	q12.1
SNP_A-2313013	A	A	275	103	314	84	4	4.55E-02	rs1440762	8	57573262	q12.1
SNP_A-2230389	C	C	261	99	280	72	4.841	2.78E-02	rs1348082	8	57577570	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1993369	T	T	292	96	322	72	4.849	2.77E-02	rs1837617	8	57580146	q12.1
SNP_A-1993372	G	G	318	96	353	67	6.942	8.40E-03	rs2055984	8	57580886	q12.1
SNP_A-2248395	T	T	272	78	319	55	6.927	8.50E-03	rs2576589	8	57588201	q12.1
SNP_A-1884828	G	G	301	53	331	35	4.907	2.67E-02	rs1973628	8	57591914	q12.1
SNP_A-2311192	A	A	412	4	416	0	4.019	4.50E-02	rs16920699	8	57593874	q12.1
SNP_A-2210742	A	A	341	21	325	35	3.879	4.89E-02	rs4737442	8	57678517	q12.1
SNP_A-1757013	T	T	327	73	306	106	6.605	1.02E-02	rs353753	8	57726498	q12.1
SNP_A-2065200	G	G	330	70	312	102	6.219	0.0126	rs1364956	8	57738405	q12.1
SNP_A-2230895	A	A	304	52	275	75	5.567	0.0183	rs114898	8	57851040	q12.1
SNP_A-2151208	C	C	334	76	303	101	4.996	2.54E-02	rs241511	8	57853713	q12.1
SNP_A-1652354	G	G	216	184	251	159	4.322	3.76E-02	rs1396122	8	57874824	q12.1
SNP_A-1745838	T	T	213	183	251	159	4.554	3.28E-02	rs6474087	8	57875781	q12.1
SNP_A-1662414	C	C	340	56	372	38	4.643	3.12E-02	rs906538	8	57894309	q12.1
SNP_A-2186316	A	A	285	127	256	158	4.922	2.65E-02	rs2317769	8	57920173	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1854251	A	A	279	117	240	142	5.093	0.024	rs2873549	8	57920323	q12.1
SNP_A-2233785	G	G	288	124	256	162	6.888	8.70E-03	rs11989947	8	57926689	q12.1
SNP_A-1879575	G	G	377	15	348	32	7.124	0.0076	rs16921146	8	57927125	q12.1
SNP_A-2298744	C	C	273	119	251	157	5.838	1.57E-02	rs11786647	8	57927246	q12.1
SNP_A-2110614	C	C	304	92	327	69	4.124	4.23E-02	rs13272502	8	57961738	q12.1
SNP_A-2274033	T	T	354	60	379	41	4.384	3.63E-02	rs7843827	8	58005810	q12.1
SNP_A-1956507	T	T	350	52	372	34	4.418	0.0356	rs7817368	8	58006460	q12.1
SNP_A-1993387	G	G	348	56	344	28	8.051	4.50E-03	rs965325	8	58007822	q12.1
SNP_A-2149534	T	T	354	56	375	37	4.482	3.43E-02	rs7831943	8	58015588	q12.1
SNP_A-1954341	C	C	295	67	339	37	11.446	7.00E-04	rs2318149	8	58377571	q12.1
SNP_A-2293240	A	A	249	105	284	72	8.445	3.70E-03	rs7013994	8	58388614	q12.1
SNP_A-1878274	T	T	339	43	338	24	4.855	0.0276	rs1996440	8	58409817	q12.1
SNP_A-1993403	A	A	262	132	303	97	8.28	4.00E-03	rs1317890	8	58452664	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251618	C	C	365	39	382	22	5.125	2.36E-02	rs16922088	8	58460626	q12.1
SNP_A-2037065	A	A	260	150	293	109	8.382	0.0038	rs13253851	8	58471311	q12.1
SNP_A-2141903	G	G	308	90	337	69	3.998	4.55E-02	rs10088084	8	58536851	q12.1
SNP_A-2225938	C	C	289	83	255	121	9.182	2.40E-03	rs1376403	8	58680947	q12.1
SNP_A-2101083	C	C	301	15	342	6	4.941	2.62E-02	rs7003082	8	58724117	q12.1
SNP_A-2305214	G	G	230	122	235	79	7.108	7.70E-03	rs10104845	8	58923004	q12.1
SNP_A-1676656	A	A	367	23	393	9	6.834	8.90E-03	rs10504241	8	59049115	q12.1
SNP_A-1753379	C	C	383	17	405	5	7.037	8.00E-03	rs10504240	8	59049901	q12.1
SNP_A-2220907	G	G	261	55	243	81	5.514	0.0189	rs1122328	8	59100304	q12.1
SNP_A-2225295	G	G	401	15	412	6	4.001	4.55E-02	rs17176439	8	59206041	q12.1
SNP_A-1811575	A	T	217	143	188	180	9.479	2.10E-03	rs7833271	8	59259287	q12.1
SNP_A-2267165	A	A	245	99	215	123	4.499	0.0339	rs1605385	8	59265550	q12.1
SNP_A-2250338	A	A	313	69	309	97	4.021	4.49E-02	rs880056	8	59297691	q12.1
SNP_A-2290273	G	G	299	35	302	62	6.253	0.0124	rs16923480	8	59515723	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2121703	T	T	224	146	267	121	5.682	1.71E-02	rs10104292	8	59633886	q12.1
SNP_A-2251265	A	A	234	154	213	191	4.633	3.14E-02	rs2726551	8	59845496	q12.1
SNP_A-2034370	A	A	305	73	312	44	6.614	0.0101	rs2634520	8	59845955	q12.1
SNP_A-2047254	T	T	370	14	367	27	4.006	0.0453	rs16923878	8	59860983	q12.1
SNP_A-2073422	C	C	395	19	409	7	5.777	1.62E-02	rs16923894	8	59862874	q12.1
SNP_A-2041627	A	A	353	5	332	0	4.671	3.07E-02	rs2693451	8	59866991	q12.1
SNP_A-2197434	G	G	258	112	247	147	4.22	4.00E-02	rs2726596	8	59872940	q12.1
SNP_A-2265251	T	T	237	77	262	56	4.543	3.31E-02	rs10957070	8	59875147	q12.1
SNP_A-1993446	C	C	354	62	377	41	5	0.0253	rs2726585	8	59956246	q12.1
SNP_A-1753495	C	C	328	72	359	53	4.11	4.26E-02	rs10504286	8	60128643	q12.1
SNP_A-2282436	G	G	271	71	291	47	5.57	0.0183	rs11784288	8	60303997	q12.1
SNP_A-1934703	A	A	319	75	342	54	4.214	4.01E-02	rs10088994	8	60348186	q12.1
SNP_A-1721111	T	T	367	31	389	17	4.644	3.12E-02	rs2326441	8	60773049	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170854	C	C	217	125	225	93	3.975	4.62E-02	rs7018304	8	60880058	q12.1
SNP_A-1993468	C	C	318	34	338	20	4.189	0.0407	rs9298021	8	60912376	q12.1
SNP_A-2201426	G	G	376	28	370	12	5.837	1.57E-02	rs7834199	8	60997427	q12.1
SNP_A-1993475	G	G	412	4	420	0	4.058	4.40E-02	rs16925485	8	61032620	q12.1
SNP_A-1919270	A	A	379	35	394	20	4.382	3.63E-02	rs16925712	8	61165748	q12.1
SNP_A-2013449	C	C	412	4	418	0	4.039	4.45E-02	rs997574	8	61261112	q12.1
SNP_A-1933373	A	A	307	11	312	2	6.246	0.0124	rs17815879	8	61540151	q12.1
SNP_A-2098259	C	C	395	19	406	8	4.633	3.14E-02	rs16927019	8	62294169	q12.2
SNP_A-1785028	G	G	379	25	392	8	8.957	0.0028	rs3864670	8	62315455	q12.2
SNP_A-2207718	T	T	379	29	395	15	4.78	2.88E-02	rs3864671	8	62315603	q12.2
SNP_A-1993515	A	A	309	7	344	0	7.702	5.50E-03	rs16927174	8	62393398	q12.2
SNP_A-1860942	G	G	250	82	294	60	6.268	0.0123	rs4738898	8	62568445	q12.3
SNP_A-2189602	C	C	252	120	287	89	6.85	8.90E-03	rs1546111	8	62567110	q12.3
SNP_A-1993520	G	G	284	132	316	100	6.12	0.0134	rs10504326	8	62571219	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1799478	G	G	278	120	307	95	4.325	3.76E-02	rs4738905	8	62606255	q12.3
SNP_A-2199555	G	G	413	1	410	8	5.436	1.97E-02	rs7013514	8	62625996	q12.3
SNP_A-2060695	C	C	359	27	328	42	4.323	3.76E-02	rs7823222	8	62690126	q12.3
SNP_A-2013461	A	A	351	43	343	69	5.729	0.0167	rs2350580	8	62716885	q12.3
SNP_A-1688546	C	C	261	139	232	168	4.445	3.50E-02	rs1495003	8	62740711	q12.3
SNP_A-2066243	A	A	351	47	350	28	4.302	3.81E-02	rs10094729	8	62798716	q12.3
SNP_A-1866593	T	T	181	167	224	154	3.859	4.95E-02	rs10957202	8	62876830	q12.3
SNP_A-2218176	G	G	296	42	327	25	5.574	1.82E-02	rs6471977	8	63012530	q12.3
SNP_A-2268455	G	G	351	37	347	57	3.957	4.67E-02	rs16928845	8	63461008	q12.3
SNP_A-1993568	C	C	377	33	356	50	4.064	4.38E-02	rs16929386	8	63753091	q12.3
SNP_A-1758349	T	T	356	20	361	37	4.483	3.42E-02	rs10504360	8	63912298	q12.3
SNP_A-2304379	C	C	372	0	330	4	4.48	3.43E-02	rs6999953	8	64193227	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839285	C	C	306	72	337	47	6.7	9.60E-03	rs4739082	8	64388446	q12.3
SNP_A-2013474	A	A	226	156	195	187	5.084	0.0241	rs7461453	8	64410935	q12.3
SNP_A-2013475	T	T	357	43	371	19	9.434	2.10E-03	rs7465412	8	64411075	q12.3
SNP_A-1993588	C	C	312	34	285	51	4.475	0.0344	rs12115114	8	64552434	q12.3
SNP_A-2125585	G	G	337	65	313	87	4.065	4.38E-02	rs2354895	8	64575540	q12.3
SNP_A-2130007	T	T	329	59	301	79	4.06	4.39E-02	rs1367812	8	64603457	q12.3
SNP_A-2127002	T	T	340	70	320	98	5.196	2.26E-02	rs6472113	8	64624186	q12.3
SNP_A-1894249	T	T	356	18	370	8	4.095	4.30E-02	rs1520933	8	64826826	q12.3
SNP_A-1993602	T	T	328	4	336	0	4.073	0.0436	rs1948035	8	65306097	q12.3
SNP_A-1846666	T	T	342	8	319	1	4.911	2.67E-02	rs10957309	8	65411497	q12.3
SNP_A-1993611	T	T	274	136	241	161	4.141	0.0419	rs7836768	8	65550021	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140997	C	C	390	14	393	5	4.23	3.97E-02	rs16931326	8	65657887	q12.3
SNP_A-2260973	T	T	367	19	333	31	3.889	4.86E-02	rs10957319	8	65711815	q12.3
SNP_A-2297709	A	A	245	161	197	187	6.548	1.05E-02	rs6997106	8	66062241	q12.3
SNP_A-1667096	G	G	247	109	298	82	7.815	5.20E-03	rs4132352	8	66106615	q13.1
SNP_A-1993616	A	A	302	56	320	38	3.968	4.64E-02	rs10504382	8	66158149	q13.1
SNP_A-1938023	G	G	279	135	312	104	5.859	0.0155	rs4581094	8	66227941	q13.1
SNP_A-2171472	C	C	269	127	301	93	7.046	7.90E-03	rs4737704	8	66235257	q13.1
SNP_A-2013485	G	G	289	47	258	70	6.183	0.0129	rs7008249	8	66240093	q13.1
SNP_A-2159278	T	T	223	187	255	161	4.041	4.44E-02	rs6472179	8	66253252	q13.1
SNP_A-1924854	C	C	372	0	331	5	5.575	1.82E-02	—	8	67152424	q13.1
SNP_A-2247859	A	A	345	17	353	7	4.253	3.92E-02	rs7831234	8	67214949	q13.1
SNP_A-1993631	G	G	371	5	384	0	5.14	2.34E-02	rs16932778	8	67373672	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1717665	G	G	393	7	412	0	7.273	7.00E-03	rs7008801	8	67497614	q13.2
SNP_A-1879764	T	T	405	7	415	1	4.603	3.19E-02	rs12541034	8	67586551	q13.1
SNP_A-1827419	A	A	408	8	419	1	5.572	0.0183	rs10095700	8	67590057	q13.1
SNP_A-1813156	G	G	361	21	389	5	10.708	1.10E-03	rs16932954	8	67597715	q13.1
SNP_A-1993636	G	G	394	20	415	3	13.091	3.00E-04	rs7012434	8	67628142	q13.1
SNP_A-1993638	C	C	397	15	412	6	4.092	4.31E-02	rs3808602	8	67740224	q13.1
SNP_A-2044319	G	G	319	63	344	44	4.27	3.88E-02	rs6472345	8	68937625	q13.2
SNP_A-1925694	G	G	361	43	387	27	4.439	3.51E-02	rs7005336	8	69068067	q13.2
SNP_A-2214931	T	T	369	47	384	28	5.093	0.024	rs16933960	8	69068694	q13.2
SNP_A-2253819	T	T	368	46	390	30	3.964	0.0465	rs16933966	8	69069314	q13.2
SNP_A-2117050	G	G	302	40	274	58	4.52	3.35E-02	rs11785911	8	69071366	q13.2
SNP_A-1836128	G	G	309	99	289	129	4.496	3.40E-02	rs4557688	8	69138659	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2166912	G	G	211	149	238	114	6.192	1.28E-02	rs1434764	8	69176632	q13.2
SNP_A-1993682	G	G	397	11	409	3	4.731	2.96E-02	rs17482603	8	69892366	q13.2
SNP_A-2134309	T	T	357	49	340	72	4.743	2.94E-02	rs16935130	8	69897584	q13.2
SNP_A-2226026	T	T	338	34	321	55	5.372	2.05E-02	rs4737917	8	69898601	q13.2
SNP_A-2123954	A	A	385	25	371	41	4.133	4.20E-02	rs10091347	8	69961636	q13.2
SNP_A-2258714	C	C	369	45	391	25	6.346	0.0118	rs7001684	8	70018288	q13.2
SNP_A-1993697	G	G	358	16	378	4	7.66	5.60E-03	rs638853	8	70176898	q13.2
SNP_A-1686422	T	T	223	169	263	147	4.422	3.55E-02	rs4737965	8	70355068	q13.3
SNP_A-1935380	G	G	353	23	353	11	4.042	4.44E-02	rs4738015	8	70738460	q13.3
SNP_A-2169022	C	C	367	23	364	10	4.801	2.85E-02	rs7819743	8	71140749	q13.3
SNP_A-1853630	A	A	397	11	417	3	4.89	0.027	rs16937074	8	71624075	q13.3
SNP_A-1895640	A	A	347	45	358	28	4.085	4.33E-02	rs1000377	8	72214140	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1728755	T	T	388	4	410	0	4.205	4.03E-02	rs10504503	8	72226419	q13.3
SNP_A-1936771	C	C	394	16	410	6	4.821	0.0281	rs1035670	8	72693563	q13.3
SNP_A-1993786	C	C	331	61	344	38	5.466	1.94E-02	rs16937848	8	72923703	q13.3
SNP_A-1993789	G	G	327	89	351	67	3.947	4.69E-02	rs10504516	8	72927929	q13.3
SNP_A-1907386	C	C	343	73	368	52	4.388	3.62E-02	rs7816487	8	72928664	q13.3
SNP_A-2189707	T	T	357	9	357	1	6.312	0.012	rs7014722	8	73039943	q13.3
SNP_A-1857911	C	C	392	16	390	30	4.093	4.31E-02	rs16938031	8	73188096	q13.3
SNP_A-2218476	C	C	361	17	362	6	5.129	0.0235	rs349352	8	73623268	q13.3
SNP_A-2068163	A	A	288	126	258	156	4.84	2.78E-02	rs10957637	8	74145558	q13.3
SNP_A-1845231	G	G	387	29	371	49	5.447	1.96E-02	rs9657104	8	75189519	q21.11
SNP_A-2248676	G	G	321	95	339	69	4.536	0.0332	rs10957694	8	75206574	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1941327	G	G	265	91	298	72	3.88	4.89E-02	rs10282976	8	75210726	q21.11
SNP_A-2130974	A	A	288	100	309	67	7.073	7.80E-03	rs10957696	8	75215851	q21.11
SNP_A-1993856	A	A	270	106	292	82	3.92	4.77E-02	rs7008430	8	75216096	q21.11
SNP_A-1933563	C	C	404	4	412	0	4.059	4.39E-02	rs4302831	8	75219862	q21.11
SNP_A-1781850	T	T	298	26	292	44	4.473	0.0344	rs2936672	8	75260998	q21.11
SNP_A-1993858	C	C	309	99	273	123	4.643	3.12E-02	rs4738438	8	75319043	q21.11
SNP_A-1688578	T	T	233	147	212	180	4.136	4.20E-02	rs4471028	8	75344937	q21.11
SNP_A-2205494	A	A	291	105	267	137	5.184	2.28E-02	rs10094189	8	75354247	q21.11
SNP_A-2093017	A	A	190	144	229	127	3.999	4.55E-02	rs4738443	8	75370208	q21.11
SNP_A-2146149	G	G	243	129	223	163	4.56	0.0327	rs12545409	8	75425707	q21.11
SNP_A-1993866	C	C	334	8	301	17	4.088	4.32E-02	rs16938934	8	75742974	q21.11
SNP_A-1993871	A	A	225	119	182	144	6.44	0.0112	rs719240	8	75986409	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1912319	G	G	312	104	277	131	5.105	2.39E-02	rs16939006	8	76043194	q21.11
SNP_A-1649980	A	A	284	38	283	71	8.497	3.60E-03	rs10504591	8	76087122	q21.13
SNP_A-2131889	A	A	308	62	290	86	4.386	3.62E-02	rs17370831	8	76203872	q21.11
SNP_A-2301737	T	T	285	67	272	92	4.034	4.46E-02	---	8	76376596	q21.11
SNP_A-2293751	C	C	246	170	282	138	5.76	1.64E-02	rs2980231	8	76459344	q21.11
SNP_A-1841840	A	A	233	177	283	133	11.047	9.00E-04	rs2980221	8	76470294	q21.11
SNP_A-1923501	C	C	326	62	346	42	4.441	3.51E-02	rs2980249	8	76489798	q21.11
SNP_A-2174814	C	C	343	55	354	34	5.002	0.0253	rs7828282	8	76564673	q21.11
SNP_A-1871258	G	G	357	11	357	1	8.197	4.20E-03	rs3779737	8	76583712	q21.11
SNP_A-2129220	G	G	240	150	205	183	6.018	1.42E-02	rs878088	8	76596138	q21.11
SNP_A-2287114	G	G	396	18	385	33	4.548	3.30E-02	rs7815941	8	76905302	q21.11
SNP_A-2305144	A	A	248	98	285	71	6.741	9.40E-03	rs10111918	8	77214736	q21.11
SNP_A-1993894	C	C	286	120	316	92	5.188	2.27E-02	rs12679759	8	77278262	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2061921	C	C	395	11	409	3	4.771	2.89E-02	rs16939309	8	77649444	q21.11
SNP_A-1993905	G	G	336	80	356	56	4.794	0.0286	rs7817733	8	77854223	q21.11
SNP_A-2030960	G	G	339	5	294	12	3.873	4.91E-02	rs13276738	8	78071992	q21.11
SNP_A-1712633	C	C	230	146	282	102	13.005	3.00E-04	rs4398888	8	78213363	q21.13
SNP_A-1810045	A	A	274	108	251	139	4.816	2.82E-02	rs4735765	8	78260360	q21.11
SNP_A-1789148	G	A	194	166	179	145	5.693	1.70E-02	rs7828279	8	78322604	q21.11
SNP_A-1993924	C	C	247	163	290	118	10.645	1.10E-03	rs7825782	8	78334295	q21.11
SNP_A-2209566	G	G	310	102	282	132	5.166	0.023	rs2310747	8	78347653	q21.11
SNP_A-2203669	A	A	311	103	282	136	5.956	0.0147	rs6473016	8	78349417	q21.11
SNP_A-2182347	G	G	235	149	274	126	4.587	3.22E-02	rs4329252	8	78360889	q21.11
SNP_A-2204064	A	A	315	85	280	114	6.24	1.25E-02	rs12682053	8	78419717	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872866	G	G	226	134	266	98	8.816	3.00E-03	rs988251	8	78487158	q21.11
SNP_A-1797137	C	C	249	159	283	125	6.243	1.25E-02	rs13258743	8	78488191	q21.11
SNP_A-1750341	C	C	335	19	334	44	9.145	2.50E-03	rs421501	8	78515242	q21.13
SNP_A-2139934	G	G	328	30	283	49	6.914	0.0086	rs17450081	8	78556704	q21.11
SNP_A-1665206	T	T	237	155	274	134	3.887	0.0487	rs1491568	8	78556866	q21.13
SNP_A-2248831	C	C	266	148	304	116	6.369	1.16E-02	rs2090635	8	78823521	q21.12
SNP_A-2281914	C	C	260	124	290	94	5.765	1.64E-02	rs1589221	8	78824141	q21.12
SNP_A-1948625	T	T	219	145	262	116	6.805	9.10E-03	rs11995179	8	78872637	q21.12
SNP_A-2312039	G	G	237	147	256	116	4.197	4.05E-02	rs1401592	8	78900891	q21.12
SNP_A-1840516	T	T	383	33	400	18	4.776	2.89E-02	rs7828090	8	79570648	q21.12
SNP_A-1794012	C	C	319	35	334	18	5.792	0.0161	---	8	79648056	q21.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2275862	C	C	375	17	373	7	3.986	4.59E-02	rs16905875	8	79714122	q21.12
SNP_A-1747231	G	G	387	3	396	12	5.1	2.39E-02	rs1870572	8	80227835	q21.13
SNP_A-2266009	A	A	291	107	308	78	4.846	2.77E-02	rs16907253	8	80952775	q21.13
SNP_A-2054129	A	A	404	0	398	4	4.04	4.44E-02	rs13439520	8	80983708	q21.13
SNP_A-2121844	G	G	409	7	403	17	4.192	4.06E-02	rs10108547	8	81008736	q21.13
SNP_A-1839151	G	G	206	158	251	141	4.367	3.67E-02	rs17459080	8	81157356	q21.13
SNP_A-1927558	T	T	192	176	231	157	4.154	4.15E-02	rs1365188	8	81206421	q21.13
SNP_A-1866154	T	T	209	167	234	134	4.943	2.62E-02	rs13280432	8	81229209	q21.13
SNP_A-2272206	G	G	182	156	221	135	4.826	2.80E-02	rs10755964	8	81240524	q21.13
SNP_A-2236657	C	C	267	47	303	31	4.943	2.62E-02	rs6988904	8	81283896	q21.13
SNP_A-1924466	C	C	343	17	278	38	12.009	5.00E-04	rs16907617	8	81438536	q21.13
SNP_A-1952692	C	C	337	35	372	20	5.299	2.13E-02	rs872218	8	81465988	q21.13
SNP_A-1788494	A	A	377	15	386	6	3.963	0.0465	rs16907781	8	81598497	q21.13
SNP_A-2156022	T	T	301	51	259	73	6.474	0.0109	rs17475818	8	81987692	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1994015	C	C	234	148	274	124	4.941	2.62E-02	rs13263982	8	82099049	q21.13
SNP_A-1943861	C	C	253	85	279	65	3.885	0.0487	rs4237094	8	82182650	q21.13
SNP_A-1729578	C	C	326	44	356	26	5.758	1.64E-02	rs201952	8	82265847	q21.13
SNP_A-1994021	C	C	337	43	360	26	4.901	2.68E-02	rs201950	8	82377396	q21.13
SNP_A-1939762	T	T	354	60	376	40	4.658	0.0309	rs169337	8	82380244	q21.13
SNP_A-2052711	A	A	230	100	192	126	6.193	1.28E-02	rs2167255	8	82515633	q21.13
SNP_A-1750309	C	C	355	43	342	64	4.285	0.0385	rs890601	8	82595399	q21.13
SNP_A-1667022	C	C	355	45	342	68	4.801	2.84E-02	rs726604	8	82603038	q21.13
SNP_A-1796507	C	C	319	25	313	47	6.419	1.13E-02	rs2912807	8	82718701	q21.13
SNP_A-2065360	T	T	340	26	315	43	5.055	0.0246	rs2955015	8	82776558	q21.13
SNP_A-2129838	G	G	391	19	408	8	4.8	2.85E-02	rs16909549	8	82822179	q21.13
SNP_A-1783500	T	T	345	45	354	28	3.992	4.57E-02	rs17783207	8	82855390	q21.13
SNP_A-2194120	A	A	372	28	364	50	6.053	1.39E-02	rs4557658	8	82984252	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1866241	G	G	337	7	337	1	4.448	3.50E-02	rs16910334	8	83461664	q21.13
SNP_A-2013558	G	G	391	19	395	7	5.481	1.92E-02	rs7843769	8	83770962	q21.13
SNP_A-1681108	G	G	242	112	228	152	5.564	0.0183	rs7837095	8	84088282	q21.13
SNP_A-2091710	G	G	343	37	365	23	3.867	4.92E-02	rs7825517	8	84120546	q21.13
SNP_A-2307498	C	C	343	39	364	20	6.737	9.40E-03	rs10958138	8	84120661	q21.13
SNP_A-2119765	G	G	344	54	342	34	3.929	4.75E-02	rs7825851	8	84120782	q21.13
SNP_A-1994066	C	C	344	38	353	21	4.93	0.0264	rs6473411	8	84155334	q21.13
SNP_A-1744951	G	G	328	60	315	85	4.391	0.0361	rs785964	8	84269809	q21.13
SNP_A-2278589	A	A	289	75	260	98	4.54	3.31E-02	rs7829784	8	84276448	q21.13
SNP_A-2296353	A	A	284	82	258	114	6.423	1.13E-02	rs2090880	8	84277905	q21.13
SNP_A-1861168	C	C	304	92	273	131	8.407	3.70E-03	rs7841219	8	84296493	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043565	T	T	278	138	248	170	5.031	2.49E-02	rs1915806	8	84373586	q21.13
SNP_A-1728099	A	A	330	70	309	103	6.809	9.10E-03	rs921145	8	84375236	q21.13
SNP_A-1686914	G	G	327	55	316	78	3.981	4.60E-02	rs7004770	8	84401181	q21.13
SNP_A-2077700	G	G	377	11	381	3	4.572	3.25E-02	rs1115354	8	84430796	q21.13
SNP_A-1934094	G	G	342	72	310	98	5.504	0.019	rs1383823	8	84488198	q21.13
SNP_A-2295746	A	A	343	21	314	34	3.995	4.56E-02	rs4739958	8	84683082	q21.13
SNP_A-1819707	A	A	374	18	388	8	4.083	4.33E-02	rs711053	8	85602980	q21.2
SNP_A-2197831	A	A	272	144	302	118	4.129	4.22E-02	rs16887456	8	87205826	q21.3
SNP_A-1933438	A	A	268	128	289	93	6.085	1.36E-02	rs4571715	8	87274060	q21.3
SNP_A-2181063	C	C	332	66	359	39	7.998	4.70E-03	---	8	87282004	q21.3
SNP_A-2065904	G	G	394	0	388	4	4.041	4.44E-02	rs16898059	8	87282118	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2257968	T	C	203	191	228	172	5.785	1.62E-02	rs4484676	8	87340892	q21.3
SNP_A-2175828	T	T	297	65	298	40	5.137	2.34E-02	rs1595207	8	87377186	q21.3
SNP_A-1914527	G	G	416	0	416	4	3.981	4.60E-02	rs16916102	8	87686716	q21.3
SNP_A-2135681	G	G	347	29	357	15	4.575	3.24E-02	rs12548374	8	87762011	q21.3
SNP_A-2097764	A	G	195	171	215	159	8.591	3.40E-03	rs2915524	8	88266138	q21.3
SNP_A-1994143	C	C	218	98	191	121	4.173	4.11E-02	rs6992170	8	88378930	q21.3
SNP_A-1878367	G	G	274	142	240	172	5.096	0.024	rs9297305	8	88424340	q21.3
SNP_A-2286190	G	G	244	122	210	148	4.962	2.59E-02	rs4961032	8	88474245	q21.3
SNP_A-2202896	T	T	325	61	350	40	5.272	2.17E-02	rs455071	8	88557354	q21.3
SNP_A-2022718	C	C	317	53	354	38	3.881	4.88E-02	rs436753	8	88599977	q21.3
SNP_A-2093232	C	C	306	52	290	80	6.173	1.30E-02	rs12543293	8	88744669	q21.3
SNP_A-1994176	C	C	295	29	304	16	3.866	4.93E-02	---	8	89780193	q21.3
SNP_A-2115006	T	T	326	46	350	22	9.323	0.0023	rs1498539	8	89912936	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1888202	T	T	274	102	235	129	5.951	0.0147	rs3947607	8	90017741	q21.3
SNP_A-2226566	A	A	400	12	410	4	4.119	0.0424	rs1240028	8	90162474	q21.3
SNP_A-1994185	C	C	401	13	412	4	4.909	2.67E-02	rs1240101	8	90180575	q21.3
SNP_A-2188118	A	A	387	13	401	3	6.479	0.0109	rs318236	8	90205799	q21.3
SNP_A-1828765	T	T	376	14	399	5	4.7	3.02E-02	rs318249	8	90275425	q21.3
SNP_A-2221081	T	T	373	39	396	20	6.787	9.20E-03	rs318256	8	90284300	q21.3
SNP_A-2048506	G	G	365	21	365	9	4.612	3.18E-02	rs7833317	8	90345058	q21.3
SNP_A-2149086	G	G	230	164	252	132	4.336	0.0373	rs10956094	8	90547673	q21.3
SNP_A-2173180	C	C	188	140	229	119	5.147	2.33E-02	rs10956095	8	90547713	q21.3
SNP_A-2128590	A	A	317	95	296	122	4.036	4.45E-02	rs17767377	8	90553403	q21.3
SNP_A-1655663	G	G	384	16	381	31	4.623	3.16E-02	rs9297690	8	90586661	q21.3
SNP_A-1906465	A	A	223	169	255	143	4.264	3.89E-02	rs4563939	8	90639425	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1994197	C	C	335	27	358	12	6.446	0.0111	rs1159858	8	90702583	q21.3
SNP_A-1994198	C	C	249	153	216	180	4.486	3.42E-02	rs1397308	8	90709838	q21.3
SNP_A-2299499	T	T	402	14	387	29	5.518	1.88E-02	rs16905331	8	91853722	q21.3
SNP_A-2094728	C	C	255	121	222	146	4.538	3.31E-02	rs6471254	8	91878147	q21.3
SNP_A-1994227	C	C	372	8	354	18	4.208	0.0402	rs16905427	8	91915161	q21.3
SNP_A-1994230	A	A	213	119	184	152	6.113	0.0134	rs1504789	8	91925351	q21.3
SNP_A-1887188	G	G	259	87	248	122	5.301	2.13E-02	rs1354520	8	91937786	q21.3
SNP_A-1911036	T	T	251	155	227	187	4.122	4.23E-02	rs9918929	8	92160886	q21.3
SNP_A-2273514	A	A	208	98	189	137	6.756	9.30E-03	rs4734009	8	92370425	q21.3
SNP_A-2274535	G	G	323	19	308	34	4.602	3.19E-02	rs10099092	8	92447958	q21.3
SNP_A-1940975	T	T	226	152	234	112	4.795	2.85E-02	rs4443623	8	92758632	q21.3
SNP_A-2061711	G	G	410	4	420	0	4.078	4.35E-02	rs10104018	8	92795093	q21.3
SNP_A-2075189	T	C	219	191	217	177	5.795	0.0161	rs10103191	8	92971608	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138503	A	G	192	162	215	157	10.521	1.20E-03	rs4734934	8	93002610	q21.3
SNP_A-2127546	C	C	324	36	354	22	4.361	3.68E-02	rs16914707	8	93078660	q21.3
SNP_A-2172363	A	A	317	89	349	63	5.941	1.48E-02	rs16915409	8	94067129	q22.1
SNP_A-2060274	C	C	306	48	325	29	5.26	0.0218	rs278593	8	94250848	q22.1
SNP_A-2291989	G	G	300	54	297	33	4.247	3.93E-02	rs278600	8	94258095	q22.1
SNP_A-1834168	A	A	346	26	355	13	4.427	3.54E-02	rs16915836	8	94368188	q22.1
SNP_A-2160453	A	A	405	9	418	2	4.617	3.17E-02	rs7822838	8	94951789	q22.1
SNP_A-2063100	C	C	300	116	324	88	4.747	0.0293	rs3018861	8	95102153	q22.1
SNP_A-2206212	T	T	361	17	380	6	5.665	1.73E-02	rs16916451	8	95155476	q22.1
SNP_A-2281322	G	G	269	145	241	177	4.698	3.02E-02	rs2978156	8	95156097	q22.1
SNP_A-2233172	G	G	243	117	220	164	8.238	4.10E-03	rs3018844	8	95156153	q22.1
SNP_A-1809337	C	C	315	95	338	70	4.593	3.21E-02	rs2607073	8	95325902	q22.1
SNP_A-2303866	G	G	394	10	381	21	4.116	4.25E-02	rs2515132	8	95407567	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2212733	T	T	305	75	281	101	4.819	2.82E-02	rs3098705	8	95585684	q22.1
SNP_A-1735138	T	T	308	80	288	114	6.384	0.0115	rs756474	8	95591533	q22.1
SNP_A-2013616	C	C	311	7	294	16	3.898	4.83E-02	rs4734281	8	95685229	q22.1
SNP_A-1939783	T	T	248	162	279	133	4.67	3.07E-02	rs3133615	8	95691039	q22.1
SNP_A-2057231	C	C	327	15	324	4	6.092	1.36E-02	rs16916972	8	95755390	q22.1
SNP_A-1824735	A	A	289	121	255	157	6.782	9.20E-03	rs297567	8	96250423	q22.1
SNP_A-1897547	G	-	211	153	186	186	4.7	3.02E-02	rs4735361	8	96417622	q22.1
SNP_A-1682730	C	C	337	29	351	13	6.375	1.16E-02	rs10504949	8	96439931	q22.1
SNP_A-1682676	A	A	356	36	380	22	4.037	4.45E-02	rs10504950	8	96440034	q22.1
SNP_A-1659206	G	G	326	70	301	93	4.237	0.0395	rs2873824	8	96551352	q22.1
SNP_A-1805025	A	A	180	150	206	114	6.508	1.07E-02	rs3133744	8	96603502	q22.1
SNP_A-2161700	C	-	237	179	209	209	4.073	0.0436	rs3104990	8	96644395	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2205996	T	T	309	59	321	31	8.588	3.40E-03	rs4366053	8	96706436	q22.1
SNP_A-2013626	A	A	303	59	338	42	4.338	0.0373	rs4492338	8	96708759	q22.1
SNP_A-1994326	C	C	311	41	367	29	4.108	4.27E-02	rs1825443	8	96803496	q22.1
SNP_A-2284207	G	G	364	6	347	15	4.177	4.10E-02	rs7821286	8	96988962	q22.1
SNP_A-2050562	T	T	382	10	405	3	4.123	4.23E-02	rs11997418	8	97056857	q22.1
SNP_A-2121450	A	A	289	109	253	135	5.035	2.48E-02	rs522744	8	97135636	q22.1
SNP_A-2122659	C	C	190	172	228	138	7.162	7.40E-03	rs1464185	8	97456593	q22.1
SNP_A-2166506	T	T	209	181	250	156	5.197	2.26E-02	rs784799	8	97470255	q22.1
SNP_A-2266203	C	C	416	0	416	4	3.981	4.60E-02	rs16894573	8	97522829	q22.1
SNP_A-1897251	T	T	329	23	325	55	12.099	5.00E-04	rs10100191	8	97628338	q22.1
SNP_A-1994355	T	T	330	46	342	28	4.545	3.30E-02	rs1898257	8	97631285	q22.1
SNP_A-1862603	C	C	238	84	203	117	8.19	4.20E-03	rs2853275	8	98078195	q22.1
SNP_A-1828978	C	C	388	26	401	13	4.548	3.30E-02	rs7825243	8	98401028	q22.1
SNP_A-1916215	C	C	368	34	353	55	5.223	0.0223	rs17741775	8	98431539	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2070591	T	T	320	94	290	120	4.615	3.17E-02	rs4735455	8	98437927	q22.1
SNP_A-1827620	C	C	272	92	243	117	4.601	3.19E-02	rs13280834	8	98441674	q22.1
SNP_A-1867200	G	G	321	89	339	65	4.187	0.0407	rs2853297	8	98476251	q22.1
SNP_A-2056746	A	A	374	28	355	45	4.449	0.0349	rs7815922	8	98649856	q22.1
SNP_A-1798837	A	A	385	27	374	44	4.187	0.0407	rs16896476	8	99056920	q22.1
SNP_A-2233328	C	C	373	19	365	35	4.747	0.0293	rs16896518	8	99078200	q22.1
SNP_A-2272015	C	C	246	132	289	97	8.723	3.10E-03	rs2514344	8	99170315	q22.2
SNP_A-2028438	G	G	310	18	302	36	5.956	0.0147	rs7461545	8	99374539	q22.2
SNP_A-2237506	T	T	408	2	388	14	9.425	2.10E-03	rs16897045	8	99570494	q22.2
SNP_A-2052759	C	C	411	1	401	9	6.518	1.07E-02	rs9642783	8	100589799	q22.2
SNP_A-2268372	G	G	226	110	252	80	6.127	1.33E-02	rs10095279	8	100864458	q22.2
SNP_A-2116375	G	G	306	54	322	28	8.512	3.50E-03	rs17420284	8	101262797	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086252	A	A	321	77	361	53	6.464	1.10E-02	rs16898297	8	101453401	q22.2
SNP_A-1914093	G	G	225	123	266	98	5.895	0.0152	rs13278272	8	101463728	q22.2
SNP_A-2177350	C	C	253	131	225	163	5.103	2.39E-02	rs2979002	8	101477217	q22.2
SNP_A-2108872	G	G	271	107	318	88	4.608	3.18E-02	rs2979001	8	101477259	q22.2
SNP_A-2201477	G	G	289	97	326	78	3.881	4.88E-02	rs1892737	8	101541858	q22.2
SNP_A-1910806	A	A	390	24	380	40	4.087	4.32E-02	rs17429734	8	101649161	q22.3
SNP_A-2140578	T	T	325	39	321	17	7.715	5.50E-03	rs3115893	8	101829525	q22.3
SNP_A-1864645	T	T	270	108	254	138	3.894	4.85E-02	rs4734492	8	101971077	q22.3
SNP_A-2269849	T	T	303	93	285	125	5.007	0.0253	rs4734493	8	101971345	q22.3
SNP_A-2173191	G	G	275	49	300	32	4.558	3.28E-02	rs3134370	8	101974856	q22.3
SNP_A-2110473	C	C	284	102	253	133	5.879	1.53E-02	rs7387625	8	101978434	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2180195	C	C	290	86	329	55	9.19	2.40E-03	rs3105454	8	101983889	q22.3
SNP_A-1853917	A	A	229	121	253	95	4.319	3.77E-02	rs1470764	8	102019214	q22.3
SNP_A-1933554	C	C	304	94	265	125	6.981	8.20E-03	rs2122922	8	102131834	q22.3
SNP_A-1800729	C	C	407	1	407	7	4.456	3.48E-02	rs16899063	8	102245364	q22.3
SNP_A-1837809	G	G	306	10	331	3	4.255	3.91E-02	rs2232687	8	102281574	q22.3
SNP_A-1864426	T	T	393	5	416	0	5.258	0.0218	rs16899114	8	102313193	q22.3
SNP_A-1799455	G	G	400	4	382	12	4.29	3.83E-02	rs961349	8	102483903	q22.3
SNP_A-2066916	T	T	384	16	406	6	4.982	2.56E-02	rs16867726	8	102550266	q22.3
SNP_A-1887937	G	A	162	148	181	137	5.299	2.13E-02	rs4392865	8	102690673	q22.3
SNP_A-1648588	A	A	285	65	285	93	3.891	4.85E-02	rs490096	8	102829473	q22.3
SNP_A-2122428	T	T	266	126	300	102	4.443	3.50E-02	rs11779882	8	103195364	q22.3
SNP_A-1994452	G	G	298	40	275	63	6.059	0.0138	rs2436964	8	103719111	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2245254	T	T	304	82	321	57	4.876	2.72E-02	rs1533182	8	104022495	q22.3
SNP_A-2116858	C	C	292	110	248	140	6.939	8.40E-03	rs2511585	8	105322890	q22.3
SNP_A-1888317	A	A	286	114	265	149	5.219	0.0223	rs2511587	8	105325461	q22.3
SNP_A-1844633	C	C	213	199	257	155	9.588	0.002	rs7010076	8	105412003	q22.3
SNP_A-2039080	G	G	349	65	367	43	4.915	2.66E-02	rs16871341	8	105440452	q22.3
SNP_A-2171294	A	A	379	9	371	21	4.865	2.74E-02	rs11784193	8	105618585	q22.3
SNP_A-2217808	G	G	305	109	339	79	6.563	0.0104	rs4461873	8	105653739	q22.3
SNP_A-1791288	G	G	321	73	346	48	6.102	0.0135	rs9297351	8	105896394	q22.3
SNP_A-2196018	A	A	317	79	349	53	6.614	0.0101	rs4734821	8	105900459	q22.3
SNP_A-1653792	C	C	331	69	362	46	5.908	1.51E-02	rs10505071	8	105954178	q22.3
SNP_A-1994523	T	T	339	71	367	47	5.973	1.45E-02	rs16872162	8	106084559	q22.3
SNP_A-2137827	T	T	331	33	304	52	5.307	0.0212	rs285857	8	106115416	q22.3
SNP_A-2270636	C	C	352	8	335	19	4.852	0.0276	rs285821	8	106172130	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2203265	G	G	357	57	374	36	5.118	2.37E-02	rs3107548	8	106174444	q22.3
SNP_A-2309136	A	A	398	14	391	27	4.141	0.0419	rs17194239	8	106195671	q22.3
SNP_A-1689805	T	T	335	61	319	85	4.257	3.91E-02	rs2342786	8	106308581	q23.1
SNP_A-1709209	A	C	216	176	217	195	4.856	0.0276	rs979646	8	106342278	q23.1
SNP_A-1750043	C	T	216	180	216	196	3.928	4.75E-02	rs1580355	8	106345535	q23.1
SNP_A-2058967	A	G	217	179	207	181	5.206	2.25E-02	rs6999452	8	106466292	q23.1
SNP_A-1814823	A	G	227	187	218	198	4.347	3.71E-02	rs6469000	8	106470472	q23.1
SNP_A-2244464	T	T	305	87	322	60	5.292	2.14E-02	rs10464844	8	106488930	q23.1
SNP_A-1947319	G	G	208	164	236	138	3.999	4.55E-02	rs1429675	8	107170799	q23.1
SNP_A-2013698	C	C	283	115	304	84	5.454	0.0195	rs6469053	8	107308956	q23.1
SNP_A-2309605	C	C	327	9	307	19	4.052	0.0441	rs7838834	8	107513890	q23.1
SNP_A-2150119	G	G	382	18	371	7	4.382	3.63E-02	rs17342815	8	107704866	q23.1
SNP_A-2084407	T	T	380	24	361	39	4.039	4.45E-02	---	8	107828733	q23.1
SNP_A-2032244	A	A	377	13	399	5	3.934	4.73E-02	rs16875182	8	107921441	q23.1
SNP_A-2261892	G	G	359	49	383	31	4.783	0.0287	rs16875208	8	107950040	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1994568	T	T	238	94	192	116	6.335	0.0118	rs13271148	8	107977379	q23.1
SNP_A-1744967	C	C	284	112	263	149	5.737	0.0166	rs720715	8	108085295	q23.1
SNP_A-2083279	T	T	338	62	364	38	6.718	9.50E-03	rs7821678	8	108149251	q23.1
SNP_A-2074030	G	G	245	143	275	101	8.774	3.10E-03	rs6997025	8	108222155	q23.1
SNP_A-2130889	C	C	295	111	263	139	4.951	2.61E-02	rs16875775	8	108238645	q23.1
SNP_A-1865555	G	G	299	69	233	85	6.239	1.25E-02	rs17368764	8	108407597	q23.1
SNP_A-2117318	C	C	324	68	307	93	4.26	0.039	rs17296616	8	108408705	q23.1
SNP_A-2234477	T	T	388	26	394	10	7.036	8.00E-03	rs16876200	8	108465505	q23.1
SNP_A-1819974	G	G	312	88	324	48	10.99	9.00E-04	rs10955454	8	108467485	q23.1
SNP_A-2058516	T	T	295	87	327	63	5.404	0.0201	rs1433192	8	108490750	q23.1
SNP_A-1758796	C	C	276	118	311	97	3.895	4.84E-02	rs10505109	8	108522454	q23.1
SNP_A-2162179	A	A	258	128	220	164	7.454	0.0063	rs17301273	8	108526968	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1881559	G	G	233	169	198	194	4.439	3.51E-02	rs10103715	8	108613382	q23.1
SNP_A-2088107	A	A	291	125	322	96	5.368	2.05E-02	rs12544388	8	108657067	q23.1
SNP_A-2057852	C	C	294	120	319	95	3.927	4.75E-02	rs281685	8	108672318	q23.1
SNP_A-1959695	C	C	277	101	299	75	4.66	0.0309	rs1283878	8	108683856	q23.1
SNP_A-1886412	A	A	411	5	420	0	5.078	2.42E-02	rs4735001	8	108792735	q23.1
SNP_A-2182526	A	A	318	40	359	25	5.04	2.48E-02	rs17405978	8	109161717	q23.1
SNP_A-2031803	C	C	368	22	346	36	3.975	4.62E-02	rs7843027	8	109431831	q23.1
SNP_A-1825597	T	T	243	133	283	107	5.604	1.79E-02	rs1979443	8	109664888	q23.1
SNP_A-1659882	T	T	227	161	274	136	5.912	1.50E-02	rs1027479	8	109682091	q23.1
SNP_A-1728495	G	G	256	144	292	120	4.37	3.66E-02	rs2173255	8	109682377	q23.1
SNP_A-1945444	A	A	370	34	383	19	4.465	3.46E-02	rs16878302	8	109701189	q23.1
SNP_A-1890527	C	C	369	37	383	21	4.67	3.07E-02	rs10090705	8	109701721	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1862384	T	T	292	84	334	60	6.401	0.0114	rs2935766	8	109727025	q23.1
SNP_A-2301230	C	C	317	85	347	57	6.872	8.80E-03	rs1909023	8	109727092	q23.1
SNP_A-1879245	T	T	313	79	339	43	11.532	7.00E-04	rs1909024	8	109727168	q23.1
SNP_A-1994631	C	C	263	143	287	113	4.518	3.35E-02	rs1391197	8	109793103	q23.1
SNP_A-2256967	C	C	241	119	275	89	6.545	1.05E-02	rs3019346	8	109794398	q23.1
SNP_A-2133033	A	A	246	132	271	99	5.838	1.57E-02	rs6469204	8	109856503	q23.1
SNP_A-1801317	A	A	249	117	291	89	6.812	9.10E-03	rs12542619	8	109924989	q23.1
SNP_A-2207139	A	A	343	61	328	84	3.906	4.81E-02	rs4469429	8	110144534	q23.1
SNP_A-1715111	G	G	228	172	262	148	4.036	4.45E-02	rs7831835	8	110761991	q23.2
SNP_A-2292759	C	C	398	12	416	2	7.464	0.0063	rs6994639	8	111010835	q23.2
SNP_A-1690886	G	G	308	72	350	54	4.522	3.35E-02	rs2060687	8	111012416	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2220852	C	C	406	10	417	3	3.897	4.84E-02	rs7844769	8	111037720	q23.2
SNP_A-1667024	C	C	376	20	374	36	4.335	0.0373	-	8	111412188	q23.2
SNP_A-2050397	C	C	386	4	388	12	3.879	4.89E-02	rs2140474	8	111442951	q23.2
SNP_A-2126325	A	A	342	60	350	40	3.912	4.80E-02	rs16880947	8	111726732	q23.2
SNP_A-1944103	C	C	256	70	259	45	4.69	3.03E-02	rs4876874	8	112815998	q23.3
SNP_A-1956729	C	C	243	151	208	184	5.962	0.0146	rs929685	8	113373346	q23.3
SNP_A-1924250	T	T	237	93	206	114	4.147	4.17E-02	rs4354335	8	114475512	q23.3
SNP_A-1739407	C	C	211	189	252	160	5.864	0.0155	rs966210	8	114872393	q23.3
SNP_A-1915475	G	G	339	37	299	55	5.371	2.05E-02	rs13248967	8	114920075	q23.3
SNP_A-1956174	A	A	370	24	395	11	5.467	1.94E-02	rs6469488	8	114954608	q23.3
SNP_A-1903983	C	C	319	75	297	99	4.091	4.31E-02	rs2884249	8	115860432	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1894671	C	C	348	16	353	5	5.748	1.65E-02	rs9918880	8	116891311	q23.3
SNP_A-1824623	A	A	385	1	391	11	8.058	4.50E-03	rs7821808	8	117186304	q23.3
SNP_A-2085603	C	C	335	37	311	61	6.769	9.30E-03	rs12550516	8	117376069	q23.3
SNP_A-1714791	T	T	270	130	307	103	5.379	2.04E-02	rs1550162	8	117520120	q23.3
SNP_A-1957163	T	T	286	130	256	160	4.764	2.91E-02	rs6469644	8	117550932	q23.3
SNP_A-1994776	T	T	287	129	240	174	10.87	0.001	rs2317380	8	117656513	q23.3
SNP_A-1930586	C	C	192	166	226	144	4.13	4.21E-02	rs10100472	8	117674116	q23.3
SNP_A-1645138	G	G	334	62	367	43	4.75	0.0293	rs10505288	8	117710379	q24.11
SNP_A-1671238	A	A	232	166	262	138	4.396	3.60E-02	rs3020160	8	117880177	q24.11
SNP_A-1825800	A	A	279	91	315	69	4.949	2.61E-02	rs7013963	8	117986441	q24.11
SNP_A-2310684	C	C	273	101	314	82	4.211	0.0402	rs7014118	8	117986493	q24.11
SNP_A-1757587	A	A	242	146	222	178	3.841	5.00E-02	rs1001646	8	117990708	q24.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1878102	T	T	233	171	263	145	3.934	4.73E-02	rs2166483	8	117993624	q24.11
SNP_A-1994786	G	G	336	0	320	4	4.173	4.11E-02	rs10505311	8	118243499	q24.11
SNP_A-2116779	A	A	349	23	331	45	7.573	5.90E-03	rs2466290	8	118262381	q24.11
SNP_A-2131398	C	C	347	25	330	46	6.617	0.0101	rs2464583	8	118281643	q24.11
SNP_A-1645520	T	T	244	148	213	193	7.798	5.20E-03	rs2023139	8	118357299	q24.11
SNP_A-2116388	T	T	338	34	322	52	4.15	4.16E-02	rs17739542	8	118440564	q24.11
SNP_A-1994793	A	A	316	18	330	8	4.126	4.22E-02	rs1948674	8	118462009	q24.11
SNP_A-2183544	G	G	246	150	204	182	6.878	8.70E-03	rs1686354	8	118474140	q24.11
SNP_A-1994796	G	G	358	52	331	75	5.204	2.25E-02	rs10505302	8	118479807	q24.11
SNP_A-2029705	G	G	227	139	195	175	6.532	0.0106	rs9297566	8	118513637	q24.11
SNP_A-2088523	G	G	244	126	268	100	4.111	4.26E-02	rs2086376	8	118599568	q24.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1956985	A	A	346	56	312	80	5.867	0.0154	rs17667915	8	118613626	q24.11
SNP_A-2198921	A	A	308	46	279	67	5.245	2.20E-02	rs17668007	8	118627407	q24.11
SNP_A-1841030	T	T	193	157	213	117	6.242	1.25E-02	rs6469697	8	118632229	q24.11
SNP_A-1915132	G	G	347	49	326	72	5.022	2.50E-02	rs755982	8	118643130	q24.11
SNP_A-1908885	T	T	287	85	249	125	10.308	1.30E-03	rs4876759	8	118908693	q24.11
SNP_A-1837451	T	T	281	81	251	121	9.478	2.10E-03	rs4546690	8	118915568	q24.11
SNP_A-2250251	C	C	282	110	311	87	4.058	4.40E-02	rs7830840	8	118957077	q24.11
SNP_A-2097355	A	A	379	1	306	6	4.714	2.99E-02	rs2451167	8	119222100	q24.12
SNP_A-1923952	T	T	300	98	279	133	5.824	1.58E-02	rs11562751	8	119238486	q24.12
SNP_A-1862372	C	C	222	110	181	129	4.934	0.0263	rs2514733	8	119249330	q24.12
SNP_A-1846517	C	C	234	148	256	116	4.735	2.96E-02	rs12541149	8	119850940	q24.12
SNP_A-1870485	C	C	401	5	394	14	4.32	3.77E-02	rs11992072	8	120072788	q24.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141477	T	T	346	8	366	2	3.892	4.85E-02	rs16891925	8	120139503	q24.12
SNP_A-1692900	G	G	365	19	356	36	5.285	2.15E-02	rs1549416	8	120139598	q24.12
SNP_A-2212681	C	C	342	16	382	6	5.558	0.0184	rs2470032	8	120440480	q24.12
SNP_A-1828056	T	T	313	41	351	25	5.395	2.02E-02	rs16892786	8	120652052	q24.12
SNP_A-2216878	A	A	273	97	246	122	4.253	3.92E-02	rs16893025	8	120782861	q24.12
SNP_A-1814479	G	G	222	130	190	158	5.185	2.28E-02	rs7017279	8	120929001	q24.12
SNP_A-1841282	C	C	228	108	235	79	3.863	4.94E-02	rs4871824	8	121074772	q24.12
SNP_A-2013768	A	A	303	49	328	28	6.695	9.70E-03	rs1543201	8	121088069	q24.12
SNP_A-1994888	T	T	273	101	306	74	5.999	0.0143	rs2037344	8	121088918	q24.12
SNP_A-2061312	A	A	275	109	305	87	3.939	4.72E-02	rs2037342	8	121089053	q24.12
SNP_A-1808348	G	G	401	9	409	1	6.479	0.0109	rs4871033	8	121136640	q24.12
SNP_A-2101406	T	T	408	8	419	1	5.572	0.0183	rs16893473	8	121137562	q24.12
SNP_A-1994893	G	G	318	92	349	69	4.65	3.11E-02	rs7822384	8	121140970	q24.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2298716	G	G	382	8	401	1	5.725	0.0167	rs6988923	8	121145061	q24.12
SNP_A-1868771	C	C	288	84	322	62	5.021	2.50E-02	rs7000609	8	121175445	q24.12
SNP_A-1714929	G	G	351	49	338	74	5.15	2.32E-02	rs2060319	8	122096140	q24.12
SNP_A-1787715	C	C	236	120	255	91	4.579	3.24E-02	rs7828673	8	122296299	q24.12
SNP_A-2140668	G	G	326	18	322	4	8.456	3.60E-03	rs10956035	8	122474983	q24.12
SNP_A-1652770	T	T	276	120	251	151	4.687	0.0304	rs1563563	8	122740602	q24.13
SNP_A-2039851	G	G	370	42	342	70	8.101	4.40E-03	rs17299925	8	122756069	q24.13
SNP_A-1888576	T	T	374	42	355	63	4.69	3.03E-02	rs17299987	8	122760376	q24.13
SNP_A-2162713	C	C	282	38	294	62	4.104	4.28E-02	rs17241305	8	122784694	q24.13
SNP_A-2093459	C	C	387	15	372	28	4.222	3.99E-02	rs6989018	8	123245696	q24.13
SNP_A-2153027	A	A	300	114	276	144	4.445	3.50E-02	rs4282579	8	123521501	q24.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1994939	C	C	292	108	271	143	5.425	1.99E-02	rs2981074	8	123530469	q24.13
SNP_A-2255341	G	G	212	136	171	165	6.975	8.30E-03	rs11784208	8	123580428	q24.13
SNP_A-1691790	A	G	224	174	205	199	3.968	4.64E-02	rs4871297	8	123662743	q24.13
SNP_A-1688658	G	G	325	13	340	2	8.382	0.0038	rs10505428	8	123812929	q24.13
SNP_A-2112076	C	C	369	17	368	4	7.793	5.20E-03	rs9649951	8	124034000	q24.13
SNP_A-2205409	T	T	349	21	344	8	5.418	1.99E-02	rs13252702	8	124223508	q24.13
SNP_A-2216622	T	T	243	163	267	127	5.42	1.99E-02	rs6996389	8	124635537	q24.13
SNP_A-2302602	A	A	195	189	210	150	4.273	3.87E-02	rs2385296	8	124655486	q24.13
SNP_A-2163411	A	A	399	17	411	7	4.34	3.72E-02	rs16898686	8	124732496	q24.13
SNP_A-2314400	G	G	237	175	270	148	4.362	3.68E-02	rs17349815	8	124815598	q24.13
SNP_A-2238624	C	C	224	188	260	146	3.975	4.62E-02	rs17258588	8	124815799	q24.13
SNP_A-1933043	G	A	204	184	230	180	6.009	1.42E-02	rs1030590	8	124823591	q24.13
SNP_A-1893824	A	A	287	69	228	84	5.355	0.0207	rs16898998	8	124968297	q24.13
SNP_A-2057110	A	A	321	65	286	86	4.682	3.05E-02	rs10094501	8	125015901	q24.13
SNP_A-2108125	A	T	165	157	191	135	6.297	0.0121	rs6470289	8	125933205	q24.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1879997	G	T	193	165	190	150	6.692	9.70E-03	rs2555723	8	126023455	q24.13
SNP_A-2239544	T	T	247	77	290	48	9.88	1.70E-03	rs10091027	8	126333533	q24.13
SNP_A-1880372	C	C	270	124	291	93	5.087	0.0241	rs7009673	8	126699341	q24.13
SNP_A-2185546	C	C	292	50	261	71	5.235	2.21E-02	rs9693804	8	126954773	q24.13
SNP_A-2050049	G	G	263	99	230	128	5.892	0.0152	rs780327	8	127132246	q24.13
SNP_A-2026657	A	A	265	45	266	72	5.032	2.49E-02	rs7006495	8	127219552	q24.13
SNP_A-2013813	T	T	313	57	363	37	6.795	9.10E-03	rs6989132	8	127608781	q24.21
SNP_A-2106182	G	G	348	38	376	24	3.996	4.56E-02	rs10090632	8	127654508	q24.21
SNP_A-2206473	G	G	416	0	416	4	3.981	4.60E-02	rs16901553	8	127666556	q24.21
SNP_A-2270859	G	G	416	0	412	4	4.019	4.50E-02	rs16901559	8	127669005	q24.21
SNP_A-2227440	G	G	343	17	332	34	5.797	0.0161	rs10101229	8	127722567	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1833719	A	A	315	17	293	31	4.783	0.0287	rs11774414	8	127722666	q24.21
SNP_A-2013814	T	T	262	108	222	140	7.348	6.70E-03	rs7011739	8	127727329	q24.21
SNP_A-1703333	A	A	276	106	315	81	5.666	1.73E-02	rs958653	8	128027258	q24.21
SNP_A-2276451	G	G	237	99	268	70	6.873	8.70E-03	rs16901922	8	128130968	q24.21
SNP_A-1846903	A	A	397	19	412	8	4.741	2.95E-02	rs16901935	8	128145727	q24.21
SNP_A-1697072	G	G	289	75	282	112	6.229	0.0126	rs1949808	8	128351127	q24.21
SNP_A-2258478	G	G	282	30	305	15	5.801	0.016	rs17450934	8	128378019	q24.21
SNP_A-2069808	G	G	288	104	294	70	5.676	0.0172	rs1447294	8	128506868	q24.21
SNP_A-2281165	C	C	332	46	305	65	4.312	3.79E-02	rs7841264	8	128535996	q24.21
SNP_A-2095013	C	C	353	25	352	42	3.985	4.59E-02	rs7829962	8	129045433	q24.21
SNP_A-1661141	G	G	347	45	378	30	4.007	0.0453	rs2909239	8	129148938	q24.21
SNP_A-1995059	G	G	383	5	367	19	8.503	3.50E-03	rs1499368	8	129163771	q24.21
SNP_A-1857757	G	G	239	155	270	112	8.63	0.0033	rs17382663	8	129172214	q24.21
SNP_A-2050234	G	G	331	49	257	65	6.813	9.00E-03	rs7008889	8	129205110	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2051530	C	C	366	50	391	29	6.389	0.0115	rs2909237	8	129260141	q24.21
SNP_A-2069937	C	C	360	42	391	25	5.355	0.0207	rs1902779	8	129267212	q24.21
SNP_A-1995076	T	T	362	46	387	29	4.611	3.18E-02	rs4288340	8	129271836	q24.21
SNP_A-2022195	C	C	351	5	372	0	5.261	0.0218	rs6987273	8	129296068	q24.21
SNP_A-2087909	C	C	375	1	374	8	5.399	2.02E-02	rs11785559	8	129369486	q24.21
SNP_A-2279104	A	A	413	3	405	15	8.059	4.50E-03	rs17806456	8	129601077	q24.21
SNP_A-1642125	C	C	369	29	355	47	4.514	3.36E-02	rs919658	8	129791597	q24.21
SNP_A-2229160	T	T	380	32	363	55	6.426	0.0112	rs6994324	8	129901338	q24.21
SNP_A-1802140	A	A	378	26	364	42	4.024	4.49E-02	—	8	129922397	q24.21
SNP_A-2239120	G	G	373	9	339	21	5.776	1.62E-02	rs4733660	8	129979812	q24.21
SNP_A-1917977	G	G	332	42	341	21	6.927	8.50E-03	rs7839409	8	130079922	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1995124	G	G	278	86	288	60	4.45	0.0349	rs1372454	8	130099312	q24.21
SNP_A-1891383	A	A	243	157	267	123	5.132	0.0235	rs4733687	8	130321411	q24.21
SNP_A-2086872	T	T	361	27	361	9	8.577	3.40E-03	rs16904074	8	130523308	q24.21
SNP_A-2267783	T	T	295	25	309	13	4.108	4.27E-02	rs2670886	8	131325860	q24.21
SNP_A-1642709	C	C	353	33	335	57	6.825	9.00E-03	rs7836215	8	131623504	q24.22
SNP_A-2287586	C	C	284	34	302	18	5.47	1.93E-02	rs10111880	8	131689369	q24.22
SNP_A-1787444	T	T	229	135	175	157	7.42	6.50E-03	rs5990380	8	131849331	q24.22
SNP_A-1995162	T	T	254	110	217	151	9.326	0.0023	rs10505564	8	131857839	q24.22
SNP_A-2089228	T	T	243	137	202	176	8.632	0.0033	rs7831104	8	131858699	q24.22
SNP_A-1938500	C	C	261	129	224	170	8.425	3.70E-03	rs7814990	8	131858748	q24.22
SNP_A-2216725	A	A	259	91	223	115	5.277	2.16E-02	rs1509854	8	131860580	q24.22
SNP_A-1935057	C	C	274	138	231	173	7.523	6.10E-03	rs3793387	8	131862883	q24.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814670	T	T	225	125	200	154	4.462	3.46E-02	rs2196315	8	131868477	q24.22
SNP_A-2146232	C	C	295	21	292	44	7.547	6.00E-03	rs12679904	8	131868589	q24.22
SNP_A-1790233	A	A	274	136	231	167	6.656	9.90E-03	rs10956553	8	131876740	q24.22
SNP_A-1800911	G	G	336	78	305	115	8.55	3.50E-03	rs4736745	8	132232756	q24.22
SNP_A-1893511	A	A	220	184	250	158	3.872	4.91E-02	rs4736746	8	132233170	q24.22
SNP_A-2089131	A	A	296	60	323	41	4.664	3.08E-02	rs6415534	8	132402402	q24.22
SNP_A-2123905	C	C	242	54	304	40	5.557	0.0184	rs6470947	8	132423461	q24.22
SNP_A-1694229	A	A	360	34	378	16	6.919	8.50E-03	rs715969	8	132430452	q24.22
SNP_A-1854437	C	C	335	19	315	33	4.334	3.74E-02	rs7014931	8	132528131	q24.22
SNP_A-2192164	G	G	407	7	417	1	4.602	3.19E-02	rs11995068	8	132612445	q24.22
SNP_A-1917082	A	A	260	112	214	146	8.75	3.10E-03	rs17626005	8	132614647	q24.22
SNP_A-1886293	G	G	397	7	417	1	4.754	0.0292	rs6997586	8	132625311	q24.22
SNP_A-2101231	A	A	302	6	327	1	3.94	4.71E-02	rs12541606	8	132808960	q24.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936664	C	C	303	83	318	60	3.978	4.61E-02	rs6471066	8	133473613	q24.22
SNP_A-2078503	C	C	308	90	311	63	4.037	4.45E-02	rs2222452	8	134054577	q24.22
SNP_A-2131979	G	G	207	171	226	136	4.48	3.43E-02	rs7816892	8	134239080	q24.22
SNP_A-1780651	G	G	277	45	241	67	6.515	1.07E-02	rs2739126	8	134249059	q24.22
SNP_A-1803744	T	T	369	45	342	74	8.088	4.50E-03	rs6983761	8	134256235	q24.22
SNP_A-1995237	A	G	204	184	234	168	9.22	2.40E-03	rs2736862	8	134497425	q24.22
SNP_A-1995238	A	A	328	2	300	8	4.095	4.30E-02	rs16904926	8	134540244	q24.22
SNP_A-1906699	G	G	275	137	304	112	3.943	4.71E-02	rs6471128	8	134575371	q24.22
SNP_A-2037911	G	G	360	44	386	28	4.34	3.72E-02	rs16904939	8	134625327	q24.22
SNP_A-1682712	G	G	364	28	387	13	6.112	0.0134	rs10505613	8	134742465	q24.22
SNP_A-2091135	G	G	247	165	217	201	5.438	1.97E-02	rs4629849	8	134870122	q24.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1995257	C	C	359	49	330	68	4.183	4.08E-02	rs17669534	8	134872017	q24.22
SNP_A-2065330	A	A	359	39	390	20	7.225	7.20E-03	rs4295695	8	135344348	q24.22
SNP_A-2312877	C	C	236	180	264	150	4.29	3.83E-02	rs7006328	8	135487749	q24.22
SNP_A-1783228	A	A	296	116	328	92	4.334	3.74E-02	rs3739422	8	135684154	q24.22
SNP_A-1886644	G	G	291	119	320	92	4.827	2.80E-02	rs16905197	8	135694274	q24.22
SNP_A-2054267	G	G	301	109	328	82	4.976	2.57E-02	rs733254	8	135707814	q24.22
SNP_A-2194412	C	C	246	112	233	145	4.05	4.42E-02	rs11996107	8	135747986	q24.22
SNP_A-2184894	T	T	351	19	341	33	3.892	4.85E-02	rs16905254	8	135911146	q24.22
SNP_A-2013894	T	T	271	77	275	51	4.597	3.20E-02	rs6992707	8	136049429	q24.22
SNP_A-2170665	A	A	358	20	357	9	3.981	4.60E-02	rs7846493	8	136136037	q24.22
SNP_A-1995288	C	C	283	93	311	61	7.948	4.80E-03	rs11776216	8	136224766	q24.22
SNP_A-2245653	G	G	274	116	245	143	4.43	3.53E-02	rs4609225	8	136800579	q24.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1843204	G	G	253	129	228	154	4.575	3.24E-02	rs7831259	8	136802435	q24.23
SNP_A-1899842	T	T	251	127	237	157	4.28	3.86E-02	rs7827685	8	136802542	q24.23
SNP_A-2300785	A	A	215	111	188	134	3.944	4.71E-02	rs2922350	8	137055200	q24.23
SNP_A-2084477	C	C	344	18	323	35	6.092	1.36E-02	rs2317729	8	137228712	q24.23
SNP_A-2043614	T	T	394	20	375	35	4.541	3.31E-02	rs16905528	8	137310055	q24.23
SNP_A-1663828	T	T	391	7	401	1	4.606	3.19E-02	rs10505662	8	137634376	q24.23
SNP_A-1958298	T	T	406	6	414	0	6.073	0.0137	rs16906170	8	137726974	q24.23
SNP_A-2191698	A	A	378	36	393	21	4.239	0.0395	rs2091923	8	138247770	q24.23
SNP_A-2154359	G	G	347	19	307	33	5.265	0.0218	rs11166686	8	138248202	q24.23
SNP_A-2045431	T	T	265	119	227	165	10.304	1.30E-03	rs4506251	8	138379880	q24.23
SNP_A-2177827	T	T	266	142	241	173	4.24	0.0395	rs10481389	8	138671999	q24.23
SNP_A-2182544	T	T	189	177	224	146	5.92	1.50E-02	---	8	138672913	q24.23
SNP_A-2098855	A	A	208	194	233	153	5.939	1.48E-02	rs4909376	8	138673540	q24.23
SNP_A-1911932	A	A	290	100	324	74	5.687	1.71E-02	---	8	138673785	q24.23
SNP_A-2184681	A	A	253	135	227	175	6.324	1.19E-02	rs11993213	8	138674409	q24.23
SNP_A-2129993	A	A	259	115	287	89	4.744	2.94E-02	rs12334660	8	138681388	q24.23
SNP_A-1783541	T	T	299	115	315	83	5.275	2.16E-02	rs4489355	8	138684814	q24.23
SNP_A-1852040	C	C	275	49	299	21	12.179	5.00E-04	rs6986084	8	138691089	q24.23
SNP_A-1920325	C	C	286	40	323	19	9.345	2.20E-03	rs7002489	8	138873579	q24.23
SNP_A-1799490	A	A	338	62	368	38	6.991	8.20E-03	rs6577839	8	138874377	q24.23
SNP_A-2151890	C	C	344	62	369	41	5.139	2.34E-02	rs7386494	8	138874970	q24.23
SNP_A-2013921	T	T	314	72	343	51	4.784	0.0287	rs6577841	8	138879056	q24.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2040462	G	G	317	81	345	57	5.338	2.09E-02	rs7840530	8	138880662	q24.23
SNP_A-2065905	T	T	312	100	337	77	3.947	0.047	rs1949140	8	138950576	q24.23
SNP_A-2177394	A	A	329	29	331	15	4.257	3.91E-02	rs2705295	8	138987482	q24.23
SNP_A-1937659	A	A	213	147	218	106	4.821	0.0281	rs12542715	8	139178860	q24.23
SNP_A-1879030	T	T	254	156	224	194	5.932	0.0149	rs17655198	8	139244364	q24.23
SNP_A-1931725	A	T	184	156	195	151	7.532	6.10E-03	rs10103726	8	139253034	q24.23
SNP_A-2165438	G	G	321	63	300	92	6.054	1.39E-02	rs6577902	8	139333022	q24.23
SNP_A-2024799	C	T	196	182	204	158	4.989	2.55E-02	rs4529468	8	139536116	q24.23
SNP_A-1814343	G	A	193	157	199	173	5.383	2.03E-02	rs4410910	8	139536136	q24.23
SNP_A-1803217	C	T	210	202	221	173	4.028	0.0448	rs17674188	8	139543743	q24.23
SNP_A-1931520	C	A	203	195	224	172	4.565	3.26E-02	rs13249380	8	139550002	q24.23
SNP_A-2186333	A	G	224	168	205	199	4.968	0.0258	rs16909195	8	139554167	q24.23
SNP_A-2013926	C	C	361	35	366	20	3.998	4.56E-02	rs4458882	8	139711848	q24.23
SNP_A-2221511	T	T	343	39	384	22	6.325	1.19E-02	rs4073002	8	139777044	q24.23
SNP_A-2192183	A	A	286	82	269	109	4.204	4.03E-02	rs12155960	8	139886087	q24.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1995417	G	G	358	42	340	62	4.305	3.80E-02	rs11166850	8	139943056	q24.23
SNP_A-2089835	T	T	349	37	328	58	5.294	2.14E-02	rs16910092	8	140162341	q24.3
SNP_A-2210354	G	G	320	10	306	2	4.894	0.027	rs16910093	8	140163078	q24.3
SNP_A-2134985	A	A	404	10	415	3	3.898	4.83E-02	rs2319092	8	140372239	q24.3
SNP_A-1719207	C	G	209	189	238	174	8.582	3.40E-03	rs2447374	8	140505119	q24.3
SNP_A-1738943	C	C	316	60	294	88	6.044	0.014	rs7465461	8	140521525	q24.3
SNP_A-1750279	G	G	332	66	321	91	3.925	4.76E-02	rs4736271	8	140521596	q24.3
SNP_A-1735282	A	A	387	11	407	3	4.898	0.0269	rs726348	8	140579815	q24.3
SNP_A-2013936	G	G	191	187	233	169	4.336	0.0373	rs2468668	8	140581239	q24.3
SNP_A-2156844	C	A	213	199	243	171	8.969	2.70E-03	rs2468677	8	140588699	q24.3
SNP_A-2121980	G	G	262	148	215	201	12.637	4.00E-04	rs10109373	8	140590988	q24.3
SNP_A-2313433	C	C	309	53	281	87	9.537	0.002	rs7018136	8	140607188	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116336	C	C	267	147	211	203	15.521	8.16E-05	rs2447395	8	140611452	q24.3
SNP_A-2193097	G	G	332	72	307	103	6.426	0.0112	rs16910856	8	140611951	q24.3
SNP_A-2123597	G	G	337	73	309	103	6.322	1.19E-02	rs4469434	8	140614144	q24.3
SNP_A-2180683	T	T	261	61	219	99	12.675	4.00E-04	rs7006579	8	140632359	q24.3
SNP_A-2295739	G	C	210	200	250	168	10.146	0.0014	rs2542464	8	140632492	q24.3
SNP_A-2144056	A	A	204	196	249	161	7.779	0.0053	rs2542463	8	140635452	q24.3
SNP_A-2140649	A	G	188	180	236	146	12.563	4.00E-04	rs2261742	8	140635804	q24.3
SNP_A-1797566	A	G	202	182	239	159	12.593	4.00E-04	rs2615404	8	140644532	q24.3
SNP_A-2228472	C	C	280	118	229	165	12.896	3.00E-04	rs4736080	8	140648574	q24.3
SNP_A-1917352	T	T	271	47	253	73	6.153	1.31E-02	rs10109997	8	140651196	q24.3
SNP_A-2285443	A	C	210	140	176	156	11.601	7.00E-04	rs6578035	8	140653283	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2294920	G	A	236	152	205	173	17.445	2.96E-05	rs4736081	8	140653370	q24.3
SNP_A-2307805	G	-	241	135	186	186	15.166	9.85E-05	rs4736082	8	140653643	q24.3
SNP_A-1935650	G	G	324	66	300	94	5.803	0.016	rs10101646	8	140654059	q24.3
SNP_A-2275790	T	C	232	138	190	184	13.761	2.00E-04	rs10875443	8	140654514	q24.3
SNP_A-2173080	G	G	265	113	209	139	8.073	4.50E-03	rs11166916	8	140654708	q24.3
SNP_A-2298404	C	T	248	150	200	194	13.72	2.00E-04	rs11787004	8	140654836	q24.3
SNP_A-2289991	A	A	315	101	283	133	6.088	1.36E-02	rs6988058	8	140674897	q24.3
SNP_A-1995448	C	C	400	10	414	2	5.531	1.87E-02	rs2319420	8	140676489	q24.3
SNP_A-2083856	C	C	404	10	417	3	3.932	4.74E-02	rs2471087	8	140685737	q24.3
SNP_A-2013941	G	A	205	199	219	163	5.139	2.34E-02	rs7825905	8	140986758	q24.3
SNP_A-2119875	T	C	185	177	208	158	4.6	3.20E-02	rs2665917	8	141032458	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2046745	G	G	205	175	220	138	4.251	3.92E-02	rs11985315	8	141212409	q24.3
SNP_A-1818686	C	C	335	81	360	60	4.008	0.0453	rs11782239	8	141238679	q24.3
SNP_A-2246189	G	G	284	78	257	105	5.331	2.09E-02	rs7017431	8	141330149	q24.3
SNP_A-1812717	G	G	262	138	302	116	4.348	3.70E-02	rs10464982	8	141349595	q24.3
SNP_A-1800553	C	C	280	108	307	75	7.146	7.50E-03	rs1879818	8	141516084	q24.3
SNP_A-2218252	C	A	214	198	232	184	4.93	0.0264	rs12386958	8	141528866	q24.3
SNP_A-2091294	A	A	193	167	220	134	5.333	2.09E-02	rs7819876	8	141528909	q24.3
SNP_A-2082217	G	G	224	178	264	144	6.825	9.00E-03	rs7820161	8	141529151	q24.3
SNP_A-1903264	C	T	184	164	204	150	7.758	0.0053	rs3735803	8	141530244	q24.3
SNP_A-2070303	G	G	343	65	367	45	4.428	3.53E-02	rs2977451	8	141603380	q24.3
SNP_A-2143830	C	C	313	43	295	63	4.301	3.81E-02	rs11167023	8	142175410	q24.3
SNP_A-2108636	C	C	364	0	334	10	10.733	1.10E-03	rs4907325	8	142695608	q24.3
SNP_A-2278984	G	G	392	16	407	5	6.024	0.0141	rs7015131	8	142815362	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2306874	G	G	371	33	382	18	4.553	3.29E-02	rs9720892	8	142840557	q24.3
SNP_A-2301839	G	G	373	31	384	16	4.927	0.0264	rs9694951	8	142855826	q24.3
SNP_A-1876964	C	C	261	133	302	104	6.356	0.0117	rs13262940	8	143656311	q24.3
SNP_A-2103952	G	G	364	18	351	33	4.643	3.12E-02	rs6476905	9	473018	p24.3
SNP_A-2161192	T	T	257	119	265	85	4.864	2.74E-02	rs9407292	9	516772	p24.3
SNP_A-2031252	T	T	332	48	317	73	5.383	2.03E-02	rs10975130	9	547340	p24.3
SNP_A-2300758	C	C	361	49	378	32	3.959	4.66E-02	rs10758793	9	650566	p24.3
SNP_A-2287179	A	A	289	93	320	72	4.122	4.23E-02	rs10739107	9	650851	p24.3
SNP_A-2277357	C	C	347	57	332	80	4.115	4.25E-02	rs10815704	9	788773	p24.3
SNP_A-2065219	C	C	278	120	315	83	9.052	2.60E-03	rs10114340	9	791375	p24.3
SNP_A-2057960	G	T	212	162	185	181	3.884	4.88E-02	rs10739166	9	847511	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1908671	G	G	281	65	292	44	4.111	4.26E-02	rs10977650	9	929738	p24.3
SNP_A-1939399	C	C	343	59	367	37	5.848	1.56E-02	rs16926587	9	940227	p24.3
SNP_A-1954543	G	G	243	157	215	185	4.004	4.54E-02	rs7869989	9	1040981	p24.3
SNP_A-2155203	T	T	360	54	339	75	4.05	4.42E-02	rs10809097	9	1047797	p24.3
SNP_A-1814773	A	A	319	33	309	53	4.671	3.07E-02	rs5008113	9	1107295	p24.3
SNP_A-1950345	A	A	254	126	290	104	4.235	3.96E-02	rs7040474	9	1107582	p24.3
SNP_A-2241928	G	G	253	109	283	83	5.178	0.0229	rs10809357	9	1113445	p24.3
SNP_A-1665380	T	T	270	126	296	100	4.185	4.08E-02	rs1337621	9	1141090	p24.3
SNP_A-2257285	C	C	215	141	253	105	8.348	3.90E-03	rs10738237	9	1148171	p24.3
SNP_A-1995518	T	T	285	131	313	105	4.171	4.11E-02	rs10511430	9	1151604	p24.3
SNP_A-2164222	T	T	216	96	201	125	4.04	4.44E-02	rs10809509	9	1152013	p24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1714887	T	T	366	32	354	58	7.471	0.0063	rs10511427	9	1196411	p24.3
SNP_A-1995521	T	A	220	164	197	185	6.036	0.014	rs4506274	9	1196487	p24.3
SNP_A-2022766	C	C	384	24	405	9	7.334	6.80E-03	rs12339290	9	1211729	p24.3
SNP_A-1995529	C	C	366	30	376	16	4.375	3.65E-02	rs10960872	9	1296855	p24.3
SNP_A-1916162	T	T	367	21	353	45	8.874	2.90E-03	rs17743398	9	1373446	p24.3
SNP_A-2307445	G	G	284	82	292	60	4.767	2.90E-02	rs7854227	9	1480407	p24.3
SNP_A-1946955	T	T	357	19	357	39	6.383	0.0115	rs11999799	9	1502519	p24.3
SNP_A-1704121	T	T	222	178	268	144	7.733	5.40E-03	rs9298820	9	2167391	p24.3
SNP_A-1995568	G	G	173	155	196	120	5.667	1.73E-02	rs10491698	9	2201628	p24.2
SNP_A-1690175	C	C	326	62	293	87	5.871	0.0154	rs10491699	9	2201865	p24.2
SNP_A-1796585	G	A	166	152	191	133	8.021	4.60E-03	rs10811646	9	2204289	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1995570	C	C	309	49	335	31	5.012	0.0252	rs2093833	9	2210796	p24.2
SNP_A-2274022	G	G	300	110	248	146	9.682	0.0019	rs10811679	9	2224701	p24.2
SNP_A-2269613	C	C	306	64	349	45	5.386	2.03E-02	rs1324205	9	2238103	p24.2
SNP_A-1923796	C	C	325	81	352	58	4.863	2.74E-02	rs17405547	9	2261325	p24.2
SNP_A-1820780	A	A	298	74	281	101	4.533	0.0332	rs10812052	9	2446879	p24.2
SNP_A-1888873	G	G	313	77	280	102	5.246	2.20E-02	rs12683430	9	2487985	p24.2
SNP_A-2301918	G	G	304	54	268	74	5.028	2.49E-02	rs10966539	9	2488434	p24.2
SNP_A-2199571	G	G	214	114	238	90	4.098	4.29E-02	rs10154469	9	2516760	p24.2
SNP_A-2288727	A	A	353	59	330	90	7.148	7.50E-03	rs588933	9	2527815	p24.2
SNP_A-1791266	G	G	285	67	254	98	7.607	5.80E-03	rs482376	9	2529495	p24.2
SNP_A-2152024	C	T	213	175	218	176	8.179	4.20E-03	rs7868173	9	2548330	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1692446	A	A	283	105	253	155	10.799	0.001	rs1576660	9	2551288	p24.2
SNP_A-1856568	C	C	350	52	389	27	9.733	0.0018	rs10967306	9	2630805	p24.2
SNP_A-1800235	G	G	356	48	334	68	4.145	4.18E-02	rs10813032	9	2923171	p24.2
SNP_A-2099200	A	A	163	159	195	137	4.344	3.71E-02	rs1501583	9	2975380	p24.2
SNP_A-2287141	G	G	229	151	258	124	4.373	3.65E-02	rs1322228	9	3159820	p24.2
SNP_A-1902619	G	G	333	49	350	32	3.991	4.57E-02	rs535614	9	3236491	p24.2
SNP_A-2096823	C	C	349	37	367	21	4.861	0.0275	rs17658838	9	3264741	p24.2
SNP_A-1995610	T	T	324	76	340	48	6.527	0.0106	rs2991304	9	3313516	p24.2
SNP_A-1719291	C	C	363	37	392	20	6.008	1.42E-02	rs1537523	9	3639097	p24.2
SNP_A-1788198	T	T	231	125	242	92	4.577	3.24E-02	rs16919564	9	3756183	p24.2
SNP_A-1922991	C	C	360	34	341	51	3.91	4.80E-02	rs16920043	9	3921254	p24.2
SNP_A-2085280	T	T	331	73	331	49	3.99	0.0458	rs10017567	9	3938457	p24.2
SNP_A-2062701	A	A	321	77	361	57	4.844	2.77E-02	rs10974260	9	3948159	p24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2234564	C	C	266	102	291	75	5.235	2.21E-02	rs10974324	9	4072768	p24.2
SNP_A-1899311	A	A	218	108	233	77	5.294	2.14E-02	rs529420	9	4117906	p24.2
SNP_A-1913548	C	C	216	122	226	90	4.321	3.76E-02	rs10974377	9	4174968	p24.2
SNP_A-1886713	C	C	274	136	235	167	6.082	0.0137	rs736893	9	4207028	p24.2
SNP_A-1957530	A	G	181	179	203	143	5.689	1.71E-02	rs10814886	9	4210076	p24.2
SNP_A-2290274	C	C	281	135	247	171	6.42	1.13E-02	rs6476827	9	4210832	p24.2
SNP_A-1945021	G	G	388	28	375	45	4.161	4.14E-02	rs17717099	9	4276932	p24.2
SNP_A-1827175	A	A	259	103	230	136	6.255	0.0124	rs4740783	9	4438088	p24.2
SNP_A-2251401	C	C	368	0	370	4	3.957	4.67E-02	rs10117872	9	4878355	p24.1
SNP_A-1876138	C	C	246	116	270	82	6.816	9.00E-03	rs4142064	9	5211818	p24.1
SNP_A-1844505	C	C	248	84	284	62	5.464	1.94E-02	rs7870536	9	5235493	p24.1
SNP_A-1699795	C	C	199	193	253	151	11.401	7.00E-04	rs10491649	9	5308770	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137147	A	A	248	84	228	114	5.239	2.21E-02	rs10758680	9	5318915	p24.1
SNP_A-2302275	T	T	254	150	296	106	10.765	0.001	rs1123960	9	5343868	p24.1
SNP_A-1788983	C	C	279	123	250	156	5.473	1.93E-02	rs1555475	9	5353068	p24.1
SNP_A-1833409	G	G	226	114	257	67	13.817	2.00E-04	rs2025167	9	5354941	p24.1
SNP_A-1995670	A	A	263	135	223	175	8.453	3.60E-03	rs9299013	9	5362724	p24.1
SNP_A-1860296	G	G	248	130	254	96	4.116	4.25E-02	rs10975090	9	5379652	p24.1
SNP_A-1889045	C	C	266	144	297	113	5.446	1.96E-02	rs10975106	9	5408152	p24.1
SNP_A-1703967	A	A	268	132	300	106	4.599	3.20E-02	rs10491646	9	5415109	p24.1
SNP_A-2137828	A	A	279	101	307	69	7.34	6.70E-03	rs911761	9	5429946	p24.1
SNP_A-1792285	A	A	334	52	355	27	8.531	3.50E-03	rs1536927	9	5571140	p24.1
SNP_A-1835480	G	G	387	29	405	15	4.845	2.77E-02	rs16923249	9	5582145	p24.1
SNP_A-2244796	T	T	339	71	371	47	6.247	0.0124	rs7865645	9	5586111	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227991	C	C	330	24	378	10	7.477	0.0063	rs10815252	9	5597230	p24.1
SNP_A-2274800	T	T	381	9	359	1	5.863	0.0155	rs7048449	9	5721315	p24.1
SNP_A-1652636	C	C	280	120	257	155	5.263	0.0218	rs9299022	9	5844323	p24.1
SNP_A-2087337	C	C	291	109	258	144	6.821	9.00E-03	rs7027341	9	5858289	p24.1
SNP_A-2261447	A	A	286	124	242	170	10.859	0.001	rs10739078	9	5865294	p24.1
SNP_A-2119620	C	C	332	4	330	0	3.952	4.68E-02	rs10739082	9	5971901	p24.1
SNP_A-1868918	C	C	324	72	288	104	7.916	4.90E-03	rs17705436	9	6300908	p24.1
SNP_A-1757333	G	G	293	105	267	143	6.853	8.80E-03	rs4742179	9	6314376	p24.1
SNP_A-1682474	C	C	313	85	281	121	7.995	4.70E-03	rs10491836	9	6321421	p24.1
SNP_A-2247257	T	T	300	50	253	75	8.289	4.00E-03	rs7850988	9	6325760	p24.1
SNP_A-1786198	T	T	302	70	270	112	11.352	8.00E-04	rs16924428	9	6341111	p24.1
SNP_A-1736999	A	A	244	136	224	168	4.038	4.45E-02	rs719725	9	6355683	p24.1
SNP_A-2047067	G	G	340	38	323	59	4.961	2.59E-02	rs4361812	9	6355737	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027983	C	C	240	132	218	164	4.384	3.63E-02	rs4419859	9	6534766	p24.1
SNP_A-2222844	G	G	398	12	416	4	4.278	3.86E-02	rs3858052	9	6760741	p24.1
SNP_A-2234928	C	C	309	107	284	136	4.496	3.40E-02	rs17593759	9	6774867	p24.1
SNP_A-1928654	G	G	330	80	358	58	4.603	3.19E-02	rs10975835	9	6787498	p24.1
SNP_A-2125288	C	C	252	158	280	130	4.196	4.05E-02	rs10815471	9	6838369	p24.1
SNP_A-2224517	T	T	390	10	372	24	6.17	1.30E-02	rs2890734	9	7025800	p24.1
SNP_A-2145646	C	C	398	8	382	22	6.857	8.80E-03	rs10976003	9	7031324	p24.1
SNP_A-2229255	T	T	400	0	396	4	4.02	4.50E-02	rs16925200	9	7035058	p24.1
SNP_A-2067495	T	T	407	7	377	21	7.836	5.10E-03	rs8181075	9	7045236	p24.1
SNP_A-1995698	T	T	356	10	377	25	5.354	0.0207	rs6477148	9	7069643	p24.1
SNP_A-2265541	C	C	364	14	371	5	4.325	3.76E-02	rs2770718	9	7253038	p24.1
SNP_A-2182338	C	C	372	42	394	24	5.522	1.88E-02	rs16926157	9	7458164	p24.1
SNP_A-1726602	G	G	394	6	412	0	6.226	0.0126	rs10511469	9	7463985	p24.1
SNP_A-1995746	T	T	395	1	393	11	8.259	4.10E-03	rs702283	9	7717062	p24.1
SNP_A-1927036	A	A	334	14	355	3	7.618	5.80E-03	rs17547957	9	7824859	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1995759	G	G	287	95	316	70	5.162	2.31E-02	rs7018802	9	8157323	p24.1
SNP_A-1923722	G	G	310	44	327	27	4.524	3.34E-02	rs1768576	9	8225898	p24.1
SNP_A-1848550	C	C	343	37	365	17	8.086	4.50E-03	rs9792404	9	8419048	p24.1
SNP_A-2043296	C	C	285	61	331	37	8.643	0.0033	rs7869958	9	8432098	p24.1
SNP_A-1723258	C	C	283	85	320	66	4.234	3.96E-02	rs1407972	9	8451714	p24.1
SNP_A-1995773	T	T	319	85	351	53	8.949	0.0028	rs2281747	9	8455598	p24.1
SNP_A-1818506	T	T	371	27	347	45	5.257	2.19E-02	rs10977148	9	8467093	p24.1
SNP_A-2174407	C	C	361	25	372	10	6.573	0.0104	rs10124277	9	8489295	p24.1
SNP_A-2091185	C	C	351	35	370	20	4.571	3.25E-02	rs4409447	9	8492387	p24.1
SNP_A-1816633	C	C	329	55	362	30	8.847	2.90E-03	rs7023008	9	8510366	p24.1
SNP_A-2014038	G	G	291	49	290	26	6.185	0.0129	rs7024591	9	8510831	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1725080	C	C	377	23	373	39	3.974	4.62E-02	rs10511499	9	8511121	p24.1
SNP_A-2049446	A	A	230	130	201	167	6.474	0.0109	rs10977176	9	8514448	p24.1
SNP_A-1836004	C	C	361	13	351	29	6.188	0.0129	rs2273998	9	8514854	p24.1
SNP_A-1874035	C	C	320	66	339	37	8.583	3.40E-03	rs7849367	9	8522140	p24.1
SNP_A-2292537	T	T	258	122	237	151	3.889	4.86E-02	rs7023351	9	8568551	p24.1
SNP_A-2306694	A	A	265	85	198	96	5.536	1.86E-02	rs10759021	9	8931696	p24.1
SNP_A-2222535	G	G	276	116	244	148	5.848	1.56E-02	rs10977393	9	8936379	p24.1
SNP_A-2136220	T	C	221	177	216	168	10.844	0.001	rs2381933	9	8962925	p24.1
SNP_A-1955903	A	A	269	53	241	73	4.612	3.17E-02	rs2381934	9	8963980	p24.1
SNP_A-2287658	C	C	306	48	324	24	8.464	3.60E-03	rs12339309	9	8964640	p24.1
SNP_A-2049572	G	G	219	111	196	142	4.978	2.57E-02	rs4742554	9	8974469	p24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2099708	A	A	270	140	237	177	6.447	0.0111	rs4380999	9	8974647	p24.1
SNP_A-1691278	A	A	213	185	248	162	4.004	4.54E-02	rs9299084	9	8983027	p24.1
SNP_A-1835674	C	C	284	102	252	124	3.921	4.77E-02	rs10977434	9	8991075	p24.1
SNP_A-2092632	T	T	203	185	237	161	4.165	4.13E-02	rs1445213	9	9172216	p23
SNP_A-1654865	T	C	199	187	224	172	5.169	0.023	rs1333107	9	9449009	p23
SNP_A-1758753	C	C	232	156	285	125	8.253	4.10E-03	rs10491614	9	9454410	p23
SNP_A-1995812	C	G	213	197	222	182	3.881	4.88E-02	rs955474	9	9455190	p23
SNP_A-2117743	C	C	215	157	254	120	8.18	4.20E-03	rs10816141	9	9465845	p23
SNP_A-1881179	T	T	329	53	341	35	3.849	4.98E-02	rs633719	9	9516138	p23
SNP_A-1739935	C	C	365	23	349	39	4.488	3.41E-02	rs2147070	9	9780306	p23
SNP_A-1819254	T	T	349	21	369	9	5.272	2.17E-02	rs10816216	9	9851006	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1707996	G	G	366	34	353	59	6.78	9.20E-03	rs10514817	9	9872403	p23
SNP_A-2025200	C	C	291	47	332	32	4.59	3.22E-02	rs10978078	9	9898821	p23
SNP_A-2262399	G	G	269	39	308	26	4.19	0.0407	rs7032996	9	9959896	p23
SNP_A-1852575	A	A	236	152	262	122	4.621	3.16E-02	rs4425814	9	9993764	p23
SNP_A-2269342	C	C	263	101	285	77	4.114	4.25E-02	rs447925	9	10079748	p23
SNP_A-2038753	G	G	324	26	300	42	4.596	3.20E-02	rs10958891	9	10114871	p23
SNP_A-1935389	A	A	292	112	307	77	6.354	0.0117	rs294868	9	10114920	p23
SNP_A-2198202	C	C	387	21	366	36	4.489	3.41E-02	rs9721595	9	10135099	p23
SNP_A-1939343	T	T	281	87	229	121	10.415	1.20E-03	rs2119589	9	10135234	p23
SNP_A-2282491	G	G	347	39	368	22	5.334	2.09E-02	rs657964	9	10416186	p23
SNP_A-2047580	A	A	258	126	290	102	4.313	0.0378	rs10217547	9	10496028	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1726034	T	T	364	20	347	51	13.695	2.00E-04	rs951099	9	10882053	p23
SNP_A-2228957	A	A	243	105	208	130	5.231	2.22E-02	rs7044282	9	11029639	p23
SNP_A-2068277	C	C	290	48	297	27	5.67	1.73E-02	rs1577119	9	11098671	p23
SNP_A-1885394	G	G	306	104	339	73	7.113	7.70E-03	rs10959536	9	11102874	p23
SNP_A-2239997	A	A	301	91	337	71	4.182	4.09E-02	rs10959538	9	11103176	p23
SNP_A-2310257	G	G	303	11	305	23	3.938	4.72E-02	rs7874270	9	11433473	p23
SNP_A-2251316	A	A	390	20	387	9	3.942	4.71E-02	rs10959895	9	11517480	p23
SNP_A-1749177	A	A	379	21	403	9	5.36	0.0206	rs10511568	9	11597135	p23
SNP_A-1841896	G	G	392	8	407	1	5.647	1.75E-02	rs10809552	9	11666182	p23
SNP_A-2124924	G	G	405	7	415	1	4.603	3.19E-02	rs7045470	9	11746234	p23
SNP_A-1914348	T	T	382	0	374	4	4.064	4.38E-02	rs10960423	9	11981732	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2076835	A	G	218	172	211	185	6.628	0.01	rs4512479	9	11986831	p23
SNP_A-2078933	T	T	295	89	309	61	5.293	2.14E-02	rs10756320	9	12018523	p23
SNP_A-1928650	G	G	400	14	391	27	4.205	4.03E-02	rs16928757	9	12347045	p23
SNP_A-1995915	A	A	402	14	389	27	4.336	0.0373	rs2890963	9	12348650	p23
SNP_A-2150301	G	G	222	148	250	122	4.159	4.14E-02	rs944522	9	12451272	p23
SNP_A-1949290	T	T	233	149	193	191	8.939	0.0028	rs12348188	9	12493842	p23
SNP_A-1805998	C	C	252	146	213	177	6.166	1.30E-02	rs791672	9	12507596	p23
SNP_A-2134454	G	G	282	132	249	159	4.512	3.36E-02	rs1408808	9	12532187	p23
SNP_A-2255736	C	C	374	20	387	9	4.389	3.62E-02	rs10733246	9	12729132	p23
SNP_A-1820706	A	A	348	14	388	6	4.027	0.0448	rs4996096	9	12746917	p23
SNP_A-1802105	C	C	321	21	269	33	4.784	0.0287	rs1536792	9	12962382	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1792758	A	A	287	115	319	85	6.185	0.0129	rs10960942	9	13083345	p23
SNP_A-2303839	C	C	281	117	251	141	3.879	4.89E-02	rs7867993	9	13125698	p23
SNP_A-2083235	C	C	375	7	326	16	4.751	0.0293	rs7039058	9	13167528	p23
SNP_A-1869436	G	G	396	4	374	14	6.003	0.0143	rs7847491	9	13175059	p23
SNP_A-2119858	A	A	340	56	353	37	4.08	4.34E-02	rs10809915	9	13199807	p23
SNP_A-1995955	C	C	406	10	393	23	5.333	2.09E-02	rs17273416	9	13204871	p23
SNP_A-1708871	C	C	348	50	385	27	8.498	3.60E-03	rs8192981	9	13671648	p23
SNP_A-2186629	T	T	264	118	286	90	4.602	3.19E-02	rs625476	9	13695973	p23
SNP_A-1846408	C	C	256	136	236	168	4.001	4.55E-02	rs1327517	9	13733702	p23
SNP_A-1943428	G	G	279	75	254	106	6.432	0.0112	rs11789440	9	13747664	p23
SNP_A-2239291	G	G	210	128	261	89	12.326	4.00E-04	rs1034166	9	13761590	p23
SNP_A-2309505	C	C	255	151	296	114	8.197	4.20E-03	rs1034165	9	13761656	p23
SNP_A-2037296	T	T	269	79	314	58	5.899	1.51E-02	rs17192702	9	13944734	p23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1793987	G	A	195	165	190	156	5.819	1.59E-02	rs7856131	9	13951462	p23
SNP_A-2121100	A	A	245	163	290	128	7.875	5.00E-03	rs1590263	9	13960315	p23
SNP_A-1829229	G	G	220	160	256	138	4.095	4.30E-02	rs7859915	9	13998652	p23
SNP_A-2265375	T	T	231	175	264	148	4.413	3.57E-02	rs7848012	9	14002182	p23
SNP_A-1719691	A	C	194	158	218	172	8.974	2.70E-03	rs1322132	9	14007543	p23
SNP_A-2172702	T	T	277	137	252	168	4.289	3.84E-02	rs480700	9	14069067	p23
SNP_A-2224495	T	T	218	112	187	139	5.253	2.19E-02	rs7034211	9	14127320	p22.3
SNP_A-2305710	G	G	247	149	270	120	4.104	4.28E-02	rs10961464	9	14282138	p22.3
SNP_A-2183600	G	G	256	154	280	126	3.855	4.96E-02	rs10810126	9	14282207	p22.3
SNP_A-2250467	C	C	345	69	324	92	3.94	4.71E-02	rs10810132	9	14328470	p22.3
SNP_A-1863010	T	T	389	13	377	25	3.977	4.61E-02	rs10961499	9	14382298	p22.3
SNP_A-2205238	C	T	217	195	218	184	3.874	4.90E-02	rs10481545	9	14386833	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1725108	C	C	236	156	217	195	4.636	3.13E-02	rs7846762	9	14412276	p22.3
SNP_A-2054541	A	A	257	101	242	132	4.228	3.98E-02	rs1008943	9	14424738	p22.3
SNP_A-2206932	C	C	269	99	246	138	7.108	7.70E-03	rs2039052	9	14425335	p22.3
SNP_A-1995996	T	T	340	76	374	46	8.977	2.70E-03	rs498591	9	14499105	p22.3
SNP_A-2153964	A	A	399	15	385	31	5.81	1.59E-02	rs4741389	9	14507555	p22.3
SNP_A-2073276	C	C	270	134	289	103	4.521	3.35E-02	rs10810175	9	14525957	p22.3
SNP_A-1842580	T	T	369	33	385	17	5.46	0.0195	rs3850440	9	14563052	p22.3
SNP_A-2123336	T	T	187	161	237	147	4.774	2.89E-02	rs7029906	9	14575052	p22.3
SNP_A-2203120	A	A	239	103	268	80	4.498	0.0339	rs7852534	9	14586528	p22.3
SNP_A-1903385	T	T	358	18	378	8	4.259	0.039	rs4741411	9	14606371	p22.3
SNP_A-2221286	G	G	372	36	338	78	17.026	3.69E-05	rs3209160	9	14608316	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1916603	C	C	377	9	347	37	18.282	0.000019055	rs10756592	9	14629392	p22.3
SNP_A-1737441	T	T	352	48	339	71	4.567	3.26E-02	rs2131882	9	14706849	p22.3
SNP_A-1996006	C	C	313	79	287	107	5.337	2.09E-02	rs4741421	9	14721449	p22.3
SNP_A-1941721	G	G	328	72	352	44	7.586	5.90E-03	rs10810242	9	14779400	p22.3
SNP_A-2145667	A	A	321	59	331	33	7.16	7.50E-03	rs4146764	9	15056888	p22.3
SNP_A-1898101	G	G	366	26	378	12	5.346	2.08E-02	rs2800572	9	15130728	p22.3
SNP_A-1996017	T	T	316	54	322	34	4.334	3.74E-02	rs3853430	9	15262230	p22.3
SNP_A-1841139	T	T	365	33	403	13	10.183	0.0014	rs2798703	9	15383063	p22.3
SNP_A-1901788	A	A	367	49	394	26	7.992	4.70E-03	rs10122299	9	15406659	p22.3
SNP_A-2303420	C	C	360	26	388	10	7.977	4.70E-03	rs2064030	9	15465447	p22.3
SNP_A-1927869	G	G	370	34	398	14	9.277	0.0023	rs741930	9	15466524	p22.3
SNP_A-1654151	C	C	334	64	375	35	10.69	1.10E-03	rs1828383	9	15515054	p22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189748	A	A	332	30	381	15	6.856	8.80E-03	rs7860339	9	15533074	p22.3
SNP_A-2151355	G	G	377	35	404	14	9.891	1.70E-03	rs9407623	9	15556222	p22.3
SNP_A-1851511	T	T	287	35	309	15	8.806	3.00E-03	rs811282	9	15568017	p22.3
SNP_A-1842650	C	C	380	32	396	16	5.663	1.73E-02	rs4741537	9	15728447	p22.3
SNP_A-2014078	T	T	370	26	396	8	10.333	1.30E-03	rs958870	9	15732241	p22.3
SNP_A-1692340	C	C	363	37	395	17	8.583	3.40E-03	rs1417974	9	15745257	p22.3
SNP_A-1744389	C	C	363	37	395	17	8.583	3.40E-03	rs1417975	9	15745674	p22.3
SNP_A-1925819	A	A	367	33	384	12	10.165	0.0014	rs10810445	9	15761541	p22.3
SNP_A-1892844	A	A	393	5	386	0	4.88	2.72E-02	rs7866899	9	15862847	p22.3
SNP_A-1857206	C	C	289	115	317	89	4.603	3.19E-02	rs11887665	9	15994012	p22.3
SNP_A-2286799	G	G	362	6	356	16	4.574	3.25E-02	rs10962312	9	16164296	p22.3
SNP_A-2265766	C	C	282	134	240	166	6.672	9.80E-03	rs7857417	9	16314261	p22.3
SNP_A-2077218	C	T	197	153	195	163	8.191	4.20E-03	rs9298760	9	16366437	p22.3
SNP_A-2211088	C	C	378	12	391	3	5.6	1.80E-02	rs16934875	9	16633147	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1996051	C	C	315	101	337	71	5.898	0.0152	rs10511625	9	16683969	p22.2
SNP_A-1996052	C	C	308	92	337	69	4.545	3.30E-02	rs4961736	9	16684210	p22.2
SNP_A-2029588	G	G	270	88	311	69	4.541	3.31E-02	rs10733314	9	16684836	p22.2
SNP_A-1996053	A	A	286	66	303	39	7.291	6.90E-03	rs1888207	9	16686187	p22.2
SNP_A-1996054	G	G	304	102	321	73	5.089	0.0241	rs10738446	9	16686510	p22.2
SNP_A-2102097	T	T	284	90	311	69	3.951	4.68E-02	rs10962542	9	16688234	p22.2
SNP_A-2205380	T	T	349	47	369	29	4.815	2.82E-02	rs4961497	9	16787461	p22.2
SNP_A-1692212	A	A	352	48	382	30	5.204	2.25E-02	rs7861010	9	16794082	p22.2
SNP_A-1829854	C	C	284	114	322	90	4.966	2.59E-02	rs10962612	9	16794167	p22.2
SNP_A-2151046	A	A	204	202	235	165	5.875	0.0154	rs1416742	9	16846883	p22.2
SNP_A-2211656	T	T	203	199	236	160	6.673	9.80E-03	rs3927680	9	16877366	p22.2
SNP_A-2124045	G	G	243	163	281	125	7.77	0.0053	rs10810661	9	16893850	p22.2
SNP_A-2081015	C	C	226	166	267	123	9.803	1.70E-03	rs7032175	9	16894080	p22.2
SNP_A-1908496	A	A	199	149	239	101	12.778	4.00E-04	rs7868583	9	16896359	p22.2
SNP_A-1943286	G	G	311	99	339	63	9.128	2.50E-03	rs10962691	9	16905105	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1918963	C	C	401	7	407	1	4.545	3.30E-02	—	9	17563561	p22.2
SNP_A-1937688	T	T	268	94	278	52	10.809	0.001	rs1998246	9	17621208	p22.2
SNP_A-2170719	G	G	370	32	381	17	4.733	2.96E-02	rs12553667	9	17626245	p22.2
SNP_A-1863333	A	A	340	6	344	0	6.018	1.42E-02	rs16935846	9	17646489	p22.2
SNP_A-1959235	A	A	342	8	307	1	4.67	3.07E-02	rs1755276	9	17932032	p22.2
SNP_A-2149477	G	G	384	32	402	18	4.313	0.0378	rs1284013	9	18030586	p22.2
SNP_A-2058071	C	T	181	157	189	155	4.919	2.66E-02	rs4961623	9	18109147	p22.2
SNP_A-2128245	C	C	370	20	396	6	8.241	4.10E-03	rs11789982	9	18172756	p22.2
SNP_A-1848770	C	C	200	154	232	120	6.584	0.0103	rs7039917	9	18251780	p22.2
SNP_A-1707071	G	G	361	39	395	15	12.074	5.00E-04	rs10511641	9	18282118	p22.2
SNP_A-1842527	C	C	256	80	229	103	4.37	3.66E-02	rs10119710	9	18315722	p22.2
SNP_A-2215080	C	C	341	47	374	30	4.955	2.60E-02	rs1411153	9	18353377	p22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1704495	C	C	339	57	374	36	6.219	0.0126	rs10511651	9	18373853	p22.2
SNP_A-1952335	G	G	227	185	257	157	4.147	4.17E-02	rs1281350	9	18463576	p22.2
SNP_A-1914971	G	G	274	130	291	99	4.463	3.46E-02	rs1341063	9	18465203	p22.2
SNP_A-1960583	A	A	311	33	278	48	4.146	4.17E-02	rs7868026	9	18517580	p22.1
SNP_A-1742743	G	G	272	128	312	100	6.002	0.0143	rs10511660	9	18520100	p22.1
SNP_A-1861942	C	C	283	121	318	96	4.797	2.85E-02	rs17209122	9	18521228	p22.1
SNP_A-1829460	A	A	243	167	210	198	5.032	2.49E-02	rs1889007	9	18596825	p22.1
SNP_A-2177004	C	C	250	146	227	183	5.028	2.49E-02	rs10810995	9	18604724	p22.1
SNP_A-1909514	T	T	326	0	314	6	6.17	1.30E-02	rs10963670	9	18605000	p22.1
SNP_A-2074418	C	C	289	127	264	156	4.083	4.33E-02	rs6475236	9	18614888	p22.1
SNP_A-1996121	A	A	264	76	291	55	4.628	0.0315	rs10511661	9	18644351	p22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2087070	G	G	356	26	337	49	7.554	6.00E-03	rs10963714	9	18655453	p22.1
SNP_A-2093039	A	A	371	9	385	21	4.204	4.03E-02	rs10963751	9	18761613	p22.1
SNP_A-1915301	A	A	221	175	252	138	6.36	0.0117	rs1897725	9	18856563	p22.1
SNP_A-2185962	G	G	398	4	345	11	4.271	3.88E-02	rs10964136	9	19424980	p22.1
SNP_A-2260987	A	A	265	71	263	105	5.132	0.0235	rs7851478	9	19643530	p22.1
SNP_A-1849257	A	A	374	0	393	5	4.729	2.97E-02	rs10964263	9	19732145	p22.1
SNP_A-1677822	G	G	385	15	378	30	4.986	2.56E-02	rs10511673	9	19868076	p22.1
SNP_A-2192149	A	A	349	19	350	6	6.564	0.0104	rs1319332	9	20182495	p21.3
SNP_A-1864387	A	A	366	32	378	18	4.109	4.27E-02	rs7046901	9	20236894	p21.3
SNP_A-2162374	T	T	373	25	382	8	8.785	3.00E-03	rs12553948	9	20253186	p21.3
SNP_A-1782231	G	G	381	31	401	15	6.058	0.0138	rs7041951	9	20265354	p21.3
SNP_A-2288833	C	C	307	9	364	2	5.661	1.73E-02	rs10964520	9	20288585	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2056021	G	G	264	76	299	59	3.855	4.96E-02	rs17177890	9	20443684	p21.3
SNP_A-1920128	T	T	389	23	406	10	5.466	1.94E-02	rs10964641	9	20631087	p21.3
SNP_A-1880359	G	G	362	52	345	73	3.918	4.78E-02	rs16938524	9	21663153	p21.3
SNP_A-2233684	C	C	333	51	315	73	4.383	3.63E-02	rs16938527	9	21663608	p21.3
SNP_A-1996213	G	G	333	43	352	24	5.915	1.50E-02	rs1377199	9	21674689	p21.3
SNP_A-1928998	C	C	198	196	232	166	5.154	2.32E-02	rs1889680	9	21685460	p21.3
SNP_A-1860184	G	A	203	199	230	174	4.466	3.46E-02	rs1452658	9	21690795	p21.3
SNP_A-1809418	A	C	184	180	210	154	4.97	0.0258	rs10811584	9	21691005	p21.3
SNP_A-2101214	T	C	192	176	212	156	7.064	7.90E-03	rs7848524	9	21691432	p21.3
SNP_A-1905466	T	T	198	120	173	167	8.656	0.0033	rs10811586	9	21691942	p21.3
SNP_A-2108548	A	A	252	150	219	197	8.441	3.70E-03	rs10811590	9	21698883	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1646060	G	A	201	193	234	168	6.808	9.10E-03	rs1335500	9	21701675	p21.3
SNP_A-1670157	C	G	192	182	214	158	5.883	1.53E-02	rs1335501	9	21701815	p21.3
SNP_A-2250746	G	T	224	184	208	192	3.852	4.97E-02	rs7847574	9	21710481	p21.3
SNP_A-2086006	A	C	205	159	190	176	4.955	2.60E-02	rs7470965	9	21717208	p21.3
SNP_A-1955171	C	T	220	192	214	178	5.13	0.0235	rs10757238	9	21722466	p21.3
SNP_A-1996215	C	T	180	164	189	151	4.288	3.84E-02	rs1414237	9	21722912	p21.3
SNP_A-1797437	G	C	213	187	214	176	5.211	0.0224	rs7021538	9	21723204	p21.3
SNP_A-2014133	G	C	217	189	222	186	5.029	2.49E-02	rs6475566	9	21723500	p21.3
SNP_A-2024528	A	G	217	191	226	190	4.652	0.031	rs4636294	9	21737803	p21.3
SNP_A-2170649	A	G	202	168	202	174	5.162	2.31E-02	rs1414242	9	21738239	p21.3
SNP_A-2081741	C	C	242	150	210	184	5.722	1.68E-02	rs1414243	9	21738433	p21.3
SNP_A-1910099	T	C	193	175	207	163	5.203	2.25E-02	rs1335508	9	21740587	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1996218	G	C	220	194	229	191	4.899	0.0269	rs7866540	9	21750396	p21.3
SNP_A-1996219	C	G	223	193	227	193	4.897	0.0269	rs9886831	9	21763167	p21.3
SNP_A-1996220	T	C	220	190	226	190	5.267	2.17E-02	rs2184551	9	21763222	p21.3
SNP_A-2156288	T	C	184	154	199	165	5.816	1.59E-02	rs7846749	9	21770251	p21.3
SNP_A-2151479	G	G	251	161	218	196	5.749	1.65E-02	rs1345024	9	21775018	p21.3
SNP_A-2297302	G	G	251	147	217	185	6.8	9.10E-03	rs10757257	9	21796564	p21.3
SNP_A-2163185	A	G	207	197	232	172	6.088	1.36E-02	rs7027989	9	21807754	p21.3
SNP_A-2096752	A	A	247	151	204	182	6.804	9.10E-03	rs3900787	9	21818110	p21.3
SNP_A-1996224	A	A	303	101	283	133	4.884	2.71E-02	rs4636295	9	21844199	p21.3
SNP_A-1842798	G	G	264	152	233	181	4.454	3.48E-02	rs7039105	9	21845096	p21.3
SNP_A-2259355	A	A	308	60	289	83	4.282	0.0385	rs4977736	9	21859079	p21.3
SNP_A-2027423	A	G	225	179	205	191	4.46	3.47E-02	rs10757272	9	22078260	p21.3
SNP_A-2035117	G	A	218	184	225	187	6.361	0.0117	rs4977574	9	22088574	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2150146	G	A	211	175	203	171	6.075	0.0137	rs2891168	9	22088619	p21.3
SNP_A-1699309	A	C	223	177	218	194	6.096	0.0135	rs1537371	9	22089568	p21.3
SNP_A-1676982	G	C	223	175	218	194	6.482	0.0109	rs1556516	9	22090176	p21.3
SNP_A-1648126	C	T	223	175	217	195	6.135	0.0132	rs10511701	9	22102599	p21.3
SNP_A-2123726	C	C	373	35	346	56	5.816	1.59E-02	rs1333053	9	22152238	p21.3
SNP_A-2266893	C	C	275	105	297	81	3.938	4.72E-02	rs613391	9	22660715	p21.3
SNP_A-2154490	T	T	250	150	278	122	4.367	3.66E-02	rs10123750	9	22718754	p21.3
SNP_A-1712015	T	T	361	33	381	19	4.263	3.89E-02	rs1999761	9	22785727	p21.3
SNP_A-1802768	A	A	350	14	307	3	5.642	1.75E-02	rs10733382	9	22954237	p21.3
SNP_A-2130853	A	A	272	66	273	37	6.97	8.30E-03	rs9407994	9	23154275	p21.3
SNP_A-2160632	T	T	263	117	279	85	5.2	2.26E-02	rs10965703	9	23204360	p21.3
SNP_A-1996247	G	G	283	109	317	81	6.008	1.42E-02	rs1339140	9	23212186	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1935195	A	A	297	107	270	134	4.311	3.79E-02	rs10738655	9	23256412	p21.3
SNP_A-1792732	G	G	302	110	269	137	4.815	2.82E-02	rs9792599	9	23257924	p21.3
SNP_A-2281849	C	C	255	113	223	137	4.359	3.68E-02	rs10156548	9	23308433	p21.3
SNP_A-1996245	G	G	337	27	341	13	4.785	0.0287	rs16907121	9	23331848	p21.3
SNP_A-1729370	C	A	189	159	205	181	4.03	4.47E-02	rs10511725	9	23416193	p21.3
SNP_A-1780683	C	C	398	18	407	5	7.429	6.40E-03	rs16907489	9	23646538	p21.3
SNP_A-2027288	G	G	361	25	352	12	4.039	4.45E-02	rs9696499	9	23681051	p21.3
SNP_A-1712527	G	G	340	42	368	26	4.688	0.0304	rs1450586	9	23996322	p21.3
SNP_A-1660371	C	C	328	26	354	14	4.321	3.76E-02	rs10511736	9	24041805	p21.3
SNP_A-1643293	C	C	347	49	375	33	4.03	4.47E-02	rs10511737	9	24041864	p21.3
SNP_A-2166101	A	A	336	72	311	95	4.129	4.22E-02	rs10124866	9	24165234	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2300576	G	G	314	58	286	78	4.161	4.14E-02	rs17698894	9	24231833	p21.3
SNP_A-2130736	A	A	388	8	380	18	3.924	4.76E-02	rs10966290	9	24332423	p21.3
SNP_A-1996292	G	G	368	36	390	22	3.94	4.72E-02	rs10511745	9	24776754	p21.3
SNP_A-2100747	G	G	282	76	290	52	4.248	3.93E-02	rs10812143	9	24933020	p21.3
SNP_A-1861473	A	A	406	4	399	13	4.821	0.0281	rs10966584	9	24943245	p21.3
SNP_A-2099410	T	T	309	55	333	33	6.392	0.0115	rs10115443	9	24976518	p21.3
SNP_A-2202893	C	C	324	28	276	40	4.029	4.47E-02	rs12337176	9	25168084	p21.3
SNP_A-2112387	A	A	335	7	277	19	7.759	0.0053	rs3118339	9	25174960	p21.3
SNP_A-2275743	T	T	400	4	369	17	8.892	2.90E-03	rs3118341	9	25175519	p21.3
SNP_A-2256590	C	C	371	1	368	10	7.328	6.80E-03	rs7022191	9	25184951	p21.3
SNP_A-2259236	A	A	411	3	400	16	9.039	2.60E-03	rs1126130	9	25199347	p21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2084394	T	T	394	4	373	17	8.542	3.50E-03	rs1998746	9	25201762	p21.3
SNP_A-2064555	C	C	412	4	405	15	6.409	0.0114	rs987434	9	25210584	p21.3
SNP_A-1889931	G	G	408	8	417	1	5.538	1.86E-02	rs17783121	9	25374959	p21.3
SNP_A-2184454	T	T	320	88	280	118	6.913	0.0086	rs7861656	9	25442963	p21.3
SNP_A-2251436	T	T	318	88	279	123	8.334	3.90E-03	rs10966920	9	25445760	p21.3
SNP_A-2116064	C	C	323	47	354	26	7.329	6.80E-03	rs546921	9	25928342	p21.2
SNP_A-2022576	A	A	394	16	404	6	4.671	3.07E-02	rs16910024	9	25978972	p21.2
SNP_A-2080176	T	T	400	16	414	6	4.767	2.90E-02	rs2891276	9	25983272	p21.2
SNP_A-2113308	A	A	364	38	369	19	6.121	0.0134	rs10812352	9	26106553	p21.2
SNP_A-1909731	T	T	350	8	357	1	5.514	0.0189	rs1529823	9	26258907	p21.2
SNP_A-2156785	T	T	330	22	317	7	6.872	8.80E-03	rs2618013	9	26304368	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2178258	A	A	207	107	243	89	4.035	4.46E-02	rs1328425	9	26447170	p21.2
SNP_A-1862588	G	G	185	157	224	98	16.783	4.19E-05	rs12554071	9	26469388	p21.2
SNP_A-1706725	C	C	201	199	238	168	5.693	1.70E-02	rs10511790	9	26495918	p21.2
SNP_A-1644256	A	A	203	157	235	133	4.237	3.96E-02	rs1854313	9	26496732	p21.2
SNP_A-1660097	T	C	207	193	231	181	4.972	0.0258	rs4111166	9	26514416	p21.2
SNP_A-1700951	G	A	199	185	227	177	5.064	2.44E-02	rs4978076	9	26514684	p21.2
SNP_A-1697074	G	G	217	163	257	141	4.554	3.28E-02	rs994390	9	26528805	p21.2
SNP_A-2266128	A	A	217	197	257	161	6.977	8.30E-03	rs1112312	9	26529976	p21.2
SNP_A-1902756	G	G	403	1	399	9	6.4	0.0114	rs10967389	9	26530641	p21.2
SNP_A-2271075	T	T	297	13	299	31	6.752	9.40E-03	rs10757627	9	26740142	p21.2
SNP_A-2041379	A	A	365	19	353	7	4.97	0.0258	—	9	26742499	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2085996	C	C	308	90	288	116	3.908	4.81E-02	rs10812520	9	27037246	p21.2
SNP_A-1960610	C	C	392	24	409	11	5.17	0.023	rs1322051	9	27175101	p21.2
SNP_A-2303002	A	A	379	35	401	19	5.318	2.11E-02	rs16911416	9	27326207	p21.2
SNP_A-2257027	A	A	201	141	229	111	5.389	2.03E-02	rs10967916	9	27365843	p21.2
SNP_A-2309779	G	G	378	4	388	0	4.084	4.33E-02	rs2764324	9	27502928	p21.2
SNP_A-1996376	C	C	408	4	420	0	4.097	4.29E-02	rs700783	9	27515522	p21.2
SNP_A-2287168	A	A	292	32	350	10	14.91	0.0001	rs10967981	9	27542193	p21.2
SNP_A-1996385	T	T	321	87	297	111	3.841	5.00E-02	rs7043861	9	27678904	p21.2
SNP_A-2202610	T	C	189	177	195	151	4.56	0.0327	rs7019732	9	27743085	p21.2
SNP_A-2122229	G	G	370	24	361	9	6.181	0.0129	rs10114706	9	27792678	p21.2
SNP_A-2143280	C	C	388	22	407	11	4.044	4.43E-02	rs4878586	9	27800414	p21.2
SNP_A-2092559	C	C	392	22	407	9	5.728	0.0167	rs7861951	9	27808130	p21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1933973	G	G	364	22	381	9	5.819	1.59E-02	rs10812667	9	27809540	p21.2
SNP_A-2268900	T	T	353	13	378	4	5.28	2.16E-02	rs17780713	9	27855212	p21.2
SNP_A-1758232	A	A	337	57	368	40	4.099	4.29E-02	rs7849119	9	27886017	p21.2
SNP_A-2092025	A	A	357	53	379	33	5.304	2.13E-02	rs10968179	9	27889983	p21.2
SNP_A-2171731	G	G	381	21	394	8	6.046	1.39E-02	rs4524882	9	28285781	p21.1
SNP_A-2044279	T	T	378	20	390	8	5.33	2.10E-02	rs4481691	9	28285916	p21.1
SNP_A-1701383	C	C	344	44	343	67	4.164	4.13E-02	rs10491896	9	28344180	p21.1
SNP_A-1714435	C	C	199	191	223	161	3.875	4.90E-02	rs10491894	9	28366487	p21.1
SNP_A-1699977	G	G	392	6	390	18	5.882	1.53E-02	rs13331877	9	28366865	p21.1
SNP_A-2179511	G	G	370	14	371	5	4.181	4.09E-02	rs10114788	9	28417026	p21.1
SNP_A-1840771	C	C	355	21	363	9	4.868	2.74E-02	rs1347791	9	28700492	p21.1
SNP_A-2238173	G	G	393	19	396	6	6.65	9.90E-03	rs16913672	9	28783442	p21.1
SNP_A-2114969	C	T	195	153	174	160	4.514	3.36E-02	rs10968773	9	28785700	p21.1
SNP_A-2035704	G	G	368	38	381	21	5.104	2.39E-02	rs16913782	9	28866158	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2052181	G	G	352	16	379	7	4.092	4.31E-02	rs1368998	9	28869953	p21.1
SNP_A-1949469	A	A	271	119	301	91	5.302	2.13E-02	rs1928655	9	29209672	p21.1
SNP_A-1957664	G	G	267	147	240	180	4.725	2.97E-02	rs10969018	9	29216791	p21.1
SNP_A-2283849	C	C	374	26	381	11	6.066	0.0138	rs17588789	9	29218231	p21.1
SNP_A-1786403	A	A	319	25	347	11	6.345	0.0118	rs10116577	9	29271634	p21.1
SNP_A-1812976	A	A	313	57	256	82	8.778	3.00E-03	rs1169752	9	29319933	p21.1
SNP_A-1942632	A	A	338	78	303	109	7.031	8.00E-03	rs1169750	9	29321763	p21.1
SNP_A-1674695	A	A	284	80	304	58	4.182	4.09E-02	rs10491663	9	29329044	p21.1
SNP_A-1732976	G	G	281	119	318	94	5.044	0.0247	rs1929829	9	29344639	p21.1
SNP_A-2155641	C	C	227	141	208	174	4.027	0.0448	rs10969134	9	29398234	p21.1
SNP_A-1684998	T	C	210	160	170	164	4.131	4.21E-02	rs4879352	9	29447656	p21.1
SNP_A-1753719	C	C	287	113	324	88	5.174	0.0229	rs10491672	9	29486811	p21.1
SNP_A-1957876	C	C	376	18	389	5	7.569	5.90E-03	rs1482073	9	29638921	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2014189	G	G	263	117	297	91	5.232	2.22E-02	rs4355871	9	29643331	p21.1
SNP_A-1725706	T	T	294	106	328	82	4.8	2.85E-02	rs953639	9	29694495	p21.1
SNP_A-1960547	C	C	406	10	417	3	3.897	4.84E-02	rs6476155	9	29807453	p21.1
SNP_A-2014190	A	A	248	108	259	77	4.859	0.0275	rs6476168	9	29889865	p21.1
SNP_A-2014191	G	G	288	128	320	98	5.662	1.73E-02	rs7848001	9	29889965	p21.1
SNP_A-1996476	A	A	203	159	232	134	4.045	4.43E-02	rs4242678	9	29918566	p21.1
SNP_A-2014194	A	A	282	130	314	104	4.564	0.0327	rs4451394	9	29918676	p21.1
SNP_A-1737665	C	C	327	73	355	53	4.245	3.94E-02	rs2502107	9	29929173	p21.1
SNP_A-2152934	G	G	289	33	312	20	3.917	4.78E-02	rs16915477	9	29981403	p21.1
SNP_A-1651890	G	G	265	135	238	172	5.786	1.62E-02	rs1361925	9	30075410	p21.1
SNP_A-2314754	C	C	262	124	224	148	4.832	2.79E-02	rs7848878	9	30079859	p21.1
SNP_A-2036842	C	C	404	0	412	4	3.904	0.0482	rs11999552	9	30341247	p21.1
SNP_A-2248976	T	T	389	7	393	1	4.515	3.36E-02	rs1335159	9	31137840	p21.1
SNP_A-2021563	G	G	178	124	164	162	4.712	3.00E-02	rs10970148	9	31143852	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1923398	T	T	334	38	314	56	4.059	4.39E-02	rs17180162	9	31625015	p21.1
SNP_A-1996526	C	C	336	28	320	44	3.946	0.047	rs895287	9	31646205	p21.1
SNP_A-1996529	C	C	323	49	300	76	6.66	9.90E-03	rs10511884	9	31668988	p21.1
SNP_A-1751507	T	T	349	25	377	13	4.536	0.0332	rs10511889	9	31973460	p21.1
SNP_A-1674036	A	A	247	139	218	168	4.548	3.30E-02	rs10511907	9	32455446	p21.1
SNP_A-1674331	A	A	395	5	412	0	5.182	2.28E-02	rs2274863	9	32477521	p21.1
SNP_A-1996550	A	A	279	71	239	91	4.974	2.57E-02	rs629566	9	32563602	p21.1
SNP_A-2097649	A	A	329	43	371	21	9.565	0.002	rs10971153	9	32808679	p21.1
SNP_A-1905375	T	T	353	55	387	31	8.14	0.0043	rs1409691	9	32816852	p21.1
SNP_A-1922761	A	A	352	52	330	74	4.551	3.29E-02	rs10813889	9	32870568	p21.1
SNP_A-1887464	G	G	360	56	338	78	4.305	3.80E-02	rs10813890	9	32876064	p21.1
SNP_A-2067865	G	G	362	0	270	12	15.697	7.44E-05	rs1360518	9	32939218	p21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2075757	A	A	353	63	321	91	6.591	1.02E-02	rs3818593	9	33110706	p21.1
SNP_A-2239069	A	A	327	83	306	110	4.431	3.53E-02	rs12342831	9	33114872	p21.1
SNP_A-1643071	G	G	359	39	353	59	3.891	4.85E-02	rs10511909	9	33122518	p21.1
SNP_A-1785357	C	C	355	15	346	4	5.933	0.0149	rs1065765	9	33125238	p21.1
SNP_A-2230961	C	C	362	12	343	25	5.031	2.49E-02	rs13285633	9	33176788	p21.1
SNP_A-2303507	T	T	346	42	350	18	9.1	2.60E-03	rs545575	9	33193602	p21.1
SNP_A-2212149	T	T	221	115	254	90	5.248	2.20E-02	rs2992817	9	33439683	p13.3
SNP_A-2206472	G	G	335	1	347	7	4.244	3.94E-02	rs12683438	9	33451299	p13.3
SNP_A-2199716	G	G	239	145	205	169	4.307	3.80E-02	rs2178824	9	33755513	p13.3
SNP_A-1828710	C	C	307	97	266	132	8.239	4.10E-03	rs1543604	9	34030797	p13.3
SNP_A-1996584	C	C	324	46	344	30	3.946	0.047	rs10511915	9	34097310	p13.3
SNP_A-2181283	G	G	341	65	345	43	4.099	4.29E-02	rs7875342	9	34319110	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2310273	G	G	366	20	330	34	4.851	0.0276	rs10972101	9	34407750	p13.3
SNP_A-2199946	C	C	335	51	314	74	4.906	2.68E-02	rs10972105	9	34409752	p13.3
SNP_A-1706453	C	C	238	42	247	101	17.35	0.000031089	rs1080750	9	34571525	p13.3
SNP_A-2114226	G	G	398	2	403	9	4.309	3.79E-02	rs2842376	9	34815149	p13.3
SNP_A-1824165	T	T	348	68	322	96	5.785	1.62E-02	rs1061677	9	34972014	p13.3
SNP_A-1799936	C	G	225	173	205	189	5.819	1.59E-02	rs885451	9	34987569	p13.3
SNP_A-1895252	G	G	241	117	201	151	7.883	5.00E-03	rs6309961	9	35093722	p13.3
SNP_A-2305270	A	G	191	175	225	151	10.796	0.001	rs10758321	9	35757753	p13.3
SNP_A-2229847	T	T	328	40	350	24	4.666	3.08E-02	rs3818556	9	36194518	p13.3
SNP_A-2281999	G	G	324	88	348	62	5.359	0.0206	rs7036926	9	36219596	p13.2
SNP_A-1825193	C	C	315	91	336	64	5.336	2.09E-02	rs2182818	9	36272084	p13.2
SNP_A-2109760	G	G	196	114	246	98	5.11	2.38E-02	rs10814373	9	36296809	p13.2
SNP_A-1908655	G	G	181	145	225	123	5.863	0.0155	rs10114094	9	36297152	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1892845	G	G	216	166	253	145	4.01	4.52E-02	rs10758368	9	36300778	p13.2
SNP_A-2308067	T	T	354	0	340	6	6.192	1.28E-02	rs2252429	9	36769081	p13.2
SNP_A-2257941	C	C	408	0	400	4	4.06	4.39E-02	rs2805380	9	36772487	p13.2
SNP_A-2297693	G	G	403	13	389	25	4.032	4.46E-02	rs10814468	9	36885144	p13.2
SNP_A-2273180	C	A	151	127	190	160	4.586	3.22E-02	rs4878668	9	36918909	p13.2
SNP_A-2263979	C	C	401	5	406	0	5.031	2.49E-02	rs2297107	9	37010361	p13.2
SNP_A-1787609	G	G	202	116	188	148	3.889	4.86E-02	rs7854466	9	37046816	p13.2
SNP_A-1804735	G	G	295	25	311	13	4.187	0.0407	rs10973207	9	37090525	p13.2
SNP_A-1876950	G	G	368	36	382	20	4.828	2.80E-02	rs17408134	9	37106493	p13.2
SNP_A-1837248	C	C	320	50	337	23	10.291	1.30E-03	rs12376809	9	37115911	p13.2
SNP_A-1886422	T	T	378	38	396	22	4.681	3.05E-02	rs17487039	9	37151736	p13.2
SNP_A-2251572	T	T	329	5	330	0	4.978	2.57E-02	rs308494	9	37267831	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1809738	G	G	246	116	250	84	4.032	4.46E-02	rs1475414	9	37516448	p13.2
SNP_A-2055823	C	C	386	4	402	0	4.144	4.18E-02	rs10973405	9	37537256	p13.2
SNP_A-1867532	C	C	398	4	390	0	3.9	4.83E-02	rs7850851	9	37918771	p13.2
SNP_A-1746797	C	C	312	88	345	67	4.326	3.75E-02	rs10511947	9	38241684	p13.1
SNP_A-2310265	C	C	329	17	334	32	4.071	0.0436	rs10973720	9	38253103	p13.2
SNP_A-1996658	A	A	276	72	317	53	5.053	0.0246	rs13729337	9	38302710	p13.2
SNP_A-2080741	G	G	401	13	415	3	6.471	1.10E-02	—	9	64214598	q12
SNP_A-2228263	G	G	215	179	248	148	5.286	2.15E-02	rs11143589	9	68585573	q13
SNP_A-1850884	A	A	380	32	379	17	4.278	3.86E-02	rs3002375	9	69028721	q21.11
SNP_A-2074395	G	G	255	89	233	117	4.746	2.94E-02	rs10869994	9	69039386	q21.11
SNP_A-1720297	G	G	362	38	349	63	6.25	0.0124	rs688933	9	69130278	q21.11
SNP_A-2091299	A	A	351	31	356	16	4.691	3.03E-02	rs11138342	9	69214705	q21.11
SNP_A-2244791	T	T	298	82	257	105	5.424	1.99E-02	rs2781542	9	69320360	q21.11
SNP_A-1936712	C	C	292	70	272	98	5.289	2.15E-02	rs4744569	9	69337395	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1797478	T	T	329	53	305	77	5.339	2.09E-02	rs10867656	9	69338341	q21.11
SNP_A-2029379	T	T	302	46	275	67	5.114	2.37E-02	rs7866199	9	69363981	q21.11
SNP_A-2174611	G	G	327	45	314	68	4.813	2.82E-02	rs7872660	9	69383051	q21.11
SNP_A-1918833	T	T	253	103	212	140	9.226	2.40E-03	rs11139338	9	69404082	q21.11
SNP_A-2039715	C	C	245	135	216	174	6.618	0.0101	rs10780527	9	69415248	q21.11
SNP_A-2210012	C	C	250	136	226	178	6.421	1.13E-02	rs10780528	9	69415305	q21.11
SNP_A-1789269	G	G	268	92	216	130	11.818	6.00E-04	rs6559643	9	69426133	q21.11
SNP_A-1814819	A	A	238	126	215	159	4.854	0.0276	rs11139511	9	69461489	q21.11
SNP_A-2291045	T	T	251	139	229	177	5.258	0.0218	rs1493050	9	69690162	q21.11
SNP_A-1996728	C	C	268	110	243	139	4.58	3.24E-02	rs10780682	9	69702385	q21.11
SNP_A-1811627	C	C	222	184	261	159	4.735	2.95E-02	rs7875361	9	69702971	q21.11
SNP_A-2240902	G	G	205	167	242	134	6.659	9.90E-03	rs10868224	9	69709217	q21.11
SNP_A-1996729	G	G	190	146	222	118	5.432	1.98E-02	rs10780685	9	69712584	q21.11
SNP_A-1857984	C	C	197	129	226	104	4.646	3.11E-02	rs6559842	9	69737934	q21.11
SNP_A-2211862	A	A	333	51	317	79	6.241	1.25E-02	rs1493056	9	69828957	q21.11
SNP_A-2220436	T	T	285	29	318	54	4.464	3.46E-02	rs951770	9	69862350	q21.11
SNP_A-1883451	A	A	334	42	339	25	4.157	4.15E-02	rs1073540	9	70059368	q21.11
SNP_A-2174190	G	G	264	94	286	70	4.387	3.62E-02	rs1927098	9	70064759	q21.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1913781	G	G	265	143	306	110	7.171	7.40E-03	rs4745013	9	70317157	q21.11
SNP_A-2076416	T	T	339	41	329	61	3.942	4.71E-02	rs4416891	9	70722520	q21.11
SNP_A-2152050	C	C	288	110	315	79	6.274	0.0123	rs7849064	9	70767708	q21.11
SNP_A-1887164	C	C	344	20	320	34	4.359	3.68E-02	rs3124516	9	70834485	q21.12
SNP_A-1915400	C	C	340	18	323	35	5.889	0.0152	rs17520103	9	70844615	q21.12
SNP_A-1839296	T	T	369	35	304	46	3.924	4.76E-02	rs649375	9	70869003	q21.12
SNP_A-1948470	A	A	292	6	312	18	5.045	0.0247	rs2309968	9	71351894	q21.13
SNP_A-2206044	A	A	219	135	210	92	4.239	0.0395	rs6560224	9	71498277	q21.13
SNP_A-2059417	T	T	367	49	388	32	4.133	4.21E-02	rs942395	9	71887840	q21.13
SNP_A-1692916	C	C	272	120	257	155	4.385	3.63E-02	rs3000646	9	72134857	q21.13
SNP_A-1854543	G	T	201	163	203	181	4.887	2.71E-02	rs753700	9	72226596	q21.13
SNP_A-1996806	A	A	175	163	201	135	4.423	3.55E-02	rs10781101	9	72276118	q21.13
SNP_A-2154491	C	T	228	186	219	197	4.945	2.62E-02	rs12004208	9	72321323	q21.13
SNP_A-2268473	A	G	223	169	200	196	4.324	3.76E-02	rs4132905	9	72326743	q21.13
SNP_A-1887819	C	-	238	176	209	209	4.691	3.03E-02	rs4373587	9	72360531	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101502	G	A	188	158	172	150	4.009	0.0453	rs13285999	9	72455259	q21.13
SNP_A-1816441	T	T	368	22	391	11	4.183	4.08E-02	rs7859898	9	72619466	q21.13
SNP_A-1900538	T	T	407	7	416	0	7.094	7.70E-03	rs17059048	9	73417810	q21.13
SNP_A-2098337	C	C	379	9	380	2	4.409	3.57E-02	rs2375762	9	73745845	q21.13
SNP_A-1996844	G	G	274	112	254	148	5.42	1.99E-02	rs2172162	9	73907002	q21.13
SNP_A-1906250	A	A	403	1	399	7	4.515	3.36E-02	rs6560370	9	73969489	q21.13
SNP_A-1905715	T	T	256	150	280	124	4.507	3.38E-02	rs4483218	9	73987618	q21.13
SNP_A-1924014	T	C	179	171	186	138	4.937	0.0263	rs11143810	9	73994203	q21.13
SNP_A-1822914	T	T	236	62	238	94	4.751	0.0293	rs4237262	9	74029371	q21.13
SNP_A-1793623	G	G	258	98	223	131	7.297	6.90E-03	rs7470366	9	74063031	q21.13
SNP_A-1898002	T	T	333	29	294	50	7.554	6.00E-03	rs2604271	9	74120966	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2307187	C	C	305	99	276	124	4.23	3.97E-02	rs2376055	9	74136745	q21.13
SNP_A-2191529	G	G	316	74	287	101	5.555	0.0184	rs517674	9	74138161	q21.13
SNP_A-2014273	A	A	390	4	398	0	4.061	4.39E-02	rs683416	9	74142929	q21.13
SNP_A-2103932	C	C	363	31	334	48	4.68	3.05E-02	rs2604270	9	74155237	q21.13
SNP_A-2306101	G	G	228	186	258	156	4.483	3.42E-02	rs10869398	9	74264533	q21.13
SNP_A-2195964	G	G	215	173	230	126	6.529	0.0106	rs10781226	9	74264984	q21.13
SNP_A-2128695	T	T	375	9	378	2	4.446	3.50E-02	rs4631535	9	74288491	q21.13
SNP_A-1785315	C	C	387	17	395	7	4.244	3.94E-02	rs17690782	9	74437076	q21.13
SNP_A-2245264	A	A	323	23	249	33	4.888	2.71E-02	rs7038344	9	74660918	q21.13
SNP_A-2130767	G	G	375	25	360	48	7.474	0.0063	rs1475717	9	74683694	q21.13
SNP_A-1996866	T	T	363	5	389	15	4.229	3.97E-02	rs773013	9	75012971	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2283421	C	C	316	74	299	103	5.041	2.48E-02	rs914660	9	75459893	q21.13
SNP_A-2224014	C	C	309	89	348	62	6.966	8.30E-03	rs12236539	9	76044952	q21.13
SNP_A-2078280	G	G	343	73	316	104	6.517	1.07E-02	rs11144794	9	76045646	q21.13
SNP_A-2134348	G	G	321	67	298	98	6.598	1.02E-02	rs11144795	9	76045806	q21.13
SNP_A-2190081	G	G	370	36	396	20	5.333	2.09E-02	rs10115735	9	76129715	q21.13
SNP_A-2181590	G	G	314	40	315	21	5.454	0.0195	rs10115755	9	76129737	q21.13
SNP_A-1664770	A	C	214	162	207	181	8.058	4.50E-03	rs4877178	9	76173999	q21.2
SNP_A-1652474	G	A	228	172	217	193	7.993	4.70E-03	rs10512069	9	76174695	q21.2
SNP_A-2155408	C	C	328	76	299	117	9.878	1.70E-03	rs10869758	9	76194930	q21.13
SNP_A-2253307	C	C	281	121	245	153	6.181	0.0129	rs2490572	9	76217199	q21.13
SNP_A-1780325	C	C	332	74	303	97	4.374	3.65E-02	rs10121699	9	76259352	q21.13
SNP_A-2280503	T	T	318	62	294	94	7.423	6.40E-03	rs7847608	9	76261981	q21.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2261083	G	G	258	82	243	109	4.059	4.39E-02	rs7388745	9	76277113	q21.13
SNP_A-1921605	T	T	352	48	358	28	5.066	2.44E-02	rs4745559	9	76386546	q21.13
SNP_A-1750383	A	A	334	62	366	42	5.131	0.0235	rs10521484	9	76423515	q21.2
SNP_A-2103078	G	G	398	4	398	0	3.98	4.60E-02	rs11144996	9	76501063	q21.2
SNP_A-2257081	A	A	223	155	242	122	4.445	3.50E-02	rs577993	9	76551425	q21.2
SNP_A-1895094	A	G	216	164	202	188	5.757	1.64E-02	rs7875530	9	77315744	q21.2
SNP_A-2178736	G	G	335	15	345	3	8.141	0.0043	rs12551471	9	77503636	q21.2
SNP_A-1801592	C	C	257	99	295	71	7.091	7.70E-03	rs4641131	9	77773806	q21.2
SNP_A-2068091	C	C	277	103	313	79	5.176	0.0229	rs10781474	9	77792532	q21.2
SNP_A-2292855	C	C	316	92	342	70	3.996	4.56E-02	rs7038332	9	77867247	q21.2
SNP_A-1996925	C	C	276	92	306	70	4.449	0.0349	rs964423	9	77896308	q21.2
SNP_A-2245376	G	G	290	70	325	47	6.318	0.012	rs10781482	9	77914394	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1996927	C	C	238	150	283	121	6.67	9.80E-03	rs9314866	9	77947503	q21.2
SNP_A-2233458	G	G	325	47	334	28	4.801	2.84E-02	rs10870048	9	77948346	q21.2
SNP_A-2098667	A	G	234	166	224	190	12.955	3.00E-04	rs7038083	9	77948549	q21.2
SNP_A-1996928	T	T	270	84	297	63	4.236	3.96E-02	rs10781494	9	77984619	q21.2
SNP_A-2045957	C	C	233	125	202	154	5.218	0.0224	rs7861244	9	78075460	q21.2
SNP_A-2169332	T	T	406	4	400	0	3.922	4.77E-02	rs11137617	9	78191209	q21.2
SNP_A-1996929	C	C	275	59	286	38	4.611	3.18E-02	rs3010739	9	78193918	q21.2
SNP_A-2139114	G	G	279	95	301	71	4.299	3.81E-02	rs1505638	9	78426450	q21.31
SNP_A-1858043	C	C	297	17	309	7	4.398	3.60E-02	rs11137864	9	78680945	q21.31
SNP_A-2243536	C	C	335	71	365	51	4.443	3.50E-02	rs11137878	9	78705304	q21.31
SNP_A-2065344	T	T	245	165	213	199	5.407	0.0201	rs984531	9	78991519	q21.31
SNP_A-2177065	A	A	296	112	323	87	4.314	0.0378	rs11138094	9	78991629	q21.31
SNP_A-1649858	G	G	235	99	228	132	3.851	4.97E-02	rs7855114	9	79015855	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1996941	A	C	228	186	244	170	16.276	5.48E-05	rs1118644	9	79131410	q21.31
SNP_A-1904364	C	C	350	52	315	77	6.562	0.0104	rs7027362	9	79137733	q21.31
SNP_A-2307968	T	T	206	198	230	164	4.39	3.62E-02	rs273439	9	79146767	q21.31
SNP_A-1833734	C	C	351	65	325	89	4.735	2.95E-02	rs1410493	9	79151806	q21.31
SNP_A-2111842	T	T	343	63	298	84	5.433	1.98E-02	rs11138143	9	79156532	q21.31
SNP_A-2137976	T	T	356	58	331	87	6.691	9.70E-03	rs7048193	9	79183011	q21.31
SNP_A-1955569	T	T	392	0	388	4	4.021	4.50E-02	rs7025706	9	79617077	q21.31
SNP_A-1996957	G	G	261	107	292	80	5.615	0.0178	rs4877519	9	79719965	q21.31
SNP_A-1862209	C	C	241	139	250	104	4.291	3.83E-02	rs267591	9	79743622	q21.31
SNP_A-2138807	G	G	245	143	216	172	4.494	3.40E-02	rs382479	9	79775742	q21.31
SNP_A-2175218	T	T	338	72	304	96	5.107	2.38E-02	rs1329577	9	79842593	q21.31
SNP_A-1949933	G	G	320	58	286	82	5.889	0.0152	rs10780348	9	79842883	q21.31
SNP_A-1895380	T	T	272	126	299	99	4.517	3.36E-02	rs17083204	9	80204873	q21.31
SNP_A-2274331	G	G	407	7	417	1	4.602	3.19E-02	rs1412762	9	80747032	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2280059	G	G	399	13	407	3	6.325	1.19E-02	rs10780470	9	80765761	q21.31
SNP_A-2119747	T	T	240	116	274	96	3.867	4.92E-02	rs11138926	9	80783263	q21.31
SNP_A-1659598	A	A	222	164	201	199	4.169	4.12E-02	rs534724	9	80800088	q21.32
SNP_A-1921746	T	T	341	39	358	24	3.98	4.61E-02	rs11139328	9	81426723	q21.32
SNP_A-2055335	A	A	240	114	198	140	6.322	1.19E-02	rs815845	9	81445644	q21.32
SNP_A-1756020	A	A	376	24	401	9	7.5	6.20E-03	rs7029848	9	82571987	q21.33
SNP_A-1707495	A	A	178	174	225	149	6.756	9.30E-03	rs726432	9	82704567	q21.33
SNP_A-1794528	C	C	394	0	394	6	5.955	0.0147	rs1847194	9	82958556	q21.32
SNP_A-1825826	G	G	259	133	220	152	3.921	4.77E-02	rs1323766	9	83041379	q21.32
SNP_A-2178660	C	C	225	143	204	176	4.25	3.92E-02	rs7041473	9	83042534	q21.32
SNP_A-1940767	C	C	325	61	283	83	5.735	0.0166	rs11139975	9	83063866	q21.32
SNP_A-1878265	G	G	262	76	216	98	6.334	0.0118	rs10867957	9	83077413	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1952073	A	A	266	148	234	182	5.546	1.85E-02	rs4877740	9	83081384	q21.32
SNP_A-2098529	A	A	375	23	394	12	3.847	4.98E-02	rs7872136	9	83131472	q21.32
SNP_A-2151324	A	A	375	23	390	10	5.41	0.02	rs1570582	9	83140066	q21.32
SNP_A-1747607	C	C	215	109	208	152	5.32	2.11E-02	rs2769612	9	83366858	q21.33
SNP_A-2072967	A	A	276	108	310	86	4.284	0.0385	rs11140198	9	83495697	q21.32
SNP_A-1997052	G	A	191	161	187	161	4.477	0.0344	rs1436932	9	83903397	q21.32
SNP_A-2216608	T	T	366	34	325	49	4.275	3.87E-02	rs17086818	9	83938595	q21.32
SNP_A-2099982	C	C	401	15	415	5	5.221	0.0223	rs12002481	9	83999352	q21.32
SNP_A-2219576	A	A	260	154	291	125	4.754	0.0292	rs6559770	9	84005935	q21.32
SNP_A-1799485	G	G	193	121	222	100	3.922	4.77E-02	rs4877821	9	84058808	q21.32
SNP_A-2097761	T	T	401	13	387	29	6.339	0.0118	rs7848051	9	84102323	q21.33
SNP_A-1874492	C	C	352	20	326	46	11.239	8.00E-04	rs7861242	9	84145096	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1863241	C	C	396	18	376	36	6.513	1.07E-02	rs12342617	9	84146464	q21.33
SNP_A-2150219	C	C	359	23	318	38	5.262	0.0218	rs10868142	9	84151169	q21.33
SNP_A-1919578	A	A	303	29	325	13	6.813	9.10E-03	rs1014836	9	84248636	q21.33
SNP_A-2282428	A	A	366	22	393	9	6.166	1.30E-02	rs4305978	9	84251930	q21.33
SNP_A-2106663	G	G	299	101	333	71	7.042	8.00E-03	rs4342694	9	84264771	q21.33
SNP_A-2131763	T	T	378	28	394	12	6.732	9.50E-03	rs13297170	9	84269987	q21.33
SNP_A-2168016	C	C	389	21	400	8	5.976	1.45E-02	rs13285387	9	84336939	q21.33
SNP_A-2309146	G	G	391	23	410	10	5.529	1.87E-02	rs7864887	9	84351637	q21.33
SNP_A-2240723	G	G	318	24	342	10	6.495	1.08E-02	rs7856875	9	84357094	q21.33
SNP_A-2139163	G	G	353	15	373	5	5.418	1.99E-02	rs17346028	9	84401901	q21.33
SNP_A-1834148	T	T	216	200	265	155	10.677	1.10E-03	rs985543	9	84480737	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1789784	G	G	216	200	265	155	10.677	1.10E-03	rs985542	9	84480799	q21.33
SNP_A-2046924	C	C	296	78	333	53	6.76	9.30E-03	rs11140709	9	84488942	q21.33
SNP_A-1904973	C	C	354	30	361	9	11.12	9.00E-04	rs1201364	9	84496932	q21.33
SNP_A-1955723	A	A	172	140	223	111	9.197	2.40E-03	rs1212171	9	84512081	q21.33
SNP_A-2037798	C	C	214	172	242	138	5.402	0.0201	rs1187329	9	84518834	q21.33
SNP_A-2206603	T	T	307	19	308	40	6.765	9.30E-03	rs10435949	9	84681175	q21.33
SNP_A-1743503	C	C	356	40	344	66	6.342	0.0118	rs1576161	9	84892055	q21.33
SNP_A-2212686	C	C	327	47	326	70	3.898	4.84E-02	rs2889963	9	84938043	q21.33
SNP_A-1950594	T	T	243	129	211	157	4.975	2.57E-02	rs329202	9	85028736	q21.33
SNP_A-1997099	G	G	349	37	383	23	4.344	3.71E-02	rs718468	9	85276628	q21.33
SNP_A-1997100	A	A	364	50	391	29	6.505	1.08E-02	rs882228	9	85277045	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1929486	G	G	358	20	351	35	4.077	4.35E-02	rs12682787	9	85352437	q21.33
SNP_A-1733080	C	C	376	6	385	21	7.716	5.50E-03	rs3739784	9	85673213	q21.33
SNP_A-1742257	T	T	356	42	338	72	8.185	4.20E-03	rs10512188	9	85726333	q21.33
SNP_A-2119310	C	C	240	152	206	188	6.399	0.0114	rs2770829	9	85753454	q21.33
SNP_A-2273322	A	A	330	0	302	6	6.49	0.0109	rs12346362	9	86298306	q21.33
SNP_A-1869657	C	T	206	176	207	181	4.078	4.35E-02	rs353785	9	86328916	q21.33
SNP_A-2025716	C	C	204	116	185	155	5.94	1.48E-02	rs12338022	9	86438470	q21.33
SNP_A-1997119	G	G	261	67	226	96	7.62	5.80E-03	rs2026340	9	86534557	q21.33
SNP_A-1997126	T	T	346	66	372	44	5.322	2.11E-02	rs10868511	9	86815867	q21.33
SNP_A-2276945	G	G	351	57	373	37	4.919	2.66E-02	rs10448319	9	86818764	q21.33
SNP_A-1887050	A	A	343	61	364	34	8.253	4.10E-03	rs4878028	9	86821842	q21.33
SNP_A-1811862	C	C	340	46	350	12	19.326	0.000011021	rs10868514	9	86823224	q21.33
SNP_A-2112983	C	C	332	50	367	35	3.892	4.85E-02	rs10868516	9	86825707	q21.33
SNP_A-1997132	T	T	306	70	296	98	4.414	0.0356	rs277739	9	86982222	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072892	A	A	312	58	305	83	4.087	4.32E-02	rs380287	9	86988040	q21.33
SNP_A-1686852	C	C	211	177	244	152	4.212	4.01E-02	rs3897826	9	87018037	q22.1
SNP_A-1681728	C	C	376	20	373	39	5.816	1.59E-02	rs4440695	9	87026204	q22.1
SNP_A-2154374	G	G	392	12	397	3	5.412	0.02	rs11141747	9	87161916	q21.33
SNP_A-1997146	G	G	227	113	190	132	4.27	3.88E-02	rs2094707	9	87327819	q21.33
SNP_A-2187517	C	C	250	106	229	149	7.519	6.10E-03	rs721936	9	87512703	q21.33
SNP_A-2235788	C	C	376	8	397	1	5.766	1.63E-02	rs1887793	9	87529165	q21.33
SNP_A-1739005	G	G	320	76	302	108	5.845	1.56E-02	rs10512197	9	87531883	q22.2
SNP_A-1652190	A	A	332	68	316	96	4.999	2.54E-02	rs10512196	9	87580265	q22.2
SNP_A-2094588	T	T	329	3	318	16	9.076	2.60E-03	rs12684240	9	87633641	q22.1
SNP_A-1789047	C	C	330	18	354	4	9.611	0.0019	rs10868659	9	87697710	q22.1
SNP_A-2173071	G	A	213	185	215	179	5.179	0.0229	rs11142017	9	87733005	q22.1
SNP_A-2073354	C	C	368	4	339	13	5.406	0.0201	rs10122903	9	87877951	q22.1
SNP_A-2305328	C	C	282	112	300	86	3.889	4.86E-02	rs529051	9	87892309	q22.1
SNP_A-2061507	C	C	364	46	384	30	3.884	4.88E-02	---	9	87933496	q22.1
SNP_A-1878443	C	C	337	51	331	75	4.219	4.00E-02	rs753826	9	88104913	q22.1
SNP_A-2298233	A	A	336	76	317	101	4.041	4.44E-02	rs17054251	9	88434544	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2026311	T	T	313	75	295	107	5.913	1.50E-02	rs1502707	9	88740102	q22.1
SNP_A-2282332	A	A	358	20	333	35	4.862	0.0275	rs7853477	9	88759802	q22.1
SNP_A-1948235	T	T	214	182	251	155	4.983	2.56E-02	rs7036867	9	88766778	q22.1
SNP_A-1802677	G	A	198	176	213	159	7.774	0.0053	rs1875620	9	88769613	q22.1
SNP_A-2204742	A	G	190	170	205	167	4.553	3.29E-02	rs11525966	9	88791490	q22.1
SNP_A-1844201	C	C	290	66	263	101	8.566	3.40E-03	rs9410429	9	88792588	q22.1
SNP_A-2229729	C	T	211	205	242	176	6.223	0.0126	rs7044951	9	88794191	q22.1
SNP_A-1921278	C	C	248	84	232	118	5.785	1.62E-02	rs4242597	9	88800649	q22.1
SNP_A-1898085	T	T	211	117	183	145	4.982	2.56E-02	rs4242598	9	88801436	q22.1
SNP_A-1941787	C	C	229	139	196	172	6.064	0.0138	rs6559326	9	88811086	q22.1
SNP_A-2295253	C	C	216	164	244	134	4.719	0.0298	rs4075163	9	88828657	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2286541	G	G	217	185	259	155	6.178	0.0129	rs6559331	9	88837423	q22.1
SNP_A-2242522	C	C	367	39	377	23	4.219	4.00E-02	rs11137503	9	88915931	q22.1
SNP_A-2088288	T	T	332	38	366	20	6.907	0.0086	rs17527617	9	88988175	q22.1
SNP_A-2028834	T	T	205	147	182	176	3.92	4.77E-02	rs7041468	9	89282678	q22.2
SNP_A-2296035	T	T	230	138	266	82	16.322	5.35E-05	rs7871577	9	89297357	q22.2
SNP_A-2190373	A	A	325	79	365	45	11.598	7.00E-04	rs4560885	9	89305894	q22.2
SNP_A-2205478	T	T	341	69	315	101	7.011	8.10E-03	rs10908927	9	89320495	q22.2
SNP_A-2281729	A	A	331	61	370	38	7.196	7.30E-03	rs10908931	9	89334831	q22.2
SNP_A-2201609	C	C	327	51	314	76	4.999	2.54E-02	rs12003997	9	89335408	q22.2
SNP_A-2287122	C	C	272	54	270	80	4.205	4.03E-02	rs17531511	9	89372591	q22.2
SNP_A-1997179	C	C	335	1	309	11	8.998	2.70E-03	rs17055074	9	89476814	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1674999	A	A	275	111	319	81	7.7	5.50E-03	rs2065438	9	89584132	q22.31
SNP_A-1961624	A	A	343	39	350	22	4.677	3.06E-02	rs9698611	9	89634340	q22.2
SNP_A-1794352	C	C	354	22	361	39	4.068	4.37E-02	rs4744515	9	89852865	q22.2
SNP_A-2203163	C	C	248	156	280	124	5.597	1.80E-02	rs920753	9	89862442	q22.2
SNP_A-2292357	C	C	335	69	366	48	5.019	2.51E-02	rs158509	9	90626004	q22.2
SNP_A-2203895	G	G	339	73	364	46	7.01	8.10E-03	rs290275	9	90626246	q22.2
SNP_A-2176006	T	T	412	4	418	0	4.039	4.45E-02	rs1675297	9	90757044	q22.2
SNP_A-2260747	T	T	408	4	416	0	4.058	4.40E-02	rs169743	9	90764698	q22.2
SNP_A-1997213	C	C	410	6	403	17	5.302	2.13E-02	rs10512205	9	90944533	q22.2
SNP_A-1997214	A	A	407	3	400	14	7.159	7.50E-03	rs16907172	9	90944701	q22.2
SNP_A-2226953	A	A	308	102	335	79	4.037	4.45E-02	rs7869771	9	91260182	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1814107	C	C	281	131	311	107	3.897	4.84E-02	rs4743835	9	91326010	q22.31
SNP_A-1884180	C	C	360	44	377	25	5.619	0.0178	rs7863503	9	91346879	q22.31
SNP_A-2079113	C	C	254	146	288	114	6.066	0.0138	rs6479351	9	91361226	q22.31
SNP_A-1828205	T	T	258	154	292	124	5.32	2.11E-02	rs6479352	9	91361265	q22.31
SNP_A-2209908	C	C	253	139	284	108	5.68	0.0172	rs16907574	9	91374028	q22.31
SNP_A-2072227	A	A	204	202	238	166	6.132	1.33E-02	rs7031729	9	91586485	q22.31
SNP_A-1821248	A	A	393	15	405	3	8.18	4.20E-03	rs17585790	9	91586538	q22.31
SNP_A-2268452	C	C	201	127	237	97	6.923	8.50E-03	rs11789730	9	91711285	q22.31
SNP_A-1837454	G	G	347	3	366	12	4.837	2.79E-02	rs7045602	9	91843788	q22.31
SNP_A-1955058	C	C	379	7	383	1	4.516	3.36E-02	rs7027257	9	91879862	q22.31
SNP_A-2096148	G	G	368	36	322	62	9.463	2.10E-03	rs7872515	9	91902095	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893917	C	C	369	39	353	59	4.417	0.0356	rs3996240	9	93701163	q22.32
SNP_A-2151513	C	C	375	5	385	15	4.622	3.16E-02	rs10732407	9	94726275	q22.32
SNP_A-1851871	A	A	396	4	390	18	8.877	2.90E-03	rs10989793	9	95482861	q22.32
SNP_A-1942377	G	G	366	38	376	22	4.357	3.69E-02	rs1970200	9	95518879	q22.32
SNP_A-2194348	A	A	241	151	220	184	4.027	0.0448	rs4743181	9	95532348	q22.32
SNP_A-2024669	A	A	356	8	363	1	5.513	0.0189	rs10979626	9	95551887	q22.32
SNP_A-2309272	A	A	267	105	241	133	4.619	3.16E-02	rs591579	9	95719799	q22.32
SNP_A-2022517	T	T	230	116	197	147	6.199	1.28E-02	rs667018	9	95743072	q22.32
SNP_A-2046511	G	A	231	183	220	196	6.261	0.0123	rs4562454	9	95920351	q22.32
SNP_A-2115015	C	C	223	117	195	163	8.975	2.70E-03	rs4743611	9	96011963	q22.32
SNP_A-1720975	T	C	209	163	206	174	8.125	4.40E-03	rs10491723	9	96307470	q22.33
SNP_A-1997292	C	C	315	95	346	68	5.907	1.51E-02	rs2026929	9	96393448	q22.33
SNP_A-2262510	A	A	325	67	342	46	4.316	0.0378	rs10816427	9	96532471	q22.33
SNP_A-1812045	A	A	329	51	366	34	4.86	0.0275	rs16919034	9	96873138	q22.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1863719	A	A	308	34	348	20	5.123	2.36E-02	rs7875800	9	96877315	q22.33
SNP_A-1942322	A	A	322	32	347	15	6.995	8.20E-03	rs10816984	9	96895339	q22.33
SNP_A-2144445	A	A	327	33	364	14	9.229	2.40E-03	rs10759417	9	96895484	q22.33
SNP_A-1876018	T	T	377	21	389	9	4.988	2.55E-02	rs732688	9	97261413	q22.33
SNP_A-2250594	T	T	388	16	408	6	4.926	0.0264	rs7024030	9	97279701	q22.33
SNP_A-1687468	G	G	299	97	342	68	7.741	5.40E-03	rs334356	9	97289210	q22.33
SNP_A-1698731	A	A	297	95	341	67	7.557	6.00E-03	rs334357	9	97289591	q22.33
SNP_A-1738955	C	C	286	108	316	80	5.66	1.74E-02	rs1875804	9	97310831	q22.33
SNP_A-2171014	T	T	306	92	273	115	4.31	3.79E-02	rs10817771	9	97404115	q22.33
SNP_A-1835581	C	C	354	62	329	91	6.393	0.0115	rs1475544	9	97413193	q22.33
SNP_A-2209711	C	T	211	157	186	184	4.292	3.83E-02	rs2149986	9	97414141	q22.33
SNP_A-2077894	C	C	213	179	246	142	6.617	0.0101	rs7875449	9	97576168	q22.33
SNP_A-2236141	G	G	224	190	258	158	5.336	2.09E-02	rs2805809	9	97576477	q22.33
SNP_A-2175157	C	C	330	42	297	69	8.256	4.10E-03	rs874610	9	97862250	q22.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2183362	G	G	301	31	267	49	5.694	1.70E-02	rs6478556	9	97921560	q22.33
SNP_A-2210167	C	C	352	56	328	88	7.881	5.00E-03	rs16912622	9	97923215	q22.33
SNP_A-1847146	T	T	328	84	306	110	4.229	3.97E-02	rs7022455	9	97946427	q22.33
SNP_A-2157672	G	G	309	55	306	82	4.575	3.25E-02	rs2795489	9	97989486	q22.33
SNP_A-2078964	G	G	283	127	316	104	3.988	0.0458	rs10818640	9	98076711	q22.33
SNP_A-2050312	C	C	300	32	301	17	4.294	3.82E-02	rs514993	9	98204703	q22.33
SNP_A-2145623	G	G	359	57	385	33	7.304	6.90E-03	rs661532	9	98217110	q22.33
SNP_A-2290197	C	C	346	42	367	15	13.362	3.00E-04	rs552989	9	98217450	q22.33
SNP_A-1792673	C	C	221	143	194	170	4.086	4.32E-02	rs550270	9	98217734	q22.33
SNP_A-2245845	T	T	365	41	377	25	4.053	0.0441	rs10986062	9	98218575	q22.33
SNP_A-2041880	T	T	328	4	370	0	4.483	3.42E-02	rs6478702	9	98248215	q22.33
SNP_A-2037992	C	C	313	53	298	76	4.383	3.63E-02	rs2184026	9	98383903	q22.33
SNP_A-1997331	G	G	228	188	252	156	4.099	4.29E-02	rs10986708	9	98393611	q22.33
SNP_A-1899963	G	G	284	76	258	98	4.007	0.0453	rs944686	9	98397176	q22.33
SNP_A-2121030	C	C	373	37	391	21	4.833	2.79E-02	rs2779541	9	98469394	q22.33
SNP_A-2146722	G	G	356	28	380	16	3.872	4.91E-02	rs10481694	9	98510187	q22.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1863209	C	C	361	27	384	14	4.706	3.01E-02	rs9299313	9	98510253	q22.33
SNP_A-1997341	C	C	365	31	390	18	4.099	4.29E-02	rs337532	9	98529964	q22.33
SNP_A-1839132	G	G	277	135	246	170	5.835	1.57E-02	rs2065597	9	98772141	q22.33
SNP_A-2029356	T	T	295	95	266	128	6.362	0.0117	rs4743299	9	98808729	q22.33
SNP_A-1920306	T	T	251	137	217	169	5.811	1.59E-02	rs4743300	9	98808794	q22.33
SNP_A-1997352	A	A	309	99	348	68	7.993	4.70E-03	rs1571590	9	98963363	q22.33
SNP_A-2108895	C	C	314	98	289	127	4.755	0.0292	rs1626179	9	99168643	q22.33
SNP_A-1862600	G	G	333	81	305	113	6.488	0.0109	rs10819657	9	99208064	q22.33
SNP_A-2254803	C	C	243	109	265	79	5.649	1.75E-02	rs7032541	9	99250417	q22.33
SNP_A-2105606	C	C	232	134	253	107	3.885	0.0487	rs7032399	9	99251022	q22.33
SNP_A-1708070	-	C	200	200	234	176	4.073	0.0436	rs2777345	9	99547556	q31.1
SNP_A-2212743	A	A	385	23	367	39	4.555	3.28E-02	rs10989019	9	100056096	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2180776	C	G	171	169	199	137	6.175	1.30E-02	rs504023	9	101257666	q31.1
SNP_A-1645874	A	A	361	37	385	23	3.915	4.78E-02	rs1448585	9	101354838	q31.1
SNP_A-1673568	T	T	352	40	386	22	6.475	0.0109	rs1375214	9	101359062	q31.1
SNP_A-1901365	T	T	226	98	272	82	4.352	3.70E-02	rs7023041	9	101422177	q31.1
SNP_A-2066266	C	C	380	22	401	9	5.938	1.48E-02	rs1535633	9	101511417	q31.1
SNP_A-1997408	C	C	310	50	292	70	3.866	4.93E-02	rs17199066	9	101536248	q31.1
SNP_A-1930223	T	T	279	63	250	84	4.496	3.40E-02	rs1885387	9	101630109	q31.1
SNP_A-2193324	C	C	373	17	377	35	5.653	1.74E-02	rs10989674	9	101717622	q31.1
SNP_A-1888719	G	G	389	13	371	25	4.171	4.11E-02	rs10820039	9	101884627	q31.1
SNP_A-1706599	A	A	372	30	398	16	4.963	2.59E-02	rs515821	9	102139677	q31.1
SNP_A-2148963	G	G	372	22	359	37	4.04	4.44E-02	rs10990003	9	102165427	q31.1
SNP_A-1910082	C	C	390	14	374	28	4.997	2.54E-02	rs16921774	9	102375940	q31.1
SNP_A-1816331	C	C	282	58	273	83	4.213	4.01E-02	rs1492596	9	102582692	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1997429	T	T	306	104	330	76	5.242	2.21E-02	rs16922174	9	102608546	q31.1
SNP_A-2079041	G	G	328	88	305	113	3.94	4.71E-02	rs1492580	9	102655527	q31.1
SNP_A-1667618	C	C	307	85	346	64	4.887	2.71E-02	rs956193	9	102746309	q31.1
SNP_A-2040366	G	G	335	1	337	7	4.412	3.57E-02	rs1417702	9	102944302	q31.1
SNP_A-1832383	A	A	388	4	392	12	3.84	5.00E-02	rs10990593	9	103018636	q31.1
SNP_A-2048095	C	A	202	142	163	161	5.483	1.92E-02	rs1448579	9	103019993	q31.1
SNP_A-2251691	A	A	349	45	386	30	4.268	3.88E-02	rs303549	9	103118948	q31.1
SNP_A-2102639	A	A	349	45	360	22	7.883	5.00E-03	rs2448842	9	103161186	q31.1
SNP_A-2293574	C	C	361	49	388	30	5.466	1.94E-02	rs445722	9	103162018	q31.1
SNP_A-2189079	T	T	364	52	388	30	6.664	9.80E-03	rs411567	9	103162523	q31.1
SNP_A-2266272	A	A	353	49	381	27	7.393	6.50E-03	rs433123	9	103171191	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2097132	T	T	358	42	376	22	6.686	9.70E-03	rs303573	9	103182707	q31.1
SNP_A-1856155	G	G	338	48	339	27	5.353	0.0207	rs303575	9	103184433	q31.1
SNP_A-1997442	G	G	329	13	335	3	6.281	1.22E-02	rs1415686	9	103315779	q31.1
SNP_A-1744891	T	T	396	6	396	16	4.423	3.55E-02	rs7040751	9	103500344	q31.1
SNP_A-1869280	G	G	353	43	329	61	3.914	4.79E-02	rs10990940	9	103610183	q31.1
SNP_A-2146283	A	A	258	110	229	135	4.256	3.91E-02	rs7863256	9	103715766	q31.1
SNP_A-2029238	C	C	410	4	414	0	4.019	4.50E-02	---	9	103954683	q31.1
SNP_A-1953137	C	C	412	4	418	0	4.039	4.45E-02	---	9	103959019	q31.1
SNP_A-2269066	A	A	406	4	414	0	4.059	4.39E-02	rs7874617	9	103963000	q31.1
SNP_A-1896462	G	G	325	89	302	116	4.381	3.63E-02	rs10121578	9	104248085	q31.1
SNP_A-2035289	C	C	315	85	285	111	4.929	0.0264	rs10820640	9	104260241	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1813888	G	G	307	97	276	130	6.441	0.0112	rs7865150	9	104291890	q31.1
SNP_A-2014432	C	C	308	96	280	122	4.429	3.53E-02	rs792260	9	104315701	q31.1
SNP_A-1997477	A	A	271	83	240	114	6.759	9.30E-03	rs1916675	9	104325959	q31.1
SNP_A-1846423	G	G	307	101	283	131	4.812	2.83E-02	rs2030625	9	104347987	q31.1
SNP_A-1875463	A	A	317	101	288	128	4.569	3.26E-02	rs955610	9	104348380	q31.1
SNP_A-2139760	A	A	280	64	249	85	4.63	3.14E-02	rs10122384	9	104438727	q31.1
SNP_A-2303094	T	T	283	69	310	42	7.797	5.20E-03	rs1357562	9	104439357	q31.1
SNP_A-1813649	T	T	305	93	273	115	3.972	4.63E-02	rs9299382	9	104439521	q31.1
SNP_A-1957211	G	G	311	77	325	51	5.402	0.0201	rs7856737	9	104441265	q31.1
SNP_A-1997482	C	C	317	83	336	54	6.566	0.0104	rs7873356	9	104443976	q31.1
SNP_A-1859979	G	G	316	88	348	66	4.563	0.0327	rs7848871	9	104452133	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2271022	C	C	293	59	261	77	3.948	4.69E-02	rs10115334	9	104453696	q31.1
SNP_A-2100682	A	A	301	73	274	104	6.676	9.80E-03	rs7038020	9	104461475	q31.1
SNP_A-1917494	A	A	313	87	333	53	8.63	0.0033	rs10991330	9	104463949	q31.1
SNP_A-2072988	G	G	291	111	315	81	5.593	1.80E-02	rs2230808	9	104642359	q31.1
SNP_A-2071924	T	T	371	9	376	2	4.483	3.42E-02	rs914544	9	104686767	q31.1
SNP_A-1997494	G	G	275	89	235	121	7.926	4.90E-03	rs1809924	9	104894024	q31.1
SNP_A-2170020	G	G	383	5	332	12	3.889	4.86E-02	rs7860321	9	105207603	q31.1
SNP_A-1828231	A	A	414	2	404	12	7.265	7.00E-03	rs16924597	9	105261333	q31.1
SNP_A-1873775	A	A	395	1	392	8	5.436	1.97E-02	rs7025543	9	105273611	q31.1
SNP_A-1807300	A	A	415	3	411	11	4.572	3.25E-02	rs12338806	9	105277115	q31.1
SNP_A-2219701	A	A	351	3	336	12	5.677	0.0172	rs4394455	9	105277421	q31.1
SNP_A-2222786	T	T	332	52	318	76	4.674	3.06E-02	rs10991669	9	105330391	q31.2
SNP_A-2119381	G	G	396	2	397	9	4.377	3.64E-02	rs10978190	9	105509799	q31.2
SNP_A-2014443	C	C	236	132	206	156	3.987	0.0458	rs966523	9	106137002	q31.2
SNP_A-1914654	C	C	321	75	298	98	3.912	4.79E-02	rs1484375	9	106147116	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2191516	C	C	333	83	303	117	7.176	7.40E-03	rs7024334	9	106151630	q31.2
SNP_A-1922175	C	C	304	112	277	143	5.004	0.0253	rs7028157	9	106152186	q31.2
SNP_A-2048670	C	C	388	6	379	15	3.963	0.0465	rs7852451	9	106188560	q31.2
SNP_A-2222177	T	T	279	33	271	63	8.752	3.10E-03	rs10978463	9	106194370	q31.2
SNP_A-2128793	A	A	369	21	354	38	5.204	2.25E-02	rs2220144	9	106217576	q31.2
SNP_A-2196178	T	T	335	75	304	104	6.197	1.28E-02	rs10816385	9	106223169	q31.2
SNP_A-1666320	G	G	300	102	333	81	3.955	4.67E-02	rs1836459	9	106279953	q31.2
SNP_A-2263964	C	C	236	128	260	100	4.578	3.24E-02	rs10118378	9	106502757	q31.2
SNP_A-1865225	G	G	254	146	230	182	4.965	2.59E-02	rs1491102	9	106547814	q31.2
SNP_A-1925308	C	C	204	190	249	157	7.43	6.40E-03	rs1352755	9	106568314	q31.2
SNP_A-2184085	G	G	351	57	359	37	4.167	4.12E-02	rs10978633	9	106615711	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1868689	A	A	338	34	355	17	6.084	1.36E-02	rs12002945	9	106969805	q31.2
SNP_A-2185269	T	T	374	4	386	0	4.106	4.27E-02	rs10116853	9	107060330	q31.2
SNP_A-1997537	C	C	319	23	342	42	3.938	4.72E-02	rs11573711	9	107165123	q31.2
SNP_A-2294784	A	A	291	95	255	117	4.4	3.59E-02	rs817870	9	107224243	q31.2
SNP_A-2144368	C	C	284	84	257	109	4.58	3.23E-02	rs1746816	9	107224881	q31.2
SNP_A-2244380	G	G	292	96	271	131	5.934	0.0149	rs1746817	9	107224936	q31.2
SNP_A-2179926	T	T	303	103	271	135	6.086	1.36E-02	rs4978923	9	107226333	q31.2
SNP_A-2253020	G	G	304	102	259	125	5.319	2.11E-02	rs12156485	9	107227002	q31.2
SNP_A-1821868	G	G	301	103	267	133	5.829	1.58E-02	rs12156453	9	107227057	q31.2
SNP_A-1791736	G	G	309	109	274	136	5	0.0253	rs1746825	9	107228111	q31.2
SNP_A-1943105	C	C	362	38	349	57	3.993	4.57E-02	rs1771715	9	107231223	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2230792	G	G	399	7	384	20	6.542	1.05E-02	rs817830	9	107233976	q31.2
SNP_A-2125476	T	T	301	89	282	122	5.535	1.86E-02	rs10978832	9	107244995	q31.2
SNP_A-2177307	G	G	336	50	334	28	5.447	1.96E-02	rs10978940	9	107451963	q31.2
SNP_A-1997549	G	G	211	201	245	167	5.676	0.0172	rs2017419	9	107461672	q31.2
SNP_A-1795814	G	G	269	71	304	50	5.502	0.019	rs10978956	9	107477435	q31.2
SNP_A-2253197	T	T	296	60	321	39	5.445	1.96E-02	rs7027436	9	107504292	q31.2
SNP_A-2044031	G	G	236	130	268	108	3.931	4.74E-02	rs10759255	9	107577506	q31.2
SNP_A-1997554	C	C	232	172	206	204	4.223	3.99E-02	rs10979067	9	107684274	q31.2
SNP_A-2241246	G	G	220	102	241	73	5.663	1.73E-02	rs4979601	9	107782337	q31.2
SNP_A-2183294	T	T	282	94	299	69	4.246	3.93E-02	rs10979231	9	107975189	q31.2
SNP_A-1832381	G	G	293	83	294	50	6.781	9.20E-03	rs10979242	9	107979947	q31.2
SNP_A-1852236	A	A	328	22	320	40	5.185	2.28E-02	rs2571501	9	107981851	q31.2
SNP_A-2211214	A	A	266	82	312	60	6.276	1.22E-02	rs10979248	9	107984083	q31.2
SNP_A-2313009	T	T	263	67	230	90	5.426	1.98E-02	rs681015	9	107994789	q31.2
SNP_A-2246600	A	A	322	84	305	111	4.078	4.34E-02	rs614851	9	107997182	q31.2
SNP_A-1856656	G	G	295	61	274	92	6.919	8.50E-03	rs607019	9	108024851	q31.2
SNP_A-2259289	T	T	292	66	275	95	5.537	1.86E-02	rs2778251	9	108027616	q31.2
SNP_A-1922611	A	A	369	17	375	7	4.194	4.06E-02	---	9	108065356	q31.2
SNP_A-1997580	A	A	319	83	320	56	4.382	3.63E-02	rs1407849	9	108144153	q31.2
SNP_A-1806741	G	G	342	34	345	19	4.065	4.38E-02	rs657749	9	108239815	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897208	T	T	317	13	308	30	6.756	9.30E-03	rs10979597	9	108736587	q31.3
SNP_A-1913693	C	C	363	43	341	63	4.456	3.48E-02	rs10979696	9	108973584	q31.3
SNP_A-1849136	G	G	262	156	211	209	13.19	3.00E-04	rs1879069	9	109071255	q31.3
SNP_A-1802282	C	C	354	64	382	40	6.585	0.0103	rs16914041	9	109071408	q31.3
SNP_A-2136753	A	A	349	3	309	13	7.361	6.70E-03	rs17793365	9	109146894	q31.3
SNP_A-1915637	C	C	269	121	255	155	4.065	4.38E-02	rs10119049	9	109446662	q31.3
SNP_A-2145382	A	A	349	55	335	77	3.875	4.90E-02	rs1358913	9	109521466	q31.3
SNP_A-2014459	G	G	313	49	294	70	4.295	3.82E-02	rs7023524	9	109611021	q31.3
SNP_A-2032199	C	C	352	26	345	47	5.859	0.0155	rs7861208	9	109931973	q31.3
SNP_A-2201154	C	C	364	36	360	56	4.058	4.40E-02	rs10980179	9	109932912	q31.3
SNP_A-2014466	T	T	310	50	309	77	4.841	2.78E-02	rs1969944	9	109983414	q31.3
SNP_A-1755492	T	T	282	108	261	149	6.857	8.80E-03	rs1037182	9	110087746	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1673330	A	A	275	127	247	167	6.769	9.30E-03	rs10513152	9	110088169	q31.3
SNP_A-2067670	G	G	378	36	361	55	4.353	3.69E-02	rs10759408	9	110148513	q31.3
SNP_A-2288827	C	C	393	23	401	9	6.162	1.30E-02	rs10118935	9	110229572	q31.3
SNP_A-1863310	G	G	344	18	363	7	5.264	0.0218	rs10817056	9	110458344	q31.3
SNP_A-1852305	A	A	328	84	357	63	4.151	4.16E-02	rs16915222	9	110482762	q31.3
SNP_A-1903934	C	C	214	128	211	171	4.007	0.0453	rs10817083	9	110553925	q31.3
SNP_A-2210671	C	C	312	32	313	53	4.512	3.36E-02	rs2821151	9	110595459	q31.3
SNP_A-1997660	G	G	319	37	300	64	7.713	5.50E-03	rs544828	9	110671392	q31.3
SNP_A-2156877	T	T	348	64	326	90	5.089	0.0241	rs498102	9	110673454	q31.3
SNP_A-1951404	T	T	325	75	347	51	5.287	2.15E-02	rs554504	9	110701019	q31.3
SNP_A-2265471	C	C	304	74	335	55	4.116	4.25E-02	rs556471	9	110701768	q31.3
SNP_A-1690061	T	T	393	9	412	2	4.728	2.97E-02	rs2025543	9	111080962	q32
SNP_A-2065733	T	T	234	132	204	162	5.116	2.37E-02	rs12338044	9	111232672	q31.3
SNP_A-1923603	A	A	238	156	198	182	5.418	1.99E-02	rs7027778	9	111398466	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2233372	C	C	239	95	225	125	4.141	4.18E-02	rs12553893	9	111496357	q31.3
SNP_A-1921715	T	T	339	33	321	55	5.97	0.0146	rs16916397	9	111648171	q31.3
SNP_A-2036622	G	G	275	139	300	106	5.454	0.0195	rs7856299	9	111669658	q31.3
SNP_A-1895540	C	C	378	22	363	41	6.014	1.42E-02	rs10817224	9	111686504	q31.3
SNP_A-2140604	C	C	285	119	251	145	4.638	3.13E-02	rs10817245	9	111786528	q31.3
SNP_A-1881347	G	G	345	23	316	40	5.662	1.73E-02	---	9	111804520	q31.3
SNP_A-2210787	T	T	317	69	303	99	5.351	0.0207	rs10981412	9	112294679	q32
SNP_A-2184860	G	G	244	82	287	59	6.645	9.90E-03	rs7852336	9	112436395	q32
SNP_A-2272744	C	C	313	59	337	35	7.014	8.10E-03	rs7864816	9	113316444	q32
SNP_A-1997724	C	C	296	114	261	143	5.428	1.98E-02	rs7868736	9	113607737	q32
SNP_A-1883562	G	G	293	105	270	132	3.996	4.56E-02	rs4979316	9	113842088	q32
SNP_A-2286797	G	G	260	116	242	150	4.66	0.0309	rs4979325	9	113859868	q32
SNP_A-2262550	C	C	252	160	282	132	4.366	3.67E-02	rs999599	9	114091149	q32
SNP_A-2218188	C	C	249	155	272	122	4.822	0.0281	rs902497	9	114091708	q32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2233348	G	G	236	124	196	142	4.233	3.97E-02	rs1535964	9	114351993	q32
SNP_A-1716301	T	T	246	144	277	111	6.103	0.0135	rs7040792	9	114625038	q33.1
SNP_A-1698805	T	T	223	153	257	123	5.648	1.75E-02	rs1885234	9	114628322	q33.1
SNP_A-1783277	C	C	169	159	186	124	4.639	3.13E-02	rs10759741	9	114744989	q32
SNP_A-1676476	T	T	329	73	304	106	6.993	8.20E-03	rs10491578	9	114759933	q33.1
SNP_A-2232780	G	G	384	4	394	0	4.083	4.33E-02	rs3789876	9	114864977	q33.1
SNP_A-2152461	G	G	326	78	294	100	4.246	3.93E-02	rs10982716	9	115216753	q33.1
SNP_A-2150104	A	A	385	31	369	49	4.385	3.63E-02	rs2900601	9	115394221	q33.1
SNP_A-1713772	A	A	351	43	384	28	4.251	3.92E-02	rs10513299	9	115481022	q33.1
SNP_A-2267453	C	C	375	39	355	59	4.63	3.14E-02	rs10982959	9	115698857	q33.1
SNP_A-1842656	C	C	374	20	386	6	7.723	5.50E-03	rs7862674	9	115753575	q33.1
SNP_A-2263825	A	A	385	17	399	7	4.397	3.60E-02	rs6478217	9	115789672	q33.1
SNP_A-1866100	C	C	325	77	275	125	15.568	7.96E-05	rs7868322	9	116256460	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098929	G	G	338	76	296	118	11.875	6.00E-04	rs3747830	9	116265541	q33.1
SNP_A-1997779	A	A	332	78	293	115	9.522	0.002	rs9299239	9	116266774	q33.1
SNP_A-2046910	C	C	366	4	376	0	4.087	4.32E-02	rs1396043	9	116272876	q33.1
SNP_A-2310915	C	C	309	29	256	42	4.855	0.0276	rs4837584	9	116357365	q33.1
SNP_A-2056848	G	G	336	78	300	114	8.788	3.00E-03	rs10983238	9	116413237	q33.1
SNP_A-2039568	C	C	340	74	359	53	3.984	4.59E-02	rs10983240	9	116414315	q33.1
SNP_A-2156608	T	T	267	135	231	177	8.212	4.20E-03	rs7856625	9	116424637	q33.1
SNP_A-2260686	G	G	335	77	301	111	7.967	4.80E-03	rs10983260	9	116444814	q33.1
SNP_A-2031791	T	T	269	137	303	99	8.12	4.40E-03	rs4837659	9	116444846	q33.1
SNP_A-2155511	C	C	257	99	222	138	8.953	0.0028	rs1885245	9	116471967	q33.1
SNP_A-2113270	G	G	366	6	354	0	5.757	1.64E-02	rs16933793	9	116489530	q33.1
SNP_A-2254283	G	G	265	129	291	95	6.295	0.0121	rs4837746	9	116502133	q33.1
SNP_A-2173690	T	T	247	133	269	93	7.585	5.90E-03	rs10983314	9	116554626	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2257603	C	T	195	159	197	155	8.622	0.0033	rs10983319	9	116563020	q33.1
SNP_A-1938457	A	G	206	198	236	170	6.769	9.30E-03	rs10983320	9	116563243	q33.1
SNP_A-1997786	A	A	235	137	209	173	5.572	0.0183	rs756118	9	116566884	q33.1
SNP_A-1997787	A	A	301	61	275	81	3.941	4.71E-02	rs894206	9	116567127	q33.1
SNP_A-1859031	C	C	213	185	237	155	3.882	4.88E-02	rs2119687	9	116606175	q33.1
SNP_A-1708899	G	G	235	165	277	135	6.269	0.0123	rs7037164	9	116667789	q33.1
SNP_A-1757645	G	G	228	166	266	128	7.835	5.10E-03	rs4412426	9	116676155	q33.1
SNP_A-1714853	T	T	261	109	302	80	7.246	7.10E-03	rs10513334	9	116676878	q33.1
SNP_A-2294459	C	C	243	61	285	43	5.553	0.0184	rs10983521	9	116943405	q33.1
SNP_A-1644902	T	G	206	196	232	182	4.337	0.0373	rs4144592	9	117354825	q33.1
SNP_A-2276801	G	G	361	57	340	82	5.107	2.38E-02	rs16905721	9	117357038	q33.1
SNP_A-1789199	C	C	306	46	280	64	4.008	0.0453	rs10983685	9	117363725	q33.1
SNP_A-2147487	G	G	347	69	321	97	5.73	0.0167	rs575321	9	117380432	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1853020	G	G	401	11	401	3	4.493	3.40E-02	rs811427	9	117384692	q33.1
SNP_A-2194017	G	G	337	49	341	27	5.966	0.0146	rs4837342	9	117391533	q33.1
SNP_A-2279565	C	C	355	59	349	35	5.058	2.45E-02	rs16905925	9	117495564	q33.1
SNP_A-1697380	T	T	353	43	342	66	4.849	2.77E-02	rs10491527	9	117552838	q33.1
SNP_A-1921392	A	A	336	70	364	50	4.376	3.65E-02	rs16906215	9	117625812	q33.1
SNP_A-2159448	T	T	276	108	249	133	3.977	4.61E-02	rs9792558	9	117649749	q33.1
SNP_A-2157502	G	G	398	4	410	0	4.1	4.29E-02	rs4837513	9	117690184	q33.1
SNP_A-2152897	A	A	376	42	358	62	4.283	0.0385	rs11793751	9	117693568	q33.1
SNP_A-2279598	C	C	228	138	203	169	4.532	3.33E-02	rs17334309	9	117697477	q33.1
SNP_A-1700576	A	A	261	139	238	176	5.167	0.023	rs2151642	9	118034032	q33.2
SNP_A-1881167	T	T	231	157	255	127	4.308	3.79E-02	rs10117037	9	118374514	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1833009	T	T	231	159	248	124	4.509	3.37E-02	rs10118743	9	118376222	q33.1
SNP_A-2033224	G	G	289	123	324	94	5.831	1.57E-02	rs10818184	9	118381274	q33.1
SNP_A-1814778	C	C	379	37	397	21	4.827	2.80E-02	rs10818263	9	118825821	q33.1
SNP_A-1839251	C	C	322	2	334	12	6.647	9.90E-03	rs230117	9	118996410	q33.1
SNP_A-2227867	C	C	352	52	333	79	6.014	1.42E-02	rs914652	9	119044925	q33.1
SNP_A-1807587	T	T	344	60	317	85	5.408	0.02	rs1332453	9	119047151	q33.1
SNP_A-1997869	G	A	226	182	219	181	8.311	3.90E-03	rs487240	9	119115689	q33.1
SNP_A-2030812	G	A	171	149	192	158	4.602	3.19E-02	rs7039577	9	119197668	q33.1
SNP_A-1892562	G	G	246	108	286	84	5.657	1.74E-02	rs10760035	9	119199663	q33.1
SNP_A-2146104	G	G	253	141	283	99	8.846	2.90E-03	rs1324623	9	119199751	q33.1
SNP_A-2162556	C	C	194	130	176	170	5.493	1.91E-02	rs1412067	9	119246795	q33.1
SNP_A-2110936	T	T	357	39	347	59	4.1	4.29E-02	rs12001595	9	119261084	q33.1
SNP_A-2262369	C	C	356	10	336	24	6.294	0.0121	rs12345648	9	119357205	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259490	C	C	370	6	382	16	4.115	4.25E-02	rs4392972	9	119540778	q33.1
SNP_A-2170407	G	G	354	18	336	32	4.368	3.66E-02	rs17386987	9	119563986	q33.1
SNP_A-2120767	G	G	325	51	361	33	5.328	2.10E-02	rs16908892	9	119578706	q33.1
SNP_A-2037602	C	C	394	24	377	43	5.758	1.64E-02	rs10984680	9	119600041	q33.2
SNP_A-1997886	G	G	262	76	261	121	7.621	5.80E-03	rs10513351	9	119606328	q33.2
SNP_A-2299794	A	A	271	137	227	175	8.472	3.60E-03	rs4837685	9	119737733	q33.2
SNP_A-2081763	A	A	276	142	234	182	8.392	0.0038	rs12553064	9	119739608	q33.2
SNP_A-2197400	G	G	276	142	238	184	8.202	4.20E-03	rs7018808	9	119749176	q33.2
SNP_A-2152323	A	A	236	110	196	152	10.431	1.20E-03	rs7851213	9	119750005	q33.2
SNP_A-1997894	G	G	263	113	226	140	5.547	1.85E-02	rs17483782	9	119752723	q33.2
SNP_A-2308979	C	C	274	50	263	73	4.309	3.79E-02	rs4837698	9	119913022	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2281305	A	A	320	24	336	10	6.149	1.31E-02	rs200549	9	120175800	q33.2
SNP_A-1869561	C	C	307	23	366	14	3.86	4.95E-02	rs846826	9	120185528	q33.2
SNP_A-2138844	C	C	407	1	403	7	4.515	3.36E-02	rs10984898	9	120218778	q33.2
SNP_A-1854315	G	G	230	112	264	88	5.077	2.42E-02	rs4836820	9	120231233	q33.2
SNP_A-1997908	G	G	334	18	346	4	9.115	2.50E-03	rs10818463	9	120385946	q33.2
SNP_A-1944050	A	A	320	58	301	87	6.252	0.0124	rs10985127	9	120863547	q33.2
SNP_A-2176211	A	A	238	152	202	176	4.515	3.36E-02	rs2302498	9	121015883	q33.2
SNP_A-2258456	G	G	234	168	206	198	4.236	3.96E-02	rs9792437	9	121044455	q33.2
SNP_A-2055683	G	G	290	84	248	122	10.267	0.0014	rs2777317	9	121448228	q33.2
SNP_A-2202593	G	G	394	16	410	6	4.821	0.0281	rs2150711	9	121505429	q33.2
SNP_A-2309057	A	C	204	166	208	192	3.917	4.78E-02	rs10739602	9	121789782	q33.2
SNP_A-2188927	C	C	231	135	269	97	9.112	2.50E-03	rs7867807	9	121817241	q33.2
SNP_A-2032115	G	G	407	5	400	14	4.319	3.77E-02	rs17263352	9	121891127	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2195582	G	G	288	32	271	49	4.085	4.33E-02	rs1213267	9	122196284	q33.2
SNP_A-1875903	T	T	319	25	317	45	5.265	0.0218	rs10115364	9	122345134	q33.2
SNP_A-2133625	G	G	363	51	382	34	3.88	4.89E-02	rs7860446	9	122412484	q33.2
SNP_A-2197705	A	A	379	9	361	21	5.191	2.27E-02	rs10818781	9	122898156	q33.2
SNP_A-2257879	C	C	361	13	356	30	6.568	0.0104	rs803714	9	122922594	q33.3
SNP_A-1857060	T	T	351	3	331	15	8.496	3.60E-03	rs2797949	9	123216639	q33.3
SNP_A-2308419	G	G	360	14	365	31	5.833	1.57E-02	rs7026808	9	123259353	q33.3
SNP_A-1886649	G	C	221	193	225	195	4.032	4.47E-02	rs12380452	9	123816671	q33.3
SNP_A-2087164	A	A	381	35	365	55	4.769	2.90E-02	rs10986181	9	123881150	q33.3
SNP_A-2079071	G	G	271	83	263	115	4.51	3.37E-02	rs10818918	9	123940064	q33.3
SNP_A-1688074	T	T	368	32	357	55	6.071	0.0137	rs10513480	9	125415451	q33.3
SNP_A-1927284	G	G	319	93	294	118	3.982	4.60E-02	rs551938	9	125502582	q33.3
SNP_A-2275751	A	A	313	9	360	2	5.416	0.02	rs7031853	9	125863535	q33.3
SNP_A-2222736	A	A	332	38	358	16	9.921	1.60E-03	rs4595229	9	125959488	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2046167	C	C	220	158	186	184	4.739	2.95E-02	rs2773377	9	126030806	q33.3
SNP_A-2062664	C	C	299	45	333	29	4.833	2.79E-02	rs2039201	9	126074416	q33.3
SNP_A-1953336	C	T	218	160	197	185	6.516	1.07E-02	rs1330154	9	126116330	q33.3
SNP_A-1809561	A	G	236	176	208	204	4.994	2.54E-02	rs6478734	9	126116940	q33.3
SNP_A-2201499	T	T	340	22	347	45	6.784	9.20E-03	rs6478740	9	126285633	q33.3
SNP_A-1932825	T	T	346	56	331	83	5.402	0.0201	rs13287122	9	126405337	q33.3
SNP_A-1788120	C	C	320	90	298	118	4.509	3.37E-02	rs11793373	9	126487097	q33.3
SNP_A-2159200	G	G	322	68	345	49	3.858	4.95E-02	rs10987427	9	126560360	q33.3
SNP_A-2151751	T	T	249	153	274	118	5.59	1.81E-02	rs4836555	9	126749582	q33.3
SNP_A-1956335	T	T	391	1	398	8	5.263	0.0218	rs17368205	9	126877775	q33.3
SNP_A-2074389	G	G	285	75	287	111	5.082	2.42E-02	rs2812293	9	127100118	q33.3
SNP_A-1998008	G	G	221	147	281	111	11.448	7.00E-04	rs7863451	9	127151798	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2240907	C	C	229	113	211	167	9.374	2.20E-03	rs4316239	9	127263040	q33.3
SNP_A-2142459	G	G	237	121	201	155	7.142	7.50E-03	rs7853047	9	127277654	q33.3
SNP_A-2149230	T	T	257	133	229	165	5.029	2.49E-02	rs7869823	9	127281643	q33.3
SNP_A-1889200	T	T	222	132	197	163	4.699	3.02E-02	rs2243906	9	127299223	q33.3
SNP_A-2243265	G	G	243	119	215	157	6.809	9.10E-03	rs2243767	9	127300942	q34.11
SNP_A-2273757	A	A	406	4	416	0	4.078	4.34E-02	rs10987737	9	127640670	q34.11
SNP_A-2208513	C	C	413	5	420	0	5.054	0.0246	rs10987776	9	127771487	q34.11
SNP_A-1820595	T	T	410	6	422	0	6.13	1.33E-02	rs10987790	9	127812389	q34.11
SNP_A-2026887	A	A	324	8	357	1	6.072	0.0137	rs2040005	9	127895540	q34.11
SNP_A-1864886	A	A	338	46	349	27	5.038	2.48E-02	rs7872702	9	127949577	q34.11
SNP_A-1740845	G	G	364	4	362	12	3.957	4.67E-02	rs1407568	9	128228146	q34.11
SNP_A-2115893	G	G	334	84	307	113	5.402	0.0201	rs10988264	9	129090024	q34.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2191089	C	C	266	80	229	99	4.305	3.80E-02	rs1556144	9	129102320	q34.11
SNP_A-2312538	C	C	274	136	315	101	7.98	4.70E-03	rs968477	9	129321415	q34.11
SNP_A-1933770	A	A	299	115	261	159	9.602	0.0019	rs7035800	9	129413299	q34.11
SNP_A-2192832	G	G	343	41	329	67	6.368	1.16E-02	rs10988454	9	129469685	q34.11
SNP_A-2051996	G	G	373	1	377	7	4.39	0.0361	rs1861783	9	129469780	q34.11
SNP_A-2301995	A	A	387	31	405	17	4.473	0.0344	rs17417877	9	129574127	q34.11
SNP_A-1938856	A	A	340	50	361	29	6.211	1.27E-02	rs4836677	9	129757016	q34.11
SNP_A-2284843	T	T	332	62	356	36	7.73	5.40E-03	rs4836678	9	129757177	q34.11
SNP_A-1938449	A	A	355	39	378	18	8.454	3.60E-03	—	9	129770134	q34.11
SNP_A-1882905	T	T	279	27	345	17	4.591	3.21E-02	rs10118313	9	129786006	q34.11
SNP_A-1795264	C	C	289	51	335	33	6.15	1.31E-02	rs2102209	9	129833088	q34.11
SNP_A-2249672	T	T	333	73	346	48	5.235	2.21E-02	rs806861	9	129867082	q34.11
SNP_A-1802559	C	C	416	2	412	10	5.334	2.09E-02	rs2417173	9	129911294	q34.11
SNP_A-2122712	G	G	415	1	408	8	5.504	0.019	rs4837463	9	129959924	q34.11
SNP_A-2107434	T	T	373	5	361	19	8.358	0.0038	rs929532	9	130043252	q34.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2032504	G	G	394	2	389	9	4.481	3.43E-02	rs10819612	9	130045800	q34.11
SNP_A-1819860	C	C	416	0	416	4	3.981	4.60E-02	rs596317	9	130386359	q34.11
SNP_A-1915415	C	C	326	34	359	19	5.399	0.0201	rs10901080	9	130388210	q34.11
SNP_A-1647108	C	C	247	111	239	155	5.7	1.70E-02	rs578802	9	130729322	q34.13
SNP_A-2314793	G	G	338	2	320	10	5.678	0.0172	rs10901297	9	130797304	q34.12
SNP_A-1710714	T	T	373	29	367	47	4.136	4.20E-02	rs10512415	9	130801124	q34.13
SNP_A-1914173	G	G	340	76	367	55	4.355	3.69E-02	rs12553392	9	131378277	q34.13
SNP_A-2268244	G	G	316	32	302	52	5.028	2.49E-02	rs2031872	9	131674772	q34.13
SNP_A-1795986	C	C	418	0	416	4	4	4.55E-02	rs7869935	9	131689726	q34.13
SNP_A-1865012	G	G	288	6	337	1	4.371	3.66E-02	rs11243606	9	131953286	q34.13
SNP_A-2195914	G	G	418	0	418	4	3.981	4.60E-02	rs7849557	9	132110925	q34.13
SNP_A-2213902	C	C	373	37	397	19	6.491	1.08E-02	rs10901163	9	132230344	q34.13
SNP_A-2195768	G	G	295	99	261	129	6.006	0.0143	rs480021	9	132360529	q34.13
SNP_A-2305756	T	T	230	188	260	160	4.085	4.33E-02	rs512165	9	132397462	q34.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1786974	G	G	208	198	237	157	6.447	0.0111	rs7864386	9	132451357	q34.13
SNP_A-1998055	G	G	330	28	287	47	6.986	8.20E-03	rs7034065	9	132529974	q34.13
SNP_A-1814587	G	G	289	97	310	72	4.414	3.57E-02	rs11243852	9	132538292	q34.13
SNP_A-2224992	C	C	388	30	370	50	5.423	1.99E-02	rs4498679	9	132566094	q34.13
SNP_A-2086102	A	A	334	38	314	72	10.872	0.001	rs6597584	9	132804981	q34.13
SNP_A-1998060	A	A	355	41	331	67	7.094	7.70E-03	rs1073123	9	132816458	q34.13
SNP_A-1791270	G	G	363	49	336	76	6.875	8.70E-03	rs7858160	9	132825736	q34.13
SNP_A-2034174	T	T	299	3	317	17	8.738	3.10E-03	rs11244024	9	133088485	q34.2
SNP_A-2272080	G	G	310	40	299	63	5.134	0.0235	rs613423	9	133165032	q34.2
SNP_A-2051988	A	A	270	56	262	88	6.387	0.0115	rs672316	9	133167679	q34.2
SNP_A-2201226	G	G	299	67	264	86	4.18	4.09E-02	rs552148	9	133183035	q34.2
SNP_A-2300435	A	A	336	8	299	17	4.216	4.01E-02	rs11244086	9	133221341	q34.2
SNP_A-1819662	G	G	366	10	362	2	5.162	2.31E-02	rs7040821	9	133293138	q34.2
SNP_A-1926126	C	C	344	60	374	42	4.255	3.91E-02	rs3025310	9	133488759	q34.2
SNP_A-2178453	T	T	365	47	351	69	4.37	3.66E-02	rs3025365	9	133512030	q34.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102698	T	T	196	158	238	134	5.594	1.80E-02	rs7027150	9	134282680	q34.2
SNP_A-1824332	T	T	260	154	219	193	7.888	5.00E-03	rs1041608	9	134295759	q34.2
SNP_A-2098900	G	G	296	102	267	127	4.203	4.04E-02	rs4917360	9	134316799	q34.2
SNP_A-2221638	C	C	393	25	407	13	4.03	4.47E-02	rs17093688	9	134350118	q34.2
SNP_A-2293633	C	C	390	10	399	3	3.867	4.92E-02	rs7033773	9	134595145	q34.2
SNP_A-2212479	C	C	296	56	278	88	7.405	6.50E-03	rs3132316	9	134653282	q34.2
SNP_A-1945676	T	T	288	90	281	123	4.339	3.72E-02	rs943423	9	134663128	q34.2
SNP_A-1809297	T	T	243	165	276	140	4.07	0.0436	rs10858265	9	134769819	q34.3
SNP_A-1782591	G	G	269	115	287	87	4.333	3.74E-02	rs11103479	9	134836368	q34.3
SNP_A-2223760	A	A	248	158	205	187	6.276	1.22E-02	rs3128606	9	134848868	q34.3
SNP_A-2277324	T	T	343	47	359	27	5.75	1.65E-02	rs7849193	9	134876769	q34.3
SNP_A-2270282	A	A	329	63	353	41	5.493	1.91E-02	rs12005720	9	134903965	q34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2174894	C	C	390	20	411	7	6.733	9.50E-03	rs3811156	9	134916966	q34.3
SNP_A-2145334	C	C	268	94	313	61	7.982	4.70E-03	rs6537958	9	135006768	q34.3
SNP_A-2053067	C	C	278	112	296	86	3.896	4.84E-02	rs2989724	9	135033862	q34.3
SNP_A-2301332	C	T	212	184	217	189	3.911	4.80E-02	rs2590504	9	135591440	q34.3
SNP_A-1895200	C	C	348	34	359	55	3.846	0.0499	rs12340697	9	135631664	q34.3
SNP_A-2199452	G	G	324	82	289	113	6.907	0.0086	rs783771	9	135686390	q34.3
SNP_A-1853902	G	G	243	147	208	196	9.472	2.10E-03	rs10858151	9	135808595	q34.3
SNP_A-2304994	A	A	280	124	311	93	6.055	1.39E-02	rs498974	9	135833496	q34.3
SNP_A-2099689	C	C	313	75	341	55	4.195	4.06E-02	rs11103223	9	136042892	q34.3
SNP_A-2250167	A	A	305	17	275	33	6.364	1.16E-02	rs7025596	9	136277422	q34.3
SNP_A-2079520	T	T	391	7	387	19	5.48	1.92E-02	rs7034799	9	136732049	q34.3
SNP_A-1902298	G	G	196	130	228	94	8.176	4.20E-03	rs945387	9	136969829	q34.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893590	C	C	219	103	197	129	4.053	0.0441	rs9411307	9	137270784	q34.3
SNP_A-2186204	G	G	335	81	309	111	5.718	1.68E-02	rs950078	9	137742653	q34.3
SNP_A-1810274	G	G	365	15	385	5	5.404	0.0201	rs3123518	9	137928408	q34.3
SNP_A-2053965	C	C	349	11	382	4	3.855	4.96E-02	rs11253096	10	580418	p15.3
SNP_A-1735146	T	T	384	16	377	35	6.967	8.30E-03	rs2790381	10	757721	p15.3
SNP_A-2237871	T	T	264	134	297	109	4.434	3.52E-02	rs10904578	10	934641	p15.3
SNP_A-1675820	C	C	288	110	322	86	4.711	3.00E-02	rs1112787	10	1600899	p15.3
SNP_A-1901878	A	A	207	107	192	138	4.091	4.31E-02	rs10794781	10	1678805	p15.3
SNP_A-2104227	C	C	390	4	410	0	4.183	4.08E-02	rs11250936	10	1967970	p15.3
SNP_A-1928292	C	C	402	0	394	4	4.061	4.39E-02	rs11250965	10	1998811	p15.3
SNP_A-1863176	C	C	393	9	402	2	4.551	3.29E-02	rs964291	10	2107537	p15.3
SNP_A-2049238	G	G	327	51	331	23	9.843	1.70E-03	rs7903764	10	2145503	p15.3
SNP_A-2269413	C	C	283	111	319	85	5.477	1.93E-02	rs11251088	10	2226687	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2199895	A	A	222	128	200	158	4.204	4.03E-02	rs7916097	10	2260448	p15.3
SNP_A-1814282	A	A	224	174	268	138	8.01	4.70E-03	rs7916063	10	2276495	p15.3
SNP_A-2138571	G	G	217	147	272	112	10.388	1.30E-03	rs17819557	10	2280244	p15.3
SNP_A-1992230	G	G	220	174	250	134	6.982	8.20E-03	rs4275540	10	2300173	p15.3
SNP_A-2281750	C	C	400	16	381	29	4.174	4.10E-02	rs12243279	10	2309476	p15.3
SNP_A-2000899	G	G	213	185	244	136	9.171	2.50E-03	rs6560806	10	2311752	p15.3
SNP_A-2290451	T	T	195	159	225	131	4.841	2.78E-02	rs7097906	10	2316129	p15.3
SNP_A-2282276	C	C	224	180	260	156	4.217	4.00E-02	rs2104473	10	2320989	p15.3
SNP_A-1992241	G	G	193	151	230	122	6.226	0.0126	rs10508226	10	2331722	p15.3
SNP_A-1892744	G	G	368	2	318	8	4.481	3.43E-02	rs6560807	10	2334268	p15.3
SNP_A-1700083	G	G	380	16	401	7	3.908	4.81E-02	rs826487	10	2398595	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2105646	C	C	398	18	412	8	4.069	4.37E-02	rs2765689	10	2440237	p15.3
SNP_A-2288438	A	A	391	21	408	8	6.17	1.30E-02	rs2458676	10	2503068	p15.3
SNP_A-1916835	A	A	365	51	386	30	6.032	0.0141	rs17158677	10	2629732	p15.3
SNP_A-1947259	A	A	285	95	333	49	18.417	1.77E-05	rs2388296	10	2631495	p15.3
SNP_A-1992352	G	G	353	39	359	21	5.265	0.0218	rs17158687	10	2635905	p15.3
SNP_A-2109938	G	A	202	150	156	150	4.606	3.19E-02	rs11251400	10	2647127	p15.3
SNP_A-2233585	G	G	204	200	239	169	5.35	0.0207	rs7080305	10	2656834	p15.3
SNP_A-2053828	G	G	211	205	247	173	5.52	1.88E-02	rs12570182	10	2659310	p15.3
SNP_A-1992361	G	G	348	48	375	27	6.844	8.90E-03	rs17158735	10	2671064	p15.3
SNP_A-1890887	T	T	257	159	214	202	9.048	2.60E-03	rs7899257	10	2685158	p15.3
SNP_A-2122138	G	G	245	105	225	145	6.701	9.60E-03	rs17182743	10	2713493	p15.3
SNP_A-1895539	T	T	323	1	304	6	3.84	5.00E-02	rs17158935	10	2761576	p15.3
SNP_A-1948712	G	G	375	37	362	58	4.795	2.85E-02	rs2454837	10	2981774	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1830878	T	T	357	9	341	25	7.896	5.00E-03	rs11251610	10	3006451	p15.2
SNP_A-2043224	T	T	376	8	366	18	3.981	4.60E-02	rs12782126	10	3026072	p15.2
SNP_A-2144073	A	A	308	52	339	35	4.542	3.31E-02	rs11251811	10	3294874	p15.2
SNP_A-1839076	G	G	373	9	365	21	4.866	2.74E-02	rs10904002	10	3305107	p15.2
SNP_A-1814362	C	C	330	10	366	0	10.919	0.001	rs7906885	10	3328183	p15.2
SNP_A-2220584	T	T	374	4	388	0	4.127	4.22E-02	rs562636	10	3339492	p15.2
SNP_A-2121111	A	A	208	188	249	167	4.431	3.53E-02	rs10795026	10	3365666	p15.2
SNP_A-2089880	C	C	335	33	299	57	8.248	4.10E-03	rs4881298	10	4174635	p15.1
SNP_A-1789943	G	G	334	22	321	37	4.066	4.38E-02	rs7913465	10	4193580	p15.1
SNP_A-1652194	A	A	287	109	321	87	4.193	4.06E-02	rs2077668	10	4465571	p15.1
SNP_A-2192665	G	G	267	97	210	114	5.875	0.0154	rs4278426	10	4528795	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209700	T	T	217	185	245	157	3.989	0.0458	rs1904667	10	4554553	p15.1
SNP_A-2163367	T	T	384	6	400	0	6.201	1.28E-02	rs10904290	10	4606862	p15.1
SNP_A-2044217	T	T	299	29	294	10	8.399	0.0038	rs313466	10	4664999	p15.1
SNP_A-1865224	G	G	348	46	332	66	3.928	4.75E-02	rs10904339	10	4813252	p15.1
SNP_A-2098430	C	C	178	170	190	126	5.402	0.0201	rs2961610	10	4825177	p15.1
SNP_A-1855550	A	A	319	9	315	21	4.73	2.96E-02	rs7090237	10	4934816	p15.1
SNP_A-2145576	A	A	402	6	402	16	4.425	3.54E-02	rs7076586	10	5081717	p15.1
SNP_A-2298533	T	T	308	20	271	33	4.648	3.11E-02	rs10904408	10	5094485	p15.1
SNP_A-2000927	G	G	354	52	328	78	6.191	1.28E-02	rs6601899	10	5108322	p15.1
SNP_A-2192903	C	C	332	76	310	102	4.532	3.33E-02	rs10795243	10	5113269	p15.1
SNP_A-2156603	C	C	344	42	338	66	4.979	2.57E-02	rs17134531	10	5236085	p15.1
SNP_A-2237088	A	A	256	54	267	85	4.498	0.0339	rs1574228	10	5302310	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1830831	C	C	338	42	325	65	5.07	2.43E-02	rs4609510	10	5330316	p15.1
SNP_A-2116591	G	G	412	4	406	12	4.039	4.45E-02	rs7895335	10	5347328	p15.1
SNP_A-1800948	C	C	321	57	289	81	5.768	1.63E-02	rs10752008	10	5374715	p15.1
SNP_A-2094861	C	C	209	199	240	150	8.618	0.0033	rs10904468	10	5376067	p15.1
SNP_A-2000931	G	G	262	106	206	124	6.059	0.0138	rs7475825	10	5378149	p15.1
SNP_A-2314859	A	A	319	71	277	91	4.794	0.0286	rs10752010	10	5380759	p15.1
SNP_A-1866569	T	T	292	70	275	95	4.211	0.0402	rs12784234	10	5394261	p15.1
SNP_A-2289824	G	G	170	142	216	126	5.072	2.43E-02	rs7896428	10	5685039	p15.1
SNP_A-2139608	C	C	279	95	254	124	4.992	2.55E-02	rs11259742	10	5687084	p15.1
SNP_A-2070290	G	G	312	100	290	130	4.641	3.12E-02	rs4747358	10	5690199	p15.1
SNP_A-2211720	C	C	270	102	244	138	6.584	0.0103	rs1544216	10	5691584	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181218	C	C	294	122	261	157	6.348	0.0118	rs7924096	10	5692243	p15.1
SNP_A-1714533	G	A	228	172	212	198	6.157	1.31E-02	rs591878	10	5939443	p15.1
SNP_A-1727595	T	T	246	142	284	120	4.25	3.92E-02	rs6602330	10	5948239	p15.1
SNP_A-2242652	G	G	236	112	201	145	7.035	8.00E-03	rs670856	10	5957363	p15.1
SNP_A-2256389	A	A	234	118	194	134	3.912	4.79E-02	rs633930	10	6017941	p15.1
SNP_A-1710808	T	T	360	40	347	65	6.015	1.42E-02	rs791590	10	6094328	p15.1
SNP_A-1834045	G	G	178	168	213	143	5.001	0.0253	rs11598648	10	6124031	p15.1
SNP_A-1920176	G	G	280	78	289	51	5.333	2.09E-02	rs10905669	10	6132099	p15.1
SNP_A-1863724	C	C	373	37	350	58	5.369	2.05E-02	rs12722489	10	6142018	p15.1
SNP_A-1827333	C	C	344	52	371	33	5.187	2.28E-02	rs12251307	10	6163501	p15.1
SNP_A-2238358	C	C	251	95	291	77	4.162	4.13E-02	rs7096344	10	6234482	p15.1
SNP_A-2190478	A	A	305	59	320	40	3.984	4.59E-02	rs1341926	10	6334450	p15.1
SNP_A-2105391	G	G	358	16	343	31	5.108	2.38E-02	rs11258455	10	6475125	p15.1
SNP_A-2116933	C	C	326	16	342	34	5.265	0.0218	rs12257237	10	6475163	p15.1
SNP_A-1906357	C	C	389	19	413	5	8.765	3.10E-03	rs961203	10	6521410	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1993470	C	C	385	15	408	6	4.285	0.0385	rs7918923	10	6540724	p15.1
SNP_A-2155816	G	G	319	97	346	72	4.79	0.0286	rs591441	10	6551392	p15.1
SNP_A-2171816	T	T	378	0	365	5	5.142	2.33E-02	rs501930	10	6573084	p15.1
SNP_A-1681172	C	C	310	78	296	110	5.365	2.05E-02	rs1327689	10	6747603	p14
SNP_A-1993560	G	G	329	69	298	104	8.594	3.40E-03	rs7896871	10	6771382	p14
SNP_A-1884875	A	A	328	66	306	104	8.943	0.0028	rs4747278	10	6771924	p14
SNP_A-1790566	A	A	217	127	191	155	4.431	3.53E-02	rs7096622	10	6821344	p14
SNP_A-1781256	T	T	398	8	418	2	3.854	4.96E-02	rs2791415	10	7000047	p14
SNP_A-1993689	G	A	189	147	187	171	4.998	2.54E-02	rs2490689	10	7009822	p14
SNP_A-2000943	A	G	213	157	205	175	9.955	1.60E-03	rs1417019	10	7017908	p14
SNP_A-1752999	G	G	229	167	268	144	4.446	3.50E-02	rs1417031	10	7022887	p14
SNP_A-2044315	C	C	357	19	387	9	4.266	3.89E-02	rs2066051	10	7047177	p14
SNP_A-2187478	A	A	251	165	211	209	8.621	0.0033	rs885045	10	7056704	p14
SNP_A-1993717	A	T	186	148	169	143	6.269	0.0123	rs885046	10	7057361	p14
SNP_A-1898490	C	C	322	52	280	70	4.796	2.85E-02	rs882778	10	7068729	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2294732	G	G	392	14	408	4	5.832	1.57E-02	rs11254933	10	7076749	p14
SNP_A-2171669	C	C	390	8	412	2	3.89	4.86E-02	rs946292	10	7077591	p14
SNP_A-1781037	A	A	303	93	332	72	3.918	4.78E-02	rs2804132	10	7080931	p14
SNP_A-2246993	C	C	252	160	226	190	3.966	4.64E-02	rs4747385	10	7096022	p14
SNP_A-1993771	A	A	399	9	397	21	4.685	0.0304	rs10508323	10	7185683	p14
SNP_A-1993776	C	C	293	109	321	83	4.793	0.0286	rs2497469	10	7201641	p14
SNP_A-2099792	A	A	374	12	376	4	3.959	4.66E-02	rs2255576	10	7554589	p14
SNP_A-2298816	T	T	308	34	321	57	4.293	3.83E-02	rs1537632	10	7657816	p14
SNP_A-1993941	A	A	313	103	282	132	5.189	2.27E-02	rs10508332	10	7717209	p14
SNP_A-1801559	T	T	273	79	244	100	3.999	4.55E-02	—	10	7723879	p14
SNP_A-1696214	C	C	272	22	358	12	6.061	0.0138	rs3740217	10	7784652	p14
SNP_A-2212865	T	T	237	129	185	137	3.85	4.97E-02	rs4749359	10	8008110	p14
SNP_A-2101428	G	G	317	13	340	4	5.281	2.16E-02	rs4749477	10	8085428	p14
SNP_A-2234210	C	C	363	5	372	0	5.089	0.0241	rs12240458	10	8094363	p14
SNP_A-1851151	A	A	355	37	386	20	6.123	1.33E-02	rs7078148	10	8265407	p14
SNP_A-1677016	G	G	355	31	350	52	5.026	2.50E-02	rs4747760	10	8277669	p14
SNP_A-1994158	G	G	292	120	262	158	6.742	9.40E-03	rs1629795	10	8286481	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2258028	G	G	311	77	330	54	4.581	3.23E-02	rs1796858	10	8320199	p14
SNP_A-2141423	C	A	212	164	214	170	11.149	8.00E-04	rs10737028	10	8364053	p14
SNP_A-2048507	G	G	254	162	226	192	4.171	4.11E-02	rs17466705	10	8366560	p14
SNP_A-1870075	C	C	275	115	301	89	4.487	3.41E-02	rs6602304	10	8525702	p14
SNP_A-2120057	G	G	202	138	236	118	3.921	4.77E-02	rs10795630	10	8552363	p14
SNP_A-1684472	T	C	220	180	214	198	3.915	4.78E-02	rs10508356	10	8567852	p14
SNP_A-2204375	T	C	213	181	214	188	4.236	3.96E-02	rs11255725	10	8591688	p14
SNP_A-1785774	C	A	213	173	205	181	5.308	0.0212	rs11255728	10	8592202	p14
SNP_A-1727515	A	A	367	15	357	33	6.806	9.10E-03	rs1325886	10	8601538	p14
SNP_A-1994303	C	C	253	131	216	170	7.967	4.80E-03	rs2765415	10	8602431	p14
SNP_A-1994306	G	G	258	152	284	116	5.961	0.0146	rs10508355	10	8602564	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800851	T	T	238	106	261	71	7.77	0.0053	rs7096441	10	8603215	p14
SNP_A-1867266	C	C	314	16	301	31	5.056	2.45E-02	rs2454056	10	8614132	p14
SNP_A-2288479	C	C	386	24	349	43	6.85	8.90E-03	rs11255738	10	8630556	p14
SNP_A-1994325	G	G	389	25	371	41	4.3	3.81E-02	rs4747803	10	8632827	p14
SNP_A-1994332	G	G	386	26	376	44	4.683	3.05E-02	rs10508358	10	8637994	p14
SNP_A-1854660	T	T	361	11	364	28	6.904	0.0086	rs7069464	10	8677428	p14
SNP_A-2153351	A	A	211	147	220	110	4.383	3.63E-02	rs4747806	10	8678241	p14
SNP_A-1905619	T	T	390	0	367	5	5.277	2.16E-02	rs17136621	10	8810870	p14
SNP_A-2246605	T	T	361	43	379	19	9.684	0.0019	rs12412730	10	9077279	p14
SNP_A-2106939	C	C	300	24	271	39	4.737	2.95E-02	rs1150037	10	9409537	p14
SNP_A-2024313	G	G	346	26	361	11	6.399	0.0114	rs12252220	10	9585313	p14
SNP_A-2109711	G	G	333	65	341	41	5.203	2.25E-02	rs11256318	10	9818034	p14
SNP_A-2231299	G	G	362	5	386	0	6.344	0.0118	rs17146401	10	9843436	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1842302	C	C	244	90	222	114	3.856	4.96E-02	rs1887038	10	9890229	p14
SNP_A-1994775	T	T	384	18	404	8	4.232	3.97E-02	rs2038922	10	9907914	p14
SNP_A-1813740	A	A	393	21	406	10	4.11	4.26E-02	rs17136681	10	9949747	p14
SNP_A-1816787	A	A	368	40	385	25	3.84	5.00E-02	rs2050775	10	9975691	p14
SNP_A-1832092	G	G	383	17	399	7	4.45	0.0349	rs10752179	10	9986664	p14
SNP_A-1994811	G	G	187	175	207	141	4.399	3.60E-02	rs12572210	10	10003207	p14
SNP_A-1748617	A	A	363	31	393	17	4.957	2.60E-02	rs10508377	10	10071183	p14
SNP_A-1895067	T	C	193	181	197	151	4.875	2.72E-02	rs2762637	10	10134843	p14
SNP_A-1915165	G	G	313	101	343	69	7.391	0.0066	rs2762659	10	10204315	p14
SNP_A-2000956	C	C	323	43	347	21	8.417	3.70E-03	rs991956	10	10211648	p14
SNP_A-2086650	C	C	358	6	343	15	4.129	4.22E-02	rs6602413	10	10308688	p14
SNP_A-2177225	G	G	353	7	348	20	6.208	1.27E-02	rs1572123	10	10315940	p14
SNP_A-1889725	T	T	393	15	395	5	4.926	2.65E-02	rs2031338	10	10626639	p14
SNP_A-1924548	A	A	277	67	252	88	4.003	4.54E-02	rs7084466	10	10655422	p14
SNP_A-2288935	A	A	320	86	352	60	6.11	0.0134	rs17148768	10	10817091	p14
SNP_A-2297373	C	C	369	41	353	65	5.712	1.69E-02	rs2255748	10	11332515	p14
SNP_A-2275805	T	T	280	82	257	113	5.627	1.58E-02	rs3847427	10	11442053	p14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2147976	G	G	242	146	219	179	4.372	3.65E-02	rs10795864	10	11458090	p14
SNP_A-1873283	T	T	305	47	299	77	6.534	0.0106	rs11257078	10	11475212	p14
SNP_A-2262929	T	T	381	31	368	50	4.639	3.12E-02	rs10905973	10	11639047	p14
SNP_A-1796657	A	A	374	24	362	46	6.987	8.20E-03	rs11257202	10	11705337	p14
SNP_A-2222780	C	C	326	86	365	55	8.941	0.0028	rs8181400	10	11753304	p14
SNP_A-1708791	A	A	321	41	310	62	4.338	0.0373	rs717799	10	11923870	p14
SNP_A-2084109	T	T	270	98	283	61	8.116	4.40E-03	rs4620613	10	12011459	p14
SNP_A-1878776	T	T	303	79	272	108	6.163	1.30E-02	rs10458820	10	12617799	p13
SNP_A-1811664	T	T	258	138	208	170	8.275	4.00E-03	rs6602593	10	12617996	p13
SNP_A-2134920	C	C	343	21	384	8	7.113	7.70E-03	rs1888669	10	12965664	p13
SNP_A-2218021	C	C	327	25	369	13	5.106	2.38E-02	rs12766004	10	13133368	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2170593	G	G	252	150	220	178	4.54	3.31E-02	rs825411	10	13209380	p13
SNP_A-1950769	C	C	287	91	261	117	4.484	3.42E-02	rs2095387	10	13223940	p13
SNP_A-1951677	A	A	286	40	310	24	4.87	2.73E-02	rs7090944	10	13246239	p13
SNP_A-1995852	G	G	362	28	401	15	5.09	0.0241	rs11258285	10	13320373	p13
SNP_A-1803604	C	C	236	80	234	112	3.991	0.0458	rs4748048	10	13726689	p13
SNP_A-1863762	G	G	322	22	279	35	4.683	3.05E-02	rs7088455	10	13893858	p13
SNP_A-2300481	C	C	319	23	327	41	4.215	4.01E-02	rs7899777	10	13915596	p13
SNP_A-2224905	G	G	397	17	411	7	4.39	0.0361	rs12780145	10	13957532	p13
SNP_A-1996055	C	C	360	16	380	6	4.956	2.60E-02	rs2610805	10	13959037	p13
SNP_A-2187521	A	G	219	197	228	188	4.622	3.16E-02	rs2698127	10	13971140	p13
SNP_A-2285357	C	C	410	6	403	17	5.302	2.13E-02	rs999856	10	14101702	p13
SNP_A-1949192	T	T	336	62	338	38	5.145	2.33E-02	rs11258843	10	14140238	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835998	C	C	359	21	393	7	8.03	4.60E-03	rs12255822	10	14159525	p13
SNP_A-2188157	C	C	299	21	332	10	4.903	2.68E-02	rs7893591	10	14171767	p13
SNP_A-1996169	A	A	238	164	275	121	9.112	2.50E-03	rs1327000	10	14197267	p13
SNP_A-1893140	A	A	385	7	384	20	6.081	0.0137	rs11258902	10	14235317	p13
SNP_A-1996201	C	C	298	98	318	66	6.71	9.60E-03	rs4750480	10	14267422	p13
SNP_A-2264946	G	G	287	85	319	63	4.828	2.80E-02	rs7919543	10	14270477	p13
SNP_A-1818578	T	T	283	91	321	69	5.083	2.42E-02	rs7068441	10	14274358	p13
SNP_A-2160775	G	G	202	194	236	166	4.772	2.89E-02	rs1228333	10	14369232	p13
SNP_A-1996279	T	T	352	64	373	45	3.915	4.78E-02	rs1218436	10	14405119	p13
SNP_A-2254220	C	C	294	28	325	13	6.656	9.90E-03	rs11259060	10	14479283	p13
SNP_A-1835842	T	T	343	3	293	11	5.813	1.59E-02	rs649005	10	14484623	p13
SNP_A-2304330	T	T	291	21	344	10	5.701	1.70E-02	rs7080073	10	14505116	p13
SNP_A-2231219	A	A	375	27	399	15	3.997	4.56E-02	rs7076985	10	14505512	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909287	T	T	383	29	388	14	5.143	2.33E-02	rs7077023	10	14505603	p13
SNP_A-2270140	C	C	226	84	223	119	4.495	3.40E-02	rs873849	10	14549813	p13
SNP_A-1826056	A	A	321	71	355	49	5.564	0.0183	rs17155533	10	14671263	p13
SNP_A-1871153	G	G	295	23	333	11	5.522	1.88E-02	rs17155568	10	14684461	p13
SNP_A-2037501	C	C	294	88	318	66	4.079	4.34E-02	rs12264162	10	14765460	p13
SNP_A-2109670	C	C	252	132	277	97	6.4	0.0114	rs4750552	10	14771455	p13
SNP_A-1898210	C	C	397	7	409	1	4.635	3.13E-02	rs7087109	10	14805163	p13
SNP_A-2088863	G	G	357	29	340	46	4.268	3.88E-02	rs17267324	10	14805582	p13
SNP_A-1933521	C	C	247	125	296	94	8.389	0.0038	rs7906952	10	15025308	p13
SNP_A-2256281	G	G	200	126	242	104	5.505	0.019	rs10906786	10	15051128	p13
SNP_A-1996456	T	T	243	143	266	114	4.265	3.89E-02	rs2298113	10	15052367	p13
SNP_A-2055882	A	A	318	50	315	77	5.001	0.0253	rs10906798	10	15100282	p13
SNP_A-1882245	A	A	220	124	253	93	6.725	9.50E-03	rs9423931	10	15297756	p13
SNP_A-1877711	T	T	342	38	383	25	4.011	4.52E-02	rs12355407	10	15544597	p13
SNP_A-2091126	C	C	327	33	342	18	4.748	0.0293	rs4750671	10	15623371	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101011	C	C	252	146	205	189	10.333	1.30E-03	rs9333117	10	15742591	p13
SNP_A-1996602	A	A	264	120	243	149	3.914	4.79E-02	rs10904611	10	15744121	p13
SNP_A-2167007	T	T	277	79	297	55	4.973	2.57E-02	rs10904617	10	15838776	p13
SNP_A-1732015	C	C	181	173	204	142	4.334	3.74E-02	rs10508502	10	16245861	p13
SNP_A-2306067	A	A	334	14	325	5	3.911	4.80E-02	rs1340130	10	16343883	p13
SNP_A-1841075	A	A	409	3	402	12	5.456	0.0195	rs1334591	10	16363537	p13
SNP_A-1723140	A	A	335	61	322	88	4.908	2.67E-02	rs902073	10	16527381	p13
SNP_A-1996678	G	G	329	51	315	73	4.125	4.23E-02	rs2000201	10	16562662	p13
SNP_A-1881410	T	T	357	7	373	1	4.716	2.99E-02	rs7079365	10	16810502	p13
SNP_A-1827147	A	A	379	11	397	3	4.863	2.74E-02	rs12098611	10	16816811	p13
SNP_A-2066225	C	C	256	96	263	69	3.931	4.74E-02	rs2603796	10	16911462	p13
SNP_A-1843661	C	C	263	111	228	134	4.46	3.47E-02	rs10904851	10	17037833	p13
SNP_A-1865891	G	G	250	124	211	159	7.607	5.80E-03	rs7906242	10	17041818	p13
SNP_A-2087601	G	G	280	118	257	149	4.505	3.38E-02	rs10904861	10	17070781	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1877968	G	G	326	32	365	15	7.701	5.50E-03	rs11254338	10	17119757	p13
SNP_A-1842301	G	G	203	165	245	145	4.593	3.21E-02	rs7088365	10	17682092	p12.33
SNP_A-2206269	T	T	217	187	248	160	4.148	4.17E-02	rs10764331	10	18491842	p12.33
SNP_A-1997092	A	A	199	185	231	155	5.023	2.50E-02	rs10764332	10	18491975	p12.33
SNP_A-2184901	C	C	258	146	281	117	4.135	4.20E-02	---	10	18651683	p12.32
SNP_A-2030670	A	A	289	25	317	13	4.689	0.0304	rs10826808	10	19346184	p12.31
SNP_A-1729296	C	C	282	114	260	150	5.561	0.0184	rs4748559	10	19471446	p12.31
SNP_A-1905018	T	T	267	111	284	76	6.64	0.01	rs3904890	10	19808713	p12.31
SNP_A-2313295	G	G	403	13	394	26	4.416	0.0356	rs7910815	10	19872053	p12.31
SNP_A-1705573	G	A	210	190	234	176	7.439	6.40E-03	rs1409737	10	19890336	p12.31
SNP_A-2045927	G	C	219	153	178	166	8.102	4.40E-03	rs10740924	10	19907692	p12.31
SNP_A-2084774	A	A	179	165	213	125	8.414	3.70E-03	rs7080370	10	19909639	p12.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1719555	G	G	392	8	391	21	5.653	1.74E-02	rs10508588	10	19918902	p12.31
SNP_A-2279081	C	C	221	187	255	153	5.829	1.58E-02	rs1326983	10	19976417	p12.31
SNP_A-2260873	C	C	375	9	277	31	18.709	0.000015227	rs7070245	10	19981014	p12.31
SNP_A-2271167	T	T	394	6	388	18	6.002	0.0143	rs2358472	10	20003009	p12.31
SNP_A-1951366	T	T	402	8	397	19	4.469	3.45E-02	rs2358473	10	20003072	p12.31
SNP_A-1794818	G	G	183	169	229	143	6.755	9.30E-03	rs7916152	10	20004919	p12.31
SNP_A-1997693	T	T	234	98	204	134	7.588	5.90E-03	rs943124	10	20192739	p12.31
SNP_A-1736857	T	T	379	21	371	41	6.361	0.0117	rs10508606	10	20280137	p12.31
SNP_A-2261322	C	C	257	159	229	191	4.52	3.35E-02	rs10764184	10	20345947	p12.31
SNP_A-1872018	G	G	181	141	208	114	4.733	2.96E-02	rs7917108	10	20713920	p12.31
SNP_A-2293193	C	C	389	3	391	13	6.076	0.0137	rs1339662	10	20836524	p12.31
SNP_A-2133611	A	A	305	101	274	124	3.932	4.74E-02	rs11012270	10	21017161	p12.31
SNP_A-2091533	T	T	235	161	255	117	7.037	8.00E-03	rs7393234	10	21057217	p12.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1998001	T	T	226	138	192	168	5.685	1.71E-02	rs1467643	10	21098922	p12.31
SNP_A-1901804	C	C	245	171	214	204	4.993	2.55E-02	rs2038915	10	21118073	p12.31
SNP_A-2190133	T	T	359	25	381	11	6.017	1.42E-02	rs788957	10	21211860	p12.31
SNP_A-2263780	A	A	370	34	395	19	4.941	2.62E-02	rs788985	10	21230699	p12.31
SNP_A-2235419	C	C	363	21	376	10	4.127	4.22E-02	rs4543885	10	21280538	p12.31
SNP_A-2159361	T	T	325	49	306	72	4.923	2.65E-02	rs4748793	10	22523017	p12.31
SNP_A-2126213	T	T	349	1	365	7	4.192	4.06E-02	rs11012972	10	22706663	p12.2
SNP_A-2046662	C	C	299	91	272	118	4.765	2.90E-02	rs12357444	10	22904043	p12.2
SNP_A-2092810	C	C	254	90	229	113	3.894	4.85E-02	rs1778338	10	22972915	p12.2
SNP_A-2196584	C	C	319	69	292	98	6.224	0.0126	rs10828389	10	23318053	p12.2
SNP_A-2172014	A	A	409	7	419	1	4.602	3.19E-02	rs16923499	10	23909713	p12.2
SNP_A-2159269	C	C	409	7	419	1	4.602	3.19E-02	rs7900373	10	23929215	p12.2
SNP_A-1946190	A	A	361	7	342	0	6.57	0.0104	rs1337320	10	23976218	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1855632	G	-	205	149	171	171	4.381	3.63E-02	rs10828594	10	24374934	p12.2
SNP_A-2167478	T	T	357	21	362	10	3.89	4.86E-02	rs16924302	10	24448404	p12.2
SNP_A-1951932	T	T	205	93	209	135	4.503	3.38E-02	rs10741050	10	24640553	p12.1
SNP_A-2175498	C	C	338	64	371	45	4.61	3.18E-02	rs6482450	10	25208126	p12.1
SNP_A-2021743	A	A	399	11	415	3	4.809	2.83E-02	rs16925223	10	25329740	p12.1
SNP_A-1792891	C	C	259	103	273	59	11.043	9.00E-04	rs4749009	10	25441711	p12.1
SNP_A-1998720	C	C	273	135	310	100	7.556	6.00E-03	rs2887041	10	25477868	p12.1
SNP_A-1906744	A	A	245	123	232	164	5.192	2.27E-02	rs10828762	10	25494756	p12.1
SNP_A-1906944	A	A	377	39	392	24	3.864	4.93E-02	rs1413394	10	25614386	p12.1
SNP_A-1998777	C	C	295	83	296	52	5.891	0.0152	rs1630323	10	25717515	p12.1
SNP_A-2283734	G	G	348	26	343	47	5.745	1.65E-02	rs1773681	10	25746982	p12.1
SNP_A-1874924	T	T	345	35	315	51	4.079	4.34E-02	rs16926240	10	26003935	p12.1
SNP_A-2247438	T	T	319	53	317	29	6.097	0.0135	rs11014745	10	26110220	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1886396	T	T	342	50	381	33	4.989	2.55E-02	rs17812509	10	26133887	p12.1
SNP_A-2001057	T	T	334	74	309	99	4.585	3.23E-02	rs7094825	10	27108316	p12.1
SNP_A-1741009	C	C	314	46	309	75	6.223	0.0126	rs2182294	10	27123075	p12.1
SNP_A-2223283	A	A	360	8	381	1	5.78	1.62E-02	rs12219637	10	27265910	p12.1
SNP_A-1957717	A	A	236	140	257	111	4.16	4.14E-02	rs882474	10	27517871	p12.1
SNP_A-2130806	G	G	331	69	311	93	4.159	4.14E-02	rs237591	10	27657795	p12.1
SNP_A-1902156	T	T	406	4	412	0	4.039	4.45E-02	rs2242356	10	27862822	p12.1
SNP_A-2041904	G	G	412	4	420	0	4.058	4.40E-02	rs17756253	10	27871257	p12.1
SNP_A-2036184	C	C	336	0	307	5	5.426	1.98E-02	rs16928617	10	28549302	p12.1
SNP_A-1943303	G	G	322	62	306	86	4.218	4.00E-02	rs10763654	10	28580644	p12.1
SNP_A-2139442	T	T	344	58	319	79	4.142	4.18E-02	rs7086943	10	28600457	p12.1
SNP_A-1710976	G	G	326	64	358	46	4.197	4.05E-02	rs787116	10	29038879	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1871618	A	A	354	12	303	25	6.465	1.10E-02	rs16929252	10	29139890	p12.1
SNP_A-2072359	T	T	341	3	301	11	5.516	1.88E-02	rs12246394	10	29192809	p12.1
SNP_A-2121635	A	A	407	1	404	10	7.331	6.80E-03	rs12267042	10	29210568	p12.1
SNP_A-2052388	C	C	307	37	330	22	4.553	3.29E-02	rs1763367	10	29340286	p12.1
SNP_A-2123189	T	T	323	47	346	26	6.826	9.00E-03	rs6481558	10	29343287	p12.1
SNP_A-2053493	T	T	338	20	309	39	7.278	7.00E-03	rs1763404	10	29383831	p12.1
SNP_A-2170053	C	C	373	39	347	61	5.76	1.64E-02	rs2783419	10	29466098	p11.23
SNP_A-2197169	T	T	305	65	283	91	5.135	2.34E-02	rs549235	10	29477846	p11.23
SNP_A-2049368	C	C	366	42	351	63	4.47	3.45E-02	rs12267702	10	29559236	p11.23
SNP_A-2285434	C	C	307	51	320	28	6.825	9.00E-03	rs10826581	10	29568066	p11.23
SNP_A-2036230	C	C	369	1	338	16	14.248	2.00E-04	rs11007506	10	29611435	p11.23
SNP_A-2095859	C	T	211	159	180	178	3.904	0.0482	rs1774950	10	29622254	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2203430	G	G	363	13	358	4	4.535	0.0332	rs11007515	10	29622453	p11.23
SNP_A-1999714	G	G	299	71	285	99	4.689	0.0304	rs1467678	10	29697279	p11.23
SNP_A-1904990	C	C	320	48	346	32	4.082	4.34E-02	rs11816750	10	29749892	p11.23
SNP_A-2061378	A	A	416	0	414	4	4	4.55E-02	rs10160200	10	29813332	p11.23
SNP_A-2272767	G	G	349	47	380	26	7.236	7.10E-03	rs4749460	10	29902974	p11.23
SNP_A-1654683	A	A	358	40	343	61	4.643	3.12E-02	rs1265446	10	29945313	p11.23
SNP_A-2201675	G	G	286	32	274	54	5.732	0.0167	rs1247456	10	29987760	p11.23
SNP_A-2247114	G	G	341	45	299	73	9.145	2.50E-03	rs10826674	10	29991633	p11.23
SNP_A-2270445	G	G	290	106	322	82	4.657	0.0309	rs1148205	10	30009185	p11.23
SNP_A-2046576	C	C	237	127	225	171	5.471	1.93E-02	rs4747691	10	30306975	p11.23
SNP_A-1999737	C	C	379	27	398	14	4.543	3.31E-02	rs16931056	10	30427021	p11.23
SNP_A-2132731	C	C	398	6	412	0	6.164	1.30E-02	rs17229307	10	30527404	p11.23
SNP_A-1924366	T	T	354	2	287	11	8.154	0.0043	rs1720618	10	30540133	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1756799	C	C	340	28	333	47	4.695	3.03E-02	rs533049	10	30540578	p11.23
SNP_A-2079300	A	A	323	25	263	45	9.454	2.10E-03	rs586594	10	30628679	p11.23
SNP_A-2100739	C	C	380	34	396	20	3.955	4.67E-02	---	10	30990735	p11.23
SNP_A-1947181	G	G	354	2	355	9	4.368	3.66E-02	rs11008345	10	31426485	p11.22
SNP_A-1809818	T	T	390	0	353	5	5.484	1.92E-02	rs1771635	10	31487985	p11.22
SNP_A-1683792	T	T	367	5	378	0	5.115	2.37E-02	rs2797894	10	31492471	p11.22
SNP_A-2026805	A	A	316	0	310	4	4.051	0.0441	rs1313045	10	31493965	p11.22
SNP_A-2290963	C	C	370	22	383	11	3.886	0.0487	rs11008400	10	31505583	p11.22
SNP_A-2241183	G	G	321	5	332	0	5.131	0.0235	---	10	31588413	p11.22
SNP_A-2036589	C	C	331	29	350	16	4.236	3.96E-02	rs7894459	10	31651262	p11.22
SNP_A-1732902	A	A	361	27	382	14	4.634	3.13E-02	rs161273	10	31749387	p11.22
SNP_A-1999760	G	G	378	6	366	0	5.765	1.63E-02	rs7896996	10	31785541	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1809907	C	C	365	19	372	8	4.527	3.34E-02	rs11008538	10	31926640	p11.22
SNP_A-2099564	T	T	219	151	258	126	5.187	2.28E-02	rs4747755	10	31928437	p11.22
SNP_A-2296486	T	T	288	128	319	101	4.748	0.0293	rs3858249	10	32069770	p11.22
SNP_A-1748375	T	T	360	36	349	55	4.058	4.40E-02	rs10508771	10	32496098	p11.22
SNP_A-2286699	G	G	348	0	302	6	6.842	8.90E-03	rs3006741	10	32905820	p11.22
SNP_A-1913865	C	C	304	34	322	16	6.998	8.20E-03	rs9418016	10	33006621	p11.22
SNP_A-1693355	A	A	284	64	307	43	5.011	0.0252	rs2070302	10	33415441	p11.22
SNP_A-2131223	A	A	408	6	418	0	6.102	0.0135	rs11009230	10	33442397	p11.22
SNP_A-1728277	C	C	339	61	373	37	7.379	0.0066	rs2180562	10	33442573	p11.22
SNP_A-1686518	G	G	339	61	374	38	6.886	8.70E-03	rs10508780	10	33443238	p11.22
SNP_A-2257663	T	C	181	155	194	148	7.616	5.80E-03	rs2666236	10	33458878	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1867990	G	G	264	118	301	85	7.767	0.0053	rs722987	10	33466245	p11.22
SNP_A-1888285	A	A	332	50	366	30	6.406	0.0114	rs4290167	10	33472549	p11.22
SNP_A-1738014	T	G	210	152	198	192	5.817	1.59E-02	rs2254826	10	33508471	p11.22
SNP_A-2153082	G	G	242	76	279	45	10.515	1.20E-03	rs734187	10	33524702	p11.22
SNP_A-2158123	A	G	198	182	224	178	4.794	0.0286	rs2247383	10	33529058	p11.22
SNP_A-2112725	T	C	205	199	237	175	5.602	1.79E-02	rs2247396	10	33529198	p11.22
SNP_A-1999791	C	T	209	185	215	175	5.24	2.21E-02	rs2247486	10	33529600	p11.22
SNP_A-2262976	G	G	388	28	397	15	4.014	4.51E-02	rs16934435	10	33697216	p11.22
SNP_A-2055276	A	C	163	157	200	144	5.495	1.91E-02	rs10740870	10	33697370	p11.22
SNP_A-2200759	G	G	300	90	270	122	6.404	0.0114	rs2785262	10	33727661	p11.22
SNP_A-1842702	C	C	211	177	260	140	9.236	2.40E-03	rs7910887	10	33730587	p11.22
SNP_A-2249435	G	G	232	180	264	154	4.045	4.43E-02	rs2785273	10	33739679	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2261756	G	G	228	172	254	138	5.051	0.0246	rs2804468	10	33742037	p11.22
SNP_A-1909258	T	T	339	7	368	0	7.519	6.10E-03	rs2804858	10	33811642	p11.22
SNP_A-1999808	A	A	310	90	350	66	5.805	0.016	rs2785245	10	33835486	p11.22
SNP_A-2293296	G	G	219	185	245	153	4.442	3.51E-02	rs3851083	10	33902733	p11.22
SNP_A-2071346	A	A	257	87	269	61	4.552	3.29E-02	rs7073701	10	34068768	p11.22
SNP_A-2089649	G	G	291	95	329	71	5.551	1.85E-02	rs7074089	10	34068914	p11.22
SNP_A-2116122	A	A	309	67	285	89	4.067	4.37E-02	rs9663087	10	34084463	p11.22
SNP_A-1999814	C	C	302	46	330	24	8.104	4.40E-03	rs1412116	10	34113154	p11.22
SNP_A-2115276	G	G	395	9	408	2	4.621	3.16E-02	rs16935052	10	34410354	p11.22
SNP_A-2232622	G	G	393	9	392	2	4.376	3.65E-02	rs7082440	10	34437069	p11.22
SNP_A-1934706	A	A	402	8	414	0	8.157	0.0043	rs12415499	10	34438526	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1793387	G	G	390	8	409	1	5.719	1.68E-02	rs773949	10	34756329	p11.21
SNP_A-2169220	T	T	275	109	309	87	4.265	3.89E-02	rs4934670	10	35141557	p11.21
SNP_A-1821931	C	C	240	146	198	164	4.307	3.80E-02	rs11009981	10	35175415	p11.21
SNP_A-2139139	T	T	245	157	277	125	5.593	1.80E-02	rs11010152	10	35607133	p11.21
SNP_A-1648008	C	C	220	130	256	108	4.484	3.42E-02	rs2474519	10	35645577	p11.21
SNP_A-1753053	A	A	244	156	280	132	4.297	3.82E-02	rs2504371	10	35680738	p11.21
SNP_A-2027073	C	C	224	134	273	117	4.622	3.16E-02	rs3003981	10	35758218	p11.21
SNP_A-2162228	T	T	245	159	283	131	5.317	2.11E-02	rs3003980	10	35763435	p11.21
SNP_A-1891805	G	G	378	36	362	58	5.452	0.0195	rs10827512	10	35855733	p11.21
SNP_A-1999879	C	C	268	126	299	103	3.925	4.76E-02	rs10827514	10	35904391	p11.21
SNP_A-1915842	T	T	300	70	271	101	7.087	7.80E-03	rs7899248	10	35918798	p11.21
SNP_A-2146454	A	A	352	64	327	85	3.861	4.94E-02	rs17511194	10	36076786	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1956638	G	G	341	53	318	82	6.987	8.20E-03	rs752431	10	36078281	p11.21
SNP_A-2314449	T	T	346	36	327	63	7.818	5.20E-03	rs11010290	10	36100315	p11.21
SNP_A-2269315	T	T	350	22	369	9	5.906	1.51E-02	rs10827555	10	36149896	p11.21
SNP_A-1952337	C	C	388	8	412	2	3.922	4.77E-02	rs772071	10	36257387	p11.21
SNP_A-1904091	C	C	391	7	404	0	7.168	7.40E-03	rs772068	10	36258019	p11.21
SNP_A-1999930	A	A	380	36	395	21	4.238	0.0395	rs12248610	10	36378221	p11.21
SNP_A-1886127	T	T	314	18	297	5	6.416	1.13E-02	rs11010473	10	36451177	p11.21
SNP_A-2187590	G	G	274	132	248	168	5.494	1.91E-02	rs2505600	10	36924912	p11.21
SNP_A-2117745	A	A	344	46	309	65	4.795	2.85E-02	rs12779376	10	37874740	p11.21
SNP_A-2000063	A	A	313	59	345	41	4.539	3.31E-02	rs2384732	10	38494927	p11.21
SNP_A-1693319	G	G	324	76	357	55	4.789	0.0286	rs10508864	10	38548925	p11.1
SNP_A-2309568	T	T	258	144	220	164	3.909	4.80E-02	rs11266166	10	41753546	q11.1
SNP_A-1932502	A	A	330	12	309	23	4	4.55E-02	rs11239769	10	42587903	q11.21
SNP_A-2274708	T	T	222	94	208	136	6.95	8.40E-03	rs1008751	10	42614580	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2217964	G	G	229	133	207	171	5.517	1.88E-02	rs2744070	10	42693206	q11.21
SNP_A-2247102	A	A	310	56	338	34	6.539	0.0106	rs788239	10	42727505	q11.21
SNP_A-1877905	C	C	321	85	281	129	11.685	6.00E-04	rs2487918	10	42745434	q11.21
SNP_A-1781273	A	A	320	86	334	58	5.5	0.019	rs2435377	10	43003606	q11.21
SNP_A-1875751	A	A	312	86	349	63	5.381	2.04E-02	rs1879310	10	43054781	q11.21
SNP_A-1878422	A	A	315	91	331	67	3.963	0.0465	rs7093409	10	43060073	q11.21
SNP_A-2113213	C	C	363	15	368	6	3.87	4.92E-02	rs11238503	10	43101097	q11.21
SNP_A-1735308	C	C	349	51	384	30	6.877	8.70E-03	rs951259	10	43485070	q11.21
SNP_A-2000209	C	C	248	78	272	54	5.471	1.93E-02	rs951260	10	43520976	q11.21
SNP_A-2202815	G	G	362	54	386	30	7.627	5.70E-03	rs11238649	10	43529347	q11.21
SNP_A-1754844	G	G	349	51	381	31	6.105	0.0135	rs7477243	10	43542313	q11.21
SNP_A-1700356	C	C	341	43	381	29	4.091	4.31E-02	rs994358	10	43542487	q11.21
SNP_A-2138605	G	G	348	36	376	18	6.955	8.40E-03	rs4948759	10	43550907	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2224171	A	A	306	66	343	43	6.706	9.60E-03	rs1335895	10	43551033	q11.21
SNP_A-2275662	A	A	348	38	381	23	4.775	2.89E-02	rs2152456	10	43558357	q11.21
SNP_A-2097667	C	C	393	15	407	5	5.226	0.0223	rs17154333	10	43572802	q11.21
SNP_A-2176717	G	G	363	43	377	25	5.01	0.0252	rs10899893	10	43572824	q11.21
SNP_A-2182632	G	G	358	50	386	32	4.885	2.71E-02	rs10899912	10	43616899	q11.21
SNP_A-1871440	T	T	412	0	416	6	5.9	1.51E-02	rs2025623	10	43701318	q11.21
SNP_A-2133169	A	A	414	0	412	4	4	4.55E-02	rs1947673	10	43705960	q11.21
SNP_A-1936190	G	G	402	10	417	1	7.595	5.90E-03	rs268329	10	43869892	q11.21
SNP_A-2176734	C	C	324	52	321	79	4.841	2.78E-02	rs1253933	10	44234390	q11.21
SNP_A-2197955	A	A	306	36	308	66	7.415	6.50E-03	rs1147952	10	44286282	q11.21
SNP_A-1875813	C	C	412	4	420	0	4.058	4.40E-02	rs6593432	10	44467292	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1901032	T	T	369	13	364	2	7.762	0.0053	rs10900105	10	44557587	q11.21
SNP_A-2174428	C	C	412	4	420	0	4.058	4.40E-02	rs17157094	10	44654956	q11.21
SNP_A-2100102	G	G	410	4	422	0	4.097	4.30E-02	rs10450473	10	44686913	q11.21
SNP_A-1927005	G	G	394	4	412	0	4.161	4.14E-02	rs10450474	10	44687234	q11.21
SNP_A-2286956	G	G	401	1	405	7	4.398	3.60E-02	rs3780900	10	45218919	q11.21
SNP_A-2035224	A	A	272	140	307	105	7.116	0.0076	rs11259760	10	47110611	q11.22
SNP_A-1934300	G	G	230	88	271	67	5.596	1.80E-02	rs11259762	10	47110763	q11.22
SNP_A-2239270	G	G	218	98	274	72	9.009	2.70E-03	rs7920880	10	47115003	q11.22
SNP_A-2122357	T	T	240	140	293	105	9.859	1.70E-03	rs7057753	10	47115440	q11.22
SNP_A-1909516	T	T	212	110	273	87	8.266	4.00E-03	rs7086842	10	47117276	q11.22
SNP_A-2125249	C	C	247	143	281	113	5.685	1.71E-02	rs7895458	10	47131895	q11.22
SNP_A-1709179	A	A	328	36	318	78	14.306	2.00E-04	rs1062225	10	48987829	q11.22
SNP_A-2000415	G	G	381	19	391	7	5.663	1.73E-02	rs17010723	10	49081449	q11.22
SNP_A-1870781	C	C	346	26	370	14	4.215	4.01E-02	rs10857548	10	49088476	q11.22
SNP_A-2301137	G	G	378	18	397	7	5.226	2.22E-02	rs17770021	10	49089981	q11.22
SNP_A-1679310	G	G	320	30	315	67	12.778	4.00E-04	rs1345107	10	49139084	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932607	G	G	320	68	299	99	6.341	0.0118	rs7909968	10	49459947	q11.22
SNP_A-2070010	G	G	282	104	315	79	5.158	2.31E-02	rs10776637	10	49589807	q11.23
SNP_A-1873127	T	T	291	117	261	149	5.475	1.93E-02	rs1904601	10	49590614	q11.23
SNP_A-2059024	C	C	315	69	292	100	6.476	0.0109	rs4838644	10	49595747	q11.23
SNP_A-1702775	G	G	391	9	412	2	4.764	2.91E-02	rs10508912	10	49731490	q11.23
SNP_A-1815332	A	A	238	136	225	175	4.387	3.62E-02	rs2663038	10	49769474	q11.23
SNP_A-2044920	A	A	397	17	414	6	5.574	1.82E-02	rs2663018	10	49817030	q11.23
SNP_A-2217995	G	G	366	16	385	5	6.16	1.31E-02	rs2663017	10	49817088	q11.23
SNP_A-2000504	G	G	399	17	416	6	5.573	1.82E-02	rs2252692	10	49863058	q11.23
SNP_A-1785112	A	A	174	170	205	147	4.113	4.26E-02	rs6537587	10	49864414	q11.23
SNP_A-1852546	C	C	364	38	372	22	4.274	3.87E-02	rs17175928	10	49967571	q11.23
SNP_A-1829592	G	G	375	11	391	3	4.824	0.0281	rs17009617	10	50123939	q11.23
SNP_A-2000541	A	A	410	4	418	0	4.058	4.40E-02	rs17009940	10	50233517	q11.23
SNP_A-1798223	C	C	337	29	354	12	7.467	0.0063	rs4253077	10	50392975	q11.23
SNP_A-1956441	T	T	356	44	372	28	3.907	4.81E-02	rs4253073	10	50393690	q11.23
SNP_A-2121086	T	T	359	57	379	39	3.912	4.79E-02	rs1880674	10	50474584	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2310809	G	G	229	187	264	158	4.88	2.72E-02	rs1917805	10	50475989	q11.23
SNP_A-1812524	G	G	331	83	301	117	7.185	7.40E-03	rs1880676	10	50494123	q11.23
SNP_A-2042036	C	C	244	168	214	196	4.114	4.25E-02	rs1258241	10	50580914	q11.23
SNP_A-2292780	A	G	189	175	220	178	3.947	0.047	rs7916489	10	50582890	q11.23
SNP_A-2214306	T	T	307	21	287	37	5.063	2.44E-02	rs7893806	10	50635209	q11.23
SNP_A-2184173	C	C	368	8	381	1	5.623	0.0177	rs10821609	10	51220923	q11.23
SNP_A-2055414	A	A	307	109	275	147	7.357	6.70E-03	rs930325	10	51702899	q11.23
SNP_A-2000631	T	T	315	77	287	101	4.518	3.35E-02	rs10508927	10	51797457	q11.23
SNP_A-2272813	T	T	281	69	267	97	4.808	2.83E-02	rs7086029	10	51837448	q11.23
SNP_A-1795415	A	A	321	81	296	106	4.355	3.69E-02	rs10825978	10	51855329	q11.23
SNP_A-2046220	C	C	226	188	259	163	3.95	4.69E-02	rs1203392	10	51874999	q11.23
SNP_A-2119569	C	C	215	185	250	154	5.449	1.96E-02	rs1203387	10	51876384	q11.23
SNP_A-2000650	C	C	202	130	213	99	3.871	4.91E-02	rs4935712	10	51929419	q11.23
SNP_A-1950431	C	C	202	140	230	114	4.47	3.45E-02	rs10826118	10	51932474	q11.23
SNP_A-2171128	C	C	306	40	328	24	4.712	2.99E-02	rs2983352	10	51961614	q11.23
SNP_A-2103178	G	G	267	115	242	144	4.454	3.48E-02	rs7916397	10	51972588	q11.23
SNP_A-2000658	A	A	285	123	257	151	4.308	3.79E-02	rs9299582	10	51974286	q11.23
SNP_A-2254893	G	G	392	4	390	0	3.96	4.66E-02	rs3001859	10	52095755	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2152279	G	G	332	38	336	22	4.094	4.30E-02	rs17501695	10	52379989	q11.23
SNP_A-2301861	G	G	282	38	327	23	5.682	1.71E-02	rs2816835	10	52422640	q11.23
SNP_A-1862335	C	C	344	64	363	43	4.627	0.0315	rs7921154	10	52546800	q11.23
SNP_A-1816782	G	G	193	163	220	132	5	0.0253	rs9415721	10	52547139	q11.23
SNP_A-2133691	G	G	341	59	357	39	4.428	3.53E-02	rs7918898	10	52551029	q11.23
SNP_A-1860308	C	C	346	56	364	38	3.903	0.0482	rs4489691	10	52551315	q11.23
SNP_A-2211985	G	G	198	180	226	130	9.262	0.0023	rs3851088	10	52600321	q21.1
SNP_A-1918686	C	C	279	39	313	19	8.552	3.50E-03	rs10996389	10	52691606	q21.1
SNP_A-2000707	C	C	374	30	385	15	5.14	2.34E-02	rs10490973	10	52693406	q21.1
SNP_A-2288343	T	C	195	177	228	164	8.581	3.40E-03	rs10822915	10	52828093	q21.1
SNP_A-1934793	C	C	352	12	387	1	10.21	0.0014	rs17629494	10	53230904	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2000760	C	C	285	121	255	149	4.565	3.26E-02	rs1937690	10	53254240	q21.1
SNP_A-1870196	T	T	289	77	275	107	4.899	0.0269	rs11000409	10	53425383	q21.1
SNP_A-2177559	C	C	377	19	398	8	4.927	0.0264	rs3862583	10	53540581	q21.1
SNP_A-2072144	C	C	316	18	351	9	3.868	4.92E-02	rs1910542	10	53691991	q21.1
SNP_A-2104880	T	T	277	85	285	59	4.352	3.70E-02	rs1194722	10	53863824	q21.1
SNP_A-1726000	A	A	232	164	276	136	6.11	0.0134	rs10508989	10	54246797	q21.1
SNP_A-2058326	A	A	374	30	362	56	7.82	5.20E-03	rs11003249	10	54320949	q21.1
SNP_A-2231256	A	A	359	41	352	66	5.517	1.88E-02	rs1343061	10	54327843	q21.1
SNP_A-1834468	G	G	327	25	340	12	4.821	0.0281	rs7087469	10	54339854	q21.1
SNP_A-2240262	T	T	296	68	284	40	5.2	2.26E-02	rs12356267	10	54363956	q21.1
SNP_A-2212968	A	A	213	203	249	173	5.156	2.32E-02	rs10066677	10	54553366	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1847798	G	G	244	146	266	114	4.758	0.0292	rs11003403	10	54554856	q21.1
SNP_A-2091569	C	C	194	186	216	146	5.566	0.0183	rs10762926	10	54555442	q21.1
SNP_A-1821587	G	G	270	100	315	61	12.861	3.00E-04	rs1871072	10	54571008	q21.1
SNP_A-2000913	C	C	236	164	272	118	9.93	1.60E-03	rs10824900	10	54572148	q21.1
SNP_A-2146208	C	C	227	113	272	76	11.21	8.00E-04	rs950899	10	54572805	q21.1
SNP_A-2152816	C	C	222	168	247	125	7.222	7.20E-03	rs4417179	10	54573992	q21.1
SNP_A-1813143	C	C	239	171	280	132	8.254	4.10E-03	rs11003413	10	54574911	q21.1
SNP_A-2152600	A	A	286	126	326	84	11.01	9.00E-04	rs10824909	10	54581212	q21.1
SNP_A-1957598	T	T	260	134	240	166	4.034	4.46E-02	rs11592074	10	54591905	q21.1
SNP_A-2057928	G	G	276	82	310	60	5.185	2.28E-02	rs10824931	10	54592005	q21.1
SNP_A-2124430	A	A	322	24	334	8	8.197	4.20E-03	rs16937420	10	54815535	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2127318	A	A	285	31	300	14	6.801	9.10E-03	rs17619615	10	54838738	q21.1
SNP_A-2179222	T	T	274	44	293	27	4.701	3.01E-02	rs16937446	10	54906079	q21.1
SNP_A-2043492	C	C	332	44	350	26	5.104	2.39E-02	rs16937596	10	55026673	q21.1
SNP_A-2000963	A	A	328	58	347	35	6.202	1.28E-02	rs767605	10	55064138	q21.1
SNP_A-2100300	C	C	332	56	317	89	7.453	0.0063	rs16937849	10	55417776	q21.1
SNP_A-2278731	C	C	327	43	308	70	6.935	8.50E-03	rs7094237	10	55417798	q21.1
SNP_A-2143116	T	T	240	160	196	182	5.238	2.21E-02	rs10825207	10	55472924	q21.1
SNP_A-2309252	A	A	217	173	248	144	4.715	2.99E-02	rs10763079	10	55605400	q21.1
SNP_A-2001032	A	A	234	174	264	144	4.637	3.13E-02	rs10490981	10	55608139	q21.1
SNP_A-1846224	A	A	380	14	360	28	5.161	2.31E-02	rs16905671	10	55615237	q21.1
SNP_A-1794184	A	A	213	145	242	118	4.615	3.17E-02	rs12774588	10	55623177	q21.1
SNP_A-2250049	A	A	374	34	337	49	4.03	4.47E-02	rs1962905	10	55632174	q21.1
SNP_A-2198160	C	C	310	34	264	52	6.277	1.22E-02	rs10740578	10	55636727	q21.1
SNP_A-1819910	C	C	308	76	324	50	5.639	1.76E-02	rs10825411	10	56296559	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1743949	G	G	388	8	410	2	3.891	4.85E-02	rs10509037	10	56767043	q21.1
SNP_A-2117794	C	T	209	157	185	175	5.254	2.19E-02	rs10763235	10	57126906	q21.1
SNP_A-1912083	C	A	219	173	202	188	4.599	3.20E-02	rs10740625	10	57153659	q21.1
SNP_A-1906624	T	C	203	163	193	175	4.597	3.20E-02	rs16907792	10	57171060	q21.1
SNP_A-2149817	G	G	216	156	241	129	3.92	4.77E-02	rs10763254	10	57172084	q21.1
SNP_A-1751103	C	C	396	4	400	14	5.336	2.09E-02	rs10509050	10	57710863	q21.1
SNP_A-1704337	T	T	394	4	393	13	4.687	0.0304	rs10509051	10	57711739	q21.1
SNP_A-1718927	T	T	392	4	395	13	4.598	3.20E-02	rs10509052	10	57714976	q21.1
SNP_A-1713217	T	T	344	0	361	7	6.608	0.0101	rs10509053	10	57717874	q21.1
SNP_A-2269447	A	A	321	67	309	93	4.207	4.03E-02	rs12098738	10	58057613	q21.1
SNP_A-2243294	A	A	362	40	347	59	3.944	0.047	rs11818464	10	58276665	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932963	G	G	341	31	350	16	4.856	0.0276	rs11005830	10	58951885	q21.1
SNP_A-1923190	A	A	412	4	405	15	6.409	0.0114	rs2393316	10	59003077	q21.1
SNP_A-2166324	C	C	213	179	238	146	4.655	0.031	rs6481297	10	59003316	q21.1
SNP_A-1911161	C	C	247	155	280	126	5.04	2.48E-02	rs6481298	10	59010736	q21.1
SNP_A-2108547	C	C	291	89	322	58	8.105	4.40E-03	rs12267635	10	59022373	q21.1
SNP_A-2221832	G	G	307	89	335	63	5.664	1.73E-02	rs17621800	10	59026621	q21.1
SNP_A-1715875	C	C	395	5	404	0	5.082	2.42E-02	rs1875592	10	59250644	q21.1
SNP_A-1828396	T	T	245	85	210	118	8.051	4.50E-03	rs11006007	10	59433431	q21.1
SNP_A-2278158	T	T	249	133	211	163	6.096	1.36E-02	rs12245596	10	59487103	q21.1
SNP_A-1796536	C	C	329	51	338	30	5.375	2.04E-02	rs1759360	10	59496497	q21.1
SNP_A-1854913	A	A	365	47	352	68	3.994	4.57E-02	rs12220092	10	59600855	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2276248	C	C	280	74	299	53	4.09	4.31E-02	rs1199096	10	59620240	q21.1
SNP_A-2001415	G	G	280	118	256	146	4.024	0.0448	rs10458675	10	60179349	q21.1
SNP_A-1844622	G	G	288	124	259	153	4.574	3.25E-02	rs10763586	10	60181765	q21.1
SNP_A-2051500	T	T	375	29	345	47	5.333	2.09E-02	rs1867551	10	60274889	q21.1
SNP_A-1954737	G	G	384	16	372	30	4.446	3.50E-02	rs11006279	10	60279459	q21.1
SNP_A-2175853	T	T	386	20	364	38	6.212	1.27E-02	rs7068824	10	60287329	q21.1
SNP_A-1961001	C	C	228	160	245	125	4.484	3.42E-02	rs11006299	10	60356426	q21.1
SNP_A-1915129	G	G	326	60	341	41	3.891	4.85E-02	rs10763596	10	60409532	q21.1
SNP_A-1835110	A	A	215	167	258	140	5.958	0.0147	rs2393526	10	60565413	q21.1
SNP_A-1872254	C	C	379	5	392	0	5.137	2.34E-02	rs11006554	10	60956910	q21.2
SNP_A-2001530	G	G	294	58	273	83	5.188	2.27E-02	rs10993988	10	61177020	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2217580	G	G	249	161	223	191	3.97	4.63E-02	rs1877796	10	61208649	q21.2
SNP_A-2287569	C	C	280	106	306	78	5.409	0.02	rs10821628	10	61413798	q21.2
SNP_A-2165125	A	A	391	17	385	31	4.052	0.0441	rs12357972	10	61577913	q21.2
SNP_A-1928103	C	C	394	16	388	32	5.26	0.0218	rs10994246	10	61611256	q21.2
SNP_A-1698123	G	G	330	70	363	51	4.315	0.0378	rs2393702	10	61949459	q21.2
SNP_A-1820900	T	T	269	123	246	152	4.04	4.44E-02	rs2170005	10	62170606	q21.2
SNP_A-2200814	C	C	247	161	211	199	6.836	8.90E-03	rs2077850	10	62576305	q21.2
SNP_A-2001189	G	G	306	4	320	0	4.155	4.15E-02	rs1915446	10	62733524	q21.2
SNP_A-2085345	C	C	363	45	385	23	7.765	0.0053	rs16916041	10	62816553	q21.2
SNP_A-1789524	C	C	335	75	368	50	6.472	1.10E-02	rs4948282	10	62950052	q21.2
SNP_A-2227591	T	T	348	64	383	37	8.818	3.00E-03	rs16916259	10	62970512	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2227790	C	C	338	52	376	26	10.51	1.20E-03	rs16916274	10	62977137	q21.2
SNP_A-1819347	C	C	300	14	367	7	3.86	4.94E-02	rs4948466	10	63006408	q21.2
SNP_A-2054682	T	T	278	50	324	28	8.884	2.90E-03	rs2393839	10	63017526	q21.2
SNP_A-2159634	A	A	339	65	379	35	11.108	9.00E-04	rs16916326	10	63022848	q21.2
SNP_A-1833996	C	C	267	107	219	141	9.138	2.50E-03	rs17286047	10	63316105	q21.2
SNP_A-2235650	C	C	274	88	251	123	6.619	0.0101	rs4948486	10	63316616	q21.2
SNP_A-1898567	G	G	285	85	267	129	8.761	3.10E-03	rs10995132	10	63798139	q21.2
SNP_A-1801228	T	T	257	121	211	143	5.574	1.82E-02	rs7923561	10	63847194	q21.2
SNP_A-1668100	G	G	361	17	350	34	5.79	0.0161	rs2251417	10	65098013	q21.3
SNP_A-1660395	A	A	371	27	367	47	5.114	2.37E-02	rs2251513	10	65098186	q21.3
SNP_A-2001902	A	A	412	4	405	15	6.409	0.0114	rs10509194	10	65142903	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2001905	A	A	248	124	213	159	6.986	8.20E-03	rs10509195	10	65193372	q21.3
SNP_A-1846122	G	G	209	167	248	130	7.932	4.90E-03	rs16918864	10	65228767	q21.3
SNP_A-2273983	T	T	344	58	323	83	5.074	2.43E-02	rs10995626	10	65228992	q21.3
SNP_A-1909095	A	A	336	44	299	63	5.096	0.024	rs1266702	10	65229969	q21.3
SNP_A-2290694	A	A	264	134	246	168	4.149	4.16E-02	rs10761796	10	65232481	q21.3
SNP_A-2139530	A	A	222	194	257	165	4.857	0.0275	rs12221149	10	65232542	q21.3
SNP_A-1825728	C	C	241	147	262	114	4.862	0.0275	rs10822226	10	65290169	q21.3
SNP_A-1923976	G	G	321	73	305	101	4.736	2.95E-02	rs7918756	10	65303906	q21.3
SNP_A-2001920	G	C	220	162	187	181	5.324	2.10E-02	rs1916411	10	65340839	q21.3
SNP_A-1866546	A	G	194	154	185	171	4.194	4.06E-02	rs7904529	10	65340894	q21.3
SNP_A-1843117	T	C	229	181	215	203	4.407	3.58E-02	rs1916408	10	65343757	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2127462	C	T	222	174	199	189	4.244	3.94E-02	rs10822247	10	65344961	q21.3
SNP_A-2001930	A	A	332	10	307	27	8.695	3.20E-03	rs867474	10	65370173	q21.3
SNP_A-2206591	G	G	206	118	247	95	5.712	1.68E-02	rs10995722	10	65388974	q21.3
SNP_A-1943973	G	G	364	38	344	60	5.499	0.019	rs1814811	10	65408085	q21.3
SNP_A-1858305	G	G	376	38	361	61	5.573	1.82E-02	rs938040	10	65408189	q21.3
SNP_A-2122103	A	A	320	14	311	27	4.227	3.98E-02	rs1078844	10	65408589	q21.3
SNP_A-2206365	C	C	310	22	293	43	7.24	7.10E-03	rs2671544	10	65409860	q21.3
SNP_A-2001202	T	T	384	28	369	47	5.093	0.024	rs2671551	10	65415222	q21.3
SNP_A-1882757	A	A	387	29	371	49	5.447	1.96E-02	rs2671470	10	65421120	q21.3
SNP_A-2212182	C	C	376	20	367	37	5.1	2.39E-02	rs12360285	10	65442680	q21.3
SNP_A-1886312	G	G	331	53	327	77	3.95	4.69E-02	rs1540484	10	65503750	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2179788	G	G	362	6	348	16	4.8	2.85E-02	rs10995844	10	65647286	q21.3
SNP_A-1668442	C	C	314	50	328	32	4.235	3.96E-02	rs2339575	10	65981881	q21.3
SNP_A-1936468	C	C	303	105	271	137	6.015	1.42E-02	rs6480000	10	66136170	q21.3
SNP_A-1795705	C	C	288	52	303	31	5.641	1.75E-02	rs16913136	10	66167200	q21.3
SNP_A-1907402	T	T	332	6	310	0	5.554	0.0184	rs11814879	10	66793311	q21.3
SNP_A-2180665	G	G	316	32	324	16	5.341	2.08E-02	rs7086740	10	66807384	q21.3
SNP_A-2001991	A	A	311	61	340	42	4.665	3.08E-02	---	10	66814396	q21.3
SNP_A-2001992	T	T	328	54	351	33	5.843	1.56E-02	---	10	66814427	q21.3
SNP_A-1875752	G	G	343	1	357	9	6.004	0.0143	rs10996591	10	67115716	q21.3
SNP_A-1688472	C	C	306	90	276	128	8.091	4.40E-03	rs3858138	10	67139598	q21.3
SNP_A-1645178	C	C	326	44	315	71	6.192	1.28E-02	rs10509251	10	67173039	q21.3
SNP_A-2024994	G	G	375	21	374	8	5.579	1.82E-02	rs12251350	10	67199962	q21.3
SNP_A-1661053	C	C	367	25	400	10	7.448	6.40E-03	rs10509247	10	67299347	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1797015	A	A	251	99	278	76	4.378	3.64E-02	rs17241218	10	67375213	q21.3
SNP_A-1855545	C	C	369	31	342	50	5.402	0.0201	rs12761845	10	67406158	q21.3
SNP_A-1924849	G	G	258	150	296	104	10.859	0.001	rs10740218	10	67455267	q21.3
SNP_A-2002056	T	T	297	109	303	79	4.12	0.0424	rs10509253	10	67491640	q21.3
SNP_A-1718329	A	A	376	24	367	47	7.321	6.80E-03	rs10509262	10	67499434	q21.3
SNP_A-1789536	G	G	256	108	224	132	4.445	3.50E-02	rs7921429	10	67510829	q21.3
SNP_A-2150212	A	A	347	49	325	75	6.152	1.31E-02	rs3911781	10	67516022	q21.3
SNP_A-2039811	T	T	329	51	293	69	4.35	3.70E-02	rs3907196	10	67555997	q21.3
SNP_A-2289806	A	A	330	28	289	55	11.224	8.00E-04	rs2394191	10	67561998	q21.3
SNP_A-2001210	C	C	328	40	282	64	8.337	3.90E-03	rs3858141	10	67571836	q21.3
SNP_A-1734498	T	T	269	127	314	96	7.542	6.00E-03	rs1911355	10	67622922	q21.3
SNP_A-2216600	T	T	340	56	372	26	12.409	4.00E-04	rs1911473	10	67679992	q21.3
SNP_A-2063990	G	G	369	31	401	15	6.584	0.0103	rs6480160	10	67769763	q21.3
SNP_A-2257246	-	-	299	29	307	11	8.053	4.50E-03	rs1948944	10	67798651	q21.3
SNP_A-2262450	G	G	383	27	346	42	4.536	0.0332	rs7897082	10	67822959	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2064049	T	T	197	155	216	124	4.112	4.26E-02	rs6480193	10	68087595	q21.3
SNP_A-1684398	C	C	368	32	360	54	5.477	1.93E-02	rs1925633	10	68144608	q21.3
SNP_A-2267266	T	T	208	188	226	142	6.141	0.0132	rs12357998	10	68160556	q21.3
SNP_A-1654205	A	A	369	31	363	49	3.923	4.76E-02	rs7073720	10	68227208	q21.3
SNP_A-2182910	T	T	377	15	368	32	6.177	0.0129	rs10762120	10	68338633	q21.3
SNP_A-1893352	T	T	316	18	322	8	3.879	4.89E-02	rs12219173	10	68359573	q21.3
SNP_A-1806397	T	T	198	190	247	155	8.701	3.20E-03	rs716546	10	68424595	q21.3
SNP_A-2149099	C	C	276	130	316	100	6.495	1.08E-02	rs716547	10	68424659	q21.3
SNP_A-2002129	T	T	200	192	221	145	6.718	9.50E-03	rs1925609	10	68424913	q21.3
SNP_A-2084845	C	C	382	16	380	30	4.089	4.32E-02	rs4484988	10	68455550	q21.3
SNP_A-2044928	A	A	340	18	326	40	8.552	3.50E-03	rs10762128	10	68461532	q21.3
SNP_A-2198561	G	G	382	34	368	52	4.01	4.52E-02	rs10762132	10	68477364	q21.3
SNP_A-2067101	C	C	349	21	293	33	4.789	0.0286	rs4745925	10	68480790	q21.3
SNP_A-1649534	T	T	340	58	317	83	5.233	2.22E-02	rs1582573	10	68753407	q21.3
SNP_A-2263836	C	C	389	7	391	1	4.485	3.42E-02	rs9414956	10	68783569	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1722630	G	G	281	115	257	151	5.765	1.63E-02	rs1969735	10	68896068	q21.3
SNP_A-2286145	C	C	394	20	379	37	5.356	0.0206	rs11815032	10	68969198	q21.3
SNP_A-2114179	A	A	416	0	418	4	3.952	0.0465	rs16924673	10	69001077	q21.3
SNP_A-1830163	T	T	343	35	315	55	5.551	1.85E-02	rs7095136	10	69114993	q21.3
SNP_A-2128660	A	A	330	50	299	69	4.37	3.66E-02	rs7893446	10	69123347	q21.3
SNP_A-2289538	C	C	271	103	253	141	6.02	0.0141	rs10823085	10	69198991	q21.3
SNP_A-2303551	A	A	396	10	387	21	4.002	4.55E-02	rs2173369	10	70098148	q21.3
SNP_A-2193246	G	G	382	2	373	13	8.169	0.0043	rs2256199	10	70423581	q22.1
SNP_A-1700500	T	T	301	69	305	99	3.898	4.84E-02	rs1599710	10	70716017	q22.1
SNP_A-1909955	A	A	326	78	302	108	5.712	1.68E-02	rs7079157	10	70789214	q22.1
SNP_A-1785158	A	A	313	81	287	113	6.36	0.0117	rs7917338	10	70801644	q22.1
SNP_A-1960517	C	C	304	84	283	115	5.454	0.0195	rs12772559	10	70854362	q22.1
SNP_A-1924016	C	C	293	51	279	77	5.42	1.99E-02	rs17569412	10	70907542	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1751683	A	A	360	6	366	18	5.621	0.0177	rs10509315	10	70927239	q22.1
SNP_A-1880767	C	C	285	47	310	26	7.068	7.80E-03	rs2018209	10	71157181	q22.1
SNP_A-1952311	C	C	302	62	273	97	9.119	2.50E-03	rs4746009	10	71302416	q22.1
SNP_A-2249805	C	C	292	96	256	136	9.241	2.40E-03	rs7071359	10	71322507	q22.1
SNP_A-2130070	A	A	401	15	412	6	4.001	4.55E-02	rs10999089	10	71457159	q22.1
SNP_A-2298798	G	G	406	4	398	14	5.63	0.0177	rs4083803	10	71623487	q22.1
SNP_A-1920712	C	C	381	5	379	17	6.424	1.13E-02	rs10999185	10	71635799	q22.1
SNP_A-1903154	A	A	386	30	374	48	4.301	3.81E-02	rs16927415	10	71700582	q22.1
SNP_A-2207220	G	G	345	7	341	1	4.38	3.64E-02	rs12253651	10	71779052	q22.1
SNP_A-1789332	G	G	270	100	250	130	4.55	3.29E-02	rs12776085	10	71970749	q22.1
SNP_A-1906175	A	A	360	12	381	27	4.713	2.99E-02	rs10999428	10	72033802	q22.1
SNP_A-1877876	C	C	272	142	244	170	4.032	4.46E-02	rs10999500	10	72170869	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2254426	T	T	352	38	353	63	5.356	0.0206	rs2541228	10	72180084	q22.1
SNP_A-2191434	A	A	328	10	333	25	5.897	0.0152	rs827312	10	72358857	q22.1
SNP_A-1923761	A	A	348	6	356	16	4.193	4.06E-02	rs827279	10	72385871	q22.1
SNP_A-2029902	T	T	368	36	357	55	4.056	4.40E-02	rs6415902	10	72449906	q22.1
SNP_A-2281664	G	G	384	12	409	3	5.874	0.0154	rs16928328	10	72462132	q22.1
SNP_A-1685750	C	C	306	94	338	72	4.383	3.63E-02	rs1234888	10	72802791	q22.1
SNP_A-2192516	A	A	346	8	370	22	5.416	0.02	rs10999865	10	72955467	q22.1
SNP_A-2002516	A	A	243	117	304	84	11.188	8.00E-04	rs10509340	10	73326988	q22.1
SNP_A-1806550	G	-	195	131	170	170	6.474	0.0109	rs1009987	10	73337354	q22.1
SNP_A-2116521	C	C	320	4	352	14	4.54	3.31E-02	rs12251048	10	73378272	q22.1
SNP_A-2243483	C	C	221	125	236	84	7.532	6.10E-03	rs4148949	10	73440657	q22.1
SNP_A-1781061	A	A	323	7	329	23	7.887	5.00E-03	rs11000205	10	73609344	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2140867	T	T	314	14	290	28	5.467	1.94E-02	rs11000413	10	74211870	q22.1
SNP_A-1782331	T	T	412	4	420	0	4.058	4.40E-02	rs2140935	10	75014704	q22.2
SNP_A-2290543	A	A	279	67	319	49	4.795	2.85E-02	rs12572101	10	75270657	q22.2
SNP_A-1796367	T	T	314	80	352	58	5.359	0.0206	rs17631000	10	75272506	q22.2
SNP_A-1946936	C	C	311	39	335	23	4.931	0.0264	rs12355771	10	75564410	q22.2
SNP_A-2290449	C	C	331	53	358	36	4.177	4.10E-02	rs9665468	10	75608844	q22.2
SNP_A-2097184	A	A	318	60	352	40	5.473	1.93E-02	rs4746214	10	76079075	q22.2
SNP_A-2169351	T	T	337	77	363	55	4.613	3.17E-02	rs946186	10	76090886	q22.2
SNP_A-2044843	C	C	340	50	375	35	3.863	4.94E-02	rs2485954	10	76176939	q22.2
SNP_A-2293108	A	A	371	33	387	13	9.014	2.70E-03	rs16932960	10	77605527	q22.2
SNP_A-2024872	T	T	397	5	404	0	5.056	2.45E-02	rs16933426	10	77783012	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2038332	G	G	409	7	402	18	4.881	2.71E-02	rs7912068	10	78193565	q22.3
SNP_A-2002763	C	C	409	7	403	17	4.192	4.06E-02	rs17231898	10	78219063	q22.3
SNP_A-1837537	T	T	356	4	345	15	6.541	1.05E-02	rs11002154	10	78826524	q22.3
SNP_A-1794415	C	C	398	12	392	24	4.002	4.54E-02	rs16934688	10	78833199	q22.3
SNP_A-2136502	G	G	328	50	309	71	4.206	4.03E-02	rs12265448	10	79039280	q22.3
SNP_A-2207658	C	C	353	1	369	13	9.589	0.002	rs10824564	10	79182555	q22.3
SNP_A-1836520	G	G	259	77	215	123	14.659	0.0001	rs2579175	10	79199539	q22.3
SNP_A-2114920	T	T	270	126	241	161	5.869	0.0154	rs2579171	10	79201567	q22.3
SNP_A-2002867	C	C	306	110	264	152	9.828	1.70E-03	rs2579170	10	79201982	q22.3
SNP_A-2125481	C	C	279	55	240	72	4.462	3.47E-02	rs2812437	10	79214081	q22.3
SNP_A-2001276	C	C	280	82	242	128	12.757	4.00E-04	rs2579158	10	79214188	q22.3
SNP_A-1885095	C	C	274	122	315	101	4.342	3.72E-02	rs2812426	10	79223567	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800324	C	C	277	95	304	62	8.143	0.0043	rs1248631	10	79252887	q22.3
SNP_A-2002872	C	C	263	91	303	71	4.75	0.0293	rs1248630	10	79253862	q22.3
SNP_A-2002873	C	C	293	81	260	102	4.185	4.08E-02	rs1261993	10	79263057	q22.3
SNP_A-2002877	G	G	297	109	248	152	11.446	7.00E-04	rs1248671	10	79273832	q22.3
SNP_A-2106932	G	G	304	110	259	155	11.238	8.00E-04	rs1272013	10	79280611	q22.3
SNP_A-2147898	G	G	228	106	221	151	5.96	0.0146	rs1248686	10	79280932	q22.3
SNP_A-1912965	T	T	273	141	243	175	5.383	2.03E-02	rs1248889	10	79369294	q22.3
SNP_A-2002925	G	G	207	129	174	156	5.363	0.0206	rs1435961	10	79890991	q22.3
SNP_A-2166947	C	C	412	4	422	0	4.077	4.35E-02	rs2140929	10	79974124	q22.3
SNP_A-1797024	C	C	412	4	422	0	4.077	4.35E-02	rs2007542	10	79986915	q22.3
SNP_A-1870672	G	G	368	48	386	30	4.584	3.23E-02	rs7082864	10	80204537	q22.3
SNP_A-2303256	A	A	298	80	335	59	5.006	0.0253	rs1371104	10	80447573	q22.3
SNP_A-2285154	C	C	284	76	316	58	3.859	4.95E-02	rs7096896	10	80471069	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2189271	C	C	294	112	322	88	4.133	4.20E-02	rs1370562	10	80495455	q22.3
SNP_A-2003003	C	C	345	65	327	93	5.324	2.10E-02	rs11002824	10	80542489	q22.3
SNP_A-1781889	A	A	291	27	311	55	6.891	8.70E-03	rs704005	10	80547096	q22.3
SNP_A-2218725	T	T	260	124	212	168	11.491	7.00E-04	rs703982	10	80612727	q22.3
SNP_A-2217619	C	C	329	83	359	63	3.929	4.75E-02	rs12161674	10	80615094	q22.3
SNP_A-1804075	C	C	331	85	358	64	3.975	4.62E-02	rs6480925	10	80621534	q22.3
SNP_A-1861788	T	T	356	44	369	27	4.284	0.0385	rs11002868	10	80638707	q22.3
SNP_A-1924599	C	C	354	26	331	43	4.913	2.67E-02	rs4979857	10	80700243	q22.3
SNP_A-2003029	A	A	164	150	192	124	4.663	3.08E-02	rs1483733	10	80800042	q22.3
SNP_A-2180486	G	G	347	21	344	38	4.652	0.031	rs11201146	10	81757317	q22.3
SNP_A-2156927	C	C	242	148	218	182	4.629	3.14E-02	rs2275191	10	81805869	q22.3
SNP_A-2109989	G	G	178	148	205	115	5.989	0.0144	rs7091565	10	81903541	q22.3
SNP_A-1656871	G	G	312	88	349	65	5.289	2.15E-02	rs1913759	10	82009337	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1741293	T	T	375	25	401	13	4.421	3.55E-02	rs9325452	10	82049618	q22.3
SNP_A-1897358	G	G	288	32	298	16	5.448	1.96E-02	rs1538818	10	82112773	q22.3
SNP_A-1783648	C	C	260	104	293	83	4.134	4.20E-02	rs6585989	10	82164741	q22.3
SNP_A-2087972	T	T	382	26	405	9	8.886	2.90E-03	rs7916618	10	82179666	q22.3
SNP_A-2003143	C	C	312	78	344	54	5.844	1.56E-02	rs1913760	10	82334656	q22.3
SNP_A-2001291	T	T	312	34	357	21	4.694	3.03E-02	rs4348832	10	82335024	q22.3
SNP_A-1880929	G	G	314	76	343	55	4.566	3.26E-02	rs4934395	10	82404699	q22.3
SNP_A-1876715	T	T	317	83	355	61	5.198	2.26E-02	rs1484170	10	82689471	q22.3
SNP_A-2112299	C	C	326	90	296	116	4.709	3.00E-02	rs1336442	10	82814402	q22.3
SNP_A-2133643	C	C	294	52	265	79	7.064	7.90E-03	rs7895483	10	82819778	q22.3
SNP_A-2104875	T	T	275	131	306	102	5.259	0.0218	rs1953661	10	82875955	q22.3
SNP_A-1939886	C	C	293	83	268	108	4.386	3.62E-02	rs10748657	10	82896757	q22.3
SNP_A-1747143	T	T	344	30	359	51	4.12	0.0424	rs10490925	10	82900389	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2072689	T	T	333	83	358	62	3.927	4.75E-02	rs10882849	10	82976666	q23.1
SNP_A-1921474	G	G	359	33	371	19	3.961	4.66E-02	rs11598449	10	83582423	q23.1
SNP_A-2274960	G	G	343	35	341	19	4.31	3.79E-02	---	10	83834819	q23.1
SNP_A-1690245	C	C	258	138	302	108	6.875	8.70E-03	rs478982	10	84250285	q23.1
SNP_A-2003301	A	A	340	44	365	27	4.875	2.72E-02	rs12413431	10	84352154	q23.1
SNP_A-1787361	C	C	366	38	354	60	5.017	2.51E-02	rs17100442	10	84413711	q23.1
SNP_A-2003325	G	G	302	88	337	57	8.524	3.50E-03	rs571797	10	84493035	q23.1
SNP_A-1863059	G	G	272	106	280	72	5.692	1.70E-02	rs513829	10	84501387	q23.1
SNP_A-1919472	T	C	191	157	198	168	5.759	1.64E-02	rs2483307	10	84554107	q23.1
SNP_A-2242548	A	A	396	18	408	8	4.02	4.50E-02	rs17100892	10	84586065	q23.1
SNP_A-2292237	T	T	245	99	285	79	4.705	3.01E-02	rs2132379	10	84597895	q23.1
SNP_A-1737878	T	T	253	145	299	109	8.813	3.00E-03	rs2348884	10	84604456	q23.1
SNP_A-1716991	T	C	201	189	224	180	3.878	4.89E-02	rs2348886	10	84606181	q23.1
SNP_A-1645688	T	A	204	156	195	185	4.724	2.97E-02	rs1339837	10	84607178	q23.1
SNP_A-1739877	T	T	279	107	321	87	4.396	3.60E-02	rs10509475	10	84877942	q23.1
SNP_A-2003352	A	A	335	37	349	21	4.695	3.03E-02	rs7900288	10	84891999	q23.1
SNP_A-2031512	C	C	219	103	272	76	8.798	3.00E-03	rs2348962	10	84920404	q23.1
SNP_A-2003357	T	T	201	149	239	125	5.111	2.38E-02	rs10787673	10	84937452	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113900	G	G	346	30	342	16	3.845	0.0499	rs7478282	10	84949364	q23.1
SNP_A-2003359	C	C	315	61	333	41	4.416	0.0356	rs1010860	10	84959623	q23.1
SNP_A-1890056	C	C	382	20	381	9	3.993	4.57E-02	rs12244098	10	85096638	q23.1
SNP_A-1798275	G	G	342	20	340	6	7.186	7.30E-03	rs10787811	10	85115163	q23.1
SNP_A-1653186	T	T	218	178	248	152	3.96	4.66E-02	rs10509480	10	85142092	q23.1
SNP_A-1825514	A	A	240	152	266	124	4.171	4.11E-02	rs10886291	10	85164129	q23.1
SNP_A-2077746	G	G	268	62	283	41	4.635	3.13E-02	rs10886387	10	85204001	q23.1
SNP_A-2304607	T	T	268	138	300	112	4.463	3.46E-02	rs1591567	10	85218196	q23.1
SNP_A-1835233	G	G	263	135	288	104	5.11	2.38E-02	rs10749314	10	85222874	q23.1
SNP_A-2003387	A	A	255	121	287	85	8.159	0.0043	rs2103203	10	85449964	q23.1
SNP_A-2076849	C	C	372	28	385	13	5.706	1.69E-02	rs11200513	10	85518470	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251450	G	G	374	26	390	14	3.915	4.78E-02	rs11200642	10	85539224	q23.1
SNP_A-1940028	A	A	383	19	396	8	4.693	3.03E-02	rs3904541	10	85547862	q23.1
SNP_A-1806265	T	T	353	25	336	46	6.61	0.0101	rs12146301	10	85571359	q23.1
SNP_A-2115097	G	G	354	0	348	4	4.046	4.43E-02	rs1110375	10	85662931	q23.1
SNP_A-2230493	G	G	284	86	313	61	5.639	1.76E-02	rs11593875	10	85681798	q23.1
SNP_A-2195920	A	A	221	147	180	168	5.037	2.48E-02	rs4281435	10	86037916	q23.1
SNP_A-2003429	A	A	305	29	341	17	4.309	3.79E-02	rs12773282	10	86092552	q23.1
SNP_A-1673848	C	C	265	91	224	120	7.22	7.20E-03	rs6585876	10	86115435	q23.1
SNP_A-1670153	G	G	282	110	263	149	6.041	0.014	rs4131709	10	86117437	q23.1
SNP_A-2182243	A	A	279	137	249	171	5.439	1.97E-02	rs2488632	10	86339557	q23.1
SNP_A-1816556	C	C	298	90	253	117	6.773	9.30E-03	rs3922702	10	86416589	q23.1
SNP_A-1744011	T	T	336	64	317	97	7.078	7.80E-03	rs10509521	10	86854026	q23.2
SNP_A-1745017	A	G	210	184	217	185	4.218	4.00E-02	rs1876895	10	86936748	q23.2
SNP_A-1668302	C	C	359	21	352	6	7.753	5.40E-03	rs869466	10	86960382	q23.2
SNP_A-1794313	A	A	347	65	314	94	6.917	8.50E-03	rs10749517	10	87169291	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2273821	A	A	368	46	341	73	7.154	7.50E-03	rs7897373	10	87169682	q23.2
SNP_A-1817044	C	C	361	37	335	55	4.412	3.57E-02	rs17105552	10	87173463	q23.2
SNP_A-1758384	T	T	364	34	395	17	6.693	9.70E-03	rs10509529	10	87490577	q23.2
SNP_A-2241003	G	G	355	25	350	48	6.869	8.80E-03	rs11201872	10	87770982	q23.2
SNP_A-2243878	A	A	365	13	341	25	4.413	3.57E-02	rs9421509	10	87814927	q23.2
SNP_A-2098891	C	C	376	18	393	5	7.704	5.50E-03	rs7912451	10	87819791	q23.2
SNP_A-1786713	T	T	364	12	369	27	5.289	2.15E-02	rs11201912	10	87900073	q23.2
SNP_A-1945052	T	T	400	16	388	32	5.497	0.019	rs11201943	10	87959142	q23.2
SNP_A-2154667	T	T	360	26	367	9	8.195	4.20E-03	rs7922658	10	88210846	q23.2
SNP_A-2003648	C	C	261	151	229	179	4.446	3.50E-02	rs2180968	10	89408710	q23.31
SNP_A-1843225	T	T	302	48	286	78	7.307	6.90E-03	rs11202586	10	89602004	q23.31
SNP_A-2050080	C	C	359	17	363	7	4.141	0.0419	rs505384	10	89913829	q23.31
SNP_A-2200276	C	C	382	30	399	17	3.947	0.047	rs7070722	10	90004201	q23.31
SNP_A-2043219	C	C	257	151	229	183	4.66	0.0309	rs14266619	10	90081520	q23.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1750357	A	A	335	63	316	94	6.499	1.08E-02	rs303519	10	90112019	q23.31
SNP_A-1880291	C	C	260	124	233	153	4.51	3.37E-02	rs10788598	10	90177092	q23.31
SNP_A-2241727	A	A	267	133	244	170	5.314	0.0212	rs10788599	10	90177904	q23.31
SNP_A-2003716	C	C	334	56	305	79	5.188	2.27E-02	rs10509552	10	90342519	q23.31
SNP_A-2003721	G	G	270	80	261	113	5.005	0.0253	rs701826	10	90407479	q23.31
SNP_A-2304227	A	A	340	66	323	91	4.339	3.72E-02	rs814626	10	90419016	q23.31
SNP_A-1671274	G	G	221	179	258	156	4.198	4.05E-02	rs2296600	10	90435016	q23.31
SNP_A-1758047	A	A	350	50	336	76	5.475	1.93E-02	rs9325604	10	90440333	q23.31
SNP_A-2003727	A	A	374	12	343	23	4.269	3.88E-02	rs17434481	10	90507130	q23.31
SNP_A-2107365	A	A	308	72	296	98	3.963	0.0465	rs303527	10	90557258	q23.31
SNP_A-1844186	A	G	222	192	223	193	4.337	0.0373	rs10887861	10	90579096	q23.31
SNP_A-1932556	T	T	222	116	270	86	8.677	3.20E-03	rs1214563	10	90592608	q23.31
SNP_A-1800605	C	C	282	126	241	175	11.114	9.00E-04	rs4498883	10	90595225	q23.31
SNP_A-2236873	T	T	262	116	226	172	13.038	3.00E-04	rs4934425	10	90599698	q23.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1642519	G	G	306	94	279	135	8.348	3.90E-03	rs10788637	10	90610385	q23.31
SNP_A-2003747	A	A	298	74	270	106	7.048	7.90E-03	rs10509557	10	90653819	q23.31
SNP_A-2060865	G	G	218	196	258	158	7.436	6.40E-03	rs4934429	10	90669033	q23.31
SNP_A-2067557	A	A	401	13	381	37	12.013	5.00E-04	rs17114337	10	90703175	q23.31
SNP_A-2003752	C	T	194	178	236	142	16.126	5.93E-05	rs1441734	10	90706817	q23.31
SNP_A-2153613	G	G	267	55	296	26	11.876	6.00E-04	rs12765241	10	90730481	q23.31
SNP_A-2261360	A	A	306	110	278	138	4.504	3.38E-02	rs7092857	10	90769298	q23.31
SNP_A-2096813	-	T	192	192	222	150	7.143	7.50E-03	rs2256329	10	90839051	q23.31
SNP_A-2288185	A	A	313	33	329	17	5.519	1.88E-02	rs11202972	10	90841799	q23.31
SNP_A-2170886	A	A	288	52	327	31	7.327	6.80E-03	rs10887911	10	90863137	q23.31
SNP_A-1881289	G	G	338	34	354	16	6.845	8.90E-03	rs11202989	10	90870906	q23.31
SNP_A-1860237	T	T	327	77	298	102	4.817	2.82E-02	rs17380509	10	90875252	q23.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1688530	G	G	391	9	412	2	4.764	2.91E-02	rs10509574	10	90928866	q23.31
SNP_A-1752681	T	T	281	85	272	114	3.843	0.0499	rs727427	10	91064961	q23.31
SNP_A-1743725	G	G	304	92	285	121	4.437	3.52E-02	rs10509579	10	91160349	q23.31
SNP_A-1755246	A	A	300	88	284	120	5.04	2.48E-02	rs2077946	10	91176036	q23.31
SNP_A-1659018	A	A	299	85	289	119	5.114	2.37E-02	rs2026550	10	91182816	q23.31
SNP_A-2273291	C	C	282	82	285	43	10.339	1.30E-03	rs7073626	10	91418384	q23.31
SNP_A-1940599	T	T	293	93	266	120	4.727	2.97E-02	rs7895379	10	91486687	q23.31
SNP_A-1896838	T	T	285	69	255	89	4.056	4.40E-02	rs1062465	10	91487611	q23.31
SNP_A-1956832	G	G	304	88	293	121	4.816	2.82E-02	rs7095818	10	91519465	q23.31
SNP_A-1749359	G	G	259	139	303	111	6.268	0.0123	rs2209672	10	91694802	q23.31
SNP_A-2247576	G	G	342	50	343	27	6.242	1.25E-02	rs12244491	10	91814824	q23.31
SNP_A-2101655	A	A	337	13	372	4	5.569	0.0183	rs1329181	10	91918169	q23.31
SNP_A-1837765	G	G	321	11	303	3	4.038	4.45E-02	rs17091368	10	91919112	q23.31
SNP_A-1749663	A	A	338	32	360	18	4.528	3.33E-02	rs10509603	10	91927954	q23.31
SNP_A-2029907	A	A	355	41	364	24	4.478	3.43E-02	rs10430648	10	91946908	q23.31
SNP_A-1926400	C	C	328	72	291	93	4.56	0.0327	rs7080786	10	92006454	q23.31
SNP_A-2202995	G	G	198	122	241	107	4.028	0.0448	rs1570991	10	92056369	q23.31
SNP_A-2281156	A	A	397	19	410	8	4.686	0.0304	rs17094054	10	92108626	q23.31
SNP_A-1746278	T	T	238	132	222	174	5.445	1.96E-02	rs1936572	10	92130666	q23.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2269867	T	T	243	157	215	189	4.652	0.031	rs1299939	10	92353074	q23.31
SNP_A-1798689	C	C	383	17	380	34	5.439	1.97E-02	rs1547851	10	92364806	q23.31
SNP_A-2001342	T	T	221	141	193	169	4.423	3.55E-02	rs2710730	10	92374388	q23.31
SNP_A-2188383	C	C	198	128	184	172	5.658	1.74E-02	rs2800166	10	92417047	q23.31
SNP_A-2051296	C	C	321	25	310	12	3.902	0.0482	rs17526697	10	92490499	q23.31
SNP_A-2176826	C	C	363	29	392	14	6.103	0.0135	rs2901127	10	92585046	q23.31
SNP_A-2281100	G	G	332	80	357	59	4.061	4.39E-02	rs10881841	10	92627133	q23.31
SNP_A-2225527	A	A	384	2	375	9	4.556	3.28E-02	rs3852497	10	92801769	q23.31
SNP_A-1780911	T	T	326	24	307	43	5.958	0.0146	rs11595274	10	92806870	q23.31
SNP_A-2190743	A	A	395	21	375	39	5.915	1.50E-02	rs11592176	10	92817968	q23.31
SNP_A-2030969	T	T	398	16	370	30	5.042	0.0247	rs11599319	10	92823738	q23.31
SNP_A-2293809	G	G	235	161	267	133	4.687	0.0304	rs7067899	10	92881044	q23.31
SNP_A-1714374	G	A	243	159	210	204	10.277	1.30E-03	rs1339822	10	94580202	q23.33
SNP_A-1649152	G	C	224	168	195	193	4.292	3.83E-02	rs1418754	10	94680140	q23.33
SNP_A-1741425	G	G	311	69	362	46	7.479	6.20E-03	rs787663	10	94736142	q23.33
SNP_A-2083019	G	G	328	48	366	24	9.828	1.70E-03	rs9420608	10	94790883	q23.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1787811	T	T	355	55	327	75	4.148	4.17E-02	rs17465590	10	94830066	q23.33
SNP_A-2110412	G	G	302	100	332	64	9.277	0.0023	rs12784076	10	94865113	q23.33
SNP_A-1943217	C	C	265	139	292	108	5.18	0.0229	rs6583860	10	94892754	q23.33
SNP_A-2228854	C	C	213	135	189	169	5.095	0.024	rs6583867	10	94928218	q23.33
SNP_A-1812579	G	A	217	175	212	196	4.287	3.84E-02	rs10882174	10	94941022	q23.33
SNP_A-2059453	C	C	243	159	210	194	5.869	0.0154	rs17382981	10	94943248	q23.33
SNP_A-1961386	T	T	195	191	239	159	7.205	7.30E-03	rs4326721	10	94948876	q23.33
SNP_A-2047522	A	T	207	201	236	166	7.266	7.00E-03	rs4918904	10	94951310	q23.33
SNP_A-2306827	G	A	214	174	210	164	9.735	0.0018	rs7910061	10	94953101	q23.33
SNP_A-2032417	A	A	213	141	196	184	5.482	1.92E-02	rs7098780	10	95042252	q23.33
SNP_A-1662598	C	C	374	20	393	9	4.563	0.0327	rs2077733	10	95045955	q23.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1941749	C	C	332	56	367	39	4.389	3.62E-02	rs787665	10	95062526	q23.33
SNP_A-2004035	A	A	261	123	235	149	3.848	4.98E-02	rs4917735	10	95067612	q23.33
SNP_A-2029005	C	C	390	4	414	0	4.224	3.99E-02	---	10	95277281	q23.33
SNP_A-2004073	A	A	221	101	213	137	4.434	3.52E-02	rs12218711	10	95461997	q23.33
SNP_A-2004076	A	A	375	41	353	65	6.094	1.36E-02	rs7094280	10	95474234	q23.33
SNP_A-2069741	A	A	368	24	337	39	4.603	3.19E-02	rs11187629	10	95479425	q23.33
SNP_A-1866073	C	C	231	183	263	153	4.747	2.94E-02	rs7078182	10	95513386	q23.33
SNP_A-1749549	C	C	340	34	347	55	4.021	4.49E-02	rs7085635	10	96752109	q24.1
SNP_A-1802666	G	G	288	108	272	138	3.874	4.90E-02	rs1934952	10	96787490	q23.33
SNP_A-1897316	C	C	307	73	335	53	4.313	0.0378	rs1934951	10	96788538	q23.33
SNP_A-2211529	T	T	324	66	349	47	4.078	4.35E-02	rs17110453	10	96819519	q23.33
SNP_A-2004147	G	G	189	173	219	145	4.666	3.08E-02	rs613340	10	96932575	q23.33
SNP_A-2164062	G	C	206	190	218	176	4.273	3.87E-02	rs11813181	10	96935525	q23.33
SNP_A-1886811	T	T	368	8	396	2	4.004	4.54E-02	rs1002788	10	97075121	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2004168	G	G	408	12	417	3	5.498	0.019	rs17110738	10	97167744	q24.1
SNP_A-2239781	C	C	313	41	329	15	12.329	4.00E-04	rs7895441	10	97329920	q24.1
SNP_A-1797348	G	G	414	0	416	4	3.962	0.0465	rs11188488	10	97549517	q24.1
SNP_A-2275488	T	T	304	58	291	89	6.389	0.0115	rs12761346	10	97965262	q24.1
SNP_A-2132399	A	A	253	109	224	140	5.617	0.0178	rs10882760	10	97992159	q24.1
SNP_A-2004243	C	C	312	50	346	28	7.768	0.0053	rs12411583	10	98171623	q24.1
SNP_A-2004244	T	T	241	163	273	133	5.028	2.49E-02	rs10509710	10	98171727	q24.1
SNP_A-2236279	A	A	232	156	271	131	4.955	2.60E-02	rs7096410	10	98173110	q24.1
SNP_A-2122521	C	C	265	137	238	164	3.871	4.91E-02	rs7923251	10	98212565	q24.1
SNP_A-2232899	G	G	263	95	233	117	4.008	0.0453	rs1937090	10	98214766	q24.1
SNP_A-2090725	A	A	268	114	317	85	5.616	0.0178	rs4919025	10	98228833	q24.1
SNP_A-2110333	C	C	299	93	284	124	4.496	3.40E-02	rs879266	10	98253535	q24.1
SNP_A-2156921	C	C	326	84	297	107	4.076	4.35E-02	rs4917743	10	98371181	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1935229	G	G	321	83	294	114	6.044	0.014	rs9633706	10	98372293	q24.1
SNP_A-1649298	T	T	369	13	371	31	6.863	8.80E-03	rs10509713	10	98780296	q24.1
SNP_A-1795873	A	A	374	44	356	64	4.143	4.18E-02	rs7084418	10	98845371	q24.1
SNP_A-2315009	C	C	271	149	236	184	6.095	1.36E-02	rs2817691	10	98849168	q24.1
SNP_A-2180223	C	C	329	91	304	118	4.471	3.45E-02	rs7894400	10	98855615	q24.1
SNP_A-1806468	C	C	316	74	300	102	4.689	3.03E-02	rs7899087	10	98856639	q24.1
SNP_A-2237952	A	A	326	88	301	119	5.596	1.80E-02	rs12256938	10	98856800	q24.1
SNP_A-2261611	C	C	305	53	285	73	3.853	4.97E-02	rs1490695	10	98857284	q24.1
SNP_A-2213511	G	G	231	139	204	168	4.41	3.57E-02	rs2636817	10	98870745	q24.1
SNP_A-1945587	C	C	243	139	212	172	5.609	1.79E-02	rs902474	10	98872364	q24.1
SNP_A-2100588	G	G	225	129	267	99	7.335	6.80E-03	rs7474809	10	98940467	q24.1
SNP_A-2052712	G	G	262	158	291	129	4.451	0.0349	rs1253407	10	98959058	q24.1
SNP_A-2046742	C	C	237	147	265	121	4.079	4.34E-02	rs2297987	10	98979444	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2253486	C	C	397	11	401	3	4.572	3.25E-02	rs2265598	10	99003595	q24.1
SNP_A-2238697	A	A	292	98	266	132	6.157	1.31E-02	rs2297988	10	99108372	q24.1
SNP_A-1809890	A	A	296	104	269	137	5.765	1.64E-02	rs7092350	10	99130208	q24.1
SNP_A-2001365	A	A	197	125	170	166	7.469	0.0063	rs7898743	10	99143530	q24.1
SNP_A-2263380	T	T	260	92	231	119	5.162	2.31E-02	rs9888026	10	99149859	q24.1
SNP_A-1935638	T	T	278	104	243	131	5.369	2.05E-02	rs10882926	10	99150680	q24.1
SNP_A-2218881	A	A	260	152	235	183	4.088	4.32E-02	rs7895646	10	99157426	q24.1
SNP_A-1848726	T	T	227	117	195	143	4.974	2.57E-02	rs10882949	10	99268169	q24.1
SNP_A-2281954	G	G	293	99	260	122	4.234	3.96E-02	rs4919129	10	99435112	q24.2
SNP_A-1809493	C	C	306	32	248	52	8.601	3.40E-03	rs4919142	10	99552201	q24.2
SNP_A-2181903	G	G	281	53	315	37	4.315	0.0378	rs894376	10	99664113	q24.2
SNP_A-1744845	T	T	224	166	271	141	5.899	1.51E-02	rs716838	10	99939999	q24.2
SNP_A-2288926	C	C	244	168	209	193	4.313	0.0378	rs10786405	10	99995272	q24.2
SNP_A-2237599	G	G	395	17	381	31	4.336	0.0373	rs4341462	10	100032427	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2236562	G	G	332	48	352	28	5.848	1.56E-02	rs10748724	10	100037965	q24.2
SNP_A-2021545	A	A	395	15	389	31	5.491	1.91E-02	rs11189569	10	100106187	q24.2
SNP_A-2124244	C	C	213	187	237	153	4.554	3.28E-02	rs2018085	10	100303032	q24.2
SNP_A-2175938	G	G	280	132	302	104	4.11	4.26E-02	rs7907389	10	100304329	q24.2
SNP_A-2268242	G	G	318	82	339	57	5.148	2.33E-02	rs603269	10	100383964	q24.2
SNP_A-2040816	A	A	273	57	293	39	4.076	4.35E-02	rs7906326	10	100516712	q24.2
SNP_A-2074129	A	A	313	65	328	44	4.349	3.70E-02	rs7098316	10	100560483	q24.2
SNP_A-1810541	A	A	367	39	355	59	4.203	4.03E-02	rs10883245	10	100750296	q24.2
SNP_A-2309656	C	C	368	16	346	30	4.855	0.0276	rs11189959	10	100829666	q24.2
SNP_A-1939184	C	C	291	23	294	40	3.989	0.0458	rs2862531	10	100972884	q24.2
SNP_A-1837505	T	C	241	175	210	208	5.602	1.79E-02	rs2494657	10	101203270	q24.2
SNP_A-2076032	G	G	336	20	301	33	4.415	0.0356	rs11190103	10	101220172	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1788529	G	G	346	54	316	74	4.359	3.68E-02	rs7074627	10	101247781	q24.2
SNP_A-2262045	T	T	306	114	271	143	5.353	0.0207	rs3184991	10	101505306	q24.2
SNP_A-1642093	C	C	389	15	376	36	8.79	3.00E-03	rs10509741	10	101581953	q24.2
SNP_A-2154553	T	T	334	12	345	31	7.34	6.70E-03	rs7358099	10	101944992	q24.31
SNP_A-1821987	G	G	395	3	384	18	10.85	0.001	rs7073610	10	101996615	q24.31
SNP_A-2004502	G	G	400	8	385	27	10.582	1.10E-03	rs7924284	10	102008079	q24.31
SNP_A-2157322	G	G	409	7	384	22	8.426	3.70E-03	rs6584356	10	102040232	q24.31
SNP_A-1819383	T	T	379	11	345	25	6.519	1.07E-02	rs2242052	10	102040504	q24.31
SNP_A-2288133	T	T	268	130	294	104	4.092	4.31E-02	rs12762598	10	102217746	q24.31
SNP_A-1819637	C	C	282	70	272	98	4.401	3.59E-02	rs2495744	10	102319399	q24.31
SNP_A-2243223	G	G	242	96	209	123	5.69	1.71E-02	rs2489013	10	102381730	q24.31
SNP_A-2208483	G	G	199	153	237	119	7.54	6.00E-03	rs2275383	10	102786764	q24.31
SNP_A-2137569	G	G	246	136	280	102	7.055	7.90E-03	rs6584411	10	102822915	q24.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2139274	C	C	303	53	259	69	4.404	3.58E-02	rs17113682	10	102835231	q24.31
SNP_A-1907183	C	C	267	119	295	89	5.717	1.68E-02	rs7920881	10	102840281	q24.31
SNP_A-2116626	G	G	400	10	375	23	5.751	1.65E-02	rs17114177	10	103477361	q24.32
SNP_A-2024878	G	G	420	0	416	6	6.014	1.42E-02	rs11191140	10	103647226	q24.32
SNP_A-2001395	A	A	258	80	276	56	4.789	0.0286	rs7069489	10	104515361	q24.32
SNP_A-2256545	A	A	283	33	267	55	5.91	1.51E-02	rs11191560	10	104859028	q24.33
SNP_A-1755552	C	C	376	8	387	19	4.031	4.47E-02	rs7895096	10	105138066	q24.33
SNP_A-2176141	C	C	385	33	400	18	4.698	3.02E-02	rs10883919	10	105577368	q24.33
SNP_A-2313642	G	A	181	169	209	167	3.87	4.92E-02	rs7100920	10	105630968	q24.33
SNP_A-2004674	A	A	242	174	276	140	5.913	1.50E-02	rs6584579	10	105635715	q24.33
SNP_A-1959098	T	T	245	171	280	134	6.817	9.00E-03	rs2475213	10	105654449	q24.33
SNP_A-2080042	T	T	339	61	359	41	4.495	3.40E-02	rs2282436	10	105787165	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2129641	C	C	415	5	422	0	5.054	0.0246	rs805703	10	105810495	q25.1
SNP_A-1843828	A	A	416	4	422	0	4.038	4.45E-02	rs548102	10	105854556	q25.1
SNP_A-1953189	A	A	266	88	272	124	3.84	5.00E-02	rs276215	10	106079372	q25.1
SNP_A-1915213	T	T	304	102	275	127	4.162	4.13E-02	rs7083064	10	106128529	q25.1
SNP_A-2092138	A	A	329	41	327	63	4.136	4.20E-02	rs11192037	10	106144133	q25.1
SNP_A-2203115	C	C	357	37	335	55	4.201	4.04E-02	rs11192196	10	106574316	q25.1
SNP_A-2222930	G	G	378	38	362	58	4.494	3.40E-02	rs11192197	10	106574743	q25.1
SNP_A-1715397	T	T	389	5	394	0	5.032	2.49E-02	rs597192	10	106582467	q25.1
SNP_A-1934629	C	C	360	6	343	19	7.149	7.50E-03	rs4917430	10	106583566	q25.1
SNP_A-2310976	G	G	367	41	357	61	3.939	4.72E-02	rs10884055	10	106596095	q25.1
SNP_A-1842080	C	C	358	22	342	48	9.895	1.70E-03	rs12357019	10	106601628	q25.1
SNP_A-2004791	A	A	384	36	365	57	5.219	0.0223	rs11192214	10	106619461	q25.1
SNP_A-2091212	A	A	334	22	304	36	4.424	3.54E-02	rs17117885	10	106645597	q25.1
SNP_A-2171309	G	G	379	31	357	51	5.531	1.87E-02	rs1525389	10	106646547	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2179865	C	C	343	53	337	77	4.086	4.32E-02	rs11192242	10	106694535	q25.1
SNP_A-2124579	G	G	337	3	343	11	4.344	3.71E-02	rs991030	10	106909554	q25.1
SNP_A-1809122	A	A	306	106	279	133	4.296	3.82E-02	rs1484245	10	106953154	q25.1
SNP_A-1716845	T	T	190	160	262	140	9.251	2.40E-03	rs7068381	10	107655269	q25.1
SNP_A-1901498	A	A	309	61	340	44	3.975	4.62E-02	rs1496080	10	107672221	q25.1
SNP_A-1956401	C	C	320	68	337	45	5.075	2.43E-02	rs477187	10	107694990	q25.1
SNP_A-2126236	A	A	269	41	317	23	7.626	5.80E-03	rs12265647	10	107760609	q25.1
SNP_A-1925730	A	A	378	36	400	22	3.925	4.76E-02	rs17119986	10	107776006	q25.1
SNP_A-1923237	A	A	349	29	372	14	5.883	1.53E-02	rs11192698	10	107811288	q25.1
SNP_A-2038634	G	G	370	26	333	49	8.752	3.10E-03	rs1411827	10	107934932	q25.1
SNP_A-2001411	A	A	303	93	309	61	5.832	1.57E-02	rs2025732	10	107969131	q25.1
SNP_A-1953093	G	G	365	37	390	22	4.519	3.35E-02	rs7096246	10	108023940	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1658992	G	G	288	114	326	86	6.15	1.31E-02	rs1023024	10	108391017	q25.1
SNP_A-2001417	G	G	398	4	406	0	4.06	4.39E-02	rs661162	10	108879710	q25.1
SNP_A-2302271	C	C	404	12	416	4	4.157	4.15E-02	rs10884422	10	108899605	q25.1
SNP_A-2191429	T	T	404	12	404	4	3.923	4.76E-02	rs11193220	10	108904738	q25.1
SNP_A-1818586	C	C	298	26	348	14	5.382	2.04E-02	rs12258901	10	108918195	q25.1
SNP_A-1839798	C	C	340	72	319	99	4.889	0.027	rs7099326	10	109173710	q25.1
SNP_A-2269392	G	G	310	14	285	27	4.948	2.61E-02	rs11193418	10	109178352	q25.1
SNP_A-2182050	A	A	409	5	416	0	5.055	0.0246	rs17122635	10	109202125	q25.1
SNP_A-2076341	T	T	364	8	388	2	3.943	4.71E-02	rs7903034	10	109202770	q25.1
SNP_A-1833560	T	T	414	6	416	0	5.986	0.0144	rs17122679	10	109206042	q25.1
SNP_A-1688316	G	G	400	4	414	0	4.119	0.0424	rs10491022	10	109799192	q25.1
SNP_A-1789860	G	G	359	53	287	79	10.463	1.20E-03	rs11193895	10	109861162	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1693144	C	C	373	31	364	50	4.445	3.50E-02	rs1928449	10	109871870	q25.1
SNP_A-1750151	G	G	380	24	365	47	7.675	5.60E-03	rs10509872	10	109906623	q25.1
SNP_A-2183396	T	T	261	149	283	119	4.17	4.12E-02	rs1329493	10	110148737	q25.1
SNP_A-2158595	A	A	350	24	340	40	4.097	4.29E-02	rs4918363	10	110158362	q25.1
SNP_A-2207504	G	G	266	148	295	121	4.204	4.03E-02	rs1831286	10	110164827	q25.1
SNP_A-2201014	A	A	253	125	291	101	4.95	2.61E-02	rs7093459	10	110170614	q25.1
SNP_A-1838490	A	A	268	116	302	94	4.149	4.17E-02	rs9332405	10	110178382	q25.1
SNP_A-1795687	C	C	377	11	360	24	5.2	2.26E-02	rs11194095	10	110186810	q25.1
SNP_A-1833724	A	A	335	15	323	31	5.762	1.64E-02	rs11194107	10	110217638	q25.1
SNP_A-2277733	T	T	273	101	264	134	4.043	4.44E-02	rs7094475	10	110224231	q25.1
SNP_A-2103483	A	A	282	136	306	108	4.174	4.11E-02	rs1332272	10	110251416	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246788	A	A	382	24	354	44	6.869	8.80E-03	rs17124681	10	110253292	q25.1
SNP_A-2276749	A	A	311	61	272	86	6.595	1.02E-02	rs1332274	10	110253388	q25.1
SNP_A-1942432	C	C	309	47	299	69	4.139	0.0419	rs1929988	10	110267905	q25.1
SNP_A-2269855	G	G	247	81	285	57	6.599	1.02E-02	rs10884668	10	110299833	q25.1
SNP_A-2049636	G	G	339	35	366	18	6.356	0.0117	rs11194202	10	110375957	q25.1
SNP_A-2118998	C	C	323	35	326	18	5.19	2.27E-02	rs11591528	10	110509337	q25.1
SNP_A-1939142	G	G	413	7	421	1	4.572	3.25E-02	rs7916577	10	110737713	q25.1
SNP_A-1806414	T	T	246	152	259	115	4.72	0.0298	rs7916127	10	110984021	q25.1
SNP_A-2055151	G	G	353	23	367	11	4.502	0.0339	rs11194526	10	111018774	q25.1
SNP_A-2196676	T	T	357	1	345	7	4.655	0.031	rs10884759	10	111128138	q25.1
SNP_A-1682256	C	C	353	29	372	12	7.542	6.00E-03	rs2145940	10	111208257	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1934220	T	T	276	128	238	152	4.621	3.16E-02	rs1039488	10	111225357	q25.1
SNP_A-2045037	C	C	214	170	245	143	4.402	3.59E-02	rs6584944	10	111242749	q25.1
SNP_A-1935115	A	A	392	4	398	0	4.041	4.44E-02	rs17794578	10	111266954	q25.1
SNP_A-2106079	A	A	269	103	236	130	5.237	2.21E-02	rs10884815	10	111378449	q25.1
SNP_A-1910938	A	A	272	140	242	172	5.028	2.49E-02	rs11596820	10	111378675	q25.1
SNP_A-2267387	T	T	416	4	422	0	4.038	4.45E-02	rs1322071	10	111536258	q25.1
SNP_A-1659506	C	C	224	136	268	112	5.721	1.68E-02	rs1935465	10	111693887	q25.2
SNP_A-1803707	G	G	304	36	323	19	5.824	1.58E-02	rs1891374	10	111956834	q25.2
SNP_A-1955756	C	C	176	168	202	142	3.969	4.63E-02	rs2855469	10	112031569	q25.2
SNP_A-2118083	T	T	276	132	300	102	4.802	2.84E-02	rs10884954	10	112121472	q25.2
SNP_A-1867343	T	C	200	182	222	182	4.196	4.05E-02	rs4918502	10	112138594	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1889613	G	T	218	194	224	188	4.37	3.66E-02	rs4918503	10	112138641	q25.2
SNP_A-1846752	G	A	228	192	226	194	5.505	0.019	rs4918508	10	112144100	q25.2
SNP_A-1660049	A	A	229	121	231	165	3.957	4.67E-02	rs2419577	10	112156207	q25.2
SNP_A-1641855	G	G	357	41	380	26	3.997	4.56E-02	rs10509929	10	112156875	q25.2
SNP_A-2272383	G	G	290	110	327	87	4.665	3.08E-02	rs11593739	10	112224209	q25.2
SNP_A-1924853	A	A	326	52	367	33	6.055	1.39E-02	rs2419571	10	112361083	q25.2
SNP_A-2138903	A	A	319	81	351	59	4.863	2.74E-02	rs4918543	10	112361326	q25.2
SNP_A-2165115	G	G	373	47	391	29	4.687	0.0304	rs11195299	10	112492132	q25.2
SNP_A-1929860	C	C	370	46	348	72	6.384	0.0115	rs12161672	10	112877461	q25.2
SNP_A-1957670	G	G	346	70	318	96	5.248	2.20E-02	rs1335713	10	112892144	q25.2
SNP_A-2256275	C	C	337	33	351	17	5.4	0.0201	rs11195448	10	112916642	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187679	A	A	301	85	326	58	6.09	1.36E-02	rs10787329	10	113072954	q25.2
SNP_A-2086538	C	C	303	81	311	43	10.547	1.20E-03	rs10787335	10	113092028	q25.2
SNP_A-1882171	T	T	289	105	311	77	5.069	2.44E-02	rs4515907	10	113099444	q25.2
SNP_A-2005307	C	C	250	166	280	140	3.888	4.86E-02	rs10509940	10	113110494	q25.2
SNP_A-1881740	C	C	305	47	269	69	6.149	0.0132	rs9421085	10	113156486	q25.2
SNP_A-2075545	C	C	335	49	307	67	3.883	4.88E-02	rs10885163	10	113156704	q25.2
SNP_A-2286586	G	G	349	53	336	78	4.842	2.78E-02	rs4396217	10	113173859	q25.2
SNP_A-2274752	G	G	401	7	376	16	4.008	0.0453	rs17129015	10	113312032	q25.2
SNP_A-2146797	A	A	371	7	357	19	5.802	0.016	rs7911321	10	113345068	q25.2
SNP_A-2303506	T	T	324	0	320	6	6.019	1.42E-02	rs17129046	10	113380246	q25.2
SNP_A-2208410	G	G	396	6	394	18	5.883	1.53E-02	rs17129063	10	113402729	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2078759	T	T	387	5	384	14	4.23	3.97E-02	rs17129087	10	113413141	q25.2
SNP_A-1935048	A	A	362	6	349	15	4.073	0.0436	rs17129107	10	113442242	q25.2
SNP_A-2005359	A	A	361	11	385	27	5.482	1.92E-02	rs1078289	10	113584783	q25.2
SNP_A-2059868	A	A	352	28	380	16	4.016	4.51E-02	rs11195742	10	113587189	q25.2
SNP_A-2005361	T	T	251	145	231	179	4.156	4.15E-02	rs11818577	10	113605087	q25.2
SNP_A-2005362	T	T	240	134	206	160	4.805	2.84E-02	rs2160794	10	113606245	q25.2
SNP_A-2074705	C	C	370	36	393	15	9.336	2.20E-03	rs10736218	10	113649683	q25.2
SNP_A-2188446	G	G	354	50	380	32	4.794	0.0286	rs10787420	10	113689173	q25.2
SNP_A-2090562	G	G	358	40	377	25	3.933	4.74E-02	rs7081632	10	113702601	q25.2
SNP_A-2195876	A	A	364	50	385	31	5.041	2.48E-02	rs7096364	10	113706092	q25.2
SNP_A-2176701	T	T	350	18	353	7	4.765	2.90E-02	rs11195861	10	114022644	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1704799	A	A	282	38	293	71	7.401	6.50E-03	rs1815239	10	114206205	q25.2
SNP_A-1833712	G	G	256	98	234	142	8.399	0.0038	rs9645551	10	114371103	q25.2
SNP_A-1874886	C	C	393	23	377	41	5.39	2.03E-02	rs11196070	10	114461555	q25.2
SNP_A-2221374	A	A	396	10	382	22	4.747	0.0293	rs11196089	10	114499280	q25.2
SNP_A-1818799	A	A	362	4	356	0	3.912	4.79E-02	rs2479117	10	114609010	q25.2
SNP_A-2198429	G	G	402	4	402	14	5.435	1.97E-02	rs7893608	10	114928707	q25.3
SNP_A-2204978	G	G	302	6	309	17	4.834	2.79E-02	rs4918811	10	115065133	q25.3
SNP_A-1751151	C	C	317	79	349	55	5.757	1.64E-02	rs2286396	10	115724974	q25.3
SNP_A-1953186	A	A	367	43	387	23	6.591	1.02E-02	rs7070157	10	115773822	q25.3
SNP_A-1871490	C	C	361	29	377	15	4.796	2.85E-02	rs12569745	10	115813735	q25.3
SNP_A-1729085	A	A	373	11	364	32	10.184	0.0014	rs727532	10	115869363	q25.3
SNP_A-1718311	C	T	206	168	212	190	4.737	2.95E-02	rs7923449	10	115968307	q25.3
SNP_A-2021567	G	G	323	87	347	59	6.21	1.27E-02	rs10885543	10	116037426	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1848642	G	G	373	43	376	26	3.962	0.0465	rs7910088	10	116162476	q25.3
SNP_A-2101272	G	G	339	35	304	52	4.786	0.0287	rs941853	10	116189165	q25.3
SNP_A-1866847	A	T	199	169	195	169	4.281	0.0385	rs10787533	10	116278053	q25.3
SNP_A-1912220	A	A	305	91	278	120	5.231	2.22E-02	rs2497719	10	116298054	q25.3
SNP_A-1780917	A	A	352	46	371	29	4.348	3.71E-02	rs11196841	10	116407357	q25.3
SNP_A-2298741	C	C	317	39	278	56	4.902	2.68E-02	rs808249	10	116456644	q25.3
SNP_A-1845912	C	C	264	98	277	69	4.989	2.55E-02	rs1537685	10	116894953	q25.3
SNP_A-2134055	T	T	266	80	247	45	5.976	1.45E-02	rs7920316	10	117261442	q25.3
SNP_A-2256760	C	C	281	105	280	74	3.994	4.57E-02	rs7895853	10	117272006	q25.3
SNP_A-1682974	T	T	393	11	411	3	4.853	0.0276	rs10510015	10	117584928	q25.3
SNP_A-2196515	G	G	238	176	278	140	7.183	7.40E-03	rs180726	10	117717708	q25.3
SNP_A-2184120	A	A	226	182	259	141	7.371	0.0066	rs180710	10	117722959	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2312628	C	C	213	137	241	95	9.048	2.60E-03	rs180708	10	117723403	q25.3
SNP_A-2005734	G	G	299	87	288	116	3.941	4.71E-02	rs7070180	10	117842460	q25.3
SNP_A-1654307	T	T	378	26	404	10	7.854	5.10E-03	rs7907051	10	117843519	q25.3
SNP_A-1644098	C	C	378	24	404	10	6.454	0.0111	rs1431486	10	117857719	q25.3
SNP_A-2072639	A	A	206	96	187	143	8.938	0.0028	rs12774375	10	118010056	q25.3
SNP_A-1869492	A	A	229	123	205	157	5.317	2.11E-02	rs11197611	10	118011735	q25.3
SNP_A-2202824	C	C	248	134	221	175	6.745	9.40E-03	rs11197612	10	118014309	q25.3
SNP_A-2005751	A	A	233	187	268	150	6.503	1.08E-02	rs758575	10	118037661	q25.3
SNP_A-1860546	A	A	259	161	291	127	5.871	0.0154	rs2577346	10	118049334	q25.3
SNP_A-1854939	A	A	244	176	275	143	5.261	0.0218	rs1860401	10	118062492	q25.3
SNP_A-2183405	C	C	390	10	407	3	4.009	0.0453	rs11817406	10	118111210	q25.3
SNP_A-1939855	A	A	366	42	395	19	9.734	0.0018	rs7087634	10	118161006	q25.3
SNP_A-2257181	C	C	355	31	393	17	5.295	2.14E-02	rs7087456	10	118162755	q25.3
SNP_A-2068845	G	G	382	18	401	5	7.765	0.0053	rs10885929	10	118177518	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2302615	G	G	400	14	417	5	4.541	3.31E-02	rs1529614	10	118195902	q25.3
SNP_A-1889184	C	C	383	15	408	4	6.919	8.50E-03	rs11197682	10	118202861	q25.3
SNP_A-2104368	A	A	378	32	392	18	4.175	4.10E-02	rs1008307	10	118450781	q25.3
SNP_A-1728559	C	C	387	17	405	7	4.498	0.0339	rs363306	10	118625117	q26.11
SNP_A-1735082	G	G	385	15	405	5	5.384	2.03E-02	rs363307	10	118626142	q26.11
SNP_A-1807068	A	A	361	5	362	0	4.98	2.56E-02	rs7903411	10	118848298	q26.11
SNP_A-2252823	G	G	336	14	363	3	7.807	5.20E-03	rs363344	10	118945554	q26.11
SNP_A-2005823	G	G	393	17	411	7	4.493	3.40E-02	rs363313	10	118957450	q26.11
SNP_A-1903639	C	C	398	18	412	6	6.237	1.25E-02	rs3858335	10	118963135	q26.11
SNP_A-2122182	C	C	389	15	413	5	5.481	1.92E-02	rs17095891	10	118963546	q26.11
SNP_A-2235515	C	C	321	61	354	42	4.868	2.74E-02	rs363278	10	119025058	q26.11
SNP_A-1829801	G	G	293	97	310	72	4.095	4.30E-02	rs181438	10	119088152	q26.11
SNP_A-1852917	T	T	288	86	256	110	4.735	2.96E-02	rs17772810	10	119147475	q26.11
SNP_A-2302580	T	T	228	128	279	103	6.928	8.50E-03	rs855767	10	119306070	q26.11
SNP_A-2179764	G	G	380	14	385	3	7.105	7.70E-03	rs242959	10	119317311	q26.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2052869	A	A	401	7	394	18	4.882	2.71E-02	rs11198317	10	119984455	q26.11
SNP_A-1853413	C	C	325	47	313	25	5.332	2.09E-02	rs1061498	10	120092408	q26.11
SNP_A-1939731	A	A	317	29	289	49	6.329	1.19E-02	rs853937	10	120152558	q26.11
SNP_A-2244177	C	C	275	29	276	60	9.223	2.40E-03	rs2225915	10	120356895	q26.11
SNP_A-2271258	T	T	376	6	369	19	6.779	9.20E-03	rs4474362	10	120375661	q26.11
SNP_A-2112119	T	T	257	133	290	110	4.042	4.44E-02	rs2787602	10	120381488	q26.11
SNP_A-1948213	G	G	308	104	284	130	3.857	4.95E-02	rs17097926	10	120418771	q26.11
SNP_A-2278652	C	C	278	60	257	83	4.518	3.35E-02	rs7919327	10	120419544	q26.11
SNP_A-1817628	T	T	283	103	266	132	3.922	4.76E-02	rs10886283	10	120422782	q26.11
SNP_A-2026554	T	T	260	156	224	190	6.014	1.42E-02	rs4752201	10	120513596	q26.11
SNP_A-2157492	G	G	237	171	205	201	4.731	2.96E-02	rs4751677	10	120599786	q26.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2081761	A	A	322	90	344	66	4.414	0.0356	rs17606601	10	121001177	q26.11
SNP_A-1809736	C	T	188	172	208	164	4.851	0.0276	rs10787948	10	121055451	q26.11
SNP_A-1664690	C	C	329	21	323	39	5.254	2.19E-02	rs1196278	10	121065619	q26.11
SNP_A-2114861	G	G	287	67	318	48	4.529	3.33E-02	rs4531379	10	121068691	q26.11
SNP_A-2133522	A	A	266	142	296	110	5.66	1.74E-02	rs915113	10	121100775	q26.11
SNP_A-1915304	A	A	357	31	326	60	10.644	1.10E-03	rs7913091	10	121199640	q26.11
SNP_A-1843172	G	G	376	40	352	68	8.032	4.60E-03	rs7896882	10	121199813	q26.11
SNP_A-1869510	T	T	379	31	357	53	6.42	1.13E-02	rs1999628	10	121207051	q26.11
SNP_A-2163419	C	C	382	34	360	58	6.908	0.0086	rs11198934	10	121207673	q26.11
SNP_A-2292817	T	T	392	12	379	31	8.571	3.40E-03	rs11198957	10	121228892	q26.11
SNP_A-2047901	G	G	382	16	368	34	6.722	9.50E-03	rs4751723	10	121228932	q26.11
SNP_A-2240071	C	C	380	12	370	24	4.128	4.22E-02	rs4751729	10	121229564	q26.11
SNP_A-1906086	C	C	382	38	401	21	5.355	0.0207	rs17099196	10	121439998	q26.11
SNP_A-2034660	G	G	340	14	351	5	4.433	3.53E-02	—	10	121527452	q26.12
SNP_A-2005978	T	T	212	206	244	166	6.47	1.10E-02	rs3781503	10	121561497	q26.12
SNP_A-1816298	C	A	217	177	206	190	3.982	4.60E-02	rs9420284	10	121595918	q26.12
SNP_A-2180204	A	A	317	77	339	55	4.404	3.58E-02	rs10749338	10	121764195	q26.12
SNP_A-1643824	G	C	224	180	225	189	7.845	5.10E-03	rs966157	10	121929866	q26.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1660265	A	T	222	178	224	186	8.318	3.90E-03	rs966158	10	121929912	q26.12
SNP_A-1701861	C	C	243	157	207	205	9.069	2.60E-03	rs10510071	10	121944326	q26.12
SNP_A-2124689	G	G	398	14	369	27	4.904	2.68E-02	rs7079630	10	122128794	q26.12
SNP_A-2099351	C	C	333	13	291	23	4.063	4.38E-02	rs7080041	10	122129025	q26.12
SNP_A-2238420	A	A	402	18	389	33	4.621	3.16E-02	rs7090223	10	122145114	q26.12
SNP_A-2197067	G	G	388	8	378	18	3.977	4.61E-02	rs7913921	10	122151784	q26.12
SNP_A-2163643	A	A	411	1	403	7	4.574	3.25E-02	rs1571099	10	122256604	q26.12
SNP_A-2124253	G	G	307	3	318	12	4.973	2.57E-02	rs4237521	10	122267201	q26.12
SNP_A-1940912	T	T	373	19	389	7	5.854	0.0155	rs11199389	10	122294432	q26.12
SNP_A-2006018	C	C	365	13	350	30	7.03	8.00E-03	rs4752432	10	122297091	q26.12
SNP_A-2232256	C	C	394	26	407	13	4.544	3.30E-02	rs11199414	10	122323419	q26.12
SNP_A-1726810	G	G	325	29	324	64	11.64	6.00E-04	rs10510084	10	122390952	q26.12
SNP_A-2067877	G	G	408	6	401	17	5.302	2.13E-02	rs11199471	10	122425887	q26.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2235377	C	C	408	6	400	16	4.62	3.16E-02	rs11199476	10	122428187	q26.12
SNP_A-2006038	T	T	350	62	368	40	5.177	0.0229	rs3011399	10	122491477	q26.12
SNP_A-2167042	C	C	348	58	374	38	5.059	2.45E-02	rs3011410	10	122495603	q26.12
SNP_A-2117854	G	G	374	28	355	53	8.167	0.0043	rs17500035	10	122528339	q26.12
SNP_A-1909351	G	G	357	27	301	53	12.016	5.00E-04	rs17100835	10	122529497	q26.12
SNP_A-1698685	T	T	398	4	414	0	4.14	0.0419	rs2250945	10	122542837	q26.12
SNP_A-1798498	G	G	409	5	420	0	5.103	2.39E-02	rs2250810	10	122869859	q26.12
SNP_A-1827691	C	C	354	4	384	0	4.314	0.0378	rs1907243	10	122890757	q26.12
SNP_A-2235924	T	T	340	8	358	2	3.862	4.94E-02	rs11199810	10	122913568	q26.12
SNP_A-2264605	T	T	414	4	420	0	4.038	4.45E-02	rs11199816	10	122934352	q26.12
SNP_A-2077605	C	C	368	22	368	10	4.314	0.0378	rs2114691	10	123188826	q26.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209390	A	A	243	155	211	189	5.611	0.0178	rs11199974	10	123204467	q26.13
SNP_A-2234867	G	G	289	93	227	133	13.889	2.00E-04	rs7911727	10	123214869	q26.13
SNP_A-2142462	C	C	308	108	274	142	6.61	0.0101	rs1619436	10	123216934	q26.13
SNP_A-1945093	T	G	196	192	229	173	4.439	3.51E-02	rs2420941	10	123219616	q26.13
SNP_A-2210841	C	C	342	0	333	5	5.097	0.024	rs2981434	10	123277693	q26.13
SNP_A-2116863	T	T	317	73	296	98	4.354	3.69E-02	rs10466158	10	123389837	q26.13
SNP_A-2166029	G	G	253	161	227	191	3.946	0.047	rs1693682	10	123453723	q26.13
SNP_A-1742487	C	C	284	100	269	133	4.671	3.07E-02	rs2420994	10	123527539	q26.13
SNP_A-1650326	G	A	218	184	221	187	5.709	1.69E-02	rs3905303	10	123739478	q26.13
SNP_A-2181276	C	C	273	89	256	118	4.415	0.0356	rs2421005	10	123868669	q26.13
SNP_A-2006169	C	C	386	22	408	10	4.989	2.55E-02	rs1113263	10	123878991	q26.13
SNP_A-2170584	C	C	193	145	230	120	5.387	2.03E-02	rs4752666	10	123938190	q26.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006182	G	G	285	133	246	170	7.378	0.0066	rs1045934	10	123980234	q26.13
SNP_A-1932851	A	A	246	116	279	87	6.195	1.28E-02	rs1555487	10	123984146	q26.13
SNP_A-2184343	T	T	286	114	248	146	6.598	1.02E-02	rs11200494	10	123985891	q26.13
SNP_A-2006187	G	A	215	149	181	171	7.92	4.90E-03	rs10887110	10	123997563	q26.13
SNP_A-2171507	T	C	201	143	176	166	6.746	9.40E-03	rs9630083	10	124007413	q26.13
SNP_A-2006189	G	G	231	145	284	108	10.537	1.20E-03	rs5017040	10	124018550	q26.13
SNP_A-2006193	C	C	288	132	321	95	7.8	5.20E-03	rs11596483	10	124027589	q26.13
SNP_A-2089800	C	T	208	158	193	165	8.36	0.0038	rs4752678	10	124029647	q26.13
SNP_A-2183713	G	A	194	132	172	166	7.226	7.20E-03	rs6585810	10	124031437	q26.13
SNP_A-2206600	T	T	242	62	292	38	9.391	2.20E-03	rs8181295	10	124031668	q26.13
SNP_A-2257697	G	G	288	132	315	85	10.907	0.001	rs17103336	10	124031691	q26.13
SNP_A-2172202	C	T	209	159	205	171	9.528	0.002	rs911775	10	124035292	q26.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2006195	C	C	259	103	308	72	9.295	0.0023	rs2104176	10	124035844	q26.13
SNP_A-2180715	A	G	171	161	208	142	8.204	4.20E-03	rs9633733	10	124046536	q26.13
SNP_A-2142787	C	T	204	184	235	163	10.663	1.10E-03	rs7907952	10	124046764	q26.13
SNP_A-2001527	G	G	408	0	416	4	3.905	0.0482	rs6585821	10	124099910	q26.13
SNP_A-2127043	A	A	400	4	404	0	4.02	4.50E-02	rs1832791	10	124635131	q26.13
SNP_A-1703737	C	C	234	150	219	191	4.58	3.24E-02	rs4980285	10	124675075	q26.13
SNP_A-2173712	C	C	410	0	404	4	4.039	4.45E-02	rs1898458	10	124902105	q26.13
SNP_A-2006276	A	A	364	24	361	43	5.079	2.42E-02	rs11248419	10	124915198	q26.13
SNP_A-2308221	A	A	243	105	201	143	9.773	0.0018	rs7090367	10	125224482	q26.13
SNP_A-1814317	G	G	237	119	210	152	5.6	1.80E-02	rs1410607	10	125229242	q26.13
SNP_A-2045381	A	A	217	147	183	167	3.891	4.85E-02	rs9423354	10	125239754	q26.13
SNP_A-2305645	G	G	342	42	328	68	6.255	0.0124	rs7916049	10	125242083	q26.13
SNP_A-1881784	A	A	259	155	225	191	6.129	1.33E-02	rs913525	10	125243227	q26.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101956	A	A	230	124	202	162	6.726	9.50E-03	rs2479901	10	125245063	q26.13
SNP_A-1947688	G	G	328	90	299	121	5.891	0.0152	rs7091074	10	125249606	q26.13
SNP_A-2034021	T	T	398	4	408	0	4.08	4.34E-02	rs841052	10	125328720	q26.13
SNP_A-1920010	T	T	392	0	390	4	4	4.55E-02	rs17608508	10	125445267	q26.13
SNP_A-1878368	C	C	413	1	408	8	5.47	1.93E-02	rs4980201	10	125453561	q26.13
SNP_A-1878205	A	A	309	55	287	87	7.889	5.00E-03	rs7920094	10	125598580	q26.13
SNP_A-2176646	G	G	304	80	282	116	7.19	7.30E-03	rs7078763	10	125853107	q26.13
SNP_A-1864666	C	C	258	80	234	110	5.855	0.0155	rs7078615	10	125853202	q26.13
SNP_A-2132622	G	G	281	49	258	68	4.043	4.44E-02	rs4511232	10	125855117	q26.13
SNP_A-1960557	T	T	233	137	278	110	6.49	1.08E-02	rs7905355	10	125914585	q26.13
SNP_A-2006360	A	A	343	9	315	21	5.622	0.0177	rs8182	10	126075966	q26.13
SNP_A-2236836	A	A	337	15	319	27	3.871	4.91E-02	rs2674348	10	126107204	q26.13
SNP_A-2305568	A	A	284	120	326	90	7.003	8.10E-03	rs17708789	10	126565839	q26.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2039528	A	A	234	92	263	69	4.924	2.65E-02	rs7099073	10	126599637	q26.13
SNP_A-2268940	A	A	359	55	383	37	4.255	3.91E-02	rs2114835	10	126620547	q26.13
SNP_A-2128949	T	T	382	22	366	46	8.735	3.10E-03	rs1077497	10	126713123	q26.13
SNP_A-1824920	C	C	352	12	343	27	5.837	1.57E-02	rs7903340	10	126730761	q26.13
SNP_A-2074011	C	C	355	45	381	27	5.34	2.08E-02	rs11244438	10	127047653	q26.13
SNP_A-1815896	T	T	196	194	231	153	7.667	5.60E-03	rs7901844	10	127152376	q26.13
SNP_A-2006465	C	C	300	60	307	33	7.354	6.70E-03	rs2027515	10	127485822	q26.2
SNP_A-1654981	T	T	261	129	305	109	4.389	3.62E-02	rs10510152	10	127598278	q26.2
SNP_A-1660751	T	T	331	65	317	89	3.919	4.78E-02	rs4357606	10	127637796	q26.2
SNP_A-2129127	G	G	324	40	358	18	9.848	1.70E-03	rs11244734	10	127646104	q26.2
SNP_A-2144822	C	C	404	4	418	0	4.118	0.0424	rs898326	10	127846374	q26.2
SNP_A-1791811	C	C	342	62	320	84	4.046	4.43E-02	rs11244956	10	128007309	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2026559	C	C	311	29	288	44	3.871	4.91E-02	rs12356119	10	128017485	q26.2
SNP_A-1912159	C	C	340	0	337	5	5.007	0.0252	rs11244965	10	128027237	q26.2
SNP_A-2058097	G	G	342	22	363	9	5.991	0.0144	rs12356932	10	128042563	q26.2
SNP_A-1665240	T	T	239	165	209	203	5.855	0.0155	rs7894577	10	128117852	q26.2
SNP_A-1881002	T	T	366	32	358	54	5.476	1.93E-02	rs7897106	10	128150520	q26.2
SNP_A-2287029	T	T	333	17	295	29	4.433	3.52E-02	rs7096562	10	128391775	q26.2
SNP_A-1739475	C	C	342	28	341	47	4.39	3.62E-02	rs1770390	10	128417417	q26.2
SNP_A-2249694	A	A	242	134	261	105	4.102	4.28E-02	rs11245125	10	128419924	q26.2
SNP_A-2096929	A	A	269	139	325	95	13.382	3.00E-04	rs9422852	10	128587576	q26.2
SNP_A-2204065	C	C	275	125	326	90	9.715	0.0018	rs9422853	10	128587723	q26.2
SNP_A-1825726	A	A	315	85	345	61	5.264	0.0218	rs9664585	10	128668007	q26.2
SNP_A-2279782	G	G	319	91	350	68	4.687	0.0304	rs12219822	10	128671775	q26.2
SNP_A-2209302	G	G	323	27	312	46	5.046	0.0247	rs2489379	10	128886566	q26.2
SNP_A-2059289	C	C	403	13	417	3	6.47	1.10E-02	rs7912795	10	129381044	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169238	C	C	339	15	321	31	6.051	1.39E-02	rs1926150	10	129441662	q26.2
SNP_A-2282680	A	A	369	35	348	54	4.666	3.08E-02	rs11018324	10	129493961	q26.2
SNP_A-2192411	A	A	358	28	343	55	8.923	0.0028	rs1926170	10	129507129	q26.2
SNP_A-2067378	G	G	370	24	345	41	5.239	2.21E-02	rs1327561	10	129514772	q26.2
SNP_A-2089696	G	G	319	51	344	30	6.366	1.16E-02	rs729598	10	129515347	q26.2
SNP_A-1815129	C	C	256	156	298	120	7.837	5.10E-03	rs7904367	10	129682011	q26.2
SNP_A-2089813	T	T	308	68	271	101	8.787	3.00E-03	rs7922406	10	129686520	q26.2
SNP_A-2082888	T	T	317	63	279	103	12.056	5.00E-04	rs7895103	10	129686948	q26.2
SNP_A-2063714	C	T	194	176	218	164	6.801	9.10E-03	rs7085243	10	129693110	q26.2
SNP_A-2088859	A	A	377	31	364	50	4.641	3.12E-02	rs7083801	10	129725918	q26.2
SNP_A-1877094	A	A	306	30	293	57	8.379	0.0038	rs11016102	10	129835144	q26.2
SNP_A-2159816	G	G	264	124	230	150	4.724	2.97E-02	rs7923707	10	130057287	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2217957	T	T	329	89	301	117	5.05	0.0246	rs7915794	10	130179509	q26.2
SNP_A-2195091	G	G	331	89	304	118	5.206	2.25E-02	rs11016274	10	130181527	q26.2
SNP_A-2298953	C	T	223	171	202	194	4.588	3.22E-02	rs10829419	10	130208207	q26.2
SNP_A-1786353	C	C	224	122	205	157	4.873	2.73E-02	rs11016297	10	130208448	q26.2
SNP_A-1834724	C	C	360	28	347	47	5.007	0.0253	rs10829454	10	130325611	q26.2
SNP_A-1787948	T	T	391	11	360	22	4.439	3.51E-02	rs748308	10	130347044	q26.2
SNP_A-2110800	C	C	364	46	343	71	5.946	0.0147	rs1327012	10	130401885	q26.2
SNP_A-1952869	C	C	397	11	397	3	4.493	3.40E-02	rs10829478	10	130402913	q26.2
SNP_A-2259756	G	G	334	28	264	38	4.323	3.76E-02	rs549879	10	130475742	q26.2
SNP_A-2234217	C	C	214	134	220	100	3.856	4.96E-02	rs5026308	10	130509357	q26.3
SNP_A-1900031	T	T	310	84	279	111	5.35	0.0207	rs942528	10	130565507	q26.3
SNP_A-2300701	C	C	336	70	359	49	4.462	3.47E-02	rs2039546	10	130598155	q26.3
SNP_A-2001584	C	C	349	11	351	27	6.307	0.012	rs7085203	10	130600913	q26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884818	G	G	242	156	264	126	4.067	4.37E-02	rs2039545	10	130636360	q26.3
SNP_A-1935353	G	G	240	110	221	139	4.021	4.49E-02	rs10764918	10	131518680	q26.3
SNP_A-1818375	A	A	411	3	406	12	5.411	0.02	rs17330838	10	131616674	q26.3
SNP_A-2006682	C	C	406	14	418	4	5.726	0.0167	rs7904588	10	131620994	q26.3
SNP_A-2310333	T	T	292	118	264	150	5.212	0.0224	rs10829675	10	131688458	q26.3
SNP_A-1863447	T	T	314	36	316	20	4.294	3.83E-02	rs7894000	10	131822686	q26.3
SNP_A-2213374	C	C	220	134	193	163	4.591	3.21E-02	rs7092451	10	131907431	q26.3
SNP_A-2213367	C	C	358	10	345	23	5.362	0.0206	rs11017192	10	131992673	q26.3
SNP_A-1902255	T	T	410	4	416	0	4.039	4.45E-02	rs10829757	10	132188935	q26.3
SNP_A-2114577	C	C	357	51	382	34	4.168	4.12E-02	rs1334914	10	132201499	q26.3
SNP_A-2266138	T	T	330	50	370	34	4.603	3.19E-02	rs7918441	10	132204958	q26.3
SNP_A-1743551	A	A	292	66	285	107	8.277	4.00E-03	rs1368665	10	132221295	q26.3
SNP_A-1952065	G	A	218	200	231	189	4.291	3.83E-02	rs12251302	10	132298115	q26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2202713	C	C	397	7	391	21	6.968	8.30E-03	rs11017456	10	132456159	q26.3
SNP_A-1863491	A	A	357	51	342	76	5.123	2.36E-02	rs7893779	10	132460301	q26.3
SNP_A-2306823	G	G	349	33	329	57	6.969	8.30E-03	rs1703728	10	132625067	q26.3
SNP_A-1887355	C	C	349	37	326	58	5.421	1.99E-02	rs12776144	10	132626509	q26.3
SNP_A-1792235	T	T	343	43	334	72	6.932	8.50E-03	rs2397738	10	132628747	q26.3
SNP_A-1827649	C	C	362	50	338	72	4.785	0.0287	rs892322	10	132630798	q26.3
SNP_A-2284031	A	A	279	65	251	97	7.777	0.0053	rs3125594	10	132637389	q26.3
SNP_A-2267973	T	T	359	49	341	75	5.837	1.57E-02	rs10829854	10	132641908	q26.3
SNP_A-1883400	A	A	186	116	174	162	6.217	1.27E-02	rs2918157	10	132906450	q26.3
SNP_A-2187092	A	A	345	5	330	20	9.333	0.0023	rs2918109	10	132968717	q26.3
SNP_A-1922068	A	A	254	164	226	196	4.459	3.47E-02	rs4372360	10	133053381	q26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181151	G	G	285	57	254	78	4.902	2.66E-02	rs9787694	10	133389289	q26.3
SNP_A-1916368	C	C	293	99	319	73	5.035	2.48E-02	rs4131689	10	133594318	q26.3
SNP_A-1931617	T	T	267	103	301	83	3.927	4.75E-02	rs10430614	10	133598630	q26.3
SNP_A-1826977	G	G	281	85	309	63	4.551	3.29E-02	rs10870271	10	133604797	q26.3
SNP_A-1829987	C	C	262	76	288	50	6.594	1.02E-02	rs3829156	10	133639376	q26.3
SNP_A-1784663	C	C	320	46	349	29	4.918	2.66E-02	rs6560704	10	133648503	q26.3
SNP_A-2264641	T	T	323	39	314	64	5.852	1.56E-02	rs7906354	10	133777077	q26.3
SNP_A-2299148	G	G	309	47	294	68	4.158	4.14E-02	rs11146323	10	133966761	q26.3
SNP_A-2298983	C	C	221	169	264	138	6.762	9.30E-03	rs10870219	10	134651068	q26.3
SNP_A-2036059	G	G	228	126	251	101	3.852	4.97E-02	rs7099794	10	134662388	q26.3
SNP_A-1703733	C	C	341	49	378	28	7.313	6.80E-03	rs2252728	10	134748649	q26.3
SNP_A-1928678	C	C	322	90	349	67	4.437	3.52E-02	rs736017	10	134806178	q26.3
SNP_A-2259588	-	A	198	198	227	151	7.894	5.00E-03	rs3008304	10	134871004	q26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2269324	A	A	326	50	357	33	4.635	3.13E-02	rs2814209	10	135171082	q26.3
SNP_A-2188173	A	A	217	129	262	104	6.353	0.0117	rs7394810	11	356710	p15.5
SNP_A-2258027	G	G	352	22	351	41	5.312	0.0212	rs1056812	11	555840	p15.5
SNP_A-1926594	C	C	385	17	412	6	5.866	0.0154	rs11246199	11	567684	p15.5
SNP_A-1887974	C	C	356	16	378	4	7.728	5.40E-03	rs11246211	11	596294	p15.5
SNP_A-1786205	C	C	404	2	400	12	7.119	0.0076	rs11604855	11	631991	p15.5
SNP_A-2100287	C	C	359	61	380	40	4.963	2.59E-02	rs7123677	11	678804	p15.5
SNP_A-1797583	G	G	386	22	371	43	7.038	8.00E-03	rs6597988	11	723072	p15.5
SNP_A-2070005	G	G	290	108	254	160	12.161	5.00E-04	rs4963059	11	1229434	p15.5
SNP_A-2265433	G	G	380	10	404	2	5.749	1.65E-02	rs6578285	11	1337340	p15.5
SNP_A-1928363	C	C	267	59	253	83	4.283	0.0385	rs7395884	11	1346492	p15.5
SNP_A-2209133	G	G	276	56	299	29	9.473	2.10E-03	rs10835060	11	1444719	p15.5
SNP_A-1854634	G	G	388	4	382	12	4.042	4.44E-02	rs1809667	11	1576435	p15.5
SNP_A-2178686	C	C	368	22	353	37	4.126	4.22E-02	rs10837859	11	1602542	p15.5
SNP_A-2304052	C	C	383	21	365	35	3.913	4.79E-02	rs12365311	11	1606463	p15.5
SNP_A-2194872	C	T	219	167	207	197	5.034	2.49E-02	rs3809101	11	1923847	p15.5

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1847365	C	T	236	182	216	204	5.227	2.22E-02	rs10769945	11	1941703	p15.5
SNP_A-1930704	C	T	201	191	229	179	4.394	0.0361	rs3890907	11	1984719	p15.5
SNP_A-2100090	A	G	205	195	231	169	6.507	1.07E-02	rs4930030	11	2043796	p15.5
SNP_A-2122448	G	G	299	89	335	65	5.603	1.79E-02	rs2651843	11	2298308	p15.5
SNP_A-2283063	T	T	316	58	331	33	7.082	7.80E-03	rs2521294	11	2305354	p15.5
SNP_A-2279707	T	T	359	33	361	17	4.873	2.73E-02	rs179407	11	2483474	p15.5
SNP_A-2096384	C	C	370	44	386	28	3.894	4.85E-02	rs7118939	11	2603196	p15.5
SNP_A-1859784	A	A	387	23	403	11	4.54	3.31E-02	rs7941377	11	2656737	p15.5
SNP_A-2222217	C	C	270	114	253	145	4.014	4.51E-02	rs231841	11	2680180	p15.5
SNP_A-1942229	C	C	265	115	241	159	7.696	5.50E-03	rs2283197	11	2682355	p15.5
SNP_A-2186983	T	T	360	30	359	15	4.668	3.07E-02	rs11024034	11	2746739	p15.5
SNP_A-1752733	T	T	306	34	314	68	9.024	2.70E-03	rs63934	11	2753371	p15.5

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2176134	A	A	396	22	407	7	7.89	5.00E-03	rs10766379	11	2782775	p15.5
SNP_A-2203798	A	A	395	23	409	5	11.796	6.00E-04	rs8181588	11	2788117	p15.5
SNP_A-2006973	G	G	396	4	373	13	5.205	2.25E-02	rs449318	11	2876762	p15.4
SNP_A-1932693	C	C	354	56	380	38	4.291	3.83E-02	rs2271580	11	3604709	p15.4
SNP_A-2304243	G	G	295	25	284	42	4.467	3.46E-02	rs6578414	11	3795065	p15.4
SNP_A-2213893	C	C	237	169	268	142	4.228	3.98E-02	rs1026231	11	3822362	p15.4
SNP_A-1823892	C	C	322	4	360	0	4.443	3.50E-02	rs11827790	11	4054828	p15.4
SNP_A-1920464	T	T	341	31	317	51	5.732	0.0167	rs11031595	11	4282368	p15.4
SNP_A-2007105	T	T	266	154	299	121	5.887	0.0152	rs10500601	11	4412531	p15.4
SNP_A-2040870	C	C	242	66	233	93	4.248	3.93E-02	rs11032345	11	4440254	p15.4
SNP_A-1781381	G	G	389	19	369	35	5.249	2.20E-02	rs10836109	11	4447884	p15.4
SNP_A-1738461	G	G	381	17	402	6	5.701	1.70E-02	rs10500604	11	4497424	p15.4
SNP_A-1741951	C	C	388	16	408	6	4.926	0.0264	rs10500605	11	4507161	p15.4
SNP_A-2144275	C	C	363	9	380	0	9.305	0.0023	rs11033047	11	4596638	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1887585	C	C	328	74	300	108	7.556	6.00E-03	rs11033126	11	4616434	p15.4
SNP_A-2007169	C	C	384	10	401	3	4.013	4.52E-02	rs16933308	11	4683016	p15.4
SNP_A-1782463	T	T	365	43	347	67	5.648	1.75E-02	rs11035102	11	4986033	p15.4
SNP_A-2231482	C	C	328	16	357	5	6.535	0.0106	rs4323861	11	5010366	p15.4
SNP_A-2133327	T	T	355	31	342	48	3.88	4.89E-02	rs2647579	11	5396863	p15.4
SNP_A-2311709	T	T	364	42	352	62	3.97	4.63E-02	rs2340653	11	5408337	p15.4
SNP_A-1720225	T	T	345	37	343	63	6.04	0.014	rs10500641	11	5433885	p15.4
SNP_A-1865964	T	T	283	123	239	143	4.486	3.42E-02	rs7101919	11	5467264	p15.4
SNP_A-2007311	T	T	353	1	317	7	5.117	2.37E-02	rs11038071	11	5529769	p15.4
SNP_A-2199591	A	A	400	14	412	4	5.728	0.0167	rs7124435	11	5658395	p15.4
SNP_A-2091939	T	T	244	172	278	136	6.418	1.13E-02	rs4357719	11	5819229	p15.4
SNP_A-1950734	G	G	238	138	267	97	8.626	0.0033	rs10769276	11	5824596	p15.4
SNP_A-1825504	T	C	212	166	194	182	4.457	3.48E-02	rs12273011	11	5853455	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2241115	T	T	236	168	209	197	3.937	4.72E-02	rs7480397	11	5858229	p15.4
SNP_A-2152938	T	T	242	174	214	206	4.395	3.60E-02	rs1377518	11	5858528	p15.4
SNP_A-2254987	G	G	265	121	290	96	4.006	0.0453	rs10838795	11	5877297	p15.4
SNP_A-1867414	T	T	251	159	279	131	4.183	4.08E-02	rs10769353	11	5911385	p15.4
SNP_A-2169691	G	G	294	64	319	41	6.052	1.39E-02	rs12274539	11	6405981	p15.4
SNP_A-1927350	G	G	286	92	246	118	5.965	0.0146	rs2857918	11	6958272	p15.4
SNP_A-1658606	C	C	294	100	278	136	5.447	1.96E-02	rs762854	11	6969203	p15.4
SNP_A-2104866	G	G	323	29	296	46	4.888	0.027	rs11041127	11	6970642	p15.4
SNP_A-2139489	C	C	254	120	214	138	4.012	4.52E-02	rs10839682	11	6989148	p15.4
SNP_A-2244719	G	G	233	113	217	145	4.178	4.09E-02	rs10839715	11	7058372	p15.4
SNP_A-1846824	A	A	352	0	342	8	8.138	0.0043	rs11041280	11	7223792	p15.4
SNP_A-1807148	A	A	343	43	355	21	7.639	5.70E-03	rs11041350	11	7375953	p15.4
SNP_A-1825105	C	C	207	191	243	163	5.016	2.51E-02	rs7126383	11	7505204	p15.4
SNP_A-2145562	G	G	177	153	205	119	6.248	0.0124	rs10769866	11	8032727	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308431	A	A	188	140	228	124	3.974	4.62E-02	rs6578921	11	8051078	p15.4
SNP_A-2211548	G	G	370	0	363	5	5.061	2.45E-02	rs7949525	11	8060386	p15.4
SNP_A-2292502	T	T	332	8	300	20	6.163	1.30E-02	rs11041777	11	8144704	p15.4
SNP_A-2115021	C	C	297	105	274	132	3.983	4.60E-02	rs439667	11	8215934	p15.4
SNP_A-1787224	C	C	412	4	418	0	4.039	4.45E-02	rs11041851	11	8272940	p15.4
SNP_A-2256230	A	A	233	155	265	131	3.989	0.0458	rs16937956	11	8361077	p15.4
SNP_A-2068702	T	T	381	13	407	5	4.013	4.51E-02	rs16938066	11	8388525	p15.4
SNP_A-2001689	T	G	183	157	177	149	4.387	3.62E-02	rs7108993	11	8403769	p15.4
SNP_A-1688160	G	G	256	116	307	85	8.884	2.90E-03	rs10500704	11	8415533	p15.4
SNP_A-1788462	A	A	365	9	391	1	6.875	8.70E-03	rs11042014	11	8598315	p15.4
SNP_A-2296830	A	A	301	41	309	19	7.882	5.00E-03	rs10743084	11	8613897	p15.4
SNP_A-1794181	C	C	237	127	211	173	8.033	4.60E-03	rs10840106	11	8658412	p15.4
SNP_A-1897250	C	G	198	178	205	161	5.583	1.81E-02	rs7117300	11	8687209	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803538	A	-	235	143	187	187	11.305	8.00E-04	rs10840114	11	8693271	p15.4
SNP_A-1836872	C	C	393	25	405	13	3.97	4.63E-02	rs1104773	11	8694171	p15.4
SNP_A-1870889	G	G	313	33	325	17	5.323	2.11E-02	rs4061049	11	8694300	p15.4
SNP_A-2235240	A	A	385	33	401	19	4.09	4.31E-02	rs4061048	11	8694326	p15.4
SNP_A-1937829	C	C	240	154	277	131	4.261	0.039	rs3812762	11	8708216	p15.4
SNP_A-2216161	A	A	266	148	224	194	9.768	0.0018	rs10769947	11	8714690	p15.4
SNP_A-2038733	G	C	187	141	181	177	3.939	4.72E-02	rs10769955	11	8741223	p15.4
SNP_A-1793836	A	A	244	164	266	134	3.89	4.86E-02	rs10743089	11	8744744	p15.4
SNP_A-2295568	G	G	257	141	221	187	9.04	2.60E-03	rs4929912	11	8773271	p15.4
SNP_A-2007586	A	A	229	111	185	141	7.957	4.80E-03	rs6484484	11	8773782	p15.4
SNP_A-2229526	C	C	258	150	212	204	9.816	1.70E-03	rs4929916	11	8781572	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944722	G	G	386	20	363	35	4.718	0.0298	rs4910466	11	9465928	p15.4
SNP_A-1799812	A	A	298	100	262	132	6.708	9.60E-03	rs7928738	11	9578687	p15.4
SNP_A-1816906	G	G	330	90	306	116	4.182	4.08E-02	rs11042440	11	9578990	p15.4
SNP_A-1785642	G	G	326	86	303	111	4.009	0.0453	rs11042441	11	9579253	p15.4
SNP_A-2114893	A	A	265	123	295	93	5.774	1.63E-02	rs10840269	11	9585378	p15.4
SNP_A-2224939	G	G	254	136	280	100	6.629	0.01	rs10770047	11	9587545	p15.4
SNP_A-2254429	T	T	260	128	227	163	6.441	0.0112	rs10840285	11	9646589	p15.4
SNP_A-2141602	A	A	334	4	284	12	5.286	2.15E-02	rs6483649	11	9717303	p15.4
SNP_A-2242016	G	G	290	94	322	62	8.237	4.10E-03	rs7115324	11	9803883	p15.4
SNP_A-2086340	C	C	326	10	287	43	22.976	1.6402E-06	rs12574467	11	9809915	p15.4
SNP_A-1676924	A	A	310	94	346	68	6.027	0.0141	rs7929338	11	9860194	p15.4
SNP_A-2173547	G	G	350	50	329	79	7.09	7.80E-03	rs2896513	11	9984119	p15.4
SNP_A-1662486	A	A	351	53	331	81	6.359	0.0117	rs10500716	11	9988620	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2126682	G	C	236	160	198	190	8.92	0.0028	rs12288355	11	10029425	p15.4
SNP_A-2259179	A	A	264	80	249	109	4.611	3.18E-02	rs11042601	11	10034179	p15.4
SNP_A-2199659	G	A	214	156	196	164	11.024	9.00E-04	rs11042617	11	10065060	p15.4
SNP_A-1936747	G	G	243	153	203	195	8.651	0.0033	rs10734652	11	10106788	p15.4
SNP_A-1725718	A	G	235	161	206	194	9.416	2.20E-03	rs7110312	11	10107422	p15.4
SNP_A-1647414	A	A	390	8	386	26	9.311	0.0023	rs10500719	11	10154151	p15.4
SNP_A-1754314	T	T	393	11	387	25	5.413	0.02	rs10500720	11	10167265	p15.4
SNP_A-2227395	A	A	357	27	322	46	6.412	1.13E-02	rs11042666	11	10183969	p15.4
SNP_A-2143109	T	C	214	190	214	172	5.588	1.81E-02	rs6484147	11	10251679	p15.4
SNP_A-1879716	T	T	236	140	191	181	9.958	1.60E-03	rs11042717	11	10260515	p15.4
SNP_A-1818598	C	C	264	130	231	157	4.694	3.03E-02	rs2923099	11	10325916	p15.4
SNP_A-1721570	A	A	376	28	363	45	4.168	4.12E-02	rs1597450	11	10334402	p15.4
SNP_A-2169257	G	G	296	42	237	59	6.639	0.01	rs11042761	11	10353619	p15.4
SNP_A-2084730	C	C	216	116	185	141	4.774	2.89E-02	rs2198010	11	10360115	p15.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2218434	C	C	408	10	399	21	3.999	4.55E-02	rs7944136	11	10618527	p15.4
SNP_A-2218109	G	G	416	4	409	13	4.819	0.0281	rs10840482	11	10716346	p15.3
SNP_A-2223278	G	G	329	15	352	4	6.942	8.40E-03	rs771373	11	10837650	p15.3
SNP_A-2210240	G	G	367	1	359	9	6.488	0.0109	rs11043025	11	10916849	p15.3
SNP_A-2239349	G	G	388	14	403	3	7.382	0.0066	rs11605707	11	10967600	p15.3
SNP_A-1957489	C	C	335	71	350	48	4.695	3.03E-02	rs1872697	11	10981358	p15.3
SNP_A-1879638	T	T	240	166	211	195	4.194	4.06E-02	rs11043079	11	11072601	p15.3
SNP_A-2279385	A	A	240	132	267	101	5.541	1.86E-02	rs10840586	11	11126384	p15.3
SNP_A-1814241	A	A	271	111	308	90	4.232	3.97E-02	rs11043121	11	11135535	p15.3
SNP_A-1838461	G	G	280	128	297	95	5.066	2.44E-02	rs10831556	11	11227427	p15.3
SNP_A-2186665	C	C	192	176	234	152	5.47	1.93E-02	rs11021731	11	11242881	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2302797	T	T	295	101	253	137	8.619	0.0033	rs10831609	11	11391027	p15.3
SNP_A-2143792	T	T	245	149	211	183	6.017	1.42E-02	rs2200565	11	11397823	p15.3
SNP_A-2034906	A	A	249	133	228	176	6.298	0.0121	rs11021844	11	11398004	p15.3
SNP_A-2312167	C	C	341	43	334	64	3.945	0.047	rs12578026	11	11402336	p15.3
SNP_A-2244265	T	T	361	43	336	72	8.19	4.20E-03	rs7946706	11	11413325	p15.3
SNP_A-2099013	G	G	400	20	385	35	4.378	3.64E-02	rs10741552	11	11496450	p15.3
SNP_A-2198203	T	T	400	18	388	32	4.098	4.29E-02	rs11021900	11	11504813	p15.3
SNP_A-2077278	C	C	339	51	293	67	4.325	3.76E-02	rs9919625	11	11549487	p15.3
SNP_A-1738214	C	C	321	71	337	47	5.188	2.27E-02	rs7117834	11	11741226	p15.3
SNP_A-1915505	T	T	391	23	409	11	4.597	3.20E-02	rs8169	11	11941430	p15.3
SNP_A-2188470	G	G	279	141	306	106	6.129	1.33E-02	rs11022119	11	12007228	p15.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897994	A	A	306	110	274	146	6.809	9.10E-03	rs11022250	11	12191983	p15.3
SNP_A-2043420	C	C	348	52	373	35	4.11	4.26E-02	rs11607178	11	12251185	p15.3
SNP_A-1705797	C	C	385	19	406	6	7.24	7.10E-03	rs10500754	11	12268309	p15.3
SNP_A-1845730	G	A	187	181	214	164	4.131	4.21E-02	rs1493964	11	12331288	p15.3
SNP_A-1935315	A	A	312	64	331	39	6.582	0.0103	rs10734193	11	12354210	p15.3
SNP_A-1795391	C	C	287	129	249	169	8.058	4.50E-03	rs10831809	11	12385952	p15.3
SNP_A-1945482	G	G	310	104	275	143	8.233	4.10E-03	rs10831810	11	12386069	p15.3
SNP_A-2069162	G	G	217	189	251	161	4.666	3.08E-02	rs7925151	11	12525695	p15.3
SNP_A-2147121	C	C	203	177	238	140	7.091	7.70E-03	rs7106819	11	12527022	p15.3
SNP_A-2275134	A	A	366	44	342	66	5.209	2.25E-02	rs4620705	11	12717185	p15.2
SNP_A-1923557	G	G	240	146	207	175	5.035	2.48E-02	rs11022491	11	12734196	p15.2
SNP_A-2232050	G	G	376	10	376	28	8.12	4.40E-03	rs11022545	11	12890259	p15.2
SNP_A-2098878	A	A	325	83	299	109	4.604	3.19E-02	rs12792409	11	12901634	p15.2
SNP_A-2215851	C	C	249	83	230	114	5.421	1.99E-02	rs10734206	11	12911273	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2106777	A	A	375	15	388	6	4.058	4.40E-02	rs10430831	11	13047020	p15.2
SNP_A-2038500	G	G	330	86	354	64	4.064	4.38E-02	rs12420514	11	13616373	p15.2
SNP_A-2171374	C	C	310	64	337	41	6.144	0.0132	rs12786409	11	13625777	p15.2
SNP_A-1899839	T	T	320	66	328	44	4.242	3.94E-02	rs17456699	11	13696409	p15.2
SNP_A-1667952	T	T	275	85	261	115	4.52	3.35E-02	rs723789	11	13728604	p15.3
SNP_A-1924510	T	T	278	140	252	170	4.16	4.14E-02	rs7112044	11	13762588	p15.2
SNP_A-1909649	G	G	323	51	336	20	13.356	3.00E-04	rs310057	11	13767203	p15.2
SNP_A-2107883	T	T	351	29	322	52	7.733	5.40E-03	rs16913463	11	13909980	p15.2
SNP_A-2093078	A	A	334	6	359	1	3.905	4.81E-02	rs11023066	11	14028641	p15.2
SNP_A-2007947	A	T	211	187	212	180	3.979	4.61E-02	rs1406356	11	14034087	p15.2
SNP_A-2308102	A	C	231	175	213	197	6.403	0.0114	rs2697827	11	14047037	p15.2
SNP_A-1929755	A	G	219	173	205	177	7.036	8.00E-03	rs2697828	11	14047498	p15.2
SNP_A-1956682	G	G	334	32	302	48	4.455	3.48E-02	rs2697833	11	14058694	p15.2
SNP_A-1940474	A	A	303	65	275	37	4.461	3.47E-02	rs4756779	11	14181880	p15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1740661	C	C	404	0	410	4	3.923	4.76E-02	rs1375953	11	14566162	p15.2
SNP_A-2007978	T	T	245	127	213	149	3.854	4.96E-02	rs1714345	11	15137499	p15.2
SNP_A-1854208	T	T	401	13	395	27	4.869	2.73E-02	rs894007	11	15838464	p15.2
SNP_A-1925449	T	T	306	40	300	64	5.145	2.33E-02	rs10832576	11	16236880	p15.1
SNP_A-1960351	C	C	218	184	241	153	3.924	4.76E-02	rs10219384	11	16285545	p15.1
SNP_A-1911773	A	A	283	123	313	91	6.29	0.0121	rs297324	11	16345860	p15.1
SNP_A-2112859	G	G	286	112	321	79	7.715	5.50E-03	rs297326	11	16346308	p15.1
SNP_A-1700372	A	A	230	170	268	130	8.228	4.10E-03	rs957476	11	16391872	p15.2
SNP_A-2119580	G	G	238	124	218	162	5.493	1.91E-02	rs7945099	11	16394550	p15.1
SNP_A-2056373	A	A	251	139	217	167	4.986	2.56E-02	rs7932807	11	16394987	p15.1
SNP_A-2049001	T	T	275	119	308	80	9.466	2.10E-03	rs10832606	11	16416136	p15.1
SNP_A-2122478	C	C	262	88	312	52	13.343	3.00E-04	rs11023945	11	16421615	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2289036	A	A	272	110	285	81	4.366	3.67E-02	rs10766384	11	17266685	p15.1
SNP_A-1923750	C	C	407	11	391	25	5.76	1.64E-02	---	11	17314047	p15.1
SNP_A-2205287	G	A	233	187	221	201	5.188	2.27E-02	rs985572	11	17458327	p15.1
SNP_A-2313742	A	A	230	186	261	157	4.404	3.58E-02	rs2190453	11	17489973	p15.1
SNP_A-1915190	A	A	230	180	260	154	3.841	5.00E-02	rs2237962	11	17491233	p15.1
SNP_A-2188320	A	A	223	177	258	150	4.697	3.02E-02	rs3765644	11	17492851	p15.1
SNP_A-1839419	G	G	192	146	239	123	6.276	1.22E-02	rs10766407	11	17493445	p15.1
SNP_A-2122260	C	C	353	65	374	44	4.652	0.031	rs10832820	11	17614464	p15.1
SNP_A-1823960	A	A	320	58	317	37	3.874	4.91E-02	rs7109072	11	17679608	p15.1
SNP_A-2280235	T	C	215	179	224	180	8.002	4.70E-03	rs4150581	11	18313846	p15.1
SNP_A-1816199	A	A	237	149	279	113	8.319	3.90E-03	rs4150615	11	18321604	p15.1
SNP_A-2105240	G	G	253	155	297	119	8.173	0.0043	rs4150622	11	18322286	p15.1
SNP_A-1825477	C	C	243	161	286	118	10.123	0.0015	rs4150673	11	18340025	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2249830	C	C	200	152	223	115	6.096	0.0135	rs4757645	11	18350421	p15.1
SNP_A-2302343	A	A	351	45	379	27	5.45	1.96E-02	rs11024688	11	18478367	p15.1
SNP_A-2154941	G	G	312	50	323	23	9.82	1.70E-03	rs12574333	11	18492791	p15.1
SNP_A-1787707	T	C	215	163	191	187	4.165	4.13E-02	rs7129164	11	18496790	p15.1
SNP_A-2189189	C	C	339	31	363	17	4.771	2.89E-02	rs11024706	11	18518767	p15.1
SNP_A-2194745	G	G	344	44	364	28	4.1	4.29E-02	rs16935575	11	18562214	p15.1
SNP_A-2237778	C	C	366	54	385	35	4.537	0.0332	rs12289223	11	18567433	p15.1
SNP_A-1859551	A	A	336	54	355	35	4.579	3.24E-02	rs6416020	11	18573760	p15.1
SNP_A-2083990	C	C	301	69	344	50	5.151	2.32E-02	rs1983124	11	18574976	p15.1
SNP_A-2080316	G	G	244	86	236	122	5.233	2.22E-02	rs11024782	11	18732907	p15.1
SNP_A-2307424	G	G	232	86	226	124	5.434	1.97E-02	rs7945401	11	19078036	p15.1
SNP_A-2123467	C	C	343	13	348	32	7.284	7.00E-03	rs10766543	11	19310510	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2218068	T	T	281	123	258	160	5.582	1.81E-02	rs2632058	11	19498694	p15.1
SNP_A-2303737	G	G	289	131	259	159	4.341	3.72E-02	rs2702715	11	19498848	p15.1
SNP_A-1885982	A	A	253	107	223	131	4.261	0.039	rs2632061	11	19500940	p15.1
SNP_A-2280219	G	G	343	75	313	105	6.372	1.16E-02	rs2632065	11	19503844	p15.1
SNP_A-2008250	A	A	330	36	309	61	7.112	7.70E-03	rs7117077	11	19510993	p15.1
SNP_A-1901666	G	G	344	54	318	80	6.066	0.0138	rs11025173	11	19519372	p15.1
SNP_A-1875066	A	A	345	57	326	80	4.38	3.64E-02	rs10833130	11	19519751	p15.1
SNP_A-1752565	C	C	367	37	357	57	4.272	3.87E-02	rs10500854	11	19524058	p15.1
SNP_A-1687130	A	A	346	58	332	82	4.282	0.0385	rs717195	11	19530078	p15.1
SNP_A-1823992	A	A	290	38	304	14	11.255	8.00E-04	rs11025290	11	19830995	p15.1
SNP_A-1804100	C	C	244	158	280	126	6.059	0.0138	rs11025319	11	19873721	p15.1
SNP_A-1959075	A	A	217	151	252	124	5.177	0.0229	rs10833189	11	19877869	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2310271	A	A	247	173	282	140	5.79	0.0161	rs2028608	11	19884920	p15.1
SNP_A-2023307	C	C	320	84	294	112	5.096	0.024	rs10732471	11	20077485	p15.1
SNP_A-2243501	T	T	313	75	291	113	8.162	0.0043	rs1470253	11	20078033	p15.1
SNP_A-2141069	C	C	316	68	295	101	6.983	8.20E-03	rs1470251	11	20078168	p15.1
SNP_A-2074706	C	C	214	106	254	82	6.096	0.0135	rs1356986	11	20286291	p15.1
SNP_A-2174456	G	G	327	63	284	96	9.747	0.0018	rs10833309	11	20334621	p15.1
SNP_A-2278020	G	G	328	68	295	99	7.497	6.20E-03	rs11025523	11	20334700	p15.1
SNP_A-2190610	A	A	378	32	381	17	4.426	3.54E-02	rs1992498	11	20528215	p15.1
SNP_A-1883591	T	T	279	121	304	94	4.458	3.47E-02	rs883377	11	20600703	p15.1
SNP_A-2231019	G	G	324	50	358	34	4.322	3.76E-02	rs9630161	11	20706233	p15.1
SNP_A-1925099	C	C	301	65	322	40	6.638	0.01	rs1465604	11	20890541	p15.1
SNP_A-2008346	C	C	407	9	421	1	6.594	1.02E-02	rs2896618	11	20903245	p15.1
SNP_A-1959426	G	G	407	13	393	25	4.03	4.47E-02	rs11025848	11	20959316	p15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2156335	T	T	407	13	389	27	5.288	2.15E-02	rs11025851	11	20960520	p15.1
SNP_A-2061012	C	C	393	11	378	26	6.373	1.16E-02	rs6483744	11	20971146	p15.1
SNP_A-2163647	C	C	200	170	236	146	4.605	3.19E-02	rs11025887	11	21019550	p15.1
SNP_A-2178727	C	C	351	19	373	9	4.049	4.42E-02	rs16907322	11	21021157	p15.1
SNP_A-1924141	A	A	202	170	237	141	5.447	1.96E-02	rs11026038	11	21324106	p15.1
SNP_A-1801109	A	A	397	23	384	38	3.9	4.83E-02	rs4475916	11	21345470	p15.1
SNP_A-2055677	C	C	341	43	325	71	7.079	7.80E-03	rs6483772	11	21459570	p15.1
SNP_A-1873134	G	A	192	152	187	175	3.945	0.047	rs12279250	11	21521655	p15.1
SNP_A-1925743	A	A	212	194	226	156	3.846	0.0499	rs4922950	11	21879703	p14.3
SNP_A-2228278	G	G	209	203	238	174	4.112	4.26E-02	rs7121300	11	21909859	p14.3
SNP_A-2223058	A	C	184	182	209	157	4.002	4.54E-02	rs6483813	11	21910098	p14.3
SNP_A-2274266	G	G	207	203	242	178	4.249	3.93E-02	rs1487837	11	21938258	p14.3
SNP_A-2155885	T	T	261	101	221	129	6.528	0.0106	rs2198999	11	21940023	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1931311	G	G	327	57	297	89	8.451	3.60E-03	rs324217	11	21940654	p14.3
SNP_A-1924781	G	G	293	79	268	116	7.946	4.80E-03	rs170488	11	21955179	p14.3
SNP_A-2157359	A	A	281	109	320	90	3.847	4.98E-02	rs324200	11	21962956	p14.3
SNP_A-2188333	T	T	333	81	292	124	11.704	6.00E-04	rs324196	11	21963604	p14.3
SNP_A-1958431	A	A	350	56	321	79	5.127	0.0235	rs11026371	11	21982348	p14.3
SNP_A-2057239	T	T	340	52	326	76	4.669	3.07E-02	rs1457893	11	22012627	p14.3
SNP_A-1662284	C	C	350	18	336	34	5.203	2.25E-02	rs10500921	11	22031845	p14.3
SNP_A-2090697	G	G	306	38	301	17	7.049	7.90E-03	rs10833705	11	22097747	p14.3
SNP_A-1826397	C	C	272	128	248	158	4.21	0.0402	rs7110597	11	22173379	p14.3
SNP_A-2001808	A	A	402	4	412	0	4.079	4.34E-02	rs7946977	11	22242002	p14.3
SNP_A-1808346	T	T	315	15	313	5	4.786	0.0287	rs10766953	11	22532667	p14.3
SNP_A-1665498	G	G	385	11	410	2	6.703	9.60E-03	rs10500938	11	22608912	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2088702	G	G	265	125	288	98	4.205	4.03E-02	rs2279240	11	22653466	p14.3
SNP_A-2095375	T	T	386	0	403	5	4.76	2.91E-02	rs11026736	11	22673795	p14.3
SNP_A-2194006	C	C	265	125	239	153	4.156	4.15E-02	rs7940885	11	22817601	p14.3
SNP_A-2193651	C	C	274	136	239	159	4.004	4.54E-02	rs4567455	11	22820102	p14.3
SNP_A-2279216	C	C	263	131	234	158	4.21	0.0402	rs4550218	11	22820234	p14.3
SNP_A-2222481	C	C	261	97	256	134	4.614	3.17E-02	rs12224304	11	22961446	p14.3
SNP_A-1818117	G	G	321	77	300	104	4.693	3.03E-02	rs10833904	11	22996587	p14.3
SNP_A-2275219	A	A	283	59	289	85	4.059	4.39E-02	rs876092	11	22999197	p14.3
SNP_A-2146909	G	G	185	175	221	135	8.331	3.90E-03	rs7929379	11	23268770	p14.3
SNP_A-1904937	C	C	307	23	327	11	4.771	2.89E-02	rs12280079	11	23283486	p14.3
SNP_A-2272770	C	C	193	187	223	161	4.085	4.33E-02	rs4400806	11	23329603	p14.3
SNP_A-2228075	C	C	202	176	229	149	3.934	4.73E-02	rs7479790	11	23353703	p14.3
SNP_A-1803640	G	G	196	136	174	170	4.874	2.73E-02	rs10834063	11	23374759	p14.3
SNP_A-1874399	C	C	240	158	205	183	4.459	3.47E-02	rs11027199	11	23377994	p14.3
SNP_A-2044667	G	G	315	57	329	37	4.511	3.37E-02	rs4581445	11	23452158	p14.3
SNP_A-1905388	G	G	312	22	264	42	9.042	2.60E-03	rs1350948	11	23474981	p14.3
SNP_A-2169855	A	A	361	53	333	79	6.246	0.0124	rs1356687	11	23476525	p14.3
SNP_A-2028497	C	C	383	7	393	1	4.609	3.18E-02	rs16911396	11	23476861	p14.3
SNP_A-2306231	C	C	314	90	348	68	4.635	3.13E-02	rs10767078	11	23487641	p14.3
SNP_A-1702275	G	G	336	64	317	89	4.593	3.21E-02	rs10500959	11	23489206	p14.3
SNP_A-2112861	G	G	236	146	246	110	4.359	3.68E-02	rs7925363	11	23540943	p14.3
SNP_A-1863110	C	C	334	42	357	17	11.354	8.00E-04	rs11027388	11	23568839	p14.3
SNP_A-1933238	A	A	294	108	315	81	4.536	0.0332	rs10834254	11	23958869	p14.3
SNP_A-1725138	A	A	276	30	351	19	5.43	1.98E-02	rs10500971	11	23963541	p14.3
SNP_A-1688716	A	A	342	58	369	37	5.623	0.0177	rs10500972	11	23964048	p14.3
SNP_A-1825179	G	G	357	59	381	39	4.843	2.78E-02	rs2955445	11	24075709	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1831310	A	A	325	75	295	101	5.273	2.17E-02	rs2957761	11	24098510	p14.3
SNP_A-1799588	A	A	296	88	258	122	8.091	4.40E-03	rs4922675	11	24098848	p14.3
SNP_A-2008662	G	G	277	75	231	99	6.773	9.30E-03	rs7122633	11	24116149	p14.3
SNP_A-2008663	A	A	290	88	251	117	6.781	9.20E-03	rs9783297	11	24116855	p14.3
SNP_A-1663578	G	G	321	79	300	112	6.236	1.25E-02	rs2947734	11	24124005	p14.3
SNP_A-2190565	A	A	357	51	330	72	4.602	3.19E-02	rs2947745	11	24128608	p14.3
SNP_A-2305329	A	A	360	50	336	78	6.933	8.50E-03	rs2957772	11	24128674	p14.3
SNP_A-2008712	G	G	238	174	213	207	4.168	4.12E-02	rs1509605	11	24533759	p14.3
SNP_A-2058383	A	A	298	66	315	39	7.276	7.00E-03	rs12290484	11	24614130	p14.3
SNP_A-1937238	C	C	295	67	258	86	4.379	3.64E-02	rs2631440	11	24692402	p14.3
SNP_A-1827102	G	G	353	5	378	0	5.315	2.11E-02	rs11028121	11	24695319	p14.3
SNP_A-2045964	C	C	348	4	376	0	4.296	3.82E-02	rs10742066	11	25019813	p14.3
SNP_A-1814158	A	A	309	85	264	108	5.648	1.75E-02	rs11028423	11	25076996	p14.3
SNP_A-2082099	G	G	306	58	293	83	4.521	3.35E-02	rs11028424	11	25077110	p14.3
SNP_A-1728237	A	A	313	81	303	109	3.889	4.86E-02	rs1900210	11	25086400	p14.3
SNP_A-2153715	A	A	253	91	221	119	5.87	0.0154	rs11028433	11	25090644	p14.3
SNP_A-2254119	C	C	328	48	329	29	4.251	3.92E-02	rs12292554	11	25694448	p14.3
SNP_A-1857236	T	T	300	100	327	67	7.639	5.70E-03	rs11028875	11	25706021	p14.3
SNP_A-1913347	G	G	302	106	335	75	7.014	8.10E-03	rs7925370	11	25707654	p14.3
SNP_A-1781423	G	G	302	102	329	73	5.956	0.0147	rs11028885	11	25714362	p14.3
SNP_A-1922318	A	A	313	101	345	73	6.043	0.014	rs10834774	11	25715397	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1646988	T	T	336	64	370	40	7.053	7.90E-03	rs10501022	11	25720130	p14.3
SNP_A-1850526	T	T	313	101	343	71	6.605	1.02E-02	rs7126987	11	25727785	p14.3
SNP_A-2142432	C	C	304	94	341	69	5.78	1.62E-02	rs7112727	11	25727828	p14.3
SNP_A-2154028	T	T	294	92	321	63	6.606	1.02E-02	rs11028909	11	25729021	p14.3
SNP_A-2098524	C	C	311	97	343	63	8.786	3.00E-03	rs12281442	11	25733667	p14.3
SNP_A-1817399	G	A	211	191	233	181	6.281	1.22E-02	rs16914584	11	25743428	p14.3
SNP_A-2221701	A	G	213	197	228	178	5.375	2.04E-02	rs10834801	11	25757624	p14.3
SNP_A-1952600	C	C	367	31	388	18	3.954	4.68E-02	rs1018022	11	25763400	p14.3
SNP_A-1740489	A	G	211	187	223	187	4.431	3.53E-02	rs1038931	11	25763962	p14.3
SNP_A-2008893	G	A	200	172	192	164	4.31	3.79E-02	rs1441483	11	25906381	p14.3
SNP_A-2065677	A	A	353	21	371	9	5.2	2.26E-02	rs10767485	11	25983851	p14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932754	C	C	330	24	309	43	6.073	0.0137	rs11029100	11	26004028	p14.2
SNP_A-2071639	G	G	348	36	326	56	5.081	2.45E-02	rs10767500	11	26005345	p14.2
SNP_A-1918568	G	G	372	38	358	60	5.13	0.0235	rs2035733	11	26006071	p14.2
SNP_A-1822859	A	A	357	35	329	51	3.934	4.73E-02	rs2171733	11	26010181	p14.2
SNP_A-1958018	A	A	345	39	321	63	6.512	1.07E-02	rs2349794	11	26010440	p14.2
SNP_A-1852687	A	A	360	46	348	70	4.995	2.54E-02	rs10767501	11	26010685	p14.2
SNP_A-2008910	A	A	363	39	346	60	4.842	2.78E-02	rs10501035	11	26017220	p14.2
SNP_A-1647462	G	G	346	32	337	53	5.121	2.36E-02	rs725853	11	26020924	p14.3
SNP_A-1709693	C	C	343	23	329	41	5.333	2.09E-02	rs725854	11	26021109	p14.3
SNP_A-2300683	G	G	366	30	351	53	6.608	1.02E-02	rs12785755	11	26026637	p14.2
SNP_A-2099712	C	C	356	22	329	41	6.71	9.60E-03	rs1994549	11	26040028	p14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2029025	A	A	337	1	287	7	5.47	1.93E-02	rs4923382	11	26696283	p14.2
SNP_A-2112226	G	G	362	26	374	12	5.348	0.0207	rs1545436	11	26767252	p14.2
SNP_A-1922709	G	G	313	79	315	51	5.151	2.32E-02	rs12363428	11	26799868	p14.2
SNP_A-2171613	C	C	223	143	268	118	5.991	0.0144	rs6484252	11	26852481	p14.2
SNP_A-2048246	G	G	378	12	376	4	3.876	4.90E-02	rs11029807	11	27031998	p14.2
SNP_A-2222009	A	A	279	137	313	105	6.179	0.0129	---	11	27152444	p14.2
SNP_A-2297564	G	G	250	78	291	57	5.787	0.0161	rs12419077	11	27165478	p14.2
SNP_A-2009040	C	C	380	20	391	9	4.329	3.75E-02	rs1442929	11	27191140	p14.2
SNP_A-2300936	C	C	343	63	369	41	5.584	1.81E-02	rs11030179	11	27973196	p14.1
SNP_A-2292540	T	T	303	49	319	29	5.517	1.88E-02	rs1525716	11	27977975	p14.1
SNP_A-1689114	G	G	330	68	362	50	3.985	4.59E-02	rs10501094	11	28065355	p14.1
SNP_A-1947958	G	G	340	66	362	46	4.256	3.91E-02	rs12280725	11	28095800	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2009127	C	C	298	46	302	26	5.204	2.25E-02	rs17244331	11	28105653	p14.1
SNP_A-1866949	C	C	347	69	368	48	4.386	3.62E-02	rs4300381	11	28269673	p14.1
SNP_A-1785636	A	A	372	2	328	10	6.295	0.0121	rs11030361	11	28499775	p14.1
SNP_A-1887365	T	T	169	159	183	123	4.394	0.0361	rs10767779	11	28990783	p14.1
SNP_A-1947705	G	G	304	96	270	128	6.58	0.0103	rs2055014	11	29152308	p14.1
SNP_A-1665386	G	G	345	39	337	63	5.417	1.99E-02	rs10501114	11	29180823	p14.1
SNP_A-2042274	C	C	338	42	363	27	4.023	4.49E-02	rs11030696	11	29390033	p14.1
SNP_A-2009274	C	C	294	86	326	60	6.235	1.25E-02	rs637678	11	30051390	p14.1
SNP_A-1667666	A	A	393	7	411	1	4.727	2.97E-02	rs4506622	11	30155398	p14.1
SNP_A-2195756	C	C	237	137	207	167	4.988	2.55E-02	rs601681	11	30190970	p14.1
SNP_A-2040371	C	C	237	167	211	201	4.572	3.25E-02	rs639403	11	30208201	p14.1
SNP_A-1855291	C	C	229	163	199	189	4.003	4.54E-02	rs6169	11	30211761	p14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2091792	C	-	223	157	169	169	5.442	1.97E-02	rs506306	11	30212443	p14.1
SNP_A-2258101	A	A	305	29	314	10	9.237	2.40E-03	rs292438	11	30696262	p14.1
SNP_A-2009379	G	G	264	62	274	42	3.877	4.89E-02	rs610865	11	30720172	p14.1
SNP_A-2025860	C	C	365	19	353	33	3.965	0.0465	rs11031630	11	32153509	p13
SNP_A-2166900	T	T	363	23	379	11	4.56	0.0327	rs9300013	11	32461118	p13
SNP_A-1945347	A	A	389	21	378	36	4.086	4.32E-02	rs17749003	11	32463509	p13
SNP_A-2162433	T	C	204	188	225	169	6.594	1.02E-02	rs10734411	11	32498360	p13
SNP_A-1849327	A	A	246	94	270	62	7.586	5.90E-03	rs7104455	11	33193166	p13
SNP_A-2142682	A	A	224	116	183	131	4.014	4.51E-02	rs11032230	11	33319442	p13
SNP_A-2182849	A	A	383	29	389	15	4.423	3.55E-02	rs11032254	11	33369699	p13
SNP_A-1934067	C	C	300	30	324	16	5.036	2.48E-02	rs4755770	11	33600980	p13
SNP_A-2301446	C	C	358	4	390	0	4.332	3.74E-02	rs12286699	11	33871577	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1905252	G	A	203	143	151	147	5.631	1.76E-02	rs7120707	11	33974532	p13
SNP_A-1839830	C	C	279	53	278	78	3.94	4.71E-02	rs3864880	11	34027509	p13
SNP_A-2075882	C	C	359	35	368	20	4.157	4.15E-02	rs11824839	11	34288896	p13
SNP_A-2240973	C	C	363	37	382	18	7.048	7.90E-03	rs16925419	11	34292263	p13
SNP_A-1801948	A	A	312	24	313	11	4.614	3.17E-02	rs17350806	11	34360958	p13
SNP_A-2080003	G	G	302	82	324	60	4.182	4.09E-02	rs7928060	11	34377506	p13
SNP_A-2072993	C	C	355	45	384	28	4.921	2.65E-02	rs7111765	11	34404069	p13
SNP_A-2135870	T	T	335	71	359	51	4.089	4.32E-02	rs7944397	11	34411885	p13
SNP_A-1756395	G	G	288	82	326	62	4.705	3.01E-02	rs769218	11	34434988	p13
SNP_A-2238106	G	G	312	102	333	69	6.877	8.70E-03	rs10836244	11	34437671	p13
SNP_A-2001886	C	C	359	39	376	24	3.96	4.66E-02	rs2274044	11	34460369	p13
SNP_A-2245214	G	G	349	41	351	23	4.735	2.96E-02	rs7949702	11	34488501	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2009686	T	C	206	172	202	174	5.096	0.024	rs3847601	11	34497225	p13
SNP_A-1719125	G	G	205	191	247	165	5.487	1.92E-02	rs836124	11	34526556	p13
SNP_A-2212224	A	A	351	63	378	40	6.117	0.0134	rs836104	11	34530393	p13
SNP_A-2310588	G	G	314	42	300	62	4.116	4.25E-02	rs891550	11	34848306	p13
SNP_A-2009781	C	C	396	0	385	5	5.109	2.38E-02	rs634096	11	35087935	p13
SNP_A-1688400	C	C	265	95	300	76	3.933	4.73E-02	rs2785175	11	35111807	p13
SNP_A-1689026	G	G	398	2	399	13	7.892	5.00E-03	rs10488808	11	35117680	p13
SNP_A-2009785	T	T	221	123	245	97	4.303	3.80E-02	rs2553809	11	35120062	p13
SNP_A-2009786	C	C	262	74	212	90	5.038	2.48E-02	rs353623	11	35128698	p13
SNP_A-2009791	T	T	373	9	364	24	6.882	8.70E-03	rs10488809	11	35152987	p13
SNP_A-1817109	C	C	378	12	364	32	9.31	0.0023	rs11033018	11	35158106	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2205809	A	A	391	23	374	42	5.927	0.0149	rs11033019	11	35158386	p13
SNP_A-1745400	C	C	314	82	346	60	4.836	2.79E-02	rs1467558	11	35193982	p13
SNP_A-2260006	G	G	260	86	289	59	6.554	1.05E-02	rs7105037	11	35215767	p13
SNP_A-1696342	G	A	215	165	194	190	3.865	4.93E-02	rs10488812	11	35225683	p13
SNP_A-1933934	C	C	224	112	239	77	6.36	0.0117	rs11033052	11	35266714	p13
SNP_A-2283973	G	G	243	81	267	39	15.328	9.04E-05	rs7107752	11	35344765	p13
SNP_A-1841482	G	G	287	129	331	87	11.295	8.00E-04	rs10836380	11	35344815	p13
SNP_A-1660023	C	C	233	161	264	136	3.993	4.57E-02	rs3945930	11	35392727	p13
SNP_A-2009828	A	A	289	125	254	158	6.099	0.0135	rs6484787	11	35446467	p13
SNP_A-1814680	T	T	355	55	326	86	8.046	4.60E-03	rs16927726	11	35545178	p13
SNP_A-1782684	C	C	360	56	328	84	7.069	7.80E-03	rs11033193	11	35559950	p13
SNP_A-2060017	G	G	369	47	353	67	3.844	0.0499	rs657607	11	35569007	p13
SNP_A-2043805	C	C	243	79	243	113	4.327	3.75E-02	rs10836438	11	35673615	p13
SNP_A-1749595	C	C	373	7	381	1	4.58	3.24E-02	rs963811	11	35673810	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1882280	A	A	360	52	336	72	4.034	4.46E-02	rs7126124	11	35718630	p13
SNP_A-2225436	A	A	251	65	292	50	4.031	4.47E-02	rs16928390	11	36070733	p13
SNP_A-1818422	C	C	382	22	410	10	5.181	2.28E-02	rs11033432	11	36087351	p13
SNP_A-2160355	G	G	402	10	418	2	5.569	0.0183	rs10001715	11	36087548	p13
SNP_A-2158061	A	G	217	197	248	168	12.077	5.00E-04	rs4755436	11	36093488	p13
SNP_A-2136624	C	T	222	170	214	174	10.84	0.001	rs7124975	11	36098490	p13
SNP_A-1683948	C	C	241	139	284	114	5.579	1.82E-02	rs10501144	11	36104243	p13
SNP_A-2224050	T	T	290	124	241	159	8.612	0.0033	rs1880709	11	36132717	p13
SNP_A-1948745	G	G	377	35	399	19	5.321	2.11E-02	rs4485080	11	36197525	p13
SNP_A-2127169	C	C	292	26	314	14	4.245	3.94E-02	rs11606476	11	36225197	p13
SNP_A-1832990	C	C	365	23	373	11	4.301	3.81E-02	rs9971578	11	36626558	p12
SNP_A-2305546	G	G	348	46	352	28	4.149	4.17E-02	rs4756340	11	36706835	p12
SNP_A-2052439	G	G	316	48	316	28	4.702	3.01E-02	rs2618296	11	37916220	p12
SNP_A-2184112	G	G	395	19	396	8	4.361	3.68E-02	rs1480053	11	38126765	p12
SNP_A-1844250	T	T	388	4	410	0	4.205	4.03E-02	rs2061640	11	38164702	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2039108	T	C	220	196	223	189	4.07	0.0436	rs11034711	11	38389637	p12
SNP_A-1688120	C	C	244	144	279	121	4.157	4.15E-02	rs10501198	11	38397554	p12
SNP_A-2010110	A	G	209	183	216	186	3.943	4.71E-02	rs1369323	11	38410997	p12
SNP_A-2067666	T	T	257	159	276	128	3.851	4.97E-02	rs7123042	11	38414672	p12
SNP_A-2089240	A	A	376	0	374	4	4	4.55E-02	rs16931787	11	38416375	p12
SNP_A-1908555	T	T	233	183	263	151	4.876	2.72E-02	rs11034845	11	38532459	p12
SNP_A-2123609	A	A	364	16	384	6	4.951	2.61E-02	rs10837012	11	38544846	p12
SNP_A-2010118	G	G	202	154	232	120	6.27	0.0123	rs10501201	11	38545355	p12
SNP_A-2010120	A	A	196	192	221	157	4.879	2.72E-02	rs10501203	11	38592016	p12
SNP_A-2046143	C	C	318	0	328	4	3.855	4.96E-02	rs6485030	11	38804228	p12
SNP_A-2234230	G	G	374	0	269	3	4.144	4.18E-02	rs10837148	11	39334824	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102400	A	A	343	11	353	3	4.71	3.00E-02	rs2089474	11	39732415	p12
SNP_A-1926949	T	T	307	11	289	23	4.722	0.0298	rs7930034	11	39946041	p12
SNP_A-2263498	T	T	291	65	271	89	4.43	3.53E-02	rs7120250	11	39948975	p12
SNP_A-2010275	A	A	360	22	376	10	4.198	4.05E-02	rs10501227	11	40262733	p12
SNP_A-2010276	T	T	301	115	333	83	6.787	9.20E-03	rs11035770	11	40275193	p12
SNP_A-1677962	T	T	270	128	315	97	7.493	6.20E-03	rs10501229	11	40321385	p12
SNP_A-1696336	T	T	269	129	309	103	5.442	1.97E-02	rs10501230	11	40321562	p12
SNP_A-2290260	T	T	233	99	201	121	4.408	3.58E-02	rs11035793	11	40326133	p12
SNP_A-2010315	T	T	339	39	351	19	7.02	8.10E-03	rs17486333	11	40512516	p12
SNP_A-2036807	G	C	215	173	191	177	4.048	4.42E-02	rs1390174	11	40595488	p12
SNP_A-1869355	A	A	339	47	350	26	6.087	1.36E-02	rs11036183	11	40978427	p12
SNP_A-2298567	G	G	301	83	277	113	5.542	1.86E-02	rs11036588	11	41805969	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1898293	G	G	259	121	220	144	4.83	2.80E-02	rs7131352	11	41830273	p12
SNP_A-1892296	G	G	328	82	296	108	5.155	2.32E-02	rs11036615	11	41850181	p12
SNP_A-1861094	A	A	268	76	266	42	7.84	5.10E-03	rs10837782	11	42128259	p12
SNP_A-2113797	A	C	160	158	203	149	4.287	3.84E-02	rs1508539	11	42332477	p12
SNP_A-1857243	G	G	205	169	239	145	4.307	3.80E-02	rs1462679	11	42383802	p12
SNP_A-2010573	T	T	318	42	281	57	3.869	4.92E-02	rs16936599	11	42391421	p12
SNP_A-2190490	G	G	252	96	224	120	4.291	3.83E-02	rs7943268	11	42512718	p12
SNP_A-2065788	G	G	311	57	282	76	3.996	4.56E-02	rs4391803	11	42656036	p12
SNP_A-2068412	G	G	288	72	246	88	3.935	4.73E-02	rs11825624	11	42702110	p12
SNP_A-2216713	T	T	319	77	289	105	5.783	1.62E-02	rs11037041	11	42707878	p12
SNP_A-2038407	G	G	331	85	301	115	5.924	0.0149	rs7102839	11	42708552	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1690685	A	A	263	119	298	98	3.965	4.64E-02	rs4132365	11	42831886	p12
SNP_A-2162944	A	A	336	58	356	38	4.745	2.94E-02	rs2114089	11	43153254	p12
SNP_A-1930422	T	T	312	30	316	14	5.631	1.76E-02	rs1318986	11	43169005	p12
SNP_A-1675952	C	C	364	2	354	12	7.282	7.00E-03	rs10501303	11	43658325	p11.2
SNP_A-2010642	G	G	227	165	263	137	5.161	2.31E-02	rs4620711	11	43670419	p11.2
SNP_A-2166435	C	C	325	83	347	55	6.357	0.0117	rs11037732	11	43885434	p11.2
SNP_A-1811071	G	G	403	13	416	4	4.952	2.61E-02	rs7947302	11	43949704	p11.2
SNP_A-2089223	C	C	331	69	360	48	4.908	2.67E-02	rs6485492	11	44010073	p11.2
SNP_A-1922367	G	G	412	0	414	4	3.962	0.0465	rs12224245	11	44027846	p11.2
SNP_A-1821502	A	A	299	61	288	36	4.768	2.90E-02	rs16937817	11	44050194	p11.2
SNP_A-2034967	T	T	363	37	386	22	4.441	3.51E-02	rs7109109	11	44203075	p11.2
SNP_A-1842119	G	G	295	61	318	40	5.224	0.0223	rs12288455	11	44249323	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187026	C	C	205	131	186	164	4.331	3.74E-02	rs4755815	11	44324957	p11.2
SNP_A-2280377	A	A	231	131	201	155	4.047	4.42E-02	rs2863089	11	44326610	p11.2
SNP_A-2184599	A	A	383	7	403	1	4.764	2.91E-02	rs4755885	11	44725608	p11.2
SNP_A-1845884	T	T	384	28	397	11	7.607	5.80E-03	rs16938081	11	44750019	p11.2
SNP_A-2082305	G	A	198	174	205	173	4.173	4.11E-02	rs11038440	11	45375689	p11.2
SNP_A-2079250	C	C	378	2	362	10	5.595	1.80E-02	rs11038633	11	45726237	p11.2
SNP_A-1733614	A	A	379	19	396	6	7.113	7.70E-03	rs2029483	11	46144163	p11.2
SNP_A-2188620	G	G	325	35	361	19	6.094	1.36E-02	rs12574668	11	46379262	p11.2
SNP_A-1789601	C	C	249	139	274	108	5.039	2.48E-02	rs4752856	11	47604618	p11.2
SNP_A-2234941	C	C	263	75	248	102	4.351	3.70E-02	rs2904315	11	48066524	p11.2
SNP_A-1807260	C	C	392	16	371	29	4.255	3.91E-02	rs7106202	11	48082307	p11.2
SNP_A-2167347	C	C	325	5	350	24	10.666	1.10E-03	rs17789571	11	48099464	p11.2
SNP_A-2102161	A	A	227	165	197	191	4.001	4.55E-02	rs1566732	11	48108070	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2286118	G	G	312	44	334	28	4.255	3.91E-02	rs10839387	11	49797292	p11.12
SNP_A-2084440	G	G	362	14	372	28	4.065	4.38E-02	rs1818894	11	49992129	p11.12
SNP_A-2048701	A	A	319	23	338	8	7.785	0.0053	rs4079913	11	50256441	p11.12
SNP_A-1808646	A	A	290	68	217	77	4.834	2.79E-02	rs10901970	11	50476835	p11.12
SNP_A-2139755	C	C	360	16	378	34	5.285	2.15E-02	rs10902344	11	51273731	p11.12
SNP_A-2258536	T	T	362	10	362	22	4.311	3.79E-02	rs924304	11	51287253	p11.12
SNP_A-2260264	T	T	340	2	328	10	5.526	1.87E-02	rs1216227	11	54924285	q11
SNP_A-2168418	T	T	335	69	368	44	7.002	8.10E-03	rs438025	11	55279960	q11
SNP_A-1902304	C	C	333	77	356	50	6.488	0.0109	rs7102394	11	55351657	q11
SNP_A-2192757	G	G	319	7	326	18	4.436	3.52E-02	rs10897379	11	55394688	q11
SNP_A-2011103	A	A	322	32	293	47	3.935	4.73E-02	rs10501340	11	55439371	q11
SNP_A-1840321	G	G	308	80	331	57	4.689	0.0304	rs17513710	11	55471771	q11
SNP_A-1948860	G	G	412	4	420	0	4.058	4.40E-02	rs11227538	11	55736854	q11
SNP_A-1909331	G	G	355	9	364	22	4.923	2.65E-02	rs7114870	11	56055687	q11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2087681	C	C	338	68	343	43	5.166	0.023	rs10896469	11	56066044	q11
SNP_A-2110663	T	T	283	85	305	63	4.093	4.31E-02	rs1397053	11	56267270	q11
SNP_A-2206577	G	G	304	52	285	81	6.799	9.10E-03	rs7942208	11	56382727	q11
SNP_A-1817599	G	G	235	149	267	121	4.923	2.65E-02	rs1938746	11	56400162	q11
SNP_A-2275718	A	A	354	60	321	85	5.846	1.56E-02	rs4939097	11	56409281	q11
SNP_A-2150560	A	A	316	72	290	94	4.011	4.52E-02	rs1792500	11	56416314	q11
SNP_A-2292252	C	C	415	1	413	7	4.486	3.42E-02	rs2510549	11	58064917	q12.1
SNP_A-2296679	C	C	415	1	413	7	4.486	3.42E-02	rs2509929	11	58163649	q12.1
SNP_A-2226652	A	A	314	72	288	102	6.275	1.22E-02	rs1938698	11	58236251	q12.1
SNP_A-1819665	T	T	327	85	305	113	4.682	3.05E-02	rs7397018	11	58249968	q12.1
SNP_A-2034429	A	A	314	90	291	115	3.918	4.78E-02	rs1938711	11	58290635	q12.1
SNP_A-2011303	C	C	294	80	260	102	4.552	3.29E-02	rs1943280	11	58368275	q12.1
SNP_A-2011309	G	G	382	2	393	9	4.201	4.04E-02	rs2856259	11	58376529	q12.1
SNP_A-2268725	G	G	315	61	288	82	4.245	3.94E-02	rs679625	11	58404807	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802104	C	C	401	13	392	26	4.416	0.0356	rs7116544	11	58411359	q12.1
SNP_A-1946817	G	G	361	47	368	28	4.702	3.01E-02	rs4938914	11	58779244	q12.1
SNP_A-2222846	C	C	303	47	326	30	4.544	3.30E-02	rs11230061	11	59248249	q12.1
SNP_A-1788564	A	A	359	5	338	14	4.696	3.02E-02	rs17154200	11	59324766	q12.1
SNP_A-1658828	A	A	367	17	368	34	5.259	0.0218	rs481560	11	59541100	q12.1
SNP_A-1959016	A	A	374	4	386	0	4.106	4.27E-02	rs1426252	11	59740362	q12.1
SNP_A-1787968	A	A	230	104	235	75	3.863	4.94E-02	rs10792267	11	59858294	q12.2
SNP_A-2011420	G	G	245	123	282	92	7.019	8.10E-03	rs950802	11	59909160	q12.2
SNP_A-2231169	G	G	402	4	387	13	5.005	0.0253	rs17615103	11	59994981	q12.2
SNP_A-2198511	C	C	345	65	374	44	5.139	2.34E-02	rs4939391	11	60046799	q12.2
SNP_A-2090185	T	T	315	55	349	35	5.928	0.0149	rs7948015	11	60075765	q12.2
SNP_A-2085848	A	A	348	58	351	33	6.273	0.0123	rs10792285	11	60090142	q12.2
SNP_A-1722734	C	C	354	20	332	48	12.188	5.00E-04	rs1080719	11	60198251	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2212159	C	C	356	38	324	58	5.488	1.91E-02	rs3016175	11	60586943	q12.2
SNP_A-2222644	A	A	212	184	233	145	5.198	2.26E-02	rs175126	11	60590200	q12.2
SNP_A-2157518	T	T	354	20	311	37	6.923	8.50E-03	rs11601370	11	60590619	q12.2
SNP_A-1837647	A	T	222	184	216	196	4.133	4.20E-02	rs675625	11	60671449	q12.2
SNP_A-1856207	T	T	314	0	309	5	5.04	2.48E-02	---	11	60977541	q12.2
SNP_A-1790027	G	G	361	23	393	11	5.089	0.0241	rs2908206	11	61043268	q12.2
SNP_A-2234693	C	C	380	30	403	13	7.353	6.70E-03	rs7943167	11	61044933	q12.2
SNP_A-1859001	T	T	385	27	405	9	9.502	2.10E-03	rs3862736	11	61047653	q12.2
SNP_A-2097352	T	C	216	172	208	186	5.604	1.79E-02	rs198464	11	61278197	q12.2
SNP_A-2204695	T	T	370	20	390	8	5.589	1.81E-02	rs2845573	11	61358484	q12.2
SNP_A-1901243	C	C	327	85	305	115	5.189	2.27E-02	rs2089925	11	61537939	q12.3
SNP_A-2248239	G	G	276	46	256	66	4.323	3.76E-02	rs6591687	11	61539224	q12.3
SNP_A-1958000	A	A	306	108	277	135	4.438	3.52E-02	rs11230882	11	61557388	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2011509	C	C	198	106	238	86	5.121	2.36E-02	rs429416	11	61586505	q12.3
SNP_A-2030806	C	C	306	42	281	63	5.242	2.21E-02	rs7114650	11	61602562	q12.3
SNP_A-2116745	C	C	369	47	395	19	12.759	4.00E-04	rs1675126	11	61662950	q12.3
SNP_A-1795709	A	A	339	71	299	113	12.09	5.00E-04	rs3781969	11	61670187	q12.3
SNP_A-1867231	C	C	251	89	245	57	4.854	0.0276	rs954237	11	61821291	q12.3
SNP_A-2247650	C	C	210	188	249	161	5.225	0.0223	rs11231027	11	61836618	q12.3
SNP_A-1913302	G	G	228	156	207	189	3.987	4.59E-02	rs2513039	11	61837268	q12.3
SNP_A-2228817	C	C	302	98	281	127	4.415	0.0356	rs12282256	11	61837433	q12.3
SNP_A-2185031	T	T	242	118	208	152	6.85	8.90E-03	rs2463833	11	61840484	q12.3
SNP_A-1784038	A	A	315	99	284	122	3.92	4.77E-02	rs11231029	11	61840579	q12.3
SNP_A-2309704	C	C	218	194	252	168	4.25	3.92E-02	rs10897253	11	61842649	q12.3
SNP_A-2188817	G	G	195	169	230	142	5.14	2.34E-02	rs11605459	11	61845323	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1756028	T	T	212	188	248	162	4.626	0.0315	rs953169	11	61858902	q12.3
SNP_A-2134827	A	A	259	79	263	115	4.49	3.41E-02	rs2958532	11	61915500	q12.3
SNP_A-1858446	T	T	255	131	223	157	4.443	3.50E-02	rs1193856	11	62770983	q12.3
SNP_A-1938157	C	C	247	161	219	189	3.922	4.76E-02	rs1404608	11	62835562	q12.3
SNP_A-2311635	C	C	389	21	401	7	7.177	7.40E-03	rs11231693	11	63619188	q13.1
SNP_A-2141608	T	T	216	152	182	176	4.524	3.34E-02	rs547484	11	63993697	q13.1
SNP_A-1682342	C	C	335	21	351	39	4.232	3.97E-02	rs1195963	11	64717230	q13.1
SNP_A-2270108	T	T	324	6	334	16	4.113	4.26E-02	rs12226602	11	65369924	q13.1
SNP_A-1793920	G	G	319	85	335	61	4.257	3.91E-02	rs3825067	11	65634995	q13.2
SNP_A-1794733	C	C	306	70	314	46	4.723	0.0298	rs918299	11	65684183	q13.2
SNP_A-2249572	A	A	313	83	324	54	5.913	1.50E-02	rs10791855	11	65720313	q13.2
SNP_A-1797549	C	T	213	161	193	189	4.241	0.0395	rs7107498	11	66476057	q13.2
SNP_A-1887896	G	G	401	5	406	0	5.031	2.49E-02	rs672432	11	67033045	q13.2
SNP_A-2096061	C	C	366	18	388	8	4.304	3.80E-02	rs2447587	11	67168406	q13.2
SNP_A-1866287	G	G	359	13	356	32	7.701	5.50E-03	rs11228033	11	67383143	q13.2
SNP_A-2042083	T	T	387	7	393	1	4.546	3.30E-02	rs11228066	11	67431419	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2011794	C	C	233	161	204	196	5.311	0.0212	rs308351	11	67488532	q13.2
SNP_A-2011805	A	C	171	167	207	147	5.723	0.0167	rs4988300	11	67845407	q13.2
SNP_A-1950649	A	A	174	134	212	116	4.412	3.57E-02	rs638076	11	67959156	q13.2
SNP_A-1815297	A	A	368	18	372	6	5.939	1.48E-02	rs3019576	11	68304836	q13.3
SNP_A-1800197	T	T	218	118	259	99	4.495	3.40E-02	rs513359	11	68426072	q13.3
SNP_A-1911521	C	C	255	139	232	180	5.957	0.0147	rs594051	11	68426263	q13.3
SNP_A-2280874	C	C	328	88	302	118	5.423	1.99E-02	rs4244842	11	68488253	q13.3
SNP_A-2212122	T	T	181	119	243	115	4.053	0.0441	rs66066675	11	68939423	q13.3
SNP_A-1899547	C	C	342	50	371	33	4.482	3.43E-02	rs4980635	11	68976688	q13.3
SNP_A-2202384	A	A	268	136	240	174	6.08	0.0137	rs7113550	11	68978949	q13.3
SNP_A-2305571	T	T	387	1	373	7	4.675	3.06E-02	rs11263468	11	69026118	q13.3
SNP_A-2172095	C	C	394	14	381	33	7.856	5.10E-03	rs2450252	11	69143453	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1661564	C	C	384	16	375	35	7.063	7.90E-03	rs633485	11	69193923	q13.3
SNP_A-2122104	C	C	344	72	316	102	6.356	0.0117	rs17323291	11	69515299	q13.3
SNP_A-1905147	T	T	316	22	280	34	3.868	4.92E-02	rs1994773	11	69515923	q13.3
SNP_A-2061853	G	G	360	34	384	20	4.279	3.86E-02	rs902870	11	69516034	q13.3
SNP_A-2177062	A	A	299	81	264	124	11.113	9.00E-04	rs4980714	11	69523168	q13.3
SNP_A-1876237	C	C	282	88	252	118	6.054	1.39E-02	rs4980715	11	69523333	q13.3
SNP_A-1953737	C	C	266	142	232	174	5.557	0.0184	rs2515267	11	69653841	q13.3
SNP_A-2114971	C	T	202	198	230	160	7.14	7.50E-03	rs25091172	11	69654072	q13.3
SNP_A-2106138	A	A	321	37	301	63	7.354	6.70E-03	rs10793024	11	69694065	q13.3
SNP_A-2093690	T	T	297	55	316	36	4.556	3.28E-02	rs570739	11	69818074	q13.3
SNP_A-2273731	T	T	261	101	241	133	4.979	2.57E-02	rs7117443	11	69857933	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1868005	A	A	299	41	310	68	4.889	0.027	rs11235967	11	69869339	q13.3
SNP_A-2217783	A	A	213	203	253	165	7.353	6.70E-03	rs682670	11	69985448	q13.3
SNP_A-1893862	T	T	287	41	320	26	4.675	3.06E-02	rs2015997	11	70341866	q13.4
SNP_A-1951786	A	A	297	35	337	21	5.051	0.0246	rs3017493	11	70343169	q13.4
SNP_A-2222950	G	G	204	114	188	166	8.406	3.70E-03	rs10897624	11	70519538	q13.4
SNP_A-1940464	T	C	203	157	203	189	5.025	2.50E-02	rs10459038	11	70524609	q13.4
SNP_A-2230015	T	T	243	153	204	182	5.786	1.62E-02	rs4945154	11	70533723	q13.4
SNP_A-1844275	G	G	264	100	272	70	4.733	2.96E-02	rs12271307	11	70549636	q13.4
SNP_A-2041419	C	C	206	152	256	110	12.057	5.00E-04	rs7123288	11	70568692	q13.4
SNP_A-1846336	G	G	227	143	266	118	5.222	0.0223	rs4312085	11	70569712	q13.4
SNP_A-1895245	G	G	229	107	205	139	5.396	2.02E-02	rs11827660	11	70671968	q13.4
SNP_A-2263654	A	A	385	23	393	11	4.298	3.82E-02	rs1792265	11	70827504	q13.4
SNP_A-2268493	G	G	214	104	208	142	4.432	3.53E-02	rs11234249	11	70964468	q13.4
SNP_A-1794508	A	A	366	38	392	22	5.037	2.48E-02	rs1028050	11	71929039	q13.4
SNP_A-1784157	G	G	343	37	346	60	4.612	3.18E-02	rs3781931	11	72004853	q13.4
SNP_A-1818456	T	T	244	56	290	42	4.353	3.69E-02	rs4944831	11	72612376	q13.4

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2177487	C	C	296	76	329	51	6.579	0.0103	rs1625496	11	72614658	q13.4
SNP_A-2165431	T	T	296	98	343	63	10.888	0.001	rs949140	11	72630991	q13.4
SNP_A-1892402	G	G	289	71	333	53	4.825	2.80E-02	rs11235706	11	72657388	q13.4
SNP_A-2304148	A	A	344	62	366	42	4.523	3.34E-02	rs11235712	11	72671847	q13.4
SNP_A-1904221	G	G	339	61	370	44	3.868	4.92E-02	rs10898915	11	72676335	q13.4
SNP_A-2301639	C	C	296	114	264	148	6.236	1.25E-02	rs2734827	11	73393925	q13.4
SNP_A-2012015	T	T	384	0	389	5	4.905	2.68E-02	rs2851712	11	73591597	q13.4
SNP_A-1926383	G	-	241	165	206	206	7.228	7.20E-03	rs612040	11	73815199	q13.4
SNP_A-2012022	C	C	202	126	166	148	4.985	2.56E-02	rs10793085	11	73830656	q13.4
SNP_A-2106764	T	T	359	13	356	4	4.582	3.23E-02	rs3781723	11	74572861	q13.4
SNP_A-1788339	A	A	252	80	291	57	6.289	0.0121	rs640927	11	75022554	q13.5

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2124325	T	T	313	3	312	14	6.965	8.30E-03	rs7101887	11	75679901	q13.5
SNP_A-1936546	A	A	398	0	390	4	4.061	4.39E-02	rs2851158	11	75724913	q13.5
SNP_A-1866479	G	G	328	34	336	18	4.931	0.0264	rs949150	11	75801477	q13.5
SNP_A-2074969	T	T	284	62	257	89	6.175	1.30E-02	rs11236909	11	76116716	q13.5
SNP_A-2173246	C	C	310	50	319	81	5.374	2.04E-02	rs10793194	11	76153377	q13.5
SNP_A-2260575	G	G	385	29	400	16	4.037	4.45E-02	rs11236998	11	76274268	q13.5
SNP_A-2021843	C	C	287	87	297	59	5.1	2.39E-02	rs11237061	11	76425847	q13.5
SNP_A-2226502	A	A	317	97	351	67	7.199	7.30E-03	rs2105803	11	76911659	q13.5
SNP_A-2200137	C	C	371	25	346	42	5.104	2.39E-02	rs4945186	11	76995927	q13.5
SNP_A-1863154	C	C	375	21	356	44	8.612	0.0033	rs1540179	11	77012587	q13.5
SNP_A-2093403	T	T	385	31	367	49	4.481	3.43E-02	—	11	77056153	q13.5
SNP_A-2204809	G	G	374	20	356	34	4.053	0.0441	rs7127803	11	77178384	q13.5
SNP_A-1872400	T	T	335	27	310	42	4.091	4.31E-02	rs7928656	11	77404931	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1924670	G	G	274	90	266	130	6.055	1.39E-02	rs977977	11	77543928	q14.1
SNP_A-2012324	C	C	356	58	375	39	4.215	4.01E-02	rs7935464	11	78494745	q14.1
SNP_A-2002065	G	G	357	59	375	39	4.519	3.35E-02	rs6592826	11	78494989	q14.1
SNP_A-2115177	C	C	338	34	360	20	4.238	0.0395	rs6592828	11	78495146	q14.1
SNP_A-2012336	A	A	273	123	241	149	4.432	3.53E-02	rs597444	11	78661621	q14.1
SNP_A-2046222	T	G	191	137	153	147	5.373	2.05E-02	rs509249	11	78664406	q14.1
SNP_A-2012375	A	A	327	61	370	42	5.443	1.97E-02	rs11237934	11	78983411	q14.1
SNP_A-2083909	T	T	409	7	419	1	4.602	3.19E-02	rs982764	11	79268635	q14.1
SNP_A-2002073	C	C	343	5	363	21	8.663	3.20E-03	rs606557	11	79342725	q14.1
SNP_A-1736571	C	C	317	57	305	97	9.623	0.0019	rs1893814	11	79494359	q14.1
SNP_A-2032669	G	G	342	64	362	44	4.272	3.87E-02	rs688477	11	79541241	q14.1
SNP_A-2076222	T	T	215	149	258	124	5.768	1.63E-02	rs1247726	11	79644830	q14.1
SNP_A-2090922	A	A	373	39	356	58	4.113	4.25E-02	rs7945479	11	79660988	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175847	T	T	398	18	379	33	4.857	0.0275	rs11232063	11	79693058	q14.1
SNP_A-2032172	G	G	243	95	278	70	5.995	0.0143	rs931103	11	79698940	q14.1
SNP_A-2239151	T	C	172	148	187	147	6.203	1.28E-02	rs11232404	11	80335038	q14.1
SNP_A-1754604	C	C	281	109	264	146	5.402	0.0201	rs1909138	11	80351696	q14.1
SNP_A-1663574	C	C	327	21	367	11	4.198	4.05E-02	rs1566241	11	80444563	q14.1
SNP_A-2275759	A	A	345	33	373	19	4.608	3.18E-02	rs7114393	11	80593158	q14.1
SNP_A-2241662	T	T	327	13	331	35	9.163	2.50E-03	rs1947594	11	80672480	q14.1
SNP_A-2099106	C	C	279	91	301	69	3.859	4.95E-02	rs6591959	11	80711817	q14.1
SNP_A-1717243	G	G	362	24	347	43	5.685	1.71E-02	rs1114556	11	81168100	q14.1
SNP_A-2095529	G	G	228	110	271	87	5.821	1.58E-02	rs11232861	11	81170733	q14.1
SNP_A-2156622	G	G	234	142	271	119	4.483	3.42E-02	rs11607556	11	81203885	q14.1
SNP_A-1882256	G	G	395	9	401	1	6.44	0.0112	rs575495	11	81477017	q14.1
SNP_A-2111373	C	C	384	28	406	12	6.97	8.30E-03	rs4944395	11	81873715	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1720857	C	C	373	27	396	14	4.687	0.0304	rs972560	11	81892500	q14.1
SNP_A-2002089	G	G	382	10	383	1	7.283	7.00E-03	rs4274219	11	81895859	q14.1
SNP_A-2099612	C	C	259	61	285	43	4.26	0.039	rs4255559	11	81898826	q14.1
SNP_A-2178688	G	G	374	40	395	23	5.142	2.34E-02	rs4471453	11	81902413	q14.1
SNP_A-1939927	G	G	376	40	395	23	5.051	0.0246	rs4280019	11	81902547	q14.1
SNP_A-1798401	G	C	203	153	173	163	5.025	2.50E-02	rs10792628	11	81955403	q14.1
SNP_A-1833324	C	C	386	26	406	10	7.597	5.80E-03	rs17143894	11	81995875	q14.1
SNP_A-2104867	A	A	352	22	362	10	4.635	3.13E-02	rs1939598	11	81999285	q14.1
SNP_A-2169283	C	C	370	16	395	7	4.016	4.51E-02	rs1790708	11	82009082	q14.1
SNP_A-2120486	T	T	376	22	404	8	7.299	6.90E-03	rs1790707	11	82009746	q14.1
SNP_A-2075290	T	T	266	80	291	51	7.519	6.10E-03	rs11825381	11	82468861	q14.1
SNP_A-2294375	C	C	325	69	355	45	6.331	1.19E-02	rs11233462	11	82491595	q14.1
SNP_A-1886401	C	C	220	166	260	146	4.113	4.26E-02	rs2512674	11	82839423	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209553	T	T	398	0	370	4	4.279	3.86E-02	rs891774	11	82853395	q14.1
SNP_A-1800544	G	G	296	92	328	64	6.646	9.90E-03	rs983590	11	83036277	q14.1
SNP_A-1912350	C	C	298	78	333	59	4.245	3.94E-02	rs7950988	11	83099929	q14.1
SNP_A-1816942	G	G	389	25	373	43	5.096	0.024	rs790364	11	83322720	q14.1
SNP_A-2284326	C	C	399	17	414	6	5.519	1.88E-02	rs4944475	11	83663059	q14.1
SNP_A-2083263	A	A	349	53	325	73	4.009	4.52E-02	rs10898233	11	83790238	q14.1
SNP_A-2066379	T	T	294	82	258	102	4.176	4.10E-02	rs10792758	11	83852697	q14.1
SNP_A-2090843	T	T	345	25	359	13	4.063	4.38E-02	rs17206578	11	84211479	q14.1
SNP_A-1720399	A	A	372	28	356	54	8.473	3.60E-03	rs10501573	11	84255411	q14.1
SNP_A-2026858	C	C	265	33	271	59	5.799	0.016	rs11600301	11	84319811	q14.1
SNP_A-2029333	A	A	231	169	261	137	5.171	0.023	rs670998	11	84379747	q14.1
SNP_A-1785255	T	T	214	184	236	150	4.354	3.69E-02	rs613315	11	84402052	q14.1
SNP_A-2295775	C	C	213	181	250	152	5.402	0.0201	rs592622	11	84402581	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2051638	A	A	232	156	269	129	5.164	2.31E-02	rs527389	11	84412643	q14.1
SNP_A-1644586	C	C	225	161	263	137	4.644	3.12E-02	rs651661	11	84414836	q14.1
SNP_A-2012868	A	A	272	122	291	91	4.969	0.0258	rs7118119	11	84465202	q14.1
SNP_A-2012871	G	G	202	186	231	157	4.394	0.0361	rs560214	11	84478951	q14.1
SNP_A-2115422	C	C	396	0	406	4	3.883	4.88E-02	rs2088018	11	84547916	q14.1
SNP_A-2012881	A	A	326	82	349	61	3.863	4.94E-02	rs10501590	11	84620725	q14.1
SNP_A-2121609	A	A	256	112	233	149	6.068	0.0138	rs450444	11	84749158	q14.1
SNP_A-1911383	C	C	349	19	342	8	4.104	4.28E-02	rs4943923	11	84944441	q14.1
SNP_A-2125991	T	C	218	196	229	185	5.265	0.0218	rs11234429	11	85217265	q14.1
SNP_A-2089471	-	T	191	191	229	151	8.111	4.40E-03	rs11234454	11	85256952	q14.1
SNP_A-2134386	A	G	203	143	191	163	11.18	8.00E-04	rs7107881	11	85320411	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1822377	C	C	292	76	294	50	4.568	3.26E-02	rs7114678	11	85333822	q14.2
SNP_A-1829668	G	G	322	74	352	44	8.962	0.0028	rs11234487	11	85335549	q14.2
SNP_A-1652856	T	T	183	175	239	155	6.936	8.40E-03	rs10501600	11	85335867	q14.2
SNP_A-1828975	T	T	278	72	263	105	6.121	0.0134	—	11	85344736	q14.2
SNP_A-1828445	A	A	329	85	304	116	5.726	0.0167	rs17744938	11	85354214	q14.2
SNP_A-1951610	T	T	384	28	403	15	4.346	3.71E-02	rs17209625	11	85364895	q14.2
SNP_A-1914271	G	G	271	117	307	75	11.384	7.00E-04	rs615887	11	85367689	q14.2
SNP_A-2252365	T	T	203	187	251	147	9.785	0.0018	rs484154	11	85383124	q14.2
SNP_A-1934857	C	C	393	9	404	2	4.587	3.22E-02	—	11	85415613	q14.2
SNP_A-1944914	G	G	326	84	303	109	4.075	4.35E-02	rs17817919	11	85432369	q14.2
SNP_A-1875020	T	C	182	124	175	149	11.484	7.00E-04	rs618001	11	85434010	q14.2
SNP_A-2012947	G	G	223	109	179	165	16.053	6.16E-05	rs597446	11	85452707	q14.2
SNP_A-2012948	G	G	314	56	353	33	7.889	5.00E-03	rs10501608	11	85455489	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287895	A	A	304	108	275	139	5.338	2.09E-02	rs536841	11	85465472	q14.2
SNP_A-2242412	T	T	281	89	247	123	7.642	5.70E-03	rs541458	11	85465999	q14.2
SNP_A-1749555	A	A	275	125	309	101	4.405	3.58E-02	rs1941375	11	85483441	q14.2
SNP_A-1705057	T	T	204	164	271	127	13	3.00E-04	rs638509	11	85511287	q14.2
SNP_A-1816650	C	C	334	30	364	14	6.846	8.90E-03	rs11234551	11	85515732	q14.2
SNP_A-1893645	G	G	287	65	315	47	4.056	4.40E-02	rs7480193	11	85539067	q14.2
SNP_A-2050001	C	C	185	171	223	123	11.236	8.00E-04	rs7113976	11	85547385	q14.2
SNP_A-2068521	C	C	357	3	350	12	5.464	1.94E-02	rs12223670	11	85605081	q14.2
SNP_A-1680600	T	T	389	11	388	24	4.654	0.031	rs10501620	11	85881439	q14.2
SNP_A-1714901	A	A	389	11	388	24	4.654	0.031	rs10501621	11	85883105	q14.2
SNP_A-2243708	T	C	172	168	197	147	4.24	0.0395	rs10751140	11	86147634	q14.2
SNP_A-1904771	T	T	274	94	235	119	5.653	1.74E-02	rs11601553	11	86176062	q14.2
SNP_A-1833802	G	G	279	103	248	128	4.482	3.43E-02	rs11234891	11	86348490	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1738705	C	C	262	126	240	160	4.824	0.0281	rs713065	11	86383828	q14.2
SNP_A-1876645	C	C	368	10	385	1	7.665	5.60E-03	rs6592334	11	86483437	q14.2
SNP_A-2100994	C	C	306	96	278	120	3.989	0.0458	rs17821321	11	86693120	q14.2
SNP_A-2013071	A	A	331	55	315	77	4.017	4.50E-02	rs17149955	11	86714943	q14.2
SNP_A-1932536	G	G	327	15	344	4	6.747	9.40E-03	rs10898703	11	86864954	q14.2
SNP_A-2161518	G	G	394	20	405	7	6.406	0.0114	rs6592369	11	86884878	q14.2
SNP_A-1942676	A	A	297	75	336	46	9.222	2.40E-03	rs7119134	11	86915803	q14.2
SNP_A-1815092	A	A	310	90	341	65	5.464	1.94E-02	rs7121003	11	86964252	q14.2
SNP_A-1823666	C	C	314	94	342	66	6.095	1.36E-02	rs7929162	11	86972967	q14.2
SNP_A-2227035	C	C	303	61	329	41	4.942	2.62E-02	rs6592394	11	86984050	q14.2
SNP_A-2013089	C	C	285	83	332	62	5.741	0.0166	rs17150418	11	87014858	q14.2
SNP_A-1881504	C	C	324	52	342	24	10.669	1.10E-03	rs7945528	11	87278296	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2147890	C	C	397	13	412	4	5	2.54E-02	rs6592443	11	87304787	q14.2
SNP_A-2075847	C	C	286	88	323	63	6.199	1.28E-02	rs890522	11	87534704	q14.2
SNP_A-1800995	G	G	288	106	317	81	4.712	2.99E-02	rs1426927	11	87535584	q14.2
SNP_A-2146612	T	T	282	112	312	86	4.909	2.67E-02	rs7111615	11	87538077	q14.2
SNP_A-2266881	C	C	297	119	328	92	4.974	2.57E-02	rs16913587	11	87542538	q14.2
SNP_A-2241972	T	T	293	123	323	93	5.628	0.0177	rs11602163	11	87548841	q14.2
SNP_A-1729346	C	C	276	122	315	91	7.006	8.10E-03	rs10501659	11	87562041	q14.2
SNP_A-1747631	C	C	277	115	309	83	6.919	8.50E-03	rs10501660	11	87574398	q14.2
SNP_A-1702765	G	G	283	117	322	90	5.86	0.0155	rs2386577	11	87579719	q14.2
SNP_A-2204633	C	C	320	10	341	3	4.147	4.17E-02	rs7478762	11	88032144	q14.3
SNP_A-2291127	T	T	393	5	406	0	5.132	0.0235	rs1499043	11	88032310	q14.3
SNP_A-2112970	T	T	374	10	359	21	4.189	0.0407	rs11018855	11	89474915	q14.3
SNP_A-2221870	T	T	337	21	312	38	5.772	1.63E-02	rs10830423	11	89526602	q14.3
SNP_A-2036132	C	C	280	80	309	59	4.513	3.36E-02	rs11018905	11	89564827	q14.3
SNP_A-2277353	C	C	304	32	280	52	5.724	0.0167	rs7479493	11	89603003	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1689911	G	G	308	36	303	65	7.567	5.90E-03	rs10501713	11	89641166	q14.3
SNP_A-1650734	A	A	380	20	376	36	4.416	0.0356	rs10501719	11	89872198	q14.3
SNP_A-2116695	G	G	210	150	234	120	4.581	3.23E-02	rs556045	11	89873859	q14.3
SNP_A-1901078	C	C	259	105	215	137	8.117	4.40E-03	rs520934	11	89875441	q14.3
SNP_A-2103418	A	G	214	150	189	171	9.268	0.0023	rs4627035	11	89880382	q14.3
SNP_A-2094780	T	-	220	140	172	172	8.801	3.00E-03	rs500264	11	89881547	q14.3
SNP_A-2084343	G	A	162	134	192	156	6.274	1.22E-02	rs558396	11	89881594	q14.3
SNP_A-2052547	C	C	208	158	239	129	5.075	2.43E-02	rs562160	11	89887386	q14.3
SNP_A-1801842	T	T	234	164	200	200	6.219	0.0126	rs4294531	11	89892792	q14.3
SNP_A-1655077	T	A	234	166	210	202	7.322	6.80E-03	rs565481	11	89919916	q14.3
SNP_A-2013400	A	A	329	27	348	12	6.28	1.22E-02	rs10501722	11	89921778	q14.3
SNP_A-2013401	G	G	223	151	180	172	5.292	2.14E-02	rs10501723	11	89922680	q14.3
SNP_A-1652838	C	G	227	163	207	185	9.509	0.002	rs570090	11	89926000	q14.3
SNP_A-2013403	A	A	215	175	241	141	5.058	2.45E-02	rs2212375	11	89948043	q14.3
SNP_A-2013406	G	G	229	183	261	151	5.156	2.32E-02	rs4635043	11	89966137	q14.3
SNP_A-2283940	G	A	238	166	213	195	10.079	0.0015	rs611622	11	89968188	q14.3
SNP_A-1823075	T	T	206	164	233	123	7.25	7.10E-03	rs609337	11	89968763	q14.3
SNP_A-2013409	A	A	223	181	253	151	4.602	3.19E-02	rs557067	11	89981859	q14.3
SNP_A-1958352	G	A	195	133	175	139	14.818	0.0001	rs509052	11	90003580	q14.3
SNP_A-2116382	A	G	245	171	215	201	9.356	2.20E-03	rs506506	11	90003811	q14.3
SNP_A-2134634	A	A	346	0	317	7	7.554	6.00E-03	rs16924273	11	90251202	q14.3
SNP_A-2013480	C	C	394	0	350	4	4.476	0.0344	rs16924449	11	90325348	q14.3
SNP_A-1730481	T	T	365	35	390	20	4.796	2.85E-02	rs10501744	11	90328419	q14.3
SNP_A-2134960	C	C	365	33	371	17	5.043	0.0247	—	11	90443017	q14.3
SNP_A-2260283	A	A	353	1	324	6	3.976	4.61E-02	rs7104107	11	90596555	q14.3
SNP_A-2205754	C	C	379	35	363	53	4.022	4.49E-02	rs10765455	11	90614434	q14.3
SNP_A-2235719	A	A	327	37	283	51	4.119	0.0424	rs7939703	11	90617039	q14.3
SNP_A-1781852	G	G	349	21	325	35	4.218	4.00E-02	rs10830716	11	90702192	q14.3
SNP_A-1831538	A	A	370	40	394	24	4.677	3.06E-02	rs16916490	11	91148600	q14.3
SNP_A-1819129	T	T	321	29	341	13	6.677	9.80E-03	rs6483153	11	91151406	q14.3
SNP_A-1846588	G	G	243	161	283	127	7.012	8.10E-03	rs10741428	11	91157828	q14.3
SNP_A-2013552	G	G	249	167	286	134	6.158	1.31E-02	rs10830772	11	91158549	q14.3
SNP_A-1688962	C	C	228	146	282	126	5.721	1.68E-02	rs6483154	11	91222287	q14.3
SNP_A-1863775	A	A	355	39	361	23	4.051	0.0441	rs765534	11	91230334	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2051597	G	G	375	5	376	14	4.135	4.20E-02	rs11019759	11	91423398	q14.3
SNP_A-1864379	A	A	255	95	281	73	4.12	0.0424	rs11019794	11	91464042	q14.3
SNP_A-2199483	C	C	295	61	260	80	4.402	3.59E-02	rs1390774	11	91472433	q14.3
SNP_A-1868441	A	A	284	102	292	68	6.012	1.42E-02	rs10830845	11	91483178	q14.3
SNP_A-1813141	G	G	343	17	352	2	11.909	6.00E-04	rs17512739	11	91739600	q14.3
SNP_A-1803484	A	A	372	6	395	1	3.845	0.0499	rs2028979	11	92291921	q21
SNP_A-1935553	G	G	363	31	379	15	5.91	1.51E-02	rs7124256	11	93009234	q21
SNP_A-2233250	T	T	227	139	208	172	4.07	0.0436	rs1395387	11	93278955	q21
SNP_A-2132759	A	A	212	134	174	154	4.652	0.031	rs1395386	11	93278979	q21
SNP_A-2091551	G	G	329	61	259	95	14.035	2.00E-04	rs16919711	11	93344289	q21
SNP_A-2013809	T	T	327	49	281	75	8.392	0.0038	rs1506658	11	93354598	q21
SNP_A-2013810	C	C	345	67	316	94	5.795	0.0161	rs2939619	11	93356828	q21
SNP_A-2013819	G	G	347	57	320	86	6.969	8.30E-03	rs1518561	11	93396497	q21
SNP_A-1754938	G	G	332	58	295	81	5.735	0.0166	rs2949865	11	93443385	q21
SNP_A-2056555	C	C	223	135	202	166	4.093	4.31E-02	rs481597	11	93709664	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2093864	A	A	410	4	416	0	4.039	4.45E-02	rs12292208	11	93841072	q21
SNP_A-1792275	G	G	382	30	358	58	9.668	0.0019	rs11805363	11	93866600	q21
SNP_A-2264919	A	A	264	110	215	133	6.261	0.0123	rs7126782	11	93963488	q21
SNP_A-1803476	G	G	384	24	394	12	4.124	4.23E-02	rs7934686	11	93992368	q21
SNP_A-1911669	G	G	384	14	405	5	4.645	3.11E-02	rs16920737	11	93994290	q21
SNP_A-2116159	T	T	231	143	252	114	4.099	4.29E-02	rs7124359	11	94008397	q21
SNP_A-2241438	A	A	396	4	397	15	6.194	1.28E-02	rs16921260	11	94399142	q21
SNP_A-1789796	G	G	394	14	380	26	3.848	4.98E-02	rs588446	11	94448093	q21
SNP_A-2143347	C	C	403	11	395	23	4.296	3.82E-02	rs653551	11	94483794	q21
SNP_A-2002150	C	C	341	9	293	21	6.501	1.08E-02	rs610520	11	94485121	q21
SNP_A-1748563	G	G	311	21	303	39	5.357	0.0206	rs641937	11	94521175	q21
SNP_A-2133425	C	C	282	130	312	104	4.385	3.63E-02	rs682533	11	94528962	q21
SNP_A-1656715	A	A	230	170	265	145	4.336	0.0373	rs976337	11	94699798	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2125234	A	A	318	80	343	55	5.575	1.82E-02	rs486829	11	94702530	q21
SNP_A-1688982	A	A	229	153	262	130	3.959	4.66E-02	rs4121863	11	94828438	q21
SNP_A-1899338	A	A	308	22	288	38	4.914	2.66E-02	rs12577444	11	94832110	q21
SNP_A-2039857	G	G	286	112	257	139	4.448	0.0349	rs2097046	11	94864637	q21
SNP_A-1871890	T	T	283	113	242	140	5.833	1.57E-02	rs2156469	11	94869049	q21
SNP_A-1867959	G	G	245	121	215	151	5.265	0.0218	rs7108412	11	94875384	q21
SNP_A-2013996	C	C	256	150	286	122	4.538	0.0332	rs1893688	11	94881727	q21
SNP_A-1826876	C	C	365	47	350	70	4.76	2.91E-02	rs11021202	11	94917555	q21
SNP_A-2243164	A	A	194	120	177	163	6.289	1.22E-02	rs1255453	11	94989283	q21
SNP_A-1644920	C	C	377	23	395	9	6.525	0.0106	rs10501833	11	95379198	q21
SNP_A-2124929	A	A	356	26	357	13	4.144	4.18E-02	rs1939483	11	95420099	q21
SNP_A-1876365	G	A	182	172	208	160	4.556	3.28E-02	rs10437580	11	95502194	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1931288	G	G	366	44	383	19	10.229	0.0014	rs16923429	11	95624950	q21
SNP_A-1735504	G	G	223	83	243	133	5.304	2.13E-02	rs2186584	11	95656813	q21
SNP_A-1895939	C	C	351	31	352	14	6.084	1.36E-02	---	11	95683668	q21
SNP_A-1669885	T	T	290	102	270	130	4.013	4.51E-02	rs557277	11	95707902	q21
SNP_A-1658586	G	G	271	97	264	134	4.851	0.0276	rs502822	11	95710642	q21
SNP_A-1712663	G	G	293	105	270	136	4.848	2.77E-02	rs483905	11	95711580	q21
SNP_A-1927397	A	A	244	100	206	128	6.501	1.08E-02	rs3847558	11	95844429	q21
SNP_A-2139953	A	A	252	162	216	196	5.993	0.0144	rs10750384	11	96274729	q21
SNP_A-2311984	G	G	254	156	225	191	5.243	2.20E-02	rs10894908	11	96344899	q21
SNP_A-2297690	C	C	303	91	322	58	7.636	5.70E-03	rs10750607	11	96463717	q22.1
SNP_A-2014197	T	T	360	26	371	13	4.494	3.40E-02	rs17129847	11	96499058	q22.1
SNP_A-2014214	T	T	356	6	340	0	5.684	1.71E-02	rs17130042	11	96720218	q22.1
SNP_A-1934428	C	T	181	173	200	148	5.214	0.0224	rs10895894	11	96906155	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1708675	C	C	276	124	310	102	3.938	4.72E-02	rs1986446	11	97336538	q22.1
SNP_A-2286954	G	G	253	101	285	59	12.788	3.00E-04	rs546546	11	97422554	q22.1
SNP_A-1745448	C	C	301	97	278	130	5.588	1.81E-02	rs561146	11	97458626	q22.1
SNP_A-1740049	T	T	302	90	282	122	5.335	2.09E-02	rs624607	11	97458718	q22.1
SNP_A-1673690	C	C	301	99	281	131	4.963	2.59E-02	rs625569	11	97458961	q22.1
SNP_A-1706859	G	G	301	97	281	131	5.517	1.88E-02	rs482657	11	97459766	q22.1
SNP_A-1737563	T	T	302	98	281	131	5.336	2.09E-02	rs639755	11	97459860	q22.1
SNP_A-2014247	C	C	280	60	308	42	4.366	3.67E-02	---	11	97474191	q22.1
SNP_A-2014248	A	A	286	98	305	71	4.841	2.78E-02	rs10501877	11	97474361	q22.1
SNP_A-1655071	A	A	281	91	269	127	5.462	1.94E-02	rs546136	11	97504479	q22.1
SNP_A-1661592	T	T	285	101	323	79	4.741	2.95E-02	rs10501878	11	97507188	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1744607	G	G	215	177	249	149	4.851	0.0276	rs2509867	11	97510276	q22.1
SNP_A-1943999	T	T	262	108	234	140	5.688	1.71E-02	rs1941837	11	97518777	q22.1
SNP_A-2014255	T	T	237	173	259	141	4.114	4.25E-02	rs1941776	11	97609815	q22.1
SNP_A-2028741	G	G	219	153	245	121	5.146	2.33E-02	rs2848519	11	97618389	q22.1
SNP_A-1939724	T	T	205	167	232	134	5.238	2.21E-02	rs2509843	11	97630614	q22.1
SNP_A-1919664	G	G	313	97	288	122	3.894	4.85E-02	rs1941783	11	97646910	q22.1
SNP_A-1914587	T	-	222	156	177	177	5.619	0.0178	rs10891921	11	97921586	q22.1
SNP_A-2295743	C	C	244	164	212	198	5.434	1.97E-02	rs4378353	11	97934598	q22.1
SNP_A-2187411	A	A	285	57	271	81	4.383	3.63E-02	rs4638281	11	97948207	q22.1
SNP_A-2061672	C	C	175	133	212	108	5.904	1.51E-02	rs10892018	11	97973277	q22.1
SNP_A-1945188	C	C	276	110	298	78	6.16	1.31E-02	rs3018592	11	98008403	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2237538	C	C	354	18	328	40	9.315	0.0023	rs11216490	11	98069327	q22.1
SNP_A-2036083	A	A	272	118	292	86	5.543	1.86E-02	rs1430469	11	98084348	q22.1
SNP_A-1830798	T	T	289	127	325	95	6.704	9.60E-03	rs2435577	11	98084455	q22.1
SNP_A-2131258	C	C	267	95	295	61	8.756	3.10E-03	rs2099201	11	98103752	q22.1
SNP_A-1947015	G	G	272	106	297	73	7.097	7.70E-03	rs963069	11	98110341	q22.1
SNP_A-1894290	G	G	402	8	417	1	5.642	1.75E-02	rs12793263	11	98158929	q22.1
SNP_A-2014309	A	A	263	93	251	125	4.434	3.52E-02	rs12362499	11	98208057	q22.1
SNP_A-1840373	G	A	229	185	223	197	5.9	1.51E-02	rs10750186	11	98438373	q22.1
SNP_A-1943347	C	C	352	30	383	13	7.779	0.0053	rs10892751	11	98451026	q22.1
SNP_A-2014336	T	T	360	42	388	20	8.811	3.00E-03	rs5008835	11	98451612	q22.1
SNP_A-2101116	A	A	345	23	363	9	6.561	0.0104	rs7120011	11	98458577	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1662090	T	T	241	157	280	106	12.628	4.00E-04	rs1940484	11	98479589	q22.1
SNP_A-1650620	T	T	239	125	287	101	6.169	1.30E-02	rs726533	11	98491609	q22.1
SNP_A-1683272	C	C	373	27	401	11	7.574	5.90E-03	rs4600174	11	98491773	q22.1
SNP_A-1837328	A	A	357	19	324	4	8.147	0.0043	rs12792189	11	98844430	q22.1
SNP_A-2253674	A	A	362	44	367	27	3.926	4.76E-02	rs11220671	11	98997685	q22.1
SNP_A-2014404	G	G	366	46	387	27	5.526	1.87E-02	rs10501920	11	98998383	q22.1
SNP_A-1940049	A	A	232	108	206	148	7.514	6.10E-03	rs1690805	11	99050585	q22.1
SNP_A-1956230	A	A	366	14	371	29	4.757	0.0292	rs12419474	11	99070312	q22.1
SNP_A-1944354	C	C	375	41	395	25	4.379	3.64E-02	rs770575	11	99389393	q22.1
SNP_A-1946376	G	G	332	54	317	79	4.919	2.66E-02	rs11222392	11	99394959	q22.1
SNP_A-1856312	A	A	261	145	237	179	4.604	3.19E-02	rs4754668	11	99484141	q22.1
SNP_A-2014481	C	C	349	31	355	17	4.05	4.42E-02	rs1833492	11	99518149	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1688832	G	G	259	129	282	98	5.129	0.0235	rs6611134	11	99997508	q22.1
SNP_A-2014541	A	A	398	0	361	5	5.473	1.93E-02	rs655175	11	100215412	q22.1
SNP_A-1682724	C	C	338	24	350	44	4.746	2.94E-02	rs1074544	11	100275701	q22.1
SNP_A-2303441	A	A	306	56	280	82	6.052	1.39E-02	rs616164	11	100327724	q22.1
SNP_A-2149882	C	C	290	40	318	22	6.367	1.16E-02	rs476308	11	100379658	q22.1
SNP_A-1684032	G	G	270	48	284	82	5.907	1.51E-02	rs521744	11	100418423	q22.1
SNP_A-2029133	A	A	410	4	414	0	4.019	4.50E-02	rs11571215	11	100439141	q22.1
SNP_A-1841952	C	C	384	16	398	6	4.776	2.89E-02	rs606386	11	100558021	q22.1
SNP_A-2014580	A	A	325	19	316	8	4.013	4.52E-02	rs2156520	11	100603330	q22.1
SNP_A-1921085	T	T	319	93	342	70	4.046	4.43E-02	rs4754743	11	100619729	q22.1
SNP_A-2230729	G	G	362	10	321	35	16.006	0.000063136	rs17096411	11	100650873	q22.1
SNP_A-1896255	C	C	386	28	375	47	4.896	0.0269	rs11224702	11	100676886	q22.1
SNP_A-1646346	G	G	362	30	332	64	13.575	2.00E-04	rs10501976	11	100686604	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805864	C	C	175	159	221	123	9.794	0.0018	rs1218918	11	100696376	q22.1
SNP_A-2087519	T	T	254	148	284	118	5.056	2.45E-02	rs11224715	11	100700084	q22.1
SNP_A-2014591	C	C	274	54	288	28	8.372	0.0038	rs12790159	11	100714240	q22.1
SNP_A-2308403	T	T	353	27	390	14	5.235	2.21E-02	rs11224733	11	100740407	q22.1
SNP_A-2281542	A	A	279	91	306	66	5.222	0.0223	rs7948518	11	100748854	q22.1
SNP_A-1733876	T	T	367	33	394	20	3.907	4.81E-02	rs10501978	11	100763961	q22.1
SNP_A-2072827	C	C	378	34	397	17	6.128	1.33E-02	rs11224760	11	100805397	q22.1
SNP_A-2312203	G	G	290	122	316	96	4.216	4.00E-02	rs2513180	11	100997840	q22.1
SNP_A-2276875	T	T	285	101	313	75	5.147	2.33E-02	rs1938861	11	101002606	q22.1
SNP_A-2014625	C	C	244	106	267	79	4.953	2.60E-02	rs1939447	11	101044894	q22.1
SNP_A-1884817	C	C	375	27	364	12	5.07	2.43E-02	rs11224967	11	101069743	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2155134	A	A	297	103	321	79	4.097	4.30E-02	rs11225308	11	101904688	q22.2
SNP_A-1888621	C	C	317	33	297	51	4.503	3.38E-02	rs1940461	11	102085618	q22.2
SNP_A-2198859	T	T	318	72	288	100	6.038	0.014	rs1892886	11	102097204	q22.2
SNP_A-2234223	G	G	379	33	382	18	4.247	3.93E-02	rs626330	11	102541001	q22.3
SNP_A-1864385	G	G	315	93	344	68	5.139	2.34E-02	rs7926763	11	102590048	q22.3
SNP_A-1704095	T	T	230	122	200	146	4.191	4.06E-02	rs1007349	11	102941313	q22.3
SNP_A-1862535	C	C	340	50	340	30	4.477	0.0344	rs7120812	11	103036338	q22.3
SNP_A-1897141	A	A	380	36	365	55	4.25	3.93E-02	rs11604394	11	103060090	q22.3
SNP_A-1797311	A	A	380	34	363	53	4.534	0.0332	rs11603978	11	103060268	q22.3
SNP_A-2124141	T	T	359	29	344	50	5.857	0.0155	rs17402181	11	103079573	q22.3
SNP_A-1744285	A	A	330	48	327	71	3.946	0.047	rs1917450	11	103095382	q22.3
SNP_A-2063893	C	C	346	18	316	36	7.16	7.50E-03	rs11225990	11	103113591	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123055	A	A	352	6	332	16	4.99	2.55E-02	rs11226015	11	103169269	q22.3
SNP_A-1860136	G	G	310	36	279	51	3.841	5.00E-02	rs2292763	11	103200146	q22.3
SNP_A-2014857	A	A	345	31	340	52	5.019	2.51E-02	rs10502019	11	103218742	q22.3
SNP_A-2014884	G	G	244	136	261	89	9.173	2.50E-03	rs361315	11	103429786	q22.3
SNP_A-2036040	T	T	215	141	266	112	8.079	4.50E-03	rs10791663	11	103434428	q22.3
SNP_A-2224865	A	A	242	150	283	117	7.2	7.30E-03	rs587116	11	103453028	q22.3
SNP_A-2014888	C	C	229	131	264	100	6.623	0.0101	rs361302	11	103455952	q22.3
SNP_A-1716749	A	A	247	153	286	124	5.767	1.63E-02	rs361262	11	103474186	q22.3
SNP_A-1655769	G	G	245	155	288	126	6.223	0.0126	rs361263	11	103474301	q22.3
SNP_A-1684296	T	T	244	154	282	122	6.411	1.13E-02	rs361266	11	103475596	q22.3
SNP_A-1658652	G	G	238	146	287	125	5.222	0.0223	rs361308	11	103482256	q22.3
SNP_A-1834112	T	T	392	18	377	33	4.704	3.01E-02	rs7950244	11	103645955	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864215	T	T	333	19	358	8	5.115	2.37E-02	rs1488964	11	103699711	q22.3
SNP_A-2241026	A	A	386	0	365	7	7.331	6.80E-03	rs530398	11	104227600	q22.3
SNP_A-2036712	A	A	397	7	379	31	15.532	8.11E-05	rs3181174	11	104381934	q22.3
SNP_A-2014985	G	G	328	46	306	68	5.009	0.0252	rs517736	11	104398767	q22.3
SNP_A-2235382	G	G	316	56	299	79	4.341	3.72E-02	rs554344	11	104400407	q22.3
SNP_A-2136349	G	G	273	67	218	90	7.97	4.80E-03	rs507509	11	104401086	q22.3
SNP_A-2258770	T	T	379	1	341	7	5.109	2.38E-02	rs497874	11	104436443	q22.3
SNP_A-1679210	A	A	342	60	329	85	4.387	3.62E-02	rs1503391	11	104450175	q22.3
SNP_A-1693214	C	C	339	57	328	84	5.037	2.48E-02	rs692897	11	104450710	q22.3
SNP_A-1737267	C	C	342	60	327	85	4.525	3.34E-02	rs692914	11	104450737	q22.3
SNP_A-1952635	C	C	217	115	238	90	3.994	4.57E-02	rs11226626	11	104523133	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839644	A	A	344	4	324	12	4.39	3.62E-02	rs1124519	11	104777474	q22.3
SNP_A-2127359	C	C	349	9	374	2	4.881	2.72E-02	rs9666259	11	104846834	q22.3
SNP_A-2090353	C	C	397	7	377	17	4.559	0.0327	rs11226774	11	104946632	q22.3
SNP_A-1836288	T	T	388	18	399	7	4.994	2.54E-02	rs11226791	11	104965252	q22.3
SNP_A-2163821	C	C	398	14	395	5	4.098	4.29E-02	rs10791780	11	105476684	q22.3
SNP_A-2015089	C	C	298	44	299	25	4.751	0.0293	rs567992	11	105767607	q22.3
SNP_A-2242201	C	C	359	49	362	30	4.264	3.89E-02	rs6588923	11	106125102	q22.3
SNP_A-2314039	A	A	285	109	307	83	4.318	3.77E-02	—	11	106218750	q22.3
SNP_A-2015115	G	G	304	92	333	65	5.959	0.0146	rs10502079	11	106224087	q22.3
SNP_A-2301044	C	C	312	74	322	50	4.546	3.30E-02	rs11211982	11	106311158	q22.3
SNP_A-1704505	G	G	292	110	325	87	4.328	3.75E-02	rs3133355	11	106389904	q22.3
SNP_A-1740623	C	C	247	95	284	56	12.645	4.00E-04	rs1388171	11	106680854	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2269477	T	T	273	55	287	33	5.752	1.65E-02	rs10890715	11	106698393	q22.3
SNP_A-2166098	A	A	352	0	361	5	4.842	2.78E-02	rs12421525	11	106916903	q22.3
SNP_A-1727090	T	T	371	13	397	3	6.807	9.10E-03	rs10502094	11	106967771	q22.3
SNP_A-2176765	G	G	269	101	261	139	4.976	2.57E-02	rs7948284	11	107088095	q22.3
SNP_A-2048689	C	C	355	51	378	34	4.078	4.34E-02	rs7937558	11	108000751	q22.3
SNP_A-1685650	T	T	312	78	351	59	4.432	3.53E-02	rs898972	11	108234110	q22.3
SNP_A-2233438	T	T	335	81	361	59	4.409	3.57E-02	rs12796331	11	108276307	q22.3
SNP_A-2021751	A	A	256	72	235	103	6.241	1.25E-02	rs10890926	11	108395145	q22.3
SNP_A-1890873	T	T	316	78	329	55	4.112	4.26E-02	rs1396918	11	108469609	q22.3
SNP_A-1813328	C	C	344	54	375	35	5.216	0.0224	rs1553769	11	108508746	q22.3
SNP_A-2259737	A	A	404	4	412	0	4.059	4.39E-02	rs12284225	11	108547884	q22.3
SNP_A-1818466	C	C	404	14	417	3	7.319	6.80E-03	rs11212973	11	108560140	q22.3
SNP_A-2218037	A	A	392	20	410	8	5.504	0.019	rs11213005	11	108624509	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246661	G	G	365	13	377	3	6.439	0.0112	rs11213021	11	108640192	q22.3
SNP_A-1818410	A	A	400	12	414	2	7.364	6.70E-03	rs11213022	11	108640347	q22.3
SNP_A-2035972	A	A	389	13	383	29	6.02	0.0141	rs1906339	11	108980770	q22.3
SNP_A-2092951	A	A	286	48	249	67	5.204	2.25E-02	rs1433560	11	109138602	q22.3
SNP_A-2016768	G	G	413	1	410	8	5.436	1.97E-02	rs17110619	11	109375271	q22.3
SNP_A-2083466	C	C	338	28	350	14	4.871	2.73E-02	rs1648156	11	109420588	q22.3
SNP_A-1958512	T	T	290	80	287	115	4.98	2.56E-02	rs7128556	11	109477438	q22.3
SNP_A-1896663	G	G	303	85	275	109	4.305	3.80E-02	rs10789752	11	109485155	q22.3
SNP_A-2054115	A	A	313	75	300	102	4.148	4.17E-02	rs689183	11	109517353	q22.3
SNP_A-1655211	T	T	301	95	283	125	4.468	3.45E-02	rs1789369	11	109532936	q22.3
SNP_A-1751767	A	A	295	89	281	125	5.788	0.0161	rs746463	11	109533593	q22.3
SNP_A-2107142	C	C	299	119	326	92	4.621	3.16E-02	rs12289680	11	110116084	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044911	C	C	337	81	361	57	4.999	2.54E-02	rs12577358	11	110117023	q23.1
SNP_A-1791275	C	C	374	10	389	3	3.982	4.60E-02	rs11213669	11	110325575	q23.1
SNP_A-2174957	G	G	265	57	244	80	4.722	0.0298	rs317519	11	110395604	q23.1
SNP_A-1708040	A	A	307	65	314	96	4.211	0.0402	rs1986684	11	110662136	q23.1
SNP_A-2018065	C	C	335	77	303	105	5.893	0.0152	rs10502139	11	110726492	q23.1
SNP_A-2002240	G	G	254	96	247	131	4.424	3.54E-02	rs4938593	11	110803463	q23.1
SNP_A-2194050	A	A	277	109	244	132	4.155	4.15E-02	rs4936453	11	110805992	q23.1
SNP_A-1691974	G	G	229	151	263	129	3.893	4.85E-02	rs1113851	11	110891810	q23.1
SNP_A-2002241	C	C	234	140	262	112	4.692	3.03E-02	rs2187388	11	110892326	q23.1
SNP_A-1856645	C	C	244	166	277	137	4.846	2.77E-02	rs2156580	11	110899538	q23.1
SNP_A-1756617	T	T	259	127	289	99	5.106	2.38E-02	rs659529	11	110974545	q23.1
SNP_A-1926089	A	A	264	126	281	95	4.624	0.0315	rs1784786	11	110991253	q23.1
SNP_A-2128121	C	C	284	132	314	106	4.326	3.75E-02	rs4630327	11	111044537	q23.1
SNP_A-2187995	G	G	266	94	293	73	3.896	4.84E-02	rs10891288	11	111057263	q23.1
SNP_A-1850662	C	C	287	121	321	99	3.928	4.75E-02	rs10789843	11	111081368	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1903297	G	G	260	106	292	80	5.441	1.97E-02	rs7937682	11	111085149	q23.1
SNP_A-2267063	C	C	249	77	300	62	4.485	3.42E-02	rs4936678	11	111130295	q23.1
SNP_A-1921781	T	T	280	134	317	101	6.908	0.0086	rs11601674	11	111139564	q23.1
SNP_A-1718183	G	G	243	105	223	139	5.322	2.11E-02	rs10502148	11	111185647	q23.1
SNP_A-2308277	T	T	289	123	255	155	5.804	0.016	rs7951256	11	111765984	q23.1
SNP_A-2238739	G	G	243	133	221	165	4.349	3.70E-02	rs12365993	11	111953103	q23.1
SNP_A-2285454	C	C	263	151	238	184	4.422	3.55E-02	rs11214256	11	111961036	q23.1
SNP_A-2266734	G	G	256	148	233	183	4.608	3.18E-02	rs10891394	11	111962843	q23.1
SNP_A-2019298	G	G	326	60	363	41	5.154	2.32E-02	rs10502162	11	112351309	q23.1
SNP_A-2019302	G	G	280	120	316	86	7.781	0.0053	rs10502163	11	112351344	q23.1
SNP_A-2139990	A	A	210	162	248	130	6.612	0.0101	rs11214441	11	112351923	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247894	G	G	268	116	288	84	5.65	1.75E-02	rs11214442	11	112352013	q23.1
SNP_A-2268149	T	T	221	179	257	147	5.833	1.57E-02	rs1940724	11	112358156	q23.1
SNP_A-1668292	C	C	334	68	373	41	8.665	3.20E-03	rs7944570	11	112383237	q23.1
SNP_A-2030349	T	T	226	186	261	151	6.15	1.31E-02	rs6589354	11	112383757	q23.1
SNP_A-1841583	C	C	352	64	375	45	4.021	4.49E-02	rs11214463	11	112398704	q23.1
SNP_A-2081900	T	T	236	114	263	89	4.534	0.0332	rs7941072	11	112398771	q23.1
SNP_A-2019407	T	T	194	170	228	138	6.059	0.0138	rs7926312	11	112399066	q23.1
SNP_A-2189086	C	C	278	114	314	78	8.939	0.0028	rs11214468	11	112402283	q23.1
SNP_A-1814603	T	T	185	167	225	147	4.627	0.0315	rs1892983	11	112404424	q23.1
SNP_A-1812077	T	T	226	178	259	145	5.617	0.0178	rs11214469	11	112405553	q23.1
SNP_A-1934006	A	A	216	166	257	135	6.619	0.0101	rs7105462	11	112417258	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2090194	T	T	229	185	261	151	5.525	1.87E-02	rs3802847	11	112417513	q23.1
SNP_A-2019872	T	T	205	161	240	130	6.034	0.014	rs4517559	11	112685412	q23.1
SNP_A-2203826	G	G	341	65	362	38	7.661	5.60E-03	rs7122454	11	112832678	q23.2
SNP_A-2314663	G	G	349	67	375	45	5.236	2.21E-02	rs10891551	11	112837505	q23.2
SNP_A-2020465	T	T	308	6	328	0	6.327	1.19E-02	---	11	113519868	q23.2
SNP_A-1867761	A	A	330	44	354	26	5.423	1.99E-02	rs660800	11	113545720	q23.2
SNP_A-2307129	G	G	331	49	357	33	3.975	4.62E-02	rs659120	11	113546098	q23.2
SNP_A-1906593	G	G	188	164	219	137	4.761	2.91E-02	rs2256292	11	113673149	q23.2
SNP_A-1822598	C	C	384	34	403	17	6.121	0.0134	rs11214938	11	113677870	q23.2
SNP_A-2186132	C	C	217	173	228	130	5.014	2.51E-02	rs3851572	11	113792426	q23.2
SNP_A-1693198	G	A	207	195	230	180	4.688	0.0304	rs536179	11	113812725	q23.2
SNP_A-1815484	C	C	291	83	306	56	5.427	1.98E-02	rs4569036	11	113841400	q23.2
SNP_A-2234596	A	A	276	134	308	110	4.037	4.45E-02	rs12421720	11	114114318	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946919	C	C	235	161	271	129	6.072	0.0137	rs7123330	11	114120247	q23.2
SNP_A-2059044	T	T	359	15	368	6	3.969	4.64E-02	---	11	114192099	q23.2
SNP_A-2125623	A	A	303	109	323	83	4.116	4.25E-02	rs2513480	11	114273476	q23.2
SNP_A-2174658	C	C	210	114	231	79	7.041	8.00E-03	rs10790060	11	114324813	q23.2
SNP_A-2243636	C	C	403	11	412	2	6.33	1.19E-02	rs10891786	11	114348619	q23.2
SNP_A-2084998	G	G	389	17	409	7	4.547	3.30E-02	rs11215392	11	114543618	q23.3
SNP_A-2002263	A	A	374	10	374	2	5.25	2.20E-02	rs6589484	11	114576024	q23.3
SNP_A-2020830	G	G	361	15	359	3	7.743	5.40E-03	rs718484	11	114922062	q23.3
SNP_A-1907770	G	G	412	4	422	0	4.077	4.35E-02	rs2250615	11	114938189	q23.3
SNP_A-1863136	A	A	407	7	403	17	4.143	4.18E-02	rs1939689	11	115267387	q23.3
SNP_A-2020847	G	G	400	2	391	9	4.552	3.29E-02	rs17118936	11	115303874	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2143125	A	A	282	60	276	88	4.681	3.05E-02	rs6589531	11	115510680	q23.3
SNP_A-1887739	A	A	355	59	340	82	3.999	4.55E-02	rs10891950	11	115662975	q23.3
SNP_A-2091270	C	C	315	51	277	67	3.931	4.74E-02	rs10891952	11	115674356	q23.3
SNP_A-2020863	A	A	242	174	211	205	4.657	0.0309	rs2174880	11	115810193	q23.3
SNP_A-1802449	C	C	377	29	356	56	9.135	2.50E-03	rs7396765	11	115819723	q23.3
SNP_A-1859678	G	G	416	0	416	4	3.981	4.60E-02	rs17490340	11	115841494	q23.3
SNP_A-2020864	T	T	204	190	233	163	3.985	4.59E-02	rs573554	11	115861070	q23.3
SNP_A-2264225	C	C	182	174	221	139	7.666	5.60E-03	rs10892001	11	116010650	q23.3
SNP_A-2283293	T	T	321	25	330	12	4.669	3.07E-02	rs17119878	11	116036689	q23.3
SNP_A-2268472	G	G	272	134	302	110	3.885	0.0487	rs1787715	11	116065535	q23.3
SNP_A-2020877	G	G	309	105	334	76	5.599	1.80E-02	rs180354	11	116105036	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920968	T	T	231	121	199	163	8.454	3.60E-03	rs108533	11	116106921	q23.3
SNP_A-1650860	T	T	298	102	333	75	5.981	1.45E-02	rs180324	11	116162984	q23.3
SNP_A-2020887	C	C	267	141	233	175	5.97	1.45E-02	rs10502221	11	116332080	q23.3
SNP_A-2020889	C	C	226	158	249	109	9.206	2.40E-03	rs7120706	11	116335297	q23.3
SNP_A-1648206	A	A	210	154	246	128	5.105	2.39E-02	rs10502222	11	116371382	q23.3
SNP_A-2002274	G	G	315	93	338	68	4.687	0.0304	rs7120449	11	116548109	q23.3
SNP_A-2169941	C	C	241	83	206	118	8.835	3.00E-03	rs1784042	11	116570686	q23.3
SNP_A-1939006	G	G	251	83	217	105	4.827	2.80E-02	rs9651682	11	116745567	q23.3
SNP_A-1868430	T	T	264	46	269	75	5.244	2.20E-02	rs7123652	11	116882728	q23.3
SNP_A-1856505	G	G	416	0	412	4	4.019	4.50E-02	rs4938408	11	116939839	q23.3
SNP_A-1694773	T	T	401	1	403	11	8.164	0.0043	rs10502226	11	116979355	q23.3
SNP_A-2232246	G	G	364	14	361	27	4.004	4.54E-02	rs11216466	11	116979790	q23.3
SNP_A-1861394	T	T	387	23	372	40	4.879	2.72E-02	rs721486	11	117062750	q23.3
SNP_A-1865665	G	G	411	3	409	11	4.533	0.0332	rs7950743	11	117118991	q23.3
SNP_A-2077529	G	G	294	22	328	10	5.625	0.0177	rs1939977	11	117119930	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2166493	G	G	377	25	374	44	4.934	0.0263	rs2226635	11	117192330	q23.3
SNP_A-1903169	A	A	351	27	342	48	5.811	1.59E-02	rs17121510	11	117381365	q23.3
SNP_A-2119668	G	G	343	15	361	5	5.372	2.05E-02	rs11216720	11	117414311	q23.3
SNP_A-2302783	C	C	289	37	324	22	5.221	0.0223	rs2276129	11	117478883	q23.3
SNP_A-1872758	T	T	398	6	382	16	4.829	2.80E-02	rs603678	11	117492601	q23.3
SNP_A-1938639	C	C	383	29	368	54	7.711	5.50E-03	rs11600901	11	117537196	q23.3
SNP_A-2226334	A	A	273	133	305	109	4.074	4.35E-02	rs12576941	11	117663212	q23.3
SNP_A-1828181	C	C	292	68	287	95	3.867	4.93E-02	rs2276424	11	117715170	q23.3
SNP_A-1871988	G	G	310	94	337	63	7.228	7.20E-03	rs10790256	11	118039292	q23.3
SNP_A-1910838	T	T	296	114	329	87	5.326	2.10E-02	rs10790261	11	118084957	q23.3
SNP_A-2311076	G	G	280	138	250	170	5.018	2.51E-02	rs10790332	11	119058888	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944791	C	C	351	47	384	32	3.934	4.73E-02	rs9633947	11	119149570	q23.3
SNP_A-1794349	G	G	286	42	355	29	5.437	1.97E-02	rs10892466	11	119166527	q23.3
SNP_A-2204161	G	G	326	84	357	61	4.978	2.57E-02	rs11217512	11	119178932	q23.3
SNP_A-2084691	C	C	250	98	277	71	5.697	1.70E-02	rs10892472	11	119188817	q23.3
SNP_A-2057714	C	C	400	18	414	8	4.068	4.37E-02	rs17123466	11	119276958	q23.3
SNP_A-2137176	T	T	349	21	375	7	7.744	5.40E-03	rs11217608	11	119355038	q23.3
SNP_A-2002300	C	C	217	93	206	134	6.32	1.19E-02	rs4938763	11	119440144	q23.3
SNP_A-2002305	A	A	350	10	362	2	5.514	0.0189	rs3897570	11	119900439	q23.3
SNP_A-2115772	A	G	184	168	186	146	4.71	3.00E-02	rs12284644	11	119955226	q23.3
SNP_A-1787843	G	G	269	87	240	118	6.335	0.0118	rs17124120	11	120010838	q23.3
SNP_A-1885224	G	G	223	193	254	162	4.722	0.0298	rs6589833	11	120067093	q23.3
SNP_A-2158049	C	C	401	9	412	2	4.584	3.23E-02	rs11218005	11	120158146	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1812638	C	C	358	2	301	9	5.685	1.71E-02	rs17124522	11	120280601	q23.3
SNP_A-1834490	G	G	301	65	326	44	5.021	2.50E-02	rs540787	11	120359689	q23.3
SNP_A-2024492	C	C	329	63	307	87	4.596	3.20E-02	rs12283211	11	120396033	q23.3
SNP_A-2193363	C	C	260	62	288	42	5.179	0.0229	rs10892713	11	120642839	q23.3
SNP_A-1850162	G	G	373	19	359	7	4.92	2.65E-02	rs4936613	11	120709811	q23.3
SNP_A-1851501	C	C	365	29	388	12	7.706	5.50E-03	rs490951	11	121185688	q23.3
SNP_A-2122656	C	C	244	80	192	114	11.656	6.00E-04	rs4102736	11	121280059	q24.1
SNP_A-2108761	A	G	224	148	196	176	12.458	4.00E-04	rs747915	11	121284874	q24.1
SNP_A-1693553	A	A	384	8	406	2	3.894	4.85E-02	rs1219425	11	121357267	q24.1
SNP_A-2151865	G	G	294	120	307	91	3.953	4.68E-02	rs564649	11	121517448	q24.1
SNP_A-1914908	G	G	273	129	299	103	4.096	4.30E-02	rs543412	11	121528137	q24.1
SNP_A-1667076	T	T	334	68	365	49	4.285	0.0385	rs511514	11	121531232	q24.1
SNP_A-1690723	G	G	328	46	360	24	8.272	4.00E-03	rs655283	11	121804988	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2021311	T	T	330	86	356	62	4.873	2.73E-02	rs10502250	11	121908673	q24.1
SNP_A-1869364	C	C	414	2	407	11	6.286	1.22E-02	rs3134403	11	122256223	q24.1
SNP_A-2152636	T	T	404	2	381	11	6.661	9.90E-03	rs3134414	11	122258390	q24.1
SNP_A-1786008	C	C	329	1	297	13	11.308	8.00E-04	rs9943528	11	122258612	q24.1
SNP_A-2244820	G	G	412	2	403	11	6.33	1.19E-02	rs3134432	11	122264276	q24.1
SNP_A-1879360	T	T	363	29	354	48	4.676	3.06E-02	rs6650181	11	122264794	q24.1
SNP_A-2048514	A	G	208	204	240	170	6.734	9.50E-03	rs10790558	11	122544050	q24.1
SNP_A-1850611	G	G	224	186	256	154	5.145	2.33E-02	rs7102292	11	122546723	q24.1
SNP_A-1904638	A	A	191	179	214	148	4.158	4.14E-02	rs7929006	11	122553372	q24.1
SNP_A-2184435	G	G	353	45	334	66	4.493	3.40E-02	rs10892983	11	122597453	q24.1
SNP_A-1781459	T	T	369	49	350	72	4.855	0.0276	rs3016380	11	122809860	q24.1
SNP_A-2157462	A	A	235	175	252	140	4.08	4.34E-02	rs2714049	11	122850730	q24.1
SNP_A-1665430	A	A	213	187	247	163	4.036	4.45E-02	rs10502268	11	123164388	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1742789	G	G	219	183	257	157	4.846	2.77E-02	rs10502270	11	123165320	q24.1
SNP_A-1714304	C	C	378	24	398	12	4.437	3.52E-02	rs10502271	11	123187074	q24.1
SNP_A-1758277	C	C	293	35	277	53	4.125	4.23E-02	rs724467	11	123218223	q24.1
SNP_A-2313312	A	A	380	28	401	13	6.009	1.42E-02	rs17127917	11	123273551	q24.1
SNP_A-2021862	T	T	245	123	263	91	5.153	2.32E-02	rs4936874	11	123375437	q24.1
SNP_A-1847651	T	T	269	59	299	41	4.61	3.18E-02	rs11219443	11	123456291	q24.1
SNP_A-1791391	A	A	385	25	376	44	5.219	0.0223	rs503326	11	123458778	q24.1
SNP_A-2150591	T	T	316	90	336	66	4.286	3.84E-02	rs12276244	11	123462367	q24.1
SNP_A-2160656	T	T	313	41	272	64	7.447	6.40E-03	rs2846226	11	123556141	q24.1
SNP_A-2134551	T	T	335	43	338	22	6.363	0.0117	rs2466625	11	123670101	q24.1
SNP_A-2022035	C	C	367	33	386	16	6.372	1.16E-02	rs2023754	11	123697566	q24.1
SNP_A-2288794	C	C	354	48	341	69	3.934	4.73E-02	rs553995	11	123700734	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1956943	G	G	284	50	295	31	4.569	3.25E-02	rs7950818	11	123890666	q24.2
SNP_A-2214952	G	G	322	84	286	112	6.053	1.39E-02	rs7103533	11	123944627	q24.2
SNP_A-1947967	C	C	285	91	271	121	4.266	3.89E-02	rs10893347	11	124568317	q24.2
SNP_A-2277049	T	T	374	10	353	23	5.644	1.75E-02	rs12290158	11	124748285	q24.2
SNP_A-1959843	C	C	405	7	385	23	9.02	2.70E-03	rs11220043	11	124763058	q24.2
SNP_A-1782393	C	T	187	147	195	171	6.002	0.0143	rs7104304	11	124788472	q24.2
SNP_A-1943632	C	T	231	175	210	198	5.715	1.68E-02	rs10893385	11	124854131	q24.2
SNP_A-2151500	G	G	334	46	300	68	5.878	1.53E-02	rs7945490	11	124945989	q24.2
SNP_A-1923810	C	C	248	156	219	187	4.598	3.20E-02	rs545673	11	124966707	q24.2
SNP_A-1870656	A	G	197	179	199	151	6.216	1.27E-02	rs515255	11	125002355	q24.2
SNP_A-1758078	T	C	221	181	227	187	7.845	5.10E-03	rs477961	11	125015030	q24.2
SNP_A-2056324	T	T	305	51	249	67	5.469	1.94E-02	rs10893412	11	125044412	q24.2
SNP_A-2240388	G	G	261	153	301	119	7.054	7.90E-03	rs565435	11	125048000	q24.2
SNP_A-2251699	A	A	305	57	285	79	4.231	3.97E-02	rs551711	11	125072338	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1896936	T	T	253	147	279	113	5.637	1.76E-02	rs555297	11	125105076	q24.2
SNP_A-2180762	A	A	223	147	192	180	5.641	1.75E-02	rs1365080	11	125108745	q24.2
SNP_A-2084360	A	A	349	1	308	6	4.191	0.0407	rs1893255	11	125121123	q24.2
SNP_A-2280207	C	C	343	17	353	7	4.31	3.79E-02	rs522690	11	125152922	q24.2
SNP_A-2022433	C	C	286	106	256	140	6.34	0.0118	rs472535	11	125290056	q24.2
SNP_A-1930133	T	T	261	61	240	88	5.718	1.68E-02	rs1144501	11	125294195	q24.2
SNP_A-2267750	G	G	339	39	353	19	7.132	0.0076	rs532721	11	125302313	q24.2
SNP_A-2115016	A	A	359	13	344	4	4.29	3.83E-02	rs11220281	11	125316889	q24.2
SNP_A-2241083	G	G	298	96	318	68	5.348	0.0207	rs658305	11	125360676	q24.2
SNP_A-2038078	T	T	384	0	374	4	4.085	4.33E-02	rs11220343	11	125458343	q24.2
SNP_A-2212744	A	A	283	111	320	88	4.686	0.0304	rs240555	11	125707295	q24.2
SNP_A-1886178	T	T	248	132	226	174	6.277	1.22E-02	rs621479	11	125913763	q24.2
SNP_A-2071323	T	T	315	31	311	51	4.544	3.30E-02	rs605344	11	125966968	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1817866	G	G	247	165	277	139	3.922	4.77E-02	rs948117	11	126299616	q24.2
SNP_A-2250137	T	T	179	161	185	121	3.994	4.57E-02	rs1784346	11	126308412	q24.2
SNP_A-2040156	G	G	347	45	373	29	4.273	3.87E-02	rs1939995	11	126356059	q24.2
SNP_A-2285596	C	C	345	57	371	37	5.155	2.32E-02	rs11220704	11	126385511	q24.2
SNP_A-1870358	C	C	288	36	339	21	6.218	0.0126	rs11220705	11	126385752	q24.2
SNP_A-2072104	G	G	317	33	300	54	5.515	0.0189	rs11220729	11	126406689	q24.2
SNP_A-1887313	G	G	359	51	340	78	6.091	1.36E-02	rs11220778	11	126488670	q24.2
SNP_A-1945477	C	C	350	52	331	73	4.053	0.0441	rs1944635	11	126494104	q24.2
SNP_A-2173170	T	T	360	48	337	73	5.919	1.50E-02	rs7952490	11	126496550	q24.2
SNP_A-1906209	T	T	339	27	331	47	5.309	0.0212	rs11220790	11	126497714	q24.2
SNP_A-2090000	C	C	353	47	339	73	5.74	0.0166	rs7941925	11	126497906	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2183273	G	G	359	11	385	3	5.055	2.45E-02	rs7126174	11	126629033	q24.2
SNP_A-2052500	C	C	276	130	308	104	4.599	3.20E-02	rs11221110	11	127304657	q24.2
SNP_A-2073100	A	A	246	114	211	141	5.45	1.96E-02	rs10750388	11	127470981	q24.2
SNP_A-1907217	T	T	376	30	401	17	4.226	3.98E-02	rs10893822	11	127530313	q24.3
SNP_A-1799297	T	T	407	9	417	1	6.517	1.07E-02	rs11221223	11	127628469	q24.3
SNP_A-1824109	C	C	343	55	329	79	4.467	3.46E-02	rs10893883	11	127879923	q24.3
SNP_A-2272241	A	A	332	12	340	26	4.576	3.24E-02	rs3935794	11	127895887	q24.3
SNP_A-2092976	G	G	384	8	387	19	4.249	3.93E-02	rs11221362	11	127955429	q24.3
SNP_A-2298810	A	A	261	147	201	173	8.442	3.70E-03	rs640060	11	128137468	q24.3
SNP_A-2023487	T	T	331	39	310	58	4.404	3.58E-02	rs7951996	11	128177718	q24.3
SNP_A-2190445	G	G	414	4	422	0	4.058	4.40E-02	rs12575389	11	128263826	q24.3
SNP_A-2054760	T	T	295	49	296	82	6.728	9.50E-03	rs4937384	11	128274418	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213504	G	G	315	39	299	63	5.975	1.45E-02	rs11221503	11	128277662	q24.3
SNP_A-2311187	A	A	307	83	278	114	6.311	0.012	rs2155548	11	128309999	q24.3
SNP_A-1951061	G	G	316	100	340	76	4.151	4.16E-02	rs11221541	11	128406451	q24.3
SNP_A-1910745	G	G	319	41	299	69	7.688	5.60E-03	rs4275640	11	128661958	q24.3
SNP_A-2077800	G	G	380	14	359	29	5.784	1.62E-02	rs4477446	11	128757186	q24.3
SNP_A-2134432	C	T	200	174	213	177	5.001	0.0253	rs10894034	11	128760828	q24.3
SNP_A-1796105	C	C	349	55	320	86	8.068	4.50E-03	rs4937426	11	128779244	q24.3
SNP_A-2257639	G	G	248	98	269	65	7.324	6.80E-03	rs10750417	11	128987385	q24.3
SNP_A-2282590	A	A	342	34	307	51	4.849	2.77E-02	rs11221846	11	129176261	q24.3
SNP_A-2235204	C	C	347	27	344	52	7.302	6.90E-03	rs10894147	11	129204066	q24.3
SNP_A-2055354	C	C	255	111	273	83	4.517	3.36E-02	rs11221874	11	129218021	q24.3
SNP_A-2187928	G	G	386	10	393	23	4.694	3.03E-02	rs2241572	11	129298658	q24.3
SNP_A-2295623	G	G	370	24	389	9	7.274	7.00E-03	rs11221912	11	129336006	q24.3
SNP_A-1958317	T	T	237	81	217	119	7.611	5.80E-03	rs982125	11	129437536	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2234400	C	C	385	19	380	34	4.156	4.15E-02	rs7117330	11	129447528	q24.3
SNP_A-1781887	G	G	382	20	377	35	4.002	4.55E-02	rs12420010	11	129449062	q24.3
SNP_A-2156008	A	G	223	181	217	201	4.161	4.14E-02	rs2291347	11	129791976	q24.3
SNP_A-2138972	C	C	315	77	350	56	4.914	2.66E-02	rs10894199	11	129814089	q24.3
SNP_A-2210085	A	A	382	30	399	17	3.947	0.047	rs11222142	11	129892968	q24.3
SNP_A-1825746	G	G	326	90	370	50	14.191	2.00E-04	rs4937559	11	130077985	q24.3
SNP_A-2176885	T	T	279	69	322	36	13.309	3.00E-04	rs4245091	11	130078028	q24.3
SNP_A-1883186	A	A	387	23	411	5	12.25	5.00E-04	rs12282812	11	130089442	q24.3
SNP_A-1852861	C	C	369	27	366	10	7.31	6.90E-03	rs7123207	11	130091025	q24.3
SNP_A-2155564	G	G	377	17	407	7	4.823	0.0281	rs12274293	11	130102791	q24.3
SNP_A-2033632	A	A	391	23	412	8	7.764	0.0053	rs7110715	11	130109257	q24.3
SNP_A-1868127	A	A	389	25	411	9	8.092	4.40E-03	rs12284994	11	130121111	q24.3
SNP_A-1827315	A	A	371	39	392	24	4.106	4.27E-02	rs6590504	11	130144888	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1841722	C	C	388	12	372	30	8.046	4.60E-03	rs647516	11	130246285	q24.3
SNP_A-2123593	C	C	322	90	301	117	4.186	0.0407	rs1347281	11	130414199	q25
SNP_A-2258139	C	T	207	197	230	172	5.778	1.62E-02	rs1793562	11	130582649	q25
SNP_A-2272062	C	C	230	176	265	137	7.315	6.80E-03	rs10791130	11	130590320	q25
SNP_A-2032281	T	T	362	46	342	68	4.809	2.83E-02	rs1108340	11	130617523	q25
SNP_A-1932975	C	C	394	18	406	8	4.021	4.49E-02	rs1543121	11	130903744	q25
SNP_A-2024665	A	A	307	95	279	121	4.463	3.46E-02	rs544166	11	131320554	q25
SNP_A-2217705	C	C	341	45	314	72	7.344	6.70E-03	rs497449	11	131335762	q25
SNP_A-2049950	A	A	304	114	337	85	5.906	1.51E-02	rs2846794	11	131374213	q25
SNP_A-2002418	G	G	313	105	340	82	3.926	4.75E-02	rs6590614	11	131455964	q25
SNP_A-1786927	C	C	336	80	315	107	4.533	0.0332	rs10791214	11	131526275	q25
SNP_A-1879610	A	A	218	150	239	121	3.981	4.60E-02	rs4128547	11	131533491	q25
SNP_A-2126408	A	A	208	172	241	149	3.944	0.047	rs3099802	11	131627725	q25
SNP_A-2024797	C	C	218	146	247	119	4.554	3.28E-02	rs718851	11	131633941	q25
SNP_A-1801685	C	C	160	154	200	132	5.64	1.76E-02	rs895925	11	131689489	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1847547	A	A	335	55	374	36	5.616	0.0178	rs2105632	11	131842137	q25
SNP_A-2024803	G	G	353	49	379	33	3.923	4.76E-02	rs2508941	11	131891191	q25
SNP_A-2229937	G	G	304	56	304	82	3.997	4.56E-02	rs11223279	11	132298389	q25
SNP_A-1829332	T	T	309	101	334	78	3.922	4.76E-02	rs11223311	11	132355945	q25
SNP_A-2190389	T	T	314	100	336	76	4.013	4.52E-02	rs11223312	11	132356227	q25
SNP_A-2219168	A	A	304	80	261	97	3.999	4.55E-02	rs7114353	11	132368892	q25
SNP_A-2196148	A	C	215	167	199	167	8.491	3.60E-03	rs7950100	11	132382880	q25
SNP_A-2002432	C	C	258	156	224	194	6.505	1.08E-02	rs4936180	11	132396933	q25
SNP_A-2311062	G	G	242	134	205	169	7.1	7.70E-03	rs4622273	11	132412382	q25
SNP_A-2276332	G	G	320	96	292	122	4.377	3.64E-02	rs11223351	11	132440691	q25
SNP_A-1913731	T	T	252	142	209	179	8.23	4.10E-03	rs476892	11	132574530	q25
SNP_A-1815339	T	T	225	163	192	190	4.63	3.14E-02	rs4073610	11	132752885	q25
SNP_A-2045955	C	C	247	169	217	201	4.702	3.01E-02	rs4638317	11	132756954	q25

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2049413	C	C	355	57	381	39	4.217	4.00E-02	rs7121227	11	132928707	q25
SNP_A-2182130	C	C	381	15	411	5	5.647	1.75E-02	rs2282603	11	133219753	q25
SNP_A-1683552	G	G	378	22	399	11	4.111	4.26E-02	rs715797	11	133234236	q25
SNP_A-1746440	C	C	297	105	333	81	4.979	2.57E-02	rs661820	11	133470304	q25
SNP_A-1784772	C	C	361	19	353	37	5.746	1.65E-02	rs11604455	11	133488076	q25
SNP_A-2224259	G	G	397	13	415	3	6.572	0.0104	rs498602	11	133635384	q25
SNP_A-2180694	A	A	380	28	358	44	4.167	4.12E-02	rs1595895	11	133674016	q25
SNP_A-2064225	G	G	344	18	331	37	6.765	9.30E-03	rs4937902	11	133875643	q25
SNP_A-2064235	T	T	355	15	334	32	6.767	9.30E-03	rs4936235	11	133882013	q25
SNP_A-2179389	A	A	194	156	227	131	4.675	3.06E-02	rs6590746	11	133917124	q25
SNP_A-1831169	G	G	365	43	393	21	8.553	3.40E-03	rs7926027	11	133971866	q25
SNP_A-2086215	G	A	222	196	223	191	4.048	4.42E-02	rs1289504	11	134157118	q25
SNP_A-2178981	C	T	222	192	226	194	4.607	3.18E-02	rs1289502	11	134159370	q25
SNP_A-2256845	C	C	376	28	365	47	4.899	0.0269	rs7305337	12	138615	p13.33
SNP_A-1882811	C	C	382	28	373	45	3.989	0.0458	rs11063291	12	479802	p13.33
SNP_A-1945411	G	G	377	13	386	2	8.168	0.0043	rs748124	12	502850	p13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181396	G	G	395	21	384	36	4.084	4.33E-02	rs11063868	12	591649	p13.33
SNP_A-2270115	C	C	283	91	312	68	4.693	3.03E-02	rs4980951	12	598971	p13.33
SNP_A-2065115	G	G	377	19	369	35	4.747	0.0293	rs11063979	12	611480	p13.33
SNP_A-2002467	G	G	252	160	216	196	6.41	1.13E-02	rs1870199	12	656499	p13.33
SNP_A-2118804	G	G	322	44	317	67	4.375	3.65E-02	rs9804992	12	859155	p13.33
SNP_A-2260355	T	T	200	116	172	144	5.123	2.36E-02	rs2107523	12	1526622	p13.33
SNP_A-1793701	T	T	396	4	412	0	4.14	0.0419	rs4140993	12	1759543	p13.33
SNP_A-2130465	A	A	374	0	372	4	4	4.55E-02	rs16930048	12	2848453	p13.33
SNP_A-2232770	C	C	273	143	313	105	8.548	3.50E-03	rs10848789	12	3065463	p13.33
SNP_A-2300655	G	G	274	92	230	110	4.494	3.40E-02	rs7304958	12	3096200	p13.33
SNP_A-2217171	T	T	279	109	253	137	4.453	3.48E-02	rs7137113	12	3096959	p13.33
SNP_A-2186521	A	A	314	14	328	4	5.837	1.57E-02	rs7954113	12	3125068	p13.32
SNP_A-2101130	T	T	371	27	388	14	4.483	3.42E-02	rs503554	12	3228467	p13.32
SNP_A-2255556	C	C	288	128	254	162	6.119	0.0134	rs581684	12	3229330	p13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1652876	C	C	359	21	348	48	10.411	1.30E-03	rs10491967	12	3238354	p13.32
SNP_A-2027267	G	G	239	139	181	177	12.045	5.00E-04	rs1860436	12	3239435	p13.32
SNP_A-1801339	T	T	240	140	207	195	10.856	0.001	rs4766088	12	3244495	p13.32
SNP_A-1932131	C	C	247	157	206	204	9.786	0.0018	rs11615232	12	3246714	p13.32
SNP_A-1910348	C	C	262	122	222	170	11.115	9.00E-04	rs650180	12	3257542	p13.32
SNP_A-1859255	T	T	247	139	225	175	4.905	2.68E-02	rs544668	12	3258265	p13.32
SNP_A-2164214	T	T	285	85	266	116	5.246	2.20E-02	rs10744601	12	3276163	p13.32
SNP_A-2304795	G	G	325	17	327	33	4.668	3.07E-02	rs17697855	12	3641923	p13.32
SNP_A-2106546	C	C	335	41	308	60	4.623	3.16E-02	rs16930752	12	3720756	p13.32
SNP_A-1881344	G	G	352	12	366	4	4.224	3.99E-02	rs17836369	12	3755299	p13.32
SNP_A-2122896	G	G	393	1	395	7	4.425	3.54E-02	rs6489530	12	4229392	p13.32
SNP_A-1899148	A	A	349	23	373	9	6.791	9.20E-03	rs16931344	12	4365348	p13.32
SNP_A-1863295	T	T	330	84	307	113	5.057	2.45E-02	rs888466	12	4403866	p13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082639	T	T	373	21	362	36	4.092	4.31E-02	rs2241282	12	4422492	p13.32
SNP_A-2108568	G	G	332	8	369	1	6.141	0.0132	rs2286577	12	4584207	p13.32
SNP_A-1828422	A	A	368	22	363	41	5.519	1.88E-02	rs7977127	12	4643571	p13.32
SNP_A-1919671	C	C	337	7	330	0	6.786	9.20E-03	rs1548	12	4676814	p13.32
SNP_A-1820024	A	G	215	165	194	182	5.065	2.44E-02	rs2286580	12	4740189	p13.32
SNP_A-1755156	C	C	368	24	358	44	5.895	0.0152	rs10492062	12	4907076	p13.32
SNP_A-2224501	C	C	367	33	341	55	6.435	0.0112	rs16933924	12	4934158	p13.32
SNP_A-1900302	C	C	255	99	248	66	4.318	3.77E-02	rs7313827	12	4962182	p13.32
SNP_A-2048444	C	C	323	39	304	58	4.297	3.82E-02	rs1157755	12	4967102	p13.32
SNP_A-1812170	G	G	198	150	225	121	4.821	0.0281	rs7964076	12	4983803	p13.32
SNP_A-1890462	C	C	355	61	383	37	6.921	8.50E-03	rs12099807	12	5000615	p13.32
SNP_A-2301777	C	C	344	58	356	38	4.292	3.83E-02	rs10849216	12	5193223	p13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2211820	G	G	280	126	310	100	4.497	3.40E-02	rs740901	12	5314401	p13.31
SNP_A-2028977	G	G	295	37	322	8	19.865	8.31E-06	rs17778948	12	5348374	p13.31
SNP_A-1714911	G	G	272	112	246	150	6.633	0.01	rs10492094	12	5348409	p13.31
SNP_A-2029004	C	C	352	64	326	90	5.387	2.03E-02	rs11063686	12	5434802	p13.31
SNP_A-2238270	C	C	357	27	383	13	5.63	0.0177	rs11609912	12	5573082	p13.31
SNP_A-2299181	C	C	199	159	242	118	10.256	0.0014	rs216312	12	5999245	p13.31
SNP_A-1886588	A	A	265	87	279	63	4.057	4.40E-02	rs11610629	12	6007717	p13.31
SNP_A-2293510	C	C	279	81	316	60	5.083	2.42E-02	rs1800380	12	6008856	p13.31
SNP_A-2025642	C	C	247	115	295	91	6.283	1.22E-02	rs216327	12	6016410	p13.31
SNP_A-1883139	C	T	175	159	203	135	10.486	1.20E-03	rs216291	12	6022134	p13.31
SNP_A-2028077	T	T	235	115	265	83	6.966	8.30E-03	rs1063857	12	6023775	p13.31
SNP_A-2203853	A	A	299	59	336	36	7.459	0.0063	rs7139057	12	6039584	p13.31
SNP_A-2213286	A	A	284	54	255	81	6.954	8.40E-03	rs11064153	12	6358711	p13.31
SNP_A-2078815	G	G	297	113	312	86	3.855	4.96E-02	rs2364493	12	6415792	p13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2139106	G	G	256	100	233	125	3.854	4.96E-02	rs4469949	12	6415872	p13.31
SNP_A-1888566	C	C	386	10	401	3	3.976	4.62E-02	rs2365031	12	6617480	p13.31
SNP_A-1801300	C	C	391	23	409	9	6.511	1.07E-02	rs11064432	12	6839002	p13.31
SNP_A-2146759	G	G	224	120	237	91	3.974	4.62E-02	rs10840686	12	8152917	p13.31
SNP_A-1733340	A	A	261	139	296	116	4.097	4.30E-02	rs2110067	12	8160264	p13.31
SNP_A-2144446	T	T	346	4	362	0	4.161	4.14E-02	rs11043718	12	8211560	p13.31
SNP_A-2290970	C	C	391	21	389	9	4.565	3.26E-02	rs12229240	12	8332082	p13.31
SNP_A-2002511	T	T	292	98	311	73	4.207	0.0402	rs4304840	12	8559164	p13.31
SNP_A-1922472	A	A	320	22	360	10	5.761	1.64E-02	rs1561555	12	8673170	p13.31
SNP_A-1791795	G	G	349	53	321	87	9.383	2.20E-03	rs4883181	12	8672912	p13.31
SNP_A-2051589	G	G	308	54	250	90	14.353	2.00E-04	rs4883182	12	8873123	p13.31
SNP_A-2002513	T	T	355	55	330	84	6.944	8.40E-03	rs7978604	12	8892984	p13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2054409	G	G	198	142	220	112	4.607	3.18E-02	rs7488933	12	8902779	p13.31
SNP_A-1708394	C	C	302	96	285	125	4.12	0.0424	rs3026252	12	9051501	p13.31
SNP_A-1742553	T	T	396	4	412	0	4.14	0.0419	rs2889717	12	9178068	p13.31
SNP_A-2308409	C	C	365	29	347	47	4.718	0.0298	rs11609486	12	9297349	p13.31
SNP_A-2235187	C	C	323	13	344	4	5.217	0.0224	rs10843579	12	9422514	p13.31
SNP_A-1908235	C	C	339	55	354	36	4.271	3.88E-02	rs4439599	12	9706049	p13.31
SNP_A-2305852	C	C	319	35	330	20	4.255	3.91E-02	rs17732859	12	9713048	p13.31
SNP_A-2102167	C	C	294	100	255	135	7.963	4.80E-03	rs2114870	12	9714407	p13.31
SNP_A-1822608	C	C	270	78	228	110	8.845	2.90E-03	rs11052372	12	9723226	p13.31
SNP_A-2031467	A	A	295	117	259	157	8.16	0.0043	rs10772079	12	9765661	p13.31
SNP_A-2244522	C	C	309	103	341	79	4.664	3.08E-02	rs4763865	12	9790776	p13.31
SNP_A-2279446	G	G	274	96	312	74	4.975	2.57E-02	rs6416258	12	9801264	p13.31
SNP_A-1959413	G	G	291	31	349	15	8.281	4.00E-03	rs10844837	12	9844069	p13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2031750	A	G	212	184	214	174	5.921	1.50E-02	rs608418	12	10023132	p13.31
SNP_A-1702595	C	C	389	11	406	2	6.516	1.07E-02	rs10492104	12	10980792	p13.2
SNP_A-1825378	A	A	277	107	251	135	4.515	3.36E-02	rs7310849	12	11058235	p13.2
SNP_A-1734858	C	C	235	97	242	144	5.237	2.21E-02	rs2900208	12	11769731	p13.2
SNP_A-1683928	A	A	249	145	223	177	4.567	3.26E-02	rs2856338	12	11796019	p13.2
SNP_A-2034823	G	G	315	83	346	62	4.372	3.65E-02	rs2909001	12	12099845	p13.2
SNP_A-1903577	G	G	264	134	296	108	4.577	3.24E-02	rs10845472	12	12129422	p13.2
SNP_A-2298260	C	C	367	45	385	29	3.885	0.0487	rs12582396	12	12627386	p13.2
SNP_A-2090535	G	G	364	16	359	5	5.455	0.0195	---	12	12681694	p13.2
SNP_A-2033745	C	C	245	161	272	130	4.693	3.03E-02	rs3759218	12	12996267	p13.1
SNP_A-1899477	A	A	226	184	248	150	4.305	3.80E-02	rs3825272	12	13046606	p13.1
SNP_A-2125388	C	C	238	178	274	144	6.117	0.0134	rs7294646	12	13093286	p13.1
SNP_A-1748491	C	C	397	3	394	18	10.551	1.20E-03	rs10505773	12	13268206	p13.1
SNP_A-2195300	G	T	237	171	217	193	9.951	1.60E-03	rs4316597	12	13339224	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2044423	C	C	307	91	334	64	5.841	1.57E-02	rs6488602	12	13370668	p13.1
SNP_A-2235654	A	A	316	100	332	72	4.779	2.88E-02	rs10744020	12	13370752	p13.1
SNP_A-2033954	T	T	347	45	317	67	5.595	1.80E-02	rs17338848	12	13377696	p13.1
SNP_A-2033975	A	A	247	121	215	147	4.69	3.03E-02	rs767839	12	13402363	p13.1
SNP_A-1728319	C	C	267	131	248	164	4.152	4.16E-02	rs10492121	12	13403627	p13.1
SNP_A-1641841	T	T	263	129	247	165	4.415	0.0356	rs1993510	12	13404741	p13.1
SNP_A-1730725	A	A	265	131	247	165	4.223	3.99E-02	-	12	13405336	p13.1
SNP_A-2178562	A	A	269	125	242	158	5.23	2.22E-02	rs2060302	12	13414016	p13.1
SNP_A-2302854	A	A	300	116	276	144	3.996	4.56E-02	rs7310876	12	13450634	p13.1
SNP_A-1888150	G	G	345	55	330	82	5.478	1.93E-02	rs7303009	12	13462559	p13.1
SNP_A-2083275	C	C	247	133	214	168	6.427	0.0112	rs11055425	12	13476784	p13.1
SNP_A-1656425	T	T	205	191	237	167	3.846	0.0499	rs2160734	12	13875616	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1834111	C	C	388	6	394	16	4.275	3.87E-02	rs11055719	12	14055747	p13.1
SNP_A-1765845	C	C	317	19	355	9	4.608	3.18E-02	rs11055738	12	14096540	p13.1
SNP_A-2138103	A	A	330	58	362	40	4.539	3.31E-02	rs2241221	12	14850658	p12.3
SNP_A-1797723	C	C	205	175	230	140	5.193	2.27E-02	rs10772807	12	14876098	p12.3
SNP_A-2297490	T	T	191	173	212	126	7.53	6.10E-03	rs2287226	12	14878363	p12.3
SNP_A-1699879	G	G	210	166	240	130	6.331	1.19E-02	rs1001096	12	14879722	p12.3
SNP_A-2260864	G	G	222	168	260	120	10.868	0.001	rs7301929	12	14893772	p12.3
SNP_A-2152512	A	A	210	166	254	122	10.895	0.001	rs7294463	12	14894575	p12.3
SNP_A-2035191	T	G	192	160	190	160	5.475	1.93E-02	rs2098434	12	14895807	p12.3
SNP_A-2035198	C	C	246	170	276	144	3.858	4.95E-02	rs10492151	12	14917332	p12.3
SNP_A-2035199	C	C	197	171	224	128	7.564	6.00E-03	rs725444	12	14920710	p12.3
SNP_A-2035204	C	C	205	149	251	115	8.822	3.00E-03	rs1544687	12	14921971	p12.3
SNP_A-1803311	T	T	185	129	216	98	6.63	0.01	rs4763403	12	14922635	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2120851	C	C	231	173	274	142	6.538	0.0106	rs6488724	12	14924028	p12.3
SNP_A-1916271	A	A	277	115	307	91	4.292	3.83E-02	rs4763407	12	14996827	p12.3
SNP_A-2204779	T	T	206	132	222	98	5.136	2.34E-02	rs12578517	12	15298452	p12.3
SNP_A-2035525	G	G	391	17	381	31	4.193	4.06E-02	rs1020851	12	15454974	p12.3
SNP_A-2035786	C	C	356	0	331	5	5.336	2.09E-02	rs16911389	12	15932868	p12.3
SNP_A-1694637	A	A	333	67	357	45	5.151	2.32E-02	rs10505790	12	16117419	p12.3
SNP_A-2117480	G	A	235	179	214	202	5.604	1.79E-02	rs10744116	12	16368136	p12.3
SNP_A-2135391	C	C	323	7	331	21	6.395	0.0114	rs10744125	12	16498124	p12.3
SNP_A-1705655	G	G	300	66	288	102	7.205	7.30E-03	rs10492193	12	16770504	p12.3
SNP_A-2074336	G	G	202	128	220	98	4.529	3.33E-02	rs10082759	12	16828087	p12.3
SNP_A-2186673	A	A	273	67	226	86	5.594	1.80E-02	rs10846428	12	16845400	p12.3
SNP_A-1894580	C	C	287	71	306	44	6.858	8.80E-03	rs7974666	12	17135652	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1898435	A	A	392	12	394	4	3.96	4.66E-02	rs16912645	12	17389157	p12.3
SNP_A-1793162	T	T	201	167	224	138	3.953	4.68E-02	rs2936207	12	17410570	p12.3
SNP_A-2158436	C	C	330	18	294	30	4.225	3.98E-02	rs10840734	12	17561056	p12.3
SNP_A-1820206	A	G	240	176	218	200	8.109	4.40E-03	rs1912879	12	17574784	p12.3
SNP_A-1878971	A	A	328	32	307	59	8.656	0.0033	rs11043491	12	17575942	p12.3
SNP_A-2021081	A	A	269	123	247	153	4.118	0.0424	rs4763476	12	17652489	p12.3
SNP_A-2137258	T	T	251	123	233	155	4.097	4.30E-02	rs2467124	12	17725821	p12.3
SNP_A-2249819	C	C	269	63	240	86	5.148	2.33E-02	rs4319561	12	17855570	p12.3
SNP_A-2229679	C	C	362	6	354	18	6.068	0.0138	rs10840935	12	18066849	p12.3
SNP_A-1798819	A	A	254	124	277	89	6.556	1.05E-02	rs7134343	12	18197747	p12.3
SNP_A-2174602	G	G	344	32	308	66	13.778	2.00E-04	rs4340104	12	18207216	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1859716	G	G	208	186	233	155	4.19	0.0407	rs11043903	12	18208260	p12.3
SNP_A-2282459	C	C	272	132	300	100	5.765	1.64E-02	rs4491292	12	18212721	p12.3
SNP_A-2120944	C	C	218	184	256	162	4.135	4.20E-02	rs4764383	12	18237964	p12.3
SNP_A-2089794	T	T	347	53	327	79	5.67	1.73E-02	rs4539389	12	18260963	p12.3
SNP_A-1815054	T	T	305	53	280	74	4.518	3.35E-02	rs12581163	12	18466821	p12.3
SNP_A-2223529	T	T	304	72	268	94	4.918	2.66E-02	rs12371624	12	18505213	p12.3
SNP_A-2037071	C	C	166	148	195	121	5.033	2.49E-02	rs1374670	12	18528429	p12.3
SNP_A-1872679	A	A	302	72	276	94	4.064	4.38E-02	rs10770370	12	18593191	p12.3
SNP_A-1814483	A	A	383	13	389	3	6.276	1.22E-02	rs7961337	12	18855833	p12.3
SNP_A-1914878	T	T	397	19	410	8	4.686	0.0304	rs16914906	12	18995227	p12.3
SNP_A-1954913	G	G	362	4	380	0	4.175	4.10E-02	rs1344716	12	19410533	p12.3
SNP_A-2191904	G	G	280	54	305	37	4.15	4.16E-02	rs751082	12	19423264	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1790556	A	A	215	201	248	172	4.588	3.22E-02	rs12581840	12	19725418	p12.3
SNP_A-1943106	A	A	385	17	394	6	5.36	0.0206	rs11044914	12	19913045	p12.2
SNP_A-2039395	A	A	394	20	381	35	4.304	3.80E-02	rs763963	12	19929686	p12.2
SNP_A-1678262	C	C	216	184	260	150	7.406	6.50E-03	rs1527260	12	19971799	p12.2
SNP_A-2188450	T	T	233	129	275	93	9.262	0.0023	rs10734694	12	19980066	p12.2
SNP_A-2076704	T	T	347	41	355	25	3.887	0.0487	rs10841428	12	20047115	p12.2
SNP_A-1870424	G	G	370	28	364	46	4.25	3.92E-02	rs2728620	12	20048750	p12.2
SNP_A-2021051	A	A	334	32	318	50	4.338	0.0373	rs2248385	12	20077657	p12.2
SNP_A-1918744	C	C	234	148	257	113	5.581	1.82E-02	rs2417849	12	20167780	p12.2
SNP_A-2038104	G	G	251	149	281	111	7.165	7.40E-03	rs2303658	12	20169697	p12.2
SNP_A-1915038	C	C	217	169	240	138	4.205	4.03E-02	rs12821841	12	20175182	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1798365	T	T	351	25	367	11	5.796	0.0161	rs7312851	12	20287520	p12.2
SNP_A-2178769	A	A	321	65	344	38	7.853	5.10E-03	rs10841527	12	20488570	p12.2
SNP_A-1861195	G	G	260	70	245	99	5.133	0.0235	rs11045323	12	20640821	p12.2
SNP_A-1711754	A	A	288	112	266	142	4.338	0.0373	rs1995409	12	21063131	p12.2
SNP_A-1853259	T	T	353	53	368	34	4.442	3.51E-02	rs11045802	12	21203587	p12.1
SNP_A-2237613	T	T	320	52	353	35	4.605	3.19E-02	rs11045986	12	21388508	p12.1
SNP_A-1861520	G	G	271	65	243	87	4.656	0.0309	rs10841833	12	21528492	p12.1
SNP_A-1814125	C	C	274	102	236	126	5.094	0.024	rs4762834	12	21549121	p12.1
SNP_A-1653524	C	C	227	173	260	148	4.104	4.28E-02	rs829080	12	21891130	p12.1
SNP_A-2297026	G	G	329	77	340	50	5.602	1.79E-02	rs10841915	12	21990928	p12.1
SNP_A-1802600	A	A	413	3	403	15	8.118	4.40E-03	rs1487429	12	22805858	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1807839	A	A	199	177	237	139	7.882	5.00E-03	rs7974864	12	22879652	p12.1
SNP_A-2242170	C	C	231	181	263	149	5.176	0.0229	rs2433642	12	22883808	p12.1
SNP_A-2043767	A	A	186	182	218	152	5.224	0.0223	rs7133927	12	22883913	p12.1
SNP_A-2238985	T	T	216	158	239	127	4.449	0.0349	rs2433643	12	22884045	p12.1
SNP_A-1851655	T	T	400	4	404	0	4.02	4.50E-02	rs4964072	12	23241057	p12.1
SNP_A-2090148	A	A	237	101	219	129	3.974	4.62E-02	rs11046932	12	23516901	p12.1
SNP_A-1931764	G	G	331	55	298	76	4.909	2.67E-02	rs1479457	12	23689385	p12.1
SNP_A-2055370	T	T	379	17	385	7	4.194	4.06E-02	rs7977312	12	23941586	p12.1
SNP_A-1874579	T	T	388	24	408	10	6.224	0.0126	—	12	24034803	p12.1
SNP_A-2289987	C	C	371	13	397	3	6.807	9.10E-03	rs12301278	12	24305559	p12.1
SNP_A-2058050	G	G	349	57	375	35	6.175	1.30E-02	rs10771099	12	24631571	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027365	A	A	332	44	357	21	9.04	2.60E-03	rs7976009	12	24636804	p12.1
SNP_A-2041291	G	G	329	85	355	61	4.929	0.0264	rs4963579	12	24671124	p12.1
SNP_A-2270083	G	G	335	53	352	32	5.588	1.81E-02	rs7974956	12	24688241	p12.1
SNP_A-2041308	C	C	210	112	257	95	4.801	2.85E-02	rs10505942	12	24690213	p12.1
SNP_A-2041321	C	C	258	148	289	117	5.383	2.03E-02	rs1487654	12	24711998	p12.1
SNP_A-1859050	C	C	289	123	316	94	5.076	2.43E-02	rs7961989	12	24714774	p12.1
SNP_A-2030202	A	A	373	13	362	26	4.493	3.40E-02	rs12830440	12	24790052	p12.1
SNP_A-2051329	C	C	289	79	297	55	4.054	0.0441	rs10771148	12	25005142	p12.1
SNP_A-2039316	C	C	292	82	300	54	5.327	2.10E-02	rs2645906	12	25008750	p12.1
SNP_A-2041909	A	A	371	31	346	48	4.45	0.0349	rs10505975	12	25367486	p12.1
SNP_A-2223938	C	C	269	85	299	63	4.766	2.90E-02	rs11048055	12	25513619	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2152783	A	A	355	57	374	36	5.232	2.22E-02	rs7978644	12	25819197	p12.1
SNP_A-1883939	C	C	366	18	365	7	4.652	0.031	rs9943745	12	25863790	p12.1
SNP_A-2224552	A	A	389	21	399	9	4.922	2.65E-02	rs16929511	12	25891187	p12.1
SNP_A-2297806	G	G	374	4	373	15	6.24	1.25E-02	rs829986	12	26009784	p12.1
SNP_A-2268642	C	G	229	187	217	201	4.046	4.43E-02	rs1480033	12	26142847	p12.1
SNP_A-2234339	C	C	352	22	324	36	4.274	3.87E-02	rs2620694	12	26153404	p12.1
SNP_A-2288652	G	G	276	74	262	110	6.744	9.40E-03	rs7972367	12	26158915	p12.1
SNP_A-1699339	C	C	255	145	232	180	4.679	3.05E-02	rs1048155	12	26164355	p12.1
SNP_A-2021679	A	A	278	116	246	150	6.295	0.0121	rs7134738	12	26249437	p12.1
SNP_A-1939513	G	G	284	64	277	91	4.235	3.96E-02	rs4963997	12	26489079	p11.23
SNP_A-2168667	T	T	275	113	236	138	5.211	0.0224	rs2170980	12	26513365	p11.23
SNP_A-2300169	T	T	313	59	287	79	3.977	4.61E-02	rs11614778	12	26566134	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2261548	A	A	301	25	270	38	3.858	4.95E-02	rs7137796	12	26586394	p11.23
SNP_A-2089399	A	A	334	74	292	98	5.764	1.64E-02	rs11611069	12	26592373	p11.23
SNP_A-1712757	C	C	373	27	395	15	3.936	4.73E-02	rs10506003	12	26597144	p11.23
SNP_A-1834080	T	T	317	47	317	71	4.12	0.0424	rs17476787	12	26650293	p11.23
SNP_A-1875755	T	T	341	37	363	21	5.054	0.0246	rs3782300	12	26685470	p11.23
SNP_A-2043299	T	T	374	38	385	19	6.415	1.13E-02	rs2880876	12	26689832	p11.23
SNP_A-2242048	C	C	313	35	364	22	4.853	0.0276	rs2306550	12	26700804	p11.23
SNP_A-1827354	T	T	199	167	217	123	6.506	1.08E-02	rs10771311	12	26954224	p11.23
SNP_A-1823140	T	T	256	142	274	112	3.972	4.63E-02	rs11048881	12	27177854	p11.23
SNP_A-1845306	C	C	220	112	254	88	5.172	0.023	rs7303320	12	27234450	p11.23
SNP_A-2092696	A	A	215	167	248	142	4.292	3.83E-02	rs10842885	12	27291048	p11.23
SNP_A-1800506	C	C	233	71	277	55	4.604	3.19E-02	rs10771326	12	27292614	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1928237	C	C	390	22	403	9	5.665	1.73E-02	rs16931982	12	27501714	p11.23
SNP_A-1724906	T	T	368	20	390	6	8.096	4.40E-03	rs306640	12	27512827	p11.23
SNP_A-2135975	T	T	337	35	322	62	7.668	5.60E-03	rs11049255	12	28027256	p11.22
SNP_A-2247019	T	T	386	2	388	12	6.967	8.30E-03	rs7957918	12	28101865	p11.22
SNP_A-2281778	T	T	373	7	375	17	3.986	4.59E-02	rs1464014	12	28616157	p11.22
SNP_A-1841264	T	G	180	160	172	136	4.992	2.55E-02	rs11049732	12	28636189	p11.22
SNP_A-2153978	G	G	254	136	287	113	4.011	4.52E-02	rs10843221	12	28659885	p11.22
SNP_A-2044783	G	G	223	131	180	164	8.138	0.0043	rs1531680	12	28840469	p11.22
SNP_A-1872286	C	A	223	183	219	191	5.678	0.0172	rs309045	12	28840592	p11.22
SNP_A-2267615	C	C	212	136	181	169	6.01	1.42E-02	rs309046	12	28840623	p11.22
SNP_A-1725758	T	T	389	5	386	20	8.834	3.00E-03	rs1480640	12	28903250	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2154527	C	C	389	9	385	21	4.742	2.94E-02	rs11049889	12	28914564	p11.22
SNP_A-1913738	C	C	404	12	396	24	4.061	4.39E-02	rs7294610	12	28915634	p11.22
SNP_A-1805294	G	G	222	160	198	190	3.896	4.84E-02	rs1021312	12	28922763	p11.22
SNP_A-2085838	T	T	284	122	319	97	4.764	2.91E-02	rs1383389	12	28923766	p11.22
SNP_A-2096864	T	T	193	123	163	149	4.988	2.55E-02	rs1383386	12	28927714	p11.22
SNP_A-1729242	G	G	235	165	208	204	5.591	1.80E-02	rs1601981	12	28961846	p11.22
SNP_A-1813123	T	T	306	88	285	115	4.292	3.83E-02	rs1387243	12	28984791	p11.22
SNP_A-2022266	G	G	247	81	225	105	4.116	4.25E-02	rs11050359	12	29715591	p11.22
SNP_A-1865281	A	A	321	57	335	35	5.475	1.93E-02	rs1549407	12	29731130	p11.22
SNP_A-1803457	G	G	339	7	361	1	4.832	2.79E-02	rs441394	12	29807560	p11.22
SNP_A-1847457	C	C	209	137	190	176	5.206	2.25E-02	rs4032492	12	30062164	p11.22
SNP_A-2257718	C	C	263	139	237	169	4.254	3.91E-02	rs11615860	12	30066479	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2290103	C	C	372	4	376	0	4.021	4.49E-02	rs11050624	12	30108687	p11.22
SNP_A-1874496	A	A	278	132	239	175	8.946	0.0028	rs12579700	12	30119734	p11.22
SNP_A-1931185	T	T	355	27	343	53	8.407	3.70E-03	rs17459648	12	30247482	p11.22
SNP_A-2255480	G	G	261	71	239	99	5.526	1.87E-02	rs4931292	12	30271808	p11.22
SNP_A-2176357	G	G	293	105	263	139	6.337	0.0118	rs7970841	12	30274289	p11.22
SNP_A-2098224	G	G	284	96	248	120	4.912	2.67E-02	rs10843669	12	30276019	p11.22
SNP_A-2046287	A	A	272	86	242	122	7.932	4.90E-03	rs977924	12	30282488	p11.22
SNP_A-2177063	C	C	332	50	371	35	4.083	4.33E-02	rs17522293	12	30313502	p11.22
SNP_A-1726374	C	C	324	20	328	36	4.034	4.46E-02	rs2700047	12	30314323	p11.22
SNP_A-2293915	T	T	353	59	379	39	4.962	2.59E-02	rs1346673	12	30327552	p11.22
SNP_A-1890201	A	A	334	64	357	45	4.058	4.40E-02	rs1731491	12	30352718	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1695783	T	T	329	71	364	46	6.987	8.20E-03	rs1320925	12	30353247	p11.22
SNP_A-1877400	A	A	331	67	360	48	4.233	3.97E-02	rs11050819	12	30364760	p11.22
SNP_A-1908015	C	C	333	65	363	47	4.009	0.0453	rs4426203	12	30366150	p11.22
SNP_A-2108176	T	T	334	66	364	44	5.611	1.79E-02	rs4564417	12	30366169	p11.22
SNP_A-2110274	T	T	302	70	337	49	5.366	2.05E-02	rs12313162	12	30366657	p11.22
SNP_A-2126752	T	T	303	51	348	34	5.453	0.0195	rs4444166	12	30375484	p11.22
SNP_A-1871453	C	C	344	68	373	45	5.811	1.59E-02	rs7977589	12	30376190	p11.22
SNP_A-2178021	C	C	334	56	355	33	6.579	0.0103	rs11050827	12	30377460	p11.22
SNP_A-2046541	A	A	331	59	351	33	7.888	5.00E-03	rs906114	12	30377530	p11.22
SNP_A-2308905	T	T	321	45	358	28	5.447	1.96E-02	rs10843721	12	30377571	p11.22
SNP_A-2107012	C	C	328	34	371	21	4.531	3.33E-02	rs16906208	12	30380098	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2089142	C	C	353	59	376	40	4.353	3.69E-02	rs17467054	12	30383823	p11.22
SNP_A-2046564	G	G	322	52	341	33	4.792	0.0286	rs7975892	12	30387886	p11.22
SNP_A-2265482	G	G	317	43	352	26	5.584	1.81E-02	rs10843724	12	30388396	p11.22
SNP_A-2046567	C	C	334	36	362	16	8.734	3.10E-03	rs10843727	12	30388891	p11.22
SNP_A-2046573	C	C	333	41	363	27	3.842	5.00E-02	rs10506067	12	30389285	p11.22
SNP_A-1854614	T	T	289	49	316	28	6.88	8.70E-03	rs11050844	12	30390159	p11.22
SNP_A-1866987	G	G	327	35	356	20	5.058	2.45E-02	rs11050846	12	30390654	p11.22
SNP_A-2154303	C	C	346	54	370	34	5.33	2.10E-02	rs7139306	12	30391138	p11.22
SNP_A-1914479	C	C	354	62	378	42	4.614	3.17E-02	rs6487902	12	30391185	p11.22
SNP_A-2074245	G	G	335	49	362	26	8.079	4.50E-03	rs12579259	12	30395202	p11.22
SNP_A-1928063	A	A	349	63	380	40	6.378	1.16E-02	rs11050857	12	30396177	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2199423	C	C	351	65	380	40	7.084	7.80E-03	rs354128	12	30396803	p11.22
SNP_A-1889548	A	A	351	59	373	41	3.889	4.86E-02	rs12582684	12	30403008	p11.22
SNP_A-2279485	T	T	325	51	339	31	5.125	2.36E-02	rs4608177	12	30403999	p11.22
SNP_A-2053938	C	C	341	51	373	31	6.133	1.33E-02	rs16906306	12	30409374	p11.22
SNP_A-2274703	C	C	345	51	366	32	4.965	2.59E-02	rs12582654	12	30409804	p11.22
SNP_A-2240310	C	C	354	62	377	43	4.143	4.18E-02	rs7299777	12	30410003	p11.22
SNP_A-1880397	T	T	340	76	374	38	14.267	2.00E-04	rs354113	12	30425805	p11.22
SNP_A-2299409	C	C	189	183	207	147	4.302	3.81E-02	rs7979416	12	30446335	p11.22
SNP_A-2213728	G	G	351	55	331	77	4.248	3.93E-02	rs1506392	12	30523465	p11.22
SNP_A-1847524	T	T	381	29	354	52	7.503	6.20E-03	rs11050927	12	30540265	p11.22
SNP_A-2289212	G	G	333	21	350	8	6.228	0.0126	rs7297184	12	30549910	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100621	C	C	259	113	291	81	7.14	7.50E-03	rs7971194	12	30599451	p11.22
SNP_A-2172881	T	T	355	49	324	76	7.228	7.20E-03	rs4931349	12	30603088	p11.21
SNP_A-2104335	C	C	358	52	327	73	4.808	2.83E-02	rs7300712	12	30610535	p11.21
SNP_A-1788441	A	A	353	53	314	86	10.071	0.0015	rs10843781	12	30611145	p11.21
SNP_A-2039950	A	G	223	191	226	180	7.448	0.0063	rs6487923	12	30673179	p11.21
SNP_A-1799475	T	C	221	189	226	178	7.889	5.00E-03	rs7327	12	30673343	p11.21
SNP_A-2263039	A	A	345	67	377	41	7.635	5.70E-03	rs33270	12	30677026	p11.21
SNP_A-2052370	T	C	201	165	204	150	11.335	8.00E-04	rs4143105	12	30682221	p11.21
SNP_A-2232100	A	G	217	185	235	179	9.424	2.10E-03	rs10771748	12	30687282	p11.21
SNP_A-1893661	G	C	219	187	231	177	9.081	2.60E-03	rs3910561	12	30691307	p11.21
SNP_A-2110630	A	A	360	20	370	6	7.654	5.70E-03	rs7974489	12	30700759	p11.21
SNP_A-2089196	G	C	206	180	223	171	7.756	5.40E-03	rs6487925	12	30701710	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2112328	C	T	210	190	235	175	7.824	5.20E-03	rs10743728	12	30707175	p11.21
SNP_A-2002635	G	A	219	157	216	172	14.797	0.0001	rs6487939	12	30791949	p11.21
SNP_A-1908717	C	T	211	137	195	165	15.561	7.99E-05	rs10771767	12	30793505	p11.21
SNP_A-1855894	T	T	353	47	368	28	5.105	2.39E-02	rs11051065	12	30810416	p11.21
SNP_A-2186032	T	T	314	66	269	83	4.348	3.70E-02	rs7312385	12	30824551	p11.21
SNP_A-2220742	C	C	330	78	306	104	4.615	3.17E-02	rs33229	12	30923612	p11.21
SNP_A-2127551	A	A	296	84	271	117	6.438	0.0112	rs1485349	12	30927043	p11.21
SNP_A-2181716	G	G	306	92	330	70	3.888	4.86E-02	rs11051137	12	30929148	p11.21
SNP_A-2281842	T	T	300	72	277	99	5.159	2.31E-02	rs10843854	12	30946411	p11.21
SNP_A-2105658	A	A	260	138	298	112	5.115	2.37E-02	rs10771781	12	30979399	p11.21
SNP_A-1872396	T	T	239	141	276	114	5.388	2.03E-02	rs10843871	12	31028407	p11.21
SNP_A-2263803	C	C	231	165	258	138	3.897	4.84E-02	rs35068	12	31039929	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2208140	C	C	277	107	237	155	11.826	6.00E-04	rs7971718	12	31202250	p11.21
SNP_A-2175905	A	A	333	41	364	18	10.261	0.0014	rs7136266	12	31243957	p11.21
SNP_A-2186365	G	G	268	118	316	92	6.56	0.0104	rs2053202	12	31284729	p11.21
SNP_A-1876978	T	C	198	158	164	136	6.891	8.70E-03	rs7313889	12	31463494	p11.21
SNP_A-1655671	A	A	356	38	387	21	5.949	0.0147	rs1259633	12	31817644	p11.21
SNP_A-2048285	C	C	369	9	372	20	3.931	4.74E-02	rs17510714	12	31997716	p11.21
SNP_A-1887656	G	G	325	61	349	43	3.924	4.76E-02	rs17587471	12	32225759	p11.21
SNP_A-2272734	A	A	276	86	249	109	4.079	4.34E-02	rs753296	12	32326780	p11.21
SNP_A-2122884	C	C	224	178	248	142	5.09	0.0241	rs1239576	12	32340866	p11.21
SNP_A-2178563	A	A	345	69	325	93	4.133	4.20E-02	---	12	32350337	p11.21
SNP_A-2232555	T	T	280	130	253	157	3.908	4.81E-02	rs7314141	12	32421314	p11.21
SNP_A-2144733	G	G	345	63	373	43	4.788	0.0287	rs12825217	12	32838827	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1947574	T	T	303	99	338	76	4.758	0.0292	rs12305595	12	33156845	p11.21
SNP_A-1680892	T	T	295	101	331	81	3.953	4.68E-02	rs7303471	12	33162179	p11.21
SNP_A-1832077	C	C	350	60	369	35	7.037	8.00E-03	rs9971778	12	33271192	p11.1
SNP_A-2028776	C	C	355	61	378	40	5.083	2.42E-02	rs4244864	12	33290320	p11.1
SNP_A-1823804	C	C	341	47	364	26	6.786	9.20E-03	rs12820860	12	33291012	p11.1
SNP_A-2049377	C	C	239	91	245	63	4.412	3.57E-02	rs6488154	12	33401684	p11.1
SNP_A-1875833	T	T	264	132	236	158	3.894	4.85E-02	rs4244865	12	33403184	p11.1
SNP_A-1909277	T	T	349	35	360	20	4.241	0.0395	rs11615703	12	33576925	p11.1
SNP_A-2168340	C	C	335	21	342	10	3.953	4.68E-02	rs7132946	12	33581116	p11.1
SNP_A-1810006	G	G	408	4	414	0	4.039	4.45E-02	rs11052776	12	33645925	p11.1
SNP_A-2023900	G	G	266	134	238	164	4.571	3.25E-02	rs717712	12	33665887	p11.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936215	C	C	406	4	416	0	4.078	4.34E-02	rs16921184	12	33683806	p11.1
SNP_A-2270886	C	T	193	185	210	162	4.242	3.94E-02	rs7954221	12	33716344	p11.1
SNP_A-2049695	G	G	363	11	392	2	6.828	9.00E-03	rs11052835	12	33720607	p11.1
SNP_A-2121217	G	G	257	109	238	148	6.12	0.0134	rs7306435	12	34374200	p11.1
SNP_A-2046054	C	C	394	22	406	10	4.68	3.05E-02	rs11183045	12	36941499	q12
SNP_A-2197255	T	T	337	9	312	2	3.875	4.90E-02	rs11183414	12	37022586	q12
SNP_A-2079990	C	C	356	18	361	7	4.827	2.80E-02	rs7488727	12	37066328	q12
SNP_A-2025855	G	G	380	32	389	17	4.653	0.031	rs10783214	12	37174489	q12
SNP_A-2137292	C	C	323	15	346	6	4.366	3.67E-02	rs7488463	12	37179686	q12
SNP_A-2295654	A	A	369	23	375	11	4.238	0.0395	rs14866343	12	37328679	q12
SNP_A-1884923	T	T	200	120	167	145	5.225	0.0223	rs11169511	12	37462069	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2236851	C	C	384	4	398	0	4.124	4.23E-02	rs1516556	12	37641948	q12
SNP_A-1786809	T	T	315	37	317	59	4.261	0.039	rs7953145	12	37852025	q12
SNP_A-2051181	T	T	385	11	397	3	4.736	2.95E-02	rs17127112	12	38082147	q12
SNP_A-2118568	C	C	374	34	380	16	6.35	0.0117	rs17127259	12	38589898	q12
SNP_A-2169869	G	G	403	5	402	14	4.187	0.0407	rs11564216	12	38766294	q12
SNP_A-1736979	A	A	395	5	398	14	4.098	4.29E-02	rs10506144	12	38776732	q12
SNP_A-2201179	T	T	312	104	339	79	4.53	3.33E-02	rs12367641	12	39376405	q12
SNP_A-2189491	A	A	389	1	395	7	4.365	3.67E-02	rs17128674	12	39399147	q12
SNP_A-1836886	C	C	400	12	382	36	12.372	4.00E-04	rs17128788	12	39458021	q12
SNP_A-2052230	C	C	209	157	233	123	5.294	2.14E-02	rs984129	12	39489064	q12
SNP_A-2286393	G	G	214	164	241	131	5.246	2.20E-02	rs1126373	12	39504736	q12
SNP_A-1858104	A	A	292	100	273	131	4.619	3.16E-02	rs287071	12	40324708	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2285652	C	C	319	33	332	14	7.889	5.00E-03	rs11181149	12	40467872	q12
SNP_A-2053569	C	C	295	89	266	112	4.084	4.33E-02	rs10491999	12	40648828	q12
SNP_A-2209630	T	T	382	8	383	1	5.4	0.0201	rs7307159	12	41302231	q12
SNP_A-2092679	T	T	331	65	349	43	4.938	0.0263	rs11610557	12	41319271	q12
SNP_A-1701167	C	C	249	151	289	123	5.659	1.74E-02	rs4480597	12	41352290	q12
SNP_A-1709335	T	T	249	151	288	124	5.307	0.0212	rs4131406	12	41352359	q12
SNP_A-2220789	G	G	236	132	272	110	4.291	3.83E-02	rs6582414	12	41354525	q12
SNP_A-1821359	C	C	203	185	229	153	4.548	3.30E-02	rs11610543	12	41420458	q12
SNP_A-2054342	G	G	361	43	387	27	4.439	3.51E-02	rs17092133	12	41534170	q12
SNP_A-2090872	C	C	345	43	359	17	11.359	8.00E-04	rs2037410	12	41536624	q12
SNP_A-2240540	G	G	307	37	315	19	5.742	0.0166	rs961687	12	41594103	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2268825	T	T	326	42	327	25	3.961	4.66E-02	rs10880392	12	41620075	q12
SNP_A-1797444	C	C	410	6	404	16	4.571	3.25E-02	rs7956756	12	41968050	q12
SNP_A-2145000	G	G	254	114	276	84	5.371	2.05E-02	rs1510522	12	42187460	q12
SNP_A-2281982	C	C	409	5	405	15	4.977	2.57E-02	rs275379	12	42216868	q12
SNP_A-2054825	A	A	410	6	403	15	3.913	4.79E-02	rs275624	12	42219751	q12
SNP_A-2300367	T	T	298	54	230	70	6.718	9.50E-03	rs7312422	12	42668776	q12
SNP_A-2055079	G	G	401	7	407	1	4.545	3.30E-02	rs7953173	12	42775023	q12
SNP_A-2266401	C	C	414	0	413	7	6.958	8.30E-03	---	12	42889177	q12
SNP_A-2209891	C	C	379	27	399	15	3.865	4.93E-02	rs17094615	12	43087894	q12
SNP_A-1804754	G	G	355	23	363	11	4.303	3.80E-02	rs7978776	12	43100050	q12
SNP_A-2055427	G	G	240	166	271	141	3.873	4.91E-02	rs6582509	12	43285940	q12
SNP_A-2055436	A	A	231	155	266	132	4.125	4.22E-02	rs4768562	12	43289609	q12
SNP_A-2261906	C	C	338	30	371	15	6.11	0.0134	rs17575480	12	43442945	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2055586	A	A	264	124	245	155	3.972	4.63E-02	rs1506678	12	43535759	q12
SNP_A-2029451	A	A	232	158	269	137	3.907	4.81E-02	—	12	43784473	q12
SNP_A-2055886	A	A	351	39	370	18	8.232	4.10E-03	rs12312846	12	44177966	q12
SNP_A-1923216	T	T	240	132	271	105	4.935	0.0263	rs11183287	12	44696400	q13.11
SNP_A-2175567	G	G	407	9	418	2	4.582	3.23E-02	rs2408467	12	44801156	q13.11
SNP_A-2098188	A	A	354	50	373	31	4.953	2.60E-02	rs3742060	12	44867576	q13.11
SNP_A-1927773	G	G	276	124	315	91	7.594	5.90E-03	rs7975820	12	45029002	q13.11
SNP_A-2056307	G	G	283	47	253	67	5.035	2.48E-02	rs4768697	12	45035232	q13.11
SNP_A-2053135	G	G	195	147	240	114	8.623	0.0033	rs9669403	12	45085167	q13.11
SNP_A-2002696	C	C	295	113	268	148	5.911	1.50E-02	rs4768727	12	45150472	q13.11
SNP_A-1908431	A	A	263	87	240	116	5.144	2.33E-02	rs11183504	12	45167037	q13.11
SNP_A-2154446	A	A	375	29	384	16	3.842	5.00E-02	rs17121410	12	45217977	q13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2064300	G	G	247	109	211	131	4.567	3.26E-02	rs2715779	12	45462714	q13.11
SNP_A-1859502	C	C	204	172	239	141	5.815	1.59E-02	rs11183672	12	45637333	q13.11
SNP_A-2039118	C	C	402	14	411	5	4.363	3.67E-02	rs17097462	12	45693664	q13.11
SNP_A-2186972	A	A	313	53	347	35	5.093	0.024	rs2408710	12	45726763	q13.11
SNP_A-2116960	G	G	361	39	382	22	5.311	0.0212	rs17097570	12	45747450	q13.11
SNP_A-1794537	A	A	217	127	233	85	7.881	5.00E-03	rs214734	12	45952914	q13.11
SNP_A-2076292	A	A	360	20	371	9	4.338	0.0373	rs214651	12	45992781	q13.11
SNP_A-2113786	C	C	255	115	220	152	7.701	5.50E-03	rs7297927	12	46057101	q13.11
SNP_A-2263476	A	A	273	71	261	111	7.978	4.70E-03	rs11183919	12	46059484	q13.11
SNP_A-1904852	A	A	315	23	346	12	4.34	3.72E-02	rs7958890	12	46226988	q13.11
SNP_A-2213006	C	C	354	50	371	33	3.881	4.88E-02	rs10783205	12	46233062	q13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864469	T	T	253	89	220	108	3.844	0.0499	rs3782908	12	46455793	q13.11
SNP_A-2299372	G	G	184	182	210	150	4.751	0.0293	rs7962898	12	46529104	q13.11
SNP_A-2137567	T	T	352	32	347	51	4.136	4.20E-02	rs2732455	12	46964262	q13.11
SNP_A-1669567	G	G	275	13	358	0	16.492	4.89E-05	rs2071380	12	47248398	q13.11
SNP_A-2119201	T	T	403	1	400	12	9.241	2.40E-03	rs17123696	12	48035042	q13.12
SNP_A-1735136	C	C	399	1	400	12	9.134	2.50E-03	rs10506284	12	48038918	q13.12
SNP_A-1883157	G	G	372	28	334	44	4.983	2.56E-02	rs15008	12	48320801	q13.12
SNP_A-2065549	C	C	391	25	407	11	5.76	1.64E-02	rs1574598	12	48571742	q13.12
SNP_A-2058114	C	C	411	1	411	7	4.457	3.48E-02	rs17261501	12	48592027	q13.12
SNP_A-2147315	A	A	385	3	370	10	3.984	4.59E-02	rs844359	12	48759700	q13.12
SNP_A-2262683	C	C	366	14	365	3	6.928	8.50E-03	rs2292218	12	50168520	q13.13
SNP_A-1835864	A	A	342	46	356	26	5.79	0.0161	rs7139087	12	50327485	q13.13
SNP_A-2024821	G	G	312	102	349	71	7.583	5.90E-03	rs4512905	12	50337397	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2198765	T	T	348	32	370	16	5.961	0.0146	rs10735837	12	50346931	q13.13
SNP_A-2092350	A	A	326	42	326	16	10.717	1.10E-03	rs11169916	12	50455698	q13.13
SNP_A-2058949	C	C	243	71	303	53	6.599	1.02E-02	rs303817	12	50462502	q13.13
SNP_A-1666152	G	G	348	50	389	23	12.029	5.00E-04	rs10506303	12	50467465	q13.13
SNP_A-2058954	C	C	355	39	386	20	7.237	7.10E-03	rs9943714	12	50468719	q13.13
SNP_A-2058957	T	T	363	49	393	27	7.483	6.20E-03	rs9943809	12	50468812	q13.13
SNP_A-1729524	A	A	275	113	311	77	9.033	2.70E-03	rs303816	12	50469752	q13.13
SNP_A-1956896	A	A	366	50	391	25	9.159	2.50E-03	rs3741705	12	50488291	q13.13
SNP_A-2267338	G	G	291	51	289	77	4.48	3.43E-02	rs706819	12	50602190	q13.13
SNP_A-1874330	G	G	349	63	375	41	5.568	0.0183	rs2293093	12	50603324	q13.13
SNP_A-1665700	T	T	271	129	313	97	7.429	6.40E-03	rs706824	12	50605518	q13.13
SNP_A-2190223	G	G	301	37	291	59	5.003	0.0253	rs11610143	12	50635338	q13.13
SNP_A-2252988	A	A	307	67	293	93	4.363	3.67E-02	rs10876222	12	50648746	q13.13
SNP_A-1936609	G	G	289	35	273	59	6.487	0.0109	rs7963204	12	50845431	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2210202	C	C	238	82	229	113	4.375	3.65E-02	rs9669529	12	50856444	q13.13
SNP_A-1843739	C	C	357	55	377	37	4.062	4.39E-02	rs10444538	12	50863752	q13.13
SNP_A-2302502	C	C	325	87	354	62	5.414	0.02	rs17653722	12	50873785	q13.13
SNP_A-2083741	T	T	288	94	261	119	4.257	3.91E-02	rs4762066	12	50877687	q13.13
SNP_A-1797041	A	A	225	89	260	70	4.401	3.59E-02	rs1894035	12	50932021	q13.13
SNP_A-1934678	C	C	374	34	398	20	4.255	3.91E-02	rs10876281	12	51052830	q13.13
SNP_A-1855331	C	C	221	115	200	146	4.584	3.23E-02	rs381518	12	51117151	q13.13
SNP_A-1833853	A	A	409	7	419	1	4.602	3.19E-02	rs3847835	12	51173889	q13.13
SNP_A-2206711	T	T	228	180	269	141	8.116	4.40E-03	rs2292503	12	51265374	q13.13
SNP_A-2273282	C	C	229	163	271	133	6.389	0.0115	rs6580890	12	51276997	q13.13
SNP_A-1944166	C	C	355	55	378	36	4.669	3.07E-02	rs7967642	12	51283300	q13.13
SNP_A-2168017	A	A	381	21	398	8	6.179	0.0129	—	12	51323683	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	P_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2214247	G	G	314	62	279	83	4.843	2.78E-02	rs11170222	12	51336102	q13.13
SNP_A-2158002	C	C	320	48	288	66	4.256	3.91E-02	rs1488697	12	51344269	q13.13
SNP_A-1947110	T	T	335	65	314	88	4.132	4.21E-02	rs936955	12	51344886	q13.13
SNP_A-1896855	T	T	359	13	381	5	3.952	4.68E-02	rs666510	12	51403960	q13.13
SNP_A-2114503	G	G	354	0	373	5	4.715	2.99E-02	rs1818763	12	51441612	q13.13
SNP_A-2256237	C	C	410	4	418	0	4.058	4.40E-02	rs6580902	12	51450456	q13.13
SNP_A-2084616	T	T	412	4	420	0	4.058	4.40E-02	rs6580903	12	51450804	q13.13
SNP_A-1910345	A	A	302	88	329	63	5.289	2.15E-02	rs4432093	12	51472389	q13.13
SNP_A-1747305	A	A	235	163	265	133	4.841	2.78E-02	rs7965628	12	51483715	q13.13
SNP_A-2041957	C	C	372	12	392	2	7.539	6.00E-03	rs872461	12	51656362	q13.13
SNP_A-2002740	T	T	303	53	338	36	4.717	2.99E-02	rs7485642	12	51677768	q13.13
SNP_A-2093222	A	A	246	80	257	57	3.878	4.89E-02	rs3741651	12	52063438	q13.13
SNP_A-2084274	C	C	364	18	365	33	4.087	4.32E-02	rs17708042	12	52355501	q13.13
SNP_A-1685406	G	C	182	138	179	165	5.275	2.16E-02	rs3910926	12	52498858	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2032872	T	T	258	86	231	113	5.154	2.32E-02	rs11170732	12	52543443	q13.13
SNP_A-2060776	C	C	380	16	385	3	8.847	2.90E-03	rs324273	12	52547734	q13.13
SNP_A-2310150	G	G	365	51	340	74	5.114	2.37E-02	rs1470321	12	52587311	q13.13
SNP_A-2291976	G	G	346	6	302	20	9.209	2.40E-03	rs11170787	12	52700427	q13.13
SNP_A-2195830	C	C	369	17	365	31	3.978	4.61E-02	rs882383	12	52887298	q13.13
SNP_A-1903315	G	G	383	19	372	34	4.386	3.62E-02	rs11170895	12	53097975	q13.13
SNP_A-1813704	C	C	382	18	376	40	8.082	4.50E-03	rs17115699	12	53365449	q13.2
SNP_A-2275303	T	T	274	134	303	107	4.478	3.43E-02	rs1153188	12	53385263	q13.2
SNP_A-2093439	A	A	384	28	375	45	3.989	0.0458	rs1274298	12	54841289	q13.2
SNP_A-2059788	A	A	304	96	332	74	4.035	4.46E-02	rs6581112	12	55560351	q13.3
SNP_A-1820745	A	A	307	101	340	78	4.518	3.35E-02	rs7315229	12	55574935	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932314	C	C	372	26	356	44	4.975	2.57E-02	rs17119301	12	55661821	q13.3
SNP_A-2026563	G	G	340	4	336	12	4.001	4.55E-02	rs17119330	12	55695506	q13.3
SNP_A-1918233	A	A	406	0	405	5	4.982	2.56E-02	rs10783813	12	55780627	q13.3
SNP_A-1810411	A	A	379	7	389	1	4.61	3.18E-02	rs1494514	12	57040057	q14.1
SNP_A-1932269	C	C	275	95	241	115	3.877	4.90E-02	rs1908329	12	57049522	q14.1
SNP_A-2151903	C	C	319	93	348	72	3.857	4.95E-02	rs3913067	12	57057845	q14.1
SNP_A-2064600	C	C	320	76	340	44	8.957	0.0028	rs4760127	12	57096291	q14.1
SNP_A-1930392	T	T	346	0	329	5	5.218	0.0224	rs17121119	12	57260991	q14.1
SNP_A-2063830	T	T	299	89	329	61	6.655	9.90E-03	rs17121185	12	57289749	q14.1
SNP_A-2209528	G	G	389	7	393	1	4.515	3.36E-02	rs17121641	12	57554996	q14.1
SNP_A-2307787	T	T	367	29	384	16	4.12	0.0424	rs11172805	12	57576546	q14.1
SNP_A-1668889	A	A	359	27	386	14	4.853	0.0276	rs1020031	12	57581720	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2268065	G	G	375	27	385	11	6.824	9.00E-03	rs11172817	12	57584374	q14.1
SNP_A-1913360	G	G	382	34	397	17	5.951	0.0147	rs11172818	12	57584557	q14.1
SNP_A-2227889	C	C	326	22	345	9	5.939	1.48E-02	rs11172833	12	57620835	q14.1
SNP_A-2293399	A	A	282	78	262	102	3.913	4.79E-02	rs1500033	12	57806597	q14.1
SNP_A-2166749	A	A	310	75	268	94	4.192	4.06E-02	rs1515904	12	57821903	q14.1
SNP_A-2275260	G	G	243	91	205	109	4.23	3.97E-02	rs11173189	12	58527083	q14.1
SNP_A-2044678	C	C	280	110	246	150	8.306	4.00E-03	rs7960213	12	58556799	q14.1
SNP_A-2083178	C	C	301	79	326	54	5.696	1.70E-02	rs10784015	12	58589090	q14.1
SNP_A-2064823	C	C	357	3	346	10	3.919	4.77E-02	rs2068673	12	58619670	q14.1
SNP_A-1860300	C	C	251	59	302	46	4.132	4.21E-02	rs11173254	12	58639528	q14.1
SNP_A-1693437	G	G	378	10	387	3	3.87	4.92E-02	rs7304826	12	58932086	q14.1
SNP_A-2217565	C	C	336	18	314	36	6.722	9.50E-03	rs2134631	12	59327013	q14.1
SNP_A-1820320	T	T	335	13	311	27	5.647	1.75E-02	rs273782	12	59353980	q14.1
SNP_A-1835185	A	A	355	41	340	60	3.878	4.89E-02	rs1032644	12	59496823	q14.1
SNP_A-2271615	A	A	252	134	276	104	4.826	2.80E-02	rs11173906	12	60031245	q14.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1932801	T	C	168	160	193	135	6.679	9.80E-03	rs10784238	12	60280462	q14.1
SNP_A-2066088	G	G	362	54	381	33	5.55	1.85E-02	rs1876276	12	60346371	q14.1
SNP_A-1943315	C	C	362	54	384	36	4.23	3.97E-02	rs4335596	12	60477213	q14.1
SNP_A-2153439	C	C	355	43	375	19	9.818	1.70E-03	rs11174192	12	60514731	q14.1
SNP_A-2130304	G	G	340	62	332	88	4.21	0.0402	rs7968617	12	60588631	q14.1
SNP_A-1929611	C	C	274	14	306	36	6.867	8.80E-03	rs11614866	12	60953345	q14.1
SNP_A-2282778	G	G	267	69	248	96	5.026	2.50E-02	rs11174412	12	60961133	q14.1
SNP_A-1941508	G	G	355	61	336	84	4.152	4.16E-02	rs11174517	12	61186024	q14.1
SNP_A-2066589	G	A	220	170	206	198	4.359	3.68E-02	rs699560	12	61354397	q14.1
SNP_A-2270627	G	G	252	130	233	165	4.571	3.25E-02	rs342153	12	61444429	q14.2
SNP_A-2207266	C	C	405	3	392	20	12.758	4.00E-04	rs681224	12	61525359	q14.2
SNP_A-1816297	C	C	329	17	335	7	4.198	4.05E-02	rs3858673	12	61606602	q14.2
SNP_A-1923085	G	G	356	20	345	41	7.272	7.00E-03	rs11174776	12	61781950	q14.2
SNP_A-1643413	T	T	340	36	296	52	4.878	2.72E-02	rs1495028	12	61801281	q14.2
SNP_A-1792379	C	C	361	29	332	44	4.041	4.44E-02	rs6581470	12	61802943	q14.2
SNP_A-2074766	G	G	364	30	332	50	6.287	1.22E-02	rs11174811	12	61826743	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2098606	A	A	384	26	366	42	4.192	4.06E-02	rs7312429	12	61875688	q14.2
SNP_A-2154306	A	A	384	6	369	15	4.11	4.26E-02	rs6581474	12	61894165	q14.2
SNP_A-2279927	G	A	194	190	237	159	8.461	3.60E-03	rs11174879	12	61909420	q14.2
SNP_A-1884762	C	C	328	70	352	48	4.944	2.62E-02	rs17099254	12	61978762	q14.2
SNP_A-2074545	C	C	324	76	335	53	4.103	4.28E-02	rs17693409	12	62057279	q14.2
SNP_A-2287668	G	G	397	19	385	33	3.949	4.69E-02	rs810872	12	62067917	q14.2
SNP_A-2067186	C	C	392	12	370	28	6.991	8.20E-03	rs522020	12	62127452	q14.2
SNP_A-2246618	A	C	212	170	202	184	4.712	3.00E-02	rs3864454	12	62404116	q14.2
SNP_A-1942652	G	A	186	168	209	133	13.062	3.00E-04	rs17099954	12	62633296	q14.2
SNP_A-1894000	C	C	214	178	257	151	5.824	1.58E-02	rs1350136	12	62637173	q14.2
SNP_A-2267955	G	A	204	200	228	176	3.895	4.84E-02	rs1947504	12	62647729	q14.2
SNP_A-1882837	G	G	223	159	198	190	4.192	4.06E-02	rs6421210	12	62704167	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783256	A	A	259	61	317	47	4.845	2.77E-02	rs10784394	12	62962104	q14.2
SNP_A-1861636	C	C	385	17	393	7	4.244	3.94E-02	rs939875	12	63555314	q14.3
SNP_A-2274048	A	A	248	154	269	123	4.197	4.05E-02	rs10748016	12	63819012	q14.3
SNP_A-1835044	G	G	265	141	291	107	5.798	0.016	rs9668269	12	63966293	q14.3
SNP_A-2068449	C	C	237	173	270	142	5.194	2.27E-02	rs10506525	12	64069645	q14.3
SNP_A-1793265	C	C	294	122	258	162	7.963	4.80E-03	rs7316273	12	64094393	q14.3
SNP_A-2294513	C	C	291	119	255	159	8.11	4.40E-03	rs3858644	12	64124796	q14.3
SNP_A-2134640	A	A	287	115	241	145	7.147	7.50E-03	rs4762098	12	64125674	q14.3
SNP_A-2203258	A	A	349	37	388	16	9.98	1.60E-03	rs10878322	12	64406085	q14.3
SNP_A-2068645	G	G	293	123	319	97	4.177	4.10E-02	rs1870566	12	64498284	q14.3
SNP_A-2002808	G	G	384	8	399	1	5.652	1.74E-02	rs726302	12	64912424	q14.3
SNP_A-1856376	A	A	332	46	329	69	4.101	4.29E-02	rs11176192	12	65131870	q14.3
SNP_A-1879771	G	G	342	2	324	8	3.875	4.90E-02	rs17102805	12	65364103	q14.3
SNP_A-2280744	A	A	407	5	420	0	5.128	0.0235	rs1152882	12	66120331	q15
SNP_A-1938138	A	A	271	135	291	107	3.872	4.91E-02	rs11176774	12	66215516	q15
SNP_A-2229108	T	T	359	47	367	29	4.227	3.98E-02	rs2700131	12	66278211	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2002822	C	C	294	118	317	91	4.334	0.0373	rs717078	12	66417943	q15
SNP_A-1827628	C	C	277	33	308	14	9.099	2.60E-03	rs12427294	12	66491647	q15
SNP_A-2176244	C	C	313	69	342	32	14.755	0.0001	rs1362463	12	66491758	q15
SNP_A-2191882	G	G	271	53	299	33	5.93	0.0149	rs1819844	12	66491871	q15
SNP_A-2313242	C	C	366	6	350	0	5.692	1.70E-02	rs10878715	12	66648248	q15
SNP_A-1703047	C	T	201	195	243	163	9.104	2.60E-03	rs7316231	12	66755909	q15
SNP_A-1667786	G	G	227	165	268	140	5.127	2.36E-02	rs10492198	12	66780095	q15
SNP_A-1910663	A	A	378	20	383	9	4.16	4.14E-02	rs10878919	12	67808247	q15
SNP_A-2164115	G	G	339	69	360	48	4.4	3.59E-02	rs6581865	12	67828056	q15
SNP_A-2091547	T	T	313	59	337	37	5.923	0.0149	rs7298726	12	67867943	q15
SNP_A-1908007	G	G	397	13	391	27	4.869	2.73E-02	rs1456232	12	67993581	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2068102	G	G	373	9	362	20	4.337	0.0373	rs10784790	12	68483390	q15
SNP_A-1676722	C	C	238	160	217	195	4.179	4.09E-02	rs438847	12	69117623	q15
SNP_A-1920994	A	A	303	59	296	92	6.4	0.0114	rs11178299	12	69248923	q15
SNP_A-2056156	G	G	342	66	309	103	9.754	0.0018	rs1431257	12	69251017	q15
SNP_A-2305100	A	A	276	128	243	155	4.63	3.14E-02	rs1561798	12	69251746	q15
SNP_A-2141534	T	T	335	79	304	116	8.482	3.60E-03	rs11615170	12	69255848	q15
SNP_A-1929018	T	T	298	56	334	28	11.296	8.00E-04	rs10879170	12	69285180	q15
SNP_A-2072690	A	A	321	95	298	122	4.195	4.05E-02	rs10506598	12	69302206	q15
SNP_A-2129113	C	C	325	89	355	61	6.545	1.05E-02	rs1372560	12	69326659	q15
SNP_A-2185181	A	A	264	76	311	61	4.054	0.0441	rs10879174	12	69327197	q15
SNP_A-2072738	C	C	253	67	296	48	5.647	1.75E-02	rs4351856	12	69334002	q15
SNP_A-1732097	C	C	277	97	329	71	7.621	5.80E-03	rs4283028	12	69337302	q15
SNP_A-2082183	A	A	328	76	347	47	7.248	7.10E-03	rs7314925	12	69369870	q15

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2265486	G	G	332	22	297	39	6.22	0.0126	rs2089975	12	69381718	q15
SNP_A-1820055	C	C	260	138	299	117	4.054	0.0441	rs11178388	12	69422879	q15
SNP_A-2099164	A	A	332	0	320	4	4.124	4.23E-02	rs11178658	12	69833277	q15
SNP_A-2261641	A	G	215	179	201	173	5.303	2.13E-02	rs17109528	12	69913844	q15
SNP_A-2002840	A	A	245	75	274	46	8.571	3.40E-03	rs4760792	12	69989253	q15
SNP_A-1831215	C	C	313	17	314	4	7.83	5.10E-03	rs1280821	12	70203113	q21.1
SNP_A-2181535	T	T	267	107	225	127	4.632	3.14E-02	rs17109801	12	70226839	q21.1
SNP_A-1814428	C	C	334	62	305	87	5.491	1.91E-02	rs17109926	12	70264995	q21.1
SNP_A-1858543	C	C	382	10	377	25	6.337	0.0118	rs11178988	12	70606698	q21.1
SNP_A-2100044	A	G	212	192	226	182	5.03	2.49E-02	rs10748186	12	70622255	q21.1
SNP_A-1833579	T	T	333	77	359	51	6.258	0.0124	rs985206	12	70787682	q21.1
SNP_A-2075428	C	C	399	5	370	14	4.852	0.0276	rs11179361	12	71473567	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2131203	T	T	326	90	352	66	4.685	0.0304	rs996877	12	71604319	q21.1
SNP_A-2298062	A	A	328	74	353	53	4.371	3.66E-02	rs2176235	12	71630009	q21.1
SNP_A-2198466	A	A	284	96	314	72	4.887	2.71E-02	rs7970369	12	71703530	q21.1
SNP_A-1714795	T	T	227	149	202	194	6.847	8.90E-03	rs952394	12	71727377	q21.1
SNP_A-1726546	G	A	217	171	221	185	8.521	3.50E-03	rs10506711	12	71730776	q21.1
SNP_A-2269762	G	A	212	154	186	184	4.97	0.0258	rs12311315	12	71807447	q21.1
SNP_A-1959979	G	G	300	88	265	119	6.79	9.20E-03	rs11179561	12	71823164	q21.1
SNP_A-1792696	A	A	252	92	211	113	5.188	2.27E-02	rs6582131	12	71853716	q21.1
SNP_A-1822061	G	G	262	100	231	135	7.14	7.50E-03	rs2176207	12	71859512	q21.1
SNP_A-2136828	T	T	310	106	274	144	7.99	4.70E-03	rs17112138	12	71887731	q21.1
SNP_A-2121348	A	A	304	100	269	141	9.069	2.60E-03	rs17112140	12	71887753	q21.1
SNP_A-2101383	A	A	237	167	206	196	4.481	3.43E-02	rs2886023	12	72460441	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1650924	C	C	386	8	387	21	5.586	1.81E-02	rs2033862	12	72497407	q21.1
SNP_A-1808246	T	T	393	9	373	19	3.968	4.64E-02	rs10748248	12	72599152	q21.1
SNP_A-1821741	T	T	366	10	366	2	5.248	2.20E-02	rs11180174	12	73378025	q21.1
SNP_A-1865799	C	A	197	177	203	165	4.559	0.0327	rs7967572	12	73396068	q21.1
SNP_A-1709675	G	G	357	23	337	51	11.089	9.00E-04	rs1589968	12	73712158	q21.1
SNP_A-1681272	C	C	341	45	354	28	4.181	4.09E-02	rs1542570	12	74284870	q21.2
SNP_A-2303101	C	C	314	74	343	47	7.3	6.90E-03	rs17115456	12	74339685	q21.2
SNP_A-1741369	G	G	236	158	214	198	5.171	0.023	rs1298362	12	74493708	q21.2
SNP_A-2076223	C	T	199	169	174	144	5.276	2.16E-02	rs1290030	12	74498851	q21.2
SNP_A-1908064	T	T	401	5	399	15	4.927	0.0264	rs11180700	12	74506263	q21.2
SNP_A-2170109	C	C	239	135	256	106	3.879	4.89E-02	rs10880034	12	74748879	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2132043	C	C	229	173	264	140	5.959	0.0146	rs10778910	12	75672825	q21.2
SNP_A-1824387	G	G	212	168	248	138	5.712	1.69E-02	rs10862666	12	75751425	q21.2
SNP_A-2233752	G	G	360	46	342	66	4.028	4.47E-02	rs12316906	12	75769186	q21.2
SNP_A-2198297	C	C	416	0	414	6	5.986	0.0144	rs772738	12	75844271	q21.2
SNP_A-2076896	T	T	320	96	346	74	3.843	5.00E-02	rs310849	12	75984171	q21.2
SNP_A-1722976	T	C	187	185	220	164	4.342	3.72E-02	rs10506759	12	76648630	q21.2
SNP_A-1660985	-	T	200	200	238	174	4.928	0.0264	rs1402319	12	76658608	q21.2
SNP_A-2272181	G	G	210	200	237	169	4.216	4.01E-02	rs1949593	12	76664342	q21.2
SNP_A-2089445	G	G	332	54	344	28	8.201	4.20E-03	rs7307970	12	76749553	q21.2
SNP_A-1822938	A	A	312	58	302	30	7.036	8.00E-03	rs1731743	12	76825859	q21.2
SNP_A-2262069	A	A	314	86	285	109	4.072	0.0436	rs2731417	12	76919591	q21.2
SNP_A-2077988	A	A	328	70	347	49	4.236	3.96E-02	rs10506769	12	76953202	q21.2
SNP_A-2149971	G	G	343	9	351	1	6.492	1.08E-02	rs17223304	12	76972681	q21.2
SNP_A-2103384	C	C	348	64	376	42	5.606	1.79E-02	rs17224126	12	76992164	q21.2
SNP_A-2086411	C	C	330	80	350	56	4.804	2.84E-02	rs438209	12	76992295	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215206	G	A	194	162	160	140	3.992	4.57E-02	rs9971904	12	77101359	q21.2
SNP_A-1726082	C	C	302	42	371	27	6.439	0.0112	rs10506781	12	77231195	q21.2
SNP_A-1910270	A	A	351	33	375	17	5.832	1.57E-02	rs17045250	12	77285380	q21.2
SNP_A-2153041	G	G	376	38	392	22	4.6	3.20E-02	rs17045291	12	77306975	q21.2
SNP_A-1896369	G	G	362	14	374	4	5.746	1.65E-02	rs1004733	12	77390508	q21.2
SNP_A-2283745	G	G	382	4	396	0	4.125	4.23E-02	rs17045709	12	77566244	q21.2
SNP_A-1918639	G	G	383	5	383	23	11.169	8.00E-04	rs12578219	12	77821396	q21.2
SNP_A-2226683	G	G	347	11	334	22	3.909	4.80E-02	—	12	77893516	q21.2
SNP_A-1827803	A	A	330	34	356	18	5.774	1.63E-02	rs17005226	12	78013283	q21.2
SNP_A-1659820	G	G	331	27	387	17	3.878	4.89E-02	rs961073	12	78058473	q21.2
SNP_A-2114569	G	G	236	162	253	123	5.307	0.0212	rs7300645	12	78186025	q21.2
SNP_A-1807372	C	C	382	26	406	14	4.158	4.14E-02	rs1526956	12	78229527	q21.2
SNP_A-1951702	G	G	326	24	338	12	4.217	4.00E-02	rs10861968	12	78287021	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2247472	G	G	311	15	316	6	3.872	4.91E-02	rs17005588	12	78311724	q21.2
SNP_A-1942817	C	C	349	9	370	2	4.801	2.84E-02	rs11114391	12	79194215	q21.31
SNP_A-2117199	A	A	388	18	376	36	6.145	0.0132	rs1163254	12	79606818	q21.31
SNP_A-2193551	C	C	364	20	344	40	7.232	7.20E-03	rs17007214	12	79614124	q21.31
SNP_A-2079711	A	A	357	53	380	36	3.922	4.77E-02	rs1305281	12	79642752	q21.31
SNP_A-1914049	T	T	214	148	241	123	3.903	0.0482	rs10862202	12	79743221	q21.31
SNP_A-2235354	A	A	246	168	216	202	5.053	0.0246	rs6539533	12	79745770	q21.31
SNP_A-1937977	G	G	288	98	255	133	7.303	6.90E-03	rs4143659	12	79746393	q21.31
SNP_A-2081658	G	G	343	49	337	25	6.654	9.90E-03	rs1920992	12	79772050	q21.31
SNP_A-1876710	C	C	230	74	288	56	6.542	1.05E-02	rs1163656	12	79839926	q21.31
SNP_A-2079971	T	T	241	127	222	158	3.96	4.66E-02	rs7974595	12	79977771	q21.31
SNP_A-1934254	C	C	275	121	229	153	7.686	5.60E-03	rs10862237	12	79995183	q21.31
SNP_A-2178223	G	G	387	9	402	2	4.66	0.0309	rs2574731	12	80031988	q21.31
SNP_A-2203986	C	C	272	96	251	123	4.124	4.23E-02	rs1435967	12	80033354	q21.31
SNP_A-2080032	C	C	400	8	407	1	5.505	0.019	rs1435965	12	80044609	q21.31
SNP_A-2034099	G	G	367	31	386	18	3.884	4.88E-02	rs10862290	12	80209337	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909893	G	G	360	18	361	5	7.158	7.50E-03	rs4573769	12	80482252	q21.31
SNP_A-1845513	C	C	293	81	273	49	4.725	2.97E-02	rs17692461	12	80674223	q21.31
SNP_A-1861901	A	A	329	9	338	0	9.121	2.50E-03	rs12319937	12	80685013	q21.31
SNP_A-1753659	A	A	328	66	353	43	5.766	1.63E-02	rs1922558	12	80704470	q21.31
SNP_A-2213967	C	C	349	47	336	72	5.321	2.11E-02	rs12307959	12	80735892	q21.31
SNP_A-2080636	C	C	373	1	338	6	4.048	4.42E-02	rs17009352	12	81123653	q21.31
SNP_A-1885516	T	T	361	7	344	16	3.844	0.0499	rs4587790	12	81301971	q21.31
SNP_A-1907808	C	C	408	6	400	16	4.62	3.16E-02	rs17775447	12	81332382	q21.31
SNP_A-2080697	A	A	314	12	270	36	14.697	0.0001	rs2731295	12	81358422	q21.31
SNP_A-1646386	A	A	345	55	332	78	4.104	4.28E-02	rs1369035	12	81906992	q21.31
SNP_A-2080974	T	T	355	49	331	71	4.868	2.74E-02	rs1682604	12	81912074	q21.31
SNP_A-2241000	T	C	192	186	214	146	7.786	0.0053	rs4084723	12	82363952	q21.31
SNP_A-2058147	T	G	176	174	203	139	6.485	0.0109	rs7316185	12	82364602	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074605	A	A	275	139	239	171	5.805	0.016	rs3112099	12	82376339	q21.31
SNP_A-1654465	C	C	269	129	243	169	6.449	0.0111	rs3112097	12	82379382	q21.31
SNP_A-2200799	T	T	218	114	188	140	4.854	0.0276	rs3103501	12	82413019	q21.31
SNP_A-2293538	C	C	246	162	212	198	6.119	0.0134	rs324804	12	82434461	q21.31
SNP_A-2081369	A	A	196	142	218	112	4.617	3.17E-02	rs7485592	12	82533255	q21.31
SNP_A-1747085	C	C	204	196	243	167	5.597	1.80E-02	rs1391072	12	82563311	q21.31
SNP_A-1735985	G	G	231	151	215	193	4.851	0.0276	rs717997	12	82636442	q21.31
SNP_A-2205779	C	C	415	1	412	8	5.436	1.97E-02	—	12	82651620	q21.31
SNP_A-2036709	G	G	313	55	315	35	4.002	4.54E-02	rs111116405	12	83341124	q21.31
SNP_A-2110290	G	G	359	43	375	25	5.109	2.38E-02	rs111116410	12	83346410	q21.31
SNP_A-2249748	C	C	351	35	374	18	6.137	0.0132	rs12231201	12	83384109	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1953438	C	C	350	36	371	21	4.513	3.36E-02	rs7970452	12	83395582	q21.31
SNP_A-1861091	C	C	317	47	348	32	3.951	4.68E-02	rs7970336	12	83396197	q21.31
SNP_A-2219709	C	C	350	40	366	20	7.004	8.10E-03	rs1459593	12	83442813	q21.31
SNP_A-2243651	G	G	365	49	389	31	4.771	2.89E-02	rs11116473	12	83482515	q21.31
SNP_A-2211578	A	A	353	43	378	24	6.198	1.28E-02	rs17012289	12	83498792	q21.31
SNP_A-1745390	G	G	386	8	399	1	5.615	0.0178	rs10506909	12	83523995	q21.31
SNP_A-2082245	C	C	272	136	311	107	5.95	0.0147	rs7302315	12	83954533	q21.31
SNP_A-1847094	A	A	263	135	297	97	8.268	4.00E-03	rs12814669	12	83966512	q21.31
SNP_A-2284283	C	C	230	92	261	71	4.511	3.37E-02	rs12231122	12	83967705	q21.31
SNP_A-1942328	A	A	358	0	332	4	4.287	3.84E-02	rs17012608	12	84059256	q21.31
SNP_A-1832537	C	C	246	100	289	83	4.099	4.29E-02	rs7966105	12	84079469	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1959158	C	C	226	190	266	152	7.47	0.0063	rs10862971	12	84238945	q21.31
SNP_A-2085837	A	A	222	176	261	141	6.994	8.20E-03	rs10779159	12	84239726	q21.31
SNP_A-1828149	T	T	227	187	258	154	5.17	0.023	rs10459170	12	84259153	q21.31
SNP_A-1901068	C	C	326	16	294	30	5.43	1.98E-02	rs1913137	12	84304593	q21.31
SNP_A-1927062	A	A	205	155	234	120	6.32	1.19E-02	rs7134486	12	84456703	q21.31
SNP_A-1938988	T	T	225	183	258	150	5.525	1.87E-02	rs1037980	12	84484115	q21.31
SNP_A-2034868	A	A	241	153	278	114	8.329	3.90E-03	rs10863019	12	84513223	q21.31
SNP_A-1947230	T	T	249	153	278	122	5.085	0.0241	rs10863023	12	84519381	q21.31
SNP_A-2084370	A	A	218	152	246	124	4.53	3.33E-02	rs2405254	12	84520087	q21.31
SNP_A-2169335	T	T	220	164	246	126	6.241	1.25E-02	rs10779186	12	84572010	q21.31
SNP_A-2195042	C	T	231	185	212	196	4.628	0.0315	rs2897093	12	84597947	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1685752	T	C	209	165	202	186	4.814	2.82E-02	rs10506924	12	84600612	q21.31
SNP_A-2082467	T	C	202	166	195	177	3.957	4.67E-02	rs7302561	12	84600708	q21.31
SNP_A-1823733	A	A	318	48	346	28	6.358	0.0117	rs7972185	12	85241252	q21.32
SNP_A-2299687	C	C	369	13	385	3	6.543	1.05E-02	rs11104005	12	85493442	q21.32
SNP_A-1947672	A	A	276	50	292	30	5.426	1.98E-02	rs7131820	12	85504044	q21.32
SNP_A-1908293	C	C	296	108	269	133	3.879	4.89E-02	rs17314381	12	85962380	q21.32
SNP_A-1939321	A	A	412	4	420	0	4.058	4.40E-02	rs17014438	12	85990370	q21.32
SNP_A-2069210	C	C	398	2	389	9	4.552	3.29E-02	rs11104341	12	86106360	q21.32
SNP_A-2194882	C	C	383	29	397	15	4.706	3.01E-02	rs17577888	12	86172681	q21.32
SNP_A-2002905	A	A	221	121	222	82	5.278	2.16E-02	rs4491334	12	86265906	q21.32
SNP_A-1917303	A	A	376	4	377	13	4.637	3.13E-02	rs1913130	12	86516994	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2288212	G	G	390	4	397	13	4.51	3.37E-02	rs790448	12	86536254	q21.32
SNP_A-2257814	T	T	246	126	216	150	3.986	4.59E-02	rs1826814	12	86539961	q21.32
SNP_A-1673210	C	C	365	23	357	41	5.025	2.50E-02	rs1436178	12	86697397	q21.32
SNP_A-1646486	G	G	361	9	349	23	6.322	1.19E-02	rs1436179	12	86697433	q21.32
SNP_A-2083419	C	C	265	135	233	163	4.667	3.07E-02	rs1436180	12	86697562	q21.32
SNP_A-1826778	C	C	386	28	369	49	6.091	1.36E-02	rs7313024	12	86703379	q21.32
SNP_A-1801681	C	C	306	102	331	79	3.899	4.83E-02	rs11104629	12	86721515	q21.32
SNP_A-1688046	C	C	371	29	361	47	4.321	3.76E-02	rs3911720	12	86723450	q21.32
SNP_A-1831604	C	C	294	74	302	48	5.2	2.26E-02	rs11104632	12	86726153	q21.32
SNP_A-1958748	G	G	241	145	281	121	4.908	2.67E-02	rs7311568	12	86747269	q21.32
SNP_A-2094314	G	G	399	7	401	1	4.485	3.42E-02	rs11104998	12	87574502	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1842231	A	A	352	18	361	5	7.44	6.40E-03	rs1881228	12	87666433	q21.33
SNP_A-2039159	C	C	292	120	317	91	4.993	2.55E-02	rs10858925	12	88649902	q21.33
SNP_A-1849541	A	A	274	84	292	58	5.243	2.20E-02	rs10858926	12	88664402	q21.33
SNP_A-1868368	G	G	235	117	280	96	5.217	0.0224	rs2056330	12	88677542	q21.33
SNP_A-2161612	T	T	275	139	306	112	4.539	3.31E-02	rs10858935	12	88725670	q21.33
SNP_A-1754758	A	A	363	33	350	62	8.776	3.10E-03	rs10506991	12	89665446	q21.33
SNP_A-2085265	C	C	390	14	400	4	5.682	1.71E-02	rs10506994	12	89844777	q21.33
SNP_A-2128692	A	A	321	87	364	54	10.303	1.30E-03	rs7968912	12	89857600	q21.33
SNP_A-2268724	G	G	314	90	352	58	9.043	2.60E-03	rs11613174	12	89858491	q21.33
SNP_A-1946680	C	C	316	80	347	45	11.229	8.00E-04	rs12820238	12	89858508	q21.33
SNP_A-1930399	G	G	353	55	383	31	7.877	5.00E-03	rs1882145	12	89865987	q21.33
SNP_A-2174813	A	A	274	74	326	50	8.081	4.50E-03	rs7961889	12	89873319	q21.33
SNP_A-1799544	C	C	339	67	377	37	10.594	1.10E-03	rs1920765	12	89887089	q21.33
SNP_A-1892574	G	G	297	69	343	41	10.007	1.60E-03	rs2408419	12	89888790	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2150445	G	G	272	64	287	35	8.603	3.40E-03	rs1950098	12	89890446	q21.33
SNP_A-2196455	C	C	279	89	315	49	13.755	2.00E-04	rs2141678	12	89899647	q21.33
SNP_A-2085329	G	G	338	74	379	37	14.659	0.0001	rs1920744	12	89905180	q21.33
SNP_A-1801093	C	C	338	62	378	38	7.684	5.60E-03	rs10859092	12	89905476	q21.33
SNP_A-1665100	T	T	344	56	380	32	8.16	0.0043	rs1920780	12	89930438	q21.33
SNP_A-1701171	T	T	329	43	371	23	7.955	4.80E-03	rs887921	12	89931160	q21.33
SNP_A-1849018	G	G	275	97	310	60	10.808	0.001	rs7302090	12	89933259	q21.33
SNP_A-2108961	T	T	343	21	373	9	5.626	0.0177	rs11105956	12	89949991	q21.33
SNP_A-1912176	T	T	301	115	340	76	10.336	1.30E-03	rs10859103	12	89963393	q21.33
SNP_A-1683986	T	T	286	110	336	78	9.071	2.60E-03	rs1920731	12	89969973	q21.33
SNP_A-1819903	C	C	350	68	372	48	4.114	4.25E-02	rs991427	12	89976890	q21.33
SNP_A-1837704	A	A	401	15	413	5	5.172	0.023	rs11105996	12	90006101	q21.33
SNP_A-2198892	T	T	396	12	404	2	7.218	7.20E-03	rs3759223	12	90009251	q21.33
SNP_A-2053784	A	A	382	30	391	13	6.748	9.40E-03	rs17018765	12	90011617	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2047444	A	A	275	89	266	122	4.55	3.29E-02	rs7312575	12	90113348	q21.33
SNP_A-1805983	C	C	405	11	412	2	6.286	1.22E-02	rs1522430	12	90132623	q21.33
SNP_A-2044983	A	A	385	13	398	4	4.961	2.59E-02	rs11106071	12	90148463	q21.33
SNP_A-2059778	A	A	407	9	418	2	4.582	3.23E-02	rs7342296	12	90276678	q21.33
SNP_A-2002924	T	C	213	179	216	174	7.391	0.0066	rs4457821	12	90497859	q21.33
SNP_A-2111113	G	G	226	144	208	178	4	4.55E-02	rs7969193	12	90548257	q21.33
SNP_A-2273674	T	T	343	69	323	93	4.137	4.20E-02	rs12321699	12	90619246	q21.33
SNP_A-2158611	G	G	345	69	325	93	4.133	4.20E-02	rs1493774	12	90634465	q21.33
SNP_A-1799571	A	A	307	47	283	71	5.858	0.0155	rs10859199	12	90662667	q21.33
SNP_A-1849205	G	G	345	71	324	94	3.86	4.94E-02	rs10777332	12	90666770	q21.33
SNP_A-1930633	C	C	332	26	307	11	4.709	3.00E-02	rs7960107	12	90764052	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2105195	C	C	360	16	374	6	4.791	0.0286	rs10859224	12	90786103	q21.33
SNP_A-2002932	G	G	263	121	225	153	6.649	9.90E-03	rs4608114	12	90887126	q21.33
SNP_A-2279726	T	C	203	181	211	177	4.054	0.0441	rs7959206	12	90922267	q21.33
SNP_A-1729810	C	C	294	50	300	82	5.845	1.56E-02	rs1836681	12	91035857	q21.33
SNP_A-1810312	A	A	392	10	385	21	3.947	0.047	rs11106556	12	91351027	q22
SNP_A-2261308	G	G	398	10	396	22	4.385	3.63E-02	rs7976259	12	91357560	q22
SNP_A-2068560	A	A	257	85	246	114	4.008	0.0453	rs7312899	12	91375326	q22
SNP_A-2313441	G	G	301	117	271	147	4.983	2.56E-02	rs10859340	12	91458658	q22
SNP_A-2086942	G	G	332	84	306	110	4.544	3.30E-02	rs11107116	12	92480972	q22
SNP_A-2254177	A	G	197	181	221	177	4.537	0.0332	rs1471816	12	92647588	q22
SNP_A-2253998	A	A	371	45	388	28	4.34	3.72E-02	rs12369836	12	92832994	q22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1854755	A	A	226	102	271	81	5.644	1.75E-02	rs10859659	12	92991353	q22
SNP_A-2087558	C	C	275	85	301	59	5.868	0.0154	rs10507035	12	93157454	q22
SNP_A-2285378	G	G	231	143	205	171	4.042	4.44E-02	rs7979054	12	93221022	q22
SNP_A-2066734	G	G	315	23	303	41	5.243	2.20E-02	rs2271979	12	93275210	q22
SNP_A-1780456	A	A	248	158	208	188	5.986	0.0144	rs1520723	12	93329462	q22
SNP_A-2215834	C	C	275	119	301	93	4.362	3.67E-02	rs12582418	12	93504899	q22
SNP_A-2044897	T	T	196	162	230	140	4.12	0.0424	rs7978852	12	93514915	q22
SNP_A-1914774	A	A	225	147	272	116	7.765	0.0053	rs6538524	12	93531749	q22
SNP_A-2037185	T	T	226	102	218	144	5.653	1.74E-02	rs7972350	12	93663073	q22
SNP_A-2114561	A	A	231	151	201	185	5.503	0.019	rs6538539	12	93697761	q22
SNP_A-2087982	T	T	265	123	240	160	5.894	0.0152	rs7961115	12	93705607	q22
SNP_A-2281917	C	C	235	157	209	191	4.764	2.91E-02	rs12579933	12	93705630	q22
SNP_A-2252437	C	C	307	49	312	26	6.631	0.01	rs10777674	12	94104052	q22
SNP_A-2248921	G	G	319	31	316	16	4.329	3.75E-02	rs7135879	12	94167871	q22
SNP_A-2258170	C	C	334	74	357	51	4.998	2.54E-02	rs11108299	12	94740722	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1954023	T	T	315	81	282	102	4.05	4.42E-02	rs2540477	12	94940022	q23.1
SNP_A-2089700	G	G	319	73	296	98	4.51	3.37E-02	rs11835965	12	95191200	q23.1
SNP_A-2180067	C	C	373	17	393	7	4.563	0.0327	rs935031	12	95363838	q23.1
SNP_A-2089067	A	A	362	24	384	12	4.522	3.35E-02	rs10507076	12	95546017	q23.1
SNP_A-2031737	C	C	364	0	326	4	4.438	3.52E-02	rs17026266	12	95962061	q23.1
SNP_A-1857171	C	C	325	21	345	9	5.306	0.0212	rs7963007	12	95974927	q23.1
SNP_A-2059198	C	C	382	26	399	11	6.446	0.0111	rs2193374	12	95980883	q23.1
SNP_A-1821186	G	G	320	38	324	20	5.334	2.09E-02	rs2193371	12	96026102	q23.1
SNP_A-1853483	T	T	240	114	210	138	4.235	3.96E-02	rs10860153	12	96044000	q23.1
SNP_A-1910233	A	A	369	7	401	1	4.967	0.0258	rs11108857	12	96055574	q23.1
SNP_A-2191774	A	A	400	6	400	16	4.424	3.54E-02	rs12228828	12	96117065	q23.1
SNP_A-2050215	A	A	395	11	414	2	6.556	1.05E-02	rs257964	12	96212914	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141848	G	G	392	8	416	2	3.919	4.78E-02	rs257955	12	96218072	q23.1
SNP_A-2196565	G	G	311	39	287	57	4.287	3.84E-02	rs10860188	12	96231750	q23.1
SNP_A-2191393	T	T	341	49	380	32	5.078	2.42E-02	rs17026860	12	96286863	q23.1
SNP_A-2126965	C	C	403	7	411	1	4.574	3.25E-02	rs11109093	12	96418337	q23.1
SNP_A-1895538	C	C	296	92	264	118	5.001	0.0253	rs12370281	12	96752101	q23.1
SNP_A-2090411	A	G	190	144	170	162	4.374	3.65E-02	rs2192792	12	96881867	q23.1
SNP_A-2211257	C	C	403	9	410	2	4.515	3.36E-02	rs12309615	12	97088416	q23.1
SNP_A-1901349	T	T	342	50	368	30	5.907	1.51E-02	rs10860307	12	97089115	q23.1
SNP_A-1816614	G	G	335	13	381	5	4.556	3.28E-02	rs12425156	12	97095034	q23.1
SNP_A-1738869	T	T	288	94	269	135	7.379	0.0066	rs1383132	12	97110987	q23.1
SNP_A-2211389	A	A	339	41	376	16	12.696	4.00E-04	rs10777915	12	97123831	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1793010	G	G	367	47	372	28	4.608	3.18E-02	rs10745826	12	97171788	q23.1
SNP_A-1860218	G	G	329	27	371	9	10.749	0.001	rs1480077	12	97188970	q23.1
SNP_A-2293710	A	A	371	29	401	17	3.902	0.0482	rs1480078	12	97190763	q23.1
SNP_A-1870295	C	C	360	36	385	17	7.606	5.80E-03	rs1351339	12	97201140	q23.1
SNP_A-1746977	C	C	380	20	408	6	8.295	4.00E-03	rs10507105	12	97214142	q23.1
SNP_A-1758301	C	C	352	40	387	25	4.625	0.0315	rs1351343	12	97214463	q23.1
SNP_A-1700305	A	A	372	28	399	15	4.636	3.13E-02	rs10492288	12	97249068	q23.1
SNP_A-2175552	A	G	208	166	193	175	4.826	2.80E-02	rs7975512	12	97301837	q23.1
SNP_A-2090804	G	G	304	58	331	41	3.932	4.74E-02	rs829894	12	97362683	q23.1
SNP_A-2027348	T	T	405	11	416	2	6.373	1.16E-02	rs17028456	12	97431582	q23.1
SNP_A-2022926	A	A	361	55	386	32	6.912	0.0086	rs17815383	12	97650910	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1877018	T	T	336	52	360	28	8.028	4.60E-03	---	12	97655354	q23.1
SNP_A-1890782	T	T	199	141	212	104	5.128	0.0235	rs2221204	12	98508302	q23.1
SNP_A-1814324	A	A	347	15	351	5	4.973	2.57E-02	rs11110050	12	98701242	q23.1
SNP_A-1959371	T	T	337	19	323	33	4.066	4.37E-02	rs2029585	12	98944855	q23.1
SNP_A-1821615	C	C	392	18	382	32	4.03	4.47E-02	rs11110283	12	99093581	q23.1
SNP_A-1702445	G	G	278	110	252	144	5.746	1.65E-02	rs1877882	12	99634667	q23.1
SNP_A-1733670	A	A	288	114	321	91	4.246	3.93E-02	rs952464	12	99653452	q23.1
SNP_A-2091662	C	C	228	150	203	181	4.306	3.80E-02	rs2222001	12	99729498	q23.1
SNP_A-2091692	C	C	225	159	276	132	6.976	8.30E-03	rs10507120	12	99752728	q23.1
SNP_A-1695203	G	G	242	90	247	137	6.038	0.014	rs938335	12	99762926	q23.1
SNP_A-2234776	G	G	291	117	258	148	5.605	1.79E-02	rs533427	12	99823331	q23.1
SNP_A-1703073	A	A	239	117	296	104	4.291	3.83E-02	rs612640	12	99828001	q23.1
SNP_A-2080797	A	A	308	100	285	129	4.521	3.35E-02	rs582147	12	99835306	q23.1
SNP_A-2168218	C	T	236	176	203	197	5.26	0.0218	rs11614937	12	100396194	q23.2
SNP_A-2210799	G	G	410	6	401	17	5.356	0.0207	rs1727080	12	100458203	q23.2
SNP_A-1670141	C	C	276	114	308	90	4.496	3.40E-02	rs6538998	12	100496048	q23.2
SNP_A-1747023	A	A	215	185	251	163	3.932	4.74E-02	rs1697485	12	100497682	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800840	G	G	212	178	235	147	4.058	4.40E-02	rs11110886	12	100506833	q23.2
SNP_A-1688240	C	C	386	16	407	7	3.902	0.0482	rs3794282	12	100568432	q23.2
SNP_A-2092407	T	T	320	26	318	46	5.109	2.38E-02	rs11111013	12	100663864	q23.2
SNP_A-2133547	C	C	215	199	246	172	4.03	4.47E-02	rs7296993	12	100903533	q23.2
SNP_A-1845389	T	T	305	95	334	68	5.784	1.62E-02	rs12578176	12	101033521	q23.2
SNP_A-2132241	C	C	336	52	365	35	4.34	3.72E-02	rs12426318	12	101137988	q23.2
SNP_A-2077859	A	A	309	93	282	118	4.191	4.06E-02	rs10860869	12	101367519	q23.2
SNP_A-2071907	C	C	306	58	270	78	4.834	2.79E-02	rs7955640	12	101470766	q23.2
SNP_A-1891954	T	T	258	140	226	180	7.037	8.00E-03	rs10778179	12	101473743	q23.2
SNP_A-1948587	C	C	259	143	229	179	5.825	1.58E-02	rs10735381	12	101477573	q23.2
SNP_A-1818877	T	T	263	145	234	182	5.802	0.016	rs10778187	12	101494144	q23.2
SNP_A-2081673	T	T	361	17	354	32	4.577	3.24E-02	rs17539564	12	101498214	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2151087	T	T	262	148	231	183	5.631	1.76E-02	rs2201521	12	101520667	q23.2
SNP_A-2120729	A	A	374	10	373	1	7.234	7.20E-03	rs7299331	12	101877396	q23.2
SNP_A-1894209	T	T	294	38	302	16	8.773	3.10E-03	rs1879251	12	101968433	q23.2
SNP_A-1661019	C	G	228	174	211	199	5.447	1.96E-02	rs10507158	12	102062701	q23.2
SNP_A-2267001	G	G	251	157	277	127	4.43	3.53E-02	rs10860949	12	102076042	q23.2
SNP_A-2050365	G	G	207	189	240	152	6.431	0.0112	rs10860951	12	102078454	q23.2
SNP_A-1911471	A	A	205	187	224	150	4.483	3.42E-02	rs7308725	12	102082557	q23.2
SNP_A-1866094	A	A	207	147	225	113	4.829	2.80E-02	rs10860955	12	102084452	q23.2
SNP_A-2230879	A	A	198	182	231	149	5.828	1.58E-02	rs11111492	12	102103558	q23.2
SNP_A-1725772	G	A	227	173	211	199	5.478	1.93E-02	rs1401994	12	102109041	q23.2
SNP_A-2275349	G	G	210	168	246	144	4.502	0.0339	rs11111498	12	102111234	q23.2
SNP_A-1792667	A	A	377	11	333	21	4.303	3.80E-02	rs17568045	12	102285781	q23.2
SNP_A-1658038	T	T	338	16	336	34	6.135	1.33E-02	rs4015536	12	102326597	q23.2
SNP_A-2093599	G	G	218	136	249	109	5.011	0.0252	rs10507166	12	102367680	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2182521	G	G	400	12	387	25	4.782	2.88E-02	rs11111634	12	102435510	q23.3
SNP_A-1857602	A	A	238	132	273	103	5.928	0.0149	rs4964629	12	102724317	q23.3
SNP_A-1808179	T	T	323	27	286	40	3.923	4.76E-02	rs11111815	12	102751254	q23.3
SNP_A-2003002	T	T	347	27	369	11	7.366	0.0066	rs7961041	12	102955663	q23.3
SNP_A-2177081	A	A	375	35	378	16	6.775	9.20E-03	rs4129848	12	103257710	q23.3
SNP_A-2022887	A	A	356	50	349	27	5.797	0.0161	rs12581164	12	103542042	q23.3
SNP_A-2096278	G	G	408	0	410	4	3.961	4.66E-02	rs11112169	12	103588127	q23.3
SNP_A-2263924	C	C	293	119	322	94	4.283	0.0385	rs312137	12	103600898	q23.3
SNP_A-2094636	C	C	289	123	261	153	4.682	3.05E-02	rs11611207	12	103705723	q23.3
SNP_A-1900627	G	G	324	32	292	56	8.118	4.40E-03	rs1196777	12	104127907	q23.3
SNP_A-2093152	A	A	392	22	405	11	3.874	4.90E-02	rs17247907	12	104254421	q23.3
SNP_A-1922535	G	G	291	89	284	60	3.949	4.69E-02	rs7302174	12	104264129	q23.3
SNP_A-2094963	C	C	283	65	326	30	15.842	6.89E-05	rs1526851	12	104388823	q23.3
SNP_A-1856189	G	G	295	101	330	74	6.046	1.39E-02	rs10861455	12	104435787	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116202	T	T	301	41	331	27	3.943	4.71E-02	rs2711734	12	104459315	q23.3
SNP_A-2306153	G	G	364	50	386	28	6.85	8.90E-03	rs2694399	12	104460141	q23.3
SNP_A-1667040	C	C	348	54	382	32	7.037	8.00E-03	rs2888856	12	104474722	q23.3
SNP_A-2087195	C	C	412	6	404	18	6.06	0.0138	rs11112601	12	104481368	q23.3
SNP_A-2161944	G	G	353	47	382	30	4.721	0.0298	rs1526844	12	104485782	q23.3
SNP_A-2255377	G	G	335	81	309	105	4.142	4.18E-02	rs4511375	12	104537911	q23.3
SNP_A-1876271	C	T	182	160	199	149	7.475	0.0063	rs4638409	12	104537959	q23.3
SNP_A-2137218	G	G	299	69	275	91	4.023	4.49E-02	rs7295594	12	104545573	q23.3
SNP_A-1850144	G	G	263	141	234	172	4.758	0.0292	rs10778417	12	104545934	q23.3
SNP_A-2199347	T	T	261	147	226	180	5.841	1.57E-02	rs2374529	12	104546498	q23.3
SNP_A-2124005	C	C	341	69	321	93	4.14	0.0419	rs11112638	12	104550818	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784561	G	G	381	35	366	54	4.338	0.0373	rs7134108	12	104569056	q23.3
SNP_A-2152374	G	G	322	42	327	25	4.152	4.16E-02	rs10746044	12	104620192	q23.3
SNP_A-2294102	T	T	282	64	254	96	7.84	5.10E-03	rs3741636	12	104638409	q23.3
SNP_A-2221515	G	G	319	93	289	121	5.139	2.34E-02	rs4338635	12	104641473	q23.3
SNP_A-1940165	A	A	287	69	234	96	8.837	3.00E-03	rs10746045	12	104646025	q23.3
SNP_A-2238432	C	C	286	56	250	80	6.441	0.0112	rs10746046	12	104647919	q23.3
SNP_A-2239156	T	T	322	94	289	129	7.271	7.00E-03	rs10735408	12	104647993	q23.3
SNP_A-2097220	G	G	330	78	310	104	4.296	3.82E-02	rs11833529	12	104664409	q23.3
SNP_A-1722642	T	T	319	79	306	106	3.97	4.63E-02	rs4600310	12	104664872	q23.3
SNP_A-1836482	T	T	295	71	273	97	4.854	0.0276	rs4509866	12	104670637	q23.3
SNP_A-2095211	T	T	226	154	203	191	4.95	2.61E-02	rs7311274	12	104709472	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1822282	A	A	250	150	286	114	7.327	6.80E-03	rs7971430	12	104801909	q23.3
SNP_A-2073022	G	G	238	108	288	90	4.985	2.56E-02	rs1421463	12	104810155	q23.3
SNP_A-1642865	A	A	362	38	342	66	8.028	4.60E-03	rs10507204	12	104817170	q23.3
SNP_A-2309574	G	G	346	36	319	53	4.212	4.01E-02	rs7956811	12	104828077	q23.3
SNP_A-1852394	A	A	369	21	398	10	4.596	3.20E-02	rs7313912	12	104929896	q23.3
SNP_A-2238623	A	A	400	18	416	6	6.295	0.0121	rs17038111	12	104995354	q23.3
SNP_A-2225220	A	A	346	20	362	8	5.483	1.92E-02	rs2075383	12	105416790	q23.3
SNP_A-2221715	C	C	330	20	332	6	7.337	6.80E-03	rs4964471	12	105482215	q23.3
SNP_A-2120338	C	C	400	12	413	3	5.589	1.81E-02	rs11113069	12	105542809	q23.3
SNP_A-2239441	C	C	383	31	361	47	3.889	4.86E-02	rs7968306	12	106273914	q23.3
SNP_A-2235331	G	G	350	36	376	22	4.128	4.22E-02	rs10861732	12	106275009	q23.3
SNP_A-1900709	A	A	377	21	355	43	8.224	4.10E-03	rs741366	12	106407562	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2124610	A	A	270	142	229	179	7.614	5.80E-03	rs4964586	12	106407958	q23.3
SNP_A-2096300	G	G	376	16	357	41	11.412	7.00E-04	rs4964217	12	106408792	q23.3
SNP_A-1819146	A	A	282	116	265	149	4.324	3.76E-02	rs7962232	12	106411481	q23.3
SNP_A-2155639	G	G	388	30	364	52	6.664	9.80E-03	rs12425559	12	106434056	q23.3
SNP_A-2073403	A	A	284	110	249	145	7.102	7.70E-03	rs11113385	12	106434646	q23.3
SNP_A-1818320	T	T	372	16	347	41	11.834	6.00E-04	rs12425238	12	106448837	q23.3
SNP_A-1942324	C	T	231	183	213	203	4.074	4.35E-02	rs10861756	12	106466079	q23.3
SNP_A-2204201	G	G	192	150	205	117	3.905	4.81E-02	rs6539389	12	106770118	q23.3
SNP_A-2003021	G	G	402	14	394	28	4.704	3.01E-02	rs4565951	12	106806569	q23.3
SNP_A-2210442	C	C	276	70	247	93	4.801	2.84E-02	rs12316047	12	106896312	q23.3
SNP_A-2174962	A	A	313	77	297	103	4.049	4.42E-02	rs7962481	12	106927172	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1930604	G	G	375	9	331	19	4.749	0.0293	rs11113879	12	107328530	q23.3
SNP_A-2213970	A	A	380	16	381	31	4.473	0.0344	rs17040591	12	107363162	q23.3
SNP_A-2181269	C	C	392	0	394	6	5.925	0.0149	rs12367818	12	107403902	q23.3
SNP_A-1642227	A	A	384	18	406	8	4.283	0.0385	rs10492251	12	107467548	q23.3
SNP_A-1810088	A	A	409	9	399	21	4.919	2.66E-02	rs11114094	12	107809093	q24.11
SNP_A-1911754	G	G	259	61	281	43	3.987	4.59E-02	rs10849968	12	108157040	q24.11
SNP_A-2231536	C	C	236	126	187	153	7.607	5.80E-03	rs10849988	12	108184387	q24.11
SNP_A-2148341	C	C	258	136	214	168	7.286	6.90E-03	rs1866065	12	108201731	q24.11
SNP_A-2092457	T	T	244	126	266	90	6.682	9.70E-03	rs1036515	12	108208340	q24.11
SNP_A-2161814	A	A	199	181	234	150	5.712	1.69E-02	rs1121314	12	108235695	q24.11
SNP_A-2248454	C	T	206	180	210	176	4.664	3.08E-02	rs10850060	12	108246410	q24.11
SNP_A-2097327	C	G	165	161	197	135	6.566	0.0104	rs4766469	12	108299610	q24.11
SNP_A-1795707	A	G	181	163	194	138	8.278	4.00E-03	rs10850131	12	108299772	q24.11
SNP_A-2230842	G	G	377	31	397	15	6.063	0.0138	rs2338102	12	108320740	q24.11
SNP_A-2003030	G	G	337	67	348	44	4.763	2.91E-02	rs7135909	12	108333818	q24.11
SNP_A-2097344	G	G	255	145	205	199	13.892	2.00E-04	rs7308864	12	108333899	q24.11
SNP_A-2097359	G	A	210	144	198	182	9.617	0.0019	rs10774708	12	108355876	q24.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1952610	G	A	211	195	243	167	10.363	1.30E-03	rs7313797	12	108358885	q24.11
SNP_A-2191042	G	G	318	54	336	22	13.706	2.00E-04	rs11066813	12	108380823	q24.11
SNP_A-2304092	G	G	388	26	349	51	9.943	1.60E-03	rs11066856	12	108385858	q24.11
SNP_A-1713544	A	G	242	160	209	205	9.395	2.20E-03	rs7311187	12	108400627	q24.11
SNP_A-2003031	G	G	265	125	282	92	5.214	0.0224	rs3815575	12	108410625	q24.11
SNP_A-1862239	T	T	238	160	274	120	8.226	4.10E-03	rs10466917	12	108440184	q24.11
SNP_A-2289014	G	G	307	75	331	43	9.497	2.10E-03	rs11067165	12	108443339	q24.11
SNP_A-2097430	T	C	241	159	210	206	9.479	2.10E-03	rs731178	12	108444398	q24.11
SNP_A-2097433	G	G	285	81	323	61	4.763	2.91E-02	rs888193	12	108450296	q24.11
SNP_A-2055975	G	C	245	161	214	202	11.507	7.00E-04	rs877710	12	108456696	q24.11
SNP_A-2236546	C	T	248	160	204	198	10.88	0.001	rs888192	12	108457817	q24.11
SNP_A-1787126	G	G	336	38	367	17	9.255	0.0023	rs7957619	12	108476599	q24.11
SNP_A-2072838	G	G	292	118	326	94	4.468	3.45E-02	rs7300998	12	108479170	q24.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2223137	C	C	237	157	202	198	7.481	6.20E-03	rs10161126	12	108505068	q24.11
SNP_A-2085738	A	G	182	176	226	162	6.185	0.0129	rs1861679	12	108517764	q24.11
SNP_A-1783830	G	G	274	46	255	69	5.258	0.0218	rs10850520	12	108537989	q24.11
SNP_A-1811132	G	G	364	26	354	42	3.858	4.95E-02	rs1344550	12	108665895	q24.11
SNP_A-2035751	T	T	328	0	306	6	6.367	1.16E-02	rs3759385	12	108912459	q24.11
SNP_A-2308733	C	C	334	12	338	4	4.001	4.55E-02	rs7960705	12	109547260	q24.11
SNP_A-2185989	G	G	338	4	342	16	6.861	8.80E-03	rs12310570	12	109751458	q24.11
SNP_A-1832759	A	A	314	76	303	103	3.949	4.69E-02	rs6489979	12	110077456	q24.11
SNP_A-2272317	G	G	320	52	335	31	5.608	1.79E-02	rs1016078	12	110872797	q24.13
SNP_A-1893604	G	G	341	23	382	12	4.602	3.19E-02	rs16942244	12	111719523	q24.13
SNP_A-2090402	A	A	320	88	350	58	7.508	6.10E-03	rs2072133	12	111871980	q24.13
SNP_A-1950644	C	C	399	5	381	17	6.916	8.50E-03	rs16942812	12	112346843	q24.13
SNP_A-2098888	A	G	182	176	205	147	5.88	1.53E-02	rs7302421	12	112542535	q24.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1783482	T	T	223	153	242	112	6.463	1.10E-02	rs565559	12	112568897	q24.13
SNP_A-1856526	G	G	329	77	298	100	4.442	3.51E-02	---	12	112596877	q24.13
SNP_A-1812908	C	C	364	10	359	23	5.072	2.43E-02	rs2075385	12	112759307	q24.13
SNP_A-2250040	A	A	227	119	249	93	4.182	4.08E-02	rs10774719	12	112807280	q24.21
SNP_A-1846353	C	C	304	90	341	71	3.965	0.0465	rs4767205	12	112982757	q24.21
SNP_A-2099348	A	A	301	99	328	74	4.767	2.90E-02	rs4767211	12	112991005	q24.21
SNP_A-2099349	C	C	318	100	346	76	4.435	3.52E-02	rs4767212	12	112991225	q24.21
SNP_A-2110920	A	A	314	102	341	75	5.232	2.22E-02	rs11066937	12	112993223	q24.21
SNP_A-2182563	G	G	252	130	226	160	5.713	1.68E-02	rs1248039	12	113347100	q24.21
SNP_A-2224245	T	T	358	42	372	26	4.028	4.47E-02	rs1403091	12	113410541	q24.21
SNP_A-1857231	C	C	360	18	400	8	4.813	2.82E-02	rs1718377	12	113486957	q24.21
SNP_A-2236759	G	G	337	11	353	3	4.852	0.0276	rs7314419	12	113697366	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1865355	A	A	305	53	306	80	4.435	3.52E-02	rs11613537	12	113849404	q24.21
SNP_A-1818967	G	G	276	96	306	74	4.309	3.79E-02	rs35486	12	113989282	q24.21
SNP_A-2230647	C	C	344	28	340	50	5.807	0.016	rs11067442	12	114054744	q24.21
SNP_A-1810303	C	C	329	35	310	54	4.621	3.16E-02	rs10850460	12	114154145	q24.21
SNP_A-1796493	A	A	349	15	360	6	4.022	4.49E-02	rs17750524	12	114265036	q24.21
SNP_A-2047549	C	C	234	148	255	119	3.967	4.64E-02	rs2133317	12	114297666	q24.21
SNP_A-2185449	C	C	310	58	280	94	10.004	1.60E-03	rs11067588	12	114318849	q24.21
SNP_A-2196978	T	T	300	80	276	108	5.149	2.33E-02	rs7295176	12	114321916	q24.21
SNP_A-2137128	C	-	212	142	184	184	7.122	0.0076	rs10850515	12	114335910	q24.21
SNP_A-2286469	C	C	255	137	285	109	4.849	2.77E-02	rs10850519	12	114391160	q24.21
SNP_A-1866238	T	T	203	147	255	121	7.505	6.20E-03	rs4767327	12	114391911	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1795588	G	G	202	134	241	97	9.354	2.20E-03	rs4767331	12	114394665	q24.21
SNP_A-1900751	G	T	190	180	208	152	6.107	0.0135	rs4767332	12	114394992	q24.21
SNP_A-1936521	A	A	205	197	243	161	6.838	8.90E-03	rs10850523	12	114395347	q24.21
SNP_A-2243643	G	G	217	199	256	162	7.003	8.10E-03	rs10850524	12	114395381	q24.21
SNP_A-2107150	A	A	197	191	219	151	5.417	1.99E-02	rs7299936	12	114396720	q24.21
SNP_A-2166019	C	C	265	135	310	100	8.612	0.0033	rs1874902	12	114413419	q24.21
SNP_A-2076015	A	A	268	146	312	104	10.389	1.30E-03	rs1874898	12	114413958	q24.21
SNP_A-2193564	G	G	202	122	250	76	15.778	7.12E-05	rs3858650	12	114421784	q24.21
SNP_A-2077642	G	G	261	147	306	110	8.821	3.00E-03	rs1463829	12	114423129	q24.21
SNP_A-1802393	T	T	255	141	291	103	8.287	4.00E-03	rs1463828	12	114423150	q24.21
SNP_A-2040771	C	C	370	44	343	65	5.025	2.50E-02	rs2133318	12	114426513	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1808141	C	C	241	157	207	191	5.902	1.51E-02	rs10774819	12	114476977	q24.21
SNP_A-1867101	A	A	327	63	291	81	3.924	4.76E-02	rs7977279	12	114477825	q24.21
SNP_A-2161148	A	A	327	39	299	59	5.246	2.20E-02	rs11067670	12	114502063	q24.21
SNP_A-2226716	C	C	229	157	205	195	5.182	2.28E-02	rs12312326	12	114507362	q24.21
SNP_A-1902146	G	G	387	13	397	3	6.378	1.16E-02	rs12426160	12	114509830	q24.21
SNP_A-2295424	C	C	266	126	244	158	4.429	3.53E-02	rs11067687	12	114530786	q24.21
SNP_A-2135963	A	A	258	110	275	83	4.182	4.08E-02	rs4767342	12	114537771	q24.21
SNP_A-2284805	A	A	295	89	306	62	4.691	3.03E-02	rs1647147	12	114663044	q24.21
SNP_A-1813131	G	G	380	36	385	21	3.859	4.95E-02	rs1647110	12	114695730	q24.21
SNP_A-2101132	A	A	286	100	270	132	4.551	3.29E-02	rs697879	12	114759538	q24.21
SNP_A-2129384	G	G	402	12	414	4	4.157	4.15E-02	rs11067813	12	114774622	q24.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2101195	A	A	379	19	364	34	4.548	3.30E-02	rs2278488	12	114866285	q24.21
SNP_A-1920627	T	T	367	13	362	26	4.285	0.0385	rs7302993	12	114962091	q24.21
SNP_A-2059920	C	C	353	19	337	37	6.151	1.31E-02	rs17580303	12	115002104	q24.21
SNP_A-2102244	G	G	392	24	374	42	5.332	2.09E-02	rs3907612	12	115144014	q24.21
SNP_A-1891609	T	T	353	9	356	20	3.921	4.77E-02	rs10850603	12	115212457	q24.21
SNP_A-2101356	C	C	230	144	278	120	5.977	1.45E-02	rs3926689	12	115293119	q24.21
SNP_A-1843676	A	A	339	9	334	20	4.159	4.14E-02	rs7975887	12	115298394	q24.21
SNP_A-2260452	T	T	366	18	362	36	5.773	1.63E-02	rs4767404	12	115331805	q24.22
SNP_A-1789748	A	A	305	33	291	57	6.584	0.0103	rs7960700	12	115502030	q24.22
SNP_A-2106109	G	G	404	4	408	0	4.02	4.50E-02	rs10850710	12	115661639	q24.22
SNP_A-2024446	A	A	328	28	322	14	4.147	4.17E-02	rs4074147	12	115866658	q24.22
SNP_A-1784177	G	G	321	31	313	51	4.779	2.88E-02	rs1093289	12	116404344	q24.22
SNP_A-1680834	T	C	209	191	227	187	4.083	4.33E-02	rs1878420	12	116464747	q24.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102264	C	C	343	25	297	45	8.079	4.50E-03	rs845753	12	116473853	q24.22
SNP_A-2102265	G	G	364	50	332	72	5.317	2.11E-02	rs816202	12	116474004	q24.22
SNP_A-2077876	G	G	377	39	395	19	7.311	6.90E-03	rs10850878	12	116544714	q24.22
SNP_A-1930226	A	A	402	0	404	4	3.961	4.66E-02	---	12	116550542	q24.22
SNP_A-2235699	C	C	284	92	295	65	4.507	3.38E-02	rs637307	12	116602579	q24.23
SNP_A-2278881	G	G	354	28	343	49	5.773	1.63E-02	rs2592283	12	116730416	q24.23
SNP_A-2305235	C	C	382	32	369	53	5.337	2.09E-02	rs2245557	12	116745950	q24.23
SNP_A-1898641	G	G	334	6	303	15	4.635	3.13E-02	rs12308535	12	116776213	q24.23
SNP_A-2287413	G	G	358	6	387	1	3.938	4.72E-02	rs11068865	12	117085969	q24.23
SNP_A-1836220	G	G	374	6	399	1	3.87	4.92E-02	rs11068898	12	117190117	q24.23
SNP_A-1805946	G	G	316	102	290	132	4.943	2.62E-02	rs905579	12	117351916	q24.23
SNP_A-2252052	A	A	349	63	367	43	4.221	3.99E-02	rs1503767	12	117352208	q24.23
SNP_A-1892719	C	C	341	29	361	13	6.644	0.01	rs10850984	12	117412547	q24.23
SNP_A-1710956	G	G	301	101	284	130	3.959	4.66E-02	rs4126012	12	117476805	q24.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116964	A	A	264	94	301	75	4.12	0.0424	rs2730562	12	117511304	q24.23
SNP_A-1940179	G	G	169	153	210	130	5.819	1.58E-02	rs2682783	12	117577289	q24.23
SNP_A-1810321	A	A	262	102	281	73	5.332	2.09E-02	rs1525976	12	117819185	q24.23
SNP_A-2107232	T	T	293	117	268	144	3.902	0.0482	rs10851061	12	117904358	q24.23
SNP_A-2039487	C	C	386	18	367	33	4.871	2.73E-02	rs11609770	12	117998943	q24.23
SNP_A-2026598	A	A	367	7	362	24	9.17	2.50E-03	rs4767780	12	118003942	q24.23
SNP_A-2227254	T	T	391	19	396	8	4.469	3.45E-02	rs11064701	12	118093721	q24.23
SNP_A-2003064	G	G	298	106	325	77	5.761	1.64E-02	rs2467020	12	118110592	q24.23
SNP_A-2245526	C	C	340	12	373	3	6.143	0.0132	rs11612180	12	118409096	q24.23
SNP_A-2205265	T	T	360	8	348	20	5.346	2.08E-02	rs1179368	12	119197425	q24.23
SNP_A-1954725	C	C	227	129	270	106	5.429	1.98E-02	rs12370780	12	119533693	q24.31
SNP_A-2201719	G	G	219	93	265	73	5.751	1.65E-02	rs10431386	12	119591646	q24.31
SNP_A-2267625	T	T	402	14	412	4	5.678	0.0172	rs10849797	12	119731647	q24.31
SNP_A-2195910	C	C	266	106	247	139	4.892	0.027	rs16996363	12	119807922	q24.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2262364	T	T	362	12	373	25	3.99	0.0458	rs535557	12	120041107	q24.31
SNP_A-2234337	T	T	332	6	267	33	23.566	0.000001207	rs11830323	12	120171851	q24.31
SNP_A-1932819	C	C	351	51	329	73	4.615	3.17E-02	rs921286	12	120690411	q24.31
SNP_A-2148745	C	C	362	0	339	5	5.299	2.13E-02	rs10847464	12	121690789	q24.31
SNP_A-2300162	G	G	264	84	247	113	4.633	3.14E-02	rs2454727	12	121725214	q24.31
SNP_A-2122086	T	T	344	70	324	94	4.092	4.31E-02	rs1106240	12	122151862	q24.31
SNP_A-2095738	G	G	334	64	306	88	4.994	2.54E-02	rs1727313	12	122165733	q24.31
SNP_A-2003081	G	G	398	20	401	9	4.107	4.27E-02	rs3759111	12	122212654	q24.31
SNP_A-1806768	T	T	347	71	323	95	4.33	3.75E-02	rs2695478	12	122214401	q24.31
SNP_A-2038087	C	C	354	14	369	5	4.526	3.34E-02	rs11057273	12	122339346	q24.31
SNP_A-1857110	C	C	273	127	242	166	6.979	8.20E-03	rs10734906	12	122732448	q24.31
SNP_A-2047865	A	A	278	138	243	175	6.72	9.50E-03	rs7132115	12	122732800	q24.31
SNP_A-2269761	G	G	259	123	229	151	4.7	3.02E-02	rs2271660	12	122744935	q24.31
SNP_A-2046385	G	G	269	145	234	186	7.471	0.0063	rs7295552	12	122748724	q24.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2237795	G	G	345	61	357	41	4.047	4.42E-02	rs11057444	12	123089430	q24.31
SNP_A-1914460	C	C	351	55	339	79	4.333	3.74E-02	rs379457	12	123127800	q24.31
SNP_A-2269332	C	C	338	48	335	77	5.901	1.51E-02	rs10846622	12	123193939	q24.31
SNP_A-2068799	T	T	325	37	311	69	9.538	0.002	rs11057495	12	123194381	q24.31
SNP_A-2211067	T	T	377	17	371	33	5.044	0.0247	rs4424765	12	123234143	q24.31
SNP_A-2277740	C	C	365	31	357	53	5.609	1.79E-02	rs10161259	12	123274610	q24.31
SNP_A-2310127	C	C	352	40	322	68	8.59	3.40E-03	rs11057556	12	123281315	q24.31
SNP_A-2198120	C	C	377	15	374	30	4.832	2.79E-02	rs1726263	12	123596523	q24.31
SNP_A-2174482	A	A	391	3	397	11	4.374	3.65E-02	rs701085	12	123680780	q24.31
SNP_A-1821793	C	C	386	24	391	11	4.782	2.88E-02	rs1672879	12	123805982	q24.31
SNP_A-1917503	C	C	363	45	390	26	5.976	1.45E-02	rs11057869	12	123869345	q24.31
SNP_A-2312468	A	A	237	97	200	114	3.889	4.86E-02	rs4375522	12	123961730	q24.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1781153	A	A	227	89	196	134	11.054	9.00E-04	rs10744187	12	123962471	q24.31
SNP_A-2126623	A	A	340	4	366	0	4.28	3.86E-02	rs7312043	12	124456595	q24.31
SNP_A-2312304	G	G	411	5	418	0	5.054	0.0246	rs16919403	12	124710743	q24.31
SNP_A-1726620	A	G	221	159	192	190	5.436	1.97E-02	rs10492041	12	124945152	q24.31
SNP_A-1959711	G	G	376	12	359	31	8.783	3.00E-03	rs225475	12	124987448	q24.31
SNP_A-1827271	A	A	394	14	373	27	4.618	3.16E-02	rs10847025	12	124988442	q24.31
SNP_A-2034718	C	C	355	13	361	1	10.287	1.30E-03	rs16920219	12	125172199	q24.31
SNP_A-2205281	G	G	411	7	421	1	4.601	3.19E-02	rs16920233	12	125176046	q24.31
SNP_A-2003092	G	G	274	108	296	80	4.972	0.0258	rs7956295	12	125245792	q24.31
SNP_A-2106242	C	C	294	116	275	147	4.116	4.25E-02	rs10492042	12	125248963	q24.31
SNP_A-1897881	T	T	390	10	380	2	5.052	0.0246	rs2021544	12	125670335	q24.32
SNP_A-1961443	G	G	331	43	299	61	4.475	0.0344	rs4765460	12	125799167	q24.32
SNP_A-2121261	C	C	213	131	190	164	4.862	0.0275	rs10847220	12	125804441	q24.32
SNP_A-1886719	T	T	397	9	388	2	4.238	0.0395	rs4765480	12	125915669	q24.32
SNP_A-1798753	C	C	379	39	359	61	5.377	2.04E-02	rs1166427	12	125948838	q24.32
SNP_A-1941865	C	C	385	29	366	52	6.992	8.20E-03	rs12426396	12	125954778	q24.32
SNP_A-2261071	G	G	303	47	281	75	7.205	7.30E-03	rs1627684	12	125963387	q24.32
SNP_A-2293161	C	C	254	110	297	91	4.39	0.0361	rs11059104	12	126406310	q24.32
SNP_A-2119686	A	A	266	100	248	136	5.693	1.70E-02	rs10847353	12	126480066	q24.32
SNP_A-2113402	G	G	232	116	213	151	5.042	0.0247	rs701057	12	126484196	q24.32
SNP_A-1882091	G	G	361	45	347	65	3.869	4.92E-02	rs755836	12	126822665	q24.32
SNP_A-2206775	C	C	359	41	334	62	5.163	2.31E-02	rs1238440	12	126825585	q24.32
SNP_A-2067485	G	G	353	63	371	41	5.082	2.42E-02	rs7300577	12	127072041	q24.32
SNP_A-1909798	T	T	379	33	363	51	4.197	4.05E-02	rs4882751	12	127389423	q24.32
SNP_A-2257092	T	T	355	47	367	25	6.797	9.10E-03	rs1683718	12	127414879	q24.32
SNP_A-2121075	G	G	355	31	389	5	20.252	6.79E-06	rs1683724	12	127426774	q24.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255403	C	C	296	74	277	101	4.711	3.00E-02	rs11059873	12	127761568	q24.32
SNP_A-1647362	A	A	258	144	232	176	4.535	0.0332	rs1386212	12	127935757	q24.33
SNP_A-1818129	G	G	278	60	278	36	5.124	2.36E-02	rs470671	12	127956638	q24.32
SNP_A-2105188	G	G	219	121	255	99	4.654	0.031	rs1616468	12	127967817	q24.32
SNP_A-1835134	A	G	159	149	199	155	4.058	4.40E-02	rs3893975	12	127999047	q24.32
SNP_A-1865014	C	C	369	5	380	0	5.114	2.37E-02	rs11060069	12	128019654	q24.32
SNP_A-2100727	G	G	359	59	381	37	5.696	1.70E-02	rs11060099	12	128055247	q24.32
SNP_A-2003117	G	G	343	41	375	25	4.981	2.56E-02	rs3851670	12	128061392	q24.32
SNP_A-1785903	G	G	375	41	397	19	8.694	3.20E-03	rs11833199	12	128120420	q24.32
SNP_A-1899964	G	G	278	78	328	54	7.582	5.90E-03	rs10847773	12	128122580	q24.32
SNP_A-2117616	A	A	276	138	249	167	4.141	0.0419	rs9805018	12	128235831	q24.32
SNP_A-1783588	G	G	226	104	194	124	3.972	4.63E-02	rs7310830	12	128240641	q24.32
SNP_A-2130328	A	C	223	191	219	191	4.366	3.67E-02	rs4760030	12	128306076	q24.33
SNP_A-2107967	T	C	203	193	220	174	3.991	4.57E-02	rs879560	12	128316376	q24.33
SNP_A-1930176	G	G	239	87	217	111	3.964	0.0465	rs7955684	12	128333185	q24.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2218321	A	A	253	89	237	119	4.57	3.25E-02	rs11060369	12	128485077	q24.33
SNP_A-1818521	T	T	368	0	360	4	4.066	4.38E-02	rs3867493	12	128528403	q24.33
SNP_A-2267634	A	A	258	104	242	134	4.029	4.47E-02	rs10744426	12	128605431	q24.33
SNP_A-2307558	C	C	387	29	371	51	6.345	0.0118	rs10847929	12	128730913	q24.33
SNP_A-2094153	C	C	388	30	368	50	5.529	1.87E-02	rs935835	12	128731897	q24.33
SNP_A-1814042	C	C	387	29	364	48	5.374	2.04E-02	rs935834	12	128731945	q24.33
SNP_A-1841152	T	T	382	22	358	38	4.966	2.59E-02	rs4760001	12	128735771	q24.33
SNP_A-2225808	G	G	387	5	370	16	6.098	0.0135	rs11060526	12	128753337	q24.33
SNP_A-1870453	T	T	254	78	237	111	5.977	1.45E-02	rs1376795	12	128805150	q24.33
SNP_A-2069933	T	T	329	53	322	82	5.694	1.70E-02	rs11060565	12	128816580	q24.33
SNP_A-1852034	A	A	268	134	278	100	4.389	3.62E-02	rs825879	12	128950830	q24.33
SNP_A-2076876	C	C	338	74	363	47	6.912	0.0086	rs1499928	12	128990812	q24.33
SNP_A-1896514	T	T	300	84	344	64	4.986	2.55E-02	rs1675869	12	129006015	q24.33
SNP_A-2073012	C	C	334	78	348	54	4.529	3.33E-02	rs10848100	12	129432902	q24.33
SNP_A-2151730	T	T	406	4	390	12	4.243	3.94E-02	rs11060928	12	129484907	q24.33
SNP_A-2176905	A	G	182	160	211	169	5.508	0.0189	rs4759753	12	129689513	q24.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2267298	C	C	228	184	262	152	5.402	0.0201	rs2632601	12	129793577	q24.33
SNP_A-2283153	G	G	349	69	371	49	4.057	4.40E-02	rs1569019	12	130101071	q24.33
SNP_A-2223583	G	G	348	70	370	50	4.003	4.54E-02	rs1976930	12	130101325	q24.33
SNP_A-2299747	A	A	331	5	311	13	3.962	0.0465	rs2280701	12	130467776	q24.33
SNP_A-1897941	C	C	355	27	374	14	4.571	3.25E-02	rs7136949	12	130488111	q24.33
SNP_A-1913289	T	T	268	94	254	126	4.596	3.20E-02	rs7485158	12	130748068	q24.33
SNP_A-1840218	A	A	325	27	309	13	3.976	4.61E-02	rs10902417	12	130803982	q24.33
SNP_A-2098671	T	T	199	127	188	176	6.163	1.30E-02	rs12310237	12	130843942	q24.33
SNP_A-2204371	A	A	349	51	379	35	3.973	4.62E-02	rs11246770	12	130873365	q24.33
SNP_A-2236989	C	C	350	62	374	30	11.849	6.00E-04	rs11246771	12	130873764	q24.33
SNP_A-2064227	A	A	343	55	377	35	5.81	1.59E-02	rs10902442	12	130899373	q24.33
SNP_A-2202205	G	G	357	21	360	6	8.154	0.0043	rs3751309	12	131767990	q24.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2104594	C	C	386	28	372	46	4.618	3.16E-02	rs5744841	12	131850057	q24.33
SNP_A-2286226	C	C	402	12	417	3	5.632	1.76E-02	rs2062162	12	132043094	q24.33
SNP_A-1727052	C	C	381	11	386	24	4.459	3.47E-02	rs1855637	13	17249443	q11
SNP_A-1698981	C	C	380	8	380	20	4.961	2.59E-02	rs2801744	13	17249794	q11
SNP_A-2313899	T	T	303	17	283	33	5.778	1.62E-02	rs4770451	13	18419975	q12.11
SNP_A-1667208	A	A	325	19	329	37	5.133	0.0235	rs2313626	13	18486150	q12.11
SNP_A-1668134	T	T	283	85	322	58	7.421	6.40E-03	rs10492508	13	18627582	q12.11
SNP_A-2303588	C	C	398	4	404	0	4.04	4.44E-02	rs3002077	13	18870977	q12.11
SNP_A-1818747	A	A	400	12	382	24	4.371	3.66E-02	rs7324021	13	19535140	q12.11
SNP_A-2100981	G	G	355	43	341	67	6.052	1.39E-02	rs9552069	13	19552610	q12.11
SNP_A-2077733	C	C	364	48	392	26	7.535	6.10E-03	rs2313477	13	19656323	q12.11
SNP_A-1876129	T	T	306	48	311	23	8.269	4.00E-03	rs2313478	13	19656460	q12.11
SNP_A-2145765	G	G	253	151	220	190	6.719	9.50E-03	rs9550627	13	19759190	q12.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2286760	T	T	233	107	197	125	3.924	4.76E-02	rs7995321	13	19822535	q12.11
SNP_A-2106668	G	G	400	14	387	31	6.618	0.0101	rs7991112	13	19922275	q12.11
SNP_A-2160113	C	T	199	181	227	173	6.495	1.08E-02	rs12873775	13	20099207	q12.11
SNP_A-1784405	T	C	204	200	239	173	5.936	1.48E-02	rs9509311	13	20107637	q12.11
SNP_A-2129433	G	G	309	43	302	22	5.715	1.68E-02	rs9315905	13	20302969	q12.11
SNP_A-1723018	C	C	325	67	313	95	4.747	0.0293	rs717265	13	20337544	q12.11
SNP_A-2150392	T	T	368	4	370	18	8.581	3.40E-03	rs9578342	13	20645976	q12.11
SNP_A-1664008	T	T	387	9	392	20	3.889	4.86E-02	rs1577359	13	20788677	q12.11
SNP_A-2150111	T	T	292	98	326	74	5.094	0.024	rs1475340	13	20895285	q12.11
SNP_A-1925306	T	T	350	30	338	52	5.983	0.0144	rs9509769	13	20981064	q12.11
SNP_A-2214052	T	T	285	91	303	61	6.279	1.22E-02	rs17680062	13	21246173	q12.11
SNP_A-1856629	G	G	310	78	328	52	5.625	0.0177	rs571828	13	21253768	q12.11
SNP_A-1882768	A	A	221	133	203	165	3.93	4.74E-02	rs9509883	13	21298032	q12.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2112682	A	A	282	42	267	69	6.761	9.30E-03	rs9509895	13	21314174	q12.11
SNP_A-1690015	T	T	337	63	369	43	5.048	0.0247	rs9317499	13	21501554	q12.12
SNP_A-1719037	G	G	352	48	378	30	5.001	0.0253	rs10507325	13	21515653	q12.12
SNP_A-1749271	C	C	348	40	378	26	3.888	4.86E-02	rs7983559	13	21516580	q12.12
SNP_A-2112919	T	T	343	53	332	76	4.102	4.28E-02	rs4769189	13	21545376	q12.11
SNP_A-1918103	C	C	293	61	327	43	4.629	3.14E-02	rs9552597	13	21588127	q12.11
SNP_A-1780830	G	G	390	24	408	10	6.152	1.31E-02	rs17076373	13	21683540	q12.11
SNP_A-2151120	C	C	374	38	401	19	7.198	7.30E-03	rs17076551	13	21767583	q12.11
SNP_A-2249791	T	T	379	3	360	10	4.067	4.37E-02	rs460453	13	21867191	q12.11
SNP_A-2041605	G	G	322	32	271	47	5.321	2.11E-02	rs12871032	13	21987687	q12.11
SNP_A-2055340	A	A	336	80	363	55	5.668	1.73E-02	rs9578484	13	22121090	q12.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113392	C	C	248	166	219	199	4.765	2.90E-02	rs314874	13	22177254	q12.11
SNP_A-2113395	A	A	249	167	219	201	5.045	0.0247	rs314873	13	22177279	q12.11
SNP_A-2113398	G	G	388	2	379	9	4.555	3.28E-02	rs17267850	13	22179711	q12.11
SNP_A-1903832	A	A	231	133	267	113	3.886	0.0487	rs431103	13	22191714	q12.11
SNP_A-2168671	A	A	224	126	256	98	5.611	1.79E-02	rs9506918	13	22227062	q12.12
SNP_A-1871447	G	G	341	45	354	28	4.181	4.09E-02	rs17077544	13	22227181	q12.12
SNP_A-1820648	C	C	241	157	259	115	6.393	0.0115	rs12428099	13	22248341	q12.12
SNP_A-1936059	G	G	247	163	274	126	6.014	1.42E-02	rs9580437	13	22248509	q12.12
SNP_A-2122876	A	A	278	132	321	91	10.62	1.10E-03	rs9506931	13	22287128	q12.12
SNP_A-2053212	C	A	235	169	219	191	10.944	9.00E-04	rs1330919	13	22294326	q12.12
SNP_A-2083870	C	C	347	19	306	38	8.234	4.10E-03	rs12431295	13	22347571	q12.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2061360	C	C	372	32	384	16	5.504	0.019	rs872273	13	22573103	q12.12
SNP_A-2179056	G	G	290	116	316	92	3.88	4.89E-02	rs9580556	13	22645255	q12.12
SNP_A-1843285	A	A	355	31	349	49	3.918	4.78E-02	rs1819342	13	22662131	q12.12
SNP_A-2241730	G	G	379	35	360	54	4.545	3.30E-02	rs2002748	13	22718684	q12.12
SNP_A-2273929	G	G	276	138	247	165	4.009	0.0453	rs4550321	13	22721888	q12.12
SNP_A-1809345	G	G	335	63	355	37	7.295	6.90E-03	rs17314986	13	22722818	q12.12
SNP_A-2021576	G	G	359	57	379	39	3.912	4.79E-02	rs17331329	13	22989459	q12.12
SNP_A-2250477	A	A	236	122	204	150	5.187	2.28E-02	rs7994077	13	23049156	q12.12
SNP_A-2195024	A	A	269	131	236	156	4.254	3.92E-02	rs7336862	13	23059031	q12.12
SNP_A-2139409	G	G	257	127	225	155	4.884	2.71E-02	rs9510783	13	23077453	q12.12
SNP_A-2024685	G	G	304	40	329	25	4.307	3.80E-02	rs8181878	13	23324511	q12.12
SNP_A-2265996	C	C	313	85	343	65	3.915	4.79E-02	rs2025304	13	23534912	q12.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2114730	G	G	357	11	352	24	4.778	2.88E-02	rs7317248	13	23625220	q12.12
SNP_A-2276238	A	A	348	10	343	21	3.89	4.86E-02	rs9511119	13	23660689	q12.12
SNP_A-2185923	T	T	238	178	267	149	4.237	0.0395	rs9551080	13	23675773	q12.12
SNP_A-2248249	T	T	224	168	250	138	4.347	3.71E-02	rs17364874	13	23685005	q12.12
SNP_A-1915745	T	T	382	4	386	0	4.021	4.49E-02	rs2027436	13	23692987	q12.12
SNP_A-2245170	G	G	378	34	398	16	6.991	8.20E-03	rs17077825	13	23829981	q12.12
SNP_A-2311238	G	G	376	4	404	0	4.274	3.87E-02	rs1539094	13	23859146	q12.12
SNP_A-2115063	G	G	354	6	382	0	6.419	1.13E-02	rs1822135	13	23906630	q12.12
SNP_A-2078463	C	C	217	125	239	97	4.54	3.31E-02	rs9511333	13	24010376	q12.12
SNP_A-2091851	G	G	326	0	330	4	3.928	4.75E-02	rs7990877	13	24015837	q12.12
SNP_A-2184785	C	C	202	118	177	143	4.044	4.43E-02	rs3783061	13	24172526	q12.12
SNP_A-2299447	C	C	290	62	298	38	5.5	0.019	rs1555716	13	24879163	q12.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2116047	A	A	411	1	411	9	6.324	1.19E-02	rs11841525	13	25134853	q12.13
SNP_A-1818724	G	G	348	64	374	38	7.564	6.00E-03	rs1048788	13	25492668	q12.13
SNP_A-1913193	A	C	211	205	244	176	6.534	0.0106	rs1048789	13	25492700	q12.13
SNP_A-2267875	G	G	329	85	358	58	6.317	0.012	rs9319303	13	25943129	q12.13
SNP_A-2296181	G	A	234	170	207	205	5.469	1.94E-02	rs12864131	13	25943939	q12.13
SNP_A-2117182	C	C	327	7	349	1	4.844	2.77E-02	rs10507369	13	26058345	q12.13
SNP_A-2066319	G	G	397	9	406	2	4.551	3.29E-02	rs17084554	13	26183805	q12.13
SNP_A-2220083	T	T	283	89	302	66	4.008	0.0453	rs2149136	13	26256780	q12.13
SNP_A-2195066	T	T	371	21	357	37	4.678	3.06E-02	rs17488034	13	26314251	q12.13
SNP_A-2087368	A	A	410	0	410	4	3.981	4.60E-02	rs7981344	13	26375106	q12.13
SNP_A-2260930	A	A	392	0	364	6	6.407	0.0114	rs7989114	13	26378201	q12.13
SNP_A-2088803	G	G	399	11	407	1	8.408	3.70E-03	rs12585453	13	26409902	q12.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1799853	C	C	318	20	327	9	4.292	3.83E-02	rs2039062	13	26463562	q12.13
SNP_A-1944024	C	C	368	12	385	3	5.701	1.70E-02	rs2094514	13	26482302	q12.13
SNP_A-1901566	G	G	295	31	319	17	4.871	2.73E-02	rs9553986	13	26767278	q12.2
SNP_A-2265182	C	C	365	3	363	11	4.529	3.33E-02	rs1333349	13	26798677	q12.2
SNP_A-2168309	A	A	314	84	291	111	4.593	3.21E-02	rs11616513	13	26845975	q12.2
SNP_A-2139197	A	A	268	106	250	138	4.567	3.26E-02	rs1218796	13	26896361	q12.2
SNP_A-1902355	G	G	337	51	324	80	6.355	0.0117	rs9554196	13	27374640	q12.2
SNP_A-2083484	G	G	312	98	345	73	5.236	2.21E-02	rs7326283	13	27377685	q12.2
SNP_A-1804463	G	G	352	64	331	89	4.712	3.00E-02	rs9551419	13	27378356	q12.2
SNP_A-2281620	A	A	268	54	237	79	6.546	1.05E-02	rs9579129	13	27382959	q12.2
SNP_A-2043321	G	G	300	62	304	36	6.241	1.25E-02	rs9513027	13	27546669	q12.2
SNP_A-2134371	G	G	337	25	330	12	4.076	4.35E-02	rs4771232	13	27706958	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2045000	A	G	193	155	184	156	6.311	0.012	rs4769612	13	28036498	q12.3
SNP_A-1805022	T	A	194	184	204	160	4.034	4.46E-02	rs9578057	13	28208467	q12.3
SNP_A-2208617	A	A	338	26	331	51	7.76	0.0053	rs2025177	13	28437451	q12.3
SNP_A-2238147	T	C	213	177	224	180	8.035	4.60E-03	rs326506	13	28506905	q12.3
SNP_A-1950171	A	A	199	131	222	100	5.319	2.11E-02	rs9508253	13	28540422	q12.3
SNP_A-2160434	C	C	290	14	344	2	10.931	9.00E-04	rs9506139	13	28797994	q12.3
SNP_A-2256387	T	T	320	94	359	61	9.223	2.40E-03	rs9550472	13	28962363	q12.3
SNP_A-2188488	G	G	376	2	380	10	5.168	0.023	rs2036973	13	29079404	q12.3
SNP_A-2103064	C	C	348	14	362	4	5.81	1.59E-02	rs17073761	13	29085009	q12.3
SNP_A-2077847	C	C	358	30	388	16	5.146	2.33E-02	rs4299006	13	29097029	q12.3
SNP_A-2166720	C	C	328	10	326	22	4.361	3.68E-02	rs17502757	13	29279204	q12.3
SNP_A-2157364	A	G	221	185	211	189	4.16	4.14E-02	rs7321345	13	29337397	q12.3
SNP_A-2122874	C	C	235	143	275	109	7.678	5.60E-03	rs503693	13	29419992	q12.3
SNP_A-2052899	A	A	253	127	217	159	6.317	0.012	rs482983	13	29593606	q12.3
SNP_A-2216648	A	A	253	127	224	168	7.277	7.00E-03	rs613712	13	29597185	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2176299	C	C	237	117	213	157	6.769	9.30E-03	rs614220	13	29597329	q12.3
SNP_A-1905145	C	C	401	5	414	0	5.13	0.0235	rs2149970	13	29685070	q12.3
SNP_A-1810911	C	C	268	48	247	81	9.078	2.60E-03	rs7983230	13	29840955	q12.3
SNP_A-1899380	A	A	283	119	265	151	4.145	4.17E-02	rs1275189	13	29844291	q12.3
SNP_A-1881529	G	G	390	2	389	13	7.943	4.80E-03	rs6490461	13	29874845	q12.3
SNP_A-1866887	A	A	185	171	232	144	7.07	7.80E-03	rs9508795	13	30022651	q12.3
SNP_A-2268282	T	T	200	192	236	158	6.27	0.0123	rs9506337	13	30022678	q12.3
SNP_A-2133511	G	G	346	14	375	5	4.893	0.027	rs17074775	13	30075774	q12.3
SNP_A-2223477	A	A	340	26	365	13	5.028	2.49E-02	rs9508822	13	30179695	q12.3
SNP_A-1738625	T	T	304	90	280	120	5.227	2.22E-02	rs9315149	13	30284846	q13.1
SNP_A-1910754	G	G	310	82	332	50	8.384	0.0038	rs17599197	13	30343890	q12.3
SNP_A-2077392	A	A	382	34	367	53	4.431	3.53E-02	rs1412203	13	30423174	q12.3
SNP_A-1838653	C	C	374	36	353	59	6.17	1.30E-02	rs4942071	13	30431165	q12.3
SNP_A-2120939	C	C	375	39	355	59	4.63	3.14E-02	rs7993586	13	30440032	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1915533	G	G	219	109	258	92	3.917	4.78E-02	rs4635202	13	30516659	q12.3
SNP_A-2121021	G	A	217	199	246	172	10.165	0.0014	rs1571187	13	30540155	q12.3
SNP_A-2121027	T	T	217	191	272	142	13.353	3.00E-04	rs9315107	13	30540858	q12.3
SNP_A-2288870	G	G	308	108	333	83	4.247	3.93E-02	rs2031725	13	30560077	q12.3
SNP_A-1882083	T	T	312	102	342	74	5.826	1.58E-02	rs12864062	13	30581392	q12.3
SNP_A-1724424	T	T	346	20	378	6	8.526	3.50E-03	rs1952994	13	30900876	q13.1
SNP_A-1841968	A	A	201	139	208	102	4.425	3.54E-02	rs277128	13	30995005	q12.3
SNP_A-1835553	T	T	336	26	326	44	4.693	3.03E-02	rs202451	13	31060903	q12.3
SNP_A-1758319	G	G	393	7	407	1	4.666	3.08E-02	-	13	31270683	q13.1
SNP_A-1754240	T	T	302	98	340	72	6.05	1.39E-02	rs797709	13	31371054	q13.1
SNP_A-1946684	T	T	295	89	259	125	8.395	0.0038	rs9566949	13	31463539	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074397	G	G	331	85	308	110	4.028	4.47E-02	rs12856583	13	31487490	q13.1
SNP_A-1870093	C	C	271	111	245	143	5.295	2.14E-02	rs416443	13	31499801	q13.1
SNP_A-2290477	A	A	254	100	224	126	4.851	0.0276	rs465023	13	31515091	q13.1
SNP_A-2086688	T	T	343	37	348	20	4.915	2.66E-02	rs12864812	13	31551377	q13.1
SNP_A-1930187	A	A	269	83	238	108	5.117	2.37E-02	rs415482	13	31557105	q13.1
SNP_A-1890859	C	C	308	82	286	106	3.874	4.91E-02	rs17634824	13	31631138	q13.1
SNP_A-2249097	G	G	189	127	171	169	5.989	0.0144	rs472817	13	31881250	q13.1
SNP_A-2195923	G	G	373	37	395	21	5.001	0.0253	rs4942947	13	32344933	q13.1
SNP_A-2122817	T	T	354	40	380	24	4.796	2.85E-02	rs2320760	13	32379793	q13.1
SNP_A-2122835	A	A	371	43	392	26	4.747	0.0293	rs4941701	13	32383476	q13.1
SNP_A-2276849	C	C	248	130	216	158	4.908	2.67E-02	rs9537595	13	32946539	q13.2
SNP_A-2054802	A	A	320	18	334	8	4.122	4.23E-02	rs9591912	13	33099168	q13.2
SNP_A-2003226	A	A	381	33	395	19	4.022	4.49E-02	rs2764015	13	33129571	q13.2
SNP_A-2235723	C	C	371	15	382	6	4.013	4.52E-02	rs5008744	13	33345299	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1904434	G	G	375	19	389	7	5.79	0.0161	rs691667	13	33588520	q13.2
SNP_A-2124312	G	G	293	87	262	112	4.825	0.0281	rs1538005	13	33658437	q13.2
SNP_A-2182350	A	A	410	4	408	12	3.962	0.0465	rs1396311	13	34166730	q13.2
SNP_A-1936993	T	T	284	78	273	107	4.329	3.75E-02	rs1508487	13	34191969	q13.2
SNP_A-2042051	C	C	336	8	319	21	6.246	1.25E-02	rs17051670	13	34347442	q13.2
SNP_A-2247742	T	T	372	44	345	75	9.073	2.60E-03	rs275968	13	35185863	q13.3
SNP_A-2125812	A	A	296	78	328	56	5.122	2.36E-02	rs1171065	13	35359822	q13.3
SNP_A-2087122	A	A	211	173	257	133	9.704	0.0018	rs9575162	13	35513122	q13.3
SNP_A-1823731	G	G	297	87	319	45	13.624	2.00E-04	rs17199136	13	35543483	q13.3
SNP_A-1942290	G	G	346	70	319	99	6.068	0.0138	rs11839572	13	35544078	q13.3
SNP_A-2095872	G	G	305	89	335	61	6.628	0.01	—	13	35546004	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1840827	C	C	312	90	286	114	3.949	4.69E-02	rs9575257	13	35557784	q13.3
SNP_A-1915295	G	G	296	114	326	86	5.362	0.0206	rs6563354	13	35594494	q13.3
SNP_A-2183026	G	G	224	134	195	159	4.118	0.0424	rs9546505	13	35612556	q13.3
SNP_A-2052791	C	C	329	69	346	48	4.177	4.10E-02	rs2296967	13	35642800	q13.3
SNP_A-1666626	G	G	329	57	369	39	5.062	2.45E-02	rs1853326	13	35796714	q13.3
SNP_A-2022830	C	C	264	98	220	144	12.738	4.00E-04	rs9547491	13	35845826	q13.3
SNP_A-1655265	T	T	240	150	205	187	6.81	9.10E-03	rs9315495	13	35885145	q13.3
SNP_A-1723260	A	A	307	93	279	133	8.242	4.10E-03	rs1028728	13	35971816	q13.3
SNP_A-1643521	C	C	224	156	268	114	10.463	1.20E-03	rs7332871	13	36028987	q13.3
SNP_A-1693913	A	A	186	106	191	173	8.354	0.0038	rs9315508	13	36067944	q13.3
SNP_A-1698669	G	G	354	46	382	24	7.935	4.80E-03	rs1570607	13	36103325	q13.3
SNP_A-1703483	A	A	358	40	345	65	6.016	1.42E-02	rs10507459	13	36234648	q13.3
SNP_A-2251992	G	G	295	49	314	30	5.162	2.31E-02	rs1571320	13	36305492	q13.3
SNP_A-1708506	G	G	348	46	334	72	5.838	1.57E-02	rs2250286	13	36380178	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2126784	G	G	402	8	406	0	8	4.70E-03	rs1998567	13	36700839	q13.3
SNP_A-2024461	C	C	333	57	346	38	4.003	4.54E-02	rs17068485	13	36799218	q13.3
SNP_A-2306347	C	C	292	46	312	24	7.571	5.90E-03	rs12431260	13	36813802	q13.3
SNP_A-1873183	C	C	348	36	353	17	6.589	0.0103	rs4245384	13	36846479	q13.3
SNP_A-2124742	T	T	378	38	401	17	8.693	3.20E-03	rs9532054	13	36895719	q13.3
SNP_A-1952178	T	T	370	28	403	11	8.507	3.50E-03	rs9532055	13	36898711	q13.3
SNP_A-1803441	A	A	379	31	400	12	8.957	0.0028	rs1407606	13	36902061	q13.3
SNP_A-2111264	C	C	333	27	346	12	6.013	1.42E-02	rs1830656	13	36902096	q13.3
SNP_A-1785430	C	C	350	62	371	37	6.905	0.0086	rs6563540	13	36906009	q13.3
SNP_A-2075671	T	T	216	130	244	82	11.988	5.00E-04	rs9547892	13	36937839	q13.3
SNP_A-1948456	C	C	377	29	404	12	7.862	5.00E-03	rs9547894	13	36938037	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2138832	A	A	269	115	303	81	7.919	4.90E-03	rs9576280	13	36958247	q13.3
SNP_A-2127077	C	C	269	87	282	58	5.742	0.0166	rs1407604	13	36992661	q13.3
SNP_A-1816944	T	T	273	109	232	154	11.008	9.00E-04	rs17255466	13	36998807	q13.3
SNP_A-2106002	C	C	236	156	260	120	5.672	0.0172	rs7997809	13	37125748	q13.3
SNP_A-2308568	T	T	335	33	372	20	4.371	3.65E-02	rs1333364	13	37193580	q13.3
SNP_A-1874774	C	C	348	32	378	16	6.322	1.19E-02	rs17203407	13	37213086	q13.3
SNP_A-2086846	C	C	365	37	385	15	9.836	1.70E-03	rs12584260	13	37238960	q13.3
SNP_A-1651846	A	A	289	77	325	53	6.35	0.0117	rs7337135	13	37256116	q13.3
SNP_A-1693260	C	C	307	89	342	70	3.843	5.00E-02	rs2184141	13	37256405	q13.3
SNP_A-2214712	T	T	225	87	200	122	7.176	7.40E-03	rs9566255	13	37276364	q13.3
SNP_A-2067646	C	C	307	87	266	110	5.201	2.26E-02	rs9576358	13	37281495	q13.3
SNP_A-2273590	C	C	277	83	250	106	4.16	4.14E-02	rs601958	13	37284764	q13.3
SNP_A-1922361	A	A	368	0	363	7	7.029	8.00E-03	rs1414646	13	37573815	q13.3
SNP_A-2228434	G	G	338	6	383	1	4.195	4.05E-02	rs11841753	13	38098826	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2165765	T	T	362	12	382	4	4.349	3.70E-02	rs7319670	13	38303170	q13.3
SNP_A-2162501	A	A	285	57	317	37	5.751	1.65E-02	rs7139901	13	38351783	q13.3
SNP_A-2187621	G	G	319	91	344	64	5.641	1.75E-02	rs2225623	13	38357484	q13.3
SNP_A-1787030	A	A	301	71	322	42	8.064	4.50E-03	rs9576634	13	38360545	q13.3
SNP_A-1644952	C	A	202	188	210	158	5.96	0.0146	rs276420	13	38370070	q14.11
SNP_A-2040458	C	C	383	19	403	5	8.632	0.0033	rs7330164	13	38393544	q13.3
SNP_A-2185521	G	G	368	24	391	9	7.435	6.40E-03	rs7989270	13	38393776	q13.3
SNP_A-2303516	C	C	371	11	403	3	5.168	0.023	rs9315631	13	38414525	q13.3
SNP_A-2305872	G	G	379	27	396	14	4.475	0.0344	rs10454604	13	38417169	q13.3
SNP_A-2128394	C	C	396	20	412	6	7.851	5.10E-03	—	13	38423339	q13.3
SNP_A-2288366	C	C	397	19	413	7	5.836	1.57E-02	rs10220044	13	38424228	q13.3
SNP_A-2180375	C	C	297	119	327	93	4.612	3.17E-02	rs2324129	13	38580032	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2083147	G	G	327	49	351	29	5.957	0.0147	rs9576735	13	38602187	q13.3
SNP_A-2084326	G	G	386	26	397	13	4.483	3.42E-02	rs17590107	13	38685335	q13.3
SNP_A-2112792	T	T	248	122	271	97	3.868	4.92E-02	rs1413057	13	38729614	q13.3
SNP_A-1758212	G	G	254	142	286	116	4.472	3.45E-02	rs1319281	13	38763706	q14.11
SNP_A-1783932	G	G	409	5	406	14	4.231	3.97E-02	---	13	39185001	q14.11
SNP_A-1697735	G	G	343	53	325	85	7.664	5.60E-03	rs9315797	13	39353352	q14.11
SNP_A-1856401	G	G	366	48	348	68	3.897	4.84E-02	rs2146368	13	39398414	q14.11
SNP_A-1851907	C	C	403	7	405	1	4.485	3.42E-02	---	13	39540620	q14.11
SNP_A-2115691	-	C	190	190	211	157	4.047	4.43E-02	rs7339301	13	39637333	q14.11
SNP_A-2129288	C	C	336	12	301	33	11.441	7.00E-04	rs9315762	13	39639907	q14.11
SNP_A-1933203	C	C	373	7	354	22	8.234	4.10E-03	rs4426233	13	39838726	q14.11
SNP_A-2223670	G	G	380	36	366	54	3.844	0.0499	rs1751852	13	39876966	q14.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1878860	C	C	350	16	342	30	4.305	3.80E-02	rs1624886	13	39878019	q14.11
SNP_A-2084665	A	A	342	52	328	76	4.668	3.07E-02	rs9594471	13	40460786	q14.11
SNP_A-1801106	A	A	346	58	326	82	4.69	3.03E-02	rs2772181	13	40530244	q14.11
SNP_A-1700107	C	A	210	190	244	168	11.211	8.00E-04	rs9315894	13	40531977	q14.11
SNP_A-1675710	C	C	333	47	331	71	4.272	3.87E-02	rs10492443	13	40532510	q14.11
SNP_A-1665548	A	A	351	45	334	70	5.777	1.62E-02	rs9315897	13	40536982	q14.11
SNP_A-1727351	G	G	375	21	362	36	4.172	4.11E-02	rs347413	13	40585040	q14.11
SNP_A-1900081	A	A	393	21	383	37	4.5	0.0339	rs4402447	13	40882742	q14.11
SNP_A-2242790	G	G	379	33	394	18	4.703	3.01E-02	rs10870761	13	41012918	q14.11
SNP_A-2053440	A	A	412	4	420	0	4.056	4.40E-02	rs17594369	13	41037516	q14.11
SNP_A-1658838	G	G	336	64	313	99	8.155	0.0043	rs727227	13	41123418	q14.11
SNP_A-2156955	G	G	247	151	225	187	4.619	3.16E-02	rs11147857	13	41170319	q14.11
SNP_A-2130183	T	T	250	154	223	187	4.691	3.03E-02	rs3945431	13	41170932	q14.11
SNP_A-1735943	A	A	335	65	305	99	8.435	3.70E-03	rs7987618	13	41183763	q14.11
SNP_A-1845068	C	C	277	113	261	147	4.518	3.35E-02	rs9590631	13	41197653	q14.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2260796	A	A	296	120	329	89	6.336	0.0118	rs1343869	13	41223871	q14.11
SNP_A-1925458	C	C	382	12	367	27	6.07	0.0138	rs3904327	13	41338981	q14.11
SNP_A-2172177	C	C	289	63	267	37	4.14	0.0419	rs9525555	13	41408305	q14.11
SNP_A-2095058	T	T	232	158	202	184	4.03	4.47E-02	rs7997862	13	41469136	q14.11
SNP_A-2201592	G	G	298	58	323	39	4.678	3.05E-02	rs1900448	13	41502241	q14.11
SNP_A-2292835	G	G	311	77	330	46	8.19	4.20E-03	rs1900447	13	41502294	q14.11
SNP_A-2091933	C	C	365	43	328	64	5.779	1.62E-02	rs9532998	13	41571336	q14.11
SNP_A-2153420	T	C	196	176	240	150	15.545	8.06E-05	rs7981733	13	41588060	q14.11
SNP_A-2268643	T	T	292	102	250	142	9.807	1.70E-03	rs668989	13	41599399	q14.11
SNP_A-2130462	A	A	297	113	249	157	11.371	7.00E-04	rs605371	13	41599717	q14.11
SNP_A-2130516	C	C	367	47	340	76	7.864	5.00E-03	rs10492444	13	41632389	q14.11
SNP_A-2308450	T	T	248	130	224	158	3.922	4.77E-02	rs12585865	13	41649707	q14.11
SNP_A-2288567	C	C	286	116	315	93	3.886	0.0487	rs9525592	13	41657253	q14.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2020973	A	A	267	87	300	56	8.635	0.0033	rs9533034	13	41682127	q14.11
SNP_A-1892026	C	C	330	84	306	110	4.385	3.62E-02	rs9562401	13	41888400	q14.11
SNP_A-2167043	A	A	290	116	264	148	5.055	0.0246	rs7998938	13	42219475	q14.11
SNP_A-2131274	G	G	329	53	289	73	5.23	2.22E-02	rs1323608	13	42266536	q14.11
SNP_A-1920149	G	G	308	34	263	47	4.072	0.0436	rs1535902	13	42269359	q14.11
SNP_A-1918679	C	C	339	67	304	98	7.71	5.50E-03	rs9562431	13	42277500	q14.11
SNP_A-2081576	G	G	347	67	314	102	8.891	2.90E-03	rs9567041	13	42277674	q14.11
SNP_A-1953642	T	T	333	37	278	56	7.01	8.10E-03	rs7990962	13	42297245	q14.11
SNP_A-1836447	A	A	221	109	235	81	4.255	3.91E-02	rs9590722	13	42355890	q14.11
SNP_A-2232370	C	C	390	16	408	6	4.874	2.73E-02	rs7316945	13	43202275	q14.11
SNP_A-2257638	A	A	400	14	413	5	4.452	0.0349	—	13	43285680	q14.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2233381	C	C	411	5	416	0	5.03	2.49E-02	rs17600693	13	43407519	q14.11
SNP_A-1783785	G	G	362	0	312	8	9.157	2.50E-03	rs9590806	13	43562976	q14.11
SNP_A-2132736	C	C	284	90	311	69	3.951	4.68E-02	rs7983067	13	43809556	q14.11
SNP_A-1957443	A	A	294	74	301	47	5.553	1.85E-02	rs4942352	13	44202415	q14.12
SNP_A-1890926	G	G	281	57	313	41	3.968	4.64E-02	rs17639733	13	44226455	q14.12
SNP_A-2121455	T	T	320	26	318	12	4.788	0.0287	rs1175384	13	44422083	q14.12
SNP_A-2275903	A	A	191	185	232	168	4.054	0.0441	rs7989500	13	44823445	q14.13
SNP_A-2286575	A	A	176	174	227	155	6.164	1.30E-02	rs7333784	13	44831243	q14.13
SNP_A-1872070	T	C	188	184	225	161	5.942	1.48E-02	rs9590898	13	44845473	q14.13
SNP_A-2242196	G	G	350	24	338	44	6.008	1.42E-02	rs9590925	13	45241230	q14.13
SNP_A-1729818	T	T	368	32	397	15	7.072	7.80E-03	rs1417205	13	45696880	q14.2
SNP_A-1818455	A	A	370	4	390	0	4.193	4.06E-02	rs12585584	13	45769866	q14.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869235	G	G	368	0	375	7	6.807	9.10E-03	rs662227	13	45952050	q14.13
SNP_A-2166651	G	G	226	106	251	81	4.653	0.031	rs7327231	13	45999484	q14.13
SNP_A-2070802	C	C	300	68	290	96	4.523	3.34E-02	rs6561323	13	46083602	q14.13
SNP_A-2081091	G	G	255	63	242	94	5.97	1.45E-02	rs9526209	13	46117781	q14.13
SNP_A-1661131	C	C	338	58	372	40	4.619	3.16E-02	rs1172484	13	46169211	q14.2
SNP_A-1883199	C	C	374	10	375	23	4.873	2.73E-02	rs17355629	13	46212173	q14.2
SNP_A-1744675	A	A	261	139	241	171	3.924	4.76E-02	rs4414373	13	46226516	q14.2
SNP_A-2112120	G	G	250	124	230	156	4.302	3.81E-02	rs11148014	13	46234326	q14.2
SNP_A-2155003	G	G	245	159	200	184	5.869	0.0154	rs1216966	13	46268543	q14.2
SNP_A-2208478	A	A	368	18	356	34	5.101	2.39E-02	rs1216973	13	46274339	q14.2
SNP_A-1908220	C	C	373	39	349	61	5.633	1.76E-02	rs11616518	13	46505958	q14.2
SNP_A-1806886	C	C	364	52	338	82	7.66	5.60E-03	rs2503308	13	46540640	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1953971	C	C	337	17	299	29	4.416	0.0356	rs11148032	13	46549366	q14.2
SNP_A-2075034	A	A	356	48	332	74	6.373	1.16E-02	rs11148033	13	46551143	q14.2
SNP_A-1903724	C	C	360	52	335	77	5.744	1.65E-02	rs9595602	13	46553724	q14.2
SNP_A-2141758	G	G	375	31	392	12	8.767	3.10E-03	rs9316278	13	46739470	q14.2
SNP_A-2192557	G	G	333	33	332	16	5.449	1.96E-02	rs9316279	13	46739616	q14.2
SNP_A-2264792	A	A	384	32	403	15	6.603	1.02E-02	rs17069824	13	46752083	q14.2
SNP_A-1812480	A	A	327	69	350	48	4.546	3.30E-02	rs6561366	13	46760888	q14.2
SNP_A-2231492	A	A	331	71	339	43	6.467	1.10E-02	rs12016712	13	46763236	q14.2
SNP_A-2096264	G	G	247	117	292	90	6.848	8.90E-03	rs11620370	13	46871144	q14.2
SNP_A-1814741	T	T	399	1	399	7	4.456	3.48E-02	rs7997096	13	46883605	q14.2
SNP_A-1866640	C	C	235	139	243	103	4.407	3.58E-02	rs17070149	13	46956401	q14.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2161266	A	A	377	5	367	15	5.134	0.0235	rs1575892	13	47001519	q14.2
SNP_A-2223317	G	G	384	18	398	8	4.077	4.35E-02	rs9567925	13	47300251	q14.2
SNP_A-1906274	A	A	364	44	379	25	5.515	0.0189	rs9568007	13	47595491	q14.2
SNP_A-1826773	A	A	409	5	416	0	5.055	0.0246	rs17071960	13	48062196	q14.2
SNP_A-1830856	A	G	201	151	197	165	9.483	2.10E-03	rs9595960	13	48151520	q14.2
SNP_A-2055077	C	-	202	150	176	176	3.862	4.94E-02	rs9535083	13	48282047	q14.2
SNP_A-2311769	A	A	219	157	235	123	4.254	3.92E-02	rs9568135	13	48415150	q14.2
SNP_A-2243481	A	A	319	57	335	35	5.604	1.79E-02	rs7338291	13	48429552	q14.2
SNP_A-2220315	G	G	272	24	287	45	4.746	2.94E-02	rs9562900	13	49039363	q14.2
SNP_A-2075777	C	C	326	46	340	28	4.651	0.031	rs2066553	13	49494334	q14.2
SNP_A-2195098	G	G	315	41	269	55	4.168	4.12E-02	rs9568405	13	49877656	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282942	C	C	362	0	356	4	4.045	4.43E-02	rs17075302	13	50556913	q14.3
SNP_A-2270404	T	T	338	70	316	96	4.793	0.0286	rs957434	13	50584167	q14.3
SNP_A-1657582	C	C	254	58	247	93	7.021	8.10E-03	rs640428	13	51200386	q14.3
SNP_A-1818669	A	A	375	5	408	0	5.403	0.0201	rs647575	13	51371717	q14.3
SNP_A-1671656	A	A	389	11	385	23	4.177	4.10E-02	rs2408930	13	51843969	q14.3
SNP_A-2112447	T	T	341	11	343	3	4.526	3.34E-02	rs7335091	13	52129455	q14.3
SNP_A-1871690	T	T	272	116	251	149	4.771	2.89E-02	rs511818	13	52297206	q14.3
SNP_A-2169754	G	G	209	167	243	119	10.352	1.30E-03	rs8181889	13	52511991	q14.3
SNP_A-2158666	C	C	320	64	340	38	7.187	7.30E-03	rs2185961	13	52521236	q14.3
SNP_A-2158892	C	C	254	132	288	100	6.542	1.05E-02	rs4886137	13	52525355	q14.3
SNP_A-2246888	C	C	258	154	281	123	4.373	3.65E-02	rs2799346	13	52533281	q14.3
SNP_A-2098661	A	A	237	147	268	118	5.071	2.43E-02	rs2806999	13	52538263	q14.3
SNP_A-2147346	T	T	220	110	192	150	7.845	5.10E-03	rs2806946	13	52543934	q14.3
SNP_A-2157317	G	G	273	111	235	135	4.926	2.65E-02	rs2806949	13	52544139	q14.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2191577	T	T	329	17	360	8	3.961	4.66E-02	rs1999800	13	53094769	q14.3
SNP_A-2061218	C	C	317	31	324	14	6.354	0.0117	rs17088901	13	53261912	q14.3
SNP_A-1901965	A	A	369	19	351	37	6.236	1.25E-02	rs4883812	13	53441517	q14.3
SNP_A-1857526	T	T	301	51	302	26	7.281	7.00E-03	rs2408987	13	53557313	q14.3
SNP_A-2250234	A	A	196	188	219	155	4.318	3.77E-02	rs2782514	13	53771363	q14.3
SNP_A-1678984	A	A	355	43	384	26	5.149	2.33E-02	rs10507601	13	53947379	q21.1
SNP_A-2067815	C	C	373	23	392	10	5.548	1.85E-02	rs1360934	13	54041755	q14.3
SNP_A-1644578	C	C	299	101	335	75	5.762	1.64E-02	rs9285210	13	55403725	q21.1
SNP_A-1666468	C	C	343	19	354	38	5.322	2.11E-02	rs9285211	13	55403828	q21.1
SNP_A-1668560	A	A	316	84	350	62	4.875	2.73E-02	rs479855	13	55493846	q21.1
SNP_A-1667204	C	C	319	81	351	61	4.169	4.12E-02	rs1936755	13	55693967	q21.1
SNP_A-1819931	G	G	384	28	358	50	7.097	7.70E-03	rs2050583	13	56458695	q21.1
SNP_A-2310515	G	G	287	115	231	173	17.73	2.55E-05	rs9569580	13	56486888	q21.1
SNP_A-2141149	C	C	286	76	209	85	5.491	1.91E-02	rs4267192	13	56500151	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2141173	C	C	390	22	370	38	4.774	2.89E-02	rs790325	13	56527759	q21.1
SNP_A-1917455	C	C	284	118	224	154	11.123	9.00E-04	rs2777625	13	56534058	q21.1
SNP_A-1853690	C	C	212	174	234	130	6.814	9.00E-03	rs9597493	13	56534695	q21.1
SNP_A-2238096	A	A	265	125	214	180	15.328	9.04E-05	rs961050	13	56558394	q21.1
SNP_A-2293045	C	C	314	86	281	117	6.559	0.0104	rs2320174	13	56558450	q21.1
SNP_A-1809442	A	A	312	88	283	113	4.503	3.38E-02	rs563765	13	56601020	q21.1
SNP_A-2141329	T	T	365	45	349	65	3.976	4.62E-02	rs3850082	13	56701186	q21.1
SNP_A-2113653	G	G	361	43	305	57	4.379	3.64E-02	rs17053900	13	56726080	q21.1
SNP_A-2083514	C	C	326	80	352	58	4.485	3.42E-02	rs6650392	13	56824884	q21.1
SNP_A-2215779	C	C	405	5	378	14	4.793	0.0286	rs17054038	13	56842302	q21.1
SNP_A-2177392	A	A	281	53	268	76	4.262	0.039	rs7399511	13	56850408	q21.1
SNP_A-1726094	G	G	244	156	283	127	5.735	0.0166	rs9317079	13	57819865	q21.2
SNP_A-1845880	C	C	319	41	309	61	3.945	0.047	rs7335173	13	58121680	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287050	G	G	284	132	247	169	7.126	0.0076	rs1333537	13	58121987	q21.1
SNP_A-2142486	A	A	252	110	202	140	8.545	3.50E-03	rs9538174	13	58189378	q21.1
SNP_A-2096785	A	A	255	147	283	111	6.401	0.0114	rs9563646	13	58232735	q21.1
SNP_A-2181153	A	A	280	86	320	68	4.132	4.21E-02	rs7492218	13	58316494	q21.1
SNP_A-2142784	C	T	211	203	235	173	6.055	1.39E-02	rs9317034	13	58443546	q21.1
SNP_A-2142823	G	G	261	129	297	105	4.603	3.19E-02	rs9285217	13	58468127	q21.1
SNP_A-2120434	A	A	278	134	309	101	6.266	0.0123	rs9538288	13	58526352	q21.2
SNP_A-1873254	G	G	289	77	276	104	4.065	4.38E-02	rs9317050	13	58565837	q21.2
SNP_A-2234176	G	G	402	4	402	0	3.98	4.60E-02	rs1547200	13	58775833	q21.2
SNP_A-2210896	T	T	306	40	299	67	6.337	0.0118	rs9591989	13	58825788	q21.2
SNP_A-2201098	A	A	317	97	289	125	4.825	2.80E-02	rs1409254	13	58836970	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2158735	G	G	256	86	222	112	5.739	0.0166	rs12584255	13	58838410	q21.2
SNP_A-1827551	G	G	255	79	234	112	6.394	0.0115	rs1326091	13	58839798	q21.2
SNP_A-2173189	T	T	240	174	268	146	3.993	4.57E-02	rs6562028	13	58863555	q21.2
SNP_A-1804808	T	T	260	96	229	121	4.795	2.85E-02	rs9598006	13	58871577	q21.2
SNP_A-1935699	A	A	247	161	281	131	5.252	2.19E-02	rs8001038	13	58928256	q21.2
SNP_A-1797541	G	G	249	143	280	112	5.585	1.81E-02	rs8000074	13	58928470	q21.2
SNP_A-2003342	C	C	263	145	294	114	5.436	1.97E-02	rs1878410	13	58935724	q21.2
SNP_A-2143397	C	C	229	105	181	139	10.062	0.0015	rs3895563	13	58954131	q21.2
SNP_A-1702763	G	G	386	14	408	4	5.989	0.0144	rs1999518	13	59132920	q21.2
SNP_A-1719091	C	C	376	24	369	43	5.278	2.16E-02	rs167272	13	59234551	q21.2
SNP_A-1720669	A	A	247	153	280	128	4.212	4.01E-02	rs2137986	13	59508567	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2003347	G	G	287	61	272	86	4.513	3.36E-02	rs7327821	13	59785590	q21.2
SNP_A-2209708	G	G	234	140	264	104	7.071	7.80E-03	rs1588759	13	60243781	q21.2
SNP_A-1798135	G	A	221	165	190	188	4.34	3.72E-02	rs3119852	13	60256371	q21.2
SNP_A-2030240	G	G	324	44	342	28	4.037	4.45E-02	rs993451	13	60285922	q21.2
SNP_A-2144560	C	C	323	27	330	14	4.145	4.17E-02	rs9317145	13	60310538	q21.2
SNP_A-2144575	G	G	288	54	251	75	5.578	1.82E-02	rs3914416	13	60317994	q21.2
SNP_A-1846483	A	A	381	11	352	22	4.393	0.0361	rs301688	13	60321333	q21.2
SNP_A-2305660	T	T	369	19	357	39	7.014	8.10E-03	rs1862201	13	60333283	q21.2
SNP_A-2144613	T	T	380	12	359	33	10.397	1.30E-03	rs301669	13	60334598	q21.2
SNP_A-1945053	T	T	263	57	251	85	5.414	0.02	rs17223208	13	60379946	q21.2
SNP_A-2144980	T	T	275	133	305	101	5.923	0.0149	rs2175953	13	60608503	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2267126	G	G	259	155	286	128	3.914	4.79E-02	rs7985761	13	60662858	q21.2
SNP_A-2145044	G	G	264	114	284	88	4.029	4.47E-02	rs3102190	13	60684722	q21.2
SNP_A-1741445	C	C	315	31	323	51	3.895	4.84E-02	rs2590492	13	60744734	q21.31
SNP_A-1650102	C	C	362	26	377	11	6.386	0.0115	rs10507678	13	60967267	q21.31
SNP_A-2116914	A	A	213	149	239	123	3.981	4.60E-02	rs9539288	13	61226415	q21.31
SNP_A-1933651	A	A	259	109	273	81	4.225	3.98E-02	rs4337196	13	61532542	q21.31
SNP_A-1735787	G	G	375	23	368	44	6.408	0.0114	rs9317297	13	61619499	q21.31
SNP_A-1906893	T	T	251	105	215	127	4.588	3.22E-02	rs417155	13	61773398	q21.31
SNP_A-1798820	C	C	333	25	331	11	5.087	0.0241	rs7319919	13	61998582	q21.31
SNP_A-2146930	T	T	341	23	309	41	6.366	1.16E-02	rs976460	13	62745339	q21.31
SNP_A-1669245	C	C	258	90	239	123	5.565	0.0183	rs1953643	13	62887946	q21.31
SNP_A-1899830	A	A	384	4	406	0	4.207	4.03E-02	rs275914	13	63331278	q21.31
SNP_A-2196981	G	G	306	90	267	121	7.128	0.0076	rs9528753	13	63878270	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137397	A	A	332	58	306	86	6.499	1.08E-02	rs4643188	13	63955813	q21.31
SNP_A-2205071	C	C	326	68	299	97	6.258	0.0124	rs1415011	13	63963642	q21.31
SNP_A-2154513	T	T	300	114	264	150	7.207	7.30E-03	rs9564177	13	63970921	q21.31
SNP_A-1956645	C	C	328	32	317	57	6.946	8.40E-03	rs9592384	13	64439315	q21.31
SNP_A-2149059	A	G	205	201	229	177	3.876	4.90E-02	rs1629705	13	64696304	q21.32
SNP_A-1937541	G	G	316	6	307	25	11.625	7.00E-04	rs7489956	13	64935051	q21.32
SNP_A-1702973	C	C	385	15	406	6	4.238	0.0395	rs10492473	13	64998943	q21.32
SNP_A-1667672	G	G	385	15	406	6	4.238	0.0395	rs964381	13	65018804	q21.32
SNP_A-1735901	T	T	202	182	240	162	4.02	4.50E-02	rs9317651	13	65579229	q21.32
SNP_A-2090770	C	C	282	50	288	28	5.877	1.53E-02	rs1442005	13	66327131	q21.32
SNP_A-1913737	C	C	354	30	340	54	7.012	8.10E-03	—	13	66384403	q21.32
SNP_A-2150712	A	A	351	29	328	54	8.304	4.00E-03	rs10492593	13	66392118	q21.32
SNP_A-2151084	A	A	208	178	225	143	4.056	4.40E-02	rs9529199	13	66660289	q21.32
SNP_A-1897530	G	G	207	183	238	146	6.275	1.22E-02	rs9541041	13	66727851	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2151248	G	G	412	2	409	9	4.446	3.50E-02	rs1173153	13	66861448	q21.32
SNP_A-2097120	A	A	358	24	354	44	5.579	1.82E-02	rs7997281	13	67084816	q21.32
SNP_A-2125059	G	G	374	34	392	18	5.341	2.08E-02	rs12100126	13	67219423	q21.32
SNP_A-2028249	G	G	384	22	365	39	5.215	0.0224	rs1475808	13	67233750	q21.32
SNP_A-2151550	C	C	362	10	393	3	4.296	3.82E-02	rs1331268	13	67259655	q21.32
SNP_A-1658752	C	C	301	89	330	66	4.7	3.02E-02	rs1438650	13	67279734	q21.33
SNP_A-1664508	C	C	347	35	363	21	3.855	4.96E-02	rs1119008	13	67617937	q21.33
SNP_A-2204724	A	A	385	7	401	1	4.701	3.02E-02	rs7320300	13	67675810	q21.33
SNP_A-2219561	T	T	262	154	287	125	4.134	4.20E-02	rs1146827	13	67717268	q21.33
SNP_A-1954709	C	C	259	115	256	78	4.866	2.74E-02	rs287397	13	68097597	q21.33
SNP_A-2143178	C	C	364	14	371	31	5.756	1.64E-02	rs1438649	13	68325735	q21.33
SNP_A-2066854	C	C	287	111	316	82	5.752	1.65E-02	rs9572034	13	68337871	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2074504	C	C	259	57	288	26	13.11	3.00E-04	rs1438646	13	68337892	q21.33
SNP_A-1719117	T	T	341	55	325	81	5.231	2.22E-02	rs9317874	13	68438973	q21.33
SNP_A-1865250	G	G	285	121	250	156	6.712	9.60E-03	rs9564518	13	68488370	q21.33
SNP_A-2214885	A	A	315	97	289	129	5.607	1.79E-02	rs4883834	13	68494810	q21.33
SNP_A-2056738	G	G	289	99	327	73	6.093	1.36E-02	rs6562554	13	68533983	q21.33
SNP_A-2288072	C	C	282	94	321	67	6.864	8.80E-03	rs2066221	13	68535126	q21.33
SNP_A-1841958	T	T	298	86	305	59	4.577	3.24E-02	rs11148798	13	68565060	q21.33
SNP_A-1851937	G	G	292	96	310	62	7.521	6.10E-03	rs1336674	13	68588559	q21.33
SNP_A-2250073	A	A	326	22	335	9	5.551	1.85E-02	rs2782463	13	68816876	q21.33
SNP_A-1724412	T	T	341	57	373	39	4.569	3.26E-02	rs9317931	13	68820552	q21.33
SNP_A-1711334	G	G	378	12	397	3	5.74	0.0166	rs10492733	13	69083667	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1655437	G	G	360	4	380	0	4.198	4.05E-02	rs7990294	13	69247277	q21.33
SNP_A-2079642	A	A	385	15	385	5	4.874	2.73E-02	rs3021374	13	69315629	q21.33
SNP_A-1951778	A	A	398	14	409	5	4.408	3.58E-02	rs2911504	13	69316650	q21.33
SNP_A-2290591	T	T	349	9	326	2	3.934	4.73E-02	rs3012107	13	69323910	q21.33
SNP_A-2066936	G	G	391	9	399	1	6.481	0.0109	rs17085605	13	69367426	q21.33
SNP_A-1924992	T	T	329	57	316	88	6.483	0.0109	rs9542167	13	69531078	q21.33
SNP_A-2127543	G	G	355	27	321	47	6.857	8.80E-03	rs9529676	13	69539187	q21.33
SNP_A-2037124	G	G	319	55	301	77	4.168	4.12E-02	rs7332679	13	69551003	q21.33
SNP_A-2126862	T	T	259	89	277	63	4.959	2.59E-02	rs4474585	13	69592698	q21.33
SNP_A-2153873	G	G	280	112	289	77	5.739	0.0166	rs9564665	13	69678281	q21.33
SNP_A-1834523	G	G	384	10	402	2	5.621	0.0177	rs9572448	13	69911753	q21.33
SNP_A-1842362	G	G	360	56	382	38	4.08	4.34E-02	rs9592718	13	69920782	q21.33
SNP_A-2027804	A	A	308	68	338	50	3.951	4.68E-02	rs8002090	13	69921512	q21.33
SNP_A-2151742	G	G	320	60	325	37	5.059	2.45E-02	rs9572471	13	69965619	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1917159	T	T	270	44	302	24	7.45	0.0063	rs9572472	13	69965775	q21.33
SNP_A-2188866	C	C	387	15	397	5	5.128	0.0235	rs17087250	13	70009633	q21.33
SNP_A-2218044	G	G	341	35	361	13	10.648	1.10E-03	rs17772532	13	70238650	q21.33
SNP_A-2154718	A	A	352	24	315	45	8.1	4.40E-03	rs17620171	13	70483115	q21.33
SNP_A-2094541	C	C	345	33	323	51	4.561	0.0327	rs7999845	13	71210958	q21.33
SNP_A-2155430	T	T	309	9	291	41	20.728	5.2934E-06	rs303945	13	71266315	q21.33
SNP_A-2224585	G	G	347	61	363	41	4.263	0.039	rs17791199	13	71574322	q21.33
SNP_A-2112555	T	T	378	26	356	48	7.2	7.30E-03	rs1362878	13	71778339	q21.33
SNP_A-1668698	C	T	209	153	203	183	7.985	4.70E-03	rs9318191	13	71933999	q22.1
SNP_A-1649786	C	C	386	4	406	0	4.185	4.08E-02	rs10492702	13	71993717	q22.1
SNP_A-2034742	C	C	281	81	284	56	3.892	4.85E-02	rs9318112	13	72169676	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2302927	C	C	247	89	251	53	7.578	5.90E-03	rs4883921	13	72496577	q22.1
SNP_A-1883316	A	C	170	134	173	157	4.412	3.57E-02	rs4885072	13	72715270	q22.1
SNP_A-1934058	A	A	383	23	397	11	4.482	3.43E-02	rs17191385	13	72796066	q22.1
SNP_A-1916467	A	A	326	46	331	27	4.716	2.99E-02	rs9592907	13	72815626	q22.1
SNP_A-2159013	G	G	373	11	371	3	4.446	3.50E-02	rs9318170	13	72838727	q22.1
SNP_A-2242750	G	G	327	89	302	118	5.037	2.48E-02	rs9573193	13	72902025	q22.1
SNP_A-2246043	G	G	403	11	414	2	6.374	1.16E-02	rs9573246	13	73024535	q22.1
SNP_A-2203492	G	A	205	153	179	165	6.084	1.36E-02	rs1034048	13	73024853	q22.1
SNP_A-2117168	A	A	197	139	225	113	4.534	0.0332	rs1034045	13	73126914	q22.1
SNP_A-2157746	C	C	290	62	319	45	3.882	4.88E-02	rs7322834	13	73537941	q22.1
SNP_A-2157939	T	T	331	83	356	62	3.932	4.74E-02	rs1156106	13	73739266	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2157942	C	C	332	84	356	62	4.148	4.17E-02	rs2184853	13	73739798	q22.1
SNP_A-1809279	A	A	193	143	204	108	4.302	3.81E-02	rs9543648	13	73923652	q22.1
SNP_A-1654171	T	T	393	7	394	18	4.665	3.08E-02	rs9318370	13	74084816	q22.2
SNP_A-1806339	A	A	293	121	263	151	4.928	0.0264	rs4885216	13	74114205	q22.1
SNP_A-2291123	C	C	348	60	317	93	8.558	3.40E-03	rs9318297	13	74114685	q22.1
SNP_A-2266981	G	G	328	56	292	82	6.858	8.80E-03	rs1887499	13	74116443	q22.1
SNP_A-2158445	A	A	343	41	298	70	10.4	1.30E-03	rs1410160	13	74126274	q22.1
SNP_A-1951318	A	A	323	87	299	119	5.82	1.58E-02	rs9593015	13	74128389	q22.1
SNP_A-2178594	A	A	338	46	315	69	5.41	0.02	rs9543739	13	74132666	q22.1
SNP_A-1678588	T	T	355	45	384	24	7.451	0.0063	rs10507846	13	74408841	q22.2
SNP_A-1720307	T	T	327	65	295	91	5.934	0.0149	rs1576867	13	74798125	q22.2
SNP_A-1744763	C	C	324	66	308	102	7.624	5.80E-03	rs10507856	13	74817824	q22.2
SNP_A-1688206	T	T	325	75	298	106	6.46	1.10E-02	rs283966	13	74879084	q22.2
SNP_A-2042546	C	C	361	5	380	16	5.076	2.43E-02	rs9600530	13	75169382	q22.2
SNP_A-2254183	C	C	407	5	399	15	5.075	2.43E-02	rs8000663	13	75186419	q22.2
SNP_A-1711578	T	T	299	33	295	59	6.676	9.80E-03	rs679090	13	75345792	q22.3
SNP_A-1795604	C	C	322	48	293	73	6.511	1.07E-02	rs11620523	13	75667133	q22.2
SNP_A-2267115	A	A	324	64	286	82	4.06	4.39E-02	rs8000953	13	75871232	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043391	T	T	322	50	306	18	12.214	5.00E-04	—	13	75877803	q22.2
SNP_A-1942637	A	A	320	60	298	90	6.701	9.60E-03	rs1572289	13	75885695	q22.2
SNP_A-1802715	G	G	321	51	293	79	7.308	6.90E-03	rs6562954	13	75887452	q22.2
SNP_A-2226365	G	G	318	58	297	87	6.434	0.0112	rs12873183	13	75898664	q22.2
SNP_A-2036218	C	C	311	55	270	76	5.702	1.69E-02	rs4885399	13	75906604	q22.2
SNP_A-2231199	T	T	339	69	311	101	7.21	7.20E-03	rs4885400	13	75908426	q22.2
SNP_A-1794139	T	T	336	68	309	93	5.007	0.0252	rs4885401	13	75908555	q22.2
SNP_A-1938264	G	G	336	62	297	87	6.349	0.0117	rs4885404	13	75912492	q22.2
SNP_A-2150524	T	T	336	62	294	82	4.956	2.60E-02	rs7985764	13	75930395	q22.2
SNP_A-2271764	G	G	298	46	266	72	7.492	6.20E-03	rs12874580	13	75930558	q22.2
SNP_A-2214126	G	G	335	71	286	96	6.884	8.70E-03	rs12858648	13	75931700	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1718141	G	G	344	38	342	62	5.154	2.32E-02	rs10507870	13	75966720	q22.3
SNP_A-2256847	A	A	331	71	299	97	5.604	1.79E-02	rs1758920	13	75969573	q22.2
SNP_A-2160393	A	A	327	67	292	90	5.164	2.31E-02	rs283976	13	75974787	q22.2
SNP_A-2160395	T	T	283	79	259	109	5.801	0.016	rs283975	13	75974819	q22.2
SNP_A-2276472	G	G	373	35	382	20	4.154	4.15E-02	rs2031942	13	76198215	q22.3
SNP_A-1894244	G	G	377	31	400	14	7.06	7.90E-03	rs621783	13	76397626	q22.3
SNP_A-2155808	C	C	387	11	401	1	8.562	3.40E-03	rs17067027	13	76437786	q22.3
SNP_A-2161969	G	G	329	23	321	43	5.96	0.0146	rs606861	13	76494409	q22.3
SNP_A-1842392	G	G	331	67	304	92	5.074	2.43E-02	rs424391	13	76512438	q22.3
SNP_A-2156578	C	C	295	39	275	61	5.536	1.86E-02	rs2185468	13	76564177	q22.3
SNP_A-1893243	A	A	370	34	382	18	5.095	0.024	rs6563005	13	76898444	q22.3
SNP_A-1807858	A	A	287	91	263	115	3.843	0.0499	rs17765211	13	76906375	q22.3
SNP_A-1817834	C	C	342	20	319	33	3.85	4.98E-02	rs4561336	13	77134721	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2161451	C	C	356	38	348	58	4.078	4.34E-02	rs1343911	13	77151328	q22.3
SNP_A-1921110	G	G	266	88	278	64	3.848	4.98E-02	rs1359391	13	77748071	q22.3
SNP_A-1878195	C	C	281	77	291	53	4.328	3.75E-02	rs9601041	13	77906949	q31.1
SNP_A-2219158	G	G	272	50	305	27	8.607	0.0033	rs7993946	13	78008550	q31.1
SNP_A-1727849	G	A	207	193	234	176	6.323	1.19E-02	rs3908811	13	78089695	q31.1
SNP_A-1738983	G	G	203	183	252	154	7.272	7.00E-03	rs10507900	13	78141534	q31.1
SNP_A-1645576	C	C	354	38	342	62	5.787	0.0161	rs2152227	13	78204088	q31.1
SNP_A-1733248	C	C	379	19	377	35	4.505	3.38E-02	rs10507903	13	78416916	q31.1
SNP_A-1934971	T	C	228	188	224	196	5.542	1.86E-02	rs944512	13	78463017	q31.1
SNP_A-2120720	C	C	374	14	385	5	4.417	0.0356	rs11149124	13	78671090	q31.1
SNP_A-2092599	A	A	360	4	386	0	4.265	3.89E-02	rs17071494	13	78945373	q31.1
SNP_A-1847004	G	G	383	17	377	7	3.889	4.86E-02	rs17071499	13	78957879	q31.1
SNP_A-2178270	G	G	403	11	418	2	6.462	1.10E-02	rs7333290	13	79121533	q31.1
SNP_A-2239158	A	A	405	11	418	2	6.417	1.13E-02	rs17071740	13	79138935	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920015	G	G	405	11	415	3	4.689	0.0304	rs17071744	13	79145771	q31.1
SNP_A-2210642	T	T	399	9	406	0	9.056	2.60E-03	rs4335681	13	79149247	q31.1
SNP_A-1874268	G	G	298	80	330	58	5.008	0.0252	rs2329130	13	79164792	q31.1
SNP_A-2115326	G	G	312	104	338	80	4.166	4.13E-02	rs2802630	13	79187117	q31.1
SNP_A-1953798	A	A	277	119	311	97	4.029	4.47E-02	rs1577406	13	79193269	q31.1
SNP_A-2028623	G	G	288	42	258	58	3.907	4.81E-02	rs1155859	13	79209606	q31.1
SNP_A-1832926	T	T	193	189	233	155	7.07	7.80E-03	rs2783085	13	79219165	q31.1
SNP_A-2190615	T	T	211	195	252	148	10.027	0.0015	rs12428029	13	79240313	q31.1
SNP_A-2052574	G	A	196	188	231	147	11.366	7.00E-04	rs7327527	13	79258401	q31.1
SNP_A-1830936	A	A	249	151	273	121	4.367	3.66E-02	rs7319612	13	79323661	q31.1
SNP_A-2122211	C	C	250	156	284	128	4.882	2.71E-02	rs7333650	13	79326008	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1915880	C	C	243	157	273	131	4.072	0.0436	rs7333880	13	79326112	q31.1
SNP_A-1907549	C	C	250	98	267	69	5.386	2.03E-02	rs9530983	13	79344288	q31.1
SNP_A-2062680	C	C	375	41	356	64	5.513	0.0189	rs6563144	13	79344705	q31.1
SNP_A-2213013	A	A	300	112	276	142	4.5	0.0339	rs3861150	13	79509141	q31.1
SNP_A-2104844	T	T	362	14	324	26	4.78	2.88E-02	rs1215445	13	79621998	q31.1
SNP_A-2238972	C	C	374	26	342	40	3.988	0.0458	rs637153	13	79654868	q31.1
SNP_A-2085570	C	C	396	12	392	24	3.943	4.71E-02	rs17072652	13	79853029	q31.1
SNP_A-1683218	A	T	175	137	188	168	5.271	2.17E-02	rs1855547	13	79955084	q31.1
SNP_A-2290931	G	G	380	2	353	9	4.915	2.66E-02	rs7994432	13	79984233	q31.1
SNP_A-1812282	T	T	364	26	337	43	5.099	2.39E-02	rs9531106	13	80188378	q31.1
SNP_A-2230118	A	A	369	15	348	30	5.568	0.0183	rs7322700	13	80547295	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2164509	T	T	382	16	395	5	5.974	1.45E-02	rs17294670	13	81194977	q31.1
SNP_A-2039615	C	C	259	81	273	55	5.125	2.36E-02	rs1983993	13	81694908	q31.1
SNP_A-1674399	C	C	261	119	308	92	6.829	9.00E-03	rs9318946	13	81860098	q31.1
SNP_A-2048853	G	G	324	14	341	5	4.605	3.19E-02	rs1536033	13	82127957	q31.1
SNP_A-1650250	C	C	374	24	370	40	3.844	0.0499	rs9319006	13	82329672	q31.1
SNP_A-1746296	A	A	266	134	245	167	4.305	3.80E-02	rs9319013	13	82422913	q31.1
SNP_A-1905023	G	G	349	63	369	41	5.206	2.25E-02	rs10162228	13	82575317	q31.1
SNP_A-2119054	A	A	216	168	258	150	4.017	4.50E-02	rs9602209	13	82998931	q31.1
SNP_A-1834535	C	C	280	38	304	22	5.154	2.32E-02	rs8000328	13	83007169	q31.1
SNP_A-2156681	T	-	201	145	178	178	4.626	0.0315	rs13331932	13	83188717	q31.1
SNP_A-2166397	C	C	248	164	212	200	6.378	1.16E-02	rs944281	13	83642608	q31.1
SNP_A-1848524	G	G	258	148	289	107	8.226	4.10E-03	rs2774070	13	83672051	q31.1
SNP_A-1858993	G	G	274	142	317	103	9.318	0.0023	rs2774065	13	83675709	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796431	C	C	288	72	273	43	4.871	2.73E-02	rs1330514	13	83826870	q31.1
SNP_A-1948072	G	G	325	25	343	9	8.009	4.70E-03	rs11620026	13	84014668	q31.1
SNP_A-1957476	A	A	273	55	273	33	4.742	2.94E-02	rs9546812	13	84164434	q31.1
SNP_A-2053928	C	T	193	189	214	164	3.886	0.0487	rs6563407	13	84183675	q31.1
SNP_A-2235088	G	G	269	133	306	106	5.309	0.0212	rs9602537	13	84190495	q31.1
SNP_A-2022848	C	C	317	37	343	21	5.3	2.13E-02	rs9531673	13	84393493	q31.1
SNP_A-1890995	T	T	402	6	406	0	6.015	1.42E-02	rs7984669	13	84692519	q31.1
SNP_A-1824283	G	G	350	24	345	41	4.294	3.83E-02	rs9575849	13	84708502	q31.1
SNP_A-1688518	G	G	288	108	266	146	6.244	1.25E-02	rs4523806	13	84723574	q31.1
SNP_A-1932760	G	G	294	18	313	7	5.334	2.09E-02	rs12867065	13	84788344	q31.1
SNP_A-2289107	A	A	336	26	333	43	3.938	4.72E-02	rs585377	13	85080141	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2298545	G	G	363	17	382	6	5.663	1.73E-02	rs1029143	13	85563006	q31.1
SNP_A-1889274	A	A	244	98	216	130	6.173	1.30E-02	rs9517334	13	85830872	q31.1
SNP_A-2158726	G	G	338	58	359	39	4.349	3.70E-02	rs7989577	13	85995724	q31.1
SNP_A-1812689	C	C	343	45	365	27	5.163	2.31E-02	rs1343558	13	86059258	q31.1
SNP_A-2110358	G	G	361	49	387	31	4.877	2.72E-02	rs7994286	13	86075116	q31.1
SNP_A-2038350	A	A	322	28	324	14	4.465	3.46E-02	rs9515731	13	86118457	q31.1
SNP_A-2276782	T	T	268	96	296	74	4.188	0.0407	rs9301725	13	86208769	q31.1
SNP_A-2168825	C	C	367	31	377	17	4.198	4.05E-02	rs10507965	13	86512691	q31.2
SNP_A-2129813	G	G	356	54	369	35	4.245	3.94E-02	rs4616156	13	86581518	q31.2
SNP_A-2156746	A	A	247	145	223	185	5.756	1.64E-02	rs1576562	13	86748319	q31.2
SNP_A-1782095	G	G	231	105	238	74	4.591	3.21E-02	rs9513196	13	86775037	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2162270	G	G	368	44	345	71	7.062	7.90E-03	rs1414169	13	87273867	q31.2
SNP_A-1830363	A	A	254	132	270	102	4.078	4.35E-02	rs1333822	13	87470328	q31.2
SNP_A-1810981	A	A	365	31	387	17	4.647	3.11E-02	rs4406933	13	87574405	q31.2
SNP_A-1722662	G	G	372	28	395	15	4.497	3.40E-02	rs314565	13	87596501	q31.2
SNP_A-1747857	C	C	371	27	396	14	4.76	2.91E-02	rs314578	13	87606326	q31.2
SNP_A-2100571	A	G	213	201	231	173	6.107	0.0135	rs2018070	13	87791958	q31.2
SNP_A-2140621	C	C	320	24	345	13	3.932	4.74E-02	rs9520372	13	87812863	q31.2
SNP_A-2279294	G	G	364	34	370	16	6.347	0.0118	rs370778	13	87860389	q31.2
SNP_A-1915675	T	T	227	153	254	122	4.989	2.55E-02	rs3963390	13	87990321	q31.2
SNP_A-1922246	G	G	242	164	276	128	6.665	9.80E-03	rs9559491	13	87991219	q31.2
SNP_A-1793004	C	C	267	129	294	94	6.712	9.60E-03	rs1334194	13	87994891	q31.2
SNP_A-2199610	T	T	412	4	420	0	4.058	4.40E-02	rs2148430	13	88154443	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2024948	C	C	286	56	291	35	4.509	3.37E-02	rs3930555	13	88357944	q31.2
SNP_A-2170323	G	G	406	10	415	3	3.863	4.94E-02	rs388287	13	88631358	q31.2
SNP_A-2170355	G	G	406	10	417	3	3.897	4.84E-02	rs375273	13	88663954	q31.2
SNP_A-1810874	T	T	384	22	392	8	6.572	0.0104	rs1504153	13	88729770	q31.2
SNP_A-1848674	C	C	412	4	420	0	4.058	4.40E-02	rs9560284	13	88744329	q31.2
SNP_A-2170545	T	T	349	31	343	49	3.916	4.78E-02	rs1472716	13	88864104	q31.3
SNP_A-2294640	A	A	353	51	320	78	7.225	7.20E-03	rs883616	13	89028058	q31.3
SNP_A-1701229	G	A	209	173	206	186	4.084	4.33E-02	rs729270	13	89066047	q31.3
SNP_A-2095918	G	G	386	6	379	17	5.305	2.13E-02	rs2148776	13	89117316	q31.3
SNP_A-1690057	G	G	329	71	312	100	5.193	2.27E-02	rs10507985	13	89207935	q31.3
SNP_A-1715719	T	T	228	172	271	141	6.6	1.02E-02	rs10507986	13	89227134	q31.3
SNP_A-1694279	G	G	235	163	276	136	5.487	1.92E-02	rs1414291	13	89236654	q31.3
SNP_A-1721750	G	G	300	100	282	130	4.293	3.83E-02	rs10507989	13	89266295	q31.3
SNP_A-1755240	G	G	215	143	275	125	6.248	0.0124	rs3928092	13	89293238	q31.3
SNP_A-2040184	G	G	358	40	385	25	4.265	3.89E-02	rs1572341	13	89305689	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1858033	A	A	393	19	373	33	4.248	3.93E-02	rs7328548	13	89307239	q31.3
SNP_A-1729500	G	G	299	57	282	84	5.53	1.87E-02	rs9284262	13	89343254	q31.3
SNP_A-1914256	C	C	216	128	241	103	4.073	0.0436	rs9301671	13	89745530	q31.3
SNP_A-2151727	C	C	377	25	388	10	6.567	0.0104	rs7329170	13	90210029	q31.3
SNP_A-2092678	C	C	233	151	259	115	6.115	0.0134	rs1572315	13	90306457	q31.3
SNP_A-2037395	G	G	296	40	278	60	4.559	3.28E-02	rs16944857	13	90312244	q31.3
SNP_A-2298589	G	G	218	148	243	115	5.409	0.02	rs9515837	13	90320308	q31.3
SNP_A-1917775	A	T	208	198	237	175	6.296	0.0121	rs9523159	13	90330869	q31.3
SNP_A-2050743	A	A	224	140	251	111	4.88	2.72E-02	rs12583307	13	90334263	q31.3
SNP_A-2136814	A	A	227	145	259	115	5.563	0.0183	rs9523165	13	90337736	q31.3
SNP_A-2171950	C	C	237	155	275	129	5.021	2.50E-02	rs13355560	13	90340598	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2027697	A	A	222	166	255	133	5.925	0.0149	rs9515851	13	90364578	q31.3
SNP_A-2144403	G	G	317	65	292	88	4.479	3.43E-02	rs7996847	13	90379613	q31.3
SNP_A-2218739	A	A	221	135	267	115	5.026	2.50E-02	rs17667370	13	90401936	q31.3
SNP_A-1831242	C	C	241	159	280	124	7.228	7.20E-03	rs17667393	13	90405321	q31.3
SNP_A-2096556	A	A	207	125	257	97	8.222	4.10E-03	rs4773607	13	90412505	q31.3
SNP_A-1780828	G	G	264	140	310	104	8.877	2.90E-03	rs4771829	13	90482406	q31.3
SNP_A-2172119	G	G	251	57	243	83	4.451	0.0349	rs958488	13	90510964	q31.3
SNP_A-1820221	T	T	328	12	323	3	5.146	2.33E-02	rs16945299	13	90587492	q31.3
SNP_A-1724684	G	G	276	112	300	82	5.593	1.80E-02	rs6492611	13	90840707	q31.3
SNP_A-1674409	A	A	184	182	216	156	4.512	3.37E-02	rs1333674	13	90902609	q31.3
SNP_A-1677620	G	G	288	106	330	80	6.173	1.30E-02	rs1413191	13	90911477	q31.3
SNP_A-2172770	C	C	366	16	399	7	4.218	4.00E-02	rs16946316	13	91082336	q31.3
SNP_A-2120366	C	C	381	27	398	12	6.135	1.33E-02	rs4773644	13	91159705	q31.3
SNP_A-2273595	C	C	206	176	247	147	6.13	1.33E-02	rs1330469	13	91346842	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1926227	A	A	263	139	288	110	4.492	3.41E-02	rs7988513	13	91682287	q31.3
SNP_A-1822745	T	T	416	0	412	4	4.019	4.50E-02	rs7995559	13	91780989	q31.3
SNP_A-1722256	G	G	383	15	375	29	4.494	3.40E-02	rs7333716	13	91890664	q31.3
SNP_A-2176368	G	G	303	103	336	80	4.474	0.0344	rs1360671	13	91962134	q31.3
SNP_A-1788581	A	A	386	30	405	15	5.437	1.97E-02	rs9301825	13	92067487	q31.3
SNP_A-1733554	C	C	232	168	268	144	4.262	0.039	rs7981536	13	92079644	q31.3
SNP_A-2308649	T	T	294	86	263	111	4.85	0.0276	rs9523845	13	92373281	q31.3
SNP_A-2173734	T	T	331	77	304	106	5.739	0.0166	rs9523851	13	92383109	q31.3
SNP_A-1653940	C	C	350	48	339	73	5.1	2.39E-02	rs1410747	13	92433153	q31.3
SNP_A-1929001	T	T	339	5	350	0	5.124	2.36E-02	rs9561235	13	92433207	q31.3
SNP_A-2173784	C	C	352	0	341	5	5.123	2.36E-02	rs16952658	13	92598378	q31.3
SNP_A-2297023	G	G	301	73	319	49	5.196	2.26E-02	rs2209880	13	92673304	q31.3
SNP_A-1816303	C	C	318	4	315	13	4.724	2.97E-02	rs7988954	13	92714354	q31.3
SNP_A-1933234	C	C	275	83	245	113	6.323	1.19E-02	rs11619543	13	92910211	q31.3
SNP_A-1824522	T	T	346	54	306	78	6.494	1.08E-02	rs1373838	13	92927597	q31.3
SNP_A-2143848	T	T	300	86	341	65	5.041	2.48E-02	rs7981060	13	92931393	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1872106	T	T	323	91	355	63	6.582	0.0103	rs12856048	13	92986151	q31.3
SNP_A-2303178	T	T	389	17	409	7	4.547	3.30E-02	rs11840833	13	93176308	q31.3
SNP_A-2036775	G	G	227	147	254	120	4.246	3.93E-02	rs9589816	13	93183430	q31.3
SNP_A-2253467	A	A	337	27	373	13	6.085	1.36E-02	rs4771882	13	93192954	q31.3
SNP_A-2256403	G	G	386	30	399	15	5.21	2.25E-02	rs9556321	13	93195621	q31.3
SNP_A-2312224	T	T	394	12	404	2	7.268	7.00E-03	rs2150127	13	93289061	q31.3
SNP_A-2174621	T	C	173	169	199	143	5.294	2.14E-02	rs2225889	13	93421163	q31.3
SNP_A-2069948	G	A	209	171	189	165	5.162	2.31E-02	rs9561487	13	93450323	q31.3
SNP_A-2174655	C	C	293	103	255	141	8.553	3.40E-03	rs7988278	13	93460576	q31.3
SNP_A-1747393	T	T	341	25	314	50	9.441	2.10E-03	rs2009772	13	93527589	q32.1
SNP_A-1937786	A	A	310	86	318	58	5.032	2.49E-02	rs9589897	13	93529659	q31.3
SNP_A-1736701	A	A	369	31	355	53	5.954	0.0147	rs1564351	13	93535723	q32.1
SNP_A-1689012	C	C	315	17	343	35	4.461	3.47E-02	rs1926657	13	93572957	q32.1
SNP_A-1818331	G	G	313	17	340	8	3.881	4.88E-02	rs17175140	13	93627157	q31.3
SNP_A-2209928	A	A	357	23	323	43	7.501	6.20E-03	rs17791768	13	93635799	q31.3
SNP_A-2089468	G	G	348	14	347	27	3.929	4.75E-02	rs17196064	13	93639724	q31.3
SNP_A-2174929	C	C	281	115	321	91	5.139	2.34E-02	rs1333261	13	93704104	q31.3
SNP_A-2174942	C	C	294	96	332	68	6.962	8.30E-03	rs9301947	13	93714027	q31.3
SNP_A-2034641	T	T	289	93	270	122	4.429	3.53E-02	rs9589960	13	93794671	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939350	A	A	372	10	368	24	5.658	1.74E-02	rs9516403	13	93813439	q32.1
SNP_A-2241683	T	T	375	33	351	57	7.193	7.30E-03	rs17196184	13	93834779	q32.1
SNP_A-2108039	T	T	359	31	333	49	4.945	2.62E-02	rs6650322	13	93867137	q32.1
SNP_A-2122424	T	T	324	48	355	31	4.817	2.82E-02	rs2389098	13	93881778	q32.1
SNP_A-1782830	A	A	327	79	352	56	4.834	2.79E-02	rs1325611	13	93892386	q32.1
SNP_A-1708176	G	G	282	60	255	87	6.317	0.012	rs723576	13	93902092	q32.1
SNP_A-2098383	A	A	343	71	318	96	4.688	0.0304	---	13	93914279	q32.1
SNP_A-2062935	C	C	333	63	306	86	4.671	3.07E-02	rs4773794	13	93919489	q32.1
SNP_A-2291878	C	C	257	151	283	123	4.108	4.27E-02	rs9301972	13	93962551	q32.1
SNP_A-2288430	A	A	266	146	295	119	4.245	3.94E-02	rs9561607	13	93975294	q32.1
SNP_A-2175204	G	G	264	148	298	118	5.421	1.99E-02	rs9301973	13	93987402	q32.1
SNP_A-1710313	G	C	208	178	227	179	7.601	5.80E-03	rs3901894	13	94104126	q32.1
SNP_A-2003487	A	T	222	192	221	181	6.032	0.014	rs6492734	13	94154733	q32.1
SNP_A-1754628	A	A	231	167	274	138	6.179	0.0129	rs2389530	13	94248755	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1954266	A	A	223	181	271	143	9	2.70E-03	rs9524640	13	94280408	q32.1
SNP_A-2162525	A	A	326	42	294	72	9.541	0.002	rs16950207	13	94291797	q32.1
SNP_A-1664222	A	A	207	193	250	162	6.577	0.0103	rs544080	13	94374210	q32.1
SNP_A-1643399	A	G	219	161	208	198	6.191	1.28E-02	rs7983589	13	94374824	q32.1
SNP_A-2063814	C	C	318	74	349	55	4.059	4.39E-02	rs9524692	13	94394271	q32.1
SNP_A-2091577	C	C	340	26	346	12	5.123	2.36E-02	rs9590151	13	94432077	q32.1
SNP_A-2122096	T	T	378	22	398	10	4.937	0.0263	rs1678365	13	94516981	q32.1
SNP_A-1835501	G	G	366	10	395	3	4.252	3.92E-02	rs1751042	13	94526324	q32.1
SNP_A-2183876	G	G	284	44	318	20	10.773	0.001	rs1751052	13	94531379	q32.1
SNP_A-1751961	C	T	216	184	223	189	5.361	0.0206	rs1327634	13	94559303	q32.1
SNP_A-2052538	G	A	206	168	212	178	6.804	9.10E-03	rs9524982	13	94946258	q32.1
SNP_A-1642557	C	C	341	57	328	80	3.99	0.0458	rs6491307	13	95152811	q32.1
SNP_A-2186352	G	T	184	128	175	171	6.026	0.0141	rs9561936	13	95158080	q32.1
SNP_A-2070808	C	C	368	16	353	31	5.099	2.39E-02	rs17266589	13	95233952	q32.1
SNP_A-1799432	C	C	369	47	351	67	3.954	4.68E-02	rs17675800	13	95624214	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1961140	G	G	209	203	239	175	4.078	4.34E-02	rs9525147	13	95645616	q32.1
SNP_A-2096283	T	G	195	183	206	160	4.618	3.16E-02	rs1327631	13	95646504	q32.1
SNP_A-2176226	A	G	194	168	209	169	5.837	1.57E-02	rs9302098	13	95666837	q32.1
SNP_A-2116113	G	A	215	183	219	183	5.777	1.62E-02	rs1927807	13	95672758	q32.1
SNP_A-2157406	T	T	208	166	247	139	5.545	1.85E-02	rs9516673	13	95835590	q32.1
SNP_A-1833775	C	C	220	190	258	154	6.784	9.20E-03	rs11069240	13	95836034	q32.1
SNP_A-1878436	C	C	212	188	249	157	5.711	1.69E-02	rs9805568	13	95836692	q32.1
SNP_A-1940444	G	G	315	33	280	48	4.249	3.93E-02	rs377676	13	95841659	q32.1
SNP_A-2064069	C	C	383	27	396	14	4.339	0.0373	rs732122	13	95897308	q32.1
SNP_A-2054387	C	C	383	15	385	5	4.924	2.65E-02	rs1328052	13	95918478	q32.1
SNP_A-2256916	C	C	399	13	409	1	10.405	1.30E-03	rs3899871	13	96003831	q32.1
SNP_A-2181299	G	G	401	15	414	6	4.045	4.43E-02	rs7334107	13	96004215	q32.1
SNP_A-2031174	G	G	311	83	339	63	3.866	4.93E-02	---	13	96286863	q32.1
SNP_A-2306458	C	C	382	32	366	50	4.289	3.84E-02	rs17771890	13	96309340	q32.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2176741	C	C	377	31	389	17	4.266	3.89E-02	rs4456365	13	96616515	q32.1
SNP_A-1720465	C	G	195	179	206	150	7.324	6.80E-03	rs4772122	13	97039027	q32.3
SNP_A-1800665	C	C	352	38	372	22	4.799	2.85E-02	rs9584701	13	97303631	q32.2
SNP_A-2299307	C	C	364	52	386	34	4.394	0.0361	rs16954586	13	97306879	q32.2
SNP_A-2277649	C	C	287	63	262	86	4.683	3.05E-02	rs7983524	13	97381381	q32.2
SNP_A-2309785	C	C	388	22	407	7	8.193	4.20E-03	rs7326592	13	97511170	q32.2
SNP_A-1788140	A	A	283	133	254	164	4.797	2.85E-02	rs7999510	13	97539314	q32.2
SNP_A-2177322	C	T	190	138	183	181	4.667	3.08E-02	rs285032	13	97584533	q32.2
SNP_A-1886028	A	A	305	111	338	78	7.456	0.0063	rs7326738	13	97720499	q32.2
SNP_A-2249923	C	C	382	6	400	0	6.233	1.25E-02	rs6110042	13	97742594	q32.2
SNP_A-1935437	G	G	332	80	364	54	6.473	1.10E-02	rs9517283	13	97861472	q32.2
SNP_A-2189403	G	G	319	65	358	46	4.995	2.54E-02	rs10450810	13	97864202	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950693	A	A	329	71	362	48	5.899	0.0152	rs7981744	13	97871063	q32.2
SNP_A-2209060	C	C	245	139	223	171	4.21	0.0402	rs9554468	13	97880603	q32.2
SNP_A-2103383	A	A	313	57	296	34	4.015	4.51E-02	rs2184903	13	98096810	q32.2
SNP_A-2217001	A	A	335	47	342	22	8.701	3.20E-03	rs12583822	13	98108399	q32.2
SNP_A-2252504	G	G	353	49	374	30	5.171	0.023	rs4412849	13	98113794	q32.2
SNP_A-2182271	A	A	354	60	373	41	4.071	0.0436	rs7996576	13	98117502	q32.2
SNP_A-1769584	G	G	355	49	379	25	8.569	3.40E-03	rs9557025	13	98120753	q32.2
SNP_A-2177757	A	A	389	21	408	8	6.237	1.25E-02	rs4646222	13	98167594	q32.2
SNP_A-2177760	T	T	312	42	336	22	7.117	0.0076	rs3782999	13	98168486	q32.2
SNP_A-2293651	C	C	374	4	380	0	4.042	4.44E-02	rs16956152	13	98411693	q32.3
SNP_A-2178048	C	C	251	81	291	57	6.753	9.40E-03	rs1410283	13	98581669	q32.3
SNP_A-2141512	G	G	239	163	217	197	4.097	4.30E-02	rs1160294	13	98731595	q32.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1692438	T	T	374	26	367	45	4.974	2.57E-02	rs10508050	13	99262718	q32.3
SNP_A-2051423	C	C	267	93	262	126	3.977	4.61E-02	rs8002771	13	100233149	q32.3
SNP_A-1927244	A	A	211	117	164	136	6.081	0.0137	rs2803215	13	100400951	q32.3
SNP_A-2129239	G	G	285	33	318	20	4.389	3.62E-02	rs2244384	13	100464872	q32.3
SNP_A-1864915	G	G	372	0	372	6	5.952	0.0147	rs17623214	13	100839361	q33.1
SNP_A-1682570	T	T	333	39	329	65	5.897	0.0152	rs1927384	13	100843751	q33.1
SNP_A-2180037	C	C	310	68	308	40	6.036	0.014	rs12876937	13	100935706	q33.1
SNP_A-2281092	A	A	280	124	300	92	5.251	2.19E-02	rs875116	13	100973899	q33.1
SNP_A-1877391	A	A	294	82	325	63	3.855	4.96E-02	rs11839966	13	101410274	q33.1
SNP_A-2089435	T	T	363	49	384	32	4.139	0.0419	rs9557800	13	101538372	q33.1
SNP_A-1817770	A	A	395	15	402	6	3.914	4.79E-02	rs9582572	13	101783900	q33.1
SNP_A-2152104	T	T	389	7	364	16	4.024	4.49E-02	rs16960147	13	101878053	q33.1
SNP_A-2289401	G	G	378	18	356	32	4.498	0.0339	rs4772481	13	101934299	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1938804	A	A	387	11	405	3	4.857	0.0275	rs17690743	13	101968388	q33.1
SNP_A-1709667	G	G	386	6	385	25	11.248	8.00E-04	rs10508128	13	102476383	q33.1
SNP_A-1654417	T	T	386	10	375	27	7.925	4.90E-03	rs10508129	13	102477544	q33.1
SNP_A-1755076	C	C	381	9	374	26	8.197	4.20E-03	rs10508130	13	102478386	q33.1
SNP_A-1674793	A	A	336	56	366	38	4.549	3.29E-02	rs9300901	13	102529393	q33.1
SNP_A-1791176	A	A	362	16	381	7	3.878	4.89E-02	rs1750410	13	102626815	q33.1
SNP_A-1755200	C	C	323	63	313	95	6.033	0.014	rs1590919	13	102713224	q33.2
SNP_A-2144909	T	T	361	29	381	15	4.948	2.61E-02	rs9586155	13	102841976	q33.1
SNP_A-1750919	A	A	290	18	332	8	5.114	2.37E-02	rs10508148	13	102965056	q33.2
SNP_A-2182318	C	C	336	68	307	89	4.037	4.45E-02	rs994513	13	102990414	q33.1
SNP_A-2043899	T	T	319	77	291	107	6.172	1.30E-02	rs9514153	13	102997576	q33.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2154974	T	T	338	76	308	108	6.954	8.40E-03	rs2390913	13	103007730	q33.1
SNP_A-2035985	A	A	371	29	381	13	6.183	0.0129	rs2027214	13	103366378	q33.1
SNP_A-2190453	T	T	328	44	345	27	4.5	0.0339	rs17368053	13	103588543	q33.1
SNP_A-2157362	T	T	326	20	341	9	4.487	3.42E-02	rs16964757	13	103883954	q33.2
SNP_A-1897366	C	C	369	19	381	7	5.73	0.0167	rs9582869	13	103903765	q33.2
SNP_A-2130119	A	A	314	76	332	50	5.784	1.62E-02	rs9586517	13	103914702	q33.2
SNP_A-1889963	G	G	303	59	315	39	4.226	3.98E-02	rs9586520	13	103918947	q33.2
SNP_A-2085441	T	T	357	23	372	10	5.425	1.99E-02	rs9582876	13	103938620	q33.2
SNP_A-1953046	G	G	359	53	372	34	4.337	0.0373	rs9586532	13	103940493	q33.2
SNP_A-1887984	C	C	370	18	395	3	11.406	7.00E-04	rs9558312	13	103960140	q33.2
SNP_A-2111597	A	A	384	32	401	13	8.386	0.0038	rs9558313	13	103960174	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2183774	G	G	344	26	356	12	5.358	0.0206	rs9558314	13	103960456	q33.2
SNP_A-2196461	G	G	227	109	249	77	6.373	1.16E-02	rs9514296	13	104045087	q33.2
SNP_A-1643377	G	G	370	30	396	16	4.967	0.0258	rs10508167	13	104170029	q33.2
SNP_A-1713019	T	T	330	70	355	51	3.851	4.97E-02	rs7991198	13	104246881	q33.2
SNP_A-1796567	G	G	221	189	261	151	7.562	6.00E-03	rs7999896	13	104366087	q33.2
SNP_A-2083368	A	A	275	55	245	73	4.041	4.44E-02	rs9519520	13	104372156	q33.2
SNP_A-1920228	C	C	293	41	284	22	4.654	0.031	rs4379936	13	104540300	q33.2
SNP_A-1828443	G	G	276	106	242	130	4.541	3.31E-02	rs9301014	13	104739059	q33.2
SNP_A-2184172	G	G	308	100	276	138	7.777	0.0053	rs10492533	13	104756698	q33.2
SNP_A-2184216	A	A	394	22	411	9	5.792	0.0161	rs7996321	13	104797243	q33.2
SNP_A-1864778	T	T	363	9	377	1	6.617	0.0101	rs9555163	13	104798955	q33.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1737171	A	A	370	8	378	22	6.002	0.0143	rs10508176	13	104872288	q33.3
SNP_A-2184273	C	C	333	1	369	11	7.246	7.10E-03	rs1557072	13	104925835	q33.2
SNP_A-1690519	G	G	303	95	284	126	4.786	0.0287	rs288740	13	105199212	q33.3
SNP_A-2003557	C	C	387	27	403	7	12.07	5.00E-04	rs2476760	13	105288687	q33.2
SNP_A-1898953	C	C	182	178	226	138	9.787	0.0018	rs9301077	13	105314455	q33.2
SNP_A-2178849	C	C	362	48	343	69	4.276	3.86E-02	rs16967647	13	105350547	q33.2
SNP_A-1802343	A	A	313	35	303	57	5.221	0.0223	rs12585559	13	105352259	q33.2
SNP_A-2034011	G	G	347	47	330	68	4.242	3.94E-02	rs16967662	13	105352545	q33.2
SNP_A-2083008	G	G	362	12	326	28	7.74	5.40E-03	rs4772736	13	105492028	q33.2
SNP_A-2139884	A	A	283	105	295	77	4.222	3.99E-02	rs7331381	13	105507616	q33.2
SNP_A-2171228	T	T	381	25	388	12	4.587	3.22E-02	rs9558721	13	105654167	q33.2
SNP_A-2081728	T	T	376	24	395	7	9.786	0.0018	rs7331798	13	105840071	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2185514	T	T	302	58	320	38	4.682	3.05E-02	rs2126735	13	105852495	q33.3
SNP_A-1829799	A	A	386	14	372	30	6.072	0.0137	rs12868185	13	105869800	q33.3
SNP_A-2185612	T	T	350	10	366	2	5.604	1.79E-02	---	13	105962224	q33.3
SNP_A-2098045	T	T	324	20	324	6	7.251	7.10E-03	rs9558798	13	106072243	q33.3
SNP_A-2185663	A	A	274	66	256	94	5.368	2.05E-02	rs1986664	13	106099421	q33.3
SNP_A-2067480	T	T	319	53	354	34	5.635	1.76E-02	rs9587180	13	106158402	q33.3
SNP_A-1828064	T	T	221	91	199	117	4.377	3.64E-02	rs508352	13	106307189	q33.3
SNP_A-1698125	C	C	202	194	241	169	4.913	2.66E-02	rs1223978	13	106473163	q33.3
SNP_A-1923771	A	A	396	4	402	0	4.04	4.44E-02	rs2796222	13	106543967	q33.3
SNP_A-2185997	C	T	189	149	179	159	5.33	2.10E-02	rs4771558	13	106667647	q33.3
SNP_A-2279199	G	A	209	179	204	174	4.701	3.02E-02	rs9634562	13	106667667	q33.3
SNP_A-1898091	C	C	270	82	243	115	6.899	0.0086	rs9555336	13	106702622	q33.3
SNP_A-1902995	T	T	361	23	354	40	4.528	3.33E-02	rs7317862	13	106704039	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2188973	C	C	309	25	301	45	5.609	1.79E-02	rs9514643	13	106714476	q33.3
SNP_A-2053460	C	C	255	149	220	182	5.864	0.0155	rs9558995	13	106735830	q33.3
SNP_A-1859149	A	A	250	152	224	190	5.473	1.93E-02	rs2147453	13	106737065	q33.3
SNP_A-2259139	T	T	277	139	309	109	5.372	2.05E-02	rs7999230	13	106749278	q33.3
SNP_A-2046082	G	G	345	25	282	40	6.493	1.08E-02	---	13	107026503	q33.3
SNP_A-1793705	C	A	226	176	207	195	4.792	0.0286	rs11618084	13	107036129	q33.3
SNP_A-2186230	T	T	402	8	402	0	7.922	4.90E-03	rs7328649	13	107126149	q33.3
SNP_A-2031276	T	T	335	15	289	31	7.628	5.70E-03	rs16971086	13	107221170	q33.3
SNP_A-2124317	C	C	400	4	414	0	4.119	0.0424	rs12585034	13	107274954	q33.3
SNP_A-2244237	G	A	214	202	233	187	4.008	0.0453	rs9520596	13	107290594	q33.3
SNP_A-2040298	G	G	270	104	244	134	5.076	2.43E-02	rs816971	13	107331904	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2197739	G	G	392	18	409	7	5.157	2.31E-02	rs16971680	13	107424932	q33.3
SNP_A-1870206	T	T	353	25	363	13	3.924	4.76E-02	rs17674880	13	107492177	q33.3
SNP_A-1739959	G	G	322	78	349	51	6.738	9.40E-03	rs2038707	13	107529850	q33.3
SNP_A-2084553	C	C	252	136	279	111	3.898	4.83E-02	rs11616923	13	107564097	q33.3
SNP_A-1868555	C	C	309	101	283	131	5.002	0.0253	rs9559260	13	107572958	q33.3
SNP_A-1959898	T	T	327	81	306	106	4.02	4.50E-02	rs12874104	13	107573024	q33.3
SNP_A-1670027	G	A	217	171	209	189	5.605	1.79E-02	rs592398	13	107577223	q33.3
SNP_A-1851766	T	T	382	6	370	0	5.767	1.63E-02	rs7987766	13	107577456	q33.3
SNP_A-2235385	A	A	319	65	349	43	5.747	1.65E-02	rs9583221	13	107605170	q33.3
SNP_A-1924102	T	T	348	64	371	41	5.774	1.63E-02	rs7981709	13	107606588	q33.3
SNP_A-2048551	G	G	344	54	367	37	3.875	4.90E-02	rs1555902	13	107654784	q33.3
SNP_A-2305513	C	C	393	13	385	25	3.852	4.97E-02	rs12856070	13	107701109	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2251502	G	G	246	116	267	87	4.914	2.66E-02	rs11069734	13	107800359	q33.3
SNP_A-2231750	G	G	333	39	342	22	4.771	2.89E-02	rs12869576	13	107877219	q33.3
SNP_A-1712181	C	C	350	18	373	7	5.381	2.04E-02	rs1410425	13	107896160	q33.3
SNP_A-1857152	G	G	301	13	318	4	5.132	0.0235	rs16972503	13	107902540	q33.3
SNP_A-2222099	C	C	302	96	278	124	4.537	0.0332	rs4771591	13	108034018	q33.3
SNP_A-1822012	T	T	396	0	392	4	4.02	4.50E-02	rs749616	13	108076294	q33.3
SNP_A-2262011	T	T	360	2	336	8	3.971	4.63E-02	rs4635193	13	108152901	q33.3
SNP_A-1799728	C	C	322	92	348	70	3.977	4.61E-02	rs10851223	13	108329517	q33.3
SNP_A-2187337	C	C	247	131	265	101	4.32	3.77E-02	rs1538221	13	108412378	q33.3
SNP_A-1877447	G	G	215	127	238	98	4.853	0.0276	rs9559451	13	108423864	q33.3
SNP_A-2187508	A	G	196	188	234	146	12.304	5.00E-04	rs1028724	13	108630183	q33.3
SNP_A-1904101	T	T	205	185	254	152	8.144	0.0043	rs2391723	13	108633315	q33.3
SNP_A-2206829	A	A	292	124	326	88	7.979	4.70E-03	rs6492172	13	108659240	q33.3
SNP_A-1933331	A	A	265	145	219	187	9.666	0.0019	rs9521239	13	108684428	q33.3
SNP_A-1867738	A	A	408	6	420	0	6.131	1.33E-02	rs9559558	13	108779727	q33.3
SNP_A-1829341	A	A	283	127	290	94	4.166	4.12E-02	rs1887638	13	108824695	q33.3
SNP_A-2092217	A	A	303	51	320	34	3.864	4.93E-02	rs9521354	13	108865125	q33.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284850	A	A	359	37	363	17	7.103	7.70E-03	rs1328244	13	108881899	q33.3
SNP_A-2266524	G	G	195	183	227	159	4.027	0.0448	rs7991365	13	109140220	q34
SNP_A-1918907	G	G	299	107	261	129	4.31	3.79E-02	rs376476	13	109353041	q34
SNP_A-1901907	A	A	220	188	262	150	7.913	4.90E-03	rs9555673	13	109587487	q34
SNP_A-2100019	T	T	225	169	264	132	7.654	5.70E-03	rs7319307	13	109591078	q34
SNP_A-2188212	G	G	272	144	312	104	9.191	2.40E-03	rs11069830	13	109619133	q34
SNP_A-2280186	T	T	246	160	202	200	8.746	3.10E-03	rs565510	13	109663502	q34
SNP_A-1875068	A	A	325	65	293	95	7.277	7.00E-03	rs9634591	13	109707920	q34
SNP_A-1806911	C	C	303	61	283	87	5.201	2.26E-02	rs9515177	13	109710635	q34
SNP_A-1798088	C	C	334	36	289	61	9.145	2.50E-03	rs9521687	13	109755663	q34
SNP_A-2287034	A	A	265	101	245	149	8.981	2.70E-03	rs1360154	13	109759469	q34
SNP_A-1861888	G	G	362	52	384	34	4.397	3.60E-02	rs7335117	13	109767925	q34
SNP_A-2182036	C	C	232	134	213	171	4.871	2.73E-02	rs4773155	13	109769067	q34
SNP_A-1810849	C	C	408	4	420	0	4.097	4.29E-02	rs6492262	13	109798753	q34
SNP_A-1867443	C	C	382	22	380	38	4.035	4.46E-02	rs3825490	13	109915985	q34
SNP_A-2240526	C	C	285	47	288	28	4.437	3.52E-02	rs2281969	13	109951659	q34
SNP_A-2229981	T	T	222	160	201	193	3.943	4.71E-02	rs9521853	13	110035261	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2311361	A	A	363	51	378	28	6.922	8.50E-03	rs2296352	13	110736890	q34
SNP_A-1913637	G	G	269	113	294	84	5.358	0.0206	rs1178819	13	110840323	q34
SNP_A-2265697	G	G	337	61	365	43	4.109	4.27E-02	rs2770254	13	110857014	q34
SNP_A-2088011	G	A	180	162	198	146	7.14	7.50E-03	rs2528763	13	110857332	q34
SNP_A-1849575	C	C	256	114	226	144	5.356	0.0207	rs1163829	13	110944195	q34
SNP_A-2234659	C	C	259	119	228	146	4.703	3.01E-02	rs9583610	13	110944668	q34
SNP_A-2142709	A	A	240	162	206	198	6.187	0.0129	rs4773392	13	111025359	q34
SNP_A-2312241	A	A	234	170	207	205	4.842	2.78E-02	rs4773396	13	111039718	q34
SNP_A-1691760	C	C	253	143	226	182	6.024	0.0141	rs2317438	13	111042662	q34
SNP_A-1794411	C	C	393	11	400	2	6.288	1.22E-02	rs7339401	13	111670854	q34
SNP_A-2263468	T	T	241	101	243	141	4.204	4.03E-02	rs9549891	13	111942258	q34
SNP_A-1659218	A	A	343	57	373	39	4.456	3.48E-02	rs2260111	13	112103258	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1913855	C	C	239	115	210	156	7.878	5.00E-03	rs8001869	13	112138235	q34
SNP_A-1917607	A	A	322	74	336	48	5.656	1.74E-02	rs3861729	13	112218952	q34
SNP_A-1810989	G	G	300	70	341	53	4.222	3.99E-02	rs9550122	13	112233546	q34
SNP_A-1830472	C	C	382	12	362	24	4.456	3.48E-02	rs9604356	13	112253464	q34
SNP_A-1937255	A	A	389	27	374	44	4.361	3.68E-02	rs7997172	13	112269197	q34
SNP_A-1902949	C	C	288	88	337	61	8.115	4.40E-03	rs9577810	13	112272390	q34
SNP_A-2142164	C	C	325	81	353	57	5.311	0.0212	rs9577814	13	112273716	q34
SNP_A-2154772	C	C	387	25	370	44	5.609	1.79E-02	rs7327665	13	112302611	q34
SNP_A-2167957	G	G	364	18	349	35	5.763	1.64E-02	rs7333030	13	112302798	q34
SNP_A-2221772	C	C	374	34	365	53	4.139	0.0419	rs9989087	13	112304035	q34
SNP_A-2217182	T	T	381	33	366	54	5.327	2.10E-02	rs9989115	13	112304065	q34
SNP_A-1794732	G	G	346	24	345	43	4.965	2.59E-02	rs9550174	13	112313564	q34
SNP_A-2050889	C	C	383	13	375	25	3.854	4.96E-02	rs7323548	13	112320879	q34
SNP_A-1811394	C	C	392	10	373	23	5.548	1.85E-02	rs2317446	13	112322678	q34
SNP_A-1916943	C	C	223	187	254	156	4.816	2.82E-02	rs9577836	13	112473196	q34
SNP_A-2276500	G	G	209	129	183	173	7.673	5.60E-03	rs282592	13	112479326	q34
SNP_A-2095073	G	G	316	16	312	4	6.835	8.90E-03	rs7325522	13	112560005	q34
SNP_A-2110390	C	C	287	113	310	88	3.991	0.0458	rs9646114	13	112630442	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2109606	G	G	244	124	224	158	4.694	3.03E-02	rs9604014	13	112755703	q34
SNP_A-2212663	T	T	287	67	329	49	4.875	2.72E-02	rs7986656	13	113157383	q34
SNP_A-2202726	C	C	343	61	371	39	5.894	0.0152	rs9577553	13	113158146	q34
SNP_A-1801904	G	G	347	49	379	31	5.219	0.0223	rs2260894	13	113189296	q34
SNP_A-1948093	A	A	351	53	374	28	8.441	3.70E-03	rs2805606	13	113200293	q34
SNP_A-1820450	C	C	345	49	378	30	5.833	1.57E-02	rs2260218	13	113200756	q34
SNP_A-2163263	C	C	352	58	372	38	4.719	0.0298	rs2260163	13	113202209	q34
SNP_A-2247668	T	T	341	57	378	36	6.333	1.19E-02	rs2490967	13	113209383	q34
SNP_A-2176794	T	T	327	49	347	29	5.722	1.68E-02	rs2490975	13	113212278	q34
SNP_A-2111340	G	G	325	37	346	22	4.422	3.55E-02	rs2258520	13	113212913	q34
SNP_A-2088897	C	C	345	69	366	48	4.389	3.62E-02	rs2479744	13	113213251	q34
SNP_A-2190443	C	C	355	57	380	36	5.573	1.82E-02	rs2258368	13	113215415	q34
SNP_A-1887692	G	G	312	72	343	53	4.172	4.11E-02	rs2260334	13	113223005	q34
SNP_A-1960213	C	C	205	129	229	101	4.712	3.00E-02	rs7399591	13	113485357	q34
SNP_A-2184222	C	C	329	55	340	34	5.005	0.0253	rs7332546	13	113600269	q34

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2212973	A	G	205	203	238	174	5.294	2.14E-02	rs7995986	13	113956904	q34
SNP_A-1851948	A	A	317	67	294	90	4.235	3.96E-02	rs9805813	13	114063361	q34
SNP_A-2216525	G	G	271	63	255	87	4.233	3.97E-02	rs10151880	14	19489537	q11.2
SNP_A-2079512	G	G	349	31	378	16	5.693	1.70E-02	rs11849055	14	19592409	q11.2
SNP_A-2191584	T	T	318	20	340	6	8.182	4.20E-03	rs2945461	14	19932910	q11.2
SNP_A-1644352	T	T	270	114	313	89	5.841	1.57E-02	rs719785	14	19968421	q11.2
SNP_A-2181529	C	C	361	27	339	43	4.302	3.81E-02	rs17211432	14	19969322	q11.2
SNP_A-1955851	T	T	360	36	339	53	3.858	4.95E-02	rs17114571	14	20225110	q11.2
SNP_A-2245322	G	G	321	29	298	52	7.385	0.0066	rs8008440	14	20226288	q11.2
SNP_A-1708849	C	C	323	9	333	21	4.251	3.92E-02	rs2075486	14	20227198	q11.2
SNP_A-2250534	T	T	401	13	389	29	6.258	0.0124	rs1999343	14	20235319	q11.2
SNP_A-1739057	G	G	222	150	199	185	4.724	2.97E-02	rs8022648	14	20282238	q11.2
SNP_A-1947165	C	C	289	65	260	90	5.542	1.86E-02	rs8005768	14	20434060	q11.2
SNP_A-1658732	C	C	228	108	250	84	4.007	0.0453	rs10483267	14	20469940	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920958	G	G	294	106	265	143	6.924	8.50E-03	rs1958399	14	20503182	q11.2
SNP_A-2003610	C	C	225	125	191	167	8.731	3.10E-03	rs2771335	14	20523213	q11.2
SNP_A-2192345	C	C	302	64	267	85	4.841	2.78E-02	rs10483251	14	20741117	q11.2
SNP_A-1940588	T	T	351	35	382	22	3.868	4.92E-02	rs17792558	14	20757234	q11.2
SNP_A-2192430	C	C	324	64	313	89	4.028	4.47E-02	rs7157052	14	20863076	q11.2
SNP_A-2247517	G	G	372	44	344	74	8.717	3.20E-03	rs17792659	14	20952489	q11.2
SNP_A-1738258	C	C	228	170	264	146	4.28	3.86E-02	rs227026	14	20989047	q11.2
SNP_A-1838226	C	T	182	148	163	137	5.656	1.74E-02	rs10135215	14	21017697	q11.2
SNP_A-1831356	T	T	289	101	324	80	4.189	0.0407	rs10129436	14	21088750	q11.2
SNP_A-1932945	T	T	246	140	196	186	12.126	5.00E-04	rs17792748	14	21091957	q11.2
SNP_A-2144744	C	C	284	96	263	131	5.951	0.0147	rs17792778	14	21108499	q11.2
SNP_A-1907047	A	A	309	107	271	147	8.784	3.00E-03	rs8018556	14	21120353	q11.2
SNP_A-2239789	T	T	234	124	260	100	3.934	4.73E-02	rs6571924	14	21123657	q11.2
SNP_A-2054940	T	T	299	93	265	139	10.992	9.00E-04	rs6571925	14	21123703	q11.2
SNP_A-2144457	A	A	235	109	195	135	6.203	1.28E-02	rs10131311	14	21331024	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936108	A	A	358	28	316	48	7.241	7.10E-03	rs17182809	14	21338108	q11.2
SNP_A-2066700	T	-	196	138	152	152	4.839	2.78E-02	rs7158561	14	21355876	q11.2
SNP_A-1907907	T	-	235	169	201	201	5.414	0.02	rs12884540	14	21371065	q11.2
SNP_A-1719751	G	G	223	177	267	145	6.955	8.40E-03	rs712486	14	21415169	q11.2
SNP_A-1956763	C	C	343	43	305	59	4.096	4.30E-02	rs732073	14	21567040	q11.2
SNP_A-2228380	C	C	398	10	408	2	5.453	0.0195	rs17183131	14	21631939	q11.2
SNP_A-2189356	C	C	252	128	286	104	4.502	3.38E-02	rs11622439	14	21925523	q11.2
SNP_A-2003619	G	G	260	102	280	68	7.268	7.00E-03	rs4389079	14	21928707	q11.2
SNP_A-1915564	T	T	267	97	233	121	4.816	2.82E-02	rs3794450	14	22045568	q11.2
SNP_A-2032293	C	C	195	127	239	107	5.315	2.11E-02	rs227003	14	22068902	q11.2
SNP_A-1888184	G	G	301	77	276	100	4.067	4.37E-02	rs6572540	14	22099119	q11.2
SNP_A-1952707	C	C	318	96	295	123	4.173	4.11E-02	rs4982641	14	22099182	q11.2
SNP_A-2193900	A	A	338	50	310	72	5.131	0.0235	rs1242940	14	22190469	q11.2
SNP_A-1848573	A	A	237	169	273	139	5.42	1.99E-02	rs1043209	14	22443826	q11.2
SNP_A-1863596	G	G	223	161	273	131	7.62	5.80E-03	rs1956880	14	22463847	q11.2
SNP_A-1808136	G	G	335	81	355	59	4.032	4.46E-02	rs10143650	14	22706113	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1900984	A	A	354	18	349	35	5.299	2.13E-02	rs221699	14	23205892	q11.2
SNP_A-1834917	G	G	378	26	384	10	7.034	8.00E-03	rs221689	14	23223883	q11.2
SNP_A-2161075	C	C	372	10	385	3	3.946	0.047	rs1958298	14	23380925	q11.2
SNP_A-1690369	T	T	360	40	387	25	4.261	0.039	rs10483291	14	23410014	q12
SNP_A-1710588	C	C	232	106	227	153	6.148	0.0132	rs1461549	14	23702428	q12
SNP_A-1675263	G	G	256	118	244	152	3.944	0.047	rs1349878	14	23711160	q12
SNP_A-2301561	G	G	362	4	368	0	4.044	4.43E-02	rs1951136	14	24020664	q11.2
SNP_A-2238044	G	G	314	82	302	112	4.475	0.0344	rs9573910	14	24170722	q11.2
SNP_A-2250845	G	G	345	41	334	68	6.544	1.05E-02	rs11626395	14	24317217	q12
SNP_A-1894098	G	G	295	113	272	142	4.187	0.0407	rs854373	14	24336974	q12
SNP_A-2195977	G	G	247	107	244	74	4.118	0.0424	rs1241615	14	24430899	q12
SNP_A-2281480	C	C	308	22	306	6	8.651	0.0033	rs8004569	14	24557656	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1658394	G	G	249	95	205	111	4.327	3.75E-02	rs10483307	14	24573107	q12
SNP_A-2281835	C	C	407	5	414	0	5.055	0.0246	rs1111763	14	24661377	q12
SNP_A-2143233	C	C	313	53	331	35	4.185	4.08E-02	rs1956948	14	24846453	q12
SNP_A-1795835	A	A	271	79	296	58	4.299	3.81E-02	rs17110559	14	25569587	q12
SNP_A-2197479	A	A	207	165	240	128	7.087	7.80E-03	rs17110711	14	25651749	q12
SNP_A-2264238	G	G	235	139	193	165	5.998	0.0143	rs11852018	14	25657577	q12
SNP_A-2022798	C	C	342	12	313	23	4.274	3.87E-02	rs17476287	14	25660180	q12
SNP_A-1807016	C	C	396	6	392	16	4.522	3.35E-02	rs8007742	14	25710774	q12
SNP_A-1664724	T	T	238	148	219	185	4.493	3.40E-02	rs202970	14	25723104	q12
SNP_A-2298011	C	C	394	12	369	23	4.032	4.46E-02	rs8008032	14	25785101	q12
SNP_A-2197788	G	G	391	5	374	14	4.56	0.0327	rs1998137	14	25945647	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2075341	A	A	396	4	410	0	4.12	0.0424	rs1950401	14	26164577	q12
SNP_A-1816848	C	C	280	40	303	21	6.801	9.10E-03	rs1950415	14	26246084	q12
SNP_A-2198236	C	C	400	10	411	3	3.899	4.83E-02	rs4983200	14	26372486	q12
SNP_A-1906783	C	C	367	5	375	15	4.664	3.08E-02	rs7145116	14	26400871	q12
SNP_A-2118092	A	A	393	11	382	26	6.218	0.0126	rs2144787	14	26449303	q12
SNP_A-1793076	A	A	286	70	309	49	4.589	3.22E-02	rs17112101	14	26553240	q12
SNP_A-2003642	T	T	363	21	368	8	5.778	1.62E-02	rs4247021	14	26613658	q12
SNP_A-1831325	T	T	301	77	276	106	5.658	1.74E-02	rs17112407	14	26793640	q12
SNP_A-1927482	C	C	368	32	344	52	5.551	1.85E-02	rs8007001	14	27817987	q12
SNP_A-2194380	T	T	212	134	185	161	4.307	3.79E-02	rs12878206	14	28089805	q12
SNP_A-1882604	T	T	259	123	204	172	14.626	0.0001	rs176297	14	28105038	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2283784	G	G	255	125	217	173	10.663	1.10E-03	rs12887727	14	28119384	q12
SNP_A-1657149	G	G	240	94	236	132	4.788	0.0287	rs2225899	14	28149293	q12
SNP_A-1645186	G	G	294	106	328	84	4.229	3.97E-02	rs226001	14	28478350	q12
SNP_A-1723938	T	T	294	106	326	82	4.637	3.13E-02	rs225998	14	28480401	q12
SNP_A-2200242	A	A	339	41	332	62	4.103	4.28E-02	rs4981678	14	28560352	q12
SNP_A-2173503	A	A	329	33	325	57	5.891	0.0152	rs1951539	14	28609859	q12
SNP_A-2200329	G	G	381	17	388	4	8.066	4.50E-03	rs1951540	14	28671763	q12
SNP_A-1646996	T	T	343	57	380	32	8.741	3.10E-03	rs10483377	14	28763710	q12
SNP_A-1736719	G	G	338	50	376	30	6.618	0.0101	rs2025052	14	28764583	q12
SNP_A-1675702	A	A	322	4	360	0	4.443	3.50E-02	rs10483376	14	28787824	q12
SNP_A-2201001	T	T	302	22	281	39	5.47	1.94E-02	rs718545	14	29559374	q12
SNP_A-2303270	G	G	358	52	386	32	5.739	0.0166	rs7148020	14	29834938	q12
SNP_A-1814193	A	A	361	53	337	83	7.4	6.50E-03	rs10149863	14	29912371	q12
SNP_A-1799854	G	G	360	56	342	78	4.054	0.0441	rs1955768	14	29918241	q12
SNP_A-2260130	T	T	357	39	344	58	3.918	4.78E-02	rs7157450	14	29918903	q12
SNP_A-2201354	T	T	384	22	376	40	5.189	2.27E-02	rs17096653	14	29928140	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134053	T	T	330	0	364	6	5.398	2.02E-02	rs1955563	14	30479094	q12
SNP_A-1679548	G	A	223	163	206	198	6.088	1.36E-02	rs4261436	14	31289521	q12
SNP_A-2301889	A	A	303	101	329	75	4.911	2.67E-02	rs1958366	14	31740857	q12
SNP_A-1934121	C	C	311	97	348	70	6.323	1.19E-02	rs17098609	14	31763927	q12
SNP_A-1691530	T	C	205	161	193	179	4.605	3.19E-02	rs1315148	14	31838148	q13.1
SNP_A-2144456	A	A	219	133	207	171	4.167	4.12E-02	rs941746	14	31974679	q12
SNP_A-1690735	G	G	382	16	407	5	6.314	0.012	rs1632578	14	32347360	q13.1
SNP_A-2203376	G	G	389	27	371	49	6.776	9.20E-03	rs17451011	14	32432681	q13.1
SNP_A-1665166	A	A	238	156	210	202	7.262	7.00E-03	rs958721	14	32448136	q13.1
SNP_A-1949060	A	A	327	49	348	30	5.218	0.0224	rs12586198	14	32511367	q13.1
SNP_A-2269612	T	T	370	0	372	4	3.957	4.67E-02	rs17100028	14	32597477	q13.1
SNP_A-2099711	G	G	357	49	391	27	7.124	0.0076	rs10140504	14	32606647	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2071941	G	G	304	44	318	70	4.083	4.33E-02	rs17100062	14	32607265	q13.1
SNP_A-1935774	C	C	371	43	355	63	4.107	4.27E-02	rs1279328	14	32646009	q13.1
SNP_A-2052725	T	T	403	13	390	30	6.915	8.50E-03	rs3910616	14	32845870	q13.1
SNP_A-2300591	T	T	271	141	235	167	4.634	3.13E-02	rs1579701	14	32887201	q13.1
SNP_A-2189854	A	A	364	16	316	32	7.329	6.80E-03	rs17100828	14	32909253	q13.1
SNP_A-2233796	A	A	389	23	373	43	6.377	1.16E-02	rs11844302	14	32930614	q13.1
SNP_A-1944776	T	T	248	130	244	92	4.081	4.34E-02	rs10142154	14	33092584	q13.1
SNP_A-2048313	C	C	242	154	202	194	8.201	4.20E-03	rs12890353	14	33094185	q13.1
SNP_A-1908535	T	T	284	106	263	137	4.635	3.13E-02	rs1998852	14	33346929	q13.1
SNP_A-2204580	C	C	223	191	250	162	3.919	4.77E-02	rs4146554	14	33353940	q13.1
SNP_A-2290535	A	A	387	11	400	2	6.426	0.0112	rs11848694	14	33390509	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2283958	T	T	400	12	415	3	5.633	1.76E-02	rs2148332	14	33401128	q13.1
SNP_A-2147884	A	A	306	12	332	4	4.568	3.26E-02	rs1680677	14	33436421	q13.1
SNP_A-1872308	C	C	398	18	413	7	5.098	2.39E-02	rs1769603	14	33467411	q13.1
SNP_A-1914227	C	C	392	12	411	3	5.728	0.0167	rs1680698	14	33472992	q13.1
SNP_A-2204640	C	C	299	89	325	67	4.165	4.13E-02	rs1769621	14	33493429	q13.1
SNP_A-1831232	T	T	277	115	302	88	4.665	3.08E-02	rs10130824	14	33493938	q13.1
SNP_A-1793297	G	G	328	30	319	51	5.373	2.04E-02	rs2035423	14	33521707	q13.1
SNP_A-2204694	C	C	310	50	338	32	5.025	2.50E-02	rs974673	14	33550265	q13.1
SNP_A-2303936	T	T	317	43	289	61	4.269	3.88E-02	rs1631523	14	33576044	q13.1
SNP_A-2119206	T	T	260	90	277	55	8.517	3.50E-03	rs11625107	14	33797878	q13.1
SNP_A-1820928	A	A	325	55	315	81	4.799	2.85E-02	rs10142667	14	34514841	q13.2
SNP_A-2205288	A	A	344	66	364	46	4.136	4.20E-02	rs10498331	14	34706120	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1797428	C	C	333	29	350	14	5.65	1.75E-02	rs7147426	14	34753236	q13.2
SNP_A-1919467	G	G	377	13	393	3	6.537	0.0106	rs1064248	14	34814590	q13.2
SNP_A-1711422	G	G	256	144	291	121	4.059	4.39E-02	rs381858	14	35029669	q13.3
SNP_A-2164373	T	T	247	113	225	145	4.858	0.0275	rs6571721	14	35043205	q13.2
SNP_A-2088555	G	G	325	27	307	43	4.164	4.13E-02	rs17103371	14	35048854	q13.2
SNP_A-1716385	T	T	246	154	286	126	5.631	1.76E-02	rs8004187	14	35130543	q13.3
SNP_A-1752273	C	C	206	112	173	145	7.111	7.70E-03	rs1179966	14	35323393	q13.3
SNP_A-2100085	G	G	355	9	353	1	6.268	0.0123	rs17103927	14	35596464	q13.2
SNP_A-2227856	A	A	257	115	241	151	4.866	2.74E-02	rs429041	14	35610887	q13.3
SNP_A-2146606	C	C	264	138	239	167	3.98	4.60E-02	rs368772	14	35610912	q13.3
SNP_A-2206193	G	G	304	66	286	96	5.915	1.50E-02	rs2415328	14	35958283	q13.3
SNP_A-1845879	G	G	297	41	292	20	6.242	1.25E-02	rs4902397	14	36010893	q13.3
SNP_A-2206383	G	G	363	49	345	69	3.843	5.00E-02	rs1950359	14	36136995	q13.3
SNP_A-2168522	A	A	245	157	271	129	4.046	4.43E-02	rs7156439	14	36170489	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2306441	G	G	251	153	279	127	3.889	4.86E-02	rs11621707	14	36184647	q13.3
SNP_A-1834650	T	T	254	150	274	120	3.966	4.64E-02	rs4899813	14	36184799	q13.3
SNP_A-1739891	G	G	219	171	243	141	4.085	4.33E-02	rs2001398	14	36566370	q21.1
SNP_A-1676678	T	T	396	4	394	12	3.961	4.66E-02	rs2415451	14	36600751	q21.1
SNP_A-1747481	G	G	341	13	348	32	7.181	7.40E-03	rs10484116	14	36842379	q21.1
SNP_A-2298602	T	T	340	2	316	12	7.732	5.40E-03	rs7154479	14	36884696	q13.3
SNP_A-1869204	A	A	252	128	284	100	5.328	2.10E-02	rs11156970	14	37341401	q21.1
SNP_A-2258363	C	C	397	19	410	8	4.686	0.0304	---	14	37538344	q21.1
SNP_A-2259050	A	A	270	82	307	63	4.416	0.0356	rs17107457	14	37608411	q21.1
SNP_A-1659108	A	A	319	81	297	115	6.508	1.07E-02	rs10483542	14	37620552	q21.1
SNP_A-1890645	A	A	395	13	385	25	3.913	4.79E-02	rs10220616	14	37780249	q21.1
SNP_A-2236544	C	C	365	13	359	27	4.866	2.74E-02	rs12323456	14	37931251	q21.1
SNP_A-2208251	G	G	269	97	250	124	3.908	4.81E-02	rs11625642	14	38247629	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2208433	T	T	351	19	293	33	6.236	1.25E-02	rs1955918	14	38510283	q21.1
SNP_A-2208440	C	C	393	21	376	44	8.472	3.60E-03	rs17108710	14	38541688	q21.1
SNP_A-2066453	T	T	199	191	225	157	4.834	2.79E-02	rs11157079	14	39158921	q21.1
SNP_A-2234369	A	A	293	87	308	60	5.142	2.33E-02	rs17769363	14	39286631	q21.1
SNP_A-1813792	C	C	406	8	398	20	5.203	2.25E-02	rs2070332	14	39571738	q21.1
SNP_A-2209139	A	A	250	144	196	162	5.887	1.53E-02	rs2899901	14	39602916	q21.1
SNP_A-1668578	T	C	189	163	189	163	3.841	5.00E-02	rs8022809	14	39784226	q21.1
SNP_A-1748175	A	G	212	182	212	180	4.891	0.027	rs3910110	14	39835994	q21.1
SNP_A-1721401	A	C	213	185	220	188	4.46	3.47E-02	rs10483528	14	39874486	q21.1
SNP_A-2285978	A	A	365	23	359	9	5.65	1.75E-02	rs1000203	14	39965858	q21.1
SNP_A-1665434	C	C	340	60	368	42	4.161	4.14E-02	rs2010155	14	40077872	q21.1
SNP_A-1648178	T	T	311	49	322	84	6.663	9.80E-03	rs10483523	14	40254131	q21.1
SNP_A-1643746	C	C	338	42	325	73	8.199	4.20E-03	rs10483522	14	40266002	q21.1
SNP_A-2209996	C	C	400	4	406	0	4.04	4.44E-02	rs2211549	14	40572975	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2174332	G	G	324	6	285	17	6.531	0.0106	rs17111772	14	40822947	q21.1
SNP_A-2175127	A	G	187	159	200	164	5.737	0.0166	rs17781156	14	40917004	q21.1
SNP_A-1867160	A	G	206	176	190	156	5.675	0.0172	rs1821019	14	40937824	q21.1
SNP_A-2098996	C	T	201	167	174	154	4.081	4.34E-02	rs7143605	14	40950477	q21.1
SNP_A-1846461	T	T	280	134	253	163	4.195	4.06E-02	rs6572094	14	41030164	q21.1
SNP_A-2210293	T	C	217	183	216	192	4.179	4.09E-02	rs1956450	14	41151632	q21.1
SNP_A-1954557	T	A	189	183	194	138	6.022	0.0141	rs8015100	14	41164982	q21.1
SNP_A-2288564	C	C	272	94	265	57	6.37	1.16E-02	rs2084347	14	41309290	q21.1
SNP_A-2141105	T	T	335	51	299	75	6.428	0.0112	rs12434724	14	41340947	q21.1
SNP_A-2127598	C	C	333	43	293	61	5.013	0.0252	rs1951877	14	41363532	q21.1
SNP_A-2030774	T	T	243	163	215	199	5.214	0.0224	rs17781474	14	41390851	q21.1
SNP_A-2174939	C	C	242	160	210	194	5.526	1.87E-02	rs12884688	14	41391684	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2234500	A	A	341	59	359	35	6.546	1.05E-02	rs17112334	14	41395425	q21.1
SNP_A-2210464	G	G	326	48	354	30	5.176	0.0229	rs10144598	14	41533770	q21.1
SNP_A-2221749	G	G	215	143	186	168	4.085	4.33E-02	rs2154294	14	41725025	q21.1
SNP_A-1877915	T	T	377	31	381	15	5.408	0.02	rs12883508	14	41901648	q21.1
SNP_A-2240423	G	G	336	52	325	31	4.128	4.22E-02	rs2083509	14	42822551	q21.2
SNP_A-2083908	C	C	398	6	390	0	5.836	1.57E-02	rs12590884	14	42861687	q21.2
SNP_A-1920414	C	C	362	0	312	4	4.609	3.18E-02	rs2201350	14	42936835	q21.2
SNP_A-2152522	A	A	245	115	205	139	5.462	1.94E-02	rs10400703	14	43093584	q21.2
SNP_A-1724386	A	A	380	18	396	8	4.131	4.21E-02	rs229712	14	43219581	q21.2
SNP_A-2066852	C	C	353	13	383	5	4.14	0.0419	rs12587864	14	43496423	q21.2
SNP_A-1807137	G	G	326	88	296	112	4.283	0.0385	rs17278886	14	43636063	q21.2
SNP_A-1653258	A	A	339	59	321	87	5.738	0.0166	rs7494280	14	44041488	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1720921	C	C	341	55	323	81	5.379	2.04E-02	rs2415902	14	44049853	q21.2
SNP_A-1840763	C	C	268	62	254	88	4.669	3.07E-02	rs8008562	14	44151337	q21.2
SNP_A-2123831	G	G	176	162	224	144	5.554	0.0184	rs1953851	14	44159355	q21.2
SNP_A-1838048	C	C	367	49	393	27	7.239	7.10E-03	rs807330	14	44239152	q21.2
SNP_A-1716685	G	G	374	26	398	14	4.17	4.12E-02	rs10483586	14	44363600	q21.2
SNP_A-1689763	G	G	374	26	398	14	4.17	4.12E-02	rs10483587	14	44363653	q21.2
SNP_A-2288463	C	C	385	25	396	8	8.869	2.90E-03	rs1593279	14	44380138	q21.2
SNP_A-2212098	T	T	285	37	330	18	8.861	2.90E-03	rs17115667	14	44403334	q21.2
SNP_A-2296469	G	G	344	14	355	5	4.431	3.53E-02	rs2295160	14	44450014	q21.2
SNP_A-2025978	C	C	386	18	392	6	6.002	0.0143	rs6572290	14	44466915	q21.2
SNP_A-2003717	T	T	378	30	378	14	5.5	0.019	rs8006685	14	44590977	q21.2
SNP_A-2230204	A	A	301	27	319	13	5.399	2.02E-02	rs1053667	14	44612788	q21.2
SNP_A-1737315	G	G	380	18	406	6	6.62	0.0101	rs860855	14	44675798	q21.2
SNP_A-1715817	G	G	341	59	375	37	6.48	0.0109	rs10498397	14	44856197	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2212415	G	G	281	123	316	92	6.502	1.08E-02	rs1266251	14	45272213	q21.2
SNP_A-1749459	A	A	269	125	241	163	6.427	0.0112	rs2050966	14	45436166	q21.3
SNP_A-2212638	G	G	230	96	188	118	5.855	0.0155	rs17726637	14	45436312	q21.2
SNP_A-1942990	C	T	214	168	204	190	4.725	2.97E-02	rs12148021	14	45457913	q21.2
SNP_A-2103534	G	A	203	165	189	171	4.278	3.86E-02	rs11850662	14	45462187	q21.2
SNP_A-1854587	G	A	218	182	210	186	4.515	3.36E-02	rs9944104	14	45491391	q21.2
SNP_A-1948412	T	T	206	122	170	152	6.677	9.80E-03	rs1951317	14	45521429	q21.2
SNP_A-2234252	G	G	383	15	400	6	4.147	4.17E-02	rs1958357	14	45623217	q21.2
SNP_A-1843884	C	C	386	8	403	1	5.686	1.71E-02	rs1754310	14	45632676	q21.2
SNP_A-2102940	G	G	310	24	294	10	4.788	0.0287	rs11157487	14	45811812	q21.2
SNP_A-2109785	C	C	285	59	326	38	6.738	9.40E-03	rs1761011	14	45974095	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2215363	C	C	269	125	304	100	4.791	0.0286	rs2933222	14	46424446	q21.3
SNP_A-1679202	T	T	381	13	376	28	5.396	2.02E-02	rs698305	14	46457086	q21.3
SNP_A-1692048	C	C	244	152	281	119	6.606	1.02E-02	rs712450	14	46457171	q21.3
SNP_A-2118330	C	C	378	0	370	4	4.064	4.38E-02	rs12435836	14	46525082	q21.3
SNP_A-2066000	T	T	350	56	356	36	4.154	4.15E-02	rs1954250	14	46564912	q21.3
SNP_A-1889728	A	G	233	183	222	198	6.579	0.0103	rs10149991	14	46638818	q21.3
SNP_A-1830350	G	T	186	184	228	164	5.451	1.96E-02	rs12588192	14	46651013	q21.3
SNP_A-1723020	C	C	336	22	339	43	6.026	0.0141	rs2416153	14	46731766	q21.3
SNP_A-1800655	C	C	355	31	374	18	3.898	4.83E-02	rs17118171	14	46753746	q21.3
SNP_A-1723638	C	C	313	69	358	52	4.422	3.55E-02	rs2261151	14	47232252	q21.3
SNP_A-1715537	A	A	331	69	362	50	4.244	3.94E-02	rs2816724	14	47242056	q21.3
SNP_A-1936795	G	G	289	99	267	131	5.196	2.26E-02	rs12893288	14	47430763	q21.3
SNP_A-2099619	C	C	380	24	349	39	4.568	3.26E-02	rs698308	14	47537844	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950428	C	C	373	37	397	21	5.085	0.0241	rs7158269	14	47775787	q21.3
SNP_A-2279881	A	A	404	0	378	8	8.459	3.60E-03	rs4381498	14	48047945	q21.3
SNP_A-2229955	G	G	177	165	198	136	3.876	4.90E-02	rs12323417	14	48080024	q21.3
SNP_A-1863234	G	G	296	66	278	94	5.329	2.10E-02	rs17120305	14	48132937	q21.3
SNP_A-1853097	G	G	346	40	357	23	4.713	2.99E-02	rs17120330	14	48143580	q21.3
SNP_A-2086351	G	G	311	25	331	13	4.319	3.77E-02	rs17120343	14	48144865	q21.3
SNP_A-2003731	T	T	289	73	316	54	3.961	4.66E-02	rs2585394	14	48251966	q21.3
SNP_A-2256294	A	A	241	127	258	96	4.619	3.16E-02	rs11628435	14	48654470	q21.3
SNP_A-2081181	A	G	193	145	184	174	5.036	2.48E-02	rs7160416	14	48845417	q21.3
SNP_A-1785527	A	A	320	64	334	44	3.956	4.67E-02	rs17772811	14	48976075	q21.3
SNP_A-1922919	T	T	299	77	297	49	4.991	2.55E-02	rs8019711	14	48985295	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897888	A	A	362	48	370	30	4.118	0.0424	rs7156155	14	49020396	q21.3
SNP_A-1835986	G	G	322	28	316	48	5.047	0.0247	rs3218791	14	49201596	q21.3
SNP_A-2193251	C	C	374	0	372	4	4	4.55E-02	rs4363775	14	49324054	q21.3
SNP_A-2214608	A	A	355	55	337	79	4.723	0.0298	rs1950510	14	49713950	q21.3
SNP_A-2129948	G	G	383	11	403	3	4.901	2.68E-02	rs4898659	14	50009206	q21.3
SNP_A-2092571	C	C	390	16	409	5	6.136	0.0132	rs2180499	14	50038960	q21.3
SNP_A-2116016	A	A	292	108	313	83	3.981	4.60E-02	rs2984272	14	50262963	q22.1
SNP_A-2266171	C	A	197	175	215	161	7.702	5.50E-03	rs4901053	14	50287324	q22.1
SNP_A-1868051	A	A	265	117	295	91	4.836	2.79E-02	rs12588703	14	50289925	q22.1
SNP_A-1739485	T	T	362	38	387	19	7.124	0.0076	rs10498438	14	50335910	q22.1
SNP_A-1677522	T	T	364	36	393	19	6.19	0.0129	rs7154422	14	50346701	q22.1
SNP_A-2196597	A	A	246	162	268	132	3.924	4.76E-02	rs9323200	14	50502582	q22.1
SNP_A-1793768	T	T	332	68	364	48	4.743	2.94E-02	rs4567626	14	50717390	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1707235	G	G	315	77	273	111	9.067	2.60E-03	rs10498445	14	50730479	q22.1
SNP_A-1645824	G	G	373	27	358	52	8.097	4.40E-03	rs708511	14	50799975	q22.1
SNP_A-1734426	C	C	264	136	229	181	8.751	3.10E-03	rs781354	14	50869364	q22.1
SNP_A-1676272	G	G	400	0	406	4	3.922	4.77E-02	rs897968	14	50869403	q22.1
SNP_A-2111461	T	T	216	168	250	138	5.401	0.0201	rs7142110	14	50878153	q22.1
SNP_A-1788330	C	C	369	35	387	21	3.909	4.80E-02	rs2356894	14	50897315	q22.1
SNP_A-1668727	A	A	380	20	376	36	4.416	0.0356	rs781381	14	50900831	q22.1
SNP_A-2047641	G	G	318	96	282	122	5.139	2.34E-02	rs17123869	14	50937357	q22.1
SNP_A-2298534	G	G	289	89	247	115	6.262	0.0123	rs17123900	14	50958296	q22.1
SNP_A-2068665	C	C	273	125	301	97	4.897	0.0269	rs7143090	14	51114532	q22.1
SNP_A-2070975	G	G	405	11	416	2	6.373	1.16E-02	rs4608255	14	51338501	q22.1
SNP_A-1796097	A	A	318	6	374	0	6.986	8.20E-03	rs17124563	14	51364273	q22.1
SNP_A-2216326	A	A	380	32	401	17	5.113	2.37E-02	rs17124692	14	51408207	q22.1
SNP_A-2050414	C	C	403	7	419	1	4.692	3.03E-02	rs1253647	14	51497862	q22.1
SNP_A-2274200	C	C	380	8	410	0	8.539	3.50E-03	rs1253651	14	51498176	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1816792	G	G	399	7	414	0	7.199	7.30E-03	rs1253653	14	51498509	q22.1
SNP_A-2023219	T	T	406	10	415	1	7.462	0.0063	rs1253654	14	51498586	q22.1
SNP_A-1893175	T	T	331	15	332	2	9.734	0.0018	rs1271518	14	51498797	q22.1
SNP_A-2081084	C	C	409	7	403	17	4.192	4.06E-02	rs12147898	14	51611212	q22.1
SNP_A-2150316	T	T	409	7	403	17	4.192	4.06E-02	rs11157875	14	51611393	q22.1
SNP_A-2141536	A	A	399	7	394	18	4.828	2.80E-02	rs1956278	14	51611889	q22.1
SNP_A-2259038	C	C	367	5	347	17	7.02	8.10E-03	rs1956281	14	51612219	q22.1
SNP_A-1838583	A	A	349	43	373	27	4.375	3.65E-02	rs10132362	14	51700801	q22.1
SNP_A-1960761	C	C	287	87	259	123	7.524	6.10E-03	---	14	51824671	q22.1
SNP_A-1689823	A	G	206	194	237	175	6.636	0.01	rs1954331	14	51877426	q22.1
SNP_A-2296218	A	G	199	183	217	167	5.683	1.71E-02	rs697812	14	51886666	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2188434	A	A	384	28	369	49	5.983	0.0144	rs17831748	14	51928181	q22.1
SNP_A-1925746	G	G	253	149	203	185	9.117	2.50E-03	rs972156	14	51975387	q22.1
SNP_A-1822676	T	T	376	14	359	27	4.495	3.40E-02	rs8004586	14	52025942	q22.1
SNP_A-1919188	C	G	214	132	191	179	13.104	3.00E-04	rs6572849	14	52047039	q22.1
SNP_A-1884056	G	G	253	143	220	174	5.329	2.10E-02	rs745080	14	52058978	q22.1
SNP_A-2103784	A	A	239	157	205	197	7.079	7.80E-03	rs2065055	14	52111299	q22.1
SNP_A-2050479	C	A	230	146	196	192	10.546	1.20E-03	rs1951448	14	52120019	q22.1
SNP_A-2217101	A	G	199	191	226	178	3.862	4.94E-02	rs2008601	14	52215806	q22.1
SNP_A-2217115	A	A	275	91	251	115	3.891	4.85E-02	rs1977232	14	52221098	q22.1
SNP_A-2278077	A	A	296	56	270	86	7.51	6.10E-03	rs10130056	14	52560972	q22.1
SNP_A-1932622	T	T	274	106	252	134	4.14	0.0419	rs10139750	14	52563872	q22.1
SNP_A-2186542	G	G	328	12	296	22	3.851	4.97E-02	rs2358080	14	52565539	q22.1
SNP_A-1832983	A	A	284	124	256	154	4.684	0.0304	rs2150541	14	52575641	q22.1
SNP_A-1866877	G	G	358	32	329	53	6.33	1.19E-02	rs2065819	14	52693414	q22.1
SNP_A-2123641	C	C	321	49	328	28	5.535	1.86E-02	rs723893	14	52866277	q22.1
SNP_A-2127431	C	G	203	193	222	166	5.655	1.74E-02	rs4901420	14	52959160	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041007	A	A	338	68	319	91	3.857	4.95E-02	rs1891550	14	53070047	q22.1
SNP_A-2260156	T	T	319	7	303	17	4.523	3.34E-02	rs17126761	14	53218192	q22.1
SNP_A-1943261	C	C	399	9	393	23	6.093	1.36E-02	rs17126771	14	53218691	q22.1
SNP_A-1896776	G	G	317	43	333	27	4.051	0.0441	rs811173	14	53671032	q22.2
SNP_A-2163361	G	G	382	32	402	18	4.387	3.62E-02	rs10150830	14	53694292	q22.2
SNP_A-1866621	C	C	384	32	399	17	4.879	2.72E-02	rs17127365	14	53718819	q22.2
SNP_A-2078676	T	T	384	32	397	17	4.803	2.84E-02	rs1951666	14	53720005	q22.2
SNP_A-2113043	G	G	285	91	314	64	6.102	0.0135	rs2143955	14	53880476	q22.2
SNP_A-2218388	A	A	205	197	238	166	5.101	2.39E-02	rs17647791	14	53884770	q22.2
SNP_A-1944531	A	A	184	180	225	153	6.037	0.014	rs17647905	14	53890225	q22.2
SNP_A-2194854	C	C	361	25	367	11	5.411	0.02	rs8016022	14	54233720	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2069873	A	A	258	146	287	115	5.22	0.0223	rs11626556	14	54258833	q22.2
SNP_A-2079683	G	G	287	55	263	81	6.012	1.42E-02	rs10144855	14	54281992	q22.2
SNP_A-1801245	C	C	368	30	365	53	5.899	1.51E-02	rs7147275	14	54303274	q22.2
SNP_A-2110089	G	G	310	96	275	123	5.344	2.08E-02	rs4898851	14	54303344	q22.2
SNP_A-1847615	T	T	324	20	299	33	3.98	4.60E-02	rs17128050	14	54413629	q22.2
SNP_A-2218842	G	G	399	15	385	35	8.207	4.20E-03	rs17128143	14	54603341	q22.3
SNP_A-1955919	A	A	374	22	343	49	11.588	7.00E-04	rs17673930	14	54877904	q22.3
SNP_A-1941876	T	T	257	151	289	123	4.717	2.99E-02	rs8019209	14	54961082	q22.3
SNP_A-2162943	T	T	265	151	295	125	4.037	4.45E-02	rs8019080	14	54961125	q22.3
SNP_A-1896563	A	A	391	9	382	20	4.272	3.87E-02	rs8004764	14	55278998	q22.3
SNP_A-2294521	A	A	291	109	264	134	3.881	4.88E-02	rs17832467	14	55365244	q22.3
SNP_A-1782065	C	C	366	22	380	10	4.758	0.0292	rs945272	14	55406398	q22.3
SNP_A-1939143	A	A	340	28	347	15	3.953	4.68E-02	rs12885303	14	55537445	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2053721	G	G	270	116	292	86	5.233	2.22E-02	rs1188690	14	55868252	q22.3
SNP_A-1904173	G	G	256	112	208	138	6.998	8.20E-03	rs12589523	14	55875192	q22.3
SNP_A-2116561	G	G	249	127	225	165	5.906	1.51E-02	rs914009	14	55876855	q22.3
SNP_A-1874939	A	A	338	12	339	27	5.416	0.02	rs17691681	14	55877470	q22.3
SNP_A-2217637	A	A	262	52	295	29	8.331	3.90E-03	rs1152501	14	55886762	q22.3
SNP_A-1852215	C	C	296	118	326	94	4.121	0.0424	rs10134600	14	56032619	q22.3
SNP_A-2220305	G	G	233	163	271	129	6.804	9.10E-03	rs10483669	14	56063987	q22.3
SNP_A-2152338	G	G	337	21	364	10	4.596	3.21E-02	rs11851219	14	56371433	q22.3
SNP_A-1827239	A	A	225	135	192	156	3.925	4.76E-02	rs1190313	14	57126010	q22.3
SNP_A-2285132	G	G	288	64	283	91	4.084	4.33E-02	rs1956680	14	57310043	q23.1
SNP_A-2075326	C	C	290	36	248	58	7.803	5.20E-03	rs1003754	14	57386669	q23.1
SNP_A-2052242	G	G	353	45	332	66	4.617	3.17E-02	rs1003753	14	57387053	q23.1
SNP_A-1921462	T	T	413	1	412	8	5.403	0.0201	rs17093968	14	57473856	q23.1
SNP_A-1868624	C	C	392	12	375	25	4.925	2.65E-02	rs17094008	14	57497859	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2282207	A	A	277	91	310	58	9.164	2.50E-03	rs8015324	14	57530795	q23.1
SNP_A-2003771	A	C	181	177	201	153	3.849	4.98E-02	rs2223934	14	57563317	q23.1
SNP_A-1652520	T	T	370	30	358	48	4.307	3.80E-02	rs10483714	14	57775387	q23.1
SNP_A-2284554	T	T	381	29	368	50	5.731	0.0167	rs856205	14	58303794	q23.1
SNP_A-1866339	C	C	342	56	369	35	5.827	1.58E-02	rs17833131	14	58321286	q23.1
SNP_A-1816729	A	A	337	9	305	1	5.562	0.0184	rs442945	14	58412902	q23.1
SNP_A-2224870	T	T	319	73	288	94	4.095	4.30E-02	rs1252915	14	58735874	q23.1
SNP_A-2111423	G	G	367	15	375	5	5.081	2.42E-02	rs1253192	14	58913159	q23.1
SNP_A-2190564	A	A	339	5	319	13	3.952	4.68E-02	rs1253107	14	59022700	q23.1
SNP_A-1929322	T	T	304	20	338	6	8.748	3.10E-03	rs1957310	14	59420454	q23.1
SNP_A-2136871	C	C	256	74	271	49	5.356	0.0207	rs12887335	14	60233783	q23.1
SNP_A-1663180	G	G	353	13	351	29	5.84	1.57E-02	rs217690	14	60394314	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1811546	G	G	404	0	407	5	4.933	0.0263	rs10133880	14	60479792	q23.1
SNP_A-1734684	C	T	211	173	222	178	8.555	3.40E-03	rs1467163	14	60632450	q23.2
SNP_A-2288081	T	T	363	29	344	52	7.021	8.10E-03	rs17098278	14	60901613	q23.1
SNP_A-2223795	C	C	386	10	371	21	4.18	4.09E-02	rs17098382	14	60986674	q23.1
SNP_A-1957981	A	A	360	0	358	4	4	4.55E-02	rs10140288	14	61031361	q23.1
SNP_A-2223910	G	G	400	4	395	15	6.356	0.0117	rs10483743	14	61080552	q23.1
SNP_A-1661622	C	C	272	126	242	168	7.574	5.90E-03	rs2101551	14	61171683	q23.2
SNP_A-2032205	G	G	336	18	346	8	3.993	4.57E-02	rs17099262	14	61377133	q23.2
SNP_A-2135251	C	C	386	18	385	7	4.661	3.08E-02	rs17099461	14	61597616	q23.2
SNP_A-2290330	G	A	213	177	220	184	6.531	0.0106	rs4435151	14	61704333	q23.2
SNP_A-2034896	G	G	258	96	224	116	4.004	4.54E-02	rs10143885	14	61717219	q23.2
SNP_A-1658254	T	T	368	22	371	9	5.335	2.09E-02	rs10498509	14	62095443	q23.2
SNP_A-2230519	G	G	275	127	240	172	9.03	2.70E-03	rs12435381	14	62249086	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2129241	G	G	259	127	216	164	8.551	3.50E-03	rs12372902	14	62253128	q23.2
SNP_A-1863705	C	C	333	9	342	2	4.569	3.26E-02	rs17223580	14	62401836	q23.2
SNP_A-2070710	A	A	356	36	363	21	3.933	4.73E-02	rs17100876	14	62766361	q23.2
SNP_A-2023473	G	G	403	13	414	4	4.908	2.67E-02	rs17178739	14	63030107	q23.2
SNP_A-2061625	A	A	286	126	309	87	7.716	5.50E-03	rs2754223	14	63044719	q23.2
SNP_A-2296791	A	A	280	104	330	70	10.42	1.20E-03	rs1255771	14	63060864	q23.2
SNP_A-2090945	G	G	262	146	306	102	11.215	8.00E-04	rs1255741	14	63099534	q23.2
SNP_A-2293899	C	C	341	25	364	8	9.46	2.10E-03	rs17101303	14	63108480	q23.2
SNP_A-2178554	T	T	358	40	374	20	6.996	8.20E-03	rs17101464	14	63469309	q23.2
SNP_A-2025286	C	C	367	47	392	28	5.594	1.80E-02	rs12586503	14	63568678	q23.2
SNP_A-2216783	G	G	306	64	316	42	4.53	3.33E-02	rs2357345	14	63582053	q23.2
SNP_A-1911163	C	C	335	65	346	40	5.883	1.53E-02	rs3829767	14	63589208	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2179442	T	T	373	41	393	21	6.974	8.30E-03	rs10140978	14	63597824	q23.2
SNP_A-2156387	A	A	359	25	384	8	9.517	0.002	rs1255973	14	63601756	q23.2
SNP_A-1829991	C	C	304	72	357	43	10.831	0.001	rs1255971	14	63604909	q23.2
SNP_A-1820813	T	T	341	67	366	48	3.98	4.61E-02	rs11158552	14	64191043	q23.3
SNP_A-2256790	G	G	312	10	342	2	5.989	0.0144	rs4899144	14	64307943	q23.3
SNP_A-2003798	G	G	406	4	406	0	3.98	4.60E-02	rs8017631	14	64366483	q23.3
SNP_A-2091173	C	C	308	70	281	97	5.603	1.79E-02	rs1256498	14	64782642	q23.3
SNP_A-2045694	A	A	278	62	251	87	5.567	0.0183	rs8004669	14	64794970	q23.3
SNP_A-2063831	T	T	338	0	315	5	5.322	2.11E-02	rs4632059	14	64933561	q23.3
SNP_A-1793527	G	G	382	16	391	5	5.862	0.0155	rs17181388	14	65187765	q23.3
SNP_A-1917076	C	C	257	155	228	188	4.89	0.027	rs12880549	14	65488852	q23.3
SNP_A-2169051	A	G	219	197	239	181	7.637	5.70E-03	rs6573644	14	65498391	q23.3
SNP_A-1932185	T	C	211	195	243	163	11.421	7.00E-04	rs7158071	14	65502314	q23.3
SNP_A-2169500	C	C	350	32	330	50	4.534	0.0332	rs17103141	14	65502724	q23.3
SNP_A-2071055	T	T	330	86	301	117	6.062	0.0138	rs17754112	14	65522927	q23.3
SNP_A-2183853	C	C	303	77	280	100	3.896	4.84E-02	rs1147443	14	65538514	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1878008	A	A	291	79	267	103	4.197	4.05E-02	rs1147442	14	65539053	q23.3
SNP_A-2021857	A	A	410	6	416	0	6.044	0.014	rs12323823	14	66434516	q23.3
SNP_A-1961289	G	G	361	49	369	31	4.015	4.51E-02	rs10138850	14	66676521	q23.3
SNP_A-2104601	G	G	393	15	406	6	4.049	4.42E-02	rs3866760	14	66702333	q23.3
SNP_A-1796085	T	T	324	10	331	3	3.844	0.0499	rs8008724	14	66916971	q23.3
SNP_A-2258032	A	A	257	95	241	125	4.334	3.74E-02	rs10146483	14	66967424	q23.3
SNP_A-2209865	G	G	252	108	226	140	5.494	1.91E-02	rs10146711	14	66967453	q23.3
SNP_A-1794783	A	A	260	132	217	155	5.2	2.26E-02	rs3742855	14	66982545	q23.3
SNP_A-1692920	A	A	329	73	363	51	5.398	2.02E-02	rs761951	14	67079527	q24.1
SNP_A-1792986	G	G	402	10	413	3	3.898	4.83E-02	rs2319843	14	67116492	q24.1
SNP_A-2103643	G	G	225	171	246	138	4.277	3.86E-02	rs7151091	14	67403902	q24.1
SNP_A-2033085	A	A	225	103	207	141	6.082	0.0137	rs11628653	14	67888729	q24.1
SNP_A-2227900	G	A	236	176	211	197	6.659	9.90E-03	rs8018477	14	67902720	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2243363	C	C	297	95	274	128	5.685	1.71E-02	rs4899241	14	67934064	q24.1
SNP_A-2227964	G	G	216	178	249	153	4.15	4.16E-02	rs10146772	14	67948122	q24.1
SNP_A-2034555	T	T	273	111	307	85	5.36	0.0206	rs4902604	14	68124238	q24.1
SNP_A-2228125	G	G	391	27	370	52	8.472	3.60E-03	rs10483814	14	68125552	q24.1
SNP_A-2270716	G	G	221	111	176	130	5.548	1.85E-02	rs10136316	14	68133274	q24.1
SNP_A-1863335	T	T	228	176	273	139	8.31	3.90E-03	rs12879200	14	68137863	q24.1
SNP_A-1854037	C	C	328	62	361	41	5.682	1.71E-02	rs6573848	14	68180283	q24.1
SNP_A-2048033	A	A	281	133	258	164	4.141	0.0419	rs1007840	14	68225853	q24.1
SNP_A-2307178	A	A	357	1	344	8	5.635	1.76E-02	rs450420	14	68256207	q24.1
SNP_A-1679150	A	A	223	111	226	154	4.051	4.42E-02	rs227438	14	68442655	q24.2
SNP_A-1943500	C	C	351	17	361	5	6.681	9.70E-03	rs730666	14	68445455	q24.1
SNP_A-2086558	T	T	250	128	231	167	6.743	9.40E-03	rs12100668	14	68863228	q24.1
SNP_A-2132179	A	A	348	70	318	102	7.3	6.90E-03	rs7152301	14	68902471	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1782127	G	G	317	49	264	68	6.279	1.22E-02	rs2061088	14	68912030	q24.1
SNP_A-2310278	A	A	325	41	292	68	8.404	3.70E-03	rs10137668	14	69018940	q24.1
SNP_A-1646172	T	T	383	19	405	9	4.01	4.52E-02	rs1205238	14	69118585	q24.2
SNP_A-2221018	C	C	319	31	351	19	3.856	4.96E-02	rs10149246	14	69175291	q24.1
SNP_A-1678830	A	C	209	179	216	182	5.204	2.25E-02	rs7144786	14	69285042	q24.2
SNP_A-1876268	T	T	326	70	361	43	8.155	0.0043	rs17107699	14	69584770	q24.2
SNP_A-2298785	G	G	240	92	259	59	7.637	5.70E-03	rs17107753	14	69610384	q24.2
SNP_A-1848886	A	A	229	107	236	76	4.474	0.0344	rs8006818	14	69657342	q24.2
SNP_A-2219952	C	C	239	117	270	72	12.326	4.00E-04	rs11622489	14	69732356	q24.2
SNP_A-1961053	G	G	261	123	232	156	5.589	1.81E-02	rs1205233	14	70202512	q24.2
SNP_A-2229802	G	G	203	139	181	171	4.42	3.55E-02	rs886600	14	70299034	q24.2
SNP_A-2292003	G	G	294	24	301	43	4.456	3.48E-02	rs2107666	14	70316660	q24.2
SNP_A-2146713	G	G	252	86	294	64	5.888	0.0152	rs11622104	14	70368767	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944375	T	T	282	112	311	87	4.539	3.31E-02	rs11626893	14	70368966	q24.2
SNP_A-2137991	T	T	361	53	384	32	5.894	0.0152	rs12882665	14	70370352	q24.2
SNP_A-2063685	A	A	358	54	384	34	5.413	0.02	rs12886420	14	70371085	q24.2
SNP_A-1751285	C	C	309	79	356	58	5.704	1.69E-02	rs728497	14	70423192	q24.2
SNP_A-2125104	A	A	344	38	328	60	5.273	2.17E-02	rs17109110	14	70716223	q24.2
SNP_A-1782598	C	C	386	28	372	46	4.618	3.16E-02	rs1990033	14	70739119	q24.2
SNP_A-2264240	C	C	248	124	224	166	6.882	8.70E-03	rs36452	14	71406022	q24.2
SNP_A-2229524	C	C	371	37	351	55	4.071	0.0436	rs2109268	14	71481608	q24.2
SNP_A-2235755	G	G	376	34	344	56	6.678	9.80E-03	rs17768231	14	71483298	q24.2
SNP_A-2063058	C	C	323	37	298	58	5.626	0.0177	rs2067854	14	71495572	q24.2
SNP_A-1912815	C	C	318	86	352	58	7.126	0.0076	rs4899409	14	71508128	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2230560	T	T	323	93	356	64	6.942	8.40E-03	rs3784056	14	71519104	q24.2
SNP_A-2230561	A	A	349	69	312	102	8.42	3.70E-03	rs10483837	14	71519244	q24.2
SNP_A-2135862	G	G	325	93	357	65	6.445	0.0111	rs17105346	14	71522224	q24.2
SNP_A-2251009	G	G	387	11	390	24	4.527	3.34E-02	rs2238276	14	71525980	q24.2
SNP_A-2140208	T	T	305	85	334	52	9.245	2.40E-03	rs11623492	14	71532310	q24.2
SNP_A-2028189	C	C	325	93	356	66	5.977	1.45E-02	rs11158927	14	71535902	q24.2
SNP_A-2146331	C	C	301	65	340	46	5.097	0.024	rs12148043	14	71542180	q24.2
SNP_A-2240827	A	A	308	74	337	47	7.323	6.80E-03	rs11628574	14	71554948	q24.2
SNP_A-1904293	G	G	325	51	302	74	5.076	2.43E-02	rs2052014	14	71557570	q24.2
SNP_A-2264435	A	A	351	49	336	70	3.989	0.0458	rs17179664	14	71647337	q24.2
SNP_A-1941698	C	C	310	38	283	17	5.723	0.0167	rs2238221	14	71769093	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2231124	G	G	386	8	397	1	5.579	1.82E-02	rs2283394	14	71848782	q24.2
SNP_A-2309494	G	G	358	40	352	62	4.482	3.42E-02	rs2239276	14	72024525	q24.2
SNP_A-2053991	G	G	375	37	354	58	5.247	2.20E-02	rs2239275	14	72024558	q24.2
SNP_A-1793092	G	G	373	39	356	62	5.591	1.81E-02	rs2239274	14	72024612	q24.2
SNP_A-1815100	T	T	370	40	351	59	4.147	4.17E-02	rs17180678	14	72024743	q24.2
SNP_A-2281465	G	C	200	150	174	168	4.468	3.45E-02	rs12878358	14	73157987	q24.3
SNP_A-2174759	A	A	223	139	242	110	4.015	4.51E-02	rs17782222	14	73408302	q24.3
SNP_A-1758029	A	A	235	167	211	203	4.619	3.16E-02	rs175072	14	73492868	q24.3
SNP_A-2232156	A	A	240	120	226	156	4.468	3.45E-02	rs2074932	14	73511437	q24.3
SNP_A-1667044	A	T	211	183	226	186	5.696	1.70E-02	rs175449	14	73580887	q24.3
SNP_A-2160067	G	G	255	115	243	149	4.036	4.45E-02	rs7157566	14	73718882	q24.3
SNP_A-2062875	C	C	186	184	242	152	9.63	0.0019	rs7153700	14	74338297	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082174	C	G	211	171	217	183	7.033	8.00E-03	rs957345	14	74345832	q24.3
SNP_A-2140046	C	-	221	145	185	185	8.019	4.60E-03	rs10148293	14	74366584	q24.3
SNP_A-2232629	G	G	172	158	207	117	9.291	0.0023	rs10483863	14	74392080	q24.3
SNP_A-1840871	A	A	245	91	224	124	5.797	0.0161	rs2300599	14	74429194	q24.3
SNP_A-2070646	-	G	176	176	214	152	5.188	2.27E-02	rs2070599	14	74430930	q24.3
SNP_A-2232670	G	G	213	145	231	99	8.276	4.00E-03	rs2159906	14	74460665	q24.3
SNP_A-2232734	A	A	245	157	205	195	7.653	5.70E-03	rs735452	14	74567737	q24.3
SNP_A-2232735	A	A	247	167	213	205	6.376	1.16E-02	rs175071	14	74567930	q24.3
SNP_A-1832156	A	A	221	189	256	158	5.318	2.11E-02	rs7156586	14	74575983	q24.3
SNP_A-2097492	A	C	225	193	231	187	6.911	0.0086	rs3742778	14	74607970	q24.3
SNP_A-1850255	C	A	177	139	181	165	4.583	3.23E-02	rs175492	14	74614973	q24.3
SNP_A-1815928	G	G	239	157	197	185	6.088	1.36E-02	rs175490	14	74615438	q24.3
SNP_A-1951897	C	C	270	126	235	149	4.166	4.12E-02	rs96358	14	74642018	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1910107	G	T	222	178	200	180	5.159	2.31E-02	rs119076	14	74642172	q24.3
SNP_A-2077479	T	C	225	193	233	187	7.256	7.10E-03	rs10146482	14	74643840	q24.3
SNP_A-2148970	G	A	210	176	199	173	4.728	2.97E-02	rs7145159	14	74653021	q24.3
SNP_A-2209369	A	C	214	190	222	186	4.426	3.54E-02	rs8003506	14	74656041	q24.3
SNP_A-2302218	C	T	191	167	206	166	5.562	0.0184	rs11623413	14	74658577	q24.3
SNP_A-1895046	C	T	219	183	210	176	6.214	1.27E-02	rs876402	14	74671615	q24.3
SNP_A-2308527	C	G	212	162	194	178	5.835	1.57E-02	rs175436	14	74678436	q24.3
SNP_A-2022306	G	T	222	194	228	188	5.559	0.0184	rs2098297	14	74688871	q24.3
SNP_A-2026513	G	A	193	179	200	160	4.053	0.0441	rs2300601	14	74709324	q24.3
SNP_A-2081607	C	C	346	44	368	24	6.555	1.05E-02	rs11159122	14	74756611	q24.3
SNP_A-1785554	C	C	240	174	270	146	4.21	0.0402	rs8018744	14	74937059	q24.3
SNP_A-2192591	G	G	289	107	297	73	5.655	1.74E-02	rs7153685	14	75019381	q24.3
SNP_A-2108483	A	G	216	194	222	184	4.425	3.54E-02	rs11626830	14	75657598	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2118270	A	A	347	35	331	53	4.054	0.0441	rs1900125	14	75727223	q24.3
SNP_A-1855667	A	A	295	113	268	140	4.176	4.10E-02	rs1900126	14	75727509	q24.3
SNP_A-2225238	T	T	266	124	242	152	3.954	4.68E-02	rs2360982	14	75764630	q24.3
SNP_A-1731871	T	T	320	82	354	60	4.948	2.61E-02	rs10483882	14	75904715	q24.3
SNP_A-2243076	C	C	317	77	299	103	4.202	4.04E-02	rs1676235	14	76088319	q24.3
SNP_A-1856757	T	T	330	74	347	53	3.88	4.89E-02	rs4903444	14	76190270	q24.3
SNP_A-1790465	G	G	388	18	383	33	4.323	3.76E-02	rs17104869	14	76318232	q24.3
SNP_A-2301800	C	C	371	5	406	0	5.434	1.98E-02	rs2242630	14	76403939	q24.3
SNP_A-1722274	C	C	351	51	334	76	5.265	0.0218	rs880373	14	76732331	q24.3
SNP_A-2053457	G	G	287	127	319	99	5.14	2.34E-02	rs10134823	14	76735478	q24.3
SNP_A-2234125	G	G	289	43	290	22	6.171	1.30E-02	rs3815625	14	76821482	q24.3
SNP_A-2272128	C	C	348	24	391	13	4.46	3.47E-02	rs8177539	14	76857512	q24.3
SNP_A-2025644	G	G	242	96	214	130	6.782	9.20E-03	rs3815628	14	76879692	q24.3
SNP_A-1833024	G	G	314	70	340	50	4.321	3.77E-02	rs17750993	14	76924168	q24.3
SNP_A-1933068	G	G	259	81	238	120	7.996	4.70E-03	rs7155063	14	76924353	q24.3
SNP_A-1940995	G	G	330	78	356	54	5.344	2.08E-02	rs17824094	14	76962714	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829562	A	A	367	17	342	38	8.879	2.90E-03	rs17751406	14	77005693	q24.3
SNP_A-2235932	T	T	383	35	363	57	5.792	0.0161	rs17751412	14	77006722	q24.3
SNP_A-1712993	C	C	280	64	259	91	5.47	1.93E-02	rs10483914	14	77187253	q24.3
SNP_A-2234458	G	G	366	52	343	79	6.292	0.0121	rs4996830	14	77194550	q24.3
SNP_A-2234476	G	G	386	30	372	48	4.393	0.0361	rs10483884	14	77219447	q24.3
SNP_A-2060261	C	C	335	83	359	61	4.186	4.08E-02	rs7157412	14	77558297	q24.3
SNP_A-2021281	C	C	184	182	221	157	5.032	2.49E-02	rs7151264	14	77565951	q24.3
SNP_A-2094584	C	C	358	60	326	90	7.492	6.20E-03	rs7156667	14	77618067	q24.3
SNP_A-1807237	A	A	340	50	359	27	7.366	0.0066	rs17106833	14	77625791	q24.3
SNP_A-2179498	A	A	329	33	342	16	6.128	1.33E-02	rs12232088	14	77659627	q24.3
SNP_A-1867872	G	G	337	69	307	101	7.416	6.50E-03	rs12588277	14	77833623	q24.3
SNP_A-2229864	C	C	368	10	366	28	8.204	4.20E-03	rs17829009	14	77952969	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1732598	A	A	334	0	314	4	4.227	3.98E-02	rs10483924	14	77982153	q31.1
SNP_A-1664872	G	G	264	82	265	49	6.779	9.20E-03	rs2216901	14	77991574	q31.1
SNP_A-1731937	A	A	222	162	262	140	4.499	0.0339	rs221418	14	78028515	q31.1
SNP_A-1714633	A	A	278	124	312	100	4.409	3.58E-02	rs7158064	14	78138496	q31.1
SNP_A-1720109	G	G	365	37	398	14	11.679	6.00E-04	rs10483933	14	78157500	q31.1
SNP_A-2235320	C	C	363	43	381	27	4.088	4.32E-02	rs17108212	14	78299155	q24.3
SNP_A-2048140	A	A	226	154	174	160	3.927	4.75E-02	rs8006983	14	78577230	q31.1
SNP_A-2038907	C	C	269	127	306	104	4.429	3.53E-02	rs7147705	14	79071849	q31.1
SNP_A-1678854	T	T	256	144	228	184	6.322	1.19E-02	rs17519	14	79077935	q31.1
SNP_A-1741661	T	T	374	6	383	19	6.253	0.0124	rs8016670	14	79086740	q31.1
SNP_A-2235989	A	A	235	171	269	143	4.747	2.94E-02	rs2543580	14	79142877	q31.1
SNP_A-2256668	G	G	216	154	255	133	4.341	3.72E-02	rs8013736	14	79145443	q31.1
SNP_A-2055638	C	C	314	82	339	61	4.021	4.49E-02	rs221488	14	79163383	q31.1
SNP_A-2133584	C	C	371	39	400	18	8.751	3.10E-03	rs17109778	14	79240326	q31.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1837384	G	G	262	150	228	184	5.82	1.58E-02	rs178379	14	79250408	q31.1
SNP_A-1906827	A	A	243	145	205	183	7.626	5.80E-03	rs178384	14	79252594	q31.1
SNP_A-2266148	G	G	287	75	293	47	5.805	0.016	rs7152384	14	79539170	q31.1
SNP_A-2215717	G	G	314	18	288	36	7.026	8.00E-03	rs1907526	14	79757632	q31.1
SNP_A-2251568	T	T	287	127	317	99	4.954	2.60E-02	rs10152064	14	79926428	q31.1
SNP_A-2236712	G	G	193	143	233	113	7.126	0.0076	rs17528984	14	80018946	q31.1
SNP_A-2236799	G	G	327	71	303	93	3.86	4.94E-02	rs10498546	14	80194089	q31.1
SNP_A-1917702	A	A	270	118	250	148	4.026	0.0448	rs2371333	14	80204045	q31.1
SNP_A-2301481	G	A	226	188	218	198	4.061	4.39E-02	rs2630271	14	80263582	q31.1
SNP_A-1808157	C	C	238	138	203	169	5.887	1.53E-02	rs2556607	14	80413947	q31.1
SNP_A-2146624	C	C	407	5	416	0	5.079	2.42E-02	rs17115590	14	81107547	q31.1
SNP_A-1856477	C	C	257	67	271	45	4.593	3.21E-02	rs1198030	14	81514028	q31.1
SNP_A-2279221	C	C	195	179	218	146	4.497	3.40E-02	rs1652591	14	81629325	q31.1
SNP_A-1725226	A	A	331	63	358	44	4.352	3.70E-02	rs1350280	14	81648764	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2259426	C	C	320	54	342	36	4.31	3.79E-02	rs799102	14	81776232	q31.1
SNP_A-1658028	T	T	366	22	366	38	3.945	0.047	rs229809	14	81903967	q31.2
SNP_A-2093925	C	C	306	98	332	72	5.036	2.48E-02	rs2372242	14	82374231	q31.2
SNP_A-2166780	T	T	313	35	333	19	5.337	2.09E-02	---	14	82374256	q31.2
SNP_A-1824779	G	G	299	85	319	59	5.295	2.14E-02	rs2372243	14	82374425	q31.2
SNP_A-1749379	G	G	387	15	409	5	5.433	1.98E-02	rs10484124	14	82490390	q31.3
SNP_A-1953570	G	G	390	16	413	7	3.944	0.047	rs7147249	14	82550373	q31.2
SNP_A-2032813	T	T	310	64	262	82	5.002	0.0253	rs17679217	14	82594395	q31.2
SNP_A-2117738	C	C	247	125	214	148	4.165	4.13E-02	rs12883055	14	82601279	q31.2
SNP_A-1879023	G	G	230	108	208	136	4.266	3.89E-02	rs2210180	14	82611426	q31.2
SNP_A-1846457	T	T	243	145	193	161	5.023	2.50E-02	rs2210181	14	82611520	q31.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2192505	A	A	390	26	409	13	4.742	2.94E-02	rs17118382	14	82848931	q31.2
SNP_A-2045005	A	A	330	20	323	5	8.37	0.0038	rs17118410	14	82859905	q31.2
SNP_A-2239785	A	A	331	19	308	34	4.981	2.56E-02	rs17118712	14	83006927	q31.2
SNP_A-1837322	A	A	296	98	262	124	5.035	2.48E-02	rs12717595	14	83236571	q31.2
SNP_A-2303300	A	A	302	114	270	144	5.274	2.16E-02	rs1952529	14	83254709	q31.2
SNP_A-2059394	T	T	348	14	312	4	4.419	3.55E-02	rs17119295	14	83475314	q31.3
SNP_A-2028681	C	C	403	13	414	4	4.908	2.67E-02	rs1511315	14	83492144	q31.3
SNP_A-1936811	G	G	390	14	408	4	5.884	1.53E-02	rs17119399	14	83535599	q31.3
SNP_A-2261084	C	C	404	12	416	4	4.157	4.15E-02	rs1531457	14	83656405	q31.3
SNP_A-2093785	G	G	241	143	258	108	5.031	2.49E-02	rs1031787	14	83764242	q31.3
SNP_A-2067949	C	C	235	127	199	151	4.857	0.0275	rs7494381	14	83953196	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1867488	A	A	332	54	365	33	6.449	0.0111	rs12897284	14	84633513	q31.3
SNP_A-1954771	A	A	366	28	355	45	4.082	4.34E-02	rs11851675	14	84660825	q31.3
SNP_A-1683166	T	T	309	57	307	93	7.151	7.50E-03	rs2022641	14	84865680	q31.3
SNP_A-1725692	A	A	219	183	260	152	6.256	0.0124	rs8023222	14	84912582	q31.3
SNP_A-1737657	T	T	332	64	339	35	7.946	4.80E-03	rs7159769	14	85310163	q31.3
SNP_A-1731179	A	A	338	64	319	89	4.59	3.22E-02	rs10498613	14	85707523	q31.3
SNP_A-2297942	C	C	353	5	358	0	5.035	2.48E-02	rs10149765	14	85789333	q31.3
SNP_A-1878683	C	C	372	6	374	0	5.984	0.0144	rs10149864	14	85789437	q31.3
SNP_A-1891555	T	T	217	187	245	147	6.308	0.012	rs804963	14	85918211	q31.3
SNP_A-2242583	C	C	183	135	224	114	5.296	2.14E-02	rs1289381	14	85929220	q31.3
SNP_A-2242587	G	G	222	184	261	153	5.923	0.0149	rs1289385	14	85929449	q31.3
SNP_A-1700638	A	A	362	18	406	8	4.338	0.0373	rs10483999	14	85938914	q31.3
SNP_A-2046068	C	C	232	168	267	131	7.029	8.00E-03	rs2185584	14	85981310	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1754108	G	G	371	31	400	14	7.338	6.80E-03	rs1959715	14	86155251	q31.3
SNP_A-1818233	A	A	303	71	334	48	5.87	0.0154	rs1362721	14	86318354	q31.3
SNP_A-2243020	C	C	300	54	342	36	5.567	0.0183	rs2111506	14	86368786	q31.3
SNP_A-2144836	G	G	260	102	291	75	5.841	1.57E-02	rs1003205	14	86383660	q31.3
SNP_A-1918962	G	G	269	105	250	134	4.083	4.33E-02	rs11629259	14	86455375	q31.3
SNP_A-2105261	C	C	409	3	409	11	4.495	3.40E-02	rs10134597	14	87177176	q31.3
SNP_A-1865084	C	C	412	4	408	12	4	4.55E-02	rs8018749	14	87178383	q31.3
SNP_A-1829506	T	T	332	84	352	62	3.895	4.84E-02	rs7151313	14	87230613	q31.3
SNP_A-2243628	A	A	378	34	398	16	6.991	8.20E-03	rs1959718	14	87250611	q31.3
SNP_A-1814876	G	G	400	2	397	11	6.198	1.28E-02	rs10148332	14	87286783	q31.3
SNP_A-2069015	C	C	197	147	214	112	4.953	2.60E-02	rs11850661	14	87417273	q31.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2244155	G	G	301	3	320	14	6.302	0.0121	rs2295739	14	87672475	q31.3
SNP_A-1878778	A	A	261	75	214	92	4.99	2.55E-02	rs2223933	14	87874319	q31.3
SNP_A-1942590	C	C	249	117	175	161	18.631	1.59E-05	rs11844638	14	87878632	q31.3
SNP_A-2214947	A	A	297	113	247	153	10.489	1.20E-03	rs11844618	14	87878704	q31.3
SNP_A-2039307	G	G	244	116	214	146	5.4	0.0201	rs12185033	14	87887777	q31.3
SNP_A-1651854	T	T	218	182	258	152	5.933	0.0149	rs394499	14	87992189	q32.11
SNP_A-2244524	T	T	362	2	342	8	3.895	4.84E-02	rs816071	14	88035137	q31.3
SNP_A-1672070	A	A	372	26	399	13	5.038	2.48E-02	rs8015271	14	88417132	q32.11
SNP_A-2201222	T	T	344	62	324	88	5.062	2.45E-02	rs17716878	14	88750773	q32.11
SNP_A-2213243	T	T	379	29	382	14	5.066	2.44E-02	rs2148407	14	88816787	q32.11
SNP_A-1723658	G	G	362	28	352	56	9.072	2.60E-03	rs1014527	14	89060829	q32.11
SNP_A-2075503	C	C	326	60	364	36	7.846	5.10E-03	rs1028721	14	89286591	q32.11
SNP_A-2027853	C	C	362	40	383	23	5.16	2.31E-02	rs17094668	14	89318281	q32.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2256677	G	G	365	47	388	28	5.497	1.91E-02	rs17126298	14	89320106	q32.11
SNP_A-1826166	A	A	354	40	375	19	8.08	4.50E-03	rs7148718	14	89322362	q32.11
SNP_A-1811877	G	G	316	0	322	4	3.902	0.0482	rs1286939	14	89411591	q32.11
SNP_A-1712323	G	G	297	103	278	132	4.084	4.33E-02	rs1951454	14	89495409	q32.11
SNP_A-1789372	C	T	203	167	208	180	5.439	1.97E-02	rs4904680	14	89891828	q32.11
SNP_A-2228345	C	T	201	169	216	178	6.386	0.0115	rs17719594	14	90002351	q32.12
SNP_A-1937081	G	G	249	87	282	64	5.409	0.02	rs2215719	14	90007493	q32.12
SNP_A-2206369	A	A	328	16	350	32	4.069	4.37E-02	rs17126830	14	90041180	q32.12
SNP_A-2169653	C	C	284	92	261	123	5.357	0.0206	rs7156252	14	90572871	q32.12
SNP_A-1934078	A	A	291	71	265	105	7.697	5.50E-03	rs11620623	14	90625300	q32.12
SNP_A-1834618	C	C	393	15	411	5	5.326	2.10E-02	rs11159993	14	90644374	q32.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2080443	C	C	316	72	292	102	6.074	0.0137	rs6575178	14	90659540	q32.12
SNP_A-2089965	T	T	244	170	210	200	4.959	2.59E-02	rs12587020	14	90748299	q32.12
SNP_A-1849163	G	G	358	0	356	4	4	4.55E-02	rs1005683	14	91062720	q32.12
SNP_A-2246223	C	C	187	177	227	157	4.531	3.33E-02	rs1743176	14	91119576	q32.12
SNP_A-2003928	G	G	340	66	314	96	6.57	0.0104	rs1704630	14	91175396	q32.12
SNP_A-2236992	C	C	335	69	367	45	6.434	0.0112	---	14	91230578	q32.12
SNP_A-2099602	C	C	348	62	386	32	11.466	7.00E-04	rs17127521	14	91261536	q32.12
SNP_A-2146875	C	C	273	89	293	61	5.845	1.56E-02	rs17805293	14	91439345	q32.12
SNP_A-2229521	A	A	396	0	356	12	13.119	3.00E-04	rs10144861	14	91535099	q32.12
SNP_A-2003932	C	C	324	16	328	34	5.821	1.58E-02	rs4904876	14	91892443	q32.12
SNP_A-2128728	A	A	393	23	378	40	4.874	2.73E-02	rs7142805	14	91893149	q32.12
SNP_A-2201363	C	C	225	113	272	78	10.652	1.10E-03	rs4904886	14	91914123	q32.12
SNP_A-2207407	G	G	234	116	274	76	11.483	7.00E-04	rs4444267	14	91917754	q32.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2080230	A	A	210	164	246	142	4.168	4.12E-02	rs10144991	14	92073484	q32.12
SNP_A-2236203	C	C	304	4	326	0	4.261	0.039	rs4499167	14	92185470	q32.12
SNP_A-2305668	C	C	412	0	410	4	4	4.55E-02	rs12434929	14	92188985	q32.12
SNP_A-2247241	G	G	361	9	382	2	4.79	0.0286	rs17128569	14	92332041	q32.12
SNP_A-2234523	A	A	331	77	309	103	4.492	3.40E-02	rs13379435	14	92628146	q32.13
SNP_A-1833637	A	A	244	116	267	89	4.569	3.26E-02	rs11850719	14	92794562	q32.13
SNP_A-1745644	C	C	204	198	242	168	5.618	0.0178	rs7145288	14	92880267	q32.13
SNP_A-1663862	G	G	315	87	354	60	7.058	7.90E-03	rs1989296	14	92895444	q32.13
SNP_A-1810156	T	T	299	89	290	54	6.081	0.0137	rs17129159	14	93276865	q32.13
SNP_A-1931164	A	A	296	72	345	47	8.248	4.10E-03	rs8003225	14	93382087	q32.13
SNP_A-1932867	G	G	334	72	378	40	11.69	6.00E-04	rs7140158	14	93388913	q32.13
SNP_A-1895153	T	T	306	82	317	55	5.181	2.28E-02	rs2236239	14	93472689	q32.13
SNP_A-1896450	T	T	209	191	244	154	6.667	9.80E-03	rs10134125	14	93750927	q32.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2126949	C	C	225	181	261	141	7.616	5.80E-03	rs4569189	14	93766441	q32.13
SNP_A-2197305	C	C	285	133	321	101	6.496	1.08E-02	rs2232704	14	93825872	q32.13
SNP_A-1844462	G	G	259	153	278	122	3.99	0.0458	rs3827896	14	93831174	q32.13
SNP_A-2248224	C	C	403	15	412	6	3.957	4.67E-02	rs10141408	14	93847114	q32.13
SNP_A-1737591	G	G	317	23	326	44	5.45	1.96E-02	rs1074925	14	93851554	q32.13
SNP_A-1836637	C	T	202	198	239	173	5.913	1.50E-02	rs732683	14	93957556	q32.13
SNP_A-1812300	G	G	288	42	264	60	4.165	4.13E-02	rs11160184	14	94007744	q32.13
SNP_A-2165860	C	C	295	107	303	73	5.667	1.73E-02	rs10139629	14	94105030	q32.13
SNP_A-2093005	A	A	335	67	301	87	4.168	4.12E-02	rs17753747	14	94212261	q32.13
SNP_A-2210145	G	G	217	141	256	120	4.467	3.46E-02	rs9323913	14	94217063	q32.13
SNP_A-2208600	T	T	405	9	416	2	4.583	3.23E-02	rs10146738	14	94349904	q32.13
SNP_A-1695325	T	T	391	1	403	7	4.28	3.86E-02	rs2145632	14	94370692	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1670876	C	C	401	1	407	7	4.369	3.66E-02	rs2180895	14	94370770	q32.2
SNP_A-2219721	A	A	311	31	334	16	5.516	1.88E-02	rs7156858	14	94396959	q32.13
SNP_A-2034419	T	T	382	32	399	15	6.519	1.07E-02	rs7157079	14	94397102	q32.13
SNP_A-1672332	G	G	326	70	315	99	4.767	2.90E-02	rs1951801	14	94480651	q32.2
SNP_A-1904564	G	G	380	8	356	18	4.373	3.65E-02	rs8011194	14	94517526	q32.13
SNP_A-2192181	T	T	280	98	295	65	6.637	0.01	rs7159427	14	94567940	q32.13
SNP_A-1961028	C	C	229	107	255	77	6.264	0.0123	rs8009967	14	94580540	q32.13
SNP_A-2222057	G	G	324	28	337	11	7.643	5.70E-03	rs17093029	14	95158512	q32.13
SNP_A-2044728	A	A	316	42	297	61	4.094	4.30E-02	rs1957937	14	95251113	q32.13
SNP_A-2209433	A	A	275	113	284	78	5.664	1.73E-02	rs4900295	14	95350903	q32.13
SNP_A-2194235	A	A	381	3	388	18	10.173	0.0014	rs3827936	14	95411127	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897306	A	A	351	3	309	13	7.425	6.40E-03	rs749951	14	95446006	q32.2
SNP_A-2107140	G	G	415	1	413	7	4.486	3.42E-02	rs3811343	14	95460180	q32.2
SNP_A-1875120	C	C	294	80	276	110	5.117	2.37E-02	rs1951302	14	95484863	q32.2
SNP_A-2163924	C	C	328	70	307	93	3.935	4.73E-02	rs1957123	14	95523364	q32.2
SNP_A-2038616	A	A	299	55	299	83	4.623	3.16E-02	rs11628218	14	95559977	q32.2
SNP_A-2039335	G	G	407	9	400	20	4.214	4.01E-02	rs10143165	14	95656921	q32.2
SNP_A-2288132	T	T	280	92	299	69	3.888	4.86E-02	rs8007059	14	95662644	q32.2
SNP_A-2096884	C	C	338	54	313	81	6.355	0.0117	rs4905462	14	95750327	q32.2
SNP_A-2123469	G	G	306	64	295	89	4.028	0.0448	rs7149784	14	96127751	q32.2
SNP_A-2251511	A	A	319	71	270	90	5.127	2.36E-02	rs17758145	14	96958336	q32.2
SNP_A-2251519	T	T	290	64	270	90	5.054	0.0246	rs11628618	14	96965028	q32.2
SNP_A-2081283	T	T	316	92	281	121	5.956	0.0147	rs10133251	14	96966822	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1880611	A	A	288	50	255	75	6.911	0.0086	rs11628827	14	96998957	q32.2
SNP_A-2121109	C	C	359	55	345	77	3.869	4.92E-02	rs4905597	14	97014266	q32.2
SNP_A-2251584	A	G	217	139	166	162	9.241	2.40E-03	rs1552126	14	97063843	q32.2
SNP_A-1842312	T	T	415	3	406	10	3.863	4.94E-02	rs234205	14	97068179	q32.2
SNP_A-2251623	C	C	412	2	407	11	6.242	1.25E-02	rs17095591	14	97121595	q32.2
SNP_A-2295575	T	T	337	11	307	23	5.159	2.31E-02	rs11160443	14	97818071	q32.2
SNP_A-2252680	T	T	296	18	341	7	6.289	0.0121	rs17595289	14	98076478	q32.2
SNP_A-2114131	C	C	287	103	332	78	6.228	0.0126	rs4900406	14	98126076	q32.2
SNP_A-2226760	T	T	277	135	312	110	4.512	3.37E-02	rs11626146	14	98141582	q32.2
SNP_A-2206454	C	C	277	133	307	101	5.912	1.50E-02	rs11627081	14	98148804	q32.2
SNP_A-2159330	G	G	414	0	410	6	6.015	1.42E-02	rs17097772	14	98286464	q32.2
SNP_A-2063194	C	C	334	48	317	73	5.527	1.87E-02	rs17613673	14	98338710	q32.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2100448	C	C	300	26	355	11	8.415	3.70E-03	rs1565615	14	98445871	q32.2
SNP_A-1849499	C	T	175	167	209	159	4.512	3.37E-02	rs1565616	14	98445982	q32.2
SNP_A-2158081	C	T	193	183	226	170	5.464	1.94E-02	rs1565618	14	98446136	q32.2
SNP_A-2253360	T	G	209	187	226	184	5.031	2.49E-02	rs11625159	14	98455360	q32.2
SNP_A-2253371	C	C	172	146	220	130	5.284	2.15E-02	rs200328	14	98458132	q32.2
SNP_A-1944260	G	G	247	147	272	114	5.295	2.14E-02	rs10130070	14	98467749	q32.2
SNP_A-2284889	T	T	212	132	228	98	5.128	0.0235	rs807450	14	98713688	q32.2
SNP_A-2205016	C	C	292	84	282	116	4.673	3.06E-02	rs2793315	14	98714475	q32.2
SNP_A-2186455	T	T	346	14	346	4	5.416	0.02	rs1257290	14	98894918	q32.2
SNP_A-1793364	C	C	305	35	305	57	4.576	3.24E-02	rs11621243	14	99207349	q32.2
SNP_A-1869456	A	A	256	120	239	153	4.241	0.0395	rs9324014	14	99283062	q32.2
SNP_A-1732648	C	C	273	129	237	175	9.38	2.20E-03	rs721910	14	99319750	q32.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1855297	C	C	230	170	264	146	4.04	4.44E-02	rs8181926	14	99353001	q32.2
SNP_A-1861009	G	G	290	82	250	116	8.753	3.10E-03	rs11849597	14	99374819	q32.2
SNP_A-2254294	C	C	274	126	308	102	4.39	3.62E-02	rs12590861	14	99377073	q32.2
SNP_A-2094766	A	A	292	106	265	131	3.941	4.71E-02	rs11160554	14	99402837	q32.2
SNP_A-1801859	G	G	258	80	234	118	8.183	4.20E-03	rs1957509	14	99403615	q32.2
SNP_A-1902141	A	A	337	75	359	51	5.262	0.0218	rs3783324	14	99419770	q32.2
SNP_A-2289968	A	A	243	99	273	75	5.003	0.0253	rs2273704	14	99453985	q32.2
SNP_A-2053011	T	T	344	4	348	0	4.023	4.49E-02	rs2400848	14	99589005	q32.2
SNP_A-1859164	C	C	359	17	348	32	4.742	2.94E-02	rs7151749	14	99615311	q32.2
SNP_A-2314406	C	C	267	95	295	67	6.235	1.25E-02	rs1212911	14	99987125	q32.2
SNP_A-2254739	G	G	317	95	289	129	6.411	1.13E-02	rs1884540	14	100370026	q32.2
SNP_A-1927066	G	G	317	71	286	118	12.964	3.00E-04	rs3783355	14	100378711	q32.2
SNP_A-2163176	C	C	291	105	306	70	6.863	8.80E-03	rs8017886	14	100524553	q32.31
SNP_A-2096367	C	C	411	7	404	18	4.881	2.72E-02	rs2400967	14	100606054	q32.31
SNP_A-1809645	A	A	381	33	391	19	3.879	4.89E-02	rs17100035	14	100750161	q32.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1795413	G	G	363	55	344	76	3.872	4.91E-02	rs12434898	14	100831794	q32.31
SNP_A-2120244	A	A	262	136	289	101	6.411	1.13E-02	rs11626278	14	100885110	q32.31
SNP_A-2207081	T	T	273	143	305	117	4.329	3.75E-02	rs11621338	14	100688333	q32.31
SNP_A-2265018	G	G	233	97	280	76	5.878	1.53E-02	rs12323822	14	100916498	q32.31
SNP_A-2117815	G	G	324	88	293	119	6.2	1.28E-02	rs9324038	14	100944102	q32.31
SNP_A-1887059	A	A	399	17	390	32	4.652	0.031	rs2151740	14	101221049	q32.31
SNP_A-2255285	A	A	392	16	390	30	4.093	4.31E-02	rs1958952	14	101231350	q32.31
SNP_A-2255311	A	A	369	11	383	3	4.785	0.0287	rs1678030	14	101389639	q32.31
SNP_A-1864349	A	A	219	127	263	101	6.529	0.0106	rs11621560	14	101626496	q32.32
SNP_A-1908218	A	A	351	23	362	10	5.286	2.15E-02	rs10130705	14	101740330	q32.32
SNP_A-2113547	T	T	314	78	329	55	4.245	3.94E-02	rs7153005	14	101768352	q32.32
SNP_A-2125578	G	G	393	23	410	10	5.462	1.94E-02	rs2183637	14	101819511	q32.32
SNP_A-2003988	A	A	299	29	282	46	4.351	3.70E-02	rs2277471	14	102094140	q32.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2051747	A	A	344	14	361	5	4.585	3.22E-02	rs1018550	14	102510035	q32.32
SNP_A-1888141	C	C	319	67	346	42	6.825	9.00E-03	rs8176373	14	102673975	q32.32
SNP_A-2081758	C	C	318	52	352	36	4.209	0.0402	rs8014278	14	102685593	q32.32
SNP_A-2132923	A	A	250	166	279	139	3.975	4.62E-02	rs4906282	14	102689266	q32.32
SNP_A-2237403	G	G	371	5	350	0	4.687	0.0304	rs2149670	14	102734430	q32.32
SNP_A-2222431	A	A	236	146	282	120	6.12	0.0134	rs8007489	14	103124325	q32.33
SNP_A-2286792	C	C	391	9	387	25	7.374	0.0066	rs10131550	14	103442852	q32.33
SNP_A-2053109	T	T	307	15	284	34	8.238	4.10E-03	rs4906396	14	103521185	q32.33
SNP_A-2170891	A	A	257	131	237	163	4.111	4.26E-02	rs11160778	14	103548493	q32.33
SNP_A-2243346	A	A	249	109	234	140	3.977	4.61E-02	rs7158069	14	103870372	q32.33
SNP_A-1782397	C	C	332	70	368	52	4.115	4.25E-02	rs8016091	14	103878757	q32.33
SNP_A-2181959	C	C	299	87	324	58	6.783	9.20E-03	rs2919622	14	104453048	q32.33
SNP_A-1864462	G	G	352	8	372	2	3.887	0.0487	---	14	105526969	q32.33
SNP_A-2257903	C	C	353	17	377	7	4.697	3.02E-02	---	14	106058906	q32.33
SNP_A-2257905	A	A	378	36	400	20	5.151	2.32E-02	---	14	106059069	q32.33
SNP_A-2263762	T	T	374	36	399	21	4.636	3.13E-02	rs17114279	14	106061045	q32.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123278	G	G	291	29	315	17	3.861	4.94E-02	---	15	18676689	q11.2
SNP_A-2240618	C	C	393	13	410	4	5.047	0.0247	rs904836	15	18810670	q11.2
SNP_A-2004012	T	T	310	24	355	13	4.68	3.05E-02	rs4983995	15	19308284	q11.2
SNP_A-2214629	T	T	332	12	305	25	5.424	1.99E-02	rs7403003	15	20539701	q11.2
SNP_A-1786714	C	C	311	37	289	63	7.544	6.00E-03	rs4778455	15	20546362	q11.2
SNP_A-2106958	A	A	210	140	235	113	4.28	3.86E-02	rs1997129	15	21205735	q11.2
SNP_A-2069309	A	A	306	44	292	64	3.981	4.60E-02	rs6576524	15	21395932	q11.2
SNP_A-2120351	A	A	305	11	308	24	4.451	0.0349	rs17116327	15	21417039	q11.2
SNP_A-2178626	T	C	189	173	209	153	7.182	7.40E-03	rs2140005	15	21560381	q11.2
SNP_A-1857420	C	C	304	76	285	107	5.679	0.0172	rs1717831	15	21578625	q11.2
SNP_A-1905167	C	G	208	184	215	183	3.962	0.0465	rs878247	15	21590066	q11.2
SNP_A-2030354	G	G	326	24	286	36	3.854	4.96E-02	rs12438636	15	21622702	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2216137	G	G	347	17	315	29	4.116	4.25E-02	rs2353497	15	21693405	q11.2
SNP_A-1820487	C	C	205	173	241	147	4.889	0.027	rs12904303	15	22591421	q11.2
SNP_A-1805941	G	G	340	62	351	37	6.242	1.25E-02	rs12442570	15	23328350	q12
SNP_A-2004033	A	A	169	151	209	137	3.904	0.0482	rs2925239	15	23332768	q12
SNP_A-2261968	T	T	391	17	393	5	6.427	0.0112	rs17115764	15	23338951	q12
SNP_A-1899161	C	C	292	100	335	71	7.624	5.80E-03	rs2906017	15	23374027	q12
SNP_A-2191895	T	T	333	79	353	53	5.661	1.74E-02	rs1976075	15	23408950	q12
SNP_A-1802649	T	T	388	24	408	12	4.426	3.54E-02	rs4906627	15	23518972	q12
SNP_A-2004037	A	A	378	26	341	49	8.713	3.20E-03	rs6576445	15	23523852	q12
SNP_A-2262261	C	C	237	143	208	172	4.56	0.0327	rs968332	15	23689108	q12
SNP_A-1753381	G	G	235	119	270	98	4.188	0.0407	rs2175462	15	23751196	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1935033	A	A	399	17	411	7	4.34	3.72E-02	rs907326	15	23780707	q12
SNP_A-2193934	C	C	410	4	405	13	4.776	2.89E-02	rs2217865	15	23997821	q12
SNP_A-2258152	G	G	369	25	363	9	6.952	8.40E-03	rs10438457	15	24579767	q12
SNP_A-2263149	C	C	334	52	322	74	3.934	4.73E-02	rs9330236	15	24900185	q12
SNP_A-2259651	A	A	306	64	282	86	4.201	4.04E-02	rs4887549	15	24907688	q12
SNP_A-2148671	A	A	273	51	254	88	10.055	0.0015	rs4887525	15	24912084	q12
SNP_A-1755362	C	C	217	149	273	139	4.042	4.44E-02	rs10519588	15	24980435	q12
SNP_A-2306670	C	T	236	178	227	191	10.652	1.10E-03	rs2286946	15	24985293	q12
SNP_A-1938029	T	C	229	187	230	188	8.46	3.60E-03	rs2286945	15	24985347	q12
SNP_A-2030332	G	C	189	145	185	163	6.484	0.0109	rs5606880	15	24989375	q12
SNP_A-2263223	T	T	375	7	405	1	4.927	0.0264	rs968671	15	25036654	q12
SNP_A-2004049	T	C	192	150	187	165	5.961	0.0146	rs6422905	15	25041181	q12
SNP_A-1855736	G	G	364	8	391	1	5.89	0.0152	rs17137668	15	25041942	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2166573	A	A	374	42	348	68	7.082	7.80E-03	rs7179956	15	25065516	q12
SNP_A-2004050	A	A	340	48	304	78	9.109	2.50E-03	rs897177	15	25069464	q12
SNP_A-2263533	G	G	328	20	331	9	4.094	4.30E-02	rs17746385	15	25585544	q12
SNP_A-2240124	C	C	308	46	288	72	6.35	0.0117	rs3101648	15	25608098	q12
SNP_A-2205501	C	C	195	185	223	155	4.517	3.36E-02	rs11074303	15	25649087	q12
SNP_A-2263685	T	T	310	52	286	76	5.466	1.94E-02	rs768547	15	25774538	q13.1
SNP_A-2263687	G	G	338	66	295	89	5.83	1.58E-02	rs768546	15	25774732	q13.1
SNP_A-2242571	T	T	288	90	271	117	3.909	4.80E-02	rs4778199	15	25780182	q13.1
SNP_A-2076436	C	C	341	69	312	104	8.326	3.90E-03	rs4778200	15	25781616	q13.1
SNP_A-2085340	A	A	367	31	350	54	6.582	0.0103	rs11263729	15	26811196	q13.1
SNP_A-2246409	A	A	367	21	361	37	4.337	0.0373	rs6493239	15	27014674	q13.1
SNP_A-2298122	T	T	382	28	348	46	5.646	1.75E-02	rs902271	15	27023816	q13.1
SNP_A-2106666	C	C	409	5	405	15	4.977	2.57E-02	rs1873278	15	27082938	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2085780	G	G	315	19	316	34	3.875	4.90E-02	rs12442802	15	27169093	q13.1
SNP_A-2233356	A	A	297	55	287	79	4.198	4.05E-02	rs4611418	15	27230795	q13.1
SNP_A-2196563	A	A	381	33	399	19	4.165	4.13E-02	rs7164004	15	27377093	q13.1
SNP_A-2179299	C	C	305	77	326	54	4.732	2.96E-02	rs817957	15	27410092	q13.1
SNP_A-1885751	T	T	400	8	399	1	5.367	2.05E-02	rs17569247	15	27463936	q13.1
SNP_A-2264617	A	A	369	19	303	31	5.353	0.0207	rs2035326	15	27785294	q13.1
SNP_A-1858352	G	G	344	46	361	29	4.263	3.89E-02	rs7176476	15	27884370	q13.1
SNP_A-2264770	T	T	326	90	350	68	3.911	4.80E-02	rs1522792	15	27999999	q13.1
SNP_A-2243630	G	G	344	24	332	44	6.01	1.42E-02	rs16954910	15	28074223	q13.2
SNP_A-2286695	C	C	384	30	367	53	6.715	9.60E-03	rs939981	15	28077598	q13.2
SNP_A-2173887	A	A	245	67	250	106	5.97	0.0146	rs11070252	15	28116500	q13.2
SNP_A-2250987	C	C	390	10	407	3	4.009	0.0453	rs2140736	15	28946504	q13.2
SNP_A-1918456	C	C	402	14	416	2	9.235	2.40E-03	rs2091236	15	28967751	q13.2
SNP_A-1645424	G	G	336	24	324	42	5.078	2.42E-02	rs10519727	15	29097931	q13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2255988	C	C	352	44	338	64	3.943	4.71E-02	rs1035706	15	29130377	q13.3
SNP_A-1902927	C	C	376	8	375	19	4.355	3.69E-02	rs12439853	15	29422035	q13.3
SNP_A-2265947	C	C	289	57	265	83	5.863	0.0155	rs12595731	15	29875174	q13.3
SNP_A-2266023	G	G	251	79	276	52	6.745	9.40E-03	rs2137857	15	30016744	q13.3
SNP_A-2297273	A	A	336	66	307	93	5.888	0.0152	rs8037084	15	30181941	q13.3
SNP_A-2309962	G	G	321	39	301	67	7.952	4.80E-03	rs2611605	15	30228925	q13.3
SNP_A-2116124	C	C	328	18	346	8	4.236	3.96E-02	rs1919360	15	30830747	q13.3
SNP_A-1909244	A	A	295	15	322	6	4.534	0.0332	rs16960230	15	30948323	q13.3
SNP_A-1689194	G	G	272	38	343	27	4.802	2.84E-02	rs1399079	15	31163206	q13.3
SNP_A-2104915	C	G	209	143	181	171	8.257	4.10E-03	rs1399074	15	31331727	q13.3
SNP_A-1935514	C	C	341	25	385	13	5.125	2.36E-02	rs17235982	15	31448195	q14
SNP_A-2267274	T	T	356	60	380	38	5.717	1.68E-02	rs10519816	15	31456613	q14
SNP_A-2032190	A	A	300	68	322	48	4.221	3.99E-02	rs4619367	15	31468929	q14
SNP_A-2266670	C	C	416	0	410	4	4.039	4.45E-02	rs2572204	15	31583002	q14
SNP_A-2144300	C	C	297	43	289	23	4.977	2.57E-02	rs1529848	15	31630671	q14
SNP_A-1785734	C	C	371	11	370	24	4.645	3.11E-02	rs8023510	15	31659730	q14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2195431	G	G	375	39	351	57	4.125	4.23E-02	rs16972837	15	31666679	q14
SNP_A-1902834	T	T	348	32	371	19	3.92	4.77E-02	rs11072570	15	31713112	q14
SNP_A-2273969	G	G	236	148	253	111	5.346	2.08E-02	rs10775211	15	31720282	q14
SNP_A-2194309	C	C	404	12	418	4	4.196	4.05E-02	rs6495238	15	31846799	q14
SNP_A-1883674	G	G	319	19	325	37	5.025	2.50E-02	rs2278316	15	31848815	q14
SNP_A-2301399	G	G	357	19	369	7	5.737	0.0166	rs4780214	15	32187977	q14
SNP_A-2191004	C	C	373	11	377	3	4.572	3.25E-02	rs7168168	15	32381077	q14
SNP_A-1853240	C	C	367	5	400	0	5.411	0.02	rs7169802	15	32381190	q14
SNP_A-2064534	G	G	314	10	312	22	4.355	3.69E-02	rs4923735	15	32757965	q14
SNP_A-1648072	G	G	358	22	381	11	4.197	4.05E-02	rs475786	15	32807194	q14
SNP_A-2143973	C	C	376	16	406	6	5.202	2.26E-02	rs11073065	15	32820343	q14
SNP_A-1862955	G	G	226	118	226	78	5.716	1.68E-02	rs664251	15	32841075	q14
SNP_A-2161357	T	T	293	87	254	110	5.124	2.36E-02	rs2015461	15	32907040	q14
SNP_A-1944398	T	T	353	23	320	36	3.939	4.72E-02	rs16961476	15	33791897	q14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1939491	A	A	357	57	384	30	9.363	2.20E-03	rs789786	15	33991803	q14
SNP_A-2229550	C	C	349	47	384	28	6.17	1.30E-02	rs789781	15	33997632	q14
SNP_A-2263977	C	C	220	196	252	158	6.205	1.27E-02	rs789774	15	34007269	q14
SNP_A-2269829	T	T	387	7	386	0	6.92	8.50E-03	rs2136721	15	34091532	q14
SNP_A-2066038	G	G	214	196	242	168	3.873	4.91E-02	rs11857996	15	34237844	q14
SNP_A-1861329	C	C	319	71	309	97	3.863	4.94E-02	rs12908082	15	34436612	q14
SNP_A-1815509	G	G	293	75	312	50	5.548	1.85E-02	rs7163854	15	34489244	q14
SNP_A-1723080	C	C	301	67	297	95	4.112	4.26E-02	rs10518884	15	34500807	q14
SNP_A-1827874	T	T	200	118	227	91	5.195	2.26E-02	rs4603514	15	34507018	q14
SNP_A-1940053	G	G	284	82	261	107	4.272	3.87E-02	rs4923720	15	34696559	q14
SNP_A-1686326	C	C	365	35	347	63	8.333	3.90E-03	rs2045014	15	34706216	q14
SNP_A-1929713	T	T	379	29	353	59	11.132	8.00E-04	rs17499823	15	34795467	q14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2131769	C	C	238	152	216	194	5.668	1.73E-02	rs6495881	15	34956569	q14
SNP_A-1646010	A	A	350	38	376	22	5.071	2.43E-02	rs10518924	15	35017621	q14
SNP_A-1886526	C	C	300	56	309	33	5.798	0.016	rs1916306	15	35068986	q14
SNP_A-2145324	T	T	373	43	394	26	4.744	2.94E-02	rs12102256	15	35077585	q14
SNP_A-2270956	T	T	392	24	368	40	4.681	3.05E-02	rs10518931	15	35282033	q14
SNP_A-1816326	A	G	190	184	207	155	4.709	3.00E-02	rs4350533	15	35334826	q14
SNP_A-2284310	G	G	357	33	348	54	5.003	0.0253	rs8027757	15	36191717	q14
SNP_A-1731483	T	T	368	32	361	53	5.016	2.51E-02	rs7179433	15	36306094	q14
SNP_A-1681994	G	G	363	27	357	49	6.099	0.0135	rs1916151	15	36310160	q14
SNP_A-1649030	C	C	367	31	361	53	5.498	0.019	rs10520054	15	36310225	q14
SNP_A-1649598	A	A	364	28	357	49	5.551	1.85E-02	rs1357382	15	36315981	q14
SNP_A-1816870	G	G	380	28	364	52	7.467	0.0063	rs4405503	15	36337109	q14
SNP_A-2271664	T	T	351	31	305	51	7.197	7.30E-03	rs1357383	15	36337334	q14
SNP_A-1898267	A	A	381	31	362	50	4.943	2.62E-02	rs2056506	15	36353614	q14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2271709	A	A	371	27	358	50	6.979	8.20E-03	rs10520056	15	36367534	q14
SNP_A-2234961	C	C	394	8	411	1	5.681	1.71E-02	rs1357384	15	36383376	q14
SNP_A-2187897	C	C	342	16	337	35	6.849	8.90E-03	rs16966730	15	36394133	q14
SNP_A-2265620	A	A	349	27	326	42	3.959	4.66E-02	rs1522764	15	36428215	q14
SNP_A-2092234	A	A	398	0	386	4	4.103	4.28E-02	rs11073319	15	36429803	q14
SNP_A-2151223	A	A	387	23	366	40	5.153	2.32E-02	rs9806705	15	36503939	q14
SNP_A-2294680	A	A	268	82	230	100	4.095	4.30E-02	rs2132157	15	36779839	q14
SNP_A-1859554	G	G	328	66	312	94	5.121	2.36E-02	rs2624272	15	36790701	q14
SNP_A-2048127	G	G	334	72	315	97	4.211	0.0402	rs2643216	15	36791101	q14
SNP_A-2235577	G	G	285	51	323	25	11.063	9.00E-04	rs2929637	15	36816858	q14
SNP_A-2163672	T	T	251	77	225	109	6.872	8.80E-03	rs6495995	15	36824425	q14
SNP_A-2285773	A	A	275	89	241	125	8.291	4.00E-03	rs9920502	15	36825314	q14
SNP_A-2139398	A	A	237	117	208	142	4.28	3.86E-02	rs4924305	15	36946641	q14

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2136678	C	C	239	177	212	208	4.093	4.30E-02	rs11070160	15	37000434	q14
SNP_A-2110236	T	T	245	163	216	190	3.885	0.0487	rs1368797	15	37015763	q14
SNP_A-1904850	T	T	245	139	198	152	4.001	4.55E-02	rs12898413	15	37021597	q14
SNP_A-2079217	G	G	290	126	321	97	5.339	2.08E-02	rs16968084	15	37152706	q14
SNP_A-2172571	T	T	220	104	250	74	6.971	8.30E-03	—	15	37165874	q14
SNP_A-2043097	A	A	279	75	280	46	5.809	1.59E-02	rs6492865	15	37313975	q14
SNP_A-2058366	G	G	307	39	291	21	4.082	4.33E-02	rs667623	15	38552652	q15.1
SNP_A-1642269	G	G	234	166	211	201	4.35	3.70E-02	rs10518697	15	38626724	q15.1
SNP_A-2300137	A	A	226	166	200	198	4.355	3.69E-02	rs17674454	15	38677116	q15.1
SNP_A-1864449	A	A	361	23	376	10	5.421	1.99E-02	rs7166182	15	39301991	q15.1
SNP_A-1659606	G	G	369	31	402	12	9.57	0.002	rs10518718	15	39340280	q15.1
SNP_A-2024482	A	A	315	61	292	82	3.95	4.69E-02	rs7164211	15	39492333	q15.1
SNP_A-2201137	C	C	367	23	398	8	8.196	4.20E-03	rs16971832	15	39551211	q15.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1812134	C	C	365	27	384	12	6.231	0.0126	rs16971834	15	39563984	q15.1
SNP_A-1673030	C	C	337	47	303	75	8.186	4.20E-03	rs4072386	15	39612911	q15.1
SNP_A-1877560	G	G	352	34	329	51	4.13	4.21E-02	rs12439488	15	39681867	q15.1
SNP_A-1871385	G	G	326	48	313	73	5.242	2.21E-02	rs2077361	15	39752165	q15.1
SNP_A-2274082	C	C	339	55	311	79	5.484	1.92E-02	rs1106934	15	39859915	q15.1
SNP_A-2305760	G	G	338	40	317	65	6.605	1.02E-02	rs1206842	15	39909909	q15.1
SNP_A-2125066	G	G	235	181	265	147	5.305	2.13E-02	rs7163310	15	40113551	q15.1
SNP_A-1833630	C	C	311	23	330	46	5.766	1.63E-02	rs1668541	15	40125529	q15.1
SNP_A-2274656	C	C	298	38	270	60	6.266	0.0123	rs2412711	15	40484523	q15.1
SNP_A-2147455	A	A	347	3	341	11	4.618	3.16E-02	rs16952474	15	40487513	q15.1
SNP_A-1838249	G	G	365	51	341	71	4.075	4.35E-02	rs17766258	15	40572429	q15.1
SNP_A-2175473	G	G	374	22	358	40	5.571	0.0183	rs16957244	15	40953321	q15.2
SNP_A-1807239	C	C	377	27	359	45	4.94	2.62E-02	rs6416436	15	41075511	q15.2
SNP_A-1895119	A	A	376	26	353	45	5.79	0.0161	rs4923955	15	41082380	q15.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2274843	C	C	375	21	352	38	5.58	1.82E-02	rs1037990	15	41086979	q15.2
SNP_A-2081101	A	A	382	2	377	11	6.243	1.25E-02	rs7174915	15	41208461	q15.2
SNP_A-1908419	T	T	382	26	369	43	4.394	0.0361	rs7183814	15	41316922	q15.2
SNP_A-1660101	T	T	331	37	338	60	4.359	3.68E-02	rs956391	15	41333549	q15.3
SNP_A-1699303	A	A	358	30	361	53	6.128	1.33E-02	rs694985	15	41529443	q15.3
SNP_A-1836923	G	G	368	28	355	45	4.173	4.11E-02	rs2447196	15	41681110	q15.3
SNP_A-1670271	T	T	366	32	358	54	5.476	1.93E-02	rs2467426	15	41705574	q15.3
SNP_A-2275229	C	C	371	25	358	42	4.525	3.34E-02	rs2447208	15	41721187	q15.3
SNP_A-1720995	A	A	367	25	366	48	6.652	9.90E-03	rs2412822	15	41939243	q15.3
SNP_A-2088192	T	T	350	20	344	36	4.491	3.41E-02	rs11070414	15	42007688	q15.3
SNP_A-2134468	G	G	393	19	413	5	8.62	0.0033	rs2706462	15	42262620	q15.3
SNP_A-1780940	G	G	396	14	411	5	4.499	0.0339	rs2447334	15	42266186	q15.3
SNP_A-2275472	C	C	249	163	282	138	4.051	4.42E-02	rs16965650	15	42746424	q21.1
SNP_A-1957983	A	A	363	19	369	35	4.177	4.10E-02	rs7182487	15	42835709	q21.1
SNP_A-1886386	A	A	196	152	245	123	7.95	4.80E-03	rs269866	15	43181698	q21.1
SNP_A-2244743	T	T	359	19	339	33	4.295	3.82E-02	rs17594910	15	43200833	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207982	G	G	335	19	342	36	4.545	3.30E-02	rs1706816	15	43247714	q21.1
SNP_A-2034939	A	A	339	77	304	114	9.068	2.60E-03	rs17553285	15	43759534	q21.1
SNP_A-2143454	T	T	327	55	290	104	17.138	3.48E-05	rs2289579	15	43767684	q21.1
SNP_A-2276872	C	C	231	87	201	111	4.936	0.0263	rs518935	15	44725701	q21.1
SNP_A-2276947	C	C	376	26	385	13	4.42	3.55E-02	rs10519075	15	44819815	q21.1
SNP_A-1690437	A	A	376	10	388	22	3.968	4.64E-02	rs10519083	15	44833152	q21.1
SNP_A-2277288	A	A	209	177	231	143	4.524	3.34E-02	rs17355071	15	45235314	q21.1
SNP_A-1857244	G	G	203	125	184	156	4.139	0.0419	rs9944240	15	45292228	q21.1
SNP_A-2229402	T	T	324	62	302	86	4.66	0.0309	rs2132661	15	45467018	q21.1
SNP_A-1869640	G	G	357	37	329	55	4.537	0.0332	rs16959537	15	45533776	q21.1
SNP_A-2195883	G	G	389	9	375	21	5.052	0.0246	rs4775692	15	45599347	q21.1
SNP_A-2256929	G	G	355	17	367	33	4.31	3.79E-02	rs12441744	15	45599488	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2231400	A	A	399	17	387	33	5.284	2.15E-02	rs8032090	15	45603611	q21.1
SNP_A-2293386	T	T	397	15	385	29	4.634	3.13E-02	rs2304413	15	45605132	q21.1
SNP_A-1788498	T	T	391	13	378	4	4.372	3.65E-02	rs16959817	15	45689739	q21.1
SNP_A-2277959	A	A	291	101	298	70	4.95	2.61E-02	rs10519143	15	45842859	q21.1
SNP_A-2234163	C	C	412	4	408	12	4	4.55E-02	rs16960341	15	45997010	q21.1
SNP_A-1744393	G	G	392	8	392	22	6.294	0.0121	rs10519163	15	46093569	q21.1
SNP_A-2157283	G	G	416	0	414	4	4	4.55E-02	rs2469585	15	46139190	q21.1
SNP_A-2300839	G	G	293	31	339	15	7.601	5.80E-03	rs11636344	15	46502529	q21.1
SNP_A-1832508	T	T	286	28	331	15	5.674	0.0172	rs16899400	15	46834784	q21.1
SNP_A-1930461	G	G	296	66	280	90	4.05	4.42E-02	rs1007662	15	47002601	q21.1
SNP_A-2278899	A	A	244	102	281	83	4.105	4.27E-02	rs17470122	15	47027116	q21.1
SNP_A-2092162	C	C	406	8	398	18	3.921	4.77E-02	rs6493344	15	47031255	q21.1
SNP_A-1879158	C	C	284	88	270	116	3.94	4.72E-02	rs4390538	15	47076438	q21.1
SNP_A-1668859	G	G	304	94	288	124	4.32	3.77E-02	rs10519208	15	47104305	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2278928	A	A	283	93	321	73	4.382	3.63E-02	rs11638981	15	47108821	q21.1
SNP_A-1833433	C	C	296	80	283	107	3.936	4.73E-02	rs16962490	15	47530920	q21.2
SNP_A-2279561	C	C	271	133	288	100	4.87	2.73E-02	rs8027678	15	48064981	q21.2
SNP_A-1729029	T	T	282	118	320	94	4.876	2.72E-02	rs2135452	15	48551182	q21.2
SNP_A-2279824	G	G	281	129	305	97	5.436	1.97E-02	rs1542958	15	48610614	q21.2
SNP_A-2190609	T	T	287	115	314	90	4.257	3.91E-02	rs1147138	15	48964928	q21.2
SNP_A-1753777	C	C	323	69	315	99	4.861	0.0275	rs2306335	15	48992184	q21.2
SNP_A-2260707	A	A	289	117	321	91	4.885	2.71E-02	rs12595526	15	49012313	q21.2
SNP_A-1810914	G	G	293	121	325	95	4.744	2.94E-02	rs1955	15	49025387	q21.2
SNP_A-2188681	A	A	281	103	328	78	6.473	1.10E-02	rs1124769	15	49139541	q21.2
SNP_A-2279977	T	T	287	101	316	72	6.256	0.0124	rs17647040	15	49143218	q21.2
SNP_A-2236427	T	T	289	113	310	86	4.355	3.69E-02	rs7170455	15	49157032	q21.2
SNP_A-2004152	A	A	291	31	322	14	7.696	5.50E-03	rs6493495	15	49405594	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2041193	C	C	308	38	326	22	4.772	2.89E-02	rs2445765	15	49422190	q21.2
SNP_A-2180644	A	A	289	45	307	27	5.044	0.0247	rs2445768	15	49422672	q21.2
SNP_A-2034303	C	C	358	36	370	16	7.809	5.20E-03	rs12441382	15	49428833	q21.2
SNP_A-2125997	T	T	365	11	378	2	6.437	0.0112	rs764530	15	49448834	q21.2
SNP_A-2115650	T	T	320	12	342	0	12.586	4.00E-04	rs16964770	15	50288963	q21.2
SNP_A-2259747	A	A	317	13	300	28	5.95	0.0147	rs1869127	15	50500862	q21.2
SNP_A-1823561	C	C	336	28	343	49	4.769	2.90E-02	rs4776053	15	50603487	q21.2
SNP_A-1949830	G	G	408	0	412	4	3.942	4.71E-02	rs1724600	15	50611009	q21.2
SNP_A-2163391	C	C	369	7	381	19	4.993	2.55E-02	rs17651731	15	50622368	q21.2
SNP_A-2163482	C	C	412	0	416	4	3.943	4.71E-02	rs8029846	15	50651431	q21.2
SNP_A-1873658	C	C	238	116	233	81	3.89	4.86E-02	rs2433285	15	50785268	q21.3
SNP_A-2281020	A	A	408	4	414	0	4.039	4.45E-02	rs16965316	15	51014051	q21.3
SNP_A-1813950	T	T	324	66	354	46	4.773	2.89E-02	rs2651515	15	51092381	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909306	G	G	362	26	347	11	5.2	2.26E-02	rs17709930	15	51094957	q21.3
SNP_A-1750821	C	C	310	40	322	66	4.661	0.0309	rs10518710	15	51174391	q21.3
SNP_A-2281257	A	A	346	24	355	11	4.923	2.65E-02	rs627359	15	51198813	q21.3
SNP_A-1758399	A	G	222	178	214	200	4.214	4.01E-02	rs1386169	15	51341800	q21.3
SNP_A-1828180	A	A	200	148	220	108	6.616	0.0101	rs11629910	15	51473913	q21.3
SNP_A-1749069	T	T	354	38	345	63	5.986	0.0144	rs1906417	15	51535967	q21.3
SNP_A-2187940	C	C	295	49	287	71	3.866	4.93E-02	rs2899517	15	51679492	q21.3
SNP_A-1695115	C	T	205	191	237	177	6.6	1.02E-02	rs4753777	15	51725287	q21.3
SNP_A-1653968	A	A	264	126	244	162	4.968	0.0258	rs956553	15	51729549	q21.3
SNP_A-2284627	T	C	217	197	229	191	4.018	4.50E-02	rs3911726	15	51752038	q21.3
SNP_A-2282151	A	A	293	119	323	93	4.631	3.14E-02	rs690487	15	51816209	q21.3
SNP_A-2282567	C	C	215	191	252	162	5.236	2.21E-02	rs991264	15	52063843	q21.3
SNP_A-2282568	T	T	255	135	282	106	4.842	2.78E-02	rs2616910	15	52063875	q21.3
SNP_A-1867058	A	A	355	43	381	27	4.452	0.0349	rs16974322	15	52297449	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1910334	A	A	411	5	422	0	5.103	2.39E-02	rs16974744	15	52612872	q21.3
SNP_A-1667052	A	T	226	164	201	199	5.34	2.08E-02	rs10518775	15	52672115	q21.3
SNP_A-1959526	T	C	232	168	202	196	6.147	0.0132	rs4396478	15	52744000	q21.3
SNP_A-2004172	T	T	378	2	361	9	4.713	2.99E-02	rs4776246	15	52776112	q21.3
SNP_A-1890139	A	G	177	145	170	144	5.277	2.16E-02	rs2414382	15	52924047	q21.3
SNP_A-2032173	A	G	189	151	180	160	4.951	2.61E-02	rs12900605	15	52924462	q21.3
SNP_A-2283613	C	C	311	51	292	72	4.179	4.09E-02	rs1915215	15	52986769	q21.3
SNP_A-1866900	C	C	359	51	330	76	6.122	1.33E-02	rs17238031	15	52995396	q21.3
SNP_A-1948381	A	A	344	64	326	90	4.796	2.85E-02	rs4126006	15	53044710	q21.3
SNP_A-1859427	C	C	359	45	379	25	6.256	0.0124	rs16976218	15	53325841	q21.3
SNP_A-2038929	C	C	393	5	402	0	5.082	2.42E-02	rs17238269	15	53427159	q21.3
SNP_A-2079413	A	A	304	104	281	133	4.409	3.57E-02	rs7182280	15	53975436	q21.3
SNP_A-1743233	G	G	232	84	225	115	4.064	4.38E-02	rs10518835	15	54062711	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2068631	T	T	416	0	418	4	3.962	0.0465	rs16977306	15	55283518	q21.3
SNP_A-2285086	G	G	382	0	353	7	7.499	6.20E-03	rs935329	15	55297253	q21.3
SNP_A-2240052	T	T	252	106	260	74	4.988	2.55E-02	rs8032560	15	55651505	q21.3
SNP_A-2285635	G	G	409	7	401	19	5.598	1.80E-02	rs16977632	15	55721601	q21.3
SNP_A-2259132	C	C	356	36	377	19	5.836	1.57E-02	rs8023670	15	55829114	q21.3
SNP_A-1783131	T	C	193	187	227	173	4.448	0.0349	rs7176749	15	55840320	q21.3
SNP_A-2162744	C	C	192	136	173	169	4.269	3.88E-02	rs2005173	15	55841041	q21.3
SNP_A-2037660	A	A	196	190	221	153	5.302	2.13E-02	rs16940262	15	56504720	q21.3
SNP_A-2063731	C	C	390	20	374	36	4.907	2.68E-02	rs11632618	15	56511998	q21.3
SNP_A-2185611	G	G	337	41	382	26	5.037	2.48E-02	rs166362	15	56520804	q21.3
SNP_A-2286756	A	A	355	59	320	80	4.748	0.0293	rs12900891	15	56543863	q21.3
SNP_A-1756088	T	T	390	10	411	3	4.08	4.34E-02	rs1869129	15	56569419	q21.3
SNP_A-2286850	T	T	383	21	401	7	7.394	6.50E-03	rs10518984	15	56615162	q21.3
SNP_A-2287165	C	C	369	15	382	4	6.588	0.0103	rs10518995	15	57083368	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287545	T	T	329	63	286	98	10.534	1.20E-03	rs11633570	15	57497872	q22.2
SNP_A-2086785	A	A	304	62	258	106	15.284	9.25E-05	rs17302379	15	57501025	q22.2
SNP_A-2193139	T	T	207	135	181	171	5.835	1.57E-02	rs4592597	15	57524016	q22.2
SNP_A-2049379	T	T	320	84	272	114	8.031	4.60E-03	rs8024880	15	57529321	q22.2
SNP_A-2264135	A	A	323	89	286	130	9.905	1.60E-03	rs4775168	15	57535955	q22.2
SNP_A-2287551	C	C	307	51	260	70	5.749	1.65E-02	rs8028913	15	57537329	q22.2
SNP_A-2094597	C	C	324	70	355	45	6.805	9.10E-03	rs2970378	15	58049895	q22.2
SNP_A-1730803	A	A	387	13	381	33	8.504	3.50E-03	rs10519008	15	58268420	q22.2
SNP_A-1713273	T	T	320	80	296	118	7.99	4.70E-03	rs1509804	15	58289547	q22.2
SNP_A-2261256	G	G	369	19	376	40	6.573	0.0104	rs17237199	15	58308597	q22.2
SNP_A-2103696	A	A	391	19	372	44	10.351	1.30E-03	rs10153040	15	58364991	q22.2
SNP_A-1807560	C	C	388	14	368	36	10.204	0.0014	rs1912260	15	58366633	q22.2
SNP_A-2239557	G	G	315	69	283	105	9.14	2.50E-03	rs11635176	15	58367625	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181512	T	T	320	80	289	101	3.889	4.86E-02	rs11634838	15	58374305	q22.2
SNP_A-2076875	T	C	165	157	193	137	6.202	1.28E-02	---	15	58704567	q22.2
SNP_A-2178571	G	G	280	76	306	56	4.134	4.20E-02	rs16942900	15	58738736	q22.2
SNP_A-2288989	G	G	288	98	272	128	4.191	4.06E-02	rs17270626	15	59005277	q22.2
SNP_A-2021339	A	A	253	163	218	200	6.367	1.16E-02	rs20111857	15	59155919	q22.2
SNP_A-2232457	G	G	351	57	374	36	5.467	1.94E-02	rs782909	15	59168791	q22.2
SNP_A-2187453	A	A	357	59	372	40	3.936	4.73E-02	rs8039380	15	59185477	q22.2
SNP_A-2244111	C	C	321	83	346	62	3.959	4.66E-02	rs782918	15	59186665	q22.2
SNP_A-2268685	C	C	321	71	350	52	4.063	4.38E-02	rs782925	15	59190716	q22.2
SNP_A-1950072	G	G	363	41	383	25	4.395	3.60E-02	rs782933	15	59198382	q22.2
SNP_A-2223200	A	A	227	169	261	135	6.171	1.30E-02	rs80320?3	15	59199434	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2030856	T	T	316	58	293	81	4.674	3.06E-02	rs12909218	15	59224481	q22.2
SNP_A-2254707	G	G	394	18	410	4	9.223	2.40E-03	rs4432213	15	59401137	q22.2
SNP_A-2094809	C	C	390	16	404	2	11.136	8.00E-04	rs4516167	15	59401313	q22.2
SNP_A-1785022	A	A	394	18	394	6	5.824	1.58E-02	rs7174511	15	59403983	q22.2
SNP_A-2173494	G	G	385	27	392	10	7.752	5.40E-03	rs12439723	15	59481935	q22.2
SNP_A-2221922	G	G	320	22	335	9	5.789	0.0161	rs10467933	15	59543035	q22.2
SNP_A-1908907	T	T	338	26	337	11	5.726	0.0167	rs3848121	15	59666856	q22.2
SNP_A-2289582	C	C	334	16	355	5	6.262	0.0123	rs10519126	15	59748312	q22.2
SNP_A-1653440	T	T	262	128	239	169	6.313	0.012	rs2414749	15	59775647	q22.2
SNP_A-1827317	A	A	258	118	228	142	4.019	4.50E-02	rs11853350	15	59834186	q22.2
SNP_A-1892204	G	G	278	130	246	160	5.053	0.0246	rs11857925	15	59837128	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2171431	G	G	278	132	238	178	9.884	1.70E-03	rs8028558	15	59843045	q22.2
SNP_A-1812874	C	C	302	78	291	107	4.336	0.0373	rs12909308	15	59856528	q22.2
SNP_A-1909736	T	T	212	122	180	174	11.175	8.00E-04	rs7342610	15	59863973	q22.2
SNP_A-2031691	T	T	390	10	374	32	11.815	6.00E-04	rs17271500	15	60215901	q22.2
SNP_A-1797263	G	G	197	129	170	164	6.071	0.0137	rs12915227	15	60226749	q22.2
SNP_A-1835809	C	C	204	196	237	171	4.094	4.30E-02	rs2611792	15	60335212	q22.2
SNP_A-1795396	G	G	228	136	251	109	4.058	4.40E-02	rs1554289	15	60355913	q22.2
SNP_A-1780875	T	T	306	18	327	7	5.386	2.03E-02	rs10851713	15	60383512	q22.2
SNP_A-2290236	C	C	323	75	361	53	5.579	1.82E-02	rs11071671	15	60549887	q22.2
SNP_A-1925714	A	A	326	90	362	54	10.884	0.001	rs1995618	15	60569558	q22.2
SNP_A-1858267	A	A	327	85	352	56	6.866	8.80E-03	rs13723347	15	60604094	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2221588	C	C	354	52	381	33	5.161	2.31E-02	rs17738685	15	60618506	q22.2
SNP_A-2279900	T	T	244	126	267	99	4.254	3.92E-02	rs11071676	15	60676953	q22.2
SNP_A-1924493	G	G	245	123	275	99	4.277	3.86E-02	rs10851714	15	60684321	q22.2
SNP_A-2108501	A	A	397	9	392	2	4.307	3.80E-02	rs16945618	15	60823364	q22.2
SNP_A-2144573	T	T	329	7	353	1	4.878	2.72E-02	rs937422	15	60868820	q22.2
SNP_A-2124811	A	A	333	43	305	63	4.917	2.66E-02	rs8026446	15	60869299	q22.2
SNP_A-2193979	A	A	376	24	366	44	5.895	0.0152	rs2270689	15	60899198	q22.2
SNP_A-2299655	C	C	229	171	199	197	3.92	4.77E-02	rs4775604	15	61110933	q22.2
SNP_A-2070541	T	T	291	39	279	61	4.944	2.62E-02	rs2937859	15	61153335	q22.2
SNP_A-1925910	C	C	414	0	413	5	4.982	2.56E-02	rs11071740	15	61382704	q22.2
SNP_A-1923115	C	C	299	109	272	140	5.117	2.37E-02	rs12438157	15	61479950	q22.2
SNP_A-2158185	C	C	306	82	326	56	5.485	1.92E-02	rs17186555	15	61768380	q22.31
SNP_A-2267688	G	G	241	123	284	90	8.501	3.60E-03	rs978363	15	61936745	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1910242	T	T	406	8	396	20	5.263	0.0218	rs16947557	15	61976354	q22.31
SNP_A-2291296	G	G	364	40	345	59	4.156	4.15E-02	rs920761	15	62002046	q22.31
SNP_A-2273677	G	G	191	163	217	135	4.282	0.0385	rs11853632	15	62004898	q22.31
SNP_A-1949997	T	T	190	178	215	149	4.093	4.31E-02	rs11071781	15	62030986	q22.31
SNP_A-2291815	T	T	355	21	335	41	7.031	8.00E-03	rs922179	15	62053050	q22.31
SNP_A-1952070	A	A	400	16	389	29	3.904	0.0482	rs1380840	15	62054718	q22.31
SNP_A-2273353	T	T	329	61	346	42	3.928	4.75E-02	rs3816385	15	62205708	q22.31
SNP_A-2162761	G	G	377	21	408	6	9.246	2.40E-03	rs17803901	15	63028754	q22.31
SNP_A-1807508	A	A	327	59	310	84	4.743	2.94E-02	rs11634367	15	63923738	q22.31
SNP_A-2004241	C	C	386	12	402	4	4.246	3.94E-02	rs8039102	15	64297672	q22.31
SNP_A-1746424	G	G	318	86	359	55	9.178	2.40E-03	rs893912	15	64644287	q22.31
SNP_A-2004246	C	C	411	7	395	21	7.313	6.80E-03	rs6494584	15	64658388	q22.31
SNP_A-2069866	G	G	216	166	243	137	4.359	3.68E-02	rs4776304	15	64672029	q22.31
SNP_A-1828362	A	A	318	22	311	39	4.672	3.07E-02	rs7359178	15	64768383	q22.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1899293	C	C	316	26	299	49	7.472	0.0063	rs2469114	15	64800818	q22.31
SNP_A-2186932	G	G	340	60	329	89	5.432	1.98E-02	rs2439398	15	64800849	q22.31
SNP_A-1801107	C	C	362	48	386	30	4.881	2.72E-02	rs4589502	15	64942123	q22.32
SNP_A-2296968	C	C	321	55	340	36	4.513	3.36E-02	rs898889	15	65001162	q22.33
SNP_A-1817699	C	C	344	76	368	54	4.527	3.34E-02	rs8040468	15	65003192	q22.33
SNP_A-1941151	G	G	337	41	358	26	3.946	0.047	rs8023420	15	65118437	q22.33
SNP_A-1830873	A	A	275	95	248	122	4.753	0.0292	rs9972423	15	65178859	q22.33
SNP_A-2226062	C	C	290	92	265	125	6.062	0.0138	rs8025083	15	65209756	q22.33
SNP_A-1888515	C	C	305	19	295	41	8.018	4.60E-03	rs2127164	15	65899091	q23
SNP_A-1866161	C	C	343	73	306	96	5.001	0.0253	rs12898654	15	65915171	q23
SNP_A-1794406	A	A	397	5	392	0	4.907	2.68E-02	rs8042999	15	66447434	q23
SNP_A-2076746	T	T	365	5	368	0	5.007	0.0252	rs12442355	15	66521047	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1863258	G	G	320	0	314	4	4.051	4.42E-02	rs1602545	15	66742162	q23
SNP_A-1802477	T	T	300	62	291	91	5.1	2.39E-02	rs11636025	15	66763048	q23
SNP_A-1863982	A	A	187	125	164	156	4.827	2.80E-02	rs6494768	15	66829553	q23
SNP_A-2293727	T	T	395	17	382	34	5.865	0.0154	rs6494777	15	66993372	q23
SNP_A-1652954	T	T	218	154	270	136	5.182	2.28E-02	rs10518826	15	67688776	q23
SNP_A-1696830	C	C	338	40	319	63	5.664	1.73E-02	rs186248	15	67788023	q23
SNP_A-2286395	C	C	231	133	209	163	4.054	0.0441	rs17315418	15	67815887	q23
SNP_A-2308990	G	G	385	31	367	53	6.174	1.30E-02	rs12912487	15	67819848	q23
SNP_A-2286643	T	T	377	31	360	52	5.686	1.71E-02	rs16953685	15	67821142	q23
SNP_A-2294204	G	G	297	45	267	75	9.096	2.60E-03	rs449734	15	67859182	q23
SNP_A-2294285	A	A	391	7	376	18	5.113	2.37E-02	rs11858882	15	67942500	q23
SNP_A-1703665	C	C	358	22	353	47	8.586	3.40E-03	rs2415068	15	67967594	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1930990	C	C	327	25	280	38	4.608	3.18E-02	rs1037422	15	67974256	q23
SNP_A-2089657	C	C	223	187	258	156	5.329	2.10E-02	rs11636597	15	68208095	q23
SNP_A-2257835	C	C	346	24	354	42	4.123	4.23E-02	rs8028949	15	68268018	q23
SNP_A-2175798	C	C	402	16	387	33	6.178	0.0129	rs16954227	15	68272168	q23
SNP_A-2306996	G	G	363	55	387	33	6.263	0.0123	rs7171666	15	68272194	q23
SNP_A-2294548	C	C	359	57	379	39	3.912	4.79E-02	rs7179693	15	68282545	q23
SNP_A-1674050	A	A	243	159	277	133	4.46	3.47E-02	rs10518906	15	68473792	q23
SNP_A-1726662	G	G	288	116	317	89	4.941	2.62E-02	rs952960	15	68474720	q23
SNP_A-1837082	C	C	316	64	295	89	4.786	0.0287	rs8027878	15	68509658	q23
SNP_A-2268241	G	G	358	34	349	51	3.899	4.83E-02	rs17699949	15	68614405	q23
SNP_A-2047491	C	C	362	16	356	32	5.254	2.19E-02	rs6494886	15	68720785	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2104861	A	A	314	84	329	61	3.917	4.78E-02	rs872474	15	69785970	q23
SNP_A-2136232	A	A	247	143	268	106	6.022	0.0141	rs1054260	15	69859611	q23
SNP_A-1904057	G	G	370	8	396	2	3.97	4.63E-02	rs7173835	15	69864701	q23
SNP_A-2295567	A	A	409	5	396	14	4.454	3.48E-02	rs1979459	15	69997816	q23
SNP_A-1890316	G	G	413	5	396	14	4.544	3.30E-02	rs2929515	15	70007042	q23
SNP_A-2303776	C	C	330	42	350	18	10.167	0.0014	rs12595464	15	70081452	q23
SNP_A-2032236	T	T	405	7	390	20	6.537	0.0106	rs2929522	15	70093036	q23
SNP_A-2077031	A	A	409	1	394	8	5.646	1.75E-02	rs12439689	15	70159870	q23
SNP_A-2025762	C	C	413	7	403	19	5.656	1.74E-02	rs16956602	15	70235165	q23
SNP_A-2062756	G	G	405	5	408	0	5.006	0.0253	rs12324744	15	70316163	q23
SNP_A-2225820	C	C	413	7	402	18	4.988	2.55E-02	rs7165735	15	70323004	q23
SNP_A-2092616	C	C	408	8	419	1	5.572	0.0183	rs2959933	15	70381766	q23
SNP_A-2138555	T	T	334	10	343	3	3.883	4.88E-02	rs2959926	15	70387117	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1927972	C	C	348	14	360	4	5.753	1.65E-02	rs9672916	15	70387481	q23
SNP_A-1787505	A	A	400	14	415	3	7.375	0.0066	rs2959925	15	70387547	q23
SNP_A-2076462	G	G	405	9	398	20	4.214	4.01E-02	rs4556749	15	70479255	q24.1
SNP_A-1799611	G	G	395	13	387	25	3.852	4.97E-02	rs16956917	15	70488831	q24.1
SNP_A-1742203	G	G	364	14	297	31	9.721	0.0018	rs4777517	15	70591660	q24.1
SNP_A-1661143	C	C	345	55	378	34	6.285	1.22E-02	rs4777529	15	70729593	q24.1
SNP_A-1781527	A	A	307	109	337	85	4.324	3.76E-02	rs730180	15	70794946	q24.1
SNP_A-2300279	C	C	333	31	355	11	10.222	0.0014	rs12594844	15	70858060	q24.1
SNP_A-1831630	C	C	338	68	363	45	5.568	0.0183	rs12594938	15	70858335	q24.1
SNP_A-2295862	G	G	383	21	345	37	4.866	2.74E-02	rs7182854	15	70866557	q24.1
SNP_A-2073821	G	G	349	39	379	25	3.977	4.61E-02	rs7178409	15	70874419	q24.1
SNP_A-1834328	C	C	325	31	358	18	4.5	0.0339	rs16957315	15	70891311	q24.1
SNP_A-2295890	C	C	329	67	356	48	4.124	4.23E-02	rs4514651	15	70909026	q24.1
SNP_A-2176559	T	T	355	63	375	41	5.197	2.26E-02	rs7497113	15	70939512	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2295907	G	G	282	68	325	43	8.231	4.10E-03	rs4640154	15	70945211	q24.1
SNP_A-2217316	C	C	314	42	349	25	5.721	1.68E-02	rs6416497	15	70947067	q24.1
SNP_A-1815971	A	A	230	118	257	95	3.958	4.67E-02	rs7183175	15	71045863	q24.1
SNP_A-2187651	T	T	401	13	355	23	3.949	4.69E-02	rs899480	15	71254389	q24.1
SNP_A-1952577	G	G	345	21	337	9	4.335	0.0373	rs3940418	15	71458570	q24.1
SNP_A-2127766	C	C	221	139	185	161	4.53	3.33E-02	rs7171755	15	71637633	q24.1
SNP_A-2023607	C	C	386	0	380	8	8.042	4.60E-03	rs8027445	15	71757671	q24.1
SNP_A-2273164	-	A	205	205	238	178	4.318	3.77E-02	rs11072430	15	71768754	q24.1
SNP_A-2095116	C	C	182	152	227	109	12.03	5.00E-04	rs7176654	15	71786059	q24.1
SNP_A-2145469	C	C	213	139	170	166	6.849	8.90E-03	rs11574495	15	71790989	q24.1
SNP_A-1809565	A	G	191	185	226	170	4.797	2.85E-02	rs7171779	15	71843376	q24.1
SNP_A-1887562	C	C	281	137	307	111	3.875	4.90E-02	rs1550434	15	72118264	q24.1
SNP_A-2212466	T	T	247	159	286	126	6.631	0.01	rs2959011	15	72398834	q24.1
SNP_A-1905125	G	G	254	134	293	103	6.755	9.40E-03	rs11072478	15	72402560	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2201375	T	T	257	123	303	103	4.694	3.03E-02	rs2959004	15	72408594	q24.1
SNP_A-2312470	C	C	256	116	298	92	5.531	1.87E-02	rs2277602	15	72409510	q24.1
SNP_A-1804274	G	G	258	132	295	103	5.974	1.45E-02	rs2959003	15	72415944	q24.1
SNP_A-1813132	G	G	290	126	322	96	5.722	0.0167	rs7174179	15	72442636	q24.1
SNP_A-2296941	C	C	362	24	380	12	4.391	0.0361	rs2469208	15	74378141	q24.2
SNP_A-1674323	T	T	372	32	395	19	3.882	4.88E-02	rs3743175	15	74412587	q24.3
SNP_A-2300138	G	G	322	32	355	19	4.376	3.64E-02	rs16968233	15	74520102	q24.3
SNP_A-1913675	C	C	385	33	404	18	4.85	0.0276	rs16968467	15	74844919	q24.3
SNP_A-2150641	A	A	383	25	358	48	8.085	4.50E-03	rs17381898	15	75191697	q24.3
SNP_A-2232802	T	T	325	31	278	54	9.061	2.60E-03	rs12913548	15	75203464	q24.3
SNP_A-2303700	T	T	371	29	333	51	7.778	0.0053	rs12903728	15	75204757	q24.3
SNP_A-2052708	C	C	299	113	319	83	5.117	2.37E-02	rs4286073	15	75673919	q24.3
SNP_A-2027421	G	G	307	111	331	81	5.547	1.85E-02	rs11638674	15	75678995	q24.3
SNP_A-1833217	G	G	277	89	295	63	4.926	2.65E-02	rs16968998	15	75684252	q24.3
SNP_A-1912099	T	T	282	92	313	71	4.189	0.0407	rs16968999	15	75684401	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2113643	A	A	232	90	211	127	6.92	8.50E-03	rs2867312	15	75689348	q24.3
SNP_A-1871919	C	C	347	69	315	101	7.57	5.90E-03	rs13313467	15	75753223	q24.3
SNP_A-1942859	A	A	290	110	261	139	4.904	2.68E-02	rs11856876	15	75760067	q24.3
SNP_A-2096639	G	G	263	59	292	42	4.159	4.14E-02	rs4624137	15	75865958	q24.3
SNP_A-2051946	A	A	315	89	339	63	5.323	2.10E-02	rs7177234	15	75876871	q24.3
SNP_A-2096294	T	T	353	13	344	34	9.308	0.0023	rs11857499	15	75918738	q24.3
SNP_A-1674613	G	G	376	2	385	11	5.922	1.50E-02	rs10519182	15	76020555	q25.1
SNP_A-2078884	A	A	297	99	268	126	4.723	0.0298	rs11072728	15	76187728	q25.1
SNP_A-2268228	C	C	197	181	239	145	7.975	4.70E-03	rs16969520	15	76204239	q25.1
SNP_A-2229445	A	G	229	169	196	194	4.813	2.83E-02	rs11857947	15	76208724	q25.1
SNP_A-2113084	T	T	398	20	371	49	13.132	3.00E-04	rs17674205	15	76248512	q25.1
SNP_A-2141208	T	T	224	180	278	132	13.15	3.00E-04	rs2280366	15	76372953	q25.1
SNP_A-1806124	C	C	401	5	414	0	5.13	0.0235	rs7172878	15	76475399	q25.1
SNP_A-2278357	C	C	413	7	420	0	7.059	7.90E-03	rs3825849	15	76476724	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2312841	A	A	276	76	233	99	6.076	0.0137	rs2869030	15	76498858	q25.1
SNP_A-1924563	T	T	298	12	309	31	7.225	7.20E-03	rs9920411	15	76577156	q25.1
SNP_A-2257371	C	C	306	74	289	99	4.016	4.51E-02	rs1564499	15	76871863	q25.1
SNP_A-2298539	G	G	332	88	298	122	7.34	6.70E-03	rs3743200	15	77061101	q25.1
SNP_A-2205781	C	C	305	85	280	116	5.804	0.016	rs7168964	15	77061746	q25.1
SNP_A-2250290	G	G	230	178	264	144	5.93	0.0149	rs1373202	15	77108843	q25.1
SNP_A-1906819	A	A	206	174	250	146	6.368	1.16E-02	rs1373201	15	77114223	q25.1
SNP_A-1796985	G	G	310	52	330	26	9.242	2.40E-03	rs1822471	15	77114282	q25.1
SNP_A-2217591	A	A	263	75	261	49	4.257	3.91E-02	rs7170146	15	77275648	q25.1
SNP_A-1688104	C	C	285	119	256	158	6.924	8.50E-03	rs1434464	15	77304993	q25.1
SNP_A-2092428	A	A	280	130	244	172	8.271	4.00E-03	rs8033304	15	77397270	q25.1
SNP_A-1941659	G	G	398	8	418	2	3.854	4.96E-02	rs3947042	15	77407173	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1816510	G	G	375	21	331	37	6.138	0.0132	rs8030533	15	77428008	q25.1
SNP_A-2004301	C	C	365	33	350	54	5.339	2.09E-02	rs6495402	15	77447479	q25.1
SNP_A-2271539	A	A	365	21	339	39	6.277	1.22E-02	rs7169738	15	77449095	q25.1
SNP_A-2218201	C	C	363	21	340	36	4.616	3.17E-02	rs7177291	15	77460866	q25.1
SNP_A-2042430	G	G	330	0	315	5	5.196	2.26E-02	rs16971125	15	77674108	q25.1
SNP_A-2298947	A	A	233	127	265	89	8.692	3.20E-03	rs8031905	15	77694156	q25.1
SNP_A-2298949	G	G	257	161	287	135	3.919	4.77E-02	rs1872825	15	77694698	q25.1
SNP_A-2077872	A	A	376	18	386	6	6.126	1.33E-02	rs16954047	15	77741808	q25.1
SNP_A-2148563	A	A	269	99	285	71	4.876	2.72E-02	rs3894754	15	77758045	q25.1
SNP_A-2283436	C	C	192	136	235	113	5.868	0.0154	rs3893384	15	77760110	q25.1
SNP_A-2251069	G	G	337	35	370	20	5.209	2.25E-02	rs3893350	15	77760689	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1651840	C	C	309	95	344	70	5.542	1.86E-02	rs1380642	15	77812690	q25.1
SNP_A-1675203	G	G	242	162	219	195	4.076	4.35E-02	rs724721	15	77815396	q25.1
SNP_A-1956444	T	T	211	181	244	134	9.155	2.50E-03	rs1074390	15	77867362	q25.1
SNP_A-2071956	C	C	245	157	219	187	4.053	0.0441	rs1675181	15	77898693	q25.1
SNP_A-1733496	A	A	376	28	365	45	4.078	4.34E-02	rs10519280	15	78108508	q25.1
SNP_A-2037820	G	G	379	5	368	0	4.824	0.0281	rs16971862	15	78311279	q25.1
SNP_A-1793131	G	G	235	163	266	136	4.336	0.0373	rs2009949	15	78339518	q25.1
SNP_A-1869628	T	T	196	152	229	131	3.918	4.78E-02	rs11072921	15	78587211	q25.1
SNP_A-2091089	C	C	188	130	241	111	6.337	0.0118	rs7162181	15	78606479	q25.1
SNP_A-2042655	A	A	218	202	266	156	10.666	1.10E-03	rs4238523	15	78616704	q25.1
SNP_A-1715159	A	A	365	21	342	48	11.293	8.00E-04	rs960170	15	78739995	q25.1
SNP_A-1675269	C	C	397	3	372	10	4.17	4.11E-02	rs2660992	15	78778531	q25.1
SNP_A-2068708	T	T	380	26	354	54	10.716	1.10E-03	rs2170879	15	78802011	q25.1
SNP_A-2119755	G	G	320	8	292	24	9.061	2.60E-03	rs2170878	15	78802036	q25.1
SNP_A-2061630	A	A	386	30	361	59	10.267	0.0014	rs8039117	15	78827651	q25.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2148606	C	C	262	84	211	111	8.386	0.0038	rs2663911	15	79207705	q25.1
SNP_A-2299664	T	T	290	110	261	141	5.35	0.0207	rs2048271	15	79214362	q25.1
SNP_A-2158176	A	A	369	41	351	63	5.085	0.0241	rs12439698	15	79217861	q25.1
SNP_A-2031572	A	A	291	127	330	88	9.524	0.002	rs859	15	79388377	q25.1
SNP_A-2299703	C	C	295	81	274	108	4.585	3.23E-02	rs1482937	15	79598554	q25.2
SNP_A-1860456	A	A	342	56	308	80	5.887	0.0152	rs1532750	15	80174831	q25.2
SNP_A-2094520	G	G	248	130	217	159	4.971	0.0258	rs4778973	15	80181060	q25.2
SNP_A-1809436	G	A	207	153	195	169	8.888	2.90E-03	rs2654216	15	80181440	q25.2
SNP_A-2195867	G	G	263	155	308	112	10.467	1.20E-03	rs2654209	15	80196782	q25.2
SNP_A-2151444	G	G	289	131	253	169	7.2	7.30E-03	rs2654208	15	80196972	q25.2
SNP_A-2138641	G	G	289	125	241	169	10.913	0.001	rs1875679	15	80200351	q25.2
SNP_A-2288576	C	C	268	70	283	45	5.694	1.70E-02	rs2665109	15	80202412	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1916298	G	G	280	130	238	170	8.734	3.10E-03	rs2134513	15	80208092	q25.2
SNP_A-2226999	G	G	292	126	325	93	6.738	9.40E-03	rs968069	15	82169903	q25.2
SNP_A-2300640	G	G	285	117	319	85	6.978	8.30E-03	rs2585063	15	82189857	q25.2
SNP_A-1680724	C	C	333	31	321	51	5.012	0.0252	rs950169	15	82426229	q25.2
SNP_A-1891451	T	T	310	90	294	120	4.47	3.45E-02	rs12148239	15	82432022	q25.2
SNP_A-1665876	G	G	365	37	353	61	5.903	1.51E-02	rs10520569	15	82449157	q25.2
SNP_A-2178305	C	C	341	71	366	50	4.509	3.37E-02	rs7166894	15	83313209	q25.3
SNP_A-2075378	T	T	304	60	303	91	5.187	2.28E-02	rs7402832	15	83931508	q25.3
SNP_A-2301474	G	G	353	25	386	12	5.529	1.87E-02	rs16943236	15	84034355	q25.3
SNP_A-2230701	T	T	368	36	382	18	6.242	1.25E-02	rs2241267	15	84079178	q25.3
SNP_A-1960875	A	A	240	114	230	148	3.842	5.00E-02	rs7497274	15	84166812	q25.3
SNP_A-1890728	C	C	350	52	364	34	4.022	4.49E-02	rs11852394	15	84307061	q25.3
SNP_A-2070277	A	A	324	34	360	20	4.873	2.73E-02	rs11858395	15	84358485	q25.3
SNP_A-1715501	C	C	274	98	261	135	5.447	1.96E-02	rs8025054	15	84545264	q25.3
SNP_A-1757831	T	T	272	74	259	101	4.208	0.0402	rs1039116	15	84546965	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2302251	A	A	249	149	226	188	5.314	0.0212	rs1908786	15	84667879	q25.3
SNP_A-2301852	A	A	288	128	262	156	3.985	4.59E-02	rs10520632	15	84806533	q25.3
SNP_A-2293604	T	C	201	177	201	167	4.532	3.33E-02	rs12443065	15	84851355	q25.3
SNP_A-1722566	G	G	207	153	196	194	3.951	4.68E-02	rs2246309	15	84925685	q25.3
SNP_A-1856520	C	C	287	65	315	47	4.056	4.40E-02	rs11630577	15	85098214	q25.3
SNP_A-2302318	A	A	304	114	332	86	5.153	2.32E-02	rs10520648	15	85419597	q25.3
SNP_A-1694573	T	T	280	120	254	158	6.284	1.22E-02	rs3844975	15	85450479	q25.3
SNP_A-2162034	G	G	348	36	323	55	4.852	0.0276	rs4887267	15	85554668	q25.3
SNP_A-2302497	C	C	340	42	314	64	5.579	1.82E-02	rs10520652	15	85562683	q25.3
SNP_A-2227274	C	C	352	46	329	65	4.009	0.0453	rs17738370	15	85564452	q25.3
SNP_A-2080237	G	G	235	171	265	143	4.292	3.83E-02	rs8030596	15	85649417	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2023067	A	A	192	172	234	138	7.784	0.0053	rs2599546	15	85662105	q25.3
SNP_A-2134973	A	A	235	181	270	148	5.731	0.0167	rs2584176	15	85663813	q25.3
SNP_A-2004337	A	A	243	63	236	92	4.77	2.90E-02	rs4390560	15	85943019	q25.3
SNP_A-2302917	A	A	248	150	225	181	3.943	4.71E-02	rs12594315	15	85959359	q25.3
SNP_A-2187413	T	T	286	116	263	147	4.539	3.31E-02	rs2069227	15	86108557	q25.3
SNP_A-2222988	A	A	212	152	223	115	4.449	0.0349	rs2348569	15	86109173	q25.3
SNP_A-2283203	G	G	325	53	305	77	5.045	0.0247	rs11856526	15	86130534	q25.3
SNP_A-1835172	A	A	326	24	306	40	4.61	3.18E-02	rs13694427	15	86131261	q25.3
SNP_A-2302959	C	C	381	29	368	46	4.06	4.39E-02	rs11632716	15	86161287	q25.3
SNP_A-1868732	G	G	221	143	204	188	5.769	1.63E-02	rs13380271	15	86300189	q25.3
SNP_A-2282959	G	G	325	73	357	49	6.144	0.0132	rs12324332	15	86350155	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1682678	T	T	351	37	321	57	5.465	1.94E-02	rs1372600	15	86594675	q25.3
SNP_A-2249899	G	G	416	0	415	5	4.982	2.56E-02	rs6496486	15	86806342	q25.3
SNP_A-2004348	G	G	262	132	273	99	4.312	0.0378	rs1470108	15	86954748	q26.1
SNP_A-2101110	A	A	376	36	378	20	4.336	0.0373	rs16942120	15	86974039	q26.1
SNP_A-1931246	C	C	299	15	310	34	6.211	1.27E-02	rs4534816	15	87066323	q26.1
SNP_A-1698383	G	G	243	137	286	118	4.18	4.09E-02	rs698621	15	87132364	q26.1
SNP_A-1820618	A	A	399	11	421	1	8.752	3.10E-03	rs11073814	15	87179888	q26.1
SNP_A-1949660	A	A	387	7	382	22	7.667	5.60E-03	rs8033823	15	87360620	q26.1
SNP_A-1787202	C	C	380	36	385	19	5.113	2.38E-02	rs2854516	15	87562492	q26.1
SNP_A-2272116	G	G	240	174	261	141	4.162	4.13E-02	rs16942893	15	87587425	q26.1
SNP_A-2303828	G	G	237	177	269	149	4.409	3.57E-02	rs3176238	15	87661431	q26.1
SNP_A-1833580	A	A	217	159	230	124	4.047	4.42E-02	rs758130	15	87674801	q26.1
SNP_A-2156106	G	G	318	22	297	37	4.478	3.43E-02	rs11073864	15	87790518	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2137165	A	A	311	33	287	51	4.768	2.90E-02	rs1371385	15	87806703	q26.1
SNP_A-1895452	G	G	288	56	268	90	8.361	0.0038	rs11635236	15	88651766	q26.1
SNP_A-1644574	C	C	363	39	351	59	4.205	4.03E-02	rs10520689	15	88680126	q26.1
SNP_A-1657844	T	T	365	37	353	59	5.12	2.36E-02	rs10520688	15	88681284	q26.1
SNP_A-2251609	C	C	359	31	347	49	4.208	0.0402	rs16944485	15	88824604	q26.1
SNP_A-2132753	T	T	350	28	343	45	3.9	4.83E-02	rs11073929	15	88839823	q26.1
SNP_A-2256283	G	C	188	146	164	138	7.122	0.0076	rs2518968	15	89108414	q26.1
SNP_A-2281604	C	C	393	21	398	10	3.891	4.85E-02	rs8031572	15	89591255	q26.1
SNP_A-2305032	G	G	238	150	208	176	4.071	0.0436	rs1079537	15	89675287	q26.1
SNP_A-1882336	A	A	233	125	195	145	4.394	0.0361	rs1125314	15	89683378	q26.1
SNP_A-2270784	T	T	362	56	330	84	7.061	7.90E-03	rs7172774	15	89956004	q26.1
SNP_A-1936636	A	A	343	43	296	80	14.458	0.0001	rs4553603	15	89964100	q26.1
SNP_A-2088267	A	A	336	74	313	105	6.107	0.0135	rs11855380	15	89968601	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1825655	G	G	276	98	310	64	9.108	2.50E-03	rs12439738	15	90336555	q26.1
SNP_A-2299468	T	T	304	44	331	29	4.028	0.0448	rs11632217	15	90617183	q26.1
SNP_A-1663620	T	T	327	77	296	118	10.042	0.0015	rs285702	15	90846239	q26.1
SNP_A-1824562	T	T	239	145	266	118	4.215	4.01E-02	rs285708	15	90922083	q26.1
SNP_A-1877688	A	A	218	106	197	133	4.058	4.40E-02	rs432364	15	90958523	q26.1
SNP_A-2141064	T	T	229	167	262	142	4.161	4.14E-02	rs8032832	15	90959099	q26.1
SNP_A-1823080	C	C	307	37	332	22	4.649	3.11E-02	rs7180285	15	91300389	q26.1
SNP_A-2306155	G	G	307	97	325	69	5.111	2.38E-02	rs10520720	15	91435728	q26.1
SNP_A-1782403	T	G	213	181	208	182	4.287	3.84E-02	rs7180858	15	91479925	q26.1
SNP_A-2302525	A	A	315	93	275	123	6.756	9.30E-03	rs6416582	15	91537949	q26.1
SNP_A-1856971	G	G	185	159	230	134	6.453	0.0111	rs7182997	15	91751147	q26.1
SNP_A-1834267	C	C	313	105	286	132	4.293	3.83E-02	rs8032634	15	91753155	q26.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1944214	C	T	232	178	205	193	5.305	2.13E-02	rs8039405	15	91753695	q26.1
SNP_A-2282955	A	C	218	182	208	176	5.886	1.53E-02	rs1489129	15	91769292	q26.1
SNP_A-2286155	T	T	340	0	330	4	4.096	4.30E-02	rs901969	15	91793974	q26.1
SNP_A-2306382	A	A	295	45	260	70	7.494	6.20E-03	rs2388299	15	91830620	q26.1
SNP_A-2255649	C	C	280	134	310	106	4.787	0.0287	rs12591369	15	92017601	q26.1
SNP_A-1914421	T	T	352	58	328	88	6.968	8.30E-03	rs11635366	15	92033956	q26.1
SNP_A-1908474	T	T	234	182	277	141	8.818	3.00E-03	rs4598857	15	92034414	q26.1
SNP_A-1730507	G	G	214	176	252	146	5.813	1.59E-02	rs1935634	15	92084978	q26.2
SNP_A-1956431	A	G	211	177	205	173	5.683	1.71E-02	rs1479808	15	92328436	q26.2
SNP_A-1817114	C	C	204	156	246	130	5.939	1.48E-02	rs12324883	15	92337454	q26.2
SNP_A-2269981	A	A	323	59	370	38	6.886	8.70E-03	rs2127462	15	92338318	q26.2
SNP_A-2230205	G	G	183	147	211	105	8.691	3.20E-03	rs11856594	15	92341785	q26.2
SNP_A-2193575	G	G	366	18	386	6	6.45	0.0111	rs2054507	15	92375012	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2127844	A	A	324	20	334	8	5.289	2.15E-02	rs6497164	15	92417120	q26.2
SNP_A-2042048	A	A	254	70	273	49	4.385	3.63E-02	rs8040967	15	92603766	q26.2
SNP_A-2144312	T	T	250	126	214	150	4.687	0.0304	rs2168349	15	92636976	q26.2
SNP_A-1715565	G	G	333	65	322	90	3.976	4.61E-02	rs3784647	15	92678818	q26.2
SNP_A-2265984	G	G	299	79	316	56	4.341	3.72E-02	---	15	92731294	q26.2
SNP_A-2313002	C	C	339	27	341	11	6.472	1.10E-02	rs17662683	15	92775531	q26.2
SNP_A-2186179	A	A	276	92	252	116	3.86	4.94E-02	rs12437763	15	92929354	q26.2
SNP_A-2085832	G	G	387	7	391	1	4.516	3.36E-02	rs17632761	15	93007376	q26.2
SNP_A-2204483	A	G	214	200	231	185	4.333	3.74E-02	rs12901421	15	93060797	q26.2
SNP_A-2135310	A	A	332	38	359	23	4.553	3.29E-02	rs4984405	15	93061175	q26.2
SNP_A-1950347	A	A	297	75	263	101	5.819	1.59E-02	rs8024991	15	93212109	q26.2
SNP_A-2307540	T	T	359	19	349	35	4.835	2.79E-02	rs1002514	15	93226233	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2307745	A	A	233	121	269	99	4.512	3.37E-02	rs186014	15	93491492	q26.2
SNP_A-2143200	G	G	303	27	318	14	4.478	3.43E-02	rs16949895	15	93596519	q26.2
SNP_A-2110243	G	G	241	81	283	61	5.463	1.94E-02	rs17555335	15	93607706	q26.2
SNP_A-1784302	A	A	227	135	201	167	4.921	2.65E-02	rs7163985	15	93689475	q26.2
SNP_A-2026012	G	G	312	46	325	27	5.16	2.31E-02	rs13329544	15	93770078	q26.2
SNP_A-2247523	C	C	338	58	358	40	3.876	4.90E-02	rs933770	15	93853726	q26.2
SNP_A-1656963	G	G	308	96	287	125	4.469	3.45E-02	rs4417514	15	94303275	q26.2
SNP_A-1756673	A	A	305	99	276	124	4.23	3.97E-02	rs10520806	15	94304812	q26.2
SNP_A-2308560	G	G	343	45	377	29	4.659	0.0309	rs12441889	15	94346766	q26.2
SNP_A-2308565	G	G	328	84	292	122	9.095	2.60E-03	rs1450496	15	94353256	q26.2
SNP_A-2308638	G	G	289	71	271	95	3.999	4.55E-02	rs10468115	15	94393358	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2181374	G	G	298	72	270	102	6.547	1.05E-02	rs4329872	15	94405177	q26.2
SNP_A-2151425	A	A	316	80	286	116	8.063	4.50E-03	rs4313763	15	94405194	q26.2
SNP_A-1847177	A	A	243	81	210	110	6.783	9.20E-03	rs8034150	15	94407225	q26.2
SNP_A-2065789	A	A	289	37	263	57	5.425	1.99E-02	rs8029545	15	94409963	q26.2
SNP_A-2147062	G	G	313	83	338	60	4.654	0.031	rs980168	15	94521758	q26.2
SNP_A-2243124	C	C	351	39	370	24	4.052	0.0441	rs2589238	15	94611871	q26.2
SNP_A-2052203	G	G	221	181	244	144	5.103	2.39E-02	rs8026716	15	94755999	q26.2
SNP_A-2024627	A	A	346	34	332	52	4.036	4.45E-02	rs2174155	15	95099450	q26.2
SNP_A-2069546	C	C	307	105	325	77	4.698	3.02E-02	rs735981	15	95251046	q26.2
SNP_A-1642495	T	T	285	59	311	35	7.256	7.10E-03	rs1828770	15	95292670	q26.2
SNP_A-1758230	A	A	300	84	327	61	4.79	0.0286	rs1849648	15	95293046	q26.2
SNP_A-2309096	T	T	413	3	405	11	4.65	3.11E-02	rs190183	15	95347713	q26.2
SNP_A-1840589	C	C	317	87	336	64	4.036	4.45E-02	rs2535484	15	95357479	q26.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1925234	T	T	291	63	308	34	8.948	0.0028	rs2670914	15	95357702	q26.2
SNP_A-1788144	T	T	295	55	312	36	4.437	3.52E-02	rs4965180	15	95716640	q26.2
SNP_A-2240329	C	C	249	139	277	113	4.168	4.12E-02	rs649034	15	95947118	q26.2
SNP_A-1788765	G	G	229	151	205	191	5.678	0.0172	rs971627	15	96152380	q26.2
SNP_A-2258159	C	C	356	30	362	50	4.207	0.0402	rs11855844	15	96462745	q26.3
SNP_A-2289485	G	G	379	11	366	2	5.824	1.58E-02	rs1552052	15	96509948	q26.3
SNP_A-2166181	G	G	295	45	294	68	3.998	4.56E-02	rs1442811	15	96619978	q26.3
SNP_A-2291860	T	C	191	153	182	168	3.932	4.74E-02	rs1982259	15	96681892	q26.3
SNP_A-1927444	C	C	310	44	294	74	7.782	0.0053	rs748933	15	96711600	q26.3
SNP_A-1798218	G	G	335	59	369	41	4.565	3.26E-02	rs6598518	15	96891353	q26.3
SNP_A-1846874	A	A	312	94	340	70	4.695	3.02E-02	rs11636483	15	96937675	q26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2106742	T	T	350	10	361	29	8.24	4.10E-03	rs8024593	15	96988019	q26.3
SNP_A-2177198	G	G	223	195	256	158	6.133	1.33E-02	rs4966008	15	97020968	q26.3
SNP_A-2090307	G	G	206	140	257	127	4.284	0.0385	rs11247361	15	97024915	q26.3
SNP_A-2146299	G	G	280	128	315	101	5.165	0.023	rs4965518	15	97865483	q26.3
SNP_A-2155234	G	G	292	30	267	45	3.961	4.66E-02	rs11857443	15	98547229	q26.3
SNP_A-2132147	G	A	185	183	200	142	5.464	1.94E-02	rs4548838	15	98578713	q26.3
SNP_A-1804277	A	A	309	51	338	34	4.504	3.38E-02	rs7170819	15	98711920	q26.3
SNP_A-1833166	A	A	253	87	251	59	4.002	4.55E-02	rs7163248	15	99150496	q26.3
SNP_A-1833514	C	C	312	6	345	1	4.055	4.40E-02	rs4264375	15	99180792	q26.3
SNP_A-2176650	G	G	294	62	304	40	4.708	3.00E-02	rs12906432	15	99231690	q26.3
SNP_A-1828658	A	A	311	93	320	64	4.981	2.56E-02	rs11630691	15	99282438	q26.3
SNP_A-1854184	C	C	371	21	357	43	7.752	5.40E-03	rs2005180	15	99536223	q26.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2311037	C	C	268	86	252	126	7.26	7.00E-03	rs752028	15	99686708	q26.3
SNP_A-1899972	G	G	291	127	265	157	4.366	3.67E-02	rs1030	15	99705317	q26.3
SNP_A-2296998	T	T	250	166	279	135	4.778	2.88E-02	rs10152756	15	99708384	q26.3
SNP_A-1838771	A	A	234	146	210	176	4.046	4.43E-02	rs10152164	15	99743186	q26.3
SNP_A-2114786	A	G	209	199	224	178	3.917	4.78E-02	rs2121206	15	99938027	q26.3
SNP_A-2131890	G	G	221	155	203	191	4.091	4.31E-02	rs2974771	16	161057	p13.3
SNP_A-2243694	A	A	336	34	338	56	4.634	3.13E-02	rs11248925	16	252636	p13.3
SNP_A-1902380	G	G	298	96	253	127	7.734	5.40E-03	rs12598318	16	1059947	p13.3
SNP_A-1877518	C	C	211	115	247	87	6.615	0.0101	rs150925	16	2264070	p13.3
SNP_A-1805926	A	A	303	107	274	146	7.35	6.70E-03	rs150928	16	2268791	p13.3
SNP_A-2195090	C	C	252	154	266	118	4.534	0.0332	rs6600193	16	2370177	p13.3
SNP_A-1911478	G	G	203	139	192	182	4.646	3.11E-02	rs1061019	16	3042177	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1943214	C	C	311	91	274	122	6.807	9.10E-03	rs1002965	16	3170473	p13.3
SNP_A-2170979	A	A	270	66	219	93	9.027	2.70E-03	rs6501153	16	3191492	p13.3
SNP_A-1938127	C	C	374	22	404	8	7.376	0.0066	rs11077325	16	3217252	p13.3
SNP_A-2313838	G	G	378	32	403	13	8.779	3.00E-03	rs9927763	16	3222276	p13.3
SNP_A-1948303	G	G	388	28	393	13	5.399	0.0201	rs11645952	16	3312482	p13.3
SNP_A-2298910	A	A	298	102	276	130	4.178	4.10E-02	rs13332500	16	3515271	p13.3
SNP_A-2314153	C	C	412	4	418	0	4.039	4.45E-02	rs1300037	16	3796446	p13.3
SNP_A-2093425	G	G	351	23	369	11	4.638	3.13E-02	rs11646632	16	4198092	p13.3
SNP_A-1884010	A	A	326	0	322	4	4.025	0.0448	rs1056333	16	4842482	p13.3
SNP_A-1862315	T	C	209	145	196	180	9.135	2.50E-03	rs2908645	16	4972911	p13.3
SNP_A-2099901	C	C	347	45	360	28	4.178	4.10E-02	rs871295	16	5156719	p13.3
SNP_A-2233380	A	A	342	52	349	33	4.133	4.20E-02	rs12149180	16	5295084	p13.3
SNP_A-1798208	T	T	329	75	356	52	5.21	2.25E-02	rs9972783	16	5310411	p13.3
SNP_A-1880295	G	G	403	7	398	0	6.855	8.80E-03	rs17137819	16	5312536	p13.3
SNP_A-2109097	T	T	290	24	311	11	5.463	1.94E-02	rs1878540	16	5323595	p13.3
SNP_A-2260526	T	T	405	13	412	4	4.82	0.0281	rs9921635	16	5332599	p13.3
SNP_A-2208318	C	C	405	13	416	4	4.907	2.67E-02	rs938756	16	5343815	p13.3
SNP_A-2004493	C	C	314	64	270	88	6.566	0.0104	rs6500689	16	5348914	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169928	G	G	345	73	317	103	6.293	0.0121	rs4786694	16	5480442	p13.3
SNP_A-2158747	C	C	351	69	327	91	3.87	4.92E-02	rs9921862	16	5598178	p13.3
SNP_A-1744063	G	G	370	22	371	39	4.337	0.0373	rs881006	16	5687796	p13.3
SNP_A-2120150	A	A	217	157	258	130	5.824	1.58E-02	rs9941024	16	5734313	p13.3
SNP_A-2304525	T	T	250	158	282	130	4.628	0.0315	rs12597642	16	5759961	p13.3
SNP_A-1824441	G	G	239	99	280	82	4.017	4.50E-02	rs7187706	16	5762457	p13.3
SNP_A-2276023	G	G	396	8	388	22	6.571	0.0104	rs12445565	16	5909866	p13.3
SNP_A-2268981	T	T	310	54	271	77	6.3	0.0121	rs7201717	16	6005281	p13.3
SNP_A-2216531	A	A	322	6	349	1	3.948	4.69E-02	rs17139361	16	6079750	p13.3
SNP_A-2136398	C	C	171	139	216	106	9.453	2.10E-03	rs2019249	16	6391866	p13.2
SNP_A-1824793	A	A	164	158	211	139	5.95	0.0147	rs2534738	16	6398444	p13.2
SNP_A-2251034	T	T	318	38	299	57	4.385	3.63E-02	rs17439057	16	6398599	p13.2
SNP_A-1875494	T	T	236	168	211	201	4.271	3.88E-02	rs9926622	16	6402232	p13.2
SNP_A-1891942	T	T	302	78	310	46	7.588	5.90E-03	---	16	6478987	p13.2
SNP_A-1789828	T	T	348	18	279	33	7.753	5.40E-03	rs11077058	16	6623076	p13.2
SNP_A-2040757	G	G	406	12	396	24	4.12	0.0424	rs9938551	16	6703909	p13.2
SNP_A-2276663	C	C	328	44	319	67	4.634	3.13E-02	rs8044559	16	6713809	p13.2
SNP_A-1943534	G	G	362	10	379	23	4.355	3.69E-02	rs2046978	16	6946142	p13.2
SNP_A-2162314	C	C	415	3	411	11	4.572	3.25E-02	---	16	7032584	p13.2
SNP_A-1782332	G	G	257	85	224	112	5.912	1.50E-02	rs12597524	16	7153100	p13.2
SNP_A-1782335	T	T	297	117	267	151	5.89	0.0152	rs12599645	16	7153393	p13.2
SNP_A-1839760	C	C	266	150	292	122	4.089	4.32E-02	rs11077152	16	7213118	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1808658	C	C	238	162	209	199	5.595	1.80E-02	rs12446629	16	7221329	p13.2
SNP_A-2149525	T	T	216	152	196	188	4.444	3.50E-02	rs8051142	16	7223015	p13.2
SNP_A-1784758	C	C	221	155	195	187	4.572	3.25E-02	rs2346611	16	7223473	p13.2
SNP_A-2037870	G	G	245	171	213	205	5.306	2.13E-02	rs7197955	16	7223623	p13.2
SNP_A-1803834	T	T	309	91	331	67	4.397	3.60E-02	rs7200633	16	7223937	p13.2
SNP_A-1802650	G	G	243	169	211	201	5.023	2.50E-02	rs11077158	16	7224553	p13.2
SNP_A-2189330	G	G	339	75	369	49	6.704	9.60E-03	rs11077164	16	7236885	p13.2
SNP_A-1874863	G	G	287	97	262	124	4.432	3.53E-02	rs4347647	16	7243446	p13.2
SNP_A-1958621	C	G	204	180	213	175	4.969	0.0258	rs4786141	16	7249036	p13.2
SNP_A-2265496	G	G	242	90	224	116	3.882	4.88E-02	rs1922593	16	7253357	p13.2
SNP_A-2128214	T	T	290	74	280	104	4.7	3.02E-02	rs8051518	16	7260516	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1715195	C	C	282	108	251	135	4.783	2.88E-02	rs1922585	16	7286620	p13.2
SNP_A-2254301	C	C	329	71	312	96	4.115	4.25E-02	rs9674069	16	7291470	p13.2
SNP_A-2208093	G	G	409	1	400	8	5.54	1.86E-02	rs17143361	16	7295259	p13.2
SNP_A-1782551	G	C	199	197	217	165	3.891	4.85E-02	rs17671597	16	7321107	p13.2
SNP_A-1840508	A	A	378	34	364	52	4.012	4.52E-02	rs8050137	16	7391457	p13.2
SNP_A-2201818	C	C	313	81	350	54	7.341	6.70E-03	rs6500960	16	7403377	p13.2
SNP_A-2297932	C	C	325	93	364	58	10.301	1.30E-03	rs7196364	16	7411668	p13.2
SNP_A-2191750	C	C	351	19	328	32	3.957	4.67E-02	rs12596133	16	7531196	p13.2
SNP_A-1783059	T	T	312	70	342	42	8.371	0.0038	rs10492760	16	7557329	p13.2
SNP_A-2023331	G	G	240	134	222	168	4.196	4.05E-02	rs2881629	16	7596300	p13.2
SNP_A-1689426	T	G	204	188	230	184	4.654	0.031	rs763650	16	7729020	p13.2
SNP_A-2285576	G	G	290	130	309	101	4.123	4.23E-02	rs8049782	16	7928299	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1838468	C	C	242	126	207	147	4.074	0.0436	rs9939373	16	7949355	p13.2
SNP_A-1804896	C	C	279	53	284	80	4.063	4.38E-02	rs3105662	16	8038365	p13.2
SNP_A-1891422	T	T	375	15	396	6	4.248	3.93E-02	rs17672815	16	8052565	p13.2
SNP_A-2246507	G	G	358	32	377	17	5.063	2.44E-02	rs17145276	16	8118121	p13.2
SNP_A-2255307	A	A	189	179	211	149	3.866	4.93E-02	rs4787138	16	8145879	p13.2
SNP_A-1796821	G	G	275	143	304	114	4.725	2.97E-02	rs8053877	16	8277804	p13.2
SNP_A-2241863	C	C	237	171	209	205	4.789	0.0286	rs29572	16	8310753	p13.2
SNP_A-1857393	T	T	251	61	282	42	5.083	2.42E-02	rs12325361	16	8358553	p13.2
SNP_A-2182119	C	C	304	36	336	22	4.518	3.35E-02	rs7185211	16	8622275	p13.2
SNP_A-2283547	A	A	319	87	341	61	5.281	2.16E-02	rs1345300	16	8671929	p13.2
SNP_A-2151476	C	C	329	49	347	31	4.529	3.33E-02	rs1731083	16	8731651	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1898544	T	T	380	0	346	4	4.367	3.66E-02	rs3743814	16	8820482	p13.2
SNP_A-2111104	T	T	251	141	219	165	3.979	4.61E-02	rs899254	16	8895689	p13.2
SNP_A-2177472	C	C	384	12	368	24	4.32	3.77E-02	rs2437716	16	8938605	p13.2
SNP_A-1781452	A	A	253	143	294	110	7.298	6.90E-03	rs9923450	16	9009889	p13.2
SNP_A-2066157	G	G	361	27	383	7	12.41	4.00E-04	rs2941346	16	9167191	p13.2
SNP_A-2148240	G	G	394	4	390	12	4.001	4.55E-02	rs8063623	16	9187171	p13.2
SNP_A-2099165	G	G	285	119	260	154	5.513	0.0189	rs2965858	16	9207809	p13.2
SNP_A-2248054	A	A	292	110	258	142	6.16	1.31E-02	rs2965859	16	9209582	p13.2
SNP_A-1784199	C	C	193	149	224	120	5.425	1.98E-02	rs2175242	16	9238393	p13.2
SNP_A-1844208	-	C	199	199	244	168	6.95	8.40E-03	rs8055943	16	9241708	p13.2
SNP_A-2140599	A	A	208	204	241	171	5.329	2.10E-02	rs2965926	16	9243757	p13.2
SNP_A-1919534	T	T	208	206	243	173	5.585	1.81E-02	rs2314293	16	9244119	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2277597	C	C	226	190	259	161	4.622	3.16E-02	rs1355269	16	9254288	p13.2
SNP_A-2023233	A	A	308	18	285	31	4.186	4.08E-02	rs1876954	16	9256780	p13.2
SNP_A-2004531	G	G	219	193	257	151	8.142	0.0043	rs2965905	16	9258321	p13.2
SNP_A-1784259	T	T	280	100	247	137	7.822	5.20E-03	rs8048358	16	9297536	p13.2
SNP_A-2268649	C	C	318	80	338	58	4.112	4.26E-02	rs2077437	16	9308671	p13.2
SNP_A-2022459	C	T	219	169	195	185	4.636	3.13E-02	rs837346	16	9320854	p13.2
SNP_A-1784336	G	G	216	126	191	159	5.265	0.0218	rs40129	16	9346193	p13.2
SNP_A-1802960	G	G	287	81	271	109	4.394	0.0361	rs4781064	16	9367687	p13.2
SNP_A-2096063	G	G	368	20	325	37	6.845	8.90E-03	rs9302525	16	9422903	p13.2
SNP_A-2053559	C	C	375	37	340	64	8.854	2.90E-03	rs12449072	16	9424955	p13.2
SNP_A-2182983	C	C	392	28	367	43	3.873	4.91E-02	rs4553629	16	9470025	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2263525	C	C	298	110	273	145	5.778	1.62E-02	rs12932123	16	9534237	p13.2
SNP_A-1934550	C	C	272	124	240	168	8.453	3.60E-03	rs9932623	16	9552891	p13.2
SNP_A-2203489	G	G	233	149	260	122	4.169	4.12E-02	rs17546809	16	9552925	p13.2
SNP_A-1957977	C	C	270	104	229	143	9.521	0.002	rs9932870	16	9553178	p13.2
SNP_A-2141905	T	T	222	168	249	139	4.282	0.0385	rs7191870	16	9558314	p13.2
SNP_A-1866469	T	G	216	178	206	178	5.579	1.82E-02	rs917955	16	9561469	p13.2
SNP_A-2208135	G	G	370	38	351	65	7.501	6.20E-03	rs12919014	16	9592915	p13.2
SNP_A-1718057	G	A	203	153	197	185	5.457	0.0195	rs1074042	16	9621355	p13.2
SNP_A-2234525	G	G	391	1	342	6	4.246	3.93E-02	rs13332245	16	9942566	p13.2
SNP_A-2246713	C	C	326	52	349	29	7.315	6.80E-03	rs3104704	16	9975453	p13.2
SNP_A-1785004	C	C	266	150	296	122	4.479	3.43E-02	rs3852745	16	10156361	p13.2
SNP_A-2062818	A	A	374	18	351	31	4.05	4.42E-02	rs17762273	16	10264902	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2270421	G	G	349	31	364	10	11.025	9.00E-04	rs11074946	16	11033404	p13.13
SNP_A-1937303	G	G	379	41	400	16	11.512	7.00E-04	rs9932114	16	11042404	p13.13
SNP_A-2082932	T	T	331	37	350	18	7.094	7.70E-03	rs11647011	16	11115591	p13.13
SNP_A-2075824	C	C	352	44	352	24	5.368	2.05E-02	rs17684919	16	11142346	p13.13
SNP_A-2115786	C	A	175	151	172	146	3.886	0.0487	rs248843	16	11195929	p13.13
SNP_A-2173401	A	A	271	113	237	147	6.722	9.50E-03	rs9935384	16	11314679	p13.13
SNP_A-1879324	A	A	347	19	320	34	5.14	2.34E-02	rs17674570	16	11713367	p13.13
SNP_A-2225432	A	A	375	25	382	12	4.587	3.22E-02	rs1583001	16	11732613	p13.13
SNP_A-1892148	A	A	302	48	305	27	5.424	1.99E-02	rs2160184	16	11801555	p13.13
SNP_A-2276971	G	G	272	124	238	152	5.062	2.45E-02	rs40311	16	11870691	p13.13
SNP_A-1786093	C	C	293	107	320	80	5.088	0.0241	rs830700	16	12163648	p13.13
SNP_A-2254212	G	G	410	4	420	0	4.078	4.35E-02	rs16959129	16	12291215	p13.13
SNP_A-2238675	C	C	410	8	413	1	5.436	1.97E-02	rs746312	16	12338030	p13.13
SNP_A-2195742	G	G	357	39	353	61	4.465	3.46E-02	rs12448282	16	12399512	p13.13
SNP_A-2279890	A	A	201	153	230	128	4.153	4.16E-02	rs7206244	16	12472733	p13.13
SNP_A-1813297	C	C	351	43	323	63	4.855	0.0276	rs9806891	16	12497677	p13.13
SNP_A-2211610	C	C	416	0	399	5	5.18	2.28E-02	rs3902080	16	12502276	p13.12
SNP_A-1851576	G	G	196	164	232	138	5.13	0.0235	rs6498314	16	12523670	p13.12
SNP_A-1684304	C	C	298	34	303	55	4.023	4.49E-02	rs10492794	16	12606289	p13.12
SNP_A-2082689	T	T	218	180	244	146	4.929	0.0264	rs3843707	16	12904289	p13.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2272577	T	T	318	92	289	119	4.836	2.79E-02	rs150077	16	13176302	p13.12
SNP_A-1958191	G	G	391	11	381	25	5.554	0.0184	rs16961475	16	13236021	p13.12
SNP_A-1787250	G	G	325	77	290	102	5.358	0.0206	rs8048671	16	13243945	p13.12
SNP_A-1787259	G	G	354	32	325	53	6.344	0.0118	rs2903251	16	13252951	p13.12
SNP_A-1719857	G	G	341	63	372	42	5.426	1.98E-02	rs10521098	16	13322188	p13.12
SNP_A-2182331	G	G	346	74	366	52	4.398	3.60E-02	rs7199581	16	13484711	p13.12
SNP_A-1793434	C	C	353	51	339	73	4.108	4.27E-02	rs16962265	16	13545495	p13.12
SNP_A-1787029	G	G	299	97	313	67	5.48	1.92E-02	rs8055219	16	13660885	p13.12
SNP_A-1804532	C	C	336	74	357	49	5.698	1.70E-02	rs17794609	16	13698966	p13.12
SNP_A-1704757	C	C	292	98	310	72	4.432	3.53E-02	rs7185124	16	13717133	p13.12
SNP_A-1788012	A	A	265	119	291	95	3.902	0.0482	rs3136189	16	13942202	p13.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1788025	C	C	244	114	268	90	3.949	4.69E-02	rs3136202	16	13945675	p13.12
SNP_A-2314721	T	T	300	28	332	16	4.305	3.80E-02	rs4781571	16	14109664	p13.12
SNP_A-2256746	G	G	376	22	402	10	5.128	0.0235	rs226781	16	14209509	p13.12
SNP_A-2087455	A	A	198	116	188	154	4.42	3.55E-02	rs9922431	16	15566149	p13.11
SNP_A-2314840	A	A	318	44	322	70	4.769	2.90E-02	rs9929598	16	15787511	p13.11
SNP_A-2004568	A	A	361	47	333	67	4.56	0.0327	rs6498577	16	15817751	p13.11
SNP_A-2082426	A	A	340	34	319	53	4.813	2.82E-02	rs35598	16	16066524	p13.11
SNP_A-2211595	G	G	383	33	336	54	7.31	6.90E-03	rs35621	16	16076109	p13.11
SNP_A-2077638	C	C	364	0	326	4	4.438	3.52E-02	rs7201980	16	16171338	p13.11
SNP_A-2080496	C	C	246	72	288	54	5.009	0.0252	rs11649230	16	16767302	p12.3
SNP_A-2107529	T	T	363	11	361	23	4.11	4.26E-02	rs16968559	16	17178134	p12.3
SNP_A-2004578	A	A	274	84	275	131	7.289	6.90E-03	rs1364319	16	17451248	p12.3
SNP_A-1876243	C	C	407	7	420	0	7.162	7.40E-03	rs7206267	16	17603923	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2043638	G	G	409	11	419	3	4.687	0.0304	rs11075381	16	17819527	p12.3
SNP_A-2144282	T	T	394	0	398	4	3.94	4.71E-02	rs4432258	16	17857597	p12.3
SNP_A-1899713	G	G	346	16	311	27	3.86	4.94E-02	rs6498783	16	18514090	p12.3
SNP_A-1861336	G	G	369	35	398	18	6.375	1.16E-02	rs2641906	16	18686949	p12.3
SNP_A-1797245	G	G	406	6	416	0	6.102	0.0135	rs7189195	16	19030244	p12.3
SNP_A-1789817	C	C	408	8	420	0	8.155	0.0043	rs16971597	16	19036276	p12.3
SNP_A-1857732	T	T	331	73	298	108	8.494	3.60E-03	rs9652587	16	19141590	p12.3
SNP_A-2180888	C	C	308	12	316	0	12.078	5.00E-04	rs9931300	16	19516503	p12.3
SNP_A-2051736	G	G	374	4	394	0	4.191	4.06E-02	rs1925522	16	19986315	p12.3
SNP_A-2037295	C	C	368	18	334	30	4.005	4.54E-02	rs12600233	16	20352824	p12.3
SNP_A-2004610	G	G	349	49	329	71	4.618	3.16E-02	rs1948567	16	20533937	p12.3
SNP_A-2192673	G	G	357	51	332	76	5.828	1.58E-02	rs163238	16	20555388	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2187087	T	T	228	62	292	52	4.185	4.08E-02	rs12448683	16	20658848	p12.3
SNP_A-2262688	C	C	328	6	310	16	4.957	2.60E-02	rs2301770	16	20709673	p12.3
SNP_A-2178664	T	T	386	8	378	20	5.207	2.25E-02	rs215884	16	21632420	p12.2
SNP_A-2113822	T	T	368	22	349	37	4.297	3.82E-02	rs215902	16	21636715	p12.2
SNP_A-1823659	T	T	270	102	253	131	3.973	4.62E-02	rs754290	16	22131010	p12.1
SNP_A-2308056	A	A	266	120	291	91	5.087	0.0241	rs1424194	16	22713810	p12.1
SNP_A-2238837	A	A	271	131	297	105	4.055	0.0441	rs4783490	16	22714326	p12.1
SNP_A-1868394	C	C	283	137	311	109	4.507	3.38E-02	rs8057434	16	22717765	p12.1
SNP_A-1821398	G	G	356	30	373	17	3.972	4.63E-02	rs7199670	16	22782739	p12.1
SNP_A-2149749	C	C	268	102	308	80	5.013	0.0252	rs208568	16	22863477	p12.1
SNP_A-2179238	G	G	263	81	290	54	6.718	9.50E-03	rs208585	16	22888259	p12.1
SNP_A-2047852	A	A	305	77	328	52	5.675	0.0172	rs430208	16	23365986	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1791977	A	A	227	67	286	54	4.87	2.73E-02	rs194802	16	23681565	p12.1
SNP_A-2245767	A	A	295	79	315	49	7.553	6.00E-03	rs2334246	16	23706433	p12.1
SNP_A-2032580	C	C	233	117	214	156	5.828	1.58E-02	rs7200013	16	23717869	p12.1
SNP_A-1829353	G	G	316	88	349	59	7.339	6.70E-03	rs187747	16	23727924	p12.1
SNP_A-1950983	T	T	299	69	335	47	5.957	0.0147	rs11649174	16	23732386	p12.1
SNP_A-1785710	A	A	188	184	233	169	4.291	3.83E-02	rs1468130	16	23790049	p12.1
SNP_A-1860175	C	C	249	157	280	128	4.763	2.91E-02	rs8051531	16	23852120	p12.1
SNP_A-2140826	C	C	184	124	227	107	4.705	3.01E-02	rs120908	16	23871593	p12.1
SNP_A-2112564	G	T	209	177	203	173	5.041	2.48E-02	rs2340988	16	23891757	p12.1
SNP_A-2238056	T	T	215	147	207	193	4.491	3.41E-02	rs1014632	16	24007245	p12.1
SNP_A-1886429	T	T	393	5	371	13	3.94	4.72E-02	rs198142	16	24106351	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2123442	G	G	272	52	246	78	6.505	1.08E-02	rs2189292	16	24248913	p12.1
SNP_A-1850989	G	G	307	89	286	126	6.797	9.10E-03	rs4788012	16	24252833	p12.1
SNP_A-2313384	T	T	300	56	336	40	4.161	4.14E-02	rs17828058	16	24259476	p12.1
SNP_A-2253651	T	T	337	17	341	5	6.478	0.0109	rs9929236	16	24265745	p12.1
SNP_A-1682460	G	G	288	98	274	130	4.432	3.53E-02	rs723722	16	24271265	p12.1
SNP_A-1889420	C	C	357	25	365	13	3.857	4.95E-02	rs1000014	16	24325037	p12.1
SNP_A-2132532	T	T	268	120	272	88	3.91	4.80E-02	rs7198632	16	24602841	p12.1
SNP_A-2309660	G	G	416	4	422	0	4.038	4.45E-02	rs12596320	16	24725006	p12.1
SNP_A-1792436	T	T	351	47	331	73	6.175	1.30E-02	rs10521128	16	24736679	p12.1
SNP_A-1792439	T	T	398	4	414	0	4.14	0.0419	rs2287785	16	24737226	p12.1
SNP_A-2293654	G	G	325	25	354	14	3.892	4.85E-02	rs8051275	16	24769228	p12.1
SNP_A-1929701	G	G	295	49	347	29	7.933	4.90E-03	rs11647310	16	24970794	p12.1
SNP_A-2263609	G	G	343	43	379	29	3.911	4.80E-02	rs10852280	16	24977046	p12.1
SNP_A-2198000	T	T	231	177	270	150	5.092	0.024	rs1076974	16	25142172	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1793057	G	G	298	98	335	77	4.368	3.66E-02	rs2979750	16	25536860	p12.1
SNP_A-1856119	T	T	375	33	374	18	4.095	4.30E-02	rs4787751	16	25661823	p12.1
SNP_A-2307950	T	T	364	8	367	19	4.237	3.96E-02	rs16975182	16	25682787	p12.1
SNP_A-2101139	T	T	224	140	199	169	4.177	4.10E-02	rs4346208	16	25933085	p12.1
SNP_A-2314120	A	G	201	199	229	171	4.522	3.35E-02	rs4520841	16	26007616	p12.1
SNP_A-2265826	C	T	221	151	192	188	7.479	6.20E-03	rs8062398	16	26050287	p12.1
SNP_A-2293122	G	G	253	165	213	205	7.758	0.0053	rs3803711	16	26055412	p12.1
SNP_A-1912940	A	A	321	91	343	65	5.043	0.0247	rs11074779	16	26358944	p12.1
SNP_A-1868959	G	G	402	0	378	10	10.494	1.20E-03	---	16	26409836	p12.1
SNP_A-1736913	A	A	248	134	234	170	4.057	4.40E-02	rs7206138	16	26471242	p12.1
SNP_A-2122492	T	T	243	155	285	129	5.408	0.02	rs237128	16	26545758	p12.1
SNP_A-2071365	T	T	323	41	331	17	9.674	0.0019	rs1866500	16	26654495	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2212223	T	T	382	0	378	6	6.016	1.42E-02	rs161162	16	26741340	p12.1
SNP_A-2004659	G	G	326	78	358	52	6.653	9.90E-03	rs4427807	16	27100192	p12.1
SNP_A-1794254	G	G	324	70	352	48	5.216	0.0224	rs1980151	16	27100220	p12.1
SNP_A-1952272	A	A	206	158	220	122	4.407	3.58E-02	rs8059713	16	27214145	p12.1
SNP_A-2131810	C	C	267	63	282	36	7.554	6.00E-03	rs11074861	16	27341819	p12.1
SNP_A-2100189	T	T	240	110	210	136	4.725	2.97E-02	rs232086	16	27444697	p12.1
SNP_A-2025441	G	G	395	23	411	11	4.534	0.0332	rs9934589	16	27677395	p11.2
SNP_A-2148778	T	T	247	109	279	85	4.828	2.80E-02	rs1363749	16	27734882	p11.2
SNP_A-1817486	T	T	216	108	187	143	6.913	0.0086	rs205360	16	28023856	p11.2
SNP_A-2116403	A	A	267	107	251	149	6.519	1.07E-02	rs205362	16	28024612	p11.2
SNP_A-1885352	C	C	288	120	255	151	5.547	1.85E-02	rs245733	16	28056946	p11.2
SNP_A-1887512	C	C	235	99	224	138	5.564	0.0183	rs13329799	16	28097074	p11.2
SNP_A-2183423	C	C	302	118	262	150	6.581	0.0103	rs7199187	16	28101161	p11.2
SNP_A-2228023	T	T	278	104	245	139	7.118	0.0076	rs7498882	16	28124106	p11.2
SNP_A-2254335	G	G	299	117	266	156	7.456	0.0063	rs9927626	16	28124175	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2048251	G	G	254	118	222	144	4.683	3.05E-02	rs9931708	16	28136132	p11.2
SNP_A-2219037	T	T	293	119	263	145	4.16	4.14E-02	rs7184239	16	28147436	p11.2
SNP_A-2242031	C	C	281	103	259	147	8.034	4.60E-03	rs4075049	16	28150790	p11.2
SNP_A-2264073	A	A	303	87	283	123	6.535	0.0106	rs9938394	16	28154169	p11.2
SNP_A-1946508	T	T	287	107	234	130	6.446	0.0111	rs12708708	16	28158034	p11.2
SNP_A-2290151	G	G	290	104	259	143	7.829	5.10E-03	rs9673810	16	28165885	p11.2
SNP_A-1751811	G	G	279	109	250	142	5.908	1.51E-02	rs3922800	16	28166303	p12.1
SNP_A-1897355	C	C	291	117	260	154	6.752	9.40E-03	rs11860882	16	28171013	p11.2
SNP_A-2175910	G	G	287	105	260	144	7.262	7.00E-03	rs7204045	16	28172173	p11.2
SNP_A-2211105	G	G	415	5	422	0	5.054	0.0246	rs12596913	16	28817123	p11.2
SNP_A-1818137	C	C	390	6	404	0	6.167	1.30E-02	rs8055762	16	29231193	p11.2
SNP_A-2148299	T	T	354	38	335	67	8.409	3.70E-03	rs17708876	16	31305967	p11.2
SNP_A-2051792	C	C	332	24	329	11	4.477	0.0344	rs1857943	16	31845956	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1797773	T	T	219	151	203	187	3.917	4.78E-02	—	16	45268370	q11.2
SNP_A-1926582	C	C	331	59	343	39	4.213	4.01E-02	rs8051205	16	46801986	q12.1
SNP_A-2298476	A	A	297	115	324	88	4.765	2.90E-02	rs1510981	16	47738037	q12.1
SNP_A-2242458	C	C	297	87	322	64	4.508	3.37E-02	rs1543957	16	47739397	q12.1
SNP_A-1918993	A	A	249	101	268	70	6.111	0.0134	rs11649147	16	47763796	q12.1
SNP_A-1898319	A	A	272	146	233	189	8.512	3.50E-03	rs9935379	16	47884582	q12.1
SNP_A-2286727	C	C	340	42	303	59	4.456	3.48E-02	rs9931454	16	47895583	q12.1
SNP_A-2208962	A	A	284	72	254	98	5.627	0.0177	rs12598711	16	47896001	q12.1
SNP_A-2072879	T	T	364	6	368	0	6.016	1.42E-02	rs152650	16	47976346	q12.1
SNP_A-2029634	A	A	202	154	247	129	6.177	0.0129	rs27807	16	47995541	q12.1
SNP_A-1783909	C	C	254	164	284	134	4.693	3.03E-02	rs152655	16	48001470	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284693	A	A	307	19	337	9	4.378	3.64E-02	rs16947390	16	48009588	q12.1
SNP_A-2230938	T	T	256	160	290	128	5.668	1.73E-02	rs193908	16	48078809	q12.1
SNP_A-2223770	C	C	252	134	280	100	6.367	1.16E-02	rs8048073	16	48329245	q12.1
SNP_A-1906880	T	T	394	12	394	26	4.922	2.65E-02	rs17284377	16	48471546	q12.1
SNP_A-1799471	G	G	313	99	341	71	5.811	1.59E-02	rs7191151	16	48779594	q12.1
SNP_A-2077095	T	T	356	52	369	29	6.641	0.01	rs9922376	16	48998680	q12.1
SNP_A-1927822	C	C	343	35	382	22	4.203	4.04E-02	rs731660	16	48998709	q12.1
SNP_A-2176598	A	A	396	4	386	0	3.88	4.89E-02	rs16946548	16	49089672	q12.1
SNP_A-1668342	A	A	372	20	375	39	5.534	1.86E-02	rs1858274	16	49102436	q12.1
SNP_A-2281659	A	A	356	52	379	31	6.028	0.0141	rs7199568	16	49121148	q12.1
SNP_A-2230131	C	C	276	130	303	101	4.895	0.0269	rs11649409	16	49440555	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1835691	T	T	319	5	332	0	5.163	2.31E-02	rs16949114	16	49534656	q12.1
SNP_A-2295582	C	C	385	25	397	11	5.624	0.0177	rs16949212	16	49607489	q12.1
SNP_A-1941663	A	A	335	39	379	25	4.624	0.0315	rs7194997	16	49937069	q12.1
SNP_A-2185512	T	T	279	113	308	80	7.055	7.90E-03	rs8053990	16	49951049	q12.1
SNP_A-1800283	G	G	339	21	363	9	5.425	1.98E-02	rs1111195	16	49973827	q12.1
SNP_A-1888319	A	A	389	19	407	9	3.901	4.83E-02	rs6499001	16	49975910	q12.1
SNP_A-1902746	C	C	397	21	412	10	4.162	4.13E-02	rs9944345	16	49976666	q12.1
SNP_A-1854816	T	T	231	117	267	97	4.114	4.25E-02	rs4784274	16	50011624	q12.1
SNP_A-2276002	G	G	264	120	289	91	5.095	0.024	rs4783832	16	50147492	q12.1
SNP_A-1941618	T	T	278	134	301	107	3.919	4.77E-02	rs8062350	16	50154538	q12.1
SNP_A-1790254	G	G	277	137	315	107	6.052	1.39E-02	rs2173454	16	50156370	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2134548	T	T	375	39	403	19	7.828	5.10E-03	rs2380107	16	50156761	q12.1
SNP_A-1781436	T	T	261	119	286	94	4.077	4.35E-02	rs1909338	16	50162643	q12.1
SNP_A-2094671	G	G	354	34	378	16	7.221	7.20E-03	rs16950037	16	50168062	q12.1
SNP_A-1958357	A	A	300	46	327	29	4.875	2.73E-02	rs17340242	16	50169726	q12.1
SNP_A-2235542	A	A	315	91	343	65	5.52	1.88E-02	rs2647979	16	50180936	q12.1
SNP_A-1800678	C	C	246	128	281	105	4.406	3.58E-02	rs1903608	16	50319100	q12.1
SNP_A-2168131	A	A	314	64	359	45	5.462	1.94E-02	rs3912519	16	50440889	q12.1
SNP_A-2247649	T	T	332	42	289	63	6.517	1.07E-02	rs1079926	16	50943957	q12.1
SNP_A-1940659	G	G	276	58	254	80	4.42	3.55E-02	rs1420537	16	51011068	q12.1
SNP_A-2228401	G	G	329	85	294	116	6.728	9.50E-03	rs3095668	16	51021188	q12.1
SNP_A-1848576	G	G	279	85	274	118	4.379	3.64E-02	rs42483	16	51022084	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1801456	A	A	301	37	265	59	7.038	8.00E-03	rs16951525	16	51274992	q12.2
SNP_A-2098356	A	G	210	172	199	181	4.111	4.26E-02	rs4784253	16	51351022	q12.2
SNP_A-1863482	A	A	347	25	372	12	5.248	2.20E-02	rs4784294	16	51695553	q12.2
SNP_A-2287349	A	A	292	110	324	86	4.523	3.34E-02	rs7187949	16	51965983	q12.2
SNP_A-1921742	C	C	269	87	247	115	4.769	2.90E-02	rs16952242	16	52031751	q12.2
SNP_A-2066673	T	T	228	82	209	119	7.135	0.0076	rs16952251	16	52040639	q12.2
SNP_A-2172181	G	A	202	188	211	169	4.132	4.21E-02	rs7204496	16	52054099	q12.2
SNP_A-2004713	A	A	294	118	259	157	7.727	5.40E-03	rs3809634	16	52095658	q12.2
SNP_A-1819739	C	C	351	49	380	26	8.16	0.0043	rs3095634	16	52098891	q12.2
SNP_A-1724214	G	G	178	158	213	139	3.979	4.61E-02	rs1124390	16	52186426	q12.1
SNP_A-1880261	C	C	350	56	325	89	8.359	0.0038	rs16952362	16	52195389	q12.2
SNP_A-2103911	T	T	322	44	300	68	5.916	1.50E-02	rs17803830	16	52200361	q12.2
SNP_A-1833662	G	G	321	23	321	11	4.024	4.49E-02	rs12447949	16	52238738	q12.2
SNP_A-1865177	C	C	385	7	405	1	4.762	2.91E-02	rs12444305	16	52258865	q12.2
SNP_A-2175099	G	G	395	21	402	10	3.945	0.047	rs16952522	16	52364999	q12.2
SNP_A-1781198	G	G	297	49	268	82	9.779	0.0018	rs9972717	16	52408805	q12.2
SNP_A-1922921	G	G	361	49	382	32	4.142	4.18E-02	rs16952728	16	52572144	q12.2
SNP_A-2004715	A	A	251	141	280	108	5.937	1.48E-02	rs8607713	16	52626966	q12.2
SNP_A-1805866	T	T	243	131	284	98	7.861	5.10E-03	rs2192872	16	52632128	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172261	G	G	313	83	271	111	6.812	9.10E-03	rs12149010	16	52665424	q12.2
SNP_A-2296169	G	G	356	36	352	20	4.073	0.0436	rs16953294	16	52859853	q12.2
SNP_A-1917478	C	C	317	49	346	30	5.704	1.69E-02	rs1866686	16	52886075	q12.2
SNP_A-1660977	A	A	251	133	279	107	4.291	3.83E-02	rs4784289	16	52892858	q12.2
SNP_A-2218898	T	C	173	161	202	130	10.727	1.10E-03	rs1562797	16	52900570	q12.2
SNP_A-2206536	G	G	336	40	372	22	6.639	0.01	rs1420294	16	52982472	q12.2
SNP_A-1782036	A	A	345	57	374	38	4.848	2.77E-02	rs16953500	16	53000379	q12.2
SNP_A-2226007	A	A	346	58	379	37	5.97	0.0146	rs13333140	16	53000587	q12.2
SNP_A-2119829	G	G	340	32	373	19	4.32	3.77E-02	rs16953503	16	53000724	q12.2
SNP_A-1802749	A	A	206	132	235	109	4.05	4.42E-02	rs933515	16	53078282	q12.2
SNP_A-2279638	C	C	304	106	255	125	4.726	2.97E-02	rs4555155	16	53445422	q12.2
SNP_A-1795427	C	C	372	40	347	59	4.472	3.45E-02	rs11076062	16	53576401	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2071024	A	A	300	110	268	140	5.398	2.02E-02	rs7198804	16	53667443	q12.2
SNP_A-1875186	C	C	311	29	354	10	11.232	8.00E-04	rs8045342	16	53695539	q12.2
SNP_A-1803186	T	T	348	56	385	35	6.406	0.0114	rs4783875	16	53700692	q12.2
SNP_A-2258853	G	G	280	108	306	84	4.148	4.17E-02	rs11645874	16	53711514	q12.2
SNP_A-1839095	C	C	270	148	238	180	5.138	2.34E-02	rs12597556	16	53763591	q12.2
SNP_A-1861589	G	G	396	14	387	5	3.965	0.0465	rs2631526	16	53798397	q12.2
SNP_A-1883686	T	T	378	26	385	13	4.353	3.69E-02	rs16954719	16	53886762	q12.2
SNP_A-1679038	G	G	366	34	392	20	4.345	3.71E-02	rs10521301	16	54070062	q12.2
SNP_A-1787253	G	G	225	147	191	171	4.455	3.48E-02	rs8050810	16	54180581	q12.2
SNP_A-2219495	C	C	236	180	270	148	5.402	0.0201	rs4578642	16	54222260	q12.2
SNP_A-1808163	T	T	212	150	243	121	5.21	2.25E-02	rs40612	16	54231821	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1803968	A	A	386	10	411	3	4.155	4.15E-02	rs36006	16	54297556	q12.2
SNP_A-1730383	C	C	231	171	267	145	4.619	3.16E-02	rs933516	16	54299686	q12.2
SNP_A-1934319	C	C	367	13	356	4	4.395	0.0361	rs4784567	16	54342924	q12.2
SNP_A-1881005	C	C	316	80	362	48	10.881	0.001	rs1585144	16	54442071	q12.2
SNP_A-1668032	G	G	327	29	306	54	8.205	4.20E-03	rs728571	16	54992695	q12.2
SNP_A-2062295	C	C	231	185	257	155	4.013	4.51E-02	rs6499837	16	55011482	q12.2
SNP_A-2292450	G	G	242	172	281	137	6.854	8.80E-03	rs9937444	16	55101059	q12.2
SNP_A-1804616	T	T	243	149	268	118	4.776	2.89E-02	rs370151	16	55118995	q12.2
SNP_A-1743595	T	T	382	20	402	8	5.575	1.82E-02	rs10521326	16	55150323	q12.2
SNP_A-2314533	G	G	384	20	354	50	14.077	2.00E-04	rs4784708	16	55261415	q12.2
SNP_A-1859880	G	G	373	45	391	29	3.879	4.89E-02	rs12596236	16	55288111	q12.2
SNP_A-2251626	C	C	328	74	300	104	6.3	0.0121	rs8044813	16	55303808	q13
SNP_A-2045445	G	G	281	71	255	97	5.285	2.15E-02	rs4784725	16	55318709	q13
SNP_A-2081648	G	G	310	52	285	75	5.21	2.25E-02	rs4783957	16	55329954	q13
SNP_A-1793291	C	C	314	42	297	23	4.121	4.23E-02	rs9927884	16	55389803	q13
SNP_A-1820053	A	A	399	17	388	34	5.778	1.62E-02	rs2399560	16	55414472	q13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1880497	G	G	223	163	255	139	3.968	4.64E-02	rs4784730	16	55422750	q13
SNP_A-1942114	T	T	329	79	296	110	6.822	9.00E-03	rs7184439	16	55425305	q13
SNP_A-1810870	C	C	311	59	287	81	4.415	0.0356	rs4368156	16	55431773	q13
SNP_A-1804292	A	A	287	59	270	82	4.219	4.00E-02	rs1529930	16	55448401	q13
SNP_A-2072813	G	G	293	95	271	121	3.967	4.64E-02	rs4329913	16	55462933	q13
SNP_A-1933956	A	A	386	20	375	35	4.23	3.97E-02	rs1114156	16	56057283	q13
SNP_A-2242851	A	A	297	29	298	54	6.544	1.05E-02	rs598486	16	56069126	q13
SNP_A-1944186	G	G	397	15	365	33	7.854	5.10E-03	rs17546208	16	56097012	q13
SNP_A-1913883	T	T	194	178	236	146	7.131	0.0076	rs1450353	16	56186072	q13
SNP_A-2246673	C	C	415	1	411	9	6.4	0.0114	rs2303784	16	56510881	q13
SNP_A-2004755	G	G	355	55	377	35	5.101	2.39E-02	rs1820237	16	56876699	q21
SNP_A-2229294	A	A	265	151	291	123	4.072	0.0436	rs1895522	16	57016539	q21
SNP_A-1792372	T	T	269	149	300	120	4.811	2.83E-02	rs4784938	16	57025354	q21
SNP_A-1870732	C	C	283	129	306	94	6.215	1.27E-02	rs3743566	16	57103286	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2102286	C	C	334	48	316	68	3.942	4.71E-02	rs961141	16	57542779	q21
SNP_A-2047416	A	A	395	7	397	1	4.485	3.42E-02	rs16960677	16	57549993	q21
SNP_A-1920614	G	G	285	99	321	75	5.266	0.0218	rs7203567	16	57761475	q21
SNP_A-1790339	C	C	218	130	232	90	6.709	9.60E-03	rs7186765	16	57938934	q21
SNP_A-2309860	A	A	216	142	250	118	4.559	0.0327	rs1580380	16	58005768	q21
SNP_A-1782636	C	C	317	89	332	60	5.747	1.65E-02	rs8057882	16	58098574	q21
SNP_A-1806619	A	A	246	92	249	57	6.666	9.80E-03	rs1482244	16	58150418	q21
SNP_A-1721816	G	G	377	25	402	12	5.195	2.27E-02	rs1107277	16	58262690	q21
SNP_A-1919070	T	T	249	151	225	181	3.882	4.88E-02	rs12921587	16	58291334	q21
SNP_A-1842219	A	A	332	44	347	27	4.396	3.60E-02	rs16961439	16	58418302	q21
SNP_A-2148410	G	G	269	45	292	28	4.846	2.77E-02	rs7198976	16	58487027	q21
SNP_A-2232372	C	C	312	40	305	17	8.041	4.60E-03	rs11866759	16	58938377	q21
SNP_A-1712749	C	C	211	189	256	158	6.867	8.80E-03	rs725517	16	59183739	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2087968	A	A	254	154	213	173	4.097	4.30E-02	rs10454068	16	59665041	q21
SNP_A-2167988	A	A	236	138	215	175	5.019	2.51E-02	rs12935144	16	59665165	q21
SNP_A-2238925	G	G	396	4	410	0	4.12	0.0424	rs7192431	16	60786238	q21
SNP_A-1909503	C	C	340	24	321	39	4.096	4.30E-02	---	16	60840996	q21
SNP_A-1808468	G	G	240	86	227	123	6.068	0.0138	rs964933	16	60905699	q21
SNP_A-1839855	G	G	355	45	378	28	4.636	3.13E-02	rs4265819	16	61174718	q21
SNP_A-2152384	C	C	346	12	373	1	9.977	1.60E-03	rs1593128	16	61210318	q21
SNP_A-1788677	C	C	289	85	328	56	8.299	4.00E-03	rs7201164	16	61224753	q21
SNP_A-1844864	G	G	340	10	318	2	4.735	2.96E-02	rs12443929	16	61307523	q21
SNP_A-2054124	A	A	309	85	352	56	8.52	3.50E-03	rs8048343	16	61359866	q21
SNP_A-1808877	C	C	306	44	337	25	6.526	0.0106	rs7498526	16	61366450	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796983	A	A	326	40	335	21	5.903	1.51E-02	rs7193666	16	61429222	q21
SNP_A-1809196	G	G	322	90	299	119	4.833	2.79E-02	rs10492812	16	61682164	q21
SNP_A-2155497	A	A	324	88	301	117	4.906	2.68E-02	rs198024	16	61719745	q21
SNP_A-1912551	G	G	371	23	374	42	4.972	0.0258	rs16965834	16	61910285	q21
SNP_A-2027615	T	T	341	39	366	24	4.326	3.75E-02	rs6498907	16	62161082	q21
SNP_A-1899731	T	T	302	98	275	127	4.996	2.54E-02	rs2965967	16	62182990	q21
SNP_A-2181329	C	C	409	5	414	0	5.03	2.49E-02	rs9783755	16	62357594	q21
SNP_A-1863682	A	A	345	59	370	40	4.477	0.0344	rs1529925	16	62608274	q21
SNP_A-1825690	G	G	320	58	299	79	3.931	4.74E-02	rs7205676	16	62728684	q21
SNP_A-2129003	C	C	387	11	380	30	8.692	3.20E-03	rs1423752	16	62770907	q21
SNP_A-1874814	G	G	221	129	177	145	4.64	3.12E-02	rs6498953	16	63220023	q21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1786702	A	A	412	4	422	0	4.077	4.35E-02	rs9925140	16	63429728	q21
SNP_A-1934049	C	C	202	136	237	107	6.199	1.28E-02	rs6416685	16	63439993	q21
SNP_A-2284002	T	T	347	57	362	38	4.098	4.29E-02	rs8052187	16	63460948	q21
SNP_A-1810664	T	T	381	13	399	5	3.846	0.0499	rs16968049	16	63499845	q21
SNP_A-1795551	G	G	340	42	346	24	4.771	2.89E-02	rs399975	16	63512665	q21
SNP_A-1932106	C	C	352	52	378	34	4.615	3.17E-02	rs6498970	16	63641805	q21
SNP_A-2254074	A	A	380	20	377	3	12.072	5.00E-04	rs11644282	16	63776188	q21
SNP_A-2061367	C	C	369	47	344	72	6.129	1.33E-02	rs1423796	16	63908802	q22.1
SNP_A-1811086	C	C	393	19	365	33	4.563	0.0327	rs861749	16	63960722	q22.1
SNP_A-2141131	G	G	301	115	276	144	4.311	3.79E-02	rs1327486	16	64249982	q22.1
SNP_A-2158131	T	T	284	126	323	97	6.157	1.31E-02	rs567959	16	64310551	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1811316	C	C	271	133	251	167	4.382	3.63E-02	rs4785849	16	64336186	q22.1
SNP_A-1690709	A	A	260	140	237	173	4.421	3.55E-02	rs4303504	16	64383668	q21
SNP_A-1907175	A	A	368	18	365	37	6.254	0.0124	rs16969587	16	64542431	q22.1
SNP_A-1811665	C	C	387	11	403	3	4.816	2.82E-02	rs1110522	16	64590238	q22.1
SNP_A-1813192	A	A	356	18	366	8	3.985	4.59E-02	rs1111223	16	64642288	q22.1
SNP_A-1811763	A	A	295	47	266	64	3.89	4.86E-02	rs7205951	16	64674213	q22.1
SNP_A-2066604	C	C	367	19	388	8	4.939	0.0263	rs11859284	16	64705074	q22.1
SNP_A-1822134	G	G	335	25	309	39	3.91	4.80E-02	rs235115	16	64770006	q22.1
SNP_A-1818773	C	C	210	118	225	87	4.808	2.83E-02	rs446170	16	64782081	q22.1
SNP_A-1834123	A	A	292	72	314	52	4.019	4.50E-02	rs2057827	16	64827396	q22.1
SNP_A-2217414	G	G	318	52	351	27	9.455	2.10E-03	rs233523	16	64842280	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1840878	A	A	280	114	256	146	4.933	0.0263	rs233537	16	64852265	q22.1
SNP_A-2139083	A	A	410	0	410	4	3.981	4.60E-02	rs9937567	16	64922254	q22.1
SNP_A-1703419	T	T	367	31	352	54	6.458	1.10E-02	rs9302570	16	65081588	q21
SNP_A-2261162	C	C	206	172	247	149	4.943	2.62E-02	rs37178	16	65146271	q22.1
SNP_A-2032712	T	T	193	183	221	149	5.328	2.10E-02	rs8051710	16	65230684	q22.1
SNP_A-1895683	C	C	216	126	235	99	3.946	0.047	rs2305311	16	65317183	q22.1
SNP_A-1672072	G	G	380	18	357	31	4.04	4.44E-02	rs163417	16	66051580	q22.1
SNP_A-1729794	C	C	338	62	372	42	5.235	2.21E-02	rs28171	16	66347740	q22.1
SNP_A-2217770	T	T	331	23	353	9	6.744	9.40E-03	rs8051517	16	66985590	q22.1
SNP_A-2065656	A	A	330	84	309	109	3.909	4.80E-02	rs6499203	16	67442894	q22.1
SNP_A-2125886	A	A	297	51	339	37	3.924	4.76E-02	rs13332128	16	67748921	q22.1
SNP_A-1924611	A	A	332	54	359	33	6.078	0.0137	rs9933019	16	67786353	q22.1
SNP_A-2236835	G	G	338	54	360	34	5.234	2.22E-02	rs17691749	16	67845516	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2197617	G	G	354	0	326	4	4.316	0.0378	rs7195995	16	68401528	q22.1
SNP_A-2195311	G	G	381	21	398	10	4.23	3.97E-02	---	16	68681849	q22.1
SNP_A-1734894	T	T	334	68	369	45	6.249	0.0124	rs10500549	16	69037272	q22.1
SNP_A-2114519	G	G	218	148	242	114	5.527	1.87E-02	rs2303792	16	69088867	q22.1
SNP_A-2231822	G	T	202	172	213	171	6.812	9.10E-03	rs2303791	16	69089255	q22.1
SNP_A-2147239	G	A	209	191	233	167	8.852	2.90E-03	rs4985534	16	69160721	q22.1
SNP_A-1894735	C	C	198	192	229	159	5.348	0.0207	rs7193968	16	69230453	q22.1
SNP_A-2180508	T	C	231	185	220	196	5.894	0.0152	rs2168608	16	69240195	q22.1
SNP_A-1841506	C	C	328	14	309	27	4.636	3.13E-02	rs2456147	16	69463141	q22.2
SNP_A-2158902	G	G	350	58	323	79	4.258	3.91E-02	rs235997	16	69841694	q22.2
SNP_A-2056103	C	C	390	6	359	15	4.515	3.36E-02	rs3096372	16	69846190	q22.2
SNP_A-2246412	C	C	396	4	389	15	6.411	1.13E-02	rs3096378	16	69887800	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1940702	T	T	397	11	382	22	3.936	4.73E-02	rs9936567	16	69931799	q22.2
SNP_A-2209063	C	C	322	10	349	1	7.981	4.70E-03	rs8060811	16	69993655	q22.2
SNP_A-2269774	A	A	288	78	258	104	5.341	2.08E-02	rs7203957	16	69993900	q22.2
SNP_A-1815236	G	G	308	70	290	96	4.531	3.33E-02	rs8056712	16	70572907	q22.2
SNP_A-2135197	T	T	269	85	249	111	4.171	4.11E-02	rs7205297	16	70583032	q22.2
SNP_A-2227101	A	A	366	8	338	18	4.519	3.35E-02	rs8058214	16	70603806	q22.2
SNP_A-1815914	T	T	268	126	317	95	8.055	4.50E-03	rs17621111	16	71708905	q22.3
SNP_A-1865033	C	C	367	39	391	23	4.811	2.83E-02	rs9923643	16	71950949	q22.3
SNP_A-2228606	A	A	361	37	372	22	3.959	4.66E-02	rs4888152	16	71959831	q22.3
SNP_A-1824857	G	G	374	44	354	66	4.945	2.62E-02	rs7189175	16	72002289	q22.3
SNP_A-2273633	A	A	373	45	353	67	4.868	2.74E-02	rs7189738	16	72002607	q22.3
SNP_A-1830682	T	T	408	4	420	0	4.097	4.29E-02	rs170594	16	72361456	q22.3
SNP_A-2142689	A	A	372	34	390	18	5.343	2.08E-02	rs2892190	16	72456853	q22.3
SNP_A-2054240	A	A	238	142	186	184	11.657	6.00E-04	rs9928459	16	72619837	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1799514	C	C	398	10	387	21	4.057	4.40E-02	rs9935622	16	72667325	q22.3
SNP_A-2179398	G	G	308	46	261	61	4.48	3.43E-02	rs17336867	16	72894605	q22.3
SNP_A-2296440	C	T	218	186	210	186	3.91	4.80E-02	rs933724	16	73464892	q22.3
SNP_A-1827749	C	C	320	66	296	88	4.073	0.0436	rs11149776	16	73484021	q22.3
SNP_A-2265109	A	A	231	163	264	128	6.405	0.0114	rs11149785	16	73535371	q22.3
SNP_A-2231240	G	G	332	32	376	20	4.164	4.13E-02	rs16951478	16	73558895	q22.3
SNP_A-2217051	A	A	305	69	339	51	4.162	4.13E-02	rs7205074	16	73777510	q22.3
SNP_A-1858642	G	G	316	18	331	7	5.164	2.31E-02	rs3094015	16	73988174	q23.1
SNP_A-1857755	A	A	334	82	359	61	3.967	4.64E-02	rs8051241	16	74180494	q23.1
SNP_A-1933585	G	G	236	178	264	150	3.958	4.66E-02	rs16943791	16	74602810	q23.1
SNP_A-1859096	G	G	318	36	310	60	5.751	1.65E-02	---	16	74773650	q23.1
SNP_A-2233107	G	G	353	63	330	86	4.325	3.76E-02	rs4888483	16	74794135	q23.1
SNP_A-2114095	A	A	349	61	330	84	4.161	4.14E-02	rs4888484	16	74794288	q23.1
SNP_A-2144157	C	C	279	73	312	52	5.171	0.023	---	16	74818662	q23.1
SNP_A-1956587	C	C	306	108	335	79	5.809	1.59E-02	rs16944012	16	74818708	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2076127	T	T	211	157	245	133	4.388	3.62E-02	rs7500315	16	74822026	q23.1
SNP_A-2283307	C	C	223	147	253	119	4.833	2.79E-02	rs7189026	16	74826020	q23.1
SNP_A-2174036	A	A	278	54	308	36	4.924	2.65E-02	rs4506927	16	75103790	q23.1
SNP_A-2058212	A	A	363	51	343	71	3.845	0.0499	rs7194038	16	75168196	q23.1
SNP_A-1918249	G	G	244	94	244	64	4.312	0.0378	rs2029962	16	75500301	q23.1
SNP_A-1818727	A	A	336	48	314	78	7.806	5.20E-03	rs1874531	16	75511507	q23.1
SNP_A-1928792	C	C	258	62	226	92	7.954	4.80E-03	rs284000	16	75580200	q23.1
SNP_A-1818835	T	T	396	14	384	30	5.984	0.0144	rs17680016	16	75588826	q23.1
SNP_A-2282130	A	A	286	132	315	105	4.471	3.45E-02	rs2220233	16	75607795	q23.1
SNP_A-2297559	C	C	231	99	189	115	4.337	0.0373	rs285004	16	75633100	q23.1
SNP_A-2112164	A	A	338	68	322	94	4.44	3.51E-02	rs9930943	16	75643536	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2088427	T	T	227	165	248	124	6.226	0.0126	rs1502433	16	75644602	q23.1
SNP_A-2294085	T	T	335	63	321	87	4.015	4.51E-02	rs17768717	16	75653688	q23.1
SNP_A-2197440	C	G	185	161	189	155	4.881	2.71E-02	rs1847161	16	75655297	q23.1
SNP_A-1943267	A	G	209	199	240	168	8.288	4.00E-03	rs285027	16	75658433	q23.1
SNP_A-2072080	A	A	177	173	215	133	8.907	0.0028	rs1385749	16	75669390	q23.1
SNP_A-1831686	G	G	185	181	211	135	7.848	5.10E-03	rs2020432	16	75669720	q23.1
SNP_A-2194644	G	G	253	123	233	159	5.088	0.0241	rs2232504	16	75786367	q23.1
SNP_A-2202467	C	C	259	159	304	112	11.743	6.00E-04	rs8061864	16	75804807	q23.1
SNP_A-2300834	G	G	195	161	211	109	8.753	3.10E-03	rs6564411	16	75805004	q23.1
SNP_A-2046979	C	C	359	25	374	12	4.869	2.73E-02	rs5027712	16	75811467	q23.1
SNP_A-2149432	T	T	367	37	381	21	4.671	3.07E-02	rs4888611	16	75811987	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2028971	A	A	344	36	342	18	5.469	1.94E-02	rs7187205	16	75815134	q23.1
SNP_A-2021748	A	A	300	88	343	61	7.448	6.40E-03	rs17769245	16	75821218	q23.1
SNP_A-2285182	G	G	337	69	362	50	3.884	0.0487	rs13335140	16	75851750	q23.1
SNP_A-1819160	C	C	240	134	228	178	5.209	2.25E-02	rs2162957	16	75854694	q23.1
SNP_A-2273129	A	A	342	66	355	43	4.972	0.0258	rs1582982	16	75859857	q23.1
SNP_A-1888625	A	A	324	58	345	39	4.376	3.65E-02	rs17701900	16	75868793	q23.1
SNP_A-2056004	A	A	324	50	351	33	4.431	3.53E-02	rs12930139	16	75870453	q23.1
SNP_A-2134289	C	C	346	68	366	48	4.01	4.52E-02	rs17712844	16	75871485	q23.1
SNP_A-1803882	T	T	309	57	352	42	4.044	4.43E-02	rs12925274	16	75878016	q23.1
SNP_A-2308363	C	G	190	142	187	153	10.052	0.0015	rs11643318	16	75880258	q23.1
SNP_A-1915694	G	G	203	183	232	156	4.079	4.34E-02	rs8061205	16	75916480	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1819356	C	C	235	167	205	197	4.518	3.35E-02	rs10514416	16	75947951	q23.1
SNP_A-2057422	T	T	331	79	359	51	7.167	7.40E-03	rs12596244	16	75987305	q23.1
SNP_A-1725504	T	T	398	4	414	0	4.14	0.0419	-	16	76126508	q23.1
SNP_A-1819688	C	C	395	21	409	9	5.039	2.48E-02	rs1841799	16	76130963	q23.1
SNP_A-1934780	C	C	385	15	376	28	4.017	4.50E-02	rs17773487	16	76320383	q23.1
SNP_A-1880355	G	G	366	26	320	56	13.733	2.00E-04	rs8058965	16	76324371	q23.1
SNP_A-1894398	C	C	319	13	329	29	5.277	2.16E-02	rs2966072	16	76382949	q23.1
SNP_A-2033338	T	T	292	102	268	134	5.288	2.15E-02	rs2914451	16	76389377	q23.1
SNP_A-2052451	A	C	212	196	231	181	5.295	2.14E-02	rs376490	16	76463159	q23.1
SNP_A-1832901	T	T	230	182	263	157	3.976	4.62E-02	rs6564480	16	76469184	q23.1
SNP_A-2125830	T	T	337	63	308	92	6.73	9.50E-03	rs440488	16	76483631	q23.1
SNP_A-1926279	C	C	300	112	321	81	5.567	0.0183	rs8060873	16	76582995	q23.1
SNP_A-1930216	G	G	300	76	318	42	9.978	1.60E-03	rs8059798	16	76583082	q23.1
SNP_A-1800309	A	A	260	82	286	48	10.037	0.0015	rs2042988	16	76586621	q23.1
SNP_A-2104362	A	A	284	100	307	77	3.884	4.88E-02	rs7192645	16	76590709	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1946727	A	A	358	48	346	72	4.831	2.80E-02	rs1073111	16	76685815	q23.1
SNP_A-2142931	A	A	222	168	256	140	4.918	2.66E-02	rs12716848	16	76725159	q23.1
SNP_A-2027197	T	T	318	86	288	110	4.379	3.64E-02	rs13338697	16	76725407	q23.1
SNP_A-2004880	A	G	196	188	221	163	5.696	1.70E-02	rs4888748	16	76730655	q23.1
SNP_A-2290850	A	G	212	202	249	171	9.244	2.40E-03	rs12716853	16	76746301	q23.1
SNP_A-1869547	C	C	355	15	342	32	6.37	1.16E-02	rs12923504	16	76760660	q23.1
SNP_A-1707649	C	C	308	44	310	68	4.229	3.97E-02	rs1502431	16	76853904	q23.1
SNP_A-1857468	C	C	364	48	391	29	5.577	1.82E-02	rs12149458	16	76960647	q23.1
SNP_A-2139854	G	G	324	72	346	46	6.431	0.0112	rs11649021	16	76963690	q23.1
SNP_A-2037509	C	C	312	86	344	62	5.374	2.04E-02	rs9930967	16	76974815	q23.1
SNP_A-2025375	C	C	273	57	300	40	4.103	4.28E-02	rs8062393	16	76975312	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2214567	C	C	385	7	397	1	4.639	3.13E-02	rs11150078	16	77024205	q23.1
SNP_A-1847897	T	T	391	21	410	8	6.235	1.25E-02	rs2738669	16	77058446	q23.1
SNP_A-1945721	C	C	277	111	318	76	9.331	0.0023	rs2667547	16	77060170	q23.1
SNP_A-1805186	C	C	260	64	299	41	7.378	0.0066	rs2247099	16	77061446	q23.1
SNP_A-1923676	C	C	390	22	412	10	4.984	2.56E-02	rs16947620	16	77063449	q23.1
SNP_A-2259917	C	C	302	76	331	49	7.155	7.50E-03	rs11150082	16	77094198	q23.1
SNP_A-2147446	A	A	278	124	309	93	6.066	0.0138	rs12443611	16	77094647	q23.1
SNP_A-1820937	G	G	393	19	396	8	4.415	0.0356	rs1397927	16	77095856	q23.1
SNP_A-1832167	A	A	347	55	369	31	7.369	0.0066	rs9923611	16	77115270	q23.1
SNP_A-1732656	G	G	343	59	372	42	3.862	4.94E-02	rs10514412	16	77122049	q23.1
SNP_A-2187106	G	G	344	54	374	32	6.802	9.10E-03	rs11150085	16	77124595	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2093293	C	C	414	2	407	13	8.107	4.40E-03	rs16948069	16	77144008	q23.1
SNP_A-1720899	C	C	260	142	224	190	9.443	2.10E-03	rs166673	16	77163307	q23.1
SNP_A-1860438	C	C	320	30	306	48	4.444	3.50E-02	rs4578663	16	77175432	q23.1
SNP_A-2132478	G	G	335	79	356	58	3.857	4.95E-02	rs11150093	16	77255388	q23.1
SNP_A-2274168	A	A	357	43	313	59	4.39	3.62E-02	rs16948408	16	77330454	q23.1
SNP_A-2216272	A	A	315	65	330	40	6.169	1.30E-02	rs2216730	16	77390953	q23.1
SNP_A-2264852	C	C	331	33	315	53	5.026	2.50E-02	rs9926713	16	77460102	q23.1
SNP_A-2179016	C	C	334	66	297	91	5.969	0.0146	rs12924818	16	77523698	q23.1
SNP_A-2265013	C	C	301	51	292	76	4.705	3.01E-02	rs2656659	16	77604802	q23.1
SNP_A-2100007	A	G	213	173	226	170	11.742	6.00E-04	rs8047597	16	77614257	q23.1
SNP_A-1930554	C	C	351	43	351	21	6.936	8.40E-03	rs16949276	16	77619263	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1904756	C	-	216	148	178	178	6.338	0.0118	rs16949333	16	77628853	q23.1
SNP_A-1822076	T	T	273	125	250	164	5.961	0.0146	rs10492901	16	77715952	q23.1
SNP_A-2088531	A	A	262	126	242	158	4.218	4.00E-02	rs8047289	16	77716326	q23.1
SNP_A-1887349	A	A	361	47	382	26	6.635	0.01	rs7200634	16	77733838	q23.1
SNP_A-1945383	C	C	255	157	222	186	4.716	2.99E-02	rs6564654	16	77778054	q23.1
SNP_A-1822200	C	C	285	117	317	89	5.487	1.92E-02	rs382888	16	77787324	q23.1
SNP_A-1753485	A	A	292	108	340	72	10.671	1.10E-03	rs4416461	16	77789477	q23.1
SNP_A-1741671	T	T	312	66	357	45	6.267	0.0123	rs8062335	16	77789801	q23.1
SNP_A-1822223	G	G	232	150	253	119	4.35	3.70E-02	rs441004	16	77794331	q23.1
SNP_A-1787986	T	T	208	160	238	134	4.296	3.82E-02	rs270443	16	77850583	q23.1
SNP_A-2135909	A	A	242	146	274	110	7.026	8.00E-03	rs906796	16	77870519	q23.1
SNP_A-2267344	G	G	293	71	316	50	4.508	3.37E-02	rs9927057	16	77918304	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2069005	A	A	222	150	264	130	4.43	3.53E-02	rs4888024	16	77996875	q23.1
SNP_A-2209843	T	T	346	30	326	50	5.595	1.80E-02	rs4380067	16	78060110	q23.1
SNP_A-1787741	A	A	397	21	375	43	8.189	4.20E-03	rs1862718	16	78075910	q23.1
SNP_A-1822641	A	A	224	108	227	77	3.99	0.0458	rs11150175	16	78138388	q23.1
SNP_A-1906063	A	A	377	35	342	58	7.216	7.20E-03	rs12598123	16	78144242	q23.1
SNP_A-1866687	G	G	274	136	305	105	5.647	1.75E-02	rs250151	16	78148780	q23.1
SNP_A-2192894	C	C	379	23	360	42	6.042	0.014	rs3784926	16	78163046	q23.1
SNP_A-2094618	T	T	192	166	235	133	7.836	5.10E-03	rs1541692	16	78166193	q23.1
SNP_A-1815488	A	A	344	68	321	95	5.249	2.20E-02	rs4889036	16	78398593	q23.1
SNP_A-2290208	C	C	310	66	277	85	3.982	4.60E-02	rs8063424	16	78424987	q23.1
SNP_A-1800030	C	C	331	87	302	116	5.471	1.93E-02	rs11150223	16	78427326	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1881744	T	T	365	23	366	6	9.634	0.0019	rs9933396	16	78434745	q23.1
SNP_A-1844947	A	A	292	88	264	112	4.269	3.88E-02	rs13338370	16	78463707	q23.1
SNP_A-1822852	A	A	407	5	402	14	4.275	3.87E-02	rs16951680	16	78526624	q23.2
SNP_A-2072002	C	C	256	104	241	135	4.128	4.22E-02	rs4888055	16	78533723	q23.2
SNP_A-1843873	T	C	207	161	180	170	4.241	0.0395	rs4145109	16	78722136	q23.2
SNP_A-2132386	C	C	332	22	343	9	5.625	0.0177	rs9941114	16	78750531	q23.2
SNP_A-2078281	G	G	309	93	279	117	4.229	3.97E-02	rs1878817	16	78905732	q23.2
SNP_A-2161617	G	G	304	84	267	113	6.584	0.0103	rs8051119	16	78907824	q23.2
SNP_A-1710660	T	T	332	66	366	46	4.987	2.55E-02	rs10514450	16	79096239	q23.1
SNP_A-1705525	A	A	389	13	409	5	3.881	4.88E-02	rs10514452	16	79157051	q23.1
SNP_A-1874537	T	T	332	24	371	9	8.208	4.20E-03	rs17823453	16	79202670	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2286750	C	C	308	102	262	132	7.243	7.10E-03	rs11150354	16	79758152	q23.2
SNP_A-2305712	A	A	300	104	275	139	6.007	0.0143	rs11150355	16	79758262	q23.2
SNP_A-1913207	A	A	310	88	281	117	5.525	1.87E-02	rs12598266	16	79758298	q23.2
SNP_A-2190359	G	G	273	95	237	117	4.554	3.28E-02	rs8058196	16	79813363	q23.2
SNP_A-2181970	T	T	394	6	404	0	6.106	0.0135	rs16955031	16	79916968	q23.2
SNP_A-2245289	G	G	296	46	278	80	9.378	2.20E-03	rs11641025	16	80142574	q23.2
SNP_A-2243407	G	G	220	134	230	102	3.86	4.95E-02	rs12444183	16	80330710	q23.2
SNP_A-2127470	G	G	199	131	180	172	5.797	0.0161	rs8045964	16	80374234	q23.2
SNP_A-1802064	C	C	291	81	319	61	4.017	4.50E-02	rs4584816	16	80378704	q23.2
SNP_A-2188133	G	G	365	51	345	75	5.116	2.37E-02	rs12598194	16	80382555	q23.2
SNP_A-2225221	G	G	340	52	323	79	5.876	0.0154	rs4078270	16	80533181	q23.2
SNP_A-2128538	A	A	344	50	309	71	5.269	2.17E-02	rs7205376	16	80539343	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1909241	A	A	352	0	316	4	4.426	3.54E-02	rs13333826	16	80620283	q23.3
SNP_A-2161300	G	G	352	18	387	5	8.377	0.0038	rs2955163	16	80685698	q23.3
SNP_A-1842058	C	C	257	105	227	133	5.148	2.33E-02	---	16	80729220	q23.3
SNP_A-1824689	A	A	394	0	373	5	5.246	2.20E-02	rs6564985	16	80741499	q23.3
SNP_A-2283846	C	C	255	119	228	154	5.913	1.50E-02	rs1862820	16	80765783	q23.3
SNP_A-1883057	A	A	386	32	404	12	9.496	2.10E-03	rs16957495	16	81070559	q23.3
SNP_A-1807448	G	G	361	21	395	9	5.718	1.68E-02	rs964745	16	81098307	q23.3
SNP_A-1825312	A	A	359	59	321	95	10.534	1.20E-03	rs3852718	16	81174137	q23.3
SNP_A-2248939	C	C	327	85	294	122	8.348	3.90E-03	rs12922128	16	81258003	q23.3
SNP_A-1825525	A	A	200	132	230	104	5.409	0.02	rs1000078	16	81340088	q23.3
SNP_A-1825554	A	A	205	169	225	137	4.082	4.33E-02	rs1350889	16	81342188	q23.3
SNP_A-1670632	A	A	384	18	378	36	5.872	0.0154	rs9319570	16	81358964	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2210009	G	G	286	44	304	24	6.425	0.0112	---	16	81359031	q23.3
SNP_A-2234137	T	C	219	195	234	188	5.831	1.57E-02	rs11646849	16	81374752	q23.3
SNP_A-2089961	T	T	387	9	372	20	4.449	0.0349	rs4783271	16	81375386	q23.3
SNP_A-1825587	T	T	361	37	367	17	7.209	7.30E-03	rs7186123	16	81379253	q23.3
SNP_A-1808960	C	C	376	42	360	62	4.175	4.10E-02	rs2549161	16	81413514	q23.3
SNP_A-1873771	A	A	347	13	337	25	3.93	4.74E-02	rs13332819	16	81699561	q23.3
SNP_A-2237239	T	T	310	50	338	34	4.062	4.39E-02	rs7203313	16	81752913	q23.3
SNP_A-1879482	C	C	294	60	291	37	4.484	3.42E-02	rs8055236	16	81769899	q23.3
SNP_A-1837441	T	T	374	44	393	27	4.536	0.0332	rs12103261	16	81785167	q23.3
SNP_A-2082866	C	C	338	74	315	101	4.957	2.60E-02	rs9938206	16	81948789	q23.3
SNP_A-1839458	T	A	227	179	203	195	3.855	4.96E-02	rs4782797	16	82056041	q23.3
SNP_A-1889700	A	T	215	165	202	196	4.194	4.06E-02	rs7206140	16	82076478	q23.3
SNP_A-1729848	G	G	321	55	320	82	4.459	3.47E-02	rs2967321	16	82083251	q23.3
SNP_A-2167357	A	A	407	11	419	3	4.727	2.97E-02	rs9928829	16	82171278	q23.3
SNP_A-1826501	C	C	370	12	318	24	5.738	0.0166	rs17686717	16	82181483	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2067087	T	T	302	116	341	81	8.565	3.40E-03	rs13337331	16	82239454	q23.3
SNP_A-1955604	A	A	301	111	336	82	6.238	1.25E-02	rs11859365	16	82241446	q23.3
SNP_A-2062801	C	C	348	44	336	66	4.485	3.42E-02	rs16961182	16	82245578	q23.3
SNP_A-2085866	G	G	232	164	209	197	4.092	4.31E-02	rs11644204	16	82268563	q23.3
SNP_A-2106922	T	T	361	57	338	78	4.019	4.50E-02	rs374476	16	82314650	q23.3
SNP_A-2266782	G	G	240	100	181	119	7.446	6.40E-03	rs691231	16	82344914	q23.3
SNP_A-1658626	C	C	371	25	369	45	5.322	2.11E-02	rs10514546	16	82400490	q23.3
SNP_A-1703009	C	C	317	85	293	121	7.061	7.90E-03	rs3852734	16	82483395	q23.3
SNP_A-1648478	C	C	230	166	268	144	4.146	4.17E-02	rs10514551	16	82483767	q23.3
SNP_A-1812228	C	C	278	68	272	102	5.785	1.62E-02	rs11149610	16	82528396	q23.3
SNP_A-1664262	T	T	230	172	266	148	4.237	0.0395	rs1462035	16	82549716	q23.3
SNP_A-1901722	G	G	307	73	338	48	6.609	0.0101	rs4782885	16	82639297	q23.3
SNP_A-1827804	G	G	213	177	243	141	6.003	0.0143	rs4082806	16	82723121	q24.1
SNP_A-1900824	G	G	277	101	264	138	5.307	0.0212	rs8063197	16	82802897	q24.1
SNP_A-2242959	A	A	322	72	297	101	5.851	1.56E-02	rs437218	16	82851668	q24.1
SNP_A-2123173	T	T	320	58	280	100	13.826	2.00E-04	rs244783	16	82917556	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1912451	C	C	333	31	360	18	4.238	0.0395	rs16963588	16	83002192	q24.1
SNP_A-1668318	T	T	334	68	360	48	4.378	3.64E-02	rs889713	16	83199024	q23.3
SNP_A-1828442	C	C	383	25	403	13	4.221	3.99E-02	---	16	83326525	q24.1
SNP_A-1755602	G	G	376	26	367	47	5.975	1.45E-02	rs10514591	16	83458314	q23.3
SNP_A-2085892	C	C	318	70	333	47	4.784	0.0287	rs11862286	16	83540736	q24.1
SNP_A-1684846	T	T	375	7	372	18	4.77	2.90E-02	rs10514600	16	83604196	q23.3
SNP_A-2299809	A	A	248	150	229	187	4.423	3.55E-02	rs12449263	16	83799710	q24.1
SNP_A-2304648	C	C	217	185	252	154	5.427	1.98E-02	rs2086829	16	83882068	q24.1
SNP_A-2099146	A	A	336	30	338	50	4.368	3.66E-02	rs8044680	16	83895156	q24.1
SNP_A-2177031	C	C	270	100	233	125	5.303	2.13E-02	rs7186617	16	83934389	q24.1
SNP_A-2293507	C	C	319	49	307	71	4.13	4.21E-02	rs2254248	16	84378807	q24.1
SNP_A-2200227	G	G	307	47	278	72	6.667	9.80E-03	rs9923691	16	84381691	q24.1
SNP_A-1912808	G	G	334	36	314	54	4.212	4.01E-02	rs1800647	16	84391661	q24.1
SNP_A-2202352	A	A	321	69	348	50	4.042	4.44E-02	rs11117418	16	84524028	q24.1
SNP_A-2152772	A	G	204	196	230	172	5.432	1.98E-02	rs2361763	16	84550635	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2305741	G	G	298	78	337	61	3.852	4.97E-02	rs4843326	16	84560559	q24.1
SNP_A-2293459	T	T	238	156	267	127	4.637	3.13E-02	rs2280381	16	84576134	q24.1
SNP_A-1834825	A	A	406	12	394	26	5.333	2.09E-02	---	16	84607271	q24.1
SNP_A-1944534	A	A	386	10	399	3	3.94	4.72E-02	rs12598047	16	84610535	q24.1
SNP_A-1736479	G	G	375	25	397	13	4.294	3.83E-02	rs721004	16	84685671	q24.1
SNP_A-2223731	A	A	308	30	304	48	3.898	4.84E-02	rs1693977	16	84848317	q24.1
SNP_A-2240887	C	C	237	119	224	154	4.198	4.05E-02	rs8049795	16	84952620	q24.1
SNP_A-2197984	C	C	209	171	255	143	6.644	9.90E-03	rs10438600	16	84953757	q24.1
SNP_A-1830306	G	G	373	17	369	7	3.934	4.73E-02	rs4843938	16	84967605	q24.1
SNP_A-1828708	C	C	370	0	340	4	4.327	3.75E-02	rs16941179	16	85000919	q24.1
SNP_A-2179615	C	C	326	38	346	22	4.84	2.78E-02	rs4843390	16	85126325	q24.1
SNP_A-1883514	A	A	209	109	188	154	7.948	4.80E-03	rs1019574	16	85283302	q24.1
SNP_A-2282875	T	T	248	138	272	106	5.221	0.0223	rs6539960	16	85293074	q24.1
SNP_A-2199886	G	G	377	9	362	22	5.751	1.65E-02	rs9933247	16	85357175	q24.1
SNP_A-2029543	A	A	300	82	276	122	8.519	3.50E-03	rs6539972	16	85377438	q24.1
SNP_A-1791480	G	G	240	86	234	118	4.105	4.28E-02	rs8046759	16	85377837	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2004984	C	C	383	17	404	4	8.53	3.50E-03	rs7190924	15	85408403	q24.1
SNP_A-1830938	A	A	392	22	410	10	4.861	0.0275	rs3922878	16	85412205	q24.1
SNP_A-1906886	G	G	398	20	414	6	7.849	5.10E-03	rs9935731	16	85415442	q24.1
SNP_A-2096624	G	G	389	19	411	9	4.003	4.54E-02	rs9926438	16	85424896	q24.1
SNP_A-1903238	A	A	404	4	418	0	4.118	0.0424	rs4372696	16	85511986	q24.1
SNP_A-2004986	G	G	396	4	395	13	4.687	0.0304	rs4240783	16	85534715	q24.1
SNP_A-1665132	T	G	207	169	213	195	4.127	4.22E-02	rs1568391	16	85736783	q24.1
SNP_A-2087060	A	A	231	121	198	146	4.788	0.0287	rs12445088	16	85763963	q24.2
SNP_A-1758475	T	C	191	149	200	186	4.623	0.0315	rs908979	16	85781471	q24.1
SNP_A-1733270	C	C	300	80	286	108	4.253	3.92E-02	rs9308365	16	85790959	q24.1
SNP_A-1693701	G	G	301	83	295	117	4.861	0.0275	rs9308366	16	85790998	q24.1
SNP_A-1826064	C	C	346	4	366	14	4.893	0.027	rs16943059	16	86172026	q24.2
SNP_A-2247423	C	C	308	4	334	0	4.309	3.79E-02	—	16	86365888	q24.2
SNP_A-1691954	A	A	280	48	262	84	9.942	1.60E-03	rs6539977	16	86605331	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2301947	C	C	391	5	393	15	4.827	2.80E-02	rs2287358	16	87773456	q24.3
SNP_A-2272182	G	G	338	38	376	18	8.749	3.10E-03	rs11542633	16	87867000	q24.3
SNP_A-2116615	C	C	344	26	297	45	7.441	6.40E-03	rs11649210	16	88334734	q24.3
SNP_A-1879141	C	C	240	158	221	197	4.58	3.23E-02	rs9893847	17	435793	p13.3
SNP_A-1882409	A	A	184	140	218	118	4.535	0.0332	rs11247571	17	855252	p13.3
SNP_A-2242026	T	T	218	186	261	159	5.665	1.73E-02	rs4790458	17	1187943	p13.3
SNP_A-1843989	A	A	231	183	265	155	4.607	3.18E-02	rs4790084	17	1229729	p13.3
SNP_A-1781411	T	T	373	1	353	9	6.757	9.30E-03	rs7504032	17	1310077	p13.3
SNP_A-2215873	A	G	190	148	179	169	4.022	4.49E-02	rs10852873	17	1551330	p13.3
SNP_A-1914204	C	C	267	137	306	104	7.129	0.0076	rs12051752	17	1584527	p13.3
SNP_A-1835807	T	T	288	74	251	93	4.245	3.94E-02	rs4790285	17	1598447	p13.3
SNP_A-2111908	G	G	266	112	242	148	5.932	0.0149	rs7216863	17	1631703	p13.3
SNP_A-1903520	C	C	286	132	313	105	4.293	3.83E-02	rs4790822	17	1636586	p13.3
SNP_A-2216935	A	A	249	131	266	90	7.393	6.50E-03	rs8073376	17	1638864	p13.3
SNP_A-2242060	G	G	275	141	306	110	5.483	1.92E-02	rs3809875	17	1650293	p13.3
SNP_A-2169813	A	A	317	61	345	37	7.041	8.00E-03	rs2230931	17	1741930	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805868	A	A	350	44	385	29	4.256	3.91E-02	rs7359575	17	1820903	p13.3
SNP_A-1816766	G	G	389	17	381	35	6.193	1.28E-02	rs11871926	17	2031462	p13.3
SNP_A-2215503	T	T	319	77	343	53	5.301	2.13E-02	rs2165796	17	2392654	p13.3
SNP_A-2157227	A	G	218	176	216	170	9.939	1.60E-03	rs7209945	17	2421679	p13.3
SNP_A-2161243	G	G	245	91	221	129	7.517	6.10E-03	rs7209407	17	2454999	p13.3
SNP_A-1947071	G	G	282	112	232	150	10.192	0.0014	rs11078280	17	2484041	p13.3
SNP_A-1948812	C	C	224	114	191	155	8.781	3.00E-03	rs7209748	17	2485263	p13.3
SNP_A-2035058	A	A	312	14	300	36	9.766	0.0018	rs2317297	17	2523841	p13.3
SNP_A-1828665	T	T	300	100	339	69	7.988	4.70E-03	rs7223411	17	2523927	p13.3
SNP_A-2259682	C	C	214	118	257	93	6.417	1.13E-02	rs11109451	17	2538781	p13.3
SNP_A-2236528	G	G	188	140	222	120	4.067	4.37E-02	rs7209772	17	2555238	p13.3
SNP_A-1853339	G	G	342	50	327	73	4.557	3.28E-02	rs4790365	17	2661001	p13.3
SNP_A-2038774	T	T	249	171	279	143	4.197	4.05E-02	rs6502656	17	2828041	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2148411	G	G	377	43	394	26	4.563	0.0327	rs4325604	17	3065758	p13.3
SNP_A-1645058	C	C	365	39	355	59	4.099	4.29E-02	rs9303166	17	3372237	p13.2
SNP_A-2052769	C	C	335	43	305	73	9.165	2.50E-03	rs7211888	17	3865855	p13.2
SNP_A-1834018	G	G	296	62	262	90	7.179	7.40E-03	rs2176324	17	3890292	p13.2
SNP_A-1794153	T	T	355	55	334	76	4.006	0.0453	rs7222392	17	3954770	p13.2
SNP_A-2277341	G	G	335	45	321	73	6.692	9.70E-03	rs7218574	17	3981429	p13.2
SNP_A-2237404	A	A	354	66	324	90	4.977	2.57E-02	rs7222860	17	4012972	p13.2
SNP_A-2313225	C	C	370	42	387	25	4.695	3.02E-02	rs2286672	17	4659581	p13.2
SNP_A-2128078	A	A	328	28	340	10	8.692	3.20E-03	rs4985683	17	5541586	p13.2
SNP_A-2068822	C	C	389	3	379	15	8.125	4.40E-03	—	17	5703980	p13.2
SNP_A-1835133	G	G	401	15	411	5	5.123	2.36E-02	rs16955281	17	5805293	p13.2
SNP_A-2296886	G	G	333	81	356	52	7.048	7.90E-03	rs8075301	17	5979493	p13.2
SNP_A-1686614	C	C	386	18	407	5	7.826	5.10E-03	rs723656	17	6066080	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2242315	A	A	275	49	315	35	4.048	4.42E-02	rs12449461	17	6077561	p13.2
SNP_A-1864711	A	A	280	46	254	76	8.619	0.0033	rs2871274	17	6099609	p13.2
SNP_A-2262707	C	C	297	109	316	82	4.326	3.75E-02	rs17655486	17	6101477	p13.2
SNP_A-2314844	C	C	281	53	272	84	6.466	1.10E-02	rs12452660	17	6102748	p13.2
SNP_A-1835574	T	T	263	123	222	164	9.323	0.0023	rs2007492	17	6374241	p13.2
SNP_A-1785276	G	G	373	35	380	18	5.395	2.02E-02	rs17804635	17	6644709	p13.1
SNP_A-2194103	G	G	316	84	295	109	3.94	4.71E-02	rs2136282	17	6644997	p13.1
SNP_A-1664416	A	A	370	28	383	13	5.707	1.69E-02	rs10491083	17	6759122	p13.1
SNP_A-2301920	A	A	284	104	253	135	5.81	1.59E-02	rs12325805	17	6852943	p13.1
SNP_A-2130977	G	G	398	0	396	4	4	4.55E-02	rs193399	17	6902996	p13.1
SNP_A-2293252	C	C	383	29	358	46	4.619	3.16E-02	rs2075760	17	7233450	p13.1
SNP_A-2168155	T	T	307	51	334	34	4.4	3.59E-02	rs4796305	17	7276779	p13.1
SNP_A-2294500	G	G	348	72	378	44	7.994	4.70E-03	rs4796418	17	7298724	p13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1836151	C	C	337	61	376	36	8.337	3.90E-03	rs3867594	17	7321405	p13.1
SNP_A-1906353	C	C	311	71	333	43	7.582	5.90E-03	rs12937610	17	7346661	p13.1
SNP_A-2265993	C	C	257	163	286	126	6.209	1.27E-02	rs11658168	17	7346858	p13.1
SNP_A-2199580	G	G	276	60	286	38	4.9	0.0269	rs7215922	17	7350936	p13.1
SNP_A-1836389	C	C	388	8	410	2	3.891	4.85E-02	rs1391765	17	8238191	p13.1
SNP_A-2056328	A	A	290	18	324	8	4.836	2.79E-02	rs2268458	17	8425299	p13.1
SNP_A-2178502	C	C	313	15	342	6	4.553	3.29E-02	rs4467126	17	8503721	p13.1
SNP_A-1805874	A	A	281	113	269	149	4.503	3.38E-02	rs8065624	17	8717568	p13.1
SNP_A-1681554	C	C	282	122	320	94	5.907	1.51E-02	rs8076457	17	9144495	p13.1
SNP_A-1837079	C	C	277	65	290	40	6.038	0.014	rs17808941	17	9271732	p13.1
SNP_A-1919100	G	G	270	150	243	179	3.973	4.62E-02	rs4791902	17	9722836	p13.1
SNP_A-1801157	T	T	254	98	243	129	3.927	4.75E-02	rs17747162	17	9920704	p13.1
SNP_A-2283409	T	T	359	11	367	3	4.66	0.0309	rs16944076	17	10856958	p12
SNP_A-2040568	A	A	401	15	408	6	3.913	4.79E-02	rs4791445	17	10857615	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1863318	C	C	393	5	386	0	4.88	2.72E-02	rs16944244	17	10967418	p12
SNP_A-1644366	A	A	203	193	237	167	4.425	3.54E-02	rs758112	17	11099019	p12
SNP_A-2240695	A	A	231	121	247	93	3.992	4.57E-02	rs17512210	17	11171191	p12
SNP_A-1835339	G	G	354	44	376	24	6.54	1.05E-02	rs205062	17	11237170	p12
SNP_A-1783642	G	G	331	89	353	65	4.443	3.50E-02	rs1513753	17	11286850	p12
SNP_A-2161127	T	T	342	64	360	44	4.16	4.14E-02	rs17699467	17	11300000	p12
SNP_A-1865253	G	G	244	116	284	92	5.454	0.0195	rs9905250	17	11675120	p12
SNP_A-1751577	T	T	399	5	412	0	5.13	0.0235	rs10521189	17	11919155	p12
SNP_A-1653452	A	A	399	5	414	0	5.155	2.32E-02	rs10521190	17	11919253	p12
SNP_A-1693218	T	T	399	5	414	0	5.155	2.32E-02	rs10521191	17	11920323	p12
SNP_A-2146686	C	C	284	60	307	41	4.446	3.50E-02	rs9907196	17	11925064	p12
SNP_A-1839297	G	G	227	129	206	164	4.931	0.0264	rs885688	17	12124724	p12
SNP_A-2102034	G	G	248	164	221	193	3.905	4.81E-02	rs4791495	17	12130882	p12
SNP_A-2250822	G	G	351	69	324	96	5.498	0.019	rs11078077	17	12412568	p12
SNP_A-2253906	C	C	263	103	226	126	4.838	2.78E-02	rs11078078	17	12412611	p12
SNP_A-2111477	T	T	361	31	378	16	5.173	0.0229	rs2322592	17	12574875	p12
SNP_A-1653568	G	G	400	4	402	12	3.883	4.88E-02	rs10491101	17	12789993	p12
SNP_A-2060705	T	T	231	109	276	92	4.331	3.74E-02	rs1024580	17	12795241	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1688808	C	C	398	0	408	6	5.811	1.59E-02	rs10521197	17	12809847	p12
SNP_A-1870147	G	G	237	171	273	129	8.377	0.0038	rs8067791	17	12972471	p12
SNP_A-2257415	G	A	193	153	176	156	5.244	2.20E-02	rs6502236	17	12975623	p12
SNP_A-2146955	T	T	348	2	365	9	4.069	4.37E-02	rs971718	17	13065774	p12
SNP_A-1937280	A	G	210	186	218	176	5.524	1.88E-02	rs8068578	17	13101373	p12
SNP_A-1789279	A	A	390	22	364	42	7.103	7.70E-03	rs929439	17	13301199	p12
SNP_A-2228787	T	T	213	109	175	141	7.762	0.0053	rs4399565	17	13407619	p12
SNP_A-2137989	C	C	375	5	352	20	9.644	0.0019	rs16948222	17	13498117	p12
SNP_A-2043217	C	C	389	9	397	1	6.481	0.0109	rs12603610	17	13766815	p12
SNP_A-2273972	G	G	334	52	300	72	4.792	0.0286	rs12946731	17	13790347	p12
SNP_A-1954408	T	T	209	149	254	118	7.707	5.50E-03	rs11652884	17	13821142	p12
SNP_A-1957268	A	A	237	179	278	140	8.027	4.60E-03	rs971030	17	13833316	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1840919	T	T	225	129	179	141	4.066	4.38E-02	rs10521257	17	13943140	p12
SNP_A-1841026	G	A	213	185	222	168	8.598	3.40E-03	rs1005322	17	14162108	p12
SNP_A-1895159	G	G	406	0	408	4	3.961	4.66E-02	rs16949443	17	14237793	p12
SNP_A-2165450	A	A	252	148	201	179	8.173	0.0043	rs12952218	17	14264098	p12
SNP_A-1838914	G	G	248	120	200	132	3.873	4.91E-02	rs11652133	17	14282208	p12
SNP_A-1958023	A	A	400	4	400	0	3.98	4.60E-02	rs6502373	17	14371616	p12
SNP_A-2193863	T	T	303	117	325	91	4.002	4.55E-02	rs885698	17	14620825	p12
SNP_A-1828874	T	C	192	182	203	153	5.113	2.37E-02	rs12452291	17	14957024	p12
SNP_A-2092801	T	T	303	55	278	80	5.705	1.69E-02	rs9916167	17	15034905	p12
SNP_A-2166416	T	T	241	85	236	116	3.842	5.00E-02	rs230923	17	15057744	p12
SNP_A-2283145	C	C	221	193	264	156	7.692	5.50E-03	rs11078296	17	15249408	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2071387	C	T	249	161	210	208	10.074	0.0015	rs4792600	17	15249569	p12
SNP_A-2249125	A	A	241	111	279	85	6.026	0.0141	rs4792606	17	15265393	p12
SNP_A-2117630	A	A	346	42	378	24	6.077	0.0137	rs2954756	17	15280008	p12
SNP_A-1788024	G	G	329	59	359	35	7.39	0.0066	rs2954760	17	15282822	p12
SNP_A-1877504	T	T	347	45	378	28	5.04	2.48E-02	rs2954762	17	15283607	p12
SNP_A-2042233	G	G	399	21	382	36	4.313	0.0378	rs4792614	17	15318098	p12
SNP_A-2156450	C	C	343	47	324	70	5.042	0.0247	rs7219850	17	15324395	p12
SNP_A-1944177	C	C	337	47	328	76	6.456	0.0111	rs7219580	17	15330707	p12
SNP_A-1944606	A	A	330	72	300	94	4.264	3.89E-02	rs8070714	17	15360336	p12
SNP_A-1723088	T	T	347	57	376	32	8.166	0.0043	rs2954750	17	15537647	p12
SNP_A-1842652	T	T	376	4	364	14	5.745	1.65E-02	rs1971159	17	15618609	p12
SNP_A-1748133	A	A	327	77	305	107	5.579	1.82E-02	rs10521309	17	15762886	p12
SNP_A-1722556	T	T	231	129	222	168	4.107	4.27E-02	rs2324027	17	15880167	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1731341	A	A	385	11	391	23	3.884	4.88E-02	rs7218218	17	16626260	p11.2
SNP_A-1865299	C	C	272	52	306	36	4.426	3.54E-02	rs2688025	17	16661466	p11.2
SNP_A-2252808	C	C	415	5	422	0	5.054	0.0246	rs6502556	17	16892430	p11.2
SNP_A-2089623	G	G	398	4	420	0	4.2	4.04E-02	rs8068587	17	16892693	p11.2
SNP_A-2261313	A	A	329	73	301	103	6.353	0.0117	rs12600635	17	17083621	p11.2
SNP_A-1824374	C	C	336	58	313	79	4.029	4.47E-02	rs9896078	17	17086944	p11.2
SNP_A-2175123	G	G	372	12	374	4	3.958	4.66E-02	rs17723136	17	17320305	p11.2
SNP_A-2173899	A	A	232	110	278	90	5.204	2.25E-02	rs4924891	17	17344599	p11.2
SNP_A-1902670	A	A	223	101	266	82	4.903	2.68E-02	rs7219976	17	17345249	p11.2
SNP_A-1843751	C	C	368	12	380	4	4.172	4.11E-02	rs16961845	17	17373181	p11.2
SNP_A-2187008	T	T	334	28	370	16	4.348	3.71E-02	rs7222358	17	17400345	p11.2
SNP_A-2259966	C	C	217	143	237	113	4.257	3.91E-02	rs8079321	17	17701514	p11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2144058	G	G	257	51	305	35	5.51	0.0189	rs2975001	17	17959081	p11.2
SNP_A-2005103	A	A	365	17	381	7	4.463	3.46E-02	rs1815570	17	20581526	p11.2
SNP_A-1866779	C	T	202	166	201	183	3.937	4.72E-02	rs9901404	17	21154375	p11.2
SNP_A-2065148	T	T	393	5	398	0	5.032	2.49E-02	rs7208486	17	21328250	p11.2
SNP_A-1926698	T	T	332	8	366	0	8.71	3.20E-03	rs7207833	17	22612417	q11.1
SNP_A-1846014	C	A	204	182	225	175	6.515	1.07E-02	rs1382048	17	22760245	q11.1
SNP_A-2304493	C	C	214	140	267	123	5.209	2.25E-02	rs2779259	17	23172411	q11.2
SNP_A-2261441	G	G	229	155	274	132	5.26	0.0218	rs2779267	17	23186621	q11.2
SNP_A-2170055	T	T	294	116	268	146	4.619	3.16E-02	rs631905	17	23907440	q11.2
SNP_A-1846058	T	T	331	59	308	88	6.504	1.08E-02	rs577451	17	23930054	q11.2
SNP_A-2060669	T	T	363	25	362	44	4.828	2.80E-02	rs4795461	17	24147942	q11.2
SNP_A-2262118	A	A	288	60	329	41	5.63	0.0177	rs12602428	17	24764399	q11.2
SNP_A-2248447	A	A	319	83	352	52	8.737	3.10E-03	rs8076005	17	25571336	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2090611	G	G	287	41	324	26	4.89	0.027	rs11080122	17	25571461	q11.2
SNP_A-1795240	T	T	332	86	360	58	6.577	0.0103	rs2020936	17	25574940	q11.2
SNP_A-1736507	C	T	217	187	221	193	4.117	4.25E-02	rs1382047	17	25881879	q11.1
SNP_A-2261357	G	G	296	36	278	56	4.906	2.68E-02	rs2111663	17	26998675	q11.2
SNP_A-2265276	C	C	268	82	286	48	9.108	2.50E-03	rs11080170	17	27145874	q11.2
SNP_A-1708643	T	T	316	14	300	28	5.076	2.43E-02	rs1400790	17	27841934	q11.2
SNP_A-1941496	T	T	367	49	349	71	4.467	3.46E-02	rs17806303	17	27855741	q11.2
SNP_A-2193502	T	T	255	141	219	175	6.387	0.0115	rs7210010	17	27929570	q11.2
SNP_A-2192286	A	T	225	157	198	194	6.901	0.0086	rs321153	17	27972666	q11.2
SNP_A-1892188	T	T	252	108	268	70	7.919	4.90E-03	rs2729352	17	28037201	q11.2
SNP_A-2177444	G	G	340	10	329	1	6.962	8.30E-03	rs9913387	17	28048704	q11.2
SNP_A-2311754	A	A	269	109	235	145	7.391	0.0066	rs12452579	17	28468812	q11.2
SNP_A-1847738	C	C	334	76	365	53	5.399	2.02E-02	rs1497363	17	28654084	q11.2
SNP_A-2026942	G	G	256	128	221	149	3.902	0.0482	rs11651326	17	28664543	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2272305	G	G	314	100	344	74	5.234	2.22E-02	rs320645	17	28673666	q11.2
SNP_A-1903166	T	T	287	67	329	47	5.715	1.68E-02	rs320628	17	28677707	q11.2
SNP_A-2213963	T	T	313	97	346	76	4.029	4.47E-02	rs11656936	17	28798812	q11.2
SNP_A-2131394	T	T	334	78	304	102	4.567	3.26E-02	rs1123024	17	28799374	q11.2
SNP_A-1819036	A	A	315	85	331	59	4.965	2.59E-02	rs3892103	17	28830073	q12
SNP_A-1882698	C	C	326	54	286	72	4.534	0.0332	rs7224103	17	28863346	q12
SNP_A-2273624	G	G	338	40	320	66	6.787	9.20E-03	rs9903659	17	28890180	q12
SNP_A-2059386	A	A	413	7	421	1	4.572	3.25E-02	rs1583390	17	28952690	q12
SNP_A-2178169	C	C	353	5	376	0	5.287	2.15E-02	rs12949709	17	28967964	q12
SNP_A-1931045	C	C	295	49	294	26	6.196	1.28E-02	rs9303665	17	29104020	q12
SNP_A-2227719	G	G	255	137	304	100	9.893	1.70E-03	rs17783671	17	29217813	q12
SNP_A-2299529	A	A	326	64	366	46	4.658	0.0309	rs6505386	17	29247841	q12
SNP_A-1784058	C	C	329	63	351	41	5.366	2.05E-02	rs6505388	17	29250417	q12
SNP_A-1856626	G	G	303	9	309	25	6.847	8.90E-03	rs4795839	17	29299877	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2005138	G	C	184	134	169	161	5.356	0.0207	rs957373	17	29482054	q12
SNP_A-1939923	A	A	268	128	226	160	7	8.20E-03	rs8069624	17	29520790	q12
SNP_A-1848744	C	C	377	35	386	20	4.153	4.16E-02	rs2003533	17	29525887	q12
SNP_A-1848955	G	G	367	23	401	11	5.141	2.34E-02	rs159316	17	29710323	q12
SNP_A-2005141	T	T	361	21	380	10	4.308	3.79E-02	rs3136680	17	29711074	q12
SNP_A-1871557	T	T	242	134	203	159	5.287	2.15E-02	rs2282692	17	29712296	q12
SNP_A-1849314	G	G	302	72	304	46	4.945	2.62E-02	rs2191054	17	29864353	q12
SNP_A-1902406	C	C	233	167	274	136	6.365	1.16E-02	rs4795966	17	30034434	q12
SNP_A-2071556	T	T	255	145	223	177	5.322	2.11E-02	rs4506952	17	30048197	q12
SNP_A-1849444	G	G	239	177	268	144	5.032	2.49E-02	rs17665518	17	30052481	q12
SNP_A-2053315	A	A	201	129	221	97	5.258	0.0218	rs11990263	17	30053750	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2307488	G	G	230	176	255	143	4.623	0.0315	rs11656182	17	30053887	q12
SNP_A-2115669	A	A	276	82	234	98	3.907	4.81E-02	rs4796063	17	30574632	q12
SNP_A-2307676	T	T	300	110	274	142	5.198	2.26E-02	rs12601614	17	30598366	q12
SNP_A-1860401	C	C	271	127	239	155	4.768	2.90E-02	rs7222370	17	30608347	q12
SNP_A-1805692	G	G	223	135	177	147	4.116	4.25E-02	rs2622524	17	30619955	q12
SNP_A-2005146	C	C	246	174	215	201	4.01	4.52E-02	rs4795078	17	30871427	q12
SNP_A-1923829	C	C	359	29	339	45	4.012	4.52E-02	rs8065894	17	30882043	q12
SNP_A-2140832	G	G	289	39	254	58	5.581	1.82E-02	rs9303692	17	31212609	q12
SNP_A-1903674	C	C	295	67	234	92	9.106	2.50E-03	rs865922	17	31315701	q12
SNP_A-1938590	G	G	350	44	358	26	4.591	3.21E-02	rs854664	17	31379891	q12
SNP_A-2128694	C	C	344	76	360	50	5.609	1.79E-02	rs854665	17	31380346	q12
SNP_A-2181947	A	A	328	40	279	59	6.339	0.0118	rs854636	17	31396931	q12
SNP_A-2071763	A	A	345	45	368	26	5.806	0.016	rs12939695	17	31471515	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1690089	G	G	309	91	290	122	4.938	0.0263	rs63954	17	31803225	q11.2
SNP_A-1732021	C	C	226	82	215	123	7.096	7.70E-03	rs727206	17	32063659	q11.2
SNP_A-1794015	A	A	313	97	289	125	4.469	3.45E-02	rs17561428	17	32109664	q12
SNP_A-2131595	A	A	331	5	330	0	4.948	2.61E-02	rs8072990	17	32150370	q12
SNP_A-1931880	G	G	404	2	402	10	5.295	2.14E-02	rs9893703	17	32249445	q12
SNP_A-2229279	C	C	362	24	351	11	4.233	3.97E-02	rs17565060	17	32301174	q12
SNP_A-1850991	G	G	239	101	283	85	3.984	4.59E-02	rs17571920	17	32322519	q12
SNP_A-1850995	G	G	283	91	322	68	5.508	0.0189	rs4795164	17	32323609	q12
SNP_A-1676082	T	T	341	63	327	87	4.012	4.52E-02	rs317343	17	32331368	q11.2
SNP_A-2239233	A	A	356	40	329	59	4.63	3.14E-02	rs11867736	17	32824490	q12
SNP_A-1904571	C	C	291	83	315	59	5.007	0.0252	rs12942606	17	32910630	q12
SNP_A-2291882	T	T	391	21	382	36	4.009	0.0453	rs11656817	17	33131012	q12
SNP_A-1678844	G	G	252	54	258	82	4.057	4.40E-02	rs4796013	17	33362752	q11.2
SNP_A-2266094	C	C	269	109	315	87	5.359	0.0206	rs7502685	17	33901979	q12
SNP_A-2228020	C	C	280	120	309	93	4.845	2.77E-02	rs10852948	17	33902029	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1851660	A	A	324	26	288	42	5.299	2.13E-02	---	17	34030362	q12
SNP_A-1894857	C	C	240	146	215	177	4.303	3.80E-02	rs16237	17	34526928	q12
SNP_A-2066216	G	G	386	16	379	31	4.773	2.89E-02	rs16968682	17	34640425	q12
SNP_A-2178191	G	G	368	0	372	4	3.936	4.73E-02	rs2060941	17	35236409	q21.1
SNP_A-2311893	C	C	406	10	395	23	5.268	2.17E-02	rs10221230	17	36310908	q21.2
SNP_A-2285691	G	G	314	80	298	108	4.41	3.57E-02	rs7214262	17	36435250	q21.2
SNP_A-2029489	T	T	366	14	365	31	6.096	0.0135	rs7223620	17	36471936	q21.2
SNP_A-2075906	G	G	301	95	272	126	5.811	1.59E-02	rs757102	17	36788472	q21.2
SNP_A-1954686	G	G	284	106	269	141	4.869	2.73E-02	rs17658000	17	36815998	q21.2
SNP_A-1801769	A	A	292	96	264	126	5.459	0.0195	rs7209968	17	36848205	q21.2
SNP_A-2246210	C	C	300	74	291	105	4.881	2.72E-02	rs17495782	17	36885866	q21.2
SNP_A-2309497	C	C	394	14	375	31	6.887	8.70E-03	rs2667945	17	38387938	q21.31
SNP_A-2223843	A	A	252	88	229	115	4.668	3.07E-02	rs9911630	17	38441868	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1853728	T	T	290	106	263	133	4.368	3.66E-02	rs8176296	17	38457117	q21.31
SNP_A-2070053	G	G	330	74	313	99	3.984	4.59E-02	rs6503369	17	38819347	q21.31
SNP_A-2185453	-	A	194	194	217	163	3.896	4.84E-02	rs231471	17	39375020	q21.31
SNP_A-1903654	G	G	368	30	369	15	4.752	0.0293	rs162430	17	39385935	q21.31
SNP_A-1663046	G	G	308	70	274	96	5.974	1.45E-02	rs8072687	17	39558963	q21.2
SNP_A-2202594	T	T	271	87	241	109	4.137	0.0419	rs3785817	17	39779191	q21.31
SNP_A-1694463	A	A	299	47	306	72	3.926	4.75E-02	rs10512485	17	39843796	q21.2
SNP_A-1879785	C	C	338	30	346	14	5.825	1.58E-02	rs1105568	17	41149210	q21.31
SNP_A-1855153	C	C	301	59	318	32	8.339	3.90E-03	rs2902662	17	41162708	q21.31
SNP_A-2210239	C	C	279	63	247	97	9.166	2.50E-03	rs3785885	17	41414477	q21.31
SNP_A-2199736	T	T	309	105	279	135	5.281	2.16E-02	rs17651507	17	41414847	q21.31
SNP_A-1849442	C	T	214	204	230	182	4.1	4.29E-02	rs758392	17	42372858	q21.32
SNP_A-2307825	A	G	198	194	213	157	4.991	2.55E-02	rs11079742	17	42375127	q21.32
SNP_A-1916012	G	G	217	173	256	124	11.172	8.00E-04	rs8081157	17	42413441	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2279876	G	G	380	10	404	2	5.749	1.65E-02	rs4468691	17	42419677	q21.32
SNP_A-2122477	G	G	277	117	326	84	9.085	2.60E-03	rs2316757	17	42421224	q21.32
SNP_A-2278461	G	A	212	188	221	173	6.568	0.0104	rs3851798	17	42421266	q21.32
SNP_A-2034805	T	T	234	70	279	49	6.752	9.40E-03	rs11651232	17	42433025	q21.32
SNP_A-1855586	A	A	199	123	157	155	8.483	3.60E-03	rs11079747	17	42433849	q21.32
SNP_A-1952332	G	G	298	98	345	63	10.867	0.001	rs1989858	17	42534323	q21.32
SNP_A-2100061	G	G	362	2	337	11	6.769	9.30E-03	rs11570570	17	42555511	q21.32
SNP_A-2087283	C	C	295	93	331	71	4.775	2.89E-02	rs11570508	17	42583559	q21.32
SNP_A-1957904	T	T	389	11	389	3	4.491	3.41E-02	rs16948092	17	43200942	q21.32
SNP_A-1856885	A	A	362	56	381	35	5.327	2.10E-02	rs10514935	17	43615673	q21.32
SNP_A-1791817	G	G	364	38	371	21	4.84	2.78E-02	rs7405452	17	44029669	q21.32
SNP_A-2034029	A	A	227	171	262	144	4.74	2.95E-02	rs11079830	17	44037629	q21.32
SNP_A-1787597	T	A	221	189	215	185	4.743	2.94E-02	rs11652932	17	44052757	q21.32
SNP_A-2083875	A	A	218	126	266	98	7.702	5.50E-03	rs3110609	17	44108542	q21.32
SNP_A-2137220	G	G	360	34	386	14	9.195	2.40E-03	rs3096645	17	44112044	q21.32
SNP_A-2053738	T	T	212	206	238	174	4.154	4.15E-02	rs4793601	17	44146800	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2208045	G	G	315	57	333	31	8.096	4.40E-03	rs2280352	17	44186025	q21.32
SNP_A-1887882	G	G	348	70	365	49	4.092	4.31E-02	rs606911	17	44263227	q21.32
SNP_A-1875670	C	C	242	84	260	60	4.59	3.22E-02	rs1554551	17	44548140	q21.32
SNP_A-2230412	A	A	284	64	263	93	6.073	0.0137	rs2671668	17	44894021	q21.32
SNP_A-2289811	C	C	383	7	401	1	4.733	2.96E-02	rs2412101	17	44896220	q21.32
SNP_A-1877203	C	C	328	82	305	107	4.138	0.0419	rs2671632	17	44899152	q21.32
SNP_A-1857671	G	G	270	100	237	131	6.303	0.0121	rs271674	17	45333985	q21.33
SNP_A-1860618	G	G	296	50	297	77	4.66	0.0309	rs271646	17	45355145	q21.33
SNP_A-2314203	A	A	326	62	331	41	3.985	4.59E-02	rs11079884	17	45431434	q21.33
SNP_A-1885218	G	G	368	32	388	18	4.405	3.58E-02	rs7215959	17	45500268	q21.33
SNP_A-1668166	G	G	258	86	315	57	10.472	1.20E-03	rs3883305	17	45570316	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2111149	A	A	342	58	354	38	4.293	3.83E-02	rs4794111	17	45652768	q21.33
SNP_A-2257119	A	A	320	64	296	92	5.94	1.48E-02	rs4794122	17	45683412	q21.33
SNP_A-1857916	G	G	254	114	259	79	5.13	0.0235	rs2254177	17	45713418	q21.33
SNP_A-2162567	T	T	389	9	376	2	4.163	4.13E-02	rs16948910	17	45770192	q21.33
SNP_A-2097932	A	A	385	7	387	1	4.485	3.42E-02	rs17715019	17	45813438	q21.33
SNP_A-2055306	C	C	219	135	254	108	5.501	0.019	rs4794145	17	45869694	q21.33
SNP_A-2248903	A	A	283	73	258	98	4.81	2.83E-02	rs7225465	17	46271158	q21.33
SNP_A-1926190	T	T	249	151	269	117	4.838	2.78E-02	rs11653728	17	46291238	q21.33
SNP_A-2111204	G	G	389	17	405	7	4.445	3.50E-02	rs7226332	17	46751872	q21.33
SNP_A-1911533	A	A	296	18	282	40	8.585	3.40E-03	rs12691063	17	46877389	q21.33
SNP_A-2276481	T	T	289	93	308	62	6.615	0.0101	rs4794257	17	46944261	q21.33
SNP_A-1858694	G	G	270	102	296	78	4.389	3.62E-02	rs728645	17	46948251	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1858741	A	A	416	0	416	6	5.957	0.0147	rs16950179	17	47062250	q21.33
SNP_A-2231759	A	A	369	17	357	31	4.277	3.86E-02	rs1263956	17	47123722	q21.33
SNP_A-2047061	C	C	415	5	420	0	5.03	2.49E-02	rs9893250	17	47256006	q21.33
SNP_A-1859055	T	-	209	155	167	167	3.856	4.96E-02	rs767326	17	47260695	q21.33
SNP_A-1959097	A	A	396	6	381	15	4.102	4.28E-02	rs7219047	17	47273970	q21.33
SNP_A-1795725	C	C	390	28	372	44	3.976	4.62E-02	rs9894418	17	47286522	q21.33
SNP_A-2260854	C	C	386	28	367	45	4.434	3.52E-02	rs9896174	17	47286597	q21.33
SNP_A-1859402	A	A	263	79	288	54	5.834	1.57E-02	rs1486745	17	47625736	q22
SNP_A-1859421	A	A	262	128	224	158	6.036	0.014	rs10514998	17	47654808	q22
SNP_A-1859433	T	T	369	33	386	16	6.281	1.22E-02	rs1503051	17	47659318	q22
SNP_A-1859447	G	G	302	112	320	84	4.399	3.60E-02	rs1393734	17	47665244	q22
SNP_A-2118556	C	C	273	131	236	154	4.3	3.81E-02	rs17678475	17	47668610	q22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1923289	A	A	346	58	332	82	4.282	0.0385	rs350011	17	47938582	q22
SNP_A-2040111	C	C	347	53	350	32	4.789	0.0286	rs12453135	17	48899896	q22
SNP_A-2312081	A	A	300	104	273	139	6.236	1.25E-02	rs1508966	17	49058483	q22
SNP_A-1952002	A	A	385	21	381	37	4.261	0.039	rs3105827	17	49066516	q22
SNP_A-1852340	C	C	251	163	288	132	5.755	1.64E-02	rs10468501	17	50081273	q22
SNP_A-2005201	G	G	307	29	292	46	4.223	3.99E-02	rs2958892	17	50233660	q22
SNP_A-2137666	G	G	321	79	337	57	3.903	0.0482	rs1017098	17	50233926	q22
SNP_A-2057223	C	C	289	79	309	57	4.222	3.99E-02	rs17817448	17	50455482	q22
SNP_A-1793125	G	G	367	37	348	58	5.142	2.34E-02	rs17817743	17	50666251	q22
SNP_A-1754394	C	C	365	39	392	22	5.579	1.82E-02	rs10515000	17	50779197	q22
SNP_A-2094994	T	T	269	135	234	174	7.338	6.80E-03	rs11868220	17	50918261	q23.1
SNP_A-2213481	G	G	216	102	258	84	4.597	3.20E-02	rs1396215	17	50963766	q23.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2032995	C	C	401	7	413	1	4.633	3.14E-02	rs8066498	17	51050928	q23.1
SNP_A-1823219	A	G	231	179	213	207	4.144	4.18E-02	rs12953204	17	51456957	q23.2
SNP_A-2092341	G	G	383	3	372	10	3.909	4.80E-02	rs17819601	17	51462287	q23.2
SNP_A-1916303	G	A	216	182	210	186	4.234	3.96E-02	rs11079206	17	51463256	q23.2
SNP_A-2162946	G	G	356	12	358	4	3.957	4.67E-02	rs1372851	17	51961071	q23.2
SNP_A-1847197	A	A	410	6	405	15	3.869	4.92E-02	rs16957703	17	52135862	q23.2
SNP_A-2255577	C	C	375	39	394	24	4.022	4.49E-02	rs9912498	17	52164441	q23.2
SNP_A-1753933	C	C	358	46	345	69	4.719	0.0298	rs1876697	17	52168372	q22
SNP_A-1924572	C	C	251	71	263	47	4.935	0.0263	rs11651692	17	52293014	q23.2
SNP_A-2142915	A	A	219	117	175	149	8.548	3.50E-03	rs7615	17	52320931	q23.2
SNP_A-1944636	A	A	329	17	362	6	6.165	1.30E-02	rs2525997	17	52326240	q23.2
SNP_A-2071227	C	C	343	37	354	18	6.653	9.90E-03	rs792402	17	52773732	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1890866	G	G	250	158	286	130	5.063	2.44E-02	rs2332933	17	52922575	q23.2
SNP_A-2213652	C	C	269	57	266	86	4.908	2.67E-02	rs2333025	17	53061936	q23.2
SNP_A-2079157	G	G	264	92	313	71	5.816	1.59E-02	rs4793565	17	53164517	q23.2
SNP_A-1727303	C	C	334	62	327	87	3.871	4.91E-02	rs1373155	17	53172211	q22
SNP_A-2046112	A	A	282	58	313	35	7.211	7.20E-03	rs3883322	17	53175398	q23.2
SNP_A-1833072	C	C	255	101	302	68	10.143	0.0014	rs8067868	17	53179948	q23.2
SNP_A-1793465	G	G	288	116	322	82	7.733	5.40E-03	rs9303396	17	53180117	q23.2
SNP_A-2194239	C	C	224	160	261	137	4.355	3.69E-02	rs9892194	17	53180824	q23.2
SNP_A-1706083	G	G	314	88	293	121	5.762	1.64E-02	rs10515075	17	53232530	q22
SNP_A-1841972	C	C	343	51	334	76	4.724	2.97E-02	rs16942405	17	53244625	q23.2
SNP_A-1864522	T	T	372	40	355	61	4.745	2.94E-02	rs722168	17	53267969	q23.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086345	T	T	172	170	214	152	4.768	2.90E-02	rs2586038	17	53271640	q23.2
SNP_A-1895041	T	T	194	162	226	134	5.338	2.09E-02	rs7222295	17	53688886	q23.2
SNP_A-1866191	G	G	368	8	359	19	4.588	3.22E-02	---	17	55293281	q23.2
SNP_A-2256145	T	T	324	36	325	17	6.356	0.0117	rs180535	17	55351797	q23.2
SNP_A-1860907	T	T	367	27	395	11	7.587	5.90E-03	rs17500797	17	55883487	q23.2
SNP_A-1729692	C	C	310	42	362	30	3.885	0.0487	rs1544508	17	56248444	q23.2
SNP_A-1896556	G	G	283	93	298	68	4.135	4.20E-02	rs8070812	17	56416350	q23.2
SNP_A-1911170	A	A	312	72	286	108	8.203	4.20E-03	rs11650989	17	56804418	q23.2
SNP_A-2169970	T	T	306	98	273	133	7.179	7.40E-03	rs8068318	17	56838548	q23.2
SNP_A-1892630	T	T	329	27	316	50	6.995	8.20E-03	rs4968433	17	56855115	q23.2
SNP_A-2210429	G	G	315	21	316	38	4.433	3.52E-02	rs1009961	17	56899557	q23.2
SNP_A-2148393	C	C	347	55	373	37	4.382	3.63E-02	rs10853034	17	56939347	q23.2
SNP_A-2135651	C	C	279	103	259	137	5.31	0.0212	rs9895941	17	58156328	q23.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1897003	G	G	366	50	394	24	10.162	0.0014	rs17686192	17	58346088	q23.3
SNP_A-1833531	T	T	358	40	394	16	11.834	6.00E-04	rs17759603	17	58352784	q23.3
SNP_A-2170839	G	G	357	41	383	23	5.897	0.0152	rs7225370	17	58388113	q23.3
SNP_A-2091532	T	C	193	145	180	170	5.019	2.51E-02	rs4267385	17	58937488	q23.3
SNP_A-1932521	G	G	370	22	350	40	5.776	1.62E-02	rs1867623	17	59690999	q23.3
SNP_A-1864796	G	G	392	24	406	12	4.241	0.0395	rs1877821	17	60605875	q24.1
SNP_A-2231301	T	T	383	37	406	16	8.987	2.70E-03	rs16961234	17	60633482	q24.1
SNP_A-2313104	A	A	328	14	374	6	4.226	3.98E-02	rs7221174	17	60663249	q24.1
SNP_A-2175696	T	T	337	25	363	9	8.36	0.0038	rs16961958	17	60692291	q24.1
SNP_A-2186104	T	T	242	150	290	110	10.405	1.30E-03	rs2869590	17	60701052	q24.1
SNP_A-2246032	A	A	242	144	284	112	7.227	7.20E-03	rs7208337	17	60719110	q24.1
SNP_A-1927748	A	A	287	107	327	73	8.983	2.70E-03	rs740856	17	60727583	q24.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1869655	C	C	312	62	343	37	7.733	5.40E-03	rs1034992	17	60782091	q24.1
SNP_A-2240488	T	T	373	9	358	2	4.114	4.25E-02	rs9675316	17	60816254	q24.1
SNP_A-1867960	T	T	322	74	344	54	3.847	4.98E-02	rs4630583	17	60842319	q24.1
SNP_A-2036834	T	T	399	9	400	2	4.412	3.57E-02	rs8073790	17	60852839	q24.1
SNP_A-1908633	G	G	330	74	353	51	5.007	0.0253	rs4790939	17	60853432	q24.1
SNP_A-2169540	T	T	370	40	394	24	4.677	3.06E-02	rs2318872	17	61313804	q24.1
SNP_A-2073701	C	C	346	68	326	94	4.725	2.97E-02	rs1420802	17	61319214	q24.1
SNP_A-1840566	C	C	382	18	357	7	3.998	4.55E-02	rs1443290	17	61462770	q24.1
SNP_A-1669681	G	G	354	42	381	27	4.075	4.35E-02	rs10491166	17	61476097	q23.3
SNP_A-1890732	C	C	308	40	325	25	3.912	4.79E-02	rs230568	17	61589572	q24.1
SNP_A-1948164	C	C	406	14	386	28	5.129	0.0235	rs8178822	17	61655991	q24.2
SNP_A-2115417	C	C	353	21	342	8	5.212	0.0224	rs4790911	17	61841377	q24.2
SNP_A-1873918	C	C	330	74	360	54	4.308	3.79E-02	rs956952	17	61948969	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1804756	A	A	294	72	323	43	8.676	3.20E-03	rs16959508	17	61949724	q24.2
SNP_A-1867144	T	T	345	13	334	4	4.372	3.65E-02	rs16959746	17	62048876	q24.2
SNP_A-1867048	T	T	242	84	233	117	4.742	2.94E-02	rs1010544	17	62117908	q24.2
SNP_A-1883468	A	A	382	30	397	15	5.289	2.15E-02	rs16960077	17	62132371	q24.2
SNP_A-1867009	G	G	300	54	336	36	5.195	2.27E-02	rs873417	17	62251823	q24.2
SNP_A-2118291	G	G	327	63	347	43	4.367	3.66E-02	rs740557	17	62451139	q24.2
SNP_A-2182510	A	A	289	111	246	152	9.843	1.70E-03	rs4790993	17	62465677	q24.2
SNP_A-2163055	A	G	206	158	203	173	8.29	4.00E-03	rs9332408	17	62539449	q24.2
SNP_A-1827686	G	G	374	4	378	0	4.021	4.49E-02	rs16960658	17	62613941	q24.2
SNP_A-1866813	T	T	293	113	256	150	7.699	5.50E-03	rs10512514	17	62642338	q24.2
SNP_A-1866807	T	T	272	80	245	115	7.603	5.80E-03	rs16960774	17	62740277	q24.2
SNP_A-1752365	G	G	374	28	356	50	6.629	0.01	rs10512501	17	62796726	q23.3
SNP_A-1868611	C	C	261	45	302	32	3.963	0.0465	rs16972793	17	63643572	q24.2
SNP_A-1668969	A	A	245	151	282	124	5.125	2.36E-02	rs718597	17	63829899	q24.1
SNP_A-1803295	T	T	403	11	393	23	4.356	3.69E-02	rs17739194	17	63852293	q24.2
SNP_A-2059554	A	A	214	190	247	161	4.739	2.95E-02	rs9915812	17	64201440	q24.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920380	T	T	244	122	218	150	4.34	3.72E-02	rs8074614	17	64261626	q24.2
SNP_A-1662054	C	C	349	45	369	27	5.052	0.0246	rs1558358	17	64820537	q24.2
SNP_A-1872806	G	G	338	80	353	57	4.11	4.26E-02	rs2028048	17	64984507	q24.3
SNP_A-1869581	C	C	201	143	240	118	5.567	0.0183	rs4968863	17	65269099	q24.3
SNP_A-2309672	A	A	225	157	251	121	5.95	0.0147	rs2057823	17	65270403	q24.3
SNP_A-1922300	T	T	232	158	255	125	4.805	2.84E-02	rs2057822	17	65270578	q24.3
SNP_A-1780986	C	G	210	192	226	170	6.931	8.50E-03	rs4968869	17	65388722	q24.3
SNP_A-2144772	A	A	265	125	299	93	6.742	9.40E-03	rs2366021	17	65395148	q24.3
SNP_A-1869702	T	T	271	123	306	98	4.827	2.80E-02	rs179919	17	65410328	q24.3
SNP_A-2179674	G	G	283	131	319	99	6.586	0.0103	rs180068	17	65469307	q24.3
SNP_A-1796008	G	G	237	175	213	207	3.884	0.0487	rs180171	17	65548869	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1895847	G	A	228	166	208	202	5.973	1.45E-02	rs8072749	17	65564546	q24.3
SNP_A-2308462	T	T	257	99	217	125	6.115	0.0134	rs236519	17	65691381	q24.3
SNP_A-1870202	C	C	288	130	305	101	3.954	4.68E-02	rs236499	17	65778101	q24.3
SNP_A-1870275	C	C	302	116	328	90	4.355	3.69E-02	rs4968892	17	65806836	q24.3
SNP_A-1955319	A	A	378	20	362	46	10.466	1.20E-03	rs17792069	17	66178578	q24.3
SNP_A-1875234	A	A	301	115	327	89	4.39	0.0361	rs8075236	17	66273420	q24.3
SNP_A-2062892	G	G	329	83	357	59	5.18	2.28E-02	rs11077526	17	66409985	q24.3
SNP_A-2217044	C	C	304	58	270	92	9.721	0.0018	rs8079714	17	66509871	q24.3
SNP_A-1850146	C	C	336	18	380	8	5.003	0.0253	rs9899007	17	66533862	q24.3
SNP_A-1870864	A	A	340	24	369	9	7.743	5.40E-03	rs1990730	17	66555445	q24.3
SNP_A-1870903	C	C	357	3	327	11	5.199	2.26E-02	rs10512560	17	66633015	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2127828	-	G	184	184	209	147	5.529	1.87E-02	rs8069925	17	66676457	q24.3
SNP_A-2157830	G	A	199	187	223	171	5.198	2.26E-02	rs2367263	17	66677883	q24.3
SNP_A-1819702	T	C	191	181	218	170	4.318	3.77E-02	rs6501447	17	66684693	q24.3
SNP_A-2184029	T	T	232	146	201	173	4.484	3.42E-02	rs17765644	17	66691087	q24.3
SNP_A-1789719	T	T	244	158	204	190	6.434	0.0112	rs11870732	17	66706836	q24.3
SNP_A-1924667	G	A	195	151	187	167	5.909	1.51E-02	rs8064388	17	66742612	q24.3
SNP_A-2282931	C	A	222	198	230	190	4.878	2.72E-02	rs8070461	17	66752467	q24.3
SNP_A-2128838	T	T	355	21	310	40	8.042	4.60E-03	rs16976490	17	66753642	q24.3
SNP_A-1905693	C	T	199	175	205	161	6.294	0.0121	rs9891216	17	66754527	q24.3
SNP_A-2280656	A	A	304	88	281	119	5.467	1.94E-02	rs1859826	17	66759520	q24.3
SNP_A-2067136	C	C	375	29	385	11	8.152	0.0043	rs12453709	17	67189132	q24.3
SNP_A-2285141	C	C	347	67	351	39	6.709	9.60E-03	rs4793378	17	67346742	q24.3
SNP_A-2021177	A	A	317	1	315	9	6.351	0.0117	rs9895035	17	67410364	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1913415	G	G	387	5	370	24	12.825	3.00E-04	rs11077582	17	67422699	q24.3
SNP_A-1828171	G	G	410	4	422	0	4.097	4.30E-02	rs2241171	17	67582386	q24.3
SNP_A-2125366	T	T	309	51	328	34	3.961	4.66E-02	rs17181232	17	67707228	q24.3
SNP_A-2083102	C	C	312	52	272	70	4.714	2.99E-02	rs9915815	17	67817495	q24.3
SNP_A-2294903	G	G	326	26	260	44	8.596	3.40E-03	rs9895115	17	67817895	q24.3
SNP_A-1915470	T	T	350	58	307	85	7.595	5.90E-03	rs9914550	17	67818013	q24.3
SNP_A-1916098	C	C	337	61	320	88	5.209	2.25E-02	rs8068003	17	67935196	q24.3
SNP_A-1871848	T	T	329	37	343	19	6.056	1.39E-02	rs7210406	17	67994648	q24.3
SNP_A-2210137	C	C	334	16	335	5	5.62	0.0178	rs4793466	17	68145659	q24.3
SNP_A-1646978	C	C	232	170	269	143	4.94	2.62E-02	rs763698	17	68233981	q24.3
SNP_A-2117661	T	T	337	77	357	55	4.238	0.0395	rs1019877	17	68257818	q24.3
SNP_A-1872026	G	G	362	42	358	20	6.972	8.30E-03	rs16977367	17	68266571	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2058876	T	T	386	24	404	12	4.367	3.66E-02	rs2060097	17	68293500	q24.3
SNP_A-2221972	G	G	344	44	375	23	7.793	5.20E-03	rs17185043	17	69004323	q25.1
SNP_A-1825122	G	G	261	157	291	129	4.367	3.66E-02	rs8077756	17	69010994	q25.1
SNP_A-2308894	C	C	284	128	232	180	14.02	2.00E-04	rs12453316	17	69027654	q25.1
SNP_A-2112947	G	G	287	69	271	101	6.134	1.33E-02	rs17191645	17	69149422	q25.1
SNP_A-1928645	G	G	248	142	229	177	4.277	3.86E-02	rs323388	17	69187154	q25.1
SNP_A-1933001	A	G	226	172	207	193	5.826	1.58E-02	rs2683191	17	69212558	q25.1
SNP_A-2106262	G	G	331	61	362	44	3.895	4.84E-02	rs17836849	17	69223351	q25.1
SNP_A-1812304	C	C	290	52	288	86	6.967	8.30E-03	rs9906978	17	69237227	q25.1
SNP_A-1895533	G	G	320	80	359	57	5.79	0.0161	rs922560	17	69362025	q25.1
SNP_A-1724538	G	G	321	79	304	106	4.28	3.86E-02	rs1073572	17	69553184	q24.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082403	G	G	380	4	404	0	4.23	3.97E-02	rs486287	17	70111636	q25.1
SNP_A-1910973	A	A	357	7	369	1	4.65	3.11E-02	rs16978145	17	70134068	q25.1
SNP_A-1808721	A	A	324	4	380	0	4.66	0.0309	rs7225923	17	70235037	q25.1
SNP_A-1873244	G	A	231	151	201	189	11.221	8.00E-04	rs2385067	17	70321665	q25.1
SNP_A-1873248	T	T	407	9	410	2	4.446	3.50E-02	rs10512600	17	70324574	q25.1
SNP_A-2305912	T	T	254	128	301	103	6.075	0.0137	rs1531564	17	70621874	q25.1
SNP_A-1878403	T	T	346	6	377	1	3.98	4.61E-02	rs7212862	17	70668091	q25.1
SNP_A-1751539	C	C	322	56	313	87	6.231	0.0126	rs4793448	17	71022270	q24.3
SNP_A-1714497	A	A	330	40	334	62	3.891	4.85E-02	rs1035076	17	71059968	q24.3
SNP_A-2196165	G	G	410	6	405	15	3.869	4.92E-02	rs7213005	17	71108024	q25.1
SNP_A-2293351	G	G	259	101	231	135	6.449	0.0111	rs4789376	17	72441593	q25.2
SNP_A-2285040	C	C	256	90	222	110	4.131	4.21E-02	rs4789378	17	72441961	q25.2
SNP_A-1818398	C	C	298	102	255	141	9.583	0.002	rs11077882	17	72465246	q25.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1794161	G	G	355	13	325	37	12.795	3.00E-04	rs3848391	17	72500435	q25.2
SNP_A-1671996	C	C	301	11	306	28	6.71	9.60E-03	rs10512597	17	73296956	q25.1
SNP_A-2223146	G	G	398	6	392	18	6.002	0.0143	rs3935192	17	73390436	q25.3
SNP_A-2179348	C	C	400	10	411	3	3.899	4.83E-02	rs17639052	17	73509831	q25.3
SNP_A-2038678	T	T	266	46	264	72	4.854	0.0276	rs4789579	17	73827026	q25.3
SNP_A-2005322	A	A	312	52	299	75	4.307	3.80E-02	rs4789575	17	73833628	q25.3
SNP_A-2203601	G	G	323	87	287	107	3.87	4.92E-02	rs2120658	17	74041888	q25.3
SNP_A-2252473	A	A	285	35	266	54	4.711	3.00E-02	rs7221694	17	74047807	q25.3
SNP_A-1836614	C	A	217	183	215	193	3.899	4.83E-02	rs12452379	17	74427053	q25.3
SNP_A-2297482	C	C	369	47	386	28	5.191	2.27E-02	rs6501275	17	74546036	q25.3
SNP_A-1839322	G	G	310	92	279	117	4.577	3.24E-02	rs8076446	17	75338179	q25.3
SNP_A-2254520	G	G	332	78	309	103	4.273	3.87E-02	rs1467979	17	75675338	q25.3
SNP_A-1956154	G	G	288	132	313	105	4.111	4.26E-02	rs12452616	17	75704676	q25.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1796490	C	C	252	106	280	82	4.515	3.36E-02	rs4889970	17	75710681	q25.3
SNP_A-2097284	C	C	271	117	298	82	7.354	6.70E-03	rs11150846	17	75713115	q25.3
SNP_A-2299110	T	T	229	183	265	151	5.67	1.73E-02	rs2269376	17	75800122	q25.3
SNP_A-1909842	C	C	330	46	355	29	4.682	3.05E-02	rs908241	17	76450273	q25.3
SNP_A-2290564	G	G	326	94	349	69	4.613	3.17E-02	rs4969398	17	76724504	q25.3
SNP_A-2202198	A	A	287	29	302	52	4.773	2.89E-02	rs9897258	17	77003846	q25.3
SNP_A-2289629	G	G	384	24	354	48	9.176	2.50E-03	rs9911383	17	77151553	q25.3
SNP_A-2213990	G	G	339	23	320	38	4.214	4.01E-02	rs1122424	17	77170931	q25.3
SNP_A-1910482	A	A	272	116	245	145	4.627	0.0315	rs3088016	17	77250454	q25.3
SNP_A-2093288	A	A	409	7	402	18	4.881	2.71E-02	rs12449687	17	77303541	q25.3
SNP_A-1955499	G	G	408	0	416	4	3.905	0.0482	rs4510078	17	77799002	q25.3
SNP_A-1717593	G	G	325	77	307	103	4.19	0.0407	rs2361701	17	78766736	q25.3
SNP_A-1916270	T	T	328	84	296	110	5.082	2.42E-02	rs551835	18	150887	p11.32
SNP_A-2074095	A	A	328	44	375	27	6.059	0.0138	rs8088001	18	277705	p11.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1737373	G	G	261	109	243	167	10.808	0.001	rs585955	18	285046	p11.32
SNP_A-2048660	G	G	410	2	405	9	4.48	3.43E-02	rs2621178	18	411412	p11.32
SNP_A-2122370	C	C	378	4	388	0	4.084	4.33E-02	rs568831	18	519676	p11.32
SNP_A-1876616	A	A	310	74	325	49	5.305	2.13E-02	rs10502289	18	666789	p11.32
SNP_A-1677586	C	C	353	47	379	31	4.083	4.33E-02	rs10502291	18	918190	p11.32
SNP_A-1876783	C	G	188	166	201	165	4.638	3.13E-02	rs4798773	18	922503	p11.32
SNP_A-1656189	C	T	224	176	216	196	5.772	1.63E-02	rs4798774	18	922569	p11.32
SNP_A-1654703	G	A	224	176	217	195	6.109	0.0135	rs4797355	18	922779	p11.32
SNP_A-1876791	G	G	357	29	366	16	3.847	4.98E-02	rs16952973	18	923897	p11.32
SNP_A-2094604	G	G	172	166	197	133	5.241	2.21E-02	rs16953197	18	935728	p11.32
SNP_A-1901681	C	C	356	10	365	3	3.876	4.90E-02	rs789040	18	1007587	p11.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1876908	T	T	326	88	359	57	8.213	4.20E-03	rs789029	18	1043252	p11.32
SNP_A-2091928	T	T	356	0	331	5	5.336	2.09E-02	rs2344674	18	1349325	p11.32
SNP_A-1676668	C	C	341	13	346	26	3.926	4.75E-02	rs718714	18	1686271	p11.32
SNP_A-1877867	C	T	236	168	207	203	6.493	1.08E-02	rs6505992	18	2019050	p11.32
SNP_A-1848526	C	A	220	194	225	193	4.04	4.44E-02	rs7229380	18	2084574	p11.32
SNP_A-2105568	T	G	198	180	210	164	5.48	1.92E-02	rs1159861	18	2160087	p11.32
SNP_A-2249088	C	C	193	119	223	97	4.304	3.80E-02	rs598444	18	2163591	p11.32
SNP_A-1873712	A	A	333	57	362	36	5.871	0.0154	rs1365237	18	2256977	p11.32
SNP_A-1660493	C	C	322	78	357	55	5.605	1.79E-02	rs621949	18	2262498	p11.32
SNP_A-2037746	C	C	316	78	301	111	5.727	0.0167	rs2682136	18	2482934	p11.32
SNP_A-1899595	G	G	245	125	211	159	6.606	1.02E-02	rs9955881	18	2507898	p11.32
SNP_A-1878357	G	G	327	69	339	47	4.261	0.039	rs8090642	18	2511311	p11.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1649012	G	C	207	189	235	173	7.855	5.10E-03	rs2165807	18	3228606	p11.31
SNP_A-2145434	T	T	368	6	358	18	6.132	1.33E-02	rs1962914	18	3416898	p11.31
SNP_A-2300253	C	C	400	16	411	5	5.911	1.50E-02	rs238137	18	3437725	p11.31
SNP_A-1903079	C	C	208	108	196	150	5.846	1.56E-02	rs1791375	18	3603827	p11.31
SNP_A-1682496	T	T	242	130	288	106	5.806	0.016	rs918174	18	3726629	p11.31
SNP_A-2145452	C	C	206	192	252	158	7.746	5.40E-03	rs3745050	18	3732572	p11.31
SNP_A-2063012	G	G	216	196	256	162	6.576	0.0103	rs11873533	18	3732713	p11.31
SNP_A-2047085	T	T	293	123	269	151	3.867	4.92E-02	rs3850801	18	3797349	p11.31
SNP_A-1787802	A	A	216	178	247	147	5.033	2.49E-02	rs12962198	18	3909493	p11.31
SNP_A-1834826	G	G	351	5	294	28	19.411	0.000010538	rs8084304	18	4175754	p11.31
SNP_A-1810701	G	A	227	183	226	192	7.368	0.0066	rs628229	18	4239393	p11.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2285844	A	A	267	87	302	56	8.851	2.90E-03	rs1940446	18	4316305	p11.31
SNP_A-1850933	C	C	339	75	369	51	5.8	0.016	rs17660772	18	4328894	p11.31
SNP_A-1816579	G	G	288	96	289	63	5.47	1.93E-02	rs9965071	18	4457751	p11.31
SNP_A-1898719	A	A	247	119	276	96	4.02	4.50E-02	rs1701495	18	4478934	p11.31
SNP_A-2160148	C	C	375	19	374	8	4.298	3.82E-02	rs11872167	18	4488302	p11.31
SNP_A-1911233	C	C	330	64	317	39	4.415	0.0356	rs1630762	18	4619150	p11.31
SNP_A-1812940	G	G	303	15	309	5	5.034	2.49E-02	rs12606610	18	4761207	p11.31
SNP_A-1827531	A	A	327	59	302	86	6.016	1.42E-02	rs6506247	18	4770620	p11.31
SNP_A-2277396	C	C	340	70	315	103	7.172	7.40E-03	rs12607104	18	4799662	p11.31
SNP_A-2083158	C	C	198	194	228	168	3.96	4.66E-02	rs1466882	18	4960506	p11.31
SNP_A-1846804	T	T	322	60	299	87	5.79	0.0161	rs6506313	18	5644289	p11.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1661488	T	T	241	151	217	183	4.243	3.94E-02	rs7243271	18	5645381	p11.31
SNP_A-2100674	G	G	362	52	388	32	5.62	0.0178	rs16948655	18	5714190	p11.31
SNP_A-1951832	G	G	279	113	317	87	5.623	0.0177	rs1917908	18	5714668	p11.31
SNP_A-1758489	G	G	271	115	310	88	6.027	0.0141	rs10502337	18	5894923	p11.31
SNP_A-1945392	C	C	324	32	349	19	4.045	4.43E-02	rs1893192	18	5937874	p11.31
SNP_A-2129402	C	C	384	30	402	16	4.654	0.031	rs4798423	18	5977484	p11.31
SNP_A-1936339	C	C	301	109	268	136	4.845	2.77E-02	rs4798426	18	5998583	p11.31
SNP_A-2211702	G	G	348	56	332	78	3.944	0.047	rs11081225	18	6011598	p11.31
SNP_A-2221415	C	C	313	77	335	53	5.173	0.0229	rs11662751	18	6078451	p11.31
SNP_A-1831885	C	C	396	20	399	9	4.106	4.27E-02	rs374509	18	6305461	p11.31
SNP_A-1920645	G	G	335	55	364	38	4.13	4.21E-02	rs7504263	18	6507834	p11.31
SNP_A-2302752	C	C	368	24	391	7	9.975	1.60E-03	rs11081245	18	6514247	p11.31
SNP_A-1803831	C	C	363	17	357	35	6.096	1.36E-02	rs12967949	18	6536179	p11.31
SNP_A-2213030	C	C	277	135	252	164	3.975	4.62E-02	rs16950474	18	6665739	p11.31
SNP_A-2280561	G	A	216	192	223	187	4.398	3.60E-02	rs7232028	18	6714958	p11.31
SNP_A-2085202	C	C	336	42	355	25	4.831	2.80E-02	rs7233825	18	6757057	p11.31
SNP_A-2229527	G	G	400	16	413	3	9.103	2.60E-03	rs524592	18	6962226	p11.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1845075	G	G	250	126	259	93	4.345	3.71E-02	rs8098365	18	7423519	p11.23
SNP_A-1882569	C	C	382	32	400	18	4.315	0.0378	rs9304003	18	7861278	p11.23
SNP_A-1841225	G	G	347	29	370	14	5.887	1.53E-02	rs9304004	18	7867629	p11.23
SNP_A-1915575	T	T	384	32	404	12	9.599	0.0019	rs17565758	18	7887307	p11.23
SNP_A-2164357	C	C	289	79	303	55	4.493	3.40E-02	rs2165412	18	7912931	p11.23
SNP_A-1783281	G	G	333	29	328	14	4.706	3.01E-02	rs17566876	18	7946629	p11.23
SNP_A-1828676	A	A	306	28	325	13	6.036	0.014	rs6506551	18	8157050	p11.23
SNP_A-2246461	G	C	195	179	198	156	4.745	2.94E-02	rs12457610	18	8200848	p11.23
SNP_A-1830576	T	T	332	46	355	29	4.576	3.24E-02	rs7505928	18	8261135	p11.23
SNP_A-2150585	C	C	408	6	402	16	4.571	3.25E-02	rs616096	18	8296371	p11.23
SNP_A-1781267	T	T	309	61	272	104	13.515	2.00E-04	rs3786385	18	8310132	p11.23
SNP_A-1674881	T	T	279	99	266	130	4.09	4.31E-02	rs2242148	18	8351185	p11.23
SNP_A-1871712	T	T	244	158	280	136	3.881	4.88E-02	rs675000	18	8415242	p11.23
SNP_A-2083016	C	C	351	61	376	42	4.321	3.76E-02	rs8084088	18	8466110	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2050435	G	G	337	41	302	64	6.763	9.30E-03	rs17497272	18	8542194	p11.22
SNP_A-2198916	T	T	259	123	248	162	4.591	3.21E-02	rs6506598	18	8553622	p11.22
SNP_A-1883215	A	A	244	92	202	120	7.359	6.70E-03	rs17582905	18	8558109	p11.22
SNP_A-1702745	G	G	235	163	271	141	3.913	4.79E-02	rs7505175	18	8617957	p11.22
SNP_A-1883315	G	G	304	78	320	50	6.345	0.0118	rs9304022	18	8677353	p11.22
SNP_A-1883344	A	A	284	120	320	84	8.499	3.60E-03	rs2160913	18	8706090	p11.22
SNP_A-1883346	C	C	193	165	221	137	4.49	3.41E-02	rs2111836	18	8706321	p11.22
SNP_A-2309761	C	T	171	163	184	130	6.244	1.25E-02	rs2160912	18	8706389	p11.22
SNP_A-1814528	G	G	242	170	274	142	4.478	3.43E-02	rs12606001	18	8772147	p11.22
SNP_A-1671450	T	T	289	111	256	154	8.853	2.90E-03	rs987850	18	9015102	p11.22
SNP_A-1916100	A	A	288	106	238	128	5.798	0.016	rs4798766	18	9076213	p11.22
SNP_A-2206380	A	A	259	105	222	138	7.306	6.90E-03	rs4797356	18	9139437	p11.22
SNP_A-2308956	C	C	322	46	293	91	15.815	6.98E-05	rs8092135	18	9264636	p11.22
SNP_A-1898123	T	T	248	166	209	199	6.268	0.0123	rs751355	18	9418420	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2309934	G	G	346	52	316	92	12.348	4.00E-04	rs11081480	18	9447938	p11.22
SNP_A-1834301	G	G	348	66	323	93	5.512	0.0189	rs167897	18	9517100	p11.22
SNP_A-1730893	C	C	371	25	364	42	4.256	3.91E-02	rs7240572	18	9520794	p11.22
SNP_A-1883892	A	A	367	13	354	26	4.568	3.26E-02	rs1942150	18	9528533	p11.22
SNP_A-2005449	T	T	292	34	247	63	12.032	5.00E-04	rs329024	18	9555132	p11.22
SNP_A-2128984	G	G	267	57	307	39	5.446	1.96E-02	rs9946612	18	9567981	p11.22
SNP_A-2005450	T	T	406	10	417	1	7.506	6.10E-03	rs623714	18	9629037	p11.22
SNP_A-1810185	A	A	192	190	233	173	4.024	4.49E-02	rs8091737	18	9740662	p11.22
SNP_A-1884103	G	G	196	184	229	161	3.966	4.64E-02	rs16955541	18	9743992	p11.22
SNP_A-1666674	A	A	399	1	403	9	6.244	1.25E-02	rs10513878	18	9880513	p11.22
SNP_A-2128559	G	G	411	1	401	7	4.604	3.19E-02	rs9957463	18	9882595	p11.22
SNP_A-1824253	T	T	386	4	408	0	4.206	4.03E-02	rs16956143	18	10028833	p11.22
SNP_A-2287215	A	A	411	5	412	0	4.982	2.56E-02	rs7229890	18	10037518	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2277408	A	A	382	4	400	0	4.166	4.12E-02	rs11872904	18	10038989	p11.22
SNP_A-1797710	C	C	329	37	357	19	6.795	9.10E-03	rs16956185	18	10042421	p11.22
SNP_A-2246918	T	T	284	90	264	118	4.415	0.0356	rs4797397	18	10045997	p11.22
SNP_A-2022539	G	G	198	126	167	151	4.834	2.79E-02	rs759278	18	10128753	p11.22
SNP_A-2298999	G	G	191	143	215	103	7.535	6.10E-03	rs481377	18	10140262	p11.22
SNP_A-2172212	C	C	283	83	257	111	5.288	2.15E-02	rs12953713	18	10208053	p11.22
SNP_A-2038200	C	C	349	47	334	72	5.458	0.0195	rs12604946	18	10262816	p11.22
SNP_A-2124296	T	T	286	94	273	125	4.276	3.86E-02	rs11080417	18	10413834	p11.22
SNP_A-1800360	T	T	331	5	324	0	4.858	0.0275	rs16974452	18	10425362	p11.22
SNP_A-2139993	A	A	375	29	350	56	9.434	2.10E-03	rs16974887	18	10545012	p11.22
SNP_A-1698925	C	C	369	31	354	58	8.327	3.90E-03	rs10502394	18	10547670	p11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1955303	T	T	295	115	269	149	5.501	0.019	rs564499	18	10556581	p11.22
SNP_A-2310943	T	T	328	28	306	46	5.119	2.37E-02	rs9956847	18	10772696	p11.22
SNP_A-2097312	G	G	244	164	270	134	4.316	0.0378	rs11665145	18	10802708	p11.22
SNP_A-1886851	C	C	387	29	400	16	3.97	4.63E-02	rs7243607	18	10939865	p11.21
SNP_A-2227223	T	T	316	26	285	41	4.577	3.24E-02	rs4797528	18	11296074	p11.21
SNP_A-2266425	C	C	375	31	362	54	6.332	1.19E-02	rs457329	18	11297693	p11.21
SNP_A-1935145	C	C	380	34	363	55	5.325	2.10E-02	rs7243042	18	11300112	p11.21
SNP_A-2142137	A	A	310	54	333	37	3.95	4.69E-02	rs370233	18	11311282	p11.21
SNP_A-1652048	G	G	363	9	354	2	4.218	4.00E-02	rs1004322	18	11506816	p11.21
SNP_A-1947876	C	C	184	166	214	142	4.081	4.34E-02	rs8095071	18	11655546	p11.21
SNP_A-1831149	A	A	316	36	272	56	6.802	9.10E-03	rs17515178	18	11677569	p11.21
SNP_A-1708018	G	G	354	40	383	25	4.36	3.68E-02	rs10502413	18	11691777	p11.21
SNP_A-1750333	C	C	357	43	388	22	7.952	4.80E-03	rs9303743	18	11702839	p11.21
SNP_A-2148660	C	C	276	80	289	47	8.303	4.00E-03	rs1786566	18	11814358	p11.21
SNP_A-1844811	C	C	408	8	419	1	5.572	0.0183	rs12457818	18	11882860	p11.21
SNP_A-2070968	A	A	309	91	286	118	4.357	3.69E-02	rs589247	18	11982725	p11.21
SNP_A-2292842	C	C	205	119	177	147	5	2.54E-02	rs6336173	18	11986337	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1859954	G	G	305	85	276	112	5.143	2.33E-02	rs627965	18	12025994	p11.21
SNP_A-2147909	C	C	293	75	241	93	5.358	0.0206	rs4797609	18	12029414	p11.21
SNP_A-2215121	G	G	336	36	323	55	4.176	4.10E-02	rs9303766	18	12290849	p11.21
SNP_A-2229699	C	C	320	82	338	56	5.311	0.0212	rs3786261	18	12352219	p11.21
SNP_A-1886633	A	A	390	10	392	2	5.293	2.14E-02	rs16973056	18	12389481	p11.21
SNP_A-1930561	T	T	362	38	362	20	5.175	0.0229	rs17615991	18	12538970	p11.21
SNP_A-2146125	T	T	356	40	327	81	14.948	0.0001	rs2542151	18	12769947	p11.21
SNP_A-1692528	T	T	322	78	348	56	4.601	3.20E-02	rs10502415	18	12799561	p11.21
SNP_A-1782372	T	T	310	58	338	36	6.311	0.012	rs17597893	18	12802061	p11.21
SNP_A-2199153	C	C	361	55	342	78	4.472	3.45E-02	rs16939895	18	12811903	p11.21
SNP_A-2294450	G	G	243	83	234	124	6.808	9.10E-03	rs7228684	18	13042473	p11.21
SNP_A-1832577	T	T	394	20	409	9	4.433	3.52E-02	rs16940084	18	13052413	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1672692	A	G	233	165	207	205	6.292	0.0121	rs1787013	18	13062979	p11.21
SNP_A-1724620	C	C	237	163	204	202	6.592	1.02E-02	rs571002	18	13080667	p11.21
SNP_A-2187401	C	T	220	166	196	186	5.313	0.0212	rs693301	18	13087207	p11.21
SNP_A-2105729	C	C	246	112	218	148	6.587	0.0103	rs12327306	18	13120681	p11.21
SNP_A-2079769	C	C	287	125	322	98	5.204	2.25E-02	rs1026330	18	13370824	p11.21
SNP_A-2094768	C	C	219	161	255	139	4.096	4.30E-02	rs3931961	18	13393109	p11.21
SNP_A-2313982	C	C	392	10	387	21	3.891	4.85E-02	rs6505813	18	13412042	p11.21
SNP_A-1883931	C	C	322	44	358	20	10.715	1.10E-03	rs3809903	18	13481039	p11.21
SNP_A-1872038	C	C	252	132	274	98	5.757	1.64E-02	rs9955173	18	13501622	p11.21
SNP_A-2240083	G	G	292	112	313	83	4.962	2.59E-02	rs11665065	18	13522208	p11.21
SNP_A-1857954	T	T	334	4	332	0	3.953	4.68E-02	rs9947231	18	13541744	p11.21
SNP_A-1843458	A	A	202	132	176	170	6.36	0.0117	rs4797793	18	13628962	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2232557	C	C	247	89	220	116	5.117	2.37E-02	rs1786510	18	13629278	p11.21
SNP_A-1887468	C	C	400	12	388	26	5.336	2.09E-02	rs17695517	18	13801006	p11.21
SNP_A-2268903	T	T	263	101	277	75	4.004	4.54E-02	rs8090695	18	13937602	p11.21
SNP_A-1693455	C	C	364	36	392	20	5.432	1.98E-02	rs10502426	18	13973649	p11.21
SNP_A-2204091	C	C	327	31	307	15	4.302	3.81E-02	rs7506352	18	14716659	p11.21
SNP_A-1877999	T	T	324	36	365	23	4.262	0.039	—	18	14717019	p11.21
SNP_A-1954238	C	C	364	32	381	17	4.975	2.57E-02	rs11080786	18	14727026	p11.21
SNP_A-1882577	T	T	298	42	298	22	5.649	1.75E-02	rs9675388	18	14727187	p11.21
SNP_A-2215835	T	T	330	26	348	14	4.028	0.0448	rs10853250	18	14729614	p11.21
SNP_A-2280344	G	G	364	32	385	17	5.136	2.34E-02	rs9963735	18	14734695	p11.21
SNP_A-2255984	A	A	339	51	330	76	4.723	0.0298	rs2384785	18	17233563	q11.1
SNP_A-2175435	T	T	347	43	328	62	3.973	4.62E-02	rs2850565	18	17510144	q11.2
SNP_A-2084637	C	C	380	26	370	42	3.854	4.96E-02	rs7231159	18	17953244	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2303811	C	C	347	19	379	9	4.344	3.71E-02	rs8086508	18	18184583	q11.2
SNP_A-1892048	G	G	313	67	349	49	4.337	0.0373	rs4572512	18	18204117	q11.2
SNP_A-1836464	G	A	208	182	215	179	4.896	0.0269	rs12958098	18	18399377	q11.2
SNP_A-1934771	G	G	230	158	200	184	4.049	4.42E-02	rs11878170	18	18414140	q11.2
SNP_A-1889774	C	T	199	177	212	178	4.064	4.38E-02	rs1521919	18	18527880	q11.2
SNP_A-1916200	G	G	400	0	404	4	3.941	4.71E-02	rs7231643	18	19011656	q11.2
SNP_A-1863212	G	G	352	42	370	26	4.208	0.0402	rs2270885	18	19312965	q11.2
SNP_A-1940869	C	C	377	9	398	2	4.776	2.89E-02	rs1788773	18	19531123	q11.2
SNP_A-2266428	G	G	331	11	358	2	6.832	9.00E-03	rs4800518	18	19694139	q11.2
SNP_A-1813779	C	C	406	8	417	1	5.572	1.82E-02	rs2337234	18	19832752	q11.2
SNP_A-2309070	C	C	316	80	327	55	4.567	3.26E-02	rs4476256	18	19944866	q11.2
SNP_A-1807039	A	A	332	42	344	26	3.956	4.67E-02	rs17259667	18	19994190	q11.2
SNP_A-2145817	T	T	412	4	405	13	4.82	0.0281	rs339868	18	20461987	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2198390	A	A	290	74	271	101	4.723	0.0298	rs9959791	18	20642397	q11.2
SNP_A-2106364	A	A	263	81	236	112	6.417	1.13E-02	rs11877115	18	20731893	q11.2
SNP_A-2090521	T	T	351	7	377	1	4.889	0.027	rs13381064	18	20745032	q11.2
SNP_A-1824274	G	G	269	133	305	105	5.474	1.93E-02	rs12608210	18	20747882	q11.2
SNP_A-1891388	C	C	234	180	267	151	4.695	3.02E-02	rs10502463	18	20815751	q11.2
SNP_A-2166583	T	T	316	86	285	111	4.727	2.97E-02	rs6508341	18	20825396	q11.2
SNP_A-1694227	C	C	300	96	276	126	5.009	0.0252	rs1941616	18	20835029	q11.2
SNP_A-1870392	C	C	380	6	408	0	6.39	0.0115	rs17188291	18	20842155	q11.2
SNP_A-2256617	C	C	300	116	273	145	4.49	3.41E-02	rs4133168	18	21066506	q11.2
SNP_A-1905754	C	C	317	97	272	140	11.235	8.00E-04	rs7234276	18	21069650	q11.2
SNP_A-2301414	G	G	209	93	193	137	7.829	5.10E-03	rs7234419	18	21069702	q11.2
SNP_A-2125449	C	C	311	67	269	93	6.924	8.50E-03	rs10432210	18	21115792	q11.2
SNP_A-2301150	T	T	232	178	269	147	5.646	1.75E-02	rs4800250	18	22064765	q11.2
SNP_A-2235168	C	C	225	173	260	140	6	0.0143	rs14478286	18	22161346	q11.2
SNP_A-1892100	C	C	235	133	186	144	4.083	4.33E-02	rs1599910	18	22271922	q11.2
SNP_A-1785975	G	G	367	19	377	7	5.668	1.73E-02	rs12953992	18	22307822	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1894707	G	G	367	47	385	29	4.694	3.03E-02	rs17604918	18	22332158	q11.2
SNP_A-2232276	A	A	406	0	400	6	6.045	1.39E-02	rs8098388	18	22334745	q11.2
SNP_A-2312578	C	C	271	137	306	108	5.512	0.0189	rs11083174	18	22361629	q11.2
SNP_A-2161309	T	C	219	167	212	190	7.077	7.80E-03	rs2186948	18	22367298	q11.2
SNP_A-1871013	G	G	405	7	394	20	6.406	0.0114	rs8083482	18	22381311	q11.2
SNP_A-2057564	C	C	378	38	359	59	5.031	2.49E-02	rs11872394	18	22612517	q11.2
SNP_A-1659192	G	A	236	164	212	196	9.753	0.0018	rs335920	18	22783999	q11.2
SNP_A-2046379	G	G	251	157	209	199	8.79	3.00E-03	rs559547	18	22787798	q11.2
SNP_A-2005536	T	T	224	140	247	105	5.924	0.0149	rs1657316	18	22803905	q11.2
SNP_A-2005537	A	A	225	141	267	107	8.161	0.0043	rs4093026	18	22804050	q11.2
SNP_A-1892840	C	C	275	113	236	162	11.582	7.00E-04	rs10502481	18	22831048	q11.2
SNP_A-2038036	A	A	241	153	280	130	4.472	3.45E-02	rs1145109	18	22833416	q11.2
SNP_A-1892862	C	C	204	142	257	109	9.878	1.70E-03	rs964008	18	22847901	q11.2
SNP_A-1841860	C	C	247	159	280	132	4.528	3.33E-02	rs1485805	18	22854673	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2040007	A	A	231	143	262	112	5.718	1.68E-02	rs720282	18	22854839	q11.2
SNP_A-1892894	G	G	359	55	340	78	4.475	0.0344	rs1941114	18	22868217	q11.2
SNP_A-1836972	A	G	238	164	208	188	11.028	9.00E-04	rs12604227	18	22874298	q11.2
SNP_A-1950457	G	G	233	145	262	120	4.037	4.45E-02	rs8084423	18	22874628	q11.2
SNP_A-2157512	C	C	349	63	365	43	4.113	4.26E-02	rs11660384	18	23055299	q11.2
SNP_A-1656687	T	T	336	62	368	44	4.27	3.88E-02	rs10502487	18	23076477	q11.2
SNP_A-1716057	T	T	337	63	368	44	4.561	0.0327	rs10502488	18	23076744	q11.2
SNP_A-1893078	T	T	385	15	377	29	4.494	3.40E-02	rs10502490	18	23189662	q11.2
SNP_A-1694647	C	C	359	29	353	51	5.78	1.62E-02	rs7242201	18	23189904	q11.2
SNP_A-2239438	A	A	334	4	346	0	4.119	0.0424	rs1941168	18	23312837	q12.1
SNP_A-2212502	A	A	244	170	264	138	3.936	4.73E-02	rs16943751	18	23402923	q12.1
SNP_A-2298614	A	A	194	164	217	131	4.838	2.78E-02	rs597591	18	23836287	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1893615	G	G	215	185	255	135	11.092	9.00E-04	rs500643	18	23883297	q12.1
SNP_A-2241432	G	G	281	103	310	74	6.174	1.30E-02	rs11564410	18	23888092	q12.1
SNP_A-1950057	T	A	198	158	189	167	5.402	0.0201	rs1148374	18	23904280	q12.1
SNP_A-1834553	T	T	173	171	205	127	8.995	2.70E-03	rs1148376	18	23906975	q12.1
SNP_A-1940630	G	G	330	54	317	77	4.172	4.11E-02	rs1231268	18	23944009	q12.1
SNP_A-2256584	A	A	256	112	216	132	4.474	0.0344	rs2191638	18	24157052	q12.1
SNP_A-1792816	C	C	350	10	344	2	5.11	2.38E-02	rs492026	18	24776123	q12.1
SNP_A-2074663	C	C	277	111	284	80	4.357	3.69E-02	rs7231282	18	24857871	q12.1
SNP_A-1853561	A	A	265	113	302	90	4.767	2.90E-02	rs11083330	18	25231071	q12.1
SNP_A-1830019	G	G	369	25	355	7	9.057	2.60E-03	rs16947039	18	25465240	q12.1
SNP_A-2149129	G	G	401	1	404	10	7.2	7.30E-03	rs16947081	18	25527456	q12.1
SNP_A-2005549	G	G	305	7	328	0	7.44	6.40E-03	rs7235884	18	25597558	q12.1
SNP_A-1929531	A	A	228	102	198	124	4.157	4.15E-02	rs1382402	18	26443129	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1895606	C	C	335	11	357	3	4.995	2.54E-02	rs10502550	18	26714645	q12.1
SNP_A-1675259	C	C	379	15	371	37	9.151	2.50E-03	rs10502551	18	26719846	q12.1
SNP_A-1895669	C	C	284	116	322	86	6.76	9.30E-03	rs12373365	18	26834409	q12.1
SNP_A-1895670	C	C	256	78	306	62	4.641	3.12E-02	rs11081674	18	26834488	q12.1
SNP_A-1822058	G	G	297	109	329	83	5.113	2.37E-02	rs11081675	18	26834675	q12.1
SNP_A-1957367	T	T	266	148	294	122	3.899	4.83E-02	rs1313586	18	26840962	q12.1
SNP_A-2107357	C	C	300	114	334	86	5.7	1.70E-02	rs12607476	18	26841275	q12.1
SNP_A-2048608	A	A	281	101	317	73	6.591	0.0103	rs1313692	18	26842863	q12.1
SNP_A-2103211	G	G	301	115	334	86	5.88	1.53E-02	rs1313591	18	26844326	q12.1
SNP_A-2263014	T	T	194	192	217	141	8.056	4.50E-03	rs276922	18	26858793	q12.1
SNP_A-2120219	A	A	203	195	239	135	13.108	3.00E-04	rs202439	18	26859713	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086099	C	G	189	183	215	145	8.175	4.20E-03	rs1313593	18	26860823	q12.1
SNP_A-2172934	C	C	338	70	365	51	3.943	4.71E-02	rs1586961	18	26875209	q12.1
SNP_A-1853049	A	A	265	143	231	167	4.065	4.38E-02	rs1469303	18	27043013	q12.1
SNP_A-1895946	G	G	334	4	283	21	14.014	2.00E-04	rs16961526	18	27080895	q12.1
SNP_A-1824512	C	C	319	33	308	54	5.123	2.36E-02	rs11081728	18	27765661	q12.1
SNP_A-1679908	A	A	367	13	343	31	8.128	4.40E-03	rs10502585	18	28051300	q12.1
SNP_A-2052424	A	A	393	17	384	32	4.653	0.031	rs9963993	18	28075158	q12.1
SNP_A-1710878	A	A	326	26	322	56	10.087	0.0015	rs10502603	18	28308502	q12.1
SNP_A-1683030	C	C	277	123	254	156	4.777	2.88E-02	rs10502604	18	28319632	q12.1
SNP_A-2308068	T	C	219	175	204	184	5.213	0.0224	rs16963478	18	28353130	q12.1
SNP_A-1934268	C	C	382	0	399	5	4.758	0.0292	rs1916650	18	28588759	q12.1
SNP_A-2304066	G	G	388	4	410	0	4.205	4.03E-02	rs16964115	18	28741896	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2005562	C	C	396	18	382	34	5.17	0.023	rs4387665	18	28845705	q12.1
SNP_A-2143811	G	G	398	18	380	38	7.555	6.00E-03	rs9960087	18	28868184	q12.1
SNP_A-2213218	T	T	356	14	330	28	5.456	0.0195	rs9950875	18	28886506	q12.1
SNP_A-2064423	G	G	370	4	375	17	7.662	5.60E-03	rs1482947	18	28899566	q12.1
SNP_A-1943627	A	A	387	11	378	26	6.142	0.0132	rs9956960	18	28918355	q12.1
SNP_A-1916267	A	A	375	9	365	23	6.24	1.25E-02	rs443593	18	28918428	q12.1
SNP_A-1884498	C	C	399	15	385	31	5.81	1.59E-02	rs271483	18	28933471	q12.1
SNP_A-1726904	A	A	383	15	381	29	4.283	0.0385	rs273024	18	28935909	q12.1
SNP_A-2037455	C	C	400	14	391	29	5.292	2.14E-02	rs271441	18	28943823	q12.1
SNP_A-1830997	T	T	404	8	394	18	3.971	4.63E-02	rs2047365	18	28954365	q12.1
SNP_A-1879121	G	G	371	3	356	10	3.993	4.57E-02	rs271467	18	29006831	q12.1
SNP_A-2025201	C	C	276	130	242	170	7.521	6.10E-03	rs9948697	18	29278608	q12.1
SNP_A-1700193	T	T	282	118	252	160	7.855	5.10E-03	rs9304121	18	29295245	q12.1
SNP_A-1748091	G	A	202	178	223	175	6.571	0.0104	rs1981360	18	29494898	q12.1
SNP_A-2074610	G	G	202	130	235	87	10.862	0.001	rs9966468	18	29787091	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2294448	G	G	221	153	270	124	7.41	6.50E-03	rs4799737	18	29861711	q12.1
SNP_A-1898353	G	G	337	75	362	50	5.894	0.0152	rs4413039	18	29916504	q12.1
SNP_A-2005569	G	G	354	6	346	16	4.631	3.14E-02	rs4073420	18	29916953	q12.1
SNP_A-2102616	T	T	261	77	289	55	5.04	2.48E-02	rs4419129	18	29917758	q12.1
SNP_A-1898453	A	A	316	2	336	10	4.775	2.89E-02	rs16965408	18	30376497	q12.1
SNP_A-1930088	A	A	276	50	250	82	8.989	2.70E-03	rs1790534	18	30663569	q12.1
SNP_A-2005574	T	T	321	61	289	81	4.305	3.80E-02	rs878767	18	30675637	q12.1
SNP_A-1695525	C	C	255	145	229	175	4.189	0.0407	rs920799	18	30864525	q12.1
SNP_A-2107243	T	T	266	142	227	185	8.72	3.10E-03	rs12958434	18	30871606	q12.1
SNP_A-2128200	C	C	273	51	302	30	6.811	9.10E-03	rs1362859	18	31172637	q12.2
SNP_A-1863252	T	T	342	38	342	22	3.924	4.76E-02	rs2909346	18	31206680	q12.2
SNP_A-1822257	G	A	206	158	202	174	7.88	5.00E-03	rs2978362	18	31213395	q12.2
SNP_A-1846252	G	A	180	168	193	145	5.356	0.0207	rs11876796	18	31217794	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2224672	G	G	289	23	287	43	5.567	0.0183	rs8095921	18	31406619	q12.2
SNP_A-2265445	G	G	255	137	276	108	4.181	4.09E-02	rs2156044	18	31642936	q12.2
SNP_A-1958672	C	C	300	52	289	31	4.004	4.54E-02	rs8092436	18	32099464	q12.2
SNP_A-2120216	A	A	313	73	299	105	5.666	1.73E-02	rs17746090	18	32195942	q12.2
SNP_A-1854699	C	C	234	158	275	131	5.581	1.82E-02	rs12606773	18	32207374	q12.2
SNP_A-2130861	T	T	293	87	335	49	13.406	3.00E-04	rs3744897	18	32209042	q12.2
SNP_A-2288561	T	T	226	152	263	113	8.534	3.50E-03	rs9967116	18	32213045	q12.2
SNP_A-2186113	A	A	253	159	296	118	9.432	2.10E-03	rs9944689	18	32213713	q12.2
SNP_A-2250235	A	A	254	160	301	119	9.963	1.60E-03	rs1398957	18	32215208	q12.2
SNP_A-2177276	A	A	311	105	354	66	11.656	6.00E-04	rs11081947	18	32224860	q12.2
SNP_A-2108841	C	C	339	77	360	50	6.328	1.19E-02	rs12606914	18	32232537	q12.2
SNP_A-2073076	G	G	305	93	340	54	12.226	5.00E-04	rs17673355	18	32233439	q12.2
SNP_A-2211134	T	T	320	6	358	0	6.647	9.90E-03	rs752520	18	32537783	q12.2
SNP_A-1953912	C	C	348	58	354	36	4.881	2.72E-02	rs12458233	18	33536199	q12.2
SNP_A-1880343	A	A	247	73	267	53	3.953	4.68E-02	rs1385029	18	33866436	q12.2
SNP_A-1900948	A	A	254	86	263	61	4.025	0.0448	rs1484092	18	33956825	q12.2
SNP_A-1822098	A	C	203	193	222	176	3.945	0.047	rs8083420	18	34074362	q12.2
SNP_A-1901062	G	G	227	159	255	133	3.936	4.72E-02	rs17628762	18	34125717	q12.2
SNP_A-1901189	C	C	253	115	266	76	7.347	6.70E-03	rs17706317	18	34234526	q12.2
SNP_A-1750387	C	C	262	138	297	115	4.106	4.27E-02	rs1196582	18	34237746	q12.2
SNP_A-1901370	A	A	255	73	249	107	5.356	0.0206	rs16970456	18	34337125	q12.2
SNP_A-2256014	G	G	337	21	338	42	6.351	0.0117	rs16970664	18	34416580	q12.2
SNP_A-1901476	C	C	376	32	355	51	4.948	2.61E-02	rs17647846	18	34421591	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960058	A	A	270	80	248	104	4.059	4.39E-02	rs1365466	18	34436438	q12.2
SNP_A-1686434	G	G	367	31	353	51	5.106	2.38E-02	rs4627439	18	34486191	q12.2
SNP_A-2230004	A	A	230	138	195	163	4.822	0.0281	rs4583326	18	34756878	q12.2
SNP_A-1715343	T	T	276	124	311	99	4.767	2.90E-02	rs10502719	18	34878964	q12.2
SNP_A-2088907	G	G	376	10	349	21	4.572	3.25E-02	rs16971709	18	35076989	q12.2
SNP_A-1743491	C	C	344	20	348	38	4.968	0.0258	rs10502721	18	35112643	q12.2
SNP_A-1901968	T	T	372	2	330	8	4.304	3.80E-02	rs1431691	18	35114145	q12.2
SNP_A-1943113	C	C	317	47	305	73	5.603	1.79E-02	rs7233056	18	35128500	q12.2
SNP_A-1655345	A	A	350	44	311	73	9.362	2.20E-03	rs10502723	18	35150359	q12.2
SNP_A-2190488	T	T	293	67	325	41	7.867	5.00E-03	rs4799278	18	35679661	q12.3
SNP_A-1902325	A	A	293	53	329	23	13.875	2.00E-04	rs11082154	18	35679897	q12.3
SNP_A-1892288	G	G	319	97	352	68	6.701	9.60E-03	rs4799520	18	35682032	q12.3
SNP_A-1933221	A	A	284	116	251	149	6.145	0.0132	rs17702736	18	35684521	q12.3
SNP_A-1902368	C	C	308	100	344	66	8.947	0.0028	rs10502727	18	35754311	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1902370	A	A	364	46	333	69	5.901	1.51E-02	rs307133	18	35754878	q12.3
SNP_A-1948085	C	C	276	30	324	18	4.855	0.0276	rs12608334	18	35755273	q12.3
SNP_A-2152767	T	T	287	91	320	62	7.27	7.00E-03	rs16972477	18	35776504	q12.3
SNP_A-2188304	A	A	293	119	261	143	3.969	4.64E-02	rs17632270	18	35809428	q12.3
SNP_A-1902438	C	C	276	76	326	44	12.245	5.00E-04	rs12960212	18	35827675	q12.3
SNP_A-1902463	C	C	307	95	276	120	4.51	3.37E-02	rs962365	18	35841228	q12.3
SNP_A-2269541	C	C	279	113	256	148	5.503	0.019	rs1433838	18	36255355	q12.3
SNP_A-2290552	G	G	335	73	308	98	4.784	0.0287	rs9965380	18	36396942	q12.3
SNP_A-2199954	T	T	317	71	277	97	6.462	1.10E-02	rs9954415	18	36397038	q12.3
SNP_A-2282388	C	C	211	139	235	109	4.869	2.73E-02	rs3884664	18	36410642	q12.3
SNP_A-2151987	T	T	272	124	233	143	3.848	4.98E-02	rs9950173	18	36447482	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1902979	T	T	247	107	206	134	6.456	0.0111	rs11082201	18	36463880	q12.3
SNP_A-1684770	G	G	286	112	260	140	4.344	3.71E-02	rs1545112	18	36471840	q12.3
SNP_A-1864108	T	T	282	104	256	130	4.145	4.17E-02	rs9945502	18	36485939	q12.3
SNP_A-2230107	C	C	296	116	272	144	4.01	4.52E-02	rs1595271	18	36490276	q12.3
SNP_A-1857843	C	C	300	116	273	145	4.49	3.41E-02	rs10084027	18	36490748	q12.3
SNP_A-1914188	G	G	258	88	225	119	6.891	8.70E-03	rs1437012	18	36497101	q12.3
SNP_A-1890000	T	T	374	40	352	60	4.662	3.08E-02	rs9954743	18	36501687	q12.3
SNP_A-2250036	A	A	283	97	251	119	4.026	0.0448	rs9956432	18	36507047	q12.3
SNP_A-1903064	T	T	297	113	268	140	4.365	3.67E-02	rs2043681	18	36511228	q12.3
SNP_A-1829989	A	A	263	101	228	124	4.646	3.11E-02	---	18	36524070	q12.3
SNP_A-2005607	C	C	273	99	231	123	5.652	1.74E-02	rs7505871	18	36530398	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1729606	C	C	371	27	365	47	5.214	0.0224	rs10502742	18	36569397	q12.3
SNP_A-1865757	T	T	392	8	372	22	7.012	8.10E-03	rs16973801	18	36693702	q12.3
SNP_A-1923435	C	C	366	12	392	4	4.476	0.0344	rs639128	18	36803484	q12.3
SNP_A-2163062	C	C	368	40	390	22	5.845	1.56E-02	rs513611	18	36820133	q12.3
SNP_A-2270317	A	A	303	75	283	99	3.972	4.63E-02	rs4243274	18	36899016	q12.3
SNP_A-1960516	T	T	378	8	373	19	4.469	3.45E-02	rs16974556	18	37212839	q12.3
SNP_A-1732848	C	C	388	12	387	25	4.392	0.0361	rs10502766	18	37373475	q12.3
SNP_A-2036778	G	G	401	11	389	25	5.622	0.0177	rs2612333	18	37384906	q12.3
SNP_A-1905981	G	G	401	9	389	21	4.982	2.56E-02	rs2587626	18	37389349	q12.3
SNP_A-1700081	T	T	348	34	351	57	4.976	2.57E-02	rs10502770	18	37415059	q12.3
SNP_A-1903752	C	C	352	28	341	45	4.087	4.32E-02	rs9304250	18	37418020	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2025942	T	T	338	0	303	5	5.53	1.87E-02	rs16975044	18	37437371	q12.3
SNP_A-1805176	T	G	207	169	214	188	5.338	2.09E-02	rs9956021	18	37682413	q12.3
SNP_A-1903951	A	A	276	122	229	149	6.553	1.05E-02	rs768343	18	37686676	q12.3
SNP_A-1918531	A	A	346	0	356	4	3.866	4.93E-02	rs1019905	18	37752231	q12.3
SNP_A-1710359	A	A	294	102	338	74	7.204	7.30E-03	rs898783	18	38152850	q12.3
SNP_A-2100808	G	G	310	46	307	23	6.705	9.60E-03	rs971293	18	38290221	q12.3
SNP_A-2082795	A	A	405	11	391	29	8.327	3.90E-03	rs11876814	18	38418544	q12.3
SNP_A-2133193	G	G	405	11	388	24	5.174	0.0229	rs11873748	18	38418765	q12.3
SNP_A-1853840	A	A	404	10	385	23	5.535	1.86E-02	rs11082282	18	38418935	q12.3
SNP_A-1744315	C	C	248	152	214	198	8.372	0.0038	rs4890428	18	38949327	q12.3
SNP_A-1958977	A	A	403	5	388	18	7.627	5.70E-03	---	18	38980974	q12.3
SNP_A-1691598	T	T	248	152	214	196	7.943	4.80E-03	rs1518148	18	38985165	q12.3
SNP_A-1862655	G	G	230	154	198	190	6.139	0.0132	rs3861290	18	39013379	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1650372	G	G	260	140	231	181	6.774	9.30E-03	rs627966	18	39174808	q12.3
SNP_A-2086461	T	T	350	52	318	70	3.942	4.71E-02	rs16977484	18	39186004	q12.3
SNP_A-2035006	C	C	301	107	266	138	6.063	0.0138	rs648087	18	39187564	q12.3
SNP_A-1893253	C	C	304	104	277	139	6.219	0.0126	rs685851	18	39188598	q12.3
SNP_A-2209295	G	G	290	90	265	129	7.821	5.20E-03	rs615111	18	39188973	q12.3
SNP_A-1794226	T	T	301	103	268	134	5.964	0.0146	rs603651	18	39189202	q12.3
SNP_A-2005622	C	C	286	118	249	147	5.653	1.74E-02	rs610325	18	39207131	q12.3
SNP_A-1758137	A	A	324	74	301	111	8.007	4.70E-03	rs687483	18	39241323	q12.3
SNP_A-2075507	A	A	309	103	278	134	5.692	1.70E-02	rs12232657	18	39244375	q12.3
SNP_A-1715177	G	G	272	128	307	105	4.21	0.0402	rs1144613	18	39250614	q12.3
SNP_A-1668811	G	G	240	160	287	125	8.314	3.90E-03	rs504693	18	39266469	q12.3
SNP_A-2074477	A	A	318	34	307	65	9.355	2.20E-03	rs12455863	18	39306233	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1840988	C	C	356	58	333	87	6.525	0.0106	rs12456239	18	39313459	q12.3
SNP_A-1653938	T	T	295	89	258	112	4.849	2.77E-02	rs8096082	18	39350243	q12.3
SNP_A-1872899	A	A	289	41	317	27	3.887	0.0487	rs1899058	18	39597116	q12.3
SNP_A-2025061	C	C	333	19	357	9	4.135	4.20E-02	rs596725	18	40028858	q12.3
SNP_A-2314182	C	C	280	66	223	81	5.298	2.13E-02	rs16978001	18	40287441	q12.3
SNP_A-2130623	T	T	321	5	354	0	5.47	1.93E-02	rs9956543	18	40673573	q12.3
SNP_A-1906520	A	A	358	56	339	81	5.037	2.48E-02	rs998124	18	40979660	q12.3
SNP_A-1852966	G	G	257	153	221	181	4.98	2.56E-02	rs12962056	18	40989943	q12.3
SNP_A-1804555	C	C	236	124	201	157	6.673	9.80E-03	rs8091576	18	40990472	q12.3
SNP_A-2121169	G	G	237	135	192	164	7.185	7.40E-03	rs11082425	18	40990866	q12.3
SNP_A-1816399	T	T	235	139	201	161	4.07	0.0436	rs8095987	18	40991282	q12.3
SNP_A-2297694	G	G	349	33	384	8	16.789	4.18E-05	rs17811812	18	40994001	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1884571	G	G	355	39	381	19	7.77	0.0053	rs17811837	18	40994089	q12.3
SNP_A-2027316	T	T	214	180	253	153	5.267	2.17E-02	rs269981	18	41038276	q12.3
SNP_A-2035714	G	G	366	18	331	31	4.562	0.0327	rs12605615	18	41056379	q12.3
SNP_A-2085107	C	C	339	29	308	46	5.069	2.44E-02	rs9973059	18	41079020	q12.3
SNP_A-2121270	T	T	334	82	359	57	5.398	2.02E-02	rs2612543	18	41270199	q12.3
SNP_A-2209962	C	C	228	178	261	149	4.779	2.88E-02	rs16978368	18	41272782	q12.3
SNP_A-1695967	C	C	321	79	357	53	6.91	0.0086	rs10502865	18	41320985	q12.3
SNP_A-2313725	C	C	314	96	345	73	4.512	3.37E-02	rs8094590	18	41357269	q12.3
SNP_A-1826844	A	A	412	2	395	11	6.511	1.07E-02	rs9955189	18	41690219	q12.3
SNP_A-2278396	C	C	331	77	345	51	5.393	2.02E-02	rs8087413	18	42378155	q21.1
SNP_A-2164705	C	C	374	38	356	62	6.161	1.31E-02	rs7241561	18	42489155	q21.1
SNP_A-1935616	T	T	314	28	290	44	4.415	0.0356	rs11874126	18	42497794	q21.1
SNP_A-1739975	T	T	327	49	328	76	4.835	2.79E-02	rs4449041	18	42586483	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1833296	A	A	408	8	399	21	5.909	1.51E-02	rs17725434	18	43105746	q21.1
SNP_A-2005641	G	G	332	4	348	0	4.167	4.12E-02	rs4510095	18	43493286	q21.1
SNP_A-2094957	T	T	272	60	293	37	6.228	0.0126	rs877354	18	43553399	q21.1
SNP_A-2238336	G	G	191	131	206	102	3.867	4.92E-02	rs9966964	18	43720605	q21.1
SNP_A-2047403	G	G	315	39	312	66	6.177	0.0129	rs4940140	18	43737588	q21.1
SNP_A-2240153	C	A	253	163	209	207	10.288	1.30E-03	rs4620750	18	43813958	q21.1
SNP_A-1911702	C	C	318	72	295	111	8.856	2.90E-03	rs10460075	18	43828638	q21.1
SNP_A-2161173	A	A	366	46	333	77	9.366	2.20E-03	rs7238127	18	43831935	q21.1
SNP_A-1938257	A	A	222	142	210	188	5.239	2.21E-02	rs7239672	18	43832126	q21.1
SNP_A-2226788	C	C	324	12	323	3	5.252	2.19E-02	rs8085875	18	43913365	q21.1
SNP_A-2005645	G	G	372	0	367	5	5.034	2.49E-02	rs4940322	18	43977335	q21.1
SNP_A-2213835	T	T	338	38	314	56	4.282	0.0385	rs12457004	18	43985005	q21.1
SNP_A-1674044	T	T	248	152	285	125	5.078	2.42E-02	rs953570	18	43986452	q21.1
SNP_A-2299856	G	G	399	5	394	14	4.275	3.87E-02	rs8096208	18	43987156	q21.1
SNP_A-2045729	C	C	335	57	313	81	4.916	2.66E-02	rs2187432	18	44041120	q21.1
SNP_A-1792038	T	T	252	122	237	159	4.707	3.00E-02	rs9947735	18	44128559	q21.1
SNP_A-1725164	C	C	330	70	309	101	6.188	0.0129	rs10502892	18	44168096	q21.1
SNP_A-1850594	A	A	308	90	289	121	4.982	2.56E-02	rs7230404	18	44198001	q21.1
SNP_A-1912425	T	T	328	22	335	43	5.79	0.0161	rs11665629	18	44398354	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1896045	G	G	335	25	314	48	7.921	4.90E-03	rs12966613	18	44405939	q21.1
SNP_A-2029641	T	T	345	71	372	46	6.354	0.0117	rs299751	18	44441259	q21.1
SNP_A-1909328	T	T	287	129	322	96	6.847	8.90E-03	rs937023	18	44637783	q21.1
SNP_A-2236534	T	T	208	186	238	134	9.844	1.70E-03	rs937021	18	44638071	q21.1
SNP_A-1789579	G	G	316	96	335	71	4.253	3.92E-02	rs1943000	18	44949547	q21.1
SNP_A-1815697	A	A	202	120	251	107	4.15	4.16E-02	rs948789	18	44954694	q21.1
SNP_A-1850750	A	A	267	135	306	104	6.597	1.02E-02	rs4939846	18	44970083	q21.1
SNP_A-1699911	T	T	268	124	298	96	5.149	2.33E-02	rs7240563	18	45015169	q21.1
SNP_A-1932439	G	G	284	40	273	71	8.284	4.00E-03	rs1788119	18	45051795	q21.1
SNP_A-2265185	C	C	265	107	292	78	5.849	1.56E-02	rs498929	18	45113522	q21.1
SNP_A-2026714	C	C	224	150	258	120	5.711	1.69E-02	rs550258	18	45114641	q21.1
SNP_A-1898706	G	G	329	17	347	5	6.974	8.30E-03	rs11082766	18	45386462	q21.1
SNP_A-1851313	A	A	347	25	369	13	4.334	3.74E-02	rs1787326	18	45714199	q21.1
SNP_A-2005649	C	C	218	146	204	186	4.392	0.0361	rs1787595	18	45715207	q21.1
SNP_A-2213553	T	T	205	177	233	149	4.195	4.05E-02	rs17659034	18	45743016	q21.1
SNP_A-2241215	G	G	390	20	374	34	3.96	4.66E-02	rs17659179	18	45765111	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1800660	A	A	390	20	371	35	4.546	3.30E-02	rs7228145	18	45775253	q21.1
SNP_A-2234668	C	C	274	106	250	140	5.67	1.73E-02	rs9961643	18	45785476	q21.1
SNP_A-2206092	A	A	332	64	319	97	6.535	0.0106	rs7244899	18	45808781	q21.1
SNP_A-2103551	G	G	318	2	299	11	6.659	9.90E-03	rs16951535	18	45885098	q21.1
SNP_A-2021542	G	G	400	2	393	9	4.516	3.36E-02	rs4939941	18	45893551	q21.1
SNP_A-1648934	T	T	372	22	361	43	6.825	9.00E-03	rs7237077	18	45896365	q21.1
SNP_A-2158756	T	T	232	180	270	144	6.872	8.80E-03	rs1705533	18	45904191	q21.1
SNP_A-2104089	C	C	297	37	303	21	4.323	3.76E-02	rs2469479	18	45905374	q21.1
SNP_A-1934815	T	T	319	47	363	27	7.49	6.20E-03	rs2469478	18	45905535	q21.1
SNP_A-1649556	G	G	376	24	362	42	5.155	2.32E-02	rs868973	18	45907380	q21.1
SNP_A-1717091	C	C	335	65	372	40	7.713	5.50E-03	rs10502906	18	45926030	q21.1
SNP_A-1740081	T	T	220	180	259	153	5.188	2.27E-02	rs1985467	18	45926248	q21.1
SNP_A-2192354	A	A	333	17	280	30	5.775	1.63E-02	rs17740343	18	45939212	q21.1
SNP_A-1892928	G	G	380	18	371	39	7.668	5.60E-03	rs17740349	18	45939513	q21.1
SNP_A-2193247	G	G	209	197	249	163	6.661	9.90E-03	rs11082808	18	45955366	q21.1
SNP_A-1910474	T	C	180	164	201	141	8.483	3.60E-03	rs8093558	18	45962382	q21.1
SNP_A-2077113	G	G	208	190	249	151	8.134	0.0043	rs12454494	18	45964695	q21.1
SNP_A-1780312	C	C	317	75	268	110	10.475	1.20E-03	rs2469480	18	45965961	q21.1
SNP_A-1815161	T	G	209	197	238	178	6.227	0.0126	rs8086036	18	45967806	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2209042	G	A	236	140	195	183	15.729	7.31E-05	rs10164183	18	45969476	q21.1
SNP_A-1724544	C	C	306	94	279	133	7.771	0.0053	rs1790440	18	45970282	q21.1
SNP_A-1786733	T	T	282	82	247	113	7.222	7.20E-03	rs1511155	18	45971240	q21.1
SNP_A-1675720	C	C	362	38	345	63	6.518	1.07E-02	rs1662897	18	45978284	q21.1
SNP_A-1660557	A	A	319	79	300	112	6.045	1.39E-02	rs1373185	18	45997838	q21.1
SNP_A-2100074	T	T	241	145	277	121	4.485	3.42E-02	rs9965706	18	46033349	q21.1
SNP_A-2273494	G	G	352	12	371	3	5.765	1.63E-02	rs8085254	18	46036147	q21.1
SNP_A-2064363	G	G	260	154	300	116	8.201	4.20E-03	rs9958001	18	46036475	q21.1
SNP_A-2190544	T	T	332	32	298	50	5.429	1.98E-02	rs2276366	18	46065303	q21.1
SNP_A-1869933	A	A	406	4	414	0	4.059	4.39E-02	rs1822461	18	46628296	q21.1
SNP_A-1942752	C	C	412	4	420	0	4.058	4.40E-02	rs16952805	18	46883911	q21.1
SNP_A-1896039	A	A	364	12	361	25	4.45	0.0349	rs8099457	18	47390464	q21.1
SNP_A-1911798	T	T	414	0	408	6	6.044	0.014	rs10502929	18	47537980	q21.1
SNP_A-1844371	A	A	329	41	347	23	5.542	1.86E-02	rs16955448	18	48523250	q21.2
SNP_A-1793994	A	A	372	6	386	16	4.069	4.37E-02	rs9953246	18	48565484	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1913667	G	G	350	4	293	17	10.23	0.0014	rs1393337	18	49259239	q21.2
SNP_A-2250997	C	C	272	132	310	100	6.851	8.90E-03	rs9956700	18	49705698	q21.2
SNP_A-1757113	A	A	272	72	296	50	4.976	2.57E-02	rs10515967	18	49713695	q21.2
SNP_A-2184022	A	A	280	70	301	47	5.275	2.16E-02	rs11660620	18	49731680	q21.2
SNP_A-1956637	C	C	298	88	317	65	4.024	4.49E-02	rs17535202	18	49751677	q21.2
SNP_A-2244241	A	A	268	72	289	47	6.02	0.0141	rs9952579	18	49762275	q21.2
SNP_A-1888348	A	A	361	55	386	32	6.912	0.0086	rs981122	18	49810530	q21.2
SNP_A-1826532	A	A	323	55	335	31	6.725	9.50E-03	rs1259812	18	49841462	q21.2
SNP_A-2059055	G	G	406	0	407	5	4.957	2.60E-02	rs1259835	18	49889422	q21.2
SNP_A-1956038	T	T	220	194	248	164	4.184	4.08E-02	rs7614	18	49935242	q21.2
SNP_A-1915421	A	A	255	115	279	83	6.164	1.30E-02	rs3017289	18	50034406	q21.2
SNP_A-1914593	T	T	277	139	303	113	3.848	4.98E-02	rs491557	18	50069340	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1914579	C	C	272	106	260	138	3.955	4.67E-02	rs2118288	18	50164312	q21.2
SNP_A-1741971	A	A	299	85	286	124	6.722	9.50E-03	rs940310	18	50167268	q21.2
SNP_A-1943078	G	G	273	113	257	149	4.928	0.0264	rs3760542	18	50190000	q21.2
SNP_A-1877389	T	T	248	108	237	141	3.967	4.64E-02	rs2140497	18	50200863	q21.2
SNP_A-2282479	G	G	387	29	403	15	4.774	2.89E-02	rs8096799	18	50376612	q21.2
SNP_A-1858631	C	C	378	22	385	7	7.743	5.40E-03	rs9945556	18	50407491	q21.2
SNP_A-1848933	C	C	215	127	193	165	5.769	1.63E-02	rs11152031	18	50684036	q21.2
SNP_A-1861954	C	C	305	93	320	62	6.234	1.25E-02	rs8092980	18	50714939	q21.2
SNP_A-2040293	A	A	273	141	245	169	4.043	4.44E-02	rs9956808	18	50767562	q21.2
SNP_A-1883893	C	C	284	122	321	87	8.119	4.40E-03	rs11661644	18	50793847	q21.2
SNP_A-1898175	G	G	282	114	289	81	4.793	0.0286	rs8088523	18	50826200	q21.2
SNP_A-1915239	C	C	216	94	258	74	5.355	0.0207	rs1944366	18	50864129	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805277	A	G	220	174	194	182	4.261	0.039	rs9952839	18	51006276	q21.2
SNP_A-1694051	A	A	292	106	330	78	6.459	1.10E-02	rs1526173	18	51012972	q21.2
SNP_A-2308283	G	A	207	203	238	160	8.621	0.0033	rs1788014	18	51037434	q21.2
SNP_A-2178963	G	G	249	133	297	97	9.671	0.0019	rs11665032	18	51037609	q21.2
SNP_A-1855785	A	A	220	178	261	131	10.599	1.10E-03	rs1261085	18	51040965	q21.2
SNP_A-2284356	G	G	275	129	309	93	7.812	5.20E-03	rs2276195	18	51047507	q21.2
SNP_A-1871354	C	C	277	139	322	98	10.455	1.20E-03	rs1942265	18	51066565	q21.2
SNP_A-1960471	A	A	202	152	246	110	11.049	9.00E-04	rs1261134	18	51082761	q21.2
SNP_A-2181168	T	C	225	181	239	153	21.485	3.57E-06	rs1788027	18	51093825	q21.2
SNP_A-1680142	C	C	374	26	398	14	4.17	4.12E-02	rs10515970	18	51129622	q21.2
SNP_A-1915497	C	C	385	29	405	15	4.918	2.66E-02	rs10515971	18	51142216	q21.2
SNP_A-2041483	A	A	394	6	373	17	5.71	1.69E-02	rs10164195	18	51177077	q21.2
SNP_A-2005674	A	A	227	187	267	149	7.532	6.10E-03	rs1660242	18	51189674	q21.2
SNP_A-1720587	G	G	389	11	410	2	6.607	1.02E-02	rs10503003	18	51343865	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1784010	C	C	375	39	390	22	5.027	2.50E-02	rs17089925	18	51551832	q21.2
SNP_A-1929294	T	T	396	20	410	8	5.381	2.04E-02	rs784240	18	51585120	q21.2
SNP_A-1916039	G	G	320	42	334	24	5.187	2.28E-02	rs2862257	18	51779297	q21.2
SNP_A-2217435	A	A	396	12	405	3	5.501	0.019	---	18	51966133	q21.2
SNP_A-2084780	C	C	239	125	249	91	4.744	2.94E-02	rs216562	18	52201691	q21.2
SNP_A-2040548	G	G	179	157	209	135	3.884	4.88E-02	rs216559	18	52201968	q21.2
SNP_A-2274150	T	T	332	78	310	104	4.449	0.0349	rs12456800	18	52268092	q21.2
SNP_A-2021115	C	C	315	57	289	77	4.056	4.40E-02	rs11872473	18	52268517	q21.2
SNP_A-2162671	T	T	354	62	328	92	6.816	9.00E-03	rs17749733	18	52272627	q21.2
SNP_A-1822048	C	C	343	55	321	81	5.68	0.0172	rs2068741	18	52292789	q21.2
SNP_A-2085200	C	C	343	59	318	80	4.098	4.29E-02	rs17541626	18	52297113	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1831560	A	A	373	25	354	40	3.938	4.72E-02	rs7237084	18	52746016	q21.31
SNP_A-1915677	C	C	201	127	188	162	3.964	0.0465	rs4800960	18	52914826	q21.31
SNP_A-2005681	C	C	255	139	299	101	9.466	2.10E-03	rs8084780	18	52990745	q21.31
SNP_A-1793714	T	T	262	148	308	106	10.638	1.10E-03	rs12605509	18	52998303	q21.31
SNP_A-2169449	A	A	274	122	315	83	10.269	0.0014	rs6566869	18	53007145	q21.31
SNP_A-1917261	A	A	280	112	316	80	7.488	6.20E-03	rs17063161	18	53012945	q21.31
SNP_A-1737581	C	C	279	121	327	79	12.578	4.00E-04	rs1468885	18	53014611	q21.31
SNP_A-1935248	T	T	253	107	302	80	7.579	5.90E-03	rs17063226	18	53024638	q21.31
SNP_A-2131580	C	C	286	126	325	89	8.852	2.90E-03	rs759555	18	53041561	q21.31
SNP_A-2091678	T	T	247	93	294	56	13.129	3.00E-04	rs2111287	18	53084560	q21.31
SNP_A-1744341	A	A	239	95	295	63	11.535	7.00E-04	rs1943394	18	53092662	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2276424	C	C	263	129	319	91	11.554	7.00E-04	rs9955714	18	53097416	q21.31
SNP_A-2295066	A	A	275	127	306	92	7.228	7.20E-03	rs9956540	18	53097523	q21.31
SNP_A-1917362	G	G	272	134	313	91	11.086	9.00E-04	rs11662857	18	53106778	q21.31
SNP_A-1917365	C	C	260	86	286	52	9.523	0.002	rs9945336	18	53106925	q21.31
SNP_A-2103753	T	T	338	72	311	97	4.817	2.82E-02	rs663460	18	53289682	q21.31
SNP_A-2197227	T	T	323	55	301	87	7.858	5.10E-03	rs7237996	18	53296505	q21.31
SNP_A-1903227	C	C	340	76	368	50	6.468	1.10E-02	rs504442	18	53296545	q21.31
SNP_A-1758623	T	T	394	4	410	0	4.141	0.0419	rs1037829	18	53360824	q21.31
SNP_A-2096937	G	G	321	37	351	17	8.611	0.0033	rs1041951	18	53391503	q21.31
SNP_A-2116254	A	A	314	36	301	65	8.248	4.10E-03	rs17686020	18	53477799	q21.31
SNP_A-1787919	G	G	313	91	346	68	4.858	0.0275	rs11659760	18	53501457	q21.31
SNP_A-2229934	T	T	312	96	281	129	6.456	0.0111	---	18	53514861	q21.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1917696	T	T	329	31	303	53	6.809	9.10E-03	rs1567389	18	53588708	q21.31
SNP_A-1917749	T	T	382	34	402	18	5.414	0.02	rs17692484	18	53687108	q21.31
SNP_A-2005696	C	C	336	0	361	5	4.623	0.0315	rs520348	18	53996224	q21.31
SNP_A-1725094	C	C	314	86	346	64	4.655	0.031	rs1553712	18	54924421	q21.32
SNP_A-1693711	T	T	379	21	404	8	6.45	0.0111	rs10503029	18	55358767	q21.32
SNP_A-1859265	A	A	259	147	289	119	4.585	3.23E-02	rs11661117	18	55422782	q21.32
SNP_A-2114085	A	A	249	133	283	109	4.425	3.54E-02	rs1429573	18	55423854	q21.32
SNP_A-1833684	G	G	262	146	294	120	4.34	3.72E-02	rs11665249	18	55424182	q21.32
SNP_A-1918935	A	A	193	171	214	138	4.408	3.58E-02	rs1864304	18	55434197	q21.32
SNP_A-2208869	T	T	213	181	247	153	4.815	2.82E-02	rs2564478	18	55434577	q21.32
SNP_A-2175357	G	G	197	153	236	136	3.846	0.0499	rs1864311	18	55437746	q21.32
SNP_A-2051968	A	A	377	39	354	64	6.787	9.20E-03	rs17698267	18	55462755	q21.32
SNP_A-2252965	A	A	237	117	230	156	4.301	3.81E-02	rs12454268	18	55533643	q21.32
SNP_A-2296024	G	G	330	28	343	15	4.181	4.09E-02	rs11872239	18	55671198	q21.32
SNP_A-2295804	C	C	322	28	351	13	6.465	1.10E-02	rs8083367	18	55730099	q21.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2082823	T	T	316	4	328	16	6.565	0.0104	rs17066440	18	55799255	q21.32
SNP_A-1911265	C	C	371	3	362	10	3.874	4.90E-02	rs4632231	18	55809733	q21.32
SNP_A-1786651	C	C	346	14	346	2	8.799	3.00E-03	rs11877823	18	55813676	q21.32
SNP_A-2272330	G	G	287	103	249	125	4.484	3.42E-02	rs7234864	18	55885837	q21.32
SNP_A-1919330	T	T	335	37	372	24	3.961	4.66E-02	rs17700028	18	55926664	q21.32
SNP_A-1751769	T	T	291	109	264	142	5.608	1.79E-02	rs492443	18	56007771	q21.32
SNP_A-2044305	T	T	240	106	215	133	4.418	0.0356	rs12957325	18	56035596	q21.32
SNP_A-2176228	C	C	327	3	313	11	4.823	0.0281	rs727406	18	56049197	q21.32
SNP_A-1749753	A	A	329	69	311	99	5.686	1.71E-02	rs1943228	18	56208903	q21.32
SNP_A-1920407	A	A	387	21	376	40	6	0.0143	rs17810343	18	56932800	q21.32
SNP_A-2165714	C	C	373	23	336	48	10.552	1.20E-03	rs2032712	18	56945896	q21.32
SNP_A-1842605	T	T	336	16	289	27	4.421	3.55E-02	rs8086823	18	57342736	q21.33
SNP_A-2259398	C	C	388	8	385	1	5.329	2.10E-02	rs8097505	18	57420886	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287906	G	G	364	38	389	23	4.396	3.60E-02	rs8096507	18	57730189	q21.33
SNP_A-1921097	C	C	201	163	225	129	5.173	0.0229	rs1030582	18	57886440	q21.33
SNP_A-1712707	G	G	223	169	257	145	4.117	0.0424	rs4274523	18	57940010	q21.33
SNP_A-2045232	C	C	217	163	250	132	5.584	1.81E-02	rs9953509	18	57982442	q21.33
SNP_A-2142367	T	T	396	4	398	0	4	4.55E-02	rs17069686	18	58092234	q21.33
SNP_A-1925644	G	G	267	105	283	75	5.199	2.26E-02	rs12606993	18	58383753	q21.33
SNP_A-1921634	C	C	316	16	306	32	5.441	1.97E-02	rs7227098	18	58646500	q21.33
SNP_A-2046868	G	G	318	18	298	34	5.549	1.85E-02	rs7230429	18	58652231	q21.33
SNP_A-2270897	C	C	377	19	358	36	5.741	0.0166	—	18	58733408	q21.33
SNP_A-1921670	A	G	220	180	213	187	5.447	1.96E-02	rs607127	18	58737929	q21.33
SNP_A-1845177	A	A	218	152	188	178	4.244	3.94E-02	rs522505	18	58747773	q21.33
SNP_A-2079173	C	T	216	200	231	189	4.011	4.52E-02	rs7239402	18	58857168	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2005730	G	A	175	157	182	146	4.44	3.51E-02	rs6567315	18	58859706	q21.33
SNP_A-1905500	A	G	227	187	222	196	5.248	2.20E-02	rs4940569	18	58915994	q21.33
SNP_A-1921840	G	G	205	159	246	134	5.519	1.88E-02	rs8098694	18	58931179	q21.33
SNP_A-1946800	C	C	354	28	331	43	3.857	4.95E-02	---	18	59184406	q21.33
SNP_A-1795239	A	G	228	178	209	193	5.373	2.04E-02	rs6567340	18	59214087	q21.33
SNP_A-2070029	A	G	169	155	177	127	6.787	9.20E-03	rs4530253	18	59231345	q21.33
SNP_A-1941811	C	T	223	155	199	195	7.016	8.10E-03	rs4941199	18	59245354	q21.33
SNP_A-1922105	G	G	398	0	404	4	3.921	4.77E-02	rs17071116	18	59276311	q21.33
SNP_A-1875225	C	C	330	60	291	87	7.223	7.20E-03	rs9945468	18	59433290	q21.33
SNP_A-2297269	G	G	351	57	321	79	4.819	0.0281	rs3180227	18	59473992	q21.33
SNP_A-1922373	T	T	305	111	276	140	4.798	2.85E-02	rs4940595	18	59530818	q21.33
SNP_A-2164814	T	T	360	4	362	12	3.871	4.91E-02	rs1155493	18	59555287	q21.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1956970	C	C	411	3	403	13	6.324	1.19E-02	rs8091131	18	59584910	q21.33
SNP_A-1959708	G	G	411	5	404	14	4.319	3.77E-02	rs17708446	18	59585089	q21.33
SNP_A-1896437	T	T	378	12	392	0	12.25	5.00E-04	rs1618922	18	59597509	q21.33
SNP_A-1868346	A	A	387	1	378	10	7.47	0.0063	rs11873703	18	59599683	q21.33
SNP_A-1891264	T	T	399	17	386	32	4.802	2.84E-02	rs6567426	18	60055343	q22.1
SNP_A-2044309	C	C	357	33	313	57	8.769	3.10E-03	rs1363011	18	60087956	q22.1
SNP_A-1809051	A	A	362	12	369	27	5.212	0.0224	rs8086719	18	60088620	q22.1
SNP_A-2163214	C	C	206	136	255	97	11.594	7.00E-04	rs11152426	18	60088953	q22.1
SNP_A-2084025	C	C	392	10	373	21	4.295	3.82E-02	rs1363013	18	60089462	q22.1
SNP_A-2113066	C	C	395	13	382	26	4.551	3.29E-02	rs1363014	18	60110147	q22.1
SNP_A-1923170	G	G	396	10	383	29	9.43	2.10E-03	rs10503088	18	60148688	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1690009	T	T	218	180	251	155	4.108	4.27E-02	rs10503090	18	60159217	q22.1
SNP_A-1923219	G	G	414	2	411	9	4.446	3.50E-02	rs10515992	18	60170704	q22.1
SNP_A-1955266	C	C	414	2	411	9	4.446	3.50E-02	rs17072919	18	60181947	q22.1
SNP_A-1846372	G	G	324	30	326	52	5.127	2.36E-02	rs1025807	18	60603427	q22.1
SNP_A-1856296	A	A	404	6	385	17	5.64	1.76E-02	rs9319685	18	60627115	q22.1
SNP_A-2152862	G	G	379	17	364	30	3.894	4.85E-02	rs1444074	18	61431805	q22.1
SNP_A-1804766	A	A	361	7	338	16	4.009	0.0453	rs1972398	18	61456486	q22.1
SNP_A-1848489	G	G	273	137	247	165	3.891	4.85E-02	rs10871590	18	61469322	q22.1
SNP_A-2057807	C	C	381	29	398	16	4.107	4.27E-02	rs2628205	18	61695345	q22.1
SNP_A-1852430	C	C	360	8	385	1	5.857	0.0155	rs2541827	18	61748263	q22.1
SNP_A-2179878	G	G	214	190	242	146	7.161	7.50E-03	rs8089989	18	61831091	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2065351	C	C	225	191	272	146	10.449	1.20E-03	rs2715349	18	61842366	q22.1
SNP_A-2070579	T	T	212	178	245	129	9.873	1.70E-03	rs2715350	18	61842405	q22.1
SNP_A-2204153	T	T	217	187	257	137	10.968	9.00E-04	rs13370501	18	61845464	q22.1
SNP_A-1707117	A	A	219	181	271	141	10.312	1.30E-03	rs2541771	18	61850212	q22.1
SNP_A-1719003	T	T	218	180	270	140	10.365	1.30E-03	rs2706624	18	61851784	q22.1
SNP_A-2163748	G	G	223	119	255	81	9.31	0.0023	rs17075694	18	61867812	q22.1
SNP_A-1924940	C	C	275	111	308	86	4.959	2.60E-02	rs4047832	18	61898500	q22.1
SNP_A-1924944	T	T	235	171	267	137	5.788	0.0161	rs2715367	18	61898993	q22.1
SNP_A-1924945	A	A	239	175	275	143	5.722	0.0167	rs2706606	18	61899757	q22.1
SNP_A-1868536	A	A	230	156	260	126	5.028	2.49E-02	rs2715281	18	61901405	q22.1
SNP_A-2189825	T	T	243	123	267	95	4.704	3.01E-02	rs2706603	18	61902017	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1691174	A	A	233	165	272	140	4.821	0.0281	rs2193295	18	61907696	q22.1
SNP_A-2204077	C	C	264	76	283	53	4.737	2.95E-02	rs8091805	18	61908145	q22.1
SNP_A-1895426	G	G	263	141	286	112	4.243	3.94E-02	rs2715282	18	61908224	q22.1
SNP_A-1905980	C	C	284	132	311	105	4.301	3.81E-02	rs9962902	18	61952681	q22.1
SNP_A-2285708	C	C	264	86	282	56	6.724	9.50E-03	rs8092179	18	61987859	q22.1
SNP_A-2130241	A	A	215	131	242	98	6.299	0.0121	rs2877964	18	61993915	q22.1
SNP_A-2043656	C	C	262	112	284	60	15.381	8.79E-05	rs1032343	18	62031073	q22.1
SNP_A-1921771	A	A	255	115	280	86	5.331	2.10E-02	rs11664818	18	62053230	q22.1
SNP_A-2170768	A	A	375	17	410	6	6.114	0.0134	rs902581	18	62063708	q22.1
SNP_A-1899735	A	A	272	118	314	86	7.905	4.90E-03	rs2172098	18	62064357	q22.1
SNP_A-1713239	A	A	237	123	292	90	10.188	0.0014	rs1388177	18	62071585	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1819093	G	G	287	83	303	57	5.126	2.36E-02	rs4558493	18	62224090	q22.1
SNP_A-2182392	G	G	296	98	321	73	4.668	3.07E-02	rs11151274	18	62226756	q22.1
SNP_A-1920154	C	C	307	107	330	78	5.333	2.09E-02	rs11660728	18	62293793	q22.1
SNP_A-2046009	C	C	301	101	322	74	4.829	2.80E-02	rs9962822	18	62327599	q22.1
SNP_A-2198756	G	G	222	116	180	146	7.609	5.80E-03	rs8087257	18	62414723	q22.1
SNP_A-1932254	C	C	354	60	378	38	5.721	1.68E-02	rs12957137	18	62479277	q22.1
SNP_A-1670882	T	T	380	18	377	35	5.224	0.0223	rs923416	18	62538172	q22.1
SNP_A-1695375	T	T	381	19	377	35	4.586	3.22E-02	rs923415	18	62538373	q22.1
SNP_A-2262956	T	T	411	5	406	14	4.275	3.87E-02	rs7231206	18	62642027	q22.1
SNP_A-2026721	T	T	251	163	281	135	4.318	3.77E-02	rs7240404	18	62692557	q22.1
SNP_A-1953424	G	G	251	163	277	135	3.906	4.81E-02	rs7238331	18	62704245	q22.1
SNP_A-2281189	T	A	225	177	204	196	3.906	4.81E-02	rs2156438	18	62868724	q22.1
SNP_A-1956997	C	C	332	34	317	17	4.56	0.0327	rs6420520	18	62960840	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1906055	T	T	372	26	366	44	4.5	0.0339	rs11877435	18	63111729	q22.1
SNP_A-1897784	T	T	258	128	192	140	6.191	1.28E-02	rs11151371	18	63326628	q22.1
SNP_A-2226128	C	C	356	18	337	33	4.911	2.67E-02	rs17827176	18	63424422	q22.1
SNP_A-1926076	T	T	373	43	400	20	9.321	0.0023	rs17077583	18	63441632	q22.1
SNP_A-1926077	G	G	235	165	268	132	5.832	1.57E-02	rs764133	18	63441694	q22.1
SNP_A-1926181	T	T	409	7	420	0	7.127	0.0076	rs17077858	18	63531966	q22.1
SNP_A-2083194	C	C	343	41	359	21	6.796	9.10E-03	rs1373365	18	63546531	q22.1
SNP_A-2165753	C	C	242	134	274	90	10.436	1.20E-03	rs12964913	18	63586223	q22.1
SNP_A-2070770	G	G	371	25	387	13	4.107	4.27E-02	rs17077963	18	63607960	q22.1
SNP_A-1868774	A	A	341	35	367	17	7.102	7.70E-03	rs519360	18	63641058	q22.1
SNP_A-1851846	C	C	409	5	420	0	5.103	2.39E-02	rs7236098	18	63737663	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1702523	A	A	396	4	412	0	4.14	0.0419	rs1350744	18	63744818	q22.1
SNP_A-1808519	A	A	410	4	416	0	4.039	4.45E-02	rs11151395	18	63748325	q22.1
SNP_A-2203199	C	C	411	5	416	0	5.03	2.49E-02	rs10439042	18	63748550	q22.1
SNP_A-1807004	C	C	408	4	416	0	4.058	4.40E-02	rs4891327	18	63761849	q22.1
SNP_A-2133109	A	A	313	43	337	27	4.455	3.48E-02	rs12965518	18	63862752	q22.1
SNP_A-2236750	A	A	312	26	314	8	9.153	2.50E-03	rs10163736	18	63883577	q22.1
SNP_A-2135966	C	C	376	12	388	4	4.168	4.12E-02	rs12604709	18	64007305	q22.1
SNP_A-2271268	G	G	258	154	281	123	4.373	3.65E-02	rs17207617	18	64099586	q22.1
SNP_A-1954105	G	G	229	125	265	105	4.011	4.52E-02	rs17207624	18	64099717	q22.1
SNP_A-1877578	T	T	211	157	236	122	5.652	1.74E-02	rs607741	18	64642928	q22.1
SNP_A-2038523	A	A	242	86	217	119	6.578	0.0103	rs9963502	18	64642967	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1839818	T	T	300	116	276	144	3.996	4.56E-02	rs12373467	18	64646852	q22.1
SNP_A-1927561	A	A	399	5	390	16	5.86	0.0155	rs1469580	18	64802946	q22.1
SNP_A-1849017	A	A	315	9	308	22	5.476	1.93E-02	rs662932	18	64807406	q22.1
SNP_A-2098059	G	G	409	7	395	21	7.244	7.10E-03	rs650388	18	64807961	q22.1
SNP_A-1798720	C	C	392	12	369	23	3.972	4.63E-02	rs8094964	18	64808329	q22.1
SNP_A-1842781	G	G	346	6	321	15	4.424	3.54E-02	rs9789236	18	64822450	q22.1
SNP_A-2099267	G	G	336	2	303	9	5.127	2.36E-02	rs649951	18	64827686	q22.1
SNP_A-1810409	C	C	408	8	398	20	5.262	0.0218	rs17080075	18	64832896	q22.1
SNP_A-1884937	G	G	373	7	379	19	5.173	0.0229	rs9954425	18	64840627	q22.1
SNP_A-1927644	A	A	396	8	387	19	4.58	3.23E-02	rs10503139	18	64851232	q22.1
SNP_A-2215793	A	A	406	6	397	21	8.391	0.0038	rs17080104	18	64854046	q22.1
SNP_A-1664970	T	T	386	2	381	11	6.243	1.25E-02	rs10503140	18	64855824	q22.1
SNP_A-1709349	C	C	392	8	393	19	4.306	3.80E-02	rs10516009	18	64857516	q22.1
SNP_A-1927659	G	G	401	5	384	16	6.086	1.36E-02	rs10503141	18	64859194	q22.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1927668	T	T	404	4	394	16	7.32	6.80E-03	rs17080145	18	64862396	q22.1
SNP_A-1697977	C	C	362	6	373	17	4.791	0.0286	rs9319771	18	64869402	q22.1
SNP_A-2060058	A	A	379	7	353	21	7.736	5.40E-03	rs8088076	18	64882697	q22.1
SNP_A-1861846	C	C	338	12	290	2	5.618	0.0178	rs9636063	18	65060131	q22.2
SNP_A-1944161	A	A	190	182	221	143	6.932	8.50E-03	rs1550597	18	65312795	q22.2
SNP_A-1912321	-	C	181	181	233	151	8.601	3.40E-03	rs1550598	18	65312915	q22.2
SNP_A-1803656	C	C	220	174	234	132	5.172	0.023	rs12967871	18	65324331	q22.2
SNP_A-2160231	C	C	401	13	383	25	4.159	4.14E-02	rs17081544	18	65541941	q22.2
SNP_A-2263731	T	T	369	37	356	56	4.071	0.0436	rs7243586	18	65574821	q22.2
SNP_A-2154151	C	C	391	9	372	20	4.565	3.26E-02	rs17081619	18	65611065	q22.2
SNP_A-2098431	G	G	316	18	303	5	6.579	0.0103	rs17062739	18	65729544	q22.2
SNP_A-2182947	C	C	387	25	403	13	4.094	4.30E-02	rs930292	18	65860098	q22.2
SNP_A-2277259	C	C	318	60	319	37	4.8	2.85E-02	—	18	65875820	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1852400	G	G	330	12	358	2	7.826	5.10E-03	rs11665422	18	65939375	q22.2
SNP_A-1960859	C	C	389	21	404	8	6.106	0.0135	rs283268	18	66036038	q22.2
SNP_A-1797833	T	T	257	159	288	130	4.669	3.07E-02	rs4891840	18	66111405	q22.2
SNP_A-2313933	C	C	252	126	267	91	5.539	1.86E-02	rs2439266	18	66180670	q22.2
SNP_A-2025786	C	C	336	14	338	4	5.47	1.93E-02	rs17082884	18	66422119	q22.2
SNP_A-1874266	T	T	378	10	391	3	3.943	4.71E-02	rs17082999	18	66510976	q22.2
SNP_A-2261317	C	C	378	24	389	11	4.981	2.56E-02	rs9319797	18	66581850	q22.2
SNP_A-2100209	T	T	367	45	393	27	5.313	0.0212	rs17083666	18	66944631	q22.3
SNP_A-2216044	G	G	302	80	329	45	10.872	0.001	rs7227144	18	66967948	q22.3
SNP_A-1865776	C	T	178	164	189	147	4.675	3.06E-02	rs8088118	18	66968691	q22.3
SNP_A-1939404	A	A	308	48	337	29	5.855	0.0155	rs8095484	18	67056335	q22.3
SNP_A-2114761	C	C	236	104	261	79	4.673	3.06E-02	rs4891443	18	67482147	q22.3
SNP_A-2034109	A	A	224	142	194	188	8.227	4.10E-03	rs8091778	18	67490728	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2029235	T	T	344	50	369	25	9.21	2.40E-03	rs4433912	18	68107569	q22.3
SNP_A-2159540	A	A	214	144	180	166	4.292	3.83E-02	rs4892004	18	68225303	q22.3
SNP_A-2040867	G	G	359	41	341	63	5.097	0.024	rs9962377	18	68256511	q22.3
SNP_A-1641755	C	C	359	39	389	23	5.092	0.024	rs1432071	18	68311274	q22.3
SNP_A-2119325	C	C	371	7	371	17	4.037	4.45E-02	rs6554316	18	68398275	q22.3
SNP_A-1887179	G	A	224	186	209	189	4.128	4.22E-02	rs7228930	18	68462221	q22.3
SNP_A-2144521	T	T	370	6	380	16	4.163	4.13E-02	rs8096871	18	68725703	q22.3
SNP_A-1793008	A	A	292	86	255	113	6.033	0.014	rs12965644	18	68737828	q22.3
SNP_A-2042907	T	T	320	96	347	73	4.204	4.03E-02	rs4516317	18	68766731	q22.3
SNP_A-2032137	C	C	281	69	310	50	4.317	3.77E-02	rs4402656	18	68766884	q22.3
SNP_A-1862250	A	A	299	79	325	59	3.935	4.73E-02	rs4528669	18	68770916	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1931786	C	C	281	81	307	61	3.918	4.78E-02	—	18	68814910	q22.3
SNP_A-2271682	T	T	395	13	406	2	8.218	4.10E-03	rs17086978	18	68954125	q22.3
SNP_A-2152932	C	C	274	90	293	65	4.619	3.16E-02	rs924698	18	68981214	q22.3
SNP_A-2080472	C	C	397	9	394	2	4.342	3.72E-02	rs1503026	18	68993586	q22.3
SNP_A-2152901	G	G	361	45	386	26	5.877	1.53E-02	rs1158869	18	68993990	q22.3
SNP_A-1883905	C	C	351	51	373	31	5.542	1.86E-02	rs17087045	18	69005326	q22.3
SNP_A-2270553	C	C	339	55	365	33	6.44	0.0112	rs1979888	18	69008386	q22.3
SNP_A-2066059	A	A	391	13	408	4	5.048	0.0246	rs1910321	18	69016281	q22.3
SNP_A-2080698	G	G	342	40	382	16	12.173	5.00E-04	rs17087084	18	69017887	q22.3
SNP_A-2203491	C	C	377	25	405	3	18.245	1.94E-05	rs12455926	18	69026751	q22.3
SNP_A-1718963	A	A	361	37	397	15	10.779	0.001	rs9319865	18	69054347	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1936242	A	A	311	55	303	85	5.896	0.0152	rs12454910	18	69155578	q22.3
SNP_A-2251535	C	C	309	57	306	36	3.948	4.69E-02	rs11873925	18	69226559	q22.3
SNP_A-1950351	G	G	349	1	354	10	7.127	0.0076	---	18	69241424	q22.3
SNP_A-2303040	G	G	265	103	224	130	6.297	0.0121	rs12966046	18	69244710	q22.3
SNP_A-1863262	A	A	318	78	336	56	4.087	4.32E-02	rs17241824	18	69255018	q22.3
SNP_A-2046807	A	A	236	126	268	102	4.471	3.45E-02	rs17751492	18	69259633	q22.3
SNP_A-1796530	A	A	204	162	232	128	5.735	0.0166	rs1942761	18	69282838	q22.3
SNP_A-2142038	C	C	312	100	288	128	4.379	3.64E-02	rs17087827	18	69377867	q22.3
SNP_A-1680408	C	C	387	9	406	2	4.732	2.96E-02	rs10514110	18	69949233	q22.3
SNP_A-1933163	T	T	311	17	304	2	11.172	8.00E-04	rs8094941	18	69959526	q22.3
SNP_A-2045997	G	G	404	10	414	2	5.451	1.96E-02	rs17088843	18	69962517	q22.3
SNP_A-1815633	A	A	400	8	411	1	5.574	1.82E-02	rs9944643	18	69963368	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2231405	T	T	351	63	378	38	7.183	7.40E-03	rs1788580	18	70063817	q22.3
SNP_A-2115012	C	C	310	38	301	59	4.477	0.0344	rs1790866	18	70066156	q22.3
SNP_A-1825994	T	T	353	57	377	39	4.121	0.0424	rs2156327	18	70070569	q22.3
SNP_A-2234085	A	A	260	42	304	24	7.281	7.00E-03	rs2156326	18	70070735	q22.3
SNP_A-1864346	T	T	365	51	336	80	7.62	5.80E-03	rs1614856	18	70087760	q22.3
SNP_A-2210673	A	A	308	42	266	62	6.212	1.27E-02	rs1790901	18	70088125	q22.3
SNP_A-1959454	G	G	337	33	310	50	4.473	0.0344	rs1582404	18	70122069	q22.3
SNP_A-2021377	A	A	324	36	297	55	5.052	0.0246	rs7237249	18	70143482	q22.3
SNP_A-2189219	G	G	294	92	290	62	4.314	0.0378	rs7242441	18	70144933	q22.3
SNP_A-2276610	C	C	393	3	367	11	5.045	0.0247	rs17089171	18	70204740	q22.3
SNP_A-1886322	C	C	399	7	379	17	4.557	3.28E-02	rs11661827	18	70224100	q22.3
SNP_A-2063170	G	G	344	56	315	77	4.512	3.37E-02	rs1256719	18	70224309	q22.3
SNP_A-1785987	G	G	406	8	398	18	3.921	4.77E-02	rs11662509	18	70224368	q22.3
SNP_A-1911788	A	A	344	64	326	88	4.229	3.97E-02	rs12957244	18	70237581	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2030894	A	A	211	167	252	136	6.673	9.80E-03	rs17089292	18	70256822	q22.3
SNP_A-2155792	G	C	179	165	193	145	5.706	1.69E-02	rs752773	18	70263267	q22.3
SNP_A-2287057	C	C	338	24	370	12	4.912	2.67E-02	rs17816304	18	70331521	q22.3
SNP_A-2065746	A	A	381	29	399	13	6.506	1.08E-02	rs17089414	18	70381698	q22.3
SNP_A-2236510	G	G	380	36	395	21	4.238	0.0395	rs17055426	18	70536292	q22.3
SNP_A-1933825	C	C	347	15	378	6	4.538	0.0332	rs10514139	18	70610211	q22.3
SNP_A-1925892	A	A	245	161	271	129	4.797	2.85E-02	rs2628123	18	70728913	q22.3
SNP_A-1691836	T	T	332	68	359	49	4.062	4.39E-02	rs2404483	18	70777662	q22.3
SNP_A-1934103	G	G	373	19	369	35	4.582	3.23E-02	rs894575	18	70945420	q22.3
SNP_A-2102104	T	T	361	39	348	60	4.614	3.17E-02	rs7239800	18	70956849	q22.3
SNP_A-2256749	C	C	395	21	413	5	10.242	0.0014	rs10163698	18	71036266	q22.3
SNP_A-2158351	C	C	318	76	344	50	6.386	0.0115	rs2639970	18	71116616	q22.3
SNP_A-1944198	G	G	376	20	375	7	6.011	1.42E-02	rs17056857	18	71199625	q22.3
SNP_A-1902819	A	A	327	45	319	69	4.817	2.82E-02	rs4542744	18	71416097	q23
SNP_A-2107445	G	G	367	27	390	12	6.388	0.0115	rs12971003	18	71427893	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2211242	G	G	288	8	341	1	6.628	0.01	rs8083887	18	71482699	q23
SNP_A-1914663	G	G	383	15	403	5	5.386	2.03E-02	rs17058173	18	71641081	q23
SNP_A-2087415	C	C	304	52	288	74	4.224	3.99E-02	rs8097673	18	71674090	q23
SNP_A-1856842	G	G	363	23	320	42	7.499	6.20E-03	rs8083828	18	71678096	q23
SNP_A-1658974	C	C	381	13	382	26	4.092	4.31E-02	rs10514191	18	71727045	q23
SNP_A-1642267	T	T	321	79	357	53	6.91	0.0086	rs10514192	18	71727224	q23
SNP_A-1853891	C	C	326	50	363	27	8.604	3.40E-03	rs17058484	18	71742254	q23
SNP_A-1654959	G	G	338	62	376	32	11.519	7.00E-04	rs10514196	18	71807075	q23
SNP_A-1694957	G	G	336	60	372	32	10.273	1.30E-03	rs10514197	18	71807149	q23
SNP_A-2276756	T	T	286	94	319	71	4.877	2.72E-02	rs17058811	18	71914488	q23
SNP_A-2041320	G	G	364	26	365	13	4.148	4.17E-02	rs17256181	18	71971008	q23
SNP_A-1732736	A	A	299	39	272	60	5.678	0.0172	rs690378	18	72208249	q23
SNP_A-2205629	A	A	278	126	258	158	4.177	4.10E-02	rs690036	18	72313005	q23
SNP_A-2099614	T	C	228	182	219	199	5.307	0.0212	rs7232061	18	72398882	q23
SNP_A-1800247	C	C	392	24	409	11	5.17	0.023	rs9953092	18	72545074	q23
SNP_A-1909808	G	G	232	126	285	107	5.452	0.0195	rs4393659	18	72561380	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1875897	T	T	271	81	288	54	5.774	1.63E-02	rs11150978	18	72570403	q23
SNP_A-2122715	T	T	251	117	278	92	4.363	3.67E-02	rs12958390	18	72574012	q23
SNP_A-2255819	G	A	238	178	219	201	7.334	6.80E-03	rs3924164	18	72578871	q23
SNP_A-2160961	C	C	393	17	412	6	5.633	1.76E-02	rs7231937	18	72620400	q23
SNP_A-2235948	A	A	277	123	248	152	4.66	0.0309	rs4890829	18	72669421	q23
SNP_A-1845692	G	G	412	4	418	0	4.039	4.45E-02	rs12406	18	72854057	q23
SNP_A-1936393	A	A	177	159	194	124	4.616	3.17E-02	rs9964845	18	72882973	q23
SNP_A-2043418	A	A	332	44	284	74	10.933	9.00E-04	rs9966136	18	73010648	q23
SNP_A-1929739	G	G	379	17	391	7	4.349	3.70E-02	rs165153	18	73477442	q23
SNP_A-2272111	G	G	310	8	307	19	4.397	3.60E-02	rs8945282	18	73598711	q23
SNP_A-1821831	G	G	303	95	274	120	4.344	3.71E-02	rs7244169	18	74109154	q23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2243069	T	T	353	49	375	31	4.695	3.02E-02	rs594517	18	74163515	q23
SNP_A-2259435	G	G	387	15	410	6	4.283	0.0385	rs11081654	18	74624200	q23
SNP_A-2223172	G	G	250	74	295	55	5.519	1.88E-02	rs11659344	18	74723926	q23
SNP_A-1931824	C	C	406	8	394	18	4.021	4.49E-02	rs3934942	18	75085557	q23
SNP_A-1795481	A	A	350	38	333	57	4.218	4.00E-02	rs9965202	18	75208922	q23
SNP_A-2095831	G	G	390	14	404	4	5.783	1.62E-02	rs4799072	18	75486965	q23
SNP_A-2216868	A	A	231	179	258	150	4.042	4.44E-02	rs585811	18	75640752	q23
SNP_A-2243575	G	G	362	46	321	75	9.235	2.40E-03	rs12604993	18	75866208	q23
SNP_A-2111507	C	C	336	56	333	33	5.071	2.43E-02	rs11081582	18	75868923	q23
SNP_A-2146029	G	G	374	28	345	47	5.858	0.0155	rs1879105	18	76028019	q23
SNP_A-1848123	G	G	309	51	267	71	5.653	1.74E-02	rs10418525	19	247458	p13.3
SNP_A-2109351	G	A	188	148	187	173	4.341	3.72E-02	rs4919910	19	460717	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2204107	G	G	269	91	321	77	3.854	4.96E-02	rs2074452	19	1058160	p13.3
SNP_A-1894698	T	T	398	18	382	32	4.243	3.94E-02	rs10423270	19	1261136	p13.3
SNP_A-2073300	C	C	373	11	371	27	6.494	1.08E-02	rs12710060	19	1261537	p13.3
SNP_A-1833487	C	C	359	41	393	21	7.75	5.40E-03	rs7251590	19	1940867	p13.3
SNP_A-2301175	T	T	236	100	257	77	3.877	4.89E-02	rs4807227	19	2269180	p13.3
SNP_A-2096585	A	A	350	70	318	100	6.822	9.00E-03	rs4806891	19	2898152	p13.3
SNP_A-2095578	T	T	313	57	268	76	5.26	0.0218	rs1614798	19	3109547	p13.3
SNP_A-1809031	G	G	257	81	298	64	4.204	4.03E-02	rs8109965	19	4147014	p13.3
SNP_A-2064926	A	A	246	98	222	136	7.125	0.0076	rs888931	19	4239555	p13.3
SNP_A-2080682	G	G	383	25	390	12	4.587	3.22E-02	rs243409	19	4342334	p13.3
SNP_A-2223279	C	C	378	8	389	1	5.582	1.81E-02	rs6510821	19	4652132	p13.3
SNP_A-1874553	C	C	297	107	330	74	7.753	5.40E-03	rs10409097	19	4795152	p13.3
SNP_A-1781361	T	T	311	51	332	34	4.064	4.38E-02	rs4807685	19	5032179	p13.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2291708	T	T	339	79	306	114	8.031	4.60E-03	rs676382	19	5420107	p13.3
SNP_A-1941065	C	C	333	63	293	97	9.736	0.0018	rs709808	19	5421410	p13.3
SNP_A-2107076	G	G	225	147	262	118	5.9	1.51E-02	rs778809	19	5781302	p13.3
SNP_A-2116181	C	C	280	108	295	85	4.757	0.0292	rs3859563	19	5784037	p13.3
SNP_A-1820156	C	C	350	52	377	29	7.514	6.10E-03	rs3760776	19	5790746	p13.3
SNP_A-1882412	C	C	249	79	283	45	11.496	7.00E-04	rs551244	19	5912883	p13.3
SNP_A-2263138	G	G	389	25	406	10	6.767	9.20E-03	---	19	6107206	p13.3
SNP_A-2108678	C	C	387	45	378	28	4.078	4.35E-02	rs344570	19	6609613	p13.3
SNP_A-2268186	G	G	270	130	229	163	7.005	8.10E-03	rs344543	19	6638414	p13.3
SNP_A-2050926	G	G	263	117	235	147	4.978	2.57E-02	rs344540	19	6638768	p13.3
SNP_A-2094614	A	A	258	90	223	119	6.519	1.07E-02	rs2305806	19	6706007	p13.3
SNP_A-1929565	G	G	368	48	349	69	4.268	3.88E-02	rs17637922	19	7034818	p13.2
SNP_A-1783341	A	A	419	1	414	8	5.47	1.93E-02	rs4804304	19	7091525	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308168	G	G	415	1	412	8	5.436	1.97E-02	rs2229434	19	7093921	p13.2
SNP_A-1805882	G	G	206	162	232	130	5.001	0.0253	rs7508679	19	7173832	p13.2
SNP_A-2038703	G	G	221	183	251	155	4.221	3.99E-02	rs7248104	19	7175431	p13.2
SNP_A-2231338	C	C	276	68	279	99	4.179	4.09E-02	rs6603141	19	8064074	p13.2
SNP_A-1880113	T	T	307	93	289	125	5.002	0.0253	rs17160495	19	8422278	p13.2
SNP_A-1881085	T	T	276	116	250	148	5.119	2.37E-02	rs2894538	19	8424415	p13.2
SNP_A-2209272	G	G	272	82	250	106	3.985	4.59E-02	rs17160520	19	8454589	p13.2
SNP_A-1903187	A	A	271	59	258	82	3.923	4.76E-02	rs2277987	19	8458273	p13.2
SNP_A-1942895	C	C	325	17	318	32	4.576	3.24E-02	rs173654	19	8775829	p13.2
SNP_A-2202077	C	C	259	143	286	116	4.152	4.16E-02	rs7245949	19	8944143	p13.2
SNP_A-1856431	T	T	267	151	290	122	3.987	0.0458	rs10402812	19	8947123	p13.2
SNP_A-1877049	C	C	199	159	239	115	10.697	1.10E-03	rs10417520	19	8963315	p13.2
SNP_A-2262555	A	A	291	51	230	66	5.779	1.62E-02	rs2191667	19	9209586	p13.2
SNP_A-2069455	A	A	378	22	333	39	6.579	0.0103	rs16979286	19	9238598	p13.2
SNP_A-2051287	C	C	298	104	273	133	4.623	0.0315	rs4322768	19	10017898	p13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1790539	G	G	315	15	311	29	4.332	3.74E-02	rs10409101	19	10482208	p13.2
SNP_A-2167965	G	G	264	126	213	161	9.39	2.20E-03	rs1053007	19	10615400	p13.2
SNP_A-1784780	A	A	285	119	251	155	6.882	8.70E-03	rs7250071	19	10626819	p13.2
SNP_A-2246120	G	G	294	112	265	143	5.268	2.17E-02	rs2738042	19	10651143	p13.2
SNP_A-2115816	G	G	251	99	229	129	4.866	2.74E-02	rs2569512	19	10651162	p13.2
SNP_A-1943740	T	T	241	131	223	183	7.839	5.10E-03	rs892086	19	10698677	p13.2
SNP_A-2150556	C	C	400	18	414	6	6.236	1.25E-02	rs2302972	19	11457297	p13.2
SNP_A-1960960	T	T	310	42	309	23	4.975	2.57E-02	rs286297	19	11655691	p13.2
SNP_A-1730831	C	C	359	45	386	28	4.816	2.82E-02	rs286300	19	11658308	p13.2
SNP_A-2091244	C	C	390	4	388	0	3.959	4.66E-02	rs448446	19	11803254	p13.2
SNP_A-2045570	A	A	284	50	287	27	6.275	1.22E-02	rs2862170	19	12425560	p13.2
SNP_A-2297176	A	A	281	119	298	90	4.341	3.72E-02	rs7248145	19	12500911	p13.2
SNP_A-2206838	G	G	303	83	276	126	9.785	0.0018	rs931067	19	13019783	p13.13
SNP_A-2272934	G	G	373	9	376	2	4.446	3.50E-02	rs11085858	19	13505719	p13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1698751	A	G	207	195	230	182	4.367	3.66E-02	-	19	14604102	p13.12
SNP_A-1796023	C	C	370	8	375	1	5.473	1.93E-02	—	19	14745841	p13.12
SNP_A-1704341	A	A	267	133	314	90	12.074	5.00E-04	rs8101893	19	14801001	p13.12
SNP_A-2030858	G	G	378	36	361	55	4.353	3.69E-02	rs7255326	19	14972506	p13.12
SNP_A-2247957	C	C	286	30	285	55	6.485	0.0109	rs10424493	19	15314418	p13.12
SNP_A-1943237	A	A	329	81	311	109	4.513	3.36E-02	rs7257156	19	15365766	p13.12
SNP_A-2210536	C	C	251	77	265	55	3.948	4.69E-02	rs3786853	19	15389983	p13.12
SNP_A-2159430	G	G	305	45	336	30	4.144	4.18E-02	rs6512041	19	15484125	p13.12
SNP_A-2151516	G	G	324	40	318	16	9.069	2.60E-03	—	19	15545121	p13.12
SNP_A-2221574	G	G	332	30	348	16	4.632	3.14E-02	rs7249167	19	15898359	p13.12
SNP_A-1782242	G	G	397	23	379	39	4.542	3.31E-02	rs4470265	19	16440900	p13.11
SNP_A-2191600	C	C	347	57	353	37	4.061	4.39E-02	rs6512146	19	16919813	p13.11
SNP_A-2280749	C	C	330	90	306	116	4.182	4.08E-02	rs4808547	19	16960638	p13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2217198	A	A	312	32	336	18	4.667	3.08E-02	rs8107156	19	16966057	p13.11
SNP_A-2222324	A	A	327	87	360	60	6.502	1.08E-02	rs11668659	19	16972699	p13.11
SNP_A-1788009	G	G	377	41	391	25	4.129	4.21E-02	rs7258100	19	17201400	p13.11
SNP_A-2303508	A	G	206	198	219	165	5.084	0.0241	rs4450527	19	17489352	p13.11
SNP_A-2173507	A	A	387	29	362	52	7.361	6.70E-03	rs10418441	19	17541101	p13.11
SNP_A-1907738	G	G	237	167	268	136	5.075	2.43E-02	rs10417130	19	17623909	p13.11
SNP_A-2263566	C	C	380	34	393	19	4.459	3.47E-02	rs845342	19	17987206	p13.11
SNP_A-2247674	A	A	275	91	224	108	5.02	2.50E-02	rs374326	19	18062266	p13.11
SNP_A-2188132	A	A	257	61	281	43	4.13	4.21E-02	rs8105176	19	18232439	p13.11
SNP_A-1873437	T	T	389	15	371	29	4.861	0.0275	rs3810444	19	18964986	p13.11
SNP_A-1748399	G	G	372	14	371	37	9.772	0.0018	rs10500212	19	19584215	p13.11
SNP_A-1799640	G	G	374	4	392	16	6.487	0.0109	rs3794996	19	19615942	p13.11
SNP_A-1937361	C	C	324	26	312	44	4.804	2.84E-02	rs7508153	19	19831113	p12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2005912	G	G	295	91	325	67	5.051	0.0246	rs8106464	19	20039694	p12
SNP_A-2118345	T	T	398	2	401	11	6.066	0.0138	rs4808270	19	20793805	p12
SNP_A-1902759	G	G	333	61	299	83	5.006	0.0253	rs10164402	19	21648247	p12
SNP_A-2047379	C	C	233	169	238	122	5.345	2.08E-02	rs12972593	19	21724414	p12
SNP_A-2136770	C	C	370	8	373	1	5.435	1.97E-02	rs13343758	19	21927834	p12
SNP_A-2086748	C	C	283	135	308	108	4.053	0.0441	rs4932824	19	23144864	p12
SNP_A-2218643	G	G	354	14	332	34	9.033	2.70E-03	rs1991826	19	23497379	p12
SNP_A-1736537	C	C	274	118	245	159	7.51	6.10E-03	rs251750	19	23839200	p12
SNP_A-1805426	C	C	390	0	372	8	8.297	4.00E-03	rs8104914	19	23850378	p12
SNP_A-1950917	A	A	334	80	305	111	6.343	0.0118	rs2195987	19	23941385	p12
SNP_A-2138758	C	C	282	44	292	24	5.902	1.51E-02	rs16968523	19	33076543	q12
SNP_A-1951484	C	C	388	0	388	4	3.98	4.61E-02	rs17620671	19	33116597	q12
SNP_A-2236127	C	C	340	20	361	9	4.665	3.08E-02	rs17770855	19	33147570	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2201357	C	C	284	62	259	83	4.169	4.12E-02	rs10401907	19	33154482	q12
SNP_A-1795676	G	G	278	50	267	75	4.932	0.0264	rs12609711	19	33165725	q12
SNP_A-1752089	G	G	324	42	289	65	6.744	9.40E-03	rs9304858	19	33171310	q12
SNP_A-1951569	G	G	321	37	290	60	6.937	8.40E-03	rs12981999	19	33171818	q12
SNP_A-1920106	T	T	373	29	402	16	4.53	3.33E-02	rs1870064	19	33496719	q12
SNP_A-1823769	A	A	377	29	397	13	6.593	1.02E-02	rs16961351	19	33544658	q12
SNP_A-2199256	G	G	362	26	387	13	4.986	2.56E-02	rs7252404	19	33581043	q12
SNP_A-1809839	A	A	380	34	403	17	6.299	0.0121	rs8101113	19	33582799	q12
SNP_A-2150953	C	C	368	18	392	8	4.356	3.69E-02	rs2108594	19	33590396	q12
SNP_A-2005940	G	G	181	161	218	138	4.921	2.65E-02	rs4805218	19	33667201	q12
SNP_A-1952167	G	G	356	14	384	4	6.191	1.28E-02	rs221764	19	33939123	q12
SNP_A-2101042	C	C	411	1	411	7	4.457	3.48E-02	rs11881661	19	34550478	q12
SNP_A-1782763	G	G	323	57	324	34	5.163	2.31E-02	rs2116878	19	34660197	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1953027	A	A	321	83	302	114	5.283	2.15E-02	rs2288895	19	34759693	q12
SNP_A-1787801	G	G	302	56	284	82	5.364	0.0206	rs11671136	19	34987473	q12
SNP_A-2228690	G	G	170	156	199	133	4.055	4.40E-02	rs255260	19	35051064	q12
SNP_A-1815473	A	A	370	16	370	6	4.415	0.0356	rs334991	19	35114453	q12
SNP_A-1953771	A	A	342	50	313	69	4.189	0.0407	rs17614350	19	35773570	q12
SNP_A-2299457	T	T	202	134	181	169	4.911	2.67E-02	rs12460988	19	35853961	q12
SNP_A-2005947	C	C	408	10	397	21	4.054	0.0441	rs7254787	19	35860699	q12
SNP_A-2005948	C	C	176	152	217	133	4.835	2.79E-02	rs4548998	19	36058906	q12
SNP_A-1721229	G	G	327	39	343	65	4.617	3.17E-02	rs278215	19	36084212	q12
SNP_A-1954080	T	T	296	116	327	93	3.997	4.56E-02	rs2279705	19	36350972	q12
SNP_A-2203497	A	A	381	29	363	47	4.699	3.02E-02	rs17496703	19	36476435	q12
SNP_A-2005955	C	C	354	4	368	0	4.135	4.20E-02	rs7254799	19	36904836	q12
SNP_A-2142527	A	A	408	6	416	0	6.073	0.0137	rs6510216	19	36938506	q12
SNP_A-1814883	T	T	416	4	420	0	4.019	4.50E-02	rs10153460	19	36956094	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1864872	G	G	234	148	260	110	6.776	9.20E-03	rs10411220	19	37367247	q13.11
SNP_A-1956500	C	C	199	195	227	139	10.212	0.0014	rs10417156	19	37502069	q13.11
SNP_A-2063475	A	A	300	50	315	29	5.897	0.0152	rs2111504	19	37609295	q13.11
SNP_A-2036389	A	A	363	37	369	19	5.653	1.74E-02	rs10426856	19	37788246	q13.11
SNP_A-2214587	C	C	228	128	234	88	5.795	0.0161	rs7253956	19	38084330	q13.11
SNP_A-1955626	G	A	181	149	180	160	4.066	4.38E-02	rs16967984	19	38540617	q13.11
SNP_A-2111453	G	C	216	170	201	189	4.37	3.66E-02	rs736682	19	38550053	q13.11
SNP_A-1955663	A	A	207	183	254	158	6.026	0.0141	rs4805877	19	38568234	q13.11
SNP_A-1870933	-	G	200	200	229	171	4.227	3.98E-02	rs2278260	19	38740148	q13.11
SNP_A-2201920	A	G	190	186	225	171	4.185	4.08E-02	rs10406663	19	38921659	q13.11
SNP_A-2076339	T	T	360	40	382	24	4.608	3.18E-02	rs17329186	19	39172751	q13.11
SNP_A-2289052	G	G	293	29	287	49	4.895	0.0269	rs11084756	19	39283595	q13.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2193656	A	A	253	133	234	170	4.852	0.0276	rs640466	19	39362565	q13.11
SNP_A-2089112	A	A	318	64	289	91	6.084	1.36E-02	rs11084766	19	39632212	q13.11
SNP_A-2082516	G	G	336	52	307	75	5.427	1.98E-02	rs11673331	19	39644343	q13.11
SNP_A-2150906	G	G	332	10	336	2	5.334	2.09E-02	rs886134	19	40355683	q13.12
SNP_A-2072047	G	G	403	15	416	2	10.148	0.0014	rs8100526	19	40718075	q13.12
SNP_A-1910055	C	C	382	22	386	10	4.441	3.51E-02	rs2162296	19	41792090	q13.12
SNP_A-1803192	-	C	192	192	225	145	8.91	0.0028	rs523979	19	42148245	q13.12
SNP_A-1957588	G	A	180	176	218	162	4.647	3.11E-02	rs1375476	19	42157015	q13.12
SNP_A-2236764	T	C	206	186	226	174	6.498	1.08E-02	rs1667337	19	42159352	q13.12
SNP_A-2185095	C	T	187	159	199	151	8.281	4.00E-03	rs1667348	19	42166959	q13.12
SNP_A-1906169	C	C	196	190	234	170	4.061	4.39E-02	rs1644666	19	42167326	q13.12
SNP_A-1653730	C	A	205	169	208	168	7.699	5.50E-03	rs1644669	19	42167867	q13.12
SNP_A-1744991	C	A	207	187	230	180	6.002	0.0143	rs1644670	19	42167901	q13.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2236221	T	C	207	187	215	159	7.73	5.40E-03	rs1667353	19	42172993	q13.12
SNP_A-2103645	C	A	181	139	167	157	4.242	3.94E-02	rs2562599	19	42208214	q13.12
SNP_A-1694765	G	C	216	188	221	191	4.12	0.0424	rs7246739	19	42223571	q13.13
SNP_A-1758587	A	G	199	169	198	168	4.905	2.68E-02	rs1818748	19	42248158	q13.13
SNP_A-1810530	C	G	204	176	208	174	5.042	0.0247	rs2385374	19	42274857	q13.12
SNP_A-2283380	A	T	189	131	166	148	9.057	2.60E-03	rs1402468	19	42312088	q13.12
SNP_A-2098459	T	T	302	74	329	49	6.231	0.0126	rs1234256	19	42409197	q13.12
SNP_A-2123175	G	G	324	82	349	57	5.425	1.98E-02	rs1530500	19	42515651	q13.12
SNP_A-2218564	A	A	345	37	321	71	11.441	7.00E-04	rs855640	19	43272184	q13.13
SNP_A-1818757	T	T	190	150	205	115	4.59	3.22E-02	rs3852911	19	43297276	q13.13
SNP_A-2091651	C	C	232	168	264	136	5.433	1.98E-02	rs332860	19	43348970	q13.13
SNP_A-2260999	G	G	280	34	276	68	10.015	1.60E-03	rs10420506	19	43362295	q13.13
SNP_A-2216295	A	A	328	52	313	79	5.731	0.0167	rs3745951	19	43509326	q13.2
SNP_A-1847752	T	T	403	1	397	7	4.545	3.30E-02	rs4802589	19	43722185	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2213574	A	A	394	26	403	13	4.416	0.0356	rs17589359	19	43887925	q13.2
SNP_A-2041658	A	A	269	77	274	110	3.902	0.0482	rs13344519	19	43978104	q13.2
SNP_A-2138153	T	T	267	67	312	48	5.67	1.73E-02	rs2241704	19	44088175	q13.2
SNP_A-1958959	C	C	358	60	334	82	4.236	3.96E-02	rs6508878	19	44778481	q13.2
SNP_A-2061127	C	C	354	34	365	17	5.789	0.0161	rs2074928	19	44920719	q13.2
SNP_A-1786217	G	G	178	144	219	103	11.04	9.00E-04	rs7251950	19	46174582	q13.2
SNP_A-2196426	T	T	344	56	324	94	9.834	1.70E-03	rs10407348	19	46645270	q13.2
SNP_A-1784922	C	C	227	85	276	68	5.113	2.37E-02	rs1195296	19	47368321	q13.2
SNP_A-2152123	G	G	340	18	346	6	6.002	0.0143	rs4803591	19	48461673	q13.31
SNP_A-2255154	C	C	393	21	399	7	6.968	8.30E-03	rs3213344	19	48752493	q13.31
SNP_A-2005986	A	A	347	9	345	21	4.668	3.07E-02	rs4251875	19	48852921	q13.31
SNP_A-2025585	T	T	344	44	327	69	5.881	1.53E-02	rs2239373	19	48854873	q13.31
SNP_A-2068276	C	C	312	102	338	76	4.838	2.78E-02	rs173202	19	48945428	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1957171	G	G	378	6	404	0	6.361	0.0117	rs8111388	19	49336893	q13.31
SNP_A-2027641	T	T	362	36	388	20	5.35	0.0207	rs2571096	19	49586004	q13.31
SNP_A-1877275	C	C	357	1	354	8	5.435	1.97E-02	rs17727898	19	49734356	q13.31
SNP_A-2144795	G	A	207	191	231	167	8.07	4.50E-03	rs10153467	19	51474417	q13.32
SNP_A-2210864	A	A	306	38	311	19	6.086	1.36E-02	rs10411556	19	51516744	q13.32
SNP_A-2033659	C	C	240	112	208	148	7.248	7.10E-03	rs404997	19	51621987	q13.32
SNP_A-1903527	G	G	230	124	195	149	5.029	2.49E-02	rs427250	19	51623902	q13.32
SNP_A-2089221	G	G	201	185	239	155	5.847	1.56E-02	rs6509283	19	51712404	q13.32
SNP_A-1961665	C	C	309	75	325	51	4.892	0.027	rs8101111	19	51726860	q13.32
SNP_A-2243557	A	A	371	45	355	65	3.97	4.63E-02	rs698705	19	52629278	q13.32
SNP_A-2173016	C	C	329	91	353	69	3.865	4.93E-02	rs3844440	19	52784719	q13.32
SNP_A-2254533	A	A	275	55	249	77	4.933	0.0264	rs2974211	19	52832120	q13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2163944	C	C	216	162	264	132	7.447	6.40E-03	rs8112377	19	53018190	q13.32
SNP_A-2291073	G	G	206	204	238	172	5.03	2.49E-02	rs4427918	19	53026777	q13.32
SNP_A-1961674	G	G	293	73	279	99	4.08	4.34E-02	rs2059815	19	53223350	q13.32
SNP_A-1872159	T	T	312	42	306	16	10.222	0.0014	rs2386983	19	53241760	q13.32
SNP_A-1961676	T	T	381	7	393	1	4.64	3.12E-02	rs445505	19	53284945	q13.32
SNP_A-1725920	G	G	286	72	257	101	6.41	1.13E-02	rs10500299	19	53413992	q13.33
SNP_A-1844258	C	C	258	92	296	74	4.006	0.0453	rs11670491	19	53980474	q13.33
SNP_A-2301476	C	C	253	95	295	75	4.902	2.68E-02	rs11881904	19	53980700	q13.33
SNP_A-1645260	C	C	375	29	367	47	4.228	3.98E-02	rs3810261	19	54914726	q13.33
SNP_A-2285102	A	A	225	167	259	137	5.329	2.10E-02	rs11083985	19	55069955	q13.33
SNP_A-2291356	G	G	278	132	246	160	4.62	3.16E-02	rs1274596	19	55665288	q13.33
SNP_A-1854878	C	C	250	168	224	198	3.866	4.93E-02	rs6509477	19	55732228	q13.33
SNP_A-2138586	G	A	205	147	157	151	5.612	0.0178	rs266863	19	56047462	q13.41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1687924	A	A	229	139	291	105	11.119	9.00E-04	rs268914	19	56134511	q13.41
SNP_A-2275689	T	T	376	44	394	28	3.972	4.63E-02	rs1654523	19	56177006	q13.41
SNP_A-2231258	C	C	404	16	392	30	4.437	3.52E-02	rs16988801	19	56195956	q13.41
SNP_A-2309731	G	G	309	109	334	84	4.21	0.0402	rs10401766	19	56234603	q13.41
SNP_A-2137120	G	G	383	37	367	55	3.858	4.95E-02	rs11671942	19	56275220	q13.41
SNP_A-2071755	T	T	346	2	323	9	4.872	2.73E-02	rs10422563	19	56325570	q13.41
SNP_A-2193228	A	A	393	27	411	11	7.135	0.0076	rs273663	19	56349412	q13.41
SNP_A-1801609	C	C	392	22	412	10	4.921	2.65E-02	rs273655	19	56363926	q13.41
SNP_A-1816512	C	C	376	36	379	19	5.026	2.50E-02	rs1566578	19	56441401	q13.41
SNP_A-2135272	T	T	376	40	390	24	4.251	3.92E-02	rs10412123	19	56454393	q13.41
SNP_A-1951607	A	A	415	5	422	0	5.054	0.0246	rs10414689	19	56488111	q13.41
SNP_A-2153437	T	T	412	6	422	0	6.101	0.0135	rs2547305	19	56639096	q13.41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2114241	A	A	283	45	253	63	4.457	3.48E-02	rs11084088	19	56756354	q13.41
SNP_A-2165729	G	G	319	85	296	110	4.06	4.39E-02	rs8111742	19	56887286	q13.41
SNP_A-2205467	T	T	303	65	326	38	7.897	5.00E-03	rs11672744	19	57145574	q13.41
SNP_A-1922626	T	T	327	85	352	64	3.861	4.94E-02	rs2015845	19	57149591	q13.41
SNP_A-1961707	C	C	253	125	305	103	5.832	1.57E-02	rs10500311	19	57189755	q13.41
SNP_A-2185724	A	A	246	148	289	111	8.697	3.20E-03	rs8112458	19	57225117	q13.41
SNP_A-1818699	G	G	300	76	339	43	11.485	7.00E-04	rs17779301	19	57231055	q13.41
SNP_A-2101385	C	C	304	92	337	67	5.55	1.85E-02	rs2043298	19	57264879	q13.41
SNP_A-1899164	G	G	359	47	334	66	4.052	0.0441	rs1025279	19	57395482	q13.41
SNP_A-2191746	A	A	382	34	362	56	5.911	1.50E-02	rs10417820	19	57418158	q13.41
SNP_A-1862491	A	A	342	8	332	20	5.286	2.15E-02	rs8113537	19	57463186	q13.41
SNP_A-1912671	G	G	281	109	323	87	4.893	0.027	rs17780009	19	57565430	q13.41
SNP_A-1909519	T	T	278	126	242	160	6.529	0.0106	rs1673917	19	57685432	q13.41

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175658	C	C	208	142	227	113	3.984	4.59E-02	rs329929	19	57693111	q13.41
SNP_A-1961716	C	C	316	22	331	11	3.991	4.57E-02	rs1019497	19	58002621	q13.41
SNP_A-1876091	C	C	369	45	384	28	4.253	3.92E-02	rs1661917	19	58197624	q13.41
SNP_A-1961720	G	G	310	30	331	17	4.191	4.06E-02	rs1650936	19	58200324	q13.41
SNP_A-2247575	G	G	359	1	349	7	4.619	3.16E-02	rs4614848	19	58385336	q13.42
SNP_A-1816994	C	C	249	125	219	149	3.977	4.61E-02	rs2617652	19	58563885	q13.42
SNP_A-2006041	G	G	250	120	280	92	5.391	2.02E-02	rs2708743	19	58649938	q13.42
SNP_A-1910764	C	C	292	80	259	117	8.905	0.0028	rs11666484	19	58661302	q13.42
SNP_A-2078672	T	T	334	80	305	115	7.555	6.00E-03	rs4801994	19	58823450	q13.42
SNP_A-1885577	C	C	392	0	392	4	3.98	4.60E-02	rs1052983	19	59416447	q13.42
SNP_A-1821561	G	G	373	23	389	9	6.456	0.0111	rs16960152	19	59424028	q13.42
SNP_A-1871847	G	G	224	114	276	102	3.852	4.97E-02	rs741584	19	59506905	q13.42
SNP_A-1938983	G	G	369	47	373	29	4.046	4.43E-02	rs2555687	19	59759666	q13.42

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1902362	T	T	318	56	349	39	4.227	3.98E-02	rs4806798	19	59858533	q13.42
SNP_A-1861897	G	G	406	6	402	16	4.522	3.35E-02	rs12461195	19	60380388	q13.42
SNP_A-2220764	T	T	371	13	362	32	8.006	4.70E-03	rs7248144	19	60988051	q13.42
SNP_A-1723992	C	C	352	52	379	33	5.166	0.023	rs7254875	19	61010979	q13.42
SNP_A-1712609	T	T	352	52	380	34	4.717	2.99E-02	rs10500321	19	61011383	q13.42
SNP_A-1946070	G	G	360	44	375	25	5.518	1.88E-02	rs4801630	19	61016671	q13.43
SNP_A-2234909	T	T	329	73	356	50	5.345	2.08E-02	rs12980766	19	61017002	q13.43
SNP_A-2255596	G	G	249	171	281	135	6.148	0.0132	rs395503	19	61061027	q13.43
SNP_A-1893355	C	C	324	88	287	125	8.668	3.20E-03	rs16986718	19	61061126	q13.43
SNP_A-2170994	G	G	266	136	292	108	4.42	3.55E-02	rs303993	19	61119156	q13.43
SNP_A-1961745	T	T	252	136	224	162	3.91	4.80E-02	rs382958	19	61131250	q13.43
SNP_A-1910786	G	G	242	140	217	173	4.758	0.0292	rs480677	19	61146700	q13.43
SNP_A-2306136	T	T	339	65	359	43	5.05	0.0246	rs11671038	19	61147259	q13.43
SNP_A-2125148	T	C	206	168	195	171	5.172	0.023	rs6510006	19	61856742	q13.43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2105445	T	T	206	202	247	169	6.569	0.0104	rs4801351	19	61857738	q13.43
SNP_A-2272174	C	C	268	114	310	86	6.722	9.50E-03	rs4483953	19	61862014	q13.43
SNP_A-1961760	C	C	332	76	338	50	4.919	2.66E-02	rs2048428	19	62177340	q13.43
SNP_A-1850395	T	T	282	66	308	38	8.679	3.20E-03	rs13343495	19	62224985	q13.43
SNP_A-2022445	T	T	339	53	359	31	6.33	1.19E-02	rs12459720	19	62232673	q13.43
SNP_A-2021972	A	A	232	160	207	195	4.749	0.0293	rs7256254	19	62305410	q13.43
SNP_A-1837997	C	C	267	83	256	128	8.271	4.00E-03	rs8103381	19	62653031	q13.43
SNP_A-2066738	A	A	286	128	258	160	4.978	2.57E-02	rs2074059	19	62677272	q13.43
SNP_A-1844431	G	G	255	59	257	95	6.276	1.22E-02	rs4801490	19	62698051	q13.43
SNP_A-1902561	C	C	369	51	388	32	4.826	2.80E-02	rs7250705	19	62759582	q13.43
SNP_A-2293249	T	T	202	124	237	93	7.195	7.30E-03	rs260500	19	63483025	q13.43
SNP_A-1893575	G	G	255	157	293	117	8.47	3.60E-03	rs260497	19	63484025	q13.43
SNP_A-2006075	G	G	212	128	263	115	4.172	4.11E-02	rs365699	19	63491464	q13.43

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2286176	G	G	394	14	405	5	4.41	3.57E-02	rs3816328	19	63753169	q13.43
SNP_A-1967425	G	G	302	32	341	17	6.132	1.33E-02	rs8124344	20	168757	p13
SNP_A-1822233	A	A	386	22	373	41	5.909	1.51E-02	rs6052239	20	401461	p13
SNP_A-1655167	A	A	377	19	365	47	11.761	6.00E-04	rs1114734	20	689894	p13
SNP_A-1967436	T	T	223	137	249	111	4.158	4.14E-02	rs673261	20	754878	p13
SNP_A-2292168	T	T	353	31	384	18	4.343	3.72E-02	rs882806	20	805271	p13
SNP_A-2121949	A	A	363	27	341	49	7.056	7.90E-03	rs882805	20	805377	p13
SNP_A-1929897	G	G	375	21	395	9	5.24	2.21E-02	rs17778888	20	1127237	p13
SNP_A-1886630	C	C	380	36	402	18	6.6	1.02E-02	rs12480258	20	1143532	p13
SNP_A-2265819	A	A	312	84	285	107	3.971	4.63E-02	rs2422601	20	1449211	p13
SNP_A-2176172	C	C	356	46	341	67	4.181	4.09E-02	rs2422604	20	1449393	p13
SNP_A-2167454	T	T	368	44	334	70	7.499	6.20E-03	rs6034006	20	1467511	p13
SNP_A-2228180	G	G	323	81	299	107	4.517	3.36E-02	rs6079605	20	1491409	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1726910	G	G	279	125	314	100	4.722	0.0298	rs3848788	20	1538066	p13
SNP_A-2259273	T	T	345	33	336	54	5.002	0.0253	rs3761269	20	1550206	p13
SNP_A-1754312	A	A	319	59	361	39	6.058	0.0138	rs202548	20	1657999	p13
SNP_A-1679304	T	T	315	29	306	48	4.676	3.06E-02	rs1438101	20	1676609	p13
SNP_A-1791966	A	A	203	199	240	172	4.933	0.0263	rs156350	20	1787408	p13
SNP_A-1897821	T	T	272	20	356	10	6.327	1.19E-02	rs727190	20	1792780	p13
SNP_A-2115287	G	G	346	28	370	16	3.889	4.86E-02	rs1438108	20	1792858	p13
SNP_A-1903006	T	T	358	36	380	18	6.636	0.01	rs4814687	20	1804533	p13
SNP_A-2124065	C	C	371	33	355	51	4.205	4.03E-02	rs6045664	20	1888145	p13
SNP_A-2210610	G	G	332	76	358	56	3.966	4.64E-02	rs2422669	20	1936025	p13
SNP_A-2136057	T	T	350	56	370	36	4.903	2.68E-02	rs1418040	20	1936382	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1804657	C	C	312	54	315	33	4.632	3.14E-02	rs2422671	20	1937383	p13
SNP_A-2181460	A	A	379	15	394	6	4.103	4.28E-02	rs2422677	20	1941052	p13
SNP_A-2099519	C	C	349	35	380	18	6.523	1.07E-02	rs6046762	20	2025456	p13
SNP_A-2060360	C	C	249	155	281	131	3.868	4.92E-02	rs6082408	20	2140516	p13
SNP_A-1667302	G	G	325	65	317	91	4.029	4.47E-02	rs6132407	20	2166630	p13
SNP_A-1869490	C	C	391	23	371	43	6.586	0.0103	rs8124987	20	2326960	p13
SNP_A-2166254	T	T	362	34	381	19	4.711	3.00E-02	rs6137946	20	2342641	p13
SNP_A-1904978	G	G	319	43	337	25	5.259	0.0218	rs1004269	20	2345656	p13
SNP_A-2175830	G	G	310	68	339	45	5.93	0.0149	rs2092631	20	2346956	p13
SNP_A-1710836	G	G	327	77	359	55	5.038	2.48E-02	rs4053458	20	2385880	p13
SNP_A-2007208	C	C	420	0	417	5	5.006	0.0253	rs6515445	20	2397143	p13
SNP_A-1929846	C	C	277	67	322	50	4.763	2.91E-02	rs6114506	20	2416296	p13
SNP_A-1744973	T	T	199	85	271	81	3.9	4.83E-02	rs4446127	20	2452788	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1873677	A	A	292	128	332	90	9.183	2.40E-03	rs16987508	20	2532331	p13
SNP_A-2159273	G	G	361	47	334	82	10.468	1.20E-03	rs12626155	20	2545560	p13
SNP_A-2247112	T	T	273	53	315	37	4.855	0.0276	rs17228085	20	2555429	p13
SNP_A-1918035	G	G	303	67	260	116	16.357	5.25E-05	rs7266145	20	2561658	p13
SNP_A-1785300	G	G	334	76	286	116	11.972	5.00E-04	rs1546931	20	2563611	p13
SNP_A-2245826	A	G	236	178	209	197	5.918	1.50E-02	rs910275	20	2563791	p13
SNP_A-1792473	T	T	320	80	288	124	10.999	9.00E-04	rs910273	20	2563882	p13
SNP_A-1808840	C	C	319	29	275	43	4.64	3.12E-02	rs6083915	20	2566140	p13
SNP_A-2039195	A	A	339	79	291	123	13.222	3.00E-04	rs6050771	20	2566308	p13
SNP_A-2126046	T	T	272	148	235	183	6.396	0.0114	rs2422818	20	2571191	p13
SNP_A-1910080	G	G	265	147	231	179	5.467	1.94E-02	rs4815449	20	2571872	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2293593	C	C	253	123	214	158	7.595	5.90E-03	rs4815453	20	2572150	p13
SNP_A-2136690	G	G	270	76	249	119	9.663	0.0019	rs6083938	20	2575497	p13
SNP_A-1853468	T	T	321	65	293	85	3.86	4.94E-02	rs1883977	20	2580010	p13
SNP_A-1682092	G	G	400	4	412	0	4.099	4.29E-02	rs6115686	20	2793326	p13
SNP_A-1838204	A	A	215	145	191	179	4.851	0.0276	rs8184236	20	2987115	p13
SNP_A-2036797	C	C	334	34	319	17	4.566	3.26E-02	rs6037567	20	3280160	p13
SNP_A-1967488	G	G	351	9	323	19	4.276	3.87E-02	rs17784288	20	3577843	p13
SNP_A-2115402	A	A	281	63	274	96	5.999	0.0143	rs6084588	20	3988923	p13
SNP_A-2044791	A	A	379	9	352	20	4.835	2.79E-02	rs6052282	20	3994188	p13
SNP_A-2195826	C	C	390	4	406	0	4.143	4.18E-02	rs1764991	20	4062848	p13
SNP_A-2197056	G	G	410	4	416	0	4.039	4.45E-02	rs1538317	20	4197122	p13
SNP_A-2070983	A	A	393	11	383	23	4.359	3.68E-02	rs297772	20	4441293	p13
SNP_A-1810282	A	A	400	14	390	28	4.774	2.89E-02	rs297774	20	4441963	p13
SNP_A-2007235	G	G	194	184	229	137	5.23	2.22E-02	rs7344639	20	4573558	p13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2308727	T	T	367	29	342	48	5.524	1.88E-02	rs6052761	20	4605017	p13
SNP_A-2133421	T	T	411	3	402	10	3.864	4.93E-02	rs7274758	20	4629310	p13
SNP_A-2062006	C	C	308	104	343	77	5.833	1.57E-02	rs6052830	20	4677789	p13
SNP_A-2234933	G	G	310	106	343	77	6.244	1.25E-02	rs7269641	20	4678559	p13
SNP_A-1867345	C	C	308	106	341	75	6.983	8.20E-03	rs6037950	20	4679022	p13
SNP_A-1864456	G	G	232	102	250	60	10.682	1.10E-03	rs2422958	20	4697289	p13
SNP_A-1796957	C	C	368	40	379	23	4.705	3.01E-02	rs6052918	20	4768603	p13
SNP_A-1908512	C	C	413	3	403	11	4.689	0.0304	rs6139641	20	5083968	p12.3
SNP_A-1806140	T	T	369	43	349	63	4.331	3.74E-02	rs6076800	20	5199101	p12.3
SNP_A-1722190	T	C	202	200	251	157	11.364	7.00E-04	rs4813744	20	5336009	p12.3
SNP_A-1967537	G	G	272	94	270	132	4.72	0.0298	rs237080	20	5760113	p12.3
SNP_A-2293429	C	C	259	81	251	111	4.128	4.22E-02	rs237096	20	5767844	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1960119	C	C	301	73	331	53	4.468	3.45E-02	rs6085298	20	5795881	p12.3
SNP_A-1895360	G	G	198	176	236	140	7.423	6.40E-03	rs1287052	20	5812948	p12.3
SNP_A-2283838	T	T	222	132	252	98	6.902	0.0086	rs1287051	20	5813420	p12.3
SNP_A-1909116	T	T	352	60	376	38	5.725	0.0167	rs236169	20	5866473	p12.3
SNP_A-1710047	C	C	393	11	411	3	4.853	0.0276	rs6117011	20	5917830	p12.3
SNP_A-2264352	T	T	285	53	301	35	4.113	4.26E-02	rs6133296	20	6114488	p12.3
SNP_A-2067717	T	T	403	1	413	7	4.313	0.0378	rs10211689	20	6223579	p12.3
SNP_A-1898324	A	A	408	4	414	0	4.039	4.45E-02	rs16992394	20	6519406	p12.3
SNP_A-2157915	A	A	393	21	382	36	4.084	4.33E-02	rs235749	20	6718144	p12.3
SNP_A-1967583	C	C	342	28	343	51	5.95	0.0147	rs13043688	20	6743944	p12.3
SNP_A-2249184	A	A	407	5	412	0	5.031	2.49E-02	rs16993000	20	6970257	p12.3
SNP_A-1929644	G	G	343	55	342	34	4.335	0.0373	rs3761883	20	6998105	p12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2313109	A	A	314	34	336	12	11.266	8.00E-04	rs971060	20	7536599	p12.3
SNP_A-2038722	C	C	309	33	331	19	4.434	3.52E-02	rs2206397	20	7539596	p12.3
SNP_A-1949452	T	T	258	58	293	37	6.565	0.0104	rs6077236	20	7573986	p12.3
SNP_A-1753921	G	G	401	3	403	11	4.455	3.48E-02	rs2223276	20	7877106	p12.3
SNP_A-1822153	A	A	242	124	226	156	3.864	4.93E-02	rs6077332	20	8145998	p12.3
SNP_A-2119967	T	T	315	97	343	71	5.21	2.25E-02	rs2745763	20	8227044	p12.3
SNP_A-1800898	C	C	283	101	295	71	5.053	0.0246	rs6055810	20	8357341	p12.3
SNP_A-1946999	G	G	395	23	407	9	6.3	0.0121	rs6140683	20	8607690	p12.3
SNP_A-2132345	G	G	255	57	243	83	4.813	2.82E-02	rs6086595	20	8712779	p12.3
SNP_A-1693881	T	T	219	133	271	119	4.361	3.68E-02	rs724088	20	9048695	p12.3
SNP_A-2149132	A	A	332	84	359	61	4.684	0.0304	rs7266736	20	9051343	p12.2
SNP_A-1967677	C	C	401	7	391	21	7.107	7.70E-03	rs16995654	20	9139578	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2030829	G	G	332	54	312	80	5.62	0.0178	rs6056523	20	9240176	p12.2
SNP_A-1900491	A	A	382	6	386	0	6.016	1.42E-02	rs16995805	20	9307138	p12.2
SNP_A-2045386	C	C	384	16	370	6	4.067	4.37E-02	rs6077544	20	9403091	p12.2
SNP_A-1784559	G	G	226	172	261	143	5.141	2.34E-02	rs2206472	20	9631789	p12.2
SNP_A-1906443	G	G	290	130	319	101	5.022	2.50E-02	rs7274775	20	9671375	p12.2
SNP_A-1967698	C	C	260	132	288	104	4.753	0.0293	rs2179473	20	9741477	p12.2
SNP_A-1791433	T	T	237	131	280	110	4.772	2.89E-02	rs6056911	20	9755661	p12.2
SNP_A-2007339	A	A	362	18	343	39	8.244	4.10E-03	rs486937	20	10007170	p12.2
SNP_A-2222329	A	A	382	16	382	2	10.642	1.10E-03	rs6032783	20	10019848	p12.2
SNP_A-2068008	G	G	286	60	312	40	5.079	2.42E-02	rs607331	20	10035230	p12.2
SNP_A-2198847	G	G	325	77	343	53	4.871	2.73E-02	rs670562	20	10038764	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2307421	A	A	302	62	302	32	8.3	4.00E-03	rs6417404	20	10051751	p12.2
SNP_A-1913493	G	G	299	55	275	77	4.665	3.08E-02	rs6131056	20	10097664	p12.2
SNP_A-1714585	C	C	319	73	343	53	4.024	0.0448	rs491244	20	10106919	p12.2
SNP_A-2154193	G	G	214	130	180	162	6.435	0.0112	rs12626080	20	10181052	p12.2
SNP_A-1839192	C	C	184	132	214	104	5.577	1.82E-02	rs362562	20	10191186	p12.2
SNP_A-1856474	T	T	277	115	290	84	4.707	3.00E-02	rs6032858	20	10299158	p12.2
SNP_A-2069014	C	C	251	135	275	95	7.716	5.50E-03	rs6039888	20	10305175	p12.2
SNP_A-2307674	C	C	250	144	283	115	5.27	2.17E-02	rs1232602	20	10546076	p12.2
SNP_A-2156300	A	A	312	52	309	77	4.218	4.00E-02	rs2143618	20	10562420	p12.2
SNP_A-2218996	T	T	288	114	320	90	4.429	3.53E-02	rs2144184	20	10839798	p12.2
SNP_A-2133354	G	G	390	12	396	4	4.041	4.44E-02	rs6040267	20	10904071	p12.2
SNP_A-2091490	A	A	337	13	361	5	4.025	0.0448	rs6033001	20	10905551	p12.2
SNP_A-2075470	A	A	320	84	341	61	4.311	3.79E-02	rs1316918	20	11590094	p12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1710135	T	T	347	55	330	80	4.978	2.57E-02	rs7261415	20	12059152	p12.1
SNP_A-2189151	T	T	366	52	349	73	3.913	4.79E-02	rs1022560	20	12085399	p12.1
SNP_A-1967787	G	G	318	82	340	60	4.144	4.18E-02	rs6033346	20	12142298	p12.1
SNP_A-1825840	G	G	317	75	333	51	4.883	2.71E-02	rs6041203	20	12153941	p12.1
SNP_A-1967793	T	T	245	91	209	113	4.932	0.0264	rs2327557	20	12221737	p12.1
SNP_A-1874088	C	C	386	4	380	0	3.918	4.78E-02	rs2224704	20	12283400	p12.1
SNP_A-2112499	G	G	385	23	375	39	4.217	4.00E-02	rs2104252	20	12286620	p12.1
SNP_A-1904644	G	G	259	125	216	154	6.649	9.90E-03	rs4814099	20	12318819	p12.1
SNP_A-1842599	C	C	319	37	302	66	8.434	3.70E-03	rs6131332	20	12328531	p12.1
SNP_A-2300716	T	T	301	63	264	84	5.066	2.44E-02	rs6041308	20	12330381	p12.1
SNP_A-2135183	G	G	306	58	286	90	7.402	6.50E-03	rs6041309	20	12331000	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1844241	G	G	354	40	377	23	5.266	2.17E-02	rs2208973	20	12342990	p12.1
SNP_A-1967799	A	A	313	47	330	28	5.257	2.19E-02	rs6074422	20	12357264	p12.1
SNP_A-2177601	C	C	324	46	290	24	4.241	0.0395	rs1076791	20	12362548	p12.1
SNP_A-1945907	G	G	345	23	373	11	4.989	2.55E-02	rs6078576	20	12366150	p12.1
SNP_A-1869446	A	A	337	25	351	11	5.729	0.0167	rs6109407	20	12371486	p12.1
SNP_A-1653106	C	C	228	166	263	143	4.028	0.0448	rs6109480	20	12554521	p12.1
SNP_A-1897497	G	G	327	69	348	48	4.423	3.55E-02	rs183191	20	12581827	p12.1
SNP_A-2007388	C	C	304	14	356	6	4.469	3.45E-02	rs2423712	20	12823977	p12.1
SNP_A-1967819	T	T	284	128	261	157	3.878	4.89E-02	rs6074520	20	12853188	p12.1
SNP_A-1948385	A	A	272	110	305	81	6.27	0.0123	rs3761893	20	12938212	p12.1
SNP_A-2167937	C	C	368	0	343	5	5.325	2.10E-02	rs1431433	20	12977764	p12.1
SNP_A-2115361	G	G	399	11	391	25	5.482	1.92E-02	rs6109693	20	13021768	p12.1
SNP_A-1967835	T	T	271	141	240	166	3.873	4.91E-02	rs6078937	20	13078096	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1950024	A	A	231	155	201	185	4.73	2.96E-02	rs6041945	20	13113181	p12.1
SNP_A-2185139	T	T	276	118	244	144	4.504	3.38E-02	rs4814213	20	13209075	p12.1
SNP_A-1967837	T	T	302	54	286	84	6.69	9.70E-03	rs719628	20	13210487	p12.1
SNP_A-1850150	C	C	351	65	376	38	7.933	4.90E-03	rs17263187	20	13237134	p12.1
SNP_A-1967840	C	C	386	20	398	8	5.327	2.10E-02	rs2145140	20	13351320	p12.1
SNP_A-2118988	G	G	233	95	202	116	4.145	4.17E-02	rs6079072	20	13383157	p12.1
SNP_A-2007394	C	C	252	106	235	135	3.886	0.0487	rs2273480	20	13412030	p12.1
SNP_A-1931348	A	A	412	0	414	4	3.962	0.0465	rs6033751	20	13462603	p12.1
SNP_A-2229238	G	G	351	35	359	19	4.748	0.0293	rs6042365	20	13733220	p12.1
SNP_A-2251522	A	A	301	85	274	112	4.968	0.0258	rs6131581	20	14373337	p12.1
SNP_A-1796818	G	G	392	16	404	6	4.721	0.0298	rs11907538	20	14638185	p12.1
SNP_A-1867906	C	C	278	62	325	39	8.092	4.40E-03	rs11087104	20	14643379	p12.1
SNP_A-2054591	A	A	348	58	378	34	7.457	0.0063	rs6079611	20	14855661	p12.1
SNP_A-1884871	C	C	285	105	314	82	4.187	0.0407	rs6135329	20	14955730	p12.1
SNP_A-2128070	G	G	357	29	325	47	5.508	0.0189	rs149819	20	15128181	p12.1
SNP_A-1967883	A	A	321	85	279	111	6.07	0.0138	rs175302	20	15167033	p12.1
SNP_A-1967885	A	A	288	88	281	119	3.99	0.0458	rs175308	20	15170775	p12.1
SNP_A-1967887	C	C	324	80	295	117	8.23	4.10E-03	rs175311	20	15171662	p12.1
SNP_A-2113766	C	C	320	86	292	118	6.281	1.22E-02	rs175312	20	15171745	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1645088	A	A	319	83	293	121	8.008	4.70E-03	rs175304	20	15215001	p12.1
SNP_A-1793935	C	C	342	50	340	28	5.459	0.0195	rs4814388	20	15423667	p12.1
SNP_A-2123067	G	G	345	45	376	22	9.148	2.50E-03	rs6131736	20	15809183	p12.1
SNP_A-1924127	G	G	336	4	368	0	4.354	3.69E-02	rs6043609	20	15834172	p12.1
SNP_A-1967922	A	A	373	27	401	13	5.674	0.0172	rs6080023	20	15847400	p12.1
SNP_A-1967923	T	T	388	26	407	11	6.516	1.07E-02	rs6080024	20	15850299	p12.1
SNP_A-2201428	A	A	376	28	391	11	7.699	5.50E-03	rs6034328	20	15850630	p12.1
SNP_A-1967924	C	C	385	21	406	10	4.34	3.72E-02	rs6135612	20	15862579	p12.1
SNP_A-1708556	T	T	373	31	401	13	8.256	4.10E-03	rs722337	20	15890220	p12.1
SNP_A-1724022	A	A	353	23	352	8	6.915	8.50E-03	rs6105492	20	15895806	p12.1
SNP_A-1646334	T	T	373	31	401	13	8.256	4.10E-03	rs6043620	20	15898710	p12.1
SNP_A-1655649	T	T	375	29	364	50	5.625	0.0177	rs10485545	20	16031666	p12.1
SNP_A-2204279	C	C	222	114	252	80	7.834	5.10E-03	rs1535597	20	16037757	p12.1
SNP_A-2070893	G	G	328	14	300	32	8.145	0.0043	rs912183	20	16059028	p12.1
SNP_A-2042462	C	C	259	139	289	115	3.865	4.93E-02	rs17726942	20	16061324	p12.1
SNP_A-2314665	A	A	285	47	271	69	4.43	3.53E-02	rs2760548	20	16064408	p12.1
SNP_A-1871807	C	C	260	154	293	127	4.521	3.35E-02	rs2327989	20	16086431	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1920096	T	T	341	45	328	66	4.144	4.18E-02	rs1890496	20	16087008	p12.1
SNP_A-1721427	C	C	327	63	308	92	5.869	0.0154	rs10485547	20	16171203	p12.1
SNP_A-2155175	A	G	186	176	198	152	4.513	3.36E-02	rs6135795	20	16482948	p12.1
SNP_A-1937608	T	T	254	82	243	129	8.905	0.0028	rs6075070	20	16484424	p12.1
SNP_A-2192404	T	C	215	187	220	188	4.44	3.51E-02	rs2277776	20	16518599	p12.1
SNP_A-2261762	C	C	282	52	324	38	3.969	4.64E-02	rs6075083	20	16533742	p12.1
SNP_A-2307304	T	T	322	48	336	30	4.43	3.53E-02	rs1105701	20	16571093	p12.1
SNP_A-2062969	G	G	210	116	250	98	4.279	3.86E-02	rs6111224	20	16577601	p12.1
SNP_A-2034009	T	T	284	64	250	96	8.559	3.40E-03	rs1885573	20	16591105	p12.1
SNP_A-1858528	A	A	322	82	338	52	6.86	8.80E-03	rs6080358	20	16591372	p12.1
SNP_A-2111734	G	G	315	43	284	74	9.818	1.70E-03	rs6080359	20	16591934	p12.1
SNP_A-2295313	G	G	324	58	303	93	8.567	3.40E-03	rs6044207	20	16598450	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1732061	A	A	215	187	248	156	5.149	2.33E-02	rs6080334	20	16599854	p12.1
SNP_A-1917743	C	C	345	5	328	0	4.721	0.0298	rs6135838	20	16603139	p12.1
SNP_A-1738048	C	C	334	70	308	104	7.619	5.80E-03	rs2328024	20	16649155	p12.1
SNP_A-1678008	G	G	382	16	384	6	4.47	3.45E-02	rs10485563	20	16808101	p12.1
SNP_A-1721754	G	G	373	31	396	18	4.015	4.51E-02	rs724053	20	16980601	p12.1
SNP_A-1753913	G	G	373	31	396	18	4.015	4.51E-02	rs763406	20	16999565	p12.1
SNP_A-1955062	T	T	298	116	321	91	3.869	4.92E-02	rs852037	20	17036787	p12.1
SNP_A-2264314	C	C	332	36	337	21	3.848	4.98E-02	rs6034754	20	17082260	p12.1
SNP_A-2152587	C	C	393	13	401	3	6.326	1.19E-02	rs852078	20	17084358	p12.1
SNP_A-1925930	G	G	347	53	379	37	3.943	4.71E-02	rs6136062	20	17237736	p12.1
SNP_A-2095443	C	C	257	155	230	190	4.971	0.0258	rs6111532	20	17328490	p12.1
SNP_A-2242760	T	T	187	147	201	115	3.918	4.78E-02	rs6044814	20	17367171	p12.1
SNP_A-2252697	T	T	246	150	196	172	6.141	0.0132	rs2269016	20	17372706	p12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1911887	G	G	220	156	266	134	5.286	2.15E-02	rs2269023	20	17381079	p12.1
SNP_A-2067421	A	A	198	174	242	146	6.516	1.07E-02	rs919189	20	17385489	p12.1
SNP_A-2267604	G	G	329	79	360	54	6.051	1.39E-02	rs2269027	20	17390908	p12.1
SNP_A-1908077	G	G	221	163	190	188	4.072	0.0436	rs2284916	20	17393535	p12.1
SNP_A-1820192	T	T	312	76	354	48	8.726	3.10E-03	rs2269032	20	17395010	p12.1
SNP_A-2223548	G	G	275	63	276	24	15.275	9.29E-05	rs16999416	20	17489830	p12.1
SNP_A-1834971	C	C	268	114	289	89	3.85	4.98E-02	rs6514828	20	17869572	p11.23
SNP_A-2239433	A	A	280	132	299	99	5.097	0.024	rs6111778	20	17921491	p11.23
SNP_A-1875411	C	C	331	59	328	34	5.699	1.70E-02	rs6105875	20	18030725	p11.23
SNP_A-1968011	G	G	349	13	354	4	4.778	2.88E-02	rs13045938	20	18087552	p11.23
SNP_A-1859197	C	C	340	32	336	16	4.808	2.83E-02	rs1022684	20	18435606	p11.23
SNP_A-2038251	G	G	303	79	321	57	4.057	4.40E-02	rs6081190	20	18461532	p11.23
SNP_A-1882504	T	T	364	20	390	8	5.791	0.0161	rs1321324	20	18712973	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2207713	C	C	351	53	328	80	6.241	1.25E-02	rs1053834	20	18742714	p11.23
SNP_A-2064394	C	C	372	34	398	16	7.281	7.00E-03	rs6045628	20	18743113	p11.23
SNP_A-1872763	G	G	318	6	326	0	6.093	1.36E-02	rs2273854	20	18975726	p11.23
SNP_A-1968055	T	T	409	5	416	0	5.055	0.0246	rs6035292	20	19239116	p11.23
SNP_A-2182133	G	G	223	143	242	112	4.346	3.71E-02	rs6081605	20	19399637	p11.23
SNP_A-2021429	C	C	300	86	277	117	5.569	0.0183	rs4814863	20	19417685	p11.23
SNP_A-1968068	T	T	354	30	337	47	4.171	4.11E-02	rs636116	20	19448070	p11.23
SNP_A-1968070	T	T	384	34	370	52	4.008	0.0453	rs2104462	20	19458010	p11.23
SNP_A-1901127	C	C	230	184	262	148	5.966	0.0146	rs3790270	20	19525156	p11.23
SNP_A-2007497	A	A	267	137	298	110	4.633	3.14E-02	rs2424239	20	19560584	p11.23
SNP_A-2007499	A	A	227	137	246	100	6.087	1.36E-02	rs6046223	20	19572009	p11.23
SNP_A-1673134	G	G	262	130	307	107	5.194	2.27E-02	rs722850	20	19605736	p11.23
SNP_A-2110730	G	G	241	167	213	197	4.195	4.06E-02	rs4814894	20	19701538	p11.23
SNP_A-2208406	A	A	350	0	352	4	3.955	4.67E-02	rs17371935	20	19754241	p11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2155098	T	T	372	0	338	4	4.375	3.65E-02	rs199542	20	19866588	p11.23
SNP_A-2027584	T	T	330	24	356	12	4.716	2.99E-02	rs16981514	20	19996908	p11.23
SNP_A-1800966	T	T	219	119	233	83	6.116	0.0134	rs9679967	20	20039322	p11.23
SNP_A-2120548	A	A	358	4	356	0	3.956	4.67E-02	rs1028435	20	20062707	p11.23
SNP_A-2305257	C	C	368	18	374	8	3.874	4.90E-02	rs964139	20	20091480	p11.23
SNP_A-2269124	C	C	335	85	369	53	9.058	2.60E-03	rs1327910	20	20208944	p11.23
SNP_A-1893906	G	G	308	44	339	19	11.356	8.00E-04	rs2145051	20	20209309	p11.23
SNP_A-1968095	G	G	174	166	204	138	4.954	2.60E-02	rs1000269	20	20246483	p11.23
SNP_A-2220562	G	G	211	201	249	171	5.482	1.92E-02	rs6046790	20	20251376	p11.23
SNP_A-1897926	G	G	390	4	404	0	4.122	4.23E-02	rs6137027	20	20348558	p11.23
SNP_A-2227114	G	G	278	88	301	61	5.784	1.62E-02	rs200371	20	22217440	p11.22
SNP_A-1905544	G	G	354	20	381	3	13.427	2.00E-04	rs1429447	20	22242822	p11.22
SNP_A-2023708	C	C	381	33	402	16	6.442	0.0111	rs418300	20	22265618	p11.22
SNP_A-1968136	C	C	379	33	401	17	5.697	1.70E-02	rs115282	20	22270363	p11.22
SNP_A-1912247	A	A	307	85	328	62	4.288	3.84E-02	rs6036119	20	22389124	p11.21
SNP_A-2213706	A	A	410	0	382	4	4.27	3.88E-02	rs1890208	20	22463122	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2130976	A	A	414	0	416	4	3.962	0.0465	rs16984209	20	22545203	p11.21
SNP_A-2307999	C	C	345	45	368	22	8.637	0.0033	---	20	23189767	p11.21
SNP_A-2076872	C	C	282	90	253	113	4.129	4.21E-02	rs6076059	20	23284261	p11.21
SNP_A-2212996	C	C	255	157	224	192	5.497	0.019	rs2249239	20	23380891	p11.21
SNP_A-2299981	C	C	382	32	402	16	5.824	1.58E-02	rs6114100	20	23393597	p11.21
SNP_A-1968174	A	A	384	36	405	17	7.366	0.0066	rs6114142	20	23409082	p11.21
SNP_A-1968175	G	G	377	35	400	16	7.74	5.40E-03	rs6137975	20	23409778	p11.21
SNP_A-1968177	A	A	354	32	391	13	9.455	2.10E-03	rs6114144	20	23410022	p11.21
SNP_A-2026840	A	A	350	0	327	5	5.31	0.0212	rs238655	20	23446207	p11.21
SNP_A-1816659	G	G	351	39	326	64	6.991	8.20E-03	rs2070856	20	23679412	p11.21
SNP_A-1825538	G	G	393	15	373	27	3.872	4.91E-02	rs4547593	20	23751448	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2007544	G	G	407	5	400	14	4.319	3.77E-02	rs2424603	20	23867101	p11.21
SNP_A-1935191	T	T	371	5	353	19	8.593	3.40E-03	rs2983541	20	23881619	p11.21
SNP_A-1856809	T	T	375	27	382	14	4.142	4.18E-02	rs6049303	20	23936563	p11.21
SNP_A-1683786	G	G	384	2	387	11	6.06	0.0138	rs1580754	20	24169028	p11.21
SNP_A-2045177	A	A	354	30	371	17	3.974	4.62E-02	rs6036726	20	24230110	p11.21
SNP_A-2007552	A	A	246	62	231	93	6.271	0.0123	rs6036754	20	24309668	p11.21
SNP_A-2171572	T	T	310	110	283	137	4.181	4.09E-02	rs13042428	20	24342770	p11.21
SNP_A-1968204	G	G	371	21	368	38	4.666	3.08E-02	rs6114732	20	24379089	p11.21
SNP_A-1680974	C	C	403	1	407	7	4.398	3.60E-02	rs10485833	20	24420449	p11.21
SNP_A-2141235	C	C	408	8	421	1	5.606	1.79E-02	rs6036924	20	24759468	p11.21
SNP_A-2256252	A	A	411	9	419	1	6.477	0.0109	rs6050013	20	24760054	p11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2060963	G	G	409	7	420	0	7.127	0.0076	rs6050016	20	24761162	p11.21
SNP_A-1791035	G	G	317	85	347	63	4.547	3.30E-02	rs6138482	20	25007442	p11.21
SNP_A-1867001	A	A	334	22	299	43	8.442	3.70E-03	rs2207634	20	25019454	p11.21
SNP_A-2254265	C	C	350	32	347	17	4.173	4.11E-02	rs1883528	20	25528959	p11.21
SNP_A-2223333	C	C	320	38	312	20	4.714	2.99E-02	rs1830542	20	28154290	q11.1
SNP_A-2276843	T	T	265	149	295	123	4.073	0.0436	rs6061015	20	29936849	q11.21
SNP_A-2179376	C	C	377	5	378	14	4.136	4.20E-02	rs880112	20	30592219	q11.21
SNP_A-2116583	C	C	182	174	211	147	4.405	3.58E-02	rs11697969	20	30702959	q11.21
SNP_A-1870553	G	G	325	33	306	52	4.819	0.0281	rs6141780	20	30726084	q11.21
SNP_A-1900027	G	G	272	90	303	55	10.098	0.0015	rs12480157	20	30726581	q11.21
SNP_A-1928059	T	T	261	89	299	63	6.826	9.00E-03	rs6057628	20	30772345	q11.21
SNP_A-2281772	A	A	242	98	268	58	11.293	8.00E-04	rs6058840	20	30782777	q11.21
SNP_A-1932435	G	G	275	103	334	68	12.153	5.00E-04	rs6057632	20	30783502	q11.21
SNP_A-1905807	G	G	290	102	330	56	15.928	6.58E-05	rs6058845	20	30787580	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2097432	T	T	295	115	337	79	9.428	2.10E-03	rs6058847	20	30787796	q11.21
SNP_A-2239741	A	A	337	43	331	65	4.207	4.03E-02	rs6141829	20	30902870	q11.21
SNP_A-1853520	T	T	406	2	405	9	4.412	3.57E-02	rs17123726	20	30911029	q11.21
SNP_A-2271377	C	C	333	17	327	33	5.035	2.48E-02	rs4911287	20	31090952	q11.21
SNP_A-2088379	C	C	347	59	369	37	5.718	1.68E-02	rs4911368	20	31885403	q11.22
SNP_A-2127028	A	A	318	20	328	8	5.292	2.14E-02	rs6088425	20	32255181	q11.22
SNP_A-1968259	T	T	244	114	207	135	4.443	3.50E-02	rs10103677	20	32932454	q11.22
SNP_A-2223650	C	C	239	135	222	172	4.568	3.26E-02	rs6058154	20	33049495	q11.22
SNP_A-1793643	G	G	206	138	236	116	3.85	4.97E-02	rs6088692	20	33102249	q11.22
SNP_A-2072958	G	G	354	48	373	31	4.15	4.16E-02	rs6060230	20	33152969	q11.22
SNP_A-1744647	T	T	307	57	301	85	4.939	0.0263	rs718404	20	33171136	q11.22
SNP_A-1904378	T	T	375	21	382	10	3.948	4.69E-02	rs6060375	20	33384389	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1655629	A	A	343	61	371	43	4.092	4.31E-02	rs2378132	20	33561712	q11.22
SNP_A-1646626	C	C	338	62	370	44	4.263	3.89E-02	rs819145	20	33577503	q11.22
SNP_A-1649210	G	G	349	55	376	38	3.991	4.57E-02	rs717593	20	34368640	q11.22
SNP_A-2221160	A	A	388	24	366	40	4.598	3.20E-02	rs6071671	20	34670015	q11.23
SNP_A-1934278	C	C	290	82	269	113	5.585	1.81E-02	rs6012560	20	35639172	q11.23
SNP_A-2286074	T	T	317	103	293	129	3.853	4.96E-02	rs6019534	20	35639821	q11.23
SNP_A-2289676	A	A	280	80	270	110	4.381	3.63E-02	rs17785937	20	35662241	q11.23
SNP_A-2146673	C	C	394	14	370	32	7.753	5.40E-03	rs6069673	20	36367793	q11.23
SNP_A-2007605	A	A	393	17	366	34	6.505	1.08E-02	rs6024822	20	36379050	q11.23
SNP_A-2007606	A	A	372	44	349	65	4.775	2.89E-02	rs6024863	20	36384404	q11.23
SNP_A-1919759	C	C	408	4	410	0	4	4.55E-02	rs5741816	20	36416396	q11.23
SNP_A-1968293	G	G	377	5	410	0	5.401	0.0201	rs11536951	20	36420935	q11.23
SNP_A-2307978	C	C	395	19	381	39	7.106	7.70E-03	rs2232599	20	36425886	q11.23
SNP_A-1954508	C	C	335	33	344	18	4.482	3.43E-02	rs6099309	20	36430763	q11.23

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1966297	G	G	311	19	324	8	4.742	2.94E-02	rs6100096	20	36595417	q11.23
SNP_A-2279597	C	C	304	92	287	121	4.259	0.039	rs2250345	20	36803336	q11.23
SNP_A-2127728	T	T	260	150	228	176	4.128	4.22E-02	rs2748666	20	36839160	q11.23
SNP_A-2033780	T	T	329	33	320	54	4.999	2.54E-02	rs16987734	20	37052118	q11.23
SNP_A-2204841	T	T	254	158	214	202	8.777	3.00E-03	rs4812357	20	37116485	q12
SNP_A-2192982	G	G	245	159	206	194	6.823	9.00E-03	rs1569538	20	37118630	q12
SNP_A-2102506	A	A	243	167	214	202	5.117	2.37E-02	rs926392	20	37123878	q12
SNP_A-1852464	A	A	245	169	214	202	5.024	2.50E-02	rs926391	20	37123899	q12
SNP_A-1860573	T	T	405	9	398	22	5.47	1.93E-02	rs2103613	20	37129934	q12
SNP_A-1823842	A	A	295	35	298	56	4.024	4.49E-02	rs16987791	20	37137226	q12
SNP_A-1968309	A	A	338	10	305	21	4.884	2.71E-02	rs724176	20	37142841	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2085493	C	C	363	39	341	65	7.168	7.40E-03	rs912180	20	37144213	q12
SNP_A-1918548	A	A	379	3	376	16	8.779	3.00E-03	rs17831740	20	37164048	q12
SNP_A-1817492	C	C	394	8	394	22	6.296	0.0121	rs6028466	20	37562416	q12
SNP_A-1968328	T	G	205	153	170	162	4.96	2.59E-02	rs6028505	20	37613924	q12
SNP_A-1650254	T	T	243	135	277	111	4.435	3.52E-02	rs1780615	20	37656548	q11.23
SNP_A-2061662	T	T	347	13	324	4	4.074	0.0436	rs13040687	20	37659343	q12
SNP_A-1968337	A	A	348	22	344	40	4.991	2.55E-02	rs292858	20	37786993	q12
SNP_A-2137509	A	A	344	22	326	38	4.745	2.94E-02	rs6028644	20	37821088	q12
SNP_A-2111187	G	G	323	55	363	39	4.321	3.76E-02	rs211857	20	37896144	q12
SNP_A-2300854	G	G	397	3	396	12	5.323	2.11E-02	rs6065178	20	38046942	q12
SNP_A-2314239	G	G	416	4	422	0	4.038	4.45E-02	rs6028872	20	38161739	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1880595	G	G	413	5	416	0	5.006	0.0253	rs6029050	20	38403254	q12
SNP_A-2212281	T	T	359	7	350	20	6.352	0.0117	rs6029067	20	38425561	q12
SNP_A-2199184	T	T	364	36	357	55	3.858	4.95E-02	rs6093375	20	38707696	q12
SNP_A-2054898	C	C	289	59	294	38	4.215	4.01E-02	rs6029319	20	38831112	q12
SNP_A-2007628	A	A	309	51	328	34	3.961	4.66E-02	rs6029361	20	38885752	q12
SNP_A-1840200	C	C	344	46	324	84	11.306	8.00E-04	rs1006325	20	39067017	q12
SNP_A-1795467	C	C	359	55	332	80	5.68	0.0172	rs6072247	20	39085306	q12
SNP_A-1674471	C	C	372	6	409	1	4.031	4.47E-02	rs211867	20	39129967	q12
SNP_A-1968378	A	A	352	58	331	81	4.447	3.50E-02	rs17264110	20	39147642	q12
SNP_A-1968379	C	C	407	9	418	2	4.582	3.23E-02	rs2076147	20	39246420	q12
SNP_A-2219840	T	T	337	49	312	74	6.044	0.014	rs17181845	20	39363443	q12
SNP_A-2301240	C	C	391	9	414	2	4.8	2.85E-02	rs2072968	20	39433330	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1870020	A	A	406	14	417	5	4.405	3.58E-02	rs16985754	20	39491955	q12
SNP_A-1834629	G	G	385	27	400	14	4.404	3.59E-02	rs6129846	20	39540728	q12
SNP_A-2247558	C	C	409	9	417	1	6.477	0.0109	rs4141780	20	39731207	q12
SNP_A-1912303	A	A	373	37	386	22	4.031	4.47E-02	rs6065400	20	39946180	q12
SNP_A-2032097	G	G	359	15	374	6	4.117	4.25E-02	rs6065406	20	39973121	q12
SNP_A-1895643	G	G	275	81	314	64	3.92	4.77E-02	rs1076666	20	40171886	q12
SNP_A-2007639	C	C	295	67	316	40	7.485	6.20E-03	rs6016688	20	40176580	q12
SNP_A-1968415	T	T	244	130	278	106	4.524	3.34E-02	rs6016745	20	40383597	q12
SNP_A-2132875	T	T	253	69	239	99	5.371	2.05E-02	rs916327	20	40445706	q12
SNP_A-2229049	C	C	324	72	294	94	4.291	3.83E-02	rs6072747	20	40505433	q12
SNP_A-1968422	T	T	262	142	235	177	5.229	2.22E-02	rs2076082	20	40510165	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2007642	T	T	268	106	233	131	4.948	2.61E-02	rs6072755	20	40533091	q12
SNP_A-1898815	C	C	306	90	281	117	4.581	3.23E-02	rs6130145	20	40536587	q12
SNP_A-2037970	G	G	350	64	323	95	7.108	7.70E-03	rs230153	20	40541070	q12
SNP_A-1968424	C	C	348	68	320	96	5.954	0.0147	rs230155	20	40543335	q12
SNP_A-2173643	G	G	366	28	352	48	5.491	1.91E-02	rs2064677	20	40608107	q12
SNP_A-1798845	C	C	298	76	259	113	9.969	1.60E-03	rs6030395	20	40714518	q12
SNP_A-1958441	A	A	300	58	266	88	8.185	4.20E-03	rs6065520	20	40715840	q12
SNP_A-1875998	A	A	387	23	364	38	4.315	0.0378	rs6072814	20	40719392	q12
SNP_A-1968429	G	G	277	141	249	169	4.02	4.50E-02	rs6016864	20	40724350	q12
SNP_A-2066039	G	G	260	108	222	140	7.076	7.80E-03	rs6102985	20	40736940	q12
SNP_A-1891280	G	G	301	97	269	129	6.327	1.19E-02	rs6065525	20	40745754	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1968430	G	G	300	96	277	137	7.735	5.40E-03	rs2425520	20	40746752	q12
SNP_A-2039986	A	A	303	101	265	129	5.827	1.58E-02	rs4810366	20	40759651	q12
SNP_A-1795122	G	G	352	62	323	91	6.743	9.40E-03	rs3092557	20	40784206	q12
SNP_A-2217303	G	G	374	14	386	4	5.74	0.0166	rs7262282	20	40905283	q12
SNP_A-1874395	T	T	363	1	342	10	7.79	0.0053	rs6016816	20	40950784	q12
SNP_A-2073831	G	G	418	0	416	6	5.986	0.0144	rs1812007	20	40956454	q12
SNP_A-1968449	C	C	397	19	385	33	3.949	4.69E-02	rs6016996	20	41313076	q13.11
SNP_A-1968451	C	C	259	139	211	187	11.97	5.00E-04	rs10485700	20	41363788	q13.11
SNP_A-1804363	C	C	218	114	243	85	5.558	0.0184	rs926292	20	41380590	q13.11
SNP_A-2156645	A	A	376	40	359	61	4.741	2.95E-02	rs6103249	20	41399350	q13.11
SNP_A-1722842	G	G	211	135	253	105	7.349	6.70E-03	rs2067084	20	41421323	q12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2246969	A	A	318	30	282	44	4.095	4.30E-02	rs6103372	20	41605279	q13.12
SNP_A-2034222	G	G	367	13	342	24	3.89	4.86E-02	rs2867726	20	41615586	q13.12
SNP_A-2206512	G	G	348	54	315	75	4.88	2.72E-02	rs1055334	20	41650061	q13.12
SNP_A-2104753	C	C	343	39	326	58	4.148	4.17E-02	rs1894668	20	41652333	q13.12
SNP_A-2228627	C	C	336	48	309	73	6.29	0.0121	rs6030975	20	41656398	q13.12
SNP_A-1834588	C	C	336	80	310	108	5.212	0.0224	rs6073143	20	41664109	q13.12
SNP_A-2007657	A	A	316	48	286	70	5.509	0.0189	rs3091647	20	41710058	q13.12
SNP_A-1668971	C	C	375	27	352	60	13.124	3.00E-04	rs10485693	20	41713416	q12
SNP_A-1858687	T	T	305	57	269	75	4.256	3.91E-02	rs826941	20	41723562	q13.12
SNP_A-2218478	A	A	336	60	319	91	6.564	0.0104	rs385345	20	41725375	q13.12
SNP_A-2276320	G	G	371	41	359	61	4.042	4.44E-02	rs387769	20	41745269	q13.12
SNP_A-2167439	A	A	374	38	353	59	5.153	2.32E-02	rs3091249	20	41789167	q13.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2232707	G	A	215	185	226	194	4.683	3.05E-02	rs3746566	20	41956979	q13.12
SNP_A-1738965	T	T	246	106	222	146	7.228	7.20E-03	rs2425524	20	42002373	q12
SNP_A-2273244	A	A	406	4	406	12	3.923	4.76E-02	rs12480895	20	42502540	q13.12
SNP_A-1672112	C	C	247	155	285	129	4.919	2.66E-02	rs2223246	20	42630572	q13.11
SNP_A-1885700	T	T	302	92	268	124	6.764	9.30E-03	rs4812861	20	42835955	q13.12
SNP_A-1787524	A	A	337	69	302	100	7.584	5.90E-03	rs1124335	20	42868827	q13.12
SNP_A-1664420	A	A	354	46	345	69	4.476	0.0344	rs1894666	20	42893074	q13.12
SNP_A-1915339	T	T	291	105	263	131	4.275	3.87E-02	rs6103892	20	42913558	q13.12
SNP_A-2141730	T	T	274	100	241	121	3.915	4.78E-02	rs6103899	20	42926331	q13.12
SNP_A-2150051	G	G	308	70	279	91	4.087	4.32E-02	rs6103901	20	42930599	q13.12
SNP_A-1860505	G	G	264	138	307	109	6.405	0.0114	rs6017444	20	42961935	q13.12
SNP_A-1880210	A	A	242	134	274	110	4.261	0.039	rs12481468	20	42965852	q13.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2313517	C	C	301	95	275	127	5.741	0.0166	rs4812873	20	42993896	q13.12
SNP_A-1866826	G	G	396	14	411	5	4.499	0.0339	rs6065890	20	43843643	q13.12
SNP_A-2250937	T	T	375	17	391	7	4.456	3.48E-02	rs12480250	20	43893783	q13.12
SNP_A-2286084	C	C	360	16	369	5	5.868	0.0154	rs1057275	20	43904683	q13.12
SNP_A-2083057	T	T	393	21	398	10	3.891	4.85E-02	rs16985456	20	44135231	q13.12
SNP_A-2204737	A	A	397	13	405	3	6.325	1.19E-02	rs17841916	20	44178129	q13.12
SNP_A-2127612	G	G	354	30	344	50	5.016	2.51E-02	rs17381472	20	44215835	q13.12
SNP_A-2086931	C	C	301	89	282	124	6.051	1.39E-02	rs966567	20	44300632	q13.12
SNP_A-1968505	G	G	352	54	369	35	4.452	0.0349	rs6094345	20	44523087	q13.12
SNP_A-2194939	A	A	283	109	260	144	5.636	1.76E-02	rs389905	20	44645862	q13.12
SNP_A-2091971	A	A	361	35	337	57	6.081	0.0137	rs3092501	20	44914354	q13.12
SNP_A-2235583	C	C	227	153	178	168	5.048	0.0247	rs6063038	20	45001830	q13.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2062101	C	C	227	175	257	149	3.926	4.75E-02	rs6063040	20	45003054	q13.12
SNP_A-1818666	A	G	220	184	215	195	3.871	4.91E-02	rs1206748	20	45006646	q13.12
SNP_A-1793695	T	T	410	4	410	0	3.981	4.60E-02	rs1210773	20	45019177	q13.12
SNP_A-1796275	C	C	352	38	370	22	4.71	3.00E-02	rs11696358	20	45321797	q13.12
SNP_A-2122167	G	G	211	195	262	150	11.325	8.00E-04	rs6066361	20	45558648	q13.12
SNP_A-1946697	C	C	299	109	328	74	7.991	4.70E-03	rs6066409	20	45673272	q13.12
SNP_A-2183170	G	G	334	38	321	63	6.257	0.0124	rs6094775	20	45739633	q13.12
SNP_A-2007702	T	T	275	145	297	115	4.231	3.97E-02	rs6018635	20	45740545	q13.12
SNP_A-1937797	G	G	316	64	291	85	3.968	4.64E-02	rs1591168	20	45760849	q13.12
SNP_A-1783538	T	T	291	107	270	140	5.018	2.51E-02	rs4810702	20	45871482	q13.13
SNP_A-2242804	T	T	255	137	230	176	5.904	1.51E-02	rs6066483	20	45871831	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1947160	T	T	368	18	347	31	3.982	4.60E-02	rs5742253	20	45898012	q13.13
SNP_A-1888082	A	A	334	30	326	58	8.477	3.60E-03	rs10021201	20	45918487	q13.13
SNP_A-2285524	G	G	359	49	333	73	5.693	1.70E-02	rs8121373	20	45927717	q13.13
SNP_A-1752611	G	G	400	4	414	0	4.119	0.0424	rs6017950	20	45956795	q13.12
SNP_A-1845687	G	G	196	192	232	168	4.446	3.50E-02	rs11698441	20	46097891	q13.13
SNP_A-2041106	C	C	237	107	219	145	5.88	1.53E-02	rs4810756	20	46099152	q13.13
SNP_A-1968548	A	A	309	81	282	112	6.193	1.28E-02	rs965220	20	46165626	q13.13
SNP_A-2089137	T	T	311	101	281	133	5.892	0.0152	rs1325760	20	46173477	q13.13
SNP_A-1920178	G	G	359	25	390	14	3.88	4.89E-02	rs11699291	20	46330350	q13.13
SNP_A-1872442	A	A	366	20	356	36	4.664	3.08E-02	rs380663	20	46402457	q13.13
SNP_A-1924379	G	G	384	12	376	28	6.405	0.0114	rs749044	20	46429137	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2281906	C	C	283	91	270	124	4.853	0.0276	rs6019284	20	46618286	q13.13
SNP_A-1904574	C	C	298	12	310	26	4.355	3.69E-02	rs729663	20	46737713	q13.13
SNP_A-2007718	C	C	324	48	305	69	4.338	0.0373	rs6019433	20	46855975	q13.13
SNP_A-1863695	A	A	377	41	359	61	4.357	3.69E-02	rs17366684	20	46903704	q13.13
SNP_A-2025205	T	T	294	4	340	0	4.593	3.21E-02	rs6019466	20	46916218	q13.13
SNP_A-2143663	G	G	334	32	309	53	6.138	0.0132	rs4809731	20	46929174	q13.13
SNP_A-2249071	C	C	406	12	390	28	6.722	9.50E-03	rs13042686	20	47468865	q13.13
SNP_A-2118411	A	C	188	158	188	152	6.361	0.0117	rs6095600	20	47700112	q13.13
SNP_A-2084909	A	A	345	67	368	46	4.64	3.12E-02	rs663890	20	47838575	q13.13
SNP_A-2271888	C	C	373	1	367	9	6.443	0.0111	rs17725005	20	48152412	q13.13
SNP_A-2213512	T	T	212	130	164	144	5.078	2.42E-02	rs6012846	20	48170921	q13.13
SNP_A-1860529	C	G	230	190	220	198	4.583	3.23E-02	rs232737	20	48197440	q13.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2064654	G	A	223	177	218	182	8.406	3.70E-03	rs232736	20	48197702	q13.13
SNP_A-2007733	T	C	207	139	170	162	8.312	3.90E-03	rs6125931	20	48228820	q13.13
SNP_A-2244520	G	G	281	135	307	99	6.567	0.0104	rs2869991	20	48497644	q13.13
SNP_A-1642331	A	A	397	7	396	18	4.72	0.0298	rs968149	20	48990967	q13.13
SNP_A-1855211	G	G	371	15	354	30	5.393	2.02E-02	rs6021011	20	49207656	q13.2
SNP_A-2120310	T	T	280	122	317	91	6.761	9.30E-03	rs2426242	20	49208757	q13.2
SNP_A-2184658	T	T	370	44	338	72	8.186	4.20E-03	rs6417290	20	49284871	q13.2
SNP_A-2051923	C	C	342	32	339	51	4.029	4.47E-02	rs1006355	20	49310261	q13.2
SNP_A-1968601	G	G	274	76	252	104	5.225	0.0223	rs880324	20	49487597	q13.2
SNP_A-1851231	A	G	203	191	219	175	3.986	4.59E-02	rs6021372	20	49728922	q13.2
SNP_A-2007745	A	A	259	105	296	86	3.925	4.76E-02	rs6067900	20	49743502	q13.2
SNP_A-2141089	T	T	290	38	292	62	4.783	0.0287	rs13045163	20	49844178	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1933210	T	T	357	31	343	53	5.961	0.0146	rs13041703	20	49854068	q13.2
SNP_A-2055918	C	C	394	8	411	1	5.681	1.71E-02	rs4809907	20	50520312	q13.2
SNP_A-1968625	G	G	399	15	410	6	4.002	4.54E-02	rs16996939	20	50713974	q13.2
SNP_A-1968628	T	T	405	15	416	6	4	4.55E-02	rs729792	20	50728253	q13.2
SNP_A-1796869	G	G	279	133	315	103	5.952	0.0147	rs241800	20	50794874	q13.2
SNP_A-2096131	C	C	350	62	367	41	4.665	3.08E-02	rs17806723	20	50797603	q13.2
SNP_A-1840681	T	T	294	92	317	43	17.766	2.50E-05	rs6022070	20	50798097	q13.2
SNP_A-1968632	G	G	192	142	212	114	3.956	4.67E-02	rs2031980	20	50909101	q13.2
SNP_A-1919145	C	C	272	104	290	78	4.205	4.03E-02	rs1923113	20	50948028	q13.2
SNP_A-1749475	C	C	365	39	347	61	5.275	2.16E-02	rs10485619	20	51137140	q13.2
SNP_A-2178445	G	G	397	9	413	1	6.639	0.01	rs6013674	20	51448213	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1707385	G	G	312	18	288	34	5.786	1.62E-02	rs3746414	20	51454801	q13.2
SNP_A-1837530	T	T	336	38	291	59	6.988	8.20E-03	rs6013694	20	51499283	q13.2
SNP_A-1922369	C	C	339	49	301	69	5.222	0.0223	rs6097439	20	51529461	q13.2
SNP_A-1930485	A	A	311	23	270	36	4.541	3.31E-02	rs6097441	20	51529517	q13.2
SNP_A-2036454	C	C	351	53	302	68	4.051	4.42E-02	rs6091687	20	51535921	q13.2
SNP_A-1934652	T	T	367	43	383	25	5.101	2.39E-02	rs16998132	20	51541073	q13.2
SNP_A-1899588	C	C	353	63	330	90	5.52	1.88E-02	rs6097457	20	51547592	q13.2
SNP_A-1792565	G	G	337	47	306	66	4.5	0.0339	rs2050275	20	51553162	q13.2
SNP_A-1885032	C	C	239	145	259	115	4.134	4.20E-02	rs6022766	20	51861627	q13.2
SNP_A-2023230	T	A	201	157	197	185	4.409	3.57E-02	rs6022811	20	51912882	q13.2
SNP_A-1921122	C	C	227	131	206	172	6.027	0.0141	rs7269891	20	51962634	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1725972	T	T	290	110	269	141	4.495	3.40E-02	rs6063858	20	51967974	q13.2
SNP_A-1679336	A	A	278	126	312	98	5.415	0.02	rs2247273	20	52204404	q13.2
SNP_A-2217993	T	T	241	149	272	116	5.978	1.45E-02	rs1570669	20	52207834	q13.2
SNP_A-1968695	A	A	218	174	274	140	9.462	2.10E-03	rs1150420	20	52400898	q13.2
SNP_A-2026788	A	A	212	166	224	124	5.182	2.28E-02	rs793034	20	52406965	q13.2
SNP_A-2055723	T	T	326	54	337	35	4.154	4.15E-02	rs8124702	20	52627603	q13.2
SNP_A-2007780	G	G	272	70	321	51	5.782	1.62E-02	rs6068912	20	52655295	q13.2
SNP_A-2007781	C	C	332	70	308	94	4.412	3.57E-02	rs873079	20	52693893	q13.2
SNP_A-2263817	A	A	213	115	180	142	5.553	1.85E-02	rs157646	20	52852160	q13.2
SNP_A-2148023	A	T	207	181	207	173	4.702	3.01E-02	rs12480339	20	52890328	q13.2
SNP_A-2241493	A	G	202	184	215	169	5.339	2.09E-02	rs6069005	20	52891949	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1898403	C	T	200	178	203	169	4.197	4.05E-02	rs6023646	20	52897721	q13.2
SNP_A-1968714	A	A	350	8	323	1	4.845	2.77E-02	rs1016884	20	52918670	q13.2
SNP_A-2278667	C	C	313	83	267	107	6.056	1.39E-02	rs1034095	20	53033569	q13.2
SNP_A-1968722	C	C	301	91	260	120	6.797	9.10E-03	rs6098360	20	53045547	q13.2
SNP_A-1954806	C	C	319	97	275	137	10.078	0.0015	rs7362603	20	53048804	q13.2
SNP_A-2117776	A	A	187	161	223	137	4.892	0.027	rs11086494	20	53228007	q13.2
SNP_A-1958951	T	T	253	155	271	113	6.479	0.0109	rs6064183	20	53249909	q13.2
SNP_A-2043835	C	C	211	155	233	125	4.216	4.00E-02	rs4811598	20	53292184	q13.2
SNP_A-2122822	G	G	254	150	275	119	4.281	0.0385	rs2767562	20	53293134	q13.2
SNP_A-2216269	A	A	197	153	233	133	4.057	4.40E-02	rs4811599	20	53307708	q13.2
SNP_A-2254210	G	G	354	28	382	12	7.281	7.00E-03	rs983425	20	53331966	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2065560	G	G	362	48	384	30	4.783	0.0287	rs17000940	20	53334694	q13.2
SNP_A-2269329	A	A	352	44	366	26	4.881	2.71E-02	rs211948	20	53371697	q13.2
SNP_A-1916960	G	G	349	37	369	17	7.965	4.80E-03	rs6064213	20	53380240	q13.2
SNP_A-1968731	T	T	339	43	366	28	4.018	4.50E-02	rs6069267	20	53429136	q13.2
SNP_A-2150866	T	T	301	7	308	18	4.413	3.57E-02	rs16984758	20	53528718	q13.31
SNP_A-1968745	A	A	385	27	398	10	8.007	4.70E-03	rs17304809	20	53622047	q13.31
SNP_A-1968767	G	G	324	94	364	56	11.948	5.00E-04	rs6024523	20	53952115	q13.31
SNP_A-1812698	T	T	339	9	349	25	6.747	9.40E-03	rs6069533	20	54036317	q13.31
SNP_A-2215649	T	T	314	52	291	77	5.714	1.68E-02	rs2208066	20	54108522	q13.31
SNP_A-1718195	G	G	303	83	277	115	6.291	0.0121	rs1499865	20	54297694	q13.2
SNP_A-2050169	C	C	375	17	346	34	6.648	9.90E-03	rs4811692	20	54370686	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1968775	C	C	410	6	420	0	6.101	0.0135	rs7260863	20	54371836	q13.31
SNP_A-2158112	G	G	404	8	413	1	5.539	1.86E-02	rs2236207	20	54400972	q13.31
SNP_A-1693809	A	A	225	179	263	149	5.625	0.0177	rs6023940	20	54491416	q13.2
SNP_A-1676106	T	T	310	42	364	26	6.161	1.31E-02	rs2870619	20	54581460	q13.2
SNP_A-1665672	A	A	351	49	384	28	7.033	8.00E-03	rs6127464	20	54581748	q13.2
SNP_A-1677440	G	G	355	45	384	26	6.1	0.0135	rs211922	20	54600656	q13.2
SNP_A-2190882	C	C	206	198	245	167	5.928	0.0149	rs6069900	20	54831367	q13.31
SNP_A-2144485	G	G	369	19	373	35	4.262	0.039	rs6025272	20	54974867	q13.31
SNP_A-2037885	C	C	406	6	403	19	6.652	9.90E-03	rs6069943	20	54975281	q13.31
SNP_A-1902059	A	A	396	8	363	19	5.305	2.13E-02	rs6069945	20	54975766	q13.31
SNP_A-2305071	C	C	345	49	332	78	6.556	1.05E-02	rs6069950	20	54999765	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1734596	A	A	306	82	340	54	7.509	6.10E-03	rs992635	20	55220837	q13.31
SNP_A-2141882	C	C	223	81	224	120	5.12	2.37E-02	rs2180780	20	55234128	q13.31
SNP_A-2249503	C	C	399	1	393	9	6.441	0.0112	rs16985477	20	55367019	q13.32
SNP_A-2088725	A	A	359	3	350	10	3.878	4.89E-02	rs2143664	20	55642619	q13.32
SNP_A-1789025	C	C	291	95	267	135	7.667	5.60E-03	rs878541	20	55714633	q13.32
SNP_A-1901742	C	C	370	34	354	52	4.116	4.25E-02	rs205791	20	55804490	q13.32
SNP_A-1832138	C	C	380	24	387	11	4.848	2.77E-02	rs4811936	20	55879082	q13.32
SNP_A-2196274	G	G	314	56	341	37	4.91	2.67E-02	rs6025929	20	55965771	q13.32
SNP_A-1854542	A	A	252	108	225	147	7.298	6.90E-03	rs6128254	20	56030413	q13.32
SNP_A-2255231	G	G	402	4	412	0	4.079	4.34E-02	rs10153988	20	56044901	q13.32
SNP_A-1826145	A	A	190	136	208	102	5.272	2.17E-02	rs4381835	20	56052150	q13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1935503	C	C	238	154	272	122	5.972	1.45E-02	rs989178	20	56054003	q13.32
SNP_A-1857387	T	T	263	151	303	107	10.312	1.30E-03	rs6026010	20	56077546	q13.32
SNP_A-2117231	G	G	263	153	299	107	10.324	1.30E-03	rs6026011	20	56077657	q13.32
SNP_A-1837011	A	A	395	13	404	4	4.866	2.74E-02	rs11696974	20	56101494	q13.32
SNP_A-2098954	C	C	392	20	402	8	5.264	0.0218	rs7265049	20	56101885	q13.32
SNP_A-1791353	C	C	416	0	412	4	4.019	4.50E-02	rs6128270	20	56115212	q13.32
SNP_A-2239417	T	T	371	7	367	21	6.892	8.70E-03	rs6026055	20	56119666	q13.32
SNP_A-1947116	C	C	376	4	382	0	4.042	4.44E-02	rs6026081	20	56151252	q13.32
SNP_A-2187495	T	T	176	166	203	141	3.954	4.68E-02	rs1537479	20	56260074	q13.32
SNP_A-2095755	T	T	187	169	223	147	4.424	3.54E-02	rs6070412	20	56298680	q13.32
SNP_A-2290381	T	T	197	175	224	144	4.723	0.0298	rs505714	20	56365964	q13.32
SNP_A-1968823	A	A	235	167	272	140	4.953	2.61E-02	rs1980576	20	56479073	q13.32
SNP_A-2111943	T	T	205	177	235	151	4.086	4.32E-02	rs4812002	20	56481756	q13.32

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2230992	T	T	388	30	373	47	4.044	4.43E-02	rs6026565	20	56872703	q13.32
SNP_A-1753027	A	G	202	184	227	187	4.102	4.28E-02	rs157103	20	56946419	q13.32
SNP_A-2228677	T	T	296	56	249	89	11.284	8.00E-04	rs2865718	20	56959807	q13.32
SNP_A-1658006	C	C	267	135	235	179	8.031	4.60E-03	rs1889331	20	57277661	q13.32
SNP_A-1904063	C	C	320	88	295	117	5.099	2.39E-02	rs4810165	20	57377928	q13.32
SNP_A-2211430	C	C	251	147	280	108	7.422	6.40E-03	rs6070848	20	57572054	q13.32
SNP_A-2207896	C	C	267	127	313	77	15.883	6.74E-05	rs3848706	20	57577582	q13.32
SNP_A-2032220	G	G	266	108	237	147	7.506	6.10E-03	rs2426791	20	57595448	q13.32
SNP_A-1828703	C	C	214	206	243	175	4.358	3.68E-02	rs2180681	20	57605741	q13.33
SNP_A-1890533	C	C	373	11	352	22	4.144	4.18E-02	rs6026992	20	57611622	q13.33
SNP_A-1819522	C	C	400	14	390	28	4.774	2.89E-02	rs6027005	20	57632613	q13.33
SNP_A-1896423	A	A	375	11	395	3	4.908	2.67E-02	rs2426803	20	57669847	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1968857	C	C	318	22	343	11	4.332	3.74E-02	rs964732	20	57936043	q13.33
SNP_A-1799809	T	T	319	69	295	97	5.641	1.75E-02	rs6071088	20	58035793	q13.33
SNP_A-1797383	C	C	359	41	333	65	6.406	0.0114	rs13039047	20	58058285	q13.33
SNP_A-1902053	A	A	331	19	337	35	4.128	4.22E-02	rs242790	20	58060281	q13.33
SNP_A-1893463	G	G	377	21	362	36	4.252	3.92E-02	rs242803	20	58071094	q13.33
SNP_A-2184275	T	T	410	10	419	3	3.862	4.94E-02	rs6015650	20	58118239	q13.33
SNP_A-2195332	C	C	411	9	418	2	4.514	3.36E-02	rs6100725	20	58120664	q13.33
SNP_A-2087045	G	G	378	4	370	16	7.265	7.00E-03	rs2145554	20	58131682	q13.33
SNP_A-1968863	G	G	405	7	415	1	4.603	3.19E-02	rs6092877	20	58145852	q13.33
SNP_A-2249935	G	G	398	14	395	5	4.098	4.29E-02	rs6015757	20	58485626	q13.33
SNP_A-1711953	G	G	241	163	217	197	4.347	3.71E-02	rs3905228	20	58791157	q13.32
SNP_A-2281508	G	G	283	49	294	28	5.785	1.62E-02	rs6128934	20	58887600	q13.33
SNP_A-1968900	G	G	229	103	267	83	4.59	3.22E-02	rs6065018	20	58951538	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2172124	C	T	215	181	214	192	3.933	4.74E-02	rs6101206	20	59050033	q13.33
SNP_A-2125693	T	T	334	76	306	104	5.581	1.82E-02	rs2865972	20	59058343	q13.33
SNP_A-2137319	G	G	296	122	326	94	5.072	2.43E-02	rs2064855	20	59058742	q13.33
SNP_A-2073655	A	A	391	5	402	0	5.108	2.38E-02	rs2427018	20	59268793	q13.33
SNP_A-2007878	C	C	337	5	382	0	5.624	0.0177	rs6587265	20	59416565	q13.33
SNP_A-1792094	A	A	227	179	272	146	7.236	7.10E-03	rs2252671	20	59422789	q13.33
SNP_A-2045968	G	C	174	138	177	147	6.876	8.70E-03	rs913551	20	59429073	q13.33
SNP_A-2301462	C	C	393	15	376	28	4.286	3.84E-02	rs2150129	20	59728259	q13.33
SNP_A-2180675	A	A	327	9	318	20	4.292	3.83E-02	rs2297193	20	59751956	q13.33
SNP_A-1831207	A	A	381	25	373	41	3.886	0.0487	rs11697808	20	59777020	q13.33
SNP_A-2301518	T	T	326	78	346	54	4.939	0.0263	rs6062064	20	60121514	q13.33
SNP_A-2195911	A	A	321	21	298	36	4.708	3.00E-02	rs2427258	20	60158303	q13.33
SNP_A-2079868	G	G	193	115	186	162	5.686	1.71E-02	rs6089336	20	60246240	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1841748	G	G	210	204	236	174	3.877	4.89E-02	rs6061245	20	60477622	q13.33
SNP_A-2310426	C	C	312	62	291	89	5.512	0.0189	rs4809480	20	60777875	q13.33
SNP_A-1940566	G	G	341	79	317	105	4.545	3.30E-02	rs6010861	20	60785447	q13.33
SNP_A-1911309	T	T	264	80	257	127	8.594	3.40E-03	rs6090280	20	61287396	q13.33
SNP_A-2108717	C	C	344	2	330	10	5.572	1.82E-02	rs6122401	20	61311662	q13.33
SNP_A-1901433	A	A	296	120	314	92	4.108	4.27E-02	rs755041	20	61416204	q13.33
SNP_A-2301679	A	A	251	155	272	118	5.538	1.86E-02	rs9680065	20	61437481	q13.33
SNP_A-1895172	A	A	314	30	347	15	6.193	1.28E-02	rs2273500	20	61457393	q13.33
SNP_A-1835778	C	C	336	14	324	28	4.879	2.72E-02	rs3746367	20	61505547	q13.33
SNP_A-1785378	C	C	364	2	361	11	6.195	1.28E-02	rs2738760	20	61724125	q13.33
SNP_A-2287617	A	A	338	28	310	44	4.567	3.26E-02	rs16984240	20	62288203	q13.33
SNP_A-2015118	A	A	383	7	411	1	4.888	2.71E-02	rs2847443	21	13517135	q11.2
SNP_A-2015159	G	G	394	0	388	4	4.041	4.44E-02	rs2822161	21	14116194	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015169	C	C	202	196	254	162	8.765	3.10E-03	rs8134986	21	14253349	q11.2
SNP_A-2015183	G	G	329	47	358	28	5.907	1.51E-02	rs7278400	21	14370431	q11.2
SNP_A-1968981	C	C	348	24	377	9	7.722	5.50E-03	rs2822560	21	14596503	q11.2
SNP_A-2015223	G	G	299	65	343	45	5.892	0.0152	rs9975944	21	14610140	q11.2
SNP_A-1748023	G	G	305	95	345	67	7.125	0.0076	rs1317731	21	14612262	q11.2
SNP_A-2015225	G	G	226	152	268	122	6.67	9.80E-03	rs954616	21	14616454	q11.2
SNP_A-2230447	C	C	369	33	386	16	6.281	1.22E-02	rs12329784	21	14627536	q11.2
SNP_A-2015228	G	G	378	28	393	15	4.217	4.00E-02	rs7283184	21	14631285	q11.2
SNP_A-2015246	A	A	367	29	352	50	5.85	1.56E-02	rs2822692	21	14777966	q11.2
SNP_A-2015256	A	G	211	165	205	197	3.94	4.71E-02	rs2822765	21	14843387	q11.2
SNP_A-2015257	A	A	330	82	293	115	7.706	5.50E-03	rs2822766	21	14843501	q11.2
SNP_A-1969003	T	T	397	17	399	7	4.094	4.30E-02	rs2822799	21	14880039	q11.2
SNP_A-2015266	T	T	350	14	356	4	5.585	1.81E-02	rs17003830	21	14929791	q11.2
SNP_A-2015283	T	T	273	85	299	57	6.697	9.70E-03	rs461408	21	15001289	q11.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1711018	C	C	309	89	348	64	6.16	1.31E-02	rs1153350	21	15008235	q11.2
SNP_A-1700137	A	A	222	164	262	120	10.102	0.0015	rs2822961	21	15146679	q11.2
SNP_A-1669665	T	T	259	109	303	89	4.712	3.00E-02	rs2223163	21	15149849	q11.2
SNP_A-2015316	A	A	242	148	210	182	5.763	1.64E-02	rs2823000	21	15288260	q11.2
SNP_A-1969053	G	G	328	78	355	53	5.833	1.57E-02	rs1474513	21	15587206	q21.1
SNP_A-1969079	A	A	348	36	365	21	4.348	3.71E-02	rs2823445	21	15979091	q21.1
SNP_A-2015448	C	C	311	85	332	62	4.279	3.86E-02	rs2823452	21	15985441	q21.1
SNP_A-2015451	C	C	355	33	389	15	7.984	4.70E-03	rs459684	21	16022146	q21.1
SNP_A-2015517	A	A	265	91	253	121	4.082	4.33E-02	rs2823760	21	16672659	q21.1
SNP_A-2015529	C	C	278	96	314	70	6.131	1.33E-02	rs1548072	21	16736632	q21.1
SNP_A-1741323	A	A	277	119	250	162	7.65	5.70E-03	rs2404139	21	17034406	q21.1
SNP_A-1722412	T	T	250	130	215	175	9.145	2.50E-03	rs2824010	21	17035400	q21.1
SNP_A-1650736	C	C	367	31	359	51	4.789	0.0286	rs1784913	21	17859951	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015653	G	G	380	32	361	57	7.467	0.0063	rs1691323	21	17867781	q21.1
SNP_A-1969174	T	T	280	108	308	78	6.167	1.30E-02	rs2824431	21	17962292	q21.1
SNP_A-2015705	C	C	231	181	260	146	5.415	0.02	rs2824549	21	18212104	q21.1
SNP_A-2015733	G	G	233	139	264	116	3.923	4.76E-02	rs157731	21	18360023	q21.1
SNP_A-1692198	G	G	209	157	258	142	4.393	0.0361	rs158030	21	18369648	q21.1
SNP_A-1969231	C	C	269	83	308	50	10.774	0.001	rs1740142	21	18853412	q21.1
SNP_A-1969232	T	T	264	140	299	97	9.899	1.70E-03	rs2824917	21	18871901	q21.1
SNP_A-2015831	T	T	252	116	287	91	5.159	2.31E-02	rs1735798	21	18878920	q21.1
SNP_A-2015835	G	G	280	136	316	102	7.027	8.00E-03	rs2824922	21	18884355	q21.1
SNP_A-2015836	A	A	261	103	292	66	9.789	0.0018	rs2824940	21	18892079	q21.1
SNP_A-1969233	A	A	277	139	318	100	9.184	2.40E-03	rs2824943	21	18895085	q21.1
SNP_A-2015837	C	C	246	110	281	71	10.706	1.10E-03	rs1569389	21	18896268	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2015839	G	G	222	112	266	80	9.092	2.60E-03	rs981203	21	18898542	q21.1
SNP_A-2015840	G	G	285	119	320	86	7.332	6.80E-03	rs981204	21	18898614	q21.1
SNP_A-2015844	G	G	269	91	310	62	8.205	4.20E-03	rs2824960	21	18916131	q21.1
SNP_A-2015851	G	G	295	107	332	70	9.918	1.60E-03	rs7276233	21	18986342	q21.1
SNP_A-1724884	G	G	366	18	395	7	5.536	1.86E-02	rs928863	21	18991242	q21.1
SNP_A-1679926	C	C	312	88	344	68	3.949	4.69E-02	rs2183559	21	18991835	q21.1
SNP_A-1969238	G	G	287	103	326	64	11.589	7.00E-04	rs2825007	21	18999450	q21.1
SNP_A-2015855	A	A	274	72	317	51	6.042	0.014	rs8127347	21	19002905	q21.1
SNP_A-2015903	A	A	374	34	351	59	7.445	6.40E-03	rs450090	21	19222929	q21.1
SNP_A-2015926	T	T	317	73	318	46	5.237	2.21E-02	rs373378	21	19316549	q21.1
SNP_A-2015935	G	G	320	92	295	119	4.466	3.46E-02	rs7281316	21	19329198	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1969256	G	G	252	138	215	161	4.446	3.50E-02	rs762004	21	19332149	q21.1
SNP_A-2016000	G	G	368	22	379	9	5.608	1.79E-02	rs9984988	21	19783029	q21.1
SNP_A-1969273	G	G	335	77	361	53	5.397	2.02E-02	rs2825627	21	19825303	q21.1
SNP_A-2016019	G	G	374	2	392	10	4.893	0.027	rs1850587	21	19991027	q21.1
SNP_A-1969287	C	C	368	32	351	49	3.97	4.63E-02	rs1401044	21	20012631	q21.1
SNP_A-1728301	A	A	379	21	374	38	4.755	0.0292	rs468280	21	20084545	q21.1
SNP_A-2016034	G	G	391	15	376	32	6.437	0.0112	rs468941	21	20095402	q21.1
SNP_A-1969291	G	G	378	26	362	44	4.97	0.0258	rs2825813	21	20113902	q21.1
SNP_A-1645004	C	C	371	25	360	42	4.434	3.52E-02	rs9975733	21	20118479	q21.1
SNP_A-1681154	C	C	373	27	364	44	4.102	4.28E-02	rs2825825	21	20119013	q21.1
SNP_A-2016047	C	C	401	5	414	0	5.13	0.0235	---	21	20185732	q21.1
SNP_A-2016048	A	A	211	135	238	100	6.744	9.40E-03	rs2825875	21	20188026	q21.1
SNP_A-1969322	G	G	288	84	256	106	4.294	3.82E-02	rs1120032	21	20804939	q21.1
SNP_A-2016179	C	C	337	27	358	12	6.355	0.0117	rs229469	21	20995095	q21.1
SNP_A-2016188	G	G	357	29	349	15	3.903	0.0482	rs460639	21	21047561	q21.1
SNP_A-2016200	A	A	260	146	226	170	4.077	4.35E-02	rs743440	21	21144691	q21.1
SNP_A-2016201	C	C	218	152	197	189	4.741	2.95E-02	rs761341	21	21157123	q21.1
SNP_A-2016203	C	C	340	50	370	26	8.801	3.00E-03	rs2826583	21	21175513	q21.1
SNP_A-2016204	C	C	301	115	332	84	6.347	0.0118	rs1119237	21	21180469	q21.1
SNP_A-1695013	C	C	279	105	319	83	4.84	2.78E-02	rs2826596	21	21183086	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1728021	C	C	288	112	320	84	5.664	1.73E-02	rs2826597	21	21183203	q21.1
SNP_A-2016238	T	T	366	4	362	0	3.935	4.73E-02	rs9975341	21	21364825	q21.1
SNP_A-2016248	C	C	185	169	204	124	6.858	8.80E-03	rs2186975	21	21431007	q21.1
SNP_A-2016249	G	G	221	147	256	110	7.89	5.00E-03	rs2826683	21	21432022	q21.1
SNP_A-2016252	C	C	238	168	272	132	6.582	0.0103	rs2826686	21	21432422	q21.1
SNP_A-2016300	T	T	334	36	337	19	5	0.0253	rs2826862	21	21787512	q21.1
SNP_A-2016304	T	T	268	84	235	113	6.411	1.13E-02	rs2826879	21	21825880	q21.1
SNP_A-1684646	G	G	333	53	366	30	7.805	5.20E-03	rs236069	21	21891171	q21.1
SNP_A-2016327	T	T	249	145	281	113	5.901	1.51E-02	rs2826995	21	22047696	q21.1
SNP_A-2103351	A	A	213	127	250	98	6.602	1.02E-02	rs12627591	21	22051715	q21.1
SNP_A-2016333	T	T	273	93	291	65	5.399	0.0201	rs2827024	21	22060126	q21.1
SNP_A-2016351	C	C	241	161	262	126	4.898	0.0269	rs2253974	21	22153703	q21.1
SNP_A-1969389	C	C	277	53	273	27	7.067	7.90E-03	rs2154721	21	22241994	q21.1
SNP_A-1969398	T	T	354	18	351	5	7.012	8.10E-03	rs2827188	21	22281685	q21.1
SNP_A-1648582	C	C	381	3	388	14	6.773	9.30E-03	rs2186427	21	22310813	q21.1
SNP_A-1969425	C	C	358	0	369	7	6.729	9.50E-03	rs2827512	21	22709180	q21.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1969434	G	G	306	106	332	80	4.694	3.03E-02	rs2827548	21	22800213	q21.1
SNP_A-2016448	C	T	224	182	214	200	3.867	4.93E-02	rs2827619	21	22878994	q21.1
SNP_A-2164250	G	G	261	63	228	80	3.845	0.0499	rs11911777	21	23126095	q21.2
SNP_A-1741823	T	T	370	26	399	13	5.112	2.38E-02	rs1506005	21	23379813	q21.2
SNP_A-1969464	T	T	320	18	365	5	8.876	2.90E-03	rs2827837	21	23380796	q21.2
SNP_A-2016509	C	C	224	136	250	104	5.643	1.75E-02	rs198123	21	23390426	q21.2
SNP_A-1643269	G	G	321	45	335	71	4.065	4.38E-02	rs2828024	21	23591708	q21.2
SNP_A-2016556	T	T	324	74	344	52	4.435	3.52E-02	rs200711	21	23735605	q21.2
SNP_A-2016560	G	G	304	60	319	39	4.766	2.90E-02	rs200672	21	23741160	q21.2
SNP_A-2016565	A	A	276	88	254	114	4.238	0.0395	rs1699983	21	23749309	q21.2
SNP_A-2016572	C	C	260	122	283	89	6.004	0.0143	rs2828206	21	23799158	q21.2
SNP_A-2016586	C	C	347	17	350	6	5.186	2.28E-02	rs1023133	21	23847927	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2016618	G	G	207	197	240	172	4.052	0.0441	rs2828470	21	24023576	q21.2
SNP_A-1969526	T	T	378	0	348	4	4.319	3.77E-02	rs8134895	21	24244881	q21.2
SNP_A-2016699	G	G	226	108	252	80	5.578	1.82E-02	rs2256546	21	24356008	q21.2
SNP_A-1969551	G	G	369	19	393	9	4.081	4.34E-02	rs8130791	21	24467318	q21.2
SNP_A-1681594	T	T	364	32	390	18	4.638	3.13E-02	rs10482950	21	24768196	q21.2
SNP_A-2016799	C	C	331	25	378	10	8.183	4.20E-03	rs17000165	21	24935356	q21.2
SNP_A-2016869	G	G	357	21	343	39	5.659	1.74E-02	rs17770242	21	25192756	q21.2
SNP_A-1729478	G	G	351	49	339	73	4.754	0.0292	rs2829484	21	25246802	q21.2
SNP_A-1726982	C	C	351	49	339	73	4.754	0.0292	rs2226351	21	25259810	q21.2
SNP_A-1701511	G	G	369	27	355	51	7.532	6.10E-03	rs2211833	21	25274750	q21.2
SNP_A-1749655	A	A	262	76	257	105	3.876	4.90E-02	rs2829531	21	25363631	q21.2
SNP_A-1741945	C	C	241	121	235	159	3.885	0.0487	rs2829562	21	25445067	q21.2
SNP_A-1750317	C	C	371	29	360	50	5.625	0.0177	rs2829620	21	25486935	q21.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1969603	G	G	371	11	359	25	5.637	1.76E-02	—	21	25499851	q21.2
SNP_A-1969606	G	G	381	29	363	57	9.433	2.10E-03	rs2829653	21	25526635	q21.2
SNP_A-1678516	C	C	358	20	353	37	4.919	2.66E-02	rs2155958	21	25631128	q21.2
SNP_A-2016933	G	G	386	14	370	26	3.919	4.78E-02	rs17000954	21	25742162	q21.2
SNP_A-2016936	G	G	357	43	381	27	4.359	3.68E-02	rs9980620	21	25754480	q21.2
SNP_A-1969620	G	G	362	42	374	26	3.941	4.71E-02	rs2829769	21	25759286	q21.2
SNP_A-1969624	T	T	346	62	367	39	5.851	1.56E-02	rs2829795	21	25841479	q21.3
SNP_A-1679812	T	T	388	12	385	27	5.605	1.79E-02	rs2409148	21	25959062	q21.3
SNP_A-2016974	C	C	393	3	387	11	4.613	3.17E-02	rs2829934	21	26127411	q21.3
SNP_A-1969635	T	T	336	0	308	4	4.334	0.0373	rs2829974	21	26182357	q21.3
SNP_A-2017035	C	C	380	12	401	3	5.785	1.62E-02	rs3787650	21	26410638	q21.3
SNP_A-2017053	A	A	340	24	344	12	3.935	4.73E-02	rs2409168	21	26495816	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017080	A	A	319	39	338	20	6.668	9.80E-03	rs8132767	21	26610103	q21.3
SNP_A-2017094	G	G	371	45	392	26	5.658	1.74E-02	rs219699	21	26700318	q21.3
SNP_A-1687674	C	C	364	36	356	56	4.26	0.039	rs2830244	21	26769135	q21.3
SNP_A-1969672	G	G	260	106	210	160	16.26	5.52E-05	rs2830249	21	26772842	q21.3
SNP_A-1969673	A	G	244	160	194	190	9.483	2.10E-03	rs966410	21	26774595	q21.3
SNP_A-1969674	A	-	237	153	185	185	8.917	0.0028	rs2830252	21	26776572	q21.3
SNP_A-1969675	G	G	250	128	298	96	8.448	3.70E-03	rs2830253	21	26777248	q21.3
SNP_A-2168473	A	A	218	134	237	101	5.146	2.33E-02	rs11088000	21	26779930	q21.3
SNP_A-2017117	C	C	355	41	336	72	8.85	2.90E-03	rs2830261	21	26795766	q21.3
SNP_A-2017155	C	C	200	188	230	154	5.453	0.0195	rs2212815	21	27049551	q21.3
SNP_A-2017159	T	T	330	84	353	61	4.423	3.55E-02	rs2830486	21	27067239	q21.3
SNP_A-2017171	C	C	341	65	344	42	4.455	3.48E-02	rs468522	21	27114559	q21.3
SNP_A-2017188	G	G	180	156	221	139	4.349	3.70E-02	rs229073	21	27214988	q21.3
SNP_A-2017193	G	G	332	70	357	49	4.593	3.21E-02	rs2830585	21	27227083	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017209	A	A	382	6	372	0	5.798	0.016	rs16979610	21	27307288	q21.3
SNP_A-1654617	C	C	293	93	331	69	5.622	0.0177	rs235947	21	27484644	q21.3
SNP_A-2017258	C	C	322	88	340	64	4.235	3.96E-02	rs2830773	21	27498278	q21.3
SNP_A-2017264	A	A	344	0	330	4	4.144	4.18E-02	rs16980155	21	27533878	q21.3
SNP_A-2017271	T	T	223	145	201	187	5.93	0.0149	rs237046	21	27565171	q21.3
SNP_A-2017300	C	C	335	71	312	96	4.555	3.28E-02	rs239671	21	27699502	q21.3
SNP_A-2017302	C	C	260	120	218	144	5.439	1.97E-02	rs2830920	21	27701047	q21.3
SNP_A-2017318	C	C	230	150	261	123	4.607	3.18E-02	rs456874	21	27761403	q21.3
SNP_A-2017362	G	G	356	52	339	73	3.924	4.76E-02	rs243730	21	28066097	q21.3
SNP_A-2017366	C	C	352	44	329	67	5.543	1.86E-02	rs1897285	21	28083843	q21.3
SNP_A-1969795	G	G	374	22	374	10	4.316	3.77E-02	rs2179019	21	28367157	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1969796	A	A	326	80	300	110	5.797	0.0161	rs2831468	21	28372435	q21.3
SNP_A-1969797	C	C	312	60	278	94	9.466	2.10E-03	rs2831474	21	28373594	q21.3
SNP_A-2017421	G	G	238	120	262	94	4.305	3.80E-02	rs2831543	21	28444918	q21.3
SNP_A-2017426	G	G	278	70	212	86	6.701	9.60E-03	rs2831639	21	28501739	q21.3
SNP_A-2017445	A	A	247	129	227	163	4.548	3.29E-02	rs2831691	21	28581025	q21.3
SNP_A-2017448	C	T	195	179	200	156	5.056	2.45E-02	rs2831702	21	28622203	q21.3
SNP_A-2017449	G	C	233	183	215	203	4.632	3.14E-02	rs2064391	21	28622299	q21.3
SNP_A-2017459	A	A	399	13	385	31	7.594	5.90E-03	rs2409300	21	28645143	q21.3
SNP_A-2017483	A	A	345	43	302	58	4.043	4.44E-02	rs17365974	21	28688667	q21.3
SNP_A-2017488	G	G	334	24	339	11	4.776	2.89E-02	rs2831779	21	28704884	q21.3
SNP_A-2017553	C	C	362	14	351	27	4.286	3.84E-02	rs11700653	21	29039190	q21.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017567	C	C	315	9	310	20	4.158	4.14E-02	rs9754234	21	29066382	q21.3
SNP_A-1969843	C	C	279	39	274	62	4.791	0.0286	rs2832131	21	29197818	q21.3
SNP_A-2017616	A	A	258	86	241	115	4.559	0.0327	rs2832213	21	29434785	q21.3
SNP_A-1969855	T	T	378	20	379	7	6.078	0.0137	rs2832233	21	29467871	q21.3
SNP_A-1969883	C	C	341	27	383	11	8.296	4.00E-03	rs363501	21	29849643	q21.3
SNP_A-1969884	T	T	370	22	400	8	7.385	0.0066	rs363497	21	29853681	q21.3
SNP_A-1969886	G	G	386	20	407	7	6.738	9.40E-03	rs363495	21	29853751	q21.3
SNP_A-2017716	A	A	361	37	345	55	3.879	4.89E-02	rs2832438	21	30059808	q21.3
SNP_A-1969921	T	C	161	159	181	131	4.405	3.58E-02	rs2832649	21	30475371	q21.3
SNP_A-2017806	C	C	395	15	401	5	5.026	2.50E-02	rs8129810	21	30521327	q22.11
SNP_A-1969925	A	A	364	40	382	24	4.429	3.53E-02	rs2832664	21	30521783	q22.11
SNP_A-2017808	C	C	360	22	387	11	4.316	0.0378	rs2832675	21	30533957	q22.11
SNP_A-2017811	T	T	363	23	361	9	5.794	0.0161	rs2832682	21	30536352	q22.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017816	C	C	377	33	401	17	5.784	1.62E-02	rs2832736	21	30561524	q22.11
SNP_A-1969932	C	C	337	21	349	9	5.01	0.0252	rs2832752	21	30576005	q22.11
SNP_A-1926817	C	C	374	24	400	12	4.633	3.14E-02	rs7276022	21	30658028	q22.11
SNP_A-1689981	A	A	253	145	293	119	5.251	2.19E-02	rs2832845	21	30678791	q22.11
SNP_A-1667884	A	G	199	171	215	165	8.059	4.50E-03	rs2832852	21	30692847	q22.11
SNP_A-2202705	T	T	196	176	223	143	5.105	2.39E-02	rs7277516	21	30703560	q22.11
SNP_A-1646828	T	T	200	176	251	151	6.817	9.00E-03	rs2832879	21	30738507	q22.11
SNP_A-1969943	G	G	180	120	226	104	4.937	0.0263	rs2832878	21	30738720	q22.11
SNP_A-1969944	A	A	204	180	226	124	9.888	1.70E-03	rs1892861	21	30740565	q22.11
SNP_A-2017846	A	A	203	175	244	138	8.114	4.40E-03	rs2252898	21	30741247	q22.11
SNP_A-1692784	A	A	209	187	254	156	6.934	8.50E-03	rs2832886	21	30746211	q22.11
SNP_A-2017847	C	C	220	178	254	136	7.976	4.70E-03	rs2832890	21	30748734	q22.11
SNP_A-2017849	A	A	198	172	224	128	7.611	5.80E-03	rs2832896	21	30755532	q22.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2017852	T	T	221	195	262	156	7.809	5.20E-03	rs2832908	21	30774051	q22.11
SNP_A-2017855	A	A	218	156	246	130	4.048	4.42E-02	rs8127561	21	30795348	q22.11
SNP_A-1672538	T	T	194	172	240	158	4.136	4.20E-02	rs722694	21	30810762	q22.11
SNP_A-1711654	C	C	396	4	412	0	4.14	0.0419	rs8131358	21	31500277	q22.11
SNP_A-2017975	G	G	368	34	386	18	5.348	0.0207	rs2256836	21	31628655	q22.11
SNP_A-1969993	A	A	338	40	348	24	4.098	4.29E-02	rs2257060	21	31630052	q22.11
SNP_A-1969994	A	A	366	40	392	20	7.515	6.10E-03	rs2257062	21	31630172	q22.11
SNP_A-1969998	T	T	373	39	390	24	3.945	0.047	rs2252002	21	31632892	q22.11
SNP_A-1710369	A	A	353	47	389	23	9.8	1.70E-03	rs2284501	21	31660909	q22.11
SNP_A-1969999	T	T	218	146	184	172	4.913	2.67E-02	rs536419	21	31676751	q22.11
SNP_A-2017991	A	A	377	21	384	10	3.948	4.69E-02	rs16988223	21	31697175	q22.11
SNP_A-2018004	G	G	297	21	276	42	7.77	0.0053	rs4816397	21	31766413	q22.11
SNP_A-1970017	A	A	254	96	219	117	4.376	3.64E-02	rs1012482	21	32104353	q22.11
SNP_A-2018040	G	G	401	1	374	6	3.896	4.84E-02	rs2833535	21	32133967	q22.11
SNP_A-2008042	T	T	230	142	206	182	5.925	0.0149	rs6517060	21	32156268	q22.11
SNP_A-2018054	C	C	309	91	342	68	4.877	2.72E-02	rs2833556	21	32207171	q22.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2018070	C	C	270	86	302	66	4.224	3.99E-02	rs16988716	21	32286740	q22.11
SNP_A-2018088	C	C	329	81	359	57	5.439	1.97E-02	rs2833637	21	32366900	q22.11
SNP_A-1970033	G	G	346	70	382	38	11.243	8.00E-04	rs17667681	21	32372187	q22.11
SNP_A-2018094	G	G	244	144	212	180	6.225	0.0126	rs2833654	21	32394310	q22.11
SNP_A-2018095	C	C	257	157	217	195	7.473	0.0063	rs2833656	21	32396727	q22.11
SNP_A-2018108	C	C	396	4	400	0	4.02	4.50E-02	rs4816423	21	32447507	q22.11
SNP_A-2018118	T	T	302	62	334	34	9.755	0.0018	rs2833709	21	32484797	q22.11
SNP_A-1904459	A	T	201	181	208	172	4.124	4.23E-02	rs9982003	21	32738460	q22.11
SNP_A-2018184	C	C	369	17	392	4	8.616	0.0033	rs1720137	21	32893657	q22.11
SNP_A-1688714	C	T	211	161	210	188	6.927	8.50E-03	rs2833933	21	32942225	q22.11
SNP_A-2018188	A	G	201	141	192	164	11.285	8.00E-04	rs844975	21	32981078	q22.11
SNP_A-1970055	G	A	201	185	239	157	12.159	5.00E-04	rs928754	21	33006701	q22.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2018193	C	C	315	33	339	19	4.509	3.37E-02	rs2154427	21	33090443	q22.11
SNP_A-2018195	C	C	279	89	313	67	4.864	2.74E-02	rs963636	21	33097435	q22.11
SNP_A-2018202	G	G	329	29	361	17	4.074	4.35E-02	rs2833978	21	33141602	q22.11
SNP_A-1888315	G	G	215	121	160	158	12.488	4.00E-04	rs11088233	21	33161938	q22.11
SNP_A-1970073	T	C	201	133	159	145	9.99	1.60E-03	rs724208	21	33413854	q22.11
SNP_A-2018234	T	T	228	152	176	164	4.942	2.62E-02	rs8129180	21	33418264	q22.11
SNP_A-1970078	A	A	319	91	284	118	5.441	1.97E-02	rs2834183	21	33603641	q22.11
SNP_A-2018298	T	T	305	87	282	120	6.037	0.014	rs914142	21	33647677	q22.11
SNP_A-2239322	T	T	290	112	268	140	3.934	4.73E-02	rs12626410	21	34235177	q22.11
SNP_A-2018393	G	G	249	109	218	134	4.579	3.24E-02	rs2834384	21	34425368	q22.11
SNP_A-1970102	A	A	406	4	402	0	3.941	4.71E-02	rs16991351	21	34482559	q22.11

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1970115	T	C	176	174	222	164	4.492	3.41E-02	rs1013063	21	34620260	q22.11
SNP_A-1970117	G	G	342	38	342	66	6.552	1.05E-02	rs723548	21	34648096	q22.11
SNP_A-1970139	A	A	394	4	392	0	3.96	4.66E-02	rs16992239	21	35046143	q22.12
SNP_A-2018516	T	T	253	139	278	110	4.534	0.0332	rs4817695	21	35141187	q22.12
SNP_A-2018528	G	G	349	31	367	13	7.816	5.20E-03	rs10460712	21	35214098	q22.12
SNP_A-2018529	T	T	322	56	354	32	7.977	4.70E-03	rs1006639	21	35218734	q22.12
SNP_A-2018531	C	C	383	15	407	5	5.489	1.91E-02	rs9982454	21	35224787	q22.12
SNP_A-1970146	C	C	391	21	412	8	6.3	0.0121	rs2834677	21	35226979	q22.12
SNP_A-1970148	G	G	376	18	399	5	7.906	4.90E-03	rs16992540	21	35234754	q22.12
SNP_A-2018557	T	T	248	158	219	193	5.247	2.20E-02	rs2242888	21	35309698	q22.12
SNP_A-2018558	G	G	248	152	225	185	4.227	3.98E-02	rs882776	21	35310157	q22.12

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1970150	T	T	366	10	352	22	4.768	2.90E-02	rs11700684	21	35331702	q22.12
SNP_A-2018561	C	C	398	14	389	31	6.449	0.0111	rs17227203	21	35337577	q22.12
SNP_A-1672074	T	T	304	88	338	60	7.053	7.90E-03	rs10483024	21	35361096	q22.12
SNP_A-2018623	A	G	228	178	203	197	3.857	4.95E-02	rs760072	21	35608734	q22.12
SNP_A-2018641	C	C	376	10	397	3	4.092	4.31E-02	rs17227476	21	35711082	q22.12
SNP_A-1970201	C	C	203	161	228	130	4.703	3.01E-02	rs1888460	21	36046912	q22.12
SNP_A-2018724	T	T	372	8	354	18	4.208	0.0402	rs2835139	21	36068075	q22.12
SNP_A-1970219	T	T	384	4	388	0	4.021	4.49E-02	rs2835262	21	36349861	q22.12
SNP_A-2018787	A	A	308	78	278	100	4.172	4.11E-02	rs9978576	21	36398229	q22.12
SNP_A-1970225	T	T	391	23	375	41	5.392	2.02E-02	---	21	36555177	q22.12
SNP_A-2018886	A	A	414	2	407	13	8.107	4.40E-03	rs16994356	21	36927512	q22.13
SNP_A-2018887	G	G	250	130	285	101	5.884	1.53E-02	rs401789	21	36928009	q22.13

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2018891	T	T	225	117	267	95	5.304	2.13E-02	rs2845789	21	36932166	q22.13
SNP_A-2018900	C	C	219	185	244	148	5.281	2.16E-02	rs9977677	21	36974655	q22.13
SNP_A-2019029	G	G	303	103	270	130	4.985	2.56E-02	rs2835833	21	37909767	q22.13
SNP_A-2019031	C	C	295	105	260	134	5.681	1.71E-02	rs2835840	21	37913191	q22.13
SNP_A-2019035	G	G	298	104	272	134	4.948	2.61E-02	rs2835852	21	37935998	q22.13
SNP_A-2019038	C	C	215	167	237	137	3.947	0.047	rs1709814	21	37938938	q22.13
SNP_A-2019045	C	C	240	138	198	158	4.724	0.0298	rs1709833	21	37959675	q22.13
SNP_A-2019047	A	A	206	166	240	136	5.551	1.85E-02	rs2835885	21	37961436	q22.13
SNP_A-2019048	C	C	210	134	242	104	6.041	0.014	rs1008542	21	37962431	q22.13
SNP_A-1970285	T	T	375	13	370	26	4.286	3.84E-02	rs2835929	21	38043123	q22.13
SNP_A-2019189	T	T	369	23	381	11	4.427	3.54E-02	rs2040234	21	38707056	q22.2
SNP_A-2019190	G	G	341	41	338	20	6.471	1.10E-02	rs9977445	21	38716301	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2019193	A	A	297	63	335	43	5.623	0.0177	rs928724	21	38728755	q22.2
SNP_A-1705491	C	C	261	89	269	129	4.398	3.60E-02	rs2836616	21	38968462	q22.2
SNP_A-2019266	G	G	265	103	248	132	3.951	4.69E-02	rs7275589	21	39041638	q22.2
SNP_A-1970352	T	T	281	99	262	134	5.595	1.80E-02	rs2210265	21	39187773	q22.2
SNP_A-2019349	G	G	268	78	235	97	3.94	4.71E-02	rs9975707	21	39330192	q22.2
SNP_A-2019362	C	C	372	2	320	10	6.516	1.07E-02	rs16997270	21	39368232	q22.2
SNP_A-2019393	T	T	364	32	374	14	7.098	7.70E-03	rs8132230	21	39505951	q22.2
SNP_A-1970373	T	T	307	23	345	11	5.472	1.93E-02	rs760166	21	39640031	q22.2
SNP_A-1970389	A	A	221	131	209	167	3.897	4.84E-02	rs550569	21	39903545	q22.2
SNP_A-2019478	C	T	214	182	218	188	4.798	2.85E-02	rs8129207	21	39992063	q22.2
SNP_A-2019534	C	C	195	167	229	145	4.083	4.33E-02	rs2837255	21	40143991	q22.2
SNP_A-2019634	T	T	388	4	402	0	4.123	4.23E-02	rs16999395	21	40446750	q22.2
SNP_A-2019682	G	A	191	133	173	171	5.74	0.0166	rs435386	21	40520243	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1970449	A	A	263	131	228	156	4.545	3.30E-02	rs7275297	21	40588469	q22.2
SNP_A-2019711	G	G	394	0	387	5	5.058	2.45E-02	rs16999671	21	40610253	q22.2
SNP_A-2019719	C	C	393	19	383	35	4.826	2.80E-02	rs2837583	21	40661862	q22.2
SNP_A-1970456	G	G	406	10	397	21	3.999	4.55E-02	rs16999738	21	40702268	q22.2
SNP_A-2019735	A	A	389	3	379	15	8.125	4.40E-03	rs16999740	21	40709211	q22.2
SNP_A-1970469	C	C	361	5	368	14	3.99	0.0458	rs17836017	21	41000639	q22.2
SNP_A-2019849	C	T	202	142	189	173	8.463	3.60E-03	rs7275921	21	41215523	q22.2
SNP_A-2019852	C	G	212	182	223	191	4.753	0.0293	rs7283882	21	41227934	q22.2
SNP_A-1688818	G	G	207	191	254	158	7.672	5.60E-03	rs2249248	21	41266902	q22.2
SNP_A-1675602	C	C	208	192	252	156	7.854	5.10E-03	rs4389398	21	41268000	q22.2
SNP_A-1747675	T	T	208	192	254	158	7.707	5.50E-03	rs1467754	21	41269518	q22.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1745045	A	A	201	185	251	157	7.219	7.20E-03	rs713112	21	41269769	q22.2
SNP_A-2019860	A	A	206	194	253	157	8.591	3.40E-03	rs7280718	21	41274122	q22.2
SNP_A-1735178	C	C	227	159	207	199	4.889	0.027	rs2837918	21	41355923	q22.2
SNP_A-1689937	T	T	233	165	209	199	4.356	3.69E-02	rs2837920	21	41356292	q22.2
SNP_A-2019893	G	G	263	93	278	56	8.911	0.0028	rs7749672	21	41409680	q22.3
SNP_A-2019917	G	G	279	75	244	100	5.772	1.63E-02	rs737288	21	41503507	q22.3
SNP_A-1970497	T	T	214	152	222	116	3.875	4.90E-02	rs3641197	21	41737239	q22.3
SNP_A-2019962	T	T	228	154	249	123	4.262	0.039	rs469483	21	41740385	q22.3
SNP_A-2019979	A	A	327	23	314	38	3.947	0.047	rs7409953	21	41807523	q22.3
SNP_A-2019992	G	G	216	170	240	140	4.12	0.0424	rs6586240	21	41898584	q22.3
SNP_A-1857835	T	T	237	135	202	176	8.148	0.0043	rs11700823	21	41994402	q22.3
SNP_A-2147952	C	C	170	168	202	140	5.275	2.16E-02	rs11701487	21	42031175	q22.3
SNP_A-1970507	C	C	254	96	275	69	5.2	2.26E-02	rs928874	21	42295594	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2020073	C	C	253	137	226	168	4.652	0.031	rs220219	21	42317483	q22.3
SNP_A-2020076	C	C	241	143	255	111	3.997	4.56E-02	rs2839447	21	42328249	q22.3
SNP_A-2020083	G	G	335	43	374	28	4.58	3.23E-02	rs220248	21	42344967	q22.3
SNP_A-2020104	C	T	189	133	180	170	6.908	0.0086	rs220169	21	42428243	q22.3
SNP_A-2020117	A	G	220	160	198	182	7.626	5.80E-03	rs3787968	21	42523456	q22.3
SNP_A-2020119	G	G	323	81	291	111	6.35	0.0117	rs3827225	21	42523848	q22.3
SNP_A-1970516	G	G	255	87	218	126	10.029	0.0015	rs915847	21	42530317	q22.3
SNP_A-1970517	G	C	218	160	209	179	10.209	0.0014	rs225444	21	42531295	q22.3
SNP_A-2020120	T	C	208	156	213	183	9.072	2.60E-03	rs225445	21	42531513	q22.3
SNP_A-2020121	A	A	270	134	237	177	7.972	4.80E-03	rs225448	21	42532899	q22.3
SNP_A-2020122	G	G	292	114	255	153	8.195	4.20E-03	rs178744	21	42535865	q22.3
SNP_A-2020123	C	C	275	75	238	120	12.964	3.00E-04	rs2839478	21	42540151	q22.3
SNP_A-2020130	G	G	349	57	330	86	6.292	0.0121	rs7275482	21	42582769	q22.3
SNP_A-2020136	A	A	390	26	405	13	4.612	3.18E-02	rs7280100	21	42615436	q22.3
SNP_A-2020142	G	G	270	72	254	114	9.032	2.70E-03	rs225333	21	42637565	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2020183	A	A	283	123	319	95	5.672	0.0172	rs412212	21	42866712	q22.3
SNP_A-2020189	G	G	282	124	311	93	5.842	1.56E-02	rs381899	21	42877191	q22.3
SNP_A-2020192	G	G	213	141	241	113	4.813	2.82E-02	rs1788449	21	42880585	q22.3
SNP_A-2020194	T	T	275	41	314	20	9.321	0.0023	rs1788421	21	42895327	q22.3
SNP_A-2020211	G	G	321	43	350	22	7.952	4.80E-03	rs2269139	21	42977018	q22.3
SNP_A-2142520	C	C	295	45	296	70	4.485	3.42E-02	rs11203161	21	43139480	q22.3
SNP_A-2020272	C	C	246	96	275	71	5.334	2.09E-02	rs234706	21	43358419	q22.3
SNP_A-2020276	G	G	333	37	296	52	4.034	4.46E-02	rs1789956	21	43392724	q22.3
SNP_A-1716941	C	C	364	32	394	14	8.054	4.50E-03	rs605781	21	43590209	q22.3
SNP_A-2020342	A	A	223	173	254	146	4.28	3.86E-02	rs2838325	21	43838712	q22.3
SNP_A-2020346	A	A	235	171	269	147	3.984	4.59E-02	rs2838331	21	43851156	q22.3
SNP_A-2008141	A	A	221	173	246	144	3.971	4.63E-02	rs2838339	21	43900178	q22.3
SNP_A-1970574	A	A	325	35	320	56	4.539	3.31E-02	rs2838407	21	44070754	q22.3
SNP_A-1658680	C	C	284	76	348	60	5.384	2.03E-02	rs2277805	21	44350385	q22.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2020493	G	G	330	84	355	61	4.556	3.28E-02	rs2838649	21	44944928	q22.3
SNP_A-2020557	C	C	388	16	381	35	6.968	8.30E-03	rs2838774	21	45334744	q22.3
SNP_A-2020558	C	C	320	10	339	1	7.764	0.0053	rs2838775	21	45335839	q22.3
SNP_A-2020567	C	C	396	18	385	35	5.565	0.0183	rs3788169	21	45405207	q22.3
SNP_A-1740519	G	G	235	125	259	95	5.207	2.25E-02	rs2838825	21	45511853	q22.3
SNP_A-1672866	G	G	286	112	324	88	5.007	0.0252	rs2838847	21	45527160	q22.3
SNP_A-2020763	G	G	392	2	389	9	4.446	3.50E-02	rs2839266	21	46709567	q22.3
SNP_A-2020786	G	G	338	10	352	22	3.853	4.97E-02	rs1892693	21	46791905	q22.3
SNP_A-2020793	C	C	357	23	374	10	5.496	1.91E-02	rs2248636	21	46810083	q22.3
SNP_A-1970657	C	C	365	17	349	33	5.479	1.93E-02	rs17432784	22	15570854	q11.1
SNP_A-2113228	A	G	200	140	182	170	7.705	5.50E-03	rs7287430	22	15682296	q11.1
SNP_A-2134988	C	C	280	36	267	55	4.22	4.00E-02	rs175152	22	15691787	q11.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1829839	T	T	240	158	204	190	5.841	1.57E-02	rs165645	22	15691900	q11.1
SNP_A-2192849	A	A	414	4	404	12	4.117	0.0424	rs5746906	22	15692887	q11.1
SNP_A-2048803	A	A	243	147	213	179	5.11	2.38E-02	rs165670	22	15693236	q11.1
SNP_A-1934911	T	T	370	14	398	4	6.167	1.30E-02	rs16982258	22	16121749	q11.1
SNP_A-2214033	T	T	385	5	372	14	4.466	3.46E-02	rs7289964	22	16265632	q11.1
SNP_A-1789709	C	C	359	33	370	18	4.557	3.28E-02	rs5746380	22	16291866	q11.1
SNP_A-2305677	A	A	345	51	349	31	4.573	3.25E-02	rs5747164	22	16304817	q11.21
SNP_A-2258008	C	C	350	48	358	26	6.382	0.0115	rs5747211	22	16365406	q11.21
SNP_A-2159655	T	T	321	77	300	106	5.227	2.22E-02	rs1003861	22	16395327	q11.21
SNP_A-2262384	A	A	331	71	306	102	6.492	1.08E-02	rs2535690	22	16527563	q11.21
SNP_A-2051526	C	C	360	20	372	8	5.34	2.08E-02	rs9605382	22	16539156	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1797048	A	A	338	54	320	76	4.195	4.05E-02	rs11538	22	16595385	q11.21
SNP_A-2212329	G	G	261	55	246	98	11.361	7.00E-04	rs439231	22	16693733	q11.21
SNP_A-2299508	C	C	374	14	401	5	4.798	2.85E-02	rs9605443	22	16801862	q11.21
SNP_A-2056951	A	A	335	13	338	4	4.726	2.97E-02	rs9605477	22	16838637	q11.21
SNP_A-1887337	G	G	307	51	327	29	6.675	9.80E-03	rs975826	22	16895136	q11.21
SNP_A-2126573	T	T	235	97	207	127	5.786	1.62E-02	rs415606	22	16895208	q11.21
SNP_A-2058280	G	G	317	87	361	53	10.992	9.00E-04	rs11705515	22	16916051	q11.21
SNP_A-2139956	C	T	169	161	220	140	10.574	1.10E-03	rs464385	22	16945562	q11.21
SNP_A-1935007	A	A	282	138	319	103	7.356	6.70E-03	rs361594	22	16951892	q11.21
SNP_A-2287527	C	C	331	53	356	30	7.278	7.00E-03	rs362250	22	16956219	q11.21
SNP_A-2119761	C	C	261	121	295	77	11.726	6.00E-04	rs467504	22	16957821	q11.21
SNP_A-1678136	C	C	371	25	361	49	7.68	5.60E-03	rs8140197	22	16987599	q11.21
SNP_A-2269001	T	T	206	126	191	161	4.254	3.92E-02	rs2073754	22	17595960	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2277809	G	G	350	4	368	0	4.181	4.09E-02	rs7286556	22	17774335	q11.21
SNP_A-1861752	A	A	270	130	242	158	4.253	3.92E-02	rs5748410	22	18092698	q11.21
SNP_A-2179301	T	T	368	24	368	8	7.67	5.60E-03	rs174699	22	18329012	q11.21
SNP_A-1825843	C	C	405	9	406	2	4.412	3.57E-02	rs9618757	22	18597195	q11.21
SNP_A-2112621	T	T	372	0	378	4	3.916	4.78E-02	rs6003460	22	19291378	q11.21
SNP_A-2209620	G	G	325	83	347	61	4.081	4.34E-02	rs7292964	22	19621101	q11.21
SNP_A-1942296	T	T	302	72	338	46	7.623	5.80E-03	rs396130	22	19682156	q11.21
SNP_A-2088195	C	C	300	62	343	45	4.681	3.05E-02	rs398577	22	19687403	q11.21
SNP_A-2086651	C	C	371	9	358	22	5.683	1.71E-02	rs9613603	22	19749852	q11.21
SNP_A-1970714	A	A	310	104	286	132	4.269	3.88E-02	rs431319	22	19773582	q11.21
SNP_A-2082153	A	A	320	90	291	113	3.938	4.72E-02	rs5994885	22	20420325	q11.21
SNP_A-1804797	T	T	327	49	293	75	7.231	7.20E-03	rs17759598	22	20446703	q11.21

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2046461	C	C	330	22	299	47	10.535	1.20E-03	rs17759796	22	20514717	q11.22
SNP_A-1895005	C	C	338	76	357	55	3.881	4.88E-02	rs240055	22	20591362	q11.22
SNP_A-1788873	G	G	361	23	389	11	4.956	2.60E-02	rs61739	22	20685204	q11.22
SNP_A-1867490	G	G	368	50	387	33	3.955	4.67E-02	rs11441033	22	20703621	q11.22
SNP_A-1813257	T	T	335	37	351	21	4.787	0.0287	rs419893	22	20711383	q11.22
SNP_A-2028330	A	A	345	5	332	0	4.778	2.88E-02	rs6000910	22	20720047	q11.22
SNP_A-1888146	T	T	408	6	403	15	3.869	4.92E-02	rs16983057	22	20779234	q11.22
SNP_A-1970745	A	G	223	185	210	190	4.14	0.0419	rs738881	22	21050926	q11.22
SNP_A-1970747	A	A	176	172	190	136	4.03	4.47E-02	rs25244	22	21075769	q11.22
SNP_A-2235655	T	T	290	78	282	106	3.846	0.0499	rs2097206	22	21238221	q11.22
SNP_A-2181892	A	A	260	142	230	174	5.072	2.43E-02	rs4300944	22	21275603	q11.22
SNP_A-2058184	A	A	254	134	217	159	4.852	0.0276	rs4822229	22	21278198	q11.22
SNP_A-1820985	C	C	264	130	304	94	8.583	3.40E-03	rs16990766	22	21347950	q11.22
SNP_A-2192407	T	T	274	134	309	97	8.023	4.60E-03	rs9612140	22	21355097	q11.22
SNP_A-1835315	T	T	195	183	256	146	11.684	6.00E-04	rs5751518	22	21366465	q11.22

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2008204	G	G	265	95	301	71	5.564	0.0183	rs4446154	22	21374357	q11.22
SNP_A-1909887	G	G	260	88	255	121	4.182	4.08E-02	rs5751559	22	21550507	q11.22
SNP_A-2177091	G	G	313	93	292	122	4.563	0.0327	rs5759503	22	21550549	q11.22
SNP_A-2181434	A	A	401	13	416	4	4.997	2.54E-02	rs756738	22	21607924	q11.22
SNP_A-1834652	G	G	369	41	374	24	4.303	3.81E-02	rs2017377	22	22086214	q11.23
SNP_A-2106853	C	C	308	82	272	116	8.068	4.50E-03	rs140156	22	22159593	q11.23
SNP_A-2096609	C	C	362	28	334	54	9.365	2.20E-03	rs2070447	22	22361117	q11.23
SNP_A-2052785	G	G	346	30	321	65	13.703	2.00E-04	rs4822443	22	22559752	q11.23
SNP_A-2207237	C	C	344	22	359	11	3.965	0.0465	rs1970980	22	22618210	q11.23
SNP_A-1811592	G	G	304	62	330	38	6.821	9.00E-03	rs762283	22	23268136	q11.23
SNP_A-1956054	A	A	291	95	320	56	11.32	8.00E-04	rs2024647	22	23643722	q11.23
SNP_A-1878842	T	T	282	118	305	91	4.369	3.66E-02	rs5760752	22	23670091	q11.23
SNP_A-2243418	T	T	341	73	372	46	7.455	0.0063	rs4140486	22	23674641	q11.23
SNP_A-2294150	A	A	305	67	318	40	6.818	9.00E-03	rs5760764	22	23689261	q11.23
SNP_A-1806029	T	T	368	18	345	7	4.024	4.49E-02	rs16980525	22	24383176	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2290732	C	C	420	0	418	4	4	4.55E-02	rs16980640	22	24460443	q12.1
SNP_A-2176133	A	A	420	0	418	4	4	4.55E-02	rs16980648	22	24460547	q12.1
SNP_A-1799542	A	A	408	10	419	3	3.897	4.84E-02	rs16980793	22	24529901	q12.1
SNP_A-1793550	A	A	196	188	227	159	4.69	3.03E-02	rs761670	22	24742510	q12.1
SNP_A-1881981	G	G	357	31	326	48	4.81	2.83E-02	rs7289355	22	24798859	q12.1
SNP_A-2041022	T	T	383	33	367	51	4.194	4.06E-02	rs8140357	22	24807396	q12.1
SNP_A-1970813	G	G	395	9	386	20	4.271	3.88E-02	rs7364171	22	24824938	q12.1
SNP_A-1693587	T	T	329	69	361	47	5.533	1.87E-02	rs134703	22	24824971	q12.1
SNP_A-1970815	A	A	300	60	339	41	5.418	1.99E-02	rs134710	22	24828556	q12.1
SNP_A-2117392	G	G	346	6	355	17	4.828	2.80E-02	rs16981470	22	24901900	q12.1
SNP_A-1795900	G	G	310	74	323	47	6.034	0.014	rs9613134	22	24946833	q12.1
SNP_A-1790584	G	G	361	11	386	2	6.734	9.50E-03	rs5761428	22	24954386	q12.1
SNP_A-2055700	G	G	390	8	380	18	3.976	4.62E-02	rs8141975	22	24989172	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2175420	G	G	348	28	342	46	4.243	3.94E-02	rs1046453	22	25165031	q12.1
SNP_A-1813708	G	G	335	47	348	30	3.98	4.61E-02	rs5761562	22	25217452	q12.1
SNP_A-2111479	A	-	243	177	207	207	5.181	2.28E-02	rs8139804	22	25254619	q12.1
SNP_A-1790527	T	T	199	139	227	105	6.525	0.0106	rs6005150	22	25447034	q12.1
SNP_A-2049819	T	C	219	187	211	175	5.86	0.0155	rs5761711	22	25454301	q12.1
SNP_A-1824143	A	A	196	156	234	136	4.282	0.0385	rs5761771	22	25538522	q12.1
SNP_A-1698001	G	G	221	183	254	158	4.047	4.42E-02	rs720914	22	25544435	q12.1
SNP_A-2060873	G	G	376	8	356	20	5.606	1.79E-02	rs9625097	22	25565143	q12.1
SNP_A-2200668	G	G	364	54	338	74	4.045	4.43E-02	rs2331312	22	25619097	q12.1
SNP_A-2200948	G	G	297	59	331	41	4.731	2.96E-02	rs5752453	22	25679749	q12.1
SNP_A-2310317	C	C	324	44	294	76	9.984	1.60E-03	rs4820741	22	25828391	q12.1
SNP_A-2276684	T	T	313	65	294	96	6.378	1.16E-02	rs4822859	22	25833412	q12.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2008232	G	G	336	70	350	46	5.127	2.36E-02	rs1056	22	25894533	q12.1
SNP_A-2056288	T	T	316	82	296	110	4.658	0.0309	rs13058659	22	25899358	q12.1
SNP_A-2173923	A	A	313	61	293	85	4.584	3.23E-02	rs9608606	22	26076638	q12.1
SNP_A-1790604	T	T	400	0	392	4	4.061	4.39E-02	rs4299423	22	26219901	q12.1
SNP_A-1884857	C	C	265	107	302	78	6.876	8.70E-03	rs2024682	22	26230380	q12.1
SNP_A-2305045	T	T	405	15	415	5	5.122	2.36E-02	rs16986873	22	27679325	q12.1
SNP_A-2069340	A	A	397	17	411	7	4.39	0.0361	rs5762919	22	27687898	q12.1
SNP_A-1970906	G	G	312	30	269	43	4.13	4.21E-02	rs5762935	22	27705706	q12.1
SNP_A-2223258	C	C	254	82	265	57	4.434	3.52E-02	rs134596	22	27794669	q12.1
SNP_A-1970910	G	G	352	34	351	17	5.241	2.21E-02	rs17523074	22	27860415	q12.1
SNP_A-2285455	T	T	313	19	327	7	5.839	1.57E-02	rs11090561	22	27897320	q12.1
SNP_A-2251425	C	C	310	34	316	16	6.326	1.19E-02	rs2527346	22	28438514	q12.2
SNP_A-2170738	T	T	322	4	312	14	5.713	1.68E-02	rs740116	22	28524953	q12.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1910339	A	A	329	65	350	44	4.695	3.02E-02	rs8139217	22	28713710	q12.2
SNP_A-2182177	G	G	314	68	323	45	4.549	3.29E-02	rs7285751	22	28718098	q12.2
SNP_A-2311756	A	A	334	68	349	43	5.835	1.57E-02	rs9614144	22	28826040	q12.2
SNP_A-2043590	G	G	370	4	368	14	5.477	1.93E-02	rs5763857	22	28904171	q12.2
SNP_A-2074896	A	A	343	9	317	21	5.542	1.86E-02	rs2412979	22	28904715	q12.2
SNP_A-1866706	G	G	369	43	391	27	4.251	3.92E-02	rs16988383	22	28917396	q12.2
SNP_A-1829575	T	T	358	46	340	66	4.031	4.47E-02	rs4820869	22	29311119	q12.2
SNP_A-2055186	A	A	329	79	327	51	4.899	0.0269	rs136233	22	29536964	q12.2
SNP_A-2211519	G	G	321	35	358	22	4.203	4.04E-02	rs5753432	22	29769724	q12.2
SNP_A-2195485	C	C	397	3	385	21	13.64	2.00E-04	rs16989540	22	30560703	q12.3
SNP_A-2101672	A	A	402	14	387	27	4.402	3.59E-02	rs5998144	22	30572798	q12.3
SNP_A-1910417	C	C	405	15	394	28	4.077	4.35E-02	rs16989600	22	30600496	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1855875	G	G	382	12	366	34	10.819	0.001	rs2235168	22	30973985	q12.3
SNP_A-1812684	C	C	382	0	332	8	9.089	2.60E-03	—	22	30981115	q12.3
SNP_A-1970957	A	A	219	141	197	179	5.331	2.10E-02	rs715542	22	31200425	q12.3
SNP_A-1970958	T	T	256	162	224	192	4.671	3.07E-02	rs1033407	22	31201201	q12.3
SNP_A-2083248	A	C	212	198	250	164	12.144	5.00E-04	rs4820079	22	31204171	q12.3
SNP_A-2201889	A	A	255	121	220	146	4.786	0.0287	rs5749450	22	31211031	q12.3
SNP_A-2287228	G	G	292	118	320	94	3.979	4.61E-02	rs11089574	22	31277989	q12.3
SNP_A-1831151	G	G	279	99	302	66	7.378	0.0066	rs9621489	22	31278013	q12.3
SNP_A-2213767	A	A	253	105	278	82	4	4.55E-02	rs4821073	22	31283195	q12.3
SNP_A-2173092	G	G	210	132	241	109	4.234	3.96E-02	rs1016741	22	31289544	q12.3
SNP_A-1781312	C	C	258	110	291	73	9.443	2.10E-03	rs1016742	22	31289603	q12.3
SNP_A-2147939	G	C	176	132	183	153	8.664	3.20E-03	rs2858731	22	31305049	q12.3
SNP_A-2150993	C	C	379	25	387	13	3.853	4.97E-02	rs5754198	22	31386785	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2058015	G	G	339	45	326	66	4.145	4.18E-02	rs13058500	22	31440433	q12.3
SNP_A-2080567	C	C	283	45	271	71	5.798	0.016	rs743742	22	31440868	q12.3
SNP_A-2297684	G	G	383	7	388	0	7.027	8.00E-03	rs3788500	22	31463945	q12.3
SNP_A-2145844	G	G	371	43	394	24	6.06	0.0138	rs5754250	22	31475805	q12.3
SNP_A-1642405	T	T	328	50	363	33	4.839	2.78E-02	rs737088	22	31512496	q12.3
SNP_A-1941765	C	C	388	22	407	11	4.044	4.43E-02	rs2267185	22	31582771	q12.3
SNP_A-2226384	G	G	333	77	314	104	4.509	3.37E-02	rs137518	22	31616296	q12.3
SNP_A-1942099	C	C	209	121	239	95	5.115	2.37E-02	rs8135220	22	31817986	q12.3
SNP_A-2049933	C	C	300	78	319	51	6.15	1.31E-02	rs2283895	22	32076417	q12.3
SNP_A-1808510	G	G	335	11	354	2	6.614	0.0101	rs16992377	22	32179937	q12.3
SNP_A-2151028	C	C	336	50	370	34	4.277	3.86E-02	rs8136529	22	32260451	q12.3
SNP_A-1957104	G	G	362	42	377	21	7.26	7.10E-03	rs17735056	22	32507811	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1811288	G	G	369	47	382	28	4.995	2.54E-02	rs5999111	22	32533124	q12.3
SNP_A-1961178	A	A	333	81	305	113	6.488	0.0109	rs13057617	22	32571618	q12.3
SNP_A-2097777	A	A	232	114	273	97	3.898	4.83E-02	rs4821194	22	32580182	q12.3
SNP_A-2041593	T	T	247	153	221	189	5.111	2.38E-02	rs17736366	22	32581775	q12.3
SNP_A-2138955	G	G	330	80	297	115	8.014	4.60E-03	rs8138735	22	32586970	q12.3
SNP_A-2281153	A	A	352	36	372	20	5.104	2.39E-02	rs5999152	22	32659156	q12.3
SNP_A-2109422	C	C	330	84	300	114	5.974	1.45E-02	rs11089650	22	33007919	q12.3
SNP_A-2183926	G	G	266	72	232	96	5.601	1.80E-02	rs5754953	22	33051594	q12.3
SNP_A-2023015	G	G	280	92	234	120	7.373	0.0066	rs169468	22	33070181	q12.3
SNP_A-1829422	T	T	226	78	233	119	5.155	2.32E-02	rs738944	22	33070230	q12.3
SNP_A-2218227	C	C	285	95	219	137	15.48	8.34E-05	rs9619426	22	33071097	q12.3
SNP_A-1862012	A	A	316	94	283	119	4.674	3.06E-02	rs738945	22	33096994	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2053100	C	C	243	161	217	191	4.007	0.0453	rs1569429	22	33114712	q12.3
SNP_A-2053710	A	G	202	182	214	174	4.65	0.031	rs425679	22	33116038	q12.3
SNP_A-2225109	G	G	220	156	199	191	4.328	3.75E-02	rs204438	22	33121986	q12.3
SNP_A-2110026	G	C	212	172	207	189	4.368	3.66E-02	rs204440	22	33122154	q12.3
SNP_A-2186869	C	C	213	115	193	149	5.074	2.43E-02	rs204443	22	33122217	q12.3
SNP_A-2079941	G	G	389	15	387	31	5.333	2.09E-02	rs5749918	22	33372697	q12.3
SNP_A-1971037	C	C	383	15	392	6	3.962	0.0465	rs5755604	22	33853056	q12.3
SNP_A-1814800	C	C	327	31	322	50	4.228	3.98E-02	rs139059	22	34243946	q12.3
SNP_A-1943868	G	G	270	126	246	160	5.034	2.48E-02	rs132617	22	34858285	q12.3
SNP_A-1889147	G	G	257	133	299	99	8.075	4.50E-03	rs132716	22	34920870	q12.3
SNP_A-1823801	C	C	308	94	287	121	4.088	4.32E-02	rs2284013	22	35414843	q12.3

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2169327	G	A	202	148	172	162	5.825	1.58E-02	rs2267361	22	35424760	q12.3
SNP_A-2092876	G	G	368	46	349	67	4.401	3.59E-02	rs1569785	22	35453095	q12.3
SNP_A-2286926	G	G	346	74	316	102	5.809	1.59E-02	rs129333	22	35477789	q12.3
SNP_A-2229307	A	A	339	65	314	94	6.227	0.0126	rs5756339	22	35490957	q12.3
SNP_A-2292136	C	C	346	74	317	101	5.429	1.98E-02	rs4821525	22	35494485	q12.3
SNP_A-1791128	C	G	213	203	231	179	4.712	3.00E-02	rs5756414	22	35655279	q12.3
SNP_A-2071966	G	A	198	192	213	161	4.569	3.26E-02	rs2239749	22	35655805	q12.3
SNP_A-2036144	C	C	325	57	309	87	6.404	0.0114	rs5756454	22	35708309	q12.3
SNP_A-2311130	C	C	331	81	359	61	3.877	4.90E-02	rs4820279	22	35991286	q13.1
SNP_A-2121243	T	T	334	2	322	10	5.529	1.87E-02	rs138465	22	37232349	q13.1
SNP_A-1673262	G	G	399	5	399	15	4.878	2.72E-02	rs138695	22	37363277	q13.1
SNP_A-1756779	A	A	396	2	395	11	6.153	1.31E-02	rs138696	22	37363533	q13.1
SNP_A-1851390	C	C	415	5	406	14	4.362	3.68E-02	rs16999297	22	37446538	q13.1

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2078096	G	G	339	5	356	0	5.212	0.0224	rs16999302	22	37450675	q13.1
SNP_A-2245450	G	G	347	43	359	27	3.841	5.00E-02	rs17298479	22	37675966	q13.1
SNP_A-2079604	T	C	238	178	210	208	4.652	0.031	rs139316	22	37824263	q13.1
SNP_A-2073202	T	T	342	76	375	45	9.456	2.10E-03	rs2281258	22	37867394	q13.1
SNP_A-1899169	T	T	241	157	204	188	5.817	1.59E-02	rs139413	22	37878272	q13.1
SNP_A-1922230	T	T	361	41	333	67	7.384	0.0066	rs6002033	22	39424327	q13.2
SNP_A-2096136	G	G	370	42	355	65	5.178	0.0229	rs6002045	22	39432218	q13.2
SNP_A-1892177	C	C	368	38	350	58	4.613	3.17E-02	rs12160628	22	39441941	q13.2
SNP_A-2153668	G	G	358	26	340	52	9.049	2.60E-03	rs17344464	22	39445684	q13.2
SNP_A-1866168	T	T	325	41	307	67	6.686	9.70E-03	rs5995935	22	39445929	q13.2
SNP_A-2305785	T	T	323	27	297	45	5.499	0.019	—	22	39448986	q13.2
SNP_A-2225774	C	C	377	41	354	62	5	0.0253	rs17344701	22	39456902	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2086569	G	G	390	22	408	10	4.863	2.74E-02	rs5758107	22	39572580	q13.2
SNP_A-1915905	A	A	323	21	347	7	7.718	5.50E-03	rs6002215	22	39704692	q13.2
SNP_A-1890540	G	G	362	0	342	4	4.209	0.0402	rs9620019	22	40785936	q13.2
SNP_A-2310386	A	A	295	117	317	87	5.125	2.36E-02	rs2839705	22	41191112	q13.2
SNP_A-2144061	C	C	335	53	368	36	4.475	0.0344	rs17003208	22	41397529	q13.2
SNP_A-2120108	C	C	336	32	379	15	7.857	5.10E-03	rs17485718	22	41432893	q13.2
SNP_A-1971128	C	C	194	118	175	147	3.995	4.56E-02	rs2038058	22	41658793	q13.2
SNP_A-2289595	A	A	327	5	291	21	11.333	8.00E-04	rs5996268	22	41795024	q13.2
SNP_A-2299577	G	G	357	21	343	37	4.689	0.0304	rs5759165	22	41818570	q13.2
SNP_A-2249839	C	C	320	28	336	14	5.051	0.0246	rs742134	22	41842773	q13.2
SNP_A-2193387	A	A	277	103	311	81	4.411	3.57E-02	rs138958	22	41908779	q13.2
SNP_A-2227439	C	C	354	38	380	24	3.902	0.0482	rs138994	22	41935306	q13.2
SNP_A-1961079	G	G	303	99	331	71	5.848	1.56E-02	rs6003121	22	41960047	q13.2

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2125149	G	G	418	0	409	5	5.079	2.42E-02	rs17003586	22	41991956	q13.2
SNP_A-2242884	T	T	401	7	391	1	4.308	3.79E-02	rs135080	22	42149069	q13.2
SNP_A-1696906	A	A	290	96	323	75	4.173	4.11E-02	rs137791	22	42336807	q13.2
SNP_A-2280447	C	C	312	76	288	100	4.233	3.97E-02	rs9614255	22	42381142	q13.2
SNP_A-1663348	A	A	278	68	250	88	3.956	4.67E-02	rs10483219	22	42387275	q13.2
SNP_A-1679974	T	T	354	50	382	32	4.895	0.0269	rs1476036	22	42416790	q13.2
SNP_A-2142803	G	G	312	84	329	55	6.318	0.012	rs4823137	22	42462250	q13.2
SNP_A-1795059	G	G	323	27	298	42	4.123	4.23E-02	rs5764066	22	42760453	q13.31
SNP_A-1665684	T	T	314	90	295	119	4.495	3.40E-02	rs10483222	22	42807244	q13.31
SNP_A-2077067	G	G	354	16	362	34	5.693	1.70E-02	rs2076507	22	42814843	q13.31
SNP_A-2277146	C	C	258	138	298	114	4.848	2.77E-02	rs9614203	22	42850275	q13.31
SNP_A-1904611	C	C	333	33	350	18	4.829	2.80E-02	rs2267613	22	42855187	q13.31
SNP_A-2265817	G	G	371	11	356	24	5.133	0.0235	rs139151	22	42919377	q13.31
SNP_A-2241027	G	G	239	169	268	142	3.998	4.56E-02	rs135396	22	43002548	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1905869	C	C	269	135	314	102	7.894	5.00E-03	rs8136631	22	43086536	q13.31
SNP_A-2103804	G	G	341	67	323	93	4.636	3.13E-02	rs129536	22	43098547	q13.31
SNP_A-2070664	T	T	254	142	290	116	4.879	2.72E-02	rs6007260	22	43434459	q13.31
SNP_A-2096917	A	A	340	8	362	2	3.932	4.74E-02	rs6006905	22	43624645	q13.31
SNP_A-1858340	T	T	222	186	253	157	4.47	3.45E-02	rs9614982	22	43637327	q13.31
SNP_A-1704349	G	G	371	33	360	54	5.113	2.37E-02	rs1028492	22	43668935	q13.31
SNP_A-2273338	T	T	272	134	232	168	6.958	8.30E-03	rs9614994	22	43682699	q13.31
SNP_A-2313307	A	A	257	71	237	111	9.017	2.70E-03	rs1005368	22	43703767	q13.31
SNP_A-1918408	C	C	370	28	361	45	3.991	0.0458	rs765330	22	43707276	q13.31
SNP_A-2061417	T	T	293	97	258	124	5.44	1.97E-02	rs132035	22	43752549	q13.31
SNP_A-1971164	T	T	309	109	283	137	4.324	3.76E-02	rs7287070	22	43761068	q13.31
SNP_A-2273696	G	G	334	60	320	90	5.984	0.0144	rs136738	22	44248556	q13.31
SNP_A-2199542	C	C	394	16	380	30	4.514	3.36E-02	rs4538310	22	44284127	q13.31
SNP_A-1902885	G	G	367	5	376	0	5.088	0.0241	rs6008534	22	45005768	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1805818	T	T	370	26	358	44	4.782	2.88E-02	rs5767240	22	45240425	q13.31
SNP_A-2080202	G	G	220	192	255	163	4.905	2.68E-02	rs3788727	22	45248785	q13.31
SNP_A-2184834	C	C	293	61	262	82	4.673	3.06E-02	rs738242	22	45268972	q13.31
SNP_A-1818154	A	A	297	105	324	78	5.158	2.31E-02	---	22	45279026	q13.31
SNP_A-2279566	A	A	317	69	294	102	7.107	7.70E-03	rs138476	22	45348833	q13.31
SNP_A-1907696	A	A	328	46	325	77	6.825	9.00E-03	rs135680	22	45414909	q13.31
SNP_A-2210428	A	A	377	9	400	2	4.812	2.83E-02	rs6007995	22	45618112	q13.31
SNP_A-1866275	C	C	411	7	401	17	4.29	3.83E-02	rs6009072	22	45674832	q13.31
SNP_A-2305324	G	G	291	49	267	69	4.399	3.60E-02	rs5766691	22	45852915	q13.31
SNP_A-1786818	T	T	298	58	270	92	9.037	2.60E-03	rs135368	22	45894528	q13.31
SNP_A-1663740	G	G	250	52	308	30	9.938	1.60E-03	rs720441	22	46402968	q13.31
SNP_A-2253365	T	T	224	148	242	110	5.744	1.65E-02	rs6008341	22	46441571	q13.31
SNP_A-1888579	G	G	262	94	246	128	5.271	2.17E-02	rs6007742	22	46479923	q13.31

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-1802935	T	T	271	111	254	152	6.217	1.27E-02	rs11090785	22	46481416	q13.31
SNP_A-2309913	C	C	233	97	259	71	5.398	2.02E-02	rs6008618	22	47015385	q13.32
SNP_A-1878070	C	C	252	158	223	195	5.572	0.0183	rs133672	22	47062102	q13.32
SNP_A-1810525	T	T	263	75	316	60	4.508	3.37E-02	rs6007864	22	47203600	q13.32
SNP_A-2140817	G	A	211	209	242	180	4.868	2.74E-02	rs4450733	22	47367021	q13.32
SNP_A-2117377	C	C	280	62	266	90	5.238	2.21E-02	rs5771917	22	47380604	q13.32
SNP_A-2073908	A	A	271	83	255	111	4.329	3.75E-02	rs9617490	22	47380849	q13.32
SNP_A-2267221	G	A	182	156	184	156	4.3	3.81E-02	rs4925430	22	47381271	q13.32
SNP_A-1867534	G	G	293	93	311	69	4.045	4.43E-02	rs132248	22	47431240	q13.32
SNP_A-1805522	G	G	299	33	355	19	6.087	1.36E-02	rs4925392	22	47476944	q13.32
SNP_A-1758612	G	G	233	67	337	39	18.056	2.15E-05	rs727080	22	47664191	q13.32
SNP_A-2243197	A	A	241	177	276	144	5.757	1.64E-02	rs2064542	22	47751777	q13.32
SNP_A-2217937	G	G	390	24	404	12	4.242	3.94E-02	rs13054825	22	47752184	q13.32
SNP_A-1877262	C	C	412	8	403	19	4.576	3.24E-02	rs739193	22	47849807	q13.33
SNP_A-2278573	T	T	212	192	238	162	4.025	0.0448	rs9627875	22	47858706	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2287973	A	C	213	159	199	187	5.903	1.51E-02	rs6009180	22	47862100	q13.33
SNP_A-1854649	G	G	291	101	269	137	6.066	0.0138	rs5769986	22	47893026	q13.33
SNP_A-1684852	G	G	296	78	276	122	9.643	0.0019	rs848741	22	47951522	q13.33
SNP_A-1786585	C	C	336	44	304	74	9.222	2.40E-03	rs2858522	22	48027438	q13.33
SNP_A-2130664	A	A	342	48	318	74	6.409	0.0114	rs7287593	22	48035642	q13.33
SNP_A-2105763	G	G	379	41	392	22	5.906	1.51E-02	rs9616300	22	48095460	q13.33
SNP_A-2264552	G	G	380	20	400	8	5.577	1.82E-02	rs5769604	22	48096012	q13.33
SNP_A-1886315	C	T	186	140	171	139	9.49	2.10E-03	rs6009689	22	48152931	q13.33
SNP_A-1866331	T	G	207	183	231	171	8.814	3.00E-03	rs6009256	22	48152992	q13.33
SNP_A-1878937	C	C	321	75	298	100	4.421	3.55E-02	rs2071893	22	48299436	q13.33
SNP_A-2122667	G	G	372	6	405	1	3.978	4.61E-02	rs5770574	22	48318828	q13.33
SNP_A-2302776	T	T	388	28	363	43	3.88	4.89E-02	rs4337585	22	48391852	q13.33
SNP_A-1901981	T	T	366	8	351	21	6.136	0.0132	rs760842	22	48400295	q13.33

Table 2

Name	Major_Allele_1	Major_Allele_2	Case_Major	Case_Minor	Control_Major	Control_Minor	Chi_Square	p_value	dbSNP_RS_ID	Chromosome	Physical_Position	Cytoband
SNP_A-2284625	A	A	371	17	357	35	6.48	0.0109	rs4824077	22	48411913	q13.33
SNP_A-2085366	C	C	325	51	335	31	4.896	0.0269	rs4824090	22	48441386	q13.33
SNP_A-1927775	A	A	390	2	391	9	4.375	3.65E-02	rs9627644	22	48622525	q13.33
SNP_A-1916764	G	G	253	153	289	119	6.636	0.01	rs5771040	22	49192534	q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2081399	acctggtattctatca[C/T]atttctgcttaacaag	C	T	NM_002074 // intron // 0 // Hs.430425 // GNB1 // 2782 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA. /// ENST00000263750 // intron // 0 // — // — // — // —	GNB1	GNB1, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), p36.33
SNP_A-1919019	ttaacgtccacaaatc[A/G]cagtcgctaggattta	A	G	NM_002074 // intron // 0 // Hs.430425 // GNB1 // 2782 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA. /// ENST00000263750 // intron // 0 // — // — // — // —	GNB1	GNB1, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), p36.33
SNP_A-2278444	gagctcactcacccat[C/T]agacgctggcaactgg	C	T	NM_002074 // intron // 0 // Hs.430425 // GNB1 // 2782 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA. /// ENST00000263750 // intron // 0 // — // — // — // —	GNB1	GNB1, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), p36.33
SNP_A-2223642	cggaggcttgtcaggt[A/C]aattaggagatgatta	A	C	NM_002074 // intron // 0 // Hs.430425 // GNB1 // 2782 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA. /// ENST00000263750 // intron // 0 // — // — // — // —	GNB1	GNB1, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), p36.33
SNP_A-1856955	tcaccaggtcttatca[A/G]tcgtcaacctggtcca	A	G	NM_002074 // intron // 0 // Hs.430425 // GNB1 // 2782 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA. /// ENST00000263750 // intron // 0 // — // — // — // —	GNB1	GNB1, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), p36.33
SNP_A-1642581	atgcaaaggctgataaaaatatttcc[A/C]agacatgctctaaatag caggcaca	A	C	NM_022114 // intron // 0 // Hs.409905 // PRDM16 // 63976 // PR domain containing 16	PRDM16	PRDM16 , rs10492941, PR domain containing 16,p36.32
SNP_A-1978484	tccccagtacttgtca[C/T]gggcttcaacgttatg	C	T	NM_080431 // downstream // 12369 // Hs.236635 // ARPM2 // 140625 // Homo sapiens actin-related protein M2 (ARPM2), mRNA. /// NM_198543 // downstream // 28802 // — // — // 0 // — /// NM_199454 // upstream // 33910 // Hs.99500 // PRDM16 // 63976 // Ho	ARPM2	ARPM2, Homo sapiens actin-related protein M2 (ARPM2), p36.32
SNP_A-1858853	tcagcaaagcaacaga[C/T]gacgaggttctcagag	C	T	NM_199454 // intron // 0 // Hs.99500 // PRDM16 // 63976 // Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, mRNA. /// NM_022114 // intron // 0 // Hs.99500 // PRDM16 // 63976 // Homo sapiens PR domain containing 16 (PRDM16), transcript	PRDM16	PRDM16, Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, p36.32
SNP_A-2098079	agagaggaggaatcaa[C/T]aatgtggacctgccta	C	T	NM_199454 // intron // 0 // Hs.99500 // PRDM16 // 63976 // Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, mRNA. /// NM_022114 // intron // 0 // Hs.99500 // PRDM16 // 63976 // Homo sapiens PR domain containing 16 (PRDM16), transcript	PRDM16	PRDM16, Homo sapiens PR domain containing 16 (PRDM16), transcript variant 2, p36.32
SNP_A-2049610	aagcttattcaggtta[C/T]cattgctatgtcttac	C	T	ENST00000361104 // intron // 0 // — // — // — // —	-	p36.32
SNP_A-1953724	tttgacttattcaaaa[A/G]agcatccccgtccagg	A	G	AB011134 // intron // 0 // Hs.509017 // KIAA0562 // 9731 // Homo sapiens mRNA for KIAA0562 protein, partial cds. /// ENST00000263739 // intron // 0 // — // — // — // —	KIAA0562	KIAA0562, Homo sapiens for KIAA0562 protein, partial cds. ,p36.32
SNP_A-1997922	aactatctaaagcagc[A/C]ctttactgacatgaaa	A	C	AB011134 // intron // 0 // Hs.509017 // KIAA0562 // 9731 // Homo sapiens mRNA for KIAA0562 protein, partial cds. /// ENST00000263739 // intron // 0 // — // — // — // — /// ENST00000335437 // intron // 0 // — // — // — // —	KIAA0562	KIAA0562, Homo sapiens for KIAA0562 protein, partial cds. ,p36.32
SNP_A-2288864	gatttaattacagtcc[C/T]gattttcagcaccatc	C	T	ENST00000332625 // upstream // 100100 // — // — // — // — /// ENST00000356772 // downstream // 8395 // — // — // — // — /// ENST00000360071 // downstream // 18057 // — // — // — // —	-	p36.32
SNP_A-2176838	caccctgaagcaggc[G/T]ctgaggcatctctgtc	G	T	NM_018836 // upstream // 532320 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 129895 // — // — // — // — /// ENST00000360071 // upstream // 121886 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2202358	ccaccaggtagaacag[A/G]atgatccactgtctcc	A	G	NM_018836 // upstream // 513290 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 148925 // --- // --- // --- // --- /// ENST00000360071 // upstream // 140916 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2254182	cttgatctcaagtcac[C/T]ggacagaggatactca	C	T	NM_018836 // upstream // 508817 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 153398 // --- // --- // --- // --- /// ENST00000360071 // upstream // 145389 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2211019	cccgcccacatctaac[C/T]ggaccagaggcagtcg	C	T	NM_018836 // upstream // 383322 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 278893 // --- // --- // --- // --- /// ENST00000360071 // upstream // 270884 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1784353	ggccccagttacaaac[C/T]aacttttctctaggag	C	T	NM_018836 // upstream // 334587 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 327628 // --- // --- // --- // --- /// ENST00000360071 // upstream // 319619 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1924023	ttagtggtaatgtcaa[C/T]ggtaacggtggtgatg	C	T	NM_018836 // upstream // 318553 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 343662 // --- // --- // --- // --- /// ENST00000360071 // upstream // 335653 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2035185	aaatgccttttaccaa[C/T]gtccagctctagaagc	C	T	NM_018836 // upstream // 254843 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 407372 // --- // --- // --- // --- /// ENST00000360071 // upstream // 399363 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2299722	gccgtaggctccagac[A/G]ctactttgttccaatc	A	G	NM_018836 // upstream // 191748 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 470467 // --- // --- // --- // --- /// ENST00000360071 // upstream // 462458 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2004332	cattgcatttcatgga[C/T]acgtctcctttgtcta	C	T	NM_018836 // upstream // 150421 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 511794 // --- // --- // --- // --- /// ENST00000360071 // upstream // 503785 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2303721	gctcagagcatcccag[A/C]ctgaagagcctcactc	A	C	NM_018836 // upstream // 136377 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 525838 // --- // --- // --- // --- /// ENST00000360071 // upstream // 517829 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2072682	acagccttcccagaaa[C/T]aggaccattcacatct	C	T	NM_018836 // upstream // 127586 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 534629 // --- // --- // --- // --- /// ENST00000360071 // upstream // 526620 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2149899	atgtcaccttgaacca[C/T]cttggcacagccggtt	C	T	NM_018836 // upstream // 127510 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 534705 // --- // --- // --- // --- /// ENST00000360071 // upstream // 526696 // --- // --- // --	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2104217	agcagagttgtccacc[A/C]agtgttggccacagtg	A	C	NM_018836 // upstream // 32573 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 629642 // — // — // — // — /// ENST00000360071 // upstream // 621633 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1999854	atggtcaccgtcttct[A/G]aaggcgtaggatcg	A	G	NM_018836 // upstream // 17805 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 644410 // — // — // — // — /// ENST00000360071 // upstream // 636401 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2297571	gccagagctgtgtcac[A/G]atcaacttaggtata	A	G	NM_018836 // upstream // 9174 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000356772 // upstream // 653041 // — // — // — // — /// ENST00000360071 // upstream // 645032 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2120497	agtccacaaaacattgc[G/T]ctccgggtgaatcctg	G	T	NM_018836 // intron // 0 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // intron // 0 // — // — // — // — /// ENST00000354985 // intron // 0 // — // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1873908	tctcagtgctgtaact[G/T]actgtcaatgagagtg	G	T	NM_018836 // intron // 0 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // intron // 0 // — // — // — // — /// ENST00000354985 // intron // 0 // — // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1822227	gtttgattatcaaga[A/G]ctaatgtatgaacata	A	G	NM_018836 // downstream // 142456 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 142456 // — // — // — // — /// ENST00000354985 // downstream // 142456 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1910067	tgtcatagaactctca[A/C]ccctgacttaacccaa	A	C	NM_018836 // downstream // 142620 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 142620 // — // — // — // — /// ENST00000354985 // downstream // 142620 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1809821	gtgagggattgcaga[A/G]cagcgaagggcatccc	A	G	NM_018836 // downstream // 151176 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 151176 // — // — // — // — /// ENST00000354985 // downstream // 151176 // — // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1871192	tcgtttttcggagaca[A/G]cggcagactgaaaacc	A	G	NM_018836 // downstream // 204774 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 204774 // — // — // — // — /// ENST00000354985 // downstream // 204774 // — // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1667950	gacgtgcacctggaaactgagatcc[A/C]agtcatctggctgtag gtttccata	A	C	NM_015102 // downstream // 650061 // Hs.434931 // NPHP4 // 261734 // nephronophthisis 4 /// NM_018836 // downstream // 468916 // Hs.25924 // SHREW1 // 55966 // transmembrane protein SHREW1	NPHP4	NPHP4, rs4475768, nephronophthisis 4, p36.32
SNP_A-2281828	gagtgagggttccata[C/T]catgttctgccatatt	C	T	NM_018836 // downstream // 293816 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 293816 // — // — // — // — /// ENST00000354985 // downstream // 293816 // — // —	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282669	gagttttgtagattgaa[C/T]gttccagaagatggca	C	T	NM_018836 // downstream // 356882 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 356882 // --- // --- // --- /// ENST00000354985 // downstream // 356882 // --- // ---	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-2078896	acccaagccaaaagcc[A/G]gagctcacgcaggca	A	G	NM_018836 // downstream // 406647 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 406647 // --- // --- // --- /// ENST00000354985 // downstream // 406647 // --- // ---	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.32
SNP_A-1827498	taactccacccaaca[C/T]aatcaglaccataaag	C	T	NM_018836 // downstream // 651560 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 651560 // --- // --- // --- /// ENST00000354985 // downstream // 651560 // --- // ---	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.31
SNP_A-2050915	aaggcgatggctctgc[A/G]aagatctgagaagacc	A	G	NM_018836 // downstream // 783893 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 783893 // --- // --- // --- /// ENST00000354985 // downstream // 783893 // --- // ---	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.31
SNP_A-2271384	gacattgggctcagat[C/G]aaatgaattcagcctc	C	G	NM_018836 // downstream // 861271 // Hs.25924 // SHREW1 // 55966 // Homo sapiens transmembrane protein SHREW1 (SHREW1), mRNA. /// ENST00000359090 // downstream // 861271 // --- // --- // --- /// ENST00000354985 // downstream // 861271 // --- // ---	SHREW1	SHREW1, Homo sapiens transmembrane protein SHREW1 (SHREW1), p36.31
SNP_A-2088032	actggctgagcggaaga[C/T]ggtgtatccctaata	C	T	NM_172130 // upstream // 30212 // Hs.440497 // KCNAB2 // 8514 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNAB2), transcript variant 2, mRNA. /// NM_003636 // upstream // 30212 // Hs.440497 // KCNAB2 // 8514	KCNAB2	KCNAB2, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNAB2), transcript variant 2, p36.31
SNP_A-1755914	ctgtaaatagcttgtcacataggac[A/G]ggatccgaaaaggag agttttgtgt	A	G	NM_007274 // intron // 0 // Hs.435092 // BACH // 11332 // brain acyl-CoA hydrolase /// NM_181862 // intron // 0 // Hs.435092 // BACH // 11332 // brain acyl-CoA hydrolase /// NM_181863 // intron // 0 // Hs.435092 // BACH // 11332 // brain acyl-CoA hydrola	BACH	BACH , rs10489536, brain acyl-CoA hydrolase p36.31
SNP_A-1676650	cttttccagcttctaaaagcacta[A/C]tactgtaaaacttaggttat ttttt	A	C	AB020640 // intron // 0 // Hs.253254 // CAMTA1 // 23261 // calmodulin binding transcription activator 1	CAMTA1	CAMTA1 , rs1396904, calmodulin binding transcription activator 1 p36.31
SNP_A-1836468	tactccagtctacaca[C/G]tgcttgatgttgttgt	C	G	NM_018198 // intron // 0 // Hs.462640 // DNAJC11 // 55735 // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 11 (DNAJC11), mRNA. /// ENST00000234490 // intron // 0 // --- // --- // --- // --- /// ENST00000294401 // intron // 0 // --- // --- // ---	DNAJC11	DNAJC11, Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 11 (DNAJC11), p36.31
SNP_A-2096412	agaccctatctcaaaa[C/G]aagcatgagcaaaact	C	G	NM_138350 // downstream // 113056 // Hs.9933 // THAP3 // 90326 // Homo sapiens hypothetical protein MGC33488, mRNA. /// BC022081 // downstream // 115052 // Hs.9933 // THAP3 // 90326 // Homo sapiens hypothetical protein MGC33488, mRNA (cDNA clon	THAP3	THAP3, Homo sapiens hypothetical protein MGC33488 (MGC33488), p36.31
SNP_A-1899466	tggaagagatactgca[C/T]ggtctgctgaacgaat	C	T	ENST00000303646 // intron // 0 // --- // --- // --- // ---	-	p36.31
SNP_A-2231290	ctattccagccttccc[A/G]aaaataatttcctgt	A	G	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.31
SNP_A-2200438	ccaacctaatacctag[C/T]agcacaaatctgatct	C	T	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.31
SNP_A-1884194	tgaaggaatgaatgaa[C/T]tgcaagtttaaatgtt	C	T	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.31
SNP_A-2146553	atgctgcacagcaacc[A/G]ctgcttggcgctgaga	A	G	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.31
SNP_A-1922613	ttagacctaattgtca[A/T]cataatgccatattaa	A	T	ENST00000303646 // intron // 0 // --- // --- // ---	-	p36.23
SNP_A-1915177	tgttcaaggcagcaaaa[C/T]ccctggacattgatgg	C	T	ENST00000303646 // intron // 0 // --- // --- // --- /// ENST00000303635 // intron // 0 // --- // --- // ---	-	p36.23
SNP_A-2298623	gcccagaaaaggtgca[C/T]ataatttgcttccaat	C	T	ENST00000303646 // intron // 0 // --- // --- // --- /// ENST00000303635 // intron // 0 // --- // --- // ---	-	p36.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1806560	gtcgttggacggtaag[A/G]acagtgcttgggtcgt	A	G	ENST00000303646 // intron // 0 // --- // --- // --- /// ENST00000303635 // intron // 0 // --- // --- // ---	-	p36.23
SNP_A-1794435	ggtccgagtcctaaaa[A/C]tgccaattcctgctgc	A	C	ENST00000054666 // intron // 0 // --- // --- // ---	-	p36.23
SNP_A-1691698	ctctgcctggttcctggagctgtcc[C/T]gataaggttgccaaptgg agcaaat	C	T	NM_018948 // upstream // 286180 // Hs.11169 // MIG-6 // 54206 // mitogen-inducible gene 6	MIG-6	MIG-6, rs4350217, mitogen-inducible gene 6,p36.23
SNP_A-2171736	caatctttcccaggac[A/C]aatttcagtgtgtcac	A	C	AF118274 // upstream // 117028 // Hs.463036 // DNB5 // 50651 // Homo sapiens DNb-5 mRNA, partial cds. /// ENST00000341781 // upstream // 154648 // --- // --- // --- /// ENST00000289877 // upstream // 117028 // --- // --- // ---	DNB5	DNB5, Homo sapiens DNb-5 partial cds. p36.23
SNP_A-1780483	ggatagctaaggtcaa[C/G]aattcaaaactaacag	C	G	NM_012102 // intron // 0 // Hs.463041 // RERE // 473 // Homo sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE), mRNA. /// ENST00000337907 // intron // 0 // --- // --- // --- /// ENST00000326676 // intron // 0 // --- // --- // ---	RERE	RERE, Homo sapiens arginine-glutamic acid dipeptide (RE) repeats (RERE), p36.23
SNP_A-1892754	tgcacagatgaactga[G/T]gaatcaataaataagt	G	T	NM_024980 // upstream // 45277 // Hs.287490 // GPR157 // 80045 // Homo sapiens G protein-coupled receptor 157 (GPR157), mRNA. /// NM_004285 // upstream // 60500 // Hs.463511 // H6PD // 9563 // Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehyd	GPR157	GPR157, Homo sapiens G protein-coupled receptor 157 (GPR157), p36.22
SNP_A-1912444	tgtgcactcaagttac[A/G]ggtctctcaggctctg	A	G	NM_025106 // downstream // 68522 // Hs.8261 // SSB1 // 80176 // Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), mRNA. /// NM_025106 // downstream // 68525 // Hs.8261 // SSB1 // 80176 // Homo sapiens SPRY domain-containing SOCS box prote	SSB1	SSB1, Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (SSB1), p36.22
SNP_A-2286423	gatgctggccccagaa[C/T]agcaggaggaacaagg	C	T	ENST00000340381 // intron // 0 // --- // --- // --- /// ENST00000340305 // intron // 0 // --- // --- // ---	-	p36.22
SNP_A-1750171	gggatgttttggcgctgggagaa[C/T]agcctcctttctgctgaa gttgcca	C	T	NM_014944 // upstream // 15579 // Hs.29665 // CLSTN1 // 22883 // calsyntenin 1 /// NM_020248 // downstream // 8171 // Hs.108222 // CTNNBIP1 // 56998 // catenin, beta interacting protein 1	CLSTN1	CLSTN1, rs10492968, calsyntenin 1 ,p36.22
SNP_A-2270634	gacagcaaatttctaa[A/G]aggctaggagtgttta	A	G	NM_183416 // intron // 0 // Hs.97858 // KIF1B // 23095 // Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, mRNA. /// NM_015074 // intron // 0 // Hs.97858 // KIF1B // 23095 // Homo sapiens kinesin family member 1B (KIF1B), transcript va	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 2, p36.22
SNP_A-1948295	tttaggatgattgaca[A/G]tggcagtacctggact	A	G	NM_015074 // intron // 0 // Hs.97858 // KIF1B // 23095 // Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, mRNA. /// AB017133 // intron // 0 // Hs.97858 // KIF1B // 23095 // Homo sapiens KIAA0591/KIF1Bbeta mRNA, complete cds. /// ENST0	KIF1B	KIF1B, Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, p36.22
SNP_A-1717751	cctcctctagaacggctggcccaac[A/G]ctttccagggctcag ccatttctc	A	G	BC051883 // intron // 0 // Hs.222219 // FLJ20321 // 54897 // hypothetical protein FLJ20321	FLJ20321	FLJ20321, rs67969, hypothetical protein FLJ20321,p36.22
SNP_A-2298739	ctagtgtagtgatgtc[G/T]atgctgtaaatatgt	G	T	NM_004565 // intron // 0 // Hs.149983 // PEX14 // 5195 // Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA. /// ENST00000270774 // intron // 0 // --- // --- // ---	PEX14	PEX14, Homo sapiens peroxisomal biogenesis factor 14 (PEX14), p36.22
SNP_A-2021932	aaaaacttgaagaaaa[C/T]gaggaagcaaaccatg	C	T	NM_004565 // intron // 0 // Hs.149983 // PEX14 // 5195 // Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA. /// ENST00000270774 // intron // 0 // --- // --- // ---	PEX14	PEX14, Homo sapiens peroxisomal biogenesis factor 14 (PEX14), p36.22
SNP_A-2281771	gagtgacagaaaatcc[A/G]ggaagtcccagaagga	A	G	NM_017766 // upstream // 36374 // Hs.222219 // FLJ20321 // 54897 // Homo sapiens hypothetical protein FLJ20321 (FLJ20321), mRNA. /// NM_173507 // downstream // 114639 // --- // FLJ37118 // 148345 // Homo sapiens hypothetical protein FLJ37118 (FLJ37118), m	FLJ20321	FLJ20321, Homo sapiens hypothetical protein FLJ20321 (FLJ20321), p36.22
SNP_A-2176916	cacctaaaatagcaaa[A/C]aacaagggcatagtg	A	C	NM_173507 // upstream // 5220 // --- // FLJ37118 // 148345 // Homo sapiens hypothetical protein FLJ37118 (FLJ37118), mRNA. /// ENST00000308835 // upstream // 5220 // --- // --- // --- // ENST00000321005 // downstream // 21467 // --- // --- // ---	FLJ37118	FLJ37118, Homo sapiens hypothetical protein FLJ37118 (FLJ37118), p36.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2291726	gcacactacttcaaaa[C/T]gctgaaattaggtatt	C	T	NM_007375 // intron // 0 // Hs.300624 // TARDBP // 23435 // Homo sapiens TAR DNA binding protein (TARDBP), mRNA. /// ENST00000240185 // intron // 0 // — // — // — // —	TARDBP	TARDBP, Homo sapiens TAR DNA binding protein (TARDBP), p36.22
SNP_A-2261658	gaaagtagggataacc[C/T]actagtcgggaggtag	C	T	ENST00000263936 // intron // 0 // — // — // — // —	-	p36.22
SNP_A-1911729	tgtgaaggcaggcaca[G/T]aaatagttaagccaca	G	T	NM_013319 // downstream // 186068 // Hs.522933 // TERE1 // 29914 // Homo sapiens transitional epithelia response protein (TERE1), mRNA. /// ENST00000240179 // downstream // 186068 // — // — // — // — /// ENST00000294484 // upstream // 5242 // —	TERE1	TERE1, Homo sapiens transitional epithelia response protein (TERE1), p36.22
SNP_A-2309196	ggaaaaatgagatgtg[A/G]atgaaagaaagaaacg	A	G	NM_198545 // intron // 0 // Hs.371716 // LOC374946 // 374946 // Homo sapiens hypothetical gene supported by AK075558; BC021286 (LOC374946), mRNA. /// ENST00000338580 // intron // 0 // — // — // — // —	LOC374946	LOC374946, Homo sapiens hypothetical gene supported by AK075558; BC021286 (LOC374946), p36.22
SNP_A-1781313	ggatgtgacagaagcc[A/G]ctgagcaatctcctcc	A	G	ENST00000312812 // CDS // 0 // — // — // — // —	-	p36.22
SNP_A-1852165	tattgtaaaaccaagc[A/G]gaggacacagaatggc	A	G	ENST00000312793 // intron // 0 // — // — // — // —	-	p36.22
SNP_A-1827473	taactcacctgagata[A/G]taaacaggcaagcgct	A	G	NM_005957 // intron // 0 // Hs.214142 // MTHFR // 4524 // Homo sapiens 5,10-methylenetetrahydrofolate reductase (NADPH) (MTHFR), mRNA. /// ENST00000323338 // intron // 0 // — // — // — // —	MTHFR	MTHFR, Homo sapiens 5,10-methylenetetrahydrofolate reductase (NADPH) (MTHFR), p36.22
SNP_A-2153521	attagcatcttaagcc[A/G]gcatcgttcatttgtc	A	G	NM_001243 // intron // 0 // Hs.1314 // TNFRSF8 // 943 // Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), transcript variant 1, mRNA. /// NM_152942 // intron // 0 // Hs.1314 // TNFRSF8 // 943 // Homo sapiens tumor necrosis fact	TNFRSF8	TNFRSF8, Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), transcript variant 1, p36.22
SNP_A-2270127	gacacaggattacaaa[C/T]gaaagcccacactgtg	C	T	NM_001243 // intron // 0 // Hs.1314 // TNFRSF8 // 943 // Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), transcript variant 1, mRNA. /// NM_152942 // intron // 0 // Hs.1314 // TNFRSF8 // 943 // Homo sapiens tumor necrosis fact	TNFRSF8	TNFRSF8, Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), transcript variant 1, p36.22
SNP_A-1735683	cctcggtacaacctgaaaaagagac[A/C]aaaattggccatttct ggtatttttt	A	C	NM_004753 // upstream // 63439 // Hs.17144 // DHRS3 // 9249 // dehydrogenase/reductase (SDR family) member 3 /// NM_152290 // upstream // 65256 // Hs.98095 // MGC35194 // 93190 // hypothetical protein MGC35194	DHRS3	DHRS3 , rs1419299, dehydrogenase,p36.21
SNP_A-2141957	atctttaattgttgga[C/T]ggaaaagaaaggaacc	C	T	NM_152290 // 3UTR // 0 // Hs.98095 // MGC35194 // 93190 // Homo sapiens hypothetical protein MGC35194 (MGC35194), mRNA. /// ENST00000288048 // 3UTR // 0 // — // — // — // —	MGC35194	MGC35194, Homo sapiens hypothetical protein MGC35194 (MGC35194), p36.21
SNP_A-2260132	gaaaatcatcccaaca[A/G]tgggtagttcctctct	A	G	AL049680 // intron // 0 // Hs.451982 // LOC343068 // 343068 // Human gene from PAC 845O24, chromosome 1, similar to preferentially expressed antigen of melanoma. /// ENST00000331684 // intron // 0 // — // — // — // —	LOC343068	LOC343068, Human gene from PAC 845O24, chromosome 1, similar to preferentially expressed antigen of melanoma, p36.21
SNP_A-1787780	gggacccctccccata[C/T]agaagtttctagaatg	C	T	ENST00000294490 // upstream // 1137 // — // — // — // — /// ENST00000341322 // upstream // 40240 // — // — // — // —	-	p36.21
SNP_A-1712855	caggtacattggaaagaacatgaaa[C/T]ttgaaataaaactca gttctgtgac	C	T	AB028949 // upstream // 621444 // Hs.368823 // KIAA1026 // 23254 // KIAA1026 protein /// NM_012231 // downstream // 152181 // Hs.413375 // PRDM2 // 7799 // PR domain containing 2, with ZNF domain /// NM_015866 // downstream // 189187 // Hs.413375 // PRDM	KIAA1026	KIAA1026 , rs725398, KIAA1026 protein ,p36.21
SNP_A-2287018	gatggttgtttggaag[G/T]catattcatttcctag	G	T	NM_198389 // downstream // 10700 // Hs.468675 // T1A-2 // 10630 // Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, mRNA. /// NM_006474 // downstream // 10700 // Hs.468675 // T1A-2 // 10630 // Homo sapiens lung	T1A-2	T1A-2, Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, p36.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802292	gtatatgttttattca[C/T]gttctcggtggcgtat	C	T	NM_198389 // downstream // 75953 // Hs.468675 // T1A-2 // 10630 // Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, mRNA. /// NM_006474 // downstream // 75953 // Hs.468675 // T1A-2 // 10630 // Homo sapiens lung	T1A-2	T1A-2, Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, p36.21
SNP_A-1999887	gcacccccccttctaa[C/T]tgtgacaatccaaagt	C	T	NM_015866 // intron // 0 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // intron // 0 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1942378	ttggcctctggaatttt[C/T]aaacctttcattggta	C	T	NM_015866 // downstream // 113508 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 76502 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain conta	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2073931	acagtgtttgaaggtg[A/G]agtacaatagaaggtg	A	G	NM_015866 // downstream // 200011 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 163005 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1719635	ctttctccagcaaggaagaaagtta[C/T]gcaaaagcacataat gaaaaacata	C	T	AB028949 // upstream // 173724 // Hs.368823 // KIAA1026 // 23254 // KIAA1026 protein /// NM_012231 // downstream // 599901 // Hs.413375 // PRDM2 // 7799 // PR domain containing 2, with ZNF domain /// NM_015866 // downstream // 636907 // Hs.413375 // PRDM	KIAA1026	KIAA1026 , rs6678924, KIAA1026 protein ,p36.21
SNP_A-2241164	ctgagcttatgagtcc[C/T]gataaaagtctacgga	C	T	NM_015866 // downstream // 331224 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 294218 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2050726	aaggcaggaacaaaga[A/G]aacaaccttgcttcta	A	G	NM_015866 // downstream // 353988 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 316982 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2041897	aactaactccaggaga[C/T]agtttagaggctgtca	C	T	NM_015866 // downstream // 534402 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 497396 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1964807	caaatacattgtagac[C/T]gagcagctgaaattgg	C	T	NM_015866 // downstream // 629403 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 592397 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1791731	gggtctggcaatgcaa[C/T]ggattgaaaataaaaa	C	T	NM_015866 // downstream // 646065 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 609059 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2104528	agcagggagaacagtg[A/G]atcagagctctgaaga	A	G	NM_015866 // downstream // 647103 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 610097 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1958749	ttttctgagcttccaa[A/C]tgatttgaggaatagg	A	C	NM_015866 // downstream // 662163 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 625157 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2059550	aatctcatcccaaaac[A/G]gcgtccaatctgccaa	A	G	NM_015866 // downstream // 663837 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 626831 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1964848	gtttaaaatgcctcat[G/T]aaaagtgcatgagcat	G	T	NM_015866 // downstream // 668020 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 631014 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-2191464	catatcttgtaagaac[A/G]ggtataaacgtctaca	A	G	NM_015866 // downstream // 668389 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 631383 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1808759	gtgaagcctcatgaac[C/T]actttgtggaagcctt	C	T	NM_015866 // downstream // 669087 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 632081 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1964852	cttcctttctattgtg[A/C]aaataccacccaatga	A	C	NM_015866 // downstream // 671740 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 634734 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1965048	gatgggggacactgac[C/T]ggtgttgagtagagga	C	T	NM_015866 // downstream // 793504 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA. /// NM_012231 // downstream // 756498 // Hs.371823 // PRDM2 // 7799 // Homo sapiens PR domain cont	PRDM2	PRDM2, Homo sapiens PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, p36.21
SNP_A-1686366	ccctatgctggcaggatcaagccaa[A/G]gctaagctctttaacttt caacact	A	G	NM_018022 // intron // 0 // Hs.30925 // FLJ10199 // 55092 // hypothetical protein FLJ10199	FLJ10199	FLJ10199 , rs10489453, hypothetical protein FLJ10199,p36.21
SNP_A-1678816	gggtaaggcagcagtaataggtctg[A/G]aaagattaacagag gctgactctaa	A	G	NM_018022 // intron // 0 // Hs.30925 // FLJ10199 // 55092 // hypothetical protein FLJ10199	FLJ10199	FLJ10199 , rs10489452, hypothetical protein FLJ10199,p36.21
SNP_A-1862219	tcatggccacctgcta[C/T]ggctcagggaaagcct	C	T	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2292495	gcactcaatgaatgaa[A/G]taacaaacattagtgg	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2075051	acatccccccaactca[G/T]gctgtagttctgcagg	G	T	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-2187234	cagggtgagaagctaac[A/G]catggaagagtcttta	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1855573	tcaataaaccatcttta[A/G]atactgtgtgcaatac	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // --- /// ENST00000303864 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1896658	tgctagttttccatca[A/G]tagacatcgttttaat	A	G	ENST00000251295 // intron // 0 // --- // --- // --- // --- /// ENST00000303864 // intron // 0 // --- // --- // --- // ---	-	p36.21
SNP_A-1806163	gtcctgaccaagtaga[C/T]gtctgtgaaatgtaga	C	T	NM_182534 // intron // 0 // Hs.447976 // FLJ23703 // 200197 // Homo sapiens hypothetical protein FLJ23703 (FLJ23703), mRNA. /// ENST00000310916 // intron // 0 // --- // --- // --- // ---	FLJ23703	FLJ23703, Homo sapiens hypothetical protein FLJ23703 (FLJ23703), p36.21
SNP_A-2171049	caatacctagaatagc[A/G]cagggcacataggaag	A	G	NM_182534 // intron // 0 // Hs.447976 // FLJ23703 // 200197 // Homo sapiens hypothetical protein FLJ23703 (FLJ23703), mRNA. /// ENST00000310916 // intron // 0 // --- // --- // --- // ---	FLJ23703	FLJ23703, Homo sapiens hypothetical protein FLJ23703 (FLJ23703), p36.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1867154	tccctgatgaatattc[C/T]aatactcttttcttag	C	T	NM_018022 // intron // 0 // Hs.465305 // FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // — // — // — // — /// ENST00000303840 // intron // 0 // — // — // — // —	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-2059674	aatctgaaaattctca[A/C]ctgaagacaaagtaaa	A	C	NM_018022 // intron // 0 // Hs.465305 // FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // — // — // — // — /// ENST00000303840 // intron // 0 // — // — // — // —	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-1814246	gtgtctgtcaccttga[C/T]gttagttgtcaccttа	C	T	NM_018022 // intron // 0 // Hs.465305 // FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // — // — // — // — /// ENST00000303840 // intron // 0 // — // — // — // —	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-2106377	agccctttcttgatca[C/T]tctgtcaaaagaaccc	C	T	NM_018022 // intron // 0 // Hs.465305 // FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // — // — // — // — /// ENST00000303840 // intron // 0 // — // — // — // —	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-1935880	ttctgttttcttttcc[A/G]gacatcttgtgatagg	A	G	NM_018022 // intron // 0 // Hs.465305 // FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // — // — // — // — /// ENST00000303840 // intron // 0 // — // — // — // —	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-2269239	gaatttaggccagaga[C/T]gccagattttcaagtt	C	T	NM_018022 // intron // 0 // Hs.465305 // FLJ10199 // 55092 // Homo sapiens hypothetical protein FLJ10199 (FLJ10199), mRNA. /// ENST00000359192 // intron // 0 // — // — // — // — /// ENST00000303840 // intron // 0 // — // — // — // —	FLJ10199	FLJ10199, Homo sapiens hypothetical protein FLJ10199 (FLJ10199), p36.21
SNP_A-1967181	ttgactttacaaatac[A/T]ctagaaaatctcagaa	A	T	NM_024329 // upstream // 10317 // Hs.465374 // EFHD2 // 79180 // Homo sapiens EF hand domain containing 2 (EFHD2), mRNA. /// ENST00000294421 // downstream // 50554 // — // — // — // — /// ENST00000314668 // downstream // 11240 // — // — // —	EFHD2	EFHD2, Homo sapiens EF hand domain containing 2 (EFHD2), p36.21
SNP_A-1857548	tcactccaattgcccc[A/G]gatgaatattggtgct	A	G	NM_024329 // upstream // 3039 // Hs.465374 // EFHD2 // 79180 // Homo sapiens EF hand domain containing 2 (EFHD2), mRNA. /// ENST00000294421 // downstream // 57832 // — // — // — // — /// ENST00000314668 // downstream // 18518 // — // — // —	EFHD2	EFHD2, Homo sapiens EF hand domain containing 2 (EFHD2), p36.21
SNP_A-1856143	tcacaaagctggacac[A/G]atacctcgtaagcctt	A	G	ENST00000251293 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-2158614	attgtatcattttcta[C/T]gtatgccatgacagga	C	T	NM_024758 // upstream // 7134 // Hs.461532 // AGMAT // 79814 // Homo sapiens agmatine ureohydrolase (agmatinase) (AGMAT), mRNA. /// ENST00000235417 // upstream // 7134 // — // — // — // — /// ENST00000270751 // upstream // 12353 // — // — // -	AGMAT	AGMAT, Homo sapiens agmatine ureohydrolase (agmatinase) (AGMAT), p36.13
SNP_A-1957325	ttttagatggcatttc[G/T]ctttgcccaaggaggt	G	T	NM_024758 // upstream // 10766 // Hs.461532 // AGMAT // 79814 // Homo sapiens agmatine ureohydrolase (agmatinase) (AGMAT), mRNA. /// ENST00000235417 // upstream // 10766 // — // — // — // — /// ENST00000270751 // upstream // 8721 // — // — //	AGMAT	AGMAT, Homo sapiens agmatine ureohydrolase (agmatinase) (AGMAT), p36.13
SNP_A-2138694	atcccagtatccaaga[A/T]gtactctgtgttgtac	A	T	ENST00000270751 // downstream // 1394 // — // — // — // — /// ENST00000320153 // upstream // 11106 // — // — // — // —	-	p36.13
SNP_A-1871939	tctacataggccaacc[C/T]gccgtgtacatgtttc	C	T	ENST00000320153 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-1817181	gttcaatctggttaca[A/G]ctagcctatatgcatt	A	G	NM_006511 // upstream // 3063 // Hs.239459 // RSC1A1 // 6248 // Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), mRNA. /// ENST00000320153 // downstream // 4834 // — // — // — // — /// ENST00000345034 // upstream // 306	RSC1A1	RSC1A1, Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), p36.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1967671	ctcttcttttgccacc[A/G]atccagttaaaaattg	A	G	NM_006511 // upstream // 1058 // Hs.239459 // RSC1A1 // 6248 // Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), mRNA. /// ENST00000320153 // downstream // 6839 // — // — // — // — /// ENST00000345034 // upstream // 105	RSC1A1	RSC1A1, Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), p36.13
SNP_A-2276046	gagagaactaaggaca[A/G]atgtaaggttgcttct	A	G	NM_006511 // downstream // 17575 // Hs.239459 // RSC1A1 // 6248 // Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), mRNA. /// ENST00000345034 // downstream // 17575 // — // — // — // — /// ENST00000235432 // upstream //	RSC1A1	RSC1A1, Homo sapiens regulatory solute carrier protein, family 1, member 1 (RSC1A1), p36.13
SNP_A-2247260	ctgtccaacggaagca[A/G]tagagcttttctcatg	A	G	ENST00000235432 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-2093789	agaagaggggctaaga[C/G]ggtacatgatgttatg	C	G	ENST00000235432 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-2113504	aggctaaaggcaatga[A/G]tagctctgccagaaaa	A	G	ENST00000235432 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-2125523	agtttatttgccaagc[G/T]gataaatgtctaaatt	G	T	NM_003443 // intron // 0 // Hs.433764 // ZBTB17 // 7709 // Homo sapiens zinc finger and BTB domain containing 17 (ZBTB17), mRNA. /// ENST00000235455 // intron // 0 // — // — // — // —	ZBTB17	ZBTB17, Homo sapiens zinc finger and BTB domain containing 17 (ZBTB17), p36.13
SNP_A-2174387	cacagaacacgatgta[A/G]gtcttcattggtgggg	A	G	NM_178840 // CDS // 0 // Hs.29190 // MGC24047 // 149563 // Homo sapiens hypothetical protein MGC24047 (MGC24047), mRNA. /// ENST00000329454 // CDS // 0 // — // — // — // —	MGC24047	MGC24047, Homo sapiens hypothetical protein MGC24047 (MGC24047), p36.13
SNP_A-2173463	cacaataaaccccaaa[C/T]ttgcaaggttctgggg	C	T	NM_014424 // intron // 0 // Hs.502612 // HSPB7 // 27129 // Homo sapiens heat shock 27kDa protein family, member 7 (cardiovascular) (HSPB7), mRNA. /// ENST00000311890 // intron // 0 // — // — // — // —	HSPB7	HSPB7, Homo sapiens heat shock 27kDa protein family, member 7 (cardiovascular) (HSPB7), p36.13
SNP_A-2030323	aaagcataggctggaa[A/G]gagtcgaggtgcacag	A	G	NM_014675 // downstream // 274 // Hs.309403 // CROCC // 9696 // Homo sapiens ciliary rootlet coiled-coil, rootletin (CROCC), mRNA. /// NM_002403 // downstream // 1274 // Hs.389137 // MFAP2 // 4237 // Homo sapiens microfibrillar-associated protein 2 (MFAP2	CROCC	CROCC, Homo sapiens ciliary rootlet coiled-coil, rootletin (CROCC), p36.13
SNP_A-2082647	acggccgacaacatca[A/G]ggtctggacggccgca	A	G	NM_007365 // upstream // 44902 // Hs.33455 // PADI2 // 11240 // Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA. /// NM_013358 // upstream // 40789 // Hs.412941 // PADI1 // 29943 // Homo sapiens peptidyl arginine deiminase, type I (PADI1),	PADI2	PADI2, Homo sapiens peptidyl arginine deiminase, type II (PADI2), p36.13
SNP_A-2296337	gcattgttataaaatc[A/G]aaacactgcaaaccac	A	G	NM_016233 // intron // 0 // Hs.149195 // PADI3 // 51702 // Homo sapiens peptidyl arginine deiminase, type III (PADI3), mRNA. /// ENST00000270733 // intron // 0 // — // — // — // —	PADI3	PADI3, Homo sapiens peptidyl arginine deiminase, type III (PADI3), p36.13
SNP_A-2023584	aaaactcttgccttca[A/C]cccagaaaggcgaagc	A	C	NM_012387 // downstream // 4206 // Hs.522969 // PADI4 // 23569 // Homo sapiens peptidyl arginine deiminase, type IV (PADI4), mRNA. /// NM_207421 // upstream // 4040 // Hs.531598 // PADI6 // 353238 // Homo sapiens peptidyl arginine deiminase, type VI (PADI	PADI4	PADI4, Homo sapiens peptidyl arginine deiminase, type IV (PADI4), p36.13
SNP_A-1814818	gtgtgtggttgagatc[A/G]ctgactctgatatcag	A	G	NM_018715 // upstream // 19516 // Hs.380857 // TD-60 // 55920 // Homo sapiens RCC1-like (TD-60), mRNA. /// ENST00000325766 // upstream // 19516 // — // — // — // — /// ENST00000290568 // upstream // 80594 // — // — // — // — /// ENST000001	TD-60	TD-60, Homo sapiens RCC1-like (TD-60), p36.13
SNP_A-2270517	gacagaccgtggacaa[A/G]ttaagtagcttggggc	A	G	ENST00000290568 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-2198998	catttggcaatggcag[G/T]agacactttggttgcc	G	T	ENST00000290568 // intron // 0 // — // — // — // —	-	p36.13
SNP_A-1941268	ttgctgtacctgacat[G/T]aggctagaggtactga	G	T	NM_030812 // upstream // 117944 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000290568 // downstream // 7170 // — // — // — // — /// ENST00000167825 // downstream // 7170 // — // — // — // —	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2170025	caagggagggaaccag[A/C]aaaagcattatcatga	A	C	NM_030812 // upstream // 75135 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000290568 // downstream // 49979 // — // — // — // — /// ENST00000167825 // downstream // 49979 // — // — // — // -	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027433	aaacattgggctggaa[A/G]gaagtgaacccccagt	A	G	NM_030812 // upstream // 58548 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000290568 // downstream // 66566 // --- // --- // --- // --- /// ENST00000167825 // downstream // 66566 // --- // --- // --- // -	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2302259	gctaaattccgactgc[A/C]aagcctttattagtgg	A	C	NM_030812 // downstream // 5943 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000235799 // downstream // 5943 // --- // --- // --- // --- /// ENST00000325482 // downstream // 6523 // --- // --- // --- // --	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2273080	gactatgcaatgacta[C/T]ggtgtttgataaaata	C	T	NM_030812 // downstream // 6581 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000235799 // downstream // 6581 // --- // --- // --- // --- /// ENST00000325482 // downstream // 7161 // --- // --- // --- // --	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2115903	agggtgtttagtagca[A/T]ccctggcctctaccca	A	T	NM_030812 // downstream // 25785 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000235799 // downstream // 25785 // --- // --- // --- // ---- /// ENST00000325482 // downstream // 26365 // --- // --- // --- //	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2188844	cagtggtatgaacaca[A/G]gccctggacatcctac	A	G	NM_030812 // downstream // 51280 // Hs.2149 // LOC81569 // 81569 // Homo sapiens actin like protein (LOC81569), mRNA. /// ENST00000235799 // downstream // 51280 // --- // --- // --- // --- /// ENST00000325482 // downstream // 51860 // --- // --- // --- //	LOC81569	LOC81569, Homo sapiens actin like protein (LOC81569), p36.13
SNP_A-2073690	acagtccaaagtcaaa[C/T]agaaccaatgttgtaa	C	T	ENST00000359853 // downstream // 4840 // --- // --- // --- // ---- /// ENST00000355895 // downstream // 5196 // --- // --- // --- // ----	-	p36.13
SNP_A-2254666	cttgcttaaggccaac[A/G]gataatggattggaat	A	G	NM_032880 // upstream // 40316 // Hs.212511 // MGC15730 // 84966 // Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA. /// ENST00000355895 // upstream // 178629 // --- // --- // --- // ---- /// ENST00000251296 // upstream // 40316 // --- // ---- /	MGC15730	MGC15730, Homo sapiens hypothetical protein MGC15730 (MGC15730), p36.13
SNP_A-2115313	aggggaggccagagaa[C/T]gcttccttcgtctgtt	C	T	NM_152375 // downstream // 14543 // Hs.406913 // FLJ38753 // 127707 // Homo sapiens hypothetical protein FLJ38753 (FLJ38753), mRNA. /// ENST00000325337 // downstream // 14543 // --- // --- // --- // --- /// ENST00000244841 // upstream // 14770 // --- // -	FLJ38753	FLJ38753, Homo sapiens hypothetical protein FLJ38753 (FLJ38753), p36.13
SNP_A-2074620	acatatacacccgcga[A/G]gagctggcgcagagga	A	G	NM_002584 // CDS // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // CDS // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 2, mRNA. /// ENST0	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-1951081	tttccatccagggaaa[C/T]gaacaagctgagtcac	C	T	NM_002584 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 2, mRNA. ///	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-2075652	acatggagctggaatc[C/T]acatctaggtatttgg	C	T	NM_002584 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 2, mRNA. ///	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-1951298	tttccctctctgtaaa[C/T]gggcagctcatacgag	C	T	NM_002584 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 2, mRNA. ///	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1952590	ttctgcctgtggtca[C/T]tactcctaagagcctg	C	T	NM_002584 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA. /// NM_013945 // intron // 0 // Hs.113253 // PAX7 // 5081 // Homo sapiens paired box gene 7 (PAX7), transcript variant 2, mRNA. ///	PAX7	PAX7, Homo sapiens paired box gene 7 (PAX7), transcript variant 1, p36.13
SNP_A-2049994	aaggaaggctcggga[C/G]tagggcacagtctgt	C	G	NM_020765 // downstream // 635 // Hs.148078 // RBAF600 // 23352 // Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000304963 // upstream // 157170 // --- // --- // --- /// ENST00000355609 // upstream // 117970 // --- //	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1786206	ggctggtctttaatccc[C/T]gaactgaatcattgga	C	T	NM_020765 // intron // 0 // Hs.148078 // RBAF600 // 23352 // Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- // --- // --- // ---	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-2208638	cccactgtggaaaacaa[G/T]gatggtcatataggga	G	T	NM_020765 // intron // 0 // Hs.148078 // RBAF600 // 23352 // Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- // --- // --- // ---	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-2254743	cttggaaagataaacc[C/T]aggctatttagagag	C	T	NM_020765 // intron // 0 // Hs.148078 // RBAF600 // 23352 // Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- // --- // --- // ---	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-2164834	caaaccatgtaattcc[A/C]aaagaaaggctgaga	A	C	NM_020765 // intron // 0 // Hs.148078 // RBAF600 // 23352 // Homo sapiens retinoblastoma-associated factor 600 (RBAF600), mRNA. /// ENST00000248008 // intron // 0 // --- // --- // --- // ---	RBAF600	RBAF600, Homo sapiens retinoblastoma-associated factor 600 (RBAF600), p36.13
SNP_A-1942629	ttggacattcgtgag[C/T]aaccaaatgccaggct	C	T	NM_012067 // CDS // 0 // Hs.6980 // AKR7A3 // 22977 // Homo sapiens aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase) (AKR7A3), mRNA. /// ENST00000062030 // CDS // 0 // --- // --- // --- // ---	AKR7A3	AKR7A3, Homo sapiens aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase) (AKR7A3), p36.13
SNP_A-2123870	agttaacatataggaccc[A/G]gaaattctactcctag	A	G	NM_017765 // intron // 0 // Hs.523036 // PQLC2 // 54896 // Homo sapiens PQ loop repeat containing 2 (PQLC2), mRNA. /// ENST00000234646 // intron // 0 // --- // --- // ---	PQLC2	PQLC2, Homo sapiens PQ loop repeat containing 2 (PQLC2), p36.13
SNP_A-2079529	accctctgctcactca[C/T]gccttggctccagcca	C	T	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// U03271 // intron // 0 // Hs.432760 // CAPZB // 832 // Human F-actin capping protein beta subunit mRNA, complete c	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-2257983	cttgtctttctgc[C/T]gactgactgggcgagt	C	T	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// U03271 // intron // 0 // Hs.432760 // CAPZB // 832 // Human F-actin capping protein beta subunit mRNA, complete c	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-1842478	taggtgctgagcaacc[C/T]gaagagaagatgacag	C	T	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// U03271 // intron // 0 // Hs.432760 // CAPZB // 832 // Human F-actin capping protein beta subunit mRNA, complete c	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-2137126	atcaggcagaaaccca[C/G]ctgctcctgctcagtc	C	G	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// U03271 // intron // 0 // Hs.432760 // CAPZB // 832 // Human F-actin capping protein beta subunit mRNA, complete c	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2237517	ctctcgggaatgtaaa[C/T]gagtgaaggtcttgat	C	T	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // — // — // — // —	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-1897118	tgctcctgtcttccaa[A/G]taacagttaaaagaaa	A	G	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // — // — // — // —	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-2192315	catcagttgggattca[G/T]tcttacatgttgtaaa	G	T	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // — // — // — // —	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-2282993	gataacttccaagaga[C/T]gtgttgcttcctgtcc	C	T	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // — // — // — // —	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-2154725	attcaaataggggata[A/C]acgtaacaataagcag	A	C	NM_004930 // intron // 0 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// ENST00000264203 // intron // 0 // — // — // — // —	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-1857001	tcaccattgccatgag[C/T]atccctttagcaagcg	C	T	NM_004930 // upstream // 60783 // Hs.432760 // CAPZB // 832 // Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /// U03271 // upstream // 126546 // Hs.432760 // CAPZB // 832 // Human F-actin capping protein beta subunit mRN	CAPZB	CAPZB, Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), p36.13
SNP_A-2184139	cagccgcttcttacaa[A/C]tcccaagaggccaaag	A	C	ENST00000304491 // 3UTR // 0 // — // — // — // —	-	p36.13
SNP_A-1788390	gggagtaagaggtgga[A/G]gaaggtgagattctag	A	G	ENST00000289815 // intron // 0 // — // — // — // —	-	p36.12
SNP_A-1892008	tgcaaaacccagaaat[A/G]accagcctggcattgt	A	G	ENST00000289815 // intron // 0 // — // — // — // —	-	p36.12
SNP_A-1921149	ttacataccacagact[A/G]aacatcattcaatctc	A	G	NM_024544 // intron // 0 // Hs.10101 // FLJ12875 // 79594 // Homo sapiens hypothetical protein FLJ12875 (FLJ12875), mRNA. /// ENST00000264198 // intron // 0 // — // — // — // —	FLJ12875	FLJ12875, Homo sapiens hypothetical protein FLJ12875 (FLJ12875), p36.12
SNP_A-2268514	gaatgggagtgagcag[A/G]acccagtctgatttta	A	G	NM_207334 // downstream // 8649 // Hs.429179 // FAM43B // 163933 // Homo sapiens family with sequence similarity 43, member B (FAM43B), mRNA. /// NM_001785 // upstream // 25380 // Hs.466910 // CDA // 978 // Homo sapiens cytidine deaminase (CDA), mRNA. ///	FAM43B	FAM43B, Homo sapiens family with sequence similarity 43, member B (FAM43B), p36.12
SNP_A-2114132	agggaaagaaccccaa[C/T]tgctcaatgagtgtct	C	T	NM_207334 // downstream // 29904 // Hs.429179 // FAM43B // 163933 // Homo sapiens family with sequence similarity 43, member B (FAM43B), mRNA. /// NM_001785 // upstream // 4125 // Hs.466910 // CDA // 978 // Homo sapiens cytidine deaminase (CDA), mRNA. ///	FAM43B	FAM43B, Homo sapiens family with sequence similarity 43, member B (FAM43B), p36.12
SNP_A-1817070	gttcaaaacagcctaa[A/G]agaccatactgaacac	A	G	NM_016287 // intron // 0 // Hs.142442 // HP1-BP74 // 50809 // Homo sapiens HP1-BP74 (HP1-BP74), mRNA. /// ENST00000360142 // intron // 0 // — // — // — // — /// ENST00000312239 // intron // 0 // — // — // — // — // —	HP1-BP74	HP1-BP74, Homo sapiens HP1-BP74 (HP1-BP74), p36.12
SNP_A-2063476	aattaataaggagaac[A/G]agaacagccaacatta	A	G	NM_001397 // upstream // 79529 // Hs.195080 // ECE1 // 1889 // Homo sapiens endothelin converting enzyme 1 (ECE1), mRNA. /// ENST00000357071 // upstream // 79745 // — // — // — // — /// ENST00000264205 // upstream // 79529 // — // — // — // —	ECE1	ECE1, Homo sapiens endothelin converting enzyme 1 (ECE1), p36.12
SNP_A-1842330	taggtagtagtaggta[C/T]agtcagacaagaacag	C	T	NM_001397 // upstream // 94824 // Hs.195080 // ECE1 // 1889 // Homo sapiens endothelin converting enzyme 1 (ECE1), mRNA. /// ENST00000357071 // upstream // 95040 // — // — // — // — /// ENST00000264205 // upstream // 94824 // — // — // — // —	ECE1	ECE1, Homo sapiens endothelin converting enzyme 1 (ECE1), p36.12
SNP_A-2049557	aagctgttgagaggaa[A/C]cctgcttatctctgat	A	C	NM_000478 // intron // 0 // Hs.75431 // ALPL // 249 // Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. /// ENST00000344573 // intron // 0 // — // — // — // —	ALPL	ALPL, Homo sapiens alkaline phosphatase, liver p36.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102609	agattgtcctgacaac[A/G]gtatttcccttggttg	A	G	NM_032236 // intron // 0 // Hs.467524 // USP48 // 84196 // Homo sapiens ubiquitin specific protease 48 (USP48), mRNA. /// ENST00000308271 // intron // 0 // --- // --- // --- // --- /// ENST00000264206 // intron // 0 // --- // --- // --- // ---	USP48	USP48, Homo sapiens ubiquitin specific protease 48 (USP48), p36.12
SNP_A-1785992	ggctgccatccagctg[C/T]aaatgcactagcactg	C	T	NM_005529 // intron // 0 // Hs.467545 // HSPG2 // 3339 // Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA. /// ENST00000270945 // intron // 0 // --- // --- // --- // ---	HSPG2	HSPG2, Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), p36.12
SNP_A-2297900	gccagtcagccaggag[A/G]aatacggacgccccca	A	G	NM_005529 // upstream // 6014 // Hs.467545 // HSPG2 // 3339 // Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA. /// ENST00000344642 // downstream // 77122 // --- // --- // --- // --- /// ENST00000270945 // upstream // 6014 // --- // -	HSPG2	HSPG2, Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), p36.12
SNP_A-1795087	ggtgacagtcccaacc[A/G]gcctagaaagatgaat	A	G	NM_001791 // intron // 0 // Hs.467637 // CDC42 // 998 // Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// ENST00000337517 // intron // 0 // --- // --- // --- // ---	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2146741	atgcttcaagacataa[A/G]ctggatcatgttctcc	A	G	NM_001791 // intron // 0 // Hs.467637 // CDC42 // 998 // Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// ENST00000337517 // intron // 0 // --- // --- // --- // --- /// ENST00000358096 // intron //	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2151483	atgttctacaggttga[C/T]gattgggaggtatagc	C	T	NM_001791 // intron // 0 // Hs.467637 // CDC42 // 998 // Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA. /// ENST00000337517 // intron // 0 // --- // --- // --- // ---	CDC42	CDC42, Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, p36.12
SNP_A-2285252	gatctctacaatggga[A/C]ctgtgacctcattcaa	A	C	NM_030761 // upstream // 16420 // Hs.302428 // WNT4 // 54361 // Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), mRNA. /// ENST00000290167 // upstream // 16420 // --- // --- // --- // --- /// ENST00000354898 // downstream // 16347	WNT4	WNT4, Homo sapiens wingless-type MMTV integration site family, member 4 (WNT4), p36.12
SNP_A-1818844	gttgagtaagctctag[C/T]agttgccagcagtttt	C	T	NM_014870 // upstream // 47081 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000354898 // upstream // 81412 // --- // --- // --- // --- /// ENST00000315432 // upstream // 47081 // --- // --- // --- // -	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2070502	acaccgtacatttaac[A/G]cagggctttcgtatcc	A	G	NM_014870 // upstream // 45601 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000354898 // upstream // 82892 // --- // --- // --- // --- /// ENST00000315432 // upstream // 45601 // --- // --- // --- // -	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2296730	gccaaatgactcagaa[A/G]ggtcaactgcctgcct	A	G	NM_014870 // upstream // 4084 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000354898 // upstream // 124409 // --- // --- // --- // --- /// ENST00000315432 // upstream // 4084 // --- // --- // --- // –	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2175725	cacattatccagatga[C/T]ggctttggaaggcaga	C	T	NM_014870 // intron // 0 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-1986940	cttaaagcctttcaaa[C/T]gcctcaatggctgctc	C	T	NM_014870 // intron // 0 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-1792137	gggtgttggccacaga[A/G]ggatatataggccatg	A	G	NM_014870 // intron // 0 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-2077347	accacaagaaccatcc[A/G]ctccttgcatttggca	A	G	NM_014870 // intron // 0 // Hs.528723 // KIAA0478 // 9923 // Homo sapiens KIAA0478 gene product (KIAA0478), mRNA. /// ENST00000315432 // intron // 0 // --- // --- // --- // ---	KIAA0478	KIAA0478, Homo sapiens KIAA0478 gene product (KIAA0478), p36.12
SNP_A-1811651	gtgctggcaacacaga[A/G]agagagtgagctatgt	A	G	NM_020526 // intron // 0 // Hs.283613 // EPHA8 // 2046 // Homo sapiens EphA8 (EPHA8), mRNA. /// ENST00000166244 // intron // 0 // --- // --- // --- // ---	EPHA8	EPHA8, Homo sapiens EphA8 (EPHA8), p36.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308314	gcttggttagcgtgca[A/G]gttaaatggaatgcgc	A	G	NM_004442 // downstream // 58824 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // downstream // 58824 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 1, mRNA. /// NM_	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-1854058	tcaaacatgggactca[C/T]caaatataaagcatgcc	C	T	NM_004442 // downstream // 67472 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // downstream // 67472 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 1, mRNA. /// NM_	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-2306194	gctggcaagtaataca[C/T]ctccatgagcaccag	C	T	NM_004442 // downstream // 70943 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // downstream // 70943 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 1, mRNA. /// NM_	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-1913373	tgtgggtgtgagagtc[C/T]acagggaacttagtt	C	T	NM_004442 // downstream // 97902 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA. /// NM_017449 // downstream // 97902 // Hs.523329 // EPHB2 // 2048 // Homo sapiens EphB2 (EPHB2), transcript variant 1, mRNA. /// NM_	EPHB2	EPHB2, Homo sapiens EphB2 (EPHB2), transcript variant 2, p36.12
SNP_A-2163486	caaaaaacacctggag[C/T]attgtagcacagtgc	C	T	NM_033631 // upstream // 69172 // Hs.454808 // LUZP1 // 7798 // Homo sapiens leucine zipper protein 1 (LUZP1), mRNA. /// NM_000864 // downstream // 14784 // Hs.121482 // HTR1D // 3352 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), mR	LUZP1	LUZP1, Homo sapiens leucine zipper protein 1 (LUZP1), p36.12
SNP_A-1850643	tattacaaatcctaaa[C/T]gcgaggcactgtgttg	C	T	NM_000864 // upstream // 18298 // Hs.121482 // HTR1D // 3352 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), mRNA. /// NM_005826 // downstream // 97267 // Hs.373763 // HNRPR // 10236 // Homo sapiens heterogeneous nuclear ribonucleopro	HTR1D	HTR1D, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), p36.12
SNP_A-1786361	ggctgttgttgttta[A/G]gttgctgtattccatc	A	G	NM_000864 // upstream // 69939 // Hs.121482 // HTR1D // 3352 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), mRNA. /// NM_005826 // downstream // 45626 // Hs.373763 // HNRPR // 10236 // Homo sapiens heterogeneous nuclear ribonucleopro	HTR1D	HTR1D, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), p36.12
SNP_A-1898138	tgctgttatacttta[C/T]ccgttcatttgtggct	C	T	NM_005826 // intron // 0 // Hs.373763 // HNRPR // 10236 // Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA. /// ENST00000302271 // intron // 0 // — // — // — // —	HNRPR	HNRPR, Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), p36.12
SNP_A-2205892	ccataggatcttcaac[C/G]accctccattcttcca	C	G	NM_030634 // upstream // 7183 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_030634 // upstream // 8287 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_138479 /	ZNF436	ZNF436, Homo sapiens zinc finger protein 436 (ZNF436), p36.12
SNP_A-2166572	caaatggtgtatcaac[A/T]gttctgcacgtgtgac	A	T	NM_030634 // upstream // 11466 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_030634 // upstream // 12570 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_138479	ZNF436	ZNF436, Homo sapiens zinc finger protein 436 (ZNF436), p36.12
SNP_A-2285512	gatctttgtaacaga[C/T]ctctctctctgcct	C	T	NM_030634 // upstream // 15441 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_030634 // upstream // 16545 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_138479	ZNF436	ZNF436, Homo sapiens zinc finger protein 436 (ZNF436), p36.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170912	caataagaagaatcag[A/T]ctcatggcggctgaag	A	T	NM_030634 // upstream // 16593 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_030634 // upstream // 17697 // Hs.293798 // ZNF436 // 80818 // Homo sapiens zinc finger protein 436 (ZNF436), mRNA. /// NM_138479	ZNF436	ZNF436, Homo sapiens zinc finger protein 436 (ZNF436), p36.12
SNP_A-1906192	tggtgaattattacca[A/C]atattgattgaagcag	A	C	NM_173065 // upstream // 92808 // Hs.221375 // IL28RA // 163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 92808 // Hs.221375 // IL28RA // 163702 // Homo	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-2112044	aggatgctggaatccc[A/G]gaattgccttcccagt	A	G	NM_173065 // upstream // 96833 // Hs.221375 // IL28RA // 163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 96833 // Hs.221375 // IL28RA // 163702 // Homo	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-2150341	atgtctgtttgccttc[C/G]ctaccacataaagact	C	G	NM_173065 // upstream // 118539 // Hs.221375 // IL28RA // 163702 // Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, mRNA. /// NM_170743 // upstream // 118539 // Hs.221375 // IL28RA // 163702 // Hom	IL28RA	IL28RA, Homo sapiens interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 3, p36.11
SNP_A-1990582	ctagaccagggagtgt[C/T]aaatgaaagaggttca	C	T	NM_178122 // intron // 0 // Hs.403187 // LOC90529 // 90529 // Homo sapiens hypothetical protein LOC90529 (LOC90529), mRNA. /// ENST00000337248 // intron // 0 // — // — // — /// ENST00000003583 // intron // 0 // — // — // —	LOC90529	LOC90529, Homo sapiens hypothetical protein LOC90529 (LOC90529), p36.11
SNP_A-2304689	gctctgcattggctaa[C/T]agatatgtatgtgggtc	C	T	NM_020448 // intron // 0 // Hs.523442 // DJ462O23.2 // 57185 // Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA. /// ENST00000358028 // intron // 0 // — // — // — /// ENST00000003912 // intron // 0 // — // — // —	DJ462O23.2	DJ462O23.2, Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), p36.11
SNP_A-2136325	atcacacacccagagaa[C/T]gacagagctggcccaa	C	T	NM_020448 // intron // 0 // Hs.523442 // DJ462O23.2 // 57185 // Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA. /// ENST00000358028 // intron // 0 // — // — // — /// ENST00000003912 // intron // 0 // — // — // —	DJ462O23.2	DJ462O23.2, Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), p36.11
SNP_A-1990698	attccatctcgtttc[A/G]atattcagagtctaca	A	G	NM_020448 // intron // 0 // Hs.523442 // DJ462O23.2 // 57185 // Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA. /// ENST00000358028 // intron // 0 // — // — // — /// ENST00000003912 // intron // 0 // — // — // —	DJ462O23.2	DJ462O23.2, Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), p36.11
SNP_A-2233813	ctcatcggctgagtca[A/G]aatcagttccagctc	A	G	NM_020448 // intron // 0 // Hs.523442 // DJ462O23.2 // 57185 // Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA. /// ENST00000358028 // intron // 0 // — // — // — /// ENST00000003912 // intron // 0 // — // — // —	DJ462O23.2	DJ462O23.2, Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), p36.11
SNP_A-2200554	ccaactgaaatcacta[C/T]ggatagcgtccttaa	C	T	NM_020448 // intron // 0 // Hs.523442 // DJ462O23.2 // 57185 // Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA. /// ENST00000358028 // intron // 0 // — // — // — /// ENST00000003912 // intron // 0 // — // — // —	DJ462O23.2	DJ462O23.2, Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), p36.11
SNP_A-1991336	ctggtgttggttccac[A/G]agaggctcagggacac	A	G	NM_013943 // downstream // 23541 // Hs.440544 // CLIC4 // 25932 // Homo sapiens chloride intracellular channel 4 (CLIC4), mRNA. /// NM_004350 // downstream // 31759 // Hs.170019 // RUNX3 // 864 // Homo sapiens runt-related transcription factor 3 (RUNX3).	CLIC4	CLIC4, Homo sapiens chloride intracellular channel 4 (CLIC4), p36.11
SNP_A-2131563	atagcagctttttca[C/T]gctgccaaaagaagaa	C	T	NM_013943 // downstream // 36871 // Hs.440544 // CLIC4 // 25932 // Homo sapiens chloride intracellular channel 4 (CLIC4), mRNA. /// NM_004350 // downstream // 18429 // Hs.170019 // RUNX3 // 864 // Homo sapiens runt-related transcription factor 3 (RUNX3).	CLIC4	CLIC4, Homo sapiens chloride intracellular channel 4 (CLIC4), p36.11
SNP_A-2184348	cagcgaccacagaaca[C/T]gaaaccaagcatgagg	C	T	ENST00000338888 // intron // 0 // — // — // — /// ENST00000308873 // intron // 0 // — // — // —	-	p36.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169223	caagatttgaactcag[A/G]catcccaacacgcaga	A	G	NM_004350 // upstream // 107144 // Hs.170019 // RUNX3 // 864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 185660 // Hs.20013 // P29 // 25949 // Homo sapiens GCIP-interacting protein p29 (P29), transcrip	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2189659	cagttttatgtaccac[G/T]cagaaagacaccgcca	G	T	NM_004350 // upstream // 120798 // Hs.170019 // RUNX3 // 864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 172006 // Hs.20013 // P29 // 25949 // Homo sapiens GCIP-interacting protein p29 (P29), transcrip	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-1991848	cttgggcctcaactca[A/C]tcacatgtgaagtc	A	C	NM_004350 // upstream // 152065 // Hs.170019 // RUNX3 // 864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 140739 // Hs.20013 // P29 // 25949 // Homo sapiens GCIP-interacting protein p29 (P29), transcrip	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2170063	caagggctcttccgcca[G/T]gggtatggtcacaggg	G	T	NM_004350 // upstream // 185356 // Hs.170019 // RUNX3 // 864 // Homo sapiens runt-related transcription factor 3 (RUNX3), mRNA. /// NM_015484 // downstream // 107448 // Hs.20013 // P29 // 25949 // Homo sapiens GCIP-interacting protein p29 (P29), transcrip	RUNX3	RUNX3, Homo sapiens runt-related transcription factor 3 (RUNX3), p36.11
SNP_A-2115093	agggctcaatccgcata[A/G]taagttctccatccat	A	G	NM_015627 // downstream // 46091 // Hs.184482 // ARH // 26119 // Homo sapiens LDL receptor adaptor protein (ARH), mRNA. /// NM_020379 // upstream // 4385 // Hs.197043 // MAN1C1 // 57134 // Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), mRNA	ARH	ARH, Homo sapiens LDL receptor adaptor protein (ARH), p36.11
SNP_A-2219947	ccttatcacaatctac[A/C]ctgaaataatacatca	A	C	NM_020379 // intron // 0 // Hs.197043 // MAN1C1 // 57134 // Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), mRNA. /// ENST00000307112 // intron // 0 // — // — // —	MAN1C1	MAN1C1, Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), p36.11
SNP_A-1956086	tttgtgagctctggaa[C/T]tcgaagtcgacttgcc	C	T	NM_020379 // intron // 0 // Hs.197043 // MAN1C1 // 57134 // Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), mRNA. /// ENST00000307112 // intron // 0 // — // — // —	MAN1C1	MAN1C1, Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), p36.11
SNP_A-1854732	tcaacatagcacatca[A/G]tacaacaatggctcat	A	G	NM_020379 // intron // 0 // Hs.197043 // MAN1C1 // 57134 // Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), mRNA. /// ENST00000307112 // intron // 0 // — // — // —	MAN1C1	MAN1C1, Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), p36.11
SNP_A-2226539	ctaagcttgtggccat[C/G]ataaggcaggaacct	C	G	NM_206926 // intron // 0 // Hs.429353 // SEPN1 // 57190 // Homo sapiens selenoprotein N, 1 (SEPN1), transcript variant 2, mRNA. /// ENST00000354177 // intron // 0 // — // — // —	SEPN1	SEPN1, Homo sapiens selenoprotein N, 1 (SEPN1), transcript variant 2, p36.11
SNP_A-1839188	tagaggaaggtctacc[A/G]aaatgaggcagaaatc	A	G	NM_004455 // downstream // 669 // Hs.150956 // EXTL1 // 2134 // Homo sapiens exostoses (multiple)-like 1 (EXTL1), mRNA. /// NM_032513 // downstream // 917 // Hs.143545 // SLC30A2 // 7780 // Homo sapiens solute carrier family 30 (zinc transporter), member	EXTL1	EXTL1, Homo sapiens exostoses (multiple)-like 1 (EXTL1), p36.11
SNP_A-2212290	ccctggctatgacaa[A/G]gagttgtgactccctc	A	G	NM_005248 // downstream // 7113 // Hs.1422 // FGR // 2268 // Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA. /// ENST00000247087 // upstream // 55523 // — // — // — // — /// ENST00000001380 // downstream //	FGR	FGR, Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), p36.11
SNP_A-1786559	ggctccctgaggaga[C/T]ggcacttcaattgaag	C	T	NM_005248 // upstream // 3089 // Hs.1422 // FGR // 2268 // Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA. /// NM_015933 // upstream // 11155 // Hs.546394 // HSPC016 // 51372 // Homo sapiens hypothetical protein HSP	FGR	FGR, Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), p36.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2050545	aaggatgtattaacaa[A/G]gtgttcactgctgtgg	A	G	NM_017638 // downstream // 27701 // Hs.479911 // MED18 // 54797 // Homo sapiens TRAP/mediator complex subunit p28b (FLJ20045). mRNA. /// NM_001269 // upstream // 278871 // Hs.469723 // CHC1 // 1104 // Homo sapiens chromosome condensation 1 (CHC1), mRNA. /	MED18	MED18, Homo sapiens TRAP.p35.3
SNP_A-2253994	cttgagaagaaaaaca[A/G]aacaaggcgagtcaca	A	G	NM_133178 // downstream // 162334 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 162334 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-2061355	aatgcccagcagtaca[C/T]acagtctctgttcagt	C	T	NM_133178 // downstream // 304648 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 304648 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.3
SNP_A-2093991	agaagctaagaaaaggg[A/G]cataaattagcaagtg	A	G	NM_133178 // downstream // 727756 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 727756 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-2080968	acctcttagtaacagc[A/G]ccacaaggtcacattt	A	G	NM_133178 // downstream // 930818 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 930818 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1781382	ggatgttgcttgttga[A/G]aaatgttgttacaaac	A	G	NM_133178 // downstream // 1195244 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1195244 // Hs.19718 // PTPRU // 10076 // Homo sapiens prote	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1842387	taggtcaggttctgtc[A/G]agtgaccagcagaagc	A	G	NM_133178 // downstream // 1237082 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1237082 // Hs.19718 // PTPRU // 10076 // Homo sapiens prote	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1803060	gtattagcaacatcac[A/G]gacattttcttattta	A	G	NM_133178 // downstream // 1237139 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1237139 // Hs.19718 // PTPRU // 10076 // Homo sapiens prote	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1999832	tgggctctgaaggaa[C/T]gcaggaatggtgaaga	C	T	NM_133178 // downstream // 1238791 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1238791 // Hs.19718 // PTPRU // 10076 // Homo sapiens prote	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-2037183	aacaaacaaaaaactga[G/T]ctctctttagattcag	G	T	NM_133178 // downstream // 1308308 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1308308 // Hs.19718 // PTPRU // 10076 // Homo sapiens prote	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2
SNP_A-1999915	tcggttctgttctaaa[C/T]gctagggatgcaaaag	C	T	NM_133178 // downstream // 1308398 // Hs.19718 // PTPRU // 10076 // Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, mRNA. /// NM_133177 // downstream // 1308398 // Hs.19718 // PTPRU // 10076 // Homo sapiens prote	PTPRU	PTPRU, Homo sapiens protein tyrosine phosphatase, receptor type, U (PTPRU), transcript variant 1, p35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1930995	ttccagtctgacatct[A/G]agagcaagcattgtga	A	G	NM_006762 // upstream // 59480 // Hs.371021 // LAPTM5 // 7805 // Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA. /// AB007937 // downstream // 52167 // Hs.158287 // SDC3 // 9672 // Homo sapiens mRNA for KIAA0468 protein,	LAPTM5	LAPTM5, Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), p35.2
SNP_A-2218066	cctgcccattttcaag[G/T]ctctggccaagtctag	G	T	NM_006762 // upstream // 106750 // Hs.371021 // LAPTM5 // 7805 // Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA. /// AB007937 // downstream // 4897 // Hs.158287 // SDC3 // 9672 // Homo sapiens mRNA for KIAA0468 protein,	LAPTM5	LAPTM5, Homo sapiens Lysosomal-associated multispanning membrane protein-5 (LAPTM5), p35.2
SNP_A-1786660	ggcttgcctgctaacc[A/G]aaacttaccacttccg	A	G	NM_024522 // upstream // 33103 // Hs.470259 // FLJ12650 // 79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 38314 // Hs.33962 // HPRP8BP // 9410 // Homo sapiens U5 snRNP-specific 40 kDa protein (hPrp8-bi	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2041225	aacctcctcattctac[A/G]cactatctccatgagt	A	G	NM_024522 // upstream // 43333 // Hs.470259 // FLJ12650 // 79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 28084 // Hs.33962 // HPRP8BP // 9410 // Homo sapiens U5 snRNP-specific 40 kDa protein (hPrp8-bi	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2165958	caaagtttaaattctg[C/G]agcatttaggattttg	C	G	NM_024522 // upstream // 69086 // Hs.470259 // FLJ12650 // 79570 // Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA. /// NM_004814 // downstream // 2331 // Hs.33962 // HPRP8BP // 9410 // Homo sapiens U5 snRNP-specific 40 kDa protein (hPrp8-bin	FLJ12650	FLJ12650, Homo sapiens hypothetical protein FLJ12650 (FLJ12650), p35.2
SNP_A-2232455	ctcacagttagcaaca[C/T]tggtataagaccccag	C	T	NM_016505 // intron // 0 // Hs.524094 // PS1D // 51538 // Homo sapiens putative S1 RNA binding domain protein (PS1D), mRNA. /// ENST00000263699 // intron // 0 // — // — // — // — /// ENST00000344147 // intron // 0 // — // — // — // —	PS1D	PS1D, Homo sapiens putative S1 RNA binding domain protein (PS1D), p35.2
SNP_A-1929512	ttcataacataacacc[A/G]attcagaaagacctac	A	G	NM_016505 // intron // 0 // Hs.524094 // PS1D // 51538 // Homo sapiens putative S1 RNA binding domain protein (PS1D), mRNA. /// ENST00000263699 // intron // 0 // — // — // — // — /// ENST00000344147 // intron // 0 // — // — // — // —	PS1D	PS1D, Homo sapiens putative S1 RNA binding domain protein (PS1D), p35.2
SNP_A-2000252	agtctgtagagtcaaa[A/C]ttcatgagttattatt	A	C	NM_016505 // intron // 0 // Hs.524094 // PS1D // 51538 // Homo sapiens putative S1 RNA binding domain protein (PS1D), mRNA. /// ENST00000263699 // intron // 0 // — // — // — // — /// ENST00000344147 // intron // 0 // — // — // — // —	PS1D	PS1D, Homo sapiens putative S1 RNA binding domain protein (PS1D), p35.2
SNP_A-2311560	ggaatgcaatacacaa[A/G]ttaagtcacactgcag	A	G	NM_016505 // 3UTR // 0 // Hs.524094 // PS1D // 51538 // Homo sapiens putative S1 RNA binding domain protein (PS1D), mRNA. /// ENST00000263699 // 3UTR // 0 // — // — // — // — /// ENST00000344147 // 3UTR // 0 // — // — // — // —	PS1D	PS1D, Homo sapiens putative S1 RNA binding domain protein (PS1D), p35.2
SNP_A-2000268	ccagactcctggatga[C/T]gagcaaggtcttctcc	C	T	NM_004102 // upstream // 9551 // Hs.112669 // FABP3 // 2170 // Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), mRNA. /// NM_178865 // upstream // 30489 // Hs.270655 // TDE2L // 347735 // Homo sapiens	FABP3	FABP3, Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), p35.2
SNP_A-2086435	actcttggttttctac[A/G]ctacctttgacaacca	A	G	NM_004102 // upstream // 12978 // Hs.112669 // FABP3 // 2170 // Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), mRNA. /// NM_178865 // upstream // 27062 // Hs.270655 // TDE2L // 347735 // Homo sapien	FABP3	FABP3, Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), p35.2
SNP_A-2043532	aactgtctcaggctaa[C/T]ggaaagaaaaatcagg	C	T	NM_004102 // upstream // 17635 // Hs.112669 // FABP3 // 2170 // Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), mRNA. /// NM_178865 // upstream // 22405 // Hs.270655 // TDE2L // 347735 // Homo sapien	FABP3	FABP3, Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), p35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2143386	atgaccataaaaccaa[C/T]acatttaggagatttg	C	T	NM_004102 // upstream // 17740 // Hs.112669 // FABP3 // 2170 // Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), mRNA. /// NM_178865 // upstream // 22300 // Hs.270655 // TDE2L // 347735 // Homo sapien	FABP3	FABP3, Homo sapiens fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), p35.2
SNP_A-2123191	agtggttgaaggggac[A/G]cattagaagctacttc	A	G	NM_178865 // downstream // 68436 // Hs.270655 // TDE2L // 347735 // Homo sapiens tumor differentially expressed 2-like (TDE2L), mRNA. /// NM_022164 // upstream // 66153 // Hs.199368 // LCN7 // 64129 // Homo sapiens lipocalin 7 (LCN7), mRNA. /// NM_022164	TDE2L	TDE2L, Homo sapiens tumor differentially expressed 2-like (TDE2L), p35.2
SNP_A-2186144	caggccccaggaacac[A/G]aaacctgacaaacagg	A	G	NM_001856 // intron // 0 // Hs.368921 // COL16A1 // 1307 // Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA. /// ENST00000271069 // intron // 0 // — // — // — // —	COL16A1	COL16A1, Homo sapiens collagen, type XVI, alpha 1 (COL16A1), p35.2
SNP_A-1865075	tccagtgcccaccaaa[C/T]gcggacacgtgagaga	C	T	NM_001703 // intron // 0 // Hs.524138 // BAI2 // 576 // Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), mRNA. /// ENST00000257070 // intron // 0 // — // — // — // —	BAI2	BAI2, Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), p35.2
SNP_A-1887389	tgagaattcagtgaaa[A/C]cagagatgtggactgt	A	C	NM_001703 // intron // 0 // Hs.524138 // BAI2 // 576 // Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), mRNA. /// ENST00000257070 // intron // 0 // — // — // — // —	BAI2	BAI2, Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), p35.2
SNP_A-2279309	gaggagcagtgggaac[A/G]aagaagaggtttccag	A	G	NM_001703 // upstream // 11697 // Hs.524138 // BAI2 // 576 // Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), mRNA. /// NM_144569 // downstream // 14692 // Hs.62604 // SPOCD1 // 90853 // Homo sapiens SPOC domain containing 1 (SPOCD1), mRNA. /	BAI2	BAI2, Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), p35.2
SNP_A-1792958	ggtacagaacaagtga[C/T]gtcatttaatcctgct	C	T	NM_144569 // intron // 0 // Hs.62604 // SPOCD1 // 90853 // Homo sapiens SPOC domain containing 1 (SPOCD1), mRNA. /// ENST00000360482 // intron // 0 // — // — // — // — /// ENST00000257100 // intron // 0 // — // — // — // — /// ENST00000319	SPOCD1	SPOCD1, Homo sapiens SPOC domain containing 1 (SPOCD1), p35.2
SNP_A-2273675	gactgcaatgtgatgg[A/G]attgtgtatgtattta	A	G	NM_144569 // upstream // 18550 // Hs.62604 // SPOCD1 // 90853 // Homo sapiens SPOC domain containing 1 (SPOCD1), mRNA. /// NM_080392 // downstream // 71892 // Hs.470477 // PTP4A2 // 8073 // Homo sapiens protein tyrosine phosphatase type IVA, member 2 (PTP	SPOCD1	SPOCD1, Homo sapiens SPOC domain containing 1 (SPOCD1), p35.2
SNP_A-2206650	ccatgacctcaagtca[A/G]acaaggccacaaggct	A	G	NM_144569 // upstream // 39376 // Hs.62604 // SPOCD1 // 90853 // Homo sapiens SPOC domain containing 1 (SPOCD1), mRNA. /// NM_080392 // downstream // 51066 // Hs.470477 // PTP4A2 // 8073 // Homo sapiens protein tyrosine phosphatase type IVA, member 2 (PTP	SPOCD1	SPOCD1, Homo sapiens SPOC domain containing 1 (SPOCD1), p35.2
SNP_A-2262406	gaaatgcgactataac[G/T]agaactcagctggctt	G	T	NM_018045 // upstream // 33526 // Hs.353454 // FLJ10276 // 55108 // Homo sapiens hypothetical protein FLJ10276 (FLJ10276), mRNA. /// NM_144621 // upstream // 42673 // Hs.546479 // ZBTB8 // 127557 // Homo sapiens zinc finger and BTB domain containing 8 (ZB	FLJ10276	FLJ10276, Homo sapiens hypothetical protein FLJ10276 (FLJ10276), p35.1
SNP_A-2064882	aattgaatggtgtaag[C/G]ctccttctaactcaaa	C	G	NM_003680 // intron // 0 // Hs.213264 // YARS // 8565 // Homo sapiens tyrosyl-tRNA synthetase (YARS), mRNA. /// ENST00000257116 // intron // 0 // — // — // — // —	YARS	YARS, Homo sapiens tyrosyl-tRNA synthetase (YARS), p35.1
SNP_A-2047615	aagatgtcacattact[G/T]agcctttaaaacctga	G	T	NM_003680 // intron // 0 // Hs.213264 // YARS // 8565 // Homo sapiens tyrosyl-tRNA synthetase (YARS), mRNA. /// ENST00000257116 // intron // 0 // — // — // — // —	YARS	YARS, Homo sapiens tyrosyl-tRNA synthetase (YARS), p35.1
SNP_A-2171870	caatgagtgaccttgc[G/T]cgaaggagaaagaccc	G	T	ENST00000291421 // intron // 0 // — // — // — // —	-	p35.1
SNP_A-1851464	tattcctctcaacaac[C/T]gtctcaggaagaggca	C	T	NM_004427 // upstream // 95941 // Hs.524271 // PHC2 // 1912 // Homo sapiens polyhomeotic-like 2 (Drosophila) (PHC2), transcript variant 2, mRNA. /// NM_198040 // upstream // 95941 // Hs.524271 // PHC2 // 1912 // Homo sapiens polyhomeotic-like 2 (Drosophil	PHC2	PHC2, Homo sapiens polyhomeotic-like 2 (Drosophila) (PHC2), transcript variant 2, p35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2050739	aaggcaggctgctagd[C/T]gaattccctctctc	C	T	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2122515	agtgctctgtgacaa[A/C]gagtgtgaggctgctg	A	C	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2026881	aaacacggatcaatccd[C/T]caatacagaaggtcca	C	T	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2084250	actagtcacttccaaa[C/T]gtgggtttcctcttg	C	T	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2171006	caatacaccaagtaccd[C/T]gcgtacctaccgccta	C	T	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // — /// ENST00000343785 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2258104	ctttaaaaatcatgat[C/G]agtccagggatctaga	C	G	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2001522	actagaagaacatccg[A/G]caaaatttggatgca	A	G	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-1649902	catgcagcacggaccatcagttcc[A/G]cttcagccatctttgat atgatgag	A	G	BC030120 // upstream // 495683 // Hs.27160 // LOC113444 // 113444 // hypothetical protein BC011880 /// NM_032884 // downstream // 69615 // Hs.194610 // MGC15882 // 84970 // hypothetical protein MGC15882 /// NM_138428 // downstream // 490003 // Hs.27160 /	LOC113444	LOC113444, rs10493056, hypothetical protein BC011880, p35.1
SNP_A-1677866	atgagtgaagttagagacatgagaa[C/T]ttattagtacttgaaac tgcaagt	C	T	BC030120 // upstream // 494831 // Hs.27160 // LOC113444 // 113444 // hypothetical protein BC011880 /// NM_032884 // downstream // 70467 // Hs.194610 // MGC15882 // 84970 // hypothetical protein MGC15882 /// NM_138428 // downstream // 489151 // Hs.27160 /	LOC113444	LOC113444, rs4653014, hypothetical protein BC011880, p35.1
SNP_A-1938453	ttgacttgaataatag[A/G]cccaaggcaagaggag	A	G	NM_052896 // intron // 0 // Hs.546470 // CSMD2 // 114784 // Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), mRNA. /// ENST00000241312 // intron // 0 // — // — // —	CSMD2	CSMD2, Homo sapiens CUB and Sushi multiple domains 2 (CSMD2), p35.1
SNP_A-2184927	cagcttaaaagacaaa[G/T]gtgcaaagaagcctct	G	T	NM_032884 // intron // 0 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// ENST00000270828 // intron // 0 // — // — // —	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2279355	gaggaggcaggtccta[A/G]agttcacacagtgtta	A	G	NM_032884 // downstream // 1401 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// ENST00000270828 // intron // 0 // — // — // —	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-1866277	tcccatcccatataca[A/C]aagcagaaatgggatg	A	C	NM_032884 // downstream // 49337 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 534518 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1)	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-1949339	ttattagatttccac[A/G]actgactcatcttct	A	G	NM_032884 // downstream // 51209 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 484710 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2145851	atgccatggtgagtca[C/T]gagttaactgtttctt	C	T	NM_032884 // downstream // 51209 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 484710 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215480	cctcactctctgggaa[G/T]gtcatcctagacag	G	T	NM_032884 // downstream // 53969 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 481950 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2002016	tcacatagctaggcca[A/G]gatttttttccatct	A	G	NM_032884 // downstream // 85375 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 450544 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2002028	ggactcaggtaaaga[C/T]aagctgcccgaaata	C	T	NM_032884 // downstream // 98821 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 437098 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-1957986	ttttcacaccatccac[C/G]aggaaatgttgtgcaaa	C	G	NM_032884 // downstream // 109045 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 426874 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2186646	cagggcacaggatgcc[G/T]cagggctgaactccag	G	T	NM_032884 // downstream // 109101 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 426818 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2045040	aagaactgtctgtggt[C/T]acagcctgggagctct	C	T	NM_032884 // downstream // 153304 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 382615 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-1796833	ggttcaggagccttca[A/T]ctataaagtgtcagaa	A	T	NM_032884 // downstream // 390131 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 145788 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2279588	gaggcaagactgaggc[C/T]actgcagaagtgggca	C	T	NM_032884 // downstream // 438337 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 97582 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2202697	ccaccttccttcaga[A/G]cacttggcgccagttg	A	G	NM_032884 // downstream // 475183 // Hs.194610 // MGC15882 // 84970 // Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA. /// NM_005268 // upstream // 60736 // Hs.198249 // GJB5 // 2709 // Homo sapiens gap junction protein, beta 5 (connexin 31.1	MGC15882	MGC15882, Homo sapiens hypothetical protein MGC15882 (MGC15882), p34.3
SNP_A-2233851	ctcatctggttaaca[A/G]tagcctgcaaacatac	A	G	AF131778 // upstream // 36698 // Hs.436393 // DLGAP3 // 58512 // Homo sapiens clone 24861 DAP-1 alpha mRNA sequence, partial cds. /// NM_153248 // downstream // 52645 // Hs.546522 // MGC14276 // 253150 // Homo sapiens hypothetical protein MGC14276 (MGC142	DLGAP3	DLGAP3, Homo sapiens clone 24861 DAP-1 alpha sequence, partial cds, p34.3
SNP_A-2227129	ctaattcacacaataaa[C/T]tcagagtgaatgcacc	C	T	NM_007167 // intron // 0 // Hs.533986 // ZNF258 // 9204 // Homo sapiens zinc finger protein 258 (ZNF258), mRNA. /// ENST00000296205 // intron // 0 // — // — // — /// ENST00000357182 // intron // 0 // — // — // — // —	ZNF258	ZNF258, Homo sapiens zinc finger protein 258 (ZNF258), p34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2165460	caaagcagataaacac[A/G]gccaaagacaaaatag	A	G	NM_007167 // intron // 0 // Hs.533986 // ZNF258 // 9204 // Homo sapiens zinc finger protein 258 (ZNF258), mRNA. /// NM_145310 // 3UTR // 0 // Hs.533986 // ZNF258 // 9204 // Homo sapiens zinc finger protein 258 (ZNF258), mRNA. /// ENST00000296205 // intron	ZNF258	ZNF258, Homo sapiens zinc finger protein 258 (ZNF258), p34.3
SNP_A-2268897	gaattattgtaaccag[C/G]ctactcaattatata	C	G	NM_012199 // intron // 0 // Hs.22867 // EIF2C1 // 26523 // Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), mRNA. /// ENST00000207451 // intron // 0 // — // — // —	EIF2C1	EIF2C1, Homo sapiens eukaryotic translation initiation factor 2C, 1 (EIF2C1), p34.3
SNP_A-1957769	tttattcagtgtaga[C/T]gaaaagagactaaaat	C	T	NM_177422 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, mRNA. /// NM_024852 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens eukaryotic transla	EIF2C3	EIF2C3, Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, p34.3
SNP_A-1848235	tatcttgttgcacaag[C/T]attattggctacctt	C	T	NM_177422 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, mRNA. /// NM_024852 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens eukaryotic transla	EIF2C3	EIF2C3, Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, p34.3
SNP_A-2003050	aattaaacaatcagca[C/T]tcattaactatacttt	C	T	NM_177422 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, mRNA. /// NM_024852 // intron // 0 // Hs.530333 // EIF2C3 // 192669 // Homo sapiens eukaryotic transla	EIF2C3	EIF2C3, Homo sapiens eukaryotic translation initiation factor 2C, 3 (EIF2C3), transcript variant 2, p34.3
SNP_A-2297919	gccagtgaaaagtgaa[A/G]cctctgaaggcagact	A	G	NM_156038 // upstream // 58153 // Hs.524517 // CSF3R // 1441 // Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, mRNA. /// NM_000760 // upstream // 58153 // Hs.524517 // CSF3R // 1441 // Homo sapiens colony st	CSF3R	CSF3R, Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, p34.3
SNP_A-2310967	ggaaggctgagaataaa[A/G]cagtagcatgtgggta	A	G	NM_156038 // upstream // 120081 // Hs.524517 // CSF3R // 1441 // Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, mRNA. /// NM_000760 // upstream // 120081 // Hs.524517 // CSF3R // 1441 // Homo sapiens colony	CSF3R	CSF3R, Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, p34.3
SNP_A-2119090	agtagatgctttgac[C/T]gccactcaggtcaaa	C	T	NM_156038 // upstream // 243160 // Hs.524517 // CSF3R // 1441 // Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, mRNA. /// NM_000760 // upstream // 243160 // Hs.524517 // CSF3R // 1441 // Homo sapiens colony	CSF3R	CSF3R, Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 2, p34.3
SNP_A-2193705	catcttggctgcggac[C/G]cttcattggaaatgga	C	G	NM_000831 // intron // 0 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// ENST00000296212 // intron // 0 // — // — // —	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-1841294	taggaagatgaaatga[C/G]tcagggcagcatctca	C	G	NM_000831 // intron // 0 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// ENST00000296212 // intron // 0 // — // — // —	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-1813646	gtgtacaaattgaaaa[A/G]gactggaaatgggcac	A	G	NM_000831 // upstream // 49795 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 390514 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ232	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2309338	ggaaaagtaggactta[C/T]agggtggcagtgctcc	C	T	NM_000831 // upstream // 96916 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 343393 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ232	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2234555	ctccactcacagata[C/T]aggaaaagaagcccaga	C	T	NM_000831 // upstream // 144893 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 295416 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ23	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-1899449	tggaagacaggacaaa[A/G]ctggaaaagctggatg	A	G	NM_000831 // upstream // 223234 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 217075 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ23	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2304796	gctctgtgtaatcaaa[A/G]tgggctgagaaagagg	A	G	NM_000831 // upstream // 280518 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 159791 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ23	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2203638	ccagaccaacctggga[C/T]gtgcctacctggcttt	C	T	NM_000831 // upstream // 303027 // Hs.2389 // GRIK3 // 2899 // Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA. /// NM_025079 // upstream // 137282 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ23	GRIK3	GRIK3, Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), p34.3
SNP_A-2004296	agcagttgaagatcac[C/G]agcagctgccttgaga	C	G	NM_025079 // downstream // 3000 // Hs.471918 // FLJ23231 // 80149 // Homo sapiens hypothetical protein FLJ23231 (FLJ23231), mRNA. /// NM_022756 // downstream // 5200 // Hs.17118 // FLJ11730 // 64769 // Homo sapiens hypothetical protein FLJ11730 (FLJ11730)	FLJ23231	FLJ23231, Homo sapiens hypothetical protein FLJ23231 (FLJ23231), p34.3
SNP_A-1890380	tgatcctcacgctcct[A/G]aaattcaacagattc	A	G	NM_024700 // intron // 0 // Hs.471951 // SNIP1 // 79753 // Homo sapiens Smad nuclear interacting protein (SNIP1), mRNA. /// ENST00000296215 // intron // 0 // — // — // —	SNIP1	SNIP1, Homo sapiens Smad nuclear interacting protein (SNIP1), p34.3
SNP_A-1825425	taaataagaaagcacc[C/G]caaatgagcaactgaa	C	G	NM_013285 // intron // 0 // Hs.75528 // GNL2 // 29889 // Homo sapiens guanine nucleotide binding protein-like 2 (nucleolar) (GNL2), mRNA. /// ENST00000257129 // intron // 0 // — // — // —	GNL2	GNL2, Homo sapiens guanine nucleotide binding protein-like 2 (nucleolar) (GNL2), p34.3
SNP_A-1859496	tcaggagaggcgcccc[G/T]aattccatgccgggtc	G	T	NM_002699 // upstream // 89658 // Hs.1837 // POU3F1 // 5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 // upstream // 89658 // — // — // — /// ENST00000324460 // upstream // 572526 // — /	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-2264586	gaagaagtgattaacc[A/G]gagagaaatgtgtagg	A	G	NM_002699 // upstream // 378205 // Hs.1837 // POU3F1 // 5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 // upstream // 378205 // — // — // — /// ENST00000324460 // upstream // 283979 // —	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-2050289	aaggagatcctatgaa[A/G]ctgggatttgtgaaa	A	G	NM_002699 // upstream // 650657 // Hs.1837 // POU3F1 // 5453 // Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), mRNA. /// ENST00000328583 // upstream // 650657 // — // — // — /// ENST00000324460 // upstream // 11527 // —	POU3F1	POU3F1, Homo sapiens POU domain, class 3, transcription factor 1 (POU3F1), p34.3
SNP_A-2311272	ggaataatgtcttcaa[A/G]tccttcccattcaaag	A	G	NM_017821 // upstream // 3374 // Hs.524626 // RHBDL2 // 54933 // Homo sapiens rhomboid, veinlet-like 2 (Drosophila) (RHBDL2), mRNA. /// NM_024595 // upstream // 61170 // Hs.293563 // FLJ12666 // 79647 // Homo sapiens hypothetical protein FLJ12666 (FLJ1266	RHBDL2	RHBDL2, Homo sapiens rhomboid, veinlet-like 2 (Drosophila) (RHBDL2), p34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138978	atccgtccagatgcac[G/T]ccttgtagtattagtt	G	T	NM_017821 // upstream // 59348 // Hs.524626 // RHBDL2 // 54933 // Homo sapiens rhomboid, veinlet-like 2 (Drosophila) (RHBDL2), mRNA. /// NM_024595 // upstream // 5196 // Hs.293563 // FLJ12666 // 79647 // Homo sapiens hypothetical protein FLJ12666 (FLJ12666	RHBDL2	RHBDL2, Homo sapiens rhomboid, veinlet-like 2 (Drosophila) (RHBDL2), p34.3
SNP_A-2049858	aaggaaatagaaaatc[A/G]ctattccagcctggac	A	G	NM_181809 // intron // 0 // Hs.494158 // BMP8A // 353500 // Homo sapiens bone morphogenetic protein 8a (BMP8A), mRNA. /// ENST00000331593 // intron // 0 // --- // --- // ---	BMP8A	BMP8A, Homo sapiens bone morphogenetic protein 8a (BMP8A), p34.3
SNP_A-1929197	ttcagggctgaacaa[C/T]agcctgctccttttg	C	T	NM_014571 // intron // 0 // Hs.472566 // HEYL // 26508 // Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA. /// ENST00000296261 // intron // 0 // --- // --- // ---	HEYL	HEYL, Homo sapiens hairy,p34.3
SNP_A-2201440	ccaatgattccatttta[C/T]gaccgtgggcaaaacc	C	T	NM_016257 // upstream // 1742 // Hs.524688 // HPCAL4 // 51440 // Homo sapiens hippocalcin like 4 (HPCAL4), mRNA. /// NM_006112 // upstream // 45702 // Hs.524690 // PPIE // 10450 // Homo sapiens peptidylprolyl isomerase E (cyclophilin E) (PPIE), transcript	HPCAL4	HPCAL4, Homo sapiens hippocalcin like 4 (HPCAL4), p34.2
SNP_A-1916197	tgttgggcacttaaacd[A/C]accctcctagcaccct	A	C	NM_006112 // downstream // 71814 // Hs.524690 // PPIE // 10450 // Homo sapiens peptidylprolyl isomerase E (cyclophilin E) (PPIE), transcript variant 1, mRNA. /// NM_203457 // downstream // 71814 // Hs.524690 // PPIE // 10450 // Homo sapiens peptidylprolyl	PPIE	PPIE, Homo sapiens peptidylprolyl isomerase E (cyclophilin E) (PPIE), transcript variant 1, p34.2
SNP_A-2210431	ccccaatttttcactc[C/T]gactaggtgttctgc	C	T	ENST00000326760 // intron // 0 // --- // --- // ---	-	p34.2
SNP_A-1870760	tcgctgaatagtaagal[A/C]aggtctgagcatggtg	A	C	NM_022733 // intron // 0 // Hs.15200 // LOC64744 // 64744 // Homo sapiens hypothetical protein AL133206 (LOC64744), mRNA. /// ENST00000196802 // intron // 0 // --- // --- // ---	LOC64744	LOC64744, Homo sapiens hypothetical protein AL133206 (LOC64744), p34.2
SNP_A-1929756	ttcatcagggaaaaaa[C/G]aggtcaagtacacaaa	C	G	NM_022733 // intron // 0 // Hs.15200 // LOC64744 // 64744 // Homo sapiens hypothetical protein AL133206 (LOC64744), mRNA. /// ENST00000196802 // intron // 0 // --- // --- // ---	LOC64744	LOC64744, Homo sapiens hypothetical protein AL133206 (LOC64744), p34.2
SNP_A-2037728	aacaagggtcccattg[C/G]caatcagtccaacaca	C	G	NM_022733 // intron // 0 // Hs.15200 // LOC64744 // 64744 // Homo sapiens hypothetical protein AL133206 (LOC64744), mRNA. /// ENST00000196802 // intron // 0 // --- // --- // ---	LOC64744	LOC64744, Homo sapiens hypothetical protein AL133206 (LOC64744), p34.2
SNP_A-1857269	tcaccttctggaacc[C/G]gaagaagaagggatg	C	G	NM_022733 // CDS // 0 // Hs.15200 // LOC64744 // 64744 // Homo sapiens hypothetical protein AL133206 (LOC64744), mRNA. /// ENST00000196802 // CDS // 0 // --- // --- // --- // ---	LOC64744	LOC64744, Homo sapiens hypothetical protein AL133206 (LOC64744), p34.2
SNP_A-2140644	atctctcagagtgtag[C/T]atttaattcactgccc	C	T	NM_133467 // upstream // 109618 // Hs.355820 // CITED4 // 163732 // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 (CITED4), mRNA. /// NM_001905 // upstream // 7947 // Hs.473087 // CTPS // 1503 // Homo sapie	CITED4	CITED4, Homo sapiens Cbp p34.2
SNP_A-2197768	cattcttttttgagcc[A/G]cattccttaagcttt	A	G	ENST00000326197 // intron // 0 // --- // --- // --- /// ENST00000337495 // intron // 0 // --- // --- // --- /// ENST00000360598 // intron // 0 // --- // --- // ---	-	p34.2
SNP_A-2164648	caaacaccagccttta[C/T]gtatggtagtctcaga	C	T	NM_001956 // downstream // 28570 // Hs.1407 // EDN2 // 1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 289309 // --- // --- // --- /// ENST00000337495 // upstream // 288778 // --- // --- // --- /// ENST0000	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2
SNP_A-2192816	catcctcacatcacca[A/G]tgagcttcagggaaag	A	G	NM_001956 // downstream // 19403 // Hs.1407 // EDN2 // 1907 // Homo sapiens endothelin 2 (EDN2), mRNA. /// ENST00000326197 // upstream // 298476 // --- // --- // --- /// ENST00000337495 // upstream // 297945 // --- // --- // --- /// ENST0000	EDN2	EDN2, Homo sapiens endothelin 2 (EDN2), p34.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209886	ccccaactccactctc[A/G]attcaggcagggcttc	A	G	NM_024503 // intron // 0 // Hs.325890 // HIVEP3 // 59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// ENST00000247584 // intron // 0 // — // — // — // —	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-1835253	tacctaatctacccaa[A/C]gtcatcgaactaataa	A	C	NM_024503 // upstream // 130932 // Hs.325890 // HIVEP3 // 59269 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA. /// NM_007102 // upstream // 321488 // Hs.32966 // GUCA2B // 2981 // Homo sapiens guanylate cycl	HIVEP3	HIVEP3, Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), p34.2
SNP_A-2065192	aattggagccaaataa[A/G]ctttcagttagcttgg	A	G	NM_173642 // downstream // 4680 // Hs.420244 // MGC47816 // 284716 // Homo sapiens hypothetical protein MGC47816 (MGC47816), mRNA. /// NM_032257 // downstream // 10884 // Hs.294009 // ZMYND12 // 84217 // Homo sapiens zinc finger, MYND domain containing 12	MGC47816	MGC47816, Homo sapiens hypothetical protein MGC47816 (MGC47816), p34.2
SNP_A-2007652	cctccaggcacagtaa[A/G]agagagaacctccagg	A	G	NM_032257 // intron // 0 // Hs.294009 // ZMYND12 // 84217 // Homo sapiens zinc finger, MYND domain containing 12 (ZMYND12), mRNA. /// ENST00000163340 // intron // 0 // — // — // — // —	ZMYND12	ZMYND12, Homo sapiens zinc finger, MYND domain containing 12 (ZMYND12), p34.2
SNP_A-2108928	agcttaggctcttaac[C/T]acttctacccatagcc	C	T	NM_018538 // intron // 0 // Hs.439437 // ERMAP // 114625 // Homo sapiens erythroblast membrane-associated protein (ERMAP), mRNA. /// ENST00000314274 // intron // 0 // — // — // — // — /// ENST00000296391 // intron // 0 // — // — // — // —	ERMAP	ERMAP, Homo sapiens erythroblast membrane-associated protein (ERMAP), p34.2
SNP_A-1854723	tcaacagttatgaaac[A/G]gcagaaccaagatgac	A	G	NM_006516 // upstream // 107030 // Hs.473721 // SLC2A1 // 6513 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /// ENST00000270929 // upstream // 107030 // — // — // — // — /// ENST00000335282 //	SLC2A1	SLC2A1, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), p34.2
SNP_A-2266041	gaaggcactagtatat[C/G]aacttcctatgccac	C	G	NM_006516 // upstream // 123756 // Hs.473721 // SLC2A1 // 6513 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /// ENST00000270929 // upstream // 123756 // — // — // — // — /// ENST00000335282 //	SLC2A1	SLC2A1, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), p34.2
SNP_A-2008128	ctgtcaagccaactaa[C/T]gttcctattgacttaa	C	T	ENST00000335282 // intron // 0 // — // — // — // —	-	p34.2
SNP_A-1801495	gtagggctgccaagag[A/G]agcaaaagatggccct	A	G	NM_152498 // intron // 0 // Hs.134451 // FLJ32000 // 149465 // Homo sapiens hypothetical protein FLJ32000 (FLJ32000), mRNA. /// ENST00000296394 // intron // 0 // — // — // — // —	FLJ32000	FLJ32000, Homo sapiens hypothetical protein FLJ32000 (FLJ32000), p34.2
SNP_A-2151912	atgtttgtatctgtta[A/G]ccaatctctctttagc	A	G	NM_152498 // downstream // 2128 // Hs.134451 // FLJ32000 // 149465 // Homo sapiens hypothetical protein FLJ32000 (FLJ32000), mRNA. /// ENST00000296394 // downstream // 2128 // — // — // — // — /// ENST00000315972 // downstream // 28510 // — // -	FLJ32000	FLJ32000, Homo sapiens hypothetical protein FLJ32000 (FLJ32000), p34.2
SNP_A-2171157	caataggccctctaac[A/G]agacaaatgaatgggg	A	G	NM_130440 // intron // 0 // Hs.272062 // PTPRF // 5792 // Homo sapiens protein tyrosine phosphatase, receptor type, F (PTPRF), transcript variant 2, mRNA. /// NM_002840 // intron // 0 // Hs.272062 // PTPRF // 5792 // Homo sapiens protein tyrosine phosphat	PTPRF	PTPRF, Homo sapiens protein tyrosine phosphatase, receptor type, F (PTPRF), transcript variant 2, p34.2
SNP_A-1926718	ttattgctttattaca[G/T]tgactagaccttccag	G	T	NM_174965 // intron // 0 // Hs.132001 // ST3GAL3 // 6487 // Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), transcript variant 3, mRNA. /// NM_174972 // intron // 0 // Hs.132001 // ST3GAL3 // 6487 // Homo sapie	ST3GAL3	ST3GAL3, Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), transcript variant 3, p34.1
SNP_A-1657251	tcagtaaatgaaccaagccatgtta[C/T]gtgaatttattgttaatat ctgaat	C	T	NM_006934 // upstream // 47357 // Hs.442590 // SLC6A9 // 6536 // solute carrier family 6 (neurotransmitter transporter, glycine), member 9 /// NM_152499 // downstream // 68158 // Hs.36567 // MGC45441 // 149473 // hypothetical protein MGC45441 /// NM_1734	SLC6A9	SLC6A9, rs10493116, solute carrier family 6 (neurotransmitter transporter, glycine), member 9 p34.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784431	ggcccttctctgtgcc[A/G]attcacacacattaa	A	G	NM_201649 // upstream // 19166 // Hs.442590 // SLC6A9 // 6536 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), transcript variant 2, mRNA. /// NM_006934 // upstream // 19400 // Hs.442590 // SLC6A9 // 6536	SLC6A9	SLC6A9, Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), transcript variant 2, p34.1
SNP_A-2129525	atacaccccccacaa[C/T]acagtcatacccgacac	C	T	NM_201649 // upstream // 20043 // Hs.442590 // SLC6A9 // 6536 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), transcript variant 2, mRNA. /// NM_006934 // upstream // 20277 // Hs.442590 // SLC6A9 // 6536	SLC6A9	SLC6A9, Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), transcript variant 2, p34.1
SNP_A-2279694	gaggcagtaactacga[A/C]ggatccatttttctc	A	C	NM_201649 // upstream // 24776 // Hs.442590 // SLC6A9 // 6536 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), transcript variant 2, mRNA. /// NM_006934 // upstream // 25010 // Hs.442590 // SLC6A9 // 6536	SLC6A9	SLC6A9, Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), transcript variant 2, p34.1
SNP_A-1757999	tacaactgtacactcaagaaaata[C/T]atccatcatctatgaca ctgaattc	C	T	NM_016501 // upstream // 186769 // - // - // - /// NM_018150 // upstream // 168148 // Hs.90375 // FLJ10597 // 55182 // hypothetical protein FLJ10597	-	-, rs1890948, - p34.1
SNP_A-2184496	cagctagaaagtttacj[A/G]gagctagaattcagac	A	G	NM_018150 // intron // 0 // Hs.456557 // FLJ10597 // 55182 // Homo sapiens hypothetical protein FLJ10597 (FLJ10597), mRNA. /// ENST00000335497 // intron // 0 // --- // --- // --- /// ENST00000355387 // intron // 0 // --- // --- // ---	FLJ10597	FLJ10597, Homo sapiens hypothetical protein FLJ10597 (FLJ10597), p34.1
SNP_A-1744333	gatgtcttccaaaacgcactgtac[C/T]gatagattaagatctaca tcagaaa	C	T	BC008498 // intron // 0 // Hs.10964 // ATPAF1 // 64756 // ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	ATPAF1, , rs631840, ATP synthase mitochondrial F1 complex assembly factor 1,p33
SNP_A-1825836	taaatgaaagcaaaac[A/G]atgcaaatatgatcat	A	G	NM_001441 // downstream // 40578 // Hs.528334 // FAAH // 2166 // Homo sapiens fatty acid amide hydrolase (FAAH), mRNA. /// NM_147192 // upstream // 52581 // Hs.375623 // DMBX1 // 127343 // Homo sapiens diencephalon/mesencephalon homeobox 1 (DMBX1), transc	FAAH	FAAH, Homo sapiens fatty acid amide hydrolase (FAAH), p33
SNP_A-2290627	gcaagaatgactgaca[C/T]gtgaatccaacttcca	C	T	NM_001441 // downstream // 88381 // Hs.528334 // FAAH // 2166 // Homo sapiens fatty acid amide hydrolase (FAAH), mRNA. /// NM_147192 // upstream // 4778 // Hs.375623 // DMBX1 // 127343 // Homo sapiens diencephalon/mesencephalon homeobox 1 (DMBX1), transcr	FAAH	FAAH, Homo sapiens fatty acid amide hydrolase (FAAH), p33
SNP_A-2299183	gccctaccagaaacag[A/C]aggatgaattgggggg	A	C	NM_022745 // intron // 0 // Hs.10964 // ATPAF1 // 64756 // Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), mRNA. /// ENST00000262750 // intron // 0 // --- // --- // ---	ATPAF1	ATPAF1, Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), p33
SNP_A-2056167	aatacctcagtgcca[C/T]gaggtaaatccaaaga	C	T	NM_022745 // intron // 0 // Hs.10964 // ATPAF1 // 64756 // Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), mRNA. /// ENST00000262750 // intron // 0 // --- // --- // ---	ATPAF1	ATPAF1, Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), p33
SNP_A-2126509	ataaaatagaaaagca[A/G]ctcataggaaaacttc	A	G	NM_022745 // intron // 0 // Hs.10964 // ATPAF1 // 64756 // Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), mRNA. /// ENST00000262750 // intron // 0 // --- // --- // ---	ATPAF1	ATPAF1, Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), p33
SNP_A-1933319	ttctaagtaccctgaa[A/T]gtaagtacctgagaga	A	T	NM_022745 // intron // 0 // Hs.10964 // ATPAF1 // 64756 // Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), mRNA. /// ENST00000262750 // intron // 0 // --- // --- // ---	ATPAF1	ATPAF1, Homo sapiens ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1), p33
SNP_A-2105026	agcatctatatgg[A/G]cactaaaatgggtgct	A	G	ENST00000294342 // intron // 0 // --- // --- // ---	-	p33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2035385	aaatggcctgagctaa[C/G]tggactgtgggagctc	C	G	NM_000778 // upstream // 78407 // Hs.1645 // CYP4A11 // 1579 // Homo sapiens cytochrome P450, family 4, subfamily A, polypeptide 11 (CYP4A11), mRNA. /// NM_178033 // upstream // 3416 // Hs.439760 // CYP4X1 // 260293 // Homo sapiens cytochrome P450, family	CYP4A11	CYP4A11, Homo sapiens cytochrome P450, family 4, subfamily A, polypeptide 11 (CYP4A11), p33
SNP_A-1960295	tttttacgtttatcca[C/T]gtgaccatttttcat	C	T	NM_178033 // intron // 0 // Hs.439760 // CYP4X1 // 260293 // Homo sapiens cytochrome P450, family 4, subfamily X, polypeptide 1 (CYP4X1), mRNA. /// ENST00000334540 // intron // 0 // --- // --- // --- // ---	CYP4X1	CYP4X1, Homo sapiens cytochrome P450, family 4, subfamily X, polypeptide 1 (CYP4X1), p33
SNP_A-2000041	tccaccaaaatcataa[A/G]ctcacttccaatgaag	A	G	NM_003189 // intron // 0 // Hs.73828 // TAL1 // 6886 // Homo sapiens T-cell acute lymphocytic leukemia 1 (TAL1), mRNA. /// ENST00000294339 // intron // 0 // --- // --- // --- // ---	TAL1	TAL1, Homo sapiens T-cell acute lymphocytic leukemia 1 (TAL1), p33
SNP_A-2131024	atagaatacaacaaag[A/C]aagactgggccttgca	A	C	NM_004474 // downstream // 46731 // Hs.166188 // FOXD2 // 2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 46731 // --- // --- // --- // --- /// ENST00000324745 // downstream // 274316 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-1883913	tgaagagagagaggaa[A/G]atttgaaccaccactg	A	G	NM_004474 // downstream // 65714 // Hs.166188 // FOXD2 // 2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 65714 // --- // --- // --- // --- /// ENST00000324745 // downstream // 255333 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-1956299	tttgtgttctatttca[A/G]cctaacatgaagggag	A	G	NM_004474 // downstream // 66217 // Hs.166188 // FOXD2 // 2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 66217 // --- // --- // --- // --- /// ENST00000324745 // downstream // 254830 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-2206282	ccatccccatccagaa[C/T]tggcacgtgctccagc	C	T	NM_004474 // downstream // 123107 // Hs.166188 // FOXD2 // 2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 123107 // --- // --- // --- // --- /// ENST00000324745 // downstream // 197940 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-1901293	tggatgggatggctga[C/T]ggctcttagaaatgcc	C	T	NM_004474 // downstream // 196189 // Hs.166188 // FOXD2 // 2306 // Homo sapiens forkhead box D2 (FOXD2), mRNA. /// ENST00000334793 // downstream // 196189 // --- // --- // --- // --- /// ENST00000324745 // downstream // 124858 // --- // --- // --- // ---	FOXD2	FOXD2, Homo sapiens forkhead box D2 (FOXD2), p33
SNP_A-2313927	ggagcgtttctgggac[C/T]gagtagaggagacact	C	T	ENST00000324745 // upstream // 19787 // --- // --- // --- // --- /// ENST00000341422 // downstream // 383215 // --- // --- // --- // ---	-	p33
SNP_A-1947261	tttaattgtgctagaa[A/G]gtcactgggatttgac	A	G	ENST00000324745 // upstream // 66830 // --- // --- // --- // --- /// ENST00000341422 // downstream // 336172 // --- // --- // --- // ---	-	p33
SNP_A-1645024	agcatagattcaatgtagtctcaat[A/C]aaaaactcagtgggttct ggcaagc	A	C	NM_019073 // intron // 0 // Hs.143251 // SPATA6 // 54558 // spermatogenesis associated 6	SPATA6	SPATA6 , rs2063712, spermatogenesis associated 6,p33
SNP_A-1903859	tgggatcctgggaaac[A/C]ccattatcagacagtg	A	C	ENST00000324745 // upstream // 341382 // --- // --- // --- // --- /// ENST00000341422 // downstream // 61620 // --- // --- // --- // ---	-	p33
SNP_A-2300632	gcctgcatcaaaatcc[C/G]attcccaggatagaaa	C	G	ENST00000341422 // CDS // 0 // --- // --- // --- // ---	-	p33
SNP_A-1951535	tttcctgaacaggtca[A/T]cgcccatttgtccata	A	T	ENST00000341422 // upstream // 22748 // --- // --- // --- // --- /// ENST00000236495 // upstream // 33190 // --- // --- // --- // ---	-	p33
SNP_A-1905163	tgggtgtcgggcaaag[A/G]aagctgctatttgtga	A	G	ENST00000341422 // upstream // 36182 // --- // --- // --- // --- /// ENST00000236495 // upstream // 19756 // --- // --- // --- // ---	-	p33
SNP_A-2098482	agagcacgaggtcatt[A/G]aaagagattaggcctg	A	G	ENST00000341422 // upstream // 37949 // --- // --- // --- // --- /// ENST00000236495 // upstream // 17989 // --- // --- // --- // ---	-	p33
SNP_A-2150456	atgtgaagctaaacac[A/G]agttcagttagagaat	A	G	NM_019073 // downstream // 29912 // Hs.408467 // SPATA6 // 54558 // Homo sapiens spermatogenesis associated 6 (SPATA6), mRNA. /// ENST00000321344 // upstream // 6169 // --- // --- // --- // --- /// ENST00000254448 // downstream // 29912 // --- // --- // -	SPATA6	SPATA6, Homo sapiens spermatogenesis associated 6 (SPATA6), p33
SNP_A-2311204	ggaagttctcatggac[A/G]atactgtgaaatatgt	A	G	NM_019073 // intron // 0 // Hs.408467 // SPATA6 // 54558 // Homo sapiens spermatogenesis associated 6 (SPATA6), mRNA. /// ENST00000254448 // intron // 0 // --- // --- // --- // ---	SPATA6	SPATA6, Homo sapiens spermatogenesis associated 6 (SPATA6), p33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2146794	atgcttgagtgctgta[A/G]agagaaaagagaagta	A	G	NM_019073 // upstream // 93393 // Hs.408467 // SPATA6 // 54558 // Homo sapiens spermatogenesis associated 6 (SPATA6), mRNA. /// NM_032785 // downstream // 18304 // Hs.144875 // FLJ14442 // 84871 // Homo sapiens hypothetical protein FLJ14442 (FLJ14442), mR	SPATA6	SPATA6, Homo sapiens spermatogenesis associated 6 (SPATA6), p33
SNP_A-2209549	cccatctgctaaaaga[A/G]aagaacaatttctgac	A	G	NM_032785 // intron // 0 // Hs.144875 // FLJ14442 // 84871 // Homo sapiens hypothetical protein FLJ14442 (FLJ14442), mRNA. /// ENST00000334103 // intron // 0 // — // — // — // —	FLJ14442	FLJ14442, Homo sapiens hypothetical protein FLJ14442 (FLJ14442), p33
SNP_A-1664052	aagtgatctcccttatgtatatgac[C/T]gcacatgtcactccattgtt aataa	C	T	NM_032785 // intron // 0 // Hs.144875 // FLJ11588 // 79656 // hypothetical protein FLJ11588	FLJ11588	FLJ11588 , rs1343426, hypothetical protein FLJ11588,p33
SNP_A-2210487	ccccctctatcaagat[A/C]aagataagtcaagatc	A	C	NM_024603 // upstream // 50090 // Hs.475348 // FLJ11588 // 79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream // 50090 // — // — // — // — /// ENST00000360752 // downstream // 332881 // — // —	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-1865067	tccagtgatcctaaca[C/G]tcaagatcacagcctg	C	G	NM_024603 // upstream // 113050 // Hs.475348 // FLJ11588 // 79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream // 113050 // — // — // — // — /// ENST00000360752 // downstream // 269921 // — // -	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-1831020	taatgaggataaattg[C/G]agaaatgaggataatg	C	G	NM_024603 // upstream // 204495 // Hs.475348 // FLJ11588 // 79656 // Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA. /// ENST00000294347 // upstream // 204495 // — // — // — // — /// ENST00000360752 // downstream // 178476 // — // -	FLJ11588	FLJ11588, Homo sapiens hypothetical protein FLJ11588 (FLJ11588), p33
SNP_A-2111518	aggaggggaccaatac[G/T]ccagcctttaaaaagt	G	T	NM_001981 // upstream // 41384 // Hs.83722 // EPS15 // 2060 // Homo sapiens epidermal growth factor receptor pathway substrate 15 (EPS15), mRNA. /// NM_148904 // upstream // 56154 // Hs.21938 // OSBPL9 // 114883 // Homo sapiens oxysterol binding protein-l	EPS15	EPS15, Homo sapiens epidermal growth factor receptor pathway substrate 15 (EPS15), p32.3
SNP_A-2306420	gctgggtgggctgata[C/T]gcagacagaaatagtc	C	T	NM_023077 // downstream // 26359 // Hs.349905 // FLJ12439 // 65260 // Homo sapiens hypothetical protein FLJ12439 (FLJ12439), mRNA. /// ENST00000329545 // downstream // 20472 // — // — // — // — /// ENST00000343491 // downstream // 3416 // — // -	FLJ12439	FLJ12439, Homo sapiens hypothetical protein FLJ12439 (FLJ12439), p32.3
SNP_A-2267982	gaatctctcctcagga[A/C]cctcataccctgcata	A	C	NM_033300 // upstream // 18121 // Hs.444637 // LRP8 // 7804 // Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, mRNA. /// NM_004631 // upstream // 18121 // Hs.444637 // LRP8 // 7804 /	LRP8	LRP8, Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, p32.3
SNP_A-2042516	aactcataaccttaac[A/G]ctttgattccttctca	A	G	NM_033300 // upstream // 103696 // Hs.444637 // LRP8 // 7804 // Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, mRNA. /// NM_004631 // upstream // 103696 // Hs.444637 // LRP8 // 7804	LRP8	LRP8, Homo sapiens low density lipoprotein receptor related protein 8, apolipoprotein e receptor (LRP8), transcript variant 2, p32.3
SNP_A-2081035	acctgaaggacgtaac[A/G]ataacaataaacatag	A	G	NM_147193 // intron // 0 // Hs.306691 // GLIS1 // 148979 // Homo sapiens GLIS family zinc finger 1 (GLIS1), mRNA. /// ENST00000312233 // intron // 0 // — // — // — // —	GLIS1	GLIS1, Homo sapiens GLIS family zinc finger 1 (GLIS1), p32.3
SNP_A-2298673	gcccagcatctgaaca[C/T]acttcttctacgggga	C	T	NM_147193 // intron // 0 // Hs.306691 // GLIS1 // 148979 // Homo sapiens GLIS family zinc finger 1 (GLIS1), mRNA. /// ENST00000312233 // intron // 0 // — // — // — // —	GLIS1	GLIS1, Homo sapiens GLIS family zinc finger 1 (GLIS1), p32.3
SNP_A-1657532	ctcaggggtccccagccagttctaa[C/T]gtatctgaaagcctgtg acccaggt	C	T	NM_018070 // intron // 0 // Hs.288801 // SSBP3 // 23648 // single stranded DNA binding protein 3 /// NM_145716 // intron // 0 // Hs.288801 // SSBP3 // 23648 // single stranded DNA binding protein 3	SSBP3	SSBP3 , rs10489565, single stranded DNA binding protein 3 ,p32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2264592	gaagaagtcaggaggc[C/G]ccgcttcgcgctaacg	C	G	NM_004872 // 5UTR // 0 // Hs.523262 // C1orf8 // 9528 // Homo sapiens chromosome 1 open reading frame 8 (C1orf8), mRNA. /// ENST00000234831 // 5UTR // 0 // — // — // —	C1orf8	C1orf8, Homo sapiens chromosome 1 open reading frame 8 (C1orf8), p32.3
SNP_A-2131109	atagacagtctcaaac[A/C]cgggaatggattgtgc	A	C	NM_145716 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /// NM_018070 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /	SSBP3	SSBP3, Homo sapiens single stranded DNA binding protein 3 (SSBP3), p32.3
SNP_A-2084201	actaggaatcttcag[C/G]caagtcgtctctat	C	G	NM_145716 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /// NM_018070 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /	SSBP3	SSBP3, Homo sapiens single stranded DNA binding protein 3 (SSBP3), p32.3
SNP_A-1879387	tctataagtgttac[A/C]ggattaaatgccatg	A	C	NM_145716 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /// NM_018070 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /	SSBP3	SSBP3, Homo sapiens single stranded DNA binding protein 3 (SSBP3), p32.3
SNP_A-2301367	gccttgagccaaaga[C/G]actagagaatagcaat	C	G	NM_145716 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /// NM_018070 // intron // 0 // Hs.175551 // SSBP3 // 23648 // Homo sapiens single stranded DNA binding protein 3 (SSBP3), mRNA. /	SSBP3	SSBP3, Homo sapiens single stranded DNA binding protein 3 (SSBP3), p32.3
SNP_A-2219558	cctgttggaccdatg[C/T]cacgggagccaggacc	C	T	NM_147161 // intron // 0 // Hs.476882 // THEA // 26027 // Homo sapiens thioesterase, adipose associated (THEA), transcript variant 2, mRNA. /// NM_015547 // intron // 0 // Hs.476882 // THEA // 26027 // Homo sapiens thioesterase, adipose associated (THEA),	THEA	THEA, Homo sapiens thioesterase, adipose associated (THEA), transcript variant 2, p32.3
SNP_A-2015679	atatgttgtactt gt[C/T]aagagccttagaaatg	C	T	NM_004623 // intron // 0 // Hs.412482 // TTC4 // 7268 // Homo sapiens tetratricopeptide repeat domain 4 (TTC4), mRNA. /// ENST00000294374 // intron // 0 // — // — // —	TTC4	TTC4, Homo sapiens tetratricopeptide repeat domain 4 (TTC4), p32.3
SNP_A-2293217	gcagagccagagttca[A/G]accggtatctgttgga	A	G	NM_004623 // downstream // 4393 // Hs.412482 // TTC4 // 7268 // Homo sapiens tetratricopeptide repeat domain 4 (TTC4), mRNA. /// NM_152268 // downstream // 9854 // Hs.380169 // DKFZp727A071 // 25973 // Homo sapiens similar to tRNA synthetase class II (DKF	TTC4	TTC4, Homo sapiens tetratricopeptide repeat domain 4 (TTC4), p32.3
SNP_A-1788580	gggatcaggaaggtgg[G/T]acctcgttttatgag	G	T	NM_152268 // upstream // 4524 // Hs.380169 // DKFZp727A071 // 25973 // Homo sapiens similar to tRNA synthetase class II (DKFZp727A071), mRNA. /// NM_017904 // downstream // 15514 // Hs.16230 // FLJ20619 // 55001 // Homo sapiens hypothetical protein FLJ206	DKFZp727A071	DKFZp727A071, Homo sapiens similar to tRNA synthetase class II (DKFZp727A071), p32.3
SNP_A-2198430	catttactgagtgcca[A/G]aacgtgcaaggaagt	A	G	NM_152607 // intron // 0 // Hs.376018 // FLJ40201 // 163747 // Homo sapiens hypothetical protein FLJ40201 (FLJ40201), mRNA. /// ENST00000358193 // intron // 0 // — // — // — /// ENST00000294377 // intron // 0 // — // — // — // —	FLJ40201	FLJ40201, Homo sapiens hypothetical protein FLJ40201 (FLJ40201), p32.3
SNP_A-2080137	accggttcctggaaaa[A/C]cgtcacttcttcaac	A	C	NM_014762 // intron // 0 // Hs.498727 // DHCR24 // 1718 // Homo sapiens 24-dehydrocholesterol reductase (DHCR24), mRNA. /// ENST00000234746 // intron // 0 // — // — // — // —	DHCR24	DHCR24, Homo sapiens 24-dehydrocholesterol reductase (DHCR24), p32.3
SNP_A-2217534	cctgacttactcacca[C/T]tgcatcccctagcacct	C	T	NM_014762 // upstream // 34637 // Hs.498727 // DHCR24 // 1718 // Homo sapiens 24-dehydrocholesterol reductase (DHCR24), mRNA. /// NM_182532 // upstream // 58937 // Hs.112554 // LOC199964 // 199964 // Homo sapiens hypothetical protein LOC199964 (LOC199964)	DHCR24	DHCR24, Homo sapiens 24-dehydrocholesterol reductase (DHCR24), p32.3
SNP_A-2087376	actgcaggtaatttac[A/G]aatggaatttctctat	A	G	NM_182532 // intron // 0 // Hs.112554 // LOC199964 // 199964 // Homo sapiens hypothetical protein LOC199964 (LOC199964), mRNA. /// ENST00000271185 // intron // 0 // — // — // — // —	LOC199964	LOC199964, Homo sapiens hypothetical protein LOC199964 (LOC199964), p32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1668518	atgagctatactgggggaacatgcc[A/G]actcaggctgatccta cagtactaa	A	G	AB028980 // upstream // 748189 // Hs.7243 // USP24 // 23358 // ubiquitin specific protease 24 /// BC020888 // downstream // 396138 // - // - // - // Homo sapiens cDNA clone IMAGE:4690950, partial cds.	USP24	USP24 , rs4497258, ubiquitin specific protease 24 p32.2
SNP_A-2134473	atatggtagacaacac[A/G]atcatcttttacaga	A	G	NM_003713 // downstream // 257172 // Hs.405156 // PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 257172 // Hs.405156 // PPAP2B // 8613 // Homo sapiens phosphatidic	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-2066349	aatttgaaccaggg[A/G]aagtgaaagttagcta	A	G	NM_003713 // downstream // 197496 // Hs.405156 // PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // downstream // 197496 // Hs.405156 // PPAP2B // 8613 // Homo sapiens phosphatidic	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-2205970	ccatatcagtgtgtca[C/G]gttttttgttttttt	C	G	NM_003713 // upstream // 22289 // Hs.405156 // PPAP2B // 8613 // Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, mRNA. /// NM_177414 // upstream // 22289 // Hs.405156 // PPAP2B // 8613 // Homo sapiens phosphatidic acid p	PPAP2B	PPAP2B, Homo sapiens phosphatidic acid phosphatase type 2B (PPAP2B), transcript variant 1, p32.2
SNP_A-2029049	aaatgtctcctatac[C/T]accactactgaggc	C	T	NM_001004303 // intron // 0 // Hs.437655 // LOC199920 // 199920 // Homo sapiens hypothetical protein LOC199920 (LOC199920), mRNA. /// ENST00000343433 // intron // 0 // -- // -- // --	LOC199920	LOC199920, Homo sapiens hypothetical protein LOC199920 (LOC199920), p32.2
SNP_A-2037225	aacaaacatttgctga[A/G]tacctatcatataata	A	G	NM_001004303 // intron // 0 // Hs.437655 // LOC199920 // 199920 // Homo sapiens hypothetical protein LOC199920 (LOC199920), mRNA. /// ENST00000343433 // intron // 0 // -- // -- // --	LOC199920	LOC199920, Homo sapiens hypothetical protein LOC199920 (LOC199920), p32.2
SNP_A-1828709	taagctgaaactacct[A/G]atgtctgagctga	A	G	NM_001004303 // intron // 0 // Hs.437655 // LOC199920 // 199920 // Homo sapiens hypothetical protein LOC199920 (LOC199920), mRNA. /// ENST00000343433 // intron // 0 // -- // -- // --	LOC199920	LOC199920, Homo sapiens hypothetical protein LOC199920 (LOC199920), p32.2
SNP_A-2199658	ccaaaaggacatagaa[A/G]caatgaaaccccagta	A	G	NM_021080 // intron // 0 // Hs.477370 // DAB1 // 1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // intron // 0 // -- // -- // --	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1945613	ttgttcttgctctaaa[C/G]cttttaataaacatt	C	G	NM_021080 // upstream // 603158 // Hs.477370 // DAB1 // 1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 603158 // -- // -- // -- // -- /// ENST00000270980 // downstream // 161909 // -- // -- // -	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-1945127	ttgtgtgatgtgagtg[C/G]atagtttgaatgggct	C	G	NM_021080 // upstream // 603827 // Hs.477370 // DAB1 // 1600 // Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA. /// ENST00000332102 // upstream // 603827 // -- // -- // -- // -- /// ENST00000270980 // downstream // 161240 // -- // -- // -	DAB1	DAB1, Homo sapiens disabled homolog 1 (Drosophila) (DAB1), p32.2
SNP_A-2169961	caaggctgaggccaca[G/T]acttgcattccaggca	G	T	NM_145243 // downstream // 416092 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream // 8148 // -- // -- // -- // -- /// ENST00000358603 // downstream // 403299 // -- // -	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-2251853	cttcatgagtcgatac[A/G]aaggtgagaatggaa	A	G	NM_145243 // downstream // 415138 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream // 9102 // -- // -- // -- // -- /// ENST00000358603 // downstream // 402345 // -- // -	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2131649	atagccagtaaagaac[C/T]gcactgaggagccagc	C	T	NM_145243 // downstream // 81932 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream // 342308 // — // — // — /// ENST00000358603 // downstream // 69139 // — // –	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-1813979	gtgtcagccactgttc[C/T]aggtagtagaggatat	C	T	NM_145243 // downstream // 43054 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream // 381186 // — // — // — /// ENST00000358603 // downstream // 30261 // — // –	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-2091695	agaaaagattatgaaa[A/G]ccttctgtaccagata	A	G	NM_145243 // downstream // 19677 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream // 404563 // — // — // — /// ENST00000358603 // downstream // 6884 // — // —	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-1945511	ttgttcattatacctta[C/T]gcttttatatgcctg	C	T	NM_145243 // downstream // 12934 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000270980 // upstream // 411306 // — // — // — /// ENST00000358603 // downstream // 141 // — // —	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.2
SNP_A-2049646	aagcttctaaagtaaa[C/T]gttgcatagtaaatat	C	T	NM_145243 // intron // 0 // Hs.425769 // OMA1 // 115209 // Homo sapiens metalloprotease related protein 1 (MPRP-1), mRNA. /// ENST00000294609 // intron // 0 // — // — // — // —	OMA1	OMA1, Homo sapiens metalloprotease related protein 1 (MPRP-1), p32.1
SNP_A-1790615	ggggctagaatgatga[C/T]agctggtagaaggtgg	C	T	NM_002353 // upstream // 71057 // Hs.23582 // TACSTD2 // 4070 // Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), mRNA. /// ENST00000330286 // upstream // T1057 // — // — // — // — /// ENST00000294610 // downstream // 6527 // -	TACSTD2	TACSTD2, Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), p32.1
SNP_A-1790716	ggggctttaagcagaaa[A/G]agtggcatatctagta	A	G	NM_002228 // downstream // 60970 // Hs.525704 // JUN // 3725 // Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), mRNA. /// ENST00000294610 // upstream // 31443 // — // — // — // — /// ENST00000315531 // downstream // 60970 // –	JUN	JUN, Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), p32.1
SNP_A-1787022	gggaaacagattcaga[C/G]agagggaggaacaggc	C	G	NM_002228 // upstream // 122504 // Hs.525704 // JUN // 3725 // Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), mRNA. /// NM_018291 // upstream // 391407 // Hs.444301 // FLJ10986 // 55277 // Homo sapiens hypothetical protein FLJ10986 (F	JUN	JUN, Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), p32.1
SNP_A-1862763	tcattcccaggcgcac[A/G]acccttgtatagtgtg	A	G	NM_002228 // upstream // 158248 // Hs.525704 // JUN // 3725 // Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), mRNA. /// NM_018291 // upstream // 355663 // Hs.444301 // FLJ10986 // 55277 // Homo sapiens hypothetical protein FLJ10986 (F	JUN	JUN, Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), p32.1
SNP_A-2074696	acatatcttgaaaact[G/T]actgtatgccaagtgt	G	T	NM_018291 // intron // 0 // Hs.444301 // FLJ10986 // 55277 // Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // — // — // — // — /// ENST00000303721 // intron // 0 // — // — // —	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-1835571	tacctacgtaagatc[A/G]cctagctgagaattgg	A	G	NM_018291 // intron // 0 // Hs.444301 // FLJ10986 // 55277 // Homo sapiens hypothetical protein FLJ10986 (FLJ10986), mRNA. /// ENST00000315089 // intron // 0 // — // — // — // — /// ENST00000303721 // intron // 0 // — // — // —	FLJ10986	FLJ10986, Homo sapiens hypothetical protein FLJ10986 (FLJ10986), p32.1
SNP_A-1744711	aaatttgagtttagagagagtta[A/G]gagttaatgaagtcaaac agagagga	A	G	NM_005595 // upstream // 762049 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 246820 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs159872, nuclear factor I,p32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829950	taataatcgtgaataa[C/T]gtggaattgctgtgat	C	T	NM_152377 // intron // 0 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// ENST00000294607 // intron // 0 // — // — // — // —	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2228473	ctacttgacttcaaaa[C/G]atactataaatatag	C	G	NM_152377 // upstream // 117787 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 890767 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1655453	gtgttctgattaaatcataaaggga[A/G]taaaaatggcataatggg aaacatcg	A	G	NM_005595 // upstream // 505430 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 503439 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs10493290, nuclear factor I,p32.1
SNP_A-1751045	cactatttagcttctgttttctgc[C/T]agtgagtaaattaaggaatg aactc	C	T	NM_005595 // upstream // 429978 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 578891 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs508507, nuclear factor I,p32.1
SNP_A-1664280	acatgtctttgcttctgggaccagg[A/C]gttgtgcagcccatcctttt ctcaa	A	C	NM_005595 // upstream // 428945 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 579924 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs554692, nuclear factor I,p32.1
SNP_A-2068187	agataaagctgtaatg[C/G]agaaaatggtttggcc	C	G	NM_152377 // upstream // 281178 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 727376 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1694803	cttatgcacttaagtagatccatca[A/G]tgaactagcctgaagga ctttccta	A	G	NM_005595 // upstream // 379431 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 629438 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs4915575, nuclear factor I,p32.1
SNP_A-1944102	ttgtcacaggccatg[A/C]acgcgtctgctttctc	A	C	NM_152377 // upstream // 294210 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 714344 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2161686	atttggtatagcgcaa[A/G]ccacgggtatagtggt	A	G	NM_152377 // upstream // 296628 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 711926 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2068500	cctaacgttgctagcc[C/G]ccttctcaaaatcttgc	C	G	NM_152377 // upstream // 322355 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 686199 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1659997	gggtgagtttgtggttctcactgga[C/G]agcatctatacagacaa acttgc	C	G	NM_005595 // upstream // 296910 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 711959 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs310186, nuclear factor I,p31.3
SNP_A-2069201	tgttctgcaaactaca[C/T]gggctgatgattgcct	C	T	NM_152377 // upstream // 497589 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 510965 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1919344	ttaagaggatgaaacc[A/G]atatcctgactaaggg	A	G	NM_152377 // upstream // 593359 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 415195 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-1662148	ttgctttggacccagctgcataaatc[C/G]aagatcctctcttaaat ccattt	C	G	NM_005595 // upstream // 65896 // Hs.173933 // NFIA // 4774 // nuclear factor I/A /// NM_152377 // upstream // 942973 // Hs.47385 // MGC34837 // 127795 // hypothetical protein MGC34837	NFIA	NFIA , rs1779866, nuclear factor I,p31.3
SNP_A-2070146	gctgtaaatcaaggca[A/C]ctgtgacatcatggtg	A	C	NM_152377 // upstream // 606744 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 401810 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2070452	gtgtcatcccagccata[C/T]aaagaaactctgaat	C	T	NM_152377 // upstream // 630876 // Hs.47385 // MGC34837 // 127795 // Homo sapiens hypothetical protein MGC34837 (MGC34837), mRNA. /// NM_005595 // upstream // 377678 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB03786	MGC34837	MGC34837, Homo sapiens hypothetical protein MGC34837 (MGC34837), p31.3
SNP_A-2035716	aaatgtgaactacca[G/T]caccatgaactgaact	G	T	NM_005595 // intron // 0 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB037860 // intron // 0 // Hs.191911 // NFIA // 4774 // Homo sapiens mRNA for KIAA1439 protein, partial cds. /// ENST00000357977 // intron // 0 // -	NFIA	NFIA, Homo sapiens nuclear factor I p31.3
SNP_A-2249832	cttaatttccaaataa[A/G]tctatctgtaacacct	A	G	NM_005595 // intron // 0 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB037860 // intron // 0 // Hs.191911 // NFIA // 4774 // Homo sapiens mRNA for KIAA1439 protein, partial cds. /// ENST00000357977 // intron // 0 // -	NFIA	NFIA, Homo sapiens nuclear factor I p31.3
SNP_A-1835166	taccctttcctctgt[A/G]aaccatgagtaacaaa	A	G	NM_005595 // downstream // 46802 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB037860 // downstream // 76615 // Hs.191911 // NFIA // 4774 // Homo sapiens mRNA for KIAA1439 protein, partial cds. /// NM_032027 // downst	NFIA	NFIA, Homo sapiens nuclear factor I p31.3
SNP_A-2034477	aaatctgaaataaata[C/T]ggcaaattactaacat	C	T	NM_005595 // downstream // 213315 // Hs.191911 // NFIA // 4774 // Homo sapiens nuclear factor I/A (NFIA), mRNA. /// AB037860 // downstream // 243128 // Hs.191911 // NFIA // 4774 // Homo sapiens mRNA for KIAA1439 protein, partial cds. /// NM_032027 // down	NFIA	NFIA, Homo sapiens nuclear factor I p31.3
SNP_A-2284365	gatatttaggtagta[A/T]ggggagaaagtatta	A	T	NM_005799 // intron // 0 // Hs.478125 // INADL // 10207 // Homo sapiens InaD-like protein (INADL), transcript variant 3, mRNA. /// NM_176878 // intron // 0 // Hs.478125 // INADL // 10207 // Homo sapiens InaD-like protein (INADL), transcript variant 4, mRN	INADL	INADL, Homo sapiens InaD-like protein (INADL), transcript variant 3, p31.3
SNP_A-2278365	gagctacagccactaa[C/T]gctggtcctcagtca	C	T	NM_181712 // upstream // 35443 // Hs.283398 // LOC163782 // 163782 // Homo sapiens hypothetical protein LOC163782 (LOC163782), mRNA. /// NM_003368 // upstream // 82153 // Hs.35086 // USP1 // 7398 // Homo sapiens ubiquitin specific protease 1 (USP1), mRNA.	LOC163782	LOC163782, Homo sapiens hypothetical protein LOC163782 (LOC163782), p31.3
SNP_A-1683822	tagaaattaaataatagagacagaaa[C/T]caagtttaagaatcttg tattaaat	C	T	NM_032852 // intron // 0 // Hs.7353 // APG4C // 84938 // APG4 autophagy 4 homolog C (S. cerevisiae) /// NM_178221 // intron // 0 // Hs.7353 // APG4C // 84938 // APG4 autophagy 4 homolog C (S. cerevisiae)	APG4C	APG4C , rs6683832, APG4 autophagy 4 homolog C (S. cerevisiae) ,p31.3
SNP_A-1753671	ctgttgaactctttctctctgtg[A/G]ttccaagtgtttgattatatac at	A	G	NM_032852 // intron // 0 // Hs.7353 // APG4C // 84938 // APG4 autophagy 4 homolog C (S. cerevisiae) /// NM_178221 // intron // 0 // Hs.7353 // APG4C // 84938 // APG4 autophagy 4 homolog C (S. cerevisiae)	APG4C	APG4C , rs2886770, APG4 autophagy 4 homolog C (S. cerevisiae) ,p31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1751609	taltataatttccttaatcagcaa[C/T]aatgactaaaacatgtgat ctaaaa	C	T	NM_012183 // upstream // 197776 // Hs.424212 // FOXD3 // 27022 // forkhead box D3 /// NM_032852 // downstream // 260905 // Hs.7353 // APG4C // 84938 // APG4 autophagy 4 homolog C (S. cerevisiae) /// NM_178221 // downstream // 260905 // Hs.7353 // APG4C /	FOXD3	FOXD3 , rs10493339, forkhead box D3 ,p31.3
SNP_A-2054037	aagttagtaaaagctc[A/G]agaaaatgttaccttt	A	G	NM_032852 // intron // 0 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // intron // 0 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S.	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2084306	actagtttggaaaaaaa[A/T]tacgaatctttatatt	A	T	NM_032852 // downstream // 7295 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 7295 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-1878152	tctgtatctccagcaa[C/T]ctgaatgtaacaggtc	C	T	NM_032852 // downstream // 83947 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 83947 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-1947985	tttagaattgctactg[C/T]atggtgataataagaa	C	T	NM_032852 // downstream // 230990 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 230990 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophag	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2314016	ggagctggatctggaa[A/G]aatgaatgagatttaa	A	G	NM_032852 // downstream // 233187 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 233187 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophag	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2074096	acagttttgattgcca[C/T]ggagaaggggaatgct	C	T	NM_032852 // downstream // 241313 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 241313 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophag	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2152004	atgttttgtttcctcaa[A/G]ctacttctctgaagg	A	G	NM_032852 // downstream // 244432 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 244432 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophag	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2093533	gaaaattacagaggca[A/G]tagaagaaaacggaat	A	G	NM_032852 // downstream // 267172 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, mRNA. /// NM_178221 // downstream // 267172 // Hs.7353 // APG4C // 84938 // Homo sapiens APG4 autophag	APG4C	APG4C, Homo sapiens APG4 autophagy 4 homolog C (S. cerevisiae) (APG4C), transcript variant 1, p31.3
SNP_A-2285397	gatctgtttacttta[C/T]cctgcccagacttagc	C	T	NM_014288 // intron // 0 // Hs.166539 // ITGB3BP // 23421 // Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA. /// ENST00000271002 // intron // 0 // — // — // — // ENST00000283568 // intron // 0 // — // — //	ITGB3BP	ITGB3BP, Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), p31.3
SNP_A-1953782	tttgagagaagactga[A/G]ctactaactgagaagt	A	G	NM_014288 // intron // 0 // Hs.166539 // ITGB3BP // 23421 // Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA. /// ENST00000271002 // intron // 0 // — // — // — // — // ENST00000283568 // intron // 0 // — // — //	ITGB3BP	ITGB3BP, Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), p31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2096297	cttgaccatcacagaa[C/T]ctaagtaaatggatag	C	T	NM_014288 // upstream // 14000 // Hs.166539 // ITGB3BP // 23421 // Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA. /// NM_006021 // upstream // 12032 // Hs.508041 // DLEU2 // 8847 // Homo sapiens deleted in lymphocytic leuk	ITGB3BP	ITGB3BP, Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), p31.3
SNP_A-1790843	ggggggctaaaccgacca[A/G]gtgtgaggattgtaaa	A	G	NM_002633 // intron // 0 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// ENST00000006941 // intron // 0 // — // — // — // —	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2132027	ataggctcattgggca[C/T]tcatgtagtatccctc	C	T	NM_002633 // intron // 0 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// ENST00000006941 // intron // 0 // — // — // — // — /// ENST00000340212 // intron // 0 // — // — // — // —	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2211354	ccctactgcacttccc[A/G]ctggtcttatttctct	A	G	NM_002633 // intron // 0 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// ENST00000006941 // intron // 0 // — // — // — // — /// ENST00000340212 // intron // 0 // — // — // — // —	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-1875088	tctctcacttacacac[A/C]ggtctgtttctacctg	A	C	NM_002633 // intron // 0 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// ENST00000006941 // intron // 0 // — // — // — // — /// ENST00000340212 // intron // 0 // — // — // — // —	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2221908	cctttttggaagtgga[C/T]gagaatggtgattcca	C	T	NM_002633 // downstream // 35304 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// NM_005012 // upstream // 78871 // Hs.436456 // ROR1 // 4919 // Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA. //	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2098023	aaccagggagccttcc[A/G]cattctcgagtcaagt	A	G	NM_002633 // downstream // 39631 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// NM_005012 // upstream // 74544 // Hs.436456 // ROR1 // 4919 // Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA. //	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2098115	gatactcagcatcttc[G/T]tcgtctcctatcactc	G	T	NM_002633 // downstream // 47570 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// NM_005012 // upstream // 66605 // Hs.436456 // ROR1 // 4919 // Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA. //	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-2098147	aaccgcagttccaaa[C/T]aacaataaaattccaag	C	T	NM_002633 // downstream // 48229 // Hs.1869 // PGM1 // 5236 // Homo sapiens phosphoglucomutase 1 (PGM1), mRNA. /// NM_005012 // upstream // 65946 // Hs.436456 // ROR1 // 4919 // Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA. //	PGM1	PGM1, Homo sapiens phosphoglucomutase 1 (PGM1), p31.3
SNP_A-1732107	ttctagggtacagttaaggtctca[C/T]ggatgttcaactaactaa atgagaa	C	T	NM_020925 // intron // 0 // Hs.24790 // KIAA1573 // 57685 // KIAA1573 protein	KIAA1573	KIAA1573 , rs10493360, KIAA1573 protein,p31.3
SNP_A-2066875	acaaaatggagtaaga[C/T]cgtgagtattcttaga	C	T	NM_152489 // downstream // 177747 // Hs.388746 // MGC35130 // 148581 // Homo sapiens hypothetical protein MGC35130 (MGC35130), mRNA. /// NM_020925 // upstream // 83824 // Hs.443891 // KIAA1573 // 57685 // Homo sapiens KIAA1573 protein (KIAA1573), mRNA. //	MGC35130	MGC35130, Homo sapiens hypothetical protein MGC35130 (MGC35130), p31.3
SNP_A-2061835	aatggatcccctcac[C/T]gtaaggagatacaaac	C	T	NM_020925 // intron // 0 // Hs.443891 // KIAA1573 // 57685 // Homo sapiens KIAA1573 protein (KIAA1573), mRNA. /// ENST00000335761 // intron // 0 // — // — // — // —	KIAA1573	KIAA1573, Homo sapiens KIAA1573 protein (KIAA1573), p31.3
SNP_A-2169450	caagcccacaaggaa[C/G]tgaagtaccagctgcc	C	G	NM_020925 // intron // 0 // Hs.443891 // KIAA1573 // 57685 // Homo sapiens KIAA1573 protein (KIAA1573), mRNA. /// ENST00000335761 // intron // 0 // — // — // — // —	KIAA1573	KIAA1573, Homo sapiens KIAA1573 protein (KIAA1573), p31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2109056	cacaggctcagatagg[C/G]agaagattagaatat	C	G	NM_020925 // downstream // 29763 // Hs.443891 // KIAA1573 // 57685 // Homo sapiens KIAA1573 protein (KIAA1573), mRNA. /// NM_020925 // downstream // 29757 // Hs.443891 // KIAA1573 // 57685 // Homo sapiens KIAA1573 protein (KIAA1573), mRNA. /// NM_018211 /	KIAA1573	KIAA1573, Homo sapiens KIAA1573 protein (KIAA1573), p31.3
SNP_A-1920931	ttacacttccttatgg[A/G]cagtttctattaatta	A	G	NM_018211 // intron // 0 // Hs.207538 // KIAA1579 // 55225 // Homo sapiens hypothetical protein FLJ10770 (KIAA1579), mRNA. /// ENST00000294428 // intron // 0 // — // — // — // —	KIAA1579	KIAA1579, Homo sapiens hypothetical protein FLJ10770 (KIAA1579), p31.3
SNP_A-2268370	gaatgccctctcctgg[A/G]aagctaggaatgttga	A	G	NM_002227 // intron // 0 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// ENST00000342505 // intron // 0 // — // — // — // — /// ENST00000294423 // intron // 0 // — // — // —	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-1886144	tgaccatctgcagac[A/G]aagaatctgtgctct	A	G	NM_002227 // intron // 0 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// ENST00000342505 // intron // 0 // — // — // — // — /// ENST00000294423 // intron // 0 // — // — // —	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-2266533	gaagtatgaaggaaga[A/C]tcaagatacagttaga	A	C	NM_002227 // upstream // 33874 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 31016 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase)	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-2286009	gatgatctaaaaccag[C/G]acagcaaatacacatg	C	G	NM_002227 // upstream // 41375 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 38517 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase)	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-1813078	gtgggtttggtggaaa[A/G]cgagcaaagcacctg	A	G	NM_002227 // upstream // 71062 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /// NM_002227 // upstream // 68204 // Hs.398570 // JAK1 // 3716 // Homo sapiens Janus kinase 1 (a protein tyrosine kinase)	JAK1	JAK1, Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), p31.3
SNP_A-2231431	ctattgggaggattaa[A/G]tcagataacgtatgta	A	G	NM_013410 // upstream // 119075 // Hs.10862 // AK3 // 205 // Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // upstream // 119075 // Hs.10862 // AK3L2 // 387851 // Homo sapi	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-2111607	aaaattggtaagccac[C/T]atcccagaaagagctc	C	T	NM_013410 // upstream // 97980 // Hs.10862 // AK3 // 205 // Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // upstream // 97980 // Hs.10862 // AK3L2 // 387851 // Homo sapien	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-2049393	aagctgactgataaaa[C/T]cgggcctaagactaat	C	T	NM_013410 // downstream // 6505 // Hs.10862 // AK3 // 205 // Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // downstream // 6505 // Hs.10862 // AK3L2 // 387851 // Homo sapi	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-2286058	gatgatgttatgaaca[A/G]taatgcttaccattta	A	G	NM_013410 // downstream // 18104 // Hs.10862 // AK3 // 205 // Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // downstream // 18104 // Hs.10862 // AK3L2 // 387851 // Homo sa	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-2248595	ctgttagtggaggaaa[A/C]ttaaccagatgaccta	A	C	NM_013410 // downstream // 21420 // Hs.10862 // AK3 // 205 // Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // downstream // 21420 // Hs.10862 // AK3L2 // 387851 // Homo sa	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2223020	cgcatatttccctgaa[A/G]cagatacatagataac	A	G	NM_013410 // downstream // 24174 // Hs.10862 // AK3 // 205 // Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001002921 // downstream // 24174 // Hs.10862 // AK3L2 // 387851 // Homo sa	AK3	AK3, Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, transcript variant 2, p31.3
SNP_A-2084149	actaggaatatttctc[A/T]ctctagttcaaaaaac	A	T	ENST00000263441 // intron // 0 // — // — // — // —	-	p31.2
SNP_A-2160984	atttcttagtaatacc[A/C]actattgctaagtgac	A	C	NM_001003679 // intron // 0 // Hs.23581 // LEPR // 3953 // Homo sapiens leptin receptor (LEPR), transcript variant 2, mRNA. /// NM_002303 // intron // 0 // Hs.23581 // LEPR // 3953 // Homo sapiens leptin receptor (LEPR), transcript variant 1, mRNA. /// EN	LEPR	LEPR, Homo sapiens leptin receptor (LEPR), transcript variant 2, p31.2
SNP_A-2000104	gttaaataaatgccag[C/T]caaaagtaactcacct	C	T	NM_002600 // intron // 0 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // — // — // — // — /// ENST00000341517 /	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2212297	ccctggggagtggaca[A/G]gtatttctagttaaaa	A	G	NM_002600 // intron // 0 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // — // — // — // — /// ENST00000341517 /	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1934901	ttctgaagttactgaa[A/G]tagttgagccccagta	A	G	NM_002600 // intron // 0 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // — // — // — // — /// ENST00000341517 /	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1735947	tgacaagttaatgtttaatttttta[C/T]gatagagcaaaggtacttta aattc	C	T	L20971 // intron // 0 // - // - // - // Human phosphodiesterase mRNA, complete cds.	-	- , rs1572930, Human phosphodiesterase mRNA, complete cds.,p31.2
SNP_A-1921172	ttacatatagattgga[A/G]ctgaaatcaagatgga	A	G	NM_002600 // intron // 0 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// ENST00000329654 // intron // 0 // — // — // — // — /// ENST00000341517 /	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2166229	caaatcactcataagc[A/G]gatgaggtttccgtga	A	G	NM_002600 // downstream // 90384 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 68632 // Hs.132121 // DKFZp761D221 // 84251 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1936692	ttcttgttatagagaa[A/G]actgttcaagctaccc	A	G	NM_002600 // downstream // 99819 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 59197 // Hs.132121 // DKFZp761D221 // 84251 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1802975	gtatgttggacaagaa[C/T]gacttgtgatcatctt	C	T	NM_002600 // downstream // 119285 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 39731 // Hs.132121 // DKFZp761D221 // 84251 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-1871513	tctaacttcttaaggt[A/G]aatgcatggctcatgt	A	G	NM_002600 // downstream // 128310 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 30706 // Hs.132121 // DKFZp761D221 // 84251 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2124281	ttccttcttaagaaa[A/T]tgttgtgccctagtt	A	T	NM_002600 // downstream // 151233 // Hs.198072 // PDE4B // 5142 // Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA. /// NM_032291 // upstream // 7783 // Hs.132121 // DKFZp761D221 // 84251 //	PDE4B	PDE4B, Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), p31.2
SNP_A-2130393	tctcagtatcagaata[C/G]aagccaagtctggcct	C	G	NM_015139 // upstream // 36450 // Hs.213642 // SLC35D1 // 23169 // Homo sapiens solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (SLC35D1), mRN /// NM_144701 // upstream // 75991 // Hs.200929 // IL23R //	SLC35D1	SLC35D1, Homo sapiens solute carrier family 35 (UDP-glucuronic acid,p31.2
SNP_A-1804219	gtcacctacagcttca[C/T]agaaaaatttttaca	C	T	NM_015139 // upstream // 89718 // Hs.213642 // SLC35D1 // 23169 // Homo sapiens solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (SLC35D1), mRN /// NM_144701 // upstream // 22723 // Hs.200929 // IL23R //	SLC35D1	SLC35D1, Homo sapiens solute carrier family 35 (UDP-glucuronic acid p31.2
SNP_A-2181569	cagagaactgtttcct[C/T]aaacgatccacttgcc	C	T	NM_144701 // intron // 0 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// ENST00000294602 // intron // 0 // — // — // — /// ENST00000347310 // intron // 0 // — // — // — // —	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2131610	attatgatgtcagcca[C/T]atttggtagtgtaatt	C	T	NM_144701 // intron // 0 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// ENST00000294602 // intron // 0 // — // — // — /// ENST00000347310 // intron // 0 // — // — // —	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2045577	aagaattattgcatca[A/G]gagttaagcacctttt	A	G	NM_144701 // intron // 0 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// ENST00000294602 // intron // 0 // — // — // — /// ENST00000347310 // intron // 0 // — // — // — // —	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-1946676	tttaacagatcattccd[A/G]aactggtaggttttt	A	G	NM_144701 // CDS // 0 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// ENST00000294602 // CDS // 0 // — // — // — /// ENST00000347310 // CDS // 0 // — // — // —	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-1916487	tgtttaagccacccaa[C/G]ccgactaagcattcct	C	G	NM_144701 // intron // 0 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// ENST00000294602 // intron // 0 // — // — // — /// ENST00000347310 // intron // 0 // — // — // — // —	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-1924276	ttataaacagctaatc[A/G]gaaccctcatttgtca	A	G	NM_144701 // downstream // 18953 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// NM_001559 // upstream // 28446 // Hs.479347 // IL12RB2 // 3595 // Homo sapiens interleukin 12 receptor, beta 2 (IL12RB2), mRNA. ///	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2087317	actgcacctggcctacf[A/G]ataatttgaagacaa	A	G	NM_144701 // downstream // 19036 // Hs.200929 // IL23R // 149233 // Homo sapiens interleukin-23 receptor (IL23R), mRNA. /// NM_001559 // upstream // 28363 // Hs.479347 // IL12RB2 // 3595 // Homo sapiens interleukin 12 receptor, beta 2 (IL12RB2), mRNA. ///	IL23R	IL23R, Homo sapiens interleukin-23 receptor (IL23R), p31.2
SNP_A-2135666	gttcctgttgataaaa[G/T]gcttagatcagtgctc	G	T	NM_001924 // downstream // 3577 // Hs.80409 // GADD45A // 1647 // Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA. /// NM_018841 // downstream // 9624 // Hs.431101 // GNG12 // 55970 // Homo sapiens guanine nucleotide binding pro	GADD45A	GADD45A, Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), p31.2
SNP_A-1946937	tttaaggtcatttagc[A/G]gataatgccctctat	A	G	NM_001924 // downstream // 10479 // Hs.80409 // GADD45A // 1647 // Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA. /// NM_018841 // downstream // 2722 // Hs.431101 // GNG12 // 55970 // Homo sapiens guanine nucleotide binding pr	GADD45A	GADD45A, Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), p31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796596	ggttactgtgtcgaaa[G/T]ggaagcggtgacgttc	G	T	NM_018841 // intron // 0 // Hs.431101 // GNG12 // 55970 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), mRNA. /// ENST00000305296 // intron // 0 // — // — // — // —	GNG12	GNG12, Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), p31.2
SNP_A-2149843	atgtcaaattggtgga[C/G]agatagacacatagat	C	G	NM_018841 // upstream // 201775 // Hs.431101 // GNG12 // 55970 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), mRNA. /// NM_004675 // downstream // 10764 // Hs.194695 // DIRAS3 // 9077 // Homo sapiens ras homolog gene fam	GNG12	GNG12, Homo sapiens guanine nucleotide binding protein (G protein), gamma 12 (GNG12), p31.2
SNP_A-1900417	tggagatgaactcaga[A/C]ctcaaggctcagctca	A	C	ENST00000294604 // CDS // 0 // — // — // — // —	-	p31.2
SNP_A-1923262	ttagcttgatgcacaa[A/G]gtcctccatgcttggc	A	G	NM_000329 // downstream // 185637 // Hs.2133 // RPE65 // 6121 // Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000294604 // upstream // 70 // — // — // — // — /// ENST00000262340 // downstream // 185637 //	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-2033274	aaatagaactactacc[A/G]ctattacttctaccac	A	G	NM_000329 // downstream // 29000 // Hs.2133 // RPE65 // 6121 // Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000294604 // upstream // 156707 // — // — // — // — /// ENST00000262340 // downstream // 29000	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-1909061	tgtatattgtgacaat[C/G]aattatattttgaaat	C	G	NM_000329 // downstream // 20426 // Hs.2133 // RPE65 // 6121 // Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000294604 // upstream // 165281 // — // — // — // — /// ENST00000262340 // downstream // 20426	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-2088457	actgtatggttatcac[G/T]gcctgaagaaatatta	G	T	NM_000329 // intron // 0 // Hs.2133 // RPE65 // 6121 // Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), mRNA. /// ENST00000262340 // intron // 0 // — // — // — // —	RPE65	RPE65, Homo sapiens retinal pigment epithelium-specific protein 65kDa (RPE65), p31.2
SNP_A-1894643	tgccacttgcaactga[C/G]tattgcagagaatttt	C	G	NM_017779 // intron // 0 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// ENST00000317877 // intron // 0 // — // — // — // — /// ENST00000262341 // intron // 0 // — // — // — // — /// ENST00000262	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-2143957	gcagtgtaaaataagc[A/G]caaggcccaggacttt	A	G	NM_017779 // intron // 0 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// ENST00000317877 // intron // 0 // — // — // — // — /// ENST00000262343 // intron // 0 // — // — // — // —	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-2144702	agggcattgaatacca[C/T]gataaaggctttatac	C	T	NM_017779 // upstream // 87765 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 1175386 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-1891630	tgattgccttttatga[C/T]cttgattcctagaagc	C	T	NM_017779 // upstream // 125955 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 1137196 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-2285185	gatctcaaattacttg[A/G]caaagatggacttta	A	G	NM_017779 // upstream // 163421 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 1099730 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2146427	tcacagacaattctcc[A/G]cttcacgtctgccctt	A	G	NM_017779 // upstream // 273673 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 989478 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-1916842	tgtttctatttctgta[A/G]aattggtgataatatc	A	G	NM_017779 // upstream // 335779 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 927372 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.2
SNP_A-2128635	ataatatgtacaatga[A/G]ctccatgaaacgagtt	A	G	NM_017779 // upstream // 871016 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 392135 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.1
SNP_A-2101649	agatgatgaatgcaac[G/T]gataaaatgtgtgggt	G	T	NM_017779 // upstream // 937134 // Hs.445098 // DEPDC1 // 55635 // Homo sapiens DEP domain containing 1 (DEPDC1), mRNA. /// NM_020794 // upstream // 326017 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000317877 //	DEPDC1	DEPDC1, Homo sapiens DEP domain containing 1 (DEPDC1), p31.1
SNP_A-1715931	taatagaatgtgatgcaagtaaaaa[A/C]atgtattttcaacatttcaaatatt	A	C	NM_020794 // intron // 0 // Hs.134228 // KIAA1365 // 57554 // densin-180	KIAA1365	KIAA1365 , rs12045965, densin-180,p31.1
SNP_A-1679464	tctctctatacagtctgctgcccga[A/C]gttagaatttagagacagcatctag	A	C	NM_020794 // intron // 0 // Hs.134228 // KIAA1365 // 57554 // densin-180	KIAA1365	KIAA1365 , rs1015819, densin-180,p31.1
SNP_A-1756683	gtcattcacacattctaacagcaga[A/G]gttactaaaacacttta accagagg	A	G	NM_004768 // intron // 0 // Hs.443458 // SFRS11 // 9295 // splicing factor, arginine/serine-rich 11	SFRS11	SFRS11 , rs10489927, splicing factor, arginine,p31.1
SNP_A-2141532	atcttagagcttaaaa[C/T]tgaaattccaaaataa	C	T	NM_020794 // intron // 0 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // — // — // — // —	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2038794	aacagcaagataccta[C/T]acaaaaaagcttacac	C	T	NM_020794 // intron // 0 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // — // — // — // —	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-1940343	ttgccacaatgtgaac[C/T]gtccctttcccaggtg	C	T	NM_020794 // intron // 0 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // — // — // — // —	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-1949730	tttcaaaagtcctaaa[A/G]cagagaagaaggttga	A	G	NM_020794 // intron // 0 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// ENST00000035383 // intron // 0 // — // — // — // —	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-1817963	gttctacagtatggca[C/T]ggagatgggtaaaaaa	C	T	NM_020794 // downstream // 13100 // Hs.479658 // LRRC7 // 57554 // Homo sapiens densin-180 (KIAA1365), mRNA. /// NM_017768 // downstream // 9471 // Hs.147836 // FLJ20331 // 55631 // Homo sapiens hypothetical protein FLJ20331 (FLJ20331), mRNA. /// ENST0000	LRRC7	LRRC7, Homo sapiens densin-180 (KIAA1365), p31.1
SNP_A-2298820	gcccatgctcttcaag[A/T]cttagatacttattct	A	T	NM_153742 // intron // 0 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // intron // 0 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cystathionine gamma-lya	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-2284752	gatcatcatggtaaaa[G/T]tatcttatcagtcaat	G	T	NM_153742 // downstream // 118886 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 118886 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cysta	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2088393	actgtactgttcacta[A/C]catattcctaagtcct	A	C	NM_153742 // downstream // 119016 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 119016 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cysta	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-1810166	gtgatcgatatggtaq[C/T]attcctcaggttatc	C	T	NM_153742 // downstream // 119744 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 119744 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cysta	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-2262452	gaaatgcagagacta[A/G]cagaagtgattacca	A	G	NM_153742 // downstream // 258656 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, mRNA. /// NM_001902 // downstream // 258656 // Hs.19904 // CTH // 1491 // Homo sapiens cystathionase (cysta	CTH	CTH, Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), transcript variant 2, p31.1
SNP_A-2183155	cagcaaccacagggaac[C/T]gaacctgcgaagcta	C	T	NM_000957 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, mRNA. /// NM_198717 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens prostaglandin E receptor 3 (	PTGER3	PTGER3, Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, p31.1
SNP_A-1955471	ttggtatttgtaaca[G/T]caggtctaaaacaagt	G	T	NM_000957 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, mRNA. /// NM_198717 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens prostaglandin E receptor 3 (	PTGER3	PTGER3, Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, p31.1
SNP_A-2168255	caactgcaaaagctag[A/C]cacaagatttaagat	A	C	NM_000957 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, mRNA. /// NM_198717 // intron // 0 // Hs.445000 // PTGER3 // 5733 // Homo sapiens prostaglandin E receptor 3 (	PTGER3	PTGER3, Homo sapiens prostaglandin E receptor 3 (subtype EP3) (PTGER3), transcript variant 1, p31.1
SNP_A-1718783	acgtataatttgagtatattctq[A/C]ctaacatttaacaaaatatat tta	A	C	NM_173808 // intron // 0 // Hs.479888 // NEGR1 // 257194 // neuronal growth regulator 1	NEGR1	NEGR1, rs1385919, neuronal growth regulator 1,p31.1
SNP_A-1791900	gggtgcaagtctcaag[C/G]ctacatgtggtgttg	C	G	NM_173808 // upstream // 98283 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 98280 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// ENS	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1868266	tcctcagactccdgta[C/T]ggtgcaattgaccact	C	T	NM_173808 // upstream // 167667 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 167664 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// E	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1938917	ttgaggtcctctgatta[C/T]agtgtaccatcccctg	C	T	NM_173808 // upstream // 487837 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 487834 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// E	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2263905	gaactaatgtcataga[A/T]gaatttctgtagtcc	A	T	NM_173808 // upstream // 645916 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 645913 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// E	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2055269	aataagagaagaagaaa[A/G]ctgaatgacaggg	A	G	NM_173808 // upstream // 1272386 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1272383 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1846754	tatcaactcaaccata[A/G]taggatgggactggg	A	G	NM_173808 // upstream // 1344318 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1344315 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1806099	gtcctcctatcatctc[C/T]ccatcctctactatc	C	T	NM_173808 // upstream // 1488480 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1488477 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2137058	atcagtttctctaaa[C/T]tgaccttcaaact	C	T	NM_173808 // upstream // 1584210 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1584207 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-2228080	ctactaaagttcttac[C/T]ggtgggagagagtagt	C	T	NM_173808 // upstream // 1596737 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. /// NM_173808 // upstream // 1596734 // Hs.146542 // NEGR1 // 257194 // Homo sapiens neuronal growth regulator 1 (NEGR1), mRNA. ///	NEGR1	NEGR1, Homo sapiens neuronal growth regulator 1 (NEGR1), p31.1
SNP_A-1717337	ctactcatgttttgatacgaataaa[A/G]ccagcgacatgctttctaa aatctt	A	G	AL834414 // upstream // 29379 // Hs.200286 // DKFZp547l048 // 127254 // hypothetical protein DKFZp547l048 /// NM_001889 // downstream // 103123 // Hs.83114 // CRYZ // 1429 // crystallin, zeta (quinone reductase)	DKFZp547l048	DKFZp547l048 , rs696699, hypothetical protein DKFZp547l048 ,p31.1
SNP_A-2238862	ctcttcaaataaggac[A/G]ctgagaggttggccgt	A	G	NM_015978 // intron // 0 // Hs.513262 // TNNI3K // 51086 // Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // intron // 0 // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-2194787	tccatacaaactacttt[A/T]aaggtagaaatattat	A	T	NM_015978 // intron // 0 // Hs.513262 // TNNI3K // 51086 // Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // intron // 0 // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-1744127	tctgactccaaagtttgtactttta[A/G]ctattgtgctaaattattaat gaa	A	G	NM_152697 // downstream // 384339 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032, rs277362, hypothetical protein MGC34032,p31.1
SNP_A-2079811	accctgccaggtcact[C/G]agggatttcataacag	C	G	NM_015978 // downstream // 8934 // Hs.513262 // TNNI3K // 51086 // Homo sapiens TNNI3 interacting kinase (TNNI3K), mRNA. /// ENST00000326637 // downstream // 8934 // --- // --- // --- // --- ENST00000294635 // upstream // 70009 // --- // --- // ---	TNNI3K	TNNI3K, Homo sapiens TNNI3 interacting kinase (TNNI3K), p31.1
SNP_A-2160576	atttccctcatgcgaa[A/C]ggaggtggataattag	A	C	ENST00000342217 // intron // 0 // --- // --- // ---	-	p31.1
SNP_A-1667262	ctttaggcccctgttatacacgagg[A/G]agacaagatatttgttgtt tactca	A	G	NM_152697 // downstream // 211950 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032, rs10493550, hypothetical protein MGC34032,p31.1
SNP_A-1690777	tagaagaaattaattgagtaaaaaa[C/T]aatctgctgttcatttgc ctaaaat	C	T	NM_152697 // downstream // 186526 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032, rs7529122, hypothetical protein MGC34032,p31.1
SNP_A-1734400	tttctaaaagattaatgtggctgat[A/G]tatttgtttcatgttaagga aaag	A	G	NM_152697 // downstream // 61872 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032, rs10493553, hypothetical protein MGC34032,p31.1
SNP_A-1723982	tactggcaggtcttagaatactaaa[C/T]gtgatttttcgaaaaagtt actttta	C	T	NM_152697 // downstream // 61721 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032, rs18523349, hypothetical protein MGC34032,p31.1
SNP_A-2102329	agattatgcagcaaaa[C/T]aagaaagaagactaagt	C	T	NM_138467 // downstream // 130685 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 232126 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// E	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2033146	aaataccacattaga[A/G]aaactgcgccatgcaa	A	G	NM_138467 // downstream // 146172 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 216639 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// E	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-1735406	atctataacacaacaaatacattc[A/G]actctttcttggatatatg agtga	A	G	AK091400 // 3UTR // 0 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032 /// AK093170 // intron // 0 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032 , rs4949821, hypothetical protein MGC34032 ,p31.1
SNP_A-1744709	caggtatgggatggaagaaggagca[C/T]gagtaaggtcaagc actaaaacatg	C	T	NM_152697 // intron // 0 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032 , rs10493561, hypothetical protein MGC34032,p31.1
SNP_A-1914997	tgttatatgttgaaga[A/G]aacaaaaataataata	A	G	NM_138467 // downstream // 196089 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 166722 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// E	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2239445	ctctttggagcaatga[A/C]agttttggaaatacat	A	C	NM_138467 // downstream // 235102 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 127709 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// E	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-1647200	aaatgcaagcagtttagaatagaag[A/T]ctaatcagaagatag agaagctttt	A	T	NM_152697 // intron // 0 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032 , rs10493569, hypothetical protein MGC34032,p31.1
SNP_A-1709059	cgacctgtaatccaatgctatctg[C/T]atggacaataaaaaaca cgccagca	C	T	NM_152697 // intron // 0 // Hs.213897 // MGC34032 // 204962 // hypothetical protein MGC34032	MGC34032	MGC34032 , rs10493570, hypothetical protein MGC34032,p31.1
SNP_A-2250512	cttaggtgagtcataa[A/G]gatgaaataggcccag	A	G	NM_138467 // downstream // 268951 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 93860 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// EN	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2313303	ggagaccaacatagaa[A/G]gagggtgattcctgga	A	G	NM_138467 // downstream // 270806 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 92005 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// EN	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-1941670	ttggaagaagtaacaa[C/T]gtaagtaccaactacc	C	T	NM_138467 // downstream // 315962 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 46849 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// EN	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2000126	agagaaacagtaactc[A/G]attccttaagtgcaa	A	G	NM_138467 // downstream // 318498 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 44313 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// EN	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-2108372	agctgcaagtttaca[C/T]agagtatttccttcag	C	T	NM_138467 // downstream // 332314 // Hs.348411 // LOC127253 // 127253 // Homo sapiens hypothetical protein BC009514 (LOC127253), mRNA. /// NM_001001933 // upstream // 30497 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// EN	LOC127253	LOC127253, Homo sapiens hypothetical protein BC009514 (LOC127253), p31.1
SNP_A-1786886	ggctttaccgtcca[A/T]aagagaactctgcatt	A	T	NM_001001933 // intron // 0 // Hs.403934 // LHX8 // 431707 // Homo sapiens LIM homeobox 8 (LHX8), mRNA. /// ENST00000359730 // intron // 0 // — // — // — /// ENST00000294638 // intron // 0 // — // — // — /// ENST00000356261 // in	LHX8	LHX8, Homo sapiens LIM homeobox 8 (LHX8), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170600	caagtgggagctaaac[A/C]aagggaatatgtagac	A	C	NM_152697 // intron // 0 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// ENST00000294639 // intron // 0 // — // — // —	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2282142	gagtgtctatggtagga[C/G]agaaaggaagttgtac	C	G	NM_152697 // intron // 0 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// ENST00000294639 // intron // 0 // — // — // —	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1689897	tgatagagagaacactggactgaaa[C/T]cttaagtatacttctg ctaattca	C	T	NM_000016 // intron // 0 // Hs.254593 // ACADM // 34 // acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	ACADM	ACADM , rs1250880, acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain,p31.1
SNP_A-1680208	cttaagatttttaatggatcaga[A/G]gaaaatcggtactaatc acttcc	A	G	NM_004582 // intron // 0 // Hs.78948 // RABGGTB // 5876 // Rab geranylgeranyltransferase, beta subunit	RABGGTB	RABGGTB , rs1146635, Rab geranylgeranyltransferase, beta subunit,p31.1
SNP_A-2206350	gctgaaatccaatatc[A/G]aaacttaaactctct	A	G	NM_152697 // upstream // 17463 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 96048 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1894544	tgccacacagtaacaa[A/G]taacttacatatctttt	A	G	NM_152697 // upstream // 28986 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 84525 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2069645	acacacaggctctgtga[C/G]agctttttctgctta	C	G	NM_152697 // upstream // 31117 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 82394 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2191689	catattcgtggcaggt[A/G]aaaagattgctgtatc	A	G	NM_152697 // upstream // 31284 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 82227 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1838639	tagacacaaatcttga[C/T]gaacacttcagccctg	C	T	NM_152697 // upstream // 31387 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 82124 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2206660	tgaccatgtatactca[C/T]attactgtttcagtct	C	T	NM_152697 // upstream // 32802 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 80709 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2129254	ataatttttagatcac[A/G]agctatatcaaatgtg	A	G	NM_152697 // upstream // 37893 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 75618 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2103311	agcaagctggacttta[A/G]catttcaaagaaggca	A	G	NM_152697 // upstream // 42697 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 70814 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-1936931	ttctttgctcatttac[A/G]cctaaaatcatgaatc	A	G	NM_152697 // upstream // 43529 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 69982 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207550	ctctttgacccaggaaa[G/T]tatgtgaatttcagga	G	T	NM_152697 // upstream // 97378 // Hs.480188 // MGC34032 // 204962 // Homo sapiens hypothetical protein MGC34032 (MGC34032), mRNA. /// NM_000016 // upstream // 16133 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 str	MGC34032	MGC34032, Homo sapiens hypothetical protein MGC34032 (MGC34032), p31.1
SNP_A-2221597	cctttgcacttgttcc[C/T]atgtaacatatttttcc	C	T	NM_000016 // intron // 0 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// ENST00000235701 // intron // 0 // — // — // — // —	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN, p31.1
SNP_A-2207767	ctttgtatccattaa[A/G]ctgtcatgaatataaa	A	G	NM_000016 // intron // 0 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// ENST00000235701 // intron // 0 // — // — // — // —	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN p31.1
SNP_A-1729868	atccctagaagattccattcaaata[A/G]caggtccattcaaac aatcaacat	A	G	NM_080868 // upstream // 92118 // Hs.125423 // ASB17 // 127247 // ankyrin repeat and SOCS box-containing 17 /// NM_152996 // upstream // 50170 // Hs.85618 // SIAT7C // 256435 // sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-ac	ASB17	ASB17, rs10493578, ankyrin repeat and SOCS box-containing 17, p31.1
SNP_A-1842968	tagtatccacagtaccg[C/G]gccacttgaattaa	C	G	NM_000016 // intron // 0 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// ENST00000235701 // intron // 0 // — // — // — // —	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN p31.1
SNP_A-1700963	ttagtacctgcaacattataggata[A/T]aggtcatactagcaggt gatgaata	A	T	NM_080868 // upstream // 105150 // Hs.125423 // ASB17 // 127247 // ankyrin repeat and SOCS box-containing 17 /// NM_152996 // upstream // 37138 // Hs.85618 // SIAT7C // 256435 // sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-a	ASB17	ASB17, rs4083965, ankyrin repeat and SOCS box-containing 17, p31.1
SNP_A-1680550	gttagatgcccatctctggactcat[C/G]aattgtggccaaaacaa cggggccc	C	G	NM_080868 // upstream // 106796 // Hs.125423 // ASB17 // 127247 // ankyrin repeat and SOCS box-containing 17 /// NM_152996 // upstream // 35492 // Hs.85618 // SIAT7C // 256435 // sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-a	ASB17	ASB17, rs10493580, ankyrin repeat and SOCS box-containing 17, p31.1
SNP_A-1813054	gtgggtgtgcacttgc[C/G]agtttgctccaggtcc	C	G	NM_000016 // downstream // 9258 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 13445 // Hs.78948 // RABGGTB // 58	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN, p31.1
SNP_A-2043557	aactgtgagtcaattg[A/G]acttatttccttata	A	G	NM_000016 // downstream // 11585 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 11118 // Hs.78948 // RABGGTB // 5	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN, p31.1
SNP_A-2042338	aactattggctaaaaa[A/G]tttgcctatattaggc	A	G	NM_000016 // downstream // 12140 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 10563 // Hs.78948 // RABGGTB // 5	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN, p31.1
SNP_A-2208385	gactatggacaagca[C/T]atggtcgcaggacttt	C	T	NM_000016 // downstream // 22563 // Hs.445040 // ACADM // 34 // Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN /// NM_004582 // upstream // 140 // Hs.78948 // RABGGTB // 587	ACADM	ACADM, Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRN, p31.1
SNP_A-2208399	gtgcttaaccctactc[C/T]accctgtctgctacca	C	T	NM_004582 // intron // 0 // Hs.78948 // RABGGTB // 5876 // Homo sapiens Rab geranylgeranyltransferase, beta subunit (RABGGTB), mRNA. /// ENST00000319942 // intron // 0 // — // — // — // —	RABGGTB	RABGGTB, Homo sapiens Rab geranylgeranyltransferase, beta subunit (RABGGTB), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2216699	cctctcctgaccttaa[A/C]agcactgatcagtagt	A	C	NM_004582 // intron // 0 // Hs.78948 // RABGGTB // 5876 // Homo sapiens Rab geranylgeranyltransferase, beta subunit (RABGGTB), mRNA. /// ENST00000319942 // intron // 0 // --- // --- // --- // ---	RABGGTB	RABGGTB, Homo sapiens Rab geranylgeranyltransferase, beta subunit (RABGGTB), p31.1
SNP_A-2197338	cattcatgttgcttta[A/G]aggaattgcaagtagc	A	G	NM_002440 // intron // 0 // Hs.216639 // MSH4 // 4438 // Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// ENST00000263187 // intron // 0 // --- // --- // --- // ---	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-2174178	cacactaacagatacc[C/T]ggagttaagacttcac	C	T	NM_002440 // intron // 0 // Hs.216639 // MSH4 // 4438 // Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// ENST00000263187 // intron // 0 // --- // --- // --- // ---	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-2160339	atttcagctttgtctt[A/T]aaagaaggagtaggat	A	T	NM_002440 // intron // 0 // Hs.216639 // MSH4 // 4438 // Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// ENST00000263187 // intron // 0 // --- // --- // --- // ---	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-2232014	ctcaacttagatggga[A/C]aaaagcctctttatgg	A	C	NM_002440 // intron // 0 // Hs.216639 // MSH4 // 4438 // Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// ENST00000263187 // intron // 0 // --- // --- // --- // ---	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-2205106	ccaggtgtgcatttaa[G/T]gttgcaactcaaagag	G	T	NM_002440 // intron // 0 // Hs.216639 // MSH4 // 4438 // Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// ENST00000263187 // intron // 0 // --- // --- // --- // ---	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-2208450	cccacccttagaata[A/G]gtatgagccacagtca	A	G	NM_002440 // downstream // 4126 // Hs.216639 // MSH4 // 4438 // Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA. /// NM_080868 // downstream // 1511 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA	MSH4	MSH4, Homo sapiens mutS homolog 4 (E. coli) (MSH4), p31.1
SNP_A-1845735	tataggttatccagaa[A/G]ctacgatttgaaagat	A	G	NM_080868 // intron // 0 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// ENST00000284142 // intron // 0 // --- // --- // --- // ---	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-1879299	tcttagctttcacgta[A/T]gtcatttctgtccaat	A	T	NM_080868 // upstream // 133 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 381241 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-ac	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2209521	cccatcgtcacgacca[C/T]gctgttcttcactcca	C	T	NM_080868 // upstream // 26324 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 355050 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2210387	aatctgctttgtggct[C/T]aaatttttgcttcaag	C	T	NM_080868 // upstream // 91972 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 289402 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2211024	tcatcttctcccacaa[A/G]tctgtctttagcggaa	A	G	NM_080868 // upstream // 140280 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 241094 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-1855364	tcaagggctcatcaaa[C/G]gctcagatgtgtccct	C	G	NM_080868 // upstream // 151859 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 229515 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2117714	aggttccttgtaaaaa[C/T]ttgccatcggccaggt	C	T	NM_080868 // upstream // 186698 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 194676 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2295408	gcatccccgtgatgaa[C/G]aaatcatgcgcattct	C	G	NM_080868 // upstream // 191881 // Hs.125423 // ASB17 // 127247 // Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA. /// NM_152996 // upstream // 189493 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N	ASB17	ASB17, Homo sapiens ankyrin repeat and SOCS box-containing 17 (ASB17), p31.1
SNP_A-2213596	cagacccagtgctaga[C/T]gtagatcccaatcaca	C	T	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-2160408	atttcatcatctggca[C/G]attagttgctggcaag	C	G	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-2084821	actcaaaatttagtac[A/G]atgcttctacttggaa	A	G	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-2024464	aaaaggaattggcgaa[A/G]atttagcataaaagat	A	G	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-1804005	gtcaattgttactaaa[C/T]ggaaaaaaatgcagag	C	T	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-1827601	taactgcatgaaccca[A/G]ataaaaaaaactgtag	A	G	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-2293268	gcagaggccaataacc[C/T]gagtaaagagacgaag	C	T	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-2214618	atggtgaatttctaac[C/T]ggaatactatgcgatc	C	T	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-2214643	tggtactactgacata[C/T]gacagaagtgatattg	C	T	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // –	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2313027	ggagaaaaagcttctg[A/G]caatattcaacaccct	A	G	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // --	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-2076029	acattatgaagacagc[A/G]aagagttaaaggtggt	A	G	NM_152996 // intron // 0 // Hs.337040 // ST6GALNAC3 // 256435 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000328299 // intron // 0 // — // — // — // --	ST6GALNAC3	ST6GALNAC3, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-2195527	catgggttcaccaggc[C/T]agacttactcctcagt	C	T	NM_030965 // upstream // 142661 // Hs.303609 // ST6GALNAC5 // 81849 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000335020 // downstream // 24242 // --- // --	ST6GALNAC5	ST6GALNAC5, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr ,p31.1
SNP_A-1749763	agacatttcacattgaaatacttga[A/C]ccaaattagcacgaggg aactggtg	A	C	NM_005482 // upstream // 53271 // Hs.293653 // PIGK // 10026 // phosphatidylinositol glycan, class K /// NM_012093 // upstream // 9905 // Hs.18268 // AK5 // 26289 // adenylate kinase 5 /// NM_174858 // upstream // 9360 // Hs.18268 // AK5 // 26289 // aden	PIGK	PIGK , rs10493537, phosphatidylinositol glycan, class K ,p31.1
SNP_A-2272145	gaccgtgtctctttaa[A/G]tattaggaatcaccttt	A	G	NM_030965 // intron // 0 // Hs.303609 // ST6GALNAC5 // 81849 // Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr /// ENST00000318803 // intron // 0 // — // — // — // —	ST6GALNAC5	ST6GALNAC5, Homo sapiens sialyltransferase 7 ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltr p31.1
SNP_A-2176940	cacctaattattttca[C/G]gcaggagtaacacatt	C	G	NM_012093 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 1, mRNA. /// E	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-1903255	tggctttatggtagcc[A/G]ctgttacgccataaac	A	G	NM_012093 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 1, mRNA. /// E	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2265224	gaagatttttatgaga[C/T]tatggggaacactttc	C	T	NM_012093 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 1, mRNA. /// E	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2222756	gtcagaaaaggatcca[C/G]ggagatataattgcag	C	G	NM_012093 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 1, mRNA. /// E	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-1843966	tagttcccatcactca[C/G]aggacaattatttgct	C	G	NM_012093 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA. /// NM_174858 // intron // 0 // Hs.18268 // AK5 // 26289 // Homo sapiens adenylate kinase 5 (AK5), transcript variant 1, mRNA. /// E	AK5	AK5, Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, p31.1
SNP_A-2265689	gaagctgataatagaa[A/G]gatgtctcggaaggag	A	G	NM_017655 // intron // 0 // Hs.13852 // GIPC2 // 54810 // Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA. /// ENST00000260524 // intron // 0 // --- // --- // --- // ---	GIPC2	GIPC2, Homo sapiens PDZ domain protein GIPC2 (GIPC2), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2037348	aacaaatatctgctag[A/G]aatgaagaagataaaa	A	G	NM_017655 // downstream // 75021 // Hs.13852 // GIPC2 // 54810 // Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA. /// NM_000959 // upstream // 278598 // Hs.292843 // PTGFR // 5737 // Homo sapiens prostaglandin F receptor (FP) (PTGFR), mRNA. /// ENST0	GIPC2	GIPC2, Homo sapiens PDZ domain protein GIPC2 (GIPC2), p31.1
SNP_A-1941548	ttgctttttagacaa[C/T]tatctggaccigttt	C	T	NM_017655 // downstream // 178814 // Hs.13852 // GIPC2 // 54810 // Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA. /// NM_000959 // upstream // 174805 // Hs.292843 // PTGFR // 5737 // Homo sapiens prostaglandin F receptor (FP) (PTGFR), mRNA. /// ENST	GIPC2	GIPC2, Homo sapiens PDZ domain protein GIPC2 (GIPC2), p31.1
SNP_A-2229606	ctaggttgcatttcct[C/T]aaatcagagtatacac	C	T	NM_006417 // downstream // 2048 // Hs.82316 // IFI44 // 10561 // Homo sapiens interferon-induced protein 44 (IFI44), mRNA. /// AY358360 // downstream // 224356 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds.	IFI44	IFI44, Homo sapiens interferon-induced protein 44 (IFI44), p31.1
SNP_A-1664318	ttattgctaatagaatatcgctatt[A/G]ttcaatgtggcaaaaatct atttt	A	G	NM_012302 // upstream // 2737572 // Hs.24212 // LPHN2 // 23266 // latrophilin 2 /// NM_022159 // upstream // 56149 // - // - // -	LPHN2	LPHN2, rs953403, latrophilin 2, p31.1
SNP_A-2233661	ctttcatcttcctacc[G/T]aattcatcaaggcaga	G	T	AY358360 // upstream // 74155 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 74155 // — // — // — // — /// ENST00000318909 // downstream // 1370250 // --- // --- //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1
SNP_A-2233778	acacctggtctaatc[A/C]catcactaagttttgt	A	C	AY358360 // upstream // 77916 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 77916 // — // — // — // — /// ENST00000318909 // downstream // 1366489 // — // — //	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1
SNP_A-1911870	tgtgacaggtctcata[C/T]gttgtatttgattac	C	T	AY358360 // upstream // 1039588 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1039588 // — // — // — // — /// ENST00000318909 // downstream // 404817 // --- // ---	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1
SNP_A-2244906	cagacactctcaatca[A/G]tgatgtggtccacaaa	A	G	AY358360 // upstream // 1042411 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1042411 // — // — // — // — /// ENST00000318909 // downstream // 401994 // — // —	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1
SNP_A-2244932	tttatgtattacagaa[A/G]aagctgtgcacagatt	A	G	AY358360 // upstream // 1042879 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1042879 // — // — // — // — /// ENST00000318909 // downstream // 401526 // — // —	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1
SNP_A-2141961	atcttacatgactact[A/G]aataaagcaatttatt	A	G	AY358360 // upstream // 1093085 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1093085 // — // — // — // — /// ENST00000318909 // downstream // 351320 // — // —	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1
SNP_A-2052245	aagtaagaaccaggga[C/T]gttgagctttgcaat	C	T	AY358360 // upstream // 1116002 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1116002 // — // — // — // — /// ENST00000318909 // downstream // 328403 // — // —	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds, p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253559	cttcttgcaataatcc[G/T]gcactaatagattcat	G	T	AY358360 // upstream // 1117596 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1117596 // --- // --- // --- // --- /// ENST00000318909 // downstream // 326809 // --- // ---	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-2000144	ggctaaaactgacata[C/T]caatttatggttacca	C	T	AY358360 // upstream // 1262734 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1262734 // --- // --- // --- // --- /// ENST00000318909 // downstream // 181671 // --- // ---	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. p31.1
SNP_A-2233367	ctcaggtcagctgcta[A/G]atggagttttcttccc	A	G	AY358360 // upstream // 1288504 // Hs.132314 // ELTD1 // 64123 // Homo sapiens clone DNA33092 ETL (UNQ202) mRNA, complete cds. /// ENST00000294631 // upstream // 1288504 // --- // --- // --- // --- /// ENST00000318909 // downstream // 155901 // --- // ---	ELTD1	ELTD1, Homo sapiens clone DNA33092 ETL (UNQ202) complete cds. ,p31.1
SNP_A-1832179	taatttgacagaatca[A/G]tagggagaggagtcac	A	G	NM_012302 // upstream // 732514 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 833141 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 833141 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1904387	tgggctttgggtacaa[C/T]taggcagctgtgctca	C	T	NM_012302 // upstream // 722905 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 823532 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 823532 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1914602	tgttaagatcctaaca[C/T]gaaaggcaatggtatt	C	T	NM_012302 // upstream // 617770 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 718397 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 718397 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2140491	atctcccacatctaag[C/G]ctgcactcaccagcaa	C	G	NM_012302 // upstream // 589131 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 689758 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 689758 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2279983	gaggctgtaggaaaca[C/T]gaaacacaacacagca	C	T	NM_012302 // upstream // 276850 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 377477 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 377477 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2066489	aatttttcttcactgg[A/T]agatgggcatcaggct	A	T	NM_012302 // upstream // 272948 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 373575 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 373575 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2060413	aatgaattttccaaca[A/G]cataaatgagcttgga	A	G	NM_012302 // upstream // 78173 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 178800 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 178800 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2198559	catttattgagtaggg[A/C]agcagccgaaaatgga	A	C	NM_012302 // upstream // 19353 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // upstream // 119980 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // upstream // 119980 //	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801146	gtagccatgtctgaaa[C/T]gacatcttatgtttga	C	T	NM_012302 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// ENST00000335786 // intron // 0 // — // — // — // — /// ENST00000360255 // intron // 0 // — // — // — // —	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2030292	aaagcaggctaatgga[A/T]tacataaaagacttgg	A	T	NM_012302 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens lectomedin-1 alpha (LEC1) mRNA, complete cds. /// ENST00000335786 // intron // 0	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2155998	attcctgtttagatta[C/G]aaaaagcctcctaaag	C	G	NM_012302 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens lectomedin-1 alpha (LEC1) mRNA, complete cds. /// ENST00000335786 // intron // 0	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2063796	aattagctattcaata[C/T]ggctgatagaaatctg	C	T	NM_012302 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // intron // 0 // Hs.24212 // LPHN2 // 23266 // Homo sapiens lectomedin-1 alpha (LEC1) mRNA, complete cds. /// ENST00000335786 // intron // 0	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2265055	gaagatagctaaccca[G/T]gattgaaaccagaatt	G	T	NM_012302 // downstream // 369355 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 368585 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 368	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1898645	tgcttgtgagcattgc[A/G]cttgggcaggctgaaa	A	G	NM_012302 // downstream // 398128 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 397358 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 397	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1878564	tctgtgtacaaaatag[A/G]acccacaaaaatattg	A	G	NM_012302 // downstream // 400736 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 399966 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 399	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1942757	ttgggccacacacaac[A/G]gatttgccataaatag	A	G	NM_012302 // downstream // 507879 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 507109 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 507	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1914025	tgtgtgctaattgata[C/T]gtagggaagcagtttc	C	T	NM_012302 // downstream // 517786 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 517016 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 517	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2156118	attcgtgcgtataaac[C/T]aggtgctattcatcag	C	T	NM_012302 // downstream // 860985 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 860215 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 860	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2264264	gaacttcaaaattcca[A/G]ggtgcaaatatattgt	A	G	NM_012302 // downstream // 881872 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 881102 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 881	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2165088	caaacttctaatggtc[A/C]aagcatcaattttgtc	A	C	NM_012302 // downstream // 888055 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 887285 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 887	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2276792	actctatctctctgac[A/G]cagaagttacgaatgc	A	G	NM_012302 // downstream // 1096547 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1095777 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 1	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-2098262	agagatctcagctaga[C/T]tattgcaacatcttcc	C	T	NM_012302 // downstream // 1383163 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1382393 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 1	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1742823	ccagttggatatcttttaacattac[C/T]accaccaacatgaacaat taagcct	C	T	NM_012302 // downstream // 1796671 // Hs.24212 // LPHN2 // 23266 // latrophilin 2 /// NM_024686 // downstream // 80835 // Hs.445826 // FLJ23033 // 79739 // hypothetical protein FLJ23033	LPHN2	LPHN2 , rs7552393, latrophilin 2 ,p31.1
SNP_A-1883581	tgaaccttcttgttgg[A/C]atatgattttatttct	A	C	NM_012302 // downstream // 1852753 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// NM_012302 // downstream // 1851983 // Hs.24212 // LPHN2 // 23266 // Homo sapiens latrophilin 2 (LPHN2), mRNA. /// AF104266 // downstream // 1	LPHN2	LPHN2, Homo sapiens latrophilin 2 (LPHN2), p31.1
SNP_A-1785625	ggctcccaccatccac[C/T]atcaacttatttactt	C	T	NM_207578 // intron // 0 // Hs.487325 // PRKACB // 5567 // Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PRKACB), transcript variant 3, mRNA. /// NM_002731 // intron // 0 // Hs.487325 // PRKACB // 5567 // Homo sapiens protein kinase, cAMP-	PRKACB	PRKACB, Homo sapiens protein kinase, cAMP-dependent, catalytic, beta (PRKACB), transcript variant 3, p31.1
SNP_A-1717837	caatctcatcagatctttataaaca[A/G]ctctgtaggatgaatattttt atttc	A	G	NM_001554 // upstream // 8225 // Hs.8867 // CYR61 // 3491 // cysteine-rich, angiogenic inducer, 61 /// NM_012137 // upstream // 107411 // Hs.380870 // DDAH1 // 23576 // dimethylarginine dimethylaminohydrolase 1	CYR61	CYR61 , rs2297139, cysteine-rich, angiogenic inducer, 61 ,p22.3
SNP_A-1806688	gtctaccctctgataa[A/T]ctccacattgaccacc	A	T	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-2300533	tcttaaatacaaccaa[A/C]cctctttaagttggca	A	C	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-1685536	ttactcggtattcctttgagagaga[A/G]tagagatgagaaagtcta ataaaac	A	G	NM_017953 // intron // 0 // Hs.5111 // FLJ20729 // 54680 // hypothetical protein FLJ20729	FLJ20729	FLJ20729 , rs952837, hypothetical protein FLJ20729,p22.3
SNP_A-1898789	tgctttgaaattaata[C/G]aagaggcaggatctca	C	G	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-1822518	gtttttctttagcttc[C/T]acagttctagcagaat	C	T	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-2300845	cagaattaaagcacac[A/G]ctcaataggatagcaa	A	G	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1855100	tcaagactttcacggc[A/G]atgaaatgaaaaaata	A	G	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-1812763	gtgggagatacagaac[A/G]gtaaacaggcaattat	A	G	NM_012137 // intron // 0 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// ENST00000284031 // intron // 0 // — // — // — // — /// ENST00000359625 // intron // 0 // — // — // — // —	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-2068094	acaagaaatggcatca[C/G]aactaaagtcctgcaa	C	G	NM_012137 // upstream // 20399 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA. /// NM_012137 // upstream // 20395 // Hs.379858 // DDAH1 // 23576 // Homo sapiens dimethylarginine dimethylaminohydrolas	DDAH1	DDAH1, Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), p22.3
SNP_A-1921745	ttactaaacttctgga[C/G]tatggggactagtatt	C	G	NM_001554 // intron // 0 // Hs.8867 // CYR61 // 3491 // Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA. /// ENST00000316642 // intron // 0 // — // — // — // — /// ENST00000271019 // intron // 0 // — // — // — // —	CYR61	CYR61, Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), p22.3
SNP_A-2047626	aagatgtgagcaaaaa[A/T]cttccctctcaaaagt	A	T	NM_001554 // downstream // 21232 // Hs.8867 // CYR61 // 3491 // Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA. /// NM_017953 // downstream // 47874 // Hs.5111 // FLJ20729 // 54680 // Homo sapiens hypothetical protein FLJ20729 (FLJ20729)	CYR61	CYR61, Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), p22.3
SNP_A-2268270	gaatgagtgaaagtca[A/G]tatgaaaacctctcag	A	G	NM_001554 // downstream // 43007 // Hs.8867 // CYR61 // 3491 // Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA. /// NM_017953 // downstream // 26099 // Hs.5111 // FLJ20729 // 54680 // Homo sapiens hypothetical protein FLJ20729 (FLJ20729)	CYR61	CYR61, Homo sapiens cysteine-rich, angiogenic inducer, 61 (CYR61), p22.3
SNP_A-2304380	aactaggttttgaata[A/G]atttctgtgcagatgt	A	G	NM_152890 // intron // 0 // Hs.47312 // COL24A1 // 255631 // Homo sapiens collagen, type XXIV, alpha 1 (COL24A1), mRNA. /// ENST00000302772 // intron // 0 // — // — // — // —	COL24A1	COL24A1, Homo sapiens collagen, type XXIV, alpha 1 (COL24A1), p22.3
SNP_A-2028601	aaactgcttgggaaaa[A/G]ggatgaaagaaaacaa	A	G	NM_152890 // intron // 0 // Hs.47312 // COL24A1 // 255631 // Homo sapiens collagen, type XXIV, alpha 1 (COL24A1), mRNA. /// ENST00000302772 // intron // 0 // — // — // — // —	COL24A1	COL24A1, Homo sapiens collagen, type XXIV, alpha 1 (COL24A1), p22.3
SNP_A-1837840	tagaaaaaatggcatc[C/T]gaacaaaagttgcttc	C	T	ENST00000294678 // intron // 0 // — // — // — // — /// ENST00000317336 // intron // 0 // — // — // — // —	-	p22.3
SNP_A-1866267	tcccatcatagcaaaa[G/T]tgttaaattgtcatca	G	T	NM_001285 // intron // 0 // Hs.194659 // CLCA1 // 1179 // Homo sapiens chloride channel, calcium activated, family member 1 (CLCA1), mRNA. /// ENST00000234701 // intron // 0 // — // — // — // — /// ENST00000353619 // intron // 0 // — // — // -	CLCA1	CLCA1, Homo sapiens chloride channel, calcium activated, family member 1 (CLCA1), p22.3
SNP_A-1956783	ttttaaatagcaatca[A/G]ctacttaaagatacac	A	G	NM_012128 // intron // 0 // Hs.546343 // CLCA4 // 22802 // Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), mRNA. /// ENST00000263723 // intron // 0 // — // — // — // —	CLCA4	CLCA4, Homo sapiens chloride channel, calcium activated, family member 4 (CLCA4), p22.3
SNP_A-1876047	tctgaatatcagggaa[A/G]gtgactcttactggtg	A	G	NM_012262 // downstream // 197839 // Hs.48823 // HS2ST1 // 9653 // Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), mRNA. /// NM_207357 // downstream // 173225 // Hs.306423 // LOC339524 // 339524 // Homo sapiens hypothetical protein LOC339524	HS2ST1	HS2ST1, Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), p22.3
SNP_A-1782087	tgcttgagtagcccta[A/G]gagtagaatatttcac	A	G	NM_006769 // downstream // 86657 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 86657 // — // — // — // — /// ENST00000234531 // upstream // 1252349 // — // — // — // — ///	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805515	gtccagcgtccaacta[A/C]aatgtatgaagtatgt	A	C	NM_006769 // downstream // 321130 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 321130 // --- // --- /// ENST00000234531 // upstream // 1017876 // --- // --- // --- // ---	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.3
SNP_A-2080152	acttgagcctccccac[A/G]ctatacatctcgtgtt	A	G	NM_006769 // downstream // 339292 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 339292 // --- // --- // --- // --- /// ENST00000234531 // upstream // 999714 // --- // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.3
SNP_A-2215820	cctcatgtcctaaatc[C/T]attcaaigtcaaatcc	C	T	NM_006769 // downstream // 486677 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 486677 // --- // --- // --- /// ENST00000234531 // upstream // 852329 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.3
SNP_A-1785447	aactgttagatcacag[C/T]aagaacagtaagctct	C	T	NM_006769 // downstream // 569217 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 569217 // --- // --- // --- /// ENST00000234531 // upstream // 769789 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.3
SNP_A-1690423	ttactgtaaagattatatgaagggat[C/T]gttatataaaatttagcac agactc	C	T	NM_006256 // upstream // 403430 // Hs.69171 // PRKCL2 // 5586 // protein kinase C-like 2 /// NM_006769 // downstream // 979891 // Hs.3844 // LMO4 // 8543 // LIM domain only 4	PRKCL2	PRKCL2 , rs10493597, protein kinase C-like 2 ,p22.2
SNP_A-1719699	aaaatggaagcaactgtgtgttcaa[C/T]agagaatttgttaacta agttatga	C	T	NM_006256 // upstream // 346339 // Hs.69171 // PRKCL2 // 5586 // protein kinase C-like 2 /// NM_006769 // downstream // 1036982 // Hs.3844 // LMO4 // 8543 // LIM domain only 4	PRKCL2	PRKCL2 , rs10489567, protein kinase C-like 2 p22.2
SNP_A-1659490	atttacttatgaggaattagaaga[C/T]gatccagagaagaaacat ttgagctg	C	T	NM_006256 // upstream // 346061 // Hs.69171 // PRKCL2 // 5586 // protein kinase C-like 2 /// NM_006769 // downstream // 1037260 // Hs.3844 // LMO4 // 8543 // LIM domain only 4	PRKCL2	PRKCL2 , rs10489568, protein kinase C-like 2 p22.2
SNP_A-1861363	tcatcagaatggccca[C/T]gagtgtcttaitgag	C	T	NM_006769 // downstream // 852758 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 852758 // --- // --- // --- /// ENST00000234531 // upstream // 486248 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1787407	agggatctgcacgtgai[A/G]ctaagcctggacaatc	A	G	NM_006769 // downstream // 882699 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 882699 // --- // --- // --- /// ENST00000234531 // upstream // 456307 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1901282	tggatggcaggactaa[C/G]taatgcaaagctggct	C	G	NM_006769 // downstream // 904117 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 904117 // --- // --- // --- /// ENST00000234531 // upstream // 434889 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2069632	acacacagatacttga[C/G]aaaaaataaatatta	C	G	NM_006769 // downstream // 917749 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 917749 // --- // --- // --- /// ENST00000234531 // upstream // 421257 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1792253	gggttccacacagaa[A/G]gacaagtagaaaaggc	A	G	NM_006769 // downstream // 929615 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 929615 // --- // --- // --- /// ENST00000234531 // upstream // 409391 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2043455	aactggtgttgaaagt[A/G]acatagactaaaaatg	A	G	NM_006769 // downstream // 932407 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 932407 // --- // --- // --- /// ENST00000234531 // upstream // 406599 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2092300	agaaagcaaagtgaccl[A/G]aaatgcagtgggttca	A	G	NM_006769 // downstream // 949170 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 949170 // --- // --- // --- /// ENST00000234531 // upstream // 389836 // --- // --- // --- // --	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1797602	ggtttcctgtgatat[A/G]taaggcagatgctgac	A	G	NM_006769 // downstream // 959413 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 959413 // --- // --- // --- /// ENST00000234531 // upstream // 379593 // --- // --- // --- // ---	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1788588	ttctttctatgcata[A/T]gtcacctaaacaaaa	A	T	NM_006769 // downstream // 993302 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 993302 // --- // --- // --- // --- /// ENST00000234531 // upstream // 345704 // --- // --- // --- // ---	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2059888	aatcttacttacttctt[C/T]aaagcttagttcaaat	C	T	NM_006769 // downstream // 1005858 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 1005858 // --- // --- // --- /// ENST00000234531 // upstream // 333148 // --- // --- // --- // ---	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-2195596	catggtcttgacacca[C/G]gttacatgaaatatga	C	G	NM_006769 // downstream // 1148669 // Hs.436792 // LMO4 // 8543 // Homo sapiens LIM domain only 4 (LMO4), mRNA. /// ENST00000271199 // downstream // 1148669 // --- // --- // --- /// ENST00000234531 // upstream // 190337 // --- // --- // --- // ---	LMO4	LMO4, Homo sapiens LIM domain only 4 (LMO4), p22.2
SNP_A-1753563	ttcaacacacctattcagtgcttca[G/T]tcaaatggaataattctac agtacc	G	T	BX537949 // downstream // 6171 // Hs.254338 // DKFZp686G0786 // 163351 // hypothetical protein DKFZp686G0786 /// NM_015350 // upstream // 175614 // Hs.387915 // TA-LRRP // 23507 // T-cell activation leucine repeat-rich protein	DKFZp686G07 86	DKFZp686G0786 , rs4658149, hypothetical protein DKFZp686G0786 ,p22.2
SNP_A-1750825	cagaaccatctatttgtccttcaa[A/G]gtacctaatttcttttccttt aa	A	G	BX537949 // downstream // 75215 // Hs.254338 // DKFZp686G0786 // 163351 // hypothetical protein DKFZp686G0786 /// NM_015350 // upstream // 106570 // Hs.387915 // TA-LRRP // 23507 // T-cell activation leucine repeat-rich protein	DKFZp686G07 86	DKFZp686G0786 , rs42596628, hypothetical protein DKFZp686G0786 ,p22.2
SNP_A-1735979	ttctatattaagaacatggaagaa[A/G]ctatattaagtacaatc aagaag	A	G	BX537949 // downstream // 97194 // Hs.254338 // DKFZp686G0786 // 163351 // hypothetical protein DKFZp686G0786 /// NM_015350 // upstream // 84591 // Hs.387915 // TA-LRRP // 23507 // T-cell activation leucine repeat-rich protein	DKFZp686G07 86	DKFZp686G0786 , rs13804116, hypothetical protein DKFZp686G0786 ,p22.2
SNP_A-2243326	ctgccttgctatagga[A/G]tcaccttggagcctca	A	G	NM_198460 // downstream // 8249 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 173536 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat-	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-1687562	aagtgtaggtcactctgacagtatat[C/T]gttaggacctgaactac tgggggtt	C	T	NM_032270 // intron // 0 // Hs.412836 // AD158 // 84230 // hypothetical protein AD158	AD158	AD158 , rs6656884, hypothetical protein AD158,p22.2
SNP_A-1805366	gtccaaggaggcccaga[A/T]gtctgaatatccactg	A	T	NM_198460 // downstream // 75170 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 106615 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2085904	actcgtggagaggtta[C/G]agaagcatcttatga	C	G	NM_198460 // downstream // 101397 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 80388 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2265277	gaagcaatgtctgag[C/T]agtcactagatggtgg	C	T	NM_198460 // downstream // 101525 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 80260 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2190925	catagcctgtttaacc[C/T]aatcccggattttcat	C	T	NM_198460 // downstream // 140815 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 40970 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2080800	acctcctggccttgaa[A/C]atgtcttgctttcatg	A	C	NM_198460 // downstream // 155676 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 26109 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2149684	atgtatcgtttcatcc[C/G]caatgatttcagtact	C	G	NM_198460 // downstream // 159456 // Hs.254338 // GBP6 // 163351 // Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), mRNA. /// NM_015350 // upstream // 22329 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat	GBP6	GBP6, Homo sapiens hypothetical protein DKFZp686G0786 (DKFZp686G0786), p22.2
SNP_A-2069841	acacagataaatatgt[C/G]aaggttaacaaatgct	C	G	NM_015350 // downstream // 3965 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA. /// NM_032270 // upstream // 35527 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differe	TA-LRRP	TA-LRRP, Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), p22.2
SNP_A-1957603	ttttatccagtaattc[A/C]atttttttcacctttga	A	C	NM_015350 // downstream // 4631 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA. /// NM_032270 // upstream // 34861 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differe	TA-LRRP	TA-LRRP, Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), p22.2
SNP_A-2238455	ctctggtttaataaag[C/T]caagaaaggttgtctt	C	T	NM_015350 // downstream // 23009 // Hs.546355 // TA-LRRP // 23507 // Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), mRNA. /// NM_032270 // upstream // 16483 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differ	TA-LRRP	TA-LRRP, Homo sapiens T-cell activation leucine repeat-rich protein (TA-LRRP), p22.2
SNP_A-2087227	actgatttctcttaaa[C/T]gactgatccagagctt	C	T	NM_032270 // intron // 0 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // — // — // — // —	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-2260059	gaaaatactcagccac[A/G]ggcttccaaaatagga	A	G	NM_032270 // intron // 0 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // — // — // — // —	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1925141	ttatcatgcttactaa[C/T]tgccagacattaaaca	C	T	NM_032270 // intron // 0 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // — // — // — // —	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1842541	taggttacattttcca[C/T]gtccaatctctacttt	C	T	NM_032270 // intron // 0 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// ENST00000302730 // intron // 0 // — // — // — // —	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-1918994	ttaacctgcatttgcc[C/T]acaagcacaccagtgt	C	T	NM_032270 // downstream // 51468 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// NM_018103 // upstream // 54424 // Hs.482087 // LRRC5 // 55144 // Homo sapiens leucine rich repeat containing 5 (L	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2
SNP_A-2162183	attttaccactctctc[C/T]gaatacatttttatt	C	T	NM_032270 // downstream // 100403 // Hs.412836 // FAD158 // 84230 // Homo sapiens factor for adipocyte differentiation 158 (FAD158), mRNA. /// NM_018103 // upstream // 5489 // Hs.482087 // LRRC5 // 55144 // Homo sapiens leucine rich repeat containing 5 (L	FAD158	FAD158, Homo sapiens factor for adipocyte differentiation 158 (FAD158), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1828248	taagagtacttcaatg[C/G]agagacagggaaggca	C	G	NM_181781 // downstream // 43689 // Hs.306221 // ZNF326 // 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 // downstream // 43689 // Hs.306221 // ZNF326 // 284695 // Homo sapiens hypothetical prot	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-1801876	tgagagtgtaggaaac[A/G]aagtaggctctgagag	A	G	NM_181781 // downstream // 362465 // Hs.306221 // ZNF326 // 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 // downstream // 362465 // Hs.306221 // ZNF326 // 284695 // Homo sapiens hypothetical pr	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-1803563	tctgaatcccacatca[C/T]cctagcaaagtttttc	C	T	NM_181781 // downstream // 516060 // Hs.306221 // ZNF326 // 284695 // Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, mRNA. /// NM_182975 // downstream // 516060 // Hs.306221 // ZNF326 // 284695 // Homo sapiens hypothetical pr	ZNF326	ZNF326, Homo sapiens hypothetical protein FLJ20403 (FLJ20403), transcript variant 2, p22.2
SNP_A-1805847	ggtatttctccatttc[C/T]aggatatgagcacatt	C	T	NM_020063 // upstream // 80216 // Hs.451956 // BARHL2 // 343472 // Homo sapiens BarH-like 2 (Drosophila) (BARHL2), mRNA. /// NM_016620 // downstream // 117849 // Hs.173001 // ZNF644 // 84146 // Homo sapiens zinc finger motif enhancer binding protein 2 (Ze	BARHL2	BARHL2, Homo sapiens BarH-like 2 (Drosophila) (BARHL2), p22.2
SNP_A-1854354	tcaaatacagctttca[A/G]agtgccttaagattaa	A	G	NM_020063 // upstream // 126730 // Hs.451956 // BARHL2 // 343472 // Homo sapiens BarH-like 2 (Drosophila) (BARHL2), mRNA. /// NM_016620 // downstream // 71335 // Hs.173001 // ZNF644 // 84146 // Homo sapiens zinc finger motif enhancer binding protein 2 (Ze	BARHL2	BARHL2, Homo sapiens BarH-like 2 (Drosophila) (BARHL2), p22.2
SNP_A-1926120	ttatgtttcttgaggc[A/C]aattttagttttcctc	A	C	NM_020063 // upstream // 129118 // Hs.451956 // BARHL2 // 343472 // Homo sapiens BarH-like 2 (Drosophila) (BARHL2), mRNA. /// NM_016620 // downstream // 68947 // Hs.173001 // ZNF644 // 84146 // Homo sapiens zinc finger motif enhancer binding protein 2 (Ze	BARHL2	BARHL2, Homo sapiens BarH-like 2 (Drosophila) (BARHL2), p22.2
SNP_A-2087173	actgatggcaccaata[C/T]cctcaacttgtaggct	C	T	NM_016620 // upstream // 133198 // Hs.173001 // ZNF644 // 84146 // Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, mRNA. /// NM_032186 // upstream // 133198 // Hs.173001 // ZNF644 // 84146 // Homo sapiens zinc fing	ZNF644	ZNF644, Homo sapiens zinc finger motif enhancer binding protein 2 (Zep-2), transcript variant 2, p22.2
SNP_A-1926310	ttattagtagacttca[A/G]actacttaggcaccag	A	G	NM_003503 // upstream // 3477 // Hs.533573 // CDC7 // 8317 // Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), mRNA. /// ENST00000329827 // upstream // 96297 // — // — // — // — /// ENST00000234626 // upstream // 3477 // — // —	CDC7	CDC7, Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), p22.2
SNP_A-2084608	actatgtgaacagcca[C/T]gtgctaggtattaggg	C	T	NM_003503 // upstream // 2705 // Hs.533573 // CDC7 // 8317 // Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), mRNA. /// ENST00000329827 // upstream // 97069 // — // — // — // — /// ENST00000234626 // upstream // 2705 // — // —	CDC7	CDC7, Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), p22.2
SNP_A-2090583	acttgtggcattatcc[A/G]caaccgtcatgtttct	A	G	NM_003503 // downstream // 8421 // Hs.533573 // CDC7 // 8317 // Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), mRNA. /// ENST00000234626 // downstream // 8421 // — // — // — // — /// ENST00000327677 // downstream // 487 // — //	CDC7	CDC7, Homo sapiens CDC7 cell division cycle 7 (S. cerevisiae) (CDC7), p22.1
SNP_A-2284942	gatcccacttaaacct[C/T]aactgagattcttgag	C	T	NM_003243 // intron // 0 // Hs.482390 // TGFBR3 // 7049 // Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFBR3), mRNA. /// ENST00000212355 // intron // 0 // — // — // — // —	TGFBR3	TGFBR3, Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFBR3), p22.1
SNP_A-2091586	agaaaacaaaaccagc[A/T]ctgattagagactcaa	A	T	NM_003243 // upstream // 51451 // Hs.482390 // TGFBR3 // 7049 // Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFBR3), mRNA. /// NM_001726 // upstream // 87255 // Hs.482520 // BRDT // 676 // Homo sapiens bromodomain, te	TGFBR3	TGFBR3, Homo sapiens transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFBR3), p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2298354	gccattctctacgaaa[C/T]attgctattacatatg	C	T	ENST00000284717 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-1877858	tctggtctctgacagg[A/T]acaaatgctaggcagg	A	T	NM_003567 // intron // 0 // Hs.36958 // BCAR3 // 8412 // Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), mRNA. /// ENST00000359912 // intron // 0 // — // — // — // —	BCAR3	BCAR3, Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), p22.1
SNP_A-2304399	gctctaaaacatcaca[A/C]aatttagaaaactaaa	A	C	NM_003567 // intron // 0 // Hs.36958 // BCAR3 // 8412 // Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), mRNA. /// ENST00000359912 // intron // 0 // — // — // — // —	BCAR3	BCAR3, Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), p22.1
SNP_A-1829059	taagggtaaacatcgc[A/G]agagagaaaaccagac	A	G	NM_003567 // intron // 0 // Hs.36958 // BCAR3 // 8412 // Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), mRNA. /// ENST00000359912 // intron // 0 // — // — // — // —	BCAR3	BCAR3, Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), p22.1
SNP_A-1652084	ccaggcttaagtgacaccacgctga[C/T]gagatattaataatga tcttaaaat	C	T	NM_000350 // intron // 0 // Hs.416707 // ABCA4 // 24 // ATP-binding cassette, sub-family A (ABC1), member 4	ABCA4	ABCA4 , rs3789405, ATP-binding cassette, sub-family A (ABC1), member 4,p22.1
SNP_A-1647442	tccagaagaaacaaacatttattga[C/G]aacttttggtgtgtgacc tgtttaa	C	G	NM_000350 // intron // 0 // Hs.416707 // ABCA4 // 24 // ATP-binding cassette, sub-family A (ABC1), member 4	ABCA4	ABCA4 , rs3789407, ATP-binding cassette, sub-family A (ABC1), member 4,p22.1
SNP_A-1807012	gtctcatcacccaaat[A/T]actgtttagatttctg	A	T	NM_002061 // intron // 0 // Hs.315562 // GCLM // 2730 // Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), mRNA. /// ENST00000263891 // intron // 0 // — // — // — // —	GCLM	GCLM, Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), p22.1
SNP_A-1830036	ggatgggctcctcacc[A/G]accattcagatctctg	A	G	NM_002061 // upstream // 70827 // Hs.315562 // GCLM // 2730 // Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), mRNA. /// ENST00000263891 // upstream // 70827 // — // — // — // — /// ENST00000294717 // downstream // 12603 // — //	GCLM	GCLM, Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), p22.1
SNP_A-2154478	attattccattgtatg[A/C]atgaactatgtaagcc	A	C	ENST00000294717 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-2152658	attaataggctgtacc[C/T]caccaataacaagctc	C	T	ENST00000294717 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-2242068	ctgatttacttatgcg[C/T]agcctccctggagaca	C	T	ENST00000294717 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-2059540	aatctcagtaaaccac[C/T]gtgacggcatctaccc	C	T	ENST00000294717 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-1893196	tgcagactagctcgtg[C/T]aaaggaggagagcgtt	C	T	NM_004815 // upstream // 25520 // Hs.483238 // PARG1 // 9411 // Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA. /// NM_004815 // upstream // 35544 // Hs.483238 // PARG1 // 9411 // Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA. /// NM_002858 /	PARG1	PARG1, Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), p22.1
SNP_A-2237408	ctctccctttgcagag[A/G]atatacgtcctctcct	A	G	NM_001993 // upstream // 53995 // Hs.62192 // F3 // 2152 // Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), mRNA. /// NM_152369 // upstream // 224580 // Hs.483423 // MGC45474 // 126969 // Homo sapiens hypothetical protein MGC4547	F3	F3, Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), p21.3
SNP_A-1870807	tcggacccaagtcagg[A/G]catctctgttttgaag	A	G	NM_001993 // upstream // 54672 // Hs.62192 // F3 // 2152 // Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), mRNA. /// NM_152369 // upstream // 223903 // Hs.483423 // MGC45474 // 126969 // Homo sapiens hypothetical protein MGC4547	F3	F3, Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), p21.3
SNP_A-2250409	cttagcgaggacctaa[G/T]catccaatgctgccaa	G	T	NM_001993 // upstream // 79049 // Hs.62192 // F3 // 2152 // Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), mRNA. /// NM_152369 // upstream // 199526 // Hs.483423 // MGC45474 // 126969 // Homo sapiens hypothetical protein MGC4547	F3	F3, Homo sapiens coagulation factor III (thromboplastin, tissue factor) (F3), p21.3
SNP_A-1727112	agacaggaatctttagtaaaatag[A/C]agtgtttttgttgtttttgc attg	A	C	NM_015485 // 3UTR // 0 // Hs.196585 // RWDD3 // 25950 // RWD domain containing 3	RWDD3	RWDD3 , rs592097, RWD domain containing 3,p21.3
SNP_A-1921269	ttacattatttaagta[C/T]gagccaaagcagatac	C	T	NM_015485 // downstream // 87780 // Hs.514092 // RWDD3 // 25950 // Homo sapiens RWD domain containing 3 (RWDD3), mRNA. /// ENST00000354428 // downstream // 87780 // — // — // — // — /// ENST00000263893 // downstream // 87780 // — // — // — // — /	RWDD3	RWDD3, Homo sapiens RWD domain containing 3 (RWDD3), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247092	ctgtcaagtacaaaac[A/G]aaactgcagaataaaa	A	G	NM_015485 // downstream // 437432 // Hs.514092 // RWDD3 // 25950 // Homo sapiens RWD domain containing 3 (RWDD3), mRNA. /// ENST00000354428 // downstream // 437432 // — // — // — // — /// ENST00000263893 // downstream // 437432 // — // — // –	RWDD3	RWDD3, Homo sapiens RWD domain containing 3 (RWDD3), p21.3
SNP_A-2081493	acctgtgaatcacaga[C/T]attacgtagaacaagc	C	T	ENST00000358225 // upstream // 268344 // — // — // — // — /// ENST00000359165 // upstream // 416131 // — // — // — // —	-	p21.3
SNP_A-1847048	cctaacagcattttca[G/T]gtagcatttcaaattt	G	T	ENST00000358225 // upstream // 276122 // — // — // — // — /// ENST00000359165 // upstream // 408353 // — // — // — // —	-	p21.3
SNP_A-1756162	atctccttttgtgattacagtaata[A/T]catcaggatagagttgaaaaaacta	A	T	NM_015485 // downstream // 1116854 // Hs.196585 // RWDD3 // 25950 // RWD domain containing 3 /// NM_021190 // upstream // 357751 // Hs.34956 // PTBP2 // 58155 // polypyrimidine tract binding protein 2	RWDD3	RWDD3 , rs10489720, RWD domain containing 3 ,p21.3
SNP_A-2088624	actgtgaccttcagta[C/T]gaggaaatagctatca	C	T	ENST00000358225 // upstream // 465924 // — // — // — // — /// ENST00000359165 // upstream // 218551 // — // — // — // —	-	p21.3
SNP_A-1709077	ttttatgagatttaatgtaactatg[C/T]attacttcagacaagatacacatat	C	T	NM_021190 // intron // 0 // Hs.34956 // PTBP2 // 58155 // polypyrimidine tract binding protein 2	PTBP2	PTBP2 , rs10489798, polypyrimidine tract binding protein 2,p21.3
SNP_A-1926824	ttatttaagctgaata[G/T]aacttttgagatgata	G	T	NM_000971 // downstream // 37469 // Hs.421257 // RPL7 // 6129 // Homo sapiens ribosomal protein L7 (RPL7), mRNA. /// ENST00000271124 // upstream // 56671 // — // — // — // — /// ENST00000260536 // downstream // 37469 // — // — // — // —	RPL7	RPL7, Homo sapiens ribosomal protein L7 (RPL7), p21.3
SNP_A-2312167	ggacagattttggcaa[A/C]taagtagagggaatat	A	C	NM_021190 // downstream // 24224 // Hs.269895 // PTBP2 // 58155 // Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), mRNA. /// NM_000110 // downstream // 238731 // Hs.335034 // DPYD // 1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD)	PTBP2	PTBP2, Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), p21.3
SNP_A-2181399	cagactcaaagcaaca[C/G]acacattgccaggccc	C	G	NM_021190 // downstream // 24521 // Hs.269895 // PTBP2 // 58155 // Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), mRNA. /// NM_000110 // downstream // 238434 // Hs.335034 // DPYD // 1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD)	PTBP2	PTBP2, Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), p21.3
SNP_A-2175840	cacatttagcaaacag[G/T]aatggaggaaccacta	G	T	NM_000110 // intron // 0 // Hs.335034 // DPYD // 1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // — // — // — // —	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-2122395	agtgcctatcccataa[C/T]aggtgacaataaatat	C	T	NM_000110 // intron // 0 // Hs.335034 // DPYD // 1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // — // — // — // —	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1731873	taccataatcaacaacttcaacata[A/G]agatcactctaccattgacctttat	A	G	NM_000110 // intron // 0 // Hs.1602 // DPYD // 1806 // dihydropyrimidine dehydrogenase	DPYD	DPYD , rs7527085, dihydropyrimidine dehydrogenase,p21.3
SNP_A-1724252	tgtcttcatattaactgtaaaatta[A/G]agtaataatggtagtttaaatttaa	A	G	NM_000110 // intron // 0 // Hs.1602 // DPYD // 1806 // dihydropyrimidine dehydrogenase	DPYD	DPYD , rs10493894, dihydropyrimidine dehydrogenase,p21.3
SNP_A-1708050	tctccttgctttctcagatctctta[G/T]gcctctaaaaaatatggtgttgtgg	G	T	NM_000110 // intron // 0 // Hs.1602 // DPYD // 1806 // dihydropyrimidine dehydrogenase	DPYD	DPYD , rs10493895, dihydropyrimidine dehydrogenase,p21.3
SNP_A-2198386	catttaatctgcatga[C/G]aaccatatgtattcct	C	G	NM_000110 // intron // 0 // Hs.335034 // DPYD // 1806 // Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA. /// ENST00000271131 // intron // 0 // — // — // — // — /// ENST00000306031 // intron // 0 // — // — // — // —	DPYD	DPYD, Homo sapiens dihydropyrimidine dehydrogenase (DPYD), p21.3
SNP_A-1851845	tattgacttgctgcta[C/T]ggtttctgaacatttt	C	T	NM_001001688 // upstream // 179268 // Hs.451802 // FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 436999 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA.	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2046999	aagagtgactaaacgg[C/T]aatgaatcacacatcc	C	T	NM_001001688 // upstream // 404461 // Hs.451802 // FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 211806 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA.	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2086927	actgagatgtggaaga[C/T]caaaggagaataagtt	C	T	NM_001001688 // upstream // 466129 // Hs.451802 // FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 150138 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA.	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-1884836	tgaatccttgaccaac[A/G]agagacaggaactgat	A	G	NM_001001688 // upstream // 469045 // Hs.451802 // FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 147222 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA.	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2159779	atttagtcacacttca[C/T]tacctccaaatatgaa	C	T	NM_001001688 // upstream // 557561 // Hs.451802 // FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 58706 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA. /	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2133273	atatataggctgtttc[A/G]ctttaaaggagtaaaa	A	G	NM_001001688 // upstream // 570739 // Hs.451802 // FLJ35409 // 400765 // Homo sapiens FLJ35409 protein (FLJ35409), mRNA. /// NM_015976 // upstream // 45528 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA. /	FLJ35409	FLJ35409, Homo sapiens FLJ35409 protein (FLJ35409), p21.3
SNP_A-2000219	ggtaacatgataaaga[A/G]taccaggaggggaagt	A	G	NM_015976 // intron // 0 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA. /// NM_152238 // intron // 0 // Hs.197015 // SNX7 // 51375 // Homo sapiens sorting nexin 7 (SNX7), transcript variant 2, mRNA. /// E	SNX7	SNX7, Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, p21.3
SNP_A-1878314	tctgtctaccagcaga[C/G]tccttttttccctcct	C	G	ENST00000263177 // intron // 0 // --- // --- // --- // ---	-	p21.3
SNP_A-1702433	ttattccaggaatgtgaggatcatt[A/C]actgtccagaaatctatta aagtaa	A	C	NM_000028 // upstream // 127922 // Hs.904 // AGL // 178 // amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // upstream // 127517 // Hs.904 // AGL // 178 // amylo-1, 6-gluco	AGL	AGL , rs953020, amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) ,p21.2
SNP_A-2144250	atgagtctatatgatg[A/C]agaaaaccatgttgtc	A	C	NM_014839 // downstream // 233471 // Hs.13245 // LPPR4 // 9890 // Homo sapiens plasticity related gene 1 (LPPR4), mRNA. /// NM_017734 // upstream // 102991 // Hs.483993 // PALMD // 54873 // Homo sapiens palmdelphin (PALMD), mRNA. /// ENST00000294644 // do	LPPR4	LPPR4, Homo sapiens plasticity related gene 1 (LPPR4), p21.2
SNP_A-2082034	accttttccttttgtga[C/G]agtgagattaagaact	C	G	NM_014839 // downstream // 251302 // Hs.13245 // LPPR4 // 9890 // Homo sapiens plasticity related gene 1 (LPPR4), mRNA. /// NM_017734 // upstream // 85160 // Hs.483993 // PALMD // 54873 // Homo sapiens palmdelphin (PALMD), mRNA. /// ENST00000294644 // dow	LPPR4	LPPR4, Homo sapiens plasticity related gene 1 (LPPR4), p21.2
SNP_A-1943945	ttgtatgaggagttga[C/G]atagctcctgaaagag	C	G	NM_000643 // upstream // 43469 // Hs.904 // AGL // 178 // Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // upstream // 43469 // Hs.904 // AGL // 178 // Homo s	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) p21.2
SNP_A-1811573	gtgctgaataatgaag[C/T]agtgtctaaaggcttg	C	T	NM_000643 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) ,p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1877368	aaagggcataataaca[G/T]aacgtacgaacattta	G	T	NM_000643 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) p21.2
SNP_A-2000232	agagtttccatcatta[C/G]caatactgagtatata	C	G	NM_000643 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) ,p21.2
SNP_A-2199176	cattttacatgactgc[C/T]attttatgtgaacaca	C	T	NM_000643 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) /// NM_000642 // intron // 0 // Hs.904 // AGL // 178 // Homo sapiens amylo	AGL	AGL, Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) p21.2
SNP_A-1718931	cacatctgttgatataggaaatcaa[C/T]cttgtaatcgtcaacctc aaagact	C	T	NM_003672 // intron // 0 // Hs.405214 // CDC14A // 8556 // CDC14 cell division cycle 14 homolog A (S. cerevisiae) /// NM_033312 // intron // 0 // Hs.405214 // CDC14A // 8556 // CDC14 cell division cycle 14 homolog A (S. cerevisiae) /// NM_033313 // intro	CDC14A	CDC14A , rs6687613, CDC14 cell division cycle 14 homolog A (S. cerevisiae) .p21.2
SNP_A-2130102	atacccaatatatgga[C/T]gggaaaagtgtagttt	C	T	NM_003729 // downstream // 35712 // Hs.484222 // RTCD1 // 8634 // Homo sapiens RNA terminal phosphate cyclase domain 1 (RTCD1), mRNA. /// NM_003672 // upstream // 25008 // Hs.533582 // CDC14A // 8556 // Homo sapiens CDC14 cell division cycle 14 homolog A	RTCD1	RTCD1, Homo sapiens RNA terminal phosphate cyclase domain 1 (RTCD1), p21.2
SNP_A-1886964	tgacttcgtaattgta[C/T]atattcatgggataca	C	T	NM_003672 // intron // 0 // Hs.533582 // CDC14A // 8556 // Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // intron // 0 // — // — // — // — /// ENST00000359262 // intr	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-1843960	tagttccagcttataa[A/G]tgagaatatgcagtat	A	G	NM_003672 // intron // 0 // Hs.533582 // CDC14A // 8556 // Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // intron // 0 // — // — // — // — /// ENST00000359262 // intr	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-2000237	attagttatgcaatgt[C/T]aaatgtgtactctttc	C	T	NM_003672 // intron // 0 // Hs.533582 // CDC14A // 8556 // Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // intron // 0 // — // — // — // — /// ENST00000359262 // intr	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-2282813	gataaactcagtgtaa[C/T]taaactgacttcccaa	C	T	NM_003672 // 3UTR // 0 // Hs.533582 // CDC14A // 8556 // Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA. /// ENST00000336454 // 3UTR // 0 // — // — // — // —	CDC14A	CDC14A, Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 1, p21.2
SNP_A-1838327	tagaaggattaagcag[A/G]cacaggttagaaggca	A	G	NM_022049 // downstream // 131211 // Hs.170053 // GPR88 // 54112 // Homo sapiens G-protein coupled receptor 88 (GPR88), mRNA. /// NM_080682 // upstream // 46518 // Hs.109225 // VCAM1 // 7412 // Homo sapiens vascular cell adhesion molecule 1 (VCAM1), trans	GPR88	GPR88, Homo sapiens G-protein coupled receptor 88 (GPR88), p21.2
SNP_A-2307506	gcttcaaaataagcca[C/T]agagagactgaatcgc	C	T	NM_015958 // upstream // 113410 // Hs.440776 // CGI-30 // 51611 // Homo sapiens CGI-30 protein (CGI-30), mRNA. /// NM_001400 // upstream // 97794 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled rece	CGI-30	CGI-30, Homo sapiens CGI-30 protein (CGI-30), p21.2
SNP_A-1887975	ggagttggccaaaaga[A/G]tagtggagagagagac	A	G	NM_001400 // downstream // 60201 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 60201 // — // — // — // — // — /// ENST00000305352	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1821837	gttttagagtcaatat[C/G]aggagtgagaaagagg	C	G	NM_001400 // downstream // 191640 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 191640 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2280913	gaggttgaatatttac[C/T]gaggccactcctgctt	C	T	NM_001400 // downstream // 201324 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 201324 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-1888890	tgccgttgagcacaga[C/T]gaagtaatcggaacac	C	T	NM_001400 // downstream // 216142 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 216142 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2251902	cttcattaatttcta[A/T]atcaacctcatgttcc	A	T	NM_001400 // downstream // 217253 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 217253 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2100758	agataggaagcagaga[G/T]aaccattagtaggtg	G	T	NM_001400 // downstream // 522706 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 522706 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2101919	agatgggagagaaattc[A/G]ccaaaaggacatatct	A	G	NM_001400 // downstream // 527891 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 527891 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2263973	gaactatttcaagca[G/T]ctgtgtccaggtatg	G	T	NM_001400 // downstream // 529049 // Hs.154210 // EDG1 // 1901 // Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /// ENST00000336722 // downstream // 529049 // --- // --- // --- /// ENST00000030535	EDG1	EDG1, Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), p21.2
SNP_A-2174214	cacaectcaagttgtc[A/C]ataagcctcttacaga	A	C	ENST00000314881 // intron // 0 // --- // --- // --- /// ENST00000359814 // intron // 0 // --- // --- // ---	-	p21.1
SNP_A-1643900	agaaaaagatgtattatctgagaaaa[C/G]atgttgctttctgttgttttt ctg	C	G	BC022531 // upstream // 372527 // Hs.335433 // OLFM3 // 118427 // olfactomedin 3 /// NM_001854 // downstream // 507920 // Hs.439168 // COL11A1 // 1301 // collagen, type XI, alpha 1 /// NM_080629 // downstream // 507920 // Hs.439168 // COL11A1 // 1301 //	OLFM3	OLFM3, rs1341913, olfactomedin 3, p21.1
SNP_A-1693415	gccagtttaaatggtgatgtacata[C/T]agaatagaggggggaaa ttgctggat	C	T	BC022531 // upstream // 373395 // Hs.335433 // OLFM3 // 118427 // olfactomedin 3 /// NM_001854 // downstream // 507052 // Hs.439168 // COL11A1 // 1301 // collagen, type XI, alpha 1 /// NM_080629 // downstream // 507052 // Hs.439168 // COL11A1 // 1301 //	OLFM3	OLFM3, rs10874598, olfactomedin 3, p21.1
SNP_A-2251752	cttcataaatatttca[A/C]ctttcctcactccct	A	C	BC022531 // upstream // 406406 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 624060 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2088476	actgtatttctatagc[A/G]aaggtcaagacccttt	A	G	BC022531 // upstream // 413870 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 616596 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-1899759	tagtcttagcaccaac[A/G]cttctaataaatgtg	A	G	BC022531 // upstream // 517906 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 512560 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-2150310	atgtctgctgttatca[C/T]ccggtcatgctaaaaa	C	T	BC022531 // upstream // 518320 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 512146 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-2191136	catagtgattgacaaat[A/T]gagttgtacagacaat	A	T	BC022531 // upstream // 525353 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 505113 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds. p21.1
SNP_A-2127314	ataaattacataaagcc[A/G]ctagcctaactatgaa	A	G	BC022531 // upstream // 528245 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 502221 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-2176975	cacctagaacttctga[C/T]ccatttgatgaatgtg	C	T	BC022531 // upstream // 537259 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 493207 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-1782250	ggcaagtcagtagataa[C/G]agcaaacttatttct	C	G	BC022531 // upstream // 555529 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 474937 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-2268942	gaattcagagctccca[G/T]gtccgctccccatgga	G	T	BC022531 // upstream // 567472 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 462984 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-1827835	taacttttctgcttta[C/T]aatcgttctcacacc	C	T	BC022531 // upstream // 580843 // Hs.484475 // OLFM3 // 118427 // Homo sapiens olfactomedin 3, mRNA (cDNA clone MGC:26675 IMAGE:4812035), complete cds. /// NM_001854 // downstream // 449623 // Hs.523446 // COL11A1 // 1301 // Homo sapiens collagen, type XI	OLFM3	OLFM3, Homo sapiens olfactomedin 3, (cDNA clone MGC:26675 IMAGE:4812035), complete cds, p21.1
SNP_A-2157474	atgatagttcctacc[C/T]agattgacagctgat	C	T	NM_004038 // downstream // 137864 // Hs.546234 // AMY1A // 276 // Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /// ENST00000332554 // downstream // 137864 // — // — // — /// ENST00000307896 // upstream // 176501 // — // — // -	AMY1A	AMY1A, Homo sapiens amylase, alpha 1A; salivary (AMY1A), p21.1
SNP_A-2233624	ctcataatgccattaa[C/T]caataacttctagtat	C	T	NM_004038 // downstream // 182558 // Hs.546234 // AMY1A // 276 // Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /// ENST00000332554 // downstream // 182558 // — // — // — /// ENST00000307896 // upstream // 131807 // — // — // -	AMY1A	AMY1A, Homo sapiens amylase, alpha 1A; salivary (AMY1A), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2118147	agtaaagacaaatcca[C/G]agtaagcagtcaatcc	C	G	NM_004038 // downstream // 183654 // Hs.546234 // AMY1A // 276 // Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /// ENST00000332554 // downstream // 183654 // — // — // — // — /// ENST00000307896 // upstream // 130711 // — // — // –	AMY1A	AMY1A, Homo sapiens amylase, alpha 1A; salivary (AMY1A), p21.1
SNP_A-2289298	gatttgtctttacttc[A/G]agtcaagtgattttgc	A	G	NM_004038 // downstream // 183673 // Hs.546234 // AMY1A // 276 // Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /// ENST00000332554 // downstream // 183673 // — // — // — // — /// ENST00000307896 // upstream // 130692 // — // — // –	AMY1A	AMY1A, Homo sapiens amylase, alpha 1A; salivary (AMY1A), p21.1
SNP_A-2157806	attgcctcagagatga[C/G]agaaaaattataatca	C	G	NM_004038 // downstream // 188242 // Hs.546234 // AMY1A // 276 // Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /// ENST00000332554 // downstream // 188242 // — // — // — // — /// ENST00000307896 // upstream // 126123 // — // — // –	AMY1A	AMY1A, Homo sapiens amylase, alpha 1A; salivary (AMY1A), p21.1
SNP_A-2199830	ccaaaccttgtatcca[A/C]tggaagtatactttag	A	C	AB023193 // upstream // 2931569 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 132310 // — // — // — // — /// ENST00000294649 // upstream // 2931569 // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p21.1
SNP_A-1896772	tgctatttactgtgga[G/T]ctgatgtctcaaactt	G	T	AB023193 // upstream // 2661920 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 401959 // — // — // — // — /// ENST00000294649 // upstream // 2661920 // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-1872138	tctactctaacaacag[C/T]caaataatatacaaag	C	T	AB023193 // upstream // 2289070 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 774809 // — // — // — // — /// ENST00000294649 // upstream // 2289070 // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. ,p21.1
SNP_A-1846534	tatattcttcaacgag[A/G]ctacataacttttgtaa	A	G	AB023193 // upstream // 1567522 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 1496357 // — // — // — // — /// ENST00000294649 // upstream // 1567522 // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-2234891	ctccatgattggccta[C/T]acctacctctctaaac	C	T	AB023193 // upstream // 1546657 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 1517222 // — // — // — // — /// ENST00000294649 // upstream // 1546657 // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-2061847	aatggatgcagcatta[C/T]agaaggcaggatggtg	C	T	AB023193 // upstream // 1042606 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2021273 // — // — // — // — /// ENST00000294649 // upstream // 1042606 // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-1681976	gaaagaacacaatgaaagtgctgta[A/G]agaatagatttaatc aagttaaatc	A	G	BC031278 // downstream // 831494 // Hs.375797 // - // - // Clone IMAGE:5295565, mRNA, partial cds /// NM_018137 // upstream // 425916 // Hs.26006 // PRMT6 // 55170 // protein arginine N-methyltransferase 6	-	- , rs10494047, Clone IMAGE:5295565, mRNA, partial cds ,p21.1
SNP_A-1912513	tgtgcatccaaatcac[C/G]cgatgaacttgatcat	C	G	AB023193 // upstream // 571326 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000307896 // downstream // 2492553 // — // — // — // — /// ENST00000294649 // upstream // 571326 // — // — // — /	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p21.1
SNP_A-1938713	ttgagcactgactaca[C/T]ccaaggagatgctaag	C	T	AB023193 // intron // 0 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// ENST00000294649 // intron // 0 // — // — // — // —	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p13.3
SNP_A-1739415	aaactcttgataaaattagaaaatg[C/T]cactaaataataagcta tgaaatgc	C	T	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // vav 3 oncogene	VAV3	VAV3 , rs10494078, vav 3 oncogene,p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207697	ccatttttctcaagac[A/G]acttctatattctcat	A	G	AB023193 // downstream // 61021 // Hs.211236 // NTNG1 // 22854 // Homo sapiens mRNA for KIAA0976 protein, partial cds. /// NM_006113 // downstream // 99562 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000294649 // d	NTNG1	NTNG1, Homo sapiens for KIAA0976 protein, partial cds. p13.3
SNP_A-1943362	taaattgaaggtgaat[C/T]agatgatccgtgtgggaa	C	T	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // — /// ENST00000343258 // intron // 0 // — // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-2081711	accttcatgagtagag[A/G]aaggacttctgaaagt	A	G	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-2135185	atattgcctctagca[A/G]caaagggatccaaatt	A	G	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-2098632	agagccagactgatca[A/C]ctatttttaaggttc	A	C	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-1945525	gctaagcactaaatcal[A/G]tcatcgagaattattc	A	G	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-1783761	ggcatttttagaatcag[A/G]agaatatcgagttga	A	G	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-1915486	tgttcctctgtcagc[A/G]tcttgtccagagaag	A	G	NM_006113 // intron // 0 // Hs.267659 // VAV3 // 10451 // Homo sapiens vav 3 oncogene (VAV3), mRNA. /// ENST00000280840 // intron // 0 // — // — // —	VAV3	VAV3, Homo sapiens vav 3 oncogene (VAV3). p13.3
SNP_A-2196540	catgttttatgggct[A/G]aatgtgtcttgcccc	A	G	NM_002790 // upstream // 4350 // Hs.485246 // PSMA5 // 5686 // Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA. /// ENST00000271308 // upstream // 4350 // — // — // — // — /// ENST00000271219 // upstream // 35713	PSMA5	PSMA5, Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), p13.3
SNP_A-2064877	aattgaatcaaactca[A/G]attggtagttgaatcc	A	G	NM_031936 // intron // 0 // Hs.514690 // GPR61 // 83873 // Homo sapiens G protein-coupled receptor 61 (GPR61), mRNA. /// ENST00000286603 // intron // 0 // — // — // — // —	GPR61	GPR61, Homo sapiens G protein-coupled receptor 61 (GPR61), p13.3
SNP_A-2061412	aatgccttgaataccc[A/G]cctgtcaaatgaagaa	A	G	NM_006492 // upstream // 38688 // Hs.169577 // ALX3 // 257 // Homo sapiens aristaless-like homeobox 3 (ALX3), mRNA. /// NM_203412 // upstream // 3146 // Hs.374027 // LOC164153 // 164153 // Homo sapiens similar to RIKEN cDNA 4930522D07 (LOC164153), mRNA. /	ALX3	ALX3, Homo sapiens aristaless-like homeobox 3 (ALX3), p13.3
SNP_A-2289520	gatttttatgtttctg[C/T]agagaagtactttct	C	T	NM_004978 // downstream // 61720 // Hs.153521 // KCNC4 // 3749 // Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 4 (KCNC4), transcript variant 1, mRNA. /// NM_153763 // downstream // 61720 // Hs.153521 // KCNC4 // 3749 // Hom	KCNC4	KCNC4, Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 4 (KCNC4), transcript variant 1. p13.3
SNP_A-1808144	gtcttggtgtggagtga[A/G]aggaaccaataatct	A	G	NM_006402 // upstream // 42785 // Hs.439815 // HBXIP // 10542 // Homo sapiens hepatitis B virus x interacting protein (HBXIP), mRNA. /// NM_032414 // upstream // 400 // Hs.514793 // PROK1 // 84432 // Homo sapiens prokineticin 1 (PROK1), mRNA. /// ENST0000	HBXIP	HBXIP, Homo sapiens hepatitis B virus x interacting protein (HBXIP), p13.3
SNP_A-1868665	tcctctgccccaagta[A/G]gatagaaggataccca	A	G	NM_006402 // upstream // 42893 // Hs.439815 // HBXIP // 10542 // Homo sapiens hepatitis B virus x interacting protein (HBXIP), mRNA. /// NM_032414 // upstream // 292 // Hs.514793 // PROK1 // 84432 // Homo sapiens prokineticin 1 (PROK1), mRNA. /// ENST0000	HBXIP	HBXIP, Homo sapiens hepatitis B virus x interacting protein (HBXIP), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1680030	ataaatttagaatgttgtctac[A/T]catacacaatatgtgctttg att	A	T	NM_000560 // downstream // 26212 // Hs.443057 // CD53 // 963 // CD53 antigen /// NM_018372 // downstream // 21057 // Hs.25245 // RIF1 // 55791 // receptor-interacting factor 1	CD53	CD53 , rs1631763, CD53 antigen ,p13.3
SNP_A-1733042	agacataatgaggctagggtaatca[C/T]gacaacacaatattg gcacaaggat	C	T	NM_000560 // downstream // 26342 // Hs.443057 // CD53 // 963 // CD53 antigen /// NM_018372 // downstream // 20927 // Hs.25245 // RIF1 // 55791 // receptor-interacting factor 1	CD53	CD53 , rs1418425, CD53 antigen ,p13.3
SNP_A-1696890	aagaccagtcttgttgaaaggcg[A/C]aatctaaaaactgttag aagaaat	A	C	NM_000560 // downstream // 27219 // Hs.443057 // CD53 // 963 // CD53 antigen /// NM_018372 // downstream // 20050 // Hs.25245 // RIF1 // 55791 // receptor-interacting factor 1	CD53	CD53 , rs1780569, CD53 antigen ,p13.3
SNP_A-2253411	cttctgttgggtcttat[C/T]atgggcttgagcag	C	T	NM_005549 // upstream // 10549 // Hs.248140 // KCNA10 // 3744 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10), mRNA. /// NM_004974 // downstream // 73819 // Hs.248139 // KCNA2 // 3737 // Homo sapiens potassium	KCNA10	KCNA10, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10), p13.3
SNP_A-2074179	acataaaatgacctcat[C/G]atcttgggtgcaag	C	G	NM_002232 // upstream // 26100 // Hs.169948 // KCNA3 // 3738 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3), mRNA. /// NM_000560 // upstream // 172397 // Hs.443057 // CD53 // 963 // Homo sapiens CD53 antigen (C	KCNA3	KCNA3, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3), p13.3
SNP_A-1961770	accctcccattcataa[C/T]ctacatacgtgcctat	C	T	NM_002232 // upstream // 45065 // Hs.169948 // KCNA3 // 3738 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3), mRNA. /// NM_000560 // upstream // 153432 // Hs.443057 // CD53 // 963 // Homo sapiens CD53 antigen (C	KCNA3	KCNA3, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3), p13.3
SNP_A-2000298	tagctagtcagtttaa[C/G]tccttaatacatatggg	C	G	NM_002232 // upstream // 125253 // Hs.169948 // KCNA3 // 3738 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3), mRNA. /// NM_000560 // upstream // 73244 // Hs.443057 // CD53 // 963 // Homo sapiens CD53 antigen (C	KCNA3	KCNA3, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3 (KCNA3), p13.3
SNP_A-1726612	aagcttctagtacttaaaataa[C/G]taaatggagtattatatat caattc	C	G	NM_001688 // downstream // 174 // Hs.81634 // ATP5F1 // 515 // ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 /// NM_174896 // upstream // 12482 // Hs.288010 // MGC24133 // 128346 // hypothetical protein MGC24133	ATP5F1	ATP5F1 , rs10489793, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 ,p13.2
SNP_A-2039242	aacagtgtagaaagca[A/T]acagagatatgctt	A	T	NM_178454 // intron // 0 // Hs.485606 // MGC54289 // 128338 // Homo sapiens hypothetical protein MGC54289 (MGC54289), mRNA. /// ENST00000286692 // intron // 0 // — // — // —	MGC54289	MGC54289, Homo sapiens hypothetical protein MGC54289 (MGC54289), p13.3
SNP_A-2195007	catgcttcatcattca[C/G]attaattatgctgatg	C	G	NM_006090 // intron // 0 // Hs.363572 // CEPT1 // 10390 // Homo sapiens choline/ethanolaminephosphotransferase (CEPT1), mRNA. /// ENST00000317584 // intron // 0 // — // — // — /// ENST00000357172 // intron // 0 // — // — // —	CEPT1	CEPT1, Homo sapiens choline,p13.3
SNP_A-1661348	tatcttttttctctttagcctgtca[C/T]actggagatccaaccacatg ctgca	C	T	NM_004980 // upstream // 182076 // Hs.414110 // KCND3 // 3752 // potassium voltage-gated channel, Shal-related subfamily, member 3 /// NM_018704 // upstream // 225007 // Hs.374649 // DKFZp547A023 // 55917 // hypothetical protein DKFZp547A023 /// NM_17219	KCND3	KCND3 , rs1155678, potassium voltage-gated channel, Shal-related subfamily, member 3 ,p13.2
SNP_A-1916196	tgttgggatgactata[C/T]acttggtaatctggg	C	T	NM_004980 // intron // 0 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // intron // 0 // Hs.414110 // KCND3 // 3752 // Homo sapiens potass	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1898265	tgcttagaggacaatc[A/G]gttatgcccacggg	A	G	NM_004980 // intron // 0 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // intron // 0 // Hs.414110 // KCND3 // 3752 // Homo sapiens potass	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2068814	acaatcaagggagccaa[C/T]gtaaattaaagttaaa	C	T	NM_004980 // upstream // 6966 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 6966 // Hs.414110 // KCND3 // 3752 // Homo sapi	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2310038	ggaaatgttgcaggac[A/C]agcaggttcacatgct	A	C	NM_004980 // upstream // 26254 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 26254 // Hs.414110 // KCND3 // 3752 // Homo sa	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2284193	gatatgtaagtaaaag[C/G]cttgtgacacttag	C	G	NM_004980 // upstream // 183017 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 183017 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1834861	taccatccagatggaat[C/T]gagcaatgagaagaggg	C	T	NM_004980 // upstream // 185916 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 185916 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1962385	ggaacaatcttgcaaat[A/G]gctgtaaagtaggaat	A	G	NM_004980 // upstream // 189323 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 189323 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2304824	gctcttacaaaatcca[A/G]attcattagcacagtt	A	G	NM_004980 // upstream // 191687 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 191687 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1852679	tatttatttttcctct[C/G]ccatctggttcacatg	C	G	NM_004980 // upstream // 193160 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 193160 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2250812	cttatcctgcccaagat[C/T]gtgaactagccaacac	C	T	NM_004980 // upstream // 200025 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 200025 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-2273588	gactgactgatagacat[A/G]gtgacagatacataga	A	G	NM_004980 // upstream // 334820 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 334820 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1962432	gttgttcatcacacta[C/G]agcatcaatttattc	C	G	NM_004980 // upstream // 355276 // Hs.414110 // KCND3 // 3752 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, mRNA. /// NM_172198 // upstream // 355276 // Hs.414110 // KCND3 // 3752 // Homo	KCND3	KCND3, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 3 (KCND3), transcript variant 1, p13.2
SNP_A-1902063	tggcatcttcattctt[A/G]aacccctaaatgccac	A	G	NM_018704 // intron // 0 // Hs.485899 // DKFZp547A023 // 55917 // Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), mRNA. /// ENST00000271277 // intron // 0 // — // — // — // —	DKFZp547A023	DKFZp547A023, Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1820594	gtttcaaccagcagtc[A/G]aatagatagattggga	A	G	NM_018704 // intron // 0 // Hs.485899 // DKFZp547A023 // 55917 // Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), mRNA. /// ENST00000271277 // intron // 0 // — // — // — // —	DKFZp547A023	DKFZp547A023, Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), p13.2
SNP_A-2239538	ctctttttctctctac[C/T]attctcaacctgtatt	C	T	NM_004185 // 3UTR // 0 // Hs.258575 // WNT2B // 7482 // Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, mRNA. /// NM_024494 // 3UTR // 0 // Hs.258575 // WNT2B // 7482 // Homo sapiens wingless-type MM	WNT2B	WNT2B, Homo sapiens wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, p13.2
SNP_A-1841793	taggccatttttattc[C/G]atgccagattacatag	C	G	NM_138728 // intron // 0 // Hs.201921 // ST7L // 54879 // Homo sapiens suppression of tumorigenicity 7 like (ST7L), transcript variant 3, mRNA. /// NM_138727 // intron // 0 // Hs.201921 // ST7L // 54879 // Homo sapiens suppression of tumorigenicity 7 like	ST7L	ST7L, Homo sapiens suppression of tumorigenicity 7 like (ST7L), transcript variant 3, p13.2
SNP_A-1785545	ggctcagtgaggttaa[C/G]acagattcagagctgt	C	G	NM_175744 // intron // 0 // Hs.502659 // RHOC // 389 // Homo sapiens ras homolog gene family, member C (RHOC), mRNA. /// ENST00000339083 // intron // 0 // — // — // — // — /// ENST00000285735 // intron // 0 // — // — // — // —	RHOC	RHOC, Homo sapiens ras homolog gene family, member C (RHOC), p13.2
SNP_A-1712863	attcttttaacctacattcagccac[A/G]ccgggaatgatgcttcttg acctga	A	G	NM_014813 // downstream // 65803 // - // - // - // - /// NM_020965 // upstream // 200226 // Hs.446369 // MAGI-3 // 260425 // membrane-associated guanylate kinase-related (MAGI-3) /// NM_152900 // upstream // 200511 // Hs.446369 // MAGI-3 // 260425 // mem	-	-, rs1324893, -,p13.2
SNP_A-2040888	aaccctaagttagatg[G/T]atatgtctggtttgtc	G	T	NM_020965 // upstream // 147853 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // upstream // 147853 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-2050449	aaggatagagactgaa[C/T]ggaaggtactggaagg	C	T	NM_020965 // upstream // 142318 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // upstream // 142318 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-1962626	cacattgcccagagac[A/G]actacagccatcagtt	A	G	NM_020965 // upstream // 13763 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // upstream // 13763 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated g	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-2132888	atataatgatctgtgc[C/T]gcaatatactataatt	C	T	NM_020965 // intron // 0 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), mRNA. /// NM_152900 // intron // 0 // Hs.486189 // MAGI-3 // 260425 // Homo sapiens membrane-associated guanylate kin	MAGI-3	MAGI-3, Homo sapiens membrane-associated guanylate kinase-related (MAGI-3) (MAGI-3), p13.2
SNP_A-1785543	ggctcagtatccctag[A/T]attctgccttaaattc	A	T	NM_205848 // intron // 0 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// ENST00000285794 // intron // 0 // — // — // — // —	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2172475	caattcaggccaagac[C/T]accctttccatcagaa	C	T	NM_205848 // intron // 0 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// ENST00000285794 // intron // 0 // — // — // — // —	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2074621	acatatacagcaaccc[A/G]cctcaaaggtttccct	A	G	NM_205848 // intron // 0 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// ENST00000285794 // intron // 0 // — // — // — // —	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2165302	caaagagagcccgtca[C/T]gtcaaagaaaccaact	C	T	NM_205848 // upstream // 79833 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// NM_033020 // downstream // 163938 // Hs.26837 // TRIM33 // 51592 // Homo sapiens tripartite motif-containing 33 (TRIM33), transcript variant b	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2000309	gcaagttcacctaca[C/T]agtgcagctccagttc	C	T	NM_205848 // upstream // 138618 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// NM_033020 // downstream // 105153 // Hs.26837 // TRIM33 // 51592 // Homo sapiens tripartite motif-containing 33 (TRIM33), transcript variant	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2159458	attacaatacccatca[A/G]aaagattaggatagaa	A	G	NM_205848 // upstream // 227164 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// NM_033020 // downstream // 16607 // Hs.26837 // TRIM33 // 51592 // Homo sapiens tripartite motif-containing 33 (TRIM33), transcript variant b	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-2055806	aatacaaaagcatgca[A/G]agacaggaaagtacaa	A	G	NM_205848 // upstream // 232271 // Hs.370963 // SYT6 // 148281 // Homo sapiens synaptotagmin VI (SYT6), mRNA. /// NM_033020 // downstream // 11500 // Hs.26837 // TRIM33 // 51592 // Homo sapiens tripartite motif-containing 33 (TRIM33), transcript variant b	SYT6	SYT6, Homo sapiens synaptotagmin VI (SYT6), p13.2
SNP_A-1733370	tccacaaaccacagagataagtgaa[C/T]cattgatgagaaccaaaatggtgtc	C	T	NM_002506 // downstream // 126630 // Hs.2561 // NGFB // 4803 // nerve growth factor, beta polypeptide /// NM_005725 // upstream // 69824 // Hs.234863 // TSPAN-2 // 10100 // tetraspan 2	NGFB	NGFB , rs10494171, nerve growth factor, beta polypeptide , p13.1
SNP_A-1925362	ttatctcctcaaaaca[A/G]caagaattctgcacct	A	G	NM_025073 // upstream // 175029 // Hs.24808 // FLJ21168 // 80143 // Homo sapiens hypothetical protein FLJ21168 (FLJ21168), mRNA. /// NM_000549 // upstream // 74158 // Hs.406687 // TSHB // 7252 // Homo sapiens thyroid stimulating hormone, beta (TSHB), mRNA	FLJ21168	FLJ21168, Homo sapiens hypothetical protein FLJ21168 (FLJ21168), p13.1
SNP_A-1810971	gtgcatttctccaaat[C/T]atctctattaagtctc	C	T	NM_005725 // upstream // 55181 // Hs.310458 // TSPAN2 // 10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 141273 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST000002	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-2050318	aaggagccaggatca[A/T]cctctgtatctgaaga	A	T	NM_005725 // upstream // 77653 // Hs.310458 // TSPAN2 // 10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 118801 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST000002	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-1963064	gccggatcttctccta[C/T]gtacctgcttcatttt	C	T	NM_005725 // upstream // 90728 // Hs.310458 // TSPAN2 // 10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 105726 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST000002	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-1963065	aaactcagtacaaaca[C/T]gcaaggcgccctttag	C	T	NM_005725 // upstream // 90832 // Hs.310458 // TSPAN2 // 10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 105622 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST000002	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1
SNP_A-1947161	tttaatgacaacttaa[C/T]gagaggagttaataag	C	T	NM_005725 // upstream // 123089 // Hs.310458 // TSPAN2 // 10100 // Homo sapiens tetraspan 2 (TSPAN-2), mRNA. /// NM_002506 // downstream // 73365 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST000002	TSPAN2	TSPAN2, Homo sapiens tetraspan 2 (TSPAN-2), p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1914703	tgttacaacacataag[A/T]ctataatgcgattcag	A	T	NM_002506 // intron // 0 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // intron // 0 // — // — // —	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-2278642	gagctggagccaagaa[A/G]gtgaaaaggaagtgag	A	G	NM_002506 // upstream // 22874 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 22874 // — // — // — // — /// ENST00000359553 // downstream // 240774 // — // — // — /// NM_002506 // upstream // 64293 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 64293 // — // — // — // — /// ENST00000359553 // downstream // 199355 // — // — // —	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-1963173	ttgtctgaccgtaa[A/T]ctgggaagctgaaatt	A	T		NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-1942655	ttgggagagcaaattc[A/G]aaaggtctgtaggaaca	A	G	NM_002506 // upstream // 232745 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 232745 // — // — // — // — /// ENST00000359553 // downstream // 30903 // — // — // —	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-1854205	tcaaagatcctgaca[A/G]gctggtatggacagt	A	G	NM_002506 // upstream // 239058 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 239058 // — // — // — // — /// ENST00000359553 // downstream // 24590 // — // — // —	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-1871433	tctaacagcagttaaa[G/T]gtgcttctttagaagg	G	T	NM_002506 // upstream // 254319 // Hs.2561 // NGFB // 4803 // Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA. /// ENST00000256655 // upstream // 254319 // — // — // — // — /// ENST00000359553 // downstream // 9329 // — // — // —	NGFB	NGFB, Homo sapiens nerve growth factor, beta polypeptide (NGFB), p13.1
SNP_A-2112005	aggatgaggttgttaa[C/T]tgggcctgtgcaggct	C	T	ENST00000359553 // intron // 0 // — // — // — // —	-	p13.1
SNP_A-2234484	ctccacatccttgtac[C/T]gagcactacttacatt	C	T	NM_138959 // intron // 0 // Hs.515130 // VANGL1 // 81839 // Homo sapiens vang-like 1 (van gogh, Drosophila) (VANGL1), mRNA. /// ENST00000355485 // intron // 0 // — // — // — // — /// ENST00000310260 // intron // 0 // — // — // — // —	VANGL1	VANGL1, Homo sapiens vang-like 1 (van gogh, Drosophila) (VANGL1), p13.1
SNP_A-1792207	gggttataaaggctta[C/T]gaagtccaacttttgg	C	T	NM_138959 // intron // 0 // Hs.515130 // VANGL1 // 81839 // Homo sapiens vang-like 1 (van gogh, Drosophila) (VANGL1), mRNA. /// ENST00000355485 // intron // 0 // — // — // — // — /// ENST00000310260 // intron // 0 // — // — // — // —	VANGL1	VANGL1, Homo sapiens vang-like 1 (van gogh, Drosophila) (VANGL1), p13.1
SNP_A-2070567	acacctgatggcttaa[G/T]gacacctaggtggcct	G	T	NM_005599 // upstream // 52160 // Hs.46296 // NHLH2 // 4808 // Homo sapiens nescient helix loop helix 2 (NHLH2), mRNA. /// NM_018420 // upstream // 83212 // Hs.125482 // SLC22A15 // 55356 // Homo sapiens solute carrier family 22 (organic cation transporte	NHLH2	NHLH2, Homo sapiens nescient helix loop helix 2 (NHLH2), p13.1
SNP_A-2156402	attctccaaaacataa[C/T]actatagcctactgt	C	T	NM_005599 // upstream // 57767 // Hs.46296 // NHLH2 // 4808 // Homo sapiens nescient helix loop helix 2 (NHLH2), mRNA. /// NM_018420 // upstream // 77605 // Hs.125482 // SLC22A15 // 55356 // Homo sapiens solute carrier family 22 (organic cation transporte	NHLH2	NHLH2, Homo sapiens nescient helix loop helix 2 (NHLH2), p13.1
SNP_A-2283952	gatatacctgaaacac[C/T]gtcaaatcatttattc	C	T	NM_152367 // downstream // 127299 // Hs.376194 // FLJ38716 // 126668 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 // upstream // 110676 // Hs.371889 // ATP1A1 // 476 // Homo sapiens ATPase, Na+/K+ transporting, alpha 1	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-2095230	agaattcttagagta[C/T]gctggcaagtgcaatt	C	T	NM_152367 // downstream // 155443 // Hs.376194 // FLJ38716 // 126668 // Homo sapiens hypothetical protein FLJ38716 (FLJ38716), mRNA. /// NM_001001586 // upstream // 82532 // Hs.371889 // ATP1A1 // 476 // Homo sapiens ATPase, Na+/K+ transporting, alpha 1 p	FLJ38716	FLJ38716, Homo sapiens hypothetical protein FLJ38716 (FLJ38716), p13.1
SNP_A-1682546	aagtagaaattcctctataaaaga[C/T]acaagagttagtcaag gaaatctat	C	T	NM_003594 // intron // 0 // Hs.201774 // TTF2 // 8458 // transcription termination factor, RNA polymerase II	TTF2	TTF2 , rs3767770, transcription termination factor, RNA polymerase II,p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251341	cttcaagggcagaaac[A/C]atgaaaaagaaagagg	A	C	NM_001767 // upstream // 3339 // Hs.523500 // CD2 // 914 // Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), mRNA. /// ENST00000295608 // upstream // 36315 // --- // --- // --- // --- // --- /// ENST00000235470 // upstream // 3339 // --- // -	CD2	CD2, Homo sapiens CD2 antigen (p50), sheep red blood cell receptor (CD2), p13.1
SNP_A-2306032	gctggaactgagttca[G/T]agtaactgtgagttat	G	T	NM_004258 // intron // 0 // Hs.74115 // IGSF2 // 9398 // Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA. /// ENST00000256652 // intron // 0 // --- // --- // --- // ---	IGSF2	IGSF2, Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), p13.1
SNP_A-2235004	ctcccaagcagactga[A/T]ccattcacatttcaac	A	T	NM_024626 // upstream // 73733 // Hs.546434 // B7-H4 // 79679 // Homo sapiens immune costimulatory protein B7-H4 (B7-H4), mRNA. /// NM_006699 // upstream // 82785 // Hs.435938 // MAN1A2 // 10905 // Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN1	B7-H4	B7-H4, Homo sapiens immune costimulatory protein B7-H4 (B7-H4), p12
SNP_A-2148257	atgggcaccctctttc[A/G]catttttttcttggc	A	G	NM_024626 // upstream // 125513 // Hs.546434 // B7-H4 // 79679 // Homo sapiens immune costimulatory protein B7-H4 (B7-H4), mRNA. /// NM_006699 // upstream // 31005 // Hs.435938 // MAN1A2 // 10905 // Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN	B7-H4	B7-H4, Homo sapiens immune costimulatory protein B7-H4 (B7-H4), p12
SNP_A-1731267	ttcaatctgtttaataaagacgtgc[C/G]aatagagtgccaaaaagcatttaaa	C	G	NM_006784 // intron // 0 // Hs.201375 // WDR3 // 10885 // WD repeat domain 3	WDR3	WDR3 , rs2273581, WD repeat domain 3,p12
SNP_A-2063902	aattatactcttctac[C/T]gaaaaatgcaaaacca	C	T	NM_006699 // downstream // 71417 // Hs.435938 // MAN1A2 // 10905 // Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA. /// NM_017709 // upstream // 8026 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, m	MAN1A2	MAN1A2, Homo sapiens mannosidase, alpha, class 1A, member 2 (MAN1A2), p12
SNP_A-2110371	aggaatgggctgatcc[C/T]gatccagaaaactaag	C	T	NM_017709 // intron // 0 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// ENST00000328500 // intron // 0 // --- // --- // --- // ---	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2098300	agagatggacttggag[A/T]cgtggttgtcattcac	A	T	NM_017709 // intron // 0 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// ENST00000328500 // intron // 0 // --- // --- // --- // ---	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2233108	ctcagcagggcttagg[A/C]atcagaaacatcagat	A	C	NM_017709 // downstream // 14832 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 226219 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1786703	ggcttgtaactgcaga[C/T]ctacttatgtattgag	C	T	NM_017709 // downstream // 105549 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 135502 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differe	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1963979	cccattgactttctgc[G/T]ctcctggatgagattt	G	T	NM_017709 // downstream // 110836 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 130215 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differe	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2253811	cttgaacttggcccac[C/T]ccaaatcagttcctat	C	T	NM_017709 // downstream // 122107 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 118944 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differe	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2038727	aacagataagtgtcta[A/G]ggaaaatcttattc	A	G	NM_017709 // downstream // 124939 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 116112 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differe	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1963988	aacacattcccaatat[C/T]ccctactcttgatggc	C	T	NM_017709 // downstream // 125985 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 115066 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differe	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1954884	ttgctttaagctggal[A/G]ggggatttgtatgt	A	G	NM_017709 // downstream // 155918 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 85133 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1963999	tgtgcttgtggcaca[G/T]ctttatcgccactat	G	T	NM_017709 // downstream // 165232 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 75819 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2203495	ccagaagacttgtca[C/G]ggtttgtgtcaggatc	C	G	NM_017709 // downstream // 186975 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 54076 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1789396	gggcccacacctacac[C/T]gagttgaccaatgtct	C	T	NM_017709 // downstream // 188379 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 52672 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2178793	cactgacatcaccaca[A/G]gttgttgctctcagtt	A	G	NM_017709 // downstream // 196315 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 44736 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-2090224	actgcaactgtcata[C/T]cacacgtgcaaaattt	C	T	NM_017709 // downstream // 218615 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 22436 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1823836	taaaatgccatgttta[A/G]caggtactactagaac	A	G	NM_017709 // downstream // 221976 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 19075 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differen	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1947810	tttactgtccaacaaa[A/C]gtatcagatcacattc	A	C	NM_017709 // downstream // 237289 // Hs.356216 // FAM46C // 54855 // Homo sapiens family with sequence similarity 46, member C (FAM46C), mRNA. /// NM_017686 // downstream // 3762 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced different	FAM46C	FAM46C, Homo sapiens family with sequence similarity 46, member C (FAM46C), p12
SNP_A-1964040	tttggaaggtttataa[C/T]agcactgttgaaggag	C	T	NM_017686 // intron // 0 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), mRNA. /// ENST00000359885 // intron // 0 // — // — // —	GDAP2	GDAP2, Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903390	tgggaactatttgaaa[A/G]tgcagcatgaaggaag	A	G	NM_017686 // intron // 0 // Hs.310809 // GDAP2 // 54834 // Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), mRNA. /// ENST00000359885 // intron // 0 // — // — // —	GDAP2	GDAP2, Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), p12
SNP_A-2285834	gatgagagaacagcaa[C/T]ggacaaaggaccaaa	C	T	NM_006784 // intron // 0 // Hs.201375 // WDR3 // 10885 // Homo sapiens WD repeat domain 3 (WDR3), mRNA. /// ENST00000349139 // intron // 0 // — // — // — /// ENST00000350446 // intron // 0 // — // — // —	WDR3	WDR3, Homo sapiens WD repeat domain 3 (WDR3), p12
SNP_A-2148762	atggtgaaatacttca[A/G]aagccttaggaagaat	A	G	NM_206996 // intron // 0 // Hs.528821 // PF6 // 200162 // Homo sapiens projection protein PF6 (PF6), mRNA. /// ENST00000286203 // intron // 0 // — // — // — /// ENST00000336338 // intron // 0 // — // — // —	PF6	PF6, Homo sapiens projection protein PF6 (PF6), p12
SNP_A-1952805	tttcgttgtcatacaa[C/T]ctgatattacttcaa	C	T	NM_206996 // intron // 0 // Hs.528821 // PF6 // 200162 // Homo sapiens projection protein PF6 (PF6), mRNA. /// ENST00000286203 // intron // 0 // — // — // — /// ENST00000336338 // intron // 0 // — // — // —	PF6	PF6, Homo sapiens projection protein PF6 (PF6), p12
SNP_A-1964071	gtatcatctggtcaca[C/T]tggtctgctagtagtt	C	T	NM_206996 // intron // 0 // Hs.528821 // PF6 // 200162 // Homo sapiens projection protein PF6 (PF6), mRNA. /// ENST00000286203 // intron // 0 // — // — // — /// ENST00000336338 // intron // 0 // — // — // —	PF6	PF6, Homo sapiens projection protein PF6 (PF6), p12
SNP_A-2224565	cgtcaatatttgcaca[C/T]ccttaacgaggccgtg	C	T	NM_006784 // downstream // 882500 // Hs.201375 // WDR3 // 10885 // Homo sapiens WD repeat domain 3 (WDR3), mRNA. /// NM_206996 // upstream // 657715 // Hs.528821 // PF6 // 200162 // Homo sapiens projection protein PF6 (PF6), mRNA. /// ENST00000349139 // d	WDR3	WDR3, Homo sapiens WD repeat domain 3 (WDR3), p12
SNP_A-2314041	ggagctttaagcaaag[C/T]attggcatgatcgggt	C	T	NM_014644 // intron // 0 // Hs.487925 // PDE4DIP // 9659 // Homo sapiens phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), transcript variant 1, mRNA. /// NM_001002812 // intron // 0 // Hs.487925 // PDE4DIP // 9659 // Homo sapiens phosphodi	PDE4DIP	PDE4DIP, Homo sapiens phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), transcript variant 1, q21.1
SNP_A-1851111	tattatttgatgaac[C/T]attgagagtaagatg	C	T	NM_022359 // intron // 0 // Hs.487925 // PDE4DIP // 9659 // Homo sapiens phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), transcript variant 3, mRNA. /// ENST00000336785 // intron // 0 // — // — // —	PDE4DIP	PDE4DIP, Homo sapiens phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP), transcript variant 3, q21.1
SNP_A-1921193	ttacatcaacctcat[A/G]agtagtattggtttgt	A	G	NM_183372 // upstream // 31268 // Hs.515837 // LOC200030 // 200030 // Homo sapiens hypothetical protein LOC200030 (LOC200030), mRNA. /// ENST00000281815 // upstream // 31268 // — // — // — /// ENST00000339388 // upstream // 31247 // — // –	LOC200030	LOC200030, Homo sapiens hypothetical protein LOC200030 (LOC200030), q21.1
SNP_A-2297123	gccacagaaattaggac[C/T]atgggagtagcttgaa	C	T	NM_004326 // upstream // 131596 // Hs.415209 // BCL9 // 607 // Homo sapiens B-cell CLL/lymphoma 9 (BCL9), mRNA. /// ENST00000310023 // downstream // 89657 // — // — // — /// ENST00000234739 // upstream // 131596 // — // — // —	BCL9	BCL9, Homo sapiens B-cell CLL q21.1
SNP_A-1966066	caattcttagaccttc[A/G]agaggacttcccagtg	A	G	NM_005266 // intron // 0 // Hs.447968 // GJA5 // 2702 // Homo sapiens gap junction protein, alpha 5, 40kDa (connexin 40) (GJA5), transcript variant A, mRNA. /// NM_181703 // intron // 0 // Hs.447968 // GJA5 // 2702 // Homo sapiens gap junction protein, al	GJA5	GJA5, Homo sapiens gap junction protein, alpha 5, 40kDa (connexin 40) (GJA5), transcript variant A, q21.1
SNP_A-2237411	ctctccgcattccccc[C/G]agtttctccctctcct	C	G	NM_005267 // upstream // 5511 // Hs.157433 // GJA8 // 2703 // Homo sapiens gap junction protein, alpha 8, 50kDa (connexin 50) (GJA8), mRNA. /// ENST00000344536 // downstream // 54995 // — // — // — /// ENST00000240986 // upstream // 5511 // -	GJA8	GJA8, Homo sapiens gap junction protein, alpha 8, 50kDa (connexin 50) (GJA8), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2163812	caaaacacatgatttc[A/G]cagaccatacagcttt	A	G	NM_207400 // downstream // 108170 // Hs.406990 // FLJ39739 // 386685 // Homo sapiens FLJ39739 protein (FLJ39739), mRNA. /// ENST00000344770 // upstream // 148800 // --- // --- // --- /// ENST00000339068 // upstream // 151307 // --- // --- // ---	FLJ39739	FLJ39739, Homo sapiens FLJ39739 protein (FLJ39739), q21.1
SNP_A-1739665	tacgtctatttataaaggcctggc[A/G]aatgaaagaactcaatg ggttttga	A	G	NM_005266 // upstream // 118657 // Hs.447968 // GJA5 // 2702 // gap junction protein, alpha 5, 40kDa (connexin 40) /// NM_005267 // upstream // 10837 // Hs.157433 // GJA8 // 2703 // gap junction protein, alpha 8, 50kDa (connexin 50) /// NM_181703 // upst	GJA5	GJA5 , rs903784, gap junction protein, alpha 5, 40kDa (connexin 40) ,q21.1
SNP_A-1781144	ggatggaaaattggac[A/C]gtcaaagagtaacagt	A	C	NM_207400 // downstream // 48928 // Hs.406990 // FLJ39739 // 386685 /// Homo sapiens FLJ39739 protein (FLJ39739), mRNA. /// ENST00000344770 // upstream // 208042 // --- // --- // --- /// ENST00000339068 // upstream // 210549 // --- // --- // ---	FLJ39739	FLJ39739, Homo sapiens FLJ39739 protein (FLJ39739), q21.1
SNP_A-2298873	gccccaatctttccaa[A/G]gaagcaggtgtttctg	A	G	NM_207400 // downstream // 43928 // Hs.406990 // FLJ39739 // 386685 /// Homo sapiens FLJ39739 protein (FLJ39739), mRNA. /// ENST00000344770 // upstream // 213042 // --- // --- // --- /// ENST00000339068 // upstream // 215549 // --- // --- // ---	FLJ39739	FLJ39739, Homo sapiens FLJ39739 protein (FLJ39739), q21.1
SNP_A-2256223	ctttagcaacatttttc[A/G]actcagtgggcactgc	A	G	NM_207400 // downstream // 36511 // Hs.406990 // FLJ39739 // 386685 /// Homo sapiens FLJ39739 protein (FLJ39739), mRNA. /// ENST00000344770 // upstream // 220459 // --- // --- // --- /// ENST00000339068 // upstream // 222966 // --- // --- // ---	FLJ39739	FLJ39739, Homo sapiens FLJ39739 protein (FLJ39739), q21.1
SNP_A-1928641	ttcactgtcaaatgc[C/T]catactgagagtatt	C	T	NM_207400 // downstream // 25543 // Hs.406990 // FLJ39739 // 386685 /// Homo sapiens FLJ39739 protein (FLJ39739), mRNA. /// ENST00000344770 // upstream // 231427 // --- // --- // --- /// ENST00000339068 // upstream // 233934 // --- // --- // ---	FLJ39739	FLJ39739, Homo sapiens FLJ39739 protein (FLJ39739), q21.1
SNP_A-1756597	ctccaaatgaatgattcatgttcag[A/G]actttcacaggtgaggg ctggaaac	A	G	NM_006697 // upstream // 768 // Hs.425144 // CRA // 10903 // cisplatin resistance associated /// NM_020205 // downstream // 5842 // Hs.8852 // ZA20D1 // 56957 // zinc finger, A20 domain containing 1 /// NM_181873 // upstream // 1252 // Hs.425144 // CRA I	CRA	CRA , rs10494363, cisplatin resistance associated ,q21.2
SNP_A-1841285	taggaagaaggggggat[C/G]aatttgaggagactg	C	G	NM_021222 // downstream // 77 // Hs.78524 // PRUNE // 58497 // Homo sapiens TcD37 homolog (HTCD37), mRNA. /// NM_138279 // upstream // 825 // Hs.534563 // BNIPL // 149428 // Homo sapiens BCL2/adenovirus E1B 19kD interacting protein like (BNIPL), mRNA. ///	PRUNE	PRUNE, Homo sapiens TcD37 homolog (HTCD37), q21.2
SNP_A-2045632	aagaatttgtgattaa[A/G]taaacatggataaaagc	A	G	NM_145796 // intron // 0 // Hs.489873 // POGZ // 23126 // Homo sapiens pogo transposable element with ZNF domain (POGZ), transcript variant 3, mRNA. /// NM_015100 // intron // 0 // Hs.489873 // POGZ // 23126 // Homo sapiens pogo transposable element with	POGZ	POGZ, Homo sapiens pogo transposable element with ZNF domain (POGZ), transcript variant 3, q21.3
SNP_A-1966628	cattaccattgtgtga[C/T]gatcacctacagtatt	C	T	NM_020127 // intron // 0 // Hs.489922 // TUFT1 // 7286 // Homo sapiens tuftelin 1 (TUFT1), mRNA. /// ENST00000342552 // intron // 0 // --- // --- // --- /// ENST00000306878 // intron // 0 // --- // --- // --- /// ENST00000353024 // intron //	TUFT1	TUFT1, Homo sapiens tuftelin 1 (TUFT1), q21.3
SNP_A-1798452	gtaaatctagaagcaa[C/T]aggtagatggttccag	C	T	NM_020127 // intron // 0 // Hs.489922 // TUFT1 // 7286 // Homo sapiens tuftelin 1 (TUFT1), mRNA. /// ENST00000342552 // intron // 0 // --- // --- // --- /// ENST00000306878 // intron // 0 // --- // --- // --- /// ENST00000353024 // intron //	TUFT1	TUFT1, Homo sapiens tuftelin 1 (TUFT1), q21.3
SNP_A-2296621	gccaaaagaaaaatgtc[A/G]atctaaaatcatgctc	A	G	NM_053055 // intron // 0 // Hs.164070 // CTMP // 117145 // Homo sapiens C-terminal modulator protein (CTMP), transcript variant 1, mRNA. /// ENST00000295348 // intron // 0 // --- // --- // ---	CTMP	CTMP, Homo sapiens C-terminal modulator protein (CTMP), transcript variant 1, q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2303782	gctcaggcagaaatac[A/C]gtaagttcaactgaat	A	C	NM_053055 // upstream // 34772 // Hs.164070 // CTMP // 117145 // Homo sapiens C-terminal modulator protein (CTMP), transcript variant 1, mRNA. /// NM_176853 // upstream // 34817 // Hs.164070 // CTMP // 117145 // Homo sapiens C-terminal modulator protein (	CTMP	CTMP, Homo sapiens C-terminal modulator protein (CTMP), transcript variant 1, q21.3
SNP_A-2298544	gcccacagcaggcaaa[A/G]gcggacctcagcagcc	A	G	NM_016190 // downstream // 28099 // Hs.242057 // C1orf10 // 49860 // Homo sapiens chromosome 1 open reading frame 10 (C1orf10), mRNA. /// ENST00000271816 // upstream // 22260 // — // — // — // — /// ENST00000271835 // downstream // 28099 // — //	C1orf10	C1orf10, Homo sapiens chromosome 1 open reading frame 10 (C1orf10), q21.3
SNP_A-2302233	gctaaatcaggccgta[A/C]actgccatcagctggg	A	C	NM_178356 // downstream // 16904 // Hs.447955 // LCE4A // 199834 // Homo sapiens late cornified envelope 4A (LCE4A), mRNA. /// NM_178354 // upstream // 50093 // — // LCE1F // 353137 // Homo sapiens late cornified envelope 1F (LCE1F), mRNA. /// ENST00000	LCE4A	LCE4A, Homo sapiens late cornified envelope 4A (LCE4A), q21.3
SNP_A-2045259	aagaaggattagcccc[A/T]gaaagtccctgaagta	A	T	NM_173080 // downstream // 10781 // — // SPRR4 // 163778 // Homo sapiens small proline rich protein 4 (SPRR4), mRNA. /// NM_005987 // upstream // 707 // Hs.46320 // SPRR1A // 6698 // Homo sapiens small proline-rich protein 1A (SPRR1A), mRNA. /// ENST000	SPRR4	SPRR4, Homo sapiens small proline rich protein 4 (SPRR4), q21.3
SNP_A-1867021	tccctcccctcttcag[C/T]ccatttcaatttagac	C	T	NM_005621 // upstream // 10610 // Hs.19413 // S100A12 // 6283 // Homo sapiens S100 calcium binding protein A12 (calgranulin C) (S100A12), mRNA. /// NM_002964 // downstream // 3824 // Hs.416073 // S100A8 // 6279 // Homo sapiens S100 calcium binding protein	S100A12	S100A12, Homo sapiens S100 calcium binding protein A12 (calgranulin C) (S100A12), q21.3
SNP_A-2257688	ctttgctttcaaaaag[C/G]cttcaggaaataaaga	C	G	NM_176823 // 5UTR // 0 // Hs.442337 // S100A7L1 // 338324 // Homo sapiens S100 calcium binding protein A7-like 1 (S100A7L1), mRNA. /// ENST00000329256 // 5UTR // 0 // — // — // — // —	S100A7L1	S100A7L1, Homo sapiens S100 calcium binding protein A7-like 1 (S100A7L1), q21.3
SNP_A-1786440	ggcttagctctgaaca[A/T]attacttcctgctcaa	A	T	NM_002249 // intron // 0 // Hs.490765 // KCNN3 // 3782 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (KCNN3), transcript varia /// NM_170782 // intron // 0 // Hs.490765 // KCNN3 // 3782 // Homo s	KCNN3	KCNN3, Homo sapiens potassium intermediate,q22
SNP_A-1967356	ctcattttgatcctca[C/G]gcacatgcttgttgtc	C	G	NM_002249 // intron // 0 // Hs.490765 // KCNN3 // 3782 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (KCNN3), transcript varia /// ENST00000271915 // intron // 0 // — // — // — // —	KCNN3	KCNN3, Homo sapiens potassium intermediate,q22
SNP_A-2243606	ctgctcagtgtcaaat[G/T]aacaggaaagtcagct	G	T	NM_002249 // intron // 0 // Hs.490765 // KCNN3 // 3782 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 (KCNN3), transcript varia /// ENST00000271915 // intron // 0 // — // — // — // —	KCNN3	KCNN3, Homo sapiens potassium intermediate q22
SNP_A-2146782	atgcttctttaactta[C/T]agtctatctccatcaa	C	T	NM_002456 // intron // 0 // Hs.89603 // MUC1 // 4582 // Homo sapiens mucin 1, transmembrane (MUC1), mRNA. /// ENST00000337604 // intron // 0 // — // — // — // —	MUC1	MUC1, Homo sapiens mucin 1, transmembrane (MUC1), q22
SNP_A-2252665	cttccttttggaaacc[C/T]acaatgccaggcaccc	C	T	NM_002456 // intron // 0 // Hs.89603 // MUC1 // 4582 // Homo sapiens mucin 1, transmembrane (MUC1), mRNA. /// NM_025058 // intron // 0 // Hs.287735 // TRIM46 // 80128 // Homo sapiens tripartite motif-containing 46 (TRIM46), mRNA. /// ENST00000337604 // in	MUC1	MUC1, Homo sapiens mucin 1, transmembrane (MUC1), q22
SNP_A-1902447	tggcctactctggtta[C/T]ggggacactgacgccc	C	T	NM_014017 // CDS // 0 // Hs.351629 // MAPBPIP // 28956 // Homo sapiens mitogen-activated protein-binding protein-interacting protein (MAPBPIP), mRNA. /// ENST00000265204 // CDS // 0 // — // — // — // —	MAPBPIP	MAPBPIP, Homo sapiens mitogen-activated protein-binding protein-interacting protein (MAPBPIP), q22
SNP_A-2099609	agaggtagcagtgaac[A/G]ggaattgtggcactgc	A	G	ENST00000292286 // intron // 0 // — // — // — // —	-	q22
SNP_A-2185830	caggatgccctcttcc[A/T]ctcagacagggacagt	A	T	ENST00000292286 // intron // 0 // — // — // — // —	-	q22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2045866	aagacatggacttcta[A/G]taattaggactgctgg	A	G	NM_005998 // intron // 0 // Hs.491494 // CCT3 // 7203 // Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), mRNA. /// ENST00000295688 // intron // 0 // --- // --- // --- // ---	CCT3	CCT3, Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), q22
SNP_A-2055555	aataatcaacaagcta[C/T]cacggaaagatctata	C	T	NM_144627 // intron // 0 // Hs.534539 // SSTK-IP // 128229 // Homo sapiens SSTK-interacting protein (SSTK-IP), mRNA. /// ENST00000295687 // intron // 0 // --- // --- // --- // ---	SSTK-IP	SSTK-IP, Homo sapiens SSTK-interacting protein (SSTK-IP), q22
SNP_A-1967491	aaaaaacagaaaggga[A/G]aggcatcacttaaaac	A	G	NM_020407 // intron // 0 // Hs.131835 // RHBG // 57127 // Homo sapiens Rhesus blood group, B glycoprotein (RHBG), mRNA. /// ENST00000255013 // intron // 0 // --- // --- // --- // ---	RHBG	RHBG, Homo sapiens Rhesus blood group, B glycoprotein (RHBG), q22
SNP_A-2309907	ggaaatatgtgtgggc[A/G]aaactaatgcctaccc	A	G	NM_006365 // upstream // 44710 // Hs.380027 // CROC4 // 10485 // Homo sapiens transcriptional activator of the c-fos promoter (CROC4), mRNA. /// NM_005920 // downstream // 2179 // Hs.314327 // MEF2D // 4209 // Homo sapiens MADS box transcription enhancer	CROC4	CROC4, Homo sapiens transcriptional activator of the c-fos promoter (CROC4), q22
SNP_A-1716727	tttcaggtactggaaaggctgacaa[C/T]aggatgactgcttgag cccaggagt	C	T	NM_005998 // intron // 0 // Hs.1708 // CCT3 // 7203 // chaperonin containing TCP1, subunit 3 (gamma)	CCT3	CCT3 , rs2764404, chaperonin containing TCP1, subunit 3 (gamma),q22
SNP_A-1651558	gactggtgaagctctaagggtcata[C/T]tatactccttccaccca cctctccc	C	T	NM_005998 // intron // 0 // Hs.1708 // CCT3 // 7203 // chaperonin containing TCP1, subunit 3 (gamma)	CCT3	CCT3 , rs2296374, chaperonin containing TCP1, subunit 3 (gamma),q22
SNP_A-1780685	ggatcagggaataaga[A/G]cttctcttctgcaagc	A	G	NM_002529 // downstream // 3855 // Hs.406293 // NTRK1 // 4914 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA. /// NM_144702 // upstream // 24214 // Hs.491734 // FLJ32884 // 149499 // Homo sapiens hypothetical protein FLJ32884	NTRK1	NTRK1, Homo sapiens neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), q23.1
SNP_A-1857436	tcactagcagacttgc[A/G]atataacaaatgcaaa	A	G	L16464 // upstream // 175694 // Hs.352672 // ETV3 // 2117 // Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 199296 // Hs.415950 // IRTA2 // 83416 // Homo sapiens immunoglobulin superfamily receptor translocation associated 2	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-1784853	ggccttcaacagactg[A/G]atggtccccacccaca	A	G	L16464 // upstream // 374194 // Hs.352672 // ETV3 // 2117 // Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 796 // Hs.415950 // IRTA2 // 83416 // Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IR	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-2291615	gcacaaggttgcaaac[C/T]agaaaaatgtatctgt	C	T	L16464 // upstream // 374710 // Hs.352672 // ETV3 // 2117 // Human ETS oncogene (PEP1) mRNA, complete cds. /// NM_031281 // downstream // 280 // Hs.415950 // IRTA2 // 83416 // Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IR	ETV3	ETV3, Human ETS oncogene (PEP1) complete cds. q23.1
SNP_A-2252301	cttccctaagaaacaa[C/T]ggaagagaaggagctt	C	T	NM_031281 // 3UTR // 0 // Hs.415950 // IRTA2 // 83416 // Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA. /// ENST00000271529 // 3UTR // 0 // --- // --- // --- // --- /// ENST00000356953 // 3UTR // 0 // --- // ---	IRTA2	IRTA2, Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), q23.1
SNP_A-1967848	tgtaggatacaaaact[C/T]agagatggaggctgtg	C	T	NM_031281 // intron // 0 // Hs.415950 // IRTA2 // 83416 // Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA. /// ENST00000271529 // intron // 0 // --- // --- // --- // --- /// ENST00000356953 // intron // 0 // ---	IRTA2	IRTA2, Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), q23.1
SNP_A-2283470	gatactagaaggtaca[C/T]gctgacttctgaaggg	C	T	NM_031281 // intron // 0 // Hs.415950 // IRTA2 // 83416 // Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), mRNA. /// ENST00000271529 // intron // 0 // --- // --- // --- // ---	IRTA2	IRTA2, Homo sapiens immunoglobulin superfamily receptor translocation associated 2 (IRTA2), q23.1
SNP_A-2285620	gatgaagaagccatta[A/T]gtatatatttgagaca	A	T	NM_031282 // intron // 0 // Hs.120260 // IRTA1 // 83417 // Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // intron // 0 // --- // --- // --- // ---	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1894633	tgccacttaagtgtta[C/T]gtctagggaaatacta	C	T	NM_031282 // intron // 0 // Hs.120260 // IRTA1 // 83417 // Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // intron // 0 // — // — // —	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1
SNP_A-1967879	atagctgaactaaacg[A/C]aaatgaaaataaatg	A	C	NM_031282 // upstream // 16431 // Hs.120260 // IRTA1 // 83417 // Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // upstream // 16431 // — // — // — // — /// ENST00000292389 // downstr	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1
SNP_A-1859266	tcagctctactaga[C/T]gtctccactggcacct	C	T	NM_031282 // upstream // 18646 // Hs.120260 // IRTA1 // 83417 // Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // upstream // 18646 // — // — // — // — /// ENST00000292389 // downstr	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1
SNP_A-2027337	aaacatgaagaaaatta[C/G]agaaaggcaagtttta	C	G	NM_031282 // upstream // 26004 // Hs.120260 // IRTA1 // 83417 // Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), mRNA. /// ENST00000271532 // upstream // 26004 // — // — // — // — /// ENST00000292389 // downstr	IRTA1	IRTA1, Homo sapiens immunoglobulin superfamily receptor translocation associated 1 (IRTA1), q23.1
SNP_A-2250932	cttatgcctgttaaa[A/C]ccagtcatatatacat	A	C	ENST00000292389 // upstream // 20717 // — // — // — // — /// ENST00000318905 // downstream // 25037 // — // — // — // — /// ENST00000304745 // downstream // 25037 // — // — // — // — /// ENST00000292392 // downstream // 45844 // –	-	q23.1
SNP_A-1693825	ggcccccaggcaggtaaatcctacta[C/T]ggaatggagagctca gactctagaa	C	T	NM_005240 // upstream // 111912 // Hs.352672 // ETV3 // 2117 // ets variant gene 3 /// NM_031281 // downstream // 263078 // Hs.415950 // IRTA2 // 83416 // immunoglobulin superfamily receptor translocation associated 2	ETV3	ETV3 , rs725377, ets variant gene 3 ,q23.1
SNP_A-1736105	agactgagtcttaataaattctca[A/G]acaattacatacttaactc aggagt	A	G	NM_031282 // intron // 0 // Hs.120260 // IRTA1 // 83417 // immunoglobulin superfamily receptor translocation associated 1	IRTA1	IRTA1 , rs2779159, immunoglobulin superfamily receptor translocation associated 1,q23.1
SNP_A-1720575	tccctcaggaaacattacataaac[A/C]aaagtgtcactggag agtagtgag	A	C	NM_031282 // intron // 0 // Hs.120260 // IRTA1 // 83417 // immunoglobulin superfamily receptor translocation associated 1	IRTA1	IRTA1 , rs2777965, immunoglobulin superfamily receptor translocation associated 1,q23.1
SNP_A-1722824	tacatccctgcagcactcaggaaaa[A/G]atgaaatggacaa cagggactctt	A	G	NM_031282 // intron // 0 // Hs.120260 // IRTA1 // 83417 // immunoglobulin superfamily receptor translocation associated 1	IRTA1	IRTA1 , rs10489674, immunoglobulin superfamily receptor translocation associated 1,q23.1
SNP_A-1724392	cccataaagcactgacaaggaccaca[A/G]actccctgtcacata gttaaaaatg	A	G	NM_031282 // upstream // 3851 // Hs.120260 // IRTA1 // 83417 // immunoglobulin superfamily receptor translocation associated 1 /// NM_052939 // downstream // 76306 // Hs.434881 // FCRH3 // 115352 // Fc receptor-like protein 3	IRTA1	IRTA1 , rs2224607, immunoglobulin superfamily receptor translocation associated 1 ,q23.1
SNP_A-2130067	ataccagtctcaaata[C/T]agcaaagagacagact	C	T	NM_018240 // intron // 0 // Hs.272234 // KIRREL // 55243 // Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA. /// ENST00000330610 // intron // 0 // — // — // — /// ENST00000359209 // intron // 0 // — // — // —	KIRREL	KIRREL, Homo sapiens kin of IRRE like (Drosophila) (KIRREL), q23.1
SNP_A-2076774	accaaaaacatctaccc[A/C]atgtgtctaggaggaa	A	C	NM_001765 // downstream // 30538 // Hs.1311 // CD1C // 911 // Homo sapiens CD1C antigen, c polypeptide (CD1C), mRNA. /// NM_001764 // downstream // 3846 // Hs.1310 // CD1B // 910 // Homo sapiens CD1B antigen, b polypeptide (CD1B), mRNA. /// ENST00000028943	CD1C	CD1C, Homo sapiens CD1C antigen, c polypeptide (CD1C), q23.1
SNP_A-1968120	taaaagaaaaatctta[C/T]gtcaattgtgaggtaa	C	T	NM_001004475 // upstream // 11572 // — // OR10T2 // 128360 // Homo sapiens olfactory receptor, family 10, subfamily T, member 2 (OR10T2), mRNA. /// ENST00000334438 // upstream // 11572 // — // — // — // — /// ENST00000314902 // downstream // 814	OR10T2	OR10T2, Homo sapiens olfactory receptor, family 10, subfamily T, member 2 (OR10T2), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2314952	ggagttcctgacacta[C/T]ggaaaactaatgagaa	C	T	NM_001005327 // upstream // 10093 // — // OR6K3 // 391114 // Homo sapiens olfactory receptor, family 6, subfamily K, member 3 (OR6K3), mRNA. /// NM_001005184 // upstream // 19683 // — // OR6K6 // 128371 // Homo sapiens olfactory receptor, family 6, su	OR6K3	OR6K3, Homo sapiens olfactory receptor, family 6, subfamily K, member 3 (OR6K3), q23.1
SNP_A-1937751	ttgaagtaatgagaag[C/G]aagagagaacacccat	C	G	NM_002432 // upstream // 13719 // Hs.153837 // MNDA // 4332 // Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA. /// ENST00000325632 // upstream // 8313 // — // — // — // — /// ENST00000295805 // upstream // 13719 // — // -	MNDA	MNDA, Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), q23.1
SNP_A-1874007	tctcatcctgaaattc[C/T]cctcatacattttcta	C	T	NM_002432 // upstream // 4612 // Hs.153837 // MNDA // 4332 // Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA. /// ENST00000325632 // upstream // 17420 // — // — // — // — /// ENST00000295805 // upstream // 4612 // — // –	MNDA	MNDA, Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), q23.1
SNP_A-2196970	cattatagaccactta[C/T]agaccaattatatcta	C	T	NM_002432 // intron // 0 // Hs.153837 // MNDA // 4332 // Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA. /// ENST00000295805 // intron // 0 // — // — // — // —	MNDA	MNDA, Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), q23.1
SNP_A-1816504	gttaggtcaatgggga[C/G]aagatattggaaaaga	C	G	NM_002432 // intron // 0 // Hs.153837 // MNDA // 4332 // Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA. /// ENST00000295805 // intron // 0 // — // — // — // —	MNDA	MNDA, Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), q23.1
SNP_A-2000384	tacagggtctaaataa[G/T]taggttacgtgccaat	G	T	NM_002432 // downstream // 33227 // Hs.153837 // MNDA // 4332 // Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA. /// NM_198929 // upstream // 48830 // Hs.224645 // PYHIN1 // 149628 // Homo sapiens interferon-inducible protein X (IF	MNDA	MNDA, Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), q23.1
SNP_A-1825368	taaataaaataaagag[A/G]aatgttcaggacacct	A	G	NM_198929 // intron // 0 // Hs.224645 // PYHIN1 // 149628 // Homo sapiens interferon-inducible protein X (IFIX), transcript variant b1, mRNA. /// NM_152501 // intron // 0 // Hs.224645 // PYHIN1 // 149628 // Homo sapiens interferon-inducible protein X (IFI	PYHIN1	PYHIN1, Homo sapiens interferon-inducible protein X (IFIX), transcript variant b1, q23.1
SNP_A-2099899	agagtcaaagctagca[C/T]gtcctctttagccatc	C	T	NM_198929 // intron // 0 // Hs.224645 // PYHIN1 // 149628 // Homo sapiens interferon-inducible protein X (IFIX), transcript variant b1, mRNA. /// NM_152501 // intron // 0 // Hs.224645 // PYHIN1 // 149628 // Homo sapiens interferon-inducible protein X (IFI	PYHIN1	PYHIN1, Homo sapiens interferon-inducible protein X (IFIX), transcript variant b1, q23.1
SNP_A-2128876	ataatgcactcacagg[C/T]actttgcaaactctag	C	T	NM_002036 // downstream // 69897 // Hs.153381 // FY // 2532 // Homo sapiens Duffy blood group (FY), mRNA. /// NM_001004467 // downstream // 2658 // — // OR10J3 // 441911 // Homo sapiens olfactory receptor, family 10, subfamily J, member 3 (OR10J3), mRNA	FY	FY, Homo sapiens Duffy blood group (FY), q23.2
SNP_A-1968464	ctacatgaggactcta[A/T]aatagttaaagtcata	A	T	NM_001004469 // upstream // 17831 // — // OR10J5 // 127385 // Homo sapiens olfactory receptor, family 10, subfamily J, member 5 (OR10J5), mRNA. /// NM_001639 // upstream // 33988 // Hs.507080 // APCS // 325 // Homo sapiens amyloid P component, serum (AP	OR10J5	OR10J5, Homo sapiens olfactory receptor, family 10, subfamily J, member 5 (OR10J5), q23.2
SNP_A-2139924	atctacagaacttcac[C/T]gcgtgtcttcatgctt	C	T	NM_001004469 // upstream // 21683 // — // OR10J5 // 127385 // Homo sapiens olfactory receptor, family 10, subfamily J, member 5 (OR10J5), mRNA. /// NM_001639 // upstream // 30136 // Hs.507080 // APCS // 325 // Homo sapiens amyloid P component, serum (AP	OR10J5	OR10J5, Homo sapiens olfactory receptor, family 10, subfamily J, member 5 (OR10J5), q23.2
SNP_A-1915603	tgttctccaggaacac[A/G]gcccctccaaagcact	A	G	X56692 // upstream // 63546 // Hs.76452 // CRP // 1401 // H.sapiens mRNA for C-reactive protein. /// NM_000567 // upstream // 63635 // Hs.76452 // CRP // 1401 // Homo sapiens C-reactive protein, pentraxin-related (CRP), mRNA. /// NM_017823 // upstream //	CRP	CRP, H.sapiens for C-reactive protein. q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1968577	gtcagtccagaattaa[C/T]ggtgtgctcggggatg	C	T	NM_033438 // upstream // 30745 // Hs.99068 // SLAMF9 // 89886 // Homo sapiens SLAM family member 9 (SLAMF9), mRNA. /// NM_145167 // downstream // 45469 // Hs.512837 // PIGM // 93183 // Homo sapiens phosphatidylinositol glycan, class M (PIGM), mRNA. /// EN	SLAMF9	SLAMF9, Homo sapiens SLAM family member 9 (SLAMF9), q23.2
SNP_A-2307565	gcttcacggaggaaga[A/G]gtcatagctgcaggaa	A	G	NM_000702 // intron // 0 // Hs.34114 // ATP1A2 // 477 // Homo sapiens ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (ATP1A2), mRNA. /// ENST00000251207 // intron // 0 // --- // --- // --- // ---	ATP1A2	ATP1A2, Homo sapiens ATPase, Na+,q23.2
SNP_A-2294519	gcagtcaggagtaaca[C/T]ggactgtgccagagag	C	T	NM_005598 // downstream // 7024 // Hs.30956 // NHLH1 // 4807 // Homo sapiens nescient helix loop helix 1 (NHLH1), mRNA. /// AB033041 // upstream // 35842 // Hs.99477 // VANGL2 // 57216 // Homo sapiens mRNA for KIAA1215 protein, partial cds. /// ENST000003	NHLH1	NHLH1, Homo sapiens nescient helix loop helix 1 (NHLH1), q23.2
SNP_A-2265899	gaaggactagacccca[A/C]gatacctgaattccct	A	C	NM_032174 // intron // 0 // Hs.321653 // FLJ12770 // 84134 // Homo sapiens hypothetical protein FLJ12770 (FLJ12770), mRNA. /// NM_005122 // intron // 0 // Hs.349642 // NR1I3 // 9970 // Homo sapiens nuclear receptor subfamily 1, group I, member 3 (NR1I3),	FLJ12770	FLJ12770, Homo sapiens hypothetical protein FLJ12770 (FLJ12770), q23.3
SNP_A-1853217	tatttgttgagcatcc[A/G]actttatcataattac	A	G	NM_021642 // upstream // 8178 // Hs.352642 // FCGR2A // 2212 // Homo sapiens Fc fragment of IgG, low affinity IIa, receptor for (CD32) (FCGR2A), mRNA. /// ENST00000357831 // downstream // 24994 // --- // --- // --- // --- /// ENST00000271450 // upstream /	FCGR2A	FCGR2A, Homo sapiens Fc fragment of IgG, low affinity IIa, receptor for (CD32) (FCGR2A), q23.3
SNP_A-1937815	ttgaataatcagagaa[A/G]attcaacacaggagat	A	G	NM_007348 // intron // 0 // Hs.492740 // ATF6 // 22926 // Homo sapiens activating transcription factor 6 (ATF6), mRNA. /// ENST00000263291 // intron // 0 // --- // --- // --- // ---	ATF6	ATF6, Homo sapiens activating transcription factor 6 (ATF6), q23.3
SNP_A-2049064	aagcgagccatgtaac[A/G]atctgggtaagaggtt	A	G	NM_007348 // intron // 0 // Hs.492740 // ATF6 // 22926 // Homo sapiens activating transcription factor 6 (ATF6), mRNA. /// ENST00000263291 // intron // 0 // --- // --- // --- // ---	ATF6	ATF6, Homo sapiens activating transcription factor 6 (ATF6), q23.3
SNP_A-1893888	tgcatactgggggctc[A/G]acaggaaagccactag	A	G	NM_015441 // intron // 0 // Hs.507515 // OLFML2B // 25903 // Homo sapiens olfactomedin-like 2B (OLFML2B), mRNA. /// ENST00000294794 // intron // 0 // --- // --- // --- // ---	OLFML2B	OLFML2B, Homo sapiens olfactomedin-like 2B (OLFML2B), q23.3
SNP_A-1652430	tcgcaaagcgggaaaaatgaaacag[C/G]ctccgacagctctttcctctttcct	C	G	NM_000569 // downstream // 11185 // Hs.372679 // FCGR3A // 2214 // Fc fragment of IgG, low affinity IIIa, receptor for (CD16) /// NM_000570 // downstream // 12349 // Hs.372679 // FCGR3A // 2214 // Fc fragment of IgG, low affinity IIIa, receptor for (CD16	FCGR3A	FCGR3A , rs412965, Fc fragment of IgG, low affinity IIIa, receptor for (CD16) ,q23.3
SNP_A-1812997	gtgggtaatcttggga[G/T]ggagtctgcaaatcaa	G	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1784130	ggccataattgctcca[A/G]gtgaaatccccaatac	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2280830	gaggtgtatcgggcct[C/T]aaagtatttttacctg	C	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2040339	aaccactgtgacatcc[A/G]gagtgcaggaaggagt	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1826221	taaattccagaatatc[C/T]atgaggagtcttggaa	C	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-2244951	ctggcacagagtatcc[A/G]agctagaaaagttaaa	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1800741	gtagaatatgtggtca[C/T]ggctatagatgtgact	C	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1969210	gctttgttaacttagc[C/T]tcttcctctatggaga	C	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1969223	gcctgagctctgaaac[G/T]ctaaataaaccacatc	G	T	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1809795	gtgaggctgcatttta[A/G]cacagtatcaatctcc	A	G	ENST00000290009 // intron // 0 // --- // --- // --- // ---	-	q23.3
SNP_A-1932810	ttccttggtgtcctac[A/G]aacttggcatattcag	A	G	NM_053282 // upstream // 34733 // Hs.350581 // EAT2 // 117157 // Homo sapiens SH2 domain-containing molecule EAT2 (EAT2), mRNA. /// NM_144624 // upstream // 51026 // --- // --- // 0 // --- /// NM_175866 // upstream // 51026 // Hs.127310 // UHMK1 // 127933	EAT2	EAT2, Homo sapiens SH2 domain-containing molecule EAT2 (EAT2), q23.3
SNP_A-1667278	ttattttccagcaggacaagatcac[C/G]ctgtttagctggtgtatcagtcagg	C	G	NM_014697 // intron // 0 // Hs.129729 // CAPON // 9722 // C-terminal PDZ domain ligand of neuronal nitric oxide synthase	CAPON	CAPON , rs10494365, C-terminal PDZ domain ligand of neuronal nitric oxide synthase,q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137000	atcagccagtgaaata[C/T]ggaatttgaccccaaa	C	T	NM_006182 // intron // 0 // Hs.275757 // DDR2 // 4921 // Homo sapiens discoidin domain receptor family, member 2 (DDR2), mRNA. /// ENST00000339627 // intron // 0 // --- // --- // --- // ---	DDR2	DDR2, Homo sapiens discoidin domain receptor family, member 2 (DDR2), q23.3
SNP_A-1689438	gtttaggtaccttgtcaagtaccttt[C/G]tcaataacacatgccaggg tccaga	C	G	NM_014697 // intron // 0 // Hs.129729 // CAPON // 9722 // C-terminal PDZ domain ligand of neuronal nitric oxide synthase	CAPON	CAPON , rs347311, C-terminal PDZ domain ligand of neuronal nitric oxide synthase,q23.3
SNP_A-1641893	atgggagggaagaattggggctaag[A/T]ccataactggcatatt tgctatctg	A	T	NM_014697 // intron // 0 // Hs.129729 // CAPON // 9722 // C-terminal PDZ domain ligand of neuronal nitric oxide synthase	CAPON	CAPON , rs3751286, C-terminal PDZ domain ligand of neuronal nitric oxide synthase,q23.3
SNP_A-2313452	ggagagccagtggtga[C/T]cagaaggtttgggtca	C	T	NM_005613 // downstream // 6636 // Hs.386726 // RGS4 // 5999 // Homo sapiens regulator of G-protein signalling 4 (RGS4), mRNA. /// NM_003617 // downstream // 59080 // Hs.24950 // RGS5 // 8490 // Homo sapiens regulator of G-protein signalling 5 (RGS5), mRN	RGS4	RGS4, Homo sapiens regulator of G-protein signalling 4 (RGS4), q23.3
SNP_A-2031880	aaagtcactctcaaga[A/G]gtcactactcactaat	A	G	NM_005613 // downstream // 6771 // Hs.386726 // RGS4 // 5999 // Homo sapiens regulator of G-protein signalling 4 (RGS4), mRNA. /// NM_003617 // downstream // 58945 // Hs.24950 // RGS5 // 8490 // Homo sapiens regulator of G-protein signalling 5 (RGS5), mRN	RGS4	RGS4, Homo sapiens regulator of G-protein signalling 4 (RGS4), q23.3
SNP_A-2283609	gatagacatctgacac[A/G]cggtctcaatccagaa	A	G	NM_145697 // downstream // 9011 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 9011 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle ass	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1949416	tttattccattgaaaa[C/T]agtgctggttactgtg	C	T	NM_145697 // downstream // 9096 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 9096 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle ass	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-2201227	ccaagtttgtaatata[C/T]aaggtgtgtttagaaa	C	T	NM_145697 // downstream // 339411 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 339411 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1688216	atgttactaattcactgggtaagtc[A/G]acggatatcccaagatgt aatgccc	A	G	NM_002585 // upstream // 1188920 // Hs.408222 // PBX1 // 5087 // pre-B-cell leukemia transcription factor 1 /// NM_031423 // downstream // 14470 // Hs.234545 // CDCA1 // 83540 // cell division cycle associated 1 /// NM_145697 // downstream // 14470 // Hs	PBX1	PBX1 , rs4448497, pre-B-cell leukemia transcription factor 1 ,q23.3
SNP_A-2314674	ggagtattgcctgata[C/T]gtagcgaaaacactgc	C	T	NM_145697 // downstream // 580126 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 580126 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1650544	tttgacttttttttcttcagggacac[C/G]agtagtataaataaatattta ctgt	C	G	NM_002585 // upstream // 1074090 // Hs.408222 // PBX1 // 5087 // pre-B-cell leukemia transcription factor 1 /// NM_031423 // downstream // 129300 // Hs.234545 // CDCA1 // 83540 // cell division cycle associated 1 /// NM_145697 // downstream // 129300 //	PBX1	PBX1 , rs9287057, pre-B-cell leukemia transcription factor 1 ,q23.3
SNP_A-1969946	ctagatttgagtgcca[C/T]ctcccaacctggaata	C	T	NM_145697 // downstream // 616825 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 616825 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2032067	aaagtgatacctggct[C/T]aatagaataacgaatt	C	T	NM_145697 // downstream // 733883 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 733883 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-2160235	atttcacatatgcacaa[C/G]cttgaggacaagaatt	C	G	NM_145697 // downstream // 882309 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 882309 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1823445	taaaagctgagctgaa[C/T]gttgccctggaagtca	C	T	NM_145697 // downstream // 1089194 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, mRNA. /// NM_031423 // downstream // 1089194 // Hs.234545 // CDCA1 // 83540 // Homo sapiens cell division cyc	CDCA1	CDCA1, Homo sapiens cell division cycle associated 1 (CDCA1), transcript variant 1, q23.3
SNP_A-1912521	tgtgcatggaacattg[A/G]aagcgtttggaacgga	A	G	NM_002585 // intron // 0 // Hs.493096 // PBX1 // 5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000340699 // intron // 0 // — // — // — // — /// ENST00000328681 // intron // 0 // — // — // — // —	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-1970271	tatggagaagcatcca[A/G]ctatgtctcaatggtt	A	G	NM_002585 // intron // 0 // Hs.493096 // PBX1 // 5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000340699 // intron // 0 // — // — // — // — /// ENST00000328681 // intron // 0 // — // — // — // —	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-1650146	agtcggcaaacattcctttgttag[G/T]aatgcaccctcacttcca aatcaga	G	T	NM_002585 // upstream // 323990 // Hs.408222 // PBX1 // 5087 // pre-B-cell leukemia transcription factor 1 /// NM_031423 // downstream // 879400 // Hs.234545 // CDCA1 // 83540 // cell division cycle associated 1 /// NM_145697 // downstream // 879400 // H	PBX1	PBX1 , rs7544769, pre-B-cell leukemia transcription factor 1 ,q23.3
SNP_A-1693134	aaaaaacacaaaagcatgctcagga[A/G]ataaatttattacac aaagtcctt	A	G	NM_002585 // upstream // 316457 // Hs.408222 // PBX1 // 5087 // pre-B-cell leukemia transcription factor 1 /// NM_031423 // downstream // 886933 // Hs.234545 // CDCA1 // 83540 // cell division cycle associated 1 /// NM_145697 // downstream // 886933 // H	PBX1	PBX1 , rs10494412, pre-B-cell leukemia transcription factor 1 ,q23.3
SNP_A-1892239	tgcaacaccgtttacc[A/G]actctgacaagccact	A	G	NM_002585 // intron // 0 // Hs.493096 // PBX1 // 5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// ENST00000340699 // intron // 0 // — // — // — // — /// ENST00000328681 // intron // 0 // — // — // — // —	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-2138036	atccaaaggtcgttaa[A/G]atggaaataagtgtcc	A	G	NM_002585 // downstream // 317650 // Hs.493096 // PBX1 // 5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// NM_177399 // downstream // 33878 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1,	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-2078173	accagtatgcaacaac[G/T]cttgccattgattctt	G	T	NM_002585 // downstream // 341001 // Hs.493096 // PBX1 // 5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// NM_177399 // downstream // 10527 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1,	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3
SNP_A-1947965	tttagaatacatagatt[C/G]atctaaaaagcacaga	C	G	NM_002585 // downstream // 346100 // Hs.493096 // PBX1 // 5087 // Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), mRNA. /// NM_177399 // downstream // 5428 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1,	PBX1	PBX1, Homo sapiens pre-B-cell leukemia transcription factor 1 (PBX1), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1970560	ccacacccactggaga[A/G]ataaggccttcaaggg	A	G	NM_177399 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-1833156	tacaccacttttgtga[A/T]atgaaaattcctgaag	A	T	NM_177399 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-1970593	tttggaggaatcaatg[A/G]agacggaattctttta	A	G	NM_177399 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-2000431	atgaattaaggtgaga[C/G]gttgggaatgaagagg	C	G	NM_177399 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // intron // 0 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-2291469	gcaattgctccattta[C/T]ggtaacctagtgttct	C	T	NM_177399 // upstream // 11679 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, mRNA. /// NM_177398 // upstream // 11679 // Hs.357630 // LMX1A // 4009 // Homo sapiens LIM homeobox tr	LMX1A	LMX1A, Homo sapiens LIM homeobox transcription factor 1, alpha (LMX1A), transcript variant 4AB, q23.3
SNP_A-2208562	cccactataatcagca[A/G]ggccattgatacccta	A	G	NM_006917 // intron // 0 // Hs.26550 // RXRG // 6258 // Homo sapiens retinoid X receptor, gamma (RXRG), mRNA. /// ENST00000271387 // intron // 0 // — // — // — // — /// ENST00000359842 // intron // 0 // --- // — // — // ---	RXRG	RXRG, Homo sapiens retinoid X receptor, gamma (RXRG), q23.3
SNP_A-2194407	catgatgtgagaatca[A/C]ggccttagagaatggt	A	C	NM_006917 // upstream // 8969 // Hs.26550 // RXRG // 6258 // Homo sapiens retinoid X receptor, gamma (RXRG), mRNA. /// NM_001005214 // upstream // 89957 // Hs.120487 // FLJ25811 // 440699 // Homo sapiens FLJ25811 protein (FLJ25811), mRNA. /// ENST00000271	RXRG	RXRG, Homo sapiens retinoid X receptor, gamma (RXRG), q23.3
SNP_A-2051071	aaggctttcagataca[A/C]cccttctttcaatcct	A	C	NM_006917 // upstream // 11622 // Hs.26550 // RXRG // 6258 // Homo sapiens retinoid X receptor, gamma (RXRG), mRNA. /// NM_001005214 // upstream // 87304 // Hs.120487 // FLJ25811 // 440699 // Homo sapiens FLJ25811 protein (FLJ25811), mRNA. /// ENST0000027	RXRG	RXRG, Homo sapiens retinoid X receptor, gamma (RXRG), q23.3
SNP_A-1970656	ctcagcctcagcatgg[A/C]agagtatatggagtta	A	C	NM_001005214 // intron // 0 // Hs.120487 // FLJ25811 // 440699 // Homo sapiens FLJ25811 protein (FLJ25811), mRNA. /// ENST00000294818 // intron // 0 // — // — // — // — // ---	FLJ25811	FLJ25811, Homo sapiens FLJ25811 protein (FLJ25811), q23.3
SNP_A-2302761	gctactgtttatcact[A/G]agcactaaacagaata	A	G	NM_001005214 // downstream // 782 // Hs.120487 // FLJ25811 // 440699 // Homo sapiens FLJ25811 protein (FLJ25811), mRNA. /// ENST00000294818 // downstream // 782 // --- // — // — // — /// ENST00000330895 // upstream // 16838 // — // — // — // -	FLJ25811	FLJ25811, Homo sapiens FLJ25811 protein (FLJ25811), q23.3
SNP_A-1970658	cttgagggtacactta[C/T]ggtgactagagttaag	C	T	NM_001005214 // downstream // 9425 // Hs.120487 // FLJ25811 // 440699 // Homo sapiens FLJ25811 protein (FLJ25811), mRNA. /// ENST00000294818 // downstream // 9425 // — // — // — // — /// ENST00000330895 // upstream // 8195 // --- // — // — //	FLJ25811	FLJ25811, Homo sapiens FLJ25811 protein (FLJ25811), q23.3
SNP_A-1970660	aaatcccaaatgctta[C/T]gtttggtcatccactg	C	T	NM_004528 // upstream // 41507 // Hs.191734 // MGST3 // 4259 // Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /// ENST00000330895 // downstream // 7228 // — // — // — // — /// ENST00000271420 // upstream // 41507 // — // —	MGST3	MGST3, Homo sapiens microsomal glutathione S-transferase 3 (MGST3), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1861176	tcatatgcaaaatgaa[C/G]gggactgggccaggtg	C	G	NM_004528 // upstream // 28300 // Hs.191734 // MGST3 // 4259 // Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /// ENST00000330895 // downstream // 20435 // — // — // — // — /// ENST00000271420 // upstream // 28300 // — // –	MGST3	MGST3, Homo sapiens microsomal glutathione S-transferase 3 (MGST3), q24.1
SNP_A-2207326	ccattctcttctggta[C/T]ctttacatgatctacc	C	T	NM_004528 // upstream // 26600 // Hs.191734 // MGST3 // 4259 // Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /// ENST00000330895 // downstream // 22135 // — // — // — // — /// ENST00000271420 // upstream // 26600 // — // –	MGST3	MGST3, Homo sapiens microsomal glutathione S-transferase 3 (MGST3), q24.1
SNP_A-2199041	catttgtacgtaggca[A/G]tcagatctttgtttct	A	G	NM_004528 // downstream // 621 // Hs.191734 // MGST3 // 4259 // Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /// NM_000696 // downstream // 5979 // Hs.2533 // ALDH9A1 // 223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1	MGST3	MGST3, Homo sapiens microsomal glutathione S-transferase 3 (MGST3), q24.1
SNP_A-1715855	tttacttttttttgaggtcattaa[A/T]aaaaaggagaagaagaatatataac	A	T	NM_002585 // downstream // 355504 // Hs.408222 // PBX1 // 5087 // pre-B-cell leukemia transcription factor 1 /// NM_177398 // downstream // 1112 // Hs.458270 // LMX1A // 4009 // LIM homeobox transcription factor 1, alpha	PBX1	PBX1 , rs1553512, pre-B-cell leukemia transcription factor 1 ,q23.3
SNP_A-2157367	attgagcacattaagc[G/T]ctctaagacccaagat	G	T	NM_000696 // intron // 0 // Hs.2533 // ALDH9A1 // 223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // intron // 0 // Hs.2533 // ALDH9A1 // 223 // Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds. //	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-1891710	tgattgtgtacaacct[A/T]aactataagctccttg	A	T	NM_000696 // intron // 0 // Hs.2533 // ALDH9A1 // 223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // intron // 0 // Hs.2533 // ALDH9A1 // 223 // Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds. //	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-1745722	aaggacaaagcaaaaatattctagc[A/G]caagagagcagacagaagcatggac	A	G	NM_177398 // intron // 0 // Hs.458270 // LMX1A // 4009 // LIM homeobox transcription factor 1, alpha	LMX1A	LMX1A , rs10494436, LIM homeobox transcription factor 1, alpha,q23.3
SNP_A-2087458	actgccaggaaatgtc[A/G]atgtccaagcgggcct	A	G	NM_000696 // CDS // 0 // Hs.2533 // ALDH9A1 // 223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // CDS // 0 // Hs.2533 // ALDH9A1 // 223 // Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds. /// ENST	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-1714146	ctcagggatatctgtaaatacatga[A/G]ggctctttttctggttgttagtgg	A	G	NM_177398 // intron // 0 // Hs.458270 // LMX1A // 4009 // LIM homeobox transcription factor 1, alpha	LMX1A	LMX1A , rs10494438, LIM homeobox transcription factor 1, alpha,q23.3
SNP_A-2023762	aaaactttttaatcca[A/G]tgcttaatgtgtgcta	A	G	NM_000696 // intron // 0 // Hs.2533 // ALDH9A1 // 223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // intron // 0 // Hs.2533 // ALDH9A1 // 223 // Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds. //	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-1663616	tcctggtccctgctttgctgatggc[C/T]ttgaagcagcctcccaagcagatga	C	T	NM_177398 // intron // 0 // Hs.458270 // LMX1A // 4009 // LIM homeobox transcription factor 1, alpha	LMX1A	LMX1A , rs1394438, LIM homeobox transcription factor 1, alpha,q23.3
SNP_A-1836094	tactactggattggtc[A/G]actataaggatgtcat	A	G	NM_000696 // upstream // 12646 // Hs.2533 // ALDH9A1 // 223 // Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA. /// U34252 // upstream // 13023 // Hs.2533 // ALDH9A1 // 223 // Human gamma-aminobutyraldehyde dehydrogenase mRNA, comp	ALDH9A1	ALDH9A1, Homo sapiens aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), q24.1
SNP_A-1659452	agaggcttcttcctctccctcctc[C/T]gtaatcattacaaacagtggatatg	C	T	BC030596 // intron // 0 // Hs.374847 // - // 400794 // Hypothetical gene supported by BC030596 (LOC400794), mRNA	-	- , rs722259, Hypothetical gene supported by BC030596 (LOC400794), mRNA,q24.1
SNP_A-1706033	ggtgaaaaactcctgggctttcag[C/G]atagaattccaccatcacatgtgag	C	G	NM_012474 // downstream // 5966 // Hs.458360 // UMPK // 7371 // uridine monophosphate kinase	UMPK	UMPK , rs10494449, uridine monophosphate kinase,q24.1
SNP_A-2041828	aactaaaataattaca[A/G]aaaagtgcaattatct	A	G	ENST00000354422 // intron // 0 // — // — // — // —	-	q24.1
SNP_A-1914076	tgtgtgggctacttca[A/G]taagcaagtctaaact	A	G	ENST00000354422 // intron // 0 // — // — // — // —	-	q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2199679	ccaaaataacattcag[A/G]ctatcttaaaatatt	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-1970761	ttgaacctcttcaaa[A/G]cagtgtttcatcatat	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-1919674	ttaaggtttaagcad[A/G]ggaatgatgtgaccag	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-2222153	cgaattagattgacaa[C/T]ggacagaagacttgaa	C	T	NM_138784 // intron // 0 // Hs.348539 // LOC116123 // 116123 // Homo sapiens hypothetical protein BC014341 (LOC116123), mRNA. /// ENST00000354422 // intron // 0 // --- // --- // --- /// ENST00000336247 // intron // 0 // --- // --- // ---	LOC116123	LOC116123, Homo sapiens hypothetical protein BC014341 (LOC116123), q24.1
SNP_A-1970824	gagactagacttggaa[A/G]taataaatgtacaatgt	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-2049924	aaggaacticaacaacta[A/G]aaacaattccaagtaa	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-1901795	tggcacctctgcgtgtc[A/G]cccatatgcagggaca	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-2000447	gttaataagggggatca[A/G]caagatggtaaaactg	A	G	ENST00000354422 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-2111338	aggagctgaatcagcc[A/G]aaactctcccctcccca	A	G	NM_032858 // downstream // 22640 // Hs.180191 // FLJ14904 // 84944 // Homo sapiens hypothetical protein FLJ14904 (FLJ14904), mRNA. /// NM_005814 // downstream // 7995 // Hs.437229 // GPA33 // 10223 // Homo sapiens glycoprotein A33 (transmembrane) (GPA33). /// NM_005814 // intron // 0 // Hs.437229 // GPA33 // 10223 // Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA. ///	FLJ14904	FLJ14904, Homo sapiens hypothetical protein FLJ14904 (FLJ14904), q24.1
SNP_A-1970901	ggaattggacagtaac[C/T]ggagaagcagctggat	C	T	ENST00000271383 // intron // 0 // --- // --- // ---	GPA33	GPA33, Homo sapiens glycoprotein A33 (transmembrane) (GPA33), q24.1
SNP_A-1970951	ctcccactgtagcaa[A/T]gtgagctttttttct	A	T	NM_002697 // intron // 0 // Hs.493649 // POU2F1 // 5451 // Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), mRNA. /// ENST00000271411 // intron // 0 // --- // --- // ---	POU2F1	POU2F1, Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), q24.2
SNP_A-2301926	gcgtacccacaatagc[A/G]aggaactctttgttt	A	G	NM_024569 // intron // 0 // Hs.493919 // MPZL1 // 9019 // Homo sapiens myelin protein zero-like 1 (MPZL1), transcript variant 2, mRNA. /// NM_003953 // intron // 0 // Hs.493919 // MPZL1 // 9019 // Homo sapiens myelin protein zero-like 1 (MPZL1), transcrip	MPZL1	MPZL1, Homo sapiens myelin protein zero-like 1 (MPZL1), transcript variant 2, q24.2
SNP_A-1706843	ccctccactaagccggtttagcaaa[C/G]agccctttcctcccag ggtcttcca	C	G	NM_052862 // intron // 0 // Hs.233125 // MGC21854 // 92241 // hypothetical protein MGC21854	MGC21854	MGC21854, rs10489194, hypothetical protein MGC21854,q24.2
SNP_A-2034097	aaatcatatttggtag[A/G]caggatttatatgatc	A	G	NM_003175 // upstream // 8393 // Hs.458346 // XCL2 // 6846 // Homo sapiens chemokine (C motif) ligand 2 (XCL2), mRNA. /// NM_002995 // upstream // 24241 // Hs.546295 // XCL1 // 6375 // Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA. /// ENST000002	XCL2	XCL2, Homo sapiens chemokine (C motif) ligand 2 (XCL2), q24.2
SNP_A-1796842	ggttcaggttcaggga[A/T]aaagatgtgtgctgac	A	T	NM_002995 // downstream // 75184 // Hs.546295 // XCL1 // 6375 // Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA. /// NM_001937 // downstream // 38208 // Hs.80552 // DPT // 1805 // Homo sapiens dermatopontin (DPT), mRNA. /// ENST00000271401 // down	XCL1	XCL1, Homo sapiens chemokine (C motif) ligand 1 (XCL1), q24.2
SNP_A-2038735	aacagatagtaaagtat[C/T]gatatatatgcaggaat	C	T	NM_002995 // downstream // 75392 // Hs.546295 // XCL1 // 6375 // Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA. /// NM_001937 // downstream // 38000 // Hs.80552 // DPT // 1805 // Homo sapiens dermatopontin (DPT), mRNA. /// ENST00000271401 // down	XCL1	XCL1, Homo sapiens chemokine (C motif) ligand 1 (XCL1), q24.2
SNP_A-2026151	aaaattcatgcctcca[A/G]attcggcaaacttg	A	G	NM_001001787 // upstream // 196594 // Hs.291196 // ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant 2, mRNA. /// NM_001677 // upstream // 196594 // Hs.291196 // ATP1B1 // 481 // Homo sapiens ATPase	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+ q24.2
SNP_A-1822822	taaaaactattccaga[C/G]actgtggaagtaaaga	C	G	NM_001001787 // upstream // 189543 // Hs.291196 // ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant 2, mRNA. /// NM_001677 // upstream // 189543 // Hs.291196 // ATP1B1 // 481 // Homo sapiens ATPase	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+ q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2122469	agtgctagaaaaatgaa[A/G]cataaagcatgaaggg	A	G	NM_001001787 // upstream // 45069 // Hs.291196 // ATP1B1 // 481 // Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant 2, mRNA. /// NM_001677 // upstream // 45069 // Hs.291196 // ATP1B1 // 481 // Homo sapiens ATPase,	ATP1B1	ATP1B1, Homo sapiens ATPase, Na+, q24.2
SNP_A-1971373	tccaaatcagtgcaaa[G/T]atctgatgcggtgggg	G	T	NM_013330 // intron // 0 // Hs.274479 // NME7 // 29922 // Homo sapiens non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (NME7), transcript variant 1, mRNA. /// NM_197972 // intron // 0 // Hs.274479 // NME7 // 29922 // Homo sapi	NME7	NME7, Homo sapiens non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) (NME7), transcript variant 1, q24.2
SNP_A-2023618	aaaactgcatacagta[C/T]aacttgcacattgagt	C	T	NM_006996 // 3UTR // 0 // Hs.30246 // SLC19A2 // 10560 // Homo sapiens solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), mRNA. /// ENST00000236137 // 3UTR // 0 // — // — // — /// ENST00000302778 // 3UTR // 0 // — // — /	SLC19A2	SLC19A2, Homo sapiens solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), q24.2
SNP_A-1931833	ttccgaagccagagga[A/G]aaatggtgctaatgtc	A	G	NM_000450 // CDS // 0 // Hs.89546 // SELE // 6401 // Homo sapiens selectin E (endothelial adhesion molecule 1) (SELE), mRNA. /// ENST00000333360 // CDS // 0 // — // — // —	SELE	SELE, Homo sapiens selectin E (endothelial adhesion molecule 1) (SELE), q24.2
SNP_A-2000468	cccacatcatattcca[A/G]ctgcttccgtttctc	A	G	ENST00000286050 // intron // 0 // — // — // —	-	q24.2
SNP_A-2055828	aatacaaatacagtga[A/G]gtctgttgcaaaata	A	G	ENST00000286050 // intron // 0 // — // — // —	-	q24.2
SNP_A-1790219	ggggagaaatcatcag[A/G]ctctccttgattgcac	A	G	NM_152281 // upstream // 114136 // Hs.183702 // FLJ11752 // 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream // 343255 // — // — // — /// ENST00000263692 // upstream // 114136 // — // — // —	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2238031	ctctgattgatataca[C/T]ggacaaatgtgcgtct	C	T	NM_152281 // upstream // 111755 // Hs.183702 // FLJ11752 // 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream // 345636 // — // — // — /// ENST00000263692 // upstream // 111755 // — // — // —	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2099979	agagtctaatttgaga[A/C]aggacatgatttcctt	A	C	NM_152281 // upstream // 34094 // Hs.183702 // FLJ11752 // 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// ENST00000286050 // upstream // 423297 // — // — // — /// ENST00000263692 // upstream // 34094 // — // — // — /	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-2240568	ctgaccctggttcca[C/T]aacaccctgaaaaatt	C	T	NM_152281 // downstream // 3447 // Hs.183702 // FLJ11752 // 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// NM_006902 // upstream // 106292 // Hs.283416 // PRRX1 // 5396 // Homo sapiens paired related homeobox 1 (PRRX1), transcript vari	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1882064	tctttgttaaggcct[C/G]aaaaatatttaaggtg	C	G	NM_152281 // downstream // 7675 // Hs.183702 // FLJ11752 // 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// NM_006902 // upstream // 102064 // Hs.283416 // PRRX1 // 5396 // Homo sapiens paired related homeobox 1 (PRRX1), transcript vari	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1928462	ttcactaactccaaga[A/G]cttgtctcccactctc	A	G	NM_152281 // downstream // 91722 // Hs.183702 // FLJ11752 // 92344 // Homo sapiens NTKL-binding protein 1 (FLJ11752), mRNA. /// NM_006902 // upstream // 18017 // Hs.283416 // PRRX1 // 5396 // Homo sapiens paired related homeobox 1 (PRRX1), transcript vari	FLJ11752	FLJ11752, Homo sapiens NTKL-binding protein 1 (FLJ11752), q24.2
SNP_A-1738807	ttaacatttaagtatctacaatact[C/G]aaaaatactgatatttaagat atatta	C	G	NM_014970 // upstream // 429780 // Hs.433442 // KIFAP3 // 22920 // kinesin-associated protein 3 /// NM_152281 // upstream // 27611 // Hs.183702 // FLJ11752 // 92344 // NTKL-binding protein 1	KIFAP3	KIFAP3, rs1537390, kinesin-associated protein 3 q24.2
SNP_A-2311665	ggaatgttgctataa[A/C]ctctgtgtatttggtc	A	C	NM_001460 // upstream // 20569 // Hs.144912 // FMO2 // 2327 // Homo sapiens flavin containing monooxygenase 2 (FMO2), mRNA. /// ENST00000236166 // downstream // 3354 // — // — // — /// ENST00000209929 // upstream // 20569 // — // — // —	FMO2	FMO2, Homo sapiens flavin containing monooxygenase 2 (FMO2), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1912445	tgtgcactggatacaa[C/T]gacggttctcatttt	C	T	NM_000261 // upstream // 31167 // Hs.436037 // MYOC // 4653 // Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), mRNA. /// NM_003762 // downstream // 16332 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated m	MYOC	MYOC, Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), q24.3
SNP_A-2298342	gccattcattgctaaa[A/G]ttgttcacctctggtga	A	G	NM_000261 // upstream // 33157 // Hs.436037 // MYOC // 4653 // Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), mRNA. /// NM_003762 // downstream // 14342 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated m	MYOC	MYOC, Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), q24.3
SNP_A-2112313	aggcaaaatcttgact[A/G]aagtgttgaggagaat	A	G	NM_000261 // upstream // 45021 // Hs.436037 // MYOC // 4653 // Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), mRNA. /// NM_003762 // downstream // 2478 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated me	MYOC	MYOC, Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), q24.3
SNP_A-2046797	aagaggagtaaagata[C/T]ggagtggagccaggcg	C	T	NM_000261 // upstream // 45111 // Hs.436037 // MYOC // 4653 // Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), mRNA. /// NM_003762 // downstream // 2388 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated me	MYOC	MYOC, Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), q24.3
SNP_A-1830975	taatgactgaaagtaa[A/C]gaaaggtgactaagtt	A	C	NM_003762 // intron // 0 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, mRNA. /// NM_201994 // intron // 0 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated membrane protein 4	VAMP4	VAMP4, Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, q24.3
SNP_A-1972239	ttaatgaatctggata[A/G]aggatttaaaagcatt	A	G	NM_003762 // upstream // 4971 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, mRNA. /// NM_201994 // upstream // 4971 // Hs.6651 // VAMP4 // 8674 // Homo sapiens vesicle-associated membrane	VAMP4	VAMP4, Homo sapiens vesicle-associated membrane protein 4 (VAMP4), transcript variant 2, q24.3
SNP_A-2234341	ctccaaatttgggaa[C/G]agctaattgtctgtga	C	G	NM_015569 // intron // 0 // Hs.494751 // DNM3 // 26052 // Homo sapiens dynamin 3 (DNM3), mRNA. /// ENST00000358155 // intron // 0 // — // — // — /// ENST00000355305 // intron // 0 // — // — // —	DNM3	DNM3, Homo sapiens dynamin 3 (DNM3), q24.3
SNP_A-1972371	aagtaccaaaagatta[C/T]cagctcagaccagggc	C	T	NM_015569 // intron // 0 // Hs.494751 // DNM3 // 26052 // Homo sapiens dynamin 3 (DNM3), mRNA. /// ENST00000358155 // intron // 0 // — // — // — /// ENST00000355305 // intron // 0 // — // — // —	DNM3	DNM3, Homo sapiens dynamin 3 (DNM3), q24.3
SNP_A-1831466	taatgttcaggctg[A/G]aaggcctattagttg	A	G	NM_139240 // downstream // 25973 // Hs.517991 // LOC92346 // 92346 // Homo sapiens LOC92346 (LOC92346), mRNA. /// NM_002642 // upstream // 50703 // Hs.188456 // PIGC // 5279 // Homo sapiens phosphatidylinositol glycan, class C (PIGC), transcript variant 2	LOC92346	LOC92346, Homo sapiens LOC92346 (LOC92346), q24.3
SNP_A-2185951	caggcacaatatgaaa[C/G]ctacaagtgccagga	C	G	NM_000639 // intron // 0 // Hs.2007 // FASLG // 356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// ENST00000305730 // intron // 0 // — // — // — /// ENST00000340030 // intron // 0 // — // — // —	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-1929570	ttcataccattctccc[C/T]gacttactgcatcat	C	T	NM_000639 // downstream // 28434 // Hs.2007 // FASLG // 356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 // downstream // 344658 // Hs.248197 // TNFSF18 // 8995 // Homo sapiens tumor necrosis factor (l	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2222598	cgagtgaatttcttta[G/T]gcagaaaagacaaaag	G	T	NM_000639 // downstream // 30813 // Hs.2007 // FASLG // 356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 // downstream // 342279 // Hs.248197 // TNFSF18 // 8995 // Homo sapiens tumor necrosis factor (l	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-1917447	tgtttgtcaaagcaa[A/G]gagtctgaaggttaac	A	G	NM_000639 // downstream // 41166 // Hs.2007 // FASLG // 356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 // downstream // 331926 // Hs.248197 // TNFSF18 // 8995 // Homo sapiens tumor necrosis factor (l	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-1934801	ttctcttttacttcataa[A/G]ctccatatgtggcttg	A	G	NM_000639 // downstream // 42846 // Hs.2007 // FASLG // 356 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), mRNA. /// NM_005092 // downstream // 330246 // Hs.248197 // TNFSF18 // 8995 // Homo sapiens tumor necrosis factor (l	FASLG	FASLG, Homo sapiens tumor necrosis factor (ligand) superfamily, member 6 (TNFSF6), q24.3
SNP_A-2308528	gcttaatatggcttta[C/T]atggatgatgcataa	C	T	NM_003326 // upstream // 92350 // Hs.181097 // TNFSF4 // 7292 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF /// NM_004905 // upstream // 177665 // Hs.120 // PRDX6 // 958	TNFSF4	TNFSF4, Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF, q25.1
SNP_A-2124605	agttccigttgtgcta[A/T]ctccatatccagccttt	A	T	NM_003326 // upstream // 150193 // Hs.181097 // TNFSF4 // 7292 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF /// NM_004905 // upstream // 119822 // Hs.120 // PRDX6 // 95	TNFSF4	TNFSF4, Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF, q25.1
SNP_A-1972692	gccttatggaatgaga[A/G]ctgtcaggaccaaagt	A	G	NM_003326 // upstream // 152968 // Hs.181097 // TNFSF4 // 7292 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF /// NM_004905 // upstream // 117047 // Hs.120 // PRDX6 // 95	TNFSF4	TNFSF4, Homo sapiens tumor necrosis factor (ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF, q25.1
SNP_A-1839575	tagatcatatctgacac[C/T]acgtctcagctgtca	C	T	NM_014656 // 3UTR // 0 // Hs.518138 // KIAA0040 // 9674 // Homo sapiens KIAA0040 gene product (KIAA0040), mRNA. /// ENST00000294692 // 3UTR // 0 // — // — // — // —	KIAA0040	KIAA0040, Homo sapiens KIAA0040 gene product (KIAA0040), q25.1
SNP_A-1843707	tagtgtcaggtacaca[C/T]agaaagagctgagaac	C	T	NM_014656 // intron // 0 // Hs.518138 // KIAA0040 // 9674 // Homo sapiens KIAA0040 gene product (KIAA0040), mRNA. /// ENST00000335817 // intron // 0 // — // — // — // —	KIAA0040	KIAA0040, Homo sapiens KIAA0040 gene product (KIAA0040), q25.1
SNP_A-1653284	tgattgctatagcacagcacttttc[A/G]atcatgaggaaaactgagt cttagaa	A	G	NM_014857 // intron // 0 // Hs.495257 // HHL // 9910 // expressed in hematopoietic cells, heart, liver	HHL	HHL , rs10489332, expressed in hematopoietic cells, heart, liver,q25.1
SNP_A-1973201	ttaaggtctgaacig[A/G]agaagagaagagagga	A	G	NM_003285 // upstream // 127223 // Hs.518149 // TNR // 7143 // Homo sapiens tenascin R (restrictin, janusin) (TNR), mRNA. /// ENST00000263525 // upstream // 127223 // — // — // — // — /// ENST00000315107 // upstream // 343325 // — // — // —	TNR	TNR, Homo sapiens tenascin R (restrictin, janusin) (TNR), q25.1
SNP_A-2235451	ctccgagaccttttag[A/G]ccaccctgaagaacac	A	G	NM_003285 // upstream // 456975 // Hs.518149 // TNR // 7143 // Homo sapiens tenascin R (restrictin, janusin) (TNR), mRNA. /// ENST00000263525 // upstream // 456975 // — // — // — // — /// ENST00000315107 // upstream // 13573 // — // — // — // — /	TNR	TNR, Homo sapiens tenascin R (restrictin, janusin) (TNR), q25.1
SNP_A-2288052	gattcaagaaactgac[A/G]aagaggcccagaggct	A	G	NM_003285 // upstream // 467554 // Hs.518149 // TNR // 7143 // Homo sapiens tenascin R (restrictin, janusin) (TNR), mRNA. /// ENST00000263525 // upstream // 467554 // — // — // — // — /// ENST00000315107 // upstream // 2994 // — // — // — // —	TNR	TNR, Homo sapiens tenascin R (restrictin, janusin) (TNR), q25.1
SNP_A-1679160	atctataaaatggtagtaataatga[C/T]accttaatcccatggtgtt ggtgag	C	T	NM_003285 // intron // 0 // Hs.54433 // TNR // 7143 // tenascin R (restrictin, janusin)	TNR	TNR , rs10489315, tenascin R (restrictin, janusin),q25.1
SNP_A-1649914	taaactatatagaaataattcaga[C/T]gatcttaataggtgtgatc tctaga	C	T	NM_003285 // intron // 0 // Hs.54433 // TNR // 7143 // tenascin R (restrictin, janusin)	TNR	TNR , rs859448, tenascin R (restrictin, janusin),q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1792899	ggtaattcctccagag[C/G]caaatgcatgtctgat	C	G	NM_020318 // intron // 0 // Hs.187284 // PAPPA2 // 60676 // Homo sapiens pappalysin 2 (PAPPA2), transcript variant 1, mRNA. /// NM_021936 // intron // 0 // Hs.187284 // PAPPA2 // 60676 // Homo sapiens pappalysin 2 (PAPPA2), transcript variant 2, mRNA. ///	PAPPA2	PAPPA2, Homo sapiens pappalysin 2 (PAPPA2), transcript variant 1, q25.2
SNP_A-1973574	tgctgggattctgagg[A/G]agatatctaggcactg	A	G	NM_004319 // intron // 0 // Hs.495897 // ASTN // 460 // Homo sapiens astrotactin (ASTN), transcript variant 1, mRNA. /// ENST00000281881 // intron // 0 // --- // --- // --- // ---	ASTN	ASTN, Homo sapiens astrotactin (ASTN), transcript variant 1, q25.2
SNP_A-2121459	agtctttttaagtcac[C/T]gccaaatccattttgc	C	T	ENST00000009954 // intron // 0 // --- // --- // --- // ---	-	q25.2
SNP_A-1798426	gtaaatcacatgcact[A/G]aaatccatgactcaga	A	G	NM_033127 // downstream // 503739 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 142635 // --- // --- // --- // --- /// ENST00000354921 // downstream // 5037	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2244212	ctggaaaagcctgaag[C/T]ctggctacaacttgcc	C	T	NM_033127 // downstream // 444973 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 201401 // --- // --- // --- // --- /// ENST00000354921 // downstream // 4449	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2143672	atgagaaaatccttca[A/G]gagtaggcttccacta	A	G	NM_033127 // downstream // 282376 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 363998 // --- // --- // --- // --- /// ENST00000354921 // downstream // 2823	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2281679	gagtctgttaaagtag[A/G]agacagggtgagaagg	A	G	NM_033127 // downstream // 282332 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 364042 // --- // --- // --- // --- /// ENST00000354921 // downstream // 2823	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-1792031	gggtgggccacgaaac[A/G]aagaggggctagcta	A	G	NM_033127 // downstream // 258911 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 387463 // --- // --- // --- // --- /// ENST00000354921 // downstream // 2589	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-1845423	tatagaaaggttatga[A/G]atttgttcctagatcc	A	G	NM_033127 // downstream // 175955 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 470419 // --- // --- // --- // --- /// ENST00000354921 // downstream // 1759	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2303310	gctatgtggcacatgc[A/G]acagggtgggaaagga	A	G	NM_033127 // downstream // 115022 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000009954 // downstream // 531352 // --- // --- // --- // --- /// ENST00000354921 // downstream // 1150	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-1751907	ctctgacaaggaaagaaatgatgag[A/G]atgagatagttctatttattaaatg	A	G	NM_021165 // downstream // 182019 // Hs.21708 // KIAA1747 // 57795 // hypothetical protein from clone 24828 /// NM_033127 // downstream // 464705 // Hs.362919 // RGPR // 89866 // regucalcin gene promotor region related protein	KIAA1747	KIAA1747 , rs12026256, hypothetical protein from clone 24828 ,q25.2
SNP_A-2215149	cctatttcccatacat[G/T]aaccactcttcttgtt	G	T	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // --- // --- // --- // --- /// ENST00000308284 // intron // 0 // --- // --- // --- // ---	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2157152	attgaaggacaggact[A/G]acatatacaatgcagc	A	G	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // --- // --- // --- // --- /// ENST00000308284 // intron // 0 // --- // --- // --- // ---	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829029	taagggagttctgaga[C/G]agaaaagatcaataiaa	C	G	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // — // — // — // — /// ENST00000308284 // intron // 0 // — // — // — //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2192987	catcgctcacaaagaa[C/T]gctctctaccctctg	C	T	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // — // — // — // — /// ENST00000308284 // intron // 0 // — // — // — //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2153629	attaggagcaattagt[A/G]aacagaatcaaaggtg	A	G	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // — // — // — // — /// ENST00000308284 // intron // 0 // — // — // — //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2297469	gccacttacgcctta[C/T]cagtttggcaaaattc	C	T	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // — // — // — // — /// ENST00000308284 // intron // 0 // — // — // — //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2103814	agcaccgactgagttat[C/T]atgaaacagaacaagg	C	T	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000354921 // intron // 0 // — // — // — // — /// ENST00000308284 // intron // 0 // — // — // — //	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2175124	cacagtgcagagatga[A/G]caaacatatagactgc	A	G	NM_033127 // intron // 0 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// ENST00000308284 // intron // 0 // — // — // — // —	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-2109339	agctttgacttgtaaa[A/G]cagcagctaaattgtc	A	G	NM_033127 // upstream // 38922 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA. /// NM_033127 // upstream // 23459 // Hs.451846 // RGPR // 89866 // Homo sapiens regucalcin gene promotor region rel	RGPR	RGPR, Homo sapiens regucalcin gene promotor region related protein (RGPR), q25.2
SNP_A-1758838	tctagctatcctgttaggttcca[C/G]gattcctagaaatgtggac ctcatg	C	G	AB067515 // intron // 0 // Hs.362919 // RGPR // 89866 // regucalcin gene promotor region related protein	RGPR	RGPR , rs1415083, regucalcin gene promotor region related protein;q25.2
SNP_A-1884325	tgaaggtaagtggaac[A/G]aaagagaaagaaggtt	A	G	NM_207467 // downstream // 144116 // Hs.369418 // FLJ35530 // 400798 // Homo sapiens FLJ35530 protein (FLJ35530), mRNA. /// NM_018037 // upstream // 32160 // Hs.496222 // RALGPS2 // 55103 // Homo sapiens Ral GEF with PH domain and SH3 binding motif 2 (RAL	FLJ35530	FLJ35530, Homo sapiens FLJ35530 protein (FLJ35530), q25.2
SNP_A-2145710	atgccaaatgtaaaaa[C/T]gaacatgaggaacatg	C	T	NM_207467 // downstream // 161170 // Hs.369418 // FLJ35530 // 400798 // Homo sapiens FLJ35530 protein (FLJ35530), mRNA. /// NM_018037 // upstream // 15106 // Hs.496222 // RALGPS2 // 55103 // Homo sapiens Ral GEF with PH domain and SH3 binding motif 2 (RAL	FLJ35530	FLJ35530, Homo sapiens FLJ35530 protein (FLJ35530), q25.2
SNP_A-2218092	cctgccgtaattcccaa[A/G]tcgacagagatatgtc	A	G	NM_207467 // downstream // 173342 // Hs.369418 // FLJ35530 // 400798 // Homo sapiens FLJ35530 protein (FLJ35530), mRNA. /// NM_018037 // upstream // 2934 // Hs.496222 // RALGPS2 // 55103 // Homo sapiens Ral GEF with PH domain and SH3 binding motif 2 (RALG	FLJ35530	FLJ35530, Homo sapiens FLJ35530 protein (FLJ35530), q25.2
SNP_A-2112656	aggcagagagtcagaa[C/T]agaaggtttaaggga	C	T	NM_018037 // intron // 0 // Hs.496222 // RALGPS2 // 55103 // Homo sapiens Ral GEF with PH domain and SH3 binding motif 2 (RALGPS2), mRNA. /// NM_152663 // intron // 0 // Hs.496222 // RALGPS2 // 55103 // Homo sapiens Ral GEF with PH domain and SH3 binding	RALGPS2	RALGPS2, Homo sapiens Ral GEF with PH domain and SH3 binding motif 2 (RALGPS2), q25.2
SNP_A-2223973	cgggcgaggtgccctcc[C/T]gctagaactcagggga	C	T	NM_182766 // intron // 0 // Hs.496400 // DKFZp686H1423 // 126859 // Homo sapiens hypothetical protein FLJ32940 (DKFZp686H1423), transcript variant 2, mRNA. /// NM_144696 // intron // 0 // Hs.496400 // DKFZp686H1423 // 126859 // Homo sapiens hypothetical p	DKFZp686H1423	DKFZp686H1423, Homo sapiens hypothetical protein FLJ32940 (DKFZp686H1423), transcript variant 2, q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783280	ggcagtctggcttcag[A/G]atcctaactcttaact	A	G	NM_173533 // intron // 0 // Hs.197354 // TDRD5 // 163589 // Homo sapiens tudor domain containing 5 (TDRD5), mRNA. /// AK092142 // intron // 0 // Hs.197354 // TDRD5 // 163589 // Homo sapiens cDNA FLJ34823 fis, clone NT2NE2008727. /// ENST00000354714 // int	TDRD5	TDRD5, Homo sapiens tudor domain containing 5 (TDRD5), q25.2
SNP_A-1974306	acctctgttggagaga[G/T]aaattctttcaagtgg	G	T	NM_033343 // intron // 0 // Hs.496545 // LHX4 // 89884 // Homo sapiens LIM homeobox 4 (LHX4), mRNA. /// ENST00000263726 // intron // 0 // --- // --- // --- // ---	LHX4	LHX4, Homo sapiens LIM homeobox 4 (LHX4), q25.2
SNP_A-2259500	gaaaacaagtttacca[A/C]gagacagagaaactcc	A	C	NM_032360 // intron // 0 // Hs.200051 // ACBD6 // 84320 // Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), mRNA. /// ENST00000258326 // intron // 0 // --- // --- // --- // ---	ACBD6	ACBD6, Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), q25.2
SNP_A-1974322	attttgaataatttgc[C/T]ataccaaccatacttg	C	T	NM_032360 // intron // 0 // Hs.200051 // ACBD6 // 84320 // Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), mRNA. /// ENST00000258326 // intron // 0 // --- // --- // --- // ---	ACBD6	ACBD6, Homo sapiens acyl-Coenzyme A binding domain containing 6 (ACBD6), q25.3
SNP_A-1948290	tttaggatacttaaca[C/T]gctcccagtgtctcac	C	T	ENST00000258314 // intron // 0 // --- // --- // --- // ---	-	q25.3
SNP_A-1801932	gtataaaataaagata[A/C]cggcacctacctccca	A	C	NM_016545 // downstream // 35580 // Hs.15725 // IER5 // 51278 // Homo sapiens immediate early response 5 (IER5), mRNA. /// ENST00000294850 // downstream // 35580 // --- // --- // --- // --- /// ENST00000319701 // upstream // 109972 // --- // --- // --- // ---	IER5	IER5, Homo sapiens immediate early response 5 (IER5), q25.3
SNP_A-2113159	aggccattgcctaacc[C/G]gagagaacaggttata	C	G	NM_016545 // downstream // 49036 // Hs.15725 // IER5 // 51278 // Homo sapiens immediate early response 5 (IER5), mRNA. /// ENST00000294850 // downstream // 49036 // --- // --- // --- // --- /// ENST00000319701 // upstream // 96516 // --- // --- // --- // ---	IER5	IER5, Homo sapiens immediate early response 5 (IER5), q25.3
SNP_A-1877039	tctgctaagaggattc[A/C]aaccagtatctgtcca	A	C	NM_016545 // downstream // 50125 // Hs.15725 // IER5 // 51278 // Homo sapiens immediate early response 5 (IER5), mRNA. /// ENST00000294850 // downstream // 50125 // --- // --- // --- // --- /// ENST00000319701 // upstream // 95427 // --- // --- // --- // ---	IER5	IER5, Homo sapiens immediate early response 5 (IER5), q25.3
SNP_A-2058801	aatcattcttttggaa[A/G]tgaatatagtatgagg	A	G	NM_000721 // intron // 0 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // intron // 0 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calcium channel, alpha-	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2092745	agaaatgcttggggtc[G/T]ctttgcttgcagaggt	G	T	NM_000721 // downstream // 333659 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 333645 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2150834	atgtggaggtaggccc[A/G]ggacacagtagagcac	A	G	NM_000721 // downstream // 363459 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 363445 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-1856347	tcacacagttaataag[C/T]aaacccaggaatgtct	C	T	NM_000721 // downstream // 410401 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 410387 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2083515	actaagttctcatcaa[C/T]ggagtgtaagtagatg	C	T	NM_000721 // downstream // 414006 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 413992 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2000533	ttcaggtcaacttaaa[A/C]ccctaatgaaataata	A	C	NM_000721 // downstream // 414570 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 414556 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2066407	aatttggagtttca[C/T]taagcatagatcctag	C	T	NM_000721 // downstream // 417279 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 417265 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2148291	atggcctaatgagaa[C/T]tgattgatcgctcga	C	T	NM_000721 // downstream // 437334 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 437320 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-1807576	gtctggcatgttgtc[A/G]agcagttatcaacctg	A	G	NM_000721 // downstream // 487867 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 487853 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-1794854	ggtcttagataattca[A/G]cttagcaattcaacca	A	G	NM_000721 // downstream // 488441 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 488427 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2251914	cttcattccatttatc[A/G]cttcaagcaattagcta	A	G	NM_000721 // downstream // 489716 // Hs.437444 // CACNA1E // 777 // Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA. /// L27745 // downstream // 489702 // Hs.437444 // CACNA1E // 777 // Homo sapiens voltage-operated calci	CACNA1E	CACNA1E, Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), q25.3
SNP_A-2284211	gatatgttgagtttc[A/C]aagaaatgagggtggt	A	C	NM_002928 // upstream // 6059 // Hs.413297 // RGS16 // 6004 // Homo sapiens regulator of G-protein signalling 16 (RGS16), mRNA. /// NM_033345 // downstream // 36190 // Hs.458417 // RGS8 // 85397 // Homo sapiens regulator of G-protein signalling 8 (RGS8),	RGS16	RGS16, Homo sapiens regulator of G-protein signalling 16 (RGS16), q25.3
SNP_A-2227823	ctaccatttttagggc[C/G]ctccatgatccaacgc	C	G	NM_002928 // upstream // 6786 // Hs.413297 // RGS16 // 6004 // Homo sapiens regulator of G-protein signalling 16 (RGS16), mRNA. /// NM_033345 // downstream // 35463 // Hs.458417 // RGS8 // 85397 // Homo sapiens regulator of G-protein signalling 8 (RGS8),	RGS16	RGS16, Homo sapiens regulator of G-protein signalling 16 (RGS16), q25.3
SNP_A-2187450	caggtttagacttatc[A/G]aacatcttgccagacc	A	G	NM_002928 // upstream // 18793 // Hs.413297 // RGS16 // 6004 // Homo sapiens regulator of G-protein signalling 16 (RGS16), mRNA. /// NM_033345 // downstream // 23456 // Hs.458417 // RGS8 // 85397 // Homo sapiens regulator of G-protein signalling 8 (RGS8),	RGS16	RGS16, Homo sapiens regulator of G-protein signalling 16 (RGS16), q25.3
SNP_A-1693250	ggtcttggaaaatcattacagtaaa[A/G]tgcagatttctaataagc cttgtttc	A	G	NM_002928 // upstream // 5552 // Hs.413297 // RGS16 // 6004 // regulator of G-protein signalling 16	RGS16	RGS16 , rs5116567, regulator of G-protein signalling 16,q25.3
SNP_A-2301183	gccttctatagcaga[C/T]ggagctgaaaggaacc	C	T	NM_015149 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), mRNA. /// ENST00000304685 // intron // 0 // — // — // —	RGL1	RGL1, Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), q25.3
SNP_A-1850998	tattatgaaaaaagcc[A/G]ctctgaacattcatgt	A	G	NM_015149 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), mRNA. /// ENST00000304685 // intron // 0 // — // — // —	RGL1	RGL1, Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2268124	gaatgaaccttcacaa[C/T]gcaggacaaagcagga	C	T	NM_015149 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), mRNA. /// AF186780 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens RGL protein (RGL) mRNA, alternatively spli	RGL1	RGL1, Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), q25.3
SNP_A-1975413	gacaccagaaactgga[A/G]gcaatatgggttccca	A	G	NM_015149 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), mRNA. /// AF186780 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens RGL protein (RGL) mRNA, alternatively spli	RGL1	RGL1, Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), q25.3
SNP_A-1975415	ccgataggcatctacc[A/G]ctgatggggactcaga	A	G	NM_015149 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), mRNA. /// AF186780 // intron // 0 // Hs.497148 // RGL1 // 23179 // Homo sapiens RGL protein (RGL) mRNA, alternatively spli	RGL1	RGL1, Homo sapiens ral guanine nucleotide dissociation stimulator-like 1 (RGL1), q25.3
SNP_A-2315045	ggataaaaatgtgcta[A/G]gcaaaatatgttggcc	A	G	ENST00000264141 // intron // 0 // — // — // — // —	-	q25.3
SNP_A-1756300	gccaaatcaatctgtaaattgtcta[C/T]gggtgagttgaaattgtaatctgag	C	T	NM_015149 // intron // 0 // Hs.79219 // RGL1 // 23179 // ral guanine nucleotide dissociation stimulator-like 1	RGL1	RGL1 , rs6658064, ral guanine nucleotide dissociation stimulator-like 1,q25.3
SNP_A-1703803	tatacttttacattttcattagtac[A/G]actcaattcccttgctctctggccc	A	G	NM_015149 // intron // 0 // Hs.79219 // RGL1 // 23179 // ral guanine nucleotide dissociation stimulator-like 1	RGL1	RGL1 , rs10494568, ral guanine nucleotide dissociation stimulator-like 1,q25.3
SNP_A-2101899	agatggctctggattg[A/C]aagtaactatatataa	A	C	NM_030806 // upstream // 34785 // Hs.497159 // C1orf21 // 81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000240780 // downstream // 278283 // — // — // — // — /// ENST00000235307 // upstream // 34785 // — //	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-2124650	agttctaatgacatta[A/G]ctacacagaaccatgc	A	G	NM_030806 // upstream // 30800 // Hs.497159 // C1orf21 // 81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000240780 // downstream // 282268 // — // — // — // — /// ENST00000235307 // upstream // 30800 // — //	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-1920203	ttaatcttcaccatta[A/T]ccctatgtaacatttt	A	T	NM_030806 // intron // 0 // Hs.497159 // C1orf21 // 81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // — // — // — // —	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-1919761	ttaagtcttccaagaa[C/T]ggttttagttggaaaa	C	T	NM_030806 // intron // 0 // Hs.497159 // C1orf21 // 81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // — // — // — // —	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-2303579	gctcacaaatgaagtc[A/G]acaggaagagatgctt	A	G	NM_030806 // intron // 0 // Hs.497159 // C1orf21 // 81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // intron // 0 // — // — // — // —	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-2172846	caattttaccactcaa[A/C]ccaggagctactactg	A	C	NM_030806 // 3UTR // 0 // Hs.497159 // C1orf21 // 81563 // Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA. /// ENST00000235307 // 3UTR // 0 // — // — // — // —	C1orf21	C1orf21, Homo sapiens chromosome 1 open reading frame 21 (C1orf21), q25.3
SNP_A-2056136	aataccgctccaaaga[G/T]atcccactatttcttt	G	T	NM_025191 // upstream // 15649 // Hs.523811 // C1orf22 // 80267 // Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA. /// NM_022083 // downstream // 20868 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (	C1orf22	C1orf22, Homo sapiens chromosome 1 open reading frame 22 (C1orf22), q25.3
SNP_A-2036035	aaattacaaatacaaa[A/G]gagaccatacttatta	A	G	NM_025191 // upstream // 23436 // Hs.523811 // C1orf22 // 80267 // Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA. /// NM_022083 // downstream // 13081 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (	C1orf22	C1orf22, Homo sapiens chromosome 1 open reading frame 22 (C1orf22), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2070562	acacctgaagtcataa[C/T]acactcaatgaaggaa	C	T	NM_025191 // upstream // 27384 // Hs.523811 // C1orf22 // 80267 // Homo sapiens chromosome 1 open reading frame 22 (C1orf22), mRNA. /// NM_022083 // downstream // 9133 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C	C1orf22	C1orf22, Homo sapiens chromosome 1 open reading frame 22 (C1orf22), q25.3
SNP_A-2180478	cagaacgtgtcctccc[A/G]caacatgatggctaaa	A	G	NM_022083 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRN	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-2158177	attggcaagacaaaca[C/T]cattaggtttcgaaca	C	T	NM_022083 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRN	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-1799507	gtaatgggcctggttc[C/T]cgtaagaattatcatt	C	T	NM_022083 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRN	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-2245984	ctggtaagtgtttggc[A/G]aaagaaggcataatga	A	G	NM_022083 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRN	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-2095641	agacacacattatcac[A/C]cccaagtaatttgtgc	A	C	NM_022083 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRN	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-1725812	attaggtgttagctaaagaatctc[A/G]cttggcataaatgtgtccc atgaat	A	G	NM_030806 // intron // 0 // Hs.12532 // C1orf21 // 81563 // chromosome 1 open reading frame 21	C1orf21	C1orf21, rs7415961, chromosome 1 open reading frame 21.q25.3
SNP_A-1666298	tttggcagaactttgagatagaacc[A/G]ctgaagtcaccctgact atctgtgt	A	G	NM_030806 // intron // 0 // Hs.12532 // C1orf21 // 81563 // chromosome 1 open reading frame 21	C1orf21	C1orf21, rs6424950, chromosome 1 open reading frame 21.q25.3
SNP_A-1859123	tcagcctcactagtaa[A/G]tgcaaatgaaggcacc	A	G	NM_022083 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRNA. /// NM_052966 // intron // 0 // Hs.518662 // C1orf24 // 116496 // Homo sapiens chromosome 1 open reading frame 24 (C1orf24), mRN	C1orf24	C1orf24, Homo sapiens chromosome 1 open reading frame 24 (C1orf24), q25.3
SNP_A-1701643	aaaatcctcatcaaacagagccgg[C/T]catattaaaacaaga aagacagaga	C	T	NM_030806 // intron // 0 // Hs.12532 // C1orf21 // 81563 // chromosome 1 open reading frame 21	C1orf21	C1orf21, rs10489721, chromosome 1 open reading frame 21.q25.3
SNP_A-1678646	ataaaatttagttgaagtactga[C/T]gaatatacaatttagtgac acattt	C	T	NM_030806 // intron // 0 // Hs.12532 // C1orf21 // 81563 // chromosome 1 open reading frame 21	C1orf21	C1orf21, rs10489722, chromosome 1 open reading frame 21.q25.3
SNP_A-1975754	ttccgggctagttta[C/T]agggaagatatgtatc	C	T	NM_007212 // intron // 0 // Hs.124186 // RNF2 // 6045 // Homo sapiens ring finger protein 2 (RNF2), mRNA. /// ENST00000240802 // intron // 0 // – // — // — // —	RNF2	RNF2, Homo sapiens ring finger protein 2 (RNF2), q25.3
SNP_A-1738367	aagtgggaaaatgtattaggcactc[A/T]atagatcctcacgtgat ataatctt	A	T	NM_030806 // intron // 0 // Hs.12532 // C1orf21 // 81563 // chromosome 1 open reading frame 21	C1orf21	C1orf21, rs2207521, chromosome 1 open reading frame 21.q25.3
SNP_A-1952651	ttctggctaaaatta[C/T]gttacttccctttggtc	C	T	NM_017673 // downstream // 3390 // Hs.134183 // C1orf26 // 54823 // Homo sapiens chromosome 1 open reading frame 26 (C1orf26), mRNA. /// NM_006469 // downstream // 1322 // Hs.497183 // IVNS1ABP // 10625 // Homo sapiens influenza virus NS1A binding protein	C1orf26	C1orf26, Homo sapiens chromosome 1 open reading frame 26 (C1orf26), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1685544	gccttctatgtttctggccaactca[A/T]cgatacaaaaacattcaccagatca	A	T	NM_022083 // intron // 0 // Hs.48778 // C1orf24 // 116496 // chromosome 1 open reading frame 24 /// NM_052966 // intron // 0 // Hs.48778 // C1orf24 // 116496 // chromosome 1 open reading frame 24	C1orf24	C1orf24 , rs689157, chromosome 1 open reading frame 24 ,q25.3
SNP_A-1975795	ttgaacagtgatgaaa[A/G]gatactctatctagct	A	G	NM_006469 // upstream // 48978 // Hs.497183 // IVNS1ABP // 10625 // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA. /// NM_031935 // upstream // 368319 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FI	IVNS1ABP	IVNS1ABP, Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, q25.3
SNP_A-2240769	ctgacttctagacact[G/T]aaaaaatctctttcat	G	T	NM_006469 // upstream // 108343 // Hs.497183 // IVNS1ABP // 10625 // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA. /// NM_031935 // upstream // 308954 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (F	IVNS1ABP	IVNS1ABP, Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, q25.3
SNP_A-2246052	ctggtattacaagcac[A/C]gtctgatagtgaatcc	A	C	NM_006469 // upstream // 202326 // Hs.497183 // IVNS1ABP // 10625 // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA. /// NM_031935 // upstream // 214971 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (F	IVNS1ABP	IVNS1ABP, Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, q25.3
SNP_A-2127835	ataagaaaagtttcac[A/G]gagtggctggaatttc	A	G	NM_006469 // upstream // 277428 // Hs.497183 // IVNS1ABP // 10625 // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA. /// NM_031935 // upstream // 139869 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (F	IVNS1ABP	IVNS1ABP, Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, q25.3
SNP_A-2000542	tgagaacaccaaatac[C/T]agtgaagatgtagagt	C	T	NM_006469 // upstream // 304092 // Hs.497183 // IVNS1ABP // 10625 // Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, mRNA. /// NM_031935 // upstream // 113205 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (F	IVNS1ABP	IVNS1ABP, Homo sapiens influenza virus NS1A binding protein (IVNS1ABP), transcript variant 1, q25.3
SNP_A-2065650	aatttagtacagtcta[C/G]gatctggtttttaggt	C	G	NM_031935 // intron // 0 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// ENST00000271588 // intron // 0 // --- // --- // --- // ---	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1790305	ggggaggtagttaaac[A/G]agtacataatacatac	A	G	NM_031935 // downstream // 29926 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 75983 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2181264	cagacccaatgttctc[C/T]gactttgaccactgca	C	T	NM_031935 // downstream // 37667 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 68242 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2214380	cctacctgtcaacgtg[A/G]aatagagaaaagtcag	A	G	NM_031935 // downstream // 41144 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 64765 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1903176	tggcttccctaggaac[A/G]gcagagataggctagc	A	G	NM_031935 // downstream // 41504 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 64405 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2139853	atctaagatgtccaga[A/G]agtggtgatttgggggg	A	G	NM_031935 // downstream // 42260 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 63649 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1908068	tgtacaatttcatata[C/T]gcccctgatactaagcc	C	T	NM_031935 // downstream // 42591 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 63318 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1932610	ttcctgtgggaaaga[C/T]tcagtggaagaaataa	C	T	NM_031935 // downstream // 43729 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 62180 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1880317	tctctttcagaaag[A/G]cctatttaatgatca	A	G	NM_031935 // downstream // 43941 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 61968 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2309548	ggaaacgcttagctact[A/G]agagtgactaggaatg	A	G	NM_031935 // downstream // 43978 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 61931 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1940288	ttgcatttgtgaata[A/G]ataagaagcagctagg	A	G	NM_031935 // downstream // 44864 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 61045 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-1894169	tgcatggctttctaaa[C/T]ttaagatgtgattca	C	T	NM_031935 // downstream // 45090 // Hs.58877 // FIBL-6 // 83872 // Homo sapiens hemicentin (FIBL-6), mRNA. /// NM_005807 // upstream // 60819 // Hs.432458 // PRG4 // 10216 // Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superf	FIBL-6	FIBL-6, Homo sapiens hemicentin (FIBL-6), q31.1
SNP_A-2076428	acatigttggcttacc[A/G]gggttacagtttctt	A	G	NM_022576 // upstream // 23920 // Hs.550 // PDC // 5132 // Homo sapiens phosducin (PDC), transcript variant 2, mRNA. /// NM_002597 // upstream // 11518 // Hs.550 // PDC // 5132 // Homo sapiens phosducin (PDC), transcript variant 1, mRNA. /// NM_022576 //	PDC	PDC, Homo sapiens phosducin (PDC), transcript variant 2, q31.1
SNP_A-1834761	taccagcaatcctgac[C/T]gtattatacctgatct	C	T	NM_022576 // upstream // 88756 // Hs.550 // PDC // 5132 // Homo sapiens phosducin (PDC), transcript variant 2, mRNA. /// NM_002597 // upstream // 76354 // Hs.550 // PDC // 5132 // Homo sapiens phosducin (PDC), transcript variant 1, mRNA. /// NM_022576 //	PDC	PDC, Homo sapiens phosducin (PDC), transcript variant 2, q31.1
SNP_A-2175747	cacattcagtgagtca[C/T]agaagccctttacctg	C	T	NM_022576 // upstream // 129477 // Hs.550 // PDC // 5132 // Homo sapiens phosducin (PDC), transcript variant 2, mRNA. /// NM_002597 // upstream // 117075 // Hs.550 // PDC // 5132 // Homo sapiens phosducin (PDC), transcript variant 1, mRNA. /// NM_022576 /	PDC	PDC, Homo sapiens phosducin (PDC), transcript variant 2, q31.1
SNP_A-1743907	cacacaggatagcaaaagttagctct[A/G]ttacagatttcacatc catgagtct	A	G	NM_003292 // downstream // 83478 // Hs.170472 // TPR // 7175 // translocated promoter region (to activated MET oncogene) /// NM_005807 // upstream // 66506 // Hs.432458 // PRG4 // 10216 // proteoglycan 4, (megakaryocyte stimulating factor, articular supe	TPR	TPR, rs586281, translocated promoter region (to activated MET oncogene), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1656691	ctttgcagagtgattaaggatcat[A/G]agattgggagattaccct gggtgat	A	G	NM_003292 // downstream // 83321 // Hs.170472 // TPR // 7175 // translocated promoter region (to activated MET oncogene) /// NM_005807 // upstream // 66349 // Hs.432458 // PRG4 // 10216 // proteoglycan 4, (megakaryocyte stimulating factor, articular supe	TPR	TPR , rs585738, translocated promoter region (to activated MET oncogene), q31.1
SNP_A-1709459	atcccttgcacccacaatggtctccaa[C/T]tgacaaagcacagta gtggaagtcc	C	T	NM_003292 // downstream // 44930 // Hs.170472 // TPR // 7175 // translocated promoter region (to activated MET oncogene) /// NM_005807 // upstream // 27958 // Hs.432458 // PRG4 // 10216 // proteoglycan 4, (megakaryocyte stimulating factor, articular supe	TPR	TPR , rs609400, translocated promoter region (to activated MET oncogene), q31.1
SNP_A-1833335	tacagaaaagtaccta[A/G]atgaactactgaaaa	A	G	NM_000963 // upstream // 104521 // Hs.196384 // PTGS2 // 5743 // Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cydooxygenase) (PTGS2), mRNA. /// NM_024420 // upstream // 44028 // Hs.497200 // PLA2G4A // 5321 // Homo s	PTGS2	PTGS2, Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G q31.1
SNP_A-1692238	tttcaagttcatttttcataatgac[C/T]agtactttaatacctgaact ggtg	C	T	NM_003292 // intron // 0 // Hs.170472 // TPR // 7175 // translocated promoter region (to activated MET oncogene)	TPR	TPR , rs3818293, translocated promoter region (to activated MET oncogene), q31.1
SNP_A-1904199	tgggcctgaaatacaa[C/T]agaaaaatgctctga	C	T	NM_024420 // intron // 0 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // intron // 0 // — // — // — // —	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2076741	acatttttagttatca[C/G]acactagagcacatga	C	G	NM_024420 // intron // 0 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // intron // 0 // — // — // — // —	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1815866	gttaatatatcaaaaaa[C/T]ggaactaataagctcc	C	T	NM_024420 // downstream // 126610 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 126610 // — // — // — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1737501	acctctatcttgaggaatcttagga[A/G]ctacatacagtgctaga aacaggct	A	G	NM_000963 // upstream // 103018 // Hs.196384 // PTGS2 // 5743 // prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) /// NM_024420 // upstream // 45531 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cyto	PTGS2	PTGS2, rs10489403, prostaglandin-endoperoxide synthase 2 (prostaglandin G,q31.1
SNP_A-1783001	ggcagcattgcagcccc[A/G]atatatagacaggagtg	A	G	NM_024420 // downstream // 476654 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 476654 // — // — // — // — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1880856	tctggttcctcttat[G/T]acaactggtgtctggt	G	T	NM_024420 // downstream // 477796 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 477796 // — // — // — // — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2239583	ctgaaaacgcattaac[C/T]ctttctctagaagtgg	C	T	NM_024420 // downstream // 585041 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 585041 // — // — // — // — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2289564	gatttttccagtata[C/T]gaaagccatttattgt	C	T	NM_024420 // downstream // 589474 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 589474 // — // — // — // — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1820248	gttaccccaatctaa[C/T]agagtttagaggagac	C	T	NM_024420 // downstream // 626586 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 626586 /// — /// — /// — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1936969	ttcttgtccttgat[A/G]acttctatagaatgcc	A	G	NM_024420 // downstream // 821198 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 821198 /// — /// — /// — /// ENST00000360968 // up	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1692498	gagtccaaatcatgcttttgtgaccat[C/T]cttttccgtaaactgtct catttc	C	T	NM_024420 // downstream // 542201 /// Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A , rs10494596, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-2257085	ctttctcagcaattgaat[G/T]atttcttctcttttgtt	G	T	NM_024420 // downstream // 1164334 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1164334 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1862436	tcatgtgtaaacctca[A/T]agtgtaaagtaatggc	A	T	NM_024420 // downstream // 1174321 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1174321 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2255922	cttaaattgcataaat[C/G]ccaatattgtatatta	C	G	NM_024420 // downstream // 1294112 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1294112 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2092767	agaaatgggtgagtac[A/C]aggctataaagaaaaa	A	C	NM_024420 // downstream // 1312534 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1312534 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2151736	atgtttaaagtagaaa[C/G]aacaatggtcaaacaa	C	G	NM_024420 // downstream // 1406412 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1406412 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2190160	cataagttcacacaag[A/C]atctccatgtgatgat	A	C	NM_024420 // downstream // 1413489 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1413489 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2151396	atgttcacaagtaaag[C/T]catctaggcctcacag	C	T	NM_024420 // downstream // 1414749 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1414749 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2000556	gaaatacaaagggtca[C/T]ctcactgtaatatgt	C	T	NM_024420 // downstream // 1424934 /// Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1424934 /// — /// — /// — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2033410	aaataggcaaaagaaa[C/G]taggaacagtccccaa	C	G	NM_024420 // downstream // 1714468 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 1714468 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1743817	tccattgataacacttattccaaaa[G/T]ctattacaattaggtggg ccagtat	G	T	NM_024420 // downstream // 1473959 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A. , rs1489261, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-2287544	gatgttttctctaa[A/G]gtacaaagcaataaac	A	G	NM_024420 // downstream // 2009587 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2009587 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1976835	agtatacactggagac[C/T]gaaaccatgatgaagt	C	T	NM_024420 // downstream // 2026280 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2026280 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1894634	tgccacttactcattc[A/G]ccttttgtgccccct	A	G	NM_024420 // downstream // 2036483 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2036483 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2159367	atttaatattctgcaa[A/C]ctgtgcttaagatat	A	C	NM_024420 // downstream // 2044658 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2044658 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2171342	caatattctgtctaaa[A/G]ctctgtaatctgaataa	A	G	NM_024420 // downstream // 2063875 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2063875 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1976870	accactgcttagcata[A/G]taattggcatttgtta	A	G	NM_024420 // downstream // 2121289 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2121289 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1801396	gtaggatttgttaagc[A/G]aaatgatagctttcag	A	G	NM_024420 // downstream // 2276533 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2276533 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2067313	acaaagtcctctctag[C/T]aagcctgtcctctgag	C	T	NM_024420 // downstream // 2281853 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2281853 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1846992	tatcagccctaccgta[G/T]tacagataacttcatt	G	T	NM_024420 // downstream // 2285013 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2285013 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A. Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2039392	aacataggacactgtc[A/G]agaatcggttgttat	A	G	NM_024420 // downstream // 2318849 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2318849 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2189148	cagttagccacaaaaa[C/T]tgctaattctacatt	C	T	NM_024420 // downstream // 2359508 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2359508 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2000559	cactttcaggtacagc[A/G]atcaaaagcagattg	A	G	NM_024420 // downstream // 2426260 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2426260 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1976936	ttacttagagcaacac[C/T]gggtatttctctta	C	T	NM_024420 // downstream // 2449414 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2449414 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-2275018	gagaactaaaactagaa[A/G]aatatgaagcagacta	A	G	NM_024420 // downstream // 2533289 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2533289 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1909593	tgtcaaaaatgatccc[A/C]cactagtggaaataag	A	C	NM_024420 // downstream // 2562135 // Hs.497200 // PLA2G4A // 5321 // Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA. /// ENST00000264143 // downstream // 2562135 // — // — // — /// ENST00000360968 //	PLA2G4A	PLA2G4A, Homo sapiens phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), q31.1
SNP_A-1720521	gtattggtgttattaaaatggcta[C/G]agaaagtggatggtaga atagatga	C	G	NM_024420 // downstream // 2252049 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A , rs6428195, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-1727423	agaccatgatgtaaaatgatatgaa[C/T]gaaggagaaaagaac aaatttgata	C	T	NM_024420 // downstream // 2351318 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A, rs10494628, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-1878643	tctgttaaaagtaagga[A/G]agttaacgcttatggc	A	G	NM_199051 // downstream // 81884 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 420858 // — // — // — // — /// ENST00000294697 // downstream // 81884 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-2071336	acacttgtacaacta[A/G]cgaacctacattgatg	A	G	NM_199051 // downstream // 74730 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 428012 // — // — // — // — /// ENST00000294697 // downstream // 74730 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1836102	tactacttgaagaaa[G/T]tttagaggttgtgtct	G	T	NM_199051 // downstream // 74141 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 428601 // — // — // — // — /// ENST00000294697 // downstream // 74141 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1908761	tgtaggtgataataa[A/G]aaggtacttggtgaaa	A	G	NM_199051 // downstream // 71585 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 431157 // — // — // — // — /// ENST00000294697 // downstream // 71585 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1977150	tattccacgtcatgca[A/G]gttatcataatcaic	A	G	NM_199051 // downstream // 68740 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 434002 // — // — // — // — /// ENST00000294697 // downstream // 68740 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977159	ccaaaatatttgagccc[A/G]aaggaagaagaagcaa	A	G	NM_199051 // downstream // 56552 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000360968 // downstream // 446190 // — // — // — /// ENST00000294697 // downstream // 56552 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1977188	ttaacagcatcttga[A/T]aggattaattcccata	A	T	NM_199051 // intron // 0 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000294697 // intron // 0 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-2271788	gaccatcaacttacaa[A/G]agcctgtgagtggtga	A	G	NM_199051 // intron // 0 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// ENST00000294697 // intron // 0 // — // — // — // —	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.1
SNP_A-1715165	acatagaatcaacctaggtgcttat[A/C]aatggtagattaattaa aaaatgg	A	C	NM_024420 // downstream // 3116647 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A , rs1529311, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-1681514	ttccctttctacattctaggaacca[A/G]aatcagcacactcggca caattat	A	G	NM_024420 // downstream // 3157540 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A , rs1935881, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-1734132	ccatgaaatgagttctatttgata[C/T]agtttgttagaacctgggg aaaatt	C	T	NM_024420 // downstream // 3157896 // Hs.211587 // PLA2G4A // 5321 // phospholipase A2, group IVA (cytosolic, calcium-dependent)	PLA2G4A	PLA2G4A , rs1935880, phospholipase A2, group IVA (cytosolic, calcium-dependent),q31.1
SNP_A-1697036	tctgccttttacgtatgttgtagg[A/C]aacctgcaatattcagataa tatga	A	C	U67037 // intron // 0 // Hs.497208 // DBCCR1L // 339479 // DBCCR1-like	DBCCR1L	DBCCR1L , rs10494631, DBCCR1-like,q31.1
SNP_A-1829362	taagtcatttctttga[C/T]gctgctttgagcatag	C	T	NM_199051 // upstream // 378777 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// NM_130782 // upstream // 1302064 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// ENST0	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.2
SNP_A-1709253	gatatttctcagataaaataatctcaa[G/T]agaagtagatcataaca ttacctga	G	T	NM_130782 // upstream // 1822761 // Hs.440890 // RGS18 // 64407 // regulator of G-protein signalling 18	RGS18	RGS18 , rs500764, regulator of G-protein signalling 18,q31.1
SNP_A-2035980	aaattaacccagtctg[C/T]attccaggccctaact	C	T	NM_199051 // upstream // 981722 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// NM_130782 // upstream // 699119 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// ENST00	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.2
SNP_A-1831205	taatgcttatatacca[A/G]cagtagaatatttagc	A	G	NM_199051 // upstream // 991766 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// NM_130782 // upstream // 689075 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// ENST00	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.2
SNP_A-1977519	tcttgagacaatctag[G/T]caacttiggaattctc	G	T	NM_199051 // upstream // 1003224 // Hs.65765 // DBCCR1L // 339479 // Homo sapiens DBCCR1-like (DBCCR1L), mRNA. /// NM_130782 // upstream // 677617 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// ENST0	DBCCR1L	DBCCR1L, Homo sapiens DBCCR1-like (DBCCR1L), q31.2
SNP_A-2062635	aatgtccagaatagqd[A/G]catttatagagacagc	A	G	NM_130782 // downstream // 12595 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 377388 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1),	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2058375	aatcacgctaaccag[G/T]agtagaatctcacatc	G	T	NM_130782 // downstream // 26329 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 363654 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1),	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2028261	aaactatctttccaaa[C/T]tcaggccaaaccaaag	C	T	NM_130782 // downstream // 69249 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 320734 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1).	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1855248	tcaagcgttcctaac[C/T]attaagacacctgaac	C	T	NM_130782 // downstream // 90088 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 299895 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1).	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2063055	aatgttcaaaactaa[C/T]tcatgccatccctct	C	T	NM_130782 // downstream // 104550 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 285433 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1977661	ggtcagttcaataaca[G/T]gagacaaagatttgg	G	T	NM_130782 // downstream // 108647 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 281336 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2282008	gagtggagcaagcaaa[A/T]agttgtgaatgggaa	A	T	NM_130782 // downstream // 126478 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 263505 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1865058	tccagtgagaggcaaa[A/G]gatattggaaatggaa	A	G	NM_130782 // downstream // 128287 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 261696 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2177101	cacctctaaacatttca[A/T]ccagttcaatatctaa	A	T	NM_130782 // downstream // 193160 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 196823 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2059828	aatcgtgaaaccacc[C/T]atgcgtactcagggac	C	T	NM_130782 // downstream // 235691 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 154292 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2156127	attcgttgaatgaata[C/T]gaatgtttggtgact	C	T	NM_130782 // downstream // 256338 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 133645 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-2135099	atattctgtggtatca[C/T]ggctaaattcaagata	C	T	NM_130782 // downstream // 264818 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 125165 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1883875	tgaagacattgaggg[A/T]aagggttaagcgact	A	T	NM_130782 // downstream // 265063 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 124920 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1)	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1818212	gtctgacgggggtga[A/G]gcctgttgttgag	A	G	NM_130782 // downstream // 323932 // Hs.440890 // RGS18 // 64407 // Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA. /// NM_002922 // upstream // 66051 // Hs.75256 // RGS1 // 5996 // Homo sapiens regulator of G-protein signalling 1 (RGS1),	RGS18	RGS18, Homo sapiens regulator of G-protein signalling 18 (RGS18), q31.2
SNP_A-1677772	aaatctcattcttgatttaatttttc[C/T]actgtgcaaatcatatatttccaac	C	T	NM_002922 // upstream // 221172 // Hs.75256 // RGS1 // 5996 // regulator of G-protein signalling 1 /// NM_130782 // downstream // 168811 // Hs.440890 // RGS18 // 64407 // regulator of G-protein signalling 18	RGS1	RGS1 , rs1936671, regulator of G-protein signalling 1, q31.2
SNP_A-2030520	aaagcctgggaaagtg[A/G]aatgtcctgaggaaa	A	G	NM_002923 // downstream // 130702 // Hs.78944 // RGS2 // 5997 // Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA. /// NM_015984 // downstream // 72792 // Hs.145469 // UCHL5 // 51377 // Homo sapiens ubiquitin carboxyl-terminal hydrolas	RGS2	RGS2, Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), q31.2
SNP_A-2075620	acatggaaaatgcaac[C/T]gaacacattagaaggt	C	T	NM_002923 // downstream // 141769 // Hs.78944 // RGS2 // 5997 // Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA. /// NM_015984 // downstream // 61725 // Hs.145469 // UCHL5 // 51377 // Homo sapiens ubiquitin carboxyl-terminal hydrolas	RGS2	RGS2, Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), q31.2
SNP_A-1829339	taagtcagaaatcagac[A/G]catttattccgctta	A	G	NM_002923 // downstream // 165426 // Hs.78944 // RGS2 // 5997 // Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA. /// NM_015984 // downstream // 38068 // Hs.145469 // UCHL5 // 51377 // Homo sapiens ubiquitin carboxyl-terminal hydrolas	RGS2	RGS2, Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), q31.2
SNP_A-2288287	gattcgccaggaacaa[C/T]gtaataaagaatcacc	C	T	NM_024529 // intron // 0 // Hs.378996 // HRPT2 // 79577 // Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), mRNA. /// ENST00000256767 // intron // 0 // — // — // —	HRPT2	HRPT2, Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), q31.2
SNP_A-1709171	agaatagaactcgatttattgataa[G/T]ggaatcaaggaaatttaactttct	G	T	NM_002923 // upstream // 95500 // Hs.78944 // RGS2 // 5997 // regulator of G-protein signalling 2, 24kDa /// NM_002927 // downstream // 53281 // Hs.17165 // RGS13 // 6003 // regulator of G-protein signalling 13 /// NM_144766 // downstream // 53281 // Hs.	RGS2	RGS2, rs2146609, regulator of G-protein signalling 2, 24kDa, q31.2
SNP_A-2247645	ctgtcttctcacct[A/C]acattagcatcactg	A	C	NM_024529 // downstream // 316027 // Hs.378996 // HRPT2 // 79577 // Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), mRNA. /// NM_003783 // upstream // 381341 // Hs.518834 // B3GALT2 // 8707 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactos	HRPT2	HRPT2, Homo sapiens hyperparathyroidism 2 (with jaw tumor) (HRPT2), q31.2
SNP_A-2099787	agagtaactgtttcca[C/T]gcaaatgccctttcca	C	T	ENST00000359327 // upstream // 125209 // — // — // — /// ENST00000356964 // upstream // 60419 // — // — // —	-	q31.2
SNP_A-1799780	gtacaagaaaaaactga[C/T]gataaaaatgcacagg	C	T	NM_198503 // downstream // 2377070 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 24643 // — // — // — /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1661914	tcaaaacagaagttcctttagca[C/T]ctgaattgtttaccagaagttta	C	T	NM_003783 // upstream // 509960 // Hs.181353 // B3GALT2 // 8707 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 /// NM_024529 // downstream // 445128 // Hs.259502 // HRPT2 // 79577 // hyperparathyroidism 2 (with jaw tumor)	B3GALT2	B3GALT2 , rs10489940, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2, q31.2
SNP_A-1880545	tcttgcaaatttcca[C/T]taataattactttcta	C	T	NM_198503 // downstream // 1812812 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 588901 // — // — // — /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2147914	atggctacagagtcaa[A/C]caacttttactggga	A	C	NM_198503 // downstream // 1802886 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 598827 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2028004	aaacgactactagatc[A/C]aaccaaaagtgtcttа	A	C	NM_198503 // downstream // 1778103 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 623610 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2154390	attattaagcatttttg[G/T]aagtgtgaacaaactg	G	T	NM_198503 // downstream // 1756525 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 645188 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2100788	agatagtcactgagaaa[C/G]tattatgtagtgtga	C	G	NM_198503 // downstream // 1748364 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 653349 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2184660	cagctctagaacaccca[A/G]aaatcacagcttctc	A	G	NM_198503 // downstream // 1727101 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 674612 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2076349	acattgctattatgaa[C/G]aacgtttgtaaaaat	C	G	NM_198503 // downstream // 1707123 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 694590 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1678226	ctggtagttttgtgagtatttcta[C/T]attcagatcaaaagatttgcgtaca	C	T	NM_003783 // upstream // 1169102 // Hs.181353 // B3GALT2 // 8707 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 /// NM_024529 // downstream // 1104270 // Hs.259502 // HRPT2 // 79577 // hyperparathyroidism 2 (with jaw tumor)	B3GALT2	B3GALT2 , rs7515996, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2, q31.3
SNP_A-1978430	tgcatgtgatgataaaa[C/T]acatcgtctaaactta	C	T	NM_198503 // downstream // 1252009 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1149704 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2207757	cccaaaaggtcttgt[A/G]aaatatgcatagtatc	A	G	NM_198503 // downstream // 1163075 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1238638 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1836040	tactacaagtccaaac[C/T]aaaacaggatagtact	C	T	NM_198503 // downstream // 750652 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1651061 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1937838	ttgaatagctgttatg[C/T]agcctaacttccagaa	C	T	NM_198503 // downstream // 701375 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1700338 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1978635	tagaatcttatttgcc[C/T]actgtttaaaaccgaa	C	T	NM_198503 // downstream // 507906 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 1893807 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1863039	tcattgttggaagcca[C/G]tcattggtatatatgt	C	G	NM_198503 // downstream // 303671 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2098042 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2044011	aacttgatagcagccaa[A/G]tcggcctgggctcagg	A	G	NM_198503 // downstream // 278026 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2123687 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1978722	gtatggcaaaccttca[A/C]gagtgagacacagcga	A	C	NM_198503 // downstream // 229719 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 2171994 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2156630	attctgccatcaagtc[A/G]cttaaagtcaagccag	A	G	NM_198503 // downstream // 94674 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000356964 // downstream // 23070039 // --- // --- // --- /// ENST00000294725 //	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-2100848	agatatatatggcaag[C/G]aagtaaaaattatctg	C	G	NM_198503 // intron // 0 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000294725 // intron // 0 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1658014	cttggaatgtctgcagtactgcacat[A/G]aagacatcctacatttttaatag	A	G	NM_003783 // upstream // 2800905 // Hs.181353 // B3GALT2 // 8707 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 /// NM_024529 // downstream // 2736073 // Hs.259502 // HRPT2 // 79577 // hyperparathyroidism 2 (with jaw tumor)	B3GALT2	B3GALT2, rs4554704, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2, q31.3
SNP_A-2287102	gatgtagtttggttgat[C/T]gaagtaaaacatggtt	C	T	NM_198503 // intron // 0 // Hs.420016 // SLICK // 343450 // Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), mRNA. /// ENST00000294725 // intron // 0 // --- // --- // ---	SLICK	SLICK, Homo sapiens sodium- and chloride-activated ATP-sensitive potassium channel (SLICK), q31.3
SNP_A-1647918	ctacactggatctccaagtttaaac[A/G]attatctggttccgattcattccgt	A	G	NM_003783 // upstream // 3269409 // Hs.181353 // B3GALT2 // 8707 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 /// NM_024529 // downstream // 3204577 // Hs.259502 // HRPT2 // 79577 // hyperparathyroidism 2 (with jaw tumor)	B3GALT2	B3GALT2, rs10494743, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2, q31.3
SNP_A-2308026	gcttgaaaaaaacata[A/G]catttcggatataaag	A	G	NM_012076 // downstream // 27070 // Hs.126135 // CRB1 // 23418 // Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, mRNA. /// NM_019049 // downstream // 4120 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ	CRB1	CRB1, Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, q31.3
SNP_A-1805656	gtccatttgctttatgt[A/G]acatcacggcttcaga	A	G	NM_012076 // downstream // 29653 // Hs.126135 // CRB1 // 23418 // Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, mRNA. /// NM_019049 // downstream // 1537 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ	CRB1	CRB1, Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), transcript variant 1, q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1979006	tcagttagctttcctg[G/T]atagccaggcaccaca	G	T	NM_019049 // intron // 0 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// ENST00000235453 // intron // 0 // — // — // — // — /// ENST00000294737 // intron // 0 // — // — // — // —	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-2126577	ataaaatgttctccaa[A/G]ttactctagaagctga	A	G	NM_019049 // intron // 0 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_144977 // intron // 0 // Hs.497279 // FAM31B // 163486 // Homo sapiens family with sequence similarity 31, member B (FAM31B),	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-2257967	ctttgtctatcctagc[C/T]aaaatagtcttctgcc	C	T	NM_019049 // upstream // 202662 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_019049 // upstream // 10530 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054)	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-2141655	atcttccaagctgggc[C/T]ctacatccctatacta	C	T	NM_019049 // upstream // 204767 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054), mRNA. /// NM_019049 // upstream // 12635 // Hs.497279 // FLJ20054 // 54530 // Homo sapiens hypothetical protein FLJ20054 (FLJ20054)	FLJ20054	FLJ20054, Homo sapiens hypothetical protein FLJ20054 (FLJ20054), q31.3
SNP_A-1952893	tttcttatactgagat[A/G]aaactgaagctcaaaa	A	G	AJ277915 // downstream // 77860 // Hs.442578 // LHX9 // 56956 // Homo sapiens partial mRNA for LIM-homeobox 9 (LHX9 gene). /// NM_020204 // downstream // 76976 // Hs.442578 // LHX9 // 56956 // Homo sapiens LIM homeobox 9 (LHX9), mRNA. /// NM_133494 // ups	LHX9	LHX9, Homo sapiens partial for LIM-homeobox 9 (LHX9 gene). q31.3
SNP_A-2231362	ctattgaaagtgacta[A/T]gtctattggtaggtct	A	T	AJ277915 // downstream // 180970 // Hs.442578 // LHX9 // 56956 // Homo sapiens partial mRNA for LIM-homeobox 9 (LHX9 gene). /// NM_020204 // downstream // 180086 // Hs.442578 // LHX9 // 56956 // Homo sapiens LIM homeobox 9 (LHX9), mRNA. /// NM_133494 // u	LHX9	LHX9, Homo sapiens partial for LIM-homeobox 9 (LHX9 gene). q31.3
SNP_A-1720263	tgttttgatcaaagtcacagattac[A/G]cttcaatatagctgccagtaaactg	A	G	NM_019049 // intron // 0 // Hs.101590 // FLJ20054 // 54530 // hypothetical protein FLJ20054 /// NM_144977 // intron // 0 // Hs.351233 // FAM31B // 163486 // family with sequence similarity 31, member B	FLJ20054	FLJ20054 , rs10494758, hypothetical protein FLJ20054 ,q31.3
SNP_A-1836193	tactatagacacatga[A/T]aaaacagcaaactgca	A	T	NM_133494 // downstream // 84626 // Hs.24119 // NEK7 // 140609 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 7 (NEK7), mRNA. /// NM_133262 // downstream // 118959 // Hs.127743 // ATP6V1G3 // 127124 // Homo sapiens ATPase, H+ transporting,	NEK7	NEK7, Homo sapiens NIMA (never in mitosis gene a)-related kinase 7 (NEK7), q31.3
SNP_A-1719405	atgctaaacagaagactggtatcta[A/T]gagtttgtaaggtgtcagattttcc	A	T	NM_002838 // upstream // 571745 // Hs.444324 // PTPRC // 5788 // protein tyrosine phosphatase, receptor type, C /// NM_020204 // downstream // 138084 // Hs.442578 // LHX9 // 56956 // LIM homeobox 9 /// NM_080921 // upstream // 571745 // Hs.444324 // PTPR	PTPRC	PTPRC , rs1233832, protein tyrosine phosphatase, receptor type, C ,q31.3
SNP_A-2219125	cctgtataacaagcct[A/G]aacatttatccctgaa	A	G	NM_080922 // downstream // 348061 // Hs.192039 // PTPRC // 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 348061 // Hs.192039 // PTPRC // 5788 // Homo sapiens protein	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3
SNP_A-1979468	tagaaggttgtatcaa[C/G]tctgctttctctgtac	C	G	NM_080922 // downstream // 399972 // Hs.192039 // PTPRC // 5788 // Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA. /// NM_002838 // downstream // 399972 // Hs.192039 // PTPRC // 5788 // Homo sapiens protein	PTPRC	PTPRC, Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1713328	gaattgtgggtttccttccactgc[A/G]catgaaacataagcaatc atttatt	A	G	NM_002838 // downstream // 469562 // Hs.444324 // PTPRC // 5788 // protein tyrosine phosphatase, receptor type, C /// NM_003822 // upstream // 800878 // Hs.183123 // NR5A2 // 2494 // nuclear receptor subfamily 5, group A, member 2 /// NM_080921 // downst	PTPRC	PTPRC , rs10494786, protein tyrosine phosphatase, receptor type, C , q32.1
SNP_A-1851704	tattcttgaaacaacc[G/T]tcagatctccaacttc	G	T	NM_003822 // intron // 0 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // intron // 0 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-2056827	aataggcaagggaaaa[C/T]ggtatgctggaatttc	C	T	NM_003822 // intron // 0 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // intron // 0 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-2031188	aaaggcatttcattccc[A/G]cctaactcctgatgac	A	G	NM_003822 // intron // 0 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // intron // 0 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-2256417	cttatgaaaataaac[A/G]caaacattctgaggat	A	G	NM_003822 // downstream // 14777 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 14777 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear re	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-2080993	acctctttactgtgaj[A/G]actctacatctgattc	A	G	NM_003822 // downstream // 19336 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 19336 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear re	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-1652378	cagatattgtctatttgaaaatttc[A/C]ctatttttgtcatcatgtttgaat ga	A	C	NM_002838 // downstream // 920620 // Hs.444324 // PTPRC // 5788 // protein tyrosine phosphatase, receptor type, C /// NM_003822 // upstream // 349820 // Hs.183123 // NR5A2 // 2494 // nuclear receptor subfamily 5, group A, member 2 /// NM_080921 // downst	PTPRC	PTPRC , rs962923, protein tyrosine phosphatase, receptor type, C , q32.1
SNP_A-1932532	ttcctggtaagagaccc[A/G]gagacccaatttcagg	A	G	NM_003822 // downstream // 138749 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 138749 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-2300052	gcctcacaaggacaaa[C/T]gtaaactcttgaacac	C	T	NM_003822 // downstream // 139505 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 139505 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-1907909	tgtaatctggtcttgaj[A/C]gcctccaggaatctgtc	A	C	NM_003822 // downstream // 153489 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, mRNA. /// NM_205860 // downstream // 153489 // Hs.33446 // NR5A2 // 2494 // Homo sapiens nuclear	NR5A2	NR5A2, Homo sapiens nuclear receptor subfamily 5, group A, member 2 (NR5A2), transcript variant 2, q32.1
SNP_A-1979852	ctcaatcgtaaaagtc[C/T]gacacggctggtcaca	C	T	NM_012482 // upstream // 33307 // Hs.59757 // ZNF281 // 23528 // Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /// D26361 // downstream // 110043 // Hs.3104 // KIF14 // 9928 // Homo sapiens KIAA0042 mRNA, partial cds. /// ENST00000294740 // upstrea	ZNF281	ZNF281, Homo sapiens zinc finger protein 281 (ZNF281), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1841271	taggaaccaggccaca[C/T]gacaggagtgagtgca	C	T	NM_012482 // upstream // 36933 // Hs.59757 // ZNF281 // 23528 // Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /// D26361 // downstream // 106417 // Hs.3104 // KIF14 // 9928 // Homo sapiens KIAA0042 mRNA, partial cds. /// ENST00000294740 // upstrea	ZNF281	ZNF281, Homo sapiens zinc finger protein 281 (ZNF281), q32.1
SNP_A-1785651	ggctcctccgaactga[C/T]atttggagatgtttt	C	T	NM_012482 // upstream // 57262 // Hs.59757 // ZNF281 // 23528 // Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /// D26361 // downstream // 86088 // Hs.3104 // KIF14 // 9928 // Homo sapiens KIAA0042 mRNA, partial cds. /// ENST00000294740 // upstream	ZNF281	ZNF281, Homo sapiens zinc finger protein 281 (ZNF281), q32.1
SNP_A-2277281	gagatccagttgaac[C/T]gtcaggctctgagaag	C	T	NM_012482 // upstream // 83651 // Hs.59757 // ZNF281 // 23528 // Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /// D26361 // downstream // 59699 // Hs.3104 // KIF14 // 9928 // Homo sapiens KIAA0042 mRNA, partial cds. /// ENST00000294740 // upstream	ZNF281	ZNF281, Homo sapiens zinc finger protein 281 (ZNF281), q32.1
SNP_A-1979871	ctttgaatctttctta[C/G]acacaggacttgagg	C	G	NM_012482 // upstream // 90504 // Hs.59757 // ZNF281 // 23528 // Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /// D26361 // downstream // 52846 // Hs.3104 // KIF14 // 9928 // Homo sapiens KIAA0042 mRNA, partial cds. /// ENST00000294740 // upstream	ZNF281	ZNF281, Homo sapiens zinc finger protein 281 (ZNF281), q32.1
SNP_A-2273037	gactatacaggtataa[A/G]aagctagctctgttta	A	G	NM_031306 // upstream // 53355 // Hs.497332 // DKFZP564B1023 // 83479 // Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA. /// NM_203459 // upstream // 16296 // Hs.23585 // KIAA1078 // 23271 // Homo sapiens KIAA1078 protein (KIAA1078)	DKFZP564B10 23	DKFZP564B1023, Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), q32.1
SNP_A-1720867	tttattcactcaggactaattacc[A/G]actttttatatgaagcagc attacg	A	G	NM_003822 // intron // 0 // Hs.183123 // NR5A2 // 2494 // nuclear receptor subfamily 5, group A, member 2	NR5A2	NR5A2 , rs7556049, nuclear receptor subfamily 5, group A, member 2,q32.1
SNP_A-1904317	tgggctgctcaggccaa[A/T]aggatttccaagtttt	A	T	NM_031306 // upstream // 64871 // Hs.497332 // DKFZP564B1023 // 83479 // Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA. /// NM_203459 // upstream // 4780 // Hs.23585 // KIAA1078 // 23271 // Homo sapiens KIAA1078 protein (KIAA1078).	DKFZP564B10 23	DKFZP564B1023, Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), q32.1
SNP_A-1979910	tcaaggtgattaggca[C/T]gatttctggccctgag	C	T	NM_031306 // upstream // 65719 // Hs.497332 // DKFZP564B1023 // 83479 // Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA. /// NM_203459 // upstream // 3932 // Hs.23585 // KIAA1078 // 23271 // Homo sapiens KIAA1078 protein (KIAA1078).	DKFZP564B10 23	DKFZP564B1023, Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), q32.1
SNP_A-1680784	atggaaagagaatacggacaaggag[A/G]cccttaggaagttg atgagaagcg	A	G	NM_003822 // downstream // 154699 // Hs.183123 // NR5A2 // 2494 // nuclear receptor subfamily 5, group A, member 2 /// NM_012482 // downstream // 76399 // Hs.59757 // ZNF281 // 23528 // zinc finger protein 281	NR5A2	NR5A2 , rs10494812, nuclear receptor subfamily 5, group A, member 2 ,q32.1
SNP_A-2031745	aaagtaggtgactttc[A/G]atcccaagtacatg	A	G	NM_018265 // downstream // 21610 // Hs.518997 // FLJ10901 // 55765 // Homo sapiens hypothetical protein FLJ10901 (FLJ10901), mRNA. /// AB007918 // downstream // 32047 // Hs.169182 // KIF21B // 23046 // Homo sapiens mRNA for KIAA0449 protein, partial cds.	FLJ10901	FLJ10901, Homo sapiens hypothetical protein FLJ10901 (FLJ10901), q32.1
SNP_A-2264597	gaagaagtgtcctcc[C/T]agtcacattcagccag	C	T	NM_000069 // intron // 0 // Hs.1294 // CACNA1S // 779 // Homo sapiens calcium channel, voltage-dependent, L type, alpha 1S subunit (CACNA1S), mRNA. /// ENST00000263942 // intron // 0 // --- // --- // --- // --- // -	CACNA1S	CACNA1S, Homo sapiens calcium channel, voltage-dependent, L type, alpha 1S subunit (CACNA1S), q32.1
SNP_A-1662940	ggagaaagaatgctaagctaattga[A/T]gacaataagaggttc acttggttga	A	T	NM_031306 // upstream // 64399 // Hs.95321 // DKFZP564B1023 // 83479 // hypothetical protein DKFZp564B1023	DKFZP564B10 23	DKFZP564B1023 , rs10494820, hypothetical protein DKFZp564B1023,q32.1
SNP_A-1653268	accaatgatatatttagaaactaa[A/G]tccggctacagtagatttt aggttgt	A	G	AB029001 // intron // 0 // Hs.23585 // KIAA1078 // 23271 // KIAA1078 protein	KIAA1078	KIAA1078 , rs2047147, KIAA1078 protein,q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1851643	tattctggatagctgg[A/G]catagctcccctctga	A	G	NM_004078 // intron // 0 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// ENST00000340006 // intron // 0 // — // — // — // —	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2272642	gacgctggtgtcagaa[A/C]gtgtgcaaggcttccg	A	C	NM_004078 // intron // 0 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// ENST00000340006 // intron // 0 // — // — // — // —	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-1810390	gtgattaagcaacatc[C/T]gagagcaaagagaggg	C	T	NM_004078 // intron // 0 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// ENST00000340006 // intron // 0 // — // — // — // —	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2260157	gaaaatctgctcagga[C/T]gtctcttagccaggct	C	T	NM_004078 // intron // 0 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// ENST00000340006 // intron // 0 // — // — // — // —	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-1879907	tcttcctacccatttg[C/T]aatcaatctcaccctc	C	T	NM_004078 // upstream // 19957 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 121243 // Hs.497369 // NAV1 // 89796 // Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST0000	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-1784546	ggcctaaatagaacga[A/G]aaaggctgactctccc	A	G	NM_004078 // upstream // 21719 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 119481 // Hs.497369 // NAV1 // 89796 // Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST0000	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2090892	actttccactcgaggc[A/G]caggaatatcattgtc	A	G	NM_004078 // upstream // 27105 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 114095 // Hs.497369 // NAV1 // 89796 // Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST0000	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2190809	catagagatgggaagt[A/C]aaatggcggttgccgg	A	C	NM_004078 // upstream // 36746 // Hs.108080 // CSRP1 // 1465 // Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /// NM_020443 // upstream // 104454 // Hs.497369 // NAV1 // 89796 // Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST0000	CSRP1	CSRP1, Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), q32.1
SNP_A-2000604	agctctgtctgggatc[C/T]gagaaggaattagaaa	C	T	NM_020443 // intron // 0 // Hs.497369 // NAV1 // 89796 // Homo sapiens neuron navigator 1 (NAV1), mRNA. /// ENST00000295624 // intron // 0 // — // — // — // — // — /// ENST00000358222 // intron // 0 // — // — // — // —	NAV1	NAV1, Homo sapiens neuron navigator 1 (NAV1), q32.1
SNP_A-1980242	ggaactggccagtcag[A/G]taagaaatacagtcta	A	G	NM_020443 // downstream // 45755 // Hs.497369 // NAV1 // 89796 // Homo sapiens neuron navigator 1 (NAV1), mRNA. /// NM_012134 // downstream // 28152 // Hs.519075 // LMOD1 // 25802 // Homo sapiens leiomodin 1 (smooth muscle) (LMOD1), mRNA. /// ENST00000295	NAV1	NAV1, Homo sapiens neuron navigator 1 (NAV1), q32.1
SNP_A-2290588	gcaagaaacctctgac[C/T]ctgaaagattaaaact	C	T	NM_004433 // downstream // 10263 // Hs.67928 // ELF3 // 1999 // Homo sapiens E74-like factor 3 (ets domain transcription factor, epithelial-specific) (ELF3), mRNA. /// NM_004767 // upstream // 96635 // Hs.132049 // GPR37L1 // 9283 // Homo sapiens G-prote	ELF3	ELF3, Homo sapiens E74-like factor 3 (ets domain transcription factor, epithelial-specific) (ELF3), q32.1
SNP_A-2128112	ataagctacgtttaga[C/T]tcattatgcatagatc	C	T	NM_080589 // upstream // 1355 // Hs.402773 // PTPN7 // 5778 // Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7), transcript variant 3, mRNA. /// NM_002832 // upstream // 1355 // Hs.402773 // PTPN7 // 5778 // Homo sapiens protein tyro	PTPN7	PTPN7, Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7), transcript variant 3, q32.1
SNP_A-2053081	aagtctaagcaaaggg[G/T]cacaacactcttggca	G	T	NM_032105 // intron // 0 // Hs.444403 // PPP1R12B // 4660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12B (PPP1R12B), transcript variant 2, mRNA. /// NM_002481 // intron // 0 // Hs.444403 // PPP1R12B // 4660 // Homo sapiens prote	PPP1R12B	PPP1R12B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12B (PPP1R12B), transcript variant 2, q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2088313	actgtaaaacgtgcca[C/T]atgatagtttgaaaac	C	T	NM_177402 // intron // 0 // Hs.447005 // SYT2 // 127833 // Homo sapiens synaptotagmin II (SYT2), mRNA. /// ENST00000317518 // intron // 0 // — // — // —	SYT2	SYT2, Homo sapiens synaptotagmin II (SYT2), q32.1
SNP_A-2197288	cattcagtccatagca[C/T]gcatttgtcaattat	C	T	NM_177402 // intron // 0 // Hs.447005 // SYT2 // 127833 // Homo sapiens synaptotagmin II (SYT2), mRNA. /// ENST00000317518 // intron // 0 // — // — // —	SYT2	SYT2, Homo sapiens synaptotagmin II (SYT2), q32.1
SNP_A-1862712	tcattcaggctctaaa[C/T]ggcaaatgagatcaga	C	T	NM_177402 // intron // 0 // Hs.447005 // SYT2 // 127833 // Homo sapiens synaptotagmin II (SYT2), mRNA. /// ENST00000317518 // intron // 0 // — // — // —	SYT2	SYT2, Homo sapiens synaptotagmin II (SYT2), q32.1
SNP_A-2284806	gatcattggaatgaag[C/T]aaaaagtgcttaatac	C	T	NM_177402 // intron // 0 // Hs.447005 // SYT2 // 127833 // Homo sapiens synaptotagmin II (SYT2), mRNA. /// ENST00000317518 // intron // 0 // — // — // —	SYT2	SYT2, Homo sapiens synaptotagmin II (SYT2), q32.1
SNP_A-2307907	gcttctgaagccatcc[G/T]aatccactggccagtt	G	T	NM_177402 // upstream // 12720 // Hs.447005 // SYT2 // 127833 // Homo sapiens synaptotagmin II (SYT2), mRNA. /// NM_006618 // downstream // 4268 // Hs.443650 // JARID1B // 10765 // Homo sapiens Jumonji, AT rich interactive domain 1B (RBP2-like) (JARID1B),	SYT2	SYT2, Homo sapiens synaptotagmin II (SYT2), q32.1
SNP_A-1980356	gaaataagtatagatat[C/T]agcaagtgccattata	C	T	NM_006618 // intron // 0 // Hs.443650 // JARID1B // 10765 // Homo sapiens Jumonji, AT rich interactive domain 1B (RBP2-like) (JARID1B), mRNA. /// ENST00000255407 // intron // 0 // — // — // — /// ENST00000235790 // intron // 0 // — // — /	JARID1B	JARID1B, Homo sapiens Jumonji, AT rich interactive domain 1B (RBP2-like) (JARID1B), q32.1
SNP_A-2207695	ccattttcgtagtgaa[C/T]tgggaagcaaggtcac	C	T	NM_000674 // intron // 0 // Hs.77867 // ADORA1 // 134 // Homo sapiens adenosine A1 receptor (ADORA1), mRNA. /// ENST00000309502 // intron // 0 // — // — // — /// ENST00000337894 // intron // 0 // — // — // — // —	ADORA1	ADORA1, Homo sapiens adenosine A1 receptor (ADORA1), q32.1
SNP_A-2192255	catcagggctgggcta[A/G]atctgacacttggtga	A	G	NM_000674 // intron // 0 // Hs.77867 // ADORA1 // 134 // Homo sapiens adenosine A1 receptor (ADORA1), mRNA. /// ENST00000309502 // intron // 0 // — // — // — /// ENST00000337894 // intron // 0 // — // — // — // —	ADORA1	ADORA1, Homo sapiens adenosine A1 receptor (ADORA1), q32.1
SNP_A-2223653	cggagtgactggaaa[C/T]gatggtatcgctgaca	C	T	NM_003465 // upstream // 74445 // Hs.201688 // CHIT1 // 1118 // Homo sapiens chitinase 1 (chitotriosidase) (CHIT1), mRNA. /// NM_006763 // upstream // 1443 // Hs.519162 // BTG2 // 7832 // Homo sapiens BTG family, member 2 (BTG2), mRNA. /// ENST00000255427	CHIT1	CHIT1, Homo sapiens chitinase 1 (chitotriosidase) (CHIT1), q32.1
SNP_A-2309014	gcttttctcatctgca[C/T]agtctgtcctccgtc	C	T	NM_003465 // upstream // 74590 // Hs.201688 // CHIT1 // 1118 // Homo sapiens chitinase 1 (chitotriosidase) (CHIT1), mRNA. /// NM_006763 // upstream // 1298 // Hs.519162 // BTG2 // 7832 // Homo sapiens BTG family, member 2 (BTG2), mRNA. /// ENST00000255427	CHIT1	CHIT1, Homo sapiens chitinase 1 (chitotriosidase) (CHIT1), q32.1
SNP_A-1790517	gggcattcatgcctg[A/G]acttaaacaatactat	A	G	NM_006763 // 3UTR // 0 // Hs.519162 // BTG2 // 7832 // Homo sapiens BTG family, member 2 (BTG2), mRNA. /// ENST00000290551 // 3UTR // 0 // — // — // — // —	BTG2	BTG2, Homo sapiens BTG family, member 2 (BTG2), q32.1
SNP_A-2218545	cctggatcctgataag[C/G]agttctgggtggagga	C	G	NM_006763 // downstream // 2448 // Hs.519162 // BTG2 // 7832 // Homo sapiens BTG family, member 2 (BTG2), mRNA. /// NM_002023 // downstream // 28582 // Hs.519168 // FMOD // 2331 // Homo sapiens fibromodulin (FMOD), mRNA. /// ENST00000290551 // downstream	BTG2	BTG2, Homo sapiens BTG family, member 2 (BTG2), q32.1
SNP_A-2279546	gaggaattgccaacaaa[A/G]tttcagtataacttct	A	G	NM_006763 // downstream // 21553 // Hs.519162 // BTG2 // 7832 // Homo sapiens BTG family, member 2 (BTG2), mRNA. /// NM_002023 // downstream // 9477 // Hs.519168 // FMOD // 2331 // Homo sapiens fibromodulin (FMOD), mRNA. /// ENST00000290551 // downstream	BTG2	BTG2, Homo sapiens BTG family, member 2 (BTG2), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2222054	cgaagagccatcaccc[C/T]gagggaacctgttttg	C	T	NM_002023 // upstream // 52646 // Hs.519168 // FMOD // 2331 // Homo sapiens fibromodulin (FMOD), mRNA. /// NM_201348 // upstream // 72003 // Hs.76494 // PRELP // 5549 // Homo sapiens proline arginine-rich end leucine-rich repeat protein (PRELP), transcrip	FMOD	FMOD, Homo sapiens fibromodulin (FMOD), q32.1
SNP_A-2269290	gaatttctctttcttc[C/T]catatctcctgttata	C	T	NM_014359 // downstream // 104339 // Hs.467538 // OPTC // 26254 // Homo sapiens opticin (OPTC), mRNA. /// M83363 // upstream // 13358 // Hs.343522 // ATP2B4 // 493 // Human plasma membrane calcium-pumping ATPase (PMCA4) mRNA, complete cds. /// NM_00100139	OPTC	OPTC, Homo sapiens opticin (OPTC), q32.1
SNP_A-1789516	gggcctgatagataca[C/T]aaattttgctccagcc	C	T	NM_014359 // downstream // 104491 // Hs.467538 // OPTC // 26254 // Homo sapiens opticin (OPTC), mRNA. /// M83363 // upstream // 13206 // Hs.343522 // ATP2B4 // 493 // Human plasma membrane calcium-pumping ATPase (PMCA4) mRNA, complete cds. /// NM_00100139	OPTC	OPTC, Homo sapiens opticin (OPTC), q32.1
SNP_A-1642993	caggccatccactacctctttatcc[C/T]gacctgaggaacgtgc acttagcgc	C	T	NM_000674 // intron // 0 // Hs.77867 // ADORA1 // 134 // adenosine A1 receptor	ADORA1	ADORA1 , rs722915, adenosine A1 receptor,q32.1
SNP_A-2268291	gaatgatcactaaaaa[A/T]cttagcaagaggaagg	A	T	NM_018208 // intron // 0 // Hs.497469 // ETNK2 // 55224 // Homo sapiens ethanolamine kinase 2 (ETNK2), mRNA. /// ENST00000306755 // intron // 0 // — // — // — // —	ETNK2	ETNK2, Homo sapiens ethanolamine kinase 2 (ETNK2), q32.1
SNP_A-2293103	gcagacccagcttaga[C/T]gattgctgcagcttgg	C	T	NM_018208 // intron // 0 // Hs.497469 // ETNK2 // 55224 // Homo sapiens ethanolamine kinase 2 (ETNK2), mRNA. /// ENST00000306755 // intron // 0 // — // — // — // —	ETNK2	ETNK2, Homo sapiens ethanolamine kinase 2 (ETNK2), q32.1
SNP_A-1675688	gggcagggacagggagagtctatac[C/T]agatgtgcatgcac atttcatatag	C	T	NM_001684 // intron // 0 // Hs.343522 // ATP2B4 // 493 // ATPase, Ca++ transporting, plasma membrane 4	ATP2B4	ATP2B4 , rs10494845, ATPase, Ca++ transporting, plasma membrane 4,q32.1
SNP_A-2175179	cacagttatttccaaa[C/G]tgtcaagaagatggta	C	G	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2233984	ctcatggtcatctcaa[A/G]ccagttcaatggaatc	A	G	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2103910	agcactcttggagctc[A/G]atctctagggtatgtg	A	G	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-1891397	tgattatggctggtgc[A/G]gagtagaccacaggag	A	G	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2235610	ctcctagctatgatga[A/G]gtgcagtaaaagtcca	A	G	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2074749	acatatgtggatggaa[C/T]atttcagaacaacttg	C	T	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1
SNP_A-2078437	accatcctgaagtacc[A/G]attctccttatcagaa	A	G	NM_014935 // intron // 0 // Hs.253146 // PLEKHA6 // 22874 // Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), mRNA. /// ENST00000272203 // intron // 0 // — // — // — // —	PLEKHA6	PLEKHA6, Homo sapiens pleckstrin homology domain containing, family A member 6 (PLEKHA6), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215261	cctcaacctactcca[A/G]agatttctccctgac	A	G	NM_002646 // intron // 0 // Hs.497487 // PIK3C2B // 5287 // Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B), mRNA. /// ENST00000255417 // intron // 0 // — // — // —	PIK3C2B	PIK3C2B, Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B), q32.1
SNP_A-2025746	aaaatgccagagcatc[A/G]aaagacaaagtggctc	A	G	NM_201630 // upstream // 13545 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 // upstream // 13545 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-2039703	aacatggctgtgtata[C/T]gaaatggtttggattt	C	T	NM_201630 // upstream // 89229 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 // upstream // 89229 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-2122311	agtgcatgctttatca[C/T]ggcctatcatctggc	C	T	NM_201630 // upstream // 114363 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 // upstream // 114363 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neurona	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-1732528	gggctggtagctgaagcagaaatca[A/G]ttatgcctgtgttgtttgt ctccca	A	G	NM_014935 // upstream // 5721 // Hs.343666 // PEPP3 // 22874 // phosphoinositol 3-phosphate-binding protein-3 /// NM_032833 // downstream // 40061 // Hs.355489 // PPP1R15B // 84919 // protein phosphatase 1, regulatory (inhibitor) subunit 15B	PEPP3	PEPP3 , rs955323, phosphoinositol 3-phosphate-binding protein-3 , q32.1
SNP_A-2185341	caggaatggaatttca[C/T]ctacgtacagtggaag	C	T	NM_201630 // upstream // 138398 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 // upstream // 138398 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neurona	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-2000618	aggtactgaaccaaac[A/T]gttctttacaaatgtt	A	T	NM_201630 // upstream // 141967 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, mRNA. /// NM_006338 // upstream // 141967 // Hs.26312 // LRRN5 // 10446 // Homo sapiens leucine rich repeat neurona	LRRN5	LRRN5, Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 2, q32.1
SNP_A-1709563	cctctctgctggactttccacctc[C/T]gttcacccacgtctcaaac tcggt	C	T	NM_002646 // intron // 0 // Hs.343329 // PIK3C2B // 5287 // phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	PIK3C2B , rs1877394, phosphoinositide-3-kinase, class 2, beta polypeptide, q32.1
SNP_A-2081698	accttcagattcaaca[A/G]acataagaacatcata	A	G	NM_030952 // intron // 0 // Hs.497512 // SNARK // 81788 // Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK), mRNA. /// ENST00000295786 // intron // 0 // — // — // —	SNARK	SNARK, Homo sapiens likely ortholog of rat SNF1 q32.1
SNP_A-2297089	gccacacaactggtaa[C/T]aaagtggcgggattta	C	T	NM_030952 // upstream // 1537 // Hs.497512 // SNARK // 81788 // Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK), mRNA. /// NM_018203 // downstream // 13228 // Hs.10414 // FLJ10748 // 55220 // Homo sapiens hypothetical protein	SNARK	SNARK, Homo sapiens likely ortholog of rat SNF1,q32.1
SNP_A-1861493	tcatccagatgattag[A/G]attctcaaaggaagt	A	G	NM_030952 // upstream // 2081 // Hs.497512 // SNARK // 81788 // Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK), mRNA. /// NM_018203 // downstream // 12684 // Hs.10414 // FLJ10748 // 55220 // Homo sapiens hypothetical protein	SNARK	SNARK, Homo sapiens likely ortholog of rat SNF1,q32.1
SNP_A-1955323	ttgggccacaatctgt[C/T]atttggtgggagtggt	C	T	NM_018203 // intron // 0 // Hs.10414 // FLJ10748 // 55220 // Homo sapiens hypothetical protein FLJ10748 (FLJ10748), mRNA. /// ENST00000294958 // intron // 0 // — // — // — // —	FLJ10748	FLJ10748, Homo sapiens hypothetical protein FLJ10748 (FLJ10748), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872841	tctatatcatgctaaa[C/T]tcctgcactgaggttc	C	T	NM_001001552 // upstream // 13053 // Hs.181245 // LEMD1 // 93273 // Homo sapiens LEM domain containing 1 (LEMD1), mRNA. /// NM_002596 // upstream // 69490 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3	LEMD1	LEMD1, Homo sapiens LEM domain containing 1 (LEMD1), q32.1
SNP_A-2280573	gaggtaggtgttatca[C/T]gaccattttacagatg	C	T	NM_001001552 // upstream // 43559 // Hs.181245 // LEMD1 // 93273 // Homo sapiens LEM domain containing 1 (LEMD1), mRNA. /// NM_002596 // upstream // 38984 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3	LEMD1	LEMD1, Homo sapiens LEM domain containing 1 (LEMD1), q32.1
SNP_A-1868273	tcctcagatgtccatc[A/T]ctatccctgttgctct	A	T	NM_001001552 // upstream // 46353 // Hs.181245 // LEMD1 // 93273 // Homo sapiens LEM domain containing 1 (LEMD1), mRNA. /// NM_002596 // upstream // 36190 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3	LEMD1	LEMD1, Homo sapiens LEM domain containing 1 (LEMD1), q32.1
SNP_A-1878562	tctgtgtaaacatcag[C/T]atcgtataaggaagaa	C	T	NM_002596 // intron // 0 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3, mRNA. /// NM_212503 // intron // 0 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript va	PCTK3	PCTK3, Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3, q32.1
SNP_A-1809586	gtgagatgacccggaa[A/G]catcttagagttagac	A	G	NM_002596 // downstream // 31169 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3, mRNA. /// NM_212503 // downstream // 31169 // Hs.445402 // PCTK3 // 5129 // Homo sapiens PCTAIRE protein kinase 3 (PCTK3	PCTK3	PCTK3, Homo sapiens PCTAIRE protein kinase 3 (PCTK3), transcript variant 3, q32.1
SNP_A-1683500	tttgctgccacctgacttgaagctc[C/T]gaccaccccagtgctact ctgctc	C	T	NM_014858 // downstream // 16086 // Hs.6360 // HUCEP11 // 9911 // cerebral protein 11 /// NM_030952 // downstream // 13855 // Hs.172012 // SNARK // 81788 // likely ortholog of rat SNF1/AMP-activated protein kinase	HUCEP11	HUCEP11 , rs1562866, cerebral protein 11 ,q32.1
SNP_A-1802599	gtatctgttcaggccc[A/G]gaatcgtcacggctca	A	G	NM_173854 // intron // 0 // Hs.20274 // SLC41A1 // 254428 // Homo sapiens solute carrier family 41, member 1 (SLC41A1), mRNA. /// ENST00000338314 // intron // 0 // — // — // — // —	SLC41A1	SLC41A1, Homo sapiens solute carrier family 41, member 1 (SLC41A1), q32.1
SNP_A-2240342	ctgaatttactgagta[C/T]agctgggaagccttga	C	T	NM_173854 // upstream // 4737 // Hs.20274 // SLC41A1 // 254428 // Homo sapiens solute carrier family 41, member 1 (SLC41A1), mRNA. /// NM_152491 // downstream // 10219 // Hs.177744 // FLJ32569 // 148811 // Homo sapiens hypothetical protein FLJ32569 (FLJ32	SLC41A1	SLC41A1, Homo sapiens solute carrier family 41, member 1 (SLC41A1), q32.1
SNP_A-2263989	gaactcacgaagaaca[C/T]tgtggctgataacaga	C	T	NM_152491 // CDS // 0 // Hs.177744 // FLJ32569 // 148811 // Homo sapiens hypothetical protein FLJ32569 (FLJ32569), mRNA. /// ENST00000342249 // CDS // 0 // — // — // — // — /// ENST00000294963 // CDS // 0 // — // — // — // —	FLJ32569	FLJ32569, Homo sapiens hypothetical protein FLJ32569 (FLJ32569), q32.1
SNP_A-1895300	tgccctctgccgtcca[A/G]aactgatattgcactg	A	G	NM_052934 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, mRNA. /// NM_134325 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens solute carrier family 26, m	SLC26A9	SLC26A9, Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, q32.1
SNP_A-1937888	ttgaatcctttcatga[A/G]gtaggcattattattc	A	G	NM_052934 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, mRNA. /// NM_134325 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens solute carrier family 26, m	SLC26A9	SLC26A9, Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, q32.1
SNP_A-2048754	aagccatggattggaa[A/G]taaatcaagagcaaaa	A	G	NM_052934 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, mRNA. /// NM_134325 // intron // 0 // Hs.164073 // SLC26A9 // 115019 // Homo sapiens solute carrier family 26, m	SLC26A9	SLC26A9, Homo sapiens solute carrier family 26, member 9 (SLC26A9), transcript variant 1, q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1876852	tctgccaacttaaagc[A/G]agattgtctggtctag	A	G	AB007925 // intron // 0 // Hs.497575 // SRGAP2 // 23380 // Homo sapiens mRNA for KIAA0456 protein, partial cds. /// ENST00000295713 // intron // 0 // — // — // — // —	SRGAP2	SRGAP2, Homo sapiens for KIAA0456 protein, partial cds. ,q32.1
SNP_A-1895602	tgcctcagagattgcc[G/T]acctgtggattaagaa	G	T	NM_000715 // downstream // 42705 // Hs.1012 // C4BPA // 722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 134021 // Hs.527653 // DAF // 1604 // Homo sapiens decay accelerating factor for compleme	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2
SNP_A-1845949	tatatacaacagaaaa[A/C]ctcaagcagttttata	A	C	NM_000715 // downstream // 101611 // Hs.1012 // C4BPA // 722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 75115 // Hs.527653 // DAF // 1604 // Homo sapiens decay accelerating factor for compleme	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2
SNP_A-1981503	cttgagataattggaa[A/G]acatggtatttctatt	A	G	NM_000715 // downstream // 106421 // Hs.1012 // C4BPA // 722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 70305 // Hs.527653 // DAF // 1604 // Homo sapiens decay accelerating factor for compleme	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2
SNP_A-1798590	gtaacaacatagtcaa[A/G]ttcagttgttaccaaa	A	G	NM_000715 // downstream // 152918 // Hs.1012 // C4BPA // 722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 23808 // Hs.527653 // DAF // 1604 // Homo sapiens decay accelerating factor for compleme	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2
SNP_A-1904398	tggggaaacaggttga[A/G]taacacagtagggagt	A	G	NM_000715 // downstream // 176110 // Hs.1012 // C4BPA // 722 // Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA. /// NM_000574 // upstream // 616 // Hs.527653 // DAF // 1604 // Homo sapiens decay accelerating factor for complement	C4BPA	C4BPA, Homo sapiens complement component 4 binding protein, alpha (C4BPA), q32.2
SNP_A-2055661	aataatgcttagcaca[C/T]agaaggagctccataa	C	T	NM_001877 // downstream // 3083 // Hs.445757 // CR2 // 1380 // Homo sapiens complement component (3d/Epstein Barr virus) receptor 2 (CR2), transcript variant 2, mRNA. /// ENST00000324539 // downstream // 3083 // — // — // — // — /// ENST00000035887	CR2	CR2, Homo sapiens complement component (3d q32.2
SNP_A-2301967	gcgtcatgtgtatcta[C/T]gtccaaattatattta	C	T	NM_172350 // intron // 0 // Hs.510402 // MCP // 4179 // Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, mRNA. /// NM_172357 // intron // 0 // Hs.510402 // MCP // 4179 // Homo sapien	MCP	MCP, Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, q32.2
SNP_A-1896003	tgccttgaggaagata[C/T]gattggaaaatcaaga	C	T	NM_172350 // 3UTR // 0 // Hs.510402 // MCP // 4179 // Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, mRNA. /// NM_172357 // 3UTR // 0 // Hs.510402 // MCP // 4179 // Homo sapiens me	MCP	MCP, Homo sapiens membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) (MCP), transcript variant n, q32.2
SNP_A-2070077	acacatatatctctgg[C/T]caccttcagagcaacc	C	T	NM_001773 // intron // 0 // Hs.374990 // CD34 // 947 // Homo sapiens CD34 antigen (CD34), mRNA. /// ENST00000356522 // intron // 0 // — // — // — // — // —	CD34	CD34, Homo sapiens CD34 antigen (CD34), q32.2
SNP_A-2027021	aaacagagatggaaga[C/T]gagacaaaaatgccat	C	T	NM_001773 // intron // 0 // Hs.374990 // CD34 // 947 // Homo sapiens CD34 antigen (CD34), mRNA. /// ENST00000356522 // intron // 0 // — // — // — // — /// ENST00000344045 // 5UTR // 0 // — // — // — // — /// ENST00000310833 // intron // 0	CD34	CD34, Homo sapiens CD34 antigen (CD34), q32.2
SNP_A-1752463	caactagctaaatacataaagcaaa[A/G]tcattaggaatttgata agcctaat	A	G	NM_000574 // downstream // 13407 // Hs.408864 // DAF // 1604 // decay accelerating factor for complement (CD55, Cromer blood group system) /// NM_025118 // downstream // 46692 // - // - // - // -	DAF	DAF , rs6540429, decay accelerating factor for complement (CD55, Cromer blood group system) ,q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800736	gtagaatagattagaa[C/T]aagaatatgctggagg	C	T	NM_025179 // intron // 0 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// ENST00000264296 // intron // 0 // --- // --- // --- // ---	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2047747	aagattgacgctatca[A/G]gcaagatcaagagtgt	A	G	NM_025179 // intron // 0 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// ENST00000264296 // intron // 0 // --- // --- // --- // ---	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1749801	ctaacctattcactcctaccataaa[G/T]gattcaagaaaactggt gtgagttt	G	T	NM_001773 // intron // 0 // Hs.374990 // CD34 // 947 // CD34 antigen	CD34	CD34 , rs6667619, CD34 antigen.q32.2
SNP_A-1982029	gcacctctgacctact[A/G]aagctatccatgaatc	A	G	NM_025179 // upstream // 510982 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 828964 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1982030	aggtcttcgtcagtta[C/T]acagtagttactgggt	C	T	NM_025179 // upstream // 511225 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 828721 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2264790	gaagacttctaaaaaac[A/G]attcaagtactgacag	A	G	NM_025179 // upstream // 521121 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 818825 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2287838	gattaggaggtagaca[A/G]tcaggctcctatgtgt	A	G	NM_025179 // upstream // 521554 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 818392 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1982031	ttgtgagcattccagg[A/C]acctctgaaaacaagc	A	C	NM_025179 // upstream // 523202 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 816744 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2277339	gagatttaacacacat[A/T]aaagagaaagccaggt	A	T	NM_025179 // upstream // 533350 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 806596 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1982032	agatcccaatgttata[C/T]ggactctttctctcc	C	T	NM_025179 // upstream // 533781 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 806165 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1982033	aactcctccaaaagaa[C/T]ggatgtctagatgaag	C	T	NM_025179 // upstream // 534049 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 805897 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2225918	ctaaatggaattcctg[A/G]acaaagtagggcaggt	A	G	NM_025179 // upstream // 595859 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 744087 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982092	ctgcactgtgaagagd[A/G]agtggtttgggaagca	A	G	NM_025179 // upstream // 724726 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 615220 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1982103	aaaaaatctttccca[C/T]catttaagtaactgca	C	T	NM_025179 // upstream // 780023 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 559923 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2190552	catacctaatgactaa[C/T]acagtgactggtgcaa	C	T	NM_025179 // upstream // 835173 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 504773 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1813021	gtgggtctctgagtca[C/T]ggcttaagtatttgg	C	T	NM_025179 // upstream // 852511 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 487435 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2243399	ctgcggaggcaagcgd[A/G]gaagaagtcattagtc	A	G	NM_025179 // upstream // 869934 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 470012 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2244884	ctggatttttcatcaga[A/G]tctaactgacctcaag	A	G	NM_025179 // upstream // 890320 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 449626 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. ///	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1830779	taatctcacagaaata[C/T]gaaagacccgcagaga	C	T	NM_025179 // upstream // 1032323 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 307623 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. //	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2285656	gatgaagtctcggaga[A/G]ggtagtgattctctgc	A	G	NM_025179 // upstream // 1039359 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 300587 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. //	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-1982187	agtgagtggcaagctct[A/T]aatttaaactctagca	A	T	NM_025179 // upstream // 1073411 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 266535 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. //	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2278977	gaggaaccagaaggggt[C/T]aatacagtcagatacc	C	T	NM_025179 // upstream // 1122975 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 216971 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. //	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2
SNP_A-2250959	cttatggttccatata[C/T]cttgctgatttttcat	C	T	NM_025179 // upstream // 1144136 // Hs.497626 // PLXNA2 // 5362 // Homo sapiens plexin A2 (PLXNA2), mRNA. /// NM_020439 // upstream // 195810 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. //	PLXNA2	PLXNA2, Homo sapiens plexin A2 (PLXNA2), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1680544	aggtgggctttataggcaaaaaaag[C/T]ctgaagaaaggaaaaacacggaacc	C	T	AY320401 // upstream // 626663 // Hs.510543 // - // 91170 // Nasopharyngeal carcinoma-associated antigen NPC-A-5 mRNA, complete cds	-	-, rs1166903, Nasopharyngeal carcinoma-associated antigen NPC-A-5 mRNA, complete cds,q32.2
SNP_A-1756182	cccaagtgagcgattcacactaaaac[A/G]ctatgttgacatatttcatgggatg	A	G	AY320401 // upstream // 548708 // Hs.510543 // - // 91170 // Nasopharyngeal carcinoma-associated antigen NPC-A-5 mRNA, complete cds	-	-, rs10494908, Nasopharyngeal carcinoma-associated antigen NPC-A-5 mRNA, complete cds,q32.2
SNP_A-2238360	ctctgggagctcctaa[C/T]ctaatgggggtgactc	C	T	NM_020439 // intron // 0 // Hs.199068 // CAMK1G // 57172 // Homo sapiens calcium/calmodulin-dependent protein kinase IG (CAMK1G), mRNA. /// ENST00000009105 // intron // 0 // — // — // —	CAMK1G	CAMK1G, Homo sapiens calcium,q32.2
SNP_A-1810371	gtgatgtggtatgaga[C/T]caggctgtacggcct	C	T	NM_015714 // downstream // 2165 // Hs.432132 // G0S2 // 50486 // Homo sapiens putative lymphocyte G0/G1 switch gene (G0S2), mRNA. /// NM_005525 // upstream // 7653 // Hs.195040 // HSD11B1 // 3290 // Homo sapiens hydroxysteroid (11-beta) dehydrogenase 1 (H	G0S2	G0S2, Homo sapiens putative lymphocyte G0,q32.2
SNP_A-2071087	acactgcccttaggac[C/G]aggcaagacaggtgcc	C	G	NM_006147 // intron // 0 // Hs.355827 // IRF6 // 3664 // Homo sapiens interferon regulatory factor 6 (IRF6), mRNA. /// ENST00000236254 // intron // 0 // — // — // — // —	IRF6	IRF6, Homo sapiens interferon regulatory factor 6 (IRF6), q32.2
SNP_A-1691658	ttaaaagaaatgcctggtcaaatag[C/T]gtagggaattactgaggaagaactt	C	T	AY320401 // downstream // 82296 // Hs.510543 // - // 91170 // Nasopharyngeal carcinoma-associated antigen NPC-A-5 mRNA, complete cds /// NM_020439 // upstream // 80118 // Hs.199068 // CAMK1G // 57172 // calcium/calmodulin-dependent protein kinase IG	-	-, rs10489336, Nasopharyngeal carcinoma-associated antigen NPC-A-5 mRNA, complete cds ,q32.2
SNP_A-2034690	aaatgaacagctgcaa[C/T]cttatatgtgagatgg	C	T	NM_018194 // intron // 0 // Hs.58650 // HHAT // 55733 // Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // — // — // — /// ENST00000308852 // intron // 0 // — // — // —	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-1684986	aggaggcaggacacagaatttccaa[C/T]gctcaggatccagctcatccaaatc	C	T	NM_025228 // intron // 0 // Hs.147434 // T3JAM // 80342 // TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator	T3JAM	T3JAM, rs10489341, TRAF3-interacting Jun N-terminal kinase (JNK)-activating modulator,q32.2
SNP_A-2046472	aagagagctacaaata[A/C]agaggtgagatccacc	A	C	NM_018194 // intron // 0 // Hs.58650 // HHAT // 55733 // Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // — // — // — /// ENST00000308852 // intron // 0 // — // — // —	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2294611	gcagtgagcaaaaaga[C/T]atgcaattcctaccgt	C	T	NM_018194 // intron // 0 // Hs.58650 // HHAT // 55733 // Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // — // — // — /// ENST00000308852 // intron // 0 // — // — // —	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2081319	acctggcagccttaa[C/T]tgaaaacattgcttga	C	T	NM_018194 // intron // 0 // Hs.58650 // HHAT // 55733 // Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // — // — // — /// ENST00000308852 // intron // 0 // — // — // —	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-1814280	gtgtcttctgtctta[C/T]gggcttttgtcttgac	C	T	NM_018194 // intron // 0 // Hs.58650 // HHAT // 55733 // Homo sapiens hedgehog acyltransferase (HHAT), mRNA. /// ENST00000261458 // intron // 0 // — // — // — /// ENST00000308852 // intron // 0 // — // — // —	HHAT	HHAT, Homo sapiens hedgehog acyltransferase (HHAT), q32.2
SNP_A-2212912	cccttgtctcagca[C/T]agattccttccacatt	C	T	NM_002238 // intron // 0 // Hs.527656 // KCNH1 // 3756 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, mRNA. /// NM_172362 // intron // 0 // Hs.527656 // KCNH1 // 3756 // Homo sapiens pot	KCNH1	KCNH1, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 1 (KCNH1), transcript variant 2, q32.2
SNP_A-1737669	tgacataagtcagtagataaaatatc[A/C]ctgcctatgtgtttcattgaaatgc	A	C	NM_018194 // upstream // 42496 // Hs.58650 // MART2 // 55733 // melanoma antigen recognized by T cells 2 /// NM_019605 // downstream // 43363 // Hs.445835 // SERTAD4 // 56256 // SERTA domain containing 4	MART2	MART2, rs645890, melanoma antigen recognized by T cells 2, q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982816	gtactgaggctatgtc[C/G]aagcacagagacagct	C	G	NM_004619 // intron // 0 // Hs.523930 // TRAF5 // 7188 // Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA. /// NM_145759 // intron // 0 // Hs.523930 // TRAF5 // 7188 // Homo sapiens TNF receptor-associated factor 5 (TRAF5	TRAF5	TRAF5, Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcript variant 1, q32.3
SNP_A-2213283	ccgctctacgacctaa[C/G]tcagctttgtggccag	C	G	NM_183059 // 3UTR // 0 // Hs.120090 // C1orf36 // 343035 // Homo sapiens chromosome 1 open reading frame 36 (C1orf36), mRNA. /// ENST00000359017 // 3UTR // 0 // — // — // — // —	C1orf36	C1orf36, Homo sapiens chromosome 1 open reading frame 36 (C1orf36), q32.3
SNP_A-2000674	gtggtagagagtgata[A/C]gtgcctcgttgcatgg	A	C	NM_183059 // upstream // 26230 // Hs.120090 // C1orf36 // 343035 // Homo sapiens chromosome 1 open reading frame 36 (C1orf36), mRNA. /// NM_021194 // downstream // 57024 // Hs.519469 // SLC30A1 // 7779 // Homo sapiens solute carrier family 30 (zinc transp	C1orf36	C1orf36, Homo sapiens chromosome 1 open reading frame 36 (C1orf36), q32.3
SNP_A-2275734	gagaccagtccctgcc[C/T]gcaaagaaattgagtc	C	T	NM_183059 // upstream // 39043 // Hs.120090 // C1orf36 // 343035 // Homo sapiens chromosome 1 open reading frame 36 (C1orf36), mRNA. /// NM_021194 // downstream // 44211 // Hs.519469 // SLC30A1 // 7779 // Homo sapiens solute carrier family 30 (zinc transp	C1orf36	C1orf36, Homo sapiens chromosome 1 open reading frame 36 (C1orf36), q32.3
SNP_A-2115387	aggggccactgggaga[C/T]cagcagaagacgccct	C	T	NM_183059 // upstream // 39968 // Hs.120090 // C1orf36 // 343035 // Homo sapiens chromosome 1 open reading frame 36 (C1orf36), mRNA. /// NM_021194 // downstream // 43286 // Hs.519469 // SLC30A1 // 7779 // Homo sapiens solute carrier family 30 (zinc transp	C1orf36	C1orf36, Homo sapiens chromosome 1 open reading frame 36 (C1orf36), q32.3
SNP_A-1883240	tgaaattcaaatttaa[G/T]ctggtgtactgctttt	G	T	NM_183059 // upstream // 40341 // Hs.120090 // C1orf36 // 343035 // Homo sapiens chromosome 1 open reading frame 36 (C1orf36), mRNA. /// NM_021194 // downstream // 42913 // Hs.519469 // SLC30A1 // 7779 // Homo sapiens solute carrier family 30 (zinc transp	C1orf36	C1orf36, Homo sapiens chromosome 1 open reading frame 36 (C1orf36), q32.3
SNP_A-2154363	attatgttgagctcta[A/G]aacaaaacactcagaa	A	G	D86960 // upstream // 79079 // Hs.497674 // LPGAT1 // 9926 // Homo sapiens mRNA for KIAA0205 gene, partial cds. /// NM_015434 // downstream // 30548 // Hs.369285 // DKFZP434B168 // 25896 // Homo sapiens DKFZP434B168 protein (DKFZP434B168), mRNA. /// ENST0	LPGAT1	LPGAT1, Homo sapiens for KIAA0205 gene, partial cds, q32.3
SNP_A-2187834	cagtagtgtttccttа[C/T]ctgcagtttttgcttt	C	T	D86960 // upstream // 108130 // Hs.497674 // LPGAT1 // 9926 // Homo sapiens mRNA for KIAA0205 gene, partial cds. /// NM_015434 // downstream // 1497 // Hs.369285 // DKFZP434B168 // 25896 // Homo sapiens DKFZP434B168 protein (DKFZP434B168), mRNA. /// ENST0	LPGAT1	LPGAT1, Homo sapiens for KIAA0205 gene, partial cds, q32.3
SNP_A-2292044	gcaccaacattggaca[C/T]tgaaggtctttttaat	C	T	NM_015434 // intron // 0 // Hs.369285 // DKFZP434B168 // 25896 // Homo sapiens DKFZP434B168 protein (DKFZP434B168), mRNA. /// ENST00000271775 // intron // 0 // — // — // — // —	DKFZP434B168	DKFZP434B168, Homo sapiens DKFZP434B168 protein (DKFZP434B168), q32.3
SNP_A-2168014	caactaacttgagaaa[A/C]ctgctgatatgaaata	A	C	NM_015434 // intron // 0 // Hs.369285 // DKFZP434B168 // 25896 // Homo sapiens DKFZP434B168 protein (DKFZP434B168), mRNA. /// ENST00000271775 // intron // 0 // — // — // — // —	DKFZP434B168	DKFZP434B168, Homo sapiens DKFZP434B168 protein (DKFZP434B168), q32.3
SNP_A-1802291	gtatatgtttccttca[A/G]cggttatttgagatgc	A	G	NM_016448 // intron // 0 // Hs.126774 // RAMP // 51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// ENST00000271754 // intron // 0 // — // — // — // — /// ENST00000318866 // intron // 0 // — // — // — // -	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-2244353	ctggaagttttattca[C/T]gtgctcttagctacta	C	T	NM_016448 // downstream // 73133 // Hs.126774 // RAMP // 51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 // upstream // 125971 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mR	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2112604	aggcacttcattgtccd[A/G]cctgatttgccctctc	A	G	NM_016448 // downstream // 75632 // Hs.126774 // RAMP // 51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 // upstream // 128470 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mR	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-1982996	ttttatataggggtg[A/T]aacctgcccatcca	A	T	NM_016448 // downstream // 153014 // Hs.126774 // RAMP // 51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 // upstream // 205852 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), m	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-1982999	tctctgagacaaaagc[A/G]aaatcttaatgttcag	A	G	NM_016448 // downstream // 153245 // Hs.126774 // RAMP // 51514 // Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA. /// NM_000982 // upstream // 206083 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), m	RAMP	RAMP, Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), q32.3
SNP_A-1895325	tgccctggagtaatta[C/T]gaagcataggcattct	C	T	NM_006243 // intron // 0 // Hs.497684 // PPP2R5A // 5525 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), mRNA. /// ENST00000261461 // intron // 0 // — // — // — // —	PPP2R5A	PPP2R5A, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A), q32.3
SNP_A-2075534	acatgcacactgggaa[C/T]cactgtctagtctc	C	T	NM_018252 // intron // 0 // Hs.445386 // FLJ10874 // 55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// ENST00000261455 // intron // 0 // — // — // —	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-2275636	gagacagctctgggtat[C/T]ggatttgagccctgcc	C	T	NM_018252 // intron // 0 // Hs.445386 // FLJ10874 // 55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// ENST00000261455 // intron // 0 // — // — // —	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-1942458	ttggctcctttctta[C/T]gagtggtgaggaaatc	C	T	NM_018252 // intron // 0 // Hs.445386 // FLJ10874 // 55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// ENST00000261455 // intron // 0 // — // — // —	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-1947313	tttacaaaggagata[C/T]gtacagcagtaactat	C	T	NM_018252 // intron // 0 // Hs.445386 // FLJ10874 // 55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// ENST00000261455 // intron // 0 // — // — // —	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-2184906	cagctgtgtttagcta[C/T]ggctttggcttgaagc	C	T	NM_018252 // upstream // 15553 // Hs.445386 // FLJ10874 // 55248 // Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA. /// NM_013349 // upstream // 2490 // Hs.461787 // SCIRP10 // 29937 // Homo sapiens secreted protein of unknown function (SPUF)	FLJ10874	FLJ10874, Homo sapiens hypothetical protein FLJ10874 (FLJ10874), q32.3
SNP_A-1892781	tgcacaggggatcta[A/G]cctctattctactgc	A	G	NM_013349 // downstream // 51151 // Hs.461787 // SCIRP10 // 29937 // Homo sapiens secreted protein of unknown function (SPUF), mRNA. /// NM_001674 // upstream // 111247 // Hs.460 // ATF3 // 467 // Homo sapiens activating transcription factor 3 (ATF3), mRN	SCIRP10	SCIRP10, Homo sapiens secreted protein of unknown function (SPUF), q32.3
SNP_A-1690207	tactacttgcatcagaatcacctat[C/G]acgcgttttaaaaagcag gttctca	C	G	NM_014873 // upstream // 1595 // - // - // - /// NM_015434 // downstream // 86097 // Hs.385548 // DKFZP434B168 // 25896 // DKFZP434B168 protein	-	-, rs4132401, - q32.3
SNP_A-1959812	ttttgtactatataca[C/G]ctagtttgaacttaaa	C	G	ENST00000356684 // intron // 0 // — // — // — // —	-	q32.3
SNP_A-1719241	ttcctcttacctcatttttggacaa[C/T]ggtcatctcagaactgaact tgaag	C	T	NM_006243 // upstream // 17751 // Hs.155079 // PPP2R5A // 5525 // protein phosphatase 2, regulatory subunit B (B56), alpha isoform /// NM_016448 // downstream // 162942 // Hs.126774 // RAMP // 51514 // RA-regulated nuclear matrix-associated protein	PPP2R5A	PPP2R5A, rs351408, protein phosphatase 2, regulatory subunit B (B56), alpha isoform, q32.3
SNP_A-2173880	cacacagcaattaaa[C/T]ggtctgaagcatgagg	C	T	NM_012424 // downstream // 142392 // Hs.30352 // RPS6KC1 // 26750 // Homo sapiens ribosomal protein S6 kinase, 52kDa, polypeptide 1 (RPS6KC1), mRNA. /// ENST00000259161 // downstream // 142392 // — // — // — // — /// ENST00000331583 // downstream	RPS6KC1	RPS6KC1, Homo sapiens ribosomal protein S6 kinase, 52kDa, polypeptide 1 (RPS6KC1), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2038302	aacacctctgtcctca[G/T]gcagtttatattcatt	G	T	NM_002763 // upstream // 460072 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// ENST00000331583 // upstream // 107388 // — // — // — // — /// ENST00000261454 // upstream // 460072 // — // — // — // —	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q32.3
SNP_A-1983384	tttttctctaagcaaa[A/C]tgtgggctaaggtaaa	A	C	NM_002763 // upstream // 170137 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// ENST00000331583 // upstream // 397323 // — // — // — // — /// ENST00000261454 // upstream // 170137 // — // — // — // —	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q32.3
SNP_A-2082027	accttttcatccccccc[A/G]atggataaacttatta	A	G	NM_002763 // upstream // 166161 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// ENST00000331583 // upstream // 401299 // — // — // — // — /// ENST00000261454 // upstream // 166161 // — // — // — // —	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q32.3
SNP_A-2058616	aatcagtcaataatta[A/T]ccatagctccattaac	A	T	NM_002763 // upstream // 19434 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// ENST00000331583 // upstream // 548026 // — // — // — // — /// ENST00000261454 // upstream // 19434 // — // — // — // —	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-1894340	tgcatttctttctcaa[C/T]acatttgtgtgcctgt	C	T	NM_002763 // downstream // 29558 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 215127 // Hs.66170 // SMYD2 // 56950 // Homo sapiens SET and MYND domain containing 2 (SMYD2), mRNA. ///	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-1853309	tattttataagcatcc[C/G]atgttttggctgcagg	C	G	NM_002763 // downstream // 151286 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 93399 // Hs.66170 // SMYD2 // 56950 // Homo sapiens SET and MYND domain containing 2 (SMYD2), mRNA. ///	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-2121564	agtgaacctttagcc[A/G]aagatgaggaagaaat	A	G	NM_002763 // downstream // 157333 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 87352 // Hs.66170 // SMYD2 // 56950 // Homo sapiens SET and MYND domain containing 2 (SMYD2), mRNA. ///	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-2116411	aggtatacggcctgac[C/T]gaactggttagccata	C	T	NM_002763 // downstream // 205719 // Hs.159437 // PROX1 // 5629 // Homo sapiens prospero-related homeobox 1 (PROX1), mRNA. /// NM_020197 // upstream // 38966 // Hs.66170 // SMYD2 // 56950 // Homo sapiens SET and MYND domain containing 2 (SMYD2), mRNA. ///	PROX1	PROX1, Homo sapiens prospero-related homeobox 1 (PROX1), q41
SNP_A-2208272	cccacacgacctggaa[C/T]tgagagcagaaagcta	C	T	NM_020197 // intron // 0 // Hs.66170 // SMYD2 // 56950 // Homo sapiens SET and MYND domain containing 2 (SMYD2), mRNA. /// ENST00000313573 // intron // 0 // — // — // — // —	SMYD2	SMYD2, Homo sapiens SET and MYND domain containing 2 (SMYD2), q41
SNP_A-2171900	caatgatggataagat[C/T]acagccgtgctaagaa	C	T	NM_005401 // intron // 0 // Hs.204749 // PTPN14 // 5784 // Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// ENST00000281894 // intron // 0 // — // — // — // —	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41
SNP_A-1712089	taggtgaggtcactgagcagacccc[A/G]catactcacagttcat gcaacccaa	A	G	NM_002763 // upstream // 160266 // Hs.159437 // PROX1 // 5629 // prospero-related homeobox 1 /// NM_012424 // downstream // 554787 // Hs.30352 // RPS6KC1 // 26750 // ribosomal protein S6 kinase, 52kDa, polypeptide 1	PROX1	PROX1 , rs10494967, prospero-related homeobox 1 ,q32.3
SNP_A-2199532	catttttttcattgaa[A/G]gtgtgccttcttttga	A	G	NM_005401 // upstream // 369072 // Hs.204749 // PTPN14 // 5784 // Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /// NM_016343 // downstream // 255802 // Hs.497741 // CENPF // 1063 // Homo sapiens centromere protein F, 350	PTPN14	PTPN14, Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1668090	ttcagtgaactgggtgtaaacaata[C/T]agatttcaaattaacaaggaaaaa	C	T	NM_005401 // intron // 0 // Hs.512667 // PTPN14 // 5784 // protein tyrosine phosphatase, non-receptor type 14	PTPN14	PTPN14, rs4465172, protein tyrosine phosphatase, non-receptor type 14,q41
SNP_A-2230115	ctatacaattccccca[A/G]attatgctaaggagca	A	G	NM_014217 // downstream // 17301 // Hs.497745 // KCNK2 // 3776 // Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), mRNA /// NM_016121 // upstream // 314273 // Hs.335139 // KCTD3 // 51133 // Homo sapiens potassium channel tetramerisation dom	KCNK2	KCNK2, Homo sapiens potassium channel, subfamily K, member 2 (KCNK2), q41
SNP_A-1899190	tggaaaatataaaatgc[A/T]cttgattctgctgtgt	A	T	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1817040	gttatttgtgtactgc[A/C]ctggcaagcaaatgcg	A	C	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2157980	attgcttcaacatagc[A/G]aagactgagtctgtgt	A	G	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1920098	ttaatcagaccattac[A/C]aaattgaataaatggc	A	C	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1828994	taaggctccaatctgc[C/G]atgttctagacataca	C	G	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2069268	acaatttgagcaggta[C/T]attgagactatatag	C	T	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1899570	tggaagggaaaatca[A/G]ggtcagaaatgaaaag	A	G	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1829878	taataagcaaccagtc[A/G]aaaagaaaatgcatct	A	G	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1781773	ggatttctctccctaa[A/G]tcgtggtctagaaata	A	G	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141680	atcttcctcatgctgal[C/T]gtcttgctacatgaa	C	T	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1984152	ctagctttcaacctgt[A/C]aactttctacatgcct	A	C	NM_007123 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // intron // 0 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosom	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2075357	acatgaactgagtttg[C/G]aataagaatgtactgc	C	G	NM_007123 // upstream // 7715 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // upstream // 7715 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2125755	agtttgattacctgtg[A/T]ataggaaggcttaag	A	T	NM_007123 // upstream // 40212 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // upstream // 40212 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2270697	gacagctaaaataaaa[C/G]aggtggcagaatatat	C	G	NM_007123 // upstream // 40912 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // upstream // 40912 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-2221449	ccttccctctatccc[C/T]attgcaccatgctgtc	C	T	NM_007123 // upstream // 46632 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // upstream // 46632 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1872497	tctagctgaacaaaga[G/T]aggtttatgcaataat	G	T	NM_007123 // upstream // 60521 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, mRNA. /// NM_206933 // upstream // 60521 // Hs.232072 // USH2A // 7399 // Homo sapiens Usher syndrome	USH2A	USH2A, Homo sapiens Usher syndrome 2A (autosomal recessive, mild) (USH2A), transcript variant 1, q41
SNP_A-1652308	gctggaatagagacttgaactgaca[A/G]ataagcataacaata ggtgtgaaactt	A	G	NM_007123 // downstream // 51563 // Hs.232072 // USH2A // 7399 // Usher syndrome 2A (autosomal recessive, mild) /// NM_016121 // downstream // 500646 // Hs.239155 // KCTD3 // 51133 // potassium channel tetramerisation domain containing 3	USH2A	USH2A , rs1811900, Usher syndrome 2A (autosomal recessive, mild) ,q41
SNP_A-1671784	aataggtgaaacttggaaggccaga[C/G]aagccagcataattt ggcacaaggg	C	G	NM_007123 // downstream // 51526 // Hs.232072 // USH2A // 7399 // Usher syndrome 2A (autosomal recessive, mild) /// NM_016121 // downstream // 500683 // Hs.239155 // KCTD3 // 51133 // potassium channel tetramerisation domain containing 3	USH2A	USH2A , rs1811901, Usher syndrome 2A (autosomal recessive, mild) ,q41
SNP_A-1916391	tgtgtctccataaa[A/C]cctaaaattcctcaga	A	C	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG),	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2286869	gatgggctgggtgaaga[C/T]gttgctttccgttgag	C	T	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG),	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2265336	gaagcagcagggccaa[A/G]tcaccactttcctgca	A	G	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG).	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2201964	ccacagatggacttaa[A/T]tgacttccaaacattg	A	T	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG).	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2246541	ctgtaaagtggtgaaa[G/T]agtaaaacctgcattt	G	T	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG).	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2232021	ctcaacttttggtcac[A/G]ctgagcaatcctctag	A	G	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG).	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2085979	actctagccctgagaa[C/T]gtaaacgctttctcag	C	T	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG).	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2216963	cctctgtaaagacaac[A/G]aacttaataaagagat	A	G	NM_001438 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // intron // 0 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG).	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-1787227	gggaatcataaaaggaa[A/G]tcccaagtgaaatgag	A	G	ENST00000360821 // intron // 0 // — // — // —	-	q41
SNP_A-1879530	tcttcaaaactcttgc[C/T]attgcagggtcttct	C	T	ENST00000360821 // intron // 0 // — // — // —	-	q41
SNP_A-1658118	tcctccttcctccttttcttggaa[A/G]ataatctgtgtcctaacttaag tat	A	G	NM_001438 // downstream // 43934 // Hs.151017 // ESRRG // 2104 // estrogen-related receptor gamma /// NM_007123 // upstream // 35922 // Hs.232072 // USH2A // 7399 // Usher syndrome 2A (autosomal recessive, mild)	ESRRG	ESRRG, rs10495023, estrogen-related receptor gamma, q41
SNP_A-1747007	taaactcttttttcggtcagtttcc[A/G]atttcatttattataatgctcta g	A	G	NM_001438 // downstream // 43646 // Hs.151017 // ESRRG // 2104 // estrogen-related receptor gamma /// NM_007123 // upstream // 36210 // Hs.232072 // USH2A // 7399 // Usher syndrome 2A (autosomal recessive, mild)	ESRRG	ESRRG, rs10495024, estrogen-related receptor gamma, q41
SNP_A-1846355	tatatggaaaatgaac[C/T]gggactgcagaagtga	C	T	NM_001438 // upstream // 455682 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 455682 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2119714	agtattcatttagctc[A/G]cttccacaattgaaac	A	G	NM_001438 // upstream // 471544 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 471544 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41
SNP_A-2077462	accacatatgtagttc[A/G]atcatcagaggtaaag	A	G	NM_001438 // upstream // 501776 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, mRNA. /// NM_206594 // upstream // 501776 // Hs.444225 // ESRRG // 2104 // Homo sapiens estrogen-related receptor	ESRRG	ESRRG, Homo sapiens estrogen-related receptor gamma (ESRRG), transcript variant 1, q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1984811	ggtatgcatagtatta[C/T]gtcagaacgacttcc	C	T	NM_003238 // intron // 0 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// ENST00000350220 // intron // 0 // — // — // — // — /// ENST00000264103 // intron // 0 // — // — // — // —	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2090841	actttcacaggtaact[C/T]aggagagagctcttcc	C	T	NM_003238 // intron // 0 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// ENST00000350220 // intron // 0 // — // — // — // — /// ENST00000264103 // intron // 0 // — // — // — // —	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2173601	cacaatttaactcagc[C/T]aagattaggtaattaa	C	T	NM_003238 // downstream // 32413 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 699835 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2313208	ggagaatgattcatta[C/T]caaatttcaacacgtg	C	T	NM_003238 // downstream // 75975 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 656273 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1798988	gtaagattcagtataac[C/G]agtacatacttagcca	C	G	NM_003238 // downstream // 168581 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 563667 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2214231	cctacaatctattaggt[C/T]ccaagttacttacaaa	C	T	NM_003238 // downstream // 491577 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 240671 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2112503	aggcacacttacctat[C/T]gctagtagtttaatc	C	T	NM_003238 // downstream // 511475 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 220773 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2213852	cctaaagccctgctc[C/G]caatggcagcttgaga	C	G	NM_003238 // downstream // 511651 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 220597 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1985056	aggatgaatttacaga[C/T]actacaggtgaagtct	C	T	NM_003238 // downstream // 602902 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 129346 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2148413	atgggtagctgaata[C/T]gctagaaatggaagaa	C	T	NM_003238 // downstream // 613843 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 118405 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-2185417	caggacagtatttgga[C/T]gttaggcttatcagac	C	T	NM_003238 // downstream // 627846 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 104402 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255182	ctggtattgtttgtct[A/C]cttgatatggcctic	A	C	NM_003238 // downstream // 628384 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 103864 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRN	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1912346	tgtgattgggtatac[A/G]agggatgtgagatagg	A	G	NM_003238 // downstream // 699843 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 32405 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1985094	gattcataatttccc[C/T]acgtagagtgtgattt	C	T	NM_003238 // downstream // 714384 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 17864 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1947831	tttactaggaagaca[A/G]aagacaggctaagatt	A	G	NM_003238 // downstream // 717930 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 14318 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1921645	ttaccttgttctggccc[A/G]cagctcatttatttca	A	G	NM_003238 // downstream // 720246 // Hs.133379 // TGFB2 // 7042 // Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA. /// NM_138794 // upstream // 12002 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA	TGFB2	TGFB2, Homo sapiens transforming growth factor, beta 2 (TGFB2), q41
SNP_A-1954086	tttgatggatcttttta[G/T]gctcgctataatctc	G	T	NM_138794 // downstream // 8922 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream // 8922 // — // — // — /// ENST00000359296 // downstream // 388868 // — // — //	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1734668	gtcatcaaactgaaactaagttgtt[C/G]ctaacattccaaggaat cagaaaga	C	G	NM_003238 // downstream // 131893 // Hs.169300 // TGFB2 // 7042 // transforming growth factor, beta 2 /// NM_138794 // upstream // 600360 // Hs.88201 // LYPLAL1 // 127018 // lysophospholipase-like 1	TGFB2	TGFB2 , rs62817, transforming growth factor, beta 2, q41
SNP_A-1985112	gagagggtaaggcatc[A/G]aagtgagaaagcaaaa	A	G	NM_138794 // downstream // 30306 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream // 30306 // — // — // — /// ENST00000359296 // downstream // 367484 // — // — /	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2161669	atttgggtatggtcac[A/G]agttagtaggggtc	A	G	NM_138794 // downstream // 78986 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream // 78986 // — // — // — /// ENST00000359296 // downstream // 318804 // — // — /	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1782797	ggcagatcaggtgtgaa[A/T]gacatcataggtatct	A	T	NM_138794 // downstream // 91991 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream // 91991 // — // — // — /// ENST00000359296 // downstream // 305799 // — // — /	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2140696	atctctgagggaatta[A/G]aggctagtctacacaa	A	G	NM_138794 // downstream // 92995 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA. /// ENST00000271607 // downstream // 92995 // — // — // — /// ENST00000359296 // downstream // 304795 // — // — /	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189285	cagttcctggctccata[A/G]ggagagagattaaata	A	G	NM_138794 // downstream // 99171 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 99171 // — // — // — // — /// ENST00000359296 // downstream // 298619 // — // — /	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2226787	ctaataatacagtcac[A/G]cttcaatgattcctgt	A	G	NM_138794 // downstream // 101147 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 101147 // — // — // — // — /// ENST00000359296 // downstream // 296643 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1868578	tcctctggataccaaaa[C/T]aggttgcggcatggga	C	T	NM_138794 // downstream // 114987 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 114987 // — // — // — // — /// ENST00000359296 // downstream // 282803 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1839069	tagagatggatagagt[A/G]aagaatttaaaaggt	A	G	NM_138794 // downstream // 138319 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 138319 // — // — // — // — /// ENST00000359296 // downstream // 259471 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1838467	tagaatccagatgctt[A/G]aaccattcaaagatta	A	G	NM_138794 // downstream // 161892 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 161892 // — // — // — // — /// ENST00000359296 // downstream // 235898 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1955916	tttgtcagttgtccca[A/G]gacttttattgtaggc	A	G	NM_138794 // downstream // 179199 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 179199 // — // — // — // — /// ENST00000359296 // downstream // 218591 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2234244	ctcatttgtgtccctg[A/G]aagagataaggagaga	A	G	NM_138794 // downstream // 186361 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 186361 // — // — // — // — /// ENST00000359296 // downstream // 211429 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2233803	ctcatcctctcttcac[A/G]cttacttctagcagc	A	G	NM_138794 // downstream // 211330 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 211330 // — // — // — // — /// ENST00000359296 // downstream // 186460 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2154785	attcaactctgtgttat[C/T]ggttatgtctgtgc	C	T	NM_138794 // downstream // 211541 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 211541 // — // — // — // — /// ENST00000359296 // downstream // 186249 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2060029	aatctttgaagtcggat[A/C]gataaaaatcaccatt	A	C	NM_138794 // downstream // 231050 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 231050 // — // — // — // — /// ENST00000359296 // downstream // 166740 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-2305216	gctgactttacagagat[C/G]attattggaggtagg	C	G	NM_138794 // downstream // 261649 // Hs.125291 // LYPLAL1 // 127018 // Homo sapiens lysophospholipase-like 1 (LYPLAL1), mRNA /// ENST00000271607 // downstream // 261649 // — // — // — // — /// ENST00000359296 // downstream // 136141 // — // —	LYPLAL1	LYPLAL1, Homo sapiens lysophospholipase-like 1 (LYPLAL1), q41
SNP_A-1758974	ttgaatctaatgtaaagcacatga[C/T]ggaaatagatttcacttat ttact	C	T	NM_003238 // downstream // 473958 // Hs.169300 // TGFB2 // 7042 // transforming growth factor, beta 2 /// NM_138794 // upstream // 258295 // Hs.88201 // LYPLAL1 // 127018 // lysophospholipase-like 1	TGFB2	TGFB2 , rs10495113, transforming growth factor, beta 2 ,q41
SNP_A-1701185	tcatgattaaggaaattgccatata[C/T]gttgatggaatgataatta aacatt	C	T	NM_003238 // downstream // 520088 // Hs.169300 // TGFB2 // 7042 // transforming growth factor, beta 2 /// NM_138794 // upstream // 212165 // Hs.88201 // LYPLAL1 // 127018 // lysophospholipase-like 1	TGFB2	TGFB2 , rs10495117, transforming growth factor, beta 2 ,q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1901913	tggcaggaaacacata[C/T]acaatttcatgacagc	C	T	NM_018713 // downstream // 256900 // Hs.519812 // SLC30A10 // 55532 // Homo sapiens solute carrier family 30 (zinc transporter), member 10 (SLC30A10), transcript variant 1, mRNA. /// ENST00000359296 // upstream // 43547 // — // — // — /// ENS	SLC30A10	SLC30A10, Homo sapiens solute carrier family 30 (zinc transporter), member 10 (SLC30A10), transcript variant 1, q41
SNP_A-2306191	gctggcaaagttaaca[C/T]ggtgtactttttcatt	C	T	NM_004446 // intron // 0 // Hs.497788 // EPRS // 2058 // Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), mRNA. /// ENST00000259146 // intron // 0 // — // — // — // —	EPRS	EPRS, Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), q41
SNP_A-2160081	atttattgcttcctac[C/T]atgttatacattggcc	C	T	NM_004446 // intron // 0 // Hs.497788 // EPRS // 2058 // Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), mRNA. /// ENST00000259146 // intron // 0 // — // — // — // —	EPRS	EPRS, Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), q41
SNP_A-1798494	gtaaatggcgctataa[A/G]taaatgtgacagcctc	A	G	NM_012414 // intron // 0 // Hs.254983 // RAB3-GAP150 // 25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // — // — // — // — /// ENST00000237724 // intron /	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2126666	ataaacagccagaact[C/G]agcaatatttcaatat	C	G	NM_012414 // intron // 0 // Hs.254983 // RAB3-GAP150 // 25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // — // — // — // — /// ENST00000237724 // intron /	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-1917116	tgtttgtcaagtcaca[A/G]tatgagcaaatctatc	A	G	NM_012414 // intron // 0 // Hs.254983 // RAB3-GAP150 // 25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // — // — // — // — /// ENST00000237724 // intron /	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-1856534	tcacagcctctgaaaa[A/G]acttccttaacacaccc	A	G	NM_012414 // intron // 0 // Hs.254983 // RAB3-GAP150 // 25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// ENST00000358951 // intron // 0 // — // — // — // — /// ENST00000237724 // intron /	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-1892747	tgcacagaatgtgaaa[C/T]cacttagtacagagac	C	T	NM_012414 // upstream // 19158 // Hs.254983 // RAB3-GAP150 // 25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// NM_018650 // upstream // 236658 // Hs.497806 // MARK1 // 4139 // Homo sapiens MAP/mi	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2063743	aattagaggcagcttta[A/G]cccaacaggtactgtg	A	G	NM_012414 // upstream // 167761 // Hs.254983 // RAB3-GAP150 // 25782 // Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA. /// NM_018650 // upstream // 88055 // Hs.497806 // MARK1 // 4139 // Homo sapiens MAP/mi	RAB3-GAP150	RAB3-GAP150, Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), q41
SNP_A-2252705	cttcgctttgtctcaa[C/T]catctgtagtttcaa	C	T	NM_022746 // downstream // 761 // Hs.497816 // FLJ22390 // 64757 // Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA. /// NM_021958 // upstream // 64253 // Hs.74870 // HLX1 // 3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA	FLJ22390	FLJ22390, Homo sapiens hypothetical protein FLJ22390 (FLJ22390), q41
SNP_A-2172389	caattagatctgcaga[A/G]atctgatcctgggaa	A	G	NM_021958 // downstream // 127005 // Hs.74870 // HLX1 // 3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 689366 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10).	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-2071016	acactgaaggtagaaa[C/T]aggaattctgtgtagg	C	T	NM_021958 // downstream // 496405 // Hs.74870 // HLX1 // 3142 // Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA. /// NM_144728 // downstream // 319966 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10).	HLX1	HLX1, Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), q41
SNP_A-1643393	tcacgatcttgcttccagcatgcte[A/G]gactcataataacttctt aacca	A	G	NM_022746 // intron // 0 // Hs.195345 // FLJ22390 // 64757 // hypothetical protein FLJ22390	FLJ22390	FLJ22390 , rs903319, hypothetical protein FLJ22390,q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1985780	tgtttctctactga[A/G]caaagcacactgttga	A	G	NM_144728 // upstream // 19257 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 19257 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosph	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2096481	agacctagaccaccta[C/T]agtataaaaagcaac	C	T	NM_144728 // upstream // 19331 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 19331 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosph	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2108731	agctgtctaccatagc[A/G]agaaaggtgctattg	A	G	NM_144728 // upstream // 38097 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 38097 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosph	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-1819465	gttgggtaacaagtgc[A/G]cagatattggtcaaa	A	G	NM_144728 // upstream // 195545 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 195545 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2146305	atgctagggacaaaga[C/T]gaggaatgagtggccc	C	T	NM_144728 // upstream // 196937 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 196937 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-1670762	gaggcaggaattactccaacttccc[A/G]aaacctcagaaaac agccctggtc	A	G	NM_007207 // downstream // 426444 // Hs.177534 // DUSP10 // 11221 // dual specificity phosphatase 10 /// NM_021958 // downstream // 389926 // Hs.74870 // HLX1 // 3142 // H2.0-like homeo box 1 (Drosophila) /// NM_144728 // downstream // 426444 // Hs.17753	DUSP10	DUSP10 , rs4846704, dual specificity phosphatase 10 ,q41
SNP_A-1928191	ttcacagactaagtta[C/T]gccgttactccaggat	C	T	NM_144728 // upstream // 365373 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 365373 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2128784	ataatctctggctaac[A/G]atgcctgtttctaatc	A	G	NM_144728 // upstream // 444785 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 444785 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-1728663	aaggcttgaacagttaaatccag[A/G]cattcctttggtgtttaa gctcc	A	G	NM_007207 // downstream // 1154437 // Hs.177534 // DUSP10 // 11221 // dual specificity phosphatase 10 /// NM_021958 // downstream // 700933 // Hs.74870 // HLX1 // 3142 // H2.0-like homeo box 1 (Drosophila) /// NM_144728 // downstream // 1154437 // Hs.17753	DUSP10	DUSP10 , rs7531435, dual specificity phosphatase 10 ,q41
SNP_A-1804147	gtcacatgctaaatgc[A/G]aattaagaaaagagag	A	G	NM_144728 // upstream // 679379 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 679379 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2238887	ctcttcacttacagtc[A/G]ctcctatgatgttatt	A	G	NM_144728 // upstream // 679805 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 679805 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247817	ctgtgagtgaggtctc[A/G]aagaactatgatgtgg	A	G	NM_144728 // upstream // 680136 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, mRNA. /// NM_144729 // upstream // 680136 // Hs.497822 // DUSP10 // 11221 // Homo sapiens dual specificity phos	DUSP10	DUSP10, Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 2, q41
SNP_A-2258710	cttttgctgagaaggc[A/T]aaggaaattctcgccc	A	T	NM_139352 // upstream // 534 // Hs.153088 // TAF1A // 9015 // Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa (TAF1A), transcript variant 2, mRNA. /// NM_139352 // upstream // 406 // Hs.153088 // TAF1A // 9015 //	TAF1A	TAF1A, Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa (TAF1A), transcript variant 2, q41
SNP_A-1757910	acccgaatgaaagtagttctcagaa[A/G]gccagaagtagttctc agagactcg	A	G	NM_007207 // upstream // 662834 // Hs.177534 // DUSP10 // 11221 // dual specificity phosphatase 10 /// NM_024746 // downstream // 117378 // Hs.123515 // FLJ13840 // 79802 // hypothetical protein FLJ13840 /// NM_144728 // upstream // 667493 // Hs.177534 /	DUSP10	DUSP10 , rs1108669, dual specificity phosphatase 10 ,q41
SNP_A-1713608	gaaaggctacagattttcttcagca[G/T]tcattattacatataataa acattt	G	T	NM_005681 // intron // 0 // Hs.153088 // TAF1A // 9015 // TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa /// NM_139352 // intron // 0 // Hs.153088 // TAF1A // 9015 // TATA box binding protein (TBP)-associated factor, RNA pol	TAF1A	TAF1A , rs10495196, TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa ,q41
SNP_A-2216984	cctctgtcttctgtcc[A/G]aaactcctatactcag	A	G	NM_152610 // downstream // 94700 // Hs.192090 // FLJ35728 // 164127 // Homo sapiens hypothetical protein FLJ35728 (FLJ35728), mRNA. /// NM_001748 // upstream // 171652 // Hs.350899 // CAPN2 // 824 // Homo sapiens calpain 2, (m/II) large subunit (CAPN2), m	FLJ35728	FLJ35728, Homo sapiens hypothetical protein FLJ35728 (FLJ35728), q42.11
SNP_A-1889310	tgagtggagcagtcta[A/G]gcagcaaggcgtggtg	A	G	NM_152610 // downstream // 95023 // Hs.192090 // FLJ35728 // 164127 // Homo sapiens hypothetical protein FLJ35728 (FLJ35728), mRNA. /// NM_001748 // upstream // 171329 // Hs.350899 // CAPN2 // 824 // Homo sapiens calpain 2, (m/II) large subunit (CAPN2), m	FLJ35728	FLJ35728, Homo sapiens hypothetical protein FLJ35728 (FLJ35728), q42.11
SNP_A-2087735	actgctttcctagcac[C/T]ccataagattcagaaa	C	T	NM_152610 // downstream // 96663 // Hs.192090 // FLJ35728 // 164127 // Homo sapiens hypothetical protein FLJ35728 (FLJ35728), mRNA. /// NM_001748 // upstream // 169689 // Hs.350899 // CAPN2 // 824 // Homo sapiens calpain 2, (m/II) large subunit (CAPN2), m	FLJ35728	FLJ35728, Homo sapiens hypothetical protein FLJ35728 (FLJ35728), q42.11
SNP_A-2111471	aggaggcccctgtaac[G/T]acttgccttcttcctg	G	T	NM_152610 // downstream // 219943 // Hs.192090 // FLJ35728 // 164127 // Homo sapiens hypothetical protein FLJ35728 (FLJ35728), mRNA. /// NM_001748 // upstream // 46409 // Hs.350899 // CAPN2 // 824 // Homo sapiens calpain 2, (m/II) large subunit (CAPN2), m	FLJ35728	FLJ35728, Homo sapiens hypothetical protein FLJ35728 (FLJ35728), q42.11
SNP_A-2128855	ataatgagtagttcaa[C/T]gaggccagcggacagc	C	T	NM_152610 // downstream // 233445 // Hs.192090 // FLJ35728 // 164127 // Homo sapiens hypothetical protein FLJ35728 (FLJ35728), mRNA. /// NM_001748 // upstream // 32907 // Hs.350899 // CAPN2 // 824 // Homo sapiens calpain 2, (m/II) large subunit (CAPN2), m	FLJ35728	FLJ35728, Homo sapiens hypothetical protein FLJ35728 (FLJ35728), q42.11
SNP_A-1868099	tcctatgaccggaaaa[A/G]cagactagtagaggcc	A	G	NM_015176 // downstream // 152 // Hs.64691 // FBXO28 // 23219 // Homo sapiens F-box protein 28 (FBXO28), mRNA. /// ENST00000272097 // downstream // 152 // — // — // — // — /// ENST00000305782 // downstream // 15787 // — // — // — // —	FBXO28	FBXO28, Homo sapiens F-box protein 28 (FBXO28), q42.12
SNP_A-2299812	gcctaagtgacatcaa[A/T]tggatcaagacaaaac	A	T	NM_152495 // intron // 0 // Hs.97338 // CNIH3 // 149111 // Homo sapiens hypothetical protein FLJ38993 (FLJ38993), mRNA. /// ENST00000272133 // intron // 0 // — // — // — // —	CNIH3	CNIH3, Homo sapiens hypothetical protein FLJ38993 (FLJ38993), q42.12
SNP_A-2101194	agatccaagtggagac[A/C]aacttttccttctct	A	C	ENST00000343412 // intron // 0 // — // — // — // —	-	q42.12
SNP_A-2301487	gcgaagggtaggtggc[A/G]aagaagagaaaagacc	A	G	ENST00000343412 // intron // 0 // — // — // — // —	-	q42.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2125384	agtttaagcagggttc[A/G]atgaagagcccaccca	A	G	NM_152608 // upstream // 41604 // Hs.520192 // FLJ35382 // 163859 // Homo sapiens hypothetical protein FLJ35382 (FLJ35382), mRNA. /// NM_005324 // upstream // 21794 // Hs.180877 // H3F3B // 3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA.	FLJ35382	FLJ35382, Homo sapiens hypothetical protein FLJ35382 (FLJ35382), q42.12
SNP_A-2314193	ggaggagtccagagga[A/G]agtaacagtggatgga	A	G	NM_005324 // downstream // 2713 // Hs.180877 // H3F3B // 3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 2713 // Hs.546259 // H3F3A // 3020 // Homo sapiens H3 histone, family 3A (H3F3A), mRNA. /// NM_022735	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q42.12
SNP_A-1807547	gtctggagaatagacc[A/G]aaggcaataagggtag	A	G	NM_005324 // downstream // 6738 // Hs.180877 // H3F3B // 3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 6738 // Hs.546259 // H3F3A // 3020 // Homo sapiens H3 histone, family 3A (H3F3A), mRNA. /// NM_022735	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q42.12
SNP_A-2086675	actgaagttcctgaaa[C/T]cttccttggaaaaatc	C	T	NM_005324 // downstream // 25449 // Hs.180877 // H3F3B // 3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 25449 // Hs.546259 // H3F3A // 3020 // Homo sapiens H3 histone, family 3A (H3F3A), mRNA. /// NM_0227	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q42.12
SNP_A-1835168	tacccttgccaacat[A/T]atcctcattaaattca	A	T	NM_022735 // intron // 0 // Hs.520207 // ACBD3 // 64746 // Homo sapiens acyl-Coenzyme A binding domain containing 3 (ACBD3), mRNA. /// ENST00000331914 // intron // 0 // --- // --- // --- // ---	ACBD3	ACBD3, Homo sapiens acyl-Coenzyme A binding domain containing 3 (ACBD3), q42.12
SNP_A-2271124	gacatcagtatttgca[A/T]agccaagttattaaag	A	T	NM_173083 // intron // 0 // Hs.120817 // LIN9 // 286826 // Homo sapiens TUDOR gene similar (TGS), mRNA. /// ENST00000328205 // intron // 0 // --- // --- // --- // --- /// ENST00000359525 // intron // 0 // --- // --- // --- // ---	LIN9	LIN9, Homo sapiens TUDOR gene similar (TGS), q42.12
SNP_A-2224431	cgtagatgacttcaac[A/G]gaccgagagaaagaag	A	G	NM_173083 // upstream // 23994 // Hs.120817 // LIN9 // 286826 // Homo sapiens TUDOR gene similar (TGS), mRNA. /// NM_001618 // downstream // 27314 // Hs.177766 // PARP1 // 142 // Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA. //	LIN9	LIN9, Homo sapiens TUDOR gene similar (TGS), q42.12
SNP_A-1959890	ttttgtctcagccaac[A/G]ggattactgggctccc	A	G	NM_002221 // intron // 0 // Hs.528087 // ITPKB // 3707 // Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), mRNA. /// ENST00000272117 // intron // 0 // --- // --- // --- // ---	ITPKB	ITPKB, Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), q42.12
SNP_A-2054862	aataaagctggtgtta[A/G]gggtatactatattta	A	G	NM_002221 // upstream // 81777 // Hs.528087 // ITPKB // 3707 // Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), mRNA. /// NM_000447 // upstream // 51986 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2),	ITPKB	ITPKB, Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), q42.13
SNP_A-1893666	tgcagtagcccttcaa[C/T]gaccttctttccccaa	C	T	NM_002221 // upstream // 127606 // Hs.528087 // ITPKB // 3707 // Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), mRNA. /// NM_000447 // upstream // 6157 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2),	ITPKB	ITPKB, Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), q42.13
SNP_A-1928465	ttcactaaggggcaga[C/T]gccaagcgcacggctc	C	T	NM_000447 // intron // 0 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, mRNA. /// NM_012486 // intron // 0 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSE	PSEN2	PSEN2, Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, q42.13
SNP_A-1891063	tgatggttagggtgaa[A/G]tgttaagactgagaaa	A	G	NM_000447 // downstream // 1358 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, mRNA. /// NM_012486 // downstream // 1358 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer d	PSEN2	PSEN2, Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, q42.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2273853	gactggggccacatac[A/G]aacaggacttcagaac	A	G	NM_000447 // downstream // 1665 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, mRNA. /// NM_012486 // downstream // 1665 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer d	PSEN2	PSEN2, Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, q42.13
SNP_A-1815300	gtgtttaacacccccca[A/G]aaagcttgtctaagta	A	G	NM_000447 // downstream // 9065 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, mRNA. /// NM_012486 // downstream // 9065 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer d	PSEN2	PSEN2, Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, q42.13
SNP_A-1853562	tatttttaagatcatc[A/G]aacaggtattctggag	A	G	NM_000447 // downstream // 38434 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, mRNA. /// NM_012486 // downstream // 38434 // Hs.25363 // PSEN2 // 5664 // Homo sapiens presenilin 2 (Alzheimer	PSEN2	PSEN2, Homo sapiens presenilin 2 (Alzheimer disease 4) (PSEN2), transcript variant 1, q42.13
SNP_A-1865632	tccattaattatatca[C/T]ctggagaacctactga	C	T	NM_020247 // intron // 0 // Hs.118241 // CABC1 // 56997 // Homo sapiens chaperone, ABC1 activity of bc1 complex like (S. pombe) (CABC1), mRNA. /// ENST00000341412 // intron // 0 // — // — // — // —	CABC1	CABC1, Homo sapiens chaperone, ABC1 activity of bc1 complex like (S. pombe) (CABC1), q42.13
SNP_A-1804995	gtcatcatgtatctta[C/G]acatattgtggtatac	C	G	NM_014826 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding prot	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-1986993	tttagttaaaatggaa[C/G]tgagaagcaaagcaga	C	G	NM_014826 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding prot	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-1898443	tgcttcgtgattatgg[C/T]agagtgtccttgactt	C	T	NM_014826 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding prot	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-1987070	tgtttaatacagagaa[A/G]tcaactgagccagatg	A	G	NM_014826 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, mRNA. /// NM_003607 // intron // 0 // Hs.35433 // CDC42BPA // 8476 // Homo sapiens CDC42 binding prot	CDC42BPA	CDC42BPA, Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant A, q42.13
SNP_A-1952154	tttctcagtctccttc[A/G]ctggatgatccttatc	A	G	ENST00000357747 // intron // 0 // — // — // — // —	-	q42.13
SNP_A-2193819	catgaaaactttctga[C/T]gagaccagagagcaga	C	T	ENST00000357747 // intron // 0 // — // — // — // —	-	q42.13
SNP_A-2099685	agaggtggaagtcgta[A/C]ctttggggtcaggccc	A	C	ENST00000357747 // intron // 0 // — // — // — // —	-	q42.13
SNP_A-1651962	gcctgcaaaggatggcctgtcagct[C/T]agcagtctgtgtgctttc tagagta	C	T	NM_003607 // intron // 0 // Hs.18586 // CDC42BPA // 8476 // CDC42 binding protein kinase alpha (DMPK-like) /// NM_014826 // intron // 0 // Hs.18586 // CDC42BPA // 8476 // CDC42 binding protein kinase alpha (DMPK-like)	CDC42BPA	CDC42BPA , rs2297419, CDC42 binding protein kinase alpha (DMPK-like) ,q42.13
SNP_A-1746408	agcatcttgtatgcagtgagtgtta[C/T]gaattttctttttgttaaaatg aat	C	T	NM_003607 // intron // 0 // Hs.18586 // CDC42BPA // 8476 // CDC42 binding protein kinase alpha (DMPK-like) /// NM_014826 // intron // 0 // Hs.18586 // CDC42BPA // 8476 // CDC42 binding protein kinase alpha (DMPK-like)	CDC42BPA	CDC42BPA , rs10495272, CDC42 binding protein kinase alpha (DMPK-like) ,q42.13
SNP_A-1743091	aagaagcaacagacgaagcatctaa[C/T]cttgtgaataaaatg attgatttag	C	T	NM_003607 // intron // 0 // Hs.18586 // CDC42BPA // 8476 // CDC42 binding protein kinase alpha (DMPK-like) /// NM_014826 // intron // 0 // Hs.18586 // CDC42BPA // 8476 // CDC42 binding protein kinase alpha (DMPK-like)	CDC42BPA	CDC42BPA , rs10495271, CDC42 binding protein kinase alpha (DMPK-like) ,q42.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2104884	agcatatacaagtatc[A/G]atagcccaatcaatca	A	G	NM_023007 // downstream // 16463 // Hs.546427 // FLJ12517 // 65094 // Homo sapiens hypothetical protein FLJ12517 (FLJ12517), mRNA. /// NM_053052 // upstream // 20225 // Hs.325081 // IMAGE3451454 // 116841 // Homo sapiens SVAP1 protein (IMAGE3451454), mRNA	FLJ12517	FLJ12517, Homo sapiens hypothetical protein FLJ12517 (FLJ12517), q42.13
SNP_A-2266341	gaaggtcctgttttcc[C/T]aaggcatttttaataa	C	T	NM_053052 // intron // 0 // Hs.325081 // IMAGE3451454 // 116841 // Homo sapiens SVAP1 protein (IMAGE3451454), mRNA. /// ENST00000272080 // intron // 0 // — // — // — // — /// ENST00000315781 // intron // 0 // — // — // — // —	IMAGE3451454	IMAGE3451454, Homo sapiens SVAP1 protein (IMAGE3451454), q42.13
SNP_A-2142662	atgaagaagggtcctc[A/G]acaaaggagcacagct	A	G	NM_183062 // intron // 0 // Hs.97604 // MPN2 // 339501 // Homo sapiens marapsin 2 (MPN2), mRNA. /// ENST00000329666 // intron // 0 // — // — // — // —	MPN2	MPN2, Homo sapiens marapsin 2 (MPN2), q42.13
SNP_A-2209036	cccagctttgggacga[A/G]caccaccttgccaccc	A	G	NM_001658 // intron // 0 // Hs.286221 // ARF1 // 375 // Homo sapiens ADP-ribosylation factor 1 (ARF1), mRNA. /// ENST00000272102 // intron // 0 // — // — // — // —	ARF1	ARF1, Homo sapiens ADP-ribosylation factor 1 (ARF1), q42.13
SNP_A-2109032	agcttccatgtccata[A/C]aaaggaggggagaagg	A	C	NM_052843 // intron // 0 // Hs.231655 // OBSCN // 84033 // Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), mRNA. /// ENST00000284548 // intron // 0 // — // — // — // —	OBSCN	OBSCN, Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), q42.13
SNP_A-1801362	gtaggagggcctagac[A/G]agaaagtaggagaaac	A	G	NM_052843 // intron // 0 // Hs.231655 // OBSCN // 84033 // Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), mRNA. /// ENST00000284548 // intron // 0 // — // — // — // —	OBSCN	OBSCN, Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), q42.13
SNP_A-1800963	gtagatactctggtca[C/T]attggattgggccctt	C	T	NM_052843 // intron // 0 // Hs.231655 // OBSCN // 84033 // Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), mRNA. /// ENST00000284548 // intron // 0 // — // — // — // — /// ENST00000359599 // intron // 0 // —	OBSCN	OBSCN, Homo sapiens obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN), q42.13
SNP_A-2058061	aatatttgtatgttta[C/T]atcttgtaactttgct	C	T	NM_021205 // downstream // 73838 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 73838 // — // — // — // — /// ENST00000323223 // upstream // 429136 // — // — /	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1823765	taaaatctaaggccca[C/T]gtaaccagtcgtttca	C	T	NM_021205 // downstream // 168501 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 168501 // — // — // — // — /// ENST00000323223 // upstream // 334473 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1897385	tgctgaagatgaccac[C/T]gcaggagggaaaggaa	C	T	NM_021205 // downstream // 191576 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 191576 // — // — // — // — /// ENST00000323223 // upstream // 311398 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1987385	atgtaataattctgga[G/T]aagccagggtacataa	G	T	NM_021205 // downstream // 209166 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 209166 // — // — // — // — /// ENST00000323223 // upstream // 293808 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-2290844	gcaaggaggtcggcga[C/T]atcacgcatccacagt	C	T	NM_021205 // downstream // 222736 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 222736 // — // — // — // — /// ENST00000323223 // upstream // 280238 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235916	ctcctgattgtcctct[A/C]aatgtgctagctagct	A	C	NM_021205 // downstream // 273839 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 273839 // — // — // — /// ENST00000323223 // upstream // 229135 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-1789850	gggctgggtgacgcac[A/G]aatcttgagtcaacag	A	G	NM_021205 // downstream // 323670 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 323670 // — // — // — /// ENST00000323223 // upstream // 179304 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-2000755	tttctgctgcagagaa[C/T]aacaacacacagtgca	C	T	NM_021205 // downstream // 460530 // Hs.435106 // RHOU // 58480 // Homo sapiens ras homolog gene family, member U (RHOU), mRNA. /// ENST00000235211 // downstream // 460530 // — // — // — /// ENST00000323223 // upstream // 42444 // — // —	RHOU	RHOU, Homo sapiens ras homolog gene family, member U (RHOU), q42.13
SNP_A-2277350	gagatttcagtgtaccc[A/C]gggatttcagggccca	A	C	NM_004578 // intron // 0 // Hs.296169 // RAB4A // 5867 // Homo sapiens RAB4A, member RAS oncogene family (RAB4A), mRNA. /// ENST00000284615 // intron // 0 // — // — // — // —	RAB4A	RAB4A, Homo sapiens RAB4A, member RAS oncogene family (RAB4A), q42.13
SNP_A-2052106	aaggtttctgtattccc[A/G]agcatatttaagtgac	A	G	NM_004578 // downstream // 13106 // Hs.296169 // RAB4A // 5867 // Homo sapiens RAB4A, member RAS oncogene family (RAB4A), mRNA. /// NM_006542 // downstream // 12375 // Hs.511754 // SPHAR // 10638 // Homo sapiens S-phase response (cyclin-related) (SPHAR).	RAB4A	RAB4A, Homo sapiens RAB4A, member RAS oncogene family (RAB4A), q42.13
SNP_A-1828092	taagacatctaaaatc[A/G]agttgacattatctct	A	G	NM_145257 // upstream // 76765 // Hs.445132 // LOC126731 // 126731 // Homo sapiens LOC126731 (LOC126731), mRNA. /// NM_005159 // downstream // 11496 // Hs.118127 // ACTC // 70 // Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA. /// NM_001100 // dow	LOC126731	LOC126731, Homo sapiens LOC126731 (LOC126731), q42.13
SNP_A-2262023	gaaatagcctctgtcc[A/G]gagagtgttgcttat	A	G	NM_145257 // upstream // 79833 // Hs.445132 // LOC126731 // 126731 // Homo sapiens LOC126731 (LOC126731), mRNA. /// NM_005159 // downstream // 8428 // Hs.118127 // ACTC // 70 // Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA. /// NM_001100 // down	LOC126731	LOC126731, Homo sapiens LOC126731 (LOC126731), q42.13
SNP_A-1859931	tcaggtcttgtgtaaa[C/T]tgatagagcaagaatt	C	T	D50923 // downstream // 117154 // Hs.533628 // KIAA0133 // 9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 289856 // Hs.300834 // GALNT2 // 2590 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13
SNP_A-2047831	aagatttgtaagtttta[C/T]agcacattaaaggatg	C	T	D50923 // downstream // 120714 // Hs.533628 // KIAA0133 // 9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 286296 // Hs.300834 // GALNT2 // 2590 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13
SNP_A-2056116	aataccattgaatacc[C/T]cacaaggacatctagg	C	T	D50923 // downstream // 125981 // Hs.533628 // KIAA0133 // 9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 281029 // Hs.300834 // GALNT2 // 2590 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13
SNP_A-1889664	tgataacggttagaac[A/G]gtacttcacgaatga	A	G	D50923 // downstream // 133352 // Hs.533628 // KIAA0133 // 9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 273658 // Hs.300834 // GALNT2 // 2590 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds. q42.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2288661	gattggataaacaata[A/G]gcagtacatatacaac	A	G	D50923 // downstream // 347701 // Hs.533628 // KIAA0133 // 9816 // Homo sapiens mRNA for KIAA0133 gene, partial cds. /// NM_004481 // upstream // 59309 // Hs.300834 // GALNT2 // 2590 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylg	KIAA0133	KIAA0133, Homo sapiens for KIAA0133 gene, partial cds, q42.13
SNP_A-2099361	agaggctaaaatgata[A/G]gctatagcacagtact	A	G	NM_024554 // upstream // 100743 // Hs.520463 // PGBD5 // 79605 // Homo sapiens piggyBac transposable element derived 5 (PGBD5), mRNA. /// NM_007357 // upstream // 164128 // Hs.211800 // COG2 // 22796 // Homo sapiens component of oligomeric golgi complex 2	PGBD5	PGBD5, Homo sapiens piggyBac transposable element derived 5 (PGBD5), q42.13
SNP_A-1908691	tgtaggcatacataaa[A/G]ctgacatgtaaactcc	A	G	NM_024554 // upstream // 187311 // Hs.520463 // PGBD5 // 79605 // Homo sapiens piggyBac transposable element derived 5 (PGBD5), mRNA. /// NM_007357 // upstream // 77560 // Hs.211800 // COG2 // 22796 // Homo sapiens component of oligomeric golgi complex 2	PGBD5	PGBD5, Homo sapiens piggyBac transposable element derived 5 (PGBD5), q42.2
SNP_A-1886668	tgactctcaaaggcac[A/G]ccctagtgtaatctct	A	G	NM_024554 // upstream // 193556 // Hs.520463 // PGBD5 // 79605 // Homo sapiens piggyBac transposable element derived 5 (PGBD5), mRNA. /// NM_007357 // upstream // 71315 // Hs.211800 // COG2 // 22796 // Homo sapiens component of oligomeric golgi complex 2	PGBD5	PGBD5, Homo sapiens piggyBac transposable element derived 5 (PGBD5), q42.2
SNP_A-1792852	ggtaatcagctgctaa[C/T]gaaaacaaccagtctg	C	T	NM_007357 // intron // 0 // Hs.211800 // COG2 // 22796 // Homo sapiens component of oligomeric golgi complex 2 (COG2), mRNA. /// ENST00000258255 // intron // 0 // — // — // — // —	COG2	COG2, Homo sapiens component of oligomeric golgi complex 2 (COG2), q42.2
SNP_A-1938818	ttgaggacttcaacac[A/G]ggcattatggccgttg	A	G	NM_000029 // intron // 0 // Hs.19383 // AGT // 183 // Homo sapiens angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8 /// ENST00000258224 // intron // 0 // — // — // —	AGT	AGT, Homo sapiens angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8, q42.2
SNP_A-1801452	gtaggcttccgttccc[A/G]cacacggaatctctcca	A	G	NM_032800 // intron // 0 // Hs.520494 // FLJ14525 // 84886 // Homo sapiens hypothetical protein FLJ14525 (FLJ14525), mRNA. /// ENST00000238200 // intron // 0 // — // — // — // — /// ENST00000355463 // intron // 0 // — // — // —	FLJ14525	FLJ14525, Homo sapiens hypothetical protein FLJ14525 (FLJ14525), q42.2
SNP_A-2000767	agtgtcagcaagaagt[A/G]aacgttgtggttgga	A	G	NM_001004342 // intron // 0 // Hs.131295 // TRIM67 // 440730 // Homo sapiens TRIM9-like protein TNL (TNL), mRNA. /// ENST00000335575 // intron // 0 // — // — // — // —	TRIM67	TRIM67, Homo sapiens TRIM9-like protein TNL (TNL), q42.2
SNP_A-1861485	tcatccacagtaccca[C/T]gcttgcaatgtccaca	C	T	NM_014236 // downstream // 14875 // Hs.498028 // GNPAT // 8443 // Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA. /// NM_175876 // downstream // 42905 // Hs.356198 // EXOC8 // 149371 // Homo sapiens exocyst complex component 8 (EXOC8), mR	GNPAT	GNPAT, Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), q42.2
SNP_A-2204457	ccagctgacttatgcd[A/G]cttgaccatttaagcc	A	G	NM_014236 // downstream // 19908 // Hs.498028 // GNPAT // 8443 // Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA. /// NM_175876 // downstream // 37872 // Hs.356198 // EXOC8 // 149371 // Homo sapiens exocyst complex component 8 (EXOC8), mR	GNPAT	GNPAT, Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), q42.2
SNP_A-2070100	acacatcaactcactat[C/T]acaaaatgtttcaca	C	T	NM_022051 // intron // 0 // Hs.444450 // EGLN1 // 54583 // Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// ENST00000357180 // intron // 0 // — // — // — // — /// ENST00000258246 // intron // 0 // — // — // — // —	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2
SNP_A-2158575	attgtagccactgata[C/T]aaccaagctcctgttt	C	T	NM_022051 // intron // 0 // Hs.444450 // EGLN1 // 54583 // Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// ENST00000357180 // intron // 0 // — // — // — // — /// ENST00000258246 // intron // 0 // — // — // — // —	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2
SNP_A-2296199	gcattctgggatcca[A/G]tcaagtgaaagaggat	A	G	NM_022051 // 5UTR // 0 // Hs.444450 // EGLN1 // 54583 // Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA. /// ENST00000258246 // 5UTR // 0 // — // — // — // —	EGLN1	EGLN1, Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), q42.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784409	ggccctattcatttca[A/C]tccaagaaggaccact	A	C	NM_005999 // intron // 0 // Hs.96247 // TSNAX // 7257 // Homo sapiens translin-associated factor X (TSNAX), mRNA. /// ENST00000261391 // intron // 0 // — // — // — // — // — /// ENST00000357874 // intron // 0 // — // — // — // —	TSNAX	TSNAX, Homo sapiens translin-associated factor X (TSNAX), q42.2
SNP_A-2101953	agatgggtgttaatgc[C/T]ccctttcttccctgtc	C	T	NM_018662 // intron // 0 // Hs.13318 // DISC1 // 27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// ENST00000295051 // intron // 0 // — // — // — // —	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2231810	ctcaaagaactcacag[A/G]caagtattgaagtcag	A	G	NM_018662 // downstream // 76170 // Hs.13318 // DISC1 // 27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 284967 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 lik	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1898440	tgcttcgggccttaaa[A/T]ccagactgctgacctc	A	T	NM_018662 // downstream // 93701 // Hs.13318 // DISC1 // 27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 267436 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 lik	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1695673	tctagatgtgcagttgtaccataaa[A/G]gactgagagtctttatcactaataa	A	G	NM_022051 // intron // 0 // Hs.130946 // EGLN1 // 54583 // egl nine homolog 1 (C. elegans)	EGLN1	EGLN1 , rs537135, egl nine homolog 1 (C. elegans),q42.2
SNP_A-2270831	gacagggctggttttg[C/T]aaatctgaagatcaca	C	T	NM_018662 // downstream // 98655 // Hs.13318 // DISC1 // 27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 262482 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 lik	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1752427	aaatagcccaggtcagcatggcttg[A/C]actatttttaactccaggtactagg	A	C	NM_022051 // intron // 0 // Hs.130946 // EGLN1 // 54583 // egl nine homolog 1 (C. elegans)	EGLN1	EGLN1 , rs545937, egl nine homolog 1 (C. elegans),q42.2
SNP_A-1668634	gtgagagttttaatcctgttgtggt[A/C]aactcgcctttcttgcttgctata	A	C	NM_022051 // intron // 0 // Hs.130946 // EGLN1 // 54583 // egl nine homolog 1 (C. elegans)	EGLN1	EGLN1 , rs546774, egl nine homolog 1 (C. elegans),q42.2
SNP_A-1699203	tcatatcttgctaacactcagtgaa[C/T]tgccctcagctgatcctctgccctg	C	T	NM_022051 // intron // 0 // Hs.130946 // EGLN1 // 54583 // egl nine homolog 1 (C. elegans)	EGLN1	EGLN1 , rs479311, egl nine homolog 1 (C. elegans),q42.2
SNP_A-1708214	ttgaaggaggaaatgaatttagaaa[C/G]gactgtgttgactcttgaggaaagc	C	G	NM_005999 // upstream // 103369 // Hs.96247 // TSNAX // 7257 // translin associated factor X /// NM_022051 // upstream // 240 // Hs.130946 // EGLN1 // 54583 // egl nine homolog 1 (C. elegans)	TSNAX	TSNAX , rs1890767, translin-associated factor X ,q42.2
SNP_A-2290879	gcaaggcttgtgtctg[A/G]aaaatactctcaaata	A	G	NM_018662 // downstream // 247042 // Hs.13318 // DISC1 // 27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 114095 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 li	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-1849565	tatgggcttcacatga[C/G]aggcatattgaacaat	C	G	NM_018662 // downstream // 360297 // Hs.13318 // DISC1 // 27185 // Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA. /// NM_020808 // downstream // 840 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 like	DISC1	DISC1, Homo sapiens disrupted in schizophrenia 1 (DISC1), q42.2
SNP_A-2114373	agggacatagaattta[C/G]acttgacacagtggag	C	G	NM_020808 // upstream // 12429 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 278323 // Hs.160373 // KIAA1383 // 54627 // Homo sapiens mRNA for KIAA1383 protei	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1889468	tgagttgaatatactg[A/T]atgagatggtggatat	A	T	NM_020808 // upstream // 18835 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 271917 // Hs.160373 // KIAA1383 // 54627 // Homo sapiens mRNA for KIAA1383 protei	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1941810	ttggaccttcagctaa[C/T]ggcatatacaaaaatt	C	T	NM_020808 // upstream // 19677 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 271075 // Hs.160373 // KIAA1383 // 54627 // Homo sapiens mRNA for KIAA1383 protei	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-2048294	aagcagagggtatgga[G/T]gagaaacacagtggac	G	T	NM_020808 // upstream // 75839 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 214913 // Hs.160373 // KIAA1383 // 54627 // Homo sapiens mRNA for KIAA1383 protei	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-2314750	ggagtctggagagtta[C/T]atttttgatgtattg	C	T	NM_020808 // upstream // 123743 // Hs.268774 // SIPA1L2 // 57568 // Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA. /// AB037804 // upstream // 167009 // Hs.160373 // KIAA1383 // 54627 // Homo sapiens mRNA for KIAA1383 prote	SIPA1L2	SIPA1L2, Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), q42.2
SNP_A-1785520	ggctcagatggagtgc[C/T]acctaagtccctggcc	C	T	AB037804 // downstream // 73509 // Hs.160373 // KIAA1383 // 54627 // Homo sapiens mRNA for KIAA1383 protein, partial cds. /// NM_032324 // upstream // 66769 // Hs.16034 // MGC13186 // 84284 // Homo sapiens hypothetical protein MGC13186 (MGC13186), mRNA. /	KIAA1383	KIAA1383, Homo sapiens for KIAA1383 protein, partial cds. ,q42.2
SNP_A-2058559	aatcagcagcattaga[C/T]agcagttataatctat	C	T	NM_014801 // intron // 0 // Hs.370605 // PCNXL2 // 80003 // Homo sapiens hypothetical protein FLJ11383 (FLJ11383), transcript variant 1, mRNA. /// NM_024938 // intron // 0 // Hs.370605 // PCNXL2 // 80003 // Homo sapiens hypothetical protein FLJ11383 (FLJ1	PCNXL2	PCNXL2, Homo sapiens hypothetical protein FLJ11383 (FLJ11383), transcript variant 1, q42.2
SNP_A-1988623	aggcataaatgagaac[A/G]aaaacattaacattgt	A	G	NM_032435 // 3UTR // 0 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// ENST00000272005 // 3UTR // 0 // — // — // — // —	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2152270	attaaatcattgacca[C/T]tggcaaccaacttaac	C	T	NM_032435 // downstream // 5624 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 224375 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1),	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2230939	ctatggctcacatgat[A/C]aaatgtaagtaaaaaa	A	C	NM_032435 // downstream // 10781 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 219218 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1),	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2130517	atactccagacctaga[A/G]atgaagaagccagcaa	A	G	NM_032435 // downstream // 43740 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 186259 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1),	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1880783	tcttggcttctcttaa[C/T]tggaacacagtggcca	C	T	NM_032435 // downstream // 100837 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 129162 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1)	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2106921	agccttgataaaataa[C/G]cagtctctccaaatgc	C	G	NM_032435 // downstream // 104237 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 125762 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1)	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2267142	gaataataggcccccc[A/G]aagagatccatgtctt	A	G	NM_032435 // downstream // 112628 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 117371 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1)	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2204884	ccagggaaggcatccc[A/G]gaaatggtacacctat	A	G	NM_032435 // downstream // 123359 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 106640 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1)	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2303195	gctatcggaatatgaa[A/C]gtaagggatgctgggc	A	C	NM_032435 // downstream // 133273 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 96726 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1),	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1958109	ttttcagtgtgttgcc[A/G]atgaaggggatgaatg	A	G	NM_032435 // downstream // 160812 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 69187 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1),	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-1873535	tctcacaacttgagac[C/T]gaaaattaagctggga	C	T	NM_032435 // downstream // 175487 // Hs.546455 // KIAA1804 // 84451 // Homo sapiens mixed lineage kinase 4 (KIAA1804), mRNA. /// NM_002245 // upstream // 54512 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1),	KIAA1804	KIAA1804, Homo sapiens mixed lineage kinase 4 (KIAA1804), q42.2
SNP_A-2286409	gatgctgatatgacag[A/C]aggccctgaaagcaat	A	C	NM_002245 // downstream // 5088 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), mRNA. /// NM_173508 // upstream // 227752 // Hs.158748 // SLC35F3 // 148641 // Homo sapiens solute carrier family 35, member F3	KCNK1	KCNK1, Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), q42.2
SNP_A-1988750	ggcttcacaactaatc[A/G]agttcctgggctggaa	A	G	NM_002245 // downstream // 109049 // Hs.208544 // KCNK1 // 3775 // Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), mRNA. /// NM_173508 // upstream // 123791 // Hs.158748 // SLC35F3 // 148641 // Homo sapiens solute carrier family 35, member	KCNK1	KCNK1, Homo sapiens potassium channel, subfamily K, member 1 (KCNK1), q42.2
SNP_A-1716193	gttctgtacaattccgtgtactact[G/T]aaatgcaaattattatcagtattag	G	T	AK074078 // intron // 0 // Hs.436455 // FLJ11383 // 80003 // hypothetical protein FLJ11383	FLJ11383	FLJ11383 , rs7550169, hypothetical protein FLJ11383,q42.2
SNP_A-1901960	tggcaggttctacgta[C/T]ggctgtgtgcattttg	C	T	NM_173508 // intron // 0 // Hs.158748 // SLC35F3 // 148641 // Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // intron // 0 // — // — // — // —	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2
SNP_A-1853688	tatttttttcagcttta[C/T]ggatgtgtaattgaca	C	T	NM_173508 // intron // 0 // Hs.158748 // SLC35F3 // 148641 // Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // intron // 0 // — // — // — // —	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2
SNP_A-1690791	tatatgcaagagaattcaaacttac[A/G]gaaaattaatgttattcaaggtcac	A	G	NM_032435 // intron // 0 // Hs.50883 // KIAA1804 // 84451 // mixed lineage kinase 4	KIAA1804	KIAA1804 , rs10489692, mixed lineage kinase 4,q42.2
SNP_A-2062039	aatgggagaataagat[A/G]aatctaccctaaggca	A	G	NM_173508 // downstream // 2194 // Hs.158748 // SLC35F3 // 148641 // Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA. /// ENST00000329010 // downstream // 2194 // — // — // — // — /// ENST00000337699 // downstream // 934 // — //	SLC35F3	SLC35F3, Homo sapiens solute carrier family 35, member F3 (SLC35F3), q42.2
SNP_A-2101289	agatcggtaagaacaa[C/T]gtgagatccagcagat	C	T	NM_005646 // upstream // 13110 // Hs.498115 // TARBP1 // 6894 // Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), mRNA. /// NM_182972 // downstream // 114819 // Hs.350268 // IRF2BP2 // 359948 // Homo sapiens interferon regulatory factor 2 binding pr	TARBP1	TARBP1, Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), q42.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2271642	gaccacgaggatgagg[A/C]atggctttgtagacag	A	C	NM_015014 // downstream // 131608 // Hs.535224 // KIAA0117 // 23029 // Homo sapiens KIAA0117 protein (KIAA0117), mRNA. /// ENST00000323183 // upstream // 154324 // --- // --- // --- // --- /// ENST00000343285 // downstream // 131608 // --- // --- // --- /	KIAA0117	KIAA0117, Homo sapiens KIAA0117 protein (KIAA0117), q42.3
SNP_A-1958192	ttttcattatgaatca[G/T]cacggtcatttagtca	G	T	NM_003193 // intron // 0 // Hs.498143 // TBCE // 6905 // Homo sapiens tubulin-specific chaperone e (TBCE), mRNA. /// ENST00000264180 // intron // 0 // --- // --- // --- // ---	TBCE	TBCE, Homo sapiens tubulin-specific chaperone e (TBCE), q42.3
SNP_A-1812701	gtgggaaaacagcagg[C/G]attgcaatttcaaaag	C	G	NM_002508 // upstream // 64124 // Hs.356624 // NID // 4811 // Homo sapiens nidogen (enactin) (NID), mRNA. /// NM_003272 // upstream // 13359 // Hs.498160 // TM7SF1 // 7107 // Homo sapiens transmembrane 7 superfamily member 1 (upregulated in kidney) (TM7SF	NID	NID, Homo sapiens nidogen (enactin) (NID), q42.3
SNP_A-1958883	ttttcttagtttaaaa[G/T]cagtgtatattgtcgt	G	T	NM_019891 // intron // 0 // Hs.424926 // ERO1LB // 56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// ENST00000264181 // intron // 0 // --- // --- // --- // --- /// ENST00000360959 // intron // 0 // --- // --- // --- // --- /// ENST0	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-2144181	atgaggtgactgctta[C/T]acaaggagatgttaca	C	T	NM_019891 // upstream // 71384 // Hs.424926 // ERO1LB // 56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// NM_080738 // upstream // 41011 // Hs.352224 // EDARADD // 128178 // Homo sapiens EDAR-associated death domain (EDARADD), tran	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-2280658	gaggtccagaagagaa[A/T]gagtgagccaggagtg	A	T	NM_019891 // upstream // 73830 // Hs.424926 // ERO1LB // 56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// NM_080738 // upstream // 38565 // Hs.352224 // EDARADD // 128178 // Homo sapiens EDAR-associated death domain (EDARADD), tran	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-2206649	ccatgaccggttctaa[A/G]gctcctgtcagtggat	A	G	NM_019891 // upstream // 73897 // Hs.424926 // ERO1LB // 56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// NM_080738 // upstream // 38498 // Hs.352224 // EDARADD // 128178 // Homo sapiens EDAR-associated death domain (EDARADD), tran	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-2179988	cactttgttgtgtgtc[A/G]actgtatgtcaataca	A	G	NM_019891 // upstream // 79095 // Hs.424926 // ERO1LB // 56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// NM_080738 // upstream // 33300 // Hs.352224 // EDARADD // 128178 // Homo sapiens EDAR-associated death domain (EDARADD), tran	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-2260578	gaaacattaccatatt[C/G]aagacagtgaacaagt	C	G	NM_019891 // upstream // 79181 // Hs.424926 // ERO1LB // 56605 // Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), mRNA. /// NM_080738 // upstream // 33214 // Hs.352224 // EDARADD // 128178 // Homo sapiens EDAR-associated death domain (EDARADD), tran	ERO1LB	ERO1LB, Homo sapiens ERO1-like beta (S. cerevisiae) (ERO1LB), q42.3
SNP_A-1784683	ggcctctgagatccac[A/G]ataccaaattagcaca	A	G	AK001221 // upstream // 22465 // Hs.209958 // FLJ10359 // 55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 59939 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // upstream	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. ,q43
SNP_A-2079595	acccggctagactcag[A/G]catgatattacgcagt	A	G	AK001221 // upstream // 31886 // Hs.209958 // FLJ10359 // 55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 50518 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // upstream	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. q43
SNP_A-2186472	cagggaagatcacaca[A/G]aggagatgtcagaagt	A	G	AK001221 // upstream // 36176 // Hs.209958 // FLJ10359 // 55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 46228 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // upstream	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. ,q43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255926	ctttaacaaatcacca[C/T]agtctggattgcttaa	C	T	AK001221 // upstream // 54452 // Hs.209958 // FLJ10359 // 55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 27952 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // upstream	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. ,q43
SNP_A-1797914	ggtttttcaaatgcac[A/G]aaggtcattttagaaa	A	G	AK001221 // upstream // 54792 // Hs.209958 // FLJ10359 // 55127 // Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. /// NM_001104 // upstream // 27612 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // upstream	FLJ10359	FLJ10359, Homo sapiens cDNA FLJ10359 fis, clone NT2RM2001243. ,q43
SNP_A-1989561	tctagtccaaagtcta[A/C]atcagccaactgaaat	A	C	NM_001104 // intron // 0 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens actinin, alpha 2 (ACTN2), mRNA. /// ENST00000264176 // intron // 0 // — // —	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-1989577	tgtaacagagacagca[C/G]aaaacattttagaaca	C	G	NM_001104 // intron // 0 // Hs.445037 // ACTN3 // 89 // Homo sapiens actinin, alpha 3 (ACTN3), mRNA. /// NM_001103 // intron // 0 // Hs.498178 // ACTN2 // 88 // Homo sapiens actinin, alpha 2 (ACTN2), mRNA. /// ENST00000264176 // intron // 0 // — // —	ACTN3	ACTN3, Homo sapiens actinin, alpha 3 (ACTN3), q43
SNP_A-2203236	ccacttatatgaggta[C/T]gtagtcaaattcacag	C	T	ENST00000333549 // downstream // 6160 // — // — // — // — /// ENST00000294915 // upstream // 71245 // — // — // — // —	-	q43
SNP_A-1758846	tatgcatgtaaaagcccttaataca[A/G]tgccagccaatgcttgccattatga	A	G	NM_003272 // downstream // 6503 // Hs.15791 // TM7SF1 // 7107 // transmembrane 7 superfamily member 1 (upregulated in kidney) /// NM_019891 // downstream // 1752 // Hs.424926 // ERO1LB // 56605 // ERO1-like beta (S. cerevisiae)	TM7SF1	TM7SF1 , rs1110423, transmembrane 7 superfamily member 1 (upregulated in kidney) ,q42.3
SNP_A-2303739	gctcagcaagcaaata[C/G]atgagacagttttggg	C	G	NM_001035 // upstream // 240928 // Hs.109514 // RYR2 // 6262 // Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000294916 // upstream // 25197 // — // — // — // — /// ENST00000355794 // upstream // 240928 // — // — // — /	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-2251403	cttcacaattgacctc[A/G]cagggttgtggtagag	A	G	NM_001035 // upstream // 159584 // Hs.109514 // RYR2 // 6262 // Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000294916 // upstream // 106541 // — // — // — // — /// ENST00000355794 // upstream // 159584 // — // — // —	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-1840379	tagcatttaaccagta[A/T]ctagtaactctgtgcg	A	T	NM_001035 // intron // 0 // Hs.109514 // RYR2 // 6262 // Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000355794 // intron // 0 // — // — // — // — /// ENST00000360064 // intron // 0 // — // — // — // —	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-2144299	atgagtgttcattgaa[C/T]tgatatctcaaagaag	C	T	NM_001035 // intron // 0 // Hs.109514 // RYR2 // 6262 // Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000355794 // intron // 0 // — // — // — // — /// ENST00000360064 // intron // 0 // — // — // — // —	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-2084614	actatgtgatagttaa[A/G]aacaagctttggtaga	A	G	NM_001035 // intron // 0 // Hs.109514 // RYR2 // 6262 // Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), mRNA. /// ENST00000355794 // intron // 0 // — // — // — // — /// ENST00000360064 // intron // 0 // — // — // — // —	RYR2	RYR2, Homo sapiens ryanodine receptor 2 (cardiac) (RYR2), q43
SNP_A-2000816	aaacactctttacacc[A/G]agttctattagcttgg	A	G	NM_021186 // upstream // 55400 // Hs.136241 // ZP4 // 57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 55400 // — // — // — // — /// ENST00000309886 // downstream // 322459 // — // — // — //	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-1856832	tcacatttaatgtgcc[C/T]ggagataaaacacagg	C	T	NM_021186 // upstream // 195549 // Hs.136241 // ZP4 // 57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 195549 // — // — // — // — /// ENST00000309886 // downstream // 182310 // — // — // —	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798011	gtaaaactacagattc[A/G]agatgctagtgaaa	A	G	NM_021186 // upstream // 343836 // Hs.136241 // ZP4 // 57829 // Homo sapiens zona pellucida glycoprotein 4 (ZP4), mRNA. /// ENST00000235643 // upstream // 343836 // — // — // — // — /// ENST00000309886 // downstream // 34023 // — // — // — // — /	ZP4	ZP4, Homo sapiens zona pellucida glycoprotein 4 (ZP4), q43
SNP_A-1725582	ctcaactgaggagacagtggataa[A/G]catacctttgaatgtc cgtgacc	A	G	NM_001035 // intron // 0 // Hs.90821 // RYR2 // 6262 // ryanodine receptor 2 (cardiac)	RYR2	RYR2 , rs939698, ryanodine receptor 2 (cardiac),q43
SNP_A-2227004	ctaatgcctaaaccaa[C/T]gatatttgatgttaa	C	T	NM_173624 // upstream // 145239 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// ENST00000309886 // upstream // 77478 // — // — // — // — /// ENST00000344214 // upstream // 145239 // — // —	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1821315	gtttgccacaactgag[G/T]atctataaaaaacagc	G	T	NM_173624 // upstream // 77998 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// ENST00000309886 // upstream // 144719 // — // — // — // — /// ENST00000344214 // upstream // 77998 // — // —	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2219796	ccttaccattcatttta[A/G]caaagcaataggatg	A	G	NM_173624 // upstream // 77615 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// ENST00000309886 // upstream // 145102 // — // — // — // — /// ENST00000344214 // upstream // 77615 // — // —	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1780931	ggatgacccaaatcgc[C/T]gatactggagccctca	C	T	NM_173624 // upstream // 77587 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// ENST00000309886 // upstream // 145130 // — // — // — // — /// ENST00000344214 // upstream // 77587 // — // —	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2285362	gatctgggggcatcta[C/T]ctccacagtcaatcca	C	T	NM_173624 // downstream // 37 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 1415233 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3), m	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2046064	aagactagatgaggaa[A/G]cgaatttgatgaagaa	A	G	NM_173624 // downstream // 128486 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 1286784 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1741903	acatacttcctaatttacatctta[C/T]atcttcacaaattttccagatt tcc	C	T	NM_000740 // upstream // 1646017 // Hs.7138 // CHRM3 // 1131 // cholinergic receptor, muscarinic 3 /// NM_021186 // upstream // 370800 // Hs.136241 // ZP4 // 57829 // zona pellucida glycoprotein 4	CHRM3	CHRM3 , rs970522, cholinergic receptor, muscarinic 3 ,q43
SNP_A-2232512	ctcaccaccaagttt[C/T]cagatgctgcatttga	C	T	NM_173624 // downstream // 606353 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 808917 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3)	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1872655	tctagtcacttcaaaa[C/T]gttagcatctatctc	C	T	NM_173624 // downstream // 608666 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 806604 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3)	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2163449	caaaaaaaagtgacag[A/G]aaagtgacctcatccc	A	G	NM_173624 // downstream // 653291 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 761979 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3)	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1666540	atcctgagaatgaaatgacccaata[C/T]ggaaagacttttgata catacagtt	C	T	NM_000740 // upstream // 1293224 // Hs.7138 // CHRM3 // 1131 // cholinergic receptor, muscarinic 3 /// NM_021186 // upstream // 723593 // Hs.136241 // ZP4 // 57829 // zona pellucida glycoprotein 4	CHRM3	CHRM3 , rs574819, cholinergic receptor, muscarinic 3 ,q43
SNP_A-2292446	gcactacagtctaagc[A/G]atctgaaacttagctt	A	G	NM_173624 // downstream // 925973 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 489297 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3)	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1823452	taaaaggaaaaaagca[A/G]ggttatgcggttggaa	A	G	NM_173624 // downstream // 1056836 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 358434 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-2096116	agacatctgtccggtg[C/T]aactgatcaatgtgag	C	T	NM_173624 // downstream // 1269784 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 145486 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1835556	tacctgttcatatcat[A/G]agtaattctaaagctc	A	G	NM_173624 // downstream // 1333524 // Hs.371796 // FLJ40504 // 284085 // Homo sapiens hypothetical protein FLJ40504 (FLJ40504), mRNA. /// NM_000740 // upstream // 81746 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3)	FLJ40504	FLJ40504, Homo sapiens hypothetical protein FLJ40504 (FLJ40504), q43
SNP_A-1990436	ctctgacagaaggaca[A/G]gattcattataccatg	A	G	NM_000740 // downstream // 65096 // Hs.7138 // CHRM3 // 1131 // Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3), mRNA. /// ENST00000255380 // downstream // 65096 // --- // --- // --- // --- /// ENST00000319953 // upstream // 33013 // — // — //	CHRM3	CHRM3, Homo sapiens cholinergic receptor, muscarinic 3 (CHRM3), q43
SNP_A-1740937	tatgtagtttcacaataatttaatc[A/G]agttgtctttcaagcaaaaa aaaaa	A	G	NM_000740 // upstream // 599480 // Hs.7138 // CHRM3 // 1131 // cholinergic receptor, muscarinic 3 /// NM_021186 // upstream // 1417337 // Hs.136241 // ZP4 // 57829 // zona pellucida glycoprotein 4	CHRM3	CHRM3 , rs4570412, cholinergic receptor, muscarinic 3 ,q43
SNP_A-1943131	ttggtcaccaaagtca[C/T]ggaagttgtagaagaa	C	T	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. q43
SNP_A-2062375	aatgtaagtagattga[A/G]tacaacatcagagaac	A	G	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-2279472	gaggatctggtagaaa[C/T]atggtagctgacttcc	C	T	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-2090153	acttgagctcgggtga[C/T]gaaggctacagtgagc	C	T	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-1786656	ggcttgcagattttgg[A/G]aagaagagtgagtgca	A	G	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-2070611	acaccttctccaatga[A/G]atctgcaccccagtct	A	G	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. ,q43
SNP_A-1845364	tatacttacagaaata[C/T]cattgtgtttaatcaa	C	T	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // — /// ENST00000330178 // intron // 0 // — // — // — // ---	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds. q43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897216	tgctctctctagaacc[A/G]cacagataaatccaat	A	G	AF218942 // intron // 0 // Hs.24889 // FMN2 // 56776 // Homo sapiens clone r56121 formin 2-like protein mRNA, partial cds. /// ENST00000319653 // intron // 0 // — // — // — // — /// ENST00000330178 // intron // 0 // — // — // — // —	FMN2	FMN2, Homo sapiens clone r56121 formin 2-like protein partial cds, q43
SNP_A-2287091	gatgtaggaaaggaaa[A/G]agagaagagactgact	A	G	NM_022469 // intron // 0 // Hs.98206 // GREM2 // 64388 // Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), mRNA. /// ENST00000318160 // intron // 0 // — // — // — // —	GREM2	GREM2, Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), q43
SNP_A-2241470	ctgagtgacagtcgaa[G/T]aggaagagcatatttc	G	T	NM_022469 // intron // 0 // Hs.98206 // GREM2 // 64388 // Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), mRNA. /// ENST00000318160 // intron // 0 // — // — // — // —	GREM2	GREM2, Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), q43
SNP_A-1885816	tgacagtctgaagtaa[C/T]cacaggactttagta	C	T	NM_022469 // intron // 0 // Hs.98206 // GREM2 // 64388 // Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), mRNA. /// ENST00000318160 // intron // 0 // — // — // — // —	GREM2	GREM2, Homo sapiens gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis) (GREM2), q43
SNP_A-1990673	ggaggcgctacagaga[C/T]ggctcaattatggcgg	C	T	NM_002924 // intron // 0 // Hs.130171 // RGS7 // 6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // — // — // — // — /// ENST00000331110 // intron // 0 // — // — // — // —	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2256631	ctttcacggttattca[C/T]ggccattcacagagtg	C	T	NM_002924 // intron // 0 // Hs.130171 // RGS7 // 6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // — // — // — // — /// ENST00000331110 // intron // 0 // — // — // — // —	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2086524	actgaaaatcactgac[A/G]aaaggcagattaacaa	A	G	NM_002924 // intron // 0 // Hs.130171 // RGS7 // 6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // — // — // — // — /// ENST00000331110 // intron // 0 // — // — // — // —	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2141806	atcttgagttaggcaa[C/T]gagtttttagatgtaa	C	T	NM_002924 // intron // 0 // Hs.130171 // RGS7 // 6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // — // — // — // — /// ENST00000331110 // intron // 0 // — // — // — // —	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-1836417	tactcatcttcctttа[C/T]ggtattcatgcattca	C	T	NM_002924 // intron // 0 // Hs.130171 // RGS7 // 6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// ENST00000348120 // intron // 0 // — // — // — // — /// ENST00000331110 // intron // 0 // — // — // — // —	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-1894569	tgccacattagataga[A/G]cagtttgcagcagact	A	G	NM_002924 // upstream // 23717 // Hs.130171 // RGS7 // 6000 // Homo sapiens regulator of G-protein signalling 7 (RGS7), mRNA. /// NM_000143 // downstream // 118110 // Hs.498239 // FH // 2271 // Homo sapiens fumarate hydratase (FH), nuclear gene encoding m	RGS7	RGS7, Homo sapiens regulator of G-protein signalling 7 (RGS7), q43
SNP_A-2272219	gacctattgtaaggga[A/G]aaaaagctgagcaaat	A	G	NM_144625 // intron // 0 // Hs.97527 // FLJ32978 // 128025 // Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// ENST00000341258 // intron // 0 // — // — // — // —	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43
SNP_A-1878873	tctgtttgaaacctaa[A/T]cctcaacgtgatggtg	A	T	NM_144625 // intron // 0 // Hs.97527 // FLJ32978 // 128025 // Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// ENST00000341258 // intron // 0 // — // — // — // —	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43
SNP_A-1797302	ggttgtaagagagaag[A/C]ccgtattccttagctt	A	C	NM_144625 // intron // 0 // Hs.97527 // FLJ32978 // 128025 // Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// ENST00000341258 // intron // 0 // — // — // — // —	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43
SNP_A-1951611	tttcctgtgagccaac[C/T]gactctgatgttatta	C	T	NM_144625 // intron // 0 // Hs.97527 // FLJ32978 // 128025 // Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// ENST00000341258 // intron // 0 // — // — // — // —	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2293602	gcagccaaattgatta[C/T]caagtgttaaataaca	C	T	NM_144625 // downstream // 10630 // Hs.97527 // FLJ32978 // 128025 // Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// NM_130398 // upstream // 36388 // Hs.498248 // EXO1 // 9156 // Homo sapiens exonuclease 1 (EXO1), transcript variant 2.	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43
SNP_A-2306859	gctgtggaagttcaga[A/C]caggaaggtgagatct	A	C	NM_144625 // downstream // 31386 // Hs.97527 // FLJ32978 // 128025 // Homo sapiens hypothetical protein FLJ32978 (FLJ32978), mRNA. /// NM_130398 // upstream // 15632 // Hs.498248 // EXO1 // 9156 // Homo sapiens exonuclease 1 (EXO1), transcript variant 2.	FLJ32978	FLJ32978, Homo sapiens hypothetical protein FLJ32978 (FLJ32978), q43
SNP_A-1758395	cctaaatatgctctgcaaggaatttt[G/T]cccaacaaaggcacttc tctagtta	G	T	NM_002924 // intron // 0 // Hs.79348 // RGS7 // 6000 // regulator of G-protein signalling 7	RGS7	RGS7 , rs4131604, regulator of G-protein signalling 7, q43
SNP_A-2268618	gaatgcatgcgaaaa[A/G]cacaggaagcagagtg	A	G	NM_001004343 // upstream // 38509 // Hs.534971 // LOC440738 // 440738 // Homo sapiens MAP1 light chain 3-like protein 2 (LOC440738), mRNA. /// ENST00000357246 // upstream // 38509 // -- // -- /// ENST00000272035 // upstream // 19503 // —	LOC440738	LOC440738, Homo sapiens MAP1 light chain 3-like protein 2 (LOC440738), q43
SNP_A-1990940	ctgctttattggttca[C/T]gaattgggcagttcca	C	T	NM_152666 // intron // 0 // Hs.498252 // FLJ40773 // 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // intron // 0 // — // — // — /// ENST00000314809 // intron // 0 // — // — // —	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2284230	gatattaatgagcaat[C/G]aaaatgtgaaagtggc	C	G	NM_152666 // intron // 0 // Hs.498252 // FLJ40773 // 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314809 // intron // 0 // — // — // —	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1669183	ctagtcctctcgaaagttaaacata[C/T]ataaagcaatagtagc caaaatgt	C	T	NM_003686 // upstream // 18203 // Hs.47504 // EXO1 // 9156 // exonuclease 1 /// NM_006027 // upstream // 18203 // Hs.47504 // EXO1 // 9156 // exonuclease 1 /// NM_130398 // upstream // 17714 // Hs.47504 // EXO1 // 9156 // exonuclease 1 /// NM_144625 // d	EXO1	EXO1 , rs10489350, exonuclease 1, q43
SNP_A-2224754	cgtcttggccttgtac[A/C]gcgttcagaaggcgac	A	C	NM_152666 // upstream // 79680 // Hs.498252 // FLJ40773 // 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream // 154920 // -- // -- // -- /// ENST00000314809 // upstream // 79680 // -- // —	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1806834	gtctatctttcccat[C/T]aggtctgttcgaaaac	C	T	NM_152666 // upstream // 229943 // Hs.498252 // FLJ40773 // 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream // 305183 // -- // -- // -- /// ENST00000314809 // upstream // 229943 // -- // -	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1991004	gcacacattgcacccaa[A/G]tgaagctaacttatgc	A	G	NM_152666 // upstream // 301159 // Hs.498252 // FLJ40773 // 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream // 376399 // -- // -- // -- /// ENST00000314809 // upstream // 301159 // -- // -	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-1838203	tagaactgggtgtcag[A/C]aactaagtgaggagag	A	C	NM_152666 // upstream // 303988 // Hs.498252 // FLJ40773 // 200150 // Homo sapiens hypothetical protein FLJ40773 (FLJ40773), mRNA. /// ENST00000314833 // upstream // 379228 // -- // -- // -- /// ENST00000314809 // upstream // 303988 // -- // -	FLJ40773	FLJ40773, Homo sapiens hypothetical protein FLJ40773 (FLJ40773), q43
SNP_A-2184339	cagcgaaaaatacaaa[A/G]gattgaatacctat	A	G	NM_006642 // intron // 0 // Hs.546337 // SDCCAG8 // 10806 // Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA. /// ENST00000355875 // intron // 0 // -- // -- // -- /// ENST00000343783 // intron // 0 // — // — // —	SDCCAG8	SDCCAG8, Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), q44

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1734358	atatctgaagtcccatttgatgc[C/T]agctccacaaacatatatt aggga	C	T	NM_014812 // downstream // 278342 // Hs.25132 // KAB // 9859 // KARP-1-binding protein /// NM_152666 // upstream // 321391 // Hs.375933 // FLJ40773 // 200150 // hypothetical protein FLJ40773	KAB	KAB , rs950125, KARP-1-binding protein q43
SNP_A-1884712	tgaatatcaaagtaat[A/C]atgctaaatgaacaag	A	C	NM_181690 // intron // 0 // Hs.498292 // AKT3 // 10000 // Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma) (AKT3), transcript variant 2, mRNA. /// NM_005465 // intron // 0 // Hs.498292 // AKT3 // 10000 // Homo sapiens v	AKT3	AKT3, Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma) (AKT3), transcript variant 2, q44
SNP_A-2187035	caggtagataaagatc[A/G]cagcaaacaaaatttg	A	G	ENST00000338317 // downstream // 91176 // — // — // — /// ENST00000308105 // upstream // 193550 // — // — // — // —	-	q44
SNP_A-1857171	tccctgcagctaccaa[C/G]gaatgactgtgtaggt	C	G	ENST00000338317 // downstream // 263017 // — // — // — /// ENST00000308105 // upstream // 21709 // — // — // —	-	q44
SNP_A-1781343	ggatgtggtaaggcca[C/G]gatttggatgctgga	C	G	NM_173807 // intron // 0 // Hs.459534 // MGC33370 // 257044 // Homo sapiens hypothetical protein MGC33370 (MGC33370), mRNA. /// ENST00000348926 // intron // 0 // — // — // — // —	MGC33370	MGC33370, Homo sapiens hypothetical protein MGC33370 (MGC33370), q44
SNP_A-2000868	gcatgaccaaaccata[A/G]tcttgatttccctac	A	G	NM_173807 // downstream // 10747 // Hs.459534 // MGC33370 // 257044 // Homo sapiens hypothetical protein MGC33370 (MGC33370), mRNA. /// NM_016076 // upstream // 1969 // Hs.498317 // PNAS-4 // 51029 // Homo sapiens CGI-146 protein (PNAS-4), mRNA. /// ENST0	MGC33370	MGC33370, Homo sapiens hypothetical protein MGC33370 (MGC33370), q44
SNP_A-1991262	tcttatcacgagtcct[A/G]cgggaaaccagctgcc	A	G	NM_031844 // upstream // 131964 // Hs.166463 // HNRPU // 3192 // Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA. /// NM_004501 // upstream // 131964 // Hs.166463 // HNRPU // 3192 /	HNRPU	HNRPU, Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, q44
SNP_A-2135288	atatgtttgatttag[A/T]ccaattctcaaactc	A	T	NM_031844 // upstream // 139728 // Hs.166463 // HNRPU // 3192 // Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA. /// NM_004501 // upstream // 139728 // Hs.166463 // HNRPU // 3192 /	HNRPU	HNRPU, Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, q44
SNP_A-1940412	ttgccataaccttagc[A/G]cattgtaagtactagg	A	G	NM_031844 // upstream // 152357 // Hs.166463 // HNRPU // 3192 // Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, mRNA. /// NM_004501 // upstream // 152357 // Hs.166463 // HNRPU // 3192 /	HNRPU	HNRPU, Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 1, q44
SNP_A-1799979	gtacataaagtaatca[A/G]actcagacaggaagta	A	G	ENST00000360484 // downstream // 61850 // — // — // — // — /// ENST00000329504 // upstream // 164673 // — // — // — // —	-	q44
SNP_A-1821958	gttttcacacatggga[A/G]gggcgagggaagctct	A	G	ENST00000360484 // downstream // 221394 // — // — // — // — /// ENST00000329504 // upstream // 5129 // — // — // — // —	-	q44
SNP_A-1991411	cccagaagaagaaata[A/G]ctatctgaacttcatc	A	G	NM_022743 // intron // 0 // Hs.546424 // SMYD3 // 64754 // Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA. /// ENST00000327801 // intron // 0 // — // — // — // —	SMYD3	SMYD3, Homo sapiens SET and MYND domain containing 3 (SMYD3), q44
SNP_A-1666890	ggggaaatctgcgtcacatgggcgga[C/T]agaaggtccctcgaa tccctcaatc	C	T	NM_178551 // 3UTR // 0 // - // - // - // -	-	-, rs1173844, -q44
SNP_A-1850582	tattaagtgttaggaa[C/G]tgtactaagtgcttta	C	G	NM_016002 // intron // 0 // Hs.498397 // CGI-49 // 51097 // Homo sapiens CGI-49 protein (CGI-49), mRNA. /// ENST00000271981 // intron // 0 // — // — // — // —	CGI-49	CGI-49, Homo sapiens CGI-49 protein (CGI-49), q44
SNP_A-2299821	gcctaatcagaatccc[C/T]ccaaaaatatagtact	C	T	NM_175865 // intron // 0 // Hs.300887 // — // 0 // Homo sapiens ELYS transcription factor-like protein TMBS62 (ELYS), mRNA. /// ENST00000283201 // intron // 0 // — // — // — // — /// ENST00000318558 // intron // 0 // — // — // — // —	-	-, Homo sapiens ELYS transcription factor-like protein TMBS62 (ELYS), q44

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2203488	ccagaagaaacgctta[C/T]acaagatgtgggaaaa	C	T	NM_207401 // upstream // 36949 // Hs.456511 // FLJ45717 // 388759 // Homo sapiens FLJ45717 protein (FLJ45717), mRNA. /// NM_003431 // downstream // 7393 // Hs.421238 // ZNF124 // 7678 // Homo sapiens zinc finger protein 124 (HZF-16) (ZNF124), mRNA. /// EN	FLJ45717	FLJ45717, Homo sapiens FLJ45717 protein (FLJ45717), q44
SNP_A-1792376	gggttgtcatttttg[C/T]agaagtcatatgatag	C	T	NM_003431 // intron // 0 // Hs.421238 // ZNF124 // 7678 // Homo sapiens zinc finger protein 124 (HZF-16) (ZNF124), mRNA. /// ENST00000360371 // intron // 0 // — // — // — // —	ZNF124	ZNF124, Homo sapiens zinc finger protein 124 (HZF-16) (ZNF124), q44
SNP_A-2299986	gcctatggcattcaca[A/G]gaaacatggcaattcc	A	G	NM_032752 // downstream // 25102 // Hs.157277 // ZNF496 // 84838 // Homo sapiens zinc finger protein 496 (ZNF496), mRNA. /// ENST00000310480 // upstream // 37368 // — // — // — // — /// ENST00000310476 // downstream // 22995 // — // — // — // —	ZNF496	ZNF496, Homo sapiens zinc finger protein 496 (ZNF496), q44
SNP_A-1876191	tctgactcctcagagc[A/G]cccgagtaagcaagtc	A	G	NM_032752 // intron // 0 // Hs.157277 // ZNF496 // 84838 // Homo sapiens zinc finger protein 496 (ZNF496), mRNA. /// ENST00000310476 // intron // 0 // — // — // — // — /// ENST00000294753 // intron // 0 // — // — // — // —	ZNF496	ZNF496, Homo sapiens zinc finger protein 496 (ZNF496), q44
SNP_A-1884075	tgaagccaggaatagc[A/G]caggtgattgcctcct	A	G	NM_183395 // intron // 0 // Hs.159483 // CIAS1 // 114548 // Homo sapiens cold autoinflammatory syndrome 1 (CIAS1), transcript variant 2, mRNA. /// NM_004895 // intron // 0 // Hs.159483 // CIAS1 // 114548 // Homo sapiens cold autoinflammatory syndrome 1 (C	CIAS1	CIAS1, Homo sapiens cold autoinflammatory syndrome 1 (CIAS1), transcript variant 2, q44
SNP_A-1884957	tgaatgataaaatgag[G/T]attgcaatttctgaag	G	T	NM_001004492 // upstream // 20728 // Hs.446999 // OR2B11 // 127623 // Homo sapiens olfactory receptor, family 2, subfamily B, member 11 (OR2B11), mRNA. /// NM_198074 // downstream // 58836 // Hs.332905 // OR2C3 // 81472 // Homo sapiens olfactory receptor,	OR2B11	OR2B11, Homo sapiens olfactory receptor, family 2, subfamily B, member 11 (OR2B11), q44
SNP_A-1819973	gttgttgcaaaagtga[C/T]gcttccctgttgttaa	C	T	NM_145278 // intron // 0 // Hs.498425 // LOC148823 // 148823 // Homo sapiens LOC148823 (LOC148823), mRNA. /// ENST00000302122 // intron // 0 // — // — // — // —	LOC148823	LOC148823, Homo sapiens LOC148823 (LOC148823), q44
SNP_A-1921939	ttactctccaaggaaa[A/G]aagatgtgttctcaaa	A	G	NM_145278 // intron // 0 // Hs.498425 // LOC148823 // 148823 // Homo sapiens LOC148823 (LOC148823), mRNA. /// ENST00000302122 // intron // 0 // — // — // — // —	LOC148823	LOC148823, Homo sapiens LOC148823 (LOC148823), q44
SNP_A-1828510	taagcagagcataatc[A/G]aaacagtgtgagttct	A	G	NM_207314 // downstream // 36745 // — // — // 0 // — /// NM_001001966 // downstream // 2447 // — // OR5AT1 // 284532 // Homo sapiens olfactory receptor, family 5, subfamily AT, member 1 (OR5AT1), mRNA. /// ENST00000319427 // downstream // 36745 //	-	q44
SNP_A-1793996	ggtcacccctctaaca[C/T]gctgtcttcacttaga	C	T	NM_001001963 // downstream // 3237 // — // OR2L8 // 391190 // Homo sapiens olfactory receptor, family 2, subfamily L, member 8 (OR2L8), mRNA. /// NM_001004491 // upstream // 12344 // — // OR2AK2 // 391191 // Homo sapiens olfactory receptor, family 2,	OR2L8	OR2L8, Homo sapiens olfactory receptor, family 2, subfamily L, member 8 (OR2L8), q44
SNP_A-2212385	ccctgtcattaagcca[C/T]gctgaacagctgacct	C	T	NM_001001918 // downstream // 9881 // — // OR5BF1 // 127066 // Homo sapiens olfactory receptor, family 5, subfamily BF, member 1 (OR5BF1), mRNA. /// NM_001004696 // upstream // 2071 // — // OR2T4 // 127074 // Homo sapiens olfactory receptor, family 2,	OR5BF1	OR5BF1, Homo sapiens olfactory receptor, family 5, subfamily BF, member 1 (OR5BF1), q44
SNP_A-2097006	agactgcccatcagtg[A/T]aaagcaacagagttga	A	T	NM_018968 // upstream // 121938 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 136308 // — // — // — // — /// ENST00000308624 // upstream // 121938 // — // — // — // —	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-1909369	tgtattacctgtccca[A/G]tggatttgattagcta	A	G	NM_018968 // upstream // 106996 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 151250 // — // — // — // — /// ENST00000308624 // upstream // 106996 // — // — // — // —	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2069302	acacaaaaaacagttac[A/G]gaagaatgcagtgacc	A	G	NM_018968 // upstream // 35454 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000295062 // downstream // 222792 // — // — // — // /// ENST00000308624 // upstream // 35454 // — // — // — // —	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2260450	gaaacaccccccactca[C/T]actgccaaaatcaaac	C	T	NM_018968 // intron // 0 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000308624 // intron // 0 // — // — // —	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2304388	gctcgtccgctccgcc[A/G]cgaatccgtttcccca	A	G	NM_018968 // intron // 0 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000308624 // intron // 0 // — // — // —	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2192909	catcctacctcggca[A/G]ctacagactcagcttg	A	G	NM_018968 // intron // 0 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// ENST00000308624 // intron // 0 // — // — // — // —	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2110760	aggacgatgtagacac[A/G]gtgaaggaaacacact	A	G	NM_018968 // downstream // 8113 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// NM_175722 // upstream // 37740 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_1	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-1835765	tacgcagatgtgcttc[A/G]ataaatctcgggccttc	A	G	NM_018968 // downstream // 11979 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// NM_175722 // upstream // 33874 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-2202564	ccacctatctcctccca[A/T]gtgacaatttcaata	A	T	NM_018968 // downstream // 26429 // Hs.148819 // SNTG2 // 54221 // Homo sapiens syntrophin, gamma 2 (SNTG2), mRNA. /// NM_175722 // upstream // 19424 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_	SNTG2	SNTG2, Homo sapiens syntrophin, gamma 2 (SNTG2), p25.3
SNP_A-1897117	tgctcctgtctcctca[A/G]aagtattccacttgg	A	G	NM_175722 // intron // 0 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5. mRNA. /// NM_175719 // intron // 0 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 2, mRNA. /// N	TPO	TPO, Homo sapiens thyroid peroxidase (TPO), transcript variant 5, p25.3
SNP_A-2113638	aggctcactcctgtc[C/T]accttttcgccttg	C	T	NM_175722 // intron // 0 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5. mRNA. /// NM_175719 // intron // 0 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 2, mRNA. /// N	TPO	TPO, Homo sapiens thyroid peroxidase (TPO), transcript variant 5, p25.3
SNP_A-1862951	tcattgcttacggact[C/T]acttacccgagcatcc	C	T	NM_175722 // downstream // 3814 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_175719 // downstream // 3814 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant	TPO	TPO, Homo sapiens thyroid peroxidase (TPO), transcript variant 5, p25.3
SNP_A-2203168	ccactgtaaatgcatg[A/G]aacttgagacttca	A	G	NM_175722 // downstream // 28381 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_175719 // downstream // 28381 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript varian	TPO	TPO, Homo sapiens thyroid peroxidase (TPO), transcript variant 5, p25.3
SNP_A-2083636	actaatttccattccc[A/G]acaacagtgtataagt	A	G	NM_175722 // downstream // 65112 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript variant 5, mRNA. /// NM_175719 // downstream // 65112 // Hs.467554 // TPO // 7173 // Homo sapiens thyroid peroxidase (TPO), transcript varian	TPO	TPO, Homo sapiens thyroid peroxidase (TPO), transcript variant 5, p25.3
SNP_A-2236381	ctcgcattgtacttga[C/T]ggtaactgatcaagg	C	T	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835042	taccccaaggcttcta[C/T]gttccggcgcaggcgg	C	T	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3
SNP_A-2076101	acattcagagatgtgc[A/G]aagtatttcaccacaa	A	G	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3
SNP_A-1881712	tctttggagagggcaa[G/T]gtagcacaacccttt	G	T	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3
SNP_A-1889635	tgataaatcccataat[A/G]aaaacgtgcagagggc	A	G	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3
SNP_A-2267656	gaatcacatacagcca[A/G]gtttgaaatgatcaca	A	G	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3
SNP_A-1722194	actttgggtcctggattaagtcaca[C/T]tttccattgtcttttctgcattgta	C	T	AB029029 // upstream // 219062 // Hs.434418 // MYT1L // 23040 // myelin transcription factor 1-like /// BC033992 // downstream // 320243 // Hs.375803 // - // - // CDNA clone IMAGE:5296578, partial cds	MYT1L	MYT1L , rs1515746, myelin transcription factor 1-like ,p25.3
SNP_A-1802265	gtatatgcattatcaa[A/G]taagagactaagtgag	A	G	ENST00000295067 // intron // 0 // — // — // — // — /// ENST00000321345 // intron // 0 // — // — // — // —	-	p25.3
SNP_A-2194248	catgaggccaacgtca[C/G]attagcttattaaatt	C	G	NM_002936 // downstream // 674304 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 106125 // — // — // — // — /// ENST00000321345 // upstream // 106185 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2243995	ctgcttcaaaaaacaa[A/C]caggtctgccaggtgg	A	C	NM_002936 // downstream // 667490 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 112939 // — // — // — // — /// ENST00000321345 // upstream // 112999 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-1961818	atggcggacacccttc[C/T]ccccatcaagcttgag	C	T	NM_002936 // downstream // 660143 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 120286 // — // — // — // — /// ENST00000321345 // upstream // 120346 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2294386	gcaggtggtggtgcac[A/G]gtgattttctaagcca	A	G	NM_002936 // downstream // 585615 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 194814 // — // — // — // — /// ENST00000321345 // upstream // 194874 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2224503	cgtatcagttgtaaac[A/G]ccctgacgaggtagcg	A	G	NM_002936 // downstream // 582471 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 197958 // — // — // — // — /// ENST00000321345 // upstream // 198018 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2071071	acactgcactgaaact[A/G]aaaaacacgatggttg	A	G	NM_002936 // downstream // 508473 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 271956 // — // — // — // — /// ENST00000321345 // upstream // 272016 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2285222	gatctccctctgaaca[C/T]ggagctgcaaggagcc	C	T	NM_002936 // downstream // 506873 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 273556 // — // — // — // — /// ENST00000321345 // upstream // 273616 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2251224	cttcaaaccataacaa[C/G]agtgatgtccaaacag	C	G	NM_002936 // downstream // 504677 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 275752 // — // — // — // — /// ENST00000321345 // upstream // 275812 // — // — // — // —	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826514	taacaagcaaggctca[C/T]ggaagagacaactag	C	T	NM_002936 // downstream // 503303 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 277126 // --- // --- // --- /// ENST00000321345 // upstream // 277186 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2171494	caatcatgcacaaaga[C/T]actgaatcaataatca	C	T	NM_002936 // downstream // 501457 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 278972 // --- // --- // --- /// ENST00000321345 // upstream // 279032 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2104801	agcataactctatag[A/C]aaagccagataaataa	A	C	NM_002936 // downstream // 501281 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 279148 // --- // --- // --- /// ENST00000321345 // upstream // 279208 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2235738	ctcctcccggtggtga[C/T]atgtttacagagaag	C	T	NM_002936 // downstream // 497298 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 283131 // --- // --- // --- /// ENST00000321345 // upstream // 283191 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-1888545	tgaggatactgattag[C/T]agttcagacattcagg	C	T	NM_002936 // downstream // 497217 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 283212 // --- // --- // --- /// ENST00000321345 // upstream // 283272 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2113474	aggcggtgattacgga[C/T]gaactcggatgatctc	C	T	NM_002936 // downstream // 372826 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 407603 // --- // --- // --- /// ENST00000321345 // upstream // 407663 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2145280	atgcacattgtcaggga[A/G]cacctaagcctccaat	A	G	NM_002936 // downstream // 372707 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 407722 // --- // --- // --- /// ENST00000321345 // upstream // 407782 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2242839	ctgccaattcaatgta[C/T]aaaacagtgacaccct	C	T	NM_002936 // downstream // 220291 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 560138 // --- // --- // --- /// ENST00000321345 // upstream // 560198 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2111207	aggagattaatcctca[C/T]agtgctagacgtgccc	C	T	NM_002936 // downstream // 101601 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// ENST00000295067 // upstream // 678828 // --- // --- // --- /// ENST00000321345 // upstream // 678888 // --- // --- // ---	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-2253590	ctcttgtggctgaac[A/G]aagacgtgttggaacc	A	G	NM_002936 // upstream // 6994 // Hs.502765 // RNASEH1 // 246243 // Homo sapiens ribonuclease H1 (RNASEH1), mRNA. /// NM_001011 // upstream // 10017 // Hs.546287 // RPS7 // 6201 // Homo sapiens ribosomal protein S7 (RPS7), mRNA. /// ENST00000315212 // upst	RNASEH1	RNASEH1, Homo sapiens ribonuclease H1 (RNASEH1), p25.3
SNP_A-1956304	ttgtgttgcagtggc[A/G]agggaatatagacctg	A	G	NM_199232 // intron // 0 // Hs.97899 // ALLC // 55821 // Homo sapiens allantoicase (ALLC), transcript variant 2, mRNA. /// NM_018436 // intron // 0 // Hs.97899 // ALLC // 55821 // Homo sapiens allantoicase (ALLC). transcript variant 1, mRNA. /// ENST00000	ALLC	ALLC, Homo sapiens allantoicase (ALLC), transcript variant 2, p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1928652	ttcactttcaacagac[A/G]aatatcttctatgcca	A	G	NM_199232 // intron // 0 // Hs.97899 // ALLC // 55821 // Homo sapiens allantoicase (ALLC), transcript variant 2, mRNA. /// NM_018436 // intron // 0 // Hs.97899 // ALLC // 55821 // Homo sapiens allantoicase (ALLC), transcript variant 1, mRNA. /// ENST00000	ALLC	ALLC, Homo sapiens allantoicase (ALLC), transcript variant 2, p25.3
SNP_A-2063064	aatgttcagaattgtc[A/G]acctcaggcaacttgc	A	G	ENST00000311817 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-1825556	taaataggtattttctc[C/T]cgagctctctatgtca	C	T	ENST00000311817 // intron // 0 // --- // --- // --- // ---	-	p25.3
SNP_A-2006097	tcattaatcaaacaca[A/C]ggtattgcattagcgt	A	C	ENST00000311817 // downstream // 21939 // --- // --- // --- // --- /// ENST00000331540 // downstream // 722854 // --- // --- // --- // ---	-	p25.3
SNP_A-1794958	ggtgaaaactgacctg[A/C]atccgctgatctttgt	A	C	ENST00000311817 // downstream // 22130 // --- // --- // --- // --- /// ENST00000331540 // downstream // 722663 // --- // --- // --- // ---	-	p25.3
SNP_A-1921271	ttacattcactatgaa[A/G]gcaaattcactgaacc	A	G	ENST00000311817 // downstream // 93928 // --- // --- // --- // --- /// ENST00000331540 // downstream // 650865 // --- // --- // --- // ---	-	p25.3
SNP_A-2197652	cattctgcaaactgcg[C/T]atcatggcctcagtct	C	T	ENST00000311817 // downstream // 107025 // --- // --- // --- // --- /// ENST00000331540 // downstream // 637768 // --- // --- // --- // ---	-	p25.3
SNP_A-1656105	ccaaaatctttaaagactttcaata[A/G]cttacaacctgtgttcatatattct	A	G	NM_003310 // downstream // 1341292 // Hs.4992 // TSSC1 // 7260 // tumor suppressing subtransferable candidate 1 /// NM_018436 // downstream // 146107 // Hs.97899 // ALLC // 55821 // allantoicase	TSSC1	TSSC1 , rs10495493, tumor suppressing subtransferable candidate 1 ,p25.3
SNP_A-1846371	tatatgggagtggaaa[A/G]ttcaaaaattcaacag	A	G	ENST00000311817 // downstream // 153560 // --- // --- // --- // --- /// ENST00000331540 // downstream // 591233 // --- // --- // --- // ---	-	p25.3
SNP_A-1684984	tccatattgacttgaaagtagctaa[C/T]tacagccaggcagagggactatcta	C	T	NM_003310 // downstream // 1331915 // Hs.4992 // TSSC1 // 7260 // tumor suppressing subtransferable candidate 1 /// NM_018436 // downstream // 155484 // Hs.97899 // ALLC // 55821 // allantoicase	TSSC1	TSSC1 , rs10495494, tumor suppressing subtransferable candidate 1 ,p25.3
SNP_A-1870455	tcgaacagatacagaa[C/G]taaaaagagcaatcac	C	G	ENST00000311817 // downstream // 277987 // --- // --- // --- // --- /// ENST00000331540 // downstream // 466806 // --- // --- // --- // ---	-	p25.3
SNP_A-2310609	ggaagagatttctgag[A/G]atggcacctaagacag	A	G	ENST00000311817 // downstream // 333067 // --- // --- // --- // --- /// ENST00000331540 // downstream // 411726 // --- // --- // --- // ---	-	p25.3
SNP_A-1889561	tgagtttgggcccagg[C/T]atgacattccattctc	C	T	ENST00000311817 // downstream // 366356 // --- // --- // --- // --- /// ENST00000331540 // downstream // 378437 // --- // --- // --- // ---	-	p25.3
SNP_A-2053304	aagtgaatgacattta[A/G]gtaggattttcctgct	A	G	ENST00000311817 // downstream // 479216 // --- // --- // --- // --- /// ENST00000331540 // downstream // 265577 // --- // --- // --- // ---	-	p25.3
SNP_A-2104140	agcagacttttaggac[C/G]ctgttgcatggtctcc	C	G	ENST00000311817 // downstream // 480313 // --- // --- // --- // --- /// ENST00000331540 // downstream // 264480 // --- // --- // --- // ---	-	p25.3
SNP_A-1909924	tgtcagagtttattct[C/G]acgtgtgcagcatcct	C	G	NM_003310 // downstream // 653495 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 21516 // --- // --- // --- // --- /// ENST00000263884 // downstream // 653495 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2040921	aaccctcctcttactg[A/T]aactcaagctgatttc	A	T	NM_003310 // downstream // 579230 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 95781 // --- // --- // --- // --- /// ENST00000263884 // downstream // 579230 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1786649	ggcttgataaaccgac[A/G]aaaataatgaaaggca	A	G	NM_003310 // downstream // 558367 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 116644 // --- // --- // --- // --- /// ENST00000263884 // downstream // 558367 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1729610	catgattcctcaaagtagtgtacct[G/T]aaacctaggaagtaaacatcaagat	G	T	NM_003310 // downstream // 565964 // Hs.4992 // TSSC1 // 7260 // tumor suppressing subtransferable candidate 1 /// NM_018436 // downstream // 921435 // Hs.97899 // ALLC // 55821 // allantoicase	TSSC1	TSSC1 , rs10495506, tumor suppressing subtransferable candidate 1 ,p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1684824	ttgattgcatattgatcaataggt[A/C]aatgtgattacaatgaaaa tcattg	A	C	NM_003310 // downstream // 557943 // Hs.4992 // TSSC1 // 7260 // tumor suppressing subtransferable candidate 1 /// NM_018436 // downstream // 929456 // Hs.97899 // ALLC // 55821 // allantoicase	TSSC1	TSSC1 , rs826015, tumor suppressing subtransferable candidate 1 p25.2
SNP_A-2074946	acatcagttctgtcaa[C/T]gtccatttgttcacat	C	T	NM_003310 // downstream // 414685 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 260326 // — // — // — // — /// ENST00000263884 // downstream // 414685 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1946431	tttaaacttttgttggd[A/G]ctttactgtagatgc	A	G	NM_003310 // downstream // 399722 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 275289 // — // — // — // — /// ENST00000263884 // downstream // 399722 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1801191	gtagctagactagcaa[C/T]taggaggaacttacag	C	T	NM_003310 // downstream // 389519 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 285492 // — // — // — // — /// ENST00000263884 // downstream // 389519 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1921774	ttactaatatcaggaa[C/T]gaaaagagtgacatct	C	T	NM_003310 // downstream // 389305 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 285706 // — // — // — // — /// ENST00000263884 // downstream // 389305 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1889375	tgagtgttcgtgttccg[C/T]ccgtgttggtgccttg	C	T	NM_003310 // downstream // 278669 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 396342 // — // — // — // — /// ENST00000263884 // downstream // 278669 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1785111	ggcgtggctgggaaca[A/G]attatgagttgagagt	A	G	NM_003310 // downstream // 275166 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 399845 // — // — // — // — /// ENST00000263884 // downstream // 275166 //	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2244455	ctggacattattacgac[C/T]gaatccagtgccttc	C	T	NM_003310 // downstream // 59142 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 615869 // — // — // — // — /// ENST00000263884 // downstream // 59142 // -	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2042814	aactctgctaacaata[C/T]atgaagcatggtgaag	C	T	NM_003310 // downstream // 31116 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000331540 // upstream // 643895 // — // — // — // — /// ENST00000263884 // downstream // 31116 // -	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2122887	agtggcctcatttgc[C/T]cgtgttgtctgtgg	C	T	NM_003310 // intron // 0 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // — // — // — // —	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2304397	gctcgtttctctgctc[A/G]cctaggatttcatgca	A	G	NM_003310 // intron // 0 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // — // — // — // —	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2113249	aggccctggtgttccc[A/G]gcgctttggcctctg	A	G	NM_003310 // intron // 0 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // — // — // — // —	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100004	agagtctggccaggaa[A/C]ccgggtgccggtggtg	A	C	NM_003310 // intron // 0 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // --- // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1961882	tggctcccttcttaac[A/G]caatcttttccaaggc	A	G	NM_003310 // intron // 0 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // --- // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-1953174	tttctttcctactcca[A/G]attgccaactttccct	A	G	NM_003310 // intron // 0 // Hs.4992 // TSSC1 // 7260 // Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), mRNA. /// ENST00000263884 // intron // 0 // --- // --- // --- // ---	TSSC1	TSSC1, Homo sapiens tumor suppressing subtransferable candidate 1 (TSSC1), p25.2
SNP_A-2093309	agaacggccgctacgc[A/C]agcaatggtgaccttt	A	C	NM_016030 // intron // 0 // Hs.252713 // TTC15 // 51112 // Homo sapiens tetratricopeptide repeat domain 15 (TTC15), mRNA. /// ENST00000304601 // intron // 0 // --- // --- // --- // --- /// ENST00000324266 // intron // 0 // --- // --- // --- // ---	TTC15	TTC15, Homo sapiens tetratricopeptide repeat domain 15 (TTC15), p25.2
SNP_A-1839232	tagaggctggtggtta[C/T]gaactgagggatgtaa	C	T	NM_016030 // downstream // 13825 // Hs.252713 // TTC15 // 51112 // Homo sapiens tetratricopeptide repeat domain 15 (TTC15), mRNA. /// NM_018269 // downstream // 4524 // Hs.502773 // MTCBP-1 // 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase	TTC15	TTC15, Homo sapiens tetratricopeptide repeat domain 15 (TTC15), p25.2
SNP_A-1961888	aaataaagagttagtg[A/C]atctttcaaattgttg	A	C	NM_018269 // upstream // 184972 // Hs.502773 // MTCBP-1 // 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), mRNA. /// NM_003108 // upstream // 536843 // Hs.432638 // SOX11 // 6664 // Homo sapiens	MTCBP-1	MTCBP-1, Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), p25.2
SNP_A-2126668	ataaacaggaaattac[A/T]ctattgattgcattgc	A	T	NM_018269 // upstream // 233422 // Hs.502773 // MTCBP-1 // 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), mRNA. /// NM_003108 // upstream // 488393 // Hs.432638 // SOX11 // 6664 // Homo sapiens	MTCBP-1	MTCBP-1, Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), p25.2
SNP_A-1729348	aggctgtgtggactgaatgcttaga[C/T]gaatcattatttatttttagacctg	C	T	NM_003108 // upstream // 245922 // Hs.432638 // SOX11 // 6664 // SRY (sex determining region Y)-box 11 /// NM_018269 // upstream // 475893 // Hs.502773 // SIPL // 55256 // SIPL protein	SOX11	SOX11 , rs10495520, SRY (sex determining region Y)-box 11 ,p25.2
SNP_A-1929967	ttcatgctatttggta[A/G]atgaaatgccccactc	A	G	NM_018269 // upstream // 694368 // Hs.502773 // MTCBP-1 // 55256 // Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), mRNA. /// NM_003108 // upstream // 27447 // Hs.432638 // SOX11 // 6664 // Homo sapiens	MTCBP-1	MTCBP-1, Homo sapiens membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1 (MTCBP-1), p25.2
SNP_A-2198539	catttattaagcacca[A/G]ctatgttcttagaaaa	A	G	NM_003108 // downstream // 69870 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 199705 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1836321	tactcaagtttcttcc[A/G]ctgtttggatcccttc	A	G	NM_003108 // downstream // 70056 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 199519 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2132168	ataggtgcccttgtta[A/G]atgtttcatgattcta	A	G	NM_003108 // downstream // 70973 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 198602 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1961916	cctcactgcttatata[A/C]ccccacattctcacct	A	C	NM_003108 // downstream // 85403 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 184172 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1961918	agcttagaggagttaa[A/G]tgatttggccaagaac	A	G	NM_003108 // downstream // 89704 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 179871 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1961919	catgtgcaactgtaa[A/G]attccaattagataa	A	G	NM_003108 // downstream // 89786 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 179789 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2069780	acacagaaagatctga[C/T]gatactgaggcgcatc	C	T	NM_003108 // downstream // 90381 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 179194 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1961921	acctgtgcacagtgga[A/G]gaacacacaggagcaa	A	G	NM_003108 // downstream // 92329 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 177246 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRNA	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1877639	tctgggaaggactaaa[C/T]cgtgagaactccacat	C	T	NM_003108 // downstream // 108957 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 160618 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2295600	gcatctttgaaaatta[C/T]cctagtggctgttctc	C	T	NM_003108 // downstream // 117258 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 152317 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1809981	gtgagttgtttgaaga[A/G]aaaggaagataaacgg	A	G	NM_003108 // downstream // 127827 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 141748 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-1961927	cttagaatagcagag[A/G]atggaattccacccag	A	G	NM_003108 // downstream // 130972 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 138603 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2095500	agacaacttgggtaa[C/G]gattcttgcagcgag	C	G	NM_003108 // downstream // 132014 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 137561 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2212616	ccctcattaatgggg[C/T]catacatttacggctg	C	T	NM_003108 // downstream // 138428 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 131147 // Hs.452443 // — // 0 // Homo sapiens hypothetical protein FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1961929	agcaatgctctgctaa[A/G]aataaatatcggaaa	A	G	NM_003108 // downstream // 144407 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 125168 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2077673	accactcaagtgccta[C/T]ggaatgtatttata	C	T	NM_003108 // downstream // 147864 // Hs.432638 // SOX11 // 6664 // Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), mRNA. /// NM_153011 // upstream // 121711 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRN	SOX11	SOX11, Homo sapiens SRY (sex determining region Y)-box 11 (SOX11), p25.2
SNP_A-2162204	atttactcaatcccc[A/G]ctgacacccacgtaga	A	G	NM_153011 // downstream // 17564 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 17564 // --- // --- // --- /// ENST00000256722 // downstream // 856513 // --- // --- // -	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-1878608	tctgtgtgtgccgaga[A/G]gtactggagatttcat	A	G	NM_153011 // downstream // 26910 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 26910 // --- // --- // --- /// ENST00000256722 // downstream // 847167 // --- // --- // -	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2069041	acaatggcgaacacac[C/T]agtataaggactaatc	C	T	NM_153011 // downstream // 515812 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 515812 // --- // --- // --- /// ENST00000256722 // downstream // 358265 // --- // --- //	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2088551	actgtctaatgcaaga[C/T]gaagggtccagaaag	C	T	NM_153011 // downstream // 543872 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 543872 // --- // --- // --- /// ENST00000256722 // downstream // 330205 // --- // --- //	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-1961965	aggctgcagaaagaca[C/G]tatctgtgcaagcggg	C	G	NM_153011 // downstream // 673635 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 673635 // --- // --- // --- /// ENST00000256722 // downstream // 200442 // --- // --- //	-	-, Homo sapiens hypothetical protein FLJ30594 (FLJ30594), p25.2
SNP_A-2117694	aggttccaggcaagca[C/T]ggccccaggtattgca	C	T	NM_153011 // downstream // 681888 // Hs.452443 // --- // 0 // Homo sapiens hypothetical protein FLJ30594 (FLJ30594), mRNA. /// ENST00000360879 // downstream // 681888 // --- // --- // --- /// ENST00000256722 // downstream // 192189 // --- // --- //	-	-, Homo sapiens hypothetical protein FLJ30594 ((FLJ30594), p25.2
SNP_A-1798308	gtaaaggagcagtaac[A/G]agggaatatctaccaa	A	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2035645	aaatgtcaagagcctat[C/G]cttcaaacagagtcaa	C	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2089027	acttaacacattttgc[A/G]gatctttccatttgaa	A	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2140670	atctctctacagtgga[C/G]tatttctctccagc	C	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2242505	ctgcagcataccaggt[C/G]aatgatcttgcaaata	C	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // --- // --- // ---	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2145958	atgccgaattctcgat[C/G]agtggccaccccaggg	C	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // — // — // — // —	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1847811	tatctccagctcctac[A/G]gcagtacccagcacac	A	G	NM_014746 // intron // 0 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // intron // 0 // — // — // — // —	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1742233	tgatgtatacacgtatacaaaaaat[A/G]aatatcaaaacttcacattgttcac	A	G	NM_014746 // intron // 0 // Hs.78894 // RNF144 // 9781 // ring finger protein 144	RNF144	RNF144 , rs389351, ring finger protein 144,p25.1
SNP_A-2186203	caggccttgctttctt[C/T]aaacctatcagctgct	C	T	NM_014746 // downstream // 67902 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 67902 // — // — // — // — /// ENST00000343152 // downstream // 737368 // — // — // —	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-2234688	ctccagctatttctac[A/G]ctattgtaacatatat	A	G	NM_014746 // downstream // 78524 // Hs.22146 // RNF144 // 9781 // Homo sapiens ring finger protein 144 (RNF144), mRNA. /// ENST00000320892 // downstream // 78524 // — // — // — // — /// ENST00000343152 // downstream // 726746 // — // — // —	RNF144	RNF144, Homo sapiens ring finger protein 144 (RNF144), p25.1
SNP_A-1708206	ccttgatttgcttgcttaatatgaa[G/T]tacttaaaatttaattttcttctct	G	T	NM_002166 // upstream // 1622191 // Hs.180919 // ID2 // 3398 // inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// NM_014746 // downstream // 15771 // Hs.78894 // RNF144 // 9781 // ring finger protein 144	ID2	ID2 , rs309275, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein ,p25.1
SNP_A-1694997	gcattcccttactctcttctcacct[A/G]caagaatttataacctcttctgaga	A	G	NM_002166 // upstream // 1621338 // Hs.180919 // ID2 // 3398 // inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// NM_014746 // downstream // 16624 // Hs.78894 // RNF144 // 9781 // ring finger protein 144	ID2	ID2 , rs309274, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein ,p25.1
SNP_A-1754986	tttttgccaaaggaaatctcaagac[G/T]ggtacagagttaaaaatgaagtaca	G	T	NM_002166 // upstream // 1619690 // Hs.180919 // ID2 // 3398 // inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// NM_014746 // downstream // 18272 // Hs.78894 // RNF144 // 9781 // ring finger protein 144	ID2	ID2 , rs309271, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein ,p25.1
SNP_A-1671558	tacctcttaatactcattttgtaga[C/T]agaaataagctttttttttcttt	C	T	NM_002166 // upstream // 1490566 // Hs.180919 // ID2 // 3398 // inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// NM_014746 // downstream // 147396 // Hs.78894 // RNF144 // 9781 // ring finger protein 144	ID2	ID2 , rs4669147, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein ,p25.1
SNP_A-2228539	ctacttttagccaca[C/T]caaatacaaaaactca	C	T	NM_207358 // downstream // 329894 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 117348 // — // — // — // — /// ENST00000358606 // downstream // 329894 // --	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-2033365	aaatagccaaaccatg[A/G]cataagggaagagcta	A	G	NM_207358 // downstream // 329842 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 117400 // — // — // — // — /// ENST00000358606 // downstream // 329842 // --	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-1891759	tgatttataaactaga[G/T]gccaatccatggctga	G	T	NM_207358 // downstream // 329657 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 117585 // --- // --- // --- // --- /// ENST00000358606 // downstream // 329657 // --	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-2302667	gctacctcccatcacc[A/G]aaatttcagatgtcag	A	G	NM_207358 // downstream // 328234 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 119008 // — // — // — // — /// ENST00000358606 // downstream // 328234 // --	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2292388	gcacgtgcaaagctgcd[A/G]gagaaaaaattgggtg	A	G	NM_207358 // downstream // 322629 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 124613 // — // — // — // — /// ENST00000358606 // downstream // 322629 // –	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2209354	cccagttttggacaaca[A/G]ccgtgtactcatgtga	A	G	NM_207358 // downstream // 321977 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 125265 // — // — // — // — /// ENST00000358606 // downstream // 321977 // –	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2206525	ccatcttcataccaaa[C/T]caactttacaaaggc	C	T	NM_207358 // downstream // 252528 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// ENST00000343152 // upstream // 194714 // — // — // — // — /// ENST00000358606 // downstream // 252528 // –	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2150090	atgtcccatgtagtta[C/T]agtattgcacaaca	C	T	NM_207358 // upstream // 137066 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 220285 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-1918630	ttaaattagctctttta[C/T]ctcacaacaaataaat	C	T	NM_207358 // upstream // 144521 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 212830 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2047730	aagattcgctggtcta[A/G]gacagaggcagagtta	A	G	NM_207358 // upstream // 144613 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 212738 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2289876	gcaaactccatgaacg[C/G]catgacttagagtt	C	G	NM_207358 // upstream // 144824 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 212527 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2195085	catggaagggaaggta[A/C]aatatcatgaggattt	A	C	NM_207358 // upstream // 144877 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 212474 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2052087	aaggttgttgagcaaa[C/G]ttctgattatcatttg	C	G	NM_207358 // upstream // 145524 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 211827 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-1962043	ttggctaaaaacttac[C/T]gagctagagttagcct	C	T	NM_207358 // upstream // 208822 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 148529 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1
SNP_A-2199246	catttttatgatcacc[A/G]agggaatggtctcaat	A	G	NM_207358 // upstream // 253528 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 103823 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789, p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1892134	tgcaaaggaacacatc[G/T]ctttatcaacaccatt	G	T	NM_207358 // upstream // 253668 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 103683 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-1889496	tgagttgggacaagaa[C/T]tcagtggcctgctggg	C	T	NM_207358 // upstream // 253844 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 103507 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant nega	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-2312192	ggacagcgggaatcca[A/G]tcagcacagttcacag	A	G	NM_207358 // upstream // 306399 // Hs.431089 // LOC339789 // 339789 // Homo sapiens hypothetical protein LOC339789 (LOC339789), mRNA. /// NM_002166 // upstream // 50952 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant negat	LOC339789	LOC339789, Homo sapiens hypothetical protein LOC339789 (LOC339789), p25.1
SNP_A-2216312	cctcctcttctatcac[C/T]attgtgttgcctcctc	C	T	NM_002166 // downstream // 12436 // Hs.180919 // ID2 // 3398 // Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA. /// ENST00000234091 // downstream // 12436 // --- // --- // --- /// ENST00000343089 //	ID2	ID2, Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), p25.1
SNP_A-1885296	tgaatttataactcac[C/G]ctgtcccttaaataa	C	G	NM_138799 // upstream // 11871 // Hs.467634 // OACT2 // 129642 // Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), mRNA. /// NM_003887 // upstream // 191147 // Hs.467662 // DDEF2 // 8853 // Homo sapiens development and differen	OACT2	OACT2, Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), p25.1
SNP_A-2141641	atcttcatgaaaagac[C/T]ggaaagatatacatcc	C	T	ENST00000351760 // intron // 0 // --- // --- // --- /// ENST00000343937 // intron // 0 // --- // --- // ---	-	p25.1
SNP_A-2284499	gatcaattgttataaa[A/T]attcactagattata	A	T	ENST00000351760 // intron // 0 // --- // --- // --- /// ENST00000343937 // intron // 0 // --- // --- // ---	-	p25.1
SNP_A-1737203	ccaaaattcataaatcttcagtac[C/T]aatattcaatgtttgaaac aaacag	C	T	NM_003183 // intron // 0 // Hs.404914 // ADAM17 // 6868 // a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme) /// NM_021832 // intron // 0 // Hs.404914 // ADAM17 // 6868 // a disintegrin and metalloproteinase	ADAM17	ADAM17 , rs4278906, a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme), p25.1
SNP_A-1896128	tgcgagtgtagatgaa[A/C]taaaaatagcaaaatg	A	C	NM_006826 // upstream // 27290 // Hs.74405 // YWHAQ // 10971 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /// NM_005680 // upstream // 185177 // Hs.128275 // TAF1B // 9014 // Homo	YWHAQ	YWHAQ, Homo sapiens tyrosine 3-monooxygenase,p25.1
SNP_A-1962075	ttcaggtccgtgtgtc[C/T]catttcactgcactgt	C	T	NM_006826 // upstream // 62922 // Hs.74405 // YWHAQ // 10971 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /// NM_005680 // upstream // 149545 // Hs.128275 // TAF1B // 9014 // Homo	YWHAQ	YWHAQ, Homo sapiens tyrosine 3-monooxygenase,p25.1
SNP_A-2253968	ctgactgcaaagcca[A/G]tgatgtatctatctcg	A	G	NM_006826 // upstream // 84631 // Hs.74405 // YWHAQ // 10971 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /// NM_005680 // upstream // 127836 // Hs.128275 // TAF1B // 9014 // Homo	YWHAQ	YWHAQ, Homo sapiens tyrosine 3-monooxygenase,p25.1
SNP_A-2029177	aaagaactaaataaac[A/G]gaaagacgtcctatgt	A	G	NM_006826 // upstream // 165929 // Hs.74405 // YWHAQ // 10971 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /// NM_005680 // upstream // 46538 // Hs.128275 // TAF1B // 9014 // Homo	YWHAQ	YWHAQ, Homo sapiens tyrosine 3-monooxygenase,p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1706689	gcatttttttttcagtgtaaatcc[A/G]ccctttattgcctccaaaaag atat	A	G	NM_005680 // upstream // 88555 // Hs.121044 // TAF1B // 9014 // TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa /// NM_006826 // upstream // 123912 // Hs.74405 // YWHAQ // 10971 // tyrosine 3-monooxygenase/tryptophan 5-monoox	TAF1B	TAF1B , rs1533388, TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa, p25.1
SNP_A-2248993	ctgttgtttgttctta[C/T]cactagtttcctgttt	C	T	NM_005680 // downstream // 15179 // Hs.128275 // TAF1B // 9014 // Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa (TAF1B), mRNA. /// NM_014552 // upstream // 2100 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens t	TAF1B	TAF1B, Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa (TAF1B), p25.1
SNP_A-2258466	ctttctactgcaagg[C/T]atcataagctaccaat	C	T	NM_014552 // intron // 0 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, mRNA. /// NM_198182 // intron // 0 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens transcription factor CP2-like 2	TFCP2L2	TFCP2L2, Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, p25.1
SNP_A-1829169	taaggttctcactccg[C/T]cctccgtgtcctgat	C	T	NM_014552 // intron // 0 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, mRNA. /// NM_198182 // intron // 0 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens transcription factor CP2-like 2	TFCP2L2	TFCP2L2, Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, p25.1
SNP_A-1819368	gttggcaggatctgca[C/G]gttgccacctgaggc	C	G	NM_014552 // intron // 0 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, mRNA. /// NM_198182 // intron // 0 // Hs.546382 // TFCP2L2 // 29841 // Homo sapiens transcription factor CP2-like 2	TFCP2L2	TFCP2L2, Homo sapiens transcription factor CP2-like 2 (TFCP2L2), transcript variant 1, p25.1
SNP_A-2266692	gaagtgagaacctctc[A/G]aaatcgatcacctatg	A	G	NM_134421 // intron // 0 // Hs.467696 // HPCAL1 // 3241 // Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, mRNA. /// NM_002149 // intron // 0 // Hs.467696 // HPCAL1 // 3241 // Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 1,	HPCAL1	HPCAL1, Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, p25.1
SNP_A-1864574	tccagaggcctggtd[A/G]cttgaaaagatgagct	A	G	NM_134421 // intron // 0 // Hs.467696 // HPCAL1 // 3241 // Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, mRNA. /// NM_002149 // intron // 0 // Hs.467696 // HPCAL1 // 3241 // Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 1,	HPCAL1	HPCAL1, Homo sapiens hippocalcin-like 1 (HPCAL1), transcript variant 2, p25.1
SNP_A-1896533	tgctactgacaggcac[C/T]gagaggctgaatggag	C	T	NM_002539 // upstream // 82572 // Hs.467701 // ODC1 // 4953 // Homo sapiens ornithine decarboxylase 1 (ODC1), mRNA. /// NM_024894 // downstream // 39869 // Hs.222494 // FLJ14075 // 79954 // Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. ///	ODC1	ODC1, Homo sapiens ornithine decarboxylase 1 (ODC1), p25.1
SNP_A-2277845	gagcatgctccttccc[A/G]aagctgattcgtggccc	A	G	NM_002539 // upstream // 82731 // Hs.467701 // ODC1 // 4953 // Homo sapiens ornithine decarboxylase 1 (ODC1), mRNA. /// NM_024894 // downstream // 39710 // Hs.222494 // FLJ14075 // 79954 // Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. ///	ODC1	ODC1, Homo sapiens ornithine decarboxylase 1 (ODC1), p25.1
SNP_A-2136942	atcagatgtgccgtct[C/G]agaacccgggcacggt	C	G	NM_002539 // upstream // 101436 // Hs.467701 // ODC1 // 4953 // Homo sapiens ornithine decarboxylase 1 (ODC1), mRNA. /// NM_024894 // downstream // 21005 // Hs.222494 // FLJ14075 // 79954 // Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. ///	ODC1	ODC1, Homo sapiens ornithine decarboxylase 1 (ODC1), p25.1
SNP_A-1812183	gtggaggagttggga[C/T]gcacttcagaagaata	C	T	NM_024894 // intron // 0 // Hs.222494 // FLJ14075 // 79954 // Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA. /// ENST00000345985 // intron // 0 // — // — // — /// ENST00000263836 // intron // 0 // — // — // —	FLJ14075	FLJ14075, Homo sapiens hypothetical protein FLJ14075 (FLJ14075), p25.1
SNP_A-1714128	ttcgtgatctgaccacaaataaa[C/G]ctggtatctctcaaact gacatct	C	G	NM_024894 // intron // 0 // Hs.235498 // FLJ14075 // 79954 // hypothetical protein FLJ14075	FLJ14075	FLJ14075 , rs6751075, hypothetical protein FLJ14075,p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1727006	tcagttgcagtcccgggtattgaa[A/G]agcatgaacagaaatg aagacaaaa	A	G	NM_024894 // intron // 0 // Hs.235498 // FLJ14075 // 79954 // hypothetical protein FLJ14075	FLJ14075	FLJ14075 , rs7600820, hypothetical protein FLJ14075,p25.1
SNP_A-2006133	ctgttctgcgaaaaag[A/C]cctcatatcttctcag	A	C	NM_144583 // downstream // 81472 // Hs.372429 // ATP6V1C2 // 245973 // Homo sapiens ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA. /// NM_005742 // upstream // 53740 // Hs.212102 // TXNDC7 // 10130 // Homo sapiens thior	ATP6V1C2	ATP6V1C2, Homo sapiens ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), p25.1
SNP_A-2280234	gagggcaggtatcaca[C/T]gtacacttccacaa	C	T	NM_144583 // downstream // 99130 // Hs.372429 // ATP6V1C2 // 245973 // Homo sapiens ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA. /// NM_005742 // upstream // 71398 // Hs.212102 // TXNDC7 // 10130 // Homo sapiens thior	ATP6V1C2	ATP6V1C2, Homo sapiens ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), p25.1
SNP_A-2006134	gctggtgggaatgtaa[A/C]gcgtgcggctgtggg	A	C	NM_002236 // downstream // 49146 // Hs.23735 // KCNF1 // 3754 // Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1), mRNA. /// NM_182586 // downstream // 135630 // Hs.329841 // FLJ33534 // 285150 // Homo sapiens hypothetical prote	KCNF1	KCNF1, Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1), p25.1
SNP_A-2176258	caccagataccacctat[C/T]gttctgtaacttctca	C	T	NM_002236 // downstream // 92903 // Hs.23735 // KCNF1 // 3754 // Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1), mRNA. /// NM_182586 // downstream // 91873 // Hs.329841 // FLJ33534 // 285150 // Homo sapiens hypothetical protei	KCNF1	KCNF1, Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1), p25.1
SNP_A-1938320	ttgactaatacagaca[A/G]ataagtgctattgttt	A	G	NM_182586 // intron // 0 // Hs.329841 // FLJ33534 // 285150 // Homo sapiens hypothetical protein FLJ33534 (FLJ33534), mRNA. /// ENST00000273641 // intron // 0 // — // — // — // —	FLJ33534	FLJ33534, Homo sapiens hypothetical protein FLJ33534 (FLJ33534), p25.1
SNP_A-2266753	gaagtggcctgagaaa[A/G]caataaagagagggcg	A	G	NM_212540 // downstream // 44928 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // downstream // 44928 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-1888162	tgagcctcaggcttac[C/G]gctaaaatgttaagtg	C	G	NM_212540 // downstream // 12511 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // downstream // 12511 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-1838342	tagaaggggcggacttg[G/T]atctgagagagaataa	G	T	NM_212540 // downstream // 9004 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // downstream // 9004 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6),	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-2080538	acctattaagacatga[C/G]cttacactctgacaac	C	G	NM_212540 // downstream // 1420 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, mRNA. /// NM_198257 // downstream // 1420 // Hs.135465 // E2F6 // 1876 // Homo sapiens E2F transcription factor 6 (E2F6),	E2F6	E2F6, Homo sapiens E2F transcription factor 6 (E2F6), transcript variant f, p25.1
SNP_A-1814487	gtgtgcatgctgttga[A/T]gtaagtagtaagagtt	A	T	NM_145693 // downstream // 35154 // Hs.467740 // LPIN1 // 23175 // Homo sapiens lipin 1 (LPIN1), mRNA. /// ENST00000256720 // downstream // 35154 // — // — // — // — /// ENST00000323501 // upstream // 161001 // — // — // — // —	LPIN1	LPIN1, Homo sapiens lipin 1 (LPIN1), p25.1
SNP_A-2266918	gaagtgtcatcaaaa[C/T]cagaagaaagtcatgg	C	T	NM_145693 // downstream // 48232 // Hs.467740 // LPIN1 // 23175 // Homo sapiens lipin 1 (LPIN1), mRNA. /// ENST00000256720 // downstream // 48232 // — // — // — // — /// ENST00000323501 // upstream // 147923 // — // — // — // —	LPIN1	LPIN1, Homo sapiens lipin 1 (LPIN1), p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2212419	ccctgtgaccagtgcd[A/G]cggagtcctgagggt	A	G	NM_145693 // downstream // 81890 // Hs.467740 // LPIN1 // 23175 // Homo sapiens lipin 1 (LPIN1), mRNA. /// ENST00000256720 // downstream // 81890 // — // — // — // — /// ENST00000323501 // upstream // 114265 // — // — // — // —	LPIN1	LPIN1, Homo sapiens lipin 1 (LPIN1), p25.1
SNP_A-1795257	ggtgagtgagagtaaa[A/G]ctagggaggaagagtt	A	G	NM_021643 // upstream // 512318 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream // 179960 // — // — // — // — /// ENST00000155926 // upstream // 512318 // — // — // —	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1962148	attgatttctgagac[A/G]actgtgctcatctcat	A	G	NM_021643 // upstream // 423524 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream // 268754 // — // — // — // — /// ENST00000155926 // upstream // 423524 // — // — // —	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1962161	caaatacctatttaca[A/T]ctcatgctctattaag	A	T	NM_021643 // upstream // 27769 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// ENST00000323501 // downstream // 664509 // — // — // — // — /// ENST00000155926 // upstream // 27769 // — // — // —	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2201491	ccaatgtaaggttgaa[A/G]tcaacaccctccatat	A	G	NM_021643 // downstream // 162353 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1728972 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2161383	atttgcaggcaaatag[A/G]aagacaaggagattat	A	G	NM_021643 // downstream // 184246 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1707079 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2032192	aaagtgtaaactgcaa[C/T]atatgctggaagtgt	C	T	NM_021643 // downstream // 227858 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1663467 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1884930	tgaatgacctgctcta[C/T]aaatggcctgcaagag	C	T	NM_021643 // downstream // 770478 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1120847 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2085250	actcagttcgaccacc[C/T]gctttatcctttggat	C	T	NM_021643 // downstream // 770564 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 1120761 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1649264	agcagccttctaaaagtgtaaaag[G/T]caagaaaatgaattct ccccagagc	G	T	NM_021643 // downstream // 885561 // Hs.155418 // TRIB2 // 28951 // tribbles homolog 2 /// NM_145175 // upstream // 1004439 // Hs.260855 // NSE1 // 151354 // NSE1	TRIB2	TRIB2, rs1510823, tribbles homolog 2, p24.3
SNP_A-2069224	acaattgtcaaggaaa[G/T]ttgttaactctgtggc	G	T	NM_021643 // downstream // 1010561 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 880764 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2089975	acttctgcttttccaj[C/T]acaacatgcacagata	C	T	NM_021643 // downstream // 1474190 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 417135 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1886143	tgaccatctactcaag[A/G]ctaaccactttcata	A	G	NM_021643 // downstream // 1690213 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 201112 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // d	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-2027340	aaacatgactaagaga[A/C]aagagagcaagtgagg	A	C	NM_021643 // downstream // 1815877 // Hs.467751 // TRIB2 // 28951 // Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), mRNA. /// NM_145175 // upstream // 75448 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// ENST00000155926 // do	TRIB2	TRIB2, Homo sapiens tribbles homolog 2 (Drosophila) (TRIB2), p24.3
SNP_A-1755752	agaaaattgatgatgccctgactctg[A/C]agctactatgggaaaa gtatttgaa	A	C	NM_021643 // downstream // 1851784 // Hs.155418 // TRB2 // 28951 // tribbles homolog 2 /// NM_145175 // upstream // 38216 // Hs.260855 // NSE1 // 151354 // NSE1	TRB2	TRB2 , rs1434977, tribbles homolog 2 ,p24.3
SNP_A-2253895	ctgacaacatgcaat[A/G]acacatgataacatta	A	G	NM_145175 // downstream // 180855 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// NM_015909 // downstream // 349730 // Hs.467759 // NAG // 51594 // Homo sapiens neuroblastoma-amplified protein (NAG), mRNA. /// ENST00000331243 // down	NSE1	NSE1, Homo sapiens NSE1 (NSE1), p24.3
SNP_A-2297714	gccagcttgtagtgaa[C/T]gctgcctggtctgggc	C	T	NM_145175 // downstream // 208381 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// NM_015909 // downstream // 322204 // Hs.467759 // NAG // 51594 // Homo sapiens neuroblastoma-amplified protein (NAG), mRNA. /// ENST00000331243 // down	NSE1	NSE1, Homo sapiens NSE1 (NSE1), p24.3
SNP_A-2035341	aaatggatgagaacaa[C/T]atataataactgtatt	C	T	NM_145175 // downstream // 450983 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// NM_015909 // downstream // 79602 // Hs.467759 // NAG // 51594 // Homo sapiens neuroblastoma-amplified protein (NAG), mRNA. /// ENST00000331243 // downs	NSE1	NSE1, Homo sapiens NSE1 (NSE1), p24.3
SNP_A-2246887	ctgtagtgatgtgttct[A/G]ataaaaagtggccagc	A	G	NM_145175 // downstream // 508299 // Hs.260855 // NSE1 // 151354 // Homo sapiens NSE1 (NSE1), mRNA. /// NM_015909 // downstream // 22286 // Hs.467759 // NAG // 51594 // Homo sapiens neuroblastoma-amplified protein (NAG), mRNA. /// ENST00000331243 // downs	NSE1	NSE1, Homo sapiens NSE1 (NSE1), p24.3
SNP_A-2218867	cctgggcaatgtgga[A/G]ccatgagaggctatgg	A	G	NM_004939 // downstream // 148887 // Hs.440599 // DDX1 // 1653 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1), mRNA. /// ENST00000233084 // downstream // 148887 // — // — // — /// ENST00000311168 // upstream // 89951 // — /	DDX1	DDX1, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1), p24.3
SNP_A-2157160	attgaaggtcattcccc[C/G]aggtcattgaacctgg	C	G	S49953 // downstream // 64958 // Hs.103989 // MYCNOS // 10408 // N-cym=DNA-binding transcriptional activator homolog {oncogene} {human, Kelly neuroblastoma cell line, mRNA, 778 nt}. /// ENST00000311168 // downstream // 4715 // — // — // — ///	MYCNOS	MYCNOS, N-cym=DNA-binding transcriptional activator homolog {oncogene} {human, Kelly neuroblastoma cell line, 778 nt}, p24.3
SNP_A-2299045	gccccctcctcttagc[A/G]ccctatctgcaggcac	A	G	S49953 // downstream // 50308 // Hs.103989 // MYCNOS // 10408 // N-cym=DNA-binding transcriptional activator homolog {oncogene} {human, Kelly neuroblastoma cell line, mRNA, 778 nt}. /// ENST00000311168 // downstream // 19365 // — // — // — // — //	MYCNOS	MYCNOS, N-cym=DNA-binding transcriptional activator homolog {oncogene} {human, Kelly neuroblastoma cell line, 778 nt}, p24.3
SNP_A-1881083	tcttaaccaagaggc[A/G]gaatattcatgatcat	A	G	S49953 // downstream // 2270 // Hs.103989 // MYCNOS // 10408 // N-cym=DNA-binding transcriptional activator homolog {oncogene} {human, Kelly neuroblastoma cell line, mRNA, 778 nt}. /// ENST00000311168 // downstream // 67403 // — // — // — ///	MYCNOS	MYCNOS, N-cym=DNA-binding transcriptional activator homolog {oncogene} {human, Kelly neuroblastoma cell line, 778 nt}, p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1888188	tgagccttcatcagac[A/T]acagatctactggcac	A	T	NM_005378 // downstream // 43795 // Hs.25960 // MYCN // 4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 571521 // Hs.467769 // FAM49A // 81553 // Homo sapiens f	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2139008	atcctaacgagaataa[C/G]gcaaggcttagcctgt	C	G	NM_005378 // downstream // 50176 // Hs.25960 // MYCN // 4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 565140 // Hs.467769 // FAM49A // 81553 // Homo sapiens f	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2045480	aagaatctctgcttta[A/G]cggaagaccgtttcg	A	G	NM_005378 // downstream // 50488 // Hs.25960 // MYCN // 4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 564828 // Hs.467769 // FAM49A // 81553 // Homo sapiens f	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2190400	catacacggtagaaga[G/T]aatatttcaaaacat	G	T	NM_005378 // downstream // 473518 // Hs.25960 // MYCN // 4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 141798 // Hs.467769 // FAM49A // 81553 // Homo sapiens	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2109529	aggaaaaggggctcaaa[C/T]ctccigtttacctgtt	C	T	NM_005378 // downstream // 539548 // Hs.25960 // MYCN // 4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 75768 // Hs.467769 // FAM49A // 81553 // Homo sapiens f	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-1816757	gttatctactttcttc[A/G]atatggattagccact	A	G	NM_005378 // downstream // 556282 // Hs.25960 // MYCN // 4613 // Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA. /// NM_030797 // downstream // 59034 // Hs.467769 // FAM49A // 81553 // Homo sapiens f	MYCN	MYCN, Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), p24.3
SNP_A-2312926	ggacttatctggcac[A/G]caatagttaaacacag	A	G	NM_030797 // upstream // 91466 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 825214 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. ///	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1895981	tgccttctaatgtgct[C/T]acatctcatactctgt	C	T	NM_030797 // upstream // 249796 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 666884 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1890212	tgatcaccctgatgaa[C/T]ggtgatatatcaaggg	C	T	NM_030797 // upstream // 290612 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 626068 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-2179223	cactgggtggagaata[C/T]ggtgtctagacgttt	C	T	NM_030797 // upstream // 311669 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 605011 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1900717	tggaggtccagagaga[A/G]acagtttacttccta	A	G	NM_030797 // upstream // 562912 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 353768 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2228528	ctactttgtaactaag[A/G]acactcttaatggtag	A	G	NM_030797 // upstream // 582910 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 333770 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. //	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1727178	agaggatagtctcaacatccttcaa[C/G]gtgacatttctttaaagatattaac	C	G	NM_003385 // upstream // 374198 // Hs.2288 // VSNL1 // 7447 // visinin-like 1 /// NM_030797 // upstream // 500676 // Hs.4863 // DKFZP566A1524 // 81553 // hypothetical protein DKFZp566A1524	VSNL1	VSNL1 , rs1507979, visinin-like 1 ,p24.2
SNP_A-1820296	gtttagaatagatggg[C/T]actttggctctatgtt	C	T	NM_030797 // upstream // 830377 // Hs.467769 // FAM49A // 81553 // Homo sapiens family with sequence similarity 49, member A (FAM49A), mRNA. /// NM_003385 // upstream // 86303 // Hs.444212 // VSNL1 // 7447 // Homo sapiens visinin-like 1 (VSNL1), mRNA. ///	FAM49A	FAM49A, Homo sapiens family with sequence similarity 49, member A (FAM49A), p24.2
SNP_A-1663662	cttcatgatccaaaggcttgtgaaa[G/T]agagagagaattatctcctctcttc	G	T	NM_003385 // downstream // 2387 // Hs.2288 // VSNL1 // 7447 // visinin-like 1 /// NM_024624 // downstream // 6303 // Hs.424559 // SMC6L1 // 79677 // SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	VSNL1	VSNL1 , rs1991315, visinin-like 1 ,p24.2
SNP_A-1880794	tcttgggaatagaggt[A/G]aaatgacggattgtaa	A	G	NM_182625 // intron // 0 // Hs.467793 // FLJ40869 // 348654 // Homo sapiens hypothetical protein FLJ40869 (FLJ40869), mRNA. /// ENST00000317402 // intron // 0 // --- // --- // --- // ---	FLJ40869	FLJ40869, Homo sapiens hypothetical protein FLJ40869 (FLJ40869), p24.2
SNP_A-2044379	aagaaaaaaaaatgca[A/G]tacggcttggaacatg	A	G	NM_182625 // intron // 0 // Hs.467793 // FLJ40869 // 348654 // Homo sapiens hypothetical protein FLJ40869 (FLJ40869), mRNA. /// ENST00000317402 // intron // 0 // --- // --- // --- // ---	FLJ40869	FLJ40869, Homo sapiens hypothetical protein FLJ40869 (FLJ40869), p24.2
SNP_A-2257612	ctttgccaggctctca[C/T]tcttctctctccggct	C	T	NM_002252 // upstream // 88938 // Hs.414489 // KCNS3 // 3790 // Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA. /// ENST00000281047 // downstream // 11768 // --- // --- // --- // --- /// ENST00000030410	KCNS3	KCNS3, Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), p24.2
SNP_A-1704279	ccaccctcacactgccccctactag[C/T]gttactgtgtccacattttaccaa	C	T	NM_002252 // upstream // 92359 // Hs.414489 // KCNS3 // 3790 // potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 /// NM_182625 // downstream // 4095 // Hs.180582 // FLJ40869 // 348654 // hypothetical protein FLJ40869	KCNS3	KCNS3 , rs750772, potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 ,p24.2
SNP_A-1785934	ggctgattaatgttac[C/T]ggagaagctgtaacta	C	T	NM_002252 // downstream // 3013 // Hs.414489 // KCNS3 // 3790 // Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA. /// NM_020905 // downstream // 618756 // Hs.288880 // RDH14 // 57665 // Homo sapiens ret	KCNS3	KCNS3, Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), p24.2
SNP_A-1725574	gacttaggaaagccaatccagtgca[C/T]agcagaataaaagtaaaaatatat	C	T	NM_002252 // intron // 0 // Hs.414489 // KCNS3 // 3790 // potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	KCNS3	KCNS3 , rs1350881, potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3,p24.2
SNP_A-1695829	ctgtgccaaaacattactgaaaaca[C/T]tactggacccttgtttgcattcatt	C	T	NM_002252 // downstream // 27004 // Hs.414489 // KCNS3 // 3790 // potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 /// NM_020905 // downstream // 594769 // Hs.288880 // RDH14 // 57665 // retinol dehydrogenase 14 (all-trans and 9-	KCNS3	KCNS3 , rs10495673, potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 ,p24.2
SNP_A-2212976	ccgaaaatgtcagaaa[A/G]tgaggagagaagaaaa	A	G	NM_020905 // upstream // 61926 // Hs.288880 // RDH14 // 57665 // Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA. /// NM_001002006 // upstream // 32988 // Hs.120319 // NT5C1B // 93034 // Homo sapiens 5'-nucleotidase, cytosolic IB	RDH14	RDH14, Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), p24.2
SNP_A-2262442	gaaatggagcagcata[C/T]gtggcataatcaatct	C	T	NM_020905 // upstream // 211208 // Hs.288880 // RDH14 // 57665 // Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA. /// NM_001002006 // upstream // 182270 // Hs.120319 // NT5C1B // 93034 // Homo sapiens 5'-nucleotidase, cytosolic	RDH14	RDH14, Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1685638	ggcaaaacatattatacttaaggca[C/T]tgcccctattttcctgataattgcg	C	T	NM_020905 // upstream // 179452 // Hs.288880 // RDH14 // 57665 // retinol dehydrogenase 14 (all-trans and 9-cis) /// NM_033253 // upstream // 150507 // Hs.120319 // NT5C1B // 93034 // 5'-nucleotidase, cytosolic IB /// NM_145260 // downstream // 629901 //	RDH14	RDH14 , rs10495692, retinol dehydrogenase 14 (all-trans and 9-cis) ,p24.2
SNP_A-2006183	gagaaggtcagtaaca[C/T]tcaacggtcaagacca	C	T	NM_020905 // upstream // 271214 // Hs.288880 // RDH14 // 57665 // Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA. /// NM_001002006 // upstream // 242276 // Hs.120319 // NT5C1B // 93034 // Homo sapiens 5'-nucleotidase, cytosolic	RDH14	RDH14, Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), p24.2
SNP_A-2054005	aagttactctgtaggc[C/T]ccctaatcaacttggc	C	T	NM_020905 // upstream // 530290 // Hs.288880 // RDH14 // 57665 // Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA. /// NM_001002006 // upstream // 501352 // Hs.120319 // NT5C1B // 93034 // Homo sapiens 5'-nucleotidase, cytosolic	RDH14	RDH14, Homo sapiens retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), p24.2
SNP_A-1962347	atctcagagaagctca[C/T]agtacaaatcatgtac	C	T	NM_145260 // upstream // 70027 // Hs.123933 // OSR1 // 130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 70027 // — // — // — // — /// ENST00000272235 // upstream // 397599 // — // — // —	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-1879390	tcttatagccacaatg[A/G]attatttgtttttatt	A	G	NM_145260 // upstream // 115490 // Hs.123933 // OSR1 // 130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 115490 // — // — // — // — /// ENST00000272235 // upstream // 352136 // — // — // -	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-2227433	ctacacgctgtcaaca[C/T]gacttacctctcacga	C	T	NM_145260 // upstream // 433325 // Hs.123933 // OSR1 // 130497 // Homo sapiens odd-skipped homolog (Drosophila) (ODD), mRNA. /// ENST00000272223 // upstream // 433325 // — // — // — // — /// ENST00000272235 // upstream // 34301 // — // — // –	OSR1	OSR1, Homo sapiens odd-skipped homolog (Drosophila) (ODD), p24.1
SNP_A-2237201	ctctcagggtactaaa[C/T]ggcagccttagctccc	C	T	ENST00000272235 // downstream // 16918 // — // — // — // — /// ENST00000333610 // downstream // 53266 // — // — // — // —	-	p24.1
SNP_A-2108084	agctctgagcacagag[G/T]actattaggttgatgc	G	T	ENST00000272235 // downstream // 46122 // — // — // — // — /// ENST00000333610 // downstream // 24062 // — // — // — // —	-	p24.1
SNP_A-1699539	cggggctcaggatccagtggctct[C/T]tacctccttttccttcacgtgggtt	C	T	NM_020779 // downstream // 53974 // Hs.145365 // WDR35 // 57539 // WD repeat domain 35 /// NM_145260 // upstream // 500659 // Hs.123933 // ODD // 130497 // odd-skipped homolog (Drosophila)	WDR35	WDR35 , rs964864, WD repeat domain 35 ,p24.1
SNP_A-1962368	tttcattatcttttcc[A/C]gaatgtcctttcacta	A	C	NM_020779 // intron // 0 // Hs.205427 // WDR35 // 57539 // Homo sapiens WD repeat domain 35 (WDR35), mRNA. /// AB037757 // intron // 0 // Hs.205427 // WDR35 // 57539 // Homo sapiens mRNA for KIAA1336 protein, partial cds. /// ENST00000281405 // intron //	WDR35	WDR35, Homo sapiens WD repeat domain 35 (WDR35), p24.1
SNP_A-2094049	agaaggaaaagattgc[C/T]actcaccacttgttac	C	T	NM_002381 // intron // 0 // Hs.6985 // MATN3 // 4148 // Homo sapiens matrilin 3 (MATN3), mRNA. /// ENST00000254354 // intron // 0 // — // — // — // —	MATN3	MATN3, Homo sapiens matrilin 3 (MATN3), p24.1
SNP_A-1736761	taaaaattttcaataatcaataata[A/G]ctgctggagaggggacaacaggtag	A	G	NM_020779 // intron // 0 // Hs.145365 // WDR35 // 57539 // WD repeat domain 35	WDR35	WDR35 , rs10495700, WD repeat domain 35,p24.1
SNP_A-1785954	ggctgcactcattgca[A/G]ggctgactagctccag	A	G	NM_014713 // upstream // 77449 // Hs.467807 // LAPTM4A // 9741 // Homo sapiens lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), mRNA. /// NM_002997 // downstream // 71665 // Hs.224607 // SDC1 // 6382 // Homo sapiens syndecan 1 (SDC1), mRNA. /	LAPTM4A	LAPTM4A, Homo sapiens lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006197	tttgataagctctgcc[A/G]aatggaaatagccacc	A	G	NM_014713 // upstream // 86575 // Hs.467807 // LAPTM4A // 9741 // Homo sapiens lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), mRNA. /// NM_002997 // downstream // 62539 // Hs.224607 // SDC1 // 6382 // Homo sapiens syndecan 1 (SDC1), mRNA. /	LAPTM4A	LAPTM4A, Homo sapiens lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), p24.1
SNP_A-2078329	accatagttctgaata[C/T]gcttagatctttattt	C	T	NM_004040 // downstream // 106699 // Hs.502876 // RHOB // 388 // Homo sapiens ras homolog gene family, member B (RHOB), mRNA. /// NM_022460 // downstream // 61685 // Hs.531785 // FLJ14249 // 64342 // Homo sapiens HS1-binding protein 3 (FLJ14249), transcri	RHOB	RHOB, Homo sapiens ras homolog gene family, member B (RHOB), p24.1
SNP_A-2282919	gataaatttagacaaa[A/G]tcagagctatgaggac	A	G	NM_004040 // downstream // 147888 // Hs.502876 // RHOB // 388 // Homo sapiens ras homolog gene family, member B (RHOB), mRNA. /// NM_022460 // downstream // 20496 // Hs.531785 // FLJ14249 // 64342 // Homo sapiens HS1-binding protein 3 (FLJ14249), transcri	RHOB	RHOB, Homo sapiens ras homolog gene family, member B (RHOB), p24.1
SNP_A-1826524	taacaaggaggtttaa[A/G]tggtgaagtatgaagt	A	G	NM_021925 // intron // 0 // Hs.187823 // FLJ21820 // 60526 // Homo sapiens hypothetical protein FLJ21820 (FLJ21820), mRNA. /// ENST00000237822 // intron // 0 // — // — // — // —	FLJ21820	FLJ21820, Homo sapiens hypothetical protein FLJ21820 (FLJ21820), p24.1
SNP_A-2208002	cccaactataattatg[A/G]atgtctctgtttttcc	A	G	NM_021925 // intron // 0 // Hs.187823 // FLJ21820 // 60526 // Homo sapiens hypothetical protein FLJ21820 (FLJ21820), mRNA. /// ENST00000237822 // intron // 0 // — // — // — // —	FLJ21820	FLJ21820, Homo sapiens hypothetical protein FLJ21820 (FLJ21820), p24.1
SNP_A-2202577	ccacctcagtactgac[A/C]attcctggctttccct	A	C	NM_000384 // upstream // 6545 // Hs.120759 // APOB // 338 // Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), mRNA. /// ENST00000233242 // upstream // 6545 // — // — // — // — /// ENST00000355709 // upstream // 87039 // — // — /	APOB	APOB, Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), p24.1
SNP_A-1879709	tcttcatactctatgc[A/G]ccattcattaatgggt	A	G	NM_000384 // upstream // 25622 // Hs.120759 // APOB // 338 // Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), mRNA. /// ENST00000233242 // upstream // 25622 // — // — // — // — /// ENST00000355709 // upstream // 67962 // — // —	APOB	APOB, Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), p24.1
SNP_A-1962391	gatattagggatacta[A/G]gcaattgtcacctact	A	G	NM_000384 // upstream // 44746 // Hs.120759 // APOB // 338 // Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), mRNA. /// ENST00000233242 // upstream // 44746 // — // — // — // — /// ENST00000355709 // upstream // 48838 // — // —	APOB	APOB, Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), p24.1
SNP_A-2159042	attgttgaataagtga[A/C]atgtttgttgaacaaa	A	C	AB067508 // upstream // 2069172 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 172882 // — // — // — // — /// ENST00000288548 // upstream // 2069172 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1685904	ctcttctattttctgaacctagtag[A/G]acatgatggagctgaagagattccc	A	G	NM_014082 // upstream // 151994 // - // - // - // - /// NM_024849 // upstream // 2340046 // - // - // - // - /// NM_025067 // upstream // 2345985 // - // - // - // -	-	- , rs10490607, - ,p24.1
SNP_A-2054680	aataaaagacactgaa[G/T]aaagataggccttta	G	T	AB067508 // upstream // 1815598 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 426456 // — // — // — // — /// ENST00000288548 // upstream // 1815598 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1947047	tttaatacacggcttc[A/T]ctataagatattatgt	A	T	AB067508 // upstream // 1687582 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 554472 // — // — // — // — /// ENST00000288548 // upstream // 1687582 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1962417	tattcttgacataagc[C/T]ctcctgaggcaggaag	C	T	AB067508 // upstream // 1387364 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 854690 // — // — // — // — /// ENST00000288548 // upstream // 1387364 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1758439	gggagttgcccctctcctttaatga[C/T]atgtaactgaattttgaacatcagg	C	T	NM_014082 // upstream // 1196330 // - // - // - // - /// NM_024849 // upstream // 1295710 // - // - // - // - /// NM_025067 // upstream // 1301649 // - // - // - // -	-	- , rs10495726, - ,p24.1
SNP_A-2207856	cccaaagggaaactcc[A/G]aaaatgtagaaaagaa	A	G	AB067508 // upstream // 951766 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1290288 // — // — // — // — /// ENST00000288548 // upstream // 951766 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1701215	tctctaagtcctcacttaagttaca[C/T]tggtgttgtgccactcttttctgaa	C	T	NM_014082 // upstream // 1244298 // - // - // - // - /// NM_024849 // upstream // 1247742 // - // - // - // - /// NM_025067 // upstream // 1253681 // - // - // - // -	-	- , rs1858124, - ,p24.1
SNP_A-1712033	tgcacattagaaaaagagtttatac[A/G]gccctcacatgagcacgcctggctt	A	G	NM_014082 // upstream // 1544543 // - // - // - // - /// NM_024849 // upstream // 947497 // - // - // - // - /// NM_025067 // upstream // 953436 // - // - // - // -	-	- , rs3849399, - ,p24.1
SNP_A-1743873	agttttagagaggacacgttgaaac[C/G]atagcagcagacctccattttccca	C	G	NM_014082 // upstream // 1545318 // - // - // - // - /// NM_024849 // upstream // 946722 // - // - // - // - /// NM_025067 // upstream // 952661 // - // - // - // -	-	- , rs4332948, - ,p24.1
SNP_A-2077762	accagaaaaagaccac[A/G]acttagaaataaagct	A	G	AB067508 // upstream // 452708 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1789346 // — // — // — // — /// ENST00000288548 // upstream // 452708 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-2145188	atgcaatgagatgaga[A/G]cctgtgaagctgcgac	A	G	AB067508 // upstream // 391397 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1850657 // — // — // — // — /// ENST00000288548 // upstream // 391397 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-2222012	cgaaccaactcaagta[C/G]gagccagaggttgtgt	C	G	AB067508 // upstream // 391349 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1850705 // — // — // — // — /// ENST00000288548 // upstream // 391349 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1737125	tatagtctaagttactagaaccaga[C/T]agccaggtgttaagttgaagaattt	C	T	NM_014082 // upstream // 1787934 // - // - // - // - /// NM_024849 // upstream // 704106 // - // - // - // - /// NM_025067 // upstream // 710045 // - // - // - // -	-	- , rs10495735, - ,p24.1
SNP_A-2290342	gcaacagtgaatttga[C/T]gttcttttattatagg	C	T	AB067508 // upstream // 382125 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1859929 // — // — // — // — /// ENST00000288548 // upstream // 382125 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-2238276	ctctggacccatctta[C/T]atttcgtatccttata	C	T	AB067508 // upstream // 381286 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1860768 // — // — // — // — /// ENST00000288548 // upstream // 381286 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1866085	tcccagagcctgaaac[C/T]gtgacaaagaggacat	C	T	AB067508 // upstream // 319456 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 1922598 // — // — // — // — /// ENST00000288548 // upstream // 319456 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-2071399	acagaaaaaaatcagc[A/G]aaactcaaagaggcag	A	G	AB067508 // upstream // 185653 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 2056401 // — // — // — // — /// ENST00000288548 // upstream // 185653 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. p24.1
SNP_A-1962445	gatgaaggtgctatta[A/G]gagatgggaatgggtg	A	G	AB067508 // upstream // 180109 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000317039 // upstream // 2061945 // — // — // — // — /// ENST00000288548 // upstream // 180109 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1938382	ttgactcctggcttca[C/G]aaactctcacaacggc	C	G	AB067508 // intron // 0 // — // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // — // — // — // —	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2103733	agcacatggtgaaaca[A/G]aagagtgttgcaacgc	A	G	AB067508 // intron // 0 // --- // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-2307536	gcttcaatggcctaca[A/G]aatagcttatctttag	A	G	AB067508 // intron // 0 // --- // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // --- // --- // --- // ---	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-1810623	gtgcaaggcccgggaa[C/T]gttctggaatcaatca	C	T	AB067508 // intron // 0 // --- // KBTBD9 // 114818 // Homo sapiens mRNA for KIAA1921 protein, partial cds. /// ENST00000288548 // intron // 0 // --- // --- // --- // --- /// ENST00000356697 // intron // 0 // --- // --- // --- // --- /// ENST00000316320 //	KBTBD9	KBTBD9, Homo sapiens for KIAA1921 protein, partial cds. ,p24.1
SNP_A-2062129	aatgggtagaggtccc[A/T]ctcagttcaggctctg	A	T	NM_016047 // intron // 0 // Hs.177861 // SF3B14 // 51639 // Homo sapiens splicing factor 3B, 14 kDa subunit (SF3B14), mRNA. /// ENST00000233468 // intron // 0 // --- // --- // --- // ---	SF3B14	SF3B14, Homo sapiens splicing factor 3B, 14 kDa subunit (SF3B14), p23.3
SNP_A-1839839	tagattcctaggccag[G/T]agttttcgttgcactt	G	T	NM_006277 // intron // 0 // Hs.432562 // ITSN2 // 50618 // Homo sapiens intersectin 2 (ITSN2), transcript variant 1, mRNA. /// NM_147152 // intron // 0 // Hs.432562 // ITSN2 // 50618 // Homo sapiens intersectin 2 (ITSN2), transcript variant 2, mRNA. /// E	ITSN2	ITSN2, Homo sapiens intersectin 2 (ITSN2), transcript variant 1, p23.3
SNP_A-1840942	tagctgacaaaagata[C/T]gatttttccactccag	C	T	NM_003743 // intron // 0 // Hs.412293 // NCOA1 // 8648 // Homo sapiens nuclear receptor coactivator 1 (NCOA1), transcript variant 1, mRNA. /// NM_147223 // intron // 0 // Hs.412293 // NCOA1 // 8648 // Homo sapiens nuclear receptor coactivator 1 (NCOA1), t	NCOA1	NCOA1, Homo sapiens nuclear receptor coactivator 1 (NCOA1), transcript variant 1, p23.3
SNP_A-1827619	taactgctttattcac[A/C]aatctctatttatcca	A	C	NM_024322 // intron // 0 // Hs.546428 // MGC11266 // 79172 // Homo sapiens hypothetical protein MGC11266 (MGC11266), mRNA. /// ENST00000260662 // intron // 0 // --- // --- // --- // ---	MGC11266	MGC11266, Homo sapiens hypothetical protein MGC11266 (MGC11266), p23.3
SNP_A-2051120	aagggaaggactgtgc[A/G]agcaactccctagccc	A	G	NM_022552 // intron // 0 // Hs.515840 // DNMT3A // 1788 // Homo sapiens DNA (cytosine-5-)-methyltransferase 3 alpha (DNMT3A), transcript variant 3, mRNA. /// NM_153759 // intron // 0 // Hs.515840 // DNMT3A // 1788 // Homo sapiens DNA (cytosine-5-)-methylt	DNMT3A	DNMT3A, Homo sapiens DNA (cytosine-5-)-methyltransferase 3 alpha (DNMT3A), transcript variant 3, p23.3
SNP_A-2207847	cccaaagctacttttc[C/T]cttgtatcctcggact	C	T	NM_033148 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 5, mRNA. /	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-1935523	ttctgggtatgcaaga[C/G]taagttcctgaacata	C	G	NM_033148 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 5, mRNA. /	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-1962479	gagtggaacggagtaa[A/G]taaagtattctggctg	A	G	NM_033148 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 5, mRNA. /	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-1902477	tggcctccggatatca[C/T]gctctcctagtttttc	C	T	NM_033148 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, mRNA. /// NM_183361 // intron // 0 // Hs.307720 // DTNB // 1838 // Homo sapiens dystrobrevin, beta (DTNB), transcript variant 5, mRNA. /	DTNB	DTNB, Homo sapiens dystrobrevin, beta (DTNB), transcript variant 3, p23.3
SNP_A-2072826	acagctggcctgcact[A/C]aaaaaaatgtctagtc	A	C	NM_018263 // intron // 0 // Hs.119815 // ASXL2 // 55252 // Homo sapiens additional sex combs like 2 (Drosophila) (ASXL2), mRNA. /// ENST00000336112 // intron // 0 // --- // --- // --- // --- /// ENST00000272341 // intron // 0 // --- // --- // --- // ---	ASXL2	ASXL2, Homo sapiens additional sex combs like 2 (Drosophila) (ASXL2), p23.3
SNP_A-1700001	cattatatgaagtagattgggatca[A/G]acttaccaatattagctgtggccgg	A	G	NM_016131 // intron // 0 // Hs.236494 // RAB10 // 10890 // RAB10, member RAS oncogene family	RAB10	RAB10 , rs10495755, RAB10, member RAS oncogene family,p23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2233419	ctcagtacacaaaaaa[A/C]aatattgccacccagg	A	C	NM_145038 // intron // 0 // Hs.393714 // MGC16372 // 92749 // Homo sapiens CG10958-like (MGC16372), mRNA. /// ENST00000288710 // intron // 0 // — // — // — /// ENST00000358114 // intron // 0 // — // — // — // —	MGC16372	MGC16372, Homo sapiens CG10958-like (MGC16372), p23.3
SNP_A-2262418	gaaatgctgctgcctat[C/T]attactgtttgtgag	C	T	NM_194248 // intron // 0 // Hs.91608 // OTOF // 9381 // Homo sapiens otoferlin (OTOF), transcript variant 1, mRNA. /// NM_194322 // intron // 0 // Hs.91608 // OTOF // 9381 // Homo sapiens otoferlin (OTOF), transcript variant 3, mRNA. /// ENST00000272371 /	OTOF	OTOF, Homo sapiens otoferlin (OTOF), transcript variant 1, p23.3
SNP_A-1886222	tgacctagtttccag[C/T]ctctttccactaattt	C	T	NM_004341 // intron // 0 // Hs.377010 // CAD // 790 // Homo sapiens carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (CAD), mRNA. /// ENST00000264705 // intron // 0 // — // — // — // —	CAD	CAD, Homo sapiens carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (CAD), p23.3
SNP_A-1693829	gtagttcaggacaggaaaggaaata[C/T]gttgtgcctgttgaggg gtcatcag	C	T	NM_013392 // intron // 0 // Hs.272736 // NRBP // 29959 // nuclear receptor binding protein	NRBP	NRBP rs780102, nuclear receptor binding protein,p23.3
SNP_A-1816236	gttactggggcttttca[C/G]aaaagagcaatggaca	C	G	NM_199191 // downstream // 22449 // Hs.258314 // BRE // 9577 // Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, mRNA. /// NM_199194 // downstream // 22449 // Hs.258314 // BRE // 9577 // Homo sapiens br	BRE	BRE, Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, p23.2
SNP_A-2249649	cttaagtcccttccaa[C/T]gctactggttactcgg	C	T	ENST00000329020 // intron // 0 // — // — // — /// ENST00000296108 // intron // 0 // — // — // —	-	p23.2
SNP_A-2216577	ccctaggctcatttca[C/T]gttacctcagatgaca	C	T	ENST00000296108 // intron // 0 // — // — // — /// ENST00000327757 // intron // 0 // — // — // —	-	p23.2
SNP_A-2253996	cttgagaatggaatgat[C/G]ctttgtactggtaaca	C	G	ENST00000296108 // intron // 0 // — // — // — /// ENST00000327757 // intron // 0 // — // — // —	-	p23.2
SNP_A-2297231	gccaccagcaactgaa[C/T]ggtttccgcacagcac	C	T	ENST00000296108 // intron // 0 // — // — // — /// ENST00000327757 // intron // 0 // — // — // —	-	p23.2
SNP_A-2229828	ctagttaaaaccgact[C/G]aggcatgtccttcagg	C	G	NM_002709 // intron // 0 // Hs.468018 // PPP1CB // 5500 // Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), transcript variant 1, mRNA. /// NM_206876 // intron // 0 // Hs.468018 // PPP1CB // 5500 // Homo sapiens protein phosph	PPP1CB	PPP1CB, Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), transcript variant 1, p23.2
SNP_A-1900844	tggagtgtaatggcaa[A/G]gtgtaagctcactgca	A	G	NM_182756 // intron // 0 // Hs.511956 // SPDY1 // 245711 // Homo sapiens speedy homolog 1 (Drosophila) (SPDY1), mRNA. /// ENST00000334056 // intron // 0 // — // — // —	SPDY1	SPDY1, Homo sapiens speedy homolog 1 (Drosophila) (SPDY1), p23.2
SNP_A-1799010	gtaagcagaagtaata[C/T]gagcatttttagagac	C	T	NM_182756 // downstream // 26279 // Hs.511956 // SPDY1 // 245711 // Homo sapiens speedy homolog 1 (Drosophila) (SPDY1), mRNA. /// NM_017910 // upstream // 6587 // Hs.468026 // FLJ20628 // 55006 // Homo sapiens hypothetical protein FLJ20628 (FLJ20628), mRN	SPDY1	SPDY1, Homo sapiens speedy homolog 1 (Drosophila) (SPDY1), p23.2
SNP_A-1807500	gtctgcggataggaga[A/G]atttaatctagtgcat	A	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // — // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2224722	cgtctgctcatctgtc[A/G]gaagtgttacaatttcc	A	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // — // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2259513	gaaaacaccaagagaa[A/G]gaagtcatacccatcc	A	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // — // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2231369	ctattgaatgattcca[C/T]gatagaaaatgtcta	C	T	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // — // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2180363	cagaaatgtgaattaa[A/G]cagaatttttttaggg	A	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // intron // 0 // — // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1780447	ggatactgaacttca[C/T]tgaaagccctctggtg	C	T	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // // intron // 0 // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2168357	caacigttcagagcta[C/G]gaacaaataggagaat	C	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // // intron // 0 // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2006243	gaggacgcttgaacac[A/G]caggcctgaaactcat	A	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // // intron // 0 // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-1928021	ttcaatgtgcatttca[C/G]attaataacgaacaat	C	G	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // // intron // 0 // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-2283959	gatatacttatatgaa[A/C]aaatgactgcttttt	A	C	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // // intron // 0 // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.2
SNP_A-1716349	cacacacacagtgtaccaggatg[C/G]agcatgtttagact cggccgttt	C	G	NM_004304 // intron // 0 // Hs.410680 // ALK // 238 // anaplastic lymphoma kinase (Ki-1)	ALK	ALK, rs4666273, anaplastic lymphoma kinase (Ki-1),p23.2
SNP_A-2194370	catgatctcttgcca[C/T]gtcaggtgacctgctc	C	T	NM_004304 // intron // 0 // Hs.196534 // ALK // 238 // Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), mRNA. /// ENST00000306036 // // intron // 0 // — // — // —	ALK	ALK, Homo sapiens anaplastic lymphoma kinase (Ki-1) (ALK), p23.1
SNP_A-1839669	tagatgatcgttattc[A/G]ctgtcaagttataata	A	G	NM_016061 // intron // 0 // Hs.515890 // YPEL5 // 51646 // Homo sapiens yippee-like 5 (Drosophila) (YPEL5), mRNA. /// ENST00000261353 // intron // 0 // — // — // —	YPEL5	YPEL5, Homo sapiens yippee-like 5 (Drosophila) (YPEL5), p23.1
SNP_A-1818946	gttgattaggaaacaa[A/G]tacttctacagtaata	A	G	NM_001002257 // intron // 0 // Hs.468048 // LYCAT // 253558 // Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, mRNA. /// NM_182551 // intron // 0 // Hs.468048 // LYCAT // 253558 // Homo sapiens acyl-CoA:lysocardioli	LYCAT	LYCAT, Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, p23.1
SNP_A-1901405	tggattcaatgccaaat[G/T]atccgacaatgagcaa	G	T	NM_001002257 // downstream // 21256 // Hs.468048 // LYCAT // 253558 // Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, mRNA. /// NM_182551 // downstream // 21256 // Hs.468048 // LYCAT // 253558 // Homo sapiens acyl-	LYCAT	LYCAT, Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, p23.1
SNP_A-2030474	aaagcccigtgaggga[A/G]gaaattgccctgtatc	A	G	NM_001002257 // downstream // 77542 // Hs.468048 // LYCAT // 253558 // Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, mRNA. /// NM_182551 // downstream // 77542 // Hs.468048 // LYCAT // 253558 // Homo sapiens acyl-	LYCAT	LYCAT, Homo sapiens acyl-CoA:lysocardiolipin acyltransferase 1 (ALCAT1), transcript variant 2, p23.1
SNP_A-2200885	ccaagcacttctgttc[A/G]cgtcatctcctttgac	A	G	NM_144575 // intron // 0 // Hs.529181 // CAPN13 // 92291 // Homo sapiens calpain 13 (CAPN13), mRNA. /// ENST00000295055 // intron // 0 // — // — // — // —	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1
SNP_A-2076045	acattattagacctca[A/G]gtgttgtgggaaatac	A	G	NM_144575 // intron // 0 // Hs.529181 // CAPN13 // 92291 // Homo sapiens calpain 13 (CAPN13), mRNA. /// ENST00000295055 // intron // 0 // — // — // — /// ENST00000359414 // intron // 0 // — // — // —	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1
SNP_A-1873788	tctcagccctgattag[A/G]cacaaagtaggatgcc	A	G	NM_144575 // intron // 0 // Hs.529181 // CAPN13 // 92291 // Homo sapiens calpain 13 (CAPN13), mRNA. /// ENST00000295055 // intron // 0 // — // — // — /// ENST00000359414 // intron // 0 // — // — // —	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1
SNP_A-1661372	gacagcctcagctcctctgttcaa[C/G]cagaagttctgactccc agtgtcct	C	G	NM_144575 // intron // 0 // Hs.325335 // CAPN13 // 92291 // calpain 13	CAPN13	CAPN13 , rs499476, calpain 13,p23.1
SNP_A-1870765	tcgctgctatcccaga[G/T]gttgcttgagaacaag	G	T	NM_144575 // upstream // 88288 // Hs.529181 // CAPN13 // 92291 // Homo sapiens calpain 13 (CAPN13), mRNA. /// BC010659 // downstream // 14742 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	CAPN13	CAPN13, Homo sapiens calpain 13 (CAPN13), p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1870519	tcgagaagggccagta[C/T]atttccagttaccta	C	T	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone .p23.1
SNP_A-1962546	tcgatggctccaagaa[A/G]ctggtgacttaggctt	A	G	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-2193305	catctcggagccaagga[C/G]agactcaaacaagagc	C	G	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-1962549	ggattcatggcaataa[C/T]gaagataaatatcaag	C	T	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-1962553	ttcaattatccaaaca[C/G]ctgtcatgaagaaagg	C	G	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone .p23.1
SNP_A-1962558	cagtggaactccagta[A/G]caatgagtgcatggtg	A	G	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone .p23.1
SNP_A-1962559	tcttaactccttcgtc[C/T]gaaagcagtgaactc	C	T	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone .p23.1
SNP_A-2069801	acacagaattagaaga[C/G]actactatgtgcaact	C	G	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-2225720	ctaaagagtatgaaac[A/G]ggatccaattgtaatt	A	G	BC010659 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA clone /// NM_024572 // intron // 0 // Hs.468058 // GALNT14 // 79623 // Ho	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone p23.1
SNP_A-1663968	cttggtgaaaggaatgtagtggaatc[A/G]ataatcattaacgagct gtctggtc	A	G	NM_024572 // intron // 0 // Hs.15830 // GALNT14 // 79623 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	GALNT14	GALNT14 . rs1862976, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14),p23.1
SNP_A-1678374	ggtcctccttttctttgtgagaaac[C/T]gtcttgggtagcctctggat gaagg	C	T	NM_024572 // intron // 0 // Hs.15830 // GALNT14 // 79623 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	GALNT14	GALNT14 . rs10490518, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14),p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1691818	ctgcatatttccctgtattagtc[A/G]ccttatccacaataatctgcaca	A	G	NM_024572 // intron // 0 // Hs.15830 // GALNT14 // 79623 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	GALNT14	GALNT14, rs3919588, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14),p23.1
SNP_A-1676156	agaggatgttattgactaaaatcag[G/T]ggtggaagtgagacagtagcattg	G	T	NM_024572 // intron // 0 // Hs.15830 // GALNT14 // 79623 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	GALNT14	GALNT14, rs1862975, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14),p23.1
SNP_A-2174009	cacacattgaagcccg[C/G]catgatgccaatcagc	C	G	BC010659 // upstream // 30940 // Hs.468058 // GALNT14 // 79623 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), mRNA (cDNA done ///NM_024572 // upstream // 30310 // Hs.468058 // GALNT14 //	GALNT14	GALNT14, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14), (cDNA clone, p23.1
SNP_A-1962569	gtggcctgtgagaaag[A/G]aaacctggactgaagt	A	G	AF214736 // downstream // 5418 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream // 5418 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH-domain containing 3 (EHD3), mRNA. /	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds, p23.1
SNP_A-1962570	cagctggctgatctga[A/G]gaactaagaggctgta	A	G	AF214736 // downstream // 5724 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream // 5724 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH-domain containing 3 (EHD3), mRNA. /	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds, p23.1
SNP_A-1962571	tcctgttagactcata[C/T]ccatgaccagagtcag	C	T	AF214736 // downstream // 5787 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream // 5787 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH-domain containing 3 (EHD3), mRNA. /	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds, p23.1
SNP_A-1891720	tgattgttcattaatg[C/T]caacaagtatttattg	C	T	AF214736 // downstream // 7057 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream // 7057 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH-domain containing 3 (EHD3), mRNA. /	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds, p23.1
SNP_A-2278873	gaggaaaagacctta[A/C]ggtgaccaactgtcct	A	C	AF214736 // downstream // 13761 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH domain containing protein 2 (EHD2) mRNA, complete cds. /// NM_014600 // downstream // 13761 // Hs.368808 // EHD3 // 30845 // Homo sapiens EH-domain containing 3 (EHD3), mRNA.	EHD3	EHD3, Homo sapiens EH domain containing protein 2 (EHD2) complete cds, p23.1
SNP_A-1795278	ggtgataaaatggaa[A/G]cttcaactgtactgt	A	G	NM_000379 // downstream // 8834 // Hs.250 // XDH // 7498 // Homo sapiens xanthine dehydrogenase (XDH), mRNA. /// ENST00000272274 // downstream // 35192 // — // — // — /// ENST00000289041 // downstream // 8834 // — // — // —	XDH	XDH, Homo sapiens xanthine dehydrogenase (XDH), p23.1
SNP_A-1676786	atttctctgctcagatctaggaag[C/T]aaaccctgcctctgctgtctctgtc	C	T	NM_000379 // downstream // 53791 // Hs.250 // XDH // 7498 // xanthine dehydrogenase /// NM_014600 // downstream // 13445 // Hs.368808 // EHD3 // 30845 // EH-domain containing 3	XDH	XDH, rs4952078, xanthine dehydrogenase, p23.1
SNP_A-1722988	gatcttagttcctgccaacctgtc[A/G]caactcaaggattaaactaaacatt	A	G	NM_000379 // downstream // 18141 // Hs.250 // XDH // 7498 // xanthine dehydrogenase /// NM_014600 // downstream // 49095 // Hs.368808 // EHD3 // 30845 // EH-domain containing 3	XDH	XDH, rs207416, xanthine dehydrogenase, p23.1
SNP_A-2058818	aatcattgaccactg[A/G]atagctccagctttga	A	G	NM_017735 // intron // 0 // Hs.468125 // FLJ20272 // 55622 // Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA. /// ENST00000317907 // intron // 0 // — // — // — // —	FLJ20272	FLJ20272, Homo sapiens hypothetical protein FLJ20272 (FLJ20272), p22.3
SNP_A-2160002	atttatgtcctgttga[C/T]agttttgttgactga	C	T	NM_017735 // intron // 0 // Hs.468125 // FLJ20272 // 55622 // Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA. /// ENST00000317907 // intron // 0 // — // — // — // —	FLJ20272	FLJ20272, Homo sapiens hypothetical protein FLJ20272 (FLJ20272), p22.3
SNP_A-1677334	ccagagatggcaccaactatgaaga[A/G]atctttggagaccacatgaagagc	A	G	NM_017735 // intron // 0 // Hs.26090 // FLJ20272 // 55622 // hypothetical protein FLJ20272	FLJ20272	FLJ20272, rs3769583, hypothetical protein FLJ20272,p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2108596	agctgggatatctgaa[C/T]gcgcccactgagttgc	C	T	NM_017735 // downstream // 56914 // Hs.468125 // FLJ20272 // 55622 // Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA. /// M34057 // upstream // 69362 // Hs.49787 // LTBP1 // 4052 // Human transforming growth factor-beta 1 binding protein mRNA	FLJ20272	FLJ20272, Homo sapiens hypothetical protein FLJ20272 (FLJ20272), p22.3
SNP_A-1945831	ttgtttaaccaacacc[C/G]cttaatggctacaggt	C	G	M34057 // intron // 0 // Hs.49787 // LTBP1 // 4052 // Human transforming growth factor-beta 1 binding protein mRNA, complete cds. /// NM_000627 // intron // 0 // Hs.49787 // LTBP1 // 4052 // Homo sapiens latent transforming growth factor beta binding prot	LTBP1	LTBP1, Human transforming growth factor-beta 1 binding protein complete cds, p22.3
SNP_A-2181407	cagactccataagaaa[C/T]gaccctacgagacaaa	C	T	M34057 // intron // 0 // Hs.49787 // LTBP1 // 4052 // Human transforming growth factor-beta 1 binding protein mRNA, complete cds. /// NM_000627 // intron // 0 // Hs.49787 // LTBP1 // 4052 // Homo sapiens latent transforming growth factor beta binding prot	LTBP1	LTBP1, Human transforming growth factor-beta 1 binding protein complete cds, p22.3
SNP_A-1695345	gaacataaaatcctaagctgaggag[A/G]actgtaagagattgc ctggtctggc	A	G	NM_000627 // intron // 0 // Hs.241257 // LTBP1 // 4052 // latent transforming growth factor beta binding protein 1	LTBP1	LTBP1 , rs4671024, latent transforming growth factor beta binding protein 1,p22.3
SNP_A-1718999	ttcttccctgctcagtagatgggaa[A/T]taccctcattgtatagaatt tctgt	A	T	NM_000627 // intron // 0 // Hs.241257 // LTBP1 // 4052 // latent transforming growth factor beta binding protein 1	LTBP1	LTBP1 , rs1993306, latent transforming growth factor beta binding protein 1,p22.3
SNP_A-1731003	ttcactccttaagacctctttaaga[A/G]caagaactatgtggaga gatcctct	A	G	NM_000627 // intron // 0 // Hs.241257 // LTBP1 // 4052 // latent transforming growth factor beta binding protein 1	LTBP1	LTBP1 , rs7569074, latent transforming growth factor beta binding protein 1,p22.3
SNP_A-1962614	ctcaggccagacccca[C/T]atttgatgtgatatgc	C	T	M34057 // downstream // 21673 // Hs.49787 // LTBP1 // 4052 // Human transforming growth factor-beta 1 binding protein mRNA, complete cds. /// NM_000627 // downstream // 21673 // Hs.49787 // LTBP1 // 4052 // Homo sapiens latent transforming growth factor b	LTBP1	LTBP1, Human transforming growth factor-beta 1 binding protein complete cds, p22.3
SNP_A-1735659	aagtgccctctactgagggatgcaa[C/T]gattcctatttctgtcact cctctc	C	T	NM_170672 // intron // 0 // Hs.24024 // RASGRP3 // 25780 // RAS guanyl releasing protein 3 (calcium and DAG-regulated)	RASGRP3	RASGRP3 , rs10495791, RAS guanyl releasing protein 3 (calcium and DAG-regulated),p22.3
SNP_A-1721277	tcacctgaaggtttgttaaagcaca[C/G]attgctgggcctcattca cagtttc	C	G	NM_015376 // downstream // 4087 // - // - // - // - /// NM_170672 // downstream // 4099 // Hs.24024 // RASGRP3 // 25780 // RAS guanyl releasing protein 3 (calcium and DAG-regulated)	-	- , rs1349119, - ,p22.3
SNP_A-1962623	agtttccagcagaata[G/T]agagaatggaggggag	G	T	NM_015475 // upstream // 115579 // Hs.468140 // DKFZP564F0522 // 25940 // Homo sapiens DKFZP564F0522 protein (DKFZP564F0522), mRNA. /// NM_207329 // downstream // 12164 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation ma	DKFZP564F0522	DKFZP564F0522, Homo sapiens DKFZP564F0522 protein (DKFZP564F0522), p22.3
SNP_A-2172287	caatgttgcagcagta[C/T]gaggaccaagagaatt	C	T	NM_207329 // upstream // 39889 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 2590666 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2282141	gagtgtctaggccaaa[C/T]gttcatcttctttatt	C	T	NM_207329 // upstream // 349901 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 2280654 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2196610	cattaaatgtgaacca[C/T]gagactaacagcacaa	C	T	NM_207329 // upstream // 615125 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 2015430 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259155	gaaaaaactttatagd[A/G]cagcaatggtctaatc	A	G	NM_207329 // upstream // 615201 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 2015354 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1742567	aggttgatttatatattggtagttta[A/G]ctttttcattataaactcaatatt ct	A	G	NM_016441 // upstream // 2035492 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1, rs10490439, cysteine-rich motor neuron 1,p22.3
SNP_A-1699951	gtgctgtcataagaaaagtgtgtaga[C/T]ctgaacaggagcatgt ctgatgtct	C	T	NM_016441 // upstream // 2019643 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1, rs10495811, cysteine-rich motor neuron 1,p22.3
SNP_A-1822900	taaaaagtaccaagcat[G/T]aaattctggaactgaa	G	T	NM_207329 // upstream // 728652 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1901903 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1962666	agattagttacatgaa[A/G]aagcttgttgaaatag	A	G	NM_207329 // upstream // 994276 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1636279 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1697635	ctggtacatcatgtgatatgagaac[C/T]atggtaggcaatcaata atgcagag	C	T	NM_016441 // upstream // 1634994 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1, rs10495827, cysteine-rich motor neuron 1,p22.3
SNP_A-2222698	cgatcctccctcta[A/C]gcagtaacctcatcgg	A	C	NM_207329 // upstream // 1066845 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1563710 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2309250	ggaaaactccctgta[C/T]actgtgaaataataa	C	T	NM_207329 // upstream // 1097153 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1533402 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1844299	tagttttcgacctta[C/T]gtaaatcacttaaatt	C	T	NM_207329 // upstream // 1104683 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1525872 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1889595	tgataaaagcctctaga[C/T]ccaacagagaactaa	C	T	NM_207329 // upstream // 1121313 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1509242 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1898631	tgcttgtatcaaaaca[C/T]atcaggtatccgataa	C	T	NM_207329 // upstream // 1133821 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1496734 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2041942	aactaataatcttcac[A/G]ggaagcccaagctct	A	G	NM_207329 // upstream // 1491491 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 1139064 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2295199	gcatattacttcagaa[C/T]tgtgcttaaccttct	C	T	NM_207329 // upstream // 1782680 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 847875 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2078980	acccacccagaataag[A/C]aaagagctgcaaatat	A	C	NM_207329 // upstream // 2068960 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 561595 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2031563	aaaggtctgggatc[A/G]aggtgtgtaatatgtg	A	G	NM_207329 // upstream // 2216625 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 413930 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1956601	ttgttgttgagaca[C/G]tcatttctctcactg	C	G	NM_207329 // upstream // 2235124 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 395431 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1962706	tctagctctctcagg[A/T]acgcattgcaaagcaa	A	T	NM_207329 // upstream // 2259881 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 370674 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2198472	catttagtaaataaaag[C/G]aagtcatagcctagtt	C	G	NM_207329 // upstream // 2276271 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 354284 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2185696	caggagtataaatcac[A/T]ctaacaacaatgtggc	A	T	NM_207329 // upstream // 2283926 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 346629 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1962709	ctttcacccgtcacc[A/T]atgttagctctaaacc	A	T	NM_207329 // upstream // 2287308 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 343247 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2162507	attttccaacatcctc[G/T]cgaatccatctgcaa	G	T	NM_207329 // upstream // 2316583 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 313972 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2052048	aaggttcccgtagaa[G/T]tgtcccctcagcagttg	G	T	NM_207329 // upstream // 2323427 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 307128 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-2161457	attgcgcgctatgca[C/T]gtgaaaaaggtctaat	C	T	NM_207329 // upstream // 2325127 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 305428 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1898201	tgcttaaattggtca[A/T]ctgtgaaatgaaggtt	A	T	NM_207329 // upstream // 2401023 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 229532 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1748265	tgagggaactctattagaagagaaa[A/T]gtctgcctttgacaatg ctatttaa	A	T	NM_016441 // upstream // 223192 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs4115339, cysteine-rich motor neuron 1,p22.3
SNP_A-2050608	aaggcaaagctatgga[A/G]acacaaaaagatcagt	A	G	NM_207329 // upstream // 2502995 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 127560 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1952683	ttctggtctttcatat[C/T]gacttagacctcaaa	C	T	NM_207329 // upstream // 2592327 // Hs.528847 // MYADML // 151325 // Homo sapiens myeloid-associated differentiation marker-like (MYADML), mRNA. /// NM_016441 // upstream // 38228 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1	MYADML	MYADML, Homo sapiens myeloid-associated differentiation marker-like (MYADML), p22.3
SNP_A-1962724	atatcagcagtaagag[A/G]gctggggacatttctt	A	G	NM_016441 // intron // 0 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // — // — // —	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1708528	tcttcatttctgacacacagctaga[A/T]gacactaccagctttctt gcagtg	A	T	NM_016441 // upstream // 7862 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs717806, cysteine-rich motor neuron 1,p22.2
SNP_A-2307648	gcttcatgtctgcta[A/G]gtacaggtcttattat	A	G	NM_016441 // intron // 0 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // — // — // —	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-2290840	gcaaggagacttggat[A/C]atttgtcaagagctag	A	C	NM_016441 // intron // 0 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // — // — // —	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1924301	ttataaaggaaggca[A/G]atatgtataagtcatt	A	G	NM_016441 // intron // 0 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // — // — // —	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1879525	tctatttttctcatc[C/T]cgtctctcacaatgg	C	T	NM_016441 // intron // 0 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // — // — // —	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1916968	tgtttgactctcggga[A/G]agctggatccgtttc	A	G	NM_016441 // intron // 0 // Hs.332847 // CRIM1 // 51232 // Homo sapiens cysteine-rich motor neuron 1 (CRIM1), mRNA. /// ENST00000280527 // intron // 0 // — // — // —	CRIM1	CRIM1, Homo sapiens cysteine-rich motor neuron 1 (CRIM1), p22.2
SNP_A-1658656	tactttttcattcattgtaacccc[C/G]aaatattatcttctcctcctg gt	C	G	NM_016441 // intron // 0 // Hs.170752 // CRIM1 // 51232 // cysteine-rich motor neuron 1	CRIM1	CRIM1 , rs848530, cysteine-rich motor neuron 1,p22.2
SNP_A-2246806	ctgtagcacctctata[A/C]actaacaatgaactat	A	C	NM_005102 // upstream // 121481 // Hs.258563 // FEZ2 // 9637 // Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), mRNA. /// NM_003162 // downstream // 129488 // Hs.43590 // STRN // 6801 // Homo sapiens striatin, calmodulin bindin	FEZ2	FEZ2, Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), p22.2
SNP_A-2267857	gaatcccctctacaa[A/G]tgaatccccacgaagc	A	G	NM_005102 // upstream // 202628 // Hs.258563 // FEZ2 // 9637 // Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), mRNA. /// NM_003162 // downstream // 48341 // Hs.43590 // STRN // 6801 // Homo sapiens striatin, calmodulin binding	FEZ2	FEZ2, Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), p22.2
SNP_A-2279944	gaggctgacacaactc[C/T]actagtatttgcttc	C	T	NM_005102 // upstream // 224096 // Hs.258563 // FEZ2 // 9637 // Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), mRNA. /// NM_003162 // downstream // 26873 // Hs.43590 // STRN // 6801 // Homo sapiens striatin, calmodulin binding	FEZ2	FEZ2, Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), p22.2
SNP_A-2275021	gagaactaaggtaaaa[C/G]gacaagacacaatgag	C	G	ENST00000233099 // intron // 0 // — // — // — /// ENST00000354531 // intron // 0 // — // — // — /// ENST00000360263 // intron // 0 // — // — // —	-	p22.2
SNP_A-1872788	tctatacgccattacc[A/T]ctaaagttiacatatt	A	T	NM_002759 // intron // 0 // Hs.131431 // EIF2AK2 // 5610 // Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /// ENST00000233057 // intron // 0 // — // — // — /// ENST00000343510 // intron // 0 //	EIF2AK2	EIF2AK2, Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284065	gatatcattccttcca[A/T]ctctctgaacatcagc	A	T	NM_002759 // intron // 0 // Hs.131431 // EIF2AK2 // 5610 // Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /// ENST00000233057 // intron // 0 // — // — // — // — /// ENST00000343510 // intron // 0 //	EIF2AK2	EIF2AK2, Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), p22.2
SNP_A-1865388	tccatccttcctcccg[C/T]attccttctcccaaag	C	T	NM_002759 // intron // 0 // Hs.131431 // EIF2AK2 // 5610 // Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /// NM_018607 // intron // 0 // Hs.433466 // PRO1853 // 55471 // Homo sapiens hypothetical protein PR	EIF2AK2	EIF2AK2, Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), p22.2
SNP_A-2037703	aacaaggagtatacag[A/T]cggatgctgatgtgtt	A	T	NM_002759 // intron // 0 // Hs.131431 // EIF2AK2 // 5610 // Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /// ENST00000233057 // intron // 0 // — // — // — // — /// ENST00000343510 // intron // 0 //	EIF2AK2	EIF2AK2, Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), p22.2
SNP_A-1793786	ggtattggcagtacta[C/T]attttaagacattttc	C	T	NM_012413 // downstream // 28758 // Hs.79033 // QPCT // 25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 241521 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector pro	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-2282032	gagtggctctcctaca[A/G]tcgtgtggcttggggt	A	G	NM_012413 // downstream // 38173 // Hs.79033 // QPCT // 25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 232106 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector pro	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-2109233	agcttgtgccttctta[C/T]ggataacccactcagg	C	T	NM_012413 // downstream // 38437 // Hs.79033 // QPCT // 25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 231842 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector pro	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-2041952	aactaatcacatggga[C/T]gcccacttcagttagc	C	T	NM_012413 // downstream // 77981 // Hs.79033 // QPCT // 25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 192298 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector pro	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-1648540	taaagagaaatgaagaaccacagta[G/T]ggagtacttttctgcattgggtagg	G	T	NM_006449 // downstream // 253259 // Hs.352554 // CDC42EP3 // 10602 // CDC42 effector protein (Rho GTPase binding) 3 /// NM_012413 // downstream // 17020 // Hs.79033 // QPCT // 25797 // glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	CDC42EP3	CDC42EP3 , rs10490445, CDC42 effector protein (Rho GTPase binding) 3 ,p22.2
SNP_A-2265577	gaagccttttagaaca[C/T]tgacaagtaaataatc	C	T	NM_012413 // downstream // 80507 // Hs.79033 // QPCT // 25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 189772 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector pro	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-1920321	ttaatgggattctgca[C/G]cacaaatctagtccct	C	G	NM_012413 // downstream // 217772 // Hs.79033 // QPCT // 25797 // Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA. /// NM_006449 // downstream // 52507 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector pro	QPCT	QPCT, Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), p22.2
SNP_A-1753153	agcgaacttgtggacgggtttgcta[C/T]agcggtgttacacttagatgaggaa	C	T	NM_006449 // upstream // 23493 // Hs.352554 // CDC42EP3 // 10602 // CDC42 effector protein (Rho GTPase binding) 3 /// NM_144713 // upstream // 254787 // Hs.9905 // FLJ32954 // 151393 // hypothetical protein FLJ32954	CDC42EP3	CDC42EP3 , rs4670762, CDC42 effector protein (Rho GTPase binding) 3 ,p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1899489	tggaagatttgcatcc[A/G]cttccacaagctgcta	A	G	NM_006449 // upstream // 157625 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA. /// NM_144713 // upstream // 120655 // Hs.532901 // FLJ32954 // 151393 // Homo sapiens hypothetical protein F	CDC42EP3	CDC42EP3, Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), p22.2
SNP_A-2301457	gcgaaaagaaccctgc[A/G]aagctatcacagagat	A	G	NM_006449 // upstream // 165268 // Hs.369574 // CDC42EP3 // 10602 // Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA. /// NM_144713 // upstream // 113012 // Hs.532901 // FLJ32954 // 151393 // Homo sapiens hypothetical protein F	CDC42EP3	CDC42EP3, Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), p22.2
SNP_A-2062351	aatgtaaccactatcc[C/T]gagaccagcaccatag	C	T	NM_173652 // intron // 0 // — // MGC34824 // 285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// ENST00000342258 // intron // 0 // — // — // — // —	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-2153826	attagttggcataaaaa[C/T]agctttcaggctttta	C	T	NM_173652 // 3UTR // 0 // — // MGC34824 // 285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// ENST00000342258 // 3UTR // 0 // — // — // — // —	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-1962812	gaacatttctgggga[A/G]aggacttcttatacaa	A	G	NM_173652 // downstream // 32995 // — // MGC34824 // 285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// NM_022374 // downstream // 81141 // Hs.190440 // ARL6IP2 // 64225 // Homo sapiens ADP-ribosylation factor-like 6 interacting	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-2183382	cagcactaattgacaa[C/T]aaataaagtgataaata	C	T	NM_173652 // downstream // 33117 // — // MGC34824 // 285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// NM_022374 // downstream // 81019 // Hs.190440 // ARL6IP2 // 64225 // Homo sapiens ADP-ribosylation factor-like 6 interacting	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-2288724	gattgtaaacaactgc[A/C]aacacaggcactagac	A	C	NM_173652 // downstream // 61504 // — // MGC34824 // 285154 // Homo sapiens hypothetical protein MGC34824 (MGC34824), mRNA. /// NM_022374 // downstream // 52632 // Hs.190440 // ARL6IP2 // 64225 // Homo sapiens ADP-ribosylation factor-like 6 interacting	MGC34824	MGC34824, Homo sapiens hypothetical protein MGC34824 (MGC34824), p22.2
SNP_A-2256507	ctttctcgactgtaa[A/C]atttctaggttgatga	A	C	NM_138394 // downstream // 10903 // Hs.445497 // HNRPLL // 92906 // Homo sapiens hypothetical protein BC008217 (LOC92906), mRNA. /// ENST00000311135 // downstream // 70262 // — // — // — // — /// ENST00000272249 // downstream // 10903 // — // —	HNRPLL	HNRPLL, Homo sapiens hypothetical protein BC008217 (LOC92906), p22.1
SNP_A-1898671	tgctttaaaacagcac[C/T]gtcggccgggcatggt	C	T	NM_003618 // intron // 0 // Hs.468239 // MAP4K3 // 8491 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// ENST00000341681 // intron // 0 // — // — // — // — /// ENST00000263881 // intron // 0 // — // —	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-2213566	ccgtcaggttctacct[G/T]aaatctatgtggagcg	G	T	NM_003618 // upstream // 155168 // Hs.468239 // MAP4K3 // 8491 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// NM_152390 // upstream // 73598 // Hs.40808 // MGC33926 // 130733 // Homo sapiens hypothetical protei	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-2116167	aggtaagtcatgtaaa[G/T]ttctttgcacagtccc	G	T	NM_003618 // upstream // 190155 // Hs.468239 // MAP4K3 // 8491 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /// NM_152390 // upstream // 38611 // Hs.40808 // MGC33926 // 130733 // Homo sapiens hypothetical protei	MAP4K3	MAP4K3, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), p22.1
SNP_A-1861878	tcatgaaatctccag[C/T]aacttttctgctctg	C	T	NM_021097 // intron // 0 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // intron // 0 // — // — // — // — /// ENST00000356676 // intron // 0 // — // —	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2155515	attcatttccagagat[C/G]actaaaaatcagagat	C	G	NM_021097 // intron // 0 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // intron // 0 // — // — // — // — /// ENST00000356676 // intron // 0 // — /	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2289949	gcaaagcagagcatca[A/G]ccttttccagcaaatcc	A	G	NM_021097 // intron // 0 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // intron // 0 // — // — // — // — /// ENST00000356676 // intron // 0 // — /	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-1962890	tgattcactgaactag[A/T]cagagtggctcagatc	A	T	NM_021097 // upstream // 67366 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 67366 // — // — // — // — /// ENST00000356676 // upstream	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2135087	atattctgaggtaggc[G/T]cattccagcatgatga	G	T	NM_021097 // upstream // 323734 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 323734 // — // — // — // — /// ENST00000356676 // upstre	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2133263	atatatactgagcaaa[A/G]taaatatctagggtac	A	G	NM_021097 // upstream // 733832 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 733832 // — // — // — // — /// ENST00000356676 // upstre	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-1909689	tgtcaagtaaaagtca[A/G]tagcctagagatgtgt	A	G	NM_021097 // upstream // 769384 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 769384 // — // — // — // — /// ENST00000356676 // upstre	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium p22.1
SNP_A-2284158	gatatgctaactatcc[G/T]gatctaatcactaccc	G	T	NM_021097 // upstream // 964827 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 964827 // — // — // — // — /// ENST00000356676 // upstre	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-1838175	tagaactcaaaactga[C/T]gaaacacaaagcaaag	C	T	NM_021097 // upstream // 1004343 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 1004343 // — // — // — // — /// ENST00000356676 // upst	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-2129664	atacagctatctgata[A/C]cagaacttgaactgga	A	C	NM_021097 // upstream // 1095422 // Hs.468274 // SLC8A1 // 6546 // Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), mRNA. /// ENST00000346579 // upstream // 1095422 // — // — // — // — /// ENST00000356676 // upst	SLC8A1	SLC8A1, Homo sapiens solute carrier family 8 (sodium,p22.1
SNP_A-1962936	tggaagtccgtacttg[C/G]cattttctcttaagtt	C	G	ENST00000238837 // upstream // 149103 // — // — // — // — /// ENST00000294964 // upstream // 54436 // — // — // — // —	-	p21
SNP_A-2068675	acaataattactctac[C/G]acaagcgttattattt	C	G	NM_019063 // upstream // 37805 // Hs.432438 // EML4 // 27436 // Homo sapiens echinoderm microtubule associated protein like 4 (EML4), mRNA. /// ENST00000294964 // downstream // 73057 // — // — // — // — /// ENST00000318522 // upstream // 37805 //	EML4	EML4, Homo sapiens echinoderm microtubule associated protein like 4 (EML4), p21
SNP_A-2178628	cactctgaaatcacta[A/T]gtcatactcccttgca	A	T	NM_012205 // upstream // 85354 // Hs.368805 // HAAO // 23498 // Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA. /// NM_006887 // downstream // 345618 // Hs.503093 // ZFP36L2 // 678 // Homo sapiens zinc finger protein 36, C3H type-like 2 (	HAAO	HAAO, Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), p21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805508	gtccagcacttgagac[A/G]ctacagagggctgcag	A	G	NM_012205 // upstream // 112375 // Hs.368805 // HAAO // 23498 // Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA. /// NM_006887 // downstream // 318597 // Hs.503093 // ZFP36L2 // 678 // Homo sapiens zinc finger protein 36, C3H type-like 2	HAAO	HAAO, Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), p21
SNP_A-2192578	catccagaatggagca[C/G]ggcatttgtcctgtcc	C	G	NM_012205 // upstream // 112693 // Hs.368805 // HAAO // 23498 // Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA. /// NM_006887 // downstream // 318279 // Hs.503093 // ZFP36L2 // 678 // Homo sapiens zinc finger protein 36, C3H type-like 2	HAAO	HAAO, Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), p21
SNP_A-2276183	gagagagagagagtat[A/G]aggtattggttcaagc	A	G	NM_012205 // upstream // 326280 // Hs.368805 // HAAO // 23498 // Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA. /// NM_006887 // downstream // 104692 // Hs.503093 // ZFP36L2 // 678 // Homo sapiens zinc finger protein 36, C3H type-like 2	HAAO	HAAO, Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), p21
SNP_A-2071772	acagaccacctttcc[A/T]agagcctggctataaa	A	T	NM_198554 // intron // 0 // Hs.369592 // THADA // 63892 // Homo sapiens thyroid adenoma associated (THADA), mRNA. /// NM_022065 // intron // 0 // Hs.369592 // THADA // 63892 // Homo sapiens thyroid adenoma associated (THADA), mRNA. /// ENST00000330266 //	THADA	THADA, Homo sapiens thyroid adenoma associated (THADA), p21
SNP_A-1673892	cgaaaatgtccctgatagtcggaga[A/T]ctcatgccagttgcctc tcaagcca	A	T	AB095948 // intron // 0 // Hs.255938 // KIAA2028 // 130271 // similar to PH (pleckstrin homology) domain	KIAA2028	KIAA2028 , rs4952999, similar to PH (pleckstrin homology) domain,p21
SNP_A-1744637	gtattcgaatgtctgaggccttcaa[C/T]atggagagtgttaataaa agtaagt	C	T	AB095948 // CDS // 0 // Hs.255938 // KIAA2028 // 130271 // similar to PH (pleckstrin homology) domain	KIAA2028	KIAA2028 , rs4953002, similar to PH (pleckstrin homology) domain,p21
SNP_A-1867683	tcctaaaactgtatac[C/T]attggttaatttttct	C	T	M92439 // intron // 0 // Hs.368084 // LRPPRC // 10128 // Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) mRNA, complete cds. /// NM_133259 // intron // 0 // Hs.368084 // LRPPRC // 10128 // Homo sapiens leucine-rich PPR-motif containing (LR	LRPPRC	LRPPRC, Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) complete cds. p21
SNP_A-2042965	aactgaagatccagaa[C/G]aggaagttagagaatc	C	G	M92439 // upstream // 88844 // Hs.368084 // LRPPRC // 10128 // Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) mRNA, complete cds. /// NM_133259 // upstream // 72769 // Hs.368084 // LRPPRC // 10128 // Homo sapiens leucine-rich PPR-motif co	LRPPRC	LRPPRC, Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) complete cds. ,p21
SNP_A-2118235	agtaaatgatggctat[A/T]atacaatgtcatggtt	A	T	M92439 // upstream // 89252 // Hs.368084 // LRPPRC // 10128 // Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) mRNA, complete cds. /// NM_133259 // upstream // 73177 // Hs.368084 // LRPPRC // 10128 // Homo sapiens leucine-rich PPR-motif co	LRPPRC	LRPPRC, Homo sapiens leucine-rich PPR-motif containing protein (LRPPRC) complete cds. ,p21
SNP_A-1962976	gctacctagggaagag[G/T]ataggatgacatcttt	G	T	NM_024766 // intron // 0 // Hs.468349 // FLJ23451 // 79823 // Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // — // — // — // —	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1781899	ggcaaaaatcaggtgg[C/T]caaaaatgtctttatc	C	T	NM_024766 // intron // 0 // Hs.468349 // FLJ23451 // 79823 // Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // — // — // — // —	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1928772	ttcagacacctgccgg[A/G]catcggggcagggtga	A	G	NM_024766 // intron // 0 // Hs.468349 // FLJ23451 // 79823 // Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// ENST00000272284 // intron // 0 // — // — // — // —	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21
SNP_A-1788425	gggagtgaaagaggaa[G/T]gagcaaagtggtcatg	G	T	NM_024766 // downstream // 59994 // Hs.468349 // FLJ23451 // 79823 // Homo sapiens hypothetical protein FLJ23451 (FLJ23451), mRNA. /// NM_005413 // upstream // 109615 // Hs.227277 // SIX3 // 6496 // Homo sapiens sine oculis homeobox homolog 3 (Drosophila)	FLJ23451	FLJ23451, Homo sapiens hypothetical protein FLJ23451 (FLJ23451), p21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2154768	attcaccaaacaaccd[A/G]aggaggagactaatga	A	G	NM_005413 // downstream // 15912 // Hs.227277 // SIX3 // 6496 // Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA. /// NM_016932 // downstream // 43995 // Hs.101937 // SIX2 // 10736 // Homo sapiens sine oculis homeobox homolog 2 (Dros	SIX3	SIX3, Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), p21
SNP_A-2147776	atggcattatggaaaaa[C/G]gtggcttgaaatat	C	G	NM_016932 // upstream // 42252 // Hs.101937 // SIX2 // 10736 // Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA. /// NM_018079 // downstream // 337026 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FL	SIX2	SIX2, Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), p21
SNP_A-1839690	tagatgccctcagtaa[A/G]tgttcagaataaat	A	G	NM_016932 // upstream // 329008 // Hs.101937 // SIX2 // 10736 // Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA. /// NM_018079 // downstream // 50270 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FL	SIX2	SIX2, Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), p21
SNP_A-1660695	actcaaattacacttacaatttttca[A/C]atatagtatctggcattca atcaag	A	C	NM_016932 // upstream // 357886 // Hs.101937 // SIX2 // 10736 // sine oculis homeobox homolog 2 (Drosophila) /// NM_018079 // downstream // 214410 // Hs.14229 // FLJ10379 // 55133 // hypothetical protein FLJ10379	SIX2	SIX2 , rs2216505, sine oculis homeobox homolog 2 (Drosophila) ,p21
SNP_A-1963010	aaatggccagcaaatg[A/G]acaaaggatcttcaa	A	G	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2222071	cgaagcagagttctta[C/T]aggtcagattgaagac	C	T	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-1827977	taagaagcatttgtga[C/T]caggctacatttctt	C	T	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-1722354	attcatgccattaactattcattac[C/T]gagccttttttgttgtcttgtttt	C	T	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // hypothetical protein FLJ10379	FLJ10379	FLJ10379, rs10490348, hypothetical protein FLJ10379,p21
SNP_A-1963013	tcagtttccgaagata[C/T]gcagctttggcgaaac	C	T	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-1927112	ttatttcaacagccca[A/C]cttcaattacaaatgt	A	C	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2236870	ctctagattaggctctc[A/G]caatatggtaaaactcc	A	G	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2244532	ctggagaaaatgtacat[A/G]aatgcacaaatactat	A	G	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2042997	aactgacaatgtagaa[A/C]gatgacagagataga	A	C	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2142002	atctttcaaggtcaa[C/T]caaaatgctatttcctt	C	T	NM_018079 // intron // 0 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// ENST00000263736 // intron // 0 // — // — // —	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-2187175	caggtctctggtataaa[C/T]ggcgtgagtaagataa	C	T	NM_018079 // upstream // 18948 // Hs.14229 // FLJ10379 // 55133 // Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA. /// NM_005400 // upstream // 21692 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// EN	FLJ10379	FLJ10379, Homo sapiens hypothetical protein FLJ10379 (FLJ10379), p21
SNP_A-1736703	agtagatgtttcagtgaactgacc[A/G]aaaatttcctgttacatag gtcaat	A	G	NM_005400 // upstream // 63234 // Hs.155281 // PRKCE // 5581 // protein kinase C, epsilon /// NM_018079 // upstream // 8866 // Hs.14229 // FLJ10379 // 55133 // hypothetical protein FLJ10379	PRKCE	PRKCE , rs6544836, protein kinase C, epsilon ,p21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1947258	tttaattggtcacgca[A/G]aagaaaggcttacatt	A	G	NM_005400 // intron // 0 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // — // — // —	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-1807533	gtctgctttgtgtca[C/T]gccagctgcctggtgc	C	T	NM_005400 // intron // 0 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // — // — // —	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-2292520	gcactccatatactg[C/T]agagctatctgaattt	C	T	NM_005400 // intron // 0 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // — // — // —	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-2236378	ctcgcatgaggccatg[C/T]catgatgatcacaggg	C	T	NM_005400 // intron // 0 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // — // — // —	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-1679796	tccagatatgatttca[G/T]ttgggccagttagatg	G	T	NM_005400 // intron // 0 // Hs.155281 // PRKCE // 5581 // protein kinase C, epsilon	PRKCE	PRKCE , rs872288, protein kinase C, epsilon,p21
SNP_A-2138342	atccagctttttggaa[C/T]gtctgttaaatagtct	C	T	NM_005400 // intron // 0 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // — // — // —	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-2220197	ccttcattcatgtcag[C/G]aaatccctaactgtgt	C	G	NM_005400 // intron // 0 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// ENST00000306156 // intron // 0 // — // — // —	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-2094853	agaatctgtgaaaaga[A/C]gtggcaactgtgctgg	A	C	NM_005400 // downstream // 65818 // Hs.97432 // PRKCE // 5581 // Homo sapiens protein kinase C, epsilon (PRKCE), mRNA. /// NM_001430 // upstream // 43617 // Hs.468410 // EPAS1 // 2034 // Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA. /// ENS	PRKCE	PRKCE, Homo sapiens protein kinase C, epsilon (PRKCE), p21
SNP_A-1845186	tataccacccccactca[A/G]gtgcaataatatttaa	A	G	NM_001430 // intron // 0 // Hs.468410 // EPAS1 // 2034 // Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA. /// ENST00000263734 // intron // 0 // — // — // —	EPAS1	EPAS1, Homo sapiens endothelial PAS domain protein 1 (EPAS1), p21
SNP_A-2185039	cagctgttaattagct[A/G]ccccctctacaaatag	A	G	NM_001430 // intron // 0 // Hs.468410 // EPAS1 // 2034 // Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA. /// ENST00000263734 // intron // 0 // — // — // —	EPAS1	EPAS1, Homo sapiens endothelial PAS domain protein 1 (EPAS1), p21
SNP_A-2307381	gcttagtgagtcagat[C/T]acaccttaatgctctt	C	T	NM_001430 // downstream // 20095 // Hs.468410 // EPAS1 // 2034 // Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA. /// ENST00000263734 // downstream // 20095 // — // — // — /// ENST00000343465 // upstream // 72795 // — // — //	EPAS1	EPAS1, Homo sapiens endothelial PAS domain protein 1 (EPAS1), p21
SNP_A-2077998	accagctattgtgaaa[A/G]ttgattataaattcac	A	G	NM_144949 // intron // 0 // Hs.468426 // SOCS5 // 9655 // Homo sapiens suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, mRNA. /// NM_014011 // intron // 0 // Hs.468426 // SOCS5 // 9655 // Homo sapiens suppressor of cytokine signaling 5 (S	SOCS5	SOCS5, Homo sapiens suppressor of cytokine signaling 5 (SOCS5), transcript variant 2, p21
SNP_A-2184001	cagccatgtgtggaaa[C/T]gtcaccctggagttct	C	T	AB032966 // intron // 0 // Hs.370603 // TTC7A // 57217 // Homo sapiens mRNA for KIAA1140 protein, partial cds. /// ENST00000319190 // intron // 0 // — // — // — /// ENST00000263737 // intron // 0 // — // — // —	TTC7A	TTC7A, Homo sapiens for KIAA1140 protein, partial cds. ,p21
SNP_A-2285049	gatcctgggagcatac[A/C]ggactcctccaaacct	A	C	AB032966 // downstream // 15595 // Hs.370603 // TTC7A // 57217 // Homo sapiens mRNA for KIAA1140 protein, partial cds. /// NM_173649 // downstream // 38711 // — // FLJ40172 // 285051 // Homo sapiens hypothetical protein FLJ40172 (FLJ40172), mRNA. /// EN	TTC7A	TTC7A, Homo sapiens for KIAA1140 protein, partial cds. ,p21
SNP_A-1784858	ggccttcatagaaaag[G/T]aattacctaaaaagaa	G	T	NM_022055 // intron // 0 // Hs.243991 // KCNK12 // 56660 // Homo sapiens potassium channel, subfamily K, member 12 (KCNK12), mRNA. /// ENST00000327876 // intron // 0 // — // — // —	KCNK12	KCNK12, Homo sapiens potassium channel, subfamily K, member 12 (KCNK12), p21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2240247	ctgaatgacagactga[A/T]acacttgctcaaaggg	A	T	NM_022055 // upstream // 106934 // Hs.243991 // KCNK12 // 56660 // Homo sapiens potassium channel, subfamily K, member 12 (KCNK12), mRNA. /// ENST00000327876 // upstream // 106934 // — // — // — // — /// ENST00000304289 // downstream // 13423 // -	KCNK12	KCNK12, Homo sapiens potassium channel, subfamily K, member 12 (KCNK12), p16.3
SNP_A-1819314	gttggagtaaagtgaa[C/T]gaaataatcagaatgt	C	T	NM_000179 // upstream // 53467 // Hs.445052 // MSH6 // 2956 // Homo sapiens mutS homolog 6 (E. coli) (MSH6), mRNA. /// NM_012167 // downstream // 77242 // Hs.284289 // FBXO11 // 80204 // Homo sapiens F-box protein 11 (FBXO11), transcript variant 3, mRNA.	MSH6	MSH6, Homo sapiens mutS homolog 6 (E. coli) (MSH6), p16.3
SNP_A-1861551	tcatcctagattaaag[A/C]ctgtattaccatgaaa	A	C	NM_000179 // downstream // 438876 // Hs.445052 // MSH6 // 2956 // Homo sapiens mutS homolog 6 (E. coli) (MSH6), mRNA. /// NM_012167 // upstream // 340146 // Hs.284289 // FBXO11 // 80204 // Homo sapiens F-box protein 11 (FBXO11), transcript variant 3, mRNA	MSH6	MSH6, Homo sapiens mutS homolog 6 (E. coli) (MSH6), p16.3
SNP_A-2104195	agcagagggtgcctaa[C/T]tgaggtcattctcagc	C	T	NM_152994 // downstream // 29678 // Hs.515985 // LOC129285 // 129285 // Homo sapiens smooth muscle myosin heavy chain 11 isoform SM1-like (LOC129285), mRNA. /// NM_172311 // upstream // 35522 // Hs.44385 // SALF // 286749 // Homo sapiens stoned B/TFIIA-al	LOC129285	LOC129285, Homo sapiens smooth muscle myosin heavy chain 11 isoform SM1-like (LOC129285), p16.3
SNP_A-1881768	tctttgtatccaataa[A/G]tcagtaacaactctac	A	G	NM_181446 // intron // 0 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // intron // 0 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FS	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-2248307	ctgtgtcagaaaccat[C/G]aagaatgcacagctga	C	G	NM_181446 // intron // 0 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // intron // 0 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FS	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-2310361	ggaactatttgatgca[C/T]tgagtaaacaagagta	C	T	NM_181446 // upstream // 34084 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 34084 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-2050103	aaggacacagtgttca[C/T]ccccctttcgcccttcc	C	T	NM_181446 // upstream // 115515 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 115515 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1908852	tgtagtgtcagtatca[A/T]gttacacagagcaaaa	A	T	NM_181446 // upstream // 278991 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 278991 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1709615	tcaaagatttattctctcaattacc[A/C]atcaaaataactaataaaaggagaa	A	C	NM_000145 // upstream // 266395 // Hs.1428 // FSHR // 2492 // follicle stimulating hormone receptor /// NM_004801 // downstream // 499463 // Hs.22998 // NRXN1 // 9378 // neurexin 1 /// NM_138735 // downstream // 499463 // Hs.22998 // NRXN1 // 9378 // neu	FSHR	FSHR , rs1527894, follicle stimulating hormone receptor ,p16.3
SNP_A-2097465	agagaacattactcca[C/T]tcacataataaagcta	C	T	NM_181446 // upstream // 396306 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 396306 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2297032	gccaattatctgactA[C/T]aggttggatgatatta	C	T	NM_181446 // upstream // 400359 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 400359 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1840294	tagcatacaatctagaA[C/T]aacacagttcttgggt	C	T	NM_181446 // upstream // 444238 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 444238 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1963152	tctcctaacaggcaag[A/C]aaaataaaagcagaat	A	C	NM_181446 // upstream // 448984 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 448984 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-2076922	accaaatagattcagg[C/T]attcaaagtcctgatg	C	T	NM_181446 // upstream // 757856 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, mRNA. /// NM_000145 // upstream // 757856 // Hs.1428 // FSHR // 2492 // Homo sapiens follicle stimulating hormon	FSHR	FSHR, Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 2, p16.3
SNP_A-1817083	gttcaaacctattcca[C/T]aagcctagtactctgc	C	T	NM_138735 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // — // — // — /// ENST00000331040 // intron // 0 // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1839613	tagatctatacaatta[A/G]cacacttgccagagc	A	G	NM_138735 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // — // — // — /// ENST00000331040 // intron // 0 // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2064139	aattcaaagacatag[G/T]aggtacaggtgggg	G	T	NM_138735 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // — // — // — /// ENST00000331040 // intron // 0 // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1889344	tgagtgtatgggaggga[A/C]cacttctgtatacct	A	C	NM_138735 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // — // — // — /// ENST00000331040 // intron // 0 // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1957545	ttttatatcacctgta[A/T]ggtcattacacttag	A	T	NM_138735 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// ENST00000342183 // intron // 0 // — // — // — /// ENST00000331040 // intron // 0 // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1686432	tctaactctcagcacatattcatag[A/T]aaaccaaagttgcaata ctgtaaaa	A	T	NM_004801 // intron // 0 // Hs.22998 // NRXN1 // 9378 // neurexin 1 /// NM_138735 // intron // 0 // Hs.22998 // NRXN1 // 9378 // neurexin 1	NRXN1	NRXN1 , rs10490231, neurexin 1 ,p16.3
SNP_A-1724654	aattagtttgtttaaagagaaga[C/T]gaggtaccctgacaaca tgatcct	C	T	NM_004801 // intron // 0 // Hs.22998 // NRXN1 // 9378 // neurexin 1 /// NM_138735 // intron // 0 // Hs.22998 // NRXN1 // 9378 // neurexin 1	NRXN1	NRXN1 , rs10490230, neurexin 1 ,p16.3
SNP_A-1698423	tggtgctgggaggctgtaagccaa[C/G]gaatctgggcaggta taacaggaac	C	G	NM_004801 // intron // 0 // Hs.22998 // NRXN1 // 9378 // neurexin 1 /// NM_138735 // intron // 0 // Hs.22998 // NRXN1 // 9378 // neurexin 1	NRXN1	NRXN1 , rs1814972, neurexin 1 ,p16.3
SNP_A-1963210	gatgtttggctaagaa[C/G]agctagattctcacaa	C	G	NM_138735 // upstream // 350670 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2971590 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2151407	atgttcagaagagtca[A/G]aaatatctttcta	A	G	NM_138735 // upstream // 363275 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2958985 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1792640	ggtaaattaagaaata[C/G]catagctgcagatgtt	C	G	NM_138735 // upstream // 457073 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2865187 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1829747	taataaaacataagcg[A/C]aacagtgaaaaactg	A	C	NM_138735 // upstream // 707751 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2614509 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2075467	acatgagtcaggaaca[A/T]cttaagattttggaa	A	T	NM_138735 // upstream // 744592 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2577668 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1690325	tcttatttttctttttgctaata[A/C]atcactgcaitcagccttaagtta	A	C	NM_004801 // upstream // 3284 // Hs.22998 // NRXN1 // 9378 // neurexin 1 /// NM_016115 // downstream // 2638231 // Hs.40763 // ASB3 // 51130 // ankyrin repeat and SOCS box-containing 3 /// NM_138735 // upstream // 683993 // Hs.22998 // NRXN1 // 9378 // n	NRXN1	NRXN1, , rs2287234, neurexin 1 ,p16.3
SNP_A-1963216	cagagagtaggagtta[G/T]gatgaggaaaaatggc	G	T	NM_138735 // upstream // 749037 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2573223 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1839253	tagaggtatgctgtac[C/T]gacaaaataatggtta	C	T	NM_138735 // upstream // 760829 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2561431 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2179725	cacttgaagtattaaa[A/G]tccaaactgtcatatt	A	G	NM_138735 // upstream // 1096322 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 2225938 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-17963111	ggtgtgtgcatactca[A/G]gaagaaagggaatgga	A	G	NM_138735 // upstream // 1354802 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1967458 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-1651394	tgattgttatcttcaaggtaaccaa[C/T]gaactgagagtgggagt gggaacag	C	T	NM_004801 // upstream // 620563 // Hs.22998 // NRXN1 // 9378 // neurexin 1 /// NM_016115 // downstream // 2020952 // Hs.40763 // ASB3 // 51130 // ankyrin repeat and SOCS box-containing 3 /// NM_138735 // upstream // 1301272 // Hs.22998 // NRXN1 // 9378 /	NRXN1	NRXN1, rs4108601, neurexin 1 ,p16.3
SNP_A-1923934	ttagtgaaagagtcaa[C/T]agtttaatagttagag	C	T	NM_138735 // upstream // 1978165 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1344095 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884504	tgaagtagtggccta[C/T]gaatgatatatcttga	C	T	NM_138735 // upstream // 2149070 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 1173190 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.3
SNP_A-2101014	agatcaaatgaagttg[A/G]aacccttaacaactc	A	G	NM_138735 // upstream // 2403336 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 918924 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1963276	caactacatagttatc[C/T]ctgagcctgcagtgct	C	T	NM_138735 // upstream // 2405644 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 916616 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2166041	caaataattaaaccaa[A/G]ccctgttgataactgc	A	G	NM_138735 // upstream // 2407702 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 914558 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1952366	ttctctgctgatca[C/T]gtgagtgctgtttggg	C	T	NM_138735 // upstream // 2926871 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 395389 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2285044	gatcctgctgtctga[C/T]aagctattatggcaga	C	T	NM_138735 // upstream // 2965742 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 356518 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1879699	tcttcataaaagttca[C/G]gtgcattcccaatctct	C	G	NM_138735 // upstream // 3094688 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 227572 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2169713	caaggaagtctccaga[C/G]gcacgcttctacatgg	C	G	NM_138735 // upstream // 3152409 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 169851 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2143719	atgagaagtctataca[A/G]caaaatctactaaata	A	G	NM_138735 // upstream // 3271689 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 50571 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (A	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-2046744	aagaggaaagcagaac[A/C]atgtgtaaaatagact	A	C	NM_138735 // upstream // 3286749 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant beta, mRNA. /// NM_145863 // downstream // 35511 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (A	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant beta, p16.2
SNP_A-1963316	taattatggaggaatt[C/T]aagcacgaagttaatg	C	T	NM_145863 // intron // 0 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 2, mRNA. /// NM_016115 // intron // 0 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-contai	ASB3	ASB3, Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 2, p16.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1850869	tattaglatttggagat[A/C]aattagagatgcatag	A	C	NM_145863 // intron // 0 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 2, mRNA. /// NM_016115 // intron // 0 // Hs.40763 // ASB3 // 51130 // Homo sapiens ankyrin repeat and SOCS box-contai	ASB3	ASB3, Homo sapiens ankyrin repeat and SOCS box-containing 3 (ASB3), transcript variant 2, p16.2
SNP_A-1744191	accagtctcatttcagcagaaatc[G/T]aagtgaggaattctatttctctta	G	T	NM_016115 // intron // 0 // Hs.40763 // ASB3 // 51130 // ankyrin repeat and SOCS box-containing 3 /// NM_145863 // intron // 0 // Hs.40763 // ASB3 // 51130 // ankyrin repeat and SOCS box-containing 3	ASB3	ASB3, rs10490472, ankyrin repeat and SOCS box-containing 3, p16.2
SNP_A-1734044	aactcttcccttccagtatcccaa[C/T]ctggctaactaggatcttactt	C	T	D38521 // downstream // 3983 // Hs.119563 // PSME4 // 23198 // proteasome (prosome, macropain) activator subunit 4 /// NM_006794 // upstream // 956 // Hs.511761 // GPR75 // 10936 // G protein-coupled receptor 75	PSME4	PSME4, rs3755113, proteasome (prosome, macropain) activator subunit 4, p16.2
SNP_A-1854506	tcaaattacacagaaa[C/T]aggcacattaaaatat	C	T	NM_014614 // intron // 0 // Hs.413801 // PSME4 // 23198 // Homo sapiens proteasome (prosome, macropain) activator subunit 4 (PSME4), mRNA. /// ENST00000185162 // intron // 0 // --- // --- // ---	PSME4	PSME4, Homo sapiens proteasome (prosome, macropain) activator subunit 4 (PSME4), p16.2
SNP_A-1963325	aaattacatgcaccca[A/G]aggtccaatttggcag	A	G	NM_014614 // upstream // 85037 // Hs.413801 // PSME4 // 23198 // Homo sapiens proteasome (prosome, macropain) activator subunit 4 (PSME4), mRNA. /// NM_138448 // upstream // 59523 // Hs.516173 // ACYP2 // 98 // Homo sapiens acylphosphatase 2, muscle type	PSME4	PSME4, Homo sapiens proteasome (prosome, macropain) activator subunit 4 (PSME4), p16.2
SNP_A-1846523	tatatctataaaaca[A/T]ccaatttgaccattta	A	T	NM_138448 // intron // 0 // Hs.516173 // ACYP2 // 98 // Homo sapiens acylphosphatase 2, muscle type (ACYP2), mRNA. /// ENST00000030536 // intron // 0 // --- // --- // ---	ACYP2	ACYP2, Homo sapiens acylphosphatase 2, muscle type (ACYP2), p16.2
SNP_A-1895085	tgcccagtgccacttg[A/G]aaaaaaatggtttagt	A	G	NM_173486 // intron // 0 // Hs.269546 // FLJ40298 // 129852 // Homo sapiens hypothetical protein FLJ40298 (FLJ40298), mRNA. /// ENST00000348914 // intron // 0 // --- // --- // --- /// ENST00000317627 // intron // 0 // --- // --- // ---	FLJ40298	FLJ40298, Homo sapiens hypothetical protein FLJ40298 (FLJ40298), p16.2
SNP_A-2276256	gagagataaaaccagg[C/G]agtaggccaacagttc	C	G	NM_173486 // CDS // 0 // Hs.269546 // FLJ40298 // 129852 // Homo sapiens hypothetical protein FLJ40298 (FLJ40298), mRNA. /// ENST00000348914 // CDS // 0 // --- // --- // --- /// ENST00000317627 // CDS // 0 // --- // --- // ---	FLJ40298	FLJ40298, Homo sapiens hypothetical protein FLJ40298 (FLJ40298), p16.2
SNP_A-2284407	gatcaaacaagatttc[A/G]ccaaaataactggtta	A	G	NM_003128 // downstream // 119902 // Hs.503178 // SPTBN1 // 6711 // Homo sapiens spectrin, beta, non-erythrocytic 1 (SPTBN1), transcript variant 1, mRNA. /// NM_003128 // downstream // 120058 // Hs.503178 // SPTBN1 // 6711 // Homo sapiens spectrin, beta,	SPTBN1	SPTBN1, Homo sapiens spectrin, beta, non-erythrocytic 1 (SPTBN1), transcript variant 1, p16.1
SNP_A-1937464	ttgaacaatttttaga[C/G]taagcaaggaaaggga	C	G	ENST00000295102 // intron // 0 // --- // --- // --- /// ENST00000343628 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-2268627	gaatgtctcagaggca[A/C]attacaagatttataa	A	C	ENST00000295102 // intron // 0 // --- // --- // --- /// ENST00000343628 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-1888634	tgaggccagaggattc[A/G]cttcttccaagatggc	A	G	ENST00000295102 // intron // 0 // --- // --- // --- /// ENST00000343628 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-1854985	tcaacttccaaaaaaa[C/T]tgaagtcagctgatca	C	T	ENST00000295102 // intron // 0 // --- // --- // --- /// ENST00000343628 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-2264205	gaactgtaagtgtcgc[C/T]aatagagatttaagat	C	T	ENST00000295102 // intron // 0 // --- // --- // --- /// ENST00000343628 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-2110202	aggaagtagttgtcat[A/G]aagctcagtcaagaga	A	G	ENST00000343628 // intron // 0 // --- // --- // --- /// ENST00000356458 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-1836992	tactggccttctaaga[A/T]gagtttaaaagtgttc	A	T	ENST00000356458 // intron // 0 // --- // --- // --- /// ENST00000343364 // intron // 0 // --- // --- // ---	-	p16.1
SNP_A-1913483	tgtggtgataataaga[C/T]ctcacaggtatcacca	C	T	ENST00000356458 // intron // 0 // --- // --- // --- /// ENST00000343364 // intron // 0 // --- // --- // ---	-	p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1646566	tttcatcaggttccaaaaatatcag[C/T]atcttgacattcttgtaaaatcttt	C	T	NM_003128 // downstream // 197980 // Hs.205401 // SPTBN1 // 6711 // spectrin, beta, non-erythrocytic 1 /// NM_007008 // downstream // 51595 // Hs.436349 // RTN4 // 57142 // reticulon 4 /// NM_020217 // downstream // 336853 // Hs.205401 // SPTBN1 // 6711	SPTBN1	SPTBN1 , rs1961245, spectrin, beta, non-erythrocytic 1 ,p16.1
SNP_A-2131511	atagcaatttttaggc[A/G]gcactgttagggcttc	A	G	ENST00000356458 // intron // 0 // --- // --- // --- // --- /// ENST00000343364 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-2313471	ggagaggagagcttta[C/T]gtgtaaccctgatcag	C	T	ENST00000356458 // intron // 0 // --- // --- // --- // --- /// ENST00000343364 // intron // 0 // --- // --- // --- // ---	-	p16.1
SNP_A-2268664	gaatgtggaacttgaa[C/T]tagacttctggaaaag	C	T	NM_018084 // upstream // 118970 // Hs.292925 // KIAA1212 // 55704 // Homo sapiens KIAA1212 (KIAA1212), mRNA. /// NM_080667 // upstream // 66244 // Hs.264208 // MGC15407 // 112942 // Homo sapiens similar to RIKEN cDNA 4931428D14 gene (MGC15407), mRNA. ///	KIAA1212	KIAA1212, Homo sapiens KIAA1212 (KIAA1212), p16.1
SNP_A-2117337	aggtgggactggacac[C/T]gaagaaagtgaccaca	C	T	NM_018084 // upstream // 157701 // Hs.292925 // KIAA1212 // 55704 // Homo sapiens KIAA1212 (KIAA1212), mRNA. /// NM_080667 // upstream // 27513 // Hs.264208 // MGC15407 // 112942 // Homo sapiens similar to RIKEN cDNA 4931428D14 gene (MGC15407), mRNA. ///	KIAA1212	KIAA1212, Homo sapiens KIAA1212 (KIAA1212), p16.1
SNP_A-1727180	ggaaaactgtatttgggttcttctc[A/G]ctataaaagggtatttttagcttca	A	G	NM_017571 // upstream // 38909 // Hs.254122 // LOC55580 // 55580 // hypothetical protein LOC55580 /// NM_018084 // upstream // 130126 // - // - // - // - /// NM_080667 // upstream // 61166 // Hs.23128 // MGC15407 // 112942 // similar to RIKEN cDNA 493142	LOC55580	LOC55580 , rs897097, hypothetical protein LOC55580 ,p16.1
SNP_A-1963361	tagcatcgattttacc[A/G]atacctcatagagtaa	A	G	NM_020463 // upstream // 5584 // Hs.516182 // KIAA1387 // 57223 // Homo sapiens KIAA1387 protein (KIAA1387), mRNA. /// NM_033109 // downstream // 12134 // Hs.388733 // PNPT1 // 87178 // Homo sapiens polyribonucleotide nucleotidyltransferase 1 (PNPT1), mRN	KIAA1387	KIAA1387, Homo sapiens KIAA1387 protein (KIAA1387), p16.1
SNP_A-1963362	gatattacagatcatg[A/G]acaaaactatttcaaa	A	G	NM_033109 // CDS // 0 // Hs.388733 // PNPT1 // 87178 // Homo sapiens polyribonucleotide nucleotidyltransferase 1 (PNPT1), mRNA. /// ENST00000260604 // CDS // 0 // --- // --- // --- // ---	PNPT1	PNPT1, Homo sapiens polyribonucleotide nucleotidyltransferase 1 (PNPT1), p16.1
SNP_A-1963366	aagacttgcaaggtga[A/G]ctacatatttccctac	A	G	NM_033109 // upstream // 89844 // Hs.388733 // PNPT1 // 87178 // Homo sapiens polyribonucleotide nucleotidyltransferase 1 (PNPT1), mRNA. /// NM_018894 // downstream // 82294 // Hs.76224 // EFEMP1 // 2202 // Homo sapiens EGF-containing fibulin-like extrace	PNPT1	PNPT1, Homo sapiens polyribonucleotide nucleotidyltransferase 1 (PNPT1), p16.1
SNP_A-1891643	tgattggaatgcttga[A/G]gttgaaacagttaagg	A	G	NM_018894 // intron // 0 // Hs.76224 // EFEMP1 // 2202 // Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, mRNA. /// NM_004105 // intron // 0 // Hs.76224 // EFEMP1 // 2202 // Homo sapiens EGF-containi	EFEMP1	EFEMP1, Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, p16.1
SNP_A-1853604	tatttttcagtgtaaa[A/T]cttgataggctgagaa	A	T	NM_018894 // intron // 0 // Hs.76224 // EFEMP1 // 2202 // Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, mRNA. /// NM_004105 // intron // 0 // Hs.76224 // EFEMP1 // 2202 // Homo sapiens EGF-containi	EFEMP1	EFEMP1, Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, p16.1
SNP_A-1939668	ttgattttctttgtag[C/G]attttttgctagttg	C	G	NM_018894 // upstream // 102042 // Hs.76224 // EFEMP1 // 2202 // Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, mRNA. /// NM_004105 // upstream // 101069 // Hs.76224 // EFEMP1 // 2202 // Homo sapien	EFEMP1	EFEMP1, Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 2, p16.1
SNP_A-1750531	tttaatagtgaaaagttaccataga[A/G]aagtgacaggagtatgtagttcttc	A	G	AK096196 // downstream // 184358 // Hs.452487 // - // - // CDNA FLJ38877 fis, clone MESAN2015277 /// NM_004105 // upstream // 67656 // Hs.76224 // EFEMP1 // 2202 // EGF-containing fibulin-like extracellular matrix protein 1 /// NM_018894 // upstream // 6	-	- , rs6545537, CDNA FLJ38877 fis, clone MESAN2015277 ,p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1724864	aacattaagaaaagatcataaatgg[A/G]aacatcatatgctgatgtggaagat	A	G	AK096196 // downstream // 184292 // Hs.452487 // - // - // CDNA FLJ38877 fis, clone MESAN2015277 /// NM_004105 // upstream // 67722 // Hs.76224 // EFEMP1 // 2202 // EGF-containing fibulin-like extracellular matrix protein 1 /// NM_018894 // upstream // 6	-	- , rs6545538, CDNA FLJ38877 fis, clone MESAN2015277 ,p16.1
SNP_A-1851797	tattgaatagttggaa[C/G]gcaaaggaaagatggg	C	G	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-2295740	gcatgattctttgcaa[A/G]tgaacttttaaattgt	A	G	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-2187544	cagtaaattcccagaa[C/T]atctgatgcactccta	C	T	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-2168798	caagaccagcccaata[C/T]acagctagagtgcaaa	C	T	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-2250660	cttataatggattaaa[A/G]agccaaggttcaaaaa	A	G	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-1963386	cagtggtcactaaata[C/T]gttgtgtttgtctgtg	C	T	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-1861948	tcatgactttaaattg[A/G]acagagtgaacatttc	A	G	ENST00000233161 // intron // 0 // — // — // — // —	-	p16.1
SNP_A-1929128	ttcaggatgcttggtc[A/G]ccagccactggacttt	A	G	NM_006296 // upstream // 1374271 // Hs.468623 // VRK2 // 7444 // Homo sapiens vaccinia related kinase 2 (VRK2), mRNA. /// NM_018062 // downstream // 1486825 // Hs.411433 // FANCL // 55120 // Homo sapiens Fanconi anemia, complementation group L (FANCL), mR	VRK2	VRK2, Homo sapiens vaccinia related kinase 2 (VRK2), p16.1
SNP_A-2091600	agaaaacagaatataa[C/T]tggaaacagacttctt	C	T	NM_018062 // intron // 0 // Hs.411433 // FANCL // 55120 // Homo sapiens Fanconi anemia, complementation group L (FANCL), mRNA. /// ENST00000233741 // intron // 0 // — // — // — // —	FANCL	FANCL, Homo sapiens Fanconi anemia, complementation group L (FANCL), p16.1
SNP_A-1963450	ctctgcttcttagtca[A/G]taagtttgtgatcttc	A	G	NM_138559 // downstream // 1898493 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 1898493 // Hs.370549 // BCL11A // 53335 // Homo sapiens B	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-1835324	tacctattgggtacta[G/T]gtatgctatctgggtg	G	T	NM_138559 // downstream // 1769190 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 1769190 // Hs.370549 // BCL11A // 53335 // Homo sapiens B	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-1963457	gactttagtttgcaag[C/T]ctggatttagagagca	C	T	NM_138559 // downstream // 1574770 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 1574770 // Hs.370549 // BCL11A // 53335 // Homo sapiens B	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-1836255	tactatgttccaaaca[A/C]tattctaagtatttta	A	C	NM_138559 // downstream // 1228049 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 1228049 // Hs.370549 // BCL11A // 53335 // Homo sapiens B	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1
SNP_A-1963470	ttgatataaacagtct[C/T]acaattcagctgatta	C	T	NM_138559 // downstream // 1107064 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 1107064 // Hs.370549 // BCL11A // 53335 // Homo sapiens B	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2052221	aagtaactaaaagtga[A/G]gacattccgatgttgt	A	G	NM_138559 // downstream // 1098605 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 1098605 // Hs.370549 // BCL11A // 53335 // Homo sapiens B	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-1859746	tcagggagaataataa[C/T]tagatgcaacaactca	C	T	NM_138559 // downstream // 917776 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 917776 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL,p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2152944	attacagccactgaga[A/T]atacataggaaactca	A	T	NM_138559 // downstream // 887901 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 887901 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2273986	gactgttaaaaatcaa[C/T]aaaatcagcatggcat	C	T	NM_138559 // downstream // 793883 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 793883 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2237321	ctctccagaactcaca[A/T]gctaatggagaagatg	A	T	NM_138559 // downstream // 523974 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 523974 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-1963497	gtgatgccaagagaga[C/T]gaggctgttcatggat	C	T	NM_138559 // downstream // 424411 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 424411 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2286759	gatggcctgagatccg[A/G]ggacaattgttggaaa	A	G	NM_138559 // downstream // 411034 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 411034 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2129899	atacatggccaggcag[A/G]aagtttccttcttcat	A	G	NM_138559 // downstream // 399876 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 399876 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-2096388	agacccatgtataatg[C/G]accagagaattgtccc	C	G	NM_138559 // downstream // 397686 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // downstream // 397686 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-c	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-1963521	tttatccactagcgc[A/G]cgtatgttacatttttg	A	G	NM_138559 // upstream // 123148 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), transcript variant 3, mRNA. /// NM_018014 // upstream // 123148 // Hs.370549 // BCL11A // 53335 // Homo sapiens B-cell	BCL11A	BCL11A, Homo sapiens B-cell CLL p16.1
SNP_A-1910781	tgtcgtcctggtataa[C/T]actgataatgattcc	C	T	NM_003400 // upstream // 37908 // Hs.370770 // XPO1 // 7514 // Homo sapiens exportin 1 (CRM1 homolog, yeast) (XPO1), mRNA. /// ENST00000195419 // upstream // 37908 // — // — // — // — /// ENST00000343147 // downstream // 133896 // — // — // —	XPO1	XPO1, Homo sapiens exportin 1 (CRM1 homolog, yeast) (XPO1), p15
SNP_A-2162824	atttgcctgtcttc[A/C]aataaagaggttgatt	A	C	ENST00000343147 // upstream // 40234 // — // — // — // — /// ENST00000340483 // upstream // 40234 // — // — // — // — /// ENST00000307507 // downstream // 73643 // — // — // — // —	-	p15
SNP_A-2284233	gatattacatagataaa[C/T]gaaagtatgaactct	C	T	NM_152516 // intron // 0 // Hs.468702 // COMMD1 // 150684 // Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 // intron // 0 // — // — // — // —	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15
SNP_A-1963535	ccaacttccaacctta[A/G]ccattatcccctacta	A	G	NM_152516 // intron // 0 // Hs.468702 // COMMD1 // 150684 // Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), mRNA. /// ENST00000311832 // intron // 0 // — // — // — // —	COMMD1	COMMD1, Homo sapiens copper metabolism (Murr1) domain containing 1 (COMMD1), p15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1745356	ttttgtatttttcagtagtttat[C/G]agtagcagtctttgtaatttttga	C	G	NM_152516 // intron // 0 // Hs.424678 // COMMD1 // 150684 // copper metabolism (Murr1) domain containing 1	COMMD1	COMMD1, rs10496096, copper metabolism (Murr1) domain containing 1,p15
SNP_A-1865857	tcccaaccaaaatctac[C/T]aacctatctgcttctc	C	T	NM_015252 // intron // 0 // Hs.271667 // EHBP1 // 23301 // Homo sapiens EH domain binding protein 1 (EHBP1), mRNA. /// ENST00000263991 // intron // 0 // — // — // — // — /// ENST00000354487 // intron // 0 // — // — // — // —	EHBP1	EHBP1, Homo sapiens EH domain binding protein 1 (EHBP1), p15
SNP_A-2085218	actcagtacagttagc[C/T]acttgtgagacttttg	C	T	NM_015252 // intron // 0 // Hs.271667 // EHBP1 // 23301 // Homo sapiens EH domain binding protein 1 (EHBP1), mRNA. /// ENST00000263991 // intron // 0 // — // — // — // — /// ENST00000354487 // intron // 0 // — // — // — // —	EHBP1	EHBP1, Homo sapiens EH domain binding protein 1 (EHBP1), p15
SNP_A-2283403	gataccatgtacaata[A/G]catcaaaaatgaagaa	A	G	NM_016516 // intron // 0 // Hs.48499 // VPS54 // 51542 // Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 1, mRNA. /// ENST00000354504 // intron // 0 // — // — // — // — /// ENST00000272322 // intron // 0 // — // —	VPS54	VPS54, Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 1, p14
SNP_A-2057412	aatatcatagacataa[C/T]gtggagccaaagaaac	C	T	NM_016516 // intron // 0 // Hs.48499 // VPS54 // 51542 // Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 1, mRNA. /// ENST00000354504 // intron // 0 // — // — // — // — /// ENST00000272322 // intron // 0 // — // —	VPS54	VPS54, Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 1, p14
SNP_A-1963553	cacaagaactcctaa[C/T]ccccagcacacatcct	C	T	NM_016516 // upstream // 45748 // Hs.48499 // VPS54 // 51542 // Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 1, mRNA. /// NM_020651 // downstream // 63100 // Hs.7886 // PELI1 // 57162 // Homo sapiens pellino homolog 1 (Dros	VPS54	VPS54, Homo sapiens vacuolar protein sorting 54 (yeast) (VPS54), transcript variant 1, p14
SNP_A-1902688	tggctacagctacgta[C/T]cttcagacttttcaat	C	T	ENST00000260642 // upstream // 87522 // — // — // — // — /// ENST00000335402 // downstream // 54259 // — // — // — // —	-	p14
SNP_A-2037592	aacaacttttagcgat[A/C]atgaatctgtgctctt	A	C	ENST00000260642 // upstream // 129061 // — // — // — // — /// ENST00000335402 // downstream // 12720 // — // — // — // —	-	p14
SNP_A-2132727	atataaacgtcacaca[C/G]aggatggctaggctga	C	G	NM_014181 // upstream // 86172 // Hs.372208 // HSPC159 // 29094 // Homo sapiens HSPC159 protein (HSPC159), mRNA. /// ENST00000335402 // upstream // 20610 // — // — // — // — /// ENST00000238875 // upstream // 86172 // — // — // — // —	HSPC159	HSPC159, Homo sapiens HSPC159 protein (HSPC159), p14
SNP_A-1930181	ttcattcatcttaaa[C/T]tccattaagtaagtgtt	C	T	NM_203437 // downstream // 184543 // Hs.468760 // AFTIPHILIN // 54812 // Homo sapiens aftiphilin protein (AFTIPHILIN), transcript variant 1, mRNA. /// NM_001002243 // downstream // 184543 // Hs.468760 // AFTIPHILIN // 54812 // Homo sapiens aftiphilin prot	AFTIPHILIN	AFTIPHILIN, Homo sapiens aftiphilin protein (AFTIPHILIN), transcript variant 1, p14
SNP_A-1896972	tgctcatgatttata[A/G]gccagaaattcagaca	A	G	NM_203437 // downstream // 392389 // Hs.468760 // AFTIPHILIN // 54812 // Homo sapiens aftiphilin protein (AFTIPHILIN), transcript variant 1, mRNA. /// NM_001002243 // downstream // 392389 // Hs.468760 // AFTIPHILIN // 54812 // Homo sapiens aftiphilin prot	AFTIPHILIN	AFTIPHILIN, Homo sapiens aftiphilin protein (AFTIPHILIN), transcript variant 1, p14
SNP_A-1841073	tagcttataaattagt[A/G]aatcaggtgtcatcac	A	G	NM_004161 // intron // 0 // Hs.310645 // RAB1A // 5861 // Homo sapiens RAB1A, member RAS oncogene family (RAB1A), mRNA. /// ENST00000356214 // intron // 0 // — // — // — // — /// ENST00000260638 // intron // 0 // — // — // — // — /// ENST0	RAB1A	RAB1A, Homo sapiens RAB1A, member RAS oncogene family (RAB1A), p14
SNP_A-1905675	tggtatctacagtaga[A/T]ccctctttttgccctt	A	T	NM_015147 // downstream // 53857 // Hs.146007 // KIAA0582 // 23177 // Homo sapiens KIAA0582 (KIAA0582), mRNA. /// NM_004161 // upstream // 29707 // Hs.310645 // RAB1A // 5861 // Homo sapiens RAB1A, member RAS oncogene family (RAB1A), mRNA. /// NM_005722 //	KIAA0582	KIAA0582, Homo sapiens KIAA0582 (KIAA0582), p14
SNP_A-1814884	gtgtgttctggaaaaa[C/T]gcctattgatactaga	C	T	NM_005722 // intron // 0 // Hs.393201 // ACTR2 // 10097 // Homo sapiens ARP2 actin-related protein 2 homolog (yeast) (ACTR2), transcript variant 2, mRNA. /// ENST00000260641 // intron // 0 // — // — // — // —	ACTR2	ACTR2, Homo sapiens ARP2 actin-related protein 2 homolog (yeast) (ACTR2), transcript variant 2, p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289773	gcaaaatgccagggac[A/G]gtaatggttccacatc	A	G	NM_181784 // intron // 0 // Hs.59332 // SPRED2 // 200734 // Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), mRNA. /// ENST00000356388 // intron // 0 // --- // --- // ---	SPRED2	SPRED2, Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), p14
SNP_A-2090962	acttctccacagcaa[A/T]gtcctaagagatac	A	T	NM_181784 // upstream // 25775 // Hs.59332 // SPRED2 // 200734 // Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), mRNA. /// ENST00000356388 // upstream // 25775 // --- // --- // --- /// ENST00000343233 // downstream // 120943 // ---	SPRED2	SPRED2, Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), p14
SNP_A-2308520	gtttagttgacctcc[C/G]agtttgtctcactgtt	C	G	NM_181784 // upstream // 145069 // Hs.59332 // SPRED2 // 200734 // Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), mRNA. /// ENST00000356388 // upstream // 145069 // --- // --- // --- /// ENST00000343233 // downstream // 1649 // ---	SPRED2	SPRED2, Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), p14
SNP_A-1859900	tcaggtatcaaaggc[A/C]gcattgtgctcaggga	A	C	NM_181784 // upstream // 146438 // Hs.59332 // SPRED2 // 200734 // Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), mRNA. /// ENST00000356388 // upstream // 146438 // --- // --- // --- /// ENST00000343233 // downstream // 280 // ---	SPRED2	SPRED2, Homo sapiens sprouty-related, EVH1 domain containing 2 (SPRED2), p14
SNP_A-2079035	acccacttctctcca[C/T]gtcttgatccatatac	C	T	NM_002398 // upstream // 868418 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 65059 // --- // --- // --- /// ENST00000272369 // upst	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2152454	attaactgggagacaq[C/T]ggcaagggcaataggg	C	T	NM_002398 // upstream // 430453 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 503024 // --- // --- /// ENST00000272369 // ups	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2099882	agagtatgctgcacaa[C/G]ggtttgcatttcagat	C	G	NM_002398 // upstream // 368626 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 564851 // --- // --- /// ENST00000272369 // ups	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2296568	gcatttttgcaaagcta[C/G]atttccctctggacc	C	G	NM_002398 // upstream // 365020 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 568457 // --- // --- /// ENST00000272369 // ups	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2028245	aaactatagcaaaaca[A/G]cctagagatcttcgtc	A	G	NM_002398 // upstream // 238541 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 694936 // --- // --- /// ENST00000272369 // ups	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2182784	cagatggcagaggcca[A/G]gaagtctccgaacaaa	A	G	NM_002398 // upstream // 45138 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000343233 // upstream // 888339 // --- // --- /// ENST00000272369 // upst	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1646416	gttactacattcaaggataaaaga[C/T]gcatttgtgataattaata ttgaaa	C	T	NM_002398 // upstream // 19151 // Hs.170177 // MEIS1 // 4211 // Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) /// NM_181784 // upstream // 984463 // Hs.173108 // SPRED2 // 200734 // sprouty-related, EVH1 domain containing 2	MEIS1	MEIS1, rs952203, Meis1, myeloid ecotropic viral integration site 1 homolog (mouse), p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006432	acaattctgttcatcc[A/G]gaccacatctttcctg	A	G	NM_002398 // intron // 0 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// ENST00000272369 // intron // 0 // — // — // — // —	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2192209	catcagccttaataac[A/G]atgtggtagaagcagg	A	G	NM_002398 // downstream // 273954 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 550598 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 pro	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-2128969	ataatgtctgtatgta[C/G]gtataatcacacatag	C	G	NM_002398 // downstream // 309838 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 514714 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 pro	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1853014	tatttgatgattcaga[G/T]aggacaagtgactttt	G	T	NM_002398 // downstream // 314297 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 510255 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 pro	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1699279	gagcagcaatttcaaagaacatagc[A/C]aaggctttcagcaat atgtaacggt	A	C	NM_002398 // downstream // 322085 // Hs.170177 // MEIS1 // 4211 // Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) /// NM_019002 // upstream // 502753 // Hs.82664 // ETAA16 // 54465 // ETAA16 protein	MEIS1	MEIS1 , rs10490198, Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) ,p14
SNP_A-2227987	ctaccttgcttgctca[G/T]atttctcaaagcctt	G	T	NM_002398 // downstream // 610222 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 214330 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 pro	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1963629	atatcccatggcatca[C/T]attcctcttcttcag	C	T	NM_002398 // downstream // 685138 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 139414 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 pro	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1963631	agtgagccttgccacc[A/G]agcattgaatatctttt	A	G	NM_002398 // downstream // 729128 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 95424 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 prot	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1726202	tcctattaagctgtgtggttgcaga[C/G]agtttgttctaaatatat gtatg	C	G	NM_002398 // downstream // 682991 // Hs.170177 // MEIS1 // 4211 // Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) /// NM_019002 // upstream // 141847 // Hs.82664 // ETAA16 // 54465 // ETAA16 protein	MEIS1	MEIS1 , rs752165, Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) ,p14
SNP_A-1842349	taggtatgcaatgtta[A/G]aaggataaatgactta	A	G	NM_002398 // downstream // 768202 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 56350 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 prot	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14
SNP_A-1815134	gtgttctcttttcaca[G/T]gcccacttctcttcca	G	T	NM_002398 // downstream // 806436 // Hs.526754 // MEIS1 // 4211 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA. /// NM_019002 // upstream // 18116 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 prot	MEIS1	MEIS1, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140454	atctccacatttgcca[C/T]tgaggattgaggactt	C	T	NM_019002 // downstream // 47035 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 584626 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mRN	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-2080620	acctcacctcattcta[C/T]gctagtctaattaatt	C	T	NM_019002 // downstream // 47415 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 584246 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mRN	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1694297	tcagacagaaaaataaactattatg[A/G]aggcacatcttttaacatttacttc	A	G	NM_006333 // downstream // 595871 // Hs.380759 // C1D // 10438 // nuclear DNA-binding protein /// NM_019002 // downstream // 35791 // Hs.82664 // ETAA16 // 54465 // ETAA16 protein /// NM_173177 // downstream // 595871 // Hs.380759 // C1D // 10438 // nucl	C1D	C1D , rs1385931, nuclear DNA-binding protein ,p14
SNP_A-1668196	aggtagataaaggtattcagtgact[C/T]aaggaaattaattatagaggaaaaa	C	T	NM_006333 // downstream // 595558 // Hs.380759 // C1D // 10438 // nuclear DNA-binding protein /// NM_019002 // downstream // 36104 // Hs.82664 // ETAA16 // 54465 // ETAA16 protein /// NM_173177 // downstream // 595558 // Hs.380759 // C1D // 10438 // nucl	C1D	C1D , rs600524, nuclear DNA-binding protein ,p14
SNP_A-1707928	tttggtgaatagcctcaaatgataa[C/T]aaggcttaacagagagcagaacact	C	T	NM_006333 // downstream // 595296 // Hs.380759 // C1D // 10438 // nuclear DNA-binding protein /// NM_019002 // downstream // 36366 // Hs.82664 // ETAA16 // 54465 // ETAA16 protein /// NM_173177 // downstream // 595296 // Hs.380759 // C1D // 10438 // nucl	C1D	C1D , rs650638, nuclear DNA-binding protein ,p14
SNP_A-2161578	atttggataaattgag[A/G]aaaactaatagccttt	A	G	NM_019002 // downstream // 112926 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 518735 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1853710	tatttttttccttgca[C/G]taccccccaagagcagt	C	G	NM_019002 // downstream // 241336 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 390325 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1881110	tctttaatgttttccc[A/G]ctgtgcttgggatgaa	A	G	NM_019002 // downstream // 248066 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 383595 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1847196	tatcatttccgaggtc[G/T]actataattctgtttc	G	T	NM_019002 // downstream // 265492 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 366169 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1915323	tgttcattcaaagcaa[A/C]caaaaattcagtaata	A	C	NM_019002 // downstream // 268095 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 363566 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-2287958	gattatggcccaaaag[C/T]aggtaagctgaagttg	C	T	NM_019002 // downstream // 361365 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 270296 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2037505	aacaaccaagccagag[C/T]aacgggtgatttgacc	C	T	NM_019002 // downstream // 531643 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 100018 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mR	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1835171	taccctttttagagtc[A/G]catctggctcccctta	A	G	NM_019002 // downstream // 563119 // Hs.353022 // ETAA16 // 54465 // Homo sapiens ETAA16 protein (ETAA16), mRNA. /// NM_173177 // downstream // 68542 // Hs.328883 // C1D // 10438 // Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 2, mRN	ETAA16	ETAA16, Homo sapiens ETAA16 protein (ETAA16), p14
SNP_A-1801030	gtagatgtattgtaga[C/T]aggttgtttgtacca	C	T	NM_015463 // intron // 0 // Hs.212885 // C2orf32 // 25927 // Homo sapiens chromosome 2 open reading frame 32 (C2orf32), mRNA. /// ENST00000263655 // intron // 0 // — // — // —	C2orf32	C2orf32, Homo sapiens chromosome 2 open reading frame 32 (C2orf32), p14
SNP_A-2061548	aatgctgggaaaactc[C/T]atcacttcacaatggc	C	T	NM_002664 // intron // 0 // Hs.468840 // PLEK // 5341 // Homo sapiens pleckstrin (PLEK), mRNA. /// ENST00000234313 // intron // 0 // — // — // - // —	PLEK	PLEK, Homo sapiens pleckstrin (PLEK), p13.3
SNP_A-2301566	gcgagtgttagaatca[C/T]gggcagatttttttt	C	T	NM_002664 // 3UTR // 0 // Hs.468840 // PLEK // 5341 // Homo sapiens pleckstrin (PLEK), mRNA. /// ENST00000234313 // 3UTR // 0 // — // — // - // —	PLEK	PLEK, Homo sapiens pleckstrin (PLEK), p13.3
SNP_A-1947035	tttaataaagatgggcc[G/T]gaactctacccagttt	G	T	D29642 // intron // 0 // Hs.531807 // ARHGAP25 // 9938 // Homo sapiens KIAA0053 mRNA, partial cds. /// ENST00000295381 // intron // 0 // — // — // — // —	ARHGAP25	ARHGAP25, Homo sapiens KIAA0053 partial cds. p13.3
SNP_A-2125986	agttttcctctctgga[G/T]acttgggtgggatgag	G	T	D29642 // intron // 0 // Hs.531807 // ARHGAP25 // 9938 // Homo sapiens KIAA0053 mRNA, partial cds. /// ENST00000295381 // intron // 0 // — // — // — // —	ARHGAP25	ARHGAP25, Homo sapiens KIAA0053 partial cds. p13.3
SNP_A-1815870	gttaatatctttctctc[A/G]cctgttaacactgttc	A	G	D29642 // downstream // 37817 // Hs.531807 // ARHGAP25 // 9938 // Homo sapiens KIAA0053 mRNA, partial cds. /// NM_014482 // downstream // 841 // Hs.158317 // BMP10 // 27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// ENST00000295381 /	ARHGAP25	ARHGAP25, Homo sapiens KIAA0053 partial cds. p13.3
SNP_A-1672250	ttcaatcatgtcctatcaatttggt[A/G]aaaagatctgtccagctcc tttac	A	G	NM_014882 // intron // 0 // - // - // -	-	-, rs10496167, -p13.3
SNP_A-1963689	tgaaacagggactcac[C/T]gagatcatgaactaag	C	T	NM_014482 // intron // 0 // Hs.158317 // BMP10 // 27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// ENST00000295379 // intron // 0 // — // — // — // —	BMP10	BMP10, Homo sapiens bone morphogenetic protein 10 (BMP10), p13.3
SNP_A-2091177	acttgtctctgttgat[C/G]tatggtcatttcattc	C	G	NM_014482 // upstream // 12281 // Hs.158317 // BMP10 // 27302 // Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA. /// NM_182536 // downstream // 61435 // Hs.16757 // GDDR // 200504 // Homo sapiens down-regulated in gastric cancer GDDR (GDDR), mRN	BMP10	BMP10, Homo sapiens bone morphogenetic protein 10 (BMP10), p13.3
SNP_A-1865869	tcccaagaaacaaacg[A/C]aagtccaagaccttac	A	C	NM_018153 // intron // 0 // Hs.165859 // ANTXR1 // 84168 // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, mRNA. /// NM_053034 // intron // 0 // Hs.165859 // ANTXR1 // 84168 // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcr	ANTXR1	ANTXR1, Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 3, p13.3
SNP_A-2140516	atctccctcttaatctc[C/T]gaccgttcctttccac	C	T	NM_053034 // intron // 0 // Hs.165859 // ANTXR1 // 84168 // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 2, mRNA. /// NM_032208 // intron // 0 // Hs.165859 // ANTXR1 // 84168 // Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcr	ANTXR1	ANTXR1, Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 2, p13.3
SNP_A-2216551	cctctaccaccacagc[A/C]atgacagtcaggtaac	A	C	NM_001153 // downstream // 1441 // Hs.422986 // ANXA4 // 307 // Homo sapiens annexin A4 (ANXA4), mRNA. /// NM_178439 // upstream // 1790 // Hs.293971 // GCL // 64395 // Homo sapiens germ cell-less homolog 1 (Drosophila) (GCL), mRNA. /// ENST00000355054 //	ANXA4	ANXA4, Homo sapiens annexin A4 (ANXA4), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2229044	ctagcatatcctggal[A/G]agcaaggtgacccggc	A	G	NM_032822 // upstream // 62606 // Hs.516077 // FLJ14668 // 84908 // Homo sapiens hypothetical protein FLJ14668 (FLJ14668), mRNA. /// NM_003236 // downstream // 82616 // Hs.170009 // TGFA // 7039 // Homo sapiens transforming growth factor, alpha (TGFA), mR	FLJ14668	FLJ14668, Homo sapiens hypothetical protein FLJ14668 (FLJ14668), p13.3
SNP_A-2218114	cctgcctcgacttggc[A/G]gatgatgtaaggaaag	A	G	NM_003236 // intron // 0 // Hs.170009 // TGFA // 7039 // Homo sapiens transforming growth factor, alpha (TGFA), mRNA. /// ENST00000295400 // intron // 0 // --- // --- // ---	TGFA	TGFA, Homo sapiens transforming growth factor, alpha (TGFA), p13.3
SNP_A-1780913	ggatgaatccagagaat[A/G]tatgctcagtgaaaaa	A	G	NM_003236 // upstream // 44531 // Hs.170009 // TGFA // 7039 // Homo sapiens transforming growth factor, alpha (TGFA), mRNA. /// NM_017482 // downstream // 63804 // Hs.188528 // ADD2 // 119 // Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-2	TGFA	TGFA, Homo sapiens transforming growth factor, alpha (TGFA), p13.3
SNP_A-1887842	tgagaigtcagcaggc[A/C]agagaaggaaaggcag	A	C	NM_017482 // intron // 0 // Hs.188528 // ADD2 // 119 // Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, mRNA. /// NM_017488 // intron // 0 // Hs.188528 // ADD2 // 119 // Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-4, mRN	ADD2	ADD2, Homo sapiens adducin 2 (beta) (ADD2), transcript variant beta-2, p13.3
SNP_A-2065461	aattgttctttttgttc[A/C]acgtgcattgtgcaac	A	C	NM_173535 // intron // 0 // --- // CLEC4F // 165530 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 13 (CLECSF13), mRNA. /// ENST00000272367 // intron // 0 // --- // --- // ---	CLEC4F	CLEC4F, Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 13 (CLECSF13), p13.3
SNP_A-1963746	tccagggggcttacctc[A/G]cacttttggacctgtt	A	G	NM_015717 // CDS // 0 // Hs.199731 // CD207 // 50489 // Homo sapiens CD207 antigen, langerin (CD207), mRNA. /// ENST00000234388 // CDS // 0 // --- // --- // ---	CD207	CD207, Homo sapiens CD207 antigen, langerin (CD207), p13.3
SNP_A-2184747	cagctgaggaactgc[C/T]gagcatgaaaggctca	C	T	NM_003494 // downstream // 58253 // Hs.252180 // DYSF // 8291 // Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// NM_019885 // downstream // 384224 // Hs.91546 // CYP26B1 // 56603 // Homo sapiens cytochrome	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-2312249	ggacagtgaaggctaa[A/G]accaaccgagactttt	A	G	NM_003494 // downstream // 111445 // Hs.252180 // DYSF // 8291 // Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// NM_019885 // downstream // 331032 // Hs.91546 // CYP26B1 // 56603 // Homo sapiens cytochrom	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-1862427	tcatgtggaactaaaa[G/T]agacctctcggtactt	G	T	NM_003494 // downstream // 149007 // Hs.252180 // DYSF // 8291 // Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// NM_019885 // downstream // 293470 // Hs.91546 // CYP26B1 // 56603 // Homo sapiens cytochrom	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-1880525	tcttgattgctctaca[A/C]attctgctgcaagatc	A	C	NM_003494 // downstream // 182487 // Hs.252180 // DYSF // 8291 // Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), mRNA. /// NM_019885 // downstream // 259990 // Hs.91546 // CYP26B1 // 56603 // Homo sapiens cytochrom	DYSF	DYSF, Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), p13.2
SNP_A-2124404	agttcaatgtatcact[A/T]agatgtcaatttgtcc	A	T	ENST00000272427 // intron // 0 // --- // --- // ---	-	p13.2
SNP_A-2283943	gatatacacatagttc[A/G]atttccttcatatag	A	G	ENST00000272427 // intron // 0 // --- // --- // ---	-	p13.2
SNP_A-1803687	gtcaaataatttccaa[C/T]agaatagatgctctaga	C	T	ENST00000272427 // intron // 0 // --- // --- // ---	-	p13.2
SNP_A-2164998	caaactctccagggaa[C/G]aaccctcaaagaggtc	C	G	ENST00000272427 // intron // 0 // --- // --- // ---	-	p13.2
SNP_A-1691100	gactagtaattaggaactatatca[C/T]gttttttccagaatttttgg agatt	C	T	AK023791 // intron // 0 // Hs.44175 // SEC15L2 // 23233 // SEC15-like 2 (S. cerevisiae)	SEC15L2	SEC15L2, rs9309464, SEC15-like 2 (S. cerevisiae),p13.2
SNP_A-1738761	tttcaatatgtctacagtacacaa[G/T]aatgatttgaaaataat aatgt	G	T	AK023791 // intron // 0 // Hs.44175 // SEC15L2 // 23233 // SEC15-like 2 (S. cerevisiae)	SEC15L2	SEC15L2, rs9309465, SEC15-like 2 (S. cerevisiae),p13.2
SNP_A-2208042	cccaagaatacgatac[A/T]caactctacataaatt	A	T	ENST00000272427 // intron // 0 // --- // --- // ---	-	p13.2
SNP_A-1871359	tctaaatatattgcta[A/T]ggggaaaactgtatag	A	T	ENST00000272427 // intron // 0 // --- // --- // ---	-	p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1736813	gttttgctgttataaacagagcaaa[C/T]gtaagtcagaagatattttttacc	C	T	AB023136 // intron // 0 // Hs.44175 // SEC15L2 // 23233 // SEC15-like 2 (S. cerevisiae)	SEC15L2	SEC15L2, rs10496185, SEC15-like 2 (S. cerevisiae),p13.2
SNP_A-2060671	aatgagattgggagta[C/T]gctgattggtgggaa	C	T	AB023136 // intron // 0 // Hs.303454 // SEC15L2 // 23233 // Homo sapiens mRNA for KIAA0919 protein, partial cds. /// ENST00000272427 // intron // 0 // --- // --- // --- /// ENST00000290144 // intron // 0 // --- // --- // ---	SEC15L2	SEC15L2, Homo sapiens for KIAA0919 protein, partial cds. p13.2
SNP_A-2172836	caatttgtgttcaag[A/G]cctataaatactgctg	A	G	AB023136 // intron // 0 // Hs.303454 // SEC15L2 // 23233 // Homo sapiens mRNA for KIAA0919 protein, partial cds. /// ENST00000272427 // intron // 0 // --- // --- // --- /// ENST00000290144 // intron // 0 // --- // --- // ---	SEC15L2	SEC15L2, Homo sapiens for KIAA0919 protein, partial cds. ,p13.2
SNP_A-2285926	gatgagtaccaaccaaa[C/T]aagtgatatcagcaat	C	T	AB023136 // intron // 0 // Hs.303454 // SEC15L2 // 23233 // Homo sapiens mRNA for KIAA0919 protein, partial cds. /// ENST00000290144 // intron // 0 // --- // --- // ---	SEC15L2	SEC15L2, Homo sapiens for KIAA0919 protein, partial cds. ,p13.2
SNP_A-1963773	tctcaagacagaaatc[A/G]gatttagacttaacct	A	G	NM_144579 // intron // 0 // Hs.368171 // SFXN5 // 94097 // Homo sapiens sideroflexin 5 (SFXN5), mRNA. /// ENST00000272433 // intron // 0 // --- // --- // ---	SFXN5	SFXN5, Homo sapiens sideroflexin 5 (SFXN5), p13.2
SNP_A-2125595	agtttccacgtctaga[A/G]aggtaaattataaaca	A	G	NM_001965 // upstream // 22075 // Hs.3052 // EGR4 // 1961 // Homo sapiens early growth response 4 (EGR4), mRNA. /// NM_015120 // upstream // 70197 // Hs.184720 // ALMS1 // 7840 // Homo sapiens Alstrom syndrome 1 (ALMS1), mRNA. /// ENST00000258092 // upstr	EGR4	EGR4, Homo sapiens early growth response 4 (EGR4), p13.2
SNP_A-2287233	gatgtcttaatttct[A/T]acctggttgccctggc	A	T	NM_015120 // intron // 0 // Hs.184720 // ALMS1 // 7840 // Homo sapiens Alstrom syndrome 1 (ALMS1), mRNA. /// ENST00000264448 // intron // 0 // --- // --- // ---	ALMS1	ALMS1, Homo sapiens Alstrom syndrome 1 (ALMS1), p13.1
SNP_A-1751809	ccgttcccaaggctactccaa[C/T]gtcgtttattaactagtcaatacca	C	T	NM_001615 // upstream // 10114 // Hs.403989 // ACTG2 // 72 // actin, gamma 2, smooth muscle, enteric /// NM_006463 // downstream // 20011 // Hs.407994 // STAMBP // 10617 // STAM binding protein	ACTG2	ACTG2, rs10519327, actin, gamma 2, smooth muscle, enteric ,p13.1
SNP_A-1946554	ttaaatatataaaaa[A/C]catgcttagctagctg	A	C	NM_021196 // intron // 0 // Hs.469033 // SLC4A5 // 57835 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, mRNA. /// NM_033323 // intron // 0 // Hs.469033 // SLC4A5 // 57835 // Homo sapiens	SLC4A5	SLC4A5, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant a, p13.1
SNP_A-2021678	aaaaacaaccattacg[C/T]cattgctatgcaaggt	C	T	NM_032603 // intron // 0 // Hs.469045 // LOXL3 // 84695 // Homo sapiens lysyl oxidase-like 3 (LOXL3), mRNA. /// ENST00000264094 // intron // 0 // --- // --- // ---	LOXL3	LOXL3, Homo sapiens lysyl oxidase-like 3 (LOXL3), p13.1
SNP_A-1818339	gttctgtggctaggaa[C/G]tccagagatagatggt	C	G	NM_138804 // intron // 0 // Hs.348645 // LOC130951 // 130951 // Homo sapiens hypothetical protein BC014602 (LOC130951), mRNA. /// ENST00000290536 // intron // 0 // --- // --- // --- /// ENST00000358434 // intron // 0 // --- // --- // ---	LOC130951	LOC130951, Homo sapiens hypothetical protein BC014602 (LOC130951), p13.1
SNP_A-2044244	aacttttctgatcctgc[A/G]aagctaaagaaccagg	A	G	NM_138804 // intron // 0 // Hs.348645 // LOC130951 // 130951 // Homo sapiens hypothetical protein BC014602 (LOC130951), mRNA. /// ENST00000290536 // intron // 0 // --- // --- // --- /// ENST00000358434 // intron // 0 // --- // --- // ---	LOC130951	LOC130951, Homo sapiens hypothetical protein BC014602 (LOC130951), p13.1
SNP_A-1929956	ttcatgcatatttttca[C/T]gtctgtacttcatcgg	C	T	NM_138804 // intron // 0 // Hs.348645 // LOC130951 // 130951 // Homo sapiens hypothetical protein BC014602 (LOC130951), mRNA. /// ENST00000290536 // intron // 0 // --- // --- // --- /// ENST00000358434 // intron // 0 // --- // --- // ---	LOC130951	LOC130951, Homo sapiens hypothetical protein BC014602 (LOC130951), p13.1
SNP_A-2289699	gcaaaagataaaaaac[C/T]gtaccaggcaggagaa	C	T	NM_138804 // intron // 0 // Hs.348645 // LOC130951 // 130951 // Homo sapiens hypothetical protein BC014602 (LOC130951), mRNA. /// ENST00000290536 // intron // 0 // --- // --- // --- /// ENST00000358434 // intron // 0 // --- // --- // ---	LOC130951	LOC130951, Homo sapiens hypothetical protein BC014602 (LOC130951), p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1855262	tcaagctcaggctttg[A/G]actcagtaggaaccaa	A	G	NM_004263 // downstream // 21657 // Hs.25887 // SEMA4F // 10505 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (S /// NM_000189 // upstream // 128940 // Hs.406266 // HK2 //	SEMA4F	SEMA4F, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (S ,p13.1
SNP_A-1963803	gctgttgtctggaaca[A/T]ggattggaaaagagca	A	T	NM_004263 // downstream // 133105 // Hs.25887 // SEMA4F // 10505 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (S /// NM_000189 // upstream // 17492 // Hs.406266 // HK2 //	SEMA4F	SEMA4F, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (S p13.1
SNP_A-2045246	aagaaggaatcgaaga[C/T]gagttagggtggatgg	C	T	NM_004263 // downstream // 149828 // Hs.25887 // SEMA4F // 10505 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (S /// NM_000189 // upstream // 769 // Hs.406266 // HK2 // 30	SEMA4F	SEMA4F, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (S p13.1
SNP_A-1847402	tatccctgaggaaaga[C/G]acagttaagcaggagg	C	G	NM_001058 // intron // 0 // Hs.200262 // TACR1 // 6869 // Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // intron // 0 // Hs.200262 // TACR1 // 6869 // Homo sapiens tachykinin receptor 1 (TACR1), transcript varia	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-2300331	gcctctccttaaaaca[G/T]aatagtggttctggag	G	T	NM_001058 // upstream // 245441 // Hs.200262 // TACR1 // 6869 // Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // upstream // 245441 // Hs.200262 // TACR1 // 6869 // Homo sapiens tachykinin receptor 1 (TACR1), tr	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-1828115	taagacctgggacttg[A/T]aactaatcccatctca	A	T	NM_001058 // upstream // 245722 // Hs.200262 // TACR1 // 6869 // Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA. /// NM_015727 // upstream // 245722 // Hs.200262 // TACR1 // 6869 // Homo sapiens tachykinin receptor 1 (TACR1), tr	TACR1	TACR1, Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, p12
SNP_A-1963831	gtgccactctttcgca[C/T]tgagtaaaagtatgtg	C	T	NM_032181 // intron // 0 // Hs.302346 // FLJ13391 // 84141 // Homo sapiens hypothetical protein FLJ13391 (FLJ13391), mRNA. /// ENST00000233712 // intron // 0 // — // — // — // —	FLJ13391	FLJ13391, Homo sapiens hypothetical protein FLJ13391 (FLJ13391), p12
SNP_A-2238829	ctcttatacaccttaa[A/C]ctcatccaccttggga	A	C	NM_032181 // upstream // 33031 // Hs.302346 // FLJ13391 // 84141 // Homo sapiens hypothetical protein FLJ13391 (FLJ13391), mRNA. /// NM_014763 // upstream // 44033 // Hs.44024 // MRPL19 // 9801 // Homo sapiens mitochondrial ribosomal protein L19 (MRPL19),	FLJ13391	FLJ13391, Homo sapiens hypothetical protein FLJ13391 (FLJ13391), p12
SNP_A-2283039	gataagcacagtttaa[C/T]ggtgtaagttgcctca	C	T	NM_032181 // upstream // 33373 // Hs.302346 // FLJ13391 // 84141 // Homo sapiens hypothetical protein FLJ13391 (FLJ13391), mRNA. /// NM_014763 // upstream // 43691 // Hs.44024 // MRPL19 // 9801 // Homo sapiens mitochondrial ribosomal protein L19 (MRPL19),	FLJ13391	FLJ13391, Homo sapiens hypothetical protein FLJ13391 (FLJ13391), p12
SNP_A-2275434	gagaatgtgaaatgca[A/G]ggatgtgagactggcc	A	G	NM_014763 // intron // 0 // Hs.44024 // MRPL19 // 9801 // Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000233713 // intron // 0 // — // — // — // — /// ENST00000358788 // i	MRPL19	MRPL19, Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), nuclear gene encoding mitochondrial protein, p12
SNP_A-2059146	aatcctcaatgaaaga[A/C]actcaacaagaataca	A	C	NM_003203 // upstream // 40953 // Hs.303808 // C2orf3 // 6936 // Homo sapiens chromosome 2 open reading frame 3 (C2orf3), mRNA. /// ENST00000321027 // upstream // 40953 // — // — // — // — /// ENST00000233047 // upstream // 36486 // — // — //	C2orf3	C2orf3, Homo sapiens chromosome 2 open reading frame 3 (C2orf3), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1899549	tggaaggaatgaagaa[A/C]ggtttcaagagccagc	A	C	NM_003203 // upstream // 92791 // Hs.303808 // C2orf3 // 6936 // Homo sapiens chromosome 2 open reading frame 3 (C2orf3), mRNA. /// ENST00000321027 // upstream // 92791 // --- // --- // --- // --- /// ENST00000233047 // upstream // 88324 // --- // --- //	C2orf3	C2orf3, Homo sapiens chromosome 2 open reading frame 3 (C2orf3), p12
SNP_A-1960911	tttttgataggaaagc[C/T]ataggttgtcagtggc	C	T	NM_024993 // downstream // 1644874 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 37986 // --- // --- // --- // --- /// ENST00000320252 // downstream // 164	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1893700	tgcagtcgttttagaa[A/G]gtaatcttggaagtga	A	G	NM_024993 // downstream // 1320842 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 362018 // --- // --- // --- // --- /// ENST00000320252 // downstream // 13	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1848932	tatgcaagtttaggaa[C/T]tgtttttctgcctgtt	C	T	NM_024993 // downstream // 1088712 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 594148 // --- // --- // --- // --- /// ENST00000320252 // downstream // 10	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1797554	ggtttccattcttccc[C/T]aagtttggtaaagtcg	C	T	NM_024993 // downstream // 558254 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 1124606 // --- // --- // --- // --- /// ENST00000320252 // downstream // 55	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963872	tatcttaaattcagtc[A/G]gagcggaaaaaacaga	A	G	NM_024993 // downstream // 350288 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 1332572 // --- // --- // --- // --- /// ENST00000320252 // downstream // 35	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2162914	attttggttgtgtcac[C/T]aagttggttagggcat	C	T	NM_024993 // downstream // 265884 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 1416976 // --- // --- // --- // --- /// ENST00000320252 // downstream // 26	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963878	ggcatatattttccaa[C/T]tgagctccaggtccaa	C	T	NM_024993 // downstream // 250147 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 1432713 // --- // --- // --- // --- /// ENST00000320252 // downstream // 25	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963879	tgtctaatgaatcaca[A/G]agtttaaatacttctt	A	G	NM_024993 // downstream // 224987 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 1457873 // --- // --- // --- // --- /// ENST00000320252 // downstream // 22	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1848160	tatcttcattctctac[A/C]atttctatccatcctt	A	C	NM_024993 // downstream // 183564 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// ENST00000358092 // downstream // 1499296 // --- // --- // --- // --- /// ENST00000320252 // downstream // 18	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1860591	tcagtttagataatag[A/C]ccccatgcagagagct	A	C	NM_024993 // upstream // 107687 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 1398145 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783420	ggcatagtgtgagaac[A/G]atgtcttaccaaatag	A	G	NM_024993 // upstream // 126175 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 1379657 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1933093	ttcgtaggtaaggaaa[C/T]aattagcagctaaga	C	T	NM_024993 // upstream // 181320 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 1324512 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1679972	ttcattacaatgtagtacttata[C/T]gctaggatacattgctgctt ataa	C	T	NM_006507 // downstream // 945074 // Hs.4158 // REG1B // 5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 620086 // Hs.285782 // LRRTM4 // 80059 // leucine-rich repeat transmembr	REG1B	REG1B , rs2861264, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-2221592	ccttgcaattgcctc[C/T]gattgaatgtgaaaaa	C	T	NM_024993 // upstream // 703950 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 801882 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1687812	taggcagacaaaaactcaagccaca[A/G]tattcacattatttgtc atatggag	A	G	NM_006507 // downstream // 719942 // Hs.4158 // REG1B // 5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 845218 // Hs.285782 // LRRTM4 // 80059 // leucine-rich repeat transmembr	REG1B	REG1B , rs1526386, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-2063403	aattaactcatcctca[C/T]gaaaagtcactctta	C	T	NM_024993 // upstream // 934534 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 571298 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2069404	acacaacattgcagaa[A/G]tcagtagttgttacaa	A	G	NM_024993 // upstream // 961718 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 544114 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2105279	agcattgcaaaaccac[C/T]gtagtcgatctgggaa	C	T	NM_024993 // upstream // 1125438 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 380394 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2025552	aaaatctgttaaatcc[A/G]gagttatttcatccat	A	G	NM_024993 // upstream // 1230053 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 275779 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2147504	atggatagcaacttaa[C/T]tgaggagtgtcaggct	C	T	NM_024993 // upstream // 1301652 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 204180 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1784579	ggcctaggagttaaga[C/T]ggcctctagaaaaaca	C	T	NM_024993 // upstream // 1375915 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 129917 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1931865	ttccggccaagtagca[A/C]atctagttttccaccc	A	C	NM_024993 // upstream // 1377820 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 128012 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1871174	tcgtttcaagaataac[A/G]gcaggtctactcttaa	A	G	NM_024993 // upstream // 1404088 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 101744 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. ///	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1758999	gcatcagaaaataaagttttaaatc[C/G]attgtattcatctattaaaatatat	C	G	NM_006507 // downstream // 218693 // Hs.4158 // REG1B // 5968 // regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) /// NM_024993 // upstream // 1346467 // Hs.285782 // LRRTM4 // 80059 // leucine-rich repeat transmemb	REG1B	REG1B , rs1521970, regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein) ,p12
SNP_A-1817220	gttcacagaactgaga[A/G]gagaaccaggcatgga	A	G	NM_024993 // upstream // 1415807 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 90025 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963907	cttatttttgcaatc[A/T]cctgcatgttaggaaa	A	T	NM_024993 // upstream // 1439014 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 66818 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963910	aggtttccatctctgc[C/G]agggtcaggtcatcac	C	G	NM_024993 // upstream // 1480153 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 25679 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963911	acccagttgtagccca[G/T]ccttgtttctgacact	G	T	NM_024993 // upstream // 1480249 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 25583 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-1963920	tccttttgtgtgcttc[A/G]atctattaaatgaaga	A	G	NM_024993 // upstream // 1487017 // Hs.285782 // LRRTM4 // 80059 // Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), mRNA. /// NM_198448 // upstream // 18815 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// E	LRRTM4	LRRTM4, Homo sapiens leucine rich repeat transmembrane neuronal 4 (LRRTM4), p12
SNP_A-2051276	aagggcaacctcacat[A/G]atacaggagaacgcat	A	G	NM_198448 // intron // 0 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// ENST00000272324 // intron // 0 // — // — // — // —	REG3G	REG3G, Homo sapiens LPPM429 (REG-III), p12
SNP_A-2066147	aatttgtggtatatga[C/T]gaaagcagtgtttaga	C	T	NM_198448 // downstream // 3871 // Hs.447084 // REG3G // 130120 // Homo sapiens LPPM429 (REG-III), mRNA. /// NM_006507 // downstream // 52656 // Hs.4158 // REG1B // 5968 // Homo sapiens regenerating islet-derived 1 beta (pancreatic stone protein, pancreat	REG3G	REG3G, Homo sapiens LPPM429 (REG-III), p12
SNP_A-2151821	atgtttcattgaagcc[A/G]agaataatgataatag	A	G	NM_002909 // downstream // 1992 // Hs.49407 // REG1A // 5967 // Homo sapiens regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein) (REG1A), mRNA. /// NM_002580 // downstream // 31596 // Hs.423 // REG3A // 5068 // Homo sa	REG1A	REG1A, Homo sapiens regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein) (REG1A), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2248322	ctgtgtcccacctctga[A/G]aaaatgcacttgaggt	A	G	NM_002580 // upstream // 111043 // Hs.423 // REG3A // 5068 // Homo sapiens pancreatitis-associated protein (PAP), transcript variant 1, mRNA. /// NM_138937 // upstream // 111043 // Hs.423 // REG3A // 5068 // Homo sapiens pancreatitis-associated protein (P	REG3A	REG3A, Homo sapiens pancreatitis-associated protein (PAP), transcript variant 1, p12
SNP_A-2050653	aaggcacaggatgtaa[A/C]aaatgagctgccacct	A	C	NM_002580 // upstream // 119857 // Hs.423 // REG3A // 5068 // Homo sapiens pancreatitis-associated protein (PAP), transcript variant 1, mRNA. /// NM_138937 // upstream // 119857 // Hs.423 // REG3A // 5068 // Homo sapiens pancreatitis-associated protein (P	REG3A	REG3A, Homo sapiens pancreatitis-associated protein (PAP), transcript variant 1, p12
SNP_A-1832054	taattgtttggagac[G/T]gcatagggagtttgg	G	T	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // — .	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1871758	tctaattaactagaaa[A/G]ctctctaagactctga	A	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1781858	ggattttgcatctgtt[A/C]aaatttcatctgcatg	A	C	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1893030	tgcactgctttctaaa[C/T]gaaaaaggcttttga	C	T	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2050577	aaggattggtaacata[A/G]ctgtactctggcaata	A	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1933645	ttctaggtagatttca[C/G]ctaacctccagagaa	C	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1804964	gtcatatttaaaagcc[A/G]cctctacttcaagt	A	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1927024	ttatttgctatagttc[A/T]cccagtgtatttgtac	A	T	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1829978	taataatttttgctgc[A/G]aagtggtataccagca	A	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2052721	aagtcaaaatctaccc[A/G]acattatttagttcag	A	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2258713	cttttgctgtttataa[C/T]aagtccctttcatcct	C	T	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — // —	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1739831	catggaagcagaaatgtccgactt[A/G]ctatgactgactctg agagtcgt	A	G	NM_004389 // intron // 0 // Hs.150917 // CTNNA2 // 1496 // catenin (cadherin-associated protein), alpha 2	CTNNA2	CTNNA2, rs1006154, catenin (cadherin-associated protein), alpha 2,p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1651136	atagctgctggctgatggtgtgta[C/T]atgaaatcttaagttagtta atag	C	T	NM_004389 // intron // 0 // Hs.150917 // CTNNA2 // 1496 // catenin (cadherin-associated protein), alpha 2	CTNNA2	CTNNA2 , rs1006155, catenin (cadherin-associated protein), alpha 2,p12
SNP_A-1920304	ttaatggaaccaatta[C/G]ctctatcaggccctgt	C	G	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — /// ENST00000343114 // intron // 0 // — // — // — /	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-2291019	gcaagtgtgcaatatg[A/T]caggcactatggaga	A	T	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — /// ENST00000343114 // intron // 0 // — // — // — /	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1963990	aagagatctaagaaggg[C/T]cccagaattagatcta	C	T	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — /// ENST00000343114 // intron // 0 // — // — // — /	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1730799	ctcccctgctgcatttaatgttta[A/G]gatatttgcaaaaagttgg cggtt	A	G	NM_004389 // intron // 0 // Hs.150917 // CTNNA2 // 1496 // catenin (cadherin-associated protein), alpha 2	CTNNA2	CTNNA2 , rs2043450, catenin (cadherin-associated protein), alpha 2,p12
SNP_A-2155301	attcataaagactcag[A/C]aatctagctatggcaa	A	C	NM_004389 // intron // 0 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// ENST00000332108 // intron // 0 // — // — // — /// ENST00000343114 // intron // 0 // — // — // — /	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1799387	gtaatcatattagtaa[C/T]agcagtggaatgaac	C	T	NM_004389 // downstream // 1171318 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// NM_178839 // upstream // 1514797 // Hs.127654 // LRRTM1 // 347730 // Homo sapiens leucine rich repeat tran	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1964045	cattttcttgccaa[A/G]aaggtaacaaattca	A	G	NM_004389 // downstream // 1521214 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// NM_178839 // upstream // 1864693 // Hs.127654 // LRRTM1 // 347730 // Homo sapiens leucine rich repeat tran	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1693391	aggctcaggtctatttcactggaaa[A/C]cctctactcatgtcttaa acacac	A	C	NM_003849 // downstream // 1812856 // Hs.270428 // SUCLG1 // 8802 // succinate-CoA ligase, GDP-forming, alpha subunit	SUCLG1	SUCLG1 , rs10496270, succinate-CoA ligase, GDP-forming, alpha subunit,p12
SNP_A-2022346	aaaaataaccatttttd[A/G]ctcttgctttattga	A	G	NM_004389 // downstream // 2066828 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// NM_178839 // upstream // 2410307 // Hs.127654 // LRRTM1 // 347730 // Homo sapiens leucine rich repeat tran	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p12
SNP_A-1744705	aggcccttgtcagccacttggctc[C/T]gctgtatttcctcacaaa tgcaccc	C	T	NM_003849 // downstream // 1525916 // Hs.270428 // SUCLG1 // 8802 // succinate-CoA ligase, GDP-forming, alpha subunit	SUCLG1	SUCLG1 , rs1582382, succinate-CoA ligase, GDP-forming, alpha subunit,p12
SNP_A-2031087	aaaggatctgctaaaa[A/G]tccgcagccaggcatg	A	G	NM_004389 // downstream // 2862206 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// NM_178839 // upstream // 3205685 // Hs.127654 // LRRTM1 // 347730 // Homo sapiens leucine rich repeat tran	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-1806786	gtctagtctgctttcta[A/G]taagctcagaacattt	A	G	NM_004389 // downstream // 3326061 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// NM_178839 // upstream // 3669540 // Hs.127654 // LRRTM1 // 347730 // Homo sapiens leucine rich repeat tran	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2
SNP_A-2111826	aggatatacacagaaaa[C/T]gtacaccaaaagtatg	C	T	NM_004389 // downstream // 3487265 // Hs.167368 // CTNNA2 // 1496 // Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA. /// NM_178839 // upstream // 3830744 // Hs.127654 // LRRTM1 // 347730 // Homo sapiens leucine rich repeat tran	CTNNA2	CTNNA2, Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2126606	ataaaatttcagatga[A/G]gactaatatcctgtgg	A	G	NM_003849 // downstream // 113576 // Hs.270428 // SUCLG1 // 8802 // Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA. /// ENST00000331369 // downstream // 17753 // — // — // — // — /// ENST00000295783 // downstream // 1	SUCLG1	SUCLG1, Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), p11.2
SNP_A-2099460	agagggactttaccaa[A/G]tggggcctctaacccc	A	G	NM_003849 // upstream // 10607 // Hs.270428 // SUCLG1 // 8802 // Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA. /// NM_173645 // upstream // 46583 // — // FLJ37357 // 284944 // Homo sapiens hypothetical protein FLJ37357 (F	SUCLG1	SUCLG1, Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), p11.2
SNP_A-2078528	accatgacagttacaa[C/T]catatgttgatatgaa	C	T	NM_173645 // intron // 0 // — // FLJ37357 // 284944 // Homo sapiens hypothetical protein FLJ37357 (FLJ37357), mRNA. /// ENST00000314395 // intron // 0 // — // — // — // —	FLJ37357	FLJ37357, Homo sapiens hypothetical protein FLJ37357 (FLJ37357), p11.2
SNP_A-1814289	gtgtcttgtgacttgg[C/T]atgatatgcagggaat	C	T	NM_173645 // downstream // 3258 // — // FLJ37357 // 284944 // Homo sapiens hypothetical protein FLJ37357 (FLJ37357), mRNA. /// ENST00000314395 // downstream // 3258 // — // — // — // — /// ENST00000306670 // upstream // 36862 // — // — // –	FLJ37357	FLJ37357, Homo sapiens hypothetical protein FLJ37357 (FLJ37357), p11.2
SNP_A-2100025	agagtgaaagctgcaa[C/T]gttgaaaaaaacatcc	C	T	NM_173645 // downstream // 19789 // — // FLJ37357 // 284944 // Homo sapiens hypothetical protein FLJ37357 (FLJ37357), mRNA. /// ENST00000314395 // downstream // 19789 // — // — // — // — /// ENST00000306670 // upstream // 20331 // — // — //	FLJ37357	FLJ37357, Homo sapiens hypothetical protein FLJ37357 (FLJ37357), p11.2
SNP_A-1913756	tgtgtcaatattaacc[C/T]aagtgatcaataactt	C	T	NM_173645 // downstream // 39785 // — // FLJ37357 // 284944 // Homo sapiens hypothetical protein FLJ37357 (FLJ37357), mRNA. /// ENST00000314395 // downstream // 39785 // — // — // — // — /// ENST00000306670 // upstream // 335 // — // — // –	FLJ37357	FLJ37357, Homo sapiens hypothetical protein FLJ37357 (FLJ37357), p11.2
SNP_A-2251796	cttcatattgataatg[C/T]attgctttcttcagga	C	T	NM_173645 // downstream // 40033 // — // FLJ37357 // 284944 // Homo sapiens hypothetical protein FLJ37357 (FLJ37357), mRNA. /// ENST00000314395 // downstream // 40033 // — // — // — // — /// ENST00000306670 // upstream // 87 // — // — // —	FLJ37357	FLJ37357, Homo sapiens hypothetical protein FLJ37357 (FLJ37357), p11.2
SNP_A-2273998	gactgtttcttatctc[G/T]gactaatccctttttt	G	T	ENST00000306670 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-2209890	ccccaactgtctcata[G/T]ggcactggcagcttca	G	T	ENST00000306670 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-2176394	caccatccaactttca[C/T]gatgggaacattttca	C	T	NM_145299 // upstream // 18179 // Hs.531817 // LOC200383 // 200383 // Homo sapiens similar to Dynein heavy chain at 16F (LOC200383). mRNA. /// ENST00000306670 // downstream // 2842 // — // — // — // — /// ENST00000272375 // upstream // 18179 // –	LOC200383	LOC200383, Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), p11.2
SNP_A-1883133	tgaaatgacgcatcat[A/T]aaatacacaggaaatt	A	T	NM_145299 // intron // 0 // Hs.531817 // LOC200383 // 200383 // Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), mRNA. /// ENST00000272375 // intron // 0 // — // — // — // —	LOC200383	LOC200383, Homo sapiens similar to Dynein heavy chain at 16F (LOC200383), p11.2
SNP_A-1964108	ctcatgtgtaaatgac[C/T]ggggttgtcgcagtggt	C	T	ENST00000237449 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-1806680	gtctacagtttctcca[A/G]gtttctttggttggca	A	G	ENST00000237449 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-2285779	gatgactccaaagcaa[C/T]tccttgcaaaacaaat	C	T	ENST00000237449 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-2198832	catttcttgaatgcaa[A/G]gttccatatgtgacct	A	G	ENST00000237449 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-2265233	gaagcaaacagagtca[A/T]taaatataagatcaat	A	T	ENST00000237449 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-1811759	gtgcttaggtctctga[A/T]caatttctagtgagtc	A	T	ENST00000237449 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-1743713	actgatacatttcaagagataaggg[C/T]cacaaggagattttca ctcaagttg	C	T	NM_031283 // intron // 0 // Hs.318517 // TCF7L1 // 83439 // transcription factor 7-like 1 (T-cell specific, HMG-box)	TCF7L1	TCF7L1 , rs10520406, transcription factor 7-like 1 (T-cell specific, HMG-box),p11.2
SNP_A-1928170	ttcacactaacatcca[C/T]cccaagtctgaattaa	C	T	NM_031283 // intron // 0 // Hs.516297 // TCF7L1 // 83439 // Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), mRNA. /// ENST00000282111 // intron // 0 // — // — // — // —	TCF7L1	TCF7L1, Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), p11.2
SNP_A-1964122	actagaaaactatcca[C/T]gttgctatctataatg	C	T	NM_031283 // intron // 0 // Hs.516297 // TCF7L1 // 83439 // Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), mRNA. /// ENST00000282111 // intron // 0 // — // — // — // —	TCF7L1	TCF7L1, Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215679	cctcagtggaaagatg[A/C]atgtgaaaaaatgttg	A	C	NM_201594 // downstream // 36774 // Hs.209542 // LOC284948 // 284948 // Homo sapiens similar to B-cell linker; B cell linker protein (LOC284948), transcript variant 2, mRNA. /// NM_198482 // downstream // 36774 // Hs.209542 // LOC284948 // 284948 // Homo	LOC284948	LOC284948, Homo sapiens similar to B-cell linker; B cell linker protein (LOC284948), transcript variant 2, p11.2
SNP_A-2271325	gacattcagaagggaa[C/G]gaacattcttgaccca	C	G	NM_000821 // upstream // 14819 // Hs.77719 // GGCX // 2677 // Homo sapiens gamma-glutamyl carboxylase (GGCX), mRNA. /// NM_003761 // upstream // 1319 // Hs.534373 // VAMP8 // 8673 // Homo sapiens vesicle-associated membrane protein 8 (endobrevin) (VAMP8),	GGCX	GGCX, Homo sapiens gamma-glutamyl carboxylase (GGCX), p11.2
SNP_A-1790562	ggggccgaggaaagta[G/T]agaggaagagaagctc	G	T	NM_006433 // downstream // 36274 // Hs.105806 // GNLY // 10578 // Homo sapiens granulysin (GNLY), transcript variant NKG5, mRNA. /// NM_012483 // downstream // 36263 // Hs.105806 // GNLY // 10578 // Homo sapiens granulysin (GNLY), transcript variant 519,	GNLY	GNLY, Homo sapiens granulysin (GNLY), transcript variant NKG5, p11.2
SNP_A-1928725	ttcagaagagggaaaa[A/G]ggccgtggaggtatat	A	G	NM_006433 // downstream // 38487 // Hs.105806 // GNLY // 10578 // Homo sapiens granulysin (GNLY), transcript variant NKG5, mRNA. /// NM_012483 // downstream // 38476 // Hs.105806 // GNLY // 10578 // Homo sapiens granulysin (GNLY), transcript variant 519,	GNLY	GNLY, Homo sapiens granulysin (GNLY), transcript variant NKG5, p11.2
SNP_A-1840923	tagctcttgttcagca[A/G]aggggaatatgagaag	A	G	NM_003896 // upstream // 56191 // Hs.415117 // ST3GAL5 // 8869 // Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), mRNA. /// NM_015425 // downstream // 81219 // Hs.26962 // POLR1A // 25885 //	ST3GAL5	ST3GAL5, Homo sapiens sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9), p11.2
SNP_A-2294362	gcaggtgactgagttc[A/G]attaaagcccctctaa	A	G	NM_017952 // intron // 0 // Hs.323489 // FLJ20758 // 55037 // Homo sapiens FLJ20758 protein (FLJ20758), mRNA. /// ENST00000254630 // intron // 0 // --- // --- // --- // ---	FLJ20758	FLJ20758, Homo sapiens FLJ20758 protein (FLJ20758), p11.2
SNP_A-1964145	actgttccattactac[A/G]caaacacatattagag	A	G	NM_022912 // 3UTR // 0 // Hs.368884 // C2orf23 // 65055 // Homo sapiens chromosome 2 open reading frame 23 (C2orf23), mRNA. /// ENST00000357263 // 3UTR // 0 // --- // --- // --- /// ENST00000165698 // 3UTR // 0 // --- // --- // --- // ---	C2orf23	C2orf23, Homo sapiens chromosome 2 open reading frame 23 (C2orf23), p11.2
SNP_A-1954718	tttgctcctcaggcag[A/C]aacaagaaagatgtgt	A	C	NM_022912 // intron // 0 // Hs.368884 // C2orf23 // 65055 // Homo sapiens chromosome 2 open reading frame 23 (C2orf23), mRNA. /// ENST00000357263 // intron // 0 // --- // --- // --- // --- /// ENST00000165698 // intron // 0 // --- // --- // --- // ---	C2orf23	C2orf23, Homo sapiens chromosome 2 open reading frame 23 (C2orf23), p11.2
SNP_A-1812246	gtggatactgacacgc[C/T]gagctgaaaagtgatt	C	T	NM_022912 // intron // 0 // Hs.368884 // C2orf23 // 65055 // Homo sapiens chromosome 2 open reading frame 23 (C2orf23), mRNA. /// ENST00000357263 // intron // 0 // --- // --- // --- // --- /// ENST00000165698 // intron // 0 // --- // --- // --- // ---	C2orf23	C2orf23, Homo sapiens chromosome 2 open reading frame 23 (C2orf23), p11.2
SNP_A-2155774	attccccccgagtaag[C/T]atagccaatagcttga	C	T	NM_016079 // intron // 0 // Hs.255015 // VPS24 // 51652 // Homo sapiens vacuolar protein sorting 24 (yeast) (VPS24), transcript variant 1, mRNA. /// ENST00000263856 // intron // 0 // --- // --- // ---	VPS24	VPS24, Homo sapiens vacuolar protein sorting 24 (yeast) (VPS24), transcript variant 1, p11.2
SNP_A-1694131	gacccttgctgtcagccaatcatcc[A/C]agcctgtgcaaattcct ggcccttt	A	C	AL832035 // intron // 0 // Hs.129982 // SMYD1 // 150572 // SET and MYND domain containing 1	SMYD1	SMYD1 , rs894198, SET and MYND domain containing 1,p11.2
SNP_A-1736727	catacagctctttgatggccatgtc[C/G]agtttgccttctttgtcttcc ctgt	C	G	NM_001443 // downstream // 7292 // Hs.380135 // FABP1 // 2168 // fatty acid binding protein 1, liver	FABP1	FABP1 , rs1530272, fatty acid binding protein 1, liver,p11.2
SNP_A-1821324	gtttgccatttataaa[A/G]cacaccattgaatcta	A	G	NM_004836 // upstream // 49899 // Hs.434326 // EIF2AK3 // 9451 // Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA. /// NM_144563 // upstream // 14206 // Hs.469264 // RPIA // 22934 // Homo sapiens ribose 5-phosphate i	EIF2AK3	EIF2AK3, Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259900	gaaaaggctgccgcat[C/G]atctcagcgaggagtg	C	G	X02990 // upstream // 74820 // Hs.546971 // --- // 0 // Human mRNA for IgM kappa light-chain variable (IV) region. /// ENST00000321577 // downstream // 7837 // --- // --- // --- // --- /// ENST00000321557 // downstream // 5864 // --- // --- // --- // ---	-	-, Human for IgM kappa light-chain variable (IV) region. ,p11.2
SNP_A-2103502	agcaatggttaacaaa[A/C]ggaggaagttggtgtt	A	C	ENST00000358611 // downstream // 17879 // --- // --- // --- // --- /// ENST00000357893 // downstream // 3850 // --- // --- // --- // --- /// ENST00000359143 // downstream // 1083027 // --- // --- // --- // ---	-	p11.2
SNP_A-1919470	ttaagccccccgtaaca[C/T]catttgcccactaaat	C	T	NM_014014 // upstream // 29135 // Hs.246112 // ASCC3L1 // 23020 // Homo sapiens activating signal cointegrator 1 complex subunit 3-like 1 (ASCC3L1), mRNA. /// NM_015341 // upstream // 1095 // Hs.308045 // BRRN1 // 23397 // Homo sapiens barren homolog (Dro	ASCC3L1	ASCC3L1, Homo sapiens activating signal cointegrator 1 complex subunit 3-like 1 (ASCC3L1), q11.2
SNP_A-1828636	taagcctgctgtgctc[A/G]gaaactgaatagtagc	A	G	NM_212481 // downstream // 25162 // Hs.920 // ARID5A // 10865 // Homo sapiens AT rich interactive domain 5A (MRF1-like) (ARID5A), transcript variant 1, mRNA. /// NM_017991 // downstream // 15385 // Hs.516341 // FLJ10081 // 55683 // Homo sapiens hypothetic	ARID5A	ARID5A, Homo sapiens AT rich interactive domain 5A (MRF1-like) (ARID5A), transcript variant 1, q11.2
SNP_A-2174210	cacactcaacaaatac[C/T]ggttgagccccggccc	C	T	NM_016490 // upstream // 22900 // Hs.107922 // LOC51252 // 51252 // Homo sapiens hypothetical protein LOC51252 (LOC51252), mRNA. /// ENST00000327896 // upstream // 22900 // --- // --- // --- // --- /// ENST00000305461 // upstream // 116416 // --- // --- /	LOC51252	LOC51252, Homo sapiens hypothetical protein LOC51252 (LOC51252), q11.2
SNP_A-1907200	tggtttctttcatcca[A/G]cctgaggcctttgcga	A	G	NM_001079 // intron // 0 // Hs.234569 // ZAP70 // 7535 // Homo sapiens zeta-chain (TCR) associated protein kinase 70kDa (ZAP70), transcript variant 1, mRNA. /// NM_207519 // intron // 0 // Hs.234569 // ZAP70 // 7535 // Homo sapiens zeta-chain (TCR) associ	ZAP70	ZAP70, Homo sapiens zeta-chain (TCR) associated protein kinase 70kDa (ZAP70), transcript variant 1, q11.2
SNP_A-1817937	gttctaacactggcca[A/C]cctttaccagccttca	A	C	NM_001079 // downstream // 15958 // Hs.234569 // ZAP70 // 7535 // Homo sapiens zeta-chain (TCR) associated protein kinase 70kDa (ZAP70), transcript variant 1, mRNA. /// NM_207519 // downstream // 15958 // Hs.234569 // ZAP70 // 7535 // Homo sapiens zeta-ch	ZAP70	ZAP70, Homo sapiens zeta-chain (TCR) associated protein kinase 70kDa (ZAP70), transcript variant 1, q11.2
SNP_A-2136365	atcacacttttgtgaa[A/G]aatgctagagagccac	A	G	D87446 // intron // 0 // Hs.469376 // RW1 // 23505 // Human mRNA for KIAA0257 gene, partial cds. /// ENST00000186436 // intron // 0 // --- // --- // --- // ---	RW1	RW1, Human for KIAA0257 gene, partial cds. ,q11.2
SNP_A-2189689	cagttttgaaaaagaa[A/G]gacacaatggaggact	A	G	D87446 // upstream // 55579 // Hs.469376 // RW1 // 23505 // Human mRNA for KIAA0257 gene, partial cds. /// NM_144992 // upstream // 143489 // Hs.269977 // MGC26733 // 200403 // Homo sapiens hypothetical protein MGC26733 (MGC26733), mRNA. /// ENST00001864	RW1	RW1, Human for KIAA0257 gene, partial cds. q11.2
SNP_A-2194552	catgcacctgaataac[C/T]aatgggtctataaata	C	T	NM_144992 // intron // 0 // Hs.269977 // MGC26733 // 200403 // Homo sapiens hypothetical protein MGC26733 (MGC26733), mRNA. /// ENST00000305068 // intron // 0 // --- // --- // --- // --- /// ENST00000355889 // intron // 0 // --- // --- // --- // ---	MGC26733	MGC26733, Homo sapiens hypothetical protein MGC26733 (MGC26733), q11.2
SNP_A-1698895	tacttttttttttttcaatcagcc[A/G]caagctttcatatcactttctgtt g	A	G	NM_018497 // intron // 0 // - // - // - // -	-	- , rs953320, -,q11.2
SNP_A-2202778	ccacgtgcctcaatta[C/T]gaatctccacgtgcct	C	T	NM_144992 // downstream // 53045 // Hs.269977 // MGC26733 // 200403 // Homo sapiens hypothetical protein MGC26733 (MGC26733), mRNA. /// NM_001298 // upstream // 24811 // Hs.234785 // CNGA3 // 1261 // Homo sapiens cyclic nucleotide gated channel alpha 3 (C	MGC26733	MGC26733, Homo sapiens hypothetical protein MGC26733 (MGC26733), q11.2
SNP_A-2168979	caagaggaaattactc[A/G]ctgatagttttcaggc	A	G	NM_001298 // intron // 0 // Hs.234785 // CNGA3 // 1261 // Homo sapiens cyclic nucleotide gated channel alpha 3 (CNGA3), mRNA. /// ENST00000272602 // intron // 0 // --- // --- // --- // ---	CNGA3	CNGA3, Homo sapiens cyclic nucleotide gated channel alpha 3 (CNGA3), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270024	gacacaagtgataaca[C/T]gttggagtgtaaagtg	C	T	NM_016503 // downstream // 43774 // Hs.346736 // MRPL30 // 51263 // Homo sapiens mitochondrial ribosomal protein L30 (MRPL30), nuclear gene encoding mitochondrial protein, transcript variant 2, mR /// NM_145212 // downstream // 43774 // Hs.346736 // MRPL3	MRPL30	MRPL30, Homo sapiens mitochondrial ribosomal protein L30 (MRPL30), nuclear gene encoding mitochondrial protein, transcript variant 2, mR ,q11.2
SNP_A-2125037	agttgcctacccccte[A/G]ctatcaaatcttgact	A	G	NM_175735 // upstream // 16887 // Hs.436468 // LYG2 // 254773 // Homo sapiens lysozyme-like (LYG2), mRNA. /// NM_174898 // downstream // 12266 // Hs.164589 // LOC129530 // 129530 // Homo sapiens hypothetical protein LOC129530 (LOC129530), mRNA. /// ENST00	LYG2	LYG2, Homo sapiens lysozyme-like (LYG2), q11.2
SNP_A-1901677	tggcaagttctttcat[C/T]acaacacaagttacat	C	T	NM_015904 // intron // 0 // Hs.158688 // EIF5B // 9669 // Homo sapiens eukaryotic translation initiation factor 5B (EIF5B), mRNA. /// ENST00000289371 // intron // 0 // — // — // — // —	EIF5B	EIF5B, Homo sapiens eukaryotic translation initiation factor 5B (EIF5B), q11.2
SNP_A-1897682	tgctgctagtccagaa[A/G]ggaatatctaatcctt	A	G	NM_016316 // intron // 0 // Hs.443077 // REV1L // 51455 // Homo sapiens REV1-like (yeast) (REV1L), mRNA. /// ENST00000258428 // intron // 0 // — // — // — // —	REV1L	REV1L, Homo sapiens REV1-like (yeast) (REV1L), q11.2
SNP_A-1817367	gttcagctagaaatac[A/G]agaggctgcaaaaaat	A	G	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2028186	aaactactgtcaggga[C/T]actccacgttagcacc	C	T	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1946373	tttaaaatttttctta[G/T]agacagcatttcacta	G	T	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1951575	tttcctgcctggcaaa[C/T]ttcattcttccttcga	C	T	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2131174	atagagaaaacgttag[A/C]cagttatgaagagcaa	A	C	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1959912	ttttgtctttgccgat[C/G]atacattttcaaacag	C	G	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-1900373	tggagagggatccacc[A/G]ggaaaaggagaagcaa	A	G	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2062284	aatggttagctttata[C/T]gtcaacctagctaggt	C	T	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2054214	aagttgaaatctcaga[C/G]aacaatctcaaatcct	C	G	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // — /// E	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2144205	atgagtaagtgcagta[C/T]aatggtaaatgtcttt	C	T	NM_002285 // intron // 0 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// ENST00000295323 // intron // 0 // — // — // — // — /// ENST00000356421 // intron // 0 // — // — // — // —	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1703649	gcagatcaccatcgctgctatta[C/T]gcgatatgtgtttctctcctgca	C	T	NM_002285 // intron // 0 // Hs.38070 // LAF4 // 3899 // lymphoid nuclear protein related to AF4	LAF4	LAF4, rs4129805, lymphoid nuclear protein related to AF4,q11.2
SNP_A-1741511	agattctgaaagcagcatttcctaa[C/T]taagaaggcccaagaaggtgacaga	C	T	NM_002285 // intron // 0 // Hs.38070 // LAF4 // 3899 // lymphoid nuclear protein related to AF4	LAF4	LAF4, rs2001722, lymphoid nuclear protein related to AF4,q11.2
SNP_A-1909823	tgtcacccatgtttcc[C/T]ccttcaatctctctacc	C	T	NM_002285 // upstream // 97509 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 81525 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. ///	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2153003	attacatatcagttta[A/G]aaatagtgacagcca	A	G	NM_002285 // upstream // 104397 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 74637 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. //	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2058346	aatcacaaatactaaaa[C/T]ctgaggctcgttctc	C	T	NM_002285 // upstream // 121668 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 57366 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. //	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2072458	acagcaggtcagagaa[C/T]ggattaagagtctggg	C	T	NM_002285 // upstream // 157855 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 21179 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. //	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2143294	atgacagccgccaaaa[A/G]gtttaaatgtgcttt	A	G	NM_002285 // upstream // 171048 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 7986 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. ///	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2299202	gccctagcgatgtcca[C/T]ggctacctcctga	C	T	NM_002285 // upstream // 174301 // Hs.444414 // LAF4 // 3899 // Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), mRNA. /// NM_198461 // downstream // 4733 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. ///	LAF4	LAF4, Homo sapiens lymphoid nuclear protein related to AF4 (LAF4), q11.2
SNP_A-2092987	agaacacaggctaacc[A/G]aaactacgcttaggct	A	G	NM_198461 // 3UTR // 0 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // 3UTR // 0 // — // — // —	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-2035740	aaatgtgcaggatgcc[A/G]ataagagctgggaggg	A	G	NM_198461 // intron // 0 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // intron // 0 // — // — // — // —	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-2049191	aagctagaaaaaaaaca[C/T]aatgtgggaagattg	C	T	NM_198461 // intron // 0 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // intron // 0 // — // — // — // —	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-2081175	acctgcaggctaagcc[A/G]aatgaaatatcagtga	A	G	NM_198461 // upstream // 43100 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // upstream // 43100 // — // — // — /// ENST00000307888 // downstream // 17650 // — // — // — // —	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-2262711	gaaatgctaatagaa[A/G]aaatctcggagcatca	A	G	NM_198461 // upstream // 50718 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // upstream // 50718 // — // — // — // — /// ENST00000307888 // downstream // 10032 // — // — // — // —	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2
SNP_A-1783665	ggcattaccccccgac[C/T]gaggcctcgtatgata	C	T	NM_198461 // upstream // 54556 // Hs.30646 // FLJ45273 // 164832 // Homo sapiens FLJ45273 protein (FLJ45273), mRNA. /// ENST00000302393 // upstream // 54556 // — // — // — // — /// ENST00000307888 // downstream // 6194 // — // — // — // —	FLJ45273	FLJ45273, Homo sapiens FLJ45273 protein (FLJ45273), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1810168	gtgatcgtgatgttaa[C/T]tgtggtggcccgtgtt	C	T	NM_004854 // downstream // 12947 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// ENST00000307888 // upstream // 8376 // --- // --- // --- /// ENST00000264249 // downstream // 12947 // --- // ---	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-2053672	aagtggccgggaaccc[A/G]aaacctgtaaatagtt	A	G	NM_004854 // downstream // 3790 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// ENST00000307888 // upstream // 17533 // --- // --- // --- /// ENST00000264249 // downstream // 3790 // --- // ---	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1718361	agtggtgttgtgcattctgtaggaa[A/G]tactgtcttactgacaga tttca	A	G	NM_002285 // upstream // 132219 // Hs.38070 // LAF4 // 3899 // lymphoid nuclear protein related to AF4 /// NM_004854 // downstream // 155136 // Hs.155553 // CHST10 // 9486 // carbohydrate sulfotransferase 10	LAF4	LAF4 , rs7597861, lymphoid nuclear protein related to AF4 ,q11.2
SNP_A-1644582	gaggatacccaaagcacaaggtccc[A/G]aactattagatgata attagaatga	A	G	NM_002285 // upstream // 132299 // Hs.38070 // LAF4 // 3899 // lymphoid nuclear protein related to AF4 /// NM_004854 // downstream // 155056 // Hs.155553 // CHST10 // 9486 // carbohydrate sulfotransferase 10	LAF4	LAF4 , rs10496346, lymphoid nuclear protein related to AF4 ,q11.2
SNP_A-1787665	gggacactaccacta[C/T]ctgacatcatattg	C	T	NM_004854 // upstream // 25092 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 120229 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// ENST00000	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1964241	ttttccagaatgcact[C/G]aggcatacatatact	C	G	NM_004854 // upstream // 29246 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 116075 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// ENST00000	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1964243	gcttgggccacctcca[C/T]gagtcgtttgtgacga	C	T	NM_004854 // upstream // 30525 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 114796 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// ENST00000	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1964244	tgtgttgctctggtaa[C/T]attccatttgagatct	C	T	NM_004854 // upstream // 30981 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 114340 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// ENST00000	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-2272051	gaccctgaaataacag[A/G]cactttcaattgctgg	A	G	NM_004854 // upstream // 31259 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 114062 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// ENST00000	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-2118587	agtaatgctaagagaa[A/G]attaacacactaagtg	A	G	NM_004854 // upstream // 93432 // Hs.516370 // CHST10 // 9486 // Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA. /// NM_024065 // upstream // 51889 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// ENST000002	CHST10	CHST10, Homo sapiens carbohydrate sulfotransferase 10 (CHST10), q11.2
SNP_A-1868640	tcctctcttgtcattc[C/T]atgttctgaagggat	C	T	NM_024065 // downstream // 150224 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 177806 // Hs.156832 // NPAS2 // 4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST0000026	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835259	tacctacaactaagaa[C/T]ccagaccaatatagtc	C	T	NM_024065 // downstream // 224807 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 103223 // Hs.156832 // NPAS2 // 4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST0000026	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-1913993	tgtgtgcaggacttaa[A/G]gccatgaggctgtgcc	A	G	NM_024065 // downstream // 231168 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 96862 // Hs.156832 // NPAS2 // 4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST00000264	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-1814554	gtgtgcttcatagaaa[A/T]taatactggataacag	A	T	NM_024065 // downstream // 291371 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 36659 // Hs.156832 // NPAS2 // 4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST00000264	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-2153358	attagaaggttctgtc[A/G]atcaacattttagaaa	A	G	NM_024065 // downstream // 310253 // Hs.469459 // PDCL3 // 79031 // Homo sapiens phosducin-like 3 (PDCL3), mRNA. /// NM_002518 // upstream // 17777 // Hs.156832 // NPAS2 // 4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST00000264	PDCL3	PDCL3, Homo sapiens phosducin-like 3 (PDCL3), q11.2
SNP_A-1822473	gtttttcatttgtttc[A/G]agaagtgccgagaaag	A	G	NM_002518 // intron // 0 // Hs.156832 // NPAS2 // 4862 // Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA. /// ENST00000335681 // intron // 0 // — // — // — // — /// ENST00000354182 // intron // 0 // — // — // — // —	NPAS2	NPAS2, Homo sapiens neuronal PAS domain protein 2 (NPAS2), q11.2
SNP_A-2104622	agcagtaccgcataga[C/T]gcccggcagtttgcac	C	T	NM_000993 // downstream // 16008 // Hs.469473 // RPL31 // 6160 // Homo sapiens ribosomal protein L31 (RPL31), mRNA. /// NM_017546 // upstream // 230490 // Hs.30819 // C2orf29 // 55571 // Homo sapiens chromosome 2 open reading frame 29 (C2orf29), mRNA. ///	RPL31	RPL31, Homo sapiens ribosomal protein L31 (RPL31), q11.2
SNP_A-1958476	ttttcctgtagattaa[C/T]tgaggcatgaggtgga	C	T	NM_000993 // downstream // 75264 // Hs.469473 // RPL31 // 6160 // Homo sapiens ribosomal protein L31 (RPL31), mRNA. /// NM_017546 // upstream // 171234 // Hs.30819 // C2orf29 // 55571 // Homo sapiens chromosome 2 open reading frame 29 (C2orf29), mRNA. ///	RPL31	RPL31, Homo sapiens ribosomal protein L31 (RPL31), q11.2
SNP_A-1859304	tcagctgtaaaaacga[A/C]ggactttctgacaccc	A	C	NM_000993 // downstream // 76183 // Hs.469473 // RPL31 // 6160 // Homo sapiens ribosomal protein L31 (RPL31), mRNA. /// NM_017546 // upstream // 170315 // Hs.30819 // C2orf29 // 55571 // Homo sapiens chromosome 2 open reading frame 29 (C2orf29), mRNA. ///	RPL31	RPL31, Homo sapiens ribosomal protein L31 (RPL31), q11.2
SNP_A-1818317	gttctgtcaaagaaaa[A/G]aggttagtgtgccatt	A	G	NM_173647 // intron // 0 // Hs.171802 // RNF149 // 284996 // Homo sapiens ring finger protein 149 (RNF149), mRNA. /// ENST00000295317 // intron // 0 // — // — // — // —	RNF149	RNF149, Homo sapiens ring finger protein 149 (RNF149), q11.2
SNP_A-1756601	aagctgtgatttggtctcatgtgcc[A/G]attaaggaagggtggtgcacaataa	A	G	NM_173647 // intron // 0 // Hs.171802 // RNF149 // 284996 // ring finger protein 149	RNF149	RNF149 , rs10496353, ring finger protein 149,q11.2
SNP_A-1823557	taaaagtgcagagtga[A/G]atgtatagcaaaattt	A	G	NM_207403 // upstream // 130452 // Hs.50607 // FLJ42986 // 389012 // Homo sapiens FLJ42986 protein (FLJ42986), mRNA. /// NM_004834 // upstream // 87695 // Hs.431550 // MAP4K4 // 9448 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4	FLJ42986	FLJ42986, Homo sapiens FLJ42986 protein (FLJ42986), q11.2
SNP_A-2050162	aaggacctcctaagac[A/G]atagatacaaaagagg	A	G	NM_207403 // upstream // 160369 // Hs.50607 // FLJ42986 // 389012 // Homo sapiens FLJ42986 protein (FLJ42986), mRNA. /// NM_004834 // upstream // 57778 // Hs.431550 // MAP4K4 // 9448 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4	FLJ42986	FLJ42986, Homo sapiens FLJ42986 protein (FLJ42986), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2068150	acaagaatttagccaa[C/T]ggccaagttagcagac	C	T	NM_004633 // upstream // 34660 // Hs.25333 // IL1R2 // 7850 // Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA. /// NM_173343 // upstream // 34660 // Hs.25333 // IL1R2 // 7850 // Homo sapiens interleukin 1 receptor, type I	IL1R2	IL1R2, Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, q11.2
SNP_A-2108422	agctgccctaatagc[A/G]atatttcaaatagtca	A	G	NM_004633 // intron // 0 // Hs.25333 // IL1R2 // 7850 // Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA. /// NM_173343 // intron // 0 // Hs.25333 // IL1R2 // 7850 // Homo sapiens interleukin 1 receptor, type II (IL1R2), t	IL1R2	IL1R2, Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, q11.2
SNP_A-1958688	tttctctctctcaac[A/G]aagcctagcacatttt	A	G	NM_004633 // downstream // 93282 // Hs.25333 // IL1R2 // 7850 // Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA. /// NM_173343 // downstream // 93282 // Hs.25333 // IL1R2 // 7850 // Homo sapiens interleukin 1 receptor, ty	IL1R2	IL1R2, Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, q11.2
SNP_A-1964281	gcatcaattgcaatga[C/T]catatggttttagcc	C	T	NM_003854 // intron // 0 // Hs.469520 // IL1RL2 // 8808 // Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), mRNA. /// ENST00000264257 // intron // 0 // — // — // — // —	IL1RL2	IL1RL2, Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), q11.2
SNP_A-1964282	ataatcactgcagcta[A/G]taatgtgctcagtctc	A	G	NM_003854 // intron // 0 // Hs.469520 // IL1RL2 // 8808 // Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), mRNA. /// ENST00000264257 // intron // 0 // — // — // — // —	IL1RL2	IL1RL2, Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), q11.2
SNP_A-2207616	ccatttgacttcctta[C/T]gtttgttaaagacacc	C	T	NM_003854 // intron // 0 // Hs.469520 // IL1RL2 // 8808 // Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), mRNA. /// ENST00000264257 // intron // 0 // — // — // — // —	IL1RL2	IL1RL2, Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), q11.2
SNP_A-2081874	accttggggtttgaac[G/T]gctcattgaaggtaat	G	T	NM_003854 // downstream // 23080 // Hs.469520 // IL1RL2 // 8808 // Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), mRNA. /// NM_016232 // upstream // 49071 // Hs.66 // IL1RL1 // 9173 // Homo sapiens interleukin 1 receptor-like 1 (IL1RL1), transcript	IL1RL2	IL1RL2, Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), q11.2
SNP_A-1689540	actgaataacattacaaactaaga[A/G]aagagtgccatttttg aatgttgc	A	G	NM_003855 // intron // 0 // Hs.159301 // IL18R1 // 8809 // interleukin 18 receptor 1	IL18R1	IL18R1, rs3213732, interleukin 18 receptor 1,q11.2
SNP_A-1743539	gtcctgcgaaatcacagtacttgcc[A/T]cttagcatctatctacac caggaaa	A	T	NM_003048 // upstream // 117661 // Hs.348255 // SLC9A2 // 6549 // solute carrier family 9 (sodium/hydrogen exchanger), isoform 2 /// NM_003853 // downstream // 49534 // Hs.158315 // IL18RAP // 8807 // interleukin 18 receptor accessory protein	SLC9A2	SLC9A2, rs2075190, solute carrier family 9 (sodium,q11.2
SNP_A-2167218	caacactgaatttaac[A/G]gatctcagaattagca	A	G	NM_032718 // upstream // 1076 // Hs.98798 // MGC11332 // 84804 // Homo sapiens hypothetical protein MGC11332 (MGC11332), mRNA. /// NM_144632 // upstream // 24146 // Hs.436203 // FLJ30294 // 130827 // Homo sapiens hypothetical protein FLJ30294 (FLJ30294).	MGC11332	MGC11332, Homo sapiens hypothetical protein MGC11332 (MGC11332), q12.1
SNP_A-2177207	cacctgctacatcatc[G/T]aagtatagtgcatccc	G	T	ENST00000354634 // upstream // 547734 // — // — // — // — /// ENST00000360991 // downstream // 961543 // — // — // — // —	-	q12.1
SNP_A-2136068	atcaagtaaccaatca[A/C]aaatcacgtctctatt	A	C	ENST00000354634 // upstream // 583529 // — // — // — // — /// ENST00000360991 // downstream // 925748 // — // — // — // —	-	q12.1
SNP_A-2304321	gctccttcattcgta[C/T]gatgtagagcaagtta	C	T	ENST00000354634 // upstream // 594548 // — // — // — // — /// ENST00000360991 // downstream // 914729 // — // — // — // —	-	q12.1
SNP_A-1952890	tttctatagaaaaca[A/T]acacgcaattacaaca	A	T	ENST00000354634 // upstream // 633777 // — // — // — // — /// ENST00000360991 // downstream // 875500 // — // — // — // —	-	q12.1
SNP_A-1874322	tctccaggcagataag[A/G]aaaaaacatacacaat	A	G	ENST00000354634 // upstream // 648399 // — // — // — // — /// ENST00000360991 // downstream // 860878 // — // — // — // —	-	q12.1
SNP_A-2080999	acctgaaaaatctctc[A/G]aggctggaacaatttg	A	G	ENST00000354634 // upstream // 791824 // — // — // — // — /// ENST00000360991 // downstream // 717453 // — // — // — // —	-	q12.1
SNP_A-2023870	aaaagaacccagaaaa[A/G]atggaatctagggcag	A	G	ENST00000354634 // upstream // 905798 // — // — // — // — /// ENST00000360991 // downstream // 603479 // — // — // — // —	-	q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1750175	cctcttccccacactttactaacaa[C/G]catattaatagggatgaagtataag	C	G	NM_006236 // upstream // 1163424 // Hs.248158 // POU3F3 // 5455 // POU domain, class 3, transcription factor 3 /// NM_144632 // downstream // 876147 // Hs.436203 // FLJ30294 // 130827 // hypothetical protein FLJ30294	POU3F3	POU3F3 , rs264962, POU domain, class 3, transcription factor 3 ,q12.1
SNP_A-1654355	atgccctaaaatagttggtaagaaa[C/T]gactttccctgttactggaaagct	C	T	NM_006236 // upstream // 1110549 // Hs.248158 // POU3F3 // 5455 // POU domain, class 3, transcription factor 3 /// NM_144632 // downstream // 929022 // Hs.436203 // FLJ30294 // 130827 // hypothetical protein FLJ30294	POU3F3	POU3F3 , rs9308868, POU domain, class 3, transcription factor 3 ,q12.1
SNP_A-2184030	cagcccaagataccaa[A/C]actccgaaggcagccc	A	C	NM_182640 // upstream // 359657 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 256815 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1800706	gtagaactgggtgaga[A/G]ggcgacataacaggcc	A	G	NM_182640 // upstream // 353979 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 262493 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1905999	tggtcggtcctcttta[C/T]aggatttttgtgagct	C	T	NM_182640 // upstream // 353918 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 262554 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1865740	tccatttagtgcatca[C/T]atctaagcaattgccc	C	T	NM_182640 // upstream // 350110 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 266362 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1869712	tccttcaactctagcc[C/T]aaaatgctggctggaa	C	T	NM_182640 // upstream // 348201 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 268271 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1878219	tctgtcactaaaacca[C/T]cactgtattctatccc	C	T	NM_182640 // upstream // 339689 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 276783 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2068910	acaatcttggagccca[A/G]ctaccacaccaacttt	A	G	NM_182640 // upstream // 306826 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 309646 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2242482	ctgcagatgttcagga[C/G]atgtaaggttgagaca	C	G	NM_182640 // upstream // 293892 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 322580 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1783651	ggcatgtgtgtaaagc[A/G]gaggggaggggagctg	A	G	NM_182640 // upstream // 293781 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 322691 // --- // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1945626	ttgttctttttactaca[A/G]ccggagtggtaaatac	A	G	NM_182640 // upstream // 291333 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 325139 // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2197575	cattctagatgatacaj[A/G]ctcttatttcagttca	A	G	NM_182640 // upstream // 291239 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 325233 // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1696136	cttatggtcagatctggaaagtta[C/T]aaaaaggtgcaaacca tcagggttt	C	T	NM_006236 // upstream // 175859 // Hs.248158 // POU3F3 // 5455 // POU domain, class 3, transcription factor 3 /// NM_144632 // downstream // 1863712 // Hs.436203 // FLJ30294 // 130827 // hypothetical protein FLJ30294	POU3F3	POU3F3 , rs2222186, POU domain, class 3, transcription factor 3 ,q12.1
SNP_A-2086322	actctgtttgtcttcc[A/C]gaaggatgcggcgcgt	A	C	NM_182640 // upstream // 174308 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000360991 // upstream // 442164 // --- // --- // --- /// ENST000	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1712773	aatttctgaaaacagaatctctcaa[C/T]taggaccttcccatgtg tgtgcca	C	T	NM_006236 // upstream // 115075 // Hs.248158 // POU3F3 // 5455 // POU domain, class 3, transcription factor 3 /// NM_144632 // downstream // 1924496 // Hs.436203 // FLJ30294 // 130827 // hypothetical protein FLJ30294	POU3F3	POU3F3 , rs2037261, POU domain, class 3, transcription factor 3 ,q12.1
SNP_A-1844072	tagttgctattgtaaa[C/T]ggaaaaatcaggaaat	C	T	NM_182640 // downstream // 14332 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 127451 // Hs.129701 // GPR45 // 11250 // Homo sapie	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1893886	tgcatactgcttatta[C/T]gagaactagttacaat	C	T	NM_182640 // downstream // 14458 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 127325 // Hs.129701 // GPR45 // 11250 // Homo sapie	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2265206	gaagattggaatatcat[C/T]gtacaaagaagtctag	C	T	NM_182640 // downstream // 29620 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 112163 // Hs.129701 // GPR45 // 11250 // Homo sapie	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-2310843	ggaagctgcaaatgga[C/T]atcaagtacactacag	C	T	NM_182640 // downstream // 29853 // Hs.469537 // MRPS9 // 64965 // Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, mRNA. /// NM_007227 // upstream // 111930 // Hs.129701 // GPR45 // 11250 // Homo sapie	MRPS9	MRPS9, Homo sapiens mitochondrial ribosomal protein S9 (MRPS9), nuclear gene encoding mitochondrial protein, q12.1
SNP_A-1927777	ttcaagcgtgtctccc[A/G]ggagcaatgtgaggag	A	G	NM_004257 // upstream // 303 // Hs.446350 // TGFBRAP1 // 9392 // Homo sapiens transforming growth factor, beta receptor associated protein 1 (TGFBRAP1), mRNA. /// NM_024093 // upstream // 28930 // Hs.303899 // MGC5508 // 79074 // Homo sapiens hypothetical	TGFBRAP1	TGFBRAP1, Homo sapiens transforming growth factor, beta receptor associated protein 1 (TGFBRAP1), q12.1
SNP_A-2134404	atatggagctgtcag[C/T]caacaaggaaatagac	C	T	NM_201555 // intron // 0 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // intron // 0 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcr	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2048401	aagcagtcacictccc[C/T]cttgagacctggcca	C	T	NM_201555 // intron // 0 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // intron // 0 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcr	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.1
SNP_A-1811751	gtgcttagataaatgc[A/G]agaaagtactacttg	A	G	NM_201555 // upstream // 55512 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream // 55512 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FH	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-2083447	actaagatgttgccac[A/G]gaaagtcagaatacag	A	G	NM_201555 // upstream // 55670 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream // 55670 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FH	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-2266508	gaagtagggtctatgg[A/G]acgccctgaccagatc	A	G	NM_201555 // upstream // 110611 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream // 110611 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1886241	tgaccgaggaaaggaa[A/G]catctcacaagctgtt	A	G	NM_201555 // upstream // 218126 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream // 218126 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1919321	ttaagagaacatttta[A/G]ctggttagaactccaa	A	G	NM_201555 // upstream // 330792 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, mRNA. /// NM_201557 // upstream // 330792 // Hs.443687 // FHL2 // 2274 // Homo sapiens four and a half LIM domains 2 (	FHL2	FHL2, Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 2, q12.2
SNP_A-1789985	gggcttgagaaaaagc[A/G]gaaaactggtctggga	A	G	NM_001004722 // intron // 0 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // intron // 0 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 1	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-2181121	cagacagcaagggaca[A/G]taaaggttagtcattc	A	G	NM_001004722 // downstream // 1341 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // downstream // 1341 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transc	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-2028823	aaacttgagctatgaa[A/G]ggccagcatcagaatc	A	G	NM_001004722 // downstream // 143282 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // downstream // 143282 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), tr	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-2053800	aagtgtatttttcaga[C/T]agctgatgttttaca	C	T	NM_001004722 // downstream // 148843 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // downstream // 148843 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), tr	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-2099133	agaggagaaacataaa[C/G]tgtcctaggagtgggg	C	G	NM_001004722 // downstream // 149850 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // downstream // 149850 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), tr	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2070493	acaccgcattgtcaaa[A/T]gggctgactccctggt	A	T	NM_001004722 // downstream // 151639 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // downstream // 151639 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), tr	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-1912496	tgtgcataatgcagaa[A/G]gaactggaacccaaag	A	G	NM_001004722 // downstream // 168313 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, mRNA. /// NM_003581 // downstream // 168313 // Hs.529244 // NCK2 // 8440 // Homo sapiens NCK adaptor protein 2 (NCK2), tr	NCK2	NCK2, Homo sapiens NCK adaptor protein 2 (NCK2), transcript variant 3, q12.2
SNP_A-1848995	tatgcaggtcctgaga[C/T]gtggagccaactaaca	C	T	NM_025076 // intron // 0 // Hs.469561 // UXS1 // 80146 // Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), mRNA. /// ENST00000283148 // intron // 0 // — // — // — // —	UXS1	UXS1, Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), q12.2
SNP_A-1828209	taagagctacccacaa[C/T]cctaaccaactgactg	C	T	NM_025076 // upstream // 77277 // Hs.469561 // UXS1 // 80146 // Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), mRNA. /// ENST00000283148 // upstream // 77277 // — // — // — // — /// ENST00000334627 // downstream // 17204 // — // — // —	UXS1	UXS1, Homo sapiens UDP-glucuronate decarboxylase 1 (UXS1), q12.2
SNP_A-2271748	gaccaggtttcccaga[A/G]tattgtcatgagcaaa	A	G	ENST00000334627 // upstream // 6401 // — // — // — // — /// ENST00000324709 // upstream // 86650 // — // — // — // — /// ENST00000359360 // downstream // 95836 // — // — // — // — /// ENST00000338161 // downstream // 107953 // —	-	q12.2
SNP_A-1871093	tcgtgggactcagaga[C/G]gctttttcgtgtcttt	C	G	ENST00000334627 // upstream // 42934 // — // — // — // — /// ENST00000324709 // upstream // 50117 // — // — // — // — /// ENST00000359360 // downstream // 59303 // — // — // — // — /// ENST00000338161 // downstream // 71420 // —	-	q12.2
SNP_A-2185408	caggacagcacgtaaa[A/G]gaacaaggcttgttcc	A	G	ENST00000304514 // intron // 0 // — // — // — // —	-	q12.2
SNP_A-2153867	attataacaatggcta[C/G]aggttctttttttcca	C	G	NM_032528 // downstream // 295560 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432 // downstream // 3437 // — // — // — // — /// ENST00000360640 // downstream //	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-2137321	atcagtttacttaatc[A/G]cagataacagagtctt	A	G	NM_032528 // downstream // 277451 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432 // downstream // 21546 // — // — // — // — /// ENST00000360640 // downstream //	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-2071925	acagagattagtaaca[A/G]ggttggtgccagtcct	A	G	NM_032528 // downstream // 98607 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432 // downstream // 200390 // — // — // — // — /// ENST00000360640 // downstream //	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-2066189	aattttaaaacctatg[A/G]caaagttgaaagtatt	A	G	NM_032528 // downstream // 94079 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432 // downstream // 204918 // — // — // — // — /// ENST00000360640 // downstream //	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-2277051	gagatgagctctttga[A/G]taggtagccaagttac	A	G	NM_032528 // downstream // 36868 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432 // downstream // 262129 // — // — // — // — /// ENST00000360640 // downstream //	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2
SNP_A-1964369	tgcaaatagttgccca[A/G]tggacaccagtgcttg	A	G	NM_032528 // downstream // 22470 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000303432 // downstream // 276527 // — // — // — // — /// ENST00000360640 // downstream //	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1693387	tgccctctcaatatcctgcaaccta[G/T]gctctcagtttcagtgttagtacta	G	T	NM_032528 // downstream // 60535 // Hs.98265 // ST6GalII // 84620 // beta-galactoside alpha-2,6-sialyltransferase II	ST6GalII	ST6GalII , rs10514794, beta-galactoside alpha-2,6-sialyltransferase II,q12.2
SNP_A-1964385	ctactggcatctagca[C/T]ggagggtccagggatg	C	T	NM_032528 // upstream // 75040 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 75980 // — // — // — // — /// ENST00000359054 // upstream // 75980	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2187802	cagtagggttgtttac[A/G]cgagtatcaccacaat	A	G	NM_032528 // upstream // 84795 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 85735 // — // — // — // — /// ENST00000359054 // upstream // 85735	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2271126	gacatcagtccggcta[C/T]acttaacctccaagtc	C	T	NM_032528 // upstream // 173819 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 174759 // — // — // — // — /// ENST00000359054 // upstream // 1747	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2082036	acctttttctccaccca[C/T]cacatagtagtaatac	C	T	NM_032528 // upstream // 285888 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 286828 // — // — // — // — /// ENST00000359054 // upstream // 2868	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-1839928	tagatttttaacagta[C/T]gtgctcatgtgaactc	C	T	NM_032528 // upstream // 438416 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 439356 // — // — // — // — /// ENST00000359054 // upstream // 4393	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2150186	atgtctaatctgtgag[A/G]aagtaaacaggttacc	A	G	NM_032528 // upstream // 659134 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 660074 // — // — // — // — /// ENST00000359054 // upstream // 6600	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-2006597	atttccagagtcgtta[C/T]agtggagatatggaag	C	T	NM_032528 // upstream // 876981 // Hs.98265 // ST6GAL2 // 84620 // Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), mRNA. /// ENST00000360640 // upstream // 877921 // — // — // — // — /// ENST00000359054 // upstream // 8779	ST6GAL2	ST6GAL2, Homo sapiens beta-galactoside alpha-2,6-sialyltransferase II (ST6GalII), q12.3
SNP_A-1921876	ttactcacagcattca[A/G]aagggaaaaaagaata	A	G	NM_021815 // upstream // 62686 // Hs.287758 // SLC5A7 // 60482 // Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA. /// ENST00000354986 // downstream // 33019 // — // — // — // — /// ENST00000264047 // upstream /	SLC5A7	SLC5A7, Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), q12.3
SNP_A-1931148	ttccatgagatattac[A/T]ctgttctgtttattga	A	T	NM_176825 // upstream // 13689 // Hs.436123 // SULT1C1 // 6819 // Homo sapiens sulfotransferase family, cytosolic, 1C, member 1 (SULT1C1), transcript variant 2, mRNA. /// NM_001056 // upstream // 14019 // Hs.436123 // SULT1C1 // 6819 // Homo sapiens sulfo	SULT1C1	SULT1C1, Homo sapiens sulfotransferase family, cytosolic, 1C, member 1 (SULT1C1), transcript variant 2, q12.3
SNP_A-1876886	tctgccagccgtgaat[C/G]agcgttcctgttgctc	C	G	ENST00000302895 // upstream // 13607 // — // — // — // — /// ENST00000309415 // upstream // 40050 // — // — // — // —	-	q13
SNP_A-1909563	tgtattttcatggcaa[A/G]aagtcaggaaacttac	A	G	ENST00000309415 // intron // 0 // — // — // — // —	-	q13
SNP_A-2265236	gaagcaaactcatcta[A/C]accagcgtttcttagt	A	C	NM_144710 // downstream // 34827 // Hs.469615 // SEPT10 // 151011 // Homo sapiens septin 10 (SEPT10), transcript variant 1, mRNA. /// NM_178584 // downstream // 34827 // Hs.469615 // SEPT10 // 151011 // Homo sapiens septin 10 (SEPT10), transcript variant	SEPT10	SEPT10, Homo sapiens septin 10 (SEPT10), transcript variant 1, q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1811631	gtgctgccttaaacaa[C/T]ttgctcattctcaagg	C	T	NM_144710 // upstream // 79130 // Hs.469615 // SEPT10 // 151011 // Homo sapiens septin 10 (SEPT10), transcript variant 1, mRNA. /// NM_178584 // upstream // 76446 // Hs.469615 // SEPT10 // 151011 // Homo sapiens septin 10 (SEPT10), transcript variant 2, m	SEPT10	SEPT10, Homo sapiens septin 10 (SEPT10), transcript variant 1, q13
SNP_A-1827100	taaccattagatagaa[A/C]tgcactggtgggggtt	A	C	ENST00000308604 // upstream // 247418 // --- // --- // --- // --- /// ENST00000295345 // upstream // 882 // --- // --- // --- // ---	-	q13
SNP_A-1810195	gtgatcttcatcaaaa[C/T]acagtgtccattgatc	C	T	AB111887 // CDS // 0 // Hs.190477 // ZC3HDC6 // 376940 // Homo sapiens mRNA for KIAA2035 protein. /// NM_198581 // CDS // 0 // Hs.190477 // ZC3HDC6 // 376940 // Homo sapiens zinc finger CCCH type domain containing 6 (ZC3HDC6), mRNA. /// ENST00000343936 //	ZC3HDC6	ZC3HDC6, Homo sapiens for KIAA2035 protein. ,q13
SNP_A-1947213	tttaatgttgcctaag[A/G]aaaaggatttggtcca	A	G	NM_032309 // downstream // 27333 // Hs.375707 // CHCHD5 // 84269 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 5 (CHCHD5), mRNA. /// NM_005415 // upstream // 29577 // Hs.546297 // SLC20A1 // 6574 // Homo sapiens solute carrier fami	CHCHD5	CHCHD5, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 5 (CHCHD5), q13
SNP_A-1690405	tccatatacggacagaggatttttc[C/T]ttgcactttatcttatgataagact	C	T	NM_032494 // intron // 0 // Hs.512785 // ZC3HDC8 // 84524 // zinc finger CCCH type domain containing 8	ZC3HDC8	ZC3HDC8 , rs2254860, zinc finger CCCH type domain containing 8,q13
SNP_A-1955078	tttggatacctctcag[A/G]atttcccatcaggacc	A	G	NM_032309 // downstream // 32258 // Hs.375707 // CHCHD5 // 84269 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 5 (CHCHD5), mRNA. /// NM_005415 // upstream // 24652 // Hs.546297 // SLC20A1 // 6574 // Homo sapiens solute carrier fami	CHCHD5	CHCHD5, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 5 (CHCHD5), q13
SNP_A-2299275	gccctccagagttcaa[C/T]aatctctagaaaggat	C	T	NM_173202 // upstream // 36564 // Hs.166371 // IL1F7 // 27178 // Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, mRNA. /// NM_014439 // upstream // 36564 // Hs.166371 // IL1F7 // 27178 // Homo sapiens interleukin 1 family	IL1F7	IL1F7, Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, q13
SNP_A-2234539	ctccacgtcactttca[A/G]ctgatgactttgtttc	A	G	NM_173202 // downstream // 39220 // Hs.166371 // IL1F7 // 27178 // Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, mRNA. /// NM_014439 // downstream // 39220 // Hs.166371 // IL1F7 // 27178 // Homo sapiens interleukin 1 fa	IL1F7	IL1F7, Homo sapiens interleukin 1 family, member 7 (zeta) (IL1F7), transcript variant 2, q13
SNP_A-2027256	aaacatagctgtaggc[A/G]ccttattacaatttct	A	G	NM_013951 // intron // 0 // Hs.469728 // PAX8 // 7849 // Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, mRNA. /// NM_013952 // intron // 0 // Hs.469728 // PAX8 // 7849 // Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8C, m	PAX8	PAX8, Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, q13
SNP_A-2144846	atgattaaacacttcc[C/T]attaggctctgtctct	C	T	NM_013951 // upstream // 156863 // Hs.469728 // PAX8 // 7849 // Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, mRNA. /// NM_013952 // upstream // 156863 // Hs.469728 // PAX8 // 7849 // Homo sapiens paired box gene 8 (PAX8), transcript va	PAX8	PAX8, Homo sapiens paired box gene 8 (PAX8), transcript variant PAX8B, q13
SNP_A-1866033	tcccactgcttctcta[A/C]atatatgccaaaccag	A	C	NM_025181 // upstream // 4930 // Hs.292509 // SLC35F5 // 80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 128207 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (ye	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1
SNP_A-1780666	ggatcacttgaggaca[A/G]tataggaaaaccctgt	A	G	NM_025181 // upstream // 32722 // Hs.292509 // SLC35F5 // 80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 100415 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (y	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2117797	aggttgccgggagcta[C/T]aatcatactactgcac	C	T	NM_025181 // upstream // 58649 // Hs.292509 // SLC35F5 // 80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 74488 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (ye	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1
SNP_A-2152711	attaatcttctgatgal[C/T]agcacaattgtcatgg	C	T	NM_025181 // upstream // 65476 // Hs.292509 // SLC35F5 // 80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 67661 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (ye	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1
SNP_A-1800861	gtagagatcatcaggg[C/T]caatgaattacatact	C	T	NM_025181 // upstream // 95488 // Hs.292509 // SLC35F5 // 80255 // Homo sapiens solute carrier family 35, member F5 (SLC35F5), mRNA. /// NM_005721 // upstream // 37649 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (ye	SLC35F5	SLC35F5, Homo sapiens solute carrier family 35, member F5 (SLC35F5), q14.1
SNP_A-2041690	aacgggacaagtggca[C/T]gaactggcagccatc	C	T	NM_005721 // downstream // 24202 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 // upstream // 459989 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-1947390	ttacaccaatattgaa[C/T]actgaagtggtgtcat	C	T	NM_005721 // downstream // 197020 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 // upstream // 287171 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP1	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-2285918	gatgaggtgtacccgaa[C/T]gtgcatttttaaagat	C	T	NM_005721 // downstream // 235652 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 // upstream // 248539 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP1	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-2157772	attgccatggtaagaa[C/T]ggtaacttctgtgag	C	T	NM_005721 // downstream // 241488 // Hs.433512 // ACTR3 // 10096 // Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA. /// NM_001004360 // upstream // 242703 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP1	ACTR3	ACTR3, Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), q14.1
SNP_A-1709403	atcaactaaaggacacacatgcata[A/C]actcaatgtgcaatg atggagtaac	A	C	NM_005721 // downstream // 69675 // Hs.433512 // ACTR3 // 10096 // ARP3 actin-related protein 3 homolog (yeast) /// NM_020868 // upstream // 414502 // Hs.91625 // DPP10 // 57628 // dipeptidylpeptidase 10	ACTR3	ACTR3, rs400960, ARP3 actin-related protein 3 homolog (yeast) q14.1
SNP_A-1964540	gcaaagttgacaagac[A/G]aacagtggagaggtgg	A	G	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1893491	tgcaggaactgggaga[C/T]ggctaagagagtggga	C	T	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1964541	aaaacatcagacgatg[A/G]aacttgatcgaaatct	A	G	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2042540	aactcatgatagatga[C/T]gcttagaagaactgaa	C	T	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1964549	ataacaaaacagggta[A/G]ggaggatagaaaatac	A	G	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1650864	tgtatatggattcctacagtaatgt[A/T]aaaaagtaatgtaattcctaaaaat	A	T	NM_020868 // intron // 0 // Hs.91625 // DPP10 // 57628 // dipeptidylpeptidase 10	DPP10	DPP10 , rs10496472, dipeptidylpeptidase 10,q14.1
SNP_A-1758900	tatgtggttataaaatcaaatggga[A/G]aaaacgactgcaatggtggaaaagg	A	G	NM_020868 // intron // 0 // Hs.91625 // DPP10 // 57628 // dipeptidylpeptidase 10	DPP10	DPP10 , rs10496473, dipeptidylpeptidase 10,q14.1
SNP_A-1804989	gtcatcaggggcatga[A/C]taatatcttaccatag	A	C	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1698043	aggagagtggctactttactggtca[A/C]ccacaatcagcaaatcattggcctc	A	C	NM_020868 // intron // 0 // Hs.91625 // DPP10 // 57628 // dipeptidylpeptidase 10	DPP10	DPP10 , rs10496484, dipeptidylpeptidase 10,q14.1
SNP_A-1822886	taaaaaggaggaaaga[C/T]tctaaaattgatgaga	C	T	NM_001004360 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // intron // 0 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript v	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2191620	catatgtgagccaaag[A/T]cctagaatacgtcatt	A	T	NM_001004360 // downstream // 166547 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 166547 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2066627	acaaaaatcaactcca[C/G]atggattagcaactta	C	G	NM_001004360 // downstream // 205681 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 205681 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2039164	aacagtatatcatgac[C/T]agtgtagatttatgtg	C	T	NM_001004360 // downstream // 214324 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 214324 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1752211	taggatagcggttgcctctgtcagc[A/G]agaagatttgtcagaatttgatgt	A	G	NM_020868 // intron // 0 // Hs.91625 // DPP10 // 57628 // dipeptidylpeptidase 10	DPP10	DPP10 , rs9308717, dipeptidylpeptidase 10,q14.1
SNP_A-2057815	aatattacattcaatc[A/G]acactgacatattaaa	A	G	NM_001004360 // downstream // 303234 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 303234 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1822062	gttttcctggctgaca[C/T]tgatgctagtagatgt	C	T	NM_001004360 // downstream // 350016 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 350016 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2156354	attctcactactctgc[A/G]atgaatgcctcagaat	A	G	NM_001004360 // downstream // 421220 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 421220 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1827723	taactagtttcacaa[A/G]gacagagacctgtct	A	G	NM_001004360 // downstream // 462455 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 462455 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1875810	tctctttgttgtaag[A/T]agagcatggtctcctc	A	T	NM_001004360 // downstream // 524187 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 524187 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1864216	tccaccctatccctaa[C/G]ttacatgcctaagat	C	G	NM_001004360 // downstream // 546703 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 546703 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2246838	ctgtaggagtttcttat[C/T]ctcattgttgctcaag	C	T	NM_001004360 // downstream // 554458 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 554458 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1884447	tgaagtctggtcaac[A/G]atctaccagagtttct	A	G	NM_001004360 // downstream // 583377 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 583377 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1964572	acgggcttggtaactg[A/T]atgttgttgttgctt	A	T	NM_001004360 // downstream // 619789 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 619789 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2314115	ggaggacatctgagtg[A/C]aaagtctggatcataa	A	C	NM_001004360 // downstream // 716530 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 716530 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2053714	aagtggggcaagactc[C/T]gaaagtaggctactat	C	T	NM_001004360 // downstream // 921379 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 921379 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DP	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2280089	gagggaatctctgtc[A/G]ctcaagaatcaatgct	A	G	NM_001004360 // downstream // 1486064 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 1486064 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2127023	ataaataaagaaacaa[G/T]agcattcatgtgcag	G	T	NM_001004360 // downstream // 1502529 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 1502529 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889785	tgatacagcagctgtg[A/G]agaatagtttggtggt	A	G	NM_001004360 // downstream // 1595911 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 1595911 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-2145135	atgcaaggtgaagaa[C/T]gcttggagcctctgc	C	T	NM_001004360 // downstream // 1611877 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 1611877 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1804416	gtcagaaatgtacaaa[A/G]gcataatgtctcatta	A	G	NM_001004360 // downstream // 1917248 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, mRNA. /// NM_020868 // downstream // 1917248 // Hs.176247 // DPP10 // 57628 // Homo sapiens dipeptidylpeptidase 10 (	DPP10	DPP10, Homo sapiens dipeptidylpeptidase 10 (DPP10), transcript variant 2, q14.1
SNP_A-1808375	gtgaaaaatatgaatg[A/C]catacgtgaacaaatg	A	C	NM_016133 // downstream // 311281 // Hs.7089 // INSIG2 // 51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 420896 // Hs.271977 // EN1 // 2019 // Homo sapiens engrailed homolog 1 (EN1), mRNA. /// ENST00000340599 /	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-1796205	ggtgtctgttccatgc[A/G]atgctgggttaccat	A	G	NM_016133 // downstream // 707681 // Hs.7089 // INSIG2 // 51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 24496 // Hs.271977 // EN1 // 2019 // Homo sapiens engrailed homolog 1 (EN1), mRNA. /// ENST00000340599 //	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-1844465	tataaaggaccacccc[A/C]ctaaacacacacatac	A	C	NM_016133 // downstream // 709869 // Hs.7089 // INSIG2 // 51141 // Homo sapiens insulin induced gene 2 (INSIG2), mRNA. /// NM_001426 // downstream // 22308 // Hs.271977 // EN1 // 2019 // Homo sapiens engrailed homolog 1 (EN1), mRNA. /// ENST00000340599 //	INSIG2	INSIG2, Homo sapiens insulin induced gene 2 (INSIG2), q14.2
SNP_A-1914501	tgttaaaaaaaaatgc[A/C]agttgccatctcccac	A	C	NM_182528 // downstream // 93573 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 16939 // -- // -- // -- /// ENST00000357803 // downstream // 61482 /	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2115991	agggttggagagttca[A/C]gaaacagctctgaagtc	A	C	NM_182528 // downstream // 73735 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 36777 // -- // -- // -- /// ENST00000357803 // downstream // 81320 /	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2171051	caatacctatttccaa[A/G]gcagtgaagaaaagca	A	G	NM_182528 // downstream // 49603 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 60909 // -- // -- // -- /// ENST00000357803 // downstream // 105452	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2177211	cacctgctctgtaacc[A/G]ccctcctgccgaact	A	G	NM_182528 // downstream // 44444 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 66068 // -- // -- // -- /// ENST00000357803 // downstream // 110611	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2117636	aggttatgaagaagac[A/G]aaaaaggatgagagct	A	G	NM_182528 // downstream // 33183 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 77329 // -- // -- // -- /// ENST00000357803 // downstream // 121872	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1964663	gcaagaagccagggac[A/C]aatggattgcaatgtt	A	C	NM_182528 // downstream // 4434 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// ENST00000359452 // upstream // 106078 // --- // --- /// --- // --- /// ENST00000357803 // downstream // 150621	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-1964664	tgaccctggatttgac[A/G]aaagctcgctcccact	A	G	NM_182528 // upstream // 16114 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 // upstream // 48805 // Hs.20805 // TSAP6 // 55240 // Homo sapiens dudulin 2 (TSAP6), mRNA. /// NM_01	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2187049	caggtagtacaccaca[C/T]agaaccagactctcag	C	T	NM_182528 // upstream // 59056 // Hs.433493 // C1QL2 // 165257 // Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), mRNA. /// NM_182915 // upstream // 5863 // Hs.20805 // TSAP6 // 55240 // Homo sapiens dudulin 2 (TSAP6), mRNA. /// NM_018	C1QL2	C1QL2, Homo sapiens complement component 1, q subcomponent-like 2 (C1QL2), q14.2
SNP_A-2159026	attgttctgctggact[A/C]agaggactaaacttat	A	C	NM_002980 // intron // 0 // Hs.42091 // SCTR // 6344 // Homo sapiens secretin receptor (SCTR), mRNA. /// ENST00000019103 // intron // 0 // --- // --- // --- // ---	SCTR	SCTR, Homo sapiens secretin receptor (SCTR), q14.2
SNP_A-2309180	ggaaaaataacccaaa[G/T]aaagagatggtggaag	G	T	NM_002980 // intron // 0 // Hs.42091 // SCTR // 6344 // Homo sapiens secretin receptor (SCTR), mRNA. /// ENST00000019103 // intron // 0 // --- // --- // --- // ---	SCTR	SCTR, Homo sapiens secretin receptor (SCTR), q14.2
SNP_A-1883494	tgaaccaacaactgcc[C/T]cctgggaagaaccctt	C	T	NM_002980 // intron // 0 // Hs.42091 // SCTR // 6344 // Homo sapiens secretin receptor (SCTR), mRNA. /// ENST00000019103 // intron // 0 // --- // --- // --- // ---	SCTR	SCTR, Homo sapiens secretin receptor (SCTR), q14.2
SNP_A-2187283	caggtggaattctgga[A/T]cctcaaaagtataaca	A	T	NM_002980 // upstream // 64780 // Hs.42091 // SCTR // 6344 // Homo sapiens secretin receptor (SCTR), mRNA. /// ENST00000019103 // upstream // 64780 // --- // --- // --- // --- /// ENST00000295220 // upstream // 15465 // --- // --- // --- // ---	SCTR	SCTR, Homo sapiens secretin receptor (SCTR), q14.2
SNP_A-1897885	tgctgggttagaagta[A/G]ctttttcaggctcact	A	G	NM_030577 // downstream // 3749 // Hs.439991 // MGC10993 // 80775 // Homo sapiens hypothetical protein MGC10993 (MGC10993), mRNA. /// NM_002830 // upstream // 73764 // Hs.469809 // PTPN4 // 5775 // Homo sapiens protein tyrosine phosphatase, non-receptor t	MGC10993	MGC10993, Homo sapiens hypothetical protein MGC10993 (MGC10993), q14.2
SNP_A-2288488	gattgaataattcaaa[C/G]agatgacgcccttgta	C	G	NM_030577 // downstream // 41893 // Hs.439991 // MGC10993 // 80775 // Homo sapiens hypothetical protein MGC10993 (MGC10993), mRNA. /// NM_002830 // upstream // 35620 // Hs.469809 // PTPN4 // 5775 // Homo sapiens protein tyrosine phosphatase, non-receptor	MGC10993	MGC10993, Homo sapiens hypothetical protein MGC10993 (MGC10993), q14.2
SNP_A-1964670	agccttacacaaagta[A/C]atcatctaacatgttt	A	C	NM_002830 // downstream // 29515 // Hs.469809 // PTPN4 // 5775 // Homo sapiens protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte) (PTPN4), mRNA. /// NM_020909 // upstream // 6117 // Hs.369232 // EPB41L5 // 57669 // Homo sapiens erythrocyte	PTPN4	PTPN4, Homo sapiens protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte) (PTPN4), q14.2
SNP_A-2168443	caacttgcatgacaaa[C/G]agtcccaaagcctaag	C	G	NM_020909 // intron // 0 // Hs.369232 // EPB41L5 // 57669 // Homo sapiens erythrocyte membrane protein band 4.1 like 5 (EPB41L5), mRNA. /// ENST00000263713 // intron // 0 // --- // --- // --- // --- /// ENST00000331393 // 3UTR // 0 // --- // --- // --- // ---	EPB41L5	EPB41L5, Homo sapiens erythrocyte membrane protein band 4.1 like 5 (EPB41L5), q14.2
SNP_A-2267825	gaatccataaaactga[C/T]agccaactcgtgggga	C	T	NM_032845 // CDS // 0 // Hs.334519 // FLJ14816 // 84931 // Homo sapiens hypothetical protein FLJ14816 (FLJ14816), mRNA. /// ENST00000314533 // CDS // 0 // --- // --- // --- // ---	FLJ14816	FLJ14816, Homo sapiens hypothetical protein FLJ14816 (FLJ14816), q14.2
SNP_A-2188784	cagtggcgactcttgc[A/G]ctgactgagtcgccaa	A	G	NM_032845 // upstream // 187744 // Hs.334519 // FLJ14816 // 84931 // Homo sapiens hypothetical protein FLJ14816 (FLJ14816), mRNA. /// NM_030381 // upstream // 143435 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), trans	FLJ14816	FLJ14816, Homo sapiens hypothetical protein FLJ14816 (FLJ14816), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2184292	cagccttccaaatcag[A/G]cactcatgttgccaat	A	G	NM_032845 // upstream // 225651 // Hs.334519 // FLJ14816 // 84931 // Homo sapiens hypothetical protein FLJ14816 (FLJ14816), mRNA. /// NM_030381 // upstream // 105528 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), trans	FLJ14816	FLJ14816, Homo sapiens hypothetical protein FLJ14816 (FLJ14816), q14.2
SNP_A-2280951	gaggtttatttggcaj[A/G]aataataaaaagcac	A	G	NM_030381 // intron // 0 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), trans	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-2029564	aaagactgcaccgttd[A/G]ccatgagattaatgaa	A	G	NM_030381 // intron // 0 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030379 // intron // 0 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), trans	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-1914697	tgttacaaaggtgcad[A/G]aaaagagcatagaggg	A	G	NM_030381 // downstream // 161603 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030381 // downstream // 161547 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-1889306	tgagtggacaataacc[A/G]gacagtccaacgaccc	A	G	NM_030381 // downstream // 163012 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, mRNA. /// NM_030381 // downstream // 162956 // Hs.111867 // GLI2 // 2736 // Homo sapiens GLI-Kruppel family member	GLI2	GLI2, Homo sapiens GLI-Kruppel family member GLI2 (GLI2), transcript variant 3, q14.2
SNP_A-1945243	ttgtgtttggcttcca[C/T]agtagaatgtttcga	C	T	NM_014553 // intron // 0 // Hs.156471 // TFCP2L1 // 29842 // Homo sapiens transcription factor CP2-like 1 (TFCP2L1), mRNA. /// ENST00000263707 // intron // 0 // --- // --- // ---	TFCP2L1	TFCP2L1, Homo sapiens transcription factor CP2-like 1 (TFCP2L1), q14.2
SNP_A-1845845	tatagtccactcaaat[A/G]tggcatgactaatttc	A	G	NM_004622 // downstream // 136678 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2120757 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1866496	tccccaggagtagac[A/G]ctaatggatacctaat	A	G	NM_004622 // downstream // 136900 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2120535 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2136012	atcaagccactcccta[A/T]acaaagcatcagatct	A	T	NM_004622 // downstream // 181005 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2076430 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964690	acctaatccttgagac[C/G]cgagctgttcagctta	C	G	NM_004622 // downstream // 183718 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2073717 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2006660	tatatgtgatttcaa[C/T]ttcctaggcaccactt	C	T	NM_004622 // downstream // 183980 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2073455 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1940267	ttgcatttccaggtta[C/T]gccaggcaacagactc	C	T	NM_004622 // downstream // 185189 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2072246 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1859889	tcaggtaccaacttcca[C/G]gttaaccagcctgg	C	G	NM_004622 // downstream // 187612 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2069823 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964691	aaaaagactggttgaa[C/T]aactgatgacctgaaa	C	T	NM_004622 // downstream // 193525 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2063910 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2216327	cctcctgatctgtcaa[A/G]gtgtctgtacacatgc	A	G	NM_004622 // downstream // 208779 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2048656 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2205297	ccagtcatgcattccaa[C/T]accctggttataatat	C	T	NM_004622 // downstream // 224450 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 2032985 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2211060	cccggactgggaaata[A/T]caggaaaaggataggg	A	T	NM_004622 // downstream // 342624 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1914811 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964694	aaatatggagcaaaga[C/T]acactacagtgaagca	C	T	NM_004622 // downstream // 487996 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1769439 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964717	gactctgggcttata[A/G]gataacatcaatttg	A	G	NM_004622 // downstream // 831056 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1426379 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1792535	ggtaaaagtgaagaaaa[G/T]catgggactgggtgg	G	T	NM_004622 // downstream // 906202 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1351233 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2188199	cagtcctgattactga[A/T]ggacgttgtttgcaac	A	T	NM_004622 // downstream // 906369 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1351066 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2179424	cactgttgaaagaga[A/G]cctagaagcagaagac	A	G	NM_004622 // downstream // 906492 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1350943 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798617	gtaacaattagtgcta[C/T]agtagaaaagacaggt	C	T	NM_004622 // downstream // 920089 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1337346 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964721	cagatcacgtagaggai[C/T]gaacctctatttttt	C	T	NM_004622 // downstream // 926366 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1331069 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2137495	atcatcaacatagaaa[A/G]ttaacagatattcag	A	G	NM_004622 // downstream // 946690 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1310745 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2199126	cattgtttcacccaa[A/G]gttatgctttataaac	A	G	NM_004622 // downstream // 964249 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1293186 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2065642	aatttaggcctgtcc[A/G]cacagattaggagtcc	A	G	NM_004622 // downstream // 964864 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1292571 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2263573	gaaccatctaacccta[C/T]gtagcttgtatatttc	C	T	NM_004622 // downstream // 1114575 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1142860 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1,	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2142672	atgaagacaaatttta[C/T]ggcacatgagagttca	C	T	NM_004622 // downstream // 1137861 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1119574 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1,	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1845901	tatataaatgtaacca[C/T]catcctgtagaagaac	C	T	NM_004622 // downstream // 1188975 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1068460 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1,	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2181685	cagagagaagttgaca[C/T]ccagtctccctaaggg	C	T	NM_004622 // downstream // 1248541 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 1008894 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1,	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1864049	tccacagaaaggaag[A/C]catcaaaattgcatgg	A	C	NM_004622 // downstream // 1278353 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 979082 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1832032	taattgtcccagaaga[A/G]caaaaactggatgtgt	A	G	NM_004622 // downstream // 1369963 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 887472 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2068167	acaagacatttcacag[A/G]agttgattacttgt	A	G	NM_004622 // downstream // 1398191 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 859244 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2045506	aagaatgatttaatga[C/T]gctaatgaaaatgt	C	T	NM_004622 // downstream // 1493370 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 764065 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1933374	ttctaatgttaaagta[C/T]atttcaccatgatct	C	T	NM_004622 // downstream // 1493467 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 763968 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964738	caaggatccatctttta[A/G]ggtgttcagtagggat	A	G	NM_004622 // downstream // 1567000 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 690435 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1964743	gagatttttcaacatc[C/T]gataacctgcatacag	C	T	NM_004622 // downstream // 1754039 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 503396 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1917263	tgttttatttttgtca[C/G]aactcagtcacataac	C	G	NM_004622 // downstream // 1819227 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 438208 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2265150	gaagatggcaaaataa[C/T]gagagaaagataaact	C	T	NM_004622 // downstream // 1888694 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 368741 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1708993	gctgtcttaaatatactcaagtgt[C/G]aaagaaatattgtttagag gtttca	C	G	NM_004622 // downstream // 1516023 // Hs.75066 // TSN // 7247 // translin /// NM_130773 // upstream // 741412 // Hs.437463 // caspr5 // 129684 // caspr5 protein /// NM_138996 // upstream // 741412 // Hs.437463 // caspr5 // 129684 // caspr5 protein	TSN	TSN, rs10496610, translin, q14.3
SNP_A-2298164	gccatctgtaaactca[C/T]gcttcggaaggatcac	C	T	NM_004622 // downstream // 1896420 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 361015 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-2262810	gaaatttatagacaa[G/T]gagaaggtgtagcta	G	T	NM_004622 // downstream // 2106210 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 151225 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3
SNP_A-1818225	gttctgatcagaaata[C/T]agtttttccaaggctg	C	T	NM_004622 // downstream // 2134810 // Hs.75066 // TSN // 7247 // Homo sapiens translin (TSN), mRNA. /// NM_130773 // upstream // 122625 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, m	TSN	TSN, Homo sapiens translin (TSN), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1690503	tatttcatgccaatagagacttaaa[A/T]agagcaacagtagctat aattacat	A	T	NM_004622 // downstream // 1850198 // Hs.75066 // TSN // 7247 // translin /// NM_130773 // upstream // 407237 // Hs.437463 // caspr5 // 129684 // caspr5 protein /// NM_138996 // upstream // 407237 // Hs.437463 // caspr5 // 129684 // caspr5 protein	TSN	TSN , rs4497882, translin ,q14.3
SNP_A-1851764	tattgaaatgtcaagc[C/T]gaatacatttgaagtt	C	T	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2235789	ctcctctcctaacaga[A/G]tagcacacactgatat	A	G	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2264179	gaactggccttgcgca[C/T]ggctctggaagcagga	C	T	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2299720	gccgtactctgagaac[A/C]atgctgtaaagcttct	A	C	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1964778	tcagaggattgtttaa[C/T]gtacacgtgtgtactc	C	T	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2006673	atatgatggtaaatga[A/G]ataatccgggcataga	A	G	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2055316	aataagcagtagagta[G/T]ctcataaacagattaa	G	T	NM_130773 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // intron // 0 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1747695	atttgcttccagaattctgctgttc[A/C]aataagtgtcatgttgtcctttaaa	A	C	NM_130773 // intron // 0 // Hs.437463 // caspr5 // 129684 // caspr5 protein /// NM_138996 // intron // 0 // Hs.437463 // caspr5 // 129684 // caspr5 protein	caspr5	caspr5 , -, caspr5 protein ,q14.3
SNP_A-1694135	tccttgaagagattatgtccctgaa[A/G]agttttaacagtattttattt agtt	A	G	NM_130773 // intron // 0 // Hs.437463 // caspr5 // 129684 // caspr5 protein /// NM_138996 // intron // 0 // Hs.437463 // caspr5 // 129684 // caspr5 protein	caspr5	caspr5 , rs2168024, caspr5 protein ,q14.3
SNP_A-1918263	ttaaagcacacaaagt[A/G]aagggctgaatctgga	A	G	NM_130773 // downstream // 1079823 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1079823 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2056721	aatagcgaagtgggta[C/T]aagcatgtttcattta	C	T	NM_130773 // downstream // 1136071 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1136071 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2220766	ccttgagtcctataca[A/T]gtggctccacaattac	A	T	NM_130773 // downstream // 1308185 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1308185 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1877762	tctgggtgcttgttcc[A/G]cttccttgtgcattcc	A	G	NM_130773 // downstream // 1314007 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1314007 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2033535	aaatatactaactgga[C/T]gaatcagcctattgat	C	T	NM_130773 // downstream // 1322102 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1322102 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-1887442	tgagacatctaaaaag[A/T]actccatccagcgttc	A	T	NM_130773 // downstream // 1336219 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1336219 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2234209	ctcatttcatggatca[A/G]tacaagataatccaga	A	G	NM_130773 // downstream // 1490170 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1490170 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2176829	caccctcaaagtcac[A/G]caaccaattctgaatt	A	G	NM_130773 // downstream // 1510811 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, mRNA. /// NM_138996 // downstream // 1510811 // Hs.21975 // CNTNAP5 // 129684 // Homo sapiens contacti	CNTNAP5	CNTNAP5, Homo sapiens contactin associated protein-like 5 (CNTNAP5), transcript variant 1, q14.3
SNP_A-2242941	ctgccatcaggagcac[A/G]ctgtgtaaccgacaag	A	G	NM_002101 // intron // 0 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // intron // 0 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2219837	ccttagaaattttcca[C/G]gtaaagaccagcattt	C	G	NM_002101 // intron // 0 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // intron // 0 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1781692	ggattgtgactcagta[C/T]gatggagagatgagat	C	T	NM_002101 // downstream // 72855 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 72855 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich bl	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1786661	ggcttgcctggcacca[C/T]tggagcaggtcttggc	C	T	NM_002101 // downstream // 77584 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 77584 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich bl	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1892696	tgcacacacaaaagaa[C/T]gccctgacaagtgcac	C	T	NM_002101 // downstream // 87214 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 87214 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich bl	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2139375	atcctgtctcactcac[C/T]gctaaccctgggcctg	C	T	NM_002101 // downstream // 89523 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 89523 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich bl	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2006677	tactcacttcgaggga[C/G]tgcataaggaaagcc	C	G	NM_002101 // downstream // 95303 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 95303 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich bl	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2006679	acagaatcaggaataa[C/T]caaaatacatgattcc	C	T	NM_002101 // downstream // 102173 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 102173 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2006680	agttaggtgctaattc[A/G]ctccggccaggcttc	A	G	NM_002101 // downstream // 102303 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 102303 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2029485	aaagaccagaaggaaa[A/G]ctaggttccaattgttt	A	G	NM_002101 // downstream // 104235 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 104235 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2095819	agacagacagctcaac[A/G]aggctactataagca	A	G	NM_002101 // downstream // 123839 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 123839 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-2252424	cttcctaggactaaga[A/G]tcgggtggaagatgggt	A	G	NM_002101 // downstream // 124310 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA. /// NM_016815 // downstream // 124310 // Hs.59138 // GYPC // 2995 // Homo sapiens glycophorin C (Gerbich	GYPC	GYPC, Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, q14.3
SNP_A-1782773	ggcagaagggtcaaca[C/G]taacaacagtcaaaa	C	G	NM_139351 // intron // 0 // Hs.193163 // BIN1 // 274 // Homo sapiens bridging integrator 1 (BIN1), transcript variant 10, mRNA. /// NM_139349 // intron // 0 // Hs.193163 // BIN1 // 274 // Homo sapiens bridging integrator 1 (BIN1), transcript variant 7, mR	BIN1	BIN1, Homo sapiens bridging integrator 1 (BIN1), transcript variant 10, q14.3
SNP_A-1723668	ggttgatcaggcttatgacgttcacg[A/G]gacccgggcagtgag tgtatgtgc	A	G	NM_004305 // intron // 0 // Hs.193163 // BIN1 // 274 // bridging integrator 1 /// NM_139343 // intron // 0 // Hs.193163 // BIN1 // 274 // bridging integrator 1 /// NM_139344 // intron // 0 // Hs.193163 // BIN1 // 274 // bridging integrator 1 /// NM_13934	BIN1	BIN1, rs873270, bridging integrator 1, q14.3
SNP_A-2293837	gcagctgcaaggtgac[C/T]atatgagtgcggagg	C	T	ENST00000272666 // intron // 0 // — // — // —	-	q14.3
SNP_A-1916013	tgttgcaggttaggga[A/G]tcaaggctgagtgtct	A	G	NM_017980 // intron // 0 // Hs.469881 // LIMS2 // 55679 // Homo sapiens LIM and senescent cell antigen-like domains 2 (LIMS2), mRNA. /// NM_005291 // intron // 0 // Hs.46453 // GPR17 // 2840 // Homo sapiens G protein-coupled receptor 17 (GPR17), mRNA. ///	LIMS2	LIMS2, Homo sapiens LIM and senescent cell antigen-like domains 2 (LIMS2), q14.3
SNP_A-2172565	caattctgaggaagaa[A/G]aaaatgctagcatgga	A	G	NM_031445 // intron // 0 // Hs.546449 // MGC4268 // 83607 // Homo sapiens hypothetical protein MGC4268 (MGC4268), mRNA. /// ENST00000272647 // intron // 0 // — // — // —	MGC4268	MGC4268, Homo sapiens hypothetical protein MGC4268 (MGC4268), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2304061	gctccaggaattcaca[A/G]ctttctcctgcatcat	A	G	NM_024545 // intron // 0 // Hs.32995 // SAP130 // 79595 // Homo sapiens mSin3A-associated protein 130 (SAP130), mRNA. /// ENST00000357702 // intron // 0 // — // — // — // — /// ENST00000259235 // intron // 0 // — // — // — // —	SAP130	SAP130, Homo sapiens mSin3A-associated protein 130 (SAP130), q14.3
SNP_A-1888840	tgaggtacaaatccaa[C/T]agagctttaatcccaa	C	T	NM_020120 // 3UTR // 0 // Hs.34180 // UGCGL1 // 56886 // Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), mRNA. /// ENST00000259253 // 3UTR // 0 // — // — // — // —	UGCGL1	UGCGL1, Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), q14.3
SNP_A-1796142	ggtgtcaccattgctc[C/T]atgattaatccagcaa	C	T	NM_020120 // downstream // 67153 // Hs.34180 // UGCGL1 // 56886 // Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), mRNA. /// NM_004807 // downstream // 9609 // Hs.512841 // HS6ST1 // 9394 // Homo sapiens heparan sulfate 6-O-sulfotra	UGCGL1	UGCGL1, Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), q14.3
SNP_A-2130151	ataccgcatccagaga[A/G]gtcgcagagccacagc	A	G	NM_004807 // intron // 0 // Hs.512841 // HS6ST1 // 9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // intron // 0 // — // — // — // —	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-2252739	cttcgtttctgtggca[C/T]gcgacagtttccacct	C	T	NM_004807 // intron // 0 // Hs.512841 // HS6ST1 // 9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // intron // 0 // — // — // — // —	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-2222537	cgaggtaagcctcaat[A/G]agcaggagacatttca	A	G	NM_004807 // upstream // 240974 // Hs.512841 // HS6ST1 // 9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // upstream // 240974 // — // — // — // — /// ENST00000356393 // downstream // 323367 // —	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-2190918	catagcccttgtcacc[A/G]cctcataaatcatttg	A	G	NM_004807 // upstream // 406975 // Hs.512841 // HS6ST1 // 9394 // Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), mRNA. /// ENST00000259241 // upstream // 406975 // — // — // — // — /// ENST00000356393 // downstream // 157366 // —	HS6ST1	HS6ST1, Homo sapiens heparan sulfate 6-O-sulfotransferase 1 (HS6ST1), q14.3
SNP_A-2155147	attcagattctatctc[A/G]agaggaacacggtctg	A	G	NM_032144 // upstream // 970898 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 125794 // — // — // — // — /// ENST00000328893 // upstream // 970898 // — // — /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q14.3
SNP_A-1898927	tgctttttaatatttc[A/G]catcaggagacatact	A	G	NM_032144 // upstream // 774371 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 322321 // — // — // — // — /// ENST00000328893 // upstream // 774371 // — // — /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-1964840	tctccaaaagacataa[C/G]gtaaagccctattcag	C	G	NM_032144 // upstream // 773399 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 323293 // — // — // — // — /// ENST00000328893 // upstream // 773399 // — // — /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2302355	gctaagcattctcaga[A/G]gacaaataaaaaccat	A	G	NM_032144 // upstream // 769601 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 327091 // — // — // — // — /// ENST00000328893 // upstream // 769601 // — // — /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2087793	actggaagttagatgt[A/T]aagagttgattgtaca	A	T	NM_032144 // upstream // 769208 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 327484 // — // — // — // — /// ENST00000328893 // upstream // 769208 // — // — /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2184260	cagcctggggaagtac[A/G]aggctcaatttagatc	A	G	NM_032144 // upstream // 766516 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 330176 // --- // --- // --- // --- /// ENST00000328893 // upstream // 766516 // --- // --- /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2294185	gcaggctgtcgcggga[C/T]gagttgatgttacagc	C	T	NM_032144 // upstream // 757645 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 339047 // --- // --- // --- // --- /// ENST00000328893 // upstream // 757645 // --- // --- /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2297770	gccaggatggttctgc[A/G]actttatgaaggaaga	A	G	NM_032144 // upstream // 705588 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 391104 // --- // --- // --- // --- /// ENST00000328893 // upstream // 705588 // --- // --- /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-1898704	tgctttagcaacacta[A/C]ctcctagacttctcag	A	C	NM_032144 // upstream // 677078 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 419614 // --- // --- // --- // --- /// ENST00000328893 // upstream // 677078 // --- // --- /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-1851185	tattcacaaatcatca[A/C]gtattgtcccaaattt	A	C	NM_032144 // upstream // 649571 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 447121 // --- // --- // --- // --- /// ENST00000328893 // upstream // 649571 // --- // --- /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2262986	gaacaataaatcacaa[A/G]taaaattggacaatac	A	G	NM_032144 // upstream // 482125 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000356393 // upstream // 614567 // --- // --- // --- // --- /// ENST00000328893 // upstream // 482125 // --- // --- /	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-1683854	tgtttcgagcttctgtgctttcaag[A/T]ctacagtaatttatcttgtgcacag	A	T	NM_004807 // upstream // 945237 // Hs.512841 // HS6ST1 // 9394 // heparan sulfate 6-O-sulfotransferase 1 /// NM_032144 // upstream // 715748 // Hs.440748 // RAB6C // 84084 // RAB6C, member RAS oncogene family	HS6ST1	HS6ST1 , rs837903, heparan sulfate 6-O-sulfotransferase 1 ,q21.1
SNP_A-1734002	tattttattttcctaattggcatac[C/T]ttttattttgttttcttgtataatt	C	T	NM_004807 // upstream // 1194954 // Hs.512841 // HS6ST1 // 9394 // heparan sulfate 6-O-sulfotransferase 1 /// NM_032144 // upstream // 466031 // Hs.440748 // RAB6C // 84084 // RAB6C, member RAS oncogene family	HS6ST1	HS6ST1 , rs1349734, heparan sulfate 6-O-sulfotransferase 1 ,q21.1
SNP_A-2006702	aggggagatgagaaca[A/G]cggggcagaaagaagg	A	G	NM_015320 // intron // 0 // Hs.469935 // ARHGEF4 // 50649 // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 4 (ARHGEF4), transcript variant 1, mRNA. /// NM_032995 // intron // 0 // Hs.469935 // ARHGEF4 // 50649 // Homo sapiens Rho guanine nucle	ARHGEF4	ARHGEF4, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 4 (ARHGEF4), transcript variant 1, q21.1
SNP_A-1951731	tttcgaacctctggga[A/C]tacatctctatggctt	A	C	ENST00000354183 // intron // 0 // --- // --- // --- // --- /// ENST00000342042 // intron // 0 // --- // --- // --- // --- /// ENST00000281893 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2034024	aaatcagagataaaga[C/T]gcaagaaagagaattc	C	T	NM_032144 // upstream // 44915 // Hs.440748 // RAB6C // 84084 // Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA. /// ENST00000320501 // upstream // 44915 // --- // --- // --- // --- /// ENST00000341700 // downstream // 15171 // --- // --- //	RAB6C	RAB6C, Homo sapiens RAB6C, member RAS oncogene family (RAB6C), q21.1
SNP_A-2276680	gagagtgcccacctcc[A/G]aggtaagagggttatt	A	G	ENST00000355473 // upstream // 155610 // --- // --- // --- // --- /// ENST00000357025 // upstream // 118118 // --- // --- // --- // ---	-	q21.2
SNP_A-1945057	ttgtgtagggaagaga[A/C]gagaaccacattgcat	A	C	NM_001508 // intron // 0 // Hs.534317 // GPR39 // 2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1808611	gtgaacagctctataa[C/T]gctcatctttattga	C	T	NM_001508 // intron // 0 // Hs.534317 // GPR39 // 2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-2212904	ccctttggccgtcaga[C/T]atacagcaagtgctca	C	T	NM_001508 // intron // 0 // Hs.534317 // GPR39 // 2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-1964877	agcataccactactta[A/G]gctgtccatatactgt	A	G	NM_001508 // intron // 0 // Hs.534317 // GPR39 // 2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-1855354	tcaaggctttgctgta[C/T]gtttgaaccactgaac	C	T	NM_001508 // intron // 0 // Hs.534317 // GPR39 // 2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-1929802	ttcatccctactcaag[A/G]ccagttaaatcagaac	A	G	NM_001508 // intron // 0 // Hs.534317 // GPR39 // 2863 // Homo sapiens G protein-coupled receptor 39 (GPR39), mRNA. /// ENST00000329321 // intron // 0 // --- // --- // --- // ---	GPR39	GPR39, Homo sapiens G protein-coupled receptor 39 (GPR39), q21.2
SNP_A-2253076	cttctctcccgcat[C/T]atcgatttcgccctct	C	T	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1964890	tgttgcctagtttaa[A/T]tcttcttgcaacatca	A	T	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1856168	tcacaaattcaccttg[A/G]cttaaattggtcaaag	A	G	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2027334	aaacatgaaacttac[A/G]attggaaaaatacaca	A	G	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1838799	tagactaagggagcgc[C/T]gagtattaaacaggtt	C	T	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1781966	ggcaaactgtgaaata[C/T]gaagcagcagtcatct	C	T	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1710912	ggggtcttatgacctatagcaaaca[A/T]gacaggtcagataattt ccttatgg	A	T	AK092189 // intron // 0 // Hs.61172 // FLJ34870 // 401013 // FLJ34870 protein	FLJ34870	FLJ34870 , rs1005941, FLJ34870 protein.q21.2
SNP_A-2308927	gcttttaagcatttag[A/G]caccatcatataaatc	A	G	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2195173	catggaggagaaaaca[C/T]ggaatagatcacacag	C	T	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2194219	catgagccagctaaag[A/G]acataggatcaagtgt	A	G	NM_207481 // intron // 0 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// ENST00000358991 // intron // 0 // --- // --- // --- // ---	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1869869	tcctctactccaagc[C/T]agagcactagaatgta	C	T	NM_207481 // upstream // 492 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 682645 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gluco	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2065186	aattggagactacttat[G/T]aggcaataatctctacc	G	T	NM_207481 // upstream // 101943 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 581194 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140985	atctgcaacatctgta[G/T]caaaggccctaatatc	G	T	NM_207481 // upstream // 102419 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 580718 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2006722	ttctaatttttcatttta[C/G]agtcacaagttgctta	C	G	NM_207481 // upstream // 403180 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 279957 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1859810	tcagggaaatccagc[C/T]gaaattttgtccatt	C	T	NM_207481 // upstream // 405028 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 278109 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-2199594	ccaaaacagtgacttc[A/G]cccgtaagaacatttt	A	G	NM_207481 // upstream // 405094 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 278043 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1964937	aggaatagaataatca[C/T]ggctgaaaatgtaatc	C	T	NM_207481 // upstream // 430596 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 252541 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1935400	ttctggagtattgtgt[A/G]aagatgagtaagagtg	A	G	NM_207481 // upstream // 450002 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 233135 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1900254	tggagaagtgacccaa[A/G]gaacaagggcgaggga	A	G	NM_207481 // upstream // 466188 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 216949 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1900304	tggagacctctgaa[A/G]ctgtctgtaagatga	A	G	NM_207481 // upstream // 466500 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 216637 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1938867	ttgaggctcatctaa[C/T]ggtagtactgatttt	C	T	NM_207481 // upstream // 490985 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 192152 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1945177	ttgtgttagaatgaca[A/G]taggcttcaaatgatc	A	G	NM_207481 // upstream // 499976 // Hs.270083 // FLJ34870 // 401013 // Homo sapiens FLJ34870 protein (FLJ34870), mRNA. /// NM_002410 // upstream // 183161 // Hs.115903 // MGAT5 // 4249 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-gl	FLJ34870	FLJ34870, Homo sapiens FLJ34870 protein (FLJ34870), q21.2
SNP_A-1652148	ctcaccagtacattcccattcataa[G/T]cctcttacctttccacca tgacc	G	T	AF251048 // downstream // 901413 // - // - // Homo sapiens connexin mRNA, complete cds. /// NM_002410 // upstream // 231133 // Hs.397624 // MGAT5 // 4249 // mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	-	- . rs6740690, Homo sapiens connexin mRNA, complete cds. q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1751917	gctttgttcattctataattcctaa[C/T]tctaatatcatcgtctccagg attc	C	T	AF251048 // downstream // 901508 // - // - // - // Homo sapiens connexin mRNA, complete cds. /// NM_002410 // upstream // 231038 // Hs.397624 // MGAT5 // 4249 // mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	-	- , rs6743570, Homo sapiens connexin mRNA, complete cds. ,q21.2
SNP_A-1964967	cctgaccatcacagac[G/T]caggtgccaagaacaa	G	T	NM_030923 // intron // 0 // Hs.369471 // DKFZP566N034 // 81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // intron // 0 // — // — // — // — /// ENST00000281924 // intron // 0 // — // — // — // — /	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-1861265	tcatattttgcaacta[A/G]ctgatcatctaacagt	A	G	NM_030923 // intron // 0 // Hs.369471 // DKFZP566N034 // 81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // intron // 0 // — // — // — // — /// ENST00000281924 // intron // 0 // — // — // — // — /	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-2212853	ccctttcctccttaaa[C/T]gttggtgaactgagag	C	T	NM_030923 // intron // 0 // Hs.369471 // DKFZP566N034 // 81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // intron // 0 // — // — // — // — /// ENST00000281924 // intron // 0 // — // — // — // — /	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-1809317	gtgactgaattaaaca[A/C]atcccaaagcctgccc	A	C	ENST00000338200 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-2195598	catggtgaaactaaaa[C/T]actcttctctactaaa	C	T	ENST00000338200 // intron // 0 // — // — // — // — /// ENST00000358529 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-2072518	acagcattgtcctatc[A/G]gaactattgtttacag	A	G	ENST00000338200 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-2229014	ctagcactgtaagata[A/G]taagagtgtgttgttc	A	G	NM_030923 // upstream // 63397 // Hs.369471 // DKFZP566N034 // 81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // upstream // 14627 // - // — // — // — /// ENST00000281924 // upstream // 63397 // -	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-2255963	ctttaagaatgtttaa[C/T]ggacaaccacttggaa	C	T	NM_030923 // upstream // 102200 // Hs.369471 // DKFZP566N034 // 81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // upstream // 53430 // - // — // — // — /// ENST00000281924 // upstream // 102200 //	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-1957159	ttttaccatttaggga[C/T]agtagtagtcaggaga	C	T	NM_030923 // upstream // 104942 // Hs.369471 // DKFZP566N034 // 81615 // Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), mRNA. /// ENST00000338200 // upstream // 56172 // - // — // — // — /// ENST00000281924 // upstream // 104942 //	DKFZP566N034	DKFZP566N034, Homo sapiens hypothetical protein DKFZp566N034 (DKFZP566N034), q21.3
SNP_A-1890052	tgatatcacaatctac[A/T]catggattgcaaccca	A	T	NM_138326 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxy	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-2223549	cggaagtatgtatgaa[C/G]aggtgatatttccact	C	G	NM_138326 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxy	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-2163386	atttttgtgagatgc[A/G]cactttactaccctc	A	G	NM_138326 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxy	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3
SNP_A-2135570	atattttctttccaac[A/C]ggcacctattatcaga	A	C	NM_138326 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), mRNA. /// BC016018 // intron // 0 // Hs.146022 // ACMSD // 130013 // Homo sapiens aminocarboxymuconate semialdehyde decarboxy	ACMSD	ACMSD, Homo sapiens aminocarboxymuconate semialdehyde decarboxylase (ACMSD), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1961121	tttttgttgttgttaa[A/G]gaatcttgctctgtcg	A	G	NM_001241 // downstream // 5122 // Hs.292754 // CCNT2 // 905 // Homo sapiens cyclin T2 (CCNT2), transcript variant a, mRNA. /// NM_058241 // downstream // 5022 // Hs.292754 // CCNT2 // 905 // Homo sapiens cyclin T2 (CCNT2), transcript variant b, mRNA. ///	CCNT2	CCNT2, Homo sapiens cyclin T2 (CCNT2), transcript variant a, q21.3
SNP_A-2157247	attgacaggacatcac[A/G]acattatgaaaatcca	A	G	NM_001241 // downstream // 6938 // Hs.292754 // CCNT2 // 905 // Homo sapiens cyclin T2 (CCNT2), transcript variant a, mRNA. /// NM_058241 // downstream // 6838 // Hs.292754 // CCNT2 // 905 // Homo sapiens cyclin T2 (CCNT2), transcript variant b, mRNA. ///	CCNT2	CCNT2, Homo sapiens cyclin T2 (CCNT2), transcript variant a, q21.3
SNP_A-1892617	tgcaattccatagctt[C/G]aaatgtctccttacag	C	G	NM_001241 // downstream // 24020 // Hs.292754 // CCNT2 // 905 // Homo sapiens cyclin T2 (CCNT2), transcript variant a, mRNA. /// NM_058241 // downstream // 23920 // Hs.292754 // CCNT2 // 905 // Homo sapiens cyclin T2 (CCNT2), transcript variant b, mRNA. /	CCNT2	CCNT2, Homo sapiens cyclin T2 (CCNT2), transcript variant a, q21.3
SNP_A-1828766	taagcttttaagtaca[A/G]tacactcttctaaaat	A	G	NM_025052 // 5UTR // 0 // Hs.503776 // FLJ23074 // 80122 // Homo sapiens hypothetical protein FLJ23074 (FLJ23074), mRNA. /// ENST00000315513 // 5UTR // 0 // — // — // — // —	FLJ23074	FLJ23074, Homo sapiens hypothetical protein FLJ23074 (FLJ23074), q21.3
SNP_A-2193719	catcttgtgactgcta[C/T]agctgaaatgactgtt	C	T	ENST00000264158 // intron // 0 // — // --- // — // —	-	q21.3
SNP_A-1906194	tggtgacaaagaaaga[A/C]cctgcttcagaaagaa	A	C	ENST00000283060 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-1782289	ggcaatacctagtgct[C/G]acaaagatatcaaatg	C	G	ENST00000283060 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-2049118	aagcgttcggcaatag[C/T]agacgtgaaaataaaa	C	T	ENST00000283060 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-1871291	tctaaactaactgaaa[C/T]gaaaagcagcagaagt	C	T	ENST00000283060 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-1815664	gttaacagagaatgcc[C/T]aaaactggaaaaacaa	C	T	ENST00000283060 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-2278323	gagcgtaggaggcagc[C/T]attttaacaatgaaaa	C	T	ENST00000283060 // intron // 0 // — // — // — // —	-	q21.3
SNP_A-2194354	catgatcactgaagac[C/T]gcaacaataaagagaa	C	T	D21852 // intron // 0 // Hs.412462 // R3HDM // 23518 // Homo sapiens KIAA0029 mRNA, partial cds. /// NM_015361 // intron // 0 // Hs.412462 // R3HDM // 23518 // Homo sapiens R3H domain (binds single-stranded nucleic acids) containing (R3HDM), mRNA. /// ENS	R3HDM	R3HDM, Homo sapiens KIAA0029 partial cds. q21.3
SNP_A-2295479	gcatctacattgatga[C/G]tatctcttactaatct	C	G	NM_014607 // intron // 0 // Hs.350806 // UBXD2 // 23190 // Homo sapiens UBX domain containing 2 (UBXD2), mRNA. /// ENST00000272638 // intron // 0 // — // — // — // ---	UBXD2	UBXD2, Homo sapiens UBX domain containing 2 (UBXD2), q21.3
SNP_A-2067262	acaaagggctcattca[A/G]cgtgatccaaaacttc	A	G	NM_002299 // CDS // 0 // Hs.2251 // LCT // 3938 // Homo sapiens lactase (LCT), mRNA. /// ENST00000264162 // CDS // 0 // — // — // — // ---	LCT	LCT, Homo sapiens lactase (LCT), q21.3
SNP_A-2045698	aagacaatattcaagg[G/T]caatctaatacagaga	G	T	NM_002299 // intron // 0 // Hs.2251 // LCT // 3938 // Homo sapiens lactase (LCT), mRNA. /// ENST00000264162 // intron // 0 // --- // --- // — // —	LCT	LCT, Homo sapiens lactase (LCT), q21.3
SNP_A-1741139	tttcttcttcaggttaatctgcatg[A/G]aaatccaaactattaattag aaggc	A	G	NM_015361 // intron // 0 // Hs.144476 // R3HDM // 23518 // R3H domain (binds single-stranded nucleic acids) containing	R3HDM	R3HDM , rs4954265, R3H domain (binds single-stranded nucleic acids) containing,q21.3
SNP_A-1745136	aatctctgatacattaatccagtgc[A/G]aaaccagtgattttcttaa actcac	A	G	NM_015361 // intron // 0 // Hs.144476 // R3HDM // 23518 // R3H domain (binds single-stranded nucleic acids) containing	R3HDM	R3HDM , rs7608702, R3H domain (binds single-stranded nucleic acids) containing,q21.3
SNP_A-1836051	tactacagagattcac[C/T]gaggtagacactgctg	C	T	NM_001349 // upstream // 63552 // Hs.503787 // DARS // 1615 // Homo sapiens aspartyl-tRNA synthetase (DARS), mRNA. /// NM_003467 // downstream // 65665 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENS	DARS	DARS, Homo sapiens aspartyl-tRNA synthetase (DARS), q21.3
SNP_A-2099998	agagtctgaataaaac[C/G]atgatagaaataagga	C	G	NM_003467 // upstream // 114239 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 114239 // --- // --- // — // — /// ENST00000272643 // upstream // 826318 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1875317	tctctgaagcacaaag[A/T]aagattacaagttcca	A	T	NM_003467 // upstream // 184924 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 184924 // --- // --- // --- // --- /// ENST00000272643 // upstream // 755633 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-1714186	ttttcatctgccttttatctgaggc[A/G]atgccaatggttttacagtac gcag	A	G	NM_001349 // upstream // 8852 // Hs.32393 // DARS // 1615 // aspartyl-tRNA synthetase /// NM_003467 // downstream // 119938 // Hs.421986 // CXCR4 // 7852 // chemokine (C-X-C motif) receptor 4	DARS	DARS , rs10496739, aspartyl-tRNA synthetase ,q21.3
SNP_A-1796653	ggttaggatttgggca[A/C]agagaatacaacagga	A	C	NM_003467 // upstream // 281843 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 281843 // --- // --- // --- // --- /// ENST00000272643 // upstream // 658714 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2292962	gcagaagctcttctgc[A/G]aataaaccatgaagtt	A	G	NM_003467 // upstream // 592113 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 592113 // --- // --- // --- // --- /// ENST00000272643 // upstream // 348444 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-2089532	acttcaagtataggta[C/T]gttgttaatgcagaaa	C	T	NM_003467 // upstream // 637769 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 637769 // --- // --- // --- // --- /// ENST00000272643 // upstream // 302788 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-1964994	tcgtttgcttactctc[C/T]gacacttgttccaaac	C	T	NM_003467 // upstream // 648535 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 648535 // --- // --- // --- // --- /// ENST00000272643 // upstream // 292022 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q21.3
SNP_A-1943413	ttggttggttatttaa[C/T]gtgaaagagatgtgta	C	T	NM_003467 // upstream // 707171 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 707171 // --- // --- // --- // --- /// ENST00000272643 // upstream // 233386 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q22.1
SNP_A-1965003	caaaggctttttagta[C/T]gtggagaagaatcaaa	C	T	NM_003467 // upstream // 794681 // Hs.421986 // CXCR4 // 7852 // Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), mRNA. /// ENST00000241393 // upstream // 794681 // --- // --- // --- // --- /// ENST00000272643 // upstream // 145876 // --- // --- /	CXCR4	CXCR4, Homo sapiens chemokine (C-X-C motif) receptor 4 (CXCR4), q22.1
SNP_A-2154076	attatcatatattctc[A/G]aactgtacttgtattt	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1965009	aaaggtaggccttcta[A/T]gctattctggagtaag	A	T	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1965010	gaaatcataggtgtag[A/G]agaaagtcagcaaagg	A	G	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1929845	ttcatctcattactgc[A/C]agtttgtacgctttga	A	C	ENST00000272643 // intron // 0 // --- // --- // --- // ---	-	q22.1
SNP_A-1745670	taaatacatagatgtgtaacacgac[C/T]gtatactcctgtacaga gctgaata	C	T	AB051466 // intron // 0 // Hs.68533 // KIAA1679 // 80731 // KIAA1679 protein	KIAA1679	KIAA1679 , rs1432216, KIAA1679 protein,q22.1
SNP_A-1693863	gcttggttcaaatctgctccatcca[C/T]aggttcctgtcctcaggat tcttca	C	T	AB051466 // intron // 0 // Hs.68533 // KIAA1679 // 80731 // KIAA1679 protein	KIAA1679	KIAA1679 , rs2375116, KIAA1679 protein,q22.1
SNP_A-1914623	tgttaagtatttcacc[A/G]acaggtacaggttata	A	G	NM_006895 // upstream // 15216 // Hs.42151 // HNMT // 3176 // Homo sapiens histamine N-methyltransferase (HNMT), mRNA. /// ENST00000272643 // downstream // 271305 // --- // --- // --- // --- /// ENST00000280097 // upstream // 15216 // --- // --- // --- //	HNMT	HNMT, Homo sapiens histamine N-methyltransferase (HNMT), q22.1
SNP_A-1881217	tctttatatctgcaca[C/T]tgtatatctgcttatg	C	T	NM_006895 // downstream // 207338 // Hs.42151 // HNMT // 3176 // Homo sapiens histamine N-methyltransferase (HNMT), mRNA. /// NM_001001664 // upstream // 279797 // Hs.333297 // LOC339745 // 339745 // Homo sapiens hypothetical protein LOC339745 (LOC339745)	HNMT	HNMT, Homo sapiens histamine N-methyltransferase (HNMT), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1757775	tctctcttccgattccatcatagaa[A/C]aaaactgaaagaaggccacagaacac	A	C	AB051466 // downstream // 200753 // Hs.68533 // KIAA1679 // 80731 // KIAA1679 protein /// NM_006895 // upstream // 85768 // Hs.42151 // HNMT // 3176 // histamine N-methyltransferase	KIAA1679	KIAA1679 , rs10496793, KIAA1679 protein ,q22.1
SNP_A-2310173	ggaacagaatgcacca[C/T]aggaacagtaagttca	C	T	NM_001001664 // downstream // 2134 // Hs.333297 // LOC339745 // 339745 // Homo sapiens hypothetical protein LOC339745 (LOC339745), mRNA. /// NM_007226 // downstream // 95561 // Hs.435019 // NXPH2 // 11249 // Homo sapiens neurexophilin 2 (NXPH2), mRNA. ///	LOC339745	LOC339745, Homo sapiens hypothetical protein LOC339745 (LOC339745), q22.1
SNP_A-2114234	agggaagacaggaaaa[A/T]catcatatgagcccag	A	T	NM_007226 // upstream // 169355 // Hs.435019 // NXPH2 // 11249 // Homo sapiens neurexophilin 2 (NXPH2), mRNA. /// ENST00000272641 // upstream // 169355 // — // — // — // ENST00000325635 // downstream // 60401 // — // — // —	NXPH2	NXPH2, Homo sapiens neurexophilin 2 (NXPH2), q22.1
SNP_A-1815953	gttaattgaagctcga[A/T]atgctaactaagaaac	A	T	NM_007226 // upstream // 208926 // Hs.435019 // NXPH2 // 11249 // Homo sapiens neurexophilin 2 (NXPH2), mRNA. /// ENST00000272641 // upstream // 208926 // — // — // — // ENST00000325635 // downstream // 20830 // — // — // —	NXPH2	NXPH2, Homo sapiens neurexophilin 2 (NXPH2), q22.1
SNP_A-1965064	ctagacatggaaaggaa[A/C]ctaatactccacagtc	A	C	NM_007226 // upstream // 215625 // Hs.435019 // NXPH2 // 11249 // Homo sapiens neurexophilin 2 (NXPH2), mRNA. /// ENST00000272641 // upstream // 215625 // — // — // — // ENST00000325635 // downstream // 14131 // — // — // —	NXPH2	NXPH2, Homo sapiens neurexophilin 2 (NXPH2), q22.1
SNP_A-2116231	aggtacatcatctgct[C/T]aatgcaccacaggtac	C	T	ENST00000325635 // CDS // 0 // — // — // —	-	q22.1
SNP_A-1925941	ttatggttcttttgta[C/T]gggagcctccaatgtc	C	T	ENST00000325635 // upstream // 28549 // — // — // — /// ENST00000355063 // upstream // 890108 // — // — // —	-	q22.1
SNP_A-1830423	taatattggtgatata[C/T]agttaatgggatttca	C	T	ENST00000325635 // upstream // 162580 // — // — // — /// ENST00000355063 // upstream // 756077 // — // — // —	-	q22.1
SNP_A-2161664	atttgggtatttaa[C/T]tgctgtatagagatag	C	T	ENST00000325635 // upstream // 194866 // — // — // — /// ENST00000355063 // upstream // 723791 // — // — // —	-	q22.1
SNP_A-2146524	atgctgagcagaaact[A/G]acctattaagacttc	A	G	ENST00000325635 // upstream // 196471 // — // — // — /// ENST00000355063 // upstream // 722186 // — // — // —	-	q22.1
SNP_A-2024793	aaaagtgaaggaatgc[C/G]acttctgaggaggtga	C	G	ENST00000325635 // upstream // 220255 // — // — // — /// ENST00000355063 // upstream // 698402 // — // — // —	-	q22.1
SNP_A-2053578	aagtgcttacatgcta[A/G]aattaggaccaggttc	A	G	ENST00000325635 // upstream // 276498 // — // — // — /// ENST00000355063 // upstream // 642159 // — // — // —	-	q22.1
SNP_A-2056564	aatagataacctcaa[A/G]aattgtgattgaggt	A	G	ENST00000325635 // upstream // 280350 // — // — // — /// ENST00000355063 // upstream // 638307 // — // — // —	-	q22.1
SNP_A-2091144	acttttgtaagctcta[G/T]attatgaacaaaacac	G	T	ENST00000325635 // upstream // 281650 // — // — // — /// ENST00000355063 // upstream // 637007 // — // — // —	-	q22.1
SNP_A-1882237	tgaaaaacttgtgaga[A/G]gaatgttaaactgcac	A	G	ENST00000325635 // upstream // 283215 // — // — // — /// ENST00000355063 // upstream // 635442 // — // — // —	-	q22.1
SNP_A-2154164	attatctgcctactca[C/G]attgatgcaaaaaaa	C	G	ENST00000325635 // upstream // 287616 // — // — // — /// ENST00000355063 // upstream // 631041 // — // — // —	-	q22.1
SNP_A-1726370	accttttagttcacaggatttctaca[C/T]aggactcttttagctccctataga	C	T	AF043467 // upstream // 71305 // Hs.435019 // NXPH2 // 11249 // neurexophilin 2 /// NM_018557 // downstream // 1379887 // Hs.417952 // LRP1B // 53353 // low density lipoprotein-related protein 1B (deleted in tumors)	NXPH2	NXPH2 , rs9287506, neurexophilin 2 ,q22.1
SNP_A-1813645	gtgtacaaatccggagt[C/G]aaaagccatcaaattc	C	G	ENST00000325635 // upstream // 343496 // — // — // — /// ENST00000355063 // upstream // 575161 // — // — // —	-	q22.1
SNP_A-1965078	aatgggacaacttaagt[C/G]caggtgcaagtaaac	C	G	ENST00000325635 // upstream // 376989 // — // — // — /// ENST00000355063 // upstream // 541668 // — // — // —	-	q22.1
SNP_A-2242480	ctgcagatgaaactac[A/C]aatccattgtctttg	A	C	ENST00000325635 // upstream // 465812 // — // — // — /// ENST00000355063 // upstream // 452845 // — // — // —	-	q22.1
SNP_A-2193199	catctcaataattacc[C/T]agtcacaggtgttaa	C	T	ENST00000325635 // upstream // 467116 // — // — // — /// ENST00000355063 // upstream // 451541 // — // — // —	-	q22.1
SNP_A-1869469	tcctgtgggtgcttta[C/T]gcattaatccacagaa	C	T	ENST00000325635 // upstream // 734973 // — // — // — /// ENST00000355063 // upstream // 183684 // — // — // —	-	q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1709849 SNP_A-1925045	ctttctcttccctgtatctatg[A/C]aatccaagaaaggtacactc cctca ttatcacagttaccct[A/C]agaagctcaggaattc	A A	C C	AF043467 // upstream // 539234 // Hs.435019 // NXPH2 // 11249 // neurexophilin 2 /// NM_018557 // downstream // 911958 // Hs.417952 // LRP1B // 53353 // low density lipoprotein-related protein 1B (deleted in tumors) ENST00000355063 // intron // 0 // — // — // —	NXPH2	NXPH2 , rs344907, neurexophilin 2 ,q22.1 q22.1
SNP_A-1820582	gtttcaaagcgaggtct[C/T]caaataaagtctgcat	C	T	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2068218	acaagataaggaaaaa[A/C]atgaagtggtctatga	A	C	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1844723	tataagcaggtttca[C/T]cttgagaatatctg	C	T	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2160897	atttctgattgggcccc[C/T]gaagttagaaaactat	C	T	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2033121	aaatacatccaatttta[G/T]gatcatttatcactaa	G	T	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1669487	catttccattcaaagaaccccctca[A/G]gctctctctagtactgat ctggtg	A	G	NM_018557 // intron // 0 // Hs.417952 // LRP1B // 53353 // low density lipoprotein-related protein 1B (deleted in tumors)	LRP1B	LRP1B , rs1385775, low density lipoprotein-related protein 1B (deleted in tumors),q22.1
SNP_A-2033004	aaataatttgagcat[A/G]aactctacaccctatt	A	G	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-2039169	aacagtcaatctcaag[A/G]aatcgccaaaatactt	A	G	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1821821	gtttacttctttaca[A/T]ctgcacaacctaagc	A	T	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1881106	tctttaatcttaaaaa[C/T]agccttagtagccagt	C	T	NM_018557 // intron // 0 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B). /// ENST00000305375 // intron // 0 // — // — // — // —	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.1
SNP_A-1754152	gaaagaagattaaaaatgtcaaaaa[A/C]ggtgctagactgtga agatgatatc	A	C	NM_018557 // intron // 0 // Hs.417952 // LRP1B // 53353 // low density lipoprotein-related protein 1B (deleted in tumors)	LRP1B	LRP1B , rs9283437, low density lipoprotein-related protein 1B (deleted in tumors),q22.1
SNP_A-1749827	atttgccaattgagaaagaatttta[A/G]aacattgtactcagtaac aatatga	A	G	NM_018557 // intron // 0 // Hs.417952 // LRP1B // 53353 // low density lipoprotein-related protein 1B (deleted in tumors)	LRP1B	LRP1B , rs3555577, low density lipoprotein-related protein 1B (deleted in tumors),q22.1
SNP_A-1820579	gtttcaaacttgaaca[A/G]ctgatccagtgtct	A	G	NM_018557 // upstream // 37324 // Hs.470117 // LRP1B // 53353 // Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), mRNA. /// NM_003937 // upstream // 709597 // Hs.470126 // KYNU // 8942 // Homo sapiens kynureninase (L-ky	LRP1B	LRP1B, Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors) (LRP1B), q22.2
SNP_A-2022405	aaaaatagatcatctg[A/G]aactgacctttatga	A	G	NM_018460 // intron // 0 // Hs.171011 // ARHGAP15 // 55843 // Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // — // — // — // —	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1758460	tcatctcgcttatcttttcatctggg[C/T]gaatgatgactgagagatcc catcc	C	T	NM_018460 // intron // 0 // Hs.433597 // ARHGAP15 // 55843 // Rho GTPase activating protein 15	ARHGAP15	ARHGAP15 , rs8272228, Rho GTPase activating protein 15,q22.2
SNP_A-1875621	tctcttatccatcat[C/T]aggtccactgcaggca	C	T	NM_018460 // intron // 0 // Hs.171011 // ARHGAP15 // 55843 // Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), mRNA. /// ENST00000295095 // intron // 0 // — // — // —	ARHGAP15	ARHGAP15, Homo sapiens Rho GTPase activating protein 15 (ARHGAP15), q22.3
SNP_A-2227328	ctacaagattttctcc[A/G]ctttatcatcagccc	A	G	NM_024659 // intron // 0 // Hs.44780 // GTDC1 // 79712 // Homo sapiens glycosyltransferase-like 1 (GTDC1), mRNA. /// ENST00000344850 // intron // 0 // — // — // — /// ENST00000241391 // intron // 0 // — // — // —	GTDC1	GTDC1, Homo sapiens glycosyltransferase-like 1 (GTDC1), q22.3
SNP_A-1965188	tttatcagtgcgtccaa[C/G]agaacaatgccagaaa	C	G	NM_024659 // intron // 0 // Hs.44780 // GTDC1 // 79712 // Homo sapiens glycosyltransferase-like 1 (GTDC1), mRNA. /// ENST00000344850 // intron // 0 // — // — // — /// ENST00000241391 // intron // 0 // — // — // —	GTDC1	GTDC1, Homo sapiens glycosyltransferase-like 1 (GTDC1), q22.3
SNP_A-2179826	cacttgttag[a/a/g]tgtgcaataacttggg	A	G	NM_014795 // intron // 0 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // intron // 0 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1836284	tactatttattgatac[A/C]cctgctgtgccaga	A	C	NM_014795 // upstream // 8643 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 8643 // — // — // — /// ENST00000359464 // upstream // 2058702 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1854404	tcaaatcatttgaagaa[A/G]tagttgtttagtgagt	A	G	NM_014795 // upstream // 152720 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 152720 // — // — // — /// ENST00000359464 // upstream // 1914625 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1707850	agatttctagaagtcaaaagtataa[C/T]tccacacaaaaagatg ttaattagt	C	T	NM_014118 // upstream // 83885 // - // - // - /// NM_014795 // downstream // 66626 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	-	-, rs2381575, -, q22.3
SNP_A-1642899	actgtggtcatgtgacaaggtcca[A/C]ctaatagaatgtgagaa gagatgta	A	C	NM_001616 // upstream // 3018733 // Hs.389846 // ACVR2 // 92 // activin A receptor, type II /// NM_014795 // upstream // 305959 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	ACVR2	ACVR2, rs706624, activin A receptor, type II, q22.3
SNP_A-1803657	gtcaaagattgggaaaa[A/G]tacattctgcttacca	A	G	NM_014795 // upstream // 735278 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 735278 // — // — // — /// ENST00000359464 // upstream // 1332067 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1894237	tgcattatggcttta[A/G]aggaagtaaaagaatc	A	G	NM_014795 // upstream // 828602 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 828602 // — // — // — /// ENST00000359464 // upstream // 1238743 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1956293	ttgtgttcagtctca[A/C]tcaaggattataactt	A	C	NM_014795 // upstream // 841731 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 841731 // — // — // — /// ENST00000359464 // upstream // 1225614 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-2100041	aggaagatatcaaatt[A/C]aagttaggagaagaaa	A	C	NM_014795 // upstream // 1244294 // Hs.34871 // ZFHX1B // 9839 // Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA. /// ENST00000303660 // upstream // 1244294 // — // — // — /// ENST00000359464 // upstream // 823051 // — // — // —	ZFHX1B	ZFHX1B, Homo sapiens zinc finger homeobox 1b (ZFHX1B), q22.3
SNP_A-1756224	ccagacccaaatatgtatcattaaa[G/T]aagtaaacctaattca aacctgatt	G	T	NM_001616 // upstream // 2152473 // Hs.389846 // ACVR2 // 92 // activin A receptor, type II /// NM_014795 // upstream // 1172219 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	ACVR2	ACVR2, rs2381762, activin A receptor, type II ,q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1728605	atatgtcttcagatcatcaatttcc[A/G]ctactcagtcattatcaag atcaag	A	G	NM_001616 // upstream // 2069552 // Hs.389846 // ACVR2 // 92 // activin A receptor, type II /// NM_014795 // upstream // 1255140 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	ACVR2	ACVR2 , rs10496989, activin A receptor, type II ,q22.3
SNP_A-1680510	tgtcttttttctttttcactcacaa[G/T]atttaaccacagttaagcatg acc	G	T	NM_001616 // upstream // 2053868 // Hs.389846 // ACVR2 // 92 // activin A receptor, type II /// NM_014795 // upstream // 1270824 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	ACVR2	ACVR2 , rs10496990, activin A receptor, type II ,q22.3
SNP_A-1703537	aataataaagaaaactgatgtcaagc[A/G]attatctgattcagatt acagtct	A	G	NM_001616 // upstream // 2031064 // Hs.389846 // ACVR2 // 92 // activin A receptor, type II /// NM_014795 // upstream // 1293628 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	ACVR2	ACVR2 , rs1228055, activin A receptor, type II ,q22.3
SNP_A-1675087	catactcacttgttcttccattca[C/T]cttgataatttgacaccatac taac	C	T	NM_001616 // upstream // 2030475 // Hs.389846 // ACVR2 // 92 // activin A receptor, type II /// NM_014795 // upstream // 1294217 // Hs.34871 // ZFHX1B // 9839 // zinc finger homeobox 1b	ACVR2	ACVR2 , rs1228054, activin A receptor, type II ,q22.3
SNP_A-2006765	gtatatggctcccgtg[A/G]atgtaaatatcagatct	A	G	NM_001616 // upstream // 1246237 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 7770 // — // — // — // — /// ENST00000241416 // upstream // 1246237 // — // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2064551	aattcctttccatgcat[G/T]ctggacccagttctt	G	T	NM_001616 // upstream // 306789 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 947218 // — // — // — // — /// ENST00000241416 // upstream // 306789 // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-1848298	tatctttttctttccac[A/G]caagatttaggcaac	A	G	NM_001616 // upstream // 299247 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 954760 // — // — // — // — /// ENST00000241416 // upstream // 299247 // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-1957279	ttttagaaccaggaaa[A/G]agtttaggctcagtga	A	G	NM_001616 // upstream // 294785 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 959222 // — // — // — // — /// ENST00000241416 // upstream // 294785 // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2289760	gcaaaatcggatagac[A/G]gtcaagtatcaaaca	A	G	NM_001616 // upstream // 289769 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 964238 // — // — // — // — /// ENST00000241416 // upstream // 289769 // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2163200	attttctgattatac[A/C]aagcaatatgggttca	A	C	NM_001616 // upstream // 278474 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 975533 // — // — // — // — /// ENST00000241416 // upstream // 278474 // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-1792061	gggtgtggtgaaagtatg[A/C]atgttcactatatagt	A	C	NM_001616 // upstream // 273241 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 980766 // — // — // — // — /// ENST00000241416 // upstream // 273241 // — // — // — /	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-1865477	tccatgaaatcttaa[C/G]ctggcggatcccttat	C	G	NM_001616 // upstream // 221853 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 1032154 // — // — // — // — /// ENST00000241416 // upstream // 221853 // — // — // —	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-2006771	ccttctgtcaacctga[C/T]atccttacatctttt	C	T	NM_001616 // upstream // 173951 // Hs.470171 // ACVR2 // 92 // Homo sapiens activin A receptor, type II (ACVR2), mRNA. /// ENST00000359464 // downstream // 1080056 // — // — // — // — /// ENST00000241416 // upstream // 173951 // — // — // —	ACVR2	ACVR2, Homo sapiens activin A receptor, type II (ACVR2), q22.3
SNP_A-1965322	gcaatttatggagcaa[A/G]tgacacgctgtaactt	A	G	NM_177964 // intron // 0 // Hs.357567 // LOC130576 // 130576 // Homo sapiens hypothetical protein LOC130576 (LOC130576), mRNA. /// ENST00000280115 // intron // 0 // — // — // — // — /// ENST00000360139 // intron // 0 // — // — // — // —	LOC130576	LOC130576, Homo sapiens hypothetical protein LOC130576 (LOC130576), q23.2
SNP_A-1808199	gtcttatactgagat[A/G]aaagatataggtggac	A	G	NM_177964 // intron // 0 // Hs.357567 // LOC130576 // 130576 // Homo sapiens hypothetical protein LOC130576 (LOC130576), mRNA. /// ENST00000280115 // intron // 0 // — // — // — // — /// ENST00000360139 // intron // 0 // — // — // — // —	LOC130576	LOC130576, Homo sapiens hypothetical protein LOC130576 (LOC130576), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1965319	aattagcaaaattcca[C/T]acacgtaactcattta	C	T	NM_177964 // intron // 0 // Hs.357567 // LOC130576 // 130576 // Homo sapiens hypothetical protein LOC130576 (LOC130576), mRNA. /// ENST00000280115 // intron // 0 // — // — // — /// ENST00000360139 // intron // 0 // — // — // —	LOC130576	LOC130576, Homo sapiens hypothetical protein LOC130576 (LOC130576), q23.2
SNP_A-2144780	atgatgtaaaactaga[A/G]acagtgaacaagaaac	A	G	NM_153041 // upstream // 57268 // Hs.470217 // FLJ32955 // 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 552327 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRN	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-2234331	ctccaaatcaccacag[C/T]aatgaccaaaggggtg	G	T	NM_153041 // upstream // 69729 // Hs.470217 // FLJ32955 // 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 539866 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRN	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-1906587	tggtgtaaagtcatgc[A/G]aaatttacttagctt	A	G	NM_153041 // upstream // 156743 // Hs.470217 // FLJ32955 // 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 452852 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mR	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-1645334	attctaaattactgggatcattcat[A/G]taaggaaatggtaagctc tgatggc	A	G	NM_005168 // downstream // 529171 // Hs.6838 // ARHE // 390 // ras homolog gene family, member E /// NM_153041 // upstream // 79833 // Hs.123533 // FLJ32955 // 150596 // hypothetical protein FLJ32955	ARHE	ARHE , rs1437965, ras homolog gene family, member E ,q23.3
SNP_A-1664342	acgcaggttatttgctctacagaa[A/C]gaacacatgaaagca gacaaaacac	A	C	NM_005168 // downstream // 474404 // Hs.6838 // ARHE // 390 // ras homolog gene family, member E /// NM_153041 // upstream // 134600 // Hs.123533 // FLJ32955 // 150596 // hypothetical protein FLJ32955	ARHE	ARHE , rs10497042, ras homolog gene family, member E ,q23.3
SNP_A-1965334	aggagaccagcaaaga[A/C]attgaaagaaagaaa	A	C	NM_153041 // upstream // 517715 // Hs.470217 // FLJ32955 // 150596 // Homo sapiens hypothetical protein FLJ32955 (FLJ32955), mRNA. /// NM_005168 // downstream // 91880 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRN	FLJ32955	FLJ32955, Homo sapiens hypothetical protein FLJ32955 (FLJ32955), q23.3
SNP_A-2215897	cctccaactcttcccc[A/G]caagcaaaaatcttag	A	G	NM_005168 // upstream // 949 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 760797 // Hs.302442 // FLJ45645 // 375287 // Homo sapiens FLJ45645 protein (FLJ45645), mRNA. /// ENST0000	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1931830	ttccctttttgtgggc[A/T]gacccatatttctag	A	T	NM_005168 // upstream // 282261 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 479485 // Hs.302442 // FLJ45645 // 375287 // Homo sapiens FLJ45645 protein (FLJ45645), mRNA. /// ENST0	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1954713	tttgctccagtctata[A/G]gagagtaatcagaatg	A	G	NM_005168 // upstream // 408165 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 353581 // Hs.302442 // FLJ45645 // 375287 // Homo sapiens FLJ45645 protein (FLJ45645), mRNA. /// ENST0	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1725642	ttacaaactgtgacaagtaaactga[A/G]agtaaaagaaactga cagaaatata	A	G	NM_004688 // downstream // 630461 // Hs.54483 // NMI // 9111 // N-myc (and STAT) interactor /// NM_005168 // upstream // 152360 // Hs.6838 // ARHE // 390 // ras homolog gene family, member E	NMI	NMI , rs7603668, N-myc (and STAT) interactor ,q23.3
SNP_A-1688566	tctcaaaatccatgcaatgtcaga[A/G]tatttctatttttggaaa ataaa	A	G	NM_004688 // downstream // 627702 // Hs.54483 // NMI // 9111 // N-myc (and STAT) interactor /// NM_005168 // upstream // 155119 // Hs.6838 // ARHE // 390 // ras homolog gene family, member E	NMI	NMI , rs9287861, N-myc (and STAT) interactor ,q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1698549	atatgaagaaaaaggtaaagaagca[G/T]aaattaaaaggata acttgaagaag	G	T	NM_004688 // downstream // 627485 // Hs.54483 // NMI // 9111 // N-myc (and STAT) interactor /// NM_005168 // upstream // 155336 // Hs.6838 // ARHE // 390 // ras homolog gene family, member E	NMI	NMI , rs2341086, N-myc (and STAT) interactor q23.3
SNP_A-2102746	agatttgcaacaaaaa[C/T]ggatggtccagctct	C	T	NM_005168 // upstream // 551964 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 209782 // Hs.302442 // FLJ45645 // 375287 // Homo sapiens FLJ45645 protein (FLJ45645), mRNA. /// ENST0	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-2080294	acctaatgcttcaag[A/T]aaataatcctatgatg	A	T	NM_005168 // upstream // 558437 // Hs.6838 // RND3 // 390 // Homo sapiens ras homolog gene family, member E (ARHE), mRNA. /// NM_198557 // downstream // 203309 // Hs.302442 // FLJ45645 // 375287 // Homo sapiens FLJ45645 protein (FLJ45645), mRNA. /// ENST0	RND3	RND3, Homo sapiens ras homolog gene family, member E (ARHE), q23.3
SNP_A-1703907	tatcccctatgctacctggctcaaa[C/T]gctgtaaaaacccaaa atgattagc	C	T	NM_004688 // downstream // 518220 // Hs.54483 // NMI // 9111 // N-myc (and STAT) interactor /// NM_005168 // upstream // 264601 // Hs.6838 // ARHE // 390 // ras homolog gene family, member E	NMI	NMI , rs10497071, N-myc (and STAT) interactor q23.3
SNP_A-1849352	tatggaatgaactaga[C/G]tatcaataagctgaaa	C	G	NM_012097 // intron // 0 // Hs.470233 // ARL5 // 26225 // Homo sapiens ADP-ribosylation factor-like 5 (ARL5), transcript variant 1, mRNA. /// NM_177985 // intron // 0 // Hs.470233 // ARL5 // 26225 // Homo sapiens ADP-ribosylation factor-like 5 (ARL5), tra	ARL5	ARL5, Homo sapiens ADP-ribosylation factor-like 5 (ARL5), transcript variant 1, q23.3
SNP_A-1713033	aaaattaagactcttattaggaaag[A/T]ccatcatctaaattgtga acaattt	A	T	X58122 // intron // 0 // Hs.386131 // NEB // 4703 // nebulin	NEB	NEB , rs10497086, nebulin,q23.3
SNP_A-1912096	tgtgaggatttaaggg[C/T]agccctaatgtgggtt	C	T	NM_052905 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 1, mRNA.	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1818372	gttcttaatgaaataa[C/T]gctggctagagccctt	C	T	NM_052905 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 1, mRNA.	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-2152095	attaaaagatacagaaa[A/G]actgggagctagaagt	A	G	NM_052905 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 1, mRNA.	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1895895	tgccigtcttgcttaa[A/G]gaatcataagactatg	A	G	NM_052905 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 1, mRNA.	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-2167563	caacatttgtagacca[C/T]gtaatatgtgcagagc	C	T	NM_052905 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 1, mRNA.	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3
SNP_A-1781652	ggattgcttgggtcta[A/G]ggggtcaagactgcgg	A	G	NM_052905 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 2, mRNA. /// NM_001004421 // intron // 0 // Hs.149566 // FMNL2 // 114793 // Homo sapiens formin-like 2 (FMNL2), transcript variant 1, mRNA.	FMNL2	FMNL2, Homo sapiens formin-like 2 (FMNL2), transcript variant 2, q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1749429	agtcaaaacagaatgttaggagcac[A/G]gctctttgagtcgagaaaattgattt	A	G	AB067489 // intron // 0 // Hs.33461 // FMNL2 // 114793 // formin-like 2	FMNL2	FMNL2 , rs4664573, formin-like 2,q23.3
SNP_A-1743669	aggttaggtgacatacaagaaacatg[C/T]ggttccacgcagtccgtcattct	C	T	AB067489 // intron // 0 // Hs.33461 // FMNL2 // 114793 // formin-like 2	FMNL2	FMNL2 , rs727327, formin-like 2,q23.3
SNP_A-1965433	cagataaatacaccta[A/G]aactggtaatcggcag	A	G	NM_152522 // downstream // 459164 // Hs.516468 // ARL6IP6 // 151188 // Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), mRNA. /// NM_019845 // downstream // 257895 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 de	ARL6IP6	ARL6IP6, Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), q23.3
SNP_A-2221742	cctttaaattatgtg[C/T]atcggtagtcttgact	C	T	NM_152522 // downstream // 527153 // Hs.516468 // ARL6IP6 // 151188 // Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), mRNA. /// NM_019845 // downstream // 189906 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 de	ARL6IP6	ARL6IP6, Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), q23.3
SNP_A-2047193	aagatacttgtccaa[A/C]cctattatgagcccag	A	C	NM_152522 // downstream // 622618 // Hs.516468 // ARL6IP6 // 151188 // Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), mRNA. /// NM_019845 // downstream // 94441 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 dep	ARL6IP6	ARL6IP6, Homo sapiens ADP-ribosylation-like factor 6-interacting protein 6 (MGC33864), q23.3
SNP_A-1806126	gtcctctcttcctgga[C/T]ggtaatcacgtttct	C	T	NM_019845 // upstream // 30536 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), mRNA. /// NM_052917 // upstream // 362851 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-gala	RPRM	RPRM, Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), q23.3
SNP_A-1948440	ttagtatgaagaata[A/G]attgtagggaaggctg	A	G	NM_019845 // upstream // 79060 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), mRNA. /// NM_052917 // upstream // 314327 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-gala	RPRM	RPRM, Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), q23.3
SNP_A-2308049	gcttgaaggaagaaaa[C/G]tatacctgggcaca	C	G	NM_019845 // upstream // 79355 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), mRNA. /// NM_052917 // upstream // 314032 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-gala	RPRM	RPRM, Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), q23.3
SNP_A-2086677	actgaagttggagaaaa[A/C]ttaggtgctaaagcag	A	C	NM_019845 // upstream // 156434 // Hs.100890 // RPRM // 56475 // Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), mRNA. /// NM_052917 // upstream // 236953 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-gal	RPRM	RPRM, Homo sapiens reprimo, TP53 dependant G2 arrest mediator candidate (RPRM), q23.3
SNP_A-1781053	ggatgcatagttgca[C/G]atacgttctctttc	C	G	NM_052917 // intron // 0 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), mRNA. /// ENST00000355685 // intron // 0 // — // — // — // —	GALNT13	GALNT13, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), q23.3
SNP_A-1644588	gtagtggtgtcatttgattccttc[G/T]cttcctccttgtgtgacttcttta	G	T	AK090913 // downstream // 849777 // Hs.470279 // - // - // CDNA FLJ33594 fis, clone BRAMY2012776 /// NM_019845 // upstream // 107266 // Hs.100890 // REPRIMO // 56475 // candidate mediator of the p53-dependent G2 arrest	-	- , rs1940253, CDNA FLJ33594 fis, clone BRAMY2012776, q23.3
SNP_A-1807804	gtctgttttgttaccg[A/G]ccagcttgctgagctg	A	G	NM_052917 // downstream // 23701 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), mRNA. /// NM_052917 // downstream // 20506 // Hs.470277 // GALNT	GALNT13	GALNT13, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044002	aactgagagagaaac[C/T]caagagaactgagaaa	C	T	NM_052917 // downstream // 99332 // Hs.470277 // GALNT13 // 114805 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), mRNA. /// NM_052917 // downstream // 96137 // Hs.470277 // GALNT	GALNT13	GALNT13, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13) (GALNT13), q24.1
SNP_A-2117987	aggtttccttcaaaa[C/T]gctatggagtgtgat	C	T	NM_002239 // intron // 0 // Hs.199776 // KCNJ3 // 3760 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 3 (KCNJ3), mRNA. /// ENST00000295101 // intron // 0 // — // — // —	KCNJ3	KCNJ3, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 3 (KCNJ3), q24.1
SNP_A-2303060	gctataaacatacaac[A/G]aaatagtctgcctttt	A	G	NM_002239 // intron // 0 // Hs.199776 // KCNJ3 // 3760 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 3 (KCNJ3), mRNA. /// ENST00000295101 // intron // 0 // — // — // —	KCNJ3	KCNJ3, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 3 (KCNJ3), q24.1
SNP_A-2282744	gataaaaatggaaaca[C/G]ctctagactaatcagg	C	G	NM_006186 // downstream // 1342909 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 1342909 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nucl	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1965484	aatgcttagaagtcaa[C/T]cagtggcttgtgaaa	C	T	NM_006186 // downstream // 1186837 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 1186837 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nucl	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2236624	ctctaaattactcaag[G/T]ccatacaaatgttatt	G	T	NM_006186 // downstream // 1161290 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 1161290 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nucl	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1965487	agccaccgaaaccgga[C/T]gatgcctcctcttaa	C	T	NM_006186 // downstream // 1093342 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 1093342 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nucl	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2142560	atgaaccaaatagcag[C/G]agagaaagtcctcatg	C	G	NM_006186 // downstream // 747686 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 747686 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclea	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1902238	tggccacttttctgta[C/T]agcaaccgaggtgata	C	T	NM_006186 // downstream // 740023 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 740023 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclea	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2081107	acctgaggagtagaga[A/T]atatgatttccagaa	A	T	NM_006186 // downstream // 731312 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 731312 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclea	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2313967	ggagctcatttcccca[A/T]cctgaaatttgaggaa	A	T	NM_006186 // downstream // 655562 // Hs.165258 // NR4A2 // 4929 // (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 655562 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclea	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1847650	tatctaatggacagccd[A/G]gaaaacccagagagac	A	G	NM_006186 // downstream // 469874 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 469874 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclea	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-1936238	ttcttcatcagttcaa[C/T]gtggtggtaatcata	C	T	NM_006186 // downstream // 52196 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA. /// NM_173171 // downstream // 52196 // Hs.165258 // NR4A2 // 4929 // Homo sapiens nuclear	NR4A2	NR4A2, Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, q24.1
SNP_A-2075173	acatctccaatacaca[C/T]aatcatttcgtttc	C	T	NM_000408 // intron // 0 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// ENST00000310454 // intron // 0 // — // — // —	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-2120071	agtcactctggacatat[A/G]tacacttcactgtta	A	G	NM_000408 // intron // 0 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// ENST00000310454 // intron // 0 // — // — // —	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-1965508	atgtaaattaaaatcc[A/T]cattatgtataagcat	A	T	NM_000408 // intron // 0 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// ENST00000310454 // intron // 0 // --- // — // — /// ENST00000358051 // intron // 0 // — // — // —	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-1876401	tctgagtggaaaaaaa[A/C]caagtagactacatat	A	C	NM_000408 // downstream // 48358 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// NM_000408 // downstream // 48537 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydro	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-2044411	aagaaaaaagagtagaat[C/T]acaaatatgcaaagtc	C	T	NM_000408 // downstream // 65852 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// NM_000408 // downstream // 66031 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydro	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-2071230	acacttaagacttcca[C/T]gtggcttcatttttc	C	T	NM_000408 // downstream // 125273 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// NM_000408 // downstream // 125452 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehyd	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-1965510	attcttattgtatcc[C/T]gagctatgcttcaaac	C	T	NM_000408 // downstream // 345485 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), mRNA. /// NM_000408 // downstream // 345664 // Hs.148266 // GPD2 // 2820 // Homo sapiens glycerol-3-phosphate dehyd	GPD2	GPD2, Homo sapiens glycerol-3-phosphate dehydrogenase 2 (mitochondrial) (GPD2), q24.1
SNP_A-1871586	tctaagcttgctccta[G/T]ggtgctcatcttgatg	G	T	NM_001105 // intron // 0 // Hs.470316 // ACVR1 // 90 // Homo sapiens activin A receptor, type I (ACVR1), mRNA. /// ENST00000263640 // intronI // 0 // — // — // —	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-2255013	cttggctgttagatc[A/G]atctccatggttaacg	A	G	NM_001105 // upstream // 70111 // Hs.470316 // ACVR1 // 90 // Homo sapiens activin A receptor, type I (ACVR1), mRNA. /// NM_173355 // upstream // 156638 // Hs.128427 // UPP2 // 151531 // Homo sapiens uridine phosphorylase 2 (UPP2), mRNA. /// ENST00000262536	ACVR1	ACVR1, Homo sapiens activin A receptor, type I (ACVR1), q24.1
SNP_A-1965533	ataatttaaagcttca[A/G]agtctggcatctgcat	A	G	NM_138803 // intron // 0 // Hs.100743 // LOC130940 // 130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // — // — // —	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-1746727	acgtataaaaccgtggatacgtta[C/T]catgtgtgtaaaagaaa aattgtaa	C	T	NM_001105 // intron // 0 // Hs.150402 // ACVR1 // 90 // activin A receptor, type I	ACVR1	ACVR1 , rs10497192, activin A receptor, type I,q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1782251	ggcaagtcatgtagga[A/G]gataagtggtaagtct	A	G	NM_138803 // intron // 0 // Hs.100743 // LOC130940 // 130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // --- // --- // --- // ---	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-2279455	gaggatattttggtaa[A/G]ggaacgaggtggcgga	A	G	NM_138803 // intron // 0 // Hs.100743 // LOC130940 // 130940 // Homo sapiens hypothetical protein BC015395 (LOC130940), mRNA. /// ENST00000283233 // intron // 0 // — // — // — // —	LOC130940	LOC130940, Homo sapiens hypothetical protein BC015395 (LOC130940), q24.1
SNP_A-2207968	cccaacatcctacata[C/T]caggtgagacttttct	C	T	NM_003628 // intron // 0 // Hs.407580 // PKP4 // 8502 // Homo sapiens plakophilin 4 (PKP4), transcript variant 1, mRNA. /// ENST00000354977 // intron // 0 // — // — // — // — /// ENST00000337068 // intron // 0 // — // — // — // — /// ENST0	PKP4	PKP4, Homo sapiens plakophilin 4 (PKP4), transcript variant 1, q24.1
SNP_A-1902202	tggccaattcagttca[C/G]aagtgctaaacctgtt	C	G	NM_003628 // downstream // 55495 // Hs.407580 // PKP4 // 8502 // Homo sapiens plakophilin 4 (PKP4), transcript variant 1, mRNA. /// ENST00000354977 // downstream // 55646 // — // — // — // — /// ENST00000337068 // downstream // 55495 // — // —	PKP4	PKP4, Homo sapiens plakophilin 4 (PKP4), transcript variant 1, q24.1
SNP_A-1794665	ggtctcagatggatcc[C/T]cgctttcctggagaag	C	T	NM_003628 // downstream // 56054 // Hs.407580 // PKP4 // 8502 // Homo sapiens plakophilin 4 (PKP4), transcript variant 1, mRNA. /// ENST00000354977 // downstream // 56205 // --- // --- // --- // --- /// ENST00000337068 // downstream // 56054 // --- // ---	PKP4	PKP4, Homo sapiens plakophilin 4 (PKP4), transcript variant 1, q24.1
SNP_A-2074993	acatcatttttgacct[G/T]aaaaaatagcaaatgt	G	T	ENST00000309950 // intron // 0 // — // — // — // —	-	q24.1
SNP_A-1679952	ggaataaacatgatacagtattaga[C/T]gaagtttataaatcaaataatttag	C	T	NM_003628 // intron // 0 // Hs.277132 // PKP4 // 8502 // plakophilin 4	PKP4	PKP4 , rs6738665, plakophilin 4,q24.1
SNP_A-1736085	tattggtgggttagttgtctgtaat[G/T]atttagttttaatttttagtgtat	G	T	NM_003628 // intron // 0 // Hs.277132 // PKP4 // 8502 // plakophilin 4	PKP4	PKP4 , rs719931, plakophilin 4,q24.1
SNP_A-2110441	aggaatttccagagga[A/T]gagcaatgggggaaga	A	T	ENST00000343761 // downstream // 232074 // — // — // — // — /// ENST00000263635 // upstream // 41559 // — // — // — // —	-	q24.2
SNP_A-2248578	ctgttagccatgtgag[A/G]atacggtagttcttcc	A	G	ENST00000343761 // downstream // 233926 // --- // --- // --- // --- /// ENST00000263635 // upstream // 39707 // --- // --- // --- // ---	-	q24.2
SNP_A-2196124	catgtgcaaaccagga[A/G]aagatgaataatccaa	A	G	ENST00000343761 // downstream // 235391 // --- // --- // --- // --- /// ENST00000263635 // upstream // 38242 // — // — // — // —	-	q24.2
SNP_A-2237161	ctctcactgatgtcac[A/G]ggttacctatgcaatc	A	G	ENST00000343761 // downstream // 244163 // — // — // — // — /// ENST00000263635 // upstream // 29470 // — // — // — // —	-	q24.2
SNP_A-2085133	actcagatctttccca[C/T]tacaggtcccgtcagg	C	T	ENST00000343761 // downstream // 260577 // — // — // — // — /// ENST00000263635 // upstream // 13056 // — // — // — // —	-	q24.2
SNP_A-1720549	ccaatgtgtgtttcccttatgcttc[C/T]gaaattgctgagttagagccctacag	C	T	AB051515 // upstream // 350763 // Hs.437362 // KIAA1728 // 85461 // KIAA1728 protein /// NM_003628 // downstream // 118931 // Hs.277132 // PKP4 // 8502 // plakophilin 4	KIAA1728	KIAA1728 , rs6722518, KIAA1728 protein ,q24.1
SNP_A-2046462	aagagagatcttgagg[C/G]atacaggcaattcctg	C	G	NM_152528 // intron // 0 // Hs.20848 // WDSAM1 // 151525 // Homo sapiens WD repeat and SAM domain containing 1 (WDSAM1), mRNA. /// ENST00000359774 // intron // 0 // --- // --- // --- // --- /// ENST00000358147 // intron // 0 // — // — // — // — // —	WDSAM1	WDSAM1, Homo sapiens WD repeat and SAM domain containing 1 (WDSAM1), q24.2
SNP_A-2226835	ctaatagctgggatta[C/G]aaggcataaaccacca	C	G	NM_152528 // upstream // 10600 // Hs.20848 // WDSAM1 // 151525 // Homo sapiens WD repeat and SAM domain containing 1 (WDSAM1), mRNA. /// NM_013450 // downstream // 21789 // Hs.470369 // BAZ2B // 29994 // Homo sapiens bromodomain adjacent to zinc finger do	WDSAM1	WDSAM1, Homo sapiens WD repeat and SAM domain containing 1 (WDSAM1), q24.2
SNP_A-1954969	tttggaagctttcaac[G/T]ctaacttttcaaactt	G	T	ENST00000355831 // intron // 0 // — // — // — // — /// ENST00000343439 // intron // 0 // — // — // — // —	-	q24.2
SNP_A-1714753	gaatttcataaatacccaacatgata[C/T]acaatagttccttagcatttgtcat	C	T	NM_152528 // intron // 0 // Hs.20848 // FLJ36175 // 151525 // hypothetical protein FLJ36175	FLJ36175	FLJ36175 , rs4665050, hypothetical protein FLJ36175,q24.2
SNP_A-2035964	aaattaaatacaacta[C/T]gtctactgccactaaa	C	T	NM_002349 // intron // 0 // Hs.153563 // LY75 // 4065 // Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /// ENST00000263636 // intron // 0 // — // — // — // —	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2
SNP_A-2094744	agaatcagaacactta[A/C]gccggaaaggacctca	A	C	NM_002349 // intron // 0 // Hs.153563 // LY75 // 4065 // Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /// ENST00000263636 // intron // 0 // — // — // — // —	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2268465	gaatggcaaagtgata[A/G]caagtgcaggcaacaa	A	G	NM_002349 // upstream // 8341 // Hs.153563 // LY75 // 4065 // Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /// NM_007366 // downstream // 27672 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENS	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2
SNP_A-2130783	atactctatacttgt[A/C]aatcattgctaatgc	A	C	NM_002349 // upstream // 8946 // Hs.153563 // LY75 // 4065 // Homo sapiens lymphocyte antigen 75 (LY75), mRNA. /// NM_007366 // downstream // 27067 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENS	LY75	LY75, Homo sapiens lymphocyte antigen 75 (LY75), q24.2
SNP_A-2160758	atttctagagtctttg[A/G]atcttagttgaactgg	A	G	NM_007366 // intron // 0 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // — // — // —	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-1805568	gtccagtggtaaaaga[C/G]aaacacgctatccct	C	G	NM_007366 // intron // 0 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // — // — // —	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-2266468	gaagtacaaattctta[C/T]acaggctgagtatcgc	C	T	NM_007366 // intron // 0 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // — // — // —	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-1831860	taattctggaaggcag[C/T]aaagaaaccgtctgga	C	T	NM_007366 // intron // 0 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // — // — // —	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-1786508	ggcttcagagctagact[G/T]atctgagttcaaatcc	G	T	NM_007366 // intron // 0 // Hs.410477 // PLA2R1 // 22925 // Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA. /// ENST00000283243 // intron // 0 // — // — // —	PLA2R1	PLA2R1, Homo sapiens phospholipase A2 receptor 1, 180kDa (PLA2R1), q24.2
SNP_A-2278960	gaggaacaaatgaagc[C/T]agggcaatgttagaac	C	T	NM_000888 // intron // 0 // Hs.470399 // ITGB6 // 3694 // Homo sapiens integrin, beta 6 (ITGB6), mRNA. /// ENST00000283249 // intron // 0 // — // — // — // —	ITGB6	ITGB6, Homo sapiens integrin, beta 6 (ITGB6), q24.2
SNP_A-1701057	atttaggtatctgtcaaatcta[C/T]aaaaggagaatcaaattg gcaagtg	C	T	NM_002349 // intron // 0 // Hs.153563 // LY75 // 4065 // lymphocyte antigen 75	LY75	LY75 , rs2292388, lymphocyte antigen 75,q24.2
SNP_A-1702663	gggagatttatttcactagctttaa[A/T]gactaagtatacctttagta gatc	A	T	NM_002349 // upstream // 21437 // Hs.153563 // LY75 // 4065 // lymphocyte antigen 75 /// NM_007366 // downstream // 14576 // Hs.410477 // PLA2R1 // 22925 // phospholipase A2 receptor 1, 180kDa /// NM_014880 // upstream // 142703 // Hs.2441 // DCL-1 // 99	LY75	LY75 , rs1877195, lymphocyte antigen 75 ,q24.2
SNP_A-1813819	gtgtatactttccac[A/C]aacatatctacagttt	A	C	NM_002897 // upstream // 89894 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 89894 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-1947279	tttaattgtatagta[A/G]gtatgaatttgctcag	A	G	NM_002897 // upstream // 109603 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 109603 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-1955592	acaggtacttaaata[A/T]gtctcattcaagtggt	A	T	NM_002897 // upstream // 238174 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 238174 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893089	tgcacttttctatctc[C/T]attcccacgagacaat	C	T	NM_002897 // upstream // 255121 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 255121 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2066859	acaaaatgaatgatga[A/G]gttaaacacccaagct	A	G	NM_002897 // upstream // 292984 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 292984 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2035658	aaatgtcatcaatcag[A/C]attttcagtaaataat	A	C	NM_002897 // upstream // 316822 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 316822 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2085300	actcatctaataattc[A/G]gaacaccatgtgttgg	A	G	NM_002897 // upstream // 316895 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 316895 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2147536	atggatctaagaagaa[A/T]ggtcgatttttcagct	A	T	NM_002897 // upstream // 335809 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 335809 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2195028	catgctttcactctag[A/G]aactttgatccagtgt	A	G	NM_002897 // upstream // 394932 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 394932 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2304448	gctctagactactcta[C/T]cattccttgtggattt	C	T	NM_002897 // upstream // 395706 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 395706 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-2311625	ggaatgtagcagtaat[A/G]agataactaagaatga	A	G	NM_002897 // upstream // 466046 // Hs.470412 // RBMS1 // 5937 // Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA. /// NM_016836 // upstream // 466046 // Hs.470412 // RBMS1 // 5937 // Homo sapiens R	RBMS1	RBMS1, Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, q24.2
SNP_A-1667816	gttgattgacaggaagagagtatga[G/T]aacacattttgtggtaataaaaatg	G	T	NM_002897 // upstream // 295241 // Hs.241567 // RBMS1 // 5937 // RNA binding motif, single stranded interacting protein 1 /// NM_004180 // upstream // 348294 // Hs.146847 // TANK // 10010 // TRAF family member-associated NFKB activator /// NM_016836 // u	RBMS1	RBMS1 , rs2123034, RNA binding motif, single stranded interacting protein 1 ,q24.2
SNP_A-1728927	atcattgtctgggttttacagatag[A/G]aaaatttaggtacatagaattatct	A	G	NM_002897 // upstream // 399289 // Hs.241567 // RBMS1 // 5937 // RNA binding motif, single stranded interacting protein 1 /// NM_004180 // upstream // 244246 // Hs.146847 // TANK // 10010 // TRAF family member-associated NFKB activator /// NM_016836 // u	RBMS1	RBMS1 , rs10497221, RNA binding motif, single stranded interacting protein 1 ,q24.2
SNP_A-1689703	tagccacagctaaactactgtgcca[A/T]tgtattaaccagtatctaattacat	A	T	NM_002897 // upstream // 430027 // Hs.241567 // RBMS1 // 5937 // RNA binding motif, single stranded interacting protein 1 /// NM_004180 // upstream // 213508 // Hs.146847 // TANK // 10010 // TRAF family member-associated NFKB activator /// NM_016836 // u	RBMS1	RBMS1 , rs997015, RNA binding motif, single stranded interacting protein 1 ,q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1965611	tatgactgcacagatc[A/G]aaagtgtcgaactcac	A	G	NM_005805 // intron // 0 // Hs.369125 // PSMD14 // 10213 // Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 (PSMD14), mRNA. /// ENST00000263639 // intron // 0 // — // — // — // —	PSMD14	PSMD14, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 (PSMD14), q24.2
SNP_A-2140021	atctagacagagaata[A/T]gctcattttcagagtc	A	T	NM_005805 // intron // 0 // Hs.369125 // PSMD14 // 10213 // Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 (PSMD14), mRNA. /// ENST00000263639 // intron // 0 // — // — // — // —	PSMD14	PSMD14, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 (PSMD14), q24.2
SNP_A-2047452	aagatgagcatcttaa[A/G]aagagcaagaacttct	A	G	NM_022058 // intron // 0 // Hs.333958 // SLC4A10 // 57282 // Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA. /// ENST00000272716 // intron // 0 // — // — // — // —	SLC4A10	SLC4A10, Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), q24.2
SNP_A-1965616	tcagttcatggactaa[C/G]gtttttatggatgata	C	G	NM_022058 // intron // 0 // Hs.333958 // SLC4A10 // 57282 // Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA. /// ENST00000272716 // intron // 0 // — // — // — // —	SLC4A10	SLC4A10, Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), q24.2
SNP_A-2299333	gccctgacataagtaa[A/G]tagagattgttaggta	A	G	NM_022058 // intron // 0 // Hs.333958 // SLC4A10 // 57282 // Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA. /// ENST00000272716 // intron // 0 // — // — // — // —	SLC4A10	SLC4A10, Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), q24.2
SNP_A-1849486	tatggccaccatactg[A/G]aaaattctggtttcgt	A	G	NM_022058 // intron // 0 // Hs.333958 // SLC4A10 // 57282 // Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA. /// ENST00000272716 // intron // 0 // — // — // — // —	SLC4A10	SLC4A10, Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), q24.2
SNP_A-1677022	ttgaaatccttttgcatctctctga[A/T]ctattgcacaaaaatttaaatcttg	A	T	NM_022058 // intron // 0 // Hs.333958 // SLC4A10 // 57282 // solute carrier family 4, sodium bicarbonate transporter-like, member 10	SLC4A10	SLC4A10 , rs10497224, solute carrier family 4, sodium bicarbonate transporter-like, member 10,q24.2
SNP_A-1714851	aagcatgagtgtaaatacagaccca[A/G]aagagtatagctcgatttcttcaag	A	G	NM_022058 // intron // 0 // Hs.333958 // SLC4A10 // 57282 // solute carrier family 4, sodium bicarbonate transporter-like, member 10	SLC4A10	SLC4A10 , rs1996266, solute carrier family 4, sodium bicarbonate transporter-like, member 10,q24.2
SNP_A-1942126	ttggattgagttgcat[C/T]aaacaaaattgaagtg	C	T	NM_033272 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens p	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1849639	tatggtcaatgacaaa[A/C]ctcacgagaagacaaa	A	C	NM_033272 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens p	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-2178663	cactctgtaatacaaa[C/T]gtcctggaagcagaga	C	T	NM_033272 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens p	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-1879625	tcttcaccttgattca[A/C]aaaaacacagctgttt	A	C	NM_033272 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // intron // 0 // Hs.470445 // KCNH7 // 90134 // Homo sapiens p	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2
SNP_A-2087090	actgatacagaatcat[A/C]aaaggcctcaggcaca	A	C	NM_033272 // upstream // 18572 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 18572 // Hs.470445 // KCNH7 // 90134 // Ho	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043936	aacttctggaatgcca[A/G]gaattgaaaagagcag	A	G	NM_033272 // upstream // 735305 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 735305 // Hs.470445 // KCNH7 // 90134 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.3
SNP_A-2057856	aatattatgctggcta[A/G]cttctgtttcttctct	A	G	NM_033272 // upstream // 741779 // Hs.470445 // KCNH7 // 90134 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, mRNA. /// NM_173162 // upstream // 741779 // Hs.470445 // KCNH7 // 90134 //	KCNH7	KCNH7, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 1, q24.3
SNP_A-2057830	aatattagaatgttag[A/G]ccaacagcaataaaat	A	G	NM_018086 // intron // 0 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// ENST00000333129 // intron // 0 // --- // --- // --- // ---	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-2049383	aagctgaataaagaca[C/T]gaaaagaaacagtgat	C	T	NM_018086 // intron // 0 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// ENST00000333129 // intron // 0 // --- // --- // --- // ---	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1965664	ttatgcattccctgag[G/T]aacatcaatagatcgc	G	T	NM_018086 // upstream // 384203 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 372617 // Hs.411881 // GRB14 // 2888 // Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST0000033	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1965671	acaaactgtagaaatc[A/T]atgacatgaaatggac	A	T	NM_018086 // upstream // 443374 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 313446 // Hs.411881 // GRB14 // 2888 // Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST0000033	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1795184	ggtgagattactacca[C/T]ctttgaagttagatgt	C	T	NM_018086 // upstream // 447627 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 309193 // Hs.411881 // GRB14 // 2888 // Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST0000033	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-2100589	agatacaggagcaaca[A/G]tcttctatacatggtt	A	G	NM_018086 // upstream // 449551 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 307269 // Hs.411881 // GRB14 // 2888 // Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST0000033	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1965674	agatcattgttgagta[C/T]gctgtcttgtatctca	C	T	NM_018086 // upstream // 506820 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 250000 // Hs.411881 // GRB14 // 2888 // Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST0000033	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1943874	ttgtatacctataaaa[A/G]tgtacattggcacaaa	A	G	NM_018086 // upstream // 550116 // Hs.170999 // FIGN // 55137 // Homo sapiens fidgetin (FIGN), mRNA. /// NM_004490 // downstream // 206704 // Hs.411881 // GRB14 // 2888 // Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA. /// ENST0000033	FIGN	FIGN, Homo sapiens fidgetin (FIGN), q24.3
SNP_A-1679570	aaccatgatctagtatatagcttat[C/T]taggaatactgtttacatta tcata	C	T	NM_004490 // downstream // 217819 // Hs.411881 // GRB14 // 2888 // growth factor receptor-bound protein 14 /// NM_018086 // upstream // 663377 // Hs.274281 // FIGN // 55137 // fidgetin	GRB14	GRB14 , rs1371178, growth factor receptor-bound protein 14 ,q24.3
SNP_A-2218798	cctgggatctaaactc[C/T]aaaacatatcctgaac	C	T	ENST00000342193 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1965681	aaattatacacgtaac[A/G]cacagtaagcattaaa	A	G	ENST00000342193 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2027137	aaacaggcctaggaac[A/G]cagaccaaagggcaaa	A	G	NM_173512 // intron // 0 // Hs.293185 // FLJ39822 // 151258 // Homo sapiens hypothetical protein FLJ39822 (FLJ39822), mRNA. /// ENST00000303735 // intron // 0 // --- // --- // --- // ---	FLJ39822	FLJ39822, Homo sapiens hypothetical protein FLJ39822 (FLJ39822), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141790	atcttgaatttttttc[C/T]actagttggtgaaaaa	C	T	NM_173512 // upstream // 20378 // Hs.293185 // FLJ39822 // 151258 // Homo sapiens hypothetical protein FLJ39822 (FLJ39822), mRNA. /// ENST00000303735 // upstream // 20378 // --- // --- // --- // --- /// ENST00000357326 // downstream // 18947 // --- // ---	FLJ39822	FLJ39822, Homo sapiens hypothetical protein FLJ39822 (FLJ39822), q24.3
SNP_A-1854585	tcaacaaaggtcaata[C/T]gaaggacgtcccaaat	C	T	NM_006920 // intron // 0 // Hs.22654 // SCN1A // 6323 // Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), mRNA. /// NM_021007 // intron // 0 // Hs.470470 // SCN2A2 // 6326 // Homo sapiens sodium channel, voltage-gated, type II, alpha 2 (	SCN1A	SCN1A, Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), q24.3
SNP_A-2197615	cattctccctgttgga[A/G]ggtggcaatagttgct	A	G	NM_006920 // intron // 0 // Hs.22654 // SCN1A // 6323 // Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), mRNA. /// NM_021007 // intron // 0 // Hs.470470 // SCN2A2 // 6326 // Homo sapiens sodium channel, voltage-gated, type II, alpha 2 (	SCN1A	SCN1A, Homo sapiens sodium channel, voltage-gated, type I, alpha (SCN1A), q24.3
SNP_A-2294507	gcagtcaaatgagtca[A/C]cctcatactaactgct	A	C	NM_024753 // intron // 0 // Hs.310672 // TTC21B // 79809 // Homo sapiens hypothetical protein FLJ11457 (FLJ11457), mRNA. /// ENST00000243344 // intron // 0 // --- // --- // --- // ---	TTC21B	TTC21B, Homo sapiens hypothetical protein FLJ11457 (FLJ11457), q24.3
SNP_A-1815172	gtgttgaagtaaaact[C/T]acattttgtgactctg	C	T	AF225985 // upstream // 69855 // --- // SCN1A // 6323 // Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) mRNA, complete cds. /// NM_002977 // downstream // 69756 // Hs.2319 // SCN9A // 6335 // Homo sapiens sodium channel, voltage-gat	SCN1A	SCN1A, Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) complete cds. q24.3
SNP_A-2128376	ataagtgtttatcatc[C/T]gagaactgattaaata	C	T	AF225985 // upstream // 82998 // --- // SCN1A // 6323 // Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) mRNA, complete cds. /// NM_002977 // downstream // 56613 // Hs.2319 // SCN9A // 6335 // Homo sapiens sodium channel, voltage-gat	SCN1A	SCN1A, Homo sapiens voltage-gated sodium channel alpha subunit SCN1A (SCN1A) complete cds. q24.3
SNP_A-2127476	ataacactgccatgta[A/G]aaaggtaaactgctga	A	G	NM_002977 // intron // 0 // Hs.2319 // SCN9A // 6335 // Homo sapiens sodium channel, voltage-gated, type IX, alpha (SCN9A), mRNA. /// ENST00000303354 // intron // 0 // --- // --- // --- // ---	SCN9A	SCN9A, Homo sapiens sodium channel, voltage-gated, type IX, alpha (SCN9A), q24.3
SNP_A-2312109	ggacacttggtaatac[A/C]ccttggaacttcagtg	A	C	NM_002976 // upstream // 323242 // Hs.182889 // SCN7A // 6332 // Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), mRNA. /// NM_002976 // upstream // 316004 // Hs.182889 // SCN7A // 6332 // Homo sapiens sodium channel, voltage-gated, ty	SCN7A	SCN7A, Homo sapiens sodium channel, voltage-gated, type VII, alpha (SCN7A), q24.3
SNP_A-1718961	aaaggacaatcgaagcaactcttga[A/G]acattctaaggttaaaaatattcag	A	G	NM_002976 // upstream // 47505 // Hs.406684 // SCN7A // 6332 // sodium channel, voltage-gated, type VII, alpha /// NM_152381 // upstream // 715603 // - // - // - // -	SCN7A	SCN7A , rs1157750, sodium channel, voltage-gated, type VII, alpha ,q24.3
SNP_A-1789625	gggctaaatggcctac[A/G]caaagccacaccgctg	A	G	ENST00000328983 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-1965727	tagtttccaacttcca[A/G]tgcagcagttatttaa	A	G	ENST00000328983 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2184296	cagccttccctcctcc[A/C]ggaagattctaggtct	A	C	ENST00000328983 // intron // 0 // --- // --- // --- // ---	-	q24.3
SNP_A-2107646	agctattgactttagc[C/T]gaatatgaattatgcc	C	T	NM_020981 // upstream // 262693 // Hs.512811 // B3GALT1 // 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 296235 // --- // --- // --- // --- /// ENST00000295237 /	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2123421	agtgtctaggtaaagc[A/G]ccatttttggagtgg	A	G	NM_020981 // upstream // 232630 // Hs.512811 // B3GALT1 // 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 326298 // --- // --- // --- // --- /// ENST00000295237 /	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2229164	ctagctcaggccagaa[C/T]cttatcactatcatca	C	T	NM_020981 // upstream // 226621 // Hs.512811 // B3GALT1 // 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 332307 // — // — // — // — /// ENST00000295237 /	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2240658	ctgactatggaaagcc[A/G]aagggcattaaagctt	A	G	NM_020981 // upstream // 180245 // Hs.512811 // B3GALT1 // 8708 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA. /// ENST00000328983 // downstream // 378683 // — // — // — // — /// ENST00000295237 /	B3GALT1	B3GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), q24.3
SNP_A-2116262	aggtactatgttctac[A/G]gattttacatgtatta	A	G	NM_013233 // intron // 0 // Hs.276271 // STK39 // 27347 // Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA. /// ENST00000355999 // intron // 0 // — // — // — // —	STK39	STK39, Homo sapiens serine threonine kinase 39 (STE20,q24.3
SNP_A-1891664	tgattggtggaagtga[C/T]gtcatgtatggtaaac	C	T	NM_052946 // intron // 0 // Hs.189780 // NOSTRIN // 115677 // Homo sapiens nitric oxide synthase trafficker (NOSTRIN), mRNA. /// ENST00000343642 // intron // 0 // — // — // — // —	NOSTRIN	NOSTRIN, Homo sapiens nitric oxide synthase trafficker (NOSTRIN), q24.3
SNP_A-1965774	cttctaaaatctccac[A/G]gacttaactagggccc	A	G	NM_021176 // downstream // 6672 // Hs.283963 // G6PC2 // 57818 // Homo sapiens glucose-6-phosphatase, catalytic, 2 (G6PC2), mRNA. /// NM_003742 // downstream // 8187 // Hs.158316 // ABCB11 // 8647 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TA	G6PC2	G6PC2, Homo sapiens glucose-6-phosphatase, catalytic, 2 (G6PC2), q24.3
SNP_A-1707762	caattatctctaagggaaagaatcc[A/G]atcataagaaagtatta atagcacc	A	G	NM_052946 // intron // 0 // Hs.416324 // NOSTRIN // 115677 // nitric oxide synthase trafficker	NOSTRIN	NOSTRIN , rs829955, nitric oxide synthase trafficker,q24.3
SNP_A-2300156	gcctccacttcttcac[G/T]ctgaccttgcttttat	G	T	NM_004525 // intron // 0 // Hs.470538 // LRP2 // 4036 // Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA. /// ENST00000263816 // intron // 0 // — // — // — // —	LRP2	LRP2, Homo sapiens low density lipoprotein-related protein 2 (LRP2), q31.1
SNP_A-1710750	gcccagttcttacctgttagcccaa[A/T]ctataagcacatggaaa ttactatt	A	T	NM_003742 // intron // 0 // Hs.158316 // ABCB11 // 8647 // ATP-binding cassette, sub-family B (MDR/TAP), member 11	ABCB11	ABCB11 , rs484066, ATP-binding cassette, sub-family B (MDR,q24.3
SNP_A-2117741	aggttcttcagaggac[A/G]ctatcgccatttgggg	A	G	NM_004525 // intron // 0 // Hs.470538 // LRP2 // 4036 // Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA. /// ENST00000263816 // intron // 0 // — // — // — // —	LRP2	LRP2, Homo sapiens low density lipoprotein-related protein 2 (LRP2), q31.1
SNP_A-1959224	ttttgaggactccata[A/C]gtaacaaataggttgg	A	C	NM_004525 // intron // 0 // Hs.470538 // LRP2 // 4036 // Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA. /// ENST00000263816 // intron // 0 // — // — // — // —	LRP2	LRP2, Homo sapiens low density lipoprotein-related protein 2 (LRP2), q31.1
SNP_A-2026211	aaaattgatactttac[A/G]gcttgacacatggttt	A	G	NM_172070 // intron // 0 // Hs.379548 // ZNF650 // 130507 // Homo sapiens similar to F10G7.10.p (KIAA2024), mRNA. /// ENST00000272793 // intron // 0 // — // — // — // —	ZNF650	ZNF650, Homo sapiens similar to F10G7.10.p (KIAA2024), q31.1
SNP_A-1920377	ttaatgtggaaaggca[C/T]ccgtattaattttcta	C	T	NM_172070 // downstream // 22636 // Hs.379548 // ZNF650 // 130507 // Homo sapiens similar to F10G7.10.p (KIAA2024), mRNA. /// NM_138995 // upstream // 94207 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // upstrea	ZNF650	ZNF650, Homo sapiens similar to F10G7.10.p (KIAA2024), q31.1
SNP_A-2297170	gccacatcagatgtcc[C/T]aaaaaggccctgggct	C	T	NM_138995 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B) mRNA, complete cds. /// ENST00000317935 // intron // 0 // -	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-1906543	tggtgggttgtcttcc[G/T]cagctttaggtttatt	G	T	NM_138995 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B) mRNA, complete cds. /// ENST00000317935 // intron // 0 // -	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1965816	actaggaaaaataaga[A/C]tagcaccagagggaac	A	C	NM_138995 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B) mRNA, complete cds. /// ENST00000317935 // intron // 0 // -	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-1965817	ctgatgtgttcaca[A/G]aagtacaagagcctat	A	G	NM_138995 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B) mRNA, complete cds. /// ENST00000317935 // intron // 0 // -	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-2140904	atctgagaggattaga[A/G]ggaacagtgcccagtg	A	G	NM_138995 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B) mRNA, complete cds. /// ENST00000317935 // intron // 0 // -	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-1785187	ggctaagtatactgga[A/G]tcatttgtaagtgct	A	G	NM_138995 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B), mRNA. /// AF369908 // intron // 0 // Hs.534101 // MYO3B // 140469 // Homo sapiens myosin IIIB (MYO3B) mRNA, complete cds. /// ENST00000317935 // intron // 0 // -	MYO3B	MYO3B, Homo sapiens myosin IIIB (MYO3B), q31.1
SNP_A-2059723	aatctgatagctgtag[C/T]atttcctaaactgtt	C	T	NM_000817 // downstream // 30720 // Hs.420036 // GAD1 // 2571 // Homo sapiens glutamate decarboxylase 1 (brain, 67kDa) (GAD1), transcript variant GAD67, mRNA. /// NM_013445 // downstream // 49097 // Hs.420036 // GAD1 // 2571 // Homo sapiens glutamate deca	GAD1	GAD1, Homo sapiens glutamate decarboxylase 1 (brain, 67kDa) (GAD1), transcript variant GAD67, q31.1
SNP_A-1847600	tatcggtttattgtc[A/C]atatctctaccagtat	A	C	NM_025000 // downstream // 15119 // Hs.413518 // FLJ13096 // 80067 // Homo sapiens hypothetical protein FLJ13096 (FLJ13096), mRNA. /// ENST00000339506 // downstream // 15119 // — // — // — /// ENST00000260968 // downstream // 19993 // — //	FLJ13096	FLJ13096, Homo sapiens hypothetical protein FLJ13096 (FLJ13096), q31.1
SNP_A-2023371	aaaacctaattggaac[C/G]ggctcgagaaagaaca	C	G	NM_024843 // intron // 0 // Hs.221941 // CYBRD1 // 79901 // Homo sapiens cytochrome b reductase 1 (CYBRD1), mRNA. /// ENST00000321348 // intron // 0 // — // — // — // —	CYBRD1	CYBRD1, Homo sapiens cytochrome b reductase 1 (CYBRD1), q31.1
SNP_A-1840030	tagcaaggtaaaggta[C/T]gttgtatgttaagtta	C	T	NM_024843 // downstream // 8240 // Hs.221941 // CYBRD1 // 79901 // Homo sapiens cytochrome b reductase 1 (CYBRD1), mRNA. /// NM_001378 // upstream // 121105 // Hs.546250 // DNCI2 // 1781 // Homo sapiens dynein, cytoplasmic, intermediate polypeptide 2 (DNC	CYBRD1	CYBRD1, Homo sapiens cytochrome b reductase 1 (CYBRD1), q31.1
SNP_A-2075060	acatcccttaaagata[C/G]agcaataaggaagcca	C	G	NM_004405 // upstream // 108279 // Hs.419 // DLX2 // 1746 // Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 216825 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // upstream // 216825 // Hs.13	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-2076256	acatttctgggactta[A/C]cccagacctactgaat	A	C	NM_004405 // upstream // 114901 // Hs.419 // DLX2 // 1746 // Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 210203 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // upstream // 210203 // Hs.13	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1
SNP_A-2269905	gacaatcatgactctd[A/C]attttcctcctccc	A	C	NM_004405 // upstream // 185242 // Hs.419 // DLX2 // 1746 // Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /// X53586 // upstream // 139862 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // upstream // 139862 // Hs.13	DLX2	DLX2, Homo sapiens distal-less homeo box 2 (DLX2), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2178882	cactgatctcttggaa[C/T]taagttaaaaggctaa	C	T	X53586 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Homo sapiens integrin, alpha 6 (ITGA6), mRNA. /// ENST00000343713 // intron // 0 // — // — // — //	ITGA6	ITGA6, Human for integrin alpha 6. q31.1
SNP_A-1965848	ttgttttatgcaatta[C/T]aaggtttgcttcatga	C	T	X53586 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Homo sapiens integrin, alpha 6 (ITGA6), mRNA. /// ENST00000343713 // intron // 0 // — // — // — //	ITGA6	ITGA6, Human for integrin alpha 6. ,q31.1
SNP_A-1965852	atcaggaatcacagga[A/G]aaataaggctttgatt	A	G	X53586 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Homo sapiens integrin, alpha 6 (ITGA6), mRNA. /// ENST00000343713 // intron // 0 // — // — // — //	ITGA6	ITGA6, Human for integrin alpha 6. ,q31.1
SNP_A-1921748	ttactaaatattccta[A/C]aactctagatggtatt	A	C	X53586 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // intron // 0 // Hs.133397 // ITGA6 // 3655 // Homo sapiens integrin, alpha 6 (ITGA6), mRNA. /// ENST00000343713 // intron // 0 // --- // --- // --- //	ITGA6	ITGA6, Human for integrin alpha 6. ,q31.1
SNP_A-1955388	tttggggttttgacac[A/G]acaattgaccagcatt	A	G	X53586 // downstream // 6382 // Hs.133397 // ITGA6 // 3655 // Human mRNA for integrin alpha 6. /// NM_000210 // downstream // 6382 // Hs.133397 // ITGA6 // 3655 // Homo sapiens integrin, alpha 6 (ITGA6), mRNA. /// NM_002610 // upstream // 43395 // Hs.4706	ITGA6	ITGA6, Human for integrin alpha 6. q31.1
SNP_A-1700612	ataaatgacaaataagctaatatag[C/T]caggcattttattagttg caatttt	C	T	NM_000210 // intron // 0 // Hs.212296 // ITGA6 // 3655 // integrin, alpha 6 /// NM_002610 // intron // 0 // Hs.433611 // PDK1 // 5163 // pyruvate dehydrogenase kinase, isoenzyme 1	ITGA6	ITGA6 , rs10497381, integrin, alpha 6 ,q31.1
SNP_A-1732516	ctaacagctgtcctctgtattaagg[C/T]catctttagcttgtcttgca aatac	C	T	NM_000210 // intron // 0 // Hs.212296 // ITGA6 // 3655 // integrin, alpha 6 /// NM_002610 // intron // 0 // Hs.433611 // PDK1 // 5163 // pyruvate dehydrogenase kinase, isoenzyme 1	ITGA6	ITGA6 , rs7596259, integrin, alpha 6 ,q31.1
SNP_A-1706853	ttattgagtagctagactcagagtc[A/G]aggccatttggaaacag ttgcttgt	A	G	NM_000210 // intron // 0 // Hs.212296 // ITGA6 // 3655 // integrin, alpha 6 /// NM_002610 // intron // 0 // Hs.433611 // PDK1 // 5163 // pyruvate dehydrogenase kinase, isoenzyme 1	ITGA6	ITGA6 , rs2272499, integrin, alpha 6 ,q31.1
SNP_A-2071583	acagaagatgagtgac[A/G]atttgccatattatct	A	G	NM_133646 // downstream // 1726 // Hs.444451 // ZAK // 51776 // Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), mRNA. /// NM_016653 // downstream // 1726 // Hs.444451 // ZAK // 51776 // Homo sapiens sterile alpha motif and	ZAK	ZAK, Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), q31.1
SNP_A-1941060	ttgctctacctttcc[A/G]acataatgaatctgtg	A	G	ENST00000325502 // upstream // 19511 // — // — // — // — /// ENST00000357595 // downstream // 252164 // — // — // — // —	-	q31.1
SNP_A-2076105	acattcaggatctagc[C/T]caggcaggtcgggaag	C	T	ENST00000325502 // upstream // 186391 // — // — // — // — /// ENST00000357595 // downstream // 85284 // — // — // — // —	-	q31.1
SNP_A-1885725	tgacagatgatgccca[C/T]gtgggactcttctcta	C	T	NM_003111 // upstream // 20837 // Hs.531587 // SP3 // 6670 // Homo sapiens Sp3 transcription factor (SP3), mRNA. /// ENST00000310015 // upstream // 20837 // — // — // — // — /// ENST00000323483 // downstream // 3598 // — // — // — // —	SP3	SP3, Homo sapiens Sp3 transcription factor (SP3), q31.1
SNP_A-1670916	ctttcctacctcgggtctctcctaa[C/G]tctaggttcacaccatatc ccatca	C	G	NM_031942 // downstream // 251719 // Hs.435733 // CDCA7 // 83879 // cell division cycle associated 7 /// NM_145810 // downstream // 251719 // Hs.435733 // CDCA7 // 83879 // cell division cycle associated 7	CDCA7	CDCA7 , rs672524, cell division cycle associated 7 ,q31.1
SNP_A-1691696	caaacattatggtaaaagagagtca[C/G]taatattttccatgcca aatgtctt	C	G	NM_031942 // downstream // 370210 // Hs.435733 // CDCA7 // 83879 // cell division cycle associated 7 /// NM_145810 // downstream // 370210 // Hs.435733 // CDCA7 // 83879 // cell division cycle associated 7	CDCA7	CDCA7 , rs10497407, cell division cycle associated 7 ,q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1684096	acctaatagaagatgaagatcctta[C/T]aggaaaacggttctcac aatacataa	C	T	NM_031942 // downstream // 502868 // Hs.435733 // CDCA7 // 83879 // cell division cycle associated 7 /// NM_145810 // downstream // 502868 // Hs.435733 // CDCA7 // 83879 // cell division cycle associated 7	CDCA7	CDCA7 , rs6729538, cell division cycle associated 7 ,q31.1
SNP_A-1938139	ttgacaggctaagaaag[A/G]cagttatggtataggc	A	G	NM_005324 // downstream // 24913 // Hs.180877 // H3F3B // 3021 // Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA. /// NM_002107 // downstream // 24913 // Hs.546259 // H3F3A // 3020 // Homo sapiens H3 histone, family 3A (H3F3A), mRNA. /// NM_0000	H3F3B	H3F3B, Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), q31.1
SNP_A-2038571	aacagaacagggtacc[A/G]gcgaagtccaagaag	A	G	NM_001689 // upstream // 21100 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 21100 // Hs.429 // ATP5G3 // 518	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc q31.1
SNP_A-1784383	ggcccctgatgaggga[A/G]ccctttggcgagctc	A	G	NM_001689 // upstream // 268322 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 268322 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc ,q31.1
SNP_A-1733166	tttatttcagtatttatcacttgaa[A/G]taggaaaaaatagcaataa ttggaa	A	G	NM_001880 // intron // 0 // Hs.80285 // ATF2 // 1386 // activating transcription factor 2	ATF2	ATF2, rs2300582, activating transcription factor 2,q31.1
SNP_A-1862285	tcatggtctgcagtaa[C/T]tgtttaaactgttc	C	T	NM_001689 // upstream // 332584 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 332584 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc ,q31.1
SNP_A-1823296	taaaactggcttgaca[A/G]ataaactctttgcat	A	G	NM_001689 // upstream // 349479 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 349479 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc ,q31.1
SNP_A-2298325	gccattagccagcatt[C/G]aatcaaaagaccatgt	C	G	NM_001689 // upstream // 349711 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 349711 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc q31.1
SNP_A-1680924	ctggttagaattgagtacttgaga[A/G]actatatgaataaattgctt gttgaa	A	G	AB051502 // downstream // 742742 // Hs.209561 // KIAA1715 // 80856 // KIAA1715 /// NM_001689 // upstream // 1306 // Hs.429 // ATP5G3 // 518 // ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	KIAA1715	KIAA1715 , rs10497435, KIAA1715 ,q31.1
SNP_A-2204882	ccagggaaagagggaat[G/T]atagggatacagaaga	G	T	NM_001689 // upstream // 555459 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 555459 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc q31.1
SNP_A-1877286	tctggaaagtatccca[C/G]tgcattaagaaatct	C	G	NM_001689 // upstream // 616111 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 616111 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc ,q31.1
SNP_A-1884341	tgaaggtgccagttgat[G/T]cacaggatgaccaccg	G	T	NM_001689 // upstream // 713991 // Hs.429 // ATP5G3 // 518 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc /// NM_001002258 // upstream // 713991 // Hs.429 // ATP5G3 // 51	ATP5G3	ATP5G3, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), nuclear gene enc q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1949354	ttattatagttgccca[C/T]gtatttctgctgcatg	C	T	NM_006554 // downstream // 261285 // Hs.470728 // MTX2 // 10651 // Homo sapiens metaxin 2 (MTX2), transcript variant 1, mRNA. /// ENST00000249442 // downstream // 261285 // --- // --- // --- /// ENST00000295549 // downstream // 30622 // --- // ---	MTX2	MTX2, Homo sapiens metaxin 2 (MTX2), transcript variant 1, q31.1
SNP_A-1789291	gggccaacgaggaaac[A/C]aaatggcagcccaga	A	C	NM_194247 // upstream // 433626 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 141243 // --- // --- // --- /// ENST00000306311 // upstream // 433626 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2238691	ctctgtttcatcacca[G/T]taataagagtaataat	G	T	NM_194247 // upstream // 420291 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 154578 // --- // --- // --- /// ENST00000306311 // upstream // 420291 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2023119	aaaacaggagaaggacf[A/G]caatttgaagaaatca	A	G	NM_194247 // upstream // 402536 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 172333 // --- // --- // --- /// ENST00000306311 // upstream // 402536 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1965969	cgataatgttagtcag[A/C]accttatgaactctct	A	C	NM_194247 // upstream // 335083 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 239786 // --- // --- // --- /// ENST00000306311 // upstream // 335083 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1965971	aaagagcttatttata[C/T]ggaatgctaatttctt	C	T	NM_194247 // upstream // 333324 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 241545 // --- // --- // --- /// ENST00000306311 // upstream // 333324 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2163186	attttctcaggaaaac[C/T]gatgaggtctttggat	C	T	NM_194247 // upstream // 308687 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 266182 // --- // --- // --- /// ENST00000306311 // upstream // 308687 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2071469	acagaaagccaacacg[A/G]agacaataatatcac	A	G	NM_194247 // upstream // 291521 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 283348 // --- // --- // --- /// ENST00000306311 // upstream // 291521 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2147193	atggacatcctcaaaa[A/C]gctcattgtcttatgg	A	C	NM_194247 // upstream // 227293 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 347576 // --- // --- // --- /// ENST00000306311 // upstream // 227293 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1965976	actctgatttaaaacc[A/G]acacagcatatcagca	A	G	NM_194247 // upstream // 165325 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 409544 // --- // --- // --- /// ENST00000306311 // upstream // 165325 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-2006859	tgagttcatcttgacc[A/G]ggggtctgacctttt	A	G	NM_194247 // upstream // 145291 // Hs.516539 // HNRPA3 // 220988 // Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA. /// ENST00000295549 // upstream // 429578 // --- // --- // --- /// ENST00000306311 // upstream // 145291 //	HNRPA3	HNRPA3, Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), q31.1
SNP_A-1655905	acatggcatcaaattctgagtaaca[A/G]ctaagagacaagtg ggcaggcagg	A	G	AF517524 // upstream // 230267 // Hs.446430 // hnRNPA3 // 220988 // heterogeneous nuclear ribonucleoprotein A3	hnRNPA3	hnRNPA3, rs10497468, heterogeneous nuclear ribonucleoprotein A3,q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1651858	tatgaaacagtatagatcttctcg[C/T]cactgcagtaccctaata ccattta	C	T	AF517524 // upstream // 152770 // Hs.446430 // hnRNPA3 // 220988 // heterogeneous nuclear ribonucleoprotein A3	hnRNPA3	hnRNPA3 , rs1919631, heterogeneous nuclear ribonucleoprotein A3,q31.1
SNP_A-1965992	tgggttcagacaacaa[A/G]gctatagaatgtgctt	A	G	NM_152517 // upstream // 37273 // Hs.447659 // FLJ30990 // 150737 // Homo sapiens hypothetical protein FLJ30990 (FLJ30990), mRNA. /// NM_152275 // downstream // 26668 // Hs.128384 // FLJ13946 // 92104 // Homo sapiens hypothetical protein FLJ13946 (FLJ1394	FLJ30990	FLJ30990, Homo sapiens hypothetical protein FLJ30990 (FLJ30990), q31.2
SNP_A-2184478	cagctaccgttgaaaac[C/T]ctttcagaggcagtgc	C	T	NM_016953 // intron // 0 // Hs.130312 // PDE11A // 50940 // Homo sapiens phosphodiesterase 11A (PDE11A), mRNA. /// ENST00000286063 // intron // 0 // — // — // — // — /// ENST00000358450 // intron // 0 // — // — // — // —	PDE11A	PDE11A, Homo sapiens phosphodiesterase 11A (PDE11A), q31.2
SNP_A-2077939	accagcattagggcta[C/T]acaatgtctaaatag	C	T	NM_173648 // intron // 0 // — // FLJ39502 // 285025 // Homo sapiens hypothetical protein FLJ39502 (FLJ39502), mRNA. /// ENST00000295723 // intron // 0 // — // — // — // — /// ENST00000343876 // intron // 0 // — // — // — // —	FLJ39502	FLJ39502, Homo sapiens hypothetical protein FLJ39502 (FLJ39502), q31.2
SNP_A-1955771	tttgtagatgggacct[C/G]aaaagtcgtatttttc	C	G	NM_178123 // upstream // 4519 // Hs.370668 // SESTD1 // 91404 // Homo sapiens SEC14 and spectrin domains 1 (SESTD1), mRNA. /// NM_152520 // downstream // 172702 // Hs.470791 // ZNF533 // 151126 // Homo sapiens zinc finger protein 533 (ZNF533), mRNA. /// N	SESTD1	SESTD1, Homo sapiens SEC14 and spectrin domains 1 (SESTD1), q31.2
SNP_A-1947624	ttacctcacgggtc[A/G]agggcaaatggaaggt	A	G	NM_178123 // upstream // 142924 // Hs.370668 // SESTD1 // 91404 // Homo sapiens SEC14 and spectrin domains 1 (SESTD1), mRNA. /// NM_152520 // downstream // 34297 // Hs.470791 // ZNF533 // 151126 // Homo sapiens zinc finger protein 533 (ZNF533), mRNA. ///	SESTD1	SESTD1, Homo sapiens SEC14 and spectrin domains 1 (SESTD1), q31.2
SNP_A-1691656	ttatagaaggaaactgctagata[C/T]aaaagttgcttgtttataa ttattc	C	T	NM_173648 // upstream // 221773 // Hs.99104 // FLJ39502 // 285025 // hypothetical protein FLJ39502 /// NM_178123 // downstream // 38876 // Hs.151414 // SESTD1 // 91404 // SEC14 and spectrin domains 1	FLJ39502	FLJ39502, rs10497532, hypothetical protein FLJ39502, q31.2
SNP_A-2209289	ccagtggaacatttac[C/T]ccatcttcaggtgtt	C	T	NM_006357 // upstream // 967956 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // upstream // 967956 // Hs.470804 // UBE2E3 // 10477 // Homo sa	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2271811	gaccatgactgttata[C/T]gcctttaatcctccca	C	T	NM_006357 // upstream // 865429 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // upstream // 865429 // Hs.470804 // UBE2E3 // 10477 // Homo sa	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1872918	tctatcccacttcaca[C/T]tgctttataagcaaaa	C	T	NM_006357 // upstream // 782668 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // upstream // 782668 // Hs.470804 // UBE2E3 // 10477 // Homo sa	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1780301	ggataaatttctccca[C/T]gaatgcagaatagta	C	T	NM_006357 // upstream // 295574 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // upstream // 295574 // Hs.470804 // UBE2E3 // 10477 // Homo sa	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1966113	ctctgttgctgagata[C/T]acagtattaaccatta	C	T	NM_006357 // intron // 0 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // intron // 0 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquiti	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1966114	tttattgagctactaq[A/G]aagttaaacaatatgc	A	G	NM_006357 // downstream // 19330 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 19330 // Hs.470804 // UBE2E3 // 10477 // Homo	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4, q31.3
SNP_A-2196174	catgtggatacataga[A/G]gttaaatttataaa	A	G	NM_006357 // downstream // 91311 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 91311 // Hs.470804 // UBE2E3 // 10477 // Homo	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2150700	atgtgcattaggttgc[C/T]gaaaagattaaatgag	C	T	NM_006357 // downstream // 110579 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 110579 // Hs.470804 // UBE2E3 // 10477 // Hom	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1834351	tacattccccatattc[C/G]agtagatgtttatc	C	G	NM_006357 // downstream // 119489 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 119489 // Hs.470804 // UBE2E3 // 10477 // Hom	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-2224136	cggtagggccacttg[C/T]aggacagcttggcagt	C	T	NM_006357 // downstream // 130378 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 130378 // Hs.470804 // UBE2E3 // 10477 // Hom	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4,q31.3
SNP_A-2175572	cacatgactgtaaaca[C/T]ataaggaagtggaatc	C	T	NM_006357 // downstream // 133846 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 133846 // Hs.470804 // UBE2E3 // 10477 // Hom	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1791927	gggtgcctgggaaaga[A/T]taaaagtgctgaggaa	A	T	NM_006357 // downstream // 264601 // Hs.470804 // UBE2E3 // 10477 // Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), transcript variant 1, mRNA. /// NM_182678 // downstream // 264601 // Hs.470804 // UBE2E3 // 10477 // Hom	UBE2E3	UBE2E3, Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4 q31.3
SNP_A-1727184	tcataaacatgccttgtttattgtc[C/T]atataactgcttttatatcatt at	C	T	NM_006357 // intron // 0 // Hs.449501 // UBE2E3 // 10477 // ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	UBE2E3	UBE2E3 , rs4077213, ubiquitin-conjugating enzyme E2E 3 (UBC4,q31.3
SNP_A-1679308	gtcatatagcttttgcctgactat[A/G]aataataaattggtatagtt agcag	A	G	NM_000885 // upstream // 200081 // Hs.528404 // ITGA4 // 3676 // integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) /// NM_006357 // downstream // 192980 // Hs.449501 // UBE2E3 // 10477 // ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homo	ITGA4	ITGA4 , rs1371617, integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor), q31.3
SNP_A-1737683	gtttctcgaaaactctaaaaatcag[A/G]ctacattctttatatgccat tgtga	A	G	NM_000885 // upstream // 115131 // Hs.528404 // ITGA4 // 3676 // integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) /// NM_006357 // downstream // 277930 // Hs.449501 // UBE2E3 // 10477 // ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homo	ITGA4	ITGA4 , rs7557202, integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor), q31.3
SNP_A-1966165	catttttccatattaag[A/G]acctaagacctacaga	A	G	NM_013436 // intron // 0 // Hs.516633 // NCKAP1 // 10787 // Homo sapiens NCK-associated protein 1 (NCKAP1), transcript variant 1, mRNA. /// NM_205842 // intron // 0 // Hs.516633 // NCKAP1 // 10787 // Homo sapiens NCK-associated protein 1 (NCKAP1), transcr	NCKAP1	NCKAP1, Homo sapiens NCK-associated protein 1 (NCKAP1), transcript variant 1, q32.1
SNP_A-1707275	tctagaaaaggcaagcttatgata[A/C]agaggagcaaatcagta gttgcctag	A	C	NM_013436 // intron // 0 // Hs.278411 // NCKAP1 // 10787 // NCK-associated protein 1	NCKAP1	NCKAP1 , rs2368351, NCK-associated protein 1,q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2070560	acacctctgactcca[A/C]agggaagccacaagtt	A	C	NM_138285 // downstream // 1172049 // Hs.180591 // NUP35 // 129401 // Homo sapiens nucleoporin 35kDa (NUP35), mRNA. /// NM_194250 // upstream // 265231 // Hs.159528 // C2orf10 // 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. ///	NUP35	NUP35, Homo sapiens nucleoporin 35kDa (NUP35), q32.1
SNP_A-1879869	tcttcccgttgtaca[C/T]acccagccttaaatt	C	T	NM_138285 // downstream // 1260804 // Hs.180591 // NUP35 // 129401 // Homo sapiens nucleoporin 35kDa (NUP35), mRNA. /// NM_194250 // upstream // 176476 // Hs.159528 // C2orf10 // 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. ///	NUP35	NUP35, Homo sapiens nucleoporin 35kDa (NUP35), q32.1
SNP_A-2267523	gaatatgctgagtttc[A/G]ctgggagccaggaagt	A	G	NM_194250 // intron // 0 // Hs.159528 // C2orf10 // 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. /// ENST00000302277 // intron // 0 // — // — // —	C2orf10	C2orf10, Homo sapiens similar to C630007C17Rik protein (LOC91752), q32.1
SNP_A-1693923	caagaaaagctgctatatttctccc[G/T]aggtacaatgcctatgtc atatgat	G	T	NM_018547 // upstream // 175791 // - // - // - // - /// NM_173651 // upstream // 964247 // Hs.376600 // FLJ34780 // 285135 // hypothetical protein FLJ34780	-	- , rs10497658, - , q32.1
SNP_A-2028848	aaacttgtacactgaa[G/T]ctataaaacttggt	G	T	NM_194250 // downstream // 403163 // Hs.159528 // C2orf10 // 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. /// ENST00000302277 // downstream // 403163 // — // — // — // — /// ENST00000325978 // upstream // 737722 // —	C2orf10	C2orf10, Homo sapiens similar to C630007C17Rik protein (LOC91752), q32.1
SNP_A-2082812	acgtaatttgcacatc[G/T]caggctgataaggag	G	T	NM_194250 // downstream // 412225 // Hs.159528 // C2orf10 // 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. /// ENST00000302277 // downstream // 412225 // — // — // — // — /// ENST00000325978 // upstream // 746784 // —	C2orf10	C2orf10, Homo sapiens similar to C630007C17Rik protein (LOC91752), q32.1
SNP_A-1885687	tgacagaatatttcca[A/T]cttcactccacagtt	A	T	NM_194250 // downstream // 412474 // Hs.159528 // C2orf10 // 91752 // Homo sapiens similar to C630007C17Rik protein (LOC91752), mRNA. /// ENST00000302277 // downstream // 412474 // — // — // — // — /// ENST00000325978 // upstream // 747033 // —	C2orf10	C2orf10, Homo sapiens similar to C630007C17Rik protein (LOC91752), q32.1
SNP_A-2284959	gatccccccacttcaa[C/T]cttgcaaagaactgga	C	T	NM_018471 // downstream // 75793 // Hs.368598 // LEREPO4 // 55854 // Homo sapiens likely ortholog of mouse immediate early response, erythropoietin 4 (LEREPO4), mRNA. /// NM_002210 // upstream // 4929 // Hs.436873 // ITGAV // 3685 // Homo sapiens integrin	LEREPO4	LEREPO4, Homo sapiens likely ortholog of mouse immediate early response, erythropoietin 4 (LEREPO4), q32.1
SNP_A-2023907	aaaagaatatgaatgc[A/T]gactggtctagctac	A	T	NM_182521 // upstream // 322050 // Hs.375054 // ZSWIM2 // 151112 // Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), mRNA. /// NM_005795 // downstream // 173885 // Hs.470882 // CALCRL // 10203 // Homo sapiens calcitonin receptor-like (CALCRL),	ZSWIM2	ZSWIM2, Homo sapiens zinc finger, SWIM domain containing 2 (ZSWIM2), q32.1
SNP_A-2290076	gcaaataatgaaaaga[A/G]gtcaagttaagtgatt	A	G	NM_005795 // intron // 0 // Hs.470882 // CALCRL // 10203 // Homo sapiens calcitonin receptor-like (CALCRL), mRNA. /// ENST00000264152 // intron // 0 // — // — // — // —	CALCRL	CALCRL, Homo sapiens calcitonin receptor-like (CALCRL), q32.1
SNP_A-1781560	ggattcctgaaattca[A/C]tcatgggtatctgagt	A	C	NM_005795 // intron // 0 // Hs.470882 // CALCRL // 10203 // Homo sapiens calcitonin receptor-like (CALCRL), mRNA. /// ENST00000264152 // intron // 0 // — // — // — // —	CALCRL	CALCRL, Homo sapiens calcitonin receptor-like (CALCRL), q32.1
SNP_A-1966228	gttaatagaccttaa[C/G]aacaacagcgaaacat	C	G	NM_005795 // intron // 0 // Hs.470882 // CALCRL // 10203 // Homo sapiens calcitonin receptor-like (CALCRL), mRNA. /// ENST00000264152 // intron // 0 // — // — // — // —	CALCRL	CALCRL, Homo sapiens calcitonin receptor-like (CALCRL), q32.1
SNP_A-1891370	tgattagtgatttcca[C/G]catttttcatatgct	C	G	NM_006287 // intron // 0 // Hs.516578 // TFPI // 7035 // Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA. /// ENST00000233156 // intron // 0 // — // — // — // — /// ENST00000339091 // intron	TFPI	TFPI, Homo sapiens tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1736021	tgtcatccagttgccggaattcata[C/T]taggcatttttcgcaagtat aatctt	C	T	NM_006287 // upstream // 563618 // Hs.102301 // TFPI // 7035 // tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) /// NM_016315 // upstream // 225469 // Hs.107056 // GULP1 // 51454 // GULP, engulfment adaptor PTB domain conta	TFPI	TFPI , rs4666753, tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) ,q32.1
SNP_A-2042579	aactccacacacatga[C/T]aatgacaatgtggtaa	C	T	NM_000090 // downstream // 73399 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 355288 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-2289546	gattttgctttacaa[A/G]agttcatacacatttt	A	G	NM_000090 // downstream // 76755 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 351932 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-2043045	aactgagagttctgga[C/T]aaaattaatgacctgt	C	T	NM_000090 // downstream // 195646 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 233041 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-2155888	attcctcaaattctgg[C/T]caaaatagaatttttc	C	T	NM_000090 // downstream // 195894 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 232793 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-1966254	tctctagctactacaa[C/T]tgattgtcctatgact	C	T	NM_000090 // downstream // 228993 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 199694 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-1877300	tctggaacttcaacta[C/T]acatatgtcagacctt	C	T	NM_000090 // downstream // 387563 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 41124 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-2089383	acttatagttggaata[G/T]tatactcagcaaaagc	G	T	NM_000090 // downstream // 405743 // Hs.443625 // COL3A1 // 1281 // Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA. /// NM_032168 // upstream // 22944 // Hs.399984 // FLJ12519 // 84128 // Homo	COL3A1	COL3A1, Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), q32.2
SNP_A-1966257	aaaagttcagagcaag[A/G]ctagaaataagagtta	A	G	NM_032168 // intron // 0 // Hs.399984 // FLJ12519 // 84128 // Homo sapiens hypothetical protein FLJ12519 (FLJ12519), mRNA. /// ENST00000314761 // intron // 0 // — // — // — // —	FLJ12519	FLJ12519, Homo sapiens hypothetical protein FLJ12519 (FLJ12519), q32.2
SNP_A-2183316	cagcacatctgcttta[A/C]actgactgactgacct	A	C	NM_032168 // downstream // 12502 // Hs.399984 // FLJ12519 // 84128 // Homo sapiens hypothetical protein FLJ12519 (FLJ12519), mRNA. /// NM_014585 // downstream // 72552 // Hs.529285 // SLC40A1 // 30061 // Homo sapiens solute carrier family 40 (iron-regulat	FLJ12519	FLJ12519, Homo sapiens hypothetical protein FLJ12519 (FLJ12519), q32.2
SNP_A-2042177	aactagtccaaagaaa[C/G]ttctggtgactgttaa	C	G	NM_032168 // downstream // 74029 // Hs.399984 // FLJ12519 // 84128 // Homo sapiens hypothetical protein FLJ12519 (FLJ12519), mRNA. /// NM_014585 // downstream // 11025 // Hs.529285 // SLC40A1 // 30061 // Homo sapiens solute carrier family 40 (iron-regulat	FLJ12519	FLJ12519, Homo sapiens hypothetical protein FLJ12519 (FLJ12519), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027694	aaaccattcattccac[G/T]gccttttcactgtcca	G	T	NM_014585 // intron // 0 // Hs.529285 // SLC40A1 // 30061 // Homo sapiens solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1), mRNA. /// ENST00000261024 // intron // 0 // — // — // — // —	SLC40A1	SLC40A1, Homo sapiens solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1), q32.2
SNP_A-1922621	ttagacctgtttaaaaa[C/T]tctaaagcacatgtta	C	T	NM_019048 // intron // 0 // Hs.101364 // NS3TP1 // 54529 // Homo sapiens HCV NS3-transactivated protein 1 (NS3TP1), mRNA. /// ENST00000260952 // intron // 0 // — // — // — // —	NS3TP1	NS3TP1, Homo sapiens HCV NS3-transactivated protein 1 (NS3TP1), q32.2
SNP_A-2143703	atgagaagaatttcac[G/T]ggccacctatcctatt	G	T	NM_016467 // intron // 0 // Hs.512600 // ORMDL1 // 94101 // Homo sapiens ORM1-like 1 (S. cerevisiae) (ORMDL1), mRNA. /// ENST00000325795 // intron // 0 // — // — // — // —	ORMDL1	ORMDL1, Homo sapiens ORM1-like 1 (S. cerevisiae) (ORMDL1), q32.2
SNP_A-1712965	cattcatattcttttccattttaa[A/C]acccagcttaatactttggaatgta	A	C	NM_032168 // intron // 0 // Hs.399984 // FLJ12519 // 84128 // hypothetical protein FLJ12519	FLJ12519	FLJ12519 , rs7419276, hypothetical protein FLJ12519,q32.2
SNP_A-1751461	caggactgactgggcttggatccag[A/G]acatgtatggtacgtgtatgttttt	A	G	NM_014585 // downstream // 69963 // Hs.409875 // SLC40A1 // 30061 // solute carrier family 40 (iron-regulated transporter), member 1 /// NM_032168 // downstream // 15091 // Hs.399984 // FLJ12519 // 84128 // hypothetical protein FLJ12519	SLC40A1	SLC40A1 , rs10497703, solute carrier family 40 (iron-regulated transporter), member 1 ,q32.2
SNP_A-2027985	aaacctttggaaaca[A/G]ggctcaatgtctcaga	A	G	NM_017694 // CDS // 0 // Hs.418581 // FLJ20160 // 54842 // Homo sapiens FLJ20160 protein (FLJ20160), mRNA. /// ENST00000281416 // CDS // 0 // — // — // — // —	FLJ20160	FLJ20160, Homo sapiens FLJ20160 protein (FLJ20160), q32.2
SNP_A-2085214	actcagtaaatagtcc[C/G]gaacggaagagaaaat	C	G	NM_017694 // intron // 0 // Hs.418581 // FLJ20160 // 54842 // Homo sapiens FLJ20160 protein (FLJ20160), mRNA. /// ENST00000281416 // intron // 0 // — // — // — // —	FLJ20160	FLJ20160, Homo sapiens FLJ20160 protein (FLJ20160), q32.2
SNP_A-1918158	ttaaactgccatagta[C/T]gcactgttatgactga	C	T	NM_017694 // intron // 0 // Hs.418581 // FLJ20160 // 54842 // Homo sapiens FLJ20160 protein (FLJ20160), mRNA. /// ENST00000281416 // intron // 0 // — // — // — // —	FLJ20160	FLJ20160, Homo sapiens FLJ20160 protein (FLJ20160), q32.2
SNP_A-2120256	agtcagtctggaaagg[A/G]aaaccaacccatttttg	A	G	NM_017694 // downstream // 6974 // Hs.418581 // FLJ20160 // 54842 // Homo sapiens FLJ20160 protein (FLJ20160), mRNA. /// ENST00000281416 // downstream // 6974 // — // — // — // — /// ENST00000341370 // downstream // 146 // — // — // — // —	FLJ20160	FLJ20160, Homo sapiens FLJ20160 protein (FLJ20160), q32.2
SNP_A-1910612	tgtcctctttgcctat[A/G]aagtgcctacttactc	A	G	NM_005966 // upstream // 72364 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // upstream // 82289 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 bind	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-2023267	aaaaccaacccgaaca[A/G]tacaatgatttcatcc	A	G	NM_005966 // upstream // 44997 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // upstream // 54922 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 bind	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-1880553	tcttgcaatccaagcg[A/G]agagagaagactggct	A	G	NM_005966 // upstream // 8265 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // upstream // 18190 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 bindi	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-2036369	aaattccttcccccaa[C/T]acagcctgcaatttttt	C	T	NM_005966 // intron // 0 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// ENST00000321041 // intron // 0 // — // — // — // —	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-1780774	ggatcgggtgctcatg[A/G]acaagtgactggctta	A	G	NM_005966 // downstream // 6340 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // downstream // 4271 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 bi	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1854509	tcaaattagagcctga[A/G]aagtctaagcaagaac	A	G	NM_005966 // downstream // 71656 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // downstream // 69587 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-2242288	ctgcaatgaagaagcg[C/T]agattttgacaatagt	C	T	NM_005966 // downstream // 113419 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // downstream // 111350 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-2057635	aatatgcattggttta[C/G]ggacaattgtatagtt	C	G	NM_005966 // downstream // 117870 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // downstream // 115801 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-1957269	ttttagaaactatgac[C/T]aggtaagaggtcggat	C	T	NM_005966 // downstream // 127968 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), mRNA. /// NM_005966 // downstream // 125899 // Hs.107474 // NAB1 // 4664 // Homo sapiens NGFI-A binding protein 1 (EGR	NAB1	NAB1, Homo sapiens NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1), q32.2
SNP_A-2084281	actagtgtaacactaa[A/G]atgctatgattaacca	A	G	NM_014905 // intron // 0 // Hs.116448 // GLS // 2744 // Homo sapiens glutaminase (GLS), mRNA. /// ENST00000320717 // intron // 0 // --- // --- // --- /// ENST00000338435 // intron // 0 // --- // --- // --- // ---	GLS	GLS, Homo sapiens glutaminase (GLS), q32.2
SNP_A-2146003	atgcctcaggttccca[C/T]gctaaatcaaaattct	C	T	NM_007315 // upstream // 3327 // Hs.470943 // STAT1 // 6772 // Homo sapiens signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant alpha, mRNA. /// NM_139266 // upstream // 3327 // Hs.470943 // STAT1 // 6772 // Homo sapiens	STAT1	STAT1, Homo sapiens signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant alpha, q32.2
SNP_A-1826477	taacaacaggatctgc[C/G]ctaattctaataggtc	C	G	NM_003151 // intron // 0 // Hs.80642 // STAT4 // 6775 // Homo sapiens signal transducer and activator of transcription 4 (STAT4), mRNA. /// ENST00000260949 // intron // 0 // --- // --- // --- // --- /// ENST00000358470 // intron // 0 // --- // --- // ---	STAT4	STAT4, Homo sapiens signal transducer and activator of transcription 4 (STAT4), q32.2
SNP_A-2181556	cagagaacaagcaaaa[C/T]tccacctaagcttaaa	C	T	NM_012223 // intron // 0 // Hs.439620 // MYO1B // 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// ENST00000339514 // intron // 0 // --- // --- // --- // --- /// ENST00000304164 // intron // 0 // --- // --- // --- // ---	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-1904358	tgggcttcaggtgaaa[C/T]gatgccatccacacat	C	T	NM_012223 // downstream // 183420 // Hs.439620 // MYO1B // 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 69400 // Hs.118183 // FLJ22833 // 64859 // Homo sapiens hypothetical protein FLJ22833 (FLJ22833), mRNA. /// ENST000003395	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-1831962	taattgctgtatacta[C/T]gactgcttttctccat	C	T	NM_012223 // downstream // 186897 // Hs.439620 // MYO1B // 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 65923 // Hs.118183 // FLJ22833 // 64859 // Homo sapiens hypothetical protein FLJ22833 (FLJ22833), mRNA. /// ENST000003395	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-2312139	ggacagagaagcgcta[A/G]gtctttacgtatcttc	A	G	NM_012223 // downstream // 198234 // Hs.439620 // MYO1B // 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 54586 // Hs.118183 // FLJ22833 // 64859 // Homo sapiens hypothetical protein FLJ22833 (FLJ22833), mRNA. /// ENST000003395	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1817162	gttcaaggcagaaaaa[C/T]cagttcttctaaggac	C	T	NM_012223 // downstream // 201964 // Hs.439620 // MYO1B // 4430 // Homo sapiens myosin IB (MYO1B), mRNA. /// NM_022837 // upstream // 50856 // Hs.118183 // FLJ22833 // 64859 // Homo sapiens hypothetical protein FLJ22833 (FLJ22833), mRNA. /// ENST000003395	MYO1B	MYO1B, Homo sapiens myosin IB (MYO1B), q32.3
SNP_A-2106862	agccttagttccatca[C/T]ctgtaatatgagggta	C	T	NM_016192 // intron // 0 // Hs.144513 // TMEFF2 // 23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // intron // 0 // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-1966310	aagaaaggacatctta[A/C]aaatgaattcctgaat	A	C	NM_016192 // intron // 0 // Hs.144513 // TMEFF2 // 23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // intron // 0 // --- // --- // ---	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-1858348	tcagacactgtagaat[A/G]agacagcaggcagagt	A	G	NM_016192 // upstream // 277436 // Hs.144513 // TMEFF2 // 23671 // Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), mRNA. /// ENST00000272771 // upstream // 277436 // --- // --- // --- // --- /// ENST0000031505	TMEFF2	TMEFF2, Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 2 (TMEFF2), q32.3
SNP_A-1913651	tgtgtagatttgtaga[C/T]aaaagatgatgtctga	C	T	ENST00000315054 // upstream // 3032 // --- // --- // --- // --- /// ENST00000354860 // upstream // 1110185 // --- // --- // --- // ---	-	q32.3
SNP_A-1877265	tctggaaaacactaga[C/T]aagctcaagtgtgaca	C	T	ENST00000315054 // upstream // 5701 // --- // --- // --- // --- /// ENST00000354860 // upstream // 1107516 // --- // --- // --- // ---	-	q32.3
SNP_A-2034526	aaatctgtacccccac[C/T]caaattagcatttgtt	C	T	ENST00000315054 // upstream // 26990 // --- // --- // --- // --- /// ENST00000354860 // upstream // 1086227 // --- // --- // --- // ---	-	q32.3
SNP_A-2091341	acttttgaggtatcca[A/G]tcaggtattttgcaga	A	G	ENST00000315054 // upstream // 42747 // --- // --- // --- // --- /// ENST00000354860 // upstream // 1070470 // --- // --- // --- // ---	-	q32.3
SNP_A-1966329	attgacagcatcaaaa[C/T]ggagggaacctggatc	C	T	ENST00000315054 // upstream // 115155 // --- // --- // --- // --- /// ENST00000354860 // upstream // 998062 // --- // --- // --- // ---	-	q32.3
SNP_A-1905579	tggtagatttcaacta[A/G]caatgtcctggtaaac	A	G	ENST00000315054 // upstream // 163285 // --- // --- // --- // --- /// ENST00000354860 // upstream // 949932 // --- // --- // --- // ---	-	q32.3
SNP_A-1679662	tgctaagagagtatagagggtgtgc[A/C]ataaactaaatctgcaggtattaag	A	C	NM_016192 // upstream // 1197318 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs2247613, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1663402	tgagatgatttggagatatatagac[C/G]atcaataatttttacagactctaga	C	G	NM_016192 // upstream // 1211284 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs2251355, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1648626	aactacaaatataataacatgttaa[C/T]acaatcttcaggatagttactgggt	C	T	NM_016192 // upstream // 1215561 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs2357647, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1709637	attctttagccttttcttaaagtaa[C/G]ctgctaagtatttacaggttaattt	C	G	NM_016192 // upstream // 1244066 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs726129, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1757493	ttccttgaccctaataatgtatcac[C/T]ctgaattgctatttttatttatgct	C	T	NM_016192 // upstream // 1244156 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs726130, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1832400	tacaaaagcttagata[C/T]gaggagacttcaaaaa	C	T	ENST00000315054 // upstream // 545406 // --- // --- // --- // --- /// ENST00000354860 // upstream // 567811 // --- // --- // --- // ---	-	q32.3
SNP_A-2162695	attttctttcctcaga[C/T]gttccttatacttatg	C	T	ENST00000315054 // upstream // 564217 // --- // --- // --- // --- /// ENST00000354860 // upstream // 549000 // --- // --- // --- // ---	-	q32.3
SNP_A-2006927	actagctccaatctgc[A/G]cattgtgagaaatttt	A	G	ENST00000315054 // upstream // 592309 // --- // --- // --- // --- /// ENST00000354860 // upstream // 520908 // --- // --- // --- // ---	-	q32.3
SNP_A-1915718	tgttcttatagtttta[C/T]gcaatttttcaacaag	C	T	ENST00000315054 // upstream // 671499 // --- // --- // --- // --- /// ENST00000354860 // upstream // 441718 // --- // --- // --- // ---	-	q32.3
SNP_A-2308873	gctttgtatgggacac[A/G]gatgatgctgagcgct	A	G	ENST00000315054 // upstream // 676425 // --- // --- // --- // --- /// ENST00000354860 // upstream // 436792 // --- // --- // --- // ---	-	q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1737726	cagcagtctctgtgaatacataattca[G/T]tctcatgtcccatcaattc ctata	G	T	NM_016192 // upstream // 1619556 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs10497745, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1950459	tttcagttcagactac[A/G]cagtattaataaata	A	G	ENST00000315054 // upstream // 1020111 /// — // — // — // — /// ENST00000354860 // upstream // 93106 // — // — // — // —	-	q32.3
SNP_A-1878237	tctgtcagtactgtaa[A/C]attgtcaggaaaaata	A	C	ENST00000354860 // downstream // 52636 // — // — // — // — /// ENST00000359634 // upstream // 1156354 // — // — // — // — ENST00000359181 // upstream // 1156354 // — // — // — // —	-	q32.3
SNP_A-2059815	aatctgtagggtacca[A/G]caagcataaaaacaca	A	G	ENST00000354860 // downstream // 164478 // — // — // — // — /// ENST00000359634 // upstream // 1044512 // — // — // — // — /// ENST00000359181 // upstream // 1044512 // — // — // — // —	-	q32.3
SNP_A-1912392	tgtgcaaatgtaagcc[A/G]agttttcataaccag	A	G	ENST00000354860 // downstream // 421627 // — // — // — // — /// ENST00000359634 // upstream // 787363 // — // — // — // — ENST00000359181 // upstream // 787363 // — // — // — // —	-	q32.3
SNP_A-2037973	aacaattgtgcctcac[C/T]accggatgctggctaa	C	T	ENST00000354860 // downstream // 472594 // — // — // — // — /// ENST00000359634 // upstream // 736396 // — // — // — // — ENST00000359181 // upstream // 736396 // — // — // — // —	-	q32.3
SNP_A-2165091	caaacttctgactcca[A/G]aactagtgatacagac	A	G	ENST00000354860 // downstream // 472815 // — // — // — // — /// ENST00000359634 // upstream // 736175 // — // — // — // — ENST00000359181 // upstream // 736175 // — // — // — // —	-	q32.3
SNP_A-2184670	cagcctctcagggaca[G/T]aatcttaagtactgac	G	T	ENST00000354860 // downstream // 498785 // — // — // — // — /// ENST00000359634 // upstream // 710205 // — // — // — // — ENST00000359181 // upstream // 710205 // — // — // — // —	-	q32.3
SNP_A-2256238	ctttagccaataggta[A/G]atcttgtaggcagt	A	G	ENST00000354860 // downstream // 538142 // — // — // — // — /// ENST00000359634 // upstream // 670848 // — // — // — // — ENST00000359181 // upstream // 670848 // — // — // — // —	-	q32.3
SNP_A-2151487	atgttctagacaagtg[A/G]agccaggttaaatcac	A	G	ENST00000354860 // downstream // 590525 // — // — // — // — /// ENST00000359634 // upstream // 618465 // — // — // — // — ENST00000359181 // upstream // 618465 // — // — // — // —	-	q32.3
SNP_A-1802552	gtatctcagctatcca[A/G]aaccttaaacccacag	A	G	ENST00000354860 // downstream // 601927 // — // — // — // — /// ENST00000359634 // upstream // 607063 // — // — // — // — ENST00000359181 // upstream // 607063 // — // — // — // — ENST00000354860 // downstream // 732569 // — // — // — // — /// ENST00000359634 // upstream // 476421 // — // — // — // — ENST00000359181 // upstream // 476421 // — // — // — // —	-	q32.3
SNP_A-1824050	taaacaagcctgcatg[A/G]acttcagccttacctt	A	G		-	q32.3
SNP_A-1659516	gaacagtaacatttgaaagcagtc[C/T]ttccttctgagaagttg gtctcaa	C	T	NM_016192 // upstream // 2776275 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2 ENST00000354860 // downstream // 961162 // — // — // — // — /// ENST00000359634 // upstream // 247828 // — // — // — // — ENST00000359181 // upstream // 247828 // — // — // — // —	TMEFF2	TMEFF2 , rs1073982, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1915828	tgttgaatacctcctc[C/T]gttcagacaaatatt	C	T		-	q32.3
SNP_A-1653278	ccacactgatgagtagggaatgcaa[A/G]catgctgaaggcag gatggttcaaa	A	G	NM_016192 // upstream // 2914879 // Hs.22791 // TMEFF2 // 23671 // transmembrane protein with EGF-like and two follistatin-like domains 2	TMEFF2	TMEFF2 , rs1965394, transmembrane protein with EGF-like and two follistatin-like domains 2,q32.3
SNP_A-1837812	tacttttttcatagtaa[C/T]ctaacaattagtcaaa	C	T	NM_018897 // intron // 0 // Hs.97403 // DNAH7 // 56171 // Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), mRNA /// ENST00000312428 // intron // 0 // — // — // — // —	DNAH7	DNAH7, Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), q32.3
SNP_A-2142516	atgaacaaggtccatc[C/T]ataaaatgtctcaaat	C	T	NM_004226 // intron // 0 // Hs.88297 // STK17B // 9262 // Homo sapiens serine/threonine kinase 17b (apoptosis-inducing) (STK17B), mRNA /// ENST00000263955 // intron // 0 // — // — // — // —	STK17B	STK17B, Homo sapiens serine q32.3
SNP_A-2063608	aatatcattgcacaca[G/T]gggagaaaaatggata	G	T	ENST00000260983 // intron // 0 // — // — // — // —	-	q32.3
SNP_A-2122834	agtggcagcagtgaaa[A/C]gctaattcaaacaggt	A	C	ENST00000260983 // intron // 0 // — // — // — // —	-	q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1817397	gttcagggactcccag[A/G]aataaccaggaccatt	A	G	NM_024989 // upstream // 32517 // Hs.229988 // PGAP1 // 80055 // Homo sapiens GPI deacylase (PGAP1), mRNA. /// NM_153697 // downstream // 35354 // Hs.432706 // LOC91526 // 91526 // Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// NM_0	PGAP1	PGAP1, Homo sapiens GPI deacylase (PGAP1), q33.1
SNP_A-1794283	ggtccaaatatattccc[C/T]ccaatttctcggttcc	C	T	NM_153697 // intron // 0 // Hs.432706 // LOC91526 // 91526 // Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), mRNA. /// ENST00000282272 // intron // 0 // --- // --- // --- /// ENST00000328737 // intron // 0 // --- // --- // ---	LOC91526	LOC91526, Homo sapiens hypothetical protein DKFZp434D2328 (LOC91526), q33.1
SNP_A-2219623	cctgtttggataaaag[A/G]attaagttcagagaag	A	G	NM_006226 // downstream // 138941 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 982163 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1745842	aaaatgaagtatctcctatctctctc[C/T]gaattctctcaagcagca ctcaaag	C	T	NM_006226 // intron // 0 // Hs.153322 // PLCL1 // 5334 // phospholipase C-like 1	PLCL1	PLCL1, rs2880366, phospholipase C-like 1,q33.1
SNP_A-1738206	cacttagtcttgttagtacaga[C/T]gaaatccaagtgataaatag gtgggt	C	T	NM_006226 // intron // 0 // Hs.153322 // PLCL1 // 5334 // phospholipase C-like 1	PLCL1	PLCL1, rs3732231, phospholipase C-like 1,q33.1
SNP_A-1966426	taggtttgtcttacttt[A/G]aaaatgcacactctta	A	G	NM_006226 // downstream // 331955 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 789149 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1785209	ggctacaagaattata[C/T]atgatgtcgcagatgt	C	T	NM_006226 // downstream // 352238 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 768866 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1950447	ttcagtggctagatat[C/T]gcctgactgtgagct	C	T	NM_006226 // downstream // 555140 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 565964 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-2273809	gactggattgtatttg[A/G]aaagcctacctctagg	A	G	NM_006226 // downstream // 569540 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 551564 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1815163	gtgttcttgtatcagg[C/T]aaagcctcctcccac	C	T	NM_006226 // downstream // 569975 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 551129 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-2060818	aatgagttatatacac[A/G]caatcttggctagtct	A	G	NM_006226 // downstream // 570537 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 550567 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-2092833	agaaattctaaatgtg[A/G]acctaaatctctgctt	A	G	NM_006226 // downstream // 622940 // Hs.153322 // PLCL1 // 5334 // Homo sapiens phospholipase C-like 1 (PLCL1), mRNA. /// NM_015265 // downstream // 498164 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000341	PLCL1	PLCL1, Homo sapiens phospholipase C-like 1 (PLCL1), q33.1
SNP_A-1651186	ttcctctacagcaatctcatttcctat[A/C]atatgacttctggtttcaac aacag	A	C	NM_006226 // downstream // 399416 // Hs.153322 // PLCL1 // 5334 // phospholipase C-like 1	PLCL1	PLCL1, rs1014226, phospholipase C-like 1,q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1707303	acttatgcatattgcttagtgccaa[C/T]gggactcttagaaatgtat ttgaga	C	T	NM_006226 // downstream // 564077 // Hs.153322 // PLCL1 // 5334 // phospholipase C-like 1	PLCL1	PLCL1 , rs1518099, phospholipase C-like 1,q33.1
SNP_A-1723486	aaacttaaaactatatttgacaaa[C/T]attaccctggcaagaattg agttta	C	T	NM_006226 // downstream // 620720 // Hs.153322 // PLCL1 // 5334 // phospholipase C-like 1	PLCL1	PLCL1 , rs1518081, phospholipase C-like 1,q33.1
SNP_A-1908618	tgtagcgtgatggtgc[C/G]aagataaaatagtagc	C	G	NM_015265 // intron // 0 // Hs.516617 // SATB2 // 23314 // Homo sapiens SATB family member 2 (SATB2), mRNA. /// ENST00000260926 // intron // 0 // --- // --- // ---	SATB2	SATB2, Homo sapiens SATB family member 2 (SATB2), q33.1
SNP_A-1966457	ctcctcagcaccaggt[A/G]aagattaggaattgca	A	G	NM_153031 // downstream // 307410 // Hs.151184 // FLJ32063 // 150538 // Homo sapiens hypothetical protein FLJ32063 (FLJ32063), mRNA. /// NM_153689 // upstream // 126961 // Hs.471040 // FLJ38973 // 205327 // Homo sapiens hypothetical protein FLJ38973 (FLJ3	FLJ32063	FLJ32063, Homo sapiens hypothetical protein FLJ32063 (FLJ32063), q33.1
SNP_A-1807959	gtcttccaagtagtaa[C/G]ccctgcctctgatc	C	G	NM_153031 // downstream // 390332 // Hs.151184 // FLJ32063 // 150538 // Homo sapiens hypothetical protein FLJ32063 (FLJ32063), mRNA. /// NM_153689 // upstream // 44039 // Hs.471040 // FLJ38973 // 205327 // Homo sapiens hypothetical protein FLJ38973 (FLJ38	FLJ32063	FLJ32063, Homo sapiens hypothetical protein FLJ32063 (FLJ32063), q33.1
SNP_A-2221995	cgaaattataaaaga[C/G]actgactagatcaat	C	G	NM_153031 // downstream // 421566 // Hs.151184 // FLJ32063 // 150538 // Homo sapiens hypothetical protein FLJ32063 (FLJ32063), mRNA. /// NM_153689 // upstream // 12805 // Hs.471040 // FLJ38973 // 205327 // Homo sapiens hypothetical protein FLJ38973 (FLJ38	FLJ32063	FLJ32063, Homo sapiens hypothetical protein FLJ32063 (FLJ32063), q33.1
SNP_A-1966466	cccaacagcagtgcaa[A/G]ctccaatgatggagt	A	G	NM_152382 // upstream // 84701 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 84937 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1966467	gtcctaattttgcaa[A/G]gacagggatatttga	A	G	NM_152382 // upstream // 125395 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 125631 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-2116569	aggtcacagagcttag[C/G]atgtagtgtggtaatc	C	G	NM_152382 // upstream // 197488 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 197724 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1862306	tcatggttcttgtatc[A/G]aagtacaattgaacat	A	G	NM_152382 // upstream // 227989 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 228225 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1748307	cataactgctggtcatggaagatta[A/C]gtttgtttatcccagttctc ccatt	A	C	NM_153031 // downstream // 360130 // Hs.511860 // FLJ32063 // 150538 // hypothetical protein FLJ32063 /// NM_153689 // upstream // 74241 // Hs.40782 // FLJ38973 // 205327 // hypothetical protein FLJ38973	FLJ32063	FLJ32063 , rs10497841, hypothetical protein FLJ32063 ,q33.1
SNP_A-2242330	ctgcacagtttcacct[A/G]acccatgcttgaacac	A	G	NM_152382 // upstream // 281616 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 281852 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-2112910	aggcatcttatatccc[A/G]ccgccatagtccaccc	A	G	NM_152382 // upstream // 310700 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 310936 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2089006	acttaaatatgttgga[C/T]tcacctatgagcaatc	C	T	NM_152382 // upstream // 322783 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 323019 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1926092	ttatgttcagaaacaa[C/T]gtcctctgctatatca	C	T	NM_152382 // upstream // 392332 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 392568 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-2253309	cttctggcctgtacta[A/T]gtgttaggaaatgtta	A	T	NM_152382 // upstream // 393048 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 393284 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-2034988	aaatgattaactgcac[A/G]ctaagagaatacattt	A	G	NM_152382 // upstream // 405789 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 406025 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1966477	tttggaagctctagag[A/G]aggatctgtttccttg	A	G	NM_152382 // upstream // 408431 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 408667 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1837611	tacttgtttggtgaaa[C/T]aggtccatctctcaca	C	T	NM_152382 // upstream // 419026 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 419262 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1966483	ctagcatgtagcagaa[C/G]caagattagaacatag	C	G	NM_152382 // upstream // 451557 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ37953), mRNA. /// NM_152382 // upstream // 451793 // Hs.204619 // FLJ37953 // 129450 // Homo sapiens hypothetical protein FLJ37953 (FLJ379	FLJ37953	FLJ37953, Homo sapiens hypothetical protein FLJ37953 (FLJ37953), q33.1
SNP_A-1869036	tcctgcagaacctcta[A/G]gtagaatttgaagagg	A	G	NM_014670 // upstream // 66061 // Hs.355983 // BZW1 // 9689 // Homo sapiens basic leucine zipper and W2 domains 1 (BZW1), mRNA. /// ENST00000358734 // downstream // 62665 // — // — // — // — /// ENST00000353957 // upstream // 65729 // — // — // — /	BZW1	BZW1, Homo sapiens basic leucine zipper and W2 domains 1 (BZW1), q33.1
SNP_A-1966497	agccactatgcccaac[A/C]aagacagtataatatt	A	C	NM_014670 // upstream // 58695 // Hs.355983 // BZW1 // 9689 // Homo sapiens basic leucine zipper and W2 domains 1 (BZW1), mRNA. /// ENST00000358734 // downstream // 70031 // — // — // — // — /// ENST00000353957 // upstream // 58363 // — // — /	BZW1	BZW1, Homo sapiens basic leucine zipper and W2 domains 1 (BZW1), q33.1
SNP_A-2110387	aggaatgttctttaca[A/G]gcgacttttgcacaa	A	G	NM_014670 // upstream // 43657 // Hs.355983 // BZW1 // 9689 // Homo sapiens basic leucine zipper and W2 domains 1 (BZW1), mRNA. /// ENST00000358734 // downstream // 85069 // — // — // — // — /// ENST00000353957 // upstream // 43325 // — // — /	BZW1	BZW1, Homo sapiens basic leucine zipper and W2 domains 1 (BZW1), q33.1
SNP_A-2286448	gatgctgtttctgaaa[C/T]tactgatatgatcata	C	T	NM_152525 // intron // 0 // Hs.335788 // ALS2CR11 // 151254 // Homo sapiens hypothetical protein FLJ25351 (FLJ25351), mRNA. /// ENST00000286195 // intron // 0 // — // — // — // — /// ENST00000316475 // intron // 0 // — // — // — // —	ALS2CR11	ALS2CR11, Homo sapiens hypothetical protein FLJ25351 (FLJ25351), q33.1
SNP_A-1948009	tttagaccatcaacga[C/G]agatgtgtagtcgggt	C	G	NM_020919 // upstream // 752 // Hs.471096 // ALS2 // 57679 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) (ALS2), mRNA. /// NM_139158 // upstream // 24708 // Hs.348711 // ALS2CR7 // 65061 // Homo sapiens amyotrophic lateral sclerosis 2 (juveni	ALS2	ALS2, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) (ALS2), q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805393	gtccaatcaaaaaacac[C/T]gcctatcatgttagct	C	T	ENST00000331807 // intron // 0 // --- // --- // --- // ---	-	q33.1
SNP_A-2079814	acctgccttaaccaat[G/T]cagtgaaggttaacat	G	T	NM_015934 // downstream // 25874 // Hs.471104 // NOP5/NOP58 // 51602 // Homo sapiens nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA. /// NM_173511 // upstream // 305448 // Hs.471130 // ALS2CR13 // 150864 // Homo sapiens amyotrophic lateral sclerosis 2 (j	NOP5	NOP5, 51602 q33.1
SNP_A-1856798	tcacattcaaaccaca[A/G]tggaactcaacctagt	A	G	NM_173511 // intron // 0 // Hs.471130 // ALS2CR13 // 150864 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (ALS2CR13), mRNA. /// ENST00000303116 // intron // 0 // --- // --- // --- /// ENST00000261012 //	ALS2CR13	ALS2CR13, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (ALS2CR13), q33.2
SNP_A-2091524	agaaaaagaggccata[C/T]taaaaaatctagactt	C	T	NM_205543 // intron // 0 // Hs.546480 // ALS2CR16 // 130029 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 16 (ALS2CR16), mRNA. /// ENST00000295849 // intron // 0 // --- // --- // ---	ALS2CR16	ALS2CR16, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 16 (ALS2CR16), q33.2
SNP_A-2049288	aagctcatagcagtaa[A/G]gaaagcaaaaagaagt	A	G	NM_205543 // 5UTR // 0 // Hs.546480 // ALS2CR16 // 130029 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 16 (ALS2CR16), mRNA. /// ENST00000295849 // 5UTR // 0 // --- // --- // ---	ALS2CR16	ALS2CR16, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 16 (ALS2CR16), q33.2
SNP_A-1844482	tataaagtctgttaca[A/G]gtttatcaaaaaatga	A	G	NM_213589 // upstream // 97297 // Hs.471162 // RAPH1 // 65059 // Homo sapiens Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 (RAPH1), transcript variant 1, mRNA. /// NM_203365 // upstream // 97278 // Hs.471162 // RAPH1 // 65059 // Homo sa	RAPH1	RAPH1, Homo sapiens Ras association (RalGDS q33.2
SNP_A-1966530	gggaagactttcaaga[C/T]aacagtcaacagaaaa	C	T	NM_006139 // intron // 0 // Hs.1987 // CD28 // 940 // Homo sapiens CD28 antigen (Tp44) (CD28), mRNA. /// ENST00000324106 // intron // 0 // --- // --- // --- /// ENST00000340642 // intron // 0 // --- // --- // --- // ---	CD28	CD28, Homo sapiens CD28 antigen (Tp44) (CD28), q33.2
SNP_A-1920299	ttaatgctgtgagtta[A/C]gtatacaagatgagta	A	C	NM_005214 // upstream // 44079 // Hs.247824 // CTLA4 // 1493 // Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA. /// ENST00000331861 // upstream // 50207 // --- // --- // --- // --- /// ENST00000302823 // upstream // 44079 // --- //	CTLA4	CTLA4, Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), q33.2
SNP_A-2137381	atcatacaagatacac[C/T]aagcatgtcaggcaga	C	T	NM_005214 // upstream // 12372 // Hs.247824 // CTLA4 // 1493 // Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA. /// ENST00000331861 // upstream // 81914 // --- // --- // --- // --- /// ENST00000302823 // upstream // 12372 // --- //	CTLA4	CTLA4, Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), q33.2
SNP_A-1966540	agatgggttctgtatg[A/G]aaaacggtctggatg	A	G	NM_005214 // downstream // 2183 // Hs.247824 // CTLA4 // 1493 // Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), mRNA. /// NM_012092 // upstream // 60605 // Hs.56247 // ICOS // 29851 // Homo sapiens inducible T-cell co-stimulator (ICOS),	CTLA4	CTLA4, Homo sapiens cytotoxic T-lymphocyte-associated protein 4 (CTLA4), q33.2
SNP_A-1728449	atatagagttcagatgagataagag[A/T]cagcatttatagccct gtgaatgt	A	T	NM_006139 // intron // 0 // Hs.1987 // CD28 // 940 // CD28 antigen (Tp44)	CD28	CD28 , rs4675360, CD28 antigen (Tp44),q33.2
SNP_A-1781825	ggatttgtttgccaaa[A/G]gtgatatcctaaatac	A	G	NM_012092 // downstream // 319469 // Hs.56247 // ICOS // 29851 // Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// NM_205863 // upstream // 264958 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) c	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.3
SNP_A-1833233	tacactacttcacgaa[A/C]aaattgcctcattcag	A	C	NM_012092 // downstream // 355349 // Hs.56247 // ICOS // 29851 // Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// NM_205863 // upstream // 229078 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) c	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814575	gtgtggaagattgatc[A/G]cagagtagtccacacg	A	G	NM_012092 // downstream // 522428 // Hs.56247 // ICOS // 29851 // Homo sapiens inducible T-cell co-stimulator (ICOS), mRNA. /// NM_205863 // upstream // 61999 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) ch	ICOS	ICOS, Homo sapiens inducible T-cell co-stimulator (ICOS), q33.3
SNP_A-1898829	tgctttggataaccga[C/T]aagaagttaaaagaaa	C	T	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-1966571	tcaggtctactattat[C/T]catcttcaagaaaagt	C	T	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2205144	ccagtaaaagttccag[G/T]agtaggccacaaagct	G	T	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-1966575	catgccatcagtgggga[A/G]gtggtaaattctgtcc	A	G	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-1914368	tgtgttgctactaatc[A/G]cttcatagctccttac	A	G	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2257942	cttgtcagcatttccc[A/G]agactttatcattaa	A	G	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-1708096	ttagatatgacttacccatagga[C/T]catttctttccaaggaaac gttaag	C	T	NM_057177 // intron // 0 // Hs.26981 // ALS2CR19 // 117583 // amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 /// NM_152526 // intron // 0 // Hs.26981 // ALS2CR19 // 117583 // amyotrophic lateral sclerosis 2 (juvenile) chromoso	ALS2CR19	ALS2CR19, rs10497880, amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 ,q33.3
SNP_A-2032101	aaagtgccaactcaga[A/G]atggagtgactgttg	A	G	NM_205863 // intron // 0 // Hs.271903 // ALS2CR19 // 117583 // Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, mRNA. /// NM_057177 // intron // 0 // Hs.271903 // ALS2CR19 // 117583	ALS2CR19	ALS2CR19, Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (ALS2CR19), transcript variant a, q33.3
SNP_A-2172047	caatggaggctttcac[A/G]cattagaaaaagaagt	A	G	NM_201264 // intron // 0 // Hs.471200 // NRP2 // 8828 // Homo sapiens neuropilin 2 (NRP2), transcript variant 6, mRNA. /// NM_003872 // intron // 0 // Hs.471200 // NRP2 // 8828 // Homo sapiens neuropilin 2 (NRP2), transcript variant 2, mRNA. /// NM_201266	NRP2	NRP2, Homo sapiens neuropilin 2 (NRP2), transcript variant 6, q33.3
SNP_A-1841101	tagcttccagccatgg[A/G]aaagacttgtgcagaa	A	G	NM_201264 // downstream // 125591 // Hs.471200 // NRP2 // 8828 // Homo sapiens neuropilin 2 (NRP2), transcript variant 6, mRNA. /// NM_003872 // downstream // 125591 // Hs.471200 // NRP2 // 8828 // Homo sapiens neuropilin 2 (NRP2), transcript variant 2, m	NRP2	NRP2, Homo sapiens neuropilin 2 (NRP2), transcript variant 6, q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1966603	acaaggatctcagaaa[A/G]ctaaaataagatgaga	A	G	ENST00000360293 // downstream // 12272 // --- // --- // --- /// ENST00000327138 // downstream // 41693 // --- // --- // ---	-	q33.3
SNP_A-2300290	gcctctaggacatata[A/C]aatgcaatatttgact	A	C	NM_003812 // intron // 0 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// ENST00000264377 // intron // 0 // --- // --- // ---	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2078241	accagttggatcatga[C/G]aaaaaagatacaacat	C	G	NM_003812 // intron // 0 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// ENST00000264377 // intron // 0 // --- // --- // ---	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2121775	agtgactgaatgaaca[C/T]actctatcaattaaa	C	T	NM_003812 // intron // 0 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// ENST00000264377 // intron // 0 // --- // --- // ---	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-1966607	tgggtcacctttcta[A/G]ccagttactaaggaag	A	G	NM_003812 // downstream // 4010 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// NM_206892 // downstream // 115664 // Hs.147816 // MDH1B // 130752 // Homo sapiens malate dehydrogenase 1B, NAD	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-1899298	tggaacacttgtgaaa[C/T]tggcagtccagagaaa	C	T	NM_003812 // downstream // 35305 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// NM_206892 // downstream // 84369 // Hs.147816 // MDH1B // 130752 // Homo sapiens malate dehydrogenase 1B, NAD	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2267284	gaatactgcaatgta[C/T]ctttgaagagtactg	C	T	NM_003812 // downstream // 86836 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// NM_206892 // downstream // 32838 // Hs.147816 // MDH1B // 130752 // Homo sapiens malate dehydrogenase 1B, NAD	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2310490	ggaagaaactaccaaa[C/T]gtatcacgcccaaagc	C	T	NM_003812 // downstream // 98956 // Hs.370287 // ADAM23 // 8745 // Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA. /// NM_206892 // downstream // 20718 // Hs.147816 // MDH1B // 130752 // Homo sapiens malate dehydrogenase 1B, NAD	ADAM23	ADAM23, Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23), q33.3
SNP_A-2278044	gagccatttttagtct[A/G]aagcaagaatgtcagt	A	G	NM_014929 // intron // 0 // Hs.84429 // KIAA0971 // 22868 // Homo sapiens KIAA0971 (KIAA0971), mRNA. /// ENST00000236980 // intron // 0 // --- // --- // --- /// ENST00000358589 // intron // 0 // --- // --- // ---	KIAA0971	KIAA0971, Homo sapiens KIAA0971 (KIAA0971), q33.3
SNP_A-1870081	tcctggttcaaagcc[C/G]cagcaagatactctgg	C	G	NM_014929 // intron // 0 // Hs.84429 // KIAA0971 // 22868 // Homo sapiens KIAA0971 (KIAA0971), mRNA. /// ENST00000236980 // intron // 0 // --- // --- // --- /// ENST00000358589 // intron // 0 // --- // --- // ---	KIAA0971	KIAA0971, Homo sapiens KIAA0971 (KIAA0971), q33.3
SNP_A-2187702	cagtactaatttcaga[A/C]gtgctgccttgctatt	A	C	NM_014929 // intron // 0 // Hs.84429 // KIAA0971 // 22868 // Homo sapiens KIAA0971 (KIAA0971), mRNA. /// ENST00000236980 // intron // 0 // --- // --- // --- /// ENST00000358589 // intron // 0 // --- // --- // ---	KIAA0971	KIAA0971, Homo sapiens KIAA0971 (KIAA0971), q33.3
SNP_A-2282148	gagtgctgtgaaatg[A/G]aagagacgattcattc	A	G	NM_014929 // downstream // 28672 // Hs.84429 // KIAA0971 // 22868 // Homo sapiens KIAA0971 (KIAA0971), mRNA. /// NM_173077 // upstream // 118420 // --- // CPO // 130749 // Homo sapiens carboxypeptidase O (CPO), mRNA. /// ENST00000236980 // downstream // 2	KIAA0971	KIAA0971, Homo sapiens KIAA0971 (KIAA0971), q33.3
SNP_A-2174029	cacaccaagcaaggta[C/T]gaagtttaatgcaatg	C	T	NM_014929 // downstream // 143676 // Hs.84429 // KIAA0971 // 22868 // , Homo sapiens KIAA0971 (KIAA0971), mRNA. /// NM_173077 // upstream // 3416 // --- // CPO // 130749 // Homo sapiens carboxypeptidase O (CPO), mRNA. /// ENST00000236980 // downstream // 14	KIAA0971	KIAA0971, Homo sapiens KIAA0971 (KIAA0971), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2252192	cttccattggttccig[A/C]agccatgtcctccaca	A	C	NM_003709 // upstream // 99477 // Hs.471221 // KLF7 // 8609 // Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA /// NM_004379 // upstream // 264768 // Hs.516646 // CREB1 // 1385 // Homo sapiens cAMP responsive element binding protein 1 (CREB1	KLF7	KLF7, Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), q33.3
SNP_A-2254599	cttgctcctgctgaat[G/T]acagggtattatcta	G	T	NM_003709 // upstream // 123597 // Hs.471221 // KLF7 // 8609 // Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA /// NM_004379 // upstream // 240648 // Hs.516646 // CREB1 // 1385 // Homo sapiens cAMP responsive element binding protein 1 (CREB	KLF7	KLF7, Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), q33.3
SNP_A-1756240	aggaacagcaggaatggtaagtga[A/G]taggaagttcaggc taagtatcaga	A	G	NM_003709 // downstream // 47652 // Hs.436708 // KLF7 // 8609 // Kruppel-like factor 7 (ubiquitous) /// NM_173077 // downstream // 63717 // Hs.434114 // CPO // 130749 // carboxypeptidase O	KLF7	KLF7, rs1990810, Kruppel-like factor 7 (ubiquitous) ,q33.3
SNP_A-1791076	ggggtgaagaaatgct[C/T]actcgccaaaaaaggc	C	T	NM_003709 // upstream // 277320 // Hs.471221 // KLF7 // 8609 // Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA /// NM_004379 // upstream // 86925 // Hs.516646 // CREB1 // 1385 // Homo sapiens cAMP responsive element binding protein 1 (CREB1	KLF7	KLF7, Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), q33.3
SNP_A-1642081	cattcacagtcacatctgacataat[C/G]aaggaatatttctactca tcttctcc	C	G	NM_003709 // intron // 0 // Hs.436708 // KLF7 // 8609 // Kruppel-like factor 7 (ubiquitous)	KLF7	KLF7, rs3791995, Kruppel-like factor 7 (ubiquitous),q33.3
SNP_A-2301718	gcgctctcagcaggac[A/G]gaaatgacgaataact	A	G	NM_005896 // upstream // 10486 // Hs.11223 // IDH1 // 3417 // Homo sapiens isocitrate dehydrogenase 1 (NADP+), soluble (IDH1), mRNA /// NM_152671 // upstream // 699 // Hs.173939 // PIP5K3 // 200576 // Homo sapiens phosphatidylinositol-3-phosphate/phospha	IDH1	IDH1, Homo sapiens isocitrate dehydrogenase 1 (NADP+), soluble (IDH1), q34
SNP_A-2226783	ctaataagtgttggtat[C/T]ggatgtagagaaattg	C	T	NM_152671 // downstream // 57278 // Hs.173939 // PIP5K3 // 200576 // Homo sapiens phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III (PIP5K3), mRNA /// NM_015040 // downstream // 4072 // Hs.173939 // PIP5K3 // 200576 // Homo sapiens	PIP5K3	PIP5K3, Homo sapiens phosphatidylinositol-3-phosphate,q34
SNP_A-1966667	ctattggctggtaatc[A/G]atatgtacctcatgca	A	G	NM_152671 // downstream // 78152 // Hs.173939 // PIP5K3 // 200576 // Homo sapiens phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III (PIP5K3), mRNA /// NM_015040 // downstream // 24946 // Hs.173939 // PIP5K3 // 200576 // Homo sapien	PIP5K3	PIP5K3, Homo sapiens phosphatidylinositol-3-phosphate q34
SNP_A-1801890	gtagtttatgctaaca[A/G]tgtcatctgtgaatgc	A	G	NM_152671 // downstream // 93917 // Hs.173939 // PIP5K3 // 200576 // Homo sapiens phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III (PIP5K3), mRNA /// NM_015040 // downstream // 40711 // Hs.173939 // PIP5K3 // 200576 // Homo sapien	PIP5K3	PIP5K3, Homo sapiens phosphatidylinositol-3-phosphate q34
SNP_A-2081326	acctggccatttttc[A/G]cagcatgggactcctc	A	G	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // — // — // — // —	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1966668	aactgttaaagggaca[A/C]gacgatgataatgtt	A	C	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // — // — // — // —	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2226345	ctaagaatagtcaaga[C/G]tatatgaagtatgtg	C	G	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // — // — // — // —	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2030429	aaagccatatttggag[A/G]agagtgaagttcctag	A	G	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // — // — // — // —	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1859999	tcagttttttcatttg[G/T]aaagatctcagggctt	G	T	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // — // — // — // —	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1966670	ttagcagaggaggtgd[A/G]actcataatagtttt	A	G	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// ENST00000272847 // intron // 0 // --- // --- // ---	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1814319	gtgtgaaagtgcctta[C/G]ggacaccctagtggtc	C	G	NM_005048 // downstream // 37325 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 892233 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcri	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1947228	tttaatcatatagaaa[A/G]cttgagtcacacaact	A	G	NM_005048 // downstream // 38022 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 891536 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcri	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2160700	atttcggaaictgaaa[A/G]aaggctttctacact	A	G	NM_005048 // downstream // 113327 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 816231 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcr	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1810858	gtgcaggtggttcata[G/T]agtctatactgaagag	G	T	NM_005048 // downstream // 154691 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 774867 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcr	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1648284	atttcaaatggccttggataagta[A/C]aggacgaaacgagag agttaaagca	A	C	NM_152671 // intron // 0 // - // - // -	-	-, rs10497897, -, q34
SNP_A-1654685	aagggtaaaacatttcagtacaca[C/T]taagaactacatatttttt aagttta	C	T	NM_005048 // intron // 0 // Hs.159499 // PTHR2 // 5746 // parathyroid hormone receptor 2	PTHR2	PTHR2, rs7564720, parathyroid hormone receptor 2,q34
SNP_A-1754800	tgattaagctttgcatggtgtaga[A/G]aaatggggcacaggtac ctggcttg	A	G	NM_002374 // upstream // 936112 // Hs.167 // MAP2 // 4133 // microtubule-associated protein 2 /// NM_005048 // downstream // 149061 // Hs.159499 // PTHR2 // 5746 // parathyroid hormone receptor 2 /// NM_031845 // upstream // 936112 // Hs.167 // MAP2 // 4	MAP2	MAP2, rs10497908, microtubule-associated protein 2, q34
SNP_A-1799295	gtaataatggctggac[A/G]ggaaaaacacagattc	A	G	NM_005048 // downstream // 706559 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 222999 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcr	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-1869272	tcctgggagcaaaccca[C/T]cttcaaccacactct	C	T	NM_005048 // downstream // 759558 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 170000 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcr	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2233577	ctcagtttgagccgta[A/C]caaacacggaccagaa	A	C	NM_005048 // downstream // 812057 // Hs.159499 // PTHR2 // 5746 // Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA. /// NM_002374 // upstream // 117501 // Hs.368281 // MAP2 // 4133 // Homo sapiens microtubule-associated protein 2 (MAP2), transcr	PTHR2	PTHR2, Homo sapiens parathyroid hormone receptor 2 (PTHR2), q34
SNP_A-2302987	gctagtaagagctcta[C/G]gaaaggcttccccaga	C	G	NM_152519 // intron // 0 // Hs.122934 // FLJ23861 // 151050 // Homo sapiens hypothetical protein FLJ23861 (FLJ23861), mRNA. /// ENST00000281772 // intron // 0 // --- // --- // ---	FLJ23861	FLJ23861, Homo sapiens hypothetical protein FLJ23861 (FLJ23861), q34
SNP_A-2261523	gaaaggcaaaggagga[A/G]attagtaatggaggg	A	G	NM_001875 // downstream // 37416 // Hs.149252 // CPS1 // 1373 // Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), mRNA. /// NM_005235 // downstream // 665570 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia	CPS1	CPS1, Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2060333	aatgaatatatagagc[A/G]agcaaagaaaggcctt	A	G	NM_001875 // downstream // 510818 // Hs.149252 // CPS1 // 1373 // Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), mRNA. /// NM_005235 // downstream // 192168 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemi	CPS1	CPS1, Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), q34
SNP_A-1703227	tatttttcctgatcccctttctac[A/G]aagtgtttaaatagagtaaaaaatg	A	G	NM_001875 // downstream // 433499 // Hs.443292 // CPS1 // 1373 // carbamoyl-phosphate synthetase 1, mitochondrial /// NM_005235 // downstream // 269487 // Hs.1939 // ERBB4 // 2066 // v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) /// NM	CPS1	CPS1 , rs10497940, carbamoyl-phosphate synthetase 1, mitochondrial q34
SNP_A-2197248	cattcagagtcagttta[A/G]taaaagtagggccagg	A	G	NM_005235 // intron // 0 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // — // — // — /// ENST00000260943 // intron // 0 // —	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2179257	cactgtaatggagaga[C/G]ctgaagtgagttact	C	G	NM_005235 // intron // 0 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// ENST00000342788 // intron // 0 // — // — // — /// ENST00000260943 // intron // 0 // —	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1720445	acaatgcaatggtatcaagcatcaa[C/T]gtgaagggtcaagaggaacctaagt	C	T	NM_005235 // intron // 0 // Hs.1939 // ERBB4 // 2066 // v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ERBB4	ERBB4 , rs1402708, v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian),q34
SNP_A-1703471	ataaaggaaaccaaataggagtaaa[A/G]aattagccgaagatcatcaaaagta	A	G	NM_005235 // intron // 0 // Hs.1939 // ERBB4 // 2066 // v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ERBB4	ERBB4 , rs7579746, v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian),q34
SNP_A-2288964	gatttatgctcctgaa[C/T]catttctctgatgaa	C	T	NM_005235 // upstream // 9977 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 458113 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-1851212	tattcacctcccagaa[C/T]gtcattaaaagaaat	C	T	NM_005235 // upstream // 79131 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 388959 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2033482	aaatagtgtgaagaaa[C/T]gcaggttgaaaaataa	C	T	NM_005235 // upstream // 79739 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 388351 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2230181	ctatactcttcaaaacd[A/G]gcatttggagtaagaa	A	G	NM_005235 // upstream // 373095 // Hs.390729 // ERBB4 // 2066 // Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA. /// NM_016260 // downstream // 94995 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger	ERBB4	ERBB4, Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), q34
SNP_A-2059718	aatctgagtccattaa[C/G]gatattcaattgtaaa	C	G	NM_016260 // intron // 0 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), mRNA. /// ENST00000342002 // intron // 0 // — // — // — /// ENST00000264190 // intron // 0 // — // — // —	ZNFN1A2	ZNFN1A2, Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), q34
SNP_A-1966798	catgttcacatctctg[A/G]agttctctctgtgca	A	G	NM_016260 // intron // 0 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), mRNA. /// ENST00000342002 // intron // 0 // — // — // — /// ENST00000264190 // intron // 0 // — // — // —	ZNFN1A2	ZNFN1A2, Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2110254	aggaataaaagagaca[A/C]ctaatgattatttaa	A	C	NM_016260 // intron // 0 // Hs.374243 // ZNFN1A2 // 22807 // Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), mRNA. /// ENST00000342002 // intron // 0 // — // — // — /// ENST00000264190 // intron // 0 // — // — // —	ZNFN1A2	ZNFN1A2, Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), q34
SNP_A-1966802	tgagggctcaaaggca[A/G]cttgacattaagaaac	A	G	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // — /// ENST00000272898 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2272155	gacctaaatttcctaag[C/T]atggcttcaaaggaac	C	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1966807	aaggctaacttatttg[C/T]attattggctaagggg	C	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2116323	aggtagcaataaattat[C/T]gaacaacgtgagtgca	C	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1914688	tgttaattggtggca[C/T]aagtggtgttgagg	C	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2180792	cagaatatgtcttgtc[G/T]cattatgttctgtatt	G	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2098266	agagatcttgaagtga[A/G]atcaatacatttctg	A	G	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2279595	gaggcaataagttgga[C/T]gactggaccatgctaa	C	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2099001	agaggaaagtacataa[A/C]cttgaaaattgagtga	A	C	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2069107	acaatgtttaccttc[A/C]agcaaaagtgtcgaaa	A	C	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2198277	cattgtgtggattgtc[A/G]gaaaactgaaaagatg	A	G	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2056068	aatacatttacttgcc[A/T]atgtggtgcggtaaga	A	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1942809	ttgggctttcatccag[A/T]agatagcatttattag	A	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2050296	aaggagatggtaagat[A/G]ataggacttccacatc	A	G	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1966812	tttgaaaacatttaaa[A/T]ctagcatggtgaaact	A	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1794851	ggtcttactgtgagaa[A/G]tgagaaaccattggag	A	G	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-2272886	gactacaagccttaa[C/T]cccagagcagaccagc	C	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // — // — // —	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2025452	aaaatcctaacactta[A/T]caaagaagagcagaact	A	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1703617	attgaagctctaaaa[G/T]gtggcaatcattgttt	G	T	NM_024532 // intron // 0 // Hs.6783 // PF20 // 79582 // PF20	PF20	PF20, rs4132244, PF20,q34
SNP_A-2297213	gccaccaagcaaggaa[A/C]aagaactggaagagct	A	C	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1966823	ggttaagactacagaa[A/T]ctctaaacaaagtct	A	T	NM_024532 // intron // 0 // Hs.471316 // SPAG16 // 79582 // Homo sapiens sperm associated antigen 16 (SPAG16), mRNA. /// ENST00000331683 // intron // 0 // --- // --- // ---	SPAG16	SPAG16, Homo sapiens sperm associated antigen 16 (SPAG16), q34
SNP_A-1949788	ttcaaaggaatggcc[C/T]cccagtgagcagcaag	C	T	NM_000465 // downstream // 134644 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 18089 // --- // --- // --- /// ENST00000260947 // downstream // 134644 // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2006998	agagttgggcgttgga[A/G]cagaccctccaggtga	A	G	NM_000465 // downstream // 124283 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 28450 // --- // --- // --- /// ENST00000260947 // downstream // 124283 // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-1966828	tcatcaaaactttcaa[C/T]ggtgcccacattgcta	C	T	NM_000465 // downstream // 121327 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 31406 // --- // --- // --- /// ENST00000260947 // downstream // 121327 // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2175331	cacatatatattgaacf[C/G]atttggatgagacg	C	G	NM_000465 // downstream // 116910 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 35823 // --- // --- // --- /// ENST00000260947 // downstream // 116910 // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2187923	cagtatgtagatgaga[C/T]tccacagattgctaga	C	T	NM_000465 // downstream // 116346 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 36387 // --- // --- // --- /// ENST00000260947 // downstream // 116346 // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-1966831	gtaaagcataaaacatt[A/G]aacaattgggagtaa	A	G	NM_000465 // downstream // 109623 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 43110 // --- // --- // --- /// ENST00000260947 // downstream // 109623 // --- // --- // ---	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-1815330	gtgtttatcctctata[A/C]atgtaggtgtagctta	A	C	NM_000465 // downstream // 99636 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 53097 // --- // --- // --- /// ENST00000260947 // downstream // 99636 // --- // --- // -	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-2279710	gaggcataattaatgaf[A/G]atagtgccaagattat	A	G	NM_000465 // downstream // 96986 // Hs.54089 // BARD1 // 580 // Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /// ENST00000312504 // downstream // 55747 // --- // --- // --- /// ENST00000260947 // downstream // 96986 // --- // --- // -	BARD1	BARD1, Homo sapiens BRCA1 associated RING domain 1 (BARD1), q35
SNP_A-1687698	cattcacagctcccctcaggcgcca[A/G]aaactttattgccagta gtagttct	A	G	NM_024532 // intron // 0 // Hs.6783 // PF20 // 79582 // PF20	PF20	PF20, rs10490503, PF20,q34
SNP_A-1966849	tggccttcatcactta[C/T]gtctgtgtcaactgt	C	T	NM_015657 // CDS // 0 // Hs.134585 // ABCA12 // 26154 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 2, mRNA. /// NM_173076 // CDS // 0 // Hs.134585 // ABCA12 // 26154 // Homo sapiens ATP-binding cassette	ABCA12	ABCA12, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 2, q35

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1961084	ttttgtctcacaggc[A/G]atgtacagaagcaacc	A	G	NM_015657 // CDS // 0 // Hs.134585 // ABCA12 // 26154 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 2, mRNA. /// NM_173076 // CDS // 0 // Hs.134585 // ABCA12 // 26154 // Homo sapiens ATP-binding cassette	ABCA12	ABCA12, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 2, q35
SNP_A-1880269	tctctctgaccatccca[A/G]tgacgtgtttaagac	A	G	NM_015657 // intron // 0 // Hs.134585 // ABCA12 // 26154 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 2, mRNA. /// NM_173076 // intron // 0 // Hs.134585 // ABCA12 // 26154 // Homo sapiens ATP-binding ca	ABCA12	ABCA12, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 2, q35
SNP_A-1730747	ttgaatttgatcatgaaagttgta[A/C]attgaagaaggtgaaattt gcatt	A	C	NM_015657 // intron // 0 // Hs.134585 // ABCA12 // 26154 // ATP-binding cassette, sub-family A (ABC1), member 12 /// NM_173076 // intron // 0 // Hs.134585 // ABCA12 // 26154 // ATP-binding cassette, sub-family A (ABC1), member 12	ABCA12	ABCA12, rs9527718, ATP-binding cassette, sub-family A (ABC1), member 12, q35
SNP_A-1645712	ttattgcatatttttggcactatgca[A/G]tagagtaigttgtcaagtaat gatt	A	G	NM_173076 // intron // 0 // Hs.134585 // ABCA12 // 26154 // ATP-binding cassette, sub-family A (ABC1), member 12	ABCA12	ABCA12, rs14664680, ATP-binding cassette, sub-family A (ABC1), member 12, q35
SNP_A-2248272	ctgtgtactagttgta[G/T]gtttatggaagaaaaa	G	T	NM_054034 // upstream // 24483 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 24483 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA. ///	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-2242459	ctgcagacttcctaca[C/T]tggaaacatcgcattt	C	T	NM_054034 // upstream // 62599 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 62599 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA. ///	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-1966855	tgctacaaatggttca[C/T]ggacctaacgaatgt	C	T	NM_054034 // upstream // 81721 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 81721 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA. ///	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-2007004	gggtttcaattaaata[C/T]gccatctttggttcc	C	T	NM_054034 // upstream // 338715 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 338715 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA. /	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-2179890	cacttttcagagaaaccc[A/G]aaagtcacagcactac	A	G	NM_054034 // upstream // 395525 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 7, mRNA. /// NM_212476 // upstream // 395525 // Hs.203717 // FN1 // 2335 // Homo sapiens fibronectin 1 (FN1), transcript variant 5, mRNA. /	FN1	FN1, Homo sapiens fibronectin 1 (FN1), transcript variant 7, q35
SNP_A-1752331	ttggatgatgggaacagcctcctga[G/T]aagtacctgaaagtga catcctcac	G	T	NM_002026 // upstream // 81444 // Hs.418138 // FN1 // 2335 // fibronectin 1 /// NM_018000 // downstream // 425291 // Hs.79741 // FLJ10116 // 55686 // hypothetical protein FLJ10116 /// NM_054034 // upstream // 81444 // Hs.418138 // FN1 // 2335 // fibronec	FN1	FN1, rs75883379, fibronectin 1, q35
SNP_A-1933868	ttctatctttgctcta[A/T]ccccgtctccttttt	A	T	NM_018000 // intron // 0 // Hs.79741 // DSU // 55686 // Homo sapiens hypothetical protein FLJ10116 (FLJ10116), mRNA. /// ENST00000236976 // intron // 0 // — // — // —	DSU	DSU, Homo sapiens hypothetical protein FLJ10116 (FLJ10116), q35
SNP_A-2031280	aaagggaatcaccacc[A/G]actctagaagtataat	A	G	NM_018000 // intron // 0 // Hs.79741 // DSU // 55686 // Homo sapiens hypothetical protein FLJ10116 (FLJ10116), mRNA. /// ENST00000236976 // intron // 0 // — // — // —	DSU	DSU, Homo sapiens hypothetical protein FLJ10116 (FLJ10116), q35
SNP_A-1966875	gcatgctctgccata[C/T]aaaaatctacctgagg	C	T	NM_018000 // intron // 0 // Hs.79741 // DSU // 55686 // Homo sapiens hypothetical protein FLJ10116 (FLJ10116), mRNA. /// ENST00000236976 // intron // 0 // — // — // —	DSU	DSU, Homo sapiens hypothetical protein FLJ10116 (FLJ10116), q35

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1700849	atgcccagcctatagttatcttta[C/T]actgaacatatttgtgtatgttttt	C	T	NM_018000 // intron // 0 // Hs.79741 // FLJ10116 // 55686 // hypothetical protein FLJ10116	FLJ10116	FLJ10116 , -, hypothetical protein FLJ10116,q35
SNP_A-2151011	atgtgtacagatagca[A/T]aagtgcaagaagagga	A	T	NM_014140 // intron // 0 // Hs.516674 // SMARCAL1 // 50485 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (SMARCAL1), mRNA. /// ENST00000357276 // intron // 0 // --- // --- // --- ///	SMARCAL1	SMARCAL1, Homo sapiens SWI,q35
SNP_A-2063398	aattaactatgctaag[C/G]actacaatttccatta	C	G	NM_014140 // intron // 0 // Hs.516674 // SMARCAL1 // 50485 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (SMARCAL1), mRNA. /// ENST00000357276 // intron // 0 // --- // --- // --- ///	SMARCAL1	SMARCAL1, Homo sapiens SWI,q35
SNP_A-2309102	gcttttctgatttcc[A/G]cagtagaatgtttaat	A	G	NM_000998 // downstream // 73387 // Hs.433701 // RPL37A // 6168 // Homo sapiens ribosomal protein L37a (RPL37A), mRNA. /// ENST00000359681 // downstream // 73387 // --- // --- // --- /// ENST00000310962 // downstream // 33409 // --- // --- // ---	RPL37A	RPL37A, Homo sapiens ribosomal protein L37a (RPL37A), q35
SNP_A-1966904	cagttccattccattg[C/T]accctatgcctctcca	C	T	NM_000599 // upstream // 97092 // Hs.369982 // IGFBP5 // 3488 // Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA. /// NM_003284 // downstream // 66823 // Hs.3017 // TNP1 // 7141 // Homo sapiens transition protein 1 (during histone	IGFBP5	IGFBP5, Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), q35
SNP_A-1885013	tgaatgcttgagaaccd[A/G]caagacctctgtgtgg	A	G	NM_000599 // upstream // 112553 // Hs.369982 // IGFBP5 // 3488 // Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA. /// NM_003284 // downstream // 51362 // Hs.3017 // TNP1 // 7141 // Homo sapiens transition protein 1 (during histon	IGFBP5	IGFBP5, Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), q35
SNP_A-1892381	tgcaagcatgaaccaa[A/G]ttacaaaccttgttaa	A	G	NM_000599 // upstream // 121376 // Hs.369982 // IGFBP5 // 3488 // Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA. /// NM_003284 // downstream // 42539 // Hs.3017 // TNP1 // 7141 // Homo sapiens transition protein 1 (during histon	IGFBP5	IGFBP5, Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), q35
SNP_A-1966917	gttttgagctgactgat[A/G]ggaaatgcagattccc	A	G	NM_022648 // downstream // 818003 // Hs.471381 // TNS // 7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 113148 // --- // --- // --- /// ENST00000355713 // downstream // 815016 // --- // --- // --- /// ENST00000	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-2259457	gaaaaattatcaggggc[A/G]agaataatataatctg	A	G	NM_022648 // downstream // 812424 // Hs.471381 // TNS // 7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 118727 // --- // --- // --- /// ENST00000355713 // downstream // 809437 // --- // --- // --- /// ENST00000	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-2118781	agtaccaaatagacaa[A/G]tcaggctgtttaccag	A	G	NM_022648 // downstream // 409869 // Hs.471381 // TNS // 7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 521282 // --- // --- // --- /// ENST00000355713 // downstream // 406882 // --- // --- // --- /// ENST00000	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-1860491	tcagttactagctgtg[C/G]aggttcttcgttgctt	C	G	NM_022648 // downstream // 407767 // Hs.471381 // TNS // 7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 523384 // --- // --- // --- /// ENST00000355713 // downstream // 404780 // --- // --- // --- /// ENST00000	TNS	TNS, Homo sapiens tensin (TNS), q35

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2240203	ctgaatatttttcca[G/T]ctgatgatttgattt	G	T	NM_022648 // downstream // 400252 // Hs.471381 // TNS // 7145 // Homo sapiens tensin (TNS), mRNA. /// ENST00000320346 // downstream // 530899 // — // — // — /// ENST00000355713 // downstream // 397265 // — // — // — /// ENST00000	TNS	TNS, Homo sapiens tensin (TNS), q35
SNP_A-1755248	cctagttggagaattctgcagacaf[A/G]tcatattccttcactatcc acaccc	A	G	NM_003284 // upstream // 27784 // Hs.3017 // TNP1 // 7141 // transition protein 1 (during histone to protamine replacement) /// NM_022648 // downstream // 527369 // Hs.512710 // TNS // 7145 // tensin	TNP1	TNP1, rs10490759, transition protein 1 (during histone to protamine replacement), q35
SNP_A-1873878	tctcagtaacggagaa[C/T]ggcttctctgggaacc	C	T	NM_000634 // upstream // 886 // Hs.194778 // IL8RA // 3577 // Homo sapiens interleukin 8 receptor, alpha (IL8RA), mRNA. /// NM_005731 // upstream // 49272 // Hs.529303 // ARPC2 // 10109 // Homo sapiens actin related protein 2/3 complex, subunit 2, 34kDa (	IL8RA	IL8RA, Homo sapiens interleukin 8 receptor, alpha (IL8RA), q35
SNP_A-2265298	gaagcaccggtcagc[A/G]agatgacatgggaggg	A	G	NM_198559 // intron // 0 // Hs.512386 // MGC50811 // 375307 // Homo sapiens hypothetical gene supported by BC052750 (MGC50811), mRNA. /// ENST00000289388 // intron // 0 // — // — // — // —	MGC50811	MGC50811, Homo sapiens hypothetical gene supported by BC052750 (MGC50811), q35
SNP_A-1788623	gggatcttctcactca[A/G]tgtaggtctctctggga	A	G	NM_000578 // CDS // 0 // Hs.471393 // SLC11A1 // 6556 // Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 (SLC11A1), mRNA. /// ENST00000233202 // CDS // 0 // — // — // — // — /// ENST00000354352 // 5	SLC11A1	SLC11A1, Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 (SLC11A1), q35
SNP_A-2045764	aagacagaagtcagga[A/G]tccaaatgctttatt	A	G	NM_015690 // intron // 0 // Hs.471404 // STK36 // 27148 // Homo sapiens serine/threonine kinase 36 (fused homolog, Drosophila) (STK36), mRNA. /// ENST00000295709 // intron // 0 // — // — // — // —	STK36	STK36, Homo sapiens serine,q35
SNP_A-2115171	agggcttaggctacaf[C/G]atattgccaataggga	C	G	NM_006522 // intron // 0 // Hs.29764 // WNT6 // 7475 // Homo sapiens wingless-type MMTV integration site family, member 6 (WNT6), mRNA. /// ENST00000233948 // intron // 0 // — // — // — // —	WNT6	WNT6, Homo sapiens wingless-type MMTV integration site family, member 6 (WNT6), q35
SNP_A-2184087	cagcccggtacctggd[A/G]aggaagtacaaccgca	A	G	NM_182847 // CDS // 0 // Hs.87469 // ACCN4 // 55515 // Homo sapiens amiloride-sensitive cation channel 4, pituitary (ACCN4), transcript variant 2, mRNA. /// NM_018674 // CDS // 0 // Hs.87469 // ACCN4 // 55515 // Homo sapiens amiloride-sensitive cation cha	ACCN4	ACCN4, Homo sapiens amiloride-sensitive cation channel 4, pituitary (ACCN4), transcript variant 2, q35
SNP_A-1966981	aaaattccaggacttaf[C/T]acattcaaaggagtgg	C	T	NM_004438 // downstream // 1458956 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 258085 // — // — // — // — /// ENST00000281821 // downstream // 1458956 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2181453	cagactggcatttccf[A/C]gaacagtctgtaagtc	A	C	NM_004438 // downstream // 1456144 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 260897 // — // — // — // — /// ENST00000281821 // downstream // 1456144 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2007026	aaaaatctccccctgal[G/T]aattcataacacaaac	G	T	NM_004438 // downstream // 1373270 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 343771 // — // — // — // — /// ENST00000281821 // downstream // 1373270 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-1844026	tagttgaaaccgtcacf[A/G]aaggcattgtatagaa	A	G	NM_004438 // downstream // 1152251 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 564790 // — // — // — // — /// ENST00000281821 // downstream // 1152251 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2258579	cttttcttgtatagac[A/C]aagcgatattctgct	A	C	NM_004438 // downstream // 970173 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 746868 // — // — // — // — /// ENST00000281821 // downstream // 970173 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1966998	agtgactggaaccg[C/T]agtagattagccacaa	C	T	NM_004438 // downstream // 898392 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 818649 // — // — // — // — /// ENST00000281821 // downstream // 898392 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2294590	gcagtgaacaaaaact[C/T]aaatctctgtattatg	C	T	NM_004438 // downstream // 895831 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 821210 // — // — // — // — /// ENST00000281821 // downstream // 895831 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2138735	atcccattcaaacata[A/T]ctacttcaaactgtat	A	T	NM_004438 // downstream // 889371 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 827670 // — // — // — // — /// ENST00000281821 // downstream // 889371 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-1831421	taatgtatagaccat[A/C]aagaattcaggatcag	A	C	NM_004438 // downstream // 866054 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 850987 // — // — // — // — /// ENST00000281821 // downstream // 866054 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2069764	acacacttctcctaa[A/C]cgctcagatttatatc	A	C	NM_004438 // downstream // 863976 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 853065 // — // — // — // — /// ENST00000281821 // downstream // 863976 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2030231	aaagcactcaagaaaa[G/T]aataagggggccaggcg	G	T	NM_004438 // downstream // 860044 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 856997 // — // — // — // — /// ENST00000281821 // downstream // 860044 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-1900813	tggagtctttgtagga[C/T]gaagacatgaggattc	C	T	NM_004438 // downstream // 837531 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 879510 // — // — // — // — /// ENST00000281821 // downstream // 837531 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2160132	atttatttttgctga[C/T]taggagtgagactggg	C	T	NM_004438 // downstream // 800106 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 916935 // — // — // — // — /// ENST00000281821 // downstream // 800106 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-1897595	tgctgcagaggtaacc[A/G]cagaaatgttctgaag	A	G	NM_004438 // downstream // 791625 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 925416 // — // — // — // — /// ENST00000281821 // downstream // 791625 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q35
SNP_A-2066348	aattttgaacaagtca[C/T]gtattgctgatggata	C	T	NM_004438 // downstream // 675916 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 1041125 // — // — // — // — /// ENST00000281821 // downstream // 675916 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q36.1
SNP_A-2250175	cttactgccctgctaa[A/G]ggtgccaatgtatgca	A	G	NM_004438 // downstream // 639509 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 1077532 // — // — // — // — /// ENST00000281821 // downstream // 639509 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q36.1
SNP_A-1748705	tgaatagtggctgggtttgagccc[A/G]agttaagacctggaaga gaaaagat	A	G	BC016981 // downstream // 840718 // Hs.244624 // EPHA4 // 2043 // EphA4	EPHA4	EPHA4 , rs1568178, EphA4,q35
SNP_A-1835692	taccttttatagacaa[A/G]gaaactgaagaacaca	A	G	NM_004438 // downstream // 431033 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 1286008 // — // — // — // — /// ENST00000281821 // downstream // 431033 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q36.1
SNP_A-2215731	cctcatatagcctag[A/C]acaaaattggcatttg	A	C	NM_004438 // downstream // 354897 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000355668 // upstream // 1362144 // — // — // — // — /// ENST00000281821 // downstream // 354897 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1866446	tccccacttagagaa[C/T]tgagcctgtcgagtta	C	T	NM_004438 // intron // 0 // Hs.371218 // EPHA4 // 2043 // Homo sapiens EphA4 (EPHA4), mRNA. /// ENST00000281821 // intron // 0 // — // — // — // —	EPHA4	EPHA4, Homo sapiens EphA4 (EPHA4), q36.1
SNP_A-1804972	gtcatcaaaccttttg[C/T]actgcaatgctgattt	C	T	ENST00000272885 // downstream // 66895 // — // — // — // — /// ENST00000358997 // upstream // 284500 // — // — // — // —	-	q36.1
SNP_A-1954912	tttgctttttccatta[C/G]cttcataaagtaacga	C	G	ENST00000272885 // downstream // 237799 // — // — // — // — /// ENST00000358997 // upstream // 113596 // — // — // — // —	-	q36.1
SNP_A-2088722	actgtggtatatgccg[C/T]agtgaaggtacgatga	C	T	ENST00000272885 // downstream // 282032 // — // — // — // — /// ENST00000358997 // upstream // 69363 // — // — // — // —	-	q36.1
SNP_A-1831851	taattctgaaattgaa[A/G]aagaaaatcatttact	A	G	NM_181461 // downstream // 169171 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 169171 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box g	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-2265658	gaagctctaaaggaag[C/T]ctatggttcactccac	C	T	NM_181461 // downstream // 148190 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 148190 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box g	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-2290506	gcaactctccaaggca[A/C]ccaaattacagccaag	A	C	NM_181461 // downstream // 147354 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 147354 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box g	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-1960637	ttttccgattgtttc[A/G]agttccatactggaga	A	G	NM_181461 // downstream // 77486 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 77486 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gen	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-1967064	caaaaatgaaggcac[A/G]aatttaagcagccttt	A	G	NM_181461 // downstream // 70946 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 70946 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gen	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-2033547	aaatatagaacccccca[C/T]gtgatccagcaattcc	C	T	NM_181461 // downstream // 54266 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 54266 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gen	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-2111105	aggagagaaggaggag[A/G]aaaccaggatatga	A	G	NM_181461 // downstream // 28184 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, mRNA. /// NM_181460 // downstream // 28184 // Hs.42146 // PAX3 // 5077 // Homo sapiens paired box gen	PAX3	PAX3, Homo sapiens paired box gene 3 (Waardenburg syndrome 1) (PAX3), transcript variant PAX3G, q36.1
SNP_A-1967073	gtgagtacataccaga[A/G]agctgctgaaaatcca	A	G	NM_152386 // intron // 0 // Hs.210043 // SGPP2 // 130367 // Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA. /// ENST00000321276 // intron // 0 // — // — // — // —	SGPP2	SGPP2, Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), q36.1
SNP_A-2314109	ggaggacaaaatacta[A/G]gcaaattaattcagga	A	G	NM_152386 // intron // 0 // Hs.210043 // SGPP2 // 130367 // Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA. /// ENST00000321276 // intron // 0 // — // — // — // —	SGPP2	SGPP2, Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), q36.1
SNP_A-2229300	ctaggactttcaaaga[C/T]gacaaaagcactaata	C	T	NM_152386 // intron // 0 // Hs.210043 // SGPP2 // 130367 // Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA. /// ENST00000321276 // intron // 0 // — // — // — // —	SGPP2	SGPP2, Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270243	gacacctcggtgaaga[C/T]ggtgacagtatttgtg	C	T	NM_152386 // intron // 0 // Hs.210043 // SGPP2 // 130367 // Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA. /// ENST00000321276 // intron // 0 // — // — // — // —	SGPP2	SGPP2, Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), q36.1
SNP_A-2251422	cttcacagctctgtta[G/T]aagcagatccttacaa	G	T	NM_152386 // downstream // 11456 // Hs.210043 // SGPP2 // 130367 // Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), mRNA. /// NM_005687 // downstream // 187 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, be	SGPP2	SGPP2, Homo sapiens sphingosine-1-phosphate phosphotase 2 (SGPP2), q36.1
SNP_A-1801529	gtaggtaccatctctg[A/G]aaaaaagctgggtctc	A	G	NM_005687 // 3UTR // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // 3UTR // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-1836599	tactctgctttacggc[A/G]cattagtcctagctag	A	G	NM_005687 // intron // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-2209814	cccattttggccaatg[C/T]ataaaactgctgatac	C	T	NM_005687 // intron // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-2283199	gataatgctgagagaa[A/T]gtaccagttgcccctt	A	T	NM_005687 // intron // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-2027278	aaacatatgagtgtca[C/T]aggaatacatcttatt	C	T	NM_005687 // intron // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-2291377	gcaatgtgacactgcc[A/G]atcttccaatcaggag	A	G	NM_005687 // intron // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-1841146	tagcttgtttgcccca[A/G]atggagaggtccgaga	A	G	NM_005687 // intron // 0 // Hs.471452 // FARSLB // 10056 // Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), mRNA. /// ENST00000281828 // intron // 0 // — // — // — // —	FARSLB	FARSLB, Homo sapiens phenylalanine-tRNA synthetase-like, beta subunit (FARSLB), q36.1
SNP_A-1859479	tcaggactttaggtaa[A/G]aggcaaatattcagta	A	G	NM_058165 // downstream // 79337 // Hs.344090 // MOGAT1 // 116255 // Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), mRNA. /// NM_004457 // upstream // 71746 // Hs.471461 // ACSL3 // 2181 // Homo sapiens acyl-CoA synthetase long-chain family m	MOGAT1	MOGAT1, Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), q36.1
SNP_A-2170160	caaggtcaatgtatca[A/C]caggtctggtttctcc	A	C	NM_058165 // downstream // 81365 // Hs.344090 // MOGAT1 // 116255 // Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), mRNA. /// NM_004457 // upstream // 69718 // Hs.471461 // ACSL3 // 2181 // Homo sapiens acyl-CoA synthetase long-chain family m	MOGAT1	MOGAT1, Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), q36.1
SNP_A-2039260	aacagttacttctctg[C/T]accatggatgacctgc	C	T	NM_058165 // downstream // 82771 // Hs.344090 // MOGAT1 // 116255 // Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), mRNA. /// NM_004457 // upstream // 68312 // Hs.471461 // ACSL3 // 2181 // Homo sapiens acyl-CoA synthetase long-chain family m	MOGAT1	MOGAT1, Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2039900	aacattgcttcaaagg[A/G]acctagaaatgctagc	A	G	NM_058165 // downstream // 98075 // Hs.344090 // MOGAT1 // 116255 // Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), mRNA. /// NM_004457 // upstream // 53008 // Hs.471461 // ACSL3 // 2181 // Homo sapiens acyl-CoA synthetase long-chain family m	MOGAT1	MOGAT1, Homo sapiens monoacylglycerol O-acyltransferase 1 (MOGAT1), q36.1
SNP_A-1821382	gtttgcttttctggaa[A/C]taaataagttgattgt	A	C	NM_080671 // downstream // 492634 // Hs.348522 // KCNE4 // 23704 // Homo sapiens potassium voltage-gated channel, Isk-related family, member 4 (KCNE4), mRNA. /// NM_003469 // downstream // 50400 // Hs.516726 // SCG2 // 7857 // Homo sapiens secretogranin I	KCNE4	KCNE4, Homo sapiens potassium voltage-gated channel, Isk-related family, member 4 (KCNE4), q36.1
SNP_A-2075038	acatccattaagcaac[A/G]gttaattctgacttaa	A	G	NM_178814 // upstream // 29862 // Hs.387648 // AP1S3 // 130340 // Homo sapiens adaptor-related protein complex 1, sigma 3 subunit (AP1S3), mRNA. /// BC021898 // upstream // 29924 // Hs.387648 // AP1S3 // 130340 // Homo sapiens adaptor-related protein comp	AP1S3	AP1S3, Homo sapiens adaptor-related protein complex 1, sigma 3 subunit (AP1S3), q36.1
SNP_A-2104957	agcatcataggtttaa[C/T]agccatactctagaag	C	T	NM_178814 // upstream // 34851 // Hs.387648 // AP1S3 // 130340 // Homo sapiens adaptor-related protein complex 1, sigma 3 subunit (AP1S3), mRNA. /// BC021898 // upstream // 34913 // Hs.387648 // AP1S3 // 130340 // Homo sapiens adaptor-related protein comp	AP1S3	AP1S3, Homo sapiens adaptor-related protein complex 1, sigma 3 subunit (AP1S3), q36.1
SNP_A-1967107	gctgctgagtttactc[C/G]atagctttcaaacctt	C	G	NM_020830 // 3UTR // 0 // Hs.368359 // WDFY1 // 57590 // Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), mRNA. /// ENST00000352510 // 3UTR // 0 // — // — // — // — /// ENST00000233055 // 3UTR // 0 // — // — // — // —	WDFY1	WDFY1, Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), q36.1
SNP_A-2063013	aatgttacacactgat[A/T]aaaagtattccagaaa	A	T	NM_020830 // intron // 0 // Hs.368359 // WDFY1 // 57590 // Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), mRNA. /// ENST00000352510 // intron // 0 // — // — // — // — /// ENST00000233055 // intron // 0 // — // — // — // —	WDFY1	WDFY1, Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), q36.1
SNP_A-2198600	catttcacacccccca[A/G]gatgaccataacaaaa	A	G	NM_020830 // intron // 0 // Hs.368359 // WDFY1 // 57590 // Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), mRNA. /// ENST00000352510 // intron // 0 // — // — // — // — /// ENST00000233055 // intron // 0 // — // — // — // —	WDFY1	WDFY1, Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), q36.1
SNP_A-1824375	taaacggatcaaccaa[A/G]tgcagtatagaatgct	A	G	NM_020830 // intron // 0 // Hs.368359 // WDFY1 // 57590 // Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), mRNA. /// ENST00000352510 // intron // 0 // — // — // — // — /// ENST00000233055 // intron // 0 // — // — // — // —	WDFY1	WDFY1, Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), q36.1
SNP_A-2104470	agcaggatggtcaaaa[C/T]taagtgagagaaaggc	C	T	NM_020830 // upstream // 4138 // Hs.368359 // WDFY1 // 57590 // Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), mRNA. /// NM_022915 // upstream // 7948 // Hs.203559 // MRPL44 // 65080 // Homo sapiens mitochondrial ribosomal protein L44 (MRPL4	WDFY1	WDFY1, Homo sapiens WD repeat and FYVE domain containing 1 (WDFY1), q36.1
SNP_A-2198694	catttccctaatgtca[A/G]tagttgcagacacttt	A	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-1967111	agcaagtttcttgcac[C/G]attttcactgatcttt	C	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-1855338	tcaaggcagcggctaa[C/G]aggacaaaatgacatg	C	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1912690	tgtgcgtcctcttcag[A/G]cctttacacgggga	A	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2046493	aagagagggccatgca[C/T]gttgtaaagccctaca	C	T	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2007047	tttaattctgccttca[A/C]aatgcctagttaaccc	A	C	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI q36.1
SNP_A-2250270	cttagaagaatggtta[C/G]acaactcacaaattga	C	G	NM_006216 // intron // 0 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// ENST00000258405 // intron // 0 // — // — // —	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2232474	ctcacatctcttgta[C/T]cacctctccgtacatt	C	T	NM_006216 // upstream // 18697 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 342446 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2023995	aaaagactggcaaacc[A/G]aataaaacctgaagtc	A	G	NM_006216 // upstream // 22318 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 338825 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-1967120	atacagggtgtcctca[A/G]agtctgggaaagaaag	A	G	NM_006216 // upstream // 43260 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 317883 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.1
SNP_A-2139215	atcctctgatggaaaa[C/G]tggttagtgcatttt	C	G	NM_006216 // upstream // 64934 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 296209 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI q36.1
SNP_A-1824438	taaactatggagtcac[A/C]gcatcattggtattca	A	C	NM_006216 // upstream // 180580 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 180563 // Hs.147585 // FLJ22	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI q36.1
SNP_A-1726634	aagcttaacattcaacattgtgctt[A/G]aacaaaactaccacta ctcaattt	A	G	NM_020830 // 3UTR // 0 // Hs.44743 // WDFY1 // 57590 // WD repeat and FYVE domain containing 1 /// NM_178350 // 3UTR // 0 // Hs.44743 // WDFY1 // 57590 // WD repeat and FYVE domain containing 1	WDFY1	WDFY1 . rs10498156, WD repeat and FYVE domain containing 1 ,q36.1
SNP_A-1677994	ctaaacaataaggaaaacaagaagca[G/T]taaattactttttccc ccaaaataa	G	T	NM_020830 // intron // 0 // Hs.44743 // WDFY1 // 57590 // WD repeat and FYVE domain containing 1 /// NM_178350 // intron // 0 // Hs.44743 // WDFY1 // 57590 // WD repeat and FYVE domain containing 1	WDFY1	WDFY1 . rs717610, WD repeat and FYVE domain containing 1 ,q36.1
SNP_A-2259198	gaaaaacaaaattcac[A/C]attctgtacatcaatc	A	C	NM_006216 // upstream // 322582 // Hs.38449 // SERPINE2 // 5270 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI /// NM_024785 // downstream // 38561 // Hs.147585 // FLJ227	SERPINE2	SERPINE2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPI ,q36.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1799259	gtaataaagtaaaata[C/G]ctcatctagaagcagg	C	G	AB014594 // intron // 0 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // intron // 0 // --- // --- // ---	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1827984	taagaaggaagtcaat[A/C]atggagtcagtttaa	A	C	AB014594 // upstream // 38966 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 38966 // --- // --- // --- // ENST00000272907 // upstream // 319645 // --- // --- // ---	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1967168	gaaagttcattgttig[C/T]ataatgatatggtttg	C	T	AB014594 // upstream // 115812 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 115812 // --- // --- // --- // ENST00000272907 // upstream // 242799 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-2027962	aaaccttcctccact[C/G]actggttcccigctg	C	G	AB014594 // upstream // 120357 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 120357 // --- // --- // --- // ENST00000272907 // upstream // 238254 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1815795	gttaagggattggcgg[A/G]aaaagagtgggatgta	A	G	AB014594 // upstream // 125335 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 125335 // --- // --- // --- // ENST00000272907 // upstream // 233276 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1839821	tagattcaaaaaaagca[C/T]gtgttagagaagtcaa	C	T	AB014594 // upstream // 125464 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 125464 // --- // --- // --- // ENST00000272907 // upstream // 233147 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1967169	tgcaagacatgctaaa[A/G]gaagtgcttcaggagg	A	G	AB014594 // upstream // 128862 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 128862 // --- // --- // --- // ENST00000272907 // upstream // 229749 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-2201109	ccaagtctacagcaaa[C/T]gaggtgcaactgtaat	C	T	AB014594 // upstream // 134014 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 134014 // --- // --- // --- // ENST00000272907 // upstream // 224597 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-2283105	gataagtttcagttaa[C/T]ccagtctatagagtc	G	T	AB014594 // upstream // 144907 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 144907 // --- // --- // --- // ENST00000272907 // upstream // 213704 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1810964	gtgcattggatgaaaa[C/T]actgaatactgtcaa	C	T	AB014594 // upstream // 155327 // Hs.46578 // DOCK10 // 55619 // Homo sapiens mRNA for KIAA0694 protein, partial cds. /// ENST00000258390 // upstream // 155327 // --- // --- // --- // ENST00000272907 // upstream // 203284 // --- // --- // -	DOCK10	DOCK10, Homo sapiens for KIAA0694 protein, partial cds. q36.2
SNP_A-1734468	tatcaagcatattgaagataatgaa[C/T]ggacctatcggatcata tcttagtt	C	T	AB040919 // upstream // 338269 // Hs.210958 // KIAA1486 // 57624 // KIAA1486 protein	KIAA1486	KIAA1486 , rs7598761, KIAA1486 protein,q36.2
SNP_A-1861073	tcatagtctaaaatgc[C/T]gaagagacataccaaa	C	T	ENST00000272907 // intron // 0 // --- // --- // ---	-	q36.3
SNP_A-2087902	actggatcataggggc[A/G]aatttatcccctgctg	A	G	ENST00000358349 // intron // 0 // --- // --- // ---	-	q36.3
SNP_A-2263512	gaaccacggagaactg[G/T]aatgagagtgatggat	G	T	ENST00000358349 // intron // 0 // --- // --- // ---	-	q36.3
SNP_A-2123330	agtgtattatcacca[C/T]gcatctcaggcaatg	C	T	ENST00000358349 // intron // 0 // --- // --- // ---	-	q36.3
SNP_A-1967219	tattgtttcctaata[C/T]gtggcttggaagggag	C	T	ENST00000358349 // intron // 0 // --- // --- // ---	-	q36.3
SNP_A-2045224	aagaagctacttatca[C/G]gaaaaaaggcaaggat	C	G	NM_000091 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, a	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-1908354	tgtactgtcattggga[A/C]aatcactaaccaga	A	C	NM_000091 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, a	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1958004	ttttcaccactgagta[C/T]gcagatctccccttg	C	T	NM_000091 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, a	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-2007068	taacaaatagcctaat[A/T]atgtaagtgaatgatt	A	T	NM_000091 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, mRNA. /// NM_031362 // intron // 0 // Hs.471525 // COL4A3 // 1285 // Homo sapiens collagen, type IV, a	COL4A3	COL4A3, Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) (COL4A3), transcript variant 1, q36.3
SNP_A-2022253	aaaaagtagaatatca[A/G]tcaccatttgcaacc	A	G	ENST00000358349 // intron // 0 // — // — // —	-	q36.3
SNP_A-1864592	tccagagttaaaggcc[G/T]gccggctaatctta	G	T	ENST00000358349 // intron // 0 // — // — // —	-	q36.3
SNP_A-1967243	gaagaaaaccacagca[C/T]tgcggagagaaagctc	C	T	ENST00000358349 // intron // 0 // — // — // —	-	q36.3
SNP_A-1949357	ttatattatctcagtga[C/T]gaccatctgttggt	C	T	NM_178821 // intron // 0 // Hs.424594 // FLJ25955 // 164781 // Homo sapiens hypothetical protein FLJ25955 (FLJ25955), mRNA. /// ENST00000358349 // intron // 0 // — // — // — // — /// ENST00000309931 // intron // 0 // — // — // —	FLJ25955	FLJ25955, Homo sapiens hypothetical protein FLJ25955 (FLJ25955), q36.3
SNP_A-1784598	ggcctcaactaaagtc[A/G]ccaactaictaiccc	A	G	ENST00000358349 // intron // 0 // — // — // —	-	q36.3
SNP_A-1944985	ttgtggtacagttaaa[C/G]taggaccacactggc	C	G	ENST00000358349 // intron // 0 // — // — // —	-	q36.3
SNP_A-2051082	aagggaaaaatgccctc[A/T]agggaacacgtgcata	A	T	ENST00000358349 // intron // 0 // — // — // —	-	q36.3
SNP_A-2155664	atccagtcacttaaa[A/T]ctgagcgctttcctt	A	T	NM_017933 // downstream // 270527 // Hs.409352 // FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000355115 // upstream // 331579 // — // — // — // — /// ENST00000343451 // downstream // 270527 // — //	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-1871348	tctaaataaaattgac[A/G]gatggactaggtccat	A	G	NM_017933 // downstream // 205199 // Hs.409352 // FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000355115 // upstream // 396907 // — // — // — // — /// ENST00000343451 // downstream // 205199 // — //	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2104191	agcagagggagaggta[A/T]cagacctgtcaggaaa	A	T	NM_017933 // intron // 0 // Hs.409352 // FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // — // — // — // — /// ENST00000354069 // intron // 0 // — // — // — // —	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-1967277	tgctgttctcttcag[A/G]atgccatgctctgtgcag	A	G	NM_017933 // intron // 0 // Hs.409352 // FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // — // — // — // — /// ENST00000354069 // intron // 0 // — // — // — // —	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2148753	atggtctgtcctaaag[C/T]agtgaatttcctaagg	C	T	NM_017933 // intron // 0 // Hs.409352 // FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // — // — // — // — /// ENST00000354069 // intron // 0 // — // — // — // —	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2151486	atgttctaccatacag[A/G]caactcaaatgtcaga	A	G	NM_017933 // intron // 0 // Hs.409352 // FLJ20701 // 55022 // Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA. /// ENST00000343451 // intron // 0 // — // — // — // — /// ENST00000354069 // intron // 0 // — // — // — // —	FLJ20701	FLJ20701, Homo sapiens hypothetical protein FLJ20701 (FLJ20701), q36.3
SNP_A-2123700	agtgttctggtctgga[C/T]gaaatgagagaactcc	C	T	NM_139072 // intron // 0 // Hs.234074 // DNER // 92737 // Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA. /// ENST00000341772 // intron // 0 // — // — // — // —	DNER	DNER, Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), q36.3
SNP_A-1735092	ctgcacttcttaaatagaacagaag[C/T]atcccctgaaaaaaata tagatctgg	C	T	NM_017933 // intron // 0 // Hs.424598 // FLJ20701 // 55022 // hypothetical protein FLJ20701	FLJ20701	FLJ20701, rs6436840, hypothetical protein FLJ20701,q36.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1837599	tacttgtgctgttcac[A/G]gaggtggtcatctcac	A	G	NM_005683 // upstream // 9212 // Hs.114545 // GPR55 // 9290 // Homo sapiens G protein-coupled receptor 55 (GPR55), mRNA. /// AK093385 // upstream // 61796 // Hs.121021 // SPATA3 // 130560 // Homo sapiens cDNA FLJ36066 fis, clone TESTI2019257. /// NM_13907	GPR55	GPR55, Homo sapiens G protein-coupled receptor 55 (GPR55), q37.1
SNP_A-2245940	ctgggttgatgaggga[C/T]gagaaggatcagggag	C	T	AK093385 // intron // 0 // Hs.121021 // SPATA3 // 130560 // Homo sapiens cDNA FLJ36066 fis, clone TESTI2019257. /// NM_139073 // intron // 0 // Hs.121021 // SPATA3 // 130560 // Homo sapiens spermatogenesis associated 3 (SPATA3), mRNA. /// ENST00000355662	SPATA3	SPATA3, Homo sapiens cDNA FLJ36066 fis, clone TESTI2019257., q37.1
SNP_A-2042821	aactctgggacggtta[C/T]ggaagattgaggttgt	C	T	NM_025139 // intron // 0 // Hs.471610 // FLJ12584 // 80210 // Homo sapiens hypothetical protein FLJ12584 (FLJ12584), mRNA. /// ENST00000349838 // intron // 0 // — // — // — /// ENST00000359743 // intron // 0 // — // — // —	FLJ12584	FLJ12584, Homo sapiens hypothetical protein FLJ12584 (FLJ12584), q37.1
SNP_A-1819182	gttgctgcatttggat[C/T]gtcttaaatattcctt	C	T	NM_152614 // downstream // 41140 // Hs.98104 // MGC35154 // 165100 // Homo sapiens hypothetical protein MGC35154 (MGC35154), mRNA. /// NM_002823 // upstream // 73104 // Hs.459927 // PTMA // 5757 // Homo sapiens prothymosin, alpha (gene sequence 28) (PTMA)	MGC35154	MGC35154, Homo sapiens hypothetical protein MGC35154 (MGC35154), q37.1
SNP_A-1866624	tccccgataagatgga[A/G]aaccagacagctccaa	A	G	NM_022730 // downstream // 44608 // Hs.335061 // COPS7B // 64708 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis) (COPS7B), mRNA. /// NM_024409 // downstream // 72093 // Hs.247916 // NPPC // 4880 // Homo sapiens natriure	COPS7B	COPS7B, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis) (COPS7B), q37.1
SNP_A-1943548	ttgtaacaaccatctc[A/C]caatactgctgagagg	A	C	NM_004846 // intron // 0 // Hs.292026 // EIF4E2 // 9470 // Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// ENST00000258416 // intron // 0 // — // — // —	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-1967339	ttagctagaaaaaatta[C/T]gtttctcctgccgct	C	T	NM_004846 // intron // 0 // Hs.292026 // EIF4E2 // 9470 // Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// ENST00000258416 // intron // 0 // — // — // —	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-2073767	acagtgaatgtgattt[A/T]aaaaggtttgtcata	A	T	NM_004846 // downstream // 7033 // Hs.292026 // EIF4E2 // 9470 // Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// NM_025202 // upstream // 57316 // Hs.516769 // EFHD1 // 80303 // Homo sapiens EF hand domain containing	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-2049507	aagctggttatgccat[A/G]gcctattaacacttaa	A	G	NM_004846 // downstream // 12649 // Hs.292026 // EIF4E2 // 9470 // Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), mRNA. /// NM_025202 // upstream // 51700 // Hs.516769 // EFHD1 // 80303 // Homo sapiens EF hand domain containing	EIF4E2	EIF4E2, Homo sapiens eukaryotic translation initiation factor 4E-like 3 (EIF4EL3), q37.1
SNP_A-1808910	gtgaatcgtttggtca[A/G]ctgttgaggacaggct	A	G	ENST00000355409 // intron // 0 // — // — // —	-	q37.1
SNP_A-2120724	agtcctagacgtgggg[C/G]tagaaattagatgaca	C	G	NM_019075 // intron // 0 // Hs.546397 // UGT1A10 // 54575 // Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), mRNA. /// NM_019076 // intron // 0 // Hs.546397 // UGT1A8 // 54576 // Homo sapiens UDP glycosyltransferase 1 family, pol	UGT1A10	UGT1A10, Homo sapiens UDP glycosyltransferase 1 family, polypeptide A10 (UGT1A10), q37.1
SNP_A-1967366	cctgcctccaccactc[A/G]ccggttatgtaaccat	A	G	NM_018410 // upstream // 54483 // Hs.532968 // DKFZp762E1312 // 55355 // Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA. /// NM_024080 // upstream // 8382 // Hs.366053 // TRPM8 // 79054 // Homo sapiens transient receptor potential c	DKFZp762E1312	DKFZp762E1312, Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), q37.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227846	ctaccccaaattattg[A/G]aagtctctctagcagc	A	G	NM_024080 // intron // 0 // Hs.366053 // TRPM8 // 79054 // Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), mRNA. /// ENST00000324695 // intron // 0 // — // — // — // — /// ENST00000355722 // intron // 0 //	TRPM8	TRPM8, Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), q37.1
SNP_A-1967368	gaccggtagaactaag[A/G]aaacgtgtcgtaatct	A	G	NM_024080 // intron // 0 // Hs.366053 // TRPM8 // 79054 // Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), mRNA. /// ENST00000324695 // intron // 0 // — // — // — // — /// ENST00000355722 // intron // 0 //	TRPM8	TRPM8, Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), q37.1
SNP_A-2268731	gaatgttttatggaca[C/T]gtcgagttaggaaaaa	C	T	NM_024080 // intron // 0 // Hs.366053 // TRPM8 // 79054 // Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), mRNA. /// ENST00000324695 // intron // 0 // — // — // — // —	TRPM8	TRPM8, Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), q37.1
SNP_A-2296498	gcatttgctgcactta[C/T]gttctagttcattaaa	C	T	NM_024080 // intron // 0 // Hs.366053 // TRPM8 // 79054 // Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), mRNA. /// ENST00000324695 // intron // 0 // — // — // — // —	TRPM8	TRPM8, Homo sapiens transient receptor potential cation channel, subfamily M, member 8 (TRPM8), q37.1
SNP_A-2103352	agcaaggtagacagta[C/T]gggatcagaacctgat	C	T	NM_006944 // intron // 0 // Hs.444488 // SPP2 // 6694 // Homo sapiens secreted phosphoprotein 2, 24kDa (SPP2), mRNA. /// ENST00000168148 // intron // 0 // — // — // — // —	SPP2	SPP2, Homo sapiens secreted phosphoprotein 2, 24kDa (SPP2), q37.1
SNP_A-1881009	tcttgttccctctttc[A/G]attccaccttcatctg	A	G	NM_006944 // downstream // 7057 // Hs.444488 // SPP2 // 6694 // Homo sapiens secreted phosphoprotein 2, 24kDa (SPP2), mRNA. /// NM_005737 // downstream // 411819 // Hs.111554 // ARL7 // 10123 // Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA. //	SPP2	SPP2, Homo sapiens secreted phosphoprotein 2, 24kDa (SPP2), q37.1
SNP_A-1860902	tcatacctagaatata[C/T]gtcgatttcagtcaag	C	T	NM_005737 // upstream // 301385 // Hs.111554 // ARL7 // 10123 // Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA. /// NM_014521 // upstream // 154071 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. ///	ARL7	ARL7, Homo sapiens ADP-ribosylation factor-like 7 (ARL7), q37.2
SNP_A-2063417	aattaagaccatcaaa[A/C]taagctccagaaagag	A	C	NM_005737 // upstream // 327925 // Hs.111554 // ARL7 // 10123 // Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA. /// NM_014521 // upstream // 127531 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. ///	ARL7	ARL7, Homo sapiens ADP-ribosylation factor-like 7 (ARL7), q37.2
SNP_A-1800856	gtagagaggagaaaaa[C/G]tggacattttacagaa	C	G	NM_005737 // upstream // 374032 // Hs.111554 // ARL7 // 10123 // Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA. /// NM_014521 // upstream // 81424 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. ///	ARL7	ARL7, Homo sapiens ADP-ribosylation factor-like 7 (ARL7), q37.2
SNP_A-1738687	actgccttagaaggtgcctgcttca[C/T]ggttggttgcctttcattggcacag	C	T	NM_005737 // upstream // 51440 // Hs.111554 // ARL7 // 10123 // ADP-ribosylation factor-like 7 /// NM_014521 // upstream // 404002 // Hs.17667 // SH3BP4 // 23677 // SH3-domain binding protein 4	ARL7	ARL7 , rs1880746, ADP-ribosylation factor-like 7 ,q37.1
SNP_A-2304974	gctgaaaaccactgac[A/C]ctatttttgtcaagac	A	C	NM_014521 // downstream // 20563 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 20629 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA.	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-1841494	taggagctgtgtgtta[C/G]gaaacagtgaggaaga	C	G	NM_014521 // downstream // 22679 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 22745 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA.	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2007121	atggtatgtctcctgc[C/T]gagcacgttcccttca	C	T	NM_014521 // downstream // 164673 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 164739 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-2141825	atcttgcaaaacagctt[A/G]acaattttatgccgcc	A	G	NM_014521 // downstream // 179295 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 179361 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-1893867	tgcatacatgtttcac[A/G]ggttgcaagcataac	A	G	NM_014521 // downstream // 180794 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 180860 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-2213718	ccgttcactatgacaa[C/G]attacctagcggtctt	C	G	NM_014521 // downstream // 181447 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 181513 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-2166328	caaatctattgaaccc[A/G]ggaaattggttcagta	A	G	NM_014521 // downstream // 216316 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 216382 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-2029631	aaagagactgcaaata[C/G]atatgacttggaggg	C	G	NM_014521 // downstream // 224226 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 224292 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-1920911	ttacactctactgtta[C/T]ggggttcaggtcagaa	C	T	NM_014521 // downstream // 292990 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 293056 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-1898421	tgcttcctccacgtcc[A/G]ctcggagtgttcttct	A	G	NM_014521 // downstream // 294093 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 294159 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-1942947	ttgggtcttctaagcc[C/T]ccatccatgtcacctg	C	T	NM_014521 // downstream // 301183 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRNA. /// NM_014521 // downstream // 301249 // Hs.516777 // SH3BP4 // 23677 // Homo sapiens SH3-domain binding protein 4 (SH3BP4), mRN	SH3BP4	SH3BP4, Homo sapiens SH3-domain binding protein 4 (SH3BP4), q37.2
SNP_A-1792569	ggtaaactaacactta[C/T]gcattgtatggaactg	C	T	NM_014914 // intron // 0 // Hs.435039 // CENTG2 // 116987 // Homo sapiens centaurin, gamma 2 (CENTG2), mRNA. /// ENST00000336665 // intron // 0 // — // — // — // — /// ENST00000358964 // intron // 0 // — // — // — // —	CENTG2	CENTG2, Homo sapiens centaurin, gamma 2 (CENTG2), q37.2
SNP_A-1893427	tgcagcgtggaatttg[A/G]aattgtggtaacagct	A	G	NM_014914 // intron // 0 // Hs.435039 // CENTG2 // 116987 // Homo sapiens centaurin, gamma 2 (CENTG2), mRNA. /// ENST00000336665 // intron // 0 // — // — // — // — /// ENST00000304032 // intron // 0 // — // — // — // —	CENTG2	CENTG2, Homo sapiens centaurin, gamma 2 (CENTG2), q37.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2071974	acagagctctctgctt[C/G]aactcaacgtcacggc	C	G	NM_024726 // upstream // 28954 // Hs.129174 // IQCA // 79781 // Homo sapiens IQ motif containing with AAA domain (IQCA), mRNA. /// NM_020311 // upstream // 33314 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /	IQCA	IQCA, Homo sapiens IQ motif containing with AAA domain (IQCA), q37.3
SNP_A-2292905	gcagaacacactcaat[A/C]acagttaatcaagtca	A	C	NM_024726 // upstream // 30709 // Hs.129174 // IQCA // 79781 // Homo sapiens IQ motif containing with AAA domain (IQCA), mRNA. /// NM_020311 // upstream // 31559 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /	IQCA	IQCA, Homo sapiens IQ motif containing with AAA domain (IQCA), q37.3
SNP_A-1902978	tggctgctgagggcac[A/G]agccccccacaaaggaa	A	G	NM_020311 // downstream // 121857 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 // downstream // 121857 // — // — // — // — /// ENST00000244820 // downstream // 351222 // — // —	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-1967391	ctatgacctgaattga[A/G]ccagaaaatgcagagt	A	G	NM_020311 // downstream // 305401 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 // downstream // 305401 // — // — // — // — /// ENST00000244820 // downstream // 167678 // — // —	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-1799618	gtaattctttgaaatc[C/G]aacagcccatttagtc	C	G	NM_020311 // downstream // 306398 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 // downstream // 306398 // — // — // — // — /// ENST00000244820 // downstream // 166681 // — // —	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-2271476	gaccaaaacattaata[A/C]ggggaagcaataaatg	A	C	NM_020311 // downstream // 312309 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 // downstream // 312309 // — // — // — // — /// ENST00000244820 // downstream // 160770 // — // —	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-1942788	ttgggctctggccaca[C/T]ggtgatttcctatcaa	C	T	NM_020311 // downstream // 456297 // Hs.471751 // CMKOR1 // 57007 // Homo sapiens chemokine orphan receptor 1 (CMKOR1), mRNA. /// ENST00000272928 // downstream // 456297 // — // — // — // — /// ENST00000244820 // downstream // 16782 // — // —	CMKOR1	CMKOR1, Homo sapiens chemokine orphan receptor 1 (CMKOR1), q37.3
SNP_A-1688398	acttagtctgaagtcttattttaaa[A/G]caattaatcagtcttatacctaagc	A	G	NM_020311 // downstream // 257404 // Hs.231853 // CMKOR1 // 57007 // chemokine orphan receptor 1	CMKOR1	CMKOR1 , rs1368208, chemokine orphan receptor 1,q37.3
SNP_A-1967397	gcgtcactcaaacctg[A/C]cagccttccaaatcac	A	C	NM_057164 // upstream // 81055 // Hs.233240 // COL6A3 // 1293 // Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 2, mRNA. /// NM_057167 // upstream // 81055 // Hs.233240 // COL6A3 // 1293 // Homo sapiens collagen, type VI, alpha 3 (CO	COL6A3	COL6A3, Homo sapiens collagen, type VI, alpha 3 (COL6A3), transcript variant 2, q37.3
SNP_A-1789600	gggcgtgacacacaca[C/G]aggcatgatctgcact	C	G	NM_198582 // intron // 0 // Hs.199821 // FLJ43374 // 377007 // Homo sapiens FLJ43374 protein (FLJ43374), mRNA. /// ENST00000305959 // intron // 0 // — // — // — // —	FLJ43374	FLJ43374, Homo sapiens FLJ43374 protein (FLJ43374), q37.3
SNP_A-1642069	gtcttcaagcattgcctcagggaca[C/T]gccaagggaacggaaaccagtccca	C	T	AF115510 // intron // 0 // Hs.512387 // LRRFIP1 // 9208 // leucine rich repeat (in FLII) interacting protein 1	LRRFIP1	LRRFIP1 , rs3754728, leucine rich repeat (in FLII) interacting protein 1,q37.3
SNP_A-2132231	atagtaactggaagag[A/C]aatttggtacccagag	A	C	NM_176799 // upstream // 13922 // Hs.92033 // ILKAP // 80895 // Homo sapiens integrin-linked kinase-associated serine/threonine phosphatase 2C (ILKAP), transcript variant 2, mRNA. /// NM_030768 // upstream // 13922 // Hs.92033 // ILKAP // 80895 // Homo sa	ILKAP	ILKAP, Homo sapiens integrin-linked kinase-associated serine,q37.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1786588	ggctttctatgattgaa[C/T]tgaggtgagccagagt	C	T	NM_018645 // downstream // 950 // Hs.42949 // HES6 // 55502 // Homo sapiens hairy and enhancer of split 6 (Drosophila) (HES6), mRNA. /// ENST00000315091 // downstream // 3763 // — // — // — /// ENST00000339726 // downstream // 3681 // — // —	HES6	HES6, Homo sapiens hairy and enhancer of split 6 (Drosophila) (HES6), q37.3
SNP_A-1929971	ttcatgctgtggcctctg[C/G]aacgaagctggcaaac	C	G	NM_022817 // 5UTR // 0 // Hs.58756 // PER2 // 8864 // Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, mRNA. /// NM_003894 // 5UTR // 0 // Hs.58756 // PER2 // 8864 // Homo sapiens period homolog 2 (Drosophila) (PER2), transcript va	PER2	PER2, Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, q37.3
SNP_A-2194848	catgctaaaagccgaa[C/T]gtacaggcctggcctg	C	T	NM_022817 // upstream // 46025 // Hs.58756 // PER2 // 8864 // Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, mRNA. /// NM_003894 // upstream // 46025 // Hs.58756 // PER2 // 8864 // Homo sapiens period homolog 2 (Drosophila) (PER2	PER2	PER2, Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, q37.3
SNP_A-1781719	ggatttaagatggctc[C/T]acattctctgacactc	C	T	NM_016114 // downstream // 130361 // Hs.516788 // ASB1 // 51665 // Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA. /// ENST00000264607 // downstream // 130361 // — // — // — /// ENST00000334138 // downstream // 269581 // -	ASB1	ASB1, Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), q37.3
SNP_A-1804439	gtcagaaggctacttc[A/T]cagagggtccattgta	A	T	NM_016114 // downstream // 181867 // Hs.516788 // ASB1 // 51665 // Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA. /// ENST00000264607 // downstream // 181867 // — // — // — /// ENST00000334138 // downstream // 218075 // -	ASB1	ASB1, Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), q37.3
SNP_A-2047571	aagatgggccaacta[C/T]ggtgaaagtgaatagg	C	T	NM_016114 // downstream // 319505 // Hs.516788 // ASB1 // 51665 // Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA. /// ENST00000264607 // downstream // 319505 // — // — // — /// ENST00000334138 // downstream // 80437 // -	ASB1	ASB1, Homo sapiens ankyrin repeat and SOCS box-containing 1 (ASB1), q37.3
SNP_A-2294252	gcagggcctgattagal[A/G]gtggctgagtgaacca	A	G	NM_001001698 // upstream // 18091 // Hs.516791 // FLJ43879 // 401039 // Homo sapiens FLJ43879 protein (FLJ43879), mRNA. /// NM_006037 // downstream // 104927 // Hs.20516 // HDAC4 // 9759 // Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /// ENST0000034	FLJ43879	FLJ43879, Homo sapiens FLJ43879 protein (FLJ43879), q37.3
SNP_A-2270560	gacagagcaggaacac[C/G]aggtgatgccaatgct	C	G	NM_006037 // intron // 0 // Hs.20516 // HDAC4 // 9759 // Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /// ENST00000345617 // intron // 0 // — // — // — /// ENST00000353446 // intron // 0 // — // — // — // —	HDAC4	HDAC4, Homo sapiens histone deacetylase 4 (HDAC4), q37.3
SNP_A-2181359	cagacgtttctctct[C/T]acagttctgaaggtga	C	T	NM_006037 // upstream // 129524 // Hs.20516 // HDAC4 // 9759 // Homo sapiens histone deacetylase 4 (HDAC4), mRNA. /// NM_207483 // upstream // 47828 // Hs.516794 // FLJ45964 // 401040 // Homo sapiens FLJ45964 protein (FLJ45964), mRNA. /// ENST00000345617	HDAC4	HDAC4, Homo sapiens histone deacetylase 4 (HDAC4), q37.3
SNP_A-1967413	cctggaatcttccccc[C/T]agatcctcacaggctg	C	T	ENST00000328627 // intron // 0 // — // — // —	-	q37.3
SNP_A-2086976	actgaggacacagaga[C/T]ctagcctcaagtggtt	C	T	ENST00000328627 // intron // 0 // — // — // —	-	q37.3
SNP_A-1831950	taattgcggacttg[A/G]aattcgttatgcattt	A	G	ENST00000328627 // intron // 0 // — // — // —	-	q37.3
SNP_A-2270273	gacacgctgtgtagc[A/G]gacacacctgagccca	A	G	ENST00000328627 // intron // 0 // — // — // —	-	q37.3
SNP_A-1746364	gctgtacaaatgctttctcgaggat[G/T]actcgcagggggtaccc tgccagga	G	T	NM_004544 // downstream // 676923 // Hs.198271 // NDUFA10 // 4705 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa /// NM_006037 // upstream // 9328 // Hs.222874 // HDAC4 // 9759 // histone deacetylase 4 /// NM_032923 // upstream // 21481	NDUFA10	NDUFA10 , rs709274, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa, q37.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829287	taagtatatgttgaac[A/G]cgggaatggccaaatg	A	G	NM_004544 // intron // 0 // Hs.277677 // NDUFA10 // 4705 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa (NDUFA10), nuclear gene encoding mitochondrial protei /// ENST00000328627 // intron // 0 // — // — // — // — ///	NDUFA10	NDUFA10, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa (NDUFA10), nuclear gene encoding mitochondrial protei q37.3
SNP_A-2175016	cacagtaagggattga[C/T]attggtattactgtgg	C	T	ENST00000328627 // intron // 0 // — // — // — // — /// ENST00000329042 // intron // 0 // — // — // — // —	-	q37.3
SNP_A-2007166	cccacccactagggac[A/G]cctttaactgatcacc	A	G	NM_148961 // upstream // 29674 // Hs.148586 // OTOS // 150677 // Homo sapiens otospiralin (OTOS), mRNA. /// NM_002081 // upstream // 265368 // Hs.328232 // GPC1 // 2817 // Homo sapiens glypican 1 (GPC1), mRNA. /// ENST00000319460 // upstream // 29674 // -	OTOS	OTOS, Homo sapiens otospiralin (OTOS), q37.3
SNP_A-2218959	cctggtccatgtcaga[C/T]cttttcaggccgggga	C	T	NM_148961 // upstream // 152681 // Hs.148586 // OTOS // 150677 // Homo sapiens otospiralin (OTOS), mRNA. /// NM_002081 // upstream // 142361 // Hs.328232 // GPC1 // 2817 // Homo sapiens glypican 1 (GPC1), mRNA. /// ENST00000319460 // upstream // 152681 //	OTOS	OTOS, Homo sapiens otospiralin (OTOS), q37.3
SNP_A-2148399	atgggggctctgcctc[A/G]aatgcctggtcagtct	A	G	NM_148961 // upstream // 159304 // Hs.148586 // OTOS // 150677 // Homo sapiens otospiralin (OTOS), mRNA. /// NM_002081 // upstream // 135738 // Hs.328232 // GPC1 // 2817 // Homo sapiens glypican 1 (GPC1), mRNA. /// ENST00000319460 // upstream // 159304 //	OTOS	OTOS, Homo sapiens otospiralin (OTOS), q37.3
SNP_A-2212691	cccttctggtaatgga[C/T]cttcctaggcagggac	C	T	NM_005301 // downstream // 1189 // Hs.239891 // GPR35 // 2859 // Homo sapiens G protein-coupled receptor 35 (GPR35), mRNA. /// NM_198998 // downstream // 43981 // Hs.534650 // AQP12 // 375318 // Homo sapiens aquaporin 12 (AQP12), mRNA. /// ENST00000319838	GPR35	GPR35, Homo sapiens G protein-coupled receptor 35 (GPR35), q37.3
SNP_A-2236223	ctccttgttgctgacc[C/G]acagcaaagcttgtct	C	G	NM_005301 // downstream // 17379 // Hs.239891 // GPR35 // 2859 // Homo sapiens G protein-coupled receptor 35 (GPR35), mRNA. /// NM_198998 // downstream // 27791 // Hs.534650 // AQP12 // 375318 // Homo sapiens aquaporin 12 (AQP12), mRNA. /// ENST0000031983	GPR35	GPR35, Homo sapiens G protein-coupled receptor 35 (GPR35), q37.3
SNP_A-1821519	gtttggtgcaccgata[G/T]gaccagtcttgtgaat	G	T	NM_198998 // downstream // 7038 // Hs.534650 // AQP12 // 375318 // Homo sapiens aquaporin 12 (AQP12), mRNA. /// NM_004321 // downstream // 8256 // Hs.516802 // KIF1A // 547 // Homo sapiens kinesin family member 1A (KIF1A), mRNA. /// ENST00000337801 // dow	AQP12	AQP12, Homo sapiens aquaporin 12 (AQP12), q37.3
SNP_A-2244434	ctggacactggaggac[A/C]aacaaatggtaccatt	A	C	ENST00000355403 // intron // 0 // — // — // — // — /// ENST00000354578 // intron // 0 // — // — // — // —	-	q37.3
SNP_A-2304225	gctcctaccgccgcac[A/G]gactttgtggacagga	A	G	ENST00000310397 // CDS // 0 // — // — // — // — /// ENST00000342631 // CDS // 0 // — // — // — // —	-	q37.3
SNP_A-1850337	tatgttgagctattca[A/C]atcaaggggactcaat	A	C	NM_182501 // 3UTR // 0 // Hs.159556 // MGC61716 // 130916 // Homo sapiens hypothetical protein MGC61716 (MGC61716), mRNA. /// ENST00000343278 // 3UTR // 0 // — // — // — // — /// ENST00000241527 // 3UTR // 0 // — // — // — // —	MGC61716	MGC61716, Homo sapiens hypothetical protein MGC61716 (MGC61716), q37.3
SNP_A-1967416	gcccacaatttaggta[C/T]gtctctggtagaagga	C	T	NM_015148 // intron // 0 // Hs.397891 // PASK // 23178 // Homo sapiens PAS domain containing serine/threonine kinase (PASK), mRNA. /// ENST00000234040 // intron // 0 // — // — // — // — /// ENST00000358649 // intron // 0 // — // — // — // –	PASK	PASK, Homo sapiens PAS domain containing serine q37.3
SNP_A-1791178	ggggttccctaagtgc[C/T]aaagtcccggccccac	C	T	NM_002712 // downstream // 15626 // Hs.36587 // PPP1R7 // 5510 // Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. /// ENST00000272983 // downstream // 15666 // — // — // — // — /// ENST00000234038 // downstream // 15626 //	PPP1R7	PPP1R7, Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), q37.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2304299	gctcctgtactgaaaa[C/T]gctcagggctacgcgg	C	T	NM_002712 // downstream // 31232 // Hs.36587 // PPP1R7 // 5510 // Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA. /// ENST00000272983 // downstream // 31272 // — // — // — // — /// ENST00000234038 // downstream // 31232 //	PPP1R7	PPP1R7, Homo sapiens protein phosphatase 1, regulatory subunit 7 (PPP1R7), q37.3
SNP_A-2305408	gctgatctggaactca[C/T]tgaagagtaaaaacat	C	T	NM_203346 // intron // 0 // Hs.471851 // HDLBP // 3069 // Homo sapiens high density lipoprotein binding protein (vigilin) (HDLBP), mRNA. /// NM_005336 // intron // 0 // Hs.471851 // HDLBP // 3069 // Homo sapiens high density lipoprotein binding protein (v	HDLBP	HDLBP, Homo sapiens high density lipoprotein binding protein (vigilin) (HDLBP), q37.3
SNP_A-2301799	gcggcaaatatgtagc[A/G]actttcagctaatcaa	A	G	NM_004404 // intron // 0 // Hs.335057 // SEPT2 // 4735 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA. /// ENST00000360051 // intron // 0 // — // — // — // — /// ENST00000336610 // intron // 0 // —	SEPT2	SEPT2, Homo sapiens neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), q37.3
SNP_A-1944557	ttgtcttttgctgtta[C/T]catctttacagtacat	C	T	ENST00000264042 // intron // 0 // — // — // — // —	-	q37.3
SNP_A-1648538	tcttccaagggctcaa[A/C]gtgtaagcaggctgga	A	C	NM_000030 // upstream // 4084 // Hs.144567 // AGXT // 189 // alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase) /// NM_004321 // upstream // 44454 // Hs.389765 // KIF1A // 547 // kinesin	AGXT	AGXT , rs4129624, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase) ,q37.3
SNP_A-1916461	tgtttaaacatggcga[A/G]cacggataactaaatg	A	G	NM_207485 // downstream // 25158 // Hs.209695 // FLJ41327 // 401045 // Homo sapiens FLJ41327 protein (FLJ41327), mRNA. /// ENST00000356827 // downstream // 25158 // — // — // — // —	FLJ41327	FLJ41327, Homo sapiens FLJ41327 protein (FLJ41327), q37.3
SNP_A-2026779	aaacacaattaaccga[C/T]gttgcagatatttcat	C	T	NM_006614 // upstream // 21006 // Hs.148909 // CHL1 // 10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // upstream // 21006 // — // — // — // —	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1855503	tcaagtgtggcaccca[A/G]gtattgtgattctaat	A	G	NM_006614 // intron // 0 // Hs.148909 // CHL1 // 10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // — // — // — // —	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2243097	ctgccctttctgccta[C/T]acctgggatctgtcaa	C	T	NM_006614 // intron // 0 // Hs.148909 // CHL1 // 10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // — // — // — // —	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1826002	taaatggggaaataac[G/T]gcttttcaaggttatt	G	T	NM_006614 // intron // 0 // Hs.148909 // CHL1 // 10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // — // — // — // —	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2153864	attataaatgaatcca[C/T]gtactcatagcacagc	C	T	NM_006614 // intron // 0 // Hs.148909 // CHL1 // 10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // — // — // — // —	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-1864787	tccagcttcataatac[A/G]cattaataataatgaa	A	G	NM_006614 // intron // 0 // Hs.148909 // CHL1 // 10752 // Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), mRNA. /// ENST00000256509 // intron // 0 // — // — // — // —	CHL1	CHL1, Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1), p26.3
SNP_A-2098842	agagctctcagggaac[C/T]ggtgaccactttggtc	C	T	NM_014461 // upstream // 139295 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000356814 // downstream // 102688 // — // — // — // — /// ENST00000350110 // upstream // 139295 // — // — // — // — /// ENS	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1901028	tggatatgatgtaaaa[A/G]gtgataagtgtggtaa	A	G	NM_014461 // upstream // 128200 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000356814 // downstream // 113783 // — // — // — // — /// ENST00000350110 // upstream // 128200 // — // — // — // — /// ENS	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1852601	tatttatccaagaata[C/T]ggaacactcagatct	C	T	NM_014461 // upstream // 94090 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000356814 // downstream // 147893 // — // — // — // — /// ENST00000350110 // upstream // 94090 // — // — // — // — /// ENST0	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2194978	catgctgttctctaca[C/T]catggtaaggaggacgg	C	T	NM_014461 // upstream // 70962 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000356814 // downstream // 171021 // — // — // — // — /// ENST00000350110 // upstream // 70962 // — // — // — // — /// ENST0	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1809275	gtgactagtctcgtat[C/T]actgtcagcgtcctct	C	T	NM_014461 // intron // 0 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000350110 // intron // 0 // — // — // — // — /// ENST00000346650 // intron // 0 // — // — // — // —	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2177900	cactaactctctaagg[G/T]aatatctttttgtcatc	G	T	NM_014461 // intron // 0 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// ENST00000350110 // intron // 0 // — // — // — // — /// ENST00000346650 // intron // 0 // — // — // — // —	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1811856	gtgctttgcttaattc[A/G]caggacagatatggat	A	G	NM_014461 // downstream // 112135 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 1055676 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1905584	tggtagcaaggaacaa[C/T]gtactggaaattgaaa	C	T	NM_014461 // downstream // 119835 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 1047976 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1971348	taactgcaattcagtat[C/G]ccttcgtatatctga	C	G	NM_014461 // downstream // 143774 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 1024037 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1961587	ttttttttctgcac[C/T]gtaaaatatgtgaagt	C	T	NM_014461 // downstream // 286570 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 881241 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1653500	tccaagacagggagataaaagttga[A/G]aacaatcggtgcaa cagagtaaaac	A	G	NM_014461 // downstream // 422336 // Hs.387300 // CNTN6 // 27255 // contactin 6 /// NM_175607 // upstream // 274633 // Hs.121115 // CNTN4 // 152330 // contactin 4 /// NM_175612 // upstream // 1213694 // Hs.121115 // CNTN4 // 152330 // contactin 4 /// NM_	CNTN6	CNTN6 , rs4684321, contactin 6 ,p26.3
SNP_A-2082443	acgcccacatagagta[C/G]agataaagggctaag	C	G	NM_014461 // downstream // 455433 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 712378 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207998	cccaactaccaggata[A/T]aaatgaagcatgttaa	A	T	NM_014461 // downstream // 634697 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 533114 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2008378	cttggtatgaaaatga[A/G]gtctccaactaaaca	A	G	NM_014461 // downstream // 637171 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 530640 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1950426	ttcagtattgtgaa[C/G]accaaaagcatgttca	C	G	NM_014461 // downstream // 779341 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 388470 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1753023	tttacgtggataacctgaccaaca[C/T]ggagtctacttttcttatt tgta	C	T	NM_175607 // intron // 0 // Hs.121115 // CNTN4 // 152330 // contactin 4	CNTN4	CNTN4 , rs1502565, contactin 4,p26.3
SNP_A-1920474	ttaattcatgtcgccca[A/G]cgtcctaaatgaaagt	A	G	NM_014461 // downstream // 1031265 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 136546 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1803194	gtaattctaaaaggaac[C/T]ggtgatatggattcca	C	T	NM_014461 // downstream // 1107287 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 60524 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-2309217	ggaaaacacggattca[C/T]gcacactgagttcttc	C	T	NM_014461 // downstream // 1163228 // Hs.387300 // CNTN6 // 27255 // Homo sapiens contactin 6 (CNTN6), mRNA. /// NM_175613 // upstream // 4583 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 /	CNTN6	CNTN6, Homo sapiens contactin 6 (CNTN6), p26.3
SNP_A-1971381	ctccctgggaagttct[A/C]acagaatgtaccaa	A	C	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// ENS	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.3
SNP_A-2183646	cagcagtggagagaca[A/G]tcttaccacatatata	A	G	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// ENS	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.3
SNP_A-1810782	gtgcagagtattcctc[A/G]gacagatacttacta	A	G	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// ENS	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.3
SNP_A-1930854	ttccagcacaaattga[C/G]acattaggctattat	C	G	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// ENS	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1879238	tcttagaagattgata[C/T]gctcatctatgtaaag	C	T	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-1944581	ttgtgaaatcaactta[C/G]taagcattagttgaat	C	G	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2008388	tgaaatgttgaagaga[C/T]gtatctgcactctcat	C	T	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2284111	gatatcttctcacacd[A/G]ctaagaatgactacta	A	G	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-1684994	catccattcaataaattgttacaga[A/G]cacctaatatggccag acgtgtca	A	G	NM_175607 // intron // 0 // Hs.121115 // CNTN4 // 152330 // contactin 4 /// NM_175613 // intron // 0 // Hs.121115 // CNTN4 // 152330 // contactin 4	CNTN4	CNTN4 , rs10510247, contactin 4 ,p26.2
SNP_A-1971396	gaggtccaacctgtta[C/T]aagaattagaatttc	C	T	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-1892596	tgcaatgttcacttgg[A/G]caccctggcggtcaat	A	G	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-2051011	aaggctggtgggtaca[A/C]gtttgatgaccatcag	A	C	NM_175613 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4 (CNTN4), transcript variant 3, mRNA. /// NM_175612 // intron // 0 // Hs.298705 // CNTN4 // 152330 // Homo sapiens contactin 4, (CNTN4), transcript variant 2, mRNA. /// NM_	CNTN4	CNTN4, Homo sapiens contactin 4 (CNTN4), transcript variant 3, p26.2
SNP_A-1816095	gttacattcatacaat[A/C]atgcacaggcaatgaa	A	C	NM_182916 // downstream // 42198 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream // 40374 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CC	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2217985	cctgcattaagtgact[C/T]agaatctagagttcct	C	T	NM_182916 // downstream // 70741 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream // 68917 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CC	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2170145	caaggtagaatgctaa[A/G]taaatgatcagtctgt	A	G	NM_182916 // downstream // 74402 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream // 72578 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CC	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903269	tggctttcttcgaggc[C/T]gagtctctaggctagt	C	T	NM_182916 // downstream // 81081 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream // 79257 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CC	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2157567	attgattgaagtataa[C/G]attgagttcctgctga	C	G	NM_182916 // downstream // 337277 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream // 335453 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase,	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-2147784	atggcatttatcctta[C/T]caatttcccaatgcct	C	T	NM_182916 // downstream // 423585 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA. /// NM_016000 // downstream // 421761 // Hs.506382 // TRNT1 // 51095 // Homo sapiens tRNA nucleotidyl transferase,	TRNT1	TRNT1, Homo sapiens tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), p26.2
SNP_A-1696500	atgtttgacataggggatagaaaga[A/T]ctggtttgtctagtggtaaagagga	A	T	NM_016000 // downstream // 575175 // Hs.506382 // TRNT1 // 51095 // tRNA nucleotidyl transferase, CCA-adding, 1 /// NM_016302 // upstream // 546338 // Hs.18925 // LOC51185 // 51185 // protein x 0001 /// NM_020873 // upstream // 119469 // Hs.126085 // LRR	TRNT1	TRNT1 , rs10510275, tRNA nucleotidyl transferase, CCA-adding, 1 ,p26.2
SNP_A-1971458	aaggacagcatttagg[C/G]aatctgcagttatata	C	G	ENST00000355003 // intron // 0 // --- // --- // --- // ---	-	p26.1
SNP_A-2246787	ctgtagatacttgtaa[C/T]gcagtggtgtttgtgt	C	T	NM_006515 // intron // 0 // Hs.475300 // SETMAR // 6419 // Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA. /// ENST00000307483 // intron // 0 // --- // --- // --- // ---	SETMAR	SETMAR, Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), p26.1
SNP_A-1699503	tttatgctgagaggaagagctgtca[A/G]gttaattaatctatctctatctat	A	G	NM_006515 // downstream // 10115 // Hs.265855 // SETMAR // 6419 // SET domain and mariner transposase fusion gene /// NM_182760 // downstream // 37278 // Hs.350475 // SUMF1 // 285362 // sulfatase modifying factor 1	SETMAR	SETMAR , rs711673, SET domain and mariner transposase fusion gene ,p26.1
SNP_A-2290012	gcaaaggtatcttccc[A/C]agtgtttcaaccaagg	A	C	NM_006515 // downstream // 17100 // Hs.475300 // SETMAR // 6419 // Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA. /// NM_182760 // downstream // 26800 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor	SETMAR	SETMAR, Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), p26.1
SNP_A-2040287	aaccaccttgacacca[A/G]aacaattcattcattc	A	G	NM_006515 // downstream // 21231 // Hs.475300 // SETMAR // 6419 // Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA. /// NM_182760 // downstream // 22669 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor	SETMAR	SETMAR, Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), p26.1
SNP_A-1909710	tgtcaatagccaaata[C/G]agcaagcggaagaaag	C	G	NM_006515 // downstream // 27664 // Hs.475300 // SETMAR // 6419 // Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA. /// NM_182760 // downstream // 16236 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor	SETMAR	SETMAR, Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), p26.1
SNP_A-2029498	aaagacccaaacactg[C/T]accttgctcataagaa	C	T	NM_182760 // intron // 0 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// ENST00000272902 // intron // 0 // --- // --- // --- // ---	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-2029544	aaagactcaagttcaa[C/T]tggacaagaggaatca	C	T	NM_182760 // intron // 0 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// ENST00000272902 // intron // 0 // --- // --- // --- // ---	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-2142670	atgaagaattgagaca[C/G]taatgttaaataaaat	C	G	NM_182760 // intron // 0 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// ENST00000272902 // intron // 0 // --- // --- // --- // ---	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-1940542	ttgccctgtctttcac[C/T]cgcatttccataaacc	C	T	NM_182760 // intron // 0 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// ENST00000272902 // intron // 0 // --- // --- // --- // ---	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1791727	gggtctgctcttgcac[A/G]gcaggagaagacttct	A	G	NM_182760 // upstream // 4628 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// D26070 // upstream // 21554 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complet	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-2122078	agtgatgatggtggaa[C/G]tgaaatatttggatta	C	G	NM_182760 // upstream // 9708 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// D26070 // upstream // 16474 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complet	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-1652666	ccatggtcaatggtagtccatcaca[C/T]tagataatatagtgtca gtgccaaa	C	T	NM_002222 // upstream // 4144 // Hs.149900 // ITPR1 // 3708 // inositol 1,4,5-triphosphate receptor, type 1 /// NM_182760 // upstream // 22044 // Hs.350475 // SUMF1 // 285362 // sulfatase modifying factor 1	ITPR1	ITPR1 , rs10510293, inositol 1,4,5-triphosphate receptor, type 1 ,p26.1
SNP_A-1971469	atccaattacactcca[C/T]aggcaattgaaatctt	C	T	NM_182760 // upstream // 22340 // Hs.350475 // SUMF1 // 285362 // Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA. /// D26070 // upstream // 3842 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complet	SUMF1	SUMF1, Homo sapiens sulfatase modifying factor 1 (SUMF1), p26.1
SNP_A-1971474	gtacaaggactaccta[C/G]attaaatgcatattgg	C	G	D26070 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. p26.1
SNP_A-1900001	tggaccactctatacc[A/G]agtcacctttgctaa	A	G	D26070 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. ,p26.1
SNP_A-1944801	ttgtgcctcttatcac[C/T]aacctggagggactca	C	T	D26070 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. p26.1
SNP_A-1907260	tggttttactgttgaa[A/T]attgctggaaacagtg	A	T	D26070 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. ,p26.1
SNP_A-2062694	aatgtctctgaaactc[A/G]aatcttctcatctgca	A	G	D26070 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Human mRNA for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. /// NM_002222 // intron // 0 // Hs.374613 // ITPR1 // 3708 // Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR	ITPR1	ITPR1, Human for type 1 inositol 1,4,5-trisphosphate receptor, complete cds. ,p26.1
SNP_A-1880914	tcttgtcaataatggc[C/T]ctgattatttgactat	C	T	NM_014674 // downstream // 87075 // Hs.224616 // EDEM1 // 9695 // Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), mRNA. /// ENST00000295399 // upstream // 118735 // --- // --- // --- // --- /// ENST00000256497 // downstream // 8707	EDEM1	EDEM1, Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), p26.1
SNP_A-2059749	aatctgcagaaaaaaa[C/G]tagcaaattcaagagc	C	G	NM_014674 // downstream // 158252 // Hs.224616 // EDEM1 // 9695 // Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), mRNA. /// ENST00000295399 // upstream // 189912 // --- // --- // --- // --- /// ENST00000256497 // downstream // 158	EDEM1	EDEM1, Homo sapiens ER degradation enhancer, mannosidase alpha-like 1 (EDEM1), p26.1
SNP_A-1737890	gtgtttcttgttactatgattgtta[G/T]gacagaaaatgcttttagaga tggg	G	T	NM_000844 // upstream // 1399740 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014674 // downstream // 241545 // - // - // - // - /// NM_181874 // upstream // 1399740 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotro	GRM7	GRM7 , rs7611998, glutamate receptor, metabotropic 7 ,p26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2087172	actgatggatacccaa[C/G]atttacaatttcttac	C	G	NM_000844 // upstream // 1295395 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1295395 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971498	caaagtcccagtctca[C/G]atcgaagtaagcccct	C	G	NM_000844 // upstream // 1295159 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1295159 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1883962	tgaagatagactctgat[C/G]atgggaagttgcatga	C	G	NM_000844 // upstream // 1286816 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1286816 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2185837	caggatggattagaga[C/G]ggggaaatgaaggcat	C	G	NM_000844 // upstream // 1278203 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1278203 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2084081	actagcaccactacag[C/G]cctcatgacctcagag	C	G	NM_000844 // upstream // 1270953 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1270953 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971502	agcacttgccagatga[C/T]gaaagatgtctgatat	C	T	NM_000844 // upstream // 1177516 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1177516 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1857144	tcacctagctcctgtt[C/T]aacacgtttgtgtacc	C	T	NM_000844 // upstream // 1117752 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 1117752 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2202551	ccacctaattcaccct[A/T]aaggactatgaaattc	A	T	NM_000844 // upstream // 908968 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 908968 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1662234	aacatcctctcttctccaactcag[A/G]acagacgtaatggctgct tattggt	A	G	NM_000844 // upstream // 768121 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014674 // downstream // 873164 // - // - // - /// NM_181874 // upstream // 768121 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropi	GRM7	GRM7 , rs10510325, glutamate receptor, metabotropic 7 , p26.1
SNP_A-1892595	tgcaatgtgtcagtta[C/T]agtttaggcactatt	C	T	NM_000844 // upstream // 704094 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 704094 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2045419	aagaatagagcgataa[A/C]attggacactggtatg	A	C	NM_000844 // upstream // 698148 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 698148 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1971529	tggattaacacaattc[A/G]ctttgaagaggctcat	A	G	NM_000844 // upstream // 658071 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 658071 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1806302	gtccttagaatcctta[A/G]gttatgtatggctaag	A	G	NM_000844 // upstream // 299010 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 299010 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1882447	tgaaaagtggtaacat[A/T]aagataaccttgaagt	A	T	NM_000844 // upstream // 260259 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 260259 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2189245	cagttcatgcctatac[A/C]agttctaactactgta	A	C	NM_000844 // upstream // 260083 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 260083 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1873120	tctattaataatgata[A/C]ctgactgtgtataaaa	A	C	NM_000844 // upstream // 238434 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 238434 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1875627	tctcttcaaacgctga[C/T]ataaccaagtccagtc	C	T	NM_000844 // upstream // 223278 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 223278 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1897965	tgctgtacctgcttgt[C/G]acaacttgagttctaa	C	G	NM_000844 // upstream // 220242 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 220242 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971554	gctccactgtaatcaa[C/T]gtgtcaatggaccacc	C	T	NM_000844 // upstream // 218032 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 218032 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971557	tgtggtaccaaaccag[A/G]aagctctgtactagct	A	G	NM_000844 // upstream // 107586 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 107586 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971558	tgatctgcagccataa[C/G]tctctaaaagttaggg	C	G	NM_000844 // upstream // 107439 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 107439 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabo	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971565	atgatgattgccagtc[A/G]gaatgaaggacaaaac	A	G	NM_000844 // upstream // 81395 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // upstream // 81395 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotr	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1696798	tgggaaaaacaattatggctaagaa[A/C]aattaagtccactggt agaaagata	A	C	NM_000844 // upstream // 69392 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014674 // downstream // 1571893 // - // - // - // - /// NM_181874 // upstream // 69392 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic	GRM7	GRM7 , rs10510341, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-2307305	gcttagaaacttagaa[A/G]caaacatacccataga	A	G	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1734076	gaggaggaagatgcagaataggcac[A/G]aaaggagtagaa aaaactagaagag	A	G	NM_000844 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_181874 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_181875 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamat	GRM7	GRM7 , rs9311980, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-2065708	aatttatgttggccca[C/T]gtatcaagtagacatt	C	T	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1819085	gttgccctgttctacc[C/T]ggcaaggacccaggca	C	T	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2138748	atccccaacattgcca[A/G]gaagacaggaatcaca	A	G	NM_000844 // CDS // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // CDS // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), tra	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2199896	ccaaagaaggcttagc[C/T]agggttcagtaaggga	C	T	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1870785	tcgcttgaggaagcag[C/G]aatgggaataatttaa	C	G	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971612	tttctcagctataagg[A/T]caatctgtaacttgaa	A	T	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1740481	ccctcccagaacctcactttgacaa[C/T]gtggctcactaattgct actgggta	C	T	NM_000844 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_181874 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_181875 // intron // 0 // Hs.83407 // GRM7 // 2917 // glutamat	GRM7	GRM7 , rs3804867, glutamate receptor, metabotropic 7 ,p26.1
SNP_A-2024809	aaaagtgcctgtgatc[A/C]gaggattctctaaagc	A	C	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1971613	atgaccatcttccaaa[C/T]gcttcagggcaatgca	C	T	NM_000844 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // intron // 0 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2100890	agatatctcctccata[A/G]taactaggacacagaa	A	G	NM_000844 // downstream // 71717 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 71717 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, meta	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1971652	aactcatttcatcacc[A/G]attcaaaagtccaatg	A	G	NM_000844 // downstream // 436604 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 436604 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2044718	aagaaaggggtataa[C/T]gagtcgtgtctaatct	C	T	NM_000844 // downstream // 438673 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 438673 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1669963	atattgtccttccctgtgagttaga[A/G]attatctccatttacaaata gaaa	A	G	NM_000844 // downstream // 389676 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 370618 // Hs.279943 // LMCD1 // 29995 // LIM and cysteine-rich domains 1 /// NM_181874 // downstream // 389676 // Hs.83407 //	GRM7	GRM7, rs2675257, glutamate receptor, metabotropic 7, p26.1
SNP_A-2114587	agggagggaattaccc[A/C]aggacgtgactaccag	A	C	NM_000844 // downstream // 445047 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 445047 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-1647834	ccacaataaaataaccaactcaaca[A/G]tggaagttacagtttt gaagaatga	A	G	NM_000844 // downstream // 390533 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 369761 // Hs.279943 // LMCD1 // 29995 // LIM and cysteine-rich domains 1 /// NM_181874 // downstream // 390533 // Hs.83407 //	GRM7	GRM7, rs10510385, glutamate receptor, metabotropic 7, p26.1
SNP_A-1667662	aagagacaaagatgcatagtataaa[C/T]gagaaataaaatcac acacattctgg	C	T	NM_000844 // downstream // 390880 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 369414 // Hs.279943 // LMCD1 // 29995 // LIM and cysteine-rich domains 1 /// NM_181874 // downstream // 390880 // Hs.83407 //	GRM7	GRM7, rs7649994, glutamate receptor, metabotropic 7, p26.1
SNP_A-1751819	cattaagttgaaataaaatccagaa[A/G]taagtaagctattgttta gaaacta	A	G	NM_000844 // downstream // 391075 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 369219 // Hs.279943 // LMCD1 // 29995 // LIM and cysteine-rich domains 1 /// NM_181874 // downstream // 391075 // Hs.83407 //	GRM7	GRM7, rs7640853, glutamate receptor, metabotropic 7, p26.1
SNP_A-1641759	tatgttagagacccctttcaggaga[C/T]ggaagcaggtatagga aaacaaaat	C	T	NM_000844 // downstream // 391198 // Hs.83407 // GRM7 // 2917 // glutamate receptor, metabotropic 7 /// NM_014583 // upstream // 369096 // Hs.279943 // LMCD1 // 29995 // LIM and cysteine-rich domains 1 /// NM_181874 // downstream // 391198 // Hs.83407 //	GRM7	GRM7, rs10510386, glutamate receptor, metabotropic 7, p26.1
SNP_A-1971659	cccagtaacctgctcc[A/G]gaacaacctgatacaa	A	G	NM_000844 // downstream // 472157 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 472157 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1971660	gttgttttctgtgcaa[A/G]tgtggaatgtagacct	A	G	NM_000844 // downstream // 472635 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 472635 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p26.1
SNP_A-2023055	aaaacagaaagagcca[C/T]gttctatcatattctc	C	T	NM_000844 // downstream // 785924 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 785924 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p25.3
SNP_A-1791344	gggtaccttgttgaca[C/T]ggctcttctacctggc	C	T	NM_000844 // downstream // 794274 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, mRNA. /// NM_181875 // downstream // 794274 // Hs.475336 // GRM7 // 2917 // Homo sapiens glutamate receptor, me	GRM7	GRM7, Homo sapiens glutamate receptor, metabotropic 7 (GRM7), transcript variant 1, p25.3
SNP_A-2310368	ggaactcacattttca[C/G]accaagtcagatattt	C	G	NM_014583 // intron // 0 // Hs.475353 // LMCD1 // 29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// ENST00000157600 // intron // 0 // — // — // — // —	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-1838290	tagaagcacaggggaa[A/G]gtgttaataaattcat	A	G	NM_014583 // intron // 0 // Hs.475353 // LMCD1 // 29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// ENST00000157600 // intron // 0 // — // — // — // —	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-1971680	caggccctggctcata[C/G]gaaatgccttagcctg	C	G	NM_014583 // intron // 0 // Hs.475353 // LMCD1 // 29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// ENST00000157600 // intron // 0 // — // — // — // —	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-2274060	gacttaggaatatcga[C/G]agaggtgcccctggga	C	G	NM_014583 // downstream // 1539 // Hs.475353 // LMCD1 // 29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// NM_015931 // downstream // 49973 // Hs.113019 // LOC51066 // 51066 // Homo sapiens fls485 (LOC51066), mRNA. /// ENST00000157	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-2121801	agtgagaacagattaa[C/T]acagtatgtgccgggc	C	T	NM_014583 // downstream // 42194 // Hs.475353 // LMCD1 // 29995 // Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), mRNA. /// NM_015931 // downstream // 9318 // Hs.113019 // LOC51066 // 51066 // Homo sapiens fls485 (LOC51066), mRNA. /// ENST00000157	LMCD1	LMCD1, Homo sapiens LIM and cysteine-rich domains 1 (LMCD1), p25.3
SNP_A-2262754	gaaatttaaagaggca[A/G]agtgattttcccaaga	A	G	NM_015931 // intron // 0 // Hs.113019 // LOC51066 // 51066 // Homo sapiens fls485 (LOC51066), mRNA. /// ENST00000341795 // intron // 0 // — // — // — // — /// ENST00000317371 // intron // 0 // — // — // — // —	LOC51066	LOC51066, Homo sapiens fls485 (LOC51066), p25.3
SNP_A-2204039	ccagatttttcccaat[A/C]agacatccacaagtca	A	C	NM_015931 // upstream // 320 // Hs.113019 // LOC51066 // 51066 // Homo sapiens fls485 (LOC51066), mRNA. /// NM_001234 // upstream // 81439 // Hs.98303 // CAV3 // 859 // Homo sapiens caveolin 3 (CAV3), transcript variant 2, mRNA. /// NM_033337 // upstream	LOC51066	LOC51066, Homo sapiens fls485 (LOC51066), p25.3
SNP_A-1874974	tctctagatagtagga[G/T]tatgtttccagaaagc	G	T	NM_000916 // upstream // 8361 // Hs.2820 // OXTR // 5021 // Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 101900 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000316793	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-2110308	aggaatcaaccacttc[A/G]aaggaagcagagagaa	A	G	NM_000916 // upstream // 9528 // Hs.2820 // OXTR // 5021 // Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 100733 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000316793	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282615	gagtttccaatttacg[A/G]acgtgctatatctctc	A	G	NM_000916 // upstream // 37042 // Hs.2820 // OXTR // 5021 // Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 73219 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000316793	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-1910869	tgtctagagtttacca[A/G]gagcacttttagtac	A	G	NM_000916 // upstream // 37493 // Hs.2820 // OXTR // 5021 // Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 72768 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000316793	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-1916983	tgtttgagtaataaaa[A/G]ctagtacttactgggc	A	G	NM_000916 // upstream // 86102 // Hs.2820 // OXTR // 5021 // Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 24159 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000316793	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-1782940	ggcagatgggagaaaa[C/T]gctaacgataagaagt	C	T	NM_000916 // upstream // 94995 // Hs.2820 // OXTR // 5021 // Homo sapiens oxytocin receptor (OXTR), mRNA. /// NM_020165 // downstream // 15266 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000316793	OXTR	OXTR, Homo sapiens oxytocin receptor (OXTR), p25.3
SNP_A-2008442	ggccaaaggcgctgaa[A/G]aacactgaggcagatt	A	G	NM_020165 // intron // 0 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000264926 // intron // 0 // --- // --- // --- // ---	RAD18	RAD18, Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), p25.3
SNP_A-1974949	tttcttagctagaata[C/G]tagagatgctttgtaa	C	G	NM_020165 // intron // 0 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000264926 // intron // 0 // --- // --- // --- // ---	RAD18	RAD18, Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), p25.3
SNP_A-2276866	gagatataattcatac[C/T]cacctgaagtgtacat	C	T	NM_020165 // intron // 0 // Hs.375684 // RAD18 // 56852 // Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), mRNA. /// ENST00000264926 // intron // 0 // --- // --- // --- // ---	RAD18	RAD18, Homo sapiens RAD18 homolog (S. cerevisiae) (RAD18), p25.3
SNP_A-1690427	tcccctcttgacccttacactggca[C/T]taaggaatacaaaagct gaggaagg	C	T	NM_014850 // intron // 0 // Hs.512860 // SRGAP2 // 9901 // SLIT-ROBO Rho GTPase activating protein 2	SRGAP2	SRGAP2 , rs370526, SLIT-ROBO Rho GTPase activating protein 2,p25.3
SNP_A-1931545	ttccccctttgagcct[C/T]agctacctcacctatc	C	T	NM_014850 // intron // 0 // Hs.475364 // SRGAP3 // 9901 // Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), mRNA. /// ENST00000356336 // intron // 0 // --- // --- // --- // --- /// ENST00000360413 // intron // 0 // --- // --- // --- // ---	SRGAP3	SRGAP3, Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), p25.3
SNP_A-1825949	taaatgctcataaaaa[G/T]atctggcaggccctct	G	T	NM_014850 // upstream // 59430 // Hs.475364 // SRGAP3 // 9901 // Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), mRNA. /// NM_015453 // upstream // 54569 // Hs.443081 // THUMPD3 // 25917 // Homo sapiens THUMP domain containing 3 (THUMPD3)	SRGAP3	SRGAP3, Homo sapiens SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2), p25.3
SNP_A-2209147	cccagggacacaaaac[C/T]agtaggtaacagattc	C	T	NM_015453 // intron // 0 // Hs.443081 // THUMPD3 // 25917 // Homo sapiens THUMP domain containing 3 (THUMPD3), mRNA. /// ENST00000345094 // intron // 0 // --- // --- // --- // ---	THUMPD3	THUMPD3, Homo sapiens THUMP domain containing 3 (THUMPD3), p25.3
SNP_A-1898647	tgcttgtgagtataga[A/G]ctaatttgtgagtact	A	G	NM_198560 // upstream // 61515 // Hs.331437 // LOC375323 // 375323 // Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), mRNA. /// NM_022485 // upstream // 34193 // Hs.475382 // FLJ22405 // 64419 // Homo sapiens hypothetical protein FLJ2	LOC375323	LOC375323, Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), p25.3
SNP_A-2127597	ataacccaagaggact[C/G]acaaggatggtgttta	C	G	NM_198560 // upstream // 67480 // Hs.331437 // LOC375323 // 375323 // Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), mRNA. /// NM_022485 // upstream // 28228 // Hs.475382 // FLJ22405 // 64419 // Homo sapiens hypothetical protein FLJ2	LOC375323	LOC375323, Homo sapiens lipoma HMGIC fusion partner-like protein 4 (LOC375323), p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2205343	ccagtctcctctttcc[A/G]caggatcagctttcac	A	G	NM_207351 // upstream // 2976 // Hs.517786 // FLJ33674 // 285368 // Homo sapiens hypothetical protein FLJ33674 (FLJ33674), mRNA. /// NM_018447 // downstream // 8583 // Hs.475392 // LOC55831 // 55831 // Homo sapiens 30 kDa protein (LOC55831), mRNA. /// ENS	FLJ33674	FLJ33674, Homo sapiens hypothetical protein FLJ33674 (FLJ33674), p25.3
SNP_A-1807655	gtctgtaaaactgcca[C/T]tagagatgtaaggaat	C	T	NM_018447 // intron // 0 // Hs.475392 // LOC55831 // 55831 // Homo sapiens 30 kDa protein (LOC55831), mRNA. /// ENST00000245046 // intron // 0 // --- // --- // --- // ---	LOC55831	LOC55831, Homo sapiens 30 kDa protein (LOC55831), p25.3
SNP_A-1879302	tcttaggacaccaaaa[C/T]tgagttattagaccag	C	T	NM_033084 // intron // 0 // Hs.208388 // FANCD2 // 2177 // Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// ENST00000287647 // intron // 0 // — // — // — // —	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-1819349	gttggcaacaaataca[C/T]gctggagttggcaagt	C	T	NM_033084 // intron // 0 // Hs.208388 // FANCD2 // 2177 // Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// ENST00000287647 // intron // 0 // — // — // — // —	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-2046409	aagagacgagcaaaga[A/G]aaataaactgattcca	A	G	NM_033084 // intron // 0 // Hs.208388 // FANCD2 // 2177 // Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), mRNA. /// NM_173472 // intron // 0 // Hs.190413 // MGC40179 // 115795 // Homo sapiens hypothetical protein MGC40179 (MGC40179), mRNA	FANCD2	FANCD2, Homo sapiens Fanconi anemia, complementation group D2 (FANCD2), p25.3
SNP_A-1934228	ttctccaagtgtttaa[C/G]agaacttggcactggt	C	G	NM_018462 // intron // 0 // Hs.517792 // C3orf10 // 55845 // Homo sapiens chromosome 3 open reading frame 10 (C3orf10), mRNA. /// ENST00000256463 // intron // 0 // — // — // — // —	C3orf10	C3orf10, Homo sapiens chromosome 3 open reading frame 10 (C3orf10), p25.3
SNP_A-2214370	cctacctctctgacca[C/G]tctttcctggcccttt	C	G	NM_001570 // intron // 0 // Hs.424542 // IRAK2 // 3656 // Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), mRNA. /// ENST00000256458 // intron // 0 // — // — // — // —	IRAK2	IRAK2, Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), p25.3
SNP_A-1814398	gtgtgaggagtcagac[A/G]gaaagaatgatctact	A	G	NM_001570 // intron // 0 // Hs.424542 // IRAK2 // 3656 // Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), mRNA. /// ENST00000256458 // intron // 0 // — // — // — // —	IRAK2	IRAK2, Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), p25.3
SNP_A-2113455	aggcgctgttgatggc[A/G]atggcattgatcagca	A	G	NM_001683 // CDS // 0 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // CDS // 0 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, pl	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2237905	ctctgacctctgctta[C/T]aattacacagaaagaa	C	T	NM_001683 // intron // 0 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // intron // 0 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporti	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-1911388	tgtcttatttcctcca[A/G]agtccttaagacagtg	A	G	NM_001683 // intron // 0 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // intron // 0 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporti	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2191545	catatgccttgtacgc[C/G]catacaccctacacac	C	G	NM_001683 // upstream // 7374 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 7374 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-1787873	gggactctgctggtca[C/T]gtaatacacacaaaag	C	T	NM_001683 // upstream // 47936 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 47936 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca+	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884552	tgaataaaagtataac[A/G]atgaccgcatagag	A	G	NM_001683 // upstream // 82421 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 82421 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca+	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2058038	aatatttcttatacaj[A/G]aacttgcattgccaa	A	G	NM_001683 // upstream // 101678 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 101678 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, C	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2102397	agattccacaagtgca[A/C]gagaagagaagttctg	A	C	NM_001683 // upstream // 131395 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, mRNA. /// NM_001001331 // upstream // 131395 // Hs.268942 // ATP2B2 // 491 // Homo sapiens ATPase, C	ATP2B2	ATP2B2, Homo sapiens ATPase, Ca++ transporting, plasma membrane 2 (ATP2B2), transcript variant 2, p25.3
SNP_A-2252490	cttcctctgaaacgtg[C/T]aaatccaaccaaacac	C	T	NM_014229 // intron // 0 // Hs.101791 // SLC6A11 // 6538 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA), member 11 (SLC6A11), mRNA. /// ENST00000254488 // intron // 0 // — // — // — // — /// ENST00000360599 // intron	SLC6A11	SLC6A11, Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA), member 11 (SLC6A11), p25.3
SNP_A-1726482	gccaatggcacattgggagctgata[C/T]ctcaccctgctctgctttgaagc	C	T	NM_003042 // intron // 0 // Hs.22003 // SLC6A1 // 6529 // solute carrier family 6 (neurotransmitter transporter, GABA), member 1	SLC6A1	SLC6A1, rs10514669, solute carrier family 6 (neurotransmitter transporter, GABA), member 1,p25.3
SNP_A-2260485	gaaacagaatgagtca[C/T]atcaaggtttaatcc	C	T	NM_003178 // intron // 0 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIb, mRNA. /// ENST00000295987 // intron // 0 // — // — // —	SYN2	SYN2, Homo sapiens synapsin II (SYN2), transcript variant IIb, p25.2
SNP_A-1811629	gtgctgcctctacaj[C/G]agcgagaatggact	C	G	NM_003178 // intron // 0 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIb, mRNA. /// NM_133625 // intron // 0 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIa, mRNA. /// ENST000	SYN2	SYN2, Homo sapiens synapsin II (SYN2), transcript variant IIb, p25.2
SNP_A-1955132	tttggcaacttgagtc[A/G]aagtctcctctaaa	A	G	NM_003178 // intron // 0 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIb, mRNA. /// NM_133625 // intron // 0 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIa, mRNA. /// NM_0032	SYN2	SYN2, Homo sapiens synapsin II (SYN2), transcript variant IIb, p25.2
SNP_A-2165736	caaagggaacagagg[G/T]aaagatatgcattgga	G	T	NM_003178 // downstream // 53609 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIb, mRNA. /// NM_133625 // downstream // 52849 // Hs.445503 // SYN2 // 6854 // Homo sapiens synapsin II (SYN2), transcript variant IIa, m	SYN2	SYN2, Homo sapiens synapsin II (SYN2), transcript variant IIb, p25.2
SNP_A-1655831	tagataaaaatatacttcacttccaj[G/T]attacactcagagacaaccaaaggc	G	T	NM_005037 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138711 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138712 // intron // 0 //	PPARG	PPARG, rs10510410, peroxisome proliferative activated receptor, gamma ,p25.2
SNP_A-1651698	gttgcctttatgagacgaaataaa[A/G]ttggatgtcactataaatggattt	A	G	NM_005037 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138711 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138712 // intron // 0 //	PPARG	PPARG, rs10510411, peroxisome proliferative activated receptor, gamma ,p25.2
SNP_A-1648728	ttaggagttattcacaaggccatta[C/T]gcttacaaaaaattatgagtcaaag	C	T	NM_005037 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138711 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138712 // intron // 0 //	PPARG	PPARG, rs10510412, peroxisome proliferative activated receptor, gamma ,p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134922	atattatttcctgcta[C/G]agttaacaaaatggga	C	G	NM_005037 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, mRNA. /// NM_138711 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens peroxisome proliferat	PPARG	PPARG, Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, p25.2
SNP_A-1946610	tttaaattacagaacg[A/G]acgggttttagtgttt	A	G	NM_005037 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, mRNA. /// NM_138711 // intron // 0 // Hs.162646 // PPARG // 5468 // Homo sapiens peroxisome proliferat	PPARG	PPARG, Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), transcript variant 4, p25.2
SNP_A-1674385	tacataagtttgcaatattaacata[A/C]ccaagaatctgtaactatttcacct	A	C	NM_005037 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_015869 // intron // 0 // Hs.387667 // PPARG // 5468 // peroxisome proliferative activated receptor, gamma /// NM_138711 // intron // 0 //	PPARG	PPARG , rs10510419, peroxisome proliferative activated receptor, gamma ,p25.2
SNP_A-1804355	gtcactggcttagaca[C/T]cgtggcagggccgggg	C	T	ENST00000342268 // intron // 0 // — // — // — // —	-	p25.2
SNP_A-2131349	atagatcagatagtaa[C/T]agcacctacctcatgg	C	T	NM_014869 // upstream // 61839 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 286938 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-2168092	caactattctgctgag[G/T]acaagtttctcaaggc	G	T	NM_014869 // upstream // 67266 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 281511 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-1815109	gtgttcggtgcatcga[C/T]gtgaattggggaggag	C	T	NM_014869 // upstream // 79352 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 269425 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-2237129	ctctcacaggggcaac[A/G]aatgcatctgaaagga	A	G	NM_014869 // upstream // 80765 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 268012 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-2211933	ccctgaagacacagaa[C/T]gtgaggtgtgctgcca	C	T	NM_014869 // upstream // 80819 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 267958 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-2208263	cccacaccaagaatcc[A/G]cacagatatttatggg	A	G	NM_014869 // upstream // 97342 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 251435 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-1971808	aggatgttctgcttca[A/G]taaagtggctcacctg	A	G	NM_014869 // upstream // 275258 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 73519 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2
SNP_A-2170713	caagttctccaatcaa[A/C]cccctcactactggga	A	C	NM_014869 // upstream // 275523 // Hs.475506 // IQSEC1 // 9922 // Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA. /// NM_024923 // downstream // 73254 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// ENST00000273	IQSEC1	IQSEC1, Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1971814	aactacgaaatccaaa[C/T]gcagggagagtggcct	C	T	NM_024923 // upstream // 39445 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// NM_024827 // upstream // 20570 // Hs.404802 // HDAC11 // 79885 // Homo sapiens histone deacetylase 11 (HDAC11), mRNA. /// ENST00000254508 //	NUP210	NUP210, Homo sapiens nucleoporin 210 (NUP210), p25.1
SNP_A-2170044	caagggcagggcagaa[A/G]tgacccgagtgcctg	A	G	NM_024923 // upstream // 46646 // Hs.475525 // NUP210 // 23225 // Homo sapiens nucleoporin 210 (NUP210), mRNA. /// NM_024827 // upstream // 13369 // Hs.404802 // HDAC11 // 79885 // Homo sapiens histone deacetylase 11 (HDAC11), mRNA. /// ENST00000254508 //	NUP210	NUP210, Homo sapiens nucleoporin 210 (NUP210), p25.1
SNP_A-1971823	gccagactgtctaaca[C/G]taggcgacggaaactc	C	G	NM_004628 // intron // 0 // Hs.475538 // XPC // 7508 // Homo sapiens xeroderma pigmentosum, complementation group C (XPC), mRNA. /// ENST00000285021 // intron // 0 // --- // --- // ---	XPC	XPC, Homo sapiens xeroderma pigmentosum, complementation group C (XPC), p25.1
SNP_A-2292891	gcagaaatgtgagctg[A/G]atcagtctcctgtatg	A	G	NM_003043 // upstream // 123871 // Hs.529488 // SLC6A6 // 6533 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (SLC6A6), mRNA. /// NM_003043 // upstream // 164856 // Hs.529488 // SLC6A6 // 6533 // Homo sapiens sol	SLC6A6	SLC6A6, Homo sapiens solute carrier family 6 (neurotransmitter transporter, taurine), member 6 (SLC6A6), p25.1
SNP_A-1645766	caaagctaaagtaagagaaatgcaaa[A/G]agcccactgttagaaa atagagatgaa	A	G	NM_016474 // intron // 0 // Hs.236257 // LOC51244 // 51244 // hypothetical protein LOC51244	LOC51244	LOC51244 , rs10510430, hypothetical protein LOC51244,p25.1
SNP_A-2041636	aacgctagaaatactg[A/G]ataacataaattaaat	A	G	NM_032137 // downstream // 3114 // Hs.506062 // C3orf20 // 84077 // Homo sapiens hypothetical protein DKFZp434N1817 (DKFZP434N1817), mRNA. /// NM_152536 // upstream // 43152 // Hs.412406 // FGD5 // 152273 // Homo sapiens FYVE, RhoGEF and PH domain contain	C3orf20	C3orf20, Homo sapiens hypothetical protein DKFZp434N1817 (DKFZP434N1817), p25.1
SNP_A-1971843	ggttcaagttatccac[A/G]gactatacctcctttt	A	G	NM_152536 // downstream // 44454 // Hs.412406 // FGD5 // 152273 // Homo sapiens FYVE, RhoGEF and PH domain containing 5 (FGD5), mRNA. /// NM_003298 // upstream // 25073 // Hs.475559 // NR2C2 // 7182 // Homo sapiens nuclear receptor subfamily 2, group C, m	FGD5	FGD5, Homo sapiens FYVE, RhoGEF and PH domain containing 5 (FGD5), p25.1
SNP_A-2297668	gccagcctgtgtcgac[A/G]aaactcgtagcagaaa	A	G	NM_004844 // intron // 0 // Hs.257761 // SH3BP5 // 9467 // Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /// ENST00000253688 // intron // 0 // --- // --- // ---	SH3BP5	SH3BP5, Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), p25.1
SNP_A-1959435	ttttgccatttttga[A/G]cgctaatgatgtatta	A	G	NM_004844 // intron // 0 // Hs.257761 // SH3BP5 // 9467 // Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /// ENST00000253688 // intron // 0 // --- // --- // ---	SH3BP5	SH3BP5, Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), p25.1
SNP_A-2145780	atgccagacacttaac[A/G]aacatcaccatattta	A	G	NM_004844 // intron // 0 // Hs.257761 // SH3BP5 // 9467 // Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /// ENST00000253688 // intron // 0 // --- // --- // ---	SH3BP5	SH3BP5, Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), p25.1
SNP_A-1793839	ggtatttgagtcaag[G/T]cggttttgagccaaa	G	T	NM_033083 // downstream // 56359 // Hs.474479 // EAF1 // 85403 // Homo sapiens ELL associated factor 1 (EAF1), mRNA. /// NM_012260 // downstream // 61769 // Hs.63290 // HPCL2 // 26061 // Homo sapiens 2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA. /// ENST000	EAF1	EAF1, Homo sapiens ELL associated factor 1 (EAF1), p25.1
SNP_A-1920655	ttacaaaacatgaccc[A/C]tctcattccttcatgt	A	C	NM_033083 // downstream // 56923 // Hs.474479 // EAF1 // 85403 // Homo sapiens ELL associated factor 1 (EAF1), mRNA. /// NM_012260 // downstream // 61205 // Hs.63290 // HPCL2 // 26061 // Homo sapiens 2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA. /// ENST000	EAF1	EAF1, Homo sapiens ELL associated factor 1 (EAF1), p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1842256	taggtaaacagaccca[C/T]gagtgtttgttaaag	C	T	NM_033083 // downstream // 71156 // Hs.474479 // EAF1 // 85403 // Homo sapiens ELL associated factor 1 (EAF1), mRNA. /// NM_012260 // downstream // 46972 // Hs.63290 // HPCL2 // 26061 // Homo sapiens 2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA. /// ENST000	EAF1	EAF1, Homo sapiens ELL associated factor 1 (EAF1), p25.1
SNP_A-2067577	acaaattctgtcaata[C/T]gtcctaccggtgacac	C	T	NM_033083 // downstream // 81208 // Hs.474479 // EAF1 // 85403 // Homo sapiens ELL associated factor 1 (EAF1), mRNA. /// NM_012260 // downstream // 36920 // Hs.63290 // HPCL2 // 26061 // Homo sapiens 2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA. /// ENST000	EAF1	EAF1, Homo sapiens ELL associated factor 1 (EAF1), p25.1
SNP_A-2162263	atttagtgctagtag[C/T]agacagtttgatggtt	C	T	NM_012260 // intron // 0 // Hs.63290 // HPCL2 // 26061 // Homo sapiens 2-hydroxyphytanoyl-CoA lyase (HPCL2), mRNA. /// ENST00000321169 // intron // 0 // --- // --- // ---	HPCL2	HPCL2, Homo sapiens 2-hydroxyphytanoyl-CoA lyase (HPCL2), p25.1
SNP_A-1855759	tcaatccatcctgcac[A/T]gtcgggcaacgtgccc	A	T	NM_000060 // downstream // 518 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 518 // --- // --- // --- /// ENST00000332754 // upstream // 231796 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2174402	cacagaactgggtgaa[C/T]taacaatgtccatgct	C	T	NM_000060 // downstream // 2701 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 2701 // --- // --- // --- /// ENST00000332754 // upstream // 229613 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2209032	cccagcttgaagcagt[C/T]acccacacaagctgat	C	T	NM_000060 // downstream // 20121 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 20121 // --- // --- // --- /// ENST00000332754 // upstream // 212193 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2077599	accacctcagtcttc[C/T]cttatccattgttct	C	T	NM_000060 // downstream // 56397 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 56397 // --- // --- // --- /// ENST00000332754 // upstream // 175917 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2008484	tgatcttgaaaatgtg[A/G]acttcattagagggtg	A	G	NM_000060 // downstream // 56520 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 56520 // --- // --- // --- /// ENST00000332754 // upstream // 175794 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-1804589	gtcagccataaaaaaa[C/G]agacccagtcatttgc	C	G	NM_000060 // downstream // 146579 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 146579 // --- // --- // --- /// ENST00000332754 // upstream // 85735 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2257337	cttcttttggttata[C/T]caagcagatggattac	C	T	NM_000060 // downstream // 196115 // Hs.517830 // BTD // 686 // Homo sapiens biotinidase (BTD), mRNA. /// ENST00000303498 // downstream // 196115 // --- // --- // --- /// ENST00000332754 // upstream // 36199 // --- // --- // ---	BTD	BTD, Homo sapiens biotinidase (BTD), p25.1
SNP_A-2008485	ccactgtgctccatca[C/T]ggaaggacacttgagt	C	T	NM_054110 // upstream // 277014 // Hs.411308 // GALNTL2 // 117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000332754 // downstream // 18304 // --- // --- // ---	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-2086232	actctgcggtcctta[A/G]aaatagaataacttct	A	G	NM_054110 // upstream // 122833 // Hs.411308 // GALNTL2 // 117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000332754 // downstream // 172485 // --- // --- // ---	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1
SNP_A-2046024	aagacgctttgcaaca[C/T]gcccagatactagaagc	C	T	NM_054110 // upstream // 122632 // Hs.411308 // GALNTL2 // 117248 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA. /// ENST00000332754 // downstream // 172686 // --- // --- // ---	GALNTL2	GALNTL2, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2107699	agctcaataaagatcc[A/G]ctattgaaaagctact	A	G	NM_015150 // intron // 0 // Hs.98910 // RAFTLIN // 23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000327152 // intron // 0 // — // — // — // — /// ENST00000334133 // intron // 0 // — // — // —	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1893505	tgcaggacagcaaaaa[A/G]tctgacaccatctgaa	A	G	NM_015150 // intron // 0 // Hs.98910 // RAFTLIN // 23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // — // — // — // —	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1849056	tatgccaactagaaaa[A/C]aacaatgcaggggga	A	C	NM_015150 // intron // 0 // Hs.98910 // RAFTLIN // 23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // — // — // — // —	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-2008491	gggtatcacgagtcac[A/G]aaatcactcagccaat	A	G	NM_015150 // intron // 0 // Hs.98910 // RAFTLIN // 23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // — // — // — // —	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1781558	ggattcctaatttgta[C/T]ctctgaacagctgaat	C	T	NM_015150 // intron // 0 // Hs.98910 // RAFTLIN // 23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // — // — // — // —	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-1956610	tttgttttaagcccccc[A/G]aagaaactcactgaca	A	G	NM_015150 // intron // 0 // Hs.98910 // RAFTLIN // 23180 // Homo sapiens raft-linking protein (RAFTLIN), mRNA. /// ENST00000334133 // intron // 0 // — // — // — // —	RAFTLIN	RAFTLIN, Homo sapiens raft-linking protein (RAFTLIN), p24.3
SNP_A-2056907	aatagtaagtgccatc[A/G]gagtaggtatatcagt	A	G	NM_001351 // upstream // 112626 // Hs.73078 // DAZL // 1618 // Homo sapiens deleted in azoospermia-like (DAZL), mRNA. /// ENST00000250863 // upstream // 112626 // — // — // — // — /// ENST00000360068 // upstream // 52178 // — // — // — // –	DAZL	DAZL, Homo sapiens deteted in azoospermia-like (DAZL), p24.3
SNP_A-1666964	catttgatttgactatatgactaga[C/T]atttacatttttttttttttttga	C	T	NM_001351 // upstream // 122262 // Hs.73078 // DAZL // 1618 // deleted in azoospermia-like /// NM_015184 // upstream // 205314 // Hs.54886 // PLCL2 // 23228 // phospholipase C-like 2	DAZL	DAZL , rs1823370, deleted in azoospermia-like ,p24.3
SNP_A-2199702	ccaaaatcactgatgg[C/G]agttaagcctggaaat	C	G	NM_001351 // upstream // 161297 // Hs.73078 // DAZL // 1618 // Homo sapiens deleted in azoospermia-like (DAZL), mRNA. /// ENST00000250863 // upstream // 161297 // — // — // — // — /// ENST00000360068 // upstream // 3507 // — // — // — // —	DAZL	DAZL, Homo sapiens deleted in azoospermia-like (DAZL), p24.3
SNP_A-2108034	agctctcagaaattta[A/G]gccatcccagctgagg	A	G	NM_015184 // upstream // 71127 // Hs.202010 // PLCL2 // 23228 // Homo sapiens phospholipase C-like 2 (PLCL2), mRNA. /// ENST00000360068 // downstream // 41971 // — // — // — // — /// ENST00000285094 // upstream // 71127 // — // — // — // —	PLCL2	PLCL2, Homo sapiens phospholipase C-like 2 (PLCL2), p24.3
SNP_A-2206323	ccatcctctcccagcc[A/G]cttttcagcttttcta	A	G	NM_015184 // intron // 0 // Hs.202010 // PLCL2 // 23228 // Homo sapiens phospholipase C-like 2 (PLCL2), mRNA. /// ENST00000285094 // intron // 0 // — // — // — // —	PLCL2	PLCL2, Homo sapiens phospholipase C-like 2 (PLCL2), p24.3
SNP_A-2299893	gcctagaggtgatcga[C/G]gtagagaaaagggagt	C	G	NM_014744 // intron // 0 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// ENST00000253692 // intron // 0 // — // — // — // —	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-2219793	ccttaccacggttcac[A/G]ctggcacactaagtct	A	G	NM_014744 // upstream // 65483 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 541553 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bind	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1935026	ttctgagtccaaataa[A/G]gtgtggagagaacgta	A	G	NM_014744 // upstream // 65668 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 541368 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bind	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1971904	ctcctcaatattctac[C/T]cagggtgtggcacaca	C	T	NM_014744 // upstream // 66466 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 540570 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bind	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1971905	tagaaataaattaccat[C/T]gtcatgtccatggca	C	T	NM_014744 // upstream // 67548 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 539488 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bind	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1901045	tggatatttcccatc[A/G]atatagctggagceca	A	G	NM_014744 // upstream // 70657 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 536379 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bind	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1971907	ccigglatttttcaca[C/T]ggggctgaggacaag	C	T	NM_014744 // upstream // 107352 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 499684 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bin	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1971908	aaaggctccctgta[C/T]ggcaagtaacgtggca	C	T	NM_014744 // upstream // 107440 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 499596 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bin	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1751919	catagaaatcactacatagtctaaa[A/T]acaacttttcatatcta attgct	A	T	NM_002971 // downstream // 500075 // Hs.416026 // SATB1 // 6304 // special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) /// NM_014744 // upstream // 107766 // Hs.115740 // TBC1D5 // 9779 // TBC1 domain family, m	SATB1	SATB1 , rs10510481, special AT-rich sequence binding protein 1 (binds to nuclear matrix,p24.3
SNP_A-1876170	tctgaccctcgcttga[A/C]cccaccactcttgct	A	C	NM_014744 // upstream // 149454 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 457582 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bin	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-1714068	gctcagttgtgctacatgttagaaa[A/C]gggcagtgatactctac ttttcag	A	C	NM_002971 // downstream // 451511 // Hs.416026 // SATB1 // 6304 // special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's) /// NM_014744 // upstream // 156330 // Hs.115740 // TBC1D5 // 9779 // TBC1 domain family, m	SATB1	SATB1 , rs10510482, special AT-rich sequence binding protein 1 (binds to nuclear matrix,p24.3
SNP_A-2269145	gaattggagctattca[A/G]ataatccactacagtc	A	G	NM_014744 // upstream // 165477 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 441559 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bin	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-2194056	catgacactcttgaga[C/T]gatagcaggttggaa	C	T	NM_014744 // upstream // 167729 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 439307 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bin	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-2299301	gcctctgacaaagac[A/G]caggtgctaaccatca	A	G	NM_014744 // upstream // 423766 // Hs.475629 // TBC1D5 // 9779 // Homo sapiens TBC1 domain family, member 5 (TBC1D5), mRNA. /// NM_002971 // downstream // 183270 // Hs.517717 // SATB1 // 6304 // Homo sapiens special AT-rich sequence binding protein 1 (bin	TBC1D5	TBC1D5, Homo sapiens TBC1 domain family, member 5 (TBC1D5), p24.3
SNP_A-2008503	cttaataaatccctg[C/T]atgcagatcctcatct	C	T	NM_144633 // upstream // 527540 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 81086 // --- // --- // --- /// ENST00000328405	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1837658	tactttcaaaagtcaa[C/T]gctcgtagtgaccaca	C	T	NM_144633 // upstream // 352081 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 256545 // — // — // — // — /// ENST00000328405	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1949317	tttattaattttacca[A/T]aagcctacagacatat	A	T	NM_144633 // upstream // 349084 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 259542 // — // — // — // — /// ENST00000328405	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2008507	ccaggtgcttgtacag[A/T]cacatggtgaaaagct	A	T	NM_144633 // upstream // 340990 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 267636 // — // — // — // — /// ENST00000328405	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1873819	tctcaggaaagctgcc[A/G]aacttatctgagagct	A	G	NM_144633 // upstream // 312591 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 296035 // — // — // — // — /// ENST00000328405	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2098602	agagcattttggcaag[C/T]ccatgattatttctaa	C	T	NM_144633 // upstream // 230061 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000335483 // downstream // 378565 // — // — // — // — /// ENST00000328405	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-2025265	aaaatatctgcagcca[G/T]tcaaaatactctcgtg	G	T	NM_144633 // intron // 0 // Hs.475656 // KCNH8 // 131096 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), mRNA. /// ENST00000328405 // intron // 0 // — // — // — // —	KCNH8	KCNH8, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 8 (KCNH8), p24.3
SNP_A-1971936	ccacttaggtggaaaa[C/G]actgacaaccaagtgg	C	G	NM_144715 // upstream // 7300 // Hs.257224 // EFHB // 151651 // Homo sapiens hypothetical protein FLJ25200 (FLJ25200), mRNA. /// NM_004162 // upstream // 5773 // Hs.475663 // RAB5A // 5868 // Homo sapiens RAB5A, member RAS oncogene family (RAB5A), mRNA. /	EFHB	EFHB, Homo sapiens hypothetical protein FLJ25200 (FLJ25200), p24.3
SNP_A-1881728	tctttgggaaaaagaa[C/T]tgagtgggctagatag	C	T	NM_004162 // intron // 0 // Hs.475663 // RAB5A // 5868 // Homo sapiens RAB5A, member RAS oncogene family (RAB5A), mRNA. /// ENST00000273047 // intron // 0 // — // — // — // —	RAB5A	RAB5A, Homo sapiens RAB5A, member RAS oncogene family (RAB5A), p24.3
SNP_A-2199677	ccaaaataaatgcatc[C/T]atctccttcacatctg	C	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-1971940	tgtagccaagagtgaa[C/T]atgatgtagcctttctt	C	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300 p24.3
SNP_A-1865788	tccatttttaggccga[A/G]gagtcttgtaaatgta	A	G	NM_003884 // CDS // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // CDS // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-2121006	agtctcacgctacaat[G/T]aactcgttatactttc	G	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300 p24.3
SNP_A-1679572	agagtatatatctgctgtgtgaagt[A/G]aaagaaccctgatagtgt tatagta	A	G	NM_003884 // intron // 0 // Hs.203475 // PCAF // 8850 // p300/CBP-associated factor	PCAF	PCAF , rs2365367, p300,p24.3
SNP_A-1929090	ttcaggaataaactga[C/T]ctgccctagttcacag	C	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300 p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287956	gattaiggatgaaggg[G/T]acaaatttatagttic	G	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-2067676	acaacaatctctctgt[C/T]atcgacatccgtgtta	C	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300,p24.3
SNP_A-2064830	aatgaaaaaacctca[C/T]gaaggccagaggaaga	C	T	NM_003884 // intron // 0 // Hs.533055 // PCAF // 8850 // Homo sapiens p300/CBP-associated factor (PCAF), mRNA. /// ENST00000263754 // intron // 0 // — // — // — // —	PCAF	PCAF, Homo sapiens p300 p24.3
SNP_A-1685912	aactacttttagaaatcttcacaaa[C/T]tcaattacctaictiactt ttgc	C	T	NM_138484 // intron // 0 // Hs.105153 // SGOL1 // 151648 // shugoshin-like 1 (S. pombe)	SGOL1	SGOL1 , rs10514674, shugoshin-like 1 (S. pombe),p24.3
SNP_A-1912335	tgtgattcatttatga[A/C]aggaaaigtgcatcat	A	C	NM_138484 // intron // 0 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // intron // 0 // — // — // — // — /// ENST00000263753 // intron // 0 // — // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2035167	aaatgcctgacatttta[A/C]aggtagaatgaggaag	A	C	NM_138484 // intron // 0 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // intron // 0 // — // — // — // — /// ENST00000263753 // intron // 0 // — // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1875690	tctcttgaactggaat[G/T]aatatgaagtagcctg	G	T	NM_138484 // upstream // 287875 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 287875 // — // — // — // — /// ENST00000263753 // upstream // 290099 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1906899	tggttccataactcaa[C/T]gtacttgttccaattc	C	T	NM_138484 // upstream // 288062 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 288062 // — // — // — // — /// ENST00000263753 // upstream // 290286 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1829308	taagtatttccactg[A/T]atgtccttgaccagaa	A	T	NM_138484 // upstream // 363401 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 363401 // — // — // — // — /// ENST00000263753 // upstream // 365625 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2091777	agaaaataagattaga[A/G]gcaagaagatcaacta	A	G	NM_138484 // upstream // 387590 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 387590 // — // — // — // — /// ENST00000263753 // upstream // 389814 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2179681	cacttctgaaaagaag[A/G]catacgcgtggtcaac	A	G	NM_138484 // upstream // 424262 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 424262 // — // — // — // — /// ENST00000263753 // upstream // 426486 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1819361	gttggcacagccttat[G/T]aggaagataatccaat	G	T	NM_138484 // upstream // 535954 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 535954 // — // — // — // — /// ENST00000263753 // upstream // 538178 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1961262	ttttttcactccaaat[C/T]gagcgatctgtgctc	C	T	NM_138484 // upstream // 836830 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 836830 // — // — // — // — /// ENST00000263753 // upstream // 839054 // — // — // —	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2091363	actttggtagacctg[C/G]actcaactatttgtag	C	G	NM_138484 // upstream // 878700 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 878700 // --- // --- // --- /// ENST00000263753 // upstream // 880924 // --- // --- // ---	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1726650	taaagtcgtagctttgtgcaccaca[A/T]ctaactgtttcaaaaattt cctaat	A	T	NM_138484 // upstream // 977611 // Hs.105153 // SGOL1 // 151648 // shugoshin-like 1 (S. pombe)	SGOL1	SGOL1 , rs1436832, shugoshin-like 1 (S. pombe),p24.3
SNP_A-1971967	tagctactctgagctc[G/T]aagactgtgagatgtc	G	T	NM_138484 // upstream // 1037087 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 1037087 // --- // --- // --- /// ENST00000263753 // upstream // 1039311 // --- // ---	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-2129322	atacaaatgtgaagta[C/T]aatcattccctgacat	C	T	NM_138484 // upstream // 1092378 // Hs.105153 // SGOL1 // 151648 // Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), mRNA. /// ENST00000306698 // upstream // 1092378 // --- // --- // --- /// ENST00000263753 // upstream // 1094602 // --- // ---	SGOL1	SGOL1, Homo sapiens shugoshin-like 1 (S. pombe) (SGOL1), p24.3
SNP_A-1971992	ataaacctggatgtca[A/G]cttacagctataaca	A	G	NM_024697 // intron // 0 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // intron // 0 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2097072	agactgtaactcaaag[A/T]agcttgtggacagagt	A	T	NM_024697 // intron // 0 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // intron // 0 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1971995	gctgacccacagaac[A/G]cagggaatgaaaggca	A	G	NM_024697 // intron // 0 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // intron // 0 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1754238	agaaaatccctctggcaaccaatac[C/T]gaccattacaatgaa cagataatta	C	T	NM_024697 // intron // 0 // Hs.99256 // FLJ22419 // 79750 // hypothetical protein FLJ22419	FLJ22419	FLJ22419 , rs3860583, hypothetical protein FLJ22419,p24.3
SNP_A-1851785	tattgaagcttacacc[G/T]catttgtgatccagt	G	T	NM_024697 // intron // 0 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // intron // 0 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1816934	gttattccaaagtgaa[C/T]gtcttaaaacaacaga	C	T	NM_024697 // upstream // 82310 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 82310 // --- // --- // --- /// ENST00000255320 // upstream // 548184 // --- // --- // -	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2106687	agcctgacagtatcaa[C/G]gttactctctaaatgc	C	G	NM_024697 // upstream // 118148 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 118148 // --- // --- // --- /// ENST00000255320 // upstream // 512346 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1972010	aatttcaaaatgaaga[C/G]agcctttgcactacc	C	G	NM_024697 // upstream // 159091 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 159091 // --- // --- // --- /// ENST00000255320 // upstream // 471403 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1972014	aatattagatatgcta[C/G]gtgtttgccttgct	C	G	NM_024697 // upstream // 227066 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 227066 // --- // --- // --- /// ENST00000255320 // upstream // 403428 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2233182	ctcagctaaatgaccc[C/T]gaaactgtagaatttt	C	T	NM_024697 // upstream // 479600 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 479600 // --- // --- // --- /// ENST00000255320 // upstream // 150894 // --- // --- // ---	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1849941	tatgtcagctcagtta[A/G]ctctctaatgcagcct	A	G	NM_024697 // upstream // 538573 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 538573 // — // — // — // — /// ENST00000255320 // upstream // 91921 // — // — //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1882062	tcttttgtgcaaaaat[A/T]atgtcctaatgtattg	A	T	NM_024697 // upstream // 543943 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 543943 // — // — // — // — /// ENST00000255320 // upstream // 86551 // — // — //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-2135617	atatttttccttctga[A/C]ctccagatactattc	A	C	NM_024697 // upstream // 571070 // Hs.21026 // ZNF659 // 79750 // Homo sapiens hypothetical protein FLJ22419 (FLJ22419), mRNA. /// ENST00000281523 // upstream // 571070 // — // — // — // — /// ENST00000255320 // upstream // 59424 // — // — //	ZNF659	ZNF659, Homo sapiens hypothetical protein FLJ22419 (FLJ22419), p24.3
SNP_A-1932268	ttcctctcagctaaa[C/G]aaaagtgtgctact	C	G	ENST00000255320 // intron // 0 // — // — // — // —	-	p24.3
SNP_A-1849632	tatggtatagccttaq[A/T]aacactgttgtcact	A	T	ENST00000255320 // intron // 0 // — // — // — // —	-	p24.3
SNP_A-1743125	tgctctggctgactcatttcatggal[A/C]cttccgttaaatttttgcctagtc	A	C	NM_024697 // upstream // 1028664 // Hs.99256 // FLJ22419 // 79750 // hypothetical protein FLJ22419 /// NM_152653 // upstream // 423328 // Hs.137047 // UBE2E2 // 7325 // ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	FLJ22419	FLJ22419 , rs296167, hypothetical protein FLJ22419 ,p24.3
SNP_A-1649684	ataaaggctcaaagtaatagaa[A/C]aggatcttaagtcagccccctgttta	A	C	NM_024697 // upstream // 1255224 // Hs.99256 // FLJ22419 // 79750 // hypothetical protein FLJ22419 /// NM_152653 // upstream // 196768 // Hs.137047 // UBE2E2 // 7325 // ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	FLJ22419	FLJ22419 , rs633464, hypothetical protein FLJ22419 ,p24.3
SNP_A-1683202	ccagttgccaaactctgggataaag[A/G]atggacaaaatacagtctctgcccc	A	G	NM_024697 // upstream // 1300758 // Hs.99256 // FLJ22419 // 79750 // hypothetical protein FLJ22419 /// NM_152653 // upstream // 151234 // Hs.137047 // UBE2E2 // 7325 // ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	FLJ22419	FLJ22419 , rs9310709, hypothetical protein FLJ22419 ,p24.3
SNP_A-1804497	gtcagagagtggagaa[C/T]gatttttctactggt	C	T	NM_152653 // intron // 0 // Hs.475688 // UBE2E2 // 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// ENST00000335798 // intron // 0 // — // — // — // —	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4 p24.3
SNP_A-2130288	atacgatggctgtctc[A/G]aaggaaagcatttgta	A	G	NM_152653 // intron // 0 // Hs.475688 // UBE2E2 // 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// ENST00000335798 // intron // 0 // — // — // — // —	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4 p24.3
SNP_A-1972053	atgataatatttagac[A/G]ctgtgacctctcagaa	A	G	NM_152653 // intron // 0 // Hs.475688 // UBE2E2 // 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// ENST00000335798 // intron // 0 // — // — // — // —	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4,p24.3
SNP_A-2277412	gagcaaacaatcatgg[A/G]atctagtcactgtgca	A	G	NM_152653 // intron // 0 // Hs.475688 // UBE2E2 // 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// ENST00000335798 // intron // 0 // — // — // — // —	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4,p24.3
SNP_A-2228543	ctacttttgctttggt[C/T]aacactatctaagcat	C	T	NM_152653 // intron // 0 // Hs.475688 // UBE2E2 // 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// ENST00000335798 // intron // 0 // — // — // — // —	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4,p24.3
SNP_A-2230203	ctatagaagtgactat[A/G]agttccatcaaatagg	A	G	NM_152653 // downstream // 112781 // Hs.475688 // UBE2E2 // 7325 // Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA. /// NM_182666 // upstream // 103336 // Hs.164853 // UBE2E1 // 7324 // Homo sapiens ubiquitin-conjug	UBE2E2	UBE2E2, Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4 p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2108400	agctgcatcacatcta[A/G]aacttttctccaagta	A	G	NM_182666 // intron // 0 // Hs.164853 // UBE2E1 // 7324 // Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast) (UBE2E1), transcript variant 2, mRNA. /// NM_003341 // intron // 0 // Hs.164853 // UBE2E1 // 7324 // Homo sapiens ubiquitin-	UBE2E1	UBE2E1, Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4 p24.2
SNP_A-2037748	aacaagtagaggtaga[C/T]ggcaattccaatgaaa	C	T	NM_182666 // intron // 0 // Hs.164853 // UBE2E1 // 7324 // Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast) (UBE2E1), transcript variant 2, mRNA. /// NM_003341 // intron // 0 // Hs.164853 // UBE2E1 // 7324 // Homo sapiens ubiquitin-	UBE2E1	UBE2E1, Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4,p24.2
SNP_A-2180967	cagaatttgaatccac[A/G]aaatttacttgggaac	A	G	NM_005126 // intron // 0 // Hs.37288 // NR1D2 // 9975 // Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA. /// ENST00000312521 // intron // 0 // — // — // — // —	NR1D2	NR1D2, Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), p24.2
SNP_A-2266915	gaagttggtctttcca[A/G]gatcattacctgctga	A	G	NM_005126 // intron // 0 // Hs.37288 // NR1D2 // 9975 // Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA. /// ENST00000312521 // intron // 0 // — // — // — // —	NR1D2	NR1D2, Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), p24.2
SNP_A-1972058	atcttggatgtcggaa[A/C]cttcaattatctgcag	A	C	NM_005126 // downstream // 15170 // Hs.37288 // NR1D2 // 9975 // Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA. /// ENST00000312521 // downstream // 15170 // — // — // — // — /// ENST00000357322 // downstream // 101699	NR1D2	NR1D2, Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), p24.2
SNP_A-2215062	cctattaagacaatga[A/T]cagatttgcaagaatg	A	T	NM_005126 // downstream // 72873 // Hs.37288 // NR1D2 // 9975 // Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA. /// ENST00000312521 // downstream // 72873 // — // — // — // — /// ENST00000357322 // downstream // 43996	NR1D2	NR1D2, Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), p24.2
SNP_A-1888586	tgaggcaagactattt[C/G]aaagatatcagcgata	C	G	NM_005126 // downstream // 88512 // Hs.37288 // NR1D2 // 9975 // Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA. /// ENST00000312521 // downstream // 88512 // — // — // — // — /// ENST00000357322 // downstream // 28357	NR1D2	NR1D2, Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), p24.2
SNP_A-1941987	ttggagtctaatgcta[A/G]ccatgtttcctcatac	A	G	NM_005126 // downstream // 107100 // Hs.37288 // NR1D2 // 9975 // Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), mRNA. /// ENST00000312521 // downstream // 107100 // — // — // — // — /// ENST00000357322 // downstream // 9769	NR1D2	NR1D2, Homo sapiens nuclear receptor subfamily 1, group D, member 2 (NR1D2), p24.2
SNP_A-1972059	cactctagttcctgaa[G/T]caattggtctgcagtg	G	T	NM_000461 // downstream // 20499 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // downstream // 21032 // Hs.187861 // THRB // 706	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1757399	caccaatctagggcagctgttccac[A/G]cagagatgcacattcg aatcagctg	A	G	NM_000461 // downstream // 21075 // Hs.203213 // THRB // 7068 // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	THRB	THRB , rs2360958, thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian),p24.2
SNP_A-1698769	taagaacaaacacccaagatttttc[A/G]acagctgtaatgctttgt gttaaca	A	G	NM_000461 // downstream // 20851 // Hs.203213 // THRB // 7068 // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	THRB	THRB , rs2063480, thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian),p24.2
SNP_A-1972063	aaaggagacgacaata[C/T]aatcagatgtattgtg	C	T	NM_000461 // intron // 0 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // — // — // — // — /// ENST0	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1972067	tttgccaggaaggaaa[C/G]aaaaacagcgaagggc	C	G	NM_000461 // intron // 0 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // — // — // — // — /// ENST0	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2297259	gccacccctttctaac[C/T]caacaactccttgacc	C	T	NM_000461 // intron // 0 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // — // — // — // — /// ENST0	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1972070	ggagagaattgcacca[A/G]ataaatgcaaaaatat	A	G	NM_000461 // intron // 0 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// ENST00000356447 // intron // 0 // — // — // — // — /// ENST0	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1745834	aaggataaagaaaactactgtatac[A/G]aattagggccacgat gtgagctgta	A	G	NM_000461 // upstream // 109795 // Hs.203213 // THRB // 7068 // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) /// NM_000965 // upstream // 823646 // Hs.436538 // RARB // 5915 // retinoic acid receptor,	THRB	THRB , rs10490835, thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) ,p24.2
SNP_A-2270964	gacagtgttttggcaa[G/T]aaaaaaatttagtttc	G	T	NM_000461 // upstream // 133657 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 133646 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1972082	catagcgccttgtaca[A/T]aggatgtcgataaatg	A	T	NM_000461 // upstream // 155190 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 155179 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2008534	ttctggaacatcaaaa[A/G]agcaatggcctaatta	A	G	NM_000461 // upstream // 178803 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 178792 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2008535	cctactgggcaaccag[A/C]ctgaatccactgtttc	A	C	NM_000461 // upstream // 178833 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 178822 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1948829	tttatatttcatttac[C/T]accagttctagttcat	C	T	NM_000461 // upstream // 259317 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 259306 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2288234	gattccctggccaaag[A/G]cagtaccaggttccaa	A	G	NM_000461 // upstream // 261223 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 261212 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2008540	actggactgtttgccc[A/G]gcatttatgccctctc	A	G	NM_000461 // upstream // 261885 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 261874 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1930947	ttccagggccctagaa[C/T]ccatttgtcactgaga	C	T	NM_000461 // upstream // 419488 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 419477 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2300254	gcctcgctcttcagat[C/G]aacctttcttcttttc	C	G	NM_000461 // upstream // 426765 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 426754 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2090409	acttggcattcagttg[C/G]aatcacctctattttt	C	G	NM_000461 // upstream // 437198 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 437187 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1908134	tgtacataaaagttca[C/T]ggaagcattgttcaca	C	T	NM_000461 // upstream // 444461 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 444450 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2313336	ggagacgtgtctagat[A/T]actgccaacaatgaca	A	T	NM_000461 // upstream // 445320 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 445309 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1972089	tctttggccatgaaaa[C/T]aatatgacaacatagc	C	T	NM_000461 // upstream // 463963 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 463952 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1972090	tggaacatcaaggaaa[A/G]atcacactgtcaatta	A	G	NM_000461 // upstream // 464923 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 464912 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1895961	tgccttcagaggccaa[A/G]cagataaccttagtga	A	G	NM_000461 // upstream // 561434 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 561423 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2300582	gcctgatggctaagca[C/T]agaggatgtttttacc	C	T	NM_000461 // upstream // 580280 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 580269 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1822258	gttttgcctggacagc[A/G]gaaaacagttatgaaa	A	G	NM_000461 // upstream // 628323 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 628312 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-2148250	atgggcacaaatagag[C/G]agaagcccactatgat	C	G	NM_000461 // upstream // 628582 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 628571 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2254763	cttggaagagtataaa[C/T]tgaactatgtcacact	C	T	NM_000461 // upstream // 632338 // Hs.187861 // THRB // 7068 // Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA. /// NM_000461 // upstream // 632327 // Hs.187861 // THRB // 7068	THRB	THRB, Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), p24.2
SNP_A-1815171	gtgttgaagacactac[A/G]gagtttattcttctct	A	G	NM_016152 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// ENST00000264330 // intron // 0 // --- // --- // --- // ---	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-1972099	ggtacacttggaaaca[C/T]aacaccatagaatgtt	C	T	NM_016152 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// ENST00000264330 // intron // 0 // --- // --- // --- // ---	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-1650526	ccatattttcttccatttttttaat[C/T]agagaggagtatttgtctgtagtcc	C	T	NM_000461 // upstream // 733751 // Hs.203213 // THRB // 7068 // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) /// NM_000965 // upstream // 199690 // Hs.436538 // RARB // 5915 // retinoic acid receptor,	THRB	THRB , rs2363594, thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) ,p24.2
SNP_A-2122555	agtgctgtaagagtca[A/G]atgtaacctctggagg	A	G	NM_016152 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// ENST00000264330 // intron // 0 // --- // --- // --- // ---	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-1662594	gtcctgagctatggtatatcccatc[A/G]aaaggtagtcattgccactcaccta	A	G	NM_000461 // upstream // 852577 // Hs.203213 // THRB // 7068 // thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) /// NM_000965 // upstream // 80864 // Hs.436538 // RARB // 5915 // retinoic acid receptor,	THRB	THRB , rs10510565, thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) ,p24.2
SNP_A-1939008	ttgagtcttgaacaaa[A/G]gtcaaccaaatgggga	A	G	NM_016152 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// ENST00000264330 // intron // 0 // --- // --- // --- // ---	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-2200732	ccaagactacagtgaa[A/G]tcggccacctctcctc	A	G	NM_016152 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// NM_000965 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcrip	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-2136180	atcaatctaacttcac[C/T]gagcaaagcttcatgc	C	T	NM_016152 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, mRNA. /// NM_000965 // intron // 0 // Hs.436538 // RARB // 5915 // Homo sapiens retinoic acid receptor, beta (RARB), transcrip	RARB	RARB, Homo sapiens retinoic acid receptor, beta (RARB), transcript variant 2, p24.2
SNP_A-2273816	gactggcaatgttccc[A/C]atgttaacaatgtaaa	A	C	NM_017897 // downstream // 478879 // Hs.55781 // FLJ20604 // 54995 // Homo sapiens hypothetical protein FLJ20604 (FLJ20604), mRNA. /// NM_052953 // upstream // 349394 // Hs.517868 // LRRC3B // 116135 // Homo sapiens leucine rich repeat containing 3B (LRRC	FLJ20604	FLJ20604, Homo sapiens hypothetical protein FLJ20604 (FLJ20604), p24.2
SNP_A-1679386	gaaatagggacctgcatttcaaagg[A/C]catccttacccaaacagggagcccc	A	C	NM_052953 // downstream // 276004 // Hs.446699 // LRP15 // 116135 // hypothetical protein LRP15 /// NM_152534 // downstream // 124137 // Hs.174379 // FLJ32685 // 152110 // hypothetical protein FLJ32685	LRP15	LRP15 , rs9310825, hypothetical protein LRP15 ,p24.1
SNP_A-1691230	gaaattgtgagtttgttttggtaga[C/T]gtaaagtgtaagaggtaaaaatgtg	C	T	NM_052953 // downstream // 310807 // Hs.446699 // LRP15 // 116135 // hypothetical protein LRP15 /// NM_152534 // downstream // 89334 // Hs.174379 // FLJ32685 // 152110 // hypothetical protein FLJ32685	LRP15	LRP15 , rs9310833, hypothetical protein LRP15 ,p24.1
SNP_A-1650982	ggtatgtatttaaaacatatgttta[G/T]aatcctgacttgaagcaacctaact	G	T	NM_052953 // downstream // 323391 // Hs.446699 // LRP15 // 116135 // hypothetical protein LRP15 /// NM_152534 // downstream // 76750 // Hs.174379 // FLJ32685 // 152110 // hypothetical protein FLJ32685	LRP15	LRP15 , rs939832, hypothetical protein LRP15 ,p24.1
SNP_A-1720359	caggtggaattagataatagaccca[A/C]gttaggttgcttcaagtcaggattc	A	C	NM_052953 // downstream // 323416 // Hs.446699 // LRP15 // 116135 // hypothetical protein LRP15 /// NM_152534 // downstream // 76725 // Hs.174379 // FLJ32685 // 152110 // hypothetical protein FLJ32685	LRP15	LRP15 , rs939833, hypothetical protein LRP15 ,p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041933	aactaagtaacaaaaa[A/T]cggcaattcaatttgt	A	T	NM_152534 // downstream // 101117 // Hs.546501 // FLJ32685 // 152110 // Homo sapiens hypothetical protein FLJ32685 (FLJ32685), mRNA. /// ENST00000358592 // downstream // 54945 // — // — // — // — /// ENST00000295720 // downstream // 49764 // — /	FLJ32685	FLJ32685, Homo sapiens hypothetical protein FLJ32685 (FLJ32685), p24.2
SNP_A-2132234	atagtaagactgtgtt[A/C]aaaaaggatgaggatg	A	C	NM_152534 // downstream // 76595 // Hs.546501 // FLJ32685 // 152110 // Homo sapiens hypothetical protein FLJ32685 (FLJ32685), mRNA. /// ENST00000358592 // downstream // 79467 // — // — // — // — /// ENST00000295720 // downstream // 25242 // — //	FLJ32685	FLJ32685, Homo sapiens hypothetical protein FLJ32685 (FLJ32685), p24.1
SNP_A-2114798	agggatttgagtggga[C/G]gaagggaaggttaagc	C	G	NM_003615 // upstream // 2415 // Hs.250072 // SLC4A7 // 9497 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA. /// NM_005442 // downstream // 257228 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesoderm	SLC4A7	SLC4A7, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), p24.1
SNP_A-2110602	aggacagtacacagaa[A/G]gactggcactgagatc	A	G	NM_005442 // upstream // 17618 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA. /// NM_182523 // upstream // 501689 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC6157	EOMES	EOMES, Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), p24.1
SNP_A-2312097	ggacactgaaaatcaa[G/T]atgccttcattggtaa	G	T	NM_005442 // upstream // 190393 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA. /// NM_182523 // upstream // 328914 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC615	EOMES	EOMES, Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), p24.1
SNP_A-1972165	ccacagtcttgctttc[A/G]atgaacttataatgtt	A	G	NM_005442 // upstream // 260142 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA. /// NM_182523 // upstream // 259165 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC615	EOMES	EOMES, Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), p24.1
SNP_A-1972168	atttgtcaaggctgca[C/G]taaaaacattttggtc	C	G	NM_005442 // upstream // 276937 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA. /// NM_182523 // upstream // 242370 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC615	EOMES	EOMES, Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), p24.1
SNP_A-1972169	ctgaattcgaaatata[C/G]ggtacttggttcgggt	C	G	NM_005442 // upstream // 276987 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA. /// NM_182523 // upstream // 242320 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC615	EOMES	EOMES, Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), p24.1
SNP_A-2169376	caagcatcaaagcaca[A/T]ctccagtctccagttc	A	T	NM_005442 // upstream // 292182 // Hs.147279 // EOMES // 8320 // Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA. /// NM_182523 // upstream // 227125 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC615	EOMES	EOMES, Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), p24.1
SNP_A-2248822	ctgttgaatctgatag[C/T]ataaaatggagcttgt	C	T	NM_182523 // downstream // 170521 // Hs.437336 // MGC61571 // 152100 // Homo sapiens hypothetical protein MGC61571 (MGC61571), mRNA. /// NM_022461 // upstream // 146557 // Hs.444724 // AZI2 // 64343 // Homo sapiens 5-azacytidine induced 2 (AZI2), transcri	MGC61571	MGC61571, Homo sapiens hypothetical protein MGC61571 (MGC61571), p24.1
SNP_A-1879401	tcttatatggttacat[G/T]aaacattgggagtctg	G	T	NM_182590 // upstream // 6401 // — // — // 0 // — /// NM_001003792 // upstream // 698800 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // u	-	p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100751	agatagctgagataga[A/G]taacaatggacacag	A	G	NM_182590 // upstream // 505168 // — // 0 // — /// NM_001003792 // upstream // 200033 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 //	-	p24.1
SNP_A-1859261	tcagctctaggcccaa[G/T]gaaactcgattctaat	G	T	NM_182590 // upstream // 516291 // — // 0 // — /// NM_001003792 // upstream // 188910 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 //	-	p24.1
SNP_A-2085318	actcatcttgaggaa[A/T]gttacaaagataatg	A	T	NM_182590 // upstream // 595117 // — // 0 // — /// NM_001003792 // upstream // 110084 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 //	-	p24.1
SNP_A-2118713	agtacactgaatcaga[C/T]actaaaaatgacactg	C	T	NM_182590 // upstream // 703213 // — // 0 // — /// NM_001003792 // upstream // 1988 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // u	-	p24.1
SNP_A-1646284	ttatgtcccaaagcttgtctgag[G/T]aaatcgacatcaggaaa ttatgttg	G	T	NM_014483 // intron // 0 // Hs.158446 // RBMS3 // 27303 // RNA binding motif, single stranded interacting protein	RBMS3	RBMS3, rs7622604, RNA binding motif, single stranded interacting protein,p24.1
SNP_A-2119463	agtatattgaataga[A/G]agttcagtacagcgt	A	G	NM_001003792 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA bindi	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2152652	attaatagcaagatta[C/T]aagtattaggttctat	C	T	NM_001003792 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA bindi	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1863373	tcatttgtacatata[A/G]gcaggagaagaattgc	A	G	NM_001003792 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA bindi	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2297573	gccagaggagatccaa[C/T]ttctcagaagggtgag	C	T	NM_001003792 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA bindi	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1929392	ttcagtggctcaccic[A/G]aaacttctaaatgaga	A	G	NM_001003792 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA bindi	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2195987	catgtctaactccaaa[A/G]ccattaatgtattaga	A	G	NM_001003792 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // intron // 0 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA bindi	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1679680	gatgaaaatcgcctctgtcttta[C/T]agagttctgagtcagaaa aattaa	C	T	NM_003242 // upstream // 203017 // Hs.82028 // TGFBR2 // 7048 // transforming growth factor, beta receptor II (70/80kDa) /// NM_014483 // downstream // 412266 // Hs.158446 // RBMS3 // 27303 // RNA binding motif, single stranded interacting protein	TGFBR2	TGFBR2 , rs1495589, transforming growth factor, beta receptor II (70,p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189978	cataacacttgtgaga[C/T]tcacctattttgttat	C	T	NM_001003792 // downstream // 504186 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // downstream // 504186 // Hs.221436 // RBMS3 // 27303 // Homo	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1899443	tggaagaatgatgatg[C/T]cacttgctgagatggg	C	T	NM_001003792 // downstream // 537606 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // downstream // 537606 // Hs.221436 // RBMS3 // 27303 // Homo	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2292681	gcactgtgtaaatgtc[C/T]gaagggccagaaagat	C	T	NM_001003792 // downstream // 548424 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // downstream // 548424 // Hs.221436 // RBMS3 // 27303 // Homo	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-2084872	actcaacccaagcaaa[G/T]ttgtcctagtgtgccc	G	T	NM_001003792 // downstream // 569875 // Hs.221436 // RBMS3 // 27303 // Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, mRNA. /// NM_001003793 // downstream // 569875 // Hs.221436 // RBMS3 // 27303 // Homo	RBMS3	RBMS3, Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), transcript variant 3, p24.1
SNP_A-1896730	tgctatgcctaggaga[A/T]gtaaagcctaaaggaa	A	T	NM_003242 // intron // 0 // Hs.82028 // TGFBR2 // 7048 // Homo sapiens transforming growth factor, beta receptor II (70/80kDa) (TGFBR2), mRNA. /// ENST00000295754 // intron // 0 // — // — // — // /// ENST00000359013 // intron // 0 // — // —	TGFBR2	TGFBR2, Homo sapiens transforming growth factor, beta receptor II (70 p24.1
SNP_A-2196130	catgtgcagcacaaca[A/G]atcaagccaggcagat	A	G	NM_003242 // intron // 0 // Hs.82028 // TGFBR2 // 7048 // Homo sapiens transforming growth factor, beta receptor II (70/80kDa) (TGFBR2), mRNA. /// ENST00000295754 // intron // 0 // — // — // — // /// ENST00000359013 // intron // 0 // — // —	TGFBR2	TGFBR2, Homo sapiens transforming growth factor, beta receptor II (70,p24.1
SNP_A-1928049	ttcaattattgtctca[C/T]gtgtacctgtaggacc	C	T	NM_207359 // upstream // 142193 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 142193 // — // — // — // — /// ENST00000344402 // upstream // 459802 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1936203	ttcttcagagaaggag[A/G]catccatgagccatta	A	G	NM_207359 // upstream // 148040 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 148040 // — // — // — // — /// ENST00000344402 // upstream // 453955 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1667296	atggtttcccaaaaacatgactgac[A/C]atgggagcctcagaa gtctctacgt	A	C	NM_003242 // downstream // 316062 // Hs.82028 // TGFBR2 // 7048 // transforming growth factor, beta receptor II (70/80kDa) /// NM_178862 // upstream // 522089 // Hs.528331 // SIMP // 201595 // source of immunodominant MHC-associated peptides	TGFBR2	TGFBR2 , rs7642265, transforming growth factor, beta receptor II (70,p24.1
SNP_A-2273061	gactatcgaggtggag[C/T]ctaaatgtaatctaaa	C	T	NM_207359 // upstream // 199101 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 199101 // — // — // — // — /// ENST00000344402 // upstream // 402894 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2186019	caggcaggaagtgcta[A/G]gggagaacacaccctg	A	G	NM_207359 // upstream // 320256 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 320256 // — // — // — // — /// ENST00000344402 // upstream // 281739 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2149608	atgtagttggcagtca[C/G]cccatagaagtgatgt	C	G	NM_207359 // upstream // 343231 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 343231 // — // — // — // — /// ENST00000344402 // upstream // 258764 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2222703	cgatcgggtacttatg[C/G]aaattctcaggatatc	C	G	NM_207359 // upstream // 468938 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 468938 // — // — // — // — /// ENST00000344402 // upstream // 133057 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1940265	ttgcatttcactgaag[C/T]aagttgccagaactct	C	T	NM_207359 // upstream // 489788 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 489788 // — // — // — // — /// ENST00000344402 // upstream // 112207 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-2301205	gccttgactaaactcc[A/T]ggaaatgagacacagc	A	T	NM_207359 // upstream // 491291 // Hs.475809 // GADL1 // 339896 // Homo sapiens glutamate decarboxylase-like 1 (GADL1), mRNA. /// ENST00000282538 // upstream // 491291 // — // — // — // — /// ENST00000344402 // upstream // 110704 // — // — //	GADL1	GADL1, Homo sapiens glutamate decarboxylase-like 1 (GADL1), p24.1
SNP_A-1711570	ctcacagggcaaataagatgtacta[C/G]tagagagccaggcaagataaaaata	C	G	NM_003242 // downstream // 677136 // Hs.82028 // TGFBR2 // 7048 // transforming growth factor, beta receptor II (70/80kDa) /// NM_178862 // upstream // 161015 // Hs.528331 // SIMP // 201595 // source of immunodominant MHC-associated peptides	TGFBR2	TGFBR2 , rs4339137, transforming growth factor, beta receptor II (70,p24.1
SNP_A-2098286	agagatgatcaaatca[C/T]ggaagtaagtgagaaa	C	T	NM_178862 // upstream // 52018 // Hs.475812 // SIMP // 201595 // Homo sapiens source of immunodominant MHC-associated peptides (SIMP), mRNA. /// ENST00000344402 // downstream // 26794 // — // — // — // — /// ENST00000354618 // downstream // 25147	SIMP	SIMP, Homo sapiens source of immunodominant MHC-associated peptides (SIMP), p24.1
SNP_A-2040953	aaccctgcaaaaggtc[A/G]cagctatttttccaca	A	G	NM_017784 // intron // 0 // Hs.150122 // OSBPL10 // 114884 // Homo sapiens oxysterol binding protein-like 10 (OSBPL10), mRNA. /// ENST00000273142 // intron // 0 // --- // --- // --- // ---	OSBPL10	OSBPL10, Homo sapiens oxysterol binding protein-like 10 (OSBPL10), p24.1
SNP_A-1951741	tttcgattctgggtac[A/C]actaacttaggcaaca	A	C	NM_015141 // downstream // 28035 // Hs.82432 // GPD1L // 23171 // Homo sapiens glycerol-3-phosphate dehydrogenase 1-like (GPD1L), mRNA. /// NM_178868 // upstream // 41931 // Hs.154986 // CKLFSF8 // 152189 // Homo sapiens chemokine-like factor super family	GPD1L	GPD1L, Homo sapiens glycerol-3-phosphate dehydrogenase 1-like (GPD1L), p23
SNP_A-1813031	gtgggtgagggaacac[C/T]aataaacagcattata	C	T	NM_178868 // intron // 0 // Hs.154986 // CKLFSF8 // 152189 // Homo sapiens chemokine-like factor super family 8 (CKLFSF8), mRNA. /// ENST00000307526 // intron // 0 // — // — // — // —	CKLFSF8	CKLFSF8, Homo sapiens chemokine-like factor super family 8 (CKLFSF8), p23
SNP_A-1972293	gactatgaatactaga[G/T]aggaaacaggagtttc	G	T	NM_178868 // intron // 0 // Hs.154986 // CKLFSF8 // 152189 // Homo sapiens chemokine-like factor super family 8 (CKLFSF8), mRNA. /// ENST00000307526 // intron // 0 // --- // --- // --- // ---	CKLFSF8	CKLFSF8, Homo sapiens chemokine-like factor super family 8 (CKLFSF8), p23
SNP_A-2105846	agccagtgtccccttc[A/G]ccaggttagacgaggt	A	G	NM_181472 // downstream // 1755 // Hs.440494 // CKLFSF7 // 112616 // Homo sapiens chemokine-like factor super family 7 (CKLFSF7), transcript variant 2, mRNA. /// NM_138410 // downstream // 1755 // Hs.440494 // CKLFSF7 // 112616 // Homo sapiens chemokine-l	CKLFSF7	CKLFSF7, Homo sapiens chemokine-like factor super family 7 (CKLFSF7), transcript variant 2, p23
SNP_A-2179214	cactggggctaaaaga[A/G]ctggagaagcagagga	A	G	NM_181472 // downstream // 1821 // Hs.440494 // CKLFSF7 // 112616 // Homo sapiens chemokine-like factor super family 7 (CKLFSF7), transcript variant 2, mRNA. /// NM_138410 // downstream // 1821 // Hs.440494 // CKLFSF7 // 112616 // Homo sapiens chemokine-l	CKLFSF7	CKLFSF7, Homo sapiens chemokine-like factor super family 7 (CKLFSF7), transcript variant 2, p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246490	cigtaaaaagccaata[A/G]agccggatgcagtggc	A	G	NM_014517 // upstream // 47645 // Hs.118041 // UBP1 // 7342 // Homo sapiens upstream binding protein 1 (LBP-1a) (UBP1), mRNA. /// ENST00000283628 // upstream // 48013 // — // — // — /// ENST00000283629 // upstream // 47645 // — // — // —	UBP1	UBP1, Homo sapiens upstream binding protein 1 (LBP-1a) (UBP1), p23
SNP_A-2221841	cctttgatgattcac[A/C]ctcttacactatatag	A	C	NM_013374 // intron // 0 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// ENST00000307296 // intron // 0 // — // — // —	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-1855518	tcaagttcaagaagga[A/C]agctcgacattgaaca	A	C	NM_013374 // intron // 0 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// ENST00000307296 // intron // 0 // — // — // —	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2024681	aaaagtacaaactgta[C/T]gacaccattgctatga	C	T	NM_013374 // downstream // 62043 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1709273 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosp	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2008602	agatactgtagcaaccc[C/T]ccctgagatttaactg	C	T	NM_013374 // downstream // 174886 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1596430 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2259866	gaaaaggaagcttcca[C/T]gagtaggcacttgacc	C	T	NM_013374 // downstream // 202858 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1568458 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2168163	caactctacccaatca[C/T]atcaggtctcctagat	C	T	NM_013374 // downstream // 402160 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1369156 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-1691188	gtatttcttaacagagcataaaaaa[A/T]ggtgttctccatgtgcca tatttt	A	T	NM_013374 // downstream // 567769 // Hs.9663 // PDCD6IP // 10015 // programmed cell death 6 interacting protein /// NM_016300 // upstream // 1235020 // Hs.376455 // ARPP-21 // 10777 // cyclic AMP-regulated phosphoprotein, 21 kD	PDCD6IP	PDCD6IP, rs1114855, programmed cell death 6 interacting protein, p23
SNP_A-2259074	cttttttctctaca[C/T]atttagtgtctggtat	C	T	NM_013374 // downstream // 669477 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1101839 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2283932	gatataaagtaggctca[A/C]aggtgtaggccatgac	A	C	NM_013374 // downstream // 689564 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1081752 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2031308	aaagggataggttaa[C/G]tcgtatgtttcaacat	C	G	NM_013374 // downstream // 742464 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 1028852 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2230244	ctatagcttaaaaaca[C/T]gaggataggttatac	C	T	NM_013374 // downstream // 797283 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 974033 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosp	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2119685	agtattactagagcta[A/C]agagagagaccgtaat	A	C	NM_013374 // downstream // 802849 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 968467 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosp	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p23
SNP_A-2284826	gatcattgtgtctta[C/T]attaacttgtcagaa	C	T	NM_013374 // downstream // 1154207 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 617109 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-2167225	caacactgctaagagc[A/G]aggagctggaaaaagg	A	G	NM_013374 // downstream // 1174220 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 597096 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1829330	taagtcaccaaagaaa[A/T]ctaacctcatctgaaa	A	T	NM_013374 // downstream // 1391191 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 380125 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1972331	ggcagagtatataccaa[C/T]gagatacaatagatg	C	T	NM_013374 // downstream // 1476950 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 294366 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1855077	tcaagacacatagaga[C/T]gaaaaatatgcaactg	C	T	NM_013374 // downstream // 1573278 // Hs.475896 // PDCD6IP // 10015 // Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA. /// NM_198399 // upstream // 198038 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phos	PDCD6IP	PDCD6IP, Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), p22.3
SNP_A-1916686	tgtttcaatttggta[C/T]gcctagtgatttggga	C	T	NM_198399 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_016300 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1928489	ttcactagttggttca[G/T]tagttatagtatgatt	G	T	NM_198399 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_016300 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2228315	ctactgcacgttggta[A/T]catactctcccaaaga	A	T	NM_198399 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_016300 // intron // 0 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1903606	tgggactgaggcaagt[A/G]accaagaatgcactat	A	G	NM_198399 // downstream // 6655 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 7025 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1972352	gagggtgatgcaacaa[A/G]catgaaggtgagggtg	A	G	NM_198399 // downstream // 9904 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 10274 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1972353	ctctatatttattgaa[C/T]gggcaggaaaacaatt	C	T	NM_198399 // downstream // 10279 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 10649 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cydi	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1834245	tacatggaatggtaag[C/T]ccagcaggtgcactat	C	T	NM_198399 // downstream // 13446 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 13816 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cydi	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2158424	attggtgtgctctcca[A/G]agaatttgtagctatt	A	G	NM_198399 // downstream // 76140 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 76510 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cydi	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1697220	aaagaactgtattttcaatccaaa[A/G]tgttcgaaatattgaaac atataat	A	G	NM_003149 // upstream // 290557 // Hs.56045 // STAC // 6769 // src homology three (SH3) and cysteine rich domain /// NM_016300 // downstream // 405257 // Hs.376455 // ARPP-21 // 10777 // cydic AMP-regulated phosphoprotein, 21 kD	STAC	STAC , rs2167488, src homology three (SH3) and cysteine rich domain ,p22.3
SNP_A-1700925	aatacactagcttttcaaagtcta[C/T]gcaaatgtgaatcagaa aagaaaca	C	T	NM_003149 // upstream // 289755 // Hs.56045 // STAC // 6769 // src homology three (SH3) and cysteine rich domain /// NM_016300 // downstream // 406059 // Hs.376455 // ARPP-21 // 10777 // cydic AMP-regulated phosphoprotein, 21 kD	STAC	STAC , rs10510672, src homology three (SH3) and cysteine rich domain ,p22.3
SNP_A-2232664	ctcacgttgtgtatcca[A/C]gttgaaggaacacta	A	C	NM_198399 // downstream // 308963 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 309333 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyc	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1972361	attggagaaggtgtga[C/T]ctgagagagctgaaaa	C	T	NM_198399 // downstream // 312500 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 312870 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyc	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1846470	tatattagtcctagccf[A/T]atgctgagaaagtttg	A	T	NM_198399 // downstream // 320657 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 321027 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyc	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1862249	tcatgggaatgtacag[A/G]aaaaacctaatatgtg	A	G	NM_198399 // downstream // 326071 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 326441 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyc	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-2091124	actttggattccctaa[C/G]tacctcaagaatgata	C	G	NM_198399 // downstream // 340989 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, mRNA. /// NM_198399 // downstream // 341359 // Hs.475902 // ARPP-21 // 10777 // Homo sapiens cyc	ARPP-21	ARPP-21, Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), transcript variant 2, p22.3
SNP_A-1887373	tgagaatgctttacig[A/C]agaatttcccaaagta	A	C	NM_003149 // downstream // 2375 // Hs.56045 // STAC // 6769 // Homo sapiens SH3 and cysteine rich domain (STAC), mRNA. /// ENST00000273183 // downstream // 2375 // --- // --- // --- /// ENST00000295943 // downstream // 162042 // --- // --- // ---	STAC	STAC, Homo sapiens SH3 and cysteine rich domain (STAC), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2127637	ataaccttctttttcta[C/T]caccttttcagtaatac	C	T	NM_003149 // downstream // 147427 // Hs.56045 // STAC // 6769 // Homo sapiens SH3 and cysteine rich domain (STAC), mRNA. /// ENST00000273183 // downstream // 147427 // — // — // — // — /// ENST00000295943 // downstream // 16990 // — // — // –	STAC	STAC, Homo sapiens SH3 and cysteine rich domain (STAC), p22.3
SNP_A-2111085	aggagactgaaaacca[C/T]gagtgtccaaagcctc	C	T	NM_002207 // intron // 0 // Hs.113157 // ITGA9 // 3680 // Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /// ENST00000264741 // intron // 0 // — // — // — // —	ITGA9	ITGA9, Homo sapiens integrin, alpha 9 (ITGA9), p22.3
SNP_A-1938839	ttgaggatgggactaa[A/G]ggctaaacttcatatt	A	G	NM_002207 // intron // 0 // Hs.113157 // ITGA9 // 3680 // Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /// ENST00000264741 // intron // 0 // — // — // — // —	ITGA9	ITGA9, Homo sapiens integrin, alpha 9 (ITGA9), p22.3
SNP_A-1972414	agtagcatgaaattag[C/G]catgttcatattaagg	C	G	NM_002207 // intron // 0 // Hs.113157 // ITGA9 // 3680 // Homo sapiens integrin, alpha 9 (ITGA9), mRNA. /// ENST00000264741 // intron // 0 // — // — // — // —	ITGA9	ITGA9, Homo sapiens integrin, alpha 9 (ITGA9), p22.3
SNP_A-1972415	ttcattctatccttca[A/G]tcaccttctatgttca	A	G	NM_005808 // intron // 0 // Hs.475963 // CTDSPL // 10217 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), mRNA. /// ENST00000273179 // intron // 0 // — // — // — // — // —	CTDSPL	CTDSPL, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), p22.3
SNP_A-2038608	aacagaatcctgaaga[C/G]ctatttgtactccatg	C	G	NM_005808 // intron // 0 // Hs.475963 // CTDSPL // 10217 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), mRNA. /// ENST00000273179 // intron // 0 // — // — // — // — // —	CTDSPL	CTDSPL, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), p22.3
SNP_A-2183485	cagcagagagacaagt[C/G]aaaaagcaactgtagt	C	G	NM_005808 // intron // 0 // Hs.475963 // CTDSPL // 10217 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), mRNA. /// ENST00000273179 // intron // 0 // — // — // — // — // —	CTDSPL	CTDSPL, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (CTDSPL), p22.3
SNP_A-1877570	tctggctacactgaaa[A/G]gcatcaaataacaagg	A	G	NM_005109 // intron // 0 // Hs.475970 // OXSR1 // 9943 // Homo sapiens oxidative-stress responsive 1 (OSR1), mRNA. /// ENST00000311806 // intron // 0 // — // — // — // —	OXSR1	OXSR1, Homo sapiens oxidative-stress responsive 1 (OSR1), p22.2
SNP_A-1848501	tatgaatgacaggttg[C/T]atttttgttttgaaaa	C	T	NM_005108 // intron // 0 // Hs.356820 // XYLB // 9942 // Homo sapiens xylulokinase homolog (H. influenzae) (XYLB), mRNA. /// ENST00000207870 // intron // 0 // — // — // — // —	XYLB	XYLB, Homo sapiens xylulokinase homolog (H. influenzae) (XYLB), p22.2
SNP_A-2307909	gcttctgacacacaca[A/C]agcatgaaaaaaaatt	A	C	NM_005108 // intron // 0 // Hs.356820 // XYLB // 9942 // Homo sapiens xylulokinase homolog (H. influenzae) (XYLB), mRNA. /// ENST00000207870 // intron // 0 // — // — // — // —	XYLB	XYLB, Homo sapiens xylulokinase homolog (H. influenzae) (XYLB), p22.2
SNP_A-2008631	cctacctttttttcgta[A/C]cctatagttctctacc	A	C	NM_194293 // upstream // 31848 // Hs.447868 // CMYA1 // 165904 // Homo sapiens cardiomyopathy associated 1 (CMYA1), mRNA. /// NM_001337 // downstream // 39054 // Hs.78913 // CX3CR1 // 1524 // Homo sapiens chemokine (C-X3-C motif) receptor 1 (CX3CR1), mRNA	CMYA1	CMYA1, Homo sapiens cardiomyopathy associated 1 (CMYA1), p22.2
SNP_A-2122233	agtgcaccgttgctca[C/T]agcacaatccctcagg	C	T	NM_006501 // downstream // 48271 // Hs.121333 // MOBP // 4336 // Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), mRNA. /// NM_182934 // downstream // 48271 // Hs.121333 // MOBP // 4336 // Homo sapiens myelin-associated oligodendrocyte	MOBP	MOBP, Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), p22.2
SNP_A-1724870	tcacaagactctaaaaagataggaa[C/T]taagaaaactacag gacaatgaaga	C	T	NM_015460 // intron // 0 // Hs.162953 // MYRIP // 25924 // myosin VIIA and Rab interacting protein	MYRIP	MYRIP , rs10510707, myosin VIIA and Rab interacting protein,p22.1
SNP_A-2095390	agacaaaaaaatаaac[A/G]ggcatataacgagtgt	A	G	NM_001248 // intron // 0 // Hs.441145 // ENTPD3 // 956 // Homo sapiens ectonucleoside triphosphate diphosphohydrolase 3 (ENTPD3), mRNA. /// ENST00000301825 // intron // 0 // — // — // — // —	ENTPD3	ENTPD3, Homo sapiens ectonucleoside triphosphate diphosphohydrolase 3 (ENTPD3), p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813994	gtgtcagtgcaggttc[A/G]acaatggtaactaatg	A	G	NM_198484 // downstream // 137584 // Hs.19977 // ZNF621 // 285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 137584 // — // — // — /// ENST00000310898 // downstream // 133204 // — // — //	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-1714150	aaaaaagaaatagagcatcttctta[C/T]ggtgaatttctatgttaag aaaagg	C	T	BC044953 // downstream // 180515 // Hs.378698 // ZNF620 // 253639 // zinc finger protein 620 /// NM_001904 // upstream // 501284 // Hs.410086 // CTNNB1 // 1499 // catenin (cadherin-associated protein), beta 1, 88kDa	ZNF620	ZNF620 , rs10510715, zinc finger protein 620 ,p22.1
SNP_A-2030053	aaagattcagctccac[A/C]aatgcactgtggatta	A	C	NM_198484 // downstream // 161875 // Hs.19977 // ZNF621 // 285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 161875 // — // — // — /// ENST00000310898 // downstream // 157495 // — // — //	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-2277280	gagattccaaaactca[G/T]tctctaaccacttat	G	T	NM_198484 // downstream // 219023 // Hs.19977 // ZNF621 // 285268 // Homo sapiens zinc finger protein 621 (ZNF621), mRNA. /// ENST00000339296 // downstream // 219023 // — // — // — /// ENST00000310898 // downstream // 214643 // — // — //	ZNF621	ZNF621, Homo sapiens zinc finger protein 621 (ZNF621), p22.1
SNP_A-1871229	tctaaaagttggagca[A/G]aactctaaattaaac	A	G	ENST00000301831 // intron // 0 // — // — // —	-	p22.1
SNP_A-1721638	atcagactccaaagcttgatcta[G/T]gctatcagacttttcaag gaaccac	G	T	AL133104 // intron // 0 // Hs.255960 // DKFZp434E1822 // 92216 // hypothetical protein DKFZp434E1822	DKFZp434E182 2	DKFZp434E1822 , rs7827387, hypothetical protein DKFZp434E1822,p22.1
SNP_A-1674761	accatcacaacgtctatcataatac[A/C]atgaatgaaccggta ctatttaaa	A	C	AL133104 // intron // 0 // Hs.255960 // DKFZp434E1822 // 92216 // hypothetical protein DKFZp434E1822	DKFZp434E182 2	DKFZp434E1822 , rs6807793, hypothetical protein DKFZp434E1822,p22.1
SNP_A-2288121	gattcagcactgctac[A/G]actggtgagttttcc	A	G	ENST00000301831 // intron // 0 // — // — // —	-	p22.1
SNP_A-1972492	cccacgcagcataggc[A/C]aaaacagtcattcagt	A	C	ENST00000301831 // intron // 0 // — // — // —	-	p22.1
SNP_A-1819483	gttggttgtcattaa[A/C]gcgtacaatttaatt	A	C	ENST00000301831 // intron // 0 // — // — // —	-	p22.1
SNP_A-2185328	caggaatgaaaactaa[A/G]aaaagaagcatacaaa	A	G	ENST00000301831 // intron // 0 // — // — // —	-	p22.1
SNP_A-1883951	tgaagagttgcataaa[C/T]gacttaaacacacat	C	T	NM_017886 // downstream // 100962 // Hs.326883 // — // 0 // Homo sapiens hypothetical protein FLJ20574 (FLJ20574), mRNA. /// ENST00000301831 // upstream // 28534 // — // — // — /// ENST00000307805 // downstream // 99210 // — // — // —	-	-, Homo sapiens hypothetical protein FLJ20574 (FLJ20574), p22.1
SNP_A-2235993	ctcctggccaaaaggaf[A/G]tattaacagacatttt	A	G	NM_017886 // downstream // 4075 // Hs.326883 // — // 0 // Homo sapiens hypothetical protein FLJ20574 (FLJ20574), mRNA. /// ENST00000301831 // upstream // 125421 // — // — // — /// ENST00000307805 // downstream // 2323 // — // — // —	-	-, Homo sapiens hypothetical protein FLJ20574 (FLJ20574), p22.1
SNP_A-2216097	cctcccagggaaaaata[C/T]gtaggaagcccactgc	C	T	AB028965 // intron // 0 // Hs.535711 // OIP106 // 22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// ENST00000327628 // intron // 0 // — // — // —	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. p22.1
SNP_A-2238475	ctctgtaagagtgaaa[G/T]taagagtggttctcac	G	T	AB028965 // intron // 0 // Hs.535711 // OIP106 // 22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// ENST00000327628 // intron // 0 // — // — // —	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. p22.1
SNP_A-1932199	ttcctccattaggcac[A/G]aggttgatttgtctag	A	G	AB028965 // 3UTR // 0 // Hs.535711 // OIP106 // 22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// ENST00000327628 // 3UTR // 0 // — // — // —	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. ,p22.1
SNP_A-2162505	attttccaaaccagaa[A/G]cgtctgggaatcaca	A	G	AB028965 // downstream // 22552 // Hs.535711 // OIP106 // 22906 // Homo sapiens mRNA for KIAA1042 protein, partial cds. /// NM_014965 // downstream // 35705 // Hs.535711 // OIP106 // 22906 // Homo sapiens OGT(O-Glc-NAc transferase)-interacting protein 106	OIP106	OIP106, Homo sapiens for KIAA1042 protein, partial cds. p22.1
SNP_A-1876396	tctgagtgaaccacc[C/T]aagctaccctcagctc	C	T	NM_004624 // downstream // 6401 // Hs.348500 // VIPR1 // 7433 // Homo sapiens vasoactive intestinal peptide receptor 1 (VIPR1), mRNA. /// NM_004206 // downstream // 4002 // Hs.445892 // SEC22L3 // 9117 // Homo sapiens SEC22 vesicle trafficking protein-lik	VIPR1	VIPR1, Homo sapiens vasoactive intestinal peptide receptor 1 (VIPR1), p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1789927	gggctctcatcaggga[A/C]aaacccagggacaata	A	C	NM_032806 // upstream // 75882 // Hs.12313 // FLJ14566 // 84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 117795 // Hs.476052 // SNRK // 54861 // Homo sapiens SNF-1 related kinase (SNRK), mRNA. /// ENST00	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1664494	atctttcaaattctttctctcatc[A/C]aatggactggttttgtctggc ctt	A	C	NM_017719 // upstream // 46945 // Hs.79025 // SNRK // 54861 // SNF-1 related kinase /// NM_032806 // upstream // 149136 // Hs.12313 // FLJ14566 // 84892 // hypothetical protein FLJ14566	SNRK	SNRK , rs10510734 SNF-1 related kinase p22.1
SNP_A-2306408	gctgggtagaaggaaag[C/G]ccaatcacctatgaca	C	G	NM_032806 // upstream // 130732 // Hs.12313 // FLJ14566 // 84892 // Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA. /// NM_017719 // upstream // 62945 // Hs.476052 // SNRK // 54861 // Homo sapiens SNF-1 related kinase (SNRK), mRNA. /// ENST00	FLJ14566	FLJ14566, Homo sapiens hypothetical protein FLJ14566 (FLJ14566), p22.1
SNP_A-1859838	tcagggtcacaaacca[C/G]aaatggcagcatggg	C	G	NM_018075 // intron // 0 // Hs.457131 // FLJ10375 // 55129 // Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA. /// ENST00000350459 // intron // 0 // — // — // — /// ENST00000292246 // intron // 0 // — // — // —	FLJ10375	FLJ10375, Homo sapiens hypothetical protein FLJ10375 (FLJ10375), p22.1
SNP_A-1922358	ttagaaaacattagac[A/G]aagcctggattca	A	G	NM_016006 // intron // 0 // Hs.19385 // ABHD5 // 51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // intron // 0 // — // — // —	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-2136541	atcacctacccagaaa[A/G]ctatctaaataccatc	A	G	NM_016006 // downstream // 62681 // Hs.19385 // ABHD5 // 51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream // 62681 // — // — // — /// ENST00000309765 // upstream // 460406 // — // — //	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-2219632	ccttaaaaagtggcca[A/G]atgacatgaacagaca	A	G	NM_016006 // downstream // 100571 // Hs.19385 // ABHD5 // 51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream // 100571 // — // — // — /// ENST00000309765 // upstream // 422516 // — // —	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-1888642	tgaggccccaccacca[C/G]gtcagtttccagtggc	C	G	NM_016006 // downstream // 141785 // Hs.19385 // ABHD5 // 51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream // 141785 // — // — // — /// ENST00000309765 // upstream // 381302 // — // —	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-1877441	tctggatcagaagaca[A/G]aaccaaattagaaatt	A	G	NM_016006 // downstream // 196078 // Hs.19385 // ABHD5 // 51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream // 196078 // — // — // — /// ENST00000309765 // upstream // 327009 // — // —	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-2223481	cgcttcttgggtcaa[C/T]aatcaaacaatactgc	C	T	NM_016006 // downstream // 490979 // Hs.19385 // ABHD5 // 51099 // Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA. /// ENST00000013894 // downstream // 490979 // — // — // — /// ENST00000309765 // upstream // 32108 // — // — /	ABHD5	ABHD5, Homo sapiens abhydrolase domain containing 5 (ABHD5), p21.33
SNP_A-2241450	ctgagtctcctcaaa[A/G]gctgtctcctaccac	A	G	NM_003278 // downstream // 33586 // Hs.476092 // CLEC3B // 7123 // Homo sapiens tetranectin (plasminogen binding protein) (TNA), mRNA. /// NM_178181 // downstream // 12622 // Hs.476093 // CDCP1 // 64866 // Homo sapiens CUB domain-containing protein 1 (CDC	CLEC3B	CLEC3B, Homo sapiens tetranectin (plasminogen binding protein) (TNA), p21.31
SNP_A-2059908	aatcttattggagtta[C/T]cttatgcacatgagtt	C	T	NM_178181 // upstream // 156142 // Hs.476093 // CDCP1 // 64866 // Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, mRNA. /// NM_022842 // upstream // 156142 // Hs.476093 // CDCP1 // 64866 // Homo sapiens CUB domain-containing pr	CDCP1	CDCP1, Homo sapiens CUB domain-containing protein 1 (CDCP1), transcript variant 2, p21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2249889	cttacaccgagcaata[C/T]aaacagtaggttacac	C	T	NM_014240 // intron // 0 // Hs.193370 // LIMD1 // 8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// ENST00000273317 // intron // 0 // --- // --- // --- // ---	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-1727240	tgtacatctgaacgagttttcacat[A/G]tgcatataccccctgtaacc accacc	A	G	NM_014240 // intron // 0 // Hs.193370 // LIMD1 // 8994 // LIM domains containing 1	LIMD1	LIMD1 , rs2118750, LIM domains containing 1,p21.31
SNP_A-1911668	tgtgaacctaccatcc[A/G]acttcaaaacagtacc	A	G	NM_014240 // downstream // 37471 // Hs.193370 // LIMD1 // 8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 37906 // Hs.413095 // SLC6A20 // 54716 // Homo sapiens solute carrier family 6 (neurotransmitter transpor	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-1972579	tgacctaccatttttg[A/T]aaatcttctcaaattc	A	T	NM_014240 // downstream // 57571 // Hs.193370 // LIMD1 // 8994 // Homo sapiens LIM domains containing 1 (LIMD1), mRNA. /// NM_020208 // downstream // 17806 // Hs.413095 // SLC6A20 // 54716 // Homo sapiens solute carrier family 6 (neurotransmitter transpor	LIMD1	LIMD1, Homo sapiens LIM domains containing 1 (LIMD1), p21.31
SNP_A-1738236	aaaagatagatgccaattatagaac[A/C]aaatttaagaaaactg ttctaaatg	A	C	NM_020208 // intron // 0 // Hs.413095 // SLC6A20 // 54716 // solute carrier family 6 (neurotransmitter transporter), member 20 /// NM_022405 // intron // 0 // Hs.413095 // SLC6A20 // 54716 // solute carrier family 6 (neurotransmitter transporter), member	SLC6A20	SLC6A20 , rs764177, solute carrier family 6 (neurotransmitter transporter), member 20 ,p21.31
SNP_A-1908319	tgtactcctggtaaaa[A/T]ccctctgatctaattc	A	T	NM_024513 // upstream // 16281 // Hs.200227 // FYCO1 // 79443 // Homo sapiens FYVE and coiled-coil domain containing 1 (FYCO1), mRNA. /// NM_006564 // downstream // 63736 // Hs.34526 // CXCR6 // 10663 // Homo sapiens chemokine (C-X-C motif) receptor 6 (CX	FYCO1	FYCO1, Homo sapiens FYVE and coiled-coil domain containing 1 (FYCO1), p21.31
SNP_A-1867667	tccgtttccagcagca[C/T]ggttctatccagcctg	C	T	NM_005283 // upstream // 31101 // Hs.248116 // XCR1 // 2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 149188 // Hs.301921 // CCR1 // 1230 // Homo sapiens chemokine (C-C motif) receptor 1 (CCR1), mRNA. ///	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-1842011	tagggagaggaagtga[C/T]gtgtttaaaagcatga	C	T	NM_005283 // upstream // 87078 // Hs.248116 // XCR1 // 2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 93211 // Hs.301921 // CCR1 // 1230 // Homo sapiens chemokine (C-C motif) receptor 1 (CCR1), mRNA. /// E	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-2116891	aggtcttactctgtgg[G/T]aatttagaaaatcaga	G	T	NM_005283 // upstream // 91402 // Hs.248116 // XCR1 // 2829 // Homo sapiens chemokine (C motif) receptor 1 (XCR1), mRNA. /// NM_001295 // downstream // 88887 // Hs.301921 // CCR1 // 1230 // Homo sapiens chemokine (C-C motif) receptor 1 (CCR1), mRNA. /// E	XCR1	XCR1, Homo sapiens chemokine (C motif) receptor 1 (XCR1), p21.31
SNP_A-1697685	gcactgaaaattgaaacatgaatta[A/G]ctgatgataatattgca atcatttg	A	G	NM_001295 // downstream // 63312 // Hs.301921 // CCR1 // 1230 // chemokine (C-C motif) receptor 1 /// NM_005283 // upstream // 116977 // Hs.248116 // XCR1 // 2829 // chemokine (C motif) receptor 1	CCR1	CCR1 , rs10510749, chemokine (C-C motif) receptor 1 ,p21.31
SNP_A-2181158	cagacagtgtgcccca[A/G]gattaggcaacaggga	A	G	NM_001837 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), t	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-2180906	cagaatgttccctagc[A/G]cttcttcccagtcagt	A	G	NM_001837 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), t	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839056	tagagatctggacaga[C/T]gtaaccttcatgttca	C	T	NM_001837 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), t	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1835635	tacattgagaaatgcc[A/C]atcggcctgtatattc	A	C	NM_001837 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // intron // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), t	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1972590	gtaccacatcctacta[C/T]gatgacgtgggcctgc	C	T	NM_001837 // CDS // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // CDS // 0 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcr	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-2284181	gatatgggcttgaata[A/T]gaaaatacctaatgat	A	T	NM_001837 // downstream // 9799 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // downstream // 9799 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) recept	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-2220032	ccttatttttgaatgg[C/T]actgaatccctataia	C	T	NM_001837 // downstream // 22763 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // downstream // 22763 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) rece	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1841881	taggctgaagattata[A/C]atgtcagctcgcaatg	A	C	NM_001837 // downstream // 23753 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // downstream // 23753 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) rece	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1972591	tccacttggttatagg[C/T]agccttgataacatct	C	T	NM_001837 // downstream // 44285 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // downstream // 44285 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) rece	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-1727451	gtgctgggtgggaaatcatgagac[C/T]cttttctgggacagga gtgtcaca	C	T	NM_000647 // upstream // 27179 // Hs.511794 // CCR2 // 1231 // chemokine (C-C motif) receptor 2 /// NM_000648 // upstream // 27179 // Hs.511794 // CCR2 // 1231 // chemokine (C-C motif) receptor 2 /// NM_001837 // downstream // 60299 // Hs.506190 // CCR3	CCR2	CCR2 , rs2888524, chemokine (C-C motif) receptor 2 ,p21.31
SNP_A-2181093	cagacacttataaata[A/C]ataggcactgttaga	A	C	NM_001837 // downstream // 77062 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // downstream // 77062 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) rece	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-2098504	agagcagagagtggaa[A/G]gttccaggtataaag	A	G	NM_001837 // downstream // 87214 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA. /// NM_178329 // downstream // 87214 // Hs.506190 // CCR3 // 1232 // Homo sapiens chemokine (C-C motif) rece	CCR3	CCR3, Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, p21.31
SNP_A-2280133	gagggagaggttttc[C/T]cagcataaccctcagc	C	T	NM_000647 // downstream // 1542 // Hs.511794 // CCR2 // 1231 // Homo sapiens chemokine (C-C motif) receptor 2 (CCR2), transcript variant A, mRNA. /// NM_000648 // downstream // 1542 // Hs.511794 // CCR2 // 1231 // Homo sapiens chemokine (C-C motif) recept	CCR2	CCR2, Homo sapiens chemokine (C-C motif) receptor 2 (CCR2), transcript variant A, p21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1794515	ggtcctgtattcatgc[C/G]aaagtcacaggggagc	C	G	NM_003965 // downstream // 9705 // Hs.458436 // CCRL2 // 9034 // Homo sapiens chemokine (C-C motif) receptor-like 2 (CCRL2), mRNA. /// NM_002343 // downstream // 16786 // Hs.529517 // LTF // 4057 // Homo sapiens lactotransferrin (LTF), mRNA. /// ENST00000	CCRL2	CCRL2, Homo sapiens chemokine (C-C motif) receptor-like 2 (CCRL2), p21.31
SNP_A-2286565	gatggacaacatatca[A/G]gccataattcaaagta	A	G	NM_003965 // downstream // 25335 // Hs.458436 // CCRL2 // 9034 // Homo sapiens chemokine (C-C motif) receptor-like 2 (CCRL2), mRNA. /// NM_002343 // downstream // 1156 // Hs.529517 // LTF // 4057 // Homo sapiens lactotransferrin (LTF), mRNA. /// ENST00000	CCRL2	CCRL2, Homo sapiens chemokine (C-C motif) receptor-like 2 (CCRL2), p21.31
SNP_A-1900517	tggagctaaaattcac[A/C]atgtgagcctccgcat	A	C	NM_024512 // upstream // 20912 // Hs.543294 // LRRC2 // 79442 // Homo sapiens leucine rich repeat containing 2 (LRRC2), mRNA. /// NM_024750 // upstream // 20912 // Hs.543294 // LRRC2 // 79442 // Homo sapiens leucine rich repeat containing 2 (LRRC2), mRNA.	LRRC2	LRRC2, Homo sapiens leucine rich repeat containing 2 (LRRC2), p21.31
SNP_A-2186048	caggcatacacgtccc[A/G]ctctctcaagaatgcc	A	G	NM_182702 // upstream // 19791 // Hs.450083 // TESSP2 // 339906 // Homo sapiens testis serine protease 2 (TESSP2), mRNA. /// NM_000258 // downstream // 3991 // Hs.517939 // MYL3 // 4634 // Homo sapiens myosin, light polypeptide 3, alkali; ventricular, ske	TESSP2	TESSP2, Homo sapiens testis serine protease 2 (TESSP2), p21.31
SNP_A-1790706	ggggcttgacctgtga[A/G]gagaagttgaggctca	A	G	ENST00000313063 // intron // 0 // — // — // — // —	-	p21.31
SNP_A-2245648	ctgggcccaggaaagc[A/G]gaagacacctttacct	A	G	NM_003458 // intron // 0 // Hs.194684 // BSN // 8927 // Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // — // — // — // —	BSN	BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-2067663	acaacaaggacaggcc[A/G]atgtgcagaagggcag	A	G	NM_003458 // intron // 0 // Hs.194684 // BSN // 8927 // Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // — // — // — // —	BSN	BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-1896623	tgctagggacttggaa[A/T]cataggaccctgtggg	A	T	NM_003458 // intron // 0 // Hs.194684 // BSN // 8927 // Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // — // — // — // —	BSN	BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-2223565	cggaatggaaacgagc[A/G]gaagaataagggaatg	A	G	NM_003458 // intron // 0 // Hs.194684 // BSN // 8927 // Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // — // — // — // —	BSN	BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-1943135	ttggtcagagcactta[A/G]cattaggtctgcttcc	A	G	NM_003458 // intron // 0 // Hs.194684 // BSN // 8927 // Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA. /// ENST00000296452 // intron // 0 // — // — // — // —	BSN	BSN, Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), p21.31
SNP_A-2071813	acagactcacagtttc[A/G]agccctgagcttatct	A	G	NM_153273 // upstream // 5687 // Hs.438691 // IHPK1 // 9807 // Homo sapiens inositol hexaphosphate kinase 1 (IHPK1), mRNA. /// ENST00000321599 // upstream // 5687 // — // — // — // — /// ENST00000343366 // downstream // 6012 // — // — // — // — /	IHPK1	IHPK1, Homo sapiens inositol hexaphosphate kinase 1 (IHPK1), p21.31
SNP_A-1750375	ggtctctcctgctttgattttagta[A/C]aagtggactctgccattctct gcct	A	C	NM_004186 // intron // 0 // Hs.32981 // SEMA3F // 6405 // sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEMA3F	SEMA3F , rs2624842, sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F,p21.31
SNP_A-1781320	ggatgtgagtccttgc[A/G]cagtggtgaaatgtag	A	G	NM_004186 // intron // 0 // Hs.32981 // SEMA3F // 6405 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), mRNA. /// ENST00000002829 // intron // 0 // – // — // — // —	SEMA3F	SEMA3F, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F (SEMA3F), p21.31
SNP_A-1972619	cttaagccaatcatga[A/G]gctcaccaggcaaggt	A	G	NM_006030 // intron // 0 // Hs.476273 // CACNA2D2 // 9254 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 2 (CACNA2D2), transcript variant 2, mRNA. /// ENST00000266039 // intron // 0 // — // — // — // — /// ENST0000036096	CACNA2D2	CACNA2D2, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.31
SNP_A-2237373	ctctcccatcaacgag[A/G]cagtaataaattaaga	A	G	NM_004635 // intron // 0 // Hs.234521 // MAPKAPK3 // 7867 // Homo sapiens mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), mRNA. /// ENST00000357955 // intron // 0 // — // — // — // — /// ENST00000266033 // intron // 0 // –	MAPKAPK3	MAPKAPK3, Homo sapiens mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), p21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1910547	tgtcctaagtcattta[C/T]actcaagtctctcatc	C	T	NM_004947 // intron // 0 // Hs.476284 // DOCK3 // 1795 // Homo sapiens dedicator of cytokinesis 3 (DOCK3), mRNA. /// ENST00000266037 // intron // 0 // --- // --- // --- // ---	DOCK3	DOCK3, Homo sapiens dedicator of cytokinesis 3 (DOCK3), p21.31
SNP_A-1700307	ccacacctagacagacagagaaaga[G/T]aaaatgtgacagt ctaagaacttaa	G	T	NM_004947 // intron // 0 // Hs.7022 // DOCK3 // 1795 // dedicator of cytokinesis 3	DOCK3	DOCK3 , rs2170177, dedicator of cytokinesis 3,p21.31
SNP_A-1957533	ttttatagtaccatca[A/G]tagtaggcggaaatga	A	G	NM_013286 // downstream // 146179 // Hs.476291 // RBM15B // 29890 // Homo sapiens chromosome 3p21.1 gene sequence (HUMAGCGB), mRNA. /// NM_014703 // upstream // 50726 // Hs.118738 // VprBP // 9730 // Homo sapiens Vpr-binding protein (VprBP), mRNA. /// NM_	RBM15B	RBM15B, Homo sapiens chromosome 3p21.1 gene sequence (HUMAGCGB), p21.2
SNP_A-2309510	ggaaacatggtgcgcc[A/G]gacgttactgcaggca	A	G	NM_000839 // downstream // 60329 // Hs.121510 // GRM2 // 2912 // Homo sapiens glutamate receptor, metabotropic 2 (GRM2), mRNA. /// NM_203424 // upstream // 82693 // Hs.412294 // IQCF2 // 389123 // Homo sapiens IQ motif containing F2 (IQCF2), mRNA. /// NM_	GRM2	GRM2, Homo sapiens glutamate receptor, metabotropic 2 (GRM2), p21.2
SNP_A-2045906	aagaccaccatccagc[C/T]caccaatcacaacttg	C	T	NM_000992 // upstream // 54082 // Hs.425125 // RPL29 // 6159 // Homo sapiens ribosomal protein L29 (RPL29), mRNA. /// NM_001947 // downstream // 364 // Hs.3843 // DUSP7 // 1849 // Homo sapiens dual specificity phosphatase 7 (DUSP7), mRNA. /// ENST00000294	RPL29	RPL29, Homo sapiens ribosomal protein L29 (RPL29), p21.2
SNP_A-2024469	aaaaggacatacatga[A/G]gaattgccaaaacgga	A	G	NM_206826 // CDS // 0 // Hs.313544 // GNL3 // 26354 // Homo sapiens nucleostemin (NS), transcript variant 3, mRNA. /// NM_014366 // CDS // 0 // Hs.313544 // GNL3 // 26354 // Homo sapiens nucleostemin (NS), transcript variant 1, mRNA. /// NM_206825 // CDS	GNL3	GNL3, Homo sapiens nucleostemin (NS), transcript variant 3, p21.1
SNP_A-2172939	cacaaaactccgtcaa[C/T]cttattatttgctact	C	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2072324	acagcaaattggaaaa[A/G]gctgaaatgcttctct	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2269474	gacaaaagcaaagcaa[A/G]gctagtgaattcaata	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2025606	aaaatgaagcaagata[A/G]aggcagctgaatactg	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2160354	atttcaggcctgtcac[A/G]aatcctgatttaccat	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2023302	aaaaccagactctaag[C/G]cccttcgacagcccag	C	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-1907176	tggtttcgattaatac[C/G]acactggtggcttcag	C	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // --- // --- // --- // ---	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2304155	gctcccctccacataa[C/T]cttcatatgccaagcc	C	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p21.1
SNP_A-1903804	tgggataatgataccc[A/C]agtactctcttgcttt	A	C	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p21.1
SNP_A-2298412	gccatttgaaaattac[A/G]agagaagaaagaaaga	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-1837035	tactggtcaacaaata[C/T]ctccacagtgactagt	C	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-2038724	aacagataaagcagta[A/C]ggacttggcctggact	A	C	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2119547	agtatcttctctgcta[G/T]gtattgccaaatccaa	G	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-1916606	tgtttataataggtaa[A/G]tgttgattgagcagag	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-1797763	ggtttgtgtgtactta[G/T]ctaatttttaaagaag	G	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-1741181	gctagacatgaaattcttcataaac[C/G]tgacctggacggtgtga ggaggagc	C	G	NM_018398 // intron // 0 // Hs.435112 // CACNA2D3 // 55799 // calcium channel, voltage-dependent, alpha 2/delta 3 subunit	CACNA2D3	CACNA2D3 , rs1526594, calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-2212587	cccttcacctctacca[A/G]agatggagtgcccact	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2174088	cacaccctgcaactac[G/T]gaatgctttcctgaac	G	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-1862114	tcatgctaagttgtaa[C/T]tggttggtttcctgaa	C	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2246472	ctggttttacctgatg[A/T]aggctgtcggggtgct	A	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2035856	aaatgttctccttgtc[A/G]ccagctttcaggaagt	A	G	NM_018398 // CDS // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // CDS // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289310	gatttgttcactcacc[A/T]atttaaacatgtttct	A	T	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2,p14.3
SNP_A-2057458	aatatccttctttatg[A/G]acgtagtgactacttt	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2093862	agaagattccatgtcc[A/G]gataataggactcagg	A	G	NM_018398 // intron // 0 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// ENST00000288197 // intron // 0 // — // — // — // —	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-1802352	gtatcaactctataaa[G/T]tcgggagcaaagtcct	G	T	NM_018398 // downstream // 12945 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// NM_020678 // upstream // 159455 // Hs.128594 // HT017 // 57408 // Homo sapiens HT017 prote	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-1791030	ggggtccaggagagct[A/C]agagaatgggtttcaa	A	C	NM_018398 // downstream // 13318 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// NM_020678 // upstream // 159828 // Hs.128594 // HT017 // 57408 // Homo sapiens HT017 prote	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2159673	atttagaggaattcca[A/G]tactcacatcaatggg	A	G	NM_018398 // downstream // 112104 // Hs.369421 // CACNA2D3 // 55799 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit (CACNA2D3), mRNA. /// NM_020678 // upstream // 258614 // Hs.128594 // HT017 // 57408 // Homo sapiens HT017 prot	CACNA2D3	CACNA2D3, Homo sapiens calcium channel, voltage-dependent, alpha 2 p14.3
SNP_A-2138986	atccgttcagggaggc[C/T]gattcacaggagtcca	C	T	NM_015576 // intron // 0 // Hs.476389 // CAST // 26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // — // — // — // —	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2266139	gaaggcttttgctttc[A/G]ctgtgaacgaggaggg	A	G	NM_015576 // intron // 0 // Hs.476389 // CAST // 26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // — // — // — // —	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-1747441	tctatgagaaagaaatattaagtaa[C/T]actgcatgtctgacattg acatgag	C	T	AB002376 // intron // 0 // Hs.476384 // CAST // 26059 // CAZ-associated structural protein	CAST	CAST , rs10510779, CAZ-associated structural protein,p14.3
SNP_A-1723756	aaacttggtttaaaaacctgaagct[A/G]agcaacctctccaaat aaacatgaa	A	G	AB002376 // intron // 0 // Hs.476384 // CAST // 26059 // CAZ-associated structural protein	CAST	CAST , rs10510780, CAZ-associated structural protein,p14.3
SNP_A-1858994	tcagcatacagtgttc[A/C]atataagcaagttcaa	A	C	NM_015576 // intron // 0 // Hs.476389 // CAST // 26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // — // — // — // —	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-1675553	caagcagattccctaagatgataaa[C/T]agagcactttatgaga ggtatgaac	C	T	AB002376 // intron // 0 // Hs.476384 // CAST // 26059 // CAZ-associated structural protein	CAST	CAST , rs9311594, CAZ-associated structural protein,p14.3
SNP_A-2231542	ctatttcagaaagatc[A/G]atgaaccgagaaagag	A	G	NM_015576 // intron // 0 // Hs.476389 // CAST // 26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // — // — // — // —	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2301045	gccttatagctggtca[A/T]gttccatggcaggtgt	A	T	NM_015576 // intron // 0 // Hs.476389 // CAST // 26059 // Homo sapiens CAZ-associated structural protein (CAST), mRNA. /// ENST00000288221 // intron // 0 // — // — // — // —	CAST	CAST, Homo sapiens CAZ-associated structural protein (CAST), p14.3
SNP_A-2204901	ccagggagatgataca[C/T]gaaataagattatatt	C	T	NM_015224 // intron // 0 // Hs.476399 // RAP140 // 23272 // Homo sapiens retinoblastoma-associated protein 140 (RAP140), mRNA. /// ENST00000355628 // intron // 0 // — // — // — // — /// ENST00000296314 // intron // 0 // — // — // — // — //	RAP140	RAP140, Homo sapiens retinoblastoma-associated protein 140 (RAP140), p14.3
SNP_A-1846186	tatatcattcatatcc[C/G]agagtgtgtcctgaaa	C	G	ENST00000338458 // intron // 0 // — // — // — // —	-	p14.3
SNP_A-1972712	cagggtttcatgatta[C/G]caagtggcagagcctg	C	G	ENST00000338458 // intron // 0 // — // — // — // —	-	p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137644	atcatgaatgtcatca[A/G]taactactaactgcca	A	G	NM_198564 // intron // 0 // Hs.128146 // FLJ44290 // 375347 // Homo sapiens FLJ44290 protein (FLJ44290), mRNA. /// ENST00000311202 // intron // 0 // — // — // — // —	FLJ44290	FLJ44290, Homo sapiens FLJ44290 protein (FLJ44290), p14.3
SNP_A-2080060	accgcacccagcaaaa[A/G]taacgatggttagatg	A	G	NM_001660 // upstream // 22183 // Hs.148330 // ARF4 // 378 // Homo sapiens ADP-ribosylation factor 4 (ARF4), mRNA. /// NM_001001794 // downstream // 5885 // Hs.530380 // MGC33692 // 414918 // Homo sapiens similar to RIKEN cDNA 1700027J05 gene (MGC33692),	ARF4	ARF4, Homo sapiens ADP-ribosylation factor 4 (ARF4), p14.3
SNP_A-2114709	agggatctgaaacaaa[C/T]tgattggaagagagga	C	T	NM_007159 // intron // 0 // Hs.476432 // SLMAP // 7871 // Homo sapiens sarcolemma associated protein (SLMAP), mRNA. /// ENST00000295952 // intron // 0 // — // — // — // — /// ENST00000295951 // intron // 0 // — // — // — // —	SLMAP	SLMAP, Homo sapiens sarcolemma associated protein (SLMAP), p14.3
SNP_A-2092471	agaaagtcttgctaaa[C/G]tgggaaggaaccttgc	C	G	NM_007159 // downstream // 45539 // Hs.476432 // SLMAP // 7871 // Homo sapiens sarcolemma associated protein (SLMAP), mRNA. /// NM_001457 // upstream // 35302 // Hs.476448 // FLNB // 2317 // Homo sapiens filamin B, beta (actin binding protein 278) (FLNB),	SLMAP	SLMAP, Homo sapiens sarcolemma associated protein (SLMAP), p14.3
SNP_A-1905818	tggtcaccatcactta[A/G]gataacgtacatataa	A	G	NM_017771 // intron // 0 // Hs.190544 // PXK // 54899 // Homo sapiens PX domain containing serine/threonine kinase (PXK), mRNA. /// ENST00000302779 // intron // 0 // — // — // — // — /// ENST00000356151 // intron // 0 // — // — // — // —	PXK	PXK, Homo sapiens PX domain containing serine p14.3
SNP_A-2304194	gctcccttgtcaaagg[A/C]aaaaaggtgcatttat	A	C	NM_017771 // intron // 0 // Hs.190544 // PXK // 54899 // Homo sapiens PX domain containing serine/threonine kinase (PXK), mRNA. /// ENST00000302779 // intron // 0 // — // — // — // — /// ENST00000356151 // intron // 0 // — // — // — // —	PXK	PXK, Homo sapiens PX domain containing serine p14.3
SNP_A-1846609	tatatttcaaagataa[C/T]tggaggaaggattcaa	C	T	NM_017771 // intron // 0 // Hs.190544 // PXK // 54899 // Homo sapiens PX domain containing serine/threonine kinase (PXK), mRNA. /// ENST00000302779 // intron // 0 // — // — // — // — /// ENST00000356151 // intron // 0 // — // — // — // —	PXK	PXK, Homo sapiens PX domain containing serine p14.3
SNP_A-1739637	gttgtagcactcatcagcaactgaa[A/G]tgatatgacttcggtgtttattgtc	A	G	NM_153331 // intron // 0 // Hs.13982 // KCTD6 // 200845 // potassium channel tetramerisation domain containing 6	KCTD6	KCTD6 , rs753819, potassium channel tetramerisation domain containing 6,p14.2
SNP_A-1972733	tcggtgtttattgtcc[A/G]tctcctctgccattcc	A	G	NM_007177 // upstream // 50929 // Hs.8022 // TU3A // 11170 // Homo sapiens TU3A protein (TU3A), mRNA. /// NM_007177 // upstream // 1083 // Hs.8022 // TU3A // 11170 // Homo sapiens TU3A protein (TU3A), mRNA. /// NM_138805 // downstream // 5255 // Hs.61265	TU3A	TU3A, Homo sapiens TU3A protein (TU3A), p14.2
SNP_A-2050187	aaggactcaagggcag[C/T]cagtatatttgggagg	C	T	NM_007177 // upstream // 55772 // Hs.8022 // TU3A // 11170 // Homo sapiens TU3A protein (TU3A), mRNA. /// NM_007177 // upstream // 5926 // Hs.8022 // TU3A // 11170 // Homo sapiens TU3A protein (TU3A), mRNA. /// NM_138805 // downstream // 412 // Hs.61265 /	TU3A	TU3A, Homo sapiens TU3A protein (TU3A), p14.2
SNP_A-2312676	ggactacttgctcaca[A/G]tgcttctgtttctggg	A	G	NM_138805 // intron // 0 // Hs.61265 // FAM3D // 131177 // Homo sapiens family with sequence similarity 3, member D (FAM3D), mRNA. /// ENST00000358781 // intron // 0 // — // — // — // —	FAM3D	FAM3D, Homo sapiens family with sequence similarity 3, member D (FAM3D), p14.2
SNP_A-2236649	ctctaactctaaataa[A/G]tgacataactgaacat	A	G	NM_198463 // upstream // 690048 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 144458 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-1972753	atcaagaactacgtgg[A/T]gacaaaagtgctataa	A	T	NM_198463 // upstream // 695096 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 139410 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1830829	taatctgcctctcta[C/T]gttctgcacattaaag	C	T	NM_198463 // upstream // 703772 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 130734 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2145194	atgcaatgggcaatgaj[A/G]tatctacgtacctgtt	A	G	NM_198463 // upstream // 722431 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 112075 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2120372	agtcatgcaagcaaga[G/T]ggtcaacgtcagatac	G	T	NM_198463 // upstream // 722519 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 111987 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2070102	acacatcaatgaaata[A/G]taaactcctggatgag	A	G	NM_198463 // upstream // 797157 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 37349 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST0000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2109846	aggaacactggcctca[A/G]taagtcttgcgagg	A	G	NM_198463 // upstream // 797984 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 36522 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST0000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-2285006	gatcctagaatattca[G/T]agccttcagtaacctt	G	T	NM_198463 // upstream // 802448 // Hs.368434 // FLJ42117 // 200844 // Homo sapiens FLJ42117 protein (FLJ42117), mRNA. /// NM_002012 // downstream // 32058 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST0000	FLJ42117	FLJ42117, Homo sapiens FLJ42117 protein (FLJ42117), p14.2
SNP_A-1859342	tcagcttctggttgaa[C/T]gagggcatgataagtt	C	T	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1972771	gaggtgggtgtgctaa[A/C]atggagatacaagcca	A	C	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1972773	gactgccacaacgaac[A/G]catttgtaggctttcc	A	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1972778	caacaatgacacaata[A/G]atgtcttagccctctag	A	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1832184	taatttgaggaactaa[C/T]ggtactagcatttaac	C	T	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1941122	ttgctcttgttgata[C/G]agccaagaggaggaaa	C	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2022904	aaaacaagagcctcta[A/C]gtactgaagtgatagg	A	C	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2046273	aagagaaagaatatgaj[A/G]gttcagcatatctcct	A	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1941427	ttgcttgaagcactaa[C/T]attcttataatgttt	C	T	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1932762	ttccttgacatgtgca[A/G]accgcaaaggaagtga	A	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1680492	gtcaccaacagaatcattattagaa[A/G]tagactgtctgaatttatg aacatgg	A	G	NM_002012 // intron // 0 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene	FHIT	FHIT , rs6788821, fragile histidine triad gene,p14.2
SNP_A-1807454	gtctgcactgagcctc[A/C]agcaatttgtcaaaat	A	C	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1972812	acactatgccaggaat[A/G]agcatctacagtgtat	A	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1880774	tcttggcttatgca[A/G]cctctagtaaaataac	A	G	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1928810	ttcagagaatagatca[C/T]gagacttctcggcctc	C	T	NM_002012 // intron // 0 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // intron // 0 // — // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1831230	taatggaatacttcat[C/T]ggcaatatatagcttt	C	T	NM_002012 // upstream // 8547 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // upstream // 8547 // — // — // — /// ENST00000240820 // downstream // 144716 // — // — // — // -	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-2252467	ctctcctcatttttgca[A/G]tgaaaccagggtgcaa	A	G	NM_002012 // upstream // 20980 // Hs.196981 // FHIT // 2272 // Homo sapiens fragile histidine triad gene (FHIT), mRNA. /// ENST00000341848 // upstream // 20980 // — // — // — // — /// ENST00000240820 // downstream // 132283 // — // — // — // —	FHIT	FHIT, Homo sapiens fragile histidine triad gene (FHIT), p14.2
SNP_A-1700221	tacagcctgtgctaagttcaaaga[A/G]gaggcagataaacttga agatttta	A	G	NM_002012 // intron // 0 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene	FHIT	FHIT , rs10510852, fragile histidine triad gene,p14.2
SNP_A-2137198	atcagtaagttgtaaa[C/T]gttagaccactatttt	C	T	NM_002841 // upstream // 860471 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 10320 // — // — // — // — /// ENST00000295874 // upstream // 860471 // -	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2281736	gagtgaacaataaatta[A/C]ctcgacatttaaaac	A	C	NM_002841 // upstream // 854951 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 15840 // — // — // — // — /// ENST00000295874 // upstream // 854951 // -	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1958173	ttttcatggtaaaagc[A/C]agagagaacactgtag	A	C	NM_002841 // upstream // 639230 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 231561 // — // — // — // — /// ENST00000295874 // upstream // 639230 //	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2243088	ctgcccttcctcataq[A/G]gcattctacatagcac	A	G	NM_002841 // upstream // 623288 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 247503 // — // — // — // — /// ENST00000295874 // upstream // 623288 //	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2008743	aatgtggttatcacca[C/T]gtaatgaagacctgcc	C	T	NM_002841 // upstream // 587079 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 283712 // — // — // — // — /// ENST00000295874 // upstream // 587079 //	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1655725	tttgggaagaattaaaagtgtgtga[C/T]gtattaaaagcagcataa tgatatt	C	T	NM_002012 // intron // 0 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene	FHIT	FHIT , rs10510860, fragile histidine triad gene,p14.2
SNP_A-2049906	aaggaaccagcatctat[C/G]aataaggagtagaaca	C	G	NM_002841 // upstream // 381700 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 489091 // --- // --- // --- /// ENST00000295874 // upstream // 381700 //	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1673018	ggaggcccagaggaaattaagtgt[A/G]gaagagatttcctag agggagtgat	A	G	M96843 // downstream // 856697 // Hs.476554 // ID2B // 84099 // inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein /// NM_002012 // upstream // 15345 // Hs.408289 // FHIT // 2272 // fragile histidine triad gene /// NM_002841 // upstr	ID2B	ID2B , rs815719, inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein ,p14.2
SNP_A-1972860	gaaataatactgaaaa[A/G]gttacgccctttgat	A	G	NM_002841 // upstream // 293355 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000240820 // upstream // 577436 // --- // --- // --- /// ENST00000295874 // upstream // 293355 //	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2053502	aagtgcatggaagaac[C/T]gcatttttgatttgtt	C	T	NM_002841 // intron // 0 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // --- // --- /// ENST00000354627 // intron // 0 // --- // --- //	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1972878	aaaatttcattcagta[C/G]caatgcctaaactgga	C	G	NM_002841 // intron // 0 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1870564	tcgagtgaaccctaca[A/T]acgtctaaaacctgtc	A	T	NM_002841 // intron // 0 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2197804	caltgaatacctgcca[A/G]ataagacatgtaacca	A	G	NM_002841 // intron // 0 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-2228144	ctactagactcagaaa[G/T]ttgacgggccctttg	G	T	NM_002841 // intron // 0 // Hs.386866 // PTPRG // 5793 // Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA. /// ENST00000295874 // intron // 0 // --- // --- // ---	PTPRG	PTPRG, Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), p14.2
SNP_A-1859097	tcagccccccaaaccc[A/G]agcgcggagcgcgctg	A	G	NM_018008 // upstream // 1350 // Hs.241523 // ZNF312 // 55079 // Homo sapiens zinc finger protein 312 (ZNF312), mRNA. /// NM_183393 // downstream // 23651 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript	ZNF312	ZNF312, Homo sapiens zinc finger protein 312 (ZNF312), p14.2
SNP_A-1972898	ccttacagggaaaaga[C/T]aacgatggctccaatg	C	T	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2230171	ctatactatattagaa[A/T]gtgtgtcaaatgcaag	A	T	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2241866	ctgatgctcggttccaa[C/T]agagaacataaactct	C	T	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2241580	ctgataagtttatcaa[C/T]ctgtgtgctgatga	C	T	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1643065	tcaggaaactgctgagatattaacc[G/T]gaaaatcatttgggtttc acttcat	G	T	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs10510884, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-1650918	ctaggaataccacctggctatgcta[C/T]agaagacaagaagctt agatttgc	C	T	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs1506746, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-1734866	ttcctagttgagtaactatttgctca[G/T]ttattctcatcatgtagta catg	G	T	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs2886937, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-1658196	caggtaaagtatggacctgtgacta[C/T]agaacattttcgtgag gggaagga	C	T	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs1561336, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-2095258	agaattggaactggca[A/G]cttaagcctggtctt	A	G	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1851943	tattgcaaaatatatat[C/G]cagagtttagacttta	C	G	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1700384	gggccatcagaattggaaggccaaa[C/G]taattcctctatgcac tgtatttaa	C	G	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs488273, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-1682684	ctttcacaaacaattgtctcatttttg[A/T]acttcctcatagtcttgtgaa gtag	A	T	AB032947 // intron // 0 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion	CADPS	CADPS , rs543060, Ca2+-dependent activator protein for secretion,p14.2
SNP_A-2164866	caaaccggttccttc[C/T]catcttcgaaaataac	C	T	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1942598	ttgggaagcactggac[C/G]gggtaggaatgtgac	C	G	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2057908	aatattctgcaggcca[C/T]tccttcaaaggtacc	C	T	NM_183393 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (C	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1720441	aaaatgccaaggatctggtactcaa[C/T]tgaagaaaaggtcat ctggaaagct	C	T	NM_003716 // upstream // 535153 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion /// NM_144642 // upstream // 433874 // Hs.26411 // SYNPR // 132204 // synaptoporin	CADPS	CADPS , rs10510892, Ca2+-dependent activator protein for secretion ,p14.2
SNP_A-2298288	gccatgtgaactctta[A/G]catcttatcctattgt	A	G	NM_183393 // upstream // 194128 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 194128 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretio	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-1840688	tagccttttcaaaga[C/T]gaccagcaaggctctc	C	T	NM_183393 // upstream // 291853 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 291853 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretio	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1748865	tgggaaaagggaagtgaggaagaaa[C/T]aggtggaaaaagc aaatacaagtga	C	T	NM_003716 // upstream // 787931 // Hs.441050 // CADPS // 8618 // Ca2+-dependent activator protein for secretion /// NM_144642 // upstream // 181096 // Hs.26411 // SYNPR // 132204 // synaptoporin	CADPS	CADPS, rs2367773, Ca2+-dependent activator protein for secretion ,p14.2
SNP_A-1972943	gtctatcaacaacaca[A/G]tcacttgtcaaatctt	A	G	NM_183393 // upstream // 493472 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, mRNA. /// NM_183394 // upstream // 493472 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretio	CADPS	CADPS, Homo sapiens Ca2+-dependent secretion activator (CADPS), transcript variant 3, p14.2
SNP_A-2281820	gagtgagcttaaaaaa[A/C]tatattgctcatgg	A	C	NM_144642 // intron // 0 // Hs.441275 // SYNPR // 132204 // Homo sapiens synaptoporin (SYNPR), mRNA. /// ENST00000295894 // intron // 0 // — // — // —	SYNPR	SYNPR, Homo sapiens synaptoporin (SYNPR), p14.2
SNP_A-1911649	tgtgaaatgtgataa[C/T]tgtggtgatttttt	C	T	NM_144642 // intron // 0 // Hs.441275 // SYNPR // 132204 // Homo sapiens synaptoporin (SYNPR), mRNA. /// ENST00000295894 // intron // 0 // — // — // —	SYNPR	SYNPR, Homo sapiens synaptoporin (SYNPR), p14.2
SNP_A-2172154	caatgtaagaaaaaaa[C/T]gcttgtatacttggat	C	T	ENST00000343837 // intron // 0 // — // — // —	-	p14.2
SNP_A-2143055	atgaatgcacatgact[C/G]aactcactacatcttg	C	G	ENST00000343837 // intron // 0 // — // — // —	-	p14.2
SNP_A-1839843	tagattctataattga[C/T]atctctcccagaggag	C	T	NM_025075 // downstream // 166300 // Hs.288151 // NIF3L1BP1 // 80145 // Homo sapiens Ngg1 interacting factor 3 like 1 binding protein 1 (NIF3L1BP1), mRNA. /// ENST00000343837 // downstream // 3476 // — // — // — /// ENST00000295896 // upstrea	NIF3L1BP1	NIF3L1BP1, Homo sapiens Ngg1 interacting factor 3 like 1 binding protein 1 (NIF3L1BP1), p14.2
SNP_A-2143624	atgacttctaatctaa[C/T]tgtctgaggtcaaggt	C	T	NM_025075 // downstream // 165592 // Hs.288151 // NIF3L1BP1 // 80145 // Homo sapiens Ngg1 interacting factor 3 like 1 binding protein 1 (NIF3L1BP1), mRNA. /// ENST00000343837 // downstream // 4184 // — // — // — /// ENST00000295896 // upstrea	NIF3L1BP1	NIF3L1BP1, Homo sapiens Ngg1 interacting factor 3 like 1 binding protein 1 (NIF3L1BP1), p14.2
SNP_A-1958094	tttcaggtaccacca[G/T]gatattgcaattatag	G	T	NM_025075 // downstream // 106302 // Hs.288151 // NIF3L1BP1 // 80145 // Homo sapiens Ngg1 interacting factor 3 like 1 binding protein 1 (NIF3L1BP1), mRNA. /// ENST00000343837 // downstream // 63474 // — // — // — /// ENST00000295896 // upstre	NIF3L1BP1	NIF3L1BP1, Homo sapiens Ngg1 interacting factor 3 like 1 binding protein 1 (NIF3L1BP1), p14.2
SNP_A-1972969	ccagttgagatgtact[C/G]agaagggcacactatc	C	G	NM_198859 // intron // 0 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // — // — // —	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2269673	gacaacatgcgtaaaa[A/G]tgcttaaaagtgaca	A	G	NM_198859 // intron // 0 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // — // — // —	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2095527	agacaagcctgtgaa[A/G]acgcacttggatggca	A	G	NM_198859 // intron // 0 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// ENST00000295902 // intron // 0 // — // — // —	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2263329	gaacatacttgaacta[C/T]aagacagcaagtagta	C	T	NM_198859 // upstream // 24296 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 265906 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2217075	cctcttcccaccgtca[C/T]gcgtcctgggtcctgg	C	T	NM_198859 // upstream // 27191 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 263011 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-1972978	ctgcaagggctttctg[C/T]tcaaatatgttatgat	C	T	NM_198859 // upstream // 34134 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 256068 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2239370	ctctttcccgaaagca[C/T]tcctcagtaatccaat	C	T	NM_198859 // upstream // 157155 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 133047 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-1959190	ttttgagaagcatggat[C/T]gaaagcgtagaatgtg	C	T	NM_198859 // upstream // 161476 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 128726 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-1972994	agacaagatcaatgaa[A/C]ctccagtggattctaa	A	C	NM_198859 // upstream // 213842 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 76360 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2277686	gagcagatggaaattc[G/T]atctagagctcagggt	G	T	NM_198859 // upstream // 271984 // Hs.148105 // PRICKLE2 // 166336 // Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), mRNA. /// NM_182920 // downstream // 18218 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (	PRICKLE2	PRICKLE2, Homo sapiens prickle-like 2 (Drosophila) (PRICKLE2), p14.1
SNP_A-2265507	gaagcccggaagcttg[A/C]acgctggcacctacac	A	C	NM_182920 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // H	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2183290	cagcacaccaaaccca[A/T]attcgctgcaccata	A	T	NM_182920 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // H	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript .p14.1
SNP_A-2303772	gctcaggagctattag[A/G]attttttgtatcga	A	G	NM_182920 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // H	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript .p14.1
SNP_A-2083737	actacagtgatcaaaa[C/T]agtctactggcataag	C	T	NM_182920 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // intron // 0 // Hs.476604 // ADAMTS9 // 56999 // H	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2091752	agaaaagtcaagttgat[A/G]aaacctgctgggcctg	A	G	NM_182920 // upstream // 38539 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 38539 // Hs.476604 // ADAMTS9 /	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript .p14.1
SNP_A-1898776	tgctttctgagtagga[G/T]acaatgagtggattg	G	T	NM_182920 // upstream // 39579 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 39579 // Hs.476604 // ADAMTS9 /	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-1817989	gttctagaccctggga[A/G]aaaaggtagacatgc	A	G	NM_182920 // upstream // 226869 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 226869 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript .p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1790083	ggggaagaagcttttа[C/T]aggatgaacatggaag	C	T	NM_182920 // upstream // 232133 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 232133 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-1973011	agactgtgggttagac[C/T]aagcataaagcattcc	C	T	NM_182920 // upstream // 234284 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 234284 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2311296	ggaatacccacttcac[A/G]atattccttgaactgt	A	G	NM_182920 // upstream // 248215 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 248215 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript p14.1
SNP_A-2058976	aatccatcattctgta[C/T]gttcagcctatctcct	C	T	NM_182920 // upstream // 250529 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 250529 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-1753165	attgcccagtagactagatttggaa[C/G]cactagaaatttagtcctgtaagac	C	G	NM_004742 // downstream // 375749 // Hs.169441 // BAIAP1 // 9223 // BAI1-associated protein 1 /// NM_020249 // upstream // 296958 // Hs.318751 // ADAMTS9 // 56999 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 moti	BAIAP1	BAIAP1 , rs10510917, BAI1-associated protein 1 ,p14.1
SNP_A-1647214	ctgacaccctattttgccttcttta[G/T]agcttcatatttatacctaaaacct	G	T	NM_004742 // downstream // 375449 // Hs.169441 // BAIAP1 // 9223 // BAI1-associated protein 1 /// NM_020249 // upstream // 297258 // Hs.318751 // ADAMTS9 // 56999 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 moti	BAIAP1	BAIAP1 , rs10514722, BAI1-associated protein 1 ,p14.1
SNP_A-1973020	atgccccaaagtggca[A/G]tcttcacagctcctct	A	G	NM_182920 // upstream // 480150 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 480150 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-1973021	acattggataactctc[C/T]acattcaggctaggca	C	T	NM_182920 // upstream // 480334 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 480334 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-1683556	tatctatgactaataagcaattata[C/T]ggagactttcccactgacaaccata	C	T	NM_004742 // downstream // 103868 // Hs.169441 // BAIAP1 // 9223 // BAI1-associated protein 1 /// NM_020249 // upstream // 568839 // Hs.318751 // ADAMTS9 // 56999 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 moti	BAIAP1	BAIAP1 , rs781300, BAI1-associated protein 1 ,p14.1
SNP_A-2072598	acagcccagactctgc[C/T]atcaaagacaactgtg	C	T	NM_182920 // upstream // 560702 // Hs.476604 // ADAMTS9 // 56999 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript /// NM_020249 // upstream // 560702 // Hs.476604 // ADAMTS9	ADAMTS9	ADAMTS9, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (ADAMTS9), transcript ,p14.1
SNP_A-1866671	tcccctcaaaggacta[C/T]gaaaatctagtaccta	C	T	NM_004742 // intron // 0 // Hs.169441 // BAIAP1 // 9223 // Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // — // — // — // — /// ENST00000295884 // intron // 0 // — // — // — // — /// ENST0000033	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2096622	agacgccttgatgaggt[C/T]acatttagagtgagat	C	T	NM_004742 // intron // 0 // Hs.169441 // BAIAP1 // 9223 // Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- /// ENST00000295884 // intron // 0 // --- // --- // --- /// ENST0000033	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-2113893	aggctgtggtcactaa[A/T]ctgtaatgcatctta	A	T	NM_004742 // intron // 0 // Hs.169441 // BAIAP1 // 9223 // Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA. /// ENST00000330909 // intron // 0 // --- // --- // --- /// ENST00000295884 // intron // 0 // --- // --- // --- /// ENST0000033	BAIAP1	BAIAP1, Homo sapiens BAI1-associated protein 1 (BAIAP1), p14.1
SNP_A-1946208	tttaaaaagaaaccaa[C/G]actaacagatgctac	C	G	NM_173471 // intron // 0 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// ENST00000354883 // intron // 0 // --- // --- // --- /// ENST00000336733 // intron // 0 // --- // --- // ---	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-1833372	tacagaagatctaggaa[G/T]agagtgtctctggaaa	G	T	NM_173471 // intron // 0 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// ENST00000354883 // intron // 0 // --- // --- // --- /// ENST00000336733 // intron // 0 // --- // --- // ---	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2150403	atgtgaaaaagcagta[C/T]gataccatcccctgaa	C	T	NM_173471 // intron // 0 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// ENST00000354883 // intron // 0 // --- // --- // --- /// ENST00000336733 // intron // 0 // --- // --- // ---	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2289923	gcaaagagatgccaaa[A/G]gaagcatttgacaaag	A	G	NM_173471 // downstream // 229853 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 107851 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2267179	gaataatttttcttgc[G/T]gagccactgagattca	G	T	NM_173471 // downstream // 477647 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 355645 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2238046	ctctgcaaagtttagcc[C/T]acggatcccctgttaaa	C	T	NM_173471 // downstream // 478521 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 356519 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2307085	gctgtttgtttctaaa[A/G]tatcaacacctggcac	A	G	NM_173471 // downstream // 511065 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 389063 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2057601	aatatgatatatcacc[A/C]attaaaaatctccaat	A	C	NM_173471 // downstream // 577883 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 455881 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2131552	atagcagatgaggtaa[C/T]ttaaagaacaaagtcc	C	T	NM_173471 // downstream // 583909 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 461907 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2032280	aaagttaattcgtatg[A/G]aaacagaagcatgctc	A	G	NM_173471 // downstream // 602789 // Hs.379386 // SLC25A26 // 115286 // Homo sapiens solute carrier family 25, member 26 (SLC25A26), mRNA. /// NM_015541 // upstream // 480787 // Hs.518055 // LRIG1 // 26018 // Homo sapiens leucine-rich repeats and immunogl	SLC25A26	SLC25A26, Homo sapiens solute carrier family 25, member 26 (SLC25A26), p14.1
SNP_A-2287944	gattatgacggcaaat[A/G]ataatgataaataata	A	G	NM_032505 // downstream // 115051 // Hs.116665 // TA-KRP // 84541 // Homo sapiens T-cell activation kelch repeat protein (TA-KRP), mRNA. /// NM_003848 // downstream // 248461 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming	TA-KRP	TA-KRP, Homo sapiens T-cell activation kelch repeat protein (TA-KRP), p14.1
SNP_A-2213551	ccglattaagaaatca[A/G]attgcatggacttt	A	G	NM_032505 // downstream // 319554 // Hs.116665 // TA-KRP // 84541 // Homo sapiens T-cell activation kelch repeat protein (TA-KRP), mRNA. /// NM_003848 // downstream // 43958 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming.	TA-KRP	TA-KRP, Homo sapiens T-cell activation kelch repeat protein (TA-KRP), p14.1
SNP_A-2313386	ggagagaaggaggaaa[C/T]caaagaaagtggcata	C	T	NM_003848 // intron // 0 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// ENST00000307241 // intron // 0 // — // — // — // — /// ENST00000307227 // intron // 0 // — // — // —	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1973112	ttctgaaaatggacca[A/T]ctcccgtctctgagcc	A	T	NM_003848 // upstream // 48930 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 301802 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1746532	gattaaagccctctgtatgtgatga[A/G]ctatctttttataatgttg aat	A	G	NM_003848 // upstream // 278425 // Hs.247309 // SUCLG2 // 8801 // succinate-CoA ligase, GDP-forming, beta subunit	SUCLG2	SUCLG2, , rs1597082, succinate-CoA ligase, GDP-forming, beta subunit,p14.1
SNP_A-1749299	tcagaggaatagaatagaatccaga[A/G]atagatccatacatg gtcaactgat	A	G	NM_003848 // upstream // 279820 // Hs.247309 // SUCLG2 // 8801 // succinate-CoA ligase, GDP-forming, beta subunit	SUCLG2	SUCLG2, , rs1597083, succinate-CoA ligase, GDP-forming, beta subunit,p14.1
SNP_A-1792914	ggtaatttggagaaata[C/T]atgagagcattgcacc	C	T	NM_003848 // upstream // 151303 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 199429 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-2193229	catctcagtaaacgac[A/T]gctctacctttctga	A	T	NM_003848 // upstream // 157394 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 193338 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1931840	ttccgagcagggcgta[C/G]ataagtggacattcca	C	G	NM_003848 // upstream // 257702 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 93030 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1973118	taaaatggctgaaatt[A/G]aaaagactcactatac	A	G	NM_003848 // upstream // 280899 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 69833 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1919055	ttaactatagatacaat[A/G]tgacagcacagttgag	A	G	NM_003848 // upstream // 310096 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 40636 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189160	cagttagtcaatggtc[A/G]agtccagatttgagca	A	G	NM_003848 // upstream // 310513 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 40219 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-1973120	cagacactggaactca[C/T]acaaatacacaaattc	C	T	NM_003848 // upstream // 311789 // Hs.186512 // SUCLG2 // 8801 // Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), mRNA. /// NM_213609 // upstream // 38943 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA.	SUCLG2	SUCLG2, Homo sapiens succinate-CoA ligase, GDP-forming, beta subunit (SUCLG2), p14.1
SNP_A-2165297	caaagagaattccaaa[A/G]taaactgcataataaa	A	G	NM_213609 // intron // 0 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// ENST00000327941 // intron // 0 // — // — // — // —	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2173570	cacaattaagcattga[G/T]gaagaggttgtttatc	G	T	NM_213609 // intron // 0 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// ENST00000327941 // intron // 0 // — // — // — // —	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2267918	gaatcgagttatttgg[A/G]attctatcctagttct	A	G	NM_213609 // intron // 0 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// ENST00000327941 // intron // 0 // — // — // — // —	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2154334	attatgtcctgagtga[A/G]agcagaaaaacgactc	A	G	NM_213609 // intron // 0 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// ENST00000327941 // intron // 0 // — // — // — // —	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2167259	caacagaatcaggaaa[C/T]catccaataagacagt	C	T	NM_213609 // downstream // 8173 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// NM_182522 // downstream // 184711 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENS	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2212447	ccctgtgtctctgctc[A/G]ctccactcaagacaga	A	G	NM_213609 // downstream // 12154 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// NM_182522 // downstream // 180730 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// EN	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2087340	actgcagacttaacta[C/G]attgacatttgaatca	C	G	NM_213609 // downstream // 179422 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// NM_182522 // downstream // 13462 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// EN	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-1876220	tctgacttggaaacaa[A/G]gaaaaaacatgaaacg	A	G	NM_213609 // downstream // 188783 // Hs.7047 // FAM19A1 // 407738 // Homo sapiens TAFA1 protein (TAFA1), mRNA. /// NM_182522 // downstream // 4101 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENS	FAM19A1	FAM19A1, Homo sapiens TAFA1 protein (TAFA1), p14.1
SNP_A-2211826	ccctctgcaagaataa[A/C]atcaaataactgttag	A	C	NM_182522 // 3UTR // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // 3UTR // 0 // — // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2291677	gcacacagcccgattc[A/C]aattatattacaaagc	A	C	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1879733	tcttcatctgtcaaac[C/G]aaaattttattagaaa	C	G	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1824824	taaagatttagtccat[A/T]acagtaaacaactatt	A	T	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1973141	acttcatagttaacaa[C/T]tgctttcaaggaatgc	C	T	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1896139	tgcgatggtatgtaaa[C/T]gaatgttgcatgacca	C	T	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2091553	agaaaaagttgtcaa[C/T]ccctgctgctcaagtg	C	T	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2147495	atggatactacgaagga[C/T]agatactgaggccat	C	T	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-2109401	agcttttaacatctgc[C/T]gagtcttaactataca	C	T	NM_182522 // intron // 0 // Hs.187873 // FAM19A4 // 151647 // Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, mRNA. /// ENST00000295569 // intron // 0 // — // — // —	FAM19A4	FAM19A4, Homo sapiens TAFA4 protein (TAFA4), transcript variant 1, p14.1
SNP_A-1973148	ctggccactgctccag[A/G]aagaaatcagagcctct	A	G	NM_006407 // downstream // 11139 // Hs.518060 // ARL6IP5 // 10550 // Homo sapiens ADP-ribosylation-like factor 6 interacting protein 5 (ARL6IP5), mRNA. /// NM_198271 // downstream // 1818 // Hs.350621 // LMOD3 // 56203 // Homo sapiens leiomodin 3 (fetal)	ARL6IP5	ARL6IP5, Homo sapiens ADP-ribosylation-like factor 6 interacting protein 5 (ARL6IP5), p14.1
SNP_A-2087557	actgcgtatgtttggat[C/T]gtgccagagagacaga	C	T	NM_198271 // intron // 0 // Hs.350621 // LMOD3 // 56203 // Homo sapiens leiomodin 3 (fetal) (LMOD3), mRNA. /// ENST00000295572 // intron // 0 // — // — // — // —	LMOD3	LMOD3, Homo sapiens leiomodin 3 (fetal) (LMOD3), p14.1
SNP_A-1904505	tgggggaggtgctgcaa[C/T]ggtaacgtaagaggtt	C	T	AB023230 // intron // 0 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // intron // 0 // — // — // — // —	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-1973153	tgctgtcttgacttga[C/G]taacagctactagata	C	G	AB023230 // intron // 0 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // intron // 0 // — // — // — // —	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-2008798	actttgctcatacta[C/T]ctattcaatcactggt	C	T	AB023230 // intron // 0 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// ENST00000264546 // intron // 0 // — // — // — // —	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-1973161	ctttaagaagtagcaa[A/C]atatcttgaagtatat	A	C	AB023230 // upstream // 160912 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 192497 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF),	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-1973162	atactctgcaccttga[A/C]gacacaacacactgta	A	C	AB023230 // upstream // 160984 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 192425 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF),	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-1811698	gtgctgtgaaacatcq[C/T]atcatgcataggacag	C	T	AB023230 // upstream // 164598 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 188811 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF),	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-2286675	gatggatgaggatgca[C/G]acctttgtaaggcagg	C	G	AB023230 // upstream // 184767 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 168642 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF),	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2230213	ctatagacttaaacct[C/T]aggattctcttagtg	C	T	AB023230 // upstream // 341500 // Hs.371681 // FRMD4B // 23150 // Homo sapiens mRNA for KIAA1013 protein, partial cds. /// NM_198159 // upstream // 11909 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), t	FRMD4B	FRMD4B, Homo sapiens for KIAA1013 protein, partial cds, p14.1
SNP_A-2035601	aaatgtaggatttgag[A/G]aaacaagctgtttgcc	A	G	NM_198159 // downstream // 56159 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 56159 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalm	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-1666784	tgttaataatataaaatagqttaata[A/T]gtgtcaattatgttaatatta aata	A	T	NM_032682 // downstream // 363092 // Hs.235860 // FOXP1 // 27086 // forkhead box P1	FOXP1	FOXP1, rs9310194, forkhead box P1,p13
SNP_A-1960215	ttttaagtgtgtggc[C/T]caatcagtttcagta	C	T	NM_198159 // downstream // 499700 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 499700 // Hs.166017 // MITF // 4286 // Homo sapiens microphtha	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-1973192	aatcctccctgatccc[A/G]aaactactgcttttt	A	G	NM_198159 // downstream // 560901 // Hs.166017 // MITF // 4286 // Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA. /// NM_198178 // downstream // 560901 // Hs.166017 // MITF // 4286 // Homo sapiens microphtha	MITF	MITF, Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, p13
SNP_A-1751637	aaaacaaaaggaaaagaaaagaaaaaa[A/G]gcttatcgcaatt ataaaagagct	A	G	NM_032682 // intron // 0 // Hs.235860 // FOXP1 // 27086 // forkhead box P1	FOXP1	FOXP1, rs2293171, forkhead box P1,p13
SNP_A-1940613	ttgcctccagggagta[C/T]gatgcttttgtgcactt	C	T	NM_032682 // intron // 0 // Hs.431498 // FOXP1 // 27086 // Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // — // — // ENST00000318789 // intron // 0 // — // — // — // — /// ENST00000342334 // int	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-1914215	tgtgtgtttactcagc[A/G]cctactgagtgtcata	A	G	NM_032682 // intron // 0 // Hs.431498 // FOXP1 // 27086 // Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // — // — // ENST00000318789 // intron // 0 // — // — // — // — /// ENST00000342334 // int	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-2044372	aacttttggtgtatat[A/T]ctcactttctgtagg	A	T	NM_032682 // intron // 0 // Hs.431498 // FOXP1 // 27086 // Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // — // — // ENST00000318789 // intron // 0 // — // — // — // — /// ENST00000356973 // int	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-2283489	gatactcctttcctagc[C/T]accgttcctggctcc	C	T	NM_032682 // intron // 0 // Hs.431498 // FOXP1 // 27086 // Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // — // — // ENST00000318789 // intron // 0 // — // — // — // — /// ENST00000356973 // int	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-1868221	tcctcacaaacccactg[C/G]agtaagattaatccca	C	G	NM_032682 // intron // 0 // Hs.431498 // FOXP1 // 27086 // Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000339693 // intron // 0 // — // — // ENST00000318789 // intron // 0 // — // — // — // — /// ENST00000356973 // int	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13
SNP_A-1679554	ttggtaaaggtgtaaataggtgtgc[A/G]atgaaagttgattaccta ataattg	A	G	NM_032682 // intron // 0 // Hs.235860 // FOXP1 // 27086 // forkhead box P1	FOXP1	FOXP1, rs830604, forkhead box P1,p13
SNP_A-2247058	ctgtatttccggaa[A/G]ggcacttgctagggggc	A	G	NM_032682 // intron // 0 // Hs.431498 // FOXP1 // 27086 // Homo sapiens forkhead box P1 (FOXP1), mRNA. /// ENST00000358280 // intron // 0 // — // — // — // — /// ENST00000318779 // intron // 0 // — // — // — // —	FOXP1	FOXP1, Homo sapiens forkhead box P1 (FOXP1), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1731295	atagctttaattatctgtctccta[A/C]atgtaactgagaaaatacaaatattg	A	C	NM_018971 // downstream // 7770 // Hs.356084 // GPR27 // 2850 // G protein-coupled receptor 27 /// NM_021935 // downstream // 8709 // Hs.528665 // PROK2 // 60675 // prokineticin 2	GPR27	GPR27 , rs1374913, G protein-coupled receptor 27 ,p13
SNP_A-2245634	ctggccaaagaccaaa[C/T]gtttaaagttcactc	C	T	ENST00000296612 // intron // 0 // — // — // —	-	p13
SNP_A-2094158	agaaggctatgcataa[A/G]tgaggaataggataaat	A	G	ENST00000296612 // intron // 0 // — // — // —	-	p13
SNP_A-1887037	tgacttttagattagga[A/T]tgtggtttctggatat	A	T	ENST00000296612 // intron // 0 // — // — // —	-	p13
SNP_A-1935169	ttctgcaggaaagagag[A/G]agagggggtttggcccct	A	G	NM_021935 // upstream // 122230 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 122230 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 precursor (PROK2) mRNA, complete cds. /// NM_0122	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2290083	gcaaatacctctatggt[A/T]cactaagtggctgcgc	A	T	NM_021935 // upstream // 122596 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 122596 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 precursor (PROK2) mRNA, complete cds. /// NM_0122	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-1885523	tgacaatccaagataa[C/T]agccaataatgagtat	C	T	NM_021935 // upstream // 403960 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 403960 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 precursor (PROK2) mRNA, complete cds. /// NM_0122	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-2008822	catgatctttctaaaa[C/T]gcaaatttgaaacaat	C	T	NM_021935 // upstream // 515651 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 (PROK2), mRNA. /// AF333025 // upstream // 515651 // Hs.528665 // PROK2 // 60675 // Homo sapiens prokineticin 2 precursor (PROK2) mRNA, complete cds. /// NM_0122	PROK2	PROK2, Homo sapiens prokineticin 2 (PROK2), p13
SNP_A-1919711	ttaagtagtagtgatat[C/G]catttcatccgatttcc	C	G	NM_012234 // upstream // 208965 // Hs.7910 // RYBP // 23429 // Homo sapiens RING1 and YY1 binding protein (RYBP), mRNA. /// NM_018130 // downstream // 93691 // Hs.528650 // SHQ1 // 55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. ///	RYBP	RYBP, Homo sapiens RING1 and YY1 binding protein (RYBP), p13
SNP_A-2079723	accctcatgagaacag[A/G]attaagtatgattaag	A	G	NM_012234 // upstream // 246853 // Hs.7910 // RYBP // 23429 // Homo sapiens RING1 and YY1 binding protein (RYBP), mRNA. /// NM_018130 // downstream // 55803 // Hs.528650 // SHQ1 // 55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. ///	RYBP	RYBP, Homo sapiens RING1 and YY1 binding protein (RYBP), p13
SNP_A-2118592	agtaatggactgctct[A/G]ctacaataattaaaac	A	G	NM_018130 // upstream // 17248 // Hs.528650 // SHQ1 // 55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // upstream // 17248 // — // — // — /// ENST00000308603 // upstream // 42663 // — // — // —	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-2223458	cgcttaaaagtctcaa[A/G]cgtgcgacttaattaa	A	G	NM_018130 // upstream // 51776 // Hs.528650 // SHQ1 // 55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // upstream // 51776 // — // — // — /// ENST00000308603 // upstream // 8135 // — // — // —	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-2024269	aaaagcatcaagctga[A/G]actttattgtgttgg	A	G	NM_018130 // upstream // 54628 // Hs.528650 // SHQ1 // 55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // upstream // 54628 // — // — // — /// ENST00000308603 // upstream // 5283 // — // — // —	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-2082369	acgcaagaccatttcc[A/G]ctacataatacaagt	A	G	NM_018130 // upstream // 54801 // Hs.528650 // SHQ1 // 55164 // Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA. /// ENST00000325599 // upstream // 54801 // — // — // — /// ENST00000308603 // upstream // 5110 // — // — // —	SHQ1	SHQ1, Homo sapiens hypothetical protein FLJ10539 (FLJ10539), p13
SNP_A-2127765	ataactggtataactc[C/T]atgctttgggaatatt	C	T	ENST00000308603 // intron // 0 // — // — // —	-	p13
SNP_A-2025685	aaaatgatagctttat[C/T]gctttagtacagagc	C	T	ENST00000308603 // intron // 0 // — // — // —	-	p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1788953	gggcaagtggtgccta[A/G]gtccagcttacatttc	A	G	NM_174907 // downstream // 263833 // Hs.431092 // PPP4R2 // 151987 // Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), mRNA. /// ENST00000295862 // downstream // 246995 // — // — // — // — /// ENST00000356692 // downstream // 263	PPP4R2	PPP4R2, Homo sapiens protein phosphatase 4, regulatory subunit 2 (PPP4R2), p13
SNP_A-1895412	tgccgctgtcttgagg[A/G]catttttctttgggctg	A	G	ENST00000263666 // intron // 0 // — // — // — // — /// ENST00000308537 // intron // 0 // — // — // — // —	-	p13
SNP_A-2301370	gcctttgatacattgg[G/T]cacattcacatgggca	G	T	ENST00000263666 // intron // 0 // — // — // — // — /// ENST00000308537 // intron // 0 // — // — // — // —	-	p13
SNP_A-1738423	ggttctaaacgacaaggtagagaga[C/T]gtgaatggaaccca aaaaagagaaa	C	T	AB029018 // upstream // 356836 // Hs.177635 // PDZRN3 // 23024 // PDZ domain containing RING finger 3 /// AB040929 // downstream // 280814 // Hs.512593 // CNTN3 // 5067 // contactin 3 (plasmacytoma associated)	PDZRN3	PDZRN3 , rs1526723, PDZ domain containing RING finger 3 ,p13
SNP_A-2008837	ctaggtgaacgtttta[C/T]agtttgggtagagaga	C	T	ENST00000263666 // upstream // 204595 // — // — // — // — /// ENST00000319719 // upstream // 428551 // — // — // — // — /// ENST00000308537 // upstream // 204676 // — // — // — // — /// ENST00000263665 // downstream // 433055 // –	-	p13
SNP_A-2209411	cccatagagatacaca[A/G]gcataaattctgtact	A	G	ENST00000263666 // upstream // 379696 // — // — // — // — /// ENST00000319719 // upstream // 603652 // — // — // — // — /// ENST00000308537 // upstream // 379777 // — // — // — // — /// ENST00000263665 // downstream // 257954 // –	-	p13
SNP_A-1947277	tttaatttgggggga[A/G]cattttggaagagata	A	G	ENST00000263666 // upstream // 485382 // — // — // — // — /// ENST00000319719 // upstream // 709338 // — // — // — // — /// ENST00000308537 // upstream // 485463 // — // — // — // — /// ENST00000263665 // downstream // 152268 // –	-	p12.3
SNP_A-1938447	ttgacttccttcaata[A/T]gttccttctaaaatgg	A	T	ENST00000263666 // upstream // 596888 // — // — // — // — /// ENST00000319719 // upstream // 820844 // — // — // — // — /// ENST00000308537 // upstream // 596969 // — // — // — // — /// ENST00000263665 // downstream // 40762 // —	-	p12.3
SNP_A-1973290	tgtacatttcattcga[A/C]ccttctgataaaaacc	A	C	ENST00000263666 // upstream // 598603 // — // — // — // — /// ENST00000319719 // upstream // 822559 // — // — // — // — /// ENST00000308537 // upstream // 598684 // — // — // — // — /// ENST00000263665 // downstream // 39047 // —	-	p12.3
SNP_A-2286490	gatgctttggcttaca[A/G]atccatttactgttaa	A	G	ENST00000263665 // intron // 0 // — // — // — // —	-	p12.3
SNP_A-2025076	aaaatacaggggaaaa[G/T]ttaatcatatcctctc	G	T	ENST00000263665 // intron // 0 // — // — // — // —	-	p12.3
SNP_A-1931074	ttccatatgagcttga[G/T]aaaaatgtgtaacctg	G	T	ENST00000263665 // intron // 0 // — // — // — // —	-	p12.3
SNP_A-1821734	gttttaaataaaagcc[A/G]aatctcaaaaggaagg	A	G	ENST00000263665 // intron // 0 // — // — // — // —	-	p12.3
SNP_A-2302718	gctactaggggaataa[C/G]tcattctggcagaccc	C	G	ENST00000263665 // intron // 0 // — // — // — // —	-	p12.3
SNP_A-1730010	atgtgttcatactctatgtgattta[A/G]agatggtgaattctgtgatg atcaa	A	G	AB040929 // upstream // 239856 // Hs.512593 // CNTN3 // 5067 // contactin 3 (plasmacytoma associated) /// AK094187 // downstream // 1003616 // Hs.512536 // - // 401075 // CDNA FLJ41782 fis, clone IMR322018192, weakly similar to ZINC FINGER PROTEIN 90	CNTN3	CNTN3 , rs4131575, contactin 3 (plasmacytoma associated) ,p12.3
SNP_A-2227099	ctaattacagcaatag[A/G]aagtgcgtgcataaac	A	G	ENST00000263665 // upstream // 187274 // — // — // — // — /// ENST00000321014 // upstream // 541677 // — // — // — // —	-	p12.3
SNP_A-2135198	atattgcttcacttga[C/T]ggtgtctcaattcttt	C	T	ENST00000263665 // upstream // 234806 // — // — // — // — /// ENST00000321014 // upstream // 494145 // — // — // — // —	-	p12.3
SNP_A-2265057	gaagataggttggttg[A/G]aattttcaggtctgag	A	G	ENST00000263665 // upstream // 234851 // — // — // — // — /// ENST00000321014 // upstream // 494100 // — // — // — // —	-	p12.3
SNP_A-1937895	ttgaatctatcactaa[C/G]tccttctctaggcgta	C	G	ENST00000263665 // upstream // 247835 // — // — // — // — /// ENST00000321014 // upstream // 481116 // — // — // — // —	-	p12.3
SNP_A-1938020	ttgaatttatgataac[A/C]agtgatactgacctaa	A	C	ENST00000263665 // upstream // 255349 // — // — // — // — /// ENST00000321014 // upstream // 473602 // — // — // — // —	-	p12.3
SNP_A-1973294	agactcggtgtggtcc[A/G]gcggctgccacctctc	A	G	ENST00000263665 // upstream // 285959 // — // — // — // — /// ENST00000321014 // upstream // 442992 // — // — // — // —	-	p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946738	tttaactaaaaggcta[C/T]ctattcaggatgaact	C	T	ENST00000263665 // upstream // 298412 // --- // --- // --- /// ENST00000321014 // upstream // 430539 // --- // --- // --- // ---	-	p12.3
SNP_A-1911767	tgtgaatactggatg[A/G]aaccactcagatggaa	A	G	ENST00000263665 // upstream // 300733 // --- // --- // --- /// ENST00000321014 // upstream // 428218 // --- // --- // --- // ---	-	p12.3
SNP_A-2192435	catcatgtctgacacc[A/C]gaagtagtacataaaa	A	C	ENST00000263665 // upstream // 473378 // --- // --- // --- /// ENST00000321014 // upstream // 255573 // --- // --- // --- // ---	-	p12.3
SNP_A-1813783	gtgtagtgctataaac[A/G]agctccataagtgcag	A	G	ENST00000263665 // upstream // 713768 // --- // --- // --- /// ENST00000321014 // upstream // 15183 // --- // --- // --- // ---	-	p12.3
SNP_A-2025658	aaaatgagatatcaag[C/G]caaactatgcatttt	C	G	ENST00000321014 // downstream // 4705 // --- // --- // --- /// ENST00000360292 // downstream // 108769 // --- // --- // --- // ---	-	p12.3
SNP_A-2200097	ccaaatatttcctta[A/G]gcttgaacatgagct	A	G	ENST00000360292 // upstream // 6141 // --- // --- // --- // --- /// ENST00000331736 // downstream // 10842 // --- // --- // --- // ---	-	p12.3
SNP_A-1938279	ttgacctgtttgatct[C/G]agagcctaatttcata	C	G	NM_012148 // downstream // 46036 // --- // DUX3 // 26582 // Homo sapiens double homeobox, 3 (DUX3), mRNA. /// NM_012149 // downstream // 46036 // --- // DUX5 // 26581 // Homo sapiens double homeobox, 5 (DUX5), mRNA. /// NM_012146 // downstream // 46036 //	DUX3	DUX3, Homo sapiens double homeobox, 3 (DUX3), p12.3
SNP_A-1816084	gttacatgattaatac[A/T]gtacaatctttgaggc	A	T	AB046788 // upstream // 995569 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 306765 // --- // --- // --- /// ENST00000332191 // upstream // 995569 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-1955714	tttgtaattgaaaaa[A/C]tatgtggcatttaat	A	C	AB046788 // upstream // 202327 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 1100007 // --- // --- // --- /// ENST00000332191 // upstream // 202327 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2049025	aagccttggactcaga[C/T]acaatagagtttaaag	C	T	AB046788 // upstream // 201474 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 1100860 // --- // --- // --- /// ENST00000332191 // upstream // 201474 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1888115	tgagccatcggataaat[A/G]tgcatgaatttcagga	A	G	AB046788 // upstream // 8032 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000349123 // upstream // 1294302 // --- // --- // --- /// ENST00000332191 // upstream // 8032 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-1946159	ttgtttttgcttagca[G/T]cttaaccactaatg	G	T	AB046788 // intron // 0 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1817376	gttcagctgttttat[C/T]acaggttgaaagtcag	C	T	AB046788 // intron // 0 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-1909341	tgtatgttgcagataa[A/T]cacatgtaagcttaa	A	T	AB046788 // intron // 0 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// ENST00000332191 // intron // 0 // --- // --- // ---	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1869426	tcctgtctggcccta[A/C]aaaattacaaatcaaa	A	C	AB046788 // downstream // 656930 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 292799 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosoph	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2214067	cctaagtctcccttta[C/T]gctatcttctaccaaa	C	T	AB046788 // downstream // 699479 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 250250 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosoph	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872629	tctaggtttattttcc[C/T]ccttgcctcaaagctt	C	T	AB046788 // downstream // 881979 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 67750 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophi	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-2049889	aaggaacaaatcaata[A/G]ggtggtagtggaagaa	A	G	AB046788 // downstream // 882581 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 67148 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophi	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. p12.3
SNP_A-1973362	aaaagcatggcttata[A/C]ctcactagacgaggca	A	C	AB046788 // downstream // 898050 // Hs.13305 // ROBO2 // 6092 // Homo sapiens mRNA for KIAA1568 protein, partial cds. /// NM_133631 // downstream // 51679 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophi	ROBO2	ROBO2, Homo sapiens for KIAA1568 protein, partial cds. ,p12.3
SNP_A-2143403	atgacccatcataaca[C/T]tgacttttttccttta	C	T	NM_002941 // intron // 0 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, mRNA. /// ENST00000305299 // intron // 0 // — // — // — // —	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, p12.3
SNP_A-2163208	atttttcttagtacga[C/T]gctctttacattgcaa	C	T	NM_002941 // intron // 0 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, mRNA. /// ENST00000305299 // intron // 0 // — // — // — // —	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, p12.3
SNP_A-2263546	gaaccaggaaagttac[C/T]gattcctgagaattca	C	T	NM_002941 // intron // 0 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, mRNA. /// ENST00000305299 // intron // 0 // — // — // — // —	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, p12.3
SNP_A-2102956	agcaaactaacagaca[C/T]atcagcctcaagatac	C	T	NM_002941 // intron // 0 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, mRNA. /// ENST00000305299 // intron // 0 // — // — // — // —	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 1, p12.3
SNP_A-2242647	ctgcataacgtcacac[A/G]cttggactgctgctgg	A	G	NM_133631 // upstream // 816486 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 245999 // Hs.13640 // ROBO1 // 6091 // Homo sapiens r	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1663956	tcctttctgaaataattttaggata[C/T]gaaaatctgtaaatgaaaaactaca	C	T	NM_000158 // downstream // 1406213 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_002941 // upstream // 493584 // Hs.301198 // ROBO1 // 6091 //	GBE1	GBE1 , rs4856497, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-2181134	cagacagctgcaagtg[C/T]agaggatttaacgaag	C	T	NM_133631 // upstream // 966504 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 396017 // Hs.13640 // ROBO1 // 6091 // Homo sapiens r	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1845979	tatatacctcttgaaa[A/C]aggcaaaggttgaagt	A	C	NM_133631 // upstream // 1087389 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 516902 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1681826	gctcatcctaaatttccataccaca[C/G]tctcttcactatttatatcttatct	C	G	NM_000158 // downstream // 1135672 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_002941 // upstream // 764125 // Hs.301198 // ROBO1 // 6091 //	GBE1	GBE1 , rs950318, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1715709	tcaccagtctatgacctcagtaca[A/T]taatctgtagtctcagttc taggt	A	T	NM_000158 // downstream // 1084953 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_002941 // upstream // 814844 // Hs.301198 // ROBO1 // 6091 //	GBE1	GBE1 , rs67644710, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-2078137	accaggtatttctctc[A/G]cttcctgagctgcaat	A	G	NM_133631 // upstream // 1291281 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 720794 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1704763	aaattgactgttgatttatatatg[C/G]cttcaagcttgatccactcat gatt	C	G	NM_000158 // downstream // 995755 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_002941 // upstream // 904042 // Hs.301198 // ROBO1 // 6091 // r	GBE1	GBE1 , rs1356030, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-2086530	actgaaacaagtaaat[A/C]atatgcatacagttgt	A	C	NM_133631 // upstream // 1342129 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 771642 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2126442	ataaaaggactaaaaa[A/C]tctatcatctttatc	A	C	NM_133631 // upstream // 1393068 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 822581 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1973385	ttctgatgctaagctc[A/C]atgcaatttacctagg	A	C	NM_133631 // upstream // 1397907 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 827420 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2261485	gaaaggaccttaggat[C/T]gtgatgaaaattaaat	C	T	NM_133631 // upstream // 1402422 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 831935 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2224613	cgtcatctgaaactac[A/G]caggacaaatgaagct	A	G	NM_133631 // upstream // 1402726 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 832239 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1822421	gttttacagctaaga[A/T]gttactaatttgggg	A	T	NM_133631 // upstream // 1427186 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 856699 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1909214	tgtatgagattctaga[A/G]gaacgtctatggatt	A	G	NM_133631 // upstream // 1476562 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 906075 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1973387	gatactaagaagatga[C/T]gagtgttctcaggca	C	T	NM_133631 // upstream // 1479495 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 909008 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044697	aagaaaggaaatgcaa[G/T]caattaaaggaatact	G	T	NM_133631 // upstream // 1482902 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 912415 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2302111	gcgtttgcttgaaaat[C/G]aatctttgtctaagt	C	G	NM_133631 // upstream // 1485044 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 914557 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2200042	ccaaagttacatggaa[A/G]ccatatttagacaaaa	A	G	NM_133631 // upstream // 1486918 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 916431 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1864610	tccagatattaaaaca[A/G]catcctgcagaagaa	A	G	NM_133631 // upstream // 1491834 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 921347 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1934754	ttctcttcgctcatag[A/C]ataatgaattactctt	A	C	NM_133631 // upstream // 1495764 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 925277 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2053504	aagtgcattacagctat[C/T]gaaactctaatcacat	C	T	NM_133631 // upstream // 1522623 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 952136 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2051721	aaggtcaaatgtgtaa[A/G]aagctgttaagattat	A	G	NM_133631 // upstream // 1536129 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 965642 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1810925	gtgcatctgagattgc[A/G]gataagaattcaaatc	A	G	NM_133631 // upstream // 1597360 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1026893 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2271219	gacatgagtacctgga[A/C]aagaaaagacagacag	A	C	NM_133631 // upstream // 1605813 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1035326 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2130656	atactggagtaggta[C/T]gcacttaatccaatat	C	T	NM_133631 // upstream // 1624104 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1053617 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2305795	gctgcctttgggtga[A/G]gtagaatgaaaattat	A	G	NM_133631 // upstream // 1624877 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1054390 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909127	tgtatcccagacgata[C/T]agttgaaatggctaga	C	T	NM_133631 // upstream // 1637503 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1067016 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1838643	tagacacacctagtaa[C/T]tgcttgggaaaaggg	C	T	NM_133631 // upstream // 1643315 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1072828 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1973398	aaaaacctcaaacaa[A/G]gcatatcaaaaaagac	A	G	NM_133631 // upstream // 1718689 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1148202 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2130118	ataccctttaataa[A/T]cataagccaaacactg	A	T	NM_133631 // upstream // 1726682 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1156195 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1973402	cctacaatgaaaaaacc[A/G]aatatcccttagcaga	A	G	NM_133631 // upstream // 1943630 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1373143 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-2275244	gagaagggtagtgagg[C/G]aaagctttaagggtc	C	G	NM_133631 // upstream // 1958977 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1388490 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1781697	ggatgtgctttgaa[C/T]aattttgtgttgcct	C	T	NM_133631 // upstream // 1974537 // Hs.13640 // ROBO1 // 6091 // Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA. /// NM_002941 // upstream // 1404050 // Hs.13640 // ROBO1 // 6091 // Homo sapiens	ROBO1	ROBO1, Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, p12.2
SNP_A-1695047	atctactgaggctaaaataagctca[A/G]tataaagatgggaata aactataga	A	G	NM_000158 // upstream // 333452 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_153184 // upstream // 2863966 // Hs.48507 // IGSF4D // 253559 //	GBE1	GBE1 , rs10511100, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-2169239	caagcaaacagatcac[C/G]atggtagaaatcagaa	C	G	NM_000158 // upstream // 726906 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type III/ NM_153184 // upstream // 2470541 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1908706	tgtagggaaactctgc[A/G]cttaacctatctctgt	A	G	NM_000158 // upstream // 758947 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type III/ NM_153184 // upstream // 2438500 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1658444	ttttttaaagctatctccaccaatc[A/G]tgtatacctgggcatatac ttagg	A	G	NM_000158 // upstream // 956043 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_153184 // upstream // 2241375 // Hs.48507 // IGSF4D // 253559 //	GBE1	GBE1 , rs1382069, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1742225	cccagaccaaagaataagctaaata[C/T]ctgagactcagag gtcagaacagg	C	T	NM_000158 // upstream // 956252 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_153184 // upstream // 2241166 // Hs.48507 // IGSF4D // 253559 //	GBE1	GBE1 , rs726174, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-1675115	gttttctctaaacataatgtattca[C/T]catccactagtcaaaaaa agcatt	C	T	NM_000158 // upstream // 969189 // Hs.1691 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_153184 // upstream // 2228229 // Hs.48507 // IGSF4D // 253559 //	GBE1	GBE1 , rs10511098, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-2162726	atttgaagacccttat[C/T]gtgtatgtatgtat	C	T	NM_000158 // upstream // 901042 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2296405 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-2199892	ccaaagaagatataga[G/T]aaagcaataaacatac	G	T	NM_000158 // upstream // 920929 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2276518 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type .p12.2
SNP_A-2282730	gataaaaacaccaaggd[A/G]cagataatcttttgtg	A	G	NM_000158 // upstream // 962242 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2235205 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1746873	tgcttgaaatattcatttctgcga[A/G]cgtatggccattgaggatt acagt	A	G	NM_000158 // upstream // 1136301 // Hs.1681 // GBE1 // 2632 // glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) /// NM_153184 // upstream // 2061117 // Hs.48507 // IGSF4D // 253559 //	GBE1	GBE1 , rs9309917, glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) ,p12.2
SNP_A-2117514	aggtgttctaaaaic[A/C]agtgataaatcaatta	A	C	NM_000158 // upstream // 1071465 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2125982 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.2
SNP_A-1973431	gtatttgcattggta[A/G]aatagcagtgcacact	A	G	NM_000158 // upstream // 1092542 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2104905 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type .p12.2
SNP_A-1816514	gttaggttatccagga[A/G]ggatcatggtgaagag	A	G	NM_000158 // upstream // 1133113 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 2064334 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type .p12.2
SNP_A-1939785	ttgcaacttatgtaa[A/G]cctaaaattattgta	A	G	NM_000158 // upstream // 2128253 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 1069194 // Hs.333991 // IGSF4D /	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1807382	gtctgacgataagcag[A/G]agaaagtcattttat	A	G	NM_000158 // upstream // 2243905 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 953542 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2008874	ttgacactgctattaa[A/G]aattgcctaagagtat	A	G	NM_000158 // upstream // 2367917 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 829530 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-2270605	gacagatcctgtaaca[A/T]ccctgtcttatttaggt	A	T	NM_000158 // upstream // 2591805 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 605642 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type .p12.1
SNP_A-2081587	acctaatccacctttac[C/G]aagaccaagcacatgg	C	G	NM_000158 // upstream // 2741279 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 456168 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-2151686	atgttgtaagtctaaat[A/G]gcaaatggctgtcaaaa	A	G	NM_000158 // upstream // 2745644 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 451803 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1973457	ctaaggaactagatca[C/T]tgagttaaaaagtcgt	C	T	NM_000158 // upstream // 2763179 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 434268 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1973460	tttccttataaattgc[C/G]catccttagatattcc	C	G	NM_000158 // upstream // 2836394 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 361053 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type p12.1
SNP_A-1929376	ttcagtgataacaaaa[A/G]caatttacgtttgaat	A	G	NM_000158 // upstream // 2866918 // Hs.436062 // GBE1 // 2632 // Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type /// NM_153184 // upstream // 330529 // Hs.333991 // IGSF4D //	GBE1	GBE1, Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type .p12.1
SNP_A-1706429	ttccaataacaactgacataaatca[A/G]gtatacaattgacttat attgtta	A	G	NM_153184 // intron // 0 // Hs.48507 // IGSF4D // 253559 // immunoglobulin superfamily, member 4D	IGSF4D	IGSF4D , rs10490896, immunoglobulin superfamily, member 4D,p12.1
SNP_A-2187656	cagtacaacataaaaac[A/G]tagctcttcttatta	A	G	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1915625	tgttctctgcatta[C/T]gaagggatacattcca	C	T	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1973466	gtcaagcaaacagtta[A/T]caaactcctgtataaa	A	T	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2257192	ctttctgctgaccaac[C/G]atttataaatgtata	C	G	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044431	aagaaaaatatcttga[C/T]ctattacctacatatg	C	T	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2028447	aaactctgaatatttta[C/G]ggttatacagaaaatt	C	G	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-2108361	agctgatttgattgt[A/G]aattagggattaaaat	A	G	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1948082	tttagagtttataca[G/T]atccacctctaaaaa	G	T	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1937463	ttgaacaattcattta[A/G]ctcaccattcaggat	A	G	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1973484	aaatcttgccctttcc[A/G]caaagtcacataagac	A	G	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // — /// ENST00000310757 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1952584	tttctgcctctagtga[A/C]agctgtttgaaaatca	A	C	NM_153184 // intron // 0 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// ENST00000345086 // intron // 0 // — // — // — /// ENST00000310757 // intron // 0 // — // — // —	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1795526	ggtgcctggcgtacac[A/G]agtttttataaccagc	A	G	NM_153184 // downstream // 323662 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// NM_014043 // upstream // 836855 // Hs.476930 // DKFZP564O123 // 25978 // Homo sapiens DKFZP564O123 protein (DKFZP5	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p12.1
SNP_A-1683594	ggttctagaaactaaatatagaaatc[A/G]caatagaatgtagcata taacactt	A	G	NM_014043 // upstream // 161982 // Hs.11449 // DKFZP564O123 // 25978 // DKFZP564O123 protein /// NM_016206 // upstream // 125792 // Hs.435013 // FLJ38507 // 389136 // colon carcinoma related protein	DKFZP564O123	DKFZP564O123 , rs979626, DKFZP564O123 protein, p12.1
SNP_A-1848438	tatgaagcagctttaa[A/C]agactgacacattctg	A	C	NM_153184 // downstream // 1055023 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// NM_014043 // upstream // 105494 // Hs.476930 // DKFZP564O123 // 25978 // Homo sapiens DKFZP564O123 protein (DKFZP	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p11.2
SNP_A-2097444	agagaacaaaagtaca[C/G]aggtagtttatcttga	C	G	NM_153184 // downstream // 1084702 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// NM_014043 // upstream // 75815 // Hs.476930 // DKFZP564O123 // 25978 // Homo sapiens DKFZP564O123 protein (DKFZP5	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p11.2
SNP_A-2180638	cagaagctgaggtcaa[C/T]gacaagtatatccagg	C	T	NM_153184 // downstream // 1112539 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA /// NM_014043 // upstream // 47978 // Hs.476930 // DKFZP564O123 // 25978 // Homo sapiens DKFZP564O123 protein (DKFZP5	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2075389	acatgaatggcttcag[A/G]caaagagagagagctt	A	G	NM_153184 // downstream // 1153624 // Hs.333991 // IGSF4D // 253559 // Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), mRNA. /// NM_014043 // upstream // 6893 // Hs.476930 // DKFZP564O123 // 25978 // Homo sapiens DKFZP564O123 protein (DKFZP56	IGSF4D	IGSF4D, Homo sapiens immunoglobulin superfamily, member 4D (IGSF4D), p11.2
SNP_A-1973510	tcctcctctgccata[C/T]gaccttgaagtgcact	C	T	NM_000306 // upstream // 24821 // Hs.89394 // POU1F1 // 5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 689342 // Hs.248136 // HTR1F // 3355 // Homo sapiens 5-hy	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.2
SNP_A-2041332	aacctgctgccttgaa[A/G]agaagaatatagtcct	A	G	NM_000306 // upstream // 44960 // Hs.89394 // POU1F1 // 5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 669203 // Hs.248136 // HTR1F // 3355 // Homo sapiens 5-hy	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.2
SNP_A-2287110	gatgtatccactacaa[C/T]tacagctctacataat	C	T	NM_000306 // upstream // 133103 // Hs.89394 // POU1F1 // 5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 581060 // Hs.248136 // HTR1F // 3355 // Homo sapiens 5-h	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.2
SNP_A-1945794	ttgttgttaatcgaag[C/T]ataaatgatctgtaac	C	T	NM_000306 // upstream // 292681 // Hs.89394 // POU1F1 // 5449 // Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), mRNA. /// NM_000866 // upstream // 421482 // Hs.248136 // HTR1F // 3355 // Homo sapiens 5-h	POU1F1	POU1F1, Homo sapiens POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1) (POU1F1), p11.2
SNP_A-2057935	aatattgagcatactg[A/C]ataagcttacaattat	A	C	NM_003663 // upstream // 114230 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 121964 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2299626	gccgcctatcattgag[A/G]caaagattcctggа	A	G	NM_003663 // upstream // 128391 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 136125 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-1800198	gtacctaatttttca[A/G]gggcttatatggagag	A	G	NM_003663 // upstream // 183111 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 190845 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2062229	aatggtgaattcagaa[A/T]cctatcacagaagctc	A	T	NM_003663 // upstream // 315731 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 323465 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-1750233	actggatctgtccaaaacaataaa[A/G]gtagtaaccctatgag tctgcaag	A	G	NM_005233 // upstream // 393942 // Hs.123642 // EPHA3 // 2042 // EphA3 /// NM_173824 // downstream // 556667 // Hs.406060 // MGC26717 // 285237 // hypothetical protein MGC26717 /// NM_182644 // upstream // 394080 // Hs.123642 // EPHA3 // 2042 // EphA3	EPHA3	EPHA3, rs1603314, EphA3, p11.1
SNP_A-1873214	tctattgtgatgtaac[A/T]gcaaaagtaggaccac	A	T	NM_003663 // upstream // 438876 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 446610 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1859546	tcaggatatttacaat[C/G]aatccaaagaggtaac	C	G	NM_003663 // upstream // 554357 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 562091 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2062339	aatgtaaaggtatgtg[C/T]acaagtagagggtgtg	C	T	NM_003663 // upstream // 573632 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 581366 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-2255818	cttgtttccaatcca[C/T]gataatctgaacatg	C	T	NM_003663 // upstream // 584805 // Hs.444818 // CGGBP1 // 8545 // Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), mRNA. /// NM_018293 // downstream // 592539 // Hs.27595 // ZNF654 // 55279 // Homo sapiens hypothetical protein FLJ10997 (FLJ1099	CGGBP1	CGGBP1, Homo sapiens CGG triplet repeat binding protein 1 (CGGBP1), p11.1
SNP_A-1883343	tgaacaatctaggcta[C/T]actcacagcaggacat	C	T	NM_005233 // intron // 0 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // intron // 0 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 2, mRNA. /// ENST00000336596 //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1973546	gatatcactaccttccc[A/G]cacaacaggtgactgg	A	G	NM_005233 // CDS // 0 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // CDS // 0 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 2, mRNA. /// ENST00000336596 // CDS //	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-2061599	aatgcttctttgggta[A/C]aatcattctcactact	A	C	NM_005233 // downstream // 104349 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // downstream // 104349 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 2, mRNA. /// E	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1876730	tctgcagcacaaagaa[C/T]aagtatagaagaatat	C	T	NM_005233 // downstream // 339664 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 1, mRNA. /// NM_182644 // downstream // 339664 // Hs.123642 // EPHA3 // 2042 // Homo sapiens EphA3 (EPHA3), transcript variant 2, mRNA. /// E	EPHA3	EPHA3, Homo sapiens EphA3 (EPHA3), transcript variant 1, p11.1
SNP_A-1937211	ttgaaaagatgagaaa[C/T]accattacgcagacaa	C	T	NM_000313 // downstream // 43478 // Hs.64016 // PROS1 // 5627 // Homo sapiens protein S (alpha) (PROS1), mRNA. /// ENST00000334663 // upstream // 4641914 // --- // --- // --- /// ENST00000348974 // downstream // 43478 // --- // --- // ---	PROS1	PROS1, Homo sapiens protein S (alpha) (PROS1), q11.2
SNP_A-1946268	tttaaaactcagagta[A/G]aagtcaagatccacac	A	G	NM_022072 // downstream // 211709 // Hs.401062 // NSUN3 // 63899 // Homo sapiens NOL1/NOP2/Sun domain family 3 (NSUN3), mRNA. /// ENST00000314622 // downstream // 211709 // --- // --- // --- /// ENST00000313754 // downstream // 168271 // --- // ---	NSUN3	NSUN3, Homo sapiens NOL1 q11.2
SNP_A-1933745	ttctatagattttta[C/T]ggaacactgtatatac	C	T	ENST00000332119 // upstream // 59474 // --- // --- // --- /// ENST00000330649 // upstream // 1352143 // --- // --- // ---	-	q11.2
SNP_A-1693395	aatagtacctatctattctagata[A/G]gtccatacacttgagaag atttac	A	G	NM_022072 // downstream // 1171087 // Hs.18740 // FLJ22609 // 63899 // hypothetical protein FLJ22609 /// NM_173655 // upstream // 2141773 // Hs.145172 // DKFZp434C1418 // 285220 // hypothetical protein DKFZp434C1418	FLJ22609	FLJ22609 , rs9288884, hypothetical protein FLJ22609 ,q11.2
SNP_A-2250565	cttagtgacaaaacca[A/G]tctttcataatatgac	A	G	ENST00000332119 // upstream // 329539 // --- // --- // --- /// ENST00000330649 // upstream // 1082078 // --- // --- // ---	-	q11.2
SNP_A-1796197	ggtgtctgaagaatta[A/G]gcagtgatagattcga	A	G	ENST00000332119 // upstream // 355596 // --- // --- // --- /// ENST00000330649 // upstream // 1056021 // --- // --- // ---	-	q11.2
SNP_A-1844699	tataagagacttgaaa[C/T]gataatcctacaggaa	C	T	ENST00000332119 // upstream // 367518 // --- // --- // --- /// ENST00000330649 // upstream // 1044099 // --- // --- // ---	-	q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225324	cgtttcattaatagtat[A/G]catactctgcacatac	A	G	ENST00000332119 // upstream // 405576 // --- // --- // --- /// ENST00000330649 // upstream // 1006041 // --- // --- // ---	-	q11.2
SNP_A-1973570	gctaagttgaacctgt[C/T]aaattgagttctcctc	C	T	ENST00000332119 // upstream // 473364 // --- // --- // --- /// ENST00000330649 // upstream // 938253 // --- // --- // ---	-	q11.2
SNP_A-2063662	aattactagacctgaa[A/C]atttacaatacacct	A	C	ENST00000332119 // upstream // 494557 // --- // --- // --- /// ENST00000330649 // upstream // 917060 // --- // --- // ---	-	q11.2
SNP_A-1834207	tacatgatttttatcc[G/T]atactcatctgtga	G	T	ENST00000332119 // upstream // 524692 // --- // --- // --- /// ENST00000330649 // upstream // 886925 // --- // --- // ---	-	q11.2
SNP_A-1888343	tgagcttaacatttta[C/G]ggagattatgaacct	C	G	ENST00000332119 // upstream // 564353 // --- // --- // --- /// ENST00000330649 // upstream // 847264 // --- // --- // ---	-	q11.2
SNP_A-1833084	tacacagtgtaagtga[C/G]ataaaaacagaaacac	C	G	ENST00000332119 // upstream // 577421 // --- // --- // --- /// ENST00000330649 // upstream // 834196 // --- // --- // ---	-	q11.2
SNP_A-1924710	ttataggtgttgatc[A/T]aaaaggacaacggagg	A	T	ENST00000332119 // upstream // 577469 // --- // --- // --- /// ENST00000330649 // upstream // 834148 // --- // --- // ---	-	q11.2
SNP_A-2279899	gaggctagaggttcaa[A/G]atcgaggtgtcagtat	A	G	ENST00000332119 // upstream // 596186 // --- // --- // --- /// ENST00000330649 // upstream // 815431 // --- // --- // ---	-	q11.2
SNP_A-2195986	catgtctaaccgtgat[A/G]agttaaaatagaacta	A	G	ENST00000332119 // upstream // 641517 // --- // --- // --- /// ENST00000330649 // upstream // 770100 // --- // --- // ---	-	q11.2
SNP_A-2132455	atagtgaatatcatta[C/T]gctccacctagatttc	C	T	ENST00000332119 // upstream // 678350 // --- // --- // --- /// ENST00000330649 // upstream // 733267 // --- // --- // ---	-	q11.2
SNP_A-1857925	tcacttctcaaaaaca[A/G]acattcacatggccaa	A	G	ENST00000332119 // upstream // 680558 // --- // --- // --- /// ENST00000330649 // upstream // 731059 // --- // --- // ---	-	q11.2
SNP_A-2048449	aagcatacatgagtat[C/G]aatagccaaatcgatc	C	G	ENST00000332119 // upstream // 1154472 // --- // --- // --- /// ENST00000330649 // upstream // 257145 // --- // --- // ---	-	q11.2
SNP_A-2256744	ctttcatgcaatttttc[C/T]atgatacctctcagt	C	T	ENST00000332119 // upstream // 1199258 // --- // --- // --- /// ENST00000330649 // upstream // 212359 // --- // --- // ---	-	q11.2
SNP_A-2258658	ctttgatggagaggcc[A/T]actttgatttgtcag	A	T	ENST00000332119 // upstream // 1363412 // --- // --- // --- /// ENST00000330649 // upstream // 48205 // --- // --- // ---	-	q11.2
SNP_A-2021760	aaaaacagtatttcga[A/G]caattaatgctgtagt	A	G	ENST00000332119 // upstream // 1404433 // --- // --- // --- /// ENST00000330649 // upstream // 7184 // --- // --- // ---	-	q11.2
SNP_A-2121198	agtctggaacttagtc[C/T]atatgtagaaatctg	C	T	ENST00000338994 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-1729822	ataattctaagaatcattgtaatct[A/G]aacttttaaaccaggtttta attgc	A	G	NM_019895 // downstream // 309639 // Hs.107393 // C3orf4 // 56650 // chromosome 3 open reading frame 4 /// NM_032778 // upstream // 233757 // Hs.23294 // MINA // 84864 // MYC induced nuclear antigen /// NM_153605 // downstream // 260879 // - // - // -	C3orf4	C3orf4, rs1024055, chromosome 3 open reading frame 4 q12.1
SNP_A-2039992	aacatttgcaatggaa[C/T]tgtgagttgaaattgg	C	T	ENST00000341450 // downstream // 24992 // --- // --- // --- /// ENST00000359776 // upstream // 60 // --- // --- // ---	-	q12.1
SNP_A-2226450	ctaagattcaaaatta[A/G]gcatcctgattccaga	A	G	NM_001004737 // upstream // 42267 // Hs.531371 // OR5K2 // 402135 // Homo sapiens olfactory receptor, family 5, subfamily K, member 2 (OR5K2), mRNA. /// NM_001004736 // upstream // 42267 // Hs.531371 // OR5K1 // 26339 // Homo sapiens olfactory receptor, 1	OR5K2	OR5K2, Homo sapiens olfactory receptor, family 5, subfamily K, member 2 (OR5K2), q12.1
SNP_A-1973606	tgtcagcaacaaagaa[A/G]gaagtgttaatgatag	A	G	NM_005290 // downstream // 67 // Hs.159900 // GPR15 // 2838 // Homo sapiens G protein-coupled receptor 15 (GPR15), mRNA. /// NM_000097 // downstream // 46265 // Hs.476982 // CPOX // 1371 // Homo sapiens coproporphyrinogen oxidase (CPOX), mRNA. /// ENST000	GPR15	GPR15, Homo sapiens G protein-coupled receptor 15 (GPR15), q12.1
SNP_A-1973619	tgacaatcctggttga[C/T]tacttctttttcaagct	C	T	NM_080927 // upstream // 92732 // Hs.203691 // DCBLD2 // 131566 // Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// NM_020351 // upstream // 644189 // Hs.134830 // COL8A1 // 1295 // Homo sapiens collagen, type VIII, alpha 1 (CO	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101984	agatggtggtttctta[A/G]ggaaaagatatatggt	A	G	NM_080927 // upstream // 713868 // Hs.203691 // DCBLD2 // 131566 // Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// NM_020351 // upstream // 23053 // Hs.134830 // COL8A1 // 1295 // Homo sapiens collagen, type VIII, alpha 1 (CO	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1
SNP_A-1973641	aggaatgaggaacaca[C/G]tcaaaatatcaagaaa	C	G	NM_080927 // upstream // 721310 // Hs.203691 // DCBLD2 // 131566 // Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// NM_020351 // upstream // 15611 // Hs.134830 // COL8A1 // 1295 // Homo sapiens collagen, type VIII, alpha 1 (CO	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1
SNP_A-1854364	tcaaatagagggtcc[A/G]aaagactgcgggctcc	A	G	NM_080927 // upstream // 727878 // Hs.203691 // DCBLD2 // 131566 // Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA. /// NM_020351 // upstream // 9043 // Hs.134830 // COL8A1 // 1295 // Homo sapiens collagen, type VIII, alpha 1 (COL	DCBLD2	DCBLD2, Homo sapiens discoidin, CUB and LCCL domain containing 2 (DCBLD2), q12.1
SNP_A-1960770	ttttctgtataaaca[C/T]tgatgaatccaggta	C	T	NM_020351 // intron // 0 // Hs.134830 // COL8A1 // 1295 // Homo sapiens collagen, type VIII, alpha 1 (COL8A1), transcript variant 2, mRNA. /// NM_001850 // intron // 0 // Hs.134830 // COL8A1 // 1295 // Homo sapiens collagen, type VIII, alpha 1 (COL8A1), t	COL8A1	COL8A1, Homo sapiens collagen, type VIII, alpha 1 (COL8A1), transcript variant 2, q12.1
SNP_A-1913913	tgtgtgaaacataccа[C/G]tgacaaaaatggtga	C	G	NM_018309 // downstream // 2072 // Hs.477003 // FLJ11046 // 55773 // Homo sapiens hypothetical protein FLJ11046 (FLJ11046), mRNA. /// NM_020202 // upstream // 8976 // Hs.439152 // NIT2 // 56954 // Homo sapiens nitrilase family, member 2 (NIT2), mRNA. ///	FLJ11046	FLJ11046, Homo sapiens hypothetical protein FLJ11046 (FLJ11046), q12.2
SNP_A-1973656	aaatgctccttactc[C/G]caacagtgtaaaccat	C	G	NM_014820 // 3UTR // 0 // Hs.227253 // TOMM70A // 9868 // Homo sapiens translocase of outer mitochondrial membrane 70 homolog A (yeast) (TOMM70A), nuclear gene encoding mitochondrial pro /// ENST00000284320 // 3UTR // 0 // — // — // — // —	TOMM70A	TOMM70A, Homo sapiens translocase of outer mitochondrial membrane 70 homolog A (yeast) (TOMM70A), nuclear gene encoding mitochondrial pro q12.2
SNP_A-1862402	tcatgtctgcaatgcc[A/G]atatccccctactcca	A	G	NM_006070 // intron // 0 // Hs.518123 // TFG // 10342 // Homo sapiens TRK-fused gene (TFG), mRNA. /// ENST00000240851 // intron // 0 // — // — // — // — // —	TFG	TFG, Homo sapiens TRK-fused gene (TFG), q12.2
SNP_A-2163612	caaaaagataatgcac[A/G]atgagattgcctacca	A	G	NM_015429 // 3UTR // 0 // Hs.477015 // ABI3BP // 25890 // Homo sapiens target of Nesh-SH3 (TARSH), mRNA. /// ENST00000284322 // 3UTR // 0 // — // — // — // —	ABI3BP	ABI3BP, Homo sapiens target of Nesh-SH3 (TARSH), q12.2
SNP_A-2069182	acaattctgcttgtta[C/T]tggattgagctaggtt	C	T	NM_015429 // intron // 0 // Hs.477015 // ABI3BP // 25890 // Homo sapiens target of Nesh-SH3 (TARSH), mRNA. /// ENST00000284322 // intron // 0 // — // — // — // —	ABI3BP	ABI3BP, Homo sapiens target of Nesh-SH3 (TARSH), q12.2
SNP_A-1922437	ttagaacactctgcta[C/T]gctattggaatgtttt	C	T	NM_015429 // upstream // 84630 // Hs.477015 // ABI3BP // 25890 // Homo sapiens target of Nesh-SH3 (TARSH), mRNA. /// NM_016247 // downstream // 148694 // Hs.272380 // IMPG2 // 50939 // Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), mRNA. /	ABI3BP	ABI3BP, Homo sapiens target of Nesh-SH3 (TARSH), q12.2
SNP_A-1790273	ggggaggaacatcaga[A/C]taacagtggacttctc	A	C	NM_016247 // intron // 0 // Hs.272380 // IMPG2 // 50939 // Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), mRNA. /// ENST00000193391 // intron // 0 // — // — // — // —	IMPG2	IMPG2, Homo sapiens interphotoreceptor matrix proteoglycan 2 (IMPG2), q12.3
SNP_A-2109984	aggaagaagttgcata[C/T]gttataggcccaacta	C	T	NM_000986 // upstream // 4108 // Hs.477028 // RPL24 // 6152 // Homo sapiens ribosomal protein L24 (RPL24), mRNA. /// ENST00000265264 // upstream // 4108 // — // — // — // — /// ENST00000360269 // upstream // 2184 // — // — // — // —	RPL24	RPL24, Homo sapiens ribosomal protein L24 (RPL24), q12.3
SNP_A-2088625	actgtgactacgataa[G/T]cttccgataaccaacg	G	T	NM_145037 // intron // 0 // Hs.130195 // FAM55C // 91775 // Homo sapiens hypothetical protein MGC15606 (MGC15606), mRNA. /// ENST00000273347 // intron // 0 // — // — // — // —	FAM55C	FAM55C, Homo sapiens hypothetical protein MGC15606 (MGC15606), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2292995	gcagaagtaataccac[A/G]gaggcgctatatgctg	A	G	NM_031419 // downstream // 86985 // Hs.319171 // NFKBIZ // 64332 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, /// NM_175056 // upstream // 487012 // Hs.352213 // LOC1313	NFKBIZ	NFKBIZ, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, q12.3
SNP_A-2294851	gcagtttttcccaacc[A/G]agcgtctacctttgat	A	G	NM_031419 // downstream // 91893 // Hs.319171 // NFKBIZ // 64332 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, /// NM_175056 // upstream // 482104 // Hs.352213 // LOC1313	NFKBIZ	NFKBIZ, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, q12.3
SNP_A-2137206	atcagtactaacacaa[C/T]tatttttacataaacc	C	T	NM_031419 // downstream // 130495 // Hs.319171 // NFKBIZ // 64332 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, /// NM_175056 // upstream // 443502 // Hs.352213 // LOC131	NFKBIZ	NFKBIZ, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, q12.3
SNP_A-1973695	aagcccactacaagga[A/T]ctgagcaacatggtca	A	T	NM_031419 // downstream // 223644 // Hs.319171 // NFKBIZ // 64332 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, /// NM_175056 // upstream // 350353 // Hs.352213 // LOC131	NFKBIZ	NFKBIZ, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (NFKBIZ), transcript variant 1, q12.3
SNP_A-2154529	attattgcctggcatc[A/G]aaaatatgggggaagg	A	G	NM_175056 // 3UTR // 0 // Hs.352213 // LOC131368 // 131368 // Homo sapiens hypothetical protein LOC131368 (LOC131368), mRNA. /// ENST00000306176 // 3UTR // 0 // --- // --- // --- // ---	LOC131368	LOC131368, Homo sapiens hypothetical protein LOC131368 (LOC131368), q12.3
SNP_A-1701721	actatttttgagcatctctttgcta[C/T]gtaaaattgtatttgctttacagat	C	T	NM_001627 // upstream // 2488077 // Hs.10247 // ALCAM // 214 // activated leukocyte cell adhesion molecule /// NM_175056 // downstream // 399428 // Hs.352213 // LOC131368 // 131368 // hypothetical protein LOC131368	ALCAM	ALCAM , rs1241287, activated leukocyte cell adhesion molecule ,q12.3
SNP_A-1860207	tcagtcccctcatccc[A/G]aagatagagtatccag	A	G	NM_175056 // downstream // 256915 // Hs.352213 // LOC131368 // 131368 // Homo sapiens hypothetical protein LOC131368 (LOC131368), mRNA. /// ENST00000306176 // downstream // 256915 // --- // --- // --- // --- /// ENST00000273343 // upstream // 504233 // ---	LOC131368	LOC131368, Homo sapiens hypothetical protein LOC131368 (LOC131368), q12.3
SNP_A-2283089	gataagtcatctagca[A/C]gtaaggctatcaatta	A	C	NM_175056 // downstream // 452338 // Hs.352213 // LOC131368 // 131368 // Homo sapiens hypothetical protein LOC131368 (LOC131368), mRNA. /// ENST00000306176 // downstream // 452338 // --- // --- // --- // --- /// ENST00000273343 // upstream // 308810 // ---	LOC131368	LOC131368, Homo sapiens hypothetical protein LOC131368 (LOC131368), q12.3
SNP_A-2129937	atacattcaaaccata[A/G]ccagctttaaactcaa	A	G	NM_175056 // downstream // 683256 // Hs.352213 // LOC131368 // 131368 // Homo sapiens hypothetical protein LOC131368 (LOC131368), mRNA. /// ENST00000306176 // downstream // 683256 // --- // --- // --- // --- /// ENST00000273343 // upstream // 77892 // ---	LOC131368	LOC131368, Homo sapiens hypothetical protein LOC131368 (LOC131368), q13.11
SNP_A-1973727	gttggctactgtactc[A/G]ctgttcataaactgtt	A	G	NM_001627 // upstream // 1681649 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 444030 // --- // --- // --- // --- /// ENST00000306107 // upstream // 1681649 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2249846	cttacaaaccttatga[G/T]agtctaaaacgagaat	G	T	NM_001627 // upstream // 1659900 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 465779 // --- // --- // --- // --- /// ENST00000306107 // upstream // 1659900 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2305962	gctgctccactggc[C/T]atcttggtctcctc	C	T	NM_001627 // upstream // 1254078 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 871601 // — // — // — // — /// ENST00000306107 // upstream // 1254078 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1973742	aggctggagtacagc[A/T]atatgcatcctggcag	A	T	NM_001627 // upstream // 1240347 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 885332 // — // — // — // — /// ENST00000306107 // upstream // 1240347 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1945650	ttgttgacagctgtta[C/T]aatacacaaggtacca	C	T	NM_001627 // upstream // 1238837 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 886842 // — // — // — // — /// ENST00000306107 // upstream // 1238837 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1953416	tttgaacatggctgtg[A/G]attaaatgataatatt	A	G	NM_001627 // upstream // 1171003 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 954676 // — // — // — // — /// ENST00000306107 // upstream // 1171003 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2139191	atcctctaacattaca[A/T]ggcaatatttcacttt	A	T	NM_001627 // upstream // 1170056 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 955623 // — // — // — // — /// ENST00000306107 // upstream // 1170056 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1973744	aatattcattaaagta[A/G]gagagctacagggtcc	A	G	NM_001627 // upstream // 1169971 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 955708 // — // — // — // — /// ENST00000306107 // upstream // 1169971 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1729548	tacttagaagcaatgtaatgatgcc[A/G]gacagttaataaactaga aaatatca	A	G	NM_001627 // upstream // 990181 // Hs.10247 // ALCAM // 214 // activated leukocyte cell adhesion molecule /// NM_175056 // downstream // 1897324 // Hs.352213 // LOC131368 // 131368 // hypothetical protein LOC131368	ALCAM	ALCAM , rs10511224, activated leukocyte cell adhesion molecule ,q13.11
SNP_A-1945495	ttgttcatagttatca[C/T]tcattgtcaacataat	C	T	NM_001627 // upstream // 1147318 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 978361 // — // — // — // — /// ENST00000306107 // upstream // 1147318 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1930451	ttccaaaatgtaaaga[C/T]ggaacaccataaaca	C	T	NM_001627 // upstream // 1133404 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 992275 // — // — // — // — /// ENST00000306107 // upstream // 1133404 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2274077	gacttatagaaattggc[C/T]atcatggaatttgcc	C	T	NM_001627 // upstream // 1133212 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 992467 // — // — // — // — /// ENST00000306107 // upstream // 1133212 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2150943	atgtgggtttatctga[A/G]catcttcctgttgggc	A	G	NM_001627 // upstream // 1114150 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA /// ENST00000273343 // downstream // 1011529 // — // — // — // - /// ENST00000306107 // upstream // 1114150 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137226	atcagtcaagtcaaag[C/G]attcttagtgatagcc	C	G	NM_001627 // upstream // 1110433 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 1015246 // — // — // — // — /// ENST00000306107 // upstream // 1110433 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2023444	aaaacggaaaatgtg[A/T]atgtgtaatgtaccac	A	T	NM_001627 // upstream // 1087788 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 1037891 // — // — // — // — /// ENST00000306107 // upstream // 1087788 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2302416	gctaagtttatccat[G/T]aaaagagaccgttag	G	T	NM_001627 // upstream // 1087165 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 1038514 // — // — // — // — /// ENST00000306107 // upstream // 1087165 //	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1929532	ttcataatcttataaa[A/G]ttccaggaagctgaat	A	G	NM_001627 // upstream // 667056 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 1458623 // — // — // — // — /// ENST00000306107 // upstream // 667056 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1973780	tcctttagttacatg[C/G]agtcatttttgtccac	C	G	NM_001627 // upstream // 100110 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// ENST00000273343 // downstream // 2025569 // — // — // — // — /// ENST00000306107 // upstream // 100110 // -	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-1687556	aaataatgataaaaagtatagtata[A/G]taagtacataaaccag taacattca	A	G	NM_170662 // intron // 0 // Hs.436986 // CBLB // 868 // Cas-Br-M (murine) ecotropic retroviral transforming sequence b	CBLB	CBLB , rs726444, Cas-Br-M (murine) ecotropic retroviral transforming sequence b,q13.11
SNP_A-2131135	atagacctatgataag[A/G]acatttccacggtatt	A	G	NM_001627 // downstream // 42409 // Hs.150693 // ALCAM // 214 // Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA. /// NM_170662 // downstream // 38967 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral	ALCAM	ALCAM, Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), q13.11
SNP_A-2079966	accctgtttcaaggc[A/G]actcagaagaggaat	A	G	NM_170662 // intron // 0 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000264122 // intron // 0 // — // - /// ENST00000346031 // intron // 0 // — // — ///	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-2144394	atgataagtagaaaaa[A/G]agaagccagcgaaaaa	A	G	NM_170662 // intron // 0 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // intron // 0 // — // — // — // — /// ENST00000264122 // intron // 0 // — // -	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-2078211	accagtgctttggtac[C/T]gctaaggctgtgattg	C	T	NM_170662 // intron // 0 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // intron // 0 // — // — // — // — /// ENST00000264122 // intron // 0 // — // -	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1846659	tatatttattccctc[A/G]actgccaggttcatta	A	G	NM_170662 // intron // 0 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // intron // 0 // — // — // — // — /// ENST00000264122 // intron // 0 // — // -	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1694411	catgaactctctttattaggaag[C/T]attgcagaacaaaaatga aactcag	G	T	NM_032600 // upstream // 1366162 // Hs.164799 // NYD-SP17 // 84692 // testes development-related NYD-SP17 /// NM_170662 // upstream // 142198 // Hs.436986 // CBLB // 868 // Cas-Br-M (murine) ecotropic retroviral transforming sequence b	NYD-SP17	NYD-SP17 , rs2127091, testes development-related NYD-SP17 ,q13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2262706	gaaattgccattgaaa[C/T]gagttaaggcctaccc	C	T	NM_170662 // upstream // 199672 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 201078 // — // — // — /// ENST00000264122 // upstream	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-2126040	agttttgagaacagat[C/T]atcaacagtgtcaaat	C	T	NM_170662 // upstream // 302275 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 303681 // — // — // — /// ENST00000264122 // upstream	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.11
SNP_A-1726970	ctttctcatctcatggaggatga[C/T]atttaaggaagatgaac attaca	C	T	NM_032600 // upstream // 848360 // Hs.164799 // NYD-SP17 // 84692 // testes development-related NYD-SP17 /// NM_170662 // upstream // 660000 // Hs.436986 // CBLB // 868 // Cas-Br-M (murine) ecotropic retroviral transforming sequence b	NYD-SP17	NYD-SP17, rs7627016, testes development-related NYD-SP17, q13.12
SNP_A-2162422	attttcaatttaaaac[A/G]ggttcattggaacata	A	G	NM_170662 // upstream // 767587 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 768993 // — // — // — /// ENST00000264122 // upstream	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.12
SNP_A-1908498	tgtaggaggtaagataa[A/G]ttagaatatgggctct	A	G	NM_170662 // upstream // 912268 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 913674 // — // — // — /// ENST00000264122 // upstream	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.12
SNP_A-1824021	taaacaaagggtaatat[A/C]attggaagagcagtag	A	C	NM_170662 // upstream // 935407 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 936813 // — // — // — /// ENST00000264122 // upstream	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.12
SNP_A-1898821	tgctttgctttcagta[A/G]cattagctgaagtaat	A	G	NM_170662 // upstream // 940816 // Hs.430589 // CBLB // 868 // Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA. /// ENST00000346031 // upstream // 942222 // — // — // — /// ENST00000264122 // upstream	CBLB	CBLB, Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), q13.12
SNP_A-2196721	cattaatttagtagcg[A/G]aactcttcatatccat	A	G	NM_032600 // upstream // 482752 // Hs.164799 // NYD-SP17 // 84692 // Homo sapiens testes development-related NYD-SP17 (NYD-SP17), mRNA. /// ENST00000355304 // upstream // 44932 // — // — // — // — /// ENST00000261058 // upstream // 482752 // — /	NYD-SP17	NYD-SP17, Homo sapiens testes development-related NYD-SP17 (NYD-SP17), q13.12
SNP_A-1730865	ctgaagaaacagttgtgaattaaaa[C/T]gagcaaatatagtaaa tattatta	C	T	NM_020235 // intron // 0 // Hs.35380 // BBX // 56987 // bobby sox homolog (Drosophila)	BBX	BBX, rs6612276, bobby sox homolog (Drosophila),q13.12
SNP_A-2184248	cagcctggattgagta[A/G]ccatttcatgctggag	A	G	NM_020235 // intron // 0 // Hs.124366 // BBX // 56987 // Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// ENST00000325839 // intron // 0 // — // — // — // — /// ENST00000325767 // intron // 0 // — // — // —	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1890297	tgatcattccatgtaa[C/T]gtgactactcaacagg	C	T	NM_020235 // downstream // 69779 // Hs.124366 // BBX // 56987 // Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA. /// NM_198793 // downstream // 167681 // Hs.446414 // CD47 // 961 // Homo sapiens CD47 antigen (Rh-related antigen, integrin-associat	BBX	BBX, Homo sapiens bobby sox homolog (Drosophila) (BBX), q13.12
SNP_A-1752045	ctaaactatcttgactgattaca[A/G]gtgtcttttcaaacttgagc tgtg	A	G	AB023217 // intron // 0 // Hs.225968 // KIAA1000 // 22989 // KIAA1000 protein	KIAA1000	KIAA1000, rs10511271, KIAA1000 protein,q13.13
SNP_A-2268564	gaatggttctagacaa[C/T]aacttttcatggaggg	C	T	NM_007072 // intron // 0 // Hs.252351 // HHLA2 // 11148 // Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA. /// ENST00000357759 // intron // 0 // — // — // — // — /// ENST00000264542 // intron // 0 // — // — // —	HHLA2	HHLA2, Homo sapiens HERV-H LTR-associating 2 (HHLA2), q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1940404	ttgccagggttaacac[A/G]gcagacagcaggcatt	A	G	NM_007072 // intron // 0 // Hs.252351 // HHLA2 // 11148 // Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA. /// ENST00000357759 // intron // 0 // — // — // — // — /// ENST00000264542 // intron // 0 // — // — // — // —	HHLA2	HHLA2, Homo sapiens HERV-H LTR-associating 2 (HHLA2), q13.13
SNP_A-1780900	ggatgaagcacttgaa[C/T]aggaatccacattaca	C	T	NM_007072 // intron // 0 // Hs.252351 // HHLA2 // 11148 // Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA. /// ENST00000357759 // intron // 0 // — // — // — // — /// ENST00000264542 // intron // 0 // — // — // — // —	HHLA2	HHLA2, Homo sapiens HERV-H LTR-associating 2 (HHLA2), q13.13
SNP_A-2188034	cagtcactgtggcaaq[C/T]aaaatgatcccacaga	C	T	ENST00000273353 // intron // 0 // — // — // —	-	q13.13
SNP_A-2068839	acaatcatcctgtca[C/T]acaatagaaggtagaa	C	T	NM_014429 // intron // 0 // Hs.278908 // MORC // 27136 // Homo sapiens microrchidia homolog (mouse) (MORC), mRNA. /// ENST00000232603 // intron // 0 // — // — // — // —	MORC	MORC, Homo sapiens microrchidia homolog (mouse) (MORC), q13.13
SNP_A-2306583	gctgtacagaaagcac[A/G]gctgggaagtctcag	A	G	NM_014429 // upstream // 33954 // Hs.278908 // MORC // 27136 // Homo sapiens microrchidia homolog (mouse) (MORC), mRNA. /// NM_138815 // downstream // 141719 // Hs.351113 // DPPA2 // 151871 // Homo sapiens hypothetical protein BC018070 (LOC151871), mRNA.	MORC	MORC, Homo sapiens microrchidia homolog (mouse) (MORC), q13.13
SNP_A-2305609	gctgcagggagctggc[G/T]aataggtagaacttgg	G	T	NM_018189 // upstream // 27104 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 27104 // — // — // — // — /// ENST00000355901 // upstream // 33842 // — // -	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2035368	aaatggcatcacacat[A/G]acgatcagagactgaa	A	G	NM_018189 // upstream // 44411 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 44411 // — // — // — // — /// ENST00000355901 // upstream // 51149 // — // -	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2312472	ggacccacttgaaaca[C/T]gagagttgatacgaag	C	T	NM_018189 // upstream // 44574 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 44574 // — // — // — // — /// ENST00000355901 // upstream // 51312 // — // -	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1847066	tatcatacaaatgtaa[A/G]acaataagagggaaaa	A	G	NM_018189 // upstream // 86824 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 86824 // — // — // — // — /// ENST00000355901 // upstream // 93562 // — // -	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1973868	gttgctagacttttaaa[A/G]acgcacaattatctgt	A	G	NM_018189 // upstream // 99854 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 99854 // — // — // — // — /// ENST00000355901 // upstream // 106592 // — // -	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2290824	gcaaggaacatttcca[A/G]gatcaactgtgtgcagg	A	G	NM_018189 // upstream // 118192 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 118192 // — // — // — // — /// ENST00000355901 // upstream // 124930 // — //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2131627	atagccaaatacaaac[A/G]gtagaactcatttaga	A	G	NM_018189 // upstream // 124447 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 124447 // — // — // — // — /// ENST00000355901 // upstream // 131185 // — //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123521	agtgtgctatagagtct[C/T]aaagtgctaaccaaaa	C	T	NM_018189 // upstream // 193303 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 193303 // --- // --- // --- /// ENST00000355901 // upstream // 200041 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1821807	gttttaccttcacag[A/G]cattacttcccaataa	A	G	NM_018189 // upstream // 243941 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 243941 // --- // --- // --- /// ENST00000355901 // upstream // 250679 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1849057	tatgccaagatgacaa[A/G]tgagaagtgcaagtgt	A	G	NM_018189 // upstream // 243975 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 243975 // --- // --- // --- /// ENST00000355901 // upstream // 250713 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1788446	gggagtgtctgtttta[C/T]gtggttaaggactgaa	C	T	NM_018189 // upstream // 246436 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 246436 // --- // --- // --- /// ENST00000355901 // upstream // 253174 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1795347	ggtgatggtataagta[A/C]gacaatgatactgtg	A	C	NM_018189 // upstream // 268234 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 268234 // --- // --- // --- /// ENST00000355901 // upstream // 274972 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-1689610	tagagaatgcaacatgtcagagata[C/G]attttcaaacaagttta accaccta	C	G	NM_015480 // upstream // 1297750 // Hs.436602 // PVRL3 // 25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 436770 // Hs.317659 // DPPA4 // 55211 // developmental pluripotency associated 4	PVRL3	PVRL3 , rs10511278, poliovirus receptor-related 3 ,q13.13
SNP_A-2008970	ggctactttctatgccq[C/G]cagttagaacttctc	C	G	NM_018189 // upstream // 275898 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 275898 // --- // --- // --- /// ENST00000355901 // upstream // 282636 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2068627	acaataaacatacaaa[C/G]caggtaacacacatag	C	G	NM_018189 // upstream // 448760 // Hs.317659 // DPPA4 // 55211 // Homo sapiens developmental pluripotency associated 4 (DPPA4), mRNA. /// ENST00000335658 // upstream // 448760 // --- // --- // --- /// ENST00000355901 // upstream // 455498 // --- //	DPPA4	DPPA4, Homo sapiens developmental pluripotency associated 4 (DPPA4), q13.13
SNP_A-2216581	cctctagtcctaagccq[A/G]cagggaatctacttc	A	G	ENST00000309365 // upstream // 34534 // --- // --- // --- /// ENST00000331815 // downstream // 940666 // --- // --- // ---	-	q13.13
SNP_A-1746947	gcagaaaacgtatatgaatccacca[C/T]gattagtctctttaaac tcagatc	C	T	NM_015480 // upstream // 897025 // Hs.436602 // PVRL3 // 25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 837495 // Hs.317659 // DPPA4 // 55211 // developmental pluripotency associated 4	PVRL3	PVRL3 , rs1903580, poliovirus receptor-related 3 ,q13.13
SNP_A-1735871	ttggcaagctacttacctctgcatc[A/G]ctctgatagagaaatga gtatcttt	A	G	NM_015480 // upstream // 877826 // Hs.436602 // PVRL3 // 25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 856694 // Hs.317659 // DPPA4 // 55211 // developmental pluripotency associated 4	PVRL3	PVRL3 , rs1993754, poliovirus receptor-related 3 ,q13.13
SNP_A-1724722	gcaccctccaaaatgtcaaagaccaa[A/T]taagaactatttgtttg ccaacaa	A	T	NM_015480 // upstream // 830631 // Hs.436602 // PVRL3 // 25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 903889 // Hs.317659 // DPPA4 // 55211 // developmental pluripotency associated 4	PVRL3	PVRL3 , rs1381365, poliovirus receptor-related 3 ,q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1701973	tggtgtttttcaataagagtttttaca[C/T]gagctaaatgatggaaaaca attaat	C	T	NM_015480 // upstream // 717666 // Hs.436602 // PVRL3 // 25945 // poliovirus receptor-related 3 /// NM_018189 // upstream // 1016854 // Hs.317659 // DPPA4 // 55211 // developmental pluripotency associated 4	PVRL3	PVRL3 , rs6795038, poliovirus receptor-related 3 q13.13
SNP_A-2231590	ctatttgaagagtgagg[A/G]aaaatgggatttctg	A	G	ENST00000309365 // upstream // 813313 // — // — // — /// ENST00000331815 // downstream // 161887 // — // — // — // —	-	q13.13
SNP_A-1973903	caagcccttataccaa[A/T]gcttactatttcaagg	A	T	ENST00000309365 // upstream // 889786 // — // — // — /// ENST00000331815 // downstream // 85414 // — // — // —	-	q13.13
SNP_A-2042678	aactcctcactcgaa[C/T]ctccaagtcagtgtct	C	T	NM_015480 // downstream // 152057 // Hs.293917 // PVRL3 // 25945 // Homo sapiens poliovirus receptor-related 3 (PVRL3), mRNA. /// NM_005816 // upstream // 255737 // Hs.142023 // CD96 // 10225 // Homo sapiens CD96 antigen (CD96), transcript variant 2, mRNA	PVRL3	PVRL3, Homo sapiens poliovirus receptor-related 3 (PVRL3), q13.13
SNP_A-1973926	aggtgttcaaatgcgg[A/G]attcgttgatactac	A	G	NM_005816 // intron // 0 // Hs.142023 // CD96 // 10225 // Homo sapiens CD96 antigen (CD96), transcript variant 2, mRNA. /// NM_198196 // intron // 0 // Hs.142023 // CD96 // 10225 // Homo sapiens CD96 antigen (CD96), transcript variant 1, mRNA. /// ENST000	CD96	CD96, Homo sapiens CD96 antigen (CD96), transcript variant 2, q13.13
SNP_A-1802857	gtatgtaaactcagtat[C/T]gtaaaaaactcagtaa	C	T	NM_153268 // intron // 0 // Hs.292419 // PLCXD2 // 257068 // Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 2 (PLCXD2), mRNA. /// ENST00000312791 // intron // 0 // — // — // —	PLCXD2	PLCXD2, Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 2 (PLCXD2), q13.2
SNP_A-2080384	acctactctaagaaa[G/T]ggactgaatcaggggg	G	T	ENST00000305815 // intron // 0 // — // — // —	-	q13.2
SNP_A-2163807	caaaacacacaaacaa[A/C]gcgaggaaagcaaggg	A	C	NM_001004196 // downstream // 20909 // Hs.79015 // CD200 // 4345 // Homo sapiens CD200 antigen (CD200), transcript variant 2, mRNA. /// NM_005944 // downstream // 20909 // Hs.79015 // CD200 // 4345 // Homo sapiens CD200 antigen (CD200), transcript variant	CD200	CD200, Homo sapiens CD200 antigen (CD200), transcript variant 2, q13.2
SNP_A-2008988	ttctagactcaagatg[C/T]aataacacaggggcag	C	T	NM_181780 // upstream // 7729 // Hs.445162 // BTLA // 151888 // Homo sapiens B and T lymphocyte associated (BTLA), mRNA. /// NM_022488 // downstream // 25612 // Hs.477126 // APG3L // 64422 // Homo sapiens APG3 autophagy 3-like (S. cerevisiae) (APG3L), mRN	BTLA	BTLA, Homo sapiens B and T lymphocyte associated (BTLA), q13.2
SNP_A-1845574	tatagcactcgactca[C/T]aataagccaataaat	C	T	NM_022488 // intron // 0 // Hs.477126 // APG3L // 64422 // Homo sapiens APG3 autophagy 3-like (S. cerevisiae) (APG3L), mRNA. /// ENST00000263290 // intron // 0 // — // — // —	APG3L	APG3L, Homo sapiens APG3 autophagy 3-like (S. cerevisiae) (APG3L), q13.2
SNP_A-2142200	atgaaaaatggcaaca[A/G]ctccaagaatataaca	A	G	NM_017945 // intron // 0 // Hs.237480 // SLC35A5 // 55032 // Homo sapiens solute carrier family 35, member A5 (SLC35A5), mRNA. /// ENST00000261034 // intron // 0 // — // — // — // —	SLC35A5	SLC35A5, Homo sapiens solute carrier family 35, member A5 (SLC35A5), q13.2
SNP_A-2242465	ctgcagagccctaaaa[C/G]ggtgtcacagccctgg	C	G	NM_199512 // upstream // 193823 // Hs.477128 // URB // 151887 // Homo sapiens steroid sensitive gene 1 (URB), transcript variant 2, mRNA. /// NM_199511 // upstream // 193823 // Hs.477128 // URB // 151887 // Homo sapiens steroid sensitive gene 1 (URB), tra	URB	URB, Homo sapiens steroid sensitive gene 1 (URB), transcript variant 2, q13.2
SNP_A-2111044	aggagaattggaaaac[G/T]ggtagagtaaaaggtt	G	T	NM_138940 // upstream // 2493 // Hs.309158 // CD200R1 // 131450 // Homo sapiens CD200 receptor 1 (CD200R1), transcript variant 3, mRNA. /// NM_170780 // upstream // 2493 // Hs.309158 // CD200R1 // 131450 // Homo sapiens CD200 receptor 1 (CD200R1), transcr	CD200R1	CD200R1, Homo sapiens CD200 receptor 1 (CD200R1), transcript variant 3, q13.2
SNP_A-2099058	agaggaagggacttac[A/G]gaattgggacccagac	A	G	NM_015412 // upstream // 16073 // Hs.477134 // C3orf17 // 25871 // Homo sapiens DKFZP434F2021 protein (DKFZP434F2021), mRNA. /// NM_033254 // upstream // 176749 // Hs.528033 // BOC // 91653 // Homo sapiens brother of CDO (BOC), mRNA. /// ENST00000314400 /	C3orf17	C3orf17, Homo sapiens DKFZP434F2021 protein (DKFZP434F2021), q13.2
SNP_A-1735598	agaatgttttccaagagttcttccc[C/T]gatggttgtatttctccctt gc	C	T	NM_033254 // intron // 0 // Hs.214099 // BOC // 91653 // brother of CDO	BOC	BOC , rs10511324, brother of CDO,q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2293406	gcagatgtaataataa[A/G]acagcattggaaattc	A	G	NM_015412 // upstream // 72875 // Hs.477134 // C3orf17 // 25871 // Homo sapiens DKFZP434F2021 protein (DKFZP434F2021), mRNA. /// NM_033254 // upstream // 119947 // Hs.528033 // BOC // 91653 // Homo sapiens brother of CDO (BOC), mRNA. /// ENST00000314400 /	C3orf17	C3orf17, Homo sapiens DKFZP434F2021 protein (DKFZP434F2021), q13.2
SNP_A-1700129	tgaatcctgtgtaaaactgactcaa[C/T]gttcccaactggattatg gactgat	C	T	AL133606 // intron // 0 // Hs.436628 // FLJ11142 // 55779 // hypothetical protein FLJ11142	FLJ11142	FLJ11142 , rs712530, hypothetical protein FLJ11142,q13.2
SNP_A-1973980	atgttctccactgaaa[C/T]aatctcttccaaacag	C	T	NM_033254 // intron // 0 // Hs.528033 // BOC // 91653 // Homo sapiens brother of CDO (BOC), mRNA. /// ENST00000355385 // intron // 0 // --- // --- // --- // --- /// ENST00000273395 // intron // 0 // --- // --- // --- // --- // ---	BOC	BOC, Homo sapiens brother of CDO (BOC), q13.2
SNP_A-2286960	gatggtcctaataacc[A/G]ctcttatttcttttat	A	G	NM_033254 // intron // 0 // Hs.528033 // BOC // 91653 // Homo sapiens brother of CDO (BOC), mRNA. /// ENST00000355385 // 3UTR // 0 // --- // --- // --- /// ENST00000273395 // intron // 0 // --- // --- // --- // --- // ---	BOC	BOC, Homo sapiens brother of CDO (BOC), q13.2
SNP_A-2113300	aggcctcacaagaaca[C/T]ccgccactgtcagagc	C	T	NM_033254 // intron // 0 // Hs.528033 // BOC // 91653 // Homo sapiens brother of CDO (BOC), mRNA. /// ENST00000273395 // intron // 0 // --- // --- // --- // --- // ---	BOC	BOC, Homo sapiens brother of CDO (BOC), q13.2
SNP_A-2008992	aagagagaatgatgta[C/T]acaagagccacagtct	C	T	NM_033254 // downstream // 2303 // Hs.528033 // BOC // 91653 // Homo sapiens brother of CDO (BOC), mRNA. /// NM_018338 // downstream // 73106 // Hs.98704 // WDR52 // 55779 // Homo sapiens hypothetical protein FLJ11142 (FLJ11142), mRNA. /// ENST00000355385	BOC	BOC, Homo sapiens brother of CDO (BOC), q13.2
SNP_A-1795893	ggtgggaggataagac[C/T]gcctttcctacgcaaa	C	T	ENST00000308346 // CDS // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2261880	gaaataactccgatga[A/G]gaaacagaagatttca	A	G	ENST00000308346 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-1743445	taacaagcttaatttttgaattggc[A/G]atatagtcacatattatgaa attca	A	G	NM_144718 // intron // 0 // Hs.72402 // LOC152185 // 152185 // hypothetical protein AY099107	LOC152185	LOC152185 , rs6769604, hypothetical protein AY099107,q13.2
SNP_A-2286449	gatgctgtttgatcga[A/T]tatccacatggttaat	A	T	NM_018338 // intron // 0 // Hs.98704 // WDR52 // 55779 // Homo sapiens hypothetical protein FLJ11142 (FLJ11142), mRNA. /// ENST00000295868 // intron // 0 // --- // --- // --- // ---	WDR52	WDR52, Homo sapiens hypothetical protein FLJ11142 (FLJ11142), q13.2
SNP_A-1668312	catatgttatgggccaaaaagttaa[C/T]atttgagtgtccacagtt gtatttt	C	T	NM_017699 // intron // 0 // Hs.272416 // FLJ20174 // 54847 // hypothetical protein FLJ20174	FLJ20174	FLJ20174 , rs7620700, hypothetical protein FLJ20174,q13.2
SNP_A-2095440	agacaaagtcaaacta[A/G]agggaattctgtaaaa	A	G	NM_144718 // intron // 0 // Hs.477144 // LOC152185 // 152185 // Homo sapiens hypothetical protein AY099107 (LOC152185), mRNA. /// ENST00000295872 // intron // 0 // --- // --- // --- // ---	LOC152185	LOC152185, Homo sapiens hypothetical protein AY099107 (LOC152185), q13.2
SNP_A-1973983	actagagtctctccaa[C/T]gtgaatcaaattgaag	C	T	NM_144718 // intron // 0 // Hs.477144 // LOC152185 // 152185 // Homo sapiens hypothetical protein AY099107 (LOC152185), mRNA. /// ENST00000295872 // intron // 0 // --- // --- // --- // ---	LOC152185	LOC152185, Homo sapiens hypothetical protein AY099107 (LOC152185), q13.2
SNP_A-1841789	taggccatactgttcc[A/G]acaatttaccaccagg	A	G	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2082510	acgctctctttcaggc[A/G]ctggtttgtcactatc	A	G	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2033314	aaatagagatgtatga[C/T]cccagacctacgatct	C	T	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2040482	aaccagtcatgtccaa[A/G]cttctgctctaaagat	A	G	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2107850	agctccaaagttaaac[A/G]atgtaggaagagctgg	A	G	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-1902881	tggctctgaatcagaa[C/T]gtaaagaacaaaattt	C	T	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826274	taaattgcatgatcaa[A/T]agacacgactgtgaaa	A	T	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2084982	actcacacctcacagc[A/C]attttagagtctccct	A	C	NM_017699 // intron // 0 // Hs.272416 // SIDT1 // 54847 // Homo sapiens SID1 transmembrane family, member 1 (SIDT1), mRNA. /// ENST00000264852 // intron // 0 // --- // --- // --- // ---	SIDT1	SIDT1, Homo sapiens SID1 transmembrane family, member 1 (SIDT1), q13.2
SNP_A-2054039	aagttagtaatcttaa[A/G]ctttgtgctaacctcc	A	G	NM_033660 // intron // 0 // Hs.121478 // DRD3 // 1814 // Homo sapiens dopamine receptor D3 (DRD3), transcript variant d, mRNA. /// NM_033659 // intron // 0 // Hs.121478 // DRD3 // 1814 // Homo sapiens dopamine receptor D3 (DRD3), transcript variant c, mRN	DRD3	DRD3, Homo sapiens dopamine receptor D3 (DRD3), transcript variant d, q13.31
SNP_A-1941167	ttgctgagtttatcta[C/T]agtgtctctaggaccc	C	T	NM_007136 // upstream // 6013 // Hs.271079 // ZNF80 // 7634 // Homo sapiens zinc finger protein 80 (pT17) (ZNF80), mRNA. /// NM_173799 // upstream // 47972 // Hs.421750 // FLJ39873 // 201633 // Homo sapiens hypothetical protein FLJ39873 (FLJ39873), mRNA.	ZNF80	ZNF80, Homo sapiens zinc finger protein 80 (pT17) (ZNF80), q13.31
SNP_A-2036847	aaatttctgcaagttc[A/G]aagtcaaatttctgca	A	G	NM_015642 // intron // 0 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // --- // --- // --- /// ENST00000355225 // intron // 0 // --- // --- // --- // ---	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2108665	agctgtaaactgcaaa[C/G]tgctgtataaaagtaa	C	G	NM_015642 // intron // 0 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // --- // --- // --- /// ENST00000355225 // intron // 0 // --- // --- // --- // ---	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2025458	aaaatcctccagagaa[G/T]agaccagtaaattcaa	G	T	NM_015642 // intron // 0 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // --- // --- // --- /// ENST00000355225 // intron // 0 // --- // --- // --- // ---	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2177333	caccttactccattac[A/G]actgcatcttaattag	A	G	NM_015642 // intron // 0 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// ENST00000357258 // intron // 0 // --- // --- // --- // --- /// ENST00000355225 // intron // 0 // --- // --- // --- // ---	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-1917341	tgttttctaggagagc[A/G]attagctaagtttagg	A	G	NM_015642 // upstream // 118763 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream // 507103 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain contain	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2263703	gaacctatctagtcaa[C/T]ggtttaattttacaaa	C	T	NM_015642 // upstream // 134686 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream // 523026 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain contain	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2097339	agagaaacacaagtca[C/T]tactagtcagtccgct	C	T	NM_015642 // upstream // 234089 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream // 622429 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain contain	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-1890323	tgatccagacaagaaa[C/G]atattatcagattatt	C	G	NM_015642 // upstream // 273392 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), mRNA. /// NM_015642 // upstream // 661732 // Hs.477166 // ZBTB20 // 26137 // Homo sapiens zinc finger and BTB domain contain	ZBTB20	ZBTB20, Homo sapiens zinc finger and BTB domain containing 20 (ZBTB20), q13.31
SNP_A-2112400	aggcaagcaaatttta[C/T]gactcttgaattaatt	C	T	NM_002045 // intron // 0 // Hs.134974 // GAP43 // 2596 // Homo sapiens growth associated protein 43 (GAP43), mRNA. /// ENST00000305124 // intron // 0 // --- // --- // --- // --- /// ENST00000358762 // intron // 0 // --- // --- // --- // ---	GAP43	GAP43, Homo sapiens growth associated protein 43 (GAP43), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974034	atgacacgtagcaata[A/G]gcacagtaaccaagct	A	G	NM_002338 // intron // 0 // Hs.477234 // LSAMP // 4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // — // — // —	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-1783560	ggcatgagagtgatta[C/T]gtagggcctattataa	C	T	NM_002338 // intron // 0 // Hs.477234 // LSAMP // 4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // — // — // —	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-2278272	gagcgaaagaagccac[C/G]ataatacagcaatgat	C	G	NM_002338 // intron // 0 // Hs.477234 // LSAMP // 4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // — // — // —	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-2303631	gctcaccttccagtc[A/G]ccattagtgctatttt	A	G	NM_002338 // intron // 0 // Hs.477234 // LSAMP // 4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // intron // 0 // — // — // —	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-1974051	tgcatggccctacctg[G/T]ctcaatttaaatgtca	G	T	NM_002338 // upstream // 152863 // Hs.477234 // LSAMP // 4045 // Homo sapiens limbic system-associated membrane protein (LSAMP), mRNA. /// ENST00000333617 // upstream // 152863 // — // — // — /// ENST00000359893 // downstream // 48003 // —	LSAMP	LSAMP, Homo sapiens limbic system-associated membrane protein (LSAMP), q13.31
SNP_A-1742239	taataatgccaccatttttatttct[C/T]acactcctcaaccccacct ctgat	C	T	NM_002338 // upstream // 571410 // Hs.528629 // LSAMP // 4045 // limbic system-associated membrane protein /// NM_152538 // downstream // 1885713 // Hs.6658 // IGSF11 // 152404 // immunoglobulin superfamily, member 11	LSAMP	LSAMP, rs871216, limbic system-associated membrane protein ,q13.31
SNP_A-1974063	ctcttataccaaata[A/G]ccaagtgtaaatacа	A	G	NM_152538 // downstream // 1934619 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 321195 // — // — // — /// ENST00000273382 // downstream // 1933099 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1644302	accaaaagctgagaaaaaaggctat[A/G]agtatcccaacgct gaatccagtca	A	G	NM_002338 // upstream // 693556 // Hs.528629 // LSAMP // 4045 // limbic system-associated membrane protein /// NM_152538 // downstream // 1763567 // Hs.6658 // IGSF11 // 152404 // immunoglobulin superfamily, member 11	LSAMP	LSAMP , rs1851236, limbic system-associated membrane protein ,q13.31
SNP_A-2094235	agaaggtgaaaataaa[A/C]tggtctcttcatgatt	A	C	NM_152538 // downstream // 1892453 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 363361 // — // — // — /// ENST00000273382 // downstream // 1890933 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1693501	ccatgcatatattgctggtttgaag[A/G]acttttagacaaaataaa acattc	A	G	NM_002338 // upstream // 779132 // Hs.528629 // LSAMP // 4045 // limbic system-associated membrane protein /// NM_152538 // downstream // 1677991 // Hs.6658 // IGSF11 // 152404 // immunoglobulin superfamily, member 11	LSAMP	LSAMP , rs1462845, limbic system-associated membrane protein ,q13.31
SNP_A-2291606	gcacaagctggtataa[A/T]aaattacatatagttg	A	T	NM_152538 // downstream // 1821921 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 433893 // — // — // — /// ENST00000273382 // downstream // 1820401 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1678750	gggattggtttaagtaatgaagtcc[A/G]caatcaatttacaagtta aggaca	A	G	NM_002338 // upstream // 830774 // Hs.528629 // LSAMP // 4045 // limbic system-associated membrane protein /// NM_152538 // downstream // 1626349 // Hs.6658 // IGSF11 // 152404 // immunoglobulin superfamily, member 11	LSAMP	LSAMP , rs7616414, limbic system-associated membrane protein ,q13.31
SNP_A-1952447	tttctgaagatattgc[A/G]acaattaattttagg	A	G	NM_152538 // downstream // 1779143 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 476671 // — // — // — /// ENST00000273382 // downstream // 1777623 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1830153	taatagatgtaagtca[A/T]gaactatggaattgtc	A	T	NM_152538 // downstream // 1657003 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 598811 // --- // --- // --- /// ENST00000273382 // downstream // 1655483 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1884408	tgaagtcaagctgcgt[A/G]aatctcaggagaagta	A	G	NM_152538 // downstream // 1648530 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 607284 // --- // --- // --- /// ENST00000273382 // downstream // 1647010 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2144129	atgaggctctgaatta[A/G]gaaccagatgtggcaa	A	G	NM_152538 // downstream // 1606936 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 648878 // --- // --- // --- /// ENST00000273382 // downstream // 1605416 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1974074	gtaaatcagtttaaa[C/G]tgctagcctaatgtt	C	G	NM_152538 // downstream // 1567388 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 688426 // --- // --- // --- /// ENST00000273382 // downstream // 1565868 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2064041	aattatgtttctctc[C/G]aactttctcaggcacc	C	G	NM_152538 // downstream // 1560017 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 695797 // --- // --- // --- /// ENST00000273382 // downstream // 1558497 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1958690	ttttctgaaactaa[C/G]tgacaatgaggcaaat	C	G	NM_152538 // downstream // 1554355 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 701459 // --- // --- // --- /// ENST00000273382 // downstream // 1552835 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2154108	attatccttgcaaat[C/G]aatcagccatgtgact	C	G	NM_152538 // downstream // 1554057 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 701757 // --- // --- // --- /// ENST00000273382 // downstream // 1552537 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2030007	aaagatgggtatttaa[C/T]ctctgcacgcagata	C	T	NM_152538 // downstream // 1517154 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 738660 // --- // --- // --- /// ENST00000273382 // downstream // 1515634 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1974075	tgtcagaagagattaa[C/T]tcaaacaggaggcagc	C	T	NM_152538 // downstream // 1474694 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 781120 // --- // --- // --- /// ENST00000273382 // downstream // 1473174 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1865995	tcccacctctcaatac[C/G]atcacttcactaagtt	C	G	NM_152538 // downstream // 1472428 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 783386 // --- // --- // --- /// ENST00000273382 // downstream // 1470908 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1960564	ttttcatatcacgta[A/G]aagttaagaaaaattc	A	G	NM_152538 // downstream // 1328023 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 927791 // --- // --- // --- /// ENST00000273382 // downstream // 1326503 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1924055	ttagtgtgaactttc[C/T]acagtatttgcatga	C	T	NM_152538 // downstream // 1274330 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 981484 // --- // --- // --- /// ENST00000273382 // downstream // 1272810 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2035907	aaatgttgcaatgga[A/G]aataagaaaggaaaga	A	G	NM_152538 // downstream // 1226028 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1029786 // --- // --- // --- /// ENST00000273382 // downstream // 1224508 /	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-1838100	tagaacaactaactaa[C/T]gcacaagtcctcattc	C	T	NM_152538 // downstream // 1210503 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1045311 // --- // --- // --- /// ENST00000273382 // downstream // 1208983 /	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.31
SNP_A-2278969	gaggaacacctgcaaa[A/C]aataacagcttagtcc	A	C	NM_152538 // downstream // 1193764 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1062050 // --- // --- // --- /// ENST00000273382 // downstream // 1192244 /	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-2167656	caaccagcactttgaa[C/T]caacataccatatggc	C	T	NM_152538 // downstream // 771982 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1483832 // --- // --- // --- /// ENST00000273382 // downstream // 770462 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-2077312	accaattccgaacaca[A/G]taatgctaagatctga	A	G	NM_152538 // downstream // 729268 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1526546 // --- // --- // --- /// ENST00000273382 // downstream // 727748 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1854556	tcaaatttgagaaatg[A/G]aagaacaacgaacctct	A	G	NM_152538 // downstream // 694104 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1561710 // --- // --- // --- /// ENST00000273382 // downstream // 692584 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-2120296	agtcataaiatttcca[C/T]gaaacttcctgaat	C	T	NM_152538 // downstream // 468335 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1787479 // --- // --- // --- /// ENST00000273382 // downstream // 466815 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1974116	cagttctggatgtcag[C/T]agtcggaaatggtttt	C	T	NM_152538 // downstream // 437057 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1818757 // --- // --- // --- /// ENST00000273382 // downstream // 435537 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1952778	tttctgttaaagttcat[C/T]cgtggcaatgtaaatt	C	T	NM_152538 // downstream // 371528 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 1884286 // --- // --- // --- /// ENST00000273382 // downstream // 370008 //	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1851916	tattgatccaatttca[A/C]agacaaggagagaggt	A	C	NM_152538 // downstream // 83896 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 2171918 // --- // --- // --- /// ENST00000273382 // downstream // 82376 // ---	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974133	agaagtggttaacagc[A/G]agacacaattaatgcc	A	G	NM_152538 // downstream // 66355 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000359893 // upstream // 2189459 // — // — // — // — /// ENST00000273382 // downstream // 64835 // –	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1974137	aaccaaagaaatcagc[A/G]gaagaccataaaaaca	A	G	NM_152538 // intron // 0 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000273382 // intron // 0 // — // — // — // — /// ENST00000354673 // intron // 0 // — // — // — // —	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1942231	ttggcacttagtcatt[G/T]aagcctacccttgtca	G	T	NM_152538 // intron // 0 // Hs.112873 // IGSF11 // 152404 // Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), mRNA. /// ENST00000273382 // intron // 0 // — // — // — // — /// ENST00000354673 // intron // 0 // — // — // — // —	IGSF11	IGSF11, Homo sapiens immunoglobulin superfamily, member 11 (IGSF11), q13.32
SNP_A-1812504	gtggcccaaagactga[C/T]aaggagcaagagatgt	C	T	NM_152539 // downstream // 21639 // Hs.351465 // FLJ32859 // 152405 // Homo sapiens hypothetical protein FLJ32859 (FLJ32859), mRNA. /// NM_006952 // upstream // 484 // Hs.271580 // UPK1B // 7348 // Homo sapiens uroplakin 1B (UPK1B), mRNA. /// ENST00000295	FLJ32859	FLJ32859, Homo sapiens hypothetical protein FLJ32859 (FLJ32859), q13.32
SNP_A-1974149	atgtgggccaagtcca[A/G]aggaaaccaccaagca	A	G	ENST00000264245 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1653654	taacattatcctcaatagagcctaa[A/G]gtatagaatacactcatt ttctcac	A	G	NM_015900 // downstream // 5193 // Hs.17752 // PLA1A // 51365 // phospholipase A1 member A /// NM_022135 // downstream // 7064 // Hs.16297 // POPDC2 // 64091 // popeye domain containing 2	PLA1A	PLA1A , rs2692618, phospholipase A1 member A ,q13.33
SNP_A-1917944	ttaaaatctagcacca[C/T]taaggaagagaagaaa	C	T	NM_022135 // intron // 0 // Hs.16297 // POPDC2 // 64091 // Homo sapiens popeye domain containing 2 (POPDC2), mRNA. /// ENST00000341124 // intron // 0 // — // — // — // — /// ENST00000264231 // intron // 0 // — // — // — // —	POPDC2	POPDC2, Homo sapiens popeye domain containing 2 (POPDC2), q13.33
SNP_A-2146539	atgctgatagaattca[A/C]gagaaaagaaatttga	A	C	NM_005694 // upstream // 16557 // Hs.534383 // COX17 // 10063 // Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, /// NM_033364 // upstream // 9073 // Hs.341906 // C3orf15 // 8	COX17	COX17, Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, q13.33
SNP_A-1897022	tgctccaatatagaga[A/G]tatcttggataatgga	A	G	NM_033364 // CDS // 0 // Hs.341906 // C3orf15 // 89876 // Homo sapiens chromosome 3 open reading frame 15 (C3orf15), mRNA. /// ENST00000273390 // CDS // 0 // — // — // — // — /// ENST00000264232 // CDS // 0 // — // — // — // —	C3orf15	C3orf15, Homo sapiens chromosome 3 open reading frame 15 (C3orf15), q13.33
SNP_A-2036631	aaattggatttgaaaa[A/G]cttggtaatgcctcat	A	G	BC012760 // intron // 0 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen synthase kinase 3 beta, mRNA (cDNA clone MGC:16182 IMAGE:3637163), complete cds. /// NM_002093 // intron // 0 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen synthase ki	GSK3B	GSK3B, Homo sapiens glycogen synthase kinase 3 beta, (cDNA clone MGC:16182 IMAGE:3637163), complete cds. ,q13.33
SNP_A-1920921	ttacactggacaagca[A/T]aaactggcacataaga	A	T	BC012760 // intron // 0 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen synthase kinase 3 beta, mRNA (cDNA clone MGC:16182 IMAGE:3637163), complete cds. /// NM_002093 // intron // 0 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen synthase ki	GSK3B	GSK3B, Homo sapiens glycogen synthase kinase 3 beta, (cDNA clone MGC:16182 IMAGE:3637163), complete cds. q13.33
SNP_A-1864328	tccactatgttcttgg[A/G]ataatattaaagaaaa	A	G	BC012760 // upstream // 10773 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen synthase kinase 3 beta, mRNA (cDNA clone MGC:16182 IMAGE:3637163), complete cds. /// NM_002093 // upstream // 11524 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen	GSK3B	GSK3B, Homo sapiens glycogen synthase kinase 3 beta, (cDNA clone MGC:16182 IMAGE:3637163), complete cds. ,q13.33
SNP_A-2089414	acttatcttcctggta[C/G]gtctgtccaccaaaag	C	G	BC012760 // upstream // 72166 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen synthase kinase 3 beta, mRNA (cDNA clone MGC:16182 IMAGE:3637163), complete cds. /// NM_002093 // upstream // 72917 // Hs.445733 // GSK3B // 2932 // Homo sapiens glycogen	GSK3B	GSK3B, Homo sapiens glycogen synthase kinase 3 beta, (cDNA clone MGC:16182 IMAGE:3637163), complete cds. ,q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1894139	tgcatgctgttttatc[A/G]ccagatagggaccatg	A	G	NM_153002 // intron // 0 // Hs.333358 // GPR156 // 165829 // Homo sapiens G protein-coupled receptor 156 (GPR156), mRNA. /// ENST00000315843 // intron // 0 // — // — // — // —	GPR156	GPR156, Homo sapiens G protein-coupled receptor 156 (GPR156), q13.33
SNP_A-1974160	ggatccaaatataagg[C/T]agtagtagtgactcag	C	T	NM_153002 // upstream // 21140 // Hs.333358 // GPR156 // 165829 // Homo sapiens G protein-coupled receptor 156 (GPR156), mRNA. /// ENST00000315843 // upstream // 21140 // — // — // — // — /// ENST00000295628 // downstream // 64849 // — // — //	GPR156	GPR156, Homo sapiens G protein-coupled receptor 156 (GPR156), q13.33
SNP_A-1974166	ttcatactttcataga[A/C]tagaacaggacagaat	A	C	NM_007085 // intron // 0 // Hs.269512 // FSTL1 // 11167 // Homo sapiens follistatin-like 1 (FSTL1), mRNA. /// ENST00000295633 // intron // 0 // — // — // — // —	FSTL1	FSTL1, Homo sapiens follistatin-like 1 (FSTL1), q13.33
SNP_A-1974171	tgggtgtcttttcacc[C/T]ggctttctggaattcc	C	T	NM_007085 // upstream // 50932 // Hs.269512 // FSTL1 // 11167 // Homo sapiens follistatin-like 1 (FSTL1), mRNA. /// NM_004547 // upstream // 94353 // Hs.304613 // NDUFB4 // 4710 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa (	FSTL1	FSTL1, Homo sapiens follistatin-like 1 (FSTL1), q13.33
SNP_A-2314491	ggagggtggaaaaaag[G/T]caagacagggtgggcc	G	T	NM_005513 // downstream // 9575 // Hs.445272 // GTF2E1 // 2960 // Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA. /// ENST00000283875 // downstream // 9575 // — // — // — // — /// ENST00000273666	GTF2E1	GTF2E1, Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), q13.33
SNP_A-1974182	taggcagcaaggccaa[A/T]agtgcatgcgttagtc	A	T	NM_005513 // downstream // 11569 // Hs.445272 // GTF2E1 // 2960 // Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA. /// ENST00000283875 // downstream // 11569 // — // — // — // — /// ENST00000027366	GTF2E1	GTF2E1, Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), q13.33
SNP_A-2218008	cctgccaacttgattc[C/T]ccacactcactttcac	C	T	NM_005513 // downstream // 73937 // Hs.445272 // GTF2E1 // 2960 // Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA. /// ENST00000283875 // downstream // 73937 // — // — // — // — /// ENST00000027366	GTF2E1	GTF2E1, Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), q13.33
SNP_A-2045296	aagaaggtactagcta[C/G]gtctaagggagagagg	C	G	NM_005513 // downstream // 85675 // Hs.445272 // GTF2E1 // 2960 // Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA. /// ENST00000283875 // downstream // 85675 // — // — // — // — /// ENST00000027366	GTF2E1	GTF2E1, Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), q13.33
SNP_A-1855968	tcaattaataagagaa[A/G]ttagagaggccaagag	A	G	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-2255110	cttggggcctaatgaa[A/G]tggaacccagtctgtc	A	G	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1807140	gtctcctgtctaaaat[A/C]agcaaacctgttgaag	A	C	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1805871	gtccctgccaaagcac[C/T]gaatccaaaatcataa	C	T	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-2280075	gagggaaggggctga[G/T]ctaatcctttcatcag	G	T	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1654005	gacccatgtaccagttttaaaggca[C/T]catctatactttatctacatgaagg	C	T	NM_006596 // downstream // 8563 // Hs.241517 // POLQ // 10721 // polymerase (DNA directed), theta /// NM_014125 // downstream // 85165 // - // - // - // -	POLQ	POLQ , rs7632907, polymerase (DNA directed), theta ,q13.33
SNP_A-1889901	tgatagatagacagac[C/T]gaaaggaatagaaaat	C	T	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1682740	aggtaattgttcaatatatatccat[C/T]aggtcaaatttgctgattatattaa	C	T	NM_006596 // intron // 0 // Hs.241517 // POLQ // 10721 // polymerase (DNA directed), theta	POLQ	POLQ , rs501099, polymerase (DNA directed), theta,q13.33
SNP_A-2090989	actttctgggctaaca[A/T]ggtcctcacacagggc	A	T	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1909572	tgtattttggctcctc[A/C]atttctgtgactttgg	A	C	ENST00000273666 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1974190	aagatgagactatgca[A/C]aggattacatggatca	A	C	NM_199420 // downstream // 9247 // Hs.241517 // POLQ // 10721 // Homo sapiens polymerase (DNA directed), theta (POLQ), transcript variant 2, mRNA. /// NM_006596 // downstream // 9247 // Hs.241517 // POLQ // 10721 // Homo sapiens polymerase (DNA directed),	POLQ	POLQ, Homo sapiens polymerase (DNA directed), theta (POLQ), transcript variant 2, q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1926565	ttattctgcataacad[A/T]atgtgcatttcttatt	A	T	NM_199420 // downstream // 727 // Hs.241517 // POLQ // 10721 // Homo sapiens polymerase (DNA directed), theta (POLQ), transcript variant 2, mRNA. /// NM_006596 // downstream // 727 // Hs.241517 // POLQ // 10721 // Homo sapiens polymerase (DNA directed), t	POLQ	POLQ, Homo sapiens polymerase (DNA directed), theta (POLQ), transcript variant 2, q13.33
SNP_A-1918793	ttaacaccttttttcd[A/G]ccaacaatatctcta	A	G	NM_016298 // intron // 0 // Hs.272564 // FBXO40 // 51725 // Homo sapiens F-box protein 40 (FBXO40), mRNA. /// ENST00000338040 // intron // 0 // — // — // — // —	FBXO40	FBXO40, Homo sapiens F-box protein 40 (FBXO40), q13.33
SNP_A-1846855	tatcacaaggcaacca[A/G]gatatatctaatttg	A	G	NM_016298 // intron // 0 // Hs.272564 // FBXO40 // 51725 // Homo sapiens F-box protein 40 (FBXO40), mRNA. /// ENST00000338040 // intron // 0 // — // — // — // —	FBXO40	FBXO40, Homo sapiens F-box protein 40 (FBXO40), q13.33
SNP_A-1670383	ccatatacctgaaaagatctgatgaa[A/G]cccagcgtgttttaaa agttcgaa	A	G	NM_006889 // CDS // 0 // Hs.27954 // CD86 // 942 // CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) /// NM_175862 // CDS // 0 // Hs.27954 // CD86 // 942 // CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	CD86	CD86 , rs1129055, CD86 antigen (CD28 antigen ligand 2, B7-2 antigen), q21.1
SNP_A-1928403	ttcacctctaagccac[A/C]ggtatcatctcttcca	A	C	NM_006889 // intron // 0 // Hs.171182 // CD86 // 942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // intron // 0 // Hs.171182 // CD86 // 942 // Homo sapiens CD86 antigen (CD28 antigen	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q13.33
SNP_A-2046445	aagagagaatcagtaa[A/G]ggatttataggcaaag	A	G	NM_006889 // downstream // 25077 // Hs.171182 // CD86 // 942 // Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, mRNA. /// NM_175862 // downstream // 25077 // Hs.171182 // CD86 // 942 // Homo sapiens CD86 antig	CD86	CD86, Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), transcript variant 2, q21.1
SNP_A-2112995	aggcatttttgcacag[A/T]ctgaccataagtatac	A	T	NM_000388 // downstream // 21152 // Hs.435615 // CASR // 846 // Homo sapiens calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism) (CASR), mRNA. /// NM_005213 // upstream // 17589 // Hs.518198 // CSTA // 1475 // Hom	CASR	CASR, Homo sapiens calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism) (CASR), q21.1
SNP_A-2141783	atctgaagctgattc[C/T]acctcaaagctgtatg	C	T	NM_005213 // intron // 0 // Hs.518198 // CSTA // 1475 // Homo sapiens cystatin A (stefin A) (CSTA), mRNA. /// ENST00000264474 // intron // 0 // — // — // — // —	CSTA	CSTA, Homo sapiens cystatin A (stefin A) (CSTA), q21.1
SNP_A-1711330	acgctgtggatgcaagagtcaatca[A/G]atgagtggtgctctat cctgtgg	A	G	NM_024610 // intron // 0 // Hs.29169 // HSPBAP1 // 79663 // HSPB (heat shock 27kDa) associated protein 1	HSPBAP1	HSPBAP1, rs10511414, HSPB (heat shock 27kDa) associated protein 1, q21.1
SNP_A-1791203	ggggtttacctattctc[C/T]accattggatggtgct	C	T	NM_031458 // upstream // 43154 // Hs.518200 // PARP9 // 83666 // Homo sapiens poly (ADP-ribose) polymerase family, member 9 (PARP9), mRNA. /// NM_138287 // downstream // 32534 // Hs.518201 // DTX3L // 151636 // Homo sapiens rhysin 2 (BBAP), mRNA. /// NM_1	PARP9	PARP9, Homo sapiens poly (ADP-ribose) polymerase family, member 9 (PARP9), q21.1
SNP_A-2043582	aactgtgtaggaatca[A/G]taaatggagagtgaaa	A	G	NM_031458 // upstream // 44526 // Hs.518200 // PARP9 // 83666 // Homo sapiens poly (ADP-ribose) polymerase family, member 9 (PARP9), mRNA. /// NM_138287 // downstream // 33906 // Hs.518201 // DTX3L // 151636 // Homo sapiens rhysin 2 (BBAP), mRNA. /// NM_1	PARP9	PARP9, Homo sapiens poly (ADP-ribose) polymerase family, member 9 (PARP9), q21.1
SNP_A-2167361	caacagggcgtgttga[C/G]attatataaataatt	C	G	NM_152615 // downstream // 21191 // Hs.120250 // PARP15 // 165631 // Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), mRNA. /// NM_017554 // upstream // 37571 // Hs.518203 // PARP14 // 54625 // Homo sapiens poly (ADP-ribose) polymeras	PARP15	PARP15, Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), q21.1
SNP_A-1844077	tagttgcttctttagt[A/G]aatgtcaagtggcatg	A	G	NM_152615 // downstream // 51044 // Hs.120250 // PARP15 // 165631 // Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), mRNA. /// NM_017554 // upstream // 7718 // Hs.518203 // PARP14 // 54625 // Homo sapiens poly (ADP-ribose) polymerase	PARP15	PARP15, Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796102	ggtgtagacaacccaa[A/C]ttcctagctggctact	A	C	NM_152615 // downstream // 51838 // Hs.120250 // PARP15 // 165631 // Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), mRNA. /// NM_017554 // upstream // 6924 // Hs.518203 // PARP14 // 54625 // Homo sapiens poly (ADP-ribose) polymerase	PARP15	PARP15, Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), q21.1
SNP_A-2224409	cgtactctccggacaa[C/T]gaaccacaaccaacgc	C	T	NM_152615 // downstream // 52063 // Hs.120250 // PARP15 // 165631 // Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), mRNA. /// NM_017554 // upstream // 6699 // Hs.518203 // PARP14 // 54625 // Homo sapiens poly (ADP-ribose) polymerase	PARP15	PARP15, Homo sapiens poly (ADP-ribose) polymerase family, member 15 (PARP15), q21.1
SNP_A-1974211	cttcatttttctgtga[C/T]gctagatactacctat	C	T	NM_017554 // intron // 0 // Hs.518203 // PARP14 // 54625 // Homo sapiens poly (ADP-ribose) polymerase family, member 14 (PARP14), mRNA. /// ENST00000310276 // intron // 0 // — // — // — // —	PARP14	PARP14, Homo sapiens poly (ADP-ribose) polymerase family, member 14 (PARP14), q21.1
SNP_A-1857223	tcacctgttcatcccc[A/G]catatcacatcatctg	A	G	NM_017554 // intron // 0 // Hs.518203 // PARP14 // 54625 // Homo sapiens poly (ADP-ribose) polymerase family, member 14 (PARP14), mRNA. /// ENST00000310276 // intron // 0 // — // — // — // —	PARP14	PARP14, Homo sapiens poly (ADP-ribose) polymerase family, member 14 (PARP14), q21.1
SNP_A-2165875	caaagtgacttacgaa[C/T]gagattgttcattgtg	C	T	AB040878 // intron // 0 // Hs.210870 // SEMA5B // 54437 // Homo sapiens mRNA for KIAA1445 protein, partial cds. /// NM_018987 // intron // 0 // Hs.210870 // SEMA5B // 54437 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like)	SEMA5B	SEMA5B, Homo sapiens for KIAA1445 protein, partial cds, q21.1
SNP_A-2135470	atatttgcttatatta[A/G]cattgatatacactag	A	G	AB040878 // intron // 0 // Hs.210870 // SEMA5B // 54437 // Homo sapiens mRNA for KIAA1445 protein, partial cds. /// NM_018987 // intron // 0 // Hs.210870 // SEMA5B // 54437 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like)	SEMA5B	SEMA5B, Homo sapiens for KIAA1445 protein, partial cds, q21.1
SNP_A-2237086	ctctcaaccgtaaaac[C/T]acacagggcagttgtg	C	T	AB040878 // intron // 0 // Hs.210870 // SEMA5B // 54437 // Homo sapiens mRNA for KIAA1445 protein, partial cds. /// NM_018987 // intron // 0 // Hs.210870 // SEMA5B // 54437 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like)	SEMA5B	SEMA5B, Homo sapiens for KIAA1445 protein, partial cds, q21.1
SNP_A-2244319	ctggaagatctcaaaac[A/G]agtccgctactcccag	A	G	NM_006810 // intron // 0 // Hs.477352 // PDIR // 10954 // Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /// ENST00000354214 // intron // 0 // — // — // — // — /// ENST00000316218 // intron // 0 // — // — // — // —	PDIR	PDIR, Homo sapiens for protein disulfide isomerase-related (PDIR), q21.1
SNP_A-1954288	tttgcaccactgatac[A/T]gtaagctctttgggggg	A	T	NM_006810 // intron // 0 // Hs.477352 // PDIR // 10954 // Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /// ENST00000354214 // intron // 0 // — // — // — // — /// ENST00000316218 // intron // 0 // — // — // — // —	PDIR	PDIR, Homo sapiens for protein disulfide isomerase-related (PDIR), q21.1
SNP_A-2080759	acctcccactgagcta[C/T]ggaatcggctttcctg	C	T	NM_006810 // intron // 0 // Hs.477352 // PDIR // 10954 // Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /// ENST00000354214 // intron // 0 // — // — // — // — /// ENST00000316218 // intron // 0 // — // — // — // —	PDIR	PDIR, Homo sapiens for protein disulfide isomerase-related (PDIR), q21.1
SNP_A-1676716	cattgtcatcattgatccatccgtc[C/T]atctccaaaaagttactca gggcct	C	T	NM_005965 // intron // 0 // Hs.386078 // MYLK // 4638 // myosin, light polypeptide kinase /// NM_053025 // intron // 0 // Hs.386078 // MYLK // 4638 // myosin, light polypeptide kinase /// NM_053026 // intron // 0 // Hs.386078 // MYLK // 4638 // myosin, l	MYLK	MYLK , rs10511420, myosin, light polypeptide kinase ,q21.1
SNP_A-1861733	tcatctggacgctgaa[C/T]ggaaagaccatcaaga	C	T	NM_053029 // CDS // 0 // Hs.477375 // MYLK // 4638 // Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, mRNA. /// NM_053028 // CDS // 0 // Hs.477375 // MYLK // 4638 // Homo sapiens myosin, light polypeptide kinase (MYLK), transcr	MYLK	MYLK, Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 4, q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936391	ttcttctcttcccaaa[C/T]gtaaccaatctaaact	C	T	NM_022757 // intron // 0 // Hs.17731 // CCDC14 // 64770 // Homo sapiens hypothetical protein FLJ12892 (FLJ12892), mRNA. /// ENST00000310351 // intron // 0 // — // — // — /// ENST00000360153 // intron // 0 // — // — // — // —	CCDC14	CCDC14, Homo sapiens hypothetical protein FLJ12892 (FLJ12892), q21.1
SNP_A-1888836	tgaggtaagtgatcac[C/G]agtgggcagggggtaa	C	G	NM_003947 // intron // 0 // Hs.8004 // HAPIP // 8997 // Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // — // — // —	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.2
SNP_A-1974240	tttcttgtagagga[A/T]catcctgtggaactga	A	T	NM_003947 // intron // 0 // Hs.8004 // HAPIP // 8997 // Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // — // — // —	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.2
SNP_A-2126558	ataaaatgcacagaga[C/T]aagacgaaggttttga	C	T	NM_003947 // intron // 0 // Hs.8004 // HAPIP // 8997 // Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // — // — // —	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.2
SNP_A-2265036	gaagatacagaatgga[C/T]tcaaggtgcaaatgga	C	T	NM_003947 // intron // 0 // Hs.8004 // HAPIP // 8997 // Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // — // — // —	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.2
SNP_A-2155114	attcagagaaggaaac[C/T]actatacactgagtaa	C	T	NM_003947 // intron // 0 // Hs.8004 // HAPIP // 8997 // Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA. /// ENST00000240874 // intron // 0 // — // — // —	HAPIP	HAPIP, Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), q21.2
SNP_A-1793433	ggtagtaaataaaaca[C/T]tggacacaacatatgc	C	T	NM_007064 // intron // 0 // Hs.162189 // TRAD // 11139 // Homo sapiens serine/threonine kinase with Dbl- and pleckstrin homology domains (TRAD), mRNA. /// ENST00000360013 // intron // 0 // — // — // — // — /// ENST00000354186 // intron // 0 // —	TRAD	TRAD, Homo sapiens serine,q21.2
SNP_A-1929905	ttcatctttctccac[A/G]gagctctcattaacc	A	G	NM_007064 // intron // 0 // Hs.162189 // TRAD // 11139 // Homo sapiens serine/threonine kinase with Dbl- and pleckstrin homology domains (TRAD), mRNA. /// ENST00000360013 // intron // 0 // — // — // — // — /// ENST00000354186 // intron // 0 // —	TRAD	TRAD, Homo sapiens serine q21.2
SNP_A-2194106	catgaccttgacttg[G/T]ataatgccttatgta	G	T	NM_007064 // intron // 0 // Hs.162189 // TRAD // 11139 // Homo sapiens serine/threonine kinase with Dbl- and pleckstrin homology domains (TRAD), mRNA. /// ENST00000354186 // intron // 0 // — // — // — // — /// ENST00000291478 // intron // 0 // —	TRAD	TRAD, Homo sapiens serine,q21.2
SNP_A-2275271	gagaagtcatgtgaca[C/G]gttttctgatttttgt	C	G	NM_000373 // intron // 0 // Hs.2057 // UMPS // 7372 // Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5-decarboxylase) (UMPS), mRNA. /// ENST00000232607 // intron // 0 // — // — // — /// ENST0	UMPS	UMPS, Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), q21.2
SNP_A-2115871	agggtggtttattaca[C/T]ggcaatatctagctaa	C	T	NM_000373 // downstream // 2892 // Hs.2057 // UMPS // 7372 // Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), mRNA. /// NM_002213 // downstream // 15276 // Hs.13155 // ITGB5 // 3693	UMPS	UMPS, Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), q21.2
SNP_A-2092352	agaaagctiatgttcc[A/G]atccatcatttaccct	A	G	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // — // — // —	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-1806659	gtctacaaaagatgta[A/C]gttaggaccaagacag	A	C	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // — // — // —	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1789222	gggcatcattctgtaa[C/T]ccctctcatttgcac	C	T	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- /// --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-2300814	gcctgggggagttatg[C/G]attggagaactggcca	C	G	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- /// --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-1809208	gtgacctaacctgacc[A/G]agtatttaatagcctt	A	G	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- /// --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-2122779	agtggattgacatgac[A/G]agattatgtgatcctg	A	G	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- /// --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-2070300	acaccaattcatataa[C/T]ggagtgctagacagct	C	T	NM_002213 // intron // 0 // Hs.13155 // ITGB5 // 3693 // Homo sapiens integrin, beta 5 (ITGB5), mRNA. /// ENST00000296181 // intron // 0 // --- /// --- // ---	ITGB5	ITGB5, Homo sapiens integrin, beta 5 (ITGB5), q21.2
SNP_A-2193836	catgaaacaggaaatc[C/T]atgtcagcaatatatg	C	T	NM_024628 // intron // 0 // Hs.477425 // SLC12A8 // 84561 // Homo sapiens solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8), mRNA. /// ENST00000314584 // intron // 0 // --- /// --- // --- /// ENST00000332979 // intron //	SLC12A8	SLC12A8, Homo sapiens solute carrier family 12 (potassium q21.2
SNP_A-1892279	tgcaaccgagagccaa[C/T]catgtgcccggtactt	C	T	NM_024628 // intron // 0 // Hs.477425 // SLC12A8 // 84561 // Homo sapiens solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8), mRNA. /// ENST00000314584 // intron // 0 // --- /// --- // --- /// ENST00000332979 // intron //	SLC12A8	SLC12A8, Homo sapiens solute carrier family 12 (potassium q21.2
SNP_A-2296627	gccaaaaggatttctg[A/G]atgccctggtgtttgc	A	G	NM_024628 // intron // 0 // Hs.477425 // SLC12A8 // 84561 // Homo sapiens solute carrier family 12 (potassium/chloride transporters), member 8 (SLC12A8), mRNA. /// ENST00000314584 // intron // 0 // --- /// --- // --- /// ENST00000332979 // intron //	SLC12A8	SLC12A8, Homo sapiens solute carrier family 12 (potassium,q21.2
SNP_A-2133630	atatcagcaacacaaa[C/T]gatttacttatgagg	C	T	NM_003794 // intron // 0 // Hs.507243 // SNX4 // 8723 // Homo sapiens sorting nexin 4 (SNX4), mRNA. /// ENST00000251775 // intron // 0 // --- /// --- // ---	SNX4	SNX4, Homo sapiens sorting nexin 4 (SNX4), q21.2
SNP_A-2305724	gctgccccctcaaccac[C/T]cctgagagaagacaac	C	T	NM_022776 // upstream // 89318 // Hs.477440 // OSBPL11 // 114885 // Homo sapiens oxysterol binding protein-like 11 (OSBPL11), mRNA. /// ENST00000296220 // upstream // 89318 // --- /// --- // --- /// ENST00000316507 // upstream // 19074 // --- /// ---	OSBPL11	OSBPL11, Homo sapiens oxysterol binding protein-like 11 (OSBPL11), q21.2
SNP_A-1723704	aagctttctactacaa[A/G]tgtaaatgactggcct	A	G	BC015413 // upstream // 24748 // Hs.194093 // ROPN1 // 54763 // ropporin, rhophilin associated protein 1 /// BC041080 // downstream // 20854 // Hs.418619 // - // - // Similar to hypothetical protein FLJ10661, clone IMAGE:4425123, mRNA	ROPN1	ROPN1 , rs2017409, ropporin, rhophilin associated protein 1 ,q21.3
SNP_A-2273653	gactgatgtctcctctc[G/T]ctctacaggcatctga	G	T	ENST00000380794 // downstream // 927 // --- /// --- /// ENST00000319373 // upstream // 16948 // --- /// ---	-	q21.2
SNP_A-1649388	ctgcctgcaggactattcattgt[C/T]aattcagttaggctgctgaattcac	C	T	NM_012190 // intron // 0 // Hs.434435 // FTHFD // 10840 // formyltetrahydrofolate dehydrogenase /// NM_144776 // intron // 0 // Hs.434435 // FTHFD // 10840 // formyltetrahydrofolate dehydrogenase	FTHFD	FTHFD, rs2365001, formyltetrahydrofolate dehydrogenase ,q21.3
SNP_A-2067848	acaaccagtcatcttc[C/T]ctccttttgtccacca	C	T	ENST00000251776 // intron // 0 // --- /// --- /// ---	-	q21.2
SNP_A-1811448	gtgctattgaacctccd[A/G]ctcatgtacacttact	A	G	NM_017836 // downstream // 4814 // Hs.506720 // SLC41A3 // 54946 // Homo sapiens solute carrier family 41, member 3 (SLC41A3), mRNA. /// ENST00000251776 // downstream // 18720 // --- /// --- /// --- /// ENST00000346785 // downstream // 4187 // --- ///	SLC41A3	SLC41A3, Homo sapiens solute carrier family 41, member 3 (SLC41A3), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2263568	gaaccatcacttctgc[C/G]aggtacagcaggattg	C	G	NM_017836 // CDS // 0 // Hs.506720 // SLC41A3 // 54946 // Homo sapiens solute carrier family 41, member 3 (SLC41A3), mRNA. /// ENST00000346785 // CDS // 0 // --- // --- // --- // --- /// ENST00000315891 // CDS // 0 // --- // --- // --- // --- /// ENST0000	SLC41A3	SLC41A3, Homo sapiens solute carrier family 41, member 3 (SLC41A3), q21.2
SNP_A-1716739	cactatcaagcagggtttattccaa[C/G]aatgaaaaagtggctta atatcagg	C	G	NM_012190 // upstream // 60843 // Hs.434435 // FTHFD // 10840 // formyltetrahydrofolate dehydrogenase /// NM_014079 // downstream // 101151 // Hs.272215 // KLF15 // 28999 // Kruppel-like factor 15 /// NM_144776 // upstream // 60843 // Hs.434435 // FTHFD	FTHFD	FTHFD , rs2197704, formyltetrahydrofolate dehydrogenase ,q21.3
SNP_A-1703283	aaaaatcttctgggtggaataagaa[A/C]atttaagatggatgaat gtgatatt	A	C	NM_012190 // upstream // 61803 // Hs.434435 // FTHFD // 10840 // formyltetrahydrofolate dehydrogenase /// NM_014079 // downstream // 100191 // Hs.272215 // KLF15 // 28999 // Kruppel-like factor 15 /// NM_144776 // upstream // 61803 // Hs.434435 // FTHFD	FTHFD	FTHFD , rs1447666, formyltetrahydrofolate dehydrogenase ,q21.3
SNP_A-2275577	gagacaccgtgtcaga[C/T]ggaagacagctctgcc	C	T	NM_017836 // upstream // 19051 // Hs.506720 // SLC41A3 // 54946 // Homo sapiens solute carrier family 41, member 3 (SLC41A3), mRNA. /// NM_144776 // downstream // 405 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), t	SLC41A3	SLC41A3, Homo sapiens solute carrier family 41, member 3 (SLC41A3), q21.2
SNP_A-2295994	gcattaaaccacccccc[C/G]acactgagtggcttgg	C	G	NM_144776 // intron // 0 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // intron // 0 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate dehydrogenase	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2077792	accagaacaatgtata[C/T]gcgttaaatttaatct	C	T	NM_144776 // intron // 0 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // intron // 0 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate dehydrogenase	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2237504	ctctcgacctcattaa[A/T]aagcatttcattagaa	A	T	NM_144776 // upstream // 23900 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 23900 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2194615	catgcagtcctggtgt[A/G]acaatcaattgaggca	A	G	NM_144776 // upstream // 28091 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 28091 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-1785247	ggctactccatggtgc[C/T]actgggatacacagcc	C	T	NM_144776 // upstream // 29342 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 29342 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-1868365	tcctcattggttcagg[C/T]cagattttattaccca	C	T	NM_144776 // upstream // 45513 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 45513 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2296379	gcatttaggaattgca[A/G]gtgaagtgctgtaaac	A	G	NM_144776 // upstream // 45584 // Hs.434435 // --- // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 45584 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2065482	aattgtttcttttgga[C/T]gtctgagaatgaaaac	C	T	NM_144776 // upstream // 46331 // Hs.434435 // — // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 46331 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2279299	gaggagcacaattcaa[C/T]gattacaccctctgtg	C	T	NM_144776 // upstream // 46469 // Hs.434435 // — // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 46469 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-2075795	acatgtacctttttctg[C/G]accaatcagctgctga	C	G	NM_144776 // upstream // 46779 // Hs.434435 // — // 0 // Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, mRNA. /// NM_012190 // upstream // 46779 // Hs.434435 // ALDH1L1 // 10840 // Homo sapiens formyltetrahydrofolate de	-	-, Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), transcript variant 2, q21.2
SNP_A-1671214	acctccatgagaggacacttgaagc[A/G]tcacactaggaactct catgggccc	A	G	NM_025112 // intron // 0 // Hs.288697 // MGC11349 // 79364 // hypothetical protein MGC11349	MGC11349	MGC11349 , rs812368, hypothetical protein MGC11349,q21.3
SNP_A-1897598	tgctgcaggaaagaaa[C/T]acaagctgctctctca	C	T	NM_014079 // upstream // 34865 // Hs.272215 // KLF15 // 28999 // Homo sapiens Kruppel-like factor 15 (KLF15), mRNA. /// NM_182628 // upstream // 2678 // Hs.458306 // FLJ40083 // 348807 // Homo sapiens hypothetical protein FLJ40083 (FLJ40083), mRNA. /// EN	KLF15	KLF15, Homo sapiens Kruppel-like factor 15 (KLF15), q21.2
SNP_A-2313538	ggagagttcgacctgc[A/G]aagagatggcagggtc	A	G	NM_182628 // intron // 0 // Hs.458306 // FLJ40083 // 348807 // Homo sapiens hypothetical protein FLJ40083 (FLJ40083), mRNA. /// ENST00000352312 // intron // 0 // — // — // — // —	FLJ40083	FLJ40083, Homo sapiens hypothetical protein FLJ40083 (FLJ40083), q21.2
SNP_A-1886989	tgacttgagaatcaga[C/T]gcagtttgactcatgg	C	T	NM_025112 // intron // 0 // Hs.440049 // MGC11349 // 79364 // Homo sapiens hypothetical protein MGC11349 (MGC11349), mRNA. /// ENST00000336332 // intron // 0 // — // — // — // —	MGC11349	MGC11349, Homo sapiens hypothetical protein MGC11349 (MGC11349), q21.2
SNP_A-1788079	gggagaggcgaaccac[A/G]aggaaggaccagggct	A	G	NM_152533 // upstream // 10651 // Hs.178210 // MGC34728 // 152065 // Homo sapiens hypothetical protein MGC34728 (MGC34728), mRNA. /// ENST00000318225 // upstream // 10651 // — // — // — // — /// ENST00000360201 // downstream // 37486 // — // —	MGC34728	MGC34728, Homo sapiens hypothetical protein MGC34728 (MGC34728), q21.2
SNP_A-1865037	tccagtccttgtctga[C/T]ggtgtccaacagccca	C	T	NM_152533 // upstream // 11604 // Hs.178210 // MGC34728 // 152065 // Homo sapiens hypothetical protein MGC34728 (MGC34728), mRNA. /// ENST00000318225 // upstream // 11604 // — // — // — // — /// ENST00000360201 // downstream // 36533 // — // —	MGC34728	MGC34728, Homo sapiens hypothetical protein MGC34728 (MGC34728), q21.2
SNP_A-2264584	gaagaaggtggttgta[A/G]gacatcgctagcaaca	A	G	NM_007283 // intron // 0 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, mRNA. /// NM_001003794 // intron // 0 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 2	MGLL	MGLL, Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, q21.3
SNP_A-1896578	tgctagaggagaaaac[A/G]agggaggactgtgatc	A	G	NM_007283 // intron // 0 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, mRNA. /// NM_001003794 // intron // 0 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 2	MGLL	MGLL, Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, q21.3
SNP_A-2294815	gcagtttattttagaa[A/T]acttccagcaagcgac	A	T	NM_007283 // intron // 0 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, mRNA. /// NM_001003794 // intron // 0 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 2	MGLL	MGLL, Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801826	gtagttaaacattagc[A/C]gagctggtaattgaac	A	C	NM_007283 // upstream // 9602 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, mRNA. /// NM_001003794 // upstream // 9602 // Hs.277035 // MGLL // 11343 // Homo sapiens monoglyceride lipase (MGLL), transcript	MGLL	MGLL, Homo sapiens monoglyceride lipase (MGLL), transcript variant 1, q21.3
SNP_A-2247337	ctgtcctaaagtaaag[A/G]aagtggagagcagttg	A	G	NM_021937 // intron // 0 // Hs.477498 // SELB // 60678 // Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // — // — // — // —	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-2009094	agatgcagagttgtac[A/G]gggtggtgataaagac	A	G	NM_021937 // intron // 0 // Hs.477498 // SELB // 60678 // Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // — // — // — // —	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-1974304	gttaccacagggccga[C/T]atggaagatggagaaa	C	T	NM_021937 // intron // 0 // Hs.477498 // SELB // 60678 // Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // — // — // — // —	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-2085653	actccctccaatggcc[C/T]ccacagggcatccatg	C	T	NM_021937 // intron // 0 // Hs.477498 // SELB // 60678 // Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // — // — // — // —	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-2210337	cccccaacatgaaagc[A/G]acgccagcaattggag	A	G	NM_021937 // intron // 0 // Hs.477498 // SELB // 60678 // Homo sapiens elongation factor for selenoprotein translation (SELB), mRNA. /// ENST00000254730 // intron // 0 // — // — // — // —	SELB	SELB, Homo sapiens elongation factor for selenoprotein translation (SELB), q21.3
SNP_A-2213480	ccggtataattccaga[C/T]tagagcctgccaatac	C	T	NM_153330 // 5UTR // 0 // Hs.518241 // DNAJB8 // 165721 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 8 (DNAJB8), mRNA. /// ENST00000319153 // 5UTR // 0 // — // — // — // —	DNAJB8	DNAJB8, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 8 (DNAJB8), q21.3
SNP_A-1893464	tgcagctgtaacacaa[G/T]gtatttgctcattctc	G	T	NM_153330 // upstream // 4850 // Hs.518241 // DNAJB8 // 165721 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 8 (DNAJB8), mRNA. /// NM_032638 // downstream // 7331 // Hs.367725 // GATA2 // 2624 // Homo sapiens GATA binding protein 2 (GATA2), mR	DNAJB8	DNAJB8, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 8 (DNAJB8), q21.3
SNP_A-2247309	ctgtcccagcaaccaa[A/C]ggatgtaagcccgtag	A	C	ENST00000314377 // CDS // 0 // — // — // — // —	-	q21.3
SNP_A-1651814	aactaaaaataaaacacataacaca[C/T]gactaggttacagtt acacctacag	C	T	NM_004637 // downstream // 1054 // Hs.356386 // RAB7 // 7879 // RAB7, member RAS oncogene family /// NM_014049 // upstream // 64464 // Hs.409209 // ACAD9 // 28976 // acyl-Coenzyme A dehydrogenase family, member 9	RAB7	RAB7 , rs3772157, RAB7, member RAS oncogene family ,q21.3
SNP_A-1942275	ttggcagtttcatact[A/G]aactaaacataccctt	A	G	NM_002950 // upstream // 21946 // Hs.518244 // RPN1 // 6184 // Homo sapiens ribophorin I (RPN1), mRNA. /// NM_004637 // upstream // 53353 // Hs.15738 // RAB7 // 7879 // Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA. /// ENST00000296255 // ups	RPN1	RPN1, Homo sapiens ribophorin I (RPN1), q21.3
SNP_A-2080402	acctagaaatttaata[C/T]agtgctctggagtctg	C	T	NM_004637 // intron // 0 // Hs.15738 // RAB7 // 7879 // Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA. /// ENST00000265062 // intron // 0 // — // — // — // —	RAB7	RAB7, Homo sapiens RAB7, member RAS oncogene family (RAB7), q21.3
SNP_A-1974308	aaagagccatggataa[C/G]tgatgggccacccagg	C	G	NM_004637 // intron // 0 // Hs.15738 // RAB7 // 7879 // Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA. /// ENST00000265062 // intron // 0 // — // — // — // —	RAB7	RAB7, Homo sapiens RAB7, member RAS oncogene family (RAB7), q21.3
SNP_A-1831143	taatgccaatttgcaa[C/G]ctgagaggggatctt	C	G	NM_004637 // downstream // 38673 // Hs.15738 // RAB7 // 7879 // Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA. /// NM_014049 // upstream // 26140 // Hs.541841 // ACAD9 // 28976 // Homo sapiens acyl-Coenzyme A dehydrogenase family, member 9 (A	RAB7	RAB7, Homo sapiens RAB7, member RAS oncogene family (RAB7), q21.3
SNP_A-1840464	tagccagcttctgtga[C/T]ctcatcatggttaatt	C	T	NM_012133 // intron // 0 // Hs.532231 // COPG2 // 26958 // Homo sapiens coatomer protein complex, subunit gamma 2 (COPG2), mRNA. /// NM_016128 // intron // 0 // Hs.518250 // COPG // 22820 // Homo sapiens coatomer protein complex, subunit gamma (COPG), mRN	COPG2	COPG2, Homo sapiens coatomer protein complex, subunit gamma 2 (COPG2), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2009105	ttggagaatctagta[C/T]gagaaacatgttcctt	C	T	NM_006026 // upstream // 16011 // Hs.75307 // H1FX // 8971 // Homo sapiens H1 histone family, member X (H1FX), mRNA. /// ENST00000333762 // upstream // 16011 // --- // --- // --- /// ENST00000332468 // downstream // 51012 // --- // --- // ---	H1FX	H1FX, Homo sapiens H1 histone family, member X (H1FX), q21.3
SNP_A-2009106	ttgttgaagtaagca[C/T]aaaatatcacatgagg	C	T	NM_006026 // upstream // 16198 // Hs.75307 // H1FX // 8971 // Homo sapiens H1 histone family, member X (H1FX), mRNA. /// ENST00000333762 // upstream // 16198 // --- // --- // --- /// ENST00000332468 // downstream // 50825 // --- // --- // ---	H1FX	H1FX, Homo sapiens H1 histone family, member X (H1FX), q21.3
SNP_A-1974316	ggctctgtggcgcta[C/T]gacacaggaatggcac	C	T	ENST00000299623 // upstream // 109306 // --- // --- // --- /// ENST00000321602 // upstream // 109306 // --- // --- // --- /// ENST00000355466 // upstream // 43370 // --- // --- // ---	-	q21.3
SNP_A-2306306	gctgggaatcatatca[A/G]tgagcatttacaagg	A	G	NM_153264 // upstream // 26959 // Hs.205403 // FLJ35880 // 256076 // Homo sapiens hypothetical protein FLJ35880 (FLJ35880), mRNA. /// ENST00000328846 // downstream // 18199 // --- // --- // --- /// ENST00000312481 // upstream // 26959 // --- // ---	FLJ35880	FLJ35880, Homo sapiens hypothetical protein FLJ35880 (FLJ35880), q21.3
SNP_A-2314145	ggaggaggagaatattc[A/G]aaatgatggtttccag	A	G	NM_153264 // CDS // 0 // Hs.205403 // FLJ35880 // 256076 // Homo sapiens hypothetical protein FLJ35880 (FLJ35880), mRNA. /// ENST00000312481 // CDS // 0 // --- // --- // ---	FLJ35880	FLJ35880, Homo sapiens hypothetical protein FLJ35880 (FLJ35880), q21.3
SNP_A-1745902	ctattatttatgtttcttattgctct[A/T]ctctcctgtggattcaaagaag cac	A	T	NM_014602 // downstream // 25302 // Hs.306747 // PIK3R4 // 30849 // phosphoinositide-3-kinase, regulatory subunit 4, p150 /// NM_153264 // downstream // 168788 // Hs.205403 // FLJ35880 // 256076 // hypothetical protein FLJ35880	PIK3R4	PIK3R4 , rs6802634, phosphoinositide-3-kinase, regulatory subunit 4, p150 ,q22.1
SNP_A-1876607	tctgatttgcagtaca[A/G]gattagtgccccttt	A	G	NM_014602 // intron // 0 // Hs.149032 // PIK3R4 // 30849 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 4, p150 (PIK3R4), mRNA. /// ENST00000356763 // intron // 0 // --- // --- // ---	PIK3R4	PIK3R4, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 4, p150 (PIK3R4), q21.3
SNP_A-2271751	gaccagtaagaagcta[C/T]gacaaggtgatgtgg	C	T	NM_024800 // intron // 0 // Hs.200813 // NEK11 // 79858 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 11 (NEK11), mRNA. /// NM_145910 // intron // 0 // Hs.200813 // NEK11 // 79858 // Homo sapiens NIMA (never in mitosis gene a)- related ki	NEK11	NEK11, Homo sapiens NIMA (never in mitosis gene a)- related kinase 11 (NEK11), q21.3
SNP_A-1974346	aaacgtagattcatggt[A/T]attatatctgactga	A	T	NM_130808 // intron // 0 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- /// ENST00000357136 // intron // 0 // --- // --- // --- /// ENST00000354260 // intron /	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1908664	tgtaggacatctaaaa[A/G]taacactgatattgac	A	G	NM_130808 // intron // 0 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- /// ENST00000357136 // intron // 0 // --- // --- // --- /// ENST00000354260 // intron /	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1908237	tgtacctcatcagcct[A/G]aatactgcttaccct	A	G	NM_130808 // intron // 0 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// ENST00000357965 // intron // 0 // --- // --- // --- /// ENST00000357136 // intron // 0 // --- // --- // --- /// ENST00000354260 // intron /	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1673128	aataacctgtatttttctctataa[C/T]ctggagtccaaaaacctc atgtca	C	T	NM_001099 // upstream // 104277 // Hs.388677 // ACPP // 55 // acid phosphatase, prostate /// NM_130808 // upstream // 178138 // Hs.199877 // CPNE4 // 131034 // copine IV	ACPP	ACPP , rs884432, acid phosphatase, prostate q22.1
SNP_A-1956175	ttgtggcaaaaatac[A/G]catggcaataccatat	A	G	NM_130808 // upstream // 122057 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 122772 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 155029 // Hs	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247251	ctgtcatttatcagca[G/T]tccatctttgtaagcc	G	T	NM_130808 // upstream // 157107 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 157822 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 119979 // Hs	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-2144689	atgatgagtgatctag[A/C]aaagctggcaattaag	A	C	NM_130808 // upstream // 162791 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 163506 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 114295 // Hs	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1932424	ttcctgcacaagcgta[G/T]gtcaagcctctgttca	G	T	NM_130808 // upstream // 164843 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 165558 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 112243 // Hs	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1929271	ttcagtacttaatcta[G/T]gttgaattgatattga	G	T	NM_130808 // upstream // 179543 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 180258 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 97543 // Hs.	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1906715	tggtgtttgaaaata[C/T]gcctgtaaattattg	C	T	NM_130808 // upstream // 179730 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 180445 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 97356 // Hs.	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1795501	ggtgccccctatgaca[C/T]actttgctcctctg	C	T	NM_130808 // upstream // 188772 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 189487 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 88314 // Hs.	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1928315	ttcagtcacctctccc[A/G]ctatgtctgggacaat	A	G	NM_130808 // upstream // 247129 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_130808 // upstream // 247844 // Hs.199877 // CPNE4 // 131034 // Homo sapiens copine IV (CPNE4), mRNA. /// NM_001099 // upstream // 29957 // Hs.	CPNE4	CPNE4, Homo sapiens copine IV (CPNE4), q22.1
SNP_A-1974380	atgtaggttctgtatc[A/G]atgtatttcttatatgg	A	G	NM_001099 // intron // 0 // Hs.433060 // ACPP // 55 // Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /// ENST00000336375 // intron // 0 // — // — /// ENST00000351273 // intron // 0 // — // — // — // —	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-1833343	tacagaaactctcccaa[A/G]aagtataactaaaaca	A	G	NM_001099 // downstream // 22051 // Hs.433060 // ACPP // 55 // Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /// NM_015268 // upstream // 82972 // — // 0 // — /// ENST00000336375 // downstream // 22051 // — // — // — // — /// EN	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-2059726	aatctgatcacatatc[A/G]agggaatttggctaa	A	G	NM_001099 // downstream // 55105 // Hs.433060 // ACPP // 55 // Homo sapiens acid phosphatase, prostate (ACPP), mRNA. /// NM_015268 // upstream // 49918 // — // 0 // — /// ENST00000336375 // downstream // 55105 // — // — // — // — /// EN	ACPP	ACPP, Homo sapiens acid phosphatase, prostate (ACPP), q22.1
SNP_A-2238720	ctcttaaatgagccaa[A/G]catacatcactaagta	A	G	NM_032169 // upstream // 511751 // Hs.441378 // FLJ12592 // 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 569295 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287021	gatggttctctgaca[C/G]tgctgaatgcaatccc	C	G	NM_032169 // upstream // 536548 // Hs.441378 // FLJ12592 // 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 594092 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-1915537	tgttctacctccccat[C/G]atcactggtgtacg	C	G	NM_032169 // upstream // 619158 // Hs.441378 // FLJ12592 // 84129 // Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), mRNA. /// NM_016557 // downstream // 676702 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1	FLJ12592	FLJ12592, Homo sapiens putative acyl-CoA dehydrogenase (FLJ12592), q22.1
SNP_A-1910946	tgtctcaaatgaaaag[G/T]cctaaccagaactgga	G	T	NM_017548 // intron // 0 // Hs.518265 // H41 // 55573 // Homo sapiens hypothetical protein H41 (H41), mRNA. /// ENST00000264993 // intron // 0 // — // — // — /// ENST00000356623 // intron // 0 // — // — // —	H41	H41, Homo sapiens hypothetical protein H41 (H41), q22.1
SNP_A-1748619	ctgtttctgaacaaggctggcttac[A/G]caaagaaagagcagta gtgtgggca	A	G	NM_016577 // intron // 0 // Hs.352530 // RAB6B // 51560 // RAB6B, member RAS oncogene family	RAB6B	RAB6B , rs2715608, RAB6B, member RAS oncogene family,q22.1
SNP_A-1974437	cctacgaccactaaaa[A/C]aatctcatgcgcaatt	A	C	NM_016577 // intron // 0 // Hs.147164 // RAB6B // 51560 // Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA. /// ENST00000285208 // intron // 0 // — // — // —	RAB6B	RAB6B, Homo sapiens RAB6B, member RAS oncogene family (RAB6B), q22.1
SNP_A-2209880	ccccaacctgaagagal[A/C]acctagatgctgaaac	A	C	NM_016577 // intron // 0 // Hs.147164 // RAB6B // 51560 // Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA. /// ENST00000285208 // intron // 0 // — // — // —	RAB6B	RAB6B, Homo sapiens RAB6B, member RAS oncogene family (RAB6B), q22.1
SNP_A-2081606	acctlacctaagaaa[C/T]gctggtgccaagagtc	C	T	NM_016577 // intron // 0 // Hs.147164 // RAB6B // 51560 // Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA. /// ENST00000285208 // intron // 0 // — // — // —	RAB6B	RAB6B, Homo sapiens RAB6B, member RAS oncogene family (RAB6B), q22.1
SNP_A-1787014	gggaaacacaatttca[C/T]aagccaaaatcagtag	C	T	NM_016577 // upstream // 14923 // Hs.147164 // RAB6B // 51560 // Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA. /// NM_025041 // downstream // 17788 // Hs.287691 // FLJ22173 // 80111 // Homo sapiens hypothetical protein FLJ22173 (FLJ22173),	RAB6B	RAB6B, Homo sapiens RAB6B, member RAS oncogene family (RAB6B), q22.1
SNP_A-2094832	agaatctcctggaggt[A/G]aaatacagattgctgg	A	G	NM_005630 // intron // 0 // Hs.518270 // SLCO2A1 // 6578 // Homo sapiens solute carrier organic anion transporter family, member 2A1 (SLCO2A1), mRNA. /// ENST00000310926 // intron // 0 // — // — // — // —	SLCO2A1	SLCO2A1, Homo sapiens solute carrier organic anion transporter family, member 2A1 (SLCO2A1), q22.1
SNP_A-1692418	ccdgctggatgcctcctgataaata[A/C]ccgggatgcaccacctt gcccttg	A	C	NM_004441 // intron // 0 // Hs.272311 // EPHB1 // 2047 // EphB1	EPHB1	EPHB1 , rs983401, EphB1,q22.2
SNP_A-1662250	gtctttataggcatggttccctaa[C/T]tgagctctagggcaggg gtcaaa	C	T	NM_004441 // intron // 0 // Hs.272311 // EPHB1 // 2047 // EphB1	EPHB1	EPHB1 , rs972234, EphB1,q22.2
SNP_A-1663672	cccaaatgactttgcatttgggcc[G/T]caaagtaacaacaaca acaaaaaaa	G	T	NM_004441 // intron // 0 // Hs.272311 // EPHB1 // 2047 // EphB1	EPHB1	EPHB1 , rs36117, EphB1,q22.2
SNP_A-2120591	agtcccaaagttatat[C/T]ctctctgttagaat	C	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329695 // intron // 0 // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2232823	ctcacttccaacctca[G/T]agagaagatatgcagc	G	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329695 // intron // 0 // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-1865671	tccattccaaagccga[A/G]caaaatcaattacgat	A	G	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-1974452	gttgtgagtttgggga[C/T]gttagtcttggcatt	C	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974453	agcaggtactgtggaa[A/G]tgaggaagaaagtccc	A	G	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-1809689	gtgagccttcaacaaa[G/T]aactctctcccaacac	G	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2068553	acaagtgaaaacagca[A/G]agaggaataagccact	A	G	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-1834162	tacatcttagtccaaa[C/T]ggaatgctgatgccaa	C	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2045768	aagacagacaagagaa[C/T]ggaataaaatggaggaa	C	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2049992	aaggaaggcatcctac[A/G]aagacagtttaaaatt	A	G	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-2291703	gcacaccaattctaac[A/T]ctaactgcagaattcc	A	T	NM_004441 // intron // 0 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// ENST00000360935 // intron // 0 // — // — // — // — /// ENST00000329895 // intron // 0 // — // — // — // — /// ENST00000358398 // intron // 0 //	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.1
SNP_A-1974474	tccagagggcctcaga[A/G]ctcaatccccttaca	A	G	NM_004441 // downstream // 152891 // Hs.116092 // EPHB1 // 2047 // Homo sapiens EphB1 (EPHB1), mRNA. /// NM_002718 // upstream // 553021 // Hs.518155 // PPP2R3A // 5523 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha (PP	EPHB1	EPHB1, Homo sapiens EphB1 (EPHB1), q22.2
SNP_A-2078318	accatagatagcaaaa[C/T]gataggcgctcagtaa	C	T	NM_000532 // intron // 0 // Hs.63788 // PCCB // 5096 // Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), mRNA. /// ENST00000251654 // intron // 0 // — // — // — // —	PCCB	PCCB, Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), q22.3
SNP_A-1974499	actttttttttcagc[A/G]actgctatctctgtg	A	G	NM_144717 // downstream // 336797 // Hs.61232 // MGC34923 // 152026 // Homo sapiens hypothetical protein MGC34923 (MGC34923), mRNA. /// NM_004189 // upstream // 416862 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SO	MGC34923	MGC34923, Homo sapiens hypothetical protein MGC34923 (MGC34923), q22.3
SNP_A-1852010	tattgcctgaagggaa[C/T]aaggaaaataaacatg	C	T	NM_144717 // downstream // 427685 // Hs.61232 // MGC34923 // 152028 // Homo sapiens hypothetical protein MGC34923 (MGC34923), mRNA. /// NM_004189 // upstream // 325974 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SO	MGC34923	MGC34923, Homo sapiens hypothetical protein MGC34923 (MGC34923), q22.3
SNP_A-2119226	agtagggaacaagaaa[G/T]gagactactgcagtta	G	T	NM_004189 // downstream // 35274 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream // 197988 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript vari	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225865	ctaaatcagaaaatgc[A/C]aatagcaacttagcta	A	C	NM_004189 // downstream // 49123 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream // 184139 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript vari	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-1931730	ttccctgcccttaacc[A/T]cagttgtacccagggc	A	T	NM_004189 // downstream // 50062 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream // 183200 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript vari	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-1887777	tgagatccctacatga[A/C]aagtggaccagcaagg	A	C	NM_004189 // downstream // 50714 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream // 182548 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript vari	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-2009148	aagctcccagttaaga[C/T]ctatgctgctagtcct	C	T	NM_004189 // downstream // 206562 // Hs.248184 // SOX14 // 8403 // Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA. /// NM_001002026 // upstream // 26700 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript vari	SOX14	SOX14, Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), q22.3
SNP_A-2311758	ggaattgaggtacaca[A/G]cagctaagaaacttgt	A	G	NM_001002026 // downstream // 25830 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript variant 2, mRNA. /// NM_016369 // downstream // 26988 // Hs.240182 // CLDN18 // 51208 // Homo sapiens claudin 18 (CLDN18), transcript varia	CLDN18	CLDN18, Homo sapiens claudin 18 (CLDN18), transcript variant 2, q22.3
SNP_A-1716203	atcttggctgaaatcaccttcccaa[A/C]tggcctgtctcctccagc cttcctc	A	C	BC037292 // intron // 0 // Hs.318921 // CHR3SYT // 83850 // chr3 synaptotagmin	CHR3SYT	CHR3SYT , rs1679177, chr3 synaptotagmin,q22.3
SNP_A-1912589	tgtgccatatattcca[A/G]taggtgatgcatgaaa	A	G	NM_012219 // intron // 0 // Hs.527021 // MRAS // 22808 // Homo sapiens muscle RAS oncogene homolog (MRAS), mRNA. /// ENST00000289104 // intron // 0 // — // — // — // — /// ENST00000360368 // intron // 0 // — // — - // — // —	MRAS	MRAS, Homo sapiens muscle RAS oncogene homolog (MRAS), q22.3
SNP_A-2009156	ctaaagcaatcactgg[A/G]atagtatcaattagga	A	G	NM_021812 // intron // 0 // Hs.512673 // BPESC1 // 60467 // Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1 (BPESC1), mRNA. /// ENST00000305608 // intron // 0 // --- // --- // --- // ---	BPESC1	BPESC1, Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1 (BPESC1), q22.3
SNP_A-2202767	ccacgtactgatcact[C/T]aacttcaacattatca	C	T	NM_021812 // 3UTR // 0 // Hs.512673 // BPESC1 // 60467 // Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1 (BPESC1), mRNA. /// ENST00000305608 // 3UTR // 0 // — // — // — // — // —	BPESC1	BPESC1, Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1 (BPESC1), q22.3
SNP_A-1663090	gctgcctgctggtggaaatctgtac[C/T]tgcattatactggagaa gcccttcc	C	T	NM_178177 // intron // 0 // Hs.14600 // NMNAT3 // 349565 // nicotinamide nucleotide adenylyltransferase 3	NMNAT3	NMNAT3 , rs211587, nicotinamide nucleotide adenylyltransferase 3,q23
SNP_A-1647966	gacacggatagtgccaggaaaatca[C/G]tctggaactctagga agggcttctc	C	G	NM_178177 // intron // 0 // Hs.14600 // NMNAT3 // 349565 // nicotinamide nucleotide adenylyltransferase 3	NMNAT3	NMNAT3 , rs211588, nicotinamide nucleotide adenylyltransferase 3,q23
SNP_A-2313314	ggagaccatagtttgg[A/G]actctgaacgtgaact	A	G	NM_178177 // intron // 0 // Hs.208673 // NMNAT3 // 349565 // Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// ENST00000339837 // intron // 0 // — // — // — // — // — /// ENST00000296202 // intron // 0 // — // — // —	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-2100432	agataacatgggccaa[A/G]ttgaaacagtttcctt	A	G	NM_178177 // intron // 0 // Hs.208673 // NMNAT3 // 349565 // Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), mRNA. /// ENST00000339837 // intron // 0 // — // — // — // — // — /// ENST00000296202 // intron // 0 // — // — // —	NMNAT3	NMNAT3, Homo sapiens nicotinamide nucleotide adenylyltransferase 3 (NMNAT3), q23
SNP_A-1698033	ataattaaggaacactatgttaggc[A/G]atgataacacaccgcc tctgggtcc	A	G	NM_022131 // upstream // 64339 // Hs.12079 // CLSTN2 // 64084 // calsyntenin 2 /// NM_025093 // upstream // 260493 // - // - // - // - /// NM_178177 // upstream // 193028 // Hs.14600 // NMNAT3 // 349565 // nicotinamide nucleotide adenylyltransferase 3	CLSTN2	CLSTN2 , rs10513087, calsyntenin 2 ,q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1706341	tgccagatggtagggatacagtaaa[C/T]agggccattgatagtt acaatggac	C	T	NM_022131 // upstream // 5881 // Hs.12079 // CLSTN2 // 64084 // calsyntenin 2 /// NM_025093 // upstream // 318951 // - // - // - /// NM_178177 // upstream // 251486 // Hs.14600 // NMNAT3 // 349565 // nicotinamide nucleotide adenylyltransferase 3	CLSTN2	CLSTN2 , rs727763, calsyntenin 2 ,q23
SNP_A-1651610	attaagcctcaatgggctacttttta[C/T]aatcccatggaaggatta atttaat	C	T	NM_022131 // intron // 0 // Hs.12079 // CLSTN2 // 64084 // calsyntenin 2	CLSTN2	CLSTN2 , rs2882426, calsyntenin 2,q23
SNP_A-1792807	ggtaagttcatttggc[A/G]gactgtaatataaaat	A	G	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1944884	ttgtggactgatgcca[A/T]taagttttaccttcag	A	T	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2243749	ctgctgagagatccag[A/T]catataagaatgaaga	A	T	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2056338	aatacttacctcccca[A/G]tactcaagtcctacca	A	G	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1974560	aggattagggctgaaa[A/G]taccaaaccttttta	A	G	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1938196	ttgacattttcagcaa[C/T]tggagtatttgttagc	C	T	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // --- // --- // --- // ---	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1830220	taataggtcaaagaaa[C/G]tattgccatgttgtgt	C	G	NM_022131 // intron // 0 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// ENST00000332210 // intron // 0 // — // — // — // —	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-2307425	gcttatcactccttca[C/T]agagactcagtagtat	C	T	NM_022131 // downstream // 8274 // Hs.158529 // CLSTN2 // 64084 // Homo sapiens calsyntenin 2 (CLSTN2), mRNA. /// NM_152616 // upstream // 101977 // Hs.343487 // TRIM42 // 287015 // Homo sapiens tripartite motif-containing 42 (TRIM42), mRNA. /// ENST00000	CLSTN2	CLSTN2, Homo sapiens calsyntenin 2 (CLSTN2), q23
SNP_A-1854504	tcaaattaagtagcta[C/T]gggcagggtgcaatga	C	T	NM_080862 // intron // 0 // Hs.477752 // SSB4 // 92369 // Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), mRNA. /// ENST00000310546 // intron // 0 // — // --- // — // —	SSB4	SSB4, Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), q23
SNP_A-1974588	tcctggcatcagatca[A/G]gatcccactgctgtga	A	G	NM_080862 // downstream // 65779 // Hs.477752 // SSB4 // 92369 // Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), mRNA. /// NM_152282 // upstream // 17468 // Hs.255491 // ACPL2 // 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), m	SSB4	SSB4, Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB4), q23
SNP_A-1641973	gtagatcaataccactctagtatta[C/T]ggcaagagatgcaatct tggtatta	C	T	AK092355 // intron // 0 // Hs.23853 // FLJ35036 // 253461 // hypothetical protein FLJ35036	FLJ35036	FLJ35036 , rs6808936, hypothetical protein FLJ35036,q23
SNP_A-2177999	cactaccctctcctta[C/T]catctattcaacacca	C	T	NM_152282 // intron // 0 // Hs.255491 // ACPL2 // 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// ENST00000286353 // intron // 0 // — // — // — // —	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-2065093	aattgcctcacttcta[C/T]ggcaagacgccagcag	C	T	NM_152282 // intron // 0 // Hs.255491 // ACPL2 // 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// ENST00000286353 // intron // 0 // — // — // — // —	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-2084259	actagtctcatccaca[C/G]tagcctttagttttaa	C	G	NM_152282 // intron // 0 // Hs.255491 // ACPL2 // 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// ENST00000286353 // intron // 0 // — // — // — // —	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2254810	cttggactgacaaaat[C/T]acagtgataggccatg	C	T	NM_152282 // downstream // 82991 // Hs.255491 // ACPL2 // 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// NM_006506 // upstream // 109190 // Hs.15999 // RASA2 // 5922 // Homo sapiens RAS p21 protein activator 2 (RASA2), mRNA. /// ENST0000	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-1798847	gtaactttgcacttgt[C/G]aatccaccagtcttcc	C	G	NM_152282 // downstream // 111960 // Hs.255491 // ACPL2 // 92370 // Homo sapiens acid phosphatase-like 2 (ACPL2), mRNA. /// NM_006506 // upstream // 80221 // Hs.15999 // RASA2 // 5922 // Homo sapiens RAS p21 protein activator 2 (RASA2), mRNA. /// ENST0000	ACPL2	ACPL2, Homo sapiens acid phosphatase-like 2 (ACPL2), q23
SNP_A-2303993	gctccaagtacggctc[C/T]attggcttattggact	C	T	NM_139209 // intron // 0 // Hs.102513 // GRK7 // 131890 // Homo sapiens G protein-coupled receptor kinase 7 (GRK7), mRNA. /// ENST00000264952 // intron // 0 // — // — // — // —	GRK7	GRK7, Homo sapiens G protein-coupled receptor kinase 7 (GRK7), q23
SNP_A-2117534	aggtgttttagaggta[C/G]aatcagtgcagcttga	C	G	NM_006286 // intron // 0 // Hs.379018 // TFDP2 // 7029 // Homo sapiens transcription factor Dp-2 (E2F dimerization partner 2) (TFDP2), mRNA. /// ENST00000344190 // intron // 0 // — // — // — // — /// ENST00000317104 // intron // 0 // — // — //	TFDP2	TFDP2, Homo sapiens transcription factor Dp-2 (E2F dimerization partner 2) (TFDP2), q23
SNP_A-2030062	aaagattctgcaatgc[A/G]caggagagtcttccag	A	G	NM_006286 // intron // 0 // Hs.379018 // TFDP2 // 7029 // Homo sapiens transcription factor Dp-2 (E2F dimerization partner 2) (TFDP2), mRNA. /// ENST00000317104 // intron // 0 // — // — // — // —	TFDP2	TFDP2, Homo sapiens transcription factor Dp-2 (E2F dimerization partner 2) (TFDP2), q23
SNP_A-1825204	taaagtatttaagata[C/T]gtgctttagatatcat	C	T	NM_013363 // upstream // 39119 // Hs.8944 // PCOLCE2 // 26577 // Homo sapiens procollagen C-endopeptidase enhancer 2 (PCOLCE2), mRNA. /// NM_198504 // downstream // 33885 // Hs.408385 // PAQR9 // 344838 // Homo sapiens progestin and adipoQ receptor family	PCOLCE2	PCOLCE2, Homo sapiens procollagen C-endopeptidase enhancer 2 (PCOLCE2), q23
SNP_A-2049281	aagctcagggggttgc[A/C]cacatttatttatttt	A	C	NM_004267 // upstream // 42736 // Hs.8786 // CHST2 // 9435 // Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2), mRNA. /// ENST00000319822 // downstream // 18943 // — // — // — // — /// ENST00000309575 // upstream // 4	CHST2	CHST2, Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2), q23
SNP_A-2241529	ctgagttgaagagcta[C/G]agatgggagttagggt	C	G	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // — // — // — // —	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium q24
SNP_A-1974635	tgacagccagaaagga[A/C]acataaatggaactca	A	C	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // — // — // — // —	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium q24
SNP_A-1712845	gttttattaaaattactaaagataa[A/G]tctgcttctagtgaacatttc ttca	A	G	NM_173653 // intron // 0 // Hs.364860 // SLC9A9 // 285195 // solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	SLC9A9	SLC9A9 , rs1242075, solute carrier family 9 (sodium,q24
SNP_A-2273954	gactgtctgtcttggc[C/T]acttatttctcttcaa	C	T	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // — // — // — // —	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium q24
SNP_A-1847515	tatccttaaagagtga[A/T]gttgccttattctaca	A	T	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // — // — // — // —	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-1974641	ctctgggagacatgag[A/G]aacatagaccaaacag	A	G	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // — // — // — // —	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974643	ccagcatcgggaactc[A/G]cacagcttggtaaatt	A	G	NM_173653 // CDS // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // CDS // 0 // --- // --- // ---	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-2120068	agtcactcccatgtaa[A/G]cacaactctcaaaacc	A	G	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // --- // --- // ---	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-1974647	tttgatgtgcaaccc[A/T]attattaatgactata	A	T	NM_173653 // intron // 0 // Hs.302257 // SLC9A9 // 285195 // Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 9 (SLC9A9), mRNA. /// ENST00000316549 // intron // 0 // --- // --- // ---	SLC9A9	SLC9A9, Homo sapiens solute carrier family 9 (sodium,q24
SNP_A-1724764	aatcagcgcaaacgtaaatatccca[A/C]ataaacctacttgtca ttgtgatc	A	C	AF130044 // upstream // 199991 // Hs.383375 // - // - // Clone FLB1825 PRO0419 mRNA, complete cds /// NM_173552 // downstream // 25070 // Hs.288954 // MGC33365 // 205428 // hypothetical protein MGC33365	-	- , rs10513238, Clone FLB1825 PRO0419 mRNA, complete cds ,q24
SNP_A-1974656	gtttcccttattgcaa[C/T]gcttaatggtagtgtt	C	T	NM_173552 // upstream // 24896 // Hs.288954 // MGC33365 // 205428 // Homo sapiens hypothetical protein MGC33365 (MGC33365), mRNA. /// ENST00000305319 // upstream // 91035 // --- // --- // --- // --- ENST00000315691 // upstream // 24896 // --- // --- /	MGC33365	MGC33365, Homo sapiens hypothetical protein MGC33365 (MGC33365), q24
SNP_A-1974659	ctttaattgctctcac[C/T]atctgcagcatagaga	C	T	NM_173552 // downstream // 44501 // Hs.288954 // MGC33365 // 205428 // Homo sapiens hypothetical protein MGC33365 (MGC33365), mRNA. /// ENST00000315691 // downstream // 44501 // --- // --- // --- // --- ENST00000360038 // downstream // 181170 // --- /	MGC33365	MGC33365, Homo sapiens hypothetical protein MGC33365 (MGC33365), q24
SNP_A-1852033	tattgctcaacgttta[G/T]actactatttttgatac	G	T	ENST00000355888 // downstream // 155889 // --- // --- // --- // --- ENST00000356397 // upstream // 1461783 // --- // --- // --- // ---	-	q24
SNP_A-1662356	aaccatgtatacctatgtgaaact[C/G]agtgtgtcatctgggtgc agaagaa	C	G	NM_018629 // upstream // 1189097 // - // - // - // -	-	- , rs10513251, - ,q24
SNP_A-2086488	actcttttgtgtaaag[A/T]caaggaaaaatatatt	A	T	ENST00000355888 // downstream // 412785 // --- // --- // --- // --- ENST00000356397 // upstream // 1204887 // --- // --- // ---	-	q24
SNP_A-1956463	ttgttgaatctgtacj[A/G]ctgagaatatcttt	A	G	ENST00000355888 // downstream // 530667 // --- // --- // --- // --- ENST00000356397 // upstream // 1087005 // --- // --- // ---	-	q24
SNP_A-2250280	cttagaatatccatgg[C/G]atcataatggctactg	C	G	ENST00000355888 // downstream // 1000300 // --- // --- // --- // --- ENST00000356397 // upstream // 617372 // --- // --- // ---	-	q24
SNP_A-2076779	accaaaaaggagcaaa[C/T]gtacaagactaacaac	C	T	ENST00000355888 // downstream // 1126770 // --- // --- // --- // --- ENST00000356397 // upstream // 490902 // --- // --- // ---	-	q24
SNP_A-2051381	aagggaagaacccag[A/C]cgaaccatttccagct	A	C	ENST00000355888 // downstream // 1126812 // --- // --- // --- // --- ENST00000356397 // upstream // 490860 // --- // --- // ---	-	q24
SNP_A-1878066	tcigtacttccattaa[C/T]atatctgatcctcaat	C	T	ENST00000355888 // downstream // 1126991 // --- // --- // --- // --- ENST00000356397 // upstream // 490681 // --- // --- // ---	-	q24
SNP_A-2077140	accaaggccatttataa[A/G]gaaatcacctccatga	A	G	ENST00000355888 // downstream // 1293500 // --- // --- // --- // --- ENST00000356397 // upstream // 324172 // --- // --- // ---	-	q24
SNP_A-1974709	tatacttaataaaata[C/T]ggtgctcaattccaag	C	T	ENST00000355888 // downstream // 1395375 // --- // --- // --- // --- ENST00000356397 // upstream // 222297 // --- // --- // ---	-	q24
SNP_A-2061685	aatggaacatatcaca[A/T]gaaatgaaacagacaa	A	T	ENST00000355888 // downstream // 1435534 // --- // --- // --- // --- ENST00000356397 // upstream // 182138 // --- // --- // ---	-	q24
SNP_A-2102629	agattgtttgtggtta[G/T]ctgccggctcctgttc	G	T	ENST00000355888 // downstream // 1534375 // --- // --- // --- // --- ENST00000356397 // upstream // 83297 // --- // --- // --- // ---	-	q24
SNP_A-1874975	tctctagcacttggag[A/G]cggtgaagaaatttgc	A	G	NM_020353 // upstream // 130519 // Hs.477869 // PLSCR4 // 57088 // Homo sapiens phospholipid scramblase 4 (PLSCR4), mRNA. /// NM_020359 // downstream // 51597 // Hs.147305 // PLSCR2 // 57047 // Homo sapiens phospholipid scramblase 2 (PLSCR2), mRNA. /// NM	PLSCR4	PLSCR4, Homo sapiens phospholipid scramblase 4 (PLSCR4), q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215119	cctattgctttggtga[A/C]aaccatgcatactcct	A	C	NM_020359 // intron // 0 // Hs.147305 // PLSCR2 // 57047 // Homo sapiens phospholipid scramblase 2 (PLSCR2), mRNA. /// ENST00000296039 // intron // 0 // — // — // — // — /// ENST00000336685 // intron // 0 // — // — // — // —	PLSCR2	PLSCR2, Homo sapiens phospholipid scramblase 2 (PLSCR2), q24
SNP_A-2069920	acacaggaagtcacaa[A/G]gggtgtctagacagat	A	G	NM_020359 // intron // 0 // Hs.147305 // PLSCR2 // 57047 // Homo sapiens phospholipid scramblase 2 (PLSCR2), mRNA. /// ENST00000296039 // intron // 0 // — // — // — // — /// ENST00000336685 // intron // 0 // — // — // — // —	PLSCR2	PLSCR2, Homo sapiens phospholipid scramblase 2 (PLSCR2), q24
SNP_A-1896181	tgcggaacttctgata[G/T]aatgctgagggcgact	G	T	NM_021105 // upstream // 16120 // Hs.130759 // PLSCR1 // 5359 // Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /// NM_032153 // downstream // 830104 // Hs.415766 // ZIC4 // 84107 // Homo sapiens Zic family member 4 (ZIC4), mRNA. /// ENST00000342 4	PLSCR1	PLSCR1, Homo sapiens phospholipid scramblase 1 (PLSCR1), q24
SNP_A-1756226	tttgcccatacaactacttaaagaa[C/T]agtggagtcacatcata catgtatg	C	T	NM_021105 // upstream // 437881 // Hs.348478 // PLSCR1 // 5359 // phospholipid scramblase 1 /// NM_032153 // downstream // 404729 // Hs.415766 // ZIC4 // 84107 // Zic family member 4	PLSCR1	PLSCR1 , rs4131188, phospholipid scramblase 1 ,q24
SNP_A-2125529	agtttcaaactaaata[C/T]caggtgtgtttataca	C	T	NM_021105 // upstream // 355159 // Hs.130759 // PLSCR1 // 5359 // Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /// NM_032153 // downstream // 491065 // Hs.415766 // ZIC4 // 84107 // Homo sapiens Zic family member 4 (ZIC4), mRNA. /// ENST00000342	PLSCR1	PLSCR1, Homo sapiens phospholipid scramblase 1 (PLSCR1), q24
SNP_A-1743915	ttaattatttctggggatcattact[C/G]aaacttaaagttccaactca cattc	C	G	NM_000685 // upstream // 965598 // Hs.197063 // AGTR1 // 185 // angiotensin II receptor, type 1 /// NM_003412 // downstream // 317719 // Hs.41154 // ZIC1 // 7545 // Zic family member 1 (odd-paired homolog, Drosophila) /// NM_004835 // upstream // 965598	AGTR1	AGTR1 , rs10513321, angiotensin II receptor, type 1 ,q24
SNP_A-1852183	tattgtacataaaaca[C/G]aaaatgtaattccagt	C	G	NM_003412 // downstream // 218419 // Hs.41154 // ZIC1 // 7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928 // downstream // 218419 // — // — // — // — /// ENST00000326920 // downstream // 5	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-2060683	aatgagcagactcaaa[A/G]aacaaatgaaagaaga	A	G	NM_003412 // downstream // 292237 // Hs.41154 // ZIC1 // 7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928 // downstream // 292237 // — // — // — // — /// ENST00000326920 // downstream // 4	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-1824601	taaagaaatgccagtg[A/G]acagtaaggattctcc	A	G	NM_003412 // downstream // 643521 // Hs.41154 // ZIC1 // 7545 // Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA. /// ENST00000282928 // downstream // 643521 // — // — // — // — /// ENST00000326920 // downstream // 1	ZIC1	ZIC1, Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), q24
SNP_A-2217520	cctgactgaagaatgg[C/G]ccaactgtaggcaaat	C	G	ENST00000326920 // upstream // 79026 // — // — // — // — /// ENST00000356128 // upstream // 232589 // — // — // — // —	-	q24
SNP_A-1677330	tttatatgtaggtagaaccttattg[G/T]aggtaatggtgaaagcca gtgagcc	G	T	NM_000685 // upstream // 257754 // Hs.197063 // AGTR1 // 185 // angiotensin II receptor, type 1 /// NM_003412 // downstream // 1025563 // Hs.41154 // ZIC1 // 7545 // Zic family member 1 (odd-paired homolog, Drosophila) /// NM_004835 // upstream // 257754	AGTR1	AGTR1 , rs4681413, angiotensin II receptor, type 1 ,q24
SNP_A-2148973	atggttcattcaaatc[A/G]cacaggtacatttcta	A	G	ENST00000326920 // upstream // 163752 // — // — // — // — /// ENST00000356128 // upstream // 147863 // — // — // — // —	-	q24
SNP_A-2274673	gagaaactgccacagg[C/T]cagaggagactaagga	C	T	ENST00000326920 // upstream // 194105 // — // — // — // — /// ENST00000356128 // upstream // 117510 // — // — // — // —	-	q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1833596	tacagctctctcttaa[C/T]gatgaagaagaggggt	C	T	NM_001870 // downstream // 10938 // Hs.646 // CPA3 // 1359 // Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), mRNA. /// ENST00000296046 // downstream // 10938 // --- // --- // --- // --- /// ENST00000339370 // downstream // 77842 // --- // --- // ---	CPA3	CPA3, Homo sapiens carboxypeptidase A3 (mast cell) (CPA3), q24
SNP_A-2089130	acttaattccatcgga[C/T]caaagtgaactaacca	C	T	NM_004130 // intron // 0 // Hs.477892 // GYG // 2992 // Homo sapiens glycogenin (GYG), mRNA. /// ENST00000353986 // intron // 0 // --- // --- // --- // --- /// ENST00000345003 // intron // 0 // --- // --- // --- // --- /// ENST00000296048 // intron // 0 /	GYG	GYG, Homo sapiens glycogenin (GYG), q24
SNP_A-1923686	ttaggttataaataaa[C/T]ggcaggtgttttctga	C	T	NM_004130 // CDS // 0 // Hs.477892 // GYG // 2992 // Homo sapiens glycogenin (GYG), mRNA. /// ENST00000353986 // CDS // 0 // --- // --- // --- // --- /// ENST00000345003 // CDS // 0 // --- // --- // --- // --- /// ENST00000296048 // CDS // 0 // --- // ---	GYG	GYG, Homo sapiens glycogenin (GYG), q24
SNP_A-1974787	ataggtgattgaggta[C/T]aggtggtctaggatca	C	T	NM_003071 // intron // 0 // Hs.3068 // SMARCA3 // 6596 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), transc /// NM_139048 // intron // 0 // Hs.3068 // SMARCA3 // 6596 // Homo s	SMARCA3	SMARCA3, Homo sapiens SWI,q24
SNP_A-2071011	acactgaactgttcta[C/T]ctcggattaaaacata	C	T	NM_003071 // intron // 0 // Hs.3068 // SMARCA3 // 6596 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), transc /// NM_139048 // intron // 0 // Hs.3068 // SMARCA3 // 6596 // Homo s	SMARCA3	SMARCA3, Homo sapiens SWI q24
SNP_A-2293211	gcagagcaagagttaa[C/T]tgtatggactgaacta	C	T	NM_003071 // upstream // 20095 // Hs.3068 // SMARCA3 // 6596 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), transc /// NM_139048 // upstream // 20095 // Hs.3068 // SMARCA3 // 65	SMARCA3	SMARCA3, Homo sapiens SWI,q24
SNP_A-1944681	ttgtgagctctggata[C/T]actaagtcccatgcca	C	T	NM_003071 // upstream // 32256 // Hs.3068 // SMARCA3 // 6596 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), transc /// NM_139048 // upstream // 32256 // Hs.3068 // SMARCA3 // 65	SMARCA3	SMARCA3, Homo sapiens SWI q24
SNP_A-2235058	ctcccagaaattataa[C/T]ggaaggaagaaggtat	C	T	NM_000096 // upstream // 23815 // Hs.282557 // CP // 1356 // Homo sapiens ceruloplasmin (ferroxidase) (CP), mRNA. /// NM_138786 // downstream // 73367 // Hs.22026 // LOC116441 // 116441 // Homo sapiens hypothetical protein BC014339 (LOC116441), mRNA. ///	CP	CP, Homo sapiens ceruloplasmin (ferroxidase) (CP), q25.1
SNP_A-2088806	actgttagaccttaag[A/G]aatgggtagaactgaa	A	G	ENST00000295907 // downstream // 6141 // --- // --- // --- // --- /// ENST00000305265 // downstream // 3289 // --- // --- // --- // ---	-	q25.1
SNP_A-2313634	ggagatgccagagact[C/T]actttaccaacattcc	C	T	ENST00000305265 // upstream // 133910 // --- // --- // --- // --- /// ENST00000355553 // upstream // 291117 // --- // --- // --- // --- /// ENST00000358223 // upstream // 291117 // --- // --- // --- // --- /// ENST00000356422 // upstream // 291783 // ---	-	q25.1
SNP_A-1923270	ttagctttatttccga[C/G]gtaatttctgccggaa	C	G	ENST00000305265 // upstream // 324788 // --- // --- // --- // --- /// ENST00000355553 // upstream // 100239 // --- // --- // --- // --- /// ENST00000358223 // upstream // 100239 // --- // --- // --- // --- /// ENST00000356422 // upstream // 100905 // ---	-	q25.1
SNP_A-1705247	taaatgagtctcaagagcaattcaa[A/G]gattataaatggttacat aactatg	A	G	NM_032025 // intron // 0 // Hs.378808 // eIF2A // 83939 // eukaryotic translation initiation factor (eIF) 2A	eIF2A	eIF2A , rs6797044, eukaryotic translation initiation factor (eIF) 2A,q25.1
SNP_A-1676282	aatatagctctctaggaagaaaggt[C/T]aatcttatcatgtgaaa aaccatta	C	T	NM_032025 // intron // 0 // Hs.378808 // eIF2A // 83939 // eukaryotic translation initiation factor (eIF) 2A	eIF2A	eIF2A , rs1522351, eukaryotic translation initiation factor (eIF) 2A,q25.1
SNP_A-2124486	agttcatactgatata[A/G]gcaagtctatcttttc	A	G	NM_014445 // intron // 0 // Hs.518326 // SERP1 // 27230 // Homo sapiens stress-associated endoplasmic reticulum protein 1 (SERP1), mRNA. /// NM_032025 // intron // 0 // Hs.378808 // eIF2A // 83939 // Homo sapiens eukaryotic translation initiation factor (	SERP1	SERP1, Homo sapiens stress-associated endoplasmic reticulum protein 1 (SERP1), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1818429	gttcatcgaaatttcaa[A/G]atatgaatcctccaat	A	G	NM_152394 // intron // 0 // Hs.147128 // MGC39662 // 131831 // Homo sapiens hypothetical protein MGC39662 (MGC39662), mRNA. /// ENST00000295910 // intron // 0 // --- // --- // --- /// ENST00000313811 // intron // 0 // --- // --- // ---	MGC39662	MGC39662, Homo sapiens hypothetical protein MGC39662 (MGC39662), q25.1
SNP_A-2180651	cagaaggactatctc[C/T]aaaagccatcctgga	C	T	NM_005067 // upstream // 29283 // Hs.477959 // SIAH2 // 6478 // Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA. /// NM_052995 // downstream // 133723 // Hs.380222 // USH3A // 7401 // Homo sapiens Usher syndrome 3A (USH3A), transcript	SIAH2	SIAH2, Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), q25.1
SNP_A-2110746	aggacctgtagagacc[A/G]acaaatctacacta	A	G	NM_005067 // upstream // 34779 // Hs.477959 // SIAH2 // 6478 // Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA. /// NM_052995 // downstream // 128227 // Hs.380222 // USH3A // 7401 // Homo sapiens Usher syndrome 3A (USH3A), transcript	SIAH2	SIAH2, Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), q25.1
SNP_A-2190748	catagaactgaaacac[A/G]gtgcagaacagaagtt	A	G	NM_005067 // upstream // 114335 // Hs.477959 // SIAH2 // 6478 // Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA. /// NM_052995 // downstream // 48671 // Hs.380222 // USH3A // 7401 // Homo sapiens Usher syndrome 3A (USH3A), transcript	SIAH2	SIAH2, Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), q25.1
SNP_A-1726900	gttgcttgagatgacaagacacctaa[A/G]aggagtgaagattatat gaattagg	A	G	NM_053002 // intron // 0 // Hs.126817 // TRALPUSH // 116931 // TRALPUSH	TRALPUSH	TRALPUSH , rs10513385, TRALPUSH,q25.1
SNP_A-1705999	agccttgtatcaattaaatcigtc[C/G]aaagagagaaccctgag gttatctg	C	G	NM_014879 // intron // 0 // Hs.2465 // GPR105 // 9934 // G protein-coupled receptor 105 /// NM_053002 // intron // 0 // Hs.126817 // TRALPUSH // 116931 // TRALPUSH	GPR105	GPR105 , rs10513390, G protein-coupled receptor 105 ,q25.1
SNP_A-2304468	gctctaggttggcttg[A/G]aactaacagaaaccca	A	G	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- /// ENST00000273432 // intron // 0 // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2284795	gatcattccagctcca[C/T]gacttgaacagtgcga	C	T	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- /// ENST00000273432 // intron // 0 // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2120573	agtccatgctaatatg[A/T]aaggcctgttcact	A	T	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- /// ENST00000273432 // intron // 0 // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2133339	atatatcagtcttagai[C/T]gaatgcttagattcag	C	T	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- /// ENST00000273432 // intron // 0 // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1878379	tctgtcttgtttcctd[A/G]cagaattagatctctt	A	G	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // intron // 0 // --- // --- /// ENST00000273432 // intron // 0 // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1747773	aatatcttgacaaagaatttaca[A/G]caaagaatgattagag ttaatgt	A	G	NM_053002 // intron // 0 // Hs.126817 // TRALPUSH // 116931 // TRALPUSH	TRALPUSH	TRALPUSH , rs2307020, TRALPUSH,q25.1
SNP_A-1974824	tttttccatctaatta[C/T]gacctccttcgccact	C	T	NM_053002 // CDS // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000309237 // CDS // 0 // --- // --- /// ENST00000273432 // CDS // 0 // --- // --- /// -	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2048106	aagcacacggctata[C/G]agagagggctgaactg	C	G	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000273432 // intron // 0 // --- // --- // ---	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2159825	attataaactgataa[C/T]gtccaaacatagtctt	C	T	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_014879 // intron // 0 // Hs.2465 // P2RY14 // 9934 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 14 (P2RY14), mRNA. /// ENST00000273432	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1974825	ctaactgaacacacgc[A/G]attttcctgcagctt	A	G	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_014879 // intron // 0 // Hs.2465 // P2RY14 // 9934 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 14 (P2RY14), mRNA. /// ENST00000273432	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1803799	gtcaagaactattcaa[A/G]gacgtatgatatggtt	A	G	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// ENST00000273432 // intron // 0 // — // — // — // —	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-1974827	gcttaaagagacccca[A/G]gtaacctcattctgtc	A	G	NM_053002 // intron // 0 // Hs.477965 // MED12L // 116931 // Homo sapiens TRALPUSH (TRALPUSH), mRNA. /// NM_023915 // intron // 0 // Hs.58561 // GPR87 // 53836 // Homo sapiens G protein-coupled receptor 87 (GPR87), mRNA. /// ENST00000273432 // intron // 0	MED12L	MED12L, Homo sapiens TRALPUSH (TRALPUSH), q25.1
SNP_A-2023924	aaaagaatggaatgaa[A/T]aaacigtgctatgt	A	T	NM_207292 // upstream // 253451 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 253451 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1868002	tcctagtatttgctta[C/T]ccaacaaagtgactgt	C	T	NM_207292 // upstream // 242423 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 242423 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2306820	gctgtgcacaaggaga[A/G]agaattctcatcttca	A	G	NM_207292 // upstream // 216230 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 216230 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2135143	atattgagacattcaa[G/T]ccaggaagaaaataggg	G	T	NM_207292 // upstream // 199365 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 199365 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2101864	agatggataattaacc[C/T]ggtaccaaaagtgtgt	C	T	NM_207292 // upstream // 131714 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 131714 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-2184664	cagctctaggaggaaa[A/G]atattcatggcacctc	A	G	NM_207292 // upstream // 122882 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 122882 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1832961	tacacaaacaattgga[A/G]atgatgtgcctaaatt	A	G	NM_207292 // upstream // 109700 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 109700 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974853	ttctttcagttcatac[A/G]acaaaataacctctaca	A	G	NM_207292 // upstream // 98644 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // upstream // 98644 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila)	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.1
SNP_A-1787440	gggaagttggtggat[C/G]agagaatgccctaggc	C	G	NM_207292 // intron // 0 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // intron // 0 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), tra	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.2
SNP_A-2252807	ctctaccttgttta[C/T]catcaacagctatatc	C	T	NM_207292 // downstream // 183488 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, mRNA. /// NM_021038 // downstream // 183488 // Hs.478000 // MBNL1 // 4154 // Homo sapiens muscleblind-like (Drosop	MBNL1	MBNL1, Homo sapiens muscleblind-like (Drosophila) (MBNL1), transcript variant 2, q25.2
SNP_A-2122305	agtgcatgacagatta[C/T]gaaagtgcagaatcaa	C	T	NM_002886 // downstream // 212771 // Hs.98643 // RAP2B // 5912 // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA. /// ENST00000323534 // downstream // 212771 // — // — // — /// ENST00000323437 // upstream // 103248 // — //	RAP2B	RAP2B, Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), q25.2
SNP_A-1974886	taaaataaaaataaaa[A/T]gacttcaagtgtacatg	A	T	NM_002886 // downstream // 281180 // Hs.98643 // RAP2B // 5912 // Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA. /// ENST00000323534 // downstream // 281180 // — // — // — // — /// ENST00000323437 // upstream // 34839 // — // -	RAP2B	RAP2B, Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), q25.2
SNP_A-2281069	gagtaatacaaattaa[C/T]acagtgccaatagaag	C	T	NM_015595 // upstream // 584367 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 584769 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2009237	tgcctgcaaatcagtc[A/G]atatagatgaggtaag	A	G	NM_015595 // upstream // 552588 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 552990 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2009238	tagcatttggacttaa[C/T]agacacaagtacatat	C	T	NM_015595 // upstream // 492571 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 492973 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1974894	catgctcaaggacagc[A/G]aaaatgagggataaga	A	G	NM_015595 // upstream // 429997 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 430399 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1745592	aagtaagaaactcagaaatgacttat[C/T]gttgagaaagacag gaaaaagtgc	C	T	NM_002886 // downstream // 773321 // Hs.98643 // RAP2B // 5912 // RAP2B, member of RAS oncogene family /// NM_015595 // upstream // 184839 // Hs.240845 // DKFZP434D146 // 26084 // DKFZP434D146 protein	RAP2B	RAP2B , rs1879558, RAP2B, member of RAS oncogene family, q25.2
SNP_A-2232080	ctcaagcaataccaca[A/C]tgaattaacaaatgaa	A	C	NM_015595 // upstream // 329303 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 329705 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974899	tattccctagggtga[A/T]aigttgaagaggcag	A	T	NM_015595 // upstream // 304392 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 304794 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1818057	gttctatttaaagac[C/T]aaacaccigtgtggt	C	T	NM_015595 // upstream // 108555 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 108957 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2028368	aaactcatttgtacca[C/T]tgaaggaatgttaac	C	T	NM_015595 // upstream // 87569 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 87971 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-1872816	tctataggccaagcaa[C/T]agttccaaagaacact	C	T	NM_015595 // upstream // 76692 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), mRNA. /// NM_015595 // upstream // 77094 // Hs.240845 // SGEF // 26084 // Homo sapiens Src homology 3	SGEF	SGEF, Homo sapiens Src homology 3 domain-containing guanine nucleotide exchange factor (SGEF), q25.2
SNP_A-2189510	cagttacaagagaaaa[A/G]tgggaccacctccacc	A	G	NM_000902 // intron // 0 // Hs.307734 // MME // 4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // intron // 0 // Hs.307734 // MME // 4311 // Homo sapie	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN, q25.2
SNP_A-1974932	gattctctctttaacc[A/C]agaaatgctctgttig	A	C	NM_000902 // intron // 0 // Hs.307734 // MME // 4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // intron // 0 // Hs.307734 // MME // 4311 // Homo sapie	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN, q25.2
SNP_A-1974933	ggattaagtgaaagag[A/C]ctcagttagaaaaata	A	C	NM_000902 // intron // 0 // Hs.307734 // MME // 4311 // Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN /// NM_007287 // intron // 0 // Hs.307734 // MME // 4311 // Homo sapie	MME	MME, Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1, mRN, q25.2
SNP_A-2237812	ctctgaaagttgctg[A/C]aaaatcacagacaaga	A	C	ENST00000232926 // intron // 0 /// — /// — /// —	-	q25.31
SNP_A-2049402	aagctgagatctaaaac[C/G]caatttgtctgactc	C	G	NM_172160 // intron // 0 // Hs.157818 // KCNAB1 // 7881 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, mRNA. /// NM_003471 // intron // 0 // Hs.157818 // KCNAB1 // 7881 // Homo sapi	KCNAB1	KCNAB1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1), transcript variant 1, q25.31
SNP_A-2163693	caaaaatcatagtgca[G/T]attatcacagtttgtc	G	T	NM_007107 // upstream // 9367 // Hs.518346 // SSR3 // 6747 // Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA. /// NM_015508 // upstream // 110096 // Hs.12813 // TIPARP // 25976 // Homo sapiens TCDD-inducibl	SSR3	SSR3, Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), q25.31
SNP_A-2087272	actgcaacttactctc[A/G]agcagagcagaaaaga	A	G	NM_001004316 // downstream // 94761 // Hs.478048 // FLJ16641 // 389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// NM_020307 // downstream // 7285 // Hs.4859 // CCNL1 // 57018 // Homo sapiens cyclin L1 (CCNL1), mRNA. /// ENST00000356539 // down	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31
SNP_A-2171598	caatccittcttgaa[C/G]agtaggtaaaatgatc	C	G	NM_001004316 // downstream // 98211 // Hs.478048 // FLJ16641 // 389170 // Homo sapiens FLJ16641 protein (FLJ16641), mRNA. /// NM_020307 // downstream // 3835 // Hs.4859 // CCNL1 // 57018 // Homo sapiens cyclin L1 (CCNL1), mRNA. /// ENST00000356539 // down	FLJ16641	FLJ16641, Homo sapiens FLJ16641 protein (FLJ16641), q25.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1670225	atctaagcataacctatgtaagctg[C/T]agagtataacgggcac tagagtcaa	C	T	NM_024621 // intron // 0 // Hs.126485 // FLJ12604 // 79674 // hypothetical protein FLJ12604	FLJ12604	FLJ12604, rs10513508, hypothetical protein FLJ12604,q25.31
SNP_A-1683182	aaggcaacaggaatcgaagaacaac[C/T]caaggaaataaat tgcctctgtcag	C	T	NM_024621 // intron // 0 // Hs.126485 // FLJ12604 // 79674 // hypothetical protein FLJ12604	FLJ12604	FLJ12604, rs1500924, hypothetical protein FLJ12604,q25.31
SNP_A-2009253	gactctcaaaaacaac[A/C]cagttaaggcaggtgt	A	C	NM_020307 // upstream // 12620 // Hs.4859 // CCNL1 // 57018 // Homo sapiens cyclin L1 (CCNL1), mRNA. /// ENST00000295926 // upstream // 12620 // — // — // — /// ENST00000295925 // upstream // 13178 // — // — // — /// ENST00000357	CCNL1	CCNL1, Homo sapiens cyclin L1 (CCNL1), q25.31
SNP_A-2165318	caaagagctaagatag[C/T]atttgcacatcaatag	C	T	NM_024621 // downstream // 4900 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 180803 // Hs.546280 // PTX3 // 5806 // Homo sapiens pentaxin-related gene, rapidly induced by IL-1	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2266012	gaaggatttgttccaa[A/G]ggatctatactctggt	A	G	NM_024621 // downstream // 4273 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // upstream // 180176 // Hs.546280 // PTX3 // 5806 // Homo sapiens pentaxin-related gene, rapidly induced by IL-1	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-1783349	ggcataaaatgcattc[C/T]aggaactgtaactcat	C	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2173931	cacacagtgcacataa[A/G]gcaatcctatgtttg	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-1974993	ccacaactgctttgaa[A/G]gacataggattaattt	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2280204	gagggatttaatacga[C/T]gaagaaagaaataggc	C	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-1889744	tgataatgaggtaccc[A/G]ggccctgatcagacat	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2120373	agtcatgcacacttaa[C/T]actatttcaaaatata	C	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.31
SNP_A-2115968	agggttcttataaaga[G/T]aaactcagcacaaatc	G	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2263026	gaacaatttgcacaaa[G/T]gccttgaaacaaaaaa	G	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-1974994	cctctctgtggctcaa[C/T]ggggaacactaataag	C	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — /// ENST00000359472 // intron // 0 // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1974995	agaataattgcttaac[A/G]gatgtgggggttccat	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-1846560	tatattggtattcaga[C/G]gacttagacaagaata	C	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2209482	ccatatcatgattaaaa[A/G]gtgaagcatcttggaa	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-1783322	ggcagtgttctgatgt[C/T]aactcattagagcagt	C	T	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2162068	atttaaatcttttttd[A/G]cacaatttgagaaaga	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2042328	aactattctaatgccat[A/C]gtaaatctcctcgct	A	C	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2302500	gctaattccagctcaa[A/C]tcctgctgctctttta	A	C	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// ENST00000354345 // intron // 0 // — // — // — // — /// ENST00000359472 // intron // 0 // — // — // — // — /// ENST0	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-2070451	acacccgatccgacta[A/G]gcgctgcaggagtcca	A	G	NM_024621 // intron // 0 // Hs.127657 // VEPH1 // 79674 // Homo sapiens hypothetical protein FLJ12604 (FLJ12604), mRNA. /// NM_002852 // intron // 0 // Hs.546280 // PTX3 // 5806 // Homo sapiens pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), m	VEPH1	VEPH1, Homo sapiens hypothetical protein FLJ12604 (FLJ12604), q25.32
SNP_A-1975023	accttgattgtctta[C/T]gctacattgacaacat	C	T	NM_022736 // downstream // 65655 // Hs.58663 // MFSD1 // 64747 // Homo sapiens hypothetical protein FLJ14153 (FLJ14153), mRNA. /// ENST00000264266 // downstream // 65655 // — // — // — // — /// ENST00000335358 // upstream // 350473 // — // — /	MFSD1	MFSD1, Homo sapiens hypothetical protein FLJ14153 (FLJ14153), q25.32
SNP_A-2119359	agtcaatttttatggat[C/G]atcaggcaaacagtat	C	G	NM_022736 // downstream // 125076 // Hs.58663 // MFSD1 // 64747 // Homo sapiens hypothetical protein FLJ14153 (FLJ14153), mRNA. /// ENST00000264266 // downstream // 125076 // — // — // — // — /// ENST00000335358 // upstream // 291052 // — // —	MFSD1	MFSD1, Homo sapiens hypothetical protein FLJ14153 (FLJ14153), q25.32
SNP_A-1975035	ataactgaggaagaaa[C/T]ctaaaatgtggtgcct	C	T	NM_014575 // intron // 0 // Hs.134665 // SCHIP1 // 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // — // — // — // —	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2075737	acatggtttaaaatc[A/C]cagttcataataggtt	A	C	NM_014575 // intron // 0 // Hs.134665 // SCHIP1 // 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // — // — // — // —	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-1889417	tgagttagtgctatca[C/T]aatccacaatatattg	C	T	NM_014575 // intron // 0 // Hs.134665 // SCHIP1 // 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // — // — // — // —	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2278847	gagctttaagcaaaa[C/T]ggaccctcgacctaa	C	T	NM_014575 // intron // 0 // Hs.134665 // SCHIP1 // 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// ENST00000337808 // intron // 0 // — // — // — // —	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140561	atctcctcaataaaac[C/T]gggggaattgatatag	C	T	NM_014575 // downstream // 53728 // Hs.134665 // SCHIP1 // 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// NM_000882 // upstream // 38338 // Hs.673 // IL12A // 3592 // Homo sapiens interleukin 12A (natural killer cell stimulato	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-2231216	ctattatgcaactatc[A/C]aaaagattgaggcaga	A	C	NM_014575 // downstream // 84514 // Hs.134665 // SCHIP1 // 29970 // Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA. /// NM_000882 // upstream // 7552 // Hs.673 // IL12A // 3592 // Homo sapiens interleukin 12A (natural killer cell stimulator	SCHIP1	SCHIP1, Homo sapiens schwannomin interacting protein 1 (SCHIP1), q25.33
SNP_A-1894630	tgccactgtgctgcaa[C/T]ctggaggacaaaaccc	C	T	NM_000882 // downstream // 41211 // Hs.673 // IL12A // 3592 // Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), /// ENST00000305579 // downstream // 41211 // --- // --- // ---	IL12A	IL12A, Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), q25.33
SNP_A-1829671	taagttggcaaaaccca[A/T]gaagttaaggccaggt	A	T	NM_000882 // downstream // 83385 // Hs.673 // IL12A // 3592 // Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), /// ENST00000305579 // downstream // 83385 // --- // --- // ---	IL12A	IL12A, Homo sapiens interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35) (IL12A), q25.33
SNP_A-1710033	gcatgactcagaaaaagttaagaac[C/G]actgatctaaagaat aagactatat	C	G	NM_025047 // downstream // 82620 // Hs.287702 // FLJ22595 // 80117 // hypothetical protein FLJ22595 /// NM_139245 // upstream // 81148 // Hs.319447 // PPM1L // 151742 // protein phosphatase 1 (formerly 2C)-like	FLJ22595	FLJ22595, rs13786663, hypothetical protein FLJ22595 ,q25.33
SNP_A-1949280	tttatgttcgtattca[A/G]gaaaggctgactctgg	A	G	NM_025047 // downstream // 122865 // Hs.287702 // FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream // 263903 // Hs.389027 // PPM1L // 151742 // Homo sapiens protein phosphatase 1 (formerly 2C)-lik	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-1949506	tttatgcttttgcca[A/G]gataaaagtgaaattt	A	G	NM_025047 // downstream // 124322 // Hs.287702 // FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream // 262446 // Hs.389027 // PPM1L // 151742 // Homo sapiens protein phosphatase 1 (formerly 2C)-lik	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-2262822	gaaatttttcaacatc[A/G]aactaaggctatcttg	A	G	NM_025047 // downstream // 138093 // Hs.287702 // FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream // 248675 // Hs.389027 // PPM1L // 151742 // Homo sapiens protein phosphatase 1 (formerly 2C)-lik	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-2255152	cttgggtttcctccca[C/T]gaagatacatatcta	C	T	NM_025047 // downstream // 138178 // Hs.287702 // FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream // 248590 // Hs.389027 // PPM1L // 151742 // Homo sapiens protein phosphatase 1 (formerly 2C)-lik	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-2173534	cacaatgattcaaata[A/C]gccaatttacagaata	A	C	NM_025047 // downstream // 145474 // Hs.287702 // FLJ22595 // 80117 // Homo sapiens hypothetical protein FLJ22595 (FLJ22595), mRNA. /// NM_139245 // upstream // 241294 // Hs.389027 // PPM1L // 151742 // Homo sapiens protein phosphatase 1 (formerly 2C)-lik	FLJ22595	FLJ22595, Homo sapiens hypothetical protein FLJ22595 (FLJ22595), q25.33
SNP_A-1747173	cagtgggtctttttctaggccaca[G/T]tcgttaggaatacagttaa ggccca	G	T	NM_139245 // intron // 0 // Hs.319447 // PPM1L // 151742 // protein phosphatase 1 (formerly 2C)-like	PPM1L	PPM1L , rs6790705, protein phosphatase 1 (formerly 2C)-like,q26.1
SNP_A-1758507	ttatccttggctacaaagatcaata[A/G]taaggatgacgccaattt gaggttg	A	G	BC027488 // downstream // 1574668 // Hs.408584 // - // 401099 // LOC401099 (LOC401099), mRNA /// NM_145035 // upstream // 230616 // Hs.369104 // ADMP // 165679 // ADMP	-	- , rs1588020, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-2300838	gcctggtatttgagta[C/G]gctgttatctgagaac	C	G	NM_001041 // downstream // 3129948 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 345033 // --- // --- // --- /// ENST00000327928 // downstream // 345033 // --- //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1657173	cagatgtgagagagtgacagaaaaa[C/T]gccaggaccccaag agactgtagaat	C	T	BC027488 // downstream // 1134483 // Hs.408584 // - // 401099 // LOC401099 (LOC401099), mRNA /// NM_145035 // upstream // 670801 // Hs.369104 // ADMP // 165679 // ADMP	-	-, rs951475, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-1837975	tagaaactggagataaa[A/G]agttaatcaaccttg	A	G	NM_001041 // downstream // 2955405 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 519576 // — // — // — // — /// ENST00000327928 // downstream // 519576 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2235563	ctcctacaagcagctat[C/G]gaaacagggggtaacta	C	G	NM_001041 // downstream // 2938651 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 536330 // — // — // — // — /// ENST00000327928 // downstream // 536330 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1975124	agatggaaacagtcct[C/G]aatacccaaatatgatt	C	G	NM_001041 // downstream // 2915739 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 559242 // — // — // — // — /// ENST00000327928 // downstream // 559242 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1827329	taacgtgagtgaaaaa[C/T]tctgttagcagatat	C	T	NM_001041 // downstream // 2797997 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 676984 // — // — // — // — /// ENST00000327928 // downstream // 676984 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1884254	tgaaggcacaagaacc[A/G]agtgatggagagagg	A	G	NM_001041 // downstream // 2786367 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 688614 // — // — // — // — /// ENST00000327928 // downstream // 688614 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1749179	ataaaagcaatgggagttgatgtaa[A/G]agaagctagtacata aggcaatgta	A	G	BC027488 // downstream // 724021 // Hs.408584 // - // 401099 // LOC401099 (LOC401099), mRNA /// NM_145035 // upstream // 1081263 // Hs.369104 // ADMP // 165679 // ADMP	-	-, rs7641366, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-1813567	gtgtaacatatgattg[C/T]agtgaagagtgagtct	C	T	NM_001041 // downstream // 2680242 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 794739 // — // — // — // — /// ENST00000327928 // downstream // 794739 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1667854	ctagctacctagcagaccttctaa[C/T]cagtagtatagagatca gtatgcat	C	T	BC027488 // downstream // 654722 // Hs.408584 // - // 401099 // LOC401099 (LOC401099), mRNA /// NM_145035 // upstream // 1150562 // Hs.369104 // ADMP // 165679 // ADMP	-	-, rs9283619, LOC401099 (LOC401099), mRNA ,q26.1
SNP_A-1887210	tgagaacacaaaggtg[A/T]aaaagtaaatcatagc	A	T	NM_001041 // downstream // 2585973 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 889008 // — // — // — // — /// ENST00000327928 // downstream // 889008 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2149276	atgtaatctgcaagtat[A/G]aaacaatgtgacctcc	A	G	NM_001041 // downstream // 2529291 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 945690 // — // — // — // — /// ENST00000327928 // downstream // 945690 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2180296	cagaaataagactgac[C/T]gcccacagctatctga	C	T	NM_001041 // downstream // 2513225 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 961756 // — // — // — // — /// ENST00000327928 // downstream // 961756 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2075971	acattagcagacacaa[A/G]atcaacttataaatgt	A	G	NM_001041 // downstream // 2477838 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 997143 // — // — // — // — /// ENST00000327928 // downstream // 997143 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1975141	ggaaataaggcaatac[A/G]agccagggacaatatt	A	G	NM_001041 // downstream // 2459733 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 1015248 // — // — // — // — /// ENST00000327928 // downstream // 1015248 // — /	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1975143	ctaggacttacaaga[C/T]gcactactggaaatc	C	T	NM_001041 // downstream // 2459192 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 1015789 // — // — // — /// ENST00000327928 // downstream // 1015789 // — /	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2197103	cattattcgttatcc[A/G]actcaaaagtttcaat	A	G	NM_001041 // downstream // 2458667 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 1016314 // — // — // — /// ENST00000327928 // downstream // 1016314 // — /	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2184232	cagcctgatggcaata[G/T]gaaagaaaacccatt	G	T	NM_001041 // downstream // 2331582 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 1143399 // — // — // — /// ENST00000327928 // downstream // 1143399 // — /	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1940587	ttgcctagatggtgtc[A/G]gaaagagccatgtagg	A	G	NM_001041 // downstream // 2306169 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 1168812 // — // — // — /// ENST00000327928 // downstream // 1168812 // — /	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1861581	tcatcgagttgctaca[C/G]attacacatttctctc	C	G	NM_001041 // downstream // 697296 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 2777685 // — // — // — /// ENST00000327928 // downstream // 2777685 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1975192	cagtcactgataaata[C/T]ggaaatgctcctacaa	C	T	NM_001041 // downstream // 410210 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 3064771 // — // — // — /// ENST00000327928 // downstream // 3064771 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2180482	cagaactactagctta[C/T]gagggtaatttagat	C	T	NM_001041 // downstream // 297831 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000345065 // downstream // 3177150 // — // — // — /// ENST00000327928 // downstream // 3177150 // — //	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1941314	ttgctgtttccgggaa[C/G]atacagcaaaatcg	C	G	NM_001041 // intron // 0 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// ENST00000264382 // intron // 0 // — // — // —	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2197156	catcaacataaacgc[A/G]catgcaagtatatgtt	A	G	NM_001041 // upstream // 39777 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// NM_014926 // downstream // 68451 // Hs.101745 // SLITRK3 // 22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1975199	catgcattaaaatttg[G/T]atcctacaaggcagaa	G	T	NM_001041 // upstream // 99686 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// NM_014926 // downstream // 8542 // Hs.101745 // SLITRK3 // 22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3)	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-2043661	aacttaagaaaacaga[C/T]ctatgaggcaggcact	C	T	NM_001041 // upstream // 107451 // Hs.429596 // SI // 6476 // Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), mRNA. /// NM_014926 // downstream // 777 // Hs.101745 // SLITRK3 // 22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3)	SI	SI, Homo sapiens sucrase-isomaltase (alpha-glucosidase) (SI), q26.1
SNP_A-1960018	tttgttcagggtagg[A/G]aagatcgtgaggatgg	A	G	NM_014926 // 3UTR // 0 // Hs.101745 // SLITRK3 // 22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), mRNA. /// ENST00000241274 // 3UTR // 0 // — // — // —	SLITRK3	SLITRK3, Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2264894	gaagagcctagaaaac[A/T]gaaagaaagccattat	A	T	NM_014926 // upstream // 529877 // Hs.101745 // SLITRK3 // 22865 // Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), mRNA. /// NM_000055 // downstream // 46347 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. ///	SLITRK3	SLITRK3, Homo sapiens SLIT and NTRK-like family, member 3 (SLITRK3), q26.1
SNP_A-2022530	aaaaatctccagtgaa[A/G]tcattccttctcatta	A	G	NM_000055 // upstream // 55901 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 55901 // — // — // — // — /// ENST00000330666 // upstream // 797972 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1799379	gtaatcagaaaggtcc[A/G]agtgaaagtcacatta	A	G	NM_000055 // upstream // 75403 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 75403 // — // — // — // — /// ENST00000330666 // upstream // 778470 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-2113505	aggctaaagggtgaaa[A/C]cacttcagattgagtg	A	C	NM_000055 // upstream // 311754 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 311754 // — // — // — // — /// ENST00000330666 // upstream // 542119 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1975212	tgccatgtgtagtgaa[A/G]tgttatatcgatttag	A	G	NM_000055 // upstream // 312228 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 312228 // — // — // — // — /// ENST00000330666 // upstream // 541645 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1939550	ttgattctagccattg[C/T]agtgtgtgtaaagtga	C	T	NM_000055 // upstream // 324761 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 324761 // — // — // — // — /// ENST00000330666 // upstream // 529112 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-1975213	taatctctggaggtag[A/C]aaccattgcttcttcg	A	C	NM_000055 // upstream // 329802 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 329802 // — // — // — // — /// ENST00000330666 // upstream // 524071 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-2098669	agagccccacataaaa[G/T]ggataaacctcaggaa	G	T	NM_000055 // upstream // 331784 // Hs.420483 // BCHE // 590 // Homo sapiens butyrylcholinesterase (BCHE), mRNA. /// ENST00000264381 // upstream // 331784 // — // — // — // — /// ENST00000330666 // upstream // 522089 // — // — // — // —	BCHE	BCHE, Homo sapiens butyrylcholinesterase (BCHE), q26.1
SNP_A-2170958	caataatattctggaa[A/G]cagcactgaagagcaa	A	G	ENST00000324629 // intron // 0 // — // — // — // —	-	q26.1
SNP_A-1844427	tataaactgctccaag[A/C]aataaagtaataatgt	A	C	NM_024687 // upstream // 65547 // Hs.478143 // FLJ23049 // 79740 // Homo sapiens hypothetical protein FLJ23049 (FLJ23049), mRNA. /// NM_006217 // downstream // 48400 // Hs.445555 // SERPINI2 // 5276 // Homo sapiens serine (or cysteine) proteinase inhibito	FLJ23049	FLJ23049, Homo sapiens hypothetical protein FLJ23049 (FLJ23049), q26.1
SNP_A-2129547	atacactacggaatac[G/T]atgcggccataaagaa	G	T	NM_024687 // upstream // 72069 // Hs.478143 // FLJ23049 // 79740 // Homo sapiens hypothetical protein FLJ23049 (FLJ23049), mRNA. /// NM_006217 // downstream // 41878 // Hs.445555 // SERPINI2 // 5276 // Homo sapiens serine (or cysteine) proteinase inhibito	FLJ23049	FLJ23049, Homo sapiens hypothetical protein FLJ23049 (FLJ23049), q26.1
SNP_A-1838221	tagaactttggaataa[A/C]gacttgaaataggatt	A	C	NM_024687 // upstream // 109267 // Hs.478143 // FLJ23049 // 79740 // Homo sapiens hypothetical protein FLJ23049 (FLJ23049), mRNA. /// NM_006217 // downstream // 4680 // Hs.445555 // SERPINI2 // 5276 // Homo sapiens serine (or cysteine) proteinase inhibito	FLJ23049	FLJ23049, Homo sapiens hypothetical protein FLJ23049 (FLJ23049), q26.1
SNP_A-1928526	ttcactctaccagaaa[C/T]gcttcacatatacatc	C	T	NM_006217 // intron // 0 // Hs.445555 // SERPINI2 // 5276 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 2 (SERPINI2), mRNA. /// ENST00000264677 // intron // 0 // — // — // — // —	SERPINI2	SERPINI2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 2 (SERPINI2), q26.1
SNP_A-2131252	atagaggaagaccttа[C/T]gatgtggctgtctatg	C	T	NM_178824 // intron // 0 // Hs.213762 // WDR49 // 151790 // Homo sapiens hypothetical protein FLJ33620 (FLJ33620), mRNA. /// ENST00000308378 // intron // 0 // — // — // — // —	WDR49	WDR49, Homo sapiens hypothetical protein FLJ33620 (FLJ33620), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215185	cctcaaaatactgcaa[A/T]ggttttctaatatatc	A	T	NM_178824 // intron // 0 // Hs.213762 // WDR49 // 151790 // Homo sapiens hypothetical protein FLJ33620 (FLJ33620), mRNA. /// ENST00000308378 // intron // 0 // --- // --- // --- /// ENST00000308351 // intron // 0 // --- // --- // ---	WDR49	WDR49, Homo sapiens hypothetical protein FLJ33620 (FLJ33620), q26.1
SNP_A-1839695	tagatgctagggatact[A/G]gaaaaaacaggatgaa	A	G	NM_005025 // intron // 0 // Hs.478153 // SERPINI1 // 5274 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2027075	aaacagcatgatagccc[A/G]actggacttacatc	A	G	NM_005025 // intron // 0 // Hs.478153 // SERPINI1 // 5274 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2216235	cctccgttgctaatggt[A/G]atgacagctaatggga	A	G	NM_005025 // intron // 0 // Hs.478153 // SERPINI1 // 5274 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // intron // 0 // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2115245	aggggaactggaagtc[A/G]cagttaggcctgaaa	A	G	NM_005025 // CDS // 0 // Hs.478153 // SERPINI1 // 5274 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// ENST00000295777 // CDS // 0 // --- // --- // ---	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2186345	caggctggagtgcaat[A/G]acacagtctcggctca	A	G	NM_005025 // downstream // 154736 // Hs.478153 // SERPINI1 // 5274 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA. /// NM_014498 // downstream // 29147 // Hs.143600 // GOLPH4 // 27333 // Homo sa	SERPINI1	SERPINI1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), q26.1
SNP_A-2058821	aatcatttggcaagat[A/G]aaacatttctctgaga	A	G	NM_014498 // upstream // 349243 // Hs.143600 // GOLPH4 // 27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 639638 // Hs.165830 // EVI1 // 2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. ///	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-2102209	agattaaactcacaaa[G/T]caataattacatatta	G	T	NM_014498 // upstream // 420078 // Hs.143600 // GOLPH4 // 27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 568803 // Hs.165830 // EVI1 // 2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. ///	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-1975246	cttatatgcttgcaat[A/C]aaaaaagtgcagaatt	A	C	NM_014498 // upstream // 822547 // Hs.143600 // GOLPH4 // 27333 // Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA. /// NM_005241 // downstream // 166334 // Hs.165830 // EVI1 // 2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. ///	GOLPH4	GOLPH4, Homo sapiens golgi phosphoprotein 4 (GOLPH4), q26.2
SNP_A-1835737	tacgagttgtcaaaaa[C/G]actcagaatggaagta	C	G	NM_005241 // upstream // 242630 // Hs.165830 // EVI1 // 2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. /// NM_032487 // downstream // 377990 // Hs.135411 // ARPM1 // 84517 // Homo sapiens actin related protein M1 (ARPM1), mRNA. ///	EVI1	EVI1, Homo sapiens ecotropic viral integration site 1 (EVI1), q26.2
SNP_A-2279761	gaggccacgttttaa[C/T]ccagctctgaaagact	C	T	NM_005241 // upstream // 355209 // Hs.165830 // EVI1 // 2122 // Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA. /// NM_032487 // downstream // 265411 // Hs.135411 // ARPM1 // 84517 // Homo sapiens actin related protein M1 (ARPM1), mRNA. ///	EVI1	EVI1, Homo sapiens ecotropic viral integration site 1 (EVI1), q26.2
SNP_A-1879857	tcttccccaagatgac[A/G]cgtgagatgacacgtg	A	G	NM_024727 // upstream // 38601 // Hs.411295 // LRRC31 // 79782 // Homo sapiens hypothetical protein FLJ23259 (FLJ23259), mRNA. /// NM_182610 // upstream // 3041 // Hs.439922 // SAMD7 // 344658 // Homo sapiens sterile alpha motif domain containing 7 (SAMD7	LRRC31	LRRC31, Homo sapiens hypothetical protein FLJ23259 (FLJ23259), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2120093	agtcacttcaccagta[C/T]gtaaacatgagttata	C	T	NM_003262 // intron // 0 // Hs.529591 // TLOC1 // 7095 // Homo sapiens translocation protein 1 (TLOC1), mRNA. /// ENST00000337002 // intron // 0 // — // — // —	TLOC1	TLOC1, Homo sapiens translocation protein 1 (TLOC1), q26.2
SNP_A-2171532	caatccaggtctacaa[C/T]gtgccagttacaatga	C	T	NM_002740 // intron // 0 // Hs.478199 // PRKCI // 5584 // Homo sapiens protein kinase C, iota (PRKCI), mRNA. /// ENST00000295797 // intron // 0 // — // — // — // —	PRKCI	PRKCI, Homo sapiens protein kinase C, iota (PRKCI), q26.2
SNP_A-2268343	gaatgcatattccaga[A/G]acttatttttgccaaa	A	G	NM_002740 // intron // 0 // Hs.478199 // PRKCI // 5584 // Homo sapiens protein kinase C, iota (PRKCI), mRNA. /// ENST00000295797 // intron // 0 // — // — // — // —	PRKCI	PRKCI, Homo sapiens protein kinase C, iota (PRKCI), q26.2
SNP_A-2290161	gcaaatgctaaaatta[A/G]gatggtaatgagtggc	A	G	NM_002740 // intron // 0 // Hs.478199 // PRKCI // 5584 // Homo sapiens protein kinase C, iota (PRKCI), mRNA. /// ENST00000295797 // intron // 0 // — // — // — // —	PRKCI	PRKCI, Homo sapiens protein kinase C, iota (PRKCI), q26.2
SNP_A-2187743	cagtagaattctattat[C/G]agagatgtaggtacta	C	G	NM_005602 // intron // 0 // Hs.31595 // CLDN11 // 5010 // Homo sapiens claudin 11 (oligodendrocyte transmembrane protein) (CLDN11), mRNA. /// ENST00000064724 // intron // 0 // — // — // — // —	CLDN11	CLDN11, Homo sapiens claudin 11 (oligodendrocyte transmembrane protein) (CLDN11), q26.2
SNP_A-1975277	agagtttgtcacaaag[A/G]aaatgttcaatgtgg	A	G	ENST00000231706 // intron // 0 // — // — // — // —	-	q26.2
SNP_A-2237328	ctctccagcttccccc[C/G]acaaagttccagacct	C	G	ENST00000231706 // upstream // 70052 // — // — // — // — /// ENST00000295830 // downstream // 210194 // — // — // — // —	-	q26.2
SNP_A-2308473	gctttacctctgccad[A/G]agctgggaggccataa	A	G	AB011123 // intron // 0 // Hs.34024 // TNIK // 23043 // Homo sapiens mRNA for KIAA0551 protein, partial cds. /// ENST00000284483 // intron // 0 // — // — // — // — /// ENST00000341852 // intron // 0 // — // — // — // — // — /// ENST00000357327	TNIK	TNIK, Homo sapiens for KIAA0551 protein, partial cds. q26.2
SNP_A-2036347	aaattcccaaacctc[A/G]caggataggctcaata	A	G	NM_002662 // intron // 0 // Hs.478230 // PLD1 // 5337 // Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), mRNA. /// ENST00000351298 // intron // 0 // — // — // — // — /// ENST00000356327 // intron // 0 // — // — // — // —	PLD1	PLD1, Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), q26.31
SNP_A-1846775	tatcaagctgcaaaac[C/T]atctacgctcctatgt	C	T	NM_002662 // intron // 0 // Hs.478230 // PLD1 // 5337 // Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), mRNA. /// ENST00000351298 // intron // 0 // — // — // — // —	PLD1	PLD1, Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), q26.31
SNP_A-1975319	tcctctcactcttagа[C/T]tcaggaaattatgtc	C	T	NM_022763 // intron // 0 // Hs.159430 // FNDC3B // 64778 // Homo sapiens FAD104 (FAD104), mRNA. /// ENST00000264609 // intron // 0 // — // — // — // — /// ENST00000336824 // intron // 0 // — // — // — // —	FNDC3B	FNDC3B, Homo sapiens FAD104 (FAD104), q26.31
SNP_A-1823068	taaaaattgttgacaa[A/T]gttaaaggtcagcttg	A	T	NM_022763 // downstream // 24230 // Hs.159430 // FNDC3B // 64778 // Homo sapiens FAD104 (FAD104), mRNA. /// NM_004122 // downstream // 20234 // Hs.248115 // GHSR // 2693 // Homo sapiens growth hormone secretagogue receptor (GHSR), transcript variant 1b, m	FNDC3B	FNDC3B, Homo sapiens FAD104 (FAD104), q26.31
SNP_A-1929430	ttcagttatcttctaq[C/T]gcctgtatttctact	C	T	NM_022763 // downstream // 24891 // Hs.159430 // FNDC3B // 64778 // Homo sapiens FAD104 (FAD104), mRNA. /// NM_004122 // downstream // 19573 // Hs.248115 // GHSR // 2693 // Homo sapiens growth hormone secretagogue receptor (GHSR), transcript variant 1b, m	FNDC3B	FNDC3B, Homo sapiens FAD104 (FAD104), q26.31
SNP_A-2278418	gagctatgaaaaatgt[C/G]acacagtacttggtga	C	G	NM_003810 // upstream // 95285 // Hs.478275 // TNFSF10 // 8743 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA. /// NM_020792 // downstream // 11882 // Hs.444099 // KIAA1363 // 57552 // Homo sapiens KIAA1363 protein (	TNFSF10	TNFSF10, Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), q26.31
SNP_A-2091520	agaaaaaagaatttaga[A/G]aactgctacaaagaaaa	A	G	NM_020792 // intron // 0 // Hs.444099 // KIAA1363 // 57552 // Homo sapiens KIAA1363 protein (KIAA1363), mRNA. /// ENST00000273512 // intron // 0 // — // — // — // —	KIAA1363	KIAA1363, Homo sapiens KIAA1363 protein (KIAA1363), q26.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2076072	acattcaacacacaga[A/G]agtaagagatcgcaga	A	G	NM_020792 // intron // 0 // Hs.444099 // KIAA1363 // 57552 // Homo sapiens KIAA1363 protein (KIAA1363), mRNA. /// ENST00000273512 // intron // 0 // — // — // —	KIAA1363	KIAA1363, Homo sapiens KIAA1363 protein (KIAA1363), q26.31
SNP_A-2312697	ggactatgggagaaac[C/T]agtactgcaatatgtt	C	T	NM_018098 // downstream // 23424 // Hs.518299 // ECT2 // 1894 // Homo sapiens epithelial cell transforming sequence 2 oncogene (ECT2), mRNA. /// NM_031955 // downstream // 44461 // Hs.444236 // SPATA16 // 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12).	ECT2	ECT2, Homo sapiens epithelial cell transforming sequence 2 oncogene (ECT2), q26.31
SNP_A-2097429	agagaaatgcaaacta[C/G]gtttagagaatgctat	C	G	NM_018098 // downstream // 26295 // Hs.518299 // ECT2 // 1894 // Homo sapiens epithelial cell transforming sequence 2 oncogene (ECT2), mRNA. /// NM_031955 // downstream // 41590 // Hs.444236 // SPATA16 // 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12).	ECT2	ECT2, Homo sapiens epithelial cell transforming sequence 2 oncogene (ECT2), q26.31
SNP_A-1850819	tattagccaatgatac[C/T]ctagtggctctgcta	C	T	NM_031955 // upstream // 317747 // Hs.444236 // SPATA16 // 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 145636 // NLGN1 // 22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000003510	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-1915159	tgttcaaatagagtga[A/G]gttgagtaagttaata	A	G	NM_031955 // upstream // 320292 // Hs.444236 // SPATA16 // 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 143091 // Hs.546345 // NLGN1 // 22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000003510	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-1894908	tgccattaatatccta[C/T]gctataaacaccactca	C	T	NM_031955 // upstream // 350686 // Hs.444236 // SPATA16 // 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 112697 // Hs.546345 // NLGN1 // 22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000003510	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-1847564	tatccttttcttctc[A/G]actatgcacaaaagaa	A	G	NM_031955 // upstream // 369790 // Hs.444236 // SPATA16 // 83893 // Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA. /// AB028993 // upstream // 93593 // Hs.546345 // NLGN1 // 22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// ENST00000035100	SPATA16	SPATA16, Homo sapiens NYD-SP12 protein (NYD-SP12), q26.31
SNP_A-1717461	gttgacaaagtaatgaatataaaga[A/T]cagacatatgaaaaa gtaacaaatt	A	T	NM_014932 // intron // 0 // Hs.71132 // NLGN1 // 22871 // neuroligin 1	NLGN1	NLGN1 , rs1345535, neuroligin 1,q26.31
SNP_A-2034317	aaatcctgatgttttc[A/G]agcaagaacaagtagc	A	G	AB028993 // downstream // 59543 // Hs.546345 // NLGN1 // 22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// NM_207015 // upstream // 754111 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (N	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds, q26.31
SNP_A-1708861	gtaaataaaaatcaaatggcataaa[C/T]gaagaagtgtgattac atcaaatac	C	T	NM_014932 // downstream // 395224 // Hs.71132 // NLGN1 // 22871 // neuroligin 1 /// NM_030921 // downstream // 2342202 // - // - // -	NLGN1	NLGN1 , rs575582, neuroligin 1 ,q26.31
SNP_A-1916597	tgtttagttgctataa[A/G]gtttgcaaagctacat	A	G	AB028993 // downstream // 703316 // Hs.546345 // NLGN1 // 22871 // Homo sapiens mRNA for KIAA1070 protein, partial cds. /// NM_207015 // upstream // 110338 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (	NLGN1	NLGN1, Homo sapiens for KIAA1070 protein, partial cds, q26.31
SNP_A-2060645	aatgagaggataaaga[C/T]actctggataaaaaac	C	T	NM_207015 // intron // 0 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 // intron // 0 // — // — // —	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-1861257	tcatatttgccaagag[A/G]acagtaaaatgataaa	A	G	NM_207015 // intron // 0 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// ENST00000316366 // intron // 0 // — // — // —	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1836618	tactctgtccaattca[A/G]tatgtatgtgttcaac	A	G	NM_207015 // downstream // 320760 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// NM_024665 // downstream // 899951 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.31
SNP_A-2077705	accactgcactcaaaac[A/G]caggttaacacagtga	A	G	NM_207015 // downstream // 587247 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// NM_024665 // downstream // 633464 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-1957119	tttacagtcctctga[A/G]aactatttatagtca	A	G	NM_207015 // downstream // 932808 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// NM_024665 // downstream // 287903 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-2245681	ctgggctcatgattca[A/C]aactactctggatttt	A	C	NM_207015 // downstream // 1149086 // Hs.416922 // NAALADL2 // 254827 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), mRNA. /// NM_024665 // downstream // 71625 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-	NAALADL2	NAALADL2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALADL2), q26.32
SNP_A-2053121	aagtctcattaaatcc[A/G]atctctgggggtgag	A	G	NM_024665 // upstream // 225191 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 224444 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2158483	attgtaagatagaaga[A/G]aacactgaacacctga	A	G	NM_024665 // upstream // 242894 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 242147 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2106048	agcccacattcgatac[A/G]atgatgtgtgtgaatg	A	G	NM_024665 // upstream // 244491 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 243744 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2169528	caagctacacgtgtga[A/G]aagcagaattgctcct	A	G	NM_024665 // upstream // 281815 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 281068 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2152563	attaaggtctcaagaaa[C/T]gaaataggctggtaca	C	T	NM_024665 // upstream // 327008 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 326261 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2108793	agctgtgtctaaactc[C/T]gaaaggagagagcat	C	T	NM_024665 // upstream // 414056 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 413309 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2114680	agggatatcgctcatg[C/T]aaattatcctgcttct	C	T	NM_024665 // upstream // 423268 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 422521 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2069358	acacaaaggaagcgta[C/T]gtaggttatttctgca	C	T	NM_024665 // upstream // 428351 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 427604 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2164224	caaaataaacatttcc[A/G]aacattctagatcaat	A	G	NM_024665 // upstream // 432623 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 431876 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1801524	gtaggtaaggaggaaa[G/T]aactgagaaactgagc	G	T	NM_024665 // upstream // 529702 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 528955 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1975445	tagcgatggtaggctc[C/T]gagcagaaaggagca	C	T	NM_024665 // upstream // 946733 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 945986 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-li	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2088322	actgtaaagcctgaac[A/C]aaaaaaatgtcagatt	A	C	NM_024665 // upstream // 1310988 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 1310241 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2103802	agcacccacatttta[A/G]ctgtcaggaaagctca	A	G	NM_024665 // upstream // 1461993 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 1461246 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2298012	gccatacagaatgaca[C/G]tgaggaatattaaaaa	C	G	NM_024665 // upstream // 1588949 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 1588202 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-1811745	gtgcttacatcacgac[C/T]ccagaagctatgggta	C	T	NM_024665 // upstream // 1598923 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), mRNA. /// NM_024665 // upstream // 1598176 // Hs.438970 // TBL1XR1 // 79718 // Homo sapiens transducin (beta)-like 1X-	TBL1XR1	TBL1XR1, Homo sapiens transducin (beta)-like 1X-linked receptor 1 (TBL1XR1), q26.32
SNP_A-2235779	ctcctctatgaagaca[A/G]catttaaaaatcaaac	A	G	NM_181361 // downstream // 119751 // Hs.478368 // KCNMB2 // 10242 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m /// NM_005832 // downstream // 119751 // Hs.478368 // KCN	KCNMB2	KCNMB2, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m q26.32
SNP_A-1900356	tggagagctgcttgaa[A/G]tatgtgtaaagacccg	A	G	NM_181361 // downstream // 120764 // Hs.478368 // KCNMB2 // 10242 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m /// NM_005832 // downstream // 120764 // Hs.478368 // KCN	KCNMB2	KCNMB2, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m q26.32
SNP_A-2250608	cttagttcagccttg[C/G]aagaatatgtctcacg	C	G	NM_181361 // downstream // 125517 // Hs.478368 // KCNMB2 // 10242 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m /// NM_005832 // downstream // 125517 // Hs.478368 // KCN	KCNMB2	KCNMB2, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m q26.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2106702	agcctgaggactctga[A/G]aaatctaaacttatt	A	G	NM_181361 // downstream // 137466 // Hs.478368 // KCNMB2 // 10242 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m /// NM_005832 // downstream // 137466 // Hs.478368 // KCN	KCNMB2	KCNMB2, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m q26.32
SNP_A-2176360	caccatacaattcctc[C/T]catcgtcatcacataa	C	T	NM_181361 // downstream // 142732 // Hs.478368 // KCNMB2 // 10242 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m /// NM_005832 // downstream // 142732 // Hs.478368 // KCN	KCNMB2	KCNMB2, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 2 (KCNMB2), transcript variant 1, m q26.32
SNP_A-2116527	aggtcaagaaaagcaa[A/T]gactaaggaattatta	A	T	NM_152240 // upstream // 20281 // Hs.386299 // WIG1 // 64393 // Homo sapiens p53 target zinc finger protein (WIG1), transcript variant 2, mRNA. /// NM_022470 // upstream // 20281 // Hs.386299 // WIG1 // 64393 // Homo sapiens p53 target zinc finger protein	WIG1	WIG1, Homo sapiens p53 target zinc finger protein (WIG1), transcript variant 2, q26.32
SNP_A-2099765	agagtaaagaaggtta[A/G]atgtgaaagtgagaga	A	G	NM_152240 // upstream // 94753 // Hs.386299 // WIG1 // 64393 // Homo sapiens p53 target zinc finger protein (WIG1), transcript variant 2, mRNA. /// NM_022470 // upstream // 94753 // Hs.386299 // WIG1 // 64393 // Homo sapiens p53 target zinc finger protein	WIG1	WIG1, Homo sapiens p53 target zinc finger protein (WIG1), transcript variant 2, q26.32
SNP_A-1683918	tgtccatggaggcctagaacacaaa[C/T]gatggaaaccttca cgcttcctg	C	T	NM_021629 // intron // 0 // Hs.48695 // GNB4 // 59345 // guanine nucleotide binding protein (G protein), beta polypeptide 4	GNB4	GNB4 , rs2287310, guanine nucleotide binding protein (G protein), beta polypeptide 4,q26.32
SNP_A-1975465	tcattctttgctacca[C/T]gagaaggtcccaggta	C	T	NM_171829 // upstream // 9657 // Hs.85701 // KCNMB3 // 27094 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M beta member 3 (KCNMB3), transcript variant 2, mR /// NM_171830 // upstream // 9657 // Hs.85701 // KCNMB3 // 270	KCNMB3	KCNMB3, Homo sapiens potassium large conductance calcium-activated channel, subfamily M beta member 3 (KCNMB3), transcript variant 2, mR q26.32
SNP_A-2165054	caaactgtaactatag[G/T]agctccatcacccaat	G	T	NM_017927 // intron // 0 // Hs.478383 // MFN1 // 55669 // Homo sapiens mitofusin 1 (MFN1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_033540 // intron // 0 // Hs.478383 // MFN1 // 55669 // Homo sapiens mitofusin 1 (MFN	MFN1	MFN1, Homo sapiens mitofusin 1 (MFN1), nuclear gene encoding mitochondrial protein, transcript variant 2, q26.32
SNP_A-2185816	caggatgactaaggct[A/G]acttcccaccatgctt	A	G	NM_021629 // upstream // 62813 // Hs.270543 // GNB4 // 59345 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA. /// NM_004301 // upstream // 48524 // Hs.435326 // ACTL6A // 86 // Homo sapiens actin-like 6A (AC	GNB4	GNB4, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), q26.33
SNP_A-2023979	aaaagaccatgagttc[A/G]ctgaatacaaagagct	A	G	NM_021629 // upstream // 69707 // Hs.270543 // GNB4 // 59345 // Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA. /// NM_004301 // upstream // 41630 // Hs.435326 // ACTL6A // 86 // Homo sapiens actin-like 6A (AC	GNB4	GNB4, Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), q26.33
SNP_A-2250182	cttactggaaaaatca[A/G]atcagaatcttgcca	A	G	NM_003940 // intron // 0 // Hs.175322 // USP13 // 8975 // Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA. /// ENST00000263966 // intron // 0 // — // — // —	USP13	USP13, Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), q26.33
SNP_A-1786068	ggctgctttggaaaac[C/T]gagagaacctcagctg	C	T	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — /// ENST00000263963 // intron // 0 // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-1975478	tcatttctttctttgga[C/T]agtcgattgctctc	C	T	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — /// ENST00000263963 // intron // 0 // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796254	ggtgtgcttgactaag[A/T]ccctgccaatggcgtg	A	T	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-1811441	gtgcatgagatcaga[C/T]ggaaaacagatgaaca	C	T	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-2159434	atttaatttcaaccag[A/G]catttactaatgaaa	A	G	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-2192929	catccttctggcaaatt[C/T]agttgagactattaaa	C	T	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-1922791	ttagagttaagcagaaa[C/T]gtgatttttgaatctag	C	T	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-2061248	aatgcatcttccctgaj[A/G]caaaagagagaggagc	A	G	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-2288940	gatttatagaattaac[A/G]acattgagagacacaa	A	G	NM_016559 // intron // 0 // Hs.478393 // PEX5L // 51555 // Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), mRNA. /// ENST00000263962 // intron // 0 // — // — // — // — /// ENST00000263963 // intron // 0 // — // — // — // —	PEX5L	PEX5L, Homo sapiens peroxisomal biogenesis factor 5-like (PEX5L), q26.33
SNP_A-1839598	tagatcctgctgaac[A/G]aatgcaatgtttctt	A	G	ENST00000273654 // intron // 0 // — // — // —	-	q26.33
SNP_A-1931417	ttccatacatatgca[A/G]acacagaagatttcaa	A	G	NM_005087 // intron // 0 // Hs.478407 // FXR1 // 8087 // Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA. /// ENST00000357559 // intron // 0 // — // — // — // — /// ENST00000305586 // intron // 0 // — // — // — // —	FXR1	FXR1, Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), q26.33
SNP_A-1975501	agctggatggtattta[C/T]aattcacgtttcttaa	C	T	NM_005087 // intron // 0 // Hs.478407 // FXR1 // 8087 // Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA. /// ENST00000357559 // intron // 0 // — // — // — // — /// ENST00000305586 // intron // 0 // — // — // — // —	FXR1	FXR1, Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), q26.33
SNP_A-2061898	aatggcacttaagcta[A/C]ctcaatttttcaagttt	A	C	NM_003106 // upstream // 715415 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ENST00000313571 // upstream // 6777 // — // — // — // — /// ENST00000325404 // upstream // 715415 // — // — // —	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2103626	agcacaccgcatatca[A/C]tcttgcagttatttg	A	C	NM_003106 // downstream // 63880 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// AB023173 // upstream // 1041947 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2104641	agcagtattaggctta[C/T]gtcaagattgagagga	C	T	NM_003106 // downstream // 140321 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// AB023173 // upstream // 965506 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-1895347	tgcccttcatctccac[C/T]gaactacttttctggat	C	T	NM_003106 // downstream // 147488 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// AB023173 // upstream // 958339 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284149	gatatgcatacggtga[C/T]acccactactgcagtg	C	T	NM_003106 // downstream // 592544 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 513283 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2251529	cttcacttgaactta[C/T]gaaaggcaccttcta	C	T	NM_003106 // downstream // 610029 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 495798 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2009367	gagagttaaaaggcaa[A/G]atacagagcaggagtc	A	G	NM_003106 // downstream // 636256 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 469571 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2009369	cccagcaacctaaaca[C/G]aaatctgaaggaatgg	C	G	NM_003106 // downstream // 796057 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 309770 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2052663	aagtatgtgcattgga[A/G]accaagaatgtacaaa	A	G	NM_003106 // downstream // 804458 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 301369 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2029045	aaagaaacttcagaca[A/G]atctcaggaagctgag	A	G	NM_003106 // downstream // 808766 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 297061 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2248403	ctgtgtgggtctcaa[C/T]actaacccagaaatac	C	T	NM_003106 // downstream // 814858 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 290969 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-1939287	ttgatctaagataaagc[A/G]aaaaaggttgtgact	A	G	NM_003106 // downstream // 1049969 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 55858 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-2032401	aaagtgttttcgctc[A/G]attccttttcattact	A	G	NM_003106 // downstream // 1053662 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 51965 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-1886535	tgactagcccagaaaa[A/C]agttagaaaatgagta	A	C	NM_003106 // downstream // 1082415 // Hs.518438 // SOX2 // 6657 // Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA. /// ABO23173 // upstream // 23412 // Hs.478429 // ATP11B // 23200 // Homo sapiens mRNA for KIAA0956 protein, partial cds. //	SOX2	SOX2, Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), q26.33
SNP_A-1884833	tgaatcctgaacccgg[G/T]ataccattgtgaaaag	G	T	NM_020166 // intron // 0 // Hs.47649 // MCCC1 // 56922 // Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA. /// ENST00000265594 // intron // 0 // --- // --- // ---	MCCC1	MCCC1, Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), q27.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1845517	tatagaggttaattca[A/G]cagacaacttatcgtg	A	G	NM_015078 // intron // 0 // Hs.405716 // MCF2L2 // 23101 // Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), mRNA. /// ENST00000328913 // intron // 0 // — // — // — // —	MCF2L2	MCF2L2, Homo sapiens MCF.2 cell line derived transforming sequence-like 2 (MCF2L2), q27.1
SNP_A-2207192	ccattatggggcagca[C/T]tgaggattttgagatt	C	T	NM_130446 // intron // 0 // Hs.333181 // KLHL6 // 89857 // Homo sapiens kelch-like 6 (Drosophila) (KLHL6), mRNA. /// ENST00000341319 // intron // 0 // — // — // — // —	KLHL6	KLHL6, Homo sapiens kelch-like 6 (Drosophila) (KLHL6), q27.1
SNP_A-2112285	aggattttgagattaa[G/T]tcagacgtgtgcttct	G	T	NM_130446 // intron // 0 // Hs.333181 // KLHL6 // 89857 // Homo sapiens kelch-like 6 (Drosophila) (KLHL6), mRNA. /// ENST00000341319 // intron // 0 // — // — // — // —	KLHL6	KLHL6, Homo sapiens kelch-like 6 (Drosophila) (KLHL6), q27.1
SNP_A-2251695	cttcagtattgctgat[C/G]aagtcacagaaacaat	C	G	NM_130446 // intron // 0 // Hs.333181 // KLHL6 // 89857 // Homo sapiens kelch-like 6 (Drosophila) (KLHL6), mRNA. /// ENST00000341319 // intron // 0 // — // — // — // —	KLHL6	KLHL6, Homo sapiens kelch-like 6 (Drosophila) (KLHL6), q27.1
SNP_A-1833435	tacagagaatcaacaa[C/T]gtggagacctacgacc	C	T	NM_130446 // CDS // 0 // Hs.333181 // KLHL6 // 89857 // Homo sapiens kelch-like 6 (Drosophila) (KLHL6), mRNA. /// ENST00000341319 // CDS // 0 // — // — // — // —	KLHL6	KLHL6, Homo sapiens kelch-like 6 (Drosophila) (KLHL6), q27.1
SNP_A-1800587	gtacttgatttgattc[C/T]cctctgtggtttcctt	C	T	NM_130446 // intron // 0 // Hs.333181 // KLHL6 // 89857 // Homo sapiens kelch-like 6 (Drosophila) (KLHL6), mRNA. /// ENST00000341319 // intron // 0 // — // — // — // —	KLHL6	KLHL6, Homo sapiens kelch-like 6 (Drosophila) (KLHL6), q27.1
SNP_A-2024505	aaaaggaggggttga[C/G]ctggaaatctgtaatt	C	G	NM_182537 // downstream // 4508 // Hs.448004 // HTR3D // 200909 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3 family member D (HTR3D), mRNA. /// NM_130770 // upstream // 9171 // Hs.352185 // HTR3C // 170572 // Homo sapiens 5-hydroxytryptamine	HTR3D	HTR3D, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3 family member D (HTR3D), q27.1
SNP_A-2081346	acctggctctgtcagt[A/T]actagctagggaagct	A	T	NM_003907 // downstream // 715 // Hs.283551 // EIF2B5 // 8893 // Homo sapiens eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa (EIF2B5), mRNA. /// ENST00000273783 // downstream // 715 // — // — // — // — /// ENST00000341606 //	EIF2B5	EIF2B5, Homo sapiens eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa (EIF2B5), q27.1
SNP_A-1932730	ttccttctcttgagaa[C/T]tggaggattcgaggac	C	T	NM_003907 // downstream // 3745 // Hs.283551 // EIF2B5 // 8893 // Homo sapiens eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa (EIF2B5), mRNA. /// ENST00000273783 // downstream // 3745 // — // — // — // — /// ENST00000341606	EIF2B5	EIF2B5, Homo sapiens eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa (EIF2B5), q27.1
SNP_A-1877549	tctggcctatgaaaaa[C/G]aatacatggcctgagg	C	G	NM_018358 // intron // 0 // Hs.361323 // ABCF3 // 55324 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA. /// ENST00000292808 // intron // 0 // — // — // — // —	ABCF3	ABCF3, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), q27.1
SNP_A-1882379	tgaaaagaaagtgttc[C/T]atgccttcctgttaga	C	T	NM_018358 // downstream // 546 // Hs.361323 // ABCF3 // 55324 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA. /// ENST00000292808 // downstream // 546 // — // — // — // — /// ENST00000342806 // upstream // 35978	ABCF3	ABCF3, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), q27.1
SNP_A-1844820	tataatacctaagtaa[C/T]acctagattgttcaaa	C	T	NM_018358 // downstream // 8157 // Hs.361323 // ABCF3 // 55324 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA. /// ENST00000292808 // downstream // 8157 // — // — // — // — /// ENST00000342806 // upstream // 283	ABCF3	ABCF3, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), q27.1
SNP_A-1975544	ggtagtcataggagaa[G/T]agatgatatagatgat	G	T	NM_018358 // downstream // 33444 // Hs.361323 // ABCF3 // 55324 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA. /// ENST00000292808 // downstream // 33444 // — // — // — // — /// ENST00000342806 // upstream // 3	ABCF3	ABCF3, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), q27.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1975545	ggaggagtgagaacca[C/T]gggcccgactcgaaag	C	T	NM_018358 // downstream // 34481 // Hs.361323 // ABCF3 // 55324 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA. /// ENST00000292808 // downstream // 34481 // — // — // — // — /// ENST00000342806 // upstream // 2	ABCF3	ABCF3, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), q27.1
SNP_A-2186143	caggccccaggaacaa[C/T]ggtctccaggctggct	C	T	NM_014693 // intron // 0 // Hs.146161 // ECE2 // 9718 // Homo sapiens endothelin converting enzyme 2 (ECE2), mRNA. /// ENST00000351385 // intron // 0 // — // — // — // —	ECE2	ECE2, Homo sapiens endothelin converting enzyme 2 (ECE2), q27.1
SNP_A-1916087	tgttgctggtgaggga[C/T]ggttgccaagtaagac	C	T	NM_014693 // intron // 0 // Hs.146161 // ECE2 // 9718 // Homo sapiens endothelin converting enzyme 2 (ECE2), mRNA. /// ENST00000351385 // intron // 0 // — // — // — // —	ECE2	ECE2, Homo sapiens endothelin converting enzyme 2 (ECE2), q27.1
SNP_A-2254550	cttgctaccatagctc[A/G]cagaagttatggagaa	A	G	NM_177978 // downstream // 45750 // Hs.166186 // CHRD // 8646 // Homo sapiens chordin (CHRD), transcript variant 2, mRNA. /// NM_177979 // downstream // 37029 // Hs.166186 // CHRD // 8646 // Homo sapiens chordin (CHRD), transcript variant 3, mRNA. /// NM_	CHRD	CHRD, Homo sapiens chordin (CHRD), transcript variant 2, q27.1
SNP_A-2280423	gagggtcagcaggaaa[A/G]gtcattgaggaccctg	A	G	NM_177978 // downstream // 74570 // Hs.166186 // CHRD // 8646 // Homo sapiens chordin (CHRD), transcript variant 2, mRNA. /// NM_177979 // downstream // 65849 // Hs.166186 // CHRD // 8646 // Homo sapiens chordin (CHRD), transcript variant 3, mRNA. /// NM_	CHRD	CHRD, Homo sapiens chordin (CHRD), transcript variant 2, q27.1
SNP_A-1789316	gggccaccaggtcaaa[A/G]gatgcaaaccccgcac	A	G	NM_004443 // CDS // 0 // Hs.2913 // EPHB3 // 2049 // Homo sapiens EphB3 (EPHB3), mRNA. /// ENST00000330394 // CDS // 0 // — // — // — // —	EPHB3	EPHB3, Homo sapiens EphB3 (EPHB3), q27.1
SNP_A-1735318	gagtctcacagacacaaccgagtag[C/T]ggagccaagatttgacccaagtctg	C	T	NM_022149 // upstream // 37779 // Hs.306123 // MAGEF1 // 64110 // melanoma antigen, family F, 1	MAGEF1	MAGEF1 , rs727272, melanoma antigen, family F, 1,q27.1
SNP_A-2009385	attaatattccatctc[A/G]acttttcctgtgtaac	A	G	NM_022149 // upstream // 39159 // Hs.306123 // MAGEF1 // 64110 // Homo sapiens melanoma antigen, family F, 1 (MAGEF1), mRNA. /// NM_015303 // upstream // 81783 // — // KIAA0804 // 23355 // — /// ENST00000317897 // upstream // 39159 // — // — // –	MAGEF1	MAGEF1, Homo sapiens melanoma antigen, family F, 1 (MAGEF1), q27.1
SNP_A-2282321	gagttattctgcaaaa[G/T]taccctcaagatacgt	G	T	NM_001966 // downstream // 19225 // Hs.429879 // EHHADH // 1962 // Homo sapiens enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (EHHADH), mRNA. /// ENST00000335012 // upstream // 18578 // — // — // — // — /// ENST00000231887 //	EHHADH	EHHADH, Homo sapiens enoyl-Coenzyme A, hydratase q27.2
SNP_A-2302193	gctaaagagagactca[A/C]catgcggttcacggaa	A	C	NM_001966 // intron // 0 // Hs.429879 // EHHADH // 1962 // Homo sapiens enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (EHHADH), mRNA. /// ENST00000231887 // intron // 0 // – – // — // — // —	EHHADH	EHHADH, Homo sapiens enoyl-Coenzyme A, hydratase,q27.2
SNP_A-1921698	ttacggaaatgaccta[C/G]aaaagtctggtgacca	C	G	NM_004721 // downstream // 258 // Hs.432898 // MAP3K13 // 9175 // Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA. /// NM_080652 // downstream // 7928 // Hs.518467 // TMEM41A // 90407 // Homo sapiens similar to RIKEN cDNA 57	MAP3K13	MAP3K13, Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), q27.2
SNP_A-1945011	ttgtggttaggtctcc[A/G]aatgaacctccttacc	A	G	NM_004721 // downstream // 6102 // Hs.432898 // MAP3K13 // 9175 // Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA. /// NM_080652 // downstream // 2084 // Hs.518467 // TMEM41A // 90407 // Homo sapiens similar to RIKEN cDNA 5	MAP3K13	MAP3K13, Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), q27.2
SNP_A-1795654	ggtgctttaaatgata[G/T]gacaaggatgctttct	G	T	NM_080652 // upstream // 1453 // Hs.518467 // TMEM41A // 90407 // Homo sapiens similar to RIKEN cDNA 5730578N08 gene (MGC15397), mRNA. /// NM_139248 // downstream // 7319 // Hs.68864 // LIPH // 200879 // Homo sapiens lipase, member H (LIPH), mRNA. /// ENS	TMEM41A	TMEM41A, Homo sapiens similar to RIKEN cDNA 5730578N08 gene (MGC15397), q27.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1877013	tctgcctttctccctaa[C/G]cctcatcctctgcac	C	G	NM_001346 // intron // 0 // Hs.171499 // DGKG // 1608 // Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA. /// ENST00000265022 // intron // 0 // — // — // — /// ENST00000344484 // intron // 0 // — // — // — // —	DGKG	DGKG, Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), q27.2
SNP_A-1934176	ttctcatggtgcttac[C/T]gactgtccagtgggac	C	T	NM_001346 // intron // 0 // Hs.171499 // DGKG // 1608 // Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA. /// ENST00000265022 // intron // 0 // — // — // — /// ENST00000344484 // intron // 0 // — // — // — // —	DGKG	DGKG, Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), q27.2
SNP_A-2073526	acagtaagccatcagc[A/T]gctgagtagtaataca	A	T	NM_001346 // upstream // 149770 // Hs.171499 // DGKG // 1608 // Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA. /// NM_017541 // downstream // 28616 // Hs.376209 // CRYGS // 1427 // Homo sapiens crystallin, gamma S (CRYGS), mRNA. /// NM_0181	DGKG	DGKG, Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), q27.3
SNP_A-2305532	gctgcaagtccttgat[G/T]ctagtaattctgcttc	G	T	NM_000893 // intron // 0 // Hs.77741 // KNG1 // 3827 // Homo sapiens kininogen 1 (KNG1), mRNA. /// K02566 // intron // 0 // Hs.77741 // KNG1 // 3827 // Human alpha-2-thiol proteinase inhibitor mRNA, complete coding sequence. /// ENST00000287611 // intron	KNG1	KNG1, Homo sapiens kininogen 1 (KNG1), q27.3
SNP_A-2026835	aaacacatggacacaa[A/G]aacatcactaaaagct	A	G	NM_001967 // intron // 0 // Hs.478553 // EIF4A2 // 1974 // Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA. /// ENST00000323963 // intron // 0 // — // — // — // — /// ENST00000356531 // intron // 0 // — // —	EIF4A2	EIF4A2, Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), q27.3
SNP_A-2208306	cccacagcctgggggta[A/G]ggtaagccctgaaacc	A	G	NM_003032 // intron // 0 // Hs.207459 // ST6GAL1 // 6480 // Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), transcript variant 2, mRNA. /// NM_173216 // intron // 0 // Hs.207459 // ST6GAL1 // 6480 // Homo sapiens s	ST6GAL1	ST6GAL1, Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), transcript variant 2, q27.3
SNP_A-1931851	ttccgcaaactctggc[A/C]aacagtctaaaatgac	A	C	NM_003032 // intron // 0 // Hs.207459 // ST6GAL1 // 6480 // Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), transcript variant 2, mRNA. /// NM_173216 // intron // 0 // Hs.207459 // ST6GAL1 // 6480 // Homo sapiens s	ST6GAL1	ST6GAL1, Homo sapiens sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), transcript variant 2, q27.3
SNP_A-1975591	tacatctggtaagtgat[C/T]ggattaaggtctcaaa	C	T	NM_001879 // intron // 0 // Hs.89983 // MASP1 // 5648 // Homo sapiens mannan-binding lectin serine protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1), transcript var /// NM_139125 // intron // 0 // Hs.89983 // MASP1 // 5648 // Homo sap	MASP1	MASP1, Homo sapiens mannan-binding lectin serine protease 1 (C4,q27.3
SNP_A-1975598	gcataagcaggatggc[A/G]actgaagggcagaatt	A	G	NM_022147 // downstream // 64004 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 233334 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000262590	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1975596	cttagcctgatttact[C/G]agatggatgttggaga	C	G	NM_022147 // downstream // 71923 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 225415 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000262590	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1905127	tgggtgctttgtgaga[A/G]tacagtctctgcagat	A	G	NM_022147 // downstream // 73935 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 223403 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000262590	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798358	gtaaagttagaatgaa[C/T]catgtgtgacaaaagg	C	T	NM_022147 // downstream // 131410 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 165928 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2074977	acatcattaggaaaa[A/C]taaaatgcagtttatc	A	C	NM_022147 // downstream // 133859 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 163479 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1659430	tccatgttgttcccccactgacat[G/T]tttcctcacttttctgtctg gaa	G	T	NM_001048 // upstream // 4649 // Hs.12409 // SST // 6750 // somatostatin /// NM_001706 // downstream // 46437 // Hs.155024 // BCL6 // 604 // B-cell CLL/lymphoma 6 (zinc finger protein 51) /// NM_138931 // downstream // 46437 // Hs.155024 // BCL6 // 604 /	SST	SST , rs1365113, somatostatin ,q27.3
SNP_A-2181518	cagacttttccataa[A/G]gtagcaatacggcgt	A	G	NM_022147 // downstream // 204302 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 93036 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1797121	ggttgacatctagaaag[A/C]cccctccatctaaaac	A	C	NM_022147 // downstream // 220985 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 76353 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2059555	aatctcatcttcactd[C/T]atggtcctccaggaat	C	T	NM_022147 // downstream // 222206 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 75132 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2059450	aatctagtacctaaaa[G/T]acttcattctgcctca	G	T	NM_022147 // downstream // 222651 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 74687 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2188759	cagtggagtgtgtaaa[C/T]gctcttcagactgtgg	C	T	NM_022147 // downstream // 230322 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 67016 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-1858766	tcagatgtttagaccc[A/G]acctcagcaacagtga	A	G	NM_022147 // downstream // 266108 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 31230 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2293966	gcaggaagttcagaaa[A/T]catcaataggttagg	A	T	NM_022147 // downstream // 277878 // Hs.43388 // IFRG28 // 64108 // Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA. /// NM_001048 // downstream // 19460 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// ENST00000259	IFRG28	IFRG28, Homo sapiens 28kD interferon responsive protein (IFRG28), q27.3
SNP_A-2203048	ccactggatgaggaaac[A/G]aggatttttccaaagc	A	G	NM_001048 // upstream // 1855 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// NM_001004312 // downstream // 26086 // Hs.452766 // RTP2 // 344892 // Homo sapiens similar to Protein MGC35450/QtsA-16602 (MGC78665), mRNA. /// ENST0000	SST	SST, Homo sapiens somatostatin (SST), q27.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1975615	ttggagtgactacctg[C/G]caatataaggagtaga	C	G	NM_001048 // upstream // 3038 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// NM_001004312 // downstream // 24903 // Hs.452766 // RTP2 // 344892 // Homo sapiens similar to Protein MGC35450/QtsA-16602 (MGC78665), mRNA. /// ENST0000	SST	SST, Homo sapiens somatostatin (SST), q27.3
SNP_A-2272355	gacctgcaagagcaaaa[A/G]aactaggcaatctgga	A	G	NM_001048 // upstream // 25582 // Hs.12409 // SST // 6750 // Homo sapiens somatostatin (SST), mRNA. /// NM_001004312 // downstream // 2359 // Hs.452766 // RTP2 // 344892 // Homo sapiens similar to Protein MGC35450/QtsA-16602 (MGC78665), mRNA. /// ENST0000	SST	SST, Homo sapiens somatostatin (SST), q27.3
SNP_A-1975628	gccatttctcatttccc[A/G]atatgccagagctggg	A	G	NM_001706 // upstream // 250578 // Hs.478588 // BCL6 // 604 // Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), transcript variant 1, mRNA. /// NM_138931 // upstream // 250578 // Hs.478588 // BCL6 // 604 // Homo sapiens B-cell CLL/lymph	BCL6	BCL6, Homo sapiens B-cell CLL q27.3
SNP_A-2145932	atgcccctagtcggct[C/T]acttgctggctgtctg	C	T	NM_001706 // upstream // 426248 // Hs.478588 // BCL6 // 604 // Homo sapiens B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), transcript variant 1, mRNA. /// NM_138931 // upstream // 426248 // Hs.478588 // BCL6 // 604 // Homo sapiens B-cell CLL/lymph	BCL6	BCL6, Homo sapiens B-cell CLL q27.3
SNP_A-2096670	agacgttaatcattgat[C/T]accaccagcagcaaat	C	T	NM_207488 // downstream // 203141 // Hs.220696 // FLJ42393 // 401105 // Homo sapiens FLJ42393 protein (FLJ42393), mRNA. /// NM_005578 // upstream // 22170 // Hs.444362 // LPP // 4026 // Homo sapiens LIM domain containing preferred translocation partner in	FLJ42393	FLJ42393, Homo sapiens FLJ42393 protein (FLJ42393), q28
SNP_A-2253700	ctgaaaacaataaa[C/T]gaagcctttggtgctg	C	T	NM_005578 // intron // 0 // Hs.444362 // LPP // 4026 // Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), mRNA. /// ENST00000312675 // intron // 0 // --- // --- // ---	LPP	LPP, Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), q28
SNP_A-2050691	aaggcagagaaaataa[C/G]gtgagcaaagacagtg	C	G	NM_005578 // intron // 0 // Hs.444362 // LPP // 4026 // Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), mRNA. /// ENST00000312675 // intron // 0 // --- // --- // ---	LPP	LPP, Homo sapiens LIM domain containing preferred translocation partner in lipoma (LPP), q28
SNP_A-1975664	gagcataaggacgacc[A/G]ctggattgaattcgga	A	G	NM_198485 // downstream // 165221 // Hs.338851 // FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 142725 // Hs.137569 // TP73L // 8626 // Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST00000034	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-1865576	tccatgtaaatgatgc[C/T]cctctaccctcaagaa	C	T	NM_198485 // downstream // 295100 // Hs.338851 // FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 12846 // Hs.137569 // TP73L // 8626 // Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST00000345	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-2240512	ctgacatttatgaccat[C/T]attttgcttttgact	C	T	NM_198485 // downstream // 298877 // Hs.338851 // FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 9069 // Hs.137569 // TP73L // 8626 // Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST0000003450	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28
SNP_A-2107247	agctaaacaaacaaac[A/G]agagatccacaggttc	A	G	NM_198485 // downstream // 303844 // Hs.338851 // FLJ41238 // 285386 // Homo sapiens FLJ41238 protein (FLJ41238), mRNA. /// NM_003722 // upstream // 4102 // Hs.137569 // TP73L // 8626 // Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST0000003450	FLJ41238	FLJ41238, Homo sapiens FLJ41238 protein (FLJ41238), q28

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2185115	caggaaaacaaaccta[C/T]agtaaatgtgttagca	C	T	NM_003722 // intron // 0 // Hs.137569 // TP73L // 8626 // Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST00000264731 // intron // 0 // — // — // — /// ENST00000320472 // intron // 0 // — // — // — // — // —	TP73L	TP73L, Homo sapiens tumor protein p73-like (TP73L), q28
SNP_A-2133490	atatatttcaaagta[C/G]ataaaggagaggaggactt	C	G	NM_003722 // intron // 0 // Hs.137569 // TP73L // 8626 // Homo sapiens tumor protein p73-like (TP73L), mRNA. /// ENST00000264731 // intron // 0 // — // — // — /// ENST00000320472 // intron // 0 // — // — // — // — // —	TP73L	TP73L, Homo sapiens tumor protein p73-like (TP73L), q28
SNP_A-1828380	taagatgtttggagtc[A/G]ccaagaaacaaagaaa	A	G	NM_018192 // intron // 0 // Hs.374191 // LEPREL1 // 55214 // Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // — // — // — // —	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-2118048	agtaaaaattcaacat[G/T]aaagtttggtaacat	G	T	NM_018192 // intron // 0 // Hs.374191 // LEPREL1 // 55214 // Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // — // — // — // —	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-1976686	gtaacttaacaattgaa[G/T]aacataacctgtatgt	G	T	NM_018192 // intron // 0 // Hs.374191 // LEPREL1 // 55214 // Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // — // — // — // —	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-2091254	actttagccaaggca[C/T]attctctgggctctca	C	T	NM_018192 // intron // 0 // Hs.374191 // LEPREL1 // 55214 // Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// ENST00000319332 // intron // 0 // — // — // — // —	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-1975696	aggatgattgaattga[C/T]gtgaatctggagaaag	C	T	NM_018192 // upstream // 37485 // Hs.374191 // LEPREL1 // 55214 // Homo sapiens leprecan-like 1 (LEPREL1), mRNA. /// NM_021101 // downstream // 147305 // Hs.439060 // CLDN1 // 9076 // Homo sapiens claudin 1 (CLDN1), mRNA. /// ENST00000319332 // upstream /	LEPREL1	LEPREL1, Homo sapiens leprecan-like 1 (LEPREL1), q28
SNP_A-1837207	tacttaaccagttagat[A/T]gaggtagtgtgaatat	A	T	NM_021101 // 3UTR // 0 // Hs.439060 // CLDN1 // 9076 // Homo sapiens claudin 1 (CLDN1), mRNA. /// ENST00000295522 // 3UTR // 0 // — // — // —	CLDN1	CLDN1, Homo sapiens claudin 1 (CLDN1), q28
SNP_A-2136895	atcagagctttgaaca[G/T]atgatccattggtccc	G	T	NM_021101 // intron // 0 // Hs.439060 // CLDN1 // 9076 // Homo sapiens claudin 1 (CLDN1), mRNA. /// ENST00000295522 // intron // 0 // — // — // — // —	CLDN1	CLDN1, Homo sapiens claudin 1 (CLDN1), q28
SNP_A-1825899	taaatgatgctccttat[C/T]attgtaaaaagattac	C	T	NM_006580 // downstream // 17062 // Hs.251391 // CLDN16 // 10686 // Homo sapiens claudin 16 (CLDN16), mRNA. /// NM_207316 // downstream // 1053 // Hs.335321 // UNQ846 // 131920 // Homo sapiens SRSR846 (UNQ846), mRNA. /// ENST00000264734 // downstream // 1	CLDN16	CLDN16, Homo sapiens claudin 16 (CLDN16), q28
SNP_A-1658738	ttattcacatattcattcagttgag[C/T]aacagttactgaatgcttac gatgt	C	T	NM_002182 // intron // 0 // Hs.143527 // IL1RAP // 3556 // interleukin 1 receptor accessory protein /// NM_134470 // intron // 0 // Hs.143527 // IL1RAP // 3556 // interleukin 1 receptor accessory protein	IL1RAP	IL1RAP , rs1015704, interleukin 1 receptor accessory protein ,q28
SNP_A-2252754	ctctctaaatgcctttg[C/T]actatctttgagttg	C	T	NM_002182 // intron // 0 // Hs.478673 // IL1RAP // 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // intron // 0 // Hs.478673 // IL1RAP // 3556 // Homo sapiens interleukin 1 receptor acces	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-2185183	caggaaattccataa[C/G]aaataaacttgcattt	C	G	NM_002182 // downstream // 136803 // Hs.478673 // IL1RAP // 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 136803 // Hs.478673 // IL1RAP // 3556 // Homo sapiens interleuki	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28
SNP_A-2227377	ctacaatgccacctta[A/G]agaaaagattccattat	A	G	NM_002182 // downstream // 551875 // Hs.478673 // IL1RAP // 3556 // Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, mRNA. /// NM_134470 // downstream // 551875 // Hs.478673 // IL1RAP // 3556 // Homo sapiens interleuki	IL1RAP	IL1RAP, Homo sapiens interleukin 1 receptor accessory protein (IL1RAP), transcript variant 1, q28

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1953764	ttgagaatctttcag[A/T]acagaggtatagcaaa	A	T	NM_198184 // intron // 0 // Hs.526794 // OSTN // 344901 // Homo sapiens osteocrin (OSTN), mRNA. /// ENST00000339051 // intron // 0 // --- // --- // --- // ---	OSTN	OSTN, Homo sapiens osteocrin (OSTN), q28
SNP_A-2124898	agttgaccatgttgaa[A/C]atccaggagccaaat	A	C	NM_198184 // intron // 0 // Hs.526794 // OSTN // 344901 // Homo sapiens osteocrin (OSTN), mRNA. /// ENST00000339051 // intron // 0 // --- // --- // --- // ---	OSTN	OSTN, Homo sapiens osteocrin (OSTN), q28
SNP_A-1798531	gtaaattcagttatcat[C/T]gtggcaacttaaaata	C	T	NM_174908 // intron // 0 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // intron // 0 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2123204	agtggtttattactta[C/T]cgataggcagcaaagg	C	T	NM_174908 // downstream // 20611 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 20611 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2221806	cctttctgatatttat[C/T]cacggctttctttgg	C	T	NM_174908 // downstream // 21260 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 21260 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2162788	attttgatttctcacc[A/G]aatacaacctctgtc	A	G	NM_174908 // downstream // 22203 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 22203 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2220854	ccttgccaaaaagccat[C/T]attaatcttagacctt	C	T	NM_174908 // downstream // 59331 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 59331 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2140735	atctctgtatagatga[C/T]gtagtttctgaatgc	C	T	NM_174908 // downstream // 59738 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 59738 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-1909319	tgtatgtggcatgaaa[G/T]agaggtccaacttat	G	T	NM_174908 // downstream // 68506 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 68506 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2113196	aggcccatgaagccac[A/G]ctaaaaatagtaacaa	A	G	NM_174908 // downstream // 78524 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 78524 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 op	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-1890568	tgatctttattgcaaa[A/T]ggcactcactctatca	A	T	NM_174908 // downstream // 107351 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 107351 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28
SNP_A-2009442	tgttctcatctcttg[A/C]aattctggatctttca	A	C	NM_174908 // downstream // 332101 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, mRNA. /// NM_178335 // downstream // 332101 // Hs.478682 // C3orf6 // 152137 // Homo sapiens chromosome 3	C3orf6	C3orf6, Homo sapiens chromosome 3 open reading frame 6 (C3orf6), transcript variant 1, q28

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308310	gcttggtgtaccctca[A/G]acagctcctgagcatc	A	G	NM_021032 // intron // 0 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcr	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2243426	ctgcgtatctttttag[A/G]atggaacagaatctt	A	G	NM_021032 // intron // 0 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcr	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-1958603	ttttctatgaagctaa[C/T]attttccagtttatat	C	T	NM_021032 // intron // 0 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // intron // 0 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcr	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-1715267	atgccaagtcaatctttctaggtc[A/G]ggtccaaacaaatactatg gagtgcc	A	G	NM_004113 // intron // 0 // Hs.343809 // FGF12 // 2257 // fibroblast growth factor 12	FGF12	FGF12 , rs3897920, fibroblast growth factor 12,q28
SNP_A-1714384	atgtgttacatacatttagttgaa[A/G]tctagcaacatatctaaga actagt	A	G	NM_004113 // intron // 0 // Hs.343809 // FGF12 // 2257 // fibroblast growth factor 12	FGF12	FGF12 , rs781424, fibroblast growth factor 12,q28
SNP_A-1664652	gagcatatatcagcaaataaacaaa[C/T]agtatgtcaggtgata ataagtgct	C	T	NM_004113 // intron // 0 // Hs.343809 // FGF12 // 2257 // fibroblast growth factor 12	FGF12	FGF12 , rs2701595, fibroblast growth factor 12,q28
SNP_A-2259619	gaaaactagattaaaa[A/G]tgccatgaggatttag	A	G	NM_021032 // upstream // 187617 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream // 187617 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (F	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2056059	aatacattactcacaa[A/G]ttacagaaagcatcta	A	G	NM_021032 // upstream // 187688 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream // 187688 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (F	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-2224775	cgtgaacgattcaata[A/G]aattttgaggatgtag	A	G	NM_021032 // upstream // 188229 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream // 188229 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (F	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-1931411	ttcccagttctatgcat[C/G]actataattatgtata	C	G	NM_021032 // upstream // 188561 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, mRNA. /// NM_004113 // upstream // 188561 // Hs.185577 // FGF12 // 2257 // Homo sapiens fibroblast growth factor 12 (F	FGF12	FGF12, Homo sapiens fibroblast growth factor 12 (FGF12), transcript variant 1, q28
SNP_A-1866842	tcccgtgtgatatagt[A/C]aacgttgaataacacc	A	C	NM_178496 // upstream // 118922 // Hs.151443 // LOC151963 // 151963 // Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), mRNA. /// NM_020386 // upstream // 204042 // Hs.36761 // HRASLS // 57110 // Homo sapiens HRAS-like suppressor (HRASLS).	LOC151963	LOC151963, Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), q29
SNP_A-1864773	tccagctgaggataccc[C/T]gagaatctcacgaac	C	T	NM_178496 // upstream // 136345 // Hs.151443 // LOC151963 // 151963 // Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), mRNA. /// NM_020386 // upstream // 186619 // Hs.36761 // HRASLS // 57110 // Homo sapiens HRAS-like suppressor (HRASLS).	LOC151963	LOC151963, Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), q29
SNP_A-1893977	tgcatcaagaagctc[A/G]cacctgaagagtatac	A	G	NM_178496 // upstream // 175339 // Hs.151443 // LOC151963 // 151963 // Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), mRNA. /// NM_020386 // upstream // 147625 // Hs.36761 // HRASLS // 57110 // Homo sapiens HRAS-like suppressor (HRASLS).	LOC151963	LOC151963, Homo sapiens similar to BcDNA:GH11415 gene product (LOC151963), q29
SNP_A-2172176	caatgtatccaaaata[C/T]ggctctatctgtgctt	C	T	ENST00000342695 // intron // 0 // --- // --- // ---	-	q29

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2144384	atgataagaataaggg[G/T]gaaacacatacctt	G	T	NM_032279 // intron // 0 // Hs.450092 // ATP13A4 // 84239 // Homo sapiens hypothetical protein DKFZp761I1011 (DKFZp761I1011), mRNA. /// ENST00000342695 // intron // 0 // — // — // — // /// ENST00000295548 // intron // 0 // — // — // -	ATP13A4	ATP13A4, Homo sapiens hypothetical protein DKFZp761I1011 (DKFZp761I1011), q29
SNP_A-2185526	caggagaaaatgttggc[A/C]attcaggctcttctg	A	C	NM_032279 // upstream // 26918 // Hs.450092 // ATP13A4 // 84239 // Homo sapiens hypothetical protein DKFZp761I1011 (DKFZp761I1011), mRNA. /// ENST00000342695 // upstream // 114477 // — // — // — // /// ENST00000295548 // upstream // 26918 // —	ATP13A4	ATP13A4, Homo sapiens hypothetical protein DKFZp761I1011 (DKFZp761I1011), q29
SNP_A-1975785	gccagaataaagtcag[C/T]ttgtgaggtaaaaga	C	T	NM_005524 // upstream // 131604 // Hs.250666 // HES1 // 3280 // Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), mRNA. /// ENST00000351516 // downstream // 307015 // — // — // — // /// ENST00000345604 // downstream // 307015 // -	HES1	HES1, Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), q29
SNP_A-1852784	tatttccacagttagc[G/T]ctgctcgatttggga	G	T	NM_005524 // upstream // 57515 // Hs.250666 // HES1 // 3280 // Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), mRNA. /// ENST00000351516 // downstream // 381104 // — // — // — // /// ENST00000345604 // downstream // 381104 // –	HES1	HES1, Homo sapiens hairy and enhancer of split 1, (Drosophila) (HES1), q29
SNP_A-1898894	tgctttctcctaaat[G/T]agcattcaccatgatg	G	T	NM_018385 // upstream // 32822 // Hs.518505 // FLJ11301 // 55341 // Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA. /// NM_152531 // downstream // 363588 // Hs.478741 // C3orf21 // 152002 // Homo sapiens hypothetical protein FLJ35155 (FLJ3515	FLJ11301	FLJ11301, Homo sapiens hypothetical protein FLJ11301 (FLJ11301), q29
SNP_A-1975807	ttccacatttaaca[G/T]taagcccatttatgc	G	T	NM_018385 // upstream // 46988 // Hs.518505 // FLJ11301 // 55341 // Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA. /// NM_152531 // downstream // 349422 // Hs.478741 // C3orf21 // 152002 // Homo sapiens hypothetical protein FLJ35155 (FLJ3515	FLJ11301	FLJ11301, Homo sapiens hypothetical protein FLJ11301 (FLJ11301), q29
SNP_A-2009475	attactgacaaatcga[C/G]acgtgctgctataaga	C	G	NM_018385 // upstream // 137521 // Hs.518505 // FLJ11301 // 55341 // Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA. /// NM_152531 // downstream // 258889 // Hs.478741 // C3orf21 // 152002 // Homo sapiens hypothetical protein FLJ35155 (FLJ351	FLJ11301	FLJ11301, Homo sapiens hypothetical protein FLJ11301 (FLJ11301), q29
SNP_A-2296324	gcattgtcttagaaaa[A/G]ggaaatcgctggtgca	A	G	NM_018385 // upstream // 158022 // Hs.518505 // FLJ11301 // 55341 // Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA. /// NM_152531 // downstream // 238388 // Hs.478741 // C3orf21 // 152002 // Homo sapiens hypothetical protein FLJ35155 (FLJ351	FLJ11301	FLJ11301, Homo sapiens hypothetical protein FLJ11301 (FLJ11301), q29
SNP_A-1868989	tcctgatggcaggtca[A/G]gttcttactcctccag	A	G	NM_152531 // intron // 0 // Hs.478741 // C3orf21 // 152002 // Homo sapiens hypothetical protein FLJ35155 (FLJ35155), mRNA. /// ENST00000310380 // intron // 0 // — // — // — // /// ENST00000356740 // intron // 0 // — // — // — /// EN	C3orf21	C3orf21, Homo sapiens hypothetical protein FLJ35155 (FLJ35155), q29
SNP_A-2204969	ccagggtgaccacca[C/T]ggattccttccctcaga	C	T	NM_152531 // intron // 0 // Hs.478741 // C3orf21 // 152002 // Homo sapiens hypothetical protein FLJ35155 (FLJ35155), mRNA. /// ENST00000310380 // intron // 0 // — // — // — // —	C3orf21	C3orf21, Homo sapiens hypothetical protein FLJ35155 (FLJ35155), q29
SNP_A-1934297	ttctcccaagagacta[A/G]gttctgtagaggcaga	A	G	NM_012287 // intron // 0 // Hs.478746 // CENTB2 // 23527 // Homo sapiens centaurin, beta 2 (CENTB2), mRNA. /// ENST00000326793 // intron // 0 // — // — // — // —	CENTB2	CENTB2, Homo sapiens centaurin, beta 2 (CENTB2), q29
SNP_A-1941094	ttgctctgcataaaga[C/T]agtagctatatacagt	C	T	NM_012287 // intron // 0 // Hs.478746 // CENTB2 // 23527 // Homo sapiens centaurin, beta 2 (CENTB2), mRNA. /// ENST00000326793 // intron // 0 // — // — // — // —	CENTB2	CENTB2, Homo sapiens centaurin, beta 2 (CENTB2), q29
SNP_A-1752539	cacaacgtaacaggatgtgaattac[C/T]ctctaagtaccatctctat atggcat	C	T	NM_003234 // intron // 0 // Hs.185726 // TFRC // 7037 // transferrin receptor (p90, CD71)	TFRC	TFRC , rs2284890, transferrin receptor (p90, CD71),q29

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1914097	tgtgtgtaattttaca[C/T]gagtggattgctatca	C	T	NM_003234 // downstream // 24526 // Hs.529618 // TFRC // 7037 // Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /// NM_003234 // downstream // 24717 // Hs.529618 // TFRC // 7037 // Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /	TFRC	TFRC, Homo sapiens transferrin receptor (p90, CD71) (TFRC), q29
SNP_A-1866540	tccccatgtacggaga[C/T]gaaagatagtaagaaa	C	T	NM_182627 // downstream // 32513 // Hs.385865 // WDR53 // 348793 // Homo sapiens hypothetical protein MGC64882 (MGC64882), mRNA. /// ENST00000342238 // upstream // 6314 // --- // --- // --- // --- /// ENST00000332629 // downstream // 32513 // --- // --- /	WDR53	WDR53, Homo sapiens hypothetical protein MGC64882 (MGC64882), q29
SNP_A-2230808	ctatgatgcgtctgct[A/G]agaagtgaacatgtgc	A	G	NM_004087 // intron // 0 // Hs.292549 // DLG1 // 1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // intron // 0 // Hs.292549 // DLG1 // 1739 // Human homolog of Drosophila discs large protein, isoform 2 (hdlg-2) mRNA, com	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1793882	ggtcaaatgaggattc[A/G]aatttgtcaacttta	A	G	NM_004087 // intron // 0 // Hs.292549 // DLG1 // 1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // intron // 0 // Hs.292549 // DLG1 // 1739 // Human homolog of Drosophila discs large protein, isoform 2 (hdlg-2) mRNA, com	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1855309	tcaaggagaacgttga[C/T]gggatgagtagaggaa	C	T	NM_004087 // upstream // 45512 // Hs.292549 // DLG1 // 1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // upstream // 46018 // Hs.292549 // DLG1 // 1739 // Human homolog of Drosophila discs large protein, isoform 2 (hdlg-	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1960693	tttttctacctgctca[A/C]gtagtacaatccctgc	A	C	NM_004087 // upstream // 148581 // Hs.292549 // DLG1 // 1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // upstream // 149087 // Hs.292549 // DLG1 // 1739 // Human homolog of Drosophila discs large protein, isoform 2 (hdl	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1866280	tcccatcctcatccct[A/G]aatagaagtggtagcc	A	G	NM_004087 // upstream // 164116 // Hs.292549 // DLG1 // 1739 // Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), mRNA. /// U13896 // upstream // 164622 // Hs.292549 // DLG1 // 1739 // Human homolog of Drosophila discs large protein, isoform 2 (hdl	DLG1	DLG1, Homo sapiens discs, large homolog 1 (Drosophila) (DLG1), q29
SNP_A-1922091	ttactgtgcaccagaa[C/T]gtactccttctgtcta	C	T	D86979 // intron // 0 // Hs.478868 // KIAA0226 // 9711 // Homo sapiens mRNA for KIAA0226 protein, partial cds. /// ENST00000273582 // intron // 0 // --- // --- // --- // ---	KIAA0226	KIAA0226, Homo sapiens for KIAA0226 protein, partial cds. ,q29
SNP_A-1868155	tcctatttactcaatg[C/G]aaatttttcaagataa	C	G	ENST00000358000 // intron // 0 // --- // --- // --- // ---	-	p16.3
SNP_A-2243706	ctgctcttcaggatga[C/T]gcctggtgtgacttga	C	T	ENST00000358000 // intron // 0 // --- // --- // --- // ---	-	p16.3
SNP_A-2281541	gagtccatgtgtgtga[A/G]gtagtcaagatcgtag	A	G	ENST00000358000 // intron // 0 // --- // --- // --- // ---	-	p16.3
SNP_A-2137417	atcatagcccactgta[C/T]ggagacacacattgtg	C	T	ENST00000358000 // intron // 0 // --- // --- // --- // ---	-	p16.3
SNP_A-2313769	ggagcagcaaatggaa[C/T]gtagttcgaagggacg	C	T	NM_194439 // intron // 0 // Hs.248290 // LOC285498 // 285498 // Homo sapiens hypothetical protein LOC285498 (LOC285498), mRNA. /// ENST00000358000 // intron // 0 // --- // --- // --- // --- /// ENST00000319237 // intron // 0 // --- // --- // --- // ---	LOC285498	LOC285498, Homo sapiens hypothetical protein LOC285498 (LOC285498), p16.3
SNP_A-2270212	gacaccagcacttgaa[C/T]gctctgcggagatttt	C	T	NM_194439 // intron // 0 // Hs.248290 // LOC285498 // 285498 // Homo sapiens hypothetical protein LOC285498 (LOC285498), mRNA. /// ENST00000358000 // intron // 0 // --- // --- // --- // --- /// ENST00000319237 // intron // 0 // --- // --- // --- // ---	LOC285498	LOC285498, Homo sapiens hypothetical protein LOC285498 (LOC285498), p16.3
SNP_A-1874824	tctcgccctgtcttca[C/T]gacatcttctcagacc	C	T	ENST00000355714 // intron // 0 // --- // --- // --- // ---	-	p16.3
SNP_A-1804094	gtcacagcagccatac[A/G]gaatgaagatgcccct	A	G	AB046863 // intron // 0 // Hs.292056 // ZFYVE28 // 57732 // Homo sapiens mRNA for KIAA1643 protein, partial cds. /// ENST00000290974 // intron // 0 // --- // --- // --- // --- /// ENST00000342540 // intron // 0 // --- // --- // --- // ---	ZFYVE28	ZFYVE28, Homo sapiens for KIAA1643 protein, partial cds. ,p16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1873633	tctcacggccccttcc[A/G]aaagctaggtggcagc	A	G	AB046863 // intron // 0 // Hs.292056 // ZFYVE28 // 57732 // Homo sapiens mRNA for KIAA1643 protein, partial cds. /// ENST00000290974 // intron // 0 // — // — // — /// ENST00000342540 // intron // 0 // — // — // — // —	ZFYVE28	ZFYVE28, Homo sapiens for KIAA1643 protein, partial cds, p16.3
SNP_A-1820953	gtttctcatccaagag[C/T]aggcgagcatgcaagg	C	T	AB046863 // intron // 0 // Hs.292056 // ZFYVE28 // 57732 // Homo sapiens mRNA for KIAA1643 protein, partial cds. /// ENST00000290974 // intron // 0 // — // — // — /// ENST00000342540 // intron // 0 // — // — // — // —	ZFYVE28	ZFYVE28, Homo sapiens for KIAA1643 protein, partial cds, p16.3
SNP_A-2065046	aattgcaccgtaacaa[C/T]taaaatatcctaatc	C	T	NM_001004056 // intron // 0 // Hs.32959 // GRK4 // 2868 // Homo sapiens G protein-coupled receptor kinase 4 (GRK4), transcript variant 2, mRNA. /// NM_182982 // intron // 0 // Hs.32959 // GRK4 // 2868 // Homo sapiens G protein-coupled receptor kinase 4 (G	GRK4	GRK4, Homo sapiens G protein-coupled receptor kinase 4 (GRK4), transcript variant 2, p16.3
SNP_A-2150779	atgtgctggtgggcag[A/G]aaggactgaacccagt	A	G	NM_002111 // intron // 0 // Hs.518450 // HD // 3064 // Homo sapiens huntingtin (Huntington disease) (HD), mRNA. /// ENST00000355072 // intron // 0 // — // — // — // —	HD	HD, Homo sapiens huntingtin (Huntington disease) (HD), p16.3
SNP_A-2106294	agccctcattgtgggg[C/T]tcacgtcactccagg	C	T	NM_173661 // downstream // 44714 // — // FLJ35424 // 285492 // Homo sapiens hypothetical protein FLJ35424 (FLJ35424), mRNA. /// ENST00000316915 // downstream // 44714 // — // — // — // — /// ENST00000358718 // downstream // 286470 // — // —	FLJ35424	FLJ35424, Homo sapiens hypothetical protein FLJ35424 (FLJ35424), p16.3
SNP_A-1906438	tggtggaaatggtcaa[A/G]tctgtcatcagaaaa	A	G	NM_173661 // downstream // 136940 // — // FLJ35424 // 285492 // Homo sapiens hypothetical protein FLJ35424 (FLJ35424), mRNA. /// ENST00000316915 // downstream // 136940 // — // — // — // — /// ENST00000358718 // downstream // 174244 // — // —	FLJ35424	FLJ35424, Homo sapiens hypothetical protein FLJ35424 (FLJ35424), p16.3
SNP_A-2259422	gaaaaatgcagacaaa[C/T]cctattaccgctcct	C	T	NM_014392 // downstream // 130829 // Hs.518595 // D4S234E // 27065 // Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// NM_016930 // upstream // 7836 // Hs.528897 // STX18 // 53407 // Homo sapiens syntaxin 18 (S	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.2
SNP_A-1915566	tgtctatgactgat[G/T]accaatgagagttgtt	G	T	NM_014392 // downstream // 303894 // Hs.518595 // D4S234E // 27065 // Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// NM_016930 // upstream // 180901 // Hs.528897 // STX18 // 53407 // Homo sapiens syntaxin 18	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.2
SNP_A-1935175	ttctgcagtgagggac[A/C]agcattagcaaggcc	A	C	NM_014392 // downstream // 366102 // Hs.518595 // D4S234E // 27065 // Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// NM_016930 // upstream // 243109 // Hs.528897 // STX18 // 53407 // Homo sapiens syntaxin 18	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.2
SNP_A-1895222	tgcccctgataccaga[A/C]catgtgagaaatattg	A	C	NM_014392 // downstream // 374032 // Hs.518595 // D4S234E // 27065 // Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// NM_016930 // upstream // 251039 // Hs.528897 // STX18 // 53407 // Homo sapiens syntaxin 18	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.2
SNP_A-2009526	taggctgacacctcat[A/T]cacggactggtgccag	A	T	NM_014392 // downstream // 428337 // Hs.518595 // D4S234E // 27065 // Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), mRNA. /// NM_016930 // upstream // 305344 // Hs.528897 // STX18 // 53407 // Homo sapiens syntaxin 18	D4S234E	D4S234E, Homo sapiens DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E), p16.2
SNP_A-2189753	cataaaaatgggccta[A/G]aatgtctatctgca	A	G	NM_002448 // downstream // 67769 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 83089 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255172	cttggtagcacaaggg[C/T]caatctgctccaacac	C	T	NM_002448 // downstream // 73889 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 76969 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1896141	tgcgattgttttgat[A/T]aaggcagcaaggacat	A	T	NM_002448 // downstream // 74064 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 76794 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2147871	atggcctctgacttgat[C/T]accttctttgttca	C	T	NM_002448 // downstream // 74192 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 76666 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2243652	ctgctcgtgtgcaggc[G/T]ctatgtcccatcaga	G	T	NM_002448 // downstream // 76229 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 74629 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1919992	ttaatagaggtcttac[C/G]aggatacagtaaatga	C	G	NM_002448 // downstream // 78641 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 72217 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2291481	gcaattgtaaatacga[C/T]ggtaaagccagccctc	C	T	NM_002448 // downstream // 79010 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 71848 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1906866	tggttcagaatgtgga[C/G]taagacatggagtgcc	C	G	NM_002448 // downstream // 83715 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 67143 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1793872	ggtcaaaggcgctaca[A/G]gaaatattaaaataat	A	G	NM_002448 // downstream // 84013 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 66845 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2090499	acttggtttgcagaaat[C/G]gaatcatgatttttgcc	C	G	NM_002448 // downstream // 84726 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 66132 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2246370	ctggttccaccattgc[A/G]ctcaacagaaggaaac	A	G	NM_002448 // downstream // 87219 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 63639 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1975853	tgtaacaagatgaaga[A/G]aagttcatgctcttgg	A	G	NM_002448 // downstream // 88327 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 62531 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2162286	atttttatataagtgga[C/T]tcatctggtgcatatt	C	T	NM_002448 // downstream // 88817 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 62041 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2262517	gaaatgtgaaaggaac[A/G]aaaaggtggccatgtg	A	G	NM_002448 // downstream // 105551 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 45307 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-2216535	cctctaatgcatcccc[A/G]ctctgaagggagact	A	G	NM_002448 // downstream // 139760 // Hs.424414 // MSX1 // 4487 // Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA. /// NM_018659 // downstream // 11098 // Hs.13872 // CYTL1 // 54360 // Homo sapiens cytokine-like protein C17 (C17), mRNA. ///	MSX1	MSX1, Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), p16.2
SNP_A-1975857	gcttgacacactgtat[A/T]ataaatccccgtttt	A	T	NM_018401 // intron // 0 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // — // — // —	STK32B	STK32B, Homo sapiens serine p16.2
SNP_A-2009531	aatcctgtttctactg[A/T]aaggcttgacacactg	A	T	NM_018401 // intron // 0 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // — // — // —	STK32B	STK32B, Homo sapiens serine p16.2
SNP_A-1936320	ttcttccatgcaatt[A/C]aaagttgtttgaaatt	A	C	NM_018401 // intron // 0 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // — // — // —	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-1901803	tggcactggcccttgga[A/G]tatcttcagaggtacc	A	G	NM_018401 // CDS // 0 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // CDS // 0 // — // — // —	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-1858015	tcactttcaatttcca[C/T]gaggagggtgcattag	C	T	NM_018401 // intron // 0 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // — // — // —	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-1794830	ggtctgtgccatctgc[A/G]aagtgctttgacattt	A	G	NM_018401 // intron // 0 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// ENST00000282908 // intron // 0 // — // — // —	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-1780431	ggatacgtctcacaga[G/T]atatattgcatgtca	G	T	NM_018401 // downstream // 4793 // Hs.133062 // STK32B // 55351 // Homo sapiens serine/threonine kinase 32B (STK32B), mRNA. /// NM_005750 // upstream // 19365 // Hs.177972 // C4orf6 // 10141 // Homo sapiens chromosome 4 open reading frame 6 (C4orf6), mRNA	STK32B	STK32B, Homo sapiens serine,p16.2
SNP_A-2300516	gcctgactgctgagga[C/T]ggccgagattttcagg	C	T	NM_014556 // intron // 0 // Hs.28051 // EVC // 2121 // Homo sapiens Ellis van Creveld syndrome (EVC), transcript variant 1, mRNA. /// NM_153717 // intron // 0 // Hs.28051 // EVC // 2121 // Homo sapiens Ellis van Creveld syndrome (EVC), transcript variant	EVC	EVC, Homo sapiens Ellis van Creveld syndrome (EVC), transcript variant 1, p16.2
SNP_A-2041048	aaccgtcagtgaaata[C/T]ctaagtcgaaggaact	C	T	NM_207405 // intron // 0 // Hs.479065 // FLJ46481 // 389197 // Homo sapiens FLJ46481 protein (FLJ46481), mRNA. /// ENST00000324058 // intron // 0 // — // — // —	FLJ46481	FLJ46481, Homo sapiens FLJ46481 protein (FLJ46481), p16.1
SNP_A-2264024	gaactcccgcggtcc[A/G]atgatgcacccagaca	A	G	NM_207405 // upstream // 4730 // Hs.479065 // FLJ46481 // 389197 // Homo sapiens FLJ46481 protein (FLJ46481), mRNA. /// ENST00000324058 // upstream // 4730 // — // — // — /// ENST00000310730 // downstream // 35339 // — // — // —	FLJ46481	FLJ46481, Homo sapiens FLJ46481 protein (FLJ46481), p16.1
SNP_A-2180109	cagaaaaggtttgccc[A/C]aaagaggtgtggccca	A	C	NM_144720 // intron // 0 // Hs.479066 // MARLIN1 // 152789 // Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), mRNA. /// ENST00000282924 // intron // 0 // — // — // —	MARLIN1	MARLIN1, Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1922106	ttactgttgaggccaa[A/G]gaatttaactcctaa	A	G	NM_144720 // intron // 0 // Hs.479066 // MARLIN1 // 152789 // Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), mRNA. /// ENST00000282924 // intron // 0 // — // — // — // —	MARLIN1	MARLIN1, Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), p16.1
SNP_A-2082225	acgagagtccagttag[A/C]aggtatgtgttaccca	A	C	NM_144720 // intron // 0 // Hs.479066 // MARLIN1 // 152789 // Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), mRNA. /// ENST00000282924 // intron // 0 // — // — // — // —	MARLIN1	MARLIN1, Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), p16.1
SNP_A-2245559	ctgggatttcgagtgc[A/G]agttggtttcaggtcc	A	G	NM_144720 // intron // 0 // Hs.479066 // MARLIN1 // 152789 // Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), mRNA. /// ENST00000282924 // intron // 0 // — // — // — // —	MARLIN1	MARLIN1, Homo sapiens multiple coiled-coil GABABR1-binding protein (MARLIN1), p16.1
SNP_A-1903751	tgggaggttgttttgc[G/T]atgagcatggctgtca	G	T	NM_181876 // intron // 0 // Hs.479069 // PPP2R2C // 5522 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m /// NM_020416 // intron // 0 // Hs.479069 // PPP2R2C // 5522 // Ho	PPP2R2C	PPP2R2C, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform (PPP2R2C), transcript variant 2, m ,p16.1
SNP_A-1905140	tgggtggctaaggcta[G/T]caacagacttcctcca	G	T	NM_152301 // upstream // 858 // Hs.518608 // PP784 // 114932 // Homo sapiens PP784 protein (PP784), transcript variant 1, mRNA. /// NM_203462 // upstream // 858 // Hs.518608 // PP784 // 114932 // Homo sapiens PP784 protein (PP784), transcript variant 2, m	PP784	PP784, Homo sapiens PP784 protein (PP784), transcript variant 1, p16.1
SNP_A-1905305	tgggtttaagagtta[C/T]agagacatttgctaa	C	T	NM_025196 // upstream // 67831 // Hs.443723 // GRPEL1 // 80273 // Homo sapiens GrpE-like 1, mitochondrial (E. coli) (GRPEL1), mRNA. /// NM_020777 // upstream // 56743 // Hs.479099 // SORCS2 // 57537 // Homo sapiens sortilin-related VPS10 domain containing	GRPEL1	GRPEL1, Homo sapiens GrpE-like 1, mitochondrial (E. coli) (GRPEL1), p16.1
SNP_A-2186816	caggggctcaaccac[A/G]ccatccaaaagcacat	A	G	NM_020777 // intron // 0 // Hs.479099 // SORCS2 // 57537 // Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron // 0 // — // — // — // —	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-1787110	gggaaaggcccagacat[C/T]gaggctcagctgagc	C	T	NM_020777 // intron // 0 // Hs.479099 // SORCS2 // 57537 // Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron // 0 // — // — // — // — /// ENST00000360303 // intron // 0 // — // — // —	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-1810491	gtgatttataaagtaa[A/G]ccttctgctgccttg	A	G	NM_020777 // intron // 0 // Hs.479099 // SORCS2 // 57537 // Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron // 0 // — // — // — // — /// ENST00000360303 // intron // 0 // — // — // —	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-2178318	cactcagcacactcaa[C/T]cctgggcaatctctct	C	T	NM_020777 // intron // 0 // Hs.479099 // SORCS2 // 57537 // Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron // 0 // — // — // — // — /// ENST00000360303 // intron // 0 // — // — // —	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-1901191	tggatgactgaatggc[A/G]gacagcaacttctacc	A	G	NM_020777 // intron // 0 // Hs.479099 // SORCS2 // 57537 // Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), mRNA. /// ENST00000329016 // intron // 0 // — // — // — // — /// ENST00000360303 // intron // 0 // — // — // —	SORCS2	SORCS2, Homo sapiens sortilin-related VPS10 domain containing receptor 2 (SORCS2), p16.1
SNP_A-1907170	tggttccctggcaac[C/T]agctctcatcctactc	C	T	NM_021638 // intron // 0 // Hs.529369 // AFAP // 60312 // Homo sapiens actin filament associated protein (AFAP), transcript variant 1, mRNA. /// NM_198595 // intron // 0 // Hs.529369 // AFAP // 60312 // Homo sapiens actin filament associated protein (AFAP	AFAP	AFAP, Homo sapiens actin filament associated protein (AFAP), transcript variant 1, p16.1
SNP_A-2223065	cgcattctgtctgtga[C/T]accgttactcccatgg	C	T	ENST00000318896 // intron // 0 // — // — // — // — /// ENST00000360559 // intron // 0 // — // — // —	-	p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2171563	caatcccttgaacagt[A/G]acgaagcacctaccat	A	G	NM_018986 // intron // 0 // Hs.479116 // SH3TC1 // 54436 // Homo sapiens SH3 domain and tetratricopeptide repeats 1 (SH3TC1), mRNA. /// ENST00000309767 // intron // 0 // — // — // — // — /// ENST00000245105 // intron // 0 // — // — // — // -	SH3TC1	SH3TC1, Homo sapiens SH3 domain and tetratricopeptide repeats 1 (SH3TC1), p16.1
SNP_A-2076208	acattctcagaaatac[A/G]acttacctaaacagac	A	G	NM_053044 // downstream // 6392 // Hs.479119 // HTRA3 // 94031 // Homo sapiens serine protease HTRA3 (HTRA3), mRNA. /// NM_003501 // downstream // 53216 // Hs.479122 // ACOX3 // 8310 // Homo sapiens acyl-Coenzyme A oxidase 3, pristanoyl (ACOX3), mRNA. ///	HTRA3	HTRA3, Homo sapiens serine protease HTRA3 (HTRA3), p16.1
SNP_A-1834667	taccacccactgctcc[A/G]caaccttccaaaaccc	A	G	NM_053044 // downstream // 15631 // Hs.479119 // HTRA3 // 94031 // Homo sapiens serine protease HTRA3 (HTRA3), mRNA. /// NM_003501 // downstream // 43977 // Hs.479122 // ACOX3 // 8310 // Homo sapiens acyl-Coenzyme A oxidase 3, pristanoyl (ACOX3), mRNA. //	HTRA3	HTRA3, Homo sapiens serine protease HTRA3 (HTRA3), p16.1
SNP_A-2246277	ctggtgggaatgacag[A/G]aaatcaggaggccagg	A	G	NM_003501 // intron // 0 // Hs.479122 // ACOX3 // 8310 // Homo sapiens acyl-Coenzyme A oxidase 3, pristanoyl (ACOX3), mRNA. /// ENST00000200383 // intron // 0 // — // — // — // — /// ENST00000356406 // intron // 0 // — // — // — // —	ACOX3	ACOX3, Homo sapiens acyl-Coenzyme A oxidase 3, pristanoyl (ACOX3), p16.1
SNP_A-2116565	aggtcacactggatga[C/T]gtaaactaaaaattaa	C	T	NM_152544 // downstream // 56002 // Hs.285317 // FLJ35725 // 152992 // Homo sapiens hypothetical protein FLJ35725 (FLJ35725), mRNA. /// NM_080819 // upstream // 47934 // Hs.350588 // GPR78 // 27201 // Homo sapiens G protein-coupled receptor 78 (GPR78), mR	FLJ35725	FLJ35725, Homo sapiens hypothetical protein FLJ35725 (FLJ35725), p16.1
SNP_A-2106197	agccccccaagtcctc[C/T]agttgcctgtgaagga	C	T	NM_152544 // downstream // 59726 // Hs.285317 // FLJ35725 // 152992 // Homo sapiens hypothetical protein FLJ35725 (FLJ35725), mRNA. /// NM_080819 // upstream // 44210 // Hs.350588 // GPR78 // 27201 // Homo sapiens G protein-coupled receptor 78 (GPR78), mR	FLJ35725	FLJ35725, Homo sapiens hypothetical protein FLJ35725 (FLJ35725), p16.1
SNP_A-1870862	tcggctaaaccaacct[A/G]agcaagcgtggaagg	A	G	NM_152544 // downstream // 60700 // Hs.285317 // FLJ35725 // 152992 // Homo sapiens hypothetical protein FLJ35725 (FLJ35725), mRNA. /// NM_080819 // upstream // 43236 // Hs.350588 // GPR78 // 27201 // Homo sapiens G protein-coupled receptor 78 (GPR78), mR	FLJ35725	FLJ35725, Homo sapiens hypothetical protein FLJ35725 (FLJ35725), p16.1
SNP_A-1859505	tcaggagattctaggc[A/T]tccaaaagtgatgtgt	A	T	NM_020041 // intron // 0 // Hs.444612 // SLC2A9 // 56606 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, mRNA. /// NM_001001290 // intron // 0 // Hs.444612 // SLC2A9 // 56606 // Homo sapi	SLC2A9	SLC2A9, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, p16.1
SNP_A-2113235	aggcccctccaatca[G/T]ctcacttgacctgtg	G	T	NM_020041 // intron // 0 // Hs.444612 // SLC2A9 // 56606 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, mRNA. /// NM_001001290 // intron // 0 // Hs.444612 // SLC2A9 // 56606 // Homo sapi	SLC2A9	SLC2A9, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), transcript variant 1, p16.1
SNP_A-2181248	cagaccagacccccac[A/G]gcaccacaggatgccc	A	G	ENST00000264785 // upstream // 24113 // — // — // — // — /// ENST00000326756 // downstream // 319909 // — // — // — // —	-	p16.1
SNP_A-2027540	aaaccaccaagtatggt[A/G]agagatcagttatgac	A	G	ENST00000264785 // upstream // 58397 // — // — // — // — /// ENST00000326756 // downstream // 285625 // — // — // — // —	-	p16.1
SNP_A-2112723	aggcagcatgttctta[A/G]caacagtcctgccct	A	G	ENST00000264785 // upstream // 109684 // — // — // — // — /// ENST00000326756 // downstream // 234338 // — // — // — // —	-	p16.1
SNP_A-1954809	tttgcgtgtggaagc[C/T]ctttagtttagatccc	C	T	ENST00000264785 // upstream // 149891 // — // — // — // — /// ENST00000326756 // downstream // 194131 // — // — // — // —	-	p16.1
SNP_A-1975955	actagaaagcatttgaj[G/T]atcatccgtctccac	G	T	ENST00000264785 // upstream // 170430 // — // — // — // — /// ENST00000326756 // downstream // 173592 // — // — // — // —	-	p16.1
SNP_A-2131108	atagacagtccagatc[A/G]ccctaatcggtgggt	A	G	ENST00000264785 // upstream // 174288 // — // — // — // — /// ENST00000326756 // downstream // 169734 // — // — // — // —	-	p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253364	cttctgtagtttgctct[A/G]caggtaacatcttgag	A	G	ENST00000326756 // downstream // 168746 // --- // --- // ---	-	p16.1
SNP_A-1975963	catcacacctcatgtga[C/T]gcttctatgctggatca	C	T	ENST00000264785 // upstream // 177846 // --- // --- // --- // --- /// ENST00000326756 // downstream // 166176 // --- // --- // --- // ---	-	p16.1
SNP_A-1975971	tgttcagatggcttga[C/T]gaaaatttcaggagca	C	T	ENST00000264785 // upstream // 223454 // --- // --- // --- // --- /// ENST00000326756 // downstream // 120568 // --- // --- // --- // ---	-	p16.1
SNP_A-2117204	aggtgctaacacaata[C/T]atgactaatgatgagg	C	T	NM_052964 // downstream // 2717 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000326756 // upstream // 40831 // --- // --- // --- // --- /// ENST00000226951 // downstream // 2717 // --- /	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2310442	ggaacttatccaaact[A/C]accigatcagaattac	A	C	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1950155	tttcactgactatgta[C/T]atgccaggcctagtct	C	T	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1975977	tacctggactattgca[C/T]tagccttctaataata	C	T	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1872439	tctagcagaagagtga[C/T]ggaaaggagtctaata	C	T	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1975983	ttagttcaccaggagg[A/G]aataatagttgaaaa	A	G	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1819519	gttggtctctgttgaa[C/G]atggcttctcaccaag	C	G	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2163861	caaaacatttttaataa[C/G]aggagggatgtcacgg	C	G	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1975987	atatataatatgctaa[C/G]aatgatgataatagcc	C	G	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1975988	taaacgaggttctga[C/G]agttaaataactgt	C	G	NM_052964 // intron // 0 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// ENST00000226951 // intron // 0 // --- // --- // ---	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1975989	gattatcacactcatg[A/C]atctgtttgttggcaa	A	C	NM_052964 // upstream // 1698 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream // 712292 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-su	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-2166922	caacaaaagaggctca[A/G]tctcaggccagctgca	A	G	NM_052964 // upstream // 2958 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream // 711032 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-su	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1825535	taaatagagtaactgat[C/T]gctttttccaacattt	C	T	NM_052964 // upstream // 7387 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream // 706603 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-su	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1680670	accagtgtttggagaacctgatcca[C/T]gatgatagttataaca gaatagta	C	T	AB110420 // intron // 0 // Hs.381351 // MIST // 116449 // mast cell immunoreceptor signal transducer	MIST	MIST , rs10516208, mast cell immunoreceptor signal transducer,p16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1975992	ctgtcagtgatcctta[A/G]caggtaagacaaattc	A	G	NM_052964 // upstream // 56800 // Hs.147851 // MIST // 116449 // Homo sapiens mast cell immunoreceptor signal transducer (MIST), mRNA. /// NM_005114 // downstream // 657190 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-s	MIST	MIST, Homo sapiens mast cell immunoreceptor signal transducer (MIST), p16.1
SNP_A-1949005	tttatctgggaacaaa[C/G]ggtggtcctgaggtca	C	G	NM_005114 // intron // 0 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// ENST00000002596 // intron // 0 // --- // --- // ---	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1821854	gtttagctgatttta[A/G]agacccccattccctca	A	G	NM_005114 // upstream // 235257 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1702703 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2035460	aaatggtagaattatc[A/G]aaatgtggtgcctact	A	G	NM_005114 // upstream // 241873 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1696087 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1846174	tatatcagttggatg[A/G]acttgcattcagtgat	A	G	NM_005114 // upstream // 593034 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1344926 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1976069	tataaattgggagaaa[G/T]aagagtgacatctat	G	T	NM_005114 // upstream // 810901 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1127059 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1976070	gaacaagatatctgca[A/G]gttttctgttcctgag	A	G	NM_005114 // upstream // 812055 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 1125905 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2250321	cttagagatcttcaag[C/G]aacatttagagggaaa	C	G	NM_005114 // upstream // 1046315 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 891645 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1901334	tggatgtgaacagtct[C/G]aagtcagttagggccg	C	G	NM_005114 // upstream // 1086408 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 851552 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2197315	cattcatccataaaaa[A/T]ctcatacacaaatatt	A	T	NM_005114 // upstream // 1155146 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 782814 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1976081	tgtcagccactatcac[A/G]ggaacttgaagcataa	A	G	NM_005114 // upstream // 1213073 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 724887 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1883328	tgaacaagaagtcact[A/G]aagagtagtcaggaaa	A	G	NM_005114 // upstream // 1239001 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 698959 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-1932627	ttccttaacaatcatc[A/T]ctttaccaaaggctat	A	T	NM_005114 // upstream // 1239579 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 698381 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2197801	cattgaagctggaggt[A/G]aaaatagcttttgtt	A	G	NM_005114 // upstream // 1260451 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 677509 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2295976	gcatgttcctctgtcc[A/T]ctgggtttcctgccaa	A	T	NM_005114 // upstream // 1438953 // Hs.507348 // HS3ST1 // 9957 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA. /// X94703 // downstream // 499007 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 //	HS3ST1	HS3ST1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), p15.33
SNP_A-2049918	aaggaactaatttcag[A/T]aactaccagtctctga	A	T	X94703 // upstream // 3974 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 // upstream // 4162 // Hs.306899 // RAB28 // 9364 // Homo sapiens RAB28, member RAS oncogene family (RAB28), mRNA. /// NM_004249 // upstream // 3981 // Hs.3068	RAB28	RAB28, H.sapiens rab28 ,p15.33
SNP_A-1835196	taccgctcttccaaag[A/G]aaatctctgtccacaa	A	G	X94703 // upstream // 4696 // Hs.306899 // RAB28 // 9364 // H.sapiens rab28 mRNA. /// NM_004249 // upstream // 4884 // Hs.306899 // RAB28 // 9364 // Homo sapiens RAB28, member RAS oncogene family (RAB28), mRNA. /// NM_004249 // upstream // 4703 // Hs.3068	RAB28	RAB28, H.sapiens rab28 p15.33
SNP_A-2224459	cgtagggttcgcatta[C/T]aaatgtctatggatct	C	T	NM_148894 // upstream // 393 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 1375801 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation ele	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1959490	tttgctaattacaga[G/T]ggtggttaataacaac	G	T	NM_148894 // upstream // 159238 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 1216956 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2198396	catttaatttcaaaac[A/T]ggtgattcattaagat	A	T	NM_148894 // upstream // 368771 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 1007423 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1665710	tatgcaatgcagaattcctggaact[C/G]aaagaaatggtagcta ggaataatc	C	G	NM_148894 // upstream // 364137 // Hs.444517 // FLJ33215 // 259282 // hypothetical protein FLJ33215 /// NM_182485 // upstream // 1012057 // Hs.44833 // CPEB2 // 132864 // cytoplasmic polyadenylation element binding protein 2 /// NM_182646 // upstream //	FLJ33215	FLJ33215 , rs572468, hypothetical protein FLJ33215 ,p15.33
SNP_A-1976142	ttgtagcagagatgt[A/G]aagatttagagatatt	A	G	NM_148894 // upstream // 523141 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 853053 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2056965	aatagctaagatcaa[C/T]ggttgagccagactg	C	T	NM_148894 // upstream // 766657 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 609537 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2064153	aattcaaatgtggata[C/T]acctaaacctaaacct	C	T	NM_148894 // upstream // 777912 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 598282 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2229654	ctagtacgtgttgaaa[C/T]tggaattcaaatgtgg	C	T	NM_148894 // upstream // 777932 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 598262 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1976160	gaattaacagagacaa[C/T]gggtgactaacatgtc	C	T	NM_148894 // upstream // 780121 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 596073 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2227774	ctaccagacttccatc[A/G]aaacaccttagaattt	A	G	NM_148894 // upstream // 808974 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 567220 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1921259	ttacattacataaaac[C/T]gtctgctagcagaccc	C	T	NM_148894 // upstream // 838150 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 538044 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-1957899	tttcaaagagtaagg[A/C]aacatggttaggccta	A	C	NM_148894 // upstream // 843306 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 532888 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2269507	gacaaacaatatggca[A/G]gatttctccgactcaa	A	G	NM_148894 // upstream // 1177866 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 198328 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2221871	ccttttgtcatcttga[C/T]ctggcttagctctcca	C	T	NM_148894 // upstream // 1245417 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 130777 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2314312	ggaggcctcaatgaaaa[A/T]ccactgccctatggga	A	T	NM_148894 // upstream // 1247734 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 128460 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33
SNP_A-2097000	agactgcattatttct[C/T]acctgatcttcagcct	C	T	NM_148894 // upstream // 1296890 // Hs.444517 // FAM44A // 259282 // Homo sapiens family with sequence similarity 44, member A (FAM44A), mRNA. /// NM_182646 // upstream // 79304 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation e	FAM44A	FAM44A, Homo sapiens family with sequence similarity 44, member A (FAM44A), p15.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102315	agattataggctttca[C/T]cactaggaattgtcgg	C	T	NM_182646 // downstream // 9635 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, mRNA. /// NM_182485 // downstream // 9635 // Hs.374216 // CPEB2 // 132864 // Homo sapiens	CPEB2	CPEB2, Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, p15.33
SNP_A-1737043	gatgggatggaacatatttaatgaa[A/C]cagaatagttgttgtcttt attggt	A	C	NM_182485 // intron // 0 // Hs.44833 // CPEB2 // 132864 // cytoplasmic polyadenylation element binding protein 2 /// NM_182646 // intron // 0 // Hs.44833 // CPEB2 // 132864 // cytoplasmic polyadenylation element binding protein 2	CPEB2	CPEB2 , rs2604580, cytoplasmic polyadenylation element binding protein 2 ,p15.33
SNP_A-1949623	tttatttgctataaaa[A/T]tgacaagaattatgat	A	T	NM_182646 // downstream // 81914 // Hs.374216 // CPEB2 // 132864 // Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, mRNA. /// NM_182485 // downstream // 81914 // Hs.374216 // CPEB2 // 132864 // Homo sapien	CPEB2	CPEB2, Homo sapiens cytoplasmic polyadenylation element binding protein 2 (CPEB2), transcript variant A, p15.33
SNP_A-1643565	agggatgggagtagaggtggcaata[C/T]agaagtagcccaag ggagatctctg	C	T	NM_031911 // upstream // 174064 // Hs.153714 // C1QTNF7 // 114905 // C1q and tumor necrosis factor related protein 7 /// NM_182485 // downstream // 95774 // Hs.44833 // CPEB2 // 132864 // cytoplasmic polyadenylation element binding protein 2 /// NM_18264	C1QTNF7	C1QTNF7 , rs1817186, C1q and tumor necrosis factor related protein 7 ,p15.33
SNP_A-2009602	tggatataaaaagctc[C/G]aggaataaatgctcgg	C	G	NM_004334 // upstream // 9058 // Hs.169998 // BST1 // 683 // Homo sapiens bone marrow stromal cell antigen 1 (BST1), mRNA. /// ENST00000328592 // downstream // 4861 // — // — // — // — /// ENST00000265016 // upstream // 9058 // — // — // — //	BST1	BST1, Homo sapiens bone marrow stromal cell antigen 1 (BST1), p15.33
SNP_A-2076265	acattcttttaaacac[C/T]gccttagaggttgccc	C	T	NM_001775 // downstream // 35902 // Hs.479214 // CD38 // 952 // Homo sapiens CD38 antigen (p45) (CD38), mRNA. /// NM_005130 // downstream // 50585 // Hs.1690 // FGFBP1 // 9982 // Homo sapiens fibroblast growth factor binding protein 1 (FGFBP1), mRNA. ///	CD38	CD38, Homo sapiens CD38 antigen (p45) (CD38), p15.32
SNP_A-2250269	cttagaagaagagcaa[A/T]gccctctaatttaaat	A	T	NM_006017 // intron // 0 // Hs.479220 // PROM1 // 8842 // Homo sapiens prominin 1 (PROM1), mRNA. /// ENST00000265014 // intron // 0 // — // — // — // —	PROM1	PROM1, Homo sapiens prominin 1 (PROM1), p15.32
SNP_A-1942423	ttggctagactcaaca[C/T]ggaaacatttttaaaa	C	T	NM_006017 // intron // 0 // Hs.479220 // PROM1 // 8842 // Homo sapiens prominin 1 (PROM1), mRNA. /// ENST00000265014 // intron // 0 // — // — // — // —	PROM1	PROM1, Homo sapiens prominin 1 (PROM1), p15.32
SNP_A-1681708	aaacaccatcatgtcaggggttaac[A/G]cttcaacacagaaat gtcaggggac	A	G	NM_006017 // intron // 0 // Hs.370052 // PROM1 // 8842 // prominin 1	PROM1	PROM1 , rs884227, prominin 1,p15.32
SNP_A-1976228	gtgcatcttatccctg[C/G]atctgtttcaacatca	C	G	NM_152684 // downstream // 172377 // Hs.445315 // FLJ39653 // 202020 // Homo sapiens hypothetical protein FLJ39653 (FLJ39653), mRNA. /// NM_001290 // downstream // 100505 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// E	FLJ39653	FLJ39653, Homo sapiens hypothetical protein FLJ39653 (FLJ39653), p15.32
SNP_A-1948052	tttagagcttcagcca[A/G]tatcttgctcctgagt	A	G	NM_001290 // intron // 0 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // intron // 0 // — // — // — // — /// ENST00000304523 // intron // 0 // — // — // — // —	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2052263	aagtaaggaaaccgta[A/C]ggctggaggctgccat	A	C	NM_001290 // upstream // 67683 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 67793 // — // — // — // — /// ENST00000304523 // upstream // 67683 // — // — // — // — /// ENS	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2201923	ccacagaagtatctca[A/T]ccattactgttaatgc	A	T	NM_001290 // upstream // 72684 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 72794 // — // — // — // — /// ENST00000304523 // upstream // 72684 // — // — // — // — /// ENS	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1925123	ttatcatagggttaga[A/G]ctgatgatcacagggg	A	G	NM_001290 // upstream // 375977 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 376087 // — // — // — // — /// ENST00000304523 // upstream // 375977 // — // — // — // — ///	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-1863463	tccaaaatggctagga[A/T]acagtagtgataggtt	A	T	NM_001290 // upstream // 419711 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 419821 // — // — // — // — /// ENST00000304523 // upstream // 419711 // — // — // — // — ///	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-1868695	tcctctgtggacccag[A/G]aaggaaagaaaaacca	A	G	NM_001290 // upstream // 549222 // Hs.23748 // LDB2 // 9079 // Homo sapiens LIM domain binding 2 (LDB2), mRNA. /// ENST00000304510 // upstream // 549332 // — // — // — // — /// ENST00000304523 // upstream // 549222 // — // — // — // — ///	LDB2	LDB2, Homo sapiens LIM domain binding 2 (LDB2), p15.32
SNP_A-2229418	ctaggccagaggacac[A/G]gggcaaccacacagga	A	G	NM_000320 // 3UTR // 0 // Hs.75438 // QDPR // 5860 // Homo sapiens quinoid dihydropteridine reductase (QDPR), mRNA. /// ENST00000281243 // 3UTR // 0 // — // — // — // —	QDPR	QDPR, Homo sapiens quinoid dihydropteridine reductase (QDPR), p15.32
SNP_A-2193055	catctaaggaggacag[A/G]cactctgcaagctact	A	G	NM_015907 // upstream // 11414 // Hs.479264 // LAP3 // 51056 // Homo sapiens leucine aminopeptidase 3 (LAP3), mRNA. /// ENST00000342925 // downstream // 38808 // — // — // — // — /// ENST00000226299 // upstream // 11414 // — // — // — // —	LAP3	LAP3, Homo sapiens leucine aminopeptidase 3 (LAP3), p15.32
SNP_A-2166417	caaatgactcaataga[C/T]gctgtgaaacaagcta	C	T	NM_022346 // CDS // 0 // Hs.479270 // HCAP-G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// ENST00000251496 // CDS // 0 // — // — // — // —	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32
SNP_A-2056403	aatagaaaatgctaac[A/G]caaataatccttcagc	A	G	NM_153686 // intron // 0 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA. /// ENST00000326877 // intron // 0 // — // — // — // —	MLR1	MLR1, Homo sapiens transcription factor MLR1 (MLR1), p15.32
SNP_A-2267287	gaatacttggagaaat[C/T]acaagggaaaagaaaa	C	T	NM_153686 // intron // 0 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA. /// ENST00000326877 // intron // 0 // — // — // — // —	MLR1	MLR1, Homo sapiens transcription factor MLR1 (MLR1), p15.32
SNP_A-2088320	actgtaaactggtgac[C/T]agaaggatagatcaca	C	T	NM_022346 // downstream // 178999 // Hs.479270 // HCAP-G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// NM_153686 // upstream // 2105 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA. //	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32
SNP_A-1914098	tgtgtgtacaaaaaaa[A/T]ttcggttcgcagatta	A	T	NM_022346 // downstream // 349376 // Hs.479270 // HCAP-G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// NM_153686 // upstream // 172482 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA.	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32
SNP_A-2297500	gccagaactcgggggа[G/T]cgtgcaaatatggggt	G	T	NM_022346 // downstream // 415671 // Hs.479270 // HCAP-G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// NM_153686 // upstream // 238777 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA.	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32
SNP_A-1914965	tgttagtttttcttga[A/G]tagcaccatctttaat	A	G	NM_022346 // downstream // 534827 // Hs.479270 // HCAP-G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// NM_153686 // upstream // 357933 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA.	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32
SNP_A-2058604	aatcaggtgtgtaaaa[G/T]agcacaacgtgtttag	G	T	NM_022346 // downstream // 535727 // Hs.479270 // HCAP-G // 64151 // Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /// NM_153686 // upstream // 358833 // Hs.446201 // MLR1 // 254251 // Homo sapiens transcription factor MLR1 (MLR1), mRNA.	HCAP-G	HCAP-G, Homo sapiens chromosome condensation protein G (HCAP-G), p15.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181072	cagacacatttcaaga[C/G]aagacacacatgtggc	C	G	NM_001001704 // downstream // 410644 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST00000359144 // downstream // 178898 // — // — // — /// ENST00000360734 // downstream // 410644 // — // — //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.32
SNP_A-1879096	tcttaattaaacactc[C/T]attgaagtgcagaga	C	T	NM_001001704 // downstream // 138976 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST00000359144 // downstream // 450566 // — // — // — /// ENST00000360734 // downstream // 138976 // — // — //	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2087162	actgatgatttatgcc[A/G]gagaaagactgtgaat	A	G	NM_001001704 // upstream // 89812 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 1080775 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2178804	cactgacggcaaaatg[A/G]aagttaatttaagagt	A	G	NM_001001704 // upstream // 89882 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 1080705 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1839464	tagatacatggagaga[A/T]cggtacccagaaaaga	A	T	NM_001001704 // upstream // 102263 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 1068324 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST00	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1824903	taaagcattcacttac[A/G]agtacagtcatgcacc	A	G	NM_001001704 // upstream // 177164 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 993423 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2111727	aggataaacatgggga[A/G]aaaatagttccacatt	A	G	NM_001001704 // upstream // 177465 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 993122 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-2202329	ccaccagaagctgaac[A/G]gatacctgaaccatgc	A	G	NM_001001704 // upstream // 192984 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 977603 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1976321	attattctaggttgta[A/T]gacctacttcaggaag	A	T	NM_001001704 // upstream // 234349 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 936238 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1921993	ttactgagataaatca[A/T]ctttgaccttcattaa	A	T	NM_001001704 // upstream // 266166 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 904421 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1976323	tctagtctctgagaca[A/G]ggcaaaaagtagaggc	A	G	NM_001001704 // upstream // 318549 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 852038 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213678	ccgtgtcattcatccc[A/G]cttcatctcaggacat	A	G	NM_001001704 // upstream // 1109230 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 61357 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1976335	aagtcgtttgagaaa[A/G]catccaagtcatagaa	A	G	NM_001001704 // upstream // 1118571 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_004787 // upstream // 52016 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST000	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), p15.31
SNP_A-1887969	tgagcaccagtttgca[C/T]atgttccaagtgtgag	C	T	NM_004787 // intron // 0 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST00000355571 // intron // 0 // — // — // — /// ENST00000273739 // intron // 0 // — // — // — // —	SLIT2	SLIT2, Homo sapiens slit homolog 2 (Drosophila) (SLIT2), p15.31
SNP_A-2082414	acgcatagacttttagc[A/G]aaggagagctgaagga	A	G	NM_004787 // intron // 0 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST00000355571 // intron // 0 // — // — // — /// ENST00000273739 // intron // 0 // — // — // — // —	SLIT2	SLIT2, Homo sapiens slit homolog 2 (Drosophila) (SLIT2), p15.31
SNP_A-1821296	gtttgcagtttaataa[C/G]acagtacaatttaata	C	G	NM_004787 // intron // 0 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST00000355571 // intron // 0 // — // — // — /// ENST00000273739 // intron // 0 // — // — // — // —	SLIT2	SLIT2, Homo sapiens slit homolog 2 (Drosophila) (SLIT2), p15.31
SNP_A-2098238	agagatattgatatta[C/T]gattgtcactgagatc	C	T	NM_004787 // intron // 0 // Hs.29802 // SLIT2 // 9353 // Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA. /// ENST00000355571 // intron // 0 // — // — // — /// ENST00000273739 // intron // 0 // — // — // — // —	SLIT2	SLIT2, Homo sapiens slit homolog 2 (Drosophila) (SLIT2), p15.31
SNP_A-1693268	accaggcatggtagcctttagacag[A/T]acatctatttttcactctc ttgaac	A	T	NM_147182 // intron // 0 // Hs.437632 // KCNIP4 // 80333 // Kv channel interacting protein 4 /// NM_147183 // intron // 0 // Hs.437632 // KCNIP4 // 80333 // Kv channel interacting protein 4	KCNIP4	KCNIP4 , rs10516369, Kv channel interacting protein 4 , p15.31
SNP_A-2009634	atataatgcagaggaa[A/G]aggactgagtcaatgt	A	G	NM_147183 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, mRNA. /// NM_147182 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, p15.31
SNP_A-2093410	agaactgaagagttac[A/G]atgaacctaggaaagt	A	G	NM_147183 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, mRNA. /// NM_147182 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 4, p15.31
SNP_A-2182437	cagataagtaccagaa[A/G]gtagcataatacacta	A	G	NM_147181 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31
SNP_A-2164972	caaactcaagtctgac[A/C]ctagatttcttctct	A	C	NM_147181 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31
SNP_A-2009639	ggacagtggatgttat[C/T]agaatgaagtgagatg	C	T	NM_147181 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, mRNA. /// NM_147182 // intron // 0 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (	KCNIP4	KCNIP4, Homo sapiens Kv channel interacting protein 4 (KCNIP4), transcript variant 2, p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2314028	ggagcttatccagcta[C/G]acagttgtcagtttg	C	G	NM_145048 // downstream // 1563245 // Hs.479298 // MGC29898 // 133015 // Homo sapiens hypothetical protein MGC29898 (MGC29898), mRNA. /// NM_147183 // upstream // 987689 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KCN	MGC29898	MGC29898, Homo sapiens hypothetical protein MGC29898 (MGC29898), p15.31
SNP_A-2075300	acatcttaaaatgt[A/G]agtagtgatcaagagt	A	G	NM_145048 // downstream // 1600008 // Hs.479298 // MGC29898 // 133015 // Homo sapiens hypothetical protein MGC29898 (MGC29898), mRNA. /// NM_147183 // upstream // 1024452 // Hs.546445 // KCNIP4 // 80333 // Homo sapiens Kv channel interacting protein 4 (KC	MGC29898	MGC29898, Homo sapiens hypothetical protein MGC29898 (MGC29898), p15.31
SNP_A-2259133	gaaaaaaatcgttaat[A/G]atacatctggatacac	A	G	BC035645 // upstream // 6568 // Hs.99195 // GPR125 // 166647 // Homo sapiens, Similar to RIKEN cDNA 3830613O22 gene, clone IMAGE:5551209, mRNA, partial cds. /// ENST00000282943 // upstream // 66796 // — // — // — /// ENST00000334304 // upstre	GPR125	GPR125, Homo sapiens, Similar to RIKEN cDNA 3830613O22 gene, clone IMAGE:5551209, partial cds, p15.31
SNP_A-1976444	gtgcttgggttcacta[C/G]agcctaaatgtgaagt	C	G	NM_020973 // downstream // 486121 // Hs.371763 // GBA3 // 57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 486333 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-2177173	cacctgagtttcaagal[A/T]attaatggaaaaaccc	A	T	NM_020973 // downstream // 528908 // Hs.371763 // GBA3 // 57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 443546 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-1727795	cttccctgtatatagtactacta[A/C]taacaagtcctaactaatca gaagt	A	C	NM_013261 // downstream // 258506 // Hs.198468 // PPARGC1A // 10891 // peroxisome proliferative activated receptor, gamma, coactivator 1, alpha /// NM_020973 // downstream // 713948 // Hs.146182 // GBA3 // 57733 // glucosidase, beta, acid 3 (cytosolic)	PPARGC1A	PPARGC1A , rs10517014, peroxisome proliferative activated receptor, gamma, coactivator 1, alpha p15.2
SNP_A-2035633	aaatgtatgttgctta[C/T]ggtacatcaatctac	C	T	NM_020973 // downstream // 893991 // Hs.371763 // GBA3 // 57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 78463 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated r	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-1976455	gttgtgcctatattaa[C/T]ggatgcctttctttt	C	T	NM_020973 // downstream // 915157 // Hs.371763 // GBA3 // 57733 // Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), mRNA. /// NM_013261 // downstream // 57297 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated r	GBA3	GBA3, Homo sapiens glucosidase, beta, acid 3 (cytosolic) (GBA3), p15.2
SNP_A-2153678	attaggggtgatggt[A/G]acaatgaaaggaagga	A	G	NM_013261 // intron // 0 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// ENST00000264867 // intron // 0 // — // — // — // —	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1942466	ttggctctgccctcaa[C/G]gatcaactgtgaaata	C	G	NM_013261 // upstream // 1879 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 635522 // Hs.5683 // DHX15 // 1665 // Homo sapiens mRN	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1924900	ttatattaaactgcca[A/G]cttaggtaggacacca	A	G	NM_013261 // upstream // 104937 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 532464 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2281529	gagtccaggctggtca[A/C]atagcttccacgtgg	A	C	NM_013261 // upstream // 118087 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 519314 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2270979	gacagttctaggaaga[A/T]aaaccatgcctcaggg	A	T	NM_013261 // upstream // 123468 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 513933 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2116007	aggattgtttgttaac[C/T]gtatcagaacctaatc	C	T	NM_013261 // upstream // 132790 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 504611 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1976474	catgactggcagagccd[A/G]aacgagggaggacgac	A	G	NM_013261 // upstream // 176096 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 461305 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2226815	ctaataccaccttctat[C/T]gactgagctgtagtga	C	T	NM_013261 // upstream // 178852 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 458549 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2229258	ctaggaagattaaggc[C/T]gatgaataaaagaaag	C	T	NM_013261 // upstream // 213909 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 423492 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1956389	tttgtatctggagaa[C/T]tatttgagacggttta	C	T	NM_013261 // upstream // 250912 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 386489 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1687490	acccaatttcctgatctaccaagca[C/T]tctagtggatgagacaa agatggtt	C	T	NM_001358 // downstream // 457038 // Hs.5683 // DHX15 // 1665 // DEAH (Asp-Glu-Ala-His) box polypeptide 15 /// NM_013261 // upstream // 180363 // Hs.198468 // PPARGC1A // 10891 // peroxisome proliferative activated receptor, gamma, coactivator 1, alpha	DHX15	DHX15 , rs2215488, DEAH (Asp-Glu-Ala-His) box polypeptide 15 ,p15.2
SNP_A-1941183	ttgctgcaaggcataa[C/T]gaggtaacatatgga	C	T	NM_013261 // upstream // 364142 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 273259 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1976489	tcagctgtttatggca[A/T]cttgagtcacagacac	A	T	NM_013261 // upstream // 370291 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 267110 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-1976490	gtcagaatttttccc[C/T]gagcatctgaacatcc	C	T	NM_013261 // upstream // 370389 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 267012 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1919670	ttaaggttcatcctgaj[A/C]aaagagacttataaat	A	C	NM_013261 // upstream // 377922 // Hs.527078 // PPARGC1A // 10891 // Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), mRNA. /// AB001636 // downstream // 259479 // Hs.5683 // DHX15 // 1665 // Homo sapiens m	PPARGC1A	PPARGC1A, Homo sapiens peroxisome proliferative activated receptor, gamma, coactivator 1, alpha (PPARGC1A), p15.2
SNP_A-2199431	cattttaaattaccc[A/T]agttgatctgtgtctg	A	T	AB001636 // upstream // 137937 // Hs.5683 // DHX15 // 1665 // Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds. /// NM_001358 // upstream // 137937 // Hs.5683 // DHX15 // 1665 // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 15 (DH	DHX15	DHX15, Homo sapiens for ATP-dependent RNA helicase #46, complete cds. p15.2
SNP_A-1956886	ttttaacttaaacac[C/T]gagcaatgtaaattca	C	T	NM_173463 // intron // 0 // Hs.106432 // DKFZp761B107 // 91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. /// ENST00000324309 // intron // 0 // — // — // —	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein (DKFZp761B107), p15.2
SNP_A-1802050	gtatacagaaaggagca[G/T]gagttccacttagggc	G	T	NM_173463 // intron // 0 // Hs.106432 // DKFZp761B107 // 91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. /// ENST00000324309 // intron // 0 // — // — // —	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein (DKFZp761B107), p15.2
SNP_A-2307600	gcttcaggacgttggaj[A/G]aagcatgaaaaagaat	A	G	NM_173463 // intron // 0 // Hs.106432 // DKFZp761B107 // 91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. /// ENST00000324309 // intron // 0 // — // — // —	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein (DKFZp761B107), p15.2
SNP_A-1976514	gcttcaaacctgcatc[G/T]gagggcagtatccgag	G	T	NM_173463 // intron // 0 // Hs.106432 // DKFZp761B107 // 91050 // Homo sapiens hypothetical protein DKFZp761B107 (DKFZp761B107), mRNA. /// ENST00000324309 // intron // 0 // — // — // —	DKFZp761B107	DKFZp761B107, Homo sapiens hypothetical protein (DKFZp761B107), p15.2
SNP_A-1866703	tcccctgagatctgac[C/T]ggcctatggcttgttt	C	T	NM_018176 // upstream // 47773 // Hs.12488 // LGI2 // 55203 // Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// NM_153825 // downstream // 42536 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver pancreas an	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-1841377	taggacaagttgatca[C/T]cttattcccaggactc	C	T	NM_018176 // upstream // 55542 // Hs.12488 // LGI2 // 55203 // Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// NM_153825 // downstream // 34767 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver pancreas an	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-2307081	gctgtttggacttcca[C/G]taaattggggcaattt	C	G	NM_018176 // upstream // 69269 // Hs.12488 // LGI2 // 55203 // Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA. /// NM_153825 // downstream // 21040 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver pancreas an	LGI2	LGI2, Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), p15.2
SNP_A-1976520	tttccagcaaactaa[C/T]gaacccaaaaggagg	C	T	NM_153825 // upstream // 50899 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver pancreas antigen (SLA/LP), mRNA. /// NM_016955 // upstream // 50744 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver panc	SLA	SLA, 51091 ,p15.2
SNP_A-1976521	ccaataataccaactc[C/T]gagattagaagttaaa	C	T	NM_153825 // upstream // 53179 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver pancreas antigen (SLA/LP), mRNA. /// NM_016955 // upstream // 53024 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver panc	SLA	SLA, 51091 ,p15.2
SNP_A-2300058	gcctcacattgaaaga[C/G]ctacctgaacaaaact	C	G	NM_153825 // upstream // 59865 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver pancreas antigen (SLA/LP), mRNA. /// NM_016955 // upstream // 59710 // Hs.253305 // SLA/LP // 51091 // Homo sapiens soluble liver antigen/liver panc	SLA	SLA, 51091 p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284389	gatcaaaaagctgtta[A/T]aattacttcagcctag	A	T	NM_018323 // downstream // 24950 // Hs.443733 // PI4K2B // 55300 // Homo sapiens phosphatidylinositol 4-kinase type-II beta (PI4K2B), mRNA. /// AK026677 // upstream // 41516 // Hs.278945 // ZCCHC4 // 29063 // Homo sapiens cDNA: FLJ23024 fis, clone LNG0168	PI4K2B	PI4K2B, Homo sapiens phosphatidylinositol 4-kinase type-II beta (PI4K2B), p15.2
SNP_A-2218844	cctggctgagtcaca[C/T]gtctagtggttggctc	C	T	NM_018323 // downstream // 29915 // Hs.443733 // PI4K2B // 55300 // Homo sapiens phosphatidylinositol 4-kinase type-II beta (PI4K2B), mRNA. /// AK026677 // upstream // 36551 // Hs.278945 // ZCCHC4 // 29063 // Homo sapiens cDNA: FLJ23024 fis, clone LNG0168	PI4K2B	PI4K2B, Homo sapiens phosphatidylinositol 4-kinase type-II beta (PI4K2B), p15.2
SNP_A-1859154	tcagcctgttaggaca[C/G]tatgttttcaagatt	C	G	AK026677 // intron // 0 // Hs.278945 // ZCCHC4 // 29063 // Homo sapiens cDNA: FLJ23024 fis, clone LNG01684. /// ENST00000358166 // intron // 0 // — // — // — /// ENST00000302874 // intron // 0 // — // — // — // —	ZCCHC4	ZCCHC4, Homo sapiens cDNA: FLJ23024 fis, clone LNG01684, p15.2
SNP_A-2063842	aattaggttatgcaaa[A/G]tcaagcaatcaaccac	A	G	AK026677 // intron // 0 // Hs.278945 // ZCCHC4 // 29063 // Homo sapiens cDNA: FLJ23024 fis, clone LNG01684. /// ENST00000358166 // intron // 0 // — // — // — /// ENST00000302874 // intron // 0 // — // — // —	ZCCHC4	ZCCHC4, Homo sapiens cDNA: FLJ23024 fis, clone LNG01684, p15.2
SNP_A-1754262	aaactgtgaaatatctatcatccta[G/T]aagaactggcatcacat tctgacat	G	T	NM_014150 // intron // 0 // - // - // -	-	-, rs316800, -,p15.2
SNP_A-2177771	cacgtcttgagacac[A/G]ccctaacacttactct	A	G	NM_015187 // intron // 0 // Hs.479384 // KIAA0746 // 23231 // Homo sapiens KIAA0746 protein (KIAA0746), mRNA. /// ENST00000264868 // intron // 0 // — // — // — // —	KIAA0746	KIAA0746, Homo sapiens KIAA0746 protein (KIAA0746), p15.2
SNP_A-2199102	catttgttactgctat[G/T]actgcaatgaagtcgg	G	T	NM_203283 // upstream // 387645 // Hs.479396 // RBPSUH // 3516 // Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, mRNA. /// NM_005349 // upstream // 387645 // Hs.479396 // RBPSUH // 3516 // Homo	RBPSUH	RBPSUH, Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, p15.2
SNP_A-2183254	cagcaatgctgaataa[A/G]ctaagccggttgcaag	A	G	NM_203283 // upstream // 386592 // Hs.479396 // RBPSUH // 3516 // Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, mRNA. /// NM_005349 // upstream // 386592 // Hs.479396 // RBPSUH // 3516 // Homo	RBPSUH	RBPSUH, Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, p15.2
SNP_A-2087702	actgcttatcatcttat[A/C]atagcagaggagctga	A	C	NM_203283 // upstream // 329152 // Hs.479396 // RBPSUH // 3516 // Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, mRNA. /// NM_005349 // upstream // 329152 // Hs.479396 // RBPSUH // 3516 // Homo	RBPSUH	RBPSUH, Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, p15.2
SNP_A-2162764	atttggaggaggata[C/T]gtggtcctagtgtgtg	C	T	NM_203283 // upstream // 248665 // Hs.479396 // RBPSUH // 3516 // Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, mRNA. /// NM_005349 // upstream // 248665 // Hs.479396 // RBPSUH // 3516 // Homo	RBPSUH	RBPSUH, Homo sapiens recombining binding protein suppressor of hairless (Drosophila) (RBPSUH), transcript variant 3, p15.2
SNP_A-2151311	atgttagtgactggaa[C/T]agatgagcatctcctt	C	T	NM_020860 // downstream // 234872 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3461170 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-2309738	ggaaaggcagtggtga[C/G]agatttcagatttgt	C	G	NM_020860 // downstream // 401450 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3294592 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1836253	tactatgtgtaacctc[A/G]agttcggaaggtctga	A	G	NM_020860 // downstream // 423118 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3272924 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1740315	tagatttcaaactcagttctattca[C/T]actaaagtccatactttca caitc	C	T	NM_002589 // upstream // 3321956 // Hs.443020 // PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_020860 // downstream // 373078 // Hs.278894 // STIM2 // 57620 // stromal interaction molecule 2 /// NM_032456 // upstream // 3321956 // Hs.443020 // P	PCDH7	PCDH7 , rs2110176, BH-protocadherin (brain-heart), p15.2
SNP_A-1953834	ttgagccatttaacc[C/G]ctctgtgactcaggtt	C	G	NM_020860 // downstream // 496606 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3199436 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1865747	tccatttcacttctaa[C/G]tctctttggtttccaa	C	G	NM_020860 // downstream // 552036 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3144006 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1726762	tagcccaggaaaggatgaaagctata[C/T]gtggaggatctatct gaagccaga	C	T	NM_002589 // upstream // 3153044 // Hs.443020 // PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_020860 // downstream // 541990 // Hs.278894 // STIM2 // 57620 // stromal interaction molecule 2 /// NM_032456 // upstream // 3153044 // Hs.443020 // P	PCDH7	PCDH7 , rs6842495, BH-protocadherin (brain-heart), p15.2
SNP_A-2254394	cttgcattctgtcttc[A/G]accctttttattaca	A	G	NM_020860 // downstream // 644800 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 3051242 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.2
SNP_A-1795969	ggtggtacatttcttc[C/T]attgcctctcccaat	C	T	NM_020860 // downstream // 1222928 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 2473114 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1682336	ttctagaatgaccatactgaaatgg[A/G]aaatttcagagatttgag attatact	A	G	NM_002589 // upstream // 2512009 // Hs.443020 // PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_020860 // downstream // 1183025 // Hs.278894 // STIM2 // 57620 // stromal interaction molecule 2 /// NM_032456 // upstream // 2512009 // Hs.443020 //	PCDH7	PCDH7 , rs3925061, BH-protocadherin (brain-heart), p15.2
SNP_A-1976610	ctttctttttgttcaga[C/T]ttgccttcccaggaaa	C	T	NM_020860 // downstream // 1712643 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1983399 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2009670	aactaaatgtctatca[A/C]agttagctaggcccaa	A	C	NM_020860 // downstream // 1762876 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1933166 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1931342	ttcccactctctgaa[C/T]gcaatatggtttaga	C	T	NM_020860 // downstream // 1767869 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1928173 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2239816	ctgaaattcatttatc[G/T]gactgagaagcttctt	G	T	NM_020860 // downstream // 1778018 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1918024 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1682416	ccctttctccattacatcatttt[C/T]ttcctagtaactagaaaactc ctga	C	T	NM_002589 // upstream // 1982159 // Hs.443020 // PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_020860 // downstream // 1712875 // Hs.278894 // STIM2 // 57620 // stromal interaction molecule 2 /// NM_032456 // upstream // 1982159 // Hs.443020 //	PCDH7	PCDH7 , rs10038905, BH-protocadherin (brain-heart) ,p15.1
SNP_A-2102455	agattctgaaatacca[C/G]gtgacaaatagtagag	C	G	NM_020860 // downstream // 1969579 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1726463 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2009673	ttaccaatgaatacta[C/T]cttctaccaattaaaa	C	T	NM_020860 // downstream // 1997797 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1698245 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1843825	tagttacagagactaa[A/C]gtaagcatgttacacat	A	C	NM_020860 // downstream // 2003158 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1692884 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2147910	atggctaaataaaagc[A/G]gcagacatgtgaatga	A	G	NM_020860 // downstream // 2003285 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1692757 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2108942	agcttagttgctttg[C/T]attaatgtaaccagtg	C	T	NM_020860 // downstream // 2212308 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1483734 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2058289	aatcaataggccatac[A/G]cattcttgcatatatg	A	G	NM_020860 // downstream // 2214917 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1481125 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1976621	tcagcttaggtctctt[C/T]aaacgtgtgcaatcat	C	T	NM_020860 // downstream // 2312027 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1384015 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1781373	ggatgttccatactaa[C/T]cctgggagaaacaat	C	T	NM_020860 // downstream // 2396738 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1299304 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2265299	gaagcaccttggaag[C/G]agatgatgagaaagaa	C	G	NM_020860 // downstream // 2396835 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1299207 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2228873	ctagatactgtagaaa[G/T]aaagcaaaatcattga	G	T	NM_020860 // downstream // 2491785 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1204257 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2199259	catttcactaaacaa[C/T]ttgctgcttgtgaatt	C	T	NM_020860 // downstream // 2563143 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1132899 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2140090	atctagtacacaaaaa[A/G]cctcacttatactag	A	G	NM_020860 // downstream // 2617032 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 1079010 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), tran	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2282231	gagttaaatacatcca[G/T]cctgatcatcaggtgc	G	T	NM_020860 // downstream // 2699362 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 996680 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1926729	ttattggccacttgal[G/T]ggctgcagtattatac	G	T	NM_020860 // downstream // 2736344 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 959698 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1915182	tgttcaataagacata[C/T]ggacaaagggaaggca	C	T	NM_020860 // downstream // 3031992 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 664050 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1826976	taacatttatcaccaa[C/T]ctgtataattacact	C	T	NM_020860 // downstream // 3170741 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 525301 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1976645	ctagaacagatgttac[C/T]aaaaatggaaacgtgg	C	T	NM_020860 // downstream // 3183351 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 512691 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2310906	ggaaggagaggaggtag[A/G]atgaacagcctgtaaa	A	G	NM_020860 // downstream // 3305241 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 390801 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2088961	acttaaaacctaatga[C/T]ggttgatatatgcagc	C	T	NM_020860 // downstream // 3398809 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 297233 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1976647	taatctcaggatgac[C/T]ggtagaaagcagcgag	C	T	NM_020860 // downstream // 3409485 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 286557 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), trans	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2144658	atgatgaattggaaaa[C/T]atggaaagatgcagat	C	T	NM_020860 // downstream // 3618540 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 77502 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transc	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-2166413	caaatgaccaatagga[A/G]gatgggttagtgacat	A	G	NM_020860 // downstream // 3651764 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 44278 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transc	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1790246	ggggagaggttgctaa[A/C]atattataggatttct	A	C	NM_020860 // downstream // 3664139 // Hs.135763 // STIM2 // 57620 // Homo sapiens stromal interaction molecule 2 (STIM2), mRNA. /// NM_032457 // upstream // 31903 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transc	STIM2	STIM2, Homo sapiens stromal interaction molecule 2 (STIM2), p15.1
SNP_A-1950353	tttcagcttctagaca[C/T]tggctgtattccttgg	C	T	NM_032457 // intron // 0 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// ENST00000333135 // intron // 0 // --- // --- // --- // ---	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2293152	gcagacttcagtgcca[G/T]acattaagtgctaaga	G	T	NM_032457 // intron // 0 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// ENST00000333135 // intron // 0 // --- // --- // --- // ---	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1976673	tgagacctttatgta[C/G]gaaaacattgcttaac	C	G	NM_032457 // downstream // 458222 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 4611226 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1929064	ttcagcttacaaacaa[A/T]ctgctttcagctctag	A	T	NM_032457 // downstream // 519608 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 4549840 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2148337	atggggaagaatgtaa[A/G]gagacaggcgtagtaa	A	G	NM_032457 // downstream // 1164270 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3905178 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1911456	tgtcttgctcgggaga[G/T]gtcattattttgctct	G	T	NM_032457 // downstream // 1228859 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3840589 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2142706	atgaagatcccagcac[A/G]atcaaactgggcaatt	A	G	NM_032457 // downstream // 1300935 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3768513 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2247017	ctgtattctattctcc[C/T]gatgtgaatttagttc	C	T	NM_032457 // downstream // 1303798 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3765650 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826217	taaattcatctgccta[C/T]gaggagctgaccattg	C	T	NM_032457 // downstream // 1304133 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3765315 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1789349	gggccagctagtaccc[A/G]agatctgtttccattc	A	G	NM_032457 // downstream // 1304545 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3764903 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2248847	ctgttgattctactaa[C/G]agtgtctccactatt	C	G	NM_032457 // downstream // 1304782 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3764666 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1798686	gtaaccaaccaagtgg[A/G]atgaacatagacaatt	A	G	NM_032457 // downstream // 1350117 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3719331 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2123321	agtgtatgccaaatg[C/T]atgtatattcaagagc	C	T	NM_032457 // downstream // 1386717 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3682731 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2056705	aatagccatgttgtta[C/T]ggagctaaagcaggg	C	T	NM_032457 // downstream // 1410030 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3659418 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1657770	gatgctctctatgaggatttaaaa[A/G]tgtgaaatcttgatcataag atttgc	A	G	NM_002589 // downstream // 1755050 // Hs.443020 // PCDH7 // 5099 // BH-protocadherin (brain-heart) /// NM_015230 // downstream // 3726031 // Hs.427719 // CENTD1 // 116984 // centaurin, delta 1 /// NM_032456 // downstream // 1760931 // Hs.443020 // PCDH7	PCDH7	PCDH7 , rs10517249, BH-protocadherin (brain-heart), p15.1
SNP_A-2038694	aacagagccttcaaca[A/G]tagtagttggaaactt	A	G	NM_032457 // downstream // 1472610 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3596838 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2229069	ctagccaagcatactg[C/T]aaaatgaatataatgc	C	T	NM_032457 // downstream // 1487059 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3582389 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-2063638	aattacctcaacttca[A/C]ctattcaaaggaaaac	A	C	NM_032457 // downstream // 1607537 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 3461911 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1
SNP_A-1976753	ttatgccatagttcca[A/G]catcttaaaattggc	A	G	NM_032457 // downstream // 3757418 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 1312030 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
				NM_032457 // downstream // 4999925 // Hs.479439 // PCDH7 // 5099 // Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, mRNA. /// NM_139182 // downstream // 69523 // Hs.479451 // CENTD1 // 116984 // Homo sapiens centaurin, delta 1 (	PCDH7	PCDH7, Homo sapiens BH-protocadherin (brain-heart) (PCDH7), transcript variant c, p14
SNP_A-1846788	tatcaagtctcaatca[C/T]ataattgacatggaaa	C	T	ENST00000357504 // downstream // 26216 // --- // --- // --- // ---	-	
SNP_A-1920198	ttaatcttataggaaa[C/T]ttgtgttcaaagtgt	C	T	ENST00000345029 // upstream // 986419 // --- // --- // --- // ---	-	p14
SNP_A-1976781	atgttaagcagaatta[C/T]ggtgacgctcaaata	C	T	ENST00000357504 // downstream // 115523 // --- // --- // --- // ---	-	p14
SNP_A-1877809	tctggtagatgtccaa[A/G]ggaagctggataattc	A	G	ENST00000345029 // upstream // 897112 // --- // --- // --- // ---	-	p14
SNP_A-2070137	acacatcttgccacga[A/T]aaccagttgctatttc	A	T	ENST00000357504 // downstream // 861028 // --- // --- // --- // ---	-	p14
SNP_A-1793857	ggtcaaaattcccaga[A/G]caaggcactgacatat	A	G	ENST00000345029 // upstream // 300902 // --- // --- // --- // ---	-	p14
SNP_A-1815156	gttgtcttcaagggaa[A/T]gttctaaacacaccat	A	T	ENST00000357504 // downstream // 325330 // --- // --- // --- // ---	-	p14
SNP_A-1710634	gttaaccgtggaagagtgaagaaga[A/G]agaagaatgcccaa gccaggtgagc	A	G	ENST00000345029 // upstream // 711733 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs1373475, KIAA1239 protein,p14
SNP_A-2070600	acacctaaaaacttat[A/G]taactcctgcttgaga	A	G	ENST00000357504 // downstream // 665216 // --- // --- // --- // ---	-	p14
SNP_A-1912867	tgtgcttcttgaaaga[C/T]ggagcctagacgtgt	C	T	ENST00000345029 // upstream // 347419 // --- // --- // --- // ---	-	p14
SNP_A-1908189	tgtaccactaacaaaa[C/T]ccacttccctctcaat	C	T	ENST00000357504 // downstream // 620816 // --- // --- // --- // ---	-	p14
SNP_A-1976814	attgtaagtcatctaa[A/T]catttatggtagaaa	A	T	ENST00000345029 // upstream // 391819 // --- // --- // --- // ---	-	p14
SNP_A-1737569	attacttcttgctacaacttcaac[G/T]atataaaagaacacccgt gtcacta	G	T	ENST00000357504 // downstream // 688988 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs724522, KIAA1239 protein,p14
SNP_A-1723392	aatcagattgattaattacaagaaa[C/T]gacttaatgacagagttt ttaaag	C	T	ENST00000345029 // upstream // 323647 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs10484215, KIAA1239 protein,p14
SNP_A-1650470	tcacccaacgctaagtatcttctgat[C/T]gcaattatatgagttgttag aaaatt	C	T	ENST00000357504 // downstream // 695127 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs10484216, KIAA1239 protein,p14
SNP_A-1854449	tcaaatgatagcggaa[C/T]gatcttcccatactta	C	T	ENST00000345029 // upstream // 317508 // --- // --- // --- // ---	-	p14
SNP_A-1686840	ggtgagcctccaaccacgaaattat[C/T]catctgctgtagttatg ataaata	C	T	ENST00000357504 // downstream // 850641 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs7678296, KIAA1239 protein,p14
SNP_A-1831943	taattgcagcaggaaa[A/G]tgtaatggcccacaag	A	G	ENST00000345029 // upstream // 161994 // --- // --- // --- // ---	-	p14
SNP_A-1713906	acctcccgcacactcattcattac[C/G]tgccattcaatagtccttg gcctg	C	G	AB033065 // upstream // 894820 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs1435385, KIAA1239 protein,p14
SNP_A-2259655	gaaaactgtactaggc[A/G]aggcccatagaataaa	A	G	AB033065 // upstream // 117815 // --- // --- // --- // ---	-	p14
SNP_A-1928004	ttcaatgcataacctcc[C/T]gataatccatccagtt	C	T	AB033065 // upstream // 262697 // Hs.4280 // KIAA1239 // 57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs7678296, KIAA1239 protein,p14
SNP_A-1729830	ttctgatcctgttaatctttagac[C/T]gtaatgcatagttgcttaagt tca	C	T	ENST00000357504 // downstream // 919415 // --- // --- // --- // ---	-	p14
SNP_A-1901959	tggcaggttcagagac[A/G]ccctttcatgagccagg gacagagaatgagttcaaatattt[A/T]aaaaaatctcagcaaa agaaccaaa	A	G	AB033065 // upstream // 93220 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs1435385, KIAA1239 protein,p14
SNP_A-1666894		A	T	AB033065 // upstream // 216837 // Hs.4280 // KIAA1239 // 57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs1369410, KIAA1239 protein,p14
SNP_A-1655151	taagggaaaacaaacaaatttaaata[A/G]taagcacaagggac agagaatgagt	A	G	ENST00000357504 // downstream // 983604 // --- // --- // --- // ---	-	p14
SNP_A-1842949	tagtatagtaaggagc[A/G]atgtaaggcatgaacc	A	G	ENST00000345029 // upstream // 29031 // --- // --- // --- // ---	KIAA1239	KIAA1239 , rs1369409, KIAA1239 protein,p14
SNP_A-1731505	ggggattacttgtaccctggttccc[G/T]gcccacattaggatatt caccaat	G	T	ENST00000357504 // downstream // 985381 // --- // --- // --- // ---	-	p14
				ENST00000345029 // upstream // 27254 // --- // --- // --- // ---		
				AB033065 // upstream // 185640 // Hs.4280 // KIAA1239 // 57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs10517405, KIAA1239 protein,p14
				ENST00000357504 // downstream // 989339 // --- // --- // --- // ---	-	p14
				ENST00000345029 // upstream // 23296 // --- // --- // --- // ---		
				AB033065 // upstream // 184937 // Hs.4280 // KIAA1239 // 57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs1369410, KIAA1239 protein,p14
				AB033065 // upstream // 184900 // Hs.4280 // KIAA1239 // 57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs1369409, KIAA1239 protein,p14
				ENST00000345029 // intron // 0 // --- // --- // --- // ---	-	p14
				AB033065 // upstream // 144013 // Hs.4280 // KIAA1239 // 57495 // KIAA1239 protein	KIAA1239	KIAA1239 , rs10517407, KIAA1239 protein,p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2228764	ctagagaactgcaccc[C/T]attcctgctgattac	C	T	NM_018302 // intron // 0 // Hs.107527 // FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ11017), mRNA. /// ENST00000333806 // intron // 0 // — // — // —	FLJ11017	FLJ11017, Homo sapiens hypothetical protein FLJ11017 (FLJ11017), p14
SNP_A-2298558	gcccacataaaatgac[A/G]aacttaatctgtaaat	A	G	ENST00000314117 // intron // 0 // — // — // —	-	p14
SNP_A-2027996	aaacgacaacctgac[A/G]ctgtttaatattcgag	A	G	ENST00000314117 // intron // 0 // — // — // —	-	p14
SNP_A-2190439	catacagtaactgatc[A/G]aaaaatggtaactatc	A	G	NM_018302 // downstream // 168692 // Hs.107527 // FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ11017), mRNA. /// NM_018302 // downstream // 168706 // Hs.107527 // FLJ11017 // 55286 // Homo sapiens hypothetical protein FLJ11017 (FLJ	FLJ11017	FLJ11017, Homo sapiens hypothetical protein FLJ11017 (FLJ11017), p14
SNP_A-2177094	cacctcgatggaatta[A/G]acatacatgtggactt	A	G	NM_015173 // intron // 0 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 // intron // 0 // — // — // — // —	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-1976844	accaaattactggctc[C/T]gaatgcaaaatgtctg	C	T	NM_015173 // intron // 0 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 // intron // 0 // — // — // — // —	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-2063089	aatgtctgattaaaa[C/T]gggctgaggaaacag	C	T	NM_015173 // intron // 0 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 // intron // 0 // — // — // — // —	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-2251687	cttcagtacaggccaa[C/T]gatggcgatccacagt	C	T	NM_015173 // intron // 0 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 // intron // 0 // — // — // — // —	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-2267901	gaatccttcatttgag[C/T]cgagccttaaggatga	C	T	NM_015173 // intron // 0 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 // intron // 0 // — // — // — // —	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-2274776	gagaaagtacagacac[A/G]gacggcttgagtcact	A	G	NM_015173 // intron // 0 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// ENST00000261439 // intron // 0 // — // — // — // —	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-2310284	ggaacccacagaggcc[A/G]gctgagatttcaattt	A	G	NM_015173 // downstream // 28866 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 496157 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor 3	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-2041579	aacgagctatatgccc[C/T]gccgtgagtaagtgc	C	T	NM_015173 // downstream // 29263 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 495760 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor 3	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-1906290	tggtgatcctgaaagc[A/G]cccgttcattcaaagt	A	G	NM_015173 // downstream // 31002 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 494021 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor 3	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2 p14
SNP_A-2204360	ccagcctggagcagtg[C/T]aagaggaaatggactg	C	T	NM_015173 // downstream // 54475 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 470548 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor 3	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102422	agattcctgcctgaaa[A/G]agggtgacatctgtcc	A	G	NM_015173 // downstream // 103830 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 421193 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-2009714	gcaaaacgccagggc[A/T]atgaaaataaattaac	A	T	NM_015173 // downstream // 114948 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 410075 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-1843407	tagtgaattcactaaa[A/C]tggtagcgacaaacc	A	C	NM_015173 // downstream // 147893 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 377130 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-2175922	caccaaaaaagaatgag[A/G]aagccgccataaacaa	A	G	NM_015173 // downstream // 218523 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 306500 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-2192229	catcaggaataggaga[A/G]ggccagttaagagca	A	G	NM_015173 // downstream // 431472 // Hs.176503 // TBC1D1 // 23216 // Homo sapiens TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA. /// NM_016531 // upstream // 93351 // Hs.298658 // KLF3 // 51274 // Homo sapiens Kruppel-like factor 3	TBC1D1	TBC1D1, Homo sapiens TBC1 (tre-2,p14
SNP_A-1651572	aatggaagaaaatattgtaaacta[C/T]ggatcttactaaggct aatataca	C	T	NM_024943 // intron // 0 // Hs.211501 // FLJ23235 // 80008 // hypothetical protein FLJ23235	FLJ23235	FLJ23235, rs2163276, hypothetical protein FLJ23235,p14
SNP_A-2120398	agtcatgtcagagtc[A/T]aaaaatttgaaagaat	A	T	NM_003359 // upstream // 16248 // Hs.28309 // UGDH // 7358 // Homo sapiens UDP-glucose dehydrogenase (UGDH), mRNA. /// NM_174921 // downstream // 7262 // Hs.205952 // LOC201895 // 201895 // Homo sapiens hypothetical protein LOC201895 (LOC201895), mRNA. //	UGDH	UGDH, Homo sapiens UDP-glucose dehydrogenase (UGDH), p14
SNP_A-1782665	ggcactgaccttatat[C/T]agctgtcagcagactc	C	T	NM_003359 // upstream // 16413 // Hs.28309 // UGDH // 7358 // Homo sapiens UDP-glucose dehydrogenase (UGDH), mRNA. /// NM_174921 // downstream // 7097 // Hs.205952 // LOC201895 // 201895 // Homo sapiens hypothetical protein LOC201895 (LOC201895), mRNA. //	UGDH	UGDH, Homo sapiens UDP-glucose dehydrogenase (UGDH), p14
SNP_A-1813109	gtggtacagaaatgga[A/G]aatggcttgagagaa	A	G	NM_174921 // intron // 0 // Hs.205952 // LOC201895 // 201895 // Homo sapiens hypothetical protein LOC201895 (LOC201895), mRNA. /// ENST00000295958 // intron // 0 // — // — // —	LOC201895	LOC201895, Homo sapiens hypothetical protein LOC201895 (LOC201895), p14
SNP_A-1834967	tacccacaggaatgac[A/T]atatttggttataggc	A	T	NM_174921 // intron // 0 // Hs.205952 // LOC201895 // 201895 // Homo sapiens hypothetical protein LOC201895 (LOC201895), mRNA. /// ENST00000295958 // intron // 0 // — // — // —	LOC201895	LOC201895, Homo sapiens hypothetical protein LOC201895 (LOC201895), p14
SNP_A-2113469	aggcggtgacttaga[C/G]gtgagtacaagccacc	C	G	NM_004310 // downstream // 1758 // Hs.160673 // RHOH // 399 // Homo sapiens ras homolog gene family, member H (RHOH), mRNA. /// NM_017581 // upstream // 108220 // Hs.272278 // CHRNA9 // 55584 // Homo sapiens cholinergic receptor, nicotinic, alpha polypept	RHOH	RHOH, Homo sapiens ras homolog gene family, member H (RHOH), p14
SNP_A-2099947	agagtccaaagctcca[G/T]gttagaggctggaagt	G	T	NM_004310 // downstream // 12352 // Hs.160673 // RHOH // 399 // Homo sapiens ras homolog gene family, member H (RHOH), mRNA. /// NM_017581 // upstream // 97626 // Hs.272278 // CHRNA9 // 55584 // Homo sapiens cholinergic receptor, nicotinic, alpha polypept	RHOH	RHOH, Homo sapiens ras homolog gene family, member H (RHOH), p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2180245	cagaaagcctgactat[G/T]aggccatcactcttac	G	T	NM_004310 // downstream // 21927 // Hs.160673 // RHOH // 399 // Homo sapiens ras homolog gene family, member H (RHOH), mRNA. /// NM_017581 // upstream // 88051 // Hs.272278 // CHRNA9 // 55584 // Homo sapiens cholinergic receptor, nicotinic, alpha polypept	RHOH	RHOH, Homo sapiens ras homolog gene family, member H (RHOH), p14
SNP_A-2294271	gcaggggagtgtaaca[C/T]ggtcagagtccaaaac	C	T	NM_004310 // downstream // 95912 // Hs.160673 // RHOH // 399 // Homo sapiens ras homolog gene family, member H (RHOH), mRNA. /// NM_017581 // upstream // 14066 // Hs.272278 // CHRNA9 // 55584 // Homo sapiens cholinergic receptor, nicotinic, alpha polypept	RHOH	RHOH, Homo sapiens ras homolog gene family, member H (RHOH), p14
SNP_A-2271376	gacattggagatggaa[C/T]gaggaagggatcctgg	C	T	NM_017581 // intron // 0 // Hs.272278 // CHRNA9 // 55584 // Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 9 (CHRNA9), mRNA. /// ENST00000310169 // intron // 0 // --- // --- // --- // ---	CHRNA9	CHRNA9, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 9 (CHRNA9), p14
SNP_A-1821029	gtttctggtaactgtg[C/T]agaatggagtttcaag	C	T	NM_017581 // downstream // 63831 // Hs.272278 // CHRNA9 // 55584 // Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 9 (CHRNA9), mRNA. /// NM_019027 // downstream // 4955 // Hs.518727 // FLJ20273 // 54502 // Homo sapiens RNA-binding protein	CHRNA9	CHRNA9, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 9 (CHRNA9), p14
SNP_A-2151446	atgttccatgttctcc[A/G]ctaatttcacttcaga	A	G	NM_019027 // intron // 0 // Hs.518727 // FLJ20273 // 54502 // Homo sapiens RNA-binding protein (FLJ20273), mRNA. /// ENST00000319592 // intron // 0 // --- // --- // --- // --- /// ENST00000295971 // intron // 0 // --- // --- // --- // ---	FLJ20273	FLJ20273, Homo sapiens RNA-binding protein (FLJ20273), p14
SNP_A-1797849	ggttttctatcacgtc[C/T]cttactcaggtttcac	C	T	NM_019027 // intron // 0 // Hs.518727 // FLJ20273 // 54502 // Homo sapiens RNA-binding protein (FLJ20273), mRNA. /// ENST00000319592 // intron // 0 // --- // --- // --- // --- /// ENST00000295971 // intron // 0 // --- // --- // --- // ---	FLJ20273	FLJ20273, Homo sapiens RNA-binding protein (FLJ20273), p14
SNP_A-2009732	ataagcattctttatg[C/T]attcgccattatactg	C	T	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-2009734	gggctactaatatgga[C/T]gtgagatgaggacctg	C	T	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-1882987	tgaaataaggagtaca[A/G]tcatctctgcctgaaa	A	G	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-1889780	tgatacactagttata[C/G]ccacaacaaccaaatg	C	G	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-2044093	aacttggcaaagagaa[A/G]tatgcagaagtcaatt	A	G	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-1921981	ttactgaagtcaccaa[A/G]ttatttttctcaacag	A	G	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14
SNP_A-2135856	atcaaatttaatccca[A/T]caattacatttaaaaa	A	T	NM_173075 // intron // 0 // Hs.479602 // APBB2 // 323 // Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), mRNA. /// ENST00000316212 // intron // 0 // --- // --- // --- // --- /// ENST00000295974 // intron /	APBB2	APBB2, Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like) (APBB2), p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1806877	gtctatttttcctctcc[A/C]agtggaaacactgcaaa	A	C	ENST00000313860 // intron // 0 // — // — // — // — /// ENST00000313875 // intron // 0 // — // — // — // —	-	p13
SNP_A-2229189	ctagctgctttgccaa[C/T]gttctgagcatcagga	C	T	NM_003924 // upstream // 126238 // Hs.87202 // PHOX2B // 8929 // Homo sapiens paired-like homeobox 2b (PHOX2B), mRNA. /// NM_018126 // upstream // 59944 // Hs.31082 // TMEM33 // 5161 // Homo sapiens transmembrane protein 33 (TMEM33), mRNA. /// ENST00002	PHOX2B	PHOX2B, Homo sapiens paired-like homeobox 2b (PHOX2B), p13
SNP_A-2051822	aaggctgattccttat[A/G]catccaggccaaaaaa	A	G	NM_207406 // upstream // 231906 // Hs.190521 // FLJ43965 // 389206 // Homo sapiens FLJ43965 protein (FLJ43965), mRNA. /// ENST00000344852 // upstream // 231906 // — // — // — // — /// ENST00000319234 // upstream // 16433 // — // — // — // —	FLJ43965	FLJ43965, Homo sapiens FLJ43965 protein (FLJ43965), p13
SNP_A-1976932	accattaattgataga[C/T]gtaggtatggcctgta	C	T	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2306970	gctgttagactgatac[A/G]aacaggtttcattcca	A	G	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1802016	gtataatcacctctac[G/T]gctctgtcttccacct	G	T	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2069774	acacagaaaagtgcta[A/G]acagtaattactctct	A	G	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1869634	tccttagaacaatgaa[A/G]ataaacaccacacat	A	G	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2238646	ctctgttacttttggc[C/T]caacaaccctaaatgc	C	T	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2282712	gagtttgcatttaaa[A/G]caatgagctgtcaaag	A	G	NM_006095 // intron // 0 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // intron // 0 // — // — // — // — /// ENST00000264449 // intron	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2125948	agttttataattcgac[A/C]aaccaaataatttttt	A	C	NM_006095 // upstream // 118240 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 118240 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2164980	caaactcaggttagaa[C/G]tatgtattcctgctac	C	G	NM_006095 // upstream // 125406 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 125406 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1976954	tgtggggaaagaatcc[C/T]gaatgatgtctagtac	C	T	NM_006095 // upstream // 247198 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 247198 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1850981	tattatcctcttcaa[A/T]caaattgtgaatcaaa	A	T	NM_006095 // upstream // 247840 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 247840 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2073060	acaggatagaaaataa[A/G]tgattcaggtcataag	A	G	NM_006095 // upstream // 253672 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 253672 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1976956	ttggtaataaattgcc[C/T]gccacaaattgcacaa	C	T	NM_006095 // upstream // 267120 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 267120 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2133212	atatagttagatgcaa[C/T]gaatcagatctaattt	C	T	NM_006095 // upstream // 281135 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 281135 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1807421	gtctgatgactagaga[A/C]gactggatggaaggtg	A	C	NM_006095 // upstream // 287280 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 287280 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1952728	tttctgtcatgagcaa[A/C]tgctgagtcagcttg	A	C	NM_006095 // upstream // 288406 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 288406 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1976960	atatatagtaaaactg[C/G]agcctacttttaatca	C	G	NM_006095 // upstream // 382161 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 382161 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1682126	gtcacctctgttcttgattgacc[C/G]atgtcagataaaaagattg ttaaaa	C	G	NM_006095 // upstream // 391718 // Hs.291385 // ATP8A1 // 10396 // ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 /// NM_182592 // downstream // 1580088 // Hs.200347 // FLJ39576 // 285525 // hypothetical protein FLJ39576	ATP8A1	ATP8A1 , rs1436469, ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 ,p13
SNP_A-2238313	ctctggcactctatc[A/G]ctagaaattgtcaggc	A	G	NM_006095 // upstream // 618223 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 618223 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2085255	actcataaaaggtcat[C/T]aagcttcacctgaac	C	T	NM_006095 // upstream // 650163 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 650163 // — // — // — // — /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803948	gtcaatattcctaca[A/T]tggcactaaaagccca	A	T	NM_006095 // upstream // 654212 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 654212 // — // — // — // /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-2286428	gatgctggtcaatcaa[G/T]aaaaacagaggcagac	G	T	NM_006095 // upstream // 667298 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 667298 // — // — // — // /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1976969	catttaataaacttca[A/G]taaatatgttggctac	A	G	NM_006095 // upstream // 709030 // Hs.435052 // ATP8A1 // 10396 // Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA. /// ENST00000340904 // upstream // 709030 // — // — // — // /// ENST00000264	ATP8A1	ATP8A1, Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), p13
SNP_A-1855733	tcaatcaatttgtgc[C/G]ctgaaaccacagtagt	C	G	NM_198353 // downstream // 249784 // Hs.479644 // KCTD8 // 386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000244249 // downstream // 25655 // — // — // — // /// ENST00000331273 // downstream	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2047468	aagatgatcaaaatac[A/G]ctagtcatggaaagg	A	G	NM_198353 // downstream // 126706 // Hs.479644 // KCTD8 // 386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000244249 // downstream // 148733 // — // — // — // /// ENST00000331273 // downstrea	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2240631	ctgacgcttagcaact[C/T]acatgaataaaatgtt	C	T	NM_198353 // downstream // 85096 // Hs.479644 // KCTD8 // 386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000244249 // downstream // 190343 // — // — // — // /// ENST00000331273 // downstream	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2234582	ctccacttacccactg[C/T]atgatattgttggtgt	C	T	NM_198353 // downstream // 77420 // Hs.479644 // KCTD8 // 386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000244249 // downstream // 198019 // — // — // — // /// ENST00000331273 // downstream	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2247981	ctgtgccttacgatga[A/C]gataagtatttgagat	A	C	NM_198353 // upstream // 86417 // Hs.479644 // KCTD8 // 386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000331273 // upstream // 86417 // — // — // — // /// ENST00000332990 // downstream // 8	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-2025987	aaaaatgttgacaatggt[A/G]aacaaagaaaaggaca	A	G	NM_198353 // upstream // 114490 // Hs.479644 // KCTD8 // 386617 // Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), mRNA. /// ENST00000331273 // upstream // 114490 // — // — // — // /// ENST00000332990 // downstream //	KCTD8	KCTD8, Homo sapiens potassium channel tetramerisation domain containing 8 (KCTD8), p13
SNP_A-1976999	tgcagtgtgcttgaac[A/C]ctagaaggttgggacc	A	C	NM_138335 // upstream // 143568 // Hs.21398 // GNPDA2 // 132789 // Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), mRNA. /// ENST00000295448 // upstream // 143568 // — // — // — // /// ENST00000330935 // downstream // 544174 // — //	GNPDA2	GNPDA2, Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), p13
SNP_A-1785088	ggcgtattggaatcc[A/G]cacacatggctattct	A	G	NM_138335 // upstream // 266175 // Hs.21398 // GNPDA2 // 132789 // Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), mRNA. /// ENST00000295448 // upstream // 266175 // — // — // — // /// ENST00000330935 // downstream // 421567 // — //	GNPDA2	GNPDA2, Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2095841	agacagagatagctcc[G/T]aagtggtagatcattc	G	T	NM_138335 // upstream // 463244 // Hs.21398 // GNPDA2 // 132789 // Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), mRNA. /// ENST00000295448 // upstream // 463244 // — // — // — /// ENST00000330935 // downstream // 224498 // — //	GNPDA2	GNPDA2, Homo sapiens glucosamine-6-phosphate deaminase 2 (GNPDA2), p13
SNP_A-1649946	tggatctcttgaatgtaggatgtaa[C/T]aataaatgtcagcaggttt taaaaa	C	T	NM_138335 // upstream // 537828 // Hs.511814 // GNPDA2 // 132789 // glucosamine-6-phosphate deaminase 2 /// NM_173536 // downstream // 775804 // Hs.375051 // GABRG1 // 2565 // gamma-aminobutyric acid (GABA) A receptor, gamma 1	GNPDA2	GNPDA2, rs10517126, glucosamine-6-phosphate deaminase 2,p13
SNP_A-1824102	taaacacctaagtata[A/G]acagaatgcatatctt	A	G	NM_173536 // downstream // 188998 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 432129 // — // — // — /// ENST00000295452 // downstream //	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-1956425	tttgttcctaaatccat[A/G]aacaagcatggccatt	A	G	NM_173536 // downstream // 186705 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 434422 // — // — // — /// ENST00000295452 // downstream //	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-2188282	cagtctccttttatcaa[C/T]acccctcacaaacacac	C	T	NM_173536 // downstream // 186505 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 434622 // — // — // — /// ENST00000295452 // downstream //	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-1977014	tgcatcaggttaaaag[C/T]ctcacctcctactta	C	T	NM_173536 // downstream // 112955 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 508172 // — // — // — /// ENST00000295452 // downstream //	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-1977015	gaaaggtcatgtagta[C/G]gaaatatgaaaagcaa	C	G	NM_173536 // downstream // 106724 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// ENST00000330935 // upstream // 514403 // — // — // — /// ENST00000295452 // downstream //	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p13
SNP_A-1919708	ttaagtaggtcaatggt[A/T]cacagaaaactgcca	A	T	NM_173536 // upstream // 37403 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// NM_000807 // downstream // 88099 // Hs.116250 // GABRA2 // 2555 // Homo sapiens gamma-aminobutyric acid (G	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p12
SNP_A-1909676	tgtcaagatggacaag[A/C]accaccatgttagccat	A	C	NM_173536 // upstream // 112655 // Hs.375051 // GABRG1 // 2565 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), mRNA. /// NM_000807 // downstream // 12847 // Hs.116250 // GABRA2 // 2555 // Homo sapiens gamma-aminobutyric acid (	GABRG1	GABRG1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 1 (GABRG1), p12
SNP_A-1948999	tttatctgaggcgata[A/G]aatccaaacgtgcaac	A	G	NM_000807 // upstream // 1764 // Hs.116250 // GABRA2 // 2555 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA. /// NM_000807 // upstream // 1215 // Hs.116250 // GABRA2 // 2555 // Homo sapiens gamma-aminobutyric acid (GABA)	GABRA2	GABRA2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), p12
SNP_A-2267713	gaatcaggcaatgcac[C/T]aattcaaggataataca	C	T	NM_000807 // upstream // 10756 // Hs.116250 // GABRA2 // 2555 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA. /// NM_000807 // upstream // 10207 // Hs.116250 // GABRA2 // 2555 // Homo sapiens gamma-aminobutyric acid (GAB	GABRA2	GABRA2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2034489	aaatctgagtcaccca[A/G]tgcacattatcacagc	A	G	NM_130902 // intron // 0 // Hs.479656 // COX7B2 // 170712 // Homo sapiens cytochrome c oxidase subunit VIIb2 (COX7B2), mRNA. /// ENST00000302930 // intron // 0 // — // — // — // — /// ENST00000355591 // intron // 0 // — // — // — // —	COX7B2	COX7B2, Homo sapiens cytochrome c oxidase subunit VIIb2 (COX7B2), p12
SNP_A-2026799	aaacacagaatactcc[A/G]gaaggtttgtcaaagt	A	G	NM_000812 // intron // 0 // Hs.27283 // GABRB1 // 2560 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), mRNA. /// ENST00000295454 // intron // 0 // — // — // — // —	GABRB1	GABRB1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), p12
SNP_A-1977046	ttagtttccattatga[C/T]gaaaagttgcaaggtt	C	T	NM_000812 // intron // 0 // Hs.27283 // GABRB1 // 2560 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), mRNA. /// ENST00000295454 // intron // 0 // — // — // — // —	GABRB1	GABRB1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), p12
SNP_A-2087996	actggccccattcttg[A/G]aagattcagattatta	A	G	NM_000812 // downstream // 2482 // Hs.27283 // GABRB1 // 2560 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), mRNA. /// NM_017845 // downstream // 21886 // Hs.23956 // COMMD8 // 54951 // Homo sapiens COMM domain containing 8 (C	GABRB1	GABRB1, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 1 (GABRB1), p12
SNP_A-1824974	taaagctctgttatgg[C/T]agggccttatttattc	C	T	NM_017845 // intron // 0 // Hs.23956 // COMMD8 // 54951 // Homo sapiens COMM domain containing 8 (COMMD8), mRNA. /// ENST00000306848 // intron // 0 // — // — // — // —	COMMD8	COMMD8, Homo sapiens COMM domain containing 8 (COMMD8), p12
SNP_A-2186974	caggtaacagagcaaa[C/G]ataaaaaaggtaggca	C	G	NM_020453 // intron // 0 // Hs.437241 // ATP10D // 57205 // Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA. /// ENST00000273859 // intron // 0 // — // — // — // —	ATP10D	ATP10D, Homo sapiens ATPase, Class V, type 10D (ATP10D), p12
SNP_A-2009776	gtgttcataacatttc[A/G]aagagctaatactagc	A	G	NM_020453 // intron // 0 // Hs.437241 // ATP10D // 57205 // Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA. /// ENST00000273859 // intron // 0 // — // — // — // —	ATP10D	ATP10D, Homo sapiens ATPase, Class V, type 10D (ATP10D), p12
SNP_A-2123719	agtgttgcctaggaga[C/T]aatttggtgaagaata	C	T	NM_020453 // intron // 0 // Hs.437241 // ATP10D // 57205 // Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA. /// ENST00000273859 // intron // 0 // — // — // — // —	ATP10D	ATP10D, Homo sapiens ATPase, Class V, type 10D (ATP10D), p12
SNP_A-2204415	ccagctcactagaaca[A/G]cgtgtacaaggattgg	A	G	NM_020453 // intron // 0 // Hs.437241 // ATP10D // 57205 // Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA. /// ENST00000273859 // intron // 0 // — // — // — // —	ATP10D	ATP10D, Homo sapiens ATPase, Class V, type 10D (ATP10D), p12
SNP_A-2313257	ggagacacatagactc[A/G]actattttggatcaac	A	G	NM_006587 // intron // 0 // Hs.518618 // CORIN // 10699 // Homo sapiens corin, serine protease (CORIN), mRNA. /// ENST00000273857 // intron // 0 // — // — // — // —	CORIN	CORIN, Homo sapiens corin, serine protease (CORIN), p12
SNP_A-1883233	tgaaattatgactcaa[C/T]ggagaatatgactgat	C	T	NM_207330 // 3UTR // 0 // Hs.134190 // LOC152519 // 152519 // Homo sapiens hypothetical protein LOC152519 (LOC152519), mRNA. /// ENST00000295461 // 3UTR // 0 // — // — // — // —	LOC152519	LOC152519, Homo sapiens hypothetical protein LOC152519 (LOC152519), p12
SNP_A-1958424	ttttcctataccttaa[C/G]caacatttgaaattac	C	G	NM_003328 // intron // 0 // Hs.479669 // TXK // 7294 // Homo sapiens TXK tyrosine kinase (TXK), mRNA. /// ENST00000264316 // intron // 0 // — // — // — // —	TXK	TXK, Homo sapiens TXK tyrosine kinase (TXK), p12
SNP_A-1977059	ggatccaggaagctac[A/G]gagagaagcagccagc	A	G	NM_003215 // 3UTR // 0 // Hs.479670 // TEC // 7006 // Homo sapiens tec protein tyrosine kinase (TEC), mRNA. /// ENST00000258070 // 3UTR // 0 // — // — // — // —	TEC	TEC, Homo sapiens tec protein tyrosine kinase (TEC), p12
SNP_A-1724044	atgaaagcacaaattagaataagaa[C/G]ctacattgtcagaatt attatttcc	C	G	NM_003328 // intron // 0 // Hs.29877 // TXK // 7294 // TXK tyrosine kinase	TXK	TXK , rs3792623, TXK tyrosine kinase,p12
SNP_A-1977063	gcaagtaatccaaata[C/T]gcaatggccaaatctg	C	T	NM_003215 // intron // 0 // Hs.479670 // TEC // 7006 // Homo sapiens tec protein tyrosine kinase (TEC), mRNA. /// ENST00000258070 // intron // 0 // — // — // — // —	TEC	TEC, Homo sapiens tec protein tyrosine kinase (TEC), p12
SNP_A-1669019	cacaagtaattgagactagaaaaaa[A/T]taatagcccaactaa cttaaattct	A	T	NM_025087 // upstream // 69870 // Hs.288462 // FLJ21511 // 80157 // hypothetical protein FLJ21511 /// NM_152398 // upstream // 9590 // Hs.95835 // MGC45416 // 132299 // hypothetical protein MGC45416	FLJ21511	FLJ21511 , rs10517231, hypothetical protein FLJ21511 ,p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2080774	acctcccctgcccagg[G/T]aagtggtactgaaaaa	G	T	NM_145263 // downstream // 176178 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 176178 // — // — // — /// ENST00000356681 // downstream // 316812 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-2210398	cccccaggcacaactg[A/G]aaacctcttttctcaa	A	G	NM_145263 // downstream // 176400 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 176400 // — // — // — /// ENST00000356681 // downstream // 316590 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-2251282	ctcaacaaagcatac[A/C]aaaacgtaaagtgggg	A	C	NM_145263 // downstream // 187718 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 187718 // — // — // — /// ENST00000356681 // downstream // 305272 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-2221098	ccttgtctcagattta[C/T]ccaagttacctctacc	C	T	NM_145263 // downstream // 201064 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 201064 // — // — // — /// ENST00000356681 // downstream // 291926 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-1826664	taacactcagttacta[C/G]gattataitcataaa	C	G	NM_145263 // downstream // 220553 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 220553 // — // — // — /// ENST00000356681 // downstream // 272437 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-2279512	gaggatgtagcaggag[A/C]aaagtaaagaaagcct	A	C	NM_145263 // downstream // 243537 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 243537 // — // — // — /// ENST00000356681 // downstream // 249453 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-1899325	tggaacatctggtttg[G/T]aaggaagccttatagg	G	T	NM_145263 // downstream // 261863 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 261863 // — // — // — /// ENST00000356681 // downstream // 231127 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-1748897	aaaggcacccctgctagccaaatgcc[A/G]atatcatgaatttgctt agagtgag	A	G	NM_145263 // downstream // 194308 // Hs.335499 // LOC132671 // 132671 // LOC132671	LOC132671	LOC132671, , rs1023941, LOC132671,q11
SNP_A-1889617	tgataaagagcatcta[C/T]ggaaaactcagctaac	C	T	NM_145263 // downstream // 361565 // Hs.527090 // LOC132671 // 132671 // Homo sapiens LOC132671 (LOC132671), mRNA /// ENST00000295213 // downstream // 361565 // — // — // — /// ENST00000356681 // downstream // 131425 // — // — // —	LOC132671	LOC132671, Homo sapiens LOC132671 (LOC132671), q11
SNP_A-1733316	ttlgaggcggaagtgaaagctgtaa[A/G]ggttagagcacaaag ggctgagagg	A	G	NM_023940 // upstream // 19318 // Hs.8035 // RASL11B // 65997 // RAS-like, family 11, member B /// NM_024534 // upstream // 97169 // Hs.518757 // FLJ12684 // 79584 // hypothetical protein FLJ12684	RASL11B	RASL11B , rs10517269, RAS-like, family 11, member B ,q12
SNP_A-2060342	aatgaatcaagtcagat[C/G]gcatttttctactc	C	G	NM_152540 // intron // 0 // Hs.302287 // SCFD2 // 152579 // Homo sapiens sec1 family domain containing 2 (SCFD2), mRNA /// ENST00000329818 // intron // 0 // — // — // — /// ENST00000339536 // intron // 0 // — // — // —	SCFD2	SCFD2, Homo sapiens sec1 family domain containing 2 (SCFD2), q12
SNP_A-2207307	ccatttaccagatac[A/G]cagacatcaccacagt	A	G	NM_152540 // intron // 0 // Hs.302287 // SCFD2 // 152579 // Homo sapiens sec1 family domain containing 2 (SCFD2), mRNA /// ENST00000329818 // intron // 0 // — // — // — /// ENST00000339536 // intron // 0 // — // — // —	SCFD2	SCFD2, Homo sapiens sec1 family domain containing 2 (SCFD2), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2109471	aggaaaaaagcaatga[A/G]gaattggtctggttga	A	G	NM_152540 // intron // 0 // Hs.302287 // SCFD2 // 152579 // Homo sapiens sec1 family domain containing 2 (SCFD2), mRNA. /// ENST00000329818 // intron // 0 // — // — // — /// ENST00000339536 // intron // 0 // — // — // —	SCFD2	SCFD2, Homo sapiens sec1 family domain containing 2 (SCFD2), q12
SNP_A-1977108	actgtatttaaggcaa[C/T]gtgaggaatagaaaac	C	T	NM_030917 // intron // 0 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// ENST00000306932 // intron // 0 // — // — // — /// ENST00000337488 // intron // 0 // — // — // —	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1977109	ttaccagtctctgtga[C/T]gtacggtcaaaaatta	C	T	NM_030917 // intron // 0 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// ENST00000306932 // intron // 0 // — // — // — /// ENST00000337488 // intron // 0 // — // — // —	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1977110	atacttgcaagaaggcc[A/G]ggcgataccatagaca	A	G	NM_030917 // intron // 0 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// ENST00000306932 // intron // 0 // — // — // — /// ENST00000337488 // intron // 0 // — // — // —	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1829310	taagtatttgttgtca[C/T]taattcataccaactc	C	T	NM_030917 // intron // 0 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// ENST00000306932 // intron // 0 // — // — // — /// ENST00000337488 // intron // 0 // — // — // — /// ENST00000	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-2121350	agtcttcttcaccttd[A/G]ctgtcctatttttgaa	A	G	NM_032622 // intron // 0 // Hs.407755 // LNX // 84708 // Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF237782 // intron // 0 // Hs.407755 // LNX // 84708 // Homo sapiens multi-PDZ-domain-containing protein mRNA, complete cds. /// ENST0000030688	LNX	LNX, Homo sapiens ligand of numb-protein X (LNX), q12
SNP_A-1751365	ctagacactatgtaatttgacccg[A/G]aatacttaaacaaaaatatagttt	A	G	NM_032622 // intron // 0 // Hs.66295 // LNX // 84708 // ligand of numb-protein X	LNX	LNX, rs13693353, ligand of numb-protein X q12
SNP_A-2139586	atcgacatttgttgaa[C/G]tgaattcaatgcccag	C	G	NM_030917 // downstream // 191733 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 93208 // Hs.407755 // LNX // 84708 // Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF23778	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1828147	taagacttagcttg[C/T]atgacagaaaggttag	C	T	NM_030917 // downstream // 222484 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 123959 // Hs.407755 // LNX // 84708 // Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF2377	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-2048856	aagcccctctcacaacc[A/G]aagtacaactgttgat	A	G	NM_030917 // downstream // 244435 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 145910 // Hs.407755 // LNX // 84708 // Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF2377	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1787055	gggaaacttgagctga[C/T]acaaaatgcaaaaagg	C	T	NM_030917 // downstream // 272945 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 174420 // Hs.407755 // LNX // 84708 // Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF2377	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12
SNP_A-1943502	ttgtaaagcaaagtga[A/G]aaacaacagctgctctg	A	G	NM_030917 // downstream // 311828 // Hs.518760 // FIP1L1 // 81608 // Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA. /// NM_032622 // upstream // 213303 // Hs.407755 // LNX // 84708 // Homo sapiens ligand of numb-protein X (LNX), mRNA. /// AF2377	FIP1L1	FIP1L1, Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2145578	atgcatatgtcatgga[A/G]gatgaatgtttcccaa	A	G	NM_133267 // downstream // 106246 // Hs.371899 // GSH-2 // 170825 // Homo sapiens homeobox protein GSH-2 (GSH-2), mRNA. /// NM_006206 // upstream // 20834 // Hs.74615 // PDGFRA // 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypep	GSH-2	GSH-2, Homo sapiens homeobox protein GSH-2 (GSH-2), q12
SNP_A-2200815	ccaagatagcacaaga[C/T]aaatgacttttaaaaa	C	T	NM_006206 // downstream // 9304 // Hs.74615 // PDGFRA // 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /// NM_000222 // upstream // 350446 // Hs.479754 // KIT // 3815 // Homo sapiens v-kit Hardy-Zuckerman	PDGFRA	PDGFRA, Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), q12
SNP_A-1889771	tgatacacaaaaggca[A/G]tgaactggaatgaaaa	A	G	NM_006206 // downstream // 308284 // Hs.74615 // PDGFRA // 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /// NM_000222 // upstream // 51466 // Hs.479754 // KIT // 3815 // Homo sapiens v-kit Hardy-Zuckerman	PDGFRA	PDGFRA, Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), q12
SNP_A-1878086	tctgtagcaaggaaca[A/C]ctctagctcttagatt	A	C	NM_006206 // downstream // 310998 // Hs.74615 // PDGFRA // 5156 // Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /// NM_000222 // upstream // 48752 // Hs.479754 // KIT // 3815 // Homo sapiens v-kit Hardy-Zuckerman	PDGFRA	PDGFRA, Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), q12
SNP_A-1977152	aatgctaagaaaggca[A/G]agctagatatttaata	A	G	NM_002253 // intron // 0 // Hs.479756 // KDR // 3791 // Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// ENST00000263923 // intron // 0 // — // — // — // —	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-1895118	tgcccattaattgagg[C/T]atttcttcacagcgtc	C	T	NM_002253 // upstream // 42589 // Hs.479756 // KDR // 3791 // Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 178058 // Hs.546432 // SRD5A2L // 79644 // Homo sapiens hypothetical p	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-1791126	ggggtggtgacctcta[C/T]aaactcttgctaccaa	C	T	NM_002253 // upstream // 55574 // Hs.479756 // KDR // 3791 // Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 165073 // Hs.546432 // SRD5A2L // 79644 // Homo sapiens hypothetical p	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-1977153	aagtgggtgatggaag[A/G]ccttagctgctatgtt	A	G	NM_002253 // upstream // 60220 // Hs.479756 // KDR // 3791 // Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 160427 // Hs.546432 // SRD5A2L // 79644 // Homo sapiens hypothetical p	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-1887723	tgagataagtctttaa[A/G]ctactatgaaatgcat	A	G	NM_002253 // upstream // 178288 // Hs.479756 // KDR // 3791 // Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA. /// NM_024592 // upstream // 42359 // Hs.546432 // SRD5A2L // 79644 // Homo sapiens hypothetical p	KDR	KDR, Homo sapiens kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), q12
SNP_A-2209421	cccatagtaatagatg[A/G]aaaaggatggacttta	A	G	NM_024592 // downstream // 9386 // Hs.546432 // SRD5A2L // 79644 // Homo sapiens hypothetical protein FLJ13352 (FLJ13352), mRNA. /// NM_018475 // upstream // 15493 // Hs.479766 // TPARL // 55858 // Homo sapiens TPA regulated locus (TPARL), mRNA. /// ENST0	SRD5A2L	SRD5A2L, Homo sapiens hypothetical protein FLJ13352 (FLJ13352), q12
SNP_A-2172232	caatgtgatttttaaa[C/G]ttaagagtcagttgaa	C	G	NM_018475 // intron // 0 // Hs.479766 // TPARL // 55858 // Homo sapiens TPA regulated locus (TPARL), mRNA. /// ENST00000257288 // intron // 0 // — // — // — // —	TPARL	TPARL, Homo sapiens TPA regulated locus (TPARL), q12
SNP_A-1977161	aaacctaatctgtcat[C/G]aagacctgctacttat	C	G	NM_004898 // intron // 0 // Hs.436975 // CLOCK // 9575 // Homo sapiens clock homolog (mouse) (CLOCK), mRNA. /// ENST00000309964 // intron // 0 // — // — // — // —	CLOCK	CLOCK, Homo sapiens clock homolog (mouse) (CLOCK), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1943277	ttggtggccttaaaaa[A/G]gtggttagatttagca	A	G	NM_004898 // intron // 0 // Hs.436975 // CLOCK // 9575 // Homo sapiens clock homolog (mouse) (CLOCK), mRNA. /// ENST00000309964 // intron // 0 // --- // --- // --- // ---	CLOCK	CLOCK, Homo sapiens clock homolog (mouse) (CLOCK), q12
SNP_A-2100732	agatagattcatgaca[C/T]tgagtttgacaataat	C	T	NM_152401 // intron // 0 // Hs.223712 // PDCL2 // 132954 // Homo sapiens phosducin-like 2 (PDCL2), mRNA. /// ENST00000295645 // intron // 0 // --- // --- // --- // ---	PDCL2	PDCL2, Homo sapiens phosducin-like 2 (PDCL2), q12
SNP_A-1718923	aaaacttcaaaactctgataaacaa[G/T]aactaaataacatgtt catggatag	G	T	NM_004898 // intron // 0 // Hs.436975 // CLOCK // 9575 // clock homolog (mouse)	CLOCK	CLOCK , rs2177127, clock homolog (mouse),q12
SNP_A-1945443	ttgttcaaaaacatca[A/T]ctattgtgattctggt	A	T	NM_006681 // intron // 0 // Hs.418367 // NMU // 10874 // Homo sapiens neuromedin U (NMU), mRNA. /// ENST00000264218 // intron // 0 // --- // --- // --- // ---	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-1946178	tttaaaaaaaaactgaa[A/G]gataacattcaatcca	A	G	NM_006681 // upstream // 70722 // Hs.418367 // NMU // 10874 // Homo sapiens neuromedin U (NMU), mRNA. /// NM_178237 // upstream // 146643 // Hs.269665 // SEC3L1 // 55763 // Homo sapiens SEC3-like 1 (S. cerevisiae) (SEC3L1), transcript variant 2, mRNA. ///	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-2009817	acctttcatcagcccc[C/G]cttctatctctgaaaa	C	G	NM_006681 // upstream // 86384 // Hs.418367 // NMU // 10874 // Homo sapiens neuromedin U (NMU), mRNA. /// NM_178237 // upstream // 130981 // Hs.269665 // SEC3L1 // 55763 // Homo sapiens SEC3-like 1 (S. cerevisiae) (SEC3L1), transcript variant 2, mRNA. ///	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-1671646	gtataagttttaaatgagtactata[A/T]gtgcttggaaatgaaaatc tgctgt	A	T	NM_006681 // upstream // 15828 // Hs.418367 // NMU // 10874 // neuromedin U /// NM_018261 // upstream // 201537 // Hs.221377 // SEC3L1 // 55763 // SEC3-like 1 (S. cerevisiae) /// NM_178237 // upstream // 201537 // Hs.221377 // SEC3L1 // 55763 // SEC3-lik	NMU	NMU , rs10517356, neuromedin U ,q12
SNP_A-1726312	aaactaagtttgtatctctgcttaa[A/G]taaccaagatgtgttgcatt tgaaa	A	G	NM_006681 // upstream // 16679 // Hs.418367 // NMU // 10874 // neuromedin U /// NM_018261 // upstream // 200686 // Hs.221377 // SEC3L1 // 55763 // SEC3-like 1 (S. cerevisiae) /// NM_178237 // upstream // 200686 // Hs.221377 // SEC3L1 // 55763 // SEC3-lik	NMU	NMU , rs1488939, neuromedin U ,q12
SNP_A-2009819	tctaatcgcttcttaa[A/G]ctaaccaatccaatcc	A	G	NM_006681 // upstream // 161589 // Hs.418367 // NMU // 10874 // Homo sapiens neuromedin U (NMU), mRNA. /// NM_178237 // upstream // 55776 // Hs.269665 // SEC3L1 // 55763 // Homo sapiens SEC3-like 1 (S. cerevisiae) (SEC3L1), transcript variant 2, mRNA. ///	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-1862953	tcattgcttggcacac[A/G]gtataagcattcaata	A	G	NM_006681 // upstream // 213351 // Hs.418367 // NMU // 10874 // Homo sapiens neuromedin U (NMU), mRNA. /// NM_178237 // upstream // 4014 // Hs.269665 // SEC3L1 // 55763 // Homo sapiens SEC3-like 1 (S. cerevisiae) (SEC3L1), transcript variant 2, mRNA. ///	NMU	NMU, Homo sapiens neuromedin U (NMU), q12
SNP_A-1670564	cagactgcttccactcccttctccc[A/G]aggactgagctctgtcat caactct	A	G	NM_006681 // upstream // 193373 // Hs.418367 // NMU // 10874 // neuromedin U /// NM_018261 // upstream // 23992 // Hs.221377 // SEC3L1 // 55763 // SEC3-like 1 (S. cerevisiae) /// NM_178237 // upstream // 23992 // Hs.221377 // SEC3L1 // 55763 // SEC3-like	NMU	NMU , rs722709, neuromedin U ,q12
SNP_A-2045210	aagaagccagttcaca[C/T]gaggccctaaggcttt	C	T	NM_025009 // downstream // 96076 // Hs.518767 // KIAA0635 // 9662 // Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000264222 // downstream // 168511 // --- // --- // --- // --- /// ENST00000257287 // downstream // 96076 // --- // --- // --- // --- ///	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-1663412	caaccacaaatattaaatacgtacc[G/T]cctagagttgaatgaa taagggcag	G	T	AB033037 // upstream // 233506 // Hs.205293 // KIAA1211 // 57482 // KIAA1211 protein /// NM_014645 // downstream // 48310 // - // - // - // -	KIAA1211	KIAA1211 , rs10517368, KIAA1211 protein ,q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1941164	ttgctgagtgcatacc[A/G]cagtgttcctgaatta	A	G	NM_025009 // downstream // 130309 // Hs.518767 // KIAA0635 // 9662 // Homo sapiens KIAA0635 (KIAA0635), mRNA. /// ENST00000264222 // downstream // 202744 // — // — // — // — /// ENST00000257287 // downstream // 130309 // — // — // — // — /	KIAA0635	KIAA0635, Homo sapiens KIAA0635 (KIAA0635), q12
SNP_A-2120346	agtcatcctttgtgcg[A/T]catcatttacaaagtt	A	T	ENST00000264229 // intron // 0 // — // — // — // —	-	q12
SNP_A-1977184	ttcgaagtctgaaaaa[C/T]tagattgcattaggat	C	T	NM_181806 // downstream // 9533 // Hs.104347 // AASDH // 132949 // Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), mRNA. /// ENST00000264229 // downstream // 943 // — // — // — // — /// ENST00000357062 // downstream // 9533 // -	AASDH	AASDH, Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), q12
SNP_A-2245954	ctgggtttgccaagaa[C/T]gtaaggtcctaactgc	C	T	NM_181806 // upstream // 2563 // Hs.104347 // AASDH // 132949 // Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), mRNA. /// NM_002703 // downstream // 3330 // Hs.331420 // PPAT // 5471 // Homo sapiens phosphoribosyl pyrophosphate amidotr	AASDH	AASDH, Homo sapiens 2-aminoadipic 6-semialdehyde dehydrogenase (NRPS998), q12
SNP_A-2153361	attagaagtttaagat[C/G]acttgaccccaaacct	C	G	NM_002703 // 3UTR // 0 // Hs.331420 // PPAT // 5471 // Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), mRNA. /// ENST00000264220 // 3UTR // 0 // — // — // — // —	PPAT	PPAT, Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), q12
SNP_A-2134716	atattaaacagcaatc[A/G]cattattttattcaat	A	G	NM_002703 // intron // 0 // Hs.331420 // PPAT // 5471 // Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), mRNA. /// ENST00000264220 // intron // 0 // — // — // — // —	PPAT	PPAT, Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), q12
SNP_A-1905110	tgggtgccaatatctc[A/T]acttcttaaagggatc	A	T	NM_002703 // intron // 0 // Hs.331420 // PPAT // 5471 // Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), mRNA. /// ENST00000264220 // intron // 0 // — // — // — // —	PPAT	PPAT, Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), q12
SNP_A-2196691	cattaatatgcttcaa[A/C]cttaatttcaatacat	A	C	NM_006947 // intron // 0 // Hs.237825 // SRP72 // 6731 // Homo sapiens signal recognition particle 72kDa (SRP72), mRNA. /// ENST00000340521 // intron // 0 // — // — // — // — /// ENST00000342756 // intron // 0 // — // — // — // —	SRP72	SRP72, Homo sapiens signal recognition particle 72kDa (SRP72), q12
SNP_A-2206950	ccatgtccccatgaag[A/T]ccgagatctcttgtcc	A	T	NM_206919 // intron // 0 // Hs.444449 // ARL9 // 132946 // Homo sapiens ADP-ribosylation factor-like 9 (ARL9), mRNA. /// ENST00000360096 // intron // 0 // — // — // — // —	ARL9	ARL9, Homo sapiens ADP-ribosylation factor-like 9 (ARL9), q12
SNP_A-1866398	tccccaactccttcca[C/T]agatgagtgatgcctg	C	T	ENST00000358277 // intron // 0 // — // — // — // —	-	q12
SNP_A-1935827	ttctgttctctctttc[G/T]cttgggaaaatagaga	G	T	ENST00000358277 // intron // 0 // — // — // — // —	-	q12
SNP_A-1953506	tttgaataacagtcat[A/G]aaatggtcatgggtca	A	G	NM_021114 // upstream // 2816 // Hs.98243 // SPINK2 // 6691 // Homo sapiens serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), mRNA. /// NM_005612 // upstream // 83329 // Hs.401145 // REST // 5978 // Homo sapiens RE1-silencing t	SPINK2	SPINK2, Homo sapiens serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), q12
SNP_A-1833309	tacacttctttgtgca[C/T]ggctcacaattcttct	C	T	NM_021114 // upstream // 45602 // Hs.98243 // SPINK2 // 6691 // Homo sapiens serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), mRNA. /// NM_005612 // upstream // 40543 // Hs.401145 // REST // 5978 // Homo sapiens RE1-silencing	SPINK2	SPINK2, Homo sapiens serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), q12
SNP_A-2292416	gcactaaatgtcactg[A/G]aggccctgaaaaaaaa	A	G	NM_000938 // downstream // 297739 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 218512 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977208	cacggcacataaagag[A/G]acagagtagacctggg	A	G	NM_000938 // downstream // 400833 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 321606 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2277718	gagcaggacttcata[A/C]gaagcttatctctc	A	C	NM_000938 // downstream // 435433 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 356206 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1848992	tatgcaggcaaataaa[C/T]gaacaaaatactcttc	C	T	NM_000938 // downstream // 443371 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 364144 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1977210	atagtatgtgcaatga[A/G]gggtacagagaagcta	A	G	NM_000938 // downstream // 546882 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 467655 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1977217	taggcttgaaaacatt[A/G]aaacagatggtgatac	A	G	NM_000938 // downstream // 629419 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 550192 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1977230	taatttctttacaaaa[A/C]ctgatagttactgata	A	C	NM_000938 // downstream // 703637 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 624410 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1977233	ttccttatcctaaaca[A/G]catctctttctatt	A	G	NM_000938 // downstream // 707315 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 628088 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1883815	tgaagaagccccttga[A/T]gctttgccctactgaa	A	T	NM_000938 // downstream // 743911 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 664684 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like growt	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1748103	cactttagaaaatagcaccatttaa[C/T]aatttcacaaaaggca gcaggtgct	C	T	NM_000938 // downstream // 705074 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 625869 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_015236	POLR2B	POLR2B , rs2048267, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12
SNP_A-1743107	agtagatttgaaaataaatctttcta[C/T]gaatgaatctaaagcgttt ctagat	C	T	NM_000938 // downstream // 758567 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 679362 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_015236	POLR2B	POLR2B , rs1509528, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12
SNP_A-1720039	gacactagtcttggcccactctata[C/G]aagtaagatcttgctag gcttgtat	C	G	NM_000938 // downstream // 760714 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 681509 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_015236	POLR2B	POLR2B , rs10517413, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977253	ttacatccaaaaata[C/T]catgtagcttgctcaa	C	T	NM_000938 // downstream // 1062588 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 983361 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like grow	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1661598	ctaaagtgttgtatatatacagaa[A/T]actgaaatgaacaagag ttcagtga	A	T	NM_000938 // downstream // 1470299 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 1391094 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs1986511, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12
SNP_A-1741995	ctccacagtaagtgagtttatttttc[C/T]acggtggctgagtttggtg ctattg	C	T	NM_000938 // downstream // 1605353 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 1526148 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs2282705, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12
SNP_A-2211205	ccctaaacatttctat[A/T]aacacaaatcacataa	A	T	NM_000938 // downstream // 1694631 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1615404 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2034355	aaatcgtcatggatat[A/G]aaattgaattgcatta	A	G	NM_000938 // downstream // 1694717 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1615490 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2139940	atctacatggttataa[A/C]tgatcgctcctactt	A	C	NM_000938 // downstream // 1727363 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1648136 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1860800	tcataatatattcaac[C/G]ctctatccagattaac	C	G	NM_000938 // downstream // 1728099 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1648872 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1977268	atggattaacataaaa[C/G]ctgacactgaaggcct	C	G	NM_000938 // downstream // 1735559 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1656332 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1939958	ttgcacttctgttttta[A/G]gtatggttgtatattt	A	G	NM_000938 // downstream // 1738644 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1659417 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-2184589	cagctcagaggagagt[A/T]aatgacaaagtatttt	A	T	NM_000938 // downstream // 1757978 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1678751 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1698825	atatttcgtgatatttcccagaaagc[A/C]gcatagtgggtaaaatct tccatttt	A	C	NM_000938 // downstream // 1702188 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 1622983 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs6843409, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1865925	tcccaatttctcact[A/T]aacttcaaataca gc	A	T	NM_000938 // downstream // 1805733 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1726506 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1932741	ttccttcttattctga[C/T]aaccatttgaataca	C	T	NM_000938 // downstream // 1910059 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1830832 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q12
SNP_A-1785197	ggctaatcctccctca[A/C]ataaaatggaatttct	A	C	NM_000938 // downstream // 1980412 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1901185 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2133942	atatctggacaagag a[A/G]gccaggcagatggaac	A	G	NM_000938 // downstream // 2007188 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 1927961 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1799680	gtaatttgcatttaa[A/G]ggttcaggcaatggag	A	G	NM_000938 // downstream // 2248342 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2169115 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2252801	cttctacagtcagaga[C/T]acagtgtaaagaaaac	C	T	NM_000938 // downstream // 2275151 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2195924 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1944870	ttgtggaagtattgga[A/G]tatagatgtatatatt	A	G	NM_000938 // downstream // 2275267 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2196040 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2160294	atttcagactggtgta[C/T]gaaagtaatgataagg	C	T	NM_000938 // downstream // 2524181 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2444954 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1821871	gttttagttaaaagaa[A/G]atggtcactgtgtttg	A	G	NM_000938 // downstream // 2621351 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2542124 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2093117	agaacatatgcaatta[A/G]caaacttaaacattag	A	G	NM_000938 // downstream // 2629063 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2549836 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1833060	tacacagatgatggaa[A/G]gaaccacacaactta	A	G	NM_000938 // downstream // 2646783 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2567556 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2065547	aatttaaggcagaccc[C/G]aaagtttgttgtctt	C	G	NM_000938 // downstream // 2651733 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2572506 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2052514	aagtaggagagaaaac[A/G]gtaggtaagaaagcaa	A	G	NM_000938 // downstream // 2656027 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2576800 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2255764	ctgtttacaggcata[C/T]gttgagtgttgaacat	C	T	NM_000938 // downstream // 2663133 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 2583906 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2040741	aaccccagagagtctgc[C/T]aaccggctctagaac	C	T	NM_000938 // downstream // 3587578 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3508351 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2254413	cttgtcatgcacaaca[C/T]tcttgtcatgcacaac	C	T	NM_000938 // downstream // 3624506 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3545279 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1894069	tgcatcttttagagc[C/G]catgacagagcagagc	C	G	NM_000938 // downstream // 3634776 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3555549 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2253665	cttctttgttctgca[A/T]aatatcigtgggattt	A	T	NM_000938 // downstream // 3770448 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3691221 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1875576	tctctgtttgtaaaat[A/C]agtaagtgctcattgt	A	C	NM_000938 // downstream // 3786492 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3707265 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2054220	aagttgaagacacaga[C/T]ggaataaaatagtggt	C	T	NM_000938 // downstream // 3858629 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3779402 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1977327	cagtatcctacagctg[C/G]aacatagtctcaggag	C	G	NM_000938 // downstream // 3864907 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3785680 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1669269	atacgctttaaataacatgctgact[C/T]aaccaatgaatgtgac tacctgg	C	T	NM_000938 // downstream // 3872999 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 3793794 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs725264, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1879898	tcttcctaaatcacaa[C/G]tacgattatctctctc	C	G	NM_000938 // downstream // 4020260 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3941033 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1895982	tgccttctagacttaa[A/G]gttagctcctctgcc	A	G	NM_000938 // downstream // 4025058 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3945831 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2163192	attttctcctcaca[A/G]tatttactctaagat	A	G	NM_000938 // downstream // 4039575 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 3960348 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2143666	atgagaaaaatgttca[C/T]gagtacagatttgtt	C	T	NM_000938 // downstream // 4115151 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 4035924 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-2311821	ggaatttccaggataat[C/T]atcagttacatgaaag	C	T	NM_000938 // downstream // 4128219 // Hs.479814 // POLR2B // 5431 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA. /// NM_001553 // upstream // 4048992 // Hs.479808 // IGFBP7 // 3490 // Homo sapiens insulin-like gro	POLR2B	POLR2B, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), q13.1
SNP_A-1745458	aaggtatattactagtaagtgaaca[A/G]tggagttaaaattatgtc ctcaatt	A	G	NM_000938 // downstream // 4082248 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 4003043 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs2129267, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-2157259	attgacatcatattac[A/G]agcccaccttgaagg	A	G	AF307080 // intron // 0 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // — // — // — /// ENST00000295349 // intron // 0 // — // — // — // —	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-2212113	ccctgcctacactaac[C/T]gtgagctatttcaaat	C	T	AF307080 // intron // 0 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// ENST00000355061 // intron // 0 // — // — // — // — // — /// ENST00000295349 // intron // 0 // — // — // — // —	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-1712487	caaaaaattgatggaaatatagga a[A/G]acaactaaggtctact tggtgtatg	A	G	NM_000938 // downstream // 4138358 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 4059153 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs1486506, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-1644932	gaaagtaaatgtttcaaagagaaaag[C/T]aatagtattaagtgttg cagagaga	C	T	NM_000938 // downstream // 4235063 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 4155858 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs1449613, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-1757541	cccattcatttattttggtatgcata[G/T]agttagtttaccttccaggat ttgc	G	T	NM_000938 // downstream // 4235828 // Hs.149353 // POLR2B // 5431 // polymerase (RNA) II (DNA directed) polypeptide B, 140kDa /// NM_001553 // upstream // 4156623 // Hs.435795 // IGFBP7 // 3490 // insulin-like growth factor binding protein 7 /// NM_01523	POLR2B	POLR2B , rs4146080, polymerase (RNA) II (DNA directed) polypeptide B, 140kDa ,q13.1
SNP_A-1739771	taccctctccacaattggaaccccca[A/G]atcggcaaacatagc aaaggaccat	A	G	NM_015236 // intron // 0 // Hs.21917 // LPHN3 // 23284 // latrophilin 3	LPHN3	LPHN3 , rs10517529, latrophilin 3,q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084017	actagagagatgtaacd[A/G]aggcagattgtgatgg	A	G	AF307080 // intron // 0 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// NM_015236 // intron // 0 // Hs.411097 // LPHN3 // 23284 // Homo sapiens latrophilin 3 (LPHN3), mRNA. /// ENST00000355061 // intron // 0 // — // — //	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-2268215	gaatgacttagagaga[A/G]gtaaatccaatcatat	A	G	AF307080 // intron // 0 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// NM_015236 // intron // 0 // Hs.411097 // LPHN3 // 23284 // Homo sapiens latrophilin 3 (LPHN3), mRNA. /// ENST00000355061 // intron // 0 // — // — //	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-1827594	taactgcagcaacagg[A/G]agtacttttagcagct	A	G	AF307080 // intron // 0 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// NM_015236 // intron // 0 // Hs.411097 // LPHN3 // 23284 // Homo sapiens latrophilin 3 (LPHN3), mRNA. /// ENST00000355061 // intron // 0 // — // — //	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-1909373	tgtattactctggctc[C/T]gagattctacattcta	C	T	AF307080 // intron // 0 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// NM_015236 // intron // 0 // Hs.411097 // LPHN3 // 23284 // Homo sapiens latrophilin 3 (LPHN3), mRNA. /// ENST00000355061 // intron // 0 // — // — //	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-2277676	gagcagagtcaccaac[A/G]cgcagcaaagaaggata	A	G	AF307080 // downstream // 14072 // — // — // 0 // Homo sapiens lectomedin-3 (LEC3) mRNA, complete cds. /// NM_015236 // downstream // 14084 // Hs.411097 // LPHN3 // 23284 // Homo sapiens latrophilin 3 (LPHN3), mRNA. /// ENST00000355061 // downstream /	-	-, Homo sapiens lectomedin-3 (LEC3) complete cds. q13.1
SNP_A-1798865	gtaagaaactactaaa[C/T]tgttccaaagtggctg	C	T	ENST00000273844 // upstream // 262247 // — // — // — /// ENST00000360919 // upstream // 2809512 // — // — // — // —	-	q13.1
SNP_A-1947911	tttagaaacatagagc[A/G]acatcattaaatctt	A	G	ENST00000273844 // upstream // 271649 // — // — // — /// ENST00000360919 // upstream // 2800110 // — // — // — // —	-	q13.1
SNP_A-1815759	gttaagataatccaaa[G/T]attgctgttttcct	G	T	ENST00000273844 // upstream // 283252 // — // — // — /// ENST00000360919 // upstream // 2788507 // — // — // — // —	-	q13.1
SNP_A-1843112	tagtcacacttaaaac[A/G]aaaacaactatgaat	A	G	ENST00000273844 // upstream // 687711 // — // — // — /// ENST00000360919 // upstream // 2384048 // — // — // — // —	-	q13.1
SNP_A-1896345	tgctaaccaagtaaaa[A/G]gtcctgaagaagcag	A	G	ENST00000273844 // upstream // 687892 // — // — // — /// ENST00000360919 // upstream // 2383867 // — // — // — // —	-	q13.1
SNP_A-2024625	aaaaggtcgctataa[A/T]gcatttcatatggact	A	T	ENST00000273844 // upstream // 953070 // — // — // — /// ENST00000360919 // upstream // 2118689 // — // — // — // —	-	q13.1
SNP_A-1977375	atgacccaaaaatagca[A/G]acgcaacattcagaga	A	G	ENST00000273844 // upstream // 961891 // — // — // — /// ENST00000360919 // upstream // 2109868 // — // — // — // —	-	q13.1
SNP_A-1783257	ggcagtactctcagca[C/T]gaacacgttagagggt	C	T	ENST00000273844 // upstream // 1063076 // — // — // — /// ENST00000360919 // upstream // 2008683 // — // — // — // —	-	q13.1
SNP_A-2026049	aaaattaattgcaaga[C/G]aaacaaaaatttacaa	C	G	ENST00000273844 // upstream // 1174228 // — // — // — /// ENST00000360919 // upstream // 1897531 // — // — // — // —	-	q13.1
SNP_A-2133307	atatatatccactgg[C/T]catatcattgaggaat	C	T	ENST00000273844 // upstream // 1343608 // — // — // — /// ENST00000360919 // upstream // 1728151 // — // — // — // —	-	q13.1
SNP_A-2177176	cacctgatcaaaccaa[A/T]ctgtgggctctacata	A	T	ENST00000273844 // upstream // 2024913 // — // — // — /// ENST00000360919 // upstream // 1046846 // — // — // — // —	-	q13.1
SNP_A-1915580	tgttctcaatggttca[A/T]agttctcaatgacttg	A	T	ENST00000273844 // upstream // 2420427 // — // — // — /// ENST00000360919 // upstream // 651332 // — // — // — // —	-	q13.1
SNP_A-1883339	tgaacaagttggtcat[A/C]aagtttgtcaaacac	A	C	ENST00000273844 // upstream // 2709423 // — // — // — /// ENST00000360919 // upstream // 362336 // — // — // — // —	-	q13.1
SNP_A-2157087	attgaaagaaaactga[C/G]agtactgctctcacct	C	G	ENST00000273844 // upstream // 2747904 // — // — // — /// ENST00000360919 // upstream // 323855 // — // — // — // —	-	q13.1
SNP_A-2066406	aatttttggagttagaa[A/G]gaactgagttgacaac	A	G	ENST00000273844 // upstream // 2768620 // — // — // — /// ENST00000360919 // upstream // 303139 // — // — // — // —	-	q13.1
SNP_A-2268543	gaatggtagaggaaag[A/G]ccatcattatcataaa	A	G	ENST00000273844 // upstream // 2830164 // — // — // — /// ENST00000360919 // upstream // 241595 // — // — // — // —	-	q13.1
SNP_A-1843768	tagtgttggtgaaaaa[A/T]cctgcttttcagcatg	A	T	ENST00000273844 // upstream // 2835681 // — // — // — /// ENST00000360919 // upstream // 236078 // — // — // — // —	-	q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829735	taagttttttcatcct[C/G]agactctaaggttag	C	G	ENST00000273844 // upstream // 2847739 /// ENST00000360919 // upstream // 224020 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 502150 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 2749329 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2030715	aaagctggttcgcaac[C/G]acaagccaacacagcc	C	G	ENST00000273844 // upstream // 2847919 /// ENST00000360919 // upstream // 223840 /// NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	-	q13.1
SNP_A-2310754	ggaagcagagggtaga[A/C]cagttattcgatgag	A	C	ENST00000273844 // upstream // 2859263 /// ENST00000360919 // upstream // 212496 /// NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	-	q13.1
SNP_A-1977413	cagtgaaacagtctac[C/T]ataatctactgaccc	C	T	ENST00000273844 // upstream // 2880828 /// ENST00000360919 // upstream // 190931 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1977415	tttccagaggattca[A/G]gaacagagtaactca	A	G	ENST00000273844 // upstream // 2881362 /// ENST00000360919 // upstream // 190397 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1977417	gaattgaatattgagg[A/G]agaaacaacttatata	A	G	ENST00000273844 // upstream // 2881606 /// ENST00000360919 // upstream // 190153 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1819819	gttgtgcaatcactgc[C/T]agtagttccaaaacat	C	T	ENST00000273844 // upstream // 2883185 /// ENST00000360919 // upstream // 188574 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1655249	tccttgtccttatcacgggtatg[A/G]aatactaataattgacac ttttgca	A	G	BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 502150 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 2749329 // Hs.21917 // LPHN3 // 23284 // latrophil	-	-, rs2349110, Clone IMAGE:4429392, mRNA, partial cds ,q13.1
SNP_A-2262299	gaaatgaagacatagg[A/G]aaaaaccacatcatta	A	G	ENST00000273844 // upstream // 2906882 /// ENST00000360919 // upstream // 164877 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2240865	ctgactcaagtgccaa[A/C]gactaatttatgggg	A	C	ENST00000273844 // upstream // 2906951 /// ENST00000360919 // upstream // 164808 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2048189	aagcactaaacagata[A/G]gctcaaggtatttta	A	G	ENST00000273844 // upstream // 2908508 /// ENST00000360919 // upstream // 163251 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1781631	ggattgattgttacta[A/T]cctcactgtattatac	A	T	ENST00000273844 // upstream // 2915060 /// ENST00000360919 // upstream // 156699 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1823883	taaaatgtctgataaa[C/T]ccaattgcagaaatta	C	T	ENST00000273844 // upstream // 2922462 /// ENST00000360919 // upstream // 149297 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2151040	atgtgtatctccctga[A/G]gattagcataggaag	A	G	ENST00000273844 // upstream // 2922528 /// ENST00000360919 // upstream // 149231 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2195351	catggctcttcaggac[A/G]ggctaattgatcagga	A	G	ENST00000273844 // upstream // 2923343 /// ENST00000360919 // upstream // 148416 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2152739	attaatgctcatgctg[C/T]agaaaaagatgcaaagg	C	T	ENST00000273844 // upstream // 2923818 /// ENST00000360919 // upstream // 147941 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-1924253	ttataaaacatcaaca[C/T]tctgtttaccattgca	C	T	ENST00000273844 // upstream // 2923884 /// ENST00000360919 // upstream // 147875 /// BC017721 // upstream // 848183 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 468370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	q13.1
SNP_A-2126062	agttttggacaatttc[C/T]aatacactgcataatt	C	T	NM_182472 // 3UTR // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// ENST00000354839 // 3UTR // 0 // — // — // —	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2075025	acatccagtcaccaaa[A/C]actgtatatttgacta	A	C	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2046208	aagacttgaataaagt[C/G]aagggcaatttagagg	C	G	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1685174	catgattatgctagaaaacctgata[C/T]agttgttaaatggttgtac tgagaa	C	T	BC017721 // upstream // 414403 // Hs.507580 // - // - // Clone IMAGE:4429392, mRNA, partial cds /// NM_004439 // downstream // 68370 // Hs.201920 // EPHA5 // 2044 // EPHA5 /// NM_015236 // downstream // 3183109 // Hs.21917 // LPHN3 // 23284 // latrophil	-	-, rs1514269, Clone IMAGE:4429392, mRNA, partial cds ,q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939833	ttgcaatcaccaacta[A/C]atccaaattgggcagt	A	C	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2194032	catgaattcattcca[C/G]atacaaagttgtct	C	G	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2009859	aaaaatctaaagatcc[A/C]accaggtccatgaggt	A	C	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1847465	tatcctccagctggtg[C/T]atattgtcaaaacagg	C	T	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2147147	atggaaatcaagctag[A/T]cattaagcatacactg	A	T	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2282851	gataaagtagtggagt[A/C]aaagtgatacagaaca	A	C	NM_182472 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // intron // 0 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000354839 //	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-2132574	atagttaaggtaaaaa[C/T]gtcacataatgctta	C	T	NM_182472 // upstream // 3723 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 3674 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST00000	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1814481	gtgtgcagttgtcccat[C/T]ggcctttggtcaagta	C	T	NM_182472 // upstream // 33396 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 33347 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST000	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.1
SNP_A-1910193	tgtcattatgacaggga[A/G]atatacgtatgaaata	A	G	NM_182472 // upstream // 181012 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 180963 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST0	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2
SNP_A-1949169	tttatggatgacttaa[A/G]tgtcctcagaaataca	A	G	NM_182472 // upstream // 221817 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 221768 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST0	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2
SNP_A-1938195	ttgacatttaatcag[A/G]ctgactgcaagcgaac	A	G	NM_182472 // upstream // 222006 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 221957 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST0	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977435	ggtattataaatattg[C/G]aacagtgacttatatg	C	G	NM_182472 // upstream // 222661 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 2, mRNA. /// NM_004439 // upstream // 222612 // Hs.479853 // EPHA5 // 2044 // Homo sapiens EphA5 (EPHA5), transcript variant 1, mRNA. /// ENST0	EPHA5	EPHA5, Homo sapiens EphA5 (EPHA5), transcript variant 2, q13.2
SNP_A-2060391	aatgaattagtcttaa[A/G]tcagaagctttattt	A	G	NM_001812 // downstream // 1154284 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 223679 // — // — // — /// ENST00000273853 // downstream // 1154284 // — // — //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-1977442	ccacatgttgcgcac[A/G]cagtttcctctgctgc	A	G	NM_001812 // downstream // 1138172 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 239791 // — // — // — /// ENST00000273853 // downstream // 1138172 // — // — //	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2114876	agggcagaattagaga[C/T]acctggtctaacatc	C	T	NM_001812 // downstream // 990014 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 387949 // — // — // — /// ENST00000273853 // downstream // 990014 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2176511	cacccacaaaccataa[C/G]aaatgatggctatgtt	C	G	NM_001812 // downstream // 652595 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 725368 // — // — // — /// ENST00000273853 // downstream // 652595 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2045272	aagaaggctggaaaaa[C/T]atgacccctcaaaaaa	C	T	NM_001812 // downstream // 652429 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 725534 // — // — // — /// ENST00000273853 // downstream // 652429 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2088668	actgtgcctgactcaa[C/T]ttcagcctcatatac	C	T	NM_001812 // downstream // 511545 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 866418 // — // — // — /// ENST00000273853 // downstream // 511545 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2191602	catatgtatatactga[G/T]gacaaagaggaagaga	G	T	NM_001812 // downstream // 410640 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 967323 // — // — // — /// ENST00000273853 // downstream // 410640 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-1714719	agcatacacggtctttaagcaagc[A/G]ccgttttcactctttgc cttcta	A	G	NM_001812 // downstream // 578942 // Hs.388457 // CENPC1 // 1060 // centromere protein C 1 /// NM_004439 // upstream // 1223745 // Hs.201920 // EPHA5 // 2044 /// NM_182472 // upstream // 1223745 // Hs.201920 // EPHA5 // 2044 // EphA5	CENPC1	CENPC1 , rs1481253, centromere protein C 1 ,q13.2
SNP_A-1820387	gttagtttagtggca[A/C]tgattaataaggcca	A	C	NM_001812 // downstream // 377440 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 1000523 // — // — // — /// ENST00000273853 // downstream // 377440 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2146997	atggaacacggagaa[C/T]gatggaactgcagggc	C	T	NM_001812 // downstream // 367023 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 1010940 // — // — // — /// ENST00000273853 // downstream // 367023 // — // — // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084322	actataaatgaatagg[A/G]ccaacataaaacgata	A	G	NM_001812 // downstream // 352707 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 1025256 // --- // --- // --- /// ENST00000273853 // downstream // 352707 // --- // --- // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-1977468	tggagaaatatgaaccf[A/T]gaaactagtataatac	A	T	NM_001812 // downstream // 282173 // Hs.479867 // CENPC1 // 1060 // Homo sapiens centromere protein C 1 (CENPC1), mRNA. /// ENST00000257675 // downstream // 1095790 // --- // --- // --- /// ENST00000273853 // downstream // 282173 // --- // --- // -	CENPC1	CENPC1, Homo sapiens centromere protein C 1 (CENPC1), q13.2
SNP_A-2039712	aacatggtttcaaac[A/G]cacagttccatttata	A	G	NM_018227 // intron // 0 // Hs.212774 // FLJ10808 // 55236 // Homo sapiens hypothetical protein FLJ10808 (FLJ10808), mRNA. /// ENST00000322244 // intron // 0 // --- // --- // ---	FLJ10808	FLJ10808, Homo sapiens hypothetical protein FLJ10808 (FLJ10808), q13.2
SNP_A-1853375	tatttcatcagtctat[C/T]accgtgaggagtggtg	C	T	NM_018227 // upstream // 28510 // Hs.212774 // FLJ10808 // 55236 // Homo sapiens hypothetical protein FLJ10808 (FLJ10808), mRNA. /// NM_000406 // downstream // 10830 // Hs.407587 // GNRHR // 2798 // Homo sapiens gonadotropin-releasing hormone receptor (GN	FLJ10808	FLJ10808, Homo sapiens hypothetical protein FLJ10808 (FLJ10808), q13.2
SNP_A-1723790	aaaacttttctgtaaaggtcagat[C/G]agtaaacaatttcagctt tataggc	C	G	NM_018227 // intron // 0 // Hs.59838 // FLJ10808 // 55236 // hypothetical protein FLJ10808	FLJ10808	FLJ10808, rs719391, hypothetical protein FLJ10808.q13.2
SNP_A-1658928	ctaatcacttagagtccataaatac[C/T]gcataggattaaggtt tgcttct	C	T	NM_018227 // intron // 0 // Hs.59838 // FLJ10808 // 55236 // hypothetical protein FLJ10808	FLJ10808	FLJ10808, rs1038428, hypothetical protein FLJ10808.q13.2
SNP_A-1977508	aaaaactgggaatgga[A/G]gtaccagcagattat	A	G	NM_024743 // upstream // 45670 // Hs.122583 // FLJ21934 // 79799 // Homo sapiens hypothetical protein FLJ21934 (FLJ21934), mRNA. /// NM_001073 // downstream // 7162 // Hs.339811 // UGT2B11 // 10720 // Homo sapiens UDP glycosyltransferase 2 family, polypep	FLJ21934	FLJ21934, Homo sapiens hypothetical protein FLJ21934 (FLJ21934), q13.2
SNP_A-2201297	ccaataggctatagaa[C/T]gatgccaacacataat	C	T	NM_001073 // intron // 0 // Hs.339811 // UGT2B11 // 10720 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11). mRNA. /// ENST00000305206 // intron // 0 // --- // --- // ---	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2
SNP_A-1856825	tcacattgctgtacaa[A/C]aagtctctataatttt	A	C	NM_001073 // intron // 0 // Hs.339811 // UGT2B11 // 10720 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11). mRNA. /// ENST00000305206 // intron // 0 // --- // --- // ---	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2
SNP_A-2272872	gactaatgtctctcta[A/C]attgcataaaactaag	A	C	NM_001073 // intron // 0 // Hs.339811 // UGT2B11 // 10720 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11). mRNA. /// ENST00000305206 // intron // 0 // --- // --- // ---	UGT2B11	UGT2B11, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11), q13.2
SNP_A-2227740	ctaccaatccagaagc[A/G]gctaggtcacatttct	A	G	NM_053039 // downstream // 137954 // Hs.137585 // UGT2B28 // 54490 // Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), mRNA. /// NM_021139 // downstream // 47164 // Hs.285887 // UGT2B4 // 7363 // Homo sapiens UDP glycosyltransfera	UGT2B28	UGT2B28, Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), q13.2
SNP_A-2208610	cccactgaatggcaag[G/T]ctaaaagaaglgctgt	G	T	NM_014465 // upstream // 23419 // Hs.129742 // SULT1B1 // 27284 // Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA. /// NM_005420 // downstream // 57087 // Hs.479898 // SULT1E1 // 6783 // Homo sapiens sulfotransferase family	SULT1B1	SULT1B1, Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), q13.3
SNP_A-1939134	ttgatactaaatctccf[A/G]ccatctgccatacaa	A	G	NM_001891 // upstream // 7715 // Hs.2242 // CSN2 // 1447 // Homo sapiens casein beta (CSN2), mRNA. /// NM_003154 // upstream // 27245 // Hs.37048 // STATH // 6779 // Homo sapiens statherin (STATH), mRNA. /// ENST00000353151 // upstream // 7715 // --- // -	CSN2	CSN2, Homo sapiens casein beta (CSN2), q13.3
SNP_A-1752741	aaatctctattgaagtactttttcaa[C/T]atagacattaaaattgctg cagtaa	C	T	NM_017855 // upstream // 2455 // Hs.143811 // APIN // 54959 // APin protein /// NM_173085 // downstream // 110856 // - // - // - // -	APIN	APIN , rs1383436, APin protein, q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1731755	gttttccatattaatatgatgatta[C/T]actagtttgcattcatttttaaaag	C	T	NM_017855 // intron // 0 // Hs.143811 // APIN // 54959 // APin protein	APIN	APIN , rs10518073, APin protein,q13.3
SNP_A-1977534	aaatgatgaactagga[A/G]tagtgcacaggtgata	A	G	NM_021225 // downstream // 48155 // Hs.479905 // PROL1 // 58503 // Homo sapiens proline rich 1 (PROL1), mRNA. /// NM_152291 // upstream // 13870 // Hs.103944 // MUC7 // 4589 // Homo sapiens mucin 7, salivary (MUC7), mRNA. /// ENST00000304904 // downstream	PROL1	PROL1, Homo sapiens proline rich 1 (PROL1), q13.3
SNP_A-2279423	gaggataaagccacca[C/T]gaaatataaaaacata	C	T	NM_020368 // downstream // 18971 // Hs.322901 // SAS10 // 57050 // Homo sapiens disrupter of silencing 10 (SAS10), mRNA. /// NM_014961 // upstream // 12457 // Hs.7972 // RIPX // 22902 // Homo sapiens rap2 interacting protein x (RIPX), mRNA. /// ENST000002	SAS10	SAS10, Homo sapiens disrupter of silencing 10 (SAS10), q13.3
SNP_A-2024667	aaaagtaacctcagac[A/G]acataacaacaaacca	A	G	NM_014961 // intron // 0 // Hs.7972 // RIPX // 22902 // Homo sapiens rap2 interacting protein x (RIPX), mRNA. /// ENST00000226328 // intron // 0 // --- // --- // ---	RIPX	RIPX, Homo sapiens rap2 interacting protein x (RIPX), q13.3
SNP_A-1707151	atttaatttggataagtatttagga[A/G]tattatcctgagttgatgtatttta	A	G	NM_002092 // downstream // 3804 // Hs.309763 // GRSF1 // 2926 // G-rich RNA sequence binding factor 1 /// NM_014961 // downstream // 22173 // Hs.7972 // RIPX // 22902 // rap2 interacting protein x	GRSF1	GRSF1 , rs2362330, G-rich RNA sequence binding factor 1 ,q13.3
SNP_A-2294811	gcagtttatcaattca[A/G]aacaagtcaggatatt	A	G	NM_000788 // downstream // 62678 // Hs.709 // DCK // 1633 // Homo sapiens deoxycytidine kinase (DCK), mRNA. /// NM_003759 // upstream // 245526 // Hs.5462 // SLC4A4 // 8671 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member	DCK	DCK, Homo sapiens deoxycytidine kinase (DCK), q13.3
SNP_A-1742409	ccctagcaatttgtctcaaatttca[C/T]gcataggatcaaaagaaaatgtttt	C	T	NM_000788 // intron // 0 // Hs.709 // DCK // 1633 // deoxycytidine kinase	DCK	DCK , rs10518080, deoxycytidine kinase,q13.3
SNP_A-1683674	aacatatgattctcttcaaaaacaa[A/G]tagcagtcaataaagtaggaatttc	A	G	NM_000788 // intron // 0 // Hs.709 // DCK // 1633 // deoxycytidine kinase	DCK	DCK , rs936868, deoxycytidine kinase,q13.3
SNP_A-2009879	taaacattacacttca[A/G]tctttgttcatgtgca	A	G	NM_003759 // intron // 0 // Hs.5462 // SLC4A4 // 8671 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), mRNA. /// ENST00000264485 // intron // 0 // — // — // — // --- /// ENST00000351898 // intron // 0 //	SLC4A4	SLC4A4, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), q13.3
SNP_A-2155365	attcatcatcttattc[A/G]cacagttattatgtat	A	G	NM_003759 // downstream // 77891 // Hs.5462 // SLC4A4 // 8671 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), mRNA. /// NM_000583 // downstream // 91723 // Hs.418497 // GC // 2638 // Homo sapiens group-specifi	SLC4A4	SLC4A4, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 4 (SLC4A4), q13.3
SNP_A-2091737	agaaaaggctgatttc[A/G]atgacaggaactctat	A	G	NM_000583 // upstream // 88791 // Hs.418497 // GC // 2638 // Homo sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// NM_053036 // upstream // 158842 // Hs.99231 // GPR74 // 10886 // Homo sapiens G protein-coupled receptor 74 (GPR	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-2204981	ccagggtatcttcaaa[A/G]tatttcccgcttataa	A	G	NM_000583 // upstream // 117590 // Hs.418497 // GC // 2638 // Homo sapiens group-specific component (vitamin D binding protein) (GC), mRNA. /// NM_053036 // upstream // 130043 // Hs.99231 // GPR74 // 10886 // Homo sapiens G protein-coupled receptor 74 (GP	GC	GC, Homo sapiens group-specific component (vitamin D binding protein) (GC), q13.3
SNP_A-1676504	gatcaagtggcaataaattagtaaa[A/T]gtcatgcaaacaaaagcaaatgatt	A	T	NM_000583 // upstream // 185144 // Hs.418497 // GC // 2638 // group-specific component (vitamin D binding protein) /// NM_004885 // upstream // 62489 // Hs.99231 // GPR74 // 10886 // G protein-coupled receptor 74 /// NM_053036 // upstream // 70059 // Hs.	GC	GC , rs10518093, group-specific component (vitamin D binding protein) ,q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2272244	gacctcagcgagatta[C/T]agactggtggagaaat	C	T	NM_014243 // intron // 0 // Hs.151435 // ADAMTS3 // 9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// ENST00000286657 // intron // 0 // — // — // — // —	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-2129055	ataattatatccaaaa[A/G]tgtctgccgtgtggta	A	G	NM_014243 // intron // 0 // Hs.151435 // ADAMTS3 // 9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// ENST00000286657 // intron // 0 // — // — // — // —	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-1808324	gtcttttcctgggtat[A/C]aggtgtactcctgggt	A	C	NM_014243 // upstream // 147964 // Hs.151435 // ADAMTS3 // 9508 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), mRNA. /// NM_173827 // downstream // 339324 // Hs.356697 // FLJ38991 //	ADAMTS3	ADAMTS3, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3 (ADAMTS3), q13.3
SNP_A-1726528	aaaatatctagagacattggaggac[A/C]actatctataaaattaaggcataga	A	C	NM_002704 // upstream // 3774 // Hs.2164 // PPBP // 5473 // pro-platelet basic protein (chemokine (C-X-C motif) ligand 7) /// NM_002994 // downstream // 4669 // Hs.89714 // CXCL5 // 6374 // chemokine (C-X-C motif) ligand 5	PPBP	PPBP , rs409336, pro-platelet basic protein (chemokine (C-X-C motif) ligand 7) ,q13.3
SNP_A-1844379	tataaaatgcaagaca[A/G]agttcagatgttttta	A	G	ENST00000359107 // intron // 0 // — // — // — // — /// ENST00000331145 // intron // 0 // — // — // — // —	-	q13.3
SNP_A-2107379	agctacagaacacggt[A/G]accatacacacttggc	A	G	NM_001657 // downstream // 63725 // Hs.270833 // AREG // 374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 254567 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ4479	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-1729222	tgaatgctgcagtgagtaatttcta[C/T]gcatattgttctgaaccatagtttg	C	T	NM_001657 // downstream // 29078 // Hs.270833 // AREG // 374 // amphiregulin (schwannoma-derived growth factor) /// NM_001729 // downstream // 313789 // Hs.73105 // BTC // 685 // betacellulin	AREG	AREG , rs1246396, amphiregulin (schwannoma-derived growth factor) ,q13.3
SNP_A-1706997	tgtttctcaaaacaaaatcaaaatt[C/G]aactatcatatgatcaagcaatacc	C	G	NM_001657 // downstream // 57212 // Hs.270833 // AREG // 374 // amphiregulin (schwannoma-derived growth factor) /// NM_001729 // downstream // 285655 // Hs.73105 // BTC // 685 // betacellulin	AREG	AREG , rs1908423, amphiregulin (schwannoma-derived growth factor) ,q13.3
SNP_A-2278906	gaggaaactcatgcta[A/C]atgaaaaaccaacaag	A	C	NM_001657 // downstream // 195265 // Hs.270833 // AREG // 374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 123027 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ447	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-2283655	gatagatcaaaaactc[A/G]gaagagacaaagctcg	A	G	NM_001657 // downstream // 271088 // Hs.270833 // AREG // 374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 47204 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ4479	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-2294869	gcataaaattctgtca[A/G]tctgttaaacttgtaa	A	G	NM_001657 // downstream // 300732 // Hs.270833 // AREG // 374 // Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /// NM_001001704 // downstream // 17560 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ4479	AREG	AREG, Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), q13.3
SNP_A-1893783	tgcagttccttccatc[A/G]agagacggagtcaatt	A	G	NM_001001704 // upstream // 7299 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// NM_001729 // downstream // 14787 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// ENST00000354875 // upstream	FLJ44796	FLJ44796, Homo sapiens FLJ44796 protein (FLJ44796), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977623	cctgaagtcaaccaca[A/G]gaatggtgagtctgg	A	G	NM_001729 // upstream // 464 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 684709 // Hs.48297 // RCHY1 // 25898 // Homo sapiens ring finger and CHY zinc finger domain containing 1 (RCHY1), mRNA. /// ENS	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-2009895	agaagacatgaagagg[A/C]aattcatgaagtagaa	A	C	NM_001729 // upstream // 43496 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 641677 // Hs.48297 // RCHY1 // 25898 // Homo sapiens ring finger and CHY zinc finger domain containing 1 (RCHY1), mRNA. /// E	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-2040153	aaccaagatatgaca[C/T]gatattgtcaggtta	C	T	NM_001729 // upstream // 340442 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 344731 // Hs.48297 // RCHY1 // 25898 // Homo sapiens ring finger and CHY zinc finger domain containing 1 (RCHY1), mRNA. ///	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-1831845	taattctccatcttaa[C/T]attctcatgccacat	C	T	NM_001729 // upstream // 495109 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 190064 // Hs.48297 // RCHY1 // 25898 // Homo sapiens ring finger and CHY zinc finger domain containing 1 (RCHY1), mRNA. ///	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-1781116	ggatgctggccaggcc[A/G]aaataatagatgccca	A	G	NM_001729 // upstream // 495227 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 189946 // Hs.48297 // RCHY1 // 25898 // Homo sapiens ring finger and CHY zinc finger domain containing 1 (RCHY1), mRNA. ///	BTC	BTC, Homo sapiens betacellulin (BTC), q13.3
SNP_A-1815131	gtgttctctgctttga[C/G]gtttggccaaaatcct	C	G	NM_001729 // upstream // 556588 // Hs.73105 // BTC // 685 // Homo sapiens betacellulin (BTC), mRNA. /// NM_015436 // downstream // 128585 // Hs.48297 // RCHY1 // 25898 // Homo sapiens ring finger and CHY zinc finger domain containing 1 (RCHY1), mRNA. ///	BTC	BTC, Homo sapiens betacellulin (BTC), q21.1
SNP_A-2201346	ccaatcagccataggcc[A/G]gaaggtgcgtaggact	A	G	NM_178497 // intron // 0 // Hs.24510 // FLJ23657 // 152816 // Homo sapiens hypothetical protein FLJ23657 (FLJ23657), mRNA. /// ENST00000311623 // intron // 0 // — // — // — // —	FLJ23657	FLJ23657, Homo sapiens hypothetical protein FLJ23657 (FLJ23657), q21.1
SNP_A-2238055	ctctgcaatatgttc[A/G]ctgtaagaatgggaaa	A	G	NM_003715 // downstream // 27310 // Hs.292689 // VDP // 8615 // Homo sapiens vesicle docking protein p115 (VDP), mRNA. /// NM_152934 // downstream // 18354 // Hs.290873 // PPEF2 // 5470 // Homo sapiens protein phosphatase, EF hand calcium-binding domain 2	VDP	VDP, Homo sapiens vesicle docking protein p115 (VDP), q21.1
SNP_A-2280336	gaggggattataggaa[A/G]gaacagcattgatacc	A	G	NM_018115 // intron // 0 // Hs.270107 // SDAD1 // 55153 // Homo sapiens SDA1 domain containing 1 (SDAD1), mRNA. /// ENST00000358408 // intron // 0 // — // — // — // — /// ENST00000356260 // intron // 0 // — // — // — // — /// ENST00000003571	SDAD1	SDAD1, Homo sapiens SDA1 domain containing 1 (SDAD1), q21.1
SNP_A-2235054	ctcccagaaaggagccc[C/T]gccttagtatcccctgc	C	T	NM_005506 // upstream // 1176 // Hs.349656 // SCARB2 // 950 // Homo sapiens scavenger receptor class B, member 2 (SCARB2), mRNA. /// ENST00000264896 // upstream // 1176 // — // — // — // — /// ENST00000339906 // upstream // 36663 // — // — // —	SCARB2	SCARB2, Homo sapiens scavenger receptor class B, member 2 (SCARB2), q21.1
SNP_A-2146121	atgccttgctgtagga[C/T]cgtggattagcagta	C	T	NM_020859 // intron // 0 // Hs.137459 // ShmL // 57619 // Homo sapiens Shroom-related protein (ShmL), mRNA. /// ENST00000264907 // intron // 0 // — // — // — // —	ShmL	ShmL, Homo sapiens Shroom-related protein (ShmL), q21.1
SNP_A-2168703	caagaatagctgaggc[A/G]atcttcaagaacaaag	A	G	NM_020859 // intron // 0 // Hs.137459 // ShmL // 57619 // Homo sapiens Shroom-related protein (ShmL), mRNA. /// ENST00000264907 // intron // 0 // — // — // — // —	ShmL	ShmL, Homo sapiens Shroom-related protein (ShmL), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872664	tctagtcctctcaggc[A/C]acgggcacttttcct	A	C	NM_020859 // intron // 0 // Hs.137459 // ShrmL // 57619 // Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // intron // 0 // --- // --- // ---	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-1942255	ttggcagctgtggaaa[A/C]cctggtaagaactgta	A	C	NM_020859 // intron // 0 // Hs.137459 // ShrmL // 57619 // Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // intron // 0 // --- // --- // ---	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-2224540	cgtattccgtcttaa[C/T]tgtgaacttccagaaag	C	T	NM_020859 // intron // 0 // Hs.137459 // ShrmL // 57619 // Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // intron // 0 // --- // --- // --- /// ENST00000296043 // intron // 0 // --- // --- // ---	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-2081964	acctttctacaagcac[A/G]catttaagcttataca	A	G	NM_020859 // intron // 0 // Hs.137459 // ShrmL // 57619 // Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // intron // 0 // --- // --- // --- /// ENST00000296043 // intron // 0 // --- // --- // ---	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-1790454	ggggcacgctcaagaa[A/T]agcacctccattaatt	A	T	NM_020859 // intron // 0 // Hs.137459 // ShrmL // 57619 // Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // intron // 0 // --- // --- // --- /// ENST00000296043 // intron // 0 // --- // --- // ---	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-2074627	acatatacccagtggaa[C/T]ggaacagataacctag	C	T	NM_020859 // downstream // 35659 // Hs.137459 // ShrmL // 57619 // Homo sapiens Shroom-related protein (ShrmL), mRNA. /// ENST00000264907 // downstream // 35659 // --- // --- // --- /// ENST00000296043 // downstream // 36285 // --- // --- // --- //	ShrmL	ShrmL, Homo sapiens Shroom-related protein (ShrmL), q21.1
SNP_A-1801094	gtagcagcaaagcgaa[C/T]gtagaaaagcagggac	C	T	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2009902	tttgttctgtggataa[A/G]aaagtggtagagcctg	A	G	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2227423	ctacaccatgcccaaa[C/G]ttgtgacctatgaaac	C	G	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2152265	attaaatattgctttt[A/G]aatggaaacgtaattt	A	G	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1977682	cagtgtctaatttctg[A/C]aattgcaaaccataac	A	C	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2146566	atgctgccctgttagal[C/T]gtgtaaagcagcccta	C	T	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1939171	ttgatagtagagtcaa[A/G]gtaaattagtaataca	A	G	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1850696	tattaccagttgtaaa[C/T]agagcagggagaagtt	C	T	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2272056	gaccctgagaatgaaa[C/T]gagggaaggaataa	C	T	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-2067268	acaaaggtacaatgcc[A/C]aatggctttcatctgt	A	C	NM_018243 // intron // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // intron // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1977684	ttcctctgtccaaagc[A/G]acatacaagtaacagg	A	G	NM_018243 // 3UTR // 0 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// ENST00000264893 // 3UTR // 0 // --- // --- // ---	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1646960	tacttgaacccaactatgcttaaa[G/T]attgaaacatttaccaaa tatcttc	G	T	NM_018243 // upstream // 15985 // Hs.386784 // FLJ10849 // 55752 // hypothetical protein FLJ10849 /// NM_020859 // downstream // 154037 // Hs.408902 // ShrmL // 57619 // Shroom-related protein	FLJ10849	FLJ10849 , rs2703137, hypothetical protein FLJ10849 .q21.1
SNP_A-1679814	ggtcatttattatgtttgtttgaa[C/G]tcaagtggcagacatagaca ctggc	C	G	NM_018243 // upstream // 15120 // Hs.386784 // FLJ10849 // 55752 // hypothetical protein FLJ10849 /// NM_020859 // downstream // 154902 // Hs.408902 // ShrmL // 57619 // Shroom-related protein	FLJ10849	FLJ10849 , rs2645690, hypothetical protein FLJ10849 .q21.1
SNP_A-2094567	agaatacactactgat[A/G]aataaaacatgaagag	A	G	NM_018243 // downstream // 8427 // Hs.128199 // SEPT11 // 55752 // Homo sapiens septin 11 (SEPT11), mRNA. /// NM_006835 // downstream // 985 // Hs.518827 // CCNI // 10983 // Homo sapiens cyclin I (CCNI). mRNA. /// ENST00000264893 // downstream // 8427 //	SEPT11	SEPT11, Homo sapiens septin 11 (SEPT11), q21.1
SNP_A-1701621	ggtacttttctccctcaaataaat[A/G]agctaaataatgaagctc attcata	A	G	NM_018243 // intron // 0 // Hs.386784 // FLJ10849 // 55752 // hypothetical protein FLJ10849	FLJ10849	FLJ10849 , rs7683005, hypothetical protein FLJ10849.q21.1
SNP_A-2166637	caaatgtgctcaatt[A/G]aagaaatgaataaattac	A	G	NM_004354 // upstream // 69135 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// ENST00000316405 // upstream // 5646 // — // — // — /// ENST00000316355 // upstream // 69135 // — // — // — /// ENST00000035440	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2275160	gagaagcatgatggca[A/G]atgaaatcttataatg	A	G	NM_004354 // intron // 0 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// ENST00000316355 // intron // 0 // — // — // — // — /// ENST00000354403 // intron // 0 // — // — // — // —	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2271298	gacattacccgtgcta[A/G]agaatataggatcag	A	G	ENST00000354403 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-1977698	tgtcaacaggataagc[A/G]cattggaccatgata	A	G	NM_004354 // downstream // 93707 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 251253 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2268100	gaatgaaacctcagaa[A/T]tggcctgtatttattt	A	T	NM_004354 // downstream // 103105 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 241855 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1977705	gtaataagctcctaa[A/G]gattccgatcccag	A	G	NM_004354 // downstream // 105967 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 238993 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-1977707	tatgatttccatgtta[C/T]gttggctttggcacag	C	T	NM_004354 // downstream // 107203 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 237757 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2237678	ctctctgattcagtaa[C/T]gctaatcctggactc	C	T	NM_004354 // downstream // 110778 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 234182 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1
SNP_A-2097809	agagactagaaagcaa[A/G]tccaattcaaatcact	A	G	NM_004354 // downstream // 113081 // Hs.13291 // CCNG2 // 901 // Homo sapiens cyclin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 231879 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cyclin G2 (CCNG2), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2083756	actacatctttcccag[A/G]ccatcacagctggatga	A	G	NM_004354 // downstream // 120895 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 224065 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-2173251	cacaactcaagcatca[A/G]aagctccatgtccaca	A	G	NM_004354 // downstream // 122350 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 222610 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1977714	agatggtaacttccac[A/T]cagaaggctatgttgg	A	T	NM_004354 // downstream // 144905 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 200055 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1804263	gtcacgatgcttaatg[C/T]cactgcattgttagc	C	T	NM_004354 // downstream // 150085 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 194875 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1712139	ctgctgtacagcaagattcatgcaa[A/G]agtctacatttttctgcttt caagta	A	G	NM_004354 // downstream // 93464 // Hs.13291 // CCNG2 // 901 // cydin G2 /// NM_006419 // upstream // 251503 // Hs.100431 // CXCL13 // 10563 // chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	CCNG2	CCNG2 , rs736600, cydin G2 ,q21.1
SNP_A-1818833	gttgaggtaaaatcac[C/T]ggaatctagtgtcata	C	T	NM_004354 // downstream // 203227 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 141733 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-2052204	aagtaacacattctgc[C/T]ctgtgctggcaattct	C	T	NM_004354 // downstream // 203323 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 141637 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1657267	ggggtgagggtaataagctcttaa[A/G]tgattcctgatcccagc tgcactga	A	G	NM_004354 // downstream // 105974 // Hs.13291 // CCNG2 // 901 // cydin G2 /// NM_006419 // upstream // 238993 // Hs.100431 // CXCL13 // 10563 // chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	CCNG2	CCNG2 , rs10518170, cyclin G2 ,q21.1
SNP_A-1977719	gactggctgacaatta[C/T]atccatgcagtgttag	C	T	NM_004354 // downstream // 209356 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 135604 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-2114961	agggccaagacaccaa[A/G]gcaggtatatgcctaa	A	G	NM_004354 // downstream // 217556 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 127404 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1908276	tgtactaaaaagctaa[A/G]cagcacttctgtggac	A	G	NM_004354 // downstream // 218473 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 126487 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2081083	acctgagatagcaaag[A/G]aagtctatagtacatt	A	G	NM_004354 // downstream // 220248 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 124712 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1844478	tataaagtagccaaag[A/G]caaagtagaatttacc	A	G	NM_004354 // downstream // 222865 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 122095 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-2251999	cttccaagcactgaca[A/G]aaatgttgtacttta	A	G	NM_004354 // downstream // 233576 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 111384 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1977721	tttgtgagctcacttat[C/T]gatgtattatgcttag	C	T	NM_004354 // downstream // 239328 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 105632 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1791156	gggtttacagtagggc[A/G]agaaaagtatgaggag	A	G	NM_004354 // downstream // 241931 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 103029 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1790943	ggggtaagtgaccgat[C/T]agtaagagattgtgct	C	T	NM_004354 // downstream // 242023 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 102937 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1886128	tgaccagttgacctca[A/T]gaacagggcccactc	A	T	NM_004354 // downstream // 242402 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 102558 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-2202168	ccacatctgtgaatga[C/T]gtagtgcaaatatctc	C	T	NM_004354 // downstream // 242487 // Hs.13291 // CCNG2 // 901 // Homo sapiens cydin G2 (CCNG2), mRNA. /// NM_006419 // upstream // 102473 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13).	CCNG2	CCNG2, Homo sapiens cydin G2 (CCNG2), q21.1
SNP_A-1705443	acaagattacctgagaatgtcatta[A/C]caatttatcgttcaattc agaaa	A	C	NM_004354 // downstream // 178982 // Hs.13291 // CCNG2 // 901 // cydin G2 /// NM_006419 // upstream // 165985 // Hs.100431 // CXCL13 // 10563 // chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	CCNG2	CCNG2 , rs10518175, cyclin G2 ,q21.1
SNP_A-1864352	tccactcggaaacagt[A/G]aggtagtacacaaaga	A	G	NM_006419 // intron // 0 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13), mRNA. /// ENST00000286758 // intron // 0 // — // — // — // —	CXCL13	CXCL13, Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13), q21.1
SNP_A-2283975	gatataggctgctcaa[C/T]tcatctccaaccgttt	C	T	NM_006419 // downstream // 50994 // Hs.100431 // CXCL13 // 10563 // Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13), mRNA. /// NM_144571 // downstream // 63179 // Hs.183085 // CNOT6L // 246175 // Homo sapiens CCR4-NOT tran	CXCL13	CXCL13, Homo sapiens chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant) (CXCL13), q21.1
SNP_A-1729194	accaactcttactaccctctgtca[A/G]aacttactaattagaatc cctgtc	A	G	NM_006419 // intron // 0 // Hs.100431 // CXCL13 // 10563 // chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	CXCL13	CXCL13 , rs355684, chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant),q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1739225	gtggttggatacaaatcttgaata[A/G]ccatctattgtggccacc atagtct	A	G	NM_006419 // intron // 0 // Hs.100431 // CXCL13 // 10563 // chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	CXCL13	CXCL13 , rs355686, chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant),q21.1
SNP_A-2063747	aattagagtggaaaggt[C/T]catggtcagagtgtt	C	T	NM_025074 // intron // 0 // Hs.369448 // FRAS1 // 80144 // Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 1, mRNA. /// NM_020875 // intron // 0 // Hs.369448 // FRAS1 // 80144 // Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 3, mRN	FRAS1	FRAS1, Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 1, q21.21
SNP_A-1858380	tcagacctacaaagac[A/G]ctatacttatagaacc	A	G	NM_025074 // intron // 0 // Hs.369448 // FRAS1 // 80144 // Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 1, mRNA. /// NM_020875 // intron // 0 // Hs.369448 // FRAS1 // 80144 // Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 3, mRN	FRAS1	FRAS1, Homo sapiens Fraser syndrome 1 (FRAS1), transcript variant 1, q21.21
SNP_A-2222745	cgatggaacactagaa[C/T]tagccttacagac	C	T	NM_005139 // intron // 0 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// ENST00000264908 // intron // 0 // --- // --- // ---	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1944785	ttgtgccactgtactg[A/G]ataagctgtagaagac	A	G	NM_005139 // intron // 0 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// ENST00000264908 // intron // 0 // --- // --- // ---	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-2117570	aggttaagtatttgtc[A/G]agcactgtatctacg	A	G	NM_005139 // downstream // 2860 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 163075 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1870032	tccttgccaattagcc[A/G]agtatctgtctttcct	A	G	NM_005139 // downstream // 5049 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 160886 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1977746	tttatcctaacctta[C/G]agcaactagctttgag	C	G	NM_005139 // downstream // 9557 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 156378 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1906948	tggttctgggaactca[A/C]attatgacctattgc	A	C	NM_005139 // downstream // 19995 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 145940 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_19	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1930163	ttcattcaatttatgc[A/G]acaccttcatcttca	A	G	NM_005139 // downstream // 72323 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 93612 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-2009921	ctccatgagaattggat[A/G]gtggtaaaaaagaact	A	G	NM_005139 // downstream // 78435 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 87500 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1875968	tctgaacttgtttcta[C/G]acacaggtaaaaaata	C	G	NM_005139 // downstream // 80247 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 85688 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920983	ttacagagtgggctaa[C/T]ggtactggattgtcc	C	T	NM_005139 // downstream // 89842 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 76093 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-2079074	acccagactgtatggc[G/T]catctagcctcatcgt	G	T	NM_005139 // downstream // 94630 // Hs.480042 // ANXA3 // 306 // Homo sapiens annexin A3 (ANXA3), mRNA. /// NM_017593 // upstream // 71305 // Hs.146551 // BMP2K // 55589 // Homo sapiens BMP2 inducible kinase (BMP2K), transcript variant 2, mRNA. /// NM_198	ANXA3	ANXA3, Homo sapiens annexin A3 (ANXA3), q21.21
SNP_A-1647602	agttacctggaaacacaaacgaaaaa[C/T]gaatgagaggaag atgaagaatagg	C	T	NM_005139 // downstream // 11760 // Hs.442733 // ANXA3 // 306 // annexin A3 /// NM_017593 // upstream // 154154 // Hs.20137 // BMP2K // 55589 // BMP2 inducible kinase /// NM_177453 // downstream // 295753 // Hs.368305 // PAQR3 // 152559 // progestin and	ANXA3	ANXA3, rs3927159, annexin A3, q21.21
SNP_A-2214609	cctagatccagtagaa[A/T]gcactttgcgcacac	A	T	NM_177453 // intron // 0 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // intron // 0 // — // — // — /// ENST00000360773 // intron // 0 // — // — // —	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1878735	tctgttctatagcata[C/T]ctggatttcagtaaag	C	T	NM_177453 // upstream // 52906 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 52950 // — // — // — /// ENST00000360773 // upstream // 52915 //	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1977755	catgtctcaagaaata[A/T]gctgcaaatatatact	A	T	NM_177453 // upstream // 76013 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 76057 // — // — // — /// ENST00000360773 // upstream // 76022 //	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1912055	tgtgagcattaaggg[C/G]aaaggcaaatgaagtg	C	G	NM_177453 // upstream // 81967 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 82011 // — // — // — /// ENST00000360773 // upstream // 81976 //	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1922721	ttagagccagacaaag[A/G]atatgcactcaacctt	A	G	NM_177453 // upstream // 247624 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 247668 // — // — // — /// ENST00000360773 // upstream // 247633	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-2116485	aggtattgaatcaacc[C/T]atgttcccatcaactg	C	T	NM_177453 // upstream // 265677 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 265721 // — // — // — /// ENST00000360773 // upstream // 265686	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-2307401	gcttatactagtccaa[A/G]taagcattaggtcata	A	G	NM_177453 // upstream // 267151 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 267195 // — // — // — /// ENST00000360773 // upstream // 267160	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-1921658	ttacctttcctgcac[G/T]ctattcccccacatga	G	T	NM_177453 // upstream // 294327 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 294371 // — // — // — /// ENST00000360773 // upstream // 294336	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1959445	ttttgccctccctacc[A/G]ctcactctacttcata	A	G	NM_177453 // upstream // 361249 // Hs.368305 // PAQR3 // 152559 // Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA. /// ENST00000342820 // upstream // 361293 // — // — // — // — /// ENST00000360773 // upstream // 361258	PAQR3	PAQR3, Homo sapiens progestin and adipoQ receptor family member III (PAQR3), q21.21
SNP_A-2289120	gatttctggatcatac[A/G]atagttaatttcagtt	A	G	NM_033214 // upstream // 30064 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 30049 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_058168 // upstream // 389244 // Hs	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1882638	tgaaaccaattaggaa[A/G]atgtaggtgaagaagc	A	G	NM_033214 // upstream // 129059 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 129044 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_058168 // upstream // 290249 //	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1915741	tgttcttcttactgta[C/T]atgaaatggctttgca	C	T	NM_033214 // upstream // 172584 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 172569 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_058168 // upstream // 246724 //	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1700364	aaaatgaaaccagtctcatccatat[C/T]attgtcactgatacaagt gcatttt	C	T	NM_033214 // upstream // 89260 // Hs.98008 // GK2 // 2712 // glycerol kinase 2 /// NM_058168 // upstream // 363811 // Hs.104215 // GDEP // 118425 // gene differentially expressed in prostate	GK2	GK2 , rs1971838, glycerol kinase 2 ,q21.21
SNP_A-1728777	ttagacacattcatcctgcaaacac[G/T]gagtattctgttcattattc tagtg	G	T	NM_033214 // upstream // 213906 // Hs.98008 // GK2 // 2712 // glycerol kinase 2 /// NM_058168 // upstream // 239165 // Hs.104215 // GDEP // 118425 // gene differentially expressed in prostate	GK2	GK2 , rs1808870, glycerol kinase 2 ,q21.21
SNP_A-1643435	ttccaataatcttggcgaattgtta[C/T]actgtaaactcagaaaatt aacatt	C	T	NM_033214 // upstream // 217882 // Hs.98008 // GK2 // 2712 // glycerol kinase 2 /// NM_058168 // upstream // 235189 // Hs.104215 // GDEP // 118425 // gene differentially expressed in prostate	GK2	GK2 , rs1866835, glycerol kinase 2 ,q21.21
SNP_A-1665202	cttcaaaattgtgtttctagcaact[C/T]actttaacttatgaacccttc attg	C	T	NM_033214 // upstream // 218447 // Hs.98008 // GK2 // 2712 // glycerol kinase 2 /// NM_058168 // upstream // 234624 // Hs.104215 // GDEP // 118425 // gene differentially expressed in prostate	GK2	GK2 , rs7677759, glycerol kinase 2 ,q21.21
SNP_A-1670161	cttgcaactaatgtaaactacctca[A/G]aataagagtcaactaa gagtaccca	A	G	NM_033214 // upstream // 241129 // Hs.98008 // GK2 // 2712 // glycerol kinase 2 /// NM_058168 // upstream // 211942 // Hs.104215 // GDEP // 118425 // gene differentially expressed in prostate	GK2	GK2 , rs10518221, glycerol kinase 2 ,q21.21
SNP_A-2240303	ctgaattatacactgt[A/T]aaagggtgaattttat	A	T	NM_033214 // upstream // 397980 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 397965 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_058168 // upstream // 21328 // H	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1847238	tatccaattaaactcc[A/T]caaggttcatattaga	A	T	NM_033214 // upstream // 402036 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_033214 // upstream // 402021 // Hs.98008 // GK2 // 2712 // Homo sapiens glycerol kinase 2 (GK2), mRNA. /// NM_058168 // upstream // 17272 // H	GK2	GK2, Homo sapiens glycerol kinase 2 (GK2), q21.21
SNP_A-1804557	gtcagcaagaagaacc[A/G]aaaaataattccttcc	A	G	NM_058168 // downstream // 2973 // Hs.104215 // GDEP // 118425 // Homo sapiens gene differentially expressed in prostate (GDEP), mRNA. /// NM_058172 // downstream // 74989 // Hs.162963 // ANTXR2 // 118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2),	GDEP	GDEP, Homo sapiens gene differentially expressed in prostate (GDEP), q21.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2305491	gctgcaaaaacctcaa[C/T]ggattacgttcaact	C	T	NM_058168 // downstream // 30085 // Hs.104215 // GDEP // 118425 // Homo sapiens gene differentially expressed in prostate (GDEP), mRNA. /// NM_058172 // downstream // 47877 // Hs.162963 // ANTXR2 // 118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2)	GDEP	GDEP, Homo sapiens gene differentially expressed in prostate (GDEP), q21.21
SNP_A-2211569	ccctcactatggtctg[A/C]aagtttatatttcccc	A	C	NM_058172 // upstream // 9581 // Hs.162963 // ANTXR2 // 118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA. /// NM_020226 // upstream // 101918 // Hs.373642 // PRDM8 // 56978 // Homo sapiens PR domain containing 8 (PRDM8), mRNA. /// AF275815 /	ANTXR2	ANTXR2, Homo sapiens anthrax toxin receptor 2 (ANTXR2), q21.21
SNP_A-2149602	atgtagttcaatctaa[A/C]acatatgtcttctca	A	C	NM_058172 // upstream // 60748 // Hs.162963 // ANTXR2 // 118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA. /// NM_020226 // upstream // 50751 // Hs.373642 // PRDM8 // 56978 // Homo sapiens PR domain containing 8 (PRDM8), mRNA. /// AF275815 /	ANTXR2	ANTXR2, Homo sapiens anthrax toxin receptor 2 (ANTXR2), q21.21
SNP_A-1977772	gtcaccctggtaatgg[G/T]aacagaaacattcagg	G	T	NM_058172 // upstream // 62916 // Hs.162963 // ANTXR2 // 118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA. /// NM_020226 // upstream // 48583 // Hs.373642 // PRDM8 // 56978 // Homo sapiens PR domain containing 8 (PRDM8), mRNA. /// AF275815 /	ANTXR2	ANTXR2, Homo sapiens anthrax toxin receptor 2 (ANTXR2), q21.21
SNP_A-1925496	ttatcttcatcttcc[A/G]cttcttcatttctc	A	G	NM_058172 // upstream // 63081 // Hs.162963 // ANTXR2 // 118429 // Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA. /// NM_020226 // upstream // 48418 // Hs.373642 // PRDM8 // 56978 // Homo sapiens PR domain containing 8 (PRDM8), mRNA. /// AF275815 /	ANTXR2	ANTXR2, Homo sapiens anthrax toxin receptor 2 (ANTXR2), q21.21
SNP_A-2113356	aggccgttatttccaa[C/T]ctctcaattactctc	C	T	NM_033143 // downstream // 40560 // Hs.37055 // FGF5 // 2250 // Homo sapiens fibroblast growth factor 5 (FGF5), transcript variant 2, mRNA. /// NM_004464 // downstream // 40560 // Hs.37055 // FGF5 // 2250 // Homo sapiens fibroblast growth factor 5 (FGF5).	FGF5	FGF5, Homo sapiens fibroblast growth factor 5 (FGF5), transcript variant 2, q21.21
SNP_A-2314457	ggagggggaatgacaca[C/T]agtgagcctgtcaaag	C	T	NM_152770 // intron // 0 // Hs.527104 // MGC35043 // 255119 // Homo sapiens hypothetical protein MGC35043 (MGC35043), mRNA. /// ENST00000358105 // intron // 0 // — // — // —	MGC35043	MGC35043, Homo sapiens hypothetical protein MGC35043 (MGC35043), q21.21
SNP_A-1869794	tccttccatagcttta[C/T]acagttaacagattaa	C	T	NM_152770 // intron // 0 // Hs.527104 // MGC35043 // 255119 // Homo sapiens hypothetical protein MGC35043 (MGC35043), mRNA. /// ENST00000358105 // intron // 0 // — // — // —	MGC35043	MGC35043, Homo sapiens hypothetical protein MGC35043 (MGC35043), q21.21
SNP_A-1852476	tatttactcaactaac[A/T]actgctaaaatcaatg	A	T	NM_152770 // intron // 0 // Hs.527104 // MGC35043 // 255119 // Homo sapiens hypothetical protein MGC35043 (MGC35043), mRNA. /// ENST00000358105 // intron // 0 // — // — // —	MGC35043	MGC35043, Homo sapiens hypothetical protein MGC35043 (MGC35043), q21.21
SNP_A-1751647	ttcttcatcattgctatgcatca[C/T]catctaaaaggctgatctg atct	C	T	NM_006259 // intron // 0 // Hs.41749 // PRKG2 // 5593 // protein kinase, cGMP-dependent, type II	PRKG2	PRKG2 , rs1112880, protein kinase, cGMP-dependent, type II,q21.21
SNP_A-2009935	aagtcggctccacagg[G/T]cattaattccactata	G	T	NM_006259 // upstream // 16336 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 205668 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1977797	catacaaccagttgac[G/T]aaacttttggacatgg	G	T	NM_006259 // upstream // 85955 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 136049 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1880617	tcttgcctggaaagaa[C/T]gtatgaggccttcta	C	T	NM_006259 // upstream // 102996 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA. /// NM_152545 // downstream // 119008 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2146423	atgctccaaaagctaa[C/T]ctttcattgataagt	C	T	NM_006259 // upstream // 143413 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 78591 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2241318	ctgagggttacagga[C/T]gagtgaccaaagtgg	C	T	NM_006259 // upstream // 145219 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 76785 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2209240	cccagtatgtggcatc[A/C]agtaagttctcaataa	A	C	NM_006259 // upstream // 145608 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 76396 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2240130	ctgaag[g/a]agcaataa[C/T]ggctgatccctgtccc	C	T	NM_006259 // upstream // 145890 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 76114 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1918409	ttaaataacctgctca[A/G]atcacaaagccgagt	A	G	NM_006259 // upstream // 146350 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 75654 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2135887	atcaacaggaaatcta[C/T]acaaactctgtaatgc	C	T	NM_006259 // upstream // 150666 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 71338 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1780701	ggatcatctagaaata[C/T]cttatggctacatct	C	T	NM_006259 // upstream // 172537 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 49467 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-2165934	caaagttatctatgca[C/T]tccaatcaacagtgag	C	T	NM_006259 // upstream // 178217 // Hs.546277 // PRKG2 // 5593 // Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA /// NM_152545 // downstream // 43787 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (R	PRKG2	PRKG2, Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), q21.21
SNP_A-1651222	ataaaaaatcaaaagtcaatagtca[A/C]ctgatactcagtctgatttagctc	A	C	NM_006259 // upstream // 91317 // Hs.41749 // PRKG2 // 5593 // protein kinase, cGMP-dependent, type II /// NM_152545 // downstream // 130687 // Hs.352552 // RASGEF1B // 153020 // RasGEF domain family, member 1B	PRKG2	PRKG2 , rs10488935, protein kinase, cGMP-dependent, type II, q21.21
SNP_A-2115652	agggtatcaagttata[C/T]gttgcagcacaccact	C	T	NM_152545 // intron // 0 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA /// ENST00000264400 // intron // 0 // — // — // — // — /// ENST00000356373 // 3UTR // 0 // — // — // — // —	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1957916	tttcaacaaatattc[A/C]acaagaactcagtcag	A	C	NM_152545 // upstream // 48593 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA /// ENST00000264400 // upstream // 48593 // — // — // — // — /// ENST00000356373 // upstream // 48610 // — // —	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100490	agataaggcagcataa[A/G]gctagacgttaatttt	A	G	NM_152545 // upstream // 164700 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // upstream // 164700 // — // — // — // — /// ENST00000356373 // upstream // 164717 // — //	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1787352	gggaagctaagcctga[C/G]attaaaaggactcggt	C	G	NM_152545 // upstream // 250863 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // upstream // 250863 // — // — // — // — /// ENST00000356373 // upstream // 250880 // — //	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-2128693	ataatcactgaaccat[A/G]acggcaggttcacatc	A	G	NM_152545 // upstream // 498991 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // upstream // 498991 // — // — // — // — /// ENST00000356373 // upstream // 499008 // — //	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1934354	ttctccgtattttacc[G/T]cacttcttgtcccagc	G	T	NM_152545 // upstream // 534127 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // upstream // 534127 // — // — // — // — /// ENST00000356373 // upstream // 534144 // — //	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1801166	gtagccttcctggaga[C/T]gatctcaccaacactt	C	T	NM_152545 // upstream // 610145 // Hs.480068 // RASGEF1B // 153020 // Homo sapiens RasGEF domain family, member 1B (RASGEF1B), mRNA. /// ENST00000264400 // upstream // 610145 // — // — // — // — /// ENST00000356373 // upstream // 610162 // — //	RASGEF1B	RASGEF1B, Homo sapiens RasGEF domain family, member 1B (RASGEF1B), q21.22
SNP_A-1852961	tatttgaaattcgcac[A/C]ctattctagtctaacc	A	C	ENST00000295471 // upstream // 98473 // — // — // — // — /// ENST00000354971 // downstream // 18765 // — // — // — // —	-	q21.22
SNP_A-2293436	gcagatttttttaaaac[C/G]aagaacattctatcct	C	G	NM_024906 // downstream // 31922 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000354971 // upstream // 14064 // — // — // — // — /// ENST00000319540 // downstream // 3361 // — // — // — // -	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2070661	acacgagctggcttaa[C/T]gggcagcctaacctgc	C	T	ENST00000319540 // intron // 0 // — // — // — // —	-	q21.22
SNP_A-1889372	tgagtgttcatagata[C/G]gcagagaggaagtcac	C	G	ENST00000319540 // intron // 0 // — // — // — // —	-	q21.22
SNP_A-2085282	actcatatataatgac[A/T]cagacaagaccgagac	A	T	ENST00000319540 // intron // 0 // — // — // — // —	-	q21.22
SNP_A-2164059	caaaagcacagtgtca[C/T]gaaatagcctgaagtg	C	T	ENST00000319540 // intron // 0 // — // — // — // —	-	q21.22
SNP_A-2048950	aagcctcggacacaaa[A/G]gagtttgtattcacac	A	G	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000319540 // intron // 0 // — // — // — // — /// ENST00000273908 // intron // 0 // — // — // — // —	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2050170	aaggaccttgtttttа[C/T]gtgtctggactagcat	C	T	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000319540 // intron // 0 // — // — // — // — /// ENST00000273908 // intron // 0 // — // — // — // —	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2155779	attccccttctggttg[A/G]agatttagtgatcagt	A	G	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000319540 // intron // 0 // — // — // — // — /// ENST00000273908 // intron // 0 // — // — // — // —	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2089949	acttctgagctggcca[C/G]ggaggaaaaagatgtg	C	G	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // — // — // — // —	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2305914	gctgctgcgtggggta[C/T]ggcattttctttctgc	C	T	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // — // — // — // —	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270490	gacagacaaccatgca[A/G]gtgatccctaaattat	A	G	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- // --- // --- /// ENST00000282709 // intron // 0 // --- // --- // --- // ---	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-2209235	cccagtagttggggaa[C/T]gagtacctggacctac	C	T	NM_024906 // intron // 0 // Hs.379191 // SCD4 // 79966 // Homo sapiens stearoyl-CoA desaturase 4 (SCD4), mRNA. /// ENST00000273908 // intron // 0 // --- // --- // --- // --- /// ENST00000282709 // intron // 0 // --- // --- // --- // ---	SCD4	SCD4, Homo sapiens stearoyl-CoA desaturase 4 (SCD4), q21.22
SNP_A-1667404	ggagattctagatttatttggtcta[A/G]ctgggaaataccctcctttt gtaaa	A	G	NM_021204 // downstream // 167631 // Hs.18442 // MASA // 58478 // E-1 enzyme /// NM_024906 // downstream // 31171 // Hs.379191 // SCD4 // 79966 // stearoyl-CoA desaturase 4	MASA	MASA , rs4693470, E-1 enzyme ,q21.22
SNP_A-1662228	cactgggagtgcttatagatgataa[A/T]tgggaatctactcctata tgtcacc	A	T	NM_021204 // downstream // 168174 // Hs.18442 // MASA // 58478 // E-1 enzyme /// NM_024906 // downstream // 30628 // Hs.379191 // SCD4 // 79966 // stearoyl-CoA desaturase 4	MASA	MASA , rs7670515, E-1 enzyme ,q21.22
SNP_A-1689951	gtgcctcatgatgattgtatgactc[A/G]cattgggatttgggctctg ggctaa	A	G	NM_021204 // downstream // 168367 // Hs.18442 // MASA // 58478 // E-1 enzyme /// NM_024906 // downstream // 30435 // Hs.379191 // SCD4 // 79966 // stearoyl-CoA desaturase 4	MASA	MASA , rs7675887, E-1 enzyme ,q21.22
SNP_A-1693789	acacacaaatttttttaatccagaa[A/G]ctacataatgatcacttta tatttt	A	G	AF389338 // 3UTR // 0 // Hs.379191 // SCD4 // 79966 // stearoyl-CoA desaturase 4	SCD4	SCD4 , rs6840, stearoyl-CoA desaturase 4,q21.22
SNP_A-2174142	cacacctttttctttcc[C/T]acctcctcagaagatg	C	T	NM_006665 // upstream // 31709 // Hs.44227 // HPSE // 10855 // Homo sapiens heparanase (HPSE), mRNA. /// NM_133636 // downstream // 40489 // Hs.480101 // HEL308 // 113510 // Homo sapiens DNA helicase HEL308 (HEL308), mRNA. /// ENST00000311412 // upstream	HPSE	HPSE, Homo sapiens heparanase (HPSE), q21.23
SNP_A-1832892	tacaatggaaaatgtc[C/T]aggttgaagcaagttc	C	T	NM_006665 // upstream // 59306 // Hs.44227 // HPSE // 10855 // Homo sapiens heparanase (HPSE), mRNA. /// NM_133636 // downstream // 12892 // Hs.480101 // HEL308 // 113510 // Homo sapiens DNA helicase HEL308 (HEL308), mRNA. /// ENST00000311412 // upstream	HPSE	HPSE, Homo sapiens heparanase (HPSE), q21.23
SNP_A-1977855	acacacttcactgcac[A/G]aagtaggaatctcaga	A	G	NM_006665 // upstream // 71676 // Hs.44227 // HPSE // 10855 // Homo sapiens heparanase (HPSE), mRNA. /// NM_133636 // downstream // 522 // Hs.480101 // HEL308 // 113510 // Homo sapiens DNA helicase HEL308 (HEL308), mRNA. /// ENST00000311412 // upstream //	HPSE	HPSE, Homo sapiens heparanase (HPSE), q21.23
SNP_A-1905382	tggtaagaactgaaac[G/T]ctctatacttacgcag	G	T	NM_032717 // downstream // 423578 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 423252 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2177445	caccttcccagcatg[A/G]caaacttacttgaaca	A	G	NM_032717 // downstream // 423944 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 423618 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2269061	gaattcttgtaaaggc[A/G]aattatcttctccaag	A	G	NM_032717 // downstream // 435953 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 435627 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2188079	cagtcatactggctga[A/G]aaaacgagaacattgt	A	G	NM_032717 // downstream // 442404 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 442078 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977872	tccctgggctccaaaa[C/T]ctgtgccagctggaaa	C	T	NM_032717 // downstream // 453597 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 453271 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1714627	tcaaaagatgggaaattgtaaccaa[A/G]tgttgaaatatgataat taactcct	A	G	AB064670 // upstream // 412018 // Hs.374681 // - // - // MRNA for OK/SW-CL.36, complete cds. /// NM_006168 // downstream // 519445 // Hs.347185 // NKX6-1 // 4825 // NK6 transcription factor related, locus 1 (Drosophila) /// NM_032717 // downstream // 368	-	- , rs1847819, MRNA for OK,q21.23
SNP_A-2262541	gaaatgtgtggaatca[C/T]agaatcattttcccag	C	T	NM_032717 // downstream // 485030 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 484704 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1757966	tctagccctcaggaagctgatttgt[A/T]aaaataccaagggttgg cctgacag	A	T	AB064670 // upstream // 505441 // Hs.374681 // - // - // MRNA for OK/SW-CL.36, complete cds. /// NM_006168 // downstream // 426022 // Hs.347185 // NKX6-1 // 4825 // NK6 transcription factor related, locus 1 (Drosophila) /// NM_032717 // downstream // 461	-	- , rs10516711, MRNA for OK,q21.23
SNP_A-2175477	cacatccttcaaatgc[A/C]agaactacaccataat	A	C	NM_032717 // downstream // 722787 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 722461 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-1787374	gggaaggagatcaaaa[C/T]ctaaagttgttacatt	C	T	NM_032717 // downstream // 736108 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA. /// NM_032717 // downstream // 735782 // Hs.99196 // MGC11324 // 84803 // Homo sapiens hypothetical protein MGC11324 (MGC113	MGC11324	MGC11324, Homo sapiens hypothetical protein MGC11324 (MGC11324), q21.23
SNP_A-2064889	aattgacaaacaaaaa[C/G]ttggatatcgctacag	C	G	NM_006168 // intron // 0 // Hs.546270 // NKX6-1 // 4825 // Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), mRNA. /// ENST00000295886 // intron // 0 // — // — // — // —	NKX6-1	NKX6-1, Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1), q21.23
SNP_A-1744339	cacaagaggtatgcctaaaagtgca[C/T]gatttccatcagaga aatggacaga	C	T	AB064670 // upstream // 892594 // Hs.374681 // - // - // MRNA for OK/SW-CL.36, complete cds. /// NM_006168 // downstream // 38869 // Hs.347185 // NKX6-1 // 4825 // NK6 transcription factor related, locus 1 (Drosophila) /// NM_032717 // downstream // 8488	-	- , rs763540, MRNA for OK,q21.23
SNP_A-2122349	agtgccataagttata[A/G]ggaggacagcagcttc	A	G	NM_031305 // upstream // 683906 // Hs.444229 // ARHGAP24 // 83478 // Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), mRNA. /// ENST00000318186 // downstream // 279334 // — // — // — // — /// ENST00000318116 // upstream // 324175 // — /	ARHGAP24	ARHGAP24, Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), q21.23
SNP_A-2090958	actttctcaaggtcaa[A/G]ttaattccaaagacat	A	G	NM_031305 // upstream // 383641 // Hs.444229 // ARHGAP24 // 83478 // Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), mRNA. /// ENST00000318186 // downstream // 579599 // — // — // — // — /// ENST00000318116 // upstream // 23910 // — //	ARHGAP24	ARHGAP24, Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), q21.23
SNP_A-2141357	atctgtggcaagaaac[C/T]gtgttcaattactaaa	C	T	ENST00000318116 // intron // 0 // — // — // — // —	-	q21.23
SNP_A-1977914	tggtctttgaactaca[A/T]aatcagaccacataga	A	T	ENST00000318116 // intron // 0 // — // — // — // —	-	q21.23
SNP_A-1977917	cttaaaggtagtccaa[C/T]cattagagggaattag	C	T	ENST00000318116 // intron // 0 // — // — // — // —	-	q21.23
SNP_A-1928721	ttcagaactatgtgtg[A/G]accagattgagtgtga	A	G	ENST00000318116 // intron // 0 // — // — // — // —	-	q21.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1977928	ttaatggcacgaccca[A/C]gaactatcaatgagtt	A	C	NM_031305 // intron // 0 // Hs.444229 // ARHGAP24 // 83478 // Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), mRNA. /// ENST00000318116 // intron // 0 // --- // --- // --- // --- /// ENST00000264343 // intron // 0 // — // — // — // —	ARHGAP24	ARHGAP24, Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), q21.23
SNP_A-2262623	gaaattcaactcttca[A/G]taaaagggaaaaacta	A	G	NM_031305 // intron // 0 // Hs.444229 // ARHGAP24 // 83478 // Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), mRNA. /// ENST00000318116 // intron // 0 // — // — // — // — /// ENST00000264343 // intron // 0 // --- // --- // --- // ---	ARHGAP24	ARHGAP24, Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), q21.23
SNP_A-2295811	gcatggagggatttaa[C/G]agcaagaagatacaat	C	G	NM_031305 // downstream // 1643 // Hs.444229 // ARHGAP24 // 83478 // Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), mRNA. /// NM_138981 // downstream // 12169 // Hs.25209 // MAPK10 // 5602 // Homo sapiens mitogen-activated protein kinase 10 (MA	ARHGAP24	ARHGAP24, Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), q21.23
SNP_A-1952665	tttctgggcactacta[C/T]gtgaatatctgcccag	C	T	NM_080684 // intron // 0 // Hs.436142 // PTPN13 // 5783 // Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript v /// NM_006264 // intron // 0 // Hs.436142 // PTPN13 // 5783 // Homo	PTPN13	PTPN13, Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1 q21.3
SNP_A-1958156	ttttcatctttctcac[A/G]ctgtatacctgagttt	A	G	NM_080684 // intron // 0 // Hs.436142 // PTPN13 // 5783 // Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript v /// NM_006264 // intron // 0 // Hs.436142 // PTPN13 // 5783 // Homo	PTPN13	PTPN13, Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1 q21.3
SNP_A-2105597	agccaccacgccccaa[C/T]agagcttcagttttac	C	T	NM_004684 // upstream // 25108 // Hs.62886 // SPARCL1 // 8404 // Homo sapiens SPARC-like 1 (mast9, hevin) (SPARCL1), mRNA. /// NM_014208 // upstream // 56447 // Hs.447902 // DSPP // 1834 // Homo sapiens dentin sialophosphoprotein (DSPP), mRNA. /// ENST000	SPARCL1	SPARCL1, Homo sapiens SPARC-like 1 (mast9, hevin) (SPARCL1), q22.1
SNP_A-1643632	tgctgtcttcttccacaggtatggc[A/G]acaatttctttcacaagctactcaa	A	G	NM_004684 // intron // 0 // Hs.75445 // SPARCL1 // 8404 // SPARC-like 1 (mast9, hevin)	SPARCL1	SPARCL1 , rs4129319, SPARC-like 1 (mast9, hevin),q22.1
SNP_A-1643461	ttacatatgaagccagtactcaaaa[A/T]aaaaaatcaaagtccataatctttc	A	T	NM_004684 // intron // 0 // Hs.75445 // SPARCL1 // 8404 // SPARC-like 1 (mast9, hevin)	SPARCL1	SPARCL1 , rs4129320, SPARC-like 1 (mast9, hevin),q22.1
SNP_A-2161139	atttgaaggagagggt[A/T]aaatcacttgaaagtg	A	T	NM_004407 // downstream // 45559 // Hs.128556 // DMP1 // 1758 // Homo sapiens dentin matrix acidic phosphoprotein (DMP1), mRNA. /// NM_004967 // upstream // 90702 // Hs.518726 // IBSP // 3381 // Homo sapiens integrin-binding sialoprotein (bone sialoprotei	DMP1	DMP1, Homo sapiens dentin matrix acidic phosphoprotein (DMP1), q22.1
SNP_A-1743077	aaccttcatagtttttgctgtttg[A/T]tttatatgaaagtggttttcctgta	A	T	NM_004407 // upstream // 2475 // Hs.93465 // DMP1 // 1758 // dentin matrix acidic phosphoprotein /// NM_014208 // downstream // 30959 // Hs.447902 // DSPP // 1834 // dentin sialophosphoprotein	DMP1	DMP1 , rs1381632, dentin matrix acidic phosphoprotein ,q22.1
SNP_A-2130845	atactttcatagaata[A/C]ggaaacatgaaatggg	A	C	NM_020203 // downstream // 79737 // Hs.189587 // MEPE // 56955 // Homo sapiens matrix, extracellular phosphoglycoprotein with ASARM motif (bone) (MEPE), mRNA. /// NM_020203 // downstream // 79761 // Hs.189587 // MEPE // 56955 // Homo sapiens matrix, extra	MEPE	MEPE, Homo sapiens matrix, extracellular phosphoglycoprotein with ASARM motif (bone) (MEPE), q22.1
SNP_A-2202971	ccactctcccaaggat[A/G]agcacccagatagcct	A	G	NM_152542 // upstream // 20675 // Hs.291000 // PPM1K // 152926 // Homo sapiens hypothetical protein DKFZp761G058 (DKFZp761G058), mRNA. /// NM_017912 // upstream // 73593 // Hs.529317 // HERC6 // 55008 // Homo sapiens hect domain and RLD 6 (HERC6), mRNA. /	PPM1K	PPM1K, Homo sapiens hypothetical protein DKFZp761G058 (DKFZp761G058), q22.1
SNP_A-1943446	ttggtttggtcccaat[C/G]aagaacattaaaaaaa	C	G	AB020721 // intron // 0 // Hs.97270 // FAM13A1 // 10144 // Homo sapiens mRNA for KIAA0914 protein, partial cds. /// ENST00000264344 // intron // 0 // --- // --- // --- // --- /// ENST00000341818 // intron // 0 // — // — // — // —	FAM13A1	FAM13A1, Homo sapiens for KIAA0914 protein, partial cds. q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1959063	ttttgaaagcatataq[A/G]gattgagcatcccaaa	A	G	NM_145715 // downstream // 55508 // Hs.58924 // TIGD2 // 166815 // Homo sapiens tigger transposable element derived 2 (TIGD2), mRNA. /// NM_198281 // downstream // 76717 // Hs.386796 // LOC285513 // 285513 // Homo sapiens hypothetical protein LOC285513 (L	TIGD2	TIGD2, Homo sapiens tigger transposable element derived 2 (TIGD2), q22.1
SNP_A-2052457	aagtagacatatatgg[A/C]aaagtcctactgcctt	A	C	NM_145715 // downstream // 100572 // Hs.58924 // TIGD2 // 166815 // Homo sapiens tigger transposable element derived 2 (TIGD2), mRNA. /// NM_198281 // downstream // 31653 // Hs.386796 // LOC285513 // 285513 // Homo sapiens hypothetical protein LOC285513 (	TIGD2	TIGD2, Homo sapiens tigger transposable element derived 2 (TIGD2), q22.1
SNP_A-2261187	gaaagaggaccctaq[A/G]cgagaaagaaatagaa	A	G	NM_198281 // upstream // 329596 // Hs.386796 // LOC285513 // 285513 // Homo sapiens hypothetical protein LOC285513 (LOC285513), mRNA. /// NM_000345 // downstream // 88165 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of a	LOC285513	LOC285513, Homo sapiens hypothetical protein LOC285513 (LOC285513), q22.1
SNP_A-2245046	ctggcatttcttttcat[C/T]gtagcatttatattaaa	C	T	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-1901147	tggatcttgtgttaac[C/T]atggatgacatttgtc	C	T	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-2059577	aatctccactaaatac[G/T]aatgactgcttatagt	G	T	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-2257906	ctttgtaggacaatta[C/T]attaatcccaaagtta	C	T	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-2252416	cttcctacttatgtcat[C/G]gtaactttgggattaa	C	G	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-1807077	gtctccattagatcat[C/T]aggtgacagtaatagt	C	T	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-1928999	ttcagcctggagtgaa[A/G]tgacagattgagaccc	A	G	NM_000345 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // intron // 0 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, a	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-2055955	aatacagagaaacagtc[A/G]actatcatcatcattt	A	G	NM_000345 // upstream // 11791 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // upstream // 13093 // Hs.271771 // SNCA // 6622 // Homo sapiens	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801078	gtagcaatcagaggtg[A/G]agactgagagcaagcg	A	G	NM_000345 // upstream // 26395 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // upstream // 27697 // Hs.271771 // SNCA // 6622 // Homo sapiens	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-2125541	agtttcaagagtggac[A/G]aaaatataaaattgc	A	G	NM_000345 // upstream // 27208 // Hs.271771 // SNCA // 6622 // Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA. /// NM_007308 // upstream // 28510 // Hs.271771 // SNCA // 6622 // Homo sapiens	SNCA	SNCA, Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, q22.1
SNP_A-1853741	tcaaaaaatgttaata[C/T]gtgctatgagaaaaca	C	T	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2234712	ctccaggacctcaaat[A/G]agagaatccctacatg	A	G	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1978024	tttataacactctgaa[A/G]tctataagctatttct	A	G	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2190194	cataatagcactgaaaa[C/G]ttaagaatgtgtccat	C	G	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2009979	aagaaactgtggaaaa[A/C]attagatttatctgca	A	C	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1978025	tgtgctataaggagaa[C/T]ttaagaaactgtggaa	C	T	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // intron // 0 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2195047	catggaaaatacctcta[A/G]tccaactgaccaaccg	A	G	NM_007351 // downstream // 35196 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 35196 // — // — // — /// ENST00000356267 // upstream // 236219 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2232037	ctcaagaatgtactgg[A/G]aaaagtcattggtaat	A	G	NM_007351 // downstream // 66044 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 66044 // — // — // — /// ENST00000356267 // upstream // 205371 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1978027	ccttgtctccggagaa[A/G]taaggaagaaggtttg	A	G	NM_007351 // downstream // 76646 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 76646 // — // — // — /// ENST00000356267 // upstream // 194769 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1883672	tgaactgaagataaaa[C/T]cccaagtcttcaggat	C	T	NM_007351 // downstream // 78772 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 78772 // — // — // — /// ENST00000356267 // upstream // 192643 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2305381	gctgatagtagtaca[A/G]gcaggaaacccacaga	A	G	NM_007351 // downstream // 81877 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 81877 // — // — // — /// ENST00000356267 // upstream // 189538 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1755762	attaaatgttttgttgatatcgt[A/G]aactgatttatccttttcttttaga	A	G	NM_007351 // intron // 0 // Hs.268107 // MMRN1 // 22915 // multimerin 1	MMRN1	MMRN1 , rs10516853, multimerin 1,q22.1
SNP_A-2279018	gaggaagagacacgaat[A/C]gtagttccagaagtgg	A	C	NM_007351 // downstream // 117394 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 117394 // — // — // — /// ENST00000356267 // upstream // 154021 // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2034816	aaatgactagaaatgc[A/T]cttgagttggactaaa	A	T	NM_007351 // downstream // 117564 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 117564 // — // — // — // — /// ENST00000356267 // upstream // 153851 // — // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1679748	ctgtgctgctttctccacctgctac[A/G]gacacttattcctcaaatct cacgt	A	G	AB051467 // upstream // 124258 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein /// NM_007351 // downstream // 49469 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680 , rs10516855, KIAA1680 protein ,q22.1
SNP_A-1711502	aaagtgatattgaagagatacacaa[C/T]gattttaatatatgtagg aagtata	C	T	AB051467 // upstream // 104951 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein /// NM_007351 // downstream // 68776 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680 , rs7661577, KIAA1680 protein ,q22.1
SNP_A-1651792	tttaaataggaataattggaaatgc[A/G]aagagttaagtgatctg gttaaagt	A	G	AB051467 // upstream // 104366 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein /// NM_007351 // downstream // 69361 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680 , rs10516857, KIAA1680 protein ,q22.1
SNP_A-1669593	tgtatctgctaactttactacagta[C/T]taccattttcgatattacttat aaa	C	T	AB051467 // upstream // 83649 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein /// NM_007351 // downstream // 90078 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680 , rs10516860, KIAA1680 protein ,q22.1
SNP_A-1748961	gagtgaataaatttttctaaatgctg[A/C]atagctccccttgaagttc tgctgc	A	C	AB051467 // upstream // 76991 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein /// NM_007351 // downstream // 96736 // Hs.268107 // MMRN1 // 22915 // multimerin 1	KIAA1680	KIAA1680 , rs722937, KIAA1680 protein ,q22.1
SNP_A-1978032	ttttctttgaagtgta[C/T]taagttctgtgagttt	C	T	NM_007351 // downstream // 240287 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 240287 // — // — // — // — /// ENST00000356267 // upstream // 31128 // — // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-1801216	gtagctccttttccta[A/T]atacctgtgagcaaca	A	T	NM_007351 // downstream // 256834 // Hs.268107 // MMRN1 // 22915 // Homo sapiens multimerin 1 (MMRN1), mRNA. /// ENST00000264790 // downstream // 256834 // — // — // — // — /// ENST00000356267 // upstream // 14581 // — // — // — // —	MMRN1	MMRN1, Homo sapiens multimerin 1 (MMRN1), q22.1
SNP_A-2202695	ccaccttgttgagata[C/T]gtgactgttgtggagg	C	T	ENST00000356267 // 5UTR // 0 // — // — // — // —	-	q22.1
SNP_A-1890244	tgatcagcttgaaaaa[C/T]gtagagggcaactcaa	C	T	NM_207491 // upstream // 402 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// NM_183049 // downstream // 604274 // Hs.518737 // TMSL3 // 7117 // Homo sapiens thymosin-like 3 (TMSL3), mRNA. /// NM_021109	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2148903	atggtgtcaaaggggа[G/T]cctcatgttcagcatt	G	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1920422	ttaattaattaagtgt[A/G]aagtaactgctcaggt	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1978033	gctgtcacaatttgta[C/T]gtttgttgggcaaaat	C	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2135083	atattctcttacatca[C/G]aaagtaagtatcaaaa	C	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2207553	ccatttcagttatcga[C/T]gatccagcccagtggc	C	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2102508	agattgacatcttcac[A/G]gaaactgcagacgtgg	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1696450	acagctacaattttccaaatataca[A/T]cacttgtttcacatgtatct agaac	A	T	AB051467 // intron // 0 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein	KIAA1680	KIAA1680 , rs1551794, KIAA1680 protein,q22.1
SNP_A-1724588	ggcattaaaagtagtcacttggttc[A/C]aacaagcattaaaaac acatgtttc	A	C	AB051467 // intron // 0 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein	KIAA1680	KIAA1680 , rs1551795, KIAA1680 protein,q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172954	cacaaaagcctgtacc[A/G]aaaacagagatgactt	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1907734	tgtaagagctggaaaa[C/T]tagtcctaagaggctg	C	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2127264	ataaatggccaaggta[A/G]cacttatgacaaatct	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2261091	gaaagacactatagga[A/G]ccgttttgattctcta	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2056312	aatactggataattac[C/T]ggccaaccaattggat	C	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1978056	tacctcctttttgtagc[A/G]ctgtaataaatcctta	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1733556	tcaaataacttccaagactccaca[C/T]tatccaacttagtgaac cttcatca	C	T	AB051467 // intron // 0 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein	KIAA1680	KIAA1680 , rs10516889, KIAA1680 protein,q22.1
SNP_A-2095257	agaattgcttgtgata[C/T]atttttgtctcattcaa	C	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1951642	tttcctagtcttcaa[A/G]tggcatctttctgtc	A	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-2247928	ctgtgcattgtcaaac[C/G]ccttaccaggacgtcc	C	G	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1700378	ttgtttaatttaaaatataatatca[C/T]ctacttgcacattatgctcta aaa	C	T	AB051467 // intron // 0 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein	KIAA1680	KIAA1680 , rs11919225, KIAA1680 protein,q22.1
SNP_A-2111029	aggagaatagggcaga[G/T]aagtatgtgaaactac	G	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1716791	gtaaagattaacaatctctaat[A/C]aacttgcattaggaaca attaaat	A	C	AB051467 // intron // 0 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein	KIAA1680	KIAA1680 , rs7672281, KIAA1680 protein,q22.1
SNP_A-1839859	tagattgatgttgcta[C/T]catataatttccaatt	C	T	NM_207491 // intron // 0 // Hs.405538 // MGC48628 // 401145 // Homo sapiens similar to KIAA1680 protein (MGC48628), mRNA. /// ENST00000333691 // intron // 0 // — // — // —	MGC48628	MGC48628, Homo sapiens similar to KIAA1680 protein (MGC48628), q22.1
SNP_A-1744691	ctcaatgacattcaggtttgccata[C/G]tggagcaagtagtgttag gccatca	C	G	AB051467 // intron // 0 // Hs.452999 // KIAA1680 // 80730 // KIAA1680 protein	KIAA1680	KIAA1680 , rs11922227, KIAA1680 protein,q22.1
SNP_A-1978065	ccatcaagacagacaa[A/C]tcaacaatactaagga	A	C	NM_001510 // upstream // 586934 // Hs.480281 // GRID2 // 2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000360030 // upstream // 23907 // — // — // — // — /// ENST00000282020 // upstream // 586934 // — // -	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.1
SNP_A-1949768	tttcaaagaagagata[C/T]cagagaatacagcttt	C	T	NM_001510 // upstream // 387462 // Hs.480281 // GRID2 // 2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000360030 // upstream // 223379 // — // — // — // — /// ENST00000282020 // upstream // 387462 // — //	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.1
SNP_A-1978085	tcatttctaaccaattg[C/T]caatacaaacacaata	C	T	NM_001510 // intron // 0 // Hs.480281 // GRID2 // 2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // — // — // —	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-2201748	ccacaatatgaaatgg[C/T]caaacaataaacaaca	C	T	NM_001510 // intron // 0 // Hs.480281 // GRID2 // 2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // — // — // —	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1853677	tatttttaatcaata[C/T]ggaaattcagcctgga	C	T	NM_001510 // intron // 0 // Hs.480281 // GRID2 // 2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-2093452	agaactgtatatgagc[C/G]atttctgaaataa	C	G	NM_001510 // intron // 0 // Hs.480281 // GRID2 // 2895 // Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), mRNA. /// ENST00000282020 // intron // 0 // --- // --- // ---	GRID2	GRID2, Homo sapiens glutamate receptor, ionotropic, delta 2 (GRID2), q22.3
SNP_A-1898746	tgctttcagcaacaaa[C/T]aaccaccaagcaataa	C	T	NM_005172 // downstream // 111403 // Hs.532680 // ATOH1 // 474 // Homo sapiens atonal homolog 1 (Drosophila) (ATOH1), mRNA. /// NM_020159 // upstream // 366328 // Hs.410406 // SMARCAD1 // 56916 // Homo sapiens SWI/SNF-related, matrix-associated actin-depen	ATOH1	ATOH1, Homo sapiens atonal homolog 1 (Drosophila) (ATOH1), q22.3
SNP_A-1814559	gtgtgcttgcaactga[A/G]gtgagaccacaaagta	A	G	NM_006457 // intron // 0 // Hs.480311 // PDLIM5 // 10611 // Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // --- // --- ENST00000318007 // intron // 0 // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1825392	taaataaataagacac[A/G]gtaaaggatcatgttt	A	G	NM_006457 // intron // 0 // Hs.480311 // PDLIM5 // 10611 // Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-2104592	agcaggtgctcactct[A/G]aaaaatacaatttaaa	A	G	NM_006457 // intron // 0 // Hs.480311 // PDLIM5 // 10611 // Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1941710	ttggaatacctcctta[A/T]atcagcacagagctt	A	T	NM_006457 // intron // 0 // Hs.480311 // PDLIM5 // 10611 // Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// ENST00000317968 // intron // 0 // --- // --- // ---	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-1978128	catccagaacttccca[C/G]atacaggcacaaacaa	C	G	NM_006457 // downstream // 5344 // Hs.480311 // PDLIM5 // 10611 // Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), mRNA. /// NM_001203 // upstream // 87152 // Hs.480321 // BMPR1B // 658 // Homo sapiens bone morphogenetic p	PDLIM5	PDLIM5, Homo sapiens LIM protein (similar to rat protein kinase C-binding enigma) (LIM), q22.3
SNP_A-2126379	ataaaacttggttctat[C/T]gaaacaatcacatcct	C	T	NM_001203 // intron // 0 // Hs.480321 // BMPR1B // 658 // Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), mRNA. /// ENST00000264568 // intron // 0 // --- // --- // ---	BMPR1B	BMPR1B, Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), q22.3
SNP_A-2230575	ctatctaccatatcacf[A/C]gagtctctactttta	A	C	NM_001203 // intron // 0 // Hs.480321 // BMPR1B // 658 // Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), mRNA. /// ENST00000264568 // intron // 0 // --- // --- // ---	BMPR1B	BMPR1B, Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), q22.3
SNP_A-1978149	aataaaaaagaaatgg[A/C]acagaaaaagctggta	A	C	NM_001203 // intron // 0 // Hs.480321 // BMPR1B // 658 // Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), mRNA. /// ENST00000264568 // intron // 0 // --- // --- // ---	BMPR1B	BMPR1B, Homo sapiens bone morphogenetic protein receptor, type IB (BMPR1B), q22.3
SNP_A-2276058	gagagaagaggcttat[C/T]agaagcagcaggcact	C	T	NM_003728 // intron // 0 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2260743	gaaacgtaataagtac[A/G]agagtgtagaggcaat	A	G	NM_003728 // intron // 0 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1978156	tacagtacaggttcac[A/G]ggcttatttcttcaca	A	G	NM_003728 // CDS // 0 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // CDS // 0 // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2061483	aatgctcaaatgtgtc[A/G]aagtgccaattgatct	A	G	NM_003728 // intron // 0 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // --- // --- // ---	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944860	ttgtgcttttcccagal[C/G]agatgaaaagtgacaa	C	G	NM_003728 // intron // 0 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // — // — // — // —	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1929622	ttcatagtggacgctg[A/G]agcctttagagtggag	A	G	NM_003728 // intron // 0 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// ENST00000331502 // intron // 0 // — // — // — // —	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1893275	tgcagatagtgtcaa[C/T]attggtgttttgca	C	T	NM_003728 // upstream // 24443 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 266792 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1888209	tgagcgctgtctactac[A/G]ccatagccattgcatt	A	G	NM_003728 // upstream // 92027 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 199208 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2149455	atgtacttttagatg[C/T]caatttcgtgtgtt	C	T	NM_003728 // upstream // 129076 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 162159 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2085076	actcactattgaacc[A/G]acaaatatttatcatg	A	G	NM_003728 // upstream // 129106 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 162129 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1978166	taaatgtggaggaaat[C/T]agaagaagtgagtgct	C	T	NM_003728 // upstream // 135491 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 155744 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1791578	gggtcaggctgaaaaa[C/G]attgataaagtcat	C	G	NM_003728 // upstream // 139782 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 151453 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2158125	attggagtagtataac[A/C]ccacctctaaagctg	A	C	NM_003728 // upstream // 140711 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 150524 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1901042	tggatatttgaaaaaa[C/T]tctgtctatctggac	C	T	NM_003728 // upstream // 143826 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 147409 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2075874	acattaaaatcaggca[C/T]taaactgtcttctga	C	T	NM_003728 // upstream // 144227 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 147008 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2222999	cgcaggtttgcttaca[C/G]tcttgggagatagaga	C	G	NM_003728 // upstream // 158065 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 133170 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141051	atctgcctagtggaca[C/T]ctcatataaatggaca	C	T	NM_003728 // upstream // 158645 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 132590 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2199310	cattttctatcacaaa[A/G]ttctgtaaaatctacc	A	G	NM_003728 // upstream // 158773 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 132462 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-2216768	cctctcttatttcctc[C/G]aatggtagtttgtagt	C	G	NM_003728 // upstream // 163837 // Hs.125605 // UNC5C // 8633 // Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), mRNA. /// NM_005390 // upstream // 127398 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2),	UNC5C	UNC5C, Homo sapiens unc-5 homolog C (C. elegans) (UNC5C), q22.3
SNP_A-1674351	catgcccttcacttacttattttac[C/T]gctggttccaacagtcagccctatt	C	T	NM_003728 // upstream // 174532 // Hs.125605 // UNC5C // 8633 // unc-5 homolog C (C. elegans) /// NM_005390 // upstream // 116549 // Hs.131361 // PDHA2 // 5161 // pyruvate dehydrogenase (lipoamide) alpha 2	UNC5C	UNC5C , rs1821742, unc-5 homolog C (C. elegans) ,q22.3
SNP_A-2173005	cacaaaccaaccctca[A/G]tcttgaatctttcttta	A	G	NM_005390 // downstream // 499994 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA. /// NM_183003 // upstream // 561336 // — // — // 0 // — /// ENST00000295266 // downstream // 499994 // — // -	PDHA2	PDHA2, Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), q22.3
SNP_A-2100833	agatatactgagaaaa[C/T]tccctgacagaactga	C	T	NM_005390 // downstream // 696561 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA. /// NM_183003 // upstream // 364769 // — // — // 0 // — /// ENST00000295266 // downstream // 696561 // — // -	PDHA2	PDHA2, Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), q22.3
SNP_A-1802533	gtatctacatataaga[A/C]ctaccctatgccaggc	A	C	NM_005390 // downstream // 748129 // Hs.131361 // PDHA2 // 5161 // Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA. /// NM_183003 // upstream // 313201 // — // — // 0 // — /// ENST00000295266 // downstream // 748129 // — // -	PDHA2	PDHA2, Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), q22.3
SNP_A-1880333	tcttgaaaatggtcta[A/G]ggatatacagcaaatg	A	G	NM_183003 // downstream // 65769 // — // — // 0 // — /// NM_174952 // downstream // 589986 // Hs.212840 // MGC46496 // 285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// ENST00000226490 // downstream // 65769 // — // — //	-	q22.3
SNP_A-2237533	ctctctaatctgtgaa[G/T]gttattttgattacta	G	T	NM_174952 // intron // 0 // Hs.212840 // MGC46496 // 285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// ENST00000295268 // intron // 0 // — // — // — // —	MGC46496	MGC46496, Homo sapiens hypothetical protein MGC46496 (MGC46496), q22.3
SNP_A-1934762	ttctcttctctgaagc[C/T]gaacacatcacaaata	C	T	NM_174952 // upstream // 30501 // Hs.212840 // MGC46496 // 285555 // Homo sapiens hypothetical protein MGC46496 (MGC46496), mRNA. /// NM_021159 // upstream // 87728 // Hs.132858 // RAP1GDS1 // 5910 // Homo sapiens RAP1, GTP-GDP dissociation stimulator 1 (	MGC46496	MGC46496, Homo sapiens hypothetical protein MGC46496 (MGC46496), q23
SNP_A-2179909	cactttcctccttcct[A/G]aattccttctgatata	A	G	NM_001968 // intron // 0 // Hs.249718 // EIF4E // 1977 // Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), mRNA. /// ENST00000280892 // intron // 0 // — // — // — // —	EIF4E	EIF4E, Homo sapiens eukaryotic translation initiation factor 4E (EIF4E), q23
SNP_A-1740385	agtagaatgttgaatcatgaaagaa[G/T]taacaacaaattgcatgcacttcac	G	T	NM_000669 // upstream // 29598 // Hs.2523 // ADH1C // 126 // alcohol dehydrogenase 1C (class I), gamma polypeptide /// NM_000673 // downstream // 29986 // Hs.389 // ADH7 // 131 // alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	ADH1C	ADH1C , rs2851292, alcohol dehydrogenase 1C (class I), gamma polypeptide ,q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1657954	agggcagacccatccagagtttaa[C/T]gtggcaacaaagtgtggttagacag	C	T	NM_000669 // upstream // 30520 // Hs.2523 // ADH1C // 126 // alcohol dehydrogenase 1C (class I), gamma polypeptide /// NM_000673 // downstream // 29064 // Hs.389 // ADH7 // 131 // alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	ADH1C	ADH1C , rs284780, alcohol dehydrogenase 1C (class I), gamma polypeptide .q23
SNP_A-1735613	tcagatttctgacacaatggtaaca[C/T]ctatccctctgcctgtgactgcca	C	T	NM_000669 // upstream // 30837 // Hs.2523 // ADH1C // 126 // alcohol dehydrogenase 1C (class I), gamma polypeptide /// NM_000673 // downstream // 28747 // Hs.389 // ADH7 // 131 // alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	ADH1C	ADH1C , rs284781, alcohol dehydrogenase 1C (class I), gamma polypeptide .q23
SNP_A-1978240	gggctgagaggagata[C/G]attcaaggccacttt	C	G	NM_000253 // intron // 0 // Hs.195799 // MTP // 4547 // Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), mRNA. /// ENST00000265517 // intron // 0 // — // — // — /// ENST00000359699 // intron // 0 // —	MTP	MTP, Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), q23
SNP_A-1753767	ttttcactgaattgctataaccaaa[C/T]ctatagttcctgttgtcctgctgtc	C	T	NM_032149 // intron // 0 // Hs.97501 // DKFZP434G072 // 84103 // hypothetical protein DKFZp434G072	DKFZP434G072	DKFZp434G072.q23
SNP_A-2213549	ccgtatgtgggtttac[A/G]gccccaacagggagta	A	G	NM_000253 // downstream // 22834 // Hs.195799 // MTP // 4547 // Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), mRNA. /// NM_014395 // upstream // 170530 // Hs.436271 // DAPP1 // 27071 // Homo sapiens dual adaptor o	MTP	MTP, Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), q23
SNP_A-2165926	caaagttacactctat[A/G]aaacacgacctgttg	A	G	NM_000253 // downstream // 31700 // Hs.195799 // MTP // 4547 // Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), mRNA. /// NM_014395 // upstream // 161664 // Hs.436271 // DAPP1 // 27071 // Homo sapiens dual adaptor o	MTP	MTP, Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), q23
SNP_A-1890478	tgatctctgcttccaa[C/T]ctaggaccagagaaat	C	T	NM_000253 // downstream // 91883 // Hs.195799 // MTP // 4547 // Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), mRNA. /// NM_014395 // upstream // 101481 // Hs.436271 // DAPP1 // 27071 // Homo sapiens dual adaptor o	MTP	MTP, Homo sapiens microsomal triglyceride transfer protein (large polypeptide, 88kDa) (MTP), q23
SNP_A-2141375	atctgtgtgagctggc[A/G]agtctatctggtctc	A	G	NM_014395 // intron // 0 // Hs.436271 // DAPP1 // 27071 // Homo sapiens dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPP1), mRNA. /// ENST00000296414 // intron // 0 // — // — // — // —	DAPP1	DAPP1, Homo sapiens dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPP1), q23
SNP_A-1924650	ttatagcaatgagaaac[G/T]aacacagaactagcat	G	T	NM_002106 // upstream // 60968 // Hs.119192 // H2AFZ // 3015 // Homo sapiens H2A histone family, member Z (H2AFZ), mRNA. /// NM_016242 // downstream // 399077 // Hs.152913 // EMCN // 51705 // Homo sapiens endomucin (EMCN), mRNA. /// ENST00000296417 // ups	H2AFZ	H2AFZ, Homo sapiens H2A histone family, member Z (H2AFZ), q23
SNP_A-2010011	tgacctgagatggtca[A/C]aaccaggcgacacatg	A	C	NM_002106 // upstream // 113768 // Hs.119192 // H2AFZ // 3015 // Homo sapiens H2A histone family, member Z (H2AFZ), mRNA. /// NM_016242 // downstream // 346277 // Hs.152913 // EMCN // 51705 // Homo sapiens endomucin (EMCN), mRNA. /// ENST00000296417 // up	H2AFZ	H2AFZ, Homo sapiens H2A histone family, member Z (H2AFZ), q23
SNP_A-1978253	agacacatttatgaaa[A/G]caaactaatatcacat	A	G	NM_002106 // upstream // 214604 // Hs.119192 // H2AFZ // 3015 // Homo sapiens H2A histone family, member Z (H2AFZ), mRNA. /// NM_016242 // downstream // 245441 // Hs.152913 // EMCN // 51705 // Homo sapiens endomucin (EMCN), mRNA. /// ENST00000296417 // up	H2AFZ	H2AFZ, Homo sapiens H2A histone family, member Z (H2AFZ), q24
SNP_A-1712253	tagctcccaactggtatgatctgaa[A/G]aatcaggcggttactaggtaggaga	A	G	NM_002106 // upstream // 197953 // Hs.119192 // H2AFZ // 3015 // H2A histone family, member Z /// NM_145244 // downstream // 37643 // Hs.107515 // DDIT4L // 115265 // DNA-damage-inducible transcript 4-like	H2AFZ	H2AFZ, rs10516461, H2A histone family, member Z .q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2261125	gaaagagaaaatagaa[C/G]tggaagctgcaggcta	C	G	NM_016242 // upstream // 32442 // Hs.152913 // EMCN // 51705 // Homo sapiens endomucin (EMCN), mRNA. /// NM_000944 // downstream // 473082 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	EMCN	EMCN, Homo sapiens endomucin (EMCN), q24
SNP_A-2238892	ctcttcagagtattga[C/T]acaacacaaggcacca	C	T	NM_016242 // upstream // 412065 // Hs.152913 // EMCN // 51705 // Homo sapiens endomucin (EMCN), mRNA. /// NM_000944 // downstream // 93459 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	EMCN	EMCN, Homo sapiens endomucin (EMCN), q24
SNP_A-2255969	cttaagatacatgca[C/T]catatgacatttagt	C	T	NM_016242 // upstream // 450059 // Hs.152913 // EMCN // 51705 // Homo sapiens endomucin (EMCN), mRNA. /// NM_000944 // downstream // 55465 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	EMCN	EMCN, Homo sapiens endomucin (EMCN), q24
SNP_A-2030935	aaaggaattactagtg[C/T]caaacgctttttgcta	C	T	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-2054727	aataaaatcagccaca[A/G]tgaaaagtaaaaatat	A	G	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1837329	tacttcaacacatttc[A/G]agttaaaagatatttc	A	G	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1845503	tatagagactccttca[C/G]tagcaaaacttttt	C	G	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-2198784	catttctgaaggcaaa[A/G]agtaaaacaagatctc	A	G	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1851113	tattatttgtttaac[A/G]ctctcattaatgctgt	A	G	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-2080771	acctcccctaccaaat[G/T]aatcagttaagtcaat	G	T	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-2286062	gatgatgtttaagttg[C/T]aaccatacacctgtac	C	T	NM_000944 // intron // 0 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// ENST00000323055 // intron // 0 // — // — // — // —	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-1666486	tccggtttcacagttg[C/T]ctgaaattgacaaacatt gtaaact	C	T	NM_000944 // intron // 0 // Hs.272458 // PPP3CA // 5530 // protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	PPP3CA	PPP3CA, rs10516469, protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha),q24
SNP_A-2194168	catgagacagttgaaa[C/T]gtctgaggagtccttg	C	T	NM_000944 // upstream // 302096 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// NM_017935 // upstream // 141447 // Hs.480400 // BANK1 // 55024 /	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2130232	ataccgtctgcagta[A/G]ctaggctccatgatgg	A	G	NM_000944 // upstream // 308423 // Hs.435512 // PPP3CA // 5530 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA. /// NM_017935 // upstream // 135120 // Hs.480400 // BANK1 // 55024 /	PPP3CA	PPP3CA, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), q24
SNP_A-2104512	agcaggcttcagagtc[A/G]cttgaaggatatgtta	A	G	NM_017935 // intron // 0 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// ENST00000322953 // intron // 0 // — // — // —	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1948031	tttagagaatttccc[A/G]aatctgatccaatacc	A	G	NM_017935 // downstream // 48482 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream // 138444 // Hs.288034 // SLC39A8 // 64116 // Homo sapiens solute carrier family 39 (	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-2305553	gctgcacagtgttccaa[C/T]ggtaccacattgtctt	C	T	NM_017935 // downstream // 70056 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream // 116870 // Hs.288034 // SLC39A8 // 64116 // Homo sapiens solute carrier family 39 (	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1942592	ttgggaaccttcctcc[A/G]aagcctcagtaaattt	A	G	NM_017935 // downstream // 88679 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream // 98247 // Hs.288034 // SLC39A8 // 64116 // Homo sapiens solute carrier family 39 (z	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-2094657	agaatatatatgttc[A/G]agaaggaatacgaaga	A	G	NM_017935 // downstream // 95870 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream // 91056 // Hs.288034 // SLC39A8 // 64116 // Homo sapiens solute carrier family 39 (z	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-2157548	attgattaagttggaa[A/C]agcagaagaaaacgtt	A	C	NM_017935 // downstream // 121394 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream // 65532 // Hs.288034 // SLC39A8 // 64116 // Homo sapiens solute carrier family 39 (	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1748831	atttattattgtctggcatagaatc[A/G]agtttaggtaagagggtag ccttca	A	G	NM_017935 // downstream // 27154 // Hs.193736 // BANK1 // 55024 // B-cell scaffold protein with ankyrin repeats 1 /// NM_022154 // downstream // 159772 // Hs.284205 // SLC39A8 // 64116 // solute carrier family 39 (zinc transporter), member 8	BANK1	BANK1, rs173218, B-cell scaffold protein with ankyrin repeats 1, q24
SNP_A-1895017	tgcccactgtgaaacc[A/C]caaataaaagtgagag	A	C	NM_017935 // downstream // 142046 // Hs.480400 // BANK1 // 55024 // Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), mRNA. /// NM_022154 // downstream // 44880 // Hs.288034 // SLC39A8 // 64116 // Homo sapiens solute carrier family 39 (	BANK1	BANK1, Homo sapiens B-cell scaffold protein with ankyrin repeats 1 (BANK1), q24
SNP_A-1676696	atgaatcaaggttatattttcttg[A/G]aagacgaaaacattacct ataccaa	A	G	NM_017935 // downstream // 158235 // Hs.193736 // BANK1 // 55024 // B-cell scaffold protein with ankyrin repeats 1 /// NM_022154 // downstream // 28691 // Hs.284205 // SLC39A8 // 64116 // solute carrier family 39 (zinc transporter), member 8	BANK1	BANK1, rs460610, B-cell scaffold protein with ankyrin repeats 1, q24
SNP_A-2173624	cacacaaaaggcatca[A/G]agttcagaaatgttcg	A	G	NM_003998 // intron // 0 // Hs.431926 // NFKB1 // 4790 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1), mRNA. /// ENST00000226574 // intron // 0 // — // — // — // —	NFKB1	NFKB1, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1), q24
SNP_A-2256913	ctttcctagtgggga[C/T]gcctaaacttcatcga	C	T	NM_001813 // upstream // 175313 // Hs.75573 // CENPE // 1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 215836 // Hs.942 // TACR3 // 6870 // Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// ENST00000265	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2090142	actgagagtaccatg[A/C]agttacaattaacat	A	C	NM_001813 // upstream // 184042 // Hs.75573 // CENPE // 1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 207107 // Hs.942 // TACR3 // 6870 // Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// ENST00000265	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24
SNP_A-1952125	ttctctcactgaaatca[C/T]atttaaatggagaaa	C	T	NM_001813 // upstream // 347096 // Hs.75573 // CENPE // 1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 44053 // Hs.942 // TACR3 // 6870 // Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// ENST00000026514	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24
SNP_A-1876501	tctgatgataccaata[A/G]acaaaggagacacacac	A	G	NM_001813 // upstream // 389691 // Hs.75573 // CENPE // 1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 1458 // Hs.942 // TACR3 // 6870 // Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// ENST00000026514	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24
SNP_A-1863960	tccaattgttacaaaat[A/T]gttcggagctaaaca	A	T	NM_001813 // upstream // 389755 // Hs.75573 // CENPE // 1062 // Homo sapiens centromere protein E, 312kDa (CENPE), mRNA. /// NM_001059 // downstream // 1394 // Hs.942 // TACR3 // 6870 // Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// ENST00000026514	CENPE	CENPE, Homo sapiens centromere protein E, 312kDa (CENPE), q24
SNP_A-2285236	gatctccttcactcca[A/C]aatgtctcatggattt	A	C	NM_001059 // upstream // 279506 // Hs.942 // TACR3 // 6870 // Homo sapiens tachykinin receptor 3 (TACR3), mRNA. /// NM_025212 // downstream // 469087 // Hs.12248 // CXXC4 // 80319 // Homo sapiens CXXC finger 4 (CXXC4), mRNA. /// ENST00000304883 // upstrea	TACR3	TACR3, Homo sapiens tachykinin receptor 3 (TACR3), q24
SNP_A-2165903	caaagtgtatactcaa[G/T]gactaattaggatgct	G	T	NM_025212 // upstream // 74801 // Hs.12248 // CXXC4 // 80319 // Homo sapiens CXXC finger 4 (CXXC4), mRNA. /// NM_017628 // upstream // 576180 // Hs.367639 // FLJ20032 // 54790 // Homo sapiens hypothetical protein FLJ20032 (FLJ20032), mRNA. /// ENST0000030	CXXC4	CXXC4, Homo sapiens CXXC finger 4 (CXXC4), q24
SNP_A-1978340	atagattagatagagc[A/G]atattatagagatgat	A	G	NM_025212 // upstream // 226034 // Hs.12248 // CXXC4 // 80319 // Homo sapiens CXXC finger 4 (CXXC4), mRNA. /// NM_017628 // upstream // 424947 // Hs.367639 // FLJ20032 // 54790 // Homo sapiens hypothetical protein FLJ20032 (FLJ20032), mRNA. /// ENST000003	CXXC4	CXXC4, Homo sapiens CXXC finger 4 (CXXC4), q24
SNP_A-1978353	ttacataaggttagaa[A/T]ttcaaatacaatcaac	A	T	NM_017628 // intron // 0 // Hs.367639 // FLJ20032 // 54790 // Homo sapiens hypothetical protein FLJ20032 (FLJ20032), mRNA. /// ENST00000305737 // intron // 0 // — // — // —	FLJ20032	FLJ20032, Homo sapiens hypothetical protein FLJ20032 (FLJ20032), q24
SNP_A-2062488	aatgtataaatgatgca[A/G]accagatcagagagag	A	G	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-1853320	tatttatctttaggg[G/T]atctgctaatcacttt	G	T	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-1978365	ttacttctcaaactat[G/T]actacgacctgccagg	G	T	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869251	tcctggctccgtagc[C/T]cggtggagtgtgcagc	C	T	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-2088025	actggctctcaaacaa[A/C]gttactctagacctg	A	C	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-1837008	tactgggattccacaac[A/G]gttaaataatttttgc	A	G	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-2143496	atgactaccatctaaa[A/G]aatagttctcggttag	A	G	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-2118277	agtaacaatttaggc[C/G]aagtatactacactca	C	G	NM_176869 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // intron // 0 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcrip	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-1691140	gaagttttttcacgaaattatagaa[C/G]aaagttacacacaatg gatctcta	C	G	NM_006903 // intron // 0 // Hs.421825 // PPA2 // 27068 // inorganic pyrophosphatase 2 /// NM_176865 // intron // 0 // - // - // - /// NM_176866 // intron // 0 // Hs.421825 // PPA2 // 27068 // inorganic pyrophosphatase 2 /// NM_176867 // intron // 0	PPA2	PPA2, rs2726526, inorganic pyrophosphatase 2 ,q24
SNP_A-1677946	aactgaaaatttataatggaaata[A/G]gaagtataactctccaa atataagc	A	G	NM_006903 // intron // 0 // Hs.421825 // PPA2 // 27068 // inorganic pyrophosphatase 2 /// NM_176865 // intron // 0 // - // - // - /// NM_176866 // intron // 0 // Hs.421825 // PPA2 // 27068 // inorganic pyrophosphatase 2 /// NM_176867 // intron // 0	PPA2	PPA2, rs923589, inorganic pyrophosphatase 2 ,q24
SNP_A-2287214	gatgtctgtgtcttcca[A/G]tgagttcctggagga	A	G	NM_176869 // upstream // 52533 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, mRNA. /// NM_176867 // upstream // 52527 // Hs.480452 // PPA2 // 27068 // Homo sapiens inorganic pyrophosphatase 2 (PPA2	PPA2	PPA2, Homo sapiens inorganic pyrophosphatase 2 (PPA2), transcript variant 1, q24
SNP_A-2199628	ccaaaagaagattggc[A/G]aaggaaggagaaaaga	A	G	NM_017700 // upstream // 24595 // Hs.272787 // FLJ20184 // 54848 // Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000326952 // upstream // 628 // — // — // — /// ENST00000265154 // upstream // 24595 // — // — // -	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24
SNP_A-2244967	ctggcaccttgaggag[A/G]agccaatctgacagga	A	G	NM_017700 // CDS // 0 // Hs.272787 // FLJ20184 // 54848 // Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000265154 // CDS // 0 // — // — // —	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24
SNP_A-1978374	gctggatatagaggta[C/G]aacctagctttgaggt	C	G	NM_017700 // intron // 0 // Hs.272787 // FLJ20184 // 54848 // Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000265154 // intron // 0 // — // — // —	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24
SNP_A-1844813	tataaatatcacagcc[A/G]ctgaaatttgtcgct	A	G	NM_017700 // intron // 0 // Hs.272787 // FLJ20184 // 54848 // Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000265154 // intron // 0 // — // — // —	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2300054	gcctcacagtctttttc[C/T]aaagctaaacagct	C	T	NM_017700 // downstream // 22433 // Hs.272787 // FLJ20184 // 54848 // Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA. /// ENST00000265154 // downstream // 22433 // — // — // — // — /// ENST00000340706 // upstream // 5085 // — // —	FLJ20184	FLJ20184, Homo sapiens hypothetical protein FLJ20184 (FLJ20184), q24
SNP_A-1978378	acacagctaattccca[A/G]catcacctaagaattc	A	G	NM_020395 // upstream // 3356 // Hs.480454 // LOC57117 // 57117 // Homo sapiens hypothetical nuclear factor SBBI22 (LOC57117), mRNA. /// NM_024751 // upstream // 5415 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ1327	LOC57117	LOC57117, Homo sapiens hypothetical nuclear factor SBBI22 (LOC57117), q24
SNP_A-2081830	accttgatgggcaaaa[C/T]ccaaattatgtttat	C	T	NM_024751 // intron // 0 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // — // — // — // — /// ENST00000360505 // intron // 0 // — // — // — // —	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-2198992	cattggatgtctcaa[C/T]gactgactctttatgc	C	T	NM_024751 // intron // 0 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // — // — // — // — /// ENST00000360505 // intron // 0 // — // — // — // —	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-1832981	tacacaacttataca[C/T]ggaatcaagttgcata	C	T	NM_024751 // intron // 0 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // — // — // — // — /// ENST00000360505 // intron // 0 // — // — // — // —	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-1870827	tcggatctcccatta[A/G]caagacatttataaga	A	G	NM_024751 // intron // 0 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // — // — // — // — /// ENST00000360505 // intron // 0 // — // — // — // —	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-2190503	cataccaaatcaacccd[A/T]cagtttcacaggaata	A	T	NM_024751 // intron // 0 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// ENST00000265150 // intron // 0 // — // — // — // — /// ENST00000360505 // intron // 0 // — // — // — // —	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-2303241	gctatgataattcaaa[C/G]gaatgtgagttcact	C	G	NM_024751 // downstream // 51982 // Hs.161429 // FLJ13273 // 79807 // Homo sapiens hypothetical protein FLJ13273 (FLJ13273), mRNA. /// NM_198278 // upstream // 19773 // Hs.518921 // LOC255743 // 255743 // Homo sapiens hypothetical protein LOC255743 (LOC25	FLJ13273	FLJ13273, Homo sapiens hypothetical protein FLJ13273 (FLJ13273), q24
SNP_A-1721199	aaaggaactaattcataggtgtga[G/T]aaattcaaagaaatgt cacttgtgt	G	T	NM_024751 // intron // 0 // Hs.126119 // FLJ13273 // 79807 // hypothetical protein FLJ13273	FLJ13273	FLJ13273 , rs10516528, hypothetical protein FLJ13273,q24
SNP_A-1728537	catccatctgatcccataaggtaa[C/T]tcatttcttacagaatttag ggcta	C	T	NM_004757 // upstream // 429556 // Hs.105656 // SCYE1 // 9255 // small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) /// NM_024751 // downstream // 63325 // Hs.126119 // FLJ13273 // 79807 // hypothetical protein FLJ13273 ///	SCYE1	SCYE1 , rs2553453, small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating), q24
SNP_A-1799303	gtaatacacacatttc[G/T]aaacacatggcataat	G	T	NM_033115 // upstream // 185779 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 153516 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24
SNP_A-2218672	cctggcctctgctcat[A/T]aataaaggcactgctg	A	T	NM_033115 // upstream // 185983 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 153720 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829867	taataagacaatgaag[C/G]ctgtaagacagttgta	C	G	NM_033115 // upstream // 189040 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 156777 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24
SNP_A-1922989	ttagcacaagtctcac[A/G]catcttcagtttata	A	G	NM_033115 // upstream // 189966 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 157703 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24
SNP_A-1954712	tttgctccagttagg[C/G]agaagcccatgcaaga	C	G	NM_033115 // upstream // 217202 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 184939 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24
SNP_A-1646944	gctaaagaaatatatgcgatgagtc[A/G]ataaatacatatttatttt caagag	A	G	NM_004757 // downstream // 126058 // Hs.105656 // SCYE1 // 9255 // small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) /// NM_014421 // downstream // 447985 // Hs.211869 // DKK2 // 27123 // dickkopf homolog 2 (Xenopus laevis)	SCYE1	SCYE1, rs10516535, small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating), q24
SNP_A-2072846	acagcttaatgataaaa[C/T]gactaatgtatgctgc	C	T	NM_033115 // upstream // 279853 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 247590 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q24
SNP_A-2178454	cactccctagacttac[A/G]ctatcttaaggcattt	A	G	NM_033115 // upstream // 589320 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 557057 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q25
SNP_A-1978400	gtttccactgaacttat[C/T]gctctgttgtgtctct	C	T	NM_033115 // upstream // 598926 // Hs.292986 // MGC16169 // 93627 // Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA. /// NM_004757 // downstream // 566663 // Hs.480465 // SCYE1 // 9255 // Homo sapiens small inducible cytokine subfamily E, mem	MGC16169	MGC16169, Homo sapiens hypothetical protein MGC16169 (MGC16169), q25
SNP_A-1831836	taattctatcaaaatat[C/T]aggttatggccaatct	C	T	NM_014421 // 3UTR // 0 // Hs.211869 // DKK2 // 27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// ENST00000285311 // 3UTR // 0 // — // — // —	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1839697	tagatgctatgatcac[A/G]gtcaacaaacatttag	A	G	NM_014421 // intron // 0 // Hs.211869 // DKK2 // 27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// ENST00000285311 // intron // 0 // — // — // —	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1953094	ttctgggtctcaagat[C/G]agaaaattgaaattat	C	G	NM_014421 // upstream // 529384 // Hs.211869 // DKK2 // 27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 47985 // Hs.368610 // PAPSS1 // 9061 // Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synth	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1929116	ttcaggagtaaacctc[C/T]attgactgatggtag	C	T	NM_014421 // upstream // 541327 // Hs.211869 // DKK2 // 27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 36042 // Hs.368610 // PAPSS1 // 9061 // Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synth	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25
SNP_A-1803534	gtatttgtttctgga[C/T]catacacattctgtga	C	T	NM_014421 // upstream // 542180 // Hs.211869 // DKK2 // 27123 // Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA. /// NM_005443 // downstream // 35189 // Hs.368610 // PAPSS1 // 9061 // Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synth	DKK2	DKK2, Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903471	tgggaagttggaaagg[C/T]cagaattggagctaac	C	T	NM_005443 // intron // 0 // Hs.368610 // PAPSS1 // 9061 // Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), mRNA. /// ENST00000265174 // intron // 0 // — // — // —	PAPSS1	PAPSS1, Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), q25
SNP_A-1681558	ctaacaaatgtctttgtgataacaa[C/T]gaagttaaatgaactga attgcta	C	T	NM_005443 // intron // 0 // Hs.3833 // PAPSS1 // 9061 // 3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	PAPSS1 , rs9307311, 3'-phosphoadenosine 5'-phosphosulfate synthase 1,q25
SNP_A-2125094	agttgtttttgtata[C/T]agtctaaggaaaaggg	C	T	NM_016269 // upstream // 49408 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 402737 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript varia	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1803520	gtatttgatcgctta[C/T]agaagctaagacggta	C	T	NM_016269 // upstream // 86583 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 365562 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript varia	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-2064260	aattcacttgaggag[C/T]attcaaagctgatcc	C	T	NM_016269 // upstream // 165535 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 286610 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript vari	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1923587	ttagggtccttccaa[C/T]ctgagactctcatct	C	T	NM_016269 // upstream // 295825 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 156320 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript vari	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1868802	tccgaaaggcagaga[A/G]ataaaatgtcactcac	A	G	NM_016269 // upstream // 372407 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 79738 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript varia	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-2038949	aacagctttacgtgca[C/T]cagtccttaatgtt	C	T	NM_016269 // upstream // 403675 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 48470 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript varia	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1978436	tcctcacagcagaaac[A/G]cagggcagagaaattt	A	G	NM_016269 // upstream // 421656 // Hs.125132 // LEF1 // 51176 // Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), mRNA. /// NM_000995 // upstream // 30489 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript varia	LEF1	LEF1, Homo sapiens lymphoid enhancer-binding factor 1 (LEF1), q25
SNP_A-1791805	gggtgacaaaaaggga[A/G]aatactctggacatag	A	G	NM_000995 // downstream // 1313 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, mRNA. /// NM_033625 // downstream // 1313 // Hs.438227 // RPL34 // 6164 // Homo sapiens ribosomal protein L34 (RPL34), trans	RPL34	RPL34, Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, q25
SNP_A-1733108	tacctcagttgtaagtagatttaa[C/T]ggtgtctacattgtttctca gctg	C	T	NM_182591 // intron // 0 // Hs.376299 // FLJ37673 // 285456 // hypothetical protein FLJ37673	FLJ37673	FLJ37673 , rs4266352, hypothetical protein FLJ37673,q25
SNP_A-1933118	ttcgtgagttagggac[A/G]aagattggtctctaa	A	G	NM_031279 // downstream // 38126 // Hs.106576 // AGXT2L1 // 64850 // Homo sapiens alanine-glyoxylate aminotransferase 2-like 1 (AGXT2L1), mRNA. /// ENST00000356182 // downstream // 36102 // — // — // — /// ENST00000355255 // downstream // 361	AGXT2L1	AGXT2L1, Homo sapiens alanine-glyoxylate aminotransferase 2-like 1 (AGXT2L1), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287766	gattactgccctcaaa[C/T]gcttctttggacagcc	C	T	NM_031279 // downstream // 35244 // Hs.106576 // AGXT2L1 // 64850 // Homo sapiens alanine-glyoxylate aminotransferase 2-like 1 (AGXT2L1), mRNA. /// ENST00000356182 // downstream // 38984 // — // — // — // — /// ENST00000355255 // downstream // 389	AGXT2L1	AGXT2L1, Homo sapiens alanine-glyoxylate aminotransferase 2-like 1 (AGXT2L1), q25
SNP_A-1919409	ttaagcaaaagaggcc[A/G]gactctatgattttat	A	G	NM_032518 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-1978449	gcctccactagcacaa[C/T]cttaattcaaagcttt	C	T	NM_032518 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-2206860	ccatggaagaattgta[A/G]gaagagacaggtcgct	A	G	NM_032518 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-2110592	aggacaggggtttaca[C/T]aactgtatacttgcaa	C	T	NM_032518 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-2242962	ctgccatggagagtaa[A/G]tgtagttcaaaagcaa	A	G	NM_032518 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // intron // 0 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-2301708	gcgctaatggctggta[A/C]atttctgaggtattgt	A	C	NM_032518 // upstream // 3231 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, mRNA. /// NM_198721 // upstream // 3231 // Hs.112925 // COL25A1 // 84570 // Homo sapiens collagen, type XXV, alpha	COL25A1	COL25A1, Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 2, q25
SNP_A-1679176	ctttgttacctaagaatgccttcca[A/C]attgtatcaggatttcaga gaaagt	A	C	NM_032518 // intron // 0 // Hs.512787 // COL25A1 // 84570 // collagen, type XXV, alpha 1	COL25A1	COL25A1 , rs2189705, collagen, type XXV, alpha 1,q25
SNP_A-1702847	tctaagtcaatagacaagtgacatt[A/T]aacatatagaacatctt gagaata	A	T	NM_032518 // intron // 0 // Hs.512787 // COL25A1 // 84570 // collagen, type XXV, alpha 1	COL25A1	COL25A1 , rs10488876, collagen, type XXV, alpha 1,q25
SNP_A-2045644	aagacaaaatataaac[A/G]atgtgagtatgcctca	A	G	NM_030821 // upstream // 42324 // Hs.480519 // PLA2G12A // 81579 // Homo sapiens phospholipase A2, group XIIA (PLA2G12A), mRNA. /// NM_018983 // upstream // 43131 // Hs.69851 // NOLA1 // 54433 // Homo sapiens nucleolar protein family A, member 1 (H/ACA sm	PLA2G12A	PLA2G12A, Homo sapiens phospholipase A2, group XIIA (PLA2G12A), q25
SNP_A-1978476	ctttctcaagaggcag[A/G]atgtaaactgaagtca	A	G	NM_198506 // intron // 0 // Hs.308127 // FLJ44691 // 345193 // Homo sapiens FLJ44691 protein (FLJ44691), mRNA. /// ENST00000327908 // intron // 0 // — // — // — // —	FLJ44691	FLJ44691, Homo sapiens FLJ44691 protein (FLJ44691), q25
SNP_A-1850736	tattactcacaatcca[A/G]taaagatgggaacatg	A	G	NM_001963 // intron // 0 // Hs.419815 // EGF // 1950 // Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), mRNA. /// ENST00000265171 // intron // 0 // — // — // — // —	EGF	EGF, Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), q25
SNP_A-1882312	tgaaaacagatgtaaa[C/G]aactatatttcaacta	C	G	NM_001963 // intron // 0 // Hs.419815 // EGF // 1950 // Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), mRNA. /// NM_024090 // 3UTR // 0 // Hs.412939 // ELOVL6 // 79071 // Homo sapiens ELOVL family member 6, elongation of long chain fatty a	EGF	EGF, Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2070329	acaccagaagagaaat[A/T]aacctaacaggccaa	A	T	NM_001537 // upstream // 145562 // Hs.250899 // HSBP1 // 3281 // Homo sapiens heat shock factor binding protein 1 (HSBP1), mRNA. /// NM_001977 // upstream // 78508 // Hs.435765 // ENPEP // 2028 // Homo sapiens glutamyl aminopeptidase (aminopeptidase A) (E	HSBP1	HSBP1, Homo sapiens heat shock factor binding protein 1 (HSBP1), q25
SNP_A-1674689	ggagatccttcttctccttaaac[C/T]gaaatcatgattccgtgtct gtggg	C	T	NM_001977 // upstream // 113779 // Hs.435765 // ENPEP // 2028 // glutamyl aminopeptidase (aminopeptidase A) /// NM_024090 // upstream // 163937 // Hs.211556 // ELOVL6 // 79071 // ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR	ENPEP	ENPEP , rs10488888, glutamyl aminopeptidase (aminopeptidase A) q25
SNP_A-2041244	aacctctcataaacca[C/T]attgttagttcagatg	C	T	NM_153426 // upstream // 283916 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 279307 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like h	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-2203280	ccacttctcctttttaa[C/T]gtgccacagatgcatg	C	T	NM_153426 // upstream // 299608 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 294999 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like h	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1960869	ttttgaatctagcaa[A/G]taattgtctcagaaat	A	G	NM_153426 // upstream // 390826 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 386217 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like h	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-1663742	aacatggctcctccacctcaacct[A/T]actataactgaattattt gcatctc	A	T	NM_000325 // upstream // 439378 // Hs.92282 // PITX2 // 5308 // paired-like homeodomain transcription factor 2 /// NM_152400 // upstream // 1083046 // Hs.23439 // FLJ39370 // 132720 // hypothetical protein FLJ39370 /// NM_153426 // upstream // 425124 //	PITX2	PITX2 , rs159440, paired-like homeodomain transcription factor 2 ,q25
SNP_A-1910094	tgtcatcagactttca[A/G]aagagcaaattcatta	A	G	NM_153426 // upstream // 562150 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, mRNA. /// NM_153426 // upstream // 557541 // Hs.92282 // PITX2 // 5308 // Homo sapiens paired-like h	PITX2	PITX2, Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 2, q25
SNP_A-2154313	attatgggtgagccaa[C/G]aaagggaaaacatcaga	C	G	NM_152400 // upstream // 536649 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 198300 // — // — // — /// ENST00000309733 // upstream // 536649 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2191220	catataatcctgcaac[A/G]actctgatagggagac	A	G	NM_152400 // upstream // 275107 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 459842 // — // — // — /// ENST00000309733 // upstream // 275107 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2159758	atttaggtaccgtatg[A/T]atctctgaattaaaat	A	T	NM_152400 // upstream // 267048 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 467901 // — // — // — /// ENST00000309733 // upstream // 267048 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2274035	gacttactataacata[C/G]ctacagtagtccagac	C	G	NM_152400 // upstream // 251258 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 483691 // — // — // — /// ENST00000309733 // upstream // 251258 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1957238	ttttacttaaggcatc[A/G]aattcagatagtcaca	A	G	NM_152400 // upstream // 191719 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 543230 // — // — // — /// ENST00000309733 // upstream // 191719 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2237616	ctctctcgcatataqc[A/G]gacaaggattctccac	A	G	NM_152400 // upstream // 161455 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 573494 // — // — // — /// ENST00000309733 // upstream // 161455 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1978537	atatcccctgttaaaa[A/T]agcgagaatatcaaag	A	T	NM_152400 // upstream // 137037 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 597912 // — // — // — /// ENST00000309733 // upstream // 137037 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1839087	tagagatttcgctgc[A/G]aacacatatagcga	A	G	NM_152400 // upstream // 103195 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 631754 // — // — // — /// ENST00000309733 // upstream // 103195 // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1728199	acacatgtcaaactggtcactagac[A/G]aggaattaaggattca acgatgaac	A	G	NM_000325 // upstream // 1325882 // Hs.92282 // PITX2 // 5308 // paired-like homeodomain transcription factor 2 /// NM_152400 // upstream // 196542 // Hs.23439 // FLJ39370 // 132720 // hypothetical protein FLJ39370 /// NM_153426 // upstream // 1311628 //	PITX2	PITX2 , rs9307376, paired-like homeodomain transcription factor 2 ,q25
SNP_A-2133496	atatatttgagttca[C/G]attcatcaattcagca	C	G	NM_152400 // upstream // 93225 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 641724 // — // — // — /// ENST00000309733 // upstream // 93225 // — // — /	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1656643	tccctcaagcttctgttcacttaa[A/G]agattattcctgaaaaat aaattg	A	G	NM_000325 // upstream // 1336160 // Hs.92282 // PITX2 // 5308 // paired-like homeodomain transcription factor 2 /// NM_152400 // upstream // 186264 // Hs.23439 // FLJ39370 // 132720 // hypothetical protein FLJ39370 /// NM_153426 // upstream // 1321906 //	PITX2	PITX2 , rs2016740, paired-like homeodomain transcription factor 2 ,q25
SNP_A-1744357	taacacccagcatcaactgtcaac[C/G]aactgagtgagccat cttggacggg	C	G	NM_000325 // upstream // 1336614 // Hs.92282 // PITX2 // 5308 // paired-like homeodomain transcription factor 2 /// NM_152400 // upstream // 185810 // Hs.23439 // FLJ39370 // 132720 // hypothetical protein FLJ39370 /// NM_153426 // upstream // 1322360 //	PITX2	PITX2 , rs877936, paired-like homeodomain transcription factor 2 ,q25
SNP_A-2124260	agttatctaagttatta[C/T]acgttttgcatcacca	C	T	NM_152400 // upstream // 66969 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 667980 // — // — // — /// ENST00000309733 // upstream // 66969 // — // — /	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1800597	gtactgtctggctca[A/G]taaggcagagataataa	A	G	NM_152400 // upstream // 50952 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 683997 // — // — // — /// ENST00000309733 // upstream // 50952 // — // — /	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1905683	tggtatctactgcca[C/T]gaagagttgttctgt	C	T	NM_152400 // upstream // 44888 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 690061 // — // — // — /// ENST00000309733 // upstream // 44888 // — // — /	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893949	tgcatatgattccagc[A/G]gattagtagatccttt	A	G	NM_152400 // upstream // 17040 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000358806 // upstream // 717909 // — // — // — // — /// ENST00000309733 // upstream // 17040 // — // — //	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1978544	ggtccatgccttttga[A/T]ctatcagtagaaatat	A	T	NM_152400 // intron // 0 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000309733 // intron // 0 // — // — // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2057213	aatatagagcgcccaa[A/G]gactttgatttccaaa	A	G	NM_152400 // intron // 0 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000309733 // intron // 0 // — // — // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1923322	ttaggaatgaagaggt[A/T]aagtcccatagcccat	A	T	NM_152400 // intron // 0 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// ENST00000309733 // intron // 0 // — // — // — // —	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-2153689	attaggtactccgagc[A/G]agtttaagggaaccat	A	G	NM_152400 // downstream // 16353 // Hs.23439 // FLJ39370 // 132720 // Homo sapiens hypothetical protein FLJ39370 (FLJ39370), mRNA. /// NM_018569 // upstream // 26361 // Hs.435991 // C4orf16 // 55435 // Homo sapiens chromosome 4 open reading frame 16 (C4or	FLJ39370	FLJ39370, Homo sapiens hypothetical protein FLJ39370 (FLJ39370), q25
SNP_A-1834416	tacatttatttccaga[A/G]gagaattaagttttgt	A	G	NM_024019 // upstream // 6089 // Hs.121810 // NEUROG2 // 63973 // Homo sapiens neurogenin 2 (NEUROG2), mRNA. /// NM_138698 // downstream // 17083 // Hs.444338 // LOC91431 // 91431 // Homo sapiens prematurely terminated mRNA decay factor-like (LOC91431), m	NEUROG2	NEUROG2, Homo sapiens neurogenin 2 (NEUROG2), q25
SNP_A-2083391	actaactatagttggc[A/G]aagacctaataaaaat	A	G	NM_138698 // CDS // 0 // Hs.444338 // LOC91431 // 91431 // Homo sapiens prematurely terminated mRNA decay factor-like (LOC91431), mRNA. /// ENST00000313239 // CDS // 0 // — // — // — // — /// ENST00000356051 // 5UTR // 0 // — // — // — // –	LOC91431	LOC91431, Homo sapiens prematurely terminated decay factor-like (LOC91431), q25
SNP_A-1803955	gtcaatcatctatcac[A/G]ctcccttaagctagaa	A	G	NM_020977 // upstream // 195044 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 195044 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript vari	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1898770	tgctttctagaccaat[A/T]aactttctcatactga	A	T	NM_020977 // upstream // 121828 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 121828 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript vari	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-2118399	agtaagcaactcattc[A/G]agatacttcagccatc	A	G	NM_020977 // upstream // 61351 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 61351 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1978548	aatgcttctaaaccaa[C/G]aaattacagaaaacat	C	G	NM_020977 // upstream // 59902 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 59902 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1978550	gtagatgtgtttgtaa[C/T]atatgttgaatgtgta	C	T	NM_020977 // upstream // 43459 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 43459 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960559	ttttcataaatgtaa[C/G]taaccgccttttaaa	C	G	NM_020977 // upstream // 40156 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 40156 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1795029	ggtgaaggtgaattac[C/T]gctatcatctactatc	C	T	NM_020977 // upstream // 32732 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 32732 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1884941	tgaatgagagggaaaaa[C/G]agaagtgagccagttc	C	G	NM_020977 // upstream // 26536 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 26536 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1922847	ttagatcattggtggg[A/G]agtttgtgaaacgaaa	A	G	NM_020977 // upstream // 26417 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 26417 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-2210503	ccccttagtatagta[C/T]gcaaagtcagcctgtc	C	T	NM_020977 // upstream // 11241 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // upstream // 11241 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript varian	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q25
SNP_A-1827105	taaccattgccttttg[C/T]atttctaggtccaga	C	T	NM_020977 // intron // 0 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 1, mRNA. /	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26
SNP_A-1834078	tacatcacctcgtcaa[A/G]atcacttagaactaa	A	G	NM_020977 // intron // 0 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA. /// NM_001148 // intron // 0 // Hs.137367 // ANK2 // 287 // Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 1, mRNA. /	ANK2	ANK2, Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, q26
SNP_A-2119867	agtcaacattaaacaa[C/T]taataagtcaacaatt	C	T	NM_172127 // intron // 0 // Hs.144114 // CAMK2D // 817 // Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA. /// NM_172128 // intron // 0 // Hs.144114 // CAMK2D // 817 // Homo sapiens calci	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-2261036	gaaagaagctaattgc[A/C]gaacagtttacagagt	A	C	NM_172127 // intron // 0 // Hs.144114 // CAMK2D // 817 // Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA. /// NM_172128 // intron // 0 // Hs.144114 // CAMK2D // 817 // Homo sapiens calci	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-1905642	tggtataaaatgaaa[C/T]gaaaatgaacaaaata	C	T	NM_172127 // intron // 0 // Hs.144114 // CAMK2D // 817 // Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA. /// NM_172128 // intron // 0 // Hs.144114 // CAMK2D // 817 // Homo sapiens calci	CAMK2D	CAMK2D, Homo sapiens calcium q26
SNP_A-1978587	ctcataatgttcaaa[A/T]tggcctttaaagct	A	T	NM_024590 // upstream // 176053 // Hs.22895 // ARSJ // 79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 443568 // Hs.144197 // UGT8 // 7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936442	ttcttctgcttgatg[A/G]aattgatgtttgtctt	A	G	NM_024590 // upstream // 181389 // Hs.22895 // ARSJ // 79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 438232 // Hs.144197 // UGT8 // 7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1789375	gggccatgacacaata[A/G]taagatgcgtaaacat	A	G	NM_024590 // upstream // 181704 // Hs.22895 // ARSJ // 79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 437917 // Hs.144197 // UGT8 // 7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1926648	ttattgagctgtctca[A/C]ctgtggctatgtttgc	A	C	NM_024590 // upstream // 210665 // Hs.22895 // ARSJ // 79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 408956 // Hs.144197 // UGT8 // 7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-2304419	gctctaagcctggcta[C/T]gtgcaagttgaggttc	C	T	NM_024590 // upstream // 289831 // Hs.22895 // ARSJ // 79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 329790 // Hs.144197 // UGT8 // 7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1715143	taattatttaaaatatcaaaacatc[C/G]aatctttttatatcatctgag tacat	C	G	NM_003360 // upstream // 368489 // Hs.274293 // UGT8 // 7368 // UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) /// NM_024590 // upstream // 327298 // Hs.22895 // FLJ23548 // 79642 // hypothetical protein FLJ23548	UGT8	UGT8 , rs10516600, UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) ,q26
SNP_A-1758819	tgaatctatctttagagtgctta[C/T]gaagtttataaattctaacct ctt	C	T	NM_003360 // upstream // 350474 // Hs.274293 // UGT8 // 7368 // UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) /// NM_024590 // upstream // 345313 // Hs.22895 // FLJ23548 // 79642 // hypothetical protein FLJ23548	UGT8	UGT8 , rs9307402, UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) ,q26
SNP_A-2164325	caaaatcataggacca[C/G]aaacgcaaaaatagac	C	G	NM_024590 // upstream // 396684 // Hs.22895 // ARSJ // 79642 // Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /// NM_003360 // upstream // 222937 // Hs.144197 // UGT8 // 7368 // Homo sapiens UDP glycosyltransferase 8 (UDP-galactose ceramide	ARSJ	ARSJ, Homo sapiens hypothetical protein FLJ23548 (FLJ23548), q26
SNP_A-1872115	tctactatttggtgaa[A/C]cttgaattccagtttt	A	C	NM_022569 // upstream // 688806 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 688806 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sulfo	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-2298432	gcccaaaaatttcatca[A/T]tctgataaacaacttc	A	T	NM_022569 // upstream // 724639 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 724639 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sulfo	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-1781032	ggatgcagaaaaacca[A/G]taattaaaggcaaatg	A	G	NM_022569 // upstream // 1049708 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1049708 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase,q26
SNP_A-2303754	gctcagccgcaataca[A/G]tagaccaccagataga	A	G	NM_022569 // upstream // 1126816 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1126816 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase,q26

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839392	tagagttcatttttc[C/T]aggatggagatctcca	C	T	NM_022569 // upstream // 1192298 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1192298 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1836439	tactcattgcatttca[C/T]ggaaaacattacaact	C	T	NM_022569 // upstream // 1435266 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1435266 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1794753	ggtctgactcctccaa[A/G]catttggtaagggtgtg	A	G	NM_022569 // upstream // 1551504 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1551504 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2137759	atcatgtgcagacaga[A/G]aaactattgtactgtg	A	G	NM_022569 // upstream // 1612830 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1612830 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2026529	aaacaaattagctttta[A/C]gggccacaataatgaa	A	C	NM_022569 // upstream // 1626504 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1626504 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2145730	atgccaatcacctgag[A/G]agtgcactgctttgt	A	G	NM_022569 // upstream // 1639078 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1639078 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1887032	tgacttaagattatc[C/G]atgtgatttgctttgc	C	G	NM_022569 // upstream // 1639307 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1639307 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2075627	acatggaaatgcctta[C/T]catattagcagattag	C	T	NM_022569 // upstream // 1681350 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1681350 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1822297	gttttggcctcttccac[A/G]ctaagtcccagaccag	A	G	NM_022569 // upstream // 1697258 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1697258 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2223447	cgctgtgaaagagaga[C/T]gaatagctcgtaaaat	C	T	NM_022569 // upstream // 1745469 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1745469 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2152019	atgttttgtatcaat[A/T]aaagcctaacagatca	A	T	NM_022569 // upstream // 1767641 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1767641 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2205564	ccagttccatgactta[C/T]cacctgcagtctaaga	C	T	NM_022569 // upstream // 1826891 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1826891 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1816190	gttactacagtctgca[A/G]cagcgtgtttctaaa	A	G	NM_022569 // upstream // 1833499 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1833499 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2172096	caatgggataactgcc[A/G]aacaatcacttgacat	A	G	NM_022569 // upstream // 1856022 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1856022 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1830138	taatagagttgcacct[C/G]aacaactggaacggtta	C	G	NM_022569 // upstream // 1856710 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1856710 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-2196834	cattactttgaacca[A/G]tgatagaagataatgt	A	G	NM_022569 // upstream // 1896414 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1896414 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1844512	tataaatattgtgta[C/T]aattggcacagagctt	C	T	NM_022569 // upstream // 1920982 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1920982 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1677610	gatttctcttctctctctcattct[C/T]acaaatgtgcacataccac atacc	C	T	NM_022569 // upstream // 1833849 // Hs.302033 // NDST4 // 64579 // N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 /// NM_152402 // downstream // 135828 // Hs.154218 // TRAM1L1 // 133022 // translocation associated membrane protein 1-like 1	NDST4	NDST4 , rs7717904, N-deacetylase,q26
SNP_A-2136044	atcaaggatagaatgat[A/G]aatgtcgataggtgt	A	G	NM_022569 // upstream // 1957069 // Hs.309539 // NDST4 // 64579 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4), mRNA. /// NM_001543 // upstream // 1957069 // Hs.222055 // NDST1 // 3340 // Homo sapiens N-deacetylase/N-sul	NDST4	NDST4, Homo sapiens N-deacetylase q26
SNP_A-1978639	tccactgtaaaggcac[A/G]atacacaaatgtcct	A	G	NM_152402 // upstream // 11959 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 937104 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotra	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1756230	gtgttagtttctgtcttataggga[C/T]gatacattatttccttgaagca aac	C	T	NM_022569 // upstream // 1910223 // Hs.302033 // NDST4 // 64579 // N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 /// NM_152402 // downstream // 59454 // Hs.154218 // TRAM1L1 // 133022 // translocation associated membrane protein 1-like 1	NDST4	NDST4 , rs10516634, N-deacetylase,q26
SNP_A-1936344	ttcttcgttgattgaa[C/T]agaattatctttaca	C	T	NM_152402 // upstream // 447961 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 501102 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2077698	accactgagaactgat[C/T]gattacaactgccaat	C	T	NM_152402 // upstream // 602180 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 346883 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1978646	catattgtatgtgaaaa[C/T]tttgaaacagtaggt	C	T	NM_152402 // upstream // 643796 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 305267 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2206310	ccatcctatctactat[C/T]actggaaagcacttaa	C	T	NM_152402 // upstream // 656471 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 292592 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1829512	taagtgctcacccat[A/T]actttgtggaaaatca	A	T	NM_152402 // upstream // 658173 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 290890 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1816699	gttatattcaaagaga[A/G]attttggtcatcctc	A	G	NM_152402 // upstream // 660971 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 288092 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2091227	actttaacatggtaa[C/T]gaggaaaaaatgagt	C	T	NM_152402 // upstream // 664681 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 284382 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1786668	ggcttgcttacaataa[A/G]ggcagatatctcagag	A	G	NM_152402 // upstream // 670838 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 278225 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1978648	tataatataaacagca[A/G]aaggatcacatacatg	A	G	NM_152402 // upstream // 694897 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 254166 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2138089	atccaagacaacagcga[G/T]gagccttaggtgactg	G	T	NM_152402 // upstream // 708447 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 240616 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1937289	ttgaaactgaagagac[A/G]catccacagaactgt	A	G	NM_152402 // upstream // 709257 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 239806 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2156392	attctcatggaattc[C/T]aaaagagcaagcacaat	C	T	NM_152402 // upstream // 711011 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 238052 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1923023	ttagcagactggacad[A/G]ccgaggaaagaatctc	A	G	NM_152402 // upstream // 720073 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 228990 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-1713458	aggcaatcacatattgtatgtgaaaa[C/T]tttgaaacagtaggtttt gtccag	C	T	NM_004784 // upstream // 305155 // Hs.20028 // NDST3 // 9348 // N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 /// NM_152402 // upstream // 643613 // Hs.154218 // TRAM1L1 // 133022 // translocation associated membrane protein 1-like 1	NDST3	NDST3 , rs1459543, N-deacetylase,q26
SNP_A-1723664	aggtttggacccacccacaatgata[C/G]agaatacatatcaac aaacactata	C	G	NM_004784 // upstream // 304837 // Hs.20028 // NDST3 // 9348 // N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 /// NM_152402 // upstream // 643931 // Hs.154218 // TRAM1L1 // 133022 // translocation associated membrane protein 1-like 1	NDST3	NDST3 , rs4269248, N-deacetylase,q26
SNP_A-1875605	tctcttagaggatgac[A/G]gtcagaaacggaggaa	A	G	NM_152402 // upstream // 756213 // Hs.154218 // TRAM1L1 // 133022 // Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), mRNA. /// NM_004784 // upstream // 192850 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotr	TRAM1L1	TRAM1L1, Homo sapiens translocation associated membrane protein 1-like 1 (TRAM1L1), q26
SNP_A-2313589	ggagatcaatatagtg[C/G]atttacatgaaggga	C	G	NM_004784 // intron // 0 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 (NDST3), mRNA. /// ENST00000296499 // intron // 0 // — // — // — // —	NDST3	NDST3, Homo sapiens N-deacetylase q26
SNP_A-1955541	tttggtgggatttgga[A/G]ctttcctcctaaca	A	G	NM_004784 // intron // 0 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 (NDST3), mRNA. /// ENST00000296499 // intron // 0 // — // — // — // —	NDST3	NDST3, Homo sapiens N-deacetylase,q26
SNP_A-2252891	cttctattaaactgcct[A/G]attatctattcaattt	A	G	NM_004784 // intron // 0 // Hs.480596 // NDST3 // 9348 // Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 (NDST3), mRNA. /// ENST00000296499 // intron // 0 // — // — // — // —	NDST3	NDST3, Homo sapiens N-deacetylase,q26
SNP_A-1657536	atcattgggacaagtggaaaatcca[C/T]ggaatacacataiat atagtaaac	C	T	NM_014822 // upstream // 142485 // Hs.409424 // SEC24D // 9871 // SEC24 related gene family, member D (S. cerevisiae)	SEC24D	SEC24D , rs955753, SEC24 related gene family, member D (S. cerevisiae),q26
SNP_A-1868990	tcctgatggtgataca[A/G]cagcattgcgaagtct	A	G	NM_001083 // upstream // 206544 // Hs.370661 // PDE5A // 8654 // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, mRNA. /// NM_033437 // upstream // 206544 // Hs.370661 // PDE5A // 8654 // Homo sapiens phosphodiesterase 5A,	PDE5A	PDE5A, Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, q27
SNP_A-2296074	gcattatccatgacct[C/T]ccaaacagaacacaca	C	T	NM_001083 // upstream // 350136 // Hs.370661 // PDE5A // 8654 // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, mRNA. /// NM_033437 // upstream // 350136 // Hs.370661 // PDE5A // 8654 // Homo sapiens phosphodiesterase 5A,	PDE5A	PDE5A, Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, q27
SNP_A-1978716	ttgtcattaaattga[A/T]gtattgtcgatggag	A	T	NM_001083 // upstream // 352655 // Hs.370661 // PDE5A // 8654 // Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, mRNA. /// NM_033437 // upstream // 352655 // Hs.370661 // PDE5A // 8654 // Homo sapiens phosphodiesterase 5A,	PDE5A	PDE5A, Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1, q27
SNP_A-2273959	gactgtgaacctactc[A/G]ctacttgaaacaatgg	A	G	NM_002358 // upstream // 72809 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 72809 // — // — // — // — /// ENST00000333047 // upstream // 72809 // —	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113422	aggcgattaagtcaaa[A/G]tgaagccttagagta	A	G	NM_002358 // upstream // 158528 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 158528 /// ENST00000333047 // upstream // 158528 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-2034670	aaatgaaatattgtga[A/G]taaaatgctgagcaag	A	G	NM_002358 // upstream // 172575 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 172575 /// ENST00000333047 // upstream // 172575 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-2029565	aaagactgctgcagag[A/G]aacaccggcaagattt	A	G	NM_002358 // upstream // 179992 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 179992 /// ENST00000333047 // upstream // 179992 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-1803978	gtcaatgtaactgctg[A/G]agatcctaacacagga	A	G	NM_002358 // upstream // 180801 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 180801 /// ENST00000333047 // upstream // 180801 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-2116228	aggtacagtatacata[C/T]agaaaagtgcatagat	C	T	NM_002358 // upstream // 182513 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 182513 /// ENST00000333047 // upstream // 182513 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27 .
SNP_A-2037257	aacaaactgatccaa[G/T]tgtaagattgtacag	G	T	NM_002358 // upstream // 208427 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 208427 /// ENST00000333047 // upstream // 208427 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-1867253	tccctggtggcaaaac[A/G]attgggaccactgac	A	G	NM_002358 // upstream // 215631 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 215631 /// ENST00000333047 // upstream // 215631 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-2108054	agctctcctctgagc[A/C]ctgttttctgtaga	A	C	NM_002358 // upstream // 216348 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 216348 /// ENST00000333047 // upstream // 216348 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-2093611	agaagaagacgatgaa[C/G]cagctgtttccataat	C	G	NM_002358 // upstream // 225691 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 225691 /// ENST00000333047 // upstream // 225691 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-1936962	ttcttgtagagctca[A/G]gtcaaatgctacttct	A	G	NM_002358 // upstream // 238514 // Hs.533185 // MAD2L1 // 4085 // Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA. /// ENST00000296509 // upstream // 238514 /// ENST00000333047 // upstream // 238514 //	MAD2L1	MAD2L1, Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), q27
SNP_A-1697683	tatttttttatgaaggacttgaaa[G/T]ttatccagagcagtattaggcc	G	T	NM_002358 // upstream // 250525 // Hs.79078 // MAD2L1 // 4085 // MAD2 mitotic arrest deficient-like 1 (yeast) /// NM_018699 // downstream // 377444 // Hs.192867 // PRDM5 // 11107 // PR domain containing 5	MAD2L1	MAD2L1 . rs2715953, MAD2 mitotic arrest deficient-like 1 (yeast) ,q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1727481	ttatgtttgaatacttaagcataaa[C/T]gttaactggatatttcccttttgc	C	T	NM_002358 // upstream // 281767 // Hs.79078 // MAD2L1 // 4085 // MAD2 mitotic arrest deficient-like 1 (yeast) /// NM_018699 // downstream // 346202 // Hs.192867 // PRDM5 // 11107 // PR domain containing 5	MAD2L1	MAD2L1 , rs950658, MAD2 mitotic arrest deficient-like 1 (yeast) ,q27
SNP_A-2221723	cctttgttgcatcccc[A/C]attttcaaaattatgc	A	C	NM_018699 // downstream // 219209 // Hs.132593 // PRDM5 // 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 132937 // — // — // — /// ENST00000264808 // downstream // 219209 // — // — // —	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1936401	ttcttctggctagta[C/T]cttatcaaatagacat	C	T	NM_018699 // downstream // 215087 // Hs.132593 // PRDM5 // 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000309746 // downstream // 137059 // — // — // — /// ENST00000264808 // downstream // 215087 // — // — // —	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1726962	taagcagatatgcttgcaaaaacaa[A/C]atcatctttacagtacatggaaaa	A	C	NM_002358 // upstream // 477470 // Hs.79078 // MAD2L1 // 4085 // MAD2 mitotic arrest deficient-like 1 (yeast) /// NM_018699 // downstream // 150499 // Hs.192867 // PRDM5 // 11107 // PR domain containing 5	MAD2L1	MAD2L1 , rs4088802, MAD2 mitotic arrest deficient-like 1 (yeast) ,q27
SNP_A-2183234	cagcaataagaaactc[A/C]gaaaggctcagggccc	A	C	NM_018699 // intron // 0 // Hs.132593 // PRDM5 // 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// ENST00000264808 // intron // 0 // — // — // —	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-1889260	tgagtgataggctcag[A/G]agaacacttacttttca	A	G	NM_018699 // upstream // 93066 // Hs.132593 // PRDM5 // 11107 // Homo sapiens PR domain containing 5 (PRDM5), mRNA. /// NM_024574 // downstream // 19703 // Hs.16026 // FLJ23191 // 79625 // Homo sapiens hypothetical protein FLJ23191 (FLJ23191), mRNA. /// E	PRDM5	PRDM5, Homo sapiens PR domain containing 5 (PRDM5), q27
SNP_A-2218634	cctggccaaatcttga[C/T]gttaatatatctgttt	C	T	NM_024574 // intron // 0 // Hs.16026 // FLJ23191 // 79625 // Homo sapiens hypothetical protein FLJ23191 (FLJ23191), mRNA. /// ENST00000309554 // intron // 0 // — // — // —	FLJ23191	FLJ23191, Homo sapiens hypothetical protein FLJ23191 (FLJ23191), q27
SNP_A-1736249	taagtagaagagcctaggatcaaata[C/G]gtctgttcaatcacaaatcccatgt	C	G	NM_024574 // upstream // 39843 // Hs.16026 // FLJ23191 // 79625 // hypothetical protein FLJ23191 /// NM_024873 // downstream // 19155 // Hs.208206 // TNIP3 // 79931 // TNFAIP3 interacting protein 3	FLJ23191	FLJ23191 , rs10518381, hypothetical protein FLJ23191 ,q27
SNP_A-2156573	attctgaatttgtgaa[C/T]gattacacccaggtta	C	T	NM_024873 // upstream // 113295 // Hs.208206 // TNIP3 // 79931 // Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), mRNA. /// NM_198179 // downstream // 51698 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA.	TNIP3	TNIP3, Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), q27
SNP_A-1688474	cagctaaaacctgaacaacgacaaa[C/G]tgaaaggactctgaccctccggcaa	C	G	AF411117 // downstream // 150949 // - // - // - // Homo sapiens G protein-coupled receptor (GPR103) mRNA, complete cds. /// NM_024873 // upstream // 14044 // Hs.208206 // TNIP3 // 79931 // TNFAIP3 interacting protein 3	-	-, rs10518384, Homo sapiens G protein-coupled receptor (GPR103) mRNA, complete cds. ,q27
SNP_A-2259084	cttttttgtatacac[A/G]gatgttgagtctgcaa	A	G	NM_024873 // upstream // 133994 // Hs.208206 // TNIP3 // 79931 // Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), mRNA. /// NM_198179 // downstream // 30999 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA.	TNIP3	TNIP3, Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), q27
SNP_A-1870222	tcctttccaatctgga[C/T]ggctttacttatttt	C	T	NM_024873 // upstream // 148494 // Hs.208206 // TNIP3 // 79931 // Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), mRNA. /// NM_198179 // downstream // 16499 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA.	TNIP3	TNIP3, Homo sapiens TNFAIP3 interacting protein 3 (TNIP3), q27
SNP_A-1782354	ggcaatgtagagatgt[C/G]acaaactggaagtcca	C	G	NM_198179 // intron // 0 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// ENST00000334383 // intron // 0 // — // — // —	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1667904	ggcacagtaagataagtgagggtga[C/T]gtaatggaaggaact ggagtctgac	C	T	AF411117 // intron // 0 // - // - // Homo sapiens G protein-coupled receptor (GPR103) mRNA, complete cds.	-	-, rs10518387, Homo sapiens G protein-coupled receptor (GPR103) mRNA, complete cds., q27
SNP_A-2200710	ccaagacaaggacccac[C/G]aggctaaaagatttt	C	G	NM_198179 // upstream // 154328 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// NM_001154 // downstream // 133018 // Hs.480653 // ANXA5 // 308 // Homo sapiens annexin A5 (ANXA5), mRNA. /// ENST00000334383	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27
SNP_A-2136889	atcagagcacataggg[A/G]aagcttattgcttagt	A	G	NM_198179 // upstream // 208047 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// NM_001154 // downstream // 79299 // Hs.480653 // ANXA5 // 308 // Homo sapiens annexin A5 (ANXA5), mRNA. /// ENST00000334383	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27
SNP_A-2010122	gcacgtggtgagattc[C/T]cttgactgtcattcaa	C	T	NM_198179 // upstream // 248997 // Hs.368977 // GPR103 // 84109 // Homo sapiens G protein-coupled receptor 103 (GPR103), mRNA. /// NM_001154 // downstream // 38349 // Hs.480653 // ANXA5 // 308 // Homo sapiens annexin A5 (ANXA5), mRNA. /// ENST00000334383	GPR103	GPR103, Homo sapiens G protein-coupled receptor 103 (GPR103), q27
SNP_A-2186517	cagggacatattgaat[A/C]aagactggataagaaa	A	C	NM_001154 // upstream // 10379 // Hs.480653 // ANXA5 // 308 // Homo sapiens annexin A5 (ANXA5), mRNA. /// NM_152399 // downstream // 51539 // Hs.27524 // FLJ30834 // 132332 // Homo sapiens hypothetical protein FLJ30834 (FLJ30834), mRNA. /// ENST00000296511	ANXA5	ANXA5, Homo sapiens annexin A5 (ANXA5), q27
SNP_A-1823548	taaaagtcttgagacg[A/C]attctgattgaatagg	A	C	NM_001154 // upstream // 54794 // Hs.480653 // ANXA5 // 308 // Homo sapiens annexin A5 (ANXA5), mRNA. /// NM_152399 // downstream // 7124 // Hs.27524 // FLJ30834 // 132332 // Homo sapiens hypothetical protein FLJ30834 (FLJ30834), mRNA. /// ENST00000296511	ANXA5	ANXA5, Homo sapiens annexin A5 (ANXA5), q27
SNP_A-2245353	ctggcttggagagaga[A/G]gcaaggactctttta	A	G	NM_152399 // upstream // 11543 // Hs.27524 // FLJ30834 // 132332 // Homo sapiens hypothetical protein FLJ30834 (FLJ30834), mRNA. /// NM_005033 // upstream // 24592 // Hs.91728 // EXOSC9 // 5393 // Homo sapiens exosome component 9 (EXOSC9), mRNA. /// NM_00	FLJ30834	FLJ30834, Homo sapiens hypothetical protein FLJ30834 (FLJ30834), q27
SNP_A-1916604	tgtttataagactcac[C/T]gtaaaatctccagact	C	T	NM_003305 // upstream // 30873 // Hs.150981 // TRPC3 // 7222 // Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), mRNA. /// ENST00000264811 // upstream // 30873 // — // — // — /// ENST00000343946 // upst	TRPC3	TRPC3, Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), q27
SNP_A-1978772	atcctcagttgcaaaa[A/G]ctctgtgtttcaggca	A	G	NM_003305 // upstream // 94086 // Hs.150981 // TRPC3 // 7222 // Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), mRNA. /// ENST00000264811 // upstream // 94086 // — // — // — /// ENST00000343946 // upst	TRPC3	TRPC3, Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), q27
SNP_A-2073688	acagtcatttccccaa[A/C]catttaggctttctgag	A	C	NM_003305 // upstream // 94441 // Hs.150981 // TRPC3 // 7222 // Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), mRNA. /// ENST00000264811 // upstream // 94441 // — // — // — /// ENST00000343946 // upst	TRPC3	TRPC3, Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), q27
SNP_A-1739261	tttgtagacaattagcaaaatttg[A/G]aagagaictgtagatga aagttagt	A	G	NM_003305 // upstream // 159617 // Hs.150981 // TRPC3 // 7222 // transient receptor potential cation channel, subfamily C, member 3	TRPC3	TRPC3, rs1405483, transient receptor potential cation channel, subfamily C, member 3,q27
SNP_A-1685606	gcacttggatggtcgaattttagc[C/T]ctatgtcacaactgactag acatta	C	T	NM_003305 // upstream // 163528 // Hs.150981 // TRPC3 // 7222 // transient receptor potential cation channel, subfamily C, member 3	TRPC3	TRPC3, rs3108397, transient receptor potential cation channel, subfamily C, member 3,q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1904559	tggggcaaataaggaa[C/G]tacattaaacctaagt	C	G	NM_145207 // intron // 0 // Hs.480672 // SPATA5 // 166378 // Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q27
SNP_A-2043979	aacttgaatatcatcc[A/G]aactgctttctcct	A	G	NM_145207 // intron // 0 // Hs.480672 // SPATA5 // 166378 // Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1
SNP_A-1824519	taaactgtgtactacc[A/G]ccatttaattaataa	A	G	NM_145207 // intron // 0 // Hs.480672 // SPATA5 // 166378 // Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1
SNP_A-2171884	caatgatagtgtttcc[A/G]aagtcatgtgggccac	A	G	NM_145207 // intron // 0 // Hs.480672 // SPATA5 // 166378 // Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// ENST00000274008 // intron // 0 // --- // --- // ---	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1
SNP_A-1906585	tggtgtaaaattgaaa[C/T]ctgtaatacgtgttat	C	T	NM_145207 // downstream // 5135 // Hs.480672 // SPATA5 // 166378 // Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// NM_005841 // upstream // 77019 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1
SNP_A-1978786	cctctttcctactgcc[A/G]aggtgatctttctcct	A	G	NM_145207 // downstream // 70007 // Hs.480672 // SPATA5 // 166378 // Homo sapiens spermatogenesis associated 5 (SPATA5), mRNA. /// NM_005841 // upstream // 12147 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling	SPATA5	SPATA5, Homo sapiens spermatogenesis associated 5 (SPATA5), q28.1
SNP_A-1922279	ttactttcatctcctc[A/G]caacatatttcccac	A	G	NM_005841 // downstream // 91755 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 91755 // Hs.436944 // SPRY1 // 10252 // Homo sa	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2273615	gactgagcccattcag[A/G]ccaaacagagtcagca	A	G	NM_005841 // downstream // 125241 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 125241 // Hs.436944 // SPRY1 // 10252 // Homo	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-1670221	ctgaaaatgtacagtggttgcatta[C/T]agccagaggtgtgctga aggtagct	C	T	AB033049 // downstream // 1168493 // Hs.28783 // KIAA1223 // 57182 // KIAA1223 protein	KIAA1223	KIAA1223 , rs896678, KIAA1223 protein,q28.1
SNP_A-1697847	ggatgggctgtcatcagtagattg[C/T]tgaaaaatattccacaa ccagttct	C	T	AB033049 // downstream // 1168294 // Hs.28783 // KIAA1223 // 57182 // KIAA1223 protein	KIAA1223	KIAA1223 , rs896676, KIAA1223 protein,q28.1
SNP_A-1685824	atgacatttatcaatgtgttttcac[A/G]aggtggtatatcgaataag gcagtt	A	G	AB033049 // downstream // 958797 // Hs.28783 // KIAA1223 // 57182 // KIAA1223 protein	KIAA1223	KIAA1223 , rs9307531, KIAA1223 protein,q28.1
SNP_A-2170991	caataattgtaacaaa[A/G]atggagttatagtac	A	G	NM_005841 // downstream // 441424 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 441424 // Hs.436944 // SPRY1 // 10252 // Homo	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-1747387	atatgctgtaatgccgtattaccac[A/G]attaagtatactgctgtac aactaa	A	G	AB033049 // downstream // 791441 // Hs.28783 // KIAA1223 // 57182 // KIAA1223 protein	KIAA1223	KIAA1223 , rs9866345, KIAA1223 protein,q28.1
SNP_A-1978800	ggaagaatgatcaaaa[C/T]acagactgcctcttca	C	T	NM_005841 // downstream // 761747 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 761747 // Hs.436944 // SPRY1 // 10252 // Homo	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-2264931	gaagaggaggtccagg[A/G]aagtgtatatttgag	A	G	NM_005841 // downstream // 812010 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 812010 // Hs.436944 // SPRY1 // 10252 // Homo	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1648592	gcttttgaaccagtctagtatt[A/C]ctggttccctcattatgagtt gat	A	C	AB033049 // downstream // 517375 // Hs.28783 // KIAA1223 // 57182 // KIAA1223 protein	KIAA1223	KIAA1223 , rs720900, KIAA1223 protein,q28.1
SNP_A-1891754	tgatttaggcaggaaa[C/T]tggcaaaagataaatc	C	T	NM_005841 // downstream // 1008009 // Hs.436944 // SPRY1 // 10252 // Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, mRNA. /// NM_199327 // downstream // 1008009 // Hs.436944 // SPRY1 // 10252 // Hom	SPRY1	SPRY1, Homo sapiens sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 1, q28.1
SNP_A-1655325	ctgaagaacccgcatggatcatac[C/T]ctgatgatttaaaccaa acaaaaga	C	T	AB033049 // downstream // 120481 // Hs.28783 // KIAA1223 // 57182 // KIAA1223 protein	KIAA1223	KIAA1223 , rs1567396, KIAA1223 protein,q28.1
SNP_A-1816816	gttatgatggaagaaa[C/T]gcactcgggttgctg	C	T	AB033049 // CDS // 0 // Hs.480694 // KIAA1223 // 57182 // Homo sapiens mRNA for KIAA1223 protein, partial cds. /// ENST00000281131 // CDS // 0 // — // — // —	KIAA1223	KIAA1223, Homo sapiens for KIAA1223 protein, partial cds, q28.1
SNP_A-1942118	ttggattcaagtacag[C/T]attgcatttatgata	C	T	ENST00000281133 // downstream // 45138 // — // — // — // — /// ENST00000357142 // upstream // 226799 // — // — // — // — /// ENST00000327537 // upstream // 226880 // — // — // — // —	-	q28.1
SNP_A-1978829	tcatatacttcatata[A/C]aatttcacttgtgcta	A	C	NM_024582 // upstream // 44318 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 28971 // — // — // — // — /// ENST00000357142 // downstream // 28971 // — // — // — // — /// ENST00000327537 // downstream // 28971 // — // — // — // —	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2045346	aagaagtgtttggca[C/G]tgattggaggcaca	C	G	NM_024582 // downstream // 26270 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 26270 // — // — // — // — /// ENST00000335110 // downstream // 26270 // — // — // — // -	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1914106	tgtgtgtagtaagatc[A/G]ctcggtctcctctta	A	G	NM_024582 // downstream // 43724 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 43724 // — // — // — // — /// ENST00000335110 // downstream // 43724 // — // — // — // -	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2033449	aaatagtaacaaagaa[C/T]gagtagttctaagt	C	T	NM_024582 // downstream // 393466 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 393466 // — // — // — // — /// ENST00000335110 // downstream // 393466 // — // — // — // — /	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2201119	ccaagtctgagacaaa[A/C]tcggaaaattatctta	A	C	NM_024582 // downstream // 395268 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 395268 // — // — // — // — /// ENST00000335110 // downstream // 395268 // — // — // — // — /	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1711640	tcttgggtgaagagggataagactc[A/C]gacacattctacagttt ctcggaga	A	C	NM_015693 // upstream // 1742229 // Hs.391481 // PDZK6 // 27152 // PDZ domain containing 6 /// NM_024582 // downstream // 397800 // Hs.25201 // FATJ // 79633 // fat-like cadherin FATJ	PDZK6	PDZK6 , rs10518476, PDZ domain containing 6 ,q28.1
SNP_A-1670001	tccacagcagtcaacttaatggtca[G/T]ataattaaagtttatgtat gtgcaa	G	T	NM_015693 // upstream // 1741040 // Hs.391481 // PDZK6 // 27152 // PDZ domain containing 6 /// NM_024582 // downstream // 398989 // Hs.25201 // FATJ // 79633 // fat-like cadherin FATJ	PDZK6	PDZK6 , rs9307579, PDZ domain containing 6 ,q28.1
SNP_A-2028795	aaacttctaggaatta[C/T]ggtagcagtgatattt	C	T	NM_024582 // downstream // 506480 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 506480 // — // — // — // — /// ENST00000335110 // downstream // 506480 // — // — // — // — /	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2238810	ctcttagccccctctc[A/G]aaaatagtctatcat	A	G	NM_024582 // downstream // 564165 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 564165 // — // — // — // — /// ENST00000335110 // downstream // 564165 // — // — // — // — /	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-2029382	aaagacaactacagag[C/T]ggtattcttcatagac	C	T	NM_024582 // downstream // 663265 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 663265 // — // — // — // — /// ENST00000335110 // downstream // 663265 // — // — // — // — /	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2272986	gactagccatttgcca[A/G]taatcataaactctgg	A	G	NM_024582 // downstream // 1001329 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 1001329 // — // — // — // — /// ENST00000335110 // downstream // 1001329 // — // — // –	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1978855	gatacagagctttcca[A/T]ctttatgttattatga	A	T	NM_024582 // downstream // 1042574 // Hs.269121 // FAT4 // 79633 // Homo sapiens fat-like cadherin FATJ (FATJ), mRNA. /// ENST00000330166 // downstream // 1042574 // — // — // — // — /// ENST00000335110 // downstream // 1042574 // — // — // –	FAT4	FAT4, Homo sapiens fat-like cadherin FATJ (FATJ), q28.1
SNP_A-1694217	tagtatctgcagtttcaggcataga[A/C]taagaggcttgaattcccctgcaga	A	C	NM_015693 // upstream // 1114106 // Hs.391481 // PDZK6 // 27152 // PDZ domain containing 6 /// NM_024582 // downstream // 1025923 // Hs.25201 // FATJ // 79633 // fat-like cadherin FATJ	PDZK6	PDZK6 , rs1397676, PDZ domain containing 6 ,q28.1
SNP_A-1647110	acaaattatgtccacaaatgtttga[C/T]acttctgcaattgagaggcaggttt	C	T	NM_015693 // upstream // 1105975 // Hs.391481 // PDZK6 // 27152 // PDZ domain containing 6 /// NM_024582 // downstream // 1034054 // Hs.25201 // FATJ // 79633 // fat-like cadherin FATJ	PDZK6	PDZK6 , rs1877169, PDZ domain containing 6 ,q28.1
SNP_A-2074553	acataggctgggatca[G/T]actcatgcatctgaga	G	T	NM_015693 // upstream // 933261 // Hs.391481 // PDZK6 // 27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 134920 // — // — // — // — /// ENST00000344124 // downstream // 134940 // — // — // —	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-1664902	gcagagaaatatttaaatatacctg[A/G]atccaaattacattttcctctact	A	G	NM_015693 // upstream // 1001540 // Hs.391481 // PDZK6 // 27152 // PDZ domain containing 6 /// NM_024582 // downstream // 1138489 // Hs.25201 // FATJ // 79633 // fat-like cadherin FATJ	PDZK6	PDZK6 , rs1160368, PDZ domain containing 6 ,q28.1
SNP_A-2283402	gataccatgcctgaaa[A/G]agaatctgaaacatta	A	G	NM_015693 // upstream // 863205 // Hs.391481 // PDZK6 // 27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 204976 // — // — // — // — /// ENST00000344124 // downstream // 204996 // — // — // —	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-2052115	aaggtttgggtctaac[A/G]cctgtgaaagaaacgg	A	G	NM_015693 // upstream // 294224 // Hs.391481 // PDZK6 // 27152 // Homo sapiens PDZ domain containing 6 (PDZK6), mRNA. /// ENST00000331863 // downstream // 773957 // — // — // — // — /// ENST00000344124 // downstream // 773977 // — // — // —	PDZK6	PDZK6, Homo sapiens PDZ domain containing 6 (PDZK6), q28.1
SNP_A-1915922	tgttgatacactttta[G/T]gtagtaccaggttttg	G	T	NM_006320 // upstream // 239012 // Hs.507910 // PGRMC2 // 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream // 283013 // Hs.12420 // PHF17 // 79960 // Homo sapiens PHD finger protein 17 (PHF17), tra	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-2228185	ctactcaagacagtac[G/T]cataagtgccaattaa	G	T	NM_006320 // upstream // 350567 // Hs.507910 // PGRMC2 // 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream // 171458 // Hs.12420 // PHF17 // 79960 // Homo sapiens PHD finger protein 17 (PHF17), tra	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-2113323	aggcctgataagggaa[C/T]ctggaaacagcatcaa	C	T	NM_006320 // upstream // 372848 // Hs.507910 // PGRMC2 // 10424 // Homo sapiens progesterone receptor membrane component 2 (PGRMC2), mRNA. /// NM_024900 // upstream // 149177 // Hs.12420 // PHF17 // 79960 // Homo sapiens PHD finger protein 17 (PHF17), tra	PGRMC2	PGRMC2, Homo sapiens progesterone receptor membrane component 2 (PGRMC2), q28.2
SNP_A-1918836	ttaacagtaatggaac[A/C]aatgtgaagcttctgc	A	C	NM_173487 // downstream // 353496 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 353496 // — // — // — // — /// ENST00000341793 // upstream // 436993 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1876502	tctgatgatataccaa[A/G]gattaagtgagtgaag	A	G	NM_173487 // downstream // 356557 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 356557 // — // — // — /// ENST00000341793 // upstream // 433932 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2060934	aatgatgcatgtaatg[A/G]attagagttgaagata	A	G	NM_173487 // downstream // 380266 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 380266 // — // — // — /// ENST00000341793 // upstream // 410223 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1850139	tatgtggaatgtggaa[G/T]ttatgttttacatgt	G	T	NM_173487 // downstream // 380335 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 380335 // — // — // — /// ENST00000341793 // upstream // 410154 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2289152	gattgaaatgacaaa[A/C]aagatatccagcaaag	A	C	NM_173487 // downstream // 381309 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 381309 // — // — // — /// ENST00000341793 // upstream // 409180 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2110019	aggaagagagcaaaga[C/T]agtaaaagcatggcct	C	T	NM_173487 // downstream // 381484 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 381484 // — // — // — /// ENST00000341793 // upstream // 409005 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1951339	ttccctctcctttaj[A/G]gcaatcatacaaataa	A	G	NM_173487 // downstream // 408581 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 408581 // — // — // — /// ENST00000341793 // upstream // 381908 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2215160	cctatttgtctgtgaa[A/G]taagttggtgtaaata	A	G	NM_173487 // downstream // 414948 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 414948 // — // — // — /// ENST00000341793 // upstream // 375541 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2124192	agttagtctgcctaga[C/T]ggggaagaacatttgg	C	T	NM_173487 // downstream // 422460 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 422460 // — // — // — /// ENST00000341793 // upstream // 368029 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2165369	caaagatcttacaaag[C/G]cttactgctgttctc	C	G	NM_173487 // downstream // 432786 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 432786 // — // — // — /// ENST00000341793 // upstream // 357703 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1978909	gcctacatgaaaaaga[A/C]cactaggatttcagtc	A	C	NM_173487 // downstream // 441243 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 441243 // — // — // — /// ENST00000341793 // upstream // 349246 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1878908	tctgttttacaccta[C/T]gccgggtcaataggat	C	T	NM_173487 // downstream // 485462 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 485462 // — // — // — /// ENST00000341793 // upstream // 305027 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2301023	gccttagatgatcaag[A/G]atagaagtatgagagg	A	G	NM_173487 // downstream // 501307 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 501307 // — // — // — /// ENST00000341793 // upstream // 289182 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-2124949	agttgagttaatttca[C/T]ccaaattgcataactg	C	T	NM_173487 // downstream // 504746 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 504746 // — // — // — /// ENST00000341793 // upstream // 285743 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1660059	gggggctgataaaaaacttaacttca[A/T]ctagtatccagtatgtgc aacatag	A	T	NM_020815 // upstream // 3617394 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 // upstream // 3617394 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_173487 // downstream // 419234 // Hs.128777 // LOC132321 // 132321 // hyp	PCDH10	PCDH10, rs642218, protocadherin 10 ,q28.2
SNP_A-1809492	gtgagacagaaaactag[A/T]ccctcaaacagtcttc	A	T	NM_173487 // downstream // 529067 // Hs.533190 // LOC132321 // 132321 // Homo sapiens hypothetical protein LOC132321 (LOC132321), mRNA. /// ENST00000281146 // downstream // 529067 // — // — // — /// ENST00000341793 // upstream // 261422 // –	LOC132321	LOC132321, Homo sapiens hypothetical protein LOC132321 (LOC132321), q28.2
SNP_A-1735765	cataacggctgtctcatttttatact[C/G]ctactaacagtgcacaaa gcttcca	C	G	NM_020815 // upstream // 3511698 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 // upstream // 3511698 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_173487 // downstream // 524930 // Hs.128777 // LOC132321 // 132321 // hyp	PCDH10	PCDH10, rs2391475, protocadherin 10 ,q28.2
SNP_A-1724602	agtaaaacttctatagtgttataa[C/T]taaagtaagcatgaatata tacaat	C	T	NM_020815 // upstream // 3141010 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 // upstream // 3141010 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_173487 // downstream // 895618 // Hs.128777 // LOC132321 // 132321 // hyp	PCDH10	PCDH10, rs10518559, protocadherin 10 ,q28.2
SNP_A-1808289	gtcttgtgagagata[A/C]cacctctacctgtgct	A	C	ENST00000341793 // downstream // 303107 // — // — // — /// ENST00000357636 // upstream // 1147054 // — // — // — /// ENST00000357643 // upstream // 1147699 // — // — // — /// ENST00000358710 // downstream // 1192173	-	q28.2
SNP_A-1949167	ttatggatagagaaa[C/G]aaaacctgcaactac	C	G	ENST00000341793 // downstream // 387053 // — // — // — /// ENST00000357636 // upstream // 1063108 // — // — // — /// ENST00000357643 // upstream // 1063753 // — // — // — /// ENST00000358710 // downstream // 1108227	-	q28.3
SNP_A-2148926	atggtgtttacaagac[A/C]gcaaaaatgttacacg	A	C	ENST00000341793 // downstream // 424905 // — // — // — /// ENST00000357636 // upstream // 1025256 // — // — // — /// ENST00000357643 // upstream // 1025901 // — // — // — /// ENST00000358710 // downstream // 1070375	-	q28.3
SNP_A-1666900	atattaattccatggctaattcaa[C/T]tattcaacaagcatcccac atcatt	C	T	NM_020815 // upstream // 2827643 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 // upstream // 2827643 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_173487 // downstream // 1208985 // Hs.128777 // LOC132321 // 132321 // hy	PCDH10	PCDH10, rs9307625, protocadherin 10 ,q28.3
SNP_A-1812433	gtggcagtaggcttat[G/T]gctgaattacttctt	G	T	ENST00000341793 // downstream // 743499 // — // — // — /// ENST00000357636 // upstream // 706662 // — // — // — /// ENST00000357643 // upstream // 707307 // — // — // — /// ENST00000358710 // downstream // 751781 //	-	q28.3
SNP_A-2148161	atgggactgactgaaaa[C/T]gtaggatgaatttact	C	T	ENST00000341793 // downstream // 783217 // — // — // — /// ENST00000357636 // upstream // 666944 // — // — // — /// ENST00000357643 // upstream // 667589 // — // — // — /// ENST00000358710 // downstream // 712063 //	-	q28.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2262394	gaaatgcatctagaca[A/G]aaaccttaacactttt	A	G	ENST00000341793 // downstream // 786952 // — // — // — /// ENST00000357636 // upstream // 663209 // — // — // — /// ENST00000357643 // upstream // 663854 // — // — // — /// ENST00000358710 // downstream // 708328 //	-	q28.3
SNP_A-1805787	gtccccgggctgtgga[A/C]atgtctttatctaca	A	C	ENST00000341793 // downstream // 902402 // — // — // — /// ENST00000357636 // upstream // 547759 // — // — // — /// ENST00000357643 // upstream // 548404 // — // — // — /// ENST00000358710 // downstream // 592878 //	-	q28.3
SNP_A-1744549	ataaccaaactaacctagcccta[A/T]catagacaaaataagc cagtttcaa	A	T	NM_020815 // upstream // 2354991 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 // upstream // 2354991 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_173487 // downstream // 1681637 // Hs.128777 // LOC132321 // 132321 // hy	PCDH10	PCDH10 , rs306388, protocadherin 10 , q28.3
SNP_A-1829393	tagctcaacagtcaa[A/G]caatatttgtatcag	A	G	ENST00000341793 // downstream // 1199753 // — // — // — /// ENST00000357636 // upstream // 250408 // — // — // — /// ENST00000357643 // upstream // 251053 // — // — // — /// ENST00000358710 // downstream // 295527 //	-	q28.3
SNP_A-2120963	agtctatatttggaca[C/T]ctttttgtgtgtg	C	T	ENST00000341793 // downstream // 1230245 // — // — // — /// ENST00000357636 // upstream // 219916 // — // — // — /// ENST00000357643 // upstream // 220561 // — // — // — /// ENST00000358710 // downstream // 265035 //	-	q28.3
SNP_A-2031756	aaagtagtcactttca[C/T]ctatggacatttgtag	C	T	ENST00000341793 // downstream // 1396416 // — // — // — /// ENST00000357636 // upstream // 53745 // — // — // — /// ENST00000357643 // upstream // 54390 // — // — // — /// ENST00000358710 // downstream // 98864 // -	-	q28.3
SNP_A-1860478	tcagttaatctttgca[C/T]atggtgataagtagga	C	T	ENST00000341793 // downstream // 1413142 // — // — // — /// ENST00000357636 // upstream // 37019 // — // — // — /// ENST00000357643 // upstream // 37664 // — // — // — /// ENST00000358710 // downstream // 82138 // -	-	q28.3
SNP_A-1934763	ttctcttctgccaaat[A/G]ataaatataatcatag	A	G	ENST00000357643 // intron // 0 // — // — // — /// ENST00000358710 // intron // 0 // — // — // —	-	q28.3
SNP_A-2264559	gaagaagcaaaataacf[A/G]tatgtgaacaagagt	A	G	ENST00000357636 // intron // 0 // — // — // — /// ENST00000360725 // intron // 0 // — // — // —	-	q28.3
SNP_A-2074214	acataagaatgttcad[C/T]aacaagcctaaaaaat	C	T	ENST00000357636 // downstream // 218553 // — // — // — /// ENST00000357643 // downstream // 150363 // — // — // — /// ENST00000358710 // upstream // 136221 // — // — // — /// ENST00000360725 // upstream // 152941 //	-	q28.3
SNP_A-2091038	actttgacaggaaaac[A/C]aaatttaactagcaaa	A	C	ENST00000357636 // downstream // 279415 // — // — // — /// ENST00000357643 // downstream // 211225 // — // — // — /// ENST00000358710 // upstream // 197083 // — // — // — /// ENST00000360725 // upstream // 213803 //	-	q28.3
SNP_A-1698831	aactgtttgaatattaaaatctta c[C/T]caaagctaaggataaaat gtccatt	C	T	NM_020815 // upstream // 942818 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 // upstream // 942818 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_173487 // downstream // 3093810 // Hs.128777 // LOC132321 // 132321 // hypo	PCDH10	PCDH10 , rs348085, protocadherin 10 , q28.3
SNP_A-2140473	atctccagctttgca[A/G]cagtaatctgacctc	A	G	NM_020815 // upstream // 716940 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // upstream // 716940 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcrip	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1896882	tgctcactggagtcac[A/C]attattggaaattcat	A	C	NM_020815 // downstream // 419694 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 419694 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1826279	taaattgcttaatata[G/T]gccctgtgcaacaaaa	G	T	NM_020815 // downstream // 423869 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 423869 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1953483	ttgaaggtgcatttta[A/G]actatcaacagacttt	A	G	NM_020815 // downstream // 424016 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 424016 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2166999	caacaacagcaagaac[C/T]aaactgaaaaataagt	C	T	NM_020815 // downstream // 438567 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 438567 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1860721	tcataacacatagtag[C/G]caggatctatttaact	C	G	NM_020815 // downstream // 473434 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 473434 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1934168	ttctcatctgtggcac[A/G]agaacaaaaataatcat	A	G	NM_020815 // downstream // 473463 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 473463 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1952465	tttctgacactgacct[C/G]aatcttctttccttt	C	G	NM_020815 // downstream // 473955 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 473955 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1814787	gtgtgtgaaactacca[G/T]gagagaagttcagttt	G	T	NM_020815 // downstream // 484304 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 484304 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2126411	ataaaagagtagataaa[C/T]agtgccacttccctt	C	T	NM_020815 // downstream // 484771 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 484771 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-2088255	actggtggccaccaaaa[C/T]gatgatttttctgaaa	C	T	NM_020815 // downstream // 505253 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA. /// NM_032961 // downstream // 505253 // Hs.192859 // PCDH10 // 57575 // Homo sapiens protocadherin 10 (PCDH10), trans	PCDH10	PCDH10, Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, q28.3
SNP_A-1717433	ttctgtatccacatggtgttgctag[A/C]agtattatatctttttggtaag agag	A	C	NM_014331 // downstream // 4679908 // Hs.6682 // SLC7A11 // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 455982 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 /	SLC7A11	SLC7A11 , rs925084, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11, q28.3
SNP_A-1716065	atgtctttactctctatatggaaaa[C/T]gaattagaaagttcacac aggtcca	C	T	NM_014331 // downstream // 4655439 // Hs.6682 // SLC7A11 // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 480451 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 /	SLC7A11	SLC7A11 , rs2660727, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11, q28.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1739469	atataatttttgctctgtctattat[C/T]actcaaacatttcaatccagtg taa	C	T	NM_014331 // downstream // 4638767 // Hs.6682 // SLC7A11 // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 497123 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 /	SLC7A11	SLC7A11, rs2724261, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 ,q28.3
SNP_A-1695039	ggatttttttaagtgatagtcttaa[A/G]gttgatcaaactactataaa aatta	A	G	NM_014331 // downstream // 4590710 // Hs.6682 // SLC7A11 // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 545180 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 /	SLC7A11	SLC7A11, rs7671017, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 ,q28.3
SNP_A-1688004	taagactatcacttaaaaaaatcca[C/G]aatcctttattcagtttt gttgt	C	G	NM_014331 // downstream // 4590683 // Hs.6682 // SLC7A11 // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 545207 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961 /	SLC7A11	SLC7A11, rs2660693, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 ,q28.3
SNP_A-2175969	caccaaatgatgataa[C/G]aaaacgttcatgata	C	G	NM_014331 // downstream // 3642851 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 326493 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1813894	gtgtatttctgccacc[G/T]gatggaccatttgtca	G	T	NM_014331 // downstream // 3642227 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 327117 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2010169	tggggagccaaagagc[A/G]atggacctatggacct	A	G	NM_014331 // downstream // 3610378 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 358966 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1918642	ttaaattcacagcaca[A/G]tgccaattacattgta	A	G	NM_014331 // downstream // 3590751 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 378593 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2214691	cctagcttccgataaa[C/T]tatgttactaaatgaa	C	T	NM_014331 // downstream // 3323264 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 646080 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1918502	ttaaatcatgtatgac[A/C]ggaaaagcagacattt	A	C	NM_014331 // downstream // 3262052 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 707292 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1803685	gtcaaataaaggaacc[A/T]ctttcgctgccacatc	A	T	NM_014331 // downstream // 3256315 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 713029 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2060799	aatgagtgagtatta[C/G]aggtaaaggctagca	C	G	NM_014331 // downstream // 3228584 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 740760 // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1692788	gtgtcaggattaagttgaattatag[A/G]acagtcaggtgatatgtg ctagagg	A	G	NM_014331 // downstream // 3433462 // Hs.6682 // SLC7A11 // 23657 // solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /// NM_020815 // downstream // 1702428 // Hs.146858 // PCDH10 // 57575 // protocadherin 10 /// NM_032961	SLC7A11	SLC7A11 , rs1354757, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 ,q28.3
SNP_A-1887154	tgagaaagagtgtggc[A/G]aggtctggaatttagt	A	G	NM_014331 // downstream // 3145476 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 823868 // — // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2093566	agaagaaagctgaaaa[A/G]gacacattctaagaag	A	G	NM_014331 // downstream // 3143033 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 826311 // — // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2125175	agttggggaatagtaa[C/T]gcaagttgaataaaac	C	T	NM_014331 // downstream // 1517909 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 2451435 // — // — // — // — /// E	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1797092	ggttgaaagtcagttt[G/T]aaaagttaggcaatag	G	T	NM_014331 // downstream // 1256521 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 2712823 // — // — // — // — /// E	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2140281	atctcaactggagtta[C/T]aatgatggtgttgttt	C	T	NM_014331 // downstream // 1245864 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 2723480 // — // — // — // — /// E	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1979057	gctacaatgtttataa[C/T]gatggtgaagaaagta	C	T	NM_014331 // downstream // 1216039 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 2753305 // — // — // — // — /// E	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2296713	gccaaatatcagaaca[C/T]tggattatacttagag	C	T	NM_014331 // downstream // 1213425 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 2755919 // — // — // — // — /// E	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1827300	taacgaggtcccgtaa[A/G]gagagtgttccattca	A	G	NM_014331 // downstream // 676125 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// ENST00000333097 // upstream // 3293219 // — // — // — // — /// EN	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1817831	gttcctgggcccctca[C/G]gcagtcagtaagtaga	C	G	NM_014331 // upstream // 96882 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 676838 // Hs.480763 // CCRN4L // 25819 // Homo sapi	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1903937	tgggattctgtgcttg[C/T]aaaaatttggggactt	C	T	NM_014331 // upstream // 99924 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 673796 // Hs.480763 // CCRN4L // 25819 // Homo sapi	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2312894	ggactgtgtgaaccaa[C/G]caggggccagttttcc	C	G	NM_014331 // upstream // 239149 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 534571 // Hs.480763 // CCRN4L // 25819 // Homo sap	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-1955649	tttgtaaattgctaca[G/T]gagtaacagtggctaa	G	T	NM_014331 // upstream // 277223 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 496497 // Hs.480763 // CCRN4L // 25819 // Homo sap	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q28.3
SNP_A-2187759	cagtagatattcaaca[A/G]aaggcaactattattg	A	G	NM_014331 // upstream // 400775 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 372945 // Hs.480763 // CCRN4L // 25819 // Homo sap	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2071376	acactttgctagatac[G/T]aattcctgcttttgag	G	T	NM_014331 // upstream // 404298 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 369422 // Hs.480763 // CCRN4L // 25819 // Homo sap	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2129429	atacaatgatatgcac[A/C]gaatgggaccagcaca	A	C	NM_014331 // upstream // 456802 // Hs.6682 // SLC7A11 // 23657 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA. /// NM_012118 // upstream // 316918 // Hs.480763 // CCRN4L // 25819 // Homo sap	SLC7A11	SLC7A11, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), q31.1
SNP_A-2194070	catgacataaatcaga[A/T]cctccgggagcaaggg	A	T	ENST00000327122 // upstream // 119039 // --- // --- // --- // --- /// ENST00000356642 // downstream // 445876 // --- // --- // --- // ---	-	q31.1
SNP_A-1925801	ttatgctttcaagtta[C/T]gtgaactagtaagatc	C	T	ENST00000327122 // upstream // 511242 // --- // --- // --- // --- /// ENST00000356642 // downstream // 53673 // --- // --- // --- // ---	-	q31.1
SNP_A-2117133	aggtgatttttaccaa[A/G]ttctgagctttgcaat	A	G	NM_021833 // upstream // 10388 // Hs.249211 // UCP1 // 7350 // Homo sapiens uncoupling protein 1 (mitochondrial, proton carrier) (UCP1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000262999 // upstream // 10388 // --- // --- // --- // --	UCP1	UCP1, Homo sapiens uncoupling protein 1 (mitochondrial, proton carrier) (UCP1), nuclear gene encoding mitochondrial protein, q31.21
SNP_A-2083488	actaaggtcattgata[A/G]cgtctctgaacaatca	A	G	ENST00000306799 // 3UTR // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-1845529	tatagataattttata[C/T]ggttgcagaaatggat	C	T	ENST00000306799 // intron // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-2189167	cagttataactgatga[A/G]cctagcaatgatgtac	A	G	ENST00000306799 // intron // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-2214943	cctatctcaaggtctc[A/C]agttggcccctggtga	A	C	ENST00000306799 // intron // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-2153898	attatacaccattcaa[A/G]gatgttgtgagtgtta	A	G	ENST00000306799 // intron // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-1979172	tccatggctgcataac[A/G]ctatttttgtatcatt	A	G	ENST00000306799 // intron // 0 // --- // --- // --- // ---	-	q31.21
SNP_A-1715521	gaaaaaacttatagtcctgtcagta[C/T]agtagcaccactgttat gttgagtg	C	T	NM_000585 // upstream // 352239 // Hs.528402 // IL15 // 3600 // interleukin 15 /// NM_014487 // downstream // 49667 // Hs.120766 // ZNF330 // 27309 // zinc finger protein 330 /// NM_172174 // upstream // 352239 // Hs.528402 // IL15 // 3600 // interleukin	IL15	IL15 , rs10519595, interleukin 15 ,q31.21
SNP_A-2077982	accagcctgtttttca[C/T]atttgtgtaactccct	C	T	NM_000585 // downstream // 24036 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant 3, mRNA. /// NM_172174 // downstream // 24036 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant 1,	IL15	IL15, Homo sapiens interleukin 15 (IL15), transcript variant 3, q31.21
SNP_A-1908772	tgtaggttggactgca[A/C]agataagtataaaacc	A	C	NM_000585 // downstream // 210308 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant 3, mRNA. /// NM_172174 // downstream // 210308 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant	IL15	IL15, Homo sapiens interleukin 15 (IL15), transcript variant 3, q31.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2157614	attgcaaatagagcta[C/T]gttgattggcctggcc	C	T	NM_000585 // downstream // 229530 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant 3, mRNA. /// NM_172174 // downstream // 229530 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant	IL15	IL15, Homo sapiens interleukin 15 (IL15), transcript variant 3, q31.21
SNP_A-1979206	tattttatatgagaaa[A/G]gatgttctatggtaaa	A	G	NM_000585 // downstream // 265121 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant 3, mRNA. /// NM_172174 // downstream // 265121 // Hs.311958 // IL15 // 3600 // Homo sapiens interleukin 15 (IL15), transcript variant	IL15	IL15, Homo sapiens interleukin 15 (IL15), transcript variant 3, q31.21
SNP_A-2301007	gccttacactacatag[A/C]atttgattatttgaaa	A	C	NM_003866 // intron // 0 // Hs.480837 // INPP4B // 8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2114822	agggcaagagctaaga[A/G]gcaaggccacatcaga	A	G	NM_003866 // intron // 0 // Hs.480837 // INPP4B // 8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2300529	gcctgagatcaagcaa[C/T]gctaggacaaccacaa	C	T	NM_003866 // intron // 0 // Hs.480837 // INPP4B // 8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-1979227	gcaacaagaattttaa[C/G]actctcaaccctctga	C	G	NM_003866 // intron // 0 // Hs.480837 // INPP4B // 8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// ENST00000262992 // intron // 0 // --- // --- // --- // ---	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-1979231	ttaaaaatcaaaagaa[A/G]tggttgagagcttatt	A	G	NM_003866 // upstream // 70673 // Hs.480837 // INPP4B // 8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// NM_207492 // upstream // 312137 // --- // --- // 0 // --- /// ENST00000262992 // upstream // 70673 // -	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-1710950	taaggccagcaaacatgtatcaagc[A/G]catattatgattcagc cactattat	A	G	NM_003866 // intron // 0 // Hs.153687 // INPP4B // 8821 // inositol polyphosphate-4-phosphatase, type II, 105kDa	INPP4B	INPP4B , rs10519642, inositol polyphosphate-4-phosphatase, type II, 105kDa,q31.21
SNP_A-1979236	caaattcattttgtca[A/G]tattgggtgacatatt	A	G	NM_003866 // upstream // 169153 // Hs.480837 // INPP4B // 8821 // Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), mRNA. /// NM_207492 // upstream // 213657 // --- // --- // 0 // --- /// ENST00000262992 // upstream // 169153 //	INPP4B	INPP4B, Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), q31.21
SNP_A-2247541	ctgtctgctttaataa[A/G]tactcgaatctatttg	A	G	NM_003601 // CDS // 0 // Hs.518857 // SMARCA5 // 8467 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (SMARCA5), mRNA. /// ENST00000283131 // CDS // 0 // --- // --- // --- // ---	SMARCA5	SMARCA5, Homo sapiens SWI q31.21
SNP_A-2126297	ataaaaattttaaaca[A/G]gctgccgtgatgtaag	A	G	NM_003601 // intron // 0 // Hs.518857 // SMARCA5 // 8467 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (SMARCA5), mRNA. /// ENST00000283131 // intron // 0 // --- // --- // --- // ---	SMARCA5	SMARCA5, Homo sapiens SWI q31.21
SNP_A-1979259	cagtgagaagggttta[A/G]caattagagacagata	A	G	ENST00000330977 // downstream // 68528 // --- // --- // --- // --- /// ENST00000329798 // downstream // 67197 // --- // --- // --- // ---	-	q31.21
SNP_A-2094289	agaagtacagaagagg[G/T]atgcaaagcccagcca	G	T	NM_002102 // downstream // 33816 // Hs.371903 // GYPE // 2996 // Homo sapiens glycophorin E (GYPE), transcript variant 1, mRNA. /// NM_198682 // downstream // 33816 // Hs.371903 // GYPE // 2996 // Homo sapiens glycophorin E (GYPE), transcript variant 2, m	GYPE	GYPE, Homo sapiens glycophorin E (GYPE), transcript variant 1, q31.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187687	cagtaccccaaataca[C/G]tggcattcacattaag	C	G	NM_002099 // upstream // 69436 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 63548 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GYPB	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2234104	ctcattcctaaactag[A/G]cattgacaagggaaa	A	G	NM_002099 // upstream // 139693 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 133805 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2255188	cttggtcattgagaa[A/G]catcaaggaaagtaaa	A	G	NM_002099 // upstream // 147575 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 141687 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1872019	tctaccctaattacag[A/G]ccaatttcatcttaac	A	G	NM_002099 // upstream // 147684 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 141796 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2080173	accgtgccctcccttg[C/T]agctctctgttggcta	C	T	NM_002099 // upstream // 201983 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 196095 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2221666	ccttttgctcctccca[A/C]tcttttcaacattaga	A	C	NM_002099 // upstream // 277827 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 271939 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2036195	aaattattaccactaa[G/T]atttgctgtcttttc	G	T	NM_002099 // upstream // 387414 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 381526 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1979279	atatcactttgccaac[C/T]ataatttttacaattc	C	T	NM_002099 // upstream // 395003 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 389115 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1939405	ttgatgctcagtcctc[C/T]gaatgacactaaatat	C	T	NM_002099 // upstream // 404274 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 398386 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1900252	tggagaagtaaaagca[A/G]gatggaatggaagaga	A	G	NM_002099 // upstream // 424824 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 418936 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-2053930	aagttaaaagccgaaa[C/T]tgtttcataacttct	C	T	NM_002099 // upstream // 429782 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 423894 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2222758	cgatggtaagcacacc[A/G]atggaagataaaaag	A	G	NM_002099 // upstream // 429959 // Hs.434973 // GYPA // 2993 // Homo sapiens glycophorin A (includes MN blood group) (GYPA), mRNA. /// NM_002100 // upstream // 424071 // Hs.434973 // GYPB // 2994 // Homo sapiens glycophorin B (includes Ss blood group) (GY	GYPA	GYPA, Homo sapiens glycophorin A (includes MN blood group) (GYPA), q31.21
SNP_A-1704941	caccggatggcataaaagtcactaa[A/C]aacagattcttcctttt atttctgg	A	C	NM_002099 // upstream // 416933 // Hs.34287 // GYPA // 2993 // glycophorin A (includes MN blood group) /// NM_002100 // upstream // 538281 // Hs.438658 // GYPB // 2994 // glycophorin B (includes Ss blood group) /// NM_022475 // upstream // 88396 // Hs.41	GYPA	GYPA , rs4834988, glycophorin A (includes MN blood group), q31.21
SNP_A-1979284	tttataaggagtaaaa[A/G]atgaggagatgaattg	A	G	NM_022475 // downstream // 208438 // Hs.507991 // HHIP // 64399 // Homo sapiens hedgehog interacting protein (HHIP), mRNA. /// NM_014885 // downstream // 47990 // Hs.480876 // ANAPC10 // 10393 // Homo sapiens anaphase promoting complex subunit 10 (ANAPC10	HHIP	HHIP, Homo sapiens hedgehog interacting protein (HHIP), q31.21
SNP_A-2084450	acatcatagtctaaa[A/G]tgccttcttactgc	A	G	NM_199324 // upstream // 83743 // Hs.270851 // HSHIN1 // 54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 // upstream // 83743 // Hs.270851 // HSHIN1 // 54726 // Homo sapiens HIV-1 induced protein HIN-1	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-2055856	aatacaagataaatcca[A/T]tcaattccaaatatc	A	T	NM_199324 // upstream // 108054 // Hs.270851 // HSHIN1 // 54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 // upstream // 108054 // Hs.270851 // HSHIN1 // 54726 // Homo sapiens HIV-1 induced protein HIN	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-2150141	atgtcctggaaaatca[A/G]cttgacttcttgtt	A	G	NM_199324 // upstream // 174852 // Hs.270851 // HSHIN1 // 54726 // Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, mRNA. /// NM_017493 // upstream // 174852 // Hs.270851 // HSHIN1 // 54726 // Homo sapiens HIV-1 induced protein HIN	HSHIN1	HSHIN1, Homo sapiens HIV-1 induced protein HIN-1 (HSHIN1), transcript variant 1, q31.21
SNP_A-1929006	ttcagccttttcacac[A/G]ccttgctataaattgc	A	G	NM_005900 // upstream // 44510 // Hs.519005 // SMAD1 // 4086 // Homo sapiens SMAD, mothers against DPP homolog 1 (Drosophila) (SMAD1), transcript variant 1, mRNA. /// NM_001003688 // upstream // 44510 // Hs.519005 // SMAD1 // 4086 // Homo sapiens SMAD, mo	SMAD1	SMAD1, Homo sapiens SMAD, mothers against DPP homolog 1 (Drosophila) (SMAD1), transcript variant 1, q31.21
SNP_A-2213433	ccgggcaaccaggtgt[C/G]atatgcggcaggcag	C	G	NM_172250 // downstream // 71637 // Hs.117747 // MMAA // 166785 // Homo sapiens methylmalonic aciduria (cobalamin deficiency) type A (MMAA), mRNA. /// NM_178835 // downstream // 30410 // Hs.133916 // LOC152485 // 152485 // Homo sapiens hypothetical protei	MMAA	MMAA, Homo sapiens methylmalonic aciduria (cobalamin deficiency) type A (MMAA), q31.21
SNP_A-2010227	tatttactaaattaa[C/T]gattgcgtttgttac	C	T	NM_007080 // intron // 0 // Hs.190520 // LSM6 // 11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // intron // 0 // — // — // —	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22
SNP_A-2292576	gcactgagacttaaaa[A/G]ttagtatggatacaat	A	G	NM_007080 // intron // 0 // Hs.190520 // LSM6 // 11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // intron // 0 // — // — // —	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22
SNP_A-1831327	taatggttgtaatggg[C/T]atactgactatgtgtc	C	T	NM_007080 // intron // 0 // Hs.190520 // LSM6 // 11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // intron // 0 // — // — // —	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22
SNP_A-1845204	tatacccaataggcca[A/G]aaaagtactggtcatc	A	G	NM_007080 // intron // 0 // Hs.190520 // LSM6 // 11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // intron // 0 // — // — // —	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944716	ttgtgatattcttggc[A/G]gagcctgcttcacacc	A	G	NM_007080 // downstream // 5198 // Hs.190520 // LSM6 // 11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // downstream // 5198 // — // — // — // — /// ENST00000335472 // downstre	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22
SNP_A-1979310	cccactctggtgttta[C/T]ggccttgtgttgcatg	C	T	NM_007080 // downstream // 41144 // Hs.190520 // LSM6 // 11157 // Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA. /// ENST00000296581 // downstream // 41144 // — // — // — // — /// ENST00000335472 // downst	LSM6	LSM6, Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), q31.22
SNP_A-2144482	atgatataactgctgc[A/G]accggcgctgccacaa	A	G	ENST00000335472 // intron // 0 // — // — // — // —	-	q31.22
SNP_A-1874276	tctccagaaatcctca[C/T]gcttaactccctcatg	C	T	ENST00000335472 // intron // 0 // — // — // — // —	-	q31.22
SNP_A-2183458	cagcagaagaattcat[C/G]agaagacaaagtcctc	C	G	ENST00000335472 // intron // 0 // — // — // — // — /// ENST00000264986 // intron // 0 // — // — // — // —	-	q31.22
SNP_A-2260380	gaaacaaatgtccaaa[A/C]ataagagaatcattta	A	C	ENST00000264986 // intron // 0 // --- // --- // --- // ---	-	q31.22
SNP_A-2176768	caccctcctggctgaa[C/T]actcctaatagtagtg	C	T	NM_004575 // upstream // 93030 // Hs.266 // POU4F2 // 5458 // Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA. /// ENST00000335472 // upstream // 35904 // --- // --- // --- // --- /// ENST00000264986 // upstream // 24011 // --- //	POU4F2	POU4F2, Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), q31.22
SNP_A-1881026	tcttgttgttgcccca[C/T]cttagaggacactcag	C	T	NM_004575 // upstream // 86774 // Hs.266 // POU4F2 // 5458 // Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA. /// ENST00000335472 // upstream // 42160 // --- // --- // --- // --- /// ENST00000264986 // upstream // 30267 // — //	POU4F2	POU4F2, Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), q31.22
SNP_A-1850764	tattacttcattgaat[G/T]actctttgccatttttt	G	T	NM_004575 // upstream // 26896 // Hs.266 // POU4F2 // 5458 // Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA. /// ENST00000335472 // upstream // 102038 // — // — // — // — /// ENST00000264986 // upstream // 90145 // — //	POU4F2	POU4F2, Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), q31.22
SNP_A-2310014	ggaaatgggagagtac[C/T]ggaggaaaatgagaaa	C	T	NM_004575 // upstream // 11045 // Hs.266 // POU4F2 // 5458 // Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA. /// ENST00000335472 // upstream // 117889 // — // — // — // — /// ENST00000264986 // upstream // 105996 // --- /	POU4F2	POU4F2, Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), q31.22
SNP_A-1911121	tgtctgaaacatcaca[A/G]tatttaggacatttta	A	G	NM_004575 // downstream // 17015 // Hs.266 // POU4F2 // 5458 // Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA. /// NM_031956 // downstream // 47547 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mR	POU4F2	POU4F2, Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), q31.22
SNP_A-2113350	aggcctgtagcataaa[A/T]ggagcatatcaccact	A	T	NM_031956 // intron // 0 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// ENST00000260021 // intron // 0 // — // — // — // — /// ENST00000325106 // intron // 0 // --- // — // — // —	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1931981	ttcctaccgcgctgaa[C/T]atggcaggaatgaaaa	C	T	NM_031956 // upstream // 56177 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 56182 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2096106	agacatctccctatac[A/G]acaattgtcctggatg	A	G	NM_031956 // upstream // 73172 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 73177 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1785181	ggctaagcatttaac[C/T]agagcatcccagact	C	T	NM_031956 // upstream // 74491 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 74496 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2285575	gatgaaatgtcttca[A/G]aacaaggcttcaggc	A	G	NM_031956 // upstream // 79332 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 79337 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2262937	gaacaacttgaaggaa[A/G]tggagcatagcctggc	A	G	NM_031956 // upstream // 80698 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 80703 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2292590	gcactgagtctggtca[A/G]aatggtaacacgtggg	A	G	NM_031956 // upstream // 82823 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 82828 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2305061	gctgaagcactgatga[A/G]agggatggagacagtg	A	G	NM_031956 // upstream // 82854 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 82859 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2151162	atgtgttgagactata[A/T]ctgggtctgcatctt	A	T	NM_031956 // upstream // 92666 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 92671 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2250025	cttacccagtggacaa[A/G]gatgatggagagactt	A	G	NM_031956 // upstream // 92716 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 92721 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2240553	ctgacccaagtaatta[C/T]aaagttagcacttgga	C	T	NM_031956 // upstream // 97944 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 97949 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 // up	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2152750	attaatgggagttgga[C/G]acaggagcaacataga	C	G	NM_031956 // upstream // 107923 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 107928 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-2240061	ctgaagctggatgcaa[C/G]agcaaggctgaaatta	C	G	NM_031956 // upstream // 392763 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 392768 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22
SNP_A-1979340	aatcttctgaaactta[C/T]acatgattcaaagaca	C	T	NM_031956 // upstream // 415353 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_031956 // upstream // 415358 // Hs.378893 // NYD-SP14 // 83894 // Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA. /// NM_001957 //	NYD-SP14	NYD-SP14, Homo sapiens NYD-SP14 protein (NYD-SP14), q31.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2279445	gaggatatacaattcc[A/C]aggcagttcttcttac	A	C	NM_001957 // downstream // 5227 // Hs.183713 // EDNRA // 1909 // Homo sapiens endothelin receptor type A (EDNRA), mRNA. /// NM_018241 // upstream // 67264 // Hs.203896 // TMEM34 // 55751 // Homo sapiens transmembrane protein 34 (TMEM34), mRNA. /// ENST000	EDNRA	EDNRA, Homo sapiens endothelin receptor type A (EDNRA), q31.23
SNP_A-2231622	ctatttgtgccataca[A/T]agaaaagtgcctgtat	A	T	NM_001957 // downstream // 6348 // Hs.183713 // EDNRA // 1909 // Homo sapiens endothelin receptor type A (EDNRA), mRNA. /// NM_018241 // upstream // 66143 // Hs.203896 // TMEM34 // 55751 // Homo sapiens transmembrane protein 34 (TMEM34), mRNA. /// ENST000	EDNRA	EDNRA, Homo sapiens endothelin receptor type A (EDNRA), q31.23
SNP_A-2058266	aatcaaggtgttacaa[C/T]aggaaatggcaaaggt	C	T	NM_001957 // downstream // 11118 // Hs.183713 // EDNRA // 1909 // Homo sapiens endothelin receptor type A (EDNRA), mRNA. /// NM_018241 // upstream // 61373 // Hs.203896 // TMEM34 // 55751 // Homo sapiens transmembrane protein 34 (TMEM34), mRNA. /// ENST00	EDNRA	EDNRA, Homo sapiens endothelin receptor type A (EDNRA), q31.23
SNP_A-1832620	tacaacaggttgaaag[G/T]agaatttaaagtacca	G	T	NM_001957 // downstream // 34071 // Hs.183713 // EDNRA // 1909 // Homo sapiens endothelin receptor type A (EDNRA), mRNA. /// NM_018241 // upstream // 38420 // Hs.203896 // TMEM34 // 55751 // Homo sapiens transmembrane protein 34 (TMEM34), mRNA. /// ENST00	EDNRA	EDNRA, Homo sapiens endothelin receptor type A (EDNRA), q31.23
SNP_A-2089220	acttactatctgacac[A/G]cttttctttcggaaag	A	G	NM_024605 // intron // 0 // Hs.368631 // ARHGAP10 // 79658 // Homo sapiens Rho GTPase activating protein 10 (ARHGAP10), mRNA. /// ENST00000336498 // intron // 0 // — // — // — // —	ARHGAP10	ARHGAP10, Homo sapiens Rho GTPase activating protein 10 (ARHGAP10), q31.23
SNP_A-1874779	tctcctttagcagtta[A/C]cactcttgctcttgta	A	C	NM_000901 // intron // 0 // Hs.163924 // NR3C2 // 4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // intron // 0 // — // — // — // — /// ENST00000355292 // intron // 0 // — // — // — //	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1979369	gaggttaaacaaaata[G/T]tatcaaggccaaagac	G	T	NM_000901 // intron // 0 // Hs.163924 // NR3C2 // 4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // intron // 0 // — // — // — // — /// ENST00000355292 // intron // 0 // — // — // — //	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1900941	tggataaggtccaaac[C/T]cttgagtctgacaatc	C	T	NM_000901 // upstream // 21879 // Hs.163924 // NR3C2 // 4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // upstream // 21879 // — // — // — // — /// ENST00000355292 // upstream // 21879 // –	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1979382	attagaatccttaaag[C/T]agaatagccttgtgag	C	T	NM_000901 // upstream // 327141 // Hs.163924 // NR3C2 // 4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // upstream // 327141 // — // — // — // — /// ENST00000355292 // upstream // 327141 //	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1684618	ggatgaacaactctgcccaaagaaa[A/G]aaccatgccgtcatc ttgaatcttt	A	G	NM_000901 // upstream // 328974 // Hs.331409 // NR3C2 // 4306 // nuclear receptor subfamily 3, group C, member 2 /// NM_152619 // upstream // 1307644 // Hs.45057 // MGC45428 // 166614 // hypothetical protein MGC45428	NR3C2	NR3C2 , rs549653, nuclear receptor subfamily 3, group C, member 2 ,q31.23
SNP_A-1683236	aactatctctcaaatactctactgg[A/T]ttgctttacatatagttaatc acca	A	T	NM_000901 // upstream // 339445 // Hs.331409 // NR3C2 // 4306 // nuclear receptor subfamily 3, group C, member 2 /// NM_152619 // upstream // 1297173 // Hs.45057 // MGC45428 // 166614 // hypothetical protein MGC45428	NR3C2	NR3C2 , rs951219, nuclear receptor subfamily 3, group C, member 2 ,q31.23
SNP_A-1737089	gagcccctgaatgggaatagaagtc[A/G]caacatatccagttc gatctgggcc	A	G	NM_000901 // upstream // 339619 // Hs.331409 // NR3C2 // 4306 // nuclear receptor subfamily 3, group C, member 2 /// NM_152619 // upstream // 1296999 // Hs.45057 // MGC45428 // 166614 // hypothetical protein MGC45428	NR3C2	NR3C2 , rs506729, nuclear receptor subfamily 3, group C, member 2 ,q31.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2156367	attctcagctagcaca[A/T]cttccattctcgggtg	A	T	NM_000901 // upstream // 585803 // Hs.163924 // NR3C2 // 4306 // Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /// ENST00000358102 // upstream // 585803 // — // — // — // — /// ENST00000355292 // upstream // 585803 //	NR3C2	NR3C2, Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), q31.23
SNP_A-1708983	atctttcttatctttgcacaatcaa[A/G]acttataaaagcctcaggg aactga	A	G	NM_000901 // upstream // 546428 // Hs.331409 // NR3C2 // 4306 // nuclear receptor subfamily 3, group C, member 2 /// NM_152619 // upstream // 1090190 // Hs.45057 // MGC45428 // 166614 // hypothetical protein MGC45428	NR3C2	NR3C2 , rs2520488, nuclear receptor subfamily 3, group C, member 2 ,q31.23
SNP_A-1824138	taaacagaagccataa[C/T]taactcctatgcttac	C	T	ENST00000335031 // intron // 0 // — // — // — // —	-	q31.23
SNP_A-2094799	agaatcctaaggcatc[A/T]aaacaatagaacactt	A	T	NM_152619 // upstream // 167188 // Hs.437045 // DCAMKL2 // 166614 // Homo sapiens hypothetical protein MGC45428 (MGC45428), mRNA. /// ENST00000335031 // upstream // 95971 // — // — // — // — /// ENST00000296550 // upstream // 167188 // — // —	DCAMKL2	DCAMKL2, Homo sapiens hypothetical protein MGC45428 (MGC45428), q31.23
SNP_A-1926034	ttatgtgcatgaaata[C/T]cttacatttttaaggc	C	T	NM_006726 // intron // 0 // Hs.480938 // LRBA // 987 // Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), mRNA. /// ENST00000356913 // intron // 0 // — // — // — // — /// ENST00000357115 // intron // 0 // — //	LRBA	LRBA, Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), q31.23
SNP_A-2026312	aaaatttccttctatc[A/G]acattaactcgccttt	A	G	NM_006726 // intron // 0 // Hs.480938 // LRBA // 987 // Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), mRNA. /// ENST00000356913 // intron // 0 // — // — // — // — /// ENST00000357115 // intron // 0 // — //	LRBA	LRBA, Homo sapiens LPS-responsive vesicle trafficking, beach and anchor containing (LRBA), q31.3
SNP_A-2273365	gactccttcttagtga[G/T]gccttctttaactacc	G	T	NM_183375 // intron // 0 // Hs.525911 // ESSPL // 345062 // Homo sapiens epidermis-specific serine protease-like protein (ESSPL), mRNA. /// ENST00000309632 // intron // 0 // — // — // — // —	ESSPL	ESSPL, Homo sapiens epidermis-specific serine protease-like protein (ESSPL), q31.3
SNP_A-2169288	caagcacactgcctac[A/G]gattagctagccctgt	A	G	NM_183375 // downstream // 508 // Hs.525911 // ESSPL // 345062 // Homo sapiens epidermis-specific serine protease-like protein (ESSPL), mRNA. /// ENST00000309632 // downstream // 508 // — // — // — // — /// ENST00000340515 // upstream // 144474 //	ESSPL	ESSPL, Homo sapiens epidermis-specific serine protease-like protein (ESSPL), q31.3
SNP_A-1979416	cagaaacatccatatg[C/T]atgcaggactatgtct	C	T	NM_004564 // intron // 0 // Hs.119316 // PET112L // 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// ENST00000263985 // intron // 0 // — // — // — // —	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2120517	agtccactttgcagat[C/G]aaccagtacaggctta	C	G	NM_004564 // upstream // 80862 // Hs.119316 // PET112L // 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 479392 // Hs.519029 // FBXW7 // 55294 // Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog,	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2028622	aaactggcacagggta[C/T]atccgaagcttgctgg	C	T	NM_004564 // upstream // 81397 // Hs.119316 // PET112L // 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 478857 // Hs.519029 // FBXW7 // 55294 // Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog,	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-2220555	ccttctgtcaaccaaa[C/T]gctcatagaatgctca	C	T	NM_004564 // upstream // 265218 // Hs.119316 // PET112L // 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 295036 // Hs.519029 // FBXW7 // 55294 // Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-1664072	gtgtaaagagatctgaaacggacaa[C/G]gaactggaagaaat gtaaaacctaa	C	G	NM_004564 // upstream // 79926 // Hs.119316 // PET112L // 5188 // PET112-like (yeast) /// NM_018315 // downstream // 481423 // Hs.312503 // FBXW7 // 55294 // F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila) /// NM_033632 // downstream /	PET112L	PET112L , rs361192, PET112-like (yeast) ,q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187547	cagtaaatttcctgcat[A/G]gcgaactcttccttg	A	G	NM_004564 // upstream // 305703 // Hs.119316 // PET112L // 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 254551 // Hs.519029 // FBXW7 // 55294 // Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-1732606	gaatcttacagaaattgtggagctg[A/G]gtaataccctcattacttttcatct	A	G	NM_004564 // upstream // 121994 // Hs.119316 // PET112L // 5188 // PET112-like (yeast) /// NM_018315 // downstream // 439355 // Hs.312503 // FBXW7 // 55294 // F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila) /// NM_033632 // downstream	PET112L	PET112L, rs901207, PET112-like (yeast), q31.3
SNP_A-2178583	cactctcactctgccc[A/G]gacagtttaagaaaagt	A	G	NM_004564 // upstream // 372201 // Hs.119316 // PET112L // 5188 // Homo sapiens PET112-like (yeast) (PET112L), mRNA. /// NM_018315 // downstream // 188053 // Hs.519029 // FBXW7 // 55294 // Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog	PET112L	PET112L, Homo sapiens PET112-like (yeast) (PET112L), q31.3
SNP_A-1661836	agatggagaaactaaagctaaggga[A/G]attaaaagatccagctaaggtcatg	A	G	AB051514 // downstream // 30125 // Hs.319946 // KIAA1727 // 85462 // KIAA1727 protein /// NM_015271 // upstream // 194655 // Hs.435734 // TRIM2 // 23321 // tripartite motif-containing 2	KIAA1727	KIAA1727, rs6837953, KIAA1727 protein, q31.3
SNP_A-2134839	atattagctctaagaa[A/G]tgatacattgcattgt	A	G	ENST00000240487 // intron // 0 // — // — // — /// ENST00000334904 // intron // 0 // — // — // — // —	-	q31.3
SNP_A-2010265	ctacttgctgcagata[C/T]ggaaagtaactgcaca	C	T	NM_173662 // intron // 0 // Hs.388364 // RNF175 // 285533 // Homo sapiens hypothetical protein LOC285533 (LOC285533), mRNA. /// ENST00000274068 // intron // 0 // — // — // — /// ENST00000360881 // intron // 0 // — // — // — // —	RNF175	RNF175, Homo sapiens hypothetical protein LOC285533 (LOC285533), q31.3
SNP_A-2036290	aaattcagtagtgtat[C/T]aggccgtagtttttt	C	T	NM_173662 // intron // 0 // Hs.388364 // RNF175 // 285533 // Homo sapiens hypothetical protein LOC285533 (LOC285533), mRNA. /// ENST00000274068 // intron // 0 // — // — // — // —	RNF175	RNF175, Homo sapiens hypothetical protein LOC285533 (LOC285533), q31.3
SNP_A-1874976	tctctagcaggtaaat[A/C]aaaaatgctatgactt	A	C	NM_003013 // intron // 0 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// ENST00000274063 // intron // 0 // — // — // — // —	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1930330	ttcatttcatagagaa[A/G]gaaagcaagacaaaga	A	G	NM_003013 // upstream // 17144 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 428396 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1961294	ttttttctggatgta[C/T]gctgaggaatagaagt	C	T	NM_003013 // upstream // 26507 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 419033 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-2268978	gaattccacaagtcag[C/T]gtccttagtatctcaa	C	T	NM_003013 // upstream // 28004 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 417536 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1794694	ggtctcctatagcatt[C/G]aagttcacaaggtgct	C	G	NM_003013 // upstream // 34567 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 410973 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-2058051	aatatttgctgaggtg[A/T]atggaaatctatcctg	A	T	NM_003013 // upstream // 34964 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 410576 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1902186	tggccaagacaagaaa[G/T]gttatcaagctgtatc	G	T	NM_003013 // upstream // 36306 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 409234 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-2094396	agaagtgccagatttc[C/T]cccagagcgtcttgtt	C	T	NM_003013 // upstream // 36578 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 408962 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1891201	tgatgtgtatggaagg[G/T]agtttgtgttctatgt	G	T	NM_003013 // upstream // 36619 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 408921 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1860868	tcatacacaatcctct[C/T]acacagaacacatggt	C	T	NM_003013 // upstream // 44973 // Hs.481022 // SFRP2 // 6423 // Homo sapiens secreted frizzled-related protein 2 (SFRP2), mRNA. /// NM_017639 // downstream // 400567 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcrip	SFRP2	SFRP2, Homo sapiens secreted frizzled-related protein 2 (SFRP2), q31.3
SNP_A-1850369	tatgttgtcttctcca[C/T]cccaaaataagacagg	C	T	NM_017639 // intron // 0 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 1, mRNA. /// NM_199348 // intron // 0 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript va	DCHS2	DCHS2, Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 1, q31.3
SNP_A-1979478	gaaatgcaagaataca[C/G]cgggagttctgcttct	C	G	NM_199348 // intron // 0 // Hs.148847 // DCHS2 // 54798 // Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 2, mRNA. /// ENST00000339452 // intron // 0 // — // — // — // —	DCHS2	DCHS2, Homo sapiens dachsous 2 (Drosophila) (DCHS2), transcript variant 2, q31.3
SNP_A-2200788	ccaagaggacaatctg[C/G]atcaagtcttcaccaa	C	G	ENST00000360952 // intron // 0 // — // — // — // —	-	q31.3
SNP_A-2209400	cccatactcacctacc[A/G]ctttgccatcacattt	A	G	ENST00000360952 // intron // 0 // — // — // — // —	-	q31.3
SNP_A-1926211	ttattaatttccttgc[A/T]cctcatagtgtatata	A	T	NM_144979 // downstream // 207037 // Hs.133095 // MGC27016 // 166863 // Homo sapiens hypothetical protein MGC27016 (MGC27016), mRNA. /// NM_000910 // upstream // 172780 // Hs.37125 // NPY2R // 4887 // Homo sapiens neuropeptide Y receptor Y2 (NPY2R), mRNA.	MGC27016	MGC27016, Homo sapiens hypothetical protein MGC27016 (MGC27016), q32.1
SNP_A-2120984	agtctattcaggctac[A/G]ataacaaactaccaca	A	G	NM_144979 // downstream // 217267 // Hs.133095 // MGC27016 // 166863 // Homo sapiens hypothetical protein MGC27016 (MGC27016), mRNA. /// NM_000910 // upstream // 162550 // Hs.37125 // NPY2R // 4887 // Homo sapiens neuropeptide Y receptor Y2 (NPY2R), mRNA.	MGC27016	MGC27016, Homo sapiens hypothetical protein MGC27016 (MGC27016), q32.1
SNP_A-1979503	atgaagatataacata[C/T]gagctgtgaatggaaa	C	T	NM_000910 // downstream // 100869 // Hs.37125 // NPY2R // 4887 // Homo sapiens neuropeptide Y receptor Y2 (NPY2R), mRNA. /// NM_024826 // downstream // 34762 // Hs.61271 // FLJ21159 // 79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA.	NPY2R	NPY2R, Homo sapiens neuropeptide Y receptor Y2 (NPY2R), q32.1
SNP_A-2235011	ctcccaatacatagta[A/G]taaacattcaggtaat	A	G	NM_024826 // upstream // 39181 // Hs.61271 // FLJ21159 // 79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA. /// Y15723 // upstream // 250575 // Hs.24258 // GUCY1A3 // 2982 // Homo sapiens mRNA for soluble guanylyl cyclase. /// NM_00085	FLJ21159	FLJ21159, Homo sapiens hypothetical protein FLJ21159 (FLJ21159), q32.1
SNP_A-2225793	ctaaagtccagatttc[A/G]aacacacactcaacta	A	G	NM_024826 // upstream // 103571 // Hs.61271 // FLJ21159 // 79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA. /// Y15723 // upstream // 186185 // Hs.24258 // GUCY1A3 // 2982 // Homo sapiens mRNA for soluble guanylyl cyclase. /// NM_0008	FLJ21159	FLJ21159, Homo sapiens hypothetical protein FLJ21159 (FLJ21159), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2203273	ccacttctactagact[A/G]aaatttccatgaagcc	A	G	NM_024826 // upstream // 155197 // Hs.61271 // FLJ21159 // 79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA. /// Y15723 // upstream // 134559 // Hs.24258 // GUCY1A3 // 2982 // Homo sapiens mRNA for soluble guanylyl cyclase. /// NM_0008	FLJ21159	FLJ21159, Homo sapiens hypothetical protein FLJ21159 (FLJ21159), q32.1
SNP_A-1979509	tctcagtaatccaact[A/G]aactgtacttcactgt	A	G	NM_024826 // upstream // 216757 // Hs.61271 // FLJ21159 // 79884 // Homo sapiens hypothetical protein FLJ21159 (FLJ21159), mRNA. /// Y15723 // upstream // 72999 // Hs.24258 // GUCY1A3 // 2982 // Homo sapiens mRNA for soluble guanylyl cyclase. /// NM_00085	FLJ21159	FLJ21159, Homo sapiens hypothetical protein FLJ21159 (FLJ21159), q32.1
SNP_A-1853971	tcaaaatgaaacacaa[C/T]gccaagcccaatgtgg	C	T	NM_000857 // downstream // 4905 // Hs.77890 // GUCY1B3 // 2983 // Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), mRNA. /// NM_017419 // downstream // 9023 // Hs.381349 // ACCN5 // 51802 // Homo sapiens amiloride-sensitive cation channel 5, i	GUCY1B3	GUCY1B3, Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), q32.1
SNP_A-1901997	tggcataaaagttgcc[A/G]gacactattaggaa	A	G	NM_000857 // downstream // 6575 // Hs.77890 // GUCY1B3 // 2983 // Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), mRNA. /// NM_017419 // downstream // 7353 // Hs.381349 // ACCN5 // 51802 // Homo sapiens amiloride-sensitive cation channel 5, i	GUCY1B3	GUCY1B3, Homo sapiens guanylate cyclase 1, soluble, beta 3 (GUCY1B3), q32.1
SNP_A-2248979	ctgttgttgaactgca[A/G]ctgggcactctacatt	A	G	NM_001334 // upstream // 41442 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 766274 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527 /	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2163651	caaaaagttacttagc[C/T]agttaaatgaatcta	C	T	NM_001334 // upstream // 41496 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 766220 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527 /	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1945847	ttgtttacaggacttg[C/G]aacgtttacatttaat	C	G	NM_001334 // upstream // 131935 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 675781 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1979519	agattaaggacactga[C/T]agttgtataattaaaa	C	T	NM_001334 // upstream // 214657 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 593059 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1979520	gatggcacattcaaaa[A/C]agatgttaaatcaagg	A	C	NM_001334 // upstream // 214897 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 592819 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2159090	attgtttgatttgaa[C/T]ggtctataaacactgg	C	T	NM_001334 // upstream // 229640 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 578076 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1667330	tttatcttatgactgcacattatca[C/T]ggaatacacaaagtcatt aatttt	C	T	NM_001334 // upstream // 18852 // Hs.75262 // CTSO // 1519 // cathepsin O /// NM_016205 // downstream // 788872 // Hs.43080 // PDGFC // 56034 // platelet derived growth factor C	CTSO	CTSO, rs6852748, cathepsin O ,q32.1
SNP_A-1752133	tttggaattcgagaaaggtcttcat[A/G]aatggaaaattgtcaaca gtgctaa	A	G	NM_001334 // upstream // 235716 // Hs.75262 // CTSO // 1519 // cathepsin O /// NM_016205 // downstream // 572008 // Hs.43080 // PDGFC // 56034 // platelet derived growth factor C	CTSO	CTSO, rs2879979, cathepsin O ,q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1979527	ctcctcattgtccaca[A/C]ctccgctagtatcga	A	C	NM_001334 // upstream // 466831 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 340885 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1979531	aaagctggtaattaaa[C/T]gcttctgatgactgaa	C	T	NM_001334 // upstream // 614858 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 192858 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1799905	gtacagactcagaaaa[C/T]gctgtgcatgcagccc	C	T	NM_001334 // upstream // 617538 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 190178 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1979532	ctctttctggaagtgg[A/T]attaagcaacacatc	A	T	NM_001334 // upstream // 622005 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 185711 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-1782755	ggcagaactggagta[C/T]gagccaatgtggacac	C	T	NM_001334 // upstream // 625790 // Hs.75262 // CTSO // 1519 // Homo sapiens cathepsin O (CTSO), mRNA. /// NM_016205 // downstream // 181926 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000281527	CTSO	CTSO, Homo sapiens cathepsin O (CTSO), q32.1
SNP_A-2265305	gaagcactcaaggtta[C/T]aagaacacaacaccct	C	T	NM_016205 // intron // 0 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000274071 // intron // 0 // --- // --- // ---	PDGFC	PDGFC, Homo sapiens platelet derived growth factor C (PDGFC), q32.1
SNP_A-1979543	ccaagaagccatctac[A/G]aaccacttttatctatg	A	G	NM_016205 // intron // 0 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000274071 // intron // 0 // --- // --- // ---	PDGFC	PDGFC, Homo sapiens platelet derived growth factor C (PDGFC), q32.1
SNP_A-2205859	ccatagatcacctgaa[C/T]gaagtaaaatatgta	C	T	NM_016205 // intron // 0 // Hs.148162 // PDGFC // 56034 // Homo sapiens platelet derived growth factor C (PDGFC), mRNA. /// ENST00000274071 // intron // 0 // --- // --- // ---	PDGFC	PDGFC, Homo sapiens platelet derived growth factor C (PDGFC), q32.1
SNP_A-2135308	atatttaatgcatcct[A/G]aacagcatgggtggag	A	G	NM_000826 // downstream // 291877 // Hs.32763 // GRIA2 // 2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 292218 // Hs.32763 // GRIA2 // 2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2.	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-1979572	ggaatgtgcaagaaaa[C/T]tggactccatgctctg	C	T	NM_000826 // downstream // 354229 // Hs.32763 // GRIA2 // 2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), mRNA. /// BC010574 // downstream // 354570 // Hs.32763 // GRIA2 // 2891 // Homo sapiens glutamate receptor, ionotropic, AMPA 2.	GRIA2	GRIA2, Homo sapiens glutamate receptor, ionotropic, AMPA 2 (GRIA2), q32.1
SNP_A-1736757	tatctactgtggctgaactgatat[A/C]cagtttgtaagaaaaaggt ctctttt	A	C	NM_000826 // downstream // 363587 // Hs.335051 // GRIA2 // 2891 // glutamate receptor, ionotropic, AMPA 2 /// NM_016613 // downstream // 397074 // Hs.323583 // DKFZp434L142 // 51313 // hypothetical protein DKFZp434L142	GRIA2	GRIA2 , rs4314333, glutamate receptor, ionotropic, AMPA 2, q32.1
SNP_A-1937896	ttgaatctcagaagcc[C/G]aaattcctggactagt	C	G	NM_021634 // upstream // 119648 // Hs.196119 // LGR7 // 59350 // Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), mRNA. /// ENST00000340501 // downstream // 123453 // --- // --- // --- /// ENST00000307765 // upstream	LGR7	LGR7, Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), q32.1
SNP_A-2206727	ccatgatgtaaaaata[C/T]acagtgtttattgatt	C	T	NM_152543 // intron // 0 // Hs.415576 // FLJ25371 // 152940 // Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // --- // --- // ---	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1929892	ttcatcttctgccaad[A/G]cttgaaaaaaggctg	A	G	NM_152543 // intron // 0 // Hs.415576 // FLJ25371 /// 152940 // Homo sapiens hypothetical protein FLJ25371 (FLJ25371), mRNA. /// ENST00000296528 // intron // 0 // — // — // — // —	FLJ25371	FLJ25371, Homo sapiens hypothetical protein FLJ25371 (FLJ25371), q32.1
SNP_A-2086581	actgaacaactccata[A/T]atttcattactgtctt	A	T	AB002311 // intron // 0 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// ENST00000264431 // intron // 0 // — // — // — // —	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.1
SNP_A-2296355	gcatttaacaaagagct[A/G]aacagttctcacacat	A	G	AB002311 // intron // 0 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// ENST00000264431 // intron // 0 // — // — // — // —	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.1
SNP_A-1823615	taaaataagagaaaag[C/T]cataaaggcagatcat	C	T	AB002311 // downstream // 98905 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1924847 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000264431	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.1
SNP_A-1979599	gacagatagtgcaggg[A/C]aatagtgtaaacaagg	A	C	AB002311 // downstream // 101732 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1922020 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1979600	cctgcactatctgtca[C/T]ggagtaacaaggagaa	C	T	AB002311 // downstream // 101750 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1922002 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1952349	tttctctgctgacaaa[A/G]gacaaaccctcttatt	A	G	AB002311 // downstream // 107282 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1916470 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2310280	ggaaccatcaaggtga[C/T]atgaatggcgaatggt	C	T	AB002311 // downstream // 109392 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1914360 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1892449	tgcaagtcggaaaata[C/G]atcaaccctgtgacct	C	G	AB002311 // downstream // 192459 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1831293 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2240024	ctgaagattacagaaa[G/T]aagaagtgaaatacat	G	T	AB002311 // downstream // 313317 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1710435 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1758426	ttttgaatgtttgttcagtgtttt[A/G]tccccagatcctaaaagttcctat	A	G	NM_014247 // downstream // 610912 // - // - // - // - /// NM_020116 // downstream // 1412838 // Hs.32452 // FSTL5 // 56884 // follistatin-like 5	-	-, rs1986432, - q32.1
SNP_A-1888424	tgaggaagagatggaa[A/G]ctgtatttcattggac	A	G	AB002311 // downstream // 878334 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 1145418 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1979619	agaaggcaacttaaaa[C/T]actcagtccccagaac	C	T	AB002311 // downstream // 1027068 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 996684 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1979620	tgtaaattaggcttaa[C/T]tgatgttggctgtgtt	C	T	AB002311 // downstream // 1027124 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 996628 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2194015	catgaatgccagatga[C/T]agtaaactctagagag	C	T	AB002311 // downstream // 1100183 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 923569 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-1937251	ttgaaaattagaccac[A/T]ggtagaatgagtatag	A	T	AB002311 // downstream // 1110351 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 913401 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2067376	acaaatactcatttgc[C/G]cttgatttgcacatcc	C	G	AB002311 // downstream // 1118235 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 905517 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-2227662	ctacatggaaaattga[A/C]gtagcaaggtaggtca	A	C	AB002311 // downstream // 1118353 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 905399 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2063220	aatgtttgtcaatatc[A/G]accaagaacaaaagtt	A	G	AB002311 // downstream // 1137777 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 885975 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1
SNP_A-2171394	caatcaactctgaagc[A/G]catcttttctcatccc	A	G	AB002311 // downstream // 1141466 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 882286 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-2262341	gaaatgagctatcacc[A/G]aaagatgtggaggaac	A	G	AB002311 // downstream // 1147826 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 875926 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-1853835	tcaaaacccatagaac[A/C]ctatgacaccaagagt	A	C	AB002311 // downstream // 1148092 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 875660 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. ,q32.1
SNP_A-2043738	aacttagtgggagaat[A/G]aattggcatggcattt	A	G	AB002311 // downstream // 1162427 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 861325 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds. q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2211402	ccctaggagatcctga[C/G]aataggttcctaagat	C	G	AB002311 // downstream // 1180378 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 843374 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.1
SNP_A-2151424	atgttcatatctttcq[A/G]ccagctagtatcagca	A	G	AB002311 // downstream // 1203872 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 819880 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.1
SNP_A-2266762	gaattaactgtccaaa[C/T]tgatacacttttttta	C	T	AB002311 // downstream // 1256991 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 766761 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.1
SNP_A-1689847	gtattgctattgcacttcttaca[A/G]caactaaagtgatctcatttt taat	A	G	NM_014247 // downstream // 1113572 // - // - // - /// NM_020116 // downstream // 910178 // Hs.32452 // FSTL5 // 56884 // follistatin-like 5	-	- , rs10517718, - ,q32.1
SNP_A-2059874	aatcttaacaggacta[C/T]cagctgaagagacaag	C	T	AB002311 // downstream // 1674151 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 349601 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.2
SNP_A-2313928	ggagcgttttaaccc[A/G]ctgcatatacacacaa	A	G	AB002311 // downstream // 1731098 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 292654 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.2
SNP_A-2261144	gaaagagagaaagtggc[A/G]cattatgaactaagca	A	G	AB002311 // downstream // 1738864 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 284888 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.2
SNP_A-2264858	gaagagagttgcagtc[A/C]aatacttagccctgct	A	C	AB002311 // downstream // 1742153 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 281599 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.2
SNP_A-1979644	ccaattattctcactc[G/T]aaggttacatcatatt	G	T	AB002311 // downstream // 1920973 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 102779 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST0000026443	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds, q32.2
SNP_A-1729472	gaaattaatctagaaatgttaaa[C/T]cgcttataggctagagt gtgtctt	C	T	NM_014247 // downstream // 1725525 // - // - // - /// NM_020116 // downstream // 298225 // Hs.32452 // FSTL5 // 56884 // follistatin-like 5	-	- , rs6825391, - ,q32.2
SNP_A-1731507	ataagctgcatagagctctccatca[A/C]aataacaaaaaaggtt tcagtgctg	A	C	NM_014247 // downstream // 1732750 // - // - // - /// NM_020116 // downstream // 291000 // Hs.32452 // FSTL5 // 56884 // follistatin-like 5	-	- , rs4505772, - ,q32.2
SNP_A-1718795	aaaatatatatgaatgacagctcta[C/T]caatatgaggttaaaag gagaaagc	C	T	NM_014247 // downstream // 1733160 // - // - // - /// NM_020116 // downstream // 290590 // Hs.32452 // FSTL5 // 56884 // follistatin-like 5	-	- , rs4446269, - ,q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2203980	ccagatgggtctgtta[C/T]gatttcagcccactg	C	T	AB002311 // downstream // 1983473 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 40279 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000264431	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds., q32.2
SNP_A-2293793	gcagctcattgcagta[A/G]gacagatttaaacaac	A	G	AB002311 // downstream // 1985903 // Hs.113912 // RAPGEF2 // 9693 // Homo sapiens mRNA for KIAA0313 gene, partial cds. /// NM_020116 // downstream // 37849 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000264431	RAPGEF2	RAPGEF2, Homo sapiens for KIAA0313 gene, partial cds., q32.2
SNP_A-1826861	taacatagacataaaac[A/G]caggcaagaacgtgt	A	G	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1920160	ttaatcctactatcc[A/G]ataagaacttggaaa	A	G	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1961349	ttttttctgtcataa[A/G]tcctaaatgccagccag	A	G	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1979658	acttgctatgtcttga[C/T]aggaataggaagaagcc	C	T	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2207773	cccaaacaaggaaata[G/T]gtaacacaagtgtggc	G	T	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1803109	gtattatctttcgaa[C/G]ttaagattttgataat	C	G	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2089999	acttcttaaaccaaa[G/T]agtgcaaaattatgtg	G	T	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1847155	tatcatgtttatagga[C/T]ccaaaatcatgtgagt	C	T	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1659168	ttggaaggaagtaggactcaaggagt[A/G]aagtattaaggtgggtttcaagga	A	G	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // follistatin-like 5	FSTL5	FSTL5 , rs10517754, follistatin-like 5,q32.2
SNP_A-2250529	cttagtacattgaaga[A/G]caagaaggcttctgta	A	G	NM_020116 // intron // 0 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// ENST00000306100 // intron // 0 // — // — // —	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2213297	ccgctgtcagaaacac[C/T]caatttatacacacac	C	T	NM_020116 // upstream // 158058 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// NM_138386 // downstream // 806581 // Hs.332844 // LOC92345 // 92345 // Homo sapiens hypothetical protein BC008207 (LOC92345), mRNA. /// ENS	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1802363	gtatcaatataaaagt[A/C]aaatggcaacacacta	A	C	NM_020116 // upstream // 185939 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// NM_138386 // downstream // 778700 // Hs.332844 // LOC92345 // 92345 // Homo sapiens hypothetical protein BC008207 (LOC92345), mRNA. /// ENS	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-2214971	cctatctttgtataac[C/T]gtccatcttttttaa	C	T	NM_020116 // upstream // 218118 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// NM_138386 // downstream // 746521 // Hs.332844 // LOC92345 // 92345 // Homo sapiens hypothetical protein BC008207 (LOC92345), mRNA. /// ENS	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1952603	ttctgctccatgaat[A/C]ataataagtcttccac	A	C	NM_020116 // upstream // 343723 // Hs.32452 // FSTL5 // 56884 // Homo sapiens follistatin-like 5 (FSTL5), mRNA. /// NM_138386 // downstream // 620916 // Hs.332844 // LOC92345 // 92345 // Homo sapiens hypothetical protein BC008207 (LOC92345), mRNA. /// ENS	FSTL5	FSTL5, Homo sapiens follistatin-like 5 (FSTL5), q32.2
SNP_A-1872054	tctacctgggaccaa[C/T]ggcacaccctatcaag	C	T	NM_138386 // upstream // 164766 // Hs.332844 // LOC92345 // 92345 // Homo sapiens hypothetical protein BC008207 (LOC92345), mRNA. /// NM_006174 // upstream // 12252 // Hs.519058 // NPY5R // 4889 // Homo sapiens neuropeptide Y receptor Y5 (NPY5R), mRNA. //	LOC92345	LOC92345, Homo sapiens hypothetical protein BC008207 (LOC92345), q32.2
SNP_A-1925016	ttatcaagagagatca[A/G]attccatcctattcac	A	G	NM_006174 // downstream // 31783 // Hs.519058 // NPY5R // 4889 // Homo sapiens neuropeptide Y receptor Y5 (NPY5R), mRNA. /// NM_032136 // downstream // 88143 // Hs.303923 // DKFZP434L1717 // 84076 // Homo sapiens similar to transketolase (DKFZP434L1717),	NPY5R	NPY5R, Homo sapiens neuropeptide Y receptor Y5 (NPY5R), q32.2
SNP_A-2034079	aaatcagttattagtc[A/T]cagttcaagatacaga	A	T	NM_006174 // downstream // 64947 // Hs.519058 // NPY5R // 4889 // Homo sapiens neuropeptide Y receptor Y5 (NPY5R), mRNA. /// NM_032136 // downstream // 54979 // Hs.303923 // DKFZP434L1717 // 84076 // Homo sapiens similar to transketolase (DKFZP434L1717),	NPY5R	NPY5R, Homo sapiens neuropeptide Y receptor Y5 (NPY5R), q32.2
SNP_A-2141379	atctgtgtgatttgaa[C/T]gctacacaccttggc	C	T	NM_017923 // intron // 0 // Hs.136900 // MARCH1 // 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// ENST00000339875 // intron // 0 // — // — // — /// ENST00000274056 // intron // 0 // — // — // —	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.2
SNP_A-1851651	tattctgtagggaaaa[A/G]agagctaacacacatg	A	G	NM_017923 // intron // 0 // Hs.136900 // MARCH1 // 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// ENST00000339875 // intron // 0 // — // — // — /// ENST00000274056 // intron // 0 // — // — // —	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.2
SNP_A-1682272	aagaagttttggagactgcatatca[C/T]accctatttaaaggttc acattta	C	T	NM_006174 // downstream // 51980 // Hs.158330 // NPY5R // 4889 // neuropeptide Y receptor Y5 /// NM_032136 // downstream // 67185 // Hs.303923 // DKFZP434L1717 // 84076 // similar to transketolase	NPY5R	NPY5R , rs1441716, neuropeptide Y receptor Y5 ,q32.2
SNP_A-2136471	atcaccaagacgatgg[A/G]actaagccattcatga	A	G	ENST00000274056 // intron // 0 // — // — // —	-	q32.3
SNP_A-2147845	atggccgcactccgcc[A/G]cagctgctccatgcac	A	G	NM_017923 // upstream // 409178 // Hs.136900 // MARCH1 // 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// NM_012403 // downstream // 174325 // Hs.518929 // ANP32C // 23520 // Homo sapiens acidic (leucine-rich) nuclear phos	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.3
SNP_A-1841356	taggaatgcgagttag[A/G]atagtagtactctca	A	G	NM_017923 // upstream // 437506 // Hs.136900 // MARCH1 // 55016 // Homo sapiens membrane-associated RING-CH protein I (MARCH-I), mRNA. /// NM_012403 // downstream // 145997 // Hs.518929 // ANP32C // 23520 // Homo sapiens acidic (leucine-rich) nuclear phos	MARCH1	MARCH1, Homo sapiens membrane-associated RING-CH protein I (MARCH-I), q32.3
SNP_A-2039952	aacatttcacttttctc[A/T]cctaaatgtgtactt	A	T	NM_012403 // upstream // 209125 // Hs.518929 // ANP32C // 23520 // Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), mRNA. /// ENST00000330241 // upstream // 209125 // — // — // — /// ENST00000357468 // u	ANP32C	ANP32C, Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member C (ANP32C), q32.3
SNP_A-1837295	tactatccacagttat[A/C]acaagaggagggata	A	C	ENST00000356562 // intron // 0 // — // — // —	-	q32.3
SNP_A-1828545	taagcatccaggaaaa[A/T]ttgtcatctgtgtcc	A	T	ENST00000356562 // intron // 0 // — // — // —	-	q32.3
SNP_A-2220812	ccttgatttaaaaaa[C/T]gttcctggctgagggc	C	T	NM_152681 // downstream // 12554 // Hs.369632 // FLJ38482 // 201931 // Homo sapiens hypothetical protein FLJ38482 (FLJ38482), mRNA. /// ENST00000322402 // downstream // 4861 // — // — // — // — /// ENST00000306480 // downstream // 12554 // — //	FLJ38482	FLJ38482, Homo sapiens hypothetical protein FLJ38482 (FLJ38482), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289739	gcaaaataagatgcca[C/T]gaggctgtcagtctgc	C	T	NM_001873 // downstream // 19193 // Hs.75360 // CPE // 1363 // Homo sapiens carboxypeptidase E (CPE), mRNA. /// ENST00000261510 // downstream // 19193 // — // — // — // — /// ENST00000359703 // downstream // 19193 // — // — // — // — /// E	CPE	CPE, Homo sapiens carboxypeptidase E (CPE), q32.3
SNP_A-1877859	tctggtctgaatccaa[C/T]gtcacctaagatttag	C	T	NM_012464 // upstream // 302846 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 19379 // — // — // — // — /// ENST00000061240 // upstream // 302846 // — // — // — // —	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1979766	ccattctcccgccaga[A/T]aaatatatgtgtatgt	A	T	NM_012464 // upstream // 297024 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 25201 // — // — // — // — /// ENST00000061240 // upstream // 297024 // — // — // — // —	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2291544	gcacaaacctcaaggg[A/G]ccacacatttggtaga	A	G	NM_012464 // upstream // 293014 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 29211 // — // — // — // — /// ENST00000061240 // upstream // 293014 // — // — // — // —	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1844856	tataatatttatagaa[A/C]ctagaattctgccttg	A	C	NM_012464 // upstream // 189047 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000306575 // upstream // 133178 // — // — // — // — /// ENST00000061240 // upstream // 189047 // — // — // — // —	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2264745	gaagaccctattagag[A/G]agctcagaaagggcct	A	G	NM_012464 // intron // 0 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// ENST00000061240 // intron // 0 // — // — // — // —	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1979789	atgattaagctgaatt[A/T]aaatcacaagataata	A	T	NM_012464 // downstream // 130732 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 515938 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2282983	gataactgagcagcaa[C/T]cgcagcttctcctgga	C	T	NM_012464 // downstream // 152108 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 494562 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1939413	ttgatgctggtaaaac[G/T]acatgatctctaaaca	G	T	NM_012464 // downstream // 154588 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 492082 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1979792	atagttttgagcatca[A/G]ggaatacattttcaga	A	G	NM_012464 // downstream // 183466 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 463204 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1787583	gggaattggcagccac[A/G]aacatattggtggtag	A	G	NM_012464 // downstream // 196572 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 450098 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-2072761	acagctatttggaaaa[C/T]ttaatgcaaattcatg	C	T	NM_012464 // downstream // 197084 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 449586 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1891455	tgattcatttctctca[C/G]aacaaggatacccatt	C	G	NM_012464 // downstream // 323839 // Hs.106513 // TLL1 // 7092 // Homo sapiens tolloid-like 1 (TLL1), mRNA. /// BC013983 // downstream // 322831 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (t	TLL1	TLL1, Homo sapiens tolloid-like 1 (TLL1), q32.3
SNP_A-1664304	ggataaagcttgttccaaccagtaa[A/G]tcaagattcttcaccaagaaccttc	A	G	NM_012464 // downstream // 176949 // Hs.129700 // TLL1 // 7092 // tolloid-like 1 /// NM_016950 // downstream // 571657 // Hs.159425 // SPOCK3 // 50859 // sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	TLL1	TLL1 , rs391309, tolloid-like 1 ,q32.3
SNP_A-1756991	acaagaaacaaaacagatttccaag[G/T]atttttgattacagccaaaaggtt	G	T	NM_012464 // downstream // 180089 // Hs.129700 // TLL1 // 7092 // tolloid-like 1 /// NM_016950 // downstream // 568517 // Hs.159425 // SPOCK3 // 50859 // sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	TLL1	TLL1 , rs453042, tolloid-like 1 ,q32.3
SNP_A-1659502	ttatgaaaaacaatatgcactacca[A/G]tggtaataagtataatagtcacaag	A	G	NM_012464 // downstream // 180613 // Hs.129700 // TLL1 // 7092 // tolloid-like 1 /// NM_016950 // downstream // 567993 // Hs.159425 // SPOCK3 // 50859 // sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	TLL1	TLL1 , rs418488, tolloid-like 1 ,q32.3
SNP_A-1665644	atagagcaaaaagtctttgtacctc[C/T]attgtattattggctaaaagcagaa	C	T	NM_012464 // downstream // 180701 // Hs.129700 // TLL1 // 7092 // tolloid-like 1 /// NM_016950 // downstream // 567905 // Hs.159425 // SPOCK3 // 50859 // sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	TLL1	TLL1 , rs411699, tolloid-like 1 ,q32.3
SNP_A-2196833	cattacttttctacaa[C/G]tcttaattacctttga	C	G	BC013983 // intron // 0 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // intron // 0 // Hs.481133 // SPOCK3 // 50859 // Hom	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1957604	ttttatccatcattta[C/T]gtagaaaaatcagaac	C	T	BC013983 // intron // 0 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // intron // 0 // Hs.481133 // SPOCK3 // 50859 // Hom	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1695723	ggcatttaggaaagagttttgcata[C/T]attaagtgtgaaataaatactggat	C	T	NM_016950 // intron // 0 // Hs.159425 // SPOCK3 // 50859 // sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	SPOCK3	SPOCK3 , rs2703843, sparc,q32.3
SNP_A-2245366	ctggctttaggatacc[A/G]acaatttatactttgc	A	G	BC013983 // upstream // 104666 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 104611 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1841266	taggaacatagttaga[A/G]tcagtcaataagtcaa	A	G	BC013983 // upstream // 132683 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 132628 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-2140029	atctagaggtctatta[C/G]aaaaacagtcaggaaa	C	G	BC013983 // upstream // 456013 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 455958 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-2262851	gaacaaaatcatgcca[C/G]tattaatgacctgtgt	C	G	BC013983 // upstream // 472726 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 472671 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc,q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2010359	tcaatttatactctca[A/C]caggaatatattatct	A	C	BC013983 // upstream // 527129 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 527074 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-2125351	agttgttgctaagttc[C/T]ctcatagctttaatat	C	T	BC013983 // upstream // 527645 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 527590 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc,q32.3
SNP_A-2150542	atgtgagacaaatcca[C/T]agtcgattgcttcctt	C	T	BC013983 // upstream // 650741 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 650686 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-1979833	ccaaagcacacaatta[C/G]atatcgatgattatgg	C	G	BC013983 // upstream // 659080 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 659025 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc q32.3
SNP_A-2241368	ctgaggtgttgggggc[A/C]caatctctgctccatt	A	C	BC013983 // upstream // 696956 // Hs.481133 // SPOCK3 // 50859 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3, mRNA (cDNA clone MGC:20285 IMAGE:4110883) /// NM_016950 // upstream // 696901 // Hs.481133 // SPOCK3 /	SPOCK3	SPOCK3, Homo sapiens sparc,q32.3
SNP_A-2232803	ctcactgtgtgcaaga[C/T]gtaagtgatttgcttg	C	T	NM_007193 // downstream // 206974 // Hs.188401 // ANXA10 // 11199 // Homo sapiens annexin A10 (ANXA10), mRNA. /// NM_007193 // downstream // 144878 // Hs.188401 // ANXA10 // 11199 // Homo sapiens annexin A10 (ANXA10), mRNA. /// NM_017631 // upstream // 75	ANXA10	ANXA10, Homo sapiens annexin A10 (ANXA10), q32.3
SNP_A-2108237	agctgaagttgcagcc[C/T]acaggtggaatttgtt	C	T	ENST00000284630 // intron // 0 // — // — // — // —	-	q32.3
SNP_A-2010364	aaaaaggtatggaaaa[G/T]ttgaggatcttgatag	G	T	NM_016081 // upstream // 44823 // Hs.151220 // KIAA0992 // 23022 // Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000284630 // upstream // 10866 // — // — // — // — /// ENST00000261509 // upstream // 44823 // — // — // — // — /// ENST0	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3
SNP_A-2038797	aacagcaaggtagaaa[G/T]taaaaagccagtcttc	G	T	NM_016081 // intron // 0 // Hs.151220 // KIAA0992 // 23022 // Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000261509 // intron // 0 // — // — // — // — /// ENST00000333488 // intron // 0 // — // — // — // —	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3
SNP_A-1813640	gtgtaatttacaagaa[C/G]acttaaagaactctca	C	G	NM_016081 // intron // 0 // Hs.151220 // KIAA0992 // 23022 // Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000261509 // intron // 0 // — // — // — // — /// ENST00000333488 // intron // 0 // — // — // — // —	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3
SNP_A-1820023	gttgtttgaaattgga[C/G]gtaaaaatagttgtct	C	G	NM_016081 // intron // 0 // Hs.151220 // KIAA0992 // 23022 // Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000261509 // intron // 0 // — // — // — // — /// ENST00000333488 // intron // 0 // — // — // — // — /// ENST00000359923 // intr	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3
SNP_A-2120878	agtcgttcaacaaata[C/T]ctatttagtcccaaag	C	T	NM_016081 // intron // 0 // Hs.151220 // KIAA0992 // 23022 // Homo sapiens palladin (KIAA0992), mRNA. /// ENST00000261509 // intron // 0 // — // — // — // — /// ENST00000333488 // intron // 0 // — // — // — // — /// ENST00000359923 // intr	KIAA0992	KIAA0992, Homo sapiens palladin (KIAA0992), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1915891	tgttgagcagtgggac[C/T]ggactttgcttataag	C	T	NM_032783 // upstream // 16591 // Hs.481166 // CBR4 // 84869 // Homo sapiens carbonic reductase 4 (CBR4), mRNA. /// NM_020870 // downstream // 89423 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// ENST00000306193	CBR4	CBR4, Homo sapiens carbonic reductase 4 (CBR4), q32.3
SNP_A-1979869	acccagaaatgcttta[C/G]gatggaggacattaca	C	G	NM_032783 // upstream // 16649 // Hs.481166 // CBR4 // 84869 // Homo sapiens carbonic reductase 4 (CBR4), mRNA. /// NM_020870 // downstream // 89365 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// ENST00000306193	CBR4	CBR4, Homo sapiens carbonic reductase 4 (CBR4), q32.3
SNP_A-1886154	tgaccattaatgttga[C/T]ggtcccctgtggcaga	C	T	NM_032783 // upstream // 16731 // Hs.481166 // CBR4 // 84869 // Homo sapiens carbonic reductase 4 (CBR4), mRNA. /// NM_020870 // downstream // 89283 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// ENST00000306193	CBR4	CBR4, Homo sapiens carbonic reductase 4 (CBR4), q32.3
SNP_A-2136381	atcacagcaaacgctt[C/T]aagagttctcaacaat	C	T	NM_032783 // upstream // 40508 // Hs.481166 // CBR4 // 84869 // Homo sapiens carbonic reductase 4 (CBR4), mRNA. /// NM_020870 // downstream // 65506 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// ENST00000306193	CBR4	CBR4, Homo sapiens carbonic reductase 4 (CBR4), q32.3
SNP_A-2312402	ggaccaatttagctga[C/T]ctcttccttgactgag	C	T	NM_032783 // upstream // 67497 // Hs.481166 // CBR4 // 84869 // Homo sapiens carbonic reductase 4 (CBR4), mRNA. /// NM_020870 // downstream // 38517 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// ENST00000306193	CBR4	CBR4, Homo sapiens carbonic reductase 4 (CBR4), q32.3
SNP_A-1740395	gtgtagcacatacgtagtataagaa[C/T]tctgttgatataatgccg cagtcat	C	T	NM_016081 // intron // 0 // Hs.194431 // KIAA0992 // 23022 // palladin	KIAA0992	KIAA0992 , rs4692552, palladin,q32.3
SNP_A-2010372	cacgtataatgagatg[C/T]cactgcaagagatcat	C	T	NM_020870 // upstream // 38065 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// NM_012224 // downstream // 84255 // Hs.481181 // NEK1 // 4750 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1),	SH3MD2	SH3MD2, Homo sapiens SH3 multiple domains 2 (SH3MD2), q33
SNP_A-1806219	gtcctggcgctgttga[A/G]ctttatgagatgacta	A	G	NM_020870 // upstream // 64566 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// NM_012224 // downstream // 57754 // Hs.481181 // NEK1 // 4750 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1),	SH3MD2	SH3MD2, Homo sapiens SH3 multiple domains 2 (SH3MD2), q33
SNP_A-2047332	aagatcatgtctgcaa[A/G]caagaactatttgact	A	G	NM_020870 // upstream // 109613 // Hs.301804 // SH3MD2 // 57630 // Homo sapiens SH3 multiple domains 2 (SH3MD2), mRNA. /// NM_012224 // downstream // 12707 // Hs.481181 // NEK1 // 4750 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1)	SH3MD2	SH3MD2, Homo sapiens SH3 multiple domains 2 (SH3MD2), q33
SNP_A-2128327	ataagtctgtgcaacc[A/G]gaaccatttttccata	A	G	NM_012224 // CDS // 0 // Hs.481181 // NEK1 // 4750 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA. /// ENST00000336047 // CDS // 0 // — // — // — // — /// ENST00000308881 // CDS // 0 // — // — // — // —	NEK1	NEK1, Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), q33
SNP_A-1887160	tgagaaaggaaggtta[C/T]agacttacacatatgc	C	T	NM_012224 // intron // 0 // Hs.481181 // NEK1 // 4750 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA. /// ENST00000336047 // intron // 0 // — // — // — // — /// ENST00000308881 // intron // 0 // — // — // — // -	NEK1	NEK1, Homo sapiens NIMA (never in mitosis gene a)-related kinase 1 (NEK1), q33
SNP_A-1819234	gttgcttgatggagtg[C/T]accaagtaaaaaagat	C	T	NM_001829 // intron // 0 // Hs.481186 // CLCN3 // 1182 // Homo sapiens chloride channel 3 (CLCN3), mRNA. /// NM_173872 // intron // 0 // Hs.481186 // CLCN3 // 1182 // Homo sapiens chloride channel 3 (CLCN3), transcript variant e, mRNA. /// ENST00000360642	CLCN3	CLCN3, Homo sapiens chloride channel 3 (CLCN3), q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1667684	cagagctgagagtggtagatggaac[C/T]attcttccaaagcatcatttcccca	C	T	AB067488 // downstream // 17833 // Hs.414410 // NEK1 // 4750 // NIMA (never in mitosis gene a)-related kinase 1 /// NM_020870 // upstream // 104511 // Hs.301804 // SH3MD2 // 57630 // SH3 multiple domains 2	NEK1	NEK1 , rs1578975, NIMA (never in mitosis gene a)-related kinase 1 ,q33
SNP_A-1707946	tggagatcgtggtggatattttccg[A/G]aagctgggactgaggcagtgccttg	A	G	NM_001829 // CDS // 0 // Hs.372528 // CLCN3 // 1182 // chloride channel 3	CLCN3	CLCN3 , rs1010713, chloride channel 3,q33
SNP_A-2246262	ctggtggcatgcataa[A/G]cccaaaggtaggggtc	A	G	NM_016228 // upstream // 98920 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 98920 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferas	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2052007	aaggttaaggttggag[G/T]agacgaaaatcaagag	G	T	NM_016228 // upstream // 138528 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 138528 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2154458	attattcagcactgga[A/T]aaagatagccttcttt	A	T	NM_016228 // upstream // 300318 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 300318 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2062366	aatgtaagcagagaga[C/T]ggatattcttgtttta	C	T	NM_016228 // upstream // 579841 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 579841 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2196685	cattaatacccaggaa[A/G]tgactcaaaccacagt	A	G	NM_016228 // upstream // 650651 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 650651 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1837690	tactttctagatacaa[C/T]ggtagatggtagtaca	C	T	NM_016228 // upstream // 726692 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 726692 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2101541	agatgactaaggcaca[C/G]tatcatttccaatttt	C	G	NM_016228 // upstream // 736257 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 736257 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1898659	tgcttgttaatgacat[A/G]aagattggtgaggatt	A	G	NM_016228 // upstream // 750220 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 750220 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-1886083	tgaccacttgctgtta[C/T]acctgctttgtggcaa	C	T	NM_016228 // upstream // 764070 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 764070 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33
SNP_A-2058578	aatcagctttgaactg[G/T]atctaagtcatccttc	G	T	NM_016228 // upstream // 779349 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 779349 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransfer	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1660669	gtaagttgttgtgaataatatcttg[A/G]agaaaacctacctggttgt agagtt	A	G	NM_016228 // upstream // 660855 // Hs.211477 // AADAT // 51166 // aminoadipate aminotransferase	AADAT	AADAT, rs2332027, aminoadipate aminotransferase,q33
SNP_A-1684036	acagacaaaggcatatgccacaaga[A/G]aggaacagagagtttc actgggtttac	A	G	NM_016228 // upstream // 776967 // Hs.211477 // AADAT // 51166 // aminoadipate aminotransferase	AADAT	AADAT, rs1560566, aminoadipate aminotransferase,q33
SNP_A-1691464	aaaatttttggttgagatcttaaaa[A/T]atttctaaataataatcccc agtaa	A	T	NM_016228 // upstream // 1108950 // Hs.211477 // AADAT // 51166 // aminoadipate aminotransferase	AADAT	AADAT, rs1491354, aminoadipate aminotransferase,q34.1
SNP_A-2272991	gactagctgtaaagga[C/G]atatatttgccctgt	C	G	NM_016228 // upstream // 1615597 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1615597 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransf	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2132617	atagttctggccacgta[A/G]aataggatgctgatac	A	G	NM_016228 // upstream // 1622702 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1622702 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransf	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2278443	gagctcacatggtaaa[G/T]gatgtctgccacctc	G	T	NM_016228 // upstream // 1650494 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1650494 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransf	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-1929300	ttcagtatgttctgaa[C/T]acacaatggctaatat	C	T	NM_016228 // upstream // 1698547 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, mRNA. /// NM_182662 // upstream // 1698547 // Hs.529735 // AADAT // 51166 // Homo sapiens aminoadipate aminotransf	AADAT	AADAT, Homo sapiens aminoadipate aminotransferase (AADAT), transcript variant 1, q34.1
SNP_A-2087887	actggagttcccactc[A/G]aatgccactaaccctc	A	G	NM_017423 // intron // 0 // Hs.127407 // GALNT7 // 51809 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA. /// ENST00000265000 // intron // 0 // — // — // —	GALNT7	GALNT7, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), q34.1
SNP_A-1783670	ggcattatatcagcaa[C/T]gtgtgtttctgctaca	C	T	NM_006792 // downstream // 18666 // Hs.534391 // MORF4 // 10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// ENST00000296508 // downstream // 57801 // — // — // — /// ENST00000305285 // downstream // 18666 // — // — // — // —	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-2302074	gcgttaatctattaat[A/G]aggcatccatcccat	A	G	NM_006792 // upstream // 365823 // Hs.534391 // MORF4 // 10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// NM_012180 // downstream // 254192 // Hs.76917 // FBXO8 // 26269 // Homo sapiens F-box protein 8 (FBXO8), mRNA. /// NM_012180 // downstream	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-1979966	tgcaatcaactacgtc[C/T]actggcttcggaattg	C	T	NM_006792 // upstream // 509191 // Hs.534391 // MORF4 // 10934 // Homo sapiens mortality factor 4 (MORF4), mRNA. /// NM_012180 // downstream // 110824 // Hs.76917 // FBXO8 // 26269 // Homo sapiens F-box protein 8 (FBXO8), mRNA. /// NM_012180 // downstream	MORF4	MORF4, Homo sapiens mortality factor 4 (MORF4), q34.1
SNP_A-2161133	atttgaagaatgccaa[A/G]tcaaatttctgagctc	A	G	NM_006529 // intron // 0 // Hs.413099 // GLRA3 // 8001 // Homo sapiens glycine receptor, alpha 3 (GLRA3), mRNA. /// ENST00000274093 // intron // 0 // — // — // — /// ENST00000340217 // intron // 0 // — // — // —	GLRA3	GLRA3, Homo sapiens glycine receptor, alpha 3 (GLRA3), q34.1
SNP_A-2128681	ataatcaagatttgca[A/G]aagtaggcaaatggat	A	G	NM_006529 // upstream // 20339 // Hs.413099 // GLRA3 // 8001 // Homo sapiens glycine receptor, alpha 3 (GLRA3), mRNA. /// NM_014269 // upstream // 68755 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29)	GLRA3	GLRA3, Homo sapiens glycine receptor, alpha 3 (GLRA3), q34.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2112379	aggcaactgctatcgaa[C/T]atccttgtcacagtt	C	T	NM_014269 // intron // 0 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // intron // 0 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a disintegrin and met	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.1
SNP_A-2106382	agccctttattccaa[C/T]caggtgtatcttcta	C	T	NM_014269 // downstream // 88106 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // downstream // 88106 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a dis	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.1
SNP_A-2299987	gcctatggtatttcca[A/C]actctccdaatcttg	A	C	NM_014269 // downstream // 433706 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // downstream // 433706 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a d	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.2
SNP_A-2271593	gaccacaagcagacaa[C/T]agtttgccacatcag	C	T	NM_014269 // downstream // 436068 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, mRNA. /// NM_021779 // downstream // 436068 // Hs.126838 // ADAM29 // 11086 // Homo sapiens a d	ADAM29	ADAM29, Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), transcript variant 1, q34.2
SNP_A-2261665	gaaagtataaaccatc[A/G]catacaagagaatccg	A	G	NM_005277 // intron // 0 // Hs.75819 // GPM6A // 2823 // Homo sapiens glycoprotein M6A (GPM6A), transcript variant 1, mRNA. /// NM_201591 // intron // 0 // Hs.75819 // GPM6A // 2823 // Homo sapiens glycoprotein M6A (GPM6A), transcript variant 2, mRNA. ///	GPM6A	GPM6A, Homo sapiens glycoprotein M6A (GPM6A), transcript variant 1, q34.2
SNP_A-1980006	gcagttagctaagaccd[A/G]ctttaatgatagggc	A	G	NM_170710 // intron // 0 // Hs.532056 // WDR17 // 116966 // Homo sapiens WD repeat domain 17 (WDR17), transcript variant 1, mRNA. /// NM_181265 // intron // 0 // Hs.532056 // WDR17 // 116966 // Homo sapiens WD repeat domain 17 (WDR17), transcript variant	WDR17	WDR17, Homo sapiens WD repeat domain 17 (WDR17), transcript variant 1, q34.2
SNP_A-2129528	atacacctatagcact[G/T]aataaaaaatactgctg	G	T	NM_080874 // intron // 0 // Hs.352364 // ASB5 // 140458 // Homo sapiens ankyrin repeat and SOCS box-containing 5 (ASB5), mRNA. /// ENST00000296525 // intron // 0 // --- // --- // ---	ASB5	ASB5, Homo sapiens ankyrin repeat and SOCS box-containing 5 (ASB5), q34.2
SNP_A-1658314	caattctaaaatttagaacaataa[C/T]tgggtcttaaatatagatt tggga	C	T	NM_005429 // intron // 0 // Hs.79141 // VEGFC // 7424 // vascular endothelial growth factor C	VEGFC	VEGFC, rs1692787, vascular endothelial growth factor C,q34.3
SNP_A-2151803	atgttcaaattatccf[G/T]agttaacgtgactggc	G	T	NM_005429 // upstream // 313059 // Hs.435215 // VEGFC // 7424 // Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA. /// NM_018248 // upstream // 204074 // Hs.405467 // NEIL3 // 55247 // Homo sapiens DNA glycosylase hFPG2 (FLJ10858), mRNA. //	VEGFC	VEGFC, Homo sapiens vascular endothelial growth factor C (VEGFC), q34.3
SNP_A-1851068	tattattctctaaaac[G/T]ctaatatggtctggct	G	T	NM_005429 // upstream // 485591 // Hs.435215 // VEGFC // 7424 // Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA. /// NM_018248 // upstream // 31542 // Hs.405467 // NEIL3 // 55247 // Homo sapiens DNA glycosylase hFPG2 (FLJ10858), mRNA. ///	VEGFC	VEGFC, Homo sapiens vascular endothelial growth factor C (VEGFC), q34.3
SNP_A-1663034	ctatcaggacacaatgaaatattta[C/G]attctgggataacaatg tactaatg	C	G	NM_005429 // upstream // 457227 // Hs.79141 // VEGFC // 7424 // vascular endothelial growth factor C /// NM_018248 // upstream // 59906 // Hs.405467 // FLJ10858 // 55247 // DNA glycosylase hFPG2	VEGFC	VEGFC , rs10520373, vascular endothelial growth factor C ,q34.3
SNP_A-2086350	actcttactcatcacc[A/G]caaatcacttattaat	A	G	NM_000027 // upstream // 522417 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 522417 // --- // --- // --- /// ENST00000356882 // downstream // 260704 // --- // --- // --- // ---	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1949448	tttattctgttgtctatA/G]cttctcaatgtttaat	A	G	NM_000027 // upstream // 638723 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 638723 // -- // -- // -- /// ENST00000356882 // downstream // 2492398 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2072634	acagcctaatgatgca[C/T]aaaaatagtgatatgt	C	T	NM_000027 // upstream // 656105 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 656105 // -- // -- // -- /// ENST00000356882 // downstream // 2475016 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1851933	tattgattgccttaag[A/C]actgcaattaactaag	A	C	NM_000027 // upstream // 669645 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 669645 // -- // -- // -- /// ENST00000356882 // downstream // 2461476 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2134856	atattag[g/c]aggctaC/T]gcgtgacattacccca	C	T	NM_000027 // upstream // 699605 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 699605 // -- // -- // -- /// ENST00000356882 // downstream // 2431516 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1900806	tggagctgtccagta[A/C]ctaatctcctgcaga	A	C	NM_000027 // upstream // 754427 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 754427 // -- // -- // -- /// ENST00000356882 // downstream // 2376694 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1853993	tcaaaatgtgcataaa[A/C]tacaggcataagttgt	A	C	NM_000027 // upstream // 813287 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 813287 // -- // -- // -- /// ENST00000356882 // downstream // 2317834 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2010440	gaaatgttactttcaa[C/G]aacttacaggaccttg	C	G	NM_000027 // upstream // 885983 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 885983 // -- // -- // -- /// ENST00000356882 // downstream // 2245138 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2084299	actagttggctccaaat[C/T]tgagaaaactgtgcac	C	T	NM_000027 // upstream // 911000 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 911000 // -- // -- // -- /// ENST00000356882 // downstream // 2220121 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2027927	aaacctgtcttaca[A/T]actcaactgaaatcat	A	T	NM_000027 // upstream // 914828 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 914828 // -- // -- // -- /// ENST00000356882 // downstream // 2216293 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2145349	atgcagaaaactaaga[C/G]acccatgaaggagaag	C	G	NM_000027 // upstream // 916832 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 916832 // -- // -- // -- /// ENST00000356882 // downstream // 2214289 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1793606	ggtatcccttaaatgaa[A/G]gaactggatgcaaatt	A	G	NM_000027 // upstream // 946698 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 946698 // -- // -- // -- /// ENST00000356882 // downstream // 2184423 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2273140	gactcaaaccccatca[A/G]tctcatgacaaagccc	A	G	NM_000027 // upstream // 1538604 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1538604 // -- // -- // -- /// ENST00000356882 // downstream // 1592517 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2112125	aggatgttcaggtga[A/T]gttctggagataatct	A	T	NM_000027 // upstream // 1581984 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1581984 // -- // -- // -- /// ENST00000356882 // downstream // 1549137 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1980071	tgttaaccaaacctacA/C]atatcatcactctaat	A	C	NM_000027 // upstream // 1598768 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1598768 // -- // -- // -- // -- /// ENST00000356882 // downstream // 1532353 // -- // -- // -- // --	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284791	gatcattaggtcatca[A/G]caaaaataaatcaatt	A	G	NM_000027 // upstream // 1646833 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 1646833 // — // — // — // — /// ENST00000356882 // downstream // 1484288 // — // — // — // –	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2010458	ttggctacatctactc[C/T]aactttgaggaaacac	C	T	NM_000027 // upstream // 2160929 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2160929 // — // — // — // — /// ENST00000356882 // downstream // 970192 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2058866	aatccaagcctttaga[C/T]cagaagtaagaataag	C	T	NM_000027 // upstream // 2186284 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2186284 // — // — // — // — /// ENST00000356882 // downstream // 944837 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1944768	ttgtgcagaggaaact[A/C]agcaatggagttcatg	A	C	NM_000027 // upstream // 2448538 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2448538 // — // — // — // — /// ENST00000356882 // downstream // 682583 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1953215	tttctttgcagtagcc[G/T]ctatggttttgaagca	G	T	NM_000027 // upstream // 2617285 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2617285 // — // — // — // — /// ENST00000356882 // downstream // 513836 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2154916	attcacaactaaagcc[A/G]ccattgaatcccatcc	A	G	NM_000027 // upstream // 2693649 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2693649 // — // — // — // — /// ENST00000356882 // downstream // 437472 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2173999	cacacattagttctcc[C/T]cagtgccatcactttg	C	T	NM_000027 // upstream // 2762907 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2762907 // — // — // — // — /// ENST00000356882 // downstream // 368214 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-2208545	cccacgtgtccaaatg[A/T]atattctgtctgacac	A	T	NM_000027 // upstream // 2784673 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2784673 // — // — // — // — /// ENST00000356882 // downstream // 346448 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1880939	tcttgtctgattatac[A/C]cctatgtgagaattca	A	C	NM_000027 // upstream // 2799161 // Hs.207776 // AGA // 175 // Homo sapiens aspartylglucosaminidase (AGA), mRNA. /// ENST00000264595 // upstream // 2799161 // — // — // — // — /// ENST00000356882 // downstream // 331960 // — // — // — // —	AGA	AGA, Homo sapiens aspartylglucosaminidase (AGA), q34.3
SNP_A-1901102	tggatccttttttcca[C/G]gtgtatgcagcaagat	C	G	NM_178838 // downstream // 960201 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 607426 // — // — // — // — /// ENST00000315302 // downstream // 960201 // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1739379	ctgccactcagttctctgtggagat[G/T]atagcaattcatgggact cagagtg	G	T	NM_000027 // upstream // 3478265 // Hs.207776 // AGA // 175 // aspartylglucosaminidase /// NM_178838 // downstream // 1220951 // Hs.175465 // LOC90768 // 90768 // hypothetical protein LOC90768	AGA	AGA , rs1879908, aspartylglucosaminidase ,q34.3
SNP_A-1654185	ctcccatagcagtgagacattacga[A/G]aaaacggtttctatggt gttcgtct	A	G	NM_000027 // upstream // 3511524 // Hs.207776 // AGA // 175 // aspartylglucosaminidase /// NM_178838 // downstream // 1187692 // Hs.175465 // LOC90768 // 90768 // hypothetical protein LOC90768	AGA	AGA , rs2309378, aspartylglucosaminidase ,q34.3
SNP_A-1980141	aagaatagagagtcag[A/G]aaattgaaaataaata	A	G	NM_178838 // downstream // 709258 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 858369 // — // — // — // — /// ENST00000315302 // downstream // 709258 // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939042	ttgagttataagggaa[A/C]aatgatgatctcagtg	A	C	NM_178838 // downstream // 700901 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 866726 // — // — // — /// ENST00000315302 // downstream // 700901 // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2042638	aactcctactgaccac[A/G]ctttccagctgagtc	A	G	NM_178838 // downstream // 678914 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 888713 // — // — // — /// ENST00000315302 // downstream // 678914 // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1980148	tgaaatttagattggg[C/T]aatttgtctggtgaa	C	T	NM_178838 // downstream // 662842 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 904785 // — // — // — /// ENST00000315302 // downstream // 662842 // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1980153	aaatgcttgattata[C/T]gacatttatggttcaa	C	T	NM_178838 // downstream // 616644 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 950983 // — // — // — /// ENST00000315302 // downstream // 616644 // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1807067	gtctccataggcactg[A/G]aaacttaccatgttc	A	G	NM_178838 // downstream // 464352 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 1103275 // — // — // — /// ENST00000315302 // downstream // 464352 // — /	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1980159	ttgcttatcaggaaga[C/G]acatttagaaagacaa	C	G	NM_178838 // downstream // 348149 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 1219478 // — // — // — /// ENST00000315302 // downstream // 348149 // — /	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1827888	taagaaaccagttcaa[C/T]agctgatgcctttgac	C	T	NM_178838 // downstream // 238236 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 1329391 // — // — // — /// ENST00000315302 // downstream // 238236 // — /	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1822540	gtttttgcagtaaata[C/T]ggaagtggatatcaag	C	T	NM_178838 // downstream // 237560 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000356882 // upstream // 1330067 // — // — // — /// ENST00000315302 // downstream // 237560 // — /	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1851659	tattctgtgctcctaa[C/T]ctttaattgattggg	C	T	NM_178838 // upstream // 4444 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000315302 // upstream // 4444 // — // — // — /// ENST00000330336 // upstream // 175111 // — // — //	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-2146253	atgctaattcccccca[C/T]gaaagatggcttaca	G	T	NM_178838 // upstream // 125818 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000315302 // upstream // 125818 // — // — // — /// ENST00000330336 // upstream // 53737 // — // —	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q34.3
SNP_A-1937905	ttgaatctttgagttta[C/T]ctggatgcatttctta	C	T	NM_178838 // upstream // 162031 // Hs.175465 // MGC45800 // 90768 // Homo sapiens hypothetical protein LOC90768 (MGC45800), mRNA. /// ENST00000315302 // upstream // 162031 // — // — // — /// ENST00000330336 // upstream // 17524 // — // —	MGC45800	MGC45800, Homo sapiens hypothetical protein LOC90768 (MGC45800), q35.1
SNP_A-2300389	gcctctggcagagcca[C/T]acttagctgaatttga	C	T	ENST00000330336 // intron // 0 // — // — // —	-	q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098566	agagcatattcactag[C/G]acattatcaggtctac	C	G	ENST00000265121 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-1846474	tatattatacatatac[A/G]gaacatctacatatttt	A	G	ENST00000265121 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-2301921	gcgtacatctcatccg[A/G]ataggagaatgcatat	A	G	ENST00000265121 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-2196548	catgttttttggtccc[C/G]catgttcccctctttt	C	G	ENST00000265121 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-2190497	catacatttcagtccc[A/G]actcacttgcttcatc	A	G	NM_001921 // intron // 0 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// ENST00000312820 // intron // 0 // — -// — // — /// ENST00000357067 // intron // 0 // — // — // — // —	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1739109	tcatgaaagcttataagctgatta[C/T]gcaataggcttaacatgc actatcc	C	T	AF195420 // intron // 0 // Hs.41793 // OD23 // 55714 // odd Oz/Ten-m homolog 3	OD23	OD23 , rs10520536, odd Oz,q35.1
SNP_A-2294630	gcagtgatgcattgca[A/G]cttcattataacaaa	A	G	NM_001921 // upstream // 105338 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 103554 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_153008 // downstream // 77079 //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1809245	gtgacgatttcacaca[A/G]gcattggaaaagaaaa	A	G	NM_001921 // upstream // 107554 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 105770 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_153008 // downstream // 74863 //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1980193	gttcatagtatctccaa[A/G]tctgcatgcttcggat	A	G	NM_001921 // upstream // 119891 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 118107 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_153008 // downstream // 62526 //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1980194	tggaggagattggaag[C/G]cttcagcaatggcctc	C	G	NM_001921 // upstream // 121136 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 119352 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_153008 // downstream // 61281 //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1980195	gatagctacactgtcc[C/G]caaaatatcacacgca	C	G	NM_001921 // upstream // 121962 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 120178 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_153008 // downstream // 60455 //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-2200631	ccaactttctgtcacc[A/G]aaaccagaagccaccc	A	G	NM_001921 // upstream // 148479 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_001921 // upstream // 146695 // Hs.183850 // DCTD // 1635 // Homo sapiens dCMP deaminase (DCTD), mRNA. /// NM_153008 // downstream // 33938 //	DCTD	DCTD, Homo sapiens dCMP deaminase (DCTD), q35.1
SNP_A-1915281	tgttcataaggtaagc[A/G]gcacatggttctttcg	A	G	NM_024949 // intron // 0 // Hs.333179 // BOMB // 80014 // Homo sapiens BH3-only member B protein (BOMB), mRNA. /// ENST00000281445 // intron // 0 // — // — // — // —	BOMB	BOMB, Homo sapiens BH3-only member B protein (BOMB), q35.1
SNP_A-1870941	tcggtatttaggtga[C/T]ctttactgttgctgtg	C	T	NM_024949 // intron // 0 // Hs.333179 // BOMB // 80014 // Homo sapiens BH3-only member B protein (BOMB), mRNA. /// ENST00000281445 // intron // 0 // — // — // — // —	BOMB	BOMB, Homo sapiens BH3-only member B protein (BOMB), q35.1
SNP_A-2264286	gaacttcctgaatcaa[A/G]gtgtggactgtccaca	A	G	NM_024949 // intron // 0 // Hs.333179 // BOMB // 80014 // Homo sapiens BH3-only member B protein (BOMB), mRNA. /// ENST00000281445 // intron // 0 // — // — // — // —	BOMB	BOMB, Homo sapiens BH3-only member B protein (BOMB), q35.1
SNP_A-1950256	ttcagacaagctctc[A/G]ataaccctggagtaga	A	G	ENST00000329738 // upstream // 32899 // — // — // — /// ENST00000357279 // upstream // 26225 // — // — // —	-	q35.1
SNP_A-2299726	gccgtcccaaaactca[G/T]atttctggagtccctt	G	T	NM_001564 // downstream // 31224 // Hs.107153 // ING2 // 3622 // Homo sapiens inhibitor of growth family, member 1-like (ING1L), mRNA. /// NM_152682 // downstream // 97602 // Hs.133337 // MGC10198 // 201965 // Homo sapiens hypothetical protein MGC10198 (M	ING2	ING2, Homo sapiens inhibitor of growth family, member 1-like (ING1L), q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1910326	tgtccagccgcataca[G/T]caattctattcacatt	G	T	NM_001564 // downstream // 47196 // Hs.107153 // ING2 // 3622 // Homo sapiens inhibitor of growth family, member 1-like (ING1L), mRNA. /// NM_152682 // downstream // 81630 // Hs.133337 // MGC10198 // 201965 // Homo sapiens hypothetical protein MGC10198 (M	ING2	ING2, Homo sapiens inhibitor of growth family, member 1-like (ING1L), q35.1
SNP_A-1898802	tgctttgatgggctag[A/G]agagaaatggtttgct	A	G	ENST00000308497 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-1923596	ttagggttagtcaata[A/G]cgccgagcctcggagg	A	G	NM_153343 // downstream // 56937 // Hs.297814 // ENPP6 // 133121 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. /// ENST00000308497 // downstream // 14048 // — // — // — // --- /// ENST00000296741 // downstream //	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase q35.1
SNP_A-1834264	tacatgtaaaattcta[C/T]agtacaggtagaggca	C	T	NM_153343 // intron // 0 // Hs.297814 // ENPP6 // 133121 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. /// ENST00000296741 // intron // 0 // — // — // — // — /// ENST00000358108 // intron // 0 // --- // --- // -	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-2188644	cagtgcatttttccac[A/G]gattacagacaaaaag	A	G	NM_153343 // intron // 0 // Hs.297814 // ENPP6 // 133121 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. /// ENST00000296741 // intron // 0 // — // — // — // — /// ENST00000358108 // intron // 0 // — // --- // -	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase q35.1
SNP_A-1947586	tttacctacacactca[C/G]cctttctattactctt	C	G	NM_153343 // intron // 0 // Hs.297814 // ENPP6 // 133121 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. /// ENST00000296741 // intron // 0 // — // --- // --- // --- /// ENST00000358108 // intron // 0 // — // — // -	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-2056554	aatagagtgtgtcaaa[A/G]acgtgcaattgatgaa	A	G	NM_153343 // intron // 0 // Hs.297814 // ENPP6 // 133121 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. /// ENST00000296741 // intron // 0 // — // — // — // — /// ENST00000358108 // intron // 0 // — // — // -	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase q35.1
SNP_A-2161180	atttgaccctgtgatg[C/T]atttatcaaaatatgg	C	T	NM_153343 // upstream // 54404 // Hs.297814 // ENPP6 // 133121 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 6 (ENPP6), mRNA. /// ENST00000296741 // upstream // 54404 // — // — // — // — /// ENST00000358108 // upstream // 54404	ENPP6	ENPP6, Homo sapiens ectonucleotide pyrophosphatase,q35.1
SNP_A-1980221	accgctgtggtctgca[A/T]ctctgacaagccccta	A	T	NM_002199 // intron // 0 // Hs.374097 // IRF2 // 3660 // Homo sapiens interferon regulatory factor 2 (IRF2), mRNA. /// ENST00000303389 // intron // 0 // --- // — // — // — // ---	IRF2	IRF2, Homo sapiens interferon regulatory factor 2 (IRF2), q35.1
SNP_A-2057323	aatatatgcaaataaa[C/T]gaaactgcggtgaaat	C	T	NM_002199 // intron // 0 // Hs.374097 // IRF2 // 3660 // Homo sapiens interferon regulatory factor 2 (IRF2), mRNA. /// ENST00000303389 // intron // 0 // --- // — // — // ---	IRF2	IRF2, Homo sapiens interferon regulatory factor 2 (IRF2), q35.1
SNP_A-1980224	gaccactttaaattca[C/T]gctgtctgatgggagg	C	T	NM_002199 // upstream // 40675 // Hs.374097 // IRF2 // 3660 // Homo sapiens interferon regulatory factor 2 (IRF2), mRNA. /// NM_004346 // downstream // 112473 // Hs.141125 // CASP3 // 836 // Homo sapiens caspase 3, apoptosis-related cysteine protease (CAS	IRF2	IRF2, Homo sapiens interferon regulatory factor 2 (IRF2), q35.1
SNP_A-1783734	ggcatttagagaaata[C/T]ggccaatgtgcaaaac	C	T	NM_024629 // intron // 0 // Hs.481307 // MLF1IP // 79682 // Homo sapiens MLF1 interacting protein (MLF1IP), mRNA. /// ENST00000281453 // intron // 0 // --- // — // --- // ---	MLF1IP	MLF1IP, Homo sapiens MLF1 interacting protein (MLF1IP), q35.1
SNP_A-2281715	gagtctttttcggtc[A/G]ctcctgcccttgttac	A	G	NM_001995 // upstream // 3625 // Hs.406678 // ACSL1 // 2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream // 17427 // Hs.406678 // ACSL1 // 2180 // Homo sapiens acyl-CoA synthetase long-chain famil	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189676	cagttttccctggaca[A/G]tatggtgccaatcaca	A	G	NM_001995 // upstream // 136991 // Hs.406678 // ACSL1 // 2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream // 150793 // Hs.406678 // ACSL1 // 2180 // Homo sapiens acyl-CoA synthetase long-chain fa	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1
SNP_A-1833553	tacagcatcctacaca[C/T]gacaatataagtaaca	C	T	NM_001995 // upstream // 146771 // Hs.406678 // ACSL1 // 2180 // Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), mRNA. /// NM_001995 // upstream // 160573 // Hs.406678 // ACSL1 // 2180 // Homo sapiens acyl-CoA synthetase long-chain fa	ACSL1	ACSL1, Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), q35.1
SNP_A-1904259	tgggctatgcctagaa[C/G]ctgtagttgatgataa	C	G	NM_031953 // intron // 0 // Hs.369091 // SNX25 // 83891 // Homo sapiens sorting nexin 25 (SNX25), mRNA. /// ENST00000264694 // intron // 0 // — // — // — // —	SNX25	SNX25, Homo sapiens sorting nexin 25 (SNX25), q35.1
SNP_A-1934507	ttctctactgccatga[C/G]ggatctaacagcactc	C	G	NM_031953 // intron // 0 // Hs.369091 // SNX25 // 83891 // Homo sapiens sorting nexin 25 (SNX25), mRNA. /// ENST00000264694 // intron // 0 // — // — // — // — /// ENST00000296779 // intron // 0 // — // — // — // —	SNX25	SNX25, Homo sapiens sorting nexin 25 (SNX25), q35.1
SNP_A-2222135	cgaatgaatgaatgaa[A/G]gctcgggtacaacagg	A	G	NM_152775 // intron // 0 // Hs.41101 // KM-HN-1 // 256309 // Homo sapiens hypothetical protein MGC33607 (MGC33607), mRNA. /// ENST00000307588 // intron // 0 // — // — // — // —	KM-HN-1	KM-HN-1, Homo sapiens hypothetical protein MGC33607 (MGC33607), q35.1
SNP_A-2107108	agcggagagcttattc[C/T]ctttcttgtcgcctat	C	T	NM_152775 // upstream // 2072 // Hs.41101 // KM-HN-1 // 256309 // Homo sapiens hypothetical protein MGC33607 (MGC33607), mRNA. /// NM_014476 // downstream // 27954 // Hs.85862 // PDLIM3 // 27295 // Homo sapiens PDZ and LIM domain 3 (PDLIM3), mRNA. /// ENS	KM-HN-1	KM-HN-1, Homo sapiens hypothetical protein MGC33607 (MGC33607), q35.1
SNP_A-2134995	atattcatctactcca[C/T]ctgtattttcacaaga	C	T	NM_014476 // upstream // 10312 // Hs.85862 // PDLIM3 // 27295 // Homo sapiens PDZ and LIM domain 3 (PDLIM3), mRNA. /// ENST00000284771 // upstream // 10329 // — // — // — // — /// ENST00000284770 // upstream // 10312 // — // — // — // — //	PDLIM3	PDLIM3, Homo sapiens PDZ and LIM domain 3 (PDLIM3), q35.1
SNP_A-1730443	agctatctagaaccattctataaat[C/T]agccttttatttgccagccatacat	C	T	NM_018409 // downstream // 72082 // Hs.42768 // DKFZp761O0113 // 55805 // hypothetical protein DKFZp761O0113 /// NM_031953 // upstream // 15804 // Hs.380726 // SNX25 // 83891 // sorting nexin 25	DKFZp761O0113	DKFZp761O0113 , rs1288547, hypothetical protein DKFZp761O0113 ,q35.1
SNP_A-1953338	tttgaaacgtaacttg[A/G]aagggctttgaaatgc	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2	ARGBP2	ARGBP2, Homo sapiens Arg q35.1
SNP_A-1807821	gtcttaagaaattact[A/G]aaagatacgactcaat	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-2032924	aaataatatgttggaa[A/G]tgataccagtgcaagg	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2	ARGBP2	ARGBP2, Homo sapiens Arg q35.1
SNP_A-1867976	tcctaggaagcaaact[C/T]accgtgttgggctctc	C	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2	ARGBP2	ARGBP2, Homo sapiens Arg q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920580	ttaatttcccaggacat[C/T]ggaataacttaaaa	C	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-1871412	tctaacaagatcctaa[A/G]tgatgacgttaatgtt	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// NM_003603 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2	ARGBP2	ARGBP2, Homo sapiens Arg q35.1
SNP_A-1980239	tagaaaatgctttccc[A/G]aatggttttcagaga	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-2010521	tcatgaaaagaaagaga[C/T]gcaggctcagagctc	C	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-1838839	tagactctccatacca[A/G]aaaaggccacaagaaa	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-2063019	aatgttacgctttga[A/G]ctgtcattgccaatgc	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-1807994	gtcttcctcatccgga[C/T]ctaggaaaggttaact	C	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg q35.1
SNP_A-1780646	ggatcaatagagtaga[A/G]gttggatggtaggga	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-2172614	caattgagattgcaaa[A/T]gttagatatgtgcaaa	A	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-2255746	cttgttggttgaagtc[A/G]aaccatggaatagagg	A	G	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg q35.1
SNP_A-2092274	agaaagatacaaggga[C/T]atgtaagtaaatggtc	C	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-1896102	tgcgaagagaagtaaa[C/T]ataaagccttcacaag	C	T	NM_021069 // intron // 0 // Hs.481342 // ARGBP2 // 8470 // Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA. /// ENST00000284776 // intron // 0 // — // — // — /// ENST00000359277 // intron // 0 // — // –	ARGBP2	ARGBP2, Homo sapiens Arg,q35.1
SNP_A-2190434	catacaggaatacaac[A/G]gctatacaagaaagaa	A	G	ENST00000333644 // intron // 0 // — // — // — // —	-	q35.2
SNP_A-1949632	tttattgtcatcaga[C/T]gctatccaggatatag	C	T	ENST00000333644 // intron // 0 // — // — // — // —	-	q35.2
SNP_A-1787307	gggaagagagaggccaa[C/T]gcaaggacacattact	C	T	ENST00000333644 // intron // 0 // — // — // — // —	-	q35.2
SNP_A-2289605	gcaaaaacagtggcaa[C/G]agtacgattgacgtga	C	G	ENST00000333644 // intron // 0 // — // — // — // —	-	q35.2
SNP_A-2141798	atctgactacattca[C/G]aattctctttttcct	C	G	ENST00000333644 // intron // 0 // — // — // — // —	-	q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1694123	gagaagaaaagctgatgacgcatga[A/G]agaggagagaatt acgggggttcaa	A	G	NM_005245 // upstream // 106167 // Hs.166994 // FAT // 2195 // FAT tumor suppressor homolog 1 (Drosophila) /// NM_174900 // upstream // 1165771 // Hs.335787 // ZFP42 // 132625 // zinc finger protein 42	FAT	FAT , rs1583219, FAT tumor suppressor homolog 1 (Drosophila), q35.2
SNP_A-1895950	tgccttatgtgagaca[C/T]cgttctctccccattt	C	T	NM_005958 // upstream // 640856 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 472466 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1936474	ttcttgaaagtcagaa[A/C]aatctaaagcaaaata	A	C	NM_005958 // upstream // 651546 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 483156 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2154783	attcaactcttggc[A/G]aaaaaacgacgccttt	A	G	NM_005958 // upstream // 654795 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 486405 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1899513	tggaagccacaaaaaa[C/G]agttgggcaaggcttg	C	G	NM_005958 // upstream // 680769 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 512379 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2126634	ataaacaatggaaaaa[A/G]gcccaactgttgttt	A	G	NM_005958 // upstream // 681145 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 512755 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2105043	agcatctggaatcaca[A/C]tggcaatcttcccaaa	A	C	NM_005958 // upstream // 681330 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 512940 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1783267	ggcagtatcatgacac[A/G]aaacaaagaacaatgg	A	G	NM_005958 // upstream // 695092 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 526702 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2010543	acacacagtgcagagc[A/C]atgagtatagtagtat	A	C	NM_005958 // upstream // 714709 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 546319 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2010544	cattcaaatccctac[A/G]cagtaagtgctcactt	A	G	NM_005958 // upstream // 714919 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 546529 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-2250196	cttactgtggtaaaac[C/T]aggccaaagtgtacag	C	T	NM_005958 // upstream // 721557 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 553167 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA. /	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2010550	tgacactttcatttaa[A/G]ggcttctatttcaagt	A	G	NM_005958 // upstream // 1257232 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 1088842 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA.	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1780417	ggatacattaattcaa[A/G]gtatagtagcacttga	A	G	NM_005958 // upstream // 1327589 // Hs.243467 // MTNR1A // 4543 // Homo sapiens melatonin receptor 1A (MTNR1A), mRNA. /// NM_005245 // upstream // 1159199 // Hs.481371 // FAT // 2195 // Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA.	MTNR1A	MTNR1A, Homo sapiens melatonin receptor 1A (MTNR1A), q35.2
SNP_A-1980266	ggttgttgaatagtaa[C/T]gaagaaatgcttctgc	C	T	NM_173553 // intron // 0 // Hs.276429 // FLJ25801 // 205860 // Homo sapiens hypothetical protein FLJ25801 (FLJ25801), mRNA. /// ENST00000326754 // intron // 0 // --- // --- // --- // ---	FLJ25801	FLJ25801, Homo sapiens hypothetical protein FLJ25801 (FLJ25801), q35.2
SNP_A-1826593	taacacaattaggatg[C/G]aagttatctttatgga	C	G	NM_178556 // downstream // 195068 // Hs.348618 // FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 // downstream // 195068 // --- // --- // --- // --- /// ENST00000321235 // upstream // 395810 // --- /	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-2074562	acataggtaacaaaaa[C/T]gtatgcataatggtgc	C	T	NM_178556 // downstream // 270921 // Hs.348618 // FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 // downstream // 270921 // --- // --- // --- // --- /// ENST00000321235 // upstream // 319957 // --- /	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-2192802	catcctactcttcaca[A/T]cttctgaaaatgtttt	A	T	NM_178556 // downstream // 296734 // Hs.348618 // FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 // downstream // 296734 // --- // --- // --- // --- /// ENST00000321235 // upstream // 294144 // --- /	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-2138433	atccatacgtgtcata[A/G]cttccctgcaagacaa	A	G	NM_178556 // downstream // 397732 // Hs.348618 // FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 // downstream // 397732 // --- // --- // --- // --- /// ENST00000321235 // upstream // 193146 // --- /	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-1887007	tgacttgcttctaatc[A/G]atagaatttggtgaat	A	G	NM_178556 // downstream // 427242 // Hs.348618 // FLJ36180 // 339976 // Homo sapiens hypothetical protein FLJ36180 (FLJ36180), mRNA. /// ENST00000332517 // downstream // 427242 // --- // --- // --- // --- /// ENST00000321235 // upstream // 163636 // --- /	FLJ36180	FLJ36180, Homo sapiens hypothetical protein FLJ36180 (FLJ36180), q35.2
SNP_A-1665052	tgaaatcagttttgctttagagaca[A/G]cataagtaggtcacctgtt ttacca	A	G	BC029568 // upstream // 1175524 // Hs.130535 // - // 401165 // Hypothetical gene supported by BC029568 (LOC401165), mRNA /// NM_178556 // downstream // 227383 // Hs.348618 // FLJ36180 // 339976 // hypothetical protein FLJ36180	-	- , rs1606234, Hypothetical gene supported by BC029568 (LOC401165), mRNA ,q35.2
SNP_A-1651106	tctgagggtgaagaaagtaaagaca[C/T]tgattaactttaggact tacgtttt	C	T	BC029568 // upstream // 1129187 // Hs.130535 // - // 401165 // Hypothetical gene supported by BC029568 (LOC401165), mRNA /// NM_178556 // downstream // 273720 // Hs.348618 // FLJ36180 // 339976 // hypothetical protein FLJ36180	-	- , rs713507, Hypothetical gene supported by BC029568 (LOC401165), mRNA ,q35.2
SNP_A-1909475	tgtattggatggtaga[C/T]gagagagaaagaacag	C	T	NM_004477 // upstream // 1188690 // Hs.203772 // FRG1 // 2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 12636 // --- // --- // --- // --- /// ENST00000226798 // upstream // 1188690 // --- // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-2117450	aggtgtgaaattcaca[A/C]cagatttccaagactt	A	C	NM_004477 // upstream // 1118850 // Hs.203772 // FRG1 // 2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 82476 // --- // --- // --- // --- /// ENST00000226798 // upstream // 1118850 // --- // --- // --- // ---	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2161125	atttgaacacagggca[A/T]tcattagaaaaaattt	A	T	NM_004477 /// upstream // 893880 // Hs.203772 // FRG1 // 2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 307446 // — // — // — /// ENST00000226798 // upstream // 893880 // — // — // — // —	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-2235584	ctcctaccttgaagca[A/T]tcttatttcagctcag	A	T	NM_004477 /// upstream // 880647 // Hs.203772 // FRG1 // 2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 320679 // — // — // — /// ENST00000226798 // upstream // 880647 // — // — // — // —	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-2086032	acttctaccagcaaca[C/T]ggtagagtttagcgc	C	T	NM_004477 /// upstream // 874944 // Hs.203772 // FRG1 // 2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 326382 // — // — // — /// ENST00000226798 // upstream // 874944 // — // — // — // —	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-1872916	tctatccatttcagca[C/T]caattggttcctagat	C	T	NM_004477 /// upstream // 736167 // Hs.203772 // FRG1 // 2483 // Homo sapiens FSHD region gene 1 (FRG1), mRNA. /// ENST00000321235 // downstream // 465159 // — // — // — /// ENST00000226798 // upstream // 736167 // — // — // — // —	FRG1	FRG1, Homo sapiens FSHD region gene 1 (FRG1), q35.2
SNP_A-1668813	atccgtcaacctctgggagaaaac[A/G]gcatttaaatctgatgtaaaatg	A	G	NM_013232 /// intron // 0 // Hs.24087 // PDCD6 // 10016 // programmed cell death 6 /// NM_020731 // intron // 0 // - // - // - // -	PDCD6	PDCD6, rs4429890, programmed cell death 6 p15.33
SNP_A-2237907	ctctgacggattacac[A/G]ctacatcttgagaaaa	A	G	NM_030782 // upstream // 14939 // Hs.444673 // CRR9 // 81037 // Homo sapiens cisplatin resistance related protein CRR9p (CRR9), mRNA. /// NM_001044 // downstream // 32971 // Hs.406 // SLC6A3 // 6531 // Homo sapiens solute carrier family 6 (neurotransmitte	CRR9	CRR9, Homo sapiens cisplatin resistance related protein CRR9p (CRR9), p15.33
SNP_A-2098871	agagctgcaagctttg[G/T]aaataagagttgctt	G	T	NM_004553 // downstream // 38489 // Hs.408257 // NDUFS6 // 4726 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA. /// NM_016358 // downstream // 22899 // Hs.196927 // IRX4 // 50805 // Homo sa	NDUFS6	NDUFS6, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), p15.33
SNP_A-1814089	gtgtccgtggtcacaa[C/T]gaaacagagaccactg	C	T	NM_004553 // downstream // 55719 // Hs.408257 // NDUFS6 // 4726 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), mRNA. /// NM_016358 // downstream // 5669 // Hs.196927 // IRX4 // 50805 // Homo sap	NDUFS6	NDUFS6, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) (NDUFS6), p15.33
SNP_A-1891196	tgatgtggtcctaaca[A/G]gaaatgggagaacttt	A	G	NM_016358 // upstream // 257875 // Hs.196927 // IRX4 // 50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 605529 // Hs.282089 // IRX2 // 153572 // Homo sapiens iroquois homeobox protein 2 (IRX2), mRNA. /// ENST	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2141788	atctgaaatgtgcagg[A/G]caactgccagagacac	A	G	NM_016358 // upstream // 314061 // Hs.196927 // IRX4 // 50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 549343 // Hs.282089 // IRX2 // 153572 // Homo sapiens iroquois homeobox protein 2 (IRX2), mRNA. /// ENST	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2206694	ccatgaggctgcacta[C/T]ggcttttctagaatcc	C	T	NM_016358 // upstream // 368967 // Hs.196927 // IRX4 // 50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 494437 // Hs.282089 // IRX2 // 153572 // Homo sapiens iroquois homeobox protein 2 (IRX2), mRNA. /// ENST	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-1882841	tgaaagcctgttccac[A/G]aagtctgagaccaaaa	A	G	NM_016358 // upstream // 369204 // Hs.196927 // IRX4 // 50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 494200 // Hs.282089 // IRX2 // 153572 // Homo sapiens iroquois homeobox protein 2 (IRX2), mRNA. /// ENST	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2263062	gaacacactcagctccl[A/G]cctctcctcagaaggc	A	G	NM_016358 // upstream // 399313 // Hs.196927 // IRX4 // 50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 464091 // Hs.282089 // IRX2 // 153572 // Homo sapiens iroquois homeobox protein 2 (IRX2), mRNA. /// ENST	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-1818222	gttctgagtcttttcaa[C/G]gacactcccattacac	C	G	NM_016358 // upstream // 816230 // Hs.196927 // IRX4 // 50805 // Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA. /// NM_033267 // downstream // 47174 // Hs.282089 // IRX2 // 153572 // Homo sapiens iroquois homeobox protein 2 (IRX2), mRNA. /// ENST0	IRX4	IRX4, Homo sapiens iroquois homeobox protein 4 (IRX4), p15.33
SNP_A-2087048	actgagtgattatatg[A/G]agaggcaaatgccact	A	G	NM_178569 // downstream // 257522 // Hs.148486 // CEI // 153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 583135 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// ENST00000334000 // dow	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-1784273	ggcccagagggaacac[G/T]ggcatggagaatagca	G	T	NM_178569 // downstream // 468070 // Hs.148486 // CEI // 153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 372587 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// ENST00000334000 // dow	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-1923542	ttagggcaagaatgtg[A/G]agaatgaaagcaccgt	A	G	NM_178569 // downstream // 632989 // Hs.148486 // CEI // 153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 207668 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// ENST00000334000 // dow	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-2260028	gaaaataagtgaaagg[A/G]cactaccaattcctcc	A	G	NM_178569 // downstream // 667489 // Hs.148486 // CEI // 153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 173168 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// ENST00000334000 // dow	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-2126446	ataaaaggataacaga[C/T]gaggcaacaaattgcc	C	T	NM_178569 // downstream // 752479 // Hs.148486 // CEI // 153571 // Homo sapiens CEI protein (CEI), mRNA. /// NM_024337 // upstream // 88178 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// ENST00000334000 // down	CEI	CEI, Homo sapiens CEI protein (CEI), p15.33
SNP_A-2052794	aagtcacctgtgcacc[C/T]ggagaagggctaattt	C	T	NM_024337 // downstream // 163569 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 1375496 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-1980364	tatggagtcacgcctg[C/T]aggatggtgatcccat	C	T	NM_024337 // downstream // 2341170 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 1304895 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2250837	cttatcccatgagta[A/G]aacaaagtaatggggc	A	G	NM_024337 // downstream // 261636 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 1277429 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 ((IRX1), p15.33
SNP_A-1919429	ttaagcacctattatg[C/G]aggcagagcttcagac	C	G	NM_024337 // downstream // 263426 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 1275639 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 ((IRX1), p15.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2054392	aagtttaatatgggcc[C/T]acagtagacttgtaaa	C	T	NM_024337 // downstream // 263693 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 1275372 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2067009	acaaaccagtgagtga[G/T]aaccatcctggatgcc	G	T	NM_024337 // downstream // 626533 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 912532 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2147310	atggagactcatgaag[A/G]actagctacattaact	A	G	NM_024337 // downstream // 664809 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 874256 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-1980378	gagacaggatctttag[C/G]aatgtagttaagtaa	C	G	NM_024337 // downstream // 665610 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 873455 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2134937	atattcaacactgaca[A/G]agtaaaatagctgaga	A	G	NM_024337 // downstream // 675997 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 863068 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2188706	cagtgctggaagcgtc[A/G]ccagctcagtgatcat	A	G	NM_024337 // downstream // 676353 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 862712 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-1827162	taacccttggaagcta[C/T]ggatctatctaatagg	C	T	NM_024337 // downstream // 676442 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 862623 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.33
SNP_A-2304174	gctcctgctgtatca[C/T]ctggtagctacacaac	C	T	NM_024337 // downstream // 1046486 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 492579 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1817408	gttcagtaagtacagc[A/G]cagagattagtatgac	A	G	NM_024337 // downstream // 1050848 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 488217 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1824926	taaagccatcttcagc[A/G]agggctgaactgaacc	A	G	NM_024337 // downstream // 1283493 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 255572 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1897387	tgctgaagcacctcac[G/T]caggatttccggcctc	G	T	NM_024337 // downstream // 1283640 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 255425 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2183747	cagcatctgtaactga[C/T]agcgggggattgtgac	C	T	NM_024337 // downstream // 1310794 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 228271 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (repro	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1935285	ttctgctccaagaaac[C/T]caccttgctcggtcca	C	T	NM_024337 // downstream // 1476797 // Hs.424156 // IRX1 // 79192 // Homo sapiens iroquois homeobox protein 1 (IRX1), mRNA. /// NM_139056 // upstream // 62268 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprol	IRX1	IRX1, Homo sapiens iroquois homeobox protein 1 (IRX1), p15.32
SNP_A-1842811	tagtacctatttcttc[A/G]acttatcttcaagcta	A	G	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1882547	tgaaaattcctcaaaa[C/T]gttaagtgtagagttt	C	T	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1980420	acaggtacaggatctc[A/G]gaatcttaagttttgg	A	G	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2140346	atctcagcaggagaga[G/T]agcagggccgtcttaa	G	T	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2238735	ctcttaagcagacgcc[A/G]cagtggaccttgaaaa	A	G	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2299449	gcccttaagcgagaaa[C/G]gaaaggtgcagtgccc	C	G	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2044432	aagaaaaatcacagaa[A/T]ctatttgaatgccaga	A	T	NM_139056 // intron // 0 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // intron // 0 // — // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1893254	tgcagagtaatgtaaa[C/T]agtatttgtgtgcctg	C	T	NM_139056 // downstream // 31052 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 31052 // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2309470	ggaaacacttatttgc[A/G]cttgtagggaaggaca	A	G	NM_139056 // downstream // 47374 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 47374 // — // — // —	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213240	ccgcccttcaatacac[A/G]gggaaatgtacatcct	A	G	NM_139056 // downstream // 68589 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 68589 // — // — //	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-1745180	gacttctccaaaaattaacttaaatc[A/G]acattcagctagtcagta tacaata	A	G	AB023164 // upstream // 60894 // Hs.5070 // KIAA0947 // 23379 // KIAA0947 protein /// NM_139056 // downstream // 96467 // Hs.352628 // ADAMTS16 // 170690 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16	KIAA0947	KIAA0947 , rs930049, KIAA0947 protein ,p15.32
SNP_A-2187429	caggttggatacttga[A/G]gacctgaaagaaataa	A	G	NM_139056 // downstream // 85115 // Hs.387861 // ADAMTS16 // 170690 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), mRNA. /// ENST00000274181 // downstream // 85115 // — // — //	ADAMTS16	ADAMTS16, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16 (ADAMTS16), p15.32
SNP_A-2300041	gcctcaagtcctggga[A/T]gcacttactattatta	A	T	NM_001001702 // downstream // 771874 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 50286 // — // — // — // — /// ENST00000321722 // downstream // 771874 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1915968	tgttgattctgaatat[C/T]acccttgtagacgctt	C	T	NM_001001702 // downstream // 744893 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 77267 // — // — // — // — /// ENST00000321722 // downstream // 744893 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2097888	agagagaaatgacatc[A/G]cttttaatttccatca	A	G	NM_001001702 // downstream // 737254 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 84906 // — // — // — // — /// ENST00000321722 // downstream // 737254 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1902851	tggctcggcagaggtc[C/T]cttctcaccttctgga	C	T	NM_001001702 // downstream // 735602 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 86558 // — // — // — // — /// ENST00000321722 // downstream // 735602 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2263592	gaaccattggtgatgg[A/G]ccatataacttcctag	A	G	NM_001001702 // downstream // 710739 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 111421 // — // — // — // — /// ENST00000321722 // downstream // 710739 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1980440	gagttgggttaggaga[A/C]caggcaaaatctatgg	A	C	NM_001001702 // downstream // 646886 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 175274 // — // — // — // — /// ENST00000321722 // downstream // 646886 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1841797	taggcccaattgccaa[A/G]aaattgtttcaacatc	A	G	NM_001001702 // downstream // 643685 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 178475 // — // — // — // — /// ENST00000321722 // downstream // 643685 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1750959	gaaaaataaaatcctcattggacaa[C/T]aattagtatcagcaag ttttgagtt	C	T	AB023164 // downstream // 247143 // Hs.5070 // KIAA0947 // 23379 // KIAA0947 protein	KIAA0947	KIAA0947 , rs2895450, KIAA0947 protein,p15.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1980459	aatgttcatcccaaac[A/G]ccatttaccagccctg	A	G	NM_001001702 // downstream // 303465 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 518695 // — // — // — // — /// ENST00000321722 // downstream // 303465 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2235966	ctcctgctggggtgaa[A/G]aaagggtcatagttct	A	G	NM_001001702 // downstream // 278119 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 544041 // — // — // — // — /// ENST00000321722 // downstream // 278119 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1680348	tgaatgcttgttattatcccagaga[A/G]ctgagaaaatgtttactggtcttta	A	G	AB023164 // downstream // 561451 // Hs.5070 // KIAA0947 // 23379 // KIAA0947 protein	KIAA0947	KIAA0947 , rs248673, KIAA0947 protein,p15.32
SNP_A-1865633	tccattacacccatga[A/G]gtacaaccaccaccta	A	G	NM_001001702 // downstream // 243114 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 579046 // — // — // — // — /// ENST00000321722 // downstream // 243114 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2243267	ctgcctgtacatgtcc[A/G]cacggttgcaatcaag	A	G	NM_001001702 // downstream // 235299 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 586861 // — // — // — // — /// ENST00000321722 // downstream // 235299 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1980470	aaaacgcttccataac[A/G]cgggctggatggaatg	A	G	NM_001001702 // downstream // 226860 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 595300 // — // — // — // — /// ENST00000321722 // downstream // 226860 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1712255	tttaatttgaagttgtgaggattgg[A/C]atagaatatgggcatctgtgccaat	A	C	AB023164 // downstream // 630686 // Hs.5070 // KIAA0947 // 23379 // KIAA0947 protein	KIAA0947	KIAA0947 , rs2398255, KIAA0947 protein,p15.32
SNP_A-2216201	cctcccttctggtgtc[A/G]ctggcaattcttggca	A	G	NM_001001702 // downstream // 169460 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 652700 // — // — // — // — /// ENST00000321722 // downstream // 169460 // — // — //	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-2083064	acgtgtttctttccaa[A/G]tgtggctgaagctata	A	G	NM_001001702 // downstream // 39383 // Hs.376760 // FLJ33360 // 401172 // Homo sapiens FLJ33360 protein (FLJ33360), mRNA. /// ENST00000296564 // downstream // 782777 // — // — // — // — /// ENST00000321722 // downstream // 39383 // — // — // -	FLJ33360	FLJ33360, Homo sapiens FLJ33360 protein (FLJ33360), p15.32
SNP_A-1980483	aaaggagcaaaattaa[A/C]cacctagagtacttaa	A	C	NM_017755 // intron // 0 // Hs.481526 // NSUN2 // 54888 // Homo sapiens NOL1/NOP2/Sun domain family 2 (NSUN2), mRNA. /// ENST00000356741 // intron // 0 // — // — // — // — /// ENST00000264670 // intron // 0 // — // — // — // —	NSUN2	NSUN2, Homo sapiens NOL1 p15.31
SNP_A-1980490	gcatgtaaaggcctta[A/G]cagaaagctgcccttg	A	G	NM_001047 // downstream // 17884 // Hs.552 // SRD5A1 // 6715 // Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA /// NM_006999 // upstream // 27169 // Hs.481542 // POLS // 110	SRD5A1	SRD5A1, Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), p15.31
SNP_A-1850078	tatgtgaggggattca[A/G]atgaaaatgcctgccc	A	G	NM_006999 // intron // 0 // Hs.481542 // POLS // 11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// ENST00000230859 // intron // 0 // — // — // — // —	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1697206	attttcataagaaaagcactgtttc[G/T]aattttaatctacaaacaactcatt	G	T	NM_006999 // intron // 0 // Hs.39488 // POLS // 11044 // polymerase (DNA directed) sigma	POLS	POLS , rs172080, polymerase (DNA directed) sigma,p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1727839	aatgattcttatgaagtttctgg[C/T]aagctgctatgtgatactat gtact	C	T	NM_006999 // downstream // 512 // Hs.39488 // POLS // 11044 // polymerase (DNA directed) sigma /// NM_020546 // upstream // 638677 // Hs.414591 // ADCY2 // 108 // adenylate cyclase 2 (brain)	POLS	POLS , rs5001282, polymerase (DNA directed) sigma ,p15.31
SNP_A-1913890	tgtgtctgtgtgcttat[C/T]atacctacacgttgcat	C	T	NM_006999 // downstream // 85702 // Hs.481542 // POLS // 11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 553503 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1796308	ggtgtgtctgaggca[C/T]agttaggtggaagaaa	C	T	NM_006999 // downstream // 86424 // Hs.481542 // POLS // 11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 552781 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1907906	tgtaatctcaagggtc[A/G]aagtggatgagaaaat	A	G	NM_006999 // downstream // 122838 // Hs.481542 // POLS // 11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 516367 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_02	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-1946081	ttgttttctgaatgat[A/T]aagatgcagagatgca	A	T	NM_006999 // downstream // 152970 // Hs.481542 // POLS // 11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 486235 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_02	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-2234834	ctccatatttcagaaa[A/C]gtcaagtctagatgg	A	C	NM_006999 // downstream // 288794 // Hs.481542 // POLS // 11044 // Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA. /// AB028983 // upstream // 350411 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_02	POLS	POLS, Homo sapiens polymerase (DNA directed) sigma (POLS), p15.31
SNP_A-2069830	acacagagattccaaa[A/G]taaatttcatttgctc	A	G	AB028983 // intron // 0 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020546 // intron // 0 // Hs.481545 // ADCY2 // 108 // Homo sapiens adenylate cyclase 2 (brain) (ADCY2), mRNA. /// ENST00000264672 // intron	ADCY2	ADCY2, Homo sapiens for KIAA1060 protein, partial cds. ,p15.31
SNP_A-1882570	tgaaacaaacagagga[A/G]gaatgtggaatccctt	A	G	AB028983 // intron // 0 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020546 // intron // 0 // Hs.481545 // ADCY2 // 108 // Homo sapiens adenylate cyclase 2 (brain) (ADCY2), mRNA. /// ENST00000264672 // intron	ADCY2	ADCY2, Homo sapiens for KIAA1060 protein, partial cds. p15.31
SNP_A-1899270	tggaaatttgcttaa[A/G]ctgtggttagagatta	A	G	AB028983 // intron // 0 // Hs.481545 // ADCY2 // 108 // Homo sapiens mRNA for KIAA1060 protein, partial cds. /// NM_020546 // intron // 0 // Hs.481545 // ADCY2 // 108 // Homo sapiens adenylate cyclase 2 (brain) (ADCY2), mRNA. /// ENST00000264672 // intron	ADCY2	ADCY2, Homo sapiens for KIAA1060 protein, partial cds. p15.31
SNP_A-1980531	ggaaactgtgccgac[A/C]attgctctacccgtt	A	C	ENST00000328830 // intron // 0 // --- // --- // ---	-	p15.31
SNP_A-2063204	aatgtttgaattggaa[A/C]ctacaaattaatactg	A	C	NM_002454 // downstream // 263517 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 263517 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1980552	ttcctaaatgccccta[A/G]atgacagcgagctcc	A	G	NM_002454 // downstream // 277601 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 277601 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920704	ttacaaatactgcaga[G/T]acacaaggattagttg	G	T	NM_002454 // downstream // 436091 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 436091 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2206423	ccatctccacattcaa[A/G]taattcctcatgttct	A	G	NM_002454 // downstream // 671843 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 671843 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1945169	ttgtgttaacgaatga[A/G]tatgaaatctatagat	A	G	NM_002454 // downstream // 725698 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 725698 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2078214	accagtggactgatac[A/G]actgatatgtttattg	A	G	NM_002454 // downstream // 732572 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 732572 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2174593	cacagatacactgcga[A/G]tagtgagaagccagag	A	G	NM_002454 // downstream // 749098 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 749098 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2075361	acatgaacttgaagga[C/T]gaggaagttgactatg	C	T	NM_002454 // downstream // 794518 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 794518 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2145326	atgcactgaccctgaa[A/G]gtttcagaaaggctg	A	G	NM_002454 // downstream // 928224 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 928224 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2086087	actctcgttgtctccc[A/G]ctaggacgattgcaat	A	G	NM_002454 // downstream // 999864 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 999864 // Hs.481551 // MTRR // 4552 // Homo	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2105554	agccacacctcatgac[A/G]agatcatttcttatat	A	G	NM_002454 // downstream // 1000711 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 1000711 // Hs.481551 // MTRR // 4552 // Ho	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1736413	aaaaggaatagtcatttctaaagta[C/T]ggtgccaltagtgttaatt tgatcg	C	T	NM_002454 // downstream // 1002081 // Hs.153792 // MTRR // 4552 // 5-methyltetrahydrofolate-homocysteine methyltransferase reductase /// NM_003966 // downstream // 135545 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1	MTRR	MTRR, rs10512994, 5-methyltetrahydrofolate-homocysteine methyltransferase reductase, p15.31
SNP_A-2010647	tccttttgccaaaga[C/G]atgcaggatgttccaa	C	G	NM_002454 // downstream // 1007300 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 1007300 // Hs.481551 // MTRR // 4552 // Ho	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041496	aacctttacatcttca[C/G]aaaaatgaggcagtaa	C	G	NM_002454 // downstream // 1008480 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 1008480 // Hs.481551 // MTRR // 4552 // Ho	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-2119645	agtatgtcctctcgta[C/T]agtcattttaaaatac	C	T	NM_002454 // downstream // 1045091 // Hs.481551 // MTRR // 4552 // Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, mRNA. /// NM_024010 // downstream // 1045091 // Hs.481551 // MTRR // 4552 // Ho	MTRR	MTRR, Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase (MTRR), transcript variant 1, p15.31
SNP_A-1980596	gcactacaatcaatga[C/T]ggaagatgcatttgga	C	T	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1826277	taaattgctcaatgtc[A/G]aaagcttgggaaaccc	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-1839775	tagatgttctgcaacc[A/G]ctgagtgctctgtaaa	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-2276694	gagagtggtctctaaa[C/T]aacaactatgtaagga	C	T	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1813841	gtgtatgattctttac[A/G]cagagcaaaagcatag	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1864158	tccacattcaaggcag[A/T]cctcacacttgctgta	A	T	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2036339	aaattccatggtgttc[A/G]gaaaatattagggtac	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1980602	tcctctgtctacatta[A/G]ctccttctttcctcct	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2254179	cttgatctaatgtcta[C/T]gcagaaaggttctagt	C	T	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1928079	ttcaatttgaactaac[A/G]atccctccccagacat	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1692506	tcccatcatgtcagaagtcacccaa[A/T]gtacggaatctatacttttagagat	A	T	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs1806111, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1657782	ccgtacattgggtgacttctgacat[C/G]atgggaatttgcaacact aaacaaa	C	G	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs1806083, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31
SNP_A-1697424	ttgctcagttgacatcagttttatg[C/T]acaaggagagtctggttta cttagc	C	T	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs1806110, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31
SNP_A-1877622	tctggctttctctgca[A/G]gtaaaatgggggctct	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-1980614	cattcttgagacttgc[A/G]gaggagagaagcgccc	A	G	NM_003966 // intron // 0 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// ENST00000264845 // intron // 0 // — // — // — // —	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31
SNP_A-1690970	atatggctgatataggaagcctgag[A/G]agtaaacagatttacc agcagtaga	A	G	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs1805960, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31
SNP_A-1665154	ttagctatgactgtattgttaccat[C/G]aaacattatgaacaggga aacagca	C	G	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs1806004, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31
SNP_A-1980628	gcaagtttcaggagca[C/T]tgctatggaaaagtac	C	T	NM_003966 // upstream // 12971 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// NM_019599 // downstream // 236216 // Hs.533930 // TAS2R1	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-1674833	acccagcaatcccactcctatgtct[A/G]tatctaagagaaagaa aatatctgt	A	G	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs953018, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31
SNP_A-1755346	gatgagctcaggaataaaacagata[A/G]ctaaggataagtcatt ttcatccag	A	G	NM_003966 // intron // 0 // Hs.528707 // SEMA5A // 9037 // sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem	SEMA5A	SEMA5A , rs10513017, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem,p15.31
SNP_A-1908719	tgtaggggaggaacaa[A/G]taaagtgagagaaagt	A	G	NM_003966 // upstream // 56820 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// NM_019599 // downstream // 192367 // Hs.533930 // TAS2R1	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2110105	aggaagctgacgctcc[A/G]acactccagatggaac	A	G	NM_003966 // upstream // 99564 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// NM_019599 // downstream // 149623 // Hs.533930 // TAS2R1	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic ,p15.31
SNP_A-2224941	cgtggactggtaatga[C/T]gaccagtgatattgag	C	T	NM_003966 // upstream // 213401 // Hs.321637 // SEMA5A // 9037 // Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic /// NM_019599 // downstream // 35786 // Hs.533930 // TAS2R1	SEMA5A	SEMA5A, Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic p15.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2313182	ggagaagtaatgtggc[G/T]cggaggaacttgagtc	G	T	NM_031916 // downstream // 2122 // Hs.381089 // ROPN1L // 83853 // Homo sapiens ropporin 1-like (ROPN1L), mRNA. /// NM_004394 // downstream // 212086 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// ENST00000274134 // d	ROPN1L	ROPN1L, Homo sapiens ropporin 1-like (ROPN1L), p15.2
SNP_A-2194837	catgcggaatgacac[A/G]gtcacactgcagaaga	A	G	NM_031916 // downstream // 56878 // Hs.381089 // ROPN1L // 83853 // Homo sapiens ropporin 1-like (ROPN1L), mRNA. /// NM_004394 // downstream // 157330 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// ENST00000274134 //	ROPN1L	ROPN1L, Homo sapiens ropporin 1-like (ROPN1L), p15.2
SNP_A-1869086	tcctgccctctccccca[C/T]ggtgctctgctgt	C	T	ENST00000296657 // intron // 0 // — // — // — /// ENST00000338956 // intron // 0 // — // — // —	-	p15.2
SNP_A-1944247	ttgtccacaactgaa[C/T]gctgacttagcacaat	C	T	ENST00000338956 // intron // 0 // — // — // —	-	p15.2
SNP_A-1810140	gtgatcattacaacaa[A/G]taacgcagaggagagg	A	G	NM_004394 // intron // 0 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// ENST00000338956 // intron // 0 // — // — // — /// ENST00000230895 // intron // 0 // — // — // — /// ENST00000360512 //	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2282884	gataaatcaagcccac[A/G]aggatcgcagaggagag	A	G	NM_004394 // upstream // 28645 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 181970 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2266992	gaataaaggaataga[A/G]gatgcaggcaaaagag	A	G	NM_004394 // upstream // 38806 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 171809 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2272469	gaccttcttttccaca[C/T]cactctgtaatgccgc	C	T	NM_004394 // upstream // 113300 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 97315 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2114993	agggccattgtattaa[C/T]ctggtgatcaagcaaa	C	T	NM_004394 // upstream // 115799 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 94816 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2028909	aaacttggaaagtga[C/G]accaagcaatcagaca	C	G	NM_004394 // upstream // 119669 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 90946 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1797364	ggttgttaaggtgtca[C/T]ctcttgaattagaatg	C	T	NM_004394 // upstream // 119837 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 90778 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2256039	cttaattcataacga[C/T]cacagacatccagttc	C	T	NM_004394 // upstream // 119982 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 90633 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2162603	atttttctcatattccaa[C/T]gttgggtaatcatct	C	T	NM_004394 // upstream // 120738 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 89877 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2266484	gaagtactgccttcaa[G/T]gaaagatccactatgt	G	T	NM_004394 // upstream // 123521 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 87094 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1867320	tcccttagaccttctc[G/T]catggattggttcc	G	T	NM_004394 // upstream // 124064 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 86551 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1886969	tgacttctcagtcaaag[C/T]ctctacatttgttta	C	T	NM_004394 // upstream // 124130 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 86485 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1789550	gggccttccagaaaga[A/G]agacaaggctcaagag	A	G	NM_004394 // upstream // 128495 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 82120 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2266675	gaagtgaacagaccaa[A/G]agacatagttcaaaa	A	G	NM_004394 // upstream // 128539 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 82076 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-1853489	tatttgctgaggggg[A/G]aaaaagatgtatttg	A	G	NM_004394 // upstream // 137583 // Hs.75189 // DAP // 1611 // Homo sapiens death-associated protein (DAP), mRNA. /// NM_001332 // downstream // 73032 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural pla	DAP	DAP, Homo sapiens death-associated protein (DAP), p15.2
SNP_A-2305073	gctgaaggttggatc[C/T]gaggatttcatttat	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2207130	ccattaattcaacaac[A/C]ctttccaagctgttt	A	C	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2178924	cactgcaaactaggaa[C/T]actgaataggagactc	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1758104	ttcacatgtagtataacactgtga[C/T]gattggcatttaatgag aggtt	C	T	NM_001332 // intron // 0 // Hs.436421 // CTNND2 // 1501 // catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	CTNND2	CTNND2, rs9312751, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein),p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1881861	tctttactcatcaaa[A/T]ctttctccttgctac	A	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1807546	gtctggagaagttgaa[A/T]gaaatgaatctccagc	A	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1950180	ttcactagcaactc[A/G]ctcttccatcatgacg	A	G	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2061623	aatgctttcaggttca[A/C]gaacaacggaaaagta	A	C	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1980697	catgttgacaagctgaa[A/G]cttcatggtttctgaa	A	G	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1980700	ttctcattttgtaagcc[C/T]gataatcattaatacca	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1980701	aaggtggatgaatgca[C/T]attcgctactaagca	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1724584	tataaaatcacttattaatctca[A/C]acaatgctatgggtagca gctact	A	C	NM_001332 // intron // 0 // Hs.436421 // CTNND2 // 1501 // catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	CTNND2	CTNND2, rs443005, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein),p15.2
SNP_A-1711436	cttttgaagaaacacattctactca[A/G]tacctcccccatggattg gcacaa	A	G	NM_001332 // intron // 0 // Hs.436421 // CTNND2 // 1501 // catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	CTNND2	CTNND2, rs445607, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein),p15.2
SNP_A-2053512	aagtgcccagagaaga[C/T]gactcaacagggaga	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1980705	gtgacatcaactcgta[C/T]atatagtttcactgtc	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2280750	gaggtgagtgggaagg[C/T]agcctaaagaggtgac	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2224767	cgtgaaacttccgq[C/T]aaggtgtgtctgattt	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2143110	atgaatgttctcagt[C/G]aaatagaataggagtt	C	G	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2308033	gcttgaaatgaactga[C/G]gcagataaaattcatg	C	G	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1980720	tgcttttcttaattca[C/T]caatgagcagtccgaa	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1720873	cacccagaataaaatctggcatttct[G/T]cccattattcccattcca ccactct	G	T	NM_001332 // intron // 0 // Hs.436421 // CTNND2 // 1501 // catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	CTNND2	CTNND2 , rs3852170, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein),p15.2
SNP_A-2090396	actiggcaagcactct[C/T]cacttaagctaatgca	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-2166121	caaataggciatgata[C/T]gtcatgctttaattgt	C	T	NM_001332 // intron // 0 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // intron // 0 // — // — // — /// ENST0	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1914783	tgttaccttcaatctc[A/G]ctcaagatctgacttt	A	G	NM_001332 // upstream // 1061475 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // upstream // 1061475 // — // — // —	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1918497	ttaaatcagaggtgga[A/G]gagtttgtataaaaaa	A	G	NM_001332 // upstream // 1073397 // Hs.314543 // CTNND2 // 1501 // Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA. /// ENST00000304623 // upstream // 1073397 // — // — // —	CTNND2	CTNND2, Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), p15.2
SNP_A-1715093	ttctaaatgtttatggttgaattcc[C/T]ggaaatatgtagaaattaca agtat	C	T	NM_001332 // upstream // 1749308 // Hs.436421 // CTNND2 // 1501 // catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) /// NM_001369 // downstream // 38621 // Hs.398124 // DNAH5 // 1767 // dynein, axonemal, heav	CTNND2	CTNND2 rs4298252, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) ,p15.2
SNP_A-1649020	atgctgcattctctttttatcattca[C/T]ctaaagaccactcatttatt aaa	C	T	NM_001332 // upstream // 1779074 // Hs.436421 // CTNND2 // 1501 // catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) /// NM_001369 // downstream // 8855 // Hs.398124 // DNAH5 // 1767 // dynein, axonemal, heavy	CTNND2	CTNND2 rs966430, catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) ,p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1952028	tttctatcttgccatc[C/T]aatctttgtccacatg	C	T	NM_001369 // downstream // 994 // Hs.212360 // DNAH5 // 1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000284293 // upstream // 52599 // --- // --- // --- // --- /// ENST00000265104 // downstream // 994 // --- // --- //	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1842300	taggtagaacaaatca[A/C]ctaagtatgtttaaag	A	C	NM_001369 // intron // 0 // Hs.212360 // DNAH5 // 1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // --- // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1674947	ggagtggggagaatgagagggtcaa[A/G]gatcttggaatgttat atgaaagga	A	G	NM_001369 // intron // 0 // Hs.398124 // DNAH5 // 1767 // dynein, axonemal, heavy polypeptide 5	DNAH5	DNAH5 , rs10513149, dynein, axonemal, heavy polypeptide 5,p15.2
SNP_A-1980781	tcatcaacttctaaca[A/C]aacctggcttaaaagg	A	C	NM_001369 // intron // 0 // Hs.212360 // DNAH5 // 1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // --- // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1844690	tataagacatcgaagg[A/G]aagtgctgacagggta	A	G	NM_001369 // intron // 0 // Hs.212360 // DNAH5 // 1767 // Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), mRNA. /// ENST00000265104 // intron // 0 // --- // --- // --- // ---	DNAH5	DNAH5, Homo sapiens dynein, axonemal, heavy polypeptide 5 (DNAH5), p15.2
SNP_A-1670880	ccacacaaagaaacttgagtttgtc[A/G]ttattgtggtgactggtc acttagg	A	G	NM_007118 // intron // 0 // Hs.367689 // TRIO // 7204 // triple functional domain (PTPRF interacting)	TRIO	TRIO , rs30617, triple functional domain (PTPRF interacting),p15.2
SNP_A-1737541	gatttaaataaaagacagtgactga[G/T]taactaaaataaatgg aaccaggtt	G	T	NM_007118 // intron // 0 // Hs.367689 // TRIO // 7204 // triple functional domain (PTPRF interacting)	TRIO	TRIO , rs247141, triple functional domain (PTPRF interacting),p15.2
SNP_A-2314914	ggagttacaaatgctg[A/G]aactcttctttaccct	A	G	NM_007118 // intron // 0 // Hs.130031 // TRIO // 7204 // Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA. /// ENST00000344204 // intron // 0 // --- // --- // --- // --- /// ENST00000322870 // intron // 0 // --- // --- // --- // ---	TRIO	TRIO, Homo sapiens triple functional domain (PTPRF interacting) (TRIO), p15.2
SNP_A-1850316	tatgttctcatttttc[C/T]agtaacttttatgct	C	T	NM_019018 // intron // 0 // Hs.528644 // FLJ11127 // 54491 // Homo sapiens hypothetical protein FLJ11127 (FLJ11127), mRNA. /// ENST00000274217 // intron // 0 // --- // --- // --- // ---	FLJ11127	FLJ11127, Homo sapiens hypothetical protein FLJ11127 (FLJ11127), p15.2
SNP_A-1890450	tgatctcatacgtgaa[A/G]tcttaaaaaaccagtc	A	G	NM_019018 // downstream // 16628 // Hs.528644 // FLJ11127 // 54491 // Homo sapiens hypothetical protein FLJ11127 (FLJ11127), mRNA. /// ENST00000274217 // downstream // 16628 // --- // --- // --- // --- /// ENST00000332977 // downstream // 24214 // --- // ---	FLJ11127	FLJ11127, Homo sapiens hypothetical protein FLJ11127 (FLJ11127), p15.2
SNP_A-2037945	aacaattactgcttga[C/T]acgacaaagtaatgtg	C	T	NM_054027 // intron // 0 // Hs.156727 // ANKH // 56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// ENST00000284268 // intron // 0 // --- // --- // --- // ---	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.2
SNP_A-2065069	aattgcatgccattcc[A/G]agtagtgtaatgaaat	A	G	NM_054027 // intron // 0 // Hs.156727 // ANKH // 56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// ENST00000284268 // intron // 0 // --- // --- // --- // ---	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.2
SNP_A-1980822	gatctaacgtcaattc[A/G]aagttctctattgaag	A	G	NM_054027 // upstream // 147784 // Hs.156727 // ANKH // 56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream // 596431 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.2
SNP_A-1980837	tgaaagagactggtaa[C/T]atgaaattgcagaaga	C	T	NM_054027 // upstream // 688961 // Hs.156727 // ANKH // 56172 // Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), mRNA. /// NM_012304 // upstream // 55254 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (F	ANKH	ANKH, Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), p15.1
SNP_A-1888842	tgaggtactatgctca[A/G]tatactaagatcagtc	A	G	NM_012304 // intron // 0 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // --- // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1
SNP_A-1980841	attgtctttaattttta[C/T]catgctcctcaaaagc	C	T	NM_012304 // intron // 0 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // --- // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2028779	aaacttccacactgtc[A/G]actttcagctttcatt	A	G	NM_012304 // intron // 0 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // --- // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1
SNP_A-2269277	gaatttccaatatgtc[C/T]ctgttgtttcacttttt	C	T	NM_012304 // intron // 0 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // --- // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1
SNP_A-1902523	tggcctggtcttcaaa[G/T]cagctaagttctcatc	G	T	NM_012304 // intron // 0 // Hs.433057 // FBXL7 // 23194 // Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA. /// ENST00000329673 // intron // 0 // --- // --- // --- // ---	FBXL7	FBXL7, Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), p15.1
SNP_A-1704467	tggcaaatgaataatcagctatcca[A/T]attggctcaaggacgatcaaggga	A	T	NM_012304 // intron // 0 // Hs.76798 // FBXL7 // 23194 // F-box and leucine-rich repeat protein 7	FBXL7	FBXL7 , rs10520822, F-box and leucine-rich repeat protein 7,p15.1
SNP_A-1958161	ttttcatgacactgaa[C/T]tgttgatgtgtctggg	C	T	NM_033414 // downstream // 178349 // Hs.60300 // ZNF622 // 90441 // Homo sapiens zinc finger protein 622 (ZNF622), mRNA. /// ENST00000332432 // upstream // 95350 // --- // --- // --- // --- /// ENST00000308683 // downstream // 178349 // --- // --- // ---	ZNF622	ZNF622, Homo sapiens zinc finger protein 622 (ZNF622), p15.1
SNP_A-1880105	tcttctccttgaggtc[C/T]gaaactatctcaaaca	C	T	NM_033414 // downstream // 164051 // Hs.60300 // ZNF622 // 90441 // Homo sapiens zinc finger protein 622 (ZNF622), mRNA. /// ENST00000332432 // upstream // 109648 // --- // --- // --- // --- /// ENST00000308683 // downstream // 164051 // --- // --- // ---	ZNF622	ZNF622, Homo sapiens zinc finger protein 622 (ZNF622), p15.1
SNP_A-1875082	tctctcacctttataa[A/G]tcgtctcattttccac	A	G	NM_033414 // downstream // 6552 // Hs.60300 // ZNF622 // 90441 // Homo sapiens zinc finger protein 622 (ZNF622), mRNA. /// ENST00000332432 // upstream // 267147 // --- // --- // --- // --- /// ENST00000308683 // downstream // 6552 // --- // --- // --- // ---	ZNF622	ZNF622, Homo sapiens zinc finger protein 622 (ZNF622), p15.1
SNP_A-1930574	ttccaagtctgtactc[A/G]atcgccctgccctcat	A	G	NM_019000 // intron // 0 // Hs.481704 // FLJ20152 // 54463 // Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-2150358	atgtcttcctggcata[A/C]cttctgaatttaactt	A	C	NM_019000 // intron // 0 // Hs.481704 // FLJ20152 // 54463 // Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-1790630	ggggctcagttactta[G/T]gagttgcatagatcca	G	T	NM_019000 // intron // 0 // Hs.481704 // FLJ20152 // 54463 // Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-1929133	ttcaggattctttcca[C/T]gtcctttggtgtagat	C	T	NM_019000 // intron // 0 // Hs.481704 // FLJ20152 // 54463 // Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-2094116	agaaggatctgcaaac[C/G]agacaggacagcggtg	C	G	NM_019000 // intron // 0 // Hs.481704 // FLJ20152 // 54463 // Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-2148472	atgggtccaaaaccaa[A/G]tcacaccatcagagtg	A	G	NM_019000 // intron // 0 // Hs.481704 // FLJ20152 // 54463 // Homo sapiens hypothetical protein FLJ20152 (FLJ20152), mRNA. /// ENST00000306320 // intron // 0 // --- // --- // --- // ---	FLJ20152	FLJ20152, Homo sapiens hypothetical protein FLJ20152 (FLJ20152), p15.1
SNP_A-1929944	ttcatgattgagccaa[C/T]gggtgtcaagtaggag	C	T	NM_012334 // intron // 0 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// ENST00000274203 // intron // 0 // --- // --- // --- // ---	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1919662	ttaaggtgaatgggca[C/T]tgatttttatgaacagc	C	T	NM_012334 // intron // 0 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// ENST00000274203 // intron // 0 // --- // --- // --- // ---	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1698567	ctaggaaggaacatttaagacgaca[A/C]aaaatctgacgtaaaggttactcca	A	C	NM_012334 // intron // 0 // Hs.61638 // MYO10 // 4651 // myosin X	MYO10	MYO10 , rs10520845, myosin X,p15.1
SNP_A-2291933	gcacatagtaggtgag[G/T]aataacaaaggcttgg	G	T	NM_012334 // intron // 0 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// ENST00000274203 // intron // 0 // --- // --- // --- // ---	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2226374	ctaagactcaaacgac[A/C]aactttctagtgaatt	A	C	NM_012334 // upstream // 63992 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 169001 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000274203 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1898579	tgcttgctcttttgac[A/G]ccagtggaagtttaaa	A	G	NM_012334 // upstream // 70000 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 162993 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000274203 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1980890	gtttactggtctgtaa[C/T]agatcctgcattagct	C	T	NM_012334 // upstream // 134333 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 98660 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000274203 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-2085706	actcctacctgtggca[A/G]tcatgaatctgttttc	A	G	NM_012334 // upstream // 197737 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 35256 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000274203 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1801227	gtagctgaaagagacc[A/C]gggtaaccatcagggc	A	C	NM_012334 // upstream // 220919 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 12074 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000274203 //	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1896086	tgcttttgccagaaa[A/G]cttcagactcgcagac	A	G	NM_012334 // upstream // 223740 // Hs.481720 // MYO10 // 4651 // Homo sapiens myosin X (MYO10), mRNA. /// NM_173669 // downstream // 9253 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000274203 // u	MYO10	MYO10, Homo sapiens myosin X (MYO10), p15.1
SNP_A-1954008	tttgatatctccttga[C/T]gtagctgaatgtcaaa	C	T	NM_173669 // intron // 0 // --- // FLJ34047 // 285696 // Homo sapiens hypothetical protein FLJ34047 (FLJ34047), mRNA. /// ENST00000339798 // intron // 0 // --- // --- // --- // ---	FLJ34047	FLJ34047, Homo sapiens hypothetical protein FLJ34047 (FLJ34047), p15.1
SNP_A-1938371	ttgactcattgactaa[G/T]gcaagctttttttttt	G	T	ENST00000322061 // upstream // 1447 // --- // --- // --- // --- /// ENST00000328167 // upstream // 130170 // --- // --- // --- // ---	-	p15.1
SNP_A-1817710	gttcccctgctactac[C/T]gctgtccaagtcacat	C	T	NM_004934 // downstream // 1470488 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 350063 // --- // --- // --- // --- /// ENST00000274170 // downstream // 1470488 // --- // --- // --- //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p15.1
SNP_A-1958085	ttttcaggaactttgg[A/G]aaaactacaggctaca	A	G	NM_004934 // downstream // 1326250 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 494301 // --- // --- // --- // --- /// ENST00000274170 // downstream // 1326250 // --- // --- // --- //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p15.1
SNP_A-2040211	aaccaatgtaatgata[C/T]ggtatgggatgatatc	C	T	NM_004934 // downstream // 1299988 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 520563 // --- // --- // --- // --- /// ENST00000274170 // downstream // 1299988 // --- // --- // --- //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p15.1
SNP_A-2143150	atgaatttaacctgga[A/G]caatgcagaatcaatt	A	G	NM_004934 // downstream // 1294768 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 525783 // --- // --- // --- // --- /// ENST00000274170 // downstream // 1294768 // --- // --- // --- //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p15.1
SNP_A-1753031	agatctgccaaagttttcacatcta[C/T]gtcatgactgttctagaacaagtag	C	T	NM_004934 // downstream // 1165644 // Hs.57691 // CDH18 // 1016 // cadherin 18, type 2 /// NM_006317 // downstream // 1023335 // Hs.511745 // BASP1 // 10409 // brain abundant, membrane attached signal protein 1	CDH18	CDH18 , rs904747, cadherin 18, type 2 ,p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1980912	ctcttaagtttggaca[A/T]gtatttgagtataagc	A	T	NM_004934 // downstream // 1003699 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 816852 // — // — // — // — /// ENST00000274170 // downstream // 1003699 // — // — // — //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2260180	gaaaatgacatcagta[C/G]cttgctagcattcttg	C	G	NM_004934 // downstream // 695956 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1124595 // — // — // — // — /// ENST00000274170 // downstream // 695956 // — // — // — // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1863519	tccaaagacgaactga[C/G]ggtgtgtgtgaacaca	C	G	NM_004934 // downstream // 689537 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1131014 // — // — // — // — /// ENST00000274170 // downstream // 689537 // — // — // — // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2118012	aggtttttcatgaacg[A/T]aaaaaaggcatgtatt	A	T	NM_004934 // downstream // 627820 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1192731 // — // — // — // — /// ENST00000274170 // downstream // 627820 // — // — // — // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1905694	tggtatgcacgtggac[A/G]cacaatagtatcataa	A	G	NM_004934 // downstream // 553309 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1267242 // — // — // — // — /// ENST00000274170 // downstream // 553309 // — // — // — // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1724732	gtctattaatcaaccttaaatgtca[A/C]caatttaaattcctcaattaaaga	A	C	NM_004934 // downstream // 524019 // Hs.57691 // CDH18 // 1016 // cadherin 18, type 2 /// NM_006317 // downstream // 1664960 // Hs.511745 // BASP1 // 10409 // brain abundant, membrane attached signal protein 1	CDH18	CDH18 , rs4131713, cadherin 18, type 2 ,p14.3
SNP_A-2055021	aataaatgcgcaagta[C/T]gaggttaaatgcttga	C	T	NM_004934 // downstream // 511379 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1309172 // — // — // — // — /// ENST00000274170 // downstream // 511379 // — // — // — // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2101758	agatgccttgatataa[A/G]agtaatctgaggctga	A	G	NM_004934 // downstream // 482313 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000333744 // upstream // 1338238 // — // — // — // — /// ENST00000274170 // downstream // 482313 // — // — // — // -	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1958340	ttttccatttttttca[A/G]agaacacatcaatttc	A	G	NM_004934 // upstream // 177842 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // upstream // 177842 // — // — // — // — /// ENST00000321978 // upstream // 1442470 // — // — // — // — /	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2044121	aacttgtatcttccaa[C/T]tgtatgtttgtaccct	C	T	NM_004934 // upstream // 623156 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // upstream // 623156 // — // — // — // — /// ENST00000321978 // upstream // 997156 // — // — // — // — //	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-2124710	agttctgaataccagg[A/T]aggacaccattaagat	A	T	NM_004934 // upstream // 1162258 // Hs.317632 // CDH18 // 1016 // Homo sapiens cadherin 18, type 2 (CDH18), mRNA. /// ENST00000274170 // upstream // 1162258 // — // — // — // — /// ENST00000321978 // upstream // 458054 // — // — // — // —	CDH18	CDH18, Homo sapiens cadherin 18, type 2 (CDH18), p14.3
SNP_A-1980956	ggcccatcaataacac[A/C]aatagcaccatgtgag	A	C	ENST00000321978 // intron // 0 // — // — // — // —	-	p14.3
SNP_A-2010729	gatttttgcatactca[A/G]tgaaacatacatattt	A	G	NM_004061 // downstream // 150352 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // upstream // 541838 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-2010731	atgctgtgactactca[C/T]acttatttactgttta	C	T	NM_004061 // intron // 0 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// ENST00000284308 // intron // 0 // — // — // — // —	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2120893	agtctaaatgcgcaga[A/G]gcatcaagtgtagaca	A	G	NM_004061 // upstream // 63048 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 416059 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (P	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-2306147	gctggagtcacttaga[C/G]agaaaaggaaagcaat	C	G	NM_004061 // upstream // 85700 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 438711 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (P	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1850636	tattaatttttcagg[C/T]cattgtttcattgatc	C	T	NM_004061 // upstream // 85996 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 439007 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (P	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1980963	aacatggtcgccaaaa[A/T]tcagagccttatgttt	A	T	NM_004061 // upstream // 93687 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 446698 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (P	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-2032533	aaataaaagtggaaaa[A/G]atcatgtcggagtgta	A	G	NM_004061 // upstream // 220530 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 573541 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-2046964	aagagtcaaagtaatc[C/T]catttccattggccag	C	T	NM_004061 // upstream // 320645 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 673656 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1831722	taattcaatcatcttc[C/T]accatgtctgtcccac	C	T	NM_004061 // upstream // 320776 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 673787 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1935456	ttctggcctgtagaga[A/C]tatgatcaatacagtt	A	C	NM_004061 // upstream // 327947 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 680958 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1 (	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1790059	ggggaacccggttacc[A/G]cagaaagcagttgaga	A	G	NM_004061 // upstream // 736815 // Hs.113684 // CDH12 // 1010 // Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), mRNA. /// NM_031887 // downstream // 1089826 // Hs.247975 // PMCHL1 // 5369 // Homo sapiens pro-melanin-concentrating hormone-like 1	CDH12	CDH12, Homo sapiens cadherin 12, type 2 (N-cadherin 2) (CDH12), p14.3
SNP_A-1980979	tggaagcagcttggga[A/T]ccacgtaacaggcaga	A	T	NM_020227 // downstream // 85678 // Hs.283096 // PRDM9 // 56979 // Homo sapiens PR domain containing 9 (PRDM9), mRNA. /// AF274347 // downstream // 71093 // Hs.406695 // PRDM7 // 11105 // Homo sapiens PR-domain zinc finger protein 7 isoform A (PRDM7) mRNA	PRDM9	PRDM9, Homo sapiens PR domain containing 9 (PRDM9), p14.2
SNP_A-1814648	gtgtgggatctttaat[A/G]actgcgacacctctgt	A	G	NM_006727 // downstream // 59625 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000317394 // downstream // 447490 // — // — // — // — /// ENST00000264463 // downstream // 59625 // — // —	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884487	tgaagtgttatatcac[A/C]gattgagaccagtaaa	A	C	NM_006727 // downstream // 35325 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// ENST00000317394 // downstream // 471790 // — // — // — // — /// ENST00000264463 // downstream // 35325 // — // —	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.2
SNP_A-2218761	cctgggaaagtattgat[C/T]ggctttcatgaggaag	C	T	NM_006727 // upstream // 47493 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 2188305 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA.	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2138383	atccagtacatgatcc[A/G]ccgtgacaatgagtag	A	G	NM_006727 // upstream // 58290 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 2177508 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA.	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1842246	taggattcgtagaata[A/T]gagtgtttagagtga	A	T	NM_006727 // upstream // 60374 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 2175424 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA.	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2173942	cacacataaattccac[A/G]gtagtattccatgatg	A	G	NM_006727 // upstream // 111693 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 2124105 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1981008	gactgccgtgtatcccc[C/T]gaagtgattaaactat	C	T	NM_006727 // upstream // 871695 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1364103 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1848600	tatgacttcttttca[A/T]ctatctgtaggtatt	A	T	NM_006727 // upstream // 953237 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1282561 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2140225	atctattcattcatca[A/G]ctaacctccctactt	A	G	NM_006727 // upstream // 998444 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 1237354 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2165163	caaagaaatcacataa[A/G]agcacaattatctcata	A	G	NM_006727 // upstream // 1300035 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 935763 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2235044	ctcccactcaggcaa[C/T]ctagcagacttgagg	C	T	NM_006727 // upstream // 1461851 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 773947 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2059730	aatctgatgagcttca[A/G]gcaaatataaagcagg	A	G	NM_006727 // upstream // 1462784 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 773014 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2094225	agaaggtagagtaaga[A/G]taaatatacatagcac	A	G	NM_006727 // upstream // 1532796 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 703002 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2177331	caccttacctttacca[C/T]acaaaggagattaaca	C	T	NM_006727 // upstream // 1810675 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 425123 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2179004	cactgccgcaagagca[A/T]taagcaaagttcacat	A	T	NM_006727 // upstream // 1858802 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 376996 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1981024	tgtgattagaagataa[C/T]tgagaacatggataaa	C	T	NM_006727 // upstream // 1925510 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 310288 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1981025	gctgcattctttgcta[C/T]ggtacataggtgccta	C	T	NM_006727 // upstream // 1929317 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 306481 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-1800612	gtactttcactcgtca[C/T]ctcctttggctgggtg	C	T	NM_006727 // upstream // 2167990 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 67808 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA.	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2249099	ctgtttctataggtgg[C/G]acccgatttatctctc	C	G	NM_006727 // upstream // 2168333 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 67465 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA.	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2055912	aatacacagaaataca[C/T]tgagtacaacattacc	C	T	NM_006727 // upstream // 2201982 // Hs.92489 // CDH10 // 1008 // Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), mRNA. /// NM_016279 // downstream // 33816 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA.	CDH10	CDH10, Homo sapiens cadherin 10, type 2 (T2-cadherin) (CDH10), p14.1
SNP_A-2187303	caggtggtaaacaagc[A/G]aaatgtactacagtgt	A	G	NM_016279 // intron // 0 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // intron // 0 // — // — // — // —	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2307471	gcttatgtttcctgta[G/T]gcttttggtaaataac	G	T	NM_016279 // upstream // 288663 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 288663 // — // — // — // — /// ENST00000333399 // upstream // 1598370 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2119380	agtataagtaggtgcc[A/G]aaaggtaggtaattgg	A	G	NM_016279 // upstream // 318764 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 318764 // — // — // — // — /// ENST00000333399 // upstream // 1568269 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1873123	tctattaatgccagga[A/G]aatcacacttcaaaat	A	G	NM_016279 // upstream // 329929 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 329929 // — // — // — // — /// ENST00000333399 // upstream // 1557104 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1925131	ttatcatctccataaa[G/T]attatcttccagacca	G	T	NM_016279 // upstream // 359063 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 359063 // — // — // — // — /// ENST00000333399 // upstream // 1527970 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1898572	tgcttgccttttcccc[A/G]caacgaggagtttctc	A	G	NM_016279 // upstream // 410130 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 410130 // — // — // — // — /// ENST00000333399 // upstream // 1476903 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2144204	atgagtaagtctacag[A/G]aataatgtcataatga	A	G	NM_016279 // upstream // 412321 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 412321 // — // — // — // — /// ENST00000333399 // upstream // 1474712 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2202887	ccactcaagaatgctg[A/G]acaatcgttaacacta	A	G	NM_016279 // upstream // 417538 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 417538 // — // — // — // — /// ENST00000333399 // upstream // 1469495 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2010765	gtgtgtcacaagacac[C/T]cttttctttcctttgt	C	T	NM_016279 // upstream // 437802 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 437802 // — // — // — // — /// ENST00000333399 // upstream // 1449231 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2114653	agggagtttagtttta[C/T]acactgttttgttccc	C	T	NM_016279 // upstream // 441300 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 441300 // — // — // — // — /// ENST00000333399 // upstream // 1445733 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1948572	tttagtttgacaaaga[A/C]gtggaatcaaaaataa	A	C	NM_016279 // upstream // 452111 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 452111 // — // — // — // — /// ENST00000333399 // upstream // 1434922 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2196580	cattaaacactaactt[C/G]aagaggattatacatt	C	G	NM_016279 // upstream // 460566 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 460566 // — // — // — // — /// ENST00000333399 // upstream // 1426467 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2146923	atggaaaatccgatac[G/T]ctgttgatccgacaag	G	T	NM_016279 // upstream // 488805 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 488805 // — // — // — // — /// ENST00000333399 // upstream // 1398228 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1981048	actgtctctgtagaac[A/G]aactgggaagaactgg	A	G	NM_016279 // upstream // 500816 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 500816 // — // — // — // — /// ENST00000333399 // upstream // 1386217 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1889278	tgagtgcattgctcta[C/T]ctaaagtactttccca	C	T	NM_016279 // upstream // 552115 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 552115 // — // — // — // — /// ENST00000333399 // upstream // 1334918 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1836234	tactatgcccattcac[C/T]gaaacagctggaaaaa	C	T	NM_016279 // upstream // 557049 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 557049 // — // — // — // — /// ENST00000333399 // upstream // 1329984 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2145889	atgcccacaggaaaac[A/C]acatgacattctgaag	A	C	NM_016279 // upstream // 580796 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 580796 // — // — // — // — /// ENST00000333399 // upstream // 1306237 // — // — // -	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-1687902	tttcttcatctgtaatataggaata[A/G]gactaaatgtgtgaattcttg tgaa	A	G	BC034574 // downstream // 644166 // Hs.453289 // - // - // Clone IMAGE:4825049, mRNA, partial cds /// NM_016279 // upstream // 1242867 // Hs.272212 // CDH9 // 1007 // cadherin 9, type 2 (T1-cadherin)	-	- , rs6880876, Clone IMAGE:4825049, mRNA, partial cds ,p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1853558	tatttttaaatcactg[A/T]acaactcataatttta	A	T	NM_016279 // upstream // 1660082 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 1660082 // — // — // — // — /// ENST00000333399 // upstream // 226951 // — // — //	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2095148	agaattacatggcaaa[A/T]caattgtaaaactgtt	A	T	NM_016279 // upstream // 1693905 // Hs.272212 // CDH9 // 1007 // Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), mRNA. /// ENST00000231021 // upstream // 1693905 // — // — // — // — /// ENST00000333399 // upstream // 193128 // — // — //	CDH9	CDH9, Homo sapiens cadherin 9, type 2 (T1-cadherin) (CDH9), p14.1
SNP_A-2159882	atttatatgccatgcc[C/G]actacttctggacaac	C	G	ENST00000333399 // downstream // 48480 // — // — // — // — /// ENST00000354793 // downstream // 1511581 // — // — // — // —	-	p14.1
SNP_A-2148776	atggtgacaaaaatca[A/G]cccgctaaagggctag	A	G	ENST00000333399 // downstream // 89729 // — // — // — // — /// ENST00000354793 // downstream // 1470332 // — // — // — // —	-	p14.1
SNP_A-2044125	aacttgtcaacacctc[G/T]atcttgaacttttggc	G	T	ENST00000333399 // downstream // 120496 // — // — // — // — /// ENST00000354793 // downstream // 1439565 // — // — // — // —	-	p14.1
SNP_A-2131163	atagactgcttgggaa[A/G]agatacacataatggg	A	G	ENST00000333399 // downstream // 321700 // — // — // — // — /// ENST00000354793 // downstream // 1238361 // — // — // — // —	-	p14.1
SNP_A-2283702	gatagcccttacaagc[A/T]gatactggagaatgaa	A	T	ENST00000333399 // downstream // 397867 // — // — // — // — /// ENST00000354793 // downstream // 1162194 // — // — // — // —	-	p13.3
SNP_A-2280653	gaggtccaagaacaaa[A/G]tataattgacccttg	A	G	ENST00000333399 // downstream // 412236 // — // — // — // — /// ENST00000354793 // downstream // 1147825 // — // — // — // —	-	p13.3
SNP_A-2079840	accctggactacattc[C/T]cctataaggctcacca	C	T	ENST00000333399 // downstream // 467358 // — // — // — // — /// ENST00000354793 // downstream // 1092703 // — // — // — // —	-	p13.3
SNP_A-1807071	gtctccatctgtgcta[A/C]cgggtcattctgttcc	A	C	ENST00000333399 // downstream // 863276 // — // — // — // — /// ENST00000354793 // downstream // 696785 // — // — // — // —	-	p13.3
SNP_A-1748445	accaaaaaaaaaaatagaacaacaa[A/G]taatttatgaacaaacaacatactc	A	G	NM_004932 // upstream // 1408649 // Hs.32963 // CDH6 // 1004 // cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	CDH6 , rs1463413, cadherin 6, type 2, K-cadherin (fetal kidney),p13.3
SNP_A-1895013	tgcccactgatgacac[A/G]gtcttgccagtcacca	A	G	ENST00000333399 // downstream // 1298723 // — // — // — // — /// ENST00000354793 // downstream // 261338 // — // — // — // —	-	p13.3
SNP_A-2131063	atagaattggattcaa[A/G]cttaattcacatgatc	A	G	NM_004932 // upstream // 671791 // Hs.171054 // CDH6 // 1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream // 32232 // — // — // — // — /// ENST00000265071 // upstream // 671791 // —	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-2293796	gcagctccactcctat[A/G]agtctgcaggatacag	A	G	NM_004932 // upstream // 619594 // Hs.171054 // CDH6 // 1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream // 84429 // — // — // — // — /// ENST00000265071 // upstream // 619594 // —	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1900030	tggacctactacagaa[A/G]agattgctgagtaagg	A	G	NM_004932 // upstream // 554136 // Hs.171054 // CDH6 // 1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream // 149887 // — // — // — // — /// ENST00000265071 // upstream // 554136 // —	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1891974	tgatttttctgagtgt[C/G]aatttttttaagtaat	C	G	NM_004932 // upstream // 286748 // Hs.171054 // CDH6 // 1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream // 417275 // — // — // — // — /// ENST00000265071 // upstream // 286748 // —	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-2220532	ccttctgccatttgaa[A/G]atatagcaagaaagta	A	G	NM_004932 // upstream // 286528 // Hs.171054 // CDH6 // 1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream // 417495 // — // — // — // — /// ENST00000265071 // upstream // 286528 // —	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1732680	tcctggaatattggttcattgtaga[C/T]gggcttacctagagggaagtatata	C	T	NM_004932 // upstream // 218559 // Hs.32963 // CDH6 // 1004 // cadherin 6, type 2, K-cadherin (fetal kidney)	CDH6	CDH6 , rs4867292, cadherin 6, type 2, K-cadherin (fetal kidney),p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1785401	ggctattcatgaggac[C/G]attgttgtggaagata	C	G	NM_004932 // upstream // 192059 // Hs.171054 // CDH6 // 1004 // Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA. /// ENST00000354793 // upstream // 511964 // — // — // — // — /// ENST00000265071 // upstream // 192059 // —	CDH6	CDH6, Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), p13.3
SNP_A-1813910	gtgtcaaaagccatca[C/T]gtactttgaatatctt	C	T	NM_013235 // intron // 0 // Hs.97997 // RNASE3L // 29102 // Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // — // — // — // — /// ENST00000265075 // intron // 0 // — // — // — // —	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-2079494	acccctattggcttca[A/G]cttggaacttttcttc	A	G	NM_013235 // intron // 0 // Hs.97997 // RNASE3L // 29102 // Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // — // — // — // — /// ENST00000265075 // intron // 0 // — // — // — // —	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-1929946	ttcatgcaaaacataa[A/G]gcaatgcagcatcttc	A	G	NM_013235 // intron // 0 // Hs.97997 // RNASE3L // 29102 // Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA. /// ENST00000344624 // intron // 0 // — // — // — // — /// ENST00000265075 // intron // 0 // — // — // — // —	RNASE3L	RNASE3L, Homo sapiens nuclear RNase III Drosha (RNASE3L), p13.3
SNP_A-1668350	agctcccagtccataactctaaata[G/T]cacatgggcacctatta ctccatat	G	T	NM_013235 // intron // 0 // Hs.438951 // RNASE3L // 29102 // nuclear RNase III Drosha	RNASE3L	RNASE3L , rs615344, nuclear RNase III Drosha,p13.3
SNP_A-2096860	agactcattccaagac[C/T]gtcctgaaaatactga	C	T	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1981141	aatctggcctggacca[A/G]gaaatctcacaaccct	A	G	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2010790	caagataaataccaaa[A/G]tatactgcaacatcca	A	G	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2254992	cttggctccagggtaa[C/T]gtgttggccttccaac	C	T	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2300706	gcctggaaagtacaca[C/T]ggtccttctgtaacac	C	T	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1680004	aatcatggacattccaaattgagac[C/T]cacaagggtttatgact acattgtc	C	T	NM_015022 // intron // 0 // Hs.287460 // PDZK3 // 23037 // PDZ domain containing 3 /// NM_178140 // intron // 0 // Hs.287460 // PDZK3 // 23037 // PDZ domain containing 3	PDZK3	PDZK3 , rs10520990, PDZ domain containing 3 ,p13.3
SNP_A-2254616	cttgctctggcaatcc[A/G]acataaggcattgagt	A	G	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1981148	gcaatcctgagtatcc[A/G]ctgtctttctcagcca	A	G	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2208396	cccaccagaatccaaa[A/T]ttcaataaaggtctc	A	T	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1894041	tgcatcgcccagggtc[A/G]ccaagtgcaaggccag	A	G	NM_015022 // CDS // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // CDS // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1805315	gtcatttttccatgga[C/T]gtctcaatgaaaaaaa	C	T	NM_015022 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // intron // 0 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript va	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2064025	aattatgtaaaattct[A/T]aaaaacagctataaat	A	T	NM_015022 // downstream // 3332 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // downstream // 3332 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3),	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-1842797	tagtacattgtaccaa[C/T]caggttatttaagga	C	T	NM_015022 // downstream // 12853 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, mRNA. /// NM_178140 // downstream // 12853 // Hs.481819 // PDZK3 // 23037 // Homo sapiens PDZ domain containing 3 (PDZK3	PDZK3	PDZK3, Homo sapiens PDZ domain containing 3 (PDZK3), transcript variant 2, p13.3
SNP_A-2021230	aaaaaaataaaaatca[C/G]aagtcaagtggtactt	C	G	NM_022130 // intron // 0 // Hs.408909 // GOLPH3 // 64083 // Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA. /// ENST00000265070 // intron // 0 // --- // --- // ---	GOLPH3	GOLPH3, Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3), p13.3
SNP_A-2062989	aatgttaaaagtacta[C/T]gatctgataattgcct	C	T	NM_006713 // intron // 0 // Hs.229641 // PC4 // 10923 // Homo sapiens activated RNA polymerase II transcription cofactor 4 (PC4), mRNA. /// ENST00000265073 // intron // 0 // --- // --- // ---	PC4	PC4, Homo sapiens activated RNA polymerase II transcription cofactor 4 (PC4), p13.3
SNP_A-2149039	atggtttcaaatatga[C/T]gcttccaactcaacag	C	T	NM_006713 // downstream // 33347 // Hs.229641 // PC4 // 10923 // Homo sapiens activated RNA polymerase II transcription cofactor 4 (PC4), mRNA. /// NM_000908 // upstream // 76256 // Hs.237028 // NPR3 // 4883 // Homo sapiens natriuretic peptide receptor C/	PC4	PC4, Homo sapiens activated RNA polymerase II transcription cofactor 4 (PC4), p13.3
SNP_A-1959825	tttgtaggtttttcat[C/T]ggaaagtctgaggcat	C	T	NM_000908 // intron // 0 // Hs.237028 // NPR3 // 4883 // Homo sapiens natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) (NPR3), mRNA. /// ENST00000265074 // intron // 0 // --- // --- // --- // ---	NPR3	NPR3, Homo sapiens natriuretic peptide receptor C,p13.3
SNP_A-1929750	ttcatcagaaccctta[C/T]gctaacctgaccacac	C	T	NM_024563 // 3UTR // 0 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// ENST00000326958 // 3UTR // 0 // --- // --- // ---	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2134190	atatgagttcaaaggc[A/G]aaaggattatttgcg	A	G	NM_024563 // downstream // 25757 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 623322 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. /// E	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-1904376	tgggcttggatttggc[A/G]gaaatctgagagtttc	A	G	NM_024563 // downstream // 80261 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 568818 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. /// E	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2309819	ggaaagtcaacgata[C/T]gtatacaaccaacagg	C	T	NM_024563 // downstream // 197940 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 451139 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. ///	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-1894613	tgccactcctatgaaa[C/T]tgtagatcacttctac	C	T	NM_024563 // downstream // 357630 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 291449 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. ///	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-1951323	tttccctgtgattatc[A/T]aaggaagtgaattctc	A	T	NM_024563 // downstream // 361428 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 287651 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. ///	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-1688164	cattctcttccctccttttgatgtag[A/C]aattatggagttttaaaattg gca	A	C	NM_003191 // upstream // 280343 // - /// - /// - /// NM_024563 // downstream // 368929 // Hs.13528 // FLJ14054 // 79614 // hypothetical protein FLJ14054 /// NM_152295 // upstream // 280347 // Hs.84131 // TARS // 6897 // threonyl-tRNA synthetase	-	-, rs1366267, -, p13.3
SNP_A-2185324	caggaatcctctattgc[C/T]acgcatttgaaagcta	C	T	NM_024563 // downstream // 437092 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 211987 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. ///	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2128527	ataatacaaaaatgc[A/G]gaaaagcaagaaagat	A	G	NM_024563 // downstream // 463637 // Hs.13528 // FLJ14054 // 79614 // Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /// NM_152295 // upstream // 185442 // Hs.481860 // TARS // 6897 // Homo sapiens threonyl-tRNA synthetase (TARS), mRNA. ///	FLJ14054	FLJ14054, Homo sapiens hypothetical protein FLJ14054 (FLJ14054), p13.3
SNP_A-2127213	ataaatgacaccaaaac[A/G]atgggggcaaggagc	A	G	NM_030955 // intron // 0 // Hs.481865 // ADAMTS12 // 81792 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // — // — // —	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-2190992	cataggaggctcttaa[A/T]agatattcaatgggtg	A	T	NM_030955 // intron // 0 // Hs.481865 // ADAMTS12 // 81792 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // — // — // —	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-2010803	tggatgccgaagctgg[A/C]agggaagaaccaagca	A	C	NM_030955 // intron // 0 // Hs.481865 // ADAMTS12 // 81792 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // — // — // —	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-1806716	gtctacttgaataaa[C/T]tggtcactgagacctc	C	T	NM_030955 // intron // 0 // Hs.481865 // ADAMTS12 // 81792 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // — // — // —	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-1801321	gtaggaagtgcgagga[C/T]atatagcagaagagtg	C	T	NM_030955 // intron // 0 // Hs.481865 // ADAMTS12 // 81792 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // — // — // —	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2179432	cactgttgtcacttta[C/T]ggagatggaagtatag	C	T	NM_030955 // intron // 0 // Hs.481865 // ADAMTS12 // 81792 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /// ENST00000352040 // intron // 0 // — // — // — // —	ADAMTS12	ADAMTS12, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), p13.3
SNP_A-2214645	cctagcaccegacaaa[A/G]actcaaaatgtgatag	A	G	NM_016180 // intron // 0 // Hs.278962 // MATP // 51151 // Homo sapiens membrane associated transporter (MATP), mRNA. /// ENST00000296589 // intron // 0 // — // — // — // — /// ENST00000342059 // intron // 0 // — // — // — // —	MATP	MATP, Homo sapiens membrane associated transporter (MATP), p13.3
SNP_A-1853234	tattttaaaacatata[C/T]agtagtcctctcttat	C	T	NM_203382 // intron // 0 // Hs.508343 // AMACR // 23600 // Homo sapiens alpha-methylacyl-CoA racemase (AMACR), transcript variant 2, mRNA. /// NM_014324 // intron // 0 // Hs.508343 // AMACR // 23600 // Homo sapiens alpha-methylacyl-CoA racemase (AMACR), t	AMACR	AMACR, Homo sapiens alpha-methylacyl-CoA racemase (AMACR), transcript variant 2, p13.3
SNP_A-1889429	tgagttatttgcaaca[C/T]tagtactacgcaagtg	C	T	NM_015577 // upstream // 31249 // Hs.431400 // RAI14 // 26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000331766 // upstream // 406820 // — // — // — // — /// ENST00000066208 // downstream // 430639 // — // — // — //	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-2128897	ataatgctttaagaac[A/G]gtcctgctcgtgcatg	A	G	NM_015577 // upstream // 30856 // Hs.431400 // RAI14 // 26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000331766 // upstream // 407213 // — // — // — // — /// ENST00000066208 // downstream // 431032 // — // — // — //	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-1981215	gctgtttgtgtgcata[A/G]ctttcaaaaacaatgt	A	G	NM_015577 // intron // 0 // Hs.431400 // RAI14 // 26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000265109 // intron // 0 // — // — // — // —	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-1981216	gtcaaaatataattca[C/T]ggcaaagcaataaaat	C	T	NM_015577 // intron // 0 // Hs.431400 // RAI14 // 26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000265109 // intron // 0 // — // — // — // —	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-1850836	tattaggaggcattac[A/G]aaaataagaaagtggt	A	G	NM_015577 // intron // 0 // Hs.431400 // RAI14 // 26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// ENST00000265109 // intron // 0 // — // — // — // —	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-2211745	ccctccttgtatcagt[C/G]aaaatcctatccactc	C	G	NM_015577 // downstream // 27714 // Hs.431400 // RAI14 // 26064 // Homo sapiens retinoic acid induced 14 (RAI14), mRNA. /// NM_133282 // downstream // 47866 // Hs.531879 // RAD1 // 5810 // Homo sapiens RAD1 homolog (S. pombe) (RAD1), transcript variant 2,	RAI14	RAI14, Homo sapiens retinoic acid induced 14 (RAI14), p13.2
SNP_A-1706709	acaattgtttgatgcttaatcttga[C/T]attaaaacctaaaacacta ctttca	C	T	BC050472 // intron // 0 // Hs.131887 // LOC134218 // 134218 // hypothetical protein LOC134218	LOC134218	LOC134218 , rs37437, hypothetical protein LOC134218,p13.2
SNP_A-2171078	caatactgttccatga[C/T]tatttcagcagaactg	C	T	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2137408	atcatagaagatgtta[A/G]cgcaccattctcatat	A	G	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2253431	cttcttaagcagaaaa[A/G]gctcttaggagagaaa	A	G	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1827780	taacttggcaaaagaa[A/G]atgttagggtccttca	A	G	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1942853	ttgggcaatgctccaa[C/T]agagtcaagggcatgt	C	T	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1855254	tcaagctagcacatcaj[A/G]tactaaaaagaaaagc	A	G	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1849911	tatgtattgccggcaa[A/G]taaagtatgtccagac	A	G	NM_000949 // intron // 0 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// ENST00000342362 // intron // 0 // — // — // — /// ENST00000325229 // intron // 0 // — // — // — // —	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2127616	ataacctaatactcc[C/T]gatcaatacacgtcc	C	T	NM_000949 // upstream // 1410 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 386002 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 2, mRNA. /// NM_0	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1741409	ctlgccaaaacctgcagtgctcaaa[C/T]gagtatcccctaacat ttcataac	C	T	NM_000949 // upstream // 36078 // Hs.212892 // PRLR // 5618 // prolactin receptor /// NM_144722 // upstream // 351437 // Hs.137422 // FLJ23577 // 79925 // KPL2 protein	PRLR	PRLR, rs10512631, prolactin receptor, p13.2
SNP_A-2267380	gaataggcaggacaaa[C/G]agaatttcctctca	C	G	NM_000949 // upstream // 75003 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 312409 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 2, mRNA. /// NM_	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2194955	catgctgcctacaga[A/C]ccactccactattcag	A	C	NM_000949 // upstream // 243032 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 144380 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 2, mRNA. /// NM	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-1836728	tactgaattcctactat[C/T]gtgaagtgcactgtcc	C	T	NM_000949 // upstream // 336659 // Hs.368587 // PRLR // 5618 // Homo sapiens prolactin receptor (PRLR), mRNA. /// NM_144722 // upstream // 50753 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 2, mRNA. /// NM_	PRLR	PRLR, Homo sapiens prolactin receptor (PRLR), p13.2
SNP_A-2266862	gaagtcttataacaca[A/G]tgtcagcttcataaag	A	G	NM_144722 // intron // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 2, mRNA. /// NM_024867 // intron // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, m	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 2, p13.2
SNP_A-2196111	catgtgatcctccaaa[C/T]agtgtaacaaggaagg	C	T	NM_024867 // intron // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // — // — // — /// ENST00000303168 // intron // 0 // — // — // — // —	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-2288086	gattcacaggtatctc[A/G]ctaaattgaaacagga	A	G	NM_024867 // CDS // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // CDS // 0 // — // — // — /// ENST00000303168 // CDS // 0 // — // — // — // —	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-1802315	gtatattggtgtcaga[A/G]tataaagtaccacat	A	G	NM_024867 // intron // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // — // — // — /// ENST00000303168 // intron // 0 // — // — // — // —	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-2266966	gaagtttgagcgggg[C/G]atgctgtgatttgatc	C	G	NM_024867 // intron // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // — // — // — /// ENST00000303168 // intron // 0 // — // — // — // — /	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2053918	aagtgtttgctgagtt[A/G]aaaataaaagcgcttt	A	G	NM_024867 // intron // 0 // Hs.298863 // FLJ23577 // 79925 // Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, mRNA. /// ENST00000356031 // intron // 0 // — // — // — // — /// ENST00000303168 // 3UTR // 0 // — // — // — // — ///	FLJ23577	FLJ23577, Homo sapiens KPL2 protein (FLJ23577), transcript variant 1, p13.2
SNP_A-2305108	gctgaatgttctctcc[A/C]acacgattacccccag	A	C	NM_145000 // upstream // 57907 // Hs.199777 // FLJ25422 // 202151 // Homo sapiens hypothetical protein FLJ25422 (FLJ25422), mRNA. /// NM_004172 // upstream // 246778 // Hs.481918 // SLC1A3 // 6507 // Homo sapiens solute carrier family 1 (glial high affini	FLJ25422	FLJ25422, Homo sapiens hypothetical protein FLJ25422 (FLJ25422), p13.2
SNP_A-2254460	cttgcccgtaagtgag[C/T]caatcctgcagatttg	C	T	NM_004172 // downstream // 47437 // Hs.481918 // SLC1A3 // 6507 // Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), mRNA. /// ENST00000265113 // downstream // 47437 // — // — // — // — /// ENST00	SLC1A3	SLC1A3, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), p13.2
SNP_A-2085225	actcagtattccagat[A/G]aaggtagccatagtgg	A	G	NM_199231 // intron // 0 // Hs.248114 // GDNF // 2668 // Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, mRNA. /// NM_199234 // intron // 0 // Hs.248114 // GDNF // 2668 // Homo sapiens glial cell derived neurotrophic fact	GDNF	GDNF, Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, p13.2
SNP_A-2107203	agcgtggctcttctca[C/T]gcattttagtcttcac	C	T	NM_199231 // upstream // 19145 // Hs.248114 // GDNF // 2668 // Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, mRNA. /// NM_199234 // upstream // 19145 // Hs.248114 // GDNF // 2668 // Homo sapiens glial cell derived neuro	GDNF	GDNF, Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant 2, p13.2
SNP_A-1749455	taagccacagcaggggctctgtgaa[C/T]cgagaaggaaaata tattgcatctg	C	T	NM_152403 // intron // 0 // Hs.20103 // FLJ39155 // 133584 // hypothetical protein FLJ39155	FLJ39155	FLJ39155 , rs3935014, hypothetical protein FLJ39155,p13.2
SNP_A-1734316	gggaaaacatttagtcccattgtaa[A/G]gattggaaagaaaag gaaaagagat	A	G	NM_152403 // intron // 0 // Hs.20103 // FLJ39155 // 133584 // hypothetical protein FLJ39155	FLJ39155	FLJ39155 , rs2956597, hypothetical protein FLJ39155,p13.2
SNP_A-2102177	agatgtttaactacat[A/G]aggtttcaaggaaata	A	G	NM_002310 // upstream // 95039 // Hs.133421 // LIFR // 3977 // Homo sapiens leukemia inhibitory factor receptor (LIFR), mRNA. /// NM_003999 // upstream // 155601 // Hs.120658 // OSMR // 9180 // Homo sapiens oncostatin M receptor (OSMR), mRNA. /// ENST0000	LIFR	LIFR, Homo sapiens leukemia inhibitory factor receptor (LIFR), p13.1
SNP_A-2112436	aggcaataaaggctcc[A/C]atacttctcccttccc	A	C	NM_003999 // intron // 0 // Hs.120658 // OSMR // 9180 // Homo sapiens oncostatin M receptor (OSMR), mRNA. /// ENST00000274276 // intron // 0 // — // — // — // —	OSMR	OSMR, Homo sapiens oncostatin M receptor (OSMR), p13.1
SNP_A-2133368	atatatcttcttgcac[A/G]ggtacacataactctt	A	G	NM_199335 // upstream // 58451 // Hs.370503 // FYB // 2533 // Homo sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// NM_001465 // upstream // 41838 // Hs.370503 // FYB // 2533 // Homo sapiens FYN binding protein (FYB-120/130) (FYB), mRNA. /// NM_	FYB	FYB, Homo sapiens FYN binding protein (FYB-120,p13.1
SNP_A-1981356	ctccacaaatgttggc[C/T]gcatgaagtgtaagag	C	T	NM_001343 // intron // 0 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// ENST00000320816 // intron // 0 // — // — // — // —	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1715019	gttttgctccctgttagatagtaaa[A/C]catataagggaacaaatc tttattt	A	C	NM_001343 // intron // 0 // Hs.81988 // DAB2 // 1601 // disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DAB2	DAB2 , rs3849763, disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila),p13.1
SNP_A-1710590	aagttaaatttacctaatgtttatt[A/G]tataccagatgtgatgctaa gacat	A	G	NM_001343 // intron // 0 // Hs.81988 // DAB2 // 1601 // disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DAB2	DAB2 , rs3849765, disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila),p13.1
SNP_A-1714903	atttgccttttattctacttggaa[A/G]ctctgctgataaagctgtttaa ggg	A	G	NM_000958 // upstream // 1178027 // Hs.199248 // PTGER4 // 5734 // prostaglandin E receptor 4 (subtype EP4) /// NM_001343 // upstream // 77265 // Hs.81988 // DAB2 // 1601 // disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	PTGER4	PTGER4 , rs10491482, prostaglandin E receptor 4 (subtype EP4) ,p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2010842	gtggaaagctaacaca[A/T]actgatgatactgttt	A	T	NM_001343 // upstream // 157820 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 1097266 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-2198095	cattgggactgactag[A/G]cagttggtgcaaccca	A	G	NM_001343 // upstream // 174537 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 1080549 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1881633	tctttgaggacactca[A/G]gattaatcacattcct	A	G	NM_001343 // upstream // 203889 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 1051197 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1799857	gtacacccaggggagg[C/T]atgctctaagttccaa	C	T	NM_001343 // upstream // 444319 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 810767 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1732638	acttggcccaggtttgaataaagcc[A/T]ccttgaccagtaaaaat tattgcta	A	T	NM_000958 // upstream // 579868 // Hs.199248 // PTGER4 // 5734 // prostaglandin E receptor 4 (subtype EP4) /// NM_001343 // upstream // 675424 // Hs.81988 // DAB2 // 1601 // disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	PTGER4	PTGER4 , rs924981, prostaglandin E receptor 4 (subtype EP4) ,p13.1
SNP_A-1882019	tcttttgccatcttac[A/G]atagtactaataactt	A	G	NM_001343 // upstream // 713123 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 541963 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-2269403	gaattttggaaatcag[A/G]acacaaaatagaggat	A	G	NM_001343 // upstream // 749500 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 505586 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1885438	tgacaaatgggaaatc[C/T]agaaattggaagttag	C	T	NM_001343 // upstream // 1103953 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 151133 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1696734	cacttacatactattacaataatga[A/T]gctgaagtatttttttagga aaacaa	A	T	NM_000958 // upstream // 92767 // Hs.199248 // PTGER4 // 5734 // prostaglandin E receptor 4 (subtype EP4) /// NM_001343 // upstream // 1162525 // Hs.81988 // DAB2 // 1601 // disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	PTGER4	PTGER4 , rs10512745, prostaglandin E receptor 4 (subtype EP4) ,p13.1
SNP_A-1981395	atcatagtcatttcac[C/T]ctccagcacacactta	C	T	NM_001343 // upstream // 1178257 // Hs.481980 // DAB2 // 1601 // Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA. /// NM_000958 // upstream // 76829 // Hs.199248 // PTGER4 // 5734 // Homo sapiens prostaglandin	DAB2	DAB2, Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), p13.1
SNP_A-1852576	tatttataacttcccc[C/T]gctactcctatagata	C	T	NM_032587 // downstream // 16833 // Hs.200242 // CARD6 // 84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream // 56389 // Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// E	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1825449	taaataataactcaa[C/T]gtgaatgatacctgga	C	T	NM_032587 // downstream // 22725 /// Hs.200242 // CARD6 // 84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream // 50497 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// E	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1
SNP_A-1891191	tgatgtggcccattccg[A/G]agaaagcttattatat	A	G	NM_032587 // downstream // 32597 /// Hs.200242 // CARD6 // 84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream // 40625 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// E	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1
SNP_A-1901441	tggattcttcagtc[A/G]acctaccctgtaat	A	G	NM_032587 // downstream // 34470 /// Hs.200242 // CARD6 // 84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream // 38752 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// E	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1
SNP_A-1940162	ttgcatatacaaatta[C/T]gtgtaagaggagaaat	C	T	NM_032587 // downstream // 34683 /// Hs.200242 // CARD6 // 84674 // Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA. /// NM_000587 // upstream // 38539 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// E	CARD6	CARD6, Homo sapiens caspase recruitment domain family, member 6 (CARD6), p13.1
SNP_A-2303799	gctcagggtgatgtgat[C/G]agcacacgcaggaaggt	C	G	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // — // — // —	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-1797846	ggttttcgtatggtac[C/T]aatgatcaaaatacct	C	T	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // — // — // —	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-2061489	aatgctcacattctgg[C/T]catgtcatatggaaaa	C	T	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // — // — // —	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-1677066	cttattataaaatgttcactggagg[A/G]aatacagaaagttatga agaaataa	A	G	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // complement component 7	C7	C7 , rs10512750, complement component 7,p13.1
SNP_A-1932286	ttcctctgaaatcccaa[A/G]attcaaccatctata	A	G	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // — // — // —	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-1981408	gtaggagatttaatgt[C/G]aaaacagcaaacgcat	C	G	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // — // — // —	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-1981409	tgagggggatggcagtc[A/T]catatgcatcttgtaa	A	T	NM_000587 // intron // 0 /// Hs.78065 // C7 // 730 // Homo sapiens complement component 7 (C7), mRNA. /// ENST00000313164 // intron // 0 // — // — // —	C7	C7, Homo sapiens complement component 7 (C7), p13.1
SNP_A-2153227	attactgatcatttcaa[C/G]atagtgggaaaacttg	C	G	NM_173489 // intron // 0 /// Hs.97714 // FLJ40243 // 133558 // Homo sapiens hypothetical protein FLJ40243 (FLJ40243), mRNA. /// ENST00000355152 // intron // 0 // — // — // — /// ENST00000296803 // intron // 0 // — // — // —	FLJ40243	FLJ40243, Homo sapiens hypothetical protein FLJ40243 (FLJ40243), p13.1
SNP_A-2125337	agttgttagactaaag[G/T]atagcagattgctgg	G	T	NM_000065 // intron // 0 /// Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// ENST00000337836 // intron // 0 // — // — // — /// ENST00000263413 // intron // 0 // — // — // —	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-1800622	gtactttaaagtcaa[C/T]aggagattattcgaat	C	T	NM_000065 // intron // 0 /// Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// ENST00000337836 // intron // 0 // — // — // — /// ENST00000263413 // intron // 0 // — // — // —	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-2031693	aaagtactactcaaggt[A/C]aagtttgagcatttt	A	C	NM_000065 // intron // 0 /// Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// ENST00000337836 // intron // 0 // — // — // — /// ENST00000263413 // intron // 0 // — // — // —	C6	C6, Homo sapiens complement component 6 (C6), p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2133566	atatcacaaaattcaa[G/T]gagtgaatgtagaaag	G	T	NM_000065 // intron // 0 // Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// ENST00000263413 // intron // 0 // — // — // —	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-1830109	taatagaaaaagaacaa[A/G]cattcaaagctttca	A	G	NM_000065 // upstream // 50716 // Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// NM_000065 // upstream // 2788 // Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// ENST00000337836 // upstream // 5	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-2070196	acacattaatcattga[A/G]tatcaaacttaaatgt	A	G	NM_000065 // upstream // 74640 // Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// NM_000065 // upstream // 26712 // Hs.481992 // C6 // 729 // Homo sapiens complement component 6 (C6), mRNA. /// ENST00000337836 // upstream //	C6	C6, Homo sapiens complement component 6 (C6), p13.1
SNP_A-1740195	gccacatctgtaactctcaaatct[C/G]aaaactaacatgtctctt taacca	C	G	NM_000065 // upstream // 203190 // Hs.1282 // C6 // 729 // complement component 6 /// NM_000436 // downstream // 313367 // Hs.177584 // OXCT // 5019 // 3-oxoacid CoA transferase	C6	C6 , rs9292806, complement component 6 ,p13.1
SNP_A-1718115	agagaaggggggaaaatattaattta[C/G]atcgaaaaaaaaaa agatgaacta	C	G	NM_000065 // upstream // 308798 // Hs.1282 // C6 // 729 // complement component 6 /// NM_000436 // downstream // 207759 // Hs.177584 // OXCT // 5019 // 3-oxoacid CoA transferase	C6	C6 , rs3851442, complement component 6 ,p13.1
SNP_A-1981435	agacttgtaattaccc[A/G]atgtgcttacatgaaa	A	G	NM_000436 // downstream // 3313 // Hs.278277 // OXCT1 // 5019 // Homo sapiens 3-oxoacid CoA transferase 1 (OXCT1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000321394 // upstream // 139101 // — // — // — /// ENST00000342023	OXCT1	OXCT1, Homo sapiens 3-oxoacid CoA transferase 1 (OXCT1), nuclear gene encoding mitochondrial protein, p13.1
SNP_A-1710457	cttgaaagattagataagttcaca[C/T]gaaatgcaagggtcca gcacttagt	C	T	NM_000436 // intron // 0 // Hs.177584 // OXCT // 5019 // 3-oxoacid CoA transferase	OXCT	OXCT, rs10512793, 3-oxoacid CoA transferase,p13.1
SNP_A-2268411	gaatgctgtgattatt[A/G]aaagaggcaatacctg	A	G	NM_000163 // upstream // 25561 // Hs.125180 // GHR // 2690 // Homo sapiens growth hormone receptor (GHR), mRNA. /// ENST00000327893 // upstream // 430285 // — // — // — /// ENST00000230882 // upstream // 25561 // — // — // — // — ///	GHR	GHR, Homo sapiens growth hormone receptor (GHR), p12
SNP_A-2213328	ccggaagcactatttta[G/T]atacactatgccacca	G	T	NM_004465 // upstream // 238026 // Hs.248049 // FGF10 // 2255 // Homo sapiens fibroblast growth factor 10 (FGF10), mRNA. /// NM_016640 // upstream // 182217 // Hs.124165 // MRPS30 // 10884 // Homo sapiens mitochondrial ribosomal protein S30 (MRPS30), nucl	FGF10	FGF10, Homo sapiens fibroblast growth factor 10 (FGF10), p12
SNP_A-1870550	tcgaggcatcaggcc[C/T]attttgtccttttatt	C	T	NM_016640 // downstream // 413982 // Hs.124165 // MRPS30 // 10884 // Homo sapiens mitochondrial ribosomal protein S30 (MRPS30), nuclear gene encoding mitochondrial protein, mRNA. /// NM_021072 // downstream // 32581 // Hs.353176 // HCN1 // 348980 // Homo	MRPS30	MRPS30, Homo sapiens mitochondrial ribosomal protein S30 (MRPS30), nuclear gene encoding mitochondrial protein, p12
SNP_A-1758245	aattctaaggctcaaaataactggt[A/G]aaactgaggttaaaattt tcaaaac	A	G	NM_016640 // downstream // 434194 // Hs.124165 // MRPS30 // 10884 // mitochondrial ribosomal protein S30 /// NM_021072 // downstream // 12369 // Hs.353176 // HCN1 // 348980 // hyperpolarization activated cyclic nucleotide-gated potassium channel 1	MRPS30	MRPS30, rs10512876, mitochondrial ribosomal protein S30 ,p12
SNP_A-1863112	tcatttagcttagag[A/G]aaatgaactttaaggc	A	G	NM_021072 // intron // 0 // Hs.353176 // HCN1 // 348980 // Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), mRNA. /// ENST00000303230 // intron // 0 // — // — // — // —	HCN1	HCN1, Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), p12
SNP_A-2135741	atcaaagaaagtctca[C/T]gacaaagtggtattc	C	T	NM_021072 // intron // 0 // Hs.353176 // HCN1 // 348980 // Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), mRNA. /// ENST00000303230 // intron // 0 // — // — // — // —	HCN1	HCN1, Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2034537	aaatctgtgtgtccaa[A/G]ctgaattcatttaacc	A	G	NM_021072 // intron // 0 // Hs.353176 // HCN1 // 348980 // Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), mRNA. /// ENST00000303230 // intron // 0 // — // — // — // —	HCN1	HCN1, Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), p12
SNP_A-2010876	tctccttcaggaaaaaa[C/T]tgttgcctaaaagta	C	T	NM_021072 // intron // 0 // Hs.353176 // HCN1 // 348980 // Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), mRNA. /// ENST00000303230 // intron // 0 // — // — // — // —	HCN1	HCN1, Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), p12
SNP_A-1836153	tactaggtgatatacа[C/G]atattccaaagactga	C	G	NM_021072 // intron // 0 // Hs.353176 // HCN1 // 348980 // Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), mRNA. /// ENST00000303230 // intron // 0 // — // — // — // —	HCN1	HCN1, Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 1 (HCN1), p12
SNP_A-2298296	gccatgtgggtaagaa[C/G]agaaattgagaaaata	C	G	NM_024615 // intron // 0 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// ENST00000281631 // intron // 0 // — // — // —	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-1933829	ttctatgtgtcctgа[C/T]taatagacttctcat	C	T	NM_024615 // intron // 0 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// ENST00000281631 // intron // 0 // — // — // — // —	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-1840815	tagctatgtatttatg[A/T]agagaaaaagcatggtg	A	T	NM_024615 // intron // 0 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// ENST00000281631 // intron // 0 // — // — // — // —	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-2179531	cacttataccatgcta[C/T]gaccaggaagtttaa	C	T	NM_024615 // intron // 0 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// ENST00000281631 // intron // 0 // — // — // — // —	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-1881076	tctttaaattgtaata[G/T]gcaggctgggcataat	G	T	NM_024615 // downstream // 144931 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// NM_002202 // upstream // 395858 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/home	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-2099108	agaggaccaccagtaa[A/G]taatttggttctggt	A	G	NM_024615 // downstream // 154855 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// NM_002202 // upstream // 385934 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/home	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-1981486	tcaccactctgttccac[A/G]gagaatttaaggaaaa	A	G	NM_024615 // downstream // 155707 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// NM_002202 // upstream // 385082 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/home	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-1981487	tttcaccatgaaaaaa[A/C]tagtgacatattcag	A	C	NM_024615 // downstream // 171623 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// NM_002202 // upstream // 369166 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/home	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1
SNP_A-1981489	tgatgctaacagcgta[A/C]gtttcttagaaaaccc	A	C	NM_024615 // downstream // 172907 // Hs.369581 // PARP8 // 79668 // Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), mRNA. /// NM_002202 // upstream // 367882 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/home	PARP8	PARP8, Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), q11.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2276015	gagagaaagccctgaa[C/T]gtatggtacaataaagc	C	T	NM_002202 // downstream // 998252 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA. /// NM_015946 // upstream // 395244 // Hs.519304 // PELO // 53918 // Homo sapiens pelota homolog (Drosophila) (	ISL1	ISL1, Homo sapiens ISL1 transcription factor, LIM q11.2
SNP_A-2022136	aaaaagctaaccaaga[C/T]ggtgttctgcttgatg	C	T	NM_002202 // downstream // 1108878 // Hs.505 // ISL1 // 3670 // Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA. /// NM_015946 // upstream // 284618 // Hs.519304 // PELO // 53918 // Homo sapiens pelota homolog (Drosophila)	ISL1	ISL1, Homo sapiens ISL1 transcription factor, LIM q11.2
SNP_A-2075296	acatcttgtattctca[A/G]tcgaacttctgctaaa	A	G	NM_181501 // intron // 0 // Hs.519304 // ITGA1 // 3672 // Homo sapiens integrin, alpha 1 (ITGA1), mRNA. /// ENST00000282588 // intron // 0 // --- // --- // --- // ---	ITGA1	ITGA1, Homo sapiens integrin, alpha 1 (ITGA1), q11.2
SNP_A-2199600	ccaaaaccacttcgaa[A/G]ttagacacacttaaaa	A	G	NM_183418 // upstream // 41954 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, mRNA. /// NM_004531 // upstream // 41954 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthesi	MOCS2	MOCS2, Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, q11.2
SNP_A-1949137	ttatgccatctgccaa[A/C]agagtattacacacca	A	C	NM_183418 // upstream // 151996 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, mRNA. /// NM_004531 // upstream // 151996 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthe	MOCS2	MOCS2, Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, q11.2
SNP_A-2226594	ctaagggacacagctg[A/G]atgacataatgtggac	A	G	NM_183418 // upstream // 158042 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, mRNA. /// NM_004531 // upstream // 158042 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthe	MOCS2	MOCS2, Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, q11.2
SNP_A-1800764	gtagaattgacaggaa[C/G]tgactaagggacacag	C	G	NM_183418 // upstream // 158062 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, mRNA. /// NM_004531 // upstream // 158062 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthe	MOCS2	MOCS2, Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, q11.2
SNP_A-1645954	gcctgtagcagccctaaattaggta[A/G]agacccagctttgttg ctttta	A	G	NM_004531 // upstream // 192625 // Hs.163645 // MOCS2 // 4338 // molybdenum cofactor synthesis 2 /// NM_006350 // upstream // 178645 // Hs.9914 // FST // 10468 // follistatin /// NM_013409 // upstream // 178645 // Hs.9914 // FST // 10468 // follistatin /	MOCS2	MOCS2, rs27313, molybdenum cofactor synthesis 2, q11.2
SNP_A-1981541	ttcaggttattgata[C/T]taagttgcacagagtg	C	T	NM_183418 // upstream // 190792 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, mRNA. /// NM_004531 // upstream // 190792 // Hs.163645 // MOCS2 // 4338 // Homo sapiens molybdenum cofactor synthe	MOCS2	MOCS2, Homo sapiens molybdenum cofactor synthesis 2 (MOCS2), transcript variant 2, q11.2
SNP_A-1691178	agctatcattataaccacatacaga[A/G]ctatacactagaaaccattccttcc	A	G	NM_002495 // intron // 0 // Hs.10758 // NDUFS4 // 4724 // NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	NDUFS4	NDUFS4, rs4453447, NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase),q11.2
SNP_A-2010885	cccaccatctggagaa[A/T]ctatgcaattcccctt	A	T	NM_002495 // downstream // 94507 // Hs.528222 // NDUFS4 // 4724 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA. /// NM_019087 // downstream // 106942 // Hs.152664 // ARFRP2 // 54622 // Homo	NDUFS4	NDUFS4, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), q11.2
SNP_A-2105888	agccatagtgaccaga[A/C]agttgaactctctatg	A	C	NM_002495 // downstream // 114397 // Hs.528222 // NDUFS4 // 4724 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA. /// NM_019087 // downstream // 87052 // Hs.152664 // ARFRP2 // 54622 // Homo	NDUFS4	NDUFS4, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2158580	atgtaggaacaaata[C/T]ctatgtgagttgaaga	C	T	NM_002495 // downstream // 187471 // Hs.528222 // NDUFS4 // 4724 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA. /// NM_019087 // downstream // 13978 // Hs.152664 // ARFRP2 // 54622 // Homo	NDUFS4	NDUFS4, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), q11.2
SNP_A-2081743	acctctctgatcccca[A/G]tagacatcaaaatcat	A	G	NM_002495 // downstream // 188261 // Hs.528222 // NDUFS4 // 4724 // Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA. /// NM_019087 // downstream // 13188 // Hs.152664 // ARFRP2 // 54622 // Homo	NDUFS4	NDUFS4, Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), q11.2
SNP_A-2295031	gcatactgtaaacacc[A/G]ataagaattgcatttt	A	G	NM_019087 // intron // 0 // Hs.152664 // ARFRP2 // 54622 // Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // — // — // —	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-1708368	ttctttctttcttatgacagaac[A/G]gtataaaacatagcaggctt atttt	A	G	NM_019087 // intron // 0 // Hs.152664 // ARFRP2 // 54622 // ADP-ribosylation factor related protein 2	ARFRP2	ARFRP2, rs9292042, ADP-ribosylation factor related protein 2,q11.2
SNP_A-2219297	ccigtcttgagctag[C/T]ctagaaaacagacgga	C	T	NM_019087 // intron // 0 // Hs.152664 // ARFRP2 // 54622 // Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // — // — // —	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-2170142	caaggtacatgggaac[A/G]ctaaagtgccggtgg	A	G	NM_019087 // intron // 0 // Hs.152664 // ARFRP2 // 54622 // Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // — // — // —	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-1836360	tactcagaaaggattc[C/G]acccacgcggcacttt	C	G	NM_019087 // intron // 0 // Hs.152664 // ARFRP2 // 54622 // Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// ENST00000332313 // intron // 0 // — // — // —	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-1681002	gagggaaagccatttgtaacagta[C/T]gtgtctttcaaatataa aatgtta	C	T	NM_019087 // intron // 0 // Hs.152664 // ARFRP2 // 54622 // ADP-ribosylation factor related protein 2	ARFRP2	ARFRP2, rs35943, ADP-ribosylation factor related protein 2,q11.2
SNP_A-2111170	cccgtgtgtttgtgggga[A/G]acaagtgactactgc	A	G	NM_019087 // upstream // 737 // Hs.152664 // ARFRP2 // 54622 // Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), mRNA. /// NM_006308 // upstream // 144305 // Hs.41707 // HSPB3 // 8988 // Homo sapiens heat shock 27kDa protein 3 (HSPB3), mRN	ARFRP2	ARFRP2, Homo sapiens ADP-ribosylation factor related protein 2 (ARFRP2), q11.2
SNP_A-2233313	ctcaggcctctccc[A/G]ggctttggatttattc	A	G	NM_006308 // downstream // 28004 // Hs.41707 // HSPB3 // 8988 // Homo sapiens heat shock 27kDa protein 3 (HSPB3), mRNA. /// NM_052870 // upstream // 33572 // Hs.432755 // SNAG1 // 112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mR	HSPB3	HSPB3, Homo sapiens heat shock 27kDa protein 3 (HSPB3), q11.2
SNP_A-1788062	gggagagaggcctgag[A/T]ccttgcaaagccagta	A	T	NM_006308 // downstream // 28021 // Hs.41707 // HSPB3 // 8988 // Homo sapiens heat shock 27kDa protein 3 (HSPB3), mRNA. /// NM_052870 // upstream // 33555 // Hs.432755 // SNAG1 // 112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mR	HSPB3	HSPB3, Homo sapiens heat shock 27kDa protein 3 (HSPB3), q11.2
SNP_A-1936165	ttcttcaactggacaa[A/G]gatgtattgagtacct	A	G	NM_052870 // downstream // 84000 // Hs.432755 // SNAG1 // 112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 // downstream // 84000 // — // — // — // — /// ENST00000326084 // downstream // 204275 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2
SNP_A-1870309	tctttggagtagaaa[A/G]tactaaatgaaactg	A	G	NM_052870 // downstream // 98806 // Hs.432755 // SNAG1 // 112574 // Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), mRNA. /// ENST00000326277 // downstream // 98806 // — // — // — // — /// ENST00000326084 // downstream // 189469 //	SNAG1	SNAG1, Homo sapiens sorting nexin associated golgi protein 1 (SNAG1), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1981606	tgattcattccttgcd[A/G]ctcatcatactgtat	A	G	NM_152623 // upstream // 51144 // Hs.529770 // FLJ37927 // 166979 // Homo sapiens CDC20-like protein (FLJ37927), mRNA. /// NM_021147 // downstream // 7000 // Hs.3041 // UNG2 // 10309 // Homo sapiens uracil-DNA glycosylase 2 (UNG2), mRNA. /// ENST00000002967	FLJ37927	FLJ37927, Homo sapiens CDC20-like protein (FLJ37927), q11.2
SNP_A-1822330	gttttgtagtagtttc[A/G]acttaaaaagtacac	A	G	NM_015360 // intron // 0 // Hs.274531 // KIAA0052 // 23517 // Homo sapiens KIAA0052 (KIAA0052), mRNA. /// ENST00000230640 // intron // 0 // — // — // —	KIAA0052	KIAA0052, Homo sapiens KIAA0052 (KIAA0052), q11.2
SNP_A-2140873	atctgacaaaatagac[C/T]gaaaaccaatacaact	C	T	NM_015360 // intron // 0 // Hs.274531 // KIAA0052 // 23517 // Homo sapiens KIAA0052 (KIAA0052), mRNA. /// ENST00000230640 // intron // 0 // — // — // — // —	KIAA0052	KIAA0052, Homo sapiens KIAA0052 (KIAA0052), q11.2
SNP_A-1783602	ggcatggagtcctggg[A/C]agagactggcagcgat	A	C	NM_024669 // intron // 0 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// ENST00000341048 // intron // 0 // — // — // — // —	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-2258789	ctttgtgccactaaa[A/G]ataatctcatagaaag	A	G	NM_024669 // intron // 0 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// ENST00000341048 // intron // 0 // — // — // —	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-1981623	tatacagtcaaattgg[C/T]agaatagcctctctc	C	T	NM_024669 // upstream // 146886 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 30511 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795)	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-2206704	ccatgagttgccccca[A/G]accaatcttctgaag	A	G	NM_024669 // upstream // 241334 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 124959 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-1981633	tattcattcattgata[C/G]attggttacttcaga	C	G	NM_024669 // upstream // 241360 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 124985 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-2129100	ataattcatttttccaa[A/T]agcaccagaaactacag	A	T	NM_024669 // upstream // 258660 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /// NM_024669 // upstream // 142285 // Hs.436214 // FLJ11795 // 79722 // Homo sapiens hypothetical protein FLJ11795 (FLJ11795	FLJ11795	FLJ11795, Homo sapiens hypothetical protein FLJ11795 (FLJ11795), q11.2
SNP_A-2203057	ccactgatggaaacac[C/T]agatgatgtgactact	C	T	AF042838 // upstream // 230999 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 118664 // — // — // — /// ENST00000264777 // upstream // 230999 // — // — // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2
SNP_A-1981650	aattatatgtgtgaga[C/T]gatctgccatgaacta	C	T	AF042838 // upstream // 211263 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 138400 // — // — // — /// ENST00000264777 // upstream // 211263 // — // — // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2
SNP_A-1733376	aggtcctccccagtatggtccttca[A/G]gaattatttcttttttgttttt c	A	G	AF042838 // upstream // 126154 // Hs.170610 // MAP3K1 // 4214 // mitogen-activated protein kinase kinase kinase 1	MAP3K1	MAP3K1, , rs9282978, mitogen-activated protein kinase kinase kinase 1,q11.2
SNP_A-1840339	tagcatgatggtaaca[A/C]aggtcataaccaccct	A	C	AF042838 // upstream // 133408 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 216255 // — // — // — /// ENST00000264777 // upstream // 133408 // — // — // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2
SNP_A-1981658	gtgtggctaaagatca[A/G]caggcccaagtggtag	A	G	AF042838 // upstream // 125283 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 224380 // — // — // — /// ENST00000264777 // upstream // 125283 // — // — // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1901276	tggatggatttggtg[A/T]caatcttgaattagaa	A	T	AF042838 // upstream // 124263 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 225400 // — // — // — // — /// ENST00000264777 // upstream // 124263 // — // — // — // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2
SNP_A-2087179	actgatgtaaagaaag[C/G]catgacttctagatg	C	G	AF042838 // upstream // 124229 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 225434 // — // — // — // — /// ENST00000264777 // upstream // 124229 // — // — // — // -	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2
SNP_A-1882316	tgaaaacagcaatatct[A/G]cagctaacacttagg	A	G	AF042838 // upstream // 18152 // Hs.508461 // MAP3K1 // 4214 // Homo sapiens MEK kinase 1 (MEKK1) mRNA, partial cds. /// ENST00000325646 // upstream // 331511 // — // — // — // — /// ENST00000264777 // upstream // 18152 // — // — // — // —	MAP3K1	MAP3K1, Homo sapiens MEK kinase 1 (MEKK1) partial cds, q11.2
SNP_A-1668632	aaagccaggactcgcaggctct[C/T]acccacaataatga accactatcta	C	T	NM_022913 // upstream // 155571 // Hs.71252 // DKFZp761C169 // 65056 // vasculin /// NM_152622 // upstream // 67413 // Hs.419195 // FLJ35954 // 166968 // hypothetical protein FLJ35954	DKFZp761C169	DKFZp761C169 , rs4700657, vasculin, q11.2
SNP_A-1937845	ttgaatatacacatta[G/T]ctattcaagttaaaag	G	T	NM_152622 // upstream // 99672 // Hs.419195 // FLJ35954 // 166968 // Homo sapiens hypothetical protein FLJ35954 (FLJ35954), mRNA. /// NM_022913 // upstream // 122322 // Hs.444279 // DKFZp761C169 // 65056 // Homo sapiens vasculin (DKFZp761C169), mRNA. ///	FLJ35954	FLJ35954, Homo sapiens hypothetical protein FLJ35954 (FLJ35954), q11.2
SNP_A-1981676	attggcaaatactaca[A/G]ccaaaatagccctcct	A	G	NM_152622 // upstream // 101748 // Hs.419195 // FLJ35954 // 166968 // Homo sapiens hypothetical protein FLJ35954 (FLJ35954), mRNA. /// NM_022913 // upstream // 120246 // Hs.444279 // DKFZp761C169 // 65056 // Homo sapiens vasculin (DKFZp761C169), mRNA. ///	FLJ35954	FLJ35954, Homo sapiens hypothetical protein FLJ35954 (FLJ35954), q11.2
SNP_A-1981677	ctcagctatcaacatc[A/G]ctgaaccacaagttgg	A	G	NM_152622 // upstream // 101813 // Hs.419195 // FLJ35954 // 166968 // Homo sapiens hypothetical protein FLJ35954 (FLJ35954), mRNA. /// NM_022913 // upstream // 120181 // Hs.444279 // DKFZp761C169 // 65056 // Homo sapiens vasculin (DKFZp761C169), mRNA. ///	FLJ35954	FLJ35954, Homo sapiens hypothetical protein FLJ35954 (FLJ35954), q11.2
SNP_A-1981679	ggtttccagaatacaa[C/T]ggctacagactggagg	C	T	NM_152622 // upstream // 102495 // Hs.419195 // FLJ35954 // 166968 // Homo sapiens hypothetical protein FLJ35954 (FLJ35954), mRNA. /// NM_022913 // upstream // 119499 // Hs.444279 // DKFZp761C169 // 65056 // Homo sapiens vasculin (DKFZp761C169), mRNA. ///	FLJ35954	FLJ35954, Homo sapiens hypothetical protein FLJ35954 (FLJ35954), q11.2
SNP_A-2150947	atgtggtagaaatttc[C/G]aggcgttaaaattgat	C	G	NM_152622 // upstream // 110197 // Hs.419195 // FLJ35954 // 166968 // Homo sapiens hypothetical protein FLJ35954 (FLJ35954), mRNA. /// NM_022913 // upstream // 111797 // Hs.444279 // DKFZp761C169 // 65056 // Homo sapiens vasculin (DKFZp761C169), mRNA. ///	FLJ35954	FLJ35954, Homo sapiens hypothetical protein FLJ35954 (FLJ35954), q11.2
SNP_A-1731549	aaaagaattcctcatgatattgtca[C/T]ctaatttttctaggtcact agagc	C	T	BC020897 // upstream // 115425 // Hs.119998 // - // - // Clone IMAGE:4714787, mRNA, partial cds /// NM_022913 // downstream // 291332 // Hs.71252 // DKFZp761C169 // 65056 // vasculin	-	-, rs1423142, Clone IMAGE:4714787, mRNA, partial cds, q11.2
SNP_A-2261733	gaaagtgcagcagtac[A/G]gatagccattaatgtt	A	G	NM_006622 // downstream // 835553 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 135727 // — // — // — // — /// ENST00000274289 // downstream // 835553 // — // — // -	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-2010905	gggagtgcaaggacaga[G/T]catagagaaggaactc	G	T	NM_006622 // downstream // 817787 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 153493 // — // — // — // — /// ENST00000274289 // downstream // 817787 // — // — // -	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2053610	aagtggaagctctcaa[A/G]cacaggaaagaatgtg	A	G	NM_006622 // downstream // 802673 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 168607 // --- // --- // --- /// ENST00000274289 // downstream // 802673 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1954624	ttgcggacactctta[A/G]caatgtttctagatca	A	G	NM_006622 // downstream // 761308 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 209972 // --- // --- // --- /// ENST00000274289 // downstream // 761308 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1981696	agtgataatagaagtc[C/T]ctgaaaagtcaaatgg	C	T	NM_006622 // downstream // 472292 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 498988 // --- // --- // --- /// ENST00000274289 // downstream // 472292 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1922011	ttactgattactgtaa[C/T]aaattcatgacagccc	C	T	NM_006622 // downstream // 467808 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 503472 // --- // --- // --- /// ENST00000274289 // downstream // 467808 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1823692	taaaatatgcaaatgg[A/C]acagaaatagattccc	A	C	NM_006622 // downstream // 452484 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 518796 // --- // --- // --- /// ENST00000274289 // downstream // 452484 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1845540	tatagatcgcaaaact[G/T]aatcttagaaaagtca	G	T	NM_006622 // downstream // 354127 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 617153 // --- // --- // --- /// ENST00000274289 // downstream // 354127 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-2163729	caaaaatggataaaaa[C/T]caatgagctaaaaatt	C	T	NM_006622 // downstream // 289568 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 681712 // --- // --- // --- /// ENST00000274289 // downstream // 289568 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-1848128	tatcttatcatctcag[A/G]cacttcagatcatctc	A	G	NM_006622 // downstream // 131909 // Hs.398157 // PLK2 // 10769 // Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA. /// ENST00000306758 // upstream // 839371 // --- // --- // --- /// ENST00000274289 // downstream // 131909 // --- // ---	PLK2	PLK2, Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), q11.2
SNP_A-2073641	acagtcaagcctactt[A/T]aagagattgtcataaa	A	T	NM_138453 // intron // 0 // Hs.482173 // RAB3C // 115827 // Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1981734	ctaggaatgaaactta[C/T]gtaggtccatgttcgg	C	T	NM_138453 // intron // 0 // Hs.482173 // RAB3C // 115827 // Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1981739	cccacctttattcata[A/G]cagacaacactatcca	A	G	NM_138453 // intron // 0 // Hs.482173 // RAB3C // 115827 // Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1981744	ctctagataaatgagat[C/T]acttccaataaaacag	C	T	NM_138453 // intron // 0 // Hs.482173 // RAB3C // 115827 // Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// ENST00000282878 // intron // 0 // --- // --- // ---	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-2125704	agtttgaactgaagat[A/G]aagagtgaacacattt	A	G	NM_138453 // downstream // 7950 // Hs.482173 // RAB3C // 115827 // Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA. /// NM_006203 // downstream // 111356 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosp	RAB3C	RAB3C, Homo sapiens RAB3C, member RAS oncogene family (RAB3C), q11.2
SNP_A-1669985	actataagaattgtaictctcggc[C/T]ctattcaaatttctcttctaa atta	C	T	NM_006203 // intron // 0 // Hs.28482 // PDE4D // 5144 // phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	PDE4D	PDE4D , rs9283720, phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila),q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1684928	tcattaaatttggtgaagccaagtc[G/T]gactataagaattgtatct ctctgg	G	T	NM_006203 // intron // 0 // Hs.28482 // PDE4D // 5144 // phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	PDE4D	PDE4D, rs9292189, phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila),q11.2
SNP_A-1785381	ggctatgctacaagaa[A/G]tccatgttaacttcac	A	G	NM_006203 // intron // 0 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // — // — // — /// ENST00000360047 /	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-1981758	atattcaataacttgc[G/T]ccataggtgacaggat	G	T	NM_006203 // intron // 0 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // — // — // — /// ENST00000360047 /	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-1981759	atggtgatagtaacca[C/T]gatcttaattcaag	C	T	NM_006203 // intron // 0 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // — // — // — /// ENST00000360047 /	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-1981765	gcgcaaacagaggaaa[C/T]ggcaaggaataagact	C	T	NM_006203 // intron // 0 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // — // — // — /// ENST00000360047 /	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-2159777	atttagtcaattggca[A/C]gtagaaaattaaaaag	A	C	NM_006203 // intron // 0 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000317118 // intron // 0 // — // — // — /// ENST00000360047 /	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q11.2
SNP_A-1928334	ttcaccagagattcca[C/T]gacttgtagttcct	C	T	NM_006203 // intron // 0 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// ENST00000340635 // intron // 0 // — // — // —	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q12.1
SNP_A-2041448	aacctccctctcca[A/G]gtgagacactgttagt	A	G	NM_006203 // upstream // 1094442 // Hs.117545 // PDE4D // 5144 // Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA. /// NM_006203 // upstream // 1035019 // Hs.117545 // PDE4D // 5144 // Homo s	PDE4D	PDE4D, Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), q12.1
SNP_A-1843663	tagtggtctttaaca[A/T]gtgttctctgaagtaa	A	T	NM_000082 // downstream // 60137 // Hs.435237 // ERCC8 // 1161 // Homo sapiens Cockayne syndrome 1 (classical) (CKN1), mRNA. /// ENST00000296596 // upstream // 26329 // — // — // — /// ENST00000265038 // downstream // 60137 // — // — // -	ERCC8	ERCC8, Homo sapiens Cockayne syndrome 1 (classical) (CKN1), q12.1
SNP_A-1797442	ggtttacttcctgataa[A/G]taatttgataagctt	A	G	NM_000082 // intron // 0 // Hs.435237 // ERCC8 // 1161 // Homo sapiens Cockayne syndrome 1 (classical) (CKN1), mRNA. /// ENST00000265038 // intron // 0 // — // — // —	ERCC8	ERCC8, Homo sapiens Cockayne syndrome 1 (classical) (CKN1), q12.1
SNP_A-1886943	tgacttcatattgaca[A/G]actgacttggaatatc	A	G	NM_174889 // intron // 0 // Hs.180848 // LOC91942 // 91942 // Homo sapiens hypothetical protein LOC91942 (LOC91942), mRNA. /// ENST00000296597 // intron // 0 // — // — // —	LOC91942	LOC91942, Homo sapiens hypothetical protein LOC91942 (LOC91942), q12.1
SNP_A-2229643	ctagtacaacacgttta[C/G]ctacaaccaaattcat	C	G	NM_152789 // downstream // 6092 // Hs.489105 // MGC40405 // 257415 // Homo sapiens hypothetical protein MGC40405 (MGC40405), mRNA. /// AB046797 // upstream // 139397 // Hs.18564 // ZSWIM6 // 57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. //	MGC40405	MGC40405, Homo sapiens hypothetical protein MGC40405 (MGC40405), q12.1
SNP_A-2079174	acccaggtgtcatgta[A/G]ccgccaataatttgga	A	G	AB046797 // intron // 0 // Hs.18564 // ZSWIM6 // 57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// ENST00000252744 // intron // 0 // — // — // —	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds, q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2216136	cctcccctaatcacta[C/T]gttcacatcatgctcc	C	T	AB046797 // downstream // 29160 // Hs.18564 // ZSWIM6 // 57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 111552 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// ENS	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. ,q12.1
SNP_A-2162546	attttcccttattcca[C/T]cagtgccactgggaga	C	T	AB046797 // downstream // 56160 // Hs.18564 // ZSWIM6 // 57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 84552 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// ENST	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. ,q12.1
SNP_A-1981826	aaaaggagtgattgta[A/G]gaagtcatataaatgg	A	G	AB046797 // downstream // 62564 // Hs.18564 // ZSWIM6 // 57688 // Homo sapiens mRNA for KIAA1577 protein, partial cds. /// NM_173667 // upstream // 78148 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// ENST	ZSWIM6	ZSWIM6, Homo sapiens for KIAA1577 protein, partial cds. ,q12.1
SNP_A-2264422	gaagaaacaaaactat[A/C]actcttcatagctgct	A	C	NM_173667 // downstream // 90263 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 509453 // Hs.113319 // KIF2 // 3796 // Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. /// E	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-1785306	ggctagggcctgttga[A/G]gactattgacatgaag	A	G	NM_173667 // downstream // 91646 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 508070 // Hs.113319 // KIF2 // 3796 // Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. /// E	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-1981844	atttcaaatgagctac[C/G]attttattgaatatct	C	G	NM_173667 // downstream // 99189 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 500527 // Hs.113319 // KIF2 // 3796 // Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. /// E	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-1981852	actagttttcctaaga[A/C]tccagctcaacttacc	A	C	NM_173667 // downstream // 417096 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 182620 // Hs.113319 // KIF2 // 3796 // Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. ///	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-1808642	gtgaacccaaaatagc[A/G]gccaatgaaagcaaac	A	G	NM_173667 // downstream // 570627 // — // FLJ37543 // 285668 // Homo sapiens hypothetical protein FLJ37543 (FLJ37543), mRNA. /// NM_004520 // upstream // 29089 // Hs.113319 // KIF2 // 3796 // Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. /// E	FLJ37543	FLJ37543, Homo sapiens hypothetical protein FLJ37543 (FLJ37543), q12.1
SNP_A-2305281	gctgagctcctgagag[A/C]aagaaatgaatgggag	A	C	NM_016338 // intron // 0 // Hs.482269 // IPO11 // 51194 // Homo sapiens importin 11 (IPO11), mRNA. /// ENST00000325324 // intron // 0 // — // — // — // —	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1
SNP_A-1652154	gcatctatagaatttaaaataccaa[A/T]gttagtatgtcatctgtag agacag	A	T	NM_016338 // intron // 0 // Hs.441043 // IPO11 // 51194 // importin 11	IPO11	IPO11 , rs32186, importin 11,q12.1
SNP_A-2205712	ccataactccaagata[C/G]gtggacatcactacag	C	G	NM_016338 // CDS // 0 // Hs.482269 // IPO11 // 51194 // Homo sapiens importin 11 (IPO11), mRNA. /// ENST00000325324 // CDS // 0 // — // — // — // —	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1
SNP_A-1929262	ttcagtaattacgtca[A/T]tcttgaactgtattgt	A	T	NM_016338 // intron // 0 // Hs.482269 // IPO11 // 51194 // Homo sapiens importin 11 (IPO11), mRNA. /// ENST00000325324 // intron // 0 // — // — // — // —	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1
SNP_A-2221876	ccttttgtttgctgga[C/T]gtcaatgcccagaaca	C	T	NM_016338 // downstream // 106957 // Hs.482269 // IPO11 // 51194 // Homo sapiens importin 11 (IPO11), mRNA. /// NM_001826 // upstream // 223055 // Hs.374378 // CKS1B // 1163 // Homo sapiens CDC28 protein kinase regulatory subunit 1B (CKS1B), mRNA. /// NM_	IPO11	IPO11, Homo sapiens importin 11 (IPO11), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1824728	taaagaggaggatcaaa[C/T]agttatctctacatg	C	T	NM_000524 // downstream // 1076867 // Hs.247940 // HTR1A // 3350 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA. /// ENST00000315260 // upstream // 106321 // --- // --- // --- /// ENST00000323865 // downstream // 1076867	HTR1A	HTR1A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), q12.1
SNP_A-1878571	tctgtgtataaggcaa[C/T]gtcacctgggaggcca	C	T	NM_178532 // intron // 0 // Hs.98890 // RNF180 // 285671 // Homo sapiens hypothetical protein LOC285671 (LOC285671), mRNA. /// ENST00000296615 // intron // 0 // --- // --- // ---	RNF180	RNF180, Homo sapiens hypothetical protein LOC285671 (LOC285671), q12.3
SNP_A-1647162	aagacttgtgacttgccgacagaac[A/C]atttaaaatagctgtttg aggaaaa	A	C	NM_173829 // intron // 0 // Hs.438642 // FLJ36754 // 285672 // hypothetical protein FLJ36754	FLJ36754	FLJ36754, rs1584164, hypothetical protein FLJ36754,q12.3
SNP_A-2143702	atgagaagaaaatctac[A/G]atgtgctaggaacttt	A	G	NM_005869 // intron // 0 // Hs.371372 // SDCCAG10 // 10283 // Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA. /// ENST00000303778 // intron // 0 // --- // --- // ---	SDCCAG10	SDCCAG10, Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), q12.3
SNP_A-2032262	aaagttaaagcctctat[C/T]gttgtctagtagact	C	T	NM_005869 // intron // 0 // Hs.371372 // SDCCAG10 // 10283 // Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA. /// ENST00000303778 // intron // 0 // --- // --- // ---	SDCCAG10	SDCCAG10, Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), q12.3
SNP_A-2285929	gatgagtaggttcgtg[G/T]agaaggataataatag	G	T	NM_015342 // intron // 0 // Hs.121432 // KIAA0073 // 23398 // Homo sapiens KIAA0073 protein (KIAA0073), mRNA. /// ENST00000261308 // intron // 0 // --- // --- // ---	KIAA0073	KIAA0073, Homo sapiens KIAA0073 protein (KIAA0073), q12.3
SNP_A-1713157	aattgaattggctcttacttacta[C/T]ggcatccatttttgaggaac gccta	C	T	NM_024941 // intron // 0 // Hs.184664 // FLJ13611 // 80006 // hypothetical protein FLJ13611	FLJ13611	FLJ13611, rs37253, hypothetical protein FLJ13611,q12.3
SNP_A-2261518	gaaaggatgcagaggga[C/G]aggacgagactgtaa	C	G	NM_033228 // intron // 0 // Hs.792 // TRIM23 // 373 // Homo sapiens tripartite motif-containing 23 (TRIM23), transcript variant gamma, mRNA. /// NM_033227 // intron // 0 // Hs.792 // TRIM23 // 373 // Homo sapiens tripartite motif-containing 23 (TRIM23), t	TRIM23	TRIM23, Homo sapiens tripartite motif-containing 23 (TRIM23), transcript variant gamma, q12.3
SNP_A-1923755	ttagtaatcagtgtca[A/G]tatcatttcatcaatt	A	G	NM_024941 // intron // 0 // Hs.482301 // FLJ13611 // 80006 // Homo sapiens hypothetical protein FLJ13611 (FLJ13611), mRNA. /// ENST00000341986 // intron // 0 // --- // --- // --- /// ENST00000231526 // intron // 0 // --- // --- // ---	FLJ13611	FLJ13611, Homo sapiens hypothetical protein FLJ13611 (FLJ13611), q12.3
SNP_A-1753871	tagcgtagttcttctatactcaa[A/C]atactgtagctgagttcat ggtgt	A	C	NM_020726 // intron // 0 // Hs.22151 // NLN // 57486 // neurolysin (metallopeptidase M3 family)	NLN	NLN , rs2247193, neurolysin (metallopeptidase M3 family),q12.3
SNP_A-2100609	agatacatttttcaca[C/T]aggagagacctaaata	C	T	NM_020726 // intron // 0 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // intron // 0 // --- // --- // ---	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1641865	aatttgttctctaatttctgaatc[A/G]aagaatttaaaaacatacatt ggaa	A	G	NM_020726 // intron // 0 // Hs.22151 // NLN // 57486 // neurolysin (metallopeptidase M3 family)	NLN	NLN , rs2561195, neurolysin (metallopeptidase M3 family),q12.3
SNP_A-2197428	catccattgttccca[G/T]attcttacattaat	G	T	NM_020726 // intron // 0 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // intron // 0 // --- // --- // ---	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2041978	aactaatttgaggaa[A/G]tgctacaccaggaatg	A	G	NM_020726 // intron // 0 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // intron // 0 // --- // --- // ---	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2115433	aggggacaaagtcta[C/T]atcaggtggcaaaacg	C	T	NM_020726 // 3UTR // 0 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// ENST00000340159 // 3UTR // 0 // --- // --- // ---	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1870006	tccttgatccaatcaa[A/C]cttcagtgagctcatg	A	C	NM_020726 // downstream // 56160 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 43485 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2280504	gaggtaacaaggatgc[A/C]caagtagattacctga	A	C	NM_020726 // downstream // 60543 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 39102 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1981943	gaaaaaggagaataaaa[A/G]gccatgtggttcattg	A	G	NM_020726 // downstream // 63260 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 36385 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2251998	cttccaagatgagtta[C/T]atattaggcaaagtga	C	T	NM_020726 // downstream // 67951 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 31694 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2145418	atgcagcatttacact[A/G]agatctgaaactgagt	A	G	NM_020726 // downstream // 69137 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 30508 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1785546	ggctcagtgcaatttc[C/T]aatacgttataatatg	C	T	NM_020726 // downstream // 71845 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 27800 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2255397	cttgtcagactaggac[C/T]gagccattctagcagc	C	T	NM_020726 // downstream // 75973 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 23672 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1907828	tgtaagtggaatgcta[C/T]tgtgtattatcatgtct	C	T	NM_020726 // downstream // 78751 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 20894 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2187830	cagtagtgagtttgca[C/T]agctcccaaatttcca	C	T	NM_020726 // downstream // 80560 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 19085 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-2034644	aaatgaaacagtgtac[A/T]ggaagctgctaataa	A	T	NM_020726 // downstream // 80685 // Hs.247460 // NLN // 57486 // Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA. /// NM_018695 // upstream // 18960 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRN	NLN	NLN, Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), q12.3
SNP_A-1906605	tggtgtatatgtgaca[A/G]ggccctaatttctaa	A	G	NM_018695 // intron // 0 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2 interacting protein (ERBB2IP), mRNA. /// AF263744 // intron // 0 // Hs.519346 // ERBB2IP // 55914 // Homo sapiens erbb2-interacting protein ERBIN mRNA, complete cds. /// ENST0	ERBB2IP	ERBB2IP, Homo sapiens erbb2 interacting protein (ERBB2IP), q12.3
SNP_A-2196014	catgtctccataggtc[A/G]ccctccagcttggcca	A	G	NM_139168 // downstream // 139297 // Hs.519347 // SFRS12 // 140890 // Homo sapiens splicing factor, arginine/serine-rich 12 (SFRS12), mRNA. /// NM_139168 // downstream // 137599 // Hs.519347 // SFRS12 // 140890 // Homo sapiens splicing factor, arginine/se	SFRS12	SFRS12, Homo sapiens splicing factor, arginine q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072771	acagctcagcaattac[A/G]ctctacataatctttt	A	G	NM_198828 // intron // 0 // Hs.482329 // LOC375449 // 375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine q12.3
SNP_A-2213839	cctaaagacctcctta[A/G]cttagtgggcaagcct	A	G	NM_198828 // intron // 0 // Hs.482329 // LOC375449 // 375449 // Homo sapiens similar to microtubule associated testis specific serine/threonine protein kinase (LOC375449), mRNA. /// ENST00000354187 // intron // 0 // --- // --- // --- // ---	LOC375449	LOC375449, Homo sapiens similar to microtubule associated testis specific serine q12.3
SNP_A-1982005	tgaaattgaggaagta[C/G]ggaggtggcctcacct	C	G	NM_005582 // upstream // 814164 // Hs.87205 // LY64 // 4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 215686 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-k	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-2285396	gatctgttgatgaatc[C/T]gaaattggaagctctg	C	T	NM_005582 // upstream // 954523 // Hs.87205 // LY64 // 4064 // Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), mRNA. /// NM_181523 // upstream // 75327 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-ki	LY64	LY64, Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kDa (mouse) (LY64), q13.1
SNP_A-1982011	agtggaaaagtaagac[A/T]ctatcgtacagggagg	A	T	NM_181523 // intron // 0 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// ENST00000274335 // intron // 0 // --- // --- // --- // ---	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2298315	gccattaagctttgta[G/T]gactgcacatgacatt	G	T	NM_181523 // intron // 0 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// ENST00000274335 // intron // 0 // --- // --- // --- // ---	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1680700	ccatcttggacttctgcctctcaga[C/T]gttaaggtgataaacttgtatggtt	C	T	NM_022902 // upstream // 774989 // Hs.438748 // SLC30A5 // 64924 // solute carrier family 30 (zinc transporter), member 5 /// NM_024055 // upstream // 774925 // Hs.438748 // SLC30A5 // 64924 // solute carrier family 30 (zinc transporter), member 5 /// NM	SLC30A5	SLC30A5 , rs391974, solute carrier family 30 (zinc transporter), member 5 ,q13.1
SNP_A-2283645	gatagagtgtcaagaa[A/G]aaacctggaaggtacc	A	G	NM_181523 // downstream // 8237 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 11485 // Hs.132225 // PIK3R1 // 5295 // Homo sa	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1982013	ggttgcccttcagcag[A/G]caattaagaaagacat	A	G	NM_181523 // downstream // 38410 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 41658 // Hs.132225 // PIK3R1 // 5295 // Homo s	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2211147	cccgtctgtataaata[C/T]gtgttcagagacttca	C	T	NM_181523 // downstream // 110057 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 113305 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2153214	attactgaagaccaaa[A/C]ggcatcatagcatgat	A	C	NM_181523 // downstream // 115558 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 118806 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1948177	tttagcataaccccac[A/G]gtagaatcaataacgg	A	G	NM_181523 // downstream // 325811 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 329059 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982019	cctttaagaagagagc[A/G]cttaaagagtaaggt	A	G	NM_181523 // downstream // 345233 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 348481 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-1982025	atgctgctcactgag[A/G]aactgagagaccagct	A	G	NM_181523 // downstream // 408867 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 412115 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2181090	cagacactgtctaact[C/T]acttggagcctgagg	C	T	NM_181523 // downstream // 507001 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 510249 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2107969	agctcctgtcactcca[C/T]tggctttgtctctgg	C	T	NM_181523 // downstream // 517289 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 520537 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2243396	ctgcggaaataagcac[A/G]aatgggctctgttgga	A	G	NM_181523 // downstream // 654553 // Hs.132225 // PIK3R1 // 5295 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, mRNA. /// NM_181524 // downstream // 657801 // Hs.132225 // PIK3R1 // 5295 // Homo	PIK3R1	PIK3R1, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1), transcript variant 1, q13.1
SNP_A-2010944	tctgtagtctagtgta[A/G]taactggctcatagta	A	G	NM_001799 // intron // 0 // Hs.184298 // CDK7 // 1022 // Homo sapiens cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) (CDK7), mRNA. /// ENST00000256443 // intron // 0 // — // — // —	CDK7	CDK7, Homo sapiens cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) (CDK7), q13.2
SNP_A-1863314	tcattttaccacttca[A/G]tcactaaagccagtaa	A	G	NM_018429 // intron // 0 // Hs.258272 // BDP1 // 55814 // Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA. /// ENST00000358731 // intron // 0 // — // — // — // —	BDP1	BDP1, Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), q13.2
SNP_A-1879532	tcttcaaaatctttac[A/G]cgattgatcttccatg	A	G	NM_018429 // CDS // 0 // Hs.258272 // BDP1 // 55814 // Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA. /// ENST00000358731 // CDS // 0 // — // — // — // — /// ENST00000320952 // CDS /	BDP1	BDP1, Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), q13.2
SNP_A-1957310	tttagagattttaa[A/G]tgttggacttaag	A	G	NM_018429 // intron // 0 // Hs.258272 // BDP1 // 55814 // Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), mRNA. /// ENST00000358731 // intron // 0 // — // — // — // — /// ENST00000320952 //	BDP1	BDP1, Homo sapiens B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB (BDP1), q13.2
SNP_A-1747513	ttaatccaggtataagaggtttag[A/G]cgttcttactatggactg catag	A	G	AB051476 // CDS // 0 // Hs.272808 // BDP1 // 55814 // B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	BDP1	BDP1, rs277941, B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB,q13.2
SNP_A-2251236	cttcaagaacctatc[C/T]aacctgttcaactatt	C	T	NM_022132 // intron // 0 // Hs.167531 // MCCC2 // 64087 // Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), mRNA. /// ENST00000340941 // intron // 0 // — // — // — // — /// ENST00000323375 // intron // 0 // — // — // — /	MCCC2	MCCC2, Homo sapiens methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (MCCC2), q13.2
SNP_A-1641991	aatcacaagtgtagtgatttaaaca[C/G]ggtatcagtggctttac gcatccat	C	G	NM_004291 // downstream // 7580 // Hs.1707 // CART // 9607 // cocaine- and amphetamine-regulated transcript /// NM_005909 // upstream // 378688 // Hs.103042 // MAP1B // 4131 // microtubule-associated protein 1B /// NM_032010 // upstream // 454867 // Hs.1	CART	CART, rs7731217, cocaine- and amphetamine-regulated transcript, q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138961	atccgcagcgtcagaag[A/G]aagctgtattgtctga	A	G	NM_004291 // downstream // 222989 // Hs.1707 // CART // 9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 163320 // Hs.335079 // MAP1B // 4131 // Homo sapiens microtubule-associated protein 1B (M	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-1846698	tatcaaaaggaaagaaa[A/G]agatgaggaaatagcat	A	G	NM_004291 // downstream // 290508 // Hs.1707 // CART // 9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 95801 // Hs.335079 // MAP1B // 4131 // Homo sapiens microtubule-associated protein 1B (MA	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-1869077	tcctgccatgagaaat[G/T]aaagtcagacaaagac	G	T	NM_004291 // downstream // 321216 // Hs.1707 // CART // 9607 // Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA. /// NM_005909 // upstream // 65093 // Hs.335079 // MAP1B // 4131 // Homo sapiens microtubule-associated protein 1B (MA	CART	CART, Homo sapiens cocaine- and amphetamine-regulated transcript (CART), q13.2
SNP_A-1860201	tcagtccagtggacaa[C/G]aaatgggagctgaatt	C	G	NM_152625 // intron // 0 // Hs.370303 // ZNF366 // 167465 // Homo sapiens zinc finger protein 366 (ZNF366), mRNA. /// ENST00000318442 // intron // 0 // --- // --- // ---	ZNF366	ZNF366, Homo sapiens zinc finger protein 366 (ZNF366), q13.2
SNP_A-2264346	gaacttactgagtaa[C/G]agaacagcttgcggga	C	G	NM_152625 // upstream // 201437 // Hs.370303 // ZNF366 // 167465 // Homo sapiens zinc finger protein 366 (ZNF366), mRNA. /// NM_002270 // upstream // 107922 // Hs.482497 // TNPO1 // 3842 // Homo sapiens transportin 1 (TNPO1), transcript variant 1, mRNA. /	ZNF366	ZNF366, Homo sapiens zinc finger protein 366 (ZNF366), q13.2
SNP_A-1982080	aagagatatagtcgct[A/G]aacactaggtcatata	A	G	NM_173490 // upstream // 23736 // Hs.162246 // LOC134285 // 134285 // Homo sapiens hypothetical protein LOC134285 (LOC134285), mRNA. /// ENST00000287761 // downstream // 58726 // --- // --- // --- /// ENST00000341845 // downstream // 6318 // --- //	LOC134285	LOC134285, Homo sapiens hypothetical protein LOC134285 (LOC134285), q13.2
SNP_A-1953163	tttcttcaattctga[C/G]ctctcccttcagttac	C	G	NM_153217 // downstream // 103119 // Hs.508588 // MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream // 220190 // Hs.529798 // BTF3 // 689 // Homo sapiens basic transcription factor 3 (BTF3), mRNA.	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-2027594	aaaccagccctaaata[A/C]acattgagaagacca	A	C	NM_153217 // downstream // 107478 // Hs.508588 // MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream // 215831 // Hs.529798 // BTF3 // 689 // Homo sapiens basic transcription factor 3 (BTF3), mRNA.	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-1787529	gggaatgagactgcta[C/T]atcatgttaagtgttt	C	T	NM_153217 // downstream // 169617 // Hs.508588 // MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream // 153692 // Hs.529798 // BTF3 // 689 // Homo sapiens basic transcription factor 3 (BTF3), mRNA.	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-1865368	tccatccctgccatta[C/T]ggtcaccttgttcatg	C	T	NM_153217 // downstream // 306914 // Hs.508588 // MGC13034 // 134288 // Homo sapiens hypothetical protein MGC13034 (MGC13034), mRNA. /// NM_001207 // upstream // 16395 // Hs.529798 // BTF3 // 689 // Homo sapiens basic transcription factor 3 (BTF3), mRNA.	MGC13034	MGC13034, Homo sapiens hypothetical protein MGC13034 (MGC13034), q13.2
SNP_A-2036586	aaatgccgagtaaca[C/T]gatttcagtaacatgt	C	T	NM_032175 // intron // 0 // Hs.406703 // FLJ12787 // 84135 // Homo sapiens Src-associated protein SAW (FLJ12787), mRNA. /// ENST00000296792 // intron // 0 // --- // --- // --- // ---	FLJ12787	FLJ12787, Homo sapiens Src-associated protein SAW (FLJ12787), q13.2
SNP_A-2122391	agtgcctacttcacag[A/G]aataacaagggaacat	A	G	ENST00000296794 // intron // 0 // --- // --- // --- // ---	-	q13.2
SNP_A-2032884	aaataataaaatgaac[C/G]aagtgcctccaaact	C	G	ENST00000296799 // intron // 0 // --- // --- // --- // --- /// ENST00000287898 // intron // 0 // --- // --- // ---	-	q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253540	cttcttcttacaaagd[C/T]acaagtcccactctca	C	T	NM_003633 // downstream // 649504 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 36719 // --- // --- // --- /// ENST00000287898 // downstream // 35914	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1791037	ggggtcctctaggctc[A/G]cccattctttcactcc	A	G	NM_003633 // downstream // 493074 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 193149 // --- // --- // --- /// ENST00000287898 // downstream // 19234	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-2170403	caagtatttggatgaa[A/C]cctgttagatggtggg	A	C	NM_003633 // downstream // 451558 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 234665 // --- // --- // --- /// ENST00000287898 // downstream // 23386	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1888158	tgagcctcaatcccac[A/G]aggaccctaagaaa	A	G	NM_003633 // downstream // 366571 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 319652 // --- // --- // --- /// ENST00000287898 // downstream // 31884	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1811532	gtgctctatgaacata[G/T]caggttactgtcatta	G	T	NM_003633 // downstream // 350874 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 335349 // --- // --- // --- /// ENST00000287898 // downstream // 33454	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-2297512	gccagaagttctaaaa[C/T]ctccaaggtatgtagc	C	T	NM_003633 // downstream // 312876 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 373347 // --- // --- // --- /// ENST00000287898 // downstream // 37254	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1851363	tattccaagctaatga[C/T]ggaagcaagattcata	C	T	NM_003633 // downstream // 250286 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 435937 // --- // --- // --- /// ENST00000287898 // downstream // 43513	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1982120	gaattttcaaagccca[A/G]attttcaatgacaagc	A	G	NM_003633 // downstream // 243850 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 442373 // --- // --- // --- /// ENST00000287898 // downstream // 44156	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1808674	gtgaactgccatatcc[C/G]agaaagtgaaactat	C	G	NM_003633 // downstream // 205211 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 481012 // --- // --- // --- /// ENST00000287898 // downstream // 48020	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-2131166	atagactgggtggaa[A/G]cttggacaaatcca	A	G	NM_003633 // downstream // 112757 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 573466 // --- // --- // --- /// ENST00000287898 // downstream // 57266	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1868972	tcctgatctgacagca[C/T]actaaaaagcattagg	C	T	NM_003633 // downstream // 111985 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 574238 // --- // --- // --- /// ENST00000287898 // downstream // 57343	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086809	actgacctggagcctc[C/T]agagcaagggtcagga	C	T	NM_003633 // downstream // 88988 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 597235 // — // — // — // — /// ENST00000287898 // downstream // 596430	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1851776	tattgaactcctacta[C/T]gtttgaggcactggag	C	T	NM_003633 // downstream // 74445 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// ENST00000296799 // downstream // 611778 // — // — // — // — /// ENST00000287898 // downstream // 610973	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-1849188	tatgctcctagttatc[A/G]caggaaaaggatacag	A	G	NM_003633 // upstream // 18102 // Hs.104925 // ENC1 // 8507 // Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), mRNA. /// NM_000521 // upstream // 26350 // Hs.69293 // HEXB // 3074 // Homo sapiens hexosaminidase B (beta polypeptide) (H	ENC1	ENC1, Homo sapiens ectodermal-neural cortex (with BTB-like domain) (ENC1), q13.3
SNP_A-2262542	gaaatgtgtggtgggg[A/C]catattagtggtgaca	A	C	NM_000859 // upstream // 966 // Hs.11899 // HMGCR // 3156 // Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA. /// ENST00000274361 // upstream // 99430 // — // — // — // — /// ENST00000343975 // upstream // 924 // — //	HMGCR	HMGCR, Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), q13.3
SNP_A-1982167	actggtaatagttccc[A/G]gagaatggctggctcc	A	G	ENST00000322285 // intron // 0 // — // — // — // —	-	q13.3
SNP_A-1839936	tagcaaaagtcattgc[A/G]agttctgaaggaaaca	A	G	ENST00000322285 // downstream // 6856 // — // — // — // — /// ENST00000306733 // upstream // 39755 // — // — // — // —	-	q13.3
SNP_A-1982169	aaagggattgcagtag[C/T]agtaggtggcatggtc	C	T	ENST00000322285 // downstream // 7978 // — // — // — // — /// ENST00000306733 // upstream // 38633 // — // — // — // —	-	q13.3
SNP_A-2023090	aaaacagataaggaaa[A/C]gctcatccacagagct	A	C	NM_006633 // intron // 0 // Hs.291030 // IQGAP2 // 10788 // Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA. /// ENST00000274364 // intron // 0 // — // — // — // —	IQGAP2	IQGAP2, Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), q13.3
SNP_A-1982177	tttccatttcacccgg[A/G]agctaactgctagaga	A	G	NM_006633 // intron // 0 // Hs.291030 // IQGAP2 // 10788 // Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA. /// NM_004101 // intron // 0 // Hs.42502 // F2RL2 // 2151 // Homo sapiens coagulation factor II (thrombin) receptor-li	IQGAP2	IQGAP2, Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), q13.3
SNP_A-1943819	ttgtaggtcatctaca[C/G]gatactattcatcttt	C	G	NM_006633 // intron // 0 // Hs.291030 // IQGAP2 // 10788 // Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA. /// ENST00000274364 // intron // 0 // — // — // — // —	IQGAP2	IQGAP2, Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), q13.3
SNP_A-2287557	gattaaaacccaacaa[A/G]ctcgagtgctggggtc	A	G	NM_001882 // intron // 0 // Hs.115617 // CRHBP // 1393 // Homo sapiens corticotropin releasing hormone binding protein (CRHBP), mRNA. /// ENST00000329238 // intron // 0 // — // — // — // — /// ENST00000274368 // intron // 0 // — // — // — //	CRHBP	CRHBP, Homo sapiens corticotropin releasing hormone binding protein (CRHBP), q13.3
SNP_A-1686850	ggcaccatcgtgggtgggagggtat[C/T]ttgcatttgtcttggtatt gccctc	C	T	NM_001882 // upstream // 29473 // Hs.115617 // CRHBP // 1393 // corticotropin releasing hormone binding protein /// NM_130772 // downstream // 45352 // Hs.352172 // S100Z // 170591 // S100Z protein	CRHBP	CRHBP , rs3903346, corticotropin releasing hormone binding protein ,q13.3
SNP_A-1931386	ttcccaggcaggtcaa[C/T]gggaaaaggttgcagg	C	T	ENST00000329238 // intron // 0 // — // — // — // —	-	q13.3
SNP_A-1834175	tacatgaaaacaaatg[A/G]caacagcttgtgggtg	A	G	NM_003719 // intron // 0 // Hs.78106 // PDE8B // 8622 // Homo sapiens phosphodiesterase 8B (PDE8B), mRNA. /// ENST00000329238 // intron // 0 // — // — // — // — /// ENST00000346042 // intron // 0 // — // — // — // — /// ENST00000340978 //	PDE8B	PDE8B, Homo sapiens phosphodiesterase 8B (PDE8B), q13.3
SNP_A-2115586	agggtaagacagaaga[C/G]tataatgcacttagtc	C	G	NM_018268 // intron // 0 // Hs.482573 // WDR41 // 55255 // Homo sapiens WD repeat domain 41 (WDR41), mRNA. /// ENST00000329238 // intron // 0 // — // — // — // — /// ENST00000296679 // intron // 0 // — // — // — // —	WDR41	WDR41, Homo sapiens WD repeat domain 41 (WDR41), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1655329	caagatagccagaaattalaatttcc[G/T]gatggagtatacaaatct gccttgg	G	T	NM_018268 // intron // 0 // Hs.16470 // FLJ10904 // 55255 // hypothetical protein FLJ10904	FLJ10904	FLJ10904, rs251470, hypothetical protein FLJ10904,q13.3
SNP_A-1982201	agaagacctaaggccg[A/C]aagtcgctgtgcagca	A	C	NM_032109 // intron // 0 // Hs.202247 // OTP // 23440 // Homo sapiens orthopedia homolog (Drosophila) (OTP), mRNA. /// ENST00000306422 // intron // 0 // --- // --- // ---	OTP	OTP, Homo sapiens orthopedia homolog (Drosophila) (OTP), q14.1
SNP_A-2168701	caagaatagcaagtgc[A/C]aaaaagcagtagctct	A	C	NM_032109 // upstream // 27752 // Hs.202247 // OTP // 23440 // Homo sapiens orthopedia homolog (Drosophila) (OTP), mRNA. /// NM_004607 // downstream // 24799 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// ENST0	OTP	OTP, Homo sapiens orthopedia homolog (Drosophila) (OTP), q14.1
SNP_A-1821849	gtttagcatttccaa[C/T]ggcatcaacaaatct	C	T	NM_004607 // intron // 0 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// ENST00000306388 // intron // 0 // --- // --- // --- // ---	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-2082248	acgaggcatttctca[C/T]agtccctgacagcaca	C	T	NM_004607 // upstream // 44927 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// NM_003664 // downstream // 181054 // Hs.532091 // AP3B1 // 8546 // Homo sapiens adaptor-related protein complex 3, beta 1 subunit (A	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-1915981	tgttgcaaaggtagaa[C/T]agaatctacttctg	C	T	NM_004607 // upstream // 47888 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// NM_003664 // downstream // 178093 // Hs.532091 // AP3B1 // 8546 // Homo sapiens adaptor-related protein complex 3, beta 1 subunit (A	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-1855862	tcaatgcactgaaaat[A/C]atctaactgggaagtt	A	C	NM_004607 // upstream // 50070 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// NM_003664 // downstream // 175911 // Hs.532091 // AP3B1 // 8546 // Homo sapiens adaptor-related protein complex 3, beta 1 subunit (A	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-1827708	taacttacactcatgta[A/C]atcagctcaggattca	A	C	NM_004607 // upstream // 57330 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// NM_003664 // downstream // 168651 // Hs.532091 // AP3B1 // 8546 // Homo sapiens adaptor-related protein complex 3, beta 1 subunit (A	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-2188855	cagtggtgagagaaaa[C/G]agaattacatttatg	C	G	NM_004607 // upstream // 176360 // Hs.291212 // TBCA // 6902 // Homo sapiens tubulin-specific chaperone a (TBCA), mRNA. /// NM_003664 // downstream // 49621 // Hs.532091 // AP3B1 // 8546 // Homo sapiens adaptor-related protein complex 3, beta 1 subunit (A	TBCA	TBCA, Homo sapiens tubulin-specific chaperone a (TBCA), q14.1
SNP_A-1982221	ctaaccaagtgaaaaa[A/T]ccaatatacacaaata	A	T	NM_052822 // 3UTR // 0 // Hs.482587 // SCAMP1 // 9522 // Homo sapiens secretory carrier membrane protein 1 (SCAMP1), transcript variant 2, mRNA. /// NM_004866 // 3UTR // 0 // Hs.482587 // SCAMP1 // 9522 // Homo sapiens secretory carrier membrane protein 1	SCAMP1	SCAMP1, Homo sapiens secretory carrier membrane protein 1 (SCAMP1), transcript variant 2, q14.1
SNP_A-1812024	gtggacaacaagaaag[A/T]ccatctactaggccaa	A	T	NM_000046 // intron // 0 // Hs.149103 // ARSB // 411 // Homo sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA. /// NM_198709 // intron // 0 // Hs.149103 // ARSB // 411 // Homo sapiens arylsulfatase B (ARSB), transcript variant 2, mRNA. /// ENST0	ARSB	ARSB, Homo sapiens arylsulfatase B (ARSB), transcript variant 1, q14.1
SNP_A-2292771	gcacttggacaggaac[C/T]acgatcatacctattg	C	T	NM_000046 // intron // 0 // Hs.149103 // ARSB // 411 // Homo sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA. /// NM_198709 // intron // 0 // Hs.149103 // ARSB // 411 // Homo sapiens arylsulfatase B (ARSB), transcript variant 2, mRNA. /// ENST0	ARSB	ARSB, Homo sapiens arylsulfatase B (ARSB), transcript variant 1, q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2135439	atatttgacaccttgg[A/G]aacttgcattaatact	A	G	NM_000046 // intron // 0 // Hs.149103 // ARSB // 411 // Homo sapiens arylsulfatase B (ARSB), transcript variant 1, mRNA. /// NM_198709 // intron // 0 // Hs.149103 // ARSB // 411 // Homo sapiens arylsulfatase B (ARSB), transcript variant 2, mRNA. /// ENST0	ARSB	ARSB, Homo sapiens arylsulfatase B (ARSB), transcript variant 1, q14.1
SNP_A-1982237	gagaccttcacacaaa[C/T]ccctatcatcacagcc	C	T	NM_013391 // intron // 0 // Hs.122082 // DMGDH // 29958 // Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000255189 // intron // 0 // — // — // —	DMGDH	DMGDH, Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, q14.1
SNP_A-2166724	caaattcattcatcaa[A/C]aacggttctctgcta	A	C	NM_013391 // intron // 0 // Hs.122082 // DMGDH // 29958 // Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000255189 // intron // 0 // — // — // — /// ENST00000315090 // intron	DMGDH	DMGDH, Homo sapiens dimethylglycine dehydrogenase (DMGDH), nuclear gene encoding mitochondrial protein, q14.1
SNP_A-2137713	atcatggagacattcc[A/G]attacattatacaca	A	G	NM_153610 // intron // 0 // Hs.482625 // — // 0 // Homo sapiens cardiomyopathy associated 5 (CMYA5), mRNA. /// ENST00000238522 // intron // 0 // — // — // —	-	-, Homo sapiens cardiomyopathy associated 5 (CMYA5), q14.1
SNP_A-2023855	aaaagaaatgtgacgc[A/T]ctctcaccaagatgct	A	T	NM_153610 // intron // 0 // Hs.482625 // — // 0 // Homo sapiens cardiomyopathy associated 5 (CMYA5), mRNA. /// ENST00000238522 // intron // 0 // — // — // —	-	-, Homo sapiens cardiomyopathy associated 5 (CMYA5), q14.1
SNP_A-2010999	agtatccatcactcaa[A/G]taacatacattgtacc	A	G	NM_003248 // upstream // 28482 // Hs.211426 // THBS4 // 7060 // Homo sapiens thrombospondin 4 (THBS4), mRNA. /// ENST00000328496 // upstream // 15553 // — // — // — /// ENST00000350881 // upstream // 28482 // — // — // —	THBS4	THBS4, Homo sapiens thrombospondin 4 (THBS4), q14.1
SNP_A-2134693	atatgtttctcttcaa[A/G]ggtggttagtctagca	A	G	NM_178276 // upstream // 15861 // Hs.439630 // C5orf12 // 256987 // Homo sapiens chromosome 5 open reading frame 12 (C5orf12), mRNA. /// ENST00000329637 // upstream // 15861 // — // — // — // — /// ENST00000327852 // upstream // 69608 // — // -	C5orf12	C5orf12, Homo sapiens chromosome 5 open reading frame 12 (C5orf12), q14.1
SNP_A-2066511	aatttttaaatgggc[A/G]aaaggcttgaaatgtc	A	G	ENST00000314295 // upstream // 1364 // — // — // — // — /// ENST00000309466 // downstream // 17728 // — // — // — // —	-	q14.1
SNP_A-1838542	tagaatgtttaatttc[A/G]cttctctcacttgaat	A	G	NM_014733 // upstream // 20517 // Hs.482660 // ZFYVE16 // 9765 // Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), mRNA. /// ENST00000313424 // upstream // 27504 // — // — // — // — /// ENST00000338008 // upstream // 20517 // — //	ZFYVE16	ZFYVE16, Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), q14.1
SNP_A-1982267	taggttgtccatattg[A/C]agctggattatgggat	A	C	NM_014733 // upstream // 9051 // Hs.482660 // ZFYVE16 // 9765 // Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), mRNA. /// ENST00000313424 // upstream // 38970 // — // — // — // — /// ENST00000338008 // upstream // 9051 // — // -	ZFYVE16	ZFYVE16, Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), q14.1
SNP_A-1754646	tctatgtatttccgcaaataaaa[C/T]cattagtaaaaagatttaa gttgt	C	T	NM_014733 // intron // 0 // Hs.438240 // ZFYVE16 // 9765 // zinc finger, FYVE domain containing 16	ZFYVE16	ZFYVE16, rs249039, zinc finger, FYVE domain containing 16,q14.1
SNP_A-1840584	tagccctactctaga[A/G]caacttagtcacatt	A	G	NM_002439 // intron // 0 // Hs.280987 // MSH3 // 4437 // Homo sapiens mutS homolog 3 (E. coli) (MSH3), mRNA. /// ENST00000265081 // intron // 0 // — // — // —	MSH3	MSH3, Homo sapiens mutS homolog 3 (E. coli) (MSH3), q14.1
SNP_A-1672178	cttaaagagtgttccagtggtcca[C/T]gtgctacaactgagagg caatgagg	C	T	AF023130 // intron // 0 // Hs.410953 // RASGRF2 // 5924 // Ras protein-specific guanine nucleotide-releasing factor 2	RASGRF2	RASGRF2, rs35000, Ras protein-specific guanine nucleotide-releasing factor 2,q14.1
SNP_A-2063709	aattagaaagacaaaa[A/G]ctatctgaacatagga	A	G	NM_006909 // intron // 0 // Hs.162129 // RASGRF2 // 5924 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 2 (RASGRF2), mRNA. /// ENST00000265080 // intron // 0 // — // — // — // — // -	RASGRF2	RASGRF2, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 2 (RASGRF2), q14.1
SNP_A-2105253	agcattcctagagtcc[A/G]attcttccatttttccc	A	G	NM_130767 // intron // 0 // Hs.439127 // CACH-1 // 134526 // Homo sapiens cytosolic acetyl-CoA hydrolase (CACH-1), mRNA. /// ENST00000307624 // intron // 0 // — // — // —	CACH-1	CACH-1, Homo sapiens cytosolic acetyl-CoA hydrolase (CACH-1), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1822665	taaaaaaagcagcacc[C/G]caattcctaaatgact	C	G	NM_012446 // upstream // 172887 // Hs.102735 // SSBP2 // 23635 // Homo sapiens single-stranded DNA binding protein 2 (SSBP2), mRNA. /// NM_031482 // upstream // 47915 // Hs.527193 // APG10L // 83734 // Homo sapiens APG10 autophagy 10-like (S. cerevisiae)	SSBP2	SSBP2, Homo sapiens single-stranded DNA binding protein 2 (SSBP2), q14.1
SNP_A-1668586	tgctatacagacttatgtttccaac[C/T]gtagccacacaacacag tgttacag	C	T	NM_031482 // intron // 0 // Hs.410732 // APG10L // 83734 // APG10 autophagy 10-like (S. cerevisiae)	APG10L	APG10L , rs6888977, APG10 autophagy 10-like (S. cerevisiae),q14.2
SNP_A-1982311	acagcagactcatcgt[A/G]acagctgcccagaaga	A	G	NM_001025 // upstream // 41026 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 733317 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1674967	tctaacctcaaatggctgagctgaa[C/G]tcctgtgatgtcaacct agttttct	C	G	NM_001025 // intron // 0 // Hs.386384 // RPS23 // 6228 // ribosomal protein S23	RPS23	RPS23 , rs226199, ribosomal protein S23,q14.2
SNP_A-2044999	aagaacgtctgagaca[C/T]gggaagtttgtccctg	C	T	NM_001025 // upstream // 108904 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 665439 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1982327	agatagaaatgcacta[A/G]atctgaagttcgcacc	A	G	NM_001025 // upstream // 378859 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 395484 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1916653	tgtttattcccagtga[C/T]tagtaaattgcatttt	C	T	NM_001025 // upstream // 414501 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 359842 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1694351	gttgttgctgctattgttattatga[C/T]gtacttggccctcttccagac ccac	C	T	NM_001025 // upstream // 384153 // Hs.386384 // RPS23 // 6228 // ribosomal protein S23 /// NM_174909 // downstream // 394153 // Hs.355606 // MGC23909 // 153339 // hypothetical protein MGC23909	RPS23	RPS23 , rs10514242, ribosomal protein S23 ,q14.2
SNP_A-1910602	tgtcctctgaggcacc[A/G]aagtttttattttgat	A	G	NM_001025 // upstream // 553305 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 221038 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1814637	gtgtggcttgaggatc[A/T]cttggtgaaatagaaa	A	T	NM_001025 // upstream // 603102 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 171241 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1874210	tctccaagctttgata[A/C]ctgtggcttaatattc	A	C	NM_001025 // upstream // 722358 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 51985 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-2270966	gacagttaataaatgc[A/G]gcaggatcccactcat	A	G	NM_001025 // upstream // 724749 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 49594 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2303251	gctatgcaagccaaca[A/T]tgtcctaatattaa	A	T	NM_001025 // upstream // 734791 // Hs.386384 // RPS23 // 6228 // Homo sapiens ribosomal protein S23 (RPS23), mRNA. /// NM_174909 // downstream // 39552 // Hs.355606 // MGC23909 // 153339 // Homo sapiens hypothetical protein MGC23909 (MGC23909), mRNA. ///	RPS23	RPS23, Homo sapiens ribosomal protein S23 (RPS23), q14.2
SNP_A-1982345	tctcctgcttaaaata[A/T]ctaaaattggagaaag	A	T	NM_022406 // intron // 0 // Hs.171190 // XRCC4 // 7518 // Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, mRNA. /// NM_003401 // intron // 0 // Hs.171190 // XRCC4 // 7518 // Homo sapiens X	XRCC4	XRCC4, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 2, q14.2
SNP_A-1678132	ttcaagtgaatactggatgccaaaaa[C/G]aacacacacacctta gagtgagttt	C	G	NM_003401 // intron // 0 // Hs.150930 // XRCC4 // 7518 // X-ray repair complementing defective repair in Chinese hamster cells 4 /// NM_022406 // intron // 0 // Hs.150930 // XRCC4 // 7518 // X-ray repair complementing defective repair in Chinese hamster	XRCC4	XRCC4, rs10514252, X-ray repair complementing defective repair in Chinese hamster cells 4, q14.2
SNP_A-1703103	caataaatggcaccatataaaacag[A/G]aactgttggagagca tttatctgt	A	G	NM_003401 // intron // 0 // Hs.150930 // XRCC4 // 7518 // X-ray repair complementing defective repair in Chinese hamster cells 4 /// NM_022406 // intron // 0 // Hs.150930 // XRCC4 // 7518 // X-ray repair complementing defective repair in Chinese hamster	XRCC4	XRCC4, rs717938, X-ray repair complementing defective repair in Chinese hamster cells 4, q14.2
SNP_A-1696856	tatttgtacaaaagtttctaagtac[A/G]caaggaggaacttgcaggt catttttt	A	G	NM_003401 // intron // 0 // Hs.150930 // XRCC4 // 7518 // X-ray repair complementing defective repair in Chinese hamster cells 4 /// NM_022406 // intron // 0 // Hs.150930 // XRCC4 // 7518 // X-ray repair complementing defective repair in Chinese hamster	XRCC4	XRCC4, rs10514253, X-ray repair complementing defective repair in Chinese hamster cells 4, q14.2
SNP_A-2086161	actctgagccattaaq[C/G]atggactgtaactcaa	C	G	NM_005711 // intron // 0 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // intron // 0 // — // — // — /// ENST00000296591 // intron // 0 // — // — /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2011023	aagtatttttaaatta[A/T]gcaacaggatgtgttt	A	T	NM_005711 // upstream // 110746 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 111153 // — // — // — /// ENST00000296591 // upstream // 110746 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2063689	aattactacatttttc[A/G]agactaatagtgccc	A	G	NM_005711 // upstream // 298463 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 298870 // — // — // — /// ENST00000296591 // upstream // 298463 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-1918143	ttaaactcaaccttag[A/C]atgtcagaaataggtat	A	C	NM_005711 // upstream // 721088 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 721495 // — // — // — /// ENST00000296591 // upstream // 721088 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2083713	actacagacactaaga[A/T]taagatatgctaacag	A	T	NM_005711 // upstream // 728341 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 728748 // — // — // — /// ENST00000296591 // upstream // 728341 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-1946918	ttaaggatgcagcta[A/G]gtgaataattacattt	A	G	NM_005711 // upstream // 728620 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 729027 // — // — // — /// ENST00000296591 // upstream // 728620 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2097113	agactgtttccaata[C/T]ggctttactacttat	C	T	NM_005711 // upstream // 739204 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 739611 // — // — // — /// ENST00000296591 // upstream // 739204 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1823782	taaaatgaaaaaaaaa[A/G]gtgtcatgatatacat	A	G	NM_005711 // upstream // 741853 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 742260 // — // — // — /// ENST00000296591 // upstream // 741853 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2287411	gatgttaccaaagcaa[C/T]catacatgaagatacа	C	T	NM_005711 // upstream // 750216 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 750623 // — // — // — /// ENST00000296591 // upstream // 750216 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2045133	aagaagaccactggtg[C/T]aatttcataagcaata	C	T	NM_005711 // upstream // 756242 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 756649 // — // — // — /// ENST00000296591 // upstream // 756242 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2060066	aatgaaaaaaagacaa[C/G]aaatgaactgagcaca	C	G	NM_005711 // upstream // 763833 // Hs.482730 // EDIL3 // 10085 // Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /// ENST00000340928 // upstream // 764240 // — // — // — /// ENST00000296591 // upstream // 763833 /	EDIL3	EDIL3, Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), q14.3
SNP_A-2071818	acagactccttaaagd[A/C]aaatgatcaiatctgt	A	C	NM_001867 // upstream // 1406903 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 165 // — // — // — /// ENST00000024	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2251517	cttcactagatttgat[A/G]gtaacaaagagatatt	A	G	NM_001867 // upstream // 1397517 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 9551 // — // — // — /// ENST000002	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1872248	tctagaaaatgtttga[C/T]aatatgcctgtttct	C	T	NM_001867 // upstream // 1309606 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 97262 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1920048	ttaatatgaaaaagtta[C/G]agtgaattctcctaat	C	G	NM_001867 // upstream // 1297613 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 109455 // — // — // — /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1734474	aggatggtttatttccaaaatacta[A/G]agtgtgttcaaatatgga aacccgc	A	G	NM_005711 // upstream // 943576 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3 , rs173540, EGF-like repeats and discoidin I-like domains 3,q14.3
SNP_A-2266313	gaaggtatagtggtgt[A/G]aaaagatatcccatac	A	G	NM_001867 // upstream // 1233889 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 173179 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1859970	tcaggttcaaacttca[C/T]gttctactctgactga	C	T	NM_001867 // upstream // 1209060 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 198008 // — // — // — /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2243763	ctgctgatatctctggt[C/G]ataaatacttctacaa	C	G	NM_001867 // upstream // 1136973 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 270095 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2033333	aaatagatccataagc[A/G]actcaagcctcttgt	A	G	NM_001867 // upstream // 1096349 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 310719 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1790883	gggggtggtaatgta[C/T]ggactaggtgaagtcc	C	T	NM_001867 // upstream // 1086865 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 320203 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2097713	agagacagcagaaaag[A/G]aataggtactccctgtt	A	G	NM_001867 // upstream // 1081945 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 325123 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2215612	cctcaggaagcttccat[A/G]tcatagtagaagacaa	A	G	NM_001867 // upstream // 1052792 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 354276 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1908236	tgtacctcatattgaa[G/T]tatcactcccagaaa	G	T	NM_001867 // upstream // 889327 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 517741 // --- // --- // --- /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2178112	cactagtgttggacta[A/G]acagcaggaaaaatat	A	G	NM_001867 // upstream // 866557 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 540511 // --- // --- // --- /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1982399	aagtgatttcattggat[C/T]atgcctgtacattaa	C	T	NM_001867 // upstream // 863604 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 543464 // --- // --- // --- /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1948420	tttagtagataacata[C/G]acctctgaagtcacta	C	G	NM_001867 // upstream // 861345 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 545723 // --- // --- // --- /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1982401	aggaaccacagctcac[G/T]attaaacaattgctga	G	T	NM_001867 // upstream // 805558 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 601510 // --- // --- // --- /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1722522	tttcatcactccatggtattaaaaa[A/G]atctcctagtttgtgatgtg taca	A	G	NM_005711 // upstream // 1403861 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3, rs1500150, EGF-like repeats and discoidin I-like domains 3,q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072465	acagcagtccaatttaCT]catttgctaccttgg	C	T	NM_001867 // upstream // 771230 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 635838 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1949598	tttatttctacgttca[A/G]cataaagctcactgc	A	G	NM_001867 // upstream // 731242 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 675826 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2132350	atagtattcactacaa[A/G]ttgacttaagaaccct	A	G	NM_001867 // upstream // 719411 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 687657 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1982403	acagcaaacagctaaa[A/G]gaagatttcagccatt	A	G	NM_001867 // upstream // 682122 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 724946 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1982404	tgaaattagccgaaa[A/G]agtatatcaaaagcaa	A	G	NM_001867 // upstream // 681555 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 725513 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2219732	ccttaatcaaaaaacaa[C/T]gaggtttgagctagta	C	T	NM_001867 // upstream // 646292 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 760776 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1670918	tagaattgatgggcaataaacggta[A/G]atgttttggactccctga taaaata	A	G	NM_005711 // upstream // 1552052 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3 , rs986943, EGF-like repeats and discoidin I-like domains 3,q14.3
SNP_A-1982405	ttagagaaaaaaaaaaa[G/T]atgcctacagaatgta	G	T	NM_001867 // upstream // 560532 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 846536 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2168096	caactatttaactgta[C/T]cttgtcgtacaaaaa	C	T	NM_001867 // upstream // 468890 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 938178 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2065322	aatgtagcctcacaa[A/T]aaaagctgggtgaaaa	A	T	NM_001867 // upstream // 468699 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 938369 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1688826	taggtattaaaaaaaatctttac[A/T]ctcatcatgctaggccag agtaggg	A	T	NM_005711 // upstream // 1748504 // Hs.441044 // EDIL3 // 10085 // EGF-like repeats and discoidin I-like domains 3	EDIL3	EDIL3 , rs1363278, EGF-like repeats and discoidin I-like domains 3,q14.3
SNP_A-2116253	aggtacggaatcaatc[C/T]atatgctgtatatttt	C	T	NM_001867 // upstream // 308781 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1098267 // — // — // — /// ENST00000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2310398	ggaactgaggaacaaa[A/G]attgaaacctggact	A	G	NM_001867 // upstream // 287470 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1119598 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2171405	caatcaagccaagaaq[C/G]aaatcaagaacacaat	C	G	NM_001867 // upstream // 277929 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1129139 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-1982408	gatggcacgttaaaga[A/G]agaaaagatggcttggt	A	G	NM_001867 // upstream // 245668 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1161400 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2132795	atataacagtagtcta[C/T]cttctgccactagctg	C	T	NM_001867 // upstream // 210906 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1196162 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2111405	aggaggacagagaaagc[G/T]atcataacataacatt	G	T	NM_001867 // upstream // 133105 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1273963 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2281062	gagtaagtcattaaaat[C/T]gctctaaccctgtatt	C	T	NM_001867 // upstream // 113043 // Hs.430075 // COX7C // 1350 // Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000338970 // upstream // 1294025 // --- // --- // --- /// ENST0000	COX7C	COX7C, Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, q14.3
SNP_A-2085631	actccccccatcaaaag[A/G]cgcatagtggctgaat	A	G	NM_001239 // upstream // 278617 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 503561 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1855046	tcaagaagagagaacg[A/G]attctaggtgagcaat	A	G	NM_001239 // upstream // 290095 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 492083 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-2302553	gctacaatgggtatag[C/G]caacctcttgaataaa	C	G	NM_001239 // upstream // 383930 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 398248 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1929691	ttcatattccaaaaaa[C/G]ttcactgtgtctctga	C	G	NM_001239 // upstream // 410833 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 371345 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1715401	aaatgtgtgctatcttacctca[A/G]attaattcaaaagggaaat taatga	A	G	NM_001239 // upstream // 387269 // Hs.514 // CCNH // 902 // cyclin H /// NM_153354 // downstream // 394920 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	CCNH	CCNH , rs1423634, cyclin H ,q14.3
SNP_A-1720081	atacatccaactgaggtataggta[A/G]tgtgcccaagaagaaa tgtctagta	A	G	NM_001239 // upstream // 451967 // Hs.514 // CCNH // 902 // cyclin H /// NM_153354 // downstream // 330222 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	CCNH	CCNH , rs9293491, cyclin H ,q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1648808	ctgtaaggtagaaattggaggtcaa[G/T]aaaaatttaaacaga ggaacagagg	G	T	NM_001239 // upstream // 481248 // Hs.514 // CCNH // 902 // cyclin H /// NM_153354 // downstream // 300941 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	CCNH	CCNH , rs10514296, cyclin H ,q14.3
SNP_A-2198078	catggcacttagaaaa[A/G]actttaatcaagttc	A	G	NM_001239 // upstream // 530695 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 251483 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-2063402	aattaactcagaagca[A/C]ctacctacaagcaagt	A	C	NM_001239 // upstream // 538156 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 244022 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1982444	attgtcatgtgcaaca[C/T]acgatttgtcaacaa	C	T	NM_001239 // upstream // 540011 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 242167 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1745476	ctttgagcacttcaaatgacacttc[G/T]atatttgtacctacacaa aggata	G	T	NM_001239 // upstream // 495285 // Hs.514 // CCNH // 902 // cyclin H /// NM_153354 // downstream // 286904 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	CCNH	CCNH , rs9293494, cyclin H ,q14.3
SNP_A-2174586	cacagagtttctacaa[A/G]gatgctgcctagtgaa	A	G	NM_001239 // upstream // 560169 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 222009 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-2057742	aatatgtgaactaata[A/G]gcataagcagaatggg	A	G	NM_001239 // upstream // 688827 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 93351 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-2089262	acttagaaggtagtga[C/T]ccaatctctcagtgat	C	T	NM_001239 // upstream // 690166 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 92012 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-2155589	attccacactaggaaa[G/T]tcataggtgctcaaac	G	T	NM_001239 // upstream // 725241 // Hs.146607 // CCNH // 902 // Homo sapiens cyclin H (CCNH), mRNA. /// NM_153354 // downstream // 56937 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000256897	CCNH	CCNH, Homo sapiens cyclin H (CCNH), q14.3
SNP_A-1721902	ggcttagaaattagagtagatataa[C/T]agagttgattaacaatg gaaaaagg	C	T	NM_001239 // upstream // 698080 // Hs.514 // CCNH // 902 // cyclin H /// NM_153354 // downstream // 84109 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	CCNH	CCNH , rs6863354, cyclin H ,q14.3
SNP_A-1758886	ctttgatactatctttgtgaaat[A/G]atacctctaatctagaatattt aa	A	G	NM_001239 // upstream // 713934 // Hs.514 // CCNH // 902 // cyclin H /// NM_153354 // downstream // 68255 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	CCNH	CCNH , rs1427920, cyclin H ,q14.3
SNP_A-2134292	atatgcatatttcata[A/G]agctagacaagatga	A	G	NM_153354 // intron // 0 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000296595 // intron // 0 // --- // --- // ---	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-1727685	ggaaattgtcctctatagatctca[C/G]taaacatttcagtaaaaa taaagc	C	G	NM_153354 // intron // 0 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	MGC33214	MGC33214 , rs33706, hypothetical protein MGC33214,q14.3
SNP_A-2173140	cacaaattagcttgaa[C/T]ggtagaaagatttata	C	T	NM_153354 // intron // 0 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// ENST00000296595 // intron // 0 // --- // --- // ---	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1886785	tgactgccaggtttag[A/G]acagatattaagaacc	A	G	NM_153354 // upstream // 2066 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 // downstream // 449435 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2,	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-2028220	aaactaggcactctca[C/T]ctgaagcgacattag	C	T	NM_153354 // upstream // 34153 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 // downstream // 417348 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2,	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-2036932	aaatttgtggctacd[A/G]gaggcagtattattct	A	G	NM_153354 // upstream // 148166 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 // downstream // 303335 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-1881338	tctttcagctctctcq[C/T]gactgactttcctgaa	C	T	NM_153354 // upstream // 148248 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 // downstream // 303253 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-2273045	gactatagcattaagat[C/T]aggaaccaggaagagg	C	T	NM_153354 // upstream // 199953 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 // downstream // 251548 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-1715955	tagatagatagataatagatagaga[C/T]taaagccttcaatact gacttca	C	T	BC036480 // downstream // 159382 // Hs.12827 // - // - // Clone IMAGE:5295779, mRNA /// NM_153354 // upstream // 236216 // Hs.379972 // MGC33214 // 153396 // hypothetical protein MGC33214	-	- , rs6860708, Clone IMAGE:5295779, mRNA , q14.3
SNP_A-2044636	aagaaagaaaaggaga[A/G]agacaggattagaag	A	G	NM_153354 // upstream // 437133 // Hs.379972 // MGC33214 // 153396 // Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA. /// NM_002397 // downstream // 14368 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2,	MGC33214	MGC33214, Homo sapiens hypothetical protein MGC33214 (MGC33214), q14.3
SNP_A-1893005	tgcactctacaaaaag[C/T]atcattctcataatag	C	T	NM_002397 // intron // 0 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// ENST00000340208 // intron // 0 // — // — // — // — /// ENST00000357034 /	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1648260	catcatttttcatttcctctactgat[C/T]ggacagttaatttgcatgtatc aac	C	T	NM_002397 // downstream // 14197 // Hs.368950 // MEF2C // 4208 // MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	MEF2C , rs639725, MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C),q14.3
SNP_A-1691740	ctttaccattatttacagagtag[C/G]cttgtgtttacttgagtaacttgt	C	G	NM_002397 // downstream // 5027 // Hs.368950 // MEF2C // 4208 // MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	MEF2C , rs40504, MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C),q14.3
SNP_A-1659959	taagatcataaaagctagagaaaga[C/G]acgcttattaaggaa acaaataatt	C	G	NM_002397 // intron // 0 // Hs.368950 // MEF2C // 4208 // MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	MEF2C , rs34321, MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C),q14.3
SNP_A-2247163	ctgtcagattcattga[A/G]caagcttaaattcagg	A	G	NM_002397 // upstream // 60156 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1450325 // Hs.528302 // CETN3 // 1070 // Homo s	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1643678	tgcagaggacaggtcagattgtgt[C/G]aaggttctatgcaaac tgcccaaga	C	G	NM_002397 // upstream // 53891 // Hs.368950 // MEF2C // 4208 // MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) /// NM_004365 // downstream // 1456966 // Hs.528302 // CETN3 // 1070 // centrin, EF-hand protein, 3 (CDC3	MEF2C	MEF2C , rs301719, MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C), q14.3
SNP_A-2065441	aattgttagttttctc[C/G]agatgtttctctaag	C	G	NM_002397 // upstream // 260857 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1249624 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-2187931	cagtatgttgagatga[C/T]aagatttgctttagc	C	T	NM_002397 // upstream // 291915 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1218566 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1982463	aaagccatcctgaaa[C/T]tgtcaggtaataggag	C	T	NM_002397 // upstream // 378278 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1132203 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-2244677	ctggaggttaggcggc[C/T]atgttcaaggttctag	C	T	NM_002397 // upstream // 383541 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1126940 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1922216	ttacttgaattctgaa[A/G]tggctgaatatttgaa	A	G	NM_002397 // upstream // 384558 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1125923 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1813703	gtgtacttatatcaa[C/T]ctgggaatgtcgtcac	C	T	NM_002397 // upstream // 385341 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1125140 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1817351	gttcagcaatccactc[C/T]attatttttaggcctct	C	T	NM_002397 // upstream // 414505 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 1095976 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1982466	cacacacattggtaga[A/T]tcctttaaggaattc	A	T	NM_002397 // upstream // 653440 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 857041 // Hs.528302 // CETN3 // 1070 // Homo s	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1881077	tctttaacaattgcca[A/T]agactcccccaacttc	A	T	NM_002397 // upstream // 679158 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 831323 // Hs.528302 // CETN3 // 1070 // Homo s	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1927596	ttcaacatataaacca[A/G]agactcattaattcct	A	G	NM_002397 // upstream // 696521 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 813960 // Hs.528302 // CETN3 // 1070 // Homo s	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098193	agagataaaggaaatc[A/G]agagagaatgtgaatt	A	G	NM_002397 // upstream // 826177 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 684304 // Hs.528302 // CETN3 // 1070 // Homo s	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1982474	tctgaagccatcccta[A/G]taaatttggcatattt	A	G	NM_002397 // upstream // 1060930 // Hs.444409 // MEF2C // 4208 // Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA. /// NM_004365 // downstream // 449551 // Hs.528302 // CETN3 // 1070 // Homo	MEF2C	MEF2C, Homo sapiens MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), q14.3
SNP_A-1677508	taaaacaacactaaaataagcaaaa[A/G]aagttcagtggggg aaaaagtcaag	A	G	NM_006467 // intron // 0 // Hs.282387 // POLR3G // 10622 // polymerase (RNA) III (DNA directed) polypeptide G (32kD)	POLR3G	POLR3G , rs4569906, polymerase (RNA) III (DNA directed) polypeptide G (32kD),q14.3
SNP_A-1911600	tgtgaaacagcctcca[C/T]tgaggttattgacaag	C	T	NM_032119 // intron // 0 // Hs.153692 // MASS1 // 84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // — // — // — // —	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-2260020	gaaaataacataggaa[A/G]tacacagaacaacaaa	A	G	NM_032119 // intron // 0 // Hs.153692 // MASS1 // 84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // — // — // — // —	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1982494	ggaagcgacacttcaa[A/T]caaaagctgcaaagaa	A	T	NM_032119 // intron // 0 // Hs.153692 // MASS1 // 84059 // Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), mRNA. /// ENST00000296619 // intron // 0 // — // — // — // — /// ENST00000296614 // 5UTR // 0 // — //	MASS1	MASS1, Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse) (MASS1), q14.3
SNP_A-1684940	ctaccaacaaagattctgacataca[C/T]ggattttctggtccaaa gaatcctt	C	T	NM_032119 // intron // 0 // Hs.153692 // MASS1 // 84059 // monogenic, audiogenic seizure susceptibility 1 homolog (mouse)	MASS1	MASS1 , rs1474119, monogenic, audiogenic seizure susceptibility 1 homolog (mouse),q14.3
SNP_A-2035529	aaatgtaaacagtcca[A/G]attaagatatgctgta	A	G	NM_020801 // upstream // 424514 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1805408 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-1982516	ttaattagtgactgaa[G/T]agtgttgaataaatat	G	T	NM_020801 // upstream // 562089 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1667833 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q14.3
SNP_A-1982521	atacctgtctctatta[C/T]ctaaaaactatccatc	C	T	NM_020801 // upstream // 1203974 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 1025948 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1947138	tttaatctgaagccca[A/G]tactcggccttgcatg	A	G	NM_020801 // upstream // 1276840 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 953082 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1714547	aaggaaaagatattaactacattat[A/T]agctgctcagaaatga attagcttg	A	T	BC010610 // downstream // 917922 // Hs.446400 // - // 401201 // Clone IMAGE:5313822, mRNA /// NM_020801 // upstream // 1270535 // Hs.24684 // ARRDC3 // 57561 // arrestin domain containing 3	-	- , rs1155697, Clone IMAGE:5313822, mRNA ,q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2185758	caggatacaaaattaa[C/T]ggacatatatcactaa	C	T	NM_020801 // upstream // 1437542 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 792380 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1927459	ttcaaataaaacaaaa[A/C]ccgtgctgaatcact	A	C	NM_020801 // upstream // 1587314 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 642608 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1756260	cacttaaaaaagatttagattta[A/G]cattgctttggaatcatttct gtt	A	G	BC010610 // downstream // 622412 // Hs.446400 // - // 401201 // Clone IMAGE:5313822, mRNA /// NM_020801 // upstream // 1566045 // Hs.24684 // ARRDC3 // 57561 // arrestin domain containing 3	-	- , rs2635182, Clone IMAGE:5313822, mRNA q14.3
SNP_A-2311178	ggaagtgggaaaagaa[C/T]gtgtatagagatttag	C	T	NM_020801 // upstream // 1629362 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 600560 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1792967	ggtacagttcagtaac[A/C]ggtgctttaacaagct	A	C	NM_020801 // upstream // 1906628 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 323294 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-2076210	acattctcataaatc[A/G]actactagaacataag	A	G	NM_020801 // upstream // 2009266 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 220656 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1982540	gttttcctgaaataaa[A/G]agctgattatatctct	A	G	NM_020801 // upstream // 2197348 // Hs.24684 // ARRDC3 // 57561 // Homo sapiens arrestin domain containing 3 (ARRDC3), mRNA. /// NM_005654 // upstream // 32574 // Hs.519445 // NR2F1 // 7025 // Homo sapiens nuclear receptor subfamily 2, group F, member 1 (	ARRDC3	ARRDC3, Homo sapiens arrestin domain containing 3 (ARRDC3), q15
SNP_A-1642771	aatccagtgctaggaagtttatttta[C/T]gttgtcccacagagatca tttctc	C	T	NM_005654 // downstream // 6920 // Hs.361748 // NR2F1 // 7025 // nuclear receptor subfamily 2, group F, member 1 /// NM_024977 // downstream // 259633 // - // - // - // - /// NM_032042 // downstream // 17035 // Hs.413417 // DKFZP564D172 // 83989 // hypot	NR2F1	NR2F1 , rs10514375, nuclear receptor subfamily 2, group F, member 1, q15
SNP_A-2177709	cacgtaacaatatgag[G/T]cagattctaatatcat	G	T	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // --- // --- // ---	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-1982542	aagactcccaggatta[A/C]agttggacttgagtag	A	C	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // --- // --- // ---	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-1735378	ctagagtgatctatgatttcaag[C/G]cttaagtaaattcagtagc cttttt	C	G	NM_032042 // intron // 0 // Hs.413417 // DKFZP564D172 // 83989 // hypothetical protein DKFZp564D172	DKFZP564D172	DKFZP564D172 , rs7717718, hypothetical protein DKFZp564D172,q15
SNP_A-2267880	gaatcctcctatttcc[C/T]cactgttcccagaatt	C	T	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // --- // --- // ---	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814023	gtgtcattccaacccaa[C/G]agtccacattgtgtct	C	G	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // —	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-1755052	agaattatatagcagaaagttataq[C/T]gatctttgataaaacaatgtaata	C	T	NM_032042 // intron // 0 // Hs.413417 // DKFZP564D172 // 83989 // hypothetical protein DKFZp564D172	DKFZP564D172	DKFZP564D172, -, hypothetical protein DKFZp564D172,q15
SNP_A-2311453	ggaatcctttgaccta[C/T]ggaactatctgctttg	C	T	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2107343	agctaatggataccaa[A/G]tgtttctaatttcacc	A	G	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2186884	cagggtcatcattacc[A/G]aacattgagtaattaa	A	G	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2021288	aaaaaaattgcacaat[A/G]aattcagttagatttc	A	G	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2033299	aaatagacaaatcaag[G/T]aactagtgtctgaccc	G	T	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2284868	gatccacatttagata[A/T]gattttggaagtgtct	A	T	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-1895530	tgcctagcctgtcgta[C/G]ctaccatcaacaaaat	C	G	NM_032042 // intron // 0 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // intron // 0 // — // — // — // — /// ENST00000341626 // intron // 0 // — // — // — // — /	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-2299624	gccgccgctgccgtca[A/G]tgctaatgacgtat	A	G	NM_032042 // upstream // 36929 // Hs.127788 // DKFZP564D172 // 83989 // Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA. /// ENST00000265139 // upstream // 36929 // - // - // — // — /// ENST00000360516 // upstream // 427971 //	DKFZP564D172	DKFZP564D172, Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), q15
SNP_A-1718341	tggaaacccagcatgtcatttagat[C/T]agaaactgtgacatac attacttgc	C	T	NM_032042 // intron // 0 // Hs.413417 // DKFZP564D172 // 83989 // hypothetical protein DKFZp564D172	DKFZP564D172	DKFZP564D172, rs10514380, hypothetical protein DKFZp564D172,q15
SNP_A-2097794	agagacgagataagca[C/T]ataaataagacccaa	C	T	ENST00000339047 // intron // 0 // — // — // — // —	-	q15
SNP_A-1883822	tgaagaagtaagatca[C/T]agaggaaaattatgca	C	T	ENST00000339047 // intron // 0 // — // — // — // —	-	q15
SNP_A-2295068	gcatagccaaatttc[G/T]acatacgtttattgag	G	T	ENST00000339047 // intron // 0 // — // — // — // —	-	q15
SNP_A-1756929	ggtactgtgccactcatacacatca[A/G]atcttcctcacgtcctc ccaatat	A	G	AB020632 // downstream // 182157 // Hs.194755 // KIAA0825 // 23004 // KIAA0825 protein /// NM_024977 // upstream // 367003 // - // - // - // - /// NM_032042 // upstream // 156069 // Hs.413417 // DKFZP564D172 // 83989 // hypothetical protein DKFZp564D172	KIAA0825	KIAA0825, rs10514382, KIAA0825 protein, q15
SNP_A-2034033	aaatcagatacatgca[C/T]aaaacagtgtctactc	C	T	NM_032290 // upstream // 4448 // Hs.482853 // ANKRD32 // 84250 // Homo sapiens ankyrin repeat domain 32 (ANKRD32), mRNA. /// ENST00000265140 // downstream // 20583 // — // — // — // — /// ENST00000357138 // upstream // 22196 // — // — // — /	ANKRD32	ANKRD32, Homo sapiens ankyrin repeat domain 32 (ANKRD32), q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1705059	aagaactaatgaactaaaaactgga[C/T]gaaaatactatccag aatgtggcaa	C	T	AL050298 // downstream // 20804 // Hs.285055 // DKFZp564C0469 // 345499 // hypothetical protein DKFZp564C0469 /// NM_032290 // upstream // 6307 // Hs.91846 // DKFZp761C121 // 84250 // hypothetical protein DKFZp761C121	DKFZp564C0469	DKFZp564C0469 , rs430555, hypothetical protein DKFZp564C0469 ,q15
SNP_A-1893019	tgcactgactggctaa[C/T]tctctctcactcttag	C	T	NM_024717 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-do	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-1931328	ttcccacagttctttta[A/T]caatatgtcagtgtcg	A	T	NM_024717 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-do	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-1982551	cctatttgattgttag[A/G]attatctgtaaaagg	A	G	NM_024717 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-do	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-2298649	gcccagactttaccac[C/T]atgcaatacatccatg	C	T	NM_024717 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-do	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-2169992	caagggaaatcagcaa[A/G]attgtatagtctctca	A	G	NM_024717 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // intron // 0 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-do	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-1872398	tctagatgtccagaaa[C/T]gaccttgaaatatgaa	C	T	NM_024717 // upstream // 6717 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // upstream // 6717 // Hs.209095 // MCTP1 // 79772 // Homo sapiens mult	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-2089474	acttatttactcatca[A/G]cttaaatgttcatctc	A	G	NM_024717 // upstream // 141478 // Hs.209095 // MCTP1 // 79772 // Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, mRNA. /// NM_001002796 // upstream // 141478 // Hs.209095 // MCTP1 // 79772 // Homo sapiens	MCTP1	MCTP1, Homo sapiens multiple C2-domains with two transmembrane regions 1 (MCTP1), transcript variant L, q15
SNP_A-2142153	atctttgtaccgtca[A/G]ctcctaccattgtaca	A	G	NM_175616 // intron // 0 // Hs.8373 // FIS // 202299 // Homo sapiens FIS (FIS), mRNA. /// ENST00000357168 // intron // 0 // — // — // — // — // — ENST00000312734 // intron // 0 // — // — // —	FIS	FIS, Homo sapiens FIS (FIS), q15
SNP_A-1924145	ttagttgatagggaaa[C/G]agtcaccaatgttgtg	C	G	NM_012081 // upstream // 332930 // Hs.192221 // ELL2 // 22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 95414 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin ty	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-2266383	gaaggtggaacagtca[C/T]tcctgacactttctg	C	T	NM_012081 // upstream // 369899 // Hs.192221 // ELL2 // 22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 58445 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin ty	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1834029	tacatatcaagaatccc[A/G]accaattaccaccacc	A	G	NM_012081 // upstream // 392048 // Hs.192221 // ELL2 // 22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 36296 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin ty	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-1900509	tggagccttctgattc[G/T]ctccagtaggaagtgg	G	T	NM_012081 // upstream // 406530 // Hs.192221 // ELL2 // 22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 21814 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin ty	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-1856562	tcacaggagaaatccc[A/G]caactatgttccttcc	A	G	NM_012081 // upstream // 418947 // Hs.192221 // ELL2 // 22936 // Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), mRNA. /// NM_000439 // downstream // 9397 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin typ	ELL2	ELL2, Homo sapiens elongation factor, RNA polymerase II, 2 (ELL2), q15
SNP_A-1713386	gtcatttggagacttgtcaaagga[C/T]agaccctaattataaaat ggaaagg	C	T	BC013579 // intron // 0 // - // - // Homo sapiens calpastatin, mRNA (cDNA clone MGC:9402 IMAGE:3878564), complete cds.	-	- , rs1995186, Homo sapiens calpastatin, mRNA (cDNA clone MGC:9402 IMAGE:3878564), complete cds, q15
SNP_A-1798950	gtaagagcttttgtcg[A/G]actgtgactccagaaa	A	G	NM_000439 // 3UTR // 0 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// ENST00000311106 // 3UTR // 0 // — // — // —	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin q15
SNP_A-1952471	ttctgactcatatgc[A/G]agactcaccgagatg	A	G	NM_000439 // intron // 0 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// ENST00000311106 // intron // 0 // — // — // —	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin,q15
SNP_A-2213265	ccgcgcttggaagaag[A/T]ctgagtagttttttac	A	T	NM_000439 // intron // 0 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// ENST00000311106 // intron // 0 // — // — // —	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin,q15
SNP_A-1930408	ttcatttttgtagagaa[A/G]gaatcagaagcaagct	A	G	NM_000439 // intron // 0 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// ENST00000311106 // intron // 0 // — // — // —	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin q15
SNP_A-2220513	ccttctcttgaacta[C/T]atggcttgaagaatt	C	T	NM_000439 // intron // 0 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// ENST00000311106 // intron // 0 // — // — // —	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin,q15
SNP_A-1668488	caacaattcatgttggattacctat[A/G]caggctgacatttcaatc tcaact	A	G	NM_000439 // intron // 0 // Hs.78977 // PCSK1 // 5122 // proprotein convertase subtilisin/kexin type 1	PCSK1	PCSK1, rs271927, proprotein convertase subtilisin,q15
SNP_A-1880669	tcttgcttaatgcacc[C/T]gaccagtgacttattt	C	T	NM_000439 // upstream // 80264 // Hs.78977 // PCSK1 // 5122 // Homo sapiens proprotein convertase subtilisin/kexin type 1 (PCSK1), mRNA. /// NM_173062 // upstream // 162025 // Hs.440961 // CAST // 831 // Homo sapiens calpastatin (CAST), transcript variant	PCSK1	PCSK1, Homo sapiens proprotein convertase subtilisin,q15
SNP_A-1982583	agacatctctggagcc[C/T]gaacaatccatttact	C	T	NM_173062 // intron // 0 // Hs.440961 // CAST // 831 // Homo sapiens calpastatin (CAST), transcript variant 4, mRNA. /// NM_173060 // intron // 0 // Hs.440961 // CAST // 831 // Homo sapiens calpastatin (CAST), transcript variant 2, mRNA. /// NM_001750 //	CAST	CAST, Homo sapiens calpastatin (CAST), transcript variant 4, q15
SNP_A-1715791	ccaaaacaagcttacatcctggtgta[C/G]gaaagtttaatattaa attataat	C	G	NM_001750 // intron // 0 // Hs.440961 // CAST // 831 // calpastatin /// NM_173060 // intron // 0 // Hs.440961 // CAST // 831 // calpastatin /// NM_173061 // intron // 0 // Hs.440961 // CAST // 831 // calpastatin /// NM_173062 // intron // 0 // Hs.440961	CAST	CAST, rs26504, calpastatin, q15
SNP_A-1724140	aacccaagaaatgtaatgcaaacaa[C/T]tgggcctgtgtcactt agtcttct	C	T	NM_016442 // intron // 0 // Hs.436186 // ARTS-1 // 51752 // type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	ARTS-1	ARTS-1, rs469736, type 1 tumor necrosis factor receptor shedding aminopeptidase regulator,q15
SNP_A-1720783	tctgtttaatattgttccatttcc[C/T]ttctctttgccctgaaggcagg ctt	C	T	NM_005575 // intron // 0 // Hs.438827 // LNPEP // 4012 // leucyl/cystinyl aminopeptidase	LNPEP	LNPEP, rs1363974, leucyl,q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1696100	ttcaaatctataaacctataaagcat[A/C]tgaaagaaaaataaac ttctttatt	A	C	NM_005575 // intron // 0 // Hs.438827 // LNPEP // 4012 // leucyl/cystinyl aminopeptidase	LNPEP	LNPEP , rs27294, leucyl,q15
SNP_A-2313697	ggagcaagcacaaca[C/T]aggctgtaatagcta	C	T	NM_153234 // intron // 0 // Hs.128188 // LIX1 // 167410 // Homo sapiens chromosome 5 open reading frame 11 (C5orf11), mRNA. /// ENST00000274382 // intron // 0 // — // — // —	LIX1	LIX1, Homo sapiens chromosome 5 open reading frame 11 (C5orf11), q15
SNP_A-1982601	gaaaattggagaaaga[A/C]caaattagagtatatt	A	C	NM_153234 // upstream // 7461 // Hs.128188 // LIX1 // 167410 // Homo sapiens chromosome 5 open reading frame 11 (C5orf11), mRNA. /// NM_018343 // downstream // 12741 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENS	LIX1	LIX1, Homo sapiens chromosome 5 open reading frame 11 (C5orf11), q15
SNP_A-2198304	cattgttctctcttta[C/T]ctccttgagttcaatt	C	T	NM_153234 // upstream // 9768 // Hs.128188 // LIX1 // 167410 // Homo sapiens chromosome 5 open reading frame 11 (C5orf11), mRNA. /// NM_018343 // downstream // 10434 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENS	LIX1	LIX1, Homo sapiens chromosome 5 open reading frame 11 (C5orf11), q15
SNP_A-1798851	gtaacttttgagggaa[C/G]aggaattggcatttc	C	G	NM_153234 // upstream // 19199 // Hs.128188 // LIX1 // 167410 // Homo sapiens chromosome 5 open reading frame 11 (C5orf11), mRNA. /// NM_018343 // downstream // 1003 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENS	LIX1	LIX1, Homo sapiens chromosome 5 open reading frame 11 (C5orf11), q15
SNP_A-2126524	ataaaatatcttacac[C/T]gaaattgaggaaataa	C	T	NM_018343 // upstream // 26531 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 26531 // — // — // — /// ENST00000308338 // upstream // 1003631 // — // — // —	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-2176514	cacccacaaggtaacc[A/G]aatcacggagccaggt	A	G	NM_018343 // upstream // 356970 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 356970 // — // — // — // — /// ENST00000308338 // upstream // 673192 // — // — // — // —	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-2198350	catttaaattgagcaa[A/G]tgctagcctttcacat	A	G	NM_018343 // upstream // 363425 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 363425 // — // — // — // — /// ENST00000308338 // upstream // 666737 // — // — // — // —	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-1931809	ttccctttaatgctta[C/G]aaagggtaacgtggta	C	G	NM_018343 // upstream // 531749 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 531749 // — // — // — // — /// ENST00000308338 // upstream // 498413 // — // — // — // —	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q15
SNP_A-2192342	catcatatatccactgg[A/C]aaaattgtcaaatagt	A	C	NM_018343 // upstream // 756256 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 756256 // — // — // — // — /// ENST00000308338 // upstream // 273906 // — // — // — // —	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q21.1
SNP_A-1889155	tgagtccatgaagtaa[C/T]actcatccacatcgg	C	T	NM_018343 // upstream // 787325 // Hs.27021 // RIOK2 // 55781 // Homo sapiens RIO kinase 2 (yeast) (RIOK2), mRNA. /// ENST00000283109 // upstream // 787325 // — // — // — // — /// ENST00000308338 // upstream // 242837 // — // — // — // —	RIOK2	RIOK2, Homo sapiens RIO kinase 2 (yeast) (RIOK2), q21.1
SNP_A-1872399	tctagatgtctgtaaa[C/T]gccatcaatacagtca	C	T	NM_173670 // upstream // 201863 // Hs.526902 // RGMB // 285704 // Homo sapiens RGM domain family, member B (RGMB), mRNA. /// ENST00000308338 // downstream // 355459 // — // — // — // — /// ENST00000308234 // upstream // 201863 // — // — // —	RGMB	RGMB, Homo sapiens RGM domain family, member B (RGMB), q21.1
SNP_A-1682854	gccataaaatgagagagtggagaaaa[C/T]aatatttgtacattg atattgca	C	T	NM_018343 // upstream // 1351070 // Hs.27021 // RIOK2 // 55781 // RIO kinase 2 (yeast) /// NM_173670 // upstream // 237130 // Hs.161394 // RGMB // 285704 // RGM domain family, member B	RIOK2	RIOK2 , rs1978419, RIO kinase 2 (yeast) ,q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982644	ggtttagaagatgata[A/G]agcacagactagagtc	A	G	NM_001270 // upstream // 95951 // Hs.519474 // CHD1 // 1105 // Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), mRNA. /// ENST00000284049 // upstream // 95951 // — // — // — // — /// ENST00000344751 // downstream // 500444 // — /	CHD1	CHD1, Homo sapiens chromodomain helicase DNA binding protein 1 (CHD1), q21.1
SNP_A-1982665	catataccaatggtga[C/T]gtgatgtaatgcgaga	C	T	ENST00000331523 // downstream // 53900 // — // — // — // — /// ENST00000336068 // downstream // 10488 // — // — // — // —	-	q21.1
SNP_A-2221140	ccttgtgtcactgttc[C/G]ccttagaatttcaagc	C	G	NM_198507 // downstream // 157481 // Hs.356108 // UNQ1912 // 345757 // Homo sapiens HGS_RE408 (UNQ1912), mRNA. /// NM_175052 // downstream // 62981 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SI	UNQ1912	UNQ1912, Homo sapiens HGS_RE408 (UNQ1912), q21.1
SNP_A-1982684	aaacatctctctacgt[G/T]aaggtaatattctgca	G	T	NM_175052 // upstream // 313034 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 313034 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2233681	ctcatatatcagaatc[A/T]ccatggtttttaattg	A	T	NM_175052 // upstream // 397013 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 397013 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2113498	aggctaaaatcctgac[C/T]atgacaaaaataaatt	C	T	NM_175052 // upstream // 419195 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 419195 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1663408	caagaaaataaatctaacccagata[A/G]ataatgcttttaactatatctgatt	A	G	AF119865 // downstream // 952449 // Hs.127648 // SLCO4C1 // 353189 // solute carrier organic anion transporter family, member 4C1 /// NM_005668 // upstream // 378275 // Hs.308628 // SIAT8D // 7903 // sialyltransferase 8D (alpha-2, 8-polysialyltransferase	SLCO4C1	SLCO4C1 , rs4415055, solute carrier organic anion transporter family, member 4C1 ,q21.1
SNP_A-2077466	accacatccaaaccaa[C/T]agccagttatcatacc	C	T	NM_175052 // upstream // 436039 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 436039 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1890366	tgatccgcccttaagc[G/T]cacaccaccttaatat	G	T	NM_175052 // upstream // 443668 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 443668 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1936876	ttctttctttccaata[C/G]agctgcagcagcaccg	C	G	NM_175052 // upstream // 467091 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 467091 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2159995	atttatgtaactctta[A/G]gcccaagaatgctatt	A	G	NM_175052 // upstream // 468155 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 468155 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213154	ccgatggtgacagcta[C/T]aacctaacatgaaaat	C	T	NM_175052 // upstream // 511897 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 511897 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1959117	tttgaagtgcgata[A/C]actgtattatgatatg	A	C	NM_175052 // upstream // 512721 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 512721 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2135408	atatttccttccttga[A/G]cctaattgcatatgcc	A	G	NM_175052 // upstream // 517903 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 517903 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2146760	atgcttccgagtattg[C/G]actaggtgtgcctggc	C	G	NM_175052 // upstream // 519869 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 519869 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1810601	gtgcaactcaaaggaat[C/T]attcagaaacatattg	C	T	NM_175052 // upstream // 522805 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 522805 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1721275	aatataggaaaatgactaatagcac[A/G]aacatcaaatcagagt ctcaaattg	A	G	AF119865 // downstream // 849056 // Hs.127648 // SLCO4C1 // 353189 // solute carrier organic anion transporter family, member 4C1 /// NM_005668 // upstream // 481668 // Hs.308628 // SIAT8D // 7903 // sialyltransferase 8D (alpha-2, 8-polysialyltransferase	SLCO4C1	SLCO4C1 , rs1037796, solute carrier organic anion transporter family, member 4C1 ,q21.1
SNP_A-2063684	aattactgtatatggat[A/C]attttgcaagttttc	A	C	NM_175052 // upstream // 725279 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 725279 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1889891	tgatagagaatggaac[C/T]gtgactaaagtaagat	C	T	NM_175052 // upstream // 966004 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 966004 // Hs.308628 // ST8SIA4 // 7903 // Homo sapie	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1708915	atgatcttggattatgttcccttga[A/G]gtaaatcccactacaaag ctgaatc	A	G	AF119865 // downstream // 359446 // Hs.127648 // SLCO4C1 // 353189 // solute carrier organic anion transporter family, member 4C1 /// NM_005668 // upstream // 971278 // Hs.308628 // SIAT8D // 7903 // sialyltransferase 8D (alpha-2, 8-polysialyltransferase	SLCO4C1	SLCO4C1 , rs7731840, solute carrier organic anion transporter family, member 4C1 ,q21.1
SNP_A-2288605	gattgcgtttagaca[C/T]gtggctgtgggggatg	C	T	NM_175052 // upstream // 1022830 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 1022830 // Hs.308628 // ST8SIA4 // 7903 // Homo sap	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1741859	actatttttgcaatttactctcctc[G/T]attgttatttaggcttacagaa tgc	G	T	AF119865 // downstream // 335573 // Hs.127648 // SLCO4C1 // 353189 // solute carrier organic anion transporter family, member 4C1 /// NM_005668 // upstream // 995151 // Hs.308628 // SIAT8D // 7903 // sialyltransferase 8D (alpha-2, 8-polysialyltransferase	SLCO4C1	SLCO4C1 , rs9285932, solute carrier organic anion transporter family, member 4C1 ,q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1822029	gttttccagactctag[A/G]acagtaatgcttaaat	A	G	NM_175052 // upstream // 1061854 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 1061854 // Hs.308628 // ST8SIA4 // 7903 // Homo sap	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1982696	taaacctactgaaaaa[A/T]tgtcaaactctaggt	A	T	NM_175052 // upstream // 1124528 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 1124528 // Hs.308628 // ST8SIA4 // 7903 // Homo sap	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-1982697	gtagcattggcataaag[C/T]agctgaaaatgcattg	C	T	NM_175052 // upstream // 1199936 // Hs.308628 // ST8SIA4 // 7903 // Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, mRNA. /// NM_005668 // upstream // 1199936 // Hs.308628 // ST8SIA4 // 7903 // Homo sap	ST8SIA4	ST8SIA4, Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialyltransferase) (SIAT8D), transcript variant 2, q21.1
SNP_A-2185873	caggattccttaccc[A/G]gcacactctaaactct	A	G	NM_180991 // upstream // 122220 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 447054 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-2291749	gcacagaaagaagaaa[A/G]agcagtcataaaggaa	A	G	NM_180991 // upstream // 203690 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 365584 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-2242763	ctgcattatacgcatc[C/T]aatggctcgagggata	C	T	NM_180991 // upstream // 368170 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 201104 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-2191083	catagtagaaaaaggat[C/T]gtttaggacaggaga	C	T	NM_180991 // upstream // 371304 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 197970 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-2177844	cacgtttgtatggtcc[A/G]gaaaactgagagcagc	A	G	NM_180991 // upstream // 371554 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 197720 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-1869878	tccttgacatctttaa[A/C]tagtaagccagcaggt	A	C	NM_180991 // upstream // 372596 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 196678 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-2097999	agagagataacaccat[C/G]actaaattcacacca	C	G	NM_180991 // upstream // 382808 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 186466 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-1870002	tccttgagtcactgta[A/T]gaagctctactttaa	A	T	NM_180991 // upstream // 468603 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 100671 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1817580	gttccaagaattatgt[C/G]aagtactgaaataaaa	C	G	NM_180991 // upstream // 493494 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 75780 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine a	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-1803935	gtcaatagagtggcca[C/T]agtaattcttccaaaa	C	T	NM_180991 // upstream // 521161 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 48113 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine a	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-2177959	cactaatgttatggta[A/C]ctttgtaggctcctga	A	C	NM_180991 // upstream // 528532 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 40742 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine a	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-1905662	tggtatcaaagtttta[C/T]cttccattgaaatcca	C	T	NM_180991 // upstream // 535455 // Hs.127648 // SLCO4C1 // 353189 // Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA. /// NM_138821 // upstream // 33819 // Hs.369430 // PAM // 5066 // Homo sapiens peptidylglycine a	SLCO4C1	SLCO4C1, Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), q21.1
SNP_A-1674443	atctgctaggttgtggcttatttca[C/T]cactgtactgaatctcactacttta	C	T	NM_000919 // upstream // 35453 // Hs.352733 // PAM // 5066 // peptidylglycine alpha-amidating monooxygenase /// NM_015216 // upstream // 289894 // Hs.26179 // KIAA0433 // 23262 // KIAA0433 protein /// NM_017676 // downstream // 257448 // Hs.24088 // FLJ2	PAM	PAM , rs468501, peptidylglycine alpha-amidating monooxygenase ,q21.1
SNP_A-1659342	tcagagtttaggagcaggagatata[C/T]gatgtgctatttttagggtcataga	C	T	U19966 // intron // 0 // Hs.352733 // PAM // 5066 // peptidylglycine alpha-amidating monooxygenase	PAM	PAM , rs9327877, peptidylglycine alpha-amidating monooxygenase,q21.1
SNP_A-1810139	gtgatcattaatgcca[A/G]aaacaaacatactgtc	A	G	ENST00000354398 // intron // 0 // — // — // — // — // —	-	q21.1
SNP_A-1982747	cttcttcatgtaatcc[A/G]gaagttagagaaagag	A	G	ENST00000359550 // downstream // 150086 // — // — // — // — // — /// ENST00000357810 // downstream // 107719 // — // — // — // — // —	-	q21.2
SNP_A-1982763	ttttgagattggctgc[A/G]ctaggttaatcttggg	A	G	NM_001962 // downstream // 2601901 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 555249 // — // — // — // — // — /// ENST00000333274 // downstream // 2601901 // — // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-1982764	aggaagctgggaaaca[C/T]taggcagaaaaatgaa	C	T	NM_001962 // downstream // 2601843 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 555307 // — // — // — // — // — /// ENST00000333274 // downstream // 2601843 // — // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-1723354	taaagccagaaaatagagataagac[A/T]gaggaaatataagaattatgtaacc	A	T	NM_001962 // downstream // 2556218 // Hs.37142 // EFNA5 // 1946 // ephrin-A5 /// NM_031438 // upstream // 1261676 // Hs.434289 // NUDT12 // 83594 // nudix (nucleoside diphosphate linked moiety X)-type motif 12	EFNA5	EFNA5 , rs58982, ephrin-A5 ,q21.2
SNP_A-2265732	gaagctgtttgtatca[A/C]gacggcaaatccctca	A	C	NM_001962 // downstream // 2495140 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 662010 // — // — // — // — // — /// ENST00000333274 // downstream // 2495140 // — // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-2295614	gcatgaaaggtactga[A/G]aaaagtgctgatattg	A	G	NM_001962 // downstream // 2349333 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 807817 // — // — // — // — // — /// ENST00000333274 // downstream // 2349333 // — // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-1953415	tttgaacatgaacata[A/T]agtaatggaagctgcc	A	T	NM_001962 // downstream // 2293272 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 863878 // — // — // — // — // — /// ENST00000333274 // downstream // 2293272 // — // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1982767	cagcagatttctaaaa[C/T]gcactcgtcttgcctt	C	T	NM_001962 // downstream // 2256796 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 900354 // — // — // — // /// ENST00000333274 // downstream // 2256796 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.2
SNP_A-2044582	aagaaaccacagactа[C/T]gattgcagaaaaaat	C	T	NM_001962 // downstream // 2222373 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 934777 // — // — // — // /// ENST00000333274 // downstream // 2222373 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1838545	tagaattaacagtaa[C/G]gttaaaataatctgat	C	G	NM_001962 // downstream // 2093402 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 1063748 // — // — // — // /// ENST00000333274 // downstream // 2093402 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1982774	cttttcatctgaatc[C/T]cgtcaacatcaactcc	C	T	NM_001962 // downstream // 899377 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2257773 // — // — // — // /// ENST00000333274 // downstream // 899377 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1831300	taatgggggattata[C/T]gaatttagaagtta	C	T	NM_001962 // downstream // 517244 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2639906 // — // — // — // /// ENST00000333274 // downstream // 517244 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2277987	gagccaggaacaagta[G/T]gaaggatgaaaaagtt	G	T	NM_001962 // downstream // 289347 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2867803 // — // — // — // /// ENST00000333274 // downstream // 289347 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2209622	cccatgctgtgtaagg[C/T]atcctctgttaaagct	C	T	NM_001962 // downstream // 262561 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2894589 // — // — // — // /// ENST00000333274 // downstream // 262561 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2041938	aactaagtgtcaaaca[C/G]ctgaggctccatagat	C	G	NM_001962 // downstream // 259854 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2897296 // — // — // — // /// ENST00000333274 // downstream // 259854 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2149499	atgtagatatagaaaa[A/G]aggctaagaacataga	A	G	NM_001962 // downstream // 215987 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2941163 // — // — // — // /// ENST00000333274 // downstream // 215987 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2172427	caattatatgctgaca[A/G]tggcaaaatggatgcc	A	G	NM_001962 // downstream // 215754 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2941396 // — // — // — // /// ENST00000333274 // downstream // 215754 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1685270	taccagactggcacaggagaagaaa[G/T]gtagtgaatactaat ttgaataccg	G	T	NM_001962 // downstream // 257201 // Hs.37142 // EFNA5 // 1946 // ephrin-A5 /// NM_031438 // upstream // 3560693 // Hs.434289 // NUDT12 // 83594 // nudix (nucleoside diphosphate linked moiety X)-type motif 12	EFNA5	EFNA5 , rs4637535, ephrin-A5 , q21.3
SNP_A-1654353	gtacacagacatggtggagcagtca[A/G]aatacatacatttaag ttctccctc	A	G	NM_001962 // downstream // 242602 // Hs.37142 // EFNA5 // 1946 // ephrin-A5 /// NM_031438 // upstream // 3575292 // Hs.434289 // NUDT12 // 83594 // nudix (nucleoside diphosphate linked moiety X)-type motif 12	EFNA5	EFNA5 , rs2410936, ephrin-A5 , q21.3
SNP_A-1982786	cttctcaaatatgta[A/C]gagatgtcagaattat	A	C	NM_001962 // downstream // 181822 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2975328 // — // — // — // /// ENST00000333274 // downstream // 181822 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1687350	gagaagaaaaatgagtatgaagtca[A/G]taggtgagaaagaa ggctgcagcac	A	G	NM_001962 // downstream // 211501 // Hs.37142 // EFNA5 // 1946 // ephrin-A5 /// NM_031438 // upstream // 3606393 // Hs.434289 // NUDT12 // 83594 // nudix (nucleoside diphosphate linked moiety X)-type motif 12	EFNA5	EFNA5 , rs10515368, ephrin-A5 , q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2162987	attttgtttaacctaa[C/T]gttctccaggctcatt	C	T	NM_001962 // downstream // 160710 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2996440 // — // — // — /// ENST00000333274 // downstream // 160710 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2042018	aactaccactcactgc[A/G]ataaaatagatttccaa	A	G	NM_001962 // downstream // 160106 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2997044 // — // — // — /// ENST00000333274 // downstream // 160106 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1982787	cacatatgcagtaaaa[G/T]taggctgtgtggga	G	T	NM_001962 // downstream // 159824 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 2997326 // — // — // — /// ENST00000333274 // downstream // 159824 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2201413	ccaatgaaacaggata[C/G]aaaggccagaaataag	C	G	NM_001962 // downstream // 155629 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 3001521 // — // — // — /// ENST00000333274 // downstream // 155629 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-2113183	aggcccacatgaacaa[A/C]aatgttatagcaatat	A	C	NM_001962 // downstream // 122702 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000357810 // upstream // 3034448 // — // — // — /// ENST00000333274 // downstream // 122702 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1982799	cagagctgaacattga[A/G]gttgattaccaataca	A	G	NM_001962 // intron // 0 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000333274 // intron // 0 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1982819	gtgagccaacattcaa[A/C]aaggtcatgctagttc	A	C	NM_001962 // intron // 0 // Hs.128518 // EFNA5 // 1946 // Homo sapiens ephrin-A5 (EFNA5), mRNA. /// ENST00000333274 // intron // 0 // — // — // — // —	EFNA5	EFNA5, Homo sapiens ephrin-A5 (EFNA5), q21.3
SNP_A-1658284	tgatgatttcactcttctaaccctg[C/T]aaaggacttgcgcatacta tcccaa	C	T	AL133602 // downstream // 168972 // Hs.179112 // FBXO13 // 64839 // F-box only protein 13 /// NM_001962 // upstream // 38378 // Hs.37142 // EFNA5 // 1946 // ephrin-A5	FBXO13	FBXO13 , -, F-box only protein 13 ,q21.3
SNP_A-2125439	agtttagaagttgcca[A/C]tctgttctaaaaaata	A	C	NM_022824 // intron // 0 // Hs.112143 // FBXL17 // 64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// ENST00000359660 // intron // 0 // — // — // — // — /// ENST00000274413 // intron // 0 // — // — // — // —	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-2254697	cttgctctcccaaggc[C/T]gcattgacattgcaag	C	T	NM_022824 // upstream // 164163 // Hs.112143 // FBXL17 // 64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 202249 // Hs.221472 // FER // 2241 // Homo sapiens fer (fps/fes related) tyrosine kinase	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1982848	gatgtgcagaacttta[C/T]aatgtattgaaatcct	C	T	NM_022824 // upstream // 317144 // Hs.112143 // FBXL17 // 64839 // Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), mRNA. /// NM_005246 // upstream // 49268 // Hs.221472 // FER // 2241 // Homo sapiens fer (fps/fes related) tyrosine kinase (	FBXL17	FBXL17, Homo sapiens F-box and leucine-rich repeat protein 17 (FBXL17), q21.3
SNP_A-1757277	aactgaggcagaagaaaattacatc[A/G]atggaaacttggat ctagacagat	A	G	AL133602 // upstream // 328811 // Hs.179112 // FBXO13 // 64839 // F-box only protein 13 /// BC011940 // downstream // 31062 // Hs.133009 // - // - // CDNA FLJ44485 fis, done UTERU2033420	FBXO13	FBXO13 , rs2174973, F-box only protein 13 ,q21.3
SNP_A-1700512	tctctgcctgtcctcttgtctgca[C/T]gatttcttgggtctcagtgac aac	C	T	AL133602 // upstream // 331292 // Hs.179112 // FBXO13 // 64839 // F-box only protein 13 /// BC011940 // downstream // 28581 // Hs.133009 // - // - // CDNA FLJ44485 fis, done UTERU2033420	FBXO13	FBXO13 , rs9326745, F-box only protein 13 ,q21.3
SNP_A-1859740	tcagggaccaaggcag[A/G]atctctttttgtctt	A	G	NM_005246 // intron // 0 // Hs.221472 // FER // 2241 // Homo sapiens fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94) (FER), mRNA. /// ENST00000281092 // intron // 0 // — // — // — // —	FER	FER, Homo sapiens fer (fps q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2046053	aagactacattcctcc[A/G]ctcctcttgcaaaggg	A	G	NM_005246 // intron // 0 // Hs.221472 // FER // 2241 // Homo sapiens fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94) (FER), mRNA. /// ENST00000281092 // intron // 0 // — // — // —	FER	FER, Homo sapiens fer (fps q21.3
SNP_A-2050223	aaggagaaaagtggca[C/G]cacatatcttcata	C	G	NM_005246 // intron // 0 // Hs.221472 // FER // 2241 // Homo sapiens fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94) (FER), mRNA. /// ENST00000281092 // intron // 0 // — // — // —	FER	FER, Homo sapiens fer (fps q21.3
SNP_A-1982865	gccaaatgatgagtaa[C/T]ataggtcaggagacaa	C	T	NM_002372 // upstream // 60500 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000340141 // downstream // 39937 // — // — // — // — /// ENST00000261483 // upstream // 60500 // — //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-2141445	atcttaaaatgaacaa[A/G]tcacctggataaacat	A	G	NM_002372 // upstream // 4432 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000340141 // downstream // 96005 // — // — // — // — /// ENST00000261483 // upstream // 4432 // — // –	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-1716315	ttcccaactactcttcaggcacc[A/G]aagattctaaatcaagc caatctcc	A	G	NM_002372 // intron // 0 // Hs.439599 // MAN2A1 // 4124 // mannosidase, alpha, class 2A, member 1	MAN2A1	MAN2A1 , rs2269197, mannosidase, alpha, class 2A, member 1,q21.3
SNP_A-1729846	atggaatactattagtcataaaaa[A/C]ctatgaaatcatatcattt gtagca	A	C	NM_002372 // intron // 0 // Hs.439599 // MAN2A1 // 4124 // mannosidase, alpha, class 2A, member 1	MAN2A1	MAN2A1 , rs2218071, mannosidase, alpha, class 2A, member 1,q21.3
SNP_A-2243907	ctgctgtctatttcta[A/T]gtaatcctctgcttag	A	T	NM_002372 // downstream // 53947 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 53947 // — // — // — // — /// ENST00000341720 // downstream // 647343 // –	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-1918949	ttaaccatcagctctg[A/T]aattatagagtaagga	A	T	NM_002372 // downstream // 218173 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 218173 // — // — // — // — /// ENST00000341720 // downstream // 483117 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q21.3
SNP_A-1739099	ctacttaatacctgatcactcaaa[A/G]tagcgagttgtagaaaa ctgtttgt	A	G	NM_002372 // downstream // 333725 // Hs.439599 // MAN2A1 // 4124 // mannosidase, alpha, class 2A, member 1 /// NM_138773 // upstream // 538171 // Hs.75639 // LOC91137 // 91137 // hypothetical protein BC017169	MAN2A1	MAN2A1 , rs10515412, mannosidase, alpha, class 2A, member 1 ,q21.3
SNP_A-2149417	atgtactccataaata[A/T]atacctacagtgtacc	A	T	NM_002372 // downstream // 433506 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 433506 // — // — // — // — /// ENST00000341720 // downstream // 267784 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-2116441	aggtatctccgaaaca[C/T]tgtggatctagagatg	C	T	NM_002372 // downstream // 463535 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 463535 // — // — // — // — /// ENST00000341720 // downstream // 237755 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-2166897	caaattttcgggttta[C/T]atggttagtgtatgtt	C	T	NM_002372 // downstream // 506103 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 506103 // — // — // — // — /// ENST00000341720 // downstream // 195187 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-1908593	tgtagccaggccaaga[C/T]gaagctcagtaagtca	C	T	NM_002372 // downstream // 547457 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 547457 // — // — // — // — /// ENST00000341720 // downstream // 153833 //	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869681	tccttatgagccttgc[A/G]gacaaagaggtatcct	A	G	NM_002372 // downstream // 629502 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 629502 // — // — // — // — /// ENST00000341720 // downstream // 71788 // -	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-1754964	ttttaaaatgtcatctttatataac[A/G]agggaaatttgacaccact aagttt	A	G	NM_002372 // downstream // 597483 // Hs.439599 // MAN2A1 // 4124 // mannosidase, alpha, class 2A, member 1 /// NM_138773 // upstream // 274413 // Hs.75639 // LOC91137 // 91137 // hypothetical protein BC017169	MAN2A1	MAN2A1 , rs1488602, mannosidase, alpha, class 2A, member 1 ,q22.1
SNP_A-2124643	agttctaaaaatcata[A/C]ggcagaaattgaaaaa	A	C	NM_002372 // downstream // 647783 // Hs.432822 // MAN2A1 // 4124 // Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA. /// ENST00000261483 // downstream // 647783 // — // — // — // — /// ENST00000341720 // downstream // 53507 // -	MAN2A1	MAN2A1, Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), q22.1
SNP_A-2011136	gatagtttggacttgg[A/C]aaaggtacactaaaga	A	C	ENST00000341720 // intron // 0 // — // — // — // —	-	q22.1
SNP_A-1889596	tgataaaaggcagtgc[G/T]aaagataaaaagggaa	G	T	ENST00000334037 // intron // 0 // — // — // — // —	-	q22.1
SNP_A-1852712	tatttcacactaacta[G/T]aattgctaacattaaa	G	T	NM_138773 // upstream // 53575 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream // 60026 // — // — // — // — /// ENST00000334037 // upstream // 18132 // — // — //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1873527	tctcaattgttattag[C/G]cctgcccttgccccag	C	G	NM_138773 // upstream // 49828 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream // 63773 // — // — // — // — /// ENST00000334037 // upstream // 21879 // — // — //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1982899	agacctattctgcatg[A/G]acccttatgatcttaa	A	G	NM_138773 // upstream // 13500 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream // 100101 // — // — // — // — /// ENST00000334037 // upstream // 58207 // — // — //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-2089165	acttacagccttccat[A/C]aattctataaaccctg	A	C	NM_138773 // upstream // 9243 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000341720 // upstream // 104358 // — // — // — // — /// ENST00000334037 // upstream // 62464 // — // — //	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1913500	tgtggttataccactg[G/T]aaacatcttgtagttt	G	T	NM_138773 // intron // 0 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// ENST00000296626 // intron // 0 // — // — // — // — /// ENST00000355943 // intron // 0 // — // — // — // —	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1725404	ttcttctaaaacacagcaccagtac[A/C]gaactgtttcttcaagttt aggact	A	C	NM_002372 // downstream // 849641 // Hs.439599 // MAN2A1 // 4124 // mannosidase, alpha, class 2A, member 1 /// NM_138773 // upstream // 22255 // Hs.75639 // LOC91137 // 91137 // hypothetical protein BC017169	MAN2A1	MAN2A1 , rs2443513, mannosidase, alpha, class 2A, member 1 ,q22.1
SNP_A-2091739	agaaaagggcctagga[C/T]gaagatacaaggcttt	C	T	NM_138773 // downstream // 191679 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// NM_138551 // upstream // 115617 // Hs.389874 // TSLP // 85480 // Homo sapiens thymic stromal lymphopoietin (TSLP), trans	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1
SNP_A-1960793	tttttcttatcctaca[C/T]gtctaatccatcacca	C	T	NM_138773 // downstream // 192541 // Hs.75639 // LOC91137 // 91137 // Homo sapiens hypothetical protein BC017169 (LOC91137), mRNA. /// NM_138551 // upstream // 114755 // Hs.389874 // TSLP // 85480 // Homo sapiens thymic stromal lymphopoietin (TSLP), trans	LOC91137	LOC91137, Homo sapiens hypothetical protein BC017169 (LOC91137), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1846344	tatatgccatatatcat[C/T]attcctttcgcaactt	C	T	NM_139281 // downstream // 79794 // Hs.533237 // WDR36 // 134430 // Homo sapiens WD repeat domain 36 (WDR36), mRNA. /// NM_001744 // upstream // 17631 // Hs.220629 // CAMK4 // 814 // Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRN	WDR36	WDR36, Homo sapiens WD repeat domain 36 (WDR36), q22.1
SNP_A-1866514	tcccccataggtctca[C/T]taaagctgaacctcct	C	T	NM_001744 // intron // 0 // Hs.220629 // CAMK4 // 814 // Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA. /// ENST00000282356 // intron // 0 // — // — // —	CAMK4	CAMK4, Homo sapiens calcium q22.1
SNP_A-1658250	aaaggcactaagaagaaaggacgga[A/G]atattacacctctg tcagacttga	A	G	NM_001744 // intron // 0 // Hs.440638 // CAMK4 // 814 // calcium/calmodulin-dependent protein kinase IV	CAMK4	CAMK4 , rs3797757, calcium,q22.1
SNP_A-1877124	tctgctgaagtgtgaa[A/T]tgtgaaggcactgccc	A	T	NM_139164 // upstream // 72741 // Hs.93842 // STARD4 // 134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream // 144104 // Hs.483067 // C5orf13 // 9315 // Homo sapiens chromosome 5 open reading fram	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-2157559	attgattcaagaaata[C/T]gtagaaggtaaaatag	C	T	NM_139164 // upstream // 82917 // Hs.93842 // STARD4 // 134429 // Homo sapiens START domain containing 4, sterol regulated (STARD4), mRNA. /// NM_004772 // downstream // 133928 // Hs.483067 // C5orf13 // 9315 // Homo sapiens chromosome 5 open reading fram	STARD4	STARD4, Homo sapiens START domain containing 4, sterol regulated (STARD4), q22.1
SNP_A-1701875	tattgggatctatacagtgtctaca[C/T]attgatgataatgccttttctct	C	T	NM_004772 // downstream // 98780 // Hs.508741 // C5orf13 // 9315 // chromosome 5 open reading frame 13 /// NM_139164 // upstream // 118056 // Hs.93842 // STARD4 // 134429 // START domain containing 4, sterol regulated	C5orf13	C5orf13 , rs1457715, chromosome 5 open reading frame 13 ,q22.1
SNP_A-2158146	attggatctgccggt[C/G]aaatggcccaagtggc	C	G	NM_004772 // upstream // 286233 // Hs.483067 // C5orf13 // 9315 // Homo sapiens chromosome 5 open reading frame 13 (C5orf13), mRNA. /// NM_053000 // upstream // 116630 // Hs.12082 // TIGA1 // 114915 // Homo sapiens TIGA1 (TIGA1), mRNA. /// NM_022140 // do	C5orf13	C5orf13, Homo sapiens chromosome 5 open reading frame 13 (C5orf13), q22.1
SNP_A-1693106	tataaatacccagtttctcaaatac[A/G]ctggaatcagctttctat attact	A	G	NM_004772 // upstream // 307151 // Hs.508741 // C5orf13 // 9315 // chromosome 5 open reading frame 13 /// NM_022140 // downstream // 100593 // Hs.104746 // EPB41L4A // 64097 // erythrocyte membrane protein band 4.1 like 4A /// NM_053000 // upstream // 96	C5orf13	C5orf13 , rs187500, chromosome 5 open reading frame 13 ,q22.1
SNP_A-2164288	caaaatataagtggac[A/G]cttctctgaggcttt	A	G	NM_004772 // upstream // 364584 // Hs.483067 // C5orf13 // 9315 // Homo sapiens chromosome 5 open reading frame 13 (C5orf13), mRNA. /// NM_053000 // upstream // 38279 // Hs.12082 // TIGA1 // 114915 // Homo sapiens TIGA1 (TIGA1), mRNA. /// NM_022140 // dow	C5orf13	C5orf13, Homo sapiens chromosome 5 open reading frame 13 (C5orf13), q22.1
SNP_A-2116851	aggtctctttgggga[C/T]gtgtgtttgaggcaa	C	T	NM_022140 // intron // 0 // Hs.421767 // EPB41L4A // 64097 // Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), mRNA. /// ENST00000359109 // intron // 0 // — // — // — /// ENST00000261485 // intron // 0 // — // — // -	EPB41L4A	EPB41L4A, Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), q22.2
SNP_A-2092149	agaaacttcttcacaa[C/G]agtcatcaaaacctg	C	G	NM_022140 // intron // 0 // Hs.421767 // EPB41L4A // 64097 // Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), mRNA. /// ENST00000261486 // intron // 0 // — // — // —	EPB41L4A	EPB41L4A, Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), q22.2
SNP_A-1792945	ggtacacaggataaca[C/T]agatttccaaaagct	C	T	NM_022140 // intron // 0 // Hs.421767 // EPB41L4A // 64097 // Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), mRNA. /// ENST00000261486 // intron // 0 // — // — // —	EPB41L4A	EPB41L4A, Homo sapiens erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1790247	ggggagagtaagctga[C/T]ggatacctctcatttt	C	T	NM_000038 // upstream // 208088 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 225071 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-2265401	gaagcatgcatgtaca[A/G]actaaaaacttttc	A	G	NM_000038 // upstream // 203910 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 220893 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1739833	tgtattgatacataaatcaatgtcca[A/G]taaattacacatatttaaa ctacag	A	G	NM_000038 // upstream // 237787 // Hs.75081 // APC // 324 // adenomatosis polyposis coli /// NM_019033 // downstream // 79148 // - // - // -	APC	APC , rs462241, adenomatosis polyposis coli ,q22.2
SNP_A-1731689	tgttataactcataaaccagccctg[A/T]attaaaataatgttataatc ctactg	A	T	NM_000038 // upstream // 226292 // Hs.75081 // APC // 324 // adenomatosis polyposis coli /// NM_019033 // downstream // 90643 // - // - // - // -	APC	APC , rs255714, adenomatosis polyposis coli ,q22.2
SNP_A-1827635	taactggcttcagaaa[C/G]agcatagtgttgggca	C	G	NM_000038 // upstream // 163507 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 180490 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1902061	tggcatctgcaggtaa[C/T]tggagctttggtact	C	T	NM_000038 // upstream // 159821 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 176804 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1812432	gtggcagtaagctgga[C/T]gggagaacacaacca	C	T	NM_000038 // upstream // 157705 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 174688 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-2011142	tagatagcatgctccat[C/G]taggacagggcccagg	C	G	NM_000038 // upstream // 101390 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 118373 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1959863	tttggcttcggtgaa[C/G]aaaaatcgcatatatc	C	G	NM_000038 // upstream // 90812 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// NM_000038 // upstream // 107795 // Hs.158932 // APC // 324 // Homo sapiens adenomatosis polyposis coli (APC), mRNA. /// ENST00000307249	APC	APC, Homo sapiens adenomatosis polyposis coli (APC), q22.2
SNP_A-1725102	gacacaaaatccctgtgcctaagc[C/G]actatgaaatagttgc acataattt	C	G	NM_000038 // upstream // 103044 // Hs.75081 // APC // 324 // adenomatosis polyposis coli /// NM_019033 // downstream // 213891 // - // - // - // -	APC	APC , rs964417, adenomatosis polyposis coli ,q22.2
SNP_A-2042130	aactagcattcagccc[A/G]gcaatcacattactgg	A	G	NM_002387 // intron // 0 // Hs.483104 // MCC // 4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// ENST00000359932 // intron // 0 // — // — // — /// ENST00000302475 // intron // 0 // — // — // — // —	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-2011149	gctgaaaacagcacac[C/T]cctatcttcccaaatt	C	T	NM_002387 // intron // 0 // Hs.483104 // MCC // 4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// ENST00000359932 // intron // 0 // — // — // — /// ENST00000302475 // intron // 0 // — // — // — // —	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-2119088	agtagatgccaatatc[C/G]catataccacataaat	C	G	NM_002387 // intron // 0 // Hs.483104 // MCC // 4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// ENST00000359932 // intron // 0 // — // — // — /// ENST00000302475 // intron // 0 // — // — // — // —	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803416	gtatttcgtaccacaa[G/T]ggctgttattcaccat	G	T	NM_002387 // intron // 0 // Hs.483104 // MCC // 4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// ENST00000359932 // intron // 0 // --- // --- // --- // --- /// ENST00000302475 // intron // 0 // --- // --- // --- // ---	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-2069589	acacacacactaagga[A/C]gcctagataaaatatg	A	C	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-2120925	agtctactctggtctc[C/G]atgagagtgaagtccc	C	G	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-1916645	tgtttattaaatgcta[G/T]ctatgtcacaggccat	G	T	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-1837453	tacttctgttcaacct[A/G]agccagaatatatagc	A	G	ENST00000359932 // intron // 0 // --- // --- // --- // ---	-	q22.2
SNP_A-2220455	ccttctatgttacaca[C/T]gaatgagaatataaag	C	T	NM_002387 // upstream // 94476 // Hs.483104 // MCC // 4163 // Homo sapiens mutated in colorectal cancers (MCC), mRNA. /// NM_032028 // downstream // 44655 // Hs.519507 // STK22D // 83942 // Homo sapiens serine/threonine kinase 22D (spermiogenesis associat	MCC	MCC, Homo sapiens mutated in colorectal cancers (MCC), q22.2
SNP_A-1731771	gtataatattctgtcttattctact[C/G]actctctcagattataatcaaaata	C	G	NM_002387 // upstream // 108062 // Hs.409515 // MCC // 4163 // mutated in colorectal cancers /// NM_032028 // downstream // 30311 // Hs.333138 // STK22D // 83942 // serine/threonine kinase 22D (spermiogenesis associated)	MCC	MCC , rs6870401, mutated in colorectal cancers ,q22.2
SNP_A-1920955	ttacagaatcaatgca[A/G]tccttctcagaatacc	A	G	NM_032028 // upstream // 48491 // Hs.519507 // STK22D // 83942 // Homo sapiens serine/threonine kinase 22D (spermiogenesis associated) (STK22D), mRNA. /// NM_022828 // upstream // 30383 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing	STK22D	STK22D, Homo sapiens serine,q22.2
SNP_A-2136447	atcacatgtacatgga[C/T]aggaaaacttttgtt	C	T	NM_032028 // upstream // 48550 // Hs.519507 // STK22D // 83942 // Homo sapiens serine/threonine kinase 22D (spermiogenesis associated) (STK22D), mRNA. /// NM_022828 // upstream // 30324 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing	STK22D	STK22D, Homo sapiens serine,q22.2
SNP_A-2161693	atttggtcagggagga[A/G]tactgttcaggaatac	A	G	NM_032028 // upstream // 74198 // Hs.519507 // STK22D // 83942 // Homo sapiens serine/threonine kinase 22D (spermiogenesis associated) (STK22D), mRNA. /// NM_022828 // upstream // 4676 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing	STK22D	STK22D, Homo sapiens serine q22.2
SNP_A-2194692	catgccaactaaattg[C/T]agtgtatgggagtgag	C	T	NM_022828 // downstream // 64143 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 702894 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-acti	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.2
SNP_A-1799016	gtaagcataggcagaa[A/G]ccatagatttaggcat	A	G	NM_022828 // downstream // 478286 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 288751 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-act	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.3
SNP_A-1821462	gtttgggaaacagaca[C/T]aagaaacacataaacc	C	T	NM_022828 // downstream // 558266 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 208771 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-act	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.3
SNP_A-1890476	tgatctctgatttcca[C/T]tgatctgttaggtgaa	C	T	NM_022828 // downstream // 650806 // Hs.231942 // YTHDC2 // 64848 // Homo sapiens YTH domain containing 2 (YTHDC2), mRNA. /// NM_021614 // upstream // 116231 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-act	YTHDC2	YTHDC2, Homo sapiens YTH domain containing 2 (YTHDC2), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2269656	gacaacagcatctcac[A/G]gcatctctaaaagaga	A	G	NM_021614 // downstream // 99208 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 99208 // Hs.98280 // KCNN2 //	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-1941790	ttggacagtcatataa[A/C]ctgattcaaactagag	A	C	NM_021614 // downstream // 129795 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 129795 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-1781901	ggcaaaacagaaataa[A/C]ctgatagctgcctttt	A	C	NM_021614 // downstream // 140542 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 140542 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate q22.3
SNP_A-1871896	tctacagaattctcca[C/T]gcaataaccacaaaat	C	T	NM_021614 // downstream // 150034 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 150034 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate q22.3
SNP_A-2120609	agtcccagatttagtg[A/G]agatgacagccctctt	A	G	NM_021614 // downstream // 231222 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 231222 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-1673626	tttgtatacatttgtatctccagca[C/T]ccaacagaatatttcgcatat agcag	C	T	NM_018700 // downstream // 436674 // Hs.429642 // TRIM36 // 55521 // tripartite motif-containing 36 /// NM_021614 // downstream // 191590 // Hs.98280 // KCNN2 // 3781 // potassium intermediate/small conductance calcium-activated channel, subfamily N, mem	TRIM36	TRIM36 , rs10491499, tripartite motif-containing 36 ,q22.3
SNP_A-1707653	ttttttttttttttttggtcaaca[A/T]aatctgtctgtgtctaacatttc	A	T	NM_018700 // downstream // 409246 // Hs.429642 // TRIM36 // 55521 // tripartite motif-containing 36 /// NM_021614 // downstream // 219018 // Hs.98280 // KCNN2 // 3781 // potassium intermediate/small conductance calcium-activated channel, subfamily N, mem	TRIM36	TRIM36 , rs7728321, tripartite motif-containing 36 ,q22.3
SNP_A-2122643	agtggaaccccagcaa[C/T]atggagatttgaggtc	C	T	NM_021614 // downstream // 342868 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 342868 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-1913268	tgtgggagctataaag[C/T]ctaaaattcatagcct	C	T	NM_021614 // downstream // 386717 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 386717 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate,q22.3
SNP_A-1983042	ccatgtctttacaaaa[G/T]ccttctcaccttgaaa	G	T	NM_021614 // downstream // 461658 // Hs.98280 // KCNN2 // 3781 // Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), transcript varia /// NM_170775 // downstream // 461658 // Hs.98280 // KCNN2 /	KCNN2	KCNN2, Homo sapiens potassium intermediate q22.3
SNP_A-2210265	ccccatggagaagtag[A/T]attaggcatttttcaaa	A	T	NM_005023 // intron // 0 // Hs.254006 // PGGT1B // 5229 // Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B), mRNA. /// ENST00000296642 // intron // 0 // — // — // — // —	PGGT1B	PGGT1B, Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1708572	cttcaggcctagctaactagactac[G/T]atgttcaatactggaga aggaagat	G	T	NM_005023 // downstream // 13745 // Hs.254006 // PGGT1B // 5229 // protein geranylgeranyltransferase type I, beta subunit /// NM_018700 // upstream // 17976 // Hs.429642 // TRIM36 // 55521 // tripartite motif-containing 36	PGGT1B	PGGT1B , rs10519400, protein geranylgeranyltransferase type I, beta subunit ,q22.3
SNP_A-1901022	tggatatcatgtaagt[A/G]acaggaatagtcatat	A	G	NM_005023 // intron // 0 // Hs.254006 // PGGT1B // 5229 // Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B), mRNA. /// ENST00000296642 // intron // 0 // — // — // — // —	PGGT1B	PGGT1B, Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B), q22.3
SNP_A-1983053	atgcaacttttgtgga[C/G]tatctgtagaaatttc	C	G	NM_020177 // upstream // 25922 // Hs.47367 // FEM1C // 56929 // Homo sapiens fem-1 homolog c (C.elegans) (FEM1C), mRNA. /// NM_021649 // downstream // 7835 // Hs.278391 // TICAM2 // 353376 // Homo sapiens toll-like receptor adaptor molecule 2 (TICAM2), mR	FEM1C	FEM1C, Homo sapiens fem-1 homolog c (C.elegans) (FEM1C), q22.3
SNP_A-2036686	aaattgtgaaagaaaa[A/G]tccttgaaactctgac	A	G	NM_021649 // 3UTR // 0 // Hs.278391 // TICAM2 // 353376 // Homo sapiens toll-like receptor adaptor molecule 2 (TICAM2), mRNA. /// ENST00000333314 // 3UTR // 0 // — // — // — // —	TICAM2	TICAM2, Homo sapiens toll-like receptor adaptor molecule 2 (TICAM2), q22.3
SNP_A-2305533	gctgcaagtctatgga[A/C]gtatttcaaagagaat	A	C	NM_001284 // downstream // 496 // Hs.406191 // AP3S1 // 1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 496 // Hs.406191 // AP3S1 // 1176 // Homo sapiens adapto	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-1912930	tgtggaacaatatcac[A/G]catattggatgacttc	A	G	NM_001284 // downstream // 35738 // Hs.406191 // AP3S1 // 1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 35738 // Hs.406191 // AP3S1 // 1176 // Homo sapiens ad	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-2024531	aaaaggcaacagcata[G/T]acagaatcaaaatatc	G	T	NM_001284 // downstream // 37488 // Hs.406191 // AP3S1 // 1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 37488 // Hs.406191 // AP3S1 // 1176 // Homo sapiens ad	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-1859159	tcagccttatgagtta[C/T]aaagccattggataat	C	T	NM_001284 // downstream // 41017 // Hs.406191 // AP3S1 // 1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 41017 // Hs.406191 // AP3S1 // 1176 // Homo sapiens ad	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-1956676	ttttaaaaactacaga[C/T]gtcagcatgtttaaac	C	T	NM_001284 // downstream // 43069 // Hs.406191 // AP3S1 // 1176 // Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, mRNA. /// NM_001002924 // downstream // 43069 // Hs.406191 // AP3S1 // 1176 // Homo sapiens ad	AP3S1	AP3S1, Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 1, q23.1
SNP_A-2096819	agactcaaactattga[G/T]gcatacttggatggat	G	T	NM_173800 // intron // 0 // Hs.98288 // FLJ90650 // 206338 // Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000274462 // intron // 0 // — // — // — // — /// ENST00000357872 // intron // 0 // — // — // — // —	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1
SNP_A-2137787	atcatgttttctgata[C/G]ctatgtattgaattaa	C	G	NM_173800 // intron // 0 // Hs.98288 // FLJ90650 // 206338 // Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000274462 // intron // 0 // — // — // — // — /// ENST00000357872 // intron // 0 // — // — // — // —	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1
SNP_A-2104684	agcagtgaaggatgca[A/T]aggattaaaataggta	A	T	NM_173800 // intron // 0 // Hs.98288 // FLJ90650 // 206338 // Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000274462 // intron // 0 // — // — // — // — /// ENST00000357872 // intron // 0 // — // — // — // —	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1892703	tgcacacagagaaaagal[C/G]aggctgttttcctctt	C	G	NM_173800 // downstream // 19353 // Hs.98288 // FLJ90650 // 206338 // Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000315861 // upstream // 84335 // --- // --- // --- /// ENST00000274462 // downstream // 19353 // --- // --- // --- /// E	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1
SNP_A-1803683	gtcaaagtttacttat[C/T]gttcatcacttctca	C	T	NM_173800 // downstream // 21048 // Hs.98288 // FLJ90650 // 206338 // Homo sapiens laeverin (FLJ90650), mRNA. /// ENST00000315861 // upstream // 86030 // --- // --- // --- /// ENST00000274462 // downstream // 21048 // --- // --- // --- /// E	FLJ90650	FLJ90650, Homo sapiens laeverin (FLJ90650), q23.1
SNP_A-1942844	ttgggagatataaagag[A/G]acgctcatggttttgt	A	G	NM_016144 // upstream // 7917 // Hs.483136 // COMMD10 // 51397 // Homo sapiens COMM domain containing 10 (COMMD10), mRNA. /// ENST00000340805 // upstream // 24825 // --- // --- // --- // ENST00000274458 // upstream // 7917 // --- // --- // --- //	COMMD10	COMMD10, Homo sapiens COMM domain containing 10 (COMMD10), q23.1
SNP_A-1983093	atgtcagctagtcacc[G/T]ccatgggacctgtg	G	T	NM_020796 // intron // 0 // Hs.156967 // SEMA6A // 57556 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA. /// ENST00000343348 // intron // 0 // --- // --- // --- /// ENST00000257414 //	SEMA6A	SEMA6A, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), q23.1
SNP_A-2190311	cataatctttctccaa[A/T]atctgaggtaaacaa	A	T	ENST00000359659 // downstream // 401645 // --- // --- // --- /// ENST00000329863 // downstream // 660488 // --- // --- // ---	-	q23.1
SNP_A-1983131	agtcagaaagccaaag[A/T]acactatggagaaata	A	T	ENST00000359659 // downstream // 542465 // --- // --- // --- /// ENST00000329863 // downstream // 519668 // --- // --- // ---	-	q23.1
SNP_A-2193902	catgaacccatatgt[A/G]aatgcggcagcaagca	A	G	ENST00000359659 // downstream // 609375 // --- // --- // --- /// ENST00000329863 // downstream // 452758 // --- // --- // ---	-	q23.1
SNP_A-1820182	gtttaatctttatgtg[C/G]aaggatagggactgtc	C	G	ENST00000359659 // downstream // 779700 // --- // --- // --- /// ENST00000329863 // downstream // 282433 // --- // --- // ---	-	q23.1
SNP_A-2157495	attgatccatctggaa[A/T]cttaaacaatgcatc	A	T	ENST00000359659 // downstream // 835778 // --- // --- // --- /// ENST00000329863 // downstream // 226355 // --- // --- // ---	-	q23.1
SNP_A-2075552	acatgcatgatttctag[C/G]aactggtgacagaatg	C	G	ENST00000359659 // downstream // 892282 // --- // --- // --- /// ENST00000329863 // downstream // 169851 // --- // --- // ---	-	q23.1
SNP_A-1906718	tggttaaaatagataa[C/G]aacagattgatagaaa	C	G	ENST00000359659 // downstream // 918261 // --- // --- // --- /// ENST00000329863 // downstream // 143872 // --- // --- // ---	-	q23.1
SNP_A-1856305	tcacacaaatccaatg[A/T]cacacaaaagtagttt	A	T	ENST00000359659 // downstream // 919540 // --- // --- // --- /// ENST00000329863 // downstream // 142593 // --- // --- // ---	-	q23.1
SNP_A-2033991	aaatcacgcttcacca[A/T]aggtatttttgttg	A	T	ENST00000359659 // downstream // 920128 // --- // --- // --- /// ENST00000329863 // downstream // 142005 // --- // --- // ---	-	q23.1
SNP_A-1802741	gtatgccaccgaatta[C/T]attcagtaacaaagcc	C	T	ENST00000359659 // downstream // 920809 // --- // --- // --- /// ENST00000329863 // downstream // 141324 // --- // --- // ---	-	q23.1
SNP_A-2109266	agctttaccctcaagg[A/C]ataaattgctatcac	A	C	ENST00000359659 // downstream // 921672 // --- // --- // --- /// ENST00000329863 // downstream // 140461 // --- // --- // ---	-	q23.1
SNP_A-1903743	tgggaggttaactac[C/T]acctgaaatgctaaga	C	T	NM_173666 // downstream // 955706 // Hs.14822 // FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream // 104815 // --- // --- // --- /// ENST00000304058 // downstream // 955706 // --- //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1802357	gtatcaggtttatac[C/G]atcacaactaacttag	C	G	NM_173666 // downstream // 869186 // Hs.14822 // FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream // 191335 // --- // --- // --- /// ENST00000304058 // downstream // 869186 // --- //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074393	acatacgctagtttgc[C/G]attcaaatgctttca	C	G	NM_173666 // downstream // 868910 // Hs.14822 // FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream // 191611 // --- // --- // --- /// ENST00000304058 // downstream // 868910 // --- //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2172541	caatctaacgcctac[C/T]gaagctgtgacttgca	C	T	NM_173666 // downstream // 856918 // Hs.14822 // FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream // 203603 // --- // --- // --- /// ENST00000304058 // downstream // 856918 // --- //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1983149	tctcatttctggctac[C/T]ggttgagagagaaatg	C	T	NM_173666 // downstream // 847799 // Hs.14822 // FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream // 212722 // --- // --- // --- /// ENST00000304058 // downstream // 847799 // --- //	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-2140967	atcgattacagctcd[A/G]ctcattgtgattatta	A	G	NM_173666 // downstream // 68335 // Hs.14822 // FLJ33977 // 285605 // Homo sapiens hypothetical protein FLJ33977 (FLJ33977), mRNA. /// ENST00000329863 // upstream // 992186 // --- // --- // --- /// ENST00000304058 // downstream // 68335 // --- // -	FLJ33977	FLJ33977, Homo sapiens hypothetical protein FLJ33977 (FLJ33977), q23.1
SNP_A-1739199	ggcaatatcatcatgcttaaccgac[C/G]agatgaaagtgttctcg atcccat	C	G	NM_020796 // upstream // 2193398 // Hs.443012 // SEMA6A // 57556 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A /// NM_173666 // downstream // 71334 // Hs.14822 // FLJ33977 // 285605 // hypothetical protein FLJ33977	SEMA6A	SEMA6A , rs10491430, sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A .q23.1
SNP_A-1751551	agaagctctgtttctgctatggccd[A/G]ctgcaagtagggaaaat cactgaca	A	G	NM_020796 // upstream // 2216242 // Hs.443012 // SEMA6A // 57556 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A /// NM_173666 // downstream // 48490 // Hs.14822 // FLJ33977 // 285605 // hypothetical protein FLJ33977	SEMA6A	SEMA6A , rs631514, sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A .q23.1
SNP_A-2265744	gaagcttagggcacd[A/G]ataaaaactatagctg	A	G	NM_005509 // intron // 0 // Hs.181042 // DMXL1 // 1657 // Homo sapiens Dmx-like 1 (DMXL1), mRNA. /// ENST00000311085 // intron // 0 // --- // --- // ---	DMXL1	DMXL1, Homo sapiens Dmx-like 1 (DMXL1), q23.1
SNP_A-1983173	cattttgcccatcal[C/G]aacctttgcagggca	C	G	NM_005509 // downstream // 33718 // Hs.181042 // DMXL1 // 1657 // Homo sapiens Dmx-like 1 (DMXL1), mRNA. /// NM_014350 // upstream // 109964 // Hs.271955 // TNFAIP8 // 25816 // Homo sapiens tumor necrosis factor, alpha-induced protein 8 (TNFAIP8), mRNA. /	DMXL1	DMXL1, Homo sapiens Dmx-like 1 (DMXL1), q23.1
SNP_A-1951461	tttcctcatccggaat[A/G]aatagtgacaatatag	A	G	NM_005509 // downstream // 44457 // Hs.181042 // DMXL1 // 1657 // Homo sapiens Dmx-like 1 (DMXL1), mRNA. /// NM_014350 // upstream // 99225 // Hs.271955 // TNFAIP8 // 25816 // Homo sapiens tumor necrosis factor, alpha-induced protein 8 (TNFAIP8), mRNA. //	DMXL1	DMXL1, Homo sapiens Dmx-like 1 (DMXL1), q23.1
SNP_A-1880973	tcttgtgagggagtc[C/G]agggagcgaaagagtg	C	G	NM_005509 // downstream // 61098 // Hs.181042 // DMXL1 // 1657 // Homo sapiens Dmx-like 1 (DMXL1), mRNA. /// NM_014350 // upstream // 82584 // Hs.271955 // TNFAIP8 // 25816 // Homo sapiens tumor necrosis factor, alpha-induced protein 8 (TNFAIP8), mRNA. //	DMXL1	DMXL1, Homo sapiens Dmx-like 1 (DMXL1), q23.1
SNP_A-1868447	tcctccctggaataaa[A/G]gaacacttggttatt	A	G	NM_182761 // downstream // 23417 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 823108 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC5	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1649326	aacttccagtaagtagagcctagca[C/T]agaagttacagattag agctgcatt	C	T	NM_182761 // downstream // 20467 // Hs.434682 // LOC340069 // 340069 // hypothetical protein LOC340069	LOC340069	LOC340069 , rs330196, hypothetical protein LOC340069,q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1700494	gatgcactgtgtccaaagacatgccd[A/G]agcttcagaggcaaa caccigtcca	A	G	NM_182761 // downstream // 24599 // Hs.434682 // LOC340069 // 340069 // hypothetical protein LOC340069	LOC340069	LOC340069, rs780429, hypothetical protein LOC340069,q23.1
SNP_A-2220299	ccttccctcctttttc[G/T]ctgagcatttaattca	G	T	NM_182761 // downstream // 156830 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 689695 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2238550	ctctgtcctggaataa[C/T]cctgcaattaggaagt	C	T	NM_182761 // downstream // 449220 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 397305 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1983207	acaccacataactaaa[C/T]gaattgttgtctacct	C	T	NM_182761 // downstream // 509660 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 336865 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2119022	agtagaccgtttaata[C/G]ctcaggtggactatta	C	G	NM_182761 // downstream // 519341 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 327184 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2125518	agtttattctgcctta[A/G]atacttgtcctcaaga	A	G	NM_182761 // downstream // 532452 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 314073 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-1680022	ttctagatgcagtgaataatcagaa[A/G]aatccccttctcacata gctcaca	A	G	NM_182761 // downstream // 554816 // Hs.434682 // LOC340069 // 340069 // hypothetical protein LOC340069	LOC340069	LOC340069, , rs2112498, hypothetical protein LOC340069,q23.1
SNP_A-2131042	atagaatgaagcaaaa[G/T]ggtgggtgcagatt	G	T	NM_182761 // downstream // 674298 // Hs.434682 // LOC340069 // 340069 // Homo sapiens hypothetical protein LOC340069 (LOC340069), mRNA. /// NM_016644 // upstream // 172227 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC	LOC340069	LOC340069, Homo sapiens hypothetical protein LOC340069 (LOC340069), q23.1
SNP_A-2041692	aacgggatcatcaa[C/G]ttaaaagaaaacaatc	C	G	NM_016644 // intron // 0 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// ENST00000330264 // intron // 0 // — // — // — // —	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2155732	attcccaaatgaagta[C/T]gaatgttggcagggga	C	T	NM_016644 // downstream // 506717 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 // upstream // 658529 // Hs.105324 // FTMT // 94033 // Homo sapiens ferritin mitochondrial (FTMT), mRNA	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-1917240	tgttttatagatgcca[A/G]aaatcagggaaccata	A	G	NM_016644 // downstream // 1078819 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 // upstream // 86427 // Hs.105324 // FTMT // 94033 // Homo sapiens ferritin mitochondrial (FTMT), mRNA	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1
SNP_A-2058916	aatccagagaatagaa[A/T]gaaatatcaggtgtca	A	T	NM_016644 // downstream // 1104048 // Hs.157461 // LOC51334 // 51334 // Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), mRNA. /// NM_177478 // upstream // 61198 // Hs.105324 // FTMT // 94033 // Homo sapiens ferritin mitochondrial (FTMT), mRNA	LOC51334	LOC51334, Homo sapiens mesenchymal stem cell protein DSC54 (LOC51334), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259609	gaaaactaacacagag[A/C]cctttccaaatcgcac	A	C	NM_005460 // downstream // 264672 // Hs.426463 // SNCAIP // 9627 // Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), mRNA. /// NM_014035 // upstream // 116850 // Hs.483200 // SNX24 // 28966 // Homo sapiens sorting nexing 24 (SNX24),	SNCAIP	SNCAIP, Homo sapiens synuclein, alpha interacting protein (synphilin) (SNCAIP), q23.2
SNP_A-2252067	cttccactgttcataa[C/T]aatcacccagggacct	C	T	NM_014035 // intron // 0 // Hs.483200 // SNX24 // 28966 // Homo sapiens sorting nexing 24 (SNX24), mRNA. /// ENST00000261369 // intron // 0 // --- // --- // ---	SNX24	SNX24, Homo sapiens sorting nexing 24 (SNX24), q23.2
SNP_A-1983269	tacagataatttctta[C/G]aacaacgtatggcatt	C	G	NM_014035 // intron // 0 // Hs.483200 // SNX24 // 28966 // Homo sapiens sorting nexing 24 (SNX24), mRNA. /// ENST00000261369 // intron // 0 // --- // --- // ---	SNX24	SNX24, Homo sapiens sorting nexing 24 (SNX24), q23.2
SNP_A-2300631	gcctgcatagtataag[A/T]aggaaaattgaaatga	A	T	NM_000943 // upstream // 17718 // Hs.110364 // PPIC // 5480 // Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), mRNA. /// AF272898 // upstream // 34695 // Hs.135118 // PRDM6 // 93166 // Homo sapiens PR-domain zinc finger protein 6 isoform A	PPIC	PPIC, Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), q23.2
SNP_A-2253950	cttgactaatagccaa[A/G]gattggtcaataactc	A	G	AF272898 // intron // 0 // Hs.135118 // PRDM6 // 93166 // Homo sapiens PR-domain zinc finger protein 6 isoform A (PRDM6) mRNA, partial cds; alternatively spliced. /// ENST00000359091 // intron // 0 // --- // --- // --- /// ENST00000261364 // intron	PRDM6	PRDM6, Homo sapiens PR-domain zinc finger protein 6 isoform A (PRDM6) partial cds; alternatively spliced. q23.2
SNP_A-2081619	accttagaatgcctca[C/T]acaagaacaacagcca	C	T	ENST00000357456 // downstream // 103577 // --- // --- // --- // --- /// ENST00000360683 // downstream // 103569 // --- // --- // --- // --- /// ENST00000345990 // downstream // 104627 // --- // --- // --- // --- /// ENST00000306315 // downstream // 917893	-	q23.2
SNP_A-1877102	tctgctctcttgaaca[A/C]ctgcttatctgtcttg	A	C	ENST00000357456 // downstream // 162358 // --- // --- // --- // --- /// ENST00000360683 // downstream // 162350 // --- // --- // --- // --- /// ENST00000345990 // downstream // 163408 // --- // --- // --- // --- /// ENST00000306315 // downstream // 859112	-	q23.2
SNP_A-2174552	cacagaggatttctca[A/C]taggttcttacagtat	A	C	ENST00000357456 // downstream // 899816 // --- // --- // --- // --- /// ENST00000360683 // downstream // 899808 // --- // --- // --- // --- /// ENST00000345990 // downstream // 900866 // --- // --- // --- // --- /// ENST00000306315 // downstream // 121654	-	q23.2
SNP_A-2116950	aggtgaaatcgtgaga[C/T]ggttgagatagcccag	C	T	ENST00000357456 // downstream // 917665 // --- // --- // --- // --- /// ENST00000360683 // downstream // 917657 // --- // --- // --- // --- /// ENST00000345990 // downstream // 918715 // --- // --- // --- // --- /// ENST00000306315 // downstream // 103805	-	q23.2
SNP_A-1808928	gtgaatgaggccattc[A/G]gaaaagaccacaaagt	A	G	NM_023927 // upstream // 1482037 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 196259 // --- // --- // --- // --- /// ENST00000285689 // upstream // 1482037 // --- // -	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2229394	ctaggcacaaaaaaaa[A/T]tttcagatgtgaaggt	A	T	NM_023927 // upstream // 1276655 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 401641 // --- // --- // --- // --- /// ENST00000285689 // upstream // 1276655 // --- // -	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2052409	aagtactcatttagaa[C/T]gctatccatctgcctt	C	T	NM_023927 // upstream // 942108 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 736188 // --- // --- // --- // --- /// ENST00000285689 // upstream // 942108 // --- // ---	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2164415	caaaatgctaagacga[A/G]tccctggtatattaac	A	G	NM_023927 // upstream // 941081 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 737215 // --- // --- // --- // --- /// ENST00000285689 // upstream // 941081 // --- // ---	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1924294	ttataaagagacctga[A/G]aaattcagagccacag	A	G	NM_023927 // upstream // 929988 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 748308 // — // — // — /// ENST00000285689 // upstream // 929988 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2075362	acatgaagaaaaactc[C/T]acgtgttgtaaatcta	C	T	NM_023927 // upstream // 926094 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 752202 // — // — // — /// ENST00000285689 // upstream // 926094 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2213183	ccgcactgcatttccc[C/G]aaaacacccctcaaca	C	G	NM_023927 // upstream // 913164 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 765132 // — // — // — /// ENST00000285689 // upstream // 913164 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1834009	tacatatacaccatgg[A/G]agactatacagccata	A	G	NM_023927 // upstream // 908306 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 769990 // — // — // — /// ENST00000285689 // upstream // 908306 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1649002	tcacttacctacatcaagatttaa[C/G]aaatgtcaaaatgttgcc atatttg	C	G	NM_023927 // upstream // 925879 // Hs.281147 // NS3TP2 // 65983 // HCV NS3-transactivated protein 2	NS3TP2	NS3TP2 , rs331693, HCV NS3-transactivated protein 2,q23.2
SNP_A-1644494	tccgttataatataatgatcagata[A/G]ctaagtataaatattatatg gctaag	A	G	NM_023927 // upstream // 924889 // Hs.281147 // NS3TP2 // 65983 // HCV NS3-transactivated protein 2	NS3TP2	NS3TP2 , rs179505, HCV NS3-transactivated protein 2,q23.2
SNP_A-2221224	ccttacaacattgaa[C/T]agaagtgagtccctg	C	T	NM_023927 // upstream // 738304 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 939992 // — // — // — /// ENST00000285689 // upstream // 738304 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1896374	tgctaagctagttacc[C/G]ctccactattgcttc	C	G	NM_023927 // upstream // 738117 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 940179 // — // — // — /// ENST00000285689 // upstream // 738117 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-2037972	aacaattggcattgtc[G/T]catctttccatttct	G	T	NM_023927 // upstream // 330310 // Hs.363558 // NS3TP2 // 65983 // Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), mRNA. /// ENST00000306315 // upstream // 1347986 // — // — // — /// ENST00000285689 // upstream // 330310 // — // —	NS3TP2	NS3TP2, Homo sapiens HCV NS3-transactivated protein 2 (NS3TP2), q23.2
SNP_A-1758355	taaagatgagaactctttactggaa[C/T]aaattagcacataaact agaagatg	C	T	NM_023927 // upstream // 319048 // Hs.281147 // NS3TP2 // 65983 // HCV NS3-transactivated protein 2	NS3TP2	NS3TP2 , rs1383555, HCV NS3-transactivated protein 2,q23.2
SNP_A-1674529	ttatgtcacaattcagtttgcaaaa[C/G]cttcaatcatctaactgtct catgg	C	G	NM_023927 // upstream // 318922 // Hs.281147 // NS3TP2 // 65983 // HCV NS3-transactivated protein 2	NS3TP2	NS3TP2 , rs1383556, HCV NS3-transactivated protein 2,q23.2
SNP_A-1922415	ttagaaatgacctaaa[C/T]gtcgaatcataagggg	C	T	NM_001182 // intron // 0 // Hs.483239 // ALDH7A1 // 501 // Homo sapiens aldehyde dehydrogenase 7 family, member A1 (ALDH7A1), mRNA. /// ENST00000297542 // intron // 0 // — // — // —	ALDH7A1	ALDH7A1, Homo sapiens aldehyde dehydrogenase 7 family, member A1 (ALDH7A1), q23.2
SNP_A-2168219	caactgaatctttga[A/C]ctctcagtggtaaaat	A	C	NM_032446 // intron // 0 // Hs.438709 // MEGF10 // 84466 // Homo sapiens MEGF10 protein (MEGF10), mRNA. /// ENST00000274473 // intron // 0 // — // — // —	MEGF10	MEGF10, Homo sapiens MEGF10 protein (MEGF10), q23.2
SNP_A-1936237	ttcttcatcagtaaaa[C/T]agaagttgtgatacca	C	T	NM_130809 // downstream // 6391 // Hs.483259 // LOC133619 // 133619 // Homo sapiens hypothetical protein MGC12103 (LOC133619), mRNA. /// ENST00000330542 // downstream // 7563 // — // — // — /// ENST00000296666 // downstream // 6391 // — // —	LOC133619	LOC133619, Homo sapiens hypothetical protein MGC12103 (LOC133619), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2229302	ctaggagactatttgg[G/T]atcagacttacctgg	G	T	ENST00000308464 // downstream // 57 /// ENST00000359805 // upstream // 103845 ///	-	q23.2
SNP_A-1813353	gtggtgggtagtgaa[A/C]ctctggagtcaatatc	A	C	ENST00000308464 // downstream // 1613 /// ENST00000359805 // upstream // 102289 ///	-	q23.2
SNP_A-1808045	gtctctgtcaattgca[C/T]acccgagtggcttcat	C	T	ENST00000308464 // downstream // 17617 /// ENST00000359805 // upstream // 86285 ///	-	q23.2
SNP_A-1892646	tgcaatttgaaagcta[C/T]gtgtatcaattgact	C	T	ENST00000308464 // downstream // 27245 /// ENST00000359805 // upstream // 76657 ///	-	q23.2
SNP_A-1656315	gaaagttactgaatactattctgta[G/T]cttgtacatatcatatgctc tagca	G	T	NM_001046 // upstream // 133293 // Hs.110736 // SLC12A2 // 6558 // solute carrier family 12 (sodium/potassium/chloride transporters), member 2 /// NM_130809 // downstream // 395418 // Hs.6614 // LOC133619 // 133619 // hypothetical protein MGC12103	SLC12A2	SLC12A2 , rs2409037, solute carrier family 12 (sodium,q23.2
SNP_A-1673022	taaacccgaggactacttgcacaa[C/T]gaaatttgcaggaaaa tgagaccct	C	T	NM_001046 // upstream // 104346 // Hs.110736 // SLC12A2 // 6558 // solute carrier family 12 (sodium/potassium/chloride transporters), member 2 /// NM_130809 // downstream // 424365 // Hs.6614 // LOC133619 // 133619 // hypothetical protein MGC12103	SLC12A2	SLC12A2 , rs9327463, solute carrier family 12 (sodium,q23.2
SNP_A-1908504	tgtagagtcctctta[C/T]gagtgaacactgagtg	C	T	NM_001046 // downstream // 27150 // Hs.162585 // SLC12A2 // 6558 // Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters), member 2 (SLC12A2), mRNA. /// NM_001999 // downstream // 41200 // Hs.519294 // FBN2 // 2201 // Homo sapiens	SLC12A2	SLC12A2, Homo sapiens solute carrier family 12 (sodium,q23.2
SNP_A-1983409	acaaatgtactgaaca[C/T]gctaaggtgaaatgat	C	T	NM_001999 // intron // 0 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 // intron // 0 // — // — // —	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-2180483	cagaactagatttcct[A/G]ctgtcattcattatgg	A	G	NM_001999 // intron // 0 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// ENST00000262464 // intron // 0 // — // — // —	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.2
SNP_A-2284333	gatatttcaaactccc[A/G]aagtccaaagcaggct	A	G	NM_001999 // upstream // 37238 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 390287 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fa	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-1938270	ttgacctcttacccaa[C/G]tcctagaacaaagtca	C	G	NM_001999 // upstream // 62086 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 365439 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fa	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-1819167	gttgctctttttgtga[A/T]cttctacacaacacag	A	T	NM_001999 // upstream // 83055 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 344470 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fa	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-2233629	ctcataatgtagcca[C/T]gttaaaaactaaaata	C	T	NM_001999 // upstream // 85680 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 341845 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fa	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-2264444	gaagaaagaagtcaag[A/T]agtctgtgagttaaac	A	T	NM_001999 // upstream // 219524 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 208001 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (f	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1697789	cacatttctgcttaacttctgcag[C/T]agagacaagagattgat gtctgga	C	T	NM_001999 // upstream // 295944 // Hs.79432 // FBN2 // 2201 // fibrillin 2 (congenital contractural arachnodactyly) /// NM_014031 // upstream // 132438 // Hs.49765 // SLC27A6 // 28965 // solute carrier family 27 (fatty acid transporter), member 6	FBN2	FBN2 , rs2310809, fibrillin 2 (congenital contractural arachnodactyly), q23.3
SNP_A-2130411	atactagaggtacaaa[C/T]ggtgttatgatgtctt	C	T	NM_001999 // upstream // 368612 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 58913 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fa	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-1983432	aatggaatatgacttta[G/T]caatgtaaagaaataa	G	T	NM_001999 // upstream // 413977 // Hs.519294 // FBN2 // 2201 // Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA. /// NM_014031 // upstream // 13548 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fa	FBN2	FBN2, Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), q23.3
SNP_A-1669563	caatattgaacagtcagagaaaaag[A/C]gagtaaccagcaaa ggaggtctatc	A	C	NM_001999 // upstream // 370714 // Hs.79432 // FBN2 // 2201 // fibrillin 2 (congenital contractural arachnodactyly) /// NM_014031 // upstream // 57668 // Hs.49765 // SLC27A6 // 28965 // solute carrier family 27 (fatty acid transporter), member 6	FBN2	FBN2 , rs2522379, fibrillin 2 (congenital contractural arachnodactyly), q23.3
SNP_A-1749717	gaaagaaagaaaagaagacagagaa[C/G]ttaagatgttaga gaaagaagcagc	C	G	NM_001999 // upstream // 371034 // Hs.79432 // FBN2 // 2201 // fibrillin 2 (congenital contractural arachnodactyly) /// NM_014031 // upstream // 57348 // Hs.49765 // SLC27A6 // 28965 // solute carrier family 27 (fatty acid transporter), member 6	FBN2	FBN2 , rs2545021, fibrillin 2 (congenital contractural arachnodactyly), q23.3
SNP_A-1983435	ccaacttcatctagcc[A/G]catgaacactgcatca	A	G	NM_014031 // intron // 0 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), mRNA. /// ENST00000262462 // intron // 0 // — // — // — // — /// ENST00000358376 // intron // 0 // —	SLC27A6	SLC27A6, Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), q23.3
SNP_A-1917505	tgttttaatgctgaa[G/T]gaagctagaaaagaga	G	T	NM_014031 // downstream // 10661 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), mRNA. /// NM_014031 // downstream // 10315 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carri	SLC27A6	SLC27A6, Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), q23.3
SNP_A-2136654	atcactcattaaccttc[A/G]ctagagcaacacaacc	A	G	NM_014031 // downstream // 15561 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), mRNA. /// NM_014031 // downstream // 15215 // Hs.49765 // SLC27A6 // 28965 // Homo sapiens solute carri	SLC27A6	SLC27A6, Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), q23.3
SNP_A-1983440	ctgatatattgcttta[A/G]ggagttgcttaaaat	A	G	NM_016048 // downstream // 27726 // Hs.483296 // ISOC1 // 51015 // Homo sapiens CGI-111 protein (CGI-111), mRNA. /// NM_133638 // upstream // 318664 // Hs.23751 // ADAMTS19 // 171019 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type)	ISOC1	ISOC1, Homo sapiens CGI-111 protein (CGI-111), q23.3
SNP_A-2131261	atagaggcatagataa[C/T]ctgagtcaggaataaa	C	T	NM_016048 // downstream // 291835 // Hs.483296 // ISOC1 // 51015 // Homo sapiens CGI-111 protein (CGI-111), mRNA. /// NM_133638 // upstream // 54555 // Hs.23751 // ADAMTS19 // 171019 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type)	ISOC1	ISOC1, Homo sapiens CGI-111 protein (CGI-111), q23.3
SNP_A-2290935	gcaagtaaataaaacc[A/G]gagatgatggtgcaat	A	G	ENST00000305031 // intron // 0 // — // — // —	-	q23.3
SNP_A-1983464	ttgtactctcttcaa[C/T]agcctggatttcctg	C	T	NM_005340 // downstream // 770613 // Hs.483305 // HINT1 // 3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// ENST00000305031 // downstream // 202887 // — // — // — // — /// ENST00000304043 // downstream // 770613	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939340	ttgatgaagaaggaca[A/G]gaggtgagaagtgac	A	G	NM_005340 // downstream // 697021 // Hs.483305 // HINT1 // 3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// ENST00000305031 // downstream // 276479 // — // — // — /// ENST00000304043 // downstream // 697021	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3
SNP_A-2185970	caggcactgcaggaac[C/G]aggcaaacttgtgcaa	C	G	NM_005340 // downstream // 609829 // Hs.483305 // HINT1 // 3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// ENST00000305031 // downstream // 363671 // — // — // — /// ENST00000304043 // downstream // 609829	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3
SNP_A-1692604	tgttccctctagctggaaattctctaa[C/T]ataccacttgaagcatggt tggtt	C	T	NM_175856 // downstream // 354719 // - // - // - /// NM_005340 // downstream // 617939 // Hs.256697 // HINT1 // 3094 // histidine triad nucleotide binding protein 1	-	- , rs2215258, - , q23.3
SNP_A-1983468	aacttctaaatttcaa[A/G]caacttcatttagtg	A	G	NM_005340 // downstream // 398300 // Hs.483305 // HINT1 // 3094 // Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA. /// ENST00000305031 // downstream // 575200 // — // — // — /// ENST00000304043 // downstream // 398300	HINT1	HINT1, Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), q23.3
SNP_A-1923561	ttaggggaaaggccaga[G/T]aagggcattcctgat	G	T	NM_181705 // downstream // 21933 // Hs.115467 // LOC90624 // 90624 // Homo sapiens hypothetical protein LOC90624 (LOC90624), mRNA. /// NM_020240 // upstream // 40830 // Hs.508829 // CDC42SE2 // 56990 // Homo sapiens CDC42 small effector 2 (CDC42SE2), mRNA	LOC90624	LOC90624, Homo sapiens hypothetical protein LOC90624 (LOC90624), q23.3
SNP_A-2199854	ccaaactctaaatcaa[C/G]gaagtggcagtcttg	C	G	NM_020240 // intron // 0 // Hs.508829 // CDC42SE2 // 56990 // Homo sapiens CDC42 small effector 2 (CDC42SE2), mRNA. /// ENST00000290044 // intron // 0 // — // — // — /// ENST00000360515 // intron // 0 // — // — // —	CDC42SE2	CDC42SE2, Homo sapiens CDC42 small effector 2 (CDC42SE2), q23.3
SNP_A-2303939	gctcatgtaccataac[A/G]attctccctcttcct	A	G	AF478567 // CDS // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 mRNA, complete cds. /// NM_016340 // CDS // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens Rap guanine nucleotide e	RAPGEF6	RAPGEF6, Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 complete cds, q23.3
SNP_A-1799007	gtaagcactattgtgt[C/G]atcaatcattaggaga	C	G	AF478567 // intron // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 mRNA, complete cds. /// NM_016340 // intron // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens Rap guanine nucleo	RAPGEF6	RAPGEF6, Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 complete cds, q23.3
SNP_A-2090005	actctctacaagaaac[G/T]gcctcaagaaaacagt	G	T	AF478567 // intron // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 mRNA, complete cds. /// NM_016340 // intron // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens Rap guanine nucleo	RAPGEF6	RAPGEF6, Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 complete cds, q23.3
SNP_A-2285411	gatctacatctgca[A/G]cctattaaatcactt	A	G	AF478567 // intron // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 mRNA, complete cds. /// NM_016340 // intron // 0 // Hs.483329 // RAPGEF6 // 51735 // Homo sapiens Rap guanine nucleo	RAPGEF6	RAPGEF6, Homo sapiens PDZ domain-containing guanine nucleotide exchange factor PDZ-GEF2 complete cds, q23.3
SNP_A-2011247	gagaagagagaaaaga[C/G]taaagaggacattgtc	C	G	NM_015256 // intron // 0 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron // 0 // — // — // — // —	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2200079	ccaaatagcacaaaac[A/G]aataggtcatggtgaa	A	G	NM_015256 // intron // 0 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron // 0 // — // — // — // — /// ENST00000357096 // intron // 0 // — // — // —	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1856533	tcacagccdatgtttc[A/G]agccctatacattctg	A	G	NM_015256 // intron // 0 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron // 0 // — // — // — // ENST00000357096 // intron // 0 // — // — // — //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-1851285	tattcatagtgagaaa[A/G]aagacttcccaaaga	A	G	NM_015256 // intron // 0 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron // 0 // — // — // — // ENST00000357096 // intron // 0 // — // — // — //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2296858	gccaagagcacttaa[A/G]cccaacatgctcacac	A	G	NM_015256 // intron // 0 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// ENST00000296869 // intron // 0 // — // — // — // ENST00000357096 // intron // 0 // — // — // — //	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-1863704	tccaacttggcactac[C/T]gtaaaiaaatattgcaa	C	T	NM_015256 // upstream // 23088 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 // upstream // 43288 // Hs.694 // IL3 // 3562 // Homo sapiens interleukin 3 (colony-stimulating factor	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2308316	gctggttgtagatga[C/T]aggagcctgaatggc	C	T	NM_015256 // upstream // 34008 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 // upstream // 32368 // Hs.694 // IL3 // 3562 // Homo sapiens interleukin 3 (colony-stimulating factor	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2235038	ctcccacccgggggcca[A/G]tcatcttgaagaagtc	A	G	NM_015256 // upstream // 65144 // Hs.14945 // ACSL6 // 23305 // Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA. /// NM_000588 // upstream // 1232 // Hs.694 // IL3 // 3562 // Homo sapiens interleukin 3 (colony-stimulating factor.	ACSL6	ACSL6, Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), q23.3
SNP_A-2096646	agacggtaagactgga[C/T]gactgtggcctgagga	C	T	NM_000588 // downstream // 3290 // Hs.694 // IL3 // 3562 // Homo sapiens interleukin 3 (colony-stimulating factor. multiple) (IL3), mRNA. /// NM_000758 // upstream // 7299 // Hs.1349 // CSF2 // 1437 // Homo sapiens colony stimulating factor 2 (granulocyte	IL3	IL3, Homo sapiens interleukin 3 (colony-stimulating factor, multiple) (IL3), q23.3
SNP_A-2217595	cctgagatgacggtta[C/T]acccctgagaagacggt	C	T	NM_000758 // downstream // 25037 // Hs.1349 // CSF2 // 1437 // Homo sapiens colony stimulating factor 2 (granulocyte-macrophage) (CSF2), mRNA. /// NM_004199 // downstream // 91407 // Hs.519568 // P4HA2 // 8974 // Homo sapiens procollagen-proline, 2-oxoglu	CSF2	CSF2, Homo sapiens colony stimulating factor 2 (granulocyte-macrophage) (CSF2), q23.3
SNP_A-2099343	agaggcctatccttd[A/G]ccacataacctggctc	A	G	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — //	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-1788463	gggagttatggtgccg[A/C]aagtgtcttttggaa	A	C	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — //	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-2303297	gctatgtaatgcgagc[A/G]agtaggagcatcacc	A	G	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — //	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-2256665	ctttcagacctgagaa[C/T]ccaacacaacgagtct	C	T	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — //	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1954772	tttgctgctatggtaa[A/G]taataagtgacctgga	A	G	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — // —	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-2139951	atctaccagttctgac[G/T]atcattgtgtgtgt	G	T	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — // —	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-1841657	taggcaaagaactcta[C/T]caaaggaacatctgtc	C	T	NM_003059 // intron // 0 // Hs.310591 // SLC22A4 // 6583 // Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA. /// ENST00000200652 // intron // 0 // — // — // — // —	SLC22A4	SLC22A4, Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), q23.3
SNP_A-1866185	tcccaggtcctagaac[A/G]gtgtctcgtccataac	A	G	ENST00000337752 // intron // 0 // — // — // — // —	-	q23.3
SNP_A-1691028	ccattatgctgtagctccatttgag[C/T]agggaccttgtctgttcact actgt	C	T	AK096941 // intron // 0 // Hs.408815 // - // 389326 // CDNA FLJ46914 fis, clone SPLEN2027852	-	- , rs725580, CDNA FLJ46914 fis, clone SPLEN2027852,q23.3
SNP_A-1949019	tttatcttcagagaaa[C/G]agtgatctggagaaaa	C	G	NM_198431 // downstream // 75367 // Hs.90093 // HSPA4 // 3308 // Homo sapiens heat shock 70kDa protein 4 (HSPA4), transcript variant 2, mRNA. /// NM_002154 // downstream // 74786 // Hs.90093 // HSPA4 // 3308 // Homo sapiens heat shock 70kDa protein 4 (HSP	HSPA4	HSPA4, Homo sapiens heat shock 70kDa protein 4 (HSPA4), transcript variant 2, q31.1
SNP_A-1939747	ttgcaaatacaaacaa[C/T]gcagtaacaaacattg	C	T	ENST00000265342 // intron // 0 // — // — // — // — /// ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2273843	gactgggacaagcgaa[C/T]gctcgtaactagtttg	C	T	ENST00000265342 // intron // 0 // — // — // — // — /// ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1851005	tattatgacacaaaac[A/G]acgacactcattagta	A	G	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1885374	tgacaaaaattgaata[C/T]ggactgtggattaggt	C	T	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1983523	atgcaggtgaccttga[A/G]ctctgattgttacgac	A	G	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2065481	aattgtttcttgccca[C/T]gagaattctggaagtg	C	T	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2216657	cctctcagttgggtcc[A/G]caacatagagagagca	A	G	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1983529	ctcattcctttctcac[A/G]acaatcttataggtag	A	G	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2104499	agcaggcgacaccgag[A/G]acactgtggtgggtgc	A	G	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1711808	gaaagtaattactctgcaatatacg[C/T]ggaatgtcttaaatgctt aaagcaa	C	T	BC024300 // intron // 0 // Hs.123420 // FSTL4 // 23105 // follistatin-like 4	FSTL4	FSTL4 , rs1363245, follistatin-like 4,q31.1
SNP_A-2280920	gaggttgataacacga[C/T]gtgagtaatggctcta	C	T	ENST00000360575 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1666938	aaaagtaagatattgtctagcaatg[A/G]acacctgggttggttcc cagctctg	A	G	BC024300 // intron // 0 // Hs.123420 // FSTL4 // 23105 // follistatin-like 4	FSTL4	FSTL4 , rs256333, follistatin-like 4,q31.1
SNP_A-1983530	tgcttaggcagagata[C/T]gattagatgagggcgt	C	T	ENST00000265342 // upstream // 301215 // — // — // — // — /// ENST00000360575 // upstream // 5268 // — // — // — // — /// ENST00000231482 // upstream // 104862 // — // — // — // —	-	q31.1
SNP_A-1849858	tatgtatacgaaaaaa[A/C]gtccagccctcgtgga	A	C	ENST00000265342 // upstream // 322161 // — // — // — // — /// ENST00000360575 // upstream // 26214 // — // — // — // — /// ENST00000231482 // upstream // 83916 // — // — // — // —	-	q31.1
SNP_A-2172911	cacaaaaacaacataa[C/T]aaggagcagagaaaaa	C	T	ENST00000265342 // upstream // 330390 // — // — // — // — /// ENST00000360575 // upstream // 34443 // — // — // — // — /// ENST00000231482 // upstream // 75687 // — // — // — // —	-	q31.1
SNP_A-1896242	tgcgtattcttcagca[C/G]tgacttttaaaatca	C	G	ENST00000265342 // upstream // 336121 // — // — // — // — /// ENST00000360575 // upstream // 40174 // — // — // — // — /// ENST00000231482 // upstream // 69956 // — // — // — // —	-	q31.1
SNP_A-2063418	aattaagagaagtaac[C/T]gtacccatcgtggtaa	C	T	ENST00000265342 // upstream // 336257 // — // — // — // — /// ENST00000360575 // upstream // 40310 // — // — // — // — /// ENST00000231482 // upstream // 69820 // — // — // — // —	-	q31.1
SNP_A-2142534	atgaacagacagacac[A/T]aaccagtatggaaaca	A	T	ENST00000265342 // upstream // 344296 // — // — // — // — /// ENST00000360575 // upstream // 48349 // — // — // — // — /// ENST00000231482 // upstream // 61781 // — // — // — // —	-	q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074983	acatcaitcaactca[C/G]cagaaaggcatgtcat	C	G	ENST00000265342 // upstream // 347013 // — // — // — /// ENST00000360575 // upstream // 51066 // — // — // — /// ENST00000231482 // upstream // 59064 // — // — // —	-	q31.1
SNP_A-1983533	aatcatttcagtgagc[A/G]aagcacttttttctt	A	G	ENST00000265342 // upstream // 349623 // — // — // — /// ENST00000360575 // upstream // 53676 // — // — // — /// ENST00000231482 // upstream // 56454 // — // — // —	-	q31.1
SNP_A-1825736	taaatcccatcattga[A/G]gcatccaattatgcta	A	G	ENST00000265342 // upstream // 352474 // — // — // — /// ENST00000360575 // upstream // 56527 // — // — // — /// ENST00000231482 // upstream // 53603 // — // — // —	-	q31.1
SNP_A-1871370	tctaaatcattgaaaa[C/T]agaagaagttcacagg	C	T	ENST00000265342 // upstream // 352834 // — // — // — /// ENST00000360575 // upstream // 56887 // — // — // — /// ENST00000231482 // upstream // 53243 // — // — // —	-	q31.1
SNP_A-2250542	cttagtatttctatca[C/T]gcagatcctaccatac	C	T	ENST00000265342 // upstream // 370627 // — // — // — /// ENST00000360575 // upstream // 74680 // — // — // — /// ENST00000231482 // upstream // 35450 // — // — // —	-	q31.1
SNP_A-1691546	atcaagtccagcaaagctgctagac[A/G]ctttctgaaggaaat atggccagg	A	G	AB028984 // upstream // 414005 // Hs.123420 // FSTL4 // 23105 // follistatin-like 4 /// NM_020199 // downstream // 224889 // Hs.283437 // C5orf15 // 56951 // chromosome 5 open reading frame 15	FSTL4	FSTL4 , rs10515461, follistatin-like 4 ,q31.1
SNP_A-1755628	agcagagaaaaggggtaaagaaaca[C/T]tgggcacgatttag ggtgggcactt	C	T	AB028984 // upstream // 414497 // Hs.123420 // FSTL4 // 23105 // follistatin-like 4 /// NM_020199 // downstream // 224397 // Hs.283437 // C5orf15 // 56951 // chromosome 5 open reading frame 15	FSTL4	FSTL4 , rs9327668, follistatin-like 4 ,q31.1
SNP_A-1983552	gtcagtaaagatgtta[C/T]gatttgtgaaagata	C	T	NM_016508 // intron // 0 // Hs.105818 // CDKL3 // 51265 // Homo sapiens cyclin-dependent kinase-like 3 (CDKL3), mRNA. /// ENST00000265334 // intron // 0 // — // — // —	CDKL3	CDKL3, Homo sapiens cyclin-dependent kinase-like 3 (CDKL3), q31.1
SNP_A-2048375	aagcaggatgggaac[A/T]gcttgacctcatcca	A	T	NM_015288 // 3UTR // 0 // Hs.483419 // PHF15 // 23338 // Homo sapiens PHD finger protein 15 (PHF15), mRNA. /// ENST00000342797 // 3UTR // 0 // — // — // —	PHF15	PHF15, Homo sapiens PHD finger protein 15 (PHF15), q31.1
SNP_A-1896115	tgcgacatatagttgaj[A/G]aagattgtaaatggtt	A	G	NM_016103 // intron // 0 // Hs.279582 // SARA2 // 51128 // Homo sapiens SAR1a gene homolog 2 (S. cerevisiae) (SARA2), mRNA. /// ENST00000282606 // intron // 0 // — // — // —	SARA2	SARA2, Homo sapiens SAR1a gene homolog 2 (S. cerevisiae) (SARA2), q31.1
SNP_A-1801554	gtaggtctgctgtaacc[C/T]atcccctgtgtctga	C	T	ENST00000322410 // intron // 0 // — // — // —	-	q31.1
SNP_A-2095889	agacagcgcgctccc[C/T]acactctgttctctgc	C	T	ENST00000322410 // intron // 0 // — // — // —	-	q31.1
SNP_A-2070953	acactcgtcaatagcc[A/G]ctaagaagcagccaga	A	G	ENST00000322410 // intron // 0 // — // — // —	-	q31.1
SNP_A-1903245	tggctttaaggaagga[A/C]gggtggaagcgagtct	A	C	NM_138609 // intron // 0 // Hs.420272 // H2AFY // 9555 // Homo sapiens H2A histone family, member Y (H2AFY), transcript variant 1, mRNA. /// NM_004893 // intron // 0 // Hs.420272 // H2AFY // 9555 // Homo sapiens H2A histone family, member Y (H2AFY), trans	H2AFY	H2AFY, Homo sapiens H2A histone family, member Y (H2AFY), transcript variant 1, q31.1
SNP_A-2112640	aggcagacagctaaag[C/G]ccaaaccaccaatgaca	C	G	NM_130848 // upstream // 9591 // Hs.152477 // DCNP1 // 140947 // Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// NM_006161 // downstream // 73088 // Hs.248149 // NEUROG1 // 4762 // Homo sapiens neurogenin 1 (NEUROG1), mRNA. /// ENST0000003	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1
SNP_A-2229922	ctagttcttctttgc[A/G]gacaggaccacctdga	A	G	NM_130848 // upstream // 10735 // Hs.152477 // DCNP1 // 140947 // Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// NM_006161 // downstream // 71944 // Hs.248149 // NEUROG1 // 4762 // Homo sapiens neurogenin 1 (NEUROG1), mRNA. /// ENST00000	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1
SNP_A-2206017	ccatatggtaaatgta[C/T]gtttaatgtcaaaega	C	T	NM_130848 // upstream // 63413 // Hs.152477 // DCNP1 // 140947 // Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// NM_006161 // downstream // 19266 // Hs.248149 // NEUROG1 // 4762 // Homo sapiens neurogenin 1 (NEUROG1), mRNA. /// ENST00000	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1954010	ttgatatgaggataa[C/T]gctgggctcataaaat	C	T	NM_130848 // upstream // 65098 // Hs.152477 // DCNP1 // 140947 // Homo sapiens dendritic cell nuclear protein 1 (DCNP1), mRNA. /// NM_006161 // downstream // 17581 // Hs.248149 // NEUROG1 // 4762 // Homo sapiens neurogenin 1 (NEUROG1), mRNA. /// ENST00000	DCNP1	DCNP1, Homo sapiens dendritic cell nuclear protein 1 (DCNP1), q31.1
SNP_A-1870699	tcgcctagtggtatg[A/C]acttggccttgaat	A	C	NM_006161 // upstream // 16053 // Hs.248149 // NEUROG1 // 4762 // Homo sapiens neurogenin 1 (NEUROG1), mRNA. /// NM_004887 // downstream // 18942 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// ENST0000	NEUROG1	NEUROG1, Homo sapiens neurogenin 1 (NEUROG1), q31.1
SNP_A-1750477	ccgagctcacttctgtcagaggaat[C/T]agtttcacaagccctttttatgt	C	T	AF106911 // intron // 0 // Hs.24395 // CXCL14 // 9547 // chemokine (C-X-C motif) ligand 14	CXCL14	CXCL14 , rs3860106, chemokine (C-X-C motif) ligand 14,q31.1
SNP_A-2111017	aggagaaggttaagta[C/T]gttgcccaaaataact	C	T	NM_004887 // upstream // 6827 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 248615 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC15332	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2307125	gcttaaaatctgggcc[A/G]cacctttggctctggg	A	G	NM_004887 // upstream // 8530 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 246912 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC15332	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2105560	agccacagcatataaa[C/G]cgttcatgttgcctgg	C	G	NM_004887 // upstream // 32748 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 222694 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-1683132	ggggtaaggtttggtgagagctc[C/T]atggacctatgacaca aattgctct	C	T	NM_004887 // intron // 0 // Hs.24395 // CXCL14 // 9547 // chemokine (C-X-C motif) ligand 14	CXCL14	CXCL14 , rs2237061, chemokine (C-X-C motif) ligand 14,q31.1
SNP_A-2284010	gatatatctgctcaaa[A/C]actttctatttttta	A	C	NM_004887 // upstream // 94259 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 161183 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2053012	aagtccggaacctca[A/G]gtgctcagtgttaacc	A	G	NM_004887 // upstream // 104486 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 150956 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC153	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2101691	agatgcaatccacagg[G/T]atgctgatccgagccc	G	T	NM_004887 // upstream // 140487 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 114955 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC153	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2154934	attcacacgaaagcac[A/G]aagatggtagatggca	A	G	NM_004887 // upstream // 168525 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 86917 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-2047526	aagatggaaatgacaa[C/T]agtccctacctgatag	C	T	NM_004887 // upstream // 168853 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 86589 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2249929	cttacaggtgataaga[C/T]ggctgccaagatttac	C	T	NM_004887 // upstream // 168883 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 86559 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-1876228	tctgagaaaagaagga[C/T]gttccatctgttactg	C	T	NM_004887 // upstream // 245107 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 10335 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-1818423	gttcttcccttactac[C/T]gctctgaggaggagag	C	T	NM_004887 // upstream // 245405 // Hs.483444 // CXCL14 // 9547 // Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), mRNA. /// NM_145282 // upstream // 10037 // Hs.412418 // LOC153328 // 153328 // Homo sapiens similar to CG4995 gene product (LOC1533	CXCL14	CXCL14, Homo sapiens chemokine (C-X-C motif) ligand 14 (CXCL14), q31.1
SNP_A-1728183	agaacagagaggatggcaaaaagga[C/G]ccatgtattcaggcggaaaggccta	C	G	NM_000358 // upstream // 31899 // Hs.421496 // TGFBI // 7045 // transforming growth factor, beta-induced, 68kDa /// NM_002302 // upstream // 42076 // Hs.512580 // LECT2 // 3950 // leukocyte cell-derived chemotaxin 2 /// NM_012159 // downstream // 55432 /	TGFBI	TGFBI , rs42258, transforming growth factor, beta-induced, 68kDa ,q31.1
SNP_A-2257870	ctttggttgattaaaa[A/C]tttgatgcatgatata	A	C	NM_020389 // intron // 0 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // intron // 0 // — // — // — // — /// ENST00000355180 // intron // 0 //	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2152470	attaacttcttcctca[C/G]ctatgaccaccagaac	C	G	NM_020389 // intron // 0 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // intron // 0 // — // — // — // — /// ENST00000355180 // intron // 0 //	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-1887598	tgagagcaataggagc[C/G]gcctgttccattagag	C	G	NM_020389 // intron // 0 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // intron // 0 // — // — // — // — /// ENST00000355180 // intron // 0 //	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2233270	ctcaggagcacagtga[A/G]gattaaataatgtcta	A	G	NM_020389 // upstream // 4549 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 4549 // — // — // — // — /// ENST00000355180 // upstr	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-1895030	tgcccagagtctatac[C/T]acattccttcctgccc	C	T	NM_020389 // upstream // 13776 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 13776 // — // — // — // — /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2202221	ccacattcattcaaca[A/G]gaaagtcgaatgttga	A	G	NM_020389 // upstream // 36102 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 36102 // — // — // — // — /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2183619	cagcagtcagtgtaga[A/G]accaggaataaaaatc	A	G	NM_020389 // upstream // 39390 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 39390 // — // — // — // — /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1868473	tcctcctcctatctg[A/G]agaaaacctggtgttag	A	G	NM_020389 // upstream // 43163 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 43163 // --- // --- // --- /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2025120	aaaatactacactcac[A/G]catttaagttggata	A	G	NM_020389 // upstream // 55792 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 55792 // --- // --- // --- /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-2299306	gccctctgtaccacaa[C/G]ggttgaaagtgtataa	C	G	NM_020389 // upstream // 57477 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 57477 // --- // --- // --- /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-1913064	tgtggataccatcgtc[C/T]ctcatttctgcttgat	C	T	NM_020389 // upstream // 59933 // Hs.283104 // TRPC7 // 57113 // Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), mRNA. /// ENST00000352189 // upstream // 59933 // --- // --- // --- /// ENST00000355180 // ups	TRPC7	TRPC7, Homo sapiens transient receptor potential cation channel, subfamily C, member 7 (TRPC7), q31.1
SNP_A-1818682	gttgaatgttattcag[C/G]caccatttttttcctt	C	G	NM_004598 // downstream // 348442 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000309810 // downstream // 197004 // --- // --- // --- /// ENST00000282822	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1892622	tgcaattctctagaga[C/T]gtacgatgttgagcat	C	T	NM_004598 // downstream // 264469 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000309810 // downstream // 280977 // --- // --- // --- /// ENST00000282822	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1784382	ggcccctgagcaaatg[C/T]agaaggttcagaagtt	C	T	NM_004598 // downstream // 121219 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000309810 // downstream // 424227 // --- // --- // --- /// ENST00000282822	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1806822	gtctatcacagatacaj[A/G]tcgggcagtaacagca	A	G	NM_004598 // intron // 0 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000282223 // intron // 0 // --- // --- // ---	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1983644	tgcatttggttaaaag[A/T]ctgctttggcatttt	A	T	NM_004598 // intron // 0 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000282223 // intron // 0 // --- // --- // ---	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1983658	aaggacataaggatag[C/T]gtcagtggtcctgaa	C	T	NM_004598 // intron // 0 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000282223 // intron // 0 // --- // --- // ---	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-2269138	gaattggaagaatcac[A/G]ggactctgatttaaa	A	G	NM_004598 // intron // 0 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000282223 // intron // 0 // --- // --- // ---	SPOCK	SPOCK, Homo sapiens sparc,q31.1
SNP_A-1795576	ggtgctatgtatgcaa[A/T]gtctgaagtgtgttta	A	T	NM_004598 // intron // 0 // Hs.124611 // SPOCK // 6695 // Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA. /// ENST00000282223 // intron // 0 // --- // --- // ---	SPOCK	SPOCK, Homo sapiens sparc,q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1705063	cttttaggtaactctcccaactcaa[A/G]atcgatagttctctgaagaattgaa	A	G	NM_004598 // intron // 0 // Hs.93029 // SPOCK // 6695 // sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican)	SPOCK	SPOCK , rs1229732, sparc,q31.1
SNP_A-2121587	agtgaagaggtaagaa[A/G]gtaacttaaatcagct	A	G	NM_139199 // intron // 0 // Hs.519337 // BRD8 // 10902 // Homo sapiens bromodomain containing 8 (BRD8), transcript variant 2, mRNA. /// ENST00000254900 // intron // 0 // — // — // — // —	BRD8	BRD8, Homo sapiens bromodomain containing 8 (BRD8), transcript variant 2, q31.2
SNP_A-2292089	gcaccagagtggcaag[A/G]ctaggccctcatgaga	A	G	NM_004134 // upstream // 80737 // Hs.184233 // HSPA9B // 3313 // Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA. /// NM_001903 // upstream // 125759 // Hs.445981 // CTNNA1 // 1495 // Homo	HSPA9B	HSPA9B, Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, q31.2
SNP_A-1874912	tctctacaaacaaaag[A/T]ctgctcttcaattccc	A	T	NM_004134 // upstream // 80836 // Hs.184233 // HSPA9B // 3313 // Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA. /// NM_001903 // upstream // 125660 // Hs.445981 // CTNNA1 // 1495 // Homo	HSPA9B	HSPA9B, Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, q31.2
SNP_A-1787748	gggaccacaggaggaa[C/T]tccatatctaacctga	C	T	NM_004134 // upstream // 81594 // Hs.184233 // HSPA9B // 3313 // Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA. /// NM_001903 // upstream // 124902 // Hs.445981 // CTNNA1 // 1495 // Homo	HSPA9B	HSPA9B, Homo sapiens heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, q31.2
SNP_A-2115284	aggggacgatgttgaa[C/T]tgacaggcagcggagg	C	T	NM_001903 // downstream // 10746 // Hs.445981 // CTNNA1 // 1495 // Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA. /// AB007876 // upstream // 71015 // Hs.114169 // LRRTM2 // 26045 // Homo sapiens KIAA0416 mRNA, partial	CTNNA1	CTNNA1, Homo sapiens catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), q31.2
SNP_A-1882178	tctttttttcccacac[C/T]gagagtcctgattctg	C	T	NM_022464 // intron // 0 // Hs.483521 // SIL1 // 64374 // Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), mRNA. /// ENST00000265195 // intron // 0 // — // — // — // —	SIL1	SIL1, Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), q31.2
SNP_A-2289981	gcaaaggagatgctca[A/G]agtcgagaatgcttag	A	G	NM_022464 // intron // 0 // Hs.483521 // SIL1 // 64374 // Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), mRNA. /// ENST00000265195 // intron // 0 // — // — // — // —	SIL1	SIL1, Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), q31.2
SNP_A-2204509	ccagcttaattgtgaa[C/G]agcctcacgtgccata	C	G	NM_022464 // upstream // 17165 // Hs.483521 // SIL1 // 64374 // Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), mRNA. /// NM_018834 // upstream // 77991 // Hs.268939 // MATR3 // 9782 // Homo sapiens matrin 3 (MATR3), mRNA. ///	SIL1	SIL1, Homo sapiens endoplasmic reticulum chaperone SIL1, homolog of yeast (SIL1), q31.2
SNP_A-1789964	gggcttgttgacaagc[A/G]gccatttgcgagacag	A	G	NM_032289 // 3UTR // 0 // Hs.21963 // PSD2 // 84249 // Homo sapiens pleckstrin and Sec7 domain containing 2 (PSD2), mRNA. /// ENST00000274710 // 3UTR // 0 // — // — // — // —	PSD2	PSD2, Homo sapiens pleckstrin and Sec7 domain containing 2 (PSD2), q31.2
SNP_A-1904719	tgggggactgcaccc[A/G]gaagctttctaaggag	A	G	NM_013981 // intron // 0 // Hs.408515 // NRG2 // 9542 // Homo sapiens neuregulin 2 (NRG2), transcript variant 2, mRNA. /// NM_013983 // intron // 0 // Hs.408515 // NRG2 // 9542 // Homo sapiens neuregulin 2 (NRG2), transcript variant 4, mRNA. /// NM_013982	NRG2	NRG2, Homo sapiens neuregulin 2 (NRG2), transcript variant 2, q31.2
SNP_A-2059272	aatcctttctccaaaa[A/G]ggctagtaacattcac	A	G	NM_013981 // intron // 0 // Hs.408515 // NRG2 // 9542 // Homo sapiens neuregulin 2 (NRG2), transcript variant 2, mRNA. /// NM_013983 // intron // 0 // Hs.408515 // NRG2 // 9542 // Homo sapiens neuregulin 2 (NRG2), transcript variant 4, mRNA. /// NM_013982	NRG2	NRG2, Homo sapiens neuregulin 2 (NRG2), transcript variant 2, q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140353	atctcagcttactaca[A/G]aaaaggaacctggtca	A	G	NM_013981 // intron // 0 // Hs.408515 // NRG2 // 9542 // Homo sapiens neuregulin 2 (NRG2), transcript variant 2, mRNA. /// NM_013983 // intron // 0 // Hs.408515 // NRG2 // 9542 // Homo sapiens neuregulin 2 (NRG2), transcript variant 4, mRNA. /// NM_013982	NRG2	NRG2, Homo sapiens neuregulin 2 (NRG2), transcript variant 2, q31.2
SNP_A-1983707	agcagcaccttctaa[A/G]cttatgccaacaggaa	A	G	NM_020690 // intron // 0 // Hs.434219 // MASK-BP3 // 404734 // Homo sapiens MASK-4E-BP3 alternate reading frame gene (MASK-BP3), mRNA. /// NM_017747 // intron // 0 // Hs.434219 // ANKHD1 // 54882 // Homo sapiens ankyrin repeat and KH domain containing 1 (	MASK-BP3	MASK-BP3, Homo sapiens MASK-4E-BP3 alternate reading frame gene (MASK-BP3), q31.3
SNP_A-2271827	gaccatgtaggctaa[A/G]tcggccaaattccaa	A	G	NM_006083 // intron // 0 // Hs.421245 // IK // 3550 // Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA. /// ENST00000261812 // intron // 0 // — // — // — // —	IK	IK, Homo sapiens IK cytokine, down-regulator of HLA II (IK), q31.3
SNP_A-1702631	atatggcatttgtataatatcct[G/T]aacagactaagacagatatcgttta	G	T	NM_018900 // intron // 0 // Hs.247734 // PCDHA5 // 56143 // protocadherin alpha 5 /// NM_018901 // intron // 0 // Hs.247734 // PCDHA5 // 56143 // protocadherin alpha 5 /// NM_018902 // intron // 0 // Hs.247734 // PCDHA5 // 56143 // protocadherin alpha 5	PCDHA5	PCDHA5, rs56003, protocadherin alpha 5, q31.3
SNP_A-2210087	ccccagattgtttca[C/T]agggcccaaacactct	C	T	NM_014005 // intron // 0 // Hs.199343 // PCDHA9 // 9752 // Homo sapiens protocadherin alpha 9 (PCDHA9), transcript variant 2, mRNA. /// NM_018909 // intron // 0 // Hs.199343 // PCDHA6 // 56142 // Homo sapiens protocadherin alpha 6 (PCDHA6), transcript var	PCDHA9	PCDHA9, Homo sapiens protocadherin alpha 9 (PCDHA9), transcript variant 2, q31.3
SNP_A-2081928	accttactctaaatc[A/G]gaatcataactcaatg	A	G	NM_013340 // downstream // 2551 // Hs.278950 // PCDHB1 // 29930 // Homo sapiens protocadherin beta 1 (PCDHB1), mRNA. /// NM_018936 // upstream // 38156 // Hs.533023 // PCDHB2 // 56133 // Homo sapiens protocadherin beta 2 (PCDHB2), mRNA. /// ENST00000030654	PCDHB1	PCDHB1, Homo sapiens protocadherin beta 1 (PCDHB1), q31.3
SNP_A-1983716	catcactgtatttcca[A/G]tgaaattaggttccag	A	G	NM_013340 // downstream // 32076 // Hs.278950 // PCDHB1 // 29930 // Homo sapiens protocadherin beta 1 (PCDHB1), mRNA. /// NM_018936 // upstream // 8631 // Hs.533023 // PCDHB2 // 56133 // Homo sapiens protocadherin beta 2 (PCDHB2), mRNA. /// ENST00000030654	PCDHB1	PCDHB1, Homo sapiens protocadherin beta 1 (PCDHB1), q31.3
SNP_A-1957646	tttatctttcttcaa[C/T]gataaggttcttgcct	C	T	NM_018937 // downstream // 15192 // Hs.508987 // PCDHB3 // 56132 // Homo sapiens protocadherin beta 3 (PCDHB3), mRNA. /// NM_018938 // upstream // 2983 // Hs.283661 // PCDHB4 // 56131 // Homo sapiens protocadherin beta 4 (PCDHB4), mRNA. /// ENST00000023113	PCDHB3	PCDHB3, Homo sapiens protocadherin beta 3 (PCDHB3), q31.3
SNP_A-1821469	gtttgggataaaatggd[A/G]gaaaacaacgcgtcat	A	G	NM_015669 // 3UTR // 0 // Hs.119693 // PCDHB5 // 26167 // Homo sapiens protocadherin beta 5 (PCDHB5), mRNA. /// ENST00000231134 // 3UTR // 0 // — // — // — // —	PCDHB5	PCDHB5, Homo sapiens protocadherin beta 5 (PCDHB5), q31.3
SNP_A-2219555	cctgttgctgtcccag[A/C]caaactgcctcattta	A	C	NM_022481 // upstream // 17561 // Hs.25277 // CENTD3 // 64411 // Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), mRNA. /// NM_002587 // downstream // 154713 // Hs.79769 // PCDH1 // 5097 // Homo sa	CENTD3	CENTD3, Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), q31.3
SNP_A-1855223	tcaagcatgcaaatcc[G/T]accatcacacatggcc	G	T	NM_022481 // upstream // 19834 // Hs.25277 // CENTD3 // 64411 // Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), mRNA. /// NM_002587 // downstream // 152440 // Hs.79769 // PCDH1 // 5097 // Homo sa	CENTD3	CENTD3, Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), q31.3
SNP_A-2041004	aacccttttctcaaact[A/G]cttccgtagtctcctg	A	G	NM_022481 // upstream // 117560 // Hs.25277 // CENTD3 // 64411 // Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), mRNA. /// NM_002587 // downstream // 54714 // Hs.79769 // PCDH1 // 5097 // Homo sa	CENTD3	CENTD3, Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187147	caggtcctgttgggta[A/G]aacatttggctttcag	A	G	NM_022481 // upstream // 145922 // Hs.25277 // CENTD3 // 64411 // Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), mRNA. /// NM_002587 // downstream // 26352 // Hs.79769 // PCDH1 // 5097 // Homo sa	CENTD3	CENTD3, Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), q31.3
SNP_A-2094333	agaagtcaatgagcaa[A/G]caatgcaacatcctta	A	G	NM_005471 // upstream // 48578 // Hs.278500 // GNPDA1 // 10007 // Homo sapiens glucosamine-6-phosphate deaminase 1 (GNPDA1), mRNA. /// NM_030571 // upstream // 47154 // Hs.9788 // NDFIP1 // 80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1)	GNPDA1	GNPDA1, Homo sapiens glucosamine-6-phosphate deaminase 1 (GNPDA1), q31.3
SNP_A-1914824	tgttactatcgaaca[A/C]atttcaagtgtcatgt	A	C	NM_030571 // downstream // 118212 // Hs.9788 // NDFIP1 // 80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 38849 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4),	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-2113862	aggctgtagtaaagta[C/T]gattgtatcactgtac	C	T	NM_030571 // downstream // 133349 // Hs.9788 // NDFIP1 // 80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 23712 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4),	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-2188596	cagtgattaaagagta[C/T]gttgtattagagata	C	T	NM_030571 // downstream // 136563 // Hs.9788 // NDFIP1 // 80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 20498 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4),	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-1898069	tgctgtgcaaagtcac[A/T]atctaatcttccaact	A	T	NM_030571 // downstream // 151445 // Hs.9788 // NDFIP1 // 80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 5616 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), m	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-2147586	atggatgttcagtacc[C/T]ggagaaaagaagccat	C	T	NM_030571 // downstream // 154695 // Hs.9788 // NDFIP1 // 80762 // Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA. /// NM_030964 // downstream // 2366 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), m	NDFIP1	NDFIP1, Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), q31.3
SNP_A-2103805	agcaccccattagttg[A/G]aaaactgtactctcca	A	G	NM_030964 // upstream // 109379 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 159178 // Hs.483635 // FGF1 // 2246 // Homo sapiens fibroblast growth factor 1 (acidic) (FGF1), tra	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-2229857	ctagttatcccaggaa[G/T]gcctaatgtcaaatag	G	T	NM_030964 // upstream // 159038 // Hs.323308 // SPRY4 // 81848 // Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA. /// NM_033137 // downstream // 109519 // Hs.483635 // FGF1 // 2246 // Homo sapiens fibroblast growth factor 1 (acidic) (FGF1), tra	SPRY4	SPRY4, Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), q31.3
SNP_A-2185859	caggatgttcacaaca[A/C]cattacttgcaatggt	A	C	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1983772	gaggaccgaagtggaaa[C/T]gcttgtagaggactag	C	T	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1856164	tcacaaatggtactccg[A/G]caagaaaaagagactg	A	G	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2228238	ctactctcagaaagga[C/T]ggcccaaattcctctc	C	T	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1820292	gtttagaacattgtac[C/T]gaaaagtcttgagcca	C	T	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1886082	tgaccacttctctttc[A/G]ctgctcttctgtctct	A	G	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1983775	gcatttctggatcacc[C/T]gaaattatctcttgca	C	T	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1868662	tcctctgcatgacaaa[A/G]tgggtccaccatcact	A	G	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2234017	ctcatgtggctattga[A/G]gaagggcatagcggct	A	G	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2262930	gaacaactctaaggta[C/T]aatcaaatgattttct	C	T	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-1758100	aaaacacaacttgaaaatcataaac[A/C]agaaagcaaaaaa gagatgatttga	A	C	NM_015071 // intron // 0 // Hs.132942 // GRAF // 23092 // GTPase regulator associated with focal adhesion kinase pp125(FAK)	GRAF	GRAF , rs245815, GTPase regulator associated with focal adhesion kinase pp125(FAK),q31.3
SNP_A-1700065	atgtggccagtttatgtgcagaata[C/T]gaagggttaggtaatattt attttg	C	T	NM_015071 // intron // 0 // Hs.132942 // GRAF // 23092 // GTPase regulator associated with focal adhesion kinase pp125(FAK)	GRAF	GRAF , rs6580266, GTPase regulator associated with focal adhesion kinase pp125(FAK),q31.3
SNP_A-1676812	acagcttctgatcattcttcaacta[C/T]atcatccaggtcctggtgt catatt	C	T	NM_015071 // intron // 0 // Hs.132942 // GRAF // 23092 // GTPase regulator associated with focal adhesion kinase pp125(FAK)	GRAF	GRAF , rs7734364, GTPase regulator associated with focal adhesion kinase pp125(FAK),q31.3
SNP_A-1933697	ttctagttgagtggag[A/G]aaaggaacttgagttt	A	G	NM_015071 // intron // 0 // Hs.293593 // ARHGAP26 // 23092 // Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA. /// ENST00000274498 // intron // 0 // — // — // — // —	ARHGAP26	ARHGAP26, Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), q31.3
SNP_A-2124947	agttgagtgtttcaga[A/G]gcataggtacttgatg	A	G	NM_000176 // upstream // 66720 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 65500 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclear	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-2030888	aaaggaagaactgtct[C/G]acaggtattgttaaca	C	G	NM_000176 // upstream // 120115 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 118895 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclea	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-2155623	attccagaatcaaagg[G/T]cctgtggatatggtaa	G	T	NM_000176 // upstream // 192865 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 191645 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclea	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1874683	tctcctgcatcatgga[C/T]agaaccagtaaataga	C	T	NM_000176 // upstream // 235050 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 233830 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclea	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1983792	gtatgtgtaccagaga[C/T]attgctattcactaa	C	T	NM_000176 // upstream // 266735 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA. /// NM_000176 // upstream // 265515 // Hs.122926 // NR3C1 // 2908 // Homo sapiens nuclea	NR3C1	NR3C1, Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), q31.3
SNP_A-1941224	ttgctggatgaattaa[A/C]cctctgtcaataatct	A	C	NM_021182 // downstream // 69068 // Hs.158320 // HB-1 // 57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 269489 // Hs.372050 // SMAP-5 // 81555 // Homo sapiens golgi membrane protein SB140 (SMAP-5),	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1983810	atatatcgtcaacatat[A/C]aagttcccaatattga	A	C	NM_021182 // downstream // 159357 // Hs.158320 // HB-1 // 57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 179200 // Hs.372050 // SMAP-5 // 81555 // Homo sapiens golgi membrane protein SB140 (SMAP-5)	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-1949955	tttcaatagttgacaa[A/T]cacagcagaaccacca	A	T	NM_021182 // downstream // 203853 // Hs.158320 // HB-1 // 57824 // Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA. /// NM_030799 // downstream // 134704 // Hs.372050 // SMAP-5 // 81555 // Homo sapiens golgi membrane protein SB140 (SMAP-5)	HB-1	HB-1, Homo sapiens minor histocompatibility antigen HB-1 (HB-1), q31.3
SNP_A-2239477	ctctttagttgcata[C/T]aagtgaatcataatcc	C	T	ENST00000327887 // intron // 0 // — // — // —	-	q31.3
SNP_A-1808021	gtcttctaatttggaa[G/T]atgcatttctatggtta	G	T	ENST00000327887 // intron // 0 // — // — // —	-	q31.3
SNP_A-1983825	tccacagtactacccaa[C/T]agagtggtcaataact	C	T	ENST00000327887 // intron // 0 // — // — // —	-	q31.3
SNP_A-1927269	ttcaaaacggactgta[A/G]gcattactaacattta	A	G	NM_182960 // downstream // 1088441 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 1088441 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypotheti	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q31.3
SNP_A-1743951	gttcaggattgagagacaatatatc[A/C]gagatttgatttactcata aaaggg	A	C	NM_138492 // downstream // 1086478 // Hs.314261 // MGC21644 // 153768 // hypothetical protein MGC21644 /// NM_138492 // downstream // 1122668 // Hs.314261 // MGC21644 // 153768 // hypothetical protein MGC21644	MGC21644	MGC21644, rs9324964, hypothetical protein MGC21644 q32
SNP_A-2053982	aagttacaaattaaaaa[A/G]agacattgcaagtga	A	G	NM_182960 // downstream // 824219 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 824219 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetica	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q31.3
SNP_A-2213556	ccgtcaatatcagcac[C/G]atacgaaggccccaag	C	G	NM_182960 // downstream // 719273 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 719273 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetica	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q31.3
SNP_A-2226013	ctaacaatacccagaa[C/G]tcacaatctctccct	C	G	NM_182960 // downstream // 280045 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 280045 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetica	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q32
SNP_A-2045696	aagacaatataattac[A/G]caagttagaaataggt	A	G	NM_182960 // downstream // 122464 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 122464 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetica	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084551	actatgccatcaacaa[A/G]tcacagcaacaatttc	A	G	NM_182960 // downstream // 57387 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 57387 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q32
SNP_A-2065237	aattggcttaggtccat[C/T]tacagtctaatcattg	C	T	NM_182960 // downstream // 55376 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, mRNA. /// NM_205846 // downstream // 55376 // Hs.314261 // MGC21644 // 153768 // Homo sapiens hypothetical	MGC21644	MGC21644, Homo sapiens hypothetical protein MGC21644 (MGC21644), transcript variant 1, q32
SNP_A-1983872	agctggattcctcag[A/C]aggacaaaatcaactg	A	C	NM_152550 // intron // 0 // Hs.443728 // SH3RF2 // 153769 // Homo sapiens SH3 domain containing ring finger 2 (SH3RF2), mRNA. /// ENST00000287018 // intron // 0 // --- // --- // --- /// ENST00000359120 // intron // 0 // --- // --- // ---	SH3RF2	SH3RF2, Homo sapiens SH3 domain containing ring finger 2 (SH3RF2), q32
SNP_A-1880577	tcttgcatggaatgaa[A/G]taggttgggtcaattt	A	G	NM_194251 // upstream // 24594 // Hs.483732 // GPR151 // 134391 // Homo sapiens G protein-coupled receptor 151 (GPR151), mRNA. /// NM_004576 // downstream // 48797 // Hs.193825 // PPP2R2B // 5521 // Homo sapiens protein phosphatase 2 (formerly 2A), regula	GPR151	GPR151, Homo sapiens G protein-coupled receptor 151 (GPR151), q32
SNP_A-1799441	gtaatgaacagaaact[A/G]acgcctcaaagaggttg	A	G	NM_194251 // upstream // 34645 // Hs.483732 // GPR151 // 134391 // Homo sapiens G protein-coupled receptor 151 (GPR151), mRNA. /// NM_004576 // downstream // 38746 // Hs.193825 // PPP2R2B // 5521 // Homo sapiens protein phosphatase 2 (formerly 2A), regula	GPR151	GPR151, Homo sapiens G protein-coupled receptor 151 (GPR151), q32
SNP_A-1748775	ctacaaagactgtgctgacaactaa[A/G]tggtgtgacctaaaagcaaaacatg	A	G	AY255557 // upstream // 28995 // Hs.483732 // GPR151 // 134391 // G protein-coupled receptor 151 /// NM_004576 // downstream // 44783 // Hs.380764 // PPP2R2B // 5521 // protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform /// N	GPR151	GPR151 , rs10515571, G protein-coupled receptor 151 ,q32
SNP_A-1670790	tgacaaagccaggcagtttagtta[A/C]agttcttatccactatcccatcat	A	C	AY255557 // upstream // 69608 // Hs.483732 // GPR151 // 134391 // G protein-coupled receptor 151 /// NM_004576 // downstream // 4170 // Hs.380764 // PPP2R2B // 5521 // protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform /// NM	GPR151	GPR151 , rs322477, G protein-coupled receptor 151 ,q32
SNP_A-2250173	cttactgccaggagaa[A/G]tgttgggcagacttat	A	G	NM_004576 // intron // 0 // Hs.193825 // PPP2R2B // 5521 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform (PPP2R2B), transcript variant 1, mR /// NM_181675 // intron // 0 // Hs.193825 // PPP2R2B // 5521 // Ho	PPP2R2B	PPP2R2B, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform (PPP2R2B), transcript variant 1, mR ,q32
SNP_A-1983908	taggcactcaattcta[A/G]atggtgcagttctgta	A	G	NM_004576 // upstream // 287297 // Hs.193825 // PPP2R2B // 5521 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform (PPP2R2B), transcript variant 1, mR /// NM_181675 // upstream // 287297 // Hs.193825 // PPP2R2B	PPP2R2B	PPP2R2B, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform (PPP2R2B), transcript variant 1, mR ,q32
SNP_A-2270840	gacaggtagagaaaag[C/T]acagagatccctgaag	C	T	NM_014790 // intron // 0 // Hs.533025 // KIAA0555 // 9832 // Homo sapiens KIAA0555 gene product (KIAA0555), mRNA. /// ENST00000333010 // intron // 0 // --- // --- // --- /// ENST00000265272 // intron // 0 // --- // --- // ---	KIAA0555	KIAA0555, Homo sapiens KIAA0555 gene product (KIAA0555), q32
SNP_A-1936810	ttctttcattggaag[C/G]atacgctgtcaaggtt	C	G	NM_014790 // upstream // 6240 // Hs.533025 // KIAA0555 // 9832 // Homo sapiens KIAA0555 gene product (KIAA0555), mRNA. /// NM_003122 // downstream // 35654 // Hs.407856 // SPINK1 // 6690 // Homo sapiens serine protease inhibitor, Kazal type 1 (SPINK1), mR	KIAA0555	KIAA0555, Homo sapiens KIAA0555 gene product (KIAA0555), q32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282437	gagttctgtaatctga[A/G]actggttcatcctttt	A	G	NM_003122 // upstream // 30210 // Hs.407856 // SPINK1 // 6690 // Homo sapiens serine protease inhibitor, Kazal type 1 (SPINK1), mRNA. /// NM_054023 // upstream // 16804 // Hs.483765 // SCGB3A2 // 117156 // Homo sapiens secretoglobin, family 3A, member 2 (	SPINK1	SPINK1, Homo sapiens serine protease inhibitor, Kazal type 1 (SPINK1), q32
SNP_A-1688638	acctcaaatctaatatgttccatac[A/T]actattttgatctttcaccacaata	A	T	NM_003122 // upstream // 1774 // Hs.407856 // SPINK1 // 6690 // serine protease inhibitor, Kazal type 1 /// NM_054023 // upstream // 45300 // Hs.54795 // SCGB3A2 // 117156 // secretoglobin, family 3A, member 2	SPINK1	SPINK1 , rs10515594, serine protease inhibitor, Kazal type 1 ,q32
SNP_A-1913948	tgtgtgagaacatggc[A/C]cactttgatgctaaaa	A	C	NM_206966 // upstream // 16300 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 141242 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2046597	aagagcaataactaag[A/G]ccaatgcttgggaatt	A	G	NM_206966 // upstream // 17676 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 139866 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2050640	aaggcaatgttgaggg[A/T]agaggttggtggggtc	A	T	NM_206966 // upstream // 47722 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 109820 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-1709971	gcctatacacattctgcatggtaca[C/G]tcatatttcaatttggaagtgtggt	C	G	NM_006846 // upstream // 110589 // Hs.331555 // SPINK5 // 11005 // serine protease inhibitor, Kazal type 5	SPINK5	SPINK5 , rs10515599, serine protease inhibitor, Kazal type 5,q33.1
SNP_A-1723856	ttgtgacactggcccaaatgtctaa[C/T]gtgatcccatgatctgcattcaata	C	T	NM_006846 // upstream // 109621 // Hs.331555 // SPINK5 // 11005 // serine protease inhibitor, Kazal type 5	SPINK5	SPINK5 , rs6580511, serine protease inhibitor, Kazal type 5,q33.1
SNP_A-1983930	agataatctgtactca[A/T]agatcagtaataccat	A	T	NM_206966 // upstream // 126010 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 31532 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-1920429	ttaattagactgtaac[A/G]aaggtgaataaaaata	A	G	NM_206966 // upstream // 133680 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 23862 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2155501	attcattgccagtaac[A/G]cccacagaactttgaa	A	G	NM_206966 // upstream // 133994 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 23548 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2127542	ataacatgttcagtgc[A/G]gaaacatacaattctt	A	G	NM_206966 // upstream // 134135 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 23407 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2291484	gcaattgtttttgaca[C/T]tggacatgatataata	C	T	NM_206966 // upstream // 145805 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 11737 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mR	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1850060	tatgtgaatgcttag[A/T]aatgggaaacgttatc	A	T	NM_206966 // upstream // 147866 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 9676 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRN	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-2025965	aaaatgtgtgcattaa[A/G]gcccttgagagtacaa	A	G	NM_206966 // upstream // 147991 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 9551 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRN	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-1710764	catagatagaatacactcgaaact[G/T]aatacaaacctgttata tttatttt	G	T	NM_006846 // upstream // 56851 // Hs.331555 // SPINK5 // 11005 // serine protease inhibitor, Kazal type 5	SPINK5	SPINK5 , rs4705049, serine protease inhibitor, Kazal type 5,q33.1
SNP_A-2151544	atgtctttcatggta[C/T]ctcccccagaacgcaa	C	T	NM_206966 // upstream // 157295 // Hs.173059 // MGC23985 // 389336 // Homo sapiens similar to AVLV472 (MGC23985), mRNA. /// NM_006846 // upstream // 247 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRNA	MGC23985	MGC23985, Homo sapiens similar to AVLV472 (MGC23985), q32
SNP_A-1746793	tgaagaattggtaaactggaagatg[A/G]cactataggaaatttcc taattctg	A	G	NM_006846 // upstream // 35476 // Hs.331555 // SPINK5 // 11005 // serine protease inhibitor, Kazal type 5	SPINK5	SPINK5 , rs10491341, serine protease inhibitor, Kazal type 5,q33.1
SNP_A-2205867	ccatagcaatgtcaga[C/G]ggactgagttcaataa	C	G	NM_006846 // intron // 0 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRNA. /// ENST00000256084 // intron // 0 // — // — // — /// ENST00000359874 // intron // 0 // — // — // —	SPINK5	SPINK5, Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), q32
SNP_A-1881426	tcttctagctttta[C/T]agaccatgctatgcaa	C	T	NM_006846 // intron // 0 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRNA. /// ENST00000256084 // intron // 0 // — // — // — /// ENST00000359874 // intron // 0 // — // — // —	SPINK5	SPINK5, Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), q32
SNP_A-2109163	agcttgcatagctgtc[A/G]ccacatgacattgact	A	G	NM_006846 // intron // 0 // Hs.331555 // SPINK5 // 11005 // Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), mRNA. /// ENST00000256084 // intron // 0 // — // — // — /// ENST00000359874 // intron // 0 // — // — // —	SPINK5	SPINK5, Homo sapiens serine protease inhibitor, Kazal type 5 (SPINK5), q32
SNP_A-2247572	ctgctgtttaaaaaa[C/G]gcctgaagtttcttg	C	G	NM_205841 // downstream // 13929 // Hs.334274 // SPINK6 // 404203 // Homo sapiens protease inhibitor H (MGC21394), mRNA. /// NM_032566 // upstream // 83362 // Hs.244569 // ECG2 // 84651 // Homo sapiens esophagus cancer-related gene-2 (ECG2), mRNA. /// ENS	SPINK6	SPINK6, Homo sapiens protease inhibitor H (MGC21394), q32
SNP_A-1787868	gggactcctagattaa[A/G]aggcctgtttgaccta	A	G	NM_205841 // downstream // 14437 // Hs.334274 // SPINK6 // 404203 // Homo sapiens protease inhibitor H (MGC21394), mRNA. /// NM_032566 // upstream // 82854 // Hs.244569 // ECG2 // 84651 // Homo sapiens esophagus cancer-related gene-2 (ECG2), mRNA. /// ENS	SPINK6	SPINK6, Homo sapiens protease inhibitor H (MGC21394), q32
SNP_A-2288804	gattgttcactatggg[C/T]atacaaaatgctactg	C	T	NM_205841 // downstream // 31049 // Hs.334274 // SPINK6 // 404203 // Homo sapiens protease inhibitor H (MGC21394), mRNA. /// NM_032566 // upstream // 66242 // Hs.244569 // ECG2 // 84651 // Homo sapiens esophagus cancer-related gene-2 (ECG2), mRNA. /// ENS	SPINK6	SPINK6, Homo sapiens protease inhibitor H (MGC21394), q32
SNP_A-2243944	ctgctgtttaacttca[C/G]aaaaatttttcattaaa	C	G	NM_032566 // downstream // 52111 // Hs.244569 // ECG2 // 84651 // Homo sapiens esophagus cancer-related gene-2 (ECG2), mRNA. /// NM_205836 // upstream // 15958 // Hs.483772 // FBXO38 // 81545 // Homo sapiens F-box protein 38 (FBXO38), transcript variant 2	ECG2	ECG2, Homo sapiens esophagus cancer-related gene-2 (ECG2), q32
SNP_A-1909150	tgtatcgataccagtc[A/C]acctatctagaaccta	A	C	NM_199453 // intron // 0 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, mRNA. /// NM_000870 // intron // 0 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-hydroxytryptamine (serotonin)	HTR4	HTR4, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, q32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1804811	gtcagtgaccaacaaag[C/T]cctgaggatgcagcac	C	T	NM_199453 // upstream // 170848 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, mRNA. /// NM_000870 // upstream // 153715 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-hydroxytryptamin	HTR4	HTR4, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, q32
SNP_A-2122414	agtgcctggcacatca[C/T]agttaattggtgtgg	C	T	NM_199453 // upstream // 180377 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, mRNA. /// NM_000870 // upstream // 163244 // Hs.483773 // HTR4 // 3360 // Homo sapiens 5-hydroxytryptamin	HTR4	HTR4, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 4 (HTR4), transcript variant g, q32
SNP_A-2304037	gctccactgagtacca[A/G]ctaacaatttctacc	A	G	NM_000024 // downstream // 73627 // Hs.2551 // ADRB2 // 154 // Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), mRNA. /// NM_024577 // downstream // 102371 // Hs.483784 // SH3TC2 // 79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. ///	ADRB2	ADRB2, Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), q32
SNP_A-2076198	acattctatatgtaaa[C/T]cgcttgctaaaactct	C	T	NM_000024 // downstream // 173011 // Hs.2551 // ADRB2 // 154 // Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), mRNA. /// NM_024577 // downstream // 2987 // Hs.483784 // SH3TC2 // 79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// E	ADRB2	ADRB2, Homo sapiens adrenergic, beta-2-, receptor, surface (ADRB2), q32
SNP_A-1896144	tgcgcaagttacaaaa[C/T]ggtgtcccctctag	C	T	NM_024577 // intron // 0 // Hs.483784 // SH3TC2 // 79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// ENST00000323829 // intron // 0 // — // — // —	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-1983967	ataaactttccaccaa[A/T]gacaatattcaacag	A	T	NM_024577 // intron // 0 // Hs.483784 // SH3TC2 // 79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// ENST00000323829 // intron // 0 // — // — // —	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-2123839	agttaaataagttgtc[A/G]aggcaagtaaagaac	A	G	NM_024577 // intron // 0 // Hs.483784 // SH3TC2 // 79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// ENST00000323829 // intron // 0 // — // — // —	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-2266601	gaagtccaacagactg[A/G]acgaatgcttggtgt	A	G	NM_024577 // upstream // 42883 // Hs.483784 // SH3TC2 // 79628 // Homo sapiens KIAA1985 protein (KIAA1985), mRNA. /// NM_014945 // upstream // 35563 // Hs.49688 // ABLIM3 // 22885 // Homo sapiens actin binding LIM protein family, member 3 (ABLIM3), mRNA.	SH3TC2	SH3TC2, Homo sapiens KIAA1985 protein (KIAA1985), q32
SNP_A-2251251	cttcaaaggaaggagc[A/G]ctttataaagactca	A	G	NM_014945 // intron // 0 // Hs.49688 // ABLIM3 // 22885 // Homo sapiens actin binding LIM protein family, member 3 (ABLIM3), mRNA. /// ENST00000356541 // intron // 0 // — // — // — /// ENST00000309868 // intron // 0 // — // — // —	ABLIM3	ABLIM3, Homo sapiens actin binding LIM protein family, member 3 (ABLIM3), q32
SNP_A-2297691	gccagctccataagat[A/G]agtggagaaactgagg	A	G	NM_014443 // upstream // 43038 // Hs.409558 // IL17B // 27190 // Homo sapiens interleukin 17B (IL17B), mRNA. /// ENST00000261796 // upstream // 43038 // — // — // — /// ENST00000354543 // upstream // 597 // — // — // — // —	IL17B	IL17B, Homo sapiens interleukin 17B (IL17B), q32
SNP_A-2158496	attgtaatagtgaaac[A/G]ggaaacaaacagtgt	A	G	NM_001892 // upstream // 34240 // Hs.442592 // CSNK1A1 // 1452 // Homo sapiens casein kinase 1, alpha 1 (CSNK1A1), mRNA. /// NM_001001669 // upstream // 31204 // Hs.256206 // FLJ41603 // 389337 // Homo sapiens FLJ41603 protein (FLJ41603), mRNA. /// ENST00	CSNK1A1	CSNK1A1, Homo sapiens casein kinase 1, alpha 1 (CSNK1A1), q32
SNP_A-1824018	taaacaaagacggcaca[C/G]ggttacacttcagaag	C	G	NM_001001669 // downstream // 79919 // Hs.256206 // FLJ41603 // 389337 // Homo sapiens FLJ41603 protein (FLJ41603), mRNA. /// NM_133263 // upstream // 15418 // Hs.483816 // PPARGC1B // 133522 // Homo sapiens peroxisome proliferative activated receptor, ga	FLJ41603	FLJ41603, Homo sapiens FLJ41603 protein (FLJ41603), q32
SNP_A-2117295	aggtggatggccattc[G/T]aagctaagtaaacagc	G	T	NM_000112 // intron // 0 // Hs.302738 // SLC26A2 // 1836 // Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2), mRNA. /// ENST00000286298 // intron // 0 // — // — // — // —	SLC26A2	SLC26A2, Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2), q32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2136559	atcagcaacacaacag[C/T]ctaccccgtcattata	C	T	D83778 // intron // 0 // Hs.200776 // KIAA0194 // 22993 // Human mRNA for KIAA0194 gene, partial cds. /// ENST00000261804 // intron // 0 // — // — // — // —	KIAA0194	KIAA0194, Human for KIAA0194 gene, partial cds. ,q32
SNP_A-1953532	ttgaatcctaacatc[A/T]ccatgtactgtgtctc	A	T	D83778 // intron // 0 // Hs.200776 // KIAA0194 // 22993 // Human mRNA for KIAA0194 gene, partial cds. /// ENST00000261804 // intron // 0 // — // — // — // —	KIAA0194	KIAA0194, Human for KIAA0194 gene, partial cds. ,q32
SNP_A-2115507	aggggtcagctgctga[C/G]ggggagtaccatgcta	C	G	NM_005211 // intron // 0 // Hs.483829 // CSF1R // 1436 // Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRN /// ENST00000286301 // intron // 0 // — // — // — // —	CSF1R	CSF1R, Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRN ,q32
SNP_A-1789093	ggtcagaggtcaggaa[A/G]ctagtggcccacaca	A	G	NM_005211 // intron // 0 // Hs.483829 // CSF1R // 1436 // Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRN /// ENST00000286301 // intron // 0 // — // — // — // —	CSF1R	CSF1R, Homo sapiens colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog (CSF1R), mRN ,q32
SNP_A-1869031	tcctgcactcctggac[C/G]aacctcggctgcaga	C	G	AB028952 // upstream // 60903 // Hs.435228 // SYNPO // 11346 // Homo sapiens mRNA for KIAA1029 protein, partial cds. /// NM_007286 // upstream // 100514 // Hs.435228 // SYNPO // 11346 // Homo sapiens synaptopodin (SYNPO), mRNA. /// ENST00000261797 // down	SYNPO	SYNPO, Homo sapiens for KIAA1029 protein, partial cds. q33.1
SNP_A-2314432	ggagggcattctcaac[A/G]cacttgcaccaggttc	A	G	AB028952 // upstream // 50600 // Hs.435228 // SYNPO // 11346 // Homo sapiens mRNA for KIAA1029 protein, partial cds. /// NM_007286 // upstream // 90211 // Hs.435228 // SYNPO // 11346 // Homo sapiens synaptopodin (SYNPO), mRNA. /// ENST00000261797 // downs	SYNPO	SYNPO, Homo sapiens for KIAA1029 protein, partial cds. q33.1
SNP_A-2147562	atggatgcatggatga[A/G]attggatgatgtatgga	A	G	AB028952 // upstream // 13952 // Hs.435228 // SYNPO // 11346 // Homo sapiens mRNA for KIAA1029 protein, partial cds. /// NM_007286 // upstream // 53563 // Hs.435228 // SYNPO // 11346 // Homo sapiens synaptopodin (SYNPO), mRNA. /// ENST00000261797 // downs	SYNPO	SYNPO, Homo sapiens for KIAA1029 protein, partial cds. q33.1
SNP_A-1915205	tgttcaccaagcaata[A/G]cctggcactaatttag	A	G	NM_016221 // upstream // 1559 // Hs.328865 // DCTN4 // 51164 // Homo sapiens dynactin 4 (p62) (DCTN4), mRNA. /// ENST00000255263 // upstream // 1559 // — // — // — // — /// ENST00000324552 // upstream // 17368 // — // — // — // —	DCTN4	DCTN4, Homo sapiens dynactin 4 (p62) (DCTN4), q33.1
SNP_A-1832364	tacaaaaaggtatgcat[A/T]tcagaaataaaaatag	A	T	NM_052860 // upstream // 49156 // Hs.134885 // ZNF300 // 91975 // Homo sapiens zinc finger protein 300 (ZNF300), mRNA. /// NM_002084 // upstream // 66221 // Hs.386793 // GPX3 // 2878 // Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA. /// ENST	ZNF300	ZNF300, Homo sapiens zinc finger protein 300 (ZNF300), q33.1
SNP_A-2279874	gaggcgggatagcccg[A/G]cgaataaaagcatgga	A	G	NM_004033 // intron // 0 // Hs.412117 // ANXA6 // 309 // Homo sapiens annexin A6 (ANXA6), transcript variant 2, mRNA. /// NM_001155 // intron // 0 // Hs.412117 // ANXA6 // 309 // Homo sapiens annexin A6 (ANXA6), transcript variant 1, mRNA. /// ENST00000035	ANXA6	ANXA6, Homo sapiens annexin A6 (ANXA6), transcript variant 2, q33.1
SNP_A-1984006	tgaaattgctctgaca[C/T]atccagtccaagcata	C	T	NM_181774 // intron // 0 // Hs.132482 // SLC36A3 // 285641 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 3 (SLC36A3), mRNA. /// ENST00000335230 // intron // 0 // — // — // — // —	SLC36A3	SLC36A3, Homo sapiens solute carrier family 36 (proton,q33.1
SNP_A-2170752	caagtgtatttcccc[G/T]ctatggtgaacatctg	G	T	NM_181776 // upstream // 7399 // Hs.483877 // SLC36A2 // 153201 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 2 (SLC36A2), mRNA. /// NM_078483 // upstream // 92645 // Hs.269004 // SLC36A1 // 206358 // Homo sapiens solute c	SLC36A2	SLC36A2, Homo sapiens solute carrier family 36 (proton q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1896249	tgcgtcccatgggtaa[A/G]gactatcatcattatt	A	G	NM_181776 // upstream // 50679 // Hs.483877 // SLC36A2 // 153201 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 2 (SLC36A2), mRNA. /// NM_078483 // upstream // 49365 // Hs.269004 // SLC36A1 // 206358 // Homo sapiens solute	SLC36A2	SLC36A2, Homo sapiens solute carrier family 36 (proton,q33.1
SNP_A-2306037	gctggaagaggttcct[A/G]aggaaaggctcaggtg	A	G	NM_078483 // intron // 0 // Hs.269004 // SLC36A1 // 206358 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 1 (SLC36A1), mRNA. /// ENST00000243389 // intron // 0 // — // — // — // —	SLC36A1	SLC36A1, Homo sapiens solute carrier family 36 (proton,q33.1
SNP_A-2099040	agaggaagactcagaa[C/T]gctctcaagaaatca	C	T	NM_078483 // intron // 0 // Hs.269004 // SLC36A1 // 206358 // Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 1 (SLC36A1), mRNA. /// ENST00000243389 // intron // 0 // — // — // — // —	SLC36A1	SLC36A1, Homo sapiens solute carrier family 36 (proton,q33.1
SNP_A-1984015	tggcatccgtaacctc[A/G]atgtagacttcagtta	A	G	NM_001447 // CDS // 0 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// ENST00000261800 // CDS // 0 // — // — // — // —	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-1818200	gttctgaagcccaata[A/G]agtggaggatagtctt	A	G	NM_001447 // CDS // 0 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// ENST00000261800 // CDS // 0 // — // — // — // —	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-1882814	tgaaagcatcagggaagg[A/G]aagatgcagagtaaca	A	G	NM_001447 // upstream // 6095 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// NM_003118 // downstream // 86424 // Hs.111779 // SPARC // 6678 // Homo sapiens secreted protein, acidic, cysteine-rich	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-2257262	cttcttcataaccac[A/G]aactgtatttccagca	A	G	NM_001447 // upstream // 27079 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// NM_003118 // downstream // 65440 // Hs.111779 // SPARC // 6678 // Homo sapiens secreted protein, acidic, cysteine-rich	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-2154681	attcaaaagtgattggt[C/G]atttgcaagacagaga	C	G	NM_001447 // upstream // 27548 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// NM_003118 // downstream // 64971 // Hs.111779 // SPARC // 6678 // Homo sapiens secreted protein, acidic, cysteine-rich	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-2087625	actgctctgaactacc[A/G]ggggatttctgtgggt	A	G	NM_001447 // upstream // 32767 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// NM_003118 // downstream // 59752 // Hs.111779 // SPARC // 6678 // Homo sapiens secreted protein, acidic, cysteine-rich	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-1677408	gttagtgacctagaggaatgaaat[C/T]agaagagaagcagat caggtggaaa	C	T	NM_001447 // intron // 0 // Hs.132158 // FAT2 // 2196 // FAT tumor suppressor homolog 2 (Drosophila)	FAT2	FAT2 , rs3846714, FAT tumor suppressor homolog 2 (Drosophila),q33.1
SNP_A-1984018	ttgatcccacactccc[A/G]agagaattagtcacta	A	G	NM_001447 // upstream // 51665 // Hs.132158 // FAT2 // 2196 // Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA. /// NM_003118 // downstream // 40854 // Hs.111779 // SPARC // 6678 // Homo sapiens secreted protein, acidic, cysteine-rich	FAT2	FAT2, Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), q33.1
SNP_A-2244327	ctggaaggaaagatgc[A/G]agcagcatagtttgc	A	G	NM_000171 // upstream // 167157 // Hs.121490 // GLRA1 // 2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA. /// NM_020167 // downstream // 299550 // Hs.283093 // NMUR2 // 56923 // Homo sapiens	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease q33.1
SNP_A-1916789	tgtttcctgcaaggtc[A/G]atttcccaggtgaaag	A	G	NM_000171 // upstream // 169531 // Hs.121490 // GLRA1 // 2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA. /// NM_020167 // downstream // 297176 // Hs.283093 // NMUR2 // 56923 // Homo sapiens	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2278047	gagcccaaacttactg[C/T]atgaacaactcccaaa	C	T	NM_000171 // upstream // 346707 // Hs.121490 // GLRA1 // 2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA. /// NM_020167 // downstream // 120000 // Hs.283093 // NMUR2 // 56923 // Homo sapiens	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease,q33.1
SNP_A-2277171	gagatggtttctcac[C/T]cctctaagccttagct	C	T	NM_000171 // upstream // 358214 // Hs.121490 // GLRA1 // 2741 // Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA. /// NM_020167 // downstream // 108493 // Hs.283093 // NMUR2 // 56923 // Homo sapiens	GLRA1	GLRA1, Homo sapiens glycine receptor, alpha 1 (startle disease q33.1
SNP_A-2147102	atggaatacagtctga[A/G]ctagccttcatgaat	A	G	NM_020167 // upstream // 155792 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 929690 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-2011347	aatttggaatcagccc[C/G]aggactcctcctatcc	C	G	NM_020167 // upstream // 265736 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 819746 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-2146482	atgctctacttgata[C/T]ccataaaggcagctt	C	T	NM_020167 // upstream // 577882 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 507600 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-1984065	taatgcttaagtgaga[A/C]caacaatttcacttt	A	C	NM_020167 // upstream // 697982 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 387500 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-1793946	ggtcaatttgactaga[C/G]ataggattgattggat	C	G	NM_020167 // upstream // 750568 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 334914 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-2301441	gccttttaaacactg[C/T]attgatgattttgtcta	C	T	NM_020167 // upstream // 766039 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 319443 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-1698947	acagtagctgccctgaggatagta[A/G]caagctcagctgtagg ttctagcag	A	G	NM_000827 // upstream // 349860 // Hs.7117 // GRIA1 // 2890 // glutamate receptor, ionotropic, AMPA 1 /// NM_020167 // upstream // 735622 // Hs.283093 // NMU2R // 56923 // neuromedin U receptor 2	GRIA1	GRIA1, rs294700, glutamate receptor, ionotropic, AMPA 1, q33.2
SNP_A-2313741	ggagcacatctgattct[A/G]acatccctcctagcac	A	G	NM_020167 // upstream // 789141 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 296341 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.1
SNP_A-1878430	tctgtgactgagaca[A/G]aggtattcaaaataat	A	G	NM_020167 // upstream // 982818 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 102664 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2304728	gctctggagggaatac[A/G]gattgtctggtaaggt	A	G	NM_020167 // upstream // 1060422 // Hs.283093 // NMUR2 // 56923 // Homo sapiens neuromedin U receptor 2 (NMUR2), mRNA. /// NM_000827 // upstream // 25060 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /	NMUR2	NMUR2, Homo sapiens neuromedin U receptor 2 (NMUR2), q33.2
SNP_A-1984082	taaaccctggagatac[C/T]gcagaaaacaaaacca	C	T	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-1984099	ttggttcctgctcccg[A/G]aacttctgtcgccatc	A	G	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-1984100	gtaagacttggcttcc[C/T]caactagatactaaga	C	T	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2100470	agataagagaatgcaa[A/G]gtgttaaagaaatctc	A	G	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-1789168	gggcagtgaactcaga[C/T]gtactttatgtgtgtt	C	T	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-1876248	tctgagaatccattca[C/T]tcatttgcaaaattaa	C	T	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2158003	attgcttgctatgtgg[A/G]aaagaatgctcctagg	A	G	NM_000827 // intron // 0 // Hs.519693 // GRIA1 // 2890 // Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), mRNA. /// ENST00000285900 // intron // 0 // — // — // — // — /// ENST00000340592 // intron // 0 // — // — // — // —	GRIA1	GRIA1, Homo sapiens glutamate receptor, ionotropic, AMPA 1 (GRIA1), q33.2
SNP_A-2288596	gattgcctcggtccaa[C/G]tctcatttattaatta	C	G	NM_005927 // downstream // 20341 // Hs.432818 // MFAP3 // 4238 // Homo sapiens microfibrillar-associated protein 3 (MFAP3), mRNA. /// NM_198321 // upstream // 115362 // Hs.34421 // GALNT10 // 55568 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polype	MFAP3	MFAP3, Homo sapiens microfibrillar-associated protein 3 (MFAP3), q33.2
SNP_A-1699923	aatttacatttgatagttacatcat[C/T]ataaaacactcagaatac catgcaa	C	T	NM_005927 // intron // 0 // Hs.432818 // MFAP3 // 4238 // microfibrillar-associated protein 3	MFAP3	MFAP3 , rs816037, microfibrillar-associated protein 3,q33.2
SNP_A-1804433	gtcagaagcaaactaa[A/G]gctgctggagagaaga	A	G	NM_198321 // intron // 0 // Hs.34421 // GALNT10 // 55568 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10) (GALNT10), transcr /// NM_017540 // intron // 0 // Hs.34421 // GALNT10 // 55568 // Ho	GALNT10	GALNT10, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10) (GALNT10), transcr q33.2
SNP_A-1883552	tgaaccgttgttcaag[C/T]acaattaaggcaaaaa	C	T	NM_004821 // upstream // 93900 // Hs.152531 // HAND1 // 9421 // Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA. /// NM_015315 // upstream // 140738 // Hs.292078 // LARP // 23367 // Homo sapiens likely ortholog of mouse la relate	HAND1	HAND1, Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), q33.2
SNP_A-1984128	gagccaaacaagacag[C/G]atggcctaaaaatgac	C	G	NM_004821 // upstream // 128489 // Hs.152531 // HAND1 // 9421 // Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA. /// NM_015315 // upstream // 106149 // Hs.292078 // LARP // 23367 // Homo sapiens likely ortholog of mouse la relat	HAND1	HAND1, Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2066729	acaaaagaagctgaca[C/G]agtaactgaaaaaag	C	G	NM_004821 // upstream // 160605 // Hs.152531 // HAND1 // 9421 // Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA. /// NM_015315 // upstream // 74033 // Hs.292078 // LARP // 23367 // Homo sapiens likely ortholog of mouse la relate	HAND1	HAND1, Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), q33.2
SNP_A-1704929	gctatctctggctgagagaaccaca[A/G]acttcaagaatgtatga ggctacct	A	G	NM_004821 // upstream // 128220 // Hs.152531 // HAND1 // 9421 // heart and neural crest derivatives expressed 1 /// NM_015315 // upstream // 106418 // Hs.6214 // LARP // 23367 // likely ortholog of mouse la related protein	HAND1	HAND1, rs1824936, heart and neural crest derivatives expressed 1 ,q33.2
SNP_A-1717023	atgaaaagagagccaaacaagacag[C/G]atggcctaaaaat gacatgccctga	C	G	NM_004821 // upstream // 128489 // Hs.152531 // HAND1 // 9421 // heart and neural crest derivatives expressed 1 /// NM_015315 // upstream // 106149 // Hs.6214 // LARP // 23367 // likely ortholog of mouse la related protein	HAND1	HAND1, rs1824935, heart and neural crest derivatives expressed 1 ,q33.2
SNP_A-1896095	tgccttttcattacc[C/T]agacaatagtgcaaca	C	T	NM_015315 // intron // 0 // Hs.292078 // LARP // 23367 // Homo sapiens likely ortholog of mouse la related protein (LARP), mRNA. /// ENST00000336314 // intron // 0 // — // — // — // —	LARP	LARP, Homo sapiens likely ortholog of mouse la related protein (LARP), q33.2
SNP_A-2233712	ctcatattgcctcctta[C/T]ggtctcgttctttcaa	C	T	ENST00000330584 // CDS // 0 // — // — // — // —	-	q33.2
SNP_A-1984143	aaaacaccgtctagtc[C/T]ataggctggcaaagta	C	T	ENST00000330584 // downstream // 204433 // — // — // — // — /// ENST00000361117 // upstream // 1062293 // — // — // — // —	-	q33.2
SNP_A-1906570	tggtggtggtgttatc[C/T]acagccttatcccac	C	T	ENST00000330584 // downstream // 221186 // — // — // — // — /// ENST00000361117 // upstream // 1045540 // — // — // — // —	-	q33.2
SNP_A-1851052	tattattattgactccc[A/G]caatgaaaacaatctt	A	G	ENST00000330584 // downstream // 234993 // — // — // — // — /// ENST00000361117 // upstream // 1031733 // — // — // — // —	-	q33.2
SNP_A-2296243	gcattgatgctacaaa[C/G]agctaaatcccacagg	C	G	ENST00000330584 // downstream // 370747 // — // — // — // — /// ENST00000361117 // upstream // 895979 // — // — // — // —	-	q33.2
SNP_A-2308153	gcttgcattctgtgca[C/T]ctgcaagcttaccacc	C	T	ENST00000330584 // downstream // 432076 // — // — // — // — /// ENST00000361117 // upstream // 834650 // — // — // — // —	-	q33.2
SNP_A-2246068	ctggtcaatttcacta[C/T]aaaaactactctaaaa	C	T	ENST00000330584 // downstream // 456805 // — // — // — // — /// ENST00000361117 // upstream // 809921 // — // — // — // —	-	q33.2
SNP_A-2268503	gaatggcttcgtgaaa[C/T]tgacigttacagctat	C	T	ENST00000330584 // downstream // 459046 // — // — // — // — /// ENST00000361117 // upstream // 807680 // — // — // — // —	-	q33.2
SNP_A-1781477	ggattagttgttcaca[C/T]gttcctgactggtaga	C	T	ENST00000330584 // downstream // 470470 // — // — // — // — /// ENST00000361117 // upstream // 796256 // — // — // — // —	-	q33.2
SNP_A-2041275	aacctgaacatgggct[C/T]aacatttttcttgaca	C	T	ENST00000330584 // downstream // 545667 // — // — // — // — /// ENST00000361117 // upstream // 721059 // — // — // — // —	-	q33.2
SNP_A-1984157	gtcaataatgtcacaa[A/G]aaggtaaggcctggtg	A	G	ENST00000330584 // downstream // 575812 // — // — // — // — /// ENST00000361117 // upstream // 690914 // — // — // — // —	-	q33.2
SNP_A-1871673	tctatagcttatgat[C/G]taggaatggacttgac	C	G	ENST00000330584 // downstream // 581174 // — // — // — // — /// ENST00000361117 // upstream // 685552 // — // — // — // —	-	q33.2
SNP_A-2091465	agaaaaaacaactgac[A/C]aatagacccacacatt	A	C	ENST00000330584 // downstream // 613094 // — // — // — // — /// ENST00000361117 // upstream // 653632 // — // — // — // —	-	q33.2
SNP_A-2128514	ataatatttagacaa[C/T]gtagtactggcatata	C	T	ENST00000330584 // downstream // 613144 // — // — // — // — /// ENST00000361117 // upstream // 653582 // — // — // — // —	-	q33.2
SNP_A-1687874	ttttacataaagctggcttcacagaa[C/T]agtatctcatttgcttctca gaaca	C	T	NM_000337 // upstream // 603899 // Hs.131380 // SGCD // 6444 // sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) /// NM_014180 // downstream // 755912 // Hs.41007 // MRPL22 // 29093 // mitochondrial ribosomal protein L22 /// NM_172244 // ups	SGCD	SGCD, rs3922737, sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) ,q33.2
SNP_A-1683330	ttacttcacctatcaaaatgaaag[A/T]ctattaagcatgccctgc cctacct	A	T	NM_000337 // upstream // 603840 // Hs.131380 // SGCD // 6444 // sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) /// NM_014180 // downstream // 755971 // Hs.41007 // MRPL22 // 29093 // mitochondrial ribosomal protein L22 /// NM_172244 // ups	SGCD	SGCD, rs3922736, sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) ,q33.2
SNP_A-2209351	cccagtttctctccca[A/G]tgatataacacagagg	A	G	ENST00000330584 // downstream // 860297 // — // — // — // — /// ENST00000361117 // upstream // 406428 // — // — // — // —	-	q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813070	gtggattgactcaga[C/T]cctgccctgctttagg	C	T	ENST00000330584 // downstream // 1136288 // --- // --- // --- /// ENST00000361117 // upstream // 130438 // --- // --- // ---	-	q33.2
SNP_A-1884458	tgaagtgaggattcca[A/G]attagagcagtggtta	A	G	ENST00000330584 // downstream // 1136390 // --- // --- // --- /// ENST00000361117 // upstream // 130336 // --- // --- // ---	-	q33.2
SNP_A-2044712	aagaaaggccattgaa[A/C]ctaaactatattaag	A	C	NM_172244 // downstream // 74937 // Hs.387207 // SGCD // 6444 // Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, mRNA. /// NM_000337 // downstream // 74937 // Hs.387207 // SGCD // 6444 // Homo sapie	SGCD	SGCD, Homo sapiens sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 2, q33.3
SNP_A-2226518	ctaagctaaggaaata[A/C]actgaaatcaaacata	A	C	NM_138379 // downstream // 38729 // Hs.334907 // TIMD4 // 91937 // Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), mRNA. /// ENST00000357900 // downstream // 28103 // --- // --- // --- /// ENST00000274532 // downstream //	TIMD4	TIMD4, Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), q33.3
SNP_A-2237497	ctctccttttatgccc[A/G]gcttcagagttcatt	A	G	NM_138379 // downstream // 636 // Hs.334907 // TIMD4 // 91937 // Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), mRNA. /// ENST00000357900 // downstream // 66196 // --- // --- // --- /// ENST00000274532 // downstream // 63	TIMD4	TIMD4, Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), q33.3
SNP_A-2076013	acattatcaagagcta[C/T]ataaaagttggtgtca	C	T	NM_138379 // intron // 0 // Hs.334907 // TIMD4 // 91937 // Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), mRNA. /// ENST00000274532 // intron // 0 // --- // --- // ---	TIMD4	TIMD4, Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), q33.3
SNP_A-1984200	acaataaagtgtgtaa[A/G]agctcaggttcaagca	A	G	NM_138379 // intron // 0 // Hs.334907 // TIMD4 // 91937 // Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), mRNA. /// ENST00000274532 // intron // 0 // --- // --- // ---	TIMD4	TIMD4, Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), q33.3
SNP_A-2041368	aacctggcttctgac[A/G]agacagatttatga	A	G	NM_004270 // upstream // 8541 // Hs.279902 // CRSP9 // 9443 // Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa (CRSP9), mRNA. /// NM_130899 // downstream // 10935 // Hs.125487 // MGC26988 // 153745 // Homo sapiens hypot	CRSP9	CRSP9, Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa (CRSP9), q33.3
SNP_A-2164339	caaaatccgcttcaca[A/G]agaacacaacttacaa	A	G	NM_004270 // upstream // 15379 // Hs.279902 // CRSP9 // 9443 // Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa (CRSP9), mRNA. /// NM_130899 // downstream // 4097 // Hs.125487 // MGC26988 // 153745 // Homo sapiens hypot	CRSP9	CRSP9, Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa (CRSP9), q33.3
SNP_A-2125528	agtttcaaaaacatca[C/T]agtgtcaacttagatg	C	T	NM_005546 // intron // 0 // Hs.483938 // ITK // 3702 // Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA. /// ENST00000231189 // intron // 0 // --- // --- // ---	ITK	ITK, Homo sapiens IL2-inducible T-cell kinase (ITK), q33.3
SNP_A-1921139	ttacataatggtaaacf[A/G]gttcaatttaataaga	A	G	ENST00000318218 // downstream // 13918 // --- // --- // --- /// ENST00000311946 // upstream // 50707 // --- // --- // ---	-	q33.3
SNP_A-1822879	taaaaagctgtctacg[C/T]agttatggagaaggga	C	T	NM_023038 // intron // 0 // Hs.483944 // ADAM19 // 8728 // Homo sapiens a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19), transcript variant 1, mRNA. /// NM_033274 // intron // 0 // Hs.483944 // ADAM19 // 8728 // Homo sapiens a disint	ADAM19	ADAM19, Homo sapiens a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19), transcript variant 1, q33.3
SNP_A-2086704	actgtgctgaaatccf[A/G]gcttcaggaccaaccg	A	G	NM_014666 // upstream // 16816 // Hs.132853 // ENTH // 9685 // Homo sapiens enthoprotin (ENTH), mRNA. /// ENST00000296951 // upstream // 16816 // --- // --- // --- /// ENST00000338871 // downstream // 110442 // --- // --- // ---	ENTH	ENTH, Homo sapiens enthoprotin (ENTH), q33.3
SNP_A-1984224	tcaatcaatacgaaccf[A/G]ccaaaccagatcactg	A	G	NM_024007 // downstream // 635661 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 75033 // --- // --- // --- /// ENST00000313708 // downstream // 635661 // --- // --- // --- ///	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2231859	ctcaaagtttcccca[G/T]tcaaaagcatttgaaa	G	T	NM_024007 // downstream // 537067 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 173627 // --- // --- // --- /// ENST00000313708 // downstream // 537067 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1817562	gttcattttcatgca[A/C]taltagccaatgtcac	A	C	NM_024007 // downstream // 520021 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 190673 // --- // --- // --- /// ENST00000313708 // downstream // 520021 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984229	gatggcccactagaaac[C/T]gaaaaggacaagaaaa	C	T	NM_024007 // downstream // 505406 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 205288 // --- // --- // --- /// ENST00000313708 // downstream // 505406 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984230	actatgaagtctctgt[A/C]agccatttaatgcaa	A	C	NM_024007 // downstream // 479149 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 231545 // --- // --- // --- /// ENST00000313708 // downstream // 479149 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2135084	atattctctctaccc[A/G]cgaaaggaaaaagact	A	G	NM_024007 // downstream // 397781 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 312913 // --- // --- // --- /// ENST00000313708 // downstream // 397781 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1795125	ggtgactcctttagtg[A/G]aagaacacatctttc	A	G	NM_024007 // downstream // 197233 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 513461 // --- // --- // --- /// ENST00000313708 // downstream // 197233 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984239	ttttctttgtagaaaa[C/T]ctaatggtcactggaa	C	T	NM_024007 // downstream // 193431 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 517263 // --- // --- // --- /// ENST00000313708 // downstream // 193431 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984240	cggtcacactataatc[C/G]ccacgagacagcagga	C	G	NM_024007 // downstream // 192750 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 517944 // --- // --- // --- /// ENST00000313708 // downstream // 192750 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2034373	aaatctaaggtgttat[C/G]aagctataagatataa	C	G	NM_024007 // downstream // 186559 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 524135 // --- // --- // --- /// ENST00000313708 // downstream // 186559 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2220617	cctctttatatcaa[G/T]gaccaggatgatacc	G	T	NM_024007 // downstream // 182733 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 527961 // --- // --- // --- /// ENST00000313708 // downstream // 182733 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984241	aatgaatggtagccad[A/G]atatttgtcctttatt	A	G	NM_024007 // downstream // 180249 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 530445 // --- // --- // --- /// ENST00000313708 // downstream // 180249 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2290830	gcaaggaaggcaaatg[C/T]acaattagtatcaggg	C	T	NM_024007 // downstream // 132765 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000338871 // upstream // 577929 // --- // --- // --- /// ENST00000313708 // downstream // 132765 // --- // --- // --- //	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1807464	gtctgcagctagcta[A/T]ggagaaatgatgactaa	A	T	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984249	aggctcatgcctggtg[A/T]caataaaggcgaatag	A	T	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2242010	ctgattcctgaaatg[A/C]agttggtggtgatggg	A	C	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2241486	ctgagtggctgccaca[A/G]ggctatgttcagcgct	A	G	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2283740	gataggaaagtaatgg[C/T]caacaactcagtaatt	C	T	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2011384	gataaatgattcacccc[C/T]gacaaaaagtcacctc	C	T	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-1984259	atccagcttcttcaca[A/G]tagtaaaaaaggaggt	A	G	NM_024007 // intron // 0 // Hs.308048 // EBF // 1879 // Homo sapiens early B-cell factor (EBF), mRNA. /// ENST00000313708 // intron // 0 // --- // --- // --- /// ENST00000336546 // intron // 0 // --- // --- // --- // ---	EBF	EBF, Homo sapiens early B-cell factor (EBF), q33.3
SNP_A-2259676	gaaaacttgagagac[A/G]atgaatactaactatg	A	G	NM_144726 // intron // 0 // Hs.349306 // FLJ31951 // 153830 // Homo sapiens hypothetical protein FLJ31951 (FLJ31951), mRNA. /// ENST00000274542 // intron // 0 // --- // --- // ---	FLJ31951	FLJ31951, Homo sapiens hypothetical protein FLJ31951 (FLJ31951), q33.3
SNP_A-1730807	cctgttaaaatctgatttctataca[A/G]atttgatgttaataatctggct cat	A	G	NM_144726 // intron // 0 // Hs.349306 // FLJ31951 // 153830 // hypothetical protein FLJ31951	FLJ31951	FLJ31951, rs10515776, hypothetical protein FLJ31951,q33.3
SNP_A-1785868	ggctgactgagactga[C/T]gtttggtgtctgaagt	C	T	NM_002187 // upstream // 271643 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 314616 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-2100510	agataataagcagtca[A/G]taaatgacagaaatta	A	G	NM_002187 // upstream // 274955 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 311304 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1820518	gttatatagaaaga[C/T]aggctgtgtcatggca	C	T	NM_002187 // upstream // 275034 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 311225 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181719	cagagaggagaccgtg[A/G]agtaggtagctgtttt	A	G	NM_002187 // upstream // 310764 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 275495 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1859915	tcaggtccaattgcaa[A/C]tccaagttagctaaat	A	C	NM_002187 // upstream // 315697 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 270562 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-2073711	acagtcgggtagaaca[C/G]caagcatgctcttaga	C	G	NM_002187 // upstream // 346743 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 239516 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-2173580	cacaattcaaaacaca[A/G]tgatgctcttccaaca	A	G	NM_002187 // upstream // 350418 // Hs.674 // IL12B // 3593 // Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), /// NM_000679 // upstream // 235841 // Hs.368632 // ADRA1B // 147	IL12B	IL12B, Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B), q33.3
SNP_A-1678364	tagcccctatagtccgctgggagca[C/T]tgaactcctgacctca ggtgatcca	C	T	NM_000679 // upstream // 20817 // Hs.416813 // ADRA1B // 147 // adrenergic, alpha-1B-, receptor /// NM_002187 // upstream // 565442 // Hs.674 // IL12B // 3593 // interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation f	ADRA1B	ADRA1B . rs2195926, adrenergic, alpha-1B-, receptor ,q33.3
SNP_A-2083240	actaaacagtgatacc[C/T]gagaaatagaaacaaa	C	T	NM_006607 // downstream // 21143 // Hs.511755 // PTTG2 // 10744 // Homo sapiens pituitary tumor-transforming 2 (PTTG2), mRNA. /// NM_004219 // downstream // 21143 // Hs.350966 // PTTG1 // 9232 // Homo sapiens pituitary tumor-transforming 1 (PTTG1), mRNA.	PTTG2	PTTG2, Homo sapiens pituitary tumor-transforming 2 (PTTG2), q33.3
SNP_A-2203940	ccagatcagtactcgc[A/G]ctcccactgtgtcact	A	G	NM_006607 // downstream // 85680 // Hs.511755 // PTTG2 // 10744 // Homo sapiens pituitary tumor-transforming 2 (PTTG2), mRNA. /// NM_004219 // downstream // 85680 // Hs.350966 // PTTG1 // 9232 // Homo sapiens pituitary tumor-transforming 1 (PTTG1), mRNA.	PTTG2	PTTG2, Homo sapiens pituitary tumor-transforming 2 (PTTG2), q33.3
SNP_A-2238698	ctctgtttctgaaaca[G/T]tagcctcaaggatgcc	G	T	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// ENST00000327245 // intron // 0 // --- // --- // --- // ---	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. ,q34
SNP_A-2022602	aaaaatgagtacttta[A/C]attcctctagctgttt	A	C	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// ENST00000327245 // intron // 0 // — // — // — // —	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. ,q34
SNP_A-1878518	tctgtggaagagtaga[C/T]gtgtcatgcccagtgc	C	T	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// ENST00000327245 // intron // 0 // — // — // — // — /// ENST00000326831 // intron // 0 // — // — // — // — /// ENST000003564	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. q34
SNP_A-1780369	ggataatgcctttggg[A/G]atgtggggtatcagtt	A	G	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// ENST00000327245 // intron // 0 // — // — // — // — /// ENST00000326831 // intron // 0 // — // — // — // — /// ENST000003564	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. ,q34
SNP_A-1872670	tctagtctgactccca[A/G]atttcacaaaagtgga	A	G	AB018258 // intron // 0 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// ENST00000327245 // intron // 0 // — // — // — // — /// ENST00000326831 // intron // 0 // — // — // — // — /// ENST000003564	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. ,q34
SNP_A-1857219	tcacctgtggccggaa[C/T]ctcaaaggagagtgat	C	T	ENST00000356494 // intron // 0 // — // — // — // —	-	q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1727891	cctgttagcggagtccctttaagga[A/G]gttagaccagtgacctttgctgtgc	A	G	NM_000813 // downstream // 576931 // Hs.103998 // GABRB2 // 2561 // gamma-aminobutyric acid (GABA) A receptor, beta 2 /// NM_021911 // downstream // 576931 // Hs.103998 // GABRB2 // 2561 // gamma-aminobutyric acid (GABA) A receptor, beta 2 /// NM_025153	GABRB2	GABRB2 , rs10515815, gamma-aminobutyric acid (GABA) A receptor, beta 2 ,q34
SNP_A-1813420	gtggttatgggtcctg[A/T]atttaatgaggtctag	A	T	AB018258 // upstream // 268271 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 337519 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (G	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. q34
SNP_A-1862585	tcattagatgtgaaga[C/T]gtagtgtgctatgcca	C	T	AB018258 // upstream // 422035 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 183755 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (G	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. q34
SNP_A-2212042	ccctgatttctttaac[C/T]gtcaaatgtggttaaa	C	T	AB018258 // upstream // 422751 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 183039 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (G	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. q34
SNP_A-1788106	gggagatacaacctaa[A/G]agacaaaataacattt	A	G	AB018258 // upstream // 423480 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 182310 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (G	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. q34
SNP_A-2149231	atgtaagccacaaaaa[A/G]gaaaccatttaattca	A	G	AB018258 // upstream // 442915 // Hs.109358 // ATP10B // 23120 // Homo sapiens mRNA for KIAA0715 protein, partial cds. /// NM_021911 // downstream // 162875 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (G	ATP10B	ATP10B, Homo sapiens for KIAA0715 protein, partial cds. ,q34
SNP_A-1984332	gatatcaagttttata[A/G]cacaagcaagactgaa	A	G	NM_021911 // upstream // 76816 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2), transcript variant 1, mRNA. /// NM_000813 // upstream // 78297 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-ami	GABRB2	GABRB2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2), transcript variant 1, q34
SNP_A-1855502	tcaagtgtgactgtta[C/T]ggctgtgctagatgtc	C	T	NM_021911 // upstream // 136458 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2), transcript variant 1, mRNA. /// NM_000813 // upstream // 137939 // Hs.87083 // GABRB2 // 2561 // Homo sapiens gamma-a	GABRB2	GABRB2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2), transcript variant 1, q34
SNP_A-2188989	cagtgtggaggacata[A/T]gaaaaggcatgagact	A	T	NM_198904 // downstream // 97430 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 1184603 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2011406	gtctttgttttactga[A/C]gttcttaggggtctca	A	C	NM_198904 // downstream // 287003 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 995030 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2011409	caggcaaagacaatat[A/G]agaaaatgttgtgtgt	A	G	NM_198904 // downstream // 618491 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 663542 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2228529	ctacttgtcagcctg[A/G]attatggaacaaagac	A	G	NM_198904 // downstream // 623371 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 658662 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1642339	tcttaaggttatcatgacctaggaa[A/G]ttaggaacagggaatga acaatgtt	A	G	NM_000816 // downstream // 614530 // Hs.7195 // GABRG2 // 2566 // gamma-aminobutyric acid (GABA) A receptor, gamma 2 /// NM_004060 // upstream // 669605 // Hs.79101 // CCNG1 // 900 // cyclin G1 /// NM_145266 // downstream // 685568 // Hs.140443 // LOC134	GABRG2	GABRG2, rs4921469, gamma-aminobutyric acid (GABA) A receptor, gamma 2, q34
SNP_A-2245073	ctggccactcctcagat[C/T]gtagaaaggggtacaa	C	T	NM_198904 // downstream // 831277 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 450756 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2049824	aaggaaacgttattcca[C/T]ctcctgcaatatctta	C	T	NM_198904 // downstream // 1117122 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 164911 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-2044109	aacttggtgattagca[C/T]gagtgtaggctacggt	C	T	NM_198904 // downstream // 1119715 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 162318 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1850317	tatgttctccaacaca[A/G]agtatcattagaagat	A	G	NM_198904 // downstream // 1149477 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 132556 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1813644	gtgtaatttgaagcaa[A/C]cttrcaaattgcattg	A	C	NM_198904 // downstream // 1247939 // Hs.7195 // GABRG2 // 2566 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, mRNA. /// NM_004060 // upstream // 34094 // Hs.79101 // CCNG1 // 900 // Homo sapiens cyclin	GABRG2	GABRG2, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2), transcript variant 1, q34
SNP_A-1828542	taagcatcagcttat[C/T]ggtattaaaaatggaa	C	T	NM_182796 // downstream // 20481 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 20481 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adeno	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1655967	tcctctttttatctaccactgaaaa[G/T]actatctgattataatttgat gcct	G	T	BC011998 // upstream // 805210 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds /// NM_013283 // downstream // 29610 // Hs.54642 // MAT2B // 27430 // methionine adenosyltransferase II, beta	-	-, rs10491405, CDNA clone IMAGE:6103129, partial cds, q34
SNP_A-1803934	gtcaatagaggtcaat[A/G]aaggtcgtaatcgttt	A	G	NM_182796 // downstream // 137043 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 137043 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2029282	aaagaataaactaaa[C/T]ggtcttccacgaaaga	C	T	NM_182796 // downstream // 137282 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 137282 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1837382	tacttccatgtgttta[C/T]acaagcaacaacagcc	C	T	NM_182796 // downstream // 224733 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 224733 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2226380	ctaagagaaaatgaca[A/G]actttacatgacagt	A	G	NM_182796 // downstream // 224765 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 224765 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1668676	tctgaactagaaaagatggccaggca[C/G]aagccaatactgaat taatttccct	C	G	BC011998 // upstream // 655452 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds /// NM_013283 // downstream // 179368 // Hs.54642 // MAT2B // 27430 // methionine adenosyltransferase II, beta	-	-, rs641436, CDNA clone IMAGE:6103129, partial cds ,q34
SNP_A-1671796	aatgaatgtgtgaatagaaaatagaa[A/C]atcgaaaagcaatttc atatactca	A	C	BC011998 // upstream // 637161 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds /// NM_013283 // downstream // 197659 // Hs.54642 // MAT2B // 27430 // methionine adenosyltransferase II, beta	-	-, rs6890173, CDNA clone IMAGE:6103129, partial cds ,q34
SNP_A-1933817	ttctatggctaaaag[G/T]acttcctagaatgaca	G	T	NM_182796 // downstream // 346667 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 346667 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2207379	ccattgatctttagca[C/T]ctttgctaaaattaa	C	T	NM_182796 // downstream // 404957 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 404957 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2284688	gatcagtcaagactta[A/G]gtgtatgcttactgat	A	G	NM_182796 // downstream // 641159 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 641159 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1984400	atattgagctctaaaa[A/T]gtgggagcaaagcta	A	T	NM_182796 // downstream // 670036 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 670036 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2032723	aaataacagtataagc[A/G]attcccaggcttaatc	A	G	NM_182796 // downstream // 683774 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 683774 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1984403	gtgttcccatgactg[C/T]aaccctgctttccaaa	C	T	NM_182796 // downstream // 865252 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 865252 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2126493	ataaaataaatgtcaa[G/T]caaagtggtgtaaggg	G	T	NM_182796 // downstream // 874016 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 874016 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2096501	agacctcaatttagga[A/G]aacatccggcgtgctt	A	G	NM_182796 // downstream // 874206 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 874206 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2066053	aatttggaaaaactac[A/C]atctactcactttcc	A	C	NM_182796 // downstream // 945182 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 945182 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine ade	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1811987	gtggaagttgacaccc[A/G]ggatattctccttct	A	G	NM_182796 // downstream // 2063090 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2063090 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1945816	ttgttgtttccacaga[C/T]taaaaatagaaaccga	C	T	NM_182796 // downstream // 2100392 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2100392 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1707764	tatgtggcagatagattttgtcccg[A/T]ccaacattctctctctcct tatct	A	T	AB032953 // upstream // 2496048 // Hs.173560 // ODZ2 // 57451 // odd Oz/ten-m homolog 2 /// BC011998 // downstream // 1019905 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds	ODZ2	ODZ2 , rs262750, odd Oz,q34
SNP_A-2099721	agaggttcagggtgga[A/C]aataaatgtggaaga	A	C	NM_182796 // downstream // 2355605 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2355605 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1647242	taacaacgtcacctgggtatctcta[C/T]gcacagcgaagtttcgg aggcactc	C	T	AB032953 // upstream // 2173082 // Hs.173560 // ODZ2 // 57451 // odd Oz/ten-m homolog 2 /// BC011998 // downstream // 1342871 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds	ODZ2	ODZ2 , rs1975525, odd Oz,q34
SNP_A-1917450	tgttttgtctagaagg[C/T]cacagaatgctgagat	C	T	NM_182796 // downstream // 2567836 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2567836 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1942595	ttgggaagagccaggg[C/T]ggaataacatagttgg	C	T	NM_182796 // downstream // 2573465 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2573465 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2231640	ctattttatggtcgca[A/G]aatataccaggacaca	A	G	NM_182796 // downstream // 2824672 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2824672 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1815084	gtgttccacattcata[C/G]gtggtgttcagaaaac	C	G	NM_182796 // downstream // 2826877 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2826877 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2178473	cactcctatgcaaaag[C/T]cactgtgaaaacactg	G	T	NM_182796 // downstream // 2827998 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2827998 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2195820	catgtaggaacaggaa[A/T]cctttctagagtatgg	A	T	NM_182796 // downstream // 2837741 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2837741 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2163205	attttctaaatgtc[A/C]ataagtggtgttaat	A	C	NM_182796 // downstream // 2948068 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 2948068 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2047561	aagatggcttcataa[C/T]gcccaaagtttaatg	C	T	NM_182796 // downstream // 3179304 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3179304 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1714178	tcagaaaagattaaagccttgggaa[A/T]gacttgcatgtggac ataaaaggg	A	T	AB032953 // upstream // 1391634 // Hs.173560 // ODZ2 // 57451 // odd Oz/ten-m homolog 2 /// BC011998 // downstream // 2124319 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds	ODZ2	ODZ2 , rs10516023, odd Oz,q34
SNP_A-1984458	gaattgttagaagaac[A/G]gaatggcaaaataatt	A	G	NM_182796 // downstream // 3287603 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3287603 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1984464	aaaacgaccagagcta[A/C]aaagtgacagcagaat	A	C	NM_182796 // downstream // 3546654 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3546654 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2133571	atatcacacagcttta[A/G]cactaattaatatcct	A	G	NM_182796 // downstream // 3552069 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3552069 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2011427	gaacataaactcggag[A/G]aaaaaatgggaggaaa	A	G	NM_182796 // downstream // 3578720 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3578720 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1698853	aattgcagggatgtgctgaacagcc[A/G]cagaaataactaaag taaaagtggc	A	G	AB032953 // upstream // 1056346 // Hs.173560 // ODZ2 // 57451 // odd Oz/ten-m homolog 2 /// BC011998 // downstream // 2459607 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds	ODZ2	ODZ2 , rs1432949, odd Oz,q34
SNP_A-1841022	tagctggttataaata[A/G]tacttctgcctctgta	A	G	NM_182796 // downstream // 3596315 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3596315 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101589	agatgagctttaatcg[A/G]aggaccaaatctgtgt	A	G	NM_182796 // downstream // 3967534 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3967534 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2039086	aacaggtcaaaagtca[C/T]caagcgaatgaacaaa	C	T	NM_182796 // downstream // 3972552 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 3972552 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2204971	ccagggtaaatggata[A/T]attgtcatagatgacc	A	T	NM_182796 // downstream // 4019404 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4019404 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1679270	gttatatatagtgaggacactgtta[C/G]aataaggtgagtgcattg ttacagt	C	G	AB032953 // upstream // 534328 // Hs.173560 // ODZ2 // 57451 // odd Oz/ten-m homolog 2 /// BC011998 // downstream // 2981625 // Hs.209560 // - // - // CDNA clone IMAGE:6103129, partial cds	ODZ2	ODZ2 , rs6881950, odd Oz,q34
SNP_A-1883226	tgaaattagagagtta[A/G]gggcttgagttaaggg	A	G	NM_182796 // downstream // 4207016 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4207016 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1886807	tgactggaaatggtag[C/T]agtgtcaagatgacta	C	T	NM_182796 // downstream // 4343629 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4343629 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1799166	gtaagtcacttgtgtc[A/T]acattaaattgtcacc	A	T	NM_182796 // downstream // 4367955 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4367955 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2089409	acttatctcatggata[A/G]aacagaggatagacta	A	G	NM_182796 // downstream // 4390521 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4390521 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-2123598	agtgtgtctttggacc[C/T]cttccaggctgtttcc	C	T	NM_182796 // downstream // 4501442 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, mRNA. /// NM_013283 // downstream // 4501442 // Hs.54642 // MAT2B // 27430 // Homo sapiens methionine a	MAT2B	MAT2B, Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant 2, q34
SNP_A-1788750	gggattaaatcaatca[C/T]actggatattgctaat	C	T	ENST00000314238 // intron // 0 // — // — // — // —	-	q34
SNP_A-2162686	attttcttggagtctc[A/G]aagatgtagattatgt	A	G	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2251037	cttattagctacgcaa[C/T]cttgggcaagttttca	C	T	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2150645	atgtgattcttcacaa[C/T]gcgcagaactctctga	C	T	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2229273	ctaggaatctttgtaa[C/T]ggattgggatactgg	C	T	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2098515	agagcagcccaggtca[C/T]gagttgtgaggcac	C	T	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-1789640	gggctacaattcatca[A/G]gatgcactggaacgtg	A	G	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-2170306	caagtaatataaaggt[A/G]acaacatttctacca	A	G	NM_015238 // intron // 0 // Hs.484047 // KIBRA // 23286 // Homo sapiens KIBRA protein (KIBRA), mRNA. /// ENST00000265293 // intron // 0 // — // — // — // —	KIBRA	KIBRA, Homo sapiens KIBRA protein (KIBRA), q34
SNP_A-1884219	tgaaggagccccaaac[A/G]aaagactggcagtttc	A	G	NM_024594 // downstream // 17895 // Hs.388400 // PANK3 // 79646 // Homo sapiens pantothenate kinase 3 (PANK3), mRNA. /// ENST00000338333 // downstream // 7248 // — // — // — /// ENST00000239231 // downstream // 17895 // — // — // -	PANK3	PANK3, Homo sapiens pantothenate kinase 3 (PANK3), q34
SNP_A-2180368	cagaaattcaggaagg[G/T]ccctctaagatatga	G	T	NM_003062 // downstream // 15391 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000310599 // downstream // 29354 // — // — // — /// ENST00000332966 // downstream // 15391 // — // — // -	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2290798	gcaagctcagaggaca[C/T]aggcttacaccagcac	C	T	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-1751137	tatgaacatcttccctttcttata[A/G]catctacctcagtttcttttatta aa	A	G	NM_003062 // intron // 0 // Hs.484063 // SLIT3 // 6586 // slit homolog 3 (Drosophila)	SLIT3	SLIT3, rs10516048, slit homolog 3 (Drosophila), q34
SNP_A-2245434	ctgggacaaatgatgc[C/T]gaggaaagagaaaacc	C	T	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2242475	ctgcagatcaaaaaaq[C/T]ggctctgcagatctgc	C	T	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2025435	aaaatccaagagtcac[C/T]gatgtccatgatttct	C	T	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-1788216	gggagctgaattctcc[A/G]gcgacagttgttgggg	A	G	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2220348	ccttcctctcaaataa[C/T]gtggagaggctctctc	C	T	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2085599	actcccaatcccgaaa[C/T]agacttcataactgca	C	T	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q34
SNP_A-2184726	cagctgaagtacgtgg[A/C]aatcccagggctcgac	A	C	NM_003062 // intron // 0 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// ENST00000332966 // intron // 0 // — // — // — // — /// ENST00000355963 // intron // 0 // — // — // — // —	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2176174	caccacgaatgaaaga[C/T]acttaaccgcattt	C	T	NM_003062 // upstream // 88788 // Hs.112631 // SLIT3 // 6586 // Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA. /// NM_017785 // upstream // 194276 // Hs.368710 // FLJ20364 // 54908 // Homo sapiens hypothetical protein FLJ20364 (FLJ20364), mRNA. /	SLIT3	SLIT3, Homo sapiens slit homolog 3 (Drosophila) (SLIT3), q35.1
SNP_A-2275247	gagaacggtgtagaaa[C/G]aaataatcaccttt	C	G	NM_004946 // intron // 0 // Hs.325528 // DOCK2 // 1794 // Homo sapiens dedicator of cytokinesis 2 (DOCK2), mRNA. /// ENST00000256935 // intron // 0 // — // — // — // —	DOCK2	DOCK2, Homo sapiens dedicator of cytokinesis 2 (DOCK2), q35.1
SNP_A-2314711	ggagtccacgtgggca[A/G]gaagctaagcagcagt	A	G	NM_004946 // intron // 0 // Hs.325528 // DOCK2 // 1794 // Homo sapiens dedicator of cytokinesis 2 (DOCK2), mRNA. /// ENST00000256935 // intron // 0 // — // — // — // —	DOCK2	DOCK2, Homo sapiens dedicator of cytokinesis 2 (DOCK2), q35.1
SNP_A-1706573	ttcttgctctgcaacttagaagata[C/T]gtaigttggtcaagtaact aaacct	C	T	NM_004946 // intron // 0 // Hs.17211 // DOCK2 // 1794 // dedicator of cytokinesis 2	DOCK2	DOCK2 , rs261004, dedicator of cytokinesis 2, q35.1
SNP_A-2291541	gcacaaaaittcaatga[C/T]gggcacaagcagaaag	C	T	NM_144769 // downstream // 1727 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 1727 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-1807179	gtctctaactcctaac[A/G]cagtgctgggtacatc	A	G	NM_144769 // downstream // 8933 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 8933 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-1944152	ttgtcagcctcaggccc[A/G]agatcaaaataagagt	A	G	NM_144769 // downstream // 70977 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 70977 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript varian	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-1891804	tgatttccttctttgt[C/G]aagtggagcaccaat	C	G	NM_144769 // downstream // 77844 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 77844 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript varian	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2055574	aataatccaagccgca[A/G]gagtttctattaaaag	A	G	NM_144769 // downstream // 88281 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 88281 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript varian	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2165138	caaagaaaaggaggaaa[A/C]catatccgagagtgga	A	C	NM_144769 // downstream // 90948 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 90948 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript varian	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2281946	gagtgctaagcagaca[A/T]taaaacaaggaagtca	A	T	NM_144769 // downstream // 91315 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 91315 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript varian	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-1952057	tttctatctgtaccg[C/T]cctgagatcagctttt	C	T	NM_144769 // downstream // 108527 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 108527 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript vari	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170177	caaggtcatttctcaa[A/G]gtctagagcatacctc	A	G	NM_144769 // downstream // 110822 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, mRNA. /// NM_012188 // downstream // 110822 // Hs.87236 // FOXI1 // 2299 // Homo sapiens forkhead box I1 (FOXI1), transcript vari	FOXI1	FOXI1, Homo sapiens forkhead box I1 (FOXI1), transcript variant 2, q35.1
SNP_A-2159067	attgtttaagtcagaa[C/T]ctcagaaccgagttat	C	T	NM_005565 // intron // 0 // Hs.304475 // LCP2 // 3937 // Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// ENST00000046794 // intron // 0 // --- // --- // --- // --- // ---	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-2189092	cagtaatagagaaagg[A/T]aaaaggcagaaggaa	A	T	NM_005565 // intron // 0 // Hs.304475 // LCP2 // 3937 // Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// ENST00000046794 // intron // 0 // --- // --- // --- // --- // ---	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-1888297	tgagctcttccatatgg[G/T]ccagagagcacaagct	G	T	NM_005565 // upstream // 2548 // Hs.304475 // LCP2 // 3937 // Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// NM_004137 // downstream // 77797 // Hs.484099 // KCNMB1 // 3779 // Homo sapiens	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-1984559	gcacccgtgtgtgtat[A/G]agcaatccaggcgcca	A	G	NM_005565 // upstream // 10502 // Hs.304475 // LCP2 // 3937 // Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), mRNA. /// NM_004137 // downstream // 69843 // Hs.484099 // KCNMB1 // 3779 // Homo sapiens	LCP2	LCP2, Homo sapiens lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) (LCP2), q35.1
SNP_A-2288264	gattcctgcaggtctg[A/G]caatctcactcttcc	A	G	NM_004137 // upstream // 110201 // Hs.484099 // KCNMB1 // 3779 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 1 (KCNMB1), mRNA. /// NM_014592 // upstream // 4738 // Hs.484111 // KCNIP1 // 30820 // Homo sapi	KCNMB1	KCNMB1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 1 (KCNMB1), q35.1
SNP_A-2295815	gcatggataaattacac[A/G]attcagagcctgctgg	A	G	NM_014592 // intron // 0 // Hs.484111 // KCNIP1 // 30820 // Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA. /// ENST00000328939 // intron // 0 // --- // --- // ---	KCNIP1	KCNIP1, Homo sapiens Kv channel interacting protein 1 (KCNIP1), q35.1
SNP_A-2034327	aaatcctaagttgat[C/T]acatctgcaaaatctc	C	T	NM_014592 // intron // 0 // Hs.484111 // KCNIP1 // 30820 // Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA. /// ENST00000328939 // intron // 0 // --- // --- // ---	KCNIP1	KCNIP1, Homo sapiens Kv channel interacting protein 1 (KCNIP1), q35.1
SNP_A-2128329	ataagtgaaagaaccc[C/T]gcacatactaggtact	C	T	NM_014592 // intron // 0 // Hs.484111 // KCNIP1 // 30820 // Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA. /// ENST00000328939 // intron // 0 // --- // --- // ---	KCNIP1	KCNIP1, Homo sapiens Kv channel interacting protein 1 (KCNIP1), q35.1
SNP_A-2170464	caagtcctctgctggg[C/T]caagaatgcagctgct	C	T	NM_014592 // intron // 0 // Hs.484111 // KCNIP1 // 30820 // Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA. /// ENST00000328939 // intron // 0 // --- // --- // ---	KCNIP1	KCNIP1, Homo sapiens Kv channel interacting protein 1 (KCNIP1), q35.1
SNP_A-2108878	agcttaagcagagggg[A/C]cttccataggcgcagca	A	C	NM_014592 // downstream // 284 // Hs.484111 // KCNIP1 // 30820 // Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA. /// NM_014211 // upstream // 47618 // Hs.26225 // GABRP // 2568 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (	KCNIP1	KCNIP1, Homo sapiens Kv channel interacting protein 1 (KCNIP1), q35.1
SNP_A-1806847	gtctatgctgaagtga[C/T]aaggatagggaaaactg	C	T	NM_014211 // intron // 0 // Hs.26225 // GABRP // 2568 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA. /// ENST00000265294 // intron // 0 // --- // --- // ---	GABRP	GABRP, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), q35.1
SNP_A-2021772	aaaaacataatcctcc[A/C]aaatgaagtcattcct	A	C	NM_014211 // intron // 0 // Hs.26225 // GABRP // 2568 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA. /// ENST00000265294 // intron // 0 // --- // --- // ---	GABRP	GABRP, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2109518	aggaaaagatttggac[A/C]cagcatacctaatcaa	A	C	NM_003862 // intron // 0 // Hs.87191 // FGF18 // 8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // intron // 0 // Hs.87191 // FGF18 // 8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcrip	FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-1866005	tcccacgccaagcagg[A/G]caagactgatgctggg	A	G	NM_003862 // downstream // 38995 // Hs.87191 // FGF18 // 8817 // Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA. /// NM_033649 // downstream // 38995 // Hs.87191 // FGF18 // 8817 // Homo sapiens fibroblast growth factor 18 (F	FGF18	FGF18, Homo sapiens fibroblast growth factor 18 (FGF18), transcript variant 1, q35.1
SNP_A-2032978	aaataattattagcaa[A/G]gtagttgaacagggac	A	G	NM_005990 // intron // 0 // Hs.519756 // STK10 // 6793 // Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /// ENST00000176763 // intron // 0 // — // — // — // —	STK10	STK10, Homo sapiens serine q35.1
SNP_A-2304516	gctctcagaaggaaag[A/G]caagcaaagagaaggc	A	G	NM_005990 // intron // 0 // Hs.519756 // STK10 // 6793 // Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /// ENST00000176763 // intron // 0 // — // — // — // —	STK10	STK10, Homo sapiens serine,q35.1
SNP_A-1795192	ggtgagcagatgtcca[C/T]aggaagggaaggagca	C	T	NM_005990 // intron // 0 // Hs.519756 // STK10 // 6793 // Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /// ENST00000176763 // intron // 0 // — // — // — // —	STK10	STK10, Homo sapiens serine q35.1
SNP_A-2270828	gacagggcctacacga[C/T]gccctttcatcatgg	C	T	NM_005990 // intron // 0 // Hs.519756 // STK10 // 6793 // Homo sapiens serine/threonine kinase 10 (STK10), mRNA. /// ENST00000176763 // intron // 0 // — // — // — // —	STK10	STK10, Homo sapiens serine,q35.1
SNP_A-2189287	cagttcctgtatatta[C/T]gtccacctttcccaaa	C	T	NM_152277 // intron // 0 // Hs.179852 // DC-UbP // 92181 // Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), mRNA. /// ENST00000306184 // intron // 0 // — // — // — // —	DC-UbP	DC-UbP, Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), q35.1
SNP_A-2052765	aagtcaatcaagggca[C/T]cagtgacaatattaac	C	T	NM_152277 // intron // 0 // Hs.179852 // DC-UbP // 92181 // Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), mRNA. /// ENST00000306184 // intron // 0 // — // — // — // —	DC-UbP	DC-UbP, Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), q35.1
SNP_A-2219601	cctgtttgtatgctca[G/T]atcattggtaagggga	G	T	NM_152277 // intron // 0 // Hs.179852 // DC-UbP // 92181 // Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), mRNA. /// ENST00000306184 // intron // 0 // — // — // — // —	DC-UbP	DC-UbP, Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), q35.1
SNP_A-2222601	cgagtgagacacttaa[C/T]ctgtaacaagagctct	C	T	NM_152277 // intron // 0 // Hs.179852 // DC-UbP // 92181 // Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), mRNA. /// ENST00000306184 // intron // 0 // — // — // — // —	DC-UbP	DC-UbP, Homo sapiens dendritic cell-derived ubiquitin-like protein (DC-UbP), q35.1
SNP_A-1809976	gtgagttgcaagacgc[C/T]gaagaatctcatgtgg	C	T	ENST00000338714 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-2143816	atgagagcttattaca[C/T]cttgtgctacagatga	C	T	ENST00000338714 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-1819104	gttgccttttttccaca[C/T]agttagcaattcttta	C	T	ENST00000338714 // intron // 0 // — // — // — // — /// ENST00000357241 // intron // 0 // — // — // — // — /// ENST00000358068 // intron // 0 // — // — - // — // —	-	q35.1
SNP_A-2298904	gccccagaactccatc[A/G]atacgctgtccccagg	A	G	ENST00000338714 // intron // 0 // — // — // — // — /// ENST00000358068 // intron // 0 // — // — // — // —	-	q35.1
SNP_A-2145643	atgcatggggtgatga[C/T]agtttgcggttgctgg	C	T	ENST00000338714 // upstream // 33957 // — // — // — // — /// ENST00000311601 // upstream // 142074 // — // — // — // — /// ENST00000357241 // upstream // 65819 // — // — // — // — /// ENST00000358068 // upstream // 33788 // — //	-	q35.1
SNP_A-2011460	tcatttgttaattatc[A/G]cagtaaacattaattc	A	G	NM_004417 // downstream // 44112 // Hs.171695 // DUSP1 // 1843 // Homo sapiens dual specificity phosphatase 1 (DUSP1), mRNA. /// ENST00000315447 // downstream // 32459 // — // — // — // — /// ENST00000239223 // downstream // 44112 // — // — //	DUSP1	DUSP1, Homo sapiens dual specificity phosphatase 1 (DUSP1), q35.1
SNP_A-2154105	attatccccattctac[A/G]gatgaggaacctgagg	A	G	ENST00000326633 // intron // 0 // — // — // — // — /// ENST00000265089 // intron // 0 // — // — // — // —	-	q35.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960070	tttgtttattgctga[A/G]atgaacgaatccttca	A	G	NM_004387 // upstream // 40736 // Hs.54473 // NKX2-5 // 1482 // Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), mRNA. /// NM_003714 // downstream // 38735 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), m	NKX2-5	NKX2-5, Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), q35.1
SNP_A-1790442	ggggcaattagatgac[A/G]atcaccagatagttga	A	G	NM_004387 // upstream // 47009 // Hs.54473 // NKX2-5 // 1482 // Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), mRNA. /// NM_003714 // downstream // 32462 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), m	NKX2-5	NKX2-5, Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), q35.1
SNP_A-2154596	attatttctagtttac[A/G]ggggactcgatgggag	A	G	NM_004387 // upstream // 57986 // Hs.54473 // NKX2-5 // 1482 // Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), mRNA. /// NM_003714 // downstream // 21485 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), m	NKX2-5	NKX2-5, Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), q35.1
SNP_A-2021541	aaaaaaatattgtctca[C/T]gatgccccccagtaag	C	T	NM_004387 // upstream // 69865 // Hs.54473 // NKX2-5 // 1482 // Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), mRNA. /// NM_003714 // downstream // 9606 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mR	NKX2-5	NKX2-5, Homo sapiens NK2 transcription factor related, locus 5 (Drosophila) (NKX2-5), q35.1
SNP_A-1878725	tctgttcccgggggcca[C/T]gggcaaactgtatagt	C	T	NM_003714 // upstream // 84115 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 194963 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2180506	cagaactgggtatggat[C/T]ggtctcagaatgctga	C	T	NM_003714 // upstream // 97409 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 181669 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1949083	ttatgagatatgagc[A/G]aatgtaaccaaggctt	A	G	NM_003714 // upstream // 114818 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 164260 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2266588	gaagtcatagccagaa[A/G]agagctacaaattagt	A	G	NM_003714 // upstream // 239691 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 39387 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1984613	attcaggtcatgatg[C/T]agtcacggaaggacgg	C	T	NM_003714 // upstream // 242509 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 36569 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1888429	tgaggaagcacagtta[A/G]gttaaccaatgcggac	A	G	NM_003714 // upstream // 244533 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 34545 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2087377	actgcaggtctgatac[A/G]gattgacaggtgccac	A	G	NM_003714 // upstream // 247755 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 31323 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209932	ccccaattaccaggaa[A/G]caatatcatctttttg	A	G	NM_003714 // upstream // 252122 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 26956 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2069415	acacaactgctgggaa[C/T]gggaaagtttcaacct	C	T	NM_003714 // upstream // 252367 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 26711 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2274161	gacttcccaattcttct[C/T]cacttagccagctgcc	C	T	NM_003714 // upstream // 255523 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 23555 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2257028	ctttctaattttgct[A/G]accigatgagtgtaca	A	G	NM_003714 // upstream // 255846 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 23432 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-2234893	ctccatgcagggagtg[A/T]caaggaatttgggacc	A	T	NM_003714 // upstream // 256147 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 22931 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1984615	agggttctctcacaaa[C/T]gaaaatgcctcaaata	C	T	NM_003714 // upstream // 263382 // Hs.233160 // STC2 // 8614 // Homo sapiens stanniocalcin 2 (STC2), mRNA. /// NM_138369 // downstream // 15696 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. //	STC2	STC2, Homo sapiens stanniocalcin 2 (STC2), q35.2
SNP_A-1743383	tacttgtctttctagctattaact[C/T]tcaattactagacatttaggg agtc	C	T	BC007436 // downstream // 50430 // Hs.425091 // LOC91272 // 91272 // hypothetical protein BC007436 /// NM_003714 // upstream // 228784 // Hs.155223 // STC2 // 8614 // stanniocalcin 2	LOC91272	LOC91272 , rs889014, hypothetical protein BC007436 ,q35.2
SNP_A-1876441	tctgatacctcagaa[A/T]gtcaatcagtaccaaa	A	T	NM_138369 // upstream // 8675 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream // 8675 // — // 0 // — /// NM_030627 // upstream // 263858 // Hs.127126 // CPEB	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-1926873	ttatttatatctttgca[A/T]cagggaagcccgagagg	A	T	NM_138369 // upstream // 168915 // Hs.425091 // FAM44B // 91272 // Homo sapiens family with sequence similarity 44, member B (FAM44B), mRNA. /// NM_175906 // upstream // 168915 // — // 0 // — /// NM_030627 // upstream // 103618 // Hs.127126 //	FAM44B	FAM44B, Homo sapiens family with sequence similarity 44, member B (FAM44B), q35.2
SNP_A-1934641	ttctctgagtgctcca[A/G]gctaccttatcaggc	A	G	NM_030627 // downstream // 9581 // Hs.127126 // CPEB4 // 80315 // Homo sapiens cytoplasmic polyadenylation element binding protein 4 (CPEB4), mRNA. /// ENST00000265085 // downstream // 9581 // — // — // — /// ENST00000334035 // downstream //	CPEB4	CPEB4, Homo sapiens cytoplasmic polyadenylation element binding protein 4 (CPEB4), q35.2
SNP_A-1658734	tgacacacttggaccattgttgg[A/C]gatgaggtcaggaaact tatttctg	A	C	NM_002449 // upstream // 568190 // Hs.89404 // MSX2 // 4488 // msh homeo box homolog 2 (Drosophila) /// NM_015980 // downstream // 47231 // Hs.70669 // HMP19 // 51617 // HMP19 protein	MSX2	MSX2 , rs1036172, msh homeo box homolog 2 (Drosophila) ,q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1984632	tggttccttgatatggt[C/T]aaaccttgctcctatg	C	T	NM_015980 // downstream // 109835 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 505588 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1984635	gattagcaagactgag[A/G]acaaatcttatatag	A	G	NM_015980 // downstream // 141785 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 473638 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1850577	tattaagtgaaatacа[A/G]catggaaacagtggag	A	G	NM_015980 // downstream // 149549 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 465874 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1941977	ttggaggtggaaatac[A/G]aggcatctaaaatatga	A	G	NM_015980 // downstream // 150960 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 464463 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1945013	ttgtggttgaaccttg[A/C]agaaatgtgttagaaa	A	C	NM_015980 // downstream // 151293 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 464130 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1984643	aatccagagtgtcccaj[A/G]gaacccaaatgcccag	A	G	NM_015980 // downstream // 175358 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 440065 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-2011471	tgtcacaggtatgaac[A/G]gaatatggatgggaag	A	G	NM_015980 // downstream // 300741 // Hs.70669 // HMP19 // 51617 // Homo sapiens HMP19 protein (HMP19), mRNA. /// NM_002449 // upstream // 314682 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// ENST0000030	HMP19	HMP19, Homo sapiens HMP19 protein (HMP19), q35.2
SNP_A-1693857	ctattgtagcttttttcagaaataa[C/G]gactcatttttagaaaaga aaaaaa	C	G	NM_000794 // downstream // 453329 // Hs.2624 // DRD1 // 1812 // dopamine receptor D1 /// NM_002449 // downstream // 256807 // Hs.89404 // MSX2 // 4488 // msh homeo box homolog 2 (Drosophila)	DRD1	DRD1, rs10516121, dopamine receptor D1, q35.2
SNP_A-1984663	agaaatggagttggca[C/T]gggcactaggaactgc	C	T	NM_002449 // downstream // 357430 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream // 352710 // Hs.2624 // DRD1 // 1812 // Homo sapiens dopamine receptor D1 (DRD1), mRNA. /// ENST00	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-1984665	aaccacataaatcaca[G/T]aaacatcagggtgtac	G	T	NM_002449 // downstream // 358706 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream // 351434 // Hs.2624 // DRD1 // 1812 // Homo sapiens dopamine receptor D1 (DRD1), mRNA. /// ENST00	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-2300461	gcctgaaaaccacatg[A/G]aacctctcggtaaat	A	G	NM_002449 // downstream // 400601 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream // 309539 // Hs.2624 // DRD1 // 1812 // Homo sapiens dopamine receptor D1 (DRD1), mRNA. /// ENST00	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835786	tacggaaagatgctca[A/G]tagtgtttgaatacag	A	G	NM_002449 // downstream // 449002 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream // 261138 // Hs.2624 // DRD1 // 1812 // Homo sapiens dopamine receptor D1 (DRD1), mRNA. /// ENST00	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-2011476	ggtgagtggtgctgac[A/C]aaatcacttcactggg	A	C	NM_002449 // downstream // 562996 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream // 147144 // Hs.2624 // DRD1 // 1812 // Homo sapiens dopamine receptor D1 (DRD1), mRNA. /// ENST00	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-1903499	tgggaatgaagcaaac[A/G]agaaggcaaacaata	A	G	NM_002449 // downstream // 607903 // Hs.89404 // MSX2 // 4488 // Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA. /// NM_000794 // downstream // 102237 // Hs.2624 // DRD1 // 1812 // Homo sapiens dopamine receptor D1 (DRD1), mRNA. /// ENST00	MSX2	MSX2, Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), q35.2
SNP_A-1897862	tgctggaaggaagaaac[A/G]agataaagcatgggga	A	G	NM_022754 // downstream // 18892 // Hs.369440 // SFXN1 // 94081 // Homo sapiens sideroflexin 1 (SFXN1), mRNA. /// NM_022304 // upstream // 135136 // Hs.247885 // HRH2 // 3274 // Homo sapiens histamine receptor H2 (HRH2), mRNA. /// ENST00000321442 // downs	SFXN1	SFXN1, Homo sapiens sideroflexin 1 (SFXN1), q35.2
SNP_A-1857118	tcaccgtaggctctgc[A/G]agattttgacgatctc	A	G	NM_022304 // downstream // 10042 // Hs.247885 // HRH2 // 3274 // Homo sapiens histamine receptor H2 (HRH2), mRNA. /// NM_006651 // upstream // 102010 // Hs.478930 // CPLX1 // 10815 // Homo sapiens complexin 1 (CPLX1), mRNA. /// NM_006650 // upstream // 10	HRH2	HRH2, Homo sapiens histamine receptor H2 (HRH2), q35.2
SNP_A-1689130	atagaaaagcatgacccaattcaaga[C/T]gtgtccttctactagat ctcaacct	C	T	BC054510 // intron // 0 // Hs.247885 // HRH2 // 3274 // histamine receptor H2	HRH2	HRH2, rs6686874, histamine receptor H2,q35.2
SNP_A-1670956	gcagtggtgtcttgatcaggag[A/G]acctaggatttggaagg gcttgaga	A	G	NM_006650 // intron // 0 // Hs.193235 // CPLX2 // 10814 // complexin 2	CPLX2	CPLX2, rs7727183, complexin 2,q35.2
SNP_A-2231260	ctattcagatcacccca[A/G]tacgtattatacaatc	A	G	ENST00000331171 // downstream // 4064 // — // — // — /// ENST00000333723 // downstream // 4049 // — // — // — /// ENST00000330220 // downstream // 4064 // — // — // — /// ENST00000253490 // upstream // 73414 // — /	-	q35.2
SNP_A-1930511	ttccaacaaagctcag[C/T]cacttcttccactat	C	T	NM_014613 // intron // 0 // Hs.484242 // ETEA // 23197 // Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), mRNA. /// ENST00000261942 // intron // 0 // — // — // —	ETEA	ETEA, Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), q35.2
SNP_A-1919369	ttaagatcactgataa[A/T]cctaccaccactgaa	A	T	NM_014613 // intron // 0 // Hs.484242 // ETEA // 23197 // Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), mRNA. /// ENST00000261942 // intron // 0 // — // — // —	ETEA	ETEA, Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), q35.2
SNP_A-2043987	aacttgaatttcccca[A/G]ctataaatgaagataa	A	G	NM_014613 // downstream // 299 // Hs.484242 // ETEA // 23197 // Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), mRNA. /// NM_014901 // downstream // 16327 // Hs.434888 // RNF44 // 22838 // Homo sapiens ring finger protein 44	ETEA	ETEA, Homo sapiens expressed in T-cells and eosinophils in atopic dermatitis (ETEA), q35.2
SNP_A-2193493	catctggatttttgca[C/G]aacccaggcgggggctg	C	G	NM_003085 // upstream // 5992 // Hs.90297 // SNCB // 6620 // Homo sapiens synuclein, beta (SNCB), transcript variant 2, mRNA. /// NM_001001502 // upstream // 5992 // Hs.90297 // SNCB // 6620 // Homo sapiens synuclein, beta (SNCB), transcript variant 1, mR	SNCB	SNCB, Homo sapiens synuclein, beta (SNCB), transcript variant 2, q35.2
SNP_A-2173404	cacaaggctgacccc[A/G]agttgtttcattctg	A	G	NM_130465 // downstream // 51753 // Hs.532129 // TM4SF17 // 26262 // Homo sapiens transmembrane 4 superfamily member 17 (TM4SF17), transcript variant 2, mRNA. /// NM_002115 // downstream // 170065 // Hs.411695 // HK3 // 3101 // Homo sapiens hexokinase 3 (	TM4SF17	TM4SF17, Homo sapiens transmembrane 4 superfamily member 17 (TM4SF17), transcript variant 2, q35.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2314369	ggaggcttgctcctca[A/C]cccgtcgtgggtcact	A	C	NM_130465 // downstream // 82452 // Hs.532129 // TM4SF17 // 26262 // Homo sapiens transmembrane 4 superfamily member 17 (TM4SF17), transcript variant 2, mRNA. /// NM_002115 // downstream // 139366 // Hs.411695 // HK3 // 3101 // Homo sapiens hexokinase 3 (	TM4SF17	TM4SF17, Homo sapiens transmembrane 4 superfamily member 17 (TM4SF17), transcript variant 2, q35.2
SNP_A-1789757	gggctctggggctcac[C/T]gcaaatggggttccca	C	T	ENST00000360800 // intron // 0 // — // — // — // — /// ENST00000329542 // intron // 0 // — // — // — // —	-	q35.2
SNP_A-1675071	agtgccaccgtgagtggttatggaa[A/G]gagttgcgatgagaag ggagctgcc	A	G	AB075856 // upstream // 37853 // - // - // - // Homo sapiens mRNA for KIAA1976 protein. /// NM_002115 // downstream // 44321 // Hs.411695 // HK3 // 3101 // hexokinase 3 (white cell)	-	- , rs691268, Homo sapiens mRNA for KIAA1976 protein. ,q35.2
SNP_A-2207454	ccattgtctgaaggaa[C/G]agaaattactgatgaa	C	G	NM_002115 // intron // 0 // Hs.411695 // HK3 // 3101 // Homo sapiens hexokinase 3 (white cell) (HK3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000292432 // intron // 0 // — // — // — // —	HK3	HK3, Homo sapiens hexokinase 3 (white cell) (HK3), nuclear gene encoding mitochondrial protein, q35.2
SNP_A-1742457	aggggagggtattaatgtaagagaa[C/T]ggtaggctaaaatca cataaataga	C	T	NM_016290 // intron // 0 // Hs.300263 // RAP80 // 51720 // receptor associated protein 80	RAP80	RAP80 , rs10516138, receptor associated protein 80,q35.2
SNP_A-2112553	aggcaccttgatctta[C/G]atttaccagacttcag	C	G	NM_016290 // intron // 0 // Hs.232721 // RAP80 // 51720 // Homo sapiens receptor associated protein 80 (RAP80), mRNA. /// ENST00000323774 // intron // 0 // — // — // — // — /// ENST00000274827 // intron // 0 // — // — // — // —	RAP80	RAP80, Homo sapiens receptor associated protein 80 (RAP80), q35.2
SNP_A-2251603	cttcagcatgcgttgc[A/G]aagtgcttgtgccctg	A	G	NM_213647 // intron // 0 // Hs.165950 // FGFR4 // 2264 // Homo sapiens fibroblast growth factor receptor 4 (FGFR4), transcript variant 3, mRNA. /// NM_002011 // intron // 0 // Hs.165950 // FGFR4 // 2264 // Homo sapiens fibroblast growth factor receptor 4	FGFR4	FGFR4, Homo sapiens fibroblast growth factor receptor 4 (FGFR4), transcript variant 3, q35.2
SNP_A-2120778	agtcctggtaaacaca[A/G]gcacatgtcagtcagg	A	G	NM_013237 // downstream // 6295 // Hs.279529 // PX19 // 27166 // Homo sapiens px19-like protein (PX19), mRNA. /// NM_031300 // upstream // 1358 // Hs.442993 // MXD3 // 83463 // Homo sapiens MAX dimerization protein 3 (MXD3), mRNA. /// NM_006816 // downstr	PX19	PX19, Homo sapiens px19-like protein (PX19), q35.3
SNP_A-2306995	gctgttcctttgtcta[G/T]aattctttcatctctc	G	T	NM_013237 // downstream // 7047 // Hs.279529 // PX19 // 27166 // Homo sapiens px19-like protein (PX19), mRNA. /// NM_031300 // upstream // 2110 // Hs.442993 // MXD3 // 83463 // Homo sapiens MAX dimerization protein 3 (MXD3), mRNA. /// NM_006816 // downstr	PX19	PX19, Homo sapiens px19-like protein (PX19), q35.3
SNP_A-2222913	cgcacctataacctca[A/G]cactttgcactttgac	A	G	NM_017838 // upstream // 27299 // Hs.27222 // NOLA2 // 55651 // Homo sapiens nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs) (NOLA2), mRNA. /// NM_022471 // downstream // 4525 // Hs.484313 // GMCL1L // 64396 // Homo sapiens germ cell-les	NOLA2	NOLA2, Homo sapiens nucleolar protein family A, member 2 (H q35.3
SNP_A-1873453	tctcaaggacaaatgc[A/G]atgccccgcagcctgt	A	G	NM_173465 // intron // 0 // Hs.413494 // COL23A1 // 91522 // Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), mRNA. /// ENST00000261955 // intron // 0 // — // — // — // — /// ENST00000332122 // intron // 0 // — // — // — // —	COL23A1	COL23A1, Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), q35.3
SNP_A-1809256	gtgacgttgccttcaa[C/G]aaataattaggggtg	C	G	NM_173465 // intron // 0 // Hs.413494 // COL23A1 // 91522 // Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), mRNA. /// ENST00000261955 // intron // 0 // — // — // — // — /// ENST00000332122 // intron // 0 // — // — // — // —	COL23A1	COL23A1, Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), q35.3
SNP_A-2262903	gaacaaatgcttttac[A/G]caaacaccttgattga	A	G	NM_173465 // intron // 0 // Hs.413494 // COL23A1 // 91522 // Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), mRNA. /// ENST00000261955 // intron // 0 // — // — // — // — /// ENST00000332122 // intron // 0 // — // — // — // —	COL23A1	COL23A1, Homo sapiens collagen, type XXIII, alpha 1 (COL23A1), q35.3
SNP_A-1656465	cctgctgtgagcccagatccaggga[A/G]ccattccatccgcaa cacactcagt	A	G	NM_173465 // intron // 0 // Hs.413494 // COL23A1 // 91522 // collagen, type XXIII, alpha 1	COL23A1	COL23A1 , rs2913838, collagen, type XXIII, alpha 1,q35.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100041	agagtgacatggtatc[C/T]gagtgtttttcggatt	C	T	NM_058230 // upstream // 49090 // Hs.533044 // ZNF354B // 117608 // Homo sapiens zinc finger protein 354B (ZNF354B), mRNA. /// ENST00000331699 // upstream // 28518 // — // — // — // — /// ENST00000322434 // upstream // 49090 // — // — // — /	ZNF354B	ZNF354B, Homo sapiens zinc finger protein 354B (ZNF354B), q35.3
SNP_A-2274038	gacttactctggtaga[A/T]ctgggatgttttgcat	A	T	NM_058230 // upstream // 32633 // Hs.533044 // ZNF354B // 117608 // Homo sapiens zinc finger protein 354B (ZNF354B), mRNA. /// ENST00000331699 // upstream // 44975 // — // — // — // — /// ENST00000322434 // upstream // 32633 // — // — // — /	ZNF354B	ZNF354B, Homo sapiens zinc finger protein 354B (ZNF354B), q35.3
SNP_A-1891606	tgattgatgcggtgta[C/T]gccattgcccacgccc	C	T	NM_000843 // CDS // 0 // Hs.248131 // GRM6 // 2916 // Homo sapiens glutamate receptor, metabotropic 6 (GRM6), mRNA. /// ENST00000319065 // CDS // 0 // — // — // — // — /// ENST00000343799 // CDS // 0 // — // — // — // — /// ENST00000231188	GRM6	GRM6, Homo sapiens glutamate receptor, metabotropic 6 (GRM6), q35.3
SNP_A-2122975	agtgggagtaggggaa[A/G]acaggcaaagttcctg	A	G	NM_014594 // intron // 0 // Hs.272328 // ZNF354C // 30832 // Homo sapiens zinc finger protein 354C (ZNF354C), mRNA. /// ENST00000315475 // intron // 0 // — // — // — // —	ZNF354C	ZNF354C, Homo sapiens zinc finger protein 354C (ZNF354C), q35.3
SNP_A-1984730	tcacatcgtggccaaa[G/T]aatgacactgtgggaa	G	T	NM_014244 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Hom	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript ,q35.3
SNP_A-2162085	attttaacatcaggaa[A/G]gttcacataaaaagtc	A	G	NM_014244 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Hom	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript ,q35.3
SNP_A-2122677	agtggaatgtttgaga[C/T]gcacaaataccttaaa	C	T	NM_014244 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Hom	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript ,q35.3
SNP_A-1826522	taacaaggaagttcat[A/G]aaaagtctagatgcaa	A	G	NM_014244 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript /// NM_021599 // intron // 0 // Hs.120330 // ADAMTS2 // 9509 // Hom	ADAMTS2	ADAMTS2, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript ,q35.3
SNP_A-2184848	cagctggtaacagagc[C/T]acaaagtgccaaatgg	C	T	NM_018434 // intron // 0 // Hs.484363 // RNF130 // 55819 // Homo sapiens ring finger protein 130 (RNF130), mRNA. /// ENST00000261947 // intron // 0 // — // — // — // —	RNF130	RNF130, Homo sapiens ring finger protein 130 (RNF130), q35.3
SNP_A-2054376	aagttgtttctacggc[C/T]aagctgggaccctaac	C	T	NM_018434 // intron // 0 // Hs.484363 // RNF130 // 55819 // Homo sapiens ring finger protein 130 (RNF130), mRNA. /// ENST00000261947 // intron // 0 // — // — // — // —	RNF130	RNF130, Homo sapiens ring finger protein 130 (RNF130), q35.3
SNP_A-1918569	ttaaatgcgaacaaac[A/G]cacttggaggaattcc	A	G	NM_005110 // upstream // 81254 // Hs.30332 // GFPT2 // 9945 // Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA. /// NM_015455 // upstream // 59985 // Hs.157606 // CNOT6 // 57472 // Homo sapiens carbon catabolite repression 4 prote	GFPT2	GFPT2, Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), q35.3
SNP_A-1902911	tggctgaagaaaacgc[A/G]accttgagacttccaa	A	G	NM_015455 // intron // 0 // Hs.157606 // CNOT6 // 57472 // Homo sapiens carbon catabolite repression 4 protein (KIAA1194), mRNA. /// ENST00000261951 // intron // 0 // — // — // — // —	CNOT6	CNOT6, Homo sapiens carbon catabolite repression 4 protein (KIAA1194), q35.3
SNP_A-2198389	catttaatggggactt[A/G]aaaacagaagctatgt	A	G	NM_015455 // downstream // 9792 // Hs.157606 // CNOT6 // 57472 // Homo sapiens carbon catabolite repression 4 protein (KIAA1194), mRNA. /// NM_052863 // downstream // 1965 // Hs.62492 // SCGB3A1 // 92304 // Homo sapiens secretoglobin, family 3A, member 1	CNOT6	CNOT6, Homo sapiens carbon catabolite repression 4 protein (KIAA1194), q35.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2272386	gacctggaaaggaac[A/G]gaattatctacagaat	A	G	ENST00000315712 // upstream // 19225 // — // — // — // — /// ENST00000307832 // downstream // 26138 // — // — // — // —	-	q35.3
SNP_A-1799900	gtacagacagattatat[C/T]gagacaggttgttgga	C	T	ENST00000315712 // upstream // 36431 // — // — // — // — /// ENST00000307832 // downstream // 8932 // — // — // — // —	-	q35.3
SNP_A-2288309	gattctaagtaactgc[A/G]acctgccgtagacgc	A	G	ENST00000315712 // upstream // 44607 // — // — // — // — /// ENST00000307832 // downstream // 756 // — // — // — // —	-	q35.3
SNP_A-2265763	gaagctgtccagttc[C/G]agggaagcagggtact	C	G	NM_002406 // downstream // 36465 // Hs.519818 // MGAT1 // 4245 // Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA. /// ENST00000307832 // upstream // 14025 // — // — // — // — /// ENST00000307	MGAT1	MGAT1, Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), q35.3
SNP_A-2080454	acctaggaatgagacc[C/T]ggctaaagactgtgct	C	T	NM_002406 // downstream // 8698 // Hs.519818 // MGAT1 // 4245 // Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA. /// ENST00000307832 // upstream // 41792 // — // — // — // — /// ENST00000307	MGAT1	MGAT1, Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), q35.3
SNP_A-1821921	gtttattcacttcat[A/G]caaggagggagagttt	A	G	NM_002406 // downstream // 8094 // Hs.519818 // MGAT1 // 4245 // Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA. /// ENST00000307832 // upstream // 42396 // — // — // — // — /// ENST00000307	MGAT1	MGAT1, Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), q35.3
SNP_A-2050841	aaggccattgcatcat[C/G]agggcgtgttccatga	C	G	NM_002406 // upstream // 29673 // Hs.519818 // MGAT1 // 4245 // Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA. /// NM_002406 // upstream // 24588 // Hs.519818 // MGAT1 // 4245 // Homo sapiens mannos	MGAT1	MGAT1, Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), q35.3
SNP_A-1913817	tgtgtccctgcattaa[C/T]acctgtggatctggtg	C	T	NM_006707 // downstream // 18547 // Hs.225949 // BTNL3 // 10917 // Homo sapiens butyrophilin-like 3 (BTNL3), transcript variant 2, mRNA. /// NM_197975 // downstream // 18547 // Hs.225949 // BTNL3 // 10917 // Homo sapiens butyrophilin-like 3 (BTNL3), trans	BTNL3	BTNL3, Homo sapiens butyrophilin-like 3 (BTNL3), transcript variant 2, q35.3
SNP_A-2034126	aaatcatgtgaaaatt[A/G]aaacctctggctgtct	A	G	NM_203296 // upstream // 14625 // Hs.487412 // TRIM7 // 81786 // Homo sapiens tripartite motif-containing 7 (TRIM7), transcript variant 3, mRNA. /// NM_203294 // upstream // 14625 // Hs.487412 // TRIM7 // 81786 // Homo sapiens tripartite motif-containing	TRIM7	TRIM7, Homo sapiens tripartite motif-containing 7 (TRIM7), transcript variant 3, q35.3
SNP_A-1984754	atttcaaaggccaggg[C/T]gatccaagctgatatt	C	T	NM_020185 // upstream // 86443 // Hs.29106 // DUSP22 // 56940 // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// ENST00000307499 // upstream // 60868 // — // — // — // — /// ENST00000344450 // upstream // 86443 // — // — // -	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3
SNP_A-1896999	tgctcattctcgtgta[A/G]ggctgcaggtttccag	A	G	NM_020185 // upstream // 78271 // Hs.29106 // DUSP22 // 56940 // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// ENST00000307499 // upstream // 69040 // — // — // — // — /// ENST00000344450 // upstream // 78271 // — // — // -	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3
SNP_A-1861626	tcatctagcctgaggg[A/G]cccttgatacatgatg	A	G	NM_020185 // upstream // 5466 // Hs.29106 // DUSP22 // 56940 // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// ENST00000307499 // upstream // 141845 // — // — // — // — /// ENST00000344450 // upstream // 5466 // — // — // —	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3
SNP_A-2275925	gagactgccggtgcta[C/G]aactgtgttcccacgt	C	G	NM_020185 // downstream // 27356 // Hs.29106 // DUSP22 // 56940 // Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA. /// NM_002460 // upstream // 13057 // Hs.401013 // IRF4 // 3662 // Homo sapiens interferon regulatory factor 4 (IRF4), mRNA. //	DUSP22	DUSP22, Homo sapiens dual specificity phosphatase 22 (DUSP22), p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869223	tcctggcacatacaaa[A/G]atgttttgttccgttgt	A	G	NM_018303 // intron // 0 // Hs.484412 // SEC5L1 // 55770 // Homo sapiens SEC5-like 1 (S. cerevisiae) (SEC5L1), mRNA. /// ENST00000230449 // intron // 0 // — // — // — /// ENST00000339727 // intron // 0 // — // — // —	SEC5L1	SEC5L1, Homo sapiens SEC5-like 1 (S. cerevisiae) (SEC5L1), p25.3
SNP_A-2233730	ctcatcaaatatctctc[C/T]ctgcccgttctctct	C	T	ENST00000339727 // intron // 0 // — // — // —	-	p25.3
SNP_A-1889530	tgagtttatctaacc[A/G]aaaagaagttcattga	A	G	ENST00000339727 // intron // 0 // — // — // —	-	p25.3
SNP_A-2092386	agaaaggagaggctgaa[C/T]aggattacgggagatt	C	T	ENST00000339727 // intron // 0 // — // — // —	-	p25.3
SNP_A-1956451	tttgttcttatcacc[A/G]aaaccatttctagta	A	G	ENST00000339727 // intron // 0 // — // — // —	-	p25.3
SNP_A-1675718	aagtttataatgacttatttggag[C/T]agtgattgatgaaaaattat tgtaa	C	T	NM_018303 // upstream // 307495 // Hs.436664 // SEC5L1 // 55770 // SEC5-like 1 (S. cerevisiae) /// NM_148959 // upstream // 343660 // Hs.436664 // SEC5L1 // 55770 // SEC5-like 1 (S. cerevisiae)	SEC5L1	SEC5L1, rs707774, SEC5-like 1 (S. cerevisiae) ,p25.3
SNP_A-2184727	cagctgaatcgaacac[A/G]gccaaccctttgaact	A	G	NM_033260 // upstream // 48272 // Hs.297452 // FOXQ1 // 94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 159222 // — // — // — /// ENST00000296839 // upstream // 48272 // — // — // —	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1896011	tgccttgctgtacctg[A/T]attgtagtgacccact	A	T	NM_033260 // upstream // 40439 // Hs.297452 // FOXQ1 // 94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 167055 // — // — // — /// ENST00000296839 // upstream // 40439 // — // — // —	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1683128	caagataaggcgccactataaaa[G/T]gattcagaaagtcc aagggctctag	G	T	AK091913 // downstream // 171970 // Hs.519831 // - // - // CDNA FLJ34594 fis, clone KIDNE2009109 /// NM_033260 // upstream // 35524 // Hs.297452 // FOXQ1 // 94234 // forkhead box Q1	-	-, rs2252693, CDNA FLJ34594 fis, clone KIDNE2009109 ,p25.3
SNP_A-1823301	taaaactgtactgtgt[A/G]acaaaactcctgttct	A	G	NM_033260 // upstream // 23213 // Hs.297452 // FOXQ1 // 94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 184281 // — // — // — /// ENST00000296839 // upstream // 23213 // — // — // —	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1787632	gggacaatcttggaga[A/C]acgtcaactgaagtgc	A	C	NM_033260 // upstream // 22749 // Hs.297452 // FOXQ1 // 94234 // Homo sapiens forkhead box Q1 (FOXQ1), mRNA. /// ENST00000314040 // downstream // 184745 // — // — // — /// ENST00000296839 // upstream // 22749 // — // — // —	FOXQ1	FOXQ1, Homo sapiens forkhead box Q1 (FOXQ1), p25.3
SNP_A-1806909	gtctcaactggtttaa[A/T]ctggacaggacctgcc	A	T	NM_001452 // downstream // 134220 // Hs.484423 // FOXF2 // 2295 // Homo sapiens forkhead box F2 (FOXF2), mRNA. /// NM_001453 // upstream // 80629 // Hs.348883 // FOXC1 // 2296 // Homo sapiens forkhead box C1 (FOXC1), mRNA. /// ENST00000259806 // downstrea	FOXF2	FOXF2, Homo sapiens forkhead box F2 (FOXF2), p25.3
SNP_A-1710157	aactatcatagaagcttcaaatgac[A/G]atagtttaccttcctttt aaatt	A	G	NM_001452 // downstream // 137284 // Hs.44481 // FOXF2 // 2295 // forkhead box F2 /// NM_001453 // upstream // 77565 // Hs.348883 // FOXC1 // 2296 // forkhead box C1	FOXF2	FOXF2, rs2317961, forkhead box F2 ,p25.3
SNP_A-2176824	caccctaacaaacccc[A/T]caagtgcaaaccataa	A	T	NM_001452 // downstream // 141444 // Hs.484423 // FOXF2 // 2295 // Homo sapiens forkhead box F2 (FOXF2), mRNA. /// NM_001453 // upstream // 73405 // Hs.348883 // FOXC1 // 2296 // Homo sapiens forkhead box C1 (FOXC1), mRNA. /// ENST00000259806 // downstrea	FOXF2	FOXF2, Homo sapiens forkhead box F2 (FOXF2), p25.3
SNP_A-1881465	tctttctaaggcagaa[A/G]agtagacacaggttct	A	G	NM_001452 // downstream // 185006 // Hs.484423 // FOXF2 // 2295 // Homo sapiens forkhead box F2 (FOXF2), mRNA. /// NM_001453 // upstream // 29843 // Hs.348883 // FOXC1 // 2296 // Homo sapiens forkhead box C1 (FOXC1), mRNA. /// ENST00000259806 // downstrea	FOXF2	FOXF2, Homo sapiens forkhead box F2 (FOXF2), p25.3
SNP_A-1806503	gtcggtttctgcata[G/T]ctctttgcccaaccaa	G	T	NM_001452 // downstream // 197814 // Hs.484423 // FOXF2 // 2295 // Homo sapiens forkhead box F2 (FOXF2), mRNA. /// NM_001453 // upstream // 17035 // Hs.348883 // FOXC1 // 2296 // Homo sapiens forkhead box C1 (FOXC1), mRNA. /// ENST00000259806 // downstrea	FOXF2	FOXF2, Homo sapiens forkhead box F2 (FOXF2), p25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1912364	tgtgatttgagacaaaa[G/T]aattccaaatgtatat	G	T	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-1936000	ttctactgttggtca[A/G]caaagagcttttcta	A	G	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-2031506	aaaggtgagaagtcca[C/T]gcttcactctctagcc	C	T	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-1934425	ttctccttcctgagca[G/T]gacttgagcaagcata	G	T	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-2270547	gacagagagggaatggt[A/G]aagaccagtcttgcac	A	G	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-1679152	ttaaaatttigaatatciacacca[C/T]ggtgtttgtaagttagctc cctа	C	T	NM_001500 // intron // 0 // Hs.105435 // GMDS // 2762 // GDP-mannose 4,6-dehydratase	GMDS	GMDS , rs10484948, GDP-mannose 4,6-dehydratase,p25.3
SNP_A-2242202	ctgcaacaaagctgaa[C/T]aaagatgaagtgcaa	C	T	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-1815011	gtgttaiattggccac[C/G]acccagagatacccag	C	G	NM_001500 // intron // 0 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// ENST00000319929 // intron // 0 // — // — // —	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.3
SNP_A-2011511	atatcgtgatgtgttat[C/T]gtcctgttgacttta	C	T	NM_001500 // upstream // 345865 // Hs.144496 // GMDS // 2762 // Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /// NM_152554 // downstream // 30436 // Hs.511871 // C6orf195 // 154386 // Homo sapiens chromosome 6 open reading frame 195 (C6orf195),	GMDS	GMDS, Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), p25.2
SNP_A-2046066	aagactagattcaagat[C/T]gagattgcttcatgtg	C	T	NM_152554 // upstream // 27841 // Hs.511871 // C6orf195 // 154386 // Homo sapiens chromosome 6 open reading frame 195 (C6orf195), mRNA. /// ENST00000296847 // upstream // 27841 // — // — // — // — /// ENST00000274643 // downstream // 1198 // — /	C6orf195	C6orf195, Homo sapiens chromosome 6 open reading frame 195 (C6orf195), p25.2
SNP_A-1809970	gtgagtctgctgct[C/T]actgttgtttgttgt	C	T	ENST00000274643 // intron // 0 // — // — // —	-	p25.2
SNP_A-2142721	atgaagattttgtca[A/C]gggctgccattacatg	A	C	NM_130395 // upstream // 61191 // Hs.236828 // WRNIP1 // 56897 // Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, mRNA. /// NM_020135 // upstream // 61191 // Hs.236828 // WRNIP1 // 56897 // Homo sapiens Werner helicase i	WRNIP1	WRNIP1, Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant 2, p25.2
SNP_A-1787199	gggaacaacaattcaa[A/G]tggctgcagatttctc	A	G	NM_000904 // downstream // 15527 // Hs.533050 // NQO2 // 4835 // Homo sapiens NAD(P)H dehydrogenase, quinone 2 (NQO2), mRNA. /// NM_000904 // downstream // 15529 // Hs.533050 // NQO2 // 4835 // Homo sapiens NAD(P)H dehydrogenase, quinone 2 (NQO2), mRNA. /	NQO2	NQO2, Homo sapiens NAD(P)H dehydrogenase, quinone 2 (NQO2), p25.2
SNP_A-1932306	ttcctctgttccacaj[A/G]cacaaaagccaacaca	A	G	NM_001069 // upstream // 7358 // Hs.512712 // TUBB2 // 7280 // Homo sapiens tubulin, beta polypeptide (TUBB), mRNA. /// NM_178012 // upstream // 7358 // Hs.300701 // MGC8685 // 347733 // Homo sapiens tubulin, beta polypeptide paralog (MGC8685), mRNA. ///	TUBB2	TUBB2, Homo sapiens tubulin, beta polypeptide (TUBB), p25.2
SNP_A-1915390	tgttccatgatcttc[C/T]cttgcaaataagcctc	C	T	ENST00000259798 // intron // 0 // — // — // — /// ENST00000332523 // intron // 0 // — // — // —	-	p25.2
SNP_A-1848114	tatcttacacatccat[G/T]agctacaactgttaac	G	T	ENST00000259798 // intron // 0 // — // — // — /// ENST00000332523 // intron // 0 // — // — // —	-	p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2075531	acatgcaatcctaaa[C/T]tccatccaggtagagg	C	T	NM_021945 // upstream // 30885 // Hs.132340 // C6orf85 // 63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 246751 // Hs.484500 // C6orf145 // 221749 // Homo sapiens chromosome 6 open reading frame 14	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-2106968	agcctttgatatttcc[A/G]gagtcaatacctgctt	A	G	NM_021945 // upstream // 36444 // Hs.132340 // C6orf85 // 63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 241192 // Hs.484500 // C6orf145 // 221749 // Homo sapiens chromosome 6 open reading frame 14	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-2114894	agggcagccaacaaca[C/G]gattaaaggctggaa	C	G	NM_021945 // upstream // 37352 // Hs.132340 // C6orf85 // 63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 240284 // Hs.484500 // C6orf145 // 221749 // Homo sapiens chromosome 6 open reading frame 14	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-1835327	tacctatttaatgact[A/G]aacccaaaactaccat	A	G	NM_021945 // upstream // 39916 // Hs.132340 // C6orf85 // 63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 237720 // Hs.484500 // C6orf145 // 221749 // Homo sapiens chromosome 6 open reading frame 14	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-2112406	aggcaagcgaccagta[C/T]gaaagacgtttgccaa	C	T	NM_021945 // upstream // 40268 // Hs.132340 // C6orf85 // 63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 237368 // Hs.484500 // C6orf145 // 221749 // Homo sapiens chromosome 6 open reading frame 14	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-2255752	cttgtgtgagagaaa[A/G]cgtgacctgttctcag	A	G	NM_021945 // upstream // 40746 // Hs.132340 // C6orf85 // 63027 // Homo sapiens chromosome 6 open reading frame 85 (C6orf85), mRNA. /// NM_183373 // downstream // 236890 // Hs.484500 // C6orf145 // 221749 // Homo sapiens chromosome 6 open reading frame 14	C6orf85	C6orf85, Homo sapiens chromosome 6 open reading frame 85 (C6orf85), p25.2
SNP_A-1984837	gtagctatccctttc[A/G]ctacaaaaatatccaa	A	G	NM_012135 // downstream // 2359 // Hs.140944 // FAM50B // 26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B). mRNA. /// ENST00000274639 // downstream // 2359 // — // — // — // — /// ENST00000331244 // upstream // 124405 //	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2
SNP_A-1984838	agctagatgacaaaga[G/T]ccacattcagacttga	G	T	NM_012135 // downstream // 2492 // Hs.140944 // FAM50B // 26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B). mRNA. /// ENST00000274639 // downstream // 2492 // — // — // — // — /// ENST00000331244 // upstream // 124272 //	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2
SNP_A-2011521	tattttatacaacaa[A/G]ttcccactcctaacat	A	G	NM_012135 // downstream // 3659 // Hs.140944 // FAM50B // 26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B). mRNA. /// ENST00000274639 // downstream // 3659 // — // — // — // — /// ENST00000331244 // upstream // 123105 //	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2
SNP_A-2069584	acacacacacatttca[A/G]ctccaggagaaactt	A	G	NM_012135 // downstream // 6340 // Hs.140944 // FAM50B // 26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B). mRNA. /// ENST00000274639 // downstream // 6340 // — // — // — // — /// ENST00000331244 // upstream // 120424 //	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2
SNP_A-2272800	gactaaattaatatca[A/T]actgaggtgagccagt	A	T	NM_012135 // downstream // 29347 // Hs.140944 // FAM50B // 26240 // Homo sapiens family with sequence similarity 50, member B (FAM50B). mRNA. /// ENST00000274639 // downstream // 29347 // — // — // — // — /// ENST00000331244 // upstream // 97417 /	FAM50B	FAM50B, Homo sapiens family with sequence similarity 50, member B (FAM50B), p25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027654	aaaccatcatctaga[A/G]tatcagaccaaaagtg	A	G	NM_003913 // intron // 0 // Hs.159014 // PRPF4B // 8899 // Homo sapiens PRP4 pre-mRNA processing factor 4 homolog B (yeast) (PRPF4B), transcript variant 1, mRNA. /// NM_176800 // intron // 0 // Hs.159014 // PRPF4B // 8899 // Homo sapiens PRP4 pre-mRNA pro	PRPF4B	PRPF4B, Homo sapiens PRP4 pre-processing factor 4 homolog B (yeast) (PRPF4B), transcript variant 1, p25.2
SNP_A-1901181	tggatgacaaatctca[C/G]aaggactctaagggat	C	G	NM_206834 // intron // 0 // Hs.519855 // C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// ENST00000333388 // intron // 0 // — // — // — // — /// ENST00000360378 // intron // 0 // — // — // — // —	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.2
SNP_A-2185938	caggcacaatcatagc[A/G]cctacaatttctcag	A	G	NM_206834 // downstream // 58878 // Hs.519855 // C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream // 516517 // Hs.269092 // CDYL // 9425 // Homo sapiens chromodomain protein, Y-like (CDYL).	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2285789	gatgactgcttgtgta[C/T]gctttggatgttgct	C	T	NM_206834 // downstream // 61137 // Hs.519855 // C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream // 514258 // Hs.269092 // CDYL // 9425 // Homo sapiens chromodomain protein, Y-like (CDYL).	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2145368	atgcagacaagattac[A/G]agaaaaagaatgcaaa	A	G	NM_206834 // downstream // 276327 // Hs.519855 // C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream // 299068 // Hs.269092 // CDYL // 9425 // Homo sapiens chromodomain protein, Y-like (CDYL)	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2107264	agctaaagctatgccc[C/G]aaatgctgtcaggcta	C	G	NM_206834 // downstream // 331203 // Hs.519855 // C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream // 244192 // Hs.269092 // CDYL // 9425 // Homo sapiens chromodomain protein, Y-like (CDYL)	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-1899685	tggaatatggcattcc[C/T]caaaaaaattaaacgt	C	T	NM_206834 // downstream // 469612 // Hs.519855 // C6orf201 // 404220 // Homo sapiens chromosome 6 open reading frame 201 (C6orf201), mRNA. /// NM_170752 // upstream // 105783 // Hs.269092 // CDYL // 9425 // Homo sapiens chromodomain protein, Y-like (CDYL)	C6orf201	C6orf201, Homo sapiens chromosome 6 open reading frame 201 (C6orf201), p25.1
SNP_A-2098415	agagcaaaggtaaaca[C/T]ggtgaaaggtcctgca	C	T	NM_006638 // upstream // 64260 // Hs.511756 // RPP40 // 10799 // Homo sapiens ribonuclease P 40kDa subunit (RPP40), mRNA. /// NM_020408 // downstream // 40129 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149)	RPP40	RPP40, Homo sapiens ribonuclease P 40kDa subunit (RPP40), p25.1
SNP_A-1789198	gggcatagaaataaga[C/T]caagtggccaaaggtg	C	T	NM_006638 // upstream // 71599 // Hs.511756 // RPP40 // 10799 // Homo sapiens ribonuclease P 40kDa subunit (RPP40), mRNA. /// NM_020408 // downstream // 32790 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149)	RPP40	RPP40, Homo sapiens ribonuclease P 40kDa subunit (RPP40), p25.1
SNP_A-2300597	gcctgcaacagggata[A/G]agaatgaacagccaga	A	G	NM_006638 // upstream // 77480 // Hs.511756 // RPP40 // 10799 // Homo sapiens ribonuclease P 40kDa subunit (RPP40), mRNA. /// NM_020408 // downstream // 26909 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149)	RPP40	RPP40, Homo sapiens ribonuclease P 40kDa subunit (RPP40), p25.1
SNP_A-1984874	atgtgtacattccaga[C/G]atccaggaaagatggc	C	G	NM_006638 // upstream // 99350 // Hs.511756 // RPP40 // 10799 // Homo sapiens ribonuclease P 40kDa subunit (RPP40), mRNA. /// NM_020408 // downstream // 5039 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149).	RPP40	RPP40, Homo sapiens ribonuclease P 40kDa subunit (RPP40), p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238676	ctctgttggtattcac[A/C]accatttcttgcatga	A	C	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1781209	ggatgggagcctcaga[C/T]gacactgggtctggg	C	T	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1984876	atatggtagctagaaa[C/T]agaggcctcttcctc	C	T	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1984877	tgacttcttcagcaaa[G/T]aaattataggaaaaa	G	T	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-2060096	aatgaaaatcaagaaa[C/T]ctagcaatggctggtg	C	T	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1784527	ggccgggaagtcaga[C/T]gtgtattataacaaga	C	T	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1953708	tttgactcttcaggga[C/T]ctagcactcttcccac	C	T	NM_020408 // intron // 0 // Hs.387755 // C6orf149 // 57128 // Homo sapiens chromosome 6 open reading frame 149 (C6orf149), mRNA. /// ENST00000330636 // intron // 0 // — // — // — // —	C6orf149	C6orf149, Homo sapiens chromosome 6 open reading frame 149 (C6orf149), p25.1
SNP_A-1818918	gttgatgcaatactgga[C/G]gtttagatttcagtca	C	G	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // —	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-1984888	gttgaagcaataaatc[A/C]aaaacccactgataat	A	C	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // — /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2179150	cactggcactgtgagc[G/T]ccttcaaaaattccta	G	T	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // — /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2165474	caaagcataaatttgta[C/T]gacggatctgtgtgtt	C	T	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // — /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2212408	ccctgtgaaaaagcca[C/G]attagacactgtgggt	C	G	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // — /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1868691	tcctctgtcatcagcg[C/T]atggaagtctgttttg	C	T	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2254284	cttgcaaatttttccaa[G/T]gctagtcaatcattat	G	T	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2245042	ctggcattgtaatcac[C/T]ggctctgttatggatt	C	T	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2131838	atagcttggactgcat[C/T]aagtgcctctgggggtt	C	T	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2215506	cctcactttgtgctcc[A/G]aacaacagtactccag	A	G	NM_006567 // intron // 0 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000274680 // intron // 0 // — // — // — // /// ENST0000	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2048530	aagcatggattctgga[C/T]accgggagtaaaagca	C	T	NM_006567 // downstream // 74912 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_016588 // downstream // 151514 // Hs.103291 // NRN1 // 51299	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-2212862	ccctttctattgagaa[C/T]cagtttctgctttgt	C	T	NM_006567 // downstream // 112898 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_016588 // downstream // 113528 // Hs.103291 // NRN1 // 5129	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-1866925	tcctagttggcattc[A/G]gaacatttttcccat	A	G	NM_006567 // downstream // 211554 // Hs.484547 // FARS2 // 10667 // Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_016588 // downstream // 14872 // Hs.103291 // NRN1 // 51299	FARS2	FARS2, Homo sapiens phenylalanine-tRNA synthetase 1 (mitochondrial) (FARS1), nuclear gene encoding mitochondrial protein, p25.1
SNP_A-1809696	gtgagctacacagaca[A/G]aagtttctccagtatg	A	G	NM_016588 // upstream // 86774 // Hs.103291 // NRN1 // 51299 // Homo sapiens neuritin 1 (NRN1), mRNA. /// NM_000129 // downstream // 49911 // Hs.335513 // F13A1 // 2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// ENST0000024	NRN1	NRN1, Homo sapiens neuritin 1 (NRN1), p25.1
SNP_A-1651132	gattatttgaggctgagatataaa[C/T]tgtctaagaagcaacca ttttctc	C	T	NM_000129 // intron // 0 // Hs.80424 // F13A1 // 2162 // coagulation factor XIII, A1 polypeptide	F13A1	F13A1, rs2274393, coagulation factor XIII, A1 polypeptide p25.1
SNP_A-2036569	aaattgcaaatgtaaa[C/T]gctttagaagacaaca	C	T	NM_000129 // intron // 0 // Hs.335513 // F13A1 // 2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// ENST00000264870 // intron // 0 // — // — // — // —	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1
SNP_A-1746348	aggagaagtctctacaaactaaaga[G/T]ctctgtaaacatctac tcaggtccc	G	T	NM_000129 // upstream // 23105 // Hs.80424 // F13A1 // 2162 // coagulation factor XIII, A1 polypeptide /// NM_004271 // upstream // 244955 // Hs.184018 // LY86 // 9450 // lymphocyte antigen 86 /// NM_173675 // downstream // 16817 // Hs.170081 // FLJ33708	F13A1	F13A1, rs9328354, coagulation factor XIII, A1 polypeptide p25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889936	tgatagctgttttcat[A/G]agtaaatataaactgt	A	G	NM_000129 // upstream // 78881 // Hs.335513 // F13A1 // 2162 // Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /// NM_173675 // downstream // 164757 // Hs.170081 // FLJ33708 // 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ	F13A1	F13A1, Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), p25.1
SNP_A-2186715	cagggctataggagccd[A/G]agttcagtgggagctc	A	G	NM_173675 // intron // 0 // Hs.170081 // FLJ33708 // 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// ENST00000322767 // intron // 0 // — // — // — // —	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-1697080	atgtcaaagcatgtgaaattaaac[A/G]ctgggccctgccaaa aaatacaat	A	G	NM_004271 // intron // 0 // Hs.184018 // LY86 // 9450 // lymphocyte antigen 86 /// NM_173675 // intron // 0 // Hs.170081 // FLJ33708 // 285780 // hypothetical protein FLJ33708	LY86	LY86, rs9328377, lymphocyte antigen 86, p25.1
SNP_A-2218980	cctggtgacagccccc[A/G]catacctgtgtcagt	A	G	NM_004271 // intron // 0 // Hs.519866 // LY86 // 9450 // Homo sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // — // — // — // —	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-1739279	tggccatcttaattagcttcctaaa[C/G]gattattacatcaaagtat gtcact	C	G	NM_004271 // intron // 0 // Hs.184018 // LY86 // 9450 // lymphocyte antigen 86	LY86	LY86, rs3804484, lymphocyte antigen 86,p25.1
SNP_A-1984952	gtttagcttccagtc[A/G]cattactctttcccag	A	G	NM_004271 // intron // 0 // Hs.519866 // LY86 // 9450 // Homo sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // — // — // — // —	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-1984953	ataaactcacaaacga[A/G]ctcaggatggactgtt	A	G	NM_004271 // intron // 0 // Hs.519866 // LY86 // 9450 // Homo sapiens lymphocyte antigen 86 (LY86), mRNA. /// ENST00000230568 // intron // 0 // — // — // — // —	LY86	LY86, Homo sapiens lymphocyte antigen 86 (LY86), p25.1
SNP_A-1864808	tccaggaaagacgatc[G/T]cctcaccaacacaagc	G	T	NM_173675 // upstream // 309329 // Hs.170081 // FLJ33708 // 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 245793 // Hs.519866 // LY86 // 9450 // Homo sapiens lymphocyte antigen 86 (LY86), mRNA. /// N	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-1905369	tggtaacatgtctgc[C/T]aggtgttcaattgttg	C	T	NM_173675 // upstream // 442781 // Hs.170081 // FLJ33708 // 285780 // Homo sapiens hypothetical protein FLJ33708 (FLJ33708), mRNA. /// NM_004271 // downstream // 379245 // Hs.519866 // LY86 // 9450 // Homo sapiens lymphocyte antigen 86 (LY86), mRNA. /// N	FLJ33708	FLJ33708, Homo sapiens hypothetical protein FLJ33708 (FLJ33708), p25.1
SNP_A-1804937	gtcataggtgctattat[C/T]gtcaaagggtatagtg	C	T	NM_205864 // intron // 0 // Hs.367936 // CAGE1 // 285782 // Homo sapiens cancer/testis antigen 3 (CTAG3), transcript variant 2, mRNA. /// NM_175745 // intron // 0 // Hs.367936 // CAGE1 // 285782 // Homo sapiens cancer/testis antigen 3 (CTAG3), transcript	CAGE1	CAGE1, Homo sapiens cancer p24.3
SNP_A-1663144	tgtagaatttatgtctttataga[A/G]ctcattgtggtgtagtgtgggc actg	A	G	NM_004415 // upstream // 44760 // Hs.349499 // DSP // 1832 // desmoplakin /// NM_031480 // downstream // 78842 // Hs.437474 // RIOK1 // 83732 // RIO kinase 1 (yeast) /// NM_153005 // downstream // 78842 // Hs.437474 // RIOK1 // 83732 // RIO kinase 1 (yea	DSP	DSP, rs823695, desmoplakin, p24.3
SNP_A-1984979	actacttgtctacata[C/T]taagaggagagctgca	C	T	NM_152551 // intron // 0 // Hs.13366 // C6orf151 // 154007 // Homo sapiens chromosome 6 open reading frame 151 (C6orf151), mRNA. /// ENST00000342415 // intron // 0 // — // — // — // —	C6orf151	C6orf151, Homo sapiens chromosome 6 open reading frame 151 (C6orf151), p24.3
SNP_A-1679784	tgctcagaatgcaagaaagcttgc[A/G]ccagaaccgttaaac attcatgaac	A	G	NM_001718 // upstream // 114972 // Hs.285671 // BMP6 // 654 // bone morphogenetic protein 6 /// NM_152551 // downstream // 2599 // Hs.13366 // C6orf151 // 154007 // chromosome 6 open reading frame 151	BMP6	BMP6, rs1044761, bone morphogenetic protein 6 p24.3
SNP_A-2047582	aagatggtgacgtgaa[C/G]caaatgcagaaagaca	C	G	NM_152551 // downstream // 1249 // Hs.13366 // C6orf151 // 154007 // Homo sapiens chromosome 6 open reading frame 151 (C6orf151), mRNA. /// ENST00000342415 // downstream // 1249 // — // — // — // — /// ENST00000305775 // upstream // 7314 // — //	C6orf151	C6orf151, Homo sapiens chromosome 6 open reading frame 151 (C6orf151), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2236932	ctctagtcaaacagcc[A/G]gaacactctctccctg	A	G	NM_001718 // intron // 0 // Hs.285671 // BMP6 // 654 // Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // — // — // — // —	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-2149507	atgtagatgttactac[C/G]ccacaagcagagggag	C	G	NM_001718 // intron // 0 // Hs.285671 // BMP6 // 654 // Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // — // — // — // —	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-2257015	ctttcgtggtttgcca[A/C]cttgagagtatgtcac	A	C	NM_001718 // intron // 0 // Hs.285671 // BMP6 // 654 // Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // — // — // — // —	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-1857627	tcactctggggcccca[C/T]gaatttgcgttgttct	C	T	NM_001718 // intron // 0 // Hs.285671 // BMP6 // 654 // Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /// ENST00000283147 // intron // 0 // — // — // — // —	BMP6	BMP6, Homo sapiens bone morphogenetic protein 6 (BMP6), p24.3
SNP_A-2083382	actaaccttgcctta[C/T]gaggtaggaggtggga	C	T	NM_022085 // intron // 0 // Hs.150837 // TXNDC5 // 81567 // Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA. /// ENST00000358251 // intron // 0 // — // — // — // —	TXNDC5	TXNDC5, Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, p24.3
SNP_A-1878303	tctgtcctgaggaaat[G/T]aagagtccagttcctg	G	T	NM_022085 // intron // 0 // Hs.150837 // TXNDC5 // 81567 // Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, mRNA. /// NM_152700 // 3UTR // 0 // — // — // 0 // — /// ENST00000358251 // intron // 0 // — // — // — //	TXNDC5	TXNDC5, Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 2, p24.3
SNP_A-1985004	cccttgacaccatcaa[C/T]gtactttcttcatcct	C	T	NM_004280 // upstream // 246125 // Hs.88977 // EEF1E1 // 9521 // Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA. /// NM_015948 // downstream // 64401 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family	EEF1E1	EEF1E1, Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), p24.3
SNP_A-1885956	tgacattagctgacca[C/T]tctgtagtccttgaaa	C	T	NM_004280 // upstream // 246448 // Hs.88977 // EEF1E1 // 9521 // Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA. /// NM_015948 // downstream // 64078 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family	EEF1E1	EEF1E1, Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), p24.3
SNP_A-1649490	aaagaatctagggtcagtaaagaaa[C/T]ctaattgttataaatcc atctttat	C	T	NM_004280 // upstream // 293967 // Hs.88977 // EEF1E1 // 9521 // eukaryotic translation elongation factor 1 epsilon 1 /// NM_015948 // downstream // 16559 // Hs.285847 // SLC35B3 // 51000 // solute carrier family 35, member B3	EEF1E1	EEF1E1 , rs9328470, eukaryotic translation elongation factor 1 epsilon 1 ,p24.3
SNP_A-1985006	cttctctgactttgac[A/G]cctacactctatttttt	A	G	NM_004280 // upstream // 295996 // Hs.88977 // EEF1E1 // 9521 // Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA. /// NM_015948 // downstream // 14530 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family	EEF1E1	EEF1E1, Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), p24.3
SNP_A-2132930	atatacaaagcattca[A/G]taaatacagaaattat	A	G	NM_015948 // upstream // 80749 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1543394 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2136683	atcactgcaacaggaa[A/T]gtaattttcaccccac	A	T	NM_015948 // upstream // 94862 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1529281 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1849667	tatggtgcaaaaccaa[C/T]aatcatagcagcctca	C	T	NM_015948 // upstream // 105073 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1519070 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1985016	aatccaaaggtacaaa[A/G]taagagtgtggctaag	A	G	NM_015948 // upstream // 115175 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1508968 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2166886	caaattttaagttttta[C/G]agtcactatattgtct	C	G	NM_015948 // upstream // 115756 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1508387 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2122606	agtgctttctctgaca[A/G]attgcatggtggatag	A	G	NM_015948 // upstream // 125634 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1498509 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1718891	cttttggaaggaaaaaaaggccata[A/G]taaatatccatttccag gattgtat	A	G	NM_015948 // upstream // 130781 // Hs.285847 // SLC35B3 // 51000 // solute carrier family 35, member B3 /// NM_153003 // downstream // 1493525 // Hs.382068 // OFCC1 // 266553 // orofacial cleft 1 candidate 1	SLC35B3	SLC35B3 , rs850179, solute carrier family 35, member B3 ,p24.3
SNP_A-1873459	tctcaaggcccttcca[A/G]tctatttctggcctat	A	G	NM_015948 // upstream // 134245 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1489898 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2198164	cattgtaatccttatc[C/G]acctacccttgacttt	C	G	NM_015948 // upstream // 154122 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1470021 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1985019	tggcagagaaagggag[A/G]ccatctttcgtgtctt	A	G	NM_015948 // upstream // 223874 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1400269 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2120213	agtcaggatgtgaaac[A/G]ccattaagtataacag	A	G	NM_015948 // upstream // 232506 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1391637 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1704335	tccaacatcactcctttgtgcgacc[A/G]gcccatgggaagctaa gatgagtcc	A	G	NM_015948 // upstream // 246541 // Hs.285847 // SLC35B3 // 51000 // solute carrier family 35, member B3 /// NM_153003 // downstream // 1377765 // Hs.382068 // OFCC1 // 266553 // orofacial cleft 1 candidate 1	SLC35B3	SLC35B3 , rs4959496, solute carrier family 35, member B3 ,p24.3
SNP_A-2011554	atcccaaatccaacac[A/G]gcatctatttgagaga	A	G	NM_015948 // upstream // 445721 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1178422 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2043930	aacttctgaggtcagc[C/T]accatatcttcctcta	C	T	NM_015948 // upstream // 460539 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1163604 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2057526	aatatctaattaaac[A/G]cacatctgagaacctt	A	G	NM_015948 // upstream // 460651 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1163492 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2121710	agtgacaggttctgaa[A/G]taaacaggcctcggt	A	G	NM_015948 // upstream // 594542 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 1029601 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2175930	caccaaaagccaagcc[A/G]attctggcaccatgct	A	G	NM_015948 // upstream // 693006 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 931137 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1935444	ttctggcattgcacaa[A/G]taataaaaaagtaatc	A	G	NM_015948 // upstream // 992941 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 631202 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1985031	aagtacttccatccaa[A/G]aggtgattgactgtac	A	G	NM_015948 // upstream // 994994 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 629149 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1731075	agttctgaaacccaaaatgtcggca[A/G]ataagcgcacatca gttaacatac	A	G	NM_015948 // upstream // 1026337 // Hs.285847 // SLC35B3 // 51000 // solute carrier family 35, member B3 /// NM_153003 // downstream // 597969 // Hs.382068 // OFCC1 // 266553 // orofacial cleft 1 candidate 1	SLC35B3	SLC35B3 , rs10484247, solute carrier family 35, member B3, p24.3
SNP_A-2023854	aaaagaaatgtcagca[A/T]aatttcagatagtat	A	T	NM_015948 // upstream // 1100943 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 523200 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1896585	tgctagatgatagcaa[C/T]gattttggagcaaca	C	T	NM_015948 // upstream // 1112186 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 511957 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2029711	aaagagctacagttat[A/G]agatagaagaggttag	A	G	NM_015948 // upstream // 1121353 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 502790 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-1947358	tttacaatagttgttaa[G/T]caattcataagggtgg	G	T	NM_015948 // upstream // 1139166 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 484977 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3
SNP_A-2011559	gtgtgttggatgatg[A/G]cagtgtttcctaaag	A	G	NM_015948 // upstream // 1396975 // Hs.285847 // SLC35B3 // 51000 // Homo sapiens solute carrier family 35, member B3 (SLC35B3), mRNA. /// NM_153003 // downstream // 227168 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFC	SLC35B3	SLC35B3, Homo sapiens solute carrier family 35, member B3 (SLC35B3), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2155997	attcctgttgagtcaa[A/G]ccaccatagaatatcc	A	G	ENST00000359382 // intron // 0 // — // — // — // — /// ENST00000336327 // intron // 0 // — // — // — // — /// ENST00000327391 // intron // 0 // — // — // — // —	-	p24.3
SNP_A-1701743	gcacaaagtaagaaaacaaggaaga[C/T]tcggagctgatctc atacctcgctg	C	T	AF520801 // intron // 0 // Hs.484608 // OFCC1 // 266553 // orofacial cleft 1 candidate 1	OFCC1	OFCC1 , rs1889211, orofacial cleft 1 candidate 1,p24.3
SNP_A-2098919	agagctgttaatgttc[C/T]ctgaagactttcctgc	C	T	NM_153003 // upstream // 102799 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), mRNA. /// NM_003220 // downstream // 234442 // Hs.519880 // TFAP2A // 7020 // Homo sapiens transcription factor AP-2 alpha (activating e	OFCC1	OFCC1, Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), p24.3
SNP_A-2153095	attacccttaaaagta[C/T]acctcccagtgaatcc	C	T	NM_153003 // upstream // 123802 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), mRNA. /// NM_003220 // downstream // 213439 // Hs.519880 // TFAP2A // 7020 // Homo sapiens transcription factor AP-2 alpha (activating e	OFCC1	OFCC1, Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), p24.3
SNP_A-2082093	acgaacgaaaaagcag[C/T]agaagctgaattgcag	C	T	NM_153003 // upstream // 125653 // Hs.532138 // OFCC1 // 266553 // Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), mRNA. /// NM_003220 // downstream // 211588 // Hs.519880 // TFAP2A // 7020 // Homo sapiens transcription factor AP-2 alpha (activating e	OFCC1	OFCC1, Homo sapiens orofacial cleft 1 candidate 1 (OFCC1), p24.3
SNP_A-1985060	actctggaaaggaaca[C/T]aagtggatataaaaag	C	T	ENST00000319549 // intron // 0 // — // — // — // —	-	p24.3
SNP_A-1955382	tttggggtcataaaac[A/G]caatctttggaaatat	A	G	NM_005906 // upstream // 22430 // Hs.446125 // MAK // 4117 // Homo sapiens male germ cell-associated kinase (MAK), mRNA. /// NM_005906 // upstream // 14780 // Hs.446125 // MAK // 4117 // Homo sapiens male germ cell-associated kinase (MAK), mRNA. /// NM_00	MAK	MAK, Homo sapiens male germ cell-associated kinase (MAK), p24.2
SNP_A-1985069	acctgtaacaatagcc[A/T]agaagtaagtaaaaac	A	T	NM_004752 // intron // 0 // Hs.227098 // GCM2 // 9247 // Homo sapiens glial cells missing homolog 2 (Drosophila) (GCM2), mRNA. /// ENST00000265009 // intron // 0 // — // — // — // —	GCM2	GCM2, Homo sapiens glial cells missing homolog 2 (Drosophila) (GCM2), p24.2
SNP_A-1985070	ctaaatgtttcaggaa[A/G]gaccttgcaaggacac	A	G	NM_194299 // CDS // 0 // Hs.95600 // LOC221711 // 221711 // Homo sapiens hypothetical protein LOC221711 (LOC221711), mRNA. /// ENST00000341041 // CDS // 0 // — // — // — // —	LOC221711	LOC221711, Homo sapiens hypothetical protein LOC221711 (LOC221711), p24.2
SNP_A-1855217	tcaagcaggagaaaga[A/G]gaatgagccaaaagca	A	G	ENST00000283141 // intron // 0 // — // — // — // —	-	p24.2
SNP_A-1800666	gtagaaagttcctctg[A/G]agttgatcacaaatta	A	G	NM_017770 // intron // 0 // Hs.408557 // ELOVL2 // 54898 // Homo sapiens elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2), mRNA. /// ENST00000354666 // intron // 0 // — // — // — // —	ELOVL2	ELOVL2, Homo sapiens elongation of very long chain fatty acids (FEN1 p24.2
SNP_A-2168061	caactagagtattgta[A/T]attggaggaaagctgt	A	T	NM_006403 // upstream // 243717 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 243717 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2112689	aggcagatggcggata[C/T]taggaataaggtctag	C	T	NM_006403 // upstream // 248231 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 248231 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-1670227	cccgactaattaaagggctaaaata[C/T]atgtatagatagttata attctaga	C	T	NM_006403 // upstream // 257303 // Hs.388589 // NEDD9 // 4739 // neural precursor cell expressed, developmentally down-regulated 9 /// NM_032744 // downstream // 223705 // Hs.97411 // C6orf105 // 84830 // chromosome 6 open reading frame 105	NEDD9	NEDD9 , rs10498678, neural precursor cell expressed, developmentally down-regulated 9 ,p24.2
SNP_A-1892665	tgcacaaatatatatc[C/G]catcccacatgctctt	C	G	NM_006403 // upstream // 264435 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 264435 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1654415	acagatgagtacagttcaatcaca[C/T]ggtggtcgactgcggct gctgtgcc	C	T	NM_006403 // upstream // 266491 // Hs.388589 // NEDD9 // 4739 // neural precursor cell expressed, developmentally down-regulated 9 /// NM_032744 // downstream // 214517 // Hs.97411 // C6orf105 // 84830 // chromosome 6 open reading frame 105	NEDD9	NEDD9, rs821545, neural precursor cell expressed, developmentally down-regulated 9 ,p24.2
SNP_A-1742629	gactccattcattacttgattctta[A/T]aaggccccacttcaacaa ggggtcc	A	T	NM_006403 // upstream // 266835 // Hs.388589 // NEDD9 // 4739 // neural precursor cell expressed, developmentally down-regulated 9 /// NM_032744 // downstream // 214173 // Hs.97411 // C6orf105 // 84830 // chromosome 6 open reading frame 105	NEDD9	NEDD9, rs687163, neural precursor cell expressed, developmentally down-regulated 9 ,p24.2
SNP_A-2157831	attgccttgaataaaa[C/T]ggagactactacta	C	T	NM_006403 // upstream // 312681 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 312681 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2011573	acccaacctctctatt[A/G]aaagtcattagcaagt	A	G	NM_006403 // upstream // 327261 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 327261 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2303139	gctatatgccctcaca[A/G]attcttctactaaact	A	G	NM_006403 // upstream // 344184 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 344184 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.2
SNP_A-2118695	agtacacaaggtcagc[A/G]gacgaaaaattcctag	A	G	NM_006403 // upstream // 366030 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 366030 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-1985096	ggcagtcaagttcaaa[A/G]ccaaacgttgaatgct	A	G	NM_006403 // upstream // 401821 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 401821 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-1693230	gtaaaaaggcagcaatgttccata[A/G]atctgcttcatactgct ggttttc	A	G	NM_006403 // upstream // 436740 // Hs.388589 // NEDD9 // 4739 // neural precursor cell expressed, developmentally down-regulated 9 /// NM_032744 // downstream // 44268 // Hs.97411 // C6orf105 // 84830 // chromosome 6 open reading frame 105	NEDD9	NEDD9, rs9296117, neural precursor cell expressed, developmentally down-regulated 9 ,p24.1
SNP_A-2215227	cctcaaatgacggtga[A/G]attccacattgatat	A	G	NM_006403 // upstream // 452160 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 452160 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-1985097	tctcttgtttgctgaa[A/G]ataagacacaaaagtt	A	G	NM_006403 // upstream // 453062 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 453062 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-2103992	agcacttgaaaagcaa[A/C]cacagtaatagtttt	A	C	NM_006403 // upstream // 453326 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 453326 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1845997	tatatagaggaggaac[A/G]caatacctgctttgtg	A	G	NM_006403 // upstream // 469072 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), mRNA. /// NM_182966 // upstream // 469072 // Hs.37982 // NEDD9 // 4739 // Homo sapiens neural precursor	NEDD9	NEDD9, Homo sapiens neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), p24.1
SNP_A-2282362	gagttcaggtttattc[C/T]aagtgaagcgggaagc	C	T	NM_032744 // intron // 0 // Hs.126409 // C6orf105 // 84830 // Homo sapiens chromosome 6 open reading frame 105 (C6orf105), mRNA. /// ENST00000229583 // intron // 0 // — // — // — // —	C6orf105	C6orf105, Homo sapiens chromosome 6 open reading frame 105 (C6orf105), p24.1
SNP_A-1961506	ttttttctgaaatga[A/T]gttgatgtatcctaag	A	T	NM_032744 // upstream // 207755 // Hs.126409 // C6orf105 // 84830 // Homo sapiens chromosome 6 open reading frame 105 (C6orf105), mRNA. /// NM_002114 // upstream // 133301 // Hs.128930 // HIVEP1 // 3096 // Homo sapiens human immunodeficiency virus type I	C6orf105	C6orf105, Homo sapiens chromosome 6 open reading frame 105 (C6orf105), p24.1
SNP_A-1919757	ttaagtctctggaaaa[A/G]aggtaacgaacgtcaa	A	G	NM_002114 // intron // 0 // Hs.128930 // HIVEP1 // 3096 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), mRNA. /// ENST00000355183 // intron // 0 // — // — // — // — /// ENST00000322552 // intron // 0 // —	HIVEP1	HIVEP1, Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), p24.1
SNP_A-2070041	acacataagcaaatag[C/T]agggaacgtgaaaggg	C	T	NM_002114 // downstream // 6136 // Hs.128930 // HIVEP1 // 3096 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), mRNA. /// NM_001955 // upstream // 119829 // Hs.511899 // EDN1 // 1906 // Homo sapiens endothelin 1 (ED	HIVEP1	HIVEP1, Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), p24.1
SNP_A-2229953	ctataaaaagcaaccc[A/G]aggagaactttcatgt	A	G	NM_002114 // downstream // 53092 // Hs.128930 // HIVEP1 // 3096 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), mRNA. /// NM_001955 // upstream // 72873 // Hs.511899 // EDN1 // 1906 // Homo sapiens endothelin 1 (ED	HIVEP1	HIVEP1, Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), p24.1
SNP_A-2107622	agctatggttgttgaa[A/G]tgtggtccctggagca	A	G	NM_002948 // downstream // 41984 // Hs.381219 // RPL15 // 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 161602 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-2203623	ccagacagtttcaaga[A/G]tcccttccgagtatga	A	G	NM_002948 // downstream // 89061 // Hs.381219 // RPL15 // 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 114525 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-2309710	ggaaagcttgcaagaa[A/C]ttagtagaacacttga	A	C	NM_002948 // downstream // 129984 // Hs.381219 // RPL15 // 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 73602 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-2100855	agatatatgataggta[C/T]gtaggtagataggtag	C	T	NM_002948 // downstream // 139583 // Hs.381219 // RPL15 // 6138 // Homo sapiens ribosomal protein L15 (RPL15), mRNA. /// AB051520 // upstream // 64003 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495	RPL15	RPL15, Homo sapiens ribosomal protein L15 (RPL15), p24.1
SNP_A-2048101	aagcaatttttaata[C/G]gtgaatctgagaagag	C	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds, p24.1
SNP_A-2084657	actattagtgatacac[A/G]gaacaagagcatggat	A	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds, p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1848836	tatgatgtcccatgcc[A/G]gcagagagtgagaaag	A	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. ,p24.1
SNP_A-1852327	tattgtttggtcatta[A/G]taaaatagtgataata	A	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-1985138	ggcagcgaataaaagc[A/G]aatcatttaaaatcat	A	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-2124295	agttatgtaaacagga[A/G]gtgcagcatagtgtct	A	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-2243237	ctgcctgatgtgctga[A/T]ctctgtacaactttgc	A	T	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. p24.1
SNP_A-2094717	agaatcaaagtcaaga[C/T]gcctcctgaatatact	C	T	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. ,p24.1
SNP_A-1872209	tctacttctctcaccc[C/G]cttcaaagccaggctt	C	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// ENST00000332995 // intron // 0 // — // — // — // —	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. ,p24.1
SNP_A-2079287	acccatttctaaaaca[A/G]gtcttgataggaatga	A	G	AB051520 // intron // 0 // Hs.436996 // PHACTR1 // 221692 // Homo sapiens mRNA for KIAA1733 protein, partial cds. /// NM_016495 // 3UTR // 0 // Hs.484678 // TBC1D7 // 51256 // Homo sapiens TBC1 domain family, member 7 (TBC1D7), mRNA. /// ENST00000332995 /	PHACTR1	PHACTR1, Homo sapiens for KIAA1733 protein, partial cds. ,p24.1
SNP_A-2218160	cctgcgagctctgtta[C/T]gaaggaaatcgaaagc	C	T	NM_016495 // intron // 0 // Hs.484678 // TBC1D7 // 51256 // Homo sapiens TBC1 domain family, member 7 (TBC1D7), mRNA. /// ENST00000343141 // intron // 0 // — // — // — // — /// ENST00000320118 // intron // 0 // — // — // — // —	TBC1D7	TBC1D7, Homo sapiens TBC1 domain family, member 7 (TBC1D7), p24.1
SNP_A-1736197	atgtcagattagagaaaccaaacaa[C/T]gtgacggtacatgtg atgaaaagct	C	T	AK057228 // intron // 0 // Hs.8645 // TBC1D7 // 51256 // TBC1 domain family, member 7	TBC1D7	TBC1D7 , rs8541, TBC1 domain family, member 7,p24.1
SNP_A-1948955	tttatcgggtggttta[C/T]aggctctttatcatgg	C	T	NM_018988 // intron // 0 // Hs.484686 // GFOD1 // 54438 // Homo sapiens glucose-fructose oxidoreductase domain containing 1 (GFOD1), mRNA. /// ENST00000274688 // intron // 0 // — // — // — // —	GFOD1	GFOD1, Homo sapiens glucose-fructose oxidoreductase domain containing 1 (GFOD1), p23
SNP_A-2082062	acgaaaactagctaga[C/T]atggtagtgcgtgctt	C	T	NM_016167 // downstream // 152027 // Hs.444852 // NOL7 // 51406 // Homo sapiens nucleolar protein 7, 27kDa (NOL7), mRNA. /// NM_005493 // upstream // 62012 // Hs.306242 // RANBP9 // 10048 // Homo sapiens RAN binding protein 9 (RANBP9), mRNA. /// NM_022102	NOL7	NOL7, Homo sapiens nucleolar protein 7, 27kDa (NOL7), p23
SNP_A-1679224	gcctaagagatttattagctaaata[C/T]atgagtagtccttgtttgg attcta	C	T	NM_152737 // intron // 0 // Hs.111164 // MGC33993 // 221687 // hypothetical protein MGC33993	MGC33993	MGC33993 , rs280171, hypothetical protein MGC33993,p23
SNP_A-2145148	atgcaaggatagggta[A/G]taattcatctctagtc	A	G	NM_152737 // downstream // 113323 // Hs.111164 // RNF182 // 221687 // Homo sapiens hypothetical protein MGC33993 (MGC33993), mRNA. /// NM_004233 // upstream // 24308 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immun	RNF182	RNF182, Homo sapiens hypothetical protein MGC33993 (MGC33993), p23
SNP_A-2147921	atggctactaggccca[C/T]gtctaacaattcctca	C	T	NM_004233 // downstream // 247453 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 861971 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189449	cagttggctgaaattat[C/G]aagaaagaaattggac	C	G	NM_004233 // downstream // 579107 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 530317 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-1916680	tgtttcaacgtgtcta[C/T]gactacctgtctttta	C	T	NM_004233 // downstream // 605286 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 504138 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2257626	cttgccctgtttttca[C/T]cttctgttacacaa	C	T	NM_004233 // downstream // 634854 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 474570 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2230160	ctatacgaagctaact[C/T]acctgtctcaggaaata	C	T	NM_004233 // downstream // 653872 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 455552 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2249821	cttaattgtcctacaa[G/T]gtctcggatacccagtt	G	T	NM_004233 // downstream // 656358 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 453066 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-1820168	gtttaataacttaga[C/T]aggtttgaagaggtgg	C	T	NM_004233 // downstream // 702947 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 406477 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-1673536	aggtgttgggaattcccgagaaagd[A/G]gatcggcattattgttattgctg	A	G	NM_004233 // downstream // 806739 // Hs.79197 // CD83 // 9308 // CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) /// NM_004973 // upstream // 302681 // Hs.40154 // JARID2 // 3720 // Jumonji, AT rich interactive domain 2	CD83	CD83 , rs4285324, CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) ,p23
SNP_A-1871957	tctacattcagatatg[C/G]agccatagaaatcagag	C	G	NM_004233 // downstream // 807754 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 301670 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2011597	tggttatttatgttg[A/G]actctttagaaactgc	A	G	NM_004233 // downstream // 842034 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 267390 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-1875418	tctctgcggcacaga[C/T]ctaaaggggatgcag	C	T	NM_004233 // downstream // 860603 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 248821 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-2113088	aggccagcagaaggaa[A/C]acaatctccctaaaa	A	C	NM_004233 // downstream // 894748 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 214676 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238621	ctctgtggtgaggata[C/T]ggttatcattgtact	C	T	NM_004233 // downstream // 904840 // Hs.484703 // CD83 // 9308 // Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), mRNA. /// NM_004973 // upstream // 204584 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT	CD83	CD83, Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83), p23
SNP_A-1911330	tgtctgttgctccaga[A/T]cgaatacaagttctta	A	T	NM_004973 // intron // 0 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // — // — // — /// ENST00000341776 // intron // 0 // — // — // —	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-2280824	gaggtggtatctcac[A/G]atgaatgcagttgatt	A	G	NM_004973 // intron // 0 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // — // — // — /// ENST00000341776 // intron // 0 // — // — // —	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-2011605	gggcctgtctcataa[C/G]ggaaaggataattat	C	G	NM_004973 // intron // 0 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // — // — // — /// ENST00000341776 // intron // 0 // — // — // —	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-1892102	tgcaaagatcaattgaf[A/G]gccaccaggagttcgc	A	G	NM_004973 // intron // 0 // Hs.269059 // JARID2 // 3720 // Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), mRNA. /// ENST00000340470 // intron // 0 // — // — // — /// ENST00000341776 // intron // 0 // — // — // —	JARID2	JARID2, Homo sapiens Jumonji, AT rich interactive domain 2 (JARID2), p22.3
SNP_A-2034612	aaatcttgagaagaa[C/T]tcatgacggaaccaca	C	T	NM_183041 // intron // 0 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 // intron // 0 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding protein 1 (DTNB	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3
SNP_A-2251582	cttcagatcaccatca[A/G]agaattgctaaatga	A	G	NM_183041 // upstream // 88059 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 // upstream // 88059 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding pro	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3
SNP_A-2257892	ctttgtacagagttga[A/G]acaggatgacatgaca	A	G	NM_183041 // upstream // 154357 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 // upstream // 154357 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding p	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3
SNP_A-2194884	catgctatccaataaa[A/G]atgatgtctttcaaac	A	G	NM_183041 // upstream // 154607 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, mRNA. /// NM_032122 // upstream // 154607 // Hs.519583 // DTNBP1 // 84062 // Homo sapiens dystrobrevin binding p	DTNBP1	DTNBP1, Homo sapiens dystrobrevin binding protein 1 (DTNBP1), transcript variant 3, p22.3
SNP_A-1874729	tctccttaatgtatccc[C/T]gaggtaagtttcctac	C	T	NM_013262 // 3UTR // 0 // Hs.484738 // MYLIP // 29116 // Homo sapiens myosin regulatory light chain interacting protein (MYLIP), mRNA. /// ENST00000356840 // 3UTR // 0 // — // — // — /// ENST00000349606 // 3UTR // 0 // — // — // — // —	MYLIP	MYLIP, Homo sapiens myosin regulatory light chain interacting protein (MYLIP), p22.3
SNP_A-2273817	gactggcagaagaaag[C/G]cttgtccatacgcagg	C	G	NM_013262 // downstream // 8648 // Hs.484738 // MYLIP // 29116 // Homo sapiens myosin regulatory light chain interacting protein (MYLIP), mRNA. /// NM_006877 // upstream // 81692 // Hs.484741 // GMPR // 2766 // Homo sapiens guanosine monophosphate reducta	MYLIP	MYLIP, Homo sapiens myosin regulatory light chain interacting protein (MYLIP), p22.3
SNP_A-2074502	acatagcaatggttgc[A/G]aggagttaatgaggta	A	G	NM_000332 // intron // 0 // Hs.434961 // ATXN1 // 6310 // Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // intron // 0 // — // — // — // — // —	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3
SNP_A-2297576	gccagaggttagaag[A/G]agaattatgtgtcttc	A	G	NM_000332 // intron // 0 // Hs.434961 // ATXN1 // 6310 // Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // intron // 0 // — // — // — // —	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1985230	tctaaacaagtgaaaa[A/C]caatagctgaaaaatt	A	C	NM_000332 // intron // 0 // Hs.434961 // ATXN1 // 6310 // Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // intron // 0 // — // — // — // — // —	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3
SNP_A-2258050	cttigtatttigaaa[A/T]gaaagtctgagcaga	A	T	NM_000332 // intron // 0 // Hs.434961 // ATXN1 // 6310 // Homo sapiens ataxin 1 (ATXN1), mRNA. /// ENST00000244769 // intron // 0 // — // — // — // — // —	ATXN1	ATXN1, Homo sapiens ataxin 1 (ATXN1), p22.3
SNP_A-1673746	tcaacttccacctctgttaactac[A/G]ctgcagaaactttgacac tgaact	A	G	NM_000332 // intron // 0 // Hs.434961 // SCA1 // 6310 // spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	SCA1	SCA1 , rs10484365, spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1),p22.3
SNP_A-1704483	gcgattcttcactggaagggatga[C/T]cagaggaggaaggagtt ggcattaat	C	T	NM_000332 // intron // 0 // Hs.434961 // SCA1 // 6310 // spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	SCA1	SCA1 , rs1150625, spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1),p22.3
SNP_A-2088632	actgtgagcagtgaaa[C/T]ctgtatctgtgcaacg	C	T	NM_006366 // intron // 0 // Hs.132902 // CAP2 // 10486 // Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), mRNA. /// ENST00000229922 // intron // 0 // — // — // — // —	CAP2	CAP2, Homo sapiens CAP, adenylate cyclase-associated protein, 2 (yeast) (CAP2), p22.3
SNP_A-1894712	tgccagccactctta[C/T]agacagcctactcacc	C	T	NM_022113 // intron // 0 // Hs.189915 // KIF13A // 63971 // Homo sapiens kinesin family member 13A (KIF13A), mRNA. /// ENST00000358380 // intron // 0 // — // — // — // — /// ENST00000259711 // intron // 0 // — // — // — // —	KIF13A	KIF13A, Homo sapiens kinesin family member 13A (KIF13A), p22.3
SNP_A-2188726	cagtgcttgcccgta[C/G]agacaattcaacaaat	C	G	NM_022113 // upstream // 92652 // Hs.189915 // KIF13A // 63971 // Homo sapiens kinesin family member 13A (KIF13A), mRNA. /// NM_198586 // downstream // 41285 // Hs.348351 // NHLRC1 // 378884 // Homo sapiens NHL repeat containing 1 (NHLRC1), mRNA. /// ENST	KIF13A	KIF13A, Homo sapiens kinesin family member 13A (KIF13A), p22.3
SNP_A-1949316	ttattaattttaatca[G/T]cagttgcgtcattgc	G	T	ENST00000297792 // intron // 0 // — // — // —	-	p22.3
SNP_A-2232117	ctcaaggctttcatca[A/C]aatgttcagttctgc	A	C	ENST00000297792 // intron // 0 // — // — // —	-	p22.3
SNP_A-1950815	tttccaaaatcgtgca[A/G]gtttctattctgtag	A	G	ENST00000297792 // intron // 0 // — // — // —	-	p22.3
SNP_A-1681126	tctcagtttgggaaacatcagaat[A/T]atcataaatggagataa ttatgtg	A	T	NM_003472 // upstream // 56300 // Hs.110713 // DEK // 7913 // DEK oncogene (DNA binding)	DEK	DEK , rs2077780, DEK oncogene (DNA binding),p22.3
SNP_A-1664478	ttatgttgtccactggaatggaaaca[A/G]aattaagaaggcctatg aatttatg	A	G	NM_003472 // upstream // 56354 // Hs.110713 // DEK // 7913 // DEK oncogene (DNA binding)	DEK	DEK , rs728471, DEK oncogene (DNA binding),p22.3
SNP_A-1737301	tcagccaaagtgtgtgccactgtct[C/G]acataaaaacgaagatg ttccctgaa	C	G	NM_003472 // upstream // 70660 // Hs.110713 // DEK // 7913 // DEK oncogene (DNA binding)	DEK	DEK , rs7757820, DEK oncogene (DNA binding),p22.3
SNP_A-2265241	gaagcaaagccccaca[A/G]ctatgtgatcttgaga	A	G	NM_182757 // intron // 0 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// ENST00000259939 // intron // 0 // — // — // — // —	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2225281	cgttggtctacagaaa[A/G]aggaatgactgcattg	A	G	NM_182757 // downstream // 7812 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1360957 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-l	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1985272	gtgcaatactttgaga[C/G]gatgatctcaatcct	C	G	NM_182757 // downstream // 17570 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1351199 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1722196	aatatctgattacaggggtaagg[A/T]gtctcatatcagtatca ngctaga	A	T	AL832329 // downstream // 17641 // Hs.432653 // IBRDC2 // 255488 // IBR domain containing 2 /// NM_001546 // upstream // 1351130 // Hs.391392 // ID4 // 3400 // inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	IBRDC2	IBRDC2 , rs4490618, IBR domain containing 2 ,p22.3
SNP_A-2248256	ctgtgtaaatcttga[A/T]taagagggcagcagca	A	T	NM_182757 // downstream // 65576 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1303193 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1985278	gggagggcagaggtac[C/T]agtagatagaggaagg	C	T	NM_182757 // downstream // 102677 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1266092 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1985280	caactcagtactctgg[C/T]cacttcatgttcat	C	T	NM_182757 // downstream // 109590 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1259179 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1758115	catctaggctaaataaattacgtaa[A/C]gaattatgttgattacttatt gtgtt	A	C	AL832329 // downstream // 135358 // Hs.432653 // IBRDC2 // 255488 // IBR domain containing 2 /// NM_001546 // upstream // 1233413 // Hs.391392 // ID4 // 3400 // inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	IBRDC2	IBRDC2 , rs10484371, IBR domain containing 2 ,p22.3
SNP_A-2076737	acatttttacatatac[A/G]aaagctgaaaaagtgc	A	G	NM_182757 // downstream // 218122 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 1150647 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2265293	gaagcacccgtctgct[A/G]acaccattagagcctt	A	G	NM_182757 // downstream // 466866 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 901903 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2111071	aggagaccaggttaga[G/T]aatgacccgggaagga	G	T	NM_182757 // downstream // 505461 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 863308 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2280838	gaggtgtcttaaaca[C/T]aagcacacataaaaca	C	T	NM_182757 // downstream // 569448 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 799321 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1985305	caccttcataatctcc[A/G]cattgccactccagc	A	G	NM_182757 // downstream // 700870 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 667899 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1985322	ccttagctgctatttta[C/T]aagtccatttcatcag	C	T	NM_182757 // downstream // 1142527 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 226242 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2028968	aaagaaaaacccagtgc[A/G]gaaatggacaataaga	A	G	NM_182757 // downstream // 1185151 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 183618 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-2132309	atagtagccataaaaa[C/T]gttctgttcttatc	C	T	NM_182757 // downstream // 1294805 // Hs.148741 // IBRDC2 // 255488 // Homo sapiens IBR domain containing 2 (IBRDC2), mRNA. /// NM_001546 // upstream // 73964 // Hs.519601 // ID4 // 3400 // Homo sapiens inhibitor of DNA binding 4, dominant negative helix-	IBRDC2	IBRDC2, Homo sapiens IBR domain containing 2 (IBRDC2), p22.3
SNP_A-1702715	tcttacctgctcaggttgtggaatc[A/G]agtctaggaattgagattct ggcat	A	G	NM_175879 // intron // 0 // - // - // -	-	- , rs10484638, - ,p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1654191	tcaaattgaggccatacaaattaat[C/G]aagtgtttctactgaagctacccaa	C	G	NM_175879 // intron // 0 // - // - // - // -	-	- , rs4537124, -,p22.3
SNP_A-1985336	acctgagccttctgca[C/T]ggtgacactgattttt	C	T	ENST00000324607 // intron // 0 // — // — // — // — /// ENST00000357722 // intron // 0 // — // — // — // —	-	p22.3
SNP_A-1686904	aattaagaagccaaacagtttacca[A/G]aaagcttggccaataactttctca	A	G	NM_175879 // intron // 0 // - // - // - // -	-	- , rs2483766, -,p22.3
SNP_A-1940830	ttgctaaccagtcgcc[A/G]gaattatcccctatag	A	G	ENST00000324607 // intron // 0 // — // — // — // — /// ENST00000357722 // intron // 0 // — // — // — // —	-	p22.3
SNP_A-2207001	ccatgtggcaccttcc[A/G]gcagtactttcaaggg	A	G	NM_001949 // intron // 0 // Hs.269408 // E2F3 // 1871 // Homo sapiens E2F transcription factor 3 (E2F3), mRNA. /// ENST00000346618 // intron // 0 // — // — // — // —	E2F3	E2F3, Homo sapiens E2F transcription factor 3 (E2F3), p22.3
SNP_A-1859466	tcaggacctttacac[A/G]atactttatccactca	A	G	NM_001949 // downstream // 28348 // Hs.269408 // E2F3 // 1871 // Homo sapiens E2F transcription factor 3 (E2F3), mRNA. /// NM_017774 // upstream // 12467 // Hs.484844 // CDKAL1 // 54901 // Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (	E2F3	E2F3, Homo sapiens E2F transcription factor 3 (E2F3), p22.3
SNP_A-2041515	aacctttgcatattcc[G/T]ctttaatgaactctga	G	T	NM_017774 // intron // 0 // Hs.484844 // CDKAL1 // 54901 // Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), mRNA. /// ENST00000274695 // intron // 0 // — // — // — // —	CDKAL1	CDKAL1, Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), p22.3
SNP_A-1985362	caatcaaattttagca[A/G]catccacgaacttaat	A	G	NM_017774 // intron // 0 // Hs.484844 // CDKAL1 // 54901 // Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), mRNA. /// ENST00000274695 // intron // 0 // — // — // — // —	CDKAL1	CDKAL1, Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), p22.3
SNP_A-1985373	aaatcagcttgtctga[C/T]ggggctacacagagaa	C	T	NM_017774 // downstream // 56585 // Hs.484844 // CDKAL1 // 54901 // Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), mRNA. /// NM_003107 // upstream // 304755 // Hs.357901 // SOX4 // 6659 // Homo sapiens SRY (sex determining regi	CDKAL1	CDKAL1, Homo sapiens CDK5 regulatory subunit associated protein 1-like 1 (CDKAL1), p22.3
SNP_A-2193180	catctatttatcctaa[A/C]cgaagacctttaaaa	A	C	NM_003107 // downstream // 323861 // Hs.357901 // SOX4 // 6659 // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA. /// NM_000948 // downstream // 364772 // Hs.1905 // PRL // 5617 // Homo sapiens prolactin (PRL), mRNA. /// ENST00000244745 //	SOX4	SOX4, Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), p22.3
SNP_A-1940898	ttgctagattgggaga[A/G]catttctactgataag	A	G	NM_003107 // downstream // 513797 // Hs.357901 // SOX4 // 6659 // Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA. /// NM_000948 // downstream // 174836 // Hs.1905 // PRL // 5617 // Homo sapiens prolactin (PRL), mRNA. /// ENST00000244745 //	SOX4	SOX4, Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), p22.3
SNP_A-1698575	cgccttctccccttctaatctcagtc[A/G]ctagttgttaccattaattaaccct	A	G	NM_000948 // downstream // 67834 // Hs.1905 // PRL // 5617 // prolactin /// NM_003107 // downstream // 620805 // Hs.357901 // SOX4 // 6659 // SRY (sex determining region Y)-box 4	PRL	PRL , rs10498708, prolactin ,p22.3
SNP_A-1780901	ggatgaagcatttaat[C/G]agtcagggaatagtaa	C	G	NM_000948 // upstream // 27898 // Hs.1905 // PRL // 5617 // Homo sapiens prolactin (PRL), mRNA. /// NM_138574 // upstream // 244177 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// ENST00000306482 // upstream // 2	PRL	PRL, Homo sapiens prolactin (PRL), p22.3
SNP_A-2157065	attgaaaagctaagtc[A/G]aggcactggtgtagaa	A	G	NM_000948 // upstream // 195968 // Hs.1905 // PRL // 5617 // Homo sapiens prolactin (PRL), mRNA. /// NM_138574 // upstream // 76107 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// ENST00000306482 // upstream // 1	PRL	PRL, Homo sapiens prolactin (PRL), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1949651	ttatttatttttttaj[A/G]catggcagctttcaga	A	G	NM_000948 // upstream // 221619 // Hs.1905 // PRL // 5617 // Homo sapiens prolactin (PRL), mRNA. /// NM_138574 // upstream // 50456 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// ENST00000306482 // upstream // 2	PRL	PRL, Homo sapiens prolactin (PRL), p22.3
SNP_A-1883480	tgaacattgcacaaag[A/G]aaaagccaatgcatca	A	G	NM_138574 // downstream // 87054 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1468736 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_01	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1929488	ttcagttttcctccca[C/T]gctttactcatgactg	C	T	NM_138574 // downstream // 258872 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1296918 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_0	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1835585	tacctatatacagga[A/G]ggatgttacacaattt	A	G	NM_138574 // downstream // 376634 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1179156 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_0	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1985411	acttattagagaaca[C/T]gggtgtccaaaataia	C	T	NM_138574 // downstream // 437555 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 1118235 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_0	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-2230370	ctatattctttatcag[A/G]caccattatcctctgt	A	G	NM_138574 // downstream // 619564 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 936226 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_01	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1985418	attattagtaaaagat[G/T]aatgtgttccaacggc	G	T	NM_138574 // downstream // 808391 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 747399 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_01	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1935707	ttctgtgaaccactga[C/T]gatttctcactgccta	C	T	NM_138574 // downstream // 1046101 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 509689 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_0	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1721451	acatgatcttgcagcaaatcttgaa[A/C]aactctatggaattaac agaacatc	A	C	NM_080723 // upstream // 479475 // Hs.49230 // VMP // 140767 // vesicular membrane protein p24 /// NM_138574 // downstream // 1074983 // Hs.97124 // PWWP1 // 154150 // PWWP domain containing 1	VMP	VMP , rs542063, vesicular membrane protein p24 p22.3
SNP_A-2115506	agggggtcagagagagc[A/G]ccttgaatcactgcca	A	G	NM_138574 // downstream // 1317028 // Hs.97124 // PWWP1 // 154150 // Homo sapiens PWWP domain containing 1 (PWWP1), mRNA. /// NM_080723 // upstream // 238762 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// NM_0	PWWP1	PWWP1, Homo sapiens PWWP domain containing 1 (PWWP1), p22.3
SNP_A-1716787	caaaagcttcacgaagttatagtca[C/T]gagcaggagacagaa atgaggaggaa	C	T	NM_080723 // upstream // 235473 // Hs.49230 // VMP // 140767 // vesicular membrane protein p24 /// NM_138574 // downstream // 1318985 // Hs.97124 // PWWP1 // 154150 // PWWP domain containing 1	VMP	VMP , rs4327688, vesicular membrane protein p24 p22.3
SNP_A-2223511	cggaaaataacacaaa[A/G]tcacgatctatgaaag	A	G	NM_080723 // 3UTR // 0 // Hs.49230 // VMP // 140767 // Homo sapiens vesicular membrane protein p24 (VMP), mRNA. /// ENST00000282902 // 3UTR // 0 // — // — // — // —	VMP	VMP, Homo sapiens vesicular membrane protein p24 (VMP), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1822515	gttttcttggctttg[A/G]atacacctgtgcagat	A	G	NM_170740 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Hom	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding .p22.2
SNP_A-2187877	cagtatatttgtggaa[C/T]gcccagcttccttct	C	T	NM_170740 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Hom	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding .p22.2
SNP_A-1826493	taacaactacttgaga[A/T]tatgtgtgtcagaaag	A	T	NM_170740 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Hom	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding .p22.2
SNP_A-1879192	tcttactccagcttta[C/T]gataacctaagggac	C	T	NM_170740 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Hom	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding p22.2
SNP_A-2267404	gaatagtagaaaaacag[C/G]aagagggtctcgatag	C	G	NM_170740 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // intron // 0 // Hs.371723 // ALDH5A1 // 7915 // Hom	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding .p22.2
SNP_A-1915017	tgttatctagctcca[C/T]gttttttcttttttg	C	T	NM_170740 // downstream // 1704 // Hs.371723 // ALDH5A1 // 7915 // Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding /// NM_001080 // downstream // 1704 // Hs.371723 // ALDH5A1	ALDH5A1	ALDH5A1, Homo sapiens aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), nuclear gene encoding .p22.2
SNP_A-1843088	tagtcaagaaactcaa[A/G]ccaacacgggtatct	A	G	ENST00000259793 // intron // 0 // — // — // —	-	p22.2
SNP_A-2187613	cagtaagttagatggc[G/T]cagagatagattgaa	G	T	NM_018473 // intron // 0 // Hs.9676 // THEM2 // 55856 // Homo sapiens thioesterase superfamily member 2 (THEM2), mRNA. /// ENST00000230048 // intron // 0 // — // — // — // —	THEM2	THEM2, Homo sapiens thioesterase superfamily member 2 (THEM2), p22.2
SNP_A-1835750	tacgatgttgccctaa[C/T]cctcagggagtgtaca	C	T	NM_018473 // intron // 0 // Hs.9676 // THEM2 // 55856 // Homo sapiens thioesterase superfamily member 2 (THEM2), mRNA. /// ENST00000230048 // intron // 0 // — // — // — // —	THEM2	THEM2, Homo sapiens thioesterase superfamily member 2 (THEM2), p22.2
SNP_A-2011650	ccagagccagtactct[C/T]aaccattaagcggaag	C	T	NM_018473 // intron // 0 // Hs.9676 // THEM2 // 55856 // Homo sapiens thioesterase superfamily member 2 (THEM2), mRNA. /// ENST00000230048 // intron // 0 // — // — // — // —	THEM2	THEM2, Homo sapiens thioesterase superfamily member 2 (THEM2), p22.2
SNP_A-2032911	aaataatactctggaa[A/G]gaagtctctgatcacc	A	G	NM_015864 // intron // 0 // Hs.484915 // C6orf32 // 9750 // Homo sapiens chromosome 6 open reading frame 32 (C6orf32), mRNA. /// ENST00000259698 // intron // 0 // — // — // — // — /// ENST00000229635 // intron // 0 // — // — // — // —	C6orf32	C6orf32, Homo sapiens chromosome 6 open reading frame 32 (C6orf32), p22.2
SNP_A-1985479	atgttccagctgtaag[A/G]agaaagcatatccttc	A	G	NM_015864 // upstream // 78215 // Hs.484915 // C6orf32 // 9750 // Homo sapiens chromosome 6 open reading frame 32 (C6orf32), mRNA. /// ENST00000259698 // upstream // 78186 // — // — // — // — /// ENST00000229635 // upstream // 78215 // — // —	C6orf32	C6orf32, Homo sapiens chromosome 6 open reading frame 32 (C6orf32), p22.2
SNP_A-1870611	tcgattaccagttgca[C/T]gtagaattacttttgt	C	T	NM_015864 // upstream // 81083 // Hs.484915 // C6orf32 // 9750 // Homo sapiens chromosome 6 open reading frame 32 (C6orf32), mRNA. /// ENST00000259698 // upstream // 81054 // — // — // — // — /// ENST00000229635 // upstream // 81083 // — // —	C6orf32	C6orf32, Homo sapiens chromosome 6 open reading frame 32 (C6orf32), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2250768	cttatcactgagcaac[A/C]atttgaggagagtcgg	A	C	NM_015864 // upstream // 85231 // Hs.484915 // C6orf32 // 9750 // Homo sapiens chromosome 6 open reading frame 32 (C6orf32), mRNA. /// ENST00000259698 // upstream // 85202 // — // — // — // — /// ENST00000229635 // upstream // 85231 // — // —	C6orf32	C6orf32, Homo sapiens chromosome 6 open reading frame 32 (C6orf32), p22.2
SNP_A-2250582	cttagtggcactgaac[A/C]aacatatttcagtgtc	A	C	ENST00000342007 // downstream // 115931 // — // — // — // — // — /// ENST00000244644 // upstream // 3887 // — // — // — // —	-	p22.2
SNP_A-1707880	ttagttgtattacggtaatcgggca[C/T]atgtcttctaaccttgatgatctca	C	T	BC040903 // intron // 0 // Hs.108412 // LOC340186 // 340186 // hypothetical protein LOC340186	LOC340186	LOC340186 , rs1983579, hypothetical protein LOC340186,p22.2
SNP_A-1809754	gtgaggacttactgta[C/T]actctcatgacttcac	C	T	ENST00000332168 // intron // 0 // — // — // — // —	-	p22.2
SNP_A-1903670	tgggagagtgtgataa[A/G]agcgggtgaggaaagt	A	G	ENST00000332168 // intron // 0 // — // — // — // —	-	p22.2
SNP_A-2087785	actggaagattccaca[A/G]acgttggaaggctagg	A	G	NM_005495 // intron // 0 // Hs.282931 // SLC17A4 // 10050 // Homo sapiens solute carrier family 17 (sodium phosphate), member 4 (SLC17A4), mRNA. /// ENST00000274755 // intron // 0 // — // — // — // —	SLC17A4	SLC17A4, Homo sapiens solute carrier family 17 (sodium phosphate), member 4 (SLC17A4), p22.2
SNP_A-1661151	aatgtgagagactgaatagagagtg[A/G]tctgaacaactaagccagggaatgt	A	G	NM_005074 // upstream // 12949 // Hs.434574 // SLC17A1 // 6568 // solute carrier family 17 (sodium phosphate), member 1 /// NM_005495 // downstream // 63306 // Hs.208556 // SLC17A4 // 10050 // solute carrier family 17 (sodium phosphate), member 4 /// NM_	SLC17A1	SLC17A1 , rs3887266, solute carrier family 17 (sodium phosphate), member 1 ,p22.2
SNP_A-1985518	agcttcacaaacacaa[C/T]tacctgttactaaaat	C	T	NM_006632 // intron // 0 // Hs.327179 // SLC17A3 // 10786 // Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3), mRNA. /// ENST00000358810 // intron // 0 // — // — // — // — /// ENST00000356028 // intron // 0 // — // –	SLC17A3	SLC17A3, Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3), p22.2
SNP_A-1985524	taatcatagcaagcta[A/G]aggcctgaatgatagt	A	G	ENST00000358910 // intron // 0 // — // — // — // —	-	p22.2
SNP_A-2058146	aatcaaacacatgtaa[A/C]aaattcattggttggg	A	C	NM_003545 // upstream // 69018 // Hs.531610 // HIST1H4E // 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 69018 // Hs.143080 // HIST1H4B // 8366 // Homo sapiens histone 1, H4b (HIST1H4B), mRNA. /// NM_021968 // upstream	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-1895062	tgcccaggctggaaaa[A/G]tgtactgttttaaacc	A	G	NM_003545 // upstream // 76943 // Hs.531610 // HIST1H4E // 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 76943 // Hs.143080 // HIST1H4B // 8366 // Homo sapiens histone 1, H4b (HIST1H4B), mRNA. /// NM_021968 // upstream	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-2092012	agaaaccactgaggaa[C/G]gttgaaatgaaaactg	C	G	NM_003545 // upstream // 79584 // Hs.531610 // HIST1H4E // 8367 // Homo sapiens histone 1, H4e (HIST1H4E), mRNA. /// NM_003544 // upstream // 79584 // Hs.143080 // HIST1H4B // 8366 // Homo sapiens histone 1, H4b (HIST1H4B), mRNA. /// NM_021968 // upstream	HIST1H4E	HIST1H4E, Homo sapiens histone 1, H4e (HIST1H4E), p22.1
SNP_A-2215001	cctatgcccaggtaca[C/G]attcaaaacagatgag	C	G	NM_007047 // intron // 0 // Hs.376046 // BTN3A2 // 11118 // Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA. /// ENST00000356386 // intron // 0 // — // — // — // — /// ENST00000317303 // intron // 0 // — // — // — // —	BTN3A2	BTN3A2, Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), p22.1
SNP_A-2105565	agccacaggaaggtta[A/G]agcagaaaaaggactg	A	G	NM_181531 // downstream // 1105 // Hs.373938 // BTN2A2 // 10385 // Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), transcript variant 2, mRNA. /// NM_006995 // downstream // 1105 // Hs.373938 // BTN2A2 // 10385 // Homo sapiens butyrophilin, su	BTN2A2	BTN2A2, Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), transcript variant 2, p22.1
SNP_A-1985528	acaagtttttggttca[A/C]agttctataggtcaga	A	C	NM_007048 // downstream // 202 // Hs.191510 // BTN3A1 // 11119 // Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, mRNA. /// NM_194441 // downstream // 2664 // Hs.191510 // BTN3A1 // 11119 // Homo sapiens butyrophilin, sub	BTN3A1	BTN3A1, Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1790429	ggggcaacctcaacc[A/G]attaagcaaaagagg	A	G	NM_007048 // downstream // 964 // Hs.191510 // BTN3A1 // 11119 // Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, mRNA. /// NM_194441 // downstream // 3426 // Hs.191510 // BTN3A1 // 11119 // Homo sapiens butyrophilin, sub	BTN3A1	BTN3A1, Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, p22.1
SNP_A-2253180	cttctgagaatataat[C/G]aatgcctttcaaggtc	C	G	NM_007048 // downstream // 1219 // Hs.191510 // BTN3A1 // 11119 // Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, mRNA. /// NM_194441 // downstream // 3681 // Hs.191510 // BTN3A1 // 11119 // Homo sapiens butyrophilin, su	BTN3A1	BTN3A1, Homo sapiens butyrophilin, subfamily 3, member A1 (BTN3A1), transcript variant 1, p22.1
SNP_A-2046272	aagagaaagaacttca[A/G]ataaacagtaaagag	A	G	NM_024018 // intron // 0 // Hs.370522 // BTN2A3 // 54718 // Homo sapiens butyrophilin, subfamily 2, member A3 (BTN2A3), mRNA. /// ENST00000244504 // intron // 0 // — // — // — /// ENST00000297020 // intron // 0 // — // — // —	BTN2A3	BTN2A3, Homo sapiens butyrophilin, subfamily 2, member A3 (BTN2A3), p22.1
SNP_A-1715909	agacaagtgtgtctaataaaggga[A/G]tagctacagtggctca gttggtaca	A	G	NM_006994 // intron // 0 // Hs.167741 // BTN3A3 // 10384 // butyrophilin, subfamily 3, member A3	BTN3A3	BTN3A3 , rs3846849, butyrophilin, subfamily 3, member A3,p22.1
SNP_A-1985530	agctatattaccttca[A/C]agactgtagtttattg	A	C	NM_197974 // downstream // 2427 // Hs.167741 // BTN3A3 // 10384 // Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), transcript variant 2, mRNA. /// NM_006994 // downstream // 2427 // Hs.167741 // BTN3A3 // 10384 // Homo sapiens butyrophilin, su	BTN3A3	BTN3A3, Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), transcript variant 2, p22.1
SNP_A-2281320	gagtatggaatctcta[C/T]ctccagccttgaggtc	C	T	NM_007049 // downstream // 2249 // Hs.519635 // BTN2A1 // 11120 // Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, mRNA. /// NM_078476 // downstream // 2249 // Hs.519635 // BTN2A1 // 11120 // Homo sapiens butyrophilin, su	BTN2A1	BTN2A1, Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, p22.1
SNP_A-1985533	ttgacgaaaagtttca[G/T]ccctacctctcaaagt	G	T	NM_007049 // downstream // 4196 // Hs.519635 // BTN2A1 // 11120 // Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, mRNA. /// NM_078476 // downstream // 4196 // Hs.519635 // BTN2A1 // 11120 // Homo sapiens butyrophilin, su	BTN2A1	BTN2A1, Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, p22.1
SNP_A-1906990	tggttgataaaactgta[A/G]gtctggaaaatttaag	A	G	NM_007049 // downstream // 17445 // Hs.519635 // BTN2A1 // 11120 // Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, mRNA. /// NM_078476 // downstream // 17445 // Hs.519635 // BTN2A1 // 11120 // Homo sapiens butyrophilin,	BTN2A1	BTN2A1, Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, p22.1
SNP_A-2217720	cctgatattgagaata[A/T]acacttgagattaga	A	T	NM_001732 // downstream // 26037 // Hs.153058 // BTN1A1 // 696 // Homo sapiens butyrophilin, subfamily 1, member A1 (BTN1A1), mRNA. /// NM_006353 // upstream // 1885 // Hs.236774 // HMGN4 // 10473 // Homo sapiens high mobility group nucleosomal binding do	BTN1A1	BTN1A1, Homo sapiens butyrophilin, subfamily 1, member A1 (BTN1A1), p22.1
SNP_A-1814746	gtgtgtatctgtctcc[C/T]acatttgtaaggtctc	C	T	NM_006353 // intron // 0 // Hs.236774 // HMGN4 // 10473 // Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), mRNA. /// ENST00000328219 // intron // 0 // — // — // —	HMGN4	HMGN4, Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), p22.1
SNP_A-2267664	gaatcacctttcggc[G/T]acggacttagggaagc	G	T	NM_006353 // downstream // 6111 // Hs.236774 // HMGN4 // 10473 // Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), mRNA. /// NM_013375 // upstream // 43907 // Hs.254406 // ABT1 // 29777 // Homo sapiens activator of basal transcriptio	HMGN4	HMGN4, Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), p22.1
SNP_A-1843049	tagtattggcagata[C/G]ataaaacaacttgga	C	G	NM_006353 // downstream // 6653 // Hs.236774 // HMGN4 // 10473 // Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), mRNA. /// NM_013375 // upstream // 43365 // Hs.254406 // ABT1 // 29777 // Homo sapiens activator of basal transcriptio	HMGN4	HMGN4, Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1658660	tgtaatgaatcaataataaatagca[C/T]tgaattaagatgtgacc attttatt	C	T	NM_006353 // downstream // 8717 // Hs.236774 // HMGN4 // 10473 // high mobility group nucleosomal binding domain 4 /// NM_013375 // upstream // 41301 // Hs.254406 // ABT1 // 29777 // activator of basal transcription 1	HMGN4	HMGN4 , rs10484442, high mobility group nucleosomal binding domain 4 ,p22.1
SNP_A-1781673	ggattgggattgttgc[A/G]aaatttgagaaactag	A	G	NM_006353 // downstream // 15324 // Hs.236774 // HMGN4 // 10473 // Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), mRNA. /// NM_013375 // upstream // 34694 // Hs.254406 // ABT1 // 29777 // Homo sapiens activator of basal transcripti	HMGN4	HMGN4, Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), p22.1
SNP_A-2021293	aaaaaaatttgtaata[C/T]gtcctcagtctgctgt	C	T	NM_006353 // downstream // 24594 // Hs.236774 // HMGN4 // 10473 // Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), mRNA. /// NM_013375 // upstream // 25424 // Hs.254406 // ABT1 // 29777 // Homo sapiens activator of basal transcripti	HMGN4	HMGN4, Homo sapiens high mobility group nucleosomal binding domain 4 (HMGN4), p22.1
SNP_A-2204670	ccaggaggaagggaac[C/T]gtaaatcgcacccttt	C	T	NM_013375 // intron // 0 // Hs.254406 // ABT1 // 29777 // Homo sapiens activator of basal transcription 1 (ABT1), mRNA. /// ENST00000274849 // intron // 0 // — // — // — // —	ABT1	ABT1, Homo sapiens activator of basal transcription 1 (ABT1), p22.1
SNP_A-1881021	tcttgttgcatgtttta[A/T]cgtttgtctgggatcc	A	T	NM_021066 // downstream // 70446 // Hs.406691 // HIST1H2AJ // 8331 // Homo sapiens histone 1, H2aj (HIST1H2AJ), mRNA. /// NM_080596 // downstream // 70446 // Hs.352225 // HIST1H2AH // 85235 // Homo sapiens histone 1, H2ah (HIST1H2AH), mRNA. /// NM_005865	HIST1H2AJ	HIST1H2AJ, Homo sapiens histone 1, H2aj (HIST1H2AJ), p22.1
SNP_A-1817270	gttcactaacacaacc[C/T]agaaattggcacctga	C	T	ENST00000323127 // downstream // 6469 // — // — // — // — /// ENST00000289514 // downstream // 33362 // — // — // — // —	-	p22.1
SNP_A-1985538	ttgcttcgtaaaagcc[A/G]ctcactaatacaacat	A	G	ENST00000323127 // downstream // 24313 // — // — // — // — /// ENST00000289514 // downstream // 15518 // — // — // — // —	-	p22.1
SNP_A-2188850	cagtggtcttcagaaa[C/T]cgcttagcagagtggc	C	T	NM_032030 // downstream // 7210 // Hs.326753 // FKSG83 // 83954 // Homo sapiens FKSG83 (FKSG83), mRNA. /// ENST00000327747 // downstream // 7210 // — // — // — // — /// ENST00000359905 // upstream // 55697 // — // — // — // —	FKSG83	FKSG83, Homo sapiens FKSG83 (FKSG83), p22.1
SNP_A-2309504	ggaaacatcaagaaat[C/G]agttgagtttgacctt	C	G	NM_032030 // downstream // 9089 // Hs.326753 // FKSG83 // 83954 // Homo sapiens FKSG83 (FKSG83), mRNA. /// ENST00000327747 // downstream // 9089 // — // — // — // — /// ENST00000359905 // upstream // 53818 // — // — // — // —	FKSG83	FKSG83, Homo sapiens FKSG83 (FKSG83), p22.1
SNP_A-2057298	aatatatcacacacat[C/T]aaaatttcaggtgcag	C	T	NM_032030 // downstream // 16902 // Hs.326753 // FKSG83 // 83954 // Homo sapiens FKSG83 (FKSG83), mRNA. /// ENST00000327747 // downstream // 16902 // — // — // — // — /// ENST00000359905 // upstream // 46005 // — // — // — // —	FKSG83	FKSG83, Homo sapiens FKSG83 (FKSG83), p22.1
SNP_A-1985540	tggcagagatctgaga[A/G]agggtgaggaaaaagt	A	G	NM_007149 // upstream // 92071 // Hs.158174 // ZNF184 // 7738 // Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA. /// NM_003519 // downstream // 242354 // Hs.137594 // HIST1H2BL // 8340 // Homo sapiens histone 1, H2bl (HIST1H2BL), mRNA.	ZNF184	ZNF184, Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), p22.1
SNP_A-2102296	agattaggcctaagag[C/G]agggtataacaccact	C	G	NM_007149 // upstream // 291361 // Hs.158174 // ZNF184 // 7738 // Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA. /// NM_003519 // downstream // 43064 // Hs.137594 // HIST1H2BL // 8340 // Homo sapiens histone 1, H2bl (HIST1H2BL), mRNA.	ZNF184	ZNF184, Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), p22.1
SNP_A-2263504	gaaccacactatctga[A/C]tcaagtgtgagcagtt	A	C	NM_003528 // downstream // 8234 // Hs.2178 // HIST2H2BE // 8349 // Homo sapiens histone 2, H2be (HIST2H2BE), mRNA. /// NM_003522 // downstream // 8234 // Hs.182137 // HIST1H2BF // 8343 // Homo sapiens histone 1, H2bf (HIST1H2BF), mRNA. /// NM_003525 // do	HIST2H2BE	HIST2H2BE, Homo sapiens histone 2, H2be (HIST2H2BE), p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787205	gggaacaagtagcaca[A/G]tgagtgtccacaggct	A	G	NM_005322 // upstream // 4005 // Hs.131956 // HIST1H1B // 3009 // Homo sapiens histone 1, H1b (HIST1H1B), mRNA. /// NM_003534 // downstream // 371 // Hs.247813 // HIST1H3G // 8355 // Homo sapiens histone 1, H3g (HIST1H3G), mRNA. /// NM_003535 // downstrea	HIST1H1B	HIST1H1B, Homo sapiens histone 1, H1b (HIST1H1B), p22.1
SNP_A-2133870	atatctatgtgggtca[A/T]ggaatgaattgcagtg	A	T	ENST00000244491 // downstream // 475 // — // — // — // — /// ENST00000303290 // upstream // 107385 // — // — // — // —	-	p22.1
SNP_A-2275446	gagaattaagtggtga[A/C]ctaaaggataaagtgt	A	C	ENST00000244491 // downstream // 24877 // — // — // — // — /// ENST00000303290 // upstream // 82983 // — // — // — // —	-	p22.1
SNP_A-1941289	ttgctgtgaacctgaa[A/C]gtgctctataaaaaga	A	C	NM_006298 // downstream // 49489 // Hs.57679 // ZNF192 // 7745 // Homo sapiens zinc finger protein 192 (ZNF192), mRNA. /// ENST00000259717 // downstream // 49489 // — // — // — // — /// ENST00000322358 // downstream // 12613 // — // — // — /	ZNF192	ZNF192, Homo sapiens zinc finger protein 192 (ZNF192), p22.1
SNP_A-2201299	ccaataggttctaata[C/T]gcaaagaatgccaaga	C	T	NM_019110 // intron // 0 // Hs.44720 // ZNF307 // 387032 // Homo sapiens zinc finger protein 307 (ZNF307), mRNA. /// ENST00000252221 // intron // 0 // — // — // — // — /// ENST00000356796 // intron // 0 // — // — - // — // —	ZNF307	ZNF307, Homo sapiens zinc finger protein 307 (ZNF307), p22.1
SNP_A-2207283	ccattcctccttgaca[C/T]tggatatgcattcttt	C	T	NM_007160 // upstream // 11912 // Hs.546313 // OR2H2 // 7932 // Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA. /// NM_030883 // upstream // 11912 // Hs.434715 // OR2H1 // 26716 // Homo sapiens olfactory receptor, family 2,	OR2H2	OR2H2, Homo sapiens olfactory receptor, family 2, subfamily H, member 2 (OR2H2), p22.1
SNP_A-1834270	tacatgtagtagttcc[A/C]ctttatcatggttttg	A	C	NM_206812 // intron // 0 // Hs.141308 // MOG // 4340 // Homo sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, mRNA. /// NM_206810 // intron // 0 // Hs.141308 // MOG // 4340 // Homo sapiens myelin oligodendrocyte glycoprotein (MOG),	MOG	MOG, Homo sapiens myelin oligodendrocyte glycoprotein (MOG), transcript variant 5, p22.1
SNP_A-1952037	tttctatgccccttta[C/T]ctctaatgtccctatt	C	T	ENST00000259885 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-1721658	attaatttttaggcagtcccacata[A/C]ggtgttaaaggccaaatg caaggaa	A	C	NM_001470 // upstream // 88794 // Hs.167017 // GABBR1 // 2550 // gamma-aminobutyric acid (GABA) B receptor, 1 /// NM_002116 // upstream // 218624 // Hs.181244 // HLA-A // 3105 // major histocompatibility complex, class I, A /// NM_002127 // upstream // 1	GABBR1	GABBR1 , rs9258170, gamma-aminobutyric acid (GABA) B receptor, 1 ,p22.1
SNP_A-2205105	ccaggtgtcctgtcca[G/T]tctcaggttggtcaca	G	T	NM_018950 // intron // 0 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// ENST00000259951 // intron // 0 // — // — // — // — /// ENST00000342322 // intron // 0 // — // — // — // –	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-2105603	agccaccatgccggcc[A/G]aaaaagcatgtaaact	A	G	NM_018950 // downstream // 5452 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 6519 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, c	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-1819018	gttgcaggtttcccca[A/G]atagagaacatcaata	A	G	NM_018950 // downstream // 8751 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 9818 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, c	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-1807008	gtctcatagttttctg[C/T]atctaaggtaagcgca	C	T	NM_018950 // downstream // 12235 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 13302 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex,	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2312287	ggacatatgatgaaaa[C/T]agggaccacagctgcc	C	T	NM_018950 // downstream // 15891 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 16958 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex,	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-1796187	ggtgtccttagatcac[C/T]ggagttaatagtagca	C	T	NM_018950 // downstream // 20925 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 21992 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex,	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-2092698	agaaatgaaatggaag[A/G]atgatctctttggtaa	A	G	NM_018950 // downstream // 30974 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /// NM_018950 // downstream // 32041 // Hs.519972 // HLA-F // 3134 // Homo sapiens major histocompatibility complex,	HLA-F	HLA-F, Homo sapiens major histocompatibility complex, class I, F (HLA-F), p22.1
SNP_A-1819319	gttggataaagagaag[A/G]attttacaggttggaa	A	G	ENST00000318669 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2222525	cgagggactcagaaga[C/G]ctggaatcagaccccc	C	G	ENST00000293569 // intron // 0 // --- // --- // --- // ---	-	p22.1
SNP_A-2122691	agtggaccatgttctc[A/G]aagtgttgtggttgtc	A	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p22.1
SNP_A-2025602	aaaatgaactaactcc[C/T]aataatttacagtagg	C	T	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p22.1
SNP_A-2302210	gctaaaggctcttatg[A/G]caacttcttaaaataa	A	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p22.1
SNP_A-2169882	caaggcaggcctgtta[C/G]aggaaagtcaggaccc	C	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p22.1
SNP_A-2294141	gcaggcctggtctcta[C/G]aagctccatgtcccga	C	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2272067	gaccctgcctcttggc[A/G]aatttcagaatctggt	A	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1789797	gggctgatccatgatg[C/T]agactggctaacttca	C	T	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2082218	acgagagatgtaagaa[C/T]tgaaggtaccattcct	C	T	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2306363	gctgggctctggcttg[A/T]atctccagaatatctc	A	T	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1929198	ttcaggggtggagtaa[A/C]aggagtctctcagttc	A	C	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2247868	ctgtgatgtaatatca[A/G]tgaaccactcatttcc	A	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2186346	caggctggatgaataa[A/G]aatcctttggcttgga	A	G	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1805077	gtcatgatcccatcct[C/T]aatgcctagacctcag	C	T	NM_002127 // intron // 0 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// ENST00000357252 // intron // 0 // --- // --- // --- // ---	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1780726	ggatccattaaccata[A/G]tagtaaagaaagtcca	A	G	NM_002127 // downstream // 187632 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// NM_002127 // downstream // 8855 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen,	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-1985586	atggtcttcagatcac[A/G]cttttagtagcaagaa	A	G	NM_002127 // downstream // 213139 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), mRNA. /// NM_002127 // downstream // 34362 // Hs.512152 // HLA-G // 3135 // Homo sapiens HLA-G histocompatibility antigen	HLA-G	HLA-G, Homo sapiens HLA-G histocompatibility antigen, class I, G (HLA-G), p21.33
SNP_A-2201632	ccaattttgtgctcaa[C/T]ctctcagtaccagggt	C	T	ENST00000354576 // 5UTR // 0 // --- // --- // --- // ---	-	p21.33
SNP_A-1908239	tgtacctccctattac[A/C]agttccttgacctgcc	A	C	NM_170781 // intron // 0 // Hs.82887 // PPP1R11 // 6992 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), transcript variant 2, mRNA. /// NM_021959 // intron // 0 // Hs.82887 // PPP1R11 // 6992 // Homo sapiens protein pho	PPP1R11	PPP1R11, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), transcript variant 2, p21.33
SNP_A-1904181	tgggccgccgctcatc[A/C]aaatgtgagtaattgt	A	C	NM_170781 // 3UTR // 0 // Hs.82887 // PPP1R11 // 6992 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), transcript variant 2, mRNA. /// NM_021959 // CDS // 0 // Hs.82887 // PPP1R11 // 6992 // Homo sapiens protein phosphat	PPP1R11	PPP1R11, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 11 (PPP1R11), transcript variant 2, p21.33
SNP_A-1849682	tatggtggttgactaa[A/G]atcagaatgaccgggg	A	G	NM_007028 // upstream // 102 // Hs.493275 // TRIM31 // 11074 // Homo sapiens tripartite motif-containing 31 (TRIM31), transcript variant 1, mRNA. /// NM_052816 // upstream // 102 // Hs.493275 // TRIM31 // 11074 // Homo sapiens tripartite motif-containing	TRIM31	TRIM31, Homo sapiens tripartite motif-containing 31 (TRIM31), transcript variant 1, p21.33
SNP_A-2011678	atgggaaggtttgtga[C/T]aaggagctttaaggat	C	T	NM_024839 // downstream // 33050 // Hs.183232 // RPP21 // 79897 // Homo sapiens ribonuclease P 21kDa subunit (RPP21), mRNA. /// ENST00000259862 // downstream // 33050 // --- // --- // --- // --- /// ENST00000334917 // downstream // 33050 // --- // --- //	RPP21	RPP21, Homo sapiens ribonuclease P 21kDa subunit (RPP21), p21.33
SNP_A-2126163	agttttttcaattca[A/G]tctacgaagccagcta	A	G	NM_024839 // downstream // 61817 // Hs.183232 // RPP21 // 79897 // Homo sapiens ribonuclease P 21kDa subunit (RPP21), mRNA. /// ENST00000259862 // downstream // 61817 // --- // --- // --- // --- /// ENST00000334917 // downstream // 61817 // --- // --- //	RPP21	RPP21, Homo sapiens ribonuclease P 21kDa subunit (RPP21), p21.33
SNP_A-2106299	agccctccccagatca[C/T]agccgtctttactatt	C	T	ENST00000329683 // downstream // 433 // --- // --- // --- // --- /// ENST00000316561 // upstream // 68895 // --- // --- // --- // ---	-	p21.33
SNP_A-2204668	ccaggaggaaccgtca[A/C]caggacacacactcat	A	C	ENST00000329683 // downstream // 3014 // --- // --- // --- // --- /// ENST00000316561 // upstream // 66314 // --- // --- // --- // ---	-	p21.33
SNP_A-2306779	gctgtgaatctgtcaa[C/T]cactgggaactggcag	C	T	ENST00000329683 // downstream // 3298 // --- // --- // --- // --- /// ENST00000316561 // upstream // 66030 // --- // --- // --- // ---	-	p21.33
SNP_A-2160421	atttcatctttaacaa[A/C]cttatacacacaaaat	A	C	ENST00000329683 // downstream // 8017 // --- // --- // --- // --- /// ENST00000316561 // upstream // 61311 // --- // --- // --- // ---	-	p21.33
SNP_A-2252536	cttcctggcaaacaac[C/T]acatagaagccttta	C	T	ENST00000329683 // downstream // 32760 // --- // --- // --- // --- /// ENST00000316561 // upstream // 36568 // --- // --- // --- // ---	-	p21.33
SNP_A-2117095	aggtgatcaacttcaa[C/T]atcaacagtggtacat	C	T	ENST00000329683 // downstream // 38092 // --- // --- // --- // --- /// ENST00000316561 // upstream // 31236 // --- // --- // --- // ---	-	p21.33
SNP_A-2270968	gacagttaattaattc[C/T]agggcatatcactgct	C	T	NM_013994 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, mRNA. /// NM_013993 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family,	DDR1	DDR1, Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, p21.33
SNP_A-1834011	tacatatactctctga[G/T]gacagctcaggtcaat	G	T	NM_013994 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, mRNA. /// NM_013993 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family,	DDR1	DDR1, Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, p21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2260001	gaaaagtttcatgcaa[C/T]gtgcagcaaagatgct	C	T	NM_013994 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, mRNA. /// NM_013993 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family,	DDR1	DDR1, Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, p21.33
SNP_A-2267163	gaataatgtttccaga[A/T]gaaagagcaagagcag	A	T	NM_013994 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, mRNA. /// NM_013993 // intron // 0 // Hs.520004 // DDR1 // 780 // Homo sapiens discoidin domain receptor family,	DDR1	DDR1, Homo sapiens discoidin domain receptor family, member 1 (DDR1), transcript variant 3, p21.33
SNP_A-2090405	acttggcagggtttaa[C/T]aaccacatccaaacca	C	T	NM_080870 // downstream // 28052 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 128953 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-1810600	gtgcaactattatcca[C/T]ccagcacaaagcccat	C	T	NM_080870 // downstream // 39928 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 117077 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-1811070	gtgccatagtgtatca[C/T]gtttcctggcccagtc	C	T	NM_080870 // downstream // 44306 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 112699 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2131300	atagagtttctatatg[C/T]cagataatatcttcaa	C	T	NM_080870 // downstream // 45204 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 111801 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-1985604	agctggtcacatctca[C/G]actttcttgccaaaac	C	G	NM_080870 // downstream // 47529 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 109476 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-1790821	gggggcacagatgcca[C/T]gtgaagatcattgtgc	C	T	NM_080870 // downstream // 50473 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 106532 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2213548	ccgtatggcctctcta[A/T]gtgtcttttatcttaa	A	T	NM_080870 // downstream // 51360 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 105645 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-1887257	tgagaagaaaatgccc[C/G]gctacgtccccttct	C	G	NM_080870 // downstream // 100115 // Hs.485071 // DPCR1 // 135656 // Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), mRNA. /// NM_014070 // downstream // 56890 // Hs.272214 // C6orf15 // 29113 // Homo sapiens chromosome 6 open reading fra	DPCR1	DPCR1, Homo sapiens diffuse panbronchiolitis critical region 1 (DPCR1), p21.33
SNP_A-2097929	agagagacccctagaa[C/T]gtttccctcaaggacc	C	T	NM_014068 // 3UTR // 0 // Hs.546515 // PSORS1C1 // 170679 // Homo sapiens psoriasis susceptibility 1 candidate 1 (PSORS1C1), mRNA. /// ENST00000259881 // 3UTR // 0 // — // — // — // —	PSORS1C1	PSORS1C1, Homo sapiens psoriasis susceptibility 1 candidate 1 (PSORS1C1), p21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2200407	ccaaccattagtgtta[A/C]aatttcctgactgatc	A	C	NM_203289 // upstream // 23875 // Hs.249184 // POU5F1 // 5460 // Homo sapiens POU domain, class 5, transcription factor 1 (POU5F1), transcript variant 2, mRNA. /// NM_002701 // upstream // 23875 // Hs.249184 // POU5F1 // 5460 // Homo sapiens POU domain, c	POU5F1	POU5F1, Homo sapiens POU domain, class 5, transcription factor 1 (POU5F1), transcript variant 2, p21.33
SNP_A-2115227	aggggaaagtgaggca[G/T]gaacacacggcacaca	G	T	NM_181717 // downstream // 20448 // Hs.61335 // HCG27 // 253018 // Homo sapiens HLA complex group 27 (HCG27), mRNA. /// NM_002117 // downstream // 44336 // Hs.534125 // HLA-C // 3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mR	HCG27	HCG27, Homo sapiens HLA complex group 27 (HCG27), p21.33
SNP_A-2140943	atctgatatataatca[C/T]catctgtattaagtt	C	T	NM_181717 // downstream // 36709 // Hs.61335 // HCG27 // 253018 // Homo sapiens HLA complex group 27 (HCG27), mRNA. /// NM_002117 // downstream // 28075 // Hs.534125 // HLA-C // 3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mR	HCG27	HCG27, Homo sapiens HLA complex group 27 (HCG27), p21.33
SNP_A-2242624	ctgcagtgctttctta[G/T]ggaaatgacagggcaa	G	T	NM_002117 // upstream // 7212 // Hs.534125 // HLA-C // 3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 75193 // Hs.77961 // HLA-B // 3106 // Homo sapiens major histocompatibility complex, cla	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-2234603	ctccagaacctatgag[A/G]aagctcttatcactca	A	G	NM_002117 // upstream // 26506 // Hs.534125 // HLA-C // 3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 55899 // Hs.77961 // HLA-B // 3106 // Homo sapiens major histocompatibility complex, cl	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-1857537	tcactcatcttagtcc[A/G]cacaagcaaagcaggt	A	G	NM_002117 // upstream // 26532 // Hs.534125 // HLA-C // 3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 55873 // Hs.77961 // HLA-B // 3106 // Homo sapiens major histocompatibility complex, cl	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-1944921	ttgtggcaatttctta[C/T]atagcaatggatagct	C	T	NM_002117 // upstream // 33125 // Hs.534125 // HLA-C // 3107 // Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA. /// NM_005514 // downstream // 49280 // Hs.77961 // HLA-B // 3106 // Homo sapiens major histocompatibility complex, cl	HLA-C	HLA-C, Homo sapiens major histocompatibility complex, class I, C (HLA-C), p21.33
SNP_A-2248558	ctgttacgcactagaa[A/C]tcccgaccctgctc	A	C	NM_004639 // intron // 0 // Hs.440900 // BAT3 // 7917 // Homo sapiens HLA-B associated transcript 3 (BAT3), transcript variant 1, mRNA. /// NM_080703 // intron // 0 // Hs.440900 // BAT3 // 7917 // Homo sapiens HLA-B associated transcript 3 (BAT3), transcr	BAT3	BAT3, Homo sapiens HLA-B associated transcript 3 (BAT3), transcript variant 1, p21.33
SNP_A-2188055	cagtcagcgctacaccg[A/G]agttgaggcagccatt	A	G	NM_181842 // upstream // 13910 // Hs.234027 // ZBTB12 // 221527 // Homo sapiens zinc finger and BTB domain containing 12 (ZBTB12), mRNA. /// NM_000063 // upstream // 11815 // Hs.408903 // C2 // 717 // Homo sapiens complement component 2 (C2), mRNA. /// EN	ZBTB12	ZBTB12, Homo sapiens zinc finger and BTB domain containing 12 (ZBTB12), p21.33
SNP_A-2225939	ctaaattaactacctat[C/T]ggccaagtcctgtctc	C	T	NM_181842 // upstream // 14188 // Hs.234027 // ZBTB12 // 221527 // Homo sapiens zinc finger and BTB domain containing 12 (ZBTB12), mRNA. /// NM_000063 // upstream // 11537 // Hs.408903 // C2 // 717 // Homo sapiens complement component 2 (C2), mRNA. /// EN	ZBTB12	ZBTB12, Homo sapiens zinc finger and BTB domain containing 12 (ZBTB12), p21.33
SNP_A-1869974	tccttgaattggccca[C/G]attggcatctctgc	C	G	NM_004557 // intron // 0 // Hs.436100 // NOTCH4 // 4855 // Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), mRNA. /// ENST00000316427 // intron // 0 // --- // --- // ---	NOTCH4	NOTCH4, Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), p21.32
SNP_A-2182330	cagagtggaagtgggat[A/G]gaaggtcttcagattt	A	G	NM_006781 // intron // 0 // Hs.57692 // C6orf10 // 10665 // Homo sapiens chromosome 6 open reading frame 10 (C6orf10), mRNA. /// ENST00000305725 // intron // 0 // --- // --- // ---	C6orf10	C6orf10, Homo sapiens chromosome 6 open reading frame 10 (C6orf10), p21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1655875	tcagagagagatcaag[A/G]aaaacgaaaaactca	A	G	-		rs2073045, p21.32
SNP_A-1684424	cttaggtctgatcaatctgctccac[A/G]caatttctaggtgatcctct gcatc	A	G	NM_006781 // 5UTR // 0 // Hs.57692 // C6orf10 // 10665 // chromosome 6 open reading frame 10	C6orf10	C6orf10 , rs2050189, chromosome 6 open reading frame 10,p21.32
SNP_A-1701785	ctttgacttctctgtgggatactgc[C/T]agattaactcaacactccc agtaca	C	T	NM_019111 // upstream // 19135 // Hs.409805 // HLA-DRA // 3122 // major histocompatibility complex, class II, DR alpha /// NM_019602 // upstream // 13679 // - // - // -	HLA-DRA	HLA-DRA , rs2213580, major histocompatibility complex, class II, DR alpha ,p21.32
SNP_A-2261465	gaaaggaaataatcaag[C/T]atttggtcagtttctt	G	T	NM_006781 // upstream // 20685 // Hs.57692 // C6orf10 // 10665 // Homo sapiens chromosome 6 open reading frame 10 (C6orf10), mRNA. /// NM_019602 // downstream // 2172 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associa	C6orf10	C6orf10, Homo sapiens chromosome 6 open reading frame 10 (C6orf10), p21.32
SNP_A-1815451	gtgttttccacaaaaa[C/T]gtcatcctggactcta	C	T	NM_006781 // upstream // 22165 // Hs.57692 // C6orf10 // 10665 // Homo sapiens chromosome 6 open reading frame 10 (C6orf10), mRNA. /// NM_019602 // downstream // 692 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associat	C6orf10	C6orf10, Homo sapiens chromosome 6 open reading frame 10 (C6orf10), p21.32
SNP_A-1650978	ttctgaacacaataaactattttgaj[A/T]gatcttgggtggaatttttg gtgtt	A	T	NM_019111 // 3UTR // 0 // Hs.409805 // HLA-DRA // 3122 // major histocompatibility complex, class II, DR alpha	HLA-DRA	HLA-DRA , rs1041885, major histocompatibility complex, class II, DR alpha,p21.32
SNP_A-1985623	gcttctctcttaaa[C/G]gtcccagcagaattct	C	G	NM_019602 // upstream // 8733 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream // 24031 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex,	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1826835	taacagttctcaacac[A/G]atcttgatcaatatc	A	G	NM_019602 // upstream // 10199 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream // 22565 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex,	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1985626	tcataggaactgaatc[C/T]gagttctaactaact	C	T	NM_019602 // upstream // 13408 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream // 19356 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex,	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1860550	tcagttgaatgcctga[C/T]tagcataaagggaac	C	T	NM_019602 // upstream // 21606 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream // 11158 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex,	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-2075637	acatggaatttccacat[A/C]atctggcagttttggg	A	C	NM_019602 // upstream // 21715 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream // 11049 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex,	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-1888575	tgaggattctaagcta[C/G]ggtggacacaacttcc	C	G	NM_019602 // upstream // 24361 // Hs.534471 // BTNL2 // 56244 // Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), mRNA. /// NM_019111 // upstream // 8403 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex,	BTNL2	BTNL2, Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2), p21.32
SNP_A-2238286	ctctggagatgagagal[C/G]aataatatcagattcc	C	G	NM_019111 // intron // 0 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA. /// ENST00000354615 // intron // 0 // — // — // —	HLA-DRA	HLA-DRA, Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), p21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2220563	ccttctgtgggggtca[C/T]gctgggtgaagaatac	C	T	NM_019111 // intron // 0 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA. /// ENST00000354615 // intron // 0 // --- // --- // --- // ---	HLA-DRA	HLA-DRA, Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), p21.32
SNP_A-2073634	acagtcaaacattaaa[A/G]tctctcatcttggctg	A	G	NM_019111 // intron // 0 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA. /// ENST00000354615 // intron // 0 // --- // --- // --- // ---	HLA-DRA	HLA-DRA, Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), p21.32
SNP_A-2112717	aggcagcatactctcc[A/C]agtgtagctttctctt	A	C	NM_019111 // intron // 0 // Hs.520048 // HLA-DRA // 3122 // Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA. /// ENST00000354615 // intron // 0 // --- // --- // --- // ---	HLA-DRA	HLA-DRA, Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), p21.32
SNP_A-2261840	gaaataaactgcataa[A/C]gcaaaaaagtaaaaat	A	C	NM_002125 // downstream // 55479 // Hs.534322 // HLA-DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 1855 // --- // --- // --- // --- /// ENST00000357619 // downstream	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-1944573	ttgtgaaagtctctac[G/T]caaaatctggggactt	G	T	NM_002125 // downstream // 54223 // Hs.534322 // HLA-DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 3111 // --- // --- // --- // --- /// ENST00000357619 // downstream	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-2072098	acagataagaatgttg[A/G]aaaatataaaatatgtg	A	G	NM_002125 // downstream // 54093 // Hs.534322 // HLA-DRB5 // 3127 // Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA. /// ENST00000355324 // upstream // 3241 // --- // --- // --- // --- /// ENST00000357619 // downstream	HLA-DRB5	HLA-DRB5, Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), p21.32
SNP_A-1758454	tagtgaacttccatgcaggccatga[C/T]aggctcatttcaaaagaagcagaaa	C	T	BC031995 // upstream // 20836 // Hs.375115 // HLA-DQB2 // 3120 // major histocompatibility complex, class II, DQ beta 2 /// NM_002120 // downstream // 28413 // Hs.1802 // HLA-DOB // 3112 // major histocompatibility complex, class II, DO beta	HLA-DQB2	HLA-DQB2 , rs719654, major histocompatibility complex, class II, DQ beta 2 ,p21.32
SNP_A-1933954	ttctcaagagatttcc[A/G]gatcttctcatggtaa	A	G	NM_020056 // intron // 0 // Hs.534320 // HLA-DQA2 // 3118 // Homo sapiens major histocompatibility complex, class II, DQ alpha 2 (HLA-DQA2), mRNA. /// ENST00000190839 // intron // 0 // --- // --- // --- // ---	HLA-DQA2	HLA-DQA2, Homo sapiens major histocompatibility complex, class II, DQ alpha 2 (HLA-DQA2), p21.32
SNP_A-1935018	ttctgaggtactccca[C/T]aattactgcttctctt	C	T	NM_002120 // intron // 0 // Hs.1802 // HLA-DOB // 3112 // Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA. /// ENST00000293722 // intron // 0 // --- // --- // --- // ---	HLA-DOB	HLA-DOB, Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB), p21.32
SNP_A-2059814	aatctgtacaacatat[A/G]actgcacctaacactg	A	G	NM_018833 // intron // 0 // Hs.502 // TAP2 // 6891 // Homo sapiens transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) (TAP2), transcript variant 2, mRNA. /// NM_000544 // intron // 0 // Hs.502 // TAP2 // 6891 // Homo sapiens transporter 2, ATP-bi	TAP2	TAP2, Homo sapiens transporter 2, ATP-binding cassette, sub-family B (MDR.p21.32
SNP_A-2229836	ctagttaatggggata[C/T]gcaatttgactgtaga	C	T	NM_002118 // downstream // 32358 // Hs.1162 // HLA-DMB // 3109 // Homo sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA. /// ENST00000357323 // upstream // 22447 // --- // --- // --- // --- /// ENST00000229825 // downstream // 3	HLA-DMB	HLA-DMB, Homo sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), p21.32
SNP_A-2050102	aaggacacagtgcaaa[C/T]accaccaaagcattta	C	T	NM_002119 // 3UTR // 0 // Hs.351874 // HLA-DOA // 3111 // Homo sapiens major histocompatibility complex, class II, DO alpha (HLA-DOA), mRNA. /// ENST00000229829 // 3UTR // 0 // --- // --- // --- // ---	HLA-DOA	HLA-DOA, Homo sapiens major histocompatibility complex, class II, DO alpha (HLA-DOA), p21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1727489	aaaitgtttagatacacaatttgaa[G/T]aaactctgtggtctaactc aaatta	G	T	NM_000544 // upstream // 295940 // Hs.502 // TAP2 // 6891 // transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) /// NM_000593 // upstream // 280711 // Hs.352018 // TAP1 // 6890 // transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) /// N	TAP2	TAP2, rs2395360, transporter 2, ATP-binding cassette, sub-family B (MDR,p21.32
SNP_A-1985655	cccagctgtgtggaccc[C/T]aagatttctcgctctc	C	T	ENST00000308461 // intron // 0 // — // — // — /// ENST00000308384 // intron // 0 // — // — // —	-	p21.32
SNP_A-1850392	tatgtttgaatttgatt[C/G]aggaggagcagttcta	C	G	ENST00000308461 // intron // 0 // — // — // — /// ENST00000308384 // CDS // 0 // — // — // —	-	p21.32
SNP_A-2205583	ccagttcttgcactac[A/G]actgattactaagtta	A	G	ENST00000304890 // intron // 0 // — // — // —	-	p21.32
SNP_A-2154723	attcaaatacggtctc[C/T]aactggtggtggacag	C	T	ENST00000304890 // intron // 0 // — // — // —	-	p21.32
SNP_A-2150633	atgtgattaggtcagc[A/G]gataagggagtattg	A	G	NM_080680 // downstream // 35293 // Hs.390171 // COL11A2 // 1302 // Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA. /// ENST00000304890 // downstream // 8250 // — // — // — /// ENST00000357486 // downstream // 3	COL11A2	COL11A2, Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, p21.32
SNP_A-1904499	tggggaggcgtttctc[A/T]ctgtatgaattattag	A	T	NM_080680 // downstream // 32505 // Hs.390171 // COL11A2 // 1302 // Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA. /// ENST00000304890 // downstream // 11038 // — // — // — /// ENST00000357486 // downstream //	COL11A2	COL11A2, Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, p21.32
SNP_A-2293289	gcagagggtatcatcc[A/G]ggagaaagagtatagg	A	G	NM_080680 // intron // 0 // Hs.390171 // COL11A2 // 1302 // Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA. /// ENST00000357486 // intron // 0 // — // — // — /// ENST00000341947 // intron // 0 // — // — // -	COL11A2	COL11A2, Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, p21.32
SNP_A-1715481	acagaaaataagtgattaaagccaa[G/T]atagtggtctaaggtc aagccaaaa	G	T	NM_022551 // intron // 0 // Hs.275865 // B3GALT4 // 8705 // UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	B3GALT4	B3GALT4, rs466886, UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4,p21.32
SNP_A-1828873	taaggaggaagcaaag[A/G]attgggaataacagtc	A	G	ENST00000311258 // downstream // 21246 // — // — // — /// ENST00000318869 // downstream // 4807 // — // — // —	-	p21.32
SNP_A-1985660	gactaaacaagatgat[G/T]acccaacatgagccag	G	T	ENST00000311258 // downstream // 22859 // — // — // — /// ENST00000318869 // downstream // 3194 // — // — // —	-	p21.32
SNP_A-2039436	aacatattacattccc[A/G]atgccgaactaagcaa	A	G	AB067525 // downstream // 51400 // — // — // 0 // Homo sapiens mRNA for KIAA1938 protein, partial cds. /// NM_152735 // downstream // 51400 // Hs.528028 // ZBTB9 // 221504 // Homo sapiens zinc finger and BTB domain containing 9 (ZBTB9), mRNA. /// NM_0	-	-, Homo sapiens for KIAA1938 protein, partial cds. ,p21.32
SNP_A-1783972	ggccactccagatgta[C/T]agactcagagaaagcc	C	T	AB067525 // downstream // 71314 // — // — // 0 // Homo sapiens mRNA for KIAA1938 protein, partial cds. /// NM_152735 // downstream // 71314 // Hs.528028 // ZBTB9 // 221504 // Homo sapiens zinc finger and BTB domain containing 9 (ZBTB9), mRNA. /// NM_0	-	-, Homo sapiens for KIAA1938 protein, partial cds. ,p21.31
SNP_A-2038264	aacaccagctgcctc[A/G]ctcttttctggaacac	A	G	NM_002224 // intron // 0 // Hs.65758 // ITPR3 // 3710 // Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA. /// ENST00000244411 // intron // 0 // — // — // —	ITPR3	ITPR3, Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), p21.31
SNP_A-1870092	tcctgtacctcaagc[A/G]gcatgaaaaccatttg	A	G	NM_032340 // upstream // 2910 // Hs.93235 // C6orf125 // 84300 // Homo sapiens chromosome 6 open reading frame 125 (C6orf125), mRNA. /// NM_054111 // downstream // 7033 // Hs.17253 // IHPK3 // 117283 // Homo sapiens inositol hexaphosphate kinase 3 (IHPK3)	C6orf125	C6orf125, Homo sapiens chromosome 6 open reading frame 125 (C6orf125), p21.31
SNP_A-2134101	atatgaatcggtcaa[C/T]gtaaccaactggac	C	T	NM_054111 // intron // 0 // Hs.17253 // IHPK3 // 117283 // Homo sapiens inositol hexaphosphate kinase 3 (IHPK3), mRNA. /// ENST00000293756 // intron // 0 // — // — // —	IHPK3	IHPK3, Homo sapiens inositol hexaphosphate kinase 3 (IHPK3), p21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116755	aggtccggaaatctca[A/G]gcaggatagtagggtg	A	G	NM_002418 // upstream // 7171 // Hs.2813 // MLN // 4295 // Homo sapiens motilin (MLN), mRNA. /// NM_000841 // downstream // 210665 // Hs.429018 // GRM4 // 2914 // Homo sapiens glutamate receptor, metabotropic 4 (GRM4), mRNA. /// ENST00000266003 // upstrea	MLN	MLN, Homo sapiens motilin (MLN), p21.31
SNP_A-2251657	cttcaggctccaggag[A/G]aactgcggacacatca	A	G	NM_000841 // intron // 0 // Hs.429018 // GRM4 // 2914 // Homo sapiens glutamate receptor, metabotropic 4 (GRM4), mRNA. /// ENST00000266007 // intron // 0 // — // — // — // —	GRM4	GRM4, Homo sapiens glutamate receptor, metabotropic 4 (GRM4), p21.31
SNP_A-2110325	aggaatccttgcatga[C/T]ggccttctacaaggaa	C	T	NM_017754 // intron // 0 // Hs.42173 // C6orf107 // 54887 // Homo sapiens chromosome 6 open reading frame 107 (C6orf107), mRNA. /// ENST00000266004 // intron // 0 // — // — // — // —	C6orf107	C6orf107, Homo sapiens chromosome 6 open reading frame 107 (C6orf107), p21.31
SNP_A-2137293	atcagtgtgtcttaaa[A/G]catctgcagagttaga	A	G	NM_015245 // intron // 0 // Hs.132639 // ANKS1 // 23294 // Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), mRNA. /// ENST00000353125 // intron // 0 // — // — // — // — /// ENST00000360359 // intron // 0 // — // -	ANKS1	ANKS1, Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1 (ANKS1), p21.31
SNP_A-1905315	tggtaaaaagacatac[A/G]gggtacaacaaatata	A	G	NM_018679 // intron // 0 // Hs.435371 // TCP11 // 6954 // Homo sapiens t-complex 11 (mouse) (TCP11), mRNA. /// ENST00000311875 // intron // 0 // — // — // — // — /// ENST00000244645 // intron // 0 // — // — // — // —	TCP11	TCP11, Homo sapiens t-complex 11 (mouse) (TCP11), p21.31
SNP_A-2051928	aaggtgcgaagacagc[A/G]agtgggctacagtgga	A	G	NM_006238 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, mRNA. /// NM_177435 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens peroxisome proliferat	PPARD	PPARD, Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, p21.31
SNP_A-1843731	tagtgtgctgttagtg[A/G]agattggtctcagatg	A	G	NM_006238 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, mRNA. /// NM_177435 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens peroxisome proliferat	PPARD	PPARD, Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, p21.31
SNP_A-1873190	tctattcttgcataga[C/T]tccagggatgctgtaa	C	T	NM_006238 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, mRNA. /// NM_177435 // intron // 0 // Hs.485196 // PPARD // 5467 // Homo sapiens peroxisome proliferat	PPARD	PPARD, Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, p21.31
SNP_A-2225530	ctaaaagctttcctta[A/C]aaatctcctgaatgct	A	C	NM_004117 // intron // 0 // Hs.407190 // FKBP5 // 2289 // Homo sapiens FK506 binding protein 5 (FKBP5), mRNA. /// ENST00000337746 // intron // 0 // — // — // — // — /// ENST00000357266 // intron // 0 // — // — // — // —	FKBP5	FKBP5, Homo sapiens FK506 binding protein 5 (FKBP5), p21.31
SNP_A-1892335	tgcaagaaactcttaa[C/T]ggtggttatgcctaag	C	T	NM_004117 // intron // 0 // Hs.407190 // FKBP5 // 2289 // Homo sapiens FK506 binding protein 5 (FKBP5), mRNA. /// ENST00000357266 // intron // 0 // — // — // — // —	FKBP5	FKBP5, Homo sapiens FK506 binding protein 5 (FKBP5), p21.31
SNP_A-2280831	gaggtgtcatgggaaa[C/T]acaatttatagccagt	C	T	NM_003137 // intron // 0 // Hs.443861 // SRPK1 // 6732 // Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA. /// ENST00000359706 // intron // 0 // — // — // — // — /// ENST00000359379 // intron // 0 // — // — // — // — /// ENST00000346162 /	SRPK1	SRPK1, Homo sapiens SFRS protein kinase 1 (SRPK1), p21.31
SNP_A-2123085	agtggtagagatggga[C/G]tcaacatgacatctca	C	G	NM_020939 // intron // 0 // Hs.372129 // CPNE5 // 57699 // Homo sapiens copine V (CPNE5), mRNA. /// ENST00000244751 // intron // 0 // — // — // — // —	CPNE5	CPNE5, Homo sapiens copine V (CPNE5), p21.2
SNP_A-2281443	gagtcaggatacgaac[A/C]caagcagttatttggg	A	C	NM_020939 // intron // 0 // Hs.372129 // CPNE5 // 57699 // Homo sapiens copine V (CPNE5), mRNA. /// ENST00000244751 // intron // 0 // — // — // — // —	CPNE5	CPNE5, Homo sapiens copine V (CPNE5), p21.2
SNP_A-1783843	ggccaagacttgtaca[C/T]ggcagaactcccactg	C	T	NM_020939 // intron // 0 // Hs.372129 // CPNE5 // 57699 // Homo sapiens copine V (CPNE5), mRNA. /// ENST00000244751 // intron // 0 // — // — // — // —	CPNE5	CPNE5, Homo sapiens copine V (CPNE5), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044556	aagaaacagaatctag[C/T]cacctggctcctgcc	C	T	NM_020939 // intron // 0 // Hs.372129 // CPNE5 // 57699 // Homo sapiens copine V (CPNE5), mRNA. /// ENST00000244751 // intron // 0 // — // — // — // —	CPNE5	CPNE5, Homo sapiens copine V (CPNE5), p21.2
SNP_A-1802711	gtatgatgacatgaat[A/G]aggaaagaccagaagtga	A	G	NM_014341 // upstream // 5044 // Hs.485262 // MTCH1 // 23787 // Homo sapiens mitochondrial carrier homolog 1 (C. elegans) (MTCH1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_173558 // upstream // 14485 // Hs.509664 // FGD2 // 221472 // Homo	MTCH1	MTCH1, Homo sapiens mitochondrial carrier homolog 1 (C. elegans) (MTCH1), nuclear gene encoding mitochondrial protein, p21.2
SNP_A-2216947	cctctgggcgcctcca[A/G]ctacacacaaagccg	A	G	NM_014341 // upstream // 13668 // Hs.485262 // MTCH1 // 23787 // Homo sapiens mitochondrial carrier homolog 1 (C. elegans) (MTCH1), nuclear gene encoding mitochondrial protein, mRNA. /// NM_173558 // upstream // 5861 // Hs.509664 // FGD2 // 221472 // Homo	MTCH1	MTCH1, Homo sapiens mitochondrial carrier homolog 1 (C. elegans) (MTCH1), nuclear gene encoding mitochondrial protein, p21.2
SNP_A-2178377	cactcatggcaggcaa[C/T]gttccctgtaggcttc	C	T	NM_173558 // intron // 0 // Hs.509664 // FGD2 // 221472 // Homo sapiens FYVE, RhoGEF and PH domain containing 2 (FGD2), mRNA. /// ENST00000274963 // intron // 0 // — // — // — // —	FGD2	FGD2, Homo sapiens FYVE, RhoGEF and PH domain containing 2 (FGD2), p21.2
SNP_A-1948987	ttatctccagatctct[A/C]aaatacagaaccgtaa	A	C	NM_002648 // upstream // 39607 // Hs.81170 // PIM1 // 5292 // Homo sapiens pim-1 oncogene (PIM1), mRNA. /// ENST00000310055 // downstream // 38797 // — // — // — // — /// ENST00000259722 // upstream // 39607 // — // — // — // —	PIM1	PIM1, Homo sapiens pim-1 oncogene (PIM1), p21.2
SNP_A-1985703	agttgtacaaaacaga[C/T]cagacataaagagcat	C	T	NM_153487 // downstream // 103317 // Hs.437993 // MDGA1 // 266727 // Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), mRNA. /// ENST00000358069 // upstream // 29269 // — // — // — // — /// ENST00000360753 // upstre	MDGA1	MDGA1, Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), p21.2
SNP_A-2103937	agcactggatgggaaa[C/T]tgtgggccctcctagg	C	T	NM_153487 // downstream // 53022 // Hs.437993 // MDGA1 // 266727 // Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), mRNA. /// ENST00000358069 // upstream // 79564 // — // — // — // — /// ENST00000360753 // upstrea	MDGA1	MDGA1, Homo sapiens MAM domain containing glycosylphosphatidylinositol anchor 1 (MDGA1), p21.2
SNP_A-1691682	agggtcactgaacaaaattagact[C/G]aatcaaagttgtgcatt tgactaca	C	G	NM_152733 // intron // 0 // Hs.159388 // BTBD9 // 114781 // BTB (POZ) domain containing 9	BTBD9	BTBD9, rs9296240, BTB (POZ) domain containing 9,p21.2
SNP_A-1655589	gatttatccccttggaagtatagga[C/G]cagctttcccagagtca tctctgt	C	G	NM_152733 // intron // 0 // Hs.159388 // BTBD9 // 114781 // BTB (POZ) domain containing 9	BTBD9	BTBD9, rs9296241, BTB (POZ) domain containing 9,p21.2
SNP_A-1673492	acccagaaaacagtaaatgtatcaa[A/G]ttaatgcatgccaattt acagtgga	A	G	NM_152733 // intron // 0 // Hs.159388 // BTBD9 // 114781 // BTB (POZ) domain containing 9	BTBD9	BTBD9, rs9296242, BTB (POZ) domain containing 9,p21.2
SNP_A-1985712	cctatcttagagaaca[A/G]tggaaaatatgtgtaag	A	G	NM_152733 // intron // 0 // Hs.116233 // BTBD9 // 114781 // Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // — // — // — // —	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-2172353	caattacacaaccaga[A/G]ctcattaattggttca	A	G	NM_152733 // intron // 0 // Hs.116233 // BTBD9 // 114781 // Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // — // — // — // —	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-2138764	atcccagtgcctaca[A/G]tagtgcctagcacata	A	G	NM_152733 // intron // 0 // Hs.116233 // BTBD9 // 114781 // Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // — // — // — // —	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-2222249	cgacccaactggtctc[A/T]agtttccatctctc	A	T	NM_152733 // intron // 0 // Hs.116233 // BTBD9 // 114781 // Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// ENST00000328403 // intron // 0 // — // — // — // —	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-1849285	tatgcttgtcaaccat[C/T]acttccactatccatc	C	T	NM_152733 // upstream // 50397 // Hs.116233 // BTBD9 // 114781 // Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA. /// NM_006708 // downstream // 27453 // Hs.268849 // GLO1 // 2739 // Homo sapiens glyoxalase I (GLO1), mRNA. /// ENST00000328403 //	BTBD9	BTBD9, Homo sapiens BTB (POZ) domain containing 9 (BTBD9), p21.2
SNP_A-1707221	cacgtgttttggaagtgaaacag[A/G]agagggtgaaaacaat gactatgaa	A	G	NM_001371 // CDS // 0 // Hs.172101 // DNAH8 // 1769 // dynein, axonemal, heavy polypeptide 8	DNAH8	DNAH8, rs874808, dynein, axonemal, heavy polypeptide 8,p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1748223	cataatcagatttttatgttagaacc[A/G]ttctggcagcaatgtgagagatgtgaa	A	G	NM_001371 // intron // 0 // Hs.172101 // DNAH8 // 1769 // dynein, axonemal, heavy polypeptide 8	DNAH8	DNAH8 , rs726108, dynein, axonemal, heavy polypeptide 8,p21.2
SNP_A-2091697	agaaaagcaaagaaga[G/T]gagttaatgcagcttg	G	T	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1676472	caggcattcagtcttgccatcctaa[A/G]aactactttgatcgaaatttatt	A	G	NM_001371 // intron // 0 // Hs.172101 // DNAH8 // 1769 // dynein, axonemal, heavy polypeptide 8	DNAH8	DNAH8 , rs4380739, dynein, axonemal, heavy polypeptide 8,p21.2
SNP_A-1854122	tcaaactctcaagaaa[A/G]gactctgattggtcca	A	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2132354	atagtattgaaccata[C/T]gaaactgttgatatcc	C	T	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2107091	agcgctctgaattcc[A/G]aactcacgtatccaac	A	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1685624	gtattagacctgatagctccaagaa[C/T]gatgatccaacaacc cacatagat	C	T	NM_001371 // intron // 0 // Hs.172101 // DNAH8 // 1769 // dynein, axonemal, heavy polypeptide 8	DNAH8	DNAH8 , rs1332014, dynein, axonemal, heavy polypeptide 8,p21.2
SNP_A-1750425	gctctctttagctgtcatagctaag[C/G]caacaatgatctttggaaactatag	C	G	NM_001371 // intron // 0 // Hs.172101 // DNAH8 // 1769 // dynein, axonemal, heavy polypeptide 8	DNAH8	DNAH8 , rs10484849, dynein, axonemal, heavy polypeptide 8,p21.2
SNP_A-2092051	agaaaccttatgtaca[C/G]agctggaatgggggac	C	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2102996	agcaaagcagtatgat[A/G]acactaaaggatataa	A	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1869759	tccttcagtgttaaag[C/G]caaatctatgttgttc	C	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2269319	gaatttgacaatattc[A/G]ctaaatcttgatctag	A	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-2098434	agagcaagaatttgaa[C/T]acaaagtgatctgact	C	T	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1985729	ccctaacgcagtccga[C/T]tgtagcaacttcagct	C	T	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2
SNP_A-1783561	ggcatgagagtttttca[A/G]agtcagcattctagct	A	G	NM_001371 // intron // 0 // Hs.520106 // DNAH8 // 1769 // Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), mRNA /// ENST00000359357 // intron // 0 // --- // --- // --- /// ENST00000355261 // intron // 0 // --- // --- // ---	DNAH8	DNAH8, Homo sapiens dynein, axonemal, heavy polypeptide 8 (DNAH8), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2179931	cactttctgcacaaa[C/T]ttatgttccagagaa	C	T	NM_003740 // upstream // 42039 // Hs.444448 // KCNK5 // 8645 // Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), mRNA. /// NM_003740 // upstream // 42014 // Hs.444448 // KCNK5 // 8645 // Homo sapiens potassium channel, subfamily K, member 5	KCNK5	KCNK5, Homo sapiens potassium channel, subfamily K, member 5 (KCNK5), p21.2
SNP_A-1802524	gtatctaagcacagac[C/T]gtaggccagcaagagt	C	T	NM_145027 // intron // 0 // Hs.434296 // C6orf102 // 221458 // Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // — // — // — // — /// ENST00000287152 // intron // 0 // — // — // —	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-2112883	aggcatcactgaattat[A/G]ctatgttcttggcagc	A	G	NM_145027 // intron // 0 // Hs.434296 // C6orf102 // 221458 // Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // — // — // — // — /// ENST00000287152 // intron // 0 // — // — // —	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-1985738	gttggaaccatcgtat[A/G]aggcttgccactatc	A	G	NM_145027 // intron // 0 // Hs.434296 // C6orf102 // 221458 // Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // — // — // — // — /// ENST00000287152 // intron // 0 // — // — // —	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-1930307	ttcatttactagttccg[G/T]catgcagtattgggct	G	T	NM_145027 // intron // 0 // Hs.434296 // C6orf102 // 221458 // Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // — // — // — // — /// ENST00000287152 // intron // 0 // — // — // —	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-1809960	gtgagttatcacattat[A/T]cacatctttattggtg	A	T	NM_145027 // intron // 0 // Hs.434296 // C6orf102 // 221458 // Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // — // — // — // — /// ENST00000287152 // intron // 0 // — // — // —	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-1799754	gtacaaatgaaatcca[A/C]ggctgttctatgatag	A	C	NM_145027 // intron // 0 // Hs.434296 // C6orf102 // 221458 // Homo sapiens chromosome 6 open reading frame 102 (C6orf102), mRNA. /// ENST00000297170 // intron // 0 // — // — // — // — /// ENST00000287152 // intron // 0 // — // — // —	C6orf102	C6orf102, Homo sapiens chromosome 6 open reading frame 102 (C6orf102), p21.2
SNP_A-2190744	catagaacctagcaga[A/G]cagaaaggagaaggaa	A	G	NM_015345 // downstream // 379803 // Hs.436590 // DAAM2 // 23500 // Homo sapiens dishevelled associated activator of morphogenesis 2 (DAAM2), mRNA. /// NM_005942 // upstream // 350271 // Hs.357128 // MOCS1 // 4337 // Homo sapiens molybdenum cofactor synth	DAAM2	DAAM2, Homo sapiens dishevelled associated activator of morphogenesis 2 (DAAM2), p21.2
SNP_A-2138812	atcccctgcagtaga[C/T]ggttgacatttaaag	C	T	NM_015345 // downstream // 428738 // Hs.436590 // DAAM2 // 23500 // Homo sapiens dishevelled associated activator of morphogenesis 2 (DAAM2), mRNA. /// NM_005942 // upstream // 399206 // Hs.357128 // MOCS1 // 4337 // Homo sapiens molybdenum cofactor synth	DAAM2	DAAM2, Homo sapiens dishevelled associated activator of morphogenesis 2 (DAAM2), p21.2
SNP_A-1870085	tccttggtcagagccc[A/G]gatcaaaatgaacctg	A	G	ENST00000359835 // intron // 0 // — // — // — // — /// ENST00000338305 // intron // 0 // — // — // —	-	p21.2
SNP_A-2210914	ccccttaggtacaga[C/T]gtgctctatccctgg	C	T	NM_173561 // downstream // 315033 // Hs.158357 // UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 // upstream // 124613 // — // — // — // — /// ENST00000338305 // upstream // 124613 // — //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-1816134	gttacccacagaggca[A/C]ccctcacacagggca	A	C	NM_173561 // downstream // 284296 // Hs.158357 // UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 // upstream // 155350 // — // — // — // — /// ENST00000338305 // upstream // 155350 // — //	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-2307261	gcttaccctgtggcc[A/G]gcaatgagccccatct	A	G	NM_173561 // downstream // 76671 // Hs.158357 // UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 // upstream // 362975 // — // — // — // — /// ENST00000338305 // upstream // 362975 // — // -	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138646	atcccactgtccagta[A/C]ctgtgattatcagtgc	A	C	NM_173561 // downstream // 44906 // Hs.158357 // UNC5CL // 222643 // Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), mRNA. /// ENST00000359835 // upstream // 394740 // --- // --- // --- /// ENST00000338305 // upstream // 394740 // --- // -	UNC5CL	UNC5CL, Homo sapiens unc-5 homolog C (C. elegans)-like (UNC5CL), p21.1
SNP_A-2048864	aagccctggacacctc[A/G]cgtttatatcaacaga	A	G	NM_006789 // upstream // 4830 // Hs.546338 // APOBEC2 // 10930 // Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2 (APOBEC2), mRNA. /// ENST00000229949 // downstream // 4307 // --- // --- // --- /// ENST00000244669 //	APOBEC2	APOBEC2, Homo sapiens apolipoprotein B editing enzyme, catalytic polypeptide-like 2 (APOBEC2), p21.1
SNP_A-1985795	gagatggcataatctg[C/G]ataagacagaggtacc	C	G	NM_006789 // intron // 0 // Hs.546338 // APOBEC2 // 10930 // Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2 (APOBEC2), mRNA. /// ENST00000244669 // intron // 0 // --- // --- // --- /// ---	APOBEC2	APOBEC2, Homo sapiens apolipoprotein B editing enzyme, catalytic polypeptide-like 2 (APOBEC2), p21.1
SNP_A-1985797	attttaagcaaggta[A/G]gtgaagtcctgtgcc	A	G	NM_145063 // intron // 0 // Hs.227457 // C6orf130 // 221443 // Homo sapiens chromosome 6 open reading frame 130 (C6orf130), mRNA. /// ENST00000244558 // intron // 0 // --- // --- // ---	C6orf130	C6orf130, Homo sapiens chromosome 6 open reading frame 130 (C6orf130), p21.1
SNP_A-2247089	ctgtcaagcgtctacl[A/G]caagctatgggctact	A	G	NM_018965 // intron // 0 // Hs.435295 // TREM2 // 54209 // Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA. /// ENST00000338469 // intron // 0 // --- // --- // --- /// ENST00000211184 // intron // 0 // --- // --- // ---	TREM2	TREM2, Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), p21.1
SNP_A-2217566	cctgagacagaaatgt[G/T]aagcaaagggtgccag	G	T	NM_018965 // upstream // 22123 // Hs.435295 // TREM2 // 54209 // Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA. /// NM_024807 // downstream // 5191 // Hs.164797 // TREML2 // 79865 // Homo sapiens triggering receptor expressed	TREM2	TREM2, Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), p21.1
SNP_A-1796201	ggtgtctgggttgtca[A/G]atgtcaaaggggagg	A	G	NM_018965 // upstream // 22324 // Hs.435295 // TREM2 // 54209 // Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA. /// NM_024807 // downstream // 4990 // Hs.164797 // TREML2 // 79865 // Homo sapiens triggering receptor expressed	TREM2	TREM2, Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), p21.1
SNP_A-2025116	aaaatacggacttgaa[G/T]ggcccagttcaattca	G	T	NM_018965 // upstream // 22708 // Hs.435295 // TREM2 // 54209 // Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA. /// NM_024807 // downstream // 4606 // Hs.164797 // TREML2 // 79865 // Homo sapiens triggering receptor expressed	TREM2	TREM2, Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), p21.1
SNP_A-2277639	gagcacttacactctc[A/G]ctaatatctattacat	A	G	NM_004828 // downstream // 106795 // Hs.194721 // NCR2 // 9436 // Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), mRNA. /// NM_138457 // upstream // 88754 // Hs.131436 // FOXP4 // 116113 // Homo sapiens forkhead box P4 (FOXP4), mRNA. /// E	NCR2	NCR2, Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), p21.1
SNP_A-2270063	gacacaccggtgagca[C/G]aaaagaaagtatacc	C	G	NM_138572 // intron // 0 // Hs.520122 // TBN // 129685 // Homo sapiens taube nuss homolog (mouse) (TBN), mRNA. /// ENST00000320973 // intron // 0 // --- // --- // ---	TBN	TBN, Homo sapiens taube nuss homolog (mouse) (TBN), p21.1
SNP_A-1789027	gggcaccttgcaaacc[A/C]agctggtcatccagtt	A	C	ENST00000356542 // intron // 0 // --- // --- // ---	-	p21.1
SNP_A-1652702	attgctttacaaacttacaggaata[A/G]acatagtgttgtaaaac atttag	A	G	NM_018415 // intron // 0 // Hs.50102 // TRERF1 // 55809 // transcriptional regulating factor 1 /// NM_033501 // intron // 0 // Hs.50102 // TRERF1 // 55809 // transcriptional regulating factor 1 /// NM_033502 // intron // 0 // Hs.50102 // TRERF1 // 55809	TRERF1	TRERF1, rs489743, transcriptional regulating factor 1 ,p21.1
SNP_A-1692174	tgccagaagatactgtatttataaa[A/G]acatgatctatataatg catatgc	A	G	NM_018415 // intron // 0 // Hs.50102 // TRERF1 // 55809 // transcriptional regulating factor 1 /// NM_033501 // intron // 0 // Hs.50102 // TRERF1 // 55809 // transcriptional regulating factor 1 /// NM_033502 // intron // 0 // Hs.50102 // TRERF1 // 55809	TRERF1	TRERF1, rs260225, transcriptional regulating factor 1 ,p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2029481	aaagaccaagtggaaa[A/G]agatgcttcagctgtt	A	G	NM_018415 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating fact	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-2245052	ctggccaaatatcaat[A/G]agcatcattcttatca	A	G	NM_018415 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating fact	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-2072803	acagctgaatcacacc[A/G]aagtacaggcactggg	A	G	NM_018415 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating fact	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-2112281	aggattttcattctgc[C/G]gaggatctgttcatgg	C	G	NM_018415 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating fact	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-1985819	gcccagtgctactaag[A/G]ctctgctaggatatct	A	G	NM_018415 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating fact	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-2247765	ctgtgactttgttggc[A/G]ccccattgtgtgatgg	A	G	NM_018415 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, mRNA. /// NM_033501 // intron // 0 // Hs.485392 // TRERF1 // 55809 // Homo sapiens transcriptional regulating fact	TRERF1	TRERF1, Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 3, p21.1
SNP_A-1843223	tagtcctaatgataaa[A/G]catgtgtgaaaaacag	A	G	NM_014345 // intron // 0 // Hs.509718 // ZNF318 // 24149 // Homo sapiens zinc finger protein 318 (ZNF318), mRNA. /// ENST00000318149 // intron // 0 // — // — // — // — /// ENST00000355402 // intron // 0 // — // — // — // — /// ENST00000304	ZNF318	ZNF318, Homo sapiens zinc finger protein 318 (ZNF318), p21.1
SNP_A-2011747	cttacaactcactaaa[C/T]tggggcagggatggct	C	T	NM_003376 // downstream // 6537 // Hs.73793 // VEGF // 7422 // Homo sapiens vascular endothelial growth factor (VEGF), mRNA. /// ENST00000324450 // downstream // 6537 // — // — // — // — /// ENST00000356655 // downstream // 4657 // — // — // -	VEGF	VEGF, Homo sapiens vascular endothelial growth factor (VEGF), p21.1
SNP_A-1823971	taaaattggctgtatt[A/G]aaatatgacgtagggt	A	G	NM_153246 // downstream // 65936 // Hs.531926 // MGC45491 // 221416 // Homo sapiens hypothetical protein MGC45491 (MGC45491), mRNA. /// NM_032111 // downstream // 42610 // Hs.311190 // MRPL14 // 64928 // Homo sapiens mitochondrial ribosomal protein L14 (M	MGC45491	MGC45491, Homo sapiens hypothetical protein MGC45491 (MGC45491), p21.1
SNP_A-1722400	taaatacctcagaactcacatgcaa[G/T]tattgacatagaggac atctttggc	G	T	NM_145026 // intron // 0 // Hs.135283 // SPATS1 // 221409 // spermatogenesis associated, serine-rich 1	SPATS1	SPATS1 , rs950230, spermatogenesis associated, serine-rich 1,p21.1
SNP_A-1919346	ttaagagtaaggctcc[A/G]acttctgtttccaaga	A	G	NM_001253 // downstream // 28360 // Hs.485471 // CDC5L // 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream // 454400 // Hs.368325 // SUPT3H // 8464 // Homo sapiens suppressor of Ty 3 homolog (S. cer	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-2298495	gcccaagcccacagga[A/C]caacttactcgtcatc	A	C	NM_001253 // downstream // 58666 // Hs.485471 // CDC5L // 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream // 424094 // Hs.368325 // SUPT3H // 8464 // Homo sapiens suppressor of Ty 3 homolog (S. cer	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1930973	ttccaggttctcatca[C/T]gttgggtcagccagta	C	T	NM_001253 // downstream // 107568 // Hs.485471 // CDC5L // 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream // 375192 // Hs.368325 // SUPT3H // 8464 // Homo sapiens suppressor of Ty 3 homolog (S. ce	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-1822347	gttttgtgaggagtaa[A/G]tggatgaatacatgta	A	G	NM_001253 // downstream // 112193 // Hs.485471 // CDC5L // 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream // 370567 // Hs.368325 // SUPT3H // 8464 // Homo sapiens suppressor of Ty 3 homolog (S. ce	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-2065095	aattgcctgttgtctt[C/T]aaatttctgcagtgct	C	T	NM_001253 // downstream // 188677 // Hs.485471 // CDC5L // 988 // Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA. /// NM_181356 // downstream // 294083 // Hs.368325 // SUPT3H // 8464 // Homo sapiens suppressor of Ty 3 homolog (S. ce	CDC5L	CDC5L, Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), p21.1
SNP_A-1791239	gggtaaaatgagaaaa[A/G]tgaatgaacaggctac	A	G	NM_004348 // intron // 0 // Hs.122116 // RUNX2 // 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // intron // 0 // — // — // — // — /// ENST00000352853 // intron // 0 // — // — // — // —	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-2242121	ctgattttggaatggc[A/C]aatgaaatctgcctct	A	C	NM_004348 // downstream // 22545 // Hs.122116 // RUNX2 // 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream // 22545 // — // — // — // — /// ENST00000352853 // downstream // 22633 // — // –	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-1985869	acaaacatggatataa[A/G]ctagtgagatctgtgt	A	G	NM_004348 // downstream // 69738 // Hs.122116 // RUNX2 // 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream // 69738 // — // — // — // — /// ENST00000352853 // downstream // 69826 // — // –	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-1827650	taactggtttttatca[A/C]tctagggtaacttgcc	A	C	NM_004348 // downstream // 197120 // Hs.122116 // RUNX2 // 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream // 197120 // — // — // — // — /// ENST00000352853 // downstream // 197208 // — //	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-2299376	gccctgctctgaatca[C/T]agcccactgacgcagg	C	T	NM_004348 // downstream // 264602 // Hs.122116 // RUNX2 // 860 // Homo sapiens runt-related transcription factor 2 (RUNX2), mRNA. /// ENST00000359524 // downstream // 264602 // — // — // — // — /// ENST00000352853 // downstream // 264690 // --- //	RUNX2	RUNX2, Homo sapiens runt-related transcription factor 2 (RUNX2), p21.1
SNP_A-1939292	ttgatctagtgaacac[A/T]cgacaaggaagtgttg	A	T	BC035968 // intron // 0 // Hs.485489 // CLIC5 // 53405 // Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 // Homo sapiens chloride intracel	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. ,p21.1
SNP_A-1881885	tcttttatgcttttaa[A/G]gattgttgaggatccc	A	G	BC035968 // intron // 0 // Hs.485489 // CLIC5 // 53405 // Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// NM_016929 // intron // 0 // Hs.485489 // CLIC5 // 53405 // Homo sapiens chloride intracel	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1
SNP_A-1985884	aaatgaagtcccattc[C/T]ccagctaccttccaat	C	T	BC035968 // intron // 0 // Hs.485489 // CLIC5 // 53405 // Homo sapiens chloride intracellular channel 5, mRNA (cDNA clone MGC:32580 IMAGE:4611102), complete cds. /// ENST00000185206 // intron // 0 // --- // --- // --- // ---	CLIC5	CLIC5, Homo sapiens chloride intracellular channel 5, (cDNA clone MGC:32580 IMAGE:4611102), complete cds. p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1985890	cagacttgttgagctg[A/G]aatattctgatcattt	A	G	NM_005822 // 3UTR // 0 // Hs.440168 // DSCR1L1 // 10231 // Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA. /// ENST00000306764 // 3UTR // 0 // — // — // — // — /// ENST00000330430 // 3UTR // 0 // — // — // — // —	DSCR1L1	DSCR1L1, Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), p21.1
SNP_A-1985892	ggaagtgaggctatgc[C/G]aagtaaaagtagctat	C	G	NM_005822 // intron // 0 // Hs.440168 // DSCR1L1 // 10231 // Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA. /// ENST00000306764 // intron // 0 // — // — // — // — /// ENST00000330430 // intron // 0 // — // — // — // —	DSCR1L1	DSCR1L1, Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), p12.3
SNP_A-1985894	gaacgtgcagataaca[C/T]gataataatcaaagga	C	T	NM_005822 // intron // 0 // Hs.440168 // DSCR1L1 // 10231 // Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA. /// ENST00000306764 // intron // 0 // — // — // — // — /// ENST00000330430 // intron // 0 // — // — // — // —	DSCR1L1	DSCR1L1, Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), p12.3
SNP_A-1709523	agacaattctagttcagttccatga[G/T]tatttctgcaacagatctagcattt	G	T	NM_014452 // downstream // 154254 // Hs.159651 // TNFRSF21 // 27242 // tumor necrosis factor receptor superfamily, member 21 /// NM_025048 // upstream // 34985 // Hs.287710 // FLJ22684 // 80118 // hypothetical protein FLJ22684	TNFRSF21	TNFRSF21 , rs10498772, tumor necrosis factor receptor superfamily, member 21 ,p12.3
SNP_A-1915729	tgttcttcatgagtaa[C/T]tggtggctaacatggc	C	T	NM_014452 // intron // 0 // Hs.443577 // TNFRSF21 // 27242 // Homo sapiens tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), mRNA. /// ENST00000296861 // intron // 0 // — // — // — // —	TNFRSF21	TNFRSF21, Homo sapiens tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), p12.3
SNP_A-2237070	ctctatttttccagaa[A/G]cctactctgtcacaat	A	G	NM_014452 // upstream // 129636 // Hs.443577 // TNFRSF21 // 27242 // Homo sapiens tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), mRNA. /// NM_012120 // upstream // 38624 // Hs.485518 // CD2AP // 23607 // Homo sapiens CD2-associated prot	TNFRSF21	TNFRSF21, Homo sapiens tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), p12.3
SNP_A-1755638	gcattttcattgctatatgatactc[C/T]aaatggaatcctatgcagacatcat	C	T	NM_000255 // downstream // 1535353 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs2022335, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-2286950	gatggtattgggaacc[A/G]actataggctaggagg	A	G	NM_181744 // downstream // 15577 // Hs.213717 // OPN5 // 221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 15577 // — // — // — // — /// ENST00000244795 // downstream // 38027 // — // — // — // —	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-1685958	ctagataagccacctgtcttctgta[C/T]gtaagccactatgtaaacctaccac	C	T	NM_000255 // downstream // 1519961 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs1536818, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-1662860	ctattcctcattaagtctttaccaa[C/T]tcagtcaatgtcatcactgaccatg	C	T	NM_000255 // downstream // 1519645 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs1576277, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-2232320	ctcaatttcataccac[C/T]gcaaaactatggtaaa	C	T	NM_181744 // downstream // 32910 // Hs.213717 // OPN5 // 221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 32910 // — // — // — // — /// ENST00000244795 // downstream // 20694 // — // — // — // —	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-1806607	gtctaacctacactta[C/G]aacattgcagattaat	C	G	NM_181744 // downstream // 41052 // Hs.213717 // OPN5 // 221391 // Homo sapiens opsin 5 (OPN5), mRNA. /// ENST00000244799 // downstream // 41052 // — // — // — // — /// ENST00000244795 // downstream // 12552 // — // — // — // —	OPN5	OPN5, Homo sapiens opsin 5 (OPN5), p12.3
SNP_A-2076274	acattgaaagccaaag[A/G]ataaaatgttggtagc	A	G	ENST00000341824 // upstream // 28496 // — // — // — // — /// ENST00000332660 // downstream // 1179798 // — // — // — // —	-	p12.3
SNP_A-1865548	tccatgctcatgccta[C/G]aaaaagtcaatattgc	C	G	ENST00000341824 // upstream // 209769 // — // — // — // — /// ENST00000332660 // downstream // 998525 // — // — // — // —	-	p12.3
SNP_A-1898323	tgcttattcataaaga[C/T]gtaggtaagtaggtag	C	T	ENST00000341824 // upstream // 211449 // — // — // — // — /// ENST00000332660 // downstream // 996845 // — // — // — // —	-	p12.3
SNP_A-1723038	ggcactaagaacacattatacaaat[A/G]aagtaaagttaccatgtaataatat	A	G	NM_000255 // downstream // 1004065 // Hs.155212 // MUT // 4594 // methylmalonyl Coenzyme A mutase	MUT	MUT , rs1013401, methylmalonyl Coenzyme A mutase,p12.3
SNP_A-2047370	aagatctatttaggaa[A/G]aacctgacaatatata	A	G	ENST00000341824 // upstream // 324111 // — // — // — // — /// ENST00000332660 // downstream // 884183 // — // — // — // —	-	p12.3
SNP_A-1884878	tgaatcttcctcagta[C/T]cccccatcgtctttgtc	C	T	ENST00000341824 // upstream // 341260 // — // — // — // — /// ENST00000332660 // downstream // 867034 // — // — // — // —	-	p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1928551	ttcactgacagaagta[C/T]gaaagaaagagacatc	C	T	ENST00000341824 // upstream // 375101 // — // — // — // — /// ENST00000332660 // downstream // 833193 // — // — // — // —	-	p12.3
SNP_A-1832976	tacacaacaactcaga[A/G]gtttgcatttgcgatg	A	G	ENST00000341824 // upstream // 395374 // — // — // — // — /// ENST00000332660 // downstream // 812920 // — // — // — // —	-	p12.3
SNP_A-1828646	taagccttgagagtaa[C/T]gtgactatgtggcctg	C	T	ENST00000341824 // upstream // 480538 // — // — // — // — /// ENST00000332660 // downstream // 727756 // — // — // — // —	-	p12.3
SNP_A-1985970	aaatggggtaagtcta[C/T]gcaaactaacttagaa	C	T	ENST00000341824 // upstream // 513847 // — // — // — // — /// ENST00000332660 // downstream // 694447 // — // — // — // —	-	p12.3
SNP_A-2215590	cctcagcctactaaac[C/T]gcttccagtccgaagg	C	T	ENST00000341824 // upstream // 551810 // — // — // — // — /// ENST00000332660 // downstream // 656484 // — // — // — // —	-	p12.3
SNP_A-2146133	atgcctttgaattgga[A/C]agttttgcctacttaa	A	C	NM_000324 // intron // 0 // Hs.120950 // RHAG // 6005 // Homo sapiens Rhesus blood group-associated glycoprotein (RHAG), mRNA. /// ENST00000274818 // intron // 0 // — // — // — // — /// ENST00000229810 // intron // 0 // — // — // — // —	RHAG	RHAG, Homo sapiens Rhesus blood group-associated glycoprotein (RHAG), p12.3
SNP_A-1706109	gaatatcttcttaaaatatccatag[G/T]atttattgtggataactctaaacat	G	T	NM_003296 // intron // 0 // Hs.2042 // CRISP2 // 7180 // cysteine-rich secretory protein 2	CRISP2	CRISP2 , rs360555, cysteine-rich secretory protein 2,p12.3
SNP_A-1823645	taaaatactcagatag[A/G]cgagtgcccacaattc	A	G	NM_000324 // upstream // 33229 // Hs.120950 // RHAG // 6005 // Homo sapiens Rhesus blood group-associated glycoprotein (RHAG), mRNA. /// NM_003296 // downstream // 22291 // Hs.2042 // CRISP2 // 7180 // Homo sapiens cysteine-rich secretory protein 2 (CRISP	RHAG	RHAG, Homo sapiens Rhesus blood group-associated glycoprotein (RHAG), p12.3
SNP_A-1696388	agagacatgtttactcttgagaaac[A/G]ctagagagagttgactggtagtagg	A	G	NM_172238 // upstream // 612093 // Hs.434107 // TFAP2BL1 // 83741 // transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1	TFAP2BL1	TFAP2BL1 , rs10498781, transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1,p12.3
SNP_A-2064705	aattctgcacaattta[C/T]gaacatagtataacaa	C	T	NM_172238 // upstream // 616898 // Hs.434107 // TFAP2D // 83741 // Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1 (TFAP2BL1), mRNA. /// ENST00000322246 // upstream // 52886 // — // — // — // — /// E	TFAP2D	TFAP2D, Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1 (TFAP2BL1), p12.3
SNP_A-2086151	actctgaattacccat[C/G]atgctttaactgttta	C	G	NM_172238 // upstream // 154968 // Hs.434107 // TFAP2D // 83741 // Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1 (TFAP2BL1), mRNA. /// ENST00000322246 // upstream // 514816 // — // — // — // — ///	TFAP2D	TFAP2D, Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1 (TFAP2BL1), p12.3
SNP_A-1851344	tattcattgcctttca[C/T]aaagtttttcttctgt	C	T	NM_172238 // upstream // 47876 // Hs.434107 // TFAP2D // 83741 // Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1 (TFAP2BL1), mRNA. /// ENST00000322246 // upstream // 621908 // — // — // — // — /// E	TFAP2D	TFAP2D, Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta)-like 1 (TFAP2BL1), p12.3
SNP_A-2282701	gagttttcagttgaaa[G/T]tgcatcctatctataa	G	T	ENST00000078131 // upstream // 278180 // — // — // — // — /// ENST00000320956 // downstream // 171324 // — // — // — // —	-	p12.3
SNP_A-1753899	aaaccaatatgagagtttagaagat[C/T]aatatttttcatttttttctattc	C	T	NM_003221 // downstream // 363567 // Hs.33102 // TFAP2B // 7021 // transcription factor AP-2 beta (activating enhancer binding protein 2 beta) /// NM_138694 // downstream // 304903 // Hs.143943 // PKHD1 // 5314 // polycystic kidney and hepatic disease 1	TFAP2B	TFAP2B , rs1327261, transcription factor AP-2 beta (activating enhancer binding protein 2 beta) ,p12.3
SNP_A-2161055	atttctttatcttgtg[C/T]aggaagattccatagt	C	T	ENST00000078131 // upstream // 292407 // — // — // — // — /// ENST00000320956 // downstream // 157097 // — // — // — // —	-	p12.3
SNP_A-1986018	cccagctgatgatgga[A/G]gtgaagtgaaatgaat	A	G	ENST00000078131 // upstream // 350000 // — // — // — // — /// ENST00000320956 // downstream // 99504 // — // — // — // —	-	p12.3
SNP_A-2287869	gattagttcatggaga[C/G]agaggccttgtgaatg	C	G	NM_138694 // downstream // 115690 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // downstream // 115690 // Hs.446118 // PKHD1 // 5314 // Homo	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-1689622	gtagggaagatagcttggcttgaac[A/C]aactttctagtactccaccaagacc	A	C	NM_138694 // intron // 0 // Hs.143943 // PKHD1 // 5314 // polycystic kidney and hepatic disease 1 (autosomal recessive) /// NM_170724 // intron // 0 // Hs.143943 // PKHD1 // 5314 // polycystic kidney and hepatic disease 1 (autosomal recessive)	PKHD1	PKHD1 , rs6921799, polycystic kidney and hepatic disease 1 (autosomal recessive) ,p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2274875	gagaaattgagaaagg[C/T]atcctaacagtattac	C	T	NM_138694 // intron // 0 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-1922698	ttagagatctgttgaa[C/G]gtcatagctgatctgt	C	G	NM_138694 // intron // 0 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2174218	cacactcaccatcttc[A/G]cttcctccattattgc	A	G	NM_138694 // intron // 0 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, mRNA. /// NM_170724 // intron // 0 // Hs.446118 // PKHD1 // 5314 // Homo sapiens polycystic	PKHD1	PKHD1, Homo sapiens polycystic kidney and hepatic disease 1 (autosomal recessive) (PKHD1), transcript variant 1, p12.2
SNP_A-2102541	agattgccattttcac[C/T]gtcccatcctatttaa	C	T	NM_002388 // upstream // 71321 // Hs.179565 // MCM3 // 4172 // Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA. /// NM_133367 // upstream // 6451 // Hs.239388 // C6orf33 // 85315 // Homo sapiens chromosome 6 open read	MCM3	MCM3, Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), p12.2
SNP_A-2170962	caataatcaagctgtg[C/T]atatcttttaaagtac	C	T	NM_133367 // intron // 0 // Hs.239388 // C6orf33 // 85315 // Homo sapiens chromosome 6 open reading frame 33 (C6orf33), mRNA. /// ENST00000304641 // intron // 0 // — // — // — // — /// ENST00000360726 // intron // 0 // — // — // — // —	C6orf33	C6orf33, Homo sapiens chromosome 6 open reading frame 33 (C6orf33), p12.2
SNP_A-2048969	aagcctgaaattcacc[A/G]agtgcagttttaatta	A	G	NM_133367 // intron // 0 // Hs.239388 // C6orf33 // 85315 // Homo sapiens chromosome 6 open reading frame 33 (C6orf33), mRNA. /// ENST00000304641 // intron // 0 // — // — // — // — /// ENST00000360726 // intron // 0 // — // — // — // —	C6orf33	C6orf33, Homo sapiens chromosome 6 open reading frame 33 (C6orf33), p12.2
SNP_A-1668943	acaaaggactattaaatttgtctac[A/G]gcgtactacttggaaca ctgacccc	A	G	NM_018100 // intron // 0 // Hs.446047 // EFHC1 // 114327 // EF-hand domain (C-terminal) containing 1	EFHC1	EFHC1 , rs2038741, EF-hand domain (C-terminal) containing 1,p12.2
SNP_A-2038711	aacagagtaaaaagac[A/T]atctaaagaatgggaa	A	T	NM_018100 // intron // 0 // Hs.403171 // EFHC1 // 114327 // Homo sapiens EF-hand domain (C-terminal) containing 1 (EFHC1), mRNA. /// ENST00000263044 // intron // 0 // — // — // — // —	EFHC1	EFHC1, Homo sapiens EF-hand domain (C-terminal) containing 1 (EFHC1), p12.2
SNP_A-2149741	atgtatgtgtgactca[C/T]ggcaaatctttgagct	C	T	NM_000847 // downstream // 8287 // Hs.102484 // GSTA3 // 2940 // Homo sapiens glutathione S-transferase A3 (GSTA3), mRNA. /// ENST00000327832 // downstream // 4187 // — // — // — // — /// ENST00000211122 // downstream // 8287 // — // — // —	GSTA3	GSTA3, Homo sapiens glutathione S-transferase A3 (GSTA3), p12.2
SNP_A-1986076	tctaaatgagcaaaaa[A/G]ccttgatcacctaggt	A	G	NM_018214 // downstream // 8819 // Hs.485581 // LRRC1 // 55227 // Homo sapiens leucine rich repeat containing 1 (LRRC1), mRNA. /// NM_025168 // downstream // 8819 // Hs.485581 // LRRC1 // 55227 // Homo sapiens leucine rich repeat containing 1 (LRRC1), mRN	LRRC1	LRRC1, Homo sapiens leucine rich repeat containing 1 (LRRC1), p12.1
SNP_A-2235000	ctcccaacttggtgga[C/T]attaactgatcctgta	C	T	NM_138569 // intron // 0 // Hs.485588 // C6orf142 // 90523 // Homo sapiens chromosome 6 open reading frame 142 (C6orf142), mRNA. /// ENST00000358276 // intron // 0 // — // — // — // — /// ENST00000274897 // intron // 0 // — // — // — // —	C6orf142	C6orf142, Homo sapiens chromosome 6 open reading frame 142 (C6orf142), p12.1
SNP_A-1986087	cagaaagtcaaggaaa[A/G]aggccacttctttagg	A	G	NM_138569 // intron // 0 // Hs.485588 // C6orf142 // 90523 // Homo sapiens chromosome 6 open reading frame 142 (C6orf142), mRNA. /// ENST00000358276 // intron // 0 // — // — // — // — /// ENST00000274897 // intron // 0 // — // — // — // —	C6orf142	C6orf142, Homo sapiens chromosome 6 open reading frame 142 (C6orf142), p12.1
SNP_A-1734824	atatgtagagggcaaaaaagggcac[A/C]aagaaaagagtag tcaatgcttcct	A	C	NM_014464 // upstream // 8032 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen /// NM_138569 // downstream // 34241 // Hs.350860 // C6orf142 // 90523 // chromosome 6 open reading frame 142	TINAG	TINAG , rs1316576, tubulointerstitial nephritis antigen ,p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909222	tgtatgatattggaca[A/G]gtctccattatctcag	A	G	NM_014464 // intron // 0 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // intron // 0 // — // — // — /// ENST00000339741 // intron // 0 // — // —, - // — // —	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1712261	tattgaacagcatcaagtgattcta[C/T]attgagaagtaaatgcat gataatg	C	T	NM_001526 // upstream // 587445 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 196759 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs10484980, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1687486	ttggaaaataaaatattggcccata[A/G]agtgcaaaggcaaaa aagttactta	A	G	NM_001526 // upstream // 584877 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 199327 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs10484981, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1642655	agtgcaggattagtggaatatacag[G/T]aaattagaagcaata aaaagcacag	G	T	NM_001526 // upstream // 578589 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 205615 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs10484982, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1748497	tacaggaaattagaagcaataaaaa[A/G]cacagtatatatgtg atgctagaaa	A	G	NM_001526 // upstream // 578569 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 205635 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs10484983, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1986099	acatatgaaagtgtct[A/G]cctaagataggctttt	A	G	NM_014464 // downstream // 146378 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 146378 // — // — // — /// ENST00000339741 // downstream // 146422 // —	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1723116	agcacctacgtattattcttgacc[A/G]attttcctcaactgcagtca tttc	A	G	NM_001526 // upstream // 516490 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 267714 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs1507109, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-2126472	ataaaagtctgtgagc[A/G]ctagaaaaaggaactt	A	G	NM_014464 // downstream // 207817 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 207817 // — // — // — /// ENST00000339741 // downstream // 207861 // —	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1703399	ttgtgacttatcagtgcctagtaca[A/G]taaaaagtatatctgtaatt tatat	A	G	NM_001526 // upstream // 477770 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 306434 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs9296762, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1986102	ttatgtcctgcatcct[A/C]acactataaagcaaga	A	C	NM_014464 // downstream // 251927 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 251927 // — // — // — /// ENST00000339741 // downstream // 251971 // —	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1717981	aaaatagtaacataaaagaaactct[C/G]actcaagaccatttac taggattgt	C	G	NM_001526 // upstream // 469047 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 315157 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs10484991, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-1664698	ttctctaacaaaaaccaacagttaa[A/G]taatagcagaaataaa aattttaa	A	G	NM_001526 // upstream // 414600 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2 /// NM_014464 // downstream // 369604 // Hs.127011 // TINAG // 27283 // tubulointerstitial nephritis antigen	HCRTR2	HCRTR2 , rs10484994, hypocretin (orexin) receptor 2 ,p12.1
SNP_A-2157445	attgagtttctgttat[C/T]gagagcatttgctttt	C	T	NM_014464 // downstream // 339268 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 339268 // — // — // — /// ENST00000339741 // downstream // 339312 // —	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2085561	actccatcattactat[G/T]aaaccctcaggcaaatt	G	T	NM_014464 // downstream // 360924 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 360924 // --- // --- // --- // --- /// ENST00000339741 // downstream // 360968 // ---	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1986108	aagggagatcatatca[A/C]gggagatttgtttatt	A	C	NM_014464 // downstream // 368890 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 368890 // --- // --- // --- // --- /// ENST00000339741 // downstream // 368934 // ---	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1794177	ggtcataacaaatctc[A/G]aaaaactcagaattta	A	G	NM_014464 // downstream // 446774 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 446774 // --- // --- // --- // --- /// ENST00000339741 // downstream // 446818 // ---	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-2298868	gccccaaggaagaaga[C/T]ggcctggtgaaataca	C	T	NM_014464 // downstream // 447732 // Hs.127011 // TINAG // 27283 // Homo sapiens tubulointerstitial nephritis antigen (TINAG), mRNA. /// ENST00000259782 // downstream // 447732 // --- // --- // --- // --- /// ENST00000339741 // downstream // 447776 // ---	TINAG	TINAG, Homo sapiens tubulointerstitial nephritis antigen (TINAG), p12.1
SNP_A-1959835	ttttgtatatgttcca[A/G]taagtcaacaaaaata	A	G	NM_001526 // intron // 0 // Hs.151624 // HCRTR2 // 3062 // Homo sapiens hypocretin (orexin) receptor 2 (HCRTR2), mRNA. /// ENST00000259784 // intron // 0 // --- // --- // --- // ---	HCRTR2	HCRTR2, Homo sapiens hypocretin (orexin) receptor 2 (HCRTR2), p12.1
SNP_A-1742599	gttaaagagtctgggatttcaagaa[C/T]tgtatttaagtgtattgccacacca	C	T	NM_001526 // downstream // 143519 // Hs.151624 // HCRTR2 // 3062 // hypocretin (orexin) receptor 2	HCRTR2	HCRTR2 , rs10498805, hypocretin (orexin) receptor 2,p12.1
SNP_A-2119491	agtatcatgtggaaga[C/T]gttaaaaatgcaaatt	C	T	NM_207410 // downstream // 10250 // Hs.526967 // UNQ9356 // 389400 // Homo sapiens IVFI9356 (UNQ9356), mRNA. /// NM_019036 // downstream // 74844 // Hs.147054 // HMGCLL1 // 54511 // Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HM	UNQ9356	UNQ9356, Homo sapiens IVFI9356 (UNQ9356), p12.1
SNP_A-1676858	gaaatttaaagaaaaggatttctaa[A/G]tactctaaaagcaactgagacagct	A	G	AL137605 // upstream // 55837 // Hs.3837 // HMGCLL1 // 54511 // 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 /// NM_021073 // downstream // 120532 // Hs.1104 // BMP5 // 653 // bone morphogenetic protein 5	HMGCLL1	HMGCLL1 , rs4128949, 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 ,p12.1
SNP_A-1907918	tgtaatgaataagata[C/G]ctacatcataaagggg	C	G	NM_019036 // upstream // 91366 // Hs.147054 // HMGCLL1 // 54511 // Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HMGCLL1), mRNA. /// NM_021073 // downstream // 84889 // Hs.296648 // BMP5 // 653 // Homo sapiens bone morphogenetic p	HMGCLL1	HMGCLL1, Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HMGCLL1), p12.1
SNP_A-2073616	acagtatgaatgcaat[A/G]accgaagagcaaagaa	A	G	NM_019036 // upstream // 163270 // Hs.147054 // HMGCLL1 // 54511 // Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HMGCLL1), mRNA. /// NM_021073 // downstream // 12985 // Hs.296648 // BMP5 // 653 // Homo sapiens bone morphogenetic	HMGCLL1	HMGCLL1, Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1 (HMGCLL1), p12.1
SNP_A-1872730	tctagtttgggtacaa[A/C]atttacttcactcact	A	C	NM_021073 // intron // 0 // Hs.296648 // BMP5 // 653 // Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA. /// ENST00000265030 // intron // 0 // --- // --- // --- // ---	BMP5	BMP5, Homo sapiens bone morphogenetic protein 5 (BMP5), p12.1
SNP_A-1986123	tgtgtcttctaaaaag[C/T]cttctaagatttgtgt	C	T	NM_021073 // upstream // 6593 // Hs.296648 // BMP5 // 653 // Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA. /// ENST00000265030 // upstream // 6593 // --- // --- // --- // --- /// ENST00000329561 // downstream // 57617 // --- // --- // --- // ---	BMP5	BMP5, Homo sapiens bone morphogenetic protein 5 (BMP5), p12.1
SNP_A-2139217	atcctctgcctttaag[C/T]ctgctcttctctgcac	C	T	NM_030820 // downstream // 98203 // Hs.47629 // COL21A1 // 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000329561 // upstream // 17764 // --- // --- // --- // --- /// ENST00000244728 // downstream // 98203 // --- // --- //	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1651296	gctttatcttaacatgtgtggggca[A/C]gattaaaggactcctaag cagatat	A	C	NM_030820 // intron // 0 // Hs.408757 // COL21A1 // 81578 // collagen, type XXI, alpha 1	COL21A1	COL21A1 , rs10484724, collagen, type XXI, alpha 1,p12.1
SNP_A-1858503	tcagagccaaagtgga[C/T]ggacaaaggcataaag	C	T	NM_030820 // intron // 0 // Hs.47629 // COL21A1 // 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000244728 // intron // 0 // — // — // — // —	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-1718801	catatgtggaaatagcactagctta[C/T]gagtttatagaagtttata ttttta	C	T	NM_030820 // intron // 0 // Hs.408757 // COL21A1 // 81578 // collagen, type XXI, alpha 1	COL21A1	COL21A1 , rs1925178, collagen, type XXI, alpha 1,p12.1
SNP_A-2159189	atttaaacatactttta[A/G]gatcacttgcactagc	A	G	NM_030820 // intron // 0 // Hs.47629 // COL21A1 // 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000244728 // intron // 0 // — // — // — // —	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-1883082	tgaaatccagtagtca[C/G]tatttttcaattattt	C	G	NM_030820 // intron // 0 // Hs.47629 // COL21A1 // 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// ENST00000244728 // intron // 0 // — // — // — // —	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-2189672	cagttttcatagctcc[A/G]actttggatttcctat	A	G	NM_030820 // upstream // 67148 // Hs.47629 // COL21A1 // 81578 // Homo sapiens collagen, type XXI, alpha 1 (COL21A1), mRNA. /// NM_183380 // downstream // 143304 // Hs.485616 // DST // 667 // Homo sapiens dystonin (DST), transcript variant 1, mRNA. /// NM	COL21A1	COL21A1, Homo sapiens collagen, type XXI, alpha 1 (COL21A1), p12.1
SNP_A-1729067	tgcctagctgctaggtacctcaaga[C/T]taagatctctccttagta gttatag	C	T	NM_015548 // intron // 0 // Hs.443518 // BPAG1 // 667 // bullous pemphigoid antigen 1, 230/240kDa	BPAG1	BPAG1 , rs10484858, bullous pemphigoid antigen 1, 230,p12.1
SNP_A-2269496	gacaaaatgacagaga[A/G]ctagtgatgatttcat	A	G	NM_183380 // intron // 0 // Hs.485616 // DST // 667 // Homo sapiens dystonin (DST), transcript variant 1, mRNA. /// M69225 // intron // 0 // Hs.485616 // DST // 667 // Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds. /// ENST00000312431 // int	DST	DST, Homo sapiens dystonin (DST), transcript variant 1, p12.1
SNP_A-1844559	tataaatttgagatac[A/G]cttttcagaaaaacat	A	G	NM_183380 // intron // 0 // Hs.485616 // DST // 667 // Homo sapiens dystonin (DST), transcript variant 1, mRNA. /// M69225 // intron // 0 // Hs.485616 // DST // 667 // Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds. /// ENST00000312431 // int	DST	DST, Homo sapiens dystonin (DST), transcript variant 1, p12.1
SNP_A-1927812	ttcaaggattggaaaa[C/G]aacagagctgcagtga	C	G	NM_016277 // upstream // 31367 // Hs.485635 // RAB23 // 51715 // Homo sapiens RAB23, member RAS oncogene family (RAB23), transcript variant 1, mRNA. /// NM_183227 // upstream // 31367 // Hs.485635 // RAB23 // 51715 // Homo sapiens RAB23, member RAS oncoge	RAB23	RAB23, Homo sapiens RAB23, member RAS oncogene family (RAB23), transcript variant 1, p12.1
SNP_A-2297582	gccagagtccttctta[C/T]cacttttatcaccctc	C	T	NM_206910 // downstream // 613343 // Hs.229414 // C6orf216 // 375513 // Homo sapiens chromosome 6 open reading frame 216 (C6orf216), transcript variant 3, mRNA. /// NM_206911 // downstream // 613343 // Hs.229414 // C6orf216 // 375513 // Homo sapiens chrom	C6orf216	C6orf216, Homo sapiens chromosome 6 open reading frame 216 (C6orf216), transcript variant 3, p11.2
SNP_A-2141183	atctggggagtaataa[C/T]aaggctcagccactct	C	T	NM_206910 // downstream // 463793 // Hs.229414 // C6orf216 // 375513 // Homo sapiens chromosome 6 open reading frame 216 (C6orf216), transcript variant 3, mRNA. /// NM_206911 // downstream // 463793 // Hs.229414 // C6orf216 // 375513 // Homo sapiens chrom	C6orf216	C6orf216, Homo sapiens chromosome 6 open reading frame 216 (C6orf216), transcript variant 3, p11.2
SNP_A-2045091	aagaagaaatccaaga[C/T]gtagtagtgttggatt	C	T	NM_206910 // downstream // 99967 // Hs.229414 // C6orf216 // 375513 // Homo sapiens chromosome 6 open reading frame 216 (C6orf216), transcript variant 3, mRNA. /// NM_206911 // downstream // 99967 // Hs.229414 // C6orf216 // 375513 // Homo sapiens chromos	C6orf216	C6orf216, Homo sapiens chromosome 6 open reading frame 216 (C6orf216), transcript variant 3, p11.2
SNP_A-1838521	tagaatgctttgtaga[C/T]ctttgggtatataccc	C	T	NM_152688 // intron // 0 // Hs.519794 // KHDRBS2 // 202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // intron // 0 // — // — // — // —	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2226340	ctaagaagtcaatatt[A/G]aaaaggcaacccaat	A	G	NM_152688 // upstream // 46757 // Hs.519794 // KHDRBS2 // 202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 46757 // — // — // — /// ENST00000336170	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2159866	atttataggatacaga[A/G]caaiatttcaatacat	A	G	NM_152688 // upstream // 121553 // Hs.519794 // KHDRBS2 // 202559 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), mRNA. /// ENST00000281156 // upstream // 121553 // — // — // — // — /// ENST00000335617	KHDRBS2	KHDRBS2, Homo sapiens KH domain containing, RNA binding, signal transduction associated 2 (KHDRBS2), q11.1
SNP_A-2060583	aatgacttaggagaa[A/C]atactggccaggagt	A	C	ENST00000237261 // upstream // 222842 // — // — // — // — /// ENST00000330816 // downstream // 671540 // — // — // — // —	-	q12
SNP_A-1727523	ttatacaatttatagatgagaaca[C/G]ggaagtacagaaaatc aaatagctt	C	G	NM_015153 // downstream // 782526 // Hs.348921 // PHF3 // 23469 // PHD finger protein 3	PHF3	PHF3 , rs10494883, PHD finger protein 3,q12
SNP_A-2252300	cttcctaaacaacat[C/G]aagtcgatgagaaact	C	G	ENST00000237261 // upstream // 753847 // — // — // — // — /// ENST00000330816 // downstream // 140535 // — // — // — // —	-	q12
SNP_A-2149892	atgtcaccattgtaga[A/T]cacagaaaaaagacac	A	T	ENST00000237253 // upstream // 244413 // — // — // — // — /// ENST00000310012 // upstream // 154601 // — // — // — // —	-	q12
SNP_A-1747625	tatctgacatactggctcttaaac[A/C]actcagctagtggcttaa gttctct	A	C	NM_015153 // downstream // 1576106 // Hs.348921 // PHF3 // 23469 // PHD finger protein 3	PHF3	PHF3 , rs10498832, PHD finger protein 3,q12
SNP_A-2072965	acaggacacagctcca[C/G]tgatgcttctagggt	C	G	NM_198283 // intron // 0 // Hs.453441 // EGFL11 // 346007 // Homo sapiens EGF-like-domain, multiple 11 (EGFL11), mRNA. /// ENST00000342421 // intron // 0 // — // — // — // —	EGFL11	EGFL11, Homo sapiens EGF-like-domain, multiple 11 (EGFL11), q12
SNP_A-1951754	tttcggatgcctgcta[A/G]atgttagaggttaaa	A	G	NM_001704 // upstream // 2073868 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 726747 // — // — // — // — /// ENST00000238918 // upstream // 2073868 // — // -	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1892530	tgcaatcaagctaaaa[C/G]ttcaaaattttgtagac	C	G	NM_001704 // upstream // 1708679 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 1091936 // — // — // — // — /// ENST00000238918 // upstream // 1708679 // — // -	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2176537	cacccactcttcagtg[C/G]agcaaagttgtggatg	C	G	NM_001704 // upstream // 1702504 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 1098111 // — // — // — // — /// ENST00000238918 // upstream // 1702504 // — // -	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1671816	agttacataaaacatcaacaattag[A/G]atatttgaaacttatatat aacagt	A	G	NM_015153 // downstream // 3426398 // Hs.348921 // PHF3 // 23469 // PHD finger protein 3	PHF3	PHF3 , rs1901926, PHD finger protein 3,q12
SNP_A-1740897	acataaatcatctgaggagtaatga[A/C]acaactgcagcccag cagaaacttg	A	C	NM_001704 // upstream // 452303 // Hs.334087 // BAI3 // 577 // brain-specific angiogenesis inhibitor 3	BAI3	BAI3 , rs10498860, brain-specific angiogenesis inhibitor 3,q12
SNP_A-2156873	atctttcatggcagaa[C/T]gttaaccaagacatg	C	T	NM_001704 // upstream // 57937 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 2742678 // — // — // — // — /// ENST00000238918 // upstream // 57937 // — // — /	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1808349	gtctttttcaatgcac[A/G]gaagtcctcaattttt	A	G	NM_001704 // upstream // 57066 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000310006 // upstream // 2743549 // — // — // — // — /// ENST00000238918 // upstream // 57066 // — // — /	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2074047	acagtttatttgcttg[A/C]actttaacgtcacta	A	C	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1837824	tacttttggttccaa[A/C]acttccaggagtttgt	A	C	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1986337	atcatcagaggtatcc[A/G]ctgctttgtaaactta	A	G	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207627	ccatttgccataatac[C/T]atccctgatgttgaa	C	T	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2051035	aaggctatgtagaaat[C/G]agttgttgtcagtcca	C	G	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2231832	ctcaaagctgcagaag[A/C]ctaaattgttctccat	A	C	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-2027159	aaacaggtcattactct[A/G]acattggaaagctact	A	G	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1986340	aaattgcaagtatctat[C/T]accatacgtttccaag	C	T	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q12
SNP_A-1814147	gtgtctaatcactcat[A/G]actgctttctaatgtg	A	G	NM_001704 // intron // 0 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// ENST00000238918 // intron // 0 // — // — // —	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q13
SNP_A-1672772	ggaccaggatgtgattgccaattctt[C/T]tccctgaaaccctcttc tcatggt	C	T	NM_001704 // downstream // 86570 // Hs.334087 // BAI3 // 577 // brain-specific angiogenesis inhibitor 3 /// NM_018368 // downstream // 199781 // Hs.439494 // C6orf209 // 55788 // chromosome 6 open reading frame 209	BAI3	BAI3 , rs1410692, brain-specific angiogenesis inhibitor 3 q13
SNP_A-2253743	cttgaaataigctttc[C/T]aaattgtctgctttct	C	T	NM_001704 // downstream // 268325 // Hs.13261 // BAI3 // 577 // Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), mRNA. /// NM_018368 // downstream // 18027 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (	BAI3	BAI3, Homo sapiens brain-specific angiogenesis inhibitor 3 (BAI3), q13
SNP_A-1703151	ctgacaattcagtattagtagatgc[C/G]aggcctgctaccctatt cttgctg	C	G	NM_018368 // intron // 0 // Hs.439494 // C6orf209 // 55788 // chromosome 6 open reading frame 209	C6orf209	C6orf209 , rs3799117, chromosome 6 open reading frame 209,q13
SNP_A-2226000	ctaacaacactgaaaaa[A/C]attgtcagtaaaaca	A	C	NM_018368 // intron // 0 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // — // — // —	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1746406	atttccaactggaaacaaattctta[C/G]ctactaggtctctagag attatct	C	G	NM_018368 // intron // 0 // Hs.439494 // C6orf209 // 55788 // chromosome 6 open reading frame 209	C6orf209	C6orf209, rs2345564, chromosome 6 open reading frame 209,q13
SNP_A-2128647	ataatattataaacga[C/T]gatacctgagaactag	C	T	NM_018368 // intron // 0 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // — // — // —	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-2295865	gcatgggctctgacaa[A/C]catttaacagtatca	A	C	NM_018368 // intron // 0 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // — // — // —	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1930953	ttccagggcttcaaa[A/T]ctcaatcagtataaac	A	T	NM_018368 // intron // 0 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // — // — // —	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1902838	tggctcctgataaccc[C/T]gcttctgtattcacga	C	T	NM_018368 // intron // 0 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // — // — // —	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-2203182	ccactgtcttgattca[C/T]gctaatgcaccagtag	C	T	NM_018368 // intron // 0 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// ENST00000302569 // intron // 0 // — // — // —	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2048977	aagcctgaggaaaaa[A/G]taggatggtcctcct	A	G	NM_018368 // upstream // 1275 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// NM_001858 // upstream // 68285 // Hs.444842 // COL19A1 // 1310 // Homo sapiens collagen, type XIX, alpha 1 (COL19A1),	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1931167	ttccatgtcatctaaa[C/T]aaataaaccatcacaa	C	T	NM_018368 // upstream // 7862 // Hs.271643 // C6orf209 // 55788 // Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA. /// NM_001858 // upstream // 61698 // Hs.444842 // COL19A1 // 1310 // Homo sapiens collagen, type XIX, alpha 1 (COL19A1),	C6orf209	C6orf209, Homo sapiens chromosome 6 open reading frame 209 (C6orf209), q13
SNP_A-1645960	caataattggaaaaatttagtgta[C/T]ctgtctcttaagcttgaggt tgata	C	T	NM_001858 // intron // 0 // Hs.437567 // COL19A1 // 1310 // collagen, type XIX, alpha 1	COL19A1	COL19A1, rs10498870, collagen, type XIX, alpha 1, q13
SNP_A-1986360	accatctttagctgca[C/T]taaggaaaagtcctgc	C	T	NM_001858 // intron // 0 // Hs.444842 // COL19A1 // 1310 // Homo sapiens collagen, type XIX, alpha 1 (COL19A1), mRNA. /// ENST00000322773 // intron // 0 // --- // --- // ---	COL19A1	COL19A1, Homo sapiens collagen, type XIX, alpha 1 (COL19A1), q13
SNP_A-1747493	catgccacttagatcttcttgaga[G/T]accctgctgcagcgagc atagttaa	G	T	NM_021940 // downstream // 265377 // Hs.410882 // SMAP1 // 60682 // stromal membrane-associated protein 1 /// NM_024576 // upstream // 161423 // Hs.16512 // OGFRL1 // 79627 // opioid growth factor receptor-like 1 /// NM_080742 // upstream // 170959 // Hs	SMAP1	SMAP1, rs1207171, stromal membrane-associated protein 1, q13
SNP_A-1801757	gtagtgaaggagaaaac[A/G]aaaggaacataaatca	A	G	NM_021940 // downstream // 231278 // Hs.485717 // SMAP1 // 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream // 136251 // Hs.4273 // B3GAT2 // 135152 // Homo sapiens beta-1,3-glucuronyltransferase 2 (gluc	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-1986390	aggcaatgacacagac[A/G]agtgagaatctgatta	A	G	NM_021940 // downstream // 262394 // Hs.485717 // SMAP1 // 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream // 167367 // Hs.4273 // B3GAT2 // 135152 // Homo sapiens beta-1,3-glucuronyltransferase 2 (gluc	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-2060141	aatgaaaggtgaggaa[A/T]caatgtagaaccagc	A	T	NM_021940 // downstream // 263851 // Hs.485717 // SMAP1 // 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream // 168824 // Hs.4273 // B3GAT2 // 135152 // Homo sapiens beta-1,3-glucuronyltransferase 2 (gluc	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-1943917	ttgtatccagcctaa[C/G]aaagggcctgacatat	C	G	NM_021940 // downstream // 418885 // Hs.485717 // SMAP1 // 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream // 323858 // Hs.4273 // B3GAT2 // 135152 // Homo sapiens beta-1,3-glucuronyltransferase 2 (gluc	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-1822304	gttttgggatgggta[A/C]agactaattcctata	A	C	NM_021940 // downstream // 420102 // Hs.485717 // SMAP1 // 60682 // Homo sapiens stromal membrane-associated protein 1 (SMAP1), mRNA. /// NM_080742 // upstream // 325075 // Hs.4273 // B3GAT2 // 135152 // Homo sapiens beta-1,3-glucuronyltransferase 2 (gluc	SMAP1	SMAP1, Homo sapiens stromal membrane-associated protein 1 (SMAP1), q13
SNP_A-2273613	gactgagcatctcctg[A/C]aagttaactagttgc	A	C	NM_024576 // downstream // 25325 // Hs.16512 // OGFRL1 // 79627 // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA. /// NM_024882 // downstream // 86873 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155	OGFRL1	OGFRL1, Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), q13
SNP_A-1902206	tggccacaactttaaa[C/G]aacagcccacttatag	C	G	NM_024576 // downstream // 29997 // Hs.16512 // OGFRL1 // 79627 // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA. /// NM_024882 // downstream // 82201 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155	OGFRL1	OGFRL1, Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1986394	ctggaagatgcctaca[C/T]gtaaggagtgtgaaga	C	T	NM_024576 // downstream // 31946 // Hs.16512 // OGFRL1 // 79627 // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA. /// NM_024882 // downstream // 80252 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155	OGFRL1	OGFRL1, Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), q13
SNP_A-1805684	gtcccacagacattaa[A/G]agcatggtgtgttta	A	G	NM_024576 // downstream // 44959 // Hs.16512 // OGFRL1 // 79627 // Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA. /// NM_024882 // downstream // 67239 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155	OGFRL1	OGFRL1, Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), q13
SNP_A-2054004	aagttactctcaaata[C/T]gaatccctgaagccaa	C	T	NM_024882 // upstream // 339871 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 126408 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocyto	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-1961402	ttttttgaggaaaaaa[A/T]tctctgactacacag	A	T	NM_024882 // upstream // 397935 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 68344 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytos	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-2024257	aaaagcaggtctaaaa[A/C]ggctacatattatatg	A	C	NM_024882 // upstream // 437098 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 29181 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytos	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-1807370	gtctgacacttctcca[C/T]gttccaagagtaatc	C	T	NM_024882 // upstream // 451193 // Hs.368337 // C6orf155 // 79940 // Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA. /// NM_014989 // upstream // 15086 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytos	C6orf155	C6orf155, Homo sapiens chromosome 6 open reading frame 155 (C6orf155), q13
SNP_A-2075090	acatcctgtgtctaa[A/T]accagactggacgtat	A	T	NM_014989 // intron // 0 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // — // — // — /// ENST00000349908 // intron // 0 // —	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-2147869	atggcctctatatgac[C/G]aaaaccaaagcacact	C	G	NM_014989 // intron // 0 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // — // — // — /// ENST00000349908 // intron // 0 // —	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-1932218	ttcctcctcaagcctat[C/T]agaagtacagcatttc	C	T	NM_014989 // intron // 0 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // — // — // — /// ENST00000349908 // intron // 0 // —	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-1833916	tacataaactatccaa[A/G]tgttcctttaagtta	A	G	NM_014989 // intron // 0 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // — // — // — /// ENST00000349908 // intron // 0 // —	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-1865895	tcccaagtatagccac[A/G]caagaggttcggactt	A	G	NM_014989 // intron // 0 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // — // — // — /// ENST00000349908 // intron // 0 // —	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13
SNP_A-2310268	ggaaccagagggcata[A/G]agatgattagaacata	A	G	NM_014989 // intron // 0 // Hs.485729 // RIMS1 // 22999 // Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, mRNA. /// ENST00000346609 // intron // 0 // — // — // — /// ENST00000349908 // intron // 0 // —	RIMS1	RIMS1, Homo sapiens regulating synaptic membrane exocytosis 1 (RIMS1), transcript variant 1, q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1685806	tttgtgtcatatgaagtcttcaca[A/C]gattaacttagacttcacaa agtta	A	C	NM_014989 // downstream // 142395 // Hs.509841 // RIMS1 // 22999 // regulating synaptic membrane exocytosis 1 /// NM_019842 // upstream // 215737 // Hs.512644 // KCNQ5 // 56479 // potassium voltage-gated channel, KQT-like subfamily, member 5	RIMS1	RIMS1 , rs10485036, regulating synaptic membrane exocytosis 1 ,q13
SNP_A-1703095	taacgcagcactccaattgttttgat[C/T]gccactgtataataggta cgttatt	C	T	NM_014989 // downstream // 195474 // Hs.509841 // RIMS1 // 22999 // regulating synaptic membrane exocytosis 1 /// NM_019842 // upstream // 162658 // Hs.512644 // KCNQ5 // 56479 // potassium voltage-gated channel, KQT-like subfamily, member 5	RIMS1	RIMS1 , rs985564, regulating synaptic membrane exocytosis 1 ,q13
SNP_A-1751853	ttttattaattgtataattgtgaaa[C/T]agtcatcatgctaagtaagct gata	C	T	NM_019842 // intron // 0 // Hs.512644 // KCNQ5 // 56479 // potassium voltage-gated channel, KQT-like subfamily, member 5	KCNQ5	KCNQ5 , rs10485213, potassium voltage-gated channel, KQT-like subfamily, member 5,q13
SNP_A-2163313	atttttaaatcaggt[A/G]aaatcaagtatgaata	A	G	NM_019842 // intron // 0 // Hs.147441 // KCNQ5 // 56479 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // — // — // — // — /// ENST00000355635 // intron // 0 // — /	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-1783384	ggcatacctaagaaaca[A/G]tgggcatatatctgtc	A	G	NM_019842 // intron // 0 // Hs.147441 // KCNQ5 // 56479 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // — // — // — // — /// ENST00000355635 // intron // 0 // — /	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-2158976	attgtatagctatca[A/T]ccattagagtttattt	A	T	NM_019842 // intron // 0 // Hs.147441 // KCNQ5 // 56479 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // — // — // — // — /// ENST00000355635 // intron // 0 // — /	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-1810836	gtgcagggagaaggat[A/G]agctgaatgaggaata	A	G	NM_019842 // intron // 0 // Hs.147441 // KCNQ5 // 56479 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA. /// ENST00000331927 // intron // 0 // — // — // — // — /// ENST00000355635 // intron // 0 // — /	KCNQ5	KCNQ5, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), q13
SNP_A-2155809	attccctagttgttac[C/T]ggccctaagaaatctt	C	T	NM_001000 // upstream // 9937 // Hs.546284 // RPL39 // 6170 // Homo sapiens ribosomal protein L39 (RPL39), mRNA. /// NM_018665 // upstream // 11548 // Hs.125507 // DDX43 // 55510 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 43 (DDX43), mRNA. ///	RPL39	RPL39, Homo sapiens ribosomal protein L39 (RPL39), q13
SNP_A-2043220	aactgcccctgtgaaggt[A/G]cagatattagcattgt	A	G	NM_133645 // intron // 0 // Hs.347614 // MTO1 // 25821 // Homo sapiens mitochondrial translation optimization 1 homolog (S. cerevisiae) (MTO1), mRNA. /// NM_012123 // intron // 0 // Hs.347614 // MTO1 // 25821 // Homo sapiens mitochondrial translation opti	MTO1	MTO1, Homo sapiens mitochondrial translation optimization 1 homolog (S. cerevisiae) (MTO1), q13
SNP_A-1986443	cagggacccgaggcac[A/C]gagcaagtaagtggat	A	C	NM_001402 // upstream // 50377 // Hs.522463 // EEF1A1 // 1915 // Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA. /// NM_001402 // upstream // 49385 // Hs.522463 // EEF1A1 // 1915 // Homo sapiens eukaryotic translation elong	EEF1A1	EEF1A1, Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), q13
SNP_A-1930065	ttcatgtgttataatg[A/G]atgttaccgatggatt	A	G	NM_012434 // intron // 0 // Hs.485760 // SLC17A5 // 26503 // Homo sapiens solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5), mRNA. /// ENST00000311342 // intron // 0 // — // — // — // —	SLC17A5	SLC17A5, Homo sapiens solute carrier family 17 (anion,q13
SNP_A-2086425	actcttgcctgaagcc[C/T]attatttctggataca	C	T	NM_012434 // intron // 0 // Hs.485760 // SLC17A5 // 26503 // Homo sapiens solute carrier family 17 (anion/sugar transporter), member 5 (SLC17A5), mRNA. /// ENST00000311342 // intron // 0 // — // — // — // —	SLC17A5	SLC17A5, Homo sapiens solute carrier family 17 (anion,q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835696	tacctttcactgtaa[C/T]agaaggaacctgatac	C	T	NM_133493 // intron // 0 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// ENST00000287097 // intron // 0 // — // — // — // —	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2269957	gacaatgtgttctagc[A/G]agttagattgcaaag	A	G	NM_133493 // intron // 0 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// ENST00000287097 // intron // 0 // — // — // — // —	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2307780	gcttcctggatgccaa[A/G]tcacttttaaaaaca	A	G	NM_133493 // downstream // 245800 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 1013451 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2185939	caggcacacacaatga[C/G]cacaggcagttaattt	C	G	NM_133493 // downstream // 263728 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 995523 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1743279	aaaaaaattaagtaatttgtagtgc[G/T]atactgggacaggtggtt tacctgg	G	T	NM_004370 // downstream // 912736 // Hs.101302 // COL12A1 // 1303 // collagen, type XII, alpha 1 /// NM_080645 // downstream // 912736 // Hs.101302 // COL12A1 // 1303 // collagen, type XII, alpha 1 /// NM_133493 // downstream // 346518 // Hs.94030 // CD1	COL12A1	COL12A1 , rs9293954, collagen, type XII, alpha 1 q13
SNP_A-1839339	tagagtcttgagtaaa[C/T]acaatgccagaatagg	C	T	NM_133493 // downstream // 317719 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 941532 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1898533	tgcttgacattgagaa[A/G]ttccttccttctctt	A	G	NM_133493 // downstream // 343111 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 916140 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1930550	ttccaagcaatagcca[A/G]tactatcagaaaatcc	A	G	NM_133493 // downstream // 344519 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 914732 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2111436	aggaggatagggcaca[C/G]gtaagagactgaggt	C	G	NM_133493 // downstream // 418850 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 840401 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1961033	ttttggttagacttc[C/T]ctacattgaaggggat	C	T	NM_133493 // downstream // 452557 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 806694 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-2173959	cacacatatcaagtag[C/T]attccaagttacatg	C	T	NM_133493 // downstream // 538044 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 721207 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2026693	aaacaatatttcaaa[C/T]gtcctcaataaaatag	C	T	NM_133493 // downstream // 586045 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 673206 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1811478	gtgctcaggaagaaaac[C/T]gtagaaaccaataata	C	T	NM_133493 // downstream // 656344 // Hs.399891 // CD109 // 135228 // Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), mRNA. /// NM_080645 // downstream // 602907 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (C	CD109	CD109, Homo sapiens CD109 antigen (Gov platelet alloantigens) (CD109), q13
SNP_A-1687604	tgagcctacitttagatatttatc[A/G]caagagagtaaacacttg attatt	A	G	NM_004370 // downstream // 304002 // Hs.101302 // COL12A1 // 1303 // collagen, type XII, alpha 1 /// NM_080645 // downstream // 304002 // Hs.101302 // COL12A1 // 1303 // collagen, type XII, alpha 1 /// NM_133493 // downstream // 955252 // Hs.94030 // CD1	COL12A1	COL12A1, , rs756258, collagen, type XII, alpha 1 q13
SNP_A-1986475	tattcttgggtcatag[A/C]aaataaatgtagaccga	A	C	NM_080645 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, mRNA. /// NM_004370 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (COL12	COL12A1	COL12A1, Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, q13
SNP_A-2036956	aaatttiatcttaccc[A/G]atacatctcaaatacc	A	G	NM_080645 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, mRNA. /// NM_004370 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (COL12	COL12A1	COL12A1, Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, q13
SNP_A-2032975	aaataattaggaaaga[C/T]aacaggtgcaacagac	C	T	NM_080645 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, mRNA. /// NM_004370 // intron // 0 // Hs.101302 // COL12A1 // 1303 // Homo sapiens collagen, type XII, alpha 1 (COL12	COL12A1	COL12A1, Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, q14.1
SNP_A-2124893	agttgacaacatgaac[C/T]ggagacaagaaataaa	C	T	NM_015687 // upstream // 38031 // Hs.526972 // FILIP1 // 27145 // Homo sapiens filamin A interacting protein 1 (FILIP1), mRNA. /// NM_015571 // upstream // 69698 // Hs.485784 // SENP6 // 26054 // Homo sapiens SUMO1/sentrin specific protease 6 (SENP6), mRN	FILIP1	FILIP1, Homo sapiens filamin A interacting protein 1 (FILIP1), q14.1
SNP_A-2238556	ctctgtctcaaaaaag[G/T]agaagagaaaagatac	G	T	NM_015571 // intron // 0 // Hs.485784 // SENP6 // 26054 // Homo sapiens SUMO1/sentrin specific protease 6 (SENP6), mRNA. /// ENST00000355433 // intron // 0 // --- // --- // --- // --- /// ENST00000327284 // intron // 0 // --- // --- // ---	SENP6	SENP6, Homo sapiens SUMO1 q14.1
SNP_A-1836223	tactatctctttaaa[C/T]ttaggagaataaagt	C	T	NM_001563 // upstream // 995 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1388617 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recepto	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1647518	aaatgaaaatggaagcacaatgtaa[C/T]aaaatctctgcaatg cagcaaaggc	C	T	NM_000863 // downstream // 1285451 // Hs.520239 // HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 104161 // Hs.129882 // IMPG1 // 3617 // interphotoreceptor matrix proteoglycan 1	HTR1B	HTR1B, rs1905974, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-2257930	ctttgtatttttccaca[C/G]ccctaacacacagtg	C	G	NM_001563 // upstream // 79151 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1310461 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2070398	acaccatttttataaa[C/G]agatgagcatccatgg	C	G	NM_001563 // upstream // 80194 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1309418 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1721191	ttcccatgtgcctctttccttctct[A/G]cagatttatctttttgcttcactc ag	A	G	NM_000863 // downstream // 1246709 // Hs.520239 // HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 142903 // Hs.129882 // IMPG1 // 3617 // interphotoreceptor matrix proteoglycan 1	HTR1B	HTR1B , rs1976109, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-2310617	ggaagagctatggtga[C/T]gttcaaattgaacag	C	T	NM_001563 // upstream // 119316 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1270296 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1872304	tctagaatctctttca[A/T]cttgcaatactaaaac	A	T	NM_001563 // upstream // 122086 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1267526 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1685654	tcactgacttgcctcatccaataaa[A/G]gtttgttctgagacaat tgggt	A	G	NM_000863 // downstream // 1193644 // Hs.520239 // HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 195968 // Hs.129882 // IMPG1 // 3617 // interphotoreceptor matrix proteoglycan 1	HTR1B	HTR1B , rs9294012, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-2030794	aaagctttgagaatca[C/T]gcacaaaaaattcagg	C	T	NM_001563 // upstream // 135334 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1254278 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2213654	ccgtggatatcctgaa[G/T]gtctgggtttttt	G	T	NM_001563 // upstream // 147229 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1242383 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2250824	cttatctaaagtttca[C/G]aacagtagagtccaa	C	G	NM_001563 // upstream // 150435 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1239177 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2122911	agtggctgacaacaaa[A/G]gtatgaggtgaggga	A	G	NM_001563 // upstream // 154627 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1234985 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1872391	tctagatgagactgac[A/G]aaggagaaagcattga	A	G	NM_001563 // upstream // 176878 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1212734 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1986488	ggcaggtctcacttcc[A/G]cattagctattgactt	A	G	NM_001563 // upstream // 178264 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1211348 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2094620	agaatagccaagtaga[C/T]agaaaaggagtgagaac	C	T	NM_001563 // upstream // 218442 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1171170 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1919407	ttaagatttttgtgaa[A/T]gttaggaagcgttccc	A	T	NM_001563 // upstream // 220098 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1169514 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2155225	attcagggaagggaga[A/G]catcaaccagaatagc	A	G	NM_001563 // upstream // 239643 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1149969 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2271039	gacataagatgtagc[A/G]ataagtagggtcaga	A	G	NM_001563 // upstream // 241462 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1148150 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1929304	ttcagtatttaaacat[G/T]acaagacatgtaacat	G	T	NM_001563 // upstream // 251759 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1137853 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2196083	catgtgaattatgaag[A/G]aaagttatgcaaatgt	A	G	NM_001563 // upstream // 274617 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1114995 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1676828	ttttacatggagttgaaggaattct[C/T]aaaaaaaataagtccagct atagaaa	C	T	NM_000863 // downstream // 1029947 // Hs.520239 // HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 359665 // Hs.129882 // IMPG1 // 3617 // interphotoreceptor matrix proteoglycan 1	HTR1B	HTR1B , rs951993, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-1785144	ggctaaagatacgaat[A/G]acttccaaaaggaaat	A	G	NM_001563 // upstream // 341468 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1048144 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2069134	acaattatcctaatta[C/G]taacaggccgttctgt	C	G	NM_001563 // upstream // 352605 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1037007 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1961052	ttttgtactaaatgc[A/G]cagtgtgaagtctta	A	G	NM_001563 // upstream // 363238 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1026374 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1838900	tagagaaaattaggta[C/T]gattcaagttcttggt	C	T	NM_001563 // upstream // 387452 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 1002160 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) rece	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1831628	taattagcagaaaaaa[C/T]agcaaaggttaagaat	C	T	NM_001563 // upstream // 391533 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 998079 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2250650	cttataactgttaaaa[C/T]tgttgctctgccttat	C	T	NM_001563 // upstream // 394730 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 994882 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1859457	tcaggacataggagca[A/G]ggaaagattttatgat	A	G	NM_001563 // upstream // 410885 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 978727 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1939584	ttgattgggaaagtga[A/T]aaatgtacatgaaatc	A	T	NM_001563 // upstream // 423901 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 965711 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2157434	attgagttaagaaaag[A/G]ataattggtgaagaat	A	G	NM_001563 // upstream // 476782 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 912830 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1705813	ggggataccacagaaataagataaa[C/T]tgtggtatgagatag gtggggaata	C	T	NM_000863 // downstream // 564094 // Hs.520239 // HTR1B // 3351 // 5-hydroxytryptamine (serotonin) receptor 1B /// NM_001563 // upstream // 825518 // Hs.129882 // IMPG1 // 3617 // interphotoreceptor matrix proteoglycan 1	HTR1B	HTR1B , rs5012256, 5-hydroxytryptamine (serotonin) receptor 1B ,q14.1
SNP_A-2097426	agagaaatgaagaaag[C/G]ctggtttaggatacca	C	G	NM_001563 // upstream // 834192 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 555420 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1827460	taactcaaaattgaac[A/G]aaaacctaaatgtaag	A	G	NM_001563 // upstream // 840789 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 548823 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2252880	cttctatgagttgtta[C/T]aaatttggcccttaca	C	T	NM_001563 // upstream // 840816 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 548796 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-1986502	tgctattgtgttagga[A/G]taccttagcactatg	A	G	NM_001563 // upstream // 855597 // Hs.129882 // IMPG1 // 3617 // Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), mRNA. /// NM_000863 // downstream // 534015 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) recep	IMPG1	IMPG1, Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1), q14.1
SNP_A-2080432	acctagattttctata[C/T]aatgggcaggagttgt	C	T	NM_000863 // upstream // 143505 // Hs.123016 // HTR1B // 3351 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B), mRNA. /// X82272 // downstream // 110951 // --- // --- // 0 // Human endogenous retrovirus env mRNA. /// ENST00000257763 //	HTR1B	HTR1B, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B), q14.1
SNP_A-1926429	ttattcaattcaccta[A/C]atctgcagagggtcca	A	C	ENST00000334883 // intron // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-1986522	tgaagaaatgagctcg[A/C]actatttggtacagtg	A	C	ENST00000334883 // intron // 0 // --- // --- // --- // ---	-	q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172926	cacaaaacactactga[A/G]aataattgaataacag	A	G	ENST00000334883 // intron // 0 // --- /// --- /// ---	-	q14.1
SNP_A-1916440	tgttgtttggtacacc[A/G]cagtgttaagtgggct	A	G	X82272 // upstream // 622941 // --- // 0 // Human endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 419556 // --- /// --- /// ENST00000357889 // upstream // 622941 // --- /// --- /// ENST00000359738 // u	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-1959842	tttgtatgtttaga[G/T]atcacataggtatata	G	T	X82272 // upstream // 650814 // --- // 0 // Human endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 447429 // --- /// --- /// ENST00000357889 // upstream // 650814 // --- /// --- /// ENST00000359738 // u	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2259878	gaaaaggagggtccaa[C/G]gatgaaataggtctt	C	G	X82272 // upstream // 939922 // --- // 0 // Human endogenous retrovirus env mRNA. /// ENST00000334883 // downstream // 736537 // --- /// --- /// ENST00000357889 // upstream // 939922 // --- /// --- /// ENST00000359738 // u	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-1986557	tagttaccgggaatca[C/T]ctaaccatgaccaaaa	C	T	NM_017934 // upstream // 49078 // Hs.511817 // PHIP // 55023 // Homo sapiens pleckstrin homology domain interacting protein (PHIP), mRNA. /// NM_138730 // downstream // 73897 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal bin	PHIP	PHIP, Homo sapiens pleckstrin homology domain interacting protein (PHIP), q14.1
SNP_A-2075887	acattaaataaaaata[A/G]catggcacaaaataca	A	G	NM_017934 // upstream // 66237 // Hs.511817 // PHIP // 55023 // Homo sapiens pleckstrin homology domain interacting protein (PHIP), mRNA. /// NM_138730 // downstream // 56738 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal bin	PHIP	PHIP, Homo sapiens pleckstrin homology domain interacting protein (PHIP), q14.1
SNP_A-1957416	tttaggtgtcattga[C/T]gttagagttctgtttt	C	T	NM_017934 // upstream // 66375 // Hs.511817 // PHIP // 55023 // Homo sapiens pleckstrin homology domain interacting protein (PHIP), mRNA. /// NM_138730 // downstream // 56600 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal bin	PHIP	PHIP, Homo sapiens pleckstrin homology domain interacting protein (PHIP), q14.1
SNP_A-1930965	ttccaggtcattcaga[A/G]agcagtcagatatac	A	G	NM_017934 // upstream // 106665 // Hs.511817 // PHIP // 55023 // Homo sapiens pleckstrin homology domain interacting protein (PHIP), mRNA. /// NM_138730 // downstream // 16310 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal bi	PHIP	PHIP, Homo sapiens pleckstrin homology domain interacting protein (PHIP), q14.1
SNP_A-1986561	ggtaactttctacaac[A/G]ggcatttagaaaccat	A	G	NM_138730 // intron // 0 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, mRNA. /// NM_004242 // intron // 0 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucle	HMGN3	HMGN3, Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, q14.1
SNP_A-2089497	acttcaaactagatgt[A/G]aagacgaataggacat	A	G	NM_138730 // upstream // 539 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, mRNA. /// NM_004242 // upstream // 539 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility gro	HMGN3	HMGN3, Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, q14.1
SNP_A-1714925	tggtttaaactgctgtttggctcaa[A/G]atagacatgtatcctggag ttgtta	A	G	NM_004242 // upstream // 94726 // Hs.77558 // HMGN3 // 9324 // high mobility group nucleosomal binding domain 3 /// NM_138730 // upstream // 94726 // Hs.77558 // HMGN3 // 9324 // high mobility group nucleosomal binding domain 3 /// NM_181714 // downstrea	HMGN3	HMGN3 , rs16760, high mobility group nucleosomal binding domain 3 ,q14.1
SNP_A-2171184	caatagtgagatccta[C/T]gtcttgaagaaggaaa	C	T	NM_138730 // upstream // 43114 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, mRNA. /// NM_004242 // upstream // 43114 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility	HMGN3	HMGN3, Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2231423	ctattggaggccagaa[C/T]acatagtaaatatata	C	T	NM_138730 // upstream // 71306 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, mRNA. /// NM_004242 // upstream // 71306 // Hs.77558 // HMGN3 // 9324 // Homo sapiens high mobility	HMGN3	HMGN3, Homo sapiens high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 2, q14.1
SNP_A-1955124	tttggcaaaatggggc[A/G]actccttgcagcagtg	A	G	ENST00000360549 // CDS // 0 // --- // --- // --- // ---	-	q14.1
SNP_A-2308014	gcttctttggatttta[C/T]ggtggctttctgattt	C	T	NM_181714 // downstream // 131206 // Hs.21945 // C6orf152 // 167691 // Homo sapiens chromosome 6 open reading frame 152 (C6orf152), mRNA. /// ENST00000360549 // upstream // 42738 // --- // --- // --- // --- /// ENST00000257791 // downstream // 131206 // -	C6orf152	C6orf152, Homo sapiens chromosome 6 open reading frame 152 (C6orf152), q14.1
SNP_A-1986562	ctaataaactgtctcc[A/G]aagctgaattgatatg	A	G	NM_181714 // downstream // 130729 // Hs.21945 // C6orf152 // 167691 // Homo sapiens chromosome 6 open reading frame 152 (C6orf152), mRNA. /// ENST00000360549 // upstream // 43215 // --- // --- // --- // --- /// ENST00000257791 // downstream // 130729 // -	C6orf152	C6orf152, Homo sapiens chromosome 6 open reading frame 152 (C6orf152), q14.1
SNP_A-2178750	cactgaagaagtttca[A/G]aaggctaaattcttct	A	G	NM_181714 // downstream // 108217 // Hs.21945 // C6orf152 // 167691 // Homo sapiens chromosome 6 open reading frame 152 (C6orf152), mRNA. /// ENST00000360549 // upstream // 65727 // --- // --- // --- // --- /// ENST00000257791 // downstream // 108217 // -	C6orf152	C6orf152, Homo sapiens chromosome 6 open reading frame 152 (C6orf152), q14.1
SNP_A-1934988	ttctgagattgtagtg[A/C]aaggtaaatctgaaat	A	C	NM_181714 // downstream // 87127 // Hs.21945 // C6orf152 // 167691 // Homo sapiens chromosome 6 open reading frame 152 (C6orf152), mRNA. /// ENST00000360549 // upstream // 86817 // --- // --- // --- // --- /// ENST00000257791 // downstream // 87127 // ---	C6orf152	C6orf152, Homo sapiens chromosome 6 open reading frame 152 (C6orf152), q14.1
SNP_A-1986565	ccacataacttcaata[C/T]ctggaatttcacaaat	C	T	NM_181714 // downstream // 69951 // Hs.21945 // C6orf152 // 167691 // Homo sapiens chromosome 6 open reading frame 152 (C6orf152), mRNA. /// ENST00000360549 // upstream // 103993 // --- // --- // --- // --- /// ENST00000257791 // downstream // 69951 // -	C6orf152	C6orf152, Homo sapiens chromosome 6 open reading frame 152 (C6orf152), q14.1
SNP_A-1726384	gggacccgttgctaaaggggtgtga[A/G]atttctctgtgcggtaataaaatgt	A	G	NM_031469 // intron // 0 // Hs.302772 // SH3BGRL2 // 83699 // SH3 domain binding glutamic acid-rich protein like 2	SH3BGRL2	SH3BGRL2 , rs723981, SH3 domain binding glutamic acid-rich protein like 2,q14.1
SNP_A-2205300	ccagtccaaaagaaaa[C/T]tatggggcacttctct	C	T	NM_031469 // downstream // 52895 // Hs.302772 // SH3BGRL2 // 83699 // Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA. /// NM_022726 // downstream // 158272 // Hs.101915 // ELOVL4 // 6785 // Homo sapiens elongation of ve	SH3BGRL2	SH3BGRL2, Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), q14.1
SNP_A-1943001	ttggtaaactcatgcc[A/G]aatattcccctgcgtc	A	G	NM_031469 // downstream // 61203 // Hs.302772 // SH3BGRL2 // 83699 // Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA. /// NM_022726 // downstream // 149964 // Hs.101915 // ELOVL4 // 6785 // Homo sapiens elongation of ve	SH3BGRL2	SH3BGRL2, Homo sapiens SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), q14.1
SNP_A-1986584	atcttggaggtcaaca[C/G]aattcaagggttggat	C	G	NM_003318 // intron // 0 // Hs.169840 // TTK // 7272 // Homo sapiens TTK protein kinase (TTK), mRNA. /// ENST00000230510 // intron // 0 // --- // --- // --- // ---	TTK	TTK, Homo sapiens TTK protein kinase (TTK), q14.1
SNP_A-1948553	tttagttgatgtttta[A/G]attgactgaattgaag	A	G	NM_183050 // downstream // 95854 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 95854 // Hs.436387 // BCKDHB	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1
SNP_A-2231191	ctattagttatggata[C/G]gaactttaaacaaaca	C	G	NM_183050 // downstream // 117384 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 117384 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2106953	agcctttaagcctgaa[A/G]tgtctacacctctcca	A	G	NM_183050 // downstream // 131940 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 131940 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1
SNP_A-1871488	tctaactatactgaaa[G/T]ttgctgacactgcaag	G	T	NM_183050 // downstream // 135978 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 135978 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-2115673	agggtcaaaatggcca[G/T]aatgcaactgtgatgt	G	T	NM_183050 // downstream // 136468 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 136468 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-2241746	ctgatccataacagcc[A/G]agaaaattctatcatc	A	G	NM_183050 // downstream // 170274 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 170274 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-2065490	aattgttttcagaatc[A/G]gagatgagaaagtgac	A	G	NM_183050 // downstream // 184406 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 184406 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1
SNP_A-1986606	agcaccattctcccga[G/T]tattcagtacttaact	G	T	NM_183050 // downstream // 197920 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 197920 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1
SNP_A-2245766	ctgggggaaaagtgac[G/T]accagaaagtgaagac	G	T	NM_183050 // downstream // 209508 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 209508 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco q14.1
SNP_A-2285586	gatgaaatttctagac[A/G]cactctggatgaaaag	A	G	NM_183050 // downstream // 276890 // Hs.436387 // BCKDHB // 594 // Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco /// NM_000056 // downstream // 276890 // Hs.436387 // BCKDH	BCKDHB	BCKDHB, Homo sapiens branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) (BCKDHB), nuclear gene enco ,q14.1
SNP_A-1685090	gagtttaattgactggttacctcta[C/T]gcagtgctagataagcat ggttcat	C	T	AF130064 // upstream // 782173 // Hs.485837 // - // - // Clone FLB7925 PRO2122 mRNA, complete cds /// NM_000056 // downstream // 423243 // Hs.1265 // BCKDHB // 594 // branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	-	- , rs10485284, Clone FLB7925 PRO2122 mRNA, complete cds ,q14.1
SNP_A-1656637	atggatttctatggatacagaaata[C/T]gaatttttagacacacca ttggaat	C	T	AF130064 // upstream // 421524 // Hs.485837 // - // - // Clone FLB7925 PRO2122 mRNA, complete cds /// NM_000056 // downstream // 783892 // Hs.1265 // BCKDHB // 594 // branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	-	- , rs1822546, Clone FLB7925 PRO2122 mRNA, complete cds ,q14.1
SNP_A-2210086	ccccagattagagaga[C/T]ggaaagtggttgttag	C	T	ENST00000355935 // intron // 0 // — // — // — // — /// ENST00000358773 // intron // 0 // — // — // — // —	-	q14.1
SNP_A-1795220	ggtgaggcatggtaaa[G/T]aaatgtctgaccataa	G	T	ENST00000355935 // intron // 0 // — // — // — // — /// ENST00000358773 // intron // 0 // — // — // — // —	-	q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796639	ggttagctgcattgta[A/C]cctgtgaagcttgaaa	A	C	ENST00000355935 // upstream // 389295 // --- // --- // --- /// ENST00000358773 // upstream // 389295 // --- // --- // --- /// ENST00000357286 // upstream // 527917 // --- // --- // --- /// ENST00000359368 // downstream // 624062 // --	-	q14.1
SNP_A-2029236	aaagaagcatcctgaa[A/T]actgactcaaatagta	A	T	NM_017633 // downstream // 113441 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000237194 // upstream // 79470 // --- // --- // --- /// ENST00000320172 // downstream // 113441	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-2055355	aataaggagcttgtca[C/T]gaaaagtgaattc	C	T	NM_017633 // downstream // 55537 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000237194 // upstream // 137374 // --- // --- // --- /// ENST00000320172 // downstream // 55537 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-2243178	ctgcctcatacctac[A/G]gacaaagaactgagc	A	G	NM_017633 // downstream // 28971 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000237194 // upstream // 163940 // --- // --- // --- /// ENST00000320172 // downstream // 28971 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-1922547	ttagaatgctgccttaa[G/T]atgggttcttccttt	G	T	NM_017633 // downstream // 22282 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000237194 // upstream // 170629 // --- // --- // --- /// ENST00000320172 // downstream // 22282 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-1946652	tttaacaagcgttgca[C/T]tgaaaacaacttatg	C	T	NM_017633 // 3UTR // 0 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000320172 // 3UTR // 0 // --- // --- // --	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-1897571	tgctgcaaaacaaata[A/G]cctcaaaatcagaagc	A	G	NM_017633 // upstream // 54170 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000320172 // upstream // 54170 // --- // --- // --- /// ENST00000306270 // downstream // 363379 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-1910502	tgtccctgacgaagc[C/T]acttggctacttgtgt	C	T	NM_017633 // upstream // 153676 // Hs.10784 // FAM46A // 55603 // Homo sapiens family with sequence similarity 46, member A (FAM46A), mRNA. /// ENST00000320172 // upstream // 153676 // --- // --- // --- /// ENST00000306270 // downstream // 263873 //	FAM46A	FAM46A, Homo sapiens family with sequence similarity 46, member A (FAM46A), q14.1
SNP_A-2058218	aatcaacctagattcc[C/T]atcaactggataaaga	C	T	NM_006670 // downstream // 141368 // Hs.82128 // TPBG // 7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 384207 // Hs.148609 // C6orf157 // 90025 // Homo sapiens chromosome 6 open reading frame 157 (C6orf157), mR	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2181785	cagagatgtgctttgc[A/G]aatggtgctatttat	A	G	NM_006670 // downstream // 295611 // Hs.82128 // TPBG // 7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 229964 // Hs.148609 // C6orf157 // 90025 // Homo sapiens chromosome 6 open reading frame 157 (C6orf157), mR	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2035206	aaatgctcaaattaca[A/G]aagctcaatccaagga	A	G	NM_006670 // downstream // 295711 // Hs.82128 // TPBG // 7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 229864 // Hs.148609 // C6orf157 // 90025 // Homo sapiens chromosome 6 open reading frame 157 (C6orf157), mR	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1986653	ctggcagatgattttc[C/T]aaagtgtcttttccat	C	T	NM_006670 // downstream // 298656 // Hs.82128 // TPBG // 7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 226919 // Hs.148609 // C6orf157 // 90025 // Homo sapiens chromosome 6 open reading frame 157 (C6orf157), mR	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-2027836	aaacctaagtgcagtg[A/G]aataacccaaatgata	A	G	NM_006670 // downstream // 309907 // Hs.82128 // TPBG // 7162 // Homo sapiens trophoblast glycoprotein (TPBG), mRNA. /// NM_198920 // downstream // 215668 // Hs.148609 // C6orf157 // 90025 // Homo sapiens chromosome 6 open reading frame 157 (C6orf157), mR	TPBG	TPBG, Homo sapiens trophoblast glycoprotein (TPBG), q14.1
SNP_A-1808984	gtgaattgagtaggcc[A/G]gatgagttggcagacc	A	G	NM_033411 // downstream // 2488 // Hs.528310 // RWDD2 // 112611 // Homo sapiens RWD domain containing 2 (RWDD2), mRNA. /// NM_002395 // downstream // 12519 // Hs.21160 // ME1 // 4199 // Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), mRNA	RWDD2	RWDD2, Homo sapiens RWD domain containing 2 (RWDD2), q14.2
SNP_A-1986670	aaattgaaaatatgac[A/T]cttaaaacaagctcaa	A	T	NM_002395 // intron // 0 // Hs.21160 // ME1 // 4199 // Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), mRNA. /// ENST00000265285 // intron // 0 // --- // --- // --- // ---	ME1	ME1, Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), q14.2
SNP_A-2249867	cttacaatggcatgga[A/T]aactcagataactggt	A	T	NM_002395 // upstream // 48724 // Hs.21160 // ME1 // 4199 // Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), mRNA. /// NM_153362 // upstream // 32874 // Hs.98381 // PRSS35 // 167681 // Homo sapiens protease, serine, 35 (PRSS35), mRNA. ///	ME1	ME1, Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), q14.2
SNP_A-2169792	caaggagggttttaaa[C/T]gtccagctgtcattat	C	T	NM_002395 // upstream // 49010 // Hs.21160 // ME1 // 4199 // Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), mRNA. /// NM_153362 // upstream // 32588 // Hs.98381 // PRSS35 // 167681 // Homo sapiens protease, serine, 35 (PRSS35), mRNA. ///	ME1	ME1, Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), q14.2
SNP_A-2161687	atttggtatatcttaa[C/T]gcttggtactaatgat	C	T	NM_153362 // intron // 0 // Hs.98381 // PRSS35 // 167681 // Homo sapiens protease, serine, 35 (PRSS35), mRNA. /// ENST00000275040 // intron // 0 // --- // --- // --- // --- // ---	PRSS35	PRSS35, Homo sapiens protease, serine, 35 (PRSS35), q14.2
SNP_A-2011887	ttgtagccagctagtc[C/T]gaagtgggggtggtcc	C	T	AB014556 // intron // 0 // Hs.368046 // SNAP91 // 9892 // Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // intron // 0 // --- // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. q14.2
SNP_A-1894876	tgccatgaaatttgac[A/G]agggattcatgtatac	A	G	AB014556 // intron // 0 // Hs.368046 // SNAP91 // 9892 // Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // intron // 0 // --- // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. q14.2
SNP_A-1835490	tacctgcttattcaca[A/G]cctgcttgaggcttat	A	G	AB014556 // intron // 0 // Hs.368046 // SNAP91 // 9892 // Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // intron // 0 // --- // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. ,q14.2
SNP_A-2277509	gagcaagttaaagaat[C/G]agaggaaaacctggag	C	G	AB014556 // upstream // 7427 // Hs.368046 // SNAP91 // 9892 // Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // upstream // 7427 // --- // --- // --- // --- // --- /// ENST00000342235 // upstream // 136690 // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. ,q14.2
SNP_A-2120208	agtcaggagtcataca[C/T]agcacagaacattgtt	C	T	AB014556 // upstream // 9261 // Hs.368046 // SNAP91 // 9892 // Homo sapiens mRNA for KIAA0656 protein, partial cds. /// ENST00000195649 // upstream // 9261 // --- // --- // --- // --- // --- /// ENST00000342235 // upstream // 134856 // --- // --- // --- // ---	SNAP91	SNAP91, Homo sapiens for KIAA0656 protein, partial cds. ,q14.2
SNP_A-1947245	tttaattctttttata[A/G]cacttagcacattaat	A	G	AJ010278 // downstream // 510962 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 9801 // --- // --- // --- // --- // --- /// ENST00000330469 // downstream // 461640 // --- // --- // --- // --- // --- ///	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2079007	acccactcaccattat[C/T]acctggcatgaaaaca	C	T	AJ010278 // downstream // 494554 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 26209 // — // — // — /// ENST00000330469 // downstream // 445232 // — // — // — // —	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1986689	accttcttcgaccact[A/G]aactaaaccacgtaca	A	G	AJ010278 // downstream // 373229 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 147534 // — // — // — // — /// ENST00000330469 // downstream // 323907 // — // — // — // —	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2095219	agaattctatattatg[C/T]atagcaaatgagccaa	C	T	AJ010278 // downstream // 362147 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 158616 // — // — // — // — /// ENST00000330469 // downstream // 312825 // — // — // — // —	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-2181861	cagagcatctcattaq[A/C]ctgtgaatatacacgt	A	C	AJ010278 // downstream // 328119 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 192644 // — // — // — // — /// ENST00000330469 // downstream // 278797 // — // — // — // —	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-2143908	atgagcaaactgaatc[A/G]ctggtagtctaaataa	A	G	AJ010278 // downstream // 305642 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 215121 // — // — // — // — /// ENST00000330469 // downstream // 256320 // — // — // — // —	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1787596	gggacaaaaaatccagat[C/T]gtgaagtggaggagag	C	T	AJ010278 // downstream // 86720 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 434043 // — // — // — // — /// ENST00000330469 // downstream // 37398 // — // — // — // — ///	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-2221077	ccttgtattgttaatt[A/T]aaggcgaaatttgggc	A	T	AJ010278 // downstream // 63207 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// ENST00000257766 // upstream // 457556 // — // — // — // — /// ENST00000330469 // downstream // 13885 // — // — // — // — ///	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1986712	atgagcttctactacc[A/G]agatgcttggaaaac	A	G	ENST00000330469 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1887315	tgagaagtaggagcat[C/T]aggatatcggtatcct	C	T	ENST00000330469 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1819649	gttgtatacccaatgca[A/G]taagtatgtacaaagc	A	G	AJ010278 // upstream // 42201 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 643709 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1715923	caaaggcatagaggaacctaaatg[A/C]aaattgctaagtaaa agaggtcagt	A	C	NM_002526 // upstream // 296496 // Hs.153952 // NT5E // 4907 // 5'-nucleotidase, ecto (CD73)	NT5E	NT5E , rs2104467, 5'-nucleotidase, ecto (CD73),q14.3
SNP_A-2110785	aggactaaacaaatga[C/T]agaggacttgcagca	C	T	AJ010278 // upstream // 358367 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 327543 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2157522	attgatgctagtattat[C/T]agttaccagtggcgta	C	T	AJ010278 // upstream // 363389 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 322521 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3
SNP_A-1812252	gtggatataacggaaa[C/T]ggagtaggatttaagg	C	T	AJ010278 // upstream // 373598 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 312312 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. ,q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2288582	gattgcagctgtctat[G/T]ctctgaatggaaaaca	G	T	AJ010278 // upstream // 402621 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 283289 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2151169	atgtgttgtacagata[A/G]atatcagggtgaggtc	A	G	AJ010278 // upstream // 514367 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 171543 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1643159	ctgaaatcatcttgatggtgactaa[A/G]gtgccctgttgagtatgtt gcaggc	A	G	NM_002526 // upstream // 94518 // Hs.153952 // NT5E // 4907 // 5'-nucleotidase, ecto (CD73)	NT5E	NT5E , rs10498953, 5'-nucleotidase, ecto (CD73),q14.3
SNP_A-2172505	caattccagtcatcat[A/G]aaacagaaatatccta	A	G	AJ010278 // upstream // 537180 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 148730 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1883256	tgaaattgaattgaca[C/G]aaaccaccagtggctc	C	G	AJ010278 // upstream // 537524 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 148386 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1903106	tggcttaaaggacccc[A/G]aatatagcttaggcca	A	G	AJ010278 // upstream // 553930 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 131980 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2118336	agtaactcaatagtta[C/T]cagtcgctttgggaa	C	T	AJ010278 // upstream // 556757 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 129153 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1870220	tcctttccaactagaa[A/G]ctcctttcagagtcaag	A	G	AJ010278 // upstream // 582828 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 103082 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 /	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-1843799	tagttaaaatgcagca[C/T]atacttcaaatcacac	C	T	AJ010278 // upstream // 586724 // Hs.251830 // TBX18 // 9096 // Homo sapiens mRNA for TBX18 protein, partial. /// NM_002526 // upstream // 99186 // Hs.153952 // NT5E // 4907 // Homo sapiens 5'-nucleotidase, ecto (CD73) (NT5E), mRNA. /// ENST00000330469 //	TBX18	TBX18, Homo sapiens for TBX18 protein, partial. q14.3
SNP_A-2078687	accattcatttttcc[A/G]atctcagacatagat	A	G	NM_006372 // upstream // 147929 // Hs.485877 // SYNCRIP // 10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 148366 // — // — // — // — /// ENST00000355238 // upstr	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3
SNP_A-2291340	gcaatggagtcctaaa[C/T]gtgaaccataaaggaa	C	T	NM_006372 // upstream // 305265 // Hs.485877 // SYNCRIP // 10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 305702 // — // — // — // — /// ENST00000355238 // upstr	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2073615	acagtatgaatcaacc[C/T]gcttctggatttcccc	C	T	NM_006372 // upstream // 352228 // Hs.485877 // SYNCRIP // 10492 // Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA. /// ENST00000257768 // upstream // 352665 // --- // --- // --- /// ENST00000355238 // upstr	SYNCRIP	SYNCRIP, Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), q14.3
SNP_A-2069095	acaatgtgatagact[A/T]aaagtataaaggaatc	A	T	NM_000865 // upstream // 620318 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 102833 // --- // --- // --- /// ENST00000305344 // upstream // 620318 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-2041156	aacctattgtttaggg[A/G]ataacaacagtaagag	A	G	NM_000865 // upstream // 574207 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 148944 // --- // --- // --- /// ENST00000305344 // upstream // 574207 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-2224527	cgtatgtgaatggaca[A/T]ctgacccaagctgca	A	T	NM_000865 // upstream // 486455 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 236696 // --- // --- // --- /// ENST00000305344 // upstream // 486455 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-1702001	taataggaatgagtcagagtggagc[C/T]gataatcggaatgagt caggtgga	C	T	NM_000865 // upstream // 355593 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E, rs2020079, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1714919	gagtgtgcaaaatgatttttgataaa[A/C]atgttgatctgggggac ctgtaag	A	C	NM_000865 // upstream // 297515 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E, rs10485361, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1673910	tataaatgacatgataaaaatcctat[C/T]gaacaactccatacta atacatttg	C	T	NM_000865 // upstream // 237768 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E, rs542732, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1986752	aaggcatagtccctgat[C/T]atgtaggcgcccataa	C	T	NM_000865 // upstream // 294968 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 428183 // --- // --- // --- /// ENST00000305344 // upstream // 294968 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-1756116	gaagtcaagctgaaaatggagagca[A/G]ctatactaaagccc aatccgaggtg	A	G	NM_000865 // upstream // 196323 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E, rs487570, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1787623	gggacaagaaccataa[C/T]ccaggcaagatatcac	C	T	NM_000865 // upstream // 226793 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 496358 // --- // --- // --- /// ENST00000305344 // upstream // 226793 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q14.3
SNP_A-1719305	gaaaagtgttagcttccaagcgtga[C/T]gaacccttcagataga ctcatcagt	C	T	NM_000865 // upstream // 163716 // Hs.1611 // HTR1E // 3354 // 5-hydroxytryptamine (serotonin) receptor 1E	HTR1E	HTR1E, rs494991, 5-hydroxytryptamine (serotonin) receptor 1E,q14.3
SNP_A-1986755	ttgctaccagaccaca[A/G]atggcactaacagaaa	A	G	NM_000865 // upstream // 155204 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 567947 // --- // --- // --- /// ENST00000305344 // upstream // 155204 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15
SNP_A-1831437	taatgtggaacttttta[C/G]acctatgtccaaatac	C	G	NM_000865 // upstream // 147106 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 576045 // --- // --- // --- /// ENST00000305344 // upstream // 147106 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15
SNP_A-1862732	tcattcattaccaaac[C/G]acactcctctgtttaa	C	G	NM_000865 // upstream // 91407 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 631744 // --- // --- // --- /// ENST00000305344 // upstream // 91407 // --- /	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2091506	agaaaaactagaacac[C/T]aaataatggcagccag	C	T	NM_000865 // upstream // 47132 // Hs.1611 // HTR1E // 3354 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA. /// ENST00000257777 // upstream // 676019 // — // — // — // — /// ENST00000305344 // upstream // 47132 // — //	HTR1E	HTR1E, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), q15
SNP_A-1840770	tagctagaaggatcaa[A/T]gacaagggtgacaccg	A	T	NM_000735 // upstream // 20485 // Hs.119689 // CGA // 1081 // Homo sapiens glycoprotein hormones, alpha polypeptide (CGA), mRNA. /// AB011102 // upstream // 39985 // Hs.485892 // ZNF292 // 23036 // Homo sapiens mRNA for KIAA0530 protein, partial cds. ///	CGA	CGA, Homo sapiens glycoprotein hormones, alpha polypeptide (CGA), q15
SNP_A-1948337	tttagggcccaggtga[A/G]atgagttaggcatcca	A	G	AB011102 // intron // 0 // Hs.485892 // ZNF292 // 23036 // Homo sapiens mRNA for KIAA0530 protein, partial cds. /// ENST00000339907 // intron // 0 // — // — // — // —	ZNF292	ZNF292, Homo sapiens for KIAA0530 protein, partial cds. ,q15
SNP_A-1853801	tcaaaaatgtgaacaa[C/T]gttggggtagtggtgt	C	T	NM_020425 // intron // 0 // Hs.70769 // C6orf162 // 57150 // Homo sapiens chromosome 6 open reading frame 162 (C6orf162), mRNA. /// ENST00000229570 // intron // 0 // — // — // — // —	C6orf162	C6orf162, Homo sapiens chromosome 6 open reading frame 162 (C6orf162), q15
SNP_A-1918865	ttaacatcacgtaaga[C/G]taatacctggtggtct	C	G	ENST00000360924 // intron // 0 // — // — // — // —	-	q15
SNP_A-1986775	aaataaactacggaaa[A/G]tccatagtagcaattg	A	G	ENST00000360924 // intron // 0 // — // — // — // —	-	q15
SNP_A-2056161	aatacctggtttgaga[A/C]atcatagtttgtgcag	A	C	NM_018064 // upstream // 91383 // Hs.485915 // C6orf166 // 55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 254198 // Hs.161241 // SPACA1 // 81833 // Homo sapiens sperm acrosome associated 1 (SPACA1)	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-1889345	tgagtgtcaacttcta[C/T]aaccttggatgacata	C	T	NM_018064 // upstream // 212511 // Hs.485915 // C6orf166 // 55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 133070 // Hs.161241 // SPACA1 // 81833 // Homo sapiens sperm acrosome associated 1 (SPACA1	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-1662210	cctggcacagaggctggaaatgagt[A/G]ggtactgctaaaaca atgtggaatg	A	G	NM_001840 // downstream // 55603 // - // - // - // - /// NM_016083 // downstream // 131820 // Hs.75110 // CNR1 // 1268 // cannabinoid receptor 1 (brain) /// NM_018064 // upstream // 305839 // Hs.201864 // C6orf166 // 55122 // chromosome 6 open reading fr	-	- , rs366676, - ,q15
SNP_A-2086312	actctgtgtccagtcc[A/G]agcttcagagaaggaa	A	G	NM_018064 // upstream // 245421 // Hs.485915 // C6orf166 // 55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 100160 // Hs.161241 // SPACA1 // 81833 // Homo sapiens sperm acrosome associated 1 (SPACA1	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-2026348	aaaattttatctatca[C/G]aggctcgtaagattca	C	G	NM_018064 // upstream // 262245 // Hs.485915 // C6orf166 // 55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 83336 // Hs.161241 // SPACA1 // 81833 // Homo sapiens sperm acrosome associated 1 (SPACA1)	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-2244288	ctggaactacaccacc[A/G]gcttatctagatctcc	A	G	NM_018064 // upstream // 279386 // Hs.485915 // C6orf166 // 55122 // Homo sapiens chromosome 6 open reading frame 166 (C6orf166), mRNA. /// NM_030960 // upstream // 66195 // Hs.161241 // SPACA1 // 81833 // Homo sapiens sperm acrosome associated 1 (SPACA1)	C6orf166	C6orf166, Homo sapiens chromosome 6 open reading frame 166 (C6orf166), q15
SNP_A-1652150	caatatagataaagctagttcaaaa[A/G]cataattaattctactaa gatttgg	A	G	NM_001840 // upstream // 25283 // - // - // - // - /// NM_003800 // downstream // 419154 // Hs.27345 // RNGTT // 8732 // RNA guanylyltransferase and 5'-phosphatase /// NM_016083 // upstream // 45789 // Hs.75110 // CNR1 // 1268 // cannabinoid receptor 1 (	-	- , rs2875547, - ,q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1986789	ataggaagcacaggtg[C/T]aaatggaaaactgcaa	C	T	NM_003800 // downstream // 287916 // Hs.127219 // RNGTT // 8732 // Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), mRNA. /// ENST00000333801 // downstream // 56838 // --- // --- // --- /// ENST00000342148 // downstream // 287916 //	RNGTT	RNGTT, Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), q15
SNP_A-1955019	ttggactagcctgag[A/G]ccagtagcagagactt	A	G	NM_003800 // downstream // 73932 // Hs.127219 // RNGTT // 8732 // Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), mRNA. /// ENST00000333801 // downstream // 270822 // --- // --- // --- /// ENST00000342148 // downstream // 73932 //	RNGTT	RNGTT, Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), q15
SNP_A-1887330	tgagaataacccaaga[C/T]gtgtttcgtgctggga	C	T	NM_003800 // downstream // 26248 // Hs.127219 // RNGTT // 8732 // Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), mRNA. /// ENST00000333801 // downstream // 318506 // --- // --- // --- /// ENST00000342148 // downstream // 26248 //	RNGTT	RNGTT, Homo sapiens RNA guanylyltransferase and 5-phosphatase (RNGTT), q15
SNP_A-1966802	gttgtttggtaataggt[A/C]actcagaaccaaagtc	A	C	NM_002042 // intron // 0 // Hs.437745 // GABRR1 // 2569 // Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 1 (GABRR1), mRNA. /// ENST00000275066 // intron // 0 // --- // --- // ---	GABRR1	GABRR1, Homo sapiens gamma-aminobutyric acid (GABA) receptor, rho 1 (GABRR1), q15
SNP_A-2096036	agacataaaaatgcca[A/C]acttaaaattgaggta	A	C	NM_012115 // downstream // 6358 // Hs.546332 // CASP8AP2 // 9994 // Homo sapiens CASP8 associated protein 2 (CASP8AP2), mRNA. /// NM_032602 // upstream // 16708 // Hs.334499 // CX62 // 84694 // Homo sapiens connexin 62 (CX62), mRNA. /// ENST00000023177 //	CASP8AP2	CASP8AP2, Homo sapiens CASP8 associated protein 2 (CASP8AP2), q15
SNP_A-2282217	gagtgtttgcacagta[C/T]agtaacatttggttgt	C	T	NM_021813 // 3UTR // 0 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // 3UTR // 0 // --- // --- // --- // ---	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2072804	acagctgaatgaacta[C/T]gattacgagaacgag	C	T	NM_021813 // intron // 0 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // intron // 0 // --- // --- // --- /// ENST00000343122 // intron // 0 //	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2283857	gatagtgagcacaagc[A/G]agcacaaacctgaaat	A	G	NM_021813 // intron // 0 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// ENST00000257749 // intron // 0 // --- // --- // --- /// ENST00000343122 // intron // 0 //	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1811895	gtggaaacaggagaag[C/T]agaattcagtttggca	C	T	NM_021813 // upstream // 132496 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 86396 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-a	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-2169249	caagcaacaacataca[A/G]atataagcgatgaat	A	G	NM_021813 // upstream // 195734 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 23158 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-a	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1794755	ggtctgactctcataa[A/G]gcttacattagaatgt	A	G	NM_021813 // upstream // 196060 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 22832 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-a	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1938545	ttgagaatctactata[A/T]gctttggcaatgttga	A	T			

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2156652	attctgctaaggcatc[A/G]ctttcttccagatgtt	A	G	NM_021813 // upstream // 197754 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 21138 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-a	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1824340	taaacctgaggacac[C/T]gagaaaaacagctgct	C	T	NM_021813 // upstream // 204179 // Hs.269764 // BACH2 // 60468 // Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /// NM_145331 // downstream // 14713 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-a	BACH2	BACH2, Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), q15
SNP_A-1816125	gttaccatgcatagaa[A/G]aagggcaaggtgcag	A	G	NM_145331 // upstream // 215730 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 215587 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitoge	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q15
SNP_A-1887947	tgagcaagtaacagat[C/T]agtttcaggaagaggc	C	T	NM_145331 // upstream // 714767 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 714624 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitoge	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q15
SNP_A-2191523	catatgatgccacttc[A/G]ctgcattctatcagtc	A	G	NM_145331 // upstream // 854542 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 854399 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitoge	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2119688	agtattagaggaagaa[C/T]agagttagaagaattc	C	T	NM_145331 // upstream // 958425 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 958282 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitoge	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2191876	catcaaatgaatcacc[A/G]catatcttgaaaaatt	A	G	NM_145331 // upstream // 1273141 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1272998 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2258062	cttgttctctgatgc[A/G]aaaaatcttcagaaac	A	G	NM_145331 // upstream // 1342231 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1342088 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1896366	tgctaagagttaggat[C/G]aagaatggcatcctac	C	G	NM_145331 // upstream // 1862385 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1862242 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1878626	tctgtgttgcagacta[A/G]aagcaaaatgcagtaa	A	G	NM_145331 // upstream // 1862655 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1862512 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2122765	agtggatcttcaaca[A/T]cttaactgaccacagt	A	T	NM_145331 // upstream // 1880983 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 1880840 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2023587	aaaactctttgtgaac[G/T]aaaaggagacaggtgt	G	T	NM_145331 // upstream // 2259180 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2259037 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1930684	ttccacattctgaagc[A/G]gcagcccaaactgtat	A	G	NM_145331 // upstream // 2270498 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2270355 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2093976	agaagcctgaactatc[C/G]aagatttgaaagatga	C	G	NM_145331 // upstream // 2431083 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2430940 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-2053037	aagtcctgggaaaaat[A/T]atttcaactcagcttt	A	T	NM_145331 // upstream // 2460304 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, mRNA. /// NM_145333 // upstream // 2460161 // Hs.485968 // MAP3K7 // 6885 // Homo sapiens mito	MAP3K7	MAP3K7, Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant B, q16.1
SNP_A-1951803	tttctaaaatccctga[C/G]aaattcctagcaacta	C	G	NM_004440 // intron // 0 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// ENST00000257785 // intron // 0 // — // — // — // —	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2098535	agagcagggattaccc[A/G]gaaaccagcaccggga	A	G	NM_004440 // upstream // 426198 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1519943 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2036174	aaattatgaggttaaa[A/G]aattgcctgttgtttg	A	G	NM_004440 // upstream // 443513 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1502628 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1909297	tgtatgtattcgaact[G/T]agaactcaaaatttta	G	T	NM_004440 // upstream // 531175 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1414966 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1986905	tgactgagctccagta[A/G]gtggcaactgacttt	A	G	NM_004440 // upstream // 547011 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1399130 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1839453	tagatacaagggacga[C/T]gagtctttgaactaag	C	T	NM_004440 // upstream // 831602 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 1114539 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2226845	ctaatagtatattcac[A/C]gaattgtaaaccttac	A	C	NM_004440 // upstream // 1292602 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 653539 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2223986	cgggctgtaatttcta[C/T]gatttgtatgagtata	C	T	NM_004440 // upstream // 1812638 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 133503 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1815281	gtgttgtgcacctgca[C/T]tatctaatcctcaat	C	T	NM_004440 // upstream // 1817243 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 128898 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-2308496	gctttagcattatagt[A/G]accttctttcacctaa	A	G	NM_004440 // upstream // 1817459 // Hs.73962 // EPHA7 // 2045 // Homo sapiens EphA7 (EPHA7), mRNA. /// NM_024641 // upstream // 128682 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000257785 // upstream //	EPHA7	EPHA7, Homo sapiens EphA7 (EPHA7), q16.1
SNP_A-1826756	taacagcgatttttaa[A/G]acagcgataaagtctg	A	G	NM_024641 // intron // 0 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000302114 // intron // 0 // — // — // — /// ENST00000358812 // intron // 0 // — // — // — /// ENST00000030213	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-2045353	aagaagttcatgagcc[A/G]aagaatggtgtagcct	A	G	NM_024641 // intron // 0 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000302114 // intron // 0 // — // — // — /// ENST00000358812 // intron // 0 // — // — // —	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-2200223	ccaaattgttgtaggaa[A/C]ggcctgctatctacag	A	C	NM_024641 // 3UTR // 0 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// ENST00000302114 // 3UTR // 0 // — // — // — /// ENST00000358812 // 3UTR // 0 // — // — // —	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1819569	gttggtttaaatgggc[C/T]acttccagaatttctg	C	T	NM_024641 // downstream // 7724 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 398819 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1986931	agaaaatacagttcca[A/G]aagcgctgactcact	A	G	NM_024641 // downstream // 237314 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 169229 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1837782	tactttttcatttcaca[C/T]gataggcttcaggcta	C	T	NM_024641 // downstream // 300836 // Hs.533323 // MANEA // 79694 // Homo sapiens mannosidase, endo-alpha (MANEA), mRNA. /// NM_006581 // upstream // 105707 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	MANEA	MANEA, Homo sapiens mannosidase, endo-alpha (MANEA), q16.1
SNP_A-1650594	aaaacataaagaagtgggaatcatg[A/C]aaatgaataaacat gatttccacag	A	C	NM_006581 // upstream // 134964 // Hs.225945 // FUT9 // 10690 // fucosyltransferase 9 (alpha (1,3) fucosyltransferase) /// NM_024641 // downstream // 371358 // Hs.46903 // MANEA // 79694 // mannosidase, endo-alpha	FUT9	FUT9 , rs590973, fucosyltransferase 9 (alpha (1,3) fucosyltransferase), q16.1
SNP_A-1758002	ttatgcagaaaaagagaatataaa[C/T]gaaggtataacaagc atgaaacttc	C	T	AB023021 // intron // 0 // Hs.225945 // FUT9 // 10690 // fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	FUT9	FUT9 , rs2147716, fucosyltransferase 9 (alpha (1,3) fucosyltransferase),q16.1
SNP_A-1717173	acaattgctaccaaagttcacagga[C/G]agttagtgtaaggaa atccagaact	C	G	AB023021 // intron // 0 // Hs.225945 // FUT9 // 10690 // fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	FUT9	FUT9 , rs4002794, fucosyltransferase 9 (alpha (1,3) fucosyltransferase),q16.1
SNP_A-1986941	tttagatatgttgagt[C/T]tctgctgctactgaa	C	T	NM_006581 // intron // 0 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// ENST00000302103 // intron // 0 // — // — // —	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2173834	cacacactgatctaca[C/T]tgaaaaaaatacaaac	C	T	NM_006581 // intron // 0 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// ENST00000302103 // intron // 0 // — // — // —	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-2251342	cttcaagggttgaaaa[A/G]tttctgctaaagaata	A	G	NM_006581 // intron // 0 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// ENST00000302103 // intron // 0 // — // — // —	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-2259663	gaaaactaagcttca[A/G]gatactataactgta	A	G	NM_006581 // intron // 0 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// ENST00000302103 // intron // 0 // — // — // —	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-1724106	aggaatataaatttttgatagtctat[C/T]gctcagtagttaggtagtct gaaaa	C	T	NM_006581 // downstream // 12743 // Hs.225945 // FUT9 // 10690 // fucosyltransferase 9 (alpha (1,3) fucosyltransferase) /// NM_015323 // upstream // 303558 // Hs.149367 // KIAA0776 // 23376 // KIAA0776	FUT9	FUT9, rs10499000, fucosyltransferase 9 (alpha (1,3) fucosyltransferase), q16.1
SNP_A-2036512	aaattgacagctgcga[C/T]gagtgctatgaagaaa	C	T	NM_006581 // downstream // 30039 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// NM_015323 // upstream // 285922 // Hs.149367 // KIAA0776 // 23376 // Homo sapiens KIAA0776 (KIAA0776), m	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-2175432	cacatcatctatgtc[A/G]aaagtcatgttaacaa	A	G	NM_006581 // downstream // 50918 // Hs.200282 // FUT9 // 10690 // Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA. /// NM_015323 // upstream // 265043 // Hs.149367 // KIAA0776 // 23376 // Homo sapiens KIAA0776 (KIAA0776), m	FUT9	FUT9, Homo sapiens fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), q16.1
SNP_A-1798603	gtaacaagtattgtta[A/C]ggatgtagaggagcag	A	C	NM_020482 // downstream // 5588 // Hs.283689 // FHL5 // 9457 // Homo sapiens four and a half LIM domains 5 (FHL5), mRNA. /// NM_030784 // downstream // 175824 // Hs.485990 // GPR63 // 81491 // Homo sapiens G protein-coupled receptor 63 (GPR63), mRNA. ///	FHL5	FHL5, Homo sapiens four and a half LIM domains 5 (FHL5), q16.1
SNP_A-1986952	gagagtgctacatcaa[C/T]ctaaaatggcttcctt	C	T	NM_020482 // downstream // 143917 // Hs.283689 // FHL5 // 9457 // Homo sapiens four and a half LIM domains 5 (FHL5), mRNA. /// NM_030784 // downstream // 37495 // Hs.485990 // GPR63 // 81491 // Homo sapiens G protein-coupled receptor 63 (GPR63), mRNA. ///	FHL5	FHL5, Homo sapiens four and a half LIM domains 5 (FHL5), q16.1
SNP_A-1986956	ctttgactgccttgc[G/T]gaagagtaacccacaa	G	T	NM_014165 // upstream // 11644 // Hs.512144 // C6orf66 // 29078 // Homo sapiens chromosome 6 open reading frame 66 (C6orf66), mRNA. /// NM_052904 // upstream // 15209 // Hs.45056 // KIAA1900 // 114792 // Homo sapiens KIAA1900 (KIAA1900), mRNA. /// ENST000	C6orf66	C6orf66, Homo sapiens chromosome 6 open reading frame 66 (C6orf66), q16.1
SNP_A-1871384	tctaaatgctgtatag[C/T]catttcatttagcagac	C	T	NM_052904 // intron // 0 // Hs.45056 // KIAA1900 // 114792 // Homo sapiens KIAA1900 (KIAA1900), mRNA. /// ENST00000334273 // intron // 0 // — // — // —	KIAA1900	KIAA1900, Homo sapiens KIAA1900 (KIAA1900), q16.1
SNP_A-2086047	actctcaggacattaa[A/T]tccttctcaacctgtg	A	T	NM_052904 // intron // 0 // Hs.45056 // KIAA1900 // 114792 // Homo sapiens KIAA1900 (KIAA1900), mRNA. /// ENST00000334273 // intron // 0 // — // — // —	KIAA1900	KIAA1900, Homo sapiens KIAA1900 (KIAA1900), q16.1
SNP_A-1796401	ggtgtttaaaaatgta[G/T]agaaaccacttgcata	G	T	NM_198468 // upstream // 294128 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 1257431 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2114263	agggaaggagtaccaa[A/C]agactgaaccatttac	A	C	NM_198468 // upstream // 400862 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 1150697 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-2191082	catagtacttgacaaa[C/T]aagagtttcataaatg	C	T	NM_198468 // upstream // 430902 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 1120657 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-2135638	atatttttgccccc[A/G]gatgttctaaagtgtt	A	G	NM_198468 // upstream // 587174 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 964385 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.1
SNP_A-1926985	ttattcttggataac[A/C]aactggagaacagaat	A	C	NM_198468 // upstream // 1197328 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 354231 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-1986978	tgctctattgtaacaa[C/T]cttgtaactggctttc	C	T	NM_198468 // upstream // 1207782 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 343777 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-1785426	ggctatttttcactca[C/T]ctatcaaggaacgtg	C	T	NM_198468 // upstream // 1218498 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 333061 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-1861298	tcatcaagcgattcat[C/T]aaatctgtgatagaac	C	T	NM_198468 // upstream // 1247426 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 304133 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2248935	ctgttgtaagtaagca[C/T]ccacttgctaaagtg	C	T	NM_198468 // upstream // 1248053 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 303506 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2049870	aaggaaatctgtattc[C/T]attcggagtgtgtgat	C	T	NM_198468 // upstream // 1504178 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 47381 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2238883	ctcttcacgaaggaaa[G/T]gagggctgttgtcttg	G	T	NM_198468 // upstream // 1542636 // Hs.444292 // C6orf167 // 253714 // Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA. /// NM_005604 // upstream // 8923 // Hs.182505 // POU3F2 // 5454 // Homo sapiens POU domain, class 3, transcription f	C6orf167	C6orf167, Homo sapiens chromosome 6 open reading frame 167 (C6orf167), q16.2
SNP_A-2129549	atacactatatataaa[C/T]gggagccaaatggca	C	T	NM_012160 // Hs.536850 // FBXL4 // 26235 // Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA. /// ENST00000229971 // upstream // 76400 // — // — // — /// ENST00000305402 // upstream // 150335 // — // -	FBXL4	FBXL4, Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), q16.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1986994	tacttattgaataaaac[A/G]aatagcagtcttacag	A	G	NM_012160 // upstream // 143344 // Hs.536850 // FBXL4 // 26235 // Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA. /// ENST00000229971 // upstream // 143344 // --- // --- // --- /// ENST00000305402 // upstream // 83391 // --- //	FBXL4	FBXL4, Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), q16.2
SNP_A-1909089	tgtatcaggatgtatc[A/T]cttgtagtgtaacagg	A	T	NM_012160 // upstream // 222472 // Hs.536850 // FBXL4 // 26235 // Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA. /// ENST00000229971 // upstream // 222472 // --- // --- // --- /// ENST00000305402 // upstream // 4263 // --- // -	FBXL4	FBXL4, Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), q16.2
SNP_A-2310763	ggaagcagtatagtca[C/T]taagagaaagagatcc	C	T	NM_012160 // upstream // 222516 // Hs.536850 // FBXL4 // 26235 // Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA. /// ENST00000229971 // upstream // 222516 // --- // --- // --- /// ENST00000305402 // upstream // 4219 // --- // -	FBXL4	FBXL4, Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), q16.2
SNP_A-2058297	aatcaatattggaggc[C/T]acttgcagatactatt	C	T	NM_032511 // downstream // 63494 // Hs.486010 // C6orf168 // 84553 // Homo sapiens chromosome 6 open reading frame 168 (C6orf168), mRNA. /// ENST00000305402 // downstream // 42189 // --- // --- // --- /// ENST00000275057 // downstream // 63494 // -	C6orf168	C6orf168, Homo sapiens chromosome 6 open reading frame 168 (C6orf168), q16.2
SNP_A-1753727	gcacctgatacaggtctgtctccc[G/T]gagcaatgcttcagttct ccacatt	G	T	NM_032511 // intron // 0 // Hs.16491 // C6orf168 // 84553 // chromosome 6 open reading frame 168	C6orf168	C6orf168, , rs4839746, chromosome 6 open reading frame 168,q16.2
SNP_A-1851572	tattctcatgagcaaa[C/G]ctgaaagtacttcca	C	G	NM_032511 // intron // 0 // Hs.486010 // C6orf168 // 84553 // Homo sapiens chromosome 6 open reading frame 168 (C6orf168), mRNA. /// ENST00000275057 // intron // 0 // --- // --- // ---	C6orf168	C6orf168, Homo sapiens chromosome 6 open reading frame 168 (C6orf168), q16.2
SNP_A-1946589	tttaaatggaatgttc[A/G]agaagtcaggtattaa	A	G	NM_032511 // intron // 0 // Hs.486010 // C6orf168 // 84553 // Homo sapiens chromosome 6 open reading frame 168 (C6orf168), mRNA. /// ENST00000275057 // intron // 0 // --- // --- // ---	C6orf168	C6orf168, Homo sapiens chromosome 6 open reading frame 168 (C6orf168), q16.2
SNP_A-2164050	caaaagatttaggta[A/C]gaacaggcagtcattg	A	C	NM_032870 // upstream // 14652 // Hs.520287 // C6orf111 // 25957 // Homo sapiens chromosome 6 open reading frame 111 (C6orf111), mRNA. /// ENST00000296888 // upstream // 14652 // --- // --- // --- /// ENST00000357695 // upstream // 4035 // --- // -	C6orf111	C6orf111, Homo sapiens chromosome 6 open reading frame 111 (C6orf111), q16.2
SNP_A-1987002	aataagagaacaggca[A/T]caadtatcttttgaat	A	T	ENST00000327681 // 3UTR // 0 // --- // --- // ---	-	q16.2
SNP_A-2112549	aggcacctgataactal[A/G]agacagctcctatatc	A	G	ENST00000327681 // intron // 0 // --- // --- // ---	-	q16.2
SNP_A-1827231	taacctgagttggga[C/G]aaaatggattaaacat	C	G	ENST00000327681 // intron // 0 // --- // --- // ---	-	q16.3
SNP_A-2284670	gatcaggccagtgcat[A/G]agtcaccttgagggtc	A	G	ENST00000329966 // intron // 0 // --- // --- // ---	-	q16.3
SNP_A-1913699	tgtgtatcaagccata[C/T]ctgggagaagaagtgg	C	T	NM_005190 // downstream // 18835 // Hs.430646 // CCNC // 892 // Homo sapiens cyclin C (CCNC), mRNA. /// ENST00000327681 // upstream // 14772 // --- // --- // --- /// ENST00000329966 // upstream // 8121 // --- // --- // --- /// ENST00000329629	CCNC	CCNC, Homo sapiens cyclin C (CCNC), q16.3
SNP_A-1873603	tctcaccagcagtgga[C/T]taatgataagcagatt	C	T	NM_021620 // downstream // 66852 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 237680 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1987008	gtctgtggaactctgg[A/T]catcagctttattaac	A	T	NM_021620 // downstream // 98486 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 205846 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-2172510	caattccatgctaaga[A/G]ataaactatggatatg	A	G	NM_021620 // downstream // 138012 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 166320 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA.	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2053822	aagtgtctgtaatagt[C/T]aaggagtctcctcatg	C	T	NM_021620 // downstream // 165139 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 139193 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA.	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1910419	tgtcccaagagaaatt[C/G]aaagactgccatggca	C	G	NM_021620 // downstream // 185490 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 118842 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA.	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1935152	ttctgcacctgtcaaa[A/G]aaccaatatcccttaac	A	G	NM_021620 // downstream // 264744 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 39588 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1987014	cctctttctctgtaga[C/T]gcttagggttcagcct	C	T	NM_021620 // downstream // 279535 // Hs.287386 // PRDM13 // 59336 // Homo sapiens PR domain containing 13 (PRDM13), mRNA. /// NM_032503 // downstream // 24797 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /	PRDM13	PRDM13, Homo sapiens PR domain containing 13 (PRDM13), q16.3
SNP_A-1742677	agtaaatacagctgtcacatattt[C/T]catttgtactggagacg acagtga	C	T	NM_005068 // intron // 0 // Hs.105925 // SIM1 // 6492 // single-minded homolog 1 (Drosophila)	SIM1	SIM1 , rs718268, single-minded homolog 1 (Drosophila), q16.3
SNP_A-1830072	taatactaataatggaa[A/C]aggcacgatgagcaaa	A	C	NM_032503 // upstream // 359869 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /// NM_005068 // downstream // 34682 // Hs.534129 // SIM1 // 6492 // Homo sapiens single-minded homolog 1 (Drosophila) (SIM1), m	GPR145	GPR145, Homo sapiens G protein-coupled receptor 145 (GPR145), q16.3
SNP_A-1987025	aaaaagactgtcaact[A/G]aaagagtgctataag	A	G	NM_032503 // upstream // 390730 // Hs.434366 // GPR145 // 84539 // Homo sapiens G protein-coupled receptor 145 (GPR145), mRNA. /// NM_005068 // downstream // 3921 // Hs.534129 // SIM1 // 6492 // Homo sapiens single-minded homolog 1 (Drosophila) (SIM1), mR	GPR145	GPR145, Homo sapiens G protein-coupled receptor 145 (GPR145), q16.3
SNP_A-1701437	ttaaaatttttaaagaaaattta[G/T]gttcacacaaaatctcaca aatatt	G	T	NM_006828 // intron // 0 // Hs.143917 // HELIC1 // 10973 // helicase, ATP binding 1	HELIC1	HELIC1 , rs240165, helicase, ATP binding 1, q16.3
SNP_A-1918240	ttaaagagcaggactat[A/G]gcacttcaattataac	A	G	NM_006828 // intron // 0 // Hs.486031 // ASCC3 // 10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// ENST00000324696 // intron // 0 // — // — // — /// ENST00000262902 // intron // 0 // — // — // –	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-1987037	tataataaagctaaag[C/G]acaaagagtgtcacct	C	G	NM_006828 // intron // 0 // Hs.486031 // ASCC3 // 10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// ENST00000324696 // intron // 0 // — // — // — /// ENST00000262902 // intron // 0 // — // — // –	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-1958915	tttctcctttaaac[A/G]acaaactagggccagg	A	G	NM_006828 // intron // 0 // Hs.486031 // ASCC3 // 10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// ENST00000324696 // intron // 0 // — // — // — /// ENST00000262902 // intron // 0 // — // — // –	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-1931258	ttccatttcacttac[A/T]actgcaaaagattga	A	T	NM_006828 // upstream // 335706 // Hs.486031 // ASCC3 // 10973 // Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), mRNA. /// NM_022091 // upstream // 322468 // Hs.486031 // DJ467N11.1 // 63921 // Homo sapiens dJ467N11.1 protein (D	ASCC3	ASCC3, Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), q16.3
SNP_A-1720675	attcaaacacacatatatatatatg[C/T]aaactatgatagaaccc cagctagt	C	T	NM_021956 // intron // 0 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // intron // 0 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2 , rs2399711, glutamate receptor, ionotropic, kainate 2, q16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2080141	accgtagactgaagga[A/C]gaaggccgattttcct	A	C	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1802231	gtatatattgaatgta[C/T]agttatgcaacttaag	C	T	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1987062	taaaccttgcataaat[A/G]aaacattttcttgtct	A	G	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1918269	ttaaagcaggaataga[A/T]caaatacatgaggctg	A	T	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2025335	aaaatcaaatattacc[A/T]ctaagtcatgtatata	A	T	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2259035	ctttttccctaaaga[A/G]gacagccctttcagaa	A	G	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2166907	caaatttttctaagc[A/C]aatatgcaaaacagca	A	C	NM_175768 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // intron // 0 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic,	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1658534	aaattcctatgaaatacaaatgaaa[C/G]ctaaatctcataatttg aatggatt	C	G	NM_021956 // downstream // 423699 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // downstream // 423699 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2 , rs479856, glutamate receptor, ionotropic, kainate 2 ,q16.3
SNP_A-1673546	tagagccctgaatgacttttctgag[A/G]atttaatctagttgcatag ctattt	A	G	NM_021956 // downstream // 482526 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // downstream // 482526 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2 , rs9322664, glutamate receptor, ionotropic, kainate 2 ,q16.3
SNP_A-2205879	ccatagctgaaaatac[A/T]atagctgaaagcatgg	A	T	NM_175768 // downstream // 442144 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 437642 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate rece	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1700482	aggatagataatttgtttcaaagta[C/T]atgtaacatttatcaattta gactg	C	T	NM_021956 // downstream // 499014 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // downstream // 499014 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2 , rs1934009, glutamate receptor, ionotropic, kainate 2 ,q16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2275458	gagaattctactaaaa[C/T]ctgggcatcaatgtat	C	T	NM_175768 // downstream // 534331 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 529829 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate rece	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1688386	aaaatcacacatttagcaatttta[G/T]ctgtttagcaataatttcca acatc	G	T	NM_021956 // downstream // 645689 // Hs.307494 // GRIK2 // 2898 // downstream // 645689 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // downstream // 645689 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2, rs10499034, glutamate receptor, ionotropic, kainate 2 ,q16.3
SNP_A-1644066	gcattggaataaaatatagtggacc[A/G]tcaacttatgatacctatt gattga	A	G	NM_021956 // downstream // 665857 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // downstream // 665857 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2, rs967405, glutamate receptor, ionotropic, kainate 2 ,q16.3
SNP_A-1704413	ttagttgtgtctcttgtcaaatcca[A/G]tatctgcttacaagagaaa cacct	A	G	NM_021956 // downstream // 682075 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2 /// NM_175768 // downstream // 682075 // Hs.307494 // GRIK2 // 2898 // glutamate receptor, ionotropic, kainate 2	GRIK2	GRIK2, rs1431213, glutamate receptor, ionotropic, kainate 2 ,q16.3
SNP_A-2158582	attgtagggatgtacc[C/G]gagttattcatgtatt	C	G	NM_175768 // downstream // 983443 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 978941 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate rece	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2118663	agtaattttgtccag[A/G]ccaatgttctagagag	A	G	NM_175768 // downstream // 1007172 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1002670 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2167770	caacccttattcttaa[A/G]gcttgcaagaggttta	A	G	NM_175768 // downstream // 1023416 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1018914 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1956917	tttaagcaatcctta[C/G]catccaacatccagta	C	G	NM_175768 // downstream // 1029786 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1025284 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2238737	ctcttaagctaagtaa[C/T]cagggctacaattagt	C	T	NM_175768 // downstream // 1031370 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1026868 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1821412	gtttggagagttctca[A/G]ataaatgaaaacagat	A	G	NM_175768 // downstream // 1038882 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1034380 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2195844	catgtatagcagctga[C/T]aacaatgtttaatat	C	T	NM_175768 // downstream // 1134410 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1129908 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2118454	agtaaggtgtcttcaa[C/T]atatgcagtttgaca	C	T	NM_175768 // downstream // 1222941 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1218439 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1959294	tttgatgtgcaaaga[A/G]attggctaaatacttt	A	G	NM_175768 // downstream // 1495932 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1491430 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2021345	aaaaaactattattca[A/C]aatacgcaaacaactg	A	C	NM_175768 // downstream // 1497192 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1492690 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1877242	tctgctttgactgcct[A/G]acaatatctttctgac	A	G	NM_175768 // downstream // 1500653 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1496151 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1842698	tagtaacattctaaact[A/G]gtattatcaggttata	A	G	NM_175768 // downstream // 1502080 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1497578 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2011963	gaaaaactgccttaaa[G/T]atgtcaactaataata	G	T	NM_175768 // downstream // 1505470 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1500968 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2043275	aactgctgtgatccaa[C/T]aagtctaagtaatata	C	T	NM_175768 // downstream // 1511766 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1507264 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2153798	attagtggtatgtgg[A/T]agaattgagttatctg	A	T	NM_175768 // downstream // 1518935 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1514433 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-2110633	aggacatcggcacagg[A/C]aaatgttcatggcga	A	C	NM_175768 // downstream // 1538046 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1533544 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1869985	tccttgagaaacaaca[A/T]ggaaaatagagcaataa	A	T	NM_175768 // downstream // 1543273 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1538771 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1884221	tgaaggagctgtagaa[A/T]agaacagatgggagtc	A	T	NM_175768 // downstream // 1702091 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1697589 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2219912	ccttagtggtcttgca[C/T]aaaatctggaacagtt	C	T	NM_175768 // downstream // 1843730 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 1839228 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1925071	ttatcacttccaaata[A/G]cctctagaaaggacat	A	G	NM_175768 // downstream // 2009696 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, mRNA. /// NM_021956 // downstream // 2005194 // Hs.98262 // GRIK2 // 2898 // Homo sapiens glutamate re	GRIK2	GRIK2, Homo sapiens glutamate receptor, ionotropic, kainate 2 (GRIK2), transcript variant 2, q16.3
SNP_A-1816926	gttattcagccagtcc[C/T]gaaaagggtaatatcc	C	T	NM_020771 // downstream // 227829 // Hs.434340 // HACE1 // 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 406711 // --- // --- // --- // --- /// ENST000003	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q16.3
SNP_A-2219789	ccttaccaaaagctaa[A/T]tgcattgtcagtagta	A	T	NM_020771 // downstream // 130710 // Hs.434340 // HACE1 // 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 503830 // --- // --- // --- // --- /// ENST000003	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q21
SNP_A-1826131	taaatgtttaccataa[A/G]taaggccacaaataaa	A	G	NM_020771 // downstream // 10601 // Hs.434340 // HACE1 // 57531 // Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), mRNA. /// ENST00000355520 // downstream // 623939 // --- // --- // --- // --- /// ENST0000035	HACE1	HACE1, Homo sapiens HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1 (HACE1), q21
SNP_A-1876903	tctgccatgtagcaaa[A/T]gatcagcttacagggc	A	T	NM_001004317 // downstream // 1143 // Hs.23616 // FLJ16517 // 389421 // Homo sapiens FLJ16517 protein (FLJ16517), mRNA. /// NM_007073 // downstream // 14737 // Hs.221660 // BVES // 11149 // Homo sapiens blood vessel epicardial substance (BVES), transcript	FLJ16517	FLJ16517, Homo sapiens FLJ16517 protein (FLJ16517), q21
SNP_A-2211778	ccctctagaaccaaac[C/T]atcaatgcaccaaggc	C	T	NM_002726 // intron // 0 // Hs.436564 // PREP // 5550 // Homo sapiens prolyl endopeptidase (PREP), mRNA. /// ENST00000229430 // intron // 0 // --- // --- // --- // ---	PREP	PREP, Homo sapiens prolyl endopeptidase (PREP), q21
SNP_A-1644142	ttttaggacacaaaggtaaagtagg[C/T]aaagatctttcaagaacttgtaatt	C	T	NM_001198 // upstream // 296690 // Hs.381140 // PRDM1 // 639 // PR domain containing 1, with ZNF domain /// NM_002726 // upstream // 386739 // Hs.433986 // PREP // 5550 // prolyl endopeptidase	PRDM1	PRDM1 , rs2202766, PR domain containing 1, with ZNF domain ,q21
SNP_A-1830032	taatacatttttgata[C/T]atggcagctgctaaat	C	T	NM_002726 // upstream // 463850 // Hs.436564 // PREP // 5550 // Homo sapiens prolyl endopeptidase (PREP), mRNA. /// NM_182907 // upstream // 219376 // Hs.436023 // PRDM1 // 639 // Homo sapiens PR domain containing 1, with ZNF domain (PRDM1), transcript va	PREP	PREP, Homo sapiens prolyl endopeptidase (PREP), q21
SNP_A-2027212	aaacagtgtgtaggcc[C/T]ctataagtatcatggg	C	T	NM_182907 // downstream // 40209 // Hs.436023 // PRDM1 // 639 // Homo sapiens PR domain containing 1, with ZNF domain (PRDM1), transcript variant 2, mRNA. /// NM_001198 // downstream // 40209 // Hs.436023 // PRDM1 // 639 // Homo sapiens PR domain containi	PRDM1	PRDM1, Homo sapiens PR domain containing 1, with ZNF domain (PRDM1), transcript variant 2, q21
SNP_A-1987135	ttggcacccactttgg[A/G]caccttatagtattt	A	G	NM_004849 // upstream // 18541 // Hs.486063 // APG5L // 9474 // Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA. /// U83115 // upstream // 168008 // Hs.486074 // AIM1 // 202 // Human non-lens beta gamma-crystallin like protein (AIM1) mRNA	APG5L	APG5L, Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2267396	gaataggtgaccatta[C/T]agttatctctaacta	C	T	NM_004849 // upstream // 72007 // Hs.486063 // APG5L // 9474 // Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA. /// U83115 // upstream // 114542 // Hs.486074 // AIM1 // 202 // Human non-lens beta gamma-crystallin like protein (AIM1) mRNA	APG5L	APG5L, Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), q21
SNP_A-2107106	agcggacacctgaaga[C/T]gaaaaggctgcaggag	C	T	NM_004849 // upstream // 87044 // Hs.486063 // APG5L // 9474 // Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA. /// U83115 // upstream // 99505 // Hs.486074 // AIM1 // 202 // Human non-lens beta gamma-crystallin like protein (AIM1) mRNA.	APG5L	APG5L, Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), q21
SNP_A-1987142	aaaatcatctgagcag[A/G]caaatataactcttt	A	G	NM_004849 // upstream // 94045 // Hs.486063 // APG5L // 9474 // Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA. /// U83115 // upstream // 92504 // Hs.486074 // AIM1 // 202 // Human non-lens beta gamma-crystallin like protein (AIM1) mRNA.	APG5L	APG5L, Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), q21
SNP_A-1987146	tcttcacaaaaaccac[A/C]gccaaaaatgtgcctt	A	C	U83115 // intron // 0 // Hs.486074 // AIM1 // 202 // Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds. /// ENST00000230041 // intron // 0 // --- // --- // ---	AIM1	AIM1, Human non-lens beta gamma-crystallin like protein (AIM1) partial cds, q21
SNP_A-1650902	agttggggagcttcaaaataaa[G/T]gctgatcatgaaaaata taatgctc	G	T	NM_016487 // upstream // 204036 // Hs.36069 // C6orf203 // 51250 // chromosome 6 open reading frame 203 /// NM_018292 // downstream // 29971 // Hs.406917 // QRSL1 // 55278 // glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	C6orf203	C6orf203, rs10485221, chromosome 6 open reading frame 203, q21
SNP_A-2275479	gagaattgtgaaaaag[A/T]ctgccctggctgttgt	A	T	NM_018292 // downstream // 27711 // Hs.406917 // QRSL1 // 55278 // Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), mRNA. /// NM_016487 // upstream // 206296 // Hs.486084 // C6orf203 // 51250 // Homo sapiens chromosome 6 open	QRSL1	QRSL1, Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), q21
SNP_A-1858556	tcagaggcccatgtta[A/G]gaaattgtatagaaac	A	G	NM_018292 // downstream // 100503 // Hs.406917 // QRSL1 // 55278 // Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), mRNA. /// NM_016487 // upstream // 133504 // Hs.486084 // C6orf203 // 51250 // Homo sapiens chromosome 6 open	QRSL1	QRSL1, Homo sapiens glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (QRSL1), q21
SNP_A-2089002	acttaaatagctaaaa[C/T]gacacacaagaaacct	C	T	NM_020381 // intron // 0 // Hs.486095 // C6orf210 // 57107 // Homo sapiens chromosome 6 open reading frame 210 (C6orf210), mRNA. /// ENST00000296990 // intron // 0 // --- // --- // ---	C6orf210	C6orf210, Homo sapiens chromosome 6 open reading frame 210 (C6orf210), q21
SNP_A-2031360	aaagggaatttgccc[A/G]acaggagataagtacc	A	G	ENST00000317357 // intron // 0 // --- // --- // ---	-	q21
SNP_A-2049429	aagctgatatcctcc[A/G]aaatgatttagtatta	A	G	ENST00000317357 // intron // 0 // --- // --- // ---	-	q21
SNP_A-1929783	ttcatcattacccaaa[C/G]tttctgtctgcccttg	C	G	ENST00000317357 // intron // 0 // --- // --- // ---	-	q21
SNP_A-1645322	aatgctaacagtgaaagtcttaggc[C/T]ataaaggtcaaagaa gtaaaggtga	C	T	NM_018013 // intron // 0 // Hs.346203 // FLJ10159 // 55084 // hypothetical protein FLJ10159	FLJ10159	FLJ10159, rs1028498, hypothetical protein FLJ10159,q21
SNP_A-1935979	ttcttaccataatagg[C/G]agcttattgtcccaca	C	G	NM_018013 // upstream // 34004 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// ENST00000317357 // downstream // 11114 // --- // --- // --- /// ENST00000230065 // upstream // 34004 // --- // --- // ---	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-2231740	ctcaaaagcagcttaa[C/G]tacgatgtaatggaag	C	G	NM_018013 // upstream // 30448 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// ENST00000317357 // downstream // 14670 // --- // --- // --- /// ENST00000230065 // upstream // 30448 // --- // --- // ---	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-1987167	catacctggtaagggg[C/T]aaagctctatggaa	C	T	NM_018013 // upstream // 26233 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// ENST00000317357 // downstream // 18885 // --- // --- // --- /// ENST00000230065 // upstream // 26233 // --- // --- // ---	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2245622	ctgggcatctcaatta[A/T]gataaaagcttccctt	A	T	NM_018013 // upstream // 2448 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// ENST00000317357 // downstream // 42670 // --- // --- // --- /// ENST00000230065 // upstream // 2448 // --- // --- // -	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-1922127	ttacttaagtgagtgd[A/G]caagaagggctccgt	A	G	NM_018013 // downstream // 14392 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 69096 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4).	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-2141388	atctgttaccagtata[C/T]aaggaagcccatgaac	C	T	NM_018013 // downstream // 19062 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 64426 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4).	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-2248667	ctgttcagajctcgc[A/G]ctagttgattagct	A	G	NM_018013 // downstream // 25327 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 58161 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4).	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-1906815	tggttatcaacccccc[A/G]cagaacacaaagcccc	A	G	NM_018013 // downstream // 26295 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 57193 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4).	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-2030916	aaaggaatatttgccc[C/T]atctcttctctcatgt	C	T	NM_018013 // downstream // 72172 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 11316 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4).	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-2220754	ccttgaggtagaatga[A/G]gactcagtgtgttggt	A	G	NM_018013 // downstream // 73735 // Hs.445244 // --- // 0 // Homo sapiens hypothetical protein FLJ10159 (FLJ10159), mRNA. /// NM_198081 // downstream // 9753 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), m	-	-, Homo sapiens hypothetical protein FLJ10159 (FLJ10159), q21
SNP_A-1987176	tcccattgctttttagal[C/T]gaagcccagactctgtt	C	T	NM_198081 // intron // 0 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), mRNA. /// ENST00000341815 // intron // 0 // --- // --- // ---	SCML4	SCML4, Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), q21
SNP_A-2178524	cactcgctgattctgal[A/G]gcttagtacttaggcc	A	G	NM_198081 // intron // 0 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), mRNA. /// ENST00000341815 // intron // 0 // --- // --- // ---	SCML4	SCML4, Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), q21
SNP_A-1987177	aagttttcttgttcatg[A/C]agtgatggcaggagga	A	C	NM_198081 // intron // 0 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), mRNA. /// ENST00000341815 // intron // 0 // --- // --- // ---	SCML4	SCML4, Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), q21
SNP_A-1987178	gtgaggaaaaaagggtc[A/G]atttgcagagatttct	A	G	NM_198081 // intron // 0 // Hs.486109 // SCML4 // 256380 // Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), mRNA. /// ENST00000341815 // intron // 0 // --- // --- // ---	SCML4	SCML4, Homo sapiens sex comb on midleg-like 4 (Drosophila) (SCML4), q21
SNP_A-1733760	tgtcacaaagccagcaccagcaaga[A/G]cgacaccgagctc ccacgctttgtt	A	G	NM_007214 // upstream // 62850 // Hs.330767 // SEC63 // 11231 // SEC63-like (S. cerevisiae) /// NM_014028 // downstream // 21827 // Hs.163724 // OSTM1 // 28962 // osteopetrosis associated transmembrane protein 1	SEC63	SEC63 , rs10484905, SEC63-like (S. cerevisiae) ,q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181295	cagacctcacagagga[A/T]gtgtcatttagaagt	A	T	NM_007214 // upstream // 41928 // Hs.529957 // SEC63 // 11231 // Homo sapiens SEC63-like (S. cerevisiae) (SEC63), mRNA. /// NM_014028 // downstream // 42703 // Hs.226780 // OSTM1 // 28962 // Homo sapiens osteopetrosis associated transmembrane protein 1 (O	SEC63	SEC63, Homo sapiens SEC63-like (S. cerevisiae) (SEC63), q21
SNP_A-1895575	tgcctattgatgctaa[A/G]tcctgaagtgatgag	A	G	NM_007214 // upstream // 52984 // Hs.529957 // SEC63 // 11231 // Homo sapiens SEC63-like (S. cerevisiae) (SEC63), mRNA. /// NM_014028 // downstream // 31647 // Hs.226780 // OSTM1 // 28962 // Homo sapiens osteopetrosis associated transmembrane protein 1 (O	SEC63	SEC63, Homo sapiens SEC63-like (S. cerevisiae) (SEC63), q21
SNP_A-2209945	ccccacaattacaaaa[C/T]aaggtctgagtgccac	C	T	NM_007214 // upstream // 78762 // Hs.529957 // SEC63 // 11231 // Homo sapiens SEC63-like (S. cerevisiae) (SEC63), mRNA. /// NM_014028 // downstream // 5869 // Hs.226780 // OSTM1 // 28962 // Homo sapiens osteopetrosis associated transmembrane protein 1 (OS	SEC63	SEC63, Homo sapiens SEC63-like (S. cerevisiae) (SEC63), q21
SNP_A-2124389	agttcaagatgcggaa[C/T]tgcaaaaattggacaa	C	T	NM_145315 // intron // 0 // Hs.259666 // LACE1 // 246269 // Homo sapiens lactation elevated 1 (LACE1). mRNA. /// ENST00000258002 // intron // 0 // — // — // — // —	LACE1	LACE1, Homo sapiens lactation elevated 1 (LACE1), q21
SNP_A-1987189	gtatttttggcgcaac[C/T]cggaactcctgagtgt	C	T	NM_001455 // downstream // 18690 // Hs.220950 // FOXO3A // 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, mRNA. /// NM_201559 // downstream // 18690 // Hs.220950 // FOXO3A // 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcrip	FOXO3A	FOXO3A, Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, q21
SNP_A-2086638	actgaagatggaaaga[A/G]cctggtacccaaatca	A	G	NM_001455 // downstream // 82088 // Hs.220950 // FOXO3A // 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, mRNA. /// NM_201559 // downstream // 82088 // Hs.220950 // FOXO3A // 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcrip	FOXO3A	FOXO3A, Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, q21
SNP_A-2059510	aatctcacaacagaaa[G/T]aattcatgagcagcct	G	T	NM_001455 // downstream // 113403 // Hs.220950 // FOXO3A // 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, mRNA. /// NM_201559 // downstream // 113403 // Hs.220950 // FOXO3A // 2309 // Homo sapiens forkhead box O3A (FOXO3A), transcr	FOXO3A	FOXO3A, Homo sapiens forkhead box O3A (FOXO3A), transcript variant 1, q21
SNP_A-2249554	cttaacttgctaattat[C/T]aaagacggagattaaa	C	T	NM_173830 // downstream // 35556 // Hs.532161 // C6orf182 // 285753 // Homo sapiens chromosome 6 open reading frame 182 (C6orf182), mRNA. /// NM_173830 // downstream // 34816 // Hs.532161 // C6orf182 // 285753 // Homo sapiens chromosome 6 open reading fra	C6orf182	C6orf182, Homo sapiens chromosome 6 open reading frame 182 (C6orf182), q21
SNP_A-2219942	ccttatatgtccaata[A/G]taaatggcacaatgtg	A	G	NM_014845 // intron // 0 // Hs.529959 // KIAA0274 // 9896 // Homo sapiens KIAA0274 (KIAA0274). mRNA. /// ENST00000230124 // intron // 0 // — // — // — // —	KIAA0274	KIAA0274, Homo sapiens KIAA0274 (KIAA0274), q21
SNP_A-1904470	tggggacttcttgc[A/G]cttgttgagagaaaac	A	G	NM_014845 // intron // 0 // Hs.529959 // KIAA0274 // 9896 // Homo sapiens KIAA0274 (KIAA0274). mRNA. /// ENST00000230124 // intron // 0 // — // — // — // —	KIAA0274	KIAA0274, Homo sapiens KIAA0274 (KIAA0274), q21
SNP_A-2156198	attctacagcttctta[C/T]atctgcaatagctgtc	C	T	NM_015891 // downstream // 1983 // Hs.428147 // CDC40 // 51362 // Homo sapiens cell division cycle 40 homolog (yeast) (CDC40), mRNA. /// NM_004032 // downstream // 157985 // Hs.195313 // DDO // 8528 // Homo sapiens D-aspartate oxidase (DDO), transcript va	CDC40	CDC40, Homo sapiens cell division cycle 40 homolog (yeast) (CDC40), q21
SNP_A-2125608	agtttccgtaaatgta[A/G]cgagaggggcgctggc	A	G	NM_033125 // intron // 0 // Hs.520319 // SLC22A16 // 85413 // Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), mRNA. /// ENST00000265599 // intron // 0 // — // — // — // — - /// ENST00000330550 // intron // 0	SLC22A16	SLC22A16, Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1987220	tgtccaatatttatca[C/T]gtctggtgtttcact	C	T	NM_033125 // upstream // 48404 // Hs.520319 // SLC22A16 // 85413 // Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), mRNA. /// NM_015076 // downstream // 84933 // Hs.193251 // CDC2L6 // 23097 // Homo sapiens cyclin	SLC22A16	SLC22A16, Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), q21
SNP_A-2163774	caaaacaaaactatct[C/G]aaacagggtctacttc	C	G	NM_033125 // upstream // 56124 // Hs.520319 // SLC22A16 // 85413 // Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), mRNA. /// NM_015076 // downstream // 77213 // Hs.193251 // CDC2L6 // 23097 // Homo sapiens cyclin	SLC22A16	SLC22A16, Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), q21
SNP_A-1894972	tgcccaagagtcctta[C/T]ctggaacctctggtct	C	T	NM_033125 // upstream // 67339 // Hs.520319 // SLC22A16 // 85413 // Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), mRNA. /// NM_015076 // downstream // 85998 // Hs.193251 // CDC2L6 // 23097 // Homo sapiens cyclin	SLC22A16	SLC22A16, Homo sapiens solute carrier family 22 (organic cation transporter), member 16 (SLC22A16), q21
SNP_A-1869241	tcctggccctctgtata[C/T]ggcctttgttagcact	C	T	NM_018593 // intron // 0 // Hs.520321 // SLC16A10 // 117247 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), mRNA. /// ENST00000318989 // intron // 0 // --- // --- // --- // ---	SLC16A10	SLC16A10, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), q21
SNP_A-2193743	catctttcactccaca[A/G]gtatttgttgaacgtc	A	G	NM_018593 // downstream // 35938 // Hs.520321 // SLC16A10 // 117247 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), mRNA. /// NM_153369 // upstream // 419 // Hs.400572 // KIAA1919 // 91749 // Homo sapiens	SLC16A10	SLC16A10, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), q21
SNP_A-2268014	gaatctggaccagaga[G/T]atatagaagatgggcc	G	T	NM_153369 // downstream // 9546 // Hs.400572 // KIAA1919 // 91749 // Homo sapiens KIAA1919 (KIAA1919), mRNA. /// NM_002912 // downstream // 22220 // Hs.232021 // REV3L // 5980 // Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (RE	KIAA1919	KIAA1919, Homo sapiens KIAA1919 (KIAA1919), q21
SNP_A-2254158	cttgatagctgcagtc[C/T]agtagcaatagaaaca	C	T	NM_153369 // downstream // 26274 // Hs.400572 // KIAA1919 // 91749 // Homo sapiens KIAA1919 (KIAA1919), mRNA. /// NM_002912 // downstream // 5492 // Hs.232021 // REV3L // 5980 // Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (RE	KIAA1919	KIAA1919, Homo sapiens KIAA1919 (KIAA1919), q21
SNP_A-2302568	gctacactgttgagaa[A/T]atgcaaattatccact	A	T	NM_002912 // intron // 0 // Hs.232021 // REV3L // 5980 // Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA. /// ENST00000359745 // intron // 0 // — // -	REV3L	REV3L, Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), q21
SNP_A-2130194	atacctcagtcattaa[C/G]ctagagaactgtttaa	C	G	NM_002912 // intron // 0 // Hs.232021 // REV3L // 5980 // Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA. /// ENST00000358835 // intron // 0 // — // — // — /// ENST00000359745 // intron // 0 // — // -	REV3L	REV3L, Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), q21
SNP_A-2238073	ctctgcagaaccctga[C/T]gaattcactgagcaaa	C	T	NM_147686 // upstream // 4423 // Hs.486228 // C6orf4 // 10758 // Homo sapiens chromosome 6 open reading frame 4 (C6orf4), transcript variant 2, mRNA. /// NM_147686 // upstream // 4625 // Hs.486228 // C6orf4 // 10758 // Homo sapiens chromosome 6 open readi	C6orf4	C6orf4, Homo sapiens chromosome 6 open reading frame 4 (C6orf4), transcript variant 2, q21
SNP_A-1744387	aactcttcacaaagggaacatgta[C/T]agagtggaacttgcc ttctattct	C	T	NM_002037 // intron // 0 // Hs.390567 // FYN // 2534 // FYN oncogene related to SRC, FGR, YES	FYN	FYN , rs1409836, FYN oncogene related to SRC, FGR, YES.q21
SNP_A-1755228	tgggtaggtacataatacttcaggt[C/T]ccaacaatactggcagt ccatttgg	C	T	NM_002037 // intron // 0 // Hs.390567 // FYN // 2534 // FYN oncogene related to SRC, FGR, YES	FYN	FYN , rs9110683, FYN oncogene related to SRC, FGR, YES.q21
SNP_A-1911502	tgtctttatcctatc[C/T]cttcatcttttttag	C	T	NM_153047 // upstream // 217655 // Hs.390567 // FYN // 2534 // Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, mRNA. /// NM_002037 // upstream // 64293 // Hs.390567 // FYN // 2534 // Homo sapiens FYN oncogene related to SRC	FYN	FYN, Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1821822	gtttlactgtagttc[A/G]ctttggctccatcta	A	G	NM_002290 // CDS // 0 // Hs.213861 // LAMA4 // 3910 // Homo sapiens laminin, alpha 4 (LAMA4), mRNA. /// ENST00000230538 // CDS // 0 // --- // --- // ---	LAMA4	LAMA4, Homo sapiens laminin, alpha 4 (LAMA4), q21
SNP_A-2122519	agtgctgaaaccaggal[C/T]ggatatggaaaaacta	C	T	NM_002290 // upstream // 73758 // Hs.213861 // LAMA4 // 3910 // Homo sapiens laminin, alpha 4 (LAMA4), mRNA. /// ENST00000230538 // upstream // 73758 // --- // --- // --- /// ENST00000243219 // upstream // 74318 // --- // --- // --- /// ENST	LAMA4	LAMA4, Homo sapiens laminin, alpha 4 (LAMA4), q21
SNP_A-2192595	catccaggacacagaa[C/T]acacggttgaatatct	C	T	ENST00000327640 // downstream // 7922 // --- // --- // --- /// ENST00000332292 // downstream // 2252 // --- // --- // ---	-	q21
SNP_A-1676568	aaagatgtctgatagaaatgtgtg[C/T]atctctggcttatctgtcc atggag	C	T	NM_002290 // upstream // 602500 // Hs.437536 // LAMA4 // 3910 // laminin, alpha 4 /// NM_002356 // upstream // 1000254 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich protein kinase C substrate	LAMA4	LAMA4 , rs10499071, laminin, alpha 4 ,q21
SNP_A-1734610	cattatgctttttgctttatgtgc[C/T]gacttctaagcatgtgcatga aaaa	C	T	NM_002290 // upstream // 605404 // Hs.437536 // LAMA4 // 3910 // laminin, alpha 4 /// NM_002356 // upstream // 997350 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich protein kinase C substrate	LAMA4	LAMA4 , rs10499070, laminin, alpha 4 ,q21
SNP_A-1726428	atttgatatgacaccctgatgaag[G/T]gtctcaaaatctatgtga ctcttcc	G	T	NM_002290 // upstream // 608890 // Hs.437536 // LAMA4 // 3910 // laminin, alpha 4 /// NM_002356 // upstream // 993864 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich protein kinase C substrate	LAMA4	LAMA4 , rs9320420, laminin, alpha 4 ,q21
SNP_A-2164004	caaaagaagattatag[G/T]actgttctttctttt	G	T	ENST00000332292 // upstream // 577766 // --- // --- // --- /// ENST00000309379 // upstream // 899423 // --- // --- // ---	-	q21
SNP_A-1728497	ctatgtacatgaaatagtgtatgtg[C/T]aacctaaaaatctgaata agctgta	C	T	NM_002290 // upstream // 801246 // Hs.437536 // LAMA4 // 3910 // laminin, alpha 4 /// NM_002356 // upstream // 801508 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich protein kinase C substrate	LAMA4	LAMA4 , rs2185710, laminin, alpha 4 ,q21
SNP_A-1676346	gctgatatctcaacaggtacttttca[C/T]atttaggctaactgaaat gtgaggt	C	T	NM_002290 // upstream // 886577 // Hs.437536 // LAMA4 // 3910 // laminin, alpha 4 /// NM_002356 // upstream // 716177 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich protein kinase C substrate	LAMA4	LAMA4 , rs2502397, laminin, alpha 4 ,q21
SNP_A-1932568	ttcctgtatgcagaaaa[A/G]agggcaatgtttaaaa	A	G	ENST00000332292 // upstream // 745508 // --- // --- // --- /// ENST00000309379 // upstream // 731681 // --- // --- // ---	-	q21
SNP_A-2245695	ctgggctgtctacccaj[A/G]caactctacagatta	A	G	ENST00000332292 // upstream // 793514 // --- // --- // --- /// ENST00000309379 // upstream // 683675 // --- // --- // ---	-	q21
SNP_A-2202090	ccacagtgattcagaat[C/T]acccacaatcaccaag	C	T	ENST00000332292 // upstream // 796848 // --- // --- // --- /// ENST00000309379 // upstream // 680341 // --- // --- // ---	-	q21
SNP_A-2193912	catgaactcattatgaj[A/C]cttcatggcttaaaat	A	C	ENST00000332292 // upstream // 797650 // --- // --- // --- /// ENST00000309379 // upstream // 679539 // --- // --- // ---	-	q21
SNP_A-1987271	aatatctacagttacct[C/T]gaaaaggctattgaat	C	T	ENST00000332292 // upstream // 808106 // --- // --- // --- /// ENST00000309379 // upstream // 669083 // --- // --- // ---	-	q21
SNP_A-1731005	tacatgacattaggtgttgttttta[A/G]gcttgtaaatgatgcaaaca tttac	A	G	NM_002290 // upstream // 1016466 // Hs.437536 // LAMA4 // 3910 // laminin, alpha 4 /// NM_002356 // upstream // 586288 // Hs.318603 // MARCKS // 4082 // myristoylated alanine-rich protein kinase C substrate	LAMA4	LAMA4 , rs2637524, laminin, alpha 4 ,q21
SNP_A-2290928	gcaaggtttgaaagaa[C/T]ggcttcaaggaaag	C	T	ENST00000332292 // upstream // 904457 // --- // --- // --- /// ENST00000309379 // upstream // 572732 // --- // --- // ---	-	q21
SNP_A-1847204	tatcatttttcatcc[A/T]aacaatgtatggaaa	A	T	ENST00000332292 // upstream // 910776 // --- // --- // --- /// ENST00000309379 // upstream // 566413 // --- // --- // ---	-	q21
SNP_A-1939646	ttgatttggttgcaaa[C/G]agccatagtaaatatca	C	G	ENST00000332292 // upstream // 957856 // --- // --- // --- /// ENST00000309379 // upstream // 519333 // --- // --- // ---	-	q21
SNP_A-1822183	gtttgaagagcaaaa[A/G]tgtctttgaatttggc	A	G	ENST00000332292 // upstream // 961605 // --- // --- // --- /// ENST00000309379 // upstream // 515584 // --- // --- // ---	-	q21
SNP_A-2076857	accaaactacatggaa[A/G]caagttgcaggttacc	A	G	ENST00000332292 // upstream // 970235 // --- // --- // --- /// ENST00000309379 // upstream // 506954 // --- // --- // ---	-	q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1799018	gtaagcatgaacaaaaa[C/T]ccttaaagaagatctg	C	T	ENST00000332292 // upstream // 1124665 // --- // --- // --- // --- /// ENST00000309379 // upstream // 352524 // --- // --- // --- // ---	-	q21
SNP_A-1879172	tcttacctctacaagat[C/T]gaatgttcctaaaaca	C	T	ENST00000332292 // upstream // 1291841 // --- // --- // --- // --- /// ENST00000309379 // upstream // 185348 // --- // --- // --- // ---	-	q21
SNP_A-2154793	attcaacttccaaaaa[C/T]gttctaaatgtcatga	C	T	ENST00000332292 // upstream // 1341932 // --- // --- // --- // --- /// ENST00000309379 // upstream // 135257 // --- // --- // --- // ---	-	q21
SNP_A-2261587	gaaagggtgtttgtaaa[A/G]taiggaggatgtatgg	A	G	NM_173673 // downstream // 13761 // --- // FLJ34503 // 285759 // Homo sapiens hypothetical protein FLJ34503 (FLJ34503), mRNA. /// NM_001527 // downstream // 7780 // Hs.3352 // HDAC2 // 3066 // Homo sapiens histone deacetylase 2 (HDAC2), mRNA. /// ENST0000	FLJ34503	FLJ34503, Homo sapiens hypothetical protein FLJ34503 (FLJ34503), q21
SNP_A-2061118	aatgcaattactatca[C/G]gccagtctagtttca	C	G	NM_153612 // upstream // 763384 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 1115303 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1800015	gtacatcattgtcagat[A/G]acctagaaaataitc	A	G	NM_153612 // upstream // 805966 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 1072721 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2079233	acccatccatttttata[C/G]ataagcagcctgaagt	C	G	NM_153612 // upstream // 829643 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 1049044 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1876538	tctgatgtctggtcta[C/T]gctacagaatgtttgt	C	T	NM_153612 // upstream // 892296 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 986391 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK)	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2276723	gagagttgagtcaacc[A/G]ggcatctatagaagagg	A	G	NM_153612 // upstream // 956045 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 922642 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK)	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2261430	gaaagctgttgagaaa[C/T]gatacacagggatgtt	C	T	NM_153612 // upstream // 962337 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 916350 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK)	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1902243	tggccagaatgagtga[A/G]gagagaaatagtttg	A	G	NM_153612 // upstream // 963492 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 915195 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK)	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2064194	aattcaatagaaactc[A/G]aagatccagactcata	A	G	NM_153612 // upstream // 965533 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 913154 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK)	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2200746	ccaagagaagaggagc[A/G]aaactaaatacttgat	A	G	NM_153612 // upstream // 1073407 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 805280 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1921546	ttacctattggattga[C/T]gttgtatctgtaattt	C	T	NM_153612 // upstream // 1073959 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 804728 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2247211	ctgtcatcattattcc[A/T]ccagacctagaagctg	A	T	NM_153612 // upstream // 1078790 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 799897 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2094995	agaatggataggacgc[C/T]gatgagtttgaggcag	C	T	NM_153612 // upstream // 1224833 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 653854 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1645592	ttgttctattccccttactttctcca[A/G]aatatacagtctctgtctctctt ct	A	G	NM_002031 // downstream // 473893 // Hs.89426 // FRK // 2444 // fyn-related kinase /// NM_153612 // upstream // 1409791 // Hs.510015 // HS3ST5 // 222537 // heparan sulfate (glucosamine) 3-O-sulfotransferase 5	FRK	FRK , rs2350791, fyn-related kinase ,q22.1
SNP_A-1739229	taatagtttctactctcagaacatc[A/G]aactgtattaatataatgtg tacct	A	G	NM_002031 // downstream // 470460 // Hs.89426 // FRK // 2444 // fyn-related kinase /// NM_153612 // upstream // 1413224 // Hs.510015 // HS3ST5 // 222537 // heparan sulfate (glucosamine) 3-O-sulfotransferase 5	FRK	FRK , rs10484297, fyn-related kinase ,q22.1
SNP_A-1692724	cattttggattcattattcagttga[A/G]atggcaattaattgaaactct ctta	A	G	NM_002031 // downstream // 456470 // Hs.89426 // FRK // 2444 // fyn-related kinase /// NM_153612 // upstream // 1427214 // Hs.510015 // HS3ST5 // 222537 // heparan sulfate (glucosamine) 3-O-sulfotransferase 5	FRK	FRK , rs2001149, fyn-related kinase ,q22.1
SNP_A-1754474	aaagcgaattattgttcttctctta[C/T]cttccgctgctttatcatggtt acc	C	T	NM_002031 // downstream // 456381 // Hs.89426 // FRK // 2444 // fyn-related kinase /// NM_153612 // upstream // 1427303 // Hs.510015 // HS3ST5 // 222537 // heparan sulfate (glucosamine) 3-O-sulfotransferase 5	FRK	FRK , rs9320535, fyn-related kinase ,q22.1
SNP_A-1987312	gatgttgtggatacaa[A/G]aaaacataaggtctca	A	G	NM_153612 // upstream // 1428120 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 450567 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2267356	gaatagcatgatgaac[G/T]ataccttgaattatag	G	T	NM_153612 // upstream // 1448401 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 430286 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2261003	gaaagaaattaaggta[C/G]agtagaaatcagagat	C	G	NM_153612 // upstream // 1490024 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 388663 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2287095	gatgtagtacacactg[A/G]actggacattttaaaa	A	G	NM_153612 // upstream // 1541023 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 337664 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2162957	attttgtgagagatga[C/T]gactgaagggaagaca	C	T	NM_153612 // upstream // 1556647 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 322040 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814558	gtgtgcttgatatgaa[C/T]aataaagaagataaaa	C	T	NM_153612 // upstream // 1591286 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 287401 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-2110956	aggagaaaagggatga[C/T]gtaaaaattgttgctg	C	T	NM_153612 // upstream // 1698243 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 180444 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1859375	tcaggaaaagtgaaaa[C/G]cactaagtctaaaaga	C	G	NM_153612 // upstream // 1746677 // Hs.210262 // HS3ST5 // 222537 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), mRNA. /// NM_002031 // downstream // 132010 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK	HS3ST5	HS3ST5, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 5 (HS3ST5), q22.1
SNP_A-1987323	catgtaactaactcaa[A/C]ttcacattaataaaca	A	C	NM_002031 // intron // 0 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK), mRNA. /// ENST00000263809 // intron // 0 // — // — // — // —	FRK	FRK, Homo sapiens fyn-related kinase (FRK), q22.1
SNP_A-2206583	ccatgaaatcctataa[C/T]gtggctttggaaataa	C	T	NM_002031 // intron // 0 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK), mRNA. /// ENST00000263809 // intron // 0 // — // — // — // —	FRK	FRK, Homo sapiens fyn-related kinase (FRK), q22.1
SNP_A-1850499	tattaaagtgccatca[C/T]gtagaagagttgttct	C	T	NM_002031 // intron // 0 // Hs.89426 // FRK // 2444 // Homo sapiens fyn-related kinase (FRK), mRNA. /// ENST00000263809 // intron // 0 // — // — // — // —	FRK	FRK, Homo sapiens fyn-related kinase (FRK), q22.1
SNP_A-2157055	attgaaaacaaaacac[C/T]gtgcagcccatgctgc	C	T	NM_013352 // intron // 0 // Hs.486292 // SART2 // 29940 // Homo sapiens squamous cell carcinoma antigen recognized by T cells 2 (SART2), mRNA. /// ENST00000359564 // intron // 0 // — // — // — // —	SART2	SART2, Homo sapiens squamous cell carcinoma antigen recognized by T cells 2 (SART2), q22.1
SNP_A-1799422	gtaatctagagccata[A/G]aagctgataatgtgaa	A	G	NM_153036 // upstream // 12039 // Hs.350750 // C6orf78 // 221301 // Homo sapiens chromosome 6 open reading frame 78 (C6orf78), mRNA. /// ENST00000310560 // upstream // 2386 // — // — // — // — /// ENST00000343644 // upstream // 12039 // --- // ---	C6orf78	C6orf78, Homo sapiens chromosome 6 open reading frame 78 (C6orf78), q22.1
SNP_A-1749847	acaacacaaagtatagaaacttaac[A/G]gaggctggacttgcc atggcataat	A	G	NM_153453 // upstream // 322514 // Hs.99324 // VGLL2 // 245806 // vestigial like 2 (Drosophila) /// NM_173560 // downstream // 10893 // Hs.352276 // RFXDC1 // 222546 // regulatory factor X domain containing 1 /// NM_182645 // upstream // 322697 // Hs.993	VGLL2	VGLL2 , rs1321364, vestigial like 2 (Drosophila) ,q22.1
SNP_A-1758637	agcatttcctggcatacaacgaata[A/G]ctaaataaaaagcttct tagaaata	A	G	NM_153453 // upstream // 235818 // Hs.99324 // VGLL2 // 245806 // vestigial like 2 (Drosophila) /// NM_173560 // downstream // 97589 // Hs.352276 // RFXDC1 // 222546 // regulatory factor X domain containing 1 /// NM_182645 // upstream // 236001 // Hs.993	VGLL2	VGLL2 , rs9320589, vestigial like 2 (Drosophila) ,q22.1
SNP_A-2171300	caatatgctaaagtta[C/T]agttaacagagtctgc	C	T	NM_173560 // downstream // 48314 // Hs.352276 // RFXDC1 // 222546 // Homo sapiens regulatory factor X domain containing 1 (RFXDC1), mRNA. /// NM_153453 // upstream // 285107 // Hs.99324 // VGLL2 // 245806 // Homo sapiens vestigial like 2 (Drosophila) (VGL	RFXDC1	RFXDC1, Homo sapiens regulatory factor X domain containing 1 (RFXDC1), q22.1
SNP_A-1691788	attatgcaggatttatcccagacat[G/T]caaggagattcaacata caaaaatc	G	T	NM_153453 // upstream // 207916 // Hs.99324 // VGLL2 // 245806 // vestigial like 2 (Drosophila) /// NM_173560 // downstream // 125491 // Hs.352276 // RFXDC1 // 222546 // regulatory factor X domain containing 1 /// NM_182645 // upstream // 208099 // Hs.99	VGLL2	VGLL2 , rs1605598, vestigial like 2 (Drosophila) ,q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1857403	tcactacaataacticc[A/G]gcatattccccatggt	A	G	NM_173560 // downstream // 94075 // Hs.352276 // RFXDC1 // 222546 // Homo sapiens regulatory factor X domain containing 1 (RFXDC1), mRNA. /// NM_153453 // upstream // 239346 // Hs.99324 // VGLL2 // 245806 // Homo sapiens vestigial like 2 (Drosophila) (VGL	RFXDC1	RFXDC1, Homo sapiens regulatory factor X domain containing 1 (RFXDC1), q22.1
SNP_A-1843178	tagtcatgatccgtta[A/T]gtcatgtcatttggg	A	T	NM_002944 // intron // 0 // Hs.1041 // ROS1 // 6098 // Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), mRNA. /// ENST00000263808 // intron // 0 // — // — // —	ROS1	ROS1, Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), q22.1
SNP_A-1918054	ttaaacacatagaaaa[C/G]gtactgacaaattccc	C	G	NM_002944 // intron // 0 // Hs.1041 // ROS1 // 6098 // Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), mRNA. /// ENST00000263808 // intron // 0 // — // — // —	ROS1	ROS1, Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), q22.1
SNP_A-2129365	atacaagaactcaaca[A/C]catcaatgaacagcat	A	C	NM_002944 // upstream // 36752 // Hs.1041 // ROS1 // 6098 // Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), mRNA. /// NM_173674 // upstream // 20045 // Hs.546534 // DCBLD1 // 285761 // Homo sapiens discoidin, CUB and LCCL domain c	ROS1	ROS1, Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), q22.1
SNP_A-1919348	ttaagatagaagtca[A/G]actcaatggtgacca	A	G	ENST00000360388 // intron // 0 // — // — // — // —	-	q22.31
SNP_A-2127786	ataacttacagtggaa[C/T]gttctggataaacaac	C	T	ENST00000360388 // intron // 0 // — // — // — // —	-	q22.31
SNP_A-2078028	acattatcttgaaatg[C/T]agcaatgaattttct	C	T	NM_206921 // intron // 0 // Hs.520349 // C6orf204 // 387119 // Homo sapiens chromosome 6 open reading frame 204 (C6orf204), mRNA. /// ENST00000229580 // intron // 0 // — // — // — // — /// ENST00000360290 // intron // 0 // — // — // — // —	C6orf204	C6orf204, Homo sapiens chromosome 6 open reading frame 204 (C6orf204), q22.31
SNP_A-2094603	agaatagacccacaac[G/T]gatgctttagggacaa	G	T	NM_014034 // downstream // 27960 // Hs.292316 // ASF1A // 25842 // Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), mRNA. /// NM_153255 // upstream // 460 // Hs.486315 // MCMDC1 // 254394 // Homo sapiens minichromosome mainte	ASF1A	ASF1A, Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), q22.31
SNP_A-2097956	agagagagagagggaa[A/G]ggagactctgtttgt	A	G	NM_014034 // downstream // 33496 // Hs.292316 // ASF1A // 25842 // Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), mRNA. /// NM_153255 // upstream // 5996 // Hs.486315 // MCMDC1 // 254394 // Homo sapiens minichromosome maint	ASF1A	ASF1A, Homo sapiens ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A), q22.31
SNP_A-2133603	atatcactctactaca[C/T]gatgctgacagtcagg	C	T	NM_024581 // intron // 0 // Hs.443789 // C6orf60 // 79632 // Homo sapiens chromosome 6 open reading frame 60 (C6orf60), mRNA. /// ENST00000338891 // intron // 0 // — // — // — // — /// ENST00000229599 // intron // 0 // — // — // — // — ///	C6orf60	C6orf60, Homo sapiens chromosome 6 open reading frame 60 (C6orf60), q22.31
SNP_A-1645344	agaaagttattctctcaatattctc[C/T]ctttgtaaattatccctattcct at	C	T	NM_024581 // intron // 0 // Hs.20537 // C6orf60 // 79632 // chromosome 6 open reading frame 60	C6orf60	C6orf60 , rs9320678, chromosome 6 open reading frame 60,q22.31
SNP_A-2039050	aacagggacagaagag[C/T]caatgaatcatattgt	C	T	NM_005907 // intron // 0 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// ENST00000265493 // intron // 0 // — // — // — // —	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1723430	ttctcagtagctaagtctctttta[C/T]gaggtccaaaataaaatac atttat	C	T	NM_005907 // upstream // 215402 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 1515055 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1 , rs2357524, mannosidase, alpha, class 1A, member 1 ,q22.31
SNP_A-2245832	ctgggttggccataa[A/G]agctgacgtcagagca	A	G	NM_005907 // upstream // 195001 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1535509 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1824713	taaagacttgaaattc[A/G]cacattcaggcattat	A	G	NM_005907 // upstream // 196923 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1533587 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1910350	tgtccagtcaatggaa[A/G]agttgtccagtcaact	A	G	NM_005907 // upstream // 197904 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1532606 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1987408	atccctaaagacaaaa[A/G]tgtgtaaatgctaatc	A	G	NM_005907 // upstream // 201294 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1529216 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2229525	ctagggttaaaaaqta[A/G]tggcttccacaccta	A	G	NM_005907 // upstream // 202125 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1528385 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1987410	tataagagcctacca[C/T]gaagagctggaagaag	C	T	NM_005907 // upstream // 214555 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1515955 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1669603	ccggcatcatgtaatttttcatccc[A/G]ccattgaaagccattgttc cgtat	A	G	NM_005907 // upstream // 287332 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 1443125 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1, rs807311, mannosidase, alpha, class 1A, member 1, q22.31
SNP_A-1987411	cttccagactccacaa[A/C]acaatgaagcatatgg	A	C	NM_005907 // upstream // 244224 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1486286 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1755960	cctcaggagttttagttgataag[C/T]attggaggcaagtgaca caggtga	C	T	NM_005907 // upstream // 420331 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 1310126 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1, rs1986402, mannosidase, alpha, class 1A, member 1, q22.31
SNP_A-2261546	gaaaggctgaaccca[C/G]agagtgcatggcatgg	C	G	NM_005907 // upstream // 367271 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1363239 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1735717	gcagttttaacctgttgtattgc[C/T]cttctctatgtcaaattgtcct gt	C	T	NM_005907 // upstream // 436634 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 1293823 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1, rs10499093, mannosidase, alpha, class 1A, member 1, q22.31
SNP_A-1678784	ttccatgtggtttcatgcaccatta[C/T]agtaatttctgctatttccttct ta	C	T	NM_005907 // upstream // 471255 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 1259202 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1, rs7751642, mannosidase, alpha, class 1A, member 1, q22.31
SNP_A-2260720	gaaaccttatcatatc[G/T]cacagctttctcctc	G	T	NM_005907 // upstream // 415507 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 1315003 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1807810	gtcttaaactcaaaca[C/T]gcagagagagcctga	C	T	NM_005907 // upstream // 422519 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 1307991 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1842806	tagtacctaactgaaa[C/T]ggtcttgagatcattc	C	T	NM_005907 // upstream // 422941 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 1307569 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2063913	aattatagcatttttat[A/T]gttttatgcatcatt	A	T	NM_005907 // upstream // 447522 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 1282988 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2197640	catctgacttgtagat[C/T]tcaaatattcaactac	C	T	NM_005907 // upstream // 463788 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 1266722 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1987413	aacataatcaggaaad[C/G]atgttttattaactc	C	G	NM_005907 // upstream // 470780 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 1259730 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1683586	tacatggagaaagatcaaagtagct[A/G]aaagtcttagaatgtg tgatttaat	A	G	NM_005907 // upstream // 868087 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 862370 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1, rs10499097, mannosidase, alpha, class 1A, member 1, q22.31
SNP_A-2108312	agctgaggtatgctggi[A/G]aaaaggcttcaaggca	A	G	NM_005907 // upstream // 935432 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 795078 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2159158	atttaaaagcagtctg[C/T]aattaaccattgaata	C	T	NM_005907 // upstream // 935513 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 794997 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1987423	tatattgtgatttaga[C/T]agaaggatgatttgg	C	T	NM_005907 // upstream // 962172 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 768338 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2036698	aaattgtggtaagaag[A/G]atccagtagcatgaac	A	G	NM_005907 // upstream // 973340 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 757170 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1855712	tcaatattccatctg[C/G]caactggaagcagtta	C	G	NM_005907 // upstream // 974760 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1). mRNA. /// NM_152730 // downstream // 755750 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1868844	tcctgaataggcacca[A/G]ataaaatcagaagaca	A	G	NM_005907 // upstream // 974933 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 755577 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2023308	aaaaccagcagttaca[A/G]ggtaagagttgttcta	A	G	NM_005907 // upstream // 1002331 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 728179 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2028950	aaagaaaaacacagtd[A/G]aaaattggtatactat	A	G	NM_005907 // upstream // 1104700 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 625810 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2204155	ccagcagatgctatga[C/T]gaaagctgagagcaga	C	T	NM_005907 // upstream // 1124163 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 606347 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1843924	tagttcaagagagtca[A/G]taagtaccaaaccctct	A	G	NM_005907 // upstream // 1132320 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 598190 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-2086213	actctgctgttgacca[C/G]accttcagcagacgtg	C	G	NM_005907 // upstream // 1503877 // Hs.102788 // MAN1A1 // 4121 // Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /// NM_152730 // downstream // 226633 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame	MAN1A1	MAN1A1, Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), q22.31
SNP_A-1751737	cataaagttcaagagttatacttca[C/T]caattcttttgtcttcagca gaga	C	T	NM_005907 // upstream // 1597216 // Hs.255149 // MAN1A1 // 4121 // mannosidase, alpha, class 1A, member 1 /// NM_152730 // downstream // 133241 // Hs.348745 // C6orf170 // 221322 // chromosome 6 open reading frame 170	MAN1A1	MAN1A1, rs7747541, mannosidase, alpha, class 1A, member 1, q22.31
SNP_A-1944034	ttgtatttttcagaatc[A/G]agggtcaaattttgtg	A	G	NM_152730 // intron // 0 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame 170 (C6orf170), mRNA. /// ENST00000314282 // intron // 0 // --- // --- // ---	C6orf170	C6orf170, Homo sapiens chromosome 6 open reading frame 170 (C6orf170), q22.31
SNP_A-1867957	tcctagcagtgtaccata[C/T]aaaattctgtcttaa	C	T	NM_152730 // upstream // 2833 // Hs.121396 // C6orf170 // 221322 // Homo sapiens chromosome 6 open reading frame 170 (C6orf170), mRNA. /// NM_000165 // upstream // 115214 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (co	C6orf170	C6orf170, Homo sapiens chromosome 6 open reading frame 170 (C6orf170), q22.31
SNP_A-1698251	acatataaataatgaacgccgatta[C/T]gtgctagcaacaccaa cttcatagg	C	T	NM_000165 // downstream // 58542 // Hs.74471 // GJA1 // 2697 // gap junction protein, alpha 1, 43kDa (connexin 43) /// NM_004506 // upstream // 891381 // Hs.158195 // HSF2 // 3298 // heat shock transcription factor 2	GJA1	GJA1, rs6569212, gap junction protein, alpha 1, 43kDa (connexin 43), q22.31
SNP_A-2089171	acttacatcatcatca[A/G]ccggatgatcgcaaag	A	G	NM_000165 // downstream // 204691 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 745232 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1697525	gttgttaaataattcatcacatgta[A/G]agtaacataaccatgacc aacaata	A	G	NM_000165 // downstream // 448876 // Hs.74471 // GJA1 // 2697 // gap junction protein, alpha 1, 43kDa (connexin 43) /// NM_004506 // upstream // 501047 // Hs.158195 // HSF2 // 3298 // heat shock transcription factor 2	GJA1	GJA1, rs9388016, gap junction protein, alpha 1, 43kDa (connexin 43), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1907385	tgtaaaatgctttgaa[A/G]atgcagactgatgcat	A	G	NM_000165 // downstream // 563026 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 386897 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2163206	atttttcttacaaaac[C/T]gtaggccaagaacaca	C	T	NM_000165 // downstream // 590445 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 359478 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1789208	gggcatatcttatggg[C/G]aggtgcttttgcttct	C	G	NM_000165 // downstream // 611330 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 338593 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1781680	ggattgtaaagataag[A/G]agagaaatggaaatga	A	G	NM_000165 // downstream // 670631 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 279292 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2129107	ataattccataagtaa[C/G]gggtgaagtcctatga	C	G	NM_000165 // downstream // 755715 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 194208 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1753737	gtatttgaaatttatgaaataagca[C/T]gtggcattcttggatagaaatattt	C	T	NM_000165 // downstream // 849443 // Hs.74471 // GJA1 // 2697 // gap junction protein, alpha 1, 43kDa (connexin 43) /// NM_004506 // upstream // 100480 // Hs.158195 // HSF2 // 3298 // heat shock transcription factor 2	GJA1	GJA1 , rs536165, gap junction protein, alpha 1, 43kDa (connexin 43) ,q22.31
SNP_A-2291916	gcacataattgtgttc[A/C]aaatgttcaattgtgc	A	C	NM_000165 // downstream // 827497 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 122426 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-2288619	gattgctgctacttac[G/T]atttccagttctgtta	G	T	NM_000165 // downstream // 839004 // Hs.74471 // GJA1 // 2697 // Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), mRNA. /// NM_004506 // upstream // 110919 // Hs.158195 // HSF2 // 3298 // Homo sapiens heat shock transcription factor	GJA1	GJA1, Homo sapiens gap junction protein, alpha 1, 43kDa (connexin 43) (GJA1), q22.31
SNP_A-1800633	gtagaaaaaatacaca[A/G]aaggatataggcttac	A	G	NM_181795 // intron // 0 // Hs.486354 // PKIB // 5570 // Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), transcript variant 1, mRNA. /// NM_032471 // intron // 0 // Hs.486354 // PKIB // 5570 // Homo sapiens protein kinase (c	PKIB	PKIB, Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), transcript variant 1, q22.31
SNP_A-2252809	cttctacgacattgca[C/T]ctaatatctgaggaca	C	T	NM_181795 // downstream // 31120 // Hs.486354 // PKIB // 5570 // Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), transcript variant 1, mRNA. /// NM_032471 // downstream // 31120 // Hs.486354 // PKIB // 5570 // Homo sapiens p	PKIB	PKIB, Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), transcript variant 1, q22.31
SNP_A-2012031	caagacttttaaccta[A/G]catcaaagaattagct	A	G	NM_006714 // downstream // 52158 // Hs.486357 // SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 52158 // --- // --- // --- // --- /// ENST00000275162 // upstream // 1340	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1809566	gtgagagttgagaata[A/G]atgtaaagaagcctgg	A	G	NM_006714 // downstream // 61012 // Hs.486357 // SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 61012 // — // — // — /// ENST00000275162 // upstream // 1252	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31
SNP_A-2310466	ggaacttcctcccaa[A/C]tggactgtgctgtct	A	C	NM_006714 // downstream // 137122 // Hs.486357 // SMPDL3A // 10924 // Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), mRNA. /// ENST00000307901 // downstream // 137122 // — // — // — /// ENST00000275162 // upstream // 49	SMPDL3A	SMPDL3A, Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), q22.31
SNP_A-2195133	catggaccctaccaaa[A/G]ttcaaatctactgct	A	G	ENST00000275162 // intron // 0 // — // — // —	-	q22.31
SNP_A-1675748	tatactgttgctccagtattaaaa[G/T]catagtcatttttgtgtttat t	G	T	NM_006073 // intron // 0 // Hs.159090 // TRDN // 10345 // triadin	TRDN	TRDN , rs9283099, triadin,q22.31
SNP_A-1828582	taagccagaggtagaa[C/T]ggtttcttctgtagc	C	T	NM_006073 // upstream // 41186 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 980029 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-1745202	cctatccaccaaatgatactaacaa[C/G]aatttgtcacttagcca ttgcaaat	C	G	NM_006073 // upstream // 105563 // Hs.159090 // TRDN // 10345 // triadin /// NM_153355 // upstream // 61783 // Hs.94181 // TCBA1 // 154215 // T-cell lymphoma breakpoint associated target 1	TRDN	TRDN , rs10495162, triadin ,q22.31
SNP_A-2115481	agggggttggagtaga[A/G]taggagggaatgatat	A	G	NM_006073 // upstream // 50802 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 970413 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-1792387	gggtttaaagccaata[A/C]aggcaaaggcaagagt	A	C	NM_006073 // upstream // 65390 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 955825 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-1787653	gggacacatacattgaa[A/G]attgacataagtagta	A	G	NM_006073 // upstream // 66538 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 954677 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-2157998	attgcttcttgctagaa[C/T]gaggcaacagtttctg	C	T	NM_006073 // upstream // 68404 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 952811 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-1655939	taggtatgtataatatattgcaag[A/G]atcacctatactactaact ggtgc	A	G	NM_006073 // upstream // 139379 // Hs.159090 // TRDN // 10345 // triadin /// NM_153355 // upstream // 27967 // Hs.94181 // TCBA1 // 154215 // T-cell lymphoma breakpoint associated target 1	TRDN	TRDN , rs9320960, triadin ,q22.31
SNP_A-1834957	tacccaatatttgttc[C/T]atgctataccctgata	C	T	NM_006073 // upstream // 86623 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 934592 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-1987486	tcctttctagataggaa[A/G]aaatctaggagcttcc	A	G	NM_006073 // upstream // 110325 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 910890 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST0	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2026523	aaacaaatgctgtgc[A/G]aaagtccagaatgtta	A	G	NM_006073 // upstream // 140319 // Hs.144744 // TRDN // 10345 // Homo sapiens triadin (TRDN), mRNA. /// NM_153355 // upstream // 880896 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST0	TRDN	TRDN, Homo sapiens triadin (TRDN), q22.31
SNP_A-2277711	gagcagctggtgtatg[C/G]actagagaatataaaagg	C	G	ENST00000355094 // intron // 0 // --- // --- // ---	-	q22.31
SNP_A-1987496	actagtccatgctaaag[G/T]ataagatgcctgggaa	G	T	ENST00000355094 // intron // 0 // --- // --- // ---	-	q22.31
SNP_A-1731511	ctttgtgtgttcatgtacaattaga[C/T]caaacatacaaatagattat gttga	C	T	NM_153355 // intron // 0 // Hs.94181 // TCBA1 // 154215 // T-cell lymphoma breakpoint associated target 1	TCBA1	TCBA1 , rs2552085, T-cell lymphoma breakpoint associated target 1,q22.31
SNP_A-1687286	ctctgtgatggaatgaatcatgtcac[C/T]gagtttgccctgatctgtt gccctg	C	T	NM_153355 // intron // 0 // Hs.94181 // TCBA1 // 154215 // T-cell lymphoma breakpoint associated target 1	TCBA1	TCBA1 , rs584197, T-cell lymphoma breakpoint associated target 1,q22.31
SNP_A-1987510	ctcacatcatttgtta[A/C]aagatttgggtgcacgt	A	C	ENST00000355094 // intron // 0 // --- // --- // ---	-	q22.31
SNP_A-1800133	gtaccatggattgcct[C/G]acctttatttttgaag	C	G	ENST00000355094 // intron // 0 // --- // --- // ---	-	q22.31
SNP_A-1871792	tctaatttaatgttta[G/T]caagtgctgtgaaata	G	T	ENST00000355094 // intron // 0 // --- // --- // ---	-	q22.31
SNP_A-2171877	caatgataacagacta[C/T]gtaaccttgagctggc	C	T	NM_153355 // intron // 0 // Hs.269722 // TCBA1 // 154215 // Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA. /// ENST00000355094 // intron // 0 // --- // --- // --- /// ENST00000340719 // intron // 0 // --- // --- // --- /	TCBA1	TCBA1, Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), q22.31
SNP_A-2235341	ctccctgacttccaaaa[A/G]ggaaacttgtagccct	A	G	NM_001003397 // intron // 0 // Hs.201482 // TPD52L1 // 7164 // Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, mRNA. /// NM_001003396 // intron // 0 // Hs.201482 // TPD52L1 // 7164 // Homo sapiens tumor protein D52-like 1 (TPD52L1).	TPD52L1	TPD52L1, Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, q22.31
SNP_A-2012054	gtgcagaatctaatac[C/T]gacttgctcccagtta	C	T	NM_001003397 // intron // 0 // Hs.201482 // TPD52L1 // 7164 // Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, mRNA. /// NM_001003396 // intron // 0 // Hs.201482 // TPD52L1 // 7164 // Homo sapiens tumor protein D52-like 1 (TPD52L1).	TPD52L1	TPD52L1, Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, q22.31
SNP_A-2155305	attcataacctcaacc[C/T]atctcaacatatcatg	C	T	NM_016063 // upstream // 48830 // Hs.32826 // C6orf74 // 51020 // Homo sapiens chromosome 6 open reading frame 74 (C6orf74), mRNA. /// NM_012259 // upstream // 398916 // Hs.144287 // HEY2 // 23493 // Homo sapiens hairy/enhancer-of-split related with YRPW	C6orf74	C6orf74, Homo sapiens chromosome 6 open reading frame 74 (C6orf74), q22.31
SNP_A-1987536	cagaaacagagaaccat[C/T]tcacgactttccaata	C	T	NM_016063 // upstream // 180838 // Hs.32826 // C6orf74 // 51020 // Homo sapiens chromosome 6 open reading frame 74 (C6orf74), mRNA. /// NM_012259 // upstream // 266908 // Hs.144287 // HEY2 // 23493 // Homo sapiens hairy/enhancer-of-split related with YRPW	C6orf74	C6orf74, Homo sapiens chromosome 6 open reading frame 74 (C6orf74), q22.31
SNP_A-2141074	atctgctcagtacata[C/T]aggttaagtgcttgt	C	T	NM_016063 // upstream // 187589 // Hs.32826 // C6orf74 // 51020 // Homo sapiens chromosome 6 open reading frame 74 (C6orf74), mRNA. /// NM_012259 // upstream // 260157 // Hs.144287 // HEY2 // 23493 // Homo sapiens hairy/enhancer-of-split related with YRPW	C6orf74	C6orf74, Homo sapiens chromosome 6 open reading frame 74 (C6orf74), q22.31
SNP_A-1870247	tccttgctgctgtga[A/C]gggaagaatggaggtg	A	C	NM_016063 // upstream // 253699 // Hs.32826 // C6orf74 // 51020 // Homo sapiens chromosome 6 open reading frame 74 (C6orf74), mRNA. /// NM_012259 // upstream // 194047 // Hs.144287 // HEY2 // 23493 // Homo sapiens hairy/enhancer-of-split related with YRPW	C6orf74	C6orf74, Homo sapiens chromosome 6 open reading frame 74 (C6orf74), q22.31
SNP_A-1691298	taaaactgaaattcatcagttaaaa[C/T]gaaaatactccggcttc aaagaacc	C	T	NM_181782 // intron // 0 // Hs.292676 // NCOA7 // 135112 // nuclear receptor coactivator 7	NCOA7	NCOA7, rs481233, nuclear receptor coactivator 7,q22.32
SNP_A-1824103	taaacacctgcaaccat[C/T]agaactgagcagacct	C	T	NM_181782 // intron // 0 // Hs.171426 // NCOA7 // 135112 // Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA. /// ENST00000355470 // intron // 0 // --- // --- // --- /// ENST00000318575 // intron // 0 // --- // --- // ---	NCOA7	NCOA7, Homo sapiens nuclear receptor coactivator 7 (NCOA7), q22.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798849	gtaactttggtattaa[C/T]gaggaccaagttgagg	C	T	NM_181782 // intron // 0 // Hs.171426 // NCOA7 // 135112 // Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA. /// ENST00000355470 // intron // 0 // — // — // — // — /// ENST00000318575 // intron // 0 // — // — // — // —	NCOA7	NCOA7, Homo sapiens nuclear receptor coactivator 7 (NCOA7), q22.32
SNP_A-2263398	gaacatgatagaacaa[A/C]acctgcaaatgtgtct	A	C	NM_181782 // intron // 0 // Hs.171426 // NCOA7 // 135112 // Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA. /// ENST00000355470 // intron // 0 // — // — // — // — /// ENST00000318575 // intron // 0 // — // — // — // — /// ENST00	NCOA7	NCOA7, Homo sapiens nuclear receptor coactivator 7 (NCOA7), q22.32
SNP_A-2282339	gagttcaaggttacag[G/T]aaactgtgattatgcc	G	T	NM_021820 // downstream // 11370 // Hs.404186 // C6orf75 // 60487 // Homo sapiens chromosome 6 open reading frame 75 (C6orf75), mRNA. /// NM_032784 // upstream // 1068031 // Hs.135254 // THSD2 // 84870 // Homo sapiens thrombospondin, type I, domain contai	C6orf75	C6orf75, Homo sapiens chromosome 6 open reading frame 75 (C6orf75), q22.32
SNP_A-2246896	ctgtagtttggagaca[C/T]gattatctatcggtga	C	T	ENST00000329722 // downstream // 7967 // — // — // — // — /// ENST00000341548 // downstream // 24488 // — // — // — // —	-	q22.33
SNP_A-2314556	ggaggtgcaggatttc[C/T]aattatctgaattctg	C	T	ENST00000329722 // downstream // 23049 // — // — // — // — /// ENST00000341548 // downstream // 9406 // — // — // — // —	-	q22.33
SNP_A-1859959	tcaggtgggtttttca[A/G]taggagaccaggaagc	A	G	ENST00000341548 // upstream // 58748 // — // — // — // — /// ENST00000309493 // downstream // 8971 // — // — // — // —	-	q22.33
SNP_A-1698753	ggcctacctaatctcactaaaattc[A/G]agaatattcaaaatttatttaatt	A	G	AK097903 // intron // 0 // Hs.380210 // C6orf190 // 387357 // chromosome 6 open reading frame 190	C6orf190	C6orf190 , rs270015, chromosome 6 open reading frame 190,q22.33
SNP_A-1946345	tttaaaatgcaacaaa[C/T]gtgatttaatcaaact	C	T	ENST00000309493 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-1742561	aaggtttgttttctgtcttgttata[G/T]acccttcatcagaatacagaagtt	G	T	AK097903 // intron // 0 // Hs.380210 // C6orf190 // 387357 // chromosome 6 open reading frame 190	C6orf190	C6orf190 , rs920992, chromosome 6 open reading frame 190,q22.33
SNP_A-2043850	aacttcatgtgttata[C/T]ctgcaggatgtacata	C	T	ENST00000309493 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-1899852	tggacaaagtgtatga[A/G]aaagtttacggctata	A	G	ENST00000309493 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-1874514	tctccctgcttaaagc[A/C]ctttactgatttgccc	A	C	ENST00000309493 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-2066579	acaaaaacataaaccc[A/C]gatagactacagatct	A	C	ENST00000309493 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-1872786	tctataccttcagaa[A/G]agactacaacaaattg	A	G	NM_002844 // downstream // 24928 // Hs.155919 // PTPRK // 5796 // Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), mRNA. /// ENST00000309493 // upstream // 42801 // — // — // — // — /// ENST00000282833 // downstream // 24928 //	PTPRK	PTPRK, Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), q22.33
SNP_A-1868919	tcctgagatgtggcaa[A/G]tgtcaaagctctgtct	A	G	NM_002844 // intron // 0 // Hs.155919 // PTPRK // 5796 // Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), mRNA. /// ENST00000282833 // intron // 0 // — // — // — // —	PTPRK	PTPRK, Homo sapiens protein tyrosine phosphatase, receptor type, K (PTPRK), q22.33
SNP_A-1677734	tacatataaatattgaataataaat[A/G]atagctgctgtttgatcaaaatgat	A	G	NM_000426 // intron // 0 // Hs.445120 // LAMA2 // 3908 // laminin, alpha 2 (merosin, congenital muscular dystrophy)	LAMA2	LAMA2 , rs265355, laminin, alpha 2 (merosin, congenital muscular dystrophy),q22.33
SNP_A-1648970	ttaaggaataaaaagaattggcaaa[G/T]cttggtgatacatgggtacttttat	G	T	NM_000426 // intron // 0 // Hs.445120 // LAMA2 // 3908 // laminin, alpha 2 (merosin, congenital muscular dystrophy)	LAMA2	LAMA2 , rs265354, laminin, alpha 2 (merosin, congenital muscular dystrophy),q22.33
SNP_A-1681738	ttctttttattccttaaagaatatc[C/T]gacaatttgctggtttgtataagtt	C	T	NM_000426 // intron // 0 // Hs.445120 // LAMA2 // 3908 // laminin, alpha 2 (merosin, congenital muscular dystrophy)	LAMA2	LAMA2 , rs265353, laminin, alpha 2 (merosin, congenital muscular dystrophy),q22.33
SNP_A-2128122	ataagctctagaaaag[C/T]agtgtttatcggtatg	C	T	NM_000426 // intron // 0 // Hs.200841 // LAMA2 // 3908 // Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA. /// Z26653 // intron // 0 // Hs.200841 // LAMA2 // 3908 // H.sapiens mRNA for laminin M chain (merosin). /// EN	LAMA2	LAMA2, Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), q22.33
SNP_A-2041536	aacgaaaacaaattta[C/G]gatgaaagaatctgtg	C	G	NM_033515 // intron // 0 // Hs.486458 // ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // intron // 0 // — // — // — // —	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2196801	cattactcacaagtac[A/G]attttagaatctatag	A	G	NM_033515 // intron // 0 // Hs.486458 // ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // intron // 0 // — // — // — // —	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-1933997	ttctcacagttaccga[C/T]gaacagctcttttca	C	T	NM_033515 // intron // 0 // Hs.486458 // ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // intron // 0 // — // — // — // —	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-2149950	atgtcagtcaaaattg[C/T]caaaattatacaagct	C	T	NM_033515 // intron // 0 // Hs.486458 // ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // intron // 0 // — // — // — // —	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-2247425	ctgtctagctctctcc[C/T]aattcaactgcagttt	C	T	NM_033515 // upstream // 35607 // Hs.486458 // ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // upstream // 35607 // — // — // — // — /// ENST00000345007 // downstream // 85487 // — // -	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-1797209	ggttgcctcttttggc[C/T]caaatatactctcagg	C	T	NM_033515 // upstream // 120926 // Hs.486458 // ARHGAP18 // 93663 // Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), mRNA. /// ENST00000275189 // upstream // 120926 // — // — // — // — /// ENST00000345007 // downstream // 168 // — // -	ARHGAP18	ARHGAP18, Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), q22.33
SNP_A-2082628	acggcacctggcggag[A/G]cagattatactatcaa	A	G	ENST00000345007 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-1906851	tggttcaatttaacaa[C/T]gtttcaaatttacaac	C	T	ENST00000345007 // intron // 0 // — // — // — // —	-	q22.33
SNP_A-2259075	ctttttttctgaatac[A/G]caggctaattggaaag	A	G	ENST00000345007 // upstream // 11219 // — // — // — // — /// ENST00000354350 // upstream // 146182 // — // — // — // — /// ENST00000355158 // upstream // 146182 // — // — // — // —	-	q22.33
SNP_A-1824019	taaacaaagcaaccca[C/T]agaggaaacaatctca	C	T	ENST00000345007 // upstream // 24741 // — // — // — // — /// ENST00000354350 // upstream // 132660 // — // — // — // — /// ENST00000355158 // upstream // 132660 // — // — // — // —	-	q22.33
SNP_A-2314684	ggagtcaagtcctaga[C/T]cttcctgtaactgatt	C	T	ENST00000345007 // upstream // 55761 // — // — // — // — /// ENST00000354350 // upstream // 101640 // — // — // — // — /// ENST00000355158 // upstream // 101640 // — // — // — // —	-	q22.33
SNP_A-1877552	tctggcctcattcctc[A/G]agacattttccctttc	A	G	ENST00000345007 // upstream // 134226 // — // — // — // — /// ENST00000354350 // upstream // 23175 // — // — // — // — /// ENST00000355158 // upstream // 23175 // — // — // — // —	-	q22.33
SNP_A-1950244	tttcagaagagtcaga[A/C]gattggattttgaata	A	C	ENST00000354350 // intron // 0 // — // — // — // — /// ENST00000355158 // intron // 0 // — // — // — // —	-	q23.1
SNP_A-2292637	gcactggctttgaccc[A/G]cagactggagtttgct	A	G	ENST00000354350 // intron // 0 // — // — // — // — /// ENST00000355158 // intron // 0 // — // — // — // —	-	q23.1
SNP_A-1828144	taagacttcaagcatc[A/G]cctttagaagcactct	A	G	NM_052913 // downstream // 140921 // Hs.172870 // KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 255361 // Hs.486470 // EPB41L2 // 2037 // Homo sapiens erythrocyte membrane protein band 4.1-like 2 (EPB41L2), m	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1
SNP_A-1920980	ttacagagtaacctgc[C/T]agcaatcctatcagca	C	T	NM_052913 // downstream // 384278 // Hs.172870 // KIAA1913 // 114801 // Homo sapiens KIAA1913 (KIAA1913), mRNA. /// NM_001431 // downstream // 12004 // Hs.486470 // EPB41L2 // 2037 // Homo sapiens erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mR	KIAA1913	KIAA1913, Homo sapiens KIAA1913 (KIAA1913), q23.1
SNP_A-1686282	acagtagagacatgtaggaataaat[C/T]aactaaaggatatgc aagacttcta	C	T	NM_016377 // intron // 0 // Hs.12835 // AKAP7 // 9465 // A kinase (PRKA) anchor protein 7	AKAP7	AKAP7 , rs10499182, A kinase (PRKA) anchor protein 7,q23.2
SNP_A-2259055	ctttttgctaaccaa[C/T]gaagttactctaaata	C	T	NM_016377 // intron // 0 // Hs.486483 // AKAP7 // 9465 // Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, mRNA. /// ENST00000263049 // intron // 0 // — // — // — // —	AKAP7	AKAP7, Homo sapiens A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1733114	ttcccgtagcttgtacttttccaa[A/G]gacatacttttcaatgaaaaactct	A	G	NM_000045 // upstream // 157754 // Hs.440934 // ARG1 // 383 // arginase, liver /// NM_004830 // downstream // 171262 // Hs.29679 // CRSP3 // 9439 // cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa /// NM_004842 // downstream // 13	ARG1	ARG1 , rs6935095, arginase, liver, q23.2
SNP_A-1748367	atagaatatttcagtatagtgactc[C/T]gaatatctaatacataaagacttga	C	T	NM_000045 // upstream // 152125 // Hs.440934 // ARG1 // 383 // arginase, liver /// NM_004830 // downstream // 165633 // Hs.29679 // CRSP3 // 9439 // cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa /// NM_004842 // downstream // 13	ARG1	ARG1 , rs983502, arginase, liver, q23.2
SNP_A-1917306	tgtttcatgaaaag[G/T]catcctctaagtgctg	G	T	NM_005021 // downstream // 21728 // Hs.486489 // ENPP3 // 5169 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3), mRNA. /// NM_030908 // upstream // 67734 // Hs.486488 // OR2A4 // 79541 // Homo sapiens olfactory receptor, family 2	ENPP3	ENPP3, Homo sapiens ectonucleotide pyrophosphatase q23.2
SNP_A-1916917	tgtttcttgatcccct[A/C]aatggcagttacatga	A	C	NM_005021 // downstream // 27758 // Hs.486489 // ENPP3 // 5169 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 3 (ENPP3), mRNA. /// NM_030908 // upstream // 73764 // Hs.486488 // OR2A4 // 79541 // Homo sapiens olfactory receptor, family 2	ENPP3	ENPP3, Homo sapiens ectonucleotide pyrophosphatase q23.2
SNP_A-1818867	gttgagtttgtctcaa[A/G]acgtgggatagaggct	A	G	NM_006208 // downstream // 49964 // Hs.527295 // ENPP1 // 5167 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1), mRNA. /// NM_001901 // downstream // 7002 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth fact	ENPP1	ENPP1, Homo sapiens ectonucleotide pyrophosphatase q23.2
SNP_A-1819906	gttgttaatggaatgc[A/G]attgtcataactaca	A	G	NM_001901 // upstream // 7386 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 337368 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST00	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2152241	attaaagtccaataac[A/G]ctattctaggctttac	A	G	NM_001901 // upstream // 29841 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 314913 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST0	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-1987684	agaaattattgctccc[A/G]aagttgtaaaagtaca	A	G	NM_001901 // upstream // 44107 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 300647 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST0	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2042610	aactcccaaatcctaa[C/T]ggcttaacacaataaa	C	T	NM_001901 // upstream // 56495 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 288259 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST0	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2159068	attgtttacatagaca[C/T]agaagaagtagatgat	C	T	NM_001901 // upstream // 56764 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 287990 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST0	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-1724718	tgctaagttgggggagtcatttta g[A/T]tgtctgcttaattaggacttagga	A	T	NM_001901 // upstream // 147408 // Hs.410037 // CTGF // 1490 // connective tissue growth factor /// NM_015529 // downstream // 197358 // Hs.6909 // MOXD1 // 26002 // monooxygenase, DBH-like 1	CTGF	CTGF , rs7230771, connective tissue growth factor q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308112	gcttgataggaattgat[A/G]attgaggtctgcagct	A	G	NM_001901 // upstream // 90504 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 254250 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST0	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2249036	ctgtttaiaatctccc[A/G]ccagactcatagaagt	A	G	NM_001901 // upstream // 128672 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 216082 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-1816686	gttatatatcaaacat[C/G]gactttatcattcatg	C	G	NM_001901 // upstream // 276050 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 68704 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST0	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2266360	gaaggtgaagtataaa[A/G]tgcaagctacaacaaa	A	G	NM_001901 // upstream // 338998 // Hs.410037 // CTGF // 1490 // Homo sapiens connective tissue growth factor (CTGF), mRNA. /// NM_015529 // downstream // 5756 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST00	CTGF	CTGF, Homo sapiens connective tissue growth factor (CTGF), q23.2
SNP_A-2042353	aactatttttaactta[C/T]gcaggtccaattaaga	C	T	NM_015529 // intron // 0 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST00000336749 // intron // 0 // — // — // — /// ENST00000309488 // intron // 0 // — // — // — // —	MOXD1	MOXD1, Homo sapiens monooxygenase, DBH-like 1 (MOXD1), q23.2
SNP_A-2012086	tgaaccaaaccaaccccq[A/G]aagttcaacaacttta	A	G	NM_015529 // intron // 0 // Hs.6909 // MOXD1 // 26002 // Homo sapiens monooxygenase, DBH-like 1 (MOXD1), mRNA. /// ENST00000336749 // intron // 0 // — // — // — /// ENST00000309488 // intron // 0 // — // — // — // —	MOXD1	MOXD1, Homo sapiens monooxygenase, DBH-like 1 (MOXD1), q23.2
SNP_A-1741807	gattcccgtaggttttgtgtagtga[C/T]ggcatttatgctaaaatgt aagtg	C	T	NM_003569 // downstream // 4421 // Hs.434916 // STX7 // 8417 // syntaxin 7 /// NM_015529 // upstream // 80530 // Hs.6909 // MOXD1 // 26002 // monooxygenase, DBH-like 1	STX7	STX7 , rs2282315, syntaxin 7 ,q23.2
SNP_A-2311891	ggacaaagatataaaa[A/C]aggagtgactgtcagt	A	C	NM_003569 // intron // 0 // Hs.520383 // STX7 // 8417 // Homo sapiens syntaxin 7 (STX7), mRNA. /// ENST00000309255 // intron // 0 // — // — // — // —	STX7	STX7, Homo sapiens syntaxin 7 (STX7), q23.2
SNP_A-1987697	gcatttctgagaact[A/T]acttaattatgggtca	A	T	NM_003569 // intron // 0 // Hs.520383 // STX7 // 8417 // Homo sapiens syntaxin 7 (STX7), mRNA. /// ENST00000309255 // intron // 0 // — // — // — // —	STX7	STX7, Homo sapiens syntaxin 7 (STX7), q23.2
SNP_A-1960438	ttttatggttggaaat[A/G]actcggcgtttttca	A	G	NM_003569 // intron // 0 // Hs.520383 // STX7 // 8417 // Homo sapiens syntaxin 7 (STX7), mRNA. /// ENST00000309255 // intron // 0 // — // — // — // —	STX7	STX7, Homo sapiens syntaxin 7 (STX7), q23.2
SNP_A-2307350	gcttaggaaaaaacta[A/G]aagtcatacaagatat	A	G	NM_003569 // intron // 0 // Hs.520383 // STX7 // 8417 // Homo sapiens syntaxin 7 (STX7), mRNA. /// ENST00000309255 // intron // 0 // — // — // — // —	STX7	STX7, Homo sapiens syntaxin 7 (STX7), q23.2
SNP_A-1788711	gggatggttgaataa[A/G]gttgttgtgaaaggg	A	G	NM_003569 // upstream // 5299 // Hs.520383 // STX7 // 8417 // Homo sapiens syntaxin 7 (STX7), mRNA. /// ENST00000309255 // upstream // 5299 // — // — // — // — /// ENST00000340640 // upstream // 19962 // — // — // — // —	STX7	STX7, Homo sapiens syntaxin 7 (STX7), q23.2
SNP_A-1955528	tttggtgcattccaga[C/T]ctgtctttcattcatg	C	T	NM_175067 // downstream // 9022 // Hs.434196 // TRAR4 // 319100 // Homo sapiens trace amine receptor 4 (TRAR4), mRNA. /// NM_175057 // downstream // 9022 // Hs.434116 // TRAR3 // 134860 // Homo sapiens trace amine receptor 3 (TRAR3), mRNA. /// NM_003967 /	TRAR4	TRAR4, Homo sapiens trace amine receptor 4 (TRAR4), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1832441	tacaaacatccttga[A/G]gcatggtttataatta	A	G	NM_001016 // downstream // 25742 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 398071 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript van	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2012088	gttatgccacctactc[A/G]gaattccacaacactg	A	G	NM_001016 // downstream // 98151 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 325662 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript van	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2237754	ctctcttcctgtgtcc[A/C]actcctccagcaaagg	A	C	NM_001016 // downstream // 102083 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 321730 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript var	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2024710	aaaagtagttgtagtc[A/T]atctctcagggtattg	A	T	NM_001016 // downstream // 102236 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 321577 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript var	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-1822851	taaaaagagaatgaaa[C/T]gcagtcatttgcaatg	C	T	NM_001016 // downstream // 104432 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 319381 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript var	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2040110	aaccaaattatgcatc[C/G]cccaattcaggaagct	C	G	NM_001016 // downstream // 106834 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 316979 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript var	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2133031	atatactaacccaaa[C/T]caccaaccaaattatt	C	T	NM_001016 // downstream // 117795 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 306018 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript var	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2030440	aaagccattgagaaaac[C/T]cttcacagcataggca	C	T	NM_001016 // downstream // 128703 // Hs.546289 // RPS12 // 6206 // Homo sapiens ribosomal protein S12 (RPS12), mRNA. /// NM_172104 // upstream // 295110 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript var	RPS12	RPS12, Homo sapiens ribosomal protein S12 (RPS12), q23.2
SNP_A-2265365	gaagcagtcagtccta[C/G]agagagtgagctgagg	C	G	NM_172104 // intron // 0 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, mRNA. /// NM_004100 // intron // 0 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4	EYA4	EYA4, Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, q23.2
SNP_A-1918618	ttaacagcaggtaacc[A/G]ccaatgctcctgcctt	A	G	NM_172104 // intron // 0 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, mRNA. /// NM_004100 // intron // 0 // Hs.102408 // EYA4 // 2070 // Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4	EYA4	EYA4, Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 3, q23.2
SNP_A-1987737	tgtaatccaacagaaa[C/T]ctctttagtgtgaccc	C	T	ENST00000308518 // upstream // 120918 // --- // --- // --- // --- /// ENST00000321920 // upstream // 34225 // --- // --- // --- // ---	-	q23.2
SNP_A-2096052	agacataatggaggta[C/T]ggcattaggtaaatac	C	T	ENST00000308518 // upstream // 124056 // --- // --- // --- // --- /// ENST00000321920 // upstream // 31087 // --- // --- // --- // ---	-	q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1657820	gtacttctgtaaatactaacactc[A/G]atgcagaaagaatgtta caaagga	A	G	NM_003206 // upstream // 17434 // Hs.78061 // TCF21 // 6943 // transcription factor 21 /// NM_153224 // downstream // 17713 // Hs.126165 // MGC34034 // 154089 // hypothetical protein MGC34034	TCF21	TCF21, rs1208261, transcription factor 21, q23.2
SNP_A-1926992	ttatttgaaccagttg[C/G]aaacaaggatctaga	C	G	ENST00000321920 // 3UTR // 0 /// — /// — /// —	-	q23.2
SNP_A-2183755	cagcatctgtttaggt[C/T]cagcaggttgtacttt	C	T	NM_198392 // upstream // 16367 // Hs.78061 // TCF21 // 6943 // Homo sapiens transcription factor 21 (TCF21), transcript variant 1, mRNA. /// NM_003206 // upstream // 16367 // Hs.78061 // TCF21 // 6943 // Homo sapiens transcription factor 21 (TCF21), trans	TCF21	TCF21, Homo sapiens transcription factor 21 (TCF21), transcript variant 1, q23.2
SNP_A-1941510	ttgctttggctactga[A/G]aagtgcaagtatgggt	A	G	NM_004865 // downstream // 82744 // Hs.486507 // TBPL1 // 9519 // Homo sapiens TBP-like 1 (TBPL1), mRNA. /// NM_145176 // upstream // 17600 // Hs.486508 // SLC2A12 // 154091 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member	TBPL1	TBPL1, Homo sapiens TBP-like 1 (TBPL1), q23.2
SNP_A-1893151	tgcagaatacacaaaaa[C/T]gtacgcaaataaatat	C	T	NM_022568 // downstream // 590115 // Hs.486520 // ALDH8A1 // 64577 /// Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 590122 // Hs.486520 // ALDH8A1 // 64577 // Homo sapiens ald	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2
SNP_A-1663882	acatggtcagattgccttaaccaca[A/C]agcctcatatgtagctta ttcgatc	A	C	BX537882 // upstream // 296997 // Hs.510078 // - // 401274 // MRNA; cDNA DKFZp686H1615 (from clone DKFZp686H1615) /// NM_022568 // downstream // 302765 // Hs.18443 // ALDH8A1 // 64577 // aldehyde dehydrogenase 8 family, member A1 /// NM_170771 // downstr	-	-, rs2223995, MRNA; cDNA DKFZp686H1615 (from clone DKFZp686H1615), q23.2
SNP_A-2260941	gaaacttaaccttt[A/C]aaaaagcaatgatgaa	A	C	NM_022568 // downstream // 331862 // Hs.486520 // ALDH8A1 // 64577 /// Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 331869 // Hs.486520 // ALDH8A1 // 64577 // Homo sapiens ald	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2
SNP_A-2080760	acctcccaggcagaac[C/G]caggtcatccacacat	C	G	NM_022568 // downstream // 258546 // Hs.486520 // ALDH8A1 // 64577 /// Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 258553 // Hs.486520 // ALDH8A1 // 64577 // Homo sapiens ald	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.2
SNP_A-1878573	tctgtgtattgacaac[C/T]atttgagtaactatg	C	T	NM_022568 // downstream // 74786 // Hs.486520 // ALDH8A1 // 64577 /// Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 74793 // Hs.486520 // ALDH8A1 // 64577 // Homo sapiens aldeh	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.3
SNP_A-2237319	ctctccactttcaaa[G/T]aattagagtgatcatt	G	T	NM_022568 // downstream // 62353 // Hs.486520 // ALDH8A1 // 64577 /// Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 62360 // Hs.486520 // ALDH8A1 // 64577 // Homo sapiens aldeh	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.3
SNP_A-2180065	cagaaaaatcataata[A/G]caatcaattctggcc	A	G	NM_022568 // downstream // 40413 // Hs.486520 // ALDH8A1 // 64577 /// Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, mRNA. /// NM_170771 // downstream // 40420 // Hs.486520 // ALDH8A1 // 64577 // Homo sapiens aldeh	ALDH8A1	ALDH8A1, Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript variant 1, q23.3
SNP_A-1744439	ggcccagagttaccaaggttataga[A/G]tagtctgaaggttata ctagtgtt	A	G	NM_017651 // intron // 0 // Hs.273294 // AHI1 // 54806 // Abelson helper integration site	AHI1	AHI1, rs6931735, Abelson helper integration site,q23.3
SNP_A-1823877	taaaatgtattaaaga[A/C]acagccctttaacat	A	C	NM_017651 // intron // 0 // Hs.386684 // AHI1 // 54806 // Homo sapiens Abelson helper integration site (AHI1), mRNA. /// ENST00000265602 // intron // 0 // — /// — /// — /// ENST00000327035 // intron // 0 // — /// — // — // —	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2154460	attattcaggatgtag[C/T]atatgcattagactgg	C	T	NM_017651 // upstream // 74671 // Hs.386684 // AHI1 // 54806 // Homo sapiens Abelson helper integration site (AHI1), mRNA. /// NM_002604 // upstream // 279296 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3
SNP_A-2115714	agggtccactcacccc[C/G]aaacctagttgcaaaa	C	G	NM_017651 // upstream // 322268 // Hs.386684 // AHI1 // 54806 // Homo sapiens Abelson helper integration site (AHI1), mRNA. /// NM_002604 // upstream // 31699 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2	AHI1	AHI1, Homo sapiens Abelson helper integration site (AHI1), q23.3
SNP_A-1955970	ttgtcgatgctatga[C/T]taaaagtaagactatg	C	T	NM_002604 // intron // 0 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA. /// NM_002603 // intron // 0 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 1,	PDE7A	PDE7A, Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, q23.3
SNP_A-1926184	ttattaagcacttgcc[A/G]cacagtagaaagtcgtt	A	G	NM_002604 // intron // 0 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA. /// NM_002603 // intron // 0 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 1,	PDE7A	PDE7A, Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, q23.3
SNP_A-2066687	acaaaaccacatggat[C/G]aaaacagatagtttcc	C	G	NM_002604 // intron // 0 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, mRNA. /// NM_002603 // intron // 0 // Hs.527119 // PDE7A // 5150 // Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 1,	PDE7A	PDE7A, Homo sapiens phosphodiesterase 7A (PDE7A), transcript variant 2, q23.3
SNP_A-1899653	tggaataatggaaaaaa[C/G]gtacaggactcatgaa	C	G	NM_181310 // upstream // 8743 // Hs.126891 // IL22RA2 // 116379 // Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, mRNA. /// NM_052962 // upstream // 8743 // Hs.126891 // IL22RA2 // 116379 // Homo sapiens interleukin 22 rece	IL22RA2	IL22RA2, Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, q23.3
SNP_A-1830546	taatcagctatagaaa[C/T]gtaacaggtgctcta	C	T	NM_181310 // upstream // 8812 // Hs.126891 // IL22RA2 // 116379 // Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, mRNA. /// NM_052962 // upstream // 8812 // Hs.126891 // IL22RA2 // 116379 // Homo sapiens interleukin 22 rece	IL22RA2	IL22RA2, Homo sapiens interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 3, q23.3
SNP_A-2095264	agaattggatgaaaca[A/C]gctgaccaaacacgta	A	C	NM_175747 // upstream // 138375 // Hs.195398 // OLIG3 // 167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 234776 // Hs.211600 // TNFAIP3 // 7128 // Homo sapiens tumor necrosis factor, alpha-induced	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3
SNP_A-1852707	tatttcaattcccaga[C/T]gattttccagctaaaa	C	T	NM_175747 // upstream // 145706 // Hs.195398 // OLIG3 // 167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 227445 // Hs.211600 // TNFAIP3 // 7128 // Homo sapiens tumor necrosis factor, alpha-induced	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3
SNP_A-2149841	atgtcaaagggaaagt[A/G]aaatctgtagagggagt	A	G	NM_175747 // upstream // 150111 // Hs.195398 // OLIG3 // 167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 223040 // Hs.211600 // TNFAIP3 // 7128 // Homo sapiens tumor necrosis factor, alpha-induced	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3
SNP_A-1899538	tggaagctgggaggg[C/T]caatttagtaaacaa	C	T	NM_175747 // upstream // 305747 // Hs.195398 // OLIG3 // 167826 // Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), mRNA. /// NM_006290 // upstream // 67404 // Hs.211600 // TNFAIP3 // 7128 // Homo sapiens tumor necrosis factor, alpha-induced p	OLIG3	OLIG3, Homo sapiens oligodendrocyte transcription factor 3 (OLIG3), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2132242	atagtaagcttgacad[A/G]gtatcagtatctaaga	A	G	NM_006290 // downstream // 18146 // Hs.211600 // TNFAIP3 // 7128 // Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA. /// ENST00000237289 // downstream // 18146 // --- // --- // --- /// ENST00000342131 // upstream // 9423	TNFAIP3	TNFAIP3, Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), q23.3
SNP_A-2136659	atcactcgaaataaga[A/G]agttcacattatttgt	A	G	NM_022121 // upstream // 91343 // Hs.520421 // PERP // 64065 // Homo sapiens PERP, TP53 apoptosis effector (PERP), mRNA. /// NM_020340 // upstream // 8302 // Hs.194408 // KIAA1244 // 57221 // Homo sapiens KIAA1244 (KIAA1244), mRNA. /// NM_021635 // downst	PERP	PERP, Homo sapiens PERP, TP53 apoptosis effector (PERP), q23.3
SNP_A-1959180	ttttgacttctacttat[C/T]ctcaacacaattctac	C	T	NM_015439 // upstream // 17876 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// ENST00000343505 // upstream // 183722 // --- // --- // --- /// ENST00000258005 // upstream // 323599 // --- // -	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-1802172	gtatagtgaaaagaac[A/G]ccgaatttgaaaccag	A	G	NM_015439 // intron // 0 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// ENST00000026464 // intron // 0 // --- // --- // --- /// ENST00000332797 // intron // 0 // --- // --- // ---	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-2012120	aacaggtggataaata[C/T]aggtcagtgagaaaaa	C	T	NM_015439 // intron // 0 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// ENST00000026464 // intron // 0 // --- // --- // --- /// ENST00000332797 // intron // 0 // --- // --- // ---	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-1987852	caaagtgtcctttcgd[C/T]ctgtcagaccctagag	C	T	NM_015439 // downstream // 1428 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// NM_016557 // upstream // 28002 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1 (C	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-2263771	gaacctaatggccaa[C/T]gtaatgatagtaagag	C	T	NM_015439 // downstream // 7786 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// NM_016557 // upstream // 21644 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1 (C	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-1987853	gcaagtatttgctgaa[C/T]gagtaaatggataatt	C	T	NM_015439 // downstream // 7887 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// NM_016557 // upstream // 21543 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1 (C	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-1783021	ggcagcccgaacttga[C/T]gtgaaatatgaaggaa	C	T	NM_015439 // downstream // 27946 // Hs.412019 // C6orf80 // 25901 // Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA. /// NM_016557 // upstream // 1484 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1 (C	C6orf80	C6orf80, Homo sapiens chromosome 6 open reading frame 80 (C6orf80), q24.1
SNP_A-1956819	ttttaaatttcccccd[A/T]acatatacataccagcca	A	T	NM_016557 // downstream // 2485 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1 (CCRL1), transcript variant 2, mRNA. /// NM_178445 // downstream // 2485 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C mot	CCRL1	CCRL1, Homo sapiens chemokine (C-C motif) receptor-like 1 (CCRL1), transcript variant 2, q24.1
SNP_A-2193263	catctccagaactgaa[A/G]gtaatgaaagaatcca	A	G	NM_016557 // downstream // 8498 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C motif) receptor-like 1 (CCRL1), transcript variant 2, mRNA. /// NM_178445 // downstream // 8498 // Hs.310512 // CCRL1 // 51554 // Homo sapiens chemokine (C-C mot	CCRL1	CCRL1, Homo sapiens chemokine (C-C motif) receptor-like 1 (CCRL1), transcript variant 2, q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1825607	taaatatctattctccd[A/G]ctataactaagctact	A	G	AF116682 // downstream // 22271 // Hs.238205 // C6orf115 // 58527 // Homo sapiens PRO2013 mRNA, complete cds. /// ENST00000275201 // downstream // 22271 // — // — // — // /// ENST00000357437 // downstream // 21501 // — // — // — // —	C6orf115	C6orf115, Homo sapiens PRO2013 complete cds. q24.1
SNP_A-1707285	ttattgctcccctgcgagctccctac[A/G]aactccccggtgcttgtc cagtttc	A	G	NM_016217 // intron // 0 // Hs.6679 // HECA // 51696 // headcase homolog (Drosophila)	HECA	HECA , rs2327935, headcase homolog (Drosophila),q24.1
SNP_A-1753753	atgtttttcagatgatcaaacacd[A/G]acctagatgcagcaaac caaatcat	A	G	NM_016217 // 3UTR // 0 // Hs.6679 // HECA // 51696 // headcase homolog (Drosophila)	HECA	HECA , rs7745259, headcase homolog (Drosophila),q24.1
SNP_A-2068863	acaatcctgagttcaa[C/T]ggtttcctgagatgtt	C	T	NM_016217 // upstream // 14159 // Hs.197644 // HECA // 51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000357437 // upstream // 33251 // — // — // — // — /// ENST00000230165 // upstream // 14159 // — // — // — // —	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-2302263	gctaaatgtacagat[A/G]aggataatacttgaaa	A	G	NM_016217 // intron // 0 // Hs.197644 // HECA // 51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // intron // 0 // — // — // — // —	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-2060167	aatgaaatgattcacal[C/T]ggagctggtagcatag	C	T	NM_016217 // intron // 0 // Hs.197644 // HECA // 51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // intron // 0 // — // — // — // —	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-1838567	tagaattccctaaaac[C/T]ggaacgataatttgg	C	T	NM_016217 // downstream // 271 // Hs.197644 // HECA // 51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // downstream // 271 // — // — // — // — /// ENST00000358430 // downstream // 58993 // — // — // — // —	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-1987873	cacctacatagaatac[C/G]aggttaaagaaatctg	C	G	NM_016217 // downstream // 8273 // Hs.197644 // HECA // 51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // downstream // 8273 // — // — // — // — /// ENST00000358430 // downstream // 50991 // — // — // — // —	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-1925011	ttatcaactgcactaa[C/T]gataatttcaagttctc	C	T	NM_016217 // downstream // 10664 // Hs.197644 // HECA // 51696 // Homo sapiens headcase homolog (Drosophila) (HECA), mRNA. /// ENST00000230165 // downstream // 10664 // — // — // — // — /// ENST00000358430 // downstream // 48600 // — // — // — // -	HECA	HECA, Homo sapiens headcase homolog (Drosophila) (HECA), q24.1
SNP_A-2308658	gctttccctttctaat[G/T]atctatgcagtataat	G	T	NM_006079 // upstream // 21184 // Hs.82071 // CITED2 // 10370 // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (CITED2), mRNA. /// ENST00000306105 // upstream // 21184 // — // — // — // — /// ENST00	CITED2	CITED2, Homo sapiens Cbp.q24.1
SNP_A-1829104	taaggtatctatggact[C/T]gaaagagagaaatgca	C	T	NM_006079 // upstream // 33921 // Hs.82071 // CITED2 // 10370 // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (CITED2), mRNA. /// ENST00000306105 // upstream // 33921 // — // — // — // — /// ENST00	CITED2	CITED2, Homo sapiens Cbp q24.1
SNP_A-1803524	gtatttgctctgctct[C/T]atattcaaacctgaat	C	T	NM_006079 // upstream // 35832 // Hs.82071 // CITED2 // 10370 // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (CITED2), mRNA. /// ENST00000306105 // upstream // 35832 // — // — // — // — /// ENST00	CITED2	CITED2, Homo sapiens Cbp q24.1
SNP_A-1951800	tttctaaaaggctcaa[C/T]cttaaacacaaaacag	C	T	NM_006079 // upstream // 136000 // Hs.82071 // CITED2 // 10370 // Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (CITED2), mRNA. /// ENST00000306105 // upstream // 136000 // — // — // — // — /// ENST	CITED2	CITED2, Homo sapiens Cbp q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1654875	tgactttgaagattaacaagctaa[A/G]tacgtaaatgatatcaa catgagaa	A	G	AK097143 // downstream // 1671724 // - // - // - // Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981. /// NM_006079 // upstream // 535342 // Hs.82071 // CITED2 // 10370 // Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	-	-, rs10484811, Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981, q24.1
SNP_A-1664928	aagtgtgatgattgtctttgtaa[A/G]cctatgaactagaatgactc acata	A	G	AK097143 // downstream // 1671326 // - // - // - // Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981. /// NM_006079 // upstream // 535740 // Hs.82071 // CITED2 // 10370 // Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	-	-, rs590585, Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981, q24.1
SNP_A-1649854	taaacaaatatatataagaagccaa[C/T]gaaaaacctgtctaa tacttcaaa	C	T	AK097143 // downstream // 976338 // - // - // - // Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981. /// NM_006079 // upstream // 1230728 // Hs.82071 // CITED2 // 10370 // Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	-	-, rs6916580, Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981, q24.1
SNP_A-1805933	gtccgataaagctaaa[C/T]ctttggccaggaaag	C	T	ENST00000358016 // upstream // 1171261 // --- // --- // --- /// ENST00000343481 // downstream // 721201 // --- // --- // ---	-	q24.1
SNP_A-2097840	agagactgcttccaga[C/T]acctaacctgtgaagc	C	T	ENST00000358016 // upstream // 1409563 // --- // --- // --- /// ENST00000343481 // downstream // 482899 // --- // --- // ---	-	q24.1
SNP_A-1726726	aatacaagcagttatttaatgtcat[C/T]gatccactgattctctttat taga	C	T	AK097143 // downstream // 370406 // - // - // - // Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981. /// NM_006079 // upstream // 1836660 // Hs.82071 // CITED2 // 10370 // Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain,	-	-, rs6570450, Homo sapiens cDNA FLJ39824 fis, clone SPLEN2011981, q24.1
SNP_A-1814199	gtgtctctcgctgata[C/T]atagtcaaacaaatga	C	T	ENST00000358016 // upstream // 1877664 // --- // --- // --- /// ENST00000343481 // downstream // 14798 // --- // --- // ---	-	q24.1
SNP_A-1856286	tcacaattataiggtg[A/T]agtctctgtaagaaag	A	T	NM_002511 // downstream // 262095 // Hs.533948 // NMBR // 4829 // Homo sapiens neuromedin B receptor (NMBR), mRNA. /// ENST00000354295 // downstream // 62305 // --- // --- // --- /// ENST00000258042 // downstream // 262095 // - // - // - // -	NMBR	NMBR, Homo sapiens neuromedin B receptor (NMBR), q24.1
SNP_A-2109561	aggaaaatgttccagg[C/T]agaagaagtagttcat	C	T	NM_002511 // downstream // 19045 // Hs.533948 // NMBR // 4829 // Homo sapiens neuromedin B receptor (NMBR), mRNA. /// ENST00000354295 // downstream // 305355 // --- // --- // --- /// ENST00000258042 // downstream // 19045 // --- // --- // --	NMBR	NMBR, Homo sapiens neuromedin B receptor (NMBR), q24.1
SNP_A-1696998	gacatgtgtactgcaggcttccaa[C/T]ttaatattcaggtttcca gcagtc	C	T	NM_016485 // downstream // 58480 // Hs.267288 // C6orf55 // 51534 // chromosome 6 open reading frame 55 /// NM_020455 // upstream // 123385 // Hs.419170 // GPR126 // 57211 // G protein-coupled receptor 126 /// NM_053057 // downstream // 83650 // - // -	C6orf55	C6orf55, rs1319584, chromosome 6 open reading frame 55, q24.2
SNP_A-2086829	actgactcaccttcat[C/G]aggttctgctcctgtg	C	G	NM_020455 // downstream // 120859 // Hs.318894 // GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126), mRNA. /// NM_198569 // downstream // 120859 // Hs.318894 // GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126).	GPR126	GPR126, Homo sapiens G protein-coupled receptor 126 (GPR126), q24.2
SNP_A-2192700	catcccagttctccaa[C/G]attgggcattcigta	C	G	NM_020455 // downstream // 270968 // Hs.318894 // GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126), mRNA. /// NM_198569 // downstream // 270968 // Hs.318894 // GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126).	GPR126	GPR126, Homo sapiens G protein-coupled receptor 126 (GPR126), q24.2
SNP_A-1665658	ctictigagtttctgagacatata[A/G]agaaaggtaggtgggag agaaagtg	A	G	NM_006734 // upstream // 5681 // Hs.75063 // HIVEP2 // 3097 // human immunodeficiency virus type I enhancer binding protein 2 /// NM_016108 // upstream // 280373 // Hs.390662 // AIG1 // 51390 // androgen-induced 1	HIVEP2	HIVEP2, rs1263343, human immunodeficiency virus type I enhancer binding protein 2, q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082994	acgtggaagctggaag[C/T]ccaatcaggcgccatt	C	T	NM_020455 // downstream // 286759 // Hs.318894 // GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126), mRNA. /// NM_198569 // downstream // 286759 // Hs.318894 // GPR126 // 57211 // Homo sapiens G protein-coupled receptor 126 (GPR126).	GPR126	GPR126, Homo sapiens G protein-coupled receptor 126 (GPR126), q24.2
SNP_A-1742833	ttatcattttagactaggaaaagata[C/T]aacacagaaagacctaa tactcaga	C	T	NM_006734 // upstream // 78016 // Hs.75063 // HIVEP2 // 3097 // human immunodeficiency virus type I enhancer binding protein 2 /// NM_016108 // upstream // 208038 // Hs.390662 // AIG1 // 51390 // androgen-induced 1	HIVEP2	HIVEP2, rs185588, human immunodeficiency virus type I enhancer binding protein 2, q24.2
SNP_A-1987927	tgacataaaatcactta[A/T]gtttctggcaaaaag	A	T	NM_006734 // upstream // 23104 // Hs.510172 // HIVEP2 // 3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 262937 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-1917324	tgtttccctcctcaga[A/C]aatccatgcagtacc	A	C	NM_006734 // upstream // 32136 // Hs.510172 // HIVEP2 // 3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 253905 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-2111456	aggaggcacttccatg[A/G]attcaaacaaagagctg	A	G	NM_006734 // upstream // 56512 // Hs.510172 // HIVEP2 // 3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 229529 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-1745450	taattagcattgcttactgtgcatt[A/G]aaaaacaaggctcagaa gaaatgat	A	G	NM_016108 // intron // 0 // Hs.390662 // AIG1 // 51390 // androgen-induced 1	AIG1	AIG1, rs3804526, androgen-induced 1,q24.2
SNP_A-1655877	attgaaaaacaaggctcagaagaaa[C/T]gatataccctctcata accttgtgt	C	T	NM_016108 // intron // 0 // Hs.390662 // AIG1 // 51390 // androgen-induced 1	AIG1	AIG1, rs3804527, androgen-induced 1,q24.2
SNP_A-2163664	caaaaatacaggttga[A/G]tatcgttggccaaaa	A	G	NM_006734 // upstream // 241564 // Hs.510172 // HIVEP2 // 3097 // Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA. /// NM_016108 // upstream // 44477 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced	HIVEP2	HIVEP2, Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), q24.2
SNP_A-2250609	cttagttcatattcag[A/G]cctcaaaacatacttg	A	G	NM_016108 // intron // 0 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// ENST00000305853 // intron // 0 // – // — // — /// ENST00000357847 // intron // 0 // — // — // — // — /// ENST00000275235 // in	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-1758423	cattaactgtgacttaactctgagt[G/T]tgaacgaaaagtacaag tattgac	G	T	NM_016108 // downstream // 56585 // Hs.390662 // AIG1 // 51390 // androgen-induced 1 /// NM_182503 // downstream // 29049 // Hs.435462 // DEADC1 // 134637 // deaminase domain containing 1	AIG1	AIG1, rs742378, androgen-induced 1, q24.2
SNP_A-1830901	taatgaaaatttggg[A/G]acagatgatcataatt	A	G	NM_016108 // downstream // 15865 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// NM_182503 // downstream // 70822 // Hs.435462 // DEADC1 // 134637 // Homo sapiens deaminase domain containing 1 (DEADC1), mRNA. /// ENST000	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-1918013	ttaaaattcttgaac[C/T]gtactcaaaattatga	C	T	NM_016108 // downstream // 15890 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// NM_182503 // downstream // 70797 // Hs.435462 // DEADC1 // 134637 // Homo sapiens deaminase domain containing 1 (DEADC1), mRNA. /// ENST000	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1921912	ttactccgtgagtgtg[A/G]aagtaagattgatct	A	G	NM_016108 // downstream // 33402 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// NM_182503 // downstream // 53285 // Hs.435462 // DEADC1 // 134637 // Homo sapiens deaminase domain containing 1 (DEADC1), mRNA. /// ENST000	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-1923704	ttaggttgtacagaag[C/T]caagatgtcaggcggg	C	T	NM_016108 // downstream // 50811 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// NM_182503 // downstream // 35876 // Hs.435462 // DEADC1 // 134637 // Homo sapiens deaminase domain containing 1 (DEADC1), mRNA. /// ENST000	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-1835901	tacgtttaaaaatgcc[C/T]aataagagtgtttcca	C	T	NM_016108 // downstream // 57837 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// NM_182503 // downstream // 28850 // Hs.435462 // DEADC1 // 134637 // Homo sapiens deaminase domain containing 1 (DEADC1), mRNA. /// ENST000	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-2067875	acaaccgccctatttg[A/T]aaacagcttcaaaaga	A	T	NM_016108 // downstream // 63077 // Hs.112783 // AIG1 // 51390 // Homo sapiens androgen-induced 1 (AIG1), mRNA. /// NM_182503 // downstream // 23610 // Hs.435462 // DEADC1 // 134637 // Homo sapiens deaminase domain containing 1 (DEADC1), mRNA. /// ENST000	AIG1	AIG1, Homo sapiens androgen-induced 1 (AIG1), q24.2
SNP_A-1705275	atcgtggattgtttccatatccac[C/T]aggatacttacattggttctc aaca	C	T	NM_014721 // upstream // 13723 // - // - // - /// NM_032020 // upstream // 82876 // Hs.17680 // FUCA2 // 2519 // fucosidase, alpha-L- 2, plasma	-	-, rs10484803, -, q24.2
SNP_A-2139775	atctaaactaatccac[A/G]cttgaaggatctaga	A	G	NM_032020 // upstream // 38853 // Hs.17680 // FUCA2 // 2519 // Homo sapiens fucosidase, alpha-L- 2, plasma (FUCA2), mRNA. /// ENST00000002165 // upstream // 38853 // — // — // — /// ENST00000341946 // upstream // 38835 // — // — // — //	FUCA2	FUCA2, Homo sapiens fucosidase, alpha-L- 2, plasma (FUCA2), q24.2
SNP_A-2188723	cagtgcttgtctactc[A/C]atgatttgatttcgga	A	C	AB014580 // downstream // 8452 // Hs.102471 // PHACTR2 // 9749 // Homo sapiens mRNA for KIAA0680 protein, partial cds. /// NM_032860 // upstream // 11230 // Hs.185675 // C6orf93 // 84946 // Homo sapiens chromosome 6 open reading frame 93 (C6orf93), mRNA.	PHACTR2	PHACTR2, Homo sapiens for KIAA0680 protein, partial cds, q24.2
SNP_A-2012137	taaaggatggtcaggga[A/G]ctcaaccaaaaccaaa	A	G	NM_006718 // intron // 0 // Hs.444975 // PLAGL1 // 5325 // Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA. /// NM_002656 // intron // 0 // Hs.444975 // PLAGL1 // 5325 // Homo sapiens pleiomorphic adenoma gene-like 1 (PL	PLAGL1	PLAGL1, Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, q24.2
SNP_A-1745826	tgtgagaatcaaatgagttagttaa[C/T]ataaagcatttaccacc aaatctgg	C	T	NM_003764 // downstream // 92483 // Hs.118958 // STX11 // 8676 // syntaxin 11 /// NM_007124 // upstream // 11632 // Hs.250607 // UTRN // 7402 // utrophin (homologous to dystrophin)	STX11	STX11, rs881854, syntaxin 11, q24.2
SNP_A-1750937	cactaaatgggcatttcatgccaa[A/C]taaaaatgtaatataatc acacaat	A	C	NM_007124 // intron // 0 // Hs.250607 // UTRN // 7402 // utrophin (homologous to dystrophin)	UTRN	UTRN, rs926397, utrophin (homologous to dystrophin),q24.2
SNP_A-1706345	agctggaagctgacttagctgcca[A/G]atgtcaatgaagcc gaaaactcct	A	G	NM_007124 // intron // 0 // Hs.250607 // UTRN // 7402 // utrophin (homologous to dystrophin)	UTRN	UTRN, rs951573, utrophin (homologous to dystrophin),q24.2
SNP_A-1666026	taatatttgtgtgtactcaaagaca[C/T]agttcttactcaacatccc aagtaa	C	T	NM_005670 // downstream // 731488 // Hs.458373 // EPM2A // 7957 // epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) /// NM_007124 // downstream // 46988 // Hs.250607 // UTRN // 7402 // utrophin (homologous to dystrophin)	EPM2A	EPM2A, rs10499239, epilepsy, progressive myoclonus type 2A, Lafora disease (laforin), q24.2
SNP_A-1987968	atttagaagtgactgc[A/G]aagtgtcatttcaacc	A	G	NM_007124 // downstream // 92425 // Hs.133135 // UTRN // 7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 681890 // Hs.486696 // EPM2A // 7957 // Homo sapiens epilepsy, progressive myoclonus type 2A, La	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1945032	ttgtgtaaagcctctaa[C/T]ctacagtggcacaact	C	T	NM_007124 // downstream // 105507 // Hs.133135 // UTRN // 7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 868808 // Hs.486696 // EPM2A // 7957 // Homo sapiens epilepsy, progressive myoclonus type 2A, L	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1721708	caagctaaacctctactaattacaa[C/T]gcctccaaacttatttca ttttggca	C	T	NM_005670 // downstream // 399776 // Hs.458373 // EPM2A // 7957 // epilepsy, progressive myoclonus type 2A, Lafora disease (laforin) /// NM_007124 // downstream // 378700 // Hs.250607 // UTRN // 7402 // utrophin (homologous to dystrophin)	EPM2A	EPM2A , rs993701, epilepsy, progressive myoclonus type 2A, Lafora disease (laforin), q24.3
SNP_A-2130109	atacccacctctcaaca[C/T]cccagttggtctctc	C	T	NM_007124 // downstream // 409006 // Hs.133135 // UTRN // 7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 365309 // Hs.486696 // EPM2A // 7957 // Homo sapiens epilepsy, progressive myoclonus type 2A, L	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1921940	ttactctccagtgatc[A/G]agaattagcaatgtgga	A	G	NM_007124 // downstream // 433696 // Hs.133135 // UTRN // 7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 340619 // Hs.486696 // EPM2A // 7957 // Homo sapiens epilepsy, progressive myoclonus type 2A, L	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.2
SNP_A-1920966	ttacagaccagggtca[A/T]gggtcaaagattttgc	A	T	NM_007124 // downstream // 580204 // Hs.133135 // UTRN // 7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 194111 // Hs.486696 // EPM2A // 7957 // Homo sapiens epilepsy, progressive myoclonus type 2A, L	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.3
SNP_A-2050057	aaggaatgtcctagag[A/C]aaatcatacacacatg	A	C	NM_007124 // downstream // 619638 // Hs.133135 // UTRN // 7402 // Homo sapiens utrophin (homologous to dystrophin) (UTRN), mRNA. /// NM_005670 // downstream // 154677 // Hs.486696 // EPM2A // 7957 // Homo sapiens epilepsy, progressive myoclonus type 2A, L	UTRN	UTRN, Homo sapiens utrophin (homologous to dystrophin) (UTRN), q24.3
SNP_A-1685210	ccttctagaacattcctatctacca[A/G]acgtaatgtagccccagt ttaattc	A	G	NM_000838 // intron // 0 // Hs.32945 // GRM1 // 2911 // glutamate receptor, metabotropic 1	GRM1	GRM1 , rs10484860, glutamate receptor, metabotropic 1 q24.3
SNP_A-1987995	gagctgagacccaaaa[G/T]aggagtcaggcttagt	G	T	NM_000838 // intron // 0 // Hs.32945 // GRM1 // 2911 // Homo sapiens glutamate receptor, metabotropic 1 (GRM1), mRNA. /// ENST00000355289 // intron // 0 // --- // --- // --- /// ENST00000282753 // intron // 0 // --- // --- // ---	GRM1	GRM1, Homo sapiens glutamate receptor, metabotropic 1 (GRM1), q24.3
SNP_A-2216740	cctctctccattaata[A/T]ctggcttgactacaaa	A	T	NM_000838 // intron // 0 // Hs.32945 // GRM1 // 2911 // Homo sapiens glutamate receptor, metabotropic 1 (GRM1), mRNA. /// ENST00000355289 // intron // 0 // --- // --- // --- /// ENST00000282753 // intron // 0 // --- // --- // ---	GRM1	GRM1, Homo sapiens glutamate receptor, metabotropic 1 (GRM1), q24.3
SNP_A-2279607	gaggcaattattgtaa[C/T]gtttctccaaaactat	C	T	NM_139244 // downstream // 191667 // Hs.93534 // STXBP5 // 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream // 765171 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2282922	gataacaaaaaataatg[C/G]aagtacacaaggata	C	G	NM_139244 // downstream // 757630 // Hs.93534 // STXBP5 // 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream // 199208 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2193744	catctttcagctgaag[G/T]attacgtgctctaa	G	T	NM_139244 // downstream // 758282 // Hs.93534 // STXBP5 // 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream // 198556 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1988045	ggtgaagcctagaaga[A/G]cactgaattgctact	A	G	NM_139244 // downstream // 768782 // Hs.93534 // STXBP5 // 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream // 188056 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2274014	gacttaactcctcac[A/G]cttcaaccttcttatc	A	G	NM_139244 // downstream // 856026 // Hs.93534 // STXBP5 // 134957 // Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), mRNA. /// NM_015278 // upstream // 100812 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH	STXBP5	STXBP5, Homo sapiens syntaxin binding protein 5 (tomosyn) (STXBP5), q24.3
SNP_A-2012152	caagctctccaagtaa[C/T]gtgatgtgcagatat	C	T	NM_015278 // intron // 0 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// ENST00000229686 // intron // 0 // — // — // — // —	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-2309569	ggaaactctaggttgc[C/G]atattttctttccag	C	G	NM_015278 // intron // 0 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// ENST00000229686 // intron // 0 // — // — // — // —	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-1952063	ttctcttgtaaactt[A/G]ggagagatcggagcta	A	G	NM_015278 // downstream // 41565 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// ENST00000229686 // intron // 0 // — // — // — // —	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-1887892	tgagatttcatttgta[A/G]agccggatggctaagt	A	G	NM_015278 // downstream // 41565 // Hs.193133 // SASH1 // 23328 // Homo sapiens SAM and SH3 domain containing 1 (SASH1), mRNA. /// NM_005715 // upstream // 153723 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST	SASH1	SASH1, Homo sapiens SAM and SH3 domain containing 1 (SASH1), q24.3
SNP_A-1794488	ggtcctgaggcataaa[C/T]gggattagtgctctta	C	T	NM_005715 // intron // 0 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // — // — // — // —	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1988068	gtacagatggagaaac[G/T]gaaataaaatcaatgc	G	T	NM_005715 // intron // 0 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // — // — // — // —	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2012155	gaggagaaaatacagc[G/T]gaataagactccaggt	G	T	NM_005715 // intron // 0 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // — // — // — // —	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1858344	tcagacacatagccat[A/G]aactcagaagtagtgt	A	G	NM_005715 // intron // 0 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // — // — // — // —	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1988070	agttgtatcaggtgc[C/T]ccattgttatccctgt	C	T	NM_005715 // intron // 0 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // — // — // — // —	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1988071	tgctgtaagatcagaat[C/T]ggaaaaagacgagccc	C	T	NM_005715 // intron // 0 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// ENST00000265363 // intron // 0 // — // — // — // —	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2046355	aagagaatgataattat[C/T]aggtgtcacagggctc	C	T	NM_005715 // downstream // 133922 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 131902 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 i	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1806529	gtcgtcaggttcttgga[C/T]agattatttaagttct	C	T	NM_005715 // downstream // 138798 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 127026 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 i	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100263	agagttgttaaacaaa[C/T]gattgcttcctacata	C	T	NM_005715 // downstream // 154462 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 111362 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 i	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1875414	tctctgcgaagacaga[A/C]tatccctcggctgtgt	A	C	NM_005715 // downstream // 162841 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 102983 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 i	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2114286	agggaagttgtgagg[A/G]aagacaaagaaacgtg	A	G	NM_005715 // downstream // 167394 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 98430 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 in	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-1868161	tcctattgacgtggt[A/G]aaagaagttacgctag	A	G	NM_005715 // downstream // 192314 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 73510 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 in	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2032105	aaagtgcctgctttaa[C/T]tggatcagctctgttt	C	T	NM_005715 // downstream // 227487 // Hs.131514 // UST // 10090 // Homo sapiens uronyl-2-sulfotransferase (UST), mRNA. /// NM_015093 // upstream // 38337 // Hs.269775 // MAP3K7IP2 // 23118 // Homo sapiens mitogen-activated protein kinase kinase kinase 7 in	UST	UST, Homo sapiens uronyl-2-sulfotransferase (UST), q25.1
SNP_A-2125284	agttgtgaaaggttca[A/G]gtgggtgctgaccctt	A	G	ENST00000325863 // intron // 0 // — // — // —	-	q25.1
SNP_A-1651114	tgtatttgaagtagcagaggagtggt[A/G]tgtgaatcatttttgattac tcagt	A	G	NM_032832 // intron // 0 // Hs.408355 // LRP11 // 84918 // low density lipoprotein receptor-related protein 11	LRP11	LRP11, rs952414, low density lipoprotein receptor-related protein 11, q25.1
SNP_A-1930889	ttccagctgaccgtga[C/T]ggacactgccgggcag	C	T	NM_032832 // CDS // 0 // Hs.408355 // LRP11 // 84918 // Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), mRNA. /// ENST00000239367 // CDS // 0 // — // — // —	LRP11	LRP11, Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), q25.1
SNP_A-2202346	ccaccagcctggttcc[A/G]agctaggattaaagag	A	G	NM_032832 // intron // 0 // Hs.408355 // LRP11 // 84918 // Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), mRNA. /// ENST00000239367 // intron // 0 // — // — // —	LRP11	LRP11, Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), q25.1
SNP_A-2078825	acccaaagaatacaaa[C/T]gttctactataaaga	C	T	NM_032832 // intron // 0 // Hs.408355 // LRP11 // 84918 // Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), mRNA. /// ENST00000239367 // intron // 0 // — // — // — // —	LRP11	LRP11, Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), q25.1
SNP_A-1988082	cattgtcctcttcaga[G/T]tctcctcaggtactg	G	T	ENST00000328043 // intron // 0 // — // — // —	-	q25.1
SNP_A-1835014	tacccatcaaaatggc[A/T]atccttaaaatttcaa	A	T	NM_032832 // upstream // 66816 // Hs.408355 // LRP11 // 84918 // Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), mRNA. /// NM_139165 // upstream // 40199 // Hs.511818 // RAET1E // 135250 // Homo sapiens retinoic acid early transc	LRP11	LRP11, Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), q25.1
SNP_A-1821848	gtttagcattcagaa[A/G]aaaatagccagtaagt	A	G	NM_024518 // upstream // 40198 // Hs.326556 // ULBP3 // 79465 // Homo sapiens UL16 binding protein 3 (ULBP3), mRNA. /// ENST00000253335 // upstream // 40198 // — // — // — // — /// ENST00000359869 // upstream // 33833 // — // — // — // — /	ULBP3	ULBP3, Homo sapiens UL16 binding protein 3 (ULBP3), q25.1
SNP_A-2069425	acacaagatcacatca[C/G]ctcactgttctaagta	C	G	ENST00000359869 // intron // 0 // — // — // — // — /// ENST00000359407 // intron // 0 // — // — // —	-	q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2048976	aagcctgagctcttta[A/C]agtgaaatatccatca	A	C	NM_203395 // upstream // 52551 // Hs.310225 // C6orf71 // 389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// ENST00000359869 // downstream // 65988 // — // — // — /// ENST00000359407 // downstream // 65988 // — // — //	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-2153579	attagctgagaggaca[C/T]ggggaagccactgctg	C	T	NM_203395 // upstream // 48303 // Hs.310225 // C6orf71 // 389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// ENST00000359869 // downstream // 70236 // — // — // — /// ENST00000359407 // downstream // 70236 // — // — //	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-1935612	ttctgtacaaagcccct[C/G]agatcatgtccacctt	C	G	NM_203395 // downstream // 2798 // Hs.310225 // C6orf71 // 389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// AB033035 // upstream // 397219 // Hs.189781 // PLEKHG1 // 57480 // Homo sapiens mRNA for KIAA1209 protein, partial cds. /// E	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-1880904	tcttgtatcttagaaa[G/T]aatcagtcaacaatgg	G	T	NM_203395 // downstream // 8492 // Hs.310225 // C6orf71 // 389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// AB033035 // upstream // 391525 // Hs.189781 // PLEKHG1 // 57480 // Homo sapiens mRNA for KIAA1209 protein, partial cds. /// E	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-2086573	actgaaatgtaatata[A/C]ccaaaatgaaacacaa	A	C	NM_203395 // downstream // 275796 // Hs.310225 // C6orf71 // 389434 // Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), mRNA. /// AB033035 // upstream // 124221 // Hs.189781 // PLEKHG1 // 57480 // Homo sapiens mRNA for KIAA1209 protein, partial cds. ///	C6orf71	C6orf71, Homo sapiens iodotyrosine dehalogenase 1 (DEHAL1), q25.1
SNP_A-1794337	ggtccagttgctcccaa[C/T]atcttagagcctgtca	C	T	AB033035 // intron // 0 // Hs.189781 // PLEKHG1 // 57480 // Homo sapiens mRNA for KIAA1209 protein, partial cds. /// ENST00000239392 // intron // 0 // — // — // — /// ENST00000358517 // intron // 0 // — // — // — // —	PLEKHG1	PLEKHG1, Homo sapiens for KIAA1209 protein, partial cds., q25.1
SNP_A-1824389	taaacgttagcgaact[C/G]acagtaagaaaagaga	C	G	NM_005100 // intron // 0 // Hs.371240 // AKAP12 // 9590 // Homo sapiens A kinase (PRKA) anchor protein (gravin) 12 (AKAP12), transcript variant 1, mRNA. /// NM_144497 // intron // 0 // Hs.371240 // AKAP12 // 9590 // Homo sapiens A kinase (PRKA) anchor pro	AKAP12	AKAP12, Homo sapiens A kinase (PRKA) anchor protein (gravin) 12 (AKAP12), transcript variant 1, q25.1
SNP_A-1642137	attagctaattccca[G/T]gaaagtaggaacacgg ggataaca	G	T	NM_017909 // intron // 0 // Hs.238270 // C6orf96 // 55005 // chromosome 6 open reading frame 96	C6orf96	C6orf96, rs3800274, chromosome 6 open reading frame 96,q25.1
SNP_A-2053985	aagttacactgtagaa[C/T]tgttcgccagtcttct	C	T	NM_020861 // upstream // 4857 // Hs.520073 // ZBTB2 // 57621 // Homo sapiens zinc finger and BTB domain containing 2 (ZBTB2), mRNA. /// NM_017909 // downstream // 8456 // Hs.486835 // C6orf96 // 55005 // Homo sapiens chromosome 6 open reading frame 96 (C6	ZBTB2	ZBTB2, Homo sapiens zinc finger and BTB domain containing 2 (ZBTB2), q25.1
SNP_A-2105131	agcatggaacggagca[C/T]ggactctgacccatat	C	T	NM_025059 // intron // 0 // Hs.130239 // C6orf97 // 80129 // Homo sapiens chromosome 6 open reading frame 97 (C6orf97), mRNA. /// ENST00000239374 // intron // 0 // — // — // — // —	C6orf97	C6orf97, Homo sapiens chromosome 6 open reading frame 97 (C6orf97), q25.1
SNP_A-1900705	tggaggtacagaaagg[C/G]atgctggaagagtgtt	C	G	NM_025059 // downstream // 5957 // Hs.130239 // C6orf97 // 80129 // Homo sapiens chromosome 6 open reading frame 97 (C6orf97), mRNA. /// ENST00000239374 // downstream // 5957 // — // — // — // — /// ENST00000322595 // upstream // 178237 // — //	C6orf97	C6orf97, Homo sapiens chromosome 6 open reading frame 97 (C6orf97), q25.1
SNP_A-1662916	gacaaaaatttgtagggaagcaaat[A/C]ccttcaaggttgagtgtct ttctggtc	A	C	NM_000125 // intron // 0 // Hs.1657 // ESR1 // 2099 // estrogen receptor 1	ESR1	ESR1, rs1884054, estrogen receptor 1,q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1988127	gggaacgttaatgtta[C/T]gacaaatctcatggga	C	T	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.1
SNP_A-2081510	acctgtggaaaatga[A/T]cacgcactgaacccca	A	T	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2287886	gattataatctctct[C/T]ccttgtggacttccc	C	T	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2140714	atctctgccagcccaa[C/T]atgtggccagaggatc	C	T	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2100512	agataataagtaaacat[C/T]gatttcaagtgaacag	C	T	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2090345	actggaaaaatacaa[A/G]tagagagaccaggtg	A	G	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2063462	aattaagttattcaca[A/G]acacatggtgctcag	A	G	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-1960717	ttttctcatccaaga[A/G]gatatgtggagtaagc	A	G	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-1932923	ttccttttgcctccac[C/T]agcttcaacactaaga	C	T	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2255961	ctttaagaatagtgag[A/G]agaactgaattggcaa	A	G	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2
SNP_A-2313986	ggagctgaaaaagcag[C/G]ccatgaatacggaatc	C	G	NM_133650 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, mRNA. /// NM_015293 // intron // 0 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat conta	SYNE1	SYNE1, Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant alpha, q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2280164	gagggaggtggaagaa[A/G]agagccatttgttgag	A	G	NM_000125 // downstream // 538863 // Hs.208124 // ESR1 // 2099 // Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// NM_133650 // upstream // 5283 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transc	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.2
SNP_A-2074836	acatcaagaccctgac[C/T]gataaaatgccccctta	C	T	NM_000125 // downstream // 538982 // Hs.208124 // ESR1 // 2099 // Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// NM_133650 // upstream // 5402 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transc	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.2
SNP_A-2264771	gaagactcagccaaaa[A/G]actatcagaactgatt	A	G	NM_000125 // downstream // 590796 // Hs.208124 // ESR1 // 2099 // Homo sapiens estrogen receptor 1 (ESR1), mRNA. /// NM_133650 // upstream // 57216 // Hs.12967 // SYNE1 // 23345 // Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), trans	ESR1	ESR1, Homo sapiens estrogen receptor 1 (ESR1), q25.2
SNP_A-1729704	cttttcagaatctctgaaggaaaa[C/T]gatacgcaacataataa attttga	C	T	NM_003381 // 3UTR // 0 // Hs.53973 // VIP // 7432 // vasoactive intestinal peptide	VIP	VIP , rs688136, vasoactive intestinal peptide,q25.2
SNP_A-2090667	acttaagatgatatg[A/G]aaatgatacacattca	A	G	NM_025107 // intron // 0 // Hs.18160 // MYCT1 // 80177 // Homo sapiens myc target 1 (MYCT1), mRNA. /// ENST00000239393 // intron // 0 // — // — // — // —	MYCT1	MYCT1, Homo sapiens myc target 1 (MYCT1), q25.2
SNP_A-1905767	tggtatttcaatgta[C/T]gatggatttatctaaa	C	T	NM_025107 // intron // 0 // Hs.18160 // MYCT1 // 80177 // Homo sapiens myc target 1 (MYCT1), mRNA. /// ENST00000239393 // intron // 0 // — // — // — // —	MYCT1	MYCT1, Homo sapiens myc target 1 (MYCT1), q25.2
SNP_A-1683060	atccctttttacagtcaactcaca[A/T]gaatagacaaattcaaaa gtatgat	A	T	NM_003381 // downstream // 193528 // Hs.53973 // VIP // 7432 // vasoactive intestinal peptide /// NM_012177 // downstream // 17234 // Hs.272027 // FBXO5 // 26271 // F-box only protein 5	VIP	VIP , rs7765062, vasoactive intestinal peptide ,q25.2
SNP_A-1677774	atgttaggatggccagatataacca[C/T]gtgagaacatagcctg gtaagtggt	C	T	NM_003381 // downstream // 194427 // Hs.53973 // VIP // 7432 // vasoactive intestinal peptide /// NM_012177 // downstream // 16335 // Hs.272027 // FBXO5 // 26271 // F-box only protein 5	VIP	VIP , rs10484864, vasoactive intestinal peptide ,q25.2
SNP_A-1940810	ttgcgtttggtgatta[C/G]aacagagaattccttg	C	G	NM_012419 // upstream // 99880 // Hs.166313 // RGS17 // 26575 // Homo sapiens regulator of G-protein signalling 17 (RGS17), mRNA. /// ENST00000206262 // upstream // 99880 // — // — // — // — /// ENST00000312401 // downstream // 51158 // — // —	RGS17	RGS17, Homo sapiens regulator of G-protein signalling 17 (RGS17), q25.2
SNP_A-1932163	ttcctcatggtcttaa[G/T]atgtcatttcatctgt	G	T	NM_000914 // upstream // 743953 // Hs.2353 // OPRM1 // 4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 859222 // Hs.146100 // PIP3-E // 26034 // Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA.	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-1915282	tgttcataataggtcc[A/G]cagtaagtaatatttg	A	G	NM_000914 // upstream // 656297 // Hs.2353 // OPRM1 // 4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // downstream // 771566 // Hs.146100 // PIP3-E // 26034 // Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA.	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-1703597	ttgtggaaaaagatagatcaggtcc[C/T]acttgaagacaaagtt gctctcaac	C	T	AY036623 // intron // 0 // Hs.2353 // OPRM1 // 4988 // opioid receptor, mu 1	OPRM1	OPRM1, rs558025, opioid receptor, mu 1,q25.2
SNP_A-1931953	ttcctaatctgtgaaa[C/T]gagatactgtattac	C	T	ENST00000337049 // intron // 0 // — // — // —	-	q25.2
SNP_A-1988215	aactcctttagtacca[C/T]gaaactaaggcaaa	C	T	NM_015553 // 3UTR // 0 // Hs.146100 // PIP3-E // 26034 // Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA. /// ENST00000337049 // intron // 0 // — // — // — // — /// ENST00000265198 // 3UTR // 0 // — // — // — // —	PIP3-E	PIP3-E, Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), q25.2
SNP_A-1988222	taaaatgccttcctca[C/T]cttgtctgctgttgga	C	T	NM_015553 // intron // 0 // Hs.146100 // PIP3-E // 26034 // Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA. /// ENST00000337049 // intron // 0 // — // — // — // — /// ENST00000265198 // intron // 0 // — // — // — // —	PIP3-E	PIP3-E, Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238419	ctctgctcactaagca[C/T]atccaggtgaatgaaa	C	T	NM_015553 // intron // 0 // Hs.146100 // PIP3-E // 26034 // Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA. /// ENST00000337049 // intron // 0 // — // — // — /// ENST00000265198 // intron // 0 // — // — // —	PIP3-E	PIP3-E, Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), q25.2
SNP_A-2249551	cttaacttcacaagccc[A/G]aacagtatagaggtaat	A	G	NM_000914 // downstream // 242987 // Hs.2353 // OPRM1 // 4988 // Homo sapiens opioid receptor, mu 1 (OPRM1), mRNA. /// NM_015553 // upstream // 5681 // Hs.146100 // PIP3-E // 26034 // Homo sapiens phosphoinositide-binding protein PIP3-E (PIP3-E), mRNA. //	OPRM1	OPRM1, Homo sapiens opioid receptor, mu 1 (OPRM1), q25.2
SNP_A-1832586	tacaaattgcataacc[A/G]cctgaaatatcctaag	A	G	NM_014892 // downstream // 177125 // Hs.227602 // RBM16 // 22828 // Homo sapiens RNA binding motif protein 16 (RBM16), mRNA. /// NM_016020 // downstream // 246490 // Hs.279908 // TFB1M // 51106 // Homo sapiens transcription factor B1, mitochondrial (TFB1M	RBM16	RBM16, Homo sapiens RNA binding motif protein 16 (RBM16), q25.2
SNP_A-2086734	actgaattgctaagga[A/C]aatagcaggcgtcacc	A	C	NM_015718 // CDS // 0 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// ENST00000159060 // CDS // 0 // — // — // —	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2053085	aagtctacagtcagaa[C/T]gttccatggtgagac	C	T	NM_015718 // upstream // 362152 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 959897 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2075738	acatgggtttccta[A/G]agaagcagcaggtgga	A	G	NM_015718 // upstream // 538274 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 783775 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2026689	aaacaatatgtcaaag[G/T]agaggaaatagtgtatt	G	T	NM_015718 // upstream // 542852 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 779197 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2275335	gagaatagaaagaaatc[A/G]ctactacatttgtgct	A	G	NM_015718 // upstream // 878920 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 443129 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2198975	catttgcttgataaac[G/T]aacaaatgtttgcatg	G	T	NM_015718 // upstream // 1092527 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 229522 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-1648068	ttgaactagtccaatctctataac[A/G]cttcttcatatcatttgactt cat	A	G	NM_015718 // upstream // 1245848 // Hs.247776 // NOX3 // 50508 // NADPH oxidase 3 /// NM_020732 // upstream // 77649 // Hs.436008 // ARID1B // 57492 // AT rich interactive domain 1B (SWI1-like) /// NM_175863 // upstream // 76990 // Hs.436008 // ARID1B //	NOX3	NOX3, rs10499278, NADPH oxidase 3, q25.3
SNP_A-1670866	ttcatatcatttgacttcatgatca[A/G]attagagaggtgactggga gaacga	A	G	NM_015718 // upstream // 1245879 // Hs.247776 // NOX3 // 50508 // NADPH oxidase 3 /// NM_020732 // upstream // 77618 // Hs.436008 // ARID1B // 57492 // AT rich interactive domain 1B (SWI1-like) /// NM_175863 // upstream // 76959 // Hs.436008 // ARID1B //	NOX3	NOX3, rs10499277, NADPH oxidase 3, q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2142622	atgaactgataataaa[C/T]ggcaagaatactaaat	C	T	NM_015718 // upstream // 1197381 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 124668 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2012206	tgctagccagaaaggaa[C/T]agctgtcacaaaaacc	C	T	NM_015718 // upstream // 1197822 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 124227 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2252233	cttcccagactaata[A/G]gtgagaatctgggga	A	G	NM_015718 // upstream // 1199613 // Hs.247776 // NOX3 // 50508 // Homo sapiens NADPH oxidase 3 (NOX3), mRNA. /// NM_175863 // upstream // 122436 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript	NOX3	NOX3, Homo sapiens NADPH oxidase 3 (NOX3), q25.3
SNP_A-2111114	aggagagagaggttgc[C/G]atcagtgaaccaagat	C	G	NM_175863 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domai	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-2235996	ctcctggcccgctgcg[C/T]attcggagtaaagcat	C	T	NM_175863 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domai	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-2073558	acagtacgaggtaggg[A/G]ccaggcattcacatga	A	G	NM_175863 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domai	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-2153491	attagcaaatgtacaaa[C/G]tcaaggcactgatctt	C	G	NM_175863 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domai	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-2126119	agttttcatgactta[C/T]cacagggtgacattcc	C	T	NM_175863 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, mRNA. /// NM_020732 // intron // 0 // Hs.291587 // ARID1B // 57492 // Homo sapiens AT rich interactive domai	ARID1B	ARID1B, Homo sapiens AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 3, q25.3
SNP_A-1687034	agaactcacttgtgaatcttagtaa[A/G]taaaggtcaatttaagttagagaaa	A	G	NM_024630 // upstream // 33976 // Hs.292541 // ZDHHC14 // 79683 // zinc finger, DHHC domain containing 14 /// NM_153746 // upstream // 33976 // Hs.292541 // ZDHHC14 // 79683 // zinc finger, DHHC domain containing 14	ZDHHC14	ZDHHC14 , rs4128492, zinc finger, DHHC domain containing 14 q25.3
SNP_A-1988288	gaagtgtatcgagca[C/T]ggaaaccggttgaaac	C	T	NM_018452 // upstream // 16456 // Hs.157212 // C6orf35 // 55836 // Homo sapiens chromosome 6 open reading frame 35 (C6orf35), mRNA. /// NM_024630 // upstream // 41472 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14	C6orf35	C6orf35, Homo sapiens chromosome 6 open reading frame 35 (C6orf35), q25.3
SNP_A-1895505	tgcctactacctgtcat[C/T]cagctcacttttatact	C	T	NM_024630 // intron // 0 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA. /// NM_153746 // intron // 0 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14	ZDHHC14	ZDHHC14, Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1650706	aagtgtgtacactaaaaaagtggatc[A/G]taactggatgtcgtgag tatgtcat	A	G	NM_024630 // intron // 0 // Hs.292541 // ZDHHC14 // 79683 // zinc finger, DHHC domain containing 14 /// NM_153746 // intron // 0 // Hs.292541 // ZDHHC14 // 79683 // zinc finger, DHHC domain containing 14	ZDHHC14	ZDHHC14 , rs589588, zinc finger, DHHC domain containing 14 ,q25.3
SNP_A-2305926	gctgctggagatcgaat[C/T]gaaatgtttggcaaga	C	T	NM_024630 // intron // 0 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA. /// NM_153746 // intron // 0 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14	ZDHHC14	ZDHHC14, Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), q25.3
SNP_A-1954429	tttgcattccacaagc[A/G]catatcggtaaggtct	A	G	NM_024630 // intron // 0 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA. /// NM_153746 // intron // 0 // Hs.187459 // ZDHHC14 // 79683 // Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14	ZDHHC14	ZDHHC14, Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), q25.3
SNP_A-1890988	tgatggctttaccaaa[C/T]ggagcagaataagaag	C	T	ENST00000356060 // intron // 0 // — // — // —	-	q25.3
SNP_A-2037389	aacaaatggtgtctta[A/G]caactggatgtttgca	A	G	ENST00000356060 // intron // 0 // — // — // —	-	q25.3
SNP_A-1808907	gtgaatccgctgctcc[A/G]agtcacctttcaacc	A	G	NM_003898 // intron // 0 // Hs.434494 // SYNJ2 // 8871 // Homo sapiens synaptojanin 2 (SYNJ2), mRNA. /// ENST00000241842 // intron // 0 // — // — // —	SYNJ2	SYNJ2, Homo sapiens synaptojanin 2 (SYNJ2), q25.3
SNP_A-2173708	cacacacacaaaagca[C/T]ggtaaacagtaaataa	C	T	NM_207118 // downstream // 8947 // Hs.356224 // GTF2H5 // 404672 // Homo sapiens general transcription factor IIH, polypeptide 5 (GTF2H5), mRNA. /// NM_020245 // upstream // 111301 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4	GTF2H5	GTF2H5, Homo sapiens general transcription factor IIH, polypeptide 5 (GTF2H5), q25.3
SNP_A-1741469	cttgaaaatgtggaatatctgaaa[C/T]caggagaagtagagga gtatacaag	C	T	NM_020245 // intron // 0 // Hs.102237 // TULP4 // 56995 // tubby like protein 4	TULP4	TULP4 , rs635995, tubby like protein 4,q25.3
SNP_A-1731735	aatatttaagttaaaacgttcgga[A/G]gctatgtcagagtcagcc aaaatta	A	G	NM_020245 // intron // 0 // Hs.102237 // TULP4 // 56995 // tubby like protein 4	TULP4	TULP4 , rs585078, tubby like protein 4,q25.3
SNP_A-1988313	aataaagaaagctaaa[C/G]atgaaaaatgctgtgc	C	G	NM_020245 // intron // 0 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // — // — // — /// ENST00000357413 // intron // 0 // — // — // — // — /// ENST00000252629 /	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1988315	tgcctagctgtaacca[C/T]ctcgttttgggaatg	C	T	NM_020245 // intron // 0 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // — // — // — /// ENST00000357413 // intron // 0 // — // — // — // — /// ENST00000252629 /	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1871150	tcgttctctgtgcccc[A/G]acagtgctatatgtag	A	G	NM_020245 // intron // 0 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // — // — // — /// ENST00000357413 // intron // 0 // — // — // — // — /// ENST00000252629 /	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1988316	ccccagtatcttgcc[C/T]aagacttgagtaataa	C	T	NM_020245 // intron // 0 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // — // — // — /// ENST00000357413 // intron // 0 // — // — // — // — /// ENST00000252629 /	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1988317	tgctagtactttatga[A/G]atagcctgtgtccctg	A	G	NM_020245 // intron // 0 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // — // — // — /// ENST00000357413 // intron // 0 // — // — // — // — /// ENST00000252629 /	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2203109	ccactgctcagctgga[A/G]aggacaaactctaggc	A	G	NM_020245 // intron // 0 // Hs.486993 // TULP4 // 56995 // Homo sapiens tubby like protein 4 (TULP4), mRNA. /// ENST00000344499 // intron // 0 // --- // --- // --- /// ENST00000357413 // intron // 0 // --- // --- // --- /// ENST00000252629 //	TULP4	TULP4, Homo sapiens tubby like protein 4 (TULP4), q25.3
SNP_A-1913360	tgtgggtccaggctc[A/G]caaataaatccctctgc	A	G	ENST00000275254 // intron // 0 // --- // --- // --- /// ENST00000314630 // intron // 0 // --- // --- // ---	-	q25.3
SNP_A-2220003	ccttattcatgtccac[A/G]cttttctgccaatagt	A	G	ENST00000275254 // intron // 0 // --- // --- // --- /// ENST00000314630 // intron // 0 // --- // --- // ---	-	q25.3
SNP_A-2177746	cacgtccacagccaga[A/G]aaatcagcaaagatcc	A	G	ENST00000275254 // intron // 0 // --- // --- // --- /// ENST00000314630 // intron // 0 // --- // --- // ---	-	q25.3
SNP_A-1938740	ttgagccaaaaaaccac[C/G]agacttcagaaacctc	C	G	ENST00000275254 // intron // 0 // --- // --- // --- /// ENST00000314630 // intron // 0 // --- // --- // ---	-	q25.3
SNP_A-1988325	acattttccgagccc[A/G]atagacaagcagattt	A	G	NM_003379 // intron // 0 // Hs.487027 // VIL2 // 7430 // Homo sapiens villin 2 (ezrin) (VIL2), mRNA. /// ENST00000337147 // intron // 0 // --- // --- // --- /// ENST00000360444 // intron // 0 // --- // --- // --- /// ENST00000356712 // intro	VIL2	VIL2, Homo sapiens villin 2 (ezrin) (VIL2), q25.3
SNP_A-1699779	caatcagcccagagcctggctccca[A/G]taacacccacaata cctgttgcatt	A	G	NM_054114 // upstream // 18592 // Hs.123581 // TAGAP // 117289 // T-cell activation GTPase activating protein /// NM_138810 // upstream // 18592 // Hs.123581 // TAGAP // 117289 // T-cell activation GTPase activating protein /// NM_152133 // upstream // 1	TAGAP	TAGAP , rs169858, T-cell activation GTPase activating protein ,q25.3
SNP_A-1692668	cagtcagagaaaaggggaccaaagc[C/T]actccgtgtactctc acattcgtca	C	T	NM_054114 // upstream // 23383 // Hs.123581 // TAGAP // 117289 // T-cell activation GTPase activating protein /// NM_138810 // upstream // 23383 // Hs.123581 // TAGAP // 117289 // T-cell activation GTPase activating protein /// NM_152133 // upstream // 2	TAGAP	TAGAP , rs212390, T-cell activation GTPase activating protein ,q25.3
SNP_A-2087552	actgcgctgaccacca[A/G]cttcaaagatggtc	A	G	ENST00000308254 // intron // 0 // --- // --- // ---	-	q25.3
SNP_A-2115479	aggggattccgaagcc[A/G]atgttcccaaacctga	A	G	ENST00000340366 // CDS // 0 // --- // --- // --- /// ENST00000329629 // CDS // 0 // --- // --- // ---	-	q25.3
SNP_A-2012218	gtttgctcccccactc[C/G]aggcttctccatctcta	C	G	NM_207501 // downstream // 291725 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 23123 // --- // --- // --- /// ENST00000297267 // downstream // 60792 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-1807843	gtcttaccggttatta[C/T]cacaatgttaccacct	C	T	NM_207501 // downstream // 285439 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 29409 // --- // --- // --- /// ENST00000297267 // downstream // 67078 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2037579	aacaacttagcaaaca[A/C]catgcatttatgagag	A	C	NM_207501 // downstream // 284944 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 29904 // --- // --- // --- /// ENST00000297267 // downstream // 67573 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2070985	acactctgcttggatc[A/G]aaagtcttagcatttt	A	G	NM_207501 // downstream // 181832 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 133016 // --- // --- // --- /// ENST00000297267 // downstream // 170685 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2294515	gcagtcactggaatga[A/G]catgcccacgctcag	A	G	NM_207501 // downstream // 164146 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 150702 // --- // --- // --- /// ENST00000297267 // downstream // 188371 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2037770	aacaagtgatttgcac[G/T]atcagtcaaggtgtgg	G	T	NM_207501 // downstream // 4284 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 310564 // --- // --- // --- /// ENST00000297267 // downstream // 348233 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2286326	gatgcgggaacttcag[A/G]aaaaaagacactcggc	A	G	NM_207501 // downstream // 4216 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 310632 // --- // --- // --- /// ENST00000297267 // downstream // 348301 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-2109851	aggaacagagaggcag[G/T]aaacaatggtctctaa	G	T	NM_207501 // downstream // 3609 // Hs.487042 // FLJ27255 // 401281 // Homo sapiens FLJ27255 protein (FLJ27255), mRNA. /// ENST00000340366 // downstream // 311239 // --- // --- // --- /// ENST00000297267 // downstream // 348908 // --- // --- // ---	FLJ27255	FLJ27255, Homo sapiens FLJ27255 protein (FLJ27255), q25.3
SNP_A-1988346	agactttgcagagata[C/T]gcggatgggtcagata	C	T	NM_152857 // downstream // 11741 // Hs.446091 // WTAP // 9589 // Homo sapiens Wilms tumor 1 associated protein (WTAP), transcript variant 2, mRNA. /// NM_152858 // downstream // 11741 // Hs.446091 // WTAP // 9589 // Homo sapiens Wilms tumor 1 associated p	WTAP	WTAP, Homo sapiens Wilms tumor 1 associated protein (WTAP), transcript variant 2, q25.3
SNP_A-2200035	ccaaagtgtaactagg[C/G]aatcaaatgggaatct	C	G	NM_173516 // downstream // 47563 // Hs.349077 // PNLDC1 // 154197 // Homo sapiens poly(A)-specific ribonuclease (PARN)-like domain containing 1 (PNLDC1), mRNA. /// NM_002377 // upstream // 38675 // Hs.99900 // MAS1 // 4142 // Homo sapiens MAS1 oncogene (M	PNLDC1	PNLDC1, Homo sapiens poly(A)-specific ribonuclease (PARN)-like domain containing 1 (PNLDC1), q25.3
SNP_A-1816194	gttactactttgaagc[A/G]agaggatgtcaagtcc	A	G	NM_000876 // intron // 0 // Hs.487062 // IGF2R // 3482 // Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA. /// ENST00000356956 // intron // 0 // --- // --- // --- // ---	IGF2R	IGF2R, Homo sapiens insulin-like growth factor 2 receptor (IGF2R), q25.3
SNP_A-2121666	agtgaattctaataac[A/T]gtctggtcgcctttgg	A	T	NM_000876 // intron // 0 // Hs.487062 // IGF2R // 3482 // Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA. /// ENST00000356956 // intron // 0 // --- // --- // --- // ---	IGF2R	IGF2R, Homo sapiens insulin-like growth factor 2 receptor (IGF2R), q25.3
SNP_A-2172282	caatgttctgtgctac[A/G]ggttcaaaggaagaaa	A	G	NM_000876 // intron // 0 // Hs.487062 // IGF2R // 3482 // Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA. /// ENST00000356956 // intron // 0 // --- // --- // --- // ---	IGF2R	IGF2R, Homo sapiens insulin-like growth factor 2 receptor (IGF2R), q25.3
SNP_A-2081665	accttattgtaacccc[A/G]ggatgctagtaaccct	A	G	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-2187171	caggtctctcttctat[A/G]aagccaggacaatgat	A	G	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-2212082	ccctgccaagcttcac[A/G]ctgttttgagaaagac	A	G	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-2012229	ctgtcatcacattatc[G/T]ctgcaattttccctgc	G	T	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-2012231	ggataatgttcccctc[C/T]gagagtctccagggtg	C	T	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-1988374	tctgccttccagccga[C/T]gcaggagctgttagtg	C	T	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803733	gtcaacaatcgggtac[A/G]ctgtctaatttaag	A	G	NM_021977 // intron // 0 // Hs.242721 // SLC22A3 // 6581 // Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA. /// ENST00000275300 // intron // 0 // --- // --- // --- // ---	SLC22A3	SLC22A3, Homo sapiens solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), q25.3
SNP_A-1961463	ttttttattgtaag[C/T]agatggacatgagaaa	C	T	NM_024492 // intron // 0 // Hs.439074 // LPAL2 // 80350 // Homo sapiens lipoprotein, Lp(a)-like 2 (LPAL2), transcript variant 1, mRNA. /// NM_145727 // intron // 0 // Hs.439074 // LPAL2 // 80350 // Homo sapiens lipoprotein, Lp(a)-like 2 (LPAL2), transcrip	LPAL2	LPAL2, Homo sapiens lipoprotein, Lp(a)-like 2 (LPAL2), transcript variant 1, q25.3
SNP_A-2272818	gactaacttaagtga[C/T]gtaagcaaaggtatca	C	T	ENST00000308192 // intron // 0 // --- // --- // --- /// ENST00000316325 // intron // 0 // --- // --- // --- /// ENST00000331087 // intron // 0 // --- // --- // --- /// ENS	-	q25.3
SNP_A-1944780	ttgtgcatcactaaaga[C/T]cgttttgacttaaa	C	T	NM_000301 // downstream // 12706 // Hs.143436 // PLG // 5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 225709 // Hs.390428 // MAP3K4 // 4216 // Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-2025992	aaaatgttggaagaac[A/C]gattcgttgcctattt	A	C	NM_000301 // downstream // 14680 // Hs.143436 // PLG // 5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 223735 // Hs.390428 // MAP3K4 // 4216 // Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-2152857	attacaaatctgcaac[A/G]agtgtatgaaaatgtg	A	G	NM_000301 // downstream // 15332 // Hs.143436 // PLG // 5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 223083 // Hs.390428 // MAP3K4 // 4216 // Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-1839788	tagattaaattgcaag[C/T]atctggacattgttta	C	T	NM_000301 // downstream // 22749 // Hs.143436 // PLG // 5340 // Homo sapiens plasminogen (PLG), mRNA. /// NM_006724 // upstream // 215666 // Hs.390428 // MAP3K4 // 4216 // Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript	PLG	PLG, Homo sapiens plasminogen (PLG), q26
SNP_A-1895407	tgccgccttgcagttc[G/T]atcagacttcgtgct	G	T	NM_020133 // intron // 0 // Hs.353175 // AGPAT4 // 56895 // Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) (AGPAT4), mRNA. /// ENST00000320285 // intron // 0 // --- // --- // --- // ---	AGPAT4	AGPAT4, Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) (AGPAT4), q26
SNP_A-2149514	atgtagcaattactga[A/T]gctttgagattttatt	A	T	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2137515	atcatcagtctcccaa[C/T]tcctctactgaatcat	C	T	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1885378	tgacaaaacgttaatg[C/G]aacaggcctgcccatg	C	G	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1708336	ngagagatggagggcagggcagttct[A/G]tagtcttcaccacagtgatctttc	A	G	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Parkinson disease (autosomal recessive, juvenile) 2, parkin /// NM_013987 // intron // 0 // Hs.132954 // PARK2 // 5071 // Parkinson disease (autosomal recessive, juvenile) 2, parkin /// NM_013988	PARK2	PARK2 , rs951196, Parkinson disease (autosomal recessive, juvenile) 2, parkin, q26
SNP_A-2127870	ataagaagccatcaaa[G/T]tacattcaaggactta	G	T	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-1920996	ttacagatgcaacata[A/T]cttacaggaggcttt	A	T	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2274121	gacttcacaatggtac[C/T]gctgacctaagcttca	C	T	NM_004562 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA. /// NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, q26
SNP_A-2131780	atagctcctacacaga[A/G]aatcaaatttaggac	A	G	NM_013988 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA. /// NM_013987 // intron // 0 // Hs.132954 // PARK2 // 5071 // Homo sapiens Parkinson di	PARK2	PARK2, Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, q26
SNP_A-2023264	aaaaccaaaggcaaag[A/T]acggcctcctgagacc	A	T	NM_206854 // downstream // 178861 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 178861 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-2247924	ctgtgcatggtgaacat[A/T]tcattgcggaaaccca	A	T	NM_206854 // downstream // 307810 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 307810 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-2160567	atttcccctacggtaa[C/T]ggttggcttattgtgg	C	T	NM_206854 // downstream // 472189 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 472189 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-1892152	tgcaaagtgctatcaa[C/T]gtattatggttaacat	C	T	NM_206854 // downstream // 472406 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 472406 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q26
SNP_A-2294066	gcaggatctctaccac[A/G]ccagctgaggaggggt	A	G	NM_206854 // downstream // 572791 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 572791 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-2157571	attgattgcctgtaat[A/G]aggcttctgaaatat	A	G	NM_206854 // downstream // 651364 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 651364 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2038385	aacactcaggttctaa[C/T]tcaggatctgtatcct	C	T	NM_206854 // downstream // 728286 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 728286 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homol	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1746144	tggctaactggaggtgagcatcta[C/T]ggcctctcattagacca ggaaaaga	C	T	NM_144980 // downstream // 804799 // Hs.144734 // C6orf118 // 168090 // chromosome 6 open reading frame 118	C6orf118	C6orf118 , rs2029870, chromosome 6 open reading frame 118.q27
SNP_A-1949406	ttattcatttataaa[C/G]acttgtagctttcac	C	G	NM_206854 // downstream // 1126128 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1126128 // Hs.510324 // QKI // 9444 // Homo sapiens quaking hom	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1939940	ttgcactgactcagac[G/T]gatttacttccagatg	G	T	NM_206854 // downstream // 1174823 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1174823 // Hs.510324 // QKI // 9444 // Homo sapiens quaking hom	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-2217982	cctgcatgttcaaaaa[C/T]gaggaatagtgccag	C	T	NM_206854 // downstream // 1217650 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1217650 // Hs.510324 // QKI // 9444 // Homo sapiens quaking hom	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1853427	tattttctgagcacta[C/T]catgaggatcagaag	C	T	NM_206854 // downstream // 1500665 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1500665 // Hs.510324 // QKI // 9444 // Homo sapiens quaking hom	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1988472	acaagccaggccagct[A/G]actatagcacagaatg	A	G	NM_206854 // downstream // 1620690 // Hs.510324 // QKI // 9444 // Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, mRNA. /// NM_206855 // downstream // 1620690 // Hs.510324 // QKI // 9444 // Homo sapiens quaking hom	QKI	QKI, Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 3, q27
SNP_A-1651116	agaatcactctttcctaaaatac[G/T]gcacaaaattctagtctt attatc	G	T	NM_006661 // upstream // 93423 // Hs.416467 // PDE10A // 10846 // phosphodiesterase 10A	PDE10A	PDE10A , rs1546141, phosphodiesterase 10A.q27
SNP_A-2173622	cacacaaaagcataad[A/G]ataacaacaacaataa	A	G	NM_006661 // upstream // 209080 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 209080 // — // — // — // — /// ENST00000343842 // upstream // 123459 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-2202884	ccactatttgaaatgat[C/T]gattatttcaagtcct	C	T	NM_006661 // upstream // 221083 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 221083 // — // — // — // — /// ENST00000343842 // upstream // 135462 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-2304458	gctctagcggcaccaa[A/G]tgggctctgcgttgta	A	G	NM_006661 // upstream // 224301 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 224301 // — // — // — // — /// ENST00000343842 // upstream // 138680 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-1783033	ggcagcctcatcacaa[C/T]gagcgttctgctctac	C	T	NM_006661 // upstream // 241637 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 241637 // — // — // — // — /// ENST00000343842 // upstream // 156016 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1788849	gggatttgctggctca[C/T]gtaatggttaagttca	C	T	NM_006661 // upstream // 314821 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 314821 // — // — // — // — /// ENST00000343842 // upstream // 229200 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-1854829	tcaaccatccttccta[A/C]ctaatatccactgtcc	A	C	NM_006661 // upstream // 318648 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 318648 // — // — // — // — /// ENST00000343842 // upstream // 233027 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-2114334	agggacaaaattcaac[C/G]ctcaacaagaggacag	C	G	NM_006661 // upstream // 318675 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 318675 // — // — // — // — /// ENST00000343842 // upstream // 233054 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-1873077	tctatgtatgtatgaa[C/T]gtggaaacacacatgg	C	T	NM_006661 // upstream // 337206 // Hs.487129 // PDE10A // 10846 // Homo sapiens phosphodiesterase 10A (PDE10A), mRNA. /// ENST00000354448 // upstream // 337206 // — // — // — // — /// ENST00000343842 // upstream // 251585 // — // — // — // -	PDE10A	PDE10A, Homo sapiens phosphodiesterase 10A (PDE10A), q27
SNP_A-2266811	gaagtgtttggtggca[A/G]cagatgctcaagacag	A	G	NM_021135 // intron // 0 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 // intron // 0 // — // — // — // —	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1867422	tccctttccataaacc[A/G]ggagatttcaccacaa	A	G	NM_021135 // intron // 0 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 // intron // 0 // — // — // — // —	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1652330	aaggaattaagcttaatgtctttaa[A/G]atgagtatataaaggag caaaaaga	A	G	NM_021135 // intron // 0 // Hs.301664 // RPS6KA2 // 6196 // ribosomal protein S6 kinase, 90kDa, polypeptide 2	RPS6KA2	RPS6KA2 , rs3799568, ribosomal protein S6 kinase, 90kDa, polypeptide 2,q27
SNP_A-1861879	tcatgaaattcttaaa[C/G]attcctgtcaccccaa	C	G	NM_021135 // intron // 0 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// ENST00000265678 // intron // 0 // — // — // — // —	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1657496	ggtggcactgcggatatttttacac[A/G]ggataatgtgacctgcc cagcctgc	A	G	NM_003730 // downstream // 154527 // Hs.388130 // RNASET2 // 8635 // ribonuclease T2 /// NM_007045 // upstream // 224324 // Hs.180296 // FGFR1OP // 11116 // FGFR1 oncogene partner /// NM_021135 // upstream // 147763 // Hs.301664 // RPS6KA2 // 6196 // rib	RNASET2	RNASET2 , rs2072641, ribonuclease T2 ,q27
SNP_A-1782689	ggcactggcttccata[A/C]atacatgctacaagat	A	C	NM_021135 // upstream // 106358 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 // downstream // 195930 // Hs.529989 // RNASET2 // 8635 // Homo sapiens ribonuclease T2 (RNASE	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2193581	catcttacaccttcta[C/T]accactttaagccagc	C	T	NM_021135 // upstream // 138404 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 // downstream // 163884 // Hs.529989 // RNASET2 // 8635 // Homo sapiens ribonuclease T2 (RNASE	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2180342	cagaaatgacagagaa[C/T]gatctcgctacaccca	C	T	NM_021135 // upstream // 148964 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 // downstream // 153324 // Hs.529989 // RNASET2 // 8635 // Homo sapiens ribonuclease T2 (RNASE	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2157503	attgatcgtttaaca[C/T]gaatgatgaggtggcg	C	T	NM_021135 // upstream // 149236 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 // downstream // 153052 // Hs.529989 // RNASET2 // 8635 // Homo sapiens ribonuclease T2 (RNASE	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-1988510	gcctatctgggtccc[A/G]gcaggtttgaagatg	A	G	NM_021135 // upstream // 155186 // Hs.147119 // RPS6KA2 // 6196 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), mRNA. /// NM_003730 // downstream // 147102 // Hs.529989 // RNASET2 // 8635 // Homo sapiens ribonuclease T2 (RNASE	RPS6KA2	RPS6KA2, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), q27
SNP_A-2138029	atccaaagataaagac[C/T]gatgtatgtggatgtt	C	T	ENST00000338250 // intron // 0 // — // — // — // — /// ENST00000341806 // intron // 0 // — // — // —	-	q27
SNP_A-1792983	ggtacattcaggctaa[C/T]ggaaaaatcctacata	C	T	ENST00000338250 // intron // 0 // — // — // — // — /// ENST00000341806 // intron // 0 // — // — // —	-	q27
SNP_A-1848464	tatgaagtgagcacaa[A/G]ctgtttgaaaacggga	A	G	ENST00000338250 // intron // 0 // — // — // — // — /// ENST00000341806 // intron // 0 // — // — // —	-	q27
SNP_A-2112277	aggatttagtcatgaa[C/T]acggtaaacatacaa	C	T	NM_024919 // upstream // 93320 // Hs.266746 // FRMD1 // 79981 // Homo sapiens FERM domain containing 1 (FRMD1), mRNA. /// NM_214462 // downstream // 134427 // Hs.248294 // DACT2 // 168002 // Homo sapiens dapper homolog 2, antagonist of beta-catenin (xenop	FRMD1	FRMD1, Homo sapiens FERM domain containing 1 (FRMD1), q27
SNP_A-2104987	agcatccaggcactga[A/C]aggatgactaagttc	A	C	NM_024919 // upstream // 127369 // Hs.266746 // FRMD1 // 79981 // Homo sapiens FERM domain containing 1 (FRMD1), mRNA. /// NM_214462 // downstream // 100378 // Hs.248294 // DACT2 // 168002 // Homo sapiens dapper homolog 2, antagonist of beta-catenin (xeno	FRMD1	FRMD1, Homo sapiens FERM domain containing 1 (FRMD1), q27
SNP_A-1988529	ctagatactatgacaa[A/G]caaggtaaatctctt	A	G	BC047583 // intron // 0 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // intron // 0 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC rela	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. q27
SNP_A-2179390	cactgtgtgtagacat[A/C]aacttgcacagtctt	A	C	BC047583 // downstream // 130408 // Hs.487200 // SMOC2 // 64094 // Homo sapiens SPARC related modular calcium binding 2, mRNA (cDNA clone MGC:48409 IMAGE:4826950), complete cds. /// NM_022138 // downstream // 130413 // Hs.487200 // SMOC2 // 64094 // Homo	SMOC2	SMOC2, Homo sapiens SPARC related modular calcium binding 2, (cDNA clone MGC:48409 IMAGE:4826950), complete cds. q27
SNP_A-1864019	tccacacatttttcat[A/G]agaaaccaagactaag	A	G	NM_003247 // downstream // 275728 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// ENST00000355855 // upstream // 89454 // — // — // — // — /// ENST00000335061 // downstream // 275728 // — // — // — // —	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-2117974	aggttttattggtaac[A/G]gccaacagctggaaat	A	G	NM_003247 // downstream // 206273 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// ENST00000355855 // upstream // 158909 // — // — // — // — /// ENST00000335061 // downstream // 206273 // — // — // — // —	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-2087937	actggcaaacctggaa[C/T]gtcaggagacaacata	C	T	NM_003247 // downstream // 156746 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// ENST00000355855 // upstream // 208436 // — // — // — // — /// ENST00000335061 // downstream // 156746 // — // — // — // —	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-1933994	ttctcaggagctca[A/C]atccctgtgaactg	A	C	NM_003247 // downstream // 51160 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// ENST00000355855 // upstream // 314022 // — // — // — // — /// ENST00000335061 // downstream // 51160 // — // — // — // —	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2210289	cccaattcacgggcca[C/T]gttccaatcggcttac	C	T	NM_003247 // upstream // 1978 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// THBS2 // downstream // 316388 // Hs.131903 // MGC43690 // 253769 // Homo sapiens hypothetical protein MGC43690 (MGC43690), mRNA. /// ENST00	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-1886953	tgacttccatcgtctal[C/T]gaagcccattccatgc	C	T	NM_003247 // upstream // 2106 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// NM_182552 // downstream // 316260 // Hs.131903 // MGC43690 // 253769 // Homo sapiens hypothetical protein MGC43690 (MGC43690), mRNA. /// ENST00	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-2248629	ctgttattcagcctac[C/T]aagtccactagaatta	C	T	NM_003247 // upstream // 34439 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// NM_182552 // downstream // 283927 // Hs.131903 // MGC43690 // 253769 // Homo sapiens hypothetical protein MGC43690 (MGC43690), mRNA. /// ENST0	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-2056505	aatcagaatgggttta[C/T]gtaagtgattttctag	C	T	NM_003247 // upstream // 64490 // Hs.371147 // THBS2 // 7058 // Homo sapiens thrombospondin 2 (THBS2), mRNA. /// NM_182552 // downstream // 253876 // Hs.131903 // MGC43690 // 253769 // Homo sapiens hypothetical protein MGC43690 (MGC43690), mRNA. /// ENST0	THBS2	THBS2, Homo sapiens thrombospondin 2 (THBS2), q27
SNP_A-2222460	cgagctctgtctaaaa[C/T]ctttgctcagctttac	C	T	NM_207502 // upstream // 264659 // Hs.287553 // C6orf122 // 401288 // Homo sapiens chromosome 6 open reading frame 122 (C6orf122), mRNA. /// NM_025002 // downstream // 260617 // Hs.546442 // C6orf208 // 80069 // Homo sapiens chromosome 6 open reading fram	C6orf122	C6orf122, Homo sapiens chromosome 6 open reading frame 122 (C6orf122), q27
SNP_A-1812767	gtgggagcaaagagaa[C/T]ggaaacatggacctgg	C	T	NM_207502 // upstream // 302367 // Hs.287553 // C6orf122 // 401288 // Homo sapiens chromosome 6 open reading frame 122 (C6orf122), mRNA. /// NM_025002 // downstream // 298325 // Hs.546442 // C6orf208 // 80069 // Homo sapiens chromosome 6 open reading fram	C6orf122	C6orf122, Homo sapiens chromosome 6 open reading frame 122 (C6orf122), q27
SNP_A-2169775	caaggagcacctgcca[A/C]agaacgagccactgag	A	C	NM_207502 // upstream // 345597 // Hs.287553 // C6orf122 // 401288 // Homo sapiens chromosome 6 open reading frame 122 (C6orf122), mRNA. /// NM_025002 // downstream // 341555 // Hs.546442 // C6orf208 // 80069 // Homo sapiens chromosome 6 open reading fram	C6orf122	C6orf122, Homo sapiens chromosome 6 open reading frame 122 (C6orf122), q27
SNP_A-2012314	tgacacctgaaatcgc[C/T]ccaacagccctaggag	C	T	NM_032448 // intron // 0 // Hs.369522 // KIAA1838 // 84498 // Homo sapiens KIAA1838 (KIAA1838), mRNA. /// ENST00000262196 // intron // 0 // — // — /// ENST00000358331 // intron // 0 // — // — // — // —	KIAA1838	KIAA1838, Homo sapiens KIAA1838 (KIAA1838), q27
SNP_A-2059621	aatctctcctcactaa[A/G]tcacaacttgataaa	A	G	NM_020223 // upstream // 139059 // Hs.134742 // FAM20C // 56975 // Homo sapiens family with sequence similarity 20, member C (FAM20C), mRNA. /// ENST00000313766 // upstream // 139059 // — // — // —	FAM20C	FAM20C, Homo sapiens family with sequence similarity 20, member C (FAM20C), p22.3
SNP_A-2027752	aaacccattcactagc[A/G]aaaactgactcaggct	A	G	NM_020223 // intron // 0 // Hs.134742 // FAM20C // 56975 // Homo sapiens family with sequence similarity 20, member C (FAM20C), mRNA. /// ENST00000313766 // intron // 0 // — // — // —	FAM20C	FAM20C, Homo sapiens family with sequence similarity 20, member C (FAM20C), p22.3
SNP_A-2082482	acgcgtaagaaccacа[C/T]aggccgggcctgccag	C	T	NM_017802 // intron // 0 // Hs.521328 // FLJ20397 // 54919 // Homo sapiens hypothetical protein FLJ20397 (FLJ20397), mRNA. /// ENST00000297440 // intron // 0 // — // — // — /// ENST00000360766 // intron // 0 // — // — // —	FLJ20397	FLJ20397, Homo sapiens hypothetical protein FLJ20397 (FLJ20397), p22.3
SNP_A-2067331	acaaagtgtcaatcaa[C/T]gttttttcaataatg	C	T	NM_025154 // intron // 0 // Hs.438072 // UNC84A // 23353 // Homo sapiens unc-84 homolog A (C. elegans) (UNC84A), mRNA. /// ENST00000359946 // intron // 0 // — // — // — /// ENST00000297445 // intron // 0 // — // — // —	UNC84A	UNC84A, Homo sapiens unc-84 homolog A (C. elegans) (UNC84A), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2260671	gaaaccctttgtaaca[G/T]cagtctcaggtccgca	G	T	NM_003550 // intron // 0 // Hs.209128 // MAD1L1 // 8379 // Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA. /// ENST00000265854 // intron // 0 // — // — // —	MAD1L1	MAD1L1, Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), p22.3
SNP_A-1854959	tcaactgctgcaggga[A/C]atgagttacaaggctc	A	C	NM_003550 // intron // 0 // Hs.209128 // MAD1L1 // 8379 // Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA. /// ENST00000265854 // intron // 0 // — // — // —	MAD1L1	MAD1L1, Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), p22.3
SNP_A-1790878	ggggggtatctcagtc[A/G]aagattatggctgga	A	G	NM_025250 // intron // 0 // Hs.440899 // TTYH3 // 80727 // Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), mRNA. /// ENST00000258796 // intron // 0 // — // — // —	TTYH3	TTYH3, Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), p22.3
SNP_A-1909312	tgtatgtgaggttta[A/T]gtctgtactctctct	A	T	NM_025250 // downstream // 9249 // Hs.440899 // TTYH3 // 80727 // Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), mRNA. /// ENST00000258796 // downstream // 9249 // — // — // — // — /// ENST00000312371 // upstream // 5480 // — // — // —	TTYH3	TTYH3, Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), p22.3
SNP_A-1935839	ttctgttgccgtgttc[A/G]agagtttggctgtcag	A	G	NM_025250 // downstream // 9901 // Hs.440899 // TTYH3 // 80727 // Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), mRNA. /// ENST00000258796 // downstream // 9901 // — // — // — // — /// ENST00000312371 // upstream // 4828 // — // — // —	TTYH3	TTYH3, Homo sapiens tweety homolog 3 (Drosophila) (TTYH3), p22.3
SNP_A-2150683	atgtgcagggacgtaa[A/C]ggagcttcaaagtgca	A	C	ENST00000312371 // 3UTR // 0 // — // — // —	-	p22.3
SNP_A-2099415	agaggcttaacaaga[C/T]aggctgaaggccgctt	C	T	NM_007353 // intron // 0 // Hs.487341 // GNA12 // 2768 // Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12), mRNA. /// ENST00000275364 // intron // 0 // — // — // — // — /// ENST00000354816 // intron // 0 // — // —	GNA12	GNA12, Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12), p22.3
SNP_A-2214798	cctagttagatgtgcat[C/T]gggcaaacgctaccat	C	T	NM_007353 // upstream // 34819 // Hs.487341 // GNA12 // 2768 // Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12), mRNA. /// NM_032415 // downstream // 27005 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment do	GNA12	GNA12, Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12), p22.3
SNP_A-1788851	gggatttggcaaatat[A/G]agcaaatgttttga	A	G	NM_007353 // upstream // 59175 // Hs.487341 // GNA12 // 2768 // Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12), mRNA. /// NM_032415 // downstream // 2649 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment dom	GNA12	GNA12, Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12), p22.2
SNP_A-2257734	ctttggaggccagacaa[C/T]gtgacctaagcgttga	C	T	NM_032415 // intron // 0 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// ENST00000356408 // intron // 0 // — // — // — // — /// ENST00000355508 // intron // 0 // — // — // —	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-1784957	ggcgagaagactgatt[C/G]aagaatgttagaaag	C	G	NM_032415 // intron // 0 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// ENST00000356408 // intron // 0 // — // — // — // — /// ENST00000355508 // intron // 0 // — // — // —	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-1908712	tgtagggataaggccg[A/G]actgacaataacagag	A	G	NM_032415 // upstream // 34375 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// NM_152744 // upstream // 223345 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SD	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-2070596	acaccgttcaaactat[C/T]cggcaagacactaatc	C	T	NM_032415 // upstream // 96492 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// NM_152744 // upstream // 161228 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SD	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2274830	gagaaatctgaaactg[A/G]agcatctatgttgttc	A	G	NM_032415 // upstream // 98498 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// NM_152744 // upstream // 159222 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SD	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-2245904	ctgggtgctgaactac[A/G]gggcacaagaatagga	A	G	NM_032415 // upstream // 224423 // Hs.300355 // CARD11 // 84433 // Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA. /// NM_152744 // upstream // 33297 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SD	CARD11	CARD11, Homo sapiens caspase recruitment domain family, member 11 (CARD11), p22.2
SNP_A-2274205	gacttctgaggctaaa[G/T]atgtataagcagtctt	G	T	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-1925837	ttatggagctctacaa[A/G]tcactgcagcgtggaa	A	G	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2214488	cctactttattctgac[A/G]aagtatgtacaagcta	A	G	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2096328	agaccagttgtttggc[A/G]gaatgtccttcagtct	A	G	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-1786631	ggcttgaagcaccaga[A/C]aagtgagtcgtccacc	A	C	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2198093	cattgggaactctaag[A/G]agactgaacaggaaga	A	G	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-1988602	aactgcaggctcagaa[A/C]gggcacaggtgcttct	A	C	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // — /// ENST00000275387 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2022832	aaaacaaaactatgca[C/T]gtggttcctgtaaact	C	T	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // — /// ENST00000275387 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2178449	cactccccaaagtgga[C/T]gcacaaactcccgctc	C	T	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // — /// ENST00000275387 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2076063	acattcaaaatggaaa[C/T]gcaaagtcccaagtgc	C	T	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // — /// ENST00000275387 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-1896617	tgctaggagtgggcac[C/T]ggtcagtattatatgc	C	T	NM_152744 // intron // 0 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // intron // 0 // — // — // — // — /// ENST00000275387 // intron // 0 // — // — // — // —	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2198637	catttcatactctgac[A/G]gctttgaaaatttggt	A	G	NM_152744 // downstream // 31243 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // downstream // 31243 // — // — // — // — /// ENST00000275387 // downstream // 30437 // — // — // -	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2282120	gagtgtattaccctga[C/T]ggcaatgctgtgcaag	C	T	NM_152744 // downstream // 76509 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // downstream // 76509 // — // — // — // — /// ENST00000275387 // downstream // 75703 // — // — // -	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2184233	cagcctgatgggctta[C/T]gcgtgcagggggacac	C	T	NM_152744 // downstream // 212918 // Hs.155959 // SDK1 // 221935 // Homo sapiens sidekick homolog 1 (chicken) (SDK1), mRNA. /// ENST00000320140 // downstream // 212918 // — // — // — // — /// ENST00000275387 // downstream // 212112 // — // — /	SDK1	SDK1, Homo sapiens sidekick homolog 1 (chicken) (SDK1), p22.2
SNP_A-2031519	aaaggtgctgatgaac[C/G]caggtaaacgcactga	C	G	ENST00000297561 // intron // 0 // — // — // — // — /// ENST00000328914 // intron // 0 // — // — // — // —	-	p22.1
SNP_A-2245724	ctggggactcgaggga[C/T]gatctggctgtcacca	C	T	BC037881 // 3UTR // 0 // Hs.379190 // MMD2 // 221938 // Homo sapiens monocyte to macrophage differentiation-associated 2, mRNA (cDNA clone IMAGE:5274201), partial cds. /// ENST00000258798 // 3UTR // 0 // - // — // — // —	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2, (cDNA clone IMAGE:5274201), partial cds. ,p22.1
SNP_A-1867562	tccggcagctaaccaa[A/G]gcaatgctgttttgtt	A	G	BC037881 // intron // 0 // Hs.379190 // MMD2 // 221938 // Homo sapiens monocyte to macrophage differentiation-associated 2, mRNA (cDNA clone IMAGE:5274201), partial cds. /// ENST00000258798 // intron // 0 // - // — // — // —	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2, (cDNA clone IMAGE:5274201), partial cds. p22.1
SNP_A-1914035	tgtgtgctggctccat[C/G]aaaagtgcagctcatg	C	G	BC037881 // intron // 0 // Hs.379190 // MMD2 // 221938 // Homo sapiens monocyte to macrophage differentiation-associated 2, mRNA (cDNA clone IMAGE:5274201), partial cds. /// ENST00000258798 // intron // 0 // - // — // — // —	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2, (cDNA clone IMAGE:5274201), partial cds. ,p22.1
SNP_A-1936575	ttcttgctgtatgcac[C/T]acctgggccgactcct	C	T	ENST00000327499 // upstream // 4332 // — // — // — // — /// ENST00000288841 // upstream // 4332 // — // — // — // — /// ENST00000328270 // upstream // 54467 // — // — // — // — /// ENST00000338845 // downstream // 52024 // — // -	-	p22.1
SNP_A-1929217	ttcaggtatgtatgat[C/G]aaggctccagctgcat	C	G	NM_003088 // upstream // 23636 // Hs.118400 // FSCN1 // 6624 // Homo sapiens fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) (FSCN1), mRNA. /// ENST00000306804 // downstream // 8244 // — // — // — // — /// ENST00000340250	FSCN1	FSCN1, Homo sapiens fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) (FSCN1), p22.1
SNP_A-2215767	cctcatctgcagcgtg[C/G]caatcagttcatagtg	C	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-1940105	ttgcagtgagctgata[C/T]tacactactgcactcc	C	T	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2269704	gacaactagaagacac[A/G]gatggcctggaagccc	A	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2231103	ctatgtttcattgttg[A/G]aatgtttggtttgagc	A	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2225597	ctaaaattaacacctg[A/G]acaaattagaattaat	A	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2105931	agccatcttcttcca[C/T]accatatttacgaaca	C	T	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2109538	aggaaaataaccaaga[C/G]aattaaaagctaaaat	C	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-1898831	tgctttggccccatca[A/C]aacttctgtgtttct	A	C	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-1913461	tgtggtgaaactatad[A/G]ggctattggacagtag	A	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-2157242	attgacagacctaag[A/G]aagcaagatgaaccca	A	G	NM_019011 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // intron // 0 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 2, mRNA.	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-1889072	tgagtagtattcgaccd[A/G]caaagatatgacacaa	A	G	NM_019011 // upstream // 6744 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, mRNA. /// NM_207116 // upstream // 6744 // Hs.487458 // TRIAD3 // 54476 // Homo sapiens TRIAD3 protein (TRIAD3), transcript varian	TRIAD3	TRIAD3, Homo sapiens TRIAD3 protein (TRIAD3), transcript variant 3, p22.1
SNP_A-1858076	tcacttttataaaca[G/T]ctactgaccaggtgcg	G	T	ENST00000326459 // intron // 0 // — // — // —	-	p22.1
SNP_A-1815061	gtgttcagccctcgac[C/T]ccaagcgcctggtaga	C	T	ENST00000326459 // intron // 0 // — // — // —	-	p22.1
SNP_A-2212493	ccctaaactacgtca[C/T]ggatgttaaggagaaa	C	T	ENST00000332446 // intron // 0 // — // — // —	-	p22.1
SNP_A-1920728	ttacaacagttcttaa[C/G]ctatggagagatatt	C	G	AB021643 // downstream // 13063 // Hs.431471 // ZNF325 // 51711 // Homo sapiens GIOT-3 mRNA for gonadotropin inducible transcription repressor-3, complete cds. /// ENST00000332446 // downstream // 873 // – // — // — /// ENST00000328239 // dow	ZNF325	ZNF325, Homo sapiens GIOT-3 for gonadotropin inducible transcription repressor-3, complete cds. ,p22.1
SNP_A-2090060	actctttttaaaaaaa[C/T]gtatcctgtcatcaca	C	T	AB021643 // downstream // 10138 // Hs.431471 // ZNF325 // 51711 // Homo sapiens GIOT-3 mRNA for gonadotropin inducible transcription repressor-3, complete cds. /// ENST00000332446 // downstream // 3798 // — // — // — /// ENST00000328239 // do	ZNF325	ZNF325, Homo sapiens GIOT-3 for gonadotropin inducible transcription repressor-3, complete cds. ,p22.1
SNP_A-1949964	tttcaatcacccaag[A/T]ccaaaatcagcactct	A	T	AB021643 // downstream // 7868 // Hs.431471 // ZNF325 // 51711 // Homo sapiens GIOT-3 mRNA for gonadotropin inducible transcription repressor-3, complete cds. /// ENST00000332446 // downstream // 6068 // — // — // — /// ENST00000328239 // dow	ZNF325	ZNF325, Homo sapiens GIOT-3 for gonadotropin inducible transcription repressor-3, complete cds. ,p22.1
SNP_A-1819735	gttgtccatttctga[A/C]ctcgcgattgttttga	A	C	AB021643 // intron // 0 // Hs.431471 // ZNF325 // 51711 // Homo sapiens GIOT-3 mRNA for gonadotropin inducible transcription repressor-3, complete cds. /// ENST00000342651 // intron // 0 // — // — // —	ZNF325	ZNF325, Homo sapiens GIOT-3 for gonadotropin inducible transcription repressor-3, complete cds. ,p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1988644	aagtgtactcgcttca[C/G]aggcacatataataat	C	G	AB021643 // upstream // 13149 // Hs.431471 // ZNF325 // 51711 // Homo sapiens GIOT-3 mRNA for gonadotropin inducible transcription repressor-3, complete cds. /// AB021643 // upstream // 7140 // Hs.431471 // ZNF325 // 51711 // Homo sapiens GIOT-3 mRNA for	ZNF325	ZNF325, Homo sapiens GIOT-3 for gonadotropin inducible transcription repressor-3, complete cds. p22.1
SNP_A-2229781	ctagtgcatcattgaa[C/G]gaaaggaatttcacac	C	G	NM_020156 // downstream // 18507 // Hs.239666 // C1GALT1 // 56913 // Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), mRNA. /// NM_019005 // upstream // 309620 // Hs.520215 // FLJ20323 // 54468 // H	C1GALT1	C1GALT1, Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), p21.3
SNP_A-1988652	ttattatttctgcta[C/T]gtctaatacaaatat	C	T	NM_020156 // downstream // 23485 // Hs.239666 // C1GALT1 // 56913 // Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), mRNA. /// NM_019005 // upstream // 304642 // Hs.520215 // FLJ20323 // 54468 // H	C1GALT1	C1GALT1, Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), p21.3
SNP_A-2118078	agtaaaaggcattagg[C/T]acctggagagcactgc	C	T	NM_020156 // downstream // 108734 // Hs.239666 // C1GALT1 // 56913 // Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), mRNA. /// NM_019005 // upstream // 219393 // Hs.520215 // FLJ20323 // 54468 //	C1GALT1	C1GALT1, Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), p21.3
SNP_A-2177762	cacgtctgagtaaact[A/G]agaaatctgaaggtag	A	G	NM_002947 // intron // 0 // Hs.487540 // RPA3 // 6119 // Homo sapiens replication protein A3, 14kDa (RPA3), mRNA. /// ENST00000223129 // intron // 0 // — // — // —	RPA3	RPA3, Homo sapiens replication protein A3, 14kDa (RPA3), p21.3
SNP_A-1988680	tactgaatgtaattta[A/G]cacttatggcaggaag	A	G	ENST00000297227 // intron // 0 // — // — // —	-	p21.3
SNP_A-2196358	catgttcaacattac[C/T]ggaaaaatcaataat	C	T	NM_002947 // upstream // 243334 // Hs.487540 // RPA3 // 6119 // Homo sapiens replication protein A3, 14kDa (RPA3), mRNA. /// ENST00000223129 // upstream // 243334 // — // — // — // — /// ENST00000297227 // downstream // 82724 // — // — // —	RPA3	RPA3, Homo sapiens replication protein A3, 14kDa (RPA3), p21.3
SNP_A-2207525	ccatttatagttaa[C/T]tgaagatacaagagat	C	T	ENST00000223145 // intron // 0 // — // — // —	-	p21.3
SNP_A-2273069	gactatgaaaaataaa[A/G]atagctatcgtccatg	A	G	NM_022307 // downstream // 10012 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // downstream // 10012 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 6	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-2082898	acgtctactagtcccaj[C/T]agaaattaaaagttaa	C	T	NM_022307 // intron // 0 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // intron // 0 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), tra	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-1819957	gttgtctatttttca[C/T]gtgagaggatggactc	C	T	NM_022307 // upstream // 62534 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream // 62534 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-1901332	tggatgtccagaaga[A/G]cacagaaaaatgtggg	A	G	NM_022307 // upstream // 111500 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream // 111500 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69k	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-1888705	aatttaccctgcctca[A/C]aaagatagtcgagagg	A	C	NM_022307 // upstream // 231051 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream // 231051 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69k	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1988719	ttgttcttaagcatca[G/T]aattggttttaagaac	G	T	NM_022307 // upstream // 448080 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream // 448080 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69k	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-1988720	cctgacctctgaggaa[C/T]tgaatgccagggtaag	C	T	NM_022307 // upstream // 449750 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, mRNA. /// NM_022308 // upstream // 449750 // Hs.487561 // ICA1 // 3382 // Homo sapiens islet cell autoantigen 1, 69k	ICA1	ICA1, Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 1, p21.3
SNP_A-2257670	ctttgctgcttcttga[A/C]cgtttttggatcttca	A	C	NM_152745 // downstream // 30435 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 30435 // — // — // — // — /// ENST00000361014 // upstream // 944036 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2129935	atacattatttcccta[C/T]accaatgaccagaaga	C	T	NM_152745 // downstream // 37428 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 37428 // — // — // — // — /// ENST00000361014 // upstream // 937043 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2305563	gctgcacctatacaaa[A/C]cctatgactcaatatt	A	C	NM_152745 // downstream // 42164 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 42164 // — // — // — // — /// ENST00000361014 // upstream // 932307 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2146105	atgccttcatatgaca[A/G]tagttcaattccccac	A	G	NM_152745 // downstream // 207788 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 207788 // — // — // — // — /// ENST00000361014 // upstream // 766683 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1885144	tgaattagccaaagag[C/G]aagatatttttcttta	C	G	NM_152745 // downstream // 222374 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 222374 // — // — // — // — /// ENST00000361014 // upstream // 752097 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1782115	ggcaacgtaattgcaa[C/G]atgacagcaggcaaaa	C	G	NM_152745 // downstream // 396449 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 396449 // — // — // — // — /// ENST00000361014 // upstream // 578022 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1988736	tctggctaaacgtaca[A/G]cactgaatcatctaat	A	G	NM_152745 // downstream // 441529 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 441529 // — // — // — // — /// ENST00000361014 // upstream // 532942 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1883798	tgaagaaattgcctta[C/G]atgatagtacatgaac	C	G	NM_152745 // downstream // 583762 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 583762 // — // — // — // — /// ENST00000361014 // upstream // 390709 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-2295875	gcatggggtagctaag[C/G]ataaaagatatagcca	C	G	NM_152745 // downstream // 584559 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 584559 // — // — // — // — /// ENST00000361014 // upstream // 389912 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1832140	taatttcagtggtttc[A/G]aaattgttgagacttt	A	G	NM_152745 // downstream // 739680 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 739680 // — // — // — // — /// ENST00000361014 // upstream // 234791 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1836515	tactccttggttgaaa[C/T]agttacctcaattctg	C	T	NM_152745 // downstream // 750600 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 750600 // — // — // — // — /// ENST00000361014 // upstream // 223871 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2159848	atttatacatgaagga[C/G]aatcagtctaccataa	C	G	NM_152745 // downstream // 768195 // Hs.487564 // NXPH1 // 30010 // Homo sapiens neurexophilin 1 (NXPH1), mRNA. /// ENST00000265579 // downstream // 768195 // — // — // — // — /// ENST00000361014 // upstream // 206276 // — // — // — // —	NXPH1	NXPH1, Homo sapiens neurexophilin 1 (NXPH1), p21.3
SNP_A-1742827	taggaggagagaaaataaaagacaa[A/G]tagcgtaagagaa acagctttgttg	A	G	NM_002489 // downstream // 1349798 // Hs.50098 // NDUFA4 // 4697 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa /// NM_152745 // downstream // 830703 // Hs.343660 // NXPH1 // 30010 // neurexophilin 1	NDUFA4	NDUFA4 , rs2708997, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa ,p21.3
SNP_A-2169209	caagattgatgtggaa[A/G]aactcagcatggtttt	A	G	NM_002489 // downstream // 1046785 // Hs.50098 // NDUFA4 // 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 158115 // — // — //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1750983	ctagtcagacgttaatttgaaccac[A/G]cacagtctaagtctaga acttgtgt	A	G	NM_002489 // downstream // 947775 // Hs.50098 // NDUFA4 // 4697 // NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa /// NM_152745 // downstream // 1232726 // Hs.343660 // NXPH1 // 30010 // neurexophilin 1	NDUFA4	NDUFA4 , rs1024538, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa ,p21.3
SNP_A-1915917	tgttgagttgggtcga[G/T]agattacattagtgtc	G	T	NM_002489 // downstream // 855810 // Hs.50098 // NDUFA4 // 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 349090 // — // — //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomptex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1889882	tgatagacaagcctca[A/G]gtgctacacattcatt	A	G	NM_002489 // downstream // 851749 // Hs.50098 // NDUFA4 // 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 353151 // — // — //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1810463	gtgattgatggtagaa[C/T]tgttgctgtagggcat	C	T	NM_002489 // downstream // 729121 // Hs.50098 // NDUFA4 // 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 475779 // — // — //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1955642	tttgtaaatgcaagga[C/T]gtttataagtcaggca	C	T	NM_002489 // downstream // 131795 // Hs.50098 // NDUFA4 // 4697 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, /// ENST00000361014 // downstream // 1073105 // — // — //	NDUFA4	NDUFA4, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), nuclear gene encoding mitochondrial protein, p21.3
SNP_A-1917136	tgtttgtggttgagga[A/T]aatccaaatgtataat	A	T	AB018326 // downstream // 30087 // Hs.159918 // PHF14 // 9678 // Homo sapiens mRNA for KIAA0783 protein, partial cds. /// ENST00000303905 // downstream // 30087 // — // — // — // — /// ENST00000262042 // downstream // 240893 // — // — // — // —	PHF14	PHF14, Homo sapiens for KIAA0783 protein, partial cds. p21.3
SNP_A-2274874	gagaaattcttcagat[C/G]aaataacagaatcatg	C	G	AB018326 // downstream // 147004 // Hs.159918 // PHF14 // 9678 // Homo sapiens mRNA for KIAA0783 protein, partial cds. /// ENST00000303905 // downstream // 147004 // — // — // — // — /// ENST00000262042 // downstream // 123976 // — // — // — // —	PHF14	PHF14, Homo sapiens for KIAA0783 protein, partial cds. ,p21.3
SNP_A-2227356	ctacaatagcaggaaa[A/C]gttagaagcaccttaa	A	C	ENST00000262042 // intron // 0 // — // — // — // — // —	-	p21.3
SNP_A-1744587	gaacagtcttctccacagtctctca[C/T]gcttcctagtcccaatca aaagctt	C	T	AB023177 // intron // 0 // Hs.23799 // KIAA0960 // 23249 // KIAA0960 protein	KIAA0960	KIAA0960 , rs10486139, KIAA0960 protein,p21.3
SNP_A-2171370	caatatttggagagaa[C/T]tgaagctaagtgcttg	C	T	ENST00000262042 // intron // 0 // — // — // — // — // —	-	p21.3
SNP_A-1819516	gttggtccttggtaga[C/T]aatattccacggagat	C	T	NM_018374 // upstream // 303402 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000357331 // downstream // 23191 // — // — // — // — // — /// ENST00000353474 // upstream // 299898 // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1907279	tggttttcccctgatc[A/G]attcagttgtcttca	A	G	NM_018374 // upstream // 238700 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000357331 // downstream // 87893 // — // -- // -- // — /// ENST00000353474 // upstream // 235196 // — // –	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-2268119	gaatgaacaaagctta[C/T]aggatctatggaacaa	C	T	NM_018374 // upstream // 237593 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000357331 // downstream // 89000 // — // -- // -- // — /// ENST00000353474 // upstream // 234089 // — // –	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-1988844	gggagaggttggtcaa[A/G]aagtatgaactttcag	A	G	NM_018374 // upstream // 37216 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000357331 // downstream // 289377 // — // -- // -- // — /// ENST00000353474 // upstream // 33712 // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-1731559	attcaacagttgacagttaaaatta[C/T]gaagccaatgttccaaa atatttaaa	C	T	NM_018374 // intron // 0 // Hs.396358 // FLJ11273 // 54664 // hypothetical protein FLJ11273	FLJ11273	FLJ11273 , rs6460898, hypothetical protein FLJ11273,p21.3
SNP_A-2038665	aacagacttggcacc[A/G]gctaggtaaacctatc	A	G	NM_018374 // upstream // 15154 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000357331 // downstream // 311439 // — // -- // -- // — /// ENST00000353474 // upstream // 11650 // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-2180355	cagaaatggtagagaaa[C/G]gtcaatacagaaaaga	C	G	NM_018374 // intron // 0 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000353474 // intron // 0 // — // — // — /// ENST00000336176 // intron // 0 // — // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-1879104	tcttaattctcataag[C/G]attgtattctcaacc	C	G	NM_018374 // intron // 0 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000353474 // intron // 0 // — // — // — /// ENST00000336176 // intron // 0 // — // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-2288474	gattgaaatttagaag[A/G]atcttggaagtctttg	A	G	NM_018374 // intron // 0 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000353474 // intron // 0 // — // — // — /// ENST00000336176 // intron // 0 // — // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-2182847	cagatgtgagctaaaaa[A/G]tcgtgacctaatgaca	A	G	NM_018374 // 3UTR // 0 // Hs.396358 // FLJ11273 // 54664 // Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /// ENST00000336176 // 3UTR // 0 // — // — // —	FLJ11273	FLJ11273, Homo sapiens hypothetical protein FLJ11273 (FLJ11273), p21.3
SNP_A-1950405	ttcaggtgatagttat[C/G]aaccagcctctcgaaa	C	G	NM_033128 // intron // 0 // Hs.326941 // SCIN // 85477 // Homo sapiens scinderin (SCIN). mRNA. /// ENST00000341757 // intron // 0 // — // -- // -- // — /// ENST00000297029 // intron // 0 // — // -- // -- // --	SCIN	SCIN, Homo sapiens scinderin (SCIN), p21.3
SNP_A-1738547	ccccatgacactgtacacacgaatg[A/C]acttgttagttaaatga attatataa	A	C	NM_033128 // intron // 0 // Hs.356726 // SCIN // 85477 // scinderin	SCIN	SCIN , rs1180398, scinderin,p21.3
SNP_A-1659951	tgttgtcattcaaagggcataagca[A/C]atgtcaaataattgaatc attgaga	A	C	NM_004956 // downstream // 1130890 // Hs.150011 // ETV1 // 2115 // ets variant gene 1 /// NM_005738 // downstream // 75397 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation factor-like 4A	ETV1	ETV1 , rs702478, ets variant gene 1 ,p21.3
SNP_A-2208915	cccagcagagattcttt[A/G]aaacttactctctcat	A	G	NM_212460 // downstream // 165704 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 165704 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1885035	tgaatggcagtgctaa[A/C]acagctataacacaag	A	C	NM_212460 // downstream // 172712 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 172712 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800358	gtactagagctggtaa[A/G]caacagaggagtacag	A	G	NM_212460 // downstream // 178261 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 178261 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1952570	ttctgccaaaatgta[C/G]aatagagccttgcaat	C	G	NM_212460 // downstream // 178756 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 178756 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1712695	tgcccigtagaaagccaagcccaaa[C/T]gctataaactccttcca aataattgc	C	T	NM_004956 // downstream // 993460 // Hs.150011 // ETV1 // 2115 // ets variant gene 1 /// NM_005738 // downstream // 212827 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation factor-like 4A	ETV1	ETV1 , rs10488238, ets variant gene 1 ,p21.3
SNP_A-2133657	atatcatacattgac[A/G]ctataaaagcaggtgtt	A	G	NM_212460 // downstream // 189216 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 189216 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2083119	acgttggccatcttcc[A/G]agacattataaaacat	A	G	NM_212460 // downstream // 203643 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 203643 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2308601	gctttcagacatcttc[C/G]agaaagcgtgtgcatct	C	G	NM_212460 // downstream // 207681 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 207681 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1920457	ttaattatgtctctggt[A/G]atagaagctatattca	A	G	NM_212460 // downstream // 212700 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 212700 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-2173843	cacacactgatttta[C/G]gcagttcagcagcaag	C	G	NM_212460 // downstream // 212855 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 212855 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1781383	ggatgttggacactga[C/G]aatgcaaaggcagggt	C	G	NM_212460 // downstream // 271988 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 271988 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1906222	tggtgactagctcaaa[A/T]gaaaaggcagagagag	A	T	NM_212460 // downstream // 398523 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 398523 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1721506	ggaaataattcttggataataacaa[A/G]ttggacctctgaaatga ataagagg	A	G	NM_004956 // downstream // 660828 // Hs.150011 // ETV1 // 2115 // ets variant gene 1 /// NM_005738 // downstream // 545459 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation factor-like 4A	ETV1	ETV1 , rs2884164, ets variant gene 1 ,p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2256694	ctttcaggaaaactagal[A/C]ctlgctctlctactcc	A	C	NM_212460 // downstream // 518153 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 518153 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.3
SNP_A-1671222	atcatattccagaataagatacatg[C/G]attcctttcaacagggta cacattt	C	G	NM_004956 // downstream // 567910 // Hs.150011 // ETV1 // 2115 // ets variant gene 1 /// NM_005738 // downstream // 638377 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation factor-like 4A	ETV1	ETV1 , rs2041656, ets variant gene 1 ,p21.3
SNP_A-1885786	tgacaggctcaaaatc[A/G]aatagacatatctttt	A	G	NM_212460 // downstream // 818361 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 818361 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2021929	aaaaactccctgtccal[A/C]agagaacttacttct	A	C	NM_212460 // downstream // 832192 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 832192 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1812660	gtggcttaaacaccaa[A/C]catcagattaatcat	A	C	NM_212460 // downstream // 840885 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 840885 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2128446	ataataaatag1gaaa[C/G]aataagctgatgtcag	C	G	NM_212460 // downstream // 848270 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 848270 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1893681	tgcagtatttcaaaaa[C/T]gacaggtttaaagta	C	T	NM_212460 // downstream // 891076 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 891076 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation fac	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1922474	ttagaagacacctggal[C/G]ataaaaataaagatt	C	G	NM_212460 // downstream // 1015047 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 1015047 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation f	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1666652	aaatctccaatcaagaatacttcac[C/T]atttaatgtgtttataac actgga	C	T	NM_004956 // downstream // 101276 // Hs.150011 // ETV1 // 2115 // ets variant gene 1 /// NM_005738 // downstream // 1105011 // Hs.245540 // ARL4A // 10124 // ADP-ribosylation factor-like 4A	ETV1	ETV1 , rs13240870, ets variant gene 1 ,p21.2
SNP_A-2152100	attaaaaggcagacaa[A/C]attgccgcatgataca	A	C	NM_212460 // downstream // 1129591 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 1129591 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation f	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1988902	cttggagaataatgaa[A/G]aagcagctttatatc	A	G	NM_212460 // downstream // 1138042 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 1138042 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation f	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2012397	aacaacagcacatagg[A/C]actttattatattat	A	C	NM_212460 // downstream // 1140974 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 1140974 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation f	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-2171986	caatgctacaaacatc[C/T]gaatagcacatttttt	C	T	NM_212460 // downstream // 1148905 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, mRNA. /// NM_005738 // downstream // 1148905 // Hs.245540 // ARL4A // 10124 // Homo sapiens ADP-ribosylation f	ARL4A	ARL4A, Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 2, p21.2
SNP_A-1923769	ttagtacactgtaaaa[A/G]gctttctgtctgagta	A	G	NM_004956 // upstream // 113491 // Hs.22634 // ETV1 // 2115 // Homo sapiens ets variant gene 1 (ETV1), mRNA. /// NM_004080 // downstream // 43439 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1,	ETV1	ETV1, Homo sapiens ets variant gene 1 (ETV1), p21.2
SNP_A-2122071	agtgatgaataaaggga[C/G]cacaggtgtaaaacag	C	G	NM_004080 // intron // 0 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // intron // 0 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB),	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-2041614	aacgcaatgattatga[C/T]cggaggcagcagttga	C	T	NM_004080 // intron // 0 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // intron // 0 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB),	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-2120357	agtcatcttctgctc[C/T]acgtggcatgacaaga	C	T	NM_004080 // intron // 0 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // intron // 0 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB),	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-1783043	ggcagcggtgagataa[A/G]acgatctgcctcacta	A	G	NM_004080 // upstream // 172701 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // upstream // 172701 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-2107293	agctaagaaagcagccd[A/G]attcataaaaatgcat	A	G	NM_004080 // upstream // 202173 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, mRNA. /// NM_145695 // upstream // 202173 // Hs.487619 // DGKB // 1607 // Homo sapiens diacylglycerol kinase, beta	DGKB	DGKB, Homo sapiens diacylglycerol kinase, beta 90kDa (DGKB), transcript variant 1, p21.2
SNP_A-2035386	aaatgcctggaatta[C/G]atggtattactgcata	C	G	NM_005924 // intron // 0 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // intron // 0 // — // — // —	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2282118	gagtgtatctctttga[C/T]gttgtgctggatataa	C	T	NM_005924 // intron // 0 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // intron // 0 // — // — // —	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2053497	aagtgcataaaaaca[C/G]gaaatctgaataagg	C	G	NM_005924 // intron // 0 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // intron // 0 // — // — // —	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-1782760	ggcagaagacttcacg[A/G]cggttccaaaggccac	A	G	NM_005924 // 5UTR // 0 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // 5UTR // 0 // — // — // —	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1729146	tcatgtgggtaagccctgaataacc[G/T]acatttctttaagctatc agcacca	G	T	NM_005924 // upstream // 43938 // Hs.77858 // MEOX2 // 4223 // mesenchyme homeo box 2 (growth arrest-specific homeo box) /// NM_015464 // downstream // 730964 // Hs.25956 // SOSTDC1 // 25928 // sclerostin domain containing 1	MEOX2	MEOX2, rs10486777, mesenchyme homeo box 2 (growth arrest-specific homeo box), p21.2
SNP_A-2133396	atatatgcttgatctc[A/T]caacttcaccatttccc	A	T	NM_005924 // upstream // 21477 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 21477 // – // – // – /// ENST00000335259 // downstream //	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-1869503	tcctgttatgtttca[C/G]tagtaaagactgataa	C	G	NM_005924 // upstream // 35963 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 35963 // – // – // – /// ENST00000335259 // downstream //	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2149857	atgtcaacttggtatt[C/T]aaactgtaagcatcaa	C	T	NM_005924 // upstream // 36015 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 36015 // – // – // – /// ENST00000335259 // downstream //	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-1826545	taacaatagaaaagcg[A/G]atagcacttggcacc	A	G	NM_005924 // upstream // 38267 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 38267 // – // – // – /// ENST00000335259 // downstream //	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2030347	aaagcatggatcataa[C/T]agtttctatttcatag	C	T	NM_005924 // upstream // 58517 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 58517 // – // – // – /// ENST00000335259 // downstream //	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2061172	aatgcagatatccatc[C/G]agaccccttcagaaac	C	G	NM_005924 // upstream // 107472 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 107472 // – // – // – /// ENST00000335259 // downstream	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-1890628	tgatgaaggactagga[C/T]caattcatggaaattc	C	T	NM_005924 // upstream // 109792 // Hs.527007 // MEOX2 // 4223 // Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), mRNA. /// ENST00000262041 // upstream // 109792 // – // – // – /// ENST00000335259 // downstream	MEOX2	MEOX2, Homo sapiens mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX2), p21.1
SNP_A-2030160	aaagcaagtcaggcaa[C/G]caaatcaaggagaagg	C	G	ENST00000335259 // intron // 0 // – // – // – // –	-	p21.1
SNP_A-2042878	aactcttcgaatctg[A/T]agggagccttgaaaac	A	T	ENST00000335259 // intron // 0 // – // – // – // –	-	p21.1
SNP_A-2134703	atatgttttagttga[C/T]ctgactcagttccca	C	T	ENST00000335259 // intron // 0 // – // – // – // –	-	p21.1
SNP_A-2163604	caaaaagacacagaag[G/T]aggtaatagaaactca	G	T	NM_014038 // intron // 0 // Hs.487635 // BZW2 // 28969 // Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), mRNA. /// ENST00000258761 // intron // 0 // – // – // – // – /// ENST00000310524 // intron // 0 // – // – // – // –	BZW2	BZW2, Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), p21.1
SNP_A-1947075	tttatataaaattaac[A/G]ctaggctgtaatctgt	A	G	NM_014038 // intron // 0 // Hs.487635 // BZW2 // 28969 // Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), mRNA. /// ENST00000258761 // intron // 0 // – // – // – // –	BZW2	BZW2, Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), p21.1
SNP_A-1650428	tgttcgttttaatttttctcagcg[C/G]ccgtcatttggtttacttcatttc a	C	G	NM_014399 // intron // 0 // Hs.364544 // TM4SF13 // 27075 // transmembrane 4 superfamily member 13	TM4SF13	TM4SF13, rs10499475, transmembrane 4 superfamily member 13 p21.1
SNP_A-1721592	ggtacactgaggaaaatataatacttta[C/T]ggctgatgtctgaaga acaaggtg	C	T	NM_006408 // upstream // 28966 // Hs.226391 // AGR2 // 10551 // anterior gradient 2 homolog (Xenopus laevis) /// NM_176813 // downstream // 25557 // Hs.100686 // BCMP11 // 155465 // breast cancer membrane protein 11	AGR2	AGR2, rs10499478, anterior gradient 2 homolog (Xenopus laevis), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1756947	gagtgcagaaacatgagtgtttgcg[A/G]cagccagctagctag attctatgtc	A	G	NM_001621 // upstream // 360518 // Hs.170087 // AHR // 196 // aryl hydrocarbon receptor /// NM_176813 // upstream // 56129 // Hs.100686 // BCMP11 // 155465 // breast cancer membrane protein 11	AHR	AHR , rs847371, aryl hydrocarbon receptor ,p21.1
SNP_A-1945725	ttgttgcttatccttg[C/T]agtccaattcgtatac	C	T	NM_176813 // upstream // 46844 // Hs.100686 // BCMP11 // 155465 // Homo sapiens breast cancer membrane protein 11 (BCMP11), mRNA. /// NM_001621 // upstream // 369789 // Hs.171189 // AHR // 196 // Homo sapiens aryl hydrocarbon receptor (AHR), mRNA. /// ENS	BCMP11	BCMP11, Homo sapiens breast cancer membrane protein 11 (BCMP11), p21.1
SNP_A-1758312	gaaaaaagtcatcattatgtaaaa[A/T]cacatcatcattattaaa catgtca	A	T	NM_001621 // downstream // 13591 // Hs.170087 // AHR // 196 // aryl hydrocarbon receptor /// NM_015132 // downstream // 433475 // Hs.269881 // SNX13 // 23161 // sorting nexin 13	AHR	AHR , rs10269143, aryl hydrocarbon receptor ,p21.1
SNP_A-2123873	agttaacatctgttga[C/T]aaagcagtcgctagat	C	T	NM_001621 // downstream // 274713 // Hs.171189 // AHR // 196 // Homo sapiens aryl hydrocarbon receptor (AHR), mRNA. /// NM_015132 // downstream // 172353 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // downs	AHR	AHR, Homo sapiens aryl hydrocarbon receptor (AHR), p21.1
SNP_A-2310423	ggaactggcttccaca[C/T]gagtaagcataaaagt	C	T	NM_001621 // downstream // 314878 // Hs.171189 // AHR // 196 // Homo sapiens aryl hydrocarbon receptor (AHR), mRNA. /// NM_015132 // downstream // 132188 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // downs	AHR	AHR, Homo sapiens aryl hydrocarbon receptor (AHR), p21.1
SNP_A-2268524	gaatgggcacctcag[A/T]agtcatcttggatca	A	T	NM_001621 // downstream // 430668 // Hs.171189 // AHR // 196 // Homo sapiens aryl hydrocarbon receptor (AHR), mRNA. /// NM_015132 // downstream // 16398 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // downst	AHR	AHR, Homo sapiens aryl hydrocarbon receptor (AHR), p21.1
SNP_A-1989030	tttagacccaaaggcc[A/G]agttataaagattc	A	G	NM_015132 // intron // 0 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// ENST00000340108 // intron // 0 // — // — // — /// ENST00000242044 // intron // 0 // — // — // —	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-1702941	gtgcccaataattgggaattgggta[A/T]acagtttaggagtca gtccagac	A	T	NM_015132 // intron // 0 // Hs.269881 // SNX13 // 23161 // sorting nexin 13	SNX13	SNX13 , rs1464804, sorting nexin 13,p21.1
SNP_A-1853875	tcaaaagattaaatga[C/G]acaactgtttgctaga	C	G	NM_015132 // upstream // 3684 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // upstream // 3702 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_175886 // downstream // 82	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-2193208	catctcaccttttgca[A/G]tgaaaaaacacaacgg	A	G	NM_015132 // upstream // 28187 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // upstream // 28205 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_175886 // downstream //	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-2147219	atggacgtgtgattca[A/T]tcctggctagtgtaat	A	T	NM_015132 // upstream // 34305 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_015132 // upstream // 34323 // Hs.487648 // SNX13 // 23161 // Homo sapiens sorting nexin 13 (SNX13), mRNA. /// NM_175886 // downstream //	SNX13	SNX13, Homo sapiens sorting nexin 13 (SNX13), p21.1
SNP_A-1989037	aattgaagtcactcca[A/C]agcaagatgtttccaa	A	C	NM_175886 // upstream // 209591 // Hs.169284 // PRPS1L1 // 221823 // Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), mRNA. /// NM_014707 // upstream // 258376 // Hs.196054 // HDAC9 // 9734 // Homo sapiens histone deacetylase 9 (HD	PRPS1L1	PRPS1L1, Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1724438	ggaatctgagcctctatcatagttcac[C/G]atgtatgacttctgctttac cacac	C	G	NM_058176 // intron // 0 // Hs.487662 // HDAC9 // 9734 // histone deacetylase 9 /// NM_058177 // intron // 0 // Hs.487662 // HDAC9 // 9734 // histone deacetylase 9 /// NM_178423 // intron // 0 // Hs.487662 // HDAC9 // 9734 // histone deacetylase 9 /// NM	HDAC9	HDAC9, rs10259495, histone deacetylase 9, p21.1
SNP_A-1714296	cctattagtcatagtatacacagta[A/G]taatagccaaaatttattg cgtgtt	A	G	NM_000474 // downstream // 51186 // Hs.66744 // TWIST1 // 7291 // twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) /// NM_014707 // downstream // 395440 // Hs.487662 // HDAC9 // 9734 // histone deacetylase 9 /// NM_058176	TWIST1	TWIST1, rs2905456, twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila), p21.1
SNP_A-1656039	aaagtatccagtccagcctaaca[C/T]gcaataaatttggctat tattact	C	T	NM_000474 // downstream // 51165 // Hs.66744 // TWIST1 // 7291 // twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) /// NM_014707 // downstream // 395461 // Hs.487662 // HDAC9 // 9734 // histone deacetylase 9 /// NM_058176	TWIST1	TWIST1, rs2521720, twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila), p21.1
SNP_A-1881271	tctttattctgtgca[A/G]ggtgggctcatagaga	A	G	NM_152898 // upstream // 71118 // Hs.381371 // FERD3L // 222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 478982 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST neighbor (TWISTNB), mRNA. /// ENST00000	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1956474	tttgttgaggacctaa[C/T]acatgctggatactgt	C	T	NM_152898 // upstream // 177413 // Hs.381371 // FERD3L // 222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 372687 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST neighbor (TWISTNB), mRNA. /// ENST0000	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1989078	cgctcagagagaatag[A/G]agttcacttgtgaata	A	G	NM_152898 // upstream // 330338 // Hs.381371 // FERD3L // 222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 219762 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST neighbor (TWISTNB), mRNA. /// ENST0000	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1839947	tagcaaagaagaaaga[A/C]gtgagagactgaaagc	A	C	NM_152898 // upstream // 335489 // Hs.381371 // FERD3L // 222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 214611 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST neighbor (TWISTNB), mRNA. /// ENST0000	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-2232674	ctcactaatagtgtga[A/G]cctggataaagctacc	A	G	NM_152898 // upstream // 425831 // Hs.381371 // FERD3L // 222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 124269 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST neighbor (TWISTNB), mRNA. /// ENST0000	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-2288509	gattgagaaactttaa[G/T]cccagggaaggactat	G	T	NM_152898 // upstream // 473854 // Hs.381371 // FERD3L // 222894 // Homo sapiens Fer3-like (Drosophila) (FERD3L), mRNA. /// NM_001002926 // downstream // 76246 // Hs.353035 // TWISTNB // 221830 // Homo sapiens TWIST neighbor (TWISTNB), mRNA. /// ENST00000	FERD3L	FERD3L, Homo sapiens Fer3-like (Drosophila) (FERD3L), p21.1
SNP_A-1658910	gtcactaaagaaaatgattattac[A/G]gagttcagaaaaatt attcaaaag	A	G	NM_152774 // intron // 0 // Hs.487670 // MGC42090 // 256130 // hypothetical protein MGC42090	MGC42090	MGC42090, rs2189571, hypothetical protein MGC42090, p21.1
SNP_A-1877484	tctggcaacagaatta[C/T]gtgagatgctgtatt	C	T	NM_000982 // downstream // 61354 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// NM_182762 // downstream // 76027 // Hs.164296 // 7A5 // 346389 // Homo sapiens putative binding protein 7a5 (7A5), mRNA. /// ENST000002	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), p21.1
SNP_A-1797328	ggttgtcatttgttcg[C/G]aagtacggcagagcct	C	G	NM_002214 // intron // 0 // Hs.285724 // ITGB8 // 3696 // Homo sapiens integrin, beta 8 (ITGB8), mRNA. /// ENST00000222573 // intron // 0 // — /// — /// —	ITGB8	ITGB8, Homo sapiens integrin, beta 8 (ITGB8), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1915699	tgttctgttctatacc[A/G]cgaggcacaatattgt	A	G	NM_002214 // downstream // 31162 // Hs.285724 // ITGB8 // 3696 // Homo sapiens integrin, beta 8 (ITGB8), mRNA. /// NM_178559 // upstream // 205464 // Hs.404102 // ABCB5 // 340273 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 5 (ABCB	ITGB8	ITGB8, Homo sapiens integrin, beta 8 (ITGB8), p21.1
SNP_A-1842984	tagtatcttccacatc[C/T]atcactgaggctaccg	C	T	NM_002214 // downstream // 138698 // Hs.285724 // ITGB8 // 3696 // Homo sapiens integrin, beta 8 (ITGB8), mRNA. /// NM_178559 // upstream // 97928 // Hs.404102 // ABCB5 // 340273 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 5 (ABCB	ITGB8	ITGB8, Homo sapiens integrin, beta 8 (ITGB8), p21.1
SNP_A-2088262	actggtgtaggcatca[A/G]acatgtaaatgaatct	A	G	NM_002214 // downstream // 184890 // Hs.285724 // ITGB8 // 3696 // Homo sapiens integrin, beta 8 (ITGB8), mRNA. /// NM_178559 // upstream // 51736 // Hs.404102 // ABCB5 // 340273 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 5 (ABCB	ITGB8	ITGB8, Homo sapiens integrin, beta 8 (ITGB8), p21.1
SNP_A-2033180	aaatacctcgaagaaa[A/G]cacagattattggaag	A	G	NM_178559 // CDS // 0 // Hs.404102 // ABCB5 // 340273 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 5 (ABCB5), mRNA. /// ENST00000258738 // CDS // 0 // --- // --- // ---	ABCB5	ABCB5, Homo sapiens ATP-binding cassette, sub-family B (MDR p21.1
SNP_A-2038543	aacagaaaccattata[A/G]gtacccaaagcagaat	A	G	NM_198956 // upstream // 26746 // Hs.195922 // SP8 // 221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream // 26746 // Hs.195922 // SP8 // 221833 // Homo sapiens Sp8 transcription factor (SP8), trans	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p21.1
SNP_A-1989115	ctcagaaagaattgac[G/T]caaatgacagcctcac	G	T	NM_198956 // upstream // 257824 // Hs.195922 // SP8 // 221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream // 257824 // Hs.195922 // SP8 // 221833 // Homo sapiens Sp8 transcription factor (SP8), tra	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-1910091	tgtcatcactcaaatg[G/T]attaagtgcttgttgg	G	T	NM_198956 // upstream // 273973 // Hs.195922 // SP8 // 221833 // Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA. /// NM_182700 // upstream // 273973 // Hs.195922 // SP8 // 221833 // Homo sapiens Sp8 transcription factor (SP8), tra	SP8	SP8, Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, p15.3
SNP_A-2280998	gagtaaacgtcatggg[C/T]cagactcgaattacta	C	T	NM_003777 // downstream // 86127 // Hs.432390 // DNAH11 // 8701 // Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// NM_018719 // upstream // 41549 // Hs.520245 // RAM2 // 55536 // Homo sapiens transcription factor RAM2 (RAM2), mRNA.	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-2309735	ggaaaggcaagaaaaa[C/G]ctgagaaattgttata	C	G	NM_003777 // downstream // 98058 // Hs.432390 // DNAH11 // 8701 // Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// NM_018719 // upstream // 53480 // Hs.520245 // RAM2 // 55536 // Homo sapiens transcription factor RAM2 (RAM2), mRNA.	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-2194022	catgaatggctggaca[C/G]agagtaagaggattga	C	G	NM_003777 // downstream // 158239 // Hs.432390 // DNAH11 // 8701 // Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// NM_018719 // upstream // 113661 // Hs.520245 // RAM2 // 55536 // Homo sapiens transcription factor RAM2 (RAM2), mRN	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3
SNP_A-1827555	taactgaagtaagtag[A/G]aggttgtagtagccca	A	G	NM_003777 // downstream // 162439 // Hs.432390 // DNAH11 // 8701 // Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), mRNA. /// NM_018719 // upstream // 117861 // Hs.520245 // RAM2 // 55536 // Homo sapiens transcription factor RAM2 (RAM2), mRN	DNAH11	DNAH11, Homo sapiens dynein, axonemal, heavy polypeptide 11 (DNAH11), p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1671004	aatgggatagtaactccctcttaa[A/G]tgagacagtgatcttaa agagcaga	A	G	BC027978 // downstream // 415111 // Hs.130210 // IL6 // 3569 // interleukin 6 (interferon, beta 2) /// NM_000600 // upstream // 416915 // Hs.512234 // IL6 // 3569 // interleukin 6 (interferon, beta 2) /// NM_012294 // upstream // 114527 // Hs.449375 // R	IL6	IL6 , rs10499552, interleukin 6 (interferon, beta 2) p15.3
SNP_A-1673378	gctaggtactattgactactaaga[A/C]gattacacccacgtccat atctgta	A	C	BC027978 // downstream // 4140?6 // Hs.130210 // IL6 // 3569 // interleukin 6 (interferon, beta 2) /// NM_000600 // upstream // 415880 // Hs.512234 // IL6 // 3569 // interleukin 6 (interferon, beta 2) /// NM_012294 // upstream // 115562 // Hs.449375 // R	IL6	IL6 , rs10499551, interleukin 6 (interferon, beta 2) p15.3
SNP_A-2291368	gcaaatgtactaaggta[A/G]gcaagttgatttctgca	A	G	NM_019059 // upstream // 36688 // Hs.112318 // TOMM7 // 54543 // Homo sapiens translocase of outer mitochondrial membrane 7 homolog (yeast) (TOMM7), mRNA. /// ENST00000358435 // upstream // 36688 // — // — // — /// ENST00000340005 // upstream	TOMM7	TOMM7, Homo sapiens translocase of outer mitochondrial membrane 7 homolog (yeast) (TOMM7), p15.3
SNP_A-2208620	cccactgcagtgcata[A/C]ggttatttatctgaca	A	C	NM_019059 // upstream // 52458 // Hs.112318 // TOMM7 // 54543 // Homo sapiens translocase of outer mitochondrial membrane 7 homolog (yeast) (TOMM7), mRNA. /// ENST00000358435 // upstream // 52458 // — // — // — /// ENST00000340005 // upstream	TOMM7	TOMM7, Homo sapiens translocase of outer mitochondrial membrane 7 homolog (yeast) (TOMM7), p15.3
SNP_A-1848538	tatgacactgaattaa[C/T]agccattagaggtgaa	C	T	NM_031414 // intron // 0 // Hs.309767 // STK31 // 56164 // Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA. /// NM_032944 // intron // 0 // Hs.309767 // STK31 // 56164 // Homo sapiens serine/threonine kinase 31 (STK31), transcr	STK31	STK31, Homo sapiens serine p15.3
SNP_A-1887026	tgacttgttgtgtatc[C/T]ctggtcttccgttac	C	T	NM_031414 // downstream // 254192 // Hs.309767 // STK31 // 56164 // mRNA. /// NM_032944 // downstream // 254192 // Hs.309767 // STK31 // 56164 // Homo sapiens serine/threonine kinase 3	STK31	STK31, Homo sapiens serine p15.3
SNP_A-2265906	gaaggacttgaatcac[C/T]ggacgtcacccaggt	C	T	NM_031414 // downstream // 297272 // Hs.309767 // STK31 // 56164 // mRNA. /// NM_032944 // downstream // 297272 // Hs.309767 // STK31 // 56164 // Homo sapiens serine/threonine kinase 3	STK31	STK31, Homo sapiens serine.p15.3
SNP_A-1715813	tccacaccagtcttaaaattgaaa[C/T]gatacatcctcatatcaa gcctgaa	C	T	NM_000905 // upstream // 20002 // Hs.1832 // NPY // 4852 // neuropeptide Y /// NM_031414 // downstream // 431676 // Hs.224355 // STK31 // 56164 // serine/threonine kinase 31 /// NM_032944 // downstream // 431681 // Hs.224355 // STK31 // 56164 // serine/t	NPY	NPY , rs16162, neuropeptide Y .p15.3
SNP_A-1894344	tgcatttgaatgttga[C/T]agttcttaccaaattt	C	T	NM_031414 // downstream // 425199 // Hs.309767 // STK31 // 56164 // Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA. /// NM_032944 // downstream // 425199 // Hs.309767 // STK31 // 56164 // Homo sapiens serine/threonine kinase 3	STK31	STK31, Homo sapiens serine p15.3
SNP_A-1880981	tcttgtgtagctttttg[C/T]agatgttgctcagcct	C	T	NM_004403 // intron // 0 // Hs.520708 // DFNA5 // 1687 // Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA. /// ENST00000342947 // intron // 0 // — // — // —	DFNA5	DFNA5, Homo sapiens deafness, autosomal dominant 5 (DFNA5), p15.3
SNP_A-2292514	gcatctccaaatcacca[C/T]acttatacagctccgc	C	T	NM_145322 // upstream // 86172 // Hs.520259 // OSBPL3 // 26031 // Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, mRNA. /// NM_145321 // upstream // 86172 // Hs.520259 // OSBPL3 // 26031 // Homo sapiens oxysterol binding prot	OSBPL3	OSBPL3, Homo sapiens oxysterol binding protein-like 3 (OSBPL3), transcript variant 4, p15.3
SNP_A-1871275	tctaaacactgagctg[A/G]aattgagacattggac	A	G	NM_022150 // upstream // 74829 // Hs.60473 // C7orf9 // 64111 // Homo sapiens chromosome 7 open reading frame 9 (C7orf9), mRNA. /// ENST00000222674 // upstream // 74829 // — // — // — /// ENST00000258728 // downstream // 386424 // — // —	C7orf9	C7orf9, Homo sapiens chromosome 7 open reading frame 9 (C7orf9), p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1648396	ttctctgaaaagtctgacagagcga[A/G]cttacctttctatttcct ccatt	A	G	NM_004289 // upstream // 360051 // Hs.404741 // NFE2L3 // 9603 // nuclear factor (erythroid-derived 2)-like 3 /// NM_022150 // upstream // 543963 // Hs.60473 // C7orf9 // 64111 // chromosome 7 open reading frame 9	NFE2L3	NFE2L3 , rs10486417, nuclear factor (erythroid-derived 2)-like 3 ,p15.2
SNP_A-2030192	aaagcacaaaacactga[C/T]agctgtaaggtaaagt	C	T	NM_004289 // upstream // 376123 // Hs.404741 // NFE2L3 // 9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream // 86158 // — // — // — /// ENST00000056233 // upstream // 376123 // –	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-1899883	tggacaatttggagcc[A/T]gcatatacgcccatct	A	T	NM_004289 // upstream // 354171 // Hs.404741 // NFE2L3 // 9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream // 108110 // — // — // — /// ENST00000056233 // upstream // 354171 // -	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-2103624	agcacaccatcgtatc[A/G]caatatcccdgaattt	A	G	NM_004289 // upstream // 321420 // Hs.404741 // NFE2L3 // 9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream // 140861 // — // — // — /// ENST00000056233 // upstream // 321420 // -	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-1798806	gtaactggcaacttca[G/T]ccttccagctgcttag	G	T	NM_004289 // upstream // 246208 // Hs.404741 // NFE2L3 // 9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream // 216073 // — // — // — /// ENST00000056233 // upstream // 246208 // -	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-2266901	gaagttgccagttact[A/G]agacagggagaatgtg	A	G	NM_004289 // upstream // 246190 // Hs.404741 // NFE2L3 // 9603 // Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA. /// ENST00000258728 // upstream // 216091 // — // — // — /// ENST00000056233 // upstream // 246190 // -	NFE2L3	NFE2L3, Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), p15.2
SNP_A-2314749	ggagtctggaccccaa[A/C]gagtccaaggcagctg	A	C	NM_013322 // intron // 0 // Hs.520714 // SNX10 // 29887 // Homo sapiens sorting nexin 10 (SNX10), mRNA. /// ENST00000338523 // intron // 0 // — // — // —	SNX10	SNX10, Homo sapiens sorting nexin 10 (SNX10), p15.2
SNP_A-2199056	catttgtcacaactcc[A/G]aaagatgtgagaaagt	A	G	D42038 // upstream // 45721 // Hs.69749 // KIAA0087 // 9808 // Homo sapiens KIAA0087 mRNA, partial cds. /// NM_003930 // downstream // 82562 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST0000002	KIAA0087	KIAA0087, Homo sapiens KIAA0087 partial cds, p15.2
SNP_A-2085951	actctacaggaacaga[C/T]gcatttggtacaaata	C	T	D42038 // upstream // 66020 // Hs.69749 // KIAA0087 // 9808 // Homo sapiens KIAA0087 mRNA, partial cds. /// NM_003930 // downstream // 62263 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST0000002	KIAA0087	KIAA0087, Homo sapiens KIAA0087 partial cds, p15.2
SNP_A-1989286	tttaaaaggccagctg[G/T]atgtttgcacatcagt	G	T	D42038 // upstream // 70500 // Hs.69749 // KIAA0087 // 9808 // Homo sapiens KIAA0087 mRNA, partial cds. /// NM_003930 // downstream // 57783 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST0000002	KIAA0087	KIAA0087, Homo sapiens KIAA0087 partial cds, p15.2
SNP_A-2107250	agctaaacacactaga[C/T]gcttttgttacactaa	C	T	NM_003930 // intron // 0 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // — // — // — // —	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2
SNP_A-1664894	gagttgaactaagcagaataaaaca[A/T]ctttaccacaataata attgcaaca	A	T	NM_003930 // intron // 0 // Hs.410745 // SCAP2 // 8935 // src family associated phosphoprotein 2	SCAP2	SCAP2, rs10085721, src family associated phosphoprotein 2,p15.2
SNP_A-2314842	ggagtgctttctcagg[A/G]aaccaaaatgtagctg	A	G	NM_003930 // intron // 0 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // — // — // — // —	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2
SNP_A-2032219	aaagtgtctagaacaa[A/G]ggtctcaaactgatag	A	G	NM_003930 // intron // 0 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // intron // 0 // — // — // — // —	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2012467	agtaagaaagatcaag[C/G]ccagacactgtgactc	C	G	NM_003930 // upstream // 40825 // Hs.200770 // SCAP2 // 8935 // Homo sapiens src family associated phosphoprotein 2 (SCAP2), mRNA. /// ENST00000345317 // upstream // 40825 // --- // --- // --- /// ENST00000338865 // downstream // 77533 // --- // --	SCAP2	SCAP2, Homo sapiens src family associated phosphoprotein 2 (SCAP2), p15.2
SNP_A-1795425	ggtgcactgatttccc[C/T]ggaggagccctgagag	C	T	NM_000522 // upstream // 3525 // Hs.414467 // HOXA13 // 3209 // Homo sapiens homeo box A13 (HOXA13), mRNA. /// NM_001989 // upstream // 39200 // Hs.369879 // EVX1 // 2128 // Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), mRNA. ///	HOXA13	HOXA13, Homo sapiens homeo box A13 (HOXA13), p15.2
SNP_A-1849398	tatggaggaggtagatg[A/T]cataatatatttgcaa	A	T	NM_001989 // downstream // 33622 // Hs.369879 // EVX1 // 2128 // Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), mRNA. /// ENST00000222761 // downstream // 33622 // --- // --- // --- /// ENST00000313812 // downstream // 1779	EVX1	EVX1, Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), p15.2
SNP_A-1795608	ggtgctggaatcagac[C/T]gaaccgttggttgaa	C	T	NM_001989 // downstream // 141898 // Hs.369879 // EVX1 // 2128 // Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), mRNA. /// ENST00000222761 // downstream // 141898 // --- // --- // --- /// ENST00000313812 // downstream // 69	EVX1	EVX1, Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), p15.2
SNP_A-1871344	tctaaagtcttggaaag[C/G]ctcctgtattgccagc	C	G	NM_001989 // downstream // 162914 // Hs.369879 // EVX1 // 2128 // Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), mRNA. /// ENST00000222761 // downstream // 162914 // --- // --- // --- /// ENST00000313812 // downstream // 48	EVX1	EVX1, Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), p15.2
SNP_A-2192263	catcaggttctcttcc[C/G]cactcgagaaaatcaa	C	G	NM_152740 // intron // 0 // Hs.406758 // HIBADH // 11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// ENST00000265395 // intron // 0 // --- // --- // ---	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-1989309	aagagttacctgtttg[A/G]agtttggaatgtactt	A	G	NM_152740 // intron // 0 // Hs.406758 // HIBADH // 11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// ENST00000265395 // intron // 0 // --- // --- // ---	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-2065699	aatttatggaagtcag[A/G]aaagagatggaatcat	A	G	NM_152740 // upstream // 25247 // Hs.406758 // HIBADH // 11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// NM_006024 // upstream // 51959 // Hs.34576 // TAX1BP1 // 8887 // Homo sapiens Tax1 (human T-cell leukemia virus type I) b	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-1795079	ggtgacactcttcact[C/G]aatgaggaacagtgac	C	G	NM_152740 // upstream // 73026 // Hs.406758 // HIBADH // 11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// NM_006024 // upstream // 4180 // Hs.34576 // TAX1BP1 // 8887 // Homo sapiens Tax1 (human T-cell leukemia virus type I) bi	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-1874163	tctcatttttaaaggc[C/T]ctcttttagattgag	C	T	NM_152740 // upstream // 73292 // Hs.406758 // HIBADH // 11112 // Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), mRNA. /// NM_006024 // upstream // 3914 // Hs.34576 // TAX1BP1 // 8887 // Homo sapiens Tax1 (human T-cell leukemia virus type I) bi	HIBADH	HIBADH, Homo sapiens 3-hydroxyisobutyrate dehydrogenase (HIBADH), p15.2
SNP_A-2296951	gccaagttacaggtac[C/T]acaaccattactgtgt	C	T	NM_006024 // intron // 0 // Hs.34576 // TAX1BP1 // 8887 // Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA. /// ENST00000265393 // intron // 0 // --- // --- // ---	TAX1BP1	TAX1BP1, Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), p15.2
SNP_A-2181832	cagagcagaaaactga[C/T]aaaaactctggttaag	C	T	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // --- // --- // --- /// ENST00000355711 // intron // 0 // --- // --- // --	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.2
SNP_A-1661938	ctgggcagattggtcacaccaagaa[C/T]gaaagggacgatatt tttcttcccc	C	T	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // juxtaposed with another zinc finger gene 1	JAZF1	JAZF1 , rs757397, juxtaposed with another zinc finger gene 1,p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1645120	atagtagtttccattgtaataaatg[C/T]ggacagactaggtatttggggact	C	T	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // juxtaposed with another zinc finger gene 1	JAZF1	JAZF1 , rs735664, juxtaposed with another zinc finger gene 1,p15.2
SNP_A-2113591	aggctagtcggtcaca[A/G]agtgtcctctatgac	A	G	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // — // — // — /// ENST00000355711 // intron // 0 // — // — // –	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.2
SNP_A-2310811	ggaagccttccgtgac[C/T]gggtcaaacttctctc	C	T	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // — // — // — /// ENST00000355711 // intron // 0 // — // — // –	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2113866	aggctgtatacttcac[A/G]agcatatctgcagcc	A	G	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // — // — // — /// ENST00000355711 // intron // 0 // — // — // –	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1883943	tgaagagtcaggtgac[A/G]cattgggagagcagag	A	G	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // — // — // — /// ENST00000355711 // intron // 0 // — // — // –	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1948121	tttagattcaaaagtc[C/G]atgtaagatttgggtc	C	G	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // — // — // — /// ENST00000355711 // intron // 0 // — // — // –	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2196998	cattatcagctcatgg[C/T]cattaaatgtttaaca	C	T	NM_175061 // intron // 0 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// ENST00000283928 // intron // 0 // — // — // — /// ENST00000355711 // intron // 0 // — // — // –	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1955949	ttgtccctagctatc[C/T]acctgtgtgtacctt	C	T	NM_175061 // upstream // 99600 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 132182 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding prot	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1796433	ggtgtttaaatggaa[A/G]ctacttcagaaaataa	A	G	NM_175061 // upstream // 121248 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 110534 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding pro	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2180426	cagaacagcttcctcc[G/T]ctatataaatcacgtgt	G	T	NM_175061 // upstream // 176245 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 55537 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding prot	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1989328	gctcccacagcattca[A/G]tacatttccagagttt	A	G	NM_175061 // upstream // 180975 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 50807 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding prot	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-2120499	agtccacaaaggaaga[C/T]catttgcttgtgtgac	C	T	NM_175061 // upstream // 195465 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 36317 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding prot	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1
SNP_A-1843339	tagtcttcaaaccatat[G/T]catgcatcagaatcac	G	T	NM_175061 // upstream // 199354 // Hs.368944 // JAZF1 // 221895 // Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), mRNA. /// NM_182899 // upstream // 32428 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding prot	JAZF1	JAZF1, Homo sapiens juxtaposed with another zinc finger gene 1 (JAZF1), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1666428	atttactctgctacataaaatctg[A/C]agatggaattgtgtactatg ctctt	A	C	NM_004904 // intron // 0 // Hs.149 // CREB5 // 9586 // cAMP responsive element binding protein 5	CREB5	CREB5 , rs10486584, cAMP responsive element binding protein 5,p15.1
SNP_A-2066960	acaaacactggcctta[A/G]ctccaatatctgcgtt	A	G	NM_182899 // intron // 0 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA. /// NM_004904 // intron // 0 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), m	CREB5	CREB5, Homo sapiens cAMP responsive element binding protein 5 (CREB5), p15.1
SNP_A-1685608	agtagttagctacccagagaaatca[A/G]tactaggtacaactgc atgattgac	A	G	NM_004904 // intron // 0 // Hs.149 // CREB5 // 9586 // cAMP responsive element binding protein 5	CREB5	CREB5 , rs10486586, cAMP responsive element binding protein 5,p15.1
SNP_A-2249778	cttaatgtaccagact[A/G]catttcaaggaatttg	A	G	NM_182899 // intron // 0 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA. /// NM_004904 // intron // 0 // Hs.437075 // CREB5 // 9586 // Homo sapiens cAMP responsive element binding protein 5 (CREB5), m	CREB5	CREB5, Homo sapiens cAMP responsive element binding protein 5 (CREB5), p15.1
SNP_A-2157910	attgctcctagtattg[G/T]acctcatttaagtga	G	T	NM_004067 // intron // 0 // Hs.203663 // CHN2 // 1124 // Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // — // — // — /// ENST00000357347 // intron // 0 // — // — // — // —	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-2073362	acaggtacctgatga[C/T]gctgaccagccgactt	C	T	NM_004067 // intron // 0 // Hs.203663 // CHN2 // 1124 // Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // — // — // — /// ENST00000357347 // intron // 0 // — // — // — // —	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-1925361	ttatctcctagaatccg[A/G]actttcacccctctc	A	G	NM_004067 // intron // 0 // Hs.203663 // CHN2 // 1124 // Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // — // — // — /// ENST00000357347 // intron // 0 // — // — // — // —	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-1816061	gttacagtggcctaaa[A/G]gctatagtggtgtatg	A	G	NM_004067 // intron // 0 // Hs.203663 // CHN2 // 1124 // Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // — // — // — /// ENST00000357347 // intron // 0 // — // — // — // —	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-1658596	tggatcaatgcacatgaacttttcc[A/C]ggctttgatccatctcca actttt	A	C	NM_004067 // intron // 0 // Hs.407520 // CHN2 // 1124 // chimerin (chimaerin) 2	CHN2	CHN2 , rs722611, chimerin (chimaerin) 2,p15.1
SNP_A-2198648	catttcatcctctcat[G/T]accttcaataataaca	G	T	NM_004067 // intron // 0 // Hs.203663 // CHN2 // 1124 // Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// ENST00000222792 // intron // 0 // — // — // — /// ENST00000357347 // intron // 0 // — // — // — // —	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-1663838	gtcacaaggcagaagtggtcaaaag[C/T]agaatttaaaagaa ccaaaacaaat	C	T	NM_175887 // intron // 0 // Hs.91109 // LOC222171 // 222171 // hypothetical protein LOC222171	LOC222171	LOC222171 , rs1362355, hypothetical protein LOC222171,p15.1
SNP_A-1919521	ttaaggaaacttctg[A/G]aagcatcactcaacac	A	G	NM_004067 // downstream // 41441 // Hs.203663 // CHN2 // 1124 // Homo sapiens chimerin (chimaerin) 2 (CHN2), mRNA. /// NM_175887 // upstream // 9057 // Hs.91109 // LOC222171 // 222171 // Homo sapiens hypothetical protein LOC222171 (LOC222171), mRNA. /// E	CHN2	CHN2, Homo sapiens chimerin (chimaerin) 2 (CHN2), p15.1
SNP_A-1959483	ttttgctaaacctgca[C/T]gttctaaaagctgaat	C	T	ENST00000333076 // intron // 0 // — // — // — /// ENST00000242140 // intron // 0 // — // — // — // —	-	p15.1
SNP_A-1692496	ttttgttttgtaggggaaatggc[A/G]catttagacaagtggtctcg ggaact	A	G	NM_014766 // intron // 0 // Hs.75137 // SCRN1 // 9805 // secernin 1	SCRN1	SCRN1 , rs10488083, secernin 1,p15.1
SNP_A-2061907	aatggcagctaccaaaa[G/T]aacctatagcaaaaat	G	T	ENST00000342263 // intron // 0 // — // — // — // —	-	p15.1
SNP_A-1850190	tatgtgtatccaacca[C/T]cgttcagaagtaagaa	C	T	ENST00000324453 // intron // 0 // — // — // — /// ENST00000354415 // intron // 0 // — // — // —	-	p15.1
SNP_A-2048866	aagccctggattccaa[C/T]gtctttaacacaaatc	C	T	NM_152793 // downstream // 12835 // Hs.200100 // Ells1 // 222166 // Homo sapiens hypothetical protein Ells1 (Ells1), mRNA. /// NM_147128 // upstream // 108712 // Hs.487869 // ZNRF2 // 223082 // Homo sapiens zinc and ring finger 2 (ZNRF2), mRNA. /// ENST00	Ells1	Ells1, Homo sapiens hypothetical protein Ells1 (Ells1), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2162623	atttctctggccaa[C/T]tcggagaaggctggct	C	T	NM_152793 // downstream // 19252 // Hs.200100 // Ells1 // 222166 // Homo sapiens hypothetical protein Ells1 (Ells1), mRNA. /// NM_147128 // upstream // 102295 // Hs.487869 // ZNRF2 // 223082 // Homo sapiens zinc and ring finger 2 (ZNRF2), mRNA. /// ENST00	Ells1	Ells1, Homo sapiens hypothetical protein Ells1 (Ells1), p15.1
SNP_A-2304983	gctgaaaatcactgac[A/G]aggtagaagaatagga	A	G	NM_152793 // downstream // 27528 // Hs.200100 // Ells1 // 222166 // Homo sapiens hypothetical protein Ells1 (Ells1), mRNA. /// NM_147128 // upstream // 94019 // Hs.487869 // ZNRF2 // 223082 // Homo sapiens zinc and ring finger 2 (ZNRF2), mRNA. /// ENST000	Ells1	Ells1, Homo sapiens hypothetical protein Ells1 (Ells1), p15.1
SNP_A-2012481	tcattgtagatatcac[C/T]gctgaggctgtctgtg	C	T	NM_152793 // downstream // 97269 // Hs.200100 // Ells1 // 222166 // Homo sapiens hypothetical protein Ells1 (Ells1), mRNA. /// NM_147128 // upstream // 24278 // Hs.487869 // ZNRF2 // 223082 // Homo sapiens zinc and ring finger 2 (ZNRF2), mRNA. /// ENST000	Ells1	Ells1, Homo sapiens hypothetical protein Ells1 (Ells1), p15.1
SNP_A-2208290	cccacagacagtgtag[A/C]aattggcagcttttt	A	C	NM_147128 // intron // 0 // Hs.487869 // ZNRF2 // 223082 // Homo sapiens zinc and ring finger 2 (ZNRF2), mRNA. /// ENST00000323037 // intron // 0 // — // — // — // — /// ENST00000319243 // intron // 0 // — // — // —	ZNRF2	ZNRF2, Homo sapiens zinc and ring finger 2 (ZNRF2), p15.1
SNP_A-1683894	tctcgtaacttcaaagagtctcaaat[A/C]gtgtcaagatcctaaga caggaaac	A	C	NM_006092 // downstream // 35838 // Hs.19405 // CARD4 // 10392 // caspase recruitment domain family, member 4 /// NM_152747 // downstream // 15904 // Hs.112423 // DKFZp586I1420 // 222161 // hypothetical protein DKFZp586I1420	CARD4	CARD4, . rs9639615, caspase recruitment domain family, member 4 ,p15.1
SNP_A-1841465	taggagagctgggga[C/T]gcctctcaaggaatga	C	T	NM_006092 // intron // 0 // Hs.405153 // CARD4 // 10392 // Homo sapiens caspase recruitment domain family, member 4 (CARD4), mRNA. /// ENST00000222823 // intron // 0 // — // — // —	CARD4	CARD4, Homo sapiens caspase recruitment domain family, member 4 (CARD4), p15.1
SNP_A-1879084	tcttaatctgccaaaa[C/T]ctggcactaatctggt	C	T	NM_006092 // intron // 0 // Hs.405153 // CARD4 // 10392 // Homo sapiens caspase recruitment domain family, member 4 (CARD4), mRNA. /// ENST00000222823 // intron // 0 // — // — // —	CARD4	CARD4, Homo sapiens caspase recruitment domain family, member 4 (CARD4), p15.1
SNP_A-2132152	ataggtcttattgtccd[A/G]cggaattggttttgtc	A	G	NM_024051 // upstream // 15224 // Hs.530024 // C7orf24 // 79017 // Homo sapiens chromosome 7 open reading frame 24 (C7orf24), mRNA. /// ENST00000005374 // upstream // 15229 // — // — // — /// ENST00000275428 // upstream // 15224 // — // —	C7orf24	C7orf24, Homo sapiens chromosome 7 open reading frame 24 (C7orf24), p14.3
SNP_A-2068234	acaagatgagccccta[A/T]acgtatctaagaatgt	A	T	NM_024051 // upstream // 51417 // Hs.530024 // C7orf24 // 79017 // Homo sapiens chromosome 7 open reading frame 24 (C7orf24), mRNA. /// ENST00000005374 // upstream // 51422 // — // — // — // — /// ENST00000275428 // upstream // 51417 // — // —	C7orf24	C7orf24, Homo sapiens chromosome 7 open reading frame 24 (C7orf24), p14.3
SNP_A-1989404	agcaccatatgctgac[C/T]aggcctgaccctctt	C	T	NM_002047 // upstream // 16707 // Hs.404321 // GARS // 2617 // Homo sapiens glycyl-tRNA synthetase (GARS), mRNA. /// ENST00000355837 // upstream // 13241 // — // — // — // — /// ENST00000265296 // upstream // 16707 // — // — // — // —	GARS	GARS, Homo sapiens glycyl-tRNA synthetase (GARS), p14.3
SNP_A-2031303	aaagggaggcgaggaa[C/T]gcaagagctcagtgtc	C	T	NM_001883 // intron // 0 // Hs.546246 // CRHR2 // 1395 // Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2), mRNA. /// ENST00000222836 // intron // 0 // — // — // — // — /// ENST00000341843 // intron // 0 // — // — // — // —	CRHR2	CRHR2, Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2), p14.3
SNP_A-1789189	gggcataaaagcagtat[C/T]gtatctcagagggagt	C	T	NM_001883 // intron // 0 // Hs.546246 // CRHR2 // 1395 // Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2), mRNA. /// ENST00000222836 // intron // 0 // — // — // — // — /// ENST00000341843 // intron // 0 // — // — // — // —	CRHR2	CRHR2, Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2), p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1791820	gggtgactcaccatca[C/T]ggggccttgcattgt	C	T	NM_000823 // downstream // 24375 // Hs.767 // GHRHR // 2692 // Homo sapiens growth hormone releasing hormone receptor (GHRHR), mRNA. /// NM_001118 // upstream // 48626 // Hs.377783 // ADCYAP1R1 // 117 // Homo sapiens adenylate cydase activating polypepti	GHRHR	GHRHR, Homo sapiens growth hormone releasing hormone receptor (GHRHR), p14.3
SNP_A-2299229	gccctattgtctgaac[A/G]ctgtttttgatgtagac	A	G	NM_022728 // upstream // 32233 // Hs.45152 // NEUROD6 // 63974 // Homo sapiens neurogenic differentiation 6 (NEUROD6), mRNA. /// NM_194300 // upstream // 144207 // Hs.224269 // LOC223075 // 223075 // Homo sapiens hypothetical protein LOC223075 (LOC223075)	NEUROD6	NEUROD6, Homo sapiens neurogenic differentiation 6 (NEUROD6), p14.3
SNP_A-2179440	cactgtttgccggcac[C/T]agatttcacaggagtt	C	T	NM_022728 // upstream // 44169 // Hs.45152 // NEUROD6 // 63974 // Homo sapiens neurogenic differentiation 6 (NEUROD6), mRNA. /// NM_194300 // upstream // 132271 // Hs.224269 // LOC223075 // 223075 // Homo sapiens hypothetical protein LOC223075 (LOC223075)	NEUROD6	NEUROD6, Homo sapiens neurogenic differentiation 6 (NEUROD6), p14.3
SNP_A-1882722	tgaaacttaggcagaa[A/G]ttatgaggctgggct	A	G	NM_022728 // upstream // 44361 // Hs.45152 // NEUROD6 // 63974 // Homo sapiens neurogenic differentiation 6 (NEUROD6), mRNA. /// NM_194300 // upstream // 132079 // Hs.224269 // LOC223075 // 223075 // Homo sapiens hypothetical protein LOC223075 (LOC223075)	NEUROD6	NEUROD6, Homo sapiens neurogenic differentiation 6 (NEUROD6), p14.3
SNP_A-2183394	cagcactcctcgttcc[A/G]gctcattggacagaac	A	G	NM_022728 // upstream // 58072 // Hs.45152 // NEUROD6 // 63974 // Homo sapiens neurogenic differentiation 6 (NEUROD6), mRNA. /// NM_194300 // upstream // 118368 // Hs.224269 // LOC223075 // 223075 // Homo sapiens hypothetical protein LOC223075 (LOC223075)	NEUROD6	NEUROD6, Homo sapiens neurogenic differentiation 6 (NEUROD6), p14.3
SNP_A-1906104	tggctctggatgtgga[C/T]ggagagcaaagaaatt	C	T	NM_194300 // intron // 0 // Hs.224269 // LOC223075 // 223075 // Homo sapiens hypothetical protein LOC223075 (LOC223075), mRNA. /// ENST00000319386 // intron // 0 // — // — // —	LOC223075	LOC223075, Homo sapiens hypothetical protein LOC223075 (LOC223075), p14.3
SNP_A-2094188	agaagggattggccac[A/G]aaaaggaaagcacagg	A	G	NM_006658 // downstream // 8294 // Hs.227011 // C7orf16 // 10842 // Homo sapiens chromosome 7 open reading frame 16 (C7orf16), mRNA. /// NM_005020 // downstream // 36270 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-depend	C7orf16	C7orf16, Homo sapiens chromosome 7 open reading frame 16 (C7orf16), p14.3
SNP_A-2124994	agttgcaaatagctca[C/T]ggaagatgaagaatga	C	T	NM_005020 // intron // 0 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 // — // — // — // ENST00000284920 // intron // 0 // — // — // — // — // — // —	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2176245	caccagacataattaa[C/T]ctgtgtaactggtact	C	T	NM_005020 // intron // 0 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 // — // — // — // — // — // —	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2196703	cattaatgcataacccaa[A/G]taagtgccigtcacct	A	G	NM_005020 // intron // 0 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 // — // — // — // — // — // —	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2174650	cacagcacaggcctca[C/T]ggaaccttcagtaata	C	T	NM_005020 // intron // 0 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 // — // — // — // — // — // — // ENST00000284920 // intron // 0 // — // — // — // —	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1665596	aaacaataaatatgagaataaatat[C/G]acaaaaatgccttgac attgacaag	C	G	NM_005020 // intron // 0 // Hs.422923 // PDE1C // 5137 // phosphodiesterase 1C, calmodulin-dependent 70kDa	PDE1C	PDE1C , rs28190, phosphodiesterase 1C, calmodulin-dependent 70kDa,p14.3
SNP_A-1738230	tattgtgaaatcacagaagtgttaa[C/G]agccagttccttttttgatc atatg	C	G	NM_005020 // intron // 0 // Hs.422923 // PDE1C // 5137 // phosphodiesterase 1C, calmodulin-dependent 70kDa	PDE1C	PDE1C , rs30568, phosphodiesterase 1C, calmodulin-dependent 70kDa,p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1825742	taaatcccgaacccaa[A/G]tagtagggaccaaggt	A	G	NM_005020 // intron // 0 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 // — // — // — /// ENST00000284920 // intron // 0 // — // — // —	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1679582	tttattctttttattggaagaggtt[A/T]ggaaataaagtactagacc ttt	A	T	NM_005020 // intron // 0 // Hs.422923 // PDE1C // 5137 // phosphodiesterase 1C, calmodulin-dependent 70kDa	PDE1C	PDE1C , rs28179, phosphodiesterase 1C, calmodulin-dependent 70kDa,p14.3
SNP_A-1834283	tacatgtgaacggac[A/C]caacttttgattgac	A	C	NM_005020 // intron // 0 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// ENST00000321453 // intron // 0 // — // — // — /// ENST00000284920 // intron // 0 // — // — // —	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1800718	gtagaagcagttgtca[C/G]tccagacctcccagga	C	G	ENST00000284920 // intron // 0 // — // — // —	-	p14.3
SNP_A-2033066	aaatacactaaagaaa[G/T]acaggaaggtgagcaa	G	T	NM_005020 // upstream // 244326 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 // upstream // 243796 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmoduli	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1989443	actccaaagcttggac[C/T]ctttccagtgtcagaa	C	T	NM_005020 // upstream // 312938 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 // upstream // 312408 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmoduli	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1989444	caaggcaagcagaga[C/T]ggatgtccagtagag	C	T	NM_005020 // upstream // 331617 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 // upstream // 331087 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmoduli	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1989446	tggcctgctcacagaa[C/G]aaaggaggagcactct	C	G	NM_005020 // upstream // 376519 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 // upstream // 375989 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmoduli	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-1852087	tattggatcacaccac[A/G]agggcaggtaaaggt	A	G	NM_005020 // upstream // 408803 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA. /// NM_005020 // upstream // 408273 // Hs.487897 // PDE1C // 5137 // Homo sapiens phosphodiesterase 1C, calmoduli	PDE1C	PDE1C, Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), p14.3
SNP_A-2189022	cagtgtattccaaaat[C/G]aggagatgaaatgaag	C	G	NM_015483 // intron // 0 // Hs.372541 // KBTBD2 // 25948 // Homo sapiens kelch repeat and BTB (POZ) domain containing 2 (KBTBD2), mRNA. /// ENST00000329714 // intron // 0 // — // — // — /// ENST00000304056 // intron // 0 // — // — // —	KBTBD2	KBTBD2, Homo sapiens kelch repeat and BTB (POZ) domain containing 2 (KBTBD2), p14.3
SNP_A-1989455	taagctgtgatgaaga[C/T]gtcccgctacgctat	C	T	ENST00000329714 // intron // 0 // — // — // —	-	p14.3
SNP_A-2259916	gaaaaggggaatttcat[C/G]gagctaacgaagtggt	C	G	NM_014451 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid hormone-responsive B1 gene (	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-1702983	agataaaccaggcttcctaactgga[A/G]atagaaaattggagc ctgagattat	A	G	NM_014451 // intron // 0 // Hs.79340 // B1 // 27241 // parathyroid hormone responsive B1 gene	B1	B1 , rs10486523, parathyroid hormone-responsive B1 gene,p14.3
SNP_A-2253449	cttcttactcacttta[C/G]gaatgggacacaatga	C	G	NM_014451 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid hormone-responsive B1 gene (	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-1676350	gatctgcaagttggcatcaggaaaaa[C/T]aaattctgtagtactct gtattaac	G	T	NM_014451 // intron // 0 // Hs.79340 // B1 // 27241 // parathyroid hormone responsive B1 gene	B1	B1 , rs6971826, parathyroid hormone-responsive B1 gene,p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225830	ctaaataccagatcaa[C/G]caagtggcttattaga	C	G	NM_014451 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, mRNA. /// NM_198428 // intron // 0 // Hs.372360 // B1 // 27241 // Homo sapiens parathyroid hormone-responsive B1 gene (	B1	B1, Homo sapiens parathyroid hormone-responsive B1 gene (B1), transcript variant 1, p14.3
SNP_A-1748881	ataggctagaatattatatagtcat[A/G]aaaaaaatacctgtatca aaaaatat	A	G	NM_014451 // downstream // 55141 // Hs.79340 // B1 // 27241 // parathyroid hormone-responsive B1 gene /// NM_017937 // upstream // 64774 // - // - // -	B1	B1 , rs2034514, parathyroid hormone-responsive B1 gene ,p14.3
SNP_A-2220092	ccttcacacctcttc[A/C]acctcctctctttgc	A	C	NM_133468 // upstream // 124536 // Hs.209226 // BMPER // 168667 // Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), mRNA. /// ENST00000311067 // downstream // 51926 // --- // --- // --- /// ENST00000297161 // upstream // 12	BMPER	BMPER, Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), p14.3
SNP_A-2161637	atttgggaatatctca[A/T]ccgttcaaatgccctg	A	T	NM_133468 // upstream // 101017 // Hs.209226 // BMPER // 168667 // Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), mRNA. /// ENST00000311067 // downstream // 75445 // --- // --- // --- /// ENST00000297161 // upstream // 10	BMPER	BMPER, Homo sapiens BMP-binding endothelial regulator precursor protein (BMPER), p14.3
SNP_A-1989507	gggaatccatctctat[C/T]gcatggcagccttacc	C	T	NM_207288 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant IX, mRNA. /// NM_	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-1945539	ttgttccctcatatca[C/G]agtagcaaacaggtca	C	G	NM_207288 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant IX, mRNA. /// NM_	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-2138315	atccagagtccactga[A/G]tcactttccgtacag	A	G	NM_207288 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant IX, mRNA. /// NM_	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-2055805	aatacaaaaattcgag[A/G]atgcttaagtccctta	A	G	NM_207288 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant VI, mRNA. /// NM_207283 // intron // 0 // Hs.487951 // AAA1 // 404744 // Homo sapiens AAA1 protein (AAA1), transcript variant IX, mRNA. /// NM_	AAA1	AAA1, Homo sapiens AAA1 protein (AAA1), transcript variant VI, p14.3
SNP_A-2183341	cagcaccatggggtcc[A/G]ccagatcatatgcctc	A	G	NM_207172 // intron // 0 // Hs.453723 // GPR154 // 387129 // Homo sapiens G protein-coupled receptor 154 (GPR154), transcript variant 1, mRNA. /// NM_207173 // intron // 0 // Hs.453723 // GPR154 // 387129 // Homo sapiens G protein-coupled receptor 154 (GP	GPR154	GPR154, Homo sapiens G protein-coupled receptor 154 (GPR154), transcript variant 1, p14.3
SNP_A-1989513	taacatcaaggactc[A/G]agtttccaaatgcagg	A	G	NM_207172 // intron // 0 // Hs.453723 // GPR154 // 387129 // Homo sapiens G protein-coupled receptor 154 (GPR154), transcript variant 1, mRNA. /// NM_207173 // intron // 0 // Hs.453723 // GPR154 // 387129 // Homo sapiens G protein-coupled receptor 154 (GP	GPR154	GPR154, Homo sapiens G protein-coupled receptor 154 (GPR154), transcript variant 1, p14.3
SNP_A-2080081	accgccttaatcatga[C/G]acatctagaagacctt	C	G	NM_207172 // intron // 0 // Hs.453723 // GPR154 // 387129 // Homo sapiens G protein-coupled receptor 154 (GPR154), transcript variant 1, mRNA. /// NM_207173 // intron // 0 // Hs.453723 // GPR154 // 387129 // Homo sapiens G protein-coupled receptor 154 (GP	GPR154	GPR154, Homo sapiens G protein-coupled receptor 154 (GPR154), transcript variant 1, p14.3
SNP_A-2225076	cgtgtgcctaattaaa[G/T]cctagtcatcctcac	G	T	ENST00000310974 // intron // 0 // --- // --- // ---	-	p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253527	cttcttctagaacaga[A/G]atctgaccaagttagt	A	G	NM_020417 // upstream // 7319 // Hs.404167 // TBX20 // 57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 371711 // Hs.424711 // FLJ22313 // 64224 // Homo sapiens hypothetical protein FLJ22313 (FLJ22313), mRNA. /// ENST00000029705	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2302035	gcgtgggacttttagat[C/T]aagtggctagaagtgc	C	T	NM_020417 // upstream // 118799 // Hs.404167 // TBX20 // 57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 260231 // Hs.424711 // FLJ22313 // 64224 // Homo sapiens hypothetical protein FLJ22313 (FLJ22313), mRNA. /// ENST00000297	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2124522	agttccacggctaaaa[A/T]gaattctgaaaatcac	A	T	NM_020417 // upstream // 148268 // Hs.404167 // TBX20 // 57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 230762 // Hs.424711 // FLJ22313 // 64224 // Homo sapiens hypothetical protein FLJ22313 (FLJ22313), mRNA. /// ENST00000297	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-2160301	atttcagaggcctggd[A/C]ataaagcactggagaa	A	C	NM_020417 // upstream // 170553 // Hs.404167 // TBX20 // 57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 208477 // Hs.424711 // FLJ22313 // 64224 // Homo sapiens hypothetical protein FLJ22313 (FLJ22313), mRNA. /// ENST00000297	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-1922403	ttagaaagtgatggaa[C/T]ggaacccatggtcatg	C	T	NM_020417 // upstream // 238168 // Hs.404167 // TBX20 // 57057 // Homo sapiens T-box 20 (TBX20), mRNA. /// NM_022373 // downstream // 140862 // Hs.424711 // FLJ22313 // 64224 // Homo sapiens hypothetical protein FLJ22313 (FLJ22313), mRNA. /// ENST00000297	TBX20	TBX20, Homo sapiens T-box 20 (TBX20), p14.2
SNP_A-1804825	gtcagtggaatctgca[C/T]ggtcttggcgaggtct	C	T	NM_001788 // intron // 0 // Hs.191346 // SEPT7 // 989 // Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), mRNA. /// ENST00000350320 // intron // 0 // — // — // —	SEPT7	SEPT7, Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), p14.2
SNP_A-2229940	ctagtttgagttaca[C/T]gaatcagaaaaagtag	C	T	NM_001788 // intron // 0 // Hs.191346 // SEPT7 // 989 // Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), mRNA. /// ENST00000350320 // intron // 0 // — // — // — // —	SEPT7	SEPT7, Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), p14.2
SNP_A-2075205	acatctcttttttcga[A/C]cccaacatgaaaccac	A	C	NM_001788 // intron // 0 // Hs.191346 // SEPT7 // 989 // Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), mRNA. /// ENST00000350320 // intron // 0 // — // — // — // —	SEPT7	SEPT7, Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), p14.2
SNP_A-2304239	gctcctcaacgctggt[C/T]cagaaagaatatcaca	C	T	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-2079822	accctcacattcatat[G/T]gtcctagaagatgaat	G	T	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-1803737	gtcaacacacacatca[A/G]tcattacagatagtgg	A	G	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-2031964	aaagtctcatttacca[C/T]gttgagttgaagttc	C	T	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-2301378	gccttgcttacctgg[C/T]attctgtaaattctga	C	T	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-1945390	ttgttatatttagcag[A/G]ccaaacatgttaata	A	G	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235247	ctcccggaccctgta[C/G]gtcaaaagcctctgac	C	G	NM_030636 // intron // 0 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// ENST00000242108 // intron // 0 // — // — // —	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-2088796	actgttacatcttcat[G/T]aaaatatggtcctaca	G	T	NM_030636 // downstream // 18241 // Hs.487994 // KIAA1706 // 80820 // Homo sapiens KIAA1706 protein (KIAA1706), mRNA. /// NM_018685 // upstream // 70045 // Hs.62180 // ANLN // 54443 // Homo sapiens anillin, actin binding protein (scraps homolog, Drosophil	KIAA1706	KIAA1706, Homo sapiens KIAA1706 protein (KIAA1706), p14.2
SNP_A-1844619	tataacctctcctta[C/T]gtaaacaacaatgtg	C	T	NM_018685 // downstream // 31238 // Hs.62180 // ANLN // 54443 // Homo sapiens anillin, actin binding protein (scraps homolog, Drosophila) (ANLN), mRNA. /// NM_001637 // downstream // 27974 // Hs.488007 // AOAH // 313 // Homo sapiens acyloxyacyl hydrolase	ANLN	ANLN, Homo sapiens anillin, actin binding protein (scraps homolog, Drosophila) (ANLN), p14.2
SNP_A-2252900	ctctatttcacttaa[G/T]acctcatctactgttt	G	T	NM_001637 // intron // 0 // Hs.488007 // AOAH // 313 // Homo sapiens acyloxyacyl hydrolase (neutrophil) (AOAH), mRNA. /// ENST00000258749 // intron // 0 // — // — // —	AOAH	AOAH, Homo sapiens acyloxyacyl hydrolase (neutrophil) (AOAH), p14.2
SNP_A-1660861	tttcacaagaaaacagcacttaag[C/G]ctctatatataatcact gttact	C	G	NM_014800 // intron // 0 // Hs.444695 // ELMO1 // 9844 // engulfment and cell motility 1 (ced-12 homolog, C. elegans)	ELMO1	ELMO1 , rs1986568, engulfment and cell motility 1 (ced-12 homolog, C. elegans),p14.1
SNP_A-2210123	ccccaggagcttctta[C/G]acatggactttgctgt	C	G	NM_014800 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment a	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.1
SNP_A-1785701	ggctctaatgtgcaaa[C/T]agattgtgtgaatttt	C	T	NM_014800 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment a	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.1
SNP_A-1812669	gtggcttcagaaatga[C/G]ggaacacggtgtgttc	C	G	NM_014800 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment a	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.1
SNP_A-2055053	aataaattcctcatta[C/T]gctaaatcagcttgag	C	T	NM_014800 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, mRNA. /// NM_130442 // intron // 0 // Hs.304578 // ELMO1 // 9844 // Homo sapiens engulfment a	ELMO1	ELMO1, Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), transcript variant 1, p14.1
SNP_A-1744095	ggctagagatggaccactattagaa[A/C]agaaaaacaaagaag aggtaataaga	A	C	NM_016616 // intron // 0 // Hs.134079 // TXNDC3 // 51314 // thioredoxin domain containing 3 (spermatozoa)	TXNDC3	TXNDC3 , rs1530822, thioredoxin domain containing 3 (spermatozoa),p14.1
SNP_A-1660307	gaatgcctctgcattgagtagagtaa[A/G]tgctcaggatgactcag gctgtttc	A	G	NM_016616 // intron // 0 // Hs.134079 // TXNDC3 // 51314 // thioredoxin domain containing 3 (spermatozoa)	TXNDC3	TXNDC3 , rs1349392, thioredoxin domain containing 3 (spermatozoa),p14.1
SNP_A-1989590	atcagcttcatgccaa[A/G]atggaagatgcgtgag	A	G	NM_016616 // intron // 0 // Hs.134079 // TXNDC3 // 51314 // Homo sapiens thioredoxin domain containing 3 (spermatozoa) (TXNDC3), mRNA. /// ENST00000199447 // intron // 0 // — // — // —	TXNDC3	TXNDC3, Homo sapiens thioredoxin domain containing 3 (spermatozoa) (TXNDC3), p14.1
SNP_A-1948890	tttatcatatctgaag[A/T]caggtgatgtaccttc	A	T	NM_017549 // intron // 0 // Hs.416007 // EPDR1 // 54749 // Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), mRNA. /// ENST00000199448 // intron // 0 // — // — // —	EPDR1	EPDR1, Homo sapiens upregulated in colorectal cancer gene 1 (UCC1), p14.1
SNP_A-2043344	aactggaggagatatc[A/G]acatgaaatgaactca	A	G	NM_001003806 // intron // 0 // Hs.534032 // TARP // 445347 // Homo sapiens TCR gamma alternate reading frame protein (TARP), nuclear gene encoding mitochondrial protein, transcript variant 2 /// ENST00000339749 // intron // 0 // — // — // — // —	TARP	TARP, Homo sapiens TCR gamma alternate reading frame protein (TARP), nuclear gene encoding mitochondrial protein, transcript variant 2 p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2182538	cagatatgttacaata[C/T]agtccagtggatctc	C	T	NM_001003806 // intron // 0 // Hs.534032 // TARP // 445347 // Homo sapiens TCR gamma alternate reading frame protein (TARP), nuclear gene encoding mitochondrial protein, transcript variant 2 /// ENST00000339749 // intron // 0 // --- // --- // --- // --- /	TARP	TARP, Homo sapiens TCR gamma alternate reading frame protein (TARP), nuclear gene encoding mitochondrial protein, transcript variant 2 p14.1
SNP_A-1828787	taaggaaagtacaaac[A/G]ccaatgaaaattatt	A	G	NM_139316 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphip	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-1817180	gttcaatctaactgta[C/T]gttgcatccactaac	C	T	NM_139316 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphip	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-2132068	ataggcaaaggagaa[C/G]acttgcacctgtattt	C	G	NM_139316 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphip	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-2022820	aaaacaaaaagctta[A/C]gccgcttgaggagggg	A	C	NM_139316 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphip	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-1820534	gttattgcatggcaa[A/T]ttatttcaaaattat	A	T	NM_139316 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphip	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-2044216	aacttttcatgatgaca[A/G]attcctgttaaatgga	A	G	NM_139316 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, mRNA. /// NM_001635 // intron // 0 // Hs.546233 // AMPH // 273 // Homo sapiens amphip	AMPH	AMPH, Homo sapiens amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) (AMPH), transcript variant 2, p14.1
SNP_A-1989624	ttataaaacattatca[A/G]tctcctcggaatcatt	A	G	NM_014396 // intron // 0 // Hs.148721 // VPS41 // 27072 // Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA. /// NM_080631 // intron // 0 // Hs.148721 // VPS41 // 27072 // Homo sapiens vacuolar protein sorting 41 (yeast	VPS41	VPS41, Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, p14.1
SNP_A-2259639	gaaaactgagatccaa[C/T]aatgaaagtaactaag	C	T	NM_014396 // intron // 0 // Hs.148721 // VPS41 // 27072 // Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA. /// NM_080631 // intron // 0 // Hs.148721 // VPS41 // 27072 // Homo sapiens vacuolar protein sorting 41 (yeast	VPS41	VPS41, Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, p14.1
SNP_A-1911527	tgtcttgaagtgtca[A/G]tgaaaactacagtatc	A	G	NM_020192 // upstream // 94833 // Hs.83313 // C7orf36 // 57002 // Homo sapiens chromosome 7 open reading frame 36 (C7orf36), mRNA. /// ENST00000341194 // downstream // 6786 // --- // --- // --- // --- /// ENST00000223273 // upstream // 94833 // --- // ---	C7orf36	C7orf36, Homo sapiens chromosome 7 open reading frame 36 (C7orf36), p14.1
SNP_A-2102662	agatttaggctctcca[C/G]ataagaaaacaattcc	C	G	NM_020192 // upstream // 94617 // Hs.83313 // C7orf36 // 57002 // Homo sapiens chromosome 7 open reading frame 36 (C7orf36), mRNA. /// ENST00000341194 // downstream // 7002 // --- // --- // --- // --- /// ENST00000223273 // upstream // 94617 // --- // ---	C7orf36	C7orf36, Homo sapiens chromosome 7 open reading frame 36 (C7orf36), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2297909	gccagtcccgtgatat[G/T]atcttcatcctgacct	G	T	NM_020192 // upstream // 91903 // Hs.83313 // C7orf36 // 57002 // Homo sapiens chromosome 7 open reading frame 36 (C7orf36), mRNA. /// ENST00000341194 // downstream // 9716 /// --- /// --- /// --- /// ENST00000223273 // upstream // 91903 /// --- /// ---	C7orf36	C7orf36, Homo sapiens chromosome 7 open reading frame 36 (C7orf36), p14.1
SNP_A-2083805	actaccatttttaca[C/T]gctgccatggctgtt	C	T	NM_020192 // upstream // 91817 // Hs.83313 // C7orf36 // 57002 // Homo sapiens chromosome 7 open reading frame 36 (C7orf36), mRNA. /// ENST00000341194 // downstream // 9802 /// --- /// --- /// --- /// ENST00000223273 // upstream // 91817 /// --- /// ---	C7orf36	C7orf36, Homo sapiens chromosome 7 open reading frame 36 (C7orf36), p14.1
SNP_A-2061583	aatgcttagaacgtgca[A/G]acaaaattacattca	A	G	NM_031267 // upstream // 105100 // Hs.233552 // CDC2L5 // 8621 // Homo sapiens cell division cycle 2-like 5 (cholinesterase-related cell division controller) (CDC2L5), transcript variant 2, mRNA /// NM_003718 // upstream // 105100 // Hs.233552 // CDC2L5 /	CDC2L5	CDC2L5, Homo sapiens cell division cycle 2-like 5 (cholinesterase-related cell division controller) (CDC2L5), transcript variant 2, p14.1
SNP_A-2101278	agatccttttggctc[C/T]caaatcatccatataa	C	T	NM_031267 // intron // 0 // Hs.233552 // CDC2L5 // 8621 // Homo sapiens cell division cycle 2-like 5 (cholinesterase-related cell division controller) (CDC2L5), transcript variant 2, mRNA /// NM_003718 // intron // 0 // Hs.233552 // CDC2L5 // 8621 // Homo	CDC2L5	CDC2L5, Homo sapiens cell division cycle 2-like 5 (cholinesterase-related cell division controller) (CDC2L5), transcript variant 2, p14.1
SNP_A-1905379	tggtaacttgaccaa[G/T]gaatgacagctaccat	G	T	NM_024728 // intron // 0 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // --- // --- /// ENST00000335693 // intron // 0 // --- // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1989669	tacttacacagggaa[C/T]gactgactgtttacag	C	T	NM_024728 // intron // 0 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // --- // --- /// ENST00000335693 // intron // 0 // --- // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2012536	tggaacgagtgaaaca[A/G]ggaaagactctgaagg	A	G	NM_024728 // intron // 0 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // --- // --- /// ENST00000335693 // intron // 0 // --- // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1855160	tcaagatcaggagacal[A/G]ggtgttcgctatatgg	A	G	NM_024728 // intron // 0 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // --- // --- /// ENST00000335693 // intron // 0 // --- // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2185100	cagctttatcattgd[A/G]cagcctgcatcccaac	A	G	NM_024728 // intron // 0 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// ENST00000309930 // intron // 0 // --- // --- // --- /// ENST00000335693 // intron // 0 // --- // --- // ---	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1989679	gtgctaagcagaataq[A/T]aaagatgtgagaca	A	T	NM_024728 // downstream // 14418 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 814015 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2254055	cttgaggaacacaaga[C/G]ggataaaacactaaca	C	G	NM_024728 // downstream // 122404 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 706029 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1904342	tgggctgtgtttcaa[C/G]aggttaaggcattctt	C	G	NM_024728 // downstream // 131718 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 696715 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2225794	ctaaagtccgctaccc[C/G]aaacttcctggagag	C	G	NM_024728 // downstream // 138943 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 689490 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1900501	tggagcctgtgccca[A/G]atctagtagggtctc	A	G	NM_024728 // downstream // 171218 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 657215 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1957422	ttttagtaacctggga[C/T]aagtgacttcgacctct	C	T	NM_024728 // downstream // 176258 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 652175 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1903498	tgggaatgaaaatgta[C/T]aatttgcagctctta	C	T	NM_024728 // downstream // 222004 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 606429 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2032297	aaagttagctctagaa[C/T]gtagattggagttca	C	T	NM_024728 // downstream // 223095 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 605338 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2162908	attttggtctgccctg[C/T]aaaaactgtcatatta	C	T	NM_024728 // downstream // 248263 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 580170 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2063897	aattatacattggtca[A/G]aggaagaaagttgaat	A	G	NM_024728 // downstream // 248871 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 579562 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1796181	ggtgtcctaggcaata[A/G]ccaatcatagatgaat	A	G	NM_024728 // downstream // 293296 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 535137 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2219616	cctgttttctagctaa[A/G]atcagtaaggagaggt	A	G	NM_024728 // downstream // 328874 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 499559 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-2145240	atgcacaccaaatacc[G/T]ggtagaggaaagataa	G	T	NM_024728 // downstream // 493826 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 334607 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1
SNP_A-1989694	tctgacttgtaatca[A/G]ccctattcataagaac	A	G	NM_024728 // downstream // 578251 // Hs.161916 // C7orf10 // 79783 // Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA. /// NM_002192 // downstream // 250182 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin A	C7orf10	C7orf10, Homo sapiens chromosome 7 open reading frame 10 (C7orf10), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1697583	tgtttctagcctagatgtctctctc[A/G]atgtccatagaaaactcaagtttagt	A	G	NM_000168 // downstream // 220579 // Hs.72916 // GLI3 // 2737 // GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) /// NM_002192 // upstream // 43042 // Hs.368667 // INHBA // 3624 // inhibin, beta A (activin A, activin AB alpha polype	GLI3	GLI3 , rs713290, GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) ,p14.1
SNP_A-1750471	ggatttccatttgctctgtaggtga[C/T]gataggatatttgaagacttaaaga	C	T	NM_000168 // downstream // 218820 // Hs.72916 // GLI3 // 2737 // GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) /// NM_002192 // upstream // 44801 // Hs.368667 // INHBA // 3624 // inhibin, beta A (activin A, activin AB alpha polype	GLI3	GLI3 , rs10486721, GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) ,p14.1
SNP_A-2290216	gcaaatgaaggctca[A/G]ggtaggaatttaatgc	A	G	NM_002192 // upstream // 19150 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 16534 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1817574	gttccaaatttagtaa[A/G]agtctgccctgcagaa	A	G	NM_002192 // upstream // 19941 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 17325 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2311219	ggaagtttctgtaata[A/G]aagcaggagaaaataa	A	G	NM_002192 // upstream // 21958 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 19342 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2281594	gagtcggtaagaatga[A/G]tcattaggctgttgta	A	G	NM_002192 // upstream // 32747 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 30131 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1989707	cctgcctggaccttcg[C/T]tatcctctctaacta	C	T	NM_002192 // upstream // 35689 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 33073 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1840323	tagcatctaacataag[A/C]ctagattcagcatata	A	C	NM_002192 // upstream // 36818 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 34202 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1822444	gtttttattgagacga[C/G]cacttagcccaagaca	C	G	NM_002192 // upstream // 37182 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 34566 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1849758	tatgtaactggtggta[A/G]cttgaactggtagga	A	G	NM_002192 // upstream // 61195 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 58579 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1989708	ataaaacagtttacca[A/G]agaatacaagtataat	A	G	NM_002192 // upstream // 71849 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 69233 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1816585	gttgaaataaattgac[C/G]aaaattgaaaacagta	C	G	NM_002192 // upstream // 81897 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 79281 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2238054	ctctgcaatagtataa[A/T]ttagccattaggactg	A	T	NM_002192 // upstream // 88255 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 85639 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2059041	aatcccatagttggaa[A/G]aaaagccaatttggaa	A	G	NM_002192 // upstream // 88468 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 85852 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-1989712	aacctgtactaagaga[A/G]gccaggagagtatcta	A	G	NM_002192 // upstream // 233285 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA. /// NM_002192 // upstream // 230669 // Hs.28792 // INHBA // 3624 // Homo sapiens inhibin, beta A (activin	INHBA	INHBA, Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), p14.1
SNP_A-2025584	aaaatgaaaaacgagc[A/G]cttctcagcttggaa	A	G	NM_000168 // intron // 0 // Hs.199338 // GLI3 // 2737 // Homo sapiens GLI Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// ENST00000265526 // intron // 0 // — // — // — /// ENST00000342298 // intron // 0 //	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-2199358	catttgcaaggttta[C/G]gcagctatagcatttt	C	G	NM_000168 // intron // 0 // Hs.199338 // GLI3 // 2737 // Homo sapiens GLI Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// ENST00000265526 // intron // 0 // — // — // — /// ENST00000342298 // intron // 0 //	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-1989721	atcaaaacactaatag[A/G]atccataaacacagac	A	G	NM_000168 // intron // 0 // Hs.199338 // GLI3 // 2737 // Homo sapiens GLI Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// ENST00000265526 // intron // 0 // — // — // — /// ENST00000342298 // intron // 0 //	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-1838600	tagacaaaaagttcta[C/T]ggaagtcgaaatgtca	C	T	NM_000168 // upstream // 241796 // Hs.199338 // GLI3 // 2737 // Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA. /// NM_024054 // downstream // 444183 // Hs.214247 // C7orf25 // 79020 // Homo sapiens chromos	GLI3	GLI3, Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), p14.1
SNP_A-2164167	caaaaggttgatagtg[A/G]aagacagtgtagggat	A	G	NM_031903 // downstream // 74474 // Hs.50252 // MRPL32 // 64983 // Homo sapiens mitochondrial ribosomal protein L32 (MRPL32), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000223324 // downstream // 74474 // — // — // — /// ENS	MRPL32	MRPL32, Homo sapiens mitochondrial ribosomal protein L32 (MRPL32), nuclear gene encoding mitochondrial protein, p14.1
SNP_A-2289399	gattttcacattacа[C/T]ccttgttctacttat	C	T	NM_031903 // downstream // 98623 // Hs.50252 // MRPL32 // 64983 // Homo sapiens mitochondrial ribosomal protein L32 (MRPL32), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000223324 // downstream // 98623 // — // — // — /// ENS	MRPL32	MRPL32, Homo sapiens mitochondrial ribosomal protein L32 (MRPL32), nuclear gene encoding mitochondrial protein, p14.1
SNP_A-1854224	tcaaagccacctcaca[C/T]acaaaatgaatctctt	C	T	NM_015052 // intron // 0 // Hs.164453 // HECW1 // 23072 // Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// ENST00000265522 // intron // 0 // — // — // —	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p13
SNP_A-2259939	gaaaagtacttcataa[C/T]gctaagttctattac	C	T	NM_015052 // intron // 0 // Hs.164453 // HECW1 // 23072 // Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// ENST00000265522 // intron // 0 // — // — // —	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1942349	ttggccattgtcaatt[G/T]aaactaaagagtagct	G	T	NM_015052 // downstream // 6654 // Hs.164453 // HECW1 // 23072 // Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), mRNA. /// NM_004760 // upstream // 13134 // Hs.268887 // STK17A // 9263 // Homo sapiens serine/threonine kinase 17a (apoptosis-in	HECW1	HECW1, Homo sapiens NEDD4-like ubiquitin-protein ligase 1 (NEDL1), p13
SNP_A-2227332	ctacaaggaaacatgg[A/G]atgtatgagtggtggg	A	G	NM_182547 // intron // 0 // Hs.510745 // TMED4 // 222068 // Homo sapiens putative NFkB activating protein HNLF (HNLF), mRNA. /// ENST00000289577 // intron // 0 // --- // --- // --- // ---	TMED4	TMED4, Homo sapiens putative NFkB activating protein HNLF (HNLF), p13
SNP_A-1989767	caaaggtttgcaggaa[A/C]gcttttgacatatggg	A	C	NM_004749 // intron // 0 // Hs.231411 // TBRG4 // 9238 // Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, mRNA. /// ENST00000355752 // intron // 0 // --- // --- // --- // --- /// ENST00000360042 // intron // 0 // --	TBRG4	TBRG4, Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, p13
SNP_A-2045798	aagacagcatgagcta[C/T]aatacggaaaatgctt	C	T	NM_005856 // downstream // 358929 // Hs.25691 // RAMP3 // 10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream // 31345 // Hs.192215 // ADCY1 // 107 // Homo sapiens adenylate cyclase 1 (brain) (	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13
SNP_A-1960310	tttttacttattagag[A/G]aaacatgaacatctat	A	G	NM_005856 // downstream // 359011 // Hs.25691 // RAMP3 // 10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream // 31263 // Hs.192215 // ADCY1 // 107 // Homo sapiens adenylate cyclase 1 (brain) (	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13
SNP_A-2141047	atctgccggacaaggg[G/T]agtatattagtcaggg	G	T	NM_005856 // downstream // 382151 // Hs.25691 // RAMP3 // 10268 // Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA. /// NM_021116 // upstream // 8123 // Hs.192215 // ADCY1 // 107 // Homo sapiens adenylate cyclase 1 (brain) (A	RAMP3	RAMP3, Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), p13
SNP_A-1732502	aattatttttttatgaaatagacatg[A/G]aaatttatgtaaaacctact aatgc	A	G	NM_000598 // upstream // 207698 // Hs.450230 // IGFBP3 // 3486 // insulin-like growth factor binding protein 3 /// NM_018510 // upstream // 652456 // - // - // - // -	IGFBP3	IGFBP3 , -, insulin-like growth factor binding protein 3 ,p13
SNP_A-1732588	attggttttcatcttattattattc[C/T]ataaatggcattagtaggtttta ca	C	T	NM_000598 // upstream // 207731 // Hs.450230 // IGFBP3 // 3486 // insulin-like growth factor binding protein 3 /// NM_018510 // upstream // 652423 // - // - // - // -	IGFBP3	IGFBP3 , rs11766636, insulin-like growth factor binding protein 3 ,p13
SNP_A-1681616	aatatttcttctcttaagacatcat[A/G]agaatacaaattacaatcc attttt	A	G	NM_000598 // upstream // 209028 // Hs.450230 // IGFBP3 // 3486 // insulin-like growth factor binding protein 3 /// NM_018510 // upstream // 651126 // - // - // - // -	IGFBP3	IGFBP3 , rs10255992, insulin-like growth factor binding protein 3 ,p13
SNP_A-2201351	ccaatcatctgttgac[G/T]ctgagctggaaatgtc	G	T	ENST00000297318 // upstream // 453780 // --- // --- // --- // --- /// ENST00000321536 // upstream // 326925 // --- // --- // --- // ---	-	p13
SNP_A-2056366	aatacttggagtaaaa[G/T]agtttctggccacagt	G	T	NM_032102 // upstream // 199103 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// ENST00000321536 // downstream // 70271 // --- // --- // --- // --- /// ENST00000328370 // upstream // 199103 // -	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-1666916	tcaaaattgaacagactgggaacac[C/T]gtgaaggcttcatca gggtattttg	C	T	NM_018510 // downstream // 192385 // - // - // - // - /// NM_022748 // downstream // 299351 // Hs.12210 // TENS1 // 64759 // tensin-like SH2 domain containing 1	-	- , rs6945120, - ,p13
SNP_A-1989805	taaaaatcatcacagt[A/T]aaaatatgcttctgtg	A	T	NM_032102 // upstream // 78599 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// ENST00000321536 // downstream // 190775 // --- // --- // --- // --- /// ENST00000328370 // upstream // 78599 // --	SRP46	SRP46, Homo sapiens Splicing factor, arginine p13
SNP_A-1905904	tggtccaaattttcta[A/T]cctgacatcatgttca	A	T	NM_032102 // downstream // 12654 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 208828 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1643946	tagtaaataaaagttggaataaaata[A/C]gtttgtcatttatatatacaggta	A	C	NM_018510 // downstream // 368333 // - // - // - /// NM_022748 // downstream // 123403 // Hs.12210 // TENS1 // 64759 // tensin-like SH2 domain containing 1	-	- , rs2728481, - ,p13
SNP_A-1914167	tgtgtgtgtctgtgta[C/T]aagggtgggagcaatt	C	T	NM_032102 // downstream // 70873 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 150609 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-1841124	tagctgatctctcca[C/T]gctatttcaccccca	C	T	NM_032102 // downstream // 74650 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 146832 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-2061617	aatgctgtgtgtgta[C/T]gctagctaggtaattc	C	T	NM_032102 // downstream // 96478 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 125004 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-1719149	ctgatacagaagttcaatttttaa[A/G]gacatgttcaatttatttcttttttca	A	G	NM_018510 // downstream // 438546 // - // - // - /// NM_022748 // downstream // 53190 // Hs.12210 // TENS1 // 64759 // tensin-like SH2 domain containing 1	-	- , rs2248842, - ,p13
SNP_A-2022745	aaaaattcaggtaaaa[G/T]ccttgaatctgaaatc	G	T	NM_032102 // downstream // 160169 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 61313 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-2171982	caatgctaaaggtttc[A/G]ctataagagggtcgtga	A	G	NM_032102 // downstream // 164060 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 57422 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-2079626	accctaacatccatga[A/G]gcaactgggccacagg	A	G	NM_032102 // downstream // 165229 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 56253 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-1989814	ctctccatttaacttta[C/T]gttcaactgcaataac	C	T	NM_032102 // downstream // 166788 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 54694 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-2012565	aatctcagtctacaaa[C/T]tgctacacctgcaaaa	C	T	NM_032102 // downstream // 178109 // Hs.476680 // SRP46 // 10929 // Homo sapiens Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA. /// NM_022748 // downstream // 43373 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containi	SRP46	SRP46, Homo sapiens Splicing factor, arginine,p13
SNP_A-2067338	acaaagttcactgcaa[A/C]ataagctgtagtgaa	A	C	NM_022748 // intron // 0 // Hs.520814 // TENS1 // 64759 // Homo sapiens tensin-like SH2 domain containing 1 (TENS1), mRNA. /// ENST00000355730 // intron // 0 // — // — // — // — /// ENST00000275514 // intron // 0 // — // — // — // —	TENS1	TENS1, Homo sapiens tensin-like SH2 domain containing 1 (TENS1), p12.3
SNP_A-2313845	ggagccagagaggtaq[C/G]atgtgccggagtgaca	C	G	NM_138295 // intron // 0 // Hs.195979 // PKD1L1 // 168507 // Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // — // — // — // —	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3
SNP_A-2022246	aaaaagtacaacctga[A/G]gtttgcagaaaggcat	A	G	NM_138295 // intron // 0 // Hs.195979 // PKD1L1 // 168507 // Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // — // — // — // —	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2088193	actggtaagattatta[A/G]agcctgaagtctgaac	A	G	NM_138295 // intron // 0 // Hs.195979 // PKD1L1 // 168507 // Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // — // — // — // —	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3
SNP_A-2036677	aaattgtccataacca[A/G]tattctgcagacttaa	A	G	NM_138295 // intron // 0 // Hs.195979 // PKD1L1 // 168507 // Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA. /// ENST00000289672 // intron // 0 // — // — // — // —	PKD1L1	PKD1L1, Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), p12.3
SNP_A-1955787	tttgtaggaccatttc[A/G]aactatgtcaaagaag	A	G	ENST00000297327 // intron // 0 // — // — // — // — /// ENST00000348904 // intron // 0 // — // — // — // —	-	p12.3
SNP_A-2073969	acagttcaggttcttc[A/G]acagagagtttgtaaa	A	G	NM_152701 // intron // 0 // Hs.226568 // ABCA13 // 154664 // Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // intron // 0 // — // — // — // —	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-1951055	tttccagttttgtcca[G/T]tccatcccagatgcac	G	T	NM_152701 // downstream // 262143 // Hs.226568 // ABCA13 // 154664 // Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // downstream // 262143 // — // — // — // — /// ENST00000336627 // dow	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-2198458	catttaggatccatta[A/G]aagttggaggttgtga	A	G	NM_152701 // downstream // 276659 // Hs.226568 // ABCA13 // 154664 // Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), mRNA. /// ENST00000319379 // downstream // 276659 // — // — // — // — /// ENST00000336627 // dow	ABCA13	ABCA13, Homo sapiens ATP binding cassette gene, sub-family A (ABC1), member 13 (ABCA13), p12.3
SNP_A-2052540	aagtagtaaatcattg[A/G]caaatacttggtagtt	A	G	NM_198570 // upstream // 750948 // Hs.455185 // UNQ739 // 375567 // Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000324993 // downstream // 95260 // — // — // — // — /// ENST00000340652 // upstream // 750948 // — // — // — // —	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-1863885	tccaatctaacctaac[C/T]ggtgttctcataagaa	C	T	NM_198570 // upstream // 692143 // Hs.455185 // UNQ739 // 375567 // Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000324993 // downstream // 154065 // — // — // — // — /// ENST00000340652 // upstream // 692143 // — // — // — // —	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-2271026	gacataaattctataa[C/G]aagtgtccatcgtttt	C	G	NM_198570 // upstream // 648297 // Hs.455185 // UNQ739 // 375567 // Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000324993 // downstream // 197911 // — // — // — // — /// ENST00000340652 // upstream // 648297 // — // — // — // —	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-1942935	ttgggtcattgtatgc[A/G]catcgttgtaactgac	A	G	NM_198570 // upstream // 527255 // Hs.455185 // UNQ739 // 375567 // Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000324993 // downstream // 318953 // — // — // — // — /// ENST00000340652 // upstream // 527255 // — // — // — // —	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-2056515	aatagagatctgagta[C/T]gactgaaaaaattaca	C	T	NM_198570 // intron // 0 // Hs.455185 // UNQ739 // 375567 // Homo sapiens PSST739 (UNQ739), mRNA. /// ENST00000340652 // intron // 0 // — // — // — // —	UNQ739	UNQ739, Homo sapiens PSST739 (UNQ739), p12.3
SNP_A-2115451	agggggcattttatta[C/T]agattgtatactacta	C	T	NM_007009 // intron // 0 // Hs.388841 // ZPBP // 11055 // Homo sapiens zona pellucida binding protein (ZPBP), mRNA. /// ENST00000046087 // intron // 0 // — // — // — // —	ZPBP	ZPBP, Homo sapiens zona pellucida binding protein (ZPBP), p12.2
SNP_A-2144374	atgataaatttgagta[C/T]ctggaaatgaaaacat	C	T	ENST00000339573 // downstream // 11693 // — // — // — // — /// ENST00000297001 // upstream // 27759 // — // — // — // —	-	p12.2
SNP_A-2216344	cctcctgctgtttata[A/G]attgcaacatccctgg	A	G	NM_006060 // intron // 0 // Hs.435949 // ZNFN1A1 // 10320 // Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), mRNA. /// ENST00000357364 // intron // 0 // — // — // — // — /// ENST00000331340 // intron // 0 // — // — // —	ZNFN1A1	ZNFN1A1, Homo sapiens zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1), p12.2
SNP_A-2189903	cataaatagttcacac[C/T]gaaggactctgtgcag	C	T	NM_000790 // intron // 0 // Hs.359698 // DDC // 1644 // Homo sapiens dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), mRNA. /// ENST00000357936 // intron // 0 // — // — // — // — /// ENST00000340197 // intron // 0 // — // — // -	DDC	DDC, Homo sapiens dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2243110	ctgccgcgacccagca[C/T]gtctgtggttgtaagg	C	T	NM_000790 // intron // 0 // Hs.359698 // DDC // 1644 // Homo sapiens dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), mRNA. /// ENST00000357936 // intron // 0 // — // — // — // — // — /// ENST00000340197 // intron // 0 // — // — // -	DDC	DDC, Homo sapiens dopa decarboxylase (aromatic L-amino acid decarboxylase) (DDC), p12.2
SNP_A-1734526	aattaaatgtgtagtaaccaccaac[A/G]gatgctaaaaaacag gaaaattaag	A	G	NM_005311 // intron // 0 // - // - // - // -	-	- , rs2715094, -,p12.2
SNP_A-2012588	ttggtgaagactacca[C/G]tgacacatttttttct	C	G	NM_001001549 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth factor receptor-bound	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-1757949	caataactaggtaatcatcttctaa[C/T]gcaatcatctacatcaat catgcac	C	T	NM_005311 // intron // 0 // - // - // - // -	-	- , rs990358, -,p12.2
SNP_A-1817645	gttccagtcttgagca[A/G]tcgtaattatattata	A	G	NM_001001549 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth factor receptor-bound	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-2214527	cctagaagccatgaag[A/G]aaaaactaacttctgt	A	G	NM_001001549 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, mRNA. /// NM_005311 // intron // 0 // Hs.164060 // GRB10 // 2887 // Homo sapiens growth factor receptor-bound	GRB10	GRB10, Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 2, p12.2
SNP_A-1660885	accctccttcctgggaccctgttca[C/T]aagtctatgcatctgtag caatgta	C	T	NM_005311 // upstream // 123483 // - // - // - // - /// NM_015198 // downstream // 99761 // Hs.99141 // COBL // 23242 // cordon-bleu homolog (mouse)	-	- , rs10486746, - ,p12.2
SNP_A-1846811	tatcaatcagaaagac[G/T]gcagccgtggcgtgga	G	T	NM_015198 // intron // 0 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // intron // 0 // — // — // — // — // — /// ENST00000265136 // intron // 0 // — // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2181045	cagacacaaaccagac[A/G]cagcttatgtaccgct	A	G	NM_015198 // intron // 0 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000265136 // intron // 0 // — // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2070634	acacctttctcatta[C/T]gtaagcataggtgctg	C	T	NM_015198 // upstream // 39827 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 165683 // — // — // — // — /// ENST00000265136 // upstream // 39827 // — // — // — // –	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2127517	ataacagtggcaaaat[A/G]atttatatacatgata	A	G	NM_015198 // upstream // 147536 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 273392 // — // — // — // — /// ENST00000265136 // upstream // 147536 // — // — // — //	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2214355	cctacctaaaaggctg[C/T]caaccatgcagaggag	C	T	NM_015198 // upstream // 299212 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 425068 // — // — // — // — /// ENST00000265136 // upstream // 299212 // — // — // — //	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1836545	tactctattagcaata[A/T]gggatgtgagcaccag	A	T	NM_015198 // upstream // 308040 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA. /// ENST00000333663 // upstream // 433896 // — // — // — // — /// ENST00000265136 // upstream // 308040 // — // — // — //	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270016	gacacaacagaaaaac[A/G]gaactcgaatctgact	A	G	NM_015198 // upstream // 309511 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 435367 // — // — // — /// ENST00000265136 // upstream // 309511 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1843528	tagtgccacaagctaa[A/C]cttttcatcgcacct	A	C	NM_015198 // upstream // 413987 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 539843 // — // — // — /// ENST00000265136 // upstream // 413987 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2079245	acccatcttccactaa[C/T]attcctagccaaat	C	T	NM_015198 // upstream // 505975 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 631831 // — // — // — /// ENST00000265136 // upstream // 505975 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1824352	taaacctcacatgta[A/C]ctttgaatgtaaaat	A	C	NM_015198 // upstream // 672569 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 798425 // — // — // — /// ENST00000265136 // upstream // 672569 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2216839	cctctgatcccgaagc[C/T]ctcactctactaacag	C	T	NM_015198 // upstream // 736025 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 861881 // — // — // — /// ENST00000265136 // upstream // 736025 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1919502	ttaagctggaagttct[A/G]acagaaagatagtggg	A	G	NM_015198 // upstream // 900730 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 1026586 // — // — // — /// ENST00000265136 // upstream // 900730 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-2102851	agcaaaaacaatggtc[A/G]attctaaactgtagg	A	G	NM_015198 // upstream // 1325342 // Hs.99141 // COBL // 23242 // Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA /// ENST00000333663 // upstream // 1451198 // — // — // — /// ENST00000265136 // upstream // 1325342 // — // — // —	COBL	COBL, Homo sapiens cordon-bleu homolog (mouse) (COBL), p12.1
SNP_A-1876874	tctgccacttacccac[C/T]gaacagtacaagtgtg	C	T	NM_182595 // upstream // 382976 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA /// ENST00000360955 // upstream // 7854 // — - // — // — // — /// ENST00000318120 // upstream // 382976	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2153246	attactggcagtagaat[C/T]gcagaagagaaactca	C	T	NM_182595 // upstream // 381844 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA /// ENST00000360955 // upstream // 8986 // — - // — // — // — /// ENST00000318120 // upstream // 381844	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1989936	attcattctaagtaa[A/G]agactcaacagtgag	A	G	NM_182595 // upstream // 381168 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA /// ENST00000360955 // upstream // 9662 // — - // — // — // — /// ENST00000318120 // upstream // 381168	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1989950	gtggctgcctttgag[A/G]gagatgttcttccct	A	G	NM_182595 // downstream // 1345 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA /// NM_182546 // upstream // 1504548 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1853178	tatttgtgagaagtta[G/T]aattctgccttgttt	G	T	NM_182595 // downstream // 13654 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1492239 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2268958	gaattcagttcttccat[A/G]ataaaatccatttttca	A	G	NM_182595 // downstream // 48603 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1457290 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2156684	atctggatgcactc[A/G]cttgaaaaacagaacc	A	G	NM_182595 // downstream // 157203 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1348690 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1927261	ttcaaaacagattatc[A/G]cacttcttcatagcta	A	G	NM_182595 // downstream // 165609 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1340284 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2048793	aagcccaattgttac[A/G]ctcaaagtatagaata	A	G	NM_182595 // downstream // 166659 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1339234 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2106762	agcctggatttttggat[C/T]ggaaattgttctccat	C	T	NM_182595 // downstream // 204001 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1301892 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1875136	tctctccagatgcaga[C/T]gtggccatgcctcttg	C	T	NM_182595 // downstream // 209414 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1296479 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2209619	cccatgctggaagcta[C/T]agtctgcttaaaacct	C	T	NM_182595 // downstream // 217725 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1288168 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1844894	tataatcttaagtgaa[C/T]gagaaacaggaaatc	C	T	NM_182595 // downstream // 224798 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1281095 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-2071784	acagacctgagactccf[A/G]gaaataagtcttcatt	A	G	NM_182595 // downstream // 229063 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 1276830 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p12.1
SNP_A-1645030	ggcaagttgtagtcttctcgttca[C/T]ctatcagttaaatttccctc catt	C	T	NM_182546 // upstream // 486897 // Hs.335933 // MGC33530 // 222008 // hypothetical protein MGC33530 /// NM_182595 // downstream // 1018634 // Hs.381970 // DKFZp564N2472 // 285877 // hypothetical protein DKFZp564N2472	MGC33530	MGC33530 , rs10499727, hypothetical protein MGC33530 , p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2184758	cagctgatggtttaat[A/C]aatccttctacataat	A	C	NM_182595 // downstream // 1111765 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 394128 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-1883061	tgaaatcaagcgatga[C/T]ggagtattgaaagatg	C	T	NM_182595 // downstream // 1123436 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 382457 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-2012605	atgctaatggaaaaca[A/G]tatgtatttgcaggca	A	G	NM_182595 // downstream // 1136090 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 369803 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protei	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-2143658	atgactttgtttagca[C/T]gagcaagtgtcaggga	C	T	NM_182595 // downstream // 1430814 // Hs.381970 // DKFZp564N2472 // 285877 // Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), mRNA. /// NM_182546 // upstream // 75079 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein	DKFZp564N2472	DKFZp564N2472, Homo sapiens hypothetical protein DKFZp564N2472 (DKFZp564N2472), p11.2
SNP_A-1849427	tatggagttttaataa[C/T]gcaatgttgccaacaa	C	T	NM_182546 // downstream // 175050 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein MGC33530 (MGC33530), mRNA. /// NM_014302 // downstream // 24679 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /	MGC33530	MGC33530, Homo sapiens hypothetical protein MGC33530 (MGC33530), p11.2
SNP_A-2158027	attgctttgaacaaga[G/T]aatttggtgaagtgag	G	T	NM_182546 // downstream // 176280 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein MGC33530 (MGC33530), mRNA. /// NM_014302 // downstream // 23449 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /	MGC33530	MGC33530, Homo sapiens hypothetical protein MGC33530 (MGC33530), p11.2
SNP_A-2249666	cttaagttatgccttg[A/G]aagcaaataatctgaa	A	G	NM_182546 // downstream // 180201 // Hs.335933 // MGC33530 // 222008 // Homo sapiens hypothetical protein MGC33530 (MGC33530), mRNA. /// NM_014302 // downstream // 19528 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /	MGC33530	MGC33530, Homo sapiens hypothetical protein MGC33530 (MGC33530), p11.2
SNP_A-1951164	tttcccaagactgctc[A/G]attcttacttcaggga	A	G	NM_014302 // upstream // 7442 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 252351 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia vi	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-2307420	gcttatattttactca[A/G]gagaggcagaagagca	A	G	NM_014302 // upstream // 18750 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 241043 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia v	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-1864517	tccagacaacagaata[C/T]tatccactggtttaaa	C	T	NM_014302 // upstream // 30502 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 229291 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia v	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-1929482	ttcagttttccttcaa[G/T]aagaaggctacgttct	G	T	NM_014302 // upstream // 69016 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 190777 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia v	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235361	ctccctgctgtgaatt[A/G]aaacttgccgaagcag	A	G	NM_014302 // upstream // 69227 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 190566 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia v	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-2249413	cttaaataaaaaagga[G/T]cactgagattcgttta	G	T	NM_014302 // upstream // 104874 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 154919 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-2137617	atcatctttatcacac[C/T]gcacagaaaacaagcc	C	T	NM_014302 // upstream // 123619 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 136174 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-1702427	tttagaagctgaaaaagtctgtcag[A/G]accatgtacaacatcc aatatccga	A	G	NM_005228 // upstream // 84173 // Hs.77432 // EGFR // 1956 // epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) /// NM_014302 // upstream // 175700 // Hs.9950 // SEC61G // 23480 // Sec61 gamma subunit	EGFR	EGFR , rs2330915, epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) ,p11.2
SNP_A-1664696	tgtttagtaaagccaagtcatacta[C/T]aggagaacacattcag atgcaagtg	C	T	NM_005228 // upstream // 81936 // Hs.77432 // EGFR // 1956 // epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) /// NM_014302 // upstream // 177937 // Hs.9950 // SEC61G // 23480 // Sec61 gamma subunit	EGFR	EGFR , rs2015549, epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) ,p11.2
SNP_A-1841884	taggctgaataaagta[C/T]cttgccctgcccactg	C	T	NM_014302 // upstream // 204572 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 55221 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia v	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-2235821	ctcctcttacccagta[C/T]atcatttccacattgc	C	T	NM_014302 // upstream // 255486 // Hs.488282 // SEC61G // 23480 // Homo sapiens Sec61 gamma subunit (SEC61G), mRNA. /// NM_201282 // upstream // 4307 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia vi	SEC61G	SEC61G, Homo sapiens Sec61 gamma subunit (SEC61G), p11.2
SNP_A-2252883	cttctatgctcacgga[A/G]gaccaaatttgccttg	A	G	NM_201282 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-2101835	agatggaaggaaaaga[C/T]gctaggaaaaaatcaa	C	T	NM_201282 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-2135346	atatttatctaaacac[A/G]atgaagcaactgcttg	A	G	NM_201282 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2166333	caaatctcagttgtta[C/T]gggcatttatagctat	C	T	NM_201282 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2281385	gagtcaagaagtaaca[C/T]cctgggaatgattggc	C	T	NM_201282 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // intron // 0 // Hs.488293 // EGFR // 1956 // Homo sap	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2152543	attaaggagatcttta[C/T]gtttttctagacacag	C	T	NM_201282 // downstream // 54040 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 54040 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-2132459	atagtgacaaataaat[A/G]aaagtgaaaggacttc	A	G	NM_201282 // downstream // 73404 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 73404 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri p11.2
SNP_A-1929477	ttcagtttgtagttta[C/T]aggagttattttgcag	C	T	NM_201282 // downstream // 76900 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 76900 // Hs.488293 // EGFR //	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2240871	ctgagaatctggtgga[C/T]aagaagccacagctca	C	T	NM_201282 // downstream // 138499 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 138499 // Hs.488293 // EGFR /	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2243730	ctgctgaacgtgttcc[A/G]cttggcaccaacacca	A	G	NM_201282 // downstream // 176077 // Hs.488293 // EGFR // 1956 // Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri /// NM_201283 // downstream // 176077 // Hs.488293 // EGFR /	EGFR	EGFR, Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), transcri ,p11.2
SNP_A-2211301	ccctacaactgaccaa[C/T]gaactggtgagtgaac	C	T	NM_018697 // intron // 0 // Hs.224282 // LANCL2 // 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // — // — // — // —	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2064488	aattcccagtggaagc[G/T]cttgctgtagaaagat	G	T	NM_018697 // intron // 0 // Hs.224282 // LANCL2 // 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // — // — // — // —	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-1934374	ttctcctcacaggcca[C/T]gtactgttttcctgat	C	T	NM_018697 // intron // 0 // Hs.224282 // LANCL2 // 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // — // — // — // —	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2063645	aattacgatattccta[C/T]acacggagcttcccct	C	T	NM_018697 // intron // 0 // Hs.224282 // LANCL2 // 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // — // — // — // —	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2139429	atccttatatttagca[C/T]ctggcaggtaatataa	C	T	NM_018697 // intron // 0 // Hs.224282 // LANCL2 // 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// ENST00000254770 // intron // 0 // — // — // — // —	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2
SNP_A-2206160	ccatcagagcacttac[A/G]cggactagaggctttt	A	G	NM_018697 // downstream // 2680 // Hs.224282 // LANCL2 // 55915 // Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA. /// NM_030796 // downstream // 34192 // Hs.488307 // DKFZP564K0822 // 81552 // Homo sapiens hypothet	LANCL2	LANCL2, Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074833	acatcaacttaccgca[A/G]gtctgagactatctcc	A	G	NM_030796 // intron // 0 // Hs.488307 // DKFZP564K0822 // 81552 // Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA. /// ENST00000285279 // intron // 0 // — // — // —	DKFZP564K0822	DKFZP564K0822, Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), p11.2
SNP_A-2281595	gagtcggtcgtcatca[A/G]ggaaagaacactgtct	A	G	NM_030796 // intron // 0 // Hs.488307 // DKFZP564K0822 // 81552 // Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA. /// ENST00000285279 // intron // 0 // — // — // —	DKFZP564K0822	DKFZP564K0822, Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), p11.2
SNP_A-2250072	cttacgatattagacc[A/T]cttactaccatcct	A	T	NM_030796 // intron // 0 // Hs.488307 // DKFZP564K0822 // 81552 // Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA. /// ENST00000285279 // intron // 0 // — // — // —	DKFZP564K0822	DKFZP564K0822, Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), p11.2
SNP_A-2202119	ccacatacagtcctg[A/C]aaagaagaggagaaaa	A	C	NM_030796 // upstream // 65419 // Hs.488307 // DKFZP564K0822 // 81552 // Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), mRNA. /// NM_182827 // downstream // 43202 // Hs.446691 // FKBP9L // 360132 // Homo sapiens FK506 binding protein 9-l	DKFZP564K0822	DKFZP564K0822, Homo sapiens hypothetical protein DKFZp564K0822 (DKFZP564K0822), p11.2
SNP_A-2120438	agtcattgctaaattc[A/C]aagtcacctgcattc	A	C	NM_207366 // intron // 0 // Hs.453629 // FLJ44060 // 346288 // Homo sapiens FLJ44060 protein (FLJ44060), mRNA. /// ENST00000275579 // intron // 0 // — // — // —	FLJ44060	FLJ44060, Homo sapiens FLJ44060 protein (FLJ44060), p11.2
SNP_A-1696540	attctgtctaagccagaacatagac[A/G]aggaaagactaaaacc ctatttgtt	A	G	NM_152746 // downstream // 135217 // - // - // -	-	-, rs2634083, -,p11.2
SNP_A-1990010	ttcttggtgcaaaaat[A/C]accatgttacctgtgt	A	C	ENST00000341775 // intron // 0 // — // — // — /// ENST00000354205 // intron // 0 // — // — // —	-	p11.2
SNP_A-1802722	gtatgcaaactcagat[C/G]aaagtgaggattatca	C	G	ENST00000341775 // intron // 0 // — // — // — /// ENST00000354205 // intron // 0 // — // — // —	-	p11.2
SNP_A-2069639	acacacagcttggtta[C/T]ctagtgatgtggtac	C	T	ENST00000341775 // intron // 0 // — // — // — /// ENST00000354205 // intron // 0 // — // — // —	-	p11.2
SNP_A-2012620	ctggtcaaagacttac[C/G]acatttctttacatttc	C	G	ENST00000341775 // intron // 0 // — // — // — /// ENST00000354205 // intron // 0 // — // — // —	-	p11.2
SNP_A-1804055	gtcacaattaaactg[A/C]aggaaggcccaggaat	A	C	AF277624 // upstream // 9666 // Hs.336957 // ZNF479 // 90827 // Homo sapiens KRAB zinc finger protein (KR19) mRNA, complete cds. /// ENST00000331162 // upstream // 9666 // — // — // — /// ENST00000332915 // downstream // 35416 // — // — // —	ZNF479	ZNF479, Homo sapiens KRAB zinc finger protein (KR19), complete cds., p11.1
SNP_A-1796524	ggttaatgaagaagaa[A/G]acacctatcctctg	A	G	ENST00000332915 // upstream // 40727 // — // — // — // — /// ENST00000297383 // upstream // 40722 // — // — // — // — /// ENST00000331027 // upstream // 30463 // — // — // — // — /// ENST00000356431 // upstream // 210172 // — // —	-	p11.1
SNP_A-2312162	ggacagatgggaggga[C/T]acagaaaagaaagcatg	C	T	ENST00000332915 // upstream // 45649 // — // — // — // — /// ENST00000297383 // upstream // 45644 // — // — // — // — /// ENST00000331027 // upstream // 25541 // — // — // — // — /// ENST00000356431 // upstream // 205250 // — // —	-	p11.1
SNP_A-1755050	cttatgtgaagaaatagtggagggaa[C/T]gaagatggtcagcttt aaactgcc	C	T	AF277624 // upstream // 5540097 // Hs.336957 // ZNF479 // 90827 // zinc finger protein 479	ZNF479	ZNF479, rs4095884, zinc finger protein 479,p11.2
SNP_A-2107060	agcgatttgagacctg[A/G]gtgaaaaagaatatat	A	G	ENST00000308532 // downstream // 3732696 // — // — // — // — /// ENST00000355326 // downstream // 560613 // — // — // — // — /// ENST00000332323 // downstream // 764557 // — // — // — // — /// ENST00000345838 // downstream // 76455	-	q11.21
SNP_A-1656697	ttctttcgattcaacagttaggtaa[C/T]actgttctgtccattctgca aatg	C	T	AF277624 // upstream // 4868508 // Hs.336957 // ZNF479 // 90827 // zinc finger protein 479	ZNF479	ZNF479, rs1595989, zinc finger protein 479,q11.21
SNP_A-2105961	agccatgtctttcttc[C/T]accacaggctgcatgg	C	T	ENST00000308532 // downstream // 4230460 // — // — // — // — /// ENST00000355326 // downstream // 62849 // — // — // — // — /// ENST00000332323 // downstream // 266793 // — // — // — // — /// ENST00000345838 // downstream // 266795	-	q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1670704	ttccctcatctggcagatgaacaaa[C/T]gatgagcctgtgagca gcctcaca	C	T	AF277624 // upstream // 4972632 // Hs.336957 // ZNF479 // 90827 // zinc finger protein 479	ZNF479	ZNF479 , rs1533823, zinc finger protein 479,q11.21
SNP_A-1912675	tgtgccttctaaaata[C/T]acgggactcactggtc	C	T	ENST00000308532 // downstream // 4255341 /// --- /// --- /// --- /// ENST00000355326 // downstream // 37968 /// --- /// --- /// --- /// ENST00000332323 // downstream // 241912 /// --- /// --- /// --- /// ENST00000345838 // downstream // 241914	-	q11.21
SNP_A-1797703	ggtttgcttgaaagta[A/G]cattaacaggccaggt	A	G	ENST00000308532 // downstream // 4262987 /// --- /// --- /// --- /// ENST00000355326 // downstream // 30322 /// --- /// --- /// --- /// ENST00000332323 // downstream // 234266 /// --- /// --- /// --- /// ENST00000345838 // downstream // 234268	-	q11.21
SNP_A-1956721	tttaaaatgagaacc[A/G]caatcagagttaaatg	A	G	ENST00000355326 // intron // 0 /// --- /// --- /// ---	-	q11.21
SNP_A-2047506	aagatgccctagtttc[A/C]aggtgtgcacgtctcc	A	C	ENST00000355326 // intron // 0 /// --- /// --- /// ---	-	q11.21
SNP_A-2246264	ctggtggccgccgtga[C/T]gcatgagcttggcctc	C	T	ENST00000345030 // intron // 0 /// --- /// --- /// ---	-	q11.21
SNP_A-2134968	atattcactggagaca[C/T]tcaccctcggctcac	C	T	ENST00000345030 // intron // 0 /// --- /// --- /// ---	-	q11.21
SNP_A-2012626	cttgtacaaagtacac[A/C]gaagactatgacacta	A	C	NM_153363 // downstream // 25036 // Hs.520884 // MGC42415 // 168417 // Homo sapiens hypothetical protein MGC42415 (MGC42415), mRNA /// NM_178558 // downstream // 227975 // Hs.180546 // FLJ90430 // 340252 // Homo sapiens hypothetical protein FLJ90430 (FLJ	MGC42415	MGC42415, Homo sapiens hypothetical protein MGC42415 (MGC42415), q11.21
SNP_A-2067241	acaaaggcatttcaaa[A/T]caataaccttaggcaa	A	T	NM_153363 // downstream // 186114 // Hs.520884 // MGC42415 // 168417 // Homo sapiens hypothetical protein MGC42415 (MGC42415), mRNA. /// NM_178558 // downstream // 66897 // Hs.180546 // FLJ90430 // 340252 // Homo sapiens hypothetical protein FLJ90430 (FLJ	MGC42415	MGC42415, Homo sapiens hypothetical protein MGC42415 (MGC42415), q11.21
SNP_A-2012630	taacaagttggctaac[A/G]agttcacatctttaa	A	G	NM_173517 // intron // 0 // Hs.427232 // VKORC1L1 // 154807 // Homo sapiens vitamin K epoxide reductase complex, subunit 1-like 1 (VKORC1L1), mRNA. /// ENST00000360768 // intron // 0 /// --- /// --- /// ---	VKORC1L1	VKORC1L1, Homo sapiens vitamin K epoxide reductase complex, subunit 1-like 1 (VKORC1L1), q11.21
SNP_A-1791753	gggtcttccggttcta[C/T]gaacacagccactgac	C	T	NM_014478 // downstream // 17795 // Hs.300684 // RCP9 // 27297 // Homo sapiens calcitonin gene-related peptide-receptor component protein (RCP9), mRNA. /// NM_003596 // upstream // 34635 // Hs.421194 // TPST1 // 8460 // Homo sapiens tyrosylprotein sulfotr	RCP9	RCP9, Homo sapiens calcitonin gene-related peptide-receptor component protein (RCP9), q11.21
SNP_A-1855416	tcaagtaagttgactg[A/G]caatttttctaagcag	A	G	NM_003596 // intron // 0 // Hs.421194 // TPST1 // 8460 // Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), mRNA. /// ENST00000304842 // intron // 0 // --- // --- // --- // ENST00000359434 // intron // 0 // --- // --- // ---	TPST1	TPST1, Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), q11.21
SNP_A-2065427	aattgtgttataaa[A/G]agaaggtgtctgtctt	A	G	NM_003596 // intron // 0 // Hs.421194 // TPST1 // 8460 // Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), mRNA. /// ENST00000304842 // intron // 0 // --- // --- // --- // ENST00000359434 // intron // 0 // --- // --- // ---	TPST1	TPST1, Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), q11.21
SNP_A-2105378	agccaaaacaacttgc[A/G]gaaaataagtctacag	A	G	NM_153033 // downstream // 10239 // Hs.520914 // KCTD7 // 154881 // Homo sapiens potassium channel tetramerisation domain containing 7 (KCTD7), mRNA. /// NM_014504 // upstream // 89664 // Hs.530053 // RABGEF1 // 27342 // Homo sapiens RAB guanine nucleotid	KCTD7	KCTD7, Homo sapiens potassium channel tetramerisation domain containing 7 (KCTD7), q11.21
SNP_A-2272581	gacgaggcttacaac[A/G]gtgatgtttgggtgag	A	G	NM_014504 // intron // 0 // Hs.530053 // RABGEF1 // 27342 // Homo sapiens RAB guanine nucleotide exchange factor (GEF) 1 (RABGEF1), mRNA. /// ENST00000284957 // intron // 0 // --- // --- // ---	RABGEF1	RABGEF1, Homo sapiens RAB guanine nucleotide exchange factor (GEF) 1 (RABGEF1), q11.21
SNP_A-1944002	ttgtattctccagtaa[C/T]gtaagaacccacttaa	C	T	NM_014504 // downstream // 100788 // Hs.530053 // RABGEF1 // 27342 // Homo sapiens RAB guanine nucleotide exchange factor (GEF) 1 (RABGEF1), mRNA. /// NM_017994 // upstream // 29619 // Hs.488478 // FLJ10099 // 55069 // Homo sapiens hypothetical protein FL	RABGEF1	RABGEF1, Homo sapiens RAB guanine nucleotide exchange factor (GEF) 1 (RABGEF1), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1751691	taaaagcacaagtctgtcctaacta[G/T]agtagtattaaaatgtg actatttt	G	T	NM_016038 // downstream // 31547 // Hs.110445 // SBDS // 51119 // Shwachman-Bodian-Diamond syndrome /// NM_017994 // downstream // 3 // Hs.287955 // FLJ10099 // 55069 // hypothetical protein FLJ10099	SBDS	SBDS , rs3800818, Shwachman-Bodian-Diamond syndrome ,q11.21
SNP_A-2108629	agctggtaaatggaag[A/G]atgaagacttgaatac	A	G	NM_015570 // upstream // 2110293 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 168335 // --- // --- // --- /// ENST00000353285 // downstream // 168335 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.21
SNP_A-1888483	tgaggaccaatttctg[A/G]caaaatttgtgaacac	A	G	NM_015570 // upstream // 2101780 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 176848 // --- // --- // --- /// ENST00000353285 // downstream // 176848 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.21
SNP_A-1888213	tgagcggtcacaaga[A/G]gagtgtcaggatcaag	A	G	NM_015570 // upstream // 2101408 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 177220 // --- // --- // --- /// ENST00000353285 // downstream // 177220 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.21
SNP_A-2153924	attatactgaggaaca[C/T]gtggaatgtaaactgt	C	T	NM_015570 // upstream // 1918682 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 359946 // --- // --- // --- /// ENST00000353285 // downstream // 359946 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2285782	gatgactctacctaad[A/G]attggagatccgtaac	A	G	NM_015570 // upstream // 1904703 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 373925 // --- // --- // --- /// ENST00000353285 // downstream // 373925 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2115750	agggtctggttacad[A/G]atagagtcatacatat	A	G	NM_015570 // upstream // 1901646 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 376982 // --- // --- // --- /// ENST00000353285 // downstream // 376982 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1912485	tgtgcagtctctatac[A/G]ccggctgaaagcagct	A	G	NM_015570 // upstream // 1901436 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 377192 // --- // --- // --- /// ENST00000353285 // downstream // 377192 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2264404	gaagaaaagaaaatta[C/T]aggactggacaggtgc	C	T	NM_015570 // upstream // 1898310 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 380318 // --- // --- // --- /// ENST00000353285 // downstream // 380318 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1883612	tgaacgttggcataca[C/G]gttgtttgagtccctg	C	G	NM_015570 // upstream // 1714090 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA /// ENST00000352103 // downstream // 564538 // --- // --- // --- /// ENST00000353285 // downstream // 564538 // --- // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1681840	taaacaggattcaagagaataaaa[A/G]ctaaagatactaga actttaatga	A	G	NM_015570 // upstream // 1457611 // Hs.296720 // AUTS2 // 26053 // autism susceptibility candidate 2 /// NM_022906 // downstream // 820696 // Hs.213392 // FLJ13195 // 64940 // hypothetical protein FLJ13195 similar to stromal antigen 3	AUTS2	AUTS2, , rs727845, autism susceptibility candidate 2 ,q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990070	ctgggaggacctgaca[A/T]agcaaccatttatcag	A	T	NM_015570 // upstream // 1236780 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1041848 // — // — // — // — /// ENST00000353285 // downstream // 1041848 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1790724	ggggctttggtttataa[C/T]gagtaatttgcataga	C	T	NM_015570 // upstream // 1223764 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1054864 // — // — // — // — /// ENST00000353285 // downstream // 1054864 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1815492	gtgttttggttgatc[A/G]cctgcttatttgtaac	A	G	NM_015570 // upstream // 1076757 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1201871 // — // — // — // — /// ENST00000353285 // downstream // 1201871 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2297317	gccacgctctttcaa[C/T]aatcgccctcgtgag	C	T	NM_015570 // upstream // 889865 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1388763 // — // — // — // — /// ENST00000353285 // downstream // 1388763 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2198266	cattgtggctgagtgc[A/G]cacctgatgaagtgc	A	G	NM_015570 // upstream // 809795 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1468833 // — // — // — // — /// ENST00000353285 // downstream // 1468833 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2259417	gaaaaatgagaggccac[A/G]caaaaggtttttc	A	G	NM_015570 // upstream // 332123 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1946505 // — // — // — // — /// ENST00000353285 // downstream // 1946505 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2107042	agcgatagcagagcat[C/T]aaccaagtgcctgacc	C	T	NM_015570 // upstream // 312716 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1965912 // — // — // — // — /// ENST00000353285 // downstream // 1965912 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2195769	catgtacctcatcaaa[C/T]atcagtaactcacaac	C	T	NM_015570 // upstream // 311083 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1967545 // — // — // — // — /// ENST00000353285 // downstream // 1967545 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2238140	ctctgccctaacttat[C/T]gcctcataaaatcagt	C	T	NM_015570 // upstream // 308394 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1970234 // — // — // — // — /// ENST00000353285 // downstream // 1970234 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1932609	ttcctgttggcaattc[A/G]aagtgttggtgtcaaa	A	G	NM_015570 // upstream // 280779 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1997849 // — // — // — // — /// ENST00000353285 // downstream // 1997849 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1813184	gtggtcaagtggatga[C/T]tcaatgacttgccagg	C	T	NM_015570 // upstream // 280304 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 1998324 // — // — // — // — /// ENST00000353285 // downstream // 1998324 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2223257	cgcgagcaaacagacc[C/T]ggcttgacctcatgtc	C	T	NM_015570 // upstream // 229448 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 2049180 // — // — // — // — /// ENST00000353285 // downstream // 2049180 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1784412	ggccctcaaagcaagt[A/G]aagctcttcctgaaaa	A	G	NM_015570 // upstream // 204280 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 2074348 // — // — // — // — /// ENST00000353285 // downstream // 2074348 // — //	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2206223	ccatcattttgagttc[A/G]ccatttttttctatgt	A	G	NM_015570 // upstream // 67606 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000352103 // downstream // 2211022 // — // — // — // — /// ENST00000353285 // downstream // 2211022 // — // -	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1731973	aatttccaaagagtagcctgattgc[C/T]ataaagccctctctgcct tcacaat	C	T	NM_015570 // intron // 0 // Hs.296720 // AUTS2 // 26053 // autism susceptibility candidate 2	AUTS2	AUTS2 , rs7809475, autism susceptibility candidate 2,q11.22
SNP_A-1758254	aagtaactctggcctttaacgttta[C/T]gagcttagcaggtctctgg ccgagg	C	T	NM_015570 // intron // 0 // Hs.296720 // AUTS2 // 26053 // autism susceptibility candidate 2	AUTS2	AUTS2 , rs740166, autism susceptibility candidate 2,q11.22
SNP_A-2262037	gaaataggtctttcat[A/G]aatctgtgagctcacc	A	G	NM_015570 // intron // 0 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000345497 // intron // 0 // — // — // — // — /// ENST00000342771 // intron // 0 // — // — - // — // —	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2150876	atgtggcctcaatagg[A/T]cagatctttaatggat	A	T	NM_015570 // intron // 0 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000345497 // intron // 0 // — // — // — // — /// ENST00000342771 // intron // 0 // — // — - // — // —	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2046625	aagagcagtgggcacc[G/T]aagtcaaaatgcagat	G	T	NM_015570 // intron // 0 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000345497 // intron // 0 // — // — // — // — /// ENST00000342771 // intron // 0 // — // — - // — // —	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2308257	gcttggctgtgttatc[C/G]aaattcttgaggctcg	C	G	NM_015570 // intron // 0 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// ENST00000345497 // intron // 0 // — // — // — // — /// ENST00000342771 // intron // 0 // — // — - // — // —	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2249118	ctgtttgaagagggaa[A/C]ctaattgtatttaaca	A	C	NM_015570 // downstream // 45364 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 296443 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2281928	gagtgccctctcatcc[A/G]ctctcagacttactcc	A	G	NM_015570 // downstream // 174199 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 167608 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome regio	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-2242466	ctgcagagccctatca[A/C]agagctcctaacacgt	A	C	NM_015570 // downstream // 333967 // Hs.21631 // AUTS2 // 26053 // Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA. /// NM_022479 // upstream // 7840 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region	AUTS2	AUTS2, Homo sapiens autism susceptibility candidate 2 (AUTS2), q11.22
SNP_A-1868027	tcctagtttttggaca[A/G]ctttgagccgaatagg	A	G	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990139	atcagatttcagcca[C/T]ggtttcaaataaact	C	T	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-1814256	gtgtctgttgttctca[C/T]ctgttaagtccatagg	C	T	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-1897903	tgctggtcatgctaga[A/G]gaagccatgtaggcca	A	G	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-1910376	tgtccatccatacttc[A/G]gaaattacttaacagt	A	G	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-2268090	gaatgaaaactgaaaa[C/T]tgagactgtaaatctg	C	T	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-1888248	tgagctagtggcaaaaa[A/T]gactggaggtggcccg	A	T	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-1835631	taccttgaaattcagc[C/T]gccttgtttttactctc	C	T	NM_022479 // intron // 0 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// ENST00000333538 // intron // 0 // — // — // —	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-2094698	agaatattaatacatc[A/G]aacaacttcatcctta	A	G	NM_022479 // downstream // 72128 // Hs.488591 // WBSCR17 // 64409 // Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), mRNA. /// NM_031468 // downstream // 2049 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA.	WBSCR17	WBSCR17, Homo sapiens Williams-Beuren syndrome chromosome region 17 (WBSCR17), q11.22
SNP_A-2169582	caagctgagaaaaaaa[A/C]ggtgcaggaaacaagg	A	C	NM_031468 // intron // 0 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // — // — // —	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2031412	aaaggttagaactac[G/T]gacctactaccatgtc	G	T	NM_031468 // intron // 0 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // — // — // —	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2126598	ataaaattggaattca[C/T]agttctgaaatcaaac	C	T	NM_031468 // intron // 0 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // — // — // —	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2057322	aatatatgatcttacl[C/G]cattcagactcatcat	C	G	NM_031468 // intron // 0 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // — // — // —	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2202626	ccacctctgttgaaca[C/T]taaagacaaaggagag	C	T	NM_031468 // intron // 0 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // — // — // —	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2304543	gctctcatttcaaaat[A/T]agggactggccttaaa	A	T	NM_031468 // intron // 0 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // intron // 0 // — // — // —	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2196497	catgtttgagtctttc[C/T]atgaatatatgctttt	C	T	NM_031468 // upstream // 91144 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // upstream // 91144 // — // — // — /// ENST00000332388 // downstream // 427479 // — // — // — /// ENST0	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2066201	aattttaacaatttaa[C/G]agtgtggtacagcttt	C	G	NM_031468 // upstream // 156987 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // upstream // 156987 // — // — // — // — /// ENST00000332388 // downstream // 493322 // — // — // — // — /// ENS	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-1868526	tcctcggttttcagga[A/G]aagttaggctagaaac	A	G	NM_031468 // upstream // 224842 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // upstream // 224842 // — // — // — // — /// ENST00000332388 // downstream // 561177 // — // — // — // — /// ENS	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-1890326	tgatccagcactgtat[C/T]aggggttatggcaaca	C	T	NM_031468 // upstream // 263310 // Hs.333274 // CALN1 // 83698 // Homo sapiens calneuron 1 (CALN1), mRNA. /// ENST00000329008 // upstream // 263310 // — // — // — // — /// ENST00000332388 // downstream // 599645 // — // — // — // — /// ENS	CALN1	CALN1, Homo sapiens calneuron 1 (CALN1), q11.22
SNP_A-2081058	acctgaccaactgtca[C/T]tctccaaagacactta	C	T	NM_012453 // intron // 0 // Hs.52515 // TBL2 // 26608 // Homo sapiens transducin (beta)-like 2 (TBL2), transcript variant 1, mRNA. /// ENST00000305632 // intron // 0 // — // — // — // —	TBL2	TBL2, Homo sapiens transducin (beta)-like 2 (TBL2), transcript variant 1, q11.23
SNP_A-2299263	gccctcatggttctta[C/T]agtttggtggcagaga	C	T	NM_182504 // downstream // 125235 // Hs.180471 // WBSCR28 // 135886 // Homo sapiens Williams-Beuren syndrome critical region 28 (WBSCR28), mRNA. /// BX537939 // upstream // 37063 // Hs.252418 // ELN // 2006 // Homo sapiens mRNA; cDNA DKFZp686F06102 (from	WBSCR28	WBSCR28, Homo sapiens Williams-Beuren syndrome critical region 28 (WBSCR28), q11.23
SNP_A-2250981	cttatgtcctgactga[C/G]catgagctgagagccg	C	G	NM_016328 // downstream // 51549 // Hs.156302 // GTF2IRD1 // 9569 // Homo sapiens GTF2I repeat domain containing 1 (GTF2IRD1), transcript variant 1, mRNA. /// NM_005685 // downstream // 51549 // Hs.156302 // GTF2IRD1 // 9569 // Homo sapiens GTF2I repeat d	GTF2IRD1	GTF2IRD1, Homo sapiens GTF2I repeat domain containing 1 (GTF2IRD1), transcript variant 1, q11.23
SNP_A-1803741	gtcaacactgcatgaa[A/G]gtaactgagggggccg	A	G	NM_005338 // intron // 0 // Hs.329266 // HIP1 // 3092 // Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA. /// ENST00000336926 // intron // 0 // — // — // — // —	HIP1	HIP1, Homo sapiens huntingtin interacting protein 1 (HIP1), q11.23
SNP_A-1838304	tagaagcgaggaaaca[A/G]tatgaggagatcaact	A	G	NM_005338 // intron // 0 // Hs.329266 // HIP1 // 3092 // Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA. /// ENST00000336926 // intron // 0 // — // — // — // —	HIP1	HIP1, Homo sapiens huntingtin interacting protein 1 (HIP1), q11.23
SNP_A-1863583	tccaaatagcttcata[A/G]gtagtaactgtgaact	A	G	NM_002991 // intron // 0 // Hs.247838 // CCL24 // 6369 // Homo sapiens chemokine (C-C motif) ligand 24 (CCL24), mRNA. /// ENST00000222902 // intron // 0 // — // — // — // —	CCL24	CCL24, Homo sapiens chemokine (C-C motif) ligand 24 (CCL24), q11.23
SNP_A-2209732	cccattccttcgaaaa[C/T]ataaatgggtcattag	C	T	NM_002991 // upstream // 52491 // Hs.247838 // CCL24 // 6369 // Homo sapiens chemokine (C-C motif) ligand 24 (CCL24), mRNA. /// NM_020684 // upstream // 12742 // Hs.488827 // RHBDL7 // 57414 // Homo sapiens rhomboid, veinlet-like 7 (Drosophila) (RHBDL7),	CCL24	CCL24, Homo sapiens chemokine (C-C motif) ligand 24 (CCL24), q11.23
SNP_A-1671884	aggctggaggtgggtttttagaagc[C/G]gactcccagagagac agtgtctaga	C	G	NM_001540 // upstream // 7931 // Hs.76067 // HSPB1 // 3315 // heat shock 27kDa protein 1 /// NM_153043 // downstream // 7374 // Hs.26309 // FLJ37078 // 222183 // hypothetical protein FLJ37078	HSPB1	HSPB1 , rs10488574, heat shock 27kDa protein 1 ,q11.23
SNP_A-2073386	acaggtcaacaattca[C/T]cctcttctcactgtct	C	T	NM_080744 // downstream // 10837 // Hs.520977 // SRCRB4D // 136853 // Homo sapiens scavenger receptor cysteine rich domain containing, group B (4 domains) (SRCRB4D), mRNA. /// NM_007155 // upstream // 19059 // Hs.130553 // ZP3 // 7784 // Homo sapiens zona	SRCRB4D	SRCRB4D, Homo sapiens scavenger receptor cysteine rich domain containing, group B (4 domains) (SRCRB4D), q11.23
SNP_A-2263000	gaacaatcactattgg[C/G]caggtacagcaatatg	C	G	ENST00000285871 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-1799822	gtacacaaacaaacta[C/T]gctttctaatgttttc	C	T	ENST00000285871 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2259788	gaaaagattagatgga[C/G]accaaaactgtgattg	C	G	ENST00000285871 // intron // 0 // — // — // — // — /// ENST00000257657 // intron // 0 // — // — // — // —	-	q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2067311	acaaagtcagtcagat[C/G]aaagttcagaccagt	C	G	NM_002835 // intron // 0 // Hs.61812 // PTPN12 // 5782 // Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /// ENST00000248594 // intron // 0 // — // — // —	PTPN12	PTPN12, Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), q11.23
SNP_A-1990207	cttgctgcagcctcta[A/C]atcagaatttggtgct	A	C	NM_002835 // intron // 0 // Hs.61812 // PTPN12 // 5782 // Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /// ENST00000248594 // intron // 0 // — // — // —	PTPN12	PTPN12, Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), q11.23
SNP_A-2104908	agcatattaccatact[C/G]aacaattgtaacacaa	C	G	NM_002835 // intron // 0 // Hs.61812 // PTPN12 // 5782 // Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /// ENST00000248594 // intron // 0 // — // — // —	PTPN12	PTPN12, Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), q11.23
SNP_A-2258541	cttttctgtagtataa[C/T]gttgtgagattcatc	C	T	NM_198467 // intron // 0 // Hs.72451 // RSBN1L // 222194 // Homo sapiens round spermatid basic protein 1-like (RSBN1L), mRNA /// ENST00000334955 // intron // 0 // — // — // —	RSBN1L	RSBN1L, Homo sapiens round spermatid basic protein 1-like (RSBN1L), q11.23
SNP_A-2183607	cagcagtaccactacat[C/T]acaagatggatgaatc	C	T	NM_198467 // intron // 0 // Hs.72451 // RSBN1L // 222194 // Homo sapiens round spermatid basic protein 1-like (RSBN1L), mRNA /// ENST00000334955 // intron // 0 // — // — // —	RSBN1L	RSBN1L, Homo sapiens round spermatid basic protein 1-like (RSBN1L), q11.23
SNP_A-1935975	ttcttacatttggctg[C/T]acttaccacaggtgct	C	T	NM_032936 // intron // 0 // Hs.19025 // C7orf35 // 85025 // Homo sapiens chromosome 7 open reading frame 35 (C7orf35), mRNA /// ENST00000257663 // intron // 0 // — // — // —	C7orf35	C7orf35, Homo sapiens chromosome 7 open reading frame 35 (C7orf35), q11.23
SNP_A-1949990	ttcaaatctagccct[C/T]aaattcatctgtggtg	C	T	ENST00000307305 // intron // 0 // — // — // — /// ENST00000275575 // intron // 0 // — // — // —	-	q11.23
SNP_A-2083838	actacctgggctatca[C/G]taacattcactcaagg	C	G	NM_020432 // intron // 0 // Hs.203965 // PHTF2 // 57157 // Homo sapiens putative homeodomain transcription factor 2 (PHTF2), mRNA /// ENST00000307305 // intron // 0 // — // — // — /// ENST00000275575 // intron // 0 // — // — // —	PHTF2	PHTF2, Homo sapiens putative homeodomain transcription factor 2 (PHTF2), q11.23
SNP_A-2221100	ccttgtctctcactta[C/T]gctttgatacactga	C	T	NM_020432 // intron // 0 // Hs.203965 // PHTF2 // 57157 // Homo sapiens putative homeodomain transcription factor 2 (PHTF2), mRNA /// ENST00000275575 // intron // 0 // — // — // — /// ENST00000248550 // intron // 0 // — // — // —	PHTF2	PHTF2, Homo sapiens putative homeodomain transcription factor 2 (PHTF2), q21.11
SNP_A-2245675	ctgggctagccattca[C/G]aaaaaaactatcaat	C	G	NM_020432 // downstream // 8131 // Hs.203965 // PHTF2 // 57157 // Homo sapiens putative homeodomain transcription factor 2 (PHTF2), mRNA /// NM_012301 // downstream // 51728 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (A	PHTF2	PHTF2, Homo sapiens putative homeodomain transcription factor 2 (PHTF2), q21.11
SNP_A-2111723	aggataaaaccatcact[A/C]ggaagaataagttcaa	A	C	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST00000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-1686004	caaatgtgacagagaaccagcatat[C/G]acagtgaataagcat gcagtctctg	C	G	NM_012301 // intron // 0 // Hs.22599 // AIP1 // 9863 // atrophin-1 interacting protein 1	AIP1	AIP1, rs14477033, atrophin-1 interacting protein 1,q21.11
SNP_A-1885907	tgacatcctcaaacac[A/G]gtgaactgaaagcaaa	A	G	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST0000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2305636	gctgcatctactagaa[A/C]ggctatatgttgttcca	A	C	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST0000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-1756078	aataaaaattggatacctttttgtaa[A/G]tatctccataaagtttcaaaa atgtg	A	G	NM_012301 // intron // 0 // Hs.22599 // AIP1 // 9863 // atrophin-1 interacting protein 1	AIP1	AIP1, rs319871, atrophin-1 interacting protein 1,q21.11
SNP_A-2226306	ctaacttttgttttat[C/G]caaccatcctcatca	C	G	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST0000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072764	acagctcaagacccgal[A/G]actatgtgcctcttttt	A	G	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST0000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-2012680	ttagcctgaagagaga[C/T]taaatttgttgaatlc	C	T	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST0000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-1990278	caatgtctgactgcal[C/T]aaataaggcagcttcc	C	T	NM_012301 // intron // 0 // Hs.488945 // AIP1 // 9863 // Homo sapiens atrophin-1 interacting protein 1 (AIP1), mRNA. /// ENST00000354212 // intron // 0 // — // — // — /// ENST00000344634 // intron // 0 // — // — // — /// ENST0000	AIP1	AIP1, Homo sapiens atrophin-1 interacting protein 1 (AIP1), q21.11
SNP_A-1673122	cacagattaccctgagagcacatc[A/G]atatatattaccaaggatacttatc	A	G	BC027852 // downstream // 1749748 // Hs.367974 // MGC34774 // 399670 // ribosomal protein L13A-like /// NM_002069 // upstream // 25625 // Hs.203862 // GNAI1 // 2770 // guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide	MGC34774	MGC34774 , rs10254386, ribosomal protein L13A-like ,q21.11
SNP_A-1818077	gttctcagagcacatg[A/G]atatatgaactggaat	A	G	NM_002069 // intron // 0 // Hs.134587 // GNAI1 // 2770 // Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), mRNA. /// ENST00000351004 // intron // 0 // — // — // —	GNAI1	GNAI1, Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), q21.11
SNP_A-1848789	tatgatccagacatca[C/T]ctttttttactgaag	C	T	NM_002069 // intron // 0 // Hs.134587 // GNAI1 // 2770 // Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), mRNA. /// ENST00000351004 // intron // 0 // — // — // —	GNAI1	GNAI1, Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), q21.11
SNP_A-2299198	gccctagataactctg[A/G]agataagttgccagtg	A	G	NM_002069 // downstream // 195205 // Hs.134587 // GNAI1 // 2770 // Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), mRNA. /// ENST00000351004 // downstream // 195205 // — // — // —	GNAI1	GNAI1, Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), q21.11
SNP_A-1919384	ttaagatggctgttaa[C/T]gaaaagataaagagata	C	T	NM_001001547 // downstream // 35960 // Hs.120949 // CD36 // 948 // Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), transcript variant 2, mRNA. /// NM_001001548 // downstream // 35960 // Hs.120949 // CD36 // 948 // Hom	CD36	CD36, Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), transcript variant 2, q21.11
SNP_A-1747683	gataaaagctcacagagcaaaggca[A/G]atagttcatactaagtagcataaag	A	G	NM_006379 // intron // 0 // Hs.171921 // SEMA3C // 10512 // sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	SEMA3C	SEMA3C , rs2886792, sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C,q21.11
SNP_A-2063945	aattatcactgacatt[A/G]aagatcacttgaatct	A	G	NM_001001547 // downstream // 56074 // Hs.120949 // CD36 // 948 // Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), transcript variant 2, mRNA. /// NM_001001548 // downstream // 56074 // Hs.120949 // CD36 // 948 // Hom	CD36	CD36, Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), transcript variant 2, q21.11
SNP_A-2299589	gccgagtgtctttgca[A/G]attggttaatcatct	A	G	NM_006379 // CDS // 0 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// ENST00000265361 // CDS // 0 // — // — // —	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1862888	tcattgaattggatta[A/C]attgtctcctccattg	A	C	NM_006379 // intron // 0 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// ENST00000265361 // intron // 0 // — // — // —	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1681622	tcttcttaaatttcattatctaaac[A/C]aattgtaaatgtatacaaaatgatt	A	C	NM_000601 // downstream // 687232 // Hs.396530 // HGF // 3082 // hepatocyte growth factor (hepapoietin A; scatter factor) /// NM_006379 // upstream // 92423 // Hs.171921 // SEMA3C // 10512 // sema domain, immunoglobulin domain (Ig), short basic domain, s	HGF	HGF , rs853042, hepatocyte growth factor (hepapoietin A; scatter factor) ,q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990320	atttaacagtaattg[A/T]aaacatcagatttagt	A	T	NM_006379 // upstream // 139876 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 642902 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1925246	ttatcctcaagcagcal[A/G]ggagttttttgcag	A	G	NM_006379 // upstream // 220033 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 562745 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-2095389	agaatttttttcacaca[C/T]aaggcgttcttcctc	C	T	NM_006379 // upstream // 404996 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 377782 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1652690	cacatctctcatcatagccagctac[A/G]acttggcagccttttctt atagtg	A	G	NM_000601 // downstream // 299423 // Hs.396530 // HGF // 3082 // hepatocyte growth factor (hepapoietin A; scatter factor) /// NM_006379 // upstream // 480232 // Hs.171921 // SEMA3C // 10512 // sema domain, immunoglobulin domain (Ig), short basic domain.	HGF	HGF , rs1023534, hepatocyte growth factor (hepapoietin A; scatter factor), q21.11
SNP_A-1990326	ttattatgtatcaaa[A/T]tcaccaaataagctct	A	T	NM_006379 // upstream // 473295 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 309483 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1847535	tatccttgaagaaaaa[C/T]gtgatgtctattaa	C	T	NM_006379 // upstream // 509936 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 272842 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1913668	tgtgtaggattgtgga[A/G]cggttgaccaagtcag	A	G	NM_006379 // upstream // 677738 // Hs.269109 // SEMA3C // 10512 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /// NM_000601 // downstream // 105040 // Hs.396530 // HGF // 3082 // Hom	SEMA3C	SEMA3C, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), q21.11
SNP_A-1847235	tatccaatgctatcaaa[G/T]gtactatatttaaac	G	T	NM_000722 // intron // 0 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// ENST00000356253 // intron // 0 // — /// ENST00000356860 // intron // 0 // —	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-1734588	tgggactcttaaattgagatctccc[A/G]ctaggcaatattatagag tcactga	A	G	NM_000722 // intron // 0 // Hs.147871 // CACNA2D1 // 781 // calcium channel, voltage-dependent, alpha 2/delta subunit 1	CACNA2D1	CACNA2D1 , rs10486949, calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-1960563	tttttcatatatacga[A/G]gtcagatccttgccac	A	G	NM_000722 // intron // 0 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// ENST00000356253 // intron // 0 // — /// ENST00000356860 // intron // 0 // —	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-1960834	ttttcctttgtgaaca[A/C]gtaaattgaaatgaaa	A	C	NM_000722 // intron // 0 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// ENST00000356253 // intron // 0 // — /// ENST00000356860 // intron // 0 // —	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2219919	ccttagttggcacctg[C/G]actacatttcaaggca	C	G	NM_000722 // intron // 0 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// ENST00000356253 // intron // 0 // — // — // — /// ENST00000356860 // intron // 0 // —	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-2040614	aaccatttcactggaaa[A/G]atatcttcaggttat	A	G	NM_000722 // intron // 0 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// ENST00000356253 // intron // 0 // — // — // — /// ENST00000356860 // intron // 0 // —	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-2151209	atgttaacaggcagta[C/G]aaaaattacctcttc	C	G	NM_000722 // intron // 0 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// ENST00000356253 // intron // 0 // — // — // — /// ENST00000356860 // intron // 0 // —	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-1746254	tcttagcagtgaacaccttgctat[C/T]aagattatttcctctgctatg agtt	C	T	AB011131 // downstream // 296393 // Hs.12376 // PCLO // 27445 // piccolo (presynaptic cytomatrix protein) /// NM_000722 // upstream // 80598 // Hs.147871 // CACNA2D1 // 781 // calcium channel, voltage-dependent, alpha 2/delta subunit 1	PCLO	PCLO , rs10486967, piccolo (presynaptic cytomatrix protein) ,q21.11
SNP_A-1671462	gaaatttgatctaaagagcactaa[C/G]atggaaggagtgagg aagacagaga	C	G	AB011131 // downstream // 252748 // Hs.12376 // PCLO // 27445 // piccolo (presynaptic cytomatrix protein) /// NM_000722 // upstream // 124243 // Hs.147871 // CACNA2D1 // 781 // calcium channel, voltage-dependent, alpha 2/delta subunit 1	PCLO	PCLO , rs9791531, piccolo (presynaptic cytomatrix protein) ,q21.11
SNP_A-2022393	aaaaatactgtattca[C/T]gtcaaaaaggatagtg	C	T	NM_000722 // upstream // 96062 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 409925 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA055	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2271278	gacatgttaaatgaca[C/T]gaagaagatgtaataa	C	T	NM_000722 // upstream // 98703 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 407284 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA055	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-2209616	cccatgctatggactg[A/G]aagaatgaatattgtt	A	G	NM_000722 // upstream // 109634 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 396353 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA05	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-1990371	ttcttgactctcctta[C/T]agttggttacttttg	C	T	NM_000722 // upstream // 159517 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 346470 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA05	CACNA2D1	CACNA2D1 Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-1658152	taggacaacatctcacaaaatcata[C/T]gttacaggaaatgcat gaacagcca	C	T	AB011131 // downstream // 154367 // Hs.12376 // PCLO // 27445 // piccolo (presynaptic cytomatrix protein) /// NM_000722 // upstream // 222624 // Hs.147871 // CACNA2D1 // 781 // calcium channel, voltage-dependent, alpha 2/delta subunit 1	PCLO	PCLO , rs916853, piccolo (presynaptic cytomatrix protein) ,q21.11
SNP_A-1702521	ctggtcttaccctagtcctatattc[C/T]acccaaaagaaataaatc aaattgc	C	T	AB011131 // downstream // 63714 // Hs.12376 // PCLO // 27445 // piccolo (presynaptic cytomatrix protein) /// NM_000722 // upstream // 313277 // Hs.147871 // CACNA2D1 // 781 // calcium channel, voltage-dependent, alpha 2/delta subunit 1	PCLO	PCLO , rs10486985, piccolo (presynaptic cytomatrix protein) ,q21.11
SNP_A-1727599	tagctcccatcacttattccaaatc[G/T]ataaaaactctaagaca gatttaa	G	T	AB011131 // downstream // 50605 // Hs.12376 // PCLO // 27445 // piccolo (presynaptic cytomatrix protein) /// NM_000722 // upstream // 326386 // Hs.147871 // CACNA2D1 // 781 // calcium channel, voltage-dependent, alpha 2/delta subunit 1	PCLO	PCLO , rs2158219, piccolo (presynaptic cytomatrix protein) ,q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903941	tgggattgatagccta[A/C]taatagaagcaaaatg	A	C	NM_000722 // upstream // 316444 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 189543 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA05	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-1707131	ggagaaaatgtgcagaaggttgaca[C/G]gttactaagaacaa actaacagtac	C	G	AB011131 // intron // 0 // Hs.12376 // PCLO // 27445 // piccolo (presynaptic cytomatrix protein)	PCLO	PCLO , rs2715158, piccolo (presynaptic cytomatrix protein),q21.11
SNP_A-1922407	ttagaaataacctaaa[C/T]gattggacaaaagtt	C	T	NM_000722 // upstream // 388141 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 117846 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA05	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2,q21.11
SNP_A-1958111	tttcagttagta[G/T]cctattaagcaaaaga	G	T	NM_000722 // upstream // 406917 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 99070 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA055	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2132324	atagtagtgtataaac[C/T]gcacatatcgtttat	C	T	NM_000722 // upstream // 430604 // Hs.282151 // CACNA2D1 // 781 // Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA. /// AB011131 // downstream // 75383 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA055	CACNA2D1	CACNA2D1, Homo sapiens calcium channel, voltage-dependent, alpha 2 q21.11
SNP_A-2213794	cctaaaatcacagttc[C/G]aagaatgtaacccttg	C	G	AB011131 // intron // 0 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA0559 protein, partial cds. /// ENST00000333891 // intron // 0 // — // — // —	PCLO	PCLO, Homo sapiens for KIAA0559 protein, partial cds. q21.11
SNP_A-1892666	tgcacaaatgtcatca[G/T]gtcctcattgtgcaaa	G	T	AB011131 // upstream // 65290 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA0559 protein, partial cds. /// AB002329 // downstream // 136024 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// ENST00000333891	PCLO	PCLO, Homo sapiens for KIAA0559 protein, partial cds. q21.11
SNP_A-2228706	ctagacaggacagtaa[A/G]cgagggagaaatttgg	A	G	AB011131 // upstream // 130790 // Hs.12376 // PCLO // 27445 // Homo sapiens mRNA for KIAA0559 protein, partial cds. /// AB002329 // downstream // 70524 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// ENST00000333891	PCLO	PCLO, Homo sapiens for KIAA0559 protein, partial cds. q21.11
SNP_A-1990398	tgcttgctgttctcac[C/T]gtagagccagcctcc	C	T	AB002329 // upstream // 71383 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 240783 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic do	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11
SNP_A-1860706	tcataaatcatagtga[A/T]gtaaaagcaggtttta	A	T	AB002329 // upstream // 73716 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 238450 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic do	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11
SNP_A-2023531	aaaactatttatttta[C/T]gtcaacctatctagcc	C	T	AB002329 // upstream // 75752 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 236414 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic do	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11
SNP_A-1835359	tacctcatttattcc[A/G]atttcatcaggtgtga	A	G	AB002329 // upstream // 75808 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 236358 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic do	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1820795	gtttcccatttttcccc[A/T]ataaagatttacaaat	A	T	AB002329 // upstream // 117193 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 194973 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic d	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11
SNP_A-2121599	agtgaagctacagaaa[A/G]gataattttggggttt	A	G	AB002329 // upstream // 299078 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 13088 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic do	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11
SNP_A-1923413	ttaggatgatgttgaa[C/T]acattgaaatggagta	C	T	AB002329 // upstream // 309591 // Hs.528721 // SEMA3E // 9723 // Homo sapiens mRNA for KIAA0331 gene, partial cds. /// NM_006080 // downstream // 2575 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic dom	SEMA3E	SEMA3E, Homo sapiens for KIAA0331 gene, partial cds. q21.11
SNP_A-1946404	tttaaacctagtgaga[A/G]caaatcatcagctatg	A	G	NM_006080 // intron // 0 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // intron // 0 // --- // --- // --- // ---	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-1943946	ttgtatgagggaaagg[A/C]aatatgatctagctgc	A	C	NM_006080 // upstream // 11524 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // upstream // 11524 // --- // --- // --- // --- ///	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-1826537	taacaagttggactga[A/G]cacattgtatctcagg	A	G	NM_006080 // upstream // 112655 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // upstream // 112655 // --- // --- // --- // --- // ---	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-2128904	ataatggaataaaaga[A/G]tagagatggagaagat	A	G	NM_006080 // upstream // 190992 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // upstream // 190992 // --- // --- // --- // --- // ---	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-2055405	aataagtagtcaaaat[G/T]agtagagtagatttgg	G	T	NM_006080 // upstream // 271188 // Hs.252451 // SEMA3A // 10371 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), mRNA. /// ENST00000265362 // upstream // 271188 // --- // --- // --- // --- // ---	SEMA3A	SEMA3A, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (SEMA3A), q21.11
SNP_A-2266102	gaaggctatgaaaaca[A/G]gtaaagaagagcctac	A	G	NM_152754 // upstream // 164181 // Hs.201340 // SEMA3D // 223117 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), mRNA. /// ENST00000284136 // upstream // 164181 // --- // --- // --- // --- // ---	SEMA3D	SEMA3D, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), q21.11
SNP_A-2146730	atgcttatagaagagc[A/G]atgacaagcaaaattt	A	G	NM_152754 // upstream // 241403 // Hs.201340 // SEMA3D // 223117 // Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), mRNA. /// ENST00000284136 // upstream // 241403 // --- // --- // --- // --- // ---	SEMA3D	SEMA3D, Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D (SEMA3D), q21.11
SNP_A-1990424	agaatagcaactggta[A/G]taataggcaaaattca	A	G	ENST00000297220 // upstream // 3661 // --- // --- // --- // --- /// ENST00000354196 // upstream // 1258869 // --- // --- // --- // --- /// ENST00000355224 // upstream // 1258869 // --- // --- // --- // ---	-	q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1662556	gctttaaaaatacatttttaaataa[A/T]gacaaatgtgatataaatcaatttt	A	T	NM_000840 // upstream // 931220 // Hs.512145 // GRM3 // 2913 // glutamate receptor, metabotropic 3 /// NM_152754 // upstream // 671580 // Hs.187319 // SEMA3D // 223117 // sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin)	GRM3	GRM3 , rs3934484, glutamate receptor, metabotropic 3 ,q21.11
SNP_A-2311138	ggaagtcttcatggaa[C/T]gttatccaagttgctt	C	T	ENST00000297220 // upstream // 1150820 // --- // --- // --- // --- /// ENST00000354196 // upstream // 111710 // --- // --- // --- // --- /// ENST00000355224 // upstream // 111710 // --- // --- // --- // ---	-	q21.11
SNP_A-1748801	agcgaagaatcacagagaaacaatc[C/T]taaactgctgaaatttcctctccca	C	T	NM_000840 // intron // 0 // Hs.512145 // GRM3 // 2913 // glutamate receptor, metabotropic 3	GRM3	GRM3 , rs727989, glutamate receptor, metabotropic 3,q21.12
SNP_A-2239694	ctgaaagaattacaca[A/G]caatatgtaaaggtag	A	G	ENST00000342973 // intron // 0 // --- // --- // --- // ---	-	q21.12
SNP_A-2216900	cctctgcttatgtttc[A/G]ctcgcaccagctgggc	A	G	NM_021145 // upstream // 5616 // Hs.489028 // DMTF1 // 9988 // Homo sapiens cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA. /// NM_024315 // downstream // 49368 // Hs.196129 // C7orf23 // 79161 // Homo sapiens chromosome 7 open reading fra	DMTF1	DMTF1, Homo sapiens cyclin D binding myb-like transcription factor 1 (DMTF1), q21.12
SNP_A-1915495	tgttcctttggccaca[C/T]tgtgatttacagttta	C	T	NM_021151 // intron // 0 // Hs.125039 // CROT // 54677 // Homo sapiens carnitine O-octanoyltransferase (CROT), mRNA. /// ENST00000331536 // intron // 0 // --- // --- // --- // ---	CROT	CROT, Homo sapiens carnitine O-octanoyltransferase (CROT), q21.12
SNP_A-2198487	catttataaatccacc[A/C]agcaaacatatgaggc	A	C	NM_000443 // intron // 0 // Hs.287827 // ABCB4 // 5244 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A, mRNA. /// NM_018849 // intron // 0 // Hs.287827 // ABCB4 // 5244 // Homo sapiens ATP-binding casse	ABCB4	ABCB4, Homo sapiens ATP-binding cassette, sub-family B (MDR,q21.12
SNP_A-1921021	ttacagcctcactggg[A/G]aatttgaccttactag	A	G	NM_000927 // intron // 0 // Hs.489033 // ABCB1 // 5243 // Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 1 (ABCB1), mRNA. /// ENST00000265724 // intron // 0 // --- // --- // --- // ---	ABCB1	ABCB1, Homo sapiens ATP-binding cassette, sub-family B (MDR,q21.12
SNP_A-1669879	tcctattaccattacctgaactaag[A/G]cctatattaatccttcaacttattac	A	G	NM_004194 // intron // 0 // Hs.256398 // ADAM22 // 53616 // a disintegrin and metalloproteinase domain 22 /// NM_016351 // intron // 0 // Hs.256398 // ADAM22 // 53616 // a disintegrin and metalloproteinase domain 22 /// NM_021721 // intron // 0 // Hs.256	ADAM22	ADAM22 , rs10487009, a disintegrin and metalloproteinase domain 22 ,q21.12
SNP_A-1990470	tatatgaacagttgaa[A/C]atttgtggattgttct	A	C	NM_016351 // intron // 0 // Hs.256398 // ADAM22 // 53616 // Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA. /// NM_021721 // intron // 0 // Hs.256398 // ADAM22 // 53616 // Homo sapiens a disintegrin and met	ADAM22	ADAM22, Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, q21.12
SNP_A-1849700	tatggttcctgggcaa[A/C]cctgagatggagattt	A	C	NM_024636 // upstream // 30363 // Hs.521008 // TNFAIP9 // 79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream // 422722 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.12
SNP_A-2028496	aaactgaactatgatg[C/G]aactacaacagatgct	C	G	NM_024636 // upstream // 30476 // Hs.521008 // TNFAIP9 // 79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream // 422609 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.12
SNP_A-1990472	agtcataaaaagggta[C/T]actgctgagactgcgt	C	T	NM_024636 // upstream // 45226 // Hs.521008 // TNFAIP9 // 79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream // 407859 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2257079	cttctcacacttac[A/G]ctccagcaattctgaa	A	G	NM_024636 // upstream // 159751 // Hs.521008 // TNFAIP9 // 79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream // 293334 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FL	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.13
SNP_A-1848305	tatcttttcttatc[A/G]aactgtcatgttgccc	A	G	NM_024636 // upstream // 173187 // Hs.521008 // TNFAIP9 // 79689 // Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), mRNA. /// NM_181646 // upstream // 279898 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FL	TNFAIP9	TNFAIP9, Homo sapiens tumor necrosis factor, alpha-induced protein 9 (TNFAIP9), q21.13
SNP_A-1812729	gtgggaatgctaatca[C/T]atctgtgtatcaacac	C	T	NM_181646 // intron // 0 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// ENST00000333190 // intron // 0 // — // — // —	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-1908057	tgtacaatagagttctt[A/T]aaacttacctcgcta	A	T	NM_181646 // intron // 0 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// ENST00000333190 // intron // 0 // — // — // —	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-2281265	gagtatataaaactaa[A/C]atctcagtggtgatca	A	C	NM_181646 // intron // 0 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// ENST00000333190 // intron // 0 // — // — // —	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-1990503	aagcagcaggaaagcag[A/C]agatcattatccaattt	A	C	NM_181646 // intron // 0 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// ENST00000333190 // intron // 0 // — // — // —	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-1809974	gtgagtgataccaa[C/T]gaagagaagaaagga	C	T	NM_181646 // downstream // 641656 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// NM_152706 // upstream // 1182971 // Hs.112877 // MGC26647 // 219557 // Homo sapiens hypothetical protein MGC26647 (MGC	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-2214495	cctagaaaaagttcta[C/T]gtactatctgaaagct	C	T	NM_181646 // downstream // 720814 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// NM_152706 // upstream // 1262129 // Hs.112877 // MGC26647 // 219557 // Homo sapiens hypothetical protein MGC26647 (MGC	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-2174177	cacactaaatctccat[C/T]accacatgtgcataca	C	T	NM_181646 // downstream // 767711 // Hs.381366 // FLJ32110 // 219578 // Homo sapiens hypothetical protein FLJ32110 (FLJ32110), mRNA. /// NM_152706 // upstream // 1309026 // Hs.112877 // MGC26647 // 219557 // Homo sapiens hypothetical protein MGC26647 (MGC	FLJ32110	FLJ32110, Homo sapiens hypothetical protein FLJ32110 (FLJ32110), q21.13
SNP_A-2212131	ccctgcgagtccctag[G/T]aagctgcctagtctt	G	T	AB020641 // intron // 0 // Hs.430742 // PFTK1 // 5218 // Homo sapiens mRNA for KIAA0834 protein, partial cds. /// ENST00000306129 // intron // 0 // — // — // — // —	PFTK1	PFTK1, Homo sapiens for KIAA0834 protein, partial cds, q21.13
SNP_A-2195552	catggtacctcaacca[A/G]tagttaacctccata	A	G	AB020641 // intron // 0 // Hs.430742 // PFTK1 // 5218 // Homo sapiens mRNA for KIAA0834 protein, partial cds. /// ENST00000306129 // intron // 0 // — // — // — // —	PFTK1	PFTK1, Homo sapiens for KIAA0834 protein, partial cds, q21.13
SNP_A-1826967	taacattgatgtttca[A/C]aaatttctatttttacc	A	C	AB020641 // intron // 0 // Hs.430742 // PFTK1 // 5218 // Homo sapiens mRNA for KIAA0834 protein, partial cds. /// NM_012395 // intron // 0 // Hs.430742 // PFTK1 // 5218 // Homo sapiens PFTAIRE protein kinase 1 (PFTK1), mRNA. /// ENST00000306129 // intron	PFTK1	PFTK1, Homo sapiens for KIAA0834 protein, partial cds, q21.13
SNP_A-1851769	tattgaaattaatgaa[C/T]agcactgaggcccaat	C	T	AB020641 // intron // 0 // Hs.430742 // PFTK1 // 5218 // Homo sapiens mRNA for KIAA0834 protein, partial cds. /// NM_012395 // intron // 0 // Hs.430742 // PFTK1 // 5218 // Homo sapiens PFTAIRE protein kinase 1 (PFTK1), mRNA. /// ENST00000306129 // intron	PFTK1	PFTK1, Homo sapiens for KIAA0834 protein, partial cds, q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990561	tccttggtgctgctcaa[A/G]gaatgcgtttattat	A	G	NM_003505 // downstream // 47783 // Hs.94234 // FZD1 // 8321 // Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), mRNA. /// NM_006980 // downstream // 556290 // Hs.532216 // MTERF // 7978 // Homo sapiens transcription termination factor, mitochondrial	FZD1	FZD1, Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), q21.13
SNP_A-1720451	ttatcatcacaaacataaccaatcac[A/C]gaaattagatttgctgtt tcaggt	A	C	NM_003505 // downstream // 276131 // Hs.94234 // FZD1 // 8321 // frizzled homolog 1 (Drosophila) /// NM_006980 // downstream // 327942 // Hs.97996 // MTERF // 7978 // transcription termination factor, mitochondrial	FZD1	FZD1, rs7787692, frizzled homolog 1 (Drosophila) ,q21.2
SNP_A-1702357	cttccttagatgttcatggccggca[C/G]cttaagaatcctaagac ctcaactc	C	G	NM_003505 // downstream // 296575 // Hs.94234 // FZD1 // 8321 // frizzled homolog 1 (Drosophila) /// NM_006980 // downstream // 307498 // Hs.97996 // MTERF // 7978 // transcription termination factor, mitochondrial	FZD1	FZD1, rs2110770, frizzled homolog 1 (Drosophila) ,q21.2
SNP_A-1862016	tcatgatgaaatatac[A/C]ctttcttgctgcccg	A	C	NM_003505 // downstream // 309567 // Hs.94234 // FZD1 // 8321 // Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), mRNA. /// NM_006980 // downstream // 294506 // Hs.532216 // MTERF // 7978 // Homo sapiens transcription termination factor, mitochondrial	FZD1	FZD1, Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), q21.2
SNP_A-2248434	ctgtgttcacaaaa[C/T]aagcttggatggaaaa	C	T	NM_003505 // downstream // 507991 // Hs.94234 // FZD1 // 8321 // Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), mRNA. /// NM_006980 // downstream // 96082 // Hs.532216 // MTERF // 7978 // Homo sapiens transcription termination factor, mitochondrial	FZD1	FZD1, Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), q21.2
SNP_A-1652086	agtagaaatgaatgtgcactaatga[A/G]cttatttctacacagtt gcacta	A	G	NM_000466 // intron // 0 // Hs.164682 // PEX1 // 5189 // peroxisome biogenesis factor 1	PEX1	PEX1, rs2066743, peroxisome biogenesis factor 1,q21.2
SNP_A-1661432	ctctcttagaaggctcctaggaaga[C/T]gtatgactacccaggta actcagtc	C	T	NM_001259 // upstream // 185027 // Hs.38481 // CDK6 // 1021 // cyclin-dependent kinase 6 /// NM_017654 // downstream // 81386 // Hs.65641 // FLJ20073 // 54809 // FLJ20073 protein	CDK6	CDK6, rs102363337, cyclin-dependent kinase 6 ,q21.2
SNP_A-1823111	taaaacaatctttctc[C/T]aatcaacgaaaaggaa	C	T	NM_024553 // intron // 0 // Hs.222282 // FLJ20097 // 55610 // Homo sapiens hypothetical protein FLJ20097 (FLJ20097), mRNA. /// ENST00000251739 // intron // 0 // — // — // — /// ENST00000317751 // intron // 0 // — // — // — /// EN	FLJ20097	FLJ20097, Homo sapiens hypothetical protein FLJ20097 (FLJ20097), q21.3
SNP_A-2160088	atttattgtcctagaa[A/G]gatgtgttctaaaga	A	G	NM_001742 // intron // 0 // Hs.489127 // CALCR // 799 // Homo sapiens calcitonin receptor (CALCR), mRNA. /// L00587 // intron // 0 // Hs.489127 // CALCR // 799 // Human calcitonin receptor mRNA, complete cds. /// ENST00000359558 // intron // 0 // — // -	CALCR	CALCR, Homo sapiens calcitonin receptor (CALCR), q21.3
SNP_A-1755358	atcaggaatacaaagaattaatct[G/T]aactaatgtgatttttgttt ggggat	G	T	L00587 // intron // 0 // Hs.640 // CALCR // 799 // calcitonin receptor	CALCR	CALCR, rs10234339, calcitonin receptor,q21.3
SNP_A-2274692	gagaaagaaataaaag[A/G]catcaagctatcttc	A	G	NM_006528 // downstream // 121200 // Hs.438231 // TFPI2 // 7980 // Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), mRNA. /// ENST00000356305 // upstream // 94117 // — // — // — /// ENST00000222543 // downstream // 121200 // — // —	TFPI2	TFPI2, Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), q21.3
SNP_A-2284225	gatattaacccatgal[A/G]gtatatgtttcacaaa	A	G	NM_006528 // downstream // 5364 // Hs.438231 // TFPI2 // 7980 // Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), mRNA. /// ENST00000356305 // upstream // 209953 // — // — // — /// ENST00000222543 // downstream // 5364 // — // — // —	TFPI2	TFPI2, Homo sapiens tissue factor pathway inhibitor 2 (TFPI2), q21.3
SNP_A-1943756	ttgtagactccaataa[C/T]tgtactgcttttga	C	T	NM_005868 // upstream // 345909 // Hs.489132 // BET1 // 10282 // Homo sapiens BET1 homolog (S. cerevisiae) (BET1), mRNA. /// NM_000089 // upstream // 44745 // Hs.489142 // COL1A2 // 1278 // Homo sapiens collagen, type I, alpha 2 (COL1A2), mRNA. /// ENST00	BET1	BET1, Homo sapiens BET1 homolog (S. cerevisiae) (BET1), q21.3
SNP_A-1740497	tttcttataacatggtctatacttcca[A/G]gccaacaacttcatgcac aatcac	A	G	NM_000089 // downstream // 12383 // Hs.232115 // COL1A2 // 1278 // collagen, type I, alpha 2 /// NM_022900 // upstream // 66450 // Hs.324725 // CAS1 // 64921 // O-acetyltransferase	COL1A2	COL1A2, rs4729134, collagen, type I, alpha 2 ,q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1736623	gctgaactccagtcatgaaccgtca[C/G]ctagctaatatctatctt ctgtgag	C	G	NM_003919 // downstream // 23454 // Hs.409798 // SGCE // 8910 // sarcoglycan, epsilon /// NM_022900 // downstream // 4809 // Hs.324725 // CAS1 // 64921 // O-acetyltransferase	SGCE	SGCE , rs10499907, sarcoglycan, epsilon ,q21.3
SNP_A-1904439	tggggaatgctttaaa[A/T]actgagacaggcagtt	A	T	NM_022900 // downstream // 20514 // Hs.260041 // CAS1 // 64921 // Homo sapiens O-acetyltransferase (CAS1), mRNA. /// NM_003919 // downstream // 7751 // Hs.371199 // SGCE // 8910 // Homo sapiens sarcoglycan, epsilon (SGCE), mRNA. /// ENST00000297273 // dow	CAS1	CAS1, Homo sapiens O-acetyltransferase (CAS1), q21.3
SNP_A-1715123	cattctttcatttattcaaattgat[G/T]aatgcgattatatggaaatta aaaa	G	T	NM_000446 // intron // 0 // Hs.282209 // PON1 // 5444 // paraoxonase 1	PON1	PON1 , rs3917498, paraoxonase 1,q21.3
SNP_A-2012726	agccttgagaaggaaa[C/G]agacatggagcaaatc	C	G	NM_000446 // upstream // 901 // Hs.370995 // PON1 // 5444 // Homo sapiens paraoxonase 1 (PON1), mRNA. /// NM_000940 // downstream // 34530 // Hs.440967 // PON3 // 5446 // Homo sapiens paraoxonase 3 (PON3), mRNA. /// ENST00000222381 // upstream // 901 // -	PON1	PON1, Homo sapiens paraoxonase 1 (PON1), q21.3
SNP_A-1801924	gtataaaaatgcacac[C/T]ccttgaaagtaccact	C	T	NM_000940 // intron // 0 // Hs.440967 // PON3 // 5446 // Homo sapiens paraoxonase 3 (PON3), mRNA. /// ENST00000265627 // intron // 0 // — // — // — // —	PON3	PON3, Homo sapiens paraoxonase 3 (PON3), q21.3
SNP_A-2191263	catatagaaatagaga[C/T]ggaatgaggagatgga	C	T	NM_000940 // intron // 0 // Hs.440967 // PON3 // 5446 // Homo sapiens paraoxonase 3 (PON3), mRNA. /// ENST00000265627 // intron // 0 // — // — // — // —	PON3	PON3, Homo sapiens paraoxonase 3 (PON3), q21.3
SNP_A-2078902	acccaagggcacaagc[A/G]ctagaaatcagtggtg	A	G	NM_000940 // CDS // 0 // Hs.440967 // PON3 // 5446 // Homo sapiens paraoxonase 3 (PON3), mRNA. /// ENST00000265627 // CDS // 0 // — // — // — // —	PON3	PON3, Homo sapiens paraoxonase 3 (PON3), q21.3
SNP_A-2228559	ctagaaacaccagtag[A/T]caccgacagaaaatag	A	T	NM_000305 // upstream // 24814 // Hs.530077 // PON2 // 5445 // Homo sapiens paraoxonase 2 (PON2), mRNA. /// AF001601 // upstream // 24848 // Hs.530077 // PON2 // 5445 // Homo sapiens paraoxonase (PON2) mRNA, complete cds. /// NM_145872 // upstream // 2617	PON2	PON2, Homo sapiens paraoxonase 2 (PON2), q21.3
SNP_A-1897120	tgctcctgtggaccaa[C/G]aagtaagaaaagtctc	C	G	NM_000305 // upstream // 45132 // Hs.530077 // PON2 // 5445 // Homo sapiens paraoxonase 2 (PON2), mRNA. /// AF001601 // upstream // 45166 // Hs.530077 // PON2 // 5445 // Homo sapiens paraoxonase (PON2) mRNA, complete cds. /// NM_145872 // upstream // 5857	PON2	PON2, Homo sapiens paraoxonase 2 (PON2), q21.3
SNP_A-1706845	gtactaaacgggaggaccaacacag[A/G]taagtgcttcccaa cccttccagac	A	G	NM_016116 // intron // 0 // Hs.413226 // ASB4 // 51666 // ankyrin repeat and SOCS box-containing 4 /// NM_145872 // intron // 0 // Hs.413226 // ASB4 // 51666 // ankyrin repeat and SOCS box-containing 4	ASB4	ASB4 , rs2158047, ankyrin repeat and SOCS box-containing 4 ,q21.3
SNP_A-1953102	tttcttgtattctaaa[A/T]gaggttatgcattgtt	A	T	NM_002612 // upstream // 88887 // Hs.8364 // PDK4 // 5166 // Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4), mRNA. /// NM_004411 // upstream // 87212 // Hs.440364 // DNCI1 // 1780 // Homo sapiens dynein, cytoplasmic, intermediate polypepti	PDK4	PDK4, Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 4 (PDK4), q21.3
SNP_A-2159202	atttaaagacatacta[A/T]catgaaccacataatg	A	T	NM_004411 // intron // 0 // Hs.440364 // DNCI1 // 1780 // Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // — // — // — // — /// ENST00000359388 // intron // 0 // — // — // — //	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-2039364	aacatactaacaggga[C/T]ggtttaaaagatgaga	C	T	NM_004411 // intron // 0 // Hs.440364 // DNCI1 // 1780 // Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // — // — // — // — /// ENST00000359388 // intron // 0 // — // — // — //	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-1722832	tactctggtcattttcttctttatc[A/G]ctgttccaagaccaccaggc aatta	A	G	NM_004411 // intron // 0 // Hs.65248 // DNCI1 // 1780 // dynein, cytoplasmic, intermediate polypeptide 1	DNCI1	DNCI1 , rs1488516, dynein, cytoplasmic, intermediate polypeptide 1,q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1952190	tttctcatttcacaaa[A/C]aacataaaggccaaag	A	C	NM_004411 // intron // 0 // Hs.440364 // DNCI1 // 1780 // Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // --- // --- // --- // --- /// ENST00000359388 // intron // 0 // --- // --- // --- // ---	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-1823464	taaaaggaatgctaga[A/G]aacatgtactaatatt	A	G	NM_004411 // intron // 0 // Hs.440364 // DNCI1 // 1780 // Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // --- // --- // --- // --- /// ENST00000359388 // intron // 0 // --- // --- // --- // ---	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-1879691	tcttcagtggctaaag[A/G]atccatgactttctga	A	G	NM_004411 // intron // 0 // Hs.440364 // DNCI1 // 1780 // Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /// ENST00000338753 // intron // 0 // --- // --- // --- // --- /// ENST00000359388 // intron // 0 // --- // --- // --- // ---	DNCI1	DNCI1, Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), q21.3
SNP_A-2262372	gaaatgattcgctgcc[G/T]cttagaggtttagagc	G	T	NM_014251 // intron // 0 // Hs.489190 // SLC25A13 // 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// ENST00000265631 // intron // 0 // --- // --- // --- // ---	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-2080444	acctagcgtataattc[A/C]attcacgcaaagtgaa	A	C	NM_014251 // intron // 0 // Hs.489190 // SLC25A13 // 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// ENST00000265631 // intron // 0 // --- // --- // --- // ---	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-1960740	tttttctgaatctaac[A/G]aagggtcttactttct	A	G	NM_014251 // intron // 0 // Hs.489190 // SLC25A13 // 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// ENST00000265631 // intron // 0 // --- // --- // --- // ---	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-2293401	gcagatggcgagaaag[A/G]aagggtaggacacagg	A	G	NM_014251 // intron // 0 // Hs.489190 // SLC25A13 // 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// ENST00000265631 // intron // 0 // --- // --- // --- // ---	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-1990664	ttgatcaaaatttgca[A/G]cactcatgtgggtcct	A	G	NM_014251 // upstream // 69029 // Hs.489190 // SLC25A13 // 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// NM_207503 // downstream // 90504 // Hs.534805 // FLJ42280 // 401388 // Homo sapiens FLJ42280 protein (FLJ42	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-1942576	ttgggaaagagagcaa[A/G]tcaggaaattcaacat	A	G	NM_014251 // upstream // 98093 // Hs.489190 // SLC25A13 // 10165 // Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA. /// NM_207503 // downstream // 61440 // Hs.534805 // FLJ42280 // 401388 // Homo sapiens FLJ42280 protein (FLJ42	SLC25A13	SLC25A13, Homo sapiens solute carrier family 25, member 13 (citrin) (SLC25A13), q21.3
SNP_A-2086187	actctgccaaccgaaa[A/G]cagcagagtttcagca	A	G	NM_006304 // upstream // 148993 // Hs.489201 // SHFM1 // 7979 // Homo sapiens split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA. /// ENST00000248566 // upstream // 148993 // --- // --- // --- // --- /// ENST00000007660 // upstream // 147283	SHFM1	SHFM1, Homo sapiens split hand,q21.3
SNP_A-1990679	tcatattctatgacac[A/G]gaacttaaaggtctca	A	G	NM_006304 // upstream // 201225 // Hs.489201 // SHFM1 // 7979 // Homo sapiens split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA. /// ENST00000248566 // upstream // 201225 // --- // --- // --- // --- /// ENST00000007660 // upstream // 95051	SHFM1	SHFM1, Homo sapiens split hand,q21.3
SNP_A-1864166	tccacatttgggttag[A/T]attatagaaggcccac	A	T	NM_006304 // upstream // 208512 // Hs.489201 // SHFM1 // 7979 // Homo sapiens split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA. /// ENST00000248566 // upstream // 208512 // --- // --- // --- // --- /// ENST00000007660 // upstream // 87764	SHFM1	SHFM1, Homo sapiens split hand,q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1916453	tgtttaaaagccaaga[A/G]gttgttatagttttaa	A	G	NM_006304 // upstream // 221781 // Hs.489201 // SHFM1 // 7979 // Homo sapiens split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA. /// ENST00000248566 // upstream // 221781 // — // — // — // — /// ENST00000007660 // upstream // 74495	SHFM1	SHFM1, Homo sapiens split hand q21.3
SNP_A-1869815	tccttcctatgaggaa[A/C]gtcacatatttgtggg	A	C	NM_006304 // upstream // 222246 // Hs.489201 // SHFM1 // 7979 // Homo sapiens split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA. /// ENST00000248566 // upstream // 222246 // — // — // — // — /// ENST00000007660 // upstream // 74030	SHFM1	SHFM1, Homo sapiens split hand q21.3
SNP_A-2075212	acatctgaaggttaac[C/T]atgtggcaatttgtac	C	T	NM_020186 // downstream // 373352 // Hs.42785 // ACN9 // 57001 // Homo sapiens ACN9 homolog (S. cerevisiae) (ACN9), mRNA. /// NM_013996 // upstream // 176952 // Hs.2563 // TAC1 // 6863 // Homo sapiens tachykinin, precursor 1 (substance K, substance P, neu	ACN9	ACN9, Homo sapiens ACN9 homolog (S. cerevisiae) (ACN9), q21.3
SNP_A-1892282	tgcaacctagagtaaa[C/G]tgagcccatagtctat	C	G	NM_013996 // downstream // 77301 // Hs.2563 // TAC1 // 6863 // Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur /// NM_013998 // downstream // 77301 // Hs.2563 // TAC1 // 6863	TAC1	TAC1, Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur q21.3
SNP_A-2092914	agaacaaattacatgg[A/T]cattcaactctcattg	A	T	NM_013996 // downstream // 78972 // Hs.2563 // TAC1 // 6863 // Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur /// NM_013998 // downstream // 78972 // Hs.2563 // TAC1 // 6863	TAC1	TAC1, Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur ,q21.3
SNP_A-2184780	cagctgccccttgga[G/T]aataggcttttattac	G	T	NM_013996 // downstream // 84532 // Hs.2563 // TAC1 // 6863 // Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur /// NM_013998 // downstream // 84532 // Hs.2563 // TAC1 // 6863	TAC1	TAC1, Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur ,q21.3
SNP_A-1912334	tgtgattcatgagtca[A/G]gtagcatctcatctaa	A	G	NM_013996 // downstream // 96106 // Hs.2563 // TAC1 // 6863 // Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur /// NM_013998 // downstream // 96106 // Hs.2563 // TAC1 // 6863	TAC1	TAC1, Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neur ,q21.3
SNP_A-2192110	catcactgtcgggatg[A/T]acccctgcacgccctc	A	T	NM_001673 // CDS // 0 // Hs.489207 // ASNS // 440 // Homo sapiens asparagine synthetase (ASNS), transcript variant 2, mRNA. /// NM_133436 // CDS // 0 // Hs.489207 // ASNS // 440 // Homo sapiens asparagine synthetase (ASNS), transcript variant 1, mRNA. ///	ASNS	ASNS, Homo sapiens asparagine synthetase (ASNS), transcript variant 2, q21.3
SNP_A-2129307	atacaaagtcatttga[C/T]ggatgtgacactgggc	C	T	NM_006188 // upstream // 28015 // Hs.510456 // OCM // 4951 // Homo sapiens oncomodulin (OCM), mRNA. /// NM_014916 // upstream // 88766 // Hs.444179 // LMTK2 // 22853 // Homo sapiens lemur tyrosine kinase 2 (LMTK2), mRNA. /// ENST00000257627 // upstream //	OCM	OCM, Homo sapiens oncomodulin (OCM), q21.3
SNP_A-1852383	tatttaacttctacac[A/G]gtatccctttatgatg	A	G	NM_018842 // intron // 0 // Hs.489237 // BAIAP2L1 // 55971 // Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), mRNA. /// ENST00000005260 // intron // 0 // — // — // — // —	BAIAP2L1	BAIAP2L1, Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), q22.1
SNP_A-1790718	ggggctttctaaacaa[C/T]gtaacccagtgcataa	C	T	NM_018842 // intron // 0 // Hs.489237 // BAIAP2L1 // 55971 // Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), mRNA. /// ENST00000005260 // intron // 0 // — // — // — // —	BAIAP2L1	BAIAP2L1, Homo sapiens insulin receptor tyrosine kinase substrate (LOC55971), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270967	gacagttaatacagat[A/G]agtccctcagccctccc	A	G	NM_002523 // downstream // 30013 // Hs.3281 // NPTX2 // 4885 // Homo sapiens neuronal pentraxin II (NPTX2), mRNA. /// NM_152913 // downstream // 154920 // Hs.270753 // DKFZp761L1417 // 222865 // Homo sapiens hypothetical protein DKFZp761L1417 (DKFZp761L14	NPTX2	NPTX2, Homo sapiens neuronal pentraxin II (NPTX2), q22.1
SNP_A-2210571	ccccgtgccccacggg[C/T]agaatcccagaggagga	C	T	NM_003496 // intron // 0 // Hs.203952 // TRRAP // 8295 // Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA. /// AF110377 // intron // 0 // Hs.203952 // TRRAP // 8295 // Homo sapiens PCAF-associated factor 400 (PAF400) mRNA	TRRAP	TRRAP, Homo sapiens transformation.q22.1
SNP_A-2023141	aaaacagtcgaagcca[A/G]gaaatcagacttgct	A	G	NM_017460 // intron // 0 // Hs.442527 // CYP3A4 // 1576 // Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide 4 (CYP3A4), transcript variant 1, mRNA. /// ENST00000354593 // intron // 0 // --- // --- // --- /// ENST00000336411 // intro	CYP3A4	CYP3A4, Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide 4 (CYP3A4), transcript variant 1, q22.1
SNP_A-1789679	gggctatgacttagtg[C/G]aagaggcaactcagga	C	G	NM_133457 // intron // 0 // Hs.131603 // EMID2 // 136227 // Homo sapiens EMI domain containing 2 (EMID2), mRNA. /// ENST00000313669 // intron // 0 // --- // --- // ---	EMID2	EMID2, Homo sapiens EMI domain containing 2 (EMID2), q22.1
SNP_A-2073506	acagtaaaacacagacq[A/C]agtttcaaaagaaaac	A	C	NM_138403 // upstream // 175446 // Hs.247831 // MYLC2PL // 93408 // Homo sapiens myosin light chain 2, precursor lymphocyte-specific (MYLC2PL), mRNA. /// NM_181552 // upstream // 11447 // Hs.438974 // CUTL1 // 1523 // Homo sapiens cut-like 1, CCAAT displa	MYLC2PL	MYLC2PL, Homo sapiens myosin light chain 2, precursor lymphocyte-specific (MYLC2PL), q22.1
SNP_A-2201451	ccaatgcatgaattaa[C/G]attcagcggagagtc	C	G	NM_182634 // intron // 0 // Hs.148768 // FLJ36166 // 349152 // Homo sapiens hypothetical protein FLJ36166 (FLJ36166), mRNA. /// ENST00000312132 // intron // 0 // --- // --- // --- /// ENST00000306389 // intron // 0 // --- // --- // --- /// E	FLJ36166	FLJ36166, Homo sapiens hypothetical protein FLJ36166 (FLJ36166), q22.1
SNP_A-2033595	aaatatatttgcagaa[C/T]actatgctgtttctca	C	T	ENST00000343529 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1990750	gctacttgtcagagga[C/T]actgaattgaagagag	C	T	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1846964	tatcagaatccattcaj[A/G]ctagcatttttggaac	A	G	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1960004	tttgttattaaaaaa[A/G]gtttgtgtatggctt	A	G	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-2023037	aaaacactggcaataa[C/T]gaggcctacctgttat	C	T	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1847665	tatctaccaccatgca[A/G]cigttaagcagggagg	A	G	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1681568	tatataaacaacctctctagga[A/T]tattcatttttcatcagtttaa cta	A	T	NM_005045 // intron // 0 // Hs.431010 // RELN // 5649 // reelin /// NM_173054 // intron // 0 // Hs.431010 // RELN // 5649 // reelin	RELN	RELN , rs10487173, reelin .q22.1
SNP_A-2140345	atctcagcaggaccac[G/T]gtgctttttctggact	G	T	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-2273945	gactgtcctattaata[C/T]ggcaaatgtagtctct	C	T	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-2066020	aatttgcacttagaa[A/G]aatctggagaattgaa	A	G	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1922961	ttagcaaccttaatca[C/T]attgctactgttccct	C	T	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-2303302	gctatgtcaaatatac[C/T]agcatggagttagga	C	T	ENST00000343529 // intron // 0 // --- // --- // --- /// ENST00000339713 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-2012759	aagatttctacataa[C/T]gttgcaggatcatctt	C	T	NM_181747 // downstream // 79735 // Hs.432948 // ORC5L // 5001 // Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, mRNA. /// NM_002553 // downstream // 79735 // Hs.432948 // ORC5L // 5001 // Homo sapiens origi	ORC5L	ORC5L, Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, q22.1
SNP_A-1744929	caaaagaactgcagatgtagttctcc[C/T]aactgtatagcacattg ctttctat	C	T	AY260763 // intron // 0 // Hs.439124 // LHFPL3 // 375612 // lipoma HMGIC fusion partner-like 3	LHFPL3	LHFPL3 , rs41027, lipoma HMGIC fusion partner-like 3.q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2238923	ctcttcattctcatta[C/T]cttttggcatatacag	C	T	NM_199000 // intron // 0 // Hs.130655 // LHFPL3 // 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // — // — // — // —	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1866034	tcccactggactataa[A/G]ctccacgagggaagaa	A	G	NM_199000 // intron // 0 // Hs.130655 // LHFPL3 // 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // — // — // — // —	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1723124	atgaaaattccttcttggtggctag[A/C]aagtttgaaaatttctgaatttatt	A	C	AY260763 // intron // 0 // Hs.439124 // LHFPL3 // 375612 // lipoma HMGIC fusion partner-like 3	LHFPL3	LHFPL3 , rs4727605, lipoma HMGIC fusion partner-like 3,q22.2
SNP_A-1901174	tggatgaatacttttc[A/T]cagtcagaaatcacta	A	T	NM_199000 // intron // 0 // Hs.130655 // LHFPL3 // 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // — // — // — // —	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1681382	aagctaaatagtaggtaaccactca[A/G]taatctggacccaggctccctgttt	A	G	AY260763 // intron // 0 // Hs.439124 // LHFPL3 // 375612 // lipoma HMGIC fusion partner-like 3	LHFPL3	LHFPL3 , rs4338031, lipoma HMGIC fusion partner-like 3,q22.2
SNP_A-2012760	tgtatatacatccaca[C/T]attgtgcggtatcagc	C	T	NM_199000 // intron // 0 // Hs.130655 // LHFPL3 // 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// ENST00000335925 // intron // 0 // — // — // — // —	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-2112194	aggattctggtcttct[A/G]acaactggttggatat	A	G	NM_199000 // downstream // 35221 // Hs.130655 // LHFPL3 // 375612 // Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), mRNA. /// NM_018682 // upstream // 223449 // Hs.380021 // MLL5 // 55904 // Homo sapiens myeloid/lymphoid or mixed-lineage leukem	LHFPL3	LHFPL3, Homo sapiens lipoma HMGIC fusion partner-like 3 (LHFPL3), q22.2
SNP_A-1906859	tggttcacccatctgt[A/G]aaaggagagtaacagc	A	G	AB033044 // intron // 0 // Hs.489603 // ATXN7L1 // 57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// ENST00000329090 // intron // 0 // — // — // — // — /// ENST00000297416 // intron // 0 // — // — // — // —	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. ,q22.3
SNP_A-1805526	gtccaggaatccttcc[A/G]gcagctccgcttcgca	A	G	AB033044 // intron // 0 // Hs.489603 // ATXN7L1 // 57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// ENST00000297416 // intron // 0 // — // — // — // —	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein,. partial cds. ,q22.3
SNP_A-1930791	ttccagaacaaaagct[C/G]aactctttcgtgtggc	C	G	AB033044 // intron // 0 // Hs.489603 // ATXN7L1 // 57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// ENST00000297416 // intron // 0 // — // — // — // —	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. ,q22.3
SNP_A-2158491	attgtaaggtgccaca[G/T]ccattaaatagcacct	G	T	AB033044 // intron // 0 // Hs.489603 // ATXN7L1 // 57485 // Homo sapiens mRNA for KIAA1218 protein, partial cds. /// NM_152749 // intron // 0 // Hs.489603 // ATXN7L4 // 222255 // Homo sapiens ataxin 7-like 1 (ATXN7L4), mRNA. /// ENST00000297416 // intron	ATXN7L1	ATXN7L1, Homo sapiens for KIAA1218 protein, partial cds. q22.3
SNP_A-1680900	ttccagataattctcaaaccacatg[A/G]caggtgttactgaatgctggcaggg	A	G	NM_152749 // intron // 0 // Hs.211068 // MGC33190 // 222255 // hypothetical protein MGC33190	MGC33190	MGC33190 , rs10487836, hypothetical protein MGC33190,q22.3
SNP_A-2152458	attaactgtcaaataa[C/G]aaaatctatggatgaa	C	G	NM_152750 // intron // 0 // Hs.202120 // FLJ23834 // 222256 // Homo sapiens hypothetical protein FLJ23834 (FLJ23834), mRNA. /// ENST00000343407 // intron // 0 // — // — // — // — /// ENST00000317716 // intron // 0 // — // — // — // —	FLJ23834	FLJ23834, Homo sapiens hypothetical protein FLJ23834 (FLJ23834), q22.3
SNP_A-2023639	aaaactggggtaaata[C/T]gttcaggaattagacc	C	T	NM_152750 // downstream // 2620 // Hs.202120 // FLJ23834 // 222256 // Homo sapiens hypothetical protein FLJ23834 (FLJ23834), mRNA. /// NM_006754 // downstream // 54453 // Hs.80919 // SYPL // 6856 // Homo sapiens synaptophysin-like protein (SYPL), transcri	FLJ23834	FLJ23834, Homo sapiens hypothetical protein FLJ23834 (FLJ23834), q22.3
SNP_A-2160068	atttattgaatgaata[C/G]gaaggataaacacacg	C	G	NM_152750 // downstream // 2960 // Hs.202120 // FLJ23834 // 222256 // Homo sapiens hypothetical protein FLJ23834 (FLJ23834), mRNA. /// NM_006754 // downstream // 54113 // Hs.80919 // SYPL // 6856 // Homo sapiens synaptophysin-like protein (SYPL), transcri	FLJ23834	FLJ23834, Homo sapiens hypothetical protein FLJ23834 (FLJ23834), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1875945	tctgaacattcttccc[A/T]gatttgaacagtgt	A	T	NM_006754 // upstream // 2508 // Hs.80919 // SYPL // 6856 // Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, mRNA. /// NM_182715 // upstream // 2508 // Hs.80919 // SYPL // 6856 // Homo sapiens synaptophysin-like protein (SYPL), trans	SYPL	SYPL, Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, q22.3
SNP_A-1808719	gtgaagaggcacttac[A/G]ctacagttgcagcaat	A	G	NM_006754 // upstream // 4852 // Hs.80919 // SYPL // 6856 // Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, mRNA. /// NM_182715 // upstream // 4852 // Hs.80919 // SYPL // 6856 // Homo sapiens synaptophysin-like protein (SYPL), trans	SYPL	SYPL, Homo sapiens synaptophysin-like protein (SYPL), transcript variant 1, q22.3
SNP_A-2092080	agaaactattctgata[C/T]ggctatttccagtg	C	T	NM_005746 // upstream // 133115 // Hs.489615 // PBEF1 // 10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 133142 // Hs.489615 // PBEF1 // 10135 // Homo sapiens pre-B-cell colony e	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-1665796	aagactcgaagaagatttcctttgc[C/G]agtggcgatcaaacat cttccact	C	G	NM_005746 // upstream // 221912 // Hs.293464 // PBEF1 // 10135 // pre-B-cell colony enhancing factor 1 /// NM_175884 // downstream // 152539 // Hs.29692 // FLJ36031 // 168455 // hypothetical protein FLJ36031	PBEF1	PBEF1, rs10486020, pre-B-cell colony enhancing factor 1 ,q22.3
SNP_A-2280031	gagggaaaagttgaaa[C/G]acacactgaactaaag	C	G	NM_005746 // upstream // 230896 // Hs.489615 // PBEF1 // 10135 // Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, mRNA. /// NM_182790 // upstream // 230923 // Hs.489615 // PBEF1 // 10135 // Homo sapiens pre-B-cell colony e	PBEF1	PBEF1, Homo sapiens pre-B-cell colony enhancing factor 1 (PBEF1), transcript variant 1, q22.3
SNP_A-1757247	acatgatcaaaagcaatataatggaa[A/G]ctagaaatctttgaac aaatagtg	A	G	NM_002649 // upstream // 166935 // Hs.32942 // PIK3CG // 5294 // phosphoinositide-3-kinase, catalytic, gamma polypeptide /// NM_175884 // upstream // 37659 // Hs.29692 // FLJ36031 // 168455 // hypothetical protein FLJ36031	PIK3CG	PIK3CG , rs342242, phosphoinositide-3-kinase, catalytic, gamma polypeptide ,q22.3
SNP_A-1718775	taagacataaatgtaaccagatcta[C/T]agttaaatgatcccct aacaacag	C	T	NM_002649 // upstream // 149278 // Hs.32942 // PIK3CG // 5294 // phosphoinositide-3-kinase, catalytic, gamma polypeptide /// NM_175884 // upstream // 55316 // Hs.29692 // FLJ36031 // 168455 // hypothetical protein FLJ36031	PIK3CG	PIK3CG , rs10274553, phosphoinositide-3-kinase, catalytic, gamma polypeptide ,q22.3
SNP_A-1781296	ggatgtctagtcttta[C/G]caggcactgtctttga	C	G	NM_002649 // upstream // 181683 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 181866 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kina	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-1725478	tagaatcaccaggtctggaactga[C/T]gggaagttgagaaag atggcaacaa	C	T	NM_002649 // upstream // 145515 // Hs.32942 // PIK3CG // 5294 // phosphoinositide-3-kinase, catalytic, gamma polypeptide /// NM_175884 // upstream // 59079 // Hs.29692 // FLJ36031 // 168455 // hypothetical protein FLJ36031	PIK3CG	PIK3CG , rs10487917, phosphoinositide-3-kinase, catalytic, gamma polypeptide ,q22.3
SNP_A-1847203	tatcattttttcagata[C/T]gtgactcaagtacca	C	T	NM_002649 // upstream // 146525 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 146708 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kina	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-1990823	tgagcctgaacctcaa[C/G]ataattaaaaccacag	C	G	NM_002649 // upstream // 133522 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 133705 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kina	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-2246987	ctgtatgtaaactgat[A/G]agcctcatgcagacgc	A	G	NM_002649 // upstream // 94964 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 95147 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2111397	aggaggaattcgccct[C/T]aacttgcttgccgcct	C	T	NM_002649 // upstream // 84891 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA. /// NM_002649 // upstream // 85074 // Hs.32942 // PIK3CG // 5294 // Homo sapiens phosphoinositide-3-kinase	PIK3CG	PIK3CG, Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), q22.3
SNP_A-1684666	tctagaagttcaatgaacctcagca[C/T]agaataaacacaatg aaatccatac	C	T	NM_002736 // intron // 0 // Hs.77439 // PRKAR2B // 5577 // protein kinase, cAMP-dependent, regulatory, type II, beta	PRKAR2B	PRKAR2B , rs717099, protein kinase, cAMP-dependent, regulatory, type II, beta,q22.3
SNP_A-2237792	ctctcttttctctcca[C/T]atataacttccctatg	C	T	NM_181733 // intron // 0 // Hs.239631 // COG5 // 10466 // Homo sapiens component of oligomeric golgi complex 5 (COG5), transcript variant 2, mRNA. /// NM_006348 // intron // 0 // Hs.239631 // COG5 // 10466 // Homo sapiens component of oligomeric golgi com	COG5	COG5, Homo sapiens component of oligomeric golgi complex 5 (COG5), transcript variant 2, q22.3
SNP_A-2268166	gaatgaatgataaatg[A/G]atgtgtaactgagcca	A	G	NM_000441 // intron // 0 // Hs.546272 // SLC26A4 // 5172 // Homo sapiens solute carrier family 26, member 4 (SLC26A4), mRNA. /// ENST00000265715 // intron // 0 // --- // --- // --- // ---	SLC26A4	SLC26A4, Homo sapiens solute carrier family 26, member 4 (SLC26A4), q31.1
SNP_A-2261826	gaaataaaagttgagc[A/G]gaacaagtaaacactc	A	G	NM_000441 // intron // 0 // Hs.546272 // SLC26A4 // 5172 // Homo sapiens solute carrier family 26, member 4 (SLC26A4), mRNA. /// ENST00000265715 // intron // 0 // --- // --- // --- // ---	SLC26A4	SLC26A4, Homo sapiens solute carrier family 26, member 4 (SLC26A4), q31.1
SNP_A-1831925	taattgatcactcacc[A/G]attttaatatagtggc	A	G	NM_000441 // intron // 0 // Hs.546272 // SLC26A4 // 5172 // Homo sapiens solute carrier family 26, member 4 (SLC26A4), mRNA. /// ENST00000265715 // intron // 0 // --- // --- // --- // ---	SLC26A4	SLC26A4, Homo sapiens solute carrier family 26, member 4 (SLC26A4), q31.1
SNP_A-2104602	agcaggttcctaacac[A/G]ctatgatatttaacag	A	G	NM_000111 // intron // 0 // Hs.1650 // SLC26A3 // 1811 // Homo sapiens solute carrier family 26, member 3 (SLC26A3), mRNA. /// ENST00000340010 // intron // 0 // --- // --- // --- // ---	SLC26A3	SLC26A3, Homo sapiens solute carrier family 26, member 3 (SLC26A3), q31.1
SNP_A-2169579	caagctgaacaaaggc[A/C]aattattacacgatat	A	C	NM_000111 // upstream // 2528 // Hs.1650 // SLC26A3 // 1811 // Homo sapiens solute carrier family 26, member 3 (SLC26A3), mRNA. /// NM_000108 // upstream // 85431 // Hs.131711 // DLD // 1738 // Homo sapiens dihydrolipoamide dehydrogenase (E3 component of	SLC26A3	SLC26A3, Homo sapiens solute carrier family 26, member 3 (SLC26A3), q31.1
SNP_A-1936669	ttcttgtccaggtgcc[G/T]cagctaagttaggtac	G	T	NM_000111 // upstream // 6381 // Hs.1650 // SLC26A3 // 1811 // Homo sapiens solute carrier family 26, member 3 (SLC26A3), mRNA. /// NM_000108 // upstream // 81578 // Hs.131711 // DLD // 1738 // Homo sapiens dihydrolipoamide dehydrogenase (E3 component of	SLC26A3	SLC26A3, Homo sapiens solute carrier family 26, member 3 (SLC26A3), q31.1
SNP_A-2244085	ctgcttgggagtttga[A/C]catggcaactcaagag	A	C	NM_007356 // intron // 0 // Hs.62022 // LAMB4 // 22798 // Homo sapiens laminin, beta 4 (LAMB4), mRNA. /// ENST00000205386 // intron // 0 // --- // --- // --- // ---	LAMB4	LAMB4, Homo sapiens laminin, beta 4 (LAMB4), q31.1
SNP_A-1990850	gaagatgttgactaat[C/G]aaatacactgtcattt	C	G	NM_005010 // intron // 0 // Hs.21422 // NRCAM // 4897 // Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA. /// ENST00000351718 // intron // 0 // --- // --- // --- // ---	NRCAM	NRCAM, Homo sapiens neuronal cell adhesion molecule (NRCAM), q31.1
SNP_A-2209216	cccaggttttatgcag[G/T]atctttatttgaaggt	G	T	NM_012328 // downstream // 169177 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 1919187 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2012794	acattgtacaactcca[C/G]aggctccttacacaga	C	G	NM_012328 // downstream // 329167 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 1759197 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1842142	taggggaagaaaggtc[C/T]agtagaaggtggtaac	C	T	NM_012328 // downstream // 614535 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 1473829 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990870	taaggatagattcctg[A/G]aacagatcctctttc	A	G	NM_012328 // downstream // 640794 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 1447570 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1715115	acaaatactttttaattcaagtaa[C/T]gtacactgcaactggata cgttctt	C	T	NM_018334 // upstream // 819488 // Hs.3781 // LRRN3 // 54674 // leucine rich repeat neuronal 3 /// NM_032549 // downstream // 391415 // Hs.89576 // IMMP2L // 83943 // IMP2 inner mitochondrial membrane protease-like (S. cerevisiae)	LRRN3	LRRN3 , rs10487317, leucine rich repeat neuronal 3 ,q31.1
SNP_A-2100338	agataaaaaacattcca[A/T]actcaaaccacagca	A	T	NM_012328 // downstream // 1696042 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 392322 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1665566	gtaagatcatgtaactactttgctt[A/G]aaatcctctcccagtttccc atctc	A	G	NM_018334 // upstream // 714213 // Hs.3781 // LRRN3 // 54674 // leucine rich repeat neuronal 3 /// NM_032549 // downstream // 286140 // Hs.89576 // IMMP2L // 83943 // IMP2 inner mitochondrial membrane protease-like (S. cerevisiae)	LRRN3	LRRN3 , rs2159700, leucine rich repeat neuronal 3 ,q31.1
SNP_A-1990891	ccctacccacactgta[C/T]gaccagctccgcagta	C	T	NM_012328 // downstream // 1771737 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 316627 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1990892	gttcttacaatgatcc[G/T]agggccctacataatc	G	T	NM_012328 // downstream // 1801615 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 286749 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2282554	gagttgttgaagaaaaa[A/G]agactggatttcaggt	A	G	NM_012328 // downstream // 1808067 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 280297 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1920487	ttaattccttgcaaga[A/G]attgtctcaaatgat	A	G	NM_012328 // downstream // 1808725 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 279639 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1786632	ggcttgaaggaaagga[A/T]gttagcaggaaccag	A	T	NM_012328 // downstream // 1812518 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 275846 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1990893	aatgaacctgagagtc[A/G]ccacttaagatactgt	A	G	NM_012328 // downstream // 1821307 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 267057 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-2091208	acttgttctggccta[C/T]agtaaagcgccttca	C	T	NM_012328 // downstream // 1942952 // Hs.6790 // DNAJB9 // 4189 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), mRNA. /// NM_032549 // downstream // 145412 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membr	DNAJB9	DNAJB9, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 9 (DNAJB9), q31.1
SNP_A-1694563	tagaataaatagaattatacctcta[C/T]gtgttataagccttctaac agccac	C	T	NM_032549 // intron // 0 // Hs.89576 // IMMP2L // 83943 // IMP2 inner mitochondrial membrane protease-like (S. cerevisiae)	IMMP2L	IMMP2L , rs10499993, IMP2 inner mitochondrial membrane protease-like (S. cerevisiae),q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082191	acgactctggactta[C/T]gttgtgcagatttagt	C	T	NM_032549 // intron // 0 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), mRNA. /// ENST00000331762 // intron // 0 // — // — // — /// ENST00000332943 // intron // 0 // –	IMMP2L	IMMP2L, Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), q31.1
SNP_A-1814956	gtgttacatctagaaaa[A/G]gctttgcctaacccaa	A	G	NM_032549 // upstream // 100167 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), mRNA. /// NM_018334 // downstream // 496210 // Hs.3781 // LRRN3 // 54674 // Homo sapiens leucine rich	IMMP2L	IMMP2L, Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), q31.1
SNP_A-2129441	atacaatgtctgaga[C/T]gaagtttgtgggttt	C	T	NM_032549 // upstream // 124317 // Hs.89576 // IMMP2L // 83943 // Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), mRNA. /// NM_018334 // downstream // 520360 // Hs.3781 // LRRN3 // 54674 // Homo sapiens leucine rich	IMMP2L	IMMP2L, Homo sapiens IMP2 inner mitochondrial membrane protease-like (S. cerevisiae) (IMMP2L), q31.1
SNP_A-2046736	aagagctttaaaggca[A/G]ggttgagctatacaag	A	G	NM_014705 // intron // 0 // Hs.118140 // DOCK4 // 9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000342288 // intron // 0 // — // — // — /// ENST00000352877 // intron // 0 // — // — // — /// ENST00000348	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-1781916	ggcaaaagtcacctca[C/G]agtttatgtagcccag	C	G	NM_014705 // intron // 0 // Hs.118140 // DOCK4 // 9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000352877 // intron // 0 // — // — // — /// ENST00000348568 // intron // 0 // — // — // — // —	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-1641945	atcctacccataatgacttagctagaa[A/T]ataaatttaaattaaagt atcatt	A	T	NM_014705 // intron // 0 // Hs.118140 // DOCK4 // 9732 // dedicator of cytokinesis 4	DOCK4	DOCK4 , rs10487339, dedicator of cytokinesis 4,q31.1
SNP_A-1990923	caaaacaaaagatggc[A/G]acgtactttgagtagc	A	G	NM_014705 // upstream // 96466 // Hs.118140 // DOCK4 // 9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000342288 // upstream // 316337 // — // — // — // — /// ENST00000352877 // upstream // 96466 // — // — // -	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-2139720	atcgtgagaacagcad[C/T]aaaggggcaaattcac	C	T	NM_014705 // upstream // 164953 // Hs.118140 // DOCK4 // 9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000342288 // upstream // 384824 // — // — // — // — /// ENST00000352877 // upstream // 164953 // — // — // — // —	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-2047341	aagatccagtactgac[C/T]gaagatttctacaac	C	T	NM_014705 // upstream // 185269 // Hs.118140 // DOCK4 // 9732 // Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA. /// ENST00000342288 // upstream // 405140 // — // — // — // — /// ENST00000352877 // upstream // 185269 // — // — // — // —	DOCK4	DOCK4, Homo sapiens dedicator of cytokinesis 4 (DOCK4), q31.1
SNP_A-2056609	aatagattactgcttg[A/T]aaagtgcttaatatat	A	T	NM_001550 // upstream // 60035 // Hs.7879 // IFRD1 // 3475 // Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA. /// Y10313 // upstream // 60249 // Hs.7879 // IFRD1 // 3475 // Homo sapiens mRNA for PC4 protein (IFRD1 gene). /// ENST0	IFRD1	IFRD1, Homo sapiens interferon-related developmental regulator 1 (IFRD1), q31.1
SNP_A-1874555	tctccgtcagaattcc[C/T]ctgcagttgtttgtgg	C	T	NM_022484 // upstream // 13645 // Hs.121847 // FLJ13576 // 64418 // Homo sapiens hypothetical protein FLJ13576 (FLJ13576), mRNA. /// NM_152556 // downstream // 18122 // Hs.489734 // FLJ31818 // 154743 // Homo sapiens hypothetical protein FLJ31818 (FLJ3181	FLJ13576	FLJ13576, Homo sapiens hypothetical protein FLJ13576 (FLJ13576), q31.1
SNP_A-1788870	gggcaaaaatcacgta[C/T]gtaagtttgggctat	C	T	NM_152556 // intron // 0 // Hs.489734 // FLJ31818 // 154743 // Homo sapiens hypothetical protein FLJ31818 (FLJ31818), mRNA. /// ENST00000297145 // intron // 0 // — // — // — // — /// ENST00000358032 // intron // 0 // — // — // —	FLJ31818	FLJ31818, Homo sapiens hypothetical protein FLJ31818 (FLJ31818), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1990936	tagtgctctagtccca[C/T]gtaacaaatcttaaaa	C	T	NM_152556 // intron // 0 // Hs.489734 // FLJ31818 // 154743 // Homo sapiens hypothetical protein FLJ31818 (FLJ31818), mRNA. /// ENST00000297145 // intron // 0 // — // — // — // — /// ENST00000358032 // intron // 0 // — // — // — // —	FLJ31818	FLJ31818, Homo sapiens hypothetical protein FLJ31818 (FLJ31818), q31.1
SNP_A-1785328	ggctagttatcccagc[A/G]aatagcgagtccigtc	A	G	NM_152556 // intron // 0 // Hs.489734 // FLJ31818 // 154743 // Homo sapiens hypothetical protein FLJ31818 (FLJ31818), mRNA. /// ENST00000297145 // intron // 0 // — // — // — // — /// ENST00000358032 // intron // 0 // — // — // — // —	FLJ31818	FLJ31818, Homo sapiens hypothetical protein FLJ31818 (FLJ31818), q31.1
SNP_A-1990937	tagttgttaccctcaa[A/G]aagctactgttacctc	A	G	NM_152556 // intron // 0 // Hs.489734 // FLJ31818 // 154743 // Homo sapiens hypothetical protein FLJ31818 (FLJ31818), mRNA. /// ENST00000297145 // intron // 0 // — // — // — // — /// ENST00000358032 // intron // 0 // — // — // — // —	FLJ31818	FLJ31818, Homo sapiens hypothetical protein FLJ31818 (FLJ31818), q31.1
SNP_A-1743199	ttccttgacaacatgtttgtacc[A/G]agctttttagtgccctttta aa	A	G	NM_018970 // downstream // 116481 // Hs.152009 // GPR85 // 54329 // G protein-coupled receptor 85 /// NM_152556 // upstream // 24055 // Hs.292478 // FLJ31818 // 154743 // hypothetical protein FLJ31818	GPR85	GPR85, , rs10500014, G protein-coupled receptor 85, q31.1
SNP_A-1794178	ggtcataacaacaaac[A/G]ctaactcatcacacac	A	G	NM_018970 // upstream // 120850 // Hs.152009 // GPR85 // 54329 // Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA. /// NM_002711 // downstream // 665757 // Hs.458309 // PPP1R3A // 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor)	GPR85	GPR85, Homo sapiens G protein-coupled receptor 85 (GPR85), q31.1
SNP_A-1990952	aaggccagatcagata[C/T]gtgcaccgatccacaa	C	T	NM_018970 // upstream // 363247 // Hs.152009 // GPR85 // 54329 // Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA. /// NM_002711 // downstream // 423360 // Hs.458309 // PPP1R3A // 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor)	GPR85	GPR85, Homo sapiens G protein-coupled receptor 85 (GPR85), q31.1
SNP_A-1926768	ttattgtcacaaatta[A/T]cagtatttttgcagtg	A	T	NM_018970 // upstream // 372810 // Hs.152009 // GPR85 // 54329 // Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA. /// NM_002711 // downstream // 413797 // Hs.458309 // PPP1R3A // 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor)	GPR85	GPR85, Homo sapiens G protein-coupled receptor 85 (GPR85), q31.1
SNP_A-2300178	gcctccatctacttta[G/T]agtgaacaggcttgta	G	T	NM_018970 // upstream // 372928 // Hs.152009 // GPR85 // 54329 // Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA. /// NM_002711 // downstream // 413679 // Hs.458309 // PPP1R3A // 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor)	GPR85	GPR85, Homo sapiens G protein-coupled receptor 85 (GPR85), q31.1
SNP_A-2254610	cttgcctataatcta[A/C]catactgtatgtccta	A	C	NM_002711 // upstream // 210123 // Hs.458309 // PPP1R3A // 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 285865 // Hs.282787 // FOXP2 /	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1
SNP_A-2289324	gattgttttactcaa[A/G]tgcactgaaaattctg	A	G	NM_002711 // upstream // 386431 // Hs.458309 // PPP1R3A // 5506 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel /// NM_014491 // upstream // 109557 // Hs.282787 // FOXP2 /	PPP1R3A	PPP1R3A, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skel ,q31.1
SNP_A-2089872	acttcttcaaacaaaac[C/T]gattgtcactttcaac	C	T	NM_014491 // intron // 0 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // intron // 0 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 4, mRNA. /	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2195367	catggctggtggcgca[A/G]gaaacttcaatcatg	A	G	NM_014491 // downstream // 15517 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 15517 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript va	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1785075	ggcggtcggtattcaa[A/C]gaatcgctctgatta	A	C	NM_014491 // downstream // 30968 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 30968 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript va	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-1894687	tgccagatatatgagc[A/G]gccctatcacagttcc	A	G	NM_014491 // downstream // 52406 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 52406 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript va	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2193310	catctctacaaatatg[A/G]aaacaaaaatagcagg	A	G	NM_014491 // downstream // 98330 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 98330 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript va	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-1790763	gggggacaggacagaaa[A/G]actgtgcgactgtgac	A	G	NM_014491 // downstream // 117665 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 117665 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-1908638	tgtagcttcatattta[A/C]ctctcactgtatgccc	A	C	NM_014491 // downstream // 124354 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 124354 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2214348	cctaccccatcactca[C/T]ggcagaaactaaggcc	C	T	NM_014491 // downstream // 124811 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 124811 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-1813949	gtgtcaccataaactta[C/G]acatgaagaacactcc	C	G	NM_014491 // downstream // 130337 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 130337 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2201052	ccaaggtgcagaacca[C/T]ccacattactgtaga	C	T	NM_014491 // downstream // 133405 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 133405 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2174638	cacagcaacatgtaca[A/G]gttaccaagtcattgt	A	G	NM_014491 // downstream // 134931 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 134931 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-1990967	gcaaaacctgaaactc[C/T]atgtaggaagctatgt	C	T	NM_014491 // downstream // 143557 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 143557 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1
SNP_A-2167241	caacactttaaaggc[A/G]atgtctgtgggtcc	A	G	NM_014491 // downstream // 176282 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, mRNA. /// NM_148900 // downstream // 176282 // Hs.282787 // FOXP2 // 93986 // Homo sapiens forkhead box P2 (FOXP2), transcript	FOXP2	FOXP2, Homo sapiens forkhead box P2 (FOXP2), transcript variant 1, q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1744617	tacacctaggtgttgctatgtcga[A/G]taattcattgtatggcaaat tcatc	A	G	AF054589 // intron // 0 // Hs.132739 // HIC // 29969 // I-mfa domain-containing protein	HIC	HIC , rs4609131, I-mfa domain-containing protein,q31.1
SNP_A-1836165	tactagtgagttcca[C/T]gaaaaatctctttat	C	T	NM_199072 // intron // 0 // Hs.546385 // HIC // 29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// ENST00000257724 // intron // 0 // — // — // —	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.1
SNP_A-2012821	acacatgatttgtgg[A/C]ataactggcctatgtt	A	C	NM_199072 // intron // 0 // Hs.546385 // HIC // 29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// ENST00000257724 // intron // 0 // — // — // —	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.1
SNP_A-1953623	ttgacatcttcacc[A/G]agcttgcagaatatct	A	G	NM_199072 // downstream // 475964 // Hs.546385 // HIC // 29969 // Homo sapiens I-mfa domain-containing protein (HIC), mRNA. /// NM_012252 // downstream // 444806 // Hs.125962 // TFEC // 22797 // Homo sapiens transcription factor EC (TFEC), mRNA. /// ENST0	HIC	HIC, Homo sapiens I-mfa domain-containing protein (HIC), q31.2
SNP_A-1895489	tgcctacacatagaca[A/G]taaacaaatgtggt	A	G	NM_015641 // intron // 0 // Hs.533391 // TES // 26136 // Homo sapiens testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA. /// NM_152629 // intron // 0 // Hs.533391 // TES // 26136 // Homo sapiens testis derived transcript (3 LIM d	TES	TES, Homo sapiens testis derived transcript (3 LIM domains) (TES), transcript variant 1, q31.2
SNP_A-1854038	tcaaacactcaccatt[A/G]aaacctcattaaatt	A	G	ENST00000357705 // CDS // 0 // — // — // — /// ENST00000358541 // CDS // 0 // — // — // —	-	q31.2
SNP_A-2282454	gagttgaaaaagcgga[A/G]acgcaagaataactt	A	G	NM_003391 // intron // 0 // Hs.128553 // WNT2 // 7472 // Homo sapiens wingless-type MMTV integration site family member 2 (WNT2), mRNA. /// ENST00000265441 // intron // 0 // — // — // —	WNT2	WNT2, Homo sapiens wingless-type MMTV integration site family member 2 (WNT2), q31.2
SNP_A-2236034	ctcctggttgttcaag[A/T]ctgttgtttgttgac	A	T	NM_033427 // upstream // 29346 // Hs.335033 // CTTNBP2 // 83992 // Homo sapiens cortactin binding protein 2 (CTTNBP2), mRNA. /// ENST00000160373 // upstream // 29346 // — // — // — /// ENST00000359953 // upstream // 252316 // — // — // –	CTTNBP2	CTTNBP2, Homo sapiens cortactin binding protein 2 (CTTNBP2), q31.31
SNP_A-1709113	cagaggaagctctccatgtaacaca[A/C]agtgcagtgaggagt gagaaccaca	A	C	NM_012281 // upstream // 1138621 // Hs.202687 // KCND2 // 3751 // potassium voltage-gated channel, Shal-related subfamily, member 2 /// NM_019644 // downstream // 892364 // Hs.371820 // ANKRD7 // 56311 // ankyrin repeat domain 7	KCND2	KCND2, rs2402460, potassium voltage-gated channel, Shal-related subfamily, member 2, q31.31
SNP_A-1959439	tttgcccagatatctc[A/G]aatgttatcttaataa	A	G	NM_019644 // downstream // 941313 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 941317 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-1991037	gaaaacagtgaactca[A/G]ggatactaattcccgg	A	G	NM_019644 // downstream // 942369 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 942373 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-2065603	aatttacttctaic[A/C]acagtgtgacatggct	A	C	NM_019644 // downstream // 1394396 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 1394400 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// N	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-2061160	aatgcagaagcttaat[A/G]atcaaaaccagggaat	A	G	NM_019644 // downstream // 1400276 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 1400280 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// N	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259856	gaaaagcttgtatttc[A/G]cactgatccttaagat	A	G	NM_019644 // downstream // 1466458 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// NM_019644 // downstream // 1466462 // Hs.371820 // ANKRD7 // 56311 // Homo sapiens ankyrin repeat domain 7 (ANKRD7), mRNA. /// N	ANKRD7	ANKRD7, Homo sapiens ankyrin repeat domain 7 (ANKRD7), q31.31
SNP_A-1880544	tcttgcaaattcagca[C/T]agtgagttctctacaa	C	T	NM_012281 // intron // 0 // Hs.21703 // KCND2 // 3751 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA. /// ENST00000331113 // intron // 0 // — // — // — // —	KCND2	KCND2, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), q31.31
SNP_A-2246640	ctgtaatcagaaataa[G/T]gcaaaaatgtctgcac	G	T	NM_012281 // intron // 0 // Hs.21703 // KCND2 // 3751 // Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA. /// ENST00000331113 // intron // 0 // — // — // — // —	KCND2	KCND2, Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), q31.31
SNP_A-2216040	cctccattccttcgac[A/G]ccaccattttaaaggg	A	G	NM_012338 // upstream // 189 // Hs.16529 // TM4SF12 // 23554 // Homo sapiens transmembrane 4 superfamily member 12 (TM4SF12), mRNA. /// NM_198267 // upstream // 92451 // Hs.489811 // ING3 // 54556 // Homo sapiens inhibitor of growth family, member 3 (ING3	TM4SF12	TM4SF12, Homo sapiens transmembrane 4 superfamily member 12 (TM4SF12), q31.31
SNP_A-1937088	ttcttttgctggcact[A/G]acttaatcacctcaat	A	G	NM_014888 // intron // 0 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// ENST00000359943 // intron // 0 // — // — // — // —	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-2139022	atcctaattgtaatta[C/T]cacctgtctgtatcag	C	T	NM_014888 // intron // 0 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// ENST00000359943 // intron // 0 // — // — // — // —	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-1892458	tgcaagtgccttatta[C/T]gcatcagtaaaacagg	C	T	NM_014888 // intron // 0 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// ENST00000359943 // intron // 0 // — // — // — // —	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-2294316	gcaggtaaggagcaca[C/T]ggttgaatctcagaga	C	T	NM_014888 // upstream // 38252 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream // 438810 // Hs.489824 // PTPRZ1 // 5803 // Homo sapiens protein tyrosine phosphatase, recep	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-2105584	agccacatgtgactac[C/T]gagtattggaaacagc	C	T	NM_014888 // upstream // 54112 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream // 422950 // Hs.489824 // PTPRZ1 // 5803 // Homo sapiens protein tyrosine phosphatase, recep	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.31
SNP_A-1991076	atcctttccctaaacc[A/G]aacagtctttctcagt	A	G	NM_014888 // upstream // 284784 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream // 192278 // Hs.489824 // PTPRZ1 // 5803 // Homo sapiens protein tyrosine phosphatase, rece	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.32
SNP_A-2267172	gaataattgctgagcc[A/G]ctaaagaagaaaatac	A	G	NM_014888 // upstream // 407858 // Hs.434053 // FAM3C // 10447 // Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA. /// NM_002851 // upstream // 69204 // Hs.489824 // PTPRZ1 // 5803 // Homo sapiens protein tyrosine phosphatase, recep	FAM3C	FAM3C, Homo sapiens family with sequence similarity 3, member C (FAM3C), q31.32
SNP_A-2288664	gattggatgcatccta[A/C]aactgatactgaccta	A	C	NM_005763 // intron // 0 // Hs.528295 // AASS // 10157 // Homo sapiens aminoadipate-semialdehyde synthase (AASS), mRNA. /// ENST00000222418 // intron // 0 // — // — // — // — /// ENST00000358954 // intron // 0 // — // — // — // —	AASS	AASS, Homo sapiens aminoadipate-semialdehyde synthase (AASS), q31.32
SNP_A-1808902	gtgaatcatttaacca[C/T]tcaaaacatagctggt	C	T	NM_017954 // intron // 0 // Hs.270432 // CADPS2 // 93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS)	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839409	tagataaaatccgcg[A/T]ataaatggttaatttg	A	T	NM_017954 // intron // 0 // Hs.270432 // CADPS2 // 93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS)	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32
SNP_A-2066052	aatttgcttctggcaa[G/T]aaatgtcctaggttcc	G	T	NM_017954 // intron // 0 // Hs.270432 // CADPS2 // 93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS)	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32
SNP_A-2160208	atttcacaaagcctta[C/T]ctcagaaaagttcatc	C	T	NM_017954 // intron // 0 // Hs.270432 // CADPS2 // 93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS)	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32
SNP_A-1793027	ggtacctgaattcaac[C/T]gttcattcaactacaa	C	T	NM_017954 // intron // 0 // Hs.270432 // CADPS2 // 93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // intron // 0 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activator (CADPS)	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32
SNP_A-2169157	caagatgaggacactg[C/T]agataggaagtaatgc	C	T	NM_017954 // upstream // 2979 // Hs.270432 // CADPS2 // 93664 // Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), mRNA. /// NM_003716 // upstream // 2979 // Hs.127013 // CADPS // 8618 // Homo sapiens Ca2+-dependent secretion activat	CADPS2	CADPS2, Homo sapiens Ca2+-dependent activator protein for secretion 2 (CADPS2), q31.32
SNP_A-2074072	acagtttgccagtgaa[C/T]gagttaccatgaggga	C	T	NM_016945 // upstream // 72861 // Hs.272395 // TAS2R16 // 50833 // Homo sapiens taste receptor, type 2, member 16 (TAS2R16), mRNA. /// NM_022444 // downstream // 45040 // Hs.489849 // SLC13A1 // 6561 // Homo sapiens solute carrier family 13 (sodium/sulfat	TAS2R16	TAS2R16, Homo sapiens taste receptor, type 2, member 16 (TAS2R16), q31.32
SNP_A-1911570	tgtgaaaacatggaga[A/C]gtgttcaggaatggag	A	C	NM_022444 // intron // 0 // Hs.489849 // SLC13A1 // 6561 // Homo sapiens solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1), mRNA. /// ENST00000194130 // intron // 0 // — // — // — // —	SLC13A1	SLC13A1, Homo sapiens solute carrier family 13 (sodium,q31.32
SNP_A-1919954	ttaatacagaaacata[A/C]aatcaagtactgcata	A	C	NM_005000 // upstream // 21255 // Hs.83916 // NDUFA5 // 4698 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa (NDUFA5), nuclear gene encoding mitochondrial protein, /// NM_080928 // upstream // 22708 // Hs.97709 // ASB15 // 142	NDUFA5	NDUFA5, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa (NDUFA5), nuclear gene encoding mitochondrial protein, q31.32
SNP_A-1933507	ttctactgacttcctа[A/C]gttttagacaaagtt	A	C	NM_080928 // downstream // 8882 // Hs.97709 // ASB15 // 142685 // Homo sapiens ankyrin repeat and SOCS box-containing 15 (ASB15), mRNA. /// NM_080928 // downstream // 9728 // Hs.97709 // ASB15 // 142685 // Homo sapiens ankyrin repeat and SOCS box-containi	ASB15	ASB15, Homo sapiens ankyrin repeat and SOCS box-containing 15 (ASB15), q31.32
SNP_A-2062015	aatgggaaagggaaaat[A/G]tcatcaagcttctctc	A	G	ENST00000343134 // upstream // 119819 // — // — // — // — /// ENST00000344163 // upstream // 119742 // — // — // — // — /// ENST00000249307 // upstream // 323711 // — // — // — // —	-	q31.33
SNP_A-1921747	ttactaaatacagcaa[C/G]gttctggcagcttcag	C	G	ENST00000343134 // upstream // 121687 // — // — // — // — /// ENST00000344163 // upstream // 121610 // — // — // — // — /// ENST00000249307 // upstream // 321843 // — // — // — // —	-	q31.33
SNP_A-2294800	gcagttgttcttccaa[C/T]tggaggccagagtgtg	C	T	ENST00000343134 // upstream // 128867 // — // — // — // — /// ENST00000344163 // upstream // 128790 // — // — // — // — /// ENST00000249307 // upstream // 314663 // — // — // —	-	q31.33
SNP_A-1948304	ttaggcaaatagagg[G/T]aaagcagaaacttc	G	T	ENST00000343134 // upstream // 294811 // — // — // — // — /// ENST00000344163 // upstream // 294734 // — // — // — // — /// ENST00000249307 // upstream // 148719 // — // — // — // —	-	q31.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227973	ctaccttacccacaaa[G/T]atagggccctccttatc	G	T	ENST00000343134 // upstream // 423845 /// ENST00000344163 // upstream // 423768 /// ENST00000249307 // upstream // 19685 /// ---	-	q31.33
SNP_A-2272695	gacgtaccatctcctat[A/C]cacactggtgtcaggg	A	C	NM_005302 // downstream // 268242 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 865 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-1890004	tgatagttggaaaat[A/G]agaatcaagctgtaac	A	G	NM_005302 // downstream // 264550 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 4557 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2145496	atgcagtaatttacca[A/G]cacgaaaatgtgacca	A	G	NM_005302 // downstream // 244740 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 24367 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-1906462	tggtggagcagacgca[A/G]agaccaaatgacttaa	A	G	NM_005302 // downstream // 239613 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 29494 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2148467	atgggtcagaaataca[C/G]ataaattgttggat	C	G	NM_005302 // downstream // 231665 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 37442 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-1826084	taaatgtgctttcaac[G/T]agcaaatcatttccaa	G	T	NM_005302 // downstream // 230797 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 38310 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2151606	atgttgcaagaagctt[G/T]aaagtggttatgaatt	G	T	NM_005302 // downstream // 152820 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 116287 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2076287	acattgaatatgggac[A/T]caaatgttctatttaa	A	T	NM_005302 // downstream // 118252 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 150855 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-2278927	gaggaaagcgagatta[C/T]actaaggtttgttaa	C	T	NM_005302 // downstream // 101818 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 167289 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-1926472	ttattcatatatagg[C/T]tccctcagcctctttc	C	T	NM_005302 // downstream // 57941 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000249307 // downstream // 211166 /// ---	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991135	tgatttgtggactca[C/T]tcgggctataaagtga	C	T	NM_005302 // intron // 0 // Hs.406094 // GPR37 // 2861 // Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), mRNA. /// ENST00000303921 // intron // 0 // — // — // —	GPR37	GPR37, Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like) (GPR37), q31.33
SNP_A-1991143	tgcaaatatgtaaaca[A/G]ggacaccttacctga	A	G	NM_015450 // upstream // 112427 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 90606 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 hom	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1911789	tgtgaatgcaaaacca[C/T]tgatgaaatgtggtac	C	T	NM_015450 // upstream // 482166 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 460345 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 ho	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1743227	gttcaatgaaaataatcaccaagta[A/G]gataaatgaagtaaaac actgcttac	A	G	NM_000845 // downstream // 570510 // Hs.449625 // GRM8 // 2918 // glutamate receptor, metabotropic 8	GRM8	GRM8 , rs1362047, glutamate receptor, metabotropic 8,q31.33
SNP_A-1718903	atgatgtctgatacatagttggg[C/T]caatttttgtgatacttatatc ctt	C	T	NM_000845 // downstream // 565635 // Hs.449625 // GRM8 // 2918 // glutamate receptor, metabotropic 8	GRM8	GRM8 , rs10487424, glutamate receptor, metabotropic 8,q31.33
SNP_A-2216282	cctcctccaacacaca[C/T]ggatggcatgagattt	C	T	NM_015450 // upstream // 962243 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 940422 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 ho	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1991169	atcatattagagacta[C/T]cttacaggacttgat	C	T	NM_015450 // upstream // 962296 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 940475 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 ho	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1910240	tgtcatttttgaagaa[G/T]gcaaccttaacccttt	G	T	NM_015450 // upstream // 1195661 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 1173840 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-2040506	aaccagtttctccagc[A/G]aggtaggaatggaaat	A	G	NM_015450 // upstream // 1328895 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), mRNA. /// NM_015450 // upstream // 1307074 // Hs.31968 // POT1 // 25913 // Homo sapiens POT1 protection of telomeres 1	POT1	POT1, Homo sapiens POT1 protection of telomeres 1 homolog (S. pombe) (POT1), q31.33
SNP_A-1991209	tttacgtcgctagta[A/G]gcagttaatcaacaat	A	G	NM_000845 // upstream // 2918 // Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// ENST00000341617 // intron // 0 // — // — // — /// ENST00000358373 // intron // 0 // — // — // — /// ENST00	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-2294924	gcataagcaattaatg[A/C]atatttgtaggctac	A	C	NM_000845 // upstream // 36167 // Hs.449625 // GRM8 // 2918 // Homo sapiens glutamate receptor, metabotropic 8 (GRM8), mRNA. /// NM_176814 // downstream // 90931 // Hs.159006 // LOC168850 // 168850 // Homo sapiens hypothetical protein LOC168850 (LOC168850	GRM8	GRM8, Homo sapiens glutamate receptor, metabotropic 8 (GRM8), q32.1
SNP_A-2119624	agtatggtgttcatac[C/G]gcaggcaatctgatc	C	G	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1695685	ttgcttggtaaatgaagttgaataa[G/T]atacacatagaagaca ttaacaa	G	T	NM_014390 // intron // 0 // Hs.511400 // SND1 // 27044 // staphylococcal nuclease domain containing 1	SND1	SND1 , rs2043981, staphylococcal nuclease domain containing 1,q32.1
SNP_A-1805899	gtccctgttggagaca[A/G]atacatgttcccaga	A	G	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113499	aggctaaacactgttta[A/G]aaggacatgatcatga	A	G	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2261267	gaaagatgtaccactg[C/G]agtataatagaagagtg	C	G	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1935924	ttctaacattatgca[A/G]catataggccaaatgg	A	G	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1917355	tgttttctctgtcaga[C/T]caatttgtttttctta	C	T	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // 3UTR // 0 // Hs.534410 // NAG8 // 27099 // Homo sapiens nasopharyngeal carcinoma associated gene protein-8 (N	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1899627	tggaagttctcattgc[C/T]ctctccatatccggga	C	T	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-1908636	tgtagcttcaaagtta[C/G]agcccctctgggtg	C	G	NM_014390 // intron // 0 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// ENST00000354725 // intron // 0 // — // — // —	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2243829	ctgctgcttagttgca[A/T]tccgatatgcctccct	A	T	NM_014390 // downstream // 125390 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // downstream // 218604 // Hs.534410 // NAG8 // 27099 // Homo sapiens nasopharyngeal carcinoma associat	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2047088	aagataaaacagatac[A/G]gattctgcctacctgc	A	G	NM_014390 // downstream // 140177 // Hs.122523 // SND1 // 27044 // Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA. /// NM_014411 // downstream // 233391 // Hs.534410 // NAG8 // 27099 // Homo sapiens nasopharyngeal carcinoma associat	SND1	SND1, Homo sapiens staphylococcal nuclease domain containing 1 (SND1), q32.1
SNP_A-2187222	caggtgaattcaggga[C/T]caaagctgtttgtgt	C	T	NM_000230 // downstream // 27312 // Hs.194236 // LEP // 3952 // Homo sapiens leptin (obesity homolog, mouse) (LEP), mRNA. /// ENST00000308868 // downstream // 27312 // — // — // — /// ENST00000328227 // downstream // 19472 // — // — // —	LEP	LEP, Homo sapiens leptin (obesity homolog, mouse) (LEP), q32.1
SNP_A-2301500	gcgacaacgacaagga[C/T]aaggcctggacaaagc	C	T	NM_018396 // downstream // 190781 // Hs.433213 // METTL2 // 55798 // Homo sapiens methyltransferase like 2 (METTL2), mRNA. /// NM_181725 // downstream // 190781 // Hs.381204 // FLJ12760 // 339175 // Homo sapiens hypothetical protein FLJ12760 (FLJ12760), m	METTL2	METTL2, Homo sapiens methyltransferase like 2 (METTL2), q32.1
SNP_A-1868108	tcctatgccatctaaat[C/G]ttgctggaaagaggtc	C	G	NM_018396 // downstream // 206655 // Hs.433213 // METTL2 // 55798 // Homo sapiens methyltransferase like 2 (METTL2), mRNA. /// NM_181725 // downstream // 206655 // Hs.381204 // FLJ12760 // 339175 // Homo sapiens hypothetical protein FLJ12760 (FLJ12760), m	METTL2	METTL2, Homo sapiens methyltransferase like 2 (METTL2), q32.1
SNP_A-1991247	tgacctcctaagggaa[A/G]taagtcctgcagaagt	A	G	ENST00000357221 // intron // 0 // — // — // —	-	q32.1
SNP_A-1834435	tacatttgaaatgtga[C/T]ggctttgccaaatgag	C	T	NM_138693 // upstream // 230746 // Hs.125240 // KLF14 // 136259 // Homo sapiens Kruppel-like factor 14 (KLF14), mRNA. /// ENST00000310992 // upstream // 230746 // — // — // — /// ENST00000318777 // downstream // 81803 // — // — // —	KLF14	KLF14, Homo sapiens KruppeHike factor 14 (KLF14), q32.3
SNP_A-1783621	ggcatgggccaatcaa[A/G]agaatttggcttacc	A	G	NM_013255 // upstream // 55379 // Hs.44693 // MKLN1 // 4289 // Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1), mRNA. /// ENST00000318777 // upstream // 225533 // — // — // — /// ENST00000352689 // upstream //	MKLN1	MKLN1, Homo sapiens muskelin 1, intracellular mediator containing kelch motifs (MKLN1), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1825260	taaagtggacaatcaa[C/T]gacgttagctgtagt	C	T	NM_005397 // upstream // 29408 // Hs.16426 // PODXL // 5420 // Homo sapiens podocalyxin-like (PODXL), mRNA. /// ENST00000032985 // upstream // 29408 // --- // --- // --- /// ENST00000305171 // downstream // 167771 // --- // --- // ---	PODXL	PODXL, Homo sapiens podocalyxin-like (PODXL), q32.3
SNP_A-1991285	ttccttgcaaaattaa[C/G]agacaggcttaaagag	C	G	ENST00000305171 // upstream // 14888 // --- // --- // --- /// ENST00000251675 // downstream // 359025 // --- // --- // --- /// ENST00000360855 // downstream // 359055 // --- // --- // --- /// ENST00000359827 // downstream // 359065 //	-	q32.3
SNP_A-2137944	atcatttccttttcag[A/G]agtctacaggtaaaaa	A	G	ENST00000305171 // upstream // 15279 // --- // --- // --- /// ENST00000251675 // downstream // 358634 // --- // --- // --- /// ENST00000360855 // downstream // 358664 // --- // --- // --- /// ENST00000359827 // downstream // 358674 //	-	q32.3
SNP_A-2247456	ctgtctcagaaaaaaa[A/G]aagtgactcaccaagt	A	G	ENST00000305171 // upstream // 19229 // --- // --- // --- /// ENST00000251675 // downstream // 354684 // --- // --- // --- /// ENST00000360855 // downstream // 354714 // --- // --- // --- /// ENST00000359827 // downstream // 354724 //	-	q32.3
SNP_A-2215321	cctcaataaccaggta[C/T]agagtgagcacaacaa	C	T	ENST00000305171 // upstream // 24013 // --- // --- // --- /// ENST00000251675 // downstream // 349900 // --- // --- // --- /// ENST00000360855 // downstream // 349930 // --- // --- // --- /// ENST00000359827 // downstream // 349940 //	-	q32.3
SNP_A-2239608	ctgaaaatagcaagta[C/T]ggtaacaacgtggag	C	T	ENST00000305171 // upstream // 58030 // --- // --- // --- /// ENST00000251675 // downstream // 315883 // --- // --- // --- /// ENST00000360855 // downstream // 315913 // --- // --- // --- /// ENST00000359827 // downstream // 315923 //	-	q32.3
SNP_A-2188313	cagtctgcaagactcg[C/T]ccagtgcagacttgc	C	T	ENST00000305171 // upstream // 86128 // --- // --- // --- /// ENST00000251675 // downstream // 287785 // --- // --- // --- /// ENST00000360855 // downstream // 287815 // --- // --- // --- /// ENST00000359827 // downstream // 287825 //	-	q32.3
SNP_A-1991292	tttcatgtggacatc[C/T]gatatatttgtcccta	C	T	ENST00000305171 // upstream // 87018 // --- // --- // --- /// ENST00000251675 // downstream // 286895 // --- // --- // --- /// ENST00000360855 // downstream // 286925 // --- // --- // --- /// ENST00000359827 // downstream // 286935 //	-	q32.3
SNP_A-2155834	attccgtgatcctgaa[C/T]actgccacccatcagt	C	T	ENST00000305171 // upstream // 158231 // --- // --- // --- /// ENST00000251675 // downstream // 215682 // --- // --- // --- /// ENST00000360855 // downstream // 215712 // --- // --- // --- /// ENST00000359827 // downstream // 215722 //	-	q32.3
SNP_A-1991299	ggcaaatctctagtta[G/T]gtagtcatatcagcag	G	T	ENST00000305171 // upstream // 290389 // --- // --- // --- /// ENST00000251675 // downstream // 83524 // --- // --- // --- /// ENST00000360855 // downstream // 83554 // --- // --- // --- /// ENST00000359827 // downstream // 83564 // -	-	q32.3
SNP_A-1991300	cctgaaacttgctgaa[C/T]gttgaagtgaaggtca	C	T	ENST00000305171 // upstream // 300096 // --- // --- // --- /// ENST00000251675 // downstream // 73817 // --- // --- // --- /// ENST00000360855 // downstream // 73847 // --- // --- // --- /// ENST00000359827 // downstream // 73857 // -	-	q32.3
SNP_A-1884063	tgaagcatcctccaag[A/C]agagatcaattaaaag	A	C	ENST00000305171 // upstream // 302158 // --- // --- // --- /// ENST00000251675 // downstream // 71755 // --- // --- // --- /// ENST00000360855 // downstream // 71785 // --- // --- // --- /// ENST00000359827 // downstream // 71795 // -	-	q32.3
SNP_A-2293905	gcagctgtttgagac[A/G]ctgaaatatgaatttt	A	G	ENST00000305171 // upstream // 309116 // --- // --- // --- /// ENST00000251675 // downstream // 64797 // --- // --- // --- /// ENST00000360855 // downstream // 64827 // --- // --- // --- /// ENST00000359827 // downstream // 64837 // -	-	q32.3
SNP_A-1794370	ggtcccaatttctgtac[C/T]gagctagctgacatta	C	T	ENST00000305171 // upstream // 309463 // --- // --- // --- /// ENST00000251675 // downstream // 64450 // --- // --- // --- /// ENST00000360855 // downstream // 64480 // --- // --- // --- /// ENST00000359827 // downstream // 64490 // -	-	q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1799933	gtacagcttgattcag[C/T]atatatccaacaccctg	C	T	ENST00000305171 // upstream // 339671 // --- // --- // --- /// ENST00000251675 // downstream // 34242 // --- // --- // --- /// ENST00000360855 // downstream // 34272 // --- // --- // --- /// ENST00000359827 // downstream // 34282 // -	-	q32.3
SNP_A-2237786	ctctctttgataactct[C/T]gagccctaaaccagtg	C	T	ENST00000305171 // upstream // 339715 // --- // --- // --- /// ENST00000251675 // downstream // 34198 // --- // --- // --- /// ENST00000360855 // downstream // 34228 // --- // --- // --- /// ENST00000359827 // downstream // 34238 // -	-	q32.3
SNP_A-2104645	agcagtcaccggaggga[A/G]ccaacggaacaaagaca	A	G	ENST00000251675 // intron // 0 // --- // --- // ---	-	q32.3
SNP_A-2086242	actctgggcccatttat[C/G]agcctacagcaggtgc	C	G	ENST00000251675 // intron // 0 // --- // --- // ---	-	q32.3
SNP_A-1880937	tctgtctgaaacata[A/C]ataactcacagacaga	A	C	NM_181775 // downstream // 244967 // Hs.272319 // DKFZp434G0625 // 91584 // Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), mRNA. /// ENST00000251675 // upstream // 11362 // --- // --- // --- /// ENST00000360855 // upstream // 8019	DKFZp434G06 25	DKFZp434G0625, Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), q32.3
SNP_A-1886012	tgaccaaaaactagaa[C/T]gtggtgcgtggctcc	C	T	NM_181775 // downstream // 31720 // Hs.272319 // DKFZp434G0625 // 91584 // Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), mRNA. /// ENST00000251675 // upstream // 224609 // --- // --- // --- /// ENST00000360855 // upstream // 2934	DKFZp434G06 25	DKFZp434G0625, Homo sapiens hypothetical protein DKFZp434G0625 (DKFZp434G0625), q32.3
SNP_A-2084931	actcaatatattatta[A/C]gagagtggctcagttt	A	C	NM_017812 // intron // 0 // Hs.131434 // CHCHD3 // 54927 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA. /// ENST00000262570 // intron // 0 // --- // --- // ---	CHCHD3	CHCHD3, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), q33
SNP_A-1817766	gttcctactacattcca[C/G]aactggttaggtcttt	C	G	NM_017812 // intron // 0 // Hs.131434 // CHCHD3 // 54927 // Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA. /// ENST00000262570 // intron // 0 // --- // --- // ---	CHCHD3	CHCHD3, Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), q33
SNP_A-2185785	caggatcaaatgtcca[A/G]tgaaattcaaccaat	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1694893	tgaaagcacctctattccagccatt[A/G]tcattatccattatcattaa tgatc	A	G	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs958408, SEC8-like 1 (S. cerevisiae),q33
SNP_A-1859907	tcaggtatttatagc[A/G]aacttctatgtagaat	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2101717	agatgcagtgaaggaa[C/G]acgtttgaaatgctcc	C	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1991332	aaagagattagaatcc[A/G]aggaaattgtggtaca	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1991334	atcactaagaaaaatc[C/T]gtagactgtgagaata	C	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1801189	gtagctacagtcacaa[A/G]ttaacaattatcaggg	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1656009	caccaatacagataatataaacgca[A/T]atgaaaacaatcaggt catcigttc	A	T	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs10488169, SEC8-like 1 (S. cerevisiae),q33
SNP_A-2078222	accagtgtaactccaa[C/T]gattaccccatcata	C	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // --- // --- // ---	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1744531	tagttattcaacatccattcaaataa[A/G]ataatatcagaaatatgc ataccac	A	G	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs2911495, SEC8-like 1 (S. cerevisiae),q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2156359	attctcactgaaatga[C/G]atggaacagaggaa	C	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2261225	gaaagatacaaagtac[G/T]gattgtgcgtgtgtct	G	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2125187	agttggtacacagcaa[A/G]tgcttaatcagtgaat	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1928827	ttcagagcctaaaata[A/G]agtggttgagtcaggg	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1792774	ggtaaggagccaaatc[A/G]agctgtctctggtgga	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2247825	ctgtgagttggaatggt[A/C]cacttctaaaaacaaa	A	C	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2291838	gcacaggaagcctgta[C/T]atggatttctctagac	C	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1947360	tttacaatcactataa[G/T]gcaggaaaatacaaa	G	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2225061	cgtgtctgcagaggca[C/T]gtgtaaagtgatgcta	C	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1757595	attacaaacctattggaaccagtg[A/T]aactcataggacccag aagaggcaa	A	T	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs6962865, SEC8-like 1 (S. cerevisiae),q33
SNP_A-1742987	tgtctggaagcctacttcaatgg[A/G]acttatcctctgtaggaat cttgca	A	G	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs6963032, SEC8-like 1 (S. cerevisiae),q33
SNP_A-2068176	acaagactggtccaaa[G/T]taaagtgccgtcgtcc	G	T	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1650442	tccttctctcattatttttgcta[C/T]ataaactctagtatcttttttttg	C	T	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs2346275, SEC8-like 1 (S. cerevisiae),q33
SNP_A-1667674	agatgtactcccaaaagctgtgtaa[A/G]gcaaaaagaaaaggg aaggcaggatt	A	G	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs2971953, SEC8-like 1 (S. cerevisiae),q33
SNP_A-2100925	agatatgtcattgaaaa[A/G]taaatggaaaaggccg	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-2138753	atcccccaccaggaaca[A/G]tgacaatgccagttct	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1707145	ggtggcaacaaagagtcatgatttta[C/T]aatctcagatgcttggg gttaatag	C	T	NM_021807 // intron // 0 // Hs.446140 // SEC8L1 // 60412 // SEC8-like 1 (S. cerevisiae)	SEC8L1	SEC8L1, rs10488421, SEC8-like 1 (S. cerevisiae),q33
SNP_A-2283991	gatatataaaagaaaac[A/G]agagtccaacaatccc	A	G	NM_021807 // intron // 0 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// ENST00000253861 // intron // 0 // — // — // —	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1844683	tataagaatgagaaaa[C/T]ggtttgcttgttcc	C	T	NM_021807 // downstream // 1466 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// NM_144648 // upstream // 60127 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRN	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2106202	agccccctgtgaataa[A/C]ccattcccaagatctt	A	C	NM_021807 // downstream // 20095 // Hs.321273 // SEC8L1 // 60412 // Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), mRNA. /// NM_144648 // upstream // 41498 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mR	SEC8L1	SEC8L1, Homo sapiens SEC8-like 1 (S. cerevisiae) (SEC8L1), q33
SNP_A-1938488	ttgagaaaaggatgaa[A/G]agcaaaagccttagat	A	G	NM_144648 // intron // 0 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// ENST00000285928 // intron // 0 // — // — // —	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1824360	taaaccctttgaatgc[A/G]agactatctgtatg	A	G	NM_144648 // intron // 0 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// ENST00000285928 // intron // 0 // — // — // —	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2263474	gaaccaagaacacagc[C/T]gaatcacagtacagga	C	T	NM_144648 // intron // 0 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// ENST00000285928 // intron // 0 // — // — // —	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1815262	gtgttggtgtatttta[C/T]ggatgcttctgtaga	C	T	NM_144648 // intron // 0 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// ENST00000285928 // intron // 0 // — // — // —	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1730555	cttaaaagtacacaccgacatgcga[G/T]atgttgctctgtcacttg ctatgtg	G	T	NM_032826 // intron // 0 // Hs.292566 // SLC35B4 // 84912 // solute carrier family 35, member B4	SLC35B4	SLC35B4, rs1619682, solute carrier family 35, member B4,q33
SNP_A-1670395	aaatgccattattgccgttgacc[A/G]ctgggagacttacctgac gcagtgc	A	G	NM_032826 // intron // 0 // Hs.292566 // SLC35B4 // 84912 // solute carrier family 35, member B4	SLC35B4	SLC35B4, rs10488428, solute carrier family 35, member B4,q33
SNP_A-1941073	ttgctctcatttttta[C/G]agttctgtttgacga	C	G	NM_144648 // downstream // 14628 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 163546 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2255440	cttgtccgactgccag[A/G]caagcaacgaggtctc	A	G	NM_144648 // downstream // 20506 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 157668 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1790678	ggggctgggtcagtca[C/T]tcaaggaagttgtcaa	C	T	NM_144648 // downstream // 21817 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 156357 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2034997	aaatgattagcaaaga[C/G]aggcatgtttccacac	C	G	NM_144648 // downstream // 29234 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 148940 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1840181	tagcagagatgcatta[C/G]aacagcaagagaaggg	C	G	NM_144648 // downstream // 30292 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 147882 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2106564	agcctcaggagataaa[C/G]ggtccatgatatgaag	C	G	NM_144648 // downstream // 39380 // Hs.149774 // FLJ32786 // 136332 // Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 138794 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1725726	gaaaatctaccatcattaccaagctc[A/G]atgaataaaatgatatag atatggca	A	G	NM_001628 // downstream // 95278 // Hs.75313 // AKR1B1 // 231 // aldo-keto reductase family 1, member B1 (aldose reductase) /// NM_032826 // upstream // 30016 // Hs.292566 // SLC35B4 // 84912 // solute carrier family 35, member B4	AKR1B1	AKR1B1, rs1362985, aldo-keto reductase family 1, member B1 (aldose reductase),q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991345	ccccaaattatgggaa[C/T]agcagatacaaggagt	C	T	NM_144648 // downstream // 58000 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 120174 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1937772	ttgaagtgataacctc[C/G]aagtagatcacaaatc	C	G	NM_144648 // downstream // 71577 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 106597 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1894951	tgcccaaaagccgtca[A/T]agccttacacaaaaaa	A	T	NM_144648 // downstream // 75582 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 102592 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1915921	tgttgataagtaagaa[A/G]gttgtcagaatcaaaa	A	G	NM_144648 // downstream // 76439 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 101735 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1865712	tccattgctgcaacca[A/G]cacctatattacttttc	A	G	NM_144648 // downstream // 76565 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 101609 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2143176	atgacaaaaattaaaa[G/T]gatgctgatactagcc	G	T	NM_144648 // downstream // 77698 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 100476 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1947058	ttaatagagagaccc[C/T]gcaaatcatttcaat	C	T	NM_144648 // downstream // 79457 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 98717 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1936040	ttcttagctgttgaga[C/T]ctatgcaagtgtttt	C	T	NM_144648 // downstream // 79647 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 98527 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2165480	caaagcatgaaaaga c[C/T]ggaattcaaaatgaag	C	T	NM_144648 // downstream // 80348 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 97826 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-2183400	cagcactgcgggatc[A/C]atctgtttcacctagg	A	C	NM_144648 // downstream // 111233 // Hs.149774 // FLJ32786 // 136332 /// Homo sapiens hypothetical protein FLJ32786 (FLJ32786), mRNA. /// NM_001628 // downstream // 66941 // Hs.521212 // AKR1B1 // 231 // Homo sapiens aldo-keto reductase family 1, member B1	FLJ32786	FLJ32786, Homo sapiens hypothetical protein FLJ32786 (FLJ32786), q33
SNP_A-1741541	tggagcaagtccatgccatcagcag[A/C]agataatttaatgtctt tgaaaaa	A	C	NM_001628 // upstream // 12173 // Hs.75313 // AKR1B1 // 231 // aldo-keto reductase family 1, member B1 (aldose reductase) /// NM_020299 // upstream // 56337 // Hs.116724 // AKR1B10 // 57016 // aldo-keto reductase family 1, member B10 (aldose reductase)	AKR1B1	AKR1B1, rs2137608, aldo-keto reductase family 1, member B1 (aldose reductase), q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2062973	aatgtgttggaaagga[C/T]gtggagaaattggagt	C	T	NM_199186 // upstream // 18971 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // upstream // 18971 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BP	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-2117033	aggtgagaaatcgctc[A/G]gaaattctcaaagccc	A	G	NM_199186 // downstream // 23953 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 23953 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1918349	ttaaagtagacactaa[A/C]gatggtgggttatcaa	A	C	NM_199186 // downstream // 32783 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 32783 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-2178698	cactcttgagttctga[A/G]gatgaacaaatgtaaa	A	G	NM_199186 // downstream // 32824 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 32824 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1991366	ggaacattgtgtctta[A/T]attcatgggcttgtac	A	T	NM_199186 // downstream // 41037 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 41037 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1853353	tatttcaagaacggc[A/G]atttcagttaattta	A	G	NM_199186 // downstream // 41435 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 41435 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1717349	gtacaaggcagctagttggtagtag[A/C]ctggaattcctttagaa agagctg	A	C	NM_004342 // intron // 0 // Hs.443811 // CALD1 // 800 // caldesmon 1 /// NM_033138 // intron // 0 // Hs.443811 // CALD1 // 800 // caldesmon 1 /// NM_033157 // intron // 0 // Hs.443811 // CALD1 // 800 // caldesmon 1	CALD1	CALD1 , rs2347896, caldesmon 1 ,q33
SNP_A-1715439	atcatcagatttaccctgcttgccca[G/T]atagcatctagtcttcact caggtt	G	T	NM_004342 // intron // 0 // Hs.443811 // CALD1 // 800 // caldesmon 1 /// NM_033138 // intron // 0 // Hs.443811 // CALD1 // 800 // caldesmon 1 /// NM_033157 // intron // 0 // Hs.443811 // CALD1 // 800 // caldesmon 1	CALD1	CALD1 , rs1377296, caldesmon 1 ,q33
SNP_A-2054407	aagtttactagagcaa[C/T]attcttcaccaaacat	C	T	NM_199186 // downstream // 64845 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 64845 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-1818542	gttcttttctgttctc[C/T]gaaagtgccttttaa	C	T	NM_199186 // downstream // 93845 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 93845 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33
SNP_A-2145207	atgcaattctaaaacc[C/T]gaaggagacaggaccc	C	T	NM_199186 // downstream // 99257 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA. /// NM_001724 // downstream // 99257 // Hs.198365 // BPGM // 669 // Homo sapiens 2,3-bisphosphoglycerate mutase	BPGM	BPGM, Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 2, q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2232890	ctcagaagagagattc[A/C]gaaatgggaggcagca	A	C	NM_182489 // downstream // 68693 // Hs.453840 // LOC346673 // 346673 // Homo sapiens STRA8 (LOC346673), mRNA. /// NM_013316 // downstream // 35700 // Hs.490224 // CNOT4 // 4850 // Homo sapiens CCR4-NOT transcription complex, subunit 4 (CNOT4), mRNA. /// B	LOC346673	LOC346673, Homo sapiens STRA8 (LOC346673), q33
SNP_A-2031643	aaagtaagtgcaagaa[A/G]ttcactaataattcaa	A	G	NM_182489 // downstream // 100144 // Hs.453840 // LOC346673 // 346673 // Homo sapiens STRA8 (LOC346673), mRNA. /// NM_013316 // downstream // 4249 // Hs.490224 // CNOT4 // 4850 // Homo sapiens CCR4-NOT transcription complex, subunit 4 (CNOT4), mRNA. /// B	LOC346673	LOC346673, Homo sapiens STRA8 (LOC346673), q33
SNP_A-1789513	gggcctgagcaaggat[A/G]acttcatgagaagggt	A	G	NM_205855 // upstream // 21777 // Hs.55200 // UNQ1940 // 389558 // Homo sapiens HWKM1940 (UNQ1940), mRNA. /// NM_145808 // downstream // 156285 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // downstream // 156287 //	UNQ1940	UNQ1940, Homo sapiens HWKM1940 (UNQ1940), q33
SNP_A-2068346	acaagctgttttttc[C/T]ctaggcaggccagcc	C	T	NM_145808 // upstream // 68972 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 68929 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 822380 // Hs.52796	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1825221	taaagtcccaccttga[A/T]aactggtcagtctccc	A	T	NM_145808 // upstream // 81943 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 81900 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 809409 // Hs.52796	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1855566	tcaagtttttagctta[C/T]gaaaatttgcacaagt	C	T	NM_145808 // upstream // 83263 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 83220 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 808089 // Hs.52796	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1642489	cacagccaaaccgtatcagtaataa[A/G]agaatgaaagtgggagggaatgatg	A	G	NM_000739 // upstream // 744622 // Hs.527965 // CHRM2 // 1129 // cholinergic receptor, muscarinic 2 /// NM_145808 // upstream // 292872 // Hs.21321 // MTPN // 136319 // myotrophin	CHRM2	CHRM2, rs2114337, cholinergic receptor, muscarinic 2, q33
SNP_A-1849523	tatgggaaactctaag[A/G]acaaaggccccaggttt	A	G	NM_145808 // upstream // 394923 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 394880 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 496429 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1696656	agatgcttagaatcttgttatctat[C/T]gtatgagggtcaattatatct - - - - - - tggg - - - - - - - - - -	C	T	NM_000739 // upstream // 526015 // Hs.527965 // CHRM2 // 1129 // cholinergic receptor, muscarinic 2 /// NM_145808 // upstream // 511479 // Hs.21321 // MTPN // 136319 // myotrophin	CHRM2	CHRM2, rs10488619, cholinergic receptor, muscarinic 2, q33
SNP_A-2135826	atcaaatctgaatgta[A/G]aagaaggtcaataaca	A	G	NM_145808 // upstream // 541952 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 541909 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 349400 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2069700	acacacgctactgtca[C/T]gtaatttcctctag	C	T	NM_145808 // upstream // 543672 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 543629 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 347680 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2262883	gaacaaggtcctaaa[G/T]agaaacaaatggaaag	G	T	NM_145808 // upstream // 550964 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 550921 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 340388 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1781389	ggatgtttctcactca[C/T]agaaaatgtgtagtgg	C	T	NM_145808 // upstream // 566508 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 566465 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 324844 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1801009	gtagatgataacatca[A/G]taacttggacgtaag	A	G	NM_145808 // upstream // 574338 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 574295 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 317014 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2236669	ctctaagcttggga[A/T]aatggcccatcactc	A	T	NM_145808 // upstream // 642380 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 642337 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 248972 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-2212453	ccctgtgttacacgg[A/G]aactggctctctcag	A	G	NM_145808 // upstream // 720381 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_145808 // upstream // 720338 // Hs.43297 // MTPN // 136319 // Homo sapiens myotrophin (MTPN), mRNA. /// NM_000739 // upstream // 170971 // Hs.527	MTPN	MTPN, Homo sapiens myotrophin (MTPN), q33
SNP_A-1725114	agattaaaagaaatagccaatggga[C/T]agtaaactggaaaat atatttgaag	C	T	NM_000739 // downstream // 130141 // Hs.527965 // CHRM2 // 1129 // cholinergic receptor, muscarinic 2 /// NM_002825 // downstream // 81188 // Hs.44 // PTN // 5764 // pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	CHRM2	CHRM2 , rs832972, cholinergic receptor, muscarinic 2 , q33
SNP_A-2216241	cctcctaacggcgcaa[A/G]aatgaatcactgacaa	A	G	NM_000739 // downstream // 89885 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 117213 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2291732	gcacactgaggaataa[G/T]agtttgtatccattg	G	T	NM_000739 // downstream // 93167 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 113931 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2275049	gagaacttagcaaaac[C/T]gaagtgtgaatttca	C	T	NM_000739 // downstream // 93428 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 113670 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-1933780	ttctatctatcgatca[A/C]gtcactcatgcctagt	A	C	NM_000739 // downstream // 93769 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 113329 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2263372	gaacatcctgagaact[A/G]aaaatacctctacaag	A	G	NM_000739 // downstream // 94584 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 112514 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2290426	gcaacctcaaagtcag[A/T]cagaagcgtgaatctc	A	T	NM_000739 // downstream // 95072 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 112026 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803092	gtattatccataatgc[A/G]cagtagccagtaaaaa	A	G	NM_000739 // downstream // 105706 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 101392 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2244328	ctggaaggaacaagca[A/C]attctctgccctgta	A	C	NM_000739 // downstream // 109669 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 97429 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-2215648	cctcaggtctagcca[A/C]atggagctcaccagag	A	C	NM_000739 // downstream // 128127 // Hs.527965 // CHRM2 // 1129 // Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, mRNA. /// NM_002825 // downstream // 78971 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin	CHRM2	CHRM2, Homo sapiens cholinergic receptor, muscarinic 2 (CHRM2), transcript variant 4, q33
SNP_A-1674189	ttgatttcctatttgtagcatca[A/C]ttgtttcattttcctctttaatggac	A	C	NM_002825 // intron // 0 // Hs.44 // PTN // 5764 // pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	PTN	PTN , rs721239, pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1),q33
SNP_A-2244634	ctggagcttggactga[A/G]actttctcaagggtgt	A	G	NM_002825 // intron // 0 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA. /// ENST00000348225 // intron // 0 // — // — // — // — /// ENST00000349992 // intro	PTN	PTN, Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), q33
SNP_A-2028096	aaacgtttcatgtata[C/T]aaggggttgagattat	C	T	NM_002825 // intron // 0 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA. /// ENST00000348225 // intron // 0 // — // — // — // — /// ENST00000349992 // intro	PTN	PTN, Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), q33
SNP_A-1832336	taattttccaactat[C/G]aaaccttgtaggtata	C	G	NM_002825 // intron // 0 // Hs.371249 // PTN // 5764 // Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA. /// ENST00000348225 // intron // 0 // — // — // — // — /// ENST00000349992 // intro	PTN	PTN, Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), q33
SNP_A-2066665	acaaaaacacgctgttc[A/G]aagagcatcaagtgag	A	G	NM_004717 // intron // 0 // Hs.242947 // DGKI // 9162 // Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // — // — // — // —	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2266701	gaagtgaggggggaaag[A/G]attgagtgtttgttt	A	G	NM_004717 // intron // 0 // Hs.242947 // DGKI // 9162 // Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA. /// ENST00000288490 // intron // 0 // — // — // — // —	DGKI	DGKI, Homo sapiens diacylglycerol kinase, iota (DGKI), q33
SNP_A-2067410	acaaatattcctgaga[C/G]ctggtactgaggtac	C	G	NM_194071 // intron // 0 // Hs.490273 // CREB3L2 // 64764 // Homo sapiens cAMP responsive element binding protein 3-like 2 (CREB3L2), mRNA. /// ENST00000330387 // intron // 0 // — // — // — // —	CREB3L2	CREB3L2, Homo sapiens cAMP responsive element binding protein 3-like 2 (CREB3L2), q34
SNP_A-2150091	atgtccccagaaagac[C/G]gttctaaaaacaaggg	C	G	NM_005989 // intron // 0 // Hs.201667 // AKR1D1 // 6718 // Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), mRNA. /// ENST00000242375 // intron // 0 // — // — // — // —	AKR1D1	AKR1D1, Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), q34
SNP_A-1687886	aggataataccaagagtttggagta[C/T]gcgccttacccagtgtt cccatgaa	C	T	NM_003852 // upstream // 96105 // Hs.183858 // TIF1 // 8805 // transcriptional intermediary factor 1 /// NM_005989 // downstream // 244743 // Hs.201667 // AKR1D1 // 6718 // aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	TIF1	TIF1 , rs357396, transcriptional intermediary factor 1, q33
SNP_A-1991469	gtgttctaaactctga[C/T]gactaatatttctgga	C	T	NM_005989 // downstream // 229812 // Hs.201667 // AKR1D1 // 6718 // Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), mRNA. /// ENST00000242375 // downstream // 229812 // — // — // — // — /// E	AKR1D1	AKR1D1, Homo sapiens aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (AKR1D1), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134149	atatgagaagataaca[A/G]ccctcattggtaatca	A	G	NM_003852 // upstream // 47617 // Hs.490287 // TIF1 // 8805 // Homo sapiens transcriptional intermediary factor 1 (TIF1), transcript variant 2, mRNA. /// NM_015905 // upstream // 47617 // Hs.490287 // TIF1 // 8805 // Homo sapiens transcriptional intermedi	TIF1	TIF1, Homo sapiens transcriptional intermediary factor 1 (TIF1), transcript variant 2, q34
SNP_A-1864829	tccaggactgtaaaat[A/G]atagctgtcttgctc	A	G	NM_020632 // intron // 0 // Hs.98967 // ATP6V0A4 // 50617 // Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 4 (ATP6V0A4), transcript variant 1, mRNA. /// NM_130840 // intron // 0 // Hs.98967 // ATP6V0A4 // 50617 // Homo sapiens ATPas	ATP6V0A4	ATP6V0A4, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 4 (ATP6V0A4), transcript variant 1, q34
SNP_A-2289901	gcaaactttgatcac[A/G]cacctaacaaaaactc	A	G	NM_024625 // intron // 0 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // intron // 0 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antivi	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-2103150	agcaacagttacctcg[A/G]ataagatggccattcc	A	G	NM_024625 // upstream // 3377 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // upstream // 3377 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH ty	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-2308767	gctttgatactgaccc[G/T]ccctgaccttatcact	G	T	NM_024625 // upstream // 5131 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // upstream // 5131 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH ty	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-1958532	ttttcggtgttaaa[A/C]tgaggctgcaacccct	A	C	NM_024625 // upstream // 8958 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // upstream // 8958 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH ty	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-2235193	ctccccctctcgatc[C/T]aagttcattgtccctg	C	T	NM_024625 // upstream // 14812 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // upstream // 14812 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-1991476	gaaaggaccaagtccg[A/C]attataaagcaacaag	A	C	NM_024625 // upstream // 22775 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, mRNA. /// NM_020119 // upstream // 22775 // Hs.133512 // ZC3HAV1 // 56829 // Homo sapiens zinc finger CCCH	ZC3HAV1	ZC3HAV1, Homo sapiens zinc finger CCCH type, antiviral 1 (ZC3HAV1), transcript variant 2, q34
SNP_A-2118945	agtagaaaaacaacatt[C/T]agtctagtgcaaaag	C	T	NM_197964 // 3UTR // 0 // Hs.370475 // HSPC268 // 154791 // Homo sapiens hypothetical protein HSPC268 (HSPC268), mRNA. /// ENST00000315967 // 3UTR // 0 // — // — // —	HSPC268	HSPC268, Homo sapiens hypothetical protein HSPC268 (HSPC268), q34
SNP_A-2060329	aatgaatagctaatgat[A/T]caccagacagtaaagg	A	T	NM_022740 // intron // 0 // Hs.397465 // HIPK2 // 28996 // Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // — // — // — /// ENST00000342645 // intron // 0 // — // — // —	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-2012943	gtggaaccaccgagca[C/G]aagttgggaacctag	C	G	NM_022740 // intron // 0 // Hs.397465 // HIPK2 // 28996 // Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // — // — // — /// ENST00000342645 // intron // 0 // — // — // —	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-1822043	gttttccctagttc[G/T]aaccctgcttaaggac	G	T	NM_022740 // intron // 0 // Hs.397465 // HIPK2 // 28996 // Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // — // — // — /// ENST00000342645 // intron // 0 // — // — // —	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2196360	catgttcaacaactaa[A/T]caaagtatttgcatcc	A	T	NM_022740 // intron // 0 // Hs.397465 // HIPK2 // 28996 // Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // — // — // — // — /// ENST00000342645 // intron // 0 // — // — // — // —	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-1888516	tgaggagctaagtcac[A/G]ctaccaatggctttt	A	G	NM_022740 // intron // 0 // Hs.397465 // HIPK2 // 28996 // Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA. /// ENST00000263551 // intron // 0 // — // — // — // — /// ENST00000342645 // intron // 0 // — // — // — // —	HIPK2	HIPK2, Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), q34
SNP_A-1747525	caatatttttattagttcagtagtc[G/T]atcagttgcacagaagaagt ggatt	G	T	NM_001061 // intron // 0 // Hs.444510 // TBXAS1 // 6916 // thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A) /// NM_030984 // intron // 0 // Hs.444510 // TBXAS1 // 6916 // thromboxane A synthase 1 (platelet, cytochrome P450, fam	TBXAS1	TBXAS1 , rs10487666, thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A) ,q34
SNP_A-1991489	acatatgctgctttc[C/T]aatctcagagacaagt	C	T	NM_022750 // upstream // 10871 // Hs.12646 // ZC3HDC1 // 64761 // Homo sapiens zinc finger CCCH type domain containing 1 (ZC3HDC1), mRNA. /// ENST00000263549 // upstream // 10871 // — // — // — // — /// ENST00000006967 // downstream // 16003 // —	ZC3HDC1	ZC3HDC1, Homo sapiens zinc finger CCCH type domain containing 1 (ZC3HDC1), q34
SNP_A-2199774	ccaaacacaggaggccd[A/G]ctatattggtgacaga	A	G	NM_013446 // downstream // 22197 // Hs.490347 // MKRN1 // 23608 // Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA. /// ENST00000275874 // downstream // 4743 // — // — // — // — /// ENST00000255977 // downstream // 22197 // — // — // —	MKRN1	MKRN1, Homo sapiens makorin, ring finger protein, 1 (MKRN1), q34
SNP_A-2276008	gagagaaacccacctg[C/G]agactcggttaggctt	C	G	ENST00000275884 // intron // 0 // — // — // — // —	-	q34
SNP_A-2046620	aagagcaggttcgccg[A/G]cagacacagagttaaa	A	G	NM_052853 // upstream // 16401 // Hs.534141 // ADCK2 // 90956 // Homo sapiens aarF domain containing kinase 2 (ADCK2), mRNA. /// ENST00000275884 // upstream // 54309 // — // — // — // — /// ENST00000072869 // upstream // 16401 // — // — // —	ADCK2	ADCK2, Homo sapiens aarF domain containing kinase 2 (ADCK2), q34
SNP_A-2140536	atcccctcatattcaa[A/T]ttctagctaagaagaa	A	T	NM_004333 // intron // 0 // Hs.490366 // BRAF // 673 // Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA. /// ENST00000288602 // intron // 0 // — // — // — // —	BRAF	BRAF, Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), q34
SNP_A-1991500	cttccatacccttaga[C/T]tcaagttttctgttta	C	T	NM_004333 // upstream // 57509 // Hs.490366 // BRAF // 673 // Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA. /// ENST00000288602 // upstream // 57509 // — // — // — // — /// ENST00000328978 // downstream // 15679 // —	BRAF	BRAF, Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), q34
SNP_A-2221815	cctttctgttaaaaa[C/T]atccacgtcctgaaca	C	T	ENST00000343093 // intron // 0 // — // — // — // —	-	q34
SNP_A-2255475	cttgtctctctaccta[C/T]gttacaacccctaga	C	T	ENST00000343093 // intron // 0 // — // — // — // —	-	q34
SNP_A-1815002	gtgttagtgtcctac[C/T]gaagatgctatgaaat	C	T	ENST00000343093 // intron // 0 // — // — // — // —	-	q34
SNP_A-1933703	ttctagtttggcacc[G/T]ctatcttctctctg	G	T	ENST00000343093 // intron // 0 // — // — // — // —	-	q34
SNP_A-2188098	cagtcatggaaatgga[A/G]gtgagagaaccacaga	A	G	ENST00000343093 // intron // 0 // — // — // — // —	-	q34
SNP_A-2240057	ctgaagctccgcaga[C/T]gagtgggggtgtacaa	C	T	ENST00000343093 // intron // 0 // — // — // — // —	-	q34
SNP_A-1878871	tctgttctgctccca[C/G]ctagtatttctccagg	C	G	NM_173677 // downstream // 51930 // — // FLJ40852 // 285962 // Homo sapiens hypothetical protein FLJ40852 (FLJ40852), mRNA. /// ENST00000297761 // upstream // 5699 // — // — // — // — /// ENST00000350383 // downstream // 51930 // — // — // -	FLJ40852	FLJ40852, Homo sapiens hypothetical protein FLJ40852 (FLJ40852), q34
SNP_A-1872412	tctagatttcatgagt[A/T]aaaagcactcagaagt	A	T	ENST00000360172 // upstream // 21420 // — // — // — // — /// ENST00000350549 // upstream // 21354 // — // — // — // — /// ENST00000352156 // upstream // 21354 // — // — // — // — /// ENST00000322797 // upstream // 24421 // — // -	-	q34
SNP_A-1939791	ttgcaagaagtgggaa[A/G]agacatggtgcaagac	A	G	NM_004668 // intron // 0 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// ENST00000312952 // intron // 0 // — // — // — // —	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113840	aggctgggaactagt[C/G]atcatcgcttaggatt	C	G	NM_004668 // intron // 0 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// ENST00000312952 // intron // 0 // — // — // —	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2062848	aatgtggagcaactac[A/G]gacatgcaaaatgala	A	G	NM_004668 // downstream // 98905 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// NM_001001317 // downstream // 79099 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST000	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2100460	agataagaaagtccaa[C/T]aaatgtggagcaacta	C	T	NM_004668 // downstream // 98923 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// NM_001001317 // downstream // 79081 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST000	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2310784	ggaagccacatctga[C/T]aaatgcagaggcaatt	C	T	NM_004668 // downstream // 102150 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// NM_001001317 // downstream // 75854 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST00	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2154361	attatgttctctaa[C/T]gaattggtaactgaca	C	T	NM_004668 // downstream // 177820 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// NM_001001317 // downstream // 184 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST0000	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-1865385	tccatcctatctaga[A/C]ggcaagaaggttgtt	A	C	NM_004668 // downstream // 177895 // Hs.122785 // MGAM // 8972 // Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA. /// NM_001001317 // downstream // 109 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST0000	MGAM	MGAM, Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), q34
SNP_A-2065925	aatttctatgatgca[A/G]aatcggtgaccttata	A	G	NM_001001317 // intron // 0 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST00000304182 // intron // 0 // — // — // —	TRY1	TRY1, Homo sapiens trypsin X3 (TRY1), q34
SNP_A-1932459	ttcctgctatagtgga[A/G]gtaagaccttatatt	A	G	NM_001001317 // upstream // 5097 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST00000304182 // upstream // 5097 // — // — // — /// ENST00000334288 // downstream // 5133 // — // — // — // —	TRY1	TRY1, Homo sapiens trypsin X3 (TRY1), q34
SNP_A-1991525	catttattcattcaaa[A/T]attaaccactagctgt	A	T	NM_001001317 // upstream // 7534 // Hs.98609 // TRY1 // 136541 // Homo sapiens trypsin X3 (TRY1), mRNA. /// ENST00000304182 // upstream // 7534 // — // — // — /// ENST00000334288 // downstream // 2696 // — // — // — // —	TRY1	TRY1, Homo sapiens trypsin X3 (TRY1), q34
SNP_A-2100733	agatagattgccctaa[C/G]atctggcttagagtac	C	G	ENST00000334288 // upstream // 23357 // — // — // — /// ENST00000358973 // upstream // 12964 // — // — // — // — /// ENST00000356506 // upstream // 25485 // — // — // — // — /// ENST00000332013 // upstream // 63742 // — // -	-	q34
SNP_A-2284184	gatatggtgataaga[A/G]gaagtcctgctcctga	A	G	NM_000420 // upstream // 2192 // Hs.368588 // KEL // 3792 // Homo sapiens Kell blood group (KEL), mRNA. /// NM_001001658 // downstream // 61592 // — // OR9A2 // 13592 // Homo sapiens olfactory receptor, family 9, subfamily A, member 2 (OR9A2), mRNA. //	KEL	KEL, Homo sapiens Kell blood group (KEL), q34
SNP_A-2094404	agaagtgctctatgat[C/T]aagaggtagtgtccaa	C	T	NM_001001667 // downstream // 300 // — // OR6V1 // 346517 // Homo sapiens olfactory receptor, family 6, subfamily V, member 1 (OR6V1), mRNA. /// AF286696 // downstream // 8950 // Hs.339818 // OR6W1P // 89883 // Homo sapiens olfactory receptor sdolf mRNA	OR6V1	OR6V1, Homo sapiens olfactory receptor, family 6, subfamily V, member 1 (OR6V1), q34
SNP_A-1757843	aatctgatatttttaaaggtacata[C/T]gatgccaatgttgccgtat agctca	C	T	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant)	CLCN1	CLCN1, rs2103193, chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1717309	agatttgaaaagtcctgtagaaaac[A/G]aaatactgtatatttttca acattt	A	G	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant)	CLCN1	CLCN1 , rs10500138, chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant),q34
SNP_A-1737457	acgatggacatccagaactggagtg[A/G]aaagaagcgttgga ataccctttca	A	G	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant)	CLCN1	CLCN1 , rs2272252, chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant),q34
SNP_A-1991555	aaatgttcaatgaatg[G/T]atgaaaattaatctgc	G	T	NM_032983 // intron // 0 // Hs.368982 // CASP2 // 835 // Homo sapiens caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) /// NM_032984 // intron // 0 // Hs.368982 // CASP2 // 835 // Homo sapi	CASP2	CASP2, Homo sapiens caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2) ,q34
SNP_A-2238872	ctcttcacacaaaaaa[A/C]caatatttgaggccga	A	C	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA. /// ENST00000343257 // intron // 0 // — // — // — // —	CLCN1	CLCN1, Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), q34
SNP_A-2259281	gaaaaagaagtgatgt[A/G]aaagagatcatctttt	A	G	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA. /// ENST00000343257 // intron // 0 // — // — // — // —	CLCN1	CLCN1, Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), q34
SNP_A-2101680	agatgatttctaaggc[C/G]cttgtagatctgaaac	C	G	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA. /// ENST00000343257 // intron // 0 // — // — // — // —	CLCN1	CLCN1, Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), q34
SNP_A-2212319	ccctggtcagtgccaa[C/T]actcataatgacttgt	C	T	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA. /// ENST00000343257 // intron // 0 // — // — // — // —	CLCN1	CLCN1, Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), q34
SNP_A-1820739	gtttccaaacttaac[C/T]ctaagctcagtctcag	C	T	NM_000083 // intron // 0 // Hs.121483 // CLCN1 // 1180 // Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA. /// ENST00000343257 // intron // 0 // — // — // — // —	CLCN1	CLCN1, Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), q34
SNP_A-1904794	tggggtcccttgtcag[A/C]aacctaatgcccctaa	A	C	NM_014690 // upstream // 4193 // Hs.135343 // KIAA0773 // 9715 // Homo sapiens KIAA0773 gene product (KIAA0773), mRNA. /// NM_003461 // upstream // 14358 // Hs.490415 // ZYX // 7791 // Homo sapiens zyxin (ZYX), mRNA. /// ENST00000324572 // upstream // 419	KIAA0773	KIAA0773, Homo sapiens KIAA0773 gene product (KIAA0773), q34
SNP_A-2074080	acagttgtatttttgc[A/G]aaggagaaaaatatga	A	G	NM_176883 // downstream // 22679 // — // TAS2R41 // 259287 // Homo sapiens taste receptor, type 2, member 41 (TAS2R41), mRNA. /// ENST00000313125 // downstream // 22679 // — // — // — // — /// ENST00000327198 // downstream // 9458 // — // —	TAS2R41	TAS2R41, Homo sapiens taste receptor, type 2, member 41 (TAS2R41), q34
SNP_A-2147090	atggaagttaaaatac[G/T]ggctagagcaaagaga	G	T	ENST00000223140 // upstream // 5227 // — // — // — // — /// ENST00000343697 // downstream // 28004 // — // — // — // —	-	q35
SNP_A-2058411	aatcaccatgctgtaa[A/G]agtagtcaaccatctc	A	G	NM_022445 // intron // 0 // Hs.490454 // TPK1 // 27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// ENST00000360057 // intron // 0 // — // — // — // — /// ENST00000355763 // intron // 0 // — // — // — // —	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-2271452	gacatttgggtagcgg[C/T]aaatttgaatcatct	C	T	NM_022445 // upstream // 70292 // Hs.490454 // TPK1 // 27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 1210544 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRN	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-1913042	tgtggaggggaaaca[A/C]cgattggaataaatgc	A	C	NM_022445 // upstream // 90256 // Hs.490454 // TPK1 // 27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 1190580 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRN	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2176938	cacctaatgggtgca[C/T]atcataaaatgtaga	C	T	NM_022445 // upstream // 350055 // Hs.490454 // TPK1 // 27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 930781 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRN	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-2073551	acagtacaggtatgta[C/T]agtttaacacaaagca	C	T	NM_022445 // upstream // 1033399 // Hs.490454 // TPK1 // 27010 // Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA. /// NM_014141 // upstream // 247437 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mR	TPK1	TPK1, Homo sapiens thiamin pyrophosphokinase 1 (TPK1), q35
SNP_A-2115656	agggtatcggcatgga[A/T]gacttaataacttggg	A	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991618	tttattacctgaac[A/G]cttctaataggacact	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991619	cactctgtctcatgat[G/T]aattccaggatctgt	G	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2033428	aaataggtagccgaa[A/G]tgaaaccaaagattaa	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991631	gtactgtaaccttcttta[C/T]ggaatccctctttttc	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1835757	tacgcaataataggaaa[C/T]ttacgtacttgttat	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2297464	gccacttgtaagcata[C/T]ggatgagatttgtct	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2076636	acatttgtgaatatca[A/G]ctctgttcttggcatc	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1722554	aataaaaataggcaaacactatata[C/T]gctgtaaacctttgga gtatcctt	C	T	NM_014141 // intron // 0 // Hs.106552 // CNTNAP2 // 26047 // contactin associated protein-like 2	CNTNAP2	CNTNAP2 , rs903900, contactin associated protein-like 2, q35
SNP_A-2302679	gctacctgtaatagac[C/T]agaatctgttggttaa	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991663	ccgaattatgacattac[C/T]atttccctcatgaaa	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1890414	tgatctaactacaggg[C/T]catggaaagctttct	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1908803	tgtagtcaattctcaa[C/T]agatgacagccatggt	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2045103	aagaagaagaaaaaaa[C/G]acatccaaatccaaaa	C	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1914046	tgtgtctttggagga[C/G]taatagggcaggaatg	C	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2159445	atttacaaaagcaggc[A/G]aatcttaaataaacac	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2249201	ctgtttgatcattcaa[C/T]gttgctttctatat	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1907989	tgtaattcctaaggat[A/G]agtctaaagttgcttg	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1827027	taaccaatcaaatgac[C/T]gtaacatctgtgctgg	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1942401	ttggcgagaaatagtc[A/G]ctgaagtcaagcagaa	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991696	ggttagctgaaaatgat[A/G]taaatgacaagaggggg	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2012992	ttctcaggtgcaaaat[C/T]agactagctattccct	G	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991704	acactcagaaaatacat[A/G]tggttatcaagaatgt	A	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2154728	attcaaatattgttat[C/G]aaagtggtgccaaaaa	C	G	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1991705	catgtcataaatacat[A/C]aatttccaagcagtca	A	C	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2150041	atgtccaacttcatggt[C/T]caaatgtaaacttttgg	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-1884657	tgaatagactcattca[C/T]ggggaagtcatgcctt	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q35
SNP_A-2144391	atgataagcgcgcaaa[C/T]ggttgtggagtgaaga	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-2170767	caagtttagtgaaata[C/T]gggaacatgtacagag	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-2238057	ctctgcaatggaatga[C/T]ggtcagaaaagaacag	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-2024588	aaaaggagtgtttta[C/T]ggacaacgaggcagca	C	T	NM_014141 // intron // 0 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// ENST00000307013 // intron // 0 // — // — // —	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-1883524	tgaaccattttgggc[A/G]cactagttcctgaggg	A	G	NM_014141 // downstream // 160237 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// NM_145304 // upstream // 14712 // Hs.352212 // C7orf33 // 202865 // Homo sapiens chromosome 7 open reading frame 33	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991722	aggcatttagatgac[A/G]gcattgcgggatctcg	A	G	NM_014141 // downstream // 173174 // Hs.446192 // CNTNAP2 // 26047 // Homo sapiens contactin associated protein-like 2 (CNTNAP2), mRNA. /// NM_145304 // upstream // 1775 // Hs.352212 // C7orf33 // 202865 // Homo sapiens chromosome 7 open reading frame 33	CNTNAP2	CNTNAP2, Homo sapiens contactin associated protein-like 2 (CNTNAP2), q36.1
SNP_A-2267485	gaatatcctaacaatc[A/G]aactctgtgccaggaa	A	G	NM_145304 // downstream // 35465 // Hs.352212 // C7orf33 // 202865 // Homo sapiens chromosome 7 open reading frame 33 (C7orf33), mRNA. /// NM_003592 // upstream // 47517 // Hs.146806 // CUL1 // 8454 // Homo sapiens cullin 1 (CUL1), mRNA. /// ENST00000003070	C7orf33	C7orf33, Homo sapiens chromosome 7 open reading frame 33 (C7orf33), q36.1
SNP_A-2067586	acaaattgcaaacagc[C/T]aatatggaaatgcgtg	C	T	NM_003592 // intron // 0 // Hs.146806 // CUL1 // 8454 // Homo sapiens cullin 1 (CUL1), mRNA. /// ENST00000325222 // intron // 0 // — // — // — // —	CUL1	CUL1, Homo sapiens cullin 1 (CUL1), q36.1
SNP_A-2225335	cgtttctaagtaaagc[A/C]cactgttccaagctta	A	C	NM_003592 // intron // 0 // Hs.146806 // CUL1 // 8454 // Homo sapiens cullin 1 (CUL1), mRNA. /// ENST00000325222 // intron // 0 // — // — // — // — /// ENST00000182065 // intron // 0 // — // — // —	CUL1	CUL1, Homo sapiens cullin 1 (CUL1), q36.1
SNP_A-1835892	tacgttccaactagat[A/G]aaaggacagcattata	A	G	NM_003592 // intron // 0 // Hs.146806 // CUL1 // 8454 // Homo sapiens cullin 1 (CUL1), mRNA. /// ENST00000325222 // intron // 0 // — // — // — // — /// ENST00000182065 // intron // 0 // — // — // —	CUL1	CUL1, Homo sapiens cullin 1 (CUL1), q36.1
SNP_A-1816275	gttacttgcaagcaga[C/T]ggatgggaagattgga	C	T	NM_004911 // intron // 0 // Hs.93659 // ERP70 // 9601 // Homo sapiens protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (ERP70), mRNA. /// ENST00000286091 // intron // 0 // — // — // —	ERP70	ERP70, Homo sapiens protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (ERP70), q36.1
SNP_A-2194161	catgagaatcaactat[A/G]atacagctgactggaa	A	G	NM_015694 // downstream // 108798 // Hs.38512 // KIAA1285 // 27153 // Homo sapiens KIAA1285 protein (KIAA1285), mRNA. /// ENST00000360977 // downstream // 37636 // — // — // — // — /// ENST00000314683 // downstream // 108798 // — // — // —	KIAA1285	KIAA1285, Homo sapiens KIAA1285 protein (KIAA1285), q36.1
SNP_A-1930750	ttccactcttaatc[A/G]ctgacctgtttcagc	A	G	NM_024910 // upstream // 20206 // Hs.520785 // FLJ12700 // 79970 // Homo sapiens hypothetical protein FLJ12700 (FLJ12700), mRNA. /// NM_032534 // upstream // 70286 // Hs.299560 // KIAA1862 // 84626 // Homo sapiens KIAA1862 protein (KIAA1862), mRNA. /// EN	FLJ12700	FLJ12700, Homo sapiens hypothetical protein FLJ12700 (FLJ12700), q36.1
SNP_A-2142050	atcttgaatcaagag[A/T]agcctcatctgattta	A	T	NM_024910 // upstream // 39311 // Hs.520785 // FLJ12700 // 79970 // Homo sapiens hypothetical protein FLJ12700 (FLJ12700), mRNA. /// NM_032534 // upstream // 51181 // Hs.299560 // KIAA1862 // 84626 // Homo sapiens KIAA1862 protein (KIAA1862), mRNA. /// EN	FLJ12700	FLJ12700, Homo sapiens hypothetical protein FLJ12700 (FLJ12700), q36.1
SNP_A-2201002	ccaaggcaacttggaa[A/G]cacttcccggacagct	A	G	NM_024910 // upstream // 63466 // Hs.520785 // FLJ12700 // 79970 // Homo sapiens hypothetical protein FLJ12700 (FLJ12700), mRNA. /// NM_032534 // upstream // 27026 // Hs.299560 // KIAA1862 // 84626 // Homo sapiens KIAA1862 protein (KIAA1862), mRNA. /// EN	FLJ12700	FLJ12700, Homo sapiens hypothetical protein FLJ12700 (FLJ12700), q36.1
SNP_A-2311720	ggaattcagtggaaac[A/C]ggtaatcagatgaaga	A	C	NM_018384 // downstream // 1815 // Hs.412331 // GIMAP5 // 55340 // Homo sapiens immune associated nucleotide 4 like 1 (mouse) (IAN4L1), mRNA. /// NM_014020 // downstream // 45839 // Hs.521295 // LR8 // 28959 // Homo sapiens LR8 protein (LR8), mRNA. /// NM	GIMAP5	GIMAP5, Homo sapiens immune associated nucleotide 4 like 1 (mouse) (IAN4L1), q36.1
SNP_A-2201768	ccacaatttaacatg[C/G]agcttaatgctaattg	C	G	NM_014020 // intron // 0 // Hs.521295 // LR8 // 28959 // Homo sapiens LR8 protein (LR8), mRNA. /// NM_014020 // 5UTR // 0 // Hs.521295 // LR8 // 28959 // Homo sapiens LR8 protein (LR8), mRNA. /// ENST00000223298 // intron // 0 // — // — // —	LR8	LR8, Homo sapiens LR8 protein (LR8), q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101333	agatctccdgtcctag[C/T]atggagactctggaga	C	T	NM_007189 // intron // 0 // Hs.438823 // ABCF2 // 10061 // Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), nuclear gene encoding mitochondrial protein, transcri /// NM_005692 // intron // 0 // Hs.438823 // ABCF2 // 10061 // Homo	ABCF2	ABCF2, Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), nuclear gene encoding mitochondrial protein, transcri ,q36.1
SNP_A-1864197	tccaccagtgggtgga[A/G]gaaggaagccaaaagg	A	G	NM_003078 // upstream // 14684 // Hs.444445 // SMARCD3 // 6604 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), transc /// NM_001003801 // upstream // 14684 // Hs.444445 // SMARCD	SMARCD3	SMARCD3, Homo sapiens SWI,q36.1
SNP_A-2178216	cactattggacaggaaa[C/G]aactatgagtcgcccc	C	G	NM_003078 // upstream // 15142 // Hs.444445 // SMARCD3 // 6604 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), transc /// NM_001003801 // upstream // 15142 // Hs.444445 // SMARCD	SMARCD3	SMARCD3, Homo sapiens SWI,q36.1
SNP_A-1837627	tactttaagccaatggt[C/G]caaaatatggtgctgt	C	G	NM_003078 // upstream // 16313 // Hs.444445 // SMARCD3 // 6604 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), transc /// NM_001003801 // upstream // 16313 // Hs.444445 // SMARCD	SMARCD3	SMARCD3, Homo sapiens SWI,q36.1
SNP_A-1812832	gtgggcaattacgcaa[A/C]cttaccctagggaa	A	C	NM_016203 // intron // 0 // Hs.131133 // PRKAG2 // 51422 // Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // — // — // — /// ENST00000287878 // intron // 0 // —	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-2191235	catatacaatggtttc[A/G]gaaaaacaatttgcta	A	G	NM_016203 // intron // 0 // Hs.131133 // PRKAG2 // 51422 // Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // — // — // — /// ENST00000287878 // intron // 0 // —	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-2036134	aaattatagcggacag[A/C]aaaaaaagtcagtgtt	A	C	NM_016203 // intron // 0 // Hs.131133 // PRKAG2 // 51422 // Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // — // — // — /// ENST00000287878 // intron // 0 // —	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-1818278	gttctggcacttccc[A/G]aaaccgtagccatcag	A	G	NM_016203 // intron // 0 // Hs.131133 // PRKAG2 // 51422 // Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000355390 // intron // 0 // — // — // — /// ENST00000287878 // intron // 0 // —	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-1991758	aagaatacatttgaag[C/T]ctgttttttcccctt	C	T	NM_016203 // intron // 0 // Hs.131133 // PRKAG2 // 51422 // Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA. /// ENST00000287878 // intron // 0 // — // — // —	PRKAG2	PRKAG2, Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), q36.1
SNP_A-1744383	acactataagcattagaatcttgaa[A/C]tagaatcttgacattatct gacttc	A	C	NM_145292 // intron // 0 // Hs.131311 // GALNT15 // 168391 // UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15	GALNT15	GALNT15 , rs11112401, UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15,q36.1
SNP_A-1944517	ttgtcttggataaaaa[G/T]gaagacgaggacaagg	G	T	NM_145292 // intron // 0 // Hs.131311 // GALNTL5 // 168391 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5 (GALNTL5), mRNA. /// ENST00000323750 // intron // 0 // — // — // — /// ENST0000	GALNTL5	GALNTL5, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 5 (GALNTL5), q36.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2163479	caaaaaacaaaatagg[C/G]atgtggatttcagagt	C	G	NM_005431 // downstream // 162902 // Hs.129727 // XRCC2 // 7516 // Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), mRNA. /// ENST00000021776 // downstream // 36339 // --- // --- // --- /// ENST00000035932	XRCC2	XRCC2, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), q36.1
SNP_A-1805509	gtccagccacagaata[A/C]attttaaggtcttg	A	C	NM_005431 // upstream // 44449 // Hs.129727 // XRCC2 // 7516 // Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), mRNA. /// ENST00000359321 // upstream // 44449 // --- // --- // --- /// ENST00000328669 //	XRCC2	XRCC2, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2), q36.1
SNP_A-2104427	agcaggaaggagtgaa[C/T]ggaaaagtagctgaga	C	T	NM_020445 // downstream // 150444 // Hs.490655 // ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 // downstream // 150836 // --- // --- // --- /// ENST00000256001 // downstream // 150444 // --- /	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2123319	agtgtatgagggaaaa[C/G]atgtgcatttagata	C	G	NM_020445 // downstream // 200507 // Hs.490655 // ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 // downstream // 200899 // --- // --- // --- /// ENST00000256001 // downstream // 200507 // --- /	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-1892812	tgcacatagacaaata[C/T]atagaagaatgaaggg	C	T	NM_020445 // downstream // 302497 // Hs.490655 // ARP3BETA // 57180 // Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA. /// ENST00000297369 // downstream // 302889 // --- // --- // --- /// ENST00000256001 // downstream // 302497 // --- /	ARP3BETA	ARP3BETA, Homo sapiens actin-related protein 3-beta (ARP3BETA), q36.2
SNP_A-2040038	aacattttctgaaca[C/T]gaaattcaaacctatc	C	T	NM_207367 // upstream // 54670 // Hs.521304 // FLJ42291 // 346547 // Homo sapiens FLJ42291 protein (FLJ42291), mRNA. /// NM_130797 // upstream // 584188 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA.	FLJ42291	FLJ42291, Homo sapiens FLJ42291 protein (FLJ42291), q36.2
SNP_A-2186181	caggcctgagagcacc[C/T]gaggagtttagattta	C	T	NM_207367 // upstream // 56146 // Hs.521304 // FLJ42291 // 346547 // Homo sapiens FLJ42291 protein (FLJ42291), mRNA. /// NM_130797 // upstream // 582712 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA.	FLJ42291	FLJ42291, Homo sapiens FLJ42291 protein (FLJ42291), q36.2
SNP_A-2070900	acactcaggcaataaa[A/G]aaaagtataaagaata	A	G	NM_207367 // upstream // 159594 // Hs.521304 // FLJ42291 // 346547 // Homo sapiens FLJ42291 protein (FLJ42291), mRNA. /// NM_130797 // upstream // 479264 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA	FLJ42291	FLJ42291, Homo sapiens FLJ42291 protein (FLJ42291), q36.2
SNP_A-2045382	aagaataaaatttctc[A/T]aatcctcaaaaatagt	A	T	NM_207367 // upstream // 159620 // Hs.521304 // FLJ42291 // 346547 // Homo sapiens FLJ42291 protein (FLJ42291), mRNA. /// NM_130797 // upstream // 479238 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA	FLJ42291	FLJ42291, Homo sapiens FLJ42291 protein (FLJ42291), q36.2
SNP_A-2192508	catccaaactagtaga[A/G]ggaaaatggaactaa	A	G	NM_207367 // upstream // 291036 // Hs.521304 // FLJ42291 // 346547 // Homo sapiens FLJ42291 protein (FLJ42291), mRNA. /// NM_130797 // upstream // 347822 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA	FLJ42291	FLJ42291, Homo sapiens FLJ42291 protein (FLJ42291), q36.2
SNP_A-2237241	ctctcatctgtggctc[A/G]caagtgctccaggaga	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991780	caaattctcgcctgga[A/G]gtcagttaagaaaaagg	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1836546	tactctattctagaca[C/T]tgaaattatgcagaga	C	T	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1786209	ggctggtgatcagggal[C/T]gatgagctttctcat	C	T	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1834253	tacatggtaaaagcaa[A/G]caacatagatgagagt	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1991786	atcaatcaatcgtaca[A/G]tcttcctttacctaaa	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1991787	ctaacttgacagccac[A/G]caagggggacagttag	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2211318	ccctacatttacagga[C/T]ggtcagctgtcccat	C	T	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1868985	tcctgatgcagacccaa[C/T]gaggatcctctgccag	C	T	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1886323	tgacctcttcaggagal[C/T]ggtgaccccgagatgt	C	T	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2161646	atttgggatcaggga[A/G]atgaatgaaatttgat	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1927809	ttcaaggatgaaaccc[A/G]ctcatggctgaagagt	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138464	atccatcaatcgctta[C/T]gactttcatgacatca	C	T	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-2176729	caccctacatgtttga[A/G]gctaataagacagttt	A	G	NM_130797 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, mRNA. /// NM_001936 // intron // 0 // Hs.490684 // DPP6 // 1804 // Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 2, m	DPP6	DPP6, Homo sapiens dipeptidylpeptidase 6 (DPP6), transcript variant 1, q36.2
SNP_A-1792252	gggttccaacattcat[C/T]atccagtttcagagac	C	T	NM_007349 // intron // 0 // Hs.443881 // PAXIP1L // 22976 // Homo sapiens PAX transcription activation domain interacting protein 1 like (PAXIP1L), mRNA. /// ENST00000323199 // intron // 0 // — // — // — // —	PAXIP1L	PAXIP1L, Homo sapiens PAX transcription activation domain interacting protein 1 like (PAXIP1L), q36.2
SNP_A-1782333	ggcaatgatgtgtcac[C/T]gtagattaatcagttg	C	T	NM_024012 // downstream // 50709 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 161375 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-1888813	tgagggtgaggaacaa[C/T]ttagaatttctgctga	C	T	NM_024012 // downstream // 57188 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 154896 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2120750	agtcctctggtgagga[C/T]gcatggtaaagagtgt	C	T	NM_024012 // downstream // 59859 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 152225 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-1922422	ttagaaattactggta[C/T]ggtcttatgtttgata	C	T	NM_024012 // downstream // 66790 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 145294 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2284918	gatccatcacagctgc[C/T]acctcggtctacttag	C	T	NM_024012 // downstream // 67840 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 144244 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2235052	ctcccacttttacccc[A/G]cgctttctcactctcc	A	G	NM_024012 // downstream // 69190 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 142894 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2093968	agaagccctccatgtc[A/G]aagtctccagctcaga	A	G	NM_024012 // downstream // 69612 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 142472 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), tr	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-2013051	cgctggatatgaagcc[A/G]ctgtgtaacacacaaa	A	G	NM_024012 // downstream // 108873 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 103211 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), t	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2095320	agaatttcagggaaaac[A/T]acaatagtgaaaacat	A	T	NM_024012 // downstream // 112017 // Hs.65791 // HTR5A // 3361 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), mRNA. /// NM_198337 // upstream // 100067 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), t	HTR5A	HTR5A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A), q36.2
SNP_A-1781608	ggattgaaccttatc[A/T]gaagggaggtttctgc	A	T	NM_198337 // intron // 0 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), transcript variant 3, mRNA. /// NM_005542 // intron // 0 // Hs.520819 // INSIG1 // 3638 // Homo sapiens insulin induced gene 1 (INSIG1), transcript va	INSIG1	INSIG1, Homo sapiens insulin induced gene 1 (INSIG1), transcript variant 3, q36.3
SNP_A-2287061	gatgtaattccctcca[C/T]gctaagcttatgaccc	C	T	NM_000193 // upstream // 26571 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 800585 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf13	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-1735677	tgatttatttattgtaacttttatca[C/T]gtcttaattccataggtttgccc	C	T	NM_000193 // upstream // 127493 // Hs.121539 // SHH // 6469 // sonic hedgehog homolog (Drosophila) /// NM_032625 // downstream // 698795 // Hs.124854 // C7orf13 // 129790 // chromosome 7 open reading frame 13	SHH	SHH , rs963932, sonic hedgehog homolog (Drosophila) , q36.3
SNP_A-2308118	gcttgatggtgcaggga[A/C]acagtaaatgcatcag	A	C	NM_000193 // upstream // 113274 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 713882 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-2081105	acctgaggaccctctc[A/G]ctcaagcatgtgggaca	A	G	NM_000193 // upstream // 114525 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 712631 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-2129992	ataccaacagacacca[C/T]agataccaacaggtg	C	T	NM_000193 // upstream // 515145 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 312011 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-2195071	catggaacatggacca[A/G]cgcaaaatcctgccat	A	G	NM_000193 // upstream // 545577 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 281579 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-1878480	tctgtgcactgtccc[A/G]cagaagctggatttgt	A	G	NM_000193 // upstream // 547639 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 279517 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-1836237	tactatgcggtctcac[C/T]gaaacatctggagcac	C	T	NM_000193 // upstream // 650376 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 176780 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-2174306	cacacttagtttgaga[A/T]gacaaatctccaagt	A	T	NM_000193 // upstream // 690595 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 136561 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf1	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1721860	cacacaagctttcacgtttacttga[C/G]attgatctagtgacagct tatcag	C	G	NM_000193 // upstream // 775965 // Hs.121539 // SHH // 6469 // sonic hedgehog homolog (Drosophila) /// NM_032625 // downstream // 50323 // Hs.124854 // C7orf13 // 129790 // chromosome 7 open reading frame 13	SHH	SHH , rs10488069, sonic hedgehog homolog (Drosophila), q36.3
SNP_A-2126068	agttttgggctgatac[A/G]aatgaagcgttatgaa	A	G	NM_000193 // upstream // 742681 // Hs.121539 // SHH // 6469 // Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA. /// NM_032625 // downstream // 84475 // Hs.124854 // C7orf13 // 129790 // Homo sapiens chromosome 7 open reading frame 13 (C7orf13	SHH	SHH, Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), q36.3
SNP_A-1754544	ctgagtgctccagcaccaatcagat[C/T]atgtatgttacttcaga agagatg	C	T	NM_030936 // intron // 0 // Hs.146037 // RNF32 // 140545 // ring finger protein 32	RNF32	RNF32 , rs2365509, ring finger protein 32, q36.3
SNP_A-1667442	gaaggctgatgtgctgatacctgac[A/G]aaagagattctaaagc aaaggcatc	A	G	NM_030936 // intron // 0 // Hs.146037 // RNF32 // 140545 // ring finger protein 32	RNF32	RNF32 , rs2365511, ring finger protein 32, q36.3
SNP_A-2050258	aaggagacattggtaa[C/T]ggaagaagaggtcgga	C	T	NM_022458 // intron // 0 // Hs.397295 // C7orf2 // 64327 // Homo sapiens chromosome 7 open reading frame 2 (C7orf2), mRNA. /// ENST00000353442 // intron // 0 // — // — // — /// ENST00000354505 // intron // 0 // — // — // — /// EN	C7orf2	C7orf2, Homo sapiens chromosome 7 open reading frame 2 (C7orf2), q36.3
SNP_A-2292766	gcactgcaggtttaa[C/T]gaatgtgaaatcagag	C	T	NM_022458 // upstream // 28893 // Hs.397295 // C7orf2 // 64327 // Homo sapiens chromosome 7 open reading frame 2 (C7orf2), mRNA. /// ENST00000353442 // upstream // 28893 // — // — // — /// ENST00000354505 // upstream // 29042 // — // — //	C7orf2	C7orf2, Homo sapiens chromosome 7 open reading frame 2 (C7orf2), q36.3
SNP_A-2076880	accaaaagcctctct[C/G]acttaaccacaaggg	C	G	ENST00000275820 // intron // 0 // — // — // —	-	q36.3
SNP_A-1852522	tatttagagtcttacc[A/G]agtgggggctctccaaa	A	G	ENST00000275820 // intron // 0 // — // — // —	-	q36.3
SNP_A-2032646	aaataaatagtatctg[A/G]aagtgccacaaatggg	A	G	NM_005515 // downstream // 33475 // Hs.37035 // HLXB9 // 3110 // Homo sapiens homeo box HB9 (HLXB9), mRNA. /// ENST00000275820 // downstream // 1088 // — // — // — // — /// ENST00000252971 // downstream // 33475 // — // — // — // —	HLXB9	HLXB9, Homo sapiens homeo box HB9 (HLXB9), q36.3
SNP_A-2082832	acgtagagactgaaca[G/T]taactgaagtgtgtgg	G	T	NM_005515 // downstream // 16362 // Hs.37035 // HLXB9 // 3110 // Homo sapiens homeo box HB9 (HLXB9), mRNA. /// ENST00000275820 // downstream // 18201 // — // — // — // — /// ENST00000252971 // downstream // 16362 // — // — // — // —	HLXB9	HLXB9, Homo sapiens homeo box HB9 (HLXB9), q36.3
SNP_A-1818966	gttgcaaacatccaca[C/T]aatatcgatttgtc	C	T	NM_005515 // downstream // 13820 // Hs.37035 // HLXB9 // 3110 // Homo sapiens homeo box HB9 (HLXB9), mRNA. /// ENST00000275820 // downstream // 20743 // — // — // — // — /// ENST00000252971 // downstream // 13820 // — // — // — // —	HLXB9	HLXB9, Homo sapiens homeo box HB9 (HLXB9), q36.3
SNP_A-1738945	taaaatacttccatttcttcaggat[C/T]cagccacctgccatgttga tacct	C	T	BC033117 // downstream // 90001 // Hs.224879 // - // - // Clone IMAGE:4634276, mRNA, partial cds /// NM_014671 // upstream // 32546 // - // - // - // -	-	-, rs724688, Clone IMAGE:4634276, mRNA, partial cds, q36.3
SNP_A-1712025	tcaaatctcacactaaagccatcta[A/C]atttgggaggaggatctg ggtgtgat	A	C	NM_014671 // intron // 0 // - // - // - // -	-	-, rs1859550, -, q36.3
SNP_A-1955155	tttggcagcccttcaa[C/T]gtgtgggaagtaggag	C	T	NM_005515 // upstream // 113974 // Hs.37035 // HLXB9 // 3110 // Homo sapiens homeo box HB9 (HLXB9), mRNA. /// ENST00000252971 // upstream // 113974 // — // — // — // — /// ENST00000351332 // upstream // 14465 // — // — // — // — /// ENST00	HLXB9	HLXB9, Homo sapiens homeo box HB9 (HLXB9), q36.3
SNP_A-2129361	atacaagaaaatggaa[C/T]ggaaaagcattggcct	C	T	NM_058246 // intron // 0 // Hs.490745 // DNAJB6 // 10049 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA. /// NM_005494 // intron // 0 // Hs.490745 // DNAJB6 // 10049 // Homo sapiens DnaJ (Hsp40) homolog, s	DNAJB6	DNAJB6, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, q36.3
SNP_A-1854769	tcaacattacgattac[A/G]aaggatgaaagtggtg	A	G	NM_058246 // downstream // 1429 // Hs.490745 // DNAJB6 // 10049 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA. /// NM_005494 // downstream // 1429 // Hs.490745 // DNAJB6 // 10049 // Homo sapiens DnaJ (Hsp	DNAJB6	DNAJB6, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, q36.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2312321	ggacatgaggtttaca[C/T]acttcattagggctcc	C	T	ENST00000360892 // intron // 0 // --- // --- // ---	-	q36.3
SNP_A-2222442	cgagcctgcaattgac[C/T]gcggaagccagtgccc	C	T	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2253841	cttgaaggcttcagaat[C/G]aggtgtaacagggatg	C	G	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-1940008	ttgcagatctgaacac[C/G]aacatcattgaccaat	C	G	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-1879478	tcttatcacctgtta[C/T]gtacatgggctctaa	C	T	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2224535	cgtattattggaaatc[A/G]caccaatttgggggtt	A	G	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2082842	acgtaggaagaataaaa[A/G]tctcatccaaacacaa	A	G	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-2228918	ctagatgccaaaaata[C/T]gtgtctcctaagctca	C	T	NM_002847 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, mRNA. /// NM_130843 // intron // 0 // Hs.490789 // PTPRN2 // 5799 // Homo sapiens protein	PTPRN2	PTPRN2, Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2 (PTPRN2), transcript variant 1, q36.3
SNP_A-1707643	aaagtttatacatcaggacatg[C/G]agagtaaatctgttat gacatgaa	C	G	NM_003382 // downstream // 73353 // Hs.170560 // VIPR2 // 7434 // vasoactive intestinal peptide receptor 2 /// NM_018051 // downstream // 8637 // Hs.445204 // FLJ10300 // 55112 // hypothetical protein FLJ10300	VIPR2	VIPR2 , rs262144, vasoactive intestinal peptide receptor 2, q36.3
SNP_A-2186481	cagggaaggaggttaa[C/G]aaggaaatgcacagat	C	G	NM_003382 // intron // 0 // Hs.490817 // VIPR2 // 7434 // Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), mRNA. /// ENST00000262178 // intron // 0 // --- // --- // ---	VIPR2	VIPR2, Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), q36.3
SNP_A-2201379	ccaatcgcatcctcca[C/T]tcaagaaagcttgact	C	T	NM_003382 // intron // 0 // Hs.490817 // VIPR2 // 7434 // Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), mRNA. /// ENST00000262178 // intron // 0 // --- // --- // ---	VIPR2	VIPR2, Homo sapiens vasoactive intestinal peptide receptor 2 (VIPR2), q36.3
SNP_A-2098297	agagatgcctcaaaa[C/T]ggtcgtcgattattct	C	T	ENST00000343993 // intron // 0 // --- // --- // ---	-	p23.3
SNP_A-1991853	tctagaggctaacccat[G/T]ctggacttggaggaa	G	T	NM_175075 // intron // 0 // Hs.289293 // INM01 // 157695 // Homo sapiens hypothetical protein INM01 (INM01), mRNA. /// ENST00000343993 // intron // 0 // --- // --- // --- /// ENST00000324079 // intron // 0 // --- // --- // ---	INM01	INM01, Homo sapiens hypothetical protein INM01 (INM01), p23.3
SNP_A-2077423	accacagccattcccaa[A/G]gtcttctccgaatggc	A	G	NM_207332 // downstream // 8084 // Hs.128130 // LOC157697 // 157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA. /// ENST00000324050 // upstream // 25012 // --- // --- // --- /// ENST00000262109 // downstream // 8084 // --- // ---	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991858	tgtgtccctatgccaa[G/T]gtgccggaaacaagtc	G	T	NM_207332 // intron // 0 // Hs.128130 // LOC157697 // 157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA /// ENST00000262109 // intron // 0 // — // — // —	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3
SNP_A-2225294	cgttgtgctcaaaata[C/T]cgcttacgtccgtctt	C	T	NM_207332 // intron // 0 // Hs.128130 // LOC157697 // 157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA /// ENST00000262109 // intron // 0 // — // — // —	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3
SNP_A-2023608	aaaactgaggagaccc[C/G]aaaaagatcagtgact	C	G	NM_207332 // intron // 0 // Hs.128130 // LOC157697 // 157697 // Homo sapiens hypothetical protein LOC157697 (LOC157697), mRNA /// ENST00000262109 // intron // 0 // — // — // —	LOC157697	LOC157697, Homo sapiens hypothetical protein LOC157697 (LOC157697), p23.3
SNP_A-2213254	ccgccttcagcccaaa[C/T]tggtggcgcatccag	C	T	ENST00000359307 // intron // 0 // — // — // —	-	p23.3
SNP_A-1947715	tttactcagagacggtg[A/G]aattaatttggcactg	A	G	ENST00000359307 // downstream // 42082 // — // — // — // — /// ENST00000358493 // upstream // 186116 // — // — // — // — /// ENST00000329590 // downstream // 138855 // — // — // — // — /// ENST00000342028 // downstream // 151189 //	-	p23.3
SNP_A-1933828	ttctatgtgtattgcaa[A/T]tcctaatttgtgttt	A	T	ENST00000359307 // downstream // 42172 // — // — // — // — /// ENST00000358493 // upstream // 186206 // — // — // — // — /// ENST00000329590 // downstream // 138945 // — // — // — // — /// ENST00000342028 // downstream // 151279 //	-	p23.3
SNP_A-1787012	gggaaacaaggagctat[C/G]gtaaggacacagcagc	C	G	ENST00000359307 // downstream // 45674 // — // — // — // — /// ENST00000358493 // upstream // 189708 // — // — // — // — /// ENST00000329590 // downstream // 142447 // — // — // — // — /// ENST00000342028 // downstream // 154781 //	-	p23.3
SNP_A-2123618	agtgtgttgacttcaa[C/T]gtcgatgacaggcagc	C	T	NM_014629 // intron // 0 // Hs.98594 // ARHGEF10 // 9639 // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA /// ENST00000339765 // intron // 0 // — // — // — // — /// ENST00000349830 // intron // 0 // — // — // -	ARHGEF10	ARHGEF10, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), p23.3
SNP_A-1881243	tctttatgcatccaca[A/G]tcattcactgtaacaa	A	G	NM_014629 // intron // 0 // Hs.98594 // ARHGEF10 // 9639 // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA /// ENST00000339765 // intron // 0 // — // — // — // — /// ENST00000349830 // intron // 0 // — // — // -	ARHGEF10	ARHGEF10, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), p23.3
SNP_A-2139929	atctacagtaaaacca[C/T]agggttgatctttggt	C	T	NM_014629 // intron // 0 // Hs.98594 // ARHGEF10 // 9639 // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA /// ENST00000339765 // intron // 0 // — // — // — // — /// ENST00000349830 // intron // 0 // — // — // -	ARHGEF10	ARHGEF10, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), p23.3
SNP_A-1945262	ttgttaaatagtggag[A/G]catttggtgtaatctt	A	G	NM_003970 // downstream // 35907 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA /// NM_033225 // downstream // 666104 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRN	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.3
SNP_A-1858481	tcagagatattcatcc[A/G]atcctcctgctacaag	A	G	NM_003970 // downstream // 178759 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA /// NM_033225 // downstream // 523252 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-2067518	acaaatgtacaggaat[A/T]aaaaaaaacatcaaaa	A	T	NM_003970 // downstream // 194893 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA /// NM_033225 // downstream // 507118 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-2182863	cagatgtgctttca[C/T]tcaataaaacatggctt	C	T	NM_003970 // downstream // 210671 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA /// NM_033225 // downstream // 491340 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175472	cacatcctgccaaata[A/T]atcagtccatgcctctg	A	T	NM_003970 // downstream // 217781 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 484230 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-1780479	ggatagcacttaaaca[C/T]tgaagaggatagagct	C	T	NM_003970 // downstream // 394906 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 307105 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-2067754	acaacaggattgaaaa[A/G]cattagccacaaagga	A	G	NM_003970 // downstream // 473811 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 228200 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-2286525	gatggaaattgattac[A/C]acaaatgaatcctctg	A	C	NM_003970 // downstream // 560083 // Hs.443683 // MYOM2 // 9172 // Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), mRNA. /// NM_033225 // downstream // 141928 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mR	MYOM2	MYOM2, Homo sapiens myomesin (M-protein) 2, 165kDa (MYOM2), p23.2
SNP_A-1731223	gaacagttctagatttcaatccaat[A/G]aagtgatttgttctactc tgcac	A	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs1979509, CUB and Sushi multiple domains 1,p23.2
SNP_A-1654813	tttctcttgtgtgaaaccgtcata[G/T]cccagaaaattagaccag ttacaat	G	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs10503190, CUB and Sushi multiple domains 1,p23.2
SNP_A-1752995	tatgaggaaaaaagaggtaattggat[A/G]gaaaacaaatataa caactctttca	A	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs7827348, CUB and Sushi multiple domains 1,p23.2
SNP_A-2301596	gcgatgccatcctcaa[A/C]gtctcttaccagtgtg	A	C	NM_033225 // intron // 0 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // — // — // — // ENST00000318252 // intron // 0 // — // — // — // ENST0	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2211691	ccctccatttatatttc[A/T]ccagcgtctcttaca	A	T	NM_033225 // intron // 0 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // — // — // — // ENST00000318252 // intron // 0 // — // — // — // ENST0	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1752307	atctttctgaaatagtgcagaat[C/T]aacatcatagaatttatgtt gtca	C	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1, rs10503201, CUB and Sushi multiple domains 1,p23.2
SNP_A-1791778	gggtgaaatattgata[A/C]atagaagggcaacaaa	A	C	NM_033225 // intron // 0 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// ENST00000335551 // intron // 0 // — // — // — // ENST00000318252 // intron // 0 // — // — // — // ENST0	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2138215	atccaccctgagttaa[C/T]tgtcttgcctcatctg	C	T	NM_033225 // upstream // 10766 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 3011178 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2229126	ctagcgacctgatga[C/G]atgagctgttacatg	C	G	NM_033225 // upstream // 26015 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2995929 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2184132	cagccgcacaaagtac[A/T]ctgcctgcacttccca	A	T	NM_033225 // upstream // 37903 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2984041 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991931	aacatggcttgaaga[C/G]aaaagtagtagagtat	C	G	NM_033225 // upstream // 212458 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2809486 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1643730	tagtggagataagatctatatgagt[C/G]aataatcagaattaatta caaatga	C	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs7015502, CUB and Sushi multiple domains 1,p23.2
SNP_A-1732686	gataaatttgatttacagcatcctat[C/T]gagacatttctacatgcat aacagt	C	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs10503212, CUB and Sushi multiple domains 1,p23.2
SNP_A-1666042	aaaacagctactgctagagactgta[C/G]aaatattctgtaaaaa cagcaaaaa	C	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs10503213, CUB and Sushi multiple domains 1,p23.2
SNP_A-1878099	tctgtaggagtagcgat[C/T]gatgaactgtttaaca	C	T	NM_033225 // upstream // 220916 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2801028 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2063301	aattaaacctgtgtca[C/G]gtgaaatgtaagaaca	C	G	NM_033225 // upstream // 329458 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2692486 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1991945	tttcattaagtactta[C/G]gattagccagtaccc	C	G	NM_033225 // upstream // 338453 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2683491 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2278117	gagccctgctttggtc[A/G]cctctagtcatgtctt	A	G	NM_033225 // upstream // 354509 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2667435 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2048755	aagccatgtgtagaaa[A/T]gtttcaaaatcatggg	A	T	NM_033225 // upstream // 360595 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2661349 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2044534	aagaaaattagaaagga[C/T]ggaagaagtgatgttt	C	T	NM_033225 // upstream // 376431 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2645513 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1718271	tagtgagtttgggttttgcaaca[C/T]gaggtcgataaatgggac ctggaga	C	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs2720811, CUB and Sushi multiple domains 1,p23.2
SNP_A-2070575	acacctgctcttgaaa[G/T]gctcctctctctccg	G	T	NM_033225 // upstream // 396343 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2625601 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1902493	tgcctgaataatgaa[A/G]gcaatttgaagctatc	A	G	NM_033225 // upstream // 396843 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2625101 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1991947	aaggggattgcttttg[G/T]acttagcattacccca	G	T	NM_033225 // upstream // 398269 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2623675 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1663590	agcagtgtgcaattatttttcaaacaa[C/T]gaggattctcccccataatc ataaaga	C	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs4477054, CUB and Sushi multiple domains 1,p23.2
SNP_A-1720303	tcttgcaaacgacccctctacataag[A/C]actaacacggaattga ggcttgcct	A	C	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs1871816, CUB and Sushi multiple domains 1,p23.2
SNP_A-1729338	ccttttcattgaaagtcttgttcac[A/G]attttatcgataaaatattgttt a	A	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs900090, CUB and Sushi multiple domains 1,p23.2
SNP_A-1720623	gatatttaatatcatagaggagttat[C/T]ggacatagtacacaca gaggagtc	C	T	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs2720887, CUB and Sushi multiple domains 1,p23.2
SNP_A-1678090	ctcccagtaagtcgaacatgaagca[A/G]atgcctactacatgg tctatagat	A	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs2720888, CUB and Sushi multiple domains 1,p23.2
SNP_A-2088225	actggtcctcgttggc[C/T]aattcaggatgtgatg	C	T	NM_033225 // upstream // 403253 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2618691 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2150562	atgtgagctcagaaga[C/G]acacagtagtctaag	C	G	NM_033225 // upstream // 410697 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2611247 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2247600	ctgtcttccaacttga[A/T]accttgtcccactgga	A	T	NM_033225 // upstream // 410859 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2611085 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1859162	tcagccttcacttgcc[A/G]aatgattggtcgttgg	A	G	NM_033225 // upstream // 420720 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2601224 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2156561	attctgaagtaactta[C/T]ggatatcaggagctga	C	T	NM_033225 // upstream // 494609 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2527335 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2170270	caaggtttaggtgat[C/G]agcatccaatttaag	C	G	NM_033225 // upstream // 496152 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2525792 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1825007	taaaggaaaattttccc[A/T]gattacacttggaaca	A	T	NM_033225 // upstream // 542376 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2479568 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1863022	tcattggctatgtc[G/T]acaatatagctaggca	G	T	NM_033225 // upstream // 602481 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2419463 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1916127	tgttggaattagcgga[C/G]aaggattttaatgcag	C	G	NM_033225 // upstream // 661948 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2359996 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2035231	aaatgctgtacattat[C/T]aggagagatagtagtt	C	T	NM_033225 // upstream // 692296 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2329648 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1890638	tgatgaagttactgac[G/T]agagaaggccagtggc	G	T	NM_033225 // upstream // 711039 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2310905 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2034958	aaatgatccatcagta[C/T]acaaaataggaagatg	C	T	NM_033225 // upstream // 713514 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2308430 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2269152	gaattggcatcttctg[A/C]aatactgtaaattaga	A	C	NM_033225 // upstream // 726972 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2294972 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2193118	catctagataaatggc[C/G]actgcgttttccactt	C	G	NM_033225 // upstream // 759750 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2262194 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1672022	aatcagcatccttcatttgaatatc[A/C]cggtttaataccaccaaagcagcac	A	C	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs1714757, CUB and Sushi multiple domains 1,p23.2
SNP_A-2128679	ataatcaaataagata[C/T]gtcacattattagcga	C	T	NM_033225 // upstream // 772882 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2249062 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2066641	acaaaaatgcaaaaat[C/G]agtacaggctgggaac	C	G	NM_033225 // upstream // 775601 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2246343 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2034314	aaatcctgagaagaaa[A/C]agttggatttgaatgt	A	C	NM_033225 // upstream // 800774 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2221170 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2288601	gattgcgacttttaac[C/G]ggttaatccactgcta	C	G	NM_033225 // upstream // 845916 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2176028 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2160669	atttcctctctctcaa[C/T]agatgtggtataagct	C	T	NM_033225 // upstream // 937859 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2084085 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2286757	gatggcctcacctgca[C/G]aatagatatcctgttg	C	G	NM_033225 // upstream // 999146 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 2022798 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1754404	ccactgatcacaaaaatcagaccta[C/G]agaggaaaataaattt atggttgtc	C	G	NM_033225 // intron // 0 // Hs.415199 // CSMD1 // 64478 // CUB and Sushi multiple domains 1	CSMD1	CSMD1 , rs1405244, CUB and Sushi multiple domains 1,p23.2
SNP_A-2276886	gagaatatggcaaagg[C/T]aaaacaggctgcaggt	C	T	NM_033225 // upstream // 1182378 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1839566 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2253268	ctctgctgtaatcca[C/G]tcttataatgcaggag	C	G	NM_033225 // upstream // 1499576 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1522368 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2118079	agtaaaagtatattgc[A/G]agagctaattagttc	A	G	NM_033225 // upstream // 1520318 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1501626 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1728467	ttgtgggaaatcattcacacctgaa[A/C]aatgaaccctctaatg tttttcta	A	C	NM_001147 // downstream // 1467161 // Hs.115181 // ANGPT2 // 285 // angiopoietin 2 /// NM_024596 // upstream // 1396040 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein FLJ12847 /// NM_033225 // upstream // 40809 // Hs.415199 // CSMD1 // 64478 //	ANGPT2	ANGPT2 , rs10503288, angiopoietin 2 ,p23.2
SNP_A-1758242	cacaattaccgagttaaaagaatgc[A/G]gcagatgtcgatattgt gggaaatc	A	G	NM_001147 // downstream // 1467122 // Hs.115181 // ANGPT2 // 285 // angiopoietin 2 /// NM_024596 // upstream // 1396001 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein FLJ12847 /// NM_033225 // upstream // 40848 // Hs.415199 // CSMD1 // 64478 //	ANGPT2	ANGPT2 , rs10503289, angiopoietin 2 ,p23.2
SNP_A-2013123	aatgctatcttccata[C/T]caaagttaaagaagga	C	T	NM_033225 // upstream // 1641204 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1380740 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1829657	taagttgacttcctct[C/T]aagcttggcatttggt	C	T	NM_033225 // upstream // 1663305 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1358639 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2256013	ctttaatatgtgcata[A/T]gtgttacgcaactctt	A	T	NM_033225 // upstream // 1669643 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1352301 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1992046	aaagacgattggataa[G/T]tgaaaacaatgacttt	G	T	NM_033225 // upstream // 1694709 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1327235 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1943942	ttgtatgacaagtgaa[A/G]atgaccataaaccac	A	G	NM_033225 // upstream // 1708170 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1313774 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2161378	atttgcagatttctaa[C/T]gccctatcagataaat	C	T	NM_033225 // upstream // 1722013 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1299931 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1858228	tcagaagacaggaaag[A/G]ataatagacacaacaa	A	G	NM_033225 // upstream // 1723513 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1298431 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1870634	tcgcagaatgaatcaa[C/T]agagaacagtagcttg	C	T	NM_033225 // upstream // 1726815 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1295129 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2160891	atttctgatattaaaa[C/G]agaccttgccaaaatt	C	G	NM_033225 // upstream // 1726884 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1295060 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2054679	aataaaagaatgttat[A/G]aagcttcagatgtcat	A	G	NM_033225 // upstream // 1733674 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1288270 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2045083	aagaagaaagaagagc[A/C]aatgtaaggcgtgcag	A	C	NM_033225 // upstream // 1848962 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1172982 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2081407	acctggtgactttaa[C/G]aaatctccattcactt	C	G	NM_033225 // upstream // 1889188 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1132756 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1798555	gtaaatttgatggaaa[C/T]gctgaagaggagag	C	T	NM_033225 // upstream // 1946914 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1075030 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2068042	acaacttccacgtgca[C/T]ctttctccctctgtga	C	T	NM_033225 // upstream // 1959393 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 1062551 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2036269	aaattcactctgaaat[C/G]aaatgtattcctcctc	C	G	NM_033225 // upstream // 2072389 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 949555 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1737611	gtctgtacatatcagcctggtccca[A/C]agaaccttgacatttag cctgtgt	A	C	NM_001147 // downstream // 989254 // Hs.115181 // ANGPT2 // 285 // angiopoietin 2 /// NM_024596 // upstream // 918133 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein FLJ12847 /// NM_033225 // upstream // 518716 // Hs.415199 // CSMD1 // 64478 //	ANGPT2	ANGPT2 , rs10503310, angiopoietin 2 ,p23.2
SNP_A-1946053	ttgtttagtttcaca[A/G]tgcctctttggaggag	A	G	NM_033225 // upstream // 2121431 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 900513 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2175745	cacattcagcatttaa[C/G]aataacagaataaaag	C	G	NM_033225 // upstream // 2121586 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 900358 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2071022	acactgaatggccccc[G/T]aatgatgaattttaa	G	T	NM_033225 // upstream // 2334281 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 687663 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2142549	atgaacatcctaccta[A/G]attttacaagggttc	A	G	NM_033225 // upstream // 2375726 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 646218 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1884193	tgaaggaatcgtgtcc[C/T]cacacttacctccaac	C	T	NM_033225 // upstream // 2417624 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 604320 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2090665	actttaactattaaac[G/T]agcgagcgtttgatgt	G	T	NM_033225 // upstream // 2498253 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 523691 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1657524	tgccaaaatgataggaatagattgg[G/T]caggaataaaatatga acattttct	G	T	NM_001147 // downstream // 534553 // Hs.115181 // ANGPT2 // 285 // angiopoietin 2 /// NM_024596 // upstream // 463432 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein FLJ12847 /// NM_033225 // upstream // 973417 // Hs.415199 // CSMD1 // 64478 //	ANGPT2	ANGPT2 , rs2703322, angiopoietin 2 ,p23.2
SNP_A-1749099	aggatattgtcgaaatatgataaa[C/T]ggccagcaggtgttagt acataaat	C	T	NM_001147 // downstream // 534098 // Hs.115181 // ANGPT2 // 285 // angiopoietin 2 /// NM_024596 // upstream // 462977 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein FLJ12847 /// NM_033225 // upstream // 973872 // Hs.415199 // CSMD1 // 64478 //	ANGPT2	ANGPT2 , rs2840500, angiopoietin 2 ,p23.2
SNP_A-1742559	tctaagatgtgttaaggtttagta[C/G]gcatctgatggacttgtaa gggaga	C	G	NM_001147 // downstream // 533682 // Hs.115181 // ANGPT2 // 285 // angiopoietin 2 /// NM_024596 // upstream // 462561 // Hs.212991 // FLJ12847 // 79648 // hypothetical protein FLJ12847 /// NM_033225 // upstream // 974288 // Hs.415199 // CSMD1 // 64478 //	ANGPT2	ANGPT2 , rs2816430, angiopoietin 2 ,p23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308680	gctttctaaactgtaa[G/T]atctgcgtcctgcttt	G	T	NM_033225 // upstream // 2559917 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 462027 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1817077	gttcaaaagctgaaaa[A/G]ccttgagtctgatgtc	A	G	NM_033225 // upstream // 2672596 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 349348 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1992108	aacttccggtatgta[C/T]gtagttcactcacatt	C	T	NM_033225 // upstream // 2749014 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 272930 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1899988	tggaccaaacgaaatc[C/T]agccttctaggttttt	C	T	NM_033225 // upstream // 2751651 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 270293 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-2080790	acctcctctaacataa[C/T]tcattcttgtcctgca	C	T	NM_033225 // upstream // 2812615 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 209329 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1992111	aatacataaatcagaa[A/G]tggtatgctgatgaaa	A	G	NM_033225 // upstream // 2900848 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 121096 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.2
SNP_A-1992117	gtaactggaacagata[C/T]gtttaagcagcgtta	C	T	NM_033225 // upstream // 3005010 // Hs.209909 // CSMD1 // 64478 // Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), mRNA. /// NM_024596 // upstream // 16934 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (	CSMD1	CSMD1, Homo sapiens CUB and Sushi multiple domains 1 (CSMD1), p23.1
SNP_A-1872272	tctagaactttccctа[A/G]atcttacaacagtagt	A	G	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // — // — // —	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2260245	gaaaatggtgatcaaa[C/G]tttattctaatcaag	C	G	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // — // — // —	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2221590	ccttgcaagaaagag[A/C]aatacctgaggcaccg	A	C	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // — // — // —	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2197566	cattctacatatacac[C/T]ctagtaacaacaagca	C	T	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// NM_001147 // intron // 0 // Hs.490892 // ANGPT2 // 285 // Homo sapiens angiopoietin 2 (ANGPT2), mRNA. /// ENST00000034468	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2204171	ccagcagcttagcaaa[C/G]ttgagggcaaacacac	C	G	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// NM_001147 // 5UTR // 0 // Hs.490892 // ANGPT2 // 285 // Homo sapiens angiopoietin 2 (ANGPT2), mRNA. /// ENST00000344683	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-1924146	ttagttgattcttgaa[C/G]cactagccaagttaca	C	G	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2212582	cccttcaagttaccgt[A/T]aagacagaagaaaagg	A	T	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-1814777	gtgtgtctgctttta[C/T]gttaatggttatgaat	C	T	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-1785608	ggctccagctcaagagg[A/G]actgaaggccgctaag	A	G	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-1886957	tgacttccgcttcaca[A/G]attttgcgtcccgta	A	G	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2155306	attcataagacagaga[C/T]acaaagagatacaaag	C	T	NM_024596 // intron // 0 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// ENST00000344683 // intron // 0 // --- // --- // ---	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2073815	acagtgccaagaggga[C/T]ggtgatacctattcat	C	T	NM_024596 // downstream // 8880 // Hs.546433 // MCPH1 // 79648 // Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), mRNA. /// NM_001147 // upstream // 141330 // Hs.490892 // ANGPT2 // 285 // Homo sapiens angiopoietin 2 (ANGPT2), mRNA. ///	MCPH1	MCPH1, Homo sapiens microcephaly, primary autosomal recessive 1 (MCPH1), p23.1
SNP_A-2179938	cacttgaatatcaacc[C/T]acggaattacaaggag	C	T	NM_018361 // intron // 0 // Hs.490899 // AGPAT5 // 55326 // Homo sapiens acid acyltransferase-epsilon (LPAAT-e), mRNA. /// ENST00000285518 // intron // 0 // --- // --- // ---	AGPAT5	AGPAT5, Homo sapiens acid acyltransferase-epsilon (LPAAT-e), p23.1
SNP_A-1992152	gaaaccagaaaagcca[A/C]aaggaggctctacca	A	C	NM_018361 // downstream // 42572 // Hs.490899 // AGPAT5 // 55326 // Homo sapiens acid acyltransferase-epsilon (LPAAT-e), mRNA. /// NM_207411 // downstream // 8965 // Hs.369771 // XRG5a // 389610 // Homo sapiens HARL2754 (UNQ2754), mRNA. /// ENST00000028551	AGPAT5	AGPAT5, Homo sapiens acid acyltransferase-epsilon (LPAAT-e), p23.1
SNP_A-2291482	gcaattgtgctccaga[C/G]gtgaaagaggcagctg	C	G	NM_207411 // intron // 0 // Hs.369771 // XRG5a // 389610 // Homo sapiens HARL2754 (UNQ2754), mRNA. /// ENST00000334706 // intron // 0 // --- // --- // ---	XRG5a	XRG5a, Homo sapiens HARL2754 (UNQ2754), p23.1
SNP_A-2308640	gctttccaggccatta[C/T]accagtttccattta	C	T	NM_005218 // upstream // 1592 // Hs.32949 // DEFB1 // 1672 // Homo sapiens defensin, beta 1 (DEFB1), mRNA. /// NM_001926 // downstream // 45100 // Hs.711 // DEFA6 // 1671 // Homo sapiens defensin, alpha 6, Paneth cell-specific (DEFA6), mRNA. /// ENST00000	DEFB1	DEFB1, Homo sapiens defensin, beta 1 (DEFB1), p23.1
SNP_A-1992163	ttctgttccacaagct[A/C]agaggaagcagaattt	A	C	NM_001925 // upstream // 21026 // Hs.2582 // DEFA4 // 1669 // Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /// ENST00000297435 // upstream // 21026 // --- // --- // --- /// ENST00000329229 // downstream // 28801 // --- // --- // ---	DEFA4	DEFA4, Homo sapiens defensin, alpha 4, corticostatin (DEFA4), p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1653808	ctgctgctgctgatgtggccac[C/T]gtgattaacgcaatcagc ccagcag	C	T	NM_001925 // upstream // 21238 // Hs.2582 // DEFA4 // 1669 // defensin, alpha 4, corticostatin /// NM_004084 // downstream // 18147 // Hs.511887 // DEFA1 // 1667 // defensin, alpha 1, myeloid-related sequence	DEFA4	DEFA4 , rs2738078, defensin, alpha 4, corticostatin p23.1
SNP_A-1707774	aagacctactaggcatttaagaa[C/T]ccactcatgtgatcgaa cgataaag	C	T	NM_001925 // upstream // 27509 // Hs.2582 // DEFA4 // 1669 // defensin, alpha 4, corticostatin /// NM_004084 // downstream // 11876 // Hs.511887 // DEFA1 // 1667 // defensin, alpha 1, myeloid-related sequence	DEFA4	DEFA4 , rs2978951, defensin, alpha 4, corticostatin p23.1
SNP_A-1713093	cccatgtgcctagtccatgtgacag[C/T]attgctttaaaaatcaat aaaaatc	C	T	NM_001925 // upstream // 28105 // Hs.2582 // DEFA4 // 1669 // defensin, alpha 4, corticostatin /// NM_004084 // downstream // 11280 // Hs.511887 // DEFA1 // 1667 // defensin, alpha 1, myeloid-related sequence	DEFA4	DEFA4 , rs2702910, defensin, alpha 4, corticostatin p23.1
SNP_A-2195497	catgggtagtagtc[C/T]cttgtaggagccagtg	C	T	NM_001925 // upstream // 31379 // Hs.2582 // DEFA4 // 1669 // Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /// ENST00000297435 // upstream // 31379 // — // — // — /// ENST00000329229 // downstream // 18448 // — // — // —	DEFA4	DEFA4, Homo sapiens defensin, alpha 4, corticostatin (DEFA4), p23.1
SNP_A-2280551	gaggtagatgtgataa[G/T]gtttctggaaatgaga	G	T	NM_001925 // upstream // 33299 // Hs.2582 // DEFA4 // 1669 // Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA. /// ENST00000297435 // upstream // 33299 // — // — // — /// ENST00000329229 // downstream // 16528 // — // — // —	DEFA4	DEFA4, Homo sapiens defensin, alpha 4, corticostatin (DEFA4), p23.1
SNP_A-2183882	cagccacaaagcagtc[C/T]atatatcaagtttctg	C	T	NM_005217 // upstream // 28693 // Hs.294176 // DEFA3 // 1668 // Homo sapiens defensin, alpha 3, neutrophil-specific (DEFA3), mRNA. /// NM_004084 // upstream // 28693 // Hs.380781 // DEFA1 // 1667 // Homo sapiens defensin, alpha 1, myeloid-related sequence	DEFA3	DEFA3, Homo sapiens defensin, alpha 3, neutrophil-specific (DEFA3), p23.1
SNP_A-2119057	agtagaggagctttg[C/T]aataacagatgtgga	C	T	ENST00000310542 // downstream // 21050 // — // — // — /// ENST00000330777 // downstream // 55550 // — // — // —	-	p23.1
SNP_A-2148466	atgggtcactgatagc[A/G]acaccgttggtccggc	A	G	ENST00000330777 // CDS // 0 // — // — // —	-	p23.1
SNP_A-2013156	ctgctggaacgatcaa[C/T]gtaattagctggacta	C	T	NM_194284 // upstream // 258497 // Hs.183617 // CLDN23 // 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// ENST00000330777 // upstream // 62223 // — // — // — /// ENST00000324612 // upstream // 258497 // — // — // —	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-2038468	aacacttatcaagtat[A/T]aaataaccaacctat	A	T	NM_194284 // upstream // 99798 // Hs.183617 // CLDN23 // 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// ENST00000330777 // upstream // 220922 // — // — // — /// ENST00000324612 // upstream // 99798 // — // — // —	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-2060944	aatgatgcttctgaag[A/T]ctgttctaataatata	A	T	NM_194284 // downstream // 58594 // Hs.183617 // CLDN23 // 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// NM_004225 // downstream // 24151 // Hs.379414 // MFHAS1 // 9258 // Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1).	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-1802481	gtatccctcatccaac[A/G]gcttaagaacttgaac	A	G	NM_194284 // downstream // 59354 // Hs.183617 // CLDN23 // 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// NM_004225 // downstream // 23391 // Hs.379414 // MFHAS1 // 9258 // Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1).	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-1992185	tcaaaaccacttccg[A/G]aattgtcaaagcactg	A	G	NM_194284 // downstream // 80338 // Hs.183617 // CLDN23 // 137075 // Homo sapiens claudin 23 (CLDN23), mRNA. /// NM_004225 // downstream // 2407 // Hs.379414 // MFHAS1 // 9258 // Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), m	CLDN23	CLDN23, Homo sapiens claudin 23 (CLDN23), p23.1
SNP_A-1813585	gtgtaagaatgggcta[A/C]acacaattcgaccaa	A	C	NM_004225 // intron // 0 // Hs.379414 // MFHAS1 // 9258 // Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), mRNA. /// ENST00000276282 // intron // 0 // — // — // — // —	MFHAS1	MFHAS1, Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1914493	tgtgttttccctta[C/G]agtacgaacagaaat	C	G	NM_004225 // intron // 0 // Hs.379414 // MFHAS1 // 9258 // Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), mRNA. /// ENST00000276282 // intron // 0 // — // — // —	MFHAS1	MFHAS1, Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), p23.1
SNP_A-2173321	cacaagagaaagttcc[C/G]agcacagagaactgca	C	G	NM_024607 // upstream // 109613 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 295630 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-int	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-1847018	tatcaggctctgaatc[A/C]aacagtcttcagccag	A	C	NM_024607 // upstream // 146188 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 259055 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-int	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2182290	cagagtctcattctaa[A/G]tgcaagcaagacagag	A	G	NM_024607 // upstream // 268849 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 136394 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-int	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2139160	atcctccagtgcaga[C/G]atctctttggaaaaa	C	G	NM_024607 // upstream // 297793 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 107450 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-int	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-1841206	taggaaaacttccaag[C/T]actgcgtcaaaacata	C	T	NM_024607 // upstream // 362353 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 42890 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-inte	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-1992219	gatcactacaaggca[A/G]tcaactacaatcttct	A	G	NM_024607 // upstream // 391483 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 13760 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-inte	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2013166	tgaattaacaggtaaa[C/G]aaggagttagtatac	C	G	NM_024607 // upstream // 394456 // Hs.458513 // PPP1R3B // 79660 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA. /// NM_003747 // upstream // 10787 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-inte	PPP1R3B	PPP1R3B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), p23.1
SNP_A-2198434	catttacttattggct[G/T]aatcctacaacataca	G	T	NM_003747 // intron // 0 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// ENST00000310430 // intron // 0 // — // — // — // —	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2189874	cataaaggtctttgaa[G/T]ccacacatttcaggcc	G	T	NM_003747 // downstream // 40368 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// NM_012331 // upstream // 231607 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfo	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-1961531	ttttttgagatctga[A/T]aaaaagacttaaaagg	A	T	NM_003747 // downstream // 183720 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// NM_012331 // upstream // 88255 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfo	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1879792	tcttccacagcttaq[C/G]aaaatcacatttaaag	C	G	NM_003747 // downstream // 253921 // Hs.370267 // TNKS // 8658 // Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA. /// NM_012331 // upstream // 18054 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfo	TNKS	TNKS, Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), p23.1
SNP_A-2186795	caggggctcacaataa[C/G]tcctgagcctgaagat	C	G	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1893389	tgcagccagatgaaaa[C/T]gtatgtgatagggagtg	C	T	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1935863	ttctgtttccaaatac[A/G]agatgctgtaagcctg	A	G	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1945368	ttgttagttctggaaaa[C/T]ttagtcaatttgcatc	C	T	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2077413	accacagcaaccatgt[A/G]aacgggctgcgccaa	A	G	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2143572	atgactggatagccaa[G/T]agcgctgtaatgctta	G	T	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-2303148	gctatcaaaaagaccc[G/T]gaaatgtatttgcttg	G	T	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1992228	tagggtgccagtgtca[A/G]aaaccagacacggatg	A	G	NM_012331 // intron // 0 // Hs.490981 // MSRA // 4482 // Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA. /// ENST00000317173 // intron // 0 // --- // --- // ---	MSRA	MSRA, Homo sapiens methionine sulfoxide reductase A (MSRA), p23.1
SNP_A-1755102	ggaggtaaaagagttaagagataga[C/T]gcaaatgctgatgtga cttcatcgat	C	T	NM_012331 // intron // 0 // Hs.26458 // MSRA // 4482 // methionine sulfoxide reductase A	MSRA	MSRA, rs10503403, methionine sulfoxide reductase A,p23.1
SNP_A-2013184	cagggtcttaagccca[C/T]ataaaagtcagagaat	C	T	ENST00000329335 // intron // 0 // --- // --- // ---	-	p23.1
SNP_A-1821455	gtttggctgctatgcc[C/T]aatgcagccacgaata	C	T	ENST00000297303 // upstream // 34460 // --- // --- // --- /// ENST00000355043 // downstream // 11828 // --- // --- // ---	-	p23.1
SNP_A-2187022	caggtactggtgtaatg[G/T]agtgtggaaaatcaag	G	T	NM_053279 // intron // 0 // Hs.124299 // C8orf13 // 83648 // Homo sapiens chromosome 8 open reading frame 13 (C8orf13), mRNA. /// ENST00000284486 // intron // 0 // --- // --- // --- /// ENST00000284481 // intron // 0 // --- // --- // ---	C8orf13	C8orf13, Homo sapiens chromosome 8 open reading frame 13 (C8orf13), p23.1
SNP_A-2086162	actctgaggcccaaag[C/T]acaccagacacagact	C	T	NM_053279 // intron // 0 // Hs.124299 // C8orf13 // 83648 // Homo sapiens chromosome 8 open reading frame 13 (C8orf13), mRNA. /// ENST00000284486 // intron // 0 // --- // --- // ---	C8orf13	C8orf13, Homo sapiens chromosome 8 open reading frame 13 (C8orf13), p23.1
SNP_A-2287071	gatgtaccagtcaaca[C/G]aggccatgggagagca	C	G	NM_212553 // upstream // 257834 // Hs.528621 // --- // 0 // Homo sapiens deubiquitinating enzyme DUB4 (DUB4), mRNA. /// NM_201402 // upstream // 257834 // Hs.531448 // DUB3 // 377630 // Homo sapiens deubiquitinating enzyme 3 (DUB3), mRNA. /// NM_032916 //	-	-, Homo sapiens deubiquitinating enzyme DUB4 (DUB4), p23.1
SNP_A-1875974	tctgaagaatctagaa[A/G]tactaagtgtgtgacc	A	G	NM_152271 // upstream // 21518 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 191710 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864222	tccaccctgatagatg[C/G]agcttgtggtaaagtc	C	G	NM_152271 // upstream // 27399 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 185829 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1
SNP_A-1919602	ttaaggccgagtgtta[C/T]gtgctgccttgacatc	C	T	NM_152271 // upstream // 32241 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 180987 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p23.1
SNP_A-1931521	ttccccattggcagac[A/G]gctatttccactcaaa	A	G	NM_152271 // upstream // 83414 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 129814 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-2231168	ctattactaagtaaaa[G/T]caaccaatctgtaaag	G	T	NM_152271 // upstream // 91861 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 121367 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-1922449	ttagaaccataagatg[A/G]atttaatgtaggtct	A	G	NM_152271 // upstream // 99553 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 113675 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-2200136	ccaaatgaaataaaaa[C/T]gtgtgaatgaatccac	C	T	NM_152271 // upstream // 112263 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 100965 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ3698	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-2297560	gccagagcactgacca[A/T]atcaaagactcccatt	A	T	NM_152271 // upstream // 138262 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 74966 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-2013205	atttgcaacaataca[A/G]atgttattaactatg	A	G	NM_152271 // upstream // 201725 // Hs.180178 // FLJ23749 // 91694 // Homo sapiens hypothetical protein FLJ23749 (FLJ23749), mRNA. /// NM_182598 // upstream // 11503 // Hs.202521 // FLJ36980 // 286032 // Homo sapiens hypothetical protein FLJ36980 (FLJ36980	FLJ23749	FLJ23749, Homo sapiens hypothetical protein FLJ23749 (FLJ23749), p22
SNP_A-2305411	gctgatctttgcatta[C/T]ctagacagagaaacaa	C	T	NM_020844 // intron // 0 // Hs.527095 // KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// ENST00000303854 // intron // 0 // — // — // — // —	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-1716461	attctaaaagggctgccgctgcgtg[C/T]caaggatttcctcctcct cattctct	C	T	NM_006094 // downstream // 13665 // Hs.8700 // DLC1 // 10395 // deleted in liver cancer 1 /// NM_024767 // downstream // 144871 // Hs.8700 // DLC1 // 10395 // deleted in liver cancer 1 /// NM_182598 // downstream // 62028 // Hs.185202 // FLJ36980 // 2860	DLC1	DLC1 , rs537330, deleted in liver cancer 1 ,p22
SNP_A-1725518	gccttacataattcccacaaaagat[C/T]ataagtgcccaaaccg agagagtgc	C	T	NM_006094 // downstream // 13578 // Hs.8700 // DLC1 // 10395 // deleted in liver cancer 1 /// NM_024767 // downstream // 144784 // Hs.8700 // DLC1 // 10395 // deleted in liver cancer 1 /// NM_182598 // downstream // 62115 // Hs.185202 // FLJ36980 // 2860	DLC1	DLC1 , rs2584561, deleted in liver cancer 1 ,p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1992291	aagataaagtcgacca[C/T]tcgtaatatttttttc	C	T	NM_020844 // downstream // 17055 // Hs.527095 // KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 40143 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2111409	aggaggacttatacca[A/C]gaagtttaaagagagg	A	C	NM_020844 // downstream // 17799 // Hs.527095 // KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 39399 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-1944723	ttgtgatgagatccca[C/G]agctgctatgcgggga	C	G	NM_020844 // downstream // 24297 // Hs.527095 // KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 32901 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2297842	gccaggtatcacttct[G/T]aaatgtttgacttgag	G	T	NM_020844 // downstream // 33841 // Hs.527095 // KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 23357 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-1992292	aaaacaagcaaactta[C/G]gttcctgataattacg	C	G	NM_020844 // downstream // 43080 // Hs.527095 // KIAA1456 // 57604 // Homo sapiens KIAA1456 protein (KIAA1456), mRNA. /// NM_006094 // downstream // 14118 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2	KIAA1456	KIAA1456, Homo sapiens KIAA1456 protein (KIAA1456), p22
SNP_A-2263189	gaacagaggtacatat[A/G]aaccagtcaccctcaa	A	G	NM_182643 // intron // 0 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// ENST00000276297 // intron // 0 // --- // --- // --- // ---	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-2152877	attacaaggaactagg[A/C]aaaagaaattgacatt	A	C	NM_182643 // intron // 0 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// ENST00000276297 // intron // 0 // --- // --- // --- // ---	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-1992304	gattatcatggcactc[A/G]atgactaccaaaaagt	A	G	NM_182643 // intron // 0 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, mRNA. /// NM_024767 // intron // 0 // Hs.134296 // DLC1 // 10395 // Homo sapiens deleted in liver cancer 1 (DLC1), transcript va	DLC1	DLC1, Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 1, p22
SNP_A-1750343	agaaaacagaatagaaagatggaga[C/T]aattgtgaggtaaaaacattttaca	C	T	NM_006094 // upstream // 430921 // Hs.8700 // DLC1 // 10395 // deleted in liver cancer 1 /// NM_024767 // upstream // 49335 // Hs.8700 // DLC1 // 10395 // deleted in liver cancer 1 /// NM_152567 // upstream // 2622 // - // - // - // - /// NM_182643 // up	DLC1	DLC1 , rs10503457, deleted in liver cancer 1 ,p22
SNP_A-1992323	aaatttgtttgcaaaa[A/G]tcagcacagaagagtt	A	G	NM_139167 // downstream // 521159 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 997 // --- // --- // --- // --- /// ENST00000329135 // downstream // 521159 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1992324	ggtcttaacgcaaaga[A/G]taatactgaagtacaa	A	G	NM_139167 // downstream // 521120 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 1036 // --- // --- // --- // --- /// ENST00000329135 // downstream // 521120 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2094003	agaagctcaacttta[C/G]aacttttcaggatctg	C	G	NM_139167 // downstream // 513920 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 8236 // --- // --- // --- // --- /// ENST00000329135 // downstream // 513920 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2177974	cactacaagtggcgga[C/G]caaaattagtaatcag	C	G	NM_139167 // downstream // 492422 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 29734 // --- // --- // --- // --- /// ENST00000329135 // downstream // 492422 // --- // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2071178	acactgtcacctaata[C/T]ccatggcttgacggga	C	T	NM_139167 // downstream // 411022 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 111134 // --- // --- // --- /// ENST00000329135 // downstream // 411022 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2206738	ccatgatttaaggtaa[G/T]gcaattatactcatat	G	T	NM_139167 // downstream // 407573 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 114583 // --- // --- // --- /// ENST00000329135 // downstream // 407573 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1905156	tgggtgtaatgcctaq[G/T]acacaaagcaaaaaca	G	T	NM_139167 // downstream // 332817 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 189339 // --- // --- // --- /// ENST00000329135 // downstream // 332817 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1896956	tgctcatcatcgttaa[C/T]caggttgaaaacatat	C	T	NM_139167 // downstream // 294172 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 227984 // --- // --- // --- /// ENST00000329135 // downstream // 294172 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2298680	gcccagccataggttc[A/C]cgtaactattctgagc	A	C	NM_139167 // downstream // 201271 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 320885 // --- // --- // --- /// ENST00000329135 // downstream // 201271 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2177792	cacgtggccactccaa[A/T]ggtatctggtatgagg	A	T	NM_139167 // downstream // 125745 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 396411 // --- // --- // --- /// ENST00000329135 // downstream // 125745 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1643886	ctctcctcacagaatctaagacctat[G/T]gcaaccatgccatttac ataaaatt	G	T	NM_139167 // downstream // 83311 // Hs.348641 // SGCZ // 137868 // sarcoglycan zeta /// NM_152567 // downstream // 438267 // - // - // - // -	SGCZ	SGCZ, rs10503473, sarcoglycan zeta ,p22
SNP_A-1716285	gataaatatagctacctatcttgaaa[A/T]atactgcagaaagtata ggcttgg	A	T	NM_139167 // downstream // 80734 // Hs.348641 // SGCZ // 137868 // sarcoglycan zeta /// NM_152567 // downstream // 440844 // - // - // - // -	SGCZ	SGCZ, rs1546696, sarcoglycan zeta ,p22
SNP_A-1992346	gctccctgagaactta[A/T]gctctatcttcaata	A	T	NM_139167 // downstream // 81824 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 440332 // --- // --- // --- /// ENST00000329135 // downstream // 81824 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2304087	gctccatcctttgtatc[A/G]cttgagtcaccacaat	A	G	NM_139167 // downstream // 80960 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 441196 // --- // --- // --- /// ENST00000329135 // downstream // 80960 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2181088	cagacactgtatcaca[C/G]ctagacctctctctt	C	G	NM_139167 // downstream // 29936 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000297324 // downstream // 492220 // --- // --- // --- /// ENST00000329135 // downstream // 29936 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1654369	tagagtgtatttatcacaaattata[A/T]gtattacacatttttcga aatgg	A	T	NM_139167 // intron // 0 // Hs.348641 // SGCZ // 137868 // sarcoglycan zeta	SGCZ	SGCZ, rs20351 41, sarcoglycan zeta,p22
SNP_A-2087818	actggacagtaacttta[A/T]agccgtatgaagagat	A	T	NM_139167 // intron // 0 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2257346	ctttgaaaaaatgtaa[C/G]tgaaaatgtgtgtga	C	G	NM_139167 // intron // 0 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1833551	tacagcagttttcaa[A/T]gttaatcattcatga	A	T	NM_139167 // intron // 0 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1814261	gtgtcttacacactc[A/G]acctttaacctctggta	A	G	NM_139167 // intron // 0 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // --- // --- // ---	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903365	tgggaaatttagatca[C/T]gagacagtacagcaca	C	T	NM_139167 // intron // 0 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// ENST00000329135 // intron // 0 // — // — // —	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1992375	aaatcgagaaacagca[C/T]gaatatgaaggagtt	C	T	NM_139167 // upstream // 16852 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 968443 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2048785	aagccatttcaaagt[C/G]aagttcagggtacctc	C	G	NM_139167 // upstream // 93113 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 892182 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2271858	gacccaaacatagtgc[A/C]aaggagattaaaaaaa	A	C	NM_139167 // upstream // 98252 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 887043 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1846960	tatcagaaggaaatga[C/T]gaggagaatcaaggaa	C	T	NM_139167 // upstream // 167796 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 817499 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1992392	tcactgatgtgcttac[A/G]aactatattcctgatt	A	G	NM_139167 // upstream // 196267 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 789028 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2256375	cttatcaagttagta[C/G]agtataaagtgctgaa	C	G	NM_139167 // upstream // 243670 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 741625 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2087580	actgctaccttgataaa[C/T]gacatagtagtttgaa	C	T	NM_139167 // upstream // 260733 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 724562 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2189505	cagtttaaggcactta[A/G]gaatcatttacattaa	A	G	NM_139167 // upstream // 274682 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 710633 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1728263	ctttggtaaaatgagttttgaccc[A/T]cctcttacagactcacaat atgtac	A	T	NM_006765 // upstream // 513032 // Hs.426324 // TUSC3 // 7991 // tumor suppressor candidate 3 /// NM_139167 // upstream // 472263 // Hs.348641 // SGCZ // 137868 // sarcoglycan zeta /// NM_178234 // upstream // 513032 // Hs.426324 // TUSC3 // 7991 // tumo	TUSC3	TUSC3 , rs4348492, tumor suppressor candidate 3 p22
SNP_A-1827606	taactgcgttgttgta[A/C]agacttgacccggt	A	C	NM_139167 // upstream // 448974 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 536321 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2055516	aataatagcattaaac[A/T]gagaaagcatgaatct	A	T	NM_139167 // upstream // 458991 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 526304 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1819395	gttggctcttggtgc[C/T]aatttcattactaig	C	T	NM_139167 // upstream // 509977 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 475318 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2283097	gataagtgatgccata[C/G]atataatagcagtaag	C	G	NM_139167 // upstream // 510460 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 474835 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1826481	taacaacatctcgaaac[A/G]ctgatttcattcccca	A	G	NM_139167 // upstream // 532522 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 452773 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2224559	cgtcaaatcgtcataa[A/C]tcaattaaccttgagg	A	C	NM_139167 // upstream // 538808 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 446487 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1992402	tctgtaggtttcattg[C/G]actatttcataccgta	C	G	NM_139167 // upstream // 561435 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 423860 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-2214101	cctaatataccacaaaa[C/T]ggacaggatggagat	C	T	NM_139167 // upstream // 563789 // Hs.195298 // SGCZ // 137868 // Homo sapiens sarcoglycan zeta (SGCZ), mRNA. /// NM_178234 // upstream // 421506 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRN	SGCZ	SGCZ, Homo sapiens sarcoglycan zeta (SGCZ), p22
SNP_A-1752559	tcatttggtaaataccaaggagca[C/T]aactgttgaatcacatg gtaagaat	C	T	NM_006765 // upstream // 70586 // Hs.426324 // TUSC3 // 7991 // tumor suppressor candidate 3 /// NM_139167 // upstream // 914709 // Hs.348641 // SGCZ // 137868 // sarcoglycan zeta /// NM_178234 // upstream // 70586 // Hs.426324 // TUSC3 // 7991 // tumor	TUSC3	TUSC3 , rs1587099, tumor suppressor candidate 3 p22
SNP_A-1992412	aaatagacggttaaag[C/G]aggatgccttgagcca	C	G	NM_178234 // intron // 0 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA. /// NM_006765 // intron // 0 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), trans	TUSC3	TUSC3, Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, p22
SNP_A-1959358	ttttgcacacagaga[A/C]gtttgcaaaatcacaa	A	C	NM_178234 // downstream // 82901 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, mRNA. /// NM_178234 // downstream // 89576 // Hs.426324 // TUSC3 // 7991 // Homo sapiens tumor suppressor candidate	TUSC3	TUSC3, Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 2, p22
SNP_A-1992430	gtcttttgaaaatgaa[A/C]taaaagaggtctatgg	A	C	NM_138716 // downstream // 43990 // Hs.446291 // MSR1 // 4481 // Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, mRNA. /// NM_138715 // downstream // 43990 // Hs.446291 // MSR1 // 4481 // Homo sapiens macrophage scavenger	MSR1	MSR1, Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AIII, p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1691980	tgatgggaataggtgatgggagaa[A/C]aaaagtatcatatatt aaatagcag	A	C	NM_138715 // intron // 0 // Hs.436887 // MSR1 // 4481 // macrophage scavenger receptor 1 /// NM_138716 // intron // 0 // Hs.436887 // MSR1 // 4481 // macrophage scavenger receptor 1	MSR1	MSR1 , rs10503574, macrophage scavenger receptor 1 ,p22
SNP_A-1935160	ttctgcagagaccaaa[C/T]agaagtaaggtattaa	C	T	NM_181723 // intron // 0 // Hs.403594 // EFHA2 // 286097 // Homo sapiens EF hand domain family A2 (EFHA2), mRNA. /// ENST00000318063 // intron // 0 // — // — // —	EFHA2	EFHA2, Homo sapiens EF hand domain family A2 (EFHA2), p22
SNP_A-1906490	tggtggccttcattac[C/T]gggtagtgtgttcctt	C	T	NM_016353 // intron // 0 // Hs.443852 // ZDHHC2 // 51201 // Homo sapiens zinc finger, DHHC domain containing 2 (ZDHHC2), mRNA. /// ENST00000262096 // intron // 0 // — // — // —	ZDHHC2	ZDHHC2, Homo sapiens zinc finger, DHHC domain containing 2 (ZDHHC2), p22
SNP_A-1644472	cacatggaaatgttcgagttcgtatt[C/T]aacatgggattgttgttttct aagc	C	T	NM_003046 // upstream // 167160 // Hs.432978 // SLC7A2 // 6542 // solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	SLC7A2	SLC7A2 , rs2898465, solute carrier family 7 (cationic amino acid transporter, y+ system), member 2,p22
SNP_A-2312831	ggactgcgcaccctgg[G/T]aatttacgcaacaga	G	T	AF073482 // intron // 0 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// ENST00000180173 // intron // 0 // — // — // —	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2013243	agacgtttctttaact[C/T]accgatttcaatctt	C	T	AF073482 // upstream // 15844 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 173891 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid t	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2218576	cctggatttggcatca[A/G]cacttagttaagtagg	A	G	AF073482 // upstream // 34150 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 155585 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid t	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-1992485	aaacatcttttttag[C/G]aaccattatacagaca	C	G	AF073482 // upstream // 34943 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 154792 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid t	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2302096	gcgttggctgctggca[C/T]aatgtttgtaatttct	C	T	AF073482 // upstream // 39046 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 150689 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid t	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2085934	actctaaccattacca[A/C]aatcatattctcatgg	A	C	AF073482 // upstream // 40257 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 149478 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid t	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2090870	actttcatcctcttta[G/T]gtaagtgaccctgaag	G	T	AF073482 // upstream // 170684 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 19051 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid t	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-1849993	tatgctacacttgca[C/T]gaactctctggagaa	C	T	AF073482 // upstream // 189237 // Hs.343873 // MTMR7 // 9108 // Homo sapiens myotubularin related protein 7 mRNA, partial cds. /// NM_003046 // upstream // 498 // Hs.448520 // SLC7A2 // 6542 // Homo sapiens solute carrier family 7 (cationic amino acid tra	MTMR7	MTMR7, Homo sapiens myotubularin related protein 7 partial cds. p22
SNP_A-2110859	aggactgatgtctta[C/T]gaggagacacacac	C	T	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1812648	gtggctggtttaaaa[G/T]cttaggatcagccggg	G	T	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-2094572	agaatacagttgatga[A/C]gcctctgaaaaac	A	C	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-2279852	gaggccttatccgg[C/T]attgaaggatctaatt	C	T	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-2022113	aaaaagcagtttcga[A/G]aattagatccttcaat	A	G	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-2162720	atttgaaatgttaaa[A/G]tgaaggctgaactggc	A	G	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-1861446	tcatcattactttttca[C/T]ggtaagaacagctatt	C	T	NM_006207 // intron // 0 // Hs.458573 // PDGFRL // 5157 // Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), mRNA. /// ENST00000251630 // intron // 0 // — // — // —	PDGFRL	PDGFRL, Homo sapiens platelet-derived growth factor receptor-like (PDGFRL), p22
SNP_A-2035664	aaatgtcattccaccca[C/G]agaggcatagaagaaa	C	G	NM_020749 // 5UTR // 0 // Hs.7946 // MTUS1 // 57509 // Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 5, mRNA. /// NM_001001925 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Homo sap	MTUS1	MTUS1, Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 5, p22
SNP_A-2085817	actcctatattcaca[A/C]tgataacatgagcatt	A	C	NM_001001925 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001001924 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Hom	MTUS1	MTUS1, Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, p22
SNP_A-2162248	atttagctgatacag[A/G]agacattgcctccaca	A	G	NM_001001925 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001001924 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Hom	MTUS1	MTUS1, Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, p22
SNP_A-1992498	gaaattgttttctga[C/T]agttggtaggttctat	C	T	NM_001001925 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_001001924 // intron // 0 // Hs.7946 // MTUS1 // 57509 // Hom	MTUS1	MTUS1, Homo sapiens mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 2, p22
SNP_A-1757769	acatgtattatcttccacgatcag[C/T]ttcaagaaccttcatgatt ctgtca	C	T	NM_004315 // intron // 0 // Hs.324808 // ASAH1 // 427 // N-acylsphingosine amidohydrolase (acid ceramidase) 1 /// NM_177924 // intron // 0 // Hs.324808 // ASAH1 // 427 // N-acylsphingosine amidohydrolase (acid ceramidase) 1	ASAH1	ASAH1 , rs966118, N-acylsphingosine amidohydrolase (acid ceramidase) 1 , p22
SNP_A-2151828	atgttcctacgtgta[C/T]aagaattcacatgagc	C	T	NM_177924 // intron // 0 // Hs.527412 // ASAH1 // 427 // Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA. /// NM_004315 // intron // 0 // Hs.527412 // ASAH1 // 427 // Homo sapiens N-acylsphingosine ami	ASAH1	ASAH1, Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1940142	ttgcataagctaaata[C/T]cagatgtctatccat	C	T	NM_177924 // upstream // 12884 // Hs.527412 // ASAH1 // 427 // Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA. /// NM_004315 // upstream // 12027 // Hs.527412 // ASAH1 // 427 // Homo sapiens N-acylsph	ASAH1	ASAH1, Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, p22
SNP_A-2221747	cctttagcttcccca[A/G]tcttccigttaacacc	A	G	NM_000662 // intron // 0 // Hs.155956 // NAT1 // 9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// ENST00000307719 // intron // 0 // --- // --- // --- /// ENST00000357526 // intron // 0 // --- // --- // --- /	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-2170381	caagtatccaaacagc[A/G]cctttaaatctagac	A	G	NM_000662 // downstream // 40614 // Hs.155956 // NAT1 // 9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// NM_000015 // upstream // 127325 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-ace	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-1933254	ttctaacataaaatga[C/T]gtgaaatgctaaaata	C	T	NM_000662 // downstream // 132954 // Hs.155956 // NAT1 // 9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// NM_000015 // upstream // 34985 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-ace	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-2297583	gccagataaacataac[C/T]gtcacactaaaggcca	C	T	NM_000662 // downstream // 133027 // Hs.155956 // NAT1 // 9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// NM_000015 // upstream // 34912 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-ace	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-1839774	tagatgttctcaaaag[C/T]ctctctggtgtggctg	C	T	NM_000662 // downstream // 162652 // Hs.155956 // NAT1 // 9 // Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /// NM_000015 // upstream // 5287 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-acet	NAT1	NAT1, Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), p22
SNP_A-2277657	gagcagacataattca[A/G]tatataacaagctgta	A	G	NM_000015 // downstream // 3864 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA. /// ENST00000286479 // downstream // 3864 // --- // --- // --- /// ENST00000327208 // downstream // 123450 //	NAT2	NAT2, Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), p22
SNP_A-1918238	ttaaagagagaattaa[C/G]gtaaaatgtgtgggtg	C	G	NM_000015 // downstream // 14618 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA. /// ENST00000286479 // downstream // 14618 // --- // --- // --- /// ENST00000327208 // downstream // 112696 /	NAT2	NAT2, Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), p22
SNP_A-1684734	ctaaaccttgtagacaagtgagtca[C/T]ctgatatgtatagaagc tgtgatat	C	T	NM_018422 // 3UTR // 0 // - // - // -	-	-, rs9741, -, p22
SNP_A-1909275	tgtatgggtgtcatcc[A/G]ggaagaactggcaata	A	G	NM_000015 // downstream // 122553 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA. /// ENST00000286479 // downstream // 122553 // --- // --- // --- /// ENST00000327208 // downstream // 4761 /	NAT2	NAT2, Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), p22
SNP_A-2188648	cagtgccaggctcaga[A/C]aatatttgtaataata	A	C	NM_000015 // downstream // 122826 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA. /// ENST00000286479 // downstream // 122826 // --- // --- // --- /// ENST00000327208 // downstream // 4488 /	NAT2	NAT2, Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), p22
SNP_A-1992532	catttttaggacaataaa[A/C]tagctgcatggtctct	A	C	NM_000015 // downstream // 125792 // Hs.2 // NAT2 // 10 // Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA. /// ENST00000286479 // downstream // 125792 // --- // --- // --- /// ENST00000327208 // downstream // 1522 /	NAT2	NAT2, Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), p22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2216861	cctctgcatctaagag[C/G]aataaaaaggttacac	C	G	NM_206909 // 3UTR // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // 3UTR // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carcinoma-associated an	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2025184	aaaatagcaggattca[G/T]tgaaaggtataaacgt	G	T	NM_206909 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carcinoma-associate	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-1992545	agaagacaggaaagca[A/G]cgccgtgctaggggaa	A	G	NM_206909 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carcinoma-associate	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2290700	gcaagagtcacccaca[A/G]tgagtctggtttaggt	A	G	AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) mRNA, complete cds. /// NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containi	PSD3	PSD3, Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) complete cds. ,p22
SNP_A-2106410	agccggaagtctgaga[C/T]ggtctgttttcaagaa	C	T	AF243495 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) mRNA, complete cds. /// NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containi	PSD3	PSD3, Homo sapiens hepatocellular carcinoma-associated antigen 67 (HCA67) complete cds. ,p22
SNP_A-1992558	cctgacaatgaaaaaa[C/T]ggtttgttcagggatt	C	T	NM_015310 // intron // 0 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 1, mRNA. /// ENST00000356574 // intron // 0 // — // — // — // —	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 1, p22
SNP_A-1797529	ggtttcagttccgcca[A/G]actctccctcagtcct	A	G	NM_206909 // upstream // 283661 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 224725 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carci	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-1787248	gggaacgctaggacca[C/T]gaggggccatcagtga	C	T	NM_206909 // upstream // 288416 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 229480 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carci	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2211836	ccctctgcctggaatg[C/T]acggtccatgtttcac	C	T	NM_206909 // upstream // 291319 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 232383 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carci	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-2173491	cacaatcatgccctaa[C/T]tcgaagacaactcagt	C	T	NM_206909 // upstream // 307422 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 248486 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carci	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p22
SNP_A-1899643	tggaataaacaaagtc[C/G]atcatgccaggcagct	C	G	NM_206909 // upstream // 418398 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 359462 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carci	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2045949	aagacccatctatgtg[A/G]aacatcagcattcctg	A	G	NM_206909 // upstream // 477103 // Hs.434255 // PSD3 // 23362 // Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA. /// AF243495 // upstream // 418167 // Hs.434255 // PSD3 // 23362 // Homo sapiens hepatocellular carci	PSD3	PSD3, Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, p21.3
SNP_A-2123316	agtgtatcctgatgtg[C/T]ataagactgaatactc	C	T	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-2051978	aaggtgtcccggaaag[C/T]agatttaatcctgtct	C	T	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-2086330	actcttaacctgaagc[A/G]caagtgacagaaaacc	A	G	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-1885985	tgacattgtagtgata[A/C]gaaaatgagatgcggg	A	C	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-2287681	gattaatgctaattcc[A/G]ctaatgagcactaatg	A	G	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-2198682	catttcccaaatgcct[C/T]agcggttgtcttaaca	C	T	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-1860485	tcagttacagtcacta[C/T]gacctcattttaaaag	C	T	NM_022071 // intron // 0 // Hs.303208 // SH2D4A // 63898 // Homo sapiens SH2 domain containing 4A (SH2D4A), mRNA. /// ENST00000265807 // intron // 0 // — // — // — // —	SH2D4A	SH2D4A, Homo sapiens SH2 domain containing 4A (SH2D4A), p21.3
SNP_A-1992579	aaaaccatgaaaaaaa[A/G]tcaagacaacttcctg	A	G	NM_018371 // intron // 0 // Hs.387794 // ChGn // 55790 // Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), mRNA. /// ENST00000311540 // intron // 0 // — // — // — // — /// ENST00000332246 // intron // 0 // — // — // -	ChGn	ChGn, Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), p21.3
SNP_A-1992580	ctttgatttctcgatt[C/T]aaaacacaagcaaaca	C	T	NM_018371 // intron // 0 // Hs.387794 // ChGn // 55790 // Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), mRNA. /// ENST00000311540 // intron // 0 // — // — // — // — /// ENST00000332246 // intron // 0 // — // — // -	ChGn	ChGn, Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), p21.3
SNP_A-1787329	gggaagatgatactga[C/T]ccaggcaagacgcatg	C	T	NM_018371 // intron // 0 // Hs.387794 // ChGn // 55790 // Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), mRNA. /// ENST00000311540 // intron // 0 // — // — // — // — /// ENST00000332246 // intron // 0 // — // — // — // -	ChGn	ChGn, Homo sapiens chondroitin beta1,4 N-acetylgalactosaminyltransferase (ChGn), p21.3
SNP_A-2209120	cccaggcctctttgca[A/G]cttggtggtctcaggt	A	G	NM_000237 // downstream // 116258 // Hs.180878 // LPL // 4023 // Homo sapiens lipoprotein lipase (LPL), mRNA. /// NM_003053 // downstream // 61345 // Hs.158322 // SLC18A1 // 6570 // Homo sapiens solute carrier family 18 (vesicular monoamine), member 1 (SL	LPL	LPL, Homo sapiens lipoprotein lipase (LPL), p21.3
SNP_A-1790940	ggggtaacaggtccca[C/T]gaaagtccaaagccca	C	T	NM_003053 // intron // 0 // Hs.158322 // SLC18A1 // 6570 // Homo sapiens solute carrier family 18 (vesicular monoamine), member 1 (SLC18A1), mRNA. /// ENST00000265808 // intron // 0 // — // — // — // — /// ENST00000276373 // intron // 0 // — //	SLC18A1	SLC18A1, Homo sapiens solute carrier family 18 (vesicular monoamine), member 1 (SLC18A1), p21.3
SNP_A-1812477	gtggccacgaacccat[C/T]agagttacagatcctc	C	T	NM_021020 // upstream // 41258 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 1395582 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1824166	taaacaggttttttca[A/G]gaactgcgagactgtt	A	G	NM_021020 // upstream // 71647 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 1365193 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2030596	aaagctagagttagaa[G/T]acgccattgagaccat	G	T	NM_021020 // upstream // 76707 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 1360133 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1992618	gaatgaagtgtttggal[A/G]accatagctcgctttt	A	G	NM_021020 // upstream // 542856 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 893984 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2143981	atgagcgattaagtgc[A/G]atttgaatgtagggaa	A	G	NM_021020 // upstream // 611776 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 825064 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1780496	ggataggggaaagctc[C/T]atgaatgtaagatctg	C	T	NM_021020 // upstream // 713857 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 722983 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1790616	ggggctagcgttgcca[C/T]ctctccctattaaact	C	T	NM_021020 // upstream // 720102 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 716738 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2235585	ctcctactagagctac[A/G]atacttttcggccctt	A	G	NM_021020 // upstream // 720136 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 716704 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1992628	caaagaaaggcaaaga[A/G]tcaagtccttgcaca	A	G	NM_021020 // upstream // 921998 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 514842 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1935012	ttctgaggcattaatc[A/G]atctaccactcctctt	A	G	NM_021020 // upstream // 1304174 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 132666 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GF	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2069245	acaatttcaacagtcc[A/G]ctaactggtttccttg	A	G	NM_021020 // upstream // 1344566 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 92274 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-1927796	ttcaaggaactcagta[A/G]atgtttgtcaagcgaa	A	G	NM_021020 // upstream // 1368638 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 68202 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2040406	aaccagcagcaatgaa[A/T]taaatgagtgaatatg	A	T	NM_021020 // upstream // 1397396 // Hs.521432 // LZTS1 // 11178 // Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA. /// NM_001495 // downstream // 39444 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFR	LZTS1	LZTS1, Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), p21.3
SNP_A-2013280	cctccctcttgctgca[A/G]aatttcccaggggtgt	A	G	NM_001495 // intron // 0 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFRA2), mRNA. /// ENST00000306793 // intron // 0 // — // — // — // —	GFRA2	GFRA2, Homo sapiens GDNF family receptor alpha 2 (GFRA2), p21.3
SNP_A-1868693	tcctctgtgcctggac[A/G]ctttgttgcttcctca	A	G	NM_001495 // upstream // 31489 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFRA2), mRNA. /// NM_201349 // downstream // 88553 // Hs.71215 // DOK2 // 9046 // Homo sapiens docking protein 2, 56kDa (DOK2), transcript variant 2	GFRA2	GFRA2, Homo sapiens GDNF family receptor alpha 2 (GFRA2), p21.3
SNP_A-1880729	tcttggatctggttga[C/G]ctctttggtccgagta	C	G	NM_001495 // upstream // 80042 // Hs.441202 // GFRA2 // 2675 // Homo sapiens GDNF family receptor alpha 2 (GFRA2), mRNA. /// NM_201349 // downstream // 40000 // Hs.71215 // DOK2 // 9046 // Homo sapiens docking protein 2, 56kDa (DOK2), transcript variant 2	GFRA2	GFRA2, Homo sapiens GDNF family receptor alpha 2 (GFRA2), p21.3
SNP_A-1656917	cctggtgactcccactcctggtgta[C/T]aagaggctccatcaatc caattatt	C	T	NM_001495 // upstream // 120185 // Hs.441202 // GFRA2 // 2675 // GDNF family receptor alpha 2 /// NM_003974 // downstream // 721 // Hs.71215 // DOK2 // 9046 // docking protein 2, 56kDa	GFRA2	GFRA2 , -, GDNF family receptor alpha 2 ,p21.3
SNP_A-1992653	tgtggaacatattacc[A/G]actttaggctagagta	A	G	NM_022897 // intron // 0 // Hs.410810 // RANBP17 // 64901 // Homo sapiens RAN binding protein 17 (RANBP17), mRNA. /// NM_015024 // intron // 0 // Hs.172685 // XPO7 // 23039 // Homo sapiens exportin 7 (XPO7), mRNA. /// ENST00000252512 // intron // 0 // —	RANBP17	RANBP17, Homo sapiens RAN binding protein 17 (RANBP17), p21.3
SNP_A-2299579	gccgaggatggcgatt[C/T]aagtaagagtagcttt	C	T	NM_006128 // intron // 0 // Hs.1274 // BMP1 // 649 // Homo sapiens bone morphogenetic protein 1 (BMP1), transcript variant BMP1-2, mRNA. /// NM_006130 // intron // 0 // Hs.1274 // BMP1 // 649 // Homo sapiens bone morphogenetic protein 1 (BMP1), transcript	BMP1	BMP1, Homo sapiens bone morphogenetic protein 1 (BMP1), transcript variant BMP1-2, p21.3
SNP_A-1697468	tatgctaagtgaaagaagtcagtca[C/T]tacagaccacatattat atgatgcc	C	T	NM_005605 // intron // 0 // Hs.75206 // PPP3CC // 5533 // protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	PPP3CC	PPP3CC , rs1116084, protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma),p21.3
SNP_A-2196663	cattaagctcttagca[C/T]agtttagtcggatacc	C	T	NM_005605 // intron // 0 // Hs.149413 // PPP3CC // 5533 // Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA. /// S46622 // intron // 0 // Hs.149413 // PPP3CC // 5533 // calcineurin A c	PPP3CC	PPP3CC, Homo sapiens protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), p21.3
SNP_A-2044441	aagaaaaatttgaaac[A/G]gttgcaatgaccagca	A	G	NM_018688 // intron // 0 // Hs.546409 // BIN3 // 55909 // Homo sapiens bridging integrator 3 (BIN3), mRNA. /// ENST00000276416 // intron // 0 // - - // — // — // —	BIN3	BIN3, Homo sapiens bridging integrator 3 (BIN3), p21.3
SNP_A-2198776	catttctcctggcatc[G/T]ctagctctttagatg	G	T	NM_144962 // intron // 0 // Hs.491242 // PEBP4 // 157310 // Homo sapiens phosphatidylethanolamine-binding protein 4 (PEBP4), mRNA. /// ENST00000256404 // intron // 0 // — // — // — // —	PEBP4	PEBP4, Homo sapiens phosphatidylethanolamine-binding protein 4 (PEBP4), p21.3
SNP_A-2099059	agaggaagggatgtga[A/G]aatacagatcatgaca	A	G	NM_144962 // intron // 0 // Hs.491242 // PEBP4 // 157310 // Homo sapiens phosphatidylethanolamine-binding protein 4 (PEBP4), mRNA. /// ENST00000256404 // intron // 0 // — // — // — // —	PEBP4	PEBP4, Homo sapiens phosphatidylethanolamine-binding protein 4 (PEBP4), p21.3
SNP_A-2136287	atcacaactcagttac[A/C]ataaaatacttgacac	A	C	NM_152272 // intron // 0 // Hs.5019 // MGC29816 // 91782 // Homo sapiens hypothetical protein MGC29816 (MGC29816), mRNA. /// NM_003840 // intron // 0 // Hs.213467 // TNFRSF10D // 8793 // Homo sapiens tumor necrosis factor receptor superfamily, member 10d,	MGC29816	MGC29816, Homo sapiens hypothetical protein MGC29816 (MGC29816), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1793467	ggtagtggcatatagg[A/G]agagacctgcaggtcc	A	G	NM_002318 // intron // 0 // Hs.116479 // LOXL2 // 4017 // Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /// ENST00000256397 // intron // 0 // — // — // — /// ENST00000356206 // intron // 0 // — // — // — // —	LOXL2	LOXL2, Homo sapiens lysyl oxidase-like 2 (LOXL2), p21.3
SNP_A-1735170	ggctgtcaagatctaacatcaccaa[A/G]gctagcccaccactc ccagtctaaa	A	G	NM_006167 // downstream // 86061 // Hs.55999 // NKX3-1 // 4824 // NK3 transcription factor related, locus 1 (Drosophila) /// NM_016612 // downstream // 20451 // Hs.283716 // MSCP // 51312 // mitochondrial solute carrier protein /// NM_018579 // downstrea	NKX3-1	NKX3-1, rs1355600, NK3 transcription factor related, locus 1 (Drosophila), p21.2
SNP_A-2259925	gaaaagtccaaatta[A/G]aggtgatggcaagcac	A	G	NM_018579 // intron // 0 // Hs.122514 // MSCP // 51312 // Homo sapiens mitochondrial solute carrier protein (MSCP), mRNA. /// NM_016612 // intron // 0 // Hs.122514 // MSCP // 51312 // Homo sapiens mitochondrial solute carrier protein (MSCP), mRNA. /// ENS	MSCP	MSCP, Homo sapiens mitochondrial solute carrier protein (MSCP), p21.2
SNP_A-1931978	ttcctaccacagactg[G/T]caaaaacatcttctgg	G	T	NM_018579 // intron // 0 // Hs.122514 // MSCP // 51312 // Homo sapiens mitochondrial solute carrier protein (MSCP), mRNA. /// NM_016612 // intron // 0 // Hs.122514 // MSCP // 51312 // Homo sapiens mitochondrial solute carrier protein (MSCP), mRNA. /// ENS	MSCP	MSCP, Homo sapiens mitochondrial solute carrier protein (MSCP), p21.2
SNP_A-1784262	ggcccagacctcaca[C/T]agtttttagagggagt	C	T	NM_018579 // downstream // 49093 // Hs.122514 // MSCP // 51312 // Homo sapiens mitochondrial solute carrier protein (MSCP), mRNA. /// NM_016612 // downstream // 49093 // Hs.122514 // MSCP // 51312 // Homo sapiens mitochondrial solute carrier protein (MSCP	MSCP	MSCP, Homo sapiens mitochondrial solute carrier protein (MSCP), p21.2
SNP_A-1671152	tgctacaactgcagacttagaaaaa[C/T]gtggtcacctttgaggt ggctaaag	C	T	NM_003155 // upstream // 100860 // Hs.25590 // STC1 // 6781 // stanniocalcin 1 /// NM_014265 // upstream // 338436 // Hs.528304 // ADAM28 // 10863 // a disintegrin and metalloproteinase domain 28 /// NM_021777 // upstream // 338444 // Hs.528304 // ADAM28	STC1	STC1, rs10503737, stanniocalcin 1, p21.2
SNP_A-2032333	aaagttccaggccta[A/G]aatgtgtatgtgtat	A	G	NM_003155 // upstream // 75419 // Hs.25590 // STC1 // 6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 363877 // Hs.528304 // ADAM28 // 10863 // Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-2273003	gactaggctgatttc[C/G]aagcactgagcctgg	C	G	NM_003155 // upstream // 110159 // Hs.25590 // STC1 // 6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 329137 // Hs.528304 // ADAM28 // 10863 // Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcrip	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-2128829	ataatgacaacatcac[A/G]cagcataactgagtat	A	G	NM_003155 // upstream // 318633 // Hs.25590 // STC1 // 6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 120663 // Hs.528304 // ADAM28 // 10863 // Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcrip	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-2129726	atacagtcactgctc[A/G]ccttcattaatgcaa	A	G	NM_003155 // upstream // 339351 // Hs.25590 // STC1 // 6781 // Homo sapiens stanniocalcin 1 (STC1), mRNA. /// NM_014265 // upstream // 99945 // Hs.528304 // ADAM28 // 10863 // Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript	STC1	STC1, Homo sapiens stanniocalcin 1 (STC1), p21.2
SNP_A-1754294	gacatttgtacagtgtgatagagaga[A/G]tacattggaaaaccaa agttcagaa	A	G	AF215824 // intron // 0 // Hs.166003 // ADAM7 // 8756 // a disintegrin and metalloproteinase domain 7	ADAM7	ADAM7, rs1492404, a disintegrin and metalloproteinase domain 7, p21.2
SNP_A-1992705	ccttgtgttatagtga[C/T]ctcaatttctggatga	C	T	ENST00000335595 // intron // 0 // — // — // —	-	p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1992707	cctcaaaaatataaaa[C/T]gactgtccagtgccca	C	T	NM_003817 // downstream // 18255 // Hs.166003 // ADAM7 // 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream // 386794 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (NE	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-1911590	tgtgaaaataggcacc[A/G]gattcaaatttatg	A	G	NM_003817 // downstream // 21728 // Hs.166003 // ADAM7 // 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream // 383321 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (NE	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-2112421	aggcaagtaccaggtt[C/G]aaattgtggtgtgat	C	G	NM_003817 // downstream // 29850 // Hs.166003 // ADAM7 // 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream // 375199 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (NE	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-2253538	ctctctctgtagctac[A/C]ctaattccaagtcatt	A	C	NM_003817 // downstream // 76886 // Hs.166003 // ADAM7 // 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream // 328163 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (NE	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-2082306	acgatcttattaatgc[A/G]gattctgggttccatt	A	G	NM_003817 // downstream // 184201 // Hs.166003 // ADAM7 // 8756 // Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), mRNA. /// NM_005382 // upstream // 220848 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (N	ADAM7	ADAM7, Homo sapiens a disintegrin and metalloproteinase domain 7 (ADAM7), p21.2
SNP_A-1992716	ctttaatagacaaaac[A/T]gcaaacatatgtaact	A	T	NM_005382 // downstream // 7232 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (NEF3), mRNA. /// NM_006158 // downstream // 26497 // Hs.521461 // NEFL // 4747 // Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRN	NEF3	NEF3, Homo sapiens neurofilament 3 (150kDa medium) (NEF3), p21.2
SNP_A-1922868	ttagatcttggttcaa[C/G]ttccagtttaaactt	C	G	NM_005382 // downstream // 10603 // Hs.458657 // NEF3 // 4741 // Homo sapiens neurofilament 3 (150kDa medium) (NEF3), mRNA. /// NM_006158 // downstream // 23126 // Hs.521461 // NEFL // 4747 // Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mR	NEF3	NEF3, Homo sapiens neurofilament 3 (150kDa medium) (NEF3), p21.2
SNP_A-2035244	aaatgcttatcccicta[C/T]cttgcaaacattaaa	C	T	NM_006158 // upstream // 5414 // Hs.521461 // NEFL // 4747 // Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRNA. /// NM_024940 // upstream // 222844 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. //	NEFL	NEFL, Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), p21.2
SNP_A-2191069	catagtaaaagctcaa[A/C]acacggcagccataat	A	C	NM_006158 // upstream // 24633 // Hs.521461 // NEFL // 4747 // Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRNA. /// NM_024940 // upstream // 203625 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. /	NEFL	NEFL, Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), p21.2
SNP_A-2252357	cttcccttctccaaaa[A/T]ccaggagcaacttgag	A	T	NM_006158 // upstream // 26099 // Hs.521461 // NEFL // 4747 // Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), mRNA. /// NM_024940 // upstream // 202159 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. /	NEFL	NEFL, Homo sapiens neurofilament, light polypeptide 68kDa (NEFL), p21.2
SNP_A-1829186	taagtaaaaagagtca[A/G]tccacatgattccaac	A	G	NM_024940 // intron // 0 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. /// ENST00000276440 // intron // 0 // — // — // —	DOCK5	DOCK5, Homo sapiens dedicator of cytokinesis 5 (DOCK5), p21.2
SNP_A-2231218	ctattatggcatcagga[A/G]aacatgacttgtgct	A	G	NM_024940 // intron // 0 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. /// ENST00000276440 // intron // 0 // — // — // — // —	DOCK5	DOCK5, Homo sapiens dedicator of cytokinesis 5 (DOCK5), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2273256	gactcatgctacacac[A/T]gcgtggatgaaccttg	A	T	NM_024940 // intron // 0 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. /// ENST00000276440 // intron // 0 // — // — // —	DOCK5	DOCK5, Homo sapiens dedicator of cytokinesis 5 (DOCK5), p21.2
SNP_A-2046726	aagagcttcaagcatc[C/T]aaaaacctggtcacct	C	T	NM_024940 // CDS // 0 // Hs.195403 // DOCK5 // 80005 // Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA. /// ENST00000276440 // CDS // 0 // — // — // — // —	DOCK5	DOCK5, Homo sapiens dedicator of cytokinesis 5 (DOCK5), p21.2
SNP_A-1893950	tgcatatgcaaatagal[A/C]ccttggcaggtgctg	A	C	NM_152562 // downstream // 157711 // Hs.33366 // CDCA2 // 157313 // Homo sapiens cell division cycle associated 2 (CDCA2), mRNA. /// NM_022659 // downstream // 178437 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// EN	CDCA2	CDCA2, Homo sapiens cell division cycle associated 2 (CDCA2), p21.2
SNP_A-2025522	aaaatctgaggtctcc[A/G]agaaaagaaaattctat	A	G	NM_152562 // downstream // 317059 // Hs.33366 // CDCA2 // 157313 // Homo sapiens cell division cycle associated 2 (CDCA2), mRNA. /// NM_022659 // downstream // 19089 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// ENS	CDCA2	CDCA2, Homo sapiens cell division cycle associated 2 (CDCA2), p21.2
SNP_A-1731875	caaagactcagttgggataagagac[A/G]aggtatccagctccc agaacaaaat	A	G	NM_002717 // upstream // 269308 // Hs.512628 // PPP2R2A // 5520 // protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform /// NM_022659 // upstream // 132404 // Hs.335246 // EBF2 // 64641 // early B-cell factor 2	PPP2R2A	PPP2R2A, rs10503781, protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform ,p21.2
SNP_A-1750361	tgttcttttcaaacctctctcta[C/T]ctggcaggttctctgacgatc cagt	C	T	NM_002717 // upstream // 262877 // Hs.512628 // PPP2R2A // 5520 // protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform /// NM_022659 // upstream // 138835 // Hs.335246 // EBF2 // 64641 // early B-cell factor 2	PPP2R2A	PPP2R2A , -, protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform ,p21.2
SNP_A-1798651	gtaacaggggtgtaaa[C/T]gccagccaatctctt	C	T	NM_022659 // upstream // 127988 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 273724 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2287478	gatgttgatgattggc[A/G]gaaggatttatatgt	A	G	NM_022659 // upstream // 167371 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 234341 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-1861770	tcatcttaatgagcca[C/T]aaatgtgtaattagca	C	T	NM_022659 // upstream // 230317 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 171395 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2174926	cacagggagttattag[A/T]cacatcaagtttccaa	A	T	NM_022659 // upstream // 261043 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 140669 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-1992755	ctaactgcgaaatgac[A/T]gagatctcatagatgt	A	T	NM_022659 // upstream // 278338 // Hs.491292 // EBF2 // 64641 // Homo sapiens early B-cell factor 2 (EBF2), mRNA. /// NM_002717 // upstream // 123374 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B	EBF2	EBF2, Homo sapiens early B-cell factor 2 (EBF2), p21.2
SNP_A-2289656	gcaaaacacacaaaat[G/T]aatagtcaagatcaag	G	T	NM_002717 // intron // 0 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (PPP2R2A), mRNA. /// ENST00000315985 // intron // 0 // — // — // —	PPP2R2A	PPP2R2A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (PPP2R2A), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2034089	aaatcatagaggtata[C/T]ggcagtttcgtggact	C	T	NM_002717 // intron // 0 // Hs.146339 // PPP2R2A // 5520 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (PPP2R2A), mRNA. /// ENST00000315985 // intron // 0 // --- // --- // --- // ---	PPP2R2A	PPP2R2A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (PPP2R2A), p21.2
SNP_A-1909371	tgtattactcatggca[C/T]gtacttatactaaaaa	C	T	NM_001386 // downstream // 69923 // Hs.173381 // DPYSL2 // 1808 // Homo sapiens dihydropyrimidinase-like 2 (DPYSL2), mRNA. /// NM_033303 // downstream // 20423 // Hs.52931 // ADRA1A // 148 // Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), transcri	DPYSL2	DPYSL2, Homo sapiens dihydropyrimidinase-like 2 (DPYSL2), p21.2
SNP_A-2243433	ctgcgtgaagaagaaa[A/T]tagatgattcatgcaa	A	T	NM_033303 // intron // 0 // Hs.52931 // ADRA1A // 148 // Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), transcript variant 2, mRNA. /// NM_033302 // intron // 0 // Hs.52931 // ADRA1A // 148 // Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A),	ADRA1A	ADRA1A, Homo sapiens adrenergic, alpha-1A-, receptor (ADRA1A), transcript variant 2, p21.2
SNP_A-1753925	attctggaaatcataggactgtgaa[A/C]aagaaaagacctgag agatctcata	A	C	NM_000680 // upstream // 210202 // Hs.52931 // ADRA1A // 148 // adrenergic, alpha-1A-, receptor /// NM_030795 // downstream // 160692 // Hs.201058 // STMN4 // 81551 // stathmin-like 4 /// NM_033302 // upstream // 210202 // Hs.52931 // ADRA1A // 148 // ad	ADRA1A	ADRA1A, rs10503809, adrenergic, alpha-1A-, receptor, p21.2
SNP_A-2071591	acagaagccacttgca[C/G]caaaaccacttacagt	C	G	NM_030795 // downstream // 191797 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 191802 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389).	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-2048090	aagcaattactaaagc[A/C]acagtgacttgaggtt	A	C	NM_030795 // downstream // 172222 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 172227 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389).	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-1912689	tgtgcgtcattcaacc[C/T]attgaggtctgcata	C	T	NM_030795 // downstream // 140160 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 140165 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389).	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-2039261	aacagttagattgcta[G/T]gattatctgttaagat	G	T	NM_030795 // downstream // 139404 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 139409 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389).	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-1686104	gaaaaagacaataactgaaataaaa[A/C]ctcaatgaatgggc tcaatagcag	A	C	NM_000680 // upstream // 268883 // Hs.52931 // ADRA1A // 148 // adrenergic, alpha-1A-, receptor /// NM_030795 // downstream // 102011 // Hs.201058 // STMN4 // 81551 // stathmin-like 4 /// NM_033302 // upstream // 268883 // Hs.52931 // ADRA1A // 148 // ad	ADRA1A	ADRA1A, rs1584233, adrenergic, alpha-1A-, receptor, p21.2
SNP_A-1677072	attgattggctgagtctaatctaag[C/T]agtgaagtaactggctg gctgttc	C	T	NM_000680 // upstream // 273452 // Hs.52931 // ADRA1A // 148 // adrenergic, alpha-1A-, receptor /// NM_030795 // downstream // 97442 // Hs.201058 // STMN4 // 81551 // stathmin-like 4 /// NM_033302 // upstream // 273452 // Hs.52931 // ADRA1A // 148 // adr	ADRA1A	ADRA1A, rs2322509, adrenergic, alpha-1A-, receptor, p21.2
SNP_A-2055751	aataaattggcactcta[C/G]aaaagggagatcttcc	C	G	NM_030795 // downstream // 112669 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 112674 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389).	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2047348	aagatccgcaccgtca[A/C]aacccatctcattaaa	A	C	NM_030795 // downstream // 112152 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 112157 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389),	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-1862093	tcatgccattactgta[A/G]ataaggcagtgtagga	A	G	NM_030795 // downstream // 92641 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 92646 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389), c	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-2289443	gattttctgcaaaacc[A/G]gatgatgagaagagac	A	G	NM_030795 // downstream // 77490 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4 (STMN4), mRNA. /// BC011520 // downstream // 77495 // Hs.201058 // STMN4 // 81551 // Homo sapiens stathmin-like 4, mRNA (cDNA clone MGC:18239 IMAGE:4157389), c	STMN4	STMN4, Homo sapiens stathmin-like 4 (STMN4), p21.2
SNP_A-2013308	ctgatcttgctgcccc[C/T]actgtttgcttgagaa	C	T	NM_173175 // intron // 0 // Hs.491322 // PTK2B // 2185 // Homo sapiens PTK2B protein tyrosine kinase 2 beta (PTK2B), transcript variant 4, mRNA. /// NM_004103 // intron // 0 // Hs.491322 // PTK2B // 2185 // Homo sapiens PTK2B protein tyrosine kinase 2 bet	PTK2B	PTK2B, Homo sapiens PTK2B protein tyrosine kinase 2 beta (PTK2B), transcript variant 4, p21.2
SNP_A-1798483	gtaaatgcaaggtaaa[A/G]ttccagcaatgggttg	A	G	NM_001979 // downstream // 34407 // Hs.212088 // EPHX2 // 2053 // Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), mRNA. /// NM_001831 // downstream // 17609 // Hs.436657 // CLU // 1191 // Homo sapiens clusterin (complement lysis inhibitor, SP-40,40	EPHX2	EPHX2, Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), p21.1
SNP_A-1820964	gtttctcctcaacctc[A/C]ctacacttattgctgt	A	C	NM_001979 // downstream // 35870 // Hs.212088 // EPHX2 // 2053 // Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), mRNA. /// NM_001831 // downstream // 16146 // Hs.436657 // CLU // 1191 // Homo sapiens clusterin (complement lysis inhibitor, SP-40,40	EPHX2	EPHX2, Homo sapiens epoxide hydrolase 2, cytoplasmic (EPHX2), p21.1
SNP_A-2096598	agacgacattggcaaa[A/G]tgactcagacccacag	A	G	NM_018246 // 3UTR // 0 // Hs.445512 // FLJ10853 // 55246 // Homo sapiens hypothetical protein FLJ10853 (FLJ10853), mRNA. /// ENST00000356537 // 3UTR // 0 // — // — // — // — /// ENST00000276395 // 3UTR // 0 // — // — // — // —	FLJ10853	FLJ10853, Homo sapiens hypothetical protein FLJ10853 (FLJ10853), p21.1
SNP_A-2149781	atgtattgcaaataaa[A/C]aaacatggaaaaatct	A	C	NM_018246 // intron // 0 // Hs.445512 // FLJ10853 // 55246 // Homo sapiens hypothetical protein FLJ10853 (FLJ10853), mRNA. /// ENST00000356537 // intron // 0 // — // — // — // — /// ENST00000276395 // intron // 0 // — // — // — // —	FLJ10853	FLJ10853, Homo sapiens hypothetical protein FLJ10853 (FLJ10853), p21.1
SNP_A-1807463	gtctgcagtcaaatga[A/G]agacgcttaaatgctg	A	G	NM_018246 // intron // 0 // Hs.445512 // FLJ10853 // 55246 // Homo sapiens hypothetical protein FLJ10853 (FLJ10853), mRNA. /// ENST00000356537 // intron // 0 // — // — // — // — /// ENST00000276395 // intron // 0 // — // — // — // —	FLJ10853	FLJ10853, Homo sapiens hypothetical protein FLJ10853 (FLJ10853), p21.1
SNP_A-1953806	tttgagatatgttctg[G/T]aaccaggttattttac	G	T	NM_018246 // intron // 0 // Hs.445512 // FLJ10853 // 55246 // Homo sapiens hypothetical protein FLJ10853 (FLJ10853), mRNA. /// ENST00000356537 // intron // 0 // — // — // — // — /// ENST00000276395 // intron // 0 // — // — // — // —	FLJ10853	FLJ10853, Homo sapiens hypothetical protein FLJ10853 (FLJ10853), p21.1
SNP_A-1956286	tttgtgtgttgtcata[A/C]gttttcaactctttcg	A	C	NM_018492 // upstream // 10939 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 21465 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-2061978	aatggctgataccaag[C/T]ctgcagtgaaaaatgc	C	T	NM_018492 // upstream // 14751 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 17653 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2260938	gaaacttggttgagcc[C/T]agaatttgaaaccag	C	T	NM_018492 // upstream // 15153 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 17251 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-2264547	gaagaagagaacatca[A/G]gcctcttggctggact	A	G	NM_018492 // upstream // 18830 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 13574 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-1795370	ggtgattctgaaacac[A/G]ctgaaggtgaagaaca	A	G	NM_018492 // upstream // 19573 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 12831 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-2305834	gctgctacatggaaca[C/T]tggctaaaagtaggca	C	T	NM_018492 // upstream // 20224 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 12180 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-2034467	aaatctctgttcacat[A/G]aaagcctgtccatgaa	A	G	NM_018492 // upstream // 21252 // Hs.104741 // PBK // 55872 // Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA. /// NM_173833 // downstream // 11152 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780)	PBK	PBK, Homo sapiens T-LAK cell-originated protein kinase (TOPK), p21.1
SNP_A-1740599	ctcagacacgcttcctaaaatcatc[A/G]gaggtgcttgcacaaat tcagctac	A	G	NM_018492 // upstream // 66469 // Hs.104741 // TOPK // 55872 // T-LAK cell-originated protein kinase /// NM_173833 // downstream // 69 // Hs.146246 // MGC45780 // 286133 // hypothetical protein MGC45780	TOPK	TOPK , rs2685370, T-LAK cell-originated protein kinase ,p21.1
SNP_A-1992817	actcgtttagaaaga[A/T]ccctaacagtttgaga	A	T	NM_173833 // intron // 0 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780), mRNA. /// ENST00000354914 // intron // 0 // — // — // —	MGC45780	MGC45780, Homo sapiens hypothetical protein MGC45780 (MGC45780), p21.1
SNP_A-2303982	gctccaaagcattgac[A/G]tagttattctaaaga	A	G	NM_173833 // intron // 0 // Hs.146246 // MGC45780 // 286133 // Homo sapiens hypothetical protein MGC45780 (MGC45780), mRNA. /// ENST00000354914 // intron // 0 // — // — // — // — /// ENST00000336537 // intron // 0 // — // — // — /// E	MGC45780	MGC45780, Homo sapiens hypothetical protein MGC45780 (MGC45780), p21.1
SNP_A-2206430	ccatctcctctattac[G/T]aaagcccctgtaagac	G	T	NM_018091 // intron // 0 // Hs.491336 // ELP3 // 55140 // Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), mRNA. /// ENST00000256398 // intron // 0 // — // — // —	ELP3	ELP3, Homo sapiens elongation protein 3 homolog (S. cerevisiae) (ELP3), p21.1
SNP_A-1955877	ttgtcaaactggaaa[A/C]acaaaacaaagcaaaa	A	C	NM_018660 // intron // 0 // Hs.435535 // ZNF395 // 55893 // Homo sapiens zinc finger protein 395 (ZNF395), mRNA. /// NM_172366 // intron // 0 // Hs.532253 // FBXO16 // 157574 // Homo sapiens F-box protein 16 (FBXO16), mRNA. /// ENST00000290163 // intron /	ZNF395	ZNF395, Homo sapiens zinc finger protein 395 (ZNF395), p21.1
SNP_A-1890015	tgatatacagcgaaaga[A/G]aaaggatgaattacag	A	G	NM_017412 // downstream // 38857 // Hs.40735 // FZD3 // 7976 // Homo sapiens frizzled homolog 3 (Drosophila) (FZD3), mRNA. /// NM_001440 // upstream // 98315 // Hs.491354 // EXTL3 // 2137 // Homo sapiens exostoses (multiple)-like 3 (EXTL3), mRNA. /// ENST	FZD3	FZD3, Homo sapiens frizzled homolog 3 (Drosophila) (FZD3), p21.1
SNP_A-1919438	ttaagcagattggcaa[A/G]ggtacgtgaggcctg	A	G	NM_018250 // intron // 0 // Hs.162397 // FLJ10871 // 55756 // Homo sapiens hypothetical protein FLJ10871 (FLJ10871), mRNA. /// ENST00000265614 // intron // 0 // — // — // —	FLJ10871	FLJ10871, Homo sapiens hypothetical protein FLJ10871 (FLJ10871), p21.1
SNP_A-2028818	aaacttgacatatgca[A/G]tcaacgttaacatcac	A	G	NM_018250 // intron // 0 // Hs.162397 // FLJ10871 // 55756 // Homo sapiens hypothetical protein FLJ10871 (FLJ10871), mRNA. /// ENST00000265614 // intron // 0 // — // — // —	FLJ10871	FLJ10871, Homo sapiens hypothetical protein FLJ10871 (FLJ10871), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1822218	gttttgagtcatttaa[G/T]gctaaccatcagagtt	G	T	NM_015254 // intron // 0 // Hs.444767 // KIF13B // 23303 // Homo sapiens kinesin family member 13B (KIF13B), mRNA /// ENST00000355514 // intron // 0 // — // — // — // — // ENST00000358297 // intron // 0 // — // — // — // ENST00000003	KIF13B	KIF13B, Homo sapiens kinesin family member 13B (KIF13B), p12
SNP_A-2087487	actgcccccagaatga[C/T]gtgagaagtccttcaa	C	T	NM_015254 // intron // 0 // Hs.444767 // KIF13B // 23303 // Homo sapiens kinesin family member 13B (KIF13B), mRNA /// ENST00000355514 // intron // 0 // — // — // — // — // ENST00000358297 // intron // 0 // — // — // — // ENST000003	KIF13B	KIF13B, Homo sapiens kinesin family member 13B (KIF13B), p12
SNP_A-1780993	ggatgatattaatccc[A/G]acatcgcagggaatgt	A	G	NM_015254 // upstream // 37086 // Hs.444767 // KIF13B // 23303 // Homo sapiens kinesin family member 13B (KIF13B), mRNA /// NM_015254 // upstream // 37025 // Hs.444767 // KIF13B // 23303 // Homo sapiens kinesin family member 13B (KIF13B), mRNA /// NM_05	KIF13B	KIF13B, Homo sapiens kinesin family member 13B (KIF13B), p12
SNP_A-1957377	ttttagctttgtagga[A/C]attttttcttctcct	A	C	NM_057158 // upstream // 99849 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 97986 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatase	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-2212835	ccctttcagctttctga[C/T]accttgtgcaagcct	C	T	NM_057158 // upstream // 147597 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 145734 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatas	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-1662586	gcttctcttgggttcctcaatgca[A/C]actctgttatggcaattatct gag	A	C	NM_001394 // upstream // 187326 // Hs.417962 // DUSP4 // 1846 // dual specificity phosphatase 4 /// NM_016127 // downstream // 560858 // Hs.279921 // MGC8721 // 51669 // hypothetical protein MGC8721 /// NM_057158 // upstream // 189189 // Hs.417962 // DUS	DUSP4	DUSP4 , rs4295704, dual specificity phosphatase 4 p12
SNP_A-2197798	cattgaagcagggaaa[G/T]aattggagcacaaagg	G	T	NM_057158 // upstream // 183293 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 181430 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatas	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-1992868	aaatactgccggtgac[A/G]gaagctgcttaatcta	A	G	NM_057158 // upstream // 207114 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA. /// NM_001394 // upstream // 205251 // Hs.417962 // DUSP4 // 1846 // Homo sapiens dual specificity phosphatas	DUSP4	DUSP4, Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, p12
SNP_A-2283286	gatacaaatcagagag[C/G]accctaaagaagccct	C	G	NM_016127 // downstream // 176638 // Hs.521487 // MGC8721 // 51669 // Homo sapiens hypothetical protein MGC8721 (MGC8721), mRNA. /// ENST00000330733 // downstream // 317457 // — // — // — // — // ENST00000256255 // downstream // 176638 // — //	MGC8721	MGC8721, Homo sapiens hypothetical protein MGC8721 (MGC8721), p12
SNP_A-2077301	accaatgttattgga[C/T]gtaaatgctactggg	C	T	NM_016127 // downstream // 89367 // Hs.521487 // MGC8721 // 51669 // Homo sapiens hypothetical protein MGC8721 (MGC8721), mRNA. /// ENST00000330733 // downstream // 404728 // — // — // — // — // ENST00000256255 // downstream // 89367 // — // –	MGC8721	MGC8721, Homo sapiens hypothetical protein MGC8721 (MGC8721), p12
SNP_A-2275396	gagaatgacttagaac[C/G]gcacgcaaaggaatt	C	G	NM_006571 // upstream // 17500 // Hs.158427 // DCTN6 // 10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// ENST00000320542 // upstream // 5865 // — // — // — // — // ENST00000221114 // upstream // 17500 // — // — // —	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308624	gctttcatttctctc[A/G]aatttgctgctctgt	A	G	NM_006571 // downstream // 18801 // Hs.158427 // DCTN6 // 10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 182183 // Hs.334587 // RBPMS // 11030 // Homo sapiens RNA binding protein with multiple splicing (RBPMS), mRNA. /// ENST	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-1798186	gtaaacctctctaaaa[A/T]tacccagaaatgcaac	A	T	NM_006571 // downstream // 134094 // Hs.158427 // DCTN6 // 10671 // Homo sapiens dynactin 6 (DCTN6), mRNA. /// NM_006867 // upstream // 66890 // Hs.334587 // RBPMS // 11030 // Homo sapiens RNA binding protein with multiple splicing (RBPMS), mRNA. /// ENST	DCTN6	DCTN6, Homo sapiens dynactin 6 (DCTN6), p12
SNP_A-2060119	aatgaaagaaaaagcc[C/T]ggagtaagctccaaca	C	T	NM_031271 // upstream // 12064 // Hs.458316 // TEX15 // 56154 // Homo sapiens testis expressed sequence 15 (TEX15), mRNA. /// NM_013357 // downstream // 170658 // Hs.373778 // PURG // 29942 // Homo sapiens purine-rich element binding protein G (PURG), mRN	TEX15	TEX15, Homo sapiens testis expressed sequence 15 (TEX15), p12
SNP_A-1856993	tcaccattacttagat[C/T]atcacaggtagggatg	C	T	NM_013962 // upstream // 409242 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1317526 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1992913	attaagtgcataaccc[A/G]aatattcagaatagaa	A	G	NM_013962 // upstream // 237005 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1145289 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1666516	gagtgtgtttcatgacagcacagaa[C/T]ttatctacttgtttattgc aatgt	C	T	NM_000553 // downstream // 374003 // Hs.512715 // WRN // 7486 // Werner syndrome /// NM_004495 // upstream // 1000529 // Hs.172816 // NRG1 // 3084 // neuregulin 1 /// NM_013357 // upstream // 514962 // Hs.512715 // WRN // 7486 // Werner syndrome /// NM_0	WRN	WRN , rs10489347, Werner syndrome ,p12
SNP_A-1916010	tgttgcagatatcttg[A/G]aacatcatttgtgctt	A	G	NM_013962 // upstream // 102829 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1011113 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1856239	tcacaataaaagttaa[C/T]tcatcttctcatctc	C	T	NM_013962 // upstream // 99380 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1007664 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-g	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1892841	tgcacatctaactact[A/G]ggacacttccttttct	A	G	NM_013962 // upstream // 96065 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 1004349 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-g	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2191788	catatttctagtgtta[C/T]ggcaatgttaacttg	C	T	NM_013962 // upstream // 88164 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 996448 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-ga	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2255315	cttgtaccctccgaag[C/G]caaaacctgagctgta	C	G	NM_013962 // upstream // 34452 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 942736 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-ga	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2054073	aagttatttagctgac[G/T]ggtaaagagtctcttt	G	T	NM_013962 // upstream // 10713 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// NM_004495 // upstream // 918997 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-ga	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2239905	ctgaacctctagagaa[C/T]acagtcaggtagatga	C	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1824788	taaagatcaacgctaa[C/T]attgcctccaaccaag	C	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1694989	cacacacagcctcaatgacctaata[A/G]gcagatttgcagagc cataacctg	A	G	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // neuregulin 1	NRG1	NRG1, rs970998, neuregulin 1,p12
SNP_A-2309931	ggaaatcatcatttgg[C/G]aattgtatttcctctt	C	G	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1847690	tatctagaaaaacataq[C/T]ggaaaaaacatccagcc	C	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1992956	atttccactccctcaq[G/T]tcaaacacatatagct	G	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2303707	gctcagacaataaaata[A/G]aaacagagtgctcagc	A	G	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1934607	ttctctctggcacttat[C/T]catttatctatttttat	C	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-2208625	cccactgctggtccaa[A/G]atctgctatcaccatt	A	G	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1992959	gagagcagttttaat[C/T]tgtgaacgtgtaagtc	C	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1992963	ttggattgcttgagac[C/T]gcatctgtatgcctat	C	T	NM_013962 // intron // 0 // Hs.453951 // NRG1 // 3084 // Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA. /// ENST00000338921 // intron // 0 // — // — // —	NRG1	NRG1, Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, p12
SNP_A-1992975	tcttagtttctacaca[C/G]gatgttcagacatatt	C	G	NM_032664 // downstream // 599150 // Hs.458713 // FUT10 // 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000339085 // downstream // 3814 // — // — /// ENST00000327671 // downstream	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12
SNP_A-2137889	atcattgcctgcagaaa[A/G]aagatggtgttaagta	A	G	NM_032664 // downstream // 385293 // Hs.458713 // FUT10 // 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000339085 // downstream // 217671 // — // — // — /// ENST00000327671 // downstrea	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12
SNP_A-1919248	ttaagaaatgtagatc[A/T]aggagctgtctaacaa	A	T	NM_032664 // downstream // 353221 // Hs.458713 // FUT10 // 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000339085 // downstream // 249743 // — // — // — /// ENST00000327671 // downstrea	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2122362	agtgcccatgttcagg[C/T]aacactaatatttgca	C	T	NM_032664 // downstream // 305830 // Hs.458713 // FUT10 // 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000339085 // downstream // 297134 // — /// — /// — /// ENST00000327671 // downstrea	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12
SNP_A-1836854	tactgcagtactctcg[A/G]acccaaggtctttcca	A	G	NM_032664 // intron // 0 // Hs.458713 // FUT10 // 84750 // Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), mRNA. /// ENST00000327671 // intron // 0 // — /// — /// — /// ENST00000335589 // intron // 0 // — /// — /	FUT10	FUT10, Homo sapiens fucosyltransferase 10 (alpha (1,3) fucosyltransferase) (FUT10), p12
SNP_A-1904330	tgggctggtgccatct[C/G]aaggtgacaatggctg	C	G	NM_024025 // upstream // 74625 // Hs.8719 // MGC1136 // 78986 // Homo sapiens hypothetical protein MGC1136 (MGC1136), mRNA. /// ENST00000256261 // upstream // 74625 // — /// — /// — /// ENST00000332498 // downstream // 294953 // — /// — /	MGC1136	MGC1136, Homo sapiens hypothetical protein MGC1136 (MGC1136), p12
SNP_A-2074965	acatcatgatagcaga[C/T]tcgccggagtaatgag	C	T	NM_152344 // downstream // 1060288 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 141234 // — /// — /// — /// ENST00000321445 // downstream // 1060288 // —	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2236674	ctctaaggacattca[C/T]ccaaatctgactctgg	C	T	NM_152344 // downstream // 918834 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 282688 // — /// — /// — /// ENST00000321445 // downstream // 918834 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2281222	gagtaggaaggaacag[C/G]ctcattaacattcata	C	G	NM_152344 // downstream // 845159 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 356363 // — /// — /// — /// ENST00000321445 // downstream // 845159 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1993015	ctatgatgctcaagta[G/T]ctaaccaggaggaaaa	G	T	NM_152344 // downstream // 844000 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 357522 // — /// — /// — /// ENST00000321445 // downstream // 844000 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1881311	tctttcacaatctagg[A/G]caaagagtatgggata	A	G	NM_152344 // downstream // 843231 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 358291 // — /// — /// — /// ENST00000321445 // downstream // 843231 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1886834	tgactgggttccaca[A/T]cctctagctttcagtt	A	T	NM_152344 // downstream // 692369 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 509153 // — /// — /// — /// ENST00000321445 // downstream // 692369 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1801244	gtagctggaaccatag[G/T]agtatgcaatcacatc	G	T	NM_152344 // downstream // 690231 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 511291 // — /// — /// — /// ENST00000321445 // downstream // 690231 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1861679	tcatctcgcctgtca[A/T]ggaatgtaagaaatcc	A	T	NM_152344 // downstream // 667883 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 533639 // — /// — /// — /// ENST00000321445 // downstream // 667883 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1953997	tttgatagagttaacc[A/G]ctttcttcttcttgat	A	G	NM_152344 // downstream // 652676 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 548846 // — // — // — // — /// ENST00000321445 // downstream // 652676 // — /	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-1648476	aaattaccaggacttaaggcaggag[G/T]catacgctaaccgtg ctgttttgtg	G	T	BC044587 // downstream // 229370 // Hs.355570 // FLJ30656 // 124801 // hypothetical protein FLJ30656 /// NM_024025 // upstream // 1694308 // Hs.8719 // MGC1136 // 78986 // hypothetical protein MGC1136	FLJ30656	FLJ30656 , rs1590095, hypothetical protein FLJ30656 ,p12
SNP_A-2074840	acatcaagggaaccta[C/G]agtggaattaaatatc	C	G	NM_152344 // downstream // 186277 // Hs.355570 // FLJ30656 // 124801 // Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA. /// ENST00000307948 // upstream // 1015245 // — // — // — // — /// ENST00000321445 // downstream // 186277 // —	FLJ30656	FLJ30656, Homo sapiens hypothetical protein FLJ30656 (FLJ30656), p12
SNP_A-2287535	gatgtttgttacacac[A/G]caattcatttcctaat	A	G	NM_080872 // downstream // 424900 // Hs.238889 // UNC5D // 137970 // Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), mRNA. /// ENST00000287272 // downstream // 424900 // — // — // — // — /// ENST00000355944 // downstream // 247157 // — // —	UNC5D	UNC5D, Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), p12
SNP_A-2283544	gatacttggaatgtcc[A/C]gactacaggaacaaag	A	C	NM_080872 // downstream // 462059 // Hs.238889 // UNC5D // 137970 // Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), mRNA. /// ENST00000287272 // downstream // 462059 // — // — // — // — /// ENST00000355944 // downstream // 209998 // — // —	UNC5D	UNC5D, Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), p12
SNP_A-2249051	ctgtttcaatattaga[C/T]gtgaagaggactgatt	C	T	NM_080872 // downstream // 478531 // Hs.238889 // UNC5D // 137970 // Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), mRNA. /// ENST00000287272 // downstream // 478531 // — // — // — // — /// ENST00000355944 // downstream // 193526 // — // —	UNC5D	UNC5D, Homo sapiens unc-5 homolog D (C. elegans) (UNC5D), p12
SNP_A-1894456	tgccaaccaatccaca[G/T]gaccaccctatttgaa	G	T	ENST00000355944 // upstream // 16136 // — // — // — // — /// ENST00000297703 // upstream // 404914 // — // — // — // —	-	p12
SNP_A-1848131	tatcttattgacatgc[C/T]cattgacagctcttac	C	T	NM_025069 // upstream // 504684 // Hs.288042 // FLJ14299 // 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream // 301795 // — // — // — // — /// ENST00000331569 // upstream // 504684 // — // -	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2195016	catgcttcttgctcca[A/G]cttaatttgtcccta	A	G	NM_025069 // upstream // 480267 // Hs.288042 // FLJ14299 // 80139 // Homo sapiens hypothetical protein FLJ14299 (FLJ14299), mRNA. /// ENST00000297703 // downstream // 326212 // — // — // — // — /// ENST00000331569 // upstream // 480267 // — // -	FLJ14299	FLJ14299, Homo sapiens hypothetical protein FLJ14299 (FLJ14299), p12
SNP_A-2174690	cacagccaaactaagc[A/G]agtagtattatagaat	A	G	NM_207412 // upstream // 172397 // Hs.546586 // FLJ43582 // 389649 // Homo sapiens FLJ43582 protein (FLJ43582), mRNA. /// NM_006283 // upstream // 86204 // Hs.279245 // TACC1 // 6867 // Homo sapiens transforming, acidic coiled-coil containing protein 1 (T	FLJ43582	FLJ43582, Homo sapiens FLJ43582 protein (FLJ43582), p11.23
SNP_A-2035616	aaatgtatacaataaa[C/T]gtgaacccagctgagt	C	T	NM_207412 // upstream // 200863 // Hs.546586 // FLJ43582 // 389649 // Homo sapiens FLJ43582 protein (FLJ43582), mRNA. /// NM_006283 // upstream // 57738 // Hs.279245 // TACC1 // 6867 // Homo sapiens transforming, acidic coiled-coil containing protein 1 (T	FLJ43582	FLJ43582, Homo sapiens FLJ43582 protein (FLJ43582), p11.23
SNP_A-1698435	catcaatttaaatcagcctcagaat[A/T]ggaatagcataatttcca ttgactc	A	T	NM_020130 // downstream // 72992 // Hs.283683 // C8orf4 // 56892 // chromosome 8 open reading frame 4 /// NM_024645 // downstream // 302679 // Hs.50929 // FLJ13842 // 79698 // hypothetical protein FLJ13842	C8orf4	C8orf4 , rs726922, chromosome 8 open reading frame 4 ,p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1925152	ttatcattcctgttac[A/C]gctagcataaaaacca	A	C	NM_020130 // downstream // 47208 // Hs.283683 // C8orf4 // 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 360627 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-2304820	gctcttaacacttttac[A/T]ccatggtttatccaac	A	T	NM_020130 // downstream // 49931 // Hs.283683 // C8orf4 // 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 358104 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1993105	ttcttttctcggtgta[C/T]attcttggtgccttg	C	T	NM_020130 // downstream // 87305 // Hs.283683 // C8orf4 // 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 320730 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1831458	taatgttagccactga[C/T]acaatacatacaattcc	C	T	NM_020130 // downstream // 205816 // Hs.283683 // C8orf4 // 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 202219 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ1	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1665272	cacagggtaacagaagagatatttcc[C/T]aaagagttggtgctttgtttgta	C	T	NM_020130 // downstream // 322719 // Hs.283683 // C8orf4 // 56892 // chromosome 8 open reading frame 4 /// NM_024645 // downstream // 52952 // Hs.50929 // FLJ13842 // 79698 // hypothetical protein FLJ13842	C8orf4	C8orf4, rs988197, chromosome 8 open reading frame 4, p11.21
SNP_A-1730727	ctttgcctctctaaagatccagtgg[A/G]catttttattggtcacagaggcct	A	G	NM_024645 // intron // 0 // Hs.50929 // FLJ13842 // 79698 // hypothetical protein FLJ13842	FLJ13842	FLJ13842, , rs2722425, hypothetical protein FLJ13842,p11.21
SNP_A-2217164	cctctgttgaaagtg[C/G]agagcaacattacagt	C	G	NM_020130 // downstream // 377689 // Hs.283683 // C8orf4 // 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 30346 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-2197416	cattccatatcctcga[C/T]gtcctgctggaacaat	C	T	NM_020130 // downstream // 388593 // Hs.283683 // C8orf4 // 56892 // Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA. /// NM_024645 // downstream // 19442 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13	C8orf4	C8orf4, Homo sapiens chromosome 8 open reading frame 4 (C8orf4), p11.21
SNP_A-1915535	tgtctaccaattaaa[G/T]acaggctaggtagaa	G	T	NM_024645 // intron // 0 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // — // — // — /// ENST00000297737 // intron // 0 // — // — // —	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-2308820	gctttggaattactaq[A/G]actcttggccatgaag	A	G	NM_024645 // intron // 0 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // — // — // — /// ENST00000297737 // intron // 0 // — // — // —	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-1854933	tcaactctcaccacaa[A/T]cctactgctcccatttt	A	T	NM_024645 // intron // 0 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// ENST00000315769 // intron // 0 // — // — // — /// ENST00000297737 // intron // 0 // — // — // —	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-1861495	tcatccagctcctaac[A/G]actgtgggatctgcct	A	G	NM_024645 // upstream // 275082 // Hs.491548 // FLJ13842 // 79698 // Homo sapiens hypothetical protein FLJ13842 (FLJ13842), mRNA. /// NM_003012 // downstream // 89058 // Hs.213424 // SFRP1 // 6422 // Homo sapiens secreted frizzled-related protein 1 (SFRP1	FLJ13842	FLJ13842, Homo sapiens hypothetical protein FLJ13842 (FLJ13842), p11.21
SNP_A-2049024	aagccttgcgctttaa[A/G]taacagggagagcttcc	A	G	NM_003012 // intron // 0 // Hs.213424 // SFRP1 // 6422 // Homo sapiens secreted frizzled-related protein 1 (SFRP1), mRNA. /// ENST00000220772 // intron // 0 // — // — // —	SFRP1	SFRP1, Homo sapiens secreted frizzled-related protein 1 (SFRP1), p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1993125	ctaatctagtctttg[C/T]aggaaatgctaagtta	C	T	NM_003012 // upstream // 144230 // Hs.213424 // SFRP1 // 6422 // Homo sapiens secreted frizzled-related protein 1 (SFRP1), mRNA. /// NM_016099 // upstream // 36859 // Hs.7953 // GOLGA7 // 51125 // Homo sapiens golgi autoantigen, golgin subfamily a, 7 (GOL	SFRP1	SFRP1, Homo sapiens secreted frizzled-related protein 1 (SFRP1), p11.21
SNP_A-2293937	gcaggaaaggaagtggi[A/C]aagtcctctgatatca	A	C	NM_016099 // downstream // 6753 // Hs.7953 // GOLGA7 // 51125 // Homo sapiens golgi autoantigen, golgin subfamily a, 7 (GOLGA7), transcript variant 1, mRNA. /// NM_001002296 // downstream // 6753 // Hs.7953 // GOLGA7 // 51125 // Homo sapiens golgi autoant	GOLGA7	GOLGA7, Homo sapiens golgi autoantigen, golgin subfamily a, 7 (GOLGA7), transcript variant 1, p11.21
SNP_A-2245267	ctggctctgggtttc[A/G]agcaagtcacattctg	A	G	NM_020475 // intron // 0 // Hs.491558 // ANK1 // 286 // Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 4, mRNA. /// NM_020476 // intron // 0 // Hs.491558 // ANK1 // 286 // Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1.	ANK1	ANK1, Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 4, p11.21
SNP_A-1993130	gctgcagacctgcaaaa[C/T]gtaatataittctgttg	C	T	NM_020475 // intron // 0 // Hs.491558 // ANK1 // 286 // Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 4, mRNA. /// NM_020476 // intron // 0 // Hs.491558 // ANK1 // 286 // Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1.	ANK1	ANK1, Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 4, p11.21
SNP_A-2304316	gctccttcacacctaa[A/G]attaaaagccctagc	A	G	NM_020475 // upstream // 53930 // Hs.491558 // ANK1 // 286 // Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 4, mRNA. /// NM_020476 // upstream // 53930 // Hs.491558 // ANK1 // 286 // Homo sapiens ankyrin 1, erythrocytic (ANK1), transcrip	ANK1	ANK1, Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 4, p11.21
SNP_A-2260856	gaaactgaggttacac[A/G]gtcggatacctgtcag	A	G	NM_001556 // intron // 0 // Hs.413513 // IKBKB // 3551 // Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB), mRNA. /// ENST00000342222 // intron // 0 // — // — // — // —	IKBKB	IKBKB, Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB), p11.21
SNP_A-2256148	ctttactgactatttc[A/G]cttttgccctggaaa	A	G	NM_006749 // upstream // 88472 // Hs.491611 // SLC20A2 // 6575 // Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA. /// NM_138436 // downstream // 77425 // Hs.546472 // LOC114926 // 114926 // Homo sapiens hypothetica	SLC20A2	SLC20A2, Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), p11.21
SNP_A-1871615	tctaagtaggtgtatt[C/G]aacaagttttggaagg	C	G	NM_001002920 // downstream // 4462579 // Hs.531579 // POTE8 // 340441 // Homo sapiens protein expressed in prostate, ovary, testis, and placenta 8 (POTE8), mRNA. /// ENST00000354247 // downstream // 44562289 // — // — // — // — /// ENST00000344403	POTE8	POTE8, Homo sapiens protein expressed in prostate, ovary, testis, and placenta 8 (POTE8), q11.1
SNP_A-1741725	ttcataagttctaacaaacctctga[C/T]agaagctgtttccagccc tttcatc	C	T	D63480 // intron // 0 // Hs.381058 // KIAA0146 // 23514 // KIAA0146 protein	KIAA0146	KIAA0146 . rs10504060, KIAA0146 protein,q11.21
SNP_A-2246716	ctgtacattgatctga[A/C]cttcattaaccttgct	A	C	NM_003350 // downstream // 196692 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 331817 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365),	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1917861	ttaaaaggcacttggc[A/G]aaaaattacaaaaata	A	G	NM_003350 // downstream // 196775 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 331734 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365),	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-2136070	atcaagtaataaataaa[C/T]gtgcaaccagctgccc	C	T	NM_003350 // downstream // 247280 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 281229 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365),	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2197371	cattcatttcttcaac[A/G]agtatttagctcctac	A	G	NM_003350 // downstream // 332929 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 195580 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365),	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1993153	ccaggtgtccagccac[C/T]cacttgtctcaggtg	C	T	NM_003350 // downstream // 383987 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 144522 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365),	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1800296	gtacggaaaagtaga[C/T]gtcaatcaggtggaaa	C	T	NM_003350 // downstream // 407824 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 120685 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365),	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1993154	ctctgaggttggttct[G/T]aatgctcacaaagcta	G	T	NM_003350 // downstream // 449808 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 78701 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), m	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1713532	gggtcctctatcaaatggcaactga[A/G]taataggaccttcctcc aactgttg	A	G	NM_003350 // downstream // 589584 // Hs.371278 // UBE2V2 // 7336 // ubiquitin-conjugating enzyme E2 variant 2 /// NM_024593 // downstream // 71935 // Hs.23245 // FLJ11767 // 79645 // hypothetical protein FLJ11767	UBE2V2	UBE2V2, rs10504066, ubiquitin-conjugating enzyme E2 variant 2 ,q11.21
SNP_A-2083022	acgtggtgtgcccaac[A/C]aggaaccacatgggc	A	C	NM_003350 // downstream // 478545 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 49964 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), m	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-2146012	atgcctcctatttttat[C/T]gcgctggctgcaccca	C	T	NM_003350 // downstream // 517423 // Hs.491695 // UBE2V2 // 7336 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA. /// NM_207504 // upstream // 11086 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), m	UBE2V2	UBE2V2, Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), q11.21
SNP_A-1916666	tgtttatttctcagcc[A/G]ctaatggattgtttga	A	G	NM_207504 // downstream // 7701 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 121087 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-1802407	gtatcaaagcacaaa[A/C]ttatgacttcacaaga	A	C	NM_207504 // downstream // 20973 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 107815 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. /	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-2013377	ttcccaaccctgctca[G/T]atgctatggaacttag	G	T	NM_207504 // downstream // 22793 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 105995 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. /	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-1811087	gtgccatggattctga[C/G]aaagcctccatctccc	C	G	NM_207504 // downstream // 29412 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 99376 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2222783	cgatgtttagatagaa[G/T]aggaacttagaaaatt	G	T	NM_207504 // downstream // 44780 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 84008 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-2295823	gcatggcacggactga[C/T]aggttacatgggaaac	C	T	NM_207504 // downstream // 44813 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 83975 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-2299425	gccctgtctcactagc[A/G]gattgaccatgagtac	A	G	NM_207504 // downstream // 48104 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 80684 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-2066375	aatttgcagaaagaa[A/T]catgcagaagtttt	A	T	NM_207504 // downstream // 48190 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 80598 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-2195398	catgggaatgctgcaa[A/G]gttaatggaagagagg	A	G	NM_207504 // downstream // 59777 // Hs.255374 // FLJ46365 // 401459 // Homo sapiens FLJ46365 protein (FLJ46365), mRNA. /// NM_024593 // downstream // 69011 // Hs.23245 // FLJ11767 // 79645 // Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA. //	FLJ46365	FLJ46365, Homo sapiens FLJ46365 protein (FLJ46365), q11.21
SNP_A-2095583	agacaatgaggtgcac[A/G]gagttaagtaggagca	A	G	NM_003068 // upstream // 29631 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 29631 // — // — // — /// ENST00000303202 // upstream // 121294 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-2270766	gacaggagcagcccac[A/G]agtcatatggccttag	A	G	NM_003068 // upstream // 46987 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 46987 // — // — // — /// ENST00000303202 // upstream // 103938 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-2166469	caaatgcaataaacac[A/G]cattctatccacact	A	G	NM_003068 // upstream // 47999 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 47999 // — // — // — /// ENST00000303202 // upstream // 102926 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-1791095	gggggtgagtcattaac[C/T]gcggtcctggtgctgg	C	T	NM_003068 // upstream // 54682 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 54882 // — // — // — /// ENST00000303202 // upstream // 96043 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-1993161	tccccacgataaaagc[A/G]cacacaaacagcaggt	A	G	NM_003068 // upstream // 63518 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 63518 // — // — // — /// ENST00000303202 // upstream // 87407 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-1993164	tcattagttagaagt[A/T]acctagctgaagttt	A	T	NM_003068 // upstream // 116822 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 116822 // — // — // — /// ENST00000303202 // upstream // 34103 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-2114221	agggaactggccatta[C/T]gaccagtggataggt	C	T	NM_003068 // upstream // 141758 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 141758 // — // — // — /// ENST00000303202 // upstream // 9167 // — // — // — //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1993166	tgccactccctattga[A/C]gtccgagttgatttta	A	C	NM_003068 // upstream // 144436 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 144436 // --- // --- // --- /// ENST00000303202 // upstream // 6489 // --- // --- // --- //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-2075969	acattagatcctagat[A/C]gtattcatcccacata	A	C	NM_003068 // upstream // 149550 // Hs.360174 // SNAI2 // 6591 // Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA. /// ENST00000020945 // upstream // 149550 // --- // --- // --- /// ENST00000303202 // upstream // 1375 // --- // --- // --- //	SNAI2	SNAI2, Homo sapiens snail homolog 2 (Drosophila) (SNAI2), q11.21
SNP_A-1993169	atgaatacaggagata[A/C]gtacatgaaggtgctc	A	C	ENST00000303202 // downstream // 35439 // --- // --- // --- /// ENST00000342478 // downstream // 629197 // --- // --- // ---	-	q11.21
SNP_A-1993171	gattgtacttgattat[C/T]gtgcaggaatttagct	C	T	ENST00000303202 // downstream // 36783 // --- // --- // --- /// ENST00000342478 // downstream // 627853 // --- // --- // ---	-	q11.21
SNP_A-1886043	tgaccaaggaagaca[C/G]aaatggctatttaaat	C	G	ENST00000303202 // downstream // 70992 // --- // --- // --- /// ENST00000342478 // downstream // 593644 // --- // --- // ---	-	q11.21
SNP_A-1849784	tatgtacaaagcagga[A/G]gaccataatatctct	A	G	ENST00000303202 // downstream // 211801 // --- // --- // --- /// ENST00000342478 // downstream // 452835 // --- // --- // ---	-	q11.21
SNP_A-2074963	acatcatcattaaacat[A/G]gaagagatgtggaatc	A	G	ENST00000303202 // downstream // 471955 // --- // --- // --- /// ENST00000342478 // downstream // 192681 // --- // --- // ---	-	q11.21
SNP_A-2053268	aagtgaacaaaaaat[A/G]agccaaagacaatgac	A	G	ENST00000303202 // downstream // 520094 // --- // --- // --- /// ENST00000342478 // downstream // 144542 // --- // --- // ---	-	q11.21
SNP_A-1804142	gtcacatgaccatgta[G/T]tacaatgtatgcatgc	G	T	ENST00000303202 // downstream // 522736 // --- // --- // --- /// ENST00000342478 // downstream // 141900 // --- // --- // ---	-	q11.21
SNP_A-1809235	gtgaccttgaaaaatg[A/G]aaggaggacatcttcc	A	G	ENST00000303202 // downstream // 523083 // --- // --- // --- /// ENST00000342478 // downstream // 141553 // --- // --- // ---	-	q11.21
SNP_A-1926140	ttattaaacatgatact[A/C]caaagtacagtgaaaa	A	C	ENST00000303202 // downstream // 530193 // --- // --- // --- /// ENST00000342478 // downstream // 134443 // --- // --- // ---	-	q11.21
SNP_A-2055569	aataatcagttgaaaa[C/T]gaaaatgtaagatatc	C	T	ENST00000303202 // downstream // 531869 // --- // --- // --- /// ENST00000342478 // downstream // 132767 // --- // --- // ---	-	q11.21
SNP_A-2117768	aggttgacttcacttc[A/G]ccatatattgatatcc	A	G	ENST00000303202 // downstream // 618571 // --- // --- // --- /// ENST00000342478 // downstream // 46065 // --- // --- // ---	-	q11.21
SNP_A-2049580	aagcttacttcttttgc[A/G]aactactcattcccag	A	G	ENST00000303202 // downstream // 641802 // --- // --- // --- /// ENST00000342478 // downstream // 22834 // --- // --- // ---	-	q11.21
SNP_A-1840615	tagcctcaatcaaata[A/C]cagcctctaagtgag	A	C	NM_018967 // upstream // 534532 // Hs.157284 // SNTG1 // 54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 118404 // --- // --- // --- /// ENST00000276467 // upstream // 534532 // --- // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-1855935	tcaatgtgataaagag[A/T]atctacgaaaacatac	A	T	NM_018967 // upstream // 362763 // Hs.157284 // SNTG1 // 54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 290173 // --- // --- // --- /// ENST00000276467 // upstream // 362763 // --- // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2057710	aatatgtaccttggag[G/T]caactatttaagcatc	G	T	NM_018967 // upstream // 14050 // Hs.157284 // SNTG1 // 54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000342478 // upstream // 638886 // --- // --- // --- /// ENST00000276467 // upstream // 14050 // --- // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-2303970	gctcatttgtaaactt[A/G]caaccaactatgtgcc	A	G	NM_018967 // intron // 0 // Hs.157284 // SNTG1 // 54212 // Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA. /// ENST00000276467 // intron // 0 // --- // --- // --- /// ENST00000338349 // intron // 0 // --- // --- // ---	SNTG1	SNTG1, Homo sapiens syntrophin, gamma 1 (SNTG1), q11.21
SNP_A-1721718	caatgcagttgaaagcagtgataaa[C/T]gcaatgggacaataa tgtaggctag	C	T	NM_014682 // intron // 0 // Hs.151449 // ST18 // 9705 // suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ST18	ST18 , rs10504137, suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein),q11.23
SNP_A-2247246	ctgtcattgataatttc[A/G]ctttcactctcaggtg	A	G	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18). mRNA. /// ENST00000276480 // intron // 0 // --- // --- // ---	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2160314	atttcagattatagaa[C/G]agcgtgcgggtttcga	C	G	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1878077	tctgtagagagccttg[A/C]acagtgtctgagattt	A	C	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2023863	aaaagaacacaacaga[C/T]atttctcagataacaa	C	T	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2061184	aatgcagcgagaaaga[C/T]atcatgaacctcaggc	C	T	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1890483	tgatctgaatgtcaaa[C/T]gatttcttctaatga	C	T	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2299009	gcccctaaatttaaa[C/G]aggcaaatggtctccc	C	G	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2260364	gaaacaaactctcata[C/T]ggatttccactaagga	C	T	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1925631	ttatgagacgactcca[A/G]gaatctttgctttgg	A	G	NM_014682 // intron // 0 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// ENST00000276480 // intron // 0 // — // — // — // —	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1884733	tgaatatgggaaacaa[C/T]atgtagtagctttatt	C	T	NM_014682 // upstream // 11403 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// NM_207413 // downstream // 113002 // Hs.527111 // UNQ9433 // 389658 // Homo sapiens RPL	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-2277879	gagcatttgaacactg[A/C]aagaattgctttgaac	A	C	NM_014682 // upstream // 15956 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// NM_207413 // downstream // 108449 // Hs.527111 // UNQ9433 // 389658 // Homo sapiens RPL	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1811919	gtggaaatgctgtaga[A/G]ggtaagtactgccaca	A	G	NM_014682 // upstream // 54181 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// NM_207413 // downstream // 70224 // Hs.527111 // UNQ9433 // 389658 // Homo sapiens RPLK	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23
SNP_A-1804503	gtcagagcacaacaca[A/G]gctatttggtttcctt	A	G	NM_014682 // upstream // 54356 // Hs.147170 // ST18 // 9705 // Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), mRNA. /// NM_207413 // downstream // 70049 // Hs.527111 // UNQ9433 // 389658 // Homo sapiens RPLK	ST18	ST18, Homo sapiens suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein) (ST18), q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1860980	tcatagactaaaacaa[C/G]agaatccigtaaaaag	C	G	NM_014781 // upstream // 80695 // Hs.196102 // RB1CC1 // 9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 143306 // Hs.248117 // GPR7 // 2831 // Homo sapiens G protein-coupled receptor 7 (GPR7), mRNA. /// ENST0	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-1993289	ggtctttctcactcaa[A/C]aatctatgcttctgt	A	C	NM_014781 // upstream // 118846 // Hs.196102 // RB1CC1 // 9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 105155 // Hs.248117 // GPR7 // 2831 // Homo sapiens G protein-coupled receptor 7 (GPR7), mRNA. /// ENST	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-1993290	ggtagaactcactacc[A/G]aggatcgttgaaacct	A	G	NM_014781 // upstream // 119016 // Hs.196102 // RB1CC1 // 9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 104985 // Hs.248117 // GPR7 // 2831 // Homo sapiens G protein-coupled receptor 7 (GPR7), mRNA. /// ENST	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-1993293	ataggaacagataaga[A/G]caccttaaagtcattt	A	G	NM_014781 // upstream // 182464 // Hs.196102 // RB1CC1 // 9821 // Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), mRNA. /// NM_005285 // upstream // 41537 // Hs.248117 // GPR7 // 2831 // Homo sapiens G protein-coupled receptor 7 (GPR7), mRNA. /// ENST0	RB1CC1	RB1CC1, Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), q11.23
SNP_A-1853157	tatttgtattctccca[A/G]atgaatgtaaaaaggt	A	G	ENST00000359239 // intron // 0 // — // — // — // ENST00000359448 // intron // 0 // — // — // —	-	q11.23
SNP_A-2050022	aaggaataccattagc[A/G]ctcttgtgaagttta	A	G	ENST00000359239 // intron // 0 // — // — // — // ENST00000359448 // intron // 0 // — // — // —	-	q11.23
SNP_A-2069606	acacacacattaacaa[C/G]actcatgtcaacacat	C	G	NM_000912 // upstream // 183631 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 280513 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 sub	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2070917	acactcatgggcttaa[C/T]gtcacacggaagtcaa	C	T	NM_000912 // upstream // 319803 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 144341 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 sub	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2021122	aaaaaaaaataaagctac[C/T]agatgtgtctttcggc	C	T	NM_000912 // upstream // 332890 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 131254 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 sub	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2082768	acggtgtcaaggcaat[C/G]agggagaaccacaac	C	G	NM_000912 // upstream // 348464 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 115680 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 sub	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2148180	atgggagagtgtgttg[C/T]agttaacggctgcagg	C	T	NM_000912 // upstream // 350844 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 113300 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 sub	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-1828966	taaggccaggaggact[A/G]aaataagcacattaga	A	G	NM_000912 // upstream // 357163 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 106981 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 sub	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2013408	tcagacaacgagaaac[G/T]gctacattaaagtaca	G	T	NM_000912 // upstream // 364788 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 99356 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 subu	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2111641	aggagtgacactgtga[A/G]aagaagtcctgagaga	A	G	NM_000912 // upstream // 376559 // Hs.89455 // OPRK1 // 4986 // Homo sapiens opioid receptor, kappa 1 (OPRK1), mRNA. /// NM_213619 // downstream // 87585 // Hs.491737 // ATP6V1H // 51606 // Homo sapiens ATPase, H+ transporting, lysosomal 50/57kDa, V1 subu	OPRK1	OPRK1, Homo sapiens opioid receptor, kappa 1 (OPRK1), q11.23
SNP_A-2013411	gcatatactgttcca[C/T]aggcatctcaaaatcc	C	T	NM_006756 // intron // 0 // Hs.491745 // TCEA1 // 6917 // Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), transcript variant 1, mRNA. /// NM_201437 // intron // 0 // Hs.491745 // TCEA1 // 6917 // Homo sapiens transcription elongation fact	TCEA1	TCEA1, Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), transcript variant 1, q11.23
SNP_A-1937129	ttcttttgaggtgat[C/G]aacatttttggaaaac	C	G	NM_006756 // upstream // 2823 // Hs.491745 // TCEA1 // 6917 // Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), transcript variant 1, mRNA. /// NM_201437 // upstream // 2823 // Hs.491745 // TCEA1 // 6917 // Homo sapiens transcription elong	TCEA1	TCEA1, Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), transcript variant 1, q11.23
SNP_A-2193907	catgaactaggtaaaa[C/T]aggccagacacaaaag	C	T	NM_014175 // downstream // 8847 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 301190 // Hs.98367 // SOX17 // 64321 // Homo sapie	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-1874519	tctcccgtgcaagac[A/G]gcaaatttctacctct	A	G	NM_014175 // downstream // 17759 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 292278 // Hs.98367 // SOX17 // 64321 // Homo sapi	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-1909326	tgtatgtgtctatgta[C/T]gggttctctcacacac	C	T	NM_014175 // downstream // 28726 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 281311 // Hs.98367 // SOX17 // 64321 // Homo sapi	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-2270422	gacagaaaataattgc[C/T]gaatttgacagtaagg	C	T	NM_014175 // downstream // 30769 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 279268 // Hs.98367 // SOX17 // 64321 // Homo sapi	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-1902075	tggcatgcttgaagta[A/T]cagattttgaatgaaa	A	T	NM_014175 // downstream // 31103 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 278934 // Hs.98367 // SOX17 // 64321 // Homo sapi	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-2185764	caggatagaccacata[C/T]aggcccacagaacaa	C	T	NM_014175 // downstream // 51012 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 259025 // Hs.98367 // SOX17 // 64321 // Homo sapi	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23
SNP_A-2120396	agtcatgtggatatcc[A/G]gctcctaacaaccact	A	G	NM_014175 // downstream // 281688 // Hs.18349 // MRPL15 // 29088 // Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, mRNA. /// NM_022454 // upstream // 28349 // Hs.98367 // SOX17 // 64321 // Homo sapi	MRPL15	MRPL15, Homo sapiens mitochondrial ribosomal protein L15 (MRPL15), nuclear gene encoding mitochondrial protein, q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116061	aggtaaaataatgca[A/T]gtgtgattcaaaagca	A	T	NM_006269 // downstream // 376937 // Hs.251687 // RP1 // 6101 // Homo sapiens retinitis pigmentosa 1 (autosomal dominant) (RP1), mRNA. /// ENST00000220676 // downstream // 376937 // --- // --- // --- /// ENST00000327381 // upstream // 95154 // ---	RP1	RP1, Homo sapiens retinitis pigmentosa 1 (autosomal dominant) (RP1), q12.1
SNP_A-1889515	tgagtttaaacagtca[C/T]ccaagacagactcagc	C	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1921685	ttacgatttgcagaa[A/T]catttaatttttgtta	A	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1643964	gtaatcttatagaaactatagcac[A/C]aaagttaaacattaaat gtgaaaat	A	C	AB067476 // intron // 0 // KIAA1889 // 114786 // KIAA1889 protein	KIAA1889	KIAA1889 , rs10504191, KIAA1889 protein,q12.1
SNP_A-1677358	aaatgatttttcaaacagtgggataa[A/C]agtattgagagaaaa gttgcattg	A	C	AB067476 // intron // 0 // Hs.411705 // KIAA1889 // 114786 // KIAA1889 protein	KIAA1889	KIAA1889 , rs10504192, KIAA1889 protein,q12.1
SNP_A-1876114	tctgacactaagagga[A/G]acatccaggcatcgca	A	G	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1820521	gtttattataacgcc[G/T]cagacttgggaatag	G	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1846689	tatcaaaacatataaga[C/T]agatagtgtgtacaac	C	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-2024891	aaaagttgtaactatt[A/T]aaccagaaaacctca	A	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1913267	tgtggagctaaagga[C/G]caaaaattgggaaagt	C	G	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1993350	gtgacctattgtgaga[C/T]ggccccctgggactgat	C	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1993351	tattaaagaagccaag[A/T]ctaagttctcaataaa	A	T	ENST00000327381 // intron // 0 // --- // --- // ---	-	q12.1
SNP_A-1993361	tgttgcagctgtccaa[C/T]ctctctggcattctag	C	T	NM_002350 // intron // 0 // Hs.491767 // LYN // 4067 // Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA. /// ENST00000276497 // intron // 0 // --- // --- // --- /// ENST00000359619 // intron // 0 // --- // --- // -	LYN	LYN, Homo sapiens v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), q12.1
SNP_A-1675319	caagccctagtctgcttattaaatc[A/G]gaattccagggggcagc ggcttgcct	A	G	AK090988 // downstream // 448692 // Hs.378857 // FLJ20421 // 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 65161 // Hs.339831 // PENK // 5179 // proenkephalin	FLJ20421	FLJ20421 , rs2670028, hypothetical protein FLJ20421 ,q12.1
SNP_A-2258228	cttttagcttcacgac[A/C]actgtcatctgcagag	A	C	NM_138969 // upstream // 80665 // Hs.170673 // RDHE2 // 195814 // Homo sapiens retinal short chain dehydrogenase reductase (RDH-E2), mRNA. /// NM_006211 // downstream // 39611 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// EN	RDHE2	RDHE2, Homo sapiens retinal short chain dehydrogenase reductase (RDH-E2), q12.1
SNP_A-1789233	gggcatgacatttggg[A/G]agcccactgtccagct	A	G	NM_138969 // upstream // 81422 // Hs.170673 // RDHE2 // 195814 // Homo sapiens retinal short chain dehydrogenase reductase (RDH-E2), mRNA. /// NM_006211 // downstream // 38854 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// EN	RDHE2	RDHE2, Homo sapiens retinal short chain dehydrogenase reductase (RDH-E2), q12.1
SNP_A-1806329	gtccttcccagaagcc[A/G]cttattcattgctgca	A	G	NM_006211 // upstream // 25771 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 25771 // --- // --- // --- /// ENST00000355927 // downstream // 489655 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1817893	gttcgattgaaattga[C/T]cattgtgaatacagtg	C	T	NM_006211 // upstream // 31797 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 31797 // --- // --- // --- /// ENST00000355927 // downstream // 483629 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1801776	gtagtgataatagccc[A/G]ataagttattattctg	A	G	NM_006211 // upstream // 34697 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 34697 // --- // --- // --- /// ENST00000355927 // downstream // 480729 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2313013	ggacttttagaaatgc[A/G]agaatatgaggaatat	A	G	NM_006211 // upstream // 52119 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 52119 // --- // --- // --- /// ENST00000355927 // downstream // 463307 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2230389	ctatcaaaaaacccta[C/T]ctcaactggacagatt	C	T	NM_006211 // upstream // 56427 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 56427 // --- // --- // --- /// ENST00000355927 // downstream // 456999 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1993369	tagatatcccaaggtc[C/T]gaattctaatgtaat	C	T	NM_006211 // upstream // 59003 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 59003 // — // — // — /// ENST00000355927 // downstream // 456423 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1993372	agccagagatgtagca[A/G]ggaagcaaaagtgcag	A	G	NM_006211 // upstream // 59743 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 59743 // — // — // — /// ENST00000355927 // downstream // 455683 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2248395	ctgtgtggcgttcatg[C/T]atctcagaggtgtag	C	T	NM_006211 // upstream // 67058 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 67058 // — // — // — /// ENST00000355927 // downstream // 448368 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1884828	tgaatcctaagttcta[A/G]ccaggacaatttcta	A	G	NM_006211 // upstream // 70771 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 70771 // — // — // — /// ENST00000355927 // downstream // 444655 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2311192	ggaagtgtgttgctaa[A/G]aatgctaaaaatttaa	A	G	NM_006211 // upstream // 72731 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 72731 // — // — // — /// ENST00000355927 // downstream // 442695 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2210742	cccctgcctcgggaca[A/C]cagaggaccagtcctc	A	C	NM_006211 // upstream // 157374 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 157374 // — // — // — // — /// ENST00000355927 // downstream // 358052 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1757013	acacatcatgatcacctagaatcca[C/T]agtttacaagccctttg gtgctgta	C	T	AK090988 // downstream // 195828 // Hs.378857 // FLJ20421 // 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 318025 // Hs.339831 // PENK // 5179 // proenkephalin	FLJ20421	FLJ20421 , rs353753, hypothetical protein FLJ20421 ,q12.1
SNP_A-2065200	aattggatatccatac[A/G]gaagaaagctagcatc	A	G	NM_006211 // upstream // 217262 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 217262 // — // — // — // — /// ENST00000355927 // downstream // 298164 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2230895	ctatgcttggccctaa[A/G]tatatcacccatcggc	A	G	NM_006211 // upstream // 329897 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 329897 // — // — // — // — /// ENST00000355927 // downstream // 185529 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2151208	atgttaacaatggtta[C/T]cgctggagaatggact	C	T	NM_006211 // upstream // 332570 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 332570 // — // — // — // — /// ENST00000355927 // downstream // 182856 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1652354	tggacactgtgggtgccatttggaca[A/G]gattcaatttatttaaat ttcac	A	G	AK090988 // downstream // 47502 // Hs.378857 // FLJ20421 // 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 466351 // Hs.339831 // PENK // 5179 // proenkephalin	FLJ20421	FLJ20421 , rs1396122, hypothetical protein FLJ20421 ,q12.1
SNP_A-1745638	ttccatcttcccttcaaatgtagcc[G/T]caatttctccagaaagtgt gtaggt	G	T	AK090988 // downstream // 46545 // Hs.378857 // FLJ20421 // 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 467308 // Hs.339831 // PENK // 5179 // proenkephalin	FLJ20421	FLJ20421 , rs6474087, hypothetical protein FLJ20421 ,q12.1
SNP_A-1662414	aggactcccgccagagctgtgggaa[C/T]cttgcttcacaatagg aaatctggt	C	T	AK090988 // downstream // 28017 // Hs.378857 // FLJ20421 // 54928 // hypothetical protein FLJ20421 /// NM_006211 // upstream // 485836 // Hs.339831 // PENK // 5179 // proenkephalin	FLJ20421	FLJ20421 , rs906538, hypothetical protein FLJ20421 ,q12.1
SNP_A-2186316	caggctgagaacatcd[A/G]aggaatagcaaggagc	A	G	NM_006211 // upstream // 399030 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 399030 // — // — // — // — /// ENST00000355927 // downstream // 116396 // — // — // — // —	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1854251	tcaaaggaaaccaaatc[A/G]aaatgcaaatcagcta	A	G	NM_006211 // upstream // 399180 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 399180 // --- // --- // --- /// ENST00000355927 // downstream // 116246 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2233785	ctcatccagaatctaa[C/G]cacatttgctctgtt	C	G	NM_006211 // upstream // 405546 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 405546 // --- // --- // --- /// ENST00000355927 // downstream // 109880 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1879575	tcttcaagcaatctta[A/G]cagaatttcagtcat	A	G	NM_006211 // upstream // 405982 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 405982 // --- // --- // --- /// ENST00000355927 // downstream // 109444 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2298744	gcccagtctccatcaa[C/G]tgttgaatctcccaat	C	G	NM_006211 // upstream // 406103 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 406103 // --- // --- // --- /// ENST00000355927 // downstream // 109323 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2110814	aggactatgagaaaga[C/T]agatgctgcggaggcc	C	T	NM_006211 // upstream // 440595 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 440595 // --- // --- // --- /// ENST00000355927 // downstream // 74831 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2274033	gacttactaagcaggа[C/T]tccttgccttctaga	C	T	NM_006211 // upstream // 484667 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 484667 // --- // --- // --- /// ENST00000355927 // downstream // 30759 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1956507	tttgttgtctgacaga[C/T]cttgcaatttaaata	C	T	NM_006211 // upstream // 485317 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 485317 // --- // --- // --- /// ENST00000355927 // downstream // 30109 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1993387	aattctaaactaagac[A/G]catacatttgagaggg	A	G	NM_006211 // upstream // 486679 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 486679 // --- // --- // --- /// ENST00000355927 // downstream // 28747 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-2149534	atgtagctctttatc[C/T]ctgtacctatcttatt	C	T	NM_006211 // upstream // 494445 // Hs.339831 // PENK // 5179 // Homo sapiens proenkephalin (PENK), mRNA. /// ENST00000314922 // upstream // 494445 // --- // --- // --- /// ENST00000355927 // downstream // 20981 // --- // --- // ---	PENK	PENK, Homo sapiens proenkephalin (PENK), q12.1
SNP_A-1954341	tttgcagctacatacaa[C/T]agggtcagagaatgtt	C	T	NM_147189 // upstream // 773098 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 17733 // --- // --- // --- /// ENST00000360707 // upstream // 692096 // --- // ---	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2293240	gcagagctggacaagt[A/G]aaaaagcagtgcagca	A	G	NM_147189 // upstream // 762055 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 28776 // --- // --- // --- /// ENST00000360707 // upstream // 681053 // --- // ---	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1878274	tctgtccagcaactca[A/T]ccatcaggtttgaaac	A	T	NM_147189 // upstream // 740852 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 49979 // --- // --- // --- /// ENST00000360707 // upstream // 659850 // --- // ---	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1993403	agtggctggatataag[A/T]ctctccccactgagag	A	T	NM_147189 // upstream // 698005 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 92826 // --- // --- // --- /// ENST00000360707 // upstream // 617003 // --- // ---	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251618	ctcagctcaacacaa[C/T]ggtttacaatctagg	C	T	NM_147189 // upstream // 690043 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 100788 // — // — // — // — /// ENST00000360707 // upstream // 609041 // — // -	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2037065	aacaaaaagttctagc[A/G]atagctgacagaatca	A	G	NM_147189 // upstream // 679358 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 111473 // — // — // — // — /// ENST00000360707 // upstream // 598356 // — // -	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2141903	atcttgtcgctcccca[A/G]catatccaaagcagc	A	G	NM_147189 // upstream // 613818 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 177013 // — // — // — // — /// ENST00000360707 // upstream // 532816 // — // -	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2225938	ctaaattaacattaaa[C/T]gtgcttgggaaagag	C	T	NM_147189 // upstream // 469722 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 321109 // — // — // — // — /// ENST00000360707 // upstream // 388720 // — // -	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2101083	agatcactcagtaaga[C/G]ctatggcttttggcca	C	G	NM_147189 // upstream // 426552 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 364279 // — // — // — // — /// ENST00000360707 // upstream // 345550 // — // -	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2305214	gctgactttaaacata[A/G]agcaggcagcatttt	A	G	NM_147189 // upstream // 227665 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000314054 // downstream // 563166 // — // — // — // — /// ENST00000360707 // upstream // 146663 // — // -	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1676656	gaagtcaccttttattggcacttta[A/G]cgttacgcataaatagga ccactgt	A	G	NM_147189 // intron // 0 // Hs.34054 // MGC39325 // 90362 // hypothetical protein MGC39325	MGC39325	MGC39325, rs10504241, hypothetical protein MGC39325,q12.1
SNP_A-1753379	gaaatgtatatgcctattcaaaaag[C/T]aaattgctacagctgct gcttctaac	C	T	NM_147189 // intron // 0 // Hs.34054 // MGC39325 // 90362 // hypothetical protein MGC39325	MGC39325	MGC39325, rs10504240, hypothetical protein MGC39325,q12.1
SNP_A-2220907	ccttgctcatctccac[A/G]aaaacatttgcccccag	A	G	ENST00000360707 // intron // 0 // — // — // —	-	q12.1
SNP_A-2225295	cgttgtttacacatca[A/G]cgtctaagaatattcc	A	G	NM_147189 // intron // 0 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 // intron // 0 // — // — // — // — /// ENST00000305595 // intron // 0 // — // — // —	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-1811575	gtgctgaatgaatata[A/T]gtctagaaagcctaat	A	T	NM_147189 // downstream // 35391 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 // downstream // 36475 // — // — // — // — /// ENST00000305595 // downstream // 35391 // — //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2267165	gaataattacaagatc[A/G]aaatccttgaggaggt	A	G	NM_147189 // downstream // 41654 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 // downstream // 42738 // — // — // — // — /// ENST00000305595 // downstream // 41654 // — //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2250338	cttagataacctgaca[A/G]gcagtcacatctctc	A	G	NM_147189 // downstream // 73795 // Hs.154652 // MGC39325 // 90362 // Homo sapiens hypothetical protein MGC39325 (MGC39325), mRNA. /// ENST00000360707 // downstream // 74879 // — // — // — // — /// ENST00000305595 // downstream // 73795 // — //	MGC39325	MGC39325, Homo sapiens hypothetical protein MGC39325 (MGC39325), q12.1
SNP_A-2290273	gcaacaatatgtggac[A/G]agtagaggtaacttt	A	G	ENST00000331398 // intron // 0 // — // — // —	-	q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2121703	agtgacactgacctaf[C/T]gcctcaaggctaacta	C	T	NM_005625 // intron // 0 // Hs.200804 // SDCBP // 6386 // Homo sapiens syndecan binding protein (syntenin) (SDCBP), mRNA. /// ENST00000260130 // intron // 0 // — // — // —	SDCBP	SDCBP, Homo sapiens syndecan binding protein (syntenin) (SDCBP), q12.1
SNP_A-2251265	cttcaaatataaggaa[A/C]gttgtcataaactgct	A	C	NM_003580 // upstream // 110556 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 110556 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2034370	aaatctaactgcattaf[A/T]cctccatccatggtcc	A	T	NM_003580 // upstream // 111015 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 111015 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2047254	aagatatcacctaac[C/T]ctaagtcataggctaa	C	T	NM_003580 // upstream // 126043 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 126043 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2073422	acaggtgaggcattag[C/T]atggaccccctgggatc	C	T	NM_003580 // upstream // 127934 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 127934 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2041627	aacgccactcttctct[A/G]aaaacaattggtatca	A	G	NM_003580 // upstream // 132051 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 132051 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2197434	cattcccagatagtcc[A/G]atgcagttagtctata	A	G	NM_003580 // upstream // 138000 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 138000 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-2265251	gaagcaaccaaactta[C/T]aaaagagctatgaaga	C	T	NM_003580 // upstream // 140207 // Hs.372000 // NSMAF // 8439 // Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /// ENST00000038176 // upstream // 140207 // — // — // — /// ENST00000360223 // downs	NSMAF	NSMAF, Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), q12.1
SNP_A-1993446	aacttttaggatttcac[C/T]gaccacaaagtatttc	C	T	ENST00000360223 // intron // 0 // — // — // — /// ENST00000356808 // intron // 0 // — // — // —	-	q12.1
SNP_A-1753495	ggttagatgtcatgtatttccgatc[C/G]gagcactgattacatagct gtcttc	C	G	NM_004056 // downstream // 1022847 // Hs.250502 // CA8 // 767 // carbonic anhydrase VIII /// NM_014729 // upstream // 46915 // - // - // - // -	CA8	CA8 , rs10504286, carbonic anhydrase VIII ,q12.1
SNP_A-2282436	gagttctgtaaagttc[A/G]atcagatccatttggc	A	G	NM_004056 // downstream // 960067 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 108476 // — // — // — /// ENST00000317995 // downstream // 960067 // — // — // — // -	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1934703	ttctctgtaagttctc[A/T]cttagcaaaaaatgc	A	T	NM_004056 // downstream // 915878 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 152665 // — // — // — /// ENST00000317995 // downstream // 915878 // — // — // — // -	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1721111	gagaataaaggaagaaaaatatcga[C/T]ccagagagtgtgatt tggaggttaa	C	T	NM_004056 // downstream // 378441 // Hs.250502 // CA8 // 767 // carbonic anhydrase VIII /// NM_014729 // upstream // 691321 // - // - // - // -	CA8	CA8 , rs2326441, carbonic anhydrase VIII ,q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170854	caataaaggactaaaaa[C/T]ataagctctgtaaaaa	C	T	NM_004056 // downstream // 384006 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 684537 // --- // --- // --- /// ENST00000317995 // downstream // 384006 // --- // --- // -	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1993468	tcagtctcccagta[C/T]gaaaattgctcaaaga	C	T	NM_004056 // downstream // 351688 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 716855 // --- // --- // --- /// ENST00000317995 // downstream // 351688 // --- // --- // -	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2201426	ccaatgaccagaaata[A/G]gtagcactgtacagct	A	G	NM_004056 // downstream // 266637 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 801906 // --- // --- // --- /// ENST00000317995 // downstream // 266637 // --- // --- // -	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1993475	aatgggatgatgct[A/G]agaactcctagttaaa	A	G	NM_004056 // downstream // 231444 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 837099 // --- // --- // --- /// ENST00000317995 // downstream // 231444 // --- // --- // -	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1919270	ttaagaagctactcac[A/G]ggatttcatttatgct	A	G	NM_004056 // downstream // 98316 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 970227 // --- // --- // --- /// ENST00000317995 // downstream // 98316 // --- // --- // --	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2013449	aatgtgacatatttga[C/T]aatgacaacacaaagg	C	T	NM_004056 // downstream // 2952 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// ENST00000301647 // downstream // 1065591 // --- // --- // --- /// ENST00000317995 // downstream // 2952 // --- // --- // --	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-1933373	ttctaatgtgtctgaa[A/G]tgcataattgttagaa	A	G	NM_004056 // upstream // 183643 // Hs.491813 // CA8 // 767 // Homo sapiens carbonic anhydrase VIII (CA8), mRNA. /// NM_002865 // upstream // 51962 // Hs.369017 // RAB2 // 5862 // Homo sapiens RAB2, member RAS oncogene family (RAB2), mRNA. /// ENST00000317	CA8	CA8, Homo sapiens carbonic anhydrase VIII (CA8), q12.1
SNP_A-2098259	agagatcctatgaaca[A/C]ctctgtctgagcatta	A	C	NM_173519 // upstream // 68935 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000355465 // upstream // 98548 // --- // --- // --- /// ENST00000354881 // upstream // 68924 // --- // --- /	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-1785028	ggcggagttcattcct[A/G]acttagggcctcatct	A	G	NM_173519 // upstream // 47649 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000355465 // upstream // 119834 // --- // --- // --- /// ENST00000354881 // upstream // 47638 // --- // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-2207718	ccatttgtcaaacaa[C/T]ttctatgtgaaacacg	C	T	NM_173519 // upstream // 47501 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000355465 // upstream // 119982 // --- // --- // --- /// ENST00000354881 // upstream // 47490 // --- // --	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-1993515	aacaatgatatcaaaa[A/G]catcttaacacaacta	A	G	NM_173519 // intron // 0 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // --- // --- // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.2
SNP_A-1860942	tcatactggcacagca[A/G]gttagtgacatgagtg	A	G	NM_173519 // intron // 0 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // --- // --- // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-2189602	cagtttgagaactaaa[C/T]gagctaatacatggaa	C	T	NM_173519 // intron // 0 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // --- // --- // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-1993520	cctcttcttgaacata[A/G]ctaacttgaggaacct	A	G	NM_173519 // intron // 0 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// ENST00000325897 // intron // 0 // --- // --- // ---	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1799478	gtaatgcacttcatac[G/T]atttctcactaactc	G	T	NM_173519 // downstream // 29499 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// NM_020164 // downstream // 133583 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transc	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-2199555	ccaaaaacatgagaaa[A/G]ccagatctccatagct	A	G	NM_173519 // downstream // 49240 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// NM_020164 // downstream // 113842 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transc	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-2060695	aatgagccttgaaaa[C/T]ataatgcaatcatatc	C	T	NM_173519 // downstream // 113370 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// NM_020164 // downstream // 49712 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transc	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-2013461	agggcctggaattcaa[A/T]atgagtaacataggg	A	T	NM_173519 // downstream // 140129 // Hs.546504 // MGC34646 // 157807 // Homo sapiens hypothetical protein MGC34646 (MGC34646), mRNA. /// NM_020164 // downstream // 22953 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transc	MGC34646	MGC34646, Homo sapiens hypothetical protein MGC34646 (MGC34646), q12.3
SNP_A-1688546	atgagaaagaacagcagggaaagta[C/T]taacatttggttccta acatcatag	C	T	NM_004318 // upstream // 63748 // Hs.413557 // ASPH // 444 // aspartate beta-hydroxylase /// NM_020164 // upstream // 88464 // Hs.413557 // ASPH // 444 // aspartate beta-hydroxylase /// NM_032466 // upstream // 63809 // Hs.413557 // ASPH // 444 // aspart	ASPH	ASPH , rs1495003, aspartate beta-hydroxylase ,q12.3
SNP_A-2066243	aatttagtgcacaac[A/G]aatttctgctgtaa	A	G	NM_020164 // upstream // 33876 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, mRNA. /// NM_032467 // upstream // 33817 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), tra	ASPH	ASPH, Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, q12.3
SNP_A-1866593	tccccccatcctagta[C/T]gcaggcaaatcctgaa	C	T	NM_020164 // upstream // 111990 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, mRNA. /// NM_032467 // upstream // 111931 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), t	ASPH	ASPH, Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, q12.3
SNP_A-2218176	cctgcgtaaggaaaaa[G/T]atctagaaaggaaagg	G	T	NM_020164 // upstream // 247690 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, mRNA. /// NM_032467 // upstream // 247631 // Hs.332422 // ASPH // 444 // Homo sapiens aspartate beta-hydroxylase (ASPH), t	ASPH	ASPH, Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 5, q12.3
SNP_A-2268455	gaatggatgaacaaac[C/T]atggtgcatgtacaga	G	T	NM_173688 // upstream // 193644 // Hs.491856 // FLJ39630 // 286183 // Homo sapiens hypothetical protein FLJ39630 (FLJ39630), mRNA. /// ENST00000330792 // upstream // 241127 // — // — // — // — /// ENST00000328472 // upstream // 193644 // — // –	FLJ39630	FLJ39630, Homo sapiens hypothetical protein FLJ39630 (FLJ39630), q12.3
SNP_A-1993568	actccctttctgagtc[C/G]aaacatacaagattc	C	G	NM_173688 // intron // 0 // Hs.491856 // FLJ39630 // 286183 // Homo sapiens hypothetical protein FLJ39630 (FLJ39630), mRNA. /// ENST00000328472 // intron // 0 // — // — // — // —	FLJ39630	FLJ39630, Homo sapiens hypothetical protein FLJ39630 (FLJ39630), q12.3
SNP_A-1758349	tgcagtacagtgaaattgagttcca[C/T]gtacttgattattagatc ctggaa	C	T	NM_173688 // intron // 0 // Hs.244376 // FLJ39630 // 286183 // hypothetical protein FLJ39630	FLJ39630	FLJ39630, rs10504360, hypothetical protein FLJ39630,q12.3
SNP_A-2304379	gctcggctctataca[C/G]ctttgagcaccctc	C	G	NM_000370 // upstream // 32075 // Hs.69049 // TTPA // 7274 // Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), mRNA. /// ENST00000260116 // upstream // 32075 // — // — // — /// ENST	TTPA	TTPA, Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839285	tagagtaccatgctaa[C/T]acaatactttgaaaag	C	T	NM_000370 // upstream // 227294 // Hs.69049 // TTPA // 7274 // Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), mRNA. /// ENST00000260116 // upstream // 227294 // --- // --- // --- /// EN	TTPA	TTPA, Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), q12.3
SNP_A-2013474	ttgaggttgatattag[A/G]ataagaggtgtctgtg	A	G	NM_000370 // upstream // 249783 // Hs.69049 // TTPA // 7274 // Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), mRNA. /// ENST00000260116 // upstream // 249783 // --- // --- // --- /// EN	TTPA	TTPA, Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), q12.3
SNP_A-2013475	acaaattactgagagc[C/T]atggaaattagatact	C	T	NM_000370 // upstream // 249923 // Hs.69049 // TTPA // 7274 // Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), mRNA. /// ENST00000260116 // upstream // 249923 // --- // --- // --- /// EN	TTPA	TTPA, Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), q12.3
SNP_A-1993588	gtttaacctctcctac[C/T]agtccacaatatcctg	C	T	NM_152414 // upstream // 1102934 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 67859 // --- // --- /// ENST00000321870 // upstream //	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2125585	agtttcatctttacac[A/G]ctatatgcctatagac	A	G	NM_152414 // upstream // 1079828 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 90965 // --- // --- /// ENST00000321870 // upstream //	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2130007	atacaagttgcttga[C/T]gtaaaattaataagac	C	T	NM_152414 // upstream // 1051911 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 118882 // --- // --- /// ENST00000321870 // upstream /	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2127002	ataaagttccaatcaa[A/T]ttagaaaatctttta	A	T	NM_152414 // upstream // 1031182 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 139611 // --- // --- /// ENST00000321870 // upstream /	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-1894249	tgcattcacttaacac[C/T]ctcatttgaaaatttt	C	T	NM_152414 // upstream // 828542 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 342251 // --- // --- /// ENST00000321870 // upstream //	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-1993602	tttttagcctattaac[A/T]cttaaatcacctactg	A	T	NM_152414 // upstream // 349271 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 821522 // --- // --- /// ENST00000321870 // upstream //	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-1846686	tatatttttctccagga[A/T]cacagcattctagtta	A	T	NM_152414 // upstream // 243871 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 926922 // --- // --- /// ENST00000321870 // upstream //	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-1993611	taatatcctcatgac[C/T]caagagtgatgccact	C	T	NM_152414 // upstream // 105347 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000310210 // downstream // 1065446 // --- // --- /// ENST00000321870 // upstream /	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140997	atctgcacataaggacc[C/T]atgacttaacacatg	C	T	NM_152414 // 3UTR // 0 // Hs.388788 // BHLHB5 // 27319 // Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), mRNA. /// ENST00000321870 // 3UTR // 0 // — // — // — // —	BHLHB5	BHLHB5, Homo sapiens basic helix-loop-helix domain containing, class B, 5 (BHLHB5), q12.3
SNP_A-2260973	gaaagaaactctaaca[C/T]ctaggcttttgtattc	C	T	NM_004820 // intron // 0 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// ENST00000310193 // intron // 0 // — // — // — // —	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q12.3
SNP_A-2297709	gccagctgggcttggaa[A/G]acctcgctagcagctt	A	G	NM_004820 // upstream // 188339 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 615389 // Hs.269542 // ARMC1 // 55156 // Homo sapiens armadillo repeat cont	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q12.3
SNP_A-1667096	cctcttcccctcctccctggca[A/G]agttccactgttcttcct cccg	A	G	NM_004820 // upstream // 345306 // Hs.144877 // CYP7B1 // 9420 // cytochrome P450, family 7, subfamily B, polypeptide 1 /// NM_018120 // downstream // 458422 // Hs.106768 // FLJ10511 // 55156 // armadillo repeat containing protein	CYP7B1	CYP7B1, rs4132352, cytochrome P450, family 7, subfamily B, polypeptide 1, q13.1
SNP_A-1993616	tagaaatacttaaca[A/C]tcatcattctaaacaa	A	C	NM_004820 // upstream // 284247 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 519481 // Hs.269542 // ARMC1 // 55156 // Homo sapiens armadillo repeat cont	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-1938023	ttgaattcatggaat[G/T]agctggatagagatca	G	T	NM_004820 // upstream // 354039 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 449689 // Hs.269542 // ARMC1 // 55156 // Homo sapiens armadillo repeat cont	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-2171472	caatcagttaggtcaa[C/T]acgaatctaacactat	C	T	NM_004820 // upstream // 361355 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 442373 // Hs.269542 // ARMC1 // 55156 // Homo sapiens armadillo repeat cont	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-2013485	tacatcagtctctcta[C/G]aaaagtcacctggagt	C	G	NM_004820 // upstream // 386191 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 437537 // Hs.269542 // ARMC1 // 55156 // Homo sapiens armadillo repeat cont	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-2159278	atttaccctctcttac[C/T]ctcctcaacaagcta	C	T	NM_004820 // upstream // 379350 // Hs.491869 // CYP7B1 // 9420 // Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), mRNA. /// NM_018120 // downstream // 424378 // Hs.269542 // ARMC1 // 55156 // Homo sapiens armadillo repeat cont	CYP7B1	CYP7B1, Homo sapiens cytochrome P450, family 7, subfamily B, polypeptide 1 (CYP7B1), q13.1
SNP_A-1924854	ttatatgaatgtgaac[A/C]gtccacaaaatatgtt	A	C	NM_033105 // intron // 0 // Hs.491885 // DNAJC5B // 85479 // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 5 beta (DNAJC5B), mRNA. /// ENST00000276570 // intron // 0 // — // — // — // —	DNAJC5B	DNAJC5B, Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 5 beta (DNAJC5B), q13.1
SNP_A-2247859	ctgtgatgctcacaca[A/G]tggaactgcctaagga	A	G	NM_184086 // intron // 0 // Hs.85524 // TRIM55 // 84675 // Homo sapiens ring finger protein 29 (RNF29), transcript variant 3, mRNA. /// NM_184087 // intron // 0 // Hs.85524 // TRIM55 // 84675 // Homo sapiens ring finger protein 29 (RNF29), transcript vari	TRIM55	TRIM55, Homo sapiens ring finger protein 29 (RNF29), transcript variant 3, q13.1
SNP_A-1993631	gtggaggagtcatatg[C/G]atcattcctcatgtga	C	G	NM_000756 // upstream // 120292 // Hs.75294 // CRH // 1392 // Homo sapiens corticotropin releasing hormone (CRH), mRNA. /// NM_015169 // upstream // 130145 // Hs.71827 // RRS1 // 23212 // Homo sapiens RRS1 ribosome biogenesis regulator homolog (S. cerevis	CRH	CRH, Homo sapiens corticotropin releasing hormone (CRH), q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1717665	agtcaatgcttgagcaggattgcaa[G/T]gagagatacatattag ggaaaacta	G	T	NM_152765 // downstream // 16914 // Hs.158798 // MGC33510 // 254778 // hypothetical protein MGC33510	MGC33510	MGC33510 , rs7008801, hypothetical protein MGC33510,q13.2
SNP_A-1879764	tcttcattctattcc[C/T]cctctttgtaactaca	C	T	NM_152765 // intron // 0 // Hs.521615 // MGC33510 // 254778 // Homo sapiens hypothetical protein MGC33510 (MGC33510), mRNA. /// ENST00000305454 // intron // 0 // — // — // —	MGC33510	MGC33510, Homo sapiens hypothetical protein MGC33510 (MGC33510), q13.1
SNP_A-1827419	taactaggctccagga[A/G]caaattgaaatgacaa	A	G	NM_152765 // intron // 0 // Hs.521615 // MGC33510 // 254778 // Homo sapiens hypothetical protein MGC33510 (MGC33510), mRNA. /// ENST00000305454 // intron // 0 // — // — // —	MGC33510	MGC33510, Homo sapiens hypothetical protein MGC33510 (MGC33510), q13.1
SNP_A-1813156	gtggtatctctaggca[C/G]ctggaaaaaagctccc	C	G	NM_152765 // downstream // 4422 // Hs.521615 // MGC33510 // 254778 // Homo sapiens hypothetical protein MGC33510 (MGC33510), mRNA. /// X66087 // downstream // 41771 // Hs.445898 // MYBL1 // 4603 // H.sapiens a-myb mRNA. /// ENST00000305454 // downstream /	MGC33510	MGC33510, Homo sapiens hypothetical protein MGC33510 (MGC33510), q13.1
SNP_A-1993636	gtggagccacttggca[G/T]tcttaagtacatcct	G	T	NM_152765 // downstream // 34849 // Hs.521615 // MGC33510 // 254778 // Homo sapiens hypothetical protein MGC33510 (MGC33510), mRNA. /// X66087 // downstream // 11344 // Hs.445898 // MYBL1 // 4603 // H.sapiens a-myb mRNA. /// ENST00000305454 // downstream	MGC33510	MGC33510, Homo sapiens hypothetical protein MGC33510 (MGC33510), q13.1
SNP_A-1993638	ggactgacaaaaatta[C/T]agcttccctgaaca	C	T	NM_025054 // CDS // 0 // Hs.205550 // VCIP135 // 80124 // Homo sapiens valosin-containing protein (p97)/p47 complex-interacting protein p135 (VCIP135), mRNA. /// ENST00000310421 // CDS // 0 // — // — // — // —	VCIP135	VCIP135, Homo sapiens valosin-containing protein (p97),q13.1
SNP_A-2044319	aactttacagacaac[A/G]caagaacacgctaaaa	A	G	NM_020361 // upstream // 116491 // Hs.133085 // CPA6 // 57094 // Homo sapiens carboxypeptidase A6 (CPA6), mRNA. /// NM_024870 // upstream // 89282 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA	CPA6	CPA6, Homo sapiens carboxypeptidase A6 (CPA6), q13.2
SNP_A-1925694	ttatgatttccaaatg[A/G]atgctattatctggaa	A	G	NM_024870 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcrip	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-2214931	cctatccttcgaatcc[C/T]agatcaaagcccactt	C	T	NM_024870 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcrip	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-2253819	cttgaagacaatgata[C/T]agctgctgatttattc	C	T	NM_024870 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcrip	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-2117050	aggtgagccaaagaca[A/G]ggaagcaatatctaca	A	G	NM_024870 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcrip	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-1836128	tactagcacatttggc[G/T]catacctctcattct	G	T	NM_024870 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcrip	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2166912	caacaaaaaagtggaa[G/T]tagcttaaagaagtat	G	T	NM_024870 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, mRNA. /// NM_025170 // intron // 0 // Hs.130356 // DEPDC2 // 80243 // Homo sapiens DEP domain containing 2 (DEPDC2), transcrip	DEPDC2	DEPDC2, Homo sapiens DEP domain containing 2 (DEPDC2), transcript variant 1, q13.2
SNP_A-1993682	ttaatatttttgattc[A/G]ccaattagaccataaa	A	G	NM_052958 // intron // 0 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// ENST00000348340 // intron // 0 // --- // --- // --- // --- /// ENST00000349492 // intron // 0 // --- // --- // --- // --- /// ENST00000337103 /	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2134309	atatgccatgctcatc[C/T]atgtaactgaatcttg	C	T	NM_052958 // downstream // 4240 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 3774 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_015170 // upst	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2226026	ctaacacatttaggat[C/T]aagcttacaaatgact	C	T	NM_052958 // downstream // 5257 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 4791 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_015170 // upst	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2123954	agttaatagacatcag[A/G]attggttccagattag	A	G	NM_052958 // downstream // 68292 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 67826 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_015170 // up	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-2258714	ctttgcttgctactc[C/T]accatttttgtatct	C	T	NM_052958 // downstream // 124944 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 124478 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_015170 //	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-1993697	cacctgtgtgtatcca[A/G]cagcaagaagactgaa	A	G	NM_052958 // downstream // 283554 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_052958 // downstream // 283088 // Hs.491941 // VEST1 // 116328 // Homo sapiens vestibule-1 protein (VEST1), mRNA. /// NM_015170 //	VEST1	VEST1, Homo sapiens vestibule-1 protein (VEST1), q13.2
SNP_A-1686422	catgactcttcccacagtgcactaa[C/T]aagtagtaaaagctgaaaggaagac	C	T	NM_015170 // upstream // 73766 // Hs.409602 // SULF1 // 23213 // sulfatase 1 /// NM_052958 // downstream // 573851 // Hs.12902 // VEST1 // 116328 // vestibule-1 protein	SULF1	SULF1 , rs4737965, sulfatase 1 ,q13.3
SNP_A-1935380	ttctggacctgagtgc[C/G]agaaggaggcccactg	C	G	NM_015170 // downstream // 2759 // Hs.409602 // SULF1 // 23213 // Homo sapiens sulfatase 1 (SULF1), mRNA. /// NM_030958 // downstream // 8669 // Hs.443609 // SLCO5A1 // 81796 // Homo sapiens solute carrier organic anion transporter family, member 5A1 (SLC	SULF1	SULF1, Homo sapiens sulfatase 1 (SULF1), q13.3
SNP_A-2169022	caagagtaaaagaaaa[C/T]gtactaaatggatgta	C	T	NM_024504 // intron // 0 // Hs.287532 // PRDM14 // 63978 // Homo sapiens PR domain containing 14 (PRDM14), mRNA. /// ENST00000276594 // intron // 0 // --- // --- // --- // ---	PRDM14	PRDM14, Homo sapiens PR domain containing 14 (PRDM14), q13.3
SNP_A-1853630	tatttttctgactgca[A/G]aaatccaactaattta	A	G	NM_006540 // upstream // 145501 // Hs.446678 // NCOA2 // 10499 // Homo sapiens nuclear receptor coactivator 2 (NCOA2), mRNA. /// NM_014294 // downstream // 24152 // Hs.491988 // TRAM1 // 23471 // Homo sapiens translocation associated membrane protein 1 (T	NCOA2	NCOA2, Homo sapiens nuclear receptor coactivator 2 (NCOA2), q13.3
SNP_A-1895640	tgcctccctcaaatca[A/C]aggccaatctgtcatt	A	C	NM_016027 // upstream // 470194 // Hs.118554 // LACTB2 // 51110 // Homo sapiens lactamase, beta 2 (LACTB2), mRNA. /// NM_172060 // downstream // 58082 // Hs.491997 // EYA1 // 2138 // Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript varia	LACTB2	LACTB2, Homo sapiens lactamase, beta 2 (LACTB2), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1728755	agttagcttcttcatcaaccacca[C/T]ggaagaaaatcctccac caaaagag	C	T	NM_000503 // intron // 0 // Hs.94210 // EYA1 // 2138 // eyes absent homolog 1 (Drosophila) /// NM_172058 // intron // 0 // Hs.94210 // EYA1 // 2138 // eyes absent homolog 1 (Drosophila) /// NM_172059 // intron // 0 // Hs.94210 // EYA1 // 2138 // eyes abs	EYA1	EYA1, rs10504503, eyes absent homolog 1 (Drosophila), q13.3
SNP_A-1936771	ttcttattacaagca[C/G]acatacaggaatagg	C	G	NM_172060 // upstream // 262141 // Hs.491997 // EYA1 // 2138 // Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, mRNA. /// NM_172059 // upstream // 262141 // Hs.491997 // EYA1 // 2138 // Homo sapiens eyes absent homolog 1 (Dro	EYA1	EYA1, Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 1, q13.3
SNP_A-1993786	ccaccacctctcagac[A/C]aggaaaggaagaaaac	A	C	BC067827 // upstream // 4452 // Hs.442619 // MSC // 9242 // Homo sapiens musculin (activated B-cell factor-1), mRNA (cDNA clone MGC:87363 IMAGE:30336424), complete cds. /// NM_005098 // upstream // 4444 // Hs.442619 // MSC // 9242 // Homo sapiens musculin	MSC	MSC, Homo sapiens musculin (activated B-cell factor-1), (cDNA clone MGC:87363 IMAGE:30336424), complete cds, q13.3
SNP_A-1993789	ctgatgagttagcctt[C/G]agaagaggagtgtaca	C	G	BC067827 // upstream // 8678 // Hs.442619 // MSC // 9242 // Homo sapiens musculin (activated B-cell factor-1), mRNA (cDNA clone MGC:87363 IMAGE:30336424), complete cds. /// NM_005098 // upstream // 8670 // Hs.442619 // MSC // 9242 // Homo sapiens musculin	MSC	MSC, Homo sapiens musculin (activated B-cell factor-1), (cDNA clone MGC:87363 IMAGE:30336424), complete cds, q13.3
SNP_A-1907386	tgtaaaatggacttaa[C/G]gacaaaatacatgaat	C	G	BC067827 // upstream // 9413 // Hs.442619 // MSC // 9242 // Homo sapiens musculin (activated B-cell factor-1), mRNA (cDNA clone MGC:87363 IMAGE:30336424), complete cds. /// NM_005098 // upstream // 9405 // Hs.442619 // MSC // 9242 // Homo sapiens musculin	MSC	MSC, Homo sapiens musculin (activated B-cell factor-1), (cDNA clone MGC:87363 IMAGE:30336424), complete cds, q13.3
SNP_A-2189707	cagttttaggacata[C/T]agtgtgctatttat	C	T	BC067827 // upstream // 120692 // Hs.442619 // MSC // 9242 // Homo sapiens musculin (activated B-cell factor-1), mRNA (cDNA clone MGC:87363 IMAGE:30336424), complete cds. /// NM_005098 // upstream // 120684 // Hs.442619 // MSC // 9242 // Homo sapiens musc	MSC	MSC, Homo sapiens musculin (activated B-cell factor-1), (cDNA clone MGC:87363 IMAGE:30336424), complete cds, q13.3
SNP_A-1857911	tcacttccaggtcaag[A/C]atgttctaaaacaaac	A	C	NM_007332 // upstream // 37723 // Hs.137674 // TRPA1 // 8989 // Homo sapiens transient receptor potential cation channel, subfamily A, member 1 (TRPA1), mRNA. /// ENST00000262209 // upstream // 37723 // — /// — /// — /// ENST00000360196 // down	TRPA1	TRPA1, Homo sapiens transient receptor potential cation channel, subfamily A, member 1 (TRPA1), q13.3
SNP_A-2218476	cctggactacacagaa[C/T]aaagaacaaagaattt	C	T	NM_004770 // upstream // 19256 // Hs.6702 // KCNB2 // 9312 // Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), mRNA. /// ENST00000356760 // upstream // 191373 // — /// — /// — /// ENST00000329185 // upstre	KCNB2	KCNB2, Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), q13.3
SNP_A-2068163	acaagacatagtaaaaa[A/T]ctccgagtatgtaac	A	T	NM_153225 // intron // 0 // Hs.439040 // RPESP // 157869 // Homo sapiens RPE-spondin (RPESP), mRNA. /// ENST00000360973 // intron // 0 // — /// — /// — /// ENST00000297354 // intron // 0 // — /// — /// —	RPESP	RPESP, Homo sapiens RPE-spondin (RPESP), q13.3
SNP_A-1845231	tatacctggtccattc[A/G]aagaattcatccacaa	A	G	NM_015364 // downstream // 85660 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 119976 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-2248676	ctgttcagtgacttcc[A/G]agagatttttccacac	A	G	NM_015364 // downstream // 102715 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 102921 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1941327	ttgcttaagaactaaa[C/G]aaaatcagagttcagt	C	G	NM_015364 // downstream // 106867 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 98769 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-2130974	atagaacattttattc[A/G]aagaaaagtcattgca	A	G	NM_015364 // downstream // 111992 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 93644 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-1993856	tgcttctcgaatgaat[A/G]aaagaatgactcaaat	A	G	NM_015364 // downstream // 112237 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 93399 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-1933563	ttctagactttaaatt[C/T]aagggtgagagataaa	C	T	NM_015364 // downstream // 116003 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 89633 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-1781850	ggattttgaatccaga[C/T]ggggagaaataaagat	C	T	NM_015364 // downstream // 157139 // Hs.69328 // LY96 // 23643 // Homo sapiens lymphocyte antigen 96 (LY96), mRNA. /// NM_020647 // downstream // 48497 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// NM_020647 // downstream	LY96	LY96, Homo sapiens lymphocyte antigen 96 (LY96), q21.11
SNP_A-1993858	taaagccttgctaaaa[C/T]gtgctaagatgctgtg	C	T	NM_020647 // intron // 0 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// ENST00000342232 // intron // 0 // — // — // — // — /// ENST00000220810 // intron // 0 // — // — // — // —	JPH1	JPH1, Homo sapiens junctophilin 1 (JPH1), q21.11
SNP_A-1688578	cttttgttctcatctataatctgga[G/T]gagattgtaacaatttttttctgt	G	T	NM_015886 // upstream // 442046 // Hs.129732 // PI15 // 51050 // protease inhibitor 15 /// NM_018972 // downstream // 18373 // Hs.168950 // GDAP1 // 54332 // ganglioside-induced differentiation-associated protein 1	PI15	PI15 , rs4471028, protease inhibitor 15 ,q21.11
SNP_A-2205494	ccagtgtcaggaacac[A/G]gagggaataaagtctg	A	G	NM_020647 // intron // 0 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// ENST00000342232 // intron // 0 // — // — // — // — /// ENST00000220810 // intron // 0 // — // — // — // —	JPH1	JPH1, Homo sapiens junctophilin 1 (JPH1), q21.11
SNP_A-2093017	agaacactctgaggac[A/G]aacactgtcttttcac	A	G	NM_020647 // intron // 0 // Hs.160574 // JPH1 // 56704 // Homo sapiens junctophilin 1 (JPH1), mRNA. /// ENST00000342232 // intron // 0 // — // — // — // — /// ENST00000220810 // intron // 0 // — // — // — // —	JPH1	JPH1, Homo sapiens junctophilin 1 (JPH1), q21.11
SNP_A-2146149	atgcgagagagcaaaa[G/T]aagagatcgcagatta	G	T	NM_018972 // intron // 0 // Hs.168950 // GDAP1 // 54332 // Homo sapiens ganglioside-induced differentiation-associated protein 1 (GDAP1), mRNA. /// ENST00000220822 // intron // 0 // — // — // — // —	GDAP1	GDAP1, Homo sapiens ganglioside-induced differentiation-associated protein 1 (GDAP1), q21.11
SNP_A-1993866	aaaaaatgcactctgg[A/C]aaaagcaatgtgtcag	A	C	NM_018972 // downstream // 303817 // Hs.168950 // GDAP1 // 54332 // Homo sapiens ganglioside-induced differentiation-associated protein 1 (GDAP1), mRNA. /// NM_015886 // upstream // 156602 // Hs.98558 // PI15 // 51050 // Homo sapiens protease inhibitor 15	GDAP1	GDAP1, Homo sapiens ganglioside-induced differentiation-associated protein 1 (GDAP1), q21.11
SNP_A-1993871	cttaatttagacatga[A/G]gatgagcagtaaattc	A	G	NM_015886 // downstream // 62194 // Hs.98558 // PI15 // 51050 // Homo sapiens protease inhibitor 15 (PI15), mRNA. /// NM_031461 // upstream // 73122 // Hs.436542 // LCRISP1 // 83690 // Homo sapiens CocoaCrisp (LOC83690), mRNA. /// ENST00000260113 // downs	PI15	PI15, Homo sapiens protease inhibitor 15 (PI15), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1912319	tgtgattataaccagc[A/G]agtatatttggcacag	A	G	NM_015886 // downstream // 118979 // Hs.98558 // PI15 // 51050 // Homo sapiens protease inhibitor 15 (PI15), mRNA. /// NM_031461 // upstream // 16337 // Hs.436542 // LCRISP1 // 83690 // Homo sapiens CocoaCrisp (LOC83690), mRNA. /// ENST00000260113 // down	PI15	PI15, Homo sapiens protease inhibitor 15 (PI15), q21.11
SNP_A-1649980	gttgttgtttctgggggcatggaa[A/G]aattgtgatttgaagtttct gttt	A	G	NM_004133 // upstream // 283111 // Hs.241529 // HNF4G // 3174 // hepatocyte nuclear factor 4, gamma /// NM_031461 // downstream // 91620 // Hs.436542 // LOC83690 // 83690 // CocoaCrisp	HNF4G	HNF4G , rs10504591, hepatocyte nuclear factor 4, gamma ,q21.13
SNP_A-2131889	ataggaagttctcaat[A/G]aattgaatcgtagcag	A	G	NM_031461 // downstream // 94526 // Hs.436542 // LCRISP1 // 83690 // Homo sapiens CocoaCrisp (LOC83690), mRNA. /// NM_004133 // upstream // 278954 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_00413	LCRISP1	LCRISP1, Homo sapiens CocoaCrisp (LOC83690), q21.11
SNP_A-2301737	gcgctgttagcaaaaa[C/T]gttactactatcagtc	C	T	NM_031461 // downstream // 267250 // Hs.436542 // LCRISP1 // 83690 // Homo sapiens CocoaCrisp (LOC83690), mRNA. /// NM_004133 // upstream // 106230 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_0041	LCRISP1	LCRISP1, Homo sapiens CocoaCrisp (LOC83690), q21.11
SNP_A-2293751	gcagctacacttgttc[A/C]atcttgtctcaagc	A	C	NM_031461 // downstream // 349998 // Hs.436542 // LCRISP1 // 83690 // Homo sapiens CocoaCrisp (LOC83690), mRNA. /// NM_004133 // upstream // 23482 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_00413	LCRISP1	LCRISP1, Homo sapiens CocoaCrisp (LOC83690), q21.11
SNP_A-1841840	taggccttggtgtaa[A/C]ctaactgtgtctgcc	A	C	NM_031461 // downstream // 360948 // Hs.436542 // LCRISP1 // 83690 // Homo sapiens CocoaCrisp (LOC83690), mRNA. /// NM_004133 // upstream // 12532 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_00413	LCRISP1	LCRISP1, Homo sapiens CocoaCrisp (LOC83690), q21.11
SNP_A-1923501	ttaggctgtaaagaaa[C/T]tgaaactctcaagccc	C	T	NM_004133 // intron // 0 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// ENST00000354370 // intron // 0 // — // — // —	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2174814	cacaggaagttccaca[C/T]agaacaacaagtcaac	C	T	NM_004133 // intron // 0 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// ENST00000354370 // intron // 0 // — // — // —	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-1871258	tctaaaattcattcgt[C/G]acatcattcactcaaa	C	G	NM_004133 // intron // 0 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// ENST00000354370 // intron // 0 // — // — // —	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2129220	ataatttgcttgtgtc[G/T]cactgtaaaatatctt	G	T	NM_004133 // intron // 0 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// ENST00000354370 // intron // 0 // — // — // —	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2287114	gatgtatgccagcttat[C/G]gatgtatctctgaaat	C	G	NM_004133 // downstream // 266185 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream // 263688 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-2305144	gctgacatagtgaccat[A/G]ctgaagtcttagagg	A	G	NM_004133 // downstream // 575619 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream // 573122 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-1993894	ctatcctggaaaaaa[C/T]tggcagctgaacaaca	C	T	NM_004133 // downstream // 639145 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream // 636648 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2061921	aatggcatatgctctat[C/T]caacgaactgaaagac	C	T	NM_004133 // downstream // 1010327 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA. /// NM_004133 // downstream // 1007830 // Hs.241529 // HNF4G // 3174 // Homo sapiens hepatocyte nuclear factor 4, gamma (HNF	HNF4G	HNF4G, Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), q21.11
SNP_A-1993905	gagaagcgtcaaggtc[A/G]cctttctcaactgagc	A	G	NM_024721 // intron // 0 // Hs.458973 // ZFHX4 // 79776 // Homo sapiens zinc finger homeodomain 4 (ZFHX4), mRNA. /// ENST00000050961 // intron // 0 // — // — // — // —	ZFHX4	ZFHX4, Homo sapiens zinc finger homeodomain 4 (ZFHX4), q21.11
SNP_A-2030960	aaaggaccattcaaag[A/G]accatgtcaaatctga	A	G	NM_000318 // intron // 0 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// ENST00000357039 // intron // 0 // — // — // — // —	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-1712633	tgctattctagaatgttattttctt[C/G]aaaacaggaatttttctcattcag	C	G	NM_000318 // upstream // 250962 // Hs.180612 // PXMP3 // 5828 // peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) /// NM_006823 // upstream // 1264935 // Hs.433700 // PKIA // 5569 // protein kinase (cAMP-dependent, catalytic) inhibitor alpha //	PXMP3	PXMP3 , rs4398888, peroxisomal membrane protein 3, 35kDa (Zellweger syndrome), q21.13
SNP_A-1810045	gtgatactgcacccaa[A/T]tacttacataaagtgg	A	T	NM_000318 // upstream // 199264 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 185480 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-1789148	gggcagggagtcagc[A/G]agagatgaacagtct	A	G	NM_000318 // upstream // 261508 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 247724 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-1993924	tcttgtcctggtcgtg[A/C]aaaaatgtaatttggc	A	C	NM_000318 // upstream // 273199 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 259415 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2209566	cccatctgctagtga[A/G]ggtatgaagacaagga	A	G	NM_000318 // upstream // 286557 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 272773 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2203669	ccagactactcagggc[A/G]atacttggaataacga	A	G	NM_000318 // upstream // 288321 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 274537 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2182347	cagagttacaggaaag[C/G]ctatggagttatttac	C	G	NM_000318 // upstream // 299793 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 286009 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-2204064	ccagcaactgatcaat[A/T]aggtggcagtaattac	A	T	NM_000318 // upstream // 358621 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 344837 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872866	tctatatttccatttc[A/G]ctataactagtatgaa	A	G	NM_000318 // upstream // 426062 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 412278 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-1797137	ggttgagagtgtctac[C/T]gattattgagaaccac	C	T	NM_000318 // upstream // 427095 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 413311 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-1750341	aaagtgtttccttgtctaataaa[C/G]agaagtctctcctcactgcacttcc	C	G	NM_000318 // upstream // 552841 // Hs.180612 // PXMP3 // 5828 // peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) /// NM_006823 // upstream // 963056 // Hs.433700 // PKIA // 5569 // protein kinase (cAMP-dependent, catalytic) inhibitor alpha ///	PXMP3	PXMP3 , rs421501, peroxisomal membrane protein 3, 35kDa (Zellweger syndrome), q21.13
SNP_A-2139934	atctacatactatcca[G/T]cctatcattaataat	G	T	NM_000318 // upstream // 495608 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 481824 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.11
SNP_A-1665206	ctggcacaggaaaattcttcaaaga[C/T]gacgtgttgaattgtagctttatac	C	T	NM_000318 // upstream // 594465 // Hs.180612 // PXMP3 // 5828 // peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) /// NM_006823 // upstream // 921432 // Hs.433700 // PKIA // 5569 // protein kinase (cAMP-dependent, catalytic) inhibitor alpha ///	PXMP3	PXMP3 , rs1491568, peroxisomal membrane protein 3, 35kDa (Zellweger syndrome), q21.13
SNP_A-2248831	ctgttgagaccttcaa[C/T]gtactggaaattctga	C	T	NM_000318 // upstream // 762425 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 748641 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-2281914	gagtgccaagatgcaa[C/T]gtacagccaaccctca	C	T	NM_000318 // upstream // 763045 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 749261 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-1948625	tttataaggagaatga[A/T]gaaacactaatgaaag	A	T	NM_000318 // upstream // 811541 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 797757 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-2312039	ggacacagcctcaaga[G/T]gtcccgagatcatatg	G	T	NM_000318 // upstream // 839795 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 826011 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-1840516	tagccatgagtgacaa[C/T]gatggaaatgctct	C	T	NM_000318 // upstream // 1509552 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 1495768 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membran	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12
SNP_A-1794012	ggtcacggagacaacc[C/T]acgaaaatgatttgtt	C	T	NM_000318 // upstream // 1586960 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), mRNA. /// NM_000318 // upstream // 1573176 // Hs.437966 // PXMP3 // 5828 // Homo sapiens peroxisomal membran	PXMP3	PXMP3, Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3), q21.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2275862	gagactaggtcaaaga[C/T]gaacttattatttctt	C	T	NM_006823 // downstream // 36127 // Hs.433700 // PKIA // 5569 // Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), transcript variant 1, mRNA. /// NM_181839 // downstream // 36127 // Hs.433700 // PKIA // 5569 // Homo sapiens	PKIA	PKIA, Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), transcript variant 1, q21.12
SNP_A-1747231	tgtaaacaaattggaaaataaaaag[G/T]accacttgagtgaaaacagatttta	G	T	NM_000880 // upstream // 460115 // Hs.72927 // IL7 // 3574 // interleukin 7 /// NM_007029 // upstream // 345529 // Hs.90005 // STMN2 // 11075 // stathmin-like 2	IL7	IL7 , rs1870572, interleukin 7 ,q21.13
SNP_A-2266009	gaaggattccctctct[A/G]aaagactgcaatatgg	A	G	NM_012258 // upstream // 110216 // Hs.234434 // HEY1 // 23462 // Homo sapiens hairy/enhancer-of-split related with YRPW motif 1 (HEY1), mRNA. /// NM_012258 // upstream // 110215 // Hs.234434 // HEY1 // 23462 // Homo sapiens hairy/enhancer-of-split related	HEY1	HEY1, Homo sapiens hairy q21.13
SNP_A-2054129	aagttccatggttatt[A/G]aagggaaatggacata	A	G	NM_012258 // upstream // 141149 // Hs.234434 // HEY1 // 23462 // Homo sapiens hairy/enhancer-of-split related with YRPW motif 1 (HEY1), mRNA. /// NM_012258 // upstream // 141148 // Hs.234434 // HEY1 // 23462 // Homo sapiens hairy/enhancer-of-split related	HEY1	HEY1, Homo sapiens hairy q21.13
SNP_A-2121844	agtgagagtccaatct[C/G]agagcattacttcttt	C	G	NM_014018 // intron // 0 // Hs.521124 // MRPS28 // 28957 // Homo sapiens mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000276585 // intron // 0 // --- // --- // --- // ---	MRPS28	MRPS28, Homo sapiens mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, q21.13
SNP_A-1839151	tagagcgtgtcacatg[A/G]atgtaaataccaaagg	A	G	NM_005079 // intron // 0 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1927558	ttcaacaatgttggaa[C/T]ggaatgaagggtagag	C	T	NM_005079 // intron // 0 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1866154	tcccaggacatagacc[A/T]ctgtagtattgtcacg	A	T	NM_005079 // intron // 0 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-2272206	gacctagtatataatc[A/G]atcaggccaagccact	A	G	NM_005079 // intron // 0 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // intron // 0 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-2236657	ctctaagaccctgcac[C/T]aacaatctgttttccc	C	T	NM_005079 // upstream // 37471 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 37471 // --- // --- // --- // --- /// ENST00000354303 // upstream // 349687 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1924466	ttataattcatctcac[A/C]ctccttgatcatcaaa	A	C	NM_005079 // upstream // 192111 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 192111 // --- // --- // --- // --- /// ENST00000354303 // upstream // 195047 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1952692	tttctggtttggccaa[C/T]tgattggatggatgat	C	T	NM_005079 // upstream // 219563 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 219563 // --- // --- // --- // --- /// ENST00000354303 // upstream // 167595 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-1788494	gggataagcacacttc[A/G]aaagatgttttctagc	A	G	NM_005079 // upstream // 352072 // Hs.368433 // TPD52 // 7163 // Homo sapiens tumor protein D52 (TPD52), mRNA. /// ENST00000263850 // upstream // 352072 // --- // --- // --- // --- /// ENST00000354303 // upstream // 35086 // --- // --- // --- // ---	TPD52	TPD52, Homo sapiens tumor protein D52 (TPD52), q21.13
SNP_A-2156022	attccttccatgtcca[C/T]agcagatgtcaaaacc	C	T	ENST00000327835 // upstream // 38121 // --- // --- // --- // --- /// ENST00000297255 // upstream // 219817 // --- // --- // --- // --- /// ENST00000331106 // upstream // 219793 // --- // --- // --- // --- /// ENST00000359469 // upstream // 39245 // --- //	-	q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1994015	gtgattttgtgaaaag[C/G]ctgttggaaacccga	C	G	NM_018440 // intron // 0 // Hs.266175 // PAG // 55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// ENST00000220597 // intron // 0 // — // — // — // —	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-1943861	ttgtataacctcccaa[C/T]gtgcctctcacaatgc	C	T	NM_018440 // upstream // 77841 // Hs.266175 // PAG // 55824 // Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA. /// NM_001444 // upstream // 172676 // Hs.408061 // FABP5 // 2171 // Homo sapiens fatty acid bi	PAG	PAG, Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), q21.13
SNP_A-1729578	gcatgaatctatcccaatagtaaca[C/T]gtacagagaggatgc aagatgctta	C	T	NM_001444 // downstream // 18877 // Hs.408061 // FABP5 // 2171 // fatty acid binding protein 5 (psoriasis-associated) /// NM_002677 // downstream // 136681 // Hs.2868 // PMP2 // 5375 // peripheral myelin protein 2	FABP5	FABP5 , rs201952, fatty acid binding protein 5 (psoriasis-associated) ,q21.13
SNP_A-1994021	gaactgctttttagca[C/G]aaaacttatccataga	C	G	NM_001444 // downstream // 17835 // Hs.408061 // FABP5 // 2171 // Homo sapiens fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA. /// NM_002677 // downstream // 137725 // Hs.2868 // PMP2 // 5375 // Homo sapiens peripheral myelin protein 2	FABP5	FABP5, Homo sapiens fatty acid binding protein 5 (psoriasis-associated) (FABP5), q21.13
SNP_A-1939762	ttgcaaatttgcgtta[C/T]gtcctggaacttcaat	C	T	NM_001444 // downstream // 20683 // Hs.408061 // FABP5 // 2171 // Homo sapiens fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA. /// NM_002677 // downstream // 134877 // Hs.2868 // PMP2 // 5375 // Homo sapiens peripheral myelin protein 2	FABP5	FABP5, Homo sapiens fatty acid binding protein 5 (psoriasis-associated) (FABP5), q21.13
SNP_A-2052711	aagtattttgaggtaa[A/C]gggccataatgtatgc	A	C	NM_002677 // 3UTR // 0 // Hs.2868 // PMP2 // 5375 // Homo sapiens peripheral myelin protein 2 (PMP2), mRNA. /// ENST00000256103 // 3UTR // 0 // — // — // — // — // —	PMP2	PMP2, Homo sapiens peripheral myelin protein 2 (PMP2), q21.13
SNP_A-1750309	cagtccaaagaggccgttctgcttc[C/T]aaatgcctactgaaagt gaaatgca	C	T	NM_001442 // upstream // 149988 // Hs.391561 // FABP4 // 2167 // fatty acid binding protein 4, adipocyte /// NM_005536 // downstream // 24759 // Hs.334022 // IMPA1 // 3612 // inositol(myo)-1(or 4)-monophosphatase 1	FABP4	FABP4 , rs890601, fatty acid binding protein 4, adipocyte ,q21.13
SNP_A-1667022	gacatatttattcaatgcaagtgtc[C/T]attctggtgaccagtcaca atttca	C	T	NM_001442 // upstream // 157627 // Hs.391561 // FABP4 // 2167 // fatty acid binding protein 4, adipocyte /// NM_005536 // downstream // 17120 // Hs.334022 // IMPA1 // 3612 // inositol(myo)-1(or 4)-monophosphatase 1	FABP4	FABP4 , rs726604, fatty acid binding protein 4, adipocyte ,q21.13
SNP_A-1796507	ggttaataaatctgaa[C/T]gacagctatcgtactc	C	T	NM_005536 // downstream // 14050 // Hs.492120 // IMPA1 // 3612 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA. /// ENST00000311489 // upstream // 16962 // — // — // — // — /// ENST00000256108 // downstream // 14050 // — //	IMPA1	IMPA1, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), q21.13
SNP_A-2065360	aattgtcagggacata[G/T]gtagtggctataggtt	G	T	NM_024699 // 3UTR // 0 // Hs.390395 // FLJ14007 // 79752 // Homo sapiens hypothetical protein FLJ14007 (FLJ14007), mRNA. /// ENST00000220669 // 3UTR // 0 // — // — // — // — // —	FLJ14007	FLJ14007, Homo sapiens hypothetical protein FLJ14007 (FLJ14007), q21.13
SNP_A-2129838	atacatatttggaacc[A/G]aacgggtacccattga	A	G	NM_152284 // intron // 0 // Hs.183861 // Shax3 // 92421 // Homo sapiens Snf7 homologue associated with Alix 3 (Shax3), mRNA. /// ENST00000297265 // intron // 0 // — // — // — // —	Shax3	Shax3, Homo sapiens Snf7 homologue associated with Alix 3 (Shax3), q21.13
SNP_A-1783500	ggcatcgggaacgtta[C/T]aaatagaaagtcccaa	C	T	NM_152284 // downstream // 21092 // Hs.183861 // Shax3 // 92421 // Homo sapiens Snf7 homologue associated with Alix 3 (Shax3), mRNA. /// NM_022133 // downstream // 18985 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript v	Shax3	Shax3, Homo sapiens Snf7 homologue associated with Alix 3 (Shax3), q21.13
SNP_A-2194120	catgactcagtttatc[A/G]cacataccatgctatt	A	G	NM_022133 // upstream // 69019 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 69019 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript vari	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1866241	tcccataaaagcacaa[A/G]ctcatcaattgaatac	A	G	NM_022133 // upstream // 546431 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 546431 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript va	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2013558	ttagtgagtcaggta[A/G]caactgcctgatctgt	A	G	NM_022133 // upstream // 855729 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 855729 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript va	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1681108	aaatgatagagaaaaagtaatatgaa[C/G]actaaatgtagaaac tgccttaaat	C	G	NM_022133 // upstream // 1285642 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152836 // upstream // 1283885 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152837 // upstream // 1283885 // Hs.310194 // SNX16 // 64089 // sorting nex	SNX16	SNX16, , rs7837095, sorting nexin 16, q21.13
SNP_A-2091710	agaaaagcaggagaaaa[C/G]tcacagaatcacttac	C	G	NM_022133 // upstream // 1205313 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1205313 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2307498	gcttatttcttggctc[C/T]attcgagatcttactc	C	T	NM_022133 // upstream // 1205428 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1205428 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2119765	agtatttcaaaatctg[C/G]caaaccgataggaata	C	G	NM_022133 // upstream // 1205549 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1205549 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1994066	gcttgtcttcttgcag[C/G]aggaaaggagatgaaa	C	G	NM_022133 // upstream // 1240101 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1240101 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1744951	ctatttgctcattggcttaaagagg[A/G]gtttattaaatacacctctga aattt	A	G	NM_022133 // upstream // 1467169 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152836 // upstream // 1465412 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152837 // upstream // 1465412 // Hs.310194 // SNX16 // 64089 // sorting nex	SNX16	SNX16, , rs7859564, sorting nexin 16, q21.13
SNP_A-2278589	gagctgatgaccagcc[A/G]aggctaacatattaca	A	G	NM_022133 // upstream // 1361215 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1361215 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2296353	gcatttaaatactaaa[A/G]gtgaatggccaattct	A	G	NM_022133 // upstream // 1362672 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1362672 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1861168	tcatatgaaccaagaa[A/C]gtgcccaaataaatag	A	C	NM_022133 // upstream // 1381260 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1381260 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043565	aactgtgcgggtgcta[C/T]attcctaccctata	C	T	NM_022133 // upstream // 1458353 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1458353 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1728099	acaaaaagtgtactgtatgcctctgt[A/T]aattcaaagttgcttttct gtaat	A	T	NM_022133 // upstream // 1572596 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152836 // upstream // 1570839 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152837 // upstream // 1570839 // Hs.310194 // SNX16 // 64089 // sorting nex	SNX16	SNX16 , rs921145, sorting nexin 16 ,q21.13
SNP_A-1686914	tgatacttctgaaaacatgacattta[C/G]gaaataaacaagaaca aaatctaag	C	G	NM_022133 // upstream // 1598541 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152836 // upstream // 1596784 // Hs.310194 // SNX16 // 64089 // sorting nexin 16 /// NM_152837 // upstream // 1596784 // Hs.310194 // SNX16 // 64089 // sorting nex	SNX16	SNX16 , rs7004770, sorting nexin 16 ,q21.13
SNP_A-2077700	accactgagggaagat[A/G]agactcccatgggga	A	G	NM_022133 // upstream // 1515563 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1515563 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1934094	ttctcagctgtattga[A/G]gaataattgacaaatt	A	G	NM_022133 // upstream // 1572965 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1572965 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-2295746	gcatgcaaagttataa[A/T]gtaagaattacagca	A	T	NM_022133 // upstream // 1767849 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 1767849 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.13
SNP_A-1819707	gttgtcactgacaaac[A/T]gtatcaattagctaat	A	T	NM_022133 // upstream // 2687747 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, mRNA. /// NM_152836 // upstream // 2687747 // Hs.492121 // SNX16 // 64089 // Homo sapiens sorting nexin 16 (SNX16), transcript	SNX16	SNX16, Homo sapiens sorting nexin 16 (SNX16), transcript variant 1, q21.2
SNP_A-2197831	cattgactgcattcca[A/G]aacctagtaaatcatg	A	G	NM_152565 // intron // 0 // Hs.436360 // ATP6V0D2 // 245972 // Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), mRNA. /// ENST00000285393 // intron // 0 // --- // --- // --- // ---	ATP6V0D2	ATP6V0D2, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), q21.3
SNP_A-1933438	ttctacattactgcta[A/G]catggccgtcattaat	A	G	NM_152565 // downstream // 38487 // Hs.436360 // ATP6V0D2 // 245972 // Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), mRNA. /// NM_138817 // downstream // 21344 // Hs.149095 // SLC7A13 // 157724 // Homo sapiens s	ATP6V0D2	ATP6V0D2, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), q21.3
SNP_A-2181063	cagacacataatttgg[A/C]aaaaagctctgattct	A	C	NM_152565 // downstream // 46431 // Hs.436360 // ATP6V0D2 // 245972 // Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), mRNA. /// NM_138817 // downstream // 13400 // Hs.149095 // SLC7A13 // 157724 // Homo sapiens s	ATP6V0D2	ATP6V0D2, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), q21.3
SNP_A-2065904	aatttctgatgtttta[A/G]agagaaattatctttt	A	G	NM_152565 // downstream // 46545 // Hs.436360 // ATP6V0D2 // 245972 // Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), mRNA. /// NM_138817 // downstream // 13286 // Hs.149095 // SLC7A13 // 157724 // Homo sapiens s	ATP6V0D2	ATP6V0D2, Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 2 (ATP6V0D2), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2257968	ctttgtctcagtttca[C/T]cattttaaagtgaggg	C	T	NM_138817 // upstream // 29172 // Hs.149095 // SLC7A13 // 157724 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 13 (SLC7A13), mRNA. /// NM_007013 // upstream // 114494 // Hs.533440 // WWP1 // 11059 // Homo sap	SLC7A13	SLC7A13, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 13 (SLC7A13), q21.3
SNP_A-2175828	cacatttaacggaata[C/T]gttttatgaccacaat	C	T	NM_138817 // upstream // 65466 // Hs.149095 // SLC7A13 // 157724 // Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 13 (SLC7A13), mRNA. /// NM_007013 // upstream // 78200 // Hs.533440 // WWP1 // 11059 // Homo sapi	SLC7A13	SLC7A13, Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 13 (SLC7A13), q21.3
SNP_A-1914527	tgttaaactctaaata[A/G]gccagattgcataaca	A	G	NM_019098 // intron // 0 // Hs.154433 // CNGB3 // 54714 // Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), mRNA. /// ENST00000320005 // intron // 0 // — // — // — // —	CNGB3	CNGB3, Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), q21.3
SNP_A-2135681	atcaaaaggaatgggg[A/G]actctatgcccagaca	A	G	NM_019098 // intron // 0 // Hs.154433 // CNGB3 // 54714 // Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), mRNA. /// ENST00000320005 // intron // 0 // — // — // — // —	CNGB3	CNGB3, Homo sapiens cyclic nucleotide gated channel beta 3 (CNGB3), q21.3
SNP_A-2097764	agagaccatgccatca[A/G]gtacaccagcagactc	A	G	NM_173538 // intron // 0 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// ENST00000319712 // intron // 0 // — // — // — // —	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-1994143	actctcttagctctag[C/T]cacttttaggaagtt	C	T	NM_173538 // intron // 0 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// ENST00000319712 // intron // 0 // — // — // — // —	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-1878367	tctgtcttatgcagtc[A/G]agagaaggactgaaat	A	G	NM_173538 // intron // 0 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// ENST00000319712 // intron // 0 // — // — // — // —	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2286190	gatgcatctagaataa[C/G]acttcccatcgccttc	C	G	NM_173538 // downstream // 39110 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 479883 // Hs.371738 // FLJ35775 // 138009 // Homo sapiens hypothetical protein FLJ35775 (FLJ35775)	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2202896	ccactcacttatgtta[C/T]agcctatggtaagtta	C	T	NM_173538 // downstream // 122219 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 396774 // Hs.371738 // FLJ35775 // 138009 // Homo sapiens hypothetical protein FLJ35775 (FLJ35775	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2022718	aaaaattagcacaaac[C/T]gtcagtgattttagac	C	T	NM_173538 // downstream // 164842 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 354151 // Hs.371738 // FLJ35775 // 138009 // Homo sapiens hypothetical protein FLJ35775 (FLJ35775	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-2093232	agaaccccgagtatga[C/T]ctgtcaataggggct	C	T	NM_173538 // downstream // 309534 // — // FLJ35802 // 168975 // Homo sapiens hypothetical protein FLJ35802 (FLJ35802), mRNA. /// NM_152418 // downstream // 209459 // Hs.371738 // FLJ35775 // 138009 // Homo sapiens hypothetical protein FLJ35775 (FLJ35775	FLJ35802	FLJ35802, Homo sapiens hypothetical protein FLJ35802 (FLJ35802), q21.3
SNP_A-1994176	atgattgtatgtgtga[C/T]gtatttcactaatatt	C	T	NM_005941 // upstream // 371301 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 371529 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2115006	agggcccctggtttaa[C/T]agaggtcatttacaat	C	T	NM_005941 // upstream // 504044 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA. /// NM_022564 // upstream // 504272 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1888202	tgagcgatcgctcaca[A/T]aggttgacatatacc	A	T	NM_005941 // upstream // 608849 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 609077 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2226566	ctaaggataacatagg[A/G]aaggttgtctaagcaa	A	G	NM_005941 // upstream // 753582 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 753810 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-1994185	ctactgaggaattatc[A/C]agagagcacaaattt	A	C	NM_005941 // upstream // 781683 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 781911 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2188118	cagtccaaatgaccta[A/T]ggtggtaatgatacaa	A	T	NM_005941 // upstream // 796907 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 797135 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-1828765	taagctttggtaatta[C/T]gtctatctacacaaaa	C	T	NM_005941 // upstream // 866533 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 866761 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2221081	ccttgtcactctaagc[C/T]gatctatcttgtacc	C	T	NM_005941 // upstream // 875408 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 875636 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2048506	aagcatgagctccaga[A/G]caaaattatttagttc	A	G	NM_005941 // upstream // 936166 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA /// NM_022564 // upstream // 936394 // Hs.546267 // MMP16 // 4325 // Homo sapiens matrix met	MMP16	MMP16, Homo sapiens matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, q21.3
SNP_A-2149086	atggttttatcggaa[A/G]tgcaaagggcatggca	A	G	NM_003821 // upstream // 291500 // Hs.103755 // RIPK2 // 8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA /// ENST00000326299 // upstream // 51879 // — // — // — /// ENST00000333197 // upstream // 51397 // –	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-2173180	cacaacacctgaagaa[C/T]agtgtgccttgaagtc	C	T	NM_003821 // upstream // 291460 // Hs.103755 // RIPK2 // 8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA /// ENST00000326299 // upstream // 51919 // — // — // — /// ENST00000333197 // upstream // 51437 // –	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-2128590	ataatagtgaatgcca[A/G]ataagtgcaatggtcc	A	G	NM_003821 // upstream // 285770 // Hs.103755 // RIPK2 // 8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA /// ENST00000326299 // upstream // 57609 // — // — // — /// ENST00000333197 // upstream // 57127 // –	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-1655663	gaagaacagggagaaaatctgggc[A/G]atgagaggagtca agtttcaaaaca	A	G	NM_003821 // upstream // 139968 // Hs.103755 // RIPK2 // 8767 // receptor-interacting serine-threonine kinase 2 /// NM_005941 // upstream // 1290590 // Hs.90800 // MMP16 // 4325 // matrix metalloproteinase 16 (membrane-inserted) /// NM_022564 // upstream	RIPK2	RIPK2 , rs9297690, receptor-interacting serine-threonine kinase 2 ,q21.3
SNP_A-1906465	tggtggatgaattcta[A/C]atgagctactgtttca	A	C	NM_003821 // upstream // 199748 // Hs.103755 // RIPK2 // 8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA /// ENST00000326299 // upstream // 143631 // — // — // — /// ENST00000333197 // upstream // 143149 //	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1994197	tccattgccccaacag[C/T]caaattgtgaccttct	C	T	NM_003821 // upstream // 136590 // Hs.103755 // RIPK2 // 8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA. /// ENST00000326299 // upstream // 206789 // — // — // — /// ENST00000333197 // upstream // 206307 //	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-1994198	ggaacgtgcaatttgd[C/T]gaacatggatcacagt	C	T	NM_003821 // upstream // 129335 // Hs.103755 // RIPK2 // 8767 // Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA. /// ENST00000326299 // upstream // 214044 // — // — // — /// ENST00000333197 // upstream // 213562 //	RIPK2	RIPK2, Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), q21.3
SNP_A-2299499	gccttgattacatac[C/T]gcttatcaggccatag	C	T	NM_022351 // upstream // 19569 // Hs.302754 // EFCBP1 // 64168 // Homo sapiens EF hand calcium binding protein 1 (EFCBP1), mRNA. /// ENST00000324979 // upstream // 126707 // — // — // — /// ENST00000242753 // upstream // 19569 // — // — /	EFCBP1	EFCBP1, Homo sapiens EF hand calcium binding protein 1 (EFCBP1), q21.3
SNP_A-2094728	agaatcaagtcaitta[C/T]gttatggtaccagaat	C	T	NM_022351 // intron // 0 // Hs.302754 // EFCBP1 // 64168 // Homo sapiens EF hand calcium binding protein 1 (EFCBP1), mRNA. /// ENST00000242753 // intron // 0 // — // — // —	EFCBP1	EFCBP1, Homo sapiens EF hand calcium binding protein 1 (EFCBP1), q21.3
SNP_A-1994227	ggaaaaatactgtccat[C/T]gaagtgagcaccatgt	C	T	NM_022351 // intron // 0 // Hs.302754 // EFCBP1 // 64168 // Homo sapiens EF hand calcium binding protein 1 (EFCBP1), mRNA. /// ENST00000242753 // intron // 0 // — // — // —	EFCBP1	EFCBP1, Homo sapiens EF hand calcium binding protein 1 (EFCBP1), q21.3
SNP_A-1994230	ggagggatggattcag[A/G]agacatgggttccaag	A	G	NM_022351 // intron // 0 // Hs.302754 // EFCBP1 // 64168 // Homo sapiens EF hand calcium binding protein 1 (EFCBP1), mRNA. /// ENST00000242753 // intron // 0 // — // — // —	EFCBP1	EFCBP1, Homo sapiens EF hand calcium binding protein 1 (EFCBP1), q21.3
SNP_A-1887188	tgagaaatgatatccc[A/G]aagtctaatccaatca	A	G	NM_022351 // intron // 0 // Hs.302754 // EFCBP1 // 64168 // Homo sapiens EF hand calcium binding protein 1 (EFCBP1), mRNA. /// ENST00000242753 // intron // 0 // — // — // —	EFCBP1	EFCBP1, Homo sapiens EF hand calcium binding protein 1 (EFCBP1), q21.3
SNP_A-1911036	tgtctccttagtgtg[C/T]atggcttaaggtatct	C	T	NM_016023 // intron // 0 // Hs.30532 // CGI-77 // 51633 // Homo sapiens CGI-77 protein (CGI-77), mRNA. /// ENST00000285420 // intron // 0 // — // — // —	CGI-77	CGI-77, Homo sapiens CGI-77 protein (CGI-77), q21.3
SNP_A-2273514	gactctgttgagcaa[A/G]tagaataaagtatgat	A	G	NM_134266 // intron // 0 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // intron // 0 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, m	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2274535	gagaaaaacagattca[A/G]aactctaaatagaaaa	A	G	NM_134266 // intron // 0 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // intron // 0 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, m	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-1940975	ttgctcaatggtcaac[C/T]gtattgctaagtgaa	C	T	NM_134266 // downstream // 282510 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 279078 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute ca	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2061711	aatggaagtcaaagtc[A/G]agatctgtaaatggca	A	G	NM_134266 // downstream // 318971 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 315539 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute ca	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2075189	acatctctatagccac[C/T]ggttcaagtttaatt	C	T	NM_134266 // downstream // 495486 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 492054 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute ca	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138503	atccatgcactgcaga[A/G]tagatgttggatagca	A	G	NM_134266 // downstream // 526488 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, mRNA. /// NM_052832 // downstream // 523056 // Hs.354013 // SLC26A7 // 115111 // Homo sapiens solute ca	SLC26A7	SLC26A7, Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 2, q21.3
SNP_A-2127546	ataacattcaaggaaa[C/T]ggggaagtatgaaaaa	C	T	NM_175635 // intron // 0 // Hs.368431 // RUNX1T1 // 862 // Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), transcript varia /// NM_175636 // intron // 0 // Hs.368431 // RUNX1T1 // 862 // Homo	RUNX1T1	RUNX1T1, Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), transcript varia ,q21.3
SNP_A-2172363	caattacatcggcaac[A/G]aaaactcattttacaa	A	G	ENST00000328621 // downstream // 99940 // — // — // — // — /// ENST00000327715 // upstream // 243935 // — // — // — // —	-	q22.1
SNP_A-2060274	aatgaagccagaattc[C/T]aaaaaacataagctaa	C	T	ENST00000328621 // downstream // 283659 // — // — // — // — /// ENST00000327715 // upstream // 60216 // — // — // — // —	-	q22.1
SNP_A-2291989	gcacatggccacagag[G/T]agacaaatgttttccg	G	T	ENST00000328621 // downstream // 290906 // — // — // — // — /// ENST00000327715 // upstream // 52969 // — // — // — // —	-	q22.1
SNP_A-1834168	tacatctttacctaaa[A/G]tgattaacaagtagcc	A	G	ENST00000327715 // downstream // 56624 // — // — // — // — /// ENST00000344692 // upstream // 359291 // — // — // — // —	-	q22.1
SNP_A-2160453	atttcatttagtggaa[A/G]atatgtatcaagttgt	A	G	NM_153704 // downstream // 53467 // Hs.116240 // MGC26979 // 91147 // Homo sapiens hypothetical protein MGC26979 (MGC26979), mRNA. /// NM_153704 // downstream // 51151 // Hs.116240 // MGC26979 // 91147 // Homo sapiens hypothetical protein MGC26979 (MGC269	MGC26979	MGC26979, Homo sapiens hypothetical protein MGC26979 (MGC26979), q22.1
SNP_A-2063100	aatgttgaaagttggc[C/T]agatgaagaaatgaag	C	T	NM_018444 // downstream // 94683 // Hs.22265 // PPM2C // 54704 // Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein /// AF155661 // downstream // 96376 // Hs.22265 // PPM2C //	PPM2C	PPM2C, Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein ,q22.1
SNP_A-2206212	ccatcattaagctaga[C/T]aaatcccagaggtcaa	C	T	NM_018444 // downstream // 148006 // Hs.22265 // PPM2C // 54704 // Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein /// AF155661 // downstream // 149699 // Hs.22265 // PPM2C /	PPM2C	PPM2C, Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein ,q22.1
SNP_A-2281322	gagtatgggatggacc[A/G]ctagtactaaagccag	A	G	NM_018444 // downstream // 148627 // Hs.22265 // PPM2C // 54704 // Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein /// AF155661 // downstream // 150320 // Hs.22265 // PPM2C /	PPM2C	PPM2C, Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein ,q22.1
SNP_A-2233172	ctcagcctttactagc[A/G]ccagtgtcttgtacaa	A	G	NM_018444 // downstream // 148683 // Hs.22265 // PPM2C // 54704 // Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein /// AF155661 // downstream // 150376 // Hs.22265 // PPM2C /	PPM2C	PPM2C, Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit (PPM2C), nuclear gene encoding mitochondrial protein ,q22.1
SNP_A-1809337	gtgactggataggaga[A/C]agccacaaaacgacaa	A	C	NM_004063 // upstream // 35916 // Hs.89436 // CDH17 // 1015 // Homo sapiens cadherin 17, LI cadherin (liver-intestine) (CDH17), mRNA. /// NM_005261 // downstream // 4761 // Hs.345139 // GEM // 2669 // Homo sapiens GTP binding protein overexpressed in skel	CDH17	CDH17, Homo sapiens cadherin 17, LI cadherin (liver-intestine) (CDH17), q22.1
SNP_A-2303866	gctcatacaaatgtga[A/G]gccattaagaaaacat	A	G	NM_005261 // upstream // 63834 // Hs.345139 // GEM // 2669 // Homo sapiens GTP binding protein overexpressed in skeletal muscle (GEM), transcript variant 1, mRNA. /// NM_181702 // upstream // 63834 // Hs.345139 // GEM // 2669 // Homo sapiens GTP binding p	GEM	GEM, Homo sapiens GTP binding protein overexpressed in skeletal muscle (GEM), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2212733	cccttgatgatctttc[C/T]cccattctgtaccccc	C	T	NM_183009 // intron // 0 // Hs.202238 // DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, mRNA. /// NM_015496 // intron // 0 // Hs.202238 // DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP4	DKFZP434I116	DKFZP434I116, Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, q22.1
SNP_A-1735138	aagatctattttagtcttcaactta[C/T]gggtctctttgggcctcagtg actt	C	T	AF132206 // downstream // 74320 // - // - // - // Homo sapiens PRO2397 mRNA, complete cds. /// NM_015496 // upstream // 96320 // Hs.50273 // DKFZP434I116 // 25962 // DKFZP434I116 protein /// NM_017697 // upstream // 23494 // Hs.24743 // FLJ20171 // 54845	-	- , rs756474, Homo sapiens PRO2397 mRNA, complete cds. ,q22.1
SNP_A-2013616	tttcaacaaatatgca[C/T]tgcactgtgagagatc	C	T	NM_183009 // upstream // 50365 // Hs.202238 // DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, mRNA. /// NM_015496 // upstream // 50365 // Hs.202238 // DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 pro	DKFZP434I116	DKFZP434I116, Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, q22.1
SNP_A-1939783	ttgcaactgttatgaa[A/T]tgcgctacaatggaag	A	T	NM_183009 // upstream // 56175 // Hs.202238 // DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, mRNA. /// NM_015496 // upstream // 56175 // Hs.202238 // DKFZP434I116 // 25962 // Homo sapiens DKFZP434I116 pro	DKFZP434I116	DKFZP434I116, Homo sapiens DKFZP434I116 protein (DKFZP434I116), transcript variant 2, q22.1
SNP_A-2057231	aatataggatcgtata[A/C]tagttttttctcttc	A	C	NM_017697 // intron // 0 // Hs.487471 // FLJ20171 // 54845 // Homo sapiens hypothetical protein FLJ20171 (FLJ20171), mRNA. /// ENST00000358397 // intron // 0 // — // — // — // — /// ENST00000314460 // intron // 0 // — // — // — // —	FLJ20171	FLJ20171, Homo sapiens hypothetical protein FLJ20171 (FLJ20171), q22.1
SNP_A-1824735	taaagagatttataag[A/G]cagatgcaccgtggag	A	G	NM_024613 // downstream // 12336 // Hs.29724 // PLEKHF2 // 79666 // Homo sapiens pleckstrin homology domain containing, family F (with FYVE domain) member 2 (PLEKHF2), mRNA. /// NM_177965 // downstream // 75946 // Hs.128189 // LOC157657 // 157657 // Homo	PLEKHF2	PLEKHF2, Homo sapiens pleckstrin homology domain containing, family F (with FYVE domain) member 2 (PLEKHF2), q22.1
SNP_A-1897547	tgctgatgtgcaagta[C/G]ataatcacagaaacca	C	G	NM_177965 // upstream // 67028 // Hs.128189 // LOC157657 // 157657 // Homo sapiens hypothetical protein LOC157657 (LOC157657), mRNA. /// ENST00000286688 // upstream // 67028 // — // — // — // — /// ENST00000357342 // downstream // 216263 // — //	LOC157657	LOC157657, Homo sapiens hypothetical protein LOC157657 (LOC157657), q22.1
SNP_A-1682730	gctgtcaccgtgaatcaggctagac[C/T]caacttgaagaaacat cctgggatc	C	T	NM_006294 // downstream // 759387 // Hs.131255 // UQCRB // 7381 // ubiquinol-cytochrome c reductase binding protein /// NM_177965 // upstream // 201911 // Hs.128189 // LOC157657 // 157657 // hypothetical protein LOC157657	UQCRB	UQCRB , rs10504949, ubiquinol-cytochrome c reductase binding protein ,q22.1
SNP_A-1682676	gcctatcctctgccatgctgtgaaa[A/C]gataacctgctttgggtg ctctgat	A	C	NM_006294 // downstream // 759284 // Hs.131255 // UQCRB // 7381 // ubiquinol-cytochrome c reductase binding protein /// NM_177965 // upstream // 202014 // Hs.128189 // LOC157657 // 157657 // hypothetical protein LOC157657	UQCRB	UQCRB , rs10504950, ubiquinol-cytochrome c reductase binding protein ,q22.1
SNP_A-1659206	gtgtgttcctgttcaaaaaacttca[A/G]gttaacatccattgtccta gagtaa	A	G	NM_006294 // downstream // 647966 // Hs.131255 // UQCRB // 7381 // ubiquinol-cytochrome c reductase binding protein /// NM_177965 // upstream // 313332 // Hs.128189 // LOC157657 // 157657 // hypothetical protein LOC157657	UQCRB	UQCRB , rs2873824, ubiquinol-cytochrome c reductase binding protein ,q22.1
SNP_A-1805025	gtcatctataaagcca[A/G]acttcattcattggaa	A	G	NM_177965 // upstream // 252908 // Hs.128189 // LOC157657 // 157657 // Homo sapiens hypothetical protein LOC157657 (LOC157657), mRNA. /// ENST00000286688 // upstream // 252908 // — // — // — // — /// ENST00000357342 // downstream // 30383 // — /	LOC157657	LOC157657, Homo sapiens hypothetical protein LOC157657 (LOC157657), q22.1
SNP_A-2161700	atttggtgcactgtca[C/G]tagcttaaagacggag	C	G	ENST00000357342 // upstream // 9332 // — // — // — // — /// ENST00000359064 // upstream // 5821 // — // — // — // — /// ENST00000332041 // downstream // 505753 // — // — // — // —	-	q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2205996	ccatatcttctatca[G/T]gaattacttgaaaa	G	T	ENST00000357342 // upstream // 71373 /// ENST00000359064 // upstream // 67862 /// ENST00000332041 // downstream // 443712	-	q22.1
SNP_A-2013626	gttcaactgcctggta[A/G]aattaaggaaaaaaag	A	G	ENST00000357342 // upstream // 73696 /// ENST00000359064 // upstream // 70185 /// ENST00000332041 // downstream // 441389	-	q22.1
SNP_A-1994326	gggaaaagtgtgacga[C/T]ggtccaacaaagagtt	C	T	ENST00000357342 // upstream // 168433 /// ENST00000359064 // upstream // 164922 /// ENST00000332041 // downstream // 346652	-	q22.1
SNP_A-2284207	gatatgtggagagggag[G/T]attgcaaggctagaga	G	T	ENST00000357342 // upstream // 353899 /// ENST00000359064 // upstream // 350388 /// ENST00000332041 // downstream // 161186	-	q22.1
SNP_A-2050562	aaggattcagaaaaca[C/T]gggtgagccagataat	C	T	ENST00000357342 // upstream // 421794 /// ENST00000359064 // upstream // 418283 /// ENST00000332041 // downstream // 93291	-	q22.1
SNP_A-2121450	agtctttccttcacaj[A/T]ataactcagagataaa	A	T	ENST00000357342 // upstream // 500573 /// ENST00000359064 // upstream // 497062 /// ENST00000332041 // downstream // 14512	-	q22.1
SNP_A-2122659	agtggaagcagtacaga[C/G]tccatgggatgcttt	C	G	NM_014754 // downstream // 40643 // Hs.292579 // PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream // 118479 // Hs.1501 // SDC2 // 6383 // Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell s	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-2166506	caaatgctctgttact[G/T]aggtacttagccttc	G	T	NM_014754 // downstream // 54305 // Hs.292579 // PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream // 104817 // Hs.1501 // SDC2 // 6383 // Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell s	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-2266203	gaagggcagaaaacaa[C/T]gaacaagaagtgggca	C	T	NM_014754 // downstream // 106879 // Hs.292579 // PTDSS1 // 9791 // Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA. /// NM_002998 // upstream // 52243 // Hs.1501 // SDC2 // 6383 // Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell s	PTDSS1	PTDSS1, Homo sapiens phosphatidylserine synthase 1 (PTDSS1), q22.1
SNP_A-1897251	tgctctgctgggtcca[C/T]aatcaatacatggaa	C	T	NM_002998 // intron // 0 // Hs.1501 // SDC2 // 6383 // Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), mRNA. /// ENST00000302190 // intron // 0 // — // — // — // —	SDC2	SDC2, Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), q22.1
SNP_A-1994355	taactctacttagc[C/T]aaaaaaagaagtgtata	C	T	NM_002998 // intron // 0 // Hs.1501 // SDC2 // 6383 // Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), mRNA. /// ENST00000302190 // intron // 0 // — // — // — // —	SDC2	SDC2, Homo sapiens syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), q22.1
SNP_A-1862603	tcattagtcataaaca[C/T]tgggggaggttactg	C	T	NM_016134 // intron // 0 // Hs.156178 // PGCP // 10404 // Homo sapiens plasma glutamate carboxypeptidase (PGCP), mRNA. /// ENST00000325141 // intron // 0 // — // — // — // — /// ENST00000220763 // intron // 0 // — // — // —	PGCP	PGCP, Homo sapiens plasma glutamate carboxypeptidase (PGCP), q22.1
SNP_A-1828978	taaggcctgtttccc[C/T]acatgacagatgaaga	C	T	NM_033512 // upstream // 41738 // Hs.173094 // TSPYL5 // 85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 324555 // Hs.377155 // LYRIC // 92140 // Homo sapiens LYRIC/3D3 (LYRIC), mRNA. /// ENST00000332128 // upstream // 41738	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-1916215	tgttgggttgttttcca[C/T]ggctagcaagatgaaa	C	T	NM_033512 // upstream // 72249 // Hs.173094 // TSPYL5 // 85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 294044 // Hs.377155 // LYRIC // 92140 // Homo sapiens LYRIC/3D3 (LYRIC), mRNA. /// ENST00000332128 // upstream // 72249	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2070591	acacctgtacatttta[C/T]ggaaggacacaggcct	C	T	NM_033512 // upstream // 78637 // Hs.173094 // TSPYL5 // 85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 287656 // Hs.377155 // LYRIC // 92140 // Homo sapiens LYRIC/3D3 (LYRIC), mRNA. /// ENST00000322128 // upstream // 78637	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-1827620	taactggaaaggccaa[C/G]agagttatttttgca	C	G	NM_033512 // upstream // 82384 // Hs.173094 // TSPYL5 // 85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 283909 // Hs.377155 // LYRIC // 92140 // Homo sapiens LYRIC/3D3 (LYRIC), mRNA. /// ENST00000322128 // upstream // 82384	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-1867200	tccctgctgtttccag[A/G]ccttttgtgcacccac	A	G	NM_033512 // upstream // 116961 // Hs.173094 // TSPYL5 // 85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 249332 // Hs.377155 // LYRIC // 92140 // Homo sapiens LYRIC/3D3 (LYRIC), mRNA. /// ENST00000322128 // upstream // 169	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-2056746	aatagctcctaaact[A/C]aactgtcagctaact	A	C	NM_033512 // upstream // 290566 // Hs.173094 // TSPYL5 // 85453 // Homo sapiens TSPY-like 5 (TSPYL5), mRNA. /// NM_178812 // upstream // 75727 // Hs.377155 // LYRIC // 92140 // Homo sapiens LYRIC/3D3 (LYRIC), mRNA. /// ENST00000322128 // upstream // 29056	TSPYL5	TSPYL5, Homo sapiens TSPY-like 5 (TSPYL5), q22.1
SNP_A-1798937	gtaagaggaggacattct[A/G]agagaaaaggtagagt	A	G	NM_002380 // intron // 0 // Hs.189445 // MATN2 // 4147 // Homo sapiens matrilin 2 (MATN2), transcript variant 1, mRNA. /// NM_030583 // intron // 0 // Hs.189445 // MATN2 // 4147 // Homo sapiens matrilin 2 (MATN2), transcript variant 2, mRNA. /// ENST00000	MATN2	MATN2, Homo sapiens matrilin 2 (MATN2), transcript variant 1, q22.1
SNP_A-2233328	ctcaggcttctaataa[C/T]ggactccagatttta	C	T	NM_002380 // intron // 0 // Hs.189445 // MATN2 // 4147 // Homo sapiens matrilin 2 (MATN2), transcript variant 1, mRNA. /// NM_030583 // intron // 0 // Hs.189445 // MATN2 // 4147 // Homo sapiens matrilin 2 (MATN2), transcript variant 2, mRNA. /// ENST00000	MATN2	MATN2, Homo sapiens matrilin 2 (MATN2), transcript variant 1, q22.1
SNP_A-2272015	gaccctaacactctcc[A/C]agtcaaatcccttat	A	C	NM_173549 // intron // 0 // Hs.171455 // FLJ39553 // 203111 // Homo sapiens hypothetical protein FLJ39553 (FLJ39553), mRNA. /// ENST00000318528 // intron // 0 // — // — // —	FLJ39553	FLJ39553, Homo sapiens hypothetical protein FLJ39553 (FLJ39553), q22.2
SNP_A-2028438	aaactctccgatttag[A/G]acaacagcaacaaata	A	G	NM_024759 // intron // 0 // Hs.309489 // FLJ13955 // 79815 // Homo sapiens hypothetical protein FLJ13955 (FLJ13955), mRNA. /// ENST00000341166 // intron // 0 // — // — // —	FLJ13955	FLJ13955, Homo sapiens hypothetical protein FLJ13955 (FLJ13955), q22.2
SNP_A-2237506	ctctcgatgcagaaac[C/T]gatttttccatttttg	C	T	NM_006281 // intron // 0 // Hs.492333 // STK3 // 6788 // Homo sapiens serine/threonine kinase 3 (STE20 homolog, yeast) (STK3), mRNA. /// ENST00000354930 // intron // 0 // — // — // —	STK3	STK3, Homo sapiens serine q22.2
SNP_A-2052759	aagtcaaggttctaaa[C/T]gtctaaaagtcactga	C	T	NM_184042 // intron // 0 // Hs.191540 // COH1 // 157680 // Homo sapiens Cohen syndrome 1 (COH1), transcript variant 2, mRNA. /// NM_181661 // intron // 0 // Hs.191540 // COH1 // 157680 // Homo sapiens Cohen syndrome 1 (COH1), transcript variant 4, mRNA. /	COH1	COH1, Homo sapiens Cohen syndrome 1 (COH1), transcript variant 2, q22.2
SNP_A-2268372	gaatgcccttgaagta[C/G]gtgggcaggctctatg	C	G	NM_152564 // intron // 0 // Hs.191540 // COH1 // 157680 // Homo sapiens Cohen syndrome 1 (COH1), transcript variant 1, mRNA. /// NM_181661 // intron // 0 // Hs.191540 // COH1 // 157680 // Homo sapiens Cohen syndrome 1 (COH1), transcript variant 4, mRNA. /	COH1	COH1, Homo sapiens Cohen syndrome 1 (COH1), transcript variant 1, q22.2
SNP_A-2116375	aggtaggtatttgaga[A/G]ccacatatgaatatta	A	G	NM_003114 // intron // 0 // Hs.492373 // SPAG1 // 6674 // Homo sapiens sperm associated antigen 1 (SPAG1), transcript variant 1, mRNA. /// NM_172218 // intron // 0 // Hs.492373 // SPAG1 // 6674 // Homo sapiens sperm associated antigen 1 (SPAG1), transcrip	SPAG1	SPAG1, Homo sapiens sperm associated antigen 1 (SPAG1), transcript variant 1, q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086252	actctggtccatttag[A/T]attggcttatgcttct	A	T	NM_183419 // upstream // 61898 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream // 61898 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), tra	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2
SNP_A-1914093	tgtgtggtttctttag[C/G]agagctggtagttg	C	G	NM_183419 // upstream // 72225 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream // 72225 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), tra	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2
SNP_A-2177350	cacctttatccacctg[A/C]aagtatgttatgttttg	A	C	NM_183419 // upstream // 85714 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream // 85714 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), tra	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2
SNP_A-2108872	agcttaacccttttggt[A/G]aatcagcgttattcca	A	G	NM_183419 // upstream // 85756 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream // 85756 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), tra	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2
SNP_A-2201477	ccaatggctaccaaaca[A/G]ctagaactaccaatagc	A	G	NM_183419 // upstream // 150355 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, mRNA. /// NM_015435 // upstream // 150355 // Hs.292882 // RNF19 // 25897 // Homo sapiens ring finger protein 19 (RNF19), t	RNF19	RNF19, Homo sapiens ring finger protein 19 (RNF19), transcript variant 1, q22.2
SNP_A-1910806	tgtctaacctcttcaa[A/G]gctatcacacaagtaa	A	G	NM_198401 // upstream // 7998 // Hs.530199 // LOC157567 // 157567 // Homo sapiens hypothetical protein LOC157567 (LOC157567), mRNA. /// NM_152628 // downstream // 5138 // Hs.436424 // MGC39715 // 169166 // Homo sapiens hypothetical protein MGC39715 (MGC39	LOC157567	LOC157567, Homo sapiens hypothetical protein LOC157567 (LOC157567), q22.3
SNP_A-2140578	atctccttttgctgtaaa[C/T]gcagcgtggtgtcata	C	T	NM_002568 // upstream // 26058 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA. /// NM_002568 // upstream // 25410 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic 1	PABPC1	PABPC1, Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), q22.3
SNP_A-1864645	tccagcaacacttaaac[C/T]gcttctgggtgacagg	C	T	NM_002568 // upstream // 167610 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA. /// NM_002568 // upstream // 166962 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic	PABPC1	PABPC1, Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), q22.3
SNP_A-2269849	gacaagttctttaacc[C/T]ctcctggtctctgtta	C	T	NM_002568 // upstream // 167878 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA. /// NM_002568 // upstream // 167230 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic	PABPC1	PABPC1, Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), q22.3
SNP_A-2173191	cacaacagtctggtga[G/T]ataggaattattatta	G	T	NM_002568 // upstream // 171389 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA. /// NM_002568 // upstream // 170741 // Hs.387804 // PABPC1 // 26986 // Homo sapiens poly(A) binding protein, cytoplasmic	PABPC1	PABPC1, Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), q22.3
SNP_A-2110473	aggacaaagactgtag[C/G]atttcactaatatgag	C	G	NM_001029 // downstream // 846 // Hs.137367 // RPS26 // 6231 // Homo sapiens ribosomal protein S26 (RPS26), mRNA. /// NM_003406 // downstream // 21656 // Hs.492407 // YWHAZ // 7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activa	RPS26	RPS26, Homo sapiens ribosomal protein S26 (RPS26), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2180195	cagaaactacaggaac[A/C]aatttctgtctgtaag	A	C	NM_001029 // downstream // 6301 // Hs.137367 // RPS26 // 6231 // Homo sapiens ribosomal protein S26 (RPS26), mRNA. /// NM_003406 // downstream // 16201 // Hs.492407 // YWHAZ // 7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activ	RPS26	RPS26, Homo sapiens ribosomal protein S26 (RPS26), q22.3
SNP_A-1853917	tcaaaagtgattctca[A/G]taagtacagcaccta	A	G	NM_003406 // intron // 0 // Hs.492407 // YWHAZ // 7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), transcript varian /// NM_145690 // intron // 0 // Hs.492407 // YWHAZ // 7534 // Homo s	YWHAZ	YWHAZ, Homo sapiens tyrosine 3-monooxygenase q22.3
SNP_A-1933554	ttctagacacctgata[C/T]ggaaaactatgttactt	C	T	NM_003406 // upstream // 98387 // Hs.492407 // YWHAZ // 7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), transcript varian /// NM_145690 // upstream // 98387 // Hs.492407 // YWHAZ // 75	YWHAZ	YWHAZ, Homo sapiens tyrosine 3-monooxygenase,q22.3
SNP_A-1800729	gtagaagtgatgtgag[C/T]agaggctttaaatgtg	C	T	NM_003406 // upstream // 211917 // Hs.492407 // YWHAZ // 7534 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), transcript varian /// NM_145690 // upstream // 211917 // Hs.492407 // YWHAZ //	YWHAZ	YWHAZ, Homo sapiens tyrosine 3-monooxygenase q22.3
SNP_A-1837809	tacttttagaaatcct[C/G]aaccttctcagtatag	C	G	NM_016096 // intron // 0 // Hs.374485 // LOC51123 // 51123 // Homo sapiens HSPC038 protein (LOC51123), mRNA. /// ENST00000311212 // intron // 0 // --- // --- // ---	LOC51123	LOC51123, Homo sapiens HSPC038 protein (LOC51123), q22.3
SNP_A-1864426	tccacttagtgcagaa[C/T]cctagaactttcctgg	C	T	NM_016096 // upstream // 26173 // Hs.374485 // LOC51123 // 51123 // Homo sapiens HSPC038 protein (LOC51123), mRNA. /// NM_024915 // upstream // 260969 // Hs.161160 // TFCP2L3 // 79977 // Homo sapiens transcription factor CP2-like 3 (TFCP2L3), mRNA. /// EN	LOC51123	LOC51123, Homo sapiens HSPC038 protein (LOC51123), q22.3
SNP_A-1799455	gtaatgactgcaggta[C/G]gagggggcctaaaggac	C	G	NM_016096 // upstream // 196883 // Hs.374485 // LOC51123 // 51123 // Homo sapiens HSPC038 protein (LOC51123), mRNA. /// NM_024915 // upstream // 90259 // Hs.161160 // TFCP2L3 // 79977 // Homo sapiens transcription factor CP2-like 3 (TFCP2L3), mRNA. /// EN	LOC51123	LOC51123, Homo sapiens HSPC038 protein (LOC51123), q22.3
SNP_A-2066916	acaaacaaaaatcctа[C/T]cttgattgcccactc	C	T	NM_016096 // upstream // 263246 // Hs.374485 // LOC51123 // 51123 // Homo sapiens HSPC038 protein (LOC51123), mRNA. /// NM_024915 // upstream // 23896 // Hs.161160 // TFCP2L3 // 79977 // Homo sapiens transcription factor CP2-like 3 (TFCP2L3), mRNA. /// EN	LOC51123	LOC51123, Homo sapiens HSPC038 protein (LOC51123), q22.3
SNP_A-1887937	tgagcaaccactgcct[A/G]aaccattggactttgg	A	G	NM_024915 // intron // 0 // Hs.161160 // TFCP2L3 // 79977 // Homo sapiens transcription factor CP2-like 3 (TFCP2L3), mRNA. /// ENST00000251808 // intron // 0 // --- // --- // ---	TFCP2L3	TFCP2L3, Homo sapiens transcription factor CP2-like 3 (TFCP2L3), q22.3
SNP_A-1648588	caaccataatgacataaacagtgaa[A/T]attgtttaacccataat tgtgata	A	T	AF251061 // intron // 0 // Hs.90063 // NCALD // 83988 // neurocalcin delta	NCALD	NCALD , rs4490096, neurocalcin delta,q22.3
SNP_A-2122428	agtgccttagtcaga[A/T]cagagaagagtagcga	A	T	NM_032041 // intron // 0 // Hs.492427 // NCALD // 83988 // Homo sapiens neurocalcin delta (NCALD), mRNA. /// ENST00000311028 // intron // 0 // --- // --- // --- /// ENST00000220931 // intron // 0 // --- // --- // ---	NCALD	NCALD, Homo sapiens neurocalcin delta (NCALD), q22.3
SNP_A-1994452	gtatttcaacagccac[A/G]aggatcctgtctacgt	A	G	NM_024410 // downstream // 76689 // Hs.159274 // ODF1 // 4956 // Homo sapiens outer dense fiber of sperm tails 1 (ODF1), mRNA. /// NM_005655 // downstream // 11086 // Hs.435001 // KLF10 // 7071 // Homo sapiens TGFB inducible early growth response (TIEG),	ODF1	ODF1, Homo sapiens outer dense fiber of sperm tails 1 (ODF1), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2245254	ctggctccttcttagc[G/T]gaaatatccccttttt	G	T	NM_015878 // upstream // 76920 // Hs.459106 // OAZIN // 51582 // Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, mRNA. /// NM_148174 // upstream // 76920 // Hs.459106 // OAZIN // 51582 // Homo sapiens ornithine decar	OAZIN	OAZIN, Homo sapiens ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, q22.3
SNP_A-2116858	aggtctgactctatca[C/T]agttaaagcgacttga	C	T	NM_014677 // intron // 0 // Hs.117767 // RIMS2 // 9699 // Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // intron // 0 // Hs.117767 // RIMS2 // 9699 // Homo sapiens regulating synaptic membrane exocytosis 2, mRNA (cDNA	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1888317	tgagctggacatgaaa[A/C]ataggcagattgggac	A	C	NM_014677 // intron // 0 // Hs.117767 // RIMS2 // 9699 // Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // intron // 0 // Hs.117767 // RIMS2 // 9699 // Homo sapiens regulating synaptic membrane exocytosis 2, mRNA (cDNA	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-1844633	tataactatagacatc[C/G]atagcttactataata	C	G	NM_014677 // downstream // 78779 // Hs.117767 // RIMS2 // 9699 // Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), mRNA. /// BC043144 // downstream // 78779 // Hs.117767 // RIMS2 // 9699 // Homo sapiens regulating synaptic membrane exocytos	RIMS2	RIMS2, Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), q22.3
SNP_A-2039080	aacaggtagaatcaaa[A/G]tcctgtatgtatgttc	A	G	NM_030788 // downstream // 2360 // Hs.208036 // TM7SF4 // 81501 // Homo sapiens transmembrane 7 superfamily member 4 (TM7SF4), mRNA. /// NM_001385 // downstream // 20377 // Hs.443161 // DPYS // 1807 // Homo sapiens dihydropyrimidinase (DPYS), mRNA. /// EN	TM7SF4	TM7SF4, Homo sapiens transmembrane 7 superfamily member 4 (TM7SF4), q22.3
SNP_A-2171294	caatatgccagagtcc[A/G]ggaagtctccaggcag	A	G	NM_013437 // intron // 0 // Hs.301974 // LRP12 // 29967 // Homo sapiens low density lipoprotein-related protein 12 (LRP12), mRNA. /// ENST00000276654 // intron // 0 // — // — // — // —	LRP12	LRP12, Homo sapiens low density lipoprotein-related protein 12 (LRP12), q22.3
SNP_A-2217808	cctgattttagtggca[C/G]ctacatgaatgtgtac	C	G	NM_013437 // intron // 0 // Hs.301974 // LRP12 // 29967 // Homo sapiens low density lipoprotein-related protein 12 (LRP12), mRNA. /// ENST00000276654 // intron // 0 // — // — // — // —	LRP12	LRP12, Homo sapiens low density lipoprotein-related protein 12 (LRP12), q22.3
SNP_A-1791288	gggtaagtgtgtaaga[A/G]agtttcagtaagagtt	A	G	NM_012082 // upstream // 604156 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 63155 // — // — // — // — /// ENST00000323713 // upstream // 604156 // — // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2196018	catgtctctaaatggg[A/G]aagtctcatgagggga	A	G	NM_012082 // upstream // 600091 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 67220 // — // — // — // — /// ENST00000323713 // upstream // 600091 // — // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-1653792	agctctcattttattagttggtata[C/T]gcagtgcttaaaggccttatgcggc	C	T	NM_012082 // upstream // 333552 // Hs.106309 // ZFPM2 // 23414 // zinc finger protein, multitype 2 /// NM_013437 // upstream // 396427 // Hs.301974 // ST7 // 29967 // suppression of tumorigenicity	ZFPM2	ZFPM2 , rs10505071, zinc finger protein, multitype 2 ,q22.3
SNP_A-1994523	tgacctcactttcctc[C/T]ctgattcatacaaatt	C	T	NM_012082 // upstream // 415991 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 251320 // — // — // — // — /// ENST00000323713 // upstream // 415991 // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2137827	atcattattatgatac[C/T]agtggttgtttcgaga	C	T	NM_012082 // upstream // 385134 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 282177 // — // — // — // — /// ENST00000323713 // upstream // 385134 // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2270636	gacagcaacataacag[C/T]catttataacaaagtc	C	T	NM_012082 // upstream // 328420 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 338891 // — // — // — // — /// ENST00000323713 // upstream // 328420 // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2203265	ccacttcctcatagca[G/T]atttttactgtgtcct	G	T	NM_012082 // upstream // 326106 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 341205 // — // — // — // — /// ENST00000323713 // upstream // 326106 // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-2309136	ggaaaaaaccttggaa[A/G]tgtaaatgcctctaag	A	G	NM_012082 // upstream // 304879 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 362432 // — // — // — // — /// ENST00000323713 // upstream // 304879 // — // —	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q22.3
SNP_A-1689805	gagagagaatatgaatgagacacaa[C/T]gtgaatgagagaga tgtcaaccatt	C	T	NM_012082 // intron // 0 // Hs.106309 // ZFPM2 // 23414 // zinc finger protein, multitype 2	ZFPM2	ZFPM2 , rs2342786, zinc finger protein, multitype 2,q23.1
SNP_A-1709209	gaaatctcacgccatttcttaaagg[A/C]atctgatggagagtagt cttaattt	A	C	NM_012082 // intron // 0 // Hs.106309 // ZFPM2 // 23414 // zinc finger protein, multitype 2	ZFPM2	ZFPM2 , rs979646, zinc finger protein, multitype 2,q23.1
SNP_A-1750043	gacagaaatagatgaattcagaaga[C/T]atttttagagatagga cttataata	C	T	NM_012082 // intron // 0 // Hs.106309 // ZFPM2 // 23414 // zinc finger protein, multitype 2	ZFPM2	ZFPM2 , rs1580355, zinc finger protein, multitype 2,q23.1
SNP_A-2058967	aatccatataacagca[A/G]aaatgaatacagtgct	A	G	NM_012082 // upstream // 34258 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 633053 // — // — // — // — /// ENST00000323713 // upstream // 34258 // — // — //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-1814823	gtgtgtgtaggcatga[A/G]gggagagacgaataga	A	G	NM_012082 // upstream // 30078 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 637233 // — // — // — // — /// ENST00000323713 // upstream // 30078 // — // — //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2244464	ctggacatttaattca[C/T]gttgctcttaaatcca	C	T	NM_012082 // upstream // 11620 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// ENST00000357114 // downstream // 655691 // — // — // — // — /// ENST00000323713 // upstream // 11620 // — // — //	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-1947319	tttacaaatatacttc[A/G]aagtgaaaaggttgca	A	G	NM_012082 // downstream // 285857 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// NM_181354 // upstream // 568459 // Hs.148778 // OXR1 // 55074 // Homo sapiens oxidation resistance 1 (OXR1), mRNA. /// ENS	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2013698	aggaggacaggagtca[C/T]ctctaatatgaaaggc	C	T	NM_012082 // downstream // 424014 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// NM_181354 // upstream // 430302 // Hs.148778 // OXR1 // 55074 // Homo sapiens oxidation resistance 1 (OXR1), mRNA. /// ENS	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2309605	ggaaagaacgagcaaa[A/C]gcaaaggcccagagga	A	C	NM_012082 // downstream // 628948 // Hs.431009 // ZFPM2 // 23414 // Homo sapiens zinc finger protein, multitype 2 (ZFPM2), mRNA. /// NM_181354 // upstream // 225368 // Hs.148778 // OXR1 // 55074 // Homo sapiens oxidation resistance 1 (OXR1), mRNA. /// ENS	ZFPM2	ZFPM2, Homo sapiens zinc finger protein, multitype 2 (ZFPM2), q23.1
SNP_A-2150119	atgtcctcagagtgcc[A/G]acttattacagaatat	A	G	ENST00000336821 // intron // 0 // — // — // — // —	-	q23.1
SNP_A-2084407	actatatgccagatac[C/T]atactaggatttgcac	C	T	NM_181354 // intron // 0 // Hs.148778 // OXR1 // 55074 // Homo sapiens oxidation resistance 1 (OXR1), mRNA. /// ENST00000312046 // intron // 0 // — // — // — // — /// ENST00000297447 // intron // 0 // — // — // — // —	OXR1	OXR1, Homo sapiens oxidation resistance 1 (OXR1), q23.1
SNP_A-2032244	aaagtgttccagagaa[A/G]tactgaaactatgggg	A	G	NM_139166 // upstream // 69793 // Hs.374668 // STARS // 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 409458 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1),	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2261892	gaaataagccttcaga[G/T]agcaataacactaaag	G	T	NM_139166 // upstream // 98392 // Hs.374668 // STARS // 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 380859 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1),	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1994568	taatattgccaaaatat[C/T]gagtcaatagccagtt	C	T	NM_139166 // upstream // 125731 // Hs.374668 // STARS // 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 353520 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1)	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1744967	aatgtctaagaagatctttacaaga[C/G]ctgagccatagaatatt acagtatt	C	G	NM_001146 // downstream // 132998 // Hs.2463 // ANGPT1 // 284 // angiopoietin 1 /// NM_139166 // upstream // 346239 // Hs.374668 // STARS // 137735 // striated muscle activator of Rho-dependent signaling /// NM_139290 // downstream // 167521 // Hs.2463 /	ANGPT1	ANGPT1 , rs720715, angiopoietin 1 ,q23.1
SNP_A-2083279	actaaagctaggtaaa[C/T]gtttggtgcagttcac	C	T	NM_139166 // upstream // 297603 // Hs.374668 // STARS // 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 181648 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1)	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2074030	acagtgttgtgaaga[A/G]aactgtgtagaacctg	A	G	NM_139166 // upstream // 370507 // Hs.374668 // STARS // 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 108744 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1)	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-2130889	atagaaaagatgtgtc[C/T]aggattgctgtatcaa	C	T	NM_139166 // upstream // 386997 // Hs.374668 // STARS // 137735 // Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), mRNA. /// NM_139290 // downstream // 92254 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1).	STARS	STARS, Homo sapiens striated muscle activator of Rho-dependent signaling (STARS), q23.1
SNP_A-1865555	tccatggaactaagaa[A/G]gctactctacagcaca	A	G	NM_139290 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 1, mRNA. ///	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2117318	aggtggccactcccaa[C/T]ggacctggataacgaa	C	T	NM_139290 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 1, mRNA. ///	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2234477	ctccacaggtttgga[A/T]gaccatgtccacctct	A	T	NM_139290 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 1, mRNA. ///	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-1819974	gttgttgcagaggccat[A/G]gatcgatttttttt	A	G	NM_139290 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 1, mRNA. ///	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2058516	aatcagacttctac[C/T]gcagcttgtctgttga	C	T	NM_001146 // upstream // 55617 // Hs.2463 // ANGPT1 // 284 // angiopoietin 1 /// NM_139290 // upstream // 55617 // Hs.2463 // ANGPT1 // 284 // angiopoietin 1 /// NM_178565 // downstream // 345674 // Hs.444834 // MGC35555 // 340419 // hypothetical protein	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-1758796	tgatggatgtatcacttggaatga[C/T]ccttaatgtcacatcatag ttggta	C	T	NM_139290 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 1, mRNA. ///	ANGPT1	ANGPT1, rs10505109, angiopoietin 1 ,q23.1
SNP_A-2162179	attttacattgtaggcd[A/T]atcigttcacacatca	A	T	NM_139290 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // intron // 0 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 1, mRNA. ///	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1881559	tctttcttgacatgaa[A/G]ataatgccgtgtaaac	A	G	NM_139290 // upstream // 33923 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 33923 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2088107	actgggcatcatatca[A/C]cctctcccaacctgga	A	C	NM_139290 // upstream // 77608 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 77608 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2057852	aatattatcctctcaa[A/C]cgctggaaattatgaa	A	C	NM_139290 // upstream // 92859 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 92859 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-1959695	tttgggtgtaggata[C/T]gacagtataggctgaa	C	T	NM_139290 // upstream // 104397 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 104397 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript varian	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-1886412	tgacgacaacgaaaaa[A/C]ggatgtccgcttatga	A	C	NM_139290 // upstream // 213276 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, mRNA. /// NM_001146 // upstream // 213276 // Hs.369675 // ANGPT1 // 284 // Homo sapiens angiopoietin 1 (ANGPT1), transcript varian	ANGPT1	ANGPT1, Homo sapiens angiopoietin 1 (ANGPT1), transcript variant 2, q23.1
SNP_A-2182526	cagatatcccttttaca[A/C]atcccaagtttcctggc	A	C	NM_178565 // intron // 0 // Hs.444834 // MGC35555 // 340419 // Homo sapiens hypothetical protein MGC35555 (MGC35555), mRNA. /// ENST00000276659 // intron // 0 // — // — // — // —	MGC35555	MGC35555, Homo sapiens hypothetical protein MGC35555 (MGC35555), q23.1
SNP_A-2031803	aaagtatcttttgta[A/C]gtttgtgagttagaca	A	C	NM_001568 // upstream // 101704 // Hs.405590 // EIF3S6 // 3646 // Homo sapiens eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA. /// NM_014673 // upstream // 93198 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA01	EIF3S6	EIF3S6, Homo sapiens eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), q23.1
SNP_A-1825597	taaatatatttcaaga[C/T]agcatttctcagtgtc	G	T	NM_014673 // downstream // 96576 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 199634 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST00	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-1659882	ctgagacaagaatagactgagatga[C/T]agaaaaaattgaattat atacaatta	C	T	BC033057 // intron // 0 // Hs.375116 // - // - // CDNA clone IMAGE:5262992, partial cds	-	-, rs10227479, CDNA clone IMAGE:5262992, partial cds,q23.1
SNP_A-1728495	gcactcacacactgtaaaggagata[A/G]gcacttaataaatatt cacaaaata	A	G	BC033057 // intron // 0 // Hs.375116 // - // - // CDNA clone IMAGE:5262992, partial cds	-	-, rs2172255, CDNA clone IMAGE:5262992, partial cds,q23.1
SNP_A-1945444	ttgtcaaaacgtaaa[A/G]aagtcatttatgtgta	A	G	NM_014673 // downstream // 132877 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 163333 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST0	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-1890527	tgatctgttgtattaa[C/T]ctcctggaaattctac	C	T	NM_014673 // downstream // 133409 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 162801 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST0	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1862384	tcatgtccaagaaaca[C/T]ggcaaaaatggggcat	C	T	NM_014673 // downstream // 158713 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 137497 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST0	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-2301230	gccttgcctgtcattc[C/T]ctacccaaaacatgg	C	T	NM_014673 // downstream // 158780 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 137430 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST0	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-1879245	tcttagaatgtctgaa[A/T]gtccatttccacaact	A	T	NM_014673 // downstream // 158856 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 137354 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST0	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-1994631	tgagcacaacaggaca[C/T]taaggcagatccatgc	C	T	NM_014673 // downstream // 224791 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 71419 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST00	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-2256967	cttcctgtaatgaga[C/T]ctgggattctgcacac	C	T	NM_014673 // downstream // 226086 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 70124 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST00	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-2133033	atatactaatggaaca[A/G]ggacatgataccata	A	G	NM_014673 // downstream // 288191 // Hs.232002 // KIAA0103 // 9694 // Homo sapiens KIAA0103 (KIAA0103), mRNA. /// NM_153015 // downstream // 8019 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// ENST000	KIAA0103	KIAA0103, Homo sapiens KIAA0103 (KIAA0103), q23.1
SNP_A-1801317	gtaggaaggagaatac[A/G]aaatctaggtttcttc	A	G	NM_153015 // upstream // 56043 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// NM_003301 // upstream // 243911 // Hs.3022 // TRHR // 7201 // Homo sapiens thyrotropin-releasing hormone receptor (TRHR).	FLJ30668	FLJ30668, Homo sapiens hypothetical protein FLJ30668 (FLJ30668), q23.1
SNP_A-2207139	ccattacgttgtggtc[A/C]ctttctgtatatagta	A	C	NM_153015 // upstream // 275588 // Hs.99439 // FLJ30668 // 157753 // Homo sapiens hypothetical protein FLJ30668 (FLJ30668), mRNA. /// NM_003301 // upstream // 24366 // Hs.3022 // TRHR // 7201 // Homo sapiens thyrotropin-releasing hormone receptor (TRHR).	FLJ30668	FLJ30668, Homo sapiens hypothetical protein FLJ30668 (FLJ30668), q23.1
SNP_A-1715111	ctatgttaacgctgaggtttagat[C/G]actgccttaaaaaataat aacatct	C	G	NM_014379 // downstream // 173827 // Hs.13285 // KCNV1 // 27012 // potassium channel, subfamily V, member 1 /// NM_017786 // upstream // 101575 // Hs.354793 // FLJ20366 // 55638 // hypothetical protein FLJ20366	KCNV1	KCNV1 , rs7831835, potassium channel, subfamily V, member 1, q23.2
SNP_A-2292759	gcacttgacgtcact[C/T]agtagatgctaaatga	C	T	NM_017786 // upstream // 310390 // Hs.390738 // FLJ20366 // 55638 // Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA. /// NM_014379 // downstream // 37576 // Hs.13285 // KCNV1 // 27012 // Homo sapiens potassium channel, subfamily V, member 1 (	FLJ20366	FLJ20366, Homo sapiens hypothetical protein FLJ20366 (FLJ20366), q23.2
SNP_A-1690886	ggaaggagaaaaggagaagaatttta[G/T]actcatagggtctt ataaggatt	G	T	NM_014379 // upstream // 66874 // Hs.13285 // KCNV1 // 27012 // potassium channel, subfamily V, member 1 /// NM_052900 // downstream // 2179328 // Hs.21034 // CSMD3 // 114788 // CUB and Sushi multiple domains 3	KCNV1	KCNV1 , rs2060687, potassium channel, subfamily V, member 1, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2220852	ccttgcatttgtaaga[C/G]aggcaaggacatagag	C	G	NM_017786 // upstream // 337275 // Hs.390738 // FLJ20366 // 55638 // Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA. /// NM_014379 // downstream // 10691 // Hs.13285 // KCNV1 // 27012 // Homo sapiens potassium channel, subfamily V, member 1 (	FLJ20366	FLJ20366, Homo sapiens hypothetical protein FLJ20366 (FLJ20366), q23.2
SNP_A-1667024	tggtgatacctggttagttgaaagaa[A/C]gcaatggttcaatggca cctaaatg	A	C	NM_014379 // upstream // 468646 // Hs.13285 // KCNV1 // 27012 // potassium channel, subfamily V, member 1 /// NM_052900 // downstream // 1779556 // Hs.21034 // CSMD3 // 114788 // CUB and Sushi multiple domains 3	KCNV1	KCNV1 , -, potassium channel, subfamily V, member 1 , q23.2
SNP_A-2050397	aaggagtcacaaagta[C/T]aaaacaacaatccaaa	C	T	NM_014379 // upstream // 386816 // Hs.13285 // KCNV1 // 27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream // 1861386 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (C	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-2126325	ataaaacatctacagc[A/C]cctgttaatacaaa	A	C	NM_014379 // upstream // 670597 // Hs.13285 // KCNV1 // 27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream // 1577605 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (C	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.2
SNP_A-1944103	ttgtcacaggtgtcag[C/T]agtagagaatataagt	C	T	NM_014379 // upstream // 1759863 // Hs.13285 // KCNV1 // 27012 // Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), mRNA. /// NM_198124 // downstream // 488339 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (C	KCNV1	KCNV1, Homo sapiens potassium channel, subfamily V, member 1 (KCNV1), q23.3
SNP_A-1956729	ttttaaaattcgtact[C/T]agcgcaatactacaa	C	T	NM_198124 // intron // 0 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // intron // 0 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSM	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-1924250	ttataaaaatgctaga[C/T]tatactgtacttgcc	C	T	NM_052900 // intron // 0 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant c, mRNA. /// NM_198123 // intron // 0 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSM	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant c, q23.3
SNP_A-1739407	cacctagtctaggatgattgttaca[C/T]gcttctagcaacaagtgc acataaa	C	T	NM_014112 // downstream // 1504914 // Hs.26102 // TRPS1 // 7227 // trichorhinophalangeal syndrome I /// NM_052900 // upstream // 466698 // Hs.21034 // CSMD3 // 114788 // CUB and Sushi multiple domains 3	TRPS1	TRPS1 , rs966210, trichorhinophalangeal syndrome I, q23.3
SNP_A-1915475	tgttcctgtcccaaaa[A/G]cttctgtagtcctte	A	G	NM_198124 // upstream // 461517 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // upstream // 401657 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-1956174	tttgtggatttcaag[A/G]agtgcctactttact	A	G	NM_198124 // upstream // 496050 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // upstream // 436190 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3
SNP_A-1903983	tgggcaacttaatcca[C/T]gaatgttgtctgtatt	C	T	NM_198124 // upstream // 1401874 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, mRNA. /// NM_052900 // upstream // 1342014 // Hs.91381 // CSMD3 // 114788 // Homo sapiens CUB and Sushi multipl	CSMD3	CSMD3, Homo sapiens CUB and Sushi multiple domains 3 (CSMD3), transcript variant b, q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1894671	tgccagagaatggcag[C/T]cacacctacctatgag	C	T	NM_014112 // upstream // 140882 // Hs.253594 // TRPS1 // 7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 834942 // Hs.492599 // EIF3S3 // 8667 // Homo sapiens eukaryotic translation initiation factor 3,	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1824623	taaagaacttctagaa[A/G]ctgaaatgacaaaaaa	A	G	NM_014112 // upstream // 435875 // Hs.253594 // TRPS1 // 7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 539949 // Hs.492599 // EIF3S3 // 8667 // Homo sapiens eukaryotic translation initiation factor 3,	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-2085603	actcccacagcaagac[C/G]acacgaaaccagcatt	C	G	NM_014112 // upstream // 625640 // Hs.253594 // TRPS1 // 7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 350184 // Hs.492599 // EIF3S3 // 8667 // Homo sapiens eukaryotic translation initiation factor 3,	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1714791	agagaaaaagtgaacattacttaca[C/T]tcaatacataggttgg ctctgcaca	C	T	NM_003756 // downstream // 93554 // Hs.127149 // EIF3S3 // 8667 // eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa /// NM_014112 // upstream // 882284 // Hs.26102 // TRPS1 // 7227 // trichorhinophalangeal syndrome I	EIF3S3	EIF3S3 , rs1550162, eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa ,q23.3
SNP_A-1957163	ttttaccctcgacccc[C/T]cattcttgttcaccat	C	T	NM_014112 // upstream // 800503 // Hs.253594 // TRPS1 // 7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 175321 // Hs.492599 // EIF3S3 // 8667 // Homo sapiens eukaryotic translation initiation factor 3,	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1994776	acatcacttctgttga[A/T]aattcactggacaaag	A	T	NM_014112 // upstream // 906084 // Hs.253594 // TRPS1 // 7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 69740 // Hs.492599 // EIF3S3 // 8667 // Homo sapiens eukaryotic translation initiation factor 3, s	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1930586	ttccaataaaaagaag[C/G]cacaacattttcctaa	C	G	NM_014112 // upstream // 923687 // Hs.253594 // TRPS1 // 7227 // Homo sapiens trichorhinophalangeal syndrome I (TRPS1), mRNA. /// NM_003756 // downstream // 52137 // Hs.492599 // EIF3S3 // 8667 // Homo sapiens eukaryotic translation initiation factor 3, s	TRPS1	TRPS1, Homo sapiens trichorhinophalangeal syndrome I (TRPS1), q23.3
SNP_A-1645138	ctaggcagtgactggtatagtttga[A/G]ctttgtctttttttatttcagac ttt	A	G	NM_003756 // intron // 0 // Hs.127149 // EIF3S3 // 8667 // eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa	EIF3S3	EIF3S3 , rs10505288, eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa,q24.11
SNP_A-1671238	agcaaaatgataacacatcaatgta[A/T]cctgaacaatagaag aaggtaattc	A	T	NM_006265 // upstream // 36588 // Hs.81848 // RAD21 // 5885 // RAD21 homolog (S. pombe) /// NM_173851 // upstream // 223978 // Hs.179082 // SLC30A8 // 169026 // solute carrier family 30 (zinc transporter), member 8	RAD21	RAD21 , rs3020160, RAD21 homolog (S. pombe) ,q24.11
SNP_A-1825800	taaatctggtctggca[A/T]agagtgcaatggaagt	A	T	NM_006265 // upstream // 30259 // Hs.81848 // RAD21 // 5885 // Homo sapiens RAD21 homolog (S. pombe) (RAD21), mRNA. /// NM_173851 // upstream // 45958 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8	RAD21	RAD21, Homo sapiens RAD21 homolog (S. pombe) (RAD21), q24.11
SNP_A-2310684	ggaagatcataacaaa[C/T]ttcagcatcctatggg	C	T	NM_006265 // upstream // 30311 // Hs.81848 // RAD21 // 5885 // Homo sapiens RAD21 homolog (S. pombe) (RAD21), mRNA. /// NM_173851 // upstream // 45906 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8	RAD21	RAD21, Homo sapiens RAD21 homolog (S. pombe) (RAD21), q24.11
SNP_A-1757587	cagatgtagacactcaatttatgac[A/G]gaagggctgctgcaga gtaatgggg	A	G	AL713790 // intron // 0 // Hs.179082 // SLC30A8 // 169026 // solute carrier family 30 (zinc transporter), member 8	SLC30A8	SLC30A8 , rs1001646, solute carrier family 30 (zinc transporter), member 8,q24.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1878102	tctgtaggatcccaaa[A/T]catttcactcactcagg	A	T	NM_006265 // upstream // 37442 // Hs.81848 // RAD21 // 5885 // Homo sapiens RAD21 homolog (S. pombe) (RAD21), mRNA. /// NM_173851 // upstream // 38775 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8	RAD21	RAD21, Homo sapiens RAD21 homolog (S. pombe) (RAD21), q24.11
SNP_A-1994786	actgtgaatacctcat[G/T]gttcttggattataag	G	T	NM_173851 // intron // 0 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// ENST00000297345 // intron // 0 // --- // --- // ---	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2116779	aggtccttgatatac[A/C]ccagaacaatttttat	A	C	NM_173851 // downstream // 4248 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 339830 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone re	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2131398	atagatgctgaagcta[C/T]ggctcagagggaaala	C	T	NM_173851 // downstream // 23510 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 320568 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone r	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-1645520	gtttctcaggtctttcaatagcta[A/T]ttttactcacttaagatttttctt	A	T	NM_080651 // upstream // 132319 // Hs.336898 // THRAP6 // 90390 // thyroid hormone receptor associated protein 6 /// NM_173851 // downstream // 215791 // Hs.179082 // SLC30A8 // 169026 // solute carrier family 30 (zinc transporter), member 8	THRAP6	THRAP6, rs2023139, thyroid hormone receptor associated protein 6, q24.11
SNP_A-2116388	aggtagtccagattta[C/T]ggatttttctctaaat	C	T	NM_173851 // downstream // 182431 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 161647 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-1994793	aagtctagctaaacca[A/C]gataaattcattgattt	A	C	NM_173851 // downstream // 203876 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 140202 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2183544	cagcagccttaaggat[A/G]aagctattgtaacaag	A	G	NM_173851 // downstream // 216007 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 126071 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-1994796	tgatgttaacctgcc[A/G]gaatttgtaatcagga	A	G	NM_173851 // downstream // 221674 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 122404 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2029705	aaagagcctctaggcc[A/G]atcttatctggagctt	A	G	NM_173851 // downstream // 255504 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 88574 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone r	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11
SNP_A-2088523	actgtccctaaattca[A/G]actcacatacctaaaa	A	G	NM_173851 // downstream // 341435 // Hs.532270 // SLC30A8 // 169026 // Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), mRNA. /// NM_080651 // upstream // 2643 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone re	SLC30A8	SLC30A8, Homo sapiens solute carrier family 30 (zinc transporter), member 8 (SLC30A8), q24.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1956985	ttttaatacagtaaca[A/G]tccaaatcctaataag	A	G	NM_080651 // intron // 0 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), mRNA. /// ENST00000297347 // intron // 0 // — // — // — // —	THRAP6	THRAP6, Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), q24.11
SNP_A-2198921	catttgcaaggatgaa[A/C]tgagataaggagctag	A	C	NM_080651 // downstream // 5727 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), mRNA. /// NM_000127 // downstream // 253725 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1),	THRAP6	THRAP6, Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), q24.11
SNP_A-1841030	tagctgtaagggatga[A/T]gagaaagtgagtatat	A	T	NM_080651 // downstream // 10549 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), mRNA. /// NM_000127 // downstream // 248903 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1)	THRAP6	THRAP6, Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), q24.11
SNP_A-1915132	tgttatttcctaagac[A/G]gattccttccagtgtc	A	G	NM_080651 // downstream // 21450 // Hs.492612 // THRAP6 // 90390 // Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), mRNA. /// NM_000127 // downstream // 238002 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1)	THRAP6	THRAP6, Homo sapiens thyroid hormone receptor associated protein 6 (THRAP6), q24.11
SNP_A-1908885	tgtagtttaagataca[C/T]gtagaaagtcattgct	C	T	NM_000127 // intron // 0 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// ENST00000333324 // intron // 0 // — // — // — // —	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.11
SNP_A-1837451	tacttctgtctggcac[G/T]cagtttgtgatctcca	G	T	NM_000127 // intron // 0 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// ENST00000333324 // intron // 0 // — // — // — // —	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.11
SNP_A-2250251	cttagaaacttgaata[C/T]cgtggaaatctaacaa	C	T	NM_000127 // intron // 0 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// ENST00000333324 // intron // 0 // — // — // — // —	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.11
SNP_A-2097355	agagaaactggcactc[A/C]acaactatttcatttg	A	C	NM_000127 // upstream // 29634 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// NM_207506 // downstream // 237308 // Hs.492653 // SAMD12 // 401474 // Homo sapiens sterile alpha motif domain containing 12 (SAMD12), mRNA	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.12
SNP_A-1923952	ttagtgactccaactc[C/T]atgtaaatctcttcaa	C	T	NM_000127 // upstream // 46020 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// NM_207506 // downstream // 220922 // Hs.492653 // SAMD12 // 401474 // Homo sapiens sterile alpha motif domain containing 12 (SAMD12), mRNA	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.12
SNP_A-1862372	tcatgtcacattgtta[C/T]gttcagttggatgtca	C	T	NM_000127 // upstream // 56864 // Hs.492618 // EXT1 // 2131 // Homo sapiens exostoses (multiple) 1 (EXT1), mRNA. /// NM_207506 // downstream // 210078 // Hs.492653 // SAMD12 // 401474 // Homo sapiens sterile alpha motif domain containing 12 (SAMD12), mRNA	EXT1	EXT1, Homo sapiens exostoses (multiple) 1 (EXT1), q24.12
SNP_A-1846517	tatattcctcacttct[A/C]aaacagctgactccta	A	C	NM_207506 // upstream // 147639 // Hs.492653 // SAMD12 // 401474 // Homo sapiens sterile alpha motif domain containing 12 (SAMD12), mRNA. /// NM_002546 // downstream // 154038 // Hs.81791 // TNFRSF11B // 4982 // Homo sapiens tumor necrosis factor receptor	SAMD12	SAMD12, Homo sapiens sterile alpha motif domain containing 12 (SAMD12), q24.12
SNP_A-1870485	tcgaatgagatacgac[A/C]aggaaatttctcacaa	A	C	NM_002546 // upstream // 39296 // Hs.81791 // TNFRSF11B // 4982 // Homo sapiens tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA. /// NM_006438 // upstream // 75839 // Hs.176615 // COLEC10 // 10584 // Homo sapiens	TNFRSF11B	TNFRSF11B, Homo sapiens tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), q24.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141477	atcttaagattgtttc[G/T]agctctatatgccctg	G	T	NM_002546 // upstream // 106011 // Hs.81791 // TNFRSF11B // 4982 // Homo sapiens tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA. /// NM_006438 // upstream // 9124 // Hs.176615 // COLEC10 // 10584 // Homo sapiens	TNFRSF11B	TNFRSF11B, Homo sapiens tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), q24.12
SNP_A-1692900	ttacctggatcatcagctttgtgag[C/G]acagggttcacctttgtcttactca	C	G	NM_006438 // downstream // 63810 // Hs.176615 // COLEC10 // 10584 // collectin sub-family member 10 (C-type lectin) /// NM_052886 // upstream // 37623 // Hs.76550 // MAL2 // 114569 // mal, T-cell differentiation protein 2	COLEC10	COLEC10 , rs1549416, collectin sub-family member 10 (C-type lectin) ,q24.12
SNP_A-2212681	cccttctccttccaca[C/T]actcacagtaatttgg	C	T	NM_052886 // downstream // 113388 // Hs.201083 // MAL2 // 114569 // Homo sapiens mal, T-cell differentiation protein 2 (MAL2), mRNA. /// NM_002514 // upstream // 57402 // Hs.235935 // NOV // 4856 // Homo sapiens nephroblastoma overexpressed gene (NOV), mR	MAL2	MAL2, Homo sapiens mal, T-cell differentiation protein 2 (MAL2), q24.12
SNP_A-1828056	taagacaaaattctgt[C/T]aagcaaggaatcattg	C	T	NM_006209 // intron // 0 // Hs.190977 // ENPP2 // 5168 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2), mRNA. /// L35594 // intron // 0 // Hs.190977 // ENPP2 // 5168 // Human autotaxin mRNA, complete cds. /// ENST000	ENPP2	ENPP2, Homo sapiens ectonucleotide pyrophosphatase,q24.12
SNP_A-2216878	cctctgcctcttggga[A/T]caccaatttactgaga	A	T	NM_006209 // upstream // 62601 // Hs.190977 // ENPP2 // 5168 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2), mRNA. /// L35594 // upstream // 62660 // Hs.190977 // ENPP2 // 5168 // Human autotaxin mRNA, complete cds.	ENPP2	ENPP2, Homo sapiens ectonucleotide pyrophosphatase,q24.12
SNP_A-1814479	gtgtgcagtcattagc[A/G]ctatccatctctagaa	A	G	NM_024094 // intron // 0 // Hs.315167 // DCC1 // 79075 // Homo sapiens defective in sister chromatid cohesion homolog 1 (S. cerevisiae) (DCC1), mRNA. /// ENST00000313655 // intron // 0 // --- // --- // --- // ---	DCC1	DCC1, Homo sapiens defective in sister chromatid cohesion homolog 1 (S. cerevisiae) (DCC1), q24.12
SNP_A-1841282	taggaagaaaagcaga[C/T]gtagccagaaagctag	C	T	NM_022783 // intron // 0 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // intron // 0 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-2013768	agctgaatggagacag[A/T]aaatagcagcaaacat	A	T	NM_022783 // intron // 0 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // intron // 0 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-1994888	atttgaagaaatccaa[C/T]gtaggcattaggaacc	C	T	NM_022783 // intron // 0 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // intron // 0 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-2061312	aatgccactaaagtta[A/G]aagatgaaggaggaga	A	G	NM_022783 // intron // 0 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // intron // 0 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-1808348	gtctttttatttttttc[C/G]agatagtgtcttgctc	C	G	NM_022783 // downstream // 4703 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream // 4703 // --- // --- // --- // --- /// ENST00000309791 // upstream // 52223 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-2101406	agatcttcagaaaata[A/T]ccgtcatttagtagac	A	T	NM_022783 // downstream // 5625 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream // 5625 // --- // --- // --- // --- /// ENST00000309791 // upstream // 51301 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-1994893	cgtttatatcttcacc[A/G]gcaatatgcattttag	A	G	NM_022783 // downstream // 9033 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream // 9033 // --- // --- // --- // --- /// ENST00000309791 // upstream // 47893 // --- // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2298716	gcccagggcctaaaac[A/G]gtcagcacaaagcctc	A	G	NM_022783 // downstream // 13124 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream // 13124 // --- // --- // --- /// ENST00000309791 // upstream // 43802 // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-1868771	tcctcttttgtcttctc[C/T]atcccaagaatctcc	C	T	NM_022783 // downstream // 43508 // Hs.303788 // DEPDC6 // 64798 // Homo sapiens DEP domain containing 6 (DEPDC6), mRNA. /// ENST00000286234 // downstream // 43508 // --- // --- // --- /// ENST00000309791 // upstream // 13418 // --- // --- // ---	DEPDC6	DEPDC6, Homo sapiens DEP domain containing 6 (DEPDC6), q24.12
SNP_A-1714929	tctaccaccacttttggcatttgatg[A/G]ctagtcactctgtaattggtgagat	A	G	NM_005328 // downstream // 485988 // Hs.159226 // HAS2 // 3037 // hyaluronan synthase 2 /// NM_021021 // upstream // 314823 // Hs.432544 // SNTB1 // 6641 // syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	HAS2	HAS2, rs2060319, hyaluronan synthase 2, q24.12
SNP_A-1787715	gggacatagaatcata[C/T]atggttgctgacttgg	C	T	NM_021021 // upstream // 402389 // Hs.371902 // SNTB1 // 6641 // Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), mRNA. /// NM_021021 // upstream // 403035 // Hs.371902 // SNTB1 // 6641 // Homo sapiens	SNTB1	SNTB1, Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), q24.12
SNP_A-2140668	atctctctaatcaata[A/G]gcaactccactgacca	A	G	NM_021021 // upstream // 581073 // Hs.371902 // SNTB1 // 6641 // Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), mRNA. /// NM_021021 // upstream // 581719 // Hs.371902 // SNTB1 // 6641 // Homo sapiens	SNTB1	SNTB1, Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), q24.12
SNP_A-1652770	aaaagtaatctaaaggtgaaggtaa[C/T]agtaaatagcagcatacagtataaat	C	T	NM_005328 // upstream // 130384 // Hs.159226 // HAS2 // 3037 // hyaluronan synthase 2 /// NM_014943 // upstream // 1009975 // Hs.30209 // ZHX2 // 22882 // zinc fingers and homeoboxes 2	HAS2	HAS2, rs1563563, hyaluronan synthase 2, q24.13
SNP_A-2039851	aacattcggtgttaca[A/G]atgatgacattcctgt	A	G	NM_005328 // upstream // 33258 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 1107101 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1888576	tgaggattgaacttta[C/T]gcttggtggtcagtaa	C	T	NM_005328 // upstream // 37565 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 1102794 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2162713	atttgaaagaactat[C/G]acaaacaaagtttaag	C	G	NM_005328 // upstream // 61883 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 1078476 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2093459	agaactgtggttaata[C/T]ggactatcaatctaga	C	T	NM_005328 // upstream // 522885 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 617474 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2153027	attacattcacagctt[A/G]aaacgggctatggtgg	A	G	NM_005328 // upstream // 798690 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 341669 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1994939	cggttttcatggttcc[A/C]acccgacctcatataa	A	C	NM_005328 // upstream // 807658 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 332701 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-2255341	cttgtagctgtgtccc[A/G]aaccagcaagatttat	A	G	NM_005328 // upstream // 857617 // Hs.159226 // HAS2 // 3037 // Homo sapiens hyaluronan synthase 2 (HAS2), mRNA. /// NM_014943 // upstream // 282742 // Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000303	HAS2	HAS2, Homo sapiens hyaluronan synthase 2 (HAS2), q24.13
SNP_A-1691790	aaacagctgttgccttcttctccac[A/G]atggaatcaaaggatcttatcacct	A	G	NM_005328 // upstream // 1052525 // Hs.159226 // HAS2 // 3037 // hyaluronan synthase 2 /// NM_014943 // upstream // 87834 // Hs.30209 // ZHX2 // 22882 // zinc fingers and homeoboxes 2	HAS2	HAS2 , rs4871297, hyaluronan synthase 2 ,q24.13
SNP_A-1688658	tggcttccttgtccttgcataggga[A/G]gaacacaggcagacggtggtaggaga	A	G	NM_014943 // intron // 0 // Hs.30209 // ZHX2 // 22882 // zinc fingers and homeoboxes 2	ZHX2	ZHX2 , rs10505428, zinc fingers and homeoboxes 2,q24.13
SNP_A-2112076	aggatgggctgcgtca[C/T]ctttgtgggggccaac	C	T	NM_014943 // CDS // 0 /// Hs.377090 // ZHX2 // 22882 // Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), mRNA. /// ENST00000314393 // CDS // 0 // --- // --- // --- // ---	ZHX2	ZHX2, Homo sapiens zinc fingers and homeoboxes 2 (ZHX2), q24.13
SNP_A-2205409	ccagtgattggtttaa[C/T]tggcttgtggcagggc	C	T	NM_145647 // intron // 0 // Hs.492716 // MGC21654 // 93594 // Homo sapiens unknown MGC21654 product (MGC21654), mRNA. /// ENST00000287380 // intron // 0 // --- // --- // --- // --- /// ENST00000309336 // intron // 0 // --- // --- // --- // ---	MGC21654	MGC21654, Homo sapiens unknown MGC21654 product (MGC21654), q24.13
SNP_A-2216622	cctctcaaagatttca[C/T]gaggtcaacaggggag	C	T	NM_058229 // upstream // 12910 // Hs.403933 // FBXO32 // 114907 // Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, mRNA. /// NM_148177 // upstream // 12910 // Hs.403933 // FBXO32 // 114907 // Homo sapiens F-box protein 32 (FBXO32), transcrip	FBXO32	FBXO32, Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, q24.13
SNP_A-2302602	gctacatagagttcca[A/C]aataactttcctctgc	A	C	NM_058229 // upstream // 32859 // Hs.403933 // FBXO32 // 114907 // Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, mRNA. /// NM_148177 // upstream // 32859 // Hs.403933 // FBXO32 // 114907 // Homo sapiens F-box protein 32 (FBXO32), transcrip	FBXO32	FBXO32, Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, q24.13
SNP_A-2163411	atttttttgtgcaaaa[A/G]taatacataacaaagg	A	G	ENST00000325995 // intron // 0 // --- // --- // --- // --- /// ENST00000352118 // intron // 0 // --- // --- // --- // --- /// ENST00000330051 // intron // 0 // --- // --- // --- // ---	-	q24.13
SNP_A-2314400	ggagggagacctagta[C/G]agccattgataaatgt	C	G	NM_001003954 // intron // 0 // Hs.181107 // ANXA13 // 312 // Homo sapiens annexin A13 (ANXA13), transcript variant 2, mRNA. /// ENST00000262219 // intron // 0 // --- // --- // --- // ---	ANXA13	ANXA13, Homo sapiens annexin A13 (ANXA13), transcript variant 2, q24.13
SNP_A-2238624	ctctgtgtacactcta[C/T]ctgcaaagctcactgg	C	T	NM_001003954 // intron // 0 // Hs.181107 // ANXA13 // 312 // Homo sapiens annexin A13 (ANXA13), transcript variant 2, mRNA. /// ENST00000262219 // intron // 0 // --- // --- // --- // ---	ANXA13	ANXA13, Homo sapiens annexin A13 (ANXA13), transcript variant 2, q24.13
SNP_A-1933043	ttcggaacatcctgca[A/G]tatagaatctcatccc	A	G	NM_001003954 // upstream // 4768 // Hs.181107 // ANXA13 // 312 // Homo sapiens annexin A13 (ANXA13), transcript variant 2, mRNA. /// NM_004306 // upstream // 26313 // Hs.181107 // ANXA13 // 312 // Homo sapiens annexin A13 (ANXA13), transcript variant 1, m	ANXA13	ANXA13, Homo sapiens annexin A13 (ANXA13), transcript variant 2, q24.13
SNP_A-1893824	tgcataaatacctgac[A/G]ctggtaggaccaccat	A	G	ENST00000356409 // intron // 0 // --- // --- // --- // ---	-	q24.13
SNP_A-2057110	aatataaattgagaaa[A/G]aagtctgctaaaatct	A	G	ENST00000356409 // upstream // 32752 // --- // --- // --- // --- /// ENST00000297628 // upstream // 31679 // --- // --- // --- // ---	-	q24.13
SNP_A-2108125	agctctgttattatcc[A/T]ccatttttgatcatgg	A	T	NM_014751 // upstream // 123365 // Hs.336994 // MTSS1 // 9788 // Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// NM_152412 // upstream // 121516 // Hs.175350 // ZNF572 // 137209 // Homo sapiens zinc finger protein 572 (ZNF572), mRNA. /// ENST00000	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1879997	tcttcgaagcttccac[G/T]ggtcatgctgcatatg	G	T	NM_014751 // upstream // 213615 // Hs.336994 // MTSS1 // 9788 // Homo sapiens metastasis suppressor 1 (MTSS1), mRNA. /// NM_152412 // upstream // 31266 // Hs.175350 // ZNF572 // 137209 // Homo sapiens zinc finger protein 572 (ZNF572), mRNA. /// ENST000003	MTSS1	MTSS1, Homo sapiens metastasis suppressor 1 (MTSS1), q24.13
SNP_A-2239544	ctcttttgctgactg[C/T]actctcctgggcaatc	C	T	NM_173685 // intron // 0 // Hs.388297 // FLJ32440 // 286053 // Homo sapiens hypothetical protein FLJ32440 (FLJ32440), mRNA. /// ENST00000287437 // intron // 0 // --- // --- // ---	FLJ32440	FLJ32440, Homo sapiens hypothetical protein FLJ32440 (FLJ32440), q24.13
SNP_A-1880372	tcttgaagtgagaaag[C/T]atccgatgggctcg	C	T	NM_025195 // downstream // 179517 // Hs.444947 // TRIB1 // 10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream // 179517 // --- // --- // --- /// ENST00000329599 // upstream // 454633 // --- // ---	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2185546	caggagacacaaaggg[A/C]aagatcctagttctct	A	C	NM_025195 // downstream // 434949 // Hs.444947 // TRIB1 // 10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream // 434949 // --- // --- // --- /// ENST00000329599 // upstream // 199201 // --- // ---	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2050049	aaggaatgagtcagaaa[A/G]gaggcaacacaggggt	A	G	NM_025195 // downstream // 612422 // Hs.444947 // TRIB1 // 10221 // Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), mRNA. /// ENST00000311922 // downstream // 612422 // --- // --- // --- /// ENST00000329599 // upstream // 21728 // --- // ---	TRIB1	TRIB1, Homo sapiens tribbles homolog 1 (Drosophila) (TRIB1), q24.13
SNP_A-2026657	aaacaagtctcagcac[A/G]ggatttaaattccaca	A	G	NM_174911 // downstream // 414317 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream // 63909 // --- // --- // --- /// ENST00000329381 // downstream // 63909 // --- // -	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.13
SNP_A-2013813	ctgtgctattggcctct[C/T]atatcctcctggacc	C	T	NM_174911 // downstream // 25088 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// ENST00000329599 // downstream // 453138 // --- // --- // --- /// ENST00000329381 // downstream // 453138 // --- // ---	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2106182	agccccatcggatgaa[C/G]attgccattgcccaaa	C	G	NM_174911 // upstream // 14860 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 842786 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, compl	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2206473	ccatctgccttataaa[A/G]aggttgacaggtgggc	A	G	NM_174911 // upstream // 26908 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 830738 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, compl	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2270859	gacaggtgggaaggca[C/G]ctttcagagaggga	C	G	NM_174911 // upstream // 29357 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 828289 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, compl	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2227440	ctacactgacttctag[C/G]acttctttcagcagct	C	G	NM_174911 // upstream // 82919 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 774727 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, compl	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1833719	tacaggtaagcacaca[A/G]tcgtaacgaacttccc	A	G	NM_174911 // upstream // 83018 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 774628 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, compl	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2013814	gactgagatttaaagc[C/T]gaacttagactgaaac	C	T	NM_174911 // upstream // 87681 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 769965 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, compl	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1703333	ttttagttggttcattaaccaaaag[A/G]gttgttgtttgccagtctttggatg	A	G	NM_174911 // upstream // 500031 // Hs.124951 // NSE2 // 157638 // breast cancer membrane protein 101	NSE2	NSE2 , rs958653, breast cancer membrane protein 101,q24.21
SNP_A-2276451	gagaggaggcaaaatg[C/G]ataggagacagtggga	C	G	NM_174911 // upstream // 491320 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 366326 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, comp	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1846903	tatcacctcagaatga[A/G]ccggaacccgtaaaga	A	G	NM_174911 // upstream // 506079 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 351567 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, comp	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-1697072	acttgtagcacataatatattgtta[C/G]ggggtgagtaaatgatcattaattg	C	G	NM_174911 // upstream // 823900 // Hs.124951 // NSE2 // 157638 // breast cancer membrane protein 101	NSE2	NSE2 , rs1949808, breast cancer membrane protein 101,q24.21
SNP_A-2258478	cttttctatttgttgg[A/G]catatgaactatagcc	A	G	NM_174911 // upstream // 738371 // Hs.124951 // NSE2 // 157638 // Homo sapiens breast cancer membrane protein 101 (NSE2), mRNA. /// AF268618 // upstream // 119275 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, comp	NSE2	NSE2, Homo sapiens breast cancer membrane protein 101 (NSE2), q24.21
SNP_A-2069808	acacagacacaaacaa[A/G]gttaggaagcattgca	A	G	AF268618 // downstream // 8495 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, complete cds. /// ENST00000311492 // downstream // 8495 // --- // --- // --- // --- /// ENST00000304908 // upstream // 310033 // --- //	POU5F1P1	POU5F1P1, Homo sapiens POU 5 domain protein (POU5FLC20) complete cds. ,q24.21
SNP_A-2281165	gagtacttgcctcata[C/T]ggcagattcttcattc	C	T	AF268618 // downstream // 37623 // Hs.450254 // POU5F1P1 // 5462 // Homo sapiens POU 5 domain protein (POU5FLC20) mRNA, complete cds. /// ENST00000311492 // downstream // 37623 // --- // --- // --- // --- /// ENST00000304908 // upstream // 280905 // --- /	POU5F1P1	POU5F1P1, Homo sapiens POU 5 domain protein (POU5FLC20) complete cds. q24.21
SNP_A-2095013	agaatggctgaatttg[C/T]actgtgagggaactca	C	T	ENST00000328323 // upstream // 15971 // --- // --- // --- // --- /// ENST00000356718 // upstream // 154006 // --- // --- // --- // ---	-	q24.21
SNP_A-1661141	ggatacagaagctgtagaaccatag[A/G]ccaatagagtttaaaacttgaaaga	A	G	AK093424 // upstream // 231380 // Hs.232771 // - // - // CDNA FLJ36105 fis, clone TESTI2021463 /// NM_145050 // downstream // 1171600 // Hs.362994 // MGC27434 // 137196 // hypothetical protein MGC27434	-	- , rs2909239, CDNA FLJ36105 fis, clone TESTI2021463 ,q24.21
SNP_A-1995059	ttttaactgtaaagta[A/G]tacattgctaagtgga	A	G	ENST00000328323 // upstream // 134309 // --- // --- // --- // --- /// ENST00000356718 // upstream // 35668 // --- // --- // --- // ---	-	q24.21
SNP_A-1857757	tcactggatgatcttg[A/G]attaactatgctcagc	A	G	ENST00000328323 // upstream // 142752 // --- // --- // --- // --- /// ENST00000356718 // upstream // 27225 // --- // --- // --- // ---	-	q24.21
SNP_A-2050234	aaggagaacccaggac[A/G]ctcctcagcctgatgg	A	G	NM_145050 // downstream // 1228977 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 // downstream // 5297 // --- // --- // --- // --- /// ENST00000311357 // downstream // 1228977 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2051530	aagggtgccatcctta[C/T]gacgaggaaggacgag	C	T	NM_145050 // downstream // 1173946 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 60328 // --- // --- // --- /// ENST00000311357 // downstream // 1173946 // -	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2069937	acacaggcactactcac[C/T]atacactcagacacat	C	T	NM_145050 // downstream // 1166875 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 67399 // --- // --- // --- /// ENST00000311357 // downstream // 1166875 // -	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1995076	tcctcctcttaatca[C/T]ccagactgctacagtt	C	T	NM_145050 // downstream // 1162251 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 72023 // --- // --- // --- /// ENST00000311357 // downstream // 1162251 // -	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2022195	aaaaaggcattgttct[C/T]agagctaggctaccta	C	T	NM_145050 // downstream // 1138019 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 96255 // --- // --- // --- /// ENST00000311357 // downstream // 1138019 // -	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2087909	actggatgcccattaa[C/G]taattcctgtactagt	C	G	NM_145050 // downstream // 1064601 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 169673 // --- // --- // --- /// ENST00000311357 // downstream // 1064601 // -	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2279104	gaggaatctgttatgt[A/G]aacttccaagcagacg	A	G	NM_145050 // downstream // 833010 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 401264 // --- // --- // --- /// ENST00000311357 // downstream // 833010 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1642125	gatcttggattaagctcacctggaa[C/T]atatgtctattaggtca tctgta	C	T	AK093424 // upstream // 874039 // Hs.232771 // - // - // CDNA FLJ36105 fis, clone TESTI2021463 /// NM_145050 // downstream // 528941 // Hs.362994 // MGC27434 // 137196 // hypothetical protein MGC27434	-	- , - , rs919658, CDNA FLJ36105 fis, clone TESTI2021463, q24.21
SNP_A-2229160	ctagctcacacttaaa[C/T]cttatattgcatttta	C	T	NM_145050 // downstream // 532749 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 701525 // --- // --- // --- /// ENST00000311357 // downstream // 532749 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1802140	gtatagcaatagcata[A/T]ctctatgtagacgcta	A	T	NM_145050 // downstream // 511690 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 722584 // --- // --- // --- /// ENST00000311357 // downstream // 511690 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2239120	ctcttgaagcaatgga[C/G]caagaaacttgtggat	C	G	NM_145050 // downstream // 454275 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 779999 // --- // --- // --- /// ENST00000311357 // downstream // 454275 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1917977	ttaaaatgtatgaaaa[A/G]ttattgtgccigtgg	A	G	NM_145050 // downstream // 354165 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA /// ENST00000356718 // downstream // 880109 // --- // --- // --- /// ENST00000311357 // downstream // 354165 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1995124	gtgctcaagatttgct[A/G]aagataatgatagatt	A	G	NM_145050 // downstream // 334775 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 // downstream // 899499 // --- // --- // --- /// ENST00000311357 // downstream // 334775 // ---	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-1891383	tgattatattaatatc[A/C]aacttcaggaccatc	A	C	NM_145050 // downstream // 112676 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// ENST00000356718 // downstream // 1121598 // --- // --- // - - /// ENST00000311357 // downstream // 112676 // -	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2086872	actgagaaatgagtga[C/T]gtgaaggagtgactag	C	T	NM_145050 // upstream // 88892 // Hs.443245 // MGC27434 // 137196 // Homo sapiens hypothetical protein MGC27434 (MGC27434), mRNA. /// NM_031415 // downstream // 306621 // Hs.133244 // MLZE // 56169 // Homo sapiens melanoma-derived leucine zipper, extra-nu	MGC27434	MGC27434, Homo sapiens hypothetical protein MGC27434 (MGC27434), q24.21
SNP_A-2267783	gaatccaaaatgaccat[C/T]gtgggtacaataaacc	C	T	NM_018482 // intron // 0 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// ENST00000357668 // intron // 0 // --- // --- // ---	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.21
SNP_A-1642709	taagctttctgtcctgaattgttt[C/G]aaaacactggacagaggtc ttccta	C	G	NM_001115 // downstream // 125632 // Hs.511773 // ADCY8 // 114 // adenylate cyclase 8 (brain) /// NM_014152 // upstream // 358136 // - // - // - // -	ADCY8	ADCY8 , rs7836215, adenylate cyclase 8 (brain) ,q24.22
SNP_A-2287586	gattaaatcattataa[C/T]aactcgataaggcagt	C	T	NM_018482 // upstream // 205970 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 427053 // Hs.106015 // DDEF1 // 50807 // Homo sapiens mRNA for KIAA1249 protein, p	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-1787444	gggaagttgtgtgtca[C/T]gcctggagtcaccagt	C	T	NM_018482 // upstream // 365932 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 587015 // Hs.106015 // DDEF1 // 50807 // Homo sapiens mRNA for KIAA1249 protein, p	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-1995162	atttcgtatatgata[C/T]gtttcccacactttc	C	T	NM_018482 // upstream // 374440 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 595523 // Hs.106015 // DDEF1 // 50807 // Homo sapiens mRNA for KIAA1249 protein, p	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-2089228	acttactctctggaa[G/T]ctgatccagatgggtg	G	T	NM_018482 // upstream // 375300 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 596383 // Hs.106015 // DDEF1 // 50807 // Homo sapiens mRNA for KIAA1249 protein, p	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-1938500	ttgagaaagcctcaag[C/T]aaacctattgaattt	C	T	NM_018482 // upstream // 375349 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 596432 // Hs.106015 // DDEF1 // 50807 // Homo sapiens mRNA for KIAA1249 protein, p	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-2216725	cctctctatccagccat[A/T]ctgaggagaaaaaagg	A	T	NM_018482 // upstream // 377181 // Hs.106015 // DDEF1 // 50807 // Homo sapiens development and differentiation enhancing factor 1 (DDEF1), mRNA. /// AB033075 // upstream // 598264 // Hs.106015 // DDEF1 // 50807 // Homo sapiens mRNA for KIAA1249 protein, p	DDEF1	DDEF1, Homo sapiens development and differentiation enhancing factor 1 (DDEF1), q24.22
SNP_A-1935057	ttctgatcaagttgca[C/T]atctgatcaagttaca	C	T	NM_001115 // intron // 0 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// ENST00000286355 // intron // 0 // --- // --- // ---	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814670	gtgtggtaagccaggc[C/T]ataagttgaaggaaaa	C	T	NM_001115 // intron // 0 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// ENST00000286355 // intron // 0 // — // — // — // —	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2146232	atgctaagagtagtgat[C/G]aagcactgaaaggtg	C	G	NM_001115 // intron // 0 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// ENST00000286355 // intron // 0 // — // — // — // —	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1790233	ggggagacaggaccac[A/G]catagtttgcagggtc	A	G	NM_001115 // intron // 0 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// ENST00000286355 // intron // 0 // — // — // — // —	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1800911	gtagaggtttgaga[G/T]ccaggctgaagagttt	G	T	NM_001115 // upstream // 108902 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 752794 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1893511	tgcaggagaacggatc[A/G]agtggaaaatttatc	A	G	NM_001115 // upstream // 109316 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 752380 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2089131	acttaattctcataac[A/G]ataaaactgatttaaa	A	G	NM_001115 // upstream // 278548 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 583148 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2123905	agttaagatgtttgca[C/T]atatattctctgtcac	C	T	NM_001115 // upstream // 299607 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 562089 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1694229	caaaggcaatagtggacctttaacc[A/C]gcacattagtcattgttt taataga	A	C	NM_001115 // upstream // 419191 // Hs.511773 // ADCY8 // 114 // adenylate cyclase 8 (brain)	ADCY8	ADCY8, rs715969, adenylate cyclase 8 (brain),q24.22
SNP_A-1854437	tcaaatgaataggaaa[C/T]aatcctttctctca	C	T	NM_001115 // upstream // 404277 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 457419 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2192164	catcagagccatcaga[A/G]tcagggtacatattga	A	G	NM_001115 // upstream // 488591 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 373105 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1917082	tgtttggcatagtccaa[A/G]tgaaaaggaagaaaga	A	G	NM_001115 // upstream // 490793 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 370903 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-1886293	tgacctcaagaaggta[C/G]aggtggatagatttga	C	G	NM_001115 // upstream // 501457 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 360239 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22
SNP_A-2101231	agatccctagaggtt[A/C]aaataatgaaatatgg	A	C	NM_001115 // upstream // 685106 // Hs.414631 // ADCY8 // 114 // Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA. /// D63477 // upstream // 176590 // Hs.204564 // KIAA0143 // 23167 // Human mRNA for KIAA0143 gene, partial cds. /// ENST00000286355 //	ADCY8	ADCY8, Homo sapiens adenylate cyclase 8 (brain) (ADCY8), q24.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936664	ttcttgtcaaagagga[C/G]agtggttcttcagctc	C	G	NM_004519 // intron // 0 // Hs.374023 // KCNQ3 // 3786 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), mRNA. /// ENST00000330569 // intron // 0 // — // — // — // —	KCNQ3	KCNQ3, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 3 (KCNQ3), q24.22
SNP_A-2078503	accatcttgttaggac[C/T]gtcaagctgtcccact	C	T	NM_003235 // intron // 0 // Hs.546309 // TG // 7038 // Homo sapiens thyroglobulin (TG), mRNA. /// ENST00000220616 // intron // 0 // — // — // — // —	TG	TG, Homo sapiens thyroglobulin (TG), q24.22
SNP_A-2131979	ataggcaagaaacaga[A/G]ctaggattgaagcctt	A	G	NM_003235 // downstream // 22757 // Hs.546309 // TG // 7038 // Homo sapiens thyroglobulin (TG), mRNA. /// NM_006748 // upstream // 55006 // Hs.75367 // SLA // 6503 // Homo sapiens Src-like-adaptor (SLA), mRNA. /// NM_006748 // upstream // 54981 // Hs.7536	TG	TG, Homo sapiens thyroglobulin (TG), q24.22
SNP_A-1780651	ggatcacagatgaacc[A/G]cctagctgagccttc	A	G	NM_003235 // downstream // 32736 // Hs.546309 // TG // 7038 // Homo sapiens thyroglobulin (TG), mRNA. /// NM_006748 // upstream // 64985 // Hs.75367 // SLA // 6503 // Homo sapiens Src-like-adaptor (SLA), mRNA. /// NM_006748 // upstream // 64960 // Hs.7536	TG	TG, Homo sapiens thyroglobulin (TG), q24.22
SNP_A-1803744	gtcaacaggaggctaa[C/T]gtcagatcttctagaa	C	T	NM_003235 // downstream // 39912 // Hs.546309 // TG // 7038 // Homo sapiens thyroglobulin (TG), mRNA. /// NM_006748 // upstream // 72161 // Hs.75367 // SLA // 6503 // Homo sapiens Src-like-adaptor (SLA), mRNA. /// NM_006748 // upstream // 72136 // Hs.7536	TG	TG, Homo sapiens thyroglobulin (TG), q24.22
SNP_A-1995237	tgttgcctatgggtga[A/G]catcatatggcccctg	A	G	NM_006096 // upstream // 118414 // Hs.372914 // NDRG1 // 10397 // Homo sapiens N-myc downstream regulated gene 1 (NDRG1), mRNA. /// NM_003033 // downstream // 42902 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alp	NDRG1	NDRG1, Homo sapiens N-myc downstream regulated gene 1 (NDRG1), q24.22
SNP_A-1995238	actactcaaaggaaca[A/T]ctgcttggaagaggc	A	T	NM_006096 // upstream // 161233 // Hs.372914 // NDRG1 // 10397 // Homo sapiens N-myc downstream regulated gene 1 (NDRG1), mRNA. /// NM_003033 // downstream // 83 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-	NDRG1	NDRG1, Homo sapiens N-myc downstream regulated gene 1 (NDRG1), q24.22
SNP_A-1906699	tggtgttggtcattta[C/G]ggagaagaggagaaga	C	G	NM_003033 // intron // 0 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // intron // 0 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2037911	aacaatggagtttaac[A/G]cagatatgaagtaatt	A	G	NM_003033 // intron // 0 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // intron // 0 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-1682712	tcatgcaaaatgtgacatagtatga[G/T]cgagggcggacagcc ttgggaacca	G	T	AB040918 // downstream // 718626 // Hs.15611 // ZNF406 // 57623 // zinc finger protein 406 /// NM_003033 // upstream // 201714 // Hs.491107 // SIAT4A // 6482 // sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) /// NM_173344 // upstream	ZNF406	ZNF406 , rs10505613, zinc finger protein 406 q24.22
SNP_A-2091135	actttggcttgacca[C/G]gtaagaatgacagagg	C	G	NM_003033 // upstream // 216778 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 216778 // Hs.374257 // ST3GAL1 // 6482 /	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1995257	agatgacatagttgat[A/C]aggaaaagtgtcttc	A	C	NM_003033 // upstream // 218673 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 218673 // Hs.374257 // ST3GAL1 // 6482 /	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2065330	aattgtatcaccattc[A/T]ctggcattagatacaa	A	T	NM_003033 // upstream // 691004 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 691004 // Hs.374257 // ST3GAL1 // 6482 /	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-2312877	ggactgtaggtaataa[C/T]agtgtcatgtagtcag	C	T	NM_003033 // upstream // 834405 // Hs.374257 // ST3GAL1 // 6482 // Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, mRNA. /// NM_173344 // upstream // 834405 // Hs.374257 // ST3GAL1 // 6482 /	ST3GAL1	ST3GAL1, Homo sapiens sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A), transcript variant 1, q24.22
SNP_A-1783228	ggcaggtgaacgagca[A/G]tagtcgcaggcgaact	A	G	NM_020863 // CDS // 0 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // CDS // 0 // — // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-1886644	tgactcctataaagcc[A/G]gagaatgaggaaaaca	A	G	NM_020863 // intron // 0 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // intron // 0 // — // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2054267	aagttgcctaagcccaa[G/T]ctagagagtacctgtt	G	T	NM_020863 // intron // 0 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // intron // 0 // — // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2194412	catgattaaggataag[C/T]ctgtctacaacaagcg	C	T	NM_020863 // intron // 0 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // intron // 0 // — // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2184894	cagctgtgctctacttt[C/T]aagaaatttgacattt	C	T	NM_020863 // upstream // 116672 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // upstream // 116672 // — // — // — // — /// ENST00000360123 // downstream // 320815 // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2013894	aagaggctgtgaataa[C/T]ggaatggtgtgtaaat	C	T	NM_020863 // upstream // 254955 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // upstream // 254955 // — // — // — // — /// ENST00000360123 // downstream // 182532 // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2170665	caagttaggccttgaa[A/G]caaaatgaagacacca	A	G	NM_020863 // upstream // 341563 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // upstream // 341563 // — // — // — // — /// ENST00000360123 // downstream // 95924 // — // — // — /	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-1995288	gtagtagtgaccataa[C/T]aagaggagaaaactcag	C	T	NM_020863 // upstream // 430292 // Hs.446172 // ZNF406 // 57623 // Homo sapiens zinc finger protein 406 (ZNF406), mRNA. /// ENST00000318135 // upstream // 430292 // — // — // — // — /// ENST00000360123 // downstream // 7195 // — // — // — // —	ZNF406	ZNF406, Homo sapiens zinc finger protein 406 (ZNF406), q24.22
SNP_A-2245653	ctgggcccctctgcctc[G/T]atgctggaagacgtgg	G	T	NM_006558 // downstream // 71551 // Hs.444558 // KHDRBS3 // 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// ENST00000355849 // downstream // 71551 // — // — // — // — /// ENST00000002540	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1843204	tagtccataaagttcc[A/G]gctcatagcaggagag	A	G	NM_006558 // downstream // 73407 // Hs.444558 // KHDRBS3 // 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// ENST00000355849 // downstream // 73407 // --- // --- // --- // --- /// ENST000002540	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.23
SNP_A-1899842	tggacaaaaccagaaa[A/T]tagtgtgatttggaca	A	T	NM_006558 // downstream // 73514 // Hs.444558 // KHDRBS3 // 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// ENST00000355849 // downstream // 73514 // --- // --- // --- // --- /// ENST000002540	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.23
SNP_A-2300785	gcctggctttgtcagc[A/G]gctacttagagaggtt	A	G	NM_006558 // downstream // 326172 // Hs.444558 // KHDRBS3 // 10656 // Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA. /// ENST00000355849 // downstream // 326172 // --- // --- // --- // --- /// ENST0000025	KHDRBS3	KHDRBS3, Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), q24.23
SNP_A-2084477	actatctactgaggcc[C/T]gagactgcatggaggg	C	T	ENST00000357315 // downstream // 83707 // --- // --- // --- // --- /// ENST00000328955 // upstream // 1549437 // --- // --- // --- // ---	-	q24.23
SNP_A-2043614	aactgttccatgatga[C/T]gtggcataaaagagag	C	T	ENST00000357315 // downstream // 165050 // --- // --- // --- // --- /// ENST00000328955 // upstream // 1468094 // --- // --- // --- // ---	-	q24.23
SNP_A-1663828	ggctcctttgaatgctttcaaggac[G/T]gagtaaagtttgtaagag gcatttc	G	T	NM_006558 // downstream // 1003474 // Hs.13565 // KHDRBS3 // 10656 // KH domain containing, RNA binding, signal transduction associated 3 /// NM_015912 // downstream // 1491785 // Hs.13497 // LOC51059 // 51059 // hypothetical protein LOC51059	KHDRBS3	KHDRBS3 , rs10505662, KH domain containing, RNA binding, signal transduction associated 3 ,q24.23
SNP_A-1958298	ttttccagtagtgaca[C/T]tgatgttgggaattag	C	T	ENST00000357315 // downstream // 581969 // --- // --- // --- // --- /// ENST00000328955 // upstream // 1051175 // --- // --- // --- // ---	-	q24.23
SNP_A-2191698	catattctgatgggac[A/G]aattggtccttgtaaa	A	G	ENST00000357315 // downstream // 1102765 // --- // --- // --- // --- /// ENST00000328955 // upstream // 530379 // --- // --- // --- // ---	-	q24.23
SNP_A-2154359	attatgttccacagaa[A/G]agcctggaagacgtat	A	G	ENST00000357315 // downstream // 1103197 // --- // --- // --- // --- /// ENST00000328955 // upstream // 529947 // --- // --- // --- // ---	-	q24.23
SNP_A-2045431	aagaatataatacaca[G/T]tggaaatcccagaggc	G	T	ENST00000357315 // downstream // 1234875 // --- // --- // --- // --- /// ENST00000328955 // upstream // 398269 // --- // --- // --- // ---	-	q24.23
SNP_A-2177827	cacgttgattttagcc[C/T]gaggaaacctatttca	C	T	ENST00000357315 // downstream // 1526994 // --- // --- // --- // --- /// ENST00000328955 // upstream // 106150 // --- // --- // --- // ---	-	q24.23
SNP_A-2182544	cagatattcctttgaa[A/T]tcctcttttggcatct	A	T	ENST00000357315 // downstream // 1527908 // --- // --- // --- // --- /// ENST00000328955 // upstream // 105236 // --- // --- // --- // ---	-	q24.23
SNP_A-2098855	agagctgaagaactga[A/C]attcagagagcttgtg	A	C	ENST00000357315 // downstream // 1528535 // --- // --- // --- // --- /// ENST00000328955 // upstream // 104609 // --- // --- // --- // ---	-	q24.23
SNP_A-1911932	tgtgactaaatgcaca[A/G]tatgaggcgttggggt	A	G	ENST00000357315 // downstream // 1528780 // --- // --- // --- // --- /// ENST00000328955 // upstream // 104364 // --- // --- // --- // ---	-	q24.23
SNP_A-2184681	cagctctggagaacac[A/G]cttttactttagtcag	A	G	ENST00000357315 // downstream // 1529404 // --- // --- // --- // --- /// ENST00000328955 // upstream // 103740 // --- // --- // --- // ---	-	q24.23
SNP_A-2129993	ataccaacagcctgga[A/C]tcactggctgagatga	A	C	ENST00000357315 // downstream // 1536383 // --- // --- // --- // --- /// ENST00000328955 // upstream // 96761 // --- // --- // --- // ---	-	q24.23
SNP_A-1783541	ggcatgaaagctccta[C/T]agcattgataaatttc	C	T	ENST00000357315 // downstream // 1539809 // --- // --- // --- // --- /// ENST00000328955 // upstream // 93335 // --- // --- // --- // ---	-	q24.23
SNP_A-1852040	tattgctcctgagctg[C/T]aaatctgtacatcatg	C	T	ENST00000357315 // downstream // 1546084 // --- // --- // --- // --- /// ENST00000328955 // upstream // 87060 // --- // --- // --- // ---	-	q24.23
SNP_A-1920325	ttaatgggtcaccaaa[C/T]ccccaaactctaccaa	C	T	ENST00000328955 // downstream // 94379 // --- // --- // --- // --- /// ENST00000276737 // downstream // 340439 // --- // --- // --- // ---	-	q24.23
SNP_A-1799490	gtaatgcctggacgta[A/G]taaagaataaagaggg	A	G	ENST00000328955 // downstream // 95177 // --- // --- // --- // --- /// ENST00000276737 // downstream // 339641 // --- // --- // --- // ---	-	q24.23
SNP_A-2151890	atgtttggaactacta[C/T]gggagccacatcatta	C	T	ENST00000328955 // downstream // 95770 // --- // --- // --- // --- /// ENST00000276737 // downstream // 339048 // --- // --- // --- // ---	-	q24.23
SNP_A-2013921	ataaagctcaatgaga[C/T]gtaatgttctgaaaca	C	T	ENST00000328955 // downstream // 99856 // --- // --- // --- // --- /// ENST00000276737 // downstream // 334962 // --- // --- // --- // ---	-	q24.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2040462	aaccaggtaataaagca[A/G]agtattcagtaggtat	A	G	ENST00000328955 // downstream // 101462 /// ENST00000276737 // downstream // 333356 ///	-	q24.23
SNP_A-2065905	aatttctgattggttg[G/T]attaggatcctgttcc	G	T	ENST00000328955 // downstream // 171376 /// ENST00000276737 // downstream // 263442 ///	-	q24.23
SNP_A-2177394	cacctgaggatagca[A/G]agaaacaaaaacaaag	A	G	ENST00000328955 // downstream // 208282 /// ENST00000276737 // downstream // 226536 ///	-	q24.23
SNP_A-1937659	ttgaagatggctaaaa[A/C]tcttgtagtgaaacc	A	C	ENST00000328955 // downstream // 400660 /// ENST00000276737 // downstream // 34158 ///	-	q24.23
SNP_A-1879030	tcttaactgtctgtga[C/T]gaatctgataaaattt	C	T	NM_015912 // upstream // 10535 // Hs.13497 // LOC51059 // 51059 // Homo sapiens hypothetical protein LOC51059 (LOC51059), mRNA. /// ENST00000160713 // upstream // 10535 /// ENST00000316225 // downstream // 87901 ///	LOC51059	LOC51059, Homo sapiens hypothetical protein LOC51059 (LOC51059), q24.23
SNP_A-1931725	ttccctgcatatgcca[A/T]gttgattaatttatt	A	T	NM_015912 // upstream // 19205 // Hs.13497 // LOC51059 // 51059 // Homo sapiens hypothetical protein LOC51059 (LOC51059), mRNA. /// ENST00000160713 // upstream // 19205 /// ENST00000316225 // downstream // 79231 ///	LOC51059	LOC51059, Homo sapiens hypothetical protein LOC51059 (LOC51059), q24.23
SNP_A-2165438	caaagcacaatgctta[A/G]atagtctgactagttt	A	G	ENST00000316225 // intron // 0 ///	-	q24.23
SNP_A-2024799	aaaagtgagactcctc[C/T]agatggactgaaacta	C	T	NM_152888 // downstream // 133545 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000316225 // upstream // 86708 /// ENST00000303045 // downstream // 133545 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-1814343	gtgtgaagccacacta[A/G]cacaaagtgagactc	A	G	NM_152888 // downstream // 133525 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000316225 // upstream // 86728 /// ENST00000303045 // downstream // 133525 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-1803217	gtattctgcacagttat[C/T]gaaaacaaaaataaat	C	T	NM_152888 // downstream // 125918 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000316225 // upstream // 94335 /// ENST00000303045 // downstream // 125918 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-1931520	ttccccattaaatacc[A/C]ggcacctcatttctcc	A	C	NM_152888 // downstream // 119659 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000316225 // upstream // 100594 /// ENST00000303045 // downstream // 119659 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2186333	caggctgccagtggaa[A/G]caatatgcacgttgtg	A	G	NM_152888 // downstream // 115494 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000316225 // upstream // 104759 /// ENST00000303045 // downstream // 115494 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2013926	tgtcaatgcaaataag[C/T]cctacatttaggcccc	C	T	NM_152888 // intron // 0 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000303045 // intron // 0 /// ENST00000341807 // intron // 0 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2221511	ccttctctcagcaaaa[G/T]ttagacacaccattct	G	T	NM_152888 // intron // 0 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000303045 // intron // 0 /// ENST00000341807 // intron // 0 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2192183	catcagcacaaagaga[A/G]gactcaccagggaga	A	G	NM_152888 // intron // 0 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000303045 // intron // 0 ///	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1995417	ggttggacctcacaat[A/G]aacagcagaacagaaa	A	G	NM_152888 // intron // 0 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// ENST00000303045 // intron // 0 // — // — // —	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.23
SNP_A-2089835	acttctaaataccaca[G/T]gaaagagaactaggagt	G	T	NM_152888 // upstream // 166923 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 531645 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2210354	cccccacactaacccag[G/T]ctcctagcacaggaag	G	T	NM_152888 // upstream // 167660 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 530908 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2134985	atattcagtgacaaaca[A/G]ctttaggagcttgaa	A	G	NM_152888 // upstream // 376821 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 321747 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1719207	gagcagttttggaggataaagacag[C/G]agttggttagatcaga tccttcatt	C	G	AF406780 // upstream // 607827 // Hs.116394 // COL22A1 // 169044 // collagen, type XXII, alpha 1 /// NM_016601 // downstream // 90741 // Hs.117010 // KCNK9 // 51305 // potassium channel, subfamily K, member 9	COL22A1	COL22A1, rs2447374, collagen, type XXII, alpha 1 q24.3
SNP_A-1738943	atctcgagaaaagtctggtcaggat[C/G]agggagaaagatctt attgggtata	C	G	AF406780 // upstream // 624233 // Hs.116394 // COL22A1 // 169044 // collagen, type XXII, alpha 1 /// NM_016601 // downstream // 74335 // Hs.117010 // KCNK9 // 51305 // potassium channel, subfamily K, member 9	COL22A1	COL22A1, rs7465461, collagen, type XXII, alpha 1 q24.3
SNP_A-1750279	aactcaggtcttctaaaatatttac[A/G]aagcaggtgagctagag agaacttc	A	G	AF406780 // upstream // 624304 // Hs.116394 // COL22A1 // 169044 // collagen, type XXII, alpha 1 /// NM_016601 // downstream // 74264 // Hs.117010 // KCNK9 // 51305 // potassium channel, subfamily K, member 9	COL22A1	COL22A1, rs4736271, collagen, type XXII, alpha 1 q24.3
SNP_A-1735282	gatttattggaaggagttggcttac[A/G]tgattgtgaggtctaggc aagtatg	A	G	AF406780 // upstream // 682523 // Hs.116394 // COL22A1 // 169044 // collagen, type XXII, alpha 1 /// NM_016601 // downstream // 16045 // Hs.117010 // KCNK9 // 51305 // potassium channel, subfamily K, member 9	COL22A1	COL22A1, rs726348, collagen, type XXII, alpha 1 q24.3
SNP_A-2013936	aatcgcagtcacataa[A/G]cttcaaaaacatggct	A	G	NM_152888 // upstream // 585821 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 112747 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2156844	atctctatctcagca[A/C]ctgttalacttaatt	A	C	NM_152888 // upstream // 593281 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 105287 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2121980	agtgagtggctctagg[G/T]catttctctggctc	G	T	NM_152888 // upstream // 595570 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 102998 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2313433	ggagagatggtaaagc[C/T]catgcaggaagaaggg	C	T	NM_152888 // upstream // 611770 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 86798 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116336	aggtagccgtttctta[C/T]ggaaacttcacactaa	C	T	NM_152888 // upstream // 616034 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 82534 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2193097	catctactgctacca[A/G]aagttgccatcagctc	A	G	NM_152888 // upstream // 616533 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 82035 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2123597	agtgtgcttacagt[A/G]aatgacagttcagaca	A	G	NM_152888 // upstream // 618726 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 79842 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2180683	cagaaggtaaaggaca[C/T]ggaactgaagcactag	C	T	NM_152888 // upstream // 636941 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 61627 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2295739	gcatgattctggaaac[C/G]aacagatagaaatagg	C	G	NM_152888 // upstream // 637074 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 61494 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2144056	atgaggaagctggtga[A/T]gtaaggaaaggtgaga	A	T	NM_152888 // upstream // 640034 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 58534 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2140649	atctctccacatgtgd[A/G]gagcatcagttttgc	A	G	NM_152888 // upstream // 640386 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 58182 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1797566	ggtttcctgagtaaaa[A/G]cagagtctaacagccc	A	G	NM_152888 // upstream // 649114 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 49454 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2228472	ctacttgactagccaa[C/T]tcattccacctctga	C	T	NM_152888 // upstream // 653156 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 45412 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1917352	tgttttctctatga[C/T]ggtagagtattggcct	C	T	NM_152888 // upstream // 655778 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 42790 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2285443	gatcttctatcaaag[A/C]agaccagccctctac	A	C	NM_152888 // upstream // 657865 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 40703 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2294920	gcataagaggacaaaa[A/G]ggaactccactgcaga	A	G	NM_152888 // upstream // 657952 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 40616 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2307805	gcttcctttttttccca[C/G]agglatlgatcccaaa	C	G	NM_152888 // upstream // 658225 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 40343 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1935650	ttctglatttcctca[G/T]aaagcaagctccacta	G	T	NM_152888 // upstream // 658641 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 39927 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2275790	gagacctatttaacca[C/T]aagctctggtttctcc	C	T	NM_152888 // upstream // 659096 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 39472 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2173080	cacaaagtgaatttaa[G/T]atgcaaggggtggat	G	T	NM_152888 // upstream // 659290 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 39278 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2298404	gccatttcaggcacaa[C/T]gtaggcagtgggtgtg	C	T	NM_152888 // upstream // 659418 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 39150 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2289991	gcaaaggattcagaca[A/G]tagcctcctcggcccc	A	G	NM_152888 // upstream // 679479 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 19089 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-1995448	gatatctttctgtcta[C/T]gctcccatctttgcc	C	T	NM_152888 // upstream // 681071 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 17497 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (K	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2083856	actactaaacacttga[C/T]acgtctattgtgtctc	C	T	NM_152888 // upstream // 690319 // Hs.117169 // COL22A1 // 169044 // Homo sapiens collagen, type XXII, alpha 1 (COL22A1), mRNA. /// NM_016601 // downstream // 8249 // Hs.493037 // KCNK9 // 51305 // Homo sapiens potassium channel, subfamily K, member 9 (KC	COL22A1	COL22A1, Homo sapiens collagen, type XXII, alpha 1 (COL22A1), q24.3
SNP_A-2013941	ctcctcatgctcacaa[A/G]tcttaagccctttc	A	G	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // — /// — // — /// ENST00000301226 // intron // 0 // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2119875	agtcaaccgaggacaa[C/T]gcctgccaaacagag	C	T	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // — /// — // — /// ENST00000301226 // intron // 0 // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2046745	aagaggaaagctacca[A/G]tcttcctgatggatac	A	G	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // --- // --- // — // — /// ENST00000301226 // intron // 0 // — // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-1818686	gttgaattattgacca[C/T]cgcccatgcaatttcc	C	T	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // --- // — // — /// ENST00000301226 // intron // 0 // — // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2246189	ctggtgaccataattc[A/G]aggcctgatttggttt	A	G	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // — // — // — /// ENST00000301226 // intron // 0 // — // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-1812717	gtgggaaccactgtgc[A/G]attttgaatgtgcggc	A	G	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // — // — // — /// ENST00000301226 // intron // 0 // — // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-1800553	gtacttagggagacaa[C/T]gctctttcaagaaaac	C	T	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // — // — // — /// ENST00000301226 // intron // 0 // --- // --- // --- // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2218252	cctgctctatccaaca[A/C]tccttgtacacagaga	A	C	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // — // — // --- /// ENST00000301226 // intron // 0 // — // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2091294	acttttcatttgtata[A/C]ggtagctgtttaggag	A	C	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // --- // — // — /// ENST00000301226 // intron // 0 // — // — // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2082217	acgagactgaataaaa[C/G]tgttcaaactgtgctc	C	G	NM_031466 // intron // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // intron // 0 // — // --- // — // — /// ENST00000301226 // intron // 0 // --- // --- // — // —	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-1903264	tggctttctaccccaa[C/T]tacgaggactgccaga	C	T	NM_031466 // CDS // 0 // Hs.26814 // T1 // 83696 // Homo sapiens Tularik gene 1 (T1), mRNA. /// ENST00000356344 // CDS // 0 // — // — // — // — /// ENST00000301226 // CDS // 0 // — // --- // --- // ---	T1	T1, Homo sapiens Tularik gene 1 (T1), q24.3
SNP_A-2070303	acaccacaccaaagta[A/G]gcggtttcccaggaag	A	G	NM_017444 // downstream // 8852 // Hs.279704 // CHRAC1 // 54108 // Homo sapiens chromatin accessibility complex 1 (CHRAC1), mRNA. /// NM_012154 // downstream // 7067 // Hs.449415 // EIF2C2 // 27161 // Homo sapiens eukaryotic translation initiation factor	CHRAC1	CHRAC1, Homo sapiens chromatin accessibility complex 1 (CHRAC1), q24.3
SNP_A-2143830	atgagagtagcagttc[C/T]caggatgttccgctac	C	T	NM_153831 // upstream // 94896 // Hs.395482 // PTK2 // 5747 // Homo sapiens PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA. /// NM_005607 // upstream // 94896 // Hs.395482 // PTK2 // 5747 // Homo sapiens PTK2 protein tyrosine kinase 2 (	PTK2	PTK2, Homo sapiens PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, q24.3
SNP_A-2108638	agctggtcagttgtga[C/T]gttttggatggcatct	C	T	NM_007079 // downstream // 184806 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, mRNA. /// NM_032611 // downstream // 184806 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens pro	PTP4A3	PTP4A3, Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, q24.3
SNP_A-2278984	gaggaacggaatgcga[A/G]cgttgtctctgttact	A	G	NM_007079 // downstream // 304560 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, mRNA. /// NM_032611 // downstream // 304560 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens pro	PTP4A3	PTP4A3, Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2306874	gctgtggcgttttcca[A/G]tcaatcatctgtgggt	A	G	NM_007079 // downstream // 329755 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, mRNA. /// NM_032611 // downstream // 329755 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens pro	PTP4A3	PTP4A3, Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, q24.3
SNP_A-2301839	gcggctgtaacgaaac[A/G]acaccgaaagtgccgt	A	G	NM_007079 // downstream // 345024 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, mRNA. /// NM_032611 // downstream // 345024 // Hs.43666 // PTP4A3 // 11156 // Homo sapiens pro	PTP4A3	PTP4A3, Homo sapiens protein tyrosine phosphatase type IVA, member 3 (PTP4A3), transcript variant 2, q24.3
SNP_A-1876964	tctgcctcctggtccc[C/T]gcagatcgcccagacc	C	T	NM_001702 // downstream // 32942 // Hs.194654 // BAI1 // 575 // Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), mRNA. /// NM_015193 // downstream // 33101 // Hs.40888 // ARC // 23237 // Homo sapiens activity-regulated cytoskeleton-associated	BAI1	BAI1, Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), q24.3
SNP_A-2103952	agcactgtgatgctgc[G/T]acagttgacctgataa	G	T	NM_203447 // downstream // 17766 // Hs.132599 // DOCK8 // 81704 // Homo sapiens dedicator of cytokinesis 8 (DOCK8), mRNA. /// NM_015158 // upstream // 21698 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript va	DOCK8	DOCK8, Homo sapiens dedicator of cytokinesis 8 (DOCK8), p24.3
SNP_A-2161192	atttgactgctttaga[C/T]ctgtgaaaatgactgt	C	T	NM_015158 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), tra	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2031252	aaaggctggcaaaata[C/T]gtatcattgttgaagc	C	T	NM_015158 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), tra	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2300758	gcctggcagtgtcaag[C/T]ctgaaacaaagcaata	C	T	NM_015158 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), tra	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2287179	gatgtcctatcacctc[A/G]ctattgggaaggggc	A	G	NM_015158 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // intron // 0 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), tra	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2277357	gagatttctaaaagca[C/T]atttcgatcaggcaca	C	T	NM_015158 // downstream // 52671 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // downstream // 52671 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 1	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2065219	aattggcatattcccc[C/T]gagactccttttgac	C	T	NM_015158 // downstream // 55273 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, mRNA. /// NM_153186 // downstream // 55273 // Hs.493272 // ANKRD15 // 23189 // Homo sapiens ankyrin repeat domain 1	ANKRD15	ANKRD15, Homo sapiens ankyrin repeat domain 15 (ANKRD15), transcript variant 1, p24.3
SNP_A-2057960	aatattggtatctata[G/T]gaagggctaaagtaac	G	T	NM_021951 // intron // 0 // Hs.98586 // DMRT1 // 1761 // Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), mRNA. /// ENST00000223955 // intron // 0 // --- // --- // --- // ---	DMRT1	DMRT1, Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1908671	tgtaggagtgtacaaa[A/G]taaaaccagaaatttt	A	G	NM_021951 // intron // 0 // Hs.98586 // DMRT1 // 1761 // Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), mRNA. /// ENST00000223955 // intron // 0 // — // — // — // —	DMRT1	DMRT1, Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), p24.3
SNP_A-1939399	ttgatgccttagactt[C/G]aaagctgtcttttgc	C	G	NM_021951 // intron // 0 // Hs.98586 // DMRT1 // 1761 // Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), mRNA. /// ENST00000223955 // intron // 0 // — // — // — // —	DMRT1	DMRT1, Homo sapiens doublesex and mab-3 related transcription factor 1 (DMRT1), p24.3
SNP_A-1954543	tttgcccttatgggac[G/T]ctaatgacaacaaaat	G	T	NM_181872 // intron // 0 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// ENST00000302441 // intron // 0 // — // — // — // —	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2155203	attcagcttgtccaa[C/T]cacgtgaaatgaagat	C	T	NM_181872 // downstream // 255 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 247 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related tra	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1814773	gtgtgtctctggtcac[A/G]atatttcatcagcca	A	G	NM_181872 // downstream // 59753 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 59745 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1950345	tttcagctctcatatt[A/G]aaaacaagtgtccttt	A	G	NM_181872 // downstream // 60040 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 60032 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2241928	ctgatgtcctctgatc[A/G]acaagtaaagtgaaaa	A	G	NM_181872 // downstream // 65903 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 65895 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1665380	aggtgtaatttccaattccattaac[G/T]gaacgagacatgaatgtt tccttaa	G	T	NM_003070 // upstream // 864252 // Hs.396404 // SMARCA2 // 6595 // SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 /// NM_006557 // downstream // 93540 // Hs.59506 // DMRT2 // 10655 // doublesex and mab-3	SMARCA2	SMARCA2 , rs1337621, SWI,p24.3
SNP_A-2257285	cttttcttttgaaag[C/T]agtcaataacagtgca	C	T	NM_181872 // downstream // 100629 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 100621 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1995518	aacaaatctgtgttta[A/T]aataagcgtaccaaat	A	T	NM_181872 // downstream // 104062 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 104054 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2164222	caaaataaaaggtgta[G/T]agcaatttcagcggat	G	T	NM_181872 // downstream // 104471 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 104463 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1714887	ccagtgatatagatggttgaaaaac[G/T]gatgattccactgtttta aaattgt	G	T	NM_003070 // upstream // 808931 // Hs.396404 // SMARCA2 // 6595 // SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 /// NM_006557 // downstream // 14886 // Hs.59506 // DMRT2 // 10655 // doublesex and mab-	SMARCA2	SMARCA2, rs10511427, SWI,p24.3
SNP_A-1995521	cttttgtgtttcttaa[A/T]aagctgctctattagg	A	T	NM_181872 // downstream // 148945 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 148937 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2022766	aaaaattgaacagagc[C/T]gctaaaaggtaltgaa	C	T	NM_181872 // downstream // 164187 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 164179 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1995529	ctaacatgcagcccgg[A/C]agatccagtgtcaggt	A	C	NM_181872 // downstream // 249313 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 249305 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1916162	tgttggatttaagtg[C/T]accctacatgcattct	C	T	NM_181872 // downstream // 325904 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 325896 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-2307445	gcttatcttttgtcagt[C/G]aaaagaaaagtttgctg	C	G	NM_181872 // downstream // 432865 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 432857 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1946955	ttaagtagaagctgal[C/T]gaaaatatcttttctca	C	T	NM_181872 // downstream // 454977 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), mRNA. /// NM_006557 // downstream // 454969 // Hs.59506 // DMRT2 // 10655 // Homo sapiens doublesex and mab-3 relat	DMRT2	DMRT2, Homo sapiens doublesex and mab-3 related transcription factor 2 (DMRT2), p24.3
SNP_A-1704121	gatagtgctgagaaagaaatcttaa[C/T]catagctgaaataaatt gtttatat	C	T	NM_003070 // intron // 0 // Hs.396404 // SMARCA2 // 6595 // SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 /// NM_139045 // intron // 0 // Hs.396404 // SMARCA2 // 6595 // SWI/SNF related, matrix associat	SMARCA2	SMARCA2, rs9298820, SWI,p24.3
SNP_A-1995568	agtaatgtgaataagt[A/G]aagtgagctttcatga	A	G	NM_139045 // downstream // 18056 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 18004 // Hs.298990 // SMARC	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-1690175	aacacaggcttctgtggaaacgca[C/G]ggaagaagcatttac actcaatcat	C	G	NM_003070 // downstream // 18246 // Hs.396404 // SMARCA2 // 6595 // SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 /// NM_003383 // upstream // 410235 // Hs.370422 // VLDLR // 7436 // very low density li	SMARCA2	SMARCA2, rs10491699, SWI,p24.2
SNP_A-1796585	ggttactcaaggtcac[A/G]atgactgagcaaactc	A	G	NM_139045 // downstream // 20717 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 20665 // Hs.298990 // SMARC	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1995570	ttacttttgtaagtaa[C/T]tgcaaacigtcttcca	C	T	NM_139045 // downstream // 27224 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 27172 // Hs.298990 // SMARC	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2
SNP_A-2274022	gacttaataaagagccd[A/G]catgagtcgcctcagc	A	G	NM_139045 // downstream // 41129 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 41077 // Hs.298990 // SMARC	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2
SNP_A-2269613	gacaaatgactgttta[C/G]actctgcaaaccatic	C	G	NM_139045 // downstream // 54531 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 54479 // Hs.298990 // SMARC	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-1923796	ttagtagaattttaa[A/C]tggctttccatggat	A	C	NM_139045 // downstream // 77753 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 77701 // Hs.298990 // SMARC	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-1820780	gtttccattgctcaad[A/G]catttttgaaattcca	A	G	NM_139045 // downstream // 263307 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 263255 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-1888873	tgaggtcccaagtgaa[C/G]agagaggcctttggac	C	G	NM_139045 // downstream // 304413 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 304361 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2301918	gcgtaagtcagggaaa[C/G]atatacattaacaaat	C	G	NM_139045 // downstream // 304862 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 304810 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2199571	ccaaaaaggcctgtca[A/G]tcagctataaatgggt	A	G	NM_139045 // downstream // 333188 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 333136 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2
SNP_A-2288727	gattgtaacacaattc[A/G]caatcaagatttgtct	A	G	NM_139045 // downstream // 344243 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 344191 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI,p24.2
SNP_A-1791266	gggtaactgaaaccaa[A/G]gaaatgactccagtat	A	G	NM_139045 // downstream // 345923 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 345871 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI p24.2
SNP_A-2152024	atgttttttggtgaa[C/T]tactcctttatcatt	C	T	NM_139045 // downstream // 364758 // Hs.298990 // SMARCA2 // 6595 // Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transc /// NM_003070 // downstream // 364706 // Hs.298990 // SMA	SMARCA2	SMARCA2, Homo sapiens SWI p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1692446	cagtctctgttaaattatccgata[A/G]catactgaaatccttgtctg tgatc	A	G	BC004474 // intron // 0 // Hs.370422 // VLDLR // 7436 // very low density lipoprotein receptor	VLDLR	VLDLR , rs1576660, very low density lipoprotein receptor,p24.2
SNP_A-1856568	tcacaggccttgaact[C/T]actgccttgaccaat	C	T	NM_003383 // intron // 0 // Hs.370422 // VLDLR // 7436 // Homo sapiens very low density lipoprotein receptor (VLDLR), mRNA. /// ENST00000317755 // intron // 0 // — // — // — /// ENST00000341908 // intron // 0 // — // — // — /// E	VLDLR	VLDLR, Homo sapiens very low density lipoprotein receptor (VLDLR), p24.2
SNP_A-1800235	gtacctgaggacccgc[A/G]acctactcctgtaccc	A	G	NM_014878 // upstream // 89076 // Hs.493309 // KIAA0020 // 9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 291478 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-2099200	agaggataaagaaaaa[A/G]gacagtaaatcaaag	A	G	NM_014878 // upstream // 141285 // Hs.493309 // KIAA0020 // 9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 239269 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-2287141	gatgtcaaggctagca[G/T]atcaaaaaagcggaga	G	T	NM_014878 // upstream // 325725 // Hs.493309 // KIAA0020 // 9933 // Homo sapiens KIAA0020 (KIAA0020), mRNA. /// NM_134428 // downstream // 54829 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3	KIAA0020	KIAA0020, Homo sapiens KIAA0020 (KIAA0020), p24.2
SNP_A-1902619	tggcagggaatctcat[G/T]aacaccatgtggctaa	G	T	NM_134428 // intron // 0 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, mRNA. /// ENST00000265775 // intron // 0 // — // — // —	RFX3	RFX3, Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, p24.2
SNP_A-2096823	agactcaacttttcaa[C/G]agacctgtttatctt	C	G	NM_134428 // intron // 0 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, mRNA. /// NM_002919 // intron // 0 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory fact	RFX3	RFX3, Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, p24.2
SNP_A-1995610	aaacttgacttgtaaa[C/T]ctaaggaaggatcaag	C	T	NM_134428 // intron // 0 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, mRNA. /// NM_002919 // intron // 0 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory fact	RFX3	RFX3. Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, p24.2
SNP_A-1719291	ggagtaggagaaacaggctagtgct[A/C]aaagcaaagtgaaa ggctgacagag	A	C	NM_002919 // upstream // 123114 // Hs.408159 // RFX3 // 5991 // regulatory factor X, 3 (influences HLA class II expression) /// NM_014095 // downstream // 167612 // - // - // - // - /// NM_134428 // upstream // 123114 // Hs.408159 // RFX3 // 5991 // regu	RFX3	RFX3 , rs1537523, regulatory factor X, 3 (influences HLA class II expression) ,p24.2
SNP_A-1788198	gggagcggtttaacaa[A/T]gactgaataaggagag	A	T	NM_134428 // upstream // 240200 // Hs.136829 // RFX3 // 5991 // Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, mRNA. /// NM_002919 // upstream // 240200 // Hs.136829 // RFX3 // 5991 // Homo sapiens r	RFX3	RFX3, Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), transcript variant 2, p24.2
SNP_A-1922991	ttagcacaatgccagt[C/T]gagggtgtgtatatgg	C	T	NM_152629 // intron // 0 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000324333 // intron // 0 // — // — // — /// ENST00000359764 // intron // 0 // — // — // — // —	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2085280	actcatagttattcaa[C/T]cactgtcatgcctgca	C	T	NM_152629 // intron // 0 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000324333 // intron // 0 // — // — // — /// ENST00000359764 // intron // 0 // — // — // — // —	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2062701	aatgtctgccatacac[A/G]actaccaagcccttag	A	G	NM_152629 // intron // 0 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000324333 // intron // 0 // — // — // — /// ENST00000359764 // intron // 0 // — // — // — // —	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2234564	ctccactctttacttg[C/G]atatctggaaacaca	C	G	NM_152629 // intron // 0 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000359764 // intron // 0 // — // — // —	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1899311	tggaacagcatccaag[A/G]aatactacttgatggc	A	G	NM_152629 // intron // 0 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// ENST00000359764 // intron // 0 // — // — // —	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1913548	tgtgtaaaatgtacct[C/G]aataaatttgtgttt	C	G	NM_152629 // upstream // 32785 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 305472 // Hs.444915 // SLC1A1 // 6505 // Homo sapiens solute carrier family 1 (neuronal/epithelial high af	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1886713	tgactcttggatttta[C/T]agaaccacaagtcctg	C	T	NM_152629 // upstream // 64845 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 273412 // Hs.444915 // SLC1A1 // 6505 // Homo sapiens solute carrier family 1 (neuronal/epithelial high af	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1957530	ttttataggactcaac[A/G]ggctgcataaaagggc	A	G	NM_152629 // upstream // 67893 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 270364 // Hs.444915 // SLC1A1 // 6505 // Homo sapiens solute carrier family 1 (neuronal/epithelial high af	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2290274	gcaacaatatgtgtct[C/G]aaattaaccaggcatg	C	G	NM_152629 // upstream // 68649 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 269608 // Hs.444915 // SLC1A1 // 6505 // Homo sapiens solute carrier family 1 (neuronal/epithelial high af	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1945021	ttgtgtttatttactg[C/G]aactttgaagcattgg	C	G	NM_152629 // upstream // 134749 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 203508 // Hs.444915 // SLC1A1 // 6505 // Homo sapiens solute carrier family 1 (neuronal/epithelial high a	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-1827175	taaccggtaccagtca[A/T]ggaaagctgggctcta	A	T	NM_152629 // upstream // 295905 // Hs.162125 // GLIS3 // 169792 // Homo sapiens GLIS family zinc finger 3 (GLIS3), mRNA. /// NM_004170 // upstream // 42352 // Hs.444915 // SLC1A1 // 6505 // Homo sapiens solute carrier family 1 (neuronal/epithelial high af	GLIS3	GLIS3, Homo sapiens GLIS family zinc finger 3 (GLIS3), p24.2
SNP_A-2251401	cttcacaattaaacta[C/T]gtgcccacctttcac	C	T	NM_005772 // downstream // 27294 // Hs.194121 // RCL1 // 10171 // Homo sapiens RNA terminal phosphate cyclase-like 1 (RCL1), mRNA. /// ENST00000239262 // downstream // 27294 // — // — // — /// ENST00000259575 // downstream // 56315 // — ///	RCL1	RCL1, Homo sapiens RNA terminal phosphate cyclase-like 1 (RCL1), p24.1
SNP_A-1876138	tctgacattccgtag[C/T]cctagacagttattat	C	T	NM_007179 // upstream // 36200 // Hs.216373 // INSL6 // 11172 // Homo sapiens insulin-like 6 (INSL6), mRNA. /// NM_002195 // upstream // 9584 // Hs.418506 // INSL4 // 3641 // Homo sapiens insulin-like 4 (placenta) (INSL4), mRNA. /// ENST00000239315 // ups	INSL6	INSL6, Homo sapiens insulin-like 6 (INSL6), p24.1
SNP_A-1844505	tataaatagatgtcca[C/T]tgagatacacaaaaaa	C	T	NM_002195 // downstream // 11515 // Hs.418506 // INSL4 // 3641 // Homo sapiens insulin-like 4 (placenta) (INSL4), mRNA. /// NM_005059 // downstream // 54375 // Hs.127032 // RLN2 // 6019 // Homo sapiens relaxin 2 (H2) (RLN2), transcript variant 2, mRNA. //	INSL4	INSL4, Homo sapiens insulin-like 4 (placenta) (INSL4), p24.1
SNP_A-1699795	tatttttttttaaataagctgggaa[A/C]aggatcagctaactcaaggaattaa	A	C	NM_005059 // upstream // 14190 // Hs.127032 // RLN2 // 6019 // relaxin 2 (H2) /// NM_006911 // downstream // 16199 // Hs.368996 // RLN1 // 6013 // relaxin 1 (H1) /// NM_134441 // upstream // 14190 // Hs.127032 // RLN2 // 6019 // relaxin 2 (H2)	RLN2	RLN2, rs10491649, relaxin 2 (H2), p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137147	atcagggctgccttac[A/G]agatttcctgaaggaa	A	G	NM_005059 // upstream // 24335 // Hs.127032 // RLN2 // 6019 // Homo sapiens relaxin 2 (H2) (RLN2), transcript variant 2, mRNA. /// NM_134441 // upstream // 24335 // Hs.127032 // RLN2 // 6019 // Homo sapiens relaxin 2 (H2) (RLN2), transcript variant 1, mRN	RLN2	RLN2, Homo sapiens relaxin 2 (H2) (RLN2), transcript variant 2, p24.1
SNP_A-2302275	gctaacactccatcac[C/T]gaatccttgacacttg	C	T	NM_006911 // upstream // 13995 // Hs.368996 // RLN1 // 6013 // Homo sapiens relaxin 1 (H1) (RLN1), mRNA. /// NM_018465 // downstream // 4105 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000	RLN1	RLN1, Homo sapiens relaxin 1 (H1) (RLN1), p24.1
SNP_A-1788983	gggcacagaaggtaac[C/T]gcggattgagagcagg	C	T	NM_018465 // intron // 0 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000223864 // intron // 0 // --- // --- // ---	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1833409	tacagacatagacaagg[A/G]atgaaattatagatat	A	G	NM_018465 // intron // 0 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000223864 // intron // 0 // --- // --- // ---	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1995670	ttctgccaagtaggca[A/C]ccctgaaggagacttg	A	C	NM_018465 // intron // 0 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000223864 // intron // 0 // --- // --- // ---	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1860296	tcagtgaatcatttgc[A/G]aagcagagaagatgag	A	G	NM_018465 // intron // 0 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000223864 // intron // 0 // --- // --- // ---	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1889045	tgagtactgatggcaa[C/G]agctttgaagatgatt	C	G	NM_018465 // intron // 0 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// ENST00000223864 // intron // 0 // --- // --- // ---	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1703967	gccccagctaatctttacattgacca[A/T]aagtgctttgcctacata gcactgc	A	T	NM_018465 // intron // 0 // Hs.416649 // C9orf46 // 55848 // chromosome 9 open reading frame 46	C9orf46	C9orf46 , rs10491646, chromosome 9 open reading frame 46,p24.1
SNP_A-2137828	atcattattatggcac[A/G]cggcagtattaagaag	A	G	NM_018465 // upstream // 2068 // Hs.534185 // C9orf46 // 55848 // Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA. /// NM_014143 // upstream // 10613 // Hs.521989 // PDCD1LG1 // 29126 // Homo sapiens programmed cell death 1 ligand 1 (PDCD1	C9orf46	C9orf46, Homo sapiens chromosome 9 open reading frame 46 (C9orf46), p24.1
SNP_A-1792285	gggttctgggactata[A/C]aaatgaatlaaaatacc	A	C	NM_025239 // downstream // 10742 // Hs.532279 // PDCD1LG2 // 80380 // Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), mRNA. /// ENST00000355984 // downstream // 10742 // --- // --- // --- /// ENST00000355062 // downstream // 10742 // ---	PDCD1LG2	PDCD1LG2, Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), p24.1
SNP_A-1835480	tacctgcatttccta[G/T]taacgacagggctttc	G	T	NM_025239 // downstream // 21747 // Hs.532279 // PDCD1LG2 // 80380 // Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), mRNA. /// ENST00000355984 // downstream // 21747 // --- // --- // --- /// ENST00000355062 // downstream // 21747 // ---	PDCD1LG2	PDCD1LG2, Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), p24.1
SNP_A-2244796	ctggatgagacagtca[C/T]gtgtattagaggtatg	C	T	NM_025239 // downstream // 25713 // Hs.532279 // PDCD1LG2 // 80380 // Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), mRNA. /// ENST00000355984 // downstream // 25713 // --- // --- // --- /// ENST00000355062 // downstream // 25713 // ---	PDCD1LG2	PDCD1LG2, Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227991	ctaccttgttcttctc[C/T]aaaagagtctttgtta	C	T	NM_025239 // downstream // 36832 // Hs.532279 // PDCD1LG2 // 80380 // Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), mRNA. /// ENST00000355984 // downstream // 36832 // --- // --- // --- // --- /// ENST00000355062 // downstream // 36832 // ---	PDCD1LG2	PDCD1LG2, Homo sapiens programmed cell death 1 ligand 2 (PDCD1LG2), p24.1
SNP_A-2274800	gagaaataatgctcac[C/T]gctgtctttaccattt	C	T	ENST00000251879 // intron // 0 // --- // --- // --- // ---	-	p24.1
SNP_A-1652636	gcctagactgaatagaagagtgtta[C/T]gatgatgagaaagca aaatctttat	C	T	NM_005511 // upstream // 36586 // Hs.154069 // MLANA // 2315 // melan-A	MLANA	MLANA , rs9299022, melan-A,p24.1
SNP_A-2087337	actgcagacaagttca[C/T]gggaaaggaaagttac	C	T	NM_005511 // upstream // 22620 // Hs.154069 // MLANA // 2315 // Homo sapiens melan-A (MLANA), mRNA. /// ENST00000251879 // downstream // 98837 // --- // --- // --- // --- /// ENST00000276898 // downstream // 91735 // --- // --- // --- // --- /// ENST00000	MLANA	MLANA, Homo sapiens melan-A (MLANA), p24.1
SNP_A-2261447	gaaaggaaagatgacc[A/C]agagttgatgggggaa	A	C	NM_005511 // upstream // 15615 // Hs.154069 // MLANA // 2315 // Homo sapiens melan-A (MLANA), mRNA. /// ENST00000251879 // downstream // 105842 // --- // --- // --- // --- /// ENST00000276898 // downstream // 98740 // --- // --- // --- // --- /// ENST0000	MLANA	MLANA, Homo sapiens melan-A (MLANA), p24.1
SNP_A-2119620	agtatggtcttttatc[C/T]cttaacaactttctgt	C	T	NM_012416 // downstream // 30389 // Hs.167496 // RANBP6 // 26953 // Homo sapiens RAN binding protein 6 (RANBP6), mRNA. /// ENST00000329294 // upstream // 27805 // --- // --- // --- // --- /// ENST00000259569 // downstream // 30389 // --- // --- // --- // --- //	RANBP6	RANBP6, Homo sapiens RAN binding protein 6 (RANBP6), p24.1
SNP_A-1868918	tcctgagatggtctag[C/G]atagaaggcctcttgg	C	G	NM_033439 // downstream // 52932 // Hs.348390 // C9orf26 // 90865 // Homo sapiens chromosome 9 open reading frame 26 (NF-HEV) (C9orf26), mRNA. /// NM_001001875 // upstream // 17467 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD-SP25	C9orf26	C9orf26, Homo sapiens chromosome 9 open reading frame 26 (NF-HEV) (C9orf26), p24.1
SNP_A-1757333	caagcattactgctatcagtcttca[G/T]atttcagtggttaagttgat cttca	G	T	NM_033439 // downstream // 66394 // Hs.348390 // C9orf26 // 90865 // chromosome 9 open reading frame 26 (NF-HEV) /// NM_033516 // upstream // 3999 // Hs.343593 // NYD-SP25 // 89882 // protein kinase NYD-SP25	C9orf26	C9orf26 , rs4742179, chromosome 9 open reading frame 26 (NF-HEV) ,p24.1
SNP_A-1682474	gacaacatgcagaggaactgagtca[A/C]aaaggaatgtataa gaatggcatat	A	C	BC033792 // 3UTR // 0 // Hs.351815 // NYD-SP25 // 89882 // protein kinase NYD-SP25	NYD-SP25	NYD-SP25 , rs10491836, protein kinase NYD-SP25,p24.1
SNP_A-2247257	ctgtcattttgctgca[A/T]gtttttatatgccat	A	T	NM_001001875 // downstream // 4846 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, mRNA. /// NM_033516 // downstream // 4846 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD-S	NYD-SP25	NYD-SP25, Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, p24.1
SNP_A-1786198	ggctggtaaatagtta[C/T]gctgggtcttaagctt	C	T	NM_001001875 // downstream // 20197 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, mRNA. /// NM_033516 // downstream // 20197 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD	NYD-SP25	NYD-SP25, Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, p24.1
SNP_A-1736999	gattatgttcaatgagatatatata[A/C]gatagcatcaataaacatt agttct	A	C	NM_014126 // downstream // 101935 // - // - // - // - /// NM_033516 // downstream // 35017 // Hs.343593 // NYD-SP25 // 89882 // protein kinase NYD-SP25 /// NM_152306 // upstream // 47468 // Hs.394916 // UHRF2 // 115426 // ubiquitin-like, containing PHD a	-	- , rs719725, - ,p24.1
SNP_A-2047067	aagagttgttatcaga[G/T]gatctcttagtgaagt	G	T	NM_001001875 // downstream // 34823 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, mRNA. /// NM_033516 // downstream // 34823 // Hs.351815 // NYD-SP25 // 89882 // Homo sapiens protein kinase NYD	NYD-SP25	NYD-SP25, Homo sapiens protein kinase NYD-SP25 (NYD-SP25), transcript variant 3, p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027983	aaacctttgcctccta[C/T]aaaagtagacagctgt	C	T	NM_152306 // downstream // 37719 // Hs.493401 // UHRF2 // 115426 // Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 2 (UHRF2), transcript variant 1, mRNA. /// NM_152306 // downstream // 37715 // Hs.493401 // UHRF2 // 115426 // Homo sa	UHRF2	UHRF2, Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 2 (UHRF2), transcript variant 1, p24.1
SNP_A-2222844	cgcaaaaaccatatac[A/G]ataccggctatattga	A	G	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2234928	ctccattaatcgttag[C/G]acatctacccagttat	C	G	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-1928654	ttcactttcgcaacct[C/G]accatcaactttgtag	C	G	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2125288	agttgtgaactgtagt[C/G]aattcatgagtgattg	C	G	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2224517	cgtatgactgtagata[C/T]gtggggtaatttctgg	C	T	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2145646	atgcatggtttatatg[C/T]agatactaagctgttt	C	T	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2229255	ctaggaagagtgaata[C/T]cttcttgtgatggtgg	C	T	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2067495	acaaatgcatccgtcc[C/T]cacagtggtgtagcac	C	T	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-1995698	gtgactttgaacaaac[G/T]acccttacctcactt	G	T	NM_015061 // intron // 0 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // intron // 0 // — // — // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2265541	gaagcctagaaccatc[C/T]gaggcagccgtcttgt	C	T	NM_015061 // downstream // 87391 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // downstream // 87391 // — // — // — // — /// ENST00000327698 // downstream // 214038 // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-2182338	cagagtggtgtctaca[A/C]agcaatgaaatgtggt	A	C	NM_015061 // downstream // 292517 // Hs.157106 // JMJD2C // 23081 // Homo sapiens jumonji domain containing 2C (JMJD2C), mRNA. /// ENST00000346931 // downstream // 292517 // — // — // — // — /// ENST00000327698 // downstream // 8912 // — // —	JMJD2C	JMJD2C, Homo sapiens jumonji domain containing 2C (JMJD2C), p24.1
SNP_A-1726602	aggttcaataggcaaacagtataaa[G/T]tggccaaccagtaaacctgtgtata	G	T	AF116709 // upstream // 646372 // - // - // - // Homo sapiens PRO2605 mRNA, complete cds. /// NM_015061 // downstream // 298338 // Hs.209292 // JMJD2C // 23081 // jumonji domain containing 2C	-	- , rs10511469, Homo sapiens PRO2605 mRNA, complete cds. ,p24.1
SNP_A-1995746	gtttaagaaaggcctc[C/T]gacttattcaagtctg	C	T	ENST00000327698 // upstream // 248814 // — // — // — // — /// ENST00000259567 // downstream // 69443 // — // — // — // — /// ENST00000360460 // downstream // 71285 // — // — // — // — /// ENST00000358227 // downstream // 71285 // -	-	p24.1
SNP_A-1927036	ttatttggccagtgcc[A/G]agaggaattgcaatca	A	G	NM_002839 // downstream // 482409 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 482409 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1995759	gcaacaaccaaatcaa[C/G]acaaatggaaaatata	C	G	NM_002839 // downstream // 149945 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 149945 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1923722	ttagtaaaaggtagaa[A/G]tctgtttacatttgtt	A	G	NM_002839 // downstream // 81370 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // downstream // 81370 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein t	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1848550	tatgacatgctaagga[C/T]gcattgcttttctcca	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2043296	aactggaaaatacaga[A/C]gtgtttttgcatcccc	A	C	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1723258	ttaaaacttttatctctggctctct[C/T]aattttgaattaaaccagtcc catc	C	T	NM_002839 // intron // 0 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // intron // 0 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130392 // intron // 0 // Hs.32307	PTPRD	PTPRD , rs1407972, protein tyrosine phosphatase, receptor type, D ,p24.1
SNP_A-1995773	agccatatattgccgc[C/T]cactttgatgtccttc	C	T	NM_002839 // CDS // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // CDS // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, r	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1818506	gttctttcagctcata[G/T]gatttggttgatatga	G	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2174407	cacagaagaaagtaga[C/T]tccatcagcaaaattg	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2091185	actttgtgactcttaa[C/T]attacggagtgccagg	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1816633	gttataattggtatcg[C/T]atctctaaccaagcgt	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2014038	aaatcaacatagtcta[A/G]taatagatgatttaac	A	G	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1725080	aaaaatccgcctatctaggcttatg[A/C]atgttatataataccaca gatatga	A	C	NM_002839 // intron // 0 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // intron // 0 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130392 // intron // 0 // Hs.32307	PTPRD	PTPRD , rs10511499, protein tyrosine phosphatase, receptor type, D p24.1
SNP_A-2049446	aagctgctaacctat[A/G]aaacaaatgctacatg	A	G	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1836004	tactaatataacaaca[C/T]ggacgctgcggcgtct	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1874035	tctcatgaaaatttaa[C/T]gaagaaagtgcattca	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2292537	gcactctcttaacata[C/T]aggtagagcatttgt	C	T	NM_002839 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // intron // 0 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphat	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2306694	gctgtcagtgagttaa[A/G]gtggctgaaacagatc	A	G	NM_002839 // upstream // 207747 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 207747 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2222535	cgagggtttgttgga[C/G]tactggctcttcttg	C	G	NM_002839 // upstream // 212430 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 212430 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2136220	atcaatgtttagaga[C/T]gttaatagactagta	C	T	NM_002839 // upstream // 238976 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 238976 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1955903	tttgtcagattcattg[A/G]aagtatgttcccat	A	G	NM_002839 // upstream // 240031 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 240031 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2287658	gattaataaacgtaag[C/T]agtatacatggtcaat	C	T	NM_002839 // upstream // 240691 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 240691 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2049572	aagcttaacacaaaat[G/T]ataaagcatcatactg	G	T	NM_002839 // upstream // 250520 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 250520 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2099708	agaggttaactgcca[A/G]ctgactgaatctattt	A	G	NM_002839 // upstream // 250698 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 250698 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-1691278	ctgtagccatctttggtagttagtc[A/G]agagaattccaacggctc aggaaga	A	G	NM_002839 // intron // 0 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // intron // 0 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130392 // intron // 0 // Hs.32307	PTPRD	PTPRD, rs9299084, protein tyrosine phosphatase, receptor type, D, p24.1
SNP_A-1835674	tacctttctccacaat[A/C]aacagaaatttgagag	A	C	NM_002839 // upstream // 267126 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, mRNA. /// NM_130391 // upstream // 267126 // Hs.446083 // PTPRD // 5789 // Homo sapiens protein tyr	PTPRD	PTPRD, Homo sapiens protein tyrosine phosphatase, receptor type, D (PTPRD), transcript variant 1, p24.1
SNP_A-2092632	agaaatcacagtaccaa[C/T]gaagtcaaataagat	C	T	NM_000550 // upstream // 3511219 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 90905 // --- // --- // --- /// ENST00000224014 // upstream // 3511219 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1654865	aatcagagttgcaggtgaatggtca[C/T]gctttaaatggaaaact gagccagg	C	T	NM_000550 // upstream // 3234440 // Hs.75219 // TYRP1 // 7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 440272 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // upstream // 440272 // Hs.32	TYRP1	TYRP1, rs1333107, tyrosinase-related protein 1 ,p23
SNP_A-1758753	tttatttagatttgtatagttactat[C/T]cattgcatttttaagctgtttaatt a	C	T	NM_000550 // upstream // 3229039 // Hs.75219 // TYRP1 // 7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 445673 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // upstream // 445673 // Hs.32	TYRP1	TYRP1, rs10491614, tyrosinase-related protein 1 ,p23
SNP_A-1995812	agctgtagaaatgtac[C/G]aggtaatcatcaatat	C	G	NM_000550 // upstream // 3228245 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 373879 // --- // --- // --- /// ENST00000224014 // upstream // 3228245 // --- // --- //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2117743	aggttcttctgatgca[C/G]atggactaagatcaca	C	G	NM_000550 // upstream // 3217590 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 384534 // --- // --- // --- /// ENST00000224014 // upstream // 3217590 // --- // --- //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1881179	tctttagcccaacttta[C/T]atttgtaaactacagt	C	T	NM_000550 // upstream // 3167297 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 434827 // --- // --- // --- /// ENST00000224014 // upstream // 3167297 // --- // --- //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1739935	tttataaaatgttatcctcctcat[C/G]atctaatttgttcctgccgct gaa	C	G	NM_000550 // upstream // 2903143 // Hs.75219 // TYRP1 // 7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 771569 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // upstream // 771569 // Hs.32	TYRP1	TYRP1, rs2147070, tyrosinase-related protein 1 ,p23
SNP_A-1819254	gttggaaaaatagaca[G/T]atagttggaagctt	G	T	NM_000550 // upstream // 2832429 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 769695 // --- // --- // --- /// ENST00000224014 // upstream // 2832429 // --- // --- //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1707996	cagaagaaaccaacttcaccatttg[A/G]atcatgatattgacca agcgttggc	A	G	NM_000550 // upstream // 2811046 // Hs.75219 // TYRP1 // 7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 863666 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // upstream // 863666 // Hs.32	TYRP1	TYRP1, rs10514817, tyrosinase-related protein 1 ,p23
SNP_A-2025200	aaaatatggcactctata[C/T]aaatgctaggtctaag	C	T	NM_000550 // upstream // 2784614 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 817510 // — // — // — /// ENST00000224014 // upstream // 2784614 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2262399	gaaatgccagaggccaa[A/G]gagaaaaatgtataca	A	G	NM_000550 // upstream // 2723539 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 878585 // — // — // — /// ENST00000224014 // upstream // 2723539 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1852575	tatttataacaactca[A/T]gtggtcctcacaacag	A	T	NM_000550 // upstream // 2689671 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 912453 // — // — // — /// ENST00000224014 // upstream // 2689671 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2269342	gaatttggccagagta[A/C]aatctgaattccagat	A	C	NM_000550 // upstream // 2603687 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 998437 // — // — // — /// ENST00000224014 // upstream // 2603687 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2038753	aacagatctatttgtg[G/T]atgtttaaaggagga	G	T	NM_000550 // upstream // 2568564 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1033560 // — // — // — /// ENST00000224014 // upstream // 2568564 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1935389	ttctggagactagtgc[A/G]ctctttgacgttctt	A	G	NM_000550 // upstream // 2568515 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1033609 // — // — // — /// ENST00000224014 // upstream // 2568515 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2198202	cattgtcacaggtaa[C/T]ctgtagatatttcg	C	T	NM_000550 // upstream // 2548336 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1053788 // — // — // — /// ENST00000224014 // upstream // 2548336 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1939343	ttgatgaagccacata[A/T]aatttcaggcagatta	A	T	NM_000550 // upstream // 2548201 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1053923 // — // — // — /// ENST00000224014 // upstream // 2548201 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2282491	gagttgctgatttag[C/G]aataacaccaagctaa	C	G	NM_000550 // upstream // 2267249 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1334875 // — // — // — /// ENST00000224014 // upstream // 2267249 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2047580	aagatggtgaacataa[A/G]atcattgaatcaagg	A	G	NM_000550 // upstream // 2187407 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1414717 // — // — // — /// ENST00000224014 // upstream // 2187407 // — // —	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1726034	ttttacaggtaatacattatttgaa[C/T]tgatattgaataaaagtatgatgtg	C	T	NM_000550 // upstream // 1801396 // Hs.75219 // TYRP1 // 7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 1873316 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // upstream // 1873316 // Hs.	TYRP1	TYRP1 , rs951099, tyrosinase-related protein 1 p23
SNP_A-2228957	ctagatttacaaaaca[A/G]tgacaacaaatataac	A	G	NM_000550 // upstream // 1653796 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 1948328 // — // — // — /// ENST00000224014 // upstream // 1653796 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2068277	acaagcacctctatgg[C/T]caccactactatgact	C	T	NM_000550 // upstream // 1584764 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2017360 // — // — // — /// ENST00000224014 // upstream // 1584764 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1885394	tgacaaacagacctac[C/G]aaaatgtgctcgacat	C	G	NM_000550 // upstream // 1580561 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2021563 // — // — // — /// ENST00000224014 // upstream // 1580561 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2239997	ctgaagagatatttgc[A/G]ctctgtatttgttgc	A	G	NM_000550 // upstream // 1580259 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2021865 // — // — // — /// ENST00000224014 // upstream // 1580259 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2310257	ggaaccaccaagtgca[C/G]gtacccaagaaaggct	C	G	NM_000550 // upstream // 1249962 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2352162 // — // — // — /// ENST00000224014 // upstream // 1249962 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2251316	cttcaagactgtaaagt[A/G]agtcaaccatttgtcc	A	G	NM_000550 // upstream // 1165955 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2436169 // — // — // — /// ENST00000224014 // upstream // 1165955 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1749177	tccttgagttgaacagcatctctcc[A/G]attacaccttgcaatatctacttgt	A	G	NM_000550 // upstream // 1086314 // Hs.75219 // TYRP1 // 7306 // tyrosinase-related protein 1 /// NM_002839 // upstream // 2588398 // Hs.323079 // PTPRD // 5789 // protein tyrosine phosphatase, receptor type, D /// NM_130391 // upstream // 2588398 // Hs.	TYRP1	TYRP1 , rs10511568, tyrosinase-related protein 1 p23
SNP_A-1841896	taggctggatatgaaa[G/T]atggaagctccagatt	G	T	NM_000550 // upstream // 1017253 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2584871 // — // — // — /// ENST00000224014 // upstream // 1017253 // — // — //	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2124924	agttgagagtcttgaa[G/T]gactgacccataagtg	G	T	NM_000550 // upstream // 937201 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2664923 // — // — // — /// ENST00000224014 // upstream // 937201 // — // — // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1914348	tgtgttctttcgataa[A/T]tatctattcagatctc	A	T	NM_000550 // upstream // 701703 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2900421 // — // — // — /// ENST00000224014 // upstream // 701703 // — // — // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2076835	accaaacaagacaaac[A/G]accgacttcactggag	A	G	NM_000550 // upstream // 696604 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2905520 // --- // --- // --- // --- /// ENST00000224014 // upstream // 696604 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2078933	acccaatgttaatgaa[A/T]tatgaaggttctactt	A	T	NM_000550 // upstream // 664912 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 2937212 // --- // --- // --- // --- /// ENST00000224014 // upstream // 664912 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1928650	ttcactttaggctatc[A/G]aattcattacacaaaa	A	G	NM_000550 // upstream // 336390 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3265734 // --- // --- // --- // --- /// ENST00000224014 // upstream // 336390 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1995915	agtgctataataagca[A/C]aagaatgcaggtgtct	A	C	NM_000550 // upstream // 334785 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3267339 // --- // --- // --- // --- /// ENST00000224014 // upstream // 334785 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2150301	atgtctgcatctttgc[G/T]cacaaaaaatatacat	G	T	NM_000550 // upstream // 232163 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3369961 // --- // --- // --- // --- /// ENST00000224014 // upstream // 232163 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1949290	tttatgtttctaaagc[C/T]ccaagttgaaggacaa	C	T	NM_000550 // upstream // 189593 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3412531 // --- // --- // --- // --- /// ENST00000224014 // upstream // 189593 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1805998	gtcctacagactgcta[C/T]gctttatatttttatt	C	T	NM_000550 // upstream // 175839 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3426285 // --- // --- // --- // --- /// ENST00000224014 // upstream // 175839 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2134454	atatgggcagctctaa[C/G]aaggaagggaaaattg	C	G	NM_000550 // upstream // 151248 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// ENST00000360531 // downstream // 3450876 // --- // --- // --- // --- /// ENST00000224014 // upstream // 151248 // --- // --- // -	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-2255736	cttgttgccattggca[C/T]caaggaaccagtttta	C	T	NM_000550 // downstream // 28883 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// NM_203403 // upstream // 35880 // Hs.445356 // C9orf150 // 286343 // Homo sapiens chromosome 9 open reading frame 150 (C9orf150)	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1820706	gtttcatcatgaggaa[A/C]ggaaaagggagctgac	A	C	NM_000550 // downstream // 46668 // Hs.270279 // TYRP1 // 7306 // Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /// NM_203403 // upstream // 18095 // Hs.445356 // C9orf150 // 286343 // Homo sapiens chromosome 9 open reading frame 150 (C9orf150)	TYRP1	TYRP1, Homo sapiens tyrosinase-related protein 1 (TYRP1), p23
SNP_A-1802105	gtatactcaatgcttg[C/T]aacttgttttaaactc	C	T	NM_203403 // downstream // 149324 // Hs.445356 // C9orf150 // 286343 // Homo sapiens chromosome 9 open reading frame 150 (C9orf150), mRNA. /// NM_003829 // downstream // 134208 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ	C9orf150	C9orf150, Homo sapiens chromosome 9 open reading frame 150 (C9orf150), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1792758	ggtaagcctggtagccd[A/G]agacaaccatgctgac	A	G	NM_203403 // downstream // 270287 // Hs.445356 // C9orf150 // 286343 // Homo sapiens chromosome 9 open reading frame 150 (C9orf150), mRNA. /// NM_003829 // downstream // 13245 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ)	C9orf150	C9orf150, Homo sapiens chromosome 9 open reading frame 150 (C9orf150), p23
SNP_A-2303839	gctcagtgatgctctat[C/T]aatttagcttcctgca	C	T	NM_003829 // intron // 0 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319198 // intron // 0 // — // — // — // /// ENST00000319217 // intron // 0 // — // — // — // /// ENST00000319217 // intron // 0 // — // —	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2083235	actaaacacagccata[A/C]aataaatagcacttt	A	C	NM_003829 // intron // 0 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319217 // intron // 0 // — // — // — // —	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1869436	tcctgtgacatttcaa[A/G]aagtatttgctatggc	A	G	NM_003829 // intron // 0 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319217 // intron // 0 // — // — // — // —	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2119858	agtcaacaagatttta[A/C]gtactgcaaaaacaaa	A	C	NM_003829 // intron // 0 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319217 // intron // 0 // — // — // — // —	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1995955	gatctgaagaggtgaa[A/C]aggtgtaggtaggagt	A	C	NM_003829 // intron // 0 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// ENST00000319217 // intron // 0 // — // — // — // —	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1708871	caaaaatgggacagttgaccagca[C/T]ataacctatttctcca ccagaaaa	C	T	NM_003829 // upstream // 431291 // Hs.169378 // MPDZ // 8777 // multiple PDZ domain protein /// NM_005596 // downstream // 405725 // Hs.302690 // NFIB // 4781 // nuclear factor I/B	MPDZ	MPDZ , rs8192981, multiple PDZ domain protein p23
SNP_A-2186629	cagggattgtctgagat[C/T]gccttgaaatgctagc	C	T	NM_003829 // upstream // 455616 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 381634 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1846408	tatatgtctgagttgt[C/G]acaaaggaggaggtt	C	G	NM_003829 // upstream // 493345 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 343905 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1943428	ttggtttattgtgaaaa[C/G]agtctcctaagattgc	C	G	NM_003829 // upstream // 507307 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 329943 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2239291	ctctttaacacacaac[A/G]cttaaatagaagtgag	A	G	NM_003829 // upstream // 521233 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 316017 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2309505	ggaaacatctgagggt[C/G]aaagacaggtagcaac	C	G	NM_003829 // upstream // 521299 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 315951 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2037296	aacaaaggagaacact[C/T]aactcgtctgcataaa	C	T	NM_003829 // upstream // 704377 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 132873 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1793987	ggtcaccaaaggaaac[A/G]cagattgtgggtagct	A	G	NM_003829 // upstream // 711105 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 126145 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2121100	agtctctgtccactca[A/G]tgagaaaattcaagcc	A	G	NM_003829 // upstream // 719958 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 117292 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // dow	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1829229	taagtaatttctgaac[A/G]cagtgatacatcctgg	A	G	NM_003829 // upstream // 758295 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 78955 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // down	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2265375	gaagcagtttcaacta[C/T]catttcatatctcactc	C	T	NM_003829 // upstream // 761825 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 75425 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // down	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-1719691	gcactgtcacctaactcccatttga[A/C]gtatttcatgttcatccaaa caggtc	A	C	NM_003829 // upstream // 767186 // Hs.169378 // MPDZ // 8777 // multiple PDZ domain protein /// NM_005596 // downstream // 69830 // Hs.302690 // NFIB // 4781 // nuclear factor I/B	MPDZ	MPDZ , rs1322132, multiple PDZ domain protein ,p23
SNP_A-2172702	caattgtgtttctaacc[C/T]cctacagcaaacaaaa	C	T	NM_003829 // upstream // 828710 // Hs.169378 // MPDZ // 8777 // Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /// NM_005596 // downstream // 8540 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_005596 // downs	MPDZ	MPDZ, Homo sapiens multiple PDZ domain protein (MPDZ), p23
SNP_A-2224495	cgtatatttgctttta[C/T]acctgaggaatgcgca	C	T	NM_005596 // intron // 0 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// ENST00000339974 // intron // 0 // — // — // — /// ENST00000276902 // intron // 0 // — // — // — // —	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2305710	gctgccatgtttcac[A/G]aaataataaccttca	A	G	NM_005596 // intron // 0 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// ENST00000339974 // intron // 0 // — // — // — /// ENST00000276902 // intron // 0 // — // — // — // —	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2183600	cagcagtaaaagtaac[A/G]catccaaagaagcact	A	G	NM_005596 // intron // 0 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// ENST00000339974 // intron // 0 // — // — // — /// ENST00000276902 // intron // 0 // — // — // — // —	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2250467	cttaggaglagaacaa[A/C]tggagtttgaacctct	A	C	NM_005596 // upstream // 24425 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 278566 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-1863010	tcattgtctatcaaca[C/T]tggtttctgaattgtg	C	T	NM_005596 // upstream // 78253 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 224738 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2205238	ccagtatcatttctg[C/T]agctgaatctaaggtg	C	T	NM_005596 // upstream // 82788 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 220203 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1725108	cagatgttaggcctctggttattggt[C/T]cactttttactgtagaacac tgatc	C	T	NM_005596 // upstream // 108557 // Hs.302690 // NFIB // 4781 // nuclear factor I/B /// NM_178566 // downstream // 194752 // Hs.21388 // ZDHHC21 // 340481 // zinc finger, DHHC domain containing 21	NFIB	NFIB , rs7846762, nuclear factor I,p22.3
SNP_A-2054541	aagtttacagcaaag[A/T]aatctaaaatcaattt	A	T	NM_005596 // upstream // 120693 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 182298 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. //	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2206932	ccatgtaccaactgaa[A/C]cacaggagaaataata	A	C	NM_005596 // upstream // 121290 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 181701 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. //	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-1995996	gtccaacacaagtaag[A/T]cctcaagaaacgcttg	A	T	NM_005596 // upstream // 195060 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 107931 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. //	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2153964	attatagtgaaacttc[A/G]cagacgtagatcaagt	A	G	NM_005596 // upstream // 203510 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 99481 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I,p22.3
SNP_A-2073276	acagggctcctagact[C/T]agtacaggattagact	C	T	NM_005596 // upstream // 221912 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 81079 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-1842580	taggttgaaggagaaat[A/T]catatccgagagaagg	A	T	NM_005596 // upstream // 259007 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 43984 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2123336	agtgtattgtcacag[G/T]aggattggtgccttgt	G	T	NM_005596 // upstream // 271007 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 31984 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2203120	ccactgctttcctac[A/C]ggaccagtgaatactc	A	C	NM_005596 // upstream // 282483 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 20508 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. ///	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-1903385	tgggaacgtacataaa[C/T]gaagcaaagcagtcat	C	T	NM_005596 // upstream // 302326 // Hs.370359 // NFIB // 4781 // Homo sapiens nuclear factor I/B (NFIB), mRNA. /// NM_178566 // downstream // 665 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. /// E	NFIB	NFIB, Homo sapiens nuclear factor I p22.3
SNP_A-2221286	cctttatgtaaggta[C/G]gtagtggtgtttac	C	G	NM_178566 // 3UTR // 0 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. /// ENST00000324876 // 3UTR // 0 // — // — // — // —	ZDHHC21	ZDHHC21, Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1916603	tgtttataaccattaa[C/G]cacactctctcgtcc	C	G	NM_178566 // intron // 0 // Hs.21388 // ZDHHC21 // 340481 // Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), mRNA. /// ENST00000324876 // intron // 0 // — // — // —	ZDHHC21	ZDHHC21, Homo sapiens zinc finger, DHHC domain containing 21 (ZDHHC21), p22.3
SNP_A-1737441	taattcaaaacacatagctttaatg[A/T]caccgtctcagagaccacttaatct	A	T	NM_005454 // downstream // 3239 // Hs.248204 // CER1 // 9350 // cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis) /// NM_178566 // upstream // 23380 // Hs.21388 // ZDHHC21 // 340481 // zinc finger, DHHC domain containing 21	CER1	CER1, rs2131882, cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis), p22.3
SNP_A-1996006	ttctctctgatgagca[C/G]cacttagaccttcaaa	C	G	NM_005454 // upstream // 8779 // Hs.248204 // CER1 // 9350 // Homo sapiens cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis) (CER1), mRNA. /// ENST00000276911 // upstream // 8779 // — // — // — // — /// ENST00000324457 // downstream /	CER1	CER1, Homo sapiens cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis) (CER1), p22.3
SNP_A-1941721	ttggaatattcaatcat[G/T]ctatggttgcttatga	G	T	ENST00000324457 // upstream // 15241 // — // — // — // — /// ENST00000355708 // upstream // 207759 // — // — // — // —	-	p22.3
SNP_A-2145667	atgcattcttatcata[A/G]acttgtgccaaagcat	A	G	NM_152574 // downstream // 104673 // Hs.130086 // C9orf52 // 158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// ENST00000355708 // downstream // 47274 // — // — // — // — /// ENST00000297615 // downstream // 104673 // -	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-1898101	tgctgtggttaattat[G/T]agagtggagccaggtg	G	T	NM_152574 // downstream // 30833 // Hs.130086 // C9orf52 // 158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// ENST00000355708 // downstream // 121114 // — // — // — // — /// ENST00000297615 // downstream // 30833 // -	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-1996017	atacatgcgtgactac[C/T]gagggccaggtgggag	C	T	NM_152574 // intron // 0 // Hs.130086 // C9orf52 // 158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// ENST00000355694 // intron // 0 // — // — // — // —	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-1841139	tagcttgtaatagaaaa[C/T]cagtctcttggtaaga	C	T	NM_152574 // upstream // 85819 // Hs.130086 // C9orf52 // 158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// NM_003084 // upstream // 29669 // Hs.546299 // SNAPC3 // 6619 // Homo sapiens small nuclear RNA activating complex, po	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-1901788	tggcactagtaatagc[A/C]gcaaagaagtggaaag	A	C	NM_152574 // upstream // 109415 // Hs.130086 // C9orf52 // 158219 // Homo sapiens chromosome 9 open reading frame 52 (C9orf52), mRNA. /// NM_003084 // upstream // 6073 // Hs.546299 // SNAPC3 // 6619 // Homo sapiens small nuclear RNA activating complex, po	C9orf52	C9orf52, Homo sapiens chromosome 9 open reading frame 52 (C9orf52), p22.3
SNP_A-2303420	gctatttccttccata[C/G]aggtgtaacatttggg	C	G	NM_033222 // intron // 0 // Hs.493516 // PSIP1 // 11168 // Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA. /// NM_021144 // intron // 0 // Hs.493516 // PSIP1 // 11168 // Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA. /// E	PSIP1	PSIP1, Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), p22.3
SNP_A-1927869	ttcaagtgaggatgta[A/G]gactttcaaattgggt	A	G	NM_033222 // intron // 0 // Hs.493516 // PSIP1 // 11168 // Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA. /// NM_021144 // intron // 0 // Hs.493516 // PSIP1 // 11168 // Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA. /// E	PSIP1	PSIP1, Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), p22.3
SNP_A-1654151	gaaatagatgattctgatgattcag[A/C]ctattttatgttctgttag	A	C	NM_003084 // downstream // 62597 // Hs.380092 // SNAPC3 // 6619 // small nuclear RNA activating complex, polypeptide 3, 50kDa /// NM_021144 // upstream // 14804 // Hs.351305 // PSIP1 // 11168 // PC4 and SFRS1 interacting protein 1 /// NM_033222 // upstre	SNAPC3	SNAPC3, rs1828383, small nuclear RNA activating complex, polypeptide 3, 50kDa ,p22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189748	cataaaaatatgtaaa[A/G]tatcctcaaagtccaa	A	G	NM_173550 // upstream // 10023 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000318382 // upstream // 15215 // --- // --- // --- // --- /// ENST00000359391 // upstream // 9821 // --- // ---	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2151355	atgttattgagcttta[A/G]gagtgttgtatattt	A	G	NM_173550 // intron // 0 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000359391 // intron // 0 // --- // --- // --- // --- /// ENST00000297641 // intron // 0 // --- // --- // --- // --- ///	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1851511	tattcgttcatttaaa[G/T]ccctgcaaaattggca	G	T	NM_173550 // intron // 0 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000359391 // intron // 0 // --- // --- // --- // --- /// ENST00000297641 // intron // 0 // --- // --- // --- // --- ///	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1842650	tagtttttttcttca[C/T]gatcggaatgttttta	C	T	NM_173550 // intron // 0 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000297641 // intron // 0 // --- // --- // --- // --- /// ENST00000285482 // intron // 0 // --- // --- // --- // ---	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2014078	catccctttactaaga[A/T]tagggacagttccagg	A	T	NM_173550 // intron // 0 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000297641 // intron // 0 // --- // --- // --- // --- /// ENST00000285482 // intron // 0 // --- // --- // --- // ---	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1692340	agctggctacttctacttcaggcat[C/T]aggattgtgttttgcaag aaggaa	C	T	NM_173550 // intron // 0 // Hs.170652 // C9orf93 // 203238 // chromosome 9 open reading frame 93	C9orf93	C9orf93, rs14179874, chromosome 9 open reading frame 93,p22.3
SNP_A-1744389	gtgaatgatccctgaagacattatg[C/T]agtgaaagaggaatggt gacaaaaga	C	T	NM_173550 // intron // 0 // Hs.170652 // C9orf93 // 203238 // chromosome 9 open reading frame 93	C9orf93	C9orf93 , rs14179975, chromosome 9 open reading frame 93,p22.3
SNP_A-1925819	ttatggaatataaaa[A/G]ctccttgtgtatcatg	A	G	NM_173550 // intron // 0 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000297641 // intron // 0 // --- // --- // --- // --- /// ENST00000285482 // intron // 0 // --- // --- // --- // ---	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1892844	tgcacattggtgacaa[A/G]aaaaagcaggagaagg	A	G	NM_173550 // intron // 0 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// ENST00000297641 // intron // 0 // --- // --- // --- // --- /// ENST00000285482 // intron // 0 // --- // --- // --- // ---	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-1857206	tcacctggtcaatgcc[C/G]atcccctgcagtgaga	C	G	NM_173550 // downstream // 32115 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream // 414567 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2286799	gatgggaaaggtgaga[A/G]gcatgttagttgaaat	A	G	NM_173550 // downstream // 202399 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream // 244283 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST0	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2265766	gaagctttacaaactat[C/T]ggtggtgatgtccagt	C	T	NM_173550 // downstream // 352364 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream // 94318 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2077218	accaataagaaaggca[C/T]ataacagtaagaaata	C	T	NM_173550 // downstream // 404540 // Hs.17267 // C9orf93 // 203238 // Homo sapiens chromosome 9 open reading frame 93 (C9orf93), mRNA. /// NM_017637 // downstream // 42142 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00	C9orf93	C9orf93, Homo sapiens chromosome 9 open reading frame 93 (C9orf93), p22.3
SNP_A-2211088	cccggctaacctcata[C/T]gtttaatcccaaatt	C	T	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // --- // --- // ---	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1996051	tttccgcggcaatcaa[C/G]agtgaagatgtattta	C	G	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1996052	ctgctttttcacata[A/C]gtttttcaatcaccct	A	C	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2029588	aaagagaaaaatgtgc[A/G]aacgcatacaaagttg	A	G	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1996053	caccccctccaattgtc[A/G]aacacattctcctaga	A	G	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1996054	catagagcacttggga[C/G]gatgagatccctttca	C	G	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2102097	agatgtgatactgcta[G/T]ggaaggcagcataatt	G	T	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2205380	ccagtgaatctcatta[C/T]gacttcaccatctttc	C	T	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1692212	gcttctgcctgctccacgctaaaga[A/G]aatgatgtacagaact atacttaca	A	G	NM_017738 // upstream // 432486 // Hs.270502 // C9orf39 // 54875 // chromosome 9 open reading frame 39 /// NM_152576 // upstream // 276351 // - // - // - // -	C9orf39	C9orf39 , rs7861010, chromosome 9 open reading frame 39 ,p22.2
SNP_A-1829854	taataactcatatgca[A/C]atctttcctcaaagag	A	C	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2151046	atgtgtattacaggga[A/G]attagataccacaggg	A	G	NM_017637 // intron // 0 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// ENST00000317612 // intron // 0 // — // — // — // —	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2211656	ccctccaaaggaagag[A/T]caatggccagatctac	A	T	NM_017637 // upstream // 16698 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 247668 // Hs.435381 // C9orf39 // 54875 // Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST000003	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2124045	agttaccatatagagg[A/G]aaaagtcagcagtcaa	A	G	NM_017637 // upstream // 33182 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 231184 // Hs.435381 // C9orf39 // 54875 // Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST000003	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-2081015	acctgaacacggacaa[C/T]ctgacaccctaattcc	C	T	NM_017637 // upstream // 33412 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 230954 // Hs.435381 // C9orf39 // 54875 // Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST000003	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1908496	tgtagaggcaggggac[A/G]catgggaagtctgtgt	A	G	NM_017637 // upstream // 35691 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 228675 // Hs.435381 // C9orf39 // 54875 // Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST000003	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2
SNP_A-1943286	ttggtggtaacctagt[C/G]aatcagaatctgcacg	C	G	NM_017637 // upstream // 44437 // Hs.435309 // BNC2 // 54796 // Homo sapiens basonuclin 2 (BNC2), mRNA. /// NM_017738 // upstream // 219929 // Hs.435381 // C9orf39 // 54875 // Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// ENST000003	BNC2	BNC2, Homo sapiens basonuclin 2 (BNC2), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1918963	ttaaccctgaacatag[C/G]attggctagtcagcc	C	G	NM_017738 // downstream // 78558 // Hs.435381 // C9orf39 // 54875 // Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA. /// NM_003026 // upstream // 5633 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. //	C9orf39	C9orf39, Homo sapiens chromosome 9 open reading frame 39 (C9orf39), p22.2
SNP_A-1937688	ttgaagccttggaaaac[C/T]gctccgttgatgaaac	C	T	NM_003026 // intron // 0 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// ENST00000315856 // intron // 0 // — // — // — // —	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2170719	caagtctgtgctaggt[A/G]cctagaaatgcattca	A	G	NM_003026 // intron // 0 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// ENST00000315856 // intron // 0 // — // — // — // —	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1863333	tcatttttcatcaagga[A/G]ctacaggcaagattat	A	G	NM_003026 // intron // 0 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// ENST00000315856 // intron // 0 // — // — // — // —	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1959235	ttttgagggacacaa[A/G]cgttcattatatagct	A	G	NM_003026 // downstream // 144912 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 532067 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2149477	atgtagaccttgatgt[C/G]aatattactgctatag	C	G	NM_003026 // downstream // 243466 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 433513 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2058071	aatatttaaaatggg[C/T]cagaacagtaatagaa	C	T	NM_003026 // downstream // 322027 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 354952 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2128245	ataaggtggttaatcaa[C/G]tccgtgcctcagtttt	C	G	NM_003026 // downstream // 385636 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 291343 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1848770	tatgatatgcgtgcca[C/G]ctacaatagttctctt	C	G	NM_003026 // downstream // 464660 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 212319 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1707071	agtgttaggcactgaaactacctaa[A/G]tcatgagctggtcattta gtaaatg	A	G	NM_003026 // downstream // 494998 // Hs.75149 // SH3GL2 // 6456 // SH3-domain GRB2-like 2 /// NM_052866 // upstream // 182049 // Hs.148564 // ADAMTSL1 // 92949 // ADAMTS-like 1 /// NM_139238 // upstream // 182049 // Hs.148564 // ADAMTSL1 // 92949 // ADAM	SH3GL2	SH3GL2 , rs10511641, SH3-domain GRB2-like 2 ,p22.2
SNP_A-1842527	taggtgttgcctgaag[C/T]ctctttttaaaaggacc	C	T	NM_003026 // downstream // 528602 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 148377 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-2215080	cctattataagccgac[A/C]agcgtatacaggattt	A	C	NM_003026 // downstream // 566257 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 110722 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mR	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1704495	aatacctttttatgaaaattgacaa[C/G]agtgctcctgaaactttac tgtaca	C	G	NM_003026 // downstream // 586733 // Hs.75149 // SH3GL2 // 6456 // SH3-domain GRB2-like 2 /// NM_052866 // upstream // 90314 // Hs.148564 // ADAMTSL1 // 92949 // ADAMTS-like 1 /// NM_139238 // upstream // 90314 // Hs.148564 // ADAMTSL1 // 92949 // ADAMTS	SH3GL2	SH3GL2 , rs10511651, SH3-domain GRB2-like 2 ,p22.2
SNP_A-1952335	tttctctcttgacttg[C/G]aaaataaaatactctat	C	G	NM_003026 // downstream // 676456 // Hs.75149 // SH3GL2 // 6456 // Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA. /// NM_052866 // upstream // 523 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA.	SH3GL2	SH3GL2, Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), p22.2
SNP_A-1914971	tgttataaatgtgacaj[A/G]gaaaaactacaatcac	A	G	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.2
SNP_A-1960583	tttttcatgtcatttc[A/G]cctcttcaggttgt	A	G	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-1742743	tatttttctgctttgtttttgtttag[C/G]aagcagtatctctgtaataatcc ct	C	G	NM_052866 // intron // 0 // Hs.148564 // ADAMTSL1 // 92949 // ADAMTS-like 1 /// NM_139238 // intron // 0 // Hs.148564 // ADAMTSL1 // 92949 // ADAMTS-like 1	ADAMTSL1	ADAMTSL1 , rs10511660, ADAMTS-like 1 ,p22.1
SNP_A-1861942	tcatgactgctgagaa[C/T]agagagtgctggccat	C	T	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-1829460	taagtgagaaccatcc[A/G]ctgctgcagtctataa	A	G	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-2177004	cacctatatgtattcg[C/T]aatagcaccataacag	C	T	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-1909514	tgtattatttttaa[C/T]tgcaaactcaggtctt	C	T	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-2074418	acatactgacaaaatg[C/G]aattgattcgttacc	C	G	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-1996121	ctggcagatgtatata[A/G]aaagataatgactcat	A	G	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3.	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2087070	actgagtttgaagttg[A/G]aagggactgtggacac	A	G	NM_052866 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // intron // 0 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 3,	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-2093039	agaacagaatcactag[A/G]cctgaagtgaaaagt	A	G	NM_052866 // downstream // 86663 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, mRNA. /// NM_139264 // downstream // 90134 // Hs.522019 // ADAMTSL1 // 92949 // Homo sapiens ADAMTS-like 1 (ADAMTSL1), trans	ADAMTSL1	ADAMTSL1, Homo sapiens ADAMTS-like 1 (ADAMTSL1), transcript variant 2, p22.1
SNP_A-1915301	tgttcatcttgaattg[A/G]aaacactttaggaaa	A	G	NM_152702 // intron // 0 // Hs.217297 // C9orf94 // 206938 // Homo sapiens chromosome 9 open reading frame 94 (C9orf94), mRNA. /// ENST00000316239 // intron // 0 // — // — // —	C9orf94	C9orf94, Homo sapiens chromosome 9 open reading frame 94 (C9orf94), p22.1
SNP_A-2185962	caggcacgtcgtaacc[A/G]cagacaggacactgac	A	G	ENST00000340967 // CDS // 0 // — // — // — // — /// ENST00000318820 // intron // 0 // — // — // —	-	p22.1
SNP_A-2260987	gaaagaaagctattggg[A/G]atgaagactattgatc	A	G	NM_020344 // intron // 0 // Hs.283014 // SLC24A2 // 25769 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA. /// ENST00000286344 // intron // 0 // — // — // — // — /// ENST00000341998 // intron	SLC24A2	SLC24A2, Homo sapiens solute carrier family 24 (sodium,p22.1
SNP_A-1849257	tatgcttatgacatca[A/G]catttatggcaatt	A	G	NM_020344 // intron // 0 // Hs.283014 // SLC24A2 // 25769 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA. /// ENST00000286344 // intron // 0 // — // — // — // — /// ENST00000341998 // intron	SLC24A2	SLC24A2, Homo sapiens solute carrier family 24 (sodium p22.1
SNP_A-1677822	ccctgtgcagaggcatttgggctc[A/G]atagatccagagtgctc cagtcaag	A	G	NM_004529 // downstream // 466892 // Hs.404 // MLLT3 // 4300 // myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 /// NM_020344 // upstream // 91150 // Hs.283014 // SLC24A2 // 25769 // solute carrier family 24	MLLT3	MLLT3, rs10511673, myeloid,p22.1
SNP_A-2192149	catcagaatcacatgg[A/G]cacttattagaaatgc	A	G	NM_004529 // downstream // 152473 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000330804 // upstream // 296521 // — // — // —	MLLT3	MLLT3, Homo sapiens myeloid p21.3
SNP_A-1864387	tccactgccaacacca[A/G]tgcaactactgagtga	A	G	NM_004529 // downstream // 98074 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000330804 // upstream // 350920 // — // — // —	MLLT3	MLLT3, Homo sapiens myeloid,p21.3
SNP_A-2162374	atttattgctgacta[C/T]ccttccaggttaacct	C	T	NM_004529 // downstream // 81782 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000330804 // upstream // 367212 // — // — // —	MLLT3	MLLT3, Homo sapiens myeloid,p21.3
SNP_A-1782231	ggcaaggtaacctag[C/G]aatttgagcagaagga	C	G	NM_004529 // downstream // 69614 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000330804 // upstream // 379380 // — // — // —	MLLT3	MLLT3, Homo sapiens myeloid p21.3
SNP_A-2288833	gatttaaaactagata[C/T]gtcttctaatatac	C	T	NM_004529 // downstream // 46383 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000330804 // upstream // 402611 // — // — // —	MLLT3	MLLT3, Homo sapiens myeloid,p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2056021	aatacatacctctcca[C/G]aacaccattactcatt	C	G	NM_004529 // intron // 0 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000304275 // intron // 0 // --- // --- // --- // --- /// ENST000	MLLT3	MLLT3, Homo sapiens myeloid p21.3
SNP_A-1920128	ttaatcattagggaaa[C/T]gcaagtgaaaactgca	C	T	NM_004529 // upstream // 18637 // Hs.493585 // MLLT3 // 4300 // Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA. /// ENST00000304275 // upstream // 18637 // --- // --- // ---	MLLT3	MLLT3, Homo sapiens myeloid p21.3
SNP_A-1880359	tcttgaacgcttcaaa[G/T]gtctcttaacacttg	G	T	NM_176891 // upstream // 191460 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 129482 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2233684	ctcatatcaagaacaa[C/T]gtgacttgatgctat	C	T	NM_176891 // upstream // 191915 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 129027 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1996213	tcatttcagtgaactc[A/G]acagtgttactgtagt	A	G	NM_176891 // upstream // 202996 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 117946 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1928998	ttcagcctgcaaagta[C/T]agattactccaggcag	C	T	NM_176891 // upstream // 213767 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 107175 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1860184	tcagtcatctatatcc[A/G]aaatgtatctgagtta	A	G	NM_176891 // upstream // 219102 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 101840 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1809418	gtgagaaaaatcagaa[A/C]tatgattgctcagaag	A	C	NM_176891 // upstream // 219312 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 101630 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2101214	agatccagttgctcca[C/T]gttgtttgttcactg	C	T	NM_176891 // upstream // 219739 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 101203 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1905466	tggtacaagctagagc[G/T]gaaacttgagtaaagc	G	T	NM_176891 // upstream // 220249 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 100693 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2108548	agctggattcgtaag[A/T]catttaggacattctg	A	T	NM_176891 // upstream // 227190 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 93752 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1646060	gggagggttaaaagtctgactcaaa[A/G]gcgcactgtcacaat agcctgggga	A	G	NM_002451 // upstream // 90960 // Hs.446152 // MTAP // 4507 // methylthioadenosine phosphorylase /// NM_176891 // upstream // 229976 // Hs.441972 // IFNT1 // 338376 // interferon tau-1	MTAP	MTAP , rs1335500, methylthioadenosine phosphorylase ,p21.3
SNP_A-1670157	gtcaaatgaatgtacacattcatct[C/G]ttcttatgggaattacatc caggaa	C	G	NM_002451 // upstream // 90820 // Hs.446152 // MTAP // 4507 // methylthioadenosine phosphorylase /// NM_176891 // upstream // 230116 // Hs.441972 // IFNT1 // 338376 // interferon tau-1	MTAP	MTAP , rs1335501, methylthioadenosine phosphorylase ,p21.3
SNP_A-2250746	cttatatttaagataa[G/T]tagcctgccacaatta	G	T	NM_176891 // upstream // 238788 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 82154 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2086006	actctattagatcttg[A/C]aacagcactctcttct	A	C	NM_176891 // upstream // 245515 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 75427 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1955171	tttggcatatgtgcaa[C/T]gagtaaattttctgta	C	T	NM_176891 // upstream // 250773 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 70169 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1996215	tcgtgtgctatattag[C/T]atttgctttatacctt	C	T	NM_176891 // upstream // 251219 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 69723 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1797437	ggtttacctgacatag[C/G]atttaactttgctttt	C	G	NM_176891 // upstream // 251511 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 69431 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2014133	agaatgtagaggcaga[C/G]gaaatacagtgaggga	C	G	NM_176891 // upstream // 251807 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 69135 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2024528	aaaaggatttaagtcc[A/G]atagtaaaaggagcga	A	G	NM_176891 // upstream // 266110 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 54832 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2170649	caagttaaagtcatcc[A/G]cagtaaaactgagaac	A	G	NM_176891 // upstream // 266546 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 54396 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2081741	accttcctgagtcata[C/G]aaagtcacttgacctc	C	G	NM_176891 // upstream // 266740 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 54202 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1910099	tgtcatccaacggaag[C/T]actgctaagccagaca	C	T	NM_176891 // upstream // 268894 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 52048 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1996218	tgtttcctctaatgaa[C/G]gggcataatactgctc	C	G	NM_176891 // upstream // 278703 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 42239 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1996219	taattaaatacaaact[C/G]agcccattacttcac	C	G	NM_176891 // upstream // 291474 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 29468 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-1996220	aacagcctaaagatga[C/T]gtgtaagagcataata	C	T	NM_176891 // upstream // 291529 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 29413 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2156288	attcatatgtgttta[C/T]gggtgtaatctctgt	C	T	NM_176891 // upstream // 298558 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 22384 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2151479	atgttctaaaaattcc[A/G]aagtcaacicttaga	A	G	NM_176891 // upstream // 303325 // Hs.441972 // IFNE1 // 338376 // Homo sapiens interferon epsilon 1 (IFNE1), mRNA. /// NM_002451 // upstream // 17617 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST000	IFNE1	IFNE1, Homo sapiens interferon epsilon 1 (IFNE1), p21.3
SNP_A-2297302	gccacctggagtgaga[A/G]aattcaagcaatctt	A	G	NM_002451 // intron // 0 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00000297736 // intron // 0 // — // — // — /// ENST00000355696 // intron // 0 // — // — // —	MTAP	MTAP, Homo sapiens methylthioadenosine phosphorylase (MTAP), p21.3
SNP_A-2163185	attttctattggctg[A/G]atgcaagtcccaggtt	A	G	NM_002451 // intron // 0 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00000297736 // intron // 0 // — // — // — /// ENST00000355696 // intron // 0 // — // — // —	MTAP	MTAP, Homo sapiens methylthioadenosine phosphorylase (MTAP), p21.3
SNP_A-2096752	agactagaaagaaaac[A/C]ggtattgccatcagat	A	C	NM_002451 // intron // 0 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00000297736 // intron // 0 // — // — // — /// ENST00000355696 // intron // 0 // — // — // —	MTAP	MTAP, Homo sapiens methylthioadenosine phosphorylase (MTAP), p21.3
SNP_A-1996224	ttcagaagcctggaa[A/G]agaactcaacacacc	A	G	NM_002451 // intron // 0 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00000297736 // intron // 0 // — // — // — /// ENST00000355696 // intron // 0 // — // — // —	MTAP	MTAP, Homo sapiens methylthioadenosine phosphorylase (MTAP), p21.3
SNP_A-1842798	tagtacattgtaggca[G/T]tagatgtgttggagaa	G	T	NM_002451 // intron // 0 // Hs.193268 // MTAP // 4507 // Homo sapiens methylthioadenosine phosphorylase (MTAP), mRNA. /// ENST00000297736 // intron // 0 // — // — // — /// ENST00000355696 // intron // 0 // — // — // —	MTAP	MTAP, Homo sapiens methylthioadenosine phosphorylase (MTAP), p21.3
SNP_A-2259355	gaaaaagtgattcaat[A/C]ataggagaaaaatga	A	C	ENST00000355696 // intron // 0 // — // — // —	-	p21.3
SNP_A-2027423	aaacattgcaacattc[A/G]cttcttacgacctttc	A	G	NM_004936 // upstream // 78948 // Hs.72901 // CDKN2B // 1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 78989 // Hs.72901 // CDKN2B // 1030 // Homo sapiens c	CDKN2B	CDKN2B, Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3
SNP_A-2035117	aaatgcattctatagc[A/G]caggatgttccagtca	A	G	NM_004936 // upstream // 89262 // Hs.72901 // CDKN2B // 1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 89303 // Hs.72901 // CDKN2B // 1030 // Homo sapiens c	CDKN2B	CDKN2B, Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2150146	atgtcctgttggaag[A/G]ccaactctgtatcagt	A	G	NM_004936 // upstream // 89307 // Hs.72901 // CDKN2B // 1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 89348 // Hs.72901 // CDKN2B // 1030 // Homo sapiens c	CDKN2B	CDKN2B, Homo sapiens cydin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3
SNP_A-1699309	tacaatcaatggcatgttataatttt[A/C]attggcagcattattgtctc ttaa	A	C	NM_004936 // upstream // 90157 // Hs.72901 // CDKN2B // 1030 // cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) /// NM_078487 // upstream // 90157 // Hs.72901 // CDKN2B // 1030 // cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	CDKN2B , rs1537371, cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) ,p21.3
SNP_A-1676982	tgcacttaaaatgggtgaaattata[C/G]cgtggaagttatacctc aataaagt	C	G	NM_004936 // upstream // 90765 // Hs.72901 // CDKN2B // 1030 // cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) /// NM_078487 // upstream // 90765 // Hs.72901 // CDKN2B // 1030 // cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	CDKN2B , rs1556516, cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) ,p21.3
SNP_A-1648126	ctcaaaacaaaggaagtgcaattta[C/T]agaaggtagtagaat aggcagataa	C	T	NM_004936 // upstream // 103188 // Hs.72901 // CDKN2B // 1030 // cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) /// NM_078487 // upstream // 103188 // Hs.72901 // CDKN2B // 1030 // cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	CDKN2B	CDKN2B , rs10511701, cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) ,p21.3
SNP_A-2123726	agtgttggaaggtcac[C/T]aataatcccaaataac	C	T	NM_004936 // upstream // 152926 // Hs.72901 // CDKN2B // 1030 // Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA. /// NM_078487 // upstream // 152967 // Hs.72901 // CDKN2B // 1030 // Homo sapiens	CDKN2B	CDKN2B, Homo sapiens cydin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, p21.3
SNP_A-2266893	gaagttgcaaaaagta[C/G]ctggcatttaggaaat	C	G	NM_022160 // downstream // 218243 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 1019390 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2154490	attattctattaggct[A/T]aaaagaaatcaattat	A	T	NM_022160 // downstream // 276282 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 961351 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1712015	tggtgacccccattcaaattcagga[C/T]catggatttccatttaatct cccca	C	T	NM_004432 // downstream // 896257 // Hs.166109 // ELAVL2 // 1993 // ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	ELAVL2	ELAVL2 , rs1999761, ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B),p21.3
SNP_A-1802768	gtatgctatcagagta[A/C]atttcaagctcaaac	A	C	NM_022160 // downstream // 511765 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 725868 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2130853	atacttctccaaaaa[A/T]aatacagtctgtctgt	A	T	NM_022160 // downstream // 711803 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 525930 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2160632	atttcctgacttattc[A/T]cttctgtatcaccagc	A	T	NM_022160 // downstream // 761888 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 475745 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1996247	ctgcattaaaggttga[G/T]tttcctagtggctca	G	T	NM_022160 // downstream // 769714 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 467919 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1935195	ttctgcatgcatggga[A/C]aagttagctccagtcc	A	C	NM_022160 // downstream // 813940 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 423693 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1792732	ggtaagaagttcagca[A/G]aattttaggatgcaaa	A	G	NM_022160 // downstream // 815452 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 422181 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2281849	gagtgatcacaaagtg[C/G]atcttagccagtgttg	C	G	NM_022160 // downstream // 865961 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 371672 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1996245	aatacagtataagtca[A/G]tcacctctccattctg	A	G	NM_022160 // downstream // 889376 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 348257 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-1729370	gaaattacatggttatcctttatagj[A/C]actgtcttattacaatttta cat	A	C	NM_004432 // downstream // 265791 // Hs.166109 // ELAVL2 // 1993 // ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	ELAVL2	ELAVL2 , rs10511725, ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B),p21.3
SNP_A-1780683	ggatcaggaaagccaa[C/T]gctgaaaaatttaagc	C	T	NM_022160 // downstream // 1204086 // Hs.371976 // DMRTA1 // 63951 // Homo sapiens DMRT-like family A1 (DMRTA1), mRNA. /// NM_004432 // downstream // 33567 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)	DMRTA1	DMRTA1, Homo sapiens DMRT-like family A1 (DMRTA1), p21.3
SNP_A-2027288	aaacatatttataaac[C/G]aaaatgtagcatcacc	C	G	NM_004432 // 3UTR // 0 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// ENST00000359598 // 3UTR // 0	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1712527	aatgcagcagctttggtgtcctgtt[G/T]aacittagtgaaaatact aattct	G	T	BC046919 // downstream // 1670646 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_004432 // upstream // 179987 // Hs.166109 // ELAVL2 // 1993 // ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (H	LOC389708	LOC389708 , rs1450586, hypothetical gene supported by BC017510; BC046919 ,p21.3
SNP_A-1660371	ctagtatagaatagatgtgaatctc[C/T]cagtagaacagtgtacag agtagggt	C	T	BC046919 // downstream // 1625163 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_004432 // upstream // 225470 // Hs.166109 // ELAVL2 // 1993 // ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (H	LOC389708	LOC389708 , rs10511736, hypothetical gene supported by BC017510; BC046919 ,p21.3
SNP_A-1643293	gagaacagctctgcaaatggacagaa[C/G]aagtcaaaagaga ccagcaataaga	C	G	BC046919 // downstream // 1625104 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_004432 // upstream // 225529 // Hs.166109 // ELAVL2 // 1993 // ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (H	LOC389708	LOC389708 , rs10511737, hypothetical gene supported by BC017510; BC046919 ,p21.3
SNP_A-2166101	caaatagactgtaaaa[A/G]ccaggataacgtcctt	A	G	NM_004432 // upstream // 353388 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 348899 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens EL	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2300576	gcctgatgaggcttga[A/G]aattaagtagaggtca	A	G	NM_004432 // upstream // 419987 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 415498 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens EL	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2130736	atacttaaiatctctc[A/C]acctcagtttgttcat	A	C	NM_004432 // upstream // 520577 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 516088 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens EL	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1996292	acgtaaagcctggtgt[A/G]aatgtttctgctattt	A	G	NM_004432 // upstream // 964908 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 960419 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens EL	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2100747	agatagctagataaata[C/G]atatacacacagctaa	C	G	NM_004432 // upstream // 1121174 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1116685 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1861473	tcatccaacaatacaa[A/G]aaatgtagcagggtca	A	G	NM_004432 // upstream // 1131399 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1126910 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2099410	agaggcgtcagtaaaa[C/T]gtggaacgtccacgg	C	T	NM_004432 // upstream // 1164672 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1160183 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2202893	ccactcacctggattat[C/T]ggcagccggtgagaat	C	T	NM_004432 // upstream // 1356238 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1351749 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2112387	aggcaagaaatgaata[A/G]agcacaagaatacaca	A	G	NM_004432 // upstream // 1363114 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1358625 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2275743	gagaccatgatattga[C/T]aaaaaccaaggtct	C	T	NM_004432 // upstream // 1363673 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1359184 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2256590	ctttcaagttctctga[C/T]tactacttgtttcca	C	T	NM_004432 // upstream // 1373105 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1368616 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2259236	gaaaaaccctaacaga[A/G]gtgtcacaattatgac	A	G	NM_004432 // upstream // 1387501 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1383012 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2084394	actatatagaagagtc[C/T]acaaaaatcgagagcaa	C	T	NM_004432 // upstream // 1389916 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1385427 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2064555	aattcgaatttgagaa[C/T]gtctctgctatagcat	C	T	NM_004432 // upstream // 1398738 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1394249 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-1889931	tgatagctattactaa[A/G]tcctagagtggatatt	A	G	NM_004432 // upstream // 1563113 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1558624 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2184454	cagctaaggaggaaaca[C/T]ggcctctgtctcag	C	T	NM_004432 // upstream // 1631117 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1626628 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2251436	cttcacataagtttga[C/T]gctttcctctgatgt	C	T	NM_004432 // upstream // 1633914 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA. /// NM_004432 // upstream // 1629425 // Hs.166109 // ELAVL2 // 1993 // Homo sapiens	ELAVL2	ELAVL2, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), p21.3
SNP_A-2116064	aggtaaaatgtatgac[C/T]ggtgccaacctacagg	C	T	NM_001004125 // upstream // 260047 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 902343 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2022576	aaaaatgaatgcataa[A/G]atgaagtaagagatgt	A	G	NM_001004125 // upstream // 310677 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 851713 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2080176	accgtgcttcgtcata[C/T]taccagaattatttt	C	T	NM_001004125 // upstream // 314977 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 847413 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2113308	aggcctcatctctaca[A/G]tcaatcaactgattc	A	G	NM_001004125 // upstream // 438258 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 724132 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1909731	tgtcaatgggccttta[A/T]ggctgtcccaaacttc	A	T	NM_001004125 // upstream // 590612 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 571778 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2156785	attctgtttattccaa[A/T]gggagaatcgctttga	A	T	NM_001004125 // upstream // 636073 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 526317 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2178258	cactcaataaaggcaa[A/G]cttcaaaatgaaatt	A	G	NM_001004125 // upstream // 778875 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 383515 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1862588	tcattagcagcatagat[A/G]ccagcttagacaatct	A	G	NM_001004125 // upstream // 801093 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 361297 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1706725	gcctcattttgtagcacctgttgca[C/T]aattaccagaaagctcc gttcagc	C	T	BC046919 // upstream // 827621 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_024828 // downstream // 335329 // Hs.178357 // C9orf82 // 79886 // chromosome 9 open reading frame 82	LOC389708	LOC389708 , rs10511790, hypothetical gene supported by BC017510; BC046919 , p21.2
SNP_A-1644256	taatgtcatacaatatttcaactca[A/C]atactgatttgccacaaa tgagag	A	C	BC046919 // upstream // 828435 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_024828 // downstream // 334515 // Hs.178357 // C9orf82 // 79886 // chromosome 9 open reading frame 82	LOC389708	LOC389708 , rs1854313, hypothetical gene supported by BC017510; BC046919 , p21.2
SNP_A-1660097	ccatttctcaattgcttgaaagaa[C/T]taaagagtcagacatga caaactgc	C	T	BC046919 // upstream // 846119 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_024828 // downstream // 316831 // Hs.178357 // C9orf82 // 79886 // chromosome 9 open reading frame 82	LOC389708	LOC389708 , rs4111166, hypothetical gene supported by BC017510; BC046919 , p21.2
SNP_A-1700951	ctctagaaatcatagaagaaacaaa[A/G]gaaagctgttttcata gactggaat	A	G	BC046919 // upstream // 846387 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_024828 // downstream // 316563 // Hs.178357 // C9orf82 // 79886 // chromosome 9 open reading frame 82	LOC389708	LOC389708 , rs4978076, hypothetical gene supported by BC017510; BC046919 , p21.2
SNP_A-1697074	caacttgaggtgagatcacatgtta[G/T]cttgtatatcttccagtctt ccaga	G	T	BC046919 // upstream // 860508 // Hs.26268 // LOC389708 // 389708 // hypothetical gene supported by BC017510; BC046919 /// NM_024828 // downstream // 302442 // Hs.178357 // C9orf82 // 79886 // chromosome 9 open reading frame 82	LOC389708	LOC389708 , rs994390, hypothetical gene supported by BC017510; BC046919 , p21.2
SNP_A-2266128	gaaggctgacttgta[A/T]gagaaaaatacttcaa	A	T	NM_001004125 // upstream // 861681 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 300709 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-1902756	tggctattagacttaa[G/T]caccatctaccggatc	G	T	NM_001004125 // upstream // 862346 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 300044 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2271075	gacatagaatttacca[C/T]ctgtacatttttaaga	C	T	NM_001004125 // upstream // 1071847 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 90543 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2
SNP_A-2041379	aacctggttggtggtg[A/G]agctcaaaataaatct	A	G	NM_001004125 // upstream // 1074204 // Hs.26268 // TUSC1 // 286319 // Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA. /// NM_024828 // downstream // 88186 // Hs.178357 // C9orf82 // 79886 // Homo sapiens chromosome 9 open reading frame 82 (C9orf8	TUSC1	TUSC1, Homo sapiens tumor suppressor candidate 1 (TUSC1), p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2085996	actctatcagcagtaa[C/T]ctcttatgtttcc	C	T	NM_025103 // intron // 0 // Hs.145402 // CCDC2 // 80173 // Homo sapiens coiled-coil domain containing 2 (CCDC2), mRNA. /// ENST00000262247 // intron // 0 // --- // --- // ---	CCDC2	CCDC2, Homo sapiens coiled-coil domain containing 2 (CCDC2), p21.2
SNP_A-1960610	tttttccagtactccc[C/T]actgacagcctcta	C	T	NM_000459 // intron // 0 // Hs.89640 // TEK // 7010 // Homo sapiens TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) (TEK), mRNA. /// ENST00000354568 // intron // 0 // --- // --- // --- /// ENST00000239259 //	TEK	TEK, Homo sapiens TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) (TEK), p21.2
SNP_A-2303002	gctagtcagtgtaaca[A/G]aatgattagtggac	A	G	NM_024761 // intron // 0 // Hs.369022 // MOBKL2B // 79817 // Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// ENST00000262244 // intron // 0 // --- // --- // --- // ---	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-2257027	ctttctaattctctgaf[A/G]aaaacttctaatctac	A	G	NM_024761 // intron // 0 // Hs.369022 // MOBKL2B // 79817 // Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// ENST00000262244 // intron // 0 // --- // --- // --- // ---	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-2309779	ggaaagtacatcagggt[G/T]atacctaagaaattt	G	T	NM_024761 // intron // 0 // Hs.369022 // MOBKL2B // 79817 // Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// ENST00000262244 // intron // 0 // --- // --- // --- // ---	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-1996376	taaagtaatgaaatac[C/T]attccacaagcatcaa	C	T	NM_024761 // intron // 0 // Hs.369022 // MOBKL2B // 79817 // Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), mRNA. /// NM_020124 // intron // 0 // Hs.546411 // IFNK // 56832 // Homo sapiens interferon, kappa (IFNK), mRNA. ///	MOBKL2B	MOBKL2B, Homo sapiens MOB1, Mps One Binder kinase activator-like 2B (yeast) (MOBKL2B), p21.2
SNP_A-2287168	gatgtccactctcacc[A/G]ctcctttcagcatag	A	G	NM_145005 // intron // 0 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // intron // 0 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading f	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-1996385	gtgggctgaaaccagat[A/T]cataagagacctaaga	A	T	NM_145005 // upstream // 121739 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 121739 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2202610	ccacctctccaacttta[C/T]ggggctcactgttacc	C	T	NM_145005 // upstream // 185920 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 185920 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2122229	agtgcaccactgaagg[A/G]acatcccaagattctt	A	G	NM_145005 // upstream // 235513 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 235513 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2143280	atgacagatatacaat[C/T]aaacaagctgtgatca	C	T	NM_145005 // upstream // 243249 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 243249 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2092559	agaaatatcacctca[C/G]gaaaagaatggagttg	C	G	NM_145005 // upstream // 250965 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 250965 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1933973	ttctcaatgactctcc[A/G]caaagtctttcattat	A	G	NM_145005 // upstream // 252375 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 252375 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2268900	gaattatttaaaggca[C/T]ctcaagtgggattga	C	T	NM_145005 // upstream // 298047 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 298047 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-1756232	cattcattgctagaaatgtaacttta[A/G]aaccagaatatttcttag acttca	A	G	NM_145005 // upstream // 322175 // Hs.23607 // C9orf72 // 203228 // chromosome 9 open reading frame 72 /// NM_152570 // downstream // 52511 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	C9orf72	C9orf72 , rs7849119, chromosome 9 open reading frame 72 ,p21.2
SNP_A-2092025	agaaaccagagagaa[A/C]gagcacagccctttag	A	C	NM_145005 // upstream // 332818 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, mRNA. /// NM_018325 // upstream // 332818 // Hs.493639 // C9orf72 // 203228 // Homo sapiens chromosome 9	C9orf72	C9orf72, Homo sapiens chromosome 9 open reading frame 72 (C9orf72), transcript variant 2, p21.2
SNP_A-2171731	caatcttgtggatttc[A/G]ctctaactgctcatgg	A	G	NM_152570 // intron // 0 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // — // — // —	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2044279	aacttgagggacata[C/T]gtaaggtgttgcaaat	C	T	NM_152570 // intron // 0 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // — // — // —	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1701383	tatgtcttaacaatttaatcagaa[C/T]catatgacgtgaacagc atttttt	C	T	NM_152570 // intron // 0 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs10491896, hypothetical protein FLJ31810,p21.1
SNP_A-1714435	catcacccacttcgtgacaaagact[A/C]actgccctagctgcct gaagtgctg	A	C	NM_152570 // intron // 0 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs10491894, hypothetical protein FLJ31810,p21.1
SNP_A-1699977	cattatatctttctacctatcaaaaa[C/G]gaagagttgaaacaaattt tcagaa	C	G	NM_152570 // intron // 0 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs1331877, hypothetical protein FLJ31810,p21.1
SNP_A-2179511	cacttagcatatagag[G/T]catttagaaaaccta	G	T	NM_152570 // intron // 0 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // intron // 0 // — // — // —	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1840771	tagctagagatatttat[C/T]gtgactaaaccacgag	C	T	NM_152570 // upstream // 40209 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 40209 // — // — // — /// ENST00000339493 // downstream // 561294 // — // –	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2238173	ctctgccttttgcggat[C/G]agttgttatttttattc	C	G	NM_152570 // upstream // 123159 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 123159 // — // — // — /// ENST00000339493 // downstream // 644244 // — //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2114969	agggccaccgattact[C/T]aggcaagaattaacat	C	T	NM_152570 // upstream // 125417 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 125417 // — // — // — /// ENST00000339493 // downstream // 646502 // — //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2035704	aaatgtctaaaaatc[A/G]caaatcactgtgcaga	A	G	NM_152570 // upstream // 205875 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 205875 // — // — // — /// ENST00000339493 // downstream // 726960 // — //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2052181	aagtaaataagtatta[G/T]gaagactaggaactgg	G	T	NM_152570 // upstream // 209670 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 209670 // --- // --- // --- /// ENST00000339493 // downstream // 730755 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1949469	tttattgaatttttaa[A/T]acaactccatggctta	A	T	NM_152570 // upstream // 549389 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 549389 // --- // --- // --- /// ENST00000339493 // downstream // 1070474 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1957664	tttatgagaagttga[C/G]attactgcctatctag	C	G	NM_152570 // upstream // 556508 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 556508 // --- // --- // --- /// ENST00000339493 // downstream // 1077593 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2283849	gatagtcctgaagtca[C/T]atttacaagtactttg	C	T	NM_152570 // upstream // 557948 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 557948 // --- // --- // --- /// ENST00000339493 // downstream // 1079033 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1786403	ggcttaatgattgtca[A/G]aacaccctccccctca	A	G	NM_152570 // upstream // 611351 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 611351 // --- // --- // --- /// ENST00000339493 // downstream // 1132436 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1812976	gtgggtagataagtta[A/T]atatgttgccaccttt	A	T	NM_152570 // upstream // 659650 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 659650 // --- // --- // --- /// ENST00000339493 // downstream // 1180735 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1942632	ttgggaccaataagtc[A/G]atctcctactgaaggt	A	G	NM_152570 // upstream // 661480 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 661480 // --- // --- // --- /// ENST00000339493 // downstream // 1182565 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1674695	tgacacatcctctactagtcatgat[A/T]aaagtgtgttttcataaa gcctg	A	T	NM_152570 // upstream // 668764 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810, rs10491663, hypothetical protein FLJ31810,p21.1
SNP_A-1732976	tacacaaataacattaaaggatgct[C/G]aatgatattagtaactg ggcaaatg	C	G	NM_152570 // upstream // 684359 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810, rs1929829, hypothetical protein FLJ31810,p21.1
SNP_A-2155641	atccagctctatgga[C/T]gaaatttttctggtg	C	T	NM_152570 // upstream // 737951 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 737951 // --- // --- // --- /// ENST00000339493 // downstream // 1259036 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1684998	ctcatagacacacatatttttgttc[C/T]atggactgggcaatgtaat cttatg	C	T	NM_152570 // upstream // 787376 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810, rs4879352, hypothetical protein FLJ31810,p21.1
SNP_A-1753719	aaatccttcttactggcgaaata[C/G]cttgcttcaatactaattta aacaa	C	G	NM_152570 // upstream // 826531 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810, rs10491672, hypothetical protein FLJ31810,p21.1
SNP_A-1957876	ttttatttttactgga[A/C]agttatgcttcaaac	A	C	NM_152570 // upstream // 978638 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 978638 // --- // --- // --- /// ENST00000339493 // downstream // 1499723 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2014189	gatcacgtgtagtag[C/G]aacatttaaccatat	C	G	NM_152570 // upstream // 983048 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 983048 // --- // --- // --- /// ENST00000339493 // downstream // 1504133 // --- //	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1725706	tacaccccagacacagaaagtagt[C/T]gagcagtgaaaaa gcatacatttt	C	T	NM_152570 // upstream // 1034215 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs953639, hypothetical protein FLJ31810,p21.1
SNP_A-1960547	ttttcaggctgaga[C/T]attgctgcaaggttgc	C	T	NM_152570 // upstream // 1147170 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1147170 // --- // --- // --- /// ENST00000339493 // downstream // 1668255 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2014190	gtctcagatcagagg[A/G]atgatttcttgtctt	A	G	NM_152570 // upstream // 1229582 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1229582 // --- // --- // --- /// ENST00000339493 // downstream // 1750667 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2014191	gaaagagaacagtcaa[A/G]atgcattcatctcac	A	G	NM_152570 // upstream // 1229682 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1229682 // --- // --- // --- /// ENST00000339493 // downstream // 1750767 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1996476	cacatgttaataattg[A/C]caactatgacaaattt	A	C	NM_152570 // upstream // 1258283 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1258283 // --- // --- // --- /// ENST00000339493 // downstream // 1779368 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2014194	ctatttcacattccaa[A/G]tacattcaagaacaa	A	G	NM_152570 // upstream // 1258393 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1258393 // --- // --- // --- /// ENST00000339493 // downstream // 1779478 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1737665	taaacaagcagaaaacattaccata[C/G]agtggaggcgctaaa tttcaccaaa	C	G	NM_152570 // upstream // 1268893 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs2502107, hypothetical protein FLJ31810,p21.1
SNP_A-2152934	attacagagacttggg[A/G]attatatcattctat	A	G	NM_152570 // upstream // 1321120 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1321120 // --- // --- // --- /// ENST00000339493 // downstream // 1842205 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-1651890	atagatatctaaaggttatttgaag[A/G]ccaatctggcatatagaa tatctt	A	G	NM_152570 // upstream // 1415130 // Hs.446325 // FLJ31810 // 158038 // hypothetical protein FLJ31810	FLJ31810	FLJ31810 , rs1361925, hypothetical protein FLJ31810,p21.1
SNP_A-2314754	ggagtctaagcaggc[C/T]ctataggtgaatcac	C	T	NM_152570 // upstream // 1419576 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1419576 // --- // --- // --- /// ENST00000339493 // downstream // 1940661 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2036842	aaatttctctggata[C/G]ctgaccatttcacta	C	G	NM_152570 // upstream // 1680964 // Hs.145642 // FLJ31810 // 158038 // Homo sapiens hypothetical protein FLJ31810 (FLJ31810), mRNA. /// ENST00000308675 // upstream // 1680964 // --- // --- // --- /// ENST00000339493 // downstream // 2202049 // ---	FLJ31810	FLJ31810, Homo sapiens hypothetical protein FLJ31810 (FLJ31810), p21.1
SNP_A-2248976	ctgttgttcctcaaat[G/T]acaacttatctgtttt	G	T	ENST00000259550 // upstream // 315617 // --- // --- // --- /// ENST00000360120 // upstream // 106203 // --- // --- // ---	-	p21.1
SNP_A-2021563	aaaaaatcagctaaac[A/G]aaaaatctcctaga	A	G	ENST00000259550 // upstream // 321629 // --- // --- // --- /// ENST00000360120 // upstream // 100191 // --- // --- // ---	-	p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1923398	ttaggataataatctc[C/T]atctggaatcaccaaa	C	T	NM_002197 // upstream // 749603 // Hs.446075 // ACO1 // 48 // Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 749635 // Hs.446075 // ACO1 // 48 // Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// ENST00000360296 // upstream	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-1996526	cccagcactacctata[C/T]aactgtactgacatat	C	T	NM_002197 // upstream // 728413 // Hs.446075 // ACO1 // 48 // Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 728445 // Hs.446075 // ACO1 // 48 // Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// ENST00000360296 // upstream	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-1996529	tggtaaacatacacta[C/T]accactgatattacca	C	T	NM_002197 // upstream // 705630 // Hs.446075 // ACO1 // 48 // Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// NM_002197 // upstream // 705662 // Hs.446075 // ACO1 // 48 // Homo sapiens aconitase 1, soluble (ACO1), mRNA. /// ENST00000360296 // upstream	ACO1	ACO1, Homo sapiens aconitase 1, soluble (ACO1), p21.1
SNP_A-1751507	tgcatctcgtgctcacgttccagac[C/T]catcaacaggaagaaa acaagaggc	C	T	AF091236 // downstream // 729202 // - // - // Homo sapiens ADP/ATP translocase mRNA, partial cds. /// NM_002197 // upstream // 401198 // Hs.319677 // ACO1 // 48 // aconitase 1, soluble	-	- , rs10511889, Homo sapiens ADP,p21.1
SNP_A-1674036	gtaaggttcatcttcatgaagttaa[A/T]ctatgtctcacacttctgtc cagta	A	T	NM_014314 // intron // 0 // Hs.438386 // RIG-I // 23586 // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	RIG-I	RIG-I , rs10511907, DEAD,p21.1
SNP_A-1674331	ctctgatgcgtcagtgatagcaac[A/G]gtcaaacacaatctgg aggaactgg	A	G	NM_014314 // CDS // 0 // Hs.438386 // RIG-I // 23586 // DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	RIG-I	RIG-I , rs2274863, DEAD,p21.1
SNP_A-1996550	gtacagatggagggac[A/G]gatgagacagctgccc	A	G	NM_182739 // upstream // 420 // Hs.493668 // NDUFB6 // 4712 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa (NDUFB6), nuclear gene encoding mitochondrial protein, /// NM_002493 // upstream // 420 // Hs.493668 // NDUFB6 // 4712	NDUFB6	NDUFB6, Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa (NDUFB6), nuclear gene encoding mitochondrial protein, p21.1
SNP_A-2097649	agagaatgtggaaaaa[A/C]aacagacatatttgc	A	C	NM_212558 // downstream // 31282 // Hs.522063 // LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 // downstream // 153930 // Hs.20158 // APTX // 54840 // Homo sapiens aprataxin (APTX), transcript variant 1,	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-1905375	tggtaacgtggatgaa[C/T]tgtatagtgaagtctg	C	T	NM_212558 // downstream // 39455 // Hs.522063 // LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 // downstream // 145757 // Hs.20158 // APTX // 54840 // Homo sapiens aprataxin (APTX), transcript variant 1,	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-1922761	ttagaggtatgacata[A/G]atgttctctttcactc	A	G	NM_212558 // downstream // 93171 // Hs.522063 // LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 // downstream // 92041 // Hs.20158 // APTX // 54840 // Homo sapiens aprataxin (APTX), transcript variant 1, m	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-1887464	tgagaccatctggcac[A/G]aaggcttcatctgtga	A	G	NM_212558 // downstream // 98667 // Hs.522063 // LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 // downstream // 86545 // Hs.20158 // APTX // 54840 // Homo sapiens aprataxin (APTX), transcript variant 1, m	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1
SNP_A-2067865	acaacccataaaacag[C/G]atggaaagctcctta	C	G	NM_212558 // downstream // 161821 // Hs.522063 // LOC401498 // 401498 // Homo sapiens similar to RIKEN A930001M12 (LOC401498), mRNA. /// NM_175073 // downstream // 23391 // Hs.20158 // APTX // 54840 // Homo sapiens aprataxin (APTX), transcript variant 1,	LOC401498	LOC401498, Homo sapiens similar to RIKEN A930001M12 (LOC401498), p21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2075757	acatggtcactaggaa[A/G]ctcttgggcctcactt	A	G	NM_001497 // intron // 0 // Hs.272011 // B4GALT1 // 2683 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// ENST00000199168 // intron // 0 // — // — // —	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-2239069	ctcttctgctgtgaga[A/G]actctaatcatgtaag	A	G	NM_001497 // intron // 0 // Hs.272011 // B4GALT1 // 2683 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// ENST00000199168 // intron // 0 // — // — // —	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-1643071	ctccaattgggaagcacactttg[C/G]agaagcactctttaggt ggtgccc	C	G	NM_001497 // intron // 0 // Hs.396798 // B4GALT1 // 2683 // UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	B4GALT1	B4GALT1, rs10511909, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1,p21.1
SNP_A-1785357	ggctatattattgca[C/T]ccagtcctgcagcgcc	C	T	NM_001497 // CDS // 0 // Hs.272011 // B4GALT1 // 2683 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// ENST00000199168 // CDS // 0 // — // — // —	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-2230961	ctatgggccaaacta[C/T]agcctcagctggcagg	C	T	NM_001497 // upstream // 19552 // Hs.272011 // B4GALT1 // 2683 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// NM_014471 // upstream // 53408 // Hs.546367 // SPINK4 // 27290 // Homo sapiens serine pro	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-2303507	gctcaacctatcaa[C/T]cctgaaggctttctgt	C	T	NM_001497 // upstream // 36366 // Hs.272011 // B4GALT1 // 2683 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA. /// NM_014471 // upstream // 36594 // Hs.546367 // SPINK4 // 27290 // Homo sapiens serine pro	B4GALT1	B4GALT1, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), p21.1
SNP_A-2212149	ccctgctcgcttctca[A/T]gaaccgtgggagccc	A	T	NM_004925 // upstream // 2093 // Hs.234642 // AQP3 // 360 // Homo sapiens aquaporin 3 (AQP3), mRNA. /// NM_139235 // downstream // 11671 // Hs.493709 // NOL6 // 65083 // Homo sapiens nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant g	AQP3	AQP3, Homo sapiens aquaporin 3 (AQP3), p13.3
SNP_A-2206472	ccatctgcctgtgctg[A/G]atggcccctgagcaaa	A	G	NM_004925 // upstream // 13709 // Hs.234642 // AQP3 // 360 // Homo sapiens aquaporin 3 (AQP3), mRNA. /// NM_139235 // downstream // 55 // Hs.493709 // NOL6 // 65083 // Homo sapiens nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant gam	AQP3	AQP3, Homo sapiens aquaporin 3 (AQP3), p13.3
SNP_A-2199716	ccaaaatgaaaaagta[A/G]cgatgctggcagttg	A	G	X72781 // intron // 0 // Hs.435699 // PRSS3 // 5646 // Homo sapiens mRNA for trypsinogen IV a-form. /// ENST00000011477 // intron // 0 // — // — // — /// ENST00000342836 // intron // 0 // — // — // —	PRSS3	PRSS3, Homo sapiens for trypsinogen IV a-form. ,p13.3
SNP_A-1828710	taagctgaacttttct[A/C]agacacctagaatgaa	A	C	NM_020867 // intron // 0 // Hs.493739 // UBAP2 // 55833 // Homo sapiens ubiquitin associated protein 2 (UBAP2), transcript variant 2, mRNA. /// NM_018449 // intron // 0 // Hs.493739 // UBAP2 // 55833 // Homo sapiens ubiquitin associated protein 2 (UBAP2),	UBAP2	UBAP2, Homo sapiens ubiquitin associated protein 2 (UBAP2), transcript variant 2, p13.3
SNP_A-1996584	gagccttgttttaaa[C/T]ggctctagtgattaa	C	T	NM_016525 // intron // 0 // Hs.268963 // UBAP1 // 51271 // Homo sapiens ubiquitin associated protein 1 (UBAP1), mRNA. /// ENST00000356235 // intron // 0 // — // — // — // — // — /// ENST00000359544 // intron // 0 // — // — // — /// ENST000	UBAP1	UBAP1, Homo sapiens ubiquitin associated protein 1 (UBAP1), p13.3
SNP_A-2181283	cagaccgaggagttg[C/G]accgaggtgagaaagg	C	G	NM_001161 // upstream // 394 // Hs.493767 // NUDT2 // 318 // Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 2 (NUDT2), transcript variant 1, mRNA. /// NM_147172 // upstream // 394 // Hs.493767 // NUDT2 // 318 // Homo sapiens nudix	NUDT2	NUDT2, Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 2 (NUDT2), transcript variant 1, p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2310273	ggaaccaggtaaatga[A/G]gactggaacagagctc	A	G	NM_147202 // intron // 0 // Hs.493771 // C9orf25 // 203259 // Homo sapiens chromosome 9 open reading frame 25 (C9orf25), mRNA. /// ENST00000297620 // intron // 0 // --- // --- // --- // --- /// ENST00000359556 // intron // 0 // --- // --- // --- // ---	C9orf25	C9orf25, Homo sapiens chromosome 9 open reading frame 25 (C9orf25), p13.3
SNP_A-2199946	ccaaagatttatgaac[C/G]agtgcaggccaggctc	C	G	NM_147202 // intron // 0 // Hs.493771 // C9orf25 // 203259 // Homo sapiens chromosome 9 open reading frame 25 (C9orf25), mRNA. /// ENST00000297620 // intron // 0 // --- // --- // --- // --- /// ENST00000359556 // intron // 0 // --- // --- // --- // ---	C9orf25	C9orf25, Homo sapiens chromosome 9 open reading frame 25 (C9orf25), p13.3
SNP_A-1706453	acaggcacctccatatcacatgcat[C/T]ctcacatgcacaatcctagaggcac	C	T	NM_001842 // intron // 0 // Hs.194774 // CNTFR // 1271 // ciliary neurotrophic factor receptor /// NM_147164 // intron // 0 // Hs.194774 // CNTFR // 1271 // ciliary neurotrophic factor receptor	CNTFR	CNTFR , rs1080750, ciliary neurotrophic factor receptor ,p13.3
SNP_A-2114226	agggaagaacaaacca[C/G]gtagacacacttagtc	C	G	NM_002989 // upstream // 115002 // Hs.57907 // CCL21 // 6366 // Homo sapiens chemokine (C-C motif) ligand 21 (CCL21), mRNA. /// ENST00000259607 // upstream // 115002 // --- // --- // --- /// ENST00000291050 // downstream // 5116 // --- // --- // --	CCL21	CCL21, Homo sapiens chemokine (C-C motif) ligand 21 (CCL21), p13.3
SNP_A-1824165	taaacaggttacagaa[A/T]ttcggctagcactaag	A	T	ENST00000338774 // 3UTR // 0 // --- // --- // --- /// ENST00000242315 // 3UTR // 0 // --- // --- // ---	-	p13.3
SNP_A-1799936	gtacaggcatggataa[C/G]gaatctctacatatct	C	G	NM_012266 // 3UTR // 0 // Hs.237506 // DNAJB5 // 25822 // Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 5 (DNAJB5), mRNA. /// ENST00000312316 // 3UTR // 0 // --- // --- // --- /// ENST00000335998 // 3UTR // 0 // --- // --- // ---	DNAJB5	DNAJB5, Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 5 (DNAJB5), p13.3
SNP_A-1895252	tgcccggtcttaaata[C/G]agtccagcaaacagcc	C	G	NM_013442 // upstream // 568 // Hs.3439 // STOML2 // 30968 // Homo sapiens stomatin (EPB72)-like 2 (STOML2), mRNA. /// NM_025182 // downstream // 387 // Hs.301696 // KIAA1539 // 80256 // Homo sapiens KIAA1539 (KIAA1539), mRNA. /// NM_025182 // downstream	STOML2	STOML2, Homo sapiens stomatin (EPB72)-like 2 (STOML2), p13.3
SNP_A-2305270	gctgagcctggacata[A/G]cctggtaagactagaa	A	G	ENST00000354349 // intron // 0 // --- // --- // ---	-	p13.3
SNP_A-2229847	ctagttactttggata[C/T]gattatagacttggtc	C	T	NM_001833 // intron // 0 // Hs.522114 // CLTA // 1211 // Homo sapiens clathrin, light polypeptide (Lca) (CLTA), transcript variant nonbrain, mRNA. /// NM_007096 // intron // 0 // Hs.522114 // CLTA // 1211 // Homo sapiens clathrin, light polypeptide (Lca)	CLTA	CLTA, Homo sapiens clathrin, light polypeptide (Lca) (CLTA), transcript variant nonbrain, p13.3
SNP_A-2281999	gagtggacgagtaaca[G/T]ctggagagaggtgtgg	G	T	NM_005476 // intron // 0 // Hs.5920 // GNE // 10020 // Homo sapiens glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (GNE), mRNA. /// ENST00000339267 // intron // 0 // --- // --- // ---	GNE	GNE, Homo sapiens glucosamine (UDP-N-acetyl)-2-epimerase,p13.2
SNP_A-1825193	taaagtagttcactta[C/G]gggtggaccatgcaac	C	G	NM_005476 // upstream // 23683 // Hs.5920 // GNE // 10020 // Homo sapiens glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (GNE), mRNA. /// ENST00000339267 // upstream // 23683 // --- // --- // --- // --- /// ENST00000310176 // downstream	GNE	GNE, Homo sapiens glucosamine (UDP-N-acetyl)-2-epimerase,p13.2
SNP_A-2109760	aggaaatcgaacccga[G/T]attgtagaagtgactt	G	T	NM_194330 // downstream // 29584 // Hs.333503 // RNF38 // 152006 // Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, mRNA. /// NM_194328 // downstream // 29584 // Hs.333503 // RNF38 // 152006 // Homo sapiens ring finger protein 38 (RNF38	RNF38	RNF38, Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, p13.2
SNP_A-1908655	tgtaggaactaccaac[A/G]aactcagctccctgca	A	G	NM_194330 // downstream // 29241 // Hs.333503 // RNF38 // 152006 // Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, mRNA. /// NM_194328 // downstream // 29241 // Hs.333503 // RNF38 // 152006 // Homo sapiens ring finger protein 38 (RNF38	RNF38	RNF38, Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1892845	tgcacatttccacaga[G/T]gtatgtttcccaagtt	G	T	NM_194330 // downstream // 25615 // Hs.333503 // RNF38 // 152006 // Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, mRNA. /// NM_194328 // downstream // 25615 // Hs.333503 // RNF38 // 152006 // Homo sapiens ring finger protein 38 (RNF38	RNF38	RNF38, Homo sapiens ring finger protein 38 (RNF38), transcript variant 5, p13.2
SNP_A-2308067	gcttgacagaaatagat[A/T]caaacctaagtccgga	A	T	NM_014791 // downstream // 101403 // Hs.184339 // MELK // 9833 // Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA. /// NM_016734 // downstream // 59456 // Hs.126365 // PAX5 // 5079 // Homo sapiens paired box gene 5 (B-cell lineage speci	MELK	MELK, Homo sapiens maternal embryonic leucine zipper kinase (MELK), p13.2
SNP_A-2257941	ctttgtcacgcattca[A/C]cctgtctctcatcaac	A	C	NM_014791 // downstream // 104809 // Hs.184339 // MELK // 9833 // Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA. /// NM_016734 // downstream // 56050 // Hs.126365 // PAX5 // 5079 // Homo sapiens paired box gene 5 (B-cell lineage speci	MELK	MELK, Homo sapiens maternal embryonic leucine zipper kinase (MELK), p13.2
SNP_A-2297693	gccagctccgggtccc[A/G]aataaaacatgtggtc	A	G	NM_016734 // intron // 0 // Hs.126365 // PAX5 // 5079 // Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0 // -- // -- // -- /// ENST00000358127 // intron // 0 // -- // -- // --	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-2273180	gactcaccagggaaat[A/C]acttactggtgttga	A	C	NM_016734 // intron // 0 // Hs.126365 // PAX5 // 5079 // Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0 // -- // -- // -- /// ENST00000358127 // intron // 0 // -- // -- // --	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-2263979	gaactcaagagtaaga[C/T]gttcttgggaatttcc	C	T	NM_016734 // intron // 0 // Hs.126365 // PAX5 // 5079 // Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), mRNA. /// ENST00000354465 // intron // 0 // -- // -- // -- /// ENST00000358127 // intron // 0 // -- // -- // --	PAX5	PAX5, Homo sapiens paired box gene 5 (B-cell lineage specific activator) (PAX5), p13.2
SNP_A-1787609	gggacaaaggaagaga[A/G]atgctgtcaaaatcat	A	G	NM_032226 // upstream // 63696 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// NM_032226 // upstream // 63817 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-1804735	gtcaggtttaatgaa[G/T]tgggataaaccacaca	G	T	NM_032226 // upstream // 19987 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// NM_032226 // upstream // 20108 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-1876950	tctgcctactgttgac[A/G]ctgaatcctgggcagt	A	G	NM_032226 // upstream // 4019 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// NM_032226 // upstream // 4140 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZC	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-1837248	tacttacagtatttggt[C/T]accgttacatgctgta	C	T	NM_032226 // intron // 0 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// ENST00000359025 // intron // 0 // -- // -- // -- /// ENST00000322831 // intron // 0 // -- // -- // --	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-1886422	tgacgatctgagctta[A/T]aatattccgtatacta	A	T	NM_032226 // intron // 0 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// ENST00000359025 // intron // 0 // -- // -- // -- /// ENST00000322831 // intron // 0 // -- // -- // --	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2
SNP_A-2251572	cttcaggaagacataa[C/T]ggaatccatagcctct	C	T	NM_032226 // intron // 0 // Hs.522118 // ZCCHC7 // 84186 // Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), mRNA. /// ENST00000359025 // intron // 0 // -- // -- // -- /// ENST00000322831 // intron // 0 // -- // -- // --	ZCCHC7	ZCCHC7, Homo sapiens zinc finger, CCHC domain containing 7 (ZCCHC7), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1809738	gtgaggaatatcataa[G/T]tagatcagtgttgggt	G	T	NM_022490 // downstream // 22755 // Hs.446334 // PAF53 // 64425 // Homo sapiens RNA polymerase I associated factor 53 (PAF53), mRNA. /// AF176705 // downstream // 5455 // Hs.130774 // FBXO10 // 26267 // Homo sapiens F-box protein FBX10 mRNA, partial cds.	PAF53	PAF53, Homo sapiens RNA polymerase I associated factor 53 (PAF53), p13.2
SNP_A-2055823	aatacaaagggataaa[C/T]cattgatgtagacaag	C	T	AF176705 // intron // 0 // Hs.130774 // FBXO10 // 26267 // Homo sapiens F-box protein FBX10 mRNA, partial cds. /// ENST00000276960 // intron // 0 // — // — // — // —	FBXO10	FBXO10, Homo sapiens F-box protein FBX10 partial cds. p13.2
SNP_A-1867532	tccgctctgtgtctta[A/C]acctttacataagggg	A	C	NM_003028 // intron // 0 // Hs.521482 // SHB // 6461 // Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// ENST00000262512 // intron // 0 // — // — // — // —	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-1746797	cccacccaatctttgcagggcttta[C/T]gactctgctccttggaca cttgcca	C	T	NM_000692 // upstream // 141018 // Hs.436219 // ALDH1B1 // 219 // aldehyde dehydrogenase 1 family, member B1 /// NM_003028 // upstream // 182476 // Hs.379206 // SHB // 6461 // SHB (Src homology 2 domain containing) adaptor protein B	ALDH1B1	ALDH1B1 , rs10511947, aldehyde dehydrogenase 1 family, member B1 ,p13.1
SNP_A-2310265	ggaaccagaagcccag[C/T]ctactctcttattgtt	C	T	NM_003028 // upstream // 194202 // Hs.521482 // SHB // 6461 // Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// NM_000692 // upstream // 129599 // Hs.436219 // ALDH1B1 // 219 // Homo sapiens aldehyde dehydrogenase 1 f	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-1996658	cacaaatagaaaactc[A/G]ctgagtcctgcttgca	A	G	NM_003028 // upstream // 243809 // Hs.521482 // SHB // 6461 // Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), mRNA. /// NM_000692 // upstream // 79992 // Hs.436219 // ALDH1B1 // 219 // Homo sapiens aldehyde dehydrogenase 1 fa	SHB	SHB, Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB), p13.2
SNP_A-2080741	acctccagctttccca[C/G]gaaacttggttggacc	C	G	ENST00000356201 // intron // 0 // — // — // — // —	-	q12
SNP_A-2228263	ctactctttcattctc[G/T]aacacagataaaatca	G	T	NM_003558 // intron // 0 // Hs.534371 // PIP5K1B // 8395 // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), mRNA. /// ENST00000265382 // intron // 0 // — // — // — // —	PIP5K1B	PIP5K1B, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), q13
SNP_A-1850884	tattagttgccttcag[A/G]acaaagaaaaggcgag	A	G	NM_201629 // intron // 0 // Hs.50382 // TJP2 // 9414 // Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), transcript variant 2, mRNA. /// NM_004817 // intron // 0 // Hs.50382 // TJP2 // 9414 // Homo sapiens tight junction protein 2 (zona oc	TJP2	TJP2, Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), transcript variant 2, q21.11
SNP_A-2074395	acatacggagtcctga[A/G]cttcaaacacatgcct	A	G	NM_201629 // intron // 0 // Hs.50382 // TJP2 // 9414 // Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), transcript variant 2, mRNA. /// NM_004817 // intron // 0 // Hs.50382 // TJP2 // 9414 // Homo sapiens tight junction protein 2 (zona oc	TJP2	TJP2, Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), transcript variant 2, q21.11
SNP_A-1720297	aagccatgcaggcttatagtatgca[A/G]ccttatatccatcagcc aaagctat	A	G	NM_024971 // intron // 0 // Hs.288911 // TRPM3 // 80036 // transient receptor potential cation channel, subfamily M, member 3	TRPM3	TRPM3 , rs688933, transient receptor potential cation channel, subfamily M, member 3,q21.11
SNP_A-2091299	acttttccatagtaac[A/G]gtgattgtgttattgg	A	G	NM_004816 // intron // 0 // Hs.118003 // C9orf61 // 9413 // Homo sapiens chromosome 9 open reading frame 61 (C9orf61), mRNA. /// ENST00000257515 // intron // 0 // — // — // — // —	C9orf61	C9orf61, Homo sapiens chromosome 9 open reading frame 61 (C9orf61), q21.11
SNP_A-2244791	ctggatgacatggctt[G/T]aacaggtgaactgcac	G	T	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-1936712	ttctttaaaaattaca[C/G]agttttgccaaatcca	C	G	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1797478	ggtttatccagctttaj[C/T]ctctttctcacacca	C	T	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2029379	aaagacaacagatataaa[C/T]cttcattaaatctaca	C	T	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2174611	cacagatgagtaacad[A/G]aaccactgatccagac	A	G	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-1918833	ttaacaggcatagaa[G/T]ctgggtcgacggtta	G	T	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2039715	aacatggtaagtgcca[C/T]atacaaacatgaacag	C	T	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2210012	ccccacggcgattgat[C/T]accaaagcctatgatt	C	T	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-1789269	gggcattgtcagtggg[A/G]aatattcttcctgaag	A	G	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-1814819	gtgtgtgtaaggttac[A/G]atggcccttgtgcaag	A	G	NM_001163 // intron // 0 // Hs.70843 // APBA1 // 320 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), mRNA. /// ENST00000265381 // intron // 0 // — // — // — // —	APBA1	APBA1, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 1 (X11) (APBA1), q21.11
SNP_A-2291045	gcaagtttgctcaattc[C/T]atatccaggcagctgt	C	T	ENST00000297751 // intron // 0 // — // — // —	-	q21.11
SNP_A-1996728	ctgttttaggtcac[C/T]ggattgcctgccacag	C	T	ENST00000297751 // CDS // 0 // — // — // —	-	q21.11
SNP_A-1811627	gtgctgccgtgttcct[C/T]agagcaagaaggttgt	C	T	ENST00000297751 // intron // 0 // — // — // —	-	q21.11
SNP_A-2240902	ctgagacattagcatc[G/T]ataaaaccttggtac	G	T	ENST00000297751 // intron // 0 // — // — // —	-	q21.11
SNP_A-1996729	taatcgatcagagatg[C/G]aagcagttcaaattgt	C	G	ENST00000297751 // intron // 0 // — // — // —	-	q21.11
SNP_A-1857984	tcactgtctgaattat[C/T]attagctttcaaatcc	C	T	ENST00000297751 // intron // 0 // — // — // —	-	q21.11
SNP_A-2211862	ccctcttaaaatttga[A/G]gaagctataaaccctc	A	G	NM_153267 // upstream // 59117 // Hs.546524 // MAMDC2 // 256691 // Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// NM_001001704 // downstream // 218673 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST0	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11
SNP_A-2220436	cctctaccatgaaca[C/T]gaagcagaagaatgaa	C	T	NM_153267 // upstream // 25724 // Hs.546524 // MAMDC2 // 256691 // Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// NM_001001704 // downstream // 185280 // Hs.34198 // FLJ44796 // 401209 // Homo sapiens FLJ44796 protein (FLJ44796), mRNA. /// ENST0	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11
SNP_A-1883451	ggcgtgcaggaagtg[A/C]gtttgaatatgtca	A	C	NM_153267 // intron // 0 // Hs.546524 // MAMDC2 // 256691 // Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// ENST00000324072 // intron // 0 // — // — // — // —	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11
SNP_A-2174190	cacactactctgtact[C/G]aaaaaacatttcaaat	C	G	NM_153267 // intron // 0 // Hs.546524 // MAMDC2 // 256691 // Homo sapiens MAM domain containing 2 (MAMDC2), mRNA. /// ENST00000324072 // intron // 0 // — // — // — // —	MAMDC2	MAMDC2, Homo sapiens MAM domain containing 2 (MAMDC2), q21.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1913781	tgtgtcaggctgcatc[A/G]atacatattcaataaa	A	G	NM_001206 // upstream // 58063 // Hs.150557 // KLF9 // 687 // Homo sapiens basic transcription element binding protein 1 (BTEB1), mRNA. /// NM_206944 // downstream // 63266 // Hs.47288 // TRPM3 // 80036 // Homo sapiens transient receptor potential cation	KLF9	KLF9, Homo sapiens basic transcription element binding protein 1 (BTEB1), q21.11
SNP_A-2076416	acattgtggcctcaag[C/T]caagtcagtatttaat	C	T	ENST00000354500 // intron // 0 // — // — // — // —	-	q21.11
SNP_A-2152050	attaaaaagtgtaaaa[C/T]gccatgaagatgaaca	C	T	ENST00000354500 // intron // 0 // — // — // — // —	-	q21.11
SNP_A-1887164	tgagaaaggtactgta[A/C]attctaaacttatgcc	A	C	ENST00000354500 // intron // 0 // — // — // — // —	-	q21.12
SNP_A-1915400	tgttcccaatgggata[C/T]attatgctgaaagatc	C	T	ENST00000354500 // intron // 0 // — // — // — // —	-	q21.12
SNP_A-1839296	tagagtataattctta[C/T]gagtgtgagctctaaa	C	T	ENST00000354500 // intron // 0 // — // — // — // —	-	q21.12
SNP_A-1948470	tttagtctgaattaca[A/C]ggtttttacctaaaag	A	C	NM_206944 // upstream // 638394 // Hs.47288 // TRPM3 // 80036 // Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, mRNA. /// NM_206945 // upstream // 638394 // Hs.47288 // TRPM3 // 80036 // Homo	TRPM3	TRPM3, Homo sapiens transient receptor potential cation channel, subfamily M, member 3 (TRPM3), transcript variant 3, q21.13
SNP_A-2206044	ccatattctcatcaga[A/T]catttgttttcagaag	A	T	NM_013390 // downstream // 29769 // Hs.494146 // TMEM2 // 23670 // Homo sapiens transmembrane protein 2 (TMEM2), mRNA. /// ENST00000325310 // upstream // 92248 // — // — // — // — /// ENST00000344560 // downstream // 29769 // — // — // — //	TMEM2	TMEM2, Homo sapiens transmembrane protein 2 (TMEM2), q21.13
SNP_A-2059417	aatctacgcttgaaaa[C/T]gcctttaaactcaatg	C	T	NM_198394 // downstream // 69917 // Hs.534190 // C9orf85 // 138241 // Homo sapiens chromosome 9 open reading frame 85 (C9orf85), transcript variant 2, mRNA. /// NM_182505 // downstream // 69917 // Hs.534190 // C9orf85 // 138241 // Homo sapiens chromosome	C9orf85	C9orf85, Homo sapiens chromosome 9 open reading frame 85 (C9orf85), transcript variant 2, q21.13
SNP_A-1692916	aaacacttgagtgtattggaatgga[C/T]aagattatagataagtattggaaa	C	T	NM_000700 // downstream // 892431 // Hs.287558 // ANXA1 // 301 // annexin A1 /// NM_006914 // upstream // 434561 // Hs.117956 // RORB // 6096 // RAR-related orphan receptor B	ANXA1	ANXA1 , rs3000646, annexin A1 ,q21.13
SNP_A-1854543	tcaaattgtcctattc[G/T]caactctaaatatgtc	G	T	NM_006007 // upstream // 17150 // Hs.406096 // ZA20D2 // 7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 234235 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRNA	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-1996806	acaagtcataagaaca[A/G]acaatctgccaagaac	A	G	NM_006007 // upstream // 66672 // Hs.406096 // ZA20D2 // 7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 184713 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRNA	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-2154491	attattctcacagata[C/T]gttttgacctcctagc	C	T	NM_006007 // upstream // 111877 // Hs.406096 // ZA20D2 // 7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 139508 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRN	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-2268473	gaatggcagacaccaa[A/G]ctatgatcttcaacag	A	G	NM_006007 // upstream // 117297 // Hs.406096 // ZA20D2 // 7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 134088 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRN	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-1887819	tgagatgcaaagataa[C/T]taagtcacagactctg	C	T	NM_006007 // upstream // 151085 // Hs.406096 // ZA20D2 // 7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 100300 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRN	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101502	agatgaatatctggta[A/G]cacctcacagaggaga	A	G	NM_006007 // upstream // 245813 // Hs.406096 // ZA20D2 // 7763 // Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), mRNA. /// NM_138691 // upstream // 5572 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRNA.	ZA20D2	ZA20D2, Homo sapiens zinc finger, A20 domain containing 2 (ZA20D2), q21.13
SNP_A-1816441	gttagcgtctgcatac[C/T]catccacaaaatggga	C	T	NM_138691 // intron // 0 // Hs.371614 // TMC1 // 117531 // Homo sapiens transmembrane channel-like 1 (TMC1), mRNA. /// ENST00000340019 // intron // 0 // — // — // — // — /// ENST00000297784 // intron // 0 // — // — // — // —	TMC1	TMC1, Homo sapiens transmembrane channel-like 1 (TMC1), q21.13
SNP_A-1900538	tggagctgattcgatc[G/T]gacaagtgttgaagct	G	T	NM_000700 // downstream // 402949 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 402949 // — // — // — // — /// ENST00000360687 // upstream // 924008 // — // — // — // — /// ENST	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2098337	agagatgtttcctgag[A/C]atatgttctaacctct	A	C	NM_000700 // downstream // 730984 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 730984 // — // — // — // — /// ENST00000360687 // upstream // 595973 // — // — // — // — /// ENST	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1996844	aagtatttaacgaaaa[A/G]ggatagacatacctca	A	G	NM_000700 // downstream // 892141 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 892141 // — // — // — // — /// ENST00000360687 // upstream // 434816 // — // — // — // — /// ENST	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1906250	tggtgagattaccaca[A/T]atgttagccactggca	A	T	NM_000700 // downstream // 954628 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 954628 // — // — // — // — /// ENST00000360687 // upstream // 372329 // — // — // — // — /// ENST	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1905715	tggtatgtgggacaaa[C/T]gaagcattctacccta	C	T	NM_000700 // downstream // 972757 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 972757 // — // — // — // — /// ENST00000360687 // upstream // 354200 // — // — // — // — /// ENST	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1924014	ttagtggcaggaacta[C/T]cttagtcattttgata	C	T	NM_000700 // downstream // 979342 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 979342 // — // — // — // — /// ENST00000360687 // upstream // 347615 // — // — // — // — /// ENST	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1822914	taaaaagtggcagaaa[C/T]tgaatagaaaaccaag	C	T	NM_000700 // downstream // 1014510 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1014510 // — // — // — // — /// ENST00000360687 // upstream // 312447 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1793623	ggtatctcagtaggtg[A/G]cacactccaacagtca	A	G	NM_000700 // downstream // 1048170 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1048170 // — // — // — // — /// ENST00000360687 // upstream // 278787 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1898002	tgctgtcacctctcac[C/T]gtgacaggtatgattt	C	T	NM_000700 // downstream // 1106105 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1106105 // — // — // — // — /// ENST00000360687 // upstream // 220852 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2307187	gcttaagcaaattatg[C/T]cagcctacgtgaagtg	C	T	NM_000700 // downstream // 1121884 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1121884 // — // — // — // — /// ENST00000360687 // upstream // 205073 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2191529	catatgcaaattacca[C/G]tctagagcagtgtttt	C	G	NM_000700 // downstream // 1123300 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1123300 // — // — // — // — /// ENST00000360687 // upstream // 203657 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2014273	gcttcttttccagaaa[A/T]atatgctatgtgattc	A	T	NM_000700 // downstream // 1128068 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1128068 // — // — // — // — /// ENST00000360687 // upstream // 198889 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2103932	agcactgctttacctg[C/G]atctcataatttttga	C	G	NM_000700 // downstream // 1140376 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1140376 // — // — // — // — /// ENST00000360687 // upstream // 186581 // — // — // — // — /// EN	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2306101	gctggacttcaaacta[A/G]accattctggattcca	A	G	NM_000700 // downstream // 1249672 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1249672 // — // — // — // — /// ENST00000360687 // upstream // 77285 // — // — // — // — /// ENS	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2195964	catgtcctaggaagta[G/T]ctttttctcatattt	G	T	NM_000700 // downstream // 1250123 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1250123 // — // — // — // — /// ENST00000360687 // upstream // 76834 // — // — // — // — /// ENS	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-2128895	ataatgctgctggcaa[C/T]tgaatttttcagtgt	C	T	NM_000700 // downstream // 1273630 // Hs.494173 // ANXA1 // 301 // Homo sapiens annexin A1 (ANXA1), mRNA. /// ENST00000257497 // downstream // 1273630 // — // — // — // — /// ENST00000360687 // upstream // 53327 // — // — // — // — /// ENS	ANXA1	ANXA1, Homo sapiens annexin A1 (ANXA1), q21.13
SNP_A-1785315	ggctagtaatggtcag[C/G]aacatgtctcaaaacc	C	G	ENST00000360687 // intron // 0 // — // — // — // — /// ENST00000354796 // intron // 0 // — // — // — // —	-	q21.13
SNP_A-2245264	ctggctctgcaatcta[A/C]ctgaagctgaaaaggg	A	C	NM_017662 // intron // 0 // Hs.272225 // TRPM6 // 140803 // Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), mRNA. /// ENST00000360774 // intron // 0 // — // — // — // — /// ENST00000262403 // intron // 0 //	TRPM6	TRPM6, Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), q21.13
SNP_A-2130767	atacttcagaagctcc[G/T]gactaaaagcctctaa	G	T	NM_017662 // intron // 0 // Hs.272225 // TRPM6 // 140803 // Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), mRNA. /// ENST00000360774 // intron // 0 // — // — // — // — /// ENST00000262403 // intron // 0 //	TRPM6	TRPM6, Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), q21.13
SNP_A-1996866	ttcactcctttaggaa[C/T]gaaatcttacctctat	C	T	NM_012383 // downstream // 21329 // Hs.494192 // OSTF1 // 26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 722204 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2283421	gataccgcaggaaaaa[C/T]gaaatgtgacacccat	C	T	NM_012383 // downstream // 468251 // Hs.494192 // OSTF1 // 26578 // Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /// NM_006200 // upstream // 275282 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5	OSTF1	OSTF1, Homo sapiens osteoclast stimulating factor 1 (OSTF1), q21.13
SNP_A-2224014	cggggctggctgacaa[C/T]aagtaacgaaccataa	C	T	NM_006200 // downstream // 7063 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 185052 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. ///	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin q21.13
SNP_A-2078280	accataagcctgctca[A/G]tcaccatctttttctcc	A	G	NM_006200 // downstream // 7757 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 184358 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. ///	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin,q21.13
SNP_A-2134348	atatgctgagctaaag[G/T]cttcatatggttatt	G	T	NM_006200 // downstream // 7917 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 184198 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. ///	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin,q21.13
SNP_A-2190081	cataagatatagatga[G/T]agaccagagaaggtg	G	T	NM_006200 // downstream // 91826 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 100269 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. //	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin q21.13
SNP_A-2181590	cagagaaggtgactgg[A/G]ccaaaaggttgagatt	A	G	NM_006200 // downstream // 91848 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 100267 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. //	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin q21.13
SNP_A-1664770	ggagagatctggaaatttcctataaa[A/C]gcaagaaagactatga actaacgca	A	C	NM_002072 // upstream // 70509 // Hs.469951 // GNAQ // 2776 // guanine nucleotide binding protein (G protein), q polypeptide	GNAQ	GNAQ , rs4877178, guanine nucleotide binding protein (G protein), q polypeptide,q21.2
SNP_A-1652474	tctagaacatgaatactatgctcac[A/G]agtaaacctgctccaa gggatactt	A	G	NM_002072 // upstream // 71205 // Hs.469951 // GNAQ // 2776 // guanine nucleotide binding protein (G protein), q polypeptide	GNAQ	GNAQ, rs10512069, guanine nucleotide binding protein (G protein), q polypeptide,q21.2
SNP_A-2155408	attcatgatttatgca[C/T]tgagtattgcagtcct	C	T	NM_006200 // downstream // 157041 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 35074 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. //	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin q21.13
SNP_A-2253307	cttctggccctttaacd[A/C]aaaacttgatgacttg	A	C	NM_006200 // downstream // 179310 // Hs.368542 // PCSK5 // 5125 // Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), mRNA. /// NM_018339 // downstream // 12805 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. //	PCSK5	PCSK5, Homo sapiens proprotein convertase subtilisin q21.13
SNP_A-1780325	ggataaagctgaggt[C/G]aacaggactggtatca	C	G	NM_018339 // upstream // 20365 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. /// NM_001490 // upstream // 44348 // Hs.521568 // GCNT1 // 2650 // Homo sapiens glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylgluc	RFK	RFK, Homo sapiens riboflavin kinase (RFK), q21.13
SNP_A-2280503	gaggtaaatgttttta[C/T]gtcaactgaacaaaac	C	T	NM_018339 // upstream // 22994 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. /// NM_001490 // upstream // 41719 // Hs.521568 // GCNT1 // 2650 // Homo sapiens glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylgluc	RFK	RFK, Homo sapiens riboflavin kinase (RFK), q21.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2261083	gaaagacaatattaaa[C/G]taaggatgggcacagt	C	G	NM_018339 // upstream // 38126 // Hs.37558 // RFK // 55312 // Homo sapiens riboflavin kinase (RFK), mRNA. /// NM_001490 // upstream // 26587 // Hs.521568 // GCNT1 // 2650 // Homo sapiens glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylgluc	RFK	RFK, Homo sapiens riboflavin kinase (RFK), q21.13
SNP_A-1921605	ttacctggtcaatgtc[C/T]atctatcctacttgac	C	T	NM_001490 // downstream // 34662 // Hs.521568 // GCNT1 // 2650 // Homo sapiens glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase) (GCNT1), mRNA. /// ENST00000335150 // downstream // 34662 // --- // --- // --- // --- /	GCNT1	GCNT1, Homo sapiens glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase) (GCNT1), q21.13
SNP_A-1750383	aaaatagagacatgacacaatatta[A/G]atttaaagccaggga cttagaagca	A	G	AB033087 // upstream // 1221231 // Hs.494269 // TLE4 // 7091 // transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) /// NM_021154 // downstream // 21389 // Hs.286049 // PSAT1 // 29968 // phosphoserine aminotransferase 1 /// NM_058179 // down	TLE4	TLE4 , rs10521484, transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) ,q21.2
SNP_A-2103078	agcaaatgcagtaatc[A/G]ctaagggtgcagatta	A	G	ENST00000223609 // intron // 0 // --- // --- // --- // ---	-	q21.2
SNP_A-2257081	ctttctcaccattaac[A/G]gagactgaaatgcaga	A	G	NM_138818 // downstream // 116312 // Hs.494217 // C9orf65 // 158471 // Homo sapiens chromosome 9 open reading frame 65 (C9orf65), mRNA. /// ENST00000223609 // upstream // 1474 // --- // --- // --- // --- /// ENST00000286521 // downstream // 116312 // ---	C9orf65	C9orf65, Homo sapiens chromosome 9 open reading frame 65 (C9orf65), q21.2
SNP_A-1895094	tgcccatacaacctca[A/G]tagctccacattactt	A	G	NM_004297 // intron // 0 // Hs.546329 // GNA14 // 9630 // Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// ENST00000286545 // intron // 0 // --- // --- // --- // ---	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-2178736	cactgaacatgaccag[G/T]aatattaattttgaac	G	T	NM_004297 // upstream // 10859 // Hs.546329 // GNA14 // 9630 // Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), mRNA. /// NM_002072 // downstream // 61118 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide bindi	GNA14	GNA14, Homo sapiens guanine nucleotide binding protein (G protein), alpha 14 (GNA14), q21.2
SNP_A-1801592	gtaggttccagtctta[C/T]cttctccctcattagc	C	T	NM_002072 // intron // 0 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // intron // 0 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2068091	acaagaaagtgttaga[C/T]aggtgttaactattgt	C	T	NM_002072 // intron // 0 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // intron // 0 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2292855	gcagaaagaacgcata[C/T]tataatgaaggagctc	C	T	NM_002072 // intron // 0 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // intron // 0 // --- // --- // --- // ---	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-1996925	tcaaatctttatccta[C/T]agggagtgctgacatt	C	T	NM_002072 // upstream // 20562 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 20562 // --- // --- // --- // --- /// ENST00000334729 // upstream //	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2245376	ctggcttttagggatg[A/G]catcaatggacttctt	A	G	NM_002072 // upstream // 38648 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 38648 // --- // --- // --- // --- /// ENST00000334729 // upstream //	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1996927	gtgccccctgaagtta[C/T]gcagtgtgatggacct	C	T	NM_002072 // upstream // 71757 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 71757 // --- // --- // --- /// ENST00000334729 // upstream //	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2233458	ctcagtctaatttac[A/G]cagcaggattgctcta	A	G	NM_002072 // upstream // 72600 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 72600 // --- // --- // --- /// ENST00000334729 // upstream //	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2098667	agagcccatgaccaca[A/G]gttttcattccgttc	A	G	NM_002072 // upstream // 72803 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 72803 // --- // --- // --- /// ENST00000334729 // upstream //	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-1996928	ctctgtctctggaga[C/T]attctgaagttccatc	C	T	NM_002072 // upstream // 108873 // Hs.269782 // GNAQ // 2776 // Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA. /// ENST00000286548 // upstream // 108873 // --- // --- // --- /// ENST00000334729 // upstream	GNAQ	GNAQ, Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), q21.2
SNP_A-2045957	aagaccctccataatc[C/T]gacttttattgaactt	C	T	ENST00000334729 // downstream // 51478 // --- // --- // --- /// ENST00000277082 // upstream // 5105 // --- // --- // ---	-	q21.2
SNP_A-2169332	caagcagagttgaaccc[C/T]cttaaatgatgcctct	C	T	NM_021154 // downstream // 16648 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // downstream // 16648 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotr	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.2
SNP_A-1996929	gactggatgaaaaaa[C/G]agtccaaagaataaga	C	G	NM_021154 // downstream // 19357 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // downstream // 19357 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotr	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.2
SNP_A-2139114	atcctcaatgtacagg[A/G]aaggaagagattggca	A	G	NM_021154 // downstream // 251889 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // downstream // 251889 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine amino	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.31
SNP_A-1858043	tcacttgagttagta[C/T]gcctctccgaggtttc	C	T	NM_021154 // downstream // 506384 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // downstream // 506384 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine amino	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.31
SNP_A-2243536	ctgctatatgatctcat[C/G]agaagtaacctaatct	C	G	NM_021154 // downstream // 530743 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, mRNA. /// NM_058179 // downstream // 530743 // Hs.494261 // PSAT1 // 29968 // Homo sapiens phosphoserine amino	PSAT1	PSAT1, Homo sapiens phosphoserine aminotransferase 1 (PSAT1), transcript variant 2, q21.31
SNP_A-2065344	aattgtatttttctga[A/T]catttgaatttagcat	A	T	ENST00000331400 // upstream // 109351 // --- // --- // --- /// ENST00000335028 // upstream // 244254 // --- // --- // ---	-	q21.31
SNP_A-2177065	cacctccactgtttc[A/T]atctcagtggagcaga	A	T	ENST00000331400 // upstream // 109461 // --- // --- // --- /// ENST00000335028 // upstream // 244144 // --- // --- // ---	-	q21.31
SNP_A-1649858	ttgagccatgttaatggaatatcct[A/G]aataagaaccccattctttttcatt	A	G	NM_005077 // downstream // 639863 // Hs.406491 // TLE1 // 7088 // transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) /// NM_007005 // downstream // 1217082 // Hs.494269 // TLE4 // 7091 // transducin-like enhancer of split 4 (E(sp1) homolog,	TLE1	TLE1, rs7855114, transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1996941	gcagtgaggttaaaac[A/C]aacgtagcatttctca	A	C	ENST00000331400 // upstream // 249242 // — // — // — /// ENST00000335028 // upstream // 104363 // — // — // — // —	-	q21.31
SNP_A-1904364	tgggcttctgatgtac[A/C]gagttgtgaggaaata	A	C	ENST00000331400 // upstream // 255565 // — // — // — /// ENST00000335028 // upstream // 98040 // — // — // — // —	-	q21.31
SNP_A-2307968	gcttctgtttagcaa[C/T]ggcagtctagcttic	C	T	ENST00000331400 // upstream // 264599 // — // — // — /// ENST00000335028 // upstream // 89006 // — // — // — // —	-	q21.31
SNP_A-1833734	tacaggtccagagttg[C/G]aagaagaactaggact	C	G	ENST00000331400 // upstream // 269638 // — // — // — /// ENST00000335028 // upstream // 83967 // — // — // — // —	-	q21.31
SNP_A-2111842	aggatatggcatgtat[C/T]aagtgtgagatttagg	C	T	ENST00000331400 // upstream // 274364 // — // — // — /// ENST00000335028 // upstream // 79241 // — // — // — // —	-	q21.31
SNP_A-2137976	atcatttatitttgca[C/T]atgagagactaataa	C	T	ENST00000331400 // upstream // 300843 // — // — // — /// ENST00000335028 // upstream // 52762 // — // — // — // —	-	q21.31
SNP_A-1955569	tttggttcatatcagc[C/T]atagagacagcaatcc	C	T	NM_007005 // downstream // 45865 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1811080 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-lik	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1996957	ttgagcattcgttcaa[G/T]catgtttccaagttat	G	T	NM_007005 // downstream // 148753 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1708192 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1862209	tcatggcacaaagttat[C/G]cagcagaatgttcaga	C	G	NM_007005 // downstream // 172410 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1684535 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2138807	atccccgtatttcac[G/T]cccctcatctgaaaac	G	T	NM_007005 // downstream // 204530 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1652415 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2175218	cacataaacaatggtc[G/T]actacttcaaactat	G	T	NM_007005 // downstream // 271381 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1585564 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1949933	ttcaagtgactggaa[A/G]aatgttgataccattg	A	G	NM_007005 // downstream // 271671 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1585274 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1895380	tgccctttctcgctgat[C/T]cttgtttaggagcctt	C	T	NM_007005 // downstream // 633661 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1223284 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2274331	gactgtaaattagta[A/G]gtgctgagattatatc	A	G	NM_007005 // downstream // 1175820 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 681125 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2280059	gagggaactgttgtaa[C/G]gcagataatctgttta	C	G	NM_007005 // downstream // 1194549 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 662396 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-2119747	agtattgtagctgaaa[C/T]tggaagttcaaccatt	C	T	NM_007005 // downstream // 1212051 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 644894 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-li	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.31
SNP_A-1659598	ggatcttaggcttccttcaatgac[A/G]aggatctctatgtctgaca ttccag	A	G	NM_152573 // downstream // 326606 // Hs.165464 // FLJ31614 // 158158 // hypothetical protein FLJ31614	FLJ31614	FLJ31614, rs534724, hypothetical protein FLJ31614,q21.32
SNP_A-1921746	ttactaaagctgatta[C/T]gctgtcatcccttcct	C	T	NM_007005 // downstream // 1855511 // Hs.444213 // TLE4 // 7091 // Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), mRNA. /// NM_005077 // downstream // 1434 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-like	TLE4	TLE4, Homo sapiens transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4), q21.32
SNP_A-2055335	aataagcgagctgtgg[A/C]atctagacaaaaacag	A	C	NM_005077 // intron // 0 // Hs.197320 // TLE1 // 7088 // Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), mRNA. /// ENST00000355495 // intron // 0 // — // — // — /// ENST00000355002 // intron // 0 // — /	TLE1	TLE1, Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), q21.32
SNP_A-1756020	agacagacccaaaataccttattccd[A/G]gaagcatcgattaggt ctgccctg	A	G	AF174394 // downstream // 103617 // Hs.532299 // - // - // Apoptotic-related protein PCAR mRNA, partial cds /// NM_022127 // upstream // 131455 // Hs.149425 // SLC28A3 // 64078 // solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	-	- , rs7029848, Apoptotic-related protein PCAR mRNA, partial cds ,q21.33
SNP_A-1707495	acaatatggaacctgaagattttt[A/G]tggcaattccaagagatt ctcaggc	A	G	NM_006180 // upstream // 37245 // Hs.439109 // NTRK2 // 4915 // neurotrophic tyrosine kinase, receptor, type 2	NTRK2	NTRK2 , rs7264432, neurotrophic tyrosine kinase, receptor, type 2,q21.33
SNP_A-1794528	ggtccttgacttccca[C/T]aacaccctaagtgttg	C	T	NM_152573 // upstream // 50959 // Hs.129136 // RASEF // 158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream // 133310 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32
SNP_A-1825826	taaatcttaccaaa[A/G]ctggaaccacaaaat	A	G	NM_152573 // upstream // 133782 // Hs.129136 // RASEF // 158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream // 50487 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32
SNP_A-2178660	cactctggctgagaa[A/C]atgcctagaacaaaa	A	C	NM_152573 // upstream // 134937 // Hs.129136 // RASEF // 158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream // 49332 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32
SNP_A-1940767	ttgcgagtcaagggaa[C/T]ccaggagttgctctct	C	T	NM_152573 // upstream // 156269 // Hs.129136 // RASEF // 158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream // 28000 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32
SNP_A-1878265	tctgtccacagagtaa[A/G]ggtcaattaggtagtg	A	G	NM_152573 // upstream // 169816 // Hs.129136 // RASEF // 158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream // 14453 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1952073	ttctcatttgtcagca[A/C]gttttgtcagtactta	A	C	NM_152573 // upstream // 173787 // Hs.129136 // RASEF // 158158 // Homo sapiens RAS and EF hand domain containing (RASEF), mRNA. /// NM_174938 // downstream // 10482 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /	RASEF	RASEF, Homo sapiens RAS and EF hand domain containing (RASEF), q21.32
SNP_A-2098529	agagcaggacccggac[A/G]gtaggaatccacaggc	A	G	NM_174938 // intron // 0 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /// ENST00000304195 // intron // 0 // — // — // —	FRMD3	FRMD3, Homo sapiens FERM domain containing 3 (FRMD3), q21.32
SNP_A-2151324	atgttatagatgagta[A/C]gctgatgatctgagaa	A	C	NM_174938 // intron // 0 // Hs.127535 // FRMD3 // 257019 // Homo sapiens FERM domain containing 3 (FRMD3), mRNA. /// ENST00000304195 // intron // 0 // — // — // —	FRMD3	FRMD3, Homo sapiens FERM domain containing 3 (FRMD3), q21.32
SNP_A-1747607	atggaacacaagacaactctaaa[C/T]gtcaccttaacgctct tctcacat	C	T	AJ437018 // upstream // 251890 // Hs.21542 // AGTPBP1 // 23287 // ATP/GTP binding protein 1 /// NM_006180 // downstream // 272330 // Hs.439109 // NTRK2 // 4915 // neurotrophic tyrosine kinase, receptor, type 2 /// NM_015239 // downstream // 251716 // Hs.	AGTPBP1	AGTPBP1, rs2769612, ATP.q21.33
SNP_A-2072967	acaggacacctacatc[A/G]gaacaagactgctttt	A	G	NM_001001551 // downstream // 7105 // Hs.530261 // C9orf103 // 414328 // Homo sapiens chromosome 9 open reading frame 103 (C9orf103), mRNA. /// NM_053067 // downstream // 8736 // Hs.9589 // UBQLN1 // 29979 // Homo sapiens ubiquilin 1 (UBQLN1), transcript	C9orf103	C9orf103, Homo sapiens chromosome 9 open reading frame 103 (C9orf103), q21.32
SNP_A-1997052	tagtcctaaaatatcc[A/G]acacaatttttgaa	A	G	NM_024945 // downstream // 54865 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76 (C9orf76), mRNA. /// NM_024945 // downstream // 54858 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76	C9orf76	C9orf76, Homo sapiens chromosome 9 open reading frame 76 (C9orf76), q21.32
SNP_A-2216608	cctctatgtcactttc[C/T]acatttttacattgt	C	T	NM_024945 // downstream // 90063 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76 (C9orf76), mRNA. /// NM_024945 // downstream // 90056 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76	C9orf76	C9orf76, Homo sapiens chromosome 9 open reading frame 76 (C9orf76), q21.32
SNP_A-2099982	agagtctaggttctaa[C/T]gcttcgtgtcaaacg	C	T	NM_024945 // downstream // 150820 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76 (C9orf76), mRNA. /// NM_024945 // downstream // 150813 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 7	C9orf76	C9orf76, Homo sapiens chromosome 9 open reading frame 76 (C9orf76), q21.32
SNP_A-2219576	cctgttacctttac[A/G]ctaactacagcccagg	A	G	NM_024945 // downstream // 157403 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76 (C9orf76), mRNA. /// NM_024945 // downstream // 157396 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 7	C9orf76	C9orf76, Homo sapiens chromosome 9 open reading frame 76 (C9orf76), q21.32
SNP_A-1799485	gtaatgccatcttgaa[A/G]ccctccagtcccaattg	A	G	NM_024945 // downstream // 210276 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76 (C9orf76), mRNA. /// NM_024945 // downstream // 210269 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 7	C9orf76	C9orf76, Homo sapiens chromosome 9 open reading frame 76 (C9orf76), q21.32
SNP_A-2097761	agagaccataattcca[G/T]agcgttgtagccccac	G	T	NM_024945 // downstream // 253791 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 76 (C9orf76), mRNA. /// NM_024945 // downstream // 253784 // Hs.284137 // C9orf76 // 80010 // Homo sapiens chromosome 9 open reading frame 7	C9orf76	C9orf76, Homo sapiens chromosome 9 open reading frame 76 (C9orf76), q21.33
SNP_A-1874492	tctccctcaagactaa[C/T]gtgggatctaccagga	C	T	NM_022127 // intron // 0 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// ENST00000356204 // intron // 0 // — // — // — // —	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1863241	tcatttgaaatgtatc[A/C]aaatgtcctcacaaac	A	C	NM_022127 // intron // 0 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// ENST00000356204 // intron // 0 // --- // --- // --- // ---	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2150219	atgtctatgagccatа[C/T]agcactatgagtagaa	C	T	NM_022127 // intron // 0 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// ENST00000356204 // intron // 0 // --- // --- // --- // ---	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-1919578	ttaaggatcatctg[A/G]acctttgaatctttt	A	G	NM_022127 // upstream // 63482 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 265611 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2282428	gagttctgatcaact[A/C]aagtagagcggaacat	A	C	NM_022127 // upstream // 66776 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 262317 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2106663	agcctcttgtaagaac[A/G]aaatatcacacagaaa	A	G	NM_022127 // upstream // 79617 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 249476 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2131763	atagctattgtgaaaa[G/T]tactgagagaattac	G	T	NM_022127 // upstream // 84833 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 244260 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2168016	caactaagccctctcc[C/T]atcttcattcaaaag	C	T	NM_022127 // upstream // 151785 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 177308 // Hs.494312 // NTRK2 // 4915 // Homo sapiens	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2309146	ggaaaaaatggcacaa[A/G]gattacttgagtcctg	A	G	NM_022127 // upstream // 166483 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 162610 // Hs.494312 // NTRK2 // 4915 // Homo sapiens	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2240723	ctgactgcagatccac[A/G]agcataaatgattgc	A	G	NM_022127 // upstream // 171940 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 157153 // Hs.494312 // NTRK2 // 4915 // Homo sapiens	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2139163	atcctccctctcgacc[A/G]caggactatttggtt	A	G	NM_022127 // upstream // 216747 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 112346 // Hs.494312 // NTRK2 // 4915 // Homo sapiens	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-1834148	tacatctgagttatca[C/T]aagagtctgagatgat	C	T	NM_022127 // upstream // 295583 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 33510 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1789784	gggctgagaactttga[C/G]agtaatctgcaaatcc	C	G	NM_022127 // upstream // 295645 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 33448 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2046924	aagagtaaacattact[C/G]aaggatttttacctcc	C	G	NM_022127 // upstream // 303788 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 25305 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-1904973	tgggtattctctgcac[C/T]ctaccaccacttctgt	C	T	NM_022127 // upstream // 311778 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 17315 // Hs.494312 // NTRK2 // 4915 // Homo sapiens n	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-1955723	ttgtacaccagaaga[A/G]ctaattatgttggaa	A	G	NM_022127 // upstream // 326927 // Hs.149425 // SLC28A3 // 64078 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), mRNA. /// NM_006180 // upstream // 2166 // Hs.494312 // NTRK2 // 4915 // Homo sapiens ne	SLC28A3	SLC28A3, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (SLC28A3), q21.33
SNP_A-2037798	aacaataaattgcaca[C/T]agagtctgtctatagga	C	T	NM_006180 // intron // 0 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // intron // 0 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine kinase type 2 tru	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-2206603	ccatgaactttccctc[G/T]aattatgctagtcaat	G	T	NM_006180 // downstream // 14212 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // downstream // 15233 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine k	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1743503	agaaaaataaggacatatgctccta[A/C]aaaaacttgtaccaa aagtttactg	A	C	NM_002048 // downstream // 124342 // Hs.65029 // GAS1 // 2619 // growth arrest-specific 1 /// NM_024617 // upstream // 500377 // - // - // - // -	GAS1	GAS1, rs1576161, growth arrest-specific 1, q21.33
SNP_A-2212686	ccctctgaaggaagg[C/T]caattcttagagatag	C	T	NM_006180 // downstream // 71080 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // downstream // 72101 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine k	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1950594	tttcatctcaaaagaa[C/T]ctaaagcttgtagtcc	C	T	NM_006180 // downstream // 161773 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // downstream // 162794 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1997099	agggaagagtgtaaa[A/G]gtaatatctctgcg	A	G	NM_006180 // downstream // 409665 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // downstream // 410686 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1997100	acataggaacatgacc[A/T]acttagcaataaggga	A	T	NM_006180 // downstream // 410082 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // downstream // 411103 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1929486	ttcagttttaaaaag[C/G]cttccagatgaacagt	C	G	NM_006180 // downstream // 485474 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA. /// AF410900 // downstream // 486495 // Hs.494312 // NTRK2 // 4915 // Homo sapiens neurotrophin receptor tyrosine	NTRK2	NTRK2, Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), q21.33
SNP_A-1733080	caacagtccaattcaaattagacct[C/T]acaaagcaaactactc tgattagg	C	T	NM_004938 // intron // 0 // Hs.244318 // DAPK1 // 1612 // death-associated protein kinase 1	DAPK1	DAPK1, rs3739784, death-associated protein kinase 1,q21.33
SNP_A-1742257	gacaagcattatgccattacgattat[C/T]gctaaaaatgaagtcc aagcacaat	C	T	NM_004938 // intron // 0 // Hs.244318 // DAPK1 // 1612 // death-associated protein kinase 1	DAPK1	DAPK1, rs10512188, death-associated protein kinase 1,q21.33
SNP_A-2119310	agtagtgttaaaactc[C/T]gagtaaggtacttcag	C	T	NM_024635 // upstream // 32161 // Hs.436098 // MAK10 // 60560 // Homo sapiens MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae) (MAK10), mRNA. /// ENST00000297820 // downstream // 59490 // — // — // — /// ENST00000257491	MAK10	MAK10, Homo sapiens MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae) (MAK10), q21.33
SNP_A-2273322	gactcccagtgatagat[A/G]gtgagtagcttcatac	A	G	NM_002048 // downstream // 491905 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 78131 // — // — // — /// ENST00000321461 // downstream // 491905 // — // — // — // -	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1869657	tccttagggtctttta[C/T]ggctgcctacccctg	C	T	NM_002048 // downstream // 461295 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 108741 // — // — // — /// ENST00000321461 // downstream // 461295 // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2025716	aaaatgcacagtgtaa[C/T]atctggaaagacgtat	C	T	NM_002048 // downstream // 351741 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 218295 // — // — // — // — /// ENST00000321461 // downstream // 351741 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1997119	aagttgtctaatca[A/G]atgaagagaaactgca	A	G	NM_002048 // downstream // 255654 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000303658 // upstream // 314382 // — // — // — // — /// ENST00000321461 // downstream // 255654 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1997126	tatctagctgggagaa[C/T]ggtgaaccggcaaaca	C	T	NM_002048 // upstream // 24619 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 24619 // — // — // — // — /// ENST00000359720 // downstream // 38694 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2276945	gagatcccttatgaag[G/T]cacttttccttttcaac	G	T	NM_002048 // upstream // 27516 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 27516 // — // — // — // — /// ENST00000359720 // downstream // 35797 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1887050	tgacttccatatttct[A/G]aagatgattcacccat	A	G	NM_002048 // upstream // 30594 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 30594 // — // — // — // — /// ENST00000359720 // downstream // 32719 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1811862	gtgcttgtaacacta[C/T]atatttcaagaggaaa	C	T	NM_002048 // upstream // 31976 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 31976 // — // — // — // — /// ENST00000359720 // downstream // 31337 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-2112983	aggcattggccaaaaa[C/T]tgcaaaaaatgaggtg	C	T	NM_002048 // upstream // 34459 // Hs.65029 // GAS1 // 2619 // Homo sapiens growth arrest-specific 1 (GAS1), mRNA. /// ENST00000321461 // upstream // 34459 // — // — // — // — /// ENST00000359720 // downstream // 28854 // — // — // — // — // —	GAS1	GAS1, Homo sapiens growth arrest-specific 1 (GAS1), q21.33
SNP_A-1997132	gctggattaggcaaga[A/T]tccggggctgtgctgca	A	T	NM_004938 // upstream // 360128 // Hs.380277 // DAPK1 // 1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream // 95768 // — // — // — // — /// ENST00000334730 // downstream // 124602 // — // — // —	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072892	acaggaaaaagtagtc[A/G]agataccatcatgtag	A	G	NM_004938 // upstream // 354310 // Hs.380277 // DAPK1 // 1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream // 101586 // --- // --- // --- /// ENST00000334730 // downstream // 130420 // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1686852	atggaatctacaaagaaagctaata[C/G]aactaacaggtgag gttagcaagtt	C	G	NM_145283 // downstream // 3702217 // Hs.309216 // C9orf121 // 158046 // chromosome 9 open reading frame 121 /// NM_182599 // upstream // 77213 // - // - // -	C9orf121	C9orf121 , rs3897826, chromosome 9 open reading frame 121, q22.1
SNP_A-1681728	taacattgaacccccaaagtgacca[C/T]ggactgatggccta gatcatccag	C	T	NM_145283 // downstream // 378384 // Hs.309216 // C9orf121 // 158046 // chromosome 9 open reading frame 121 /// NM_182599 // upstream // 69046 // - // - // -	C9orf121	C9orf121 , rs4440695, chromosome 9 open reading frame 121, q22.1
SNP_A-2154374	attattaaaagcaaic[A/G]atgcattatgaaaatg	A	G	NM_004938 // upstream // 180434 // Hs.380277 // DAPK1 // 1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream // 275462 // --- // --- // --- /// ENST00000334730 // downstream // 304296 // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1997146	ttgccttagaaatagc[A/G]ataaacaagaatgta	A	G	NM_004938 // upstream // 14531 // Hs.380277 // DAPK1 // 1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000359720 // upstream // 441365 // --- // --- // --- /// ENST00000334730 // downstream // 470199 // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2187517	cagtaaagattctcat[C/T]aggtgccaaattctag	C	T	NM_004938 // intron // 0 // Hs.380277 // DAPK1 // 1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-2235788	ctcctctccgcgggaa[C/T]aggaatggctcttca	C	T	NM_004938 // intron // 0 // Hs.380277 // DAPK1 // 1612 // Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA. /// ENST00000358077 // intron // 0 // --- // --- // ---	DAPK1	DAPK1, Homo sapiens death-associated protein kinase 1 (DAPK1), q21.33
SNP_A-1739005	tgggattcagtcagatgtcagatac[A/G]aggttagtgaggagc ctgccaggg	A	G	NM_024077 // downstream // 86017 // Hs.288141 // SBP2 // 79048 // SECIS binding protein 2	SBP2	SBP2, rs10512197, SECIS binding protein 2,q22.2
SNP_A-1652190	gggctacagagactccaggctggtc[A/G]atcagtgacagaaat ttgagttccc	A	G	NM_006705 // upstream // 131071 // Hs.9701 // GADD45G // 10912 // growth arrest and DNA-damage-inducible, gamma	GADD45G	GADD45G , rs10512196, growth arrest and DNA-damage-inducible, gamma,q22.2
SNP_A-2094588	agaatacgaaggcata[C/T]atgtgttgttctcag	C	T	ENST00000335499 // downstream // 47219 // --- // --- // --- /// ENST00000354530 // upstream // 56137 // --- // --- // ---	-	q22.1
SNP_A-1789047	gggcactgcaggggag[A/C]acagcgctcaggctgg	A	C	ENST00000354530 // downstream // 5920 // --- // --- // --- /// ENST00000330282 // downstream // 4862 // --- // --- // ---	-	q22.1
SNP_A-2173071	cacaaaggtgacttcc[A/G]cgcccaggagaatgtg	A	G	NM_178828 // CDS // 0 // Hs.130672 // C9orf79 // 286234 // Homo sapiens chromosome 9 open reading frame 79 (C9orf79), mRNA. /// ENST00000325643 // CDS // 0 // --- // --- // ---	C9orf79	C9orf79, Homo sapiens chromosome 9 open reading frame 79 (C9orf79), q22.1
SNP_A-2073354	acaggtaataacgaaac[C/T]accaaggttaattgga	C	T	ENST00000324915 // downstream // 16796 // --- // --- // --- /// ENST00000324915 // downstream // 96150 // --- // --- // ---	-	q22.1
SNP_A-2305328	gctgaggttgcatgga[C/T]attgcagtgagtccat	C	T	ENST00000324930 // downstream // 31154 // --- // --- // --- /// ENST00000324915 // downstream // 81792 // --- // --- // ---	-	q22.1
SNP_A-2061507	aatgctctgctgggg[C/T]aatctcatcataggc	C	T	ENST00000324930 // downstream // 72341 // --- // --- // --- /// ENST00000324915 // downstream // 40605 // --- // --- // ---	-	q22.1
SNP_A-1878443	tctgtgagcaggaaac[C/T]ggctaaccaatcggct	C	T	NM_006717 // upstream // 127975 // Hs.146804 // SPIN // 10927 // Homo sapiens spindlin (SPIN), mRNA. /// ENST00000324915 // upstream // 129880 // --- // --- // --- /// ENST00000223559 // upstream // 127975 // --- // --- // ---	SPIN	SPIN, Homo sapiens spindlin (SPIN), q22.1
SNP_A-2298233	gccatgccctatcca[A/G]tgtcaatgtacagtg	A	G	NM_145283 // downstream // 18883 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 400921 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2026311	aaaatttccigttgta[C/T]atttcccatacagctt	C	T	NM_145283 // downstream // 324441 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 95363 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2282332	gagttatttttgttccf[A/G]atgggtctcagagat	A	G	NM_145283 // downstream // 344141 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 75663 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1948235	ttagctgcaatgtta[C/T]aggccagaaagttcac	C	T	NM_145283 // downstream // 351117 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 68687 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1802677	gtatgagagcccacaa[A/G]tatttagtttatgaa	A	G	NM_145283 // downstream // 353952 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 65852 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2204742	ccaggcaatgaatccc[A/G]agaaatttgcctttca	A	G	NM_145283 // downstream // 375829 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 43975 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1844201	tagtttctcctggtcc[C/T]gaaatcattataagta	C	T	NM_145283 // downstream // 376927 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 42877 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2229729	ctagtccttccagaaa[C/T]gttgccaagtacagag	C	T	NM_145283 // downstream // 378530 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 41274 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1921278	ttacattctcagagga[C/T]gctcacagcctagatc	C	T	NM_145283 // downstream // 384988 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 34816 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1898085	tgctgtggactcctgg[C/T]aaagcctgctgtccca	C	T	NM_145283 // downstream // 385775 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 34029 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-1941787	ttggacactttcaat[C/G]atgactcttgaagcag	C	G	NM_145283 // downstream // 395425 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 24379 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fr	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1
SNP_A-2295253	gcatcaacaaaacttca[A/C]ctggacaaggcacccc	A	C	NM_145283 // downstream // 412996 // Hs.494395 // C9orf121 // 158046 // Homo sapiens chromosome 9 open reading frame 121 (C9orf121), mRNA. /// NM_001001938 // upstream // 6808 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading fra	C9orf121	C9orf121, Homo sapiens chromosome 9 open reading frame 121 (C9orf121), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2286541	gatggaagtgatttca[A/G]aggcccaaagtgagtg	A	G	NM_001001938 // 3UTR // 0 // Hs.546252 // C9orf47 // 286223 // Homo sapiens chromosome 9 open reading frame 47 (C9orf47), mRNA. /// NM_005226 // intron // 0 // Hs.546252 // EDG3 // 1903 // Homo sapiens endothelial differentiation, sphingolipid G-protein-c	C9orf47	C9orf47, Homo sapiens chromosome 9 open reading frame 47 (C9orf47), q22.1
SNP_A-2242522	ctgcagcgaggcttca[C/T]ggacactattctggca	C	T	NM_016848 // intron // 0 // Hs.137570 // SHC3 // 53358 // Homo sapiens src homology 2 domain containing transforming protein C3 (SHC3), mRNA. /// ENST00000277153 // intron // 0 // — // — // —	SHC3	SHC3, Homo sapiens src homology 2 domain containing transforming protein C3 (SHC3), q22.1
SNP_A-2088288	actggtggtcagagga[C/T]ggctttaggggctgaa	C	T	NM_016848 // intron // 0 // Hs.137570 // SHC3 // 53358 // Homo sapiens src homology 2 domain containing transforming protein C3 (SHC3), mRNA. /// ENST00000277153 // intron // 0 // — // — // —	SHC3	SHC3, Homo sapiens src homology 2 domain containing transforming protein C3 (SHC3), q22.1
SNP_A-2028834	aaacttgccttcatggt[C/T]cacaaaaggctcccag	C	T	NM_006378 // intron // 0 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// ENST00000343780 // intron // 0 // — // — // — ///	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S ,q22.2
SNP_A-2296035	gcattactctgactaaa[C/T]gatgaacaatgtgagc	C	T	NM_006378 // intron // 0 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// ENST00000343780 // intron // 0 // — // — // — ///	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S ,q22.2
SNP_A-2190373	catacaatttggagccd[A/C]gagtgctgctttatct	A	C	NM_006378 // intron // 0 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// ENST00000356444 // intron // 0 // — // — // —	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S ,q22.2
SNP_A-2205478	ccagtggtgaccggaa[A/T]gaagcaaccttcctaa	A	T	NM_006378 // intron // 0 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// ENST00000356444 // intron // 0 // — // — // —	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S ,q22.2
SNP_A-2281729	gagtgaaaggagctag[A/T]caaaagagtatgcaga	A	T	NM_006378 // intron // 0 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// ENST00000356444 // intron // 0 // — // — // —	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S q22.2
SNP_A-2201609	ccaatttatttcgaat[C/T]atctgtggctgctttt	C	T	NM_006378 // intron // 0 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// ENST00000356444 // intron // 0 // — // — // —	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S q22.2
SNP_A-2287122	gatgtatgttgccata[C/T]gcactttcattctct	C	T	NM_006378 // upstream // 72169 // Hs.511748 // SEMA4D // 10507 // Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S /// NM_006378 // upstream // 30149 // Hs.511748 // SEMA4D //	SEMA4D	SEMA4D, Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (S ,q22.2
SNP_A-1997179	tctgtcaggatgtgac[C/T]gctgtttaagcgat	C	T	NM_006705 // downstream // 25797 // Hs.9701 // GADD45G // 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 25797 // — // — // — /// ENST00000332111 // upstream // 581098	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1674999	caataccctagttgaccagttcaa[A/T]ctttccctgcacttgaatg ctacta	A	T	NM_004560 // downstream // 242161 // Hs.208080 // ROR2 // 4920 // receptor tyrosine kinase-like orphan receptor 2 /// NM_005384 // upstream // 56761 // Hs.79334 // NFIL3 // 4783 // nuclear factor, interleukin 3 regulated	ROR2	ROR2 , rs2065438, receptor tyrosine kinase-like orphan receptor 2, q22.31
SNP_A-1961624	ttttttttctgccaa[A/T]atttatagctgccctg	A	T	NM_006705 // downstream // 183323 // Hs.9701 // GADD45G // 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 183323 // — // — // — /// ENST00000332111 // upstream // 4235	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-1794352	ggtccatgcagccacaC/T]ctctgcaccctgatgtc	C	T	NM_006705 // downstream // 401848 // Hs.9701 // GADD45G // 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 401848 // — // — // — /// ENST00000332111 // upstream // 2050	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-2203163	ccactggtatctgcta[C/T]gaaggaaaggagaaat	C	T	NM_006705 // downstream // 411425 // Hs.9701 // GADD45G // 10912 // Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), mRNA. /// ENST00000252506 // downstream // 411425 // — // — // — /// ENST00000332111 // upstream // 1954	GADD45G	GADD45G, Homo sapiens growth arrest and DNA-damage-inducible, gamma (GADD45G), q22.2
SNP_A-2292357	gcacgctttcaaataa[C/G]actcccagggcttgac	C	G	NM_017594 // upstream // 141342 // Hs.165636 // DIRAS2 // 54769 // Homo sapiens DIRAS family, GTP-binding RAS-like 2 (DIRAS2), mRNA. /// NM_003177 // upstream // 17621 // Hs.371720 // SYK // 6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// ENS	DIRAS2	DIRAS2, Homo sapiens DIRAS family, GTP-binding RAS-like 2 (DIRAS2), q22.2
SNP_A-2203895	ccagataaaaggtcac[A/G]attcctggtgcctggt	A	G	NM_017594 // upstream // 141584 // Hs.165636 // DIRAS2 // 54769 // Homo sapiens DIRAS family, GTP-binding RAS-like 2 (DIRAS2), mRNA. /// NM_003177 // upstream // 17379 // Hs.371720 // SYK // 6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// ENS	DIRAS2	DIRAS2, Homo sapiens DIRAS family, GTP-binding RAS-like 2 (DIRAS2), q22.2
SNP_A-2176006	caccaactgcatgcac[A/T]attggaatcgcgtttc	A	T	NM_003177 // downstream // 19020 // Hs.371720 // SYK // 6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 298627 // Hs.175905 // AUH // 549 // Homo sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nucl	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2260747	gaaacgctagctccc[G/T]ctcgtgtcaattgtct	G	T	NM_003177 // downstream // 26674 // Hs.371720 // SYK // 6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 290973 // Hs.175905 // AUH // 549 // Homo sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nucl	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-1997213	gataggaacaaaaaaa[C/T]ctcattagagtcacaa	C	T	NM_003177 // downstream // 206509 // Hs.371720 // SYK // 6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 111138 // Hs.175905 // AUH // 549 // Homo sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuc	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-1997214	gtaacttactggcctc[A/G]aggataggcctctggt	A	G	NM_003177 // downstream // 206677 // Hs.371720 // SYK // 6850 // Homo sapiens spleen tyrosine kinase (SYK), mRNA. /// NM_001698 // downstream // 110970 // Hs.175905 // AUH // 549 // Homo sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuc	SYK	SYK, Homo sapiens spleen tyrosine kinase (SYK), q22.2
SNP_A-2226953	ctaatctgaaatctta[A/C]aaggacaccaacaatc	A	C	NM_005384 // intron // 0 // Hs.79334 // NFIL3 // 4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// ENST00000297689 // intron // 0 // — // — // — // —	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1814107	gtgtcctgaatcccaa[C/T]gtctgtagcgggacat	C	T	NM_005384 // upstream // 60493 // Hs.79334 // NFIL3 // 4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 238429 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan recep	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-1884180	tgaaggaacgtattat[C/G]agtcctgagaaaaca	C	G	NM_005384 // upstream // 81362 // Hs.79334 // NFIL3 // 4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 217560 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan recep	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-2079113	acccagcccgttgta[C/T]ctctttctgggtatgt	C	T	NM_005384 // upstream // 95709 // Hs.79334 // NFIL3 // 4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 203213 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan recep	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-1828205	taagagccgggacaaa[C/T]tgataaatgagctgaa	C	T	NM_005384 // upstream // 95748 // Hs.79334 // NFIL3 // 4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 203174 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan recep	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-2209908	ccccaagggcgtagaa[A/C]atccagacagtgaga	A	C	NM_005384 // upstream // 108511 // Hs.79334 // NFIL3 // 4783 // Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), mRNA. /// NM_004560 // downstream // 190411 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan rece	NFIL3	NFIL3, Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), q22.31
SNP_A-2072227	acagatgtggcaaaaa[A/C]atccacttgatccaac	A	C	NM_004560 // intron // 0 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), mRNA. /// ENST00000303641 // intron // 0 // — // — // —	ROR2	ROR2, Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), q22.31
SNP_A-1821248	gtttgatatcataaaaa[A/C]tcaagtcagcagaac	A	C	NM_004560 // intron // 0 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), mRNA. /// ENST00000303641 // intron // 0 // — // — // —	ROR2	ROR2, Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), q22.31
SNP_A-2268452	gaatggataagcgaac[C/T]gtgaacccctatacaa	C	T	NM_004560 // intron // 0 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), mRNA. /// ENST00000303641 // intron // 0 // — // — // —	ROR2	ROR2, Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), q22.31
SNP_A-1837454	tacttcttaacaaaaa[A/G]atgtagccagaagatt	A	G	NM_004560 // upstream // 51789 // Hs.98255 // ROR2 // 4920 // Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), mRNA. /// NM_006415 // downstream // 29194 // Hs.90458 // SPTLC1 // 10558 // Homo sapiens serine palmitoyltransferase, long	ROR2	ROR2, Homo sapiens receptor tyrosine kinase-like orphan receptor 2 (ROR2), q22.31
SNP_A-1955058	tttggagggagccaca[C/T]attgacccaatgggag	C	T	NM_006415 // intron // 0 // Hs.90458 // SPTLC1 // 10558 // Homo sapiens serine palmitoyltransferase, long chain base subunit 1 (SPTLC1), transcript variant 1, mRNA. /// NM_178324 // intron // 0 // Hs.90458 // SPTLC1 // 10558 // Homo sapiens serine palmito	SPTLC1	SPTLC1, Homo sapiens serine palmitoyltransferase, long chain base subunit 1 (SPTLC1), transcript variant 1, q22.31
SNP_A-2096148	agacatggactacagcd[A/G]gcacaatatgaaagtg	A	G	NM_006415 // intron // 0 // Hs.90458 // SPTLC1 // 10558 // Homo sapiens serine palmitoyltransferase, long chain base subunit 1 (SPTLC1), transcript variant 1, mRNA. /// NM_178324 // intron // 0 // Hs.90458 // SPTLC1 // 10558 // Homo sapiens serine palmito	SPTLC1	SPTLC1, Homo sapiens serine palmitoyltransferase, long chain base subunit 1 (SPTLC1), transcript variant 1, q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893917	tgcataggtcttaccc[C/G]agctacagggctgagg	C	G	NM_024517 // downstream // 179745 // Hs.211441 // PHF2 // 5253 // Homo sapiens PHD finger protein 2 (PHF2), transcript variant 2, mRNA. /// NM_005392 // downstream // 179742 // Hs.211441 // PHF2 // 5253 // Homo sapiens PHD finger protein 2 (PHF2), transcr	PHF2	PHF2, Homo sapiens PHD finger protein 2 (PHF2), transcript variant 2, q22.32
SNP_A-2151513	atgttcigaccaaata[C/G]acattaaggctaactt	C	G	NM_032823 // intron // 0 // Hs.434253 // C9orf3 // 84909 // Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA. /// ENST00000277198 // intron // 0 // — // — // — /// ENST00000311678 // intron // 0 // — // — // — /// EN	C9orf3	C9orf3, Homo sapiens chromosome 9 open reading frame 3 (C9orf3), q22.32
SNP_A-1851871	tattgaggaaatagccc[A/T]acagaaaattcaaaga	A	T	NM_000264 // upstream // 132663 // Hs.494538 // PTCH // 5727 // Homo sapiens patched homolog (Drosophila) (PTCH), mRNA. /// ENST00000331920 // upstream // 132663 // — // — // — /// ENST00000334720 // upstream // 131299 // — // — // — //	PTCH	PTCH, Homo sapiens patched homolog (Drosophila) (PTCH), q22.32
SNP_A-1942377	ttggcctcgcaaagct[A/G]agcctctaatatact	A	G	NM_000264 // upstream // 166681 // Hs.494538 // PTCH // 5727 // Homo sapiens patched homolog (Drosophila) (PTCH), mRNA. /// ENST00000331920 // upstream // 168681 // — // — // — /// ENST00000334720 // upstream // 95281 // — // — // — //	PTCH	PTCH, Homo sapiens patched homolog (Drosophila) (PTCH), q22.32
SNP_A-2194348	catgatatttgtgaaa[A/G]atcctaacagtcacct	A	G	NM_000264 // upstream // 182150 // Hs.494538 // PTCH // 5727 // Homo sapiens patched homolog (Drosophila) (PTCH), mRNA. /// ENST00000331920 // upstream // 182150 // — // — // — /// ENST00000334720 // upstream // 81812 // — // — // — //	PTCH	PTCH, Homo sapiens patched homolog (Drosophila) (PTCH), q22.32
SNP_A-2024669	aaaagtaagagtggac[A/G]gggttgattttccat	A	G	NM_000264 // upstream // 201689 // Hs.494538 // PTCH // 5727 // Homo sapiens patched homolog (Drosophila) (PTCH), mRNA. /// ENST00000331920 // upstream // 201689 // — // — // — /// ENST00000334720 // upstream // 62273 // — // — // — //	PTCH	PTCH, Homo sapiens patched homolog (Drosophila) (PTCH), q22.32
SNP_A-2309272	ggaaaagacaaaaaac[A/C]agtggacatgataatt	A	C	ENST00000288985 // intron // 0 // — // — // — //	-	q22.32
SNP_A-2022517	aaaaatcgggttgaca[C/T]tgaactctatctgca	C	T	ENST00000288985 // intron // 0 // — // — // — //	-	q22.32
SNP_A-2046511	aagagagttaacagag[A/G]atggaaatccgatggg	A	G	NM_020207 // downstream // 63951 // Hs.494552 // C9orf102 // 56959 // Homo sapiens chromosome 9 open reading frame 102 (C9orf102), mRNA. /// NM_138497 // upstream // 16697 // — // — // 0 // — /// ENST00000288985 // downstream // 111354 // — // —	C9orf102	C9orf102, Homo sapiens chromosome 9 open reading frame 102 (C9orf102), q22.32
SNP_A-2115015	agggccggatttctaaa[C/T]gctgtaggtcaccctg	C	T	NM_138497 // downstream // 68215 // — // — // 0 // — /// NM_000197 // downstream // 65181 // Hs.477 // HSD17B3 // 3293 // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 3 (HSD17B3), mRNA. /// ENST00000297959 // downstream // 68215 // — // —	-	q22.32
SNP_A-1720975	tattctatggttccgtatgtgggc[C/T]ctttaagaaatggattctag agcct	C	T	NM_003389 // intron // 0 // Hs.439725 // CORO2A // 7464 // coronin, actin binding protein, 2A /// NM_052820 // intron // 0 // Hs.439725 // CORO2A // 7464 // coronin, actin binding protein, 2A	CORO2A	CORO2A , rs10491723, coronin, actin binding protein, 2A, q22.33
SNP_A-1997292	actaaacatgctacga[C/T]gcacaagatagcctcc	C	T	NM_033332 // intron // 0 // Hs.40582 // CDC14B // 8555 // Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 3, mRNA. /// NM_003671 // intron // 0 // — // CDC14B // 8555 // Homo sapiens CDC14 cell division c	CDC14B	CDC14B, Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 3, q22.33
SNP_A-2262510	gaaatgtcctgttttta[A/T]gtgactgaaaaatctt	A	T	AB023189 // downstream // 65231 // Hs.75264 // ZNF510 // 22869 // Homo sapiens mRNA for KIAA0972 protein, partial cds. /// ENST00000289028 // upstream // 35353 // — // — // — // — /// ENST00000223428 // downstream // 65231 // — // — // — //	ZNF510	ZNF510, Homo sapiens for KIAA0972 protein, partial cds. q22.33
SNP_A-1812045	gtggacataggctatc[A/G]aaggtttttggata	A	G	NM_032318 // upstream // 72404 // Hs.534502 // HIATL2 // 84278 // Homo sapiens hippocampus abundant gene transcript-like 2 (HIATL2), mRNA. /// NM_001333 // downstream // 1356 // Hs.87417 // CTSL2 // 1515 // Homo sapiens cathepsin L2 (CTSL2), mRNA. /// NM_	HIATL2	HIATL2, Homo sapiens hippocampus abundant gene transcript-like 2 (HIATL2), q22.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1863719	tccaagaatcaatcac[A/G]gtgatgctccaatt	A	G	NM_001333 // intron // 0 // Hs.87417 // CTSL2 // 1515 // Homo sapiens cathepsin L2 (CTSL2), mRNA. /// ENST00000259470 // intron // 0 // — // — /// ENST00000343150 // intron // 0 // — // — // — // —	CTSL2	CTSL2, Homo sapiens cathepsin L2 (CTSL2), q22.33
SNP_A-1942322	ttggccactagcctca[A/G]agctacgcacaaagga	A	G	NM_001333 // upstream // 14192 // Hs.87417 // CTSL2 // 1515 // Homo sapiens cathepsin L2 (CTSL2), mRNA. /// NM_001333 // upstream // 15459 // Hs.87417 // CTSL2 // 1515 // Homo sapiens cathepsin L2 (CTSL2), mRNA. /// ENST00000259470 // upstream // 14192 //	CTSL2	CTSL2, Homo sapiens cathepsin L2 (CTSL2), q22.33
SNP_A-2144445	atgatactggctccat[A/G]aatgaacaattccttc	A	G	NM_001333 // upstream // 14337 // Hs.87417 // CTSL2 // 1515 // Homo sapiens cathepsin L2 (CTSL2), mRNA. /// NM_001333 // upstream // 15604 // Hs.87417 // CTSL2 // 1515 // Homo sapiens cathepsin L2 (CTSL2), mRNA. /// ENST00000259470 // upstream // 14337 //	CTSL2	CTSL2, Homo sapiens cathepsin L2 (CTSL2), q22.33
SNP_A-1876018	tctgaagtccacactc[C/T]gaatgaatgccaggga	C	T	NM_014290 // intron // 0 // Hs.193842 // TDRD7 // 23424 // Homo sapiens tudor domain containing 7 (TDRD7), mRNA. /// ENST00000360763 // intron // 0 // — // — // — /// ENST00000355295 // intron // 0 // — // — // — // —	TDRD7	TDRD7, Homo sapiens tudor domain containing 7 (TDRD7), q22.33
SNP_A-2250594	cttagtgttataaaac[G/T]gcttagacctctgtca	G	T	NM_014290 // intron // 0 // Hs.193842 // TDRD7 // 23424 // Homo sapiens tudor domain containing 7 (TDRD7), mRNA. /// ENST00000360763 // intron // 0 // — // — // — /// ENST00000355295 // intron // 0 // — // — // — // —	TDRD7	TDRD7, Homo sapiens tudor domain containing 7 (TDRD7), q22.33
SNP_A-1687468	actgttcctgagtaaacattaaaa[A/G]tactccatctaaaaagct agaagtt	A	G	NM_004612 // intron // 0 // Hs.28005 // TGFBR1 // 7046 // transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TGFBR1	TGFBR1, rs334356, transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa),q22.33
SNP_A-1698731	tacttagtttcaaggtgtgggtgga[A/T]tatcaactcagggaagtg gcttgtg	A	T	NM_004612 // intron // 0 // Hs.28005 // TGFBR1 // 7046 // transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	TGFBR1	TGFBR1, rs334357, transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa),q22.33
SNP_A-1738955	aagaagcgcctaagcacctctatga[C/T]ggacctaagaaccg agaaatgaat	C	T	NM_004612 // downstream // 18686 // Hs.28005 // TGFBR1 // 7046 // transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) /// NM_033087 // downstream // 48661 // Hs.40919 // ALG2 // 85365 // asparagine-linked glycosyla	TGFBR1	TGFBR1, rs1875804, transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa), q22.33
SNP_A-2171014	caatacagccaaagaa[C/T]gatcaggcctccatta	C	T	NM_003275 // intron // 0 // Hs.404289 // TMOD1 // 7111 // Homo sapiens tropomodulin 1 (TMOD1), mRNA. /// ENST00000358692 // intron // 0 // — // — // — // — /// ENST00000259365 // intron // 0 // — // — // — // —	TMOD1	TMOD1, Homo sapiens tropomodulin 1 (TMOD1), q22.33
SNP_A-1835581	tacctttagctgaatac[A/C]ctggttcaaaaacatt	A	C	NM_003275 // intron // 0 // Hs.404289 // TMOD1 // 7111 // Homo sapiens tropomodulin 1 (TMOD1), mRNA. /// ENST00000358692 // intron // 0 // — // — // — // — /// ENST00000259365 // intron // 0 // — // — // — // —	TMOD1	TMOD1, Homo sapiens tropomodulin 1 (TMOD1), q22.33
SNP_A-2209711	cccattcaaagctctc[C/T]gactcctaacccccttt	C	T	NM_003275 // intron // 0 // Hs.404289 // TMOD1 // 7111 // Homo sapiens tropomodulin 1 (TMOD1), mRNA. /// ENST00000358692 // intron // 0 // — // — // — // — /// ENST00000259365 // intron // 0 // — // — // — // —	TMOD1	TMOD1, Homo sapiens tropomodulin 1 (TMOD1), q22.33
SNP_A-2077894	accagatgcatgcaag[C/T]ctggcagtttacagat	C	T	ENST00000338182 // downstream // 33736 // — // — // — // — /// ENST00000342013 // upstream // 118924 // — // — // — // — /// ENST00000313408 // upstream // 119077 // — // — // — // —	-	q22.33
SNP_A-2236141	ctccttccacagcaga[A/G]tacatgtgaacttgtg	A	G	ENST00000338182 // downstream // 34045 // — // — // — // — /// ENST00000342013 // upstream // 118615 // — // — // — // — /// ENST00000313408 // upstream // 118768 // — // — // — // —	-	q22.33
SNP_A-2175157	cacagtgtgaaattat[A/C]ataagagttgtagttg	A	C	NM_006401 // downstream // 4982 // Hs.494604 // ANP32B // 10541 // Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member B (ANP32B), mRNA. /// NM_018946 // upstream // 36318 // Hs.522310 // NANS // 54187 // Homo sapiens N-acetylneura	ANP32B	ANP32B, Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member B (ANP32B), q22.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2183362	cagcaccttgagtggg[A/G]acggagatacactgaa	A	G	NM_018946 // intron // 0 // Hs.522310 // NANS // 54187 // Homo sapiens N-acetylneuraminic acid synthase (sialic acid synthase) (NANS), mRNA. /// ENST00000210444 // intron // 0 // — // — // — /// ENST00000344494 // intron // 0 // — // — //	NANS	NANS, Homo sapiens N-acetylneuraminic acid synthase (sialic acid synthase) (NANS), q22.33
SNP_A-2210167	ccccagtacctctaga[A/C]tccagaatatgtaaca	A	C	NM_018946 // intron // 0 // Hs.522310 // NANS // 54187 // Homo sapiens N-acetylneuraminic acid synthase (sialic acid synthase) (NANS), mRNA. /// ENST00000210444 // intron // 0 // — // — // — /// ENST00000344494 // 3UTR // 0 // — // — // -	NANS	NANS, Homo sapiens N-acetylneuraminic acid synthase (sialic acid synthase) (NANS), q22.33
SNP_A-1847146	tatcatggtcatgaaaa[C/T]aaggaagtacgccatc	C	T	NM_033221 // intron // 0 // Hs.370530 // TRIM14 // 9830 // Homo sapiens tripartite motif-containing 14 (TRIM14), transcript variant 4, mRNA. /// NM_033220 // intron // 0 // Hs.370530 // TRIM14 // 9830 // Homo sapiens tripartite motif-containing 14 (TRIM14	TRIM14	TRIM14, Homo sapiens tripartite motif-containing 14 (TRIM14), transcript variant 4, q22.33
SNP_A-2157672	attgcagataaacaac[A/G]aatatttagcataag	A	G	NM_003389 // intron // 0 // Hs.113094 // CORO2A // 7464 // Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA. /// NM_052820 // intron // 0 // Hs.113094 // CORO2A // 7464 // Homo sapiens coronin, actin binding protein, 2A	CORO2A	CORO2A, Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, q22.33
SNP_A-2078964	acccacagtgagctc[A/G]acacgaggaaagtaac	A	G	AY026527 // intron // 0 // Hs.371016 // TBC1D2 // 55357 // Homo sapiens prostate antigen PARIS-1 mRNA, complete cds. /// ENST00000210447 // intron // 0 // — // — // — /// ENST00000342112 // intron // 0 // — // — // — /// ENST0000	TBC1D2	TBC1D2, Homo sapiens prostate antigen PARIS-1 complete cds, q22.33
SNP_A-2050312	aaggagcagagggggag[C/T]cgatgtgagagacagc	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2145623	atgcatgagaagttgt[A/G]aagaacaaggaatggc	A	G	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2290197	gcaaattaaggaagag[C/T]cacagagagaactgga	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1792673	ggtaacatattggaaa[A/C]cagaatcattagaacc	A	C	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2245845	ctgggtaagacctgta[C/T]agaaaatcttctgg	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2041880	aactaacacatgtgaa[C/T]tgaagccaagataagc	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2037992	aacacaaaagagacaa[C/T]gcttttactgatgag	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1997331	ctacgaggcctcttta[C/G]ggagccgggacattta	C	G	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1899963	tggacatcctgcttta[A/G]aatgatgtccctgcct	A	G	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2121030	agtctcattaggaaaa[C/T]ctgaccaacagtgtaa	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-2146722	atgcttaggcaagccc[G/T]gcagcgtccaatggtt	G	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // — // — // —	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1863209	tcatttctagctttaa[C/T]atttcagtgtgaaaaa	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // --- // --- // --- // ---	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1997341	tctgcctcttttcaca[C/T]ctactccctctaaggc	C	T	NM_005458 // intron // 0 // Hs.198612 // GPR51 // 9568 // Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA. /// ENST00000259455 // intron // 0 // --- // --- // --- // ---	GPR51	GPR51, Homo sapiens G protein-coupled receptor 51 (GPR51), q22.33
SNP_A-1839132	tagagccctcatgtaa[A/G]gtgccgcacattccct	A	G	NM_003774 // downstream // 81212 // Hs.534374 // GALNT4 // 8693 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), mRNA. /// NM_024642 // downstream // 81212 // Hs.47099 // GALNT12 // 7	GALNT4	GALNT4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), q22.33
SNP_A-2029356	aaagaattctaatgaa[A/T]gccagtagttgtcaca	A	T	NM_003774 // downstream // 117800 // Hs.534374 // GALNT4 // 8693 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), mRNA. /// NM_024642 // downstream // 117800 // Hs.47099 // GALNT12 //	GALNT4	GALNT4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), q22.33
SNP_A-1920306	ttaatggactctagac[A/T]agcgtgattgtatgcc	A	T	NM_003774 // downstream // 117865 // Hs.534374 // GALNT4 // 8693 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), mRNA. /// NM_024642 // downstream // 117865 // Hs.47099 // GALNT12 //	GALNT4	GALNT4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) (GALNT4), q22.33
SNP_A-1997352	gtaaggcagattactc[A/G]gaagaactggggtaga	A	G	NM_004612 // intron // 0 // Hs.494622 // TGFBR1 // 7046 // Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBR1), mRNA. /// ENST00000262458 // intron // 0 // --- // --- // --- // ---	TGFBR1	TGFBR1, Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBR1), q22.33
SNP_A-2108895	agcttaccccacggaa[A/C]gtttacagtgcccagt	A	C	NM_173199 // upstream // 495049 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 495049 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear re	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-1862600	tcattaggcactttgc[A/G]gagaccagatgctttg	A	G	NM_173199 // upstream // 455628 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 455628 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear re	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-2254803	cttggacggagcccct[C/T]agacagcaagatcacc	C	T	NM_173199 // upstream // 413275 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 413275 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear re	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-2105606	agccacccacccatta[A/C]atcagtggctcacagc	A	C	NM_173199 // upstream // 412670 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, mRNA. /// NM_006981 // upstream // 412670 // Hs.279522 // NR4A3 // 8013 // Homo sapiens nuclear re	NR4A3	NR4A3, Homo sapiens nuclear receptor subfamily 4, group A, member 3 (NR4A3), transcript variant 4, q22.33
SNP_A-1708070	aaaggcaccatcatccattacccta[C/T]agtctcaaagcagcaatcatcctgt	C	T	NM_003452 // intron // 0 // Hs.50123 // ZNF189 // 7743 // zinc finger protein 189	ZNF189	ZNF189 , rs2777345, zinc finger protein 189,q31.1
SNP_A-2212743	cccttgcatgggtcaa[A/G]atagataacagaccag	A	G	NM_183245 // intron // 0 // Hs.270443 // INVS // 27130 // Homo sapiens inversin (INVS), transcript variant 2, mRNA. /// NM_014425 // intron // 0 // Hs.270443 // INVS // 27130 // Homo sapiens inversin (INVS), transcript variant 1, mRNA. /// ENST00000262456	INVS	INVS, Homo sapiens inversin (INVS), transcript variant 2, q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2180776	cagaatacatttctct[C/G]acacttgagaccctgg	C	G	NM_197977 // downstream // 5169 // Hs.50123 // ZNF189 // 7743 // Homo sapiens zinc finger protein 189 (ZNF189), mRNA. /// NM_003452 // downstream // 5169 // Hs.50123 // ZNF189 // 7743 // Homo sapiens zinc finger protein 189 (ZNF189), mRNA. /// NM_000035 /	ZNF189	ZNF189, Homo sapiens zinc finger protein 189 (ZNF189), q31.1
SNP_A-1645874	aggaaaatatgaagattactttgca[A/T]aatattggatatgtgctgtggcaga	A	T	NM_001340 // downstream // 194230 // Hs.3232 // CYLC2 // 1539 // cylicin, basic protein of sperm head cytoskeleton 2 /// NM_006444 // upstream // 881607 // Hs.119023 // SMC2L1 // 10592 // SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	CYLC2	CYLC2 , rs1448585, cylicin, basic protein of sperm head cytoskeleton 2 ,q31.1
SNP_A-1673568	tgattactctggtacatagtaacaa[C/T]gtggctatgtagctcctgtcaccac	C	T	NM_001340 // downstream // 198454 // Hs.3232 // CYLC2 // 1539 // cylicin, basic protein of sperm head cytoskeleton 2 /// NM_006444 // upstream // 877383 // Hs.119023 // SMC2L1 // 10592 // SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	CYLC2	CYLC2 , rs1375214, cylicin, basic protein of sperm head cytoskeleton 2 ,q31.1
SNP_A-1901365	tggattaacatacgaa[A/T]agcgcctgtcaactga	A	T	ENST00000356894 // intron // 0 // --- // --- // --- // --- /// ENST00000354581 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-2066266	aattttattataagca[C/T]caaagtcaactgctag	C	T	ENST00000356894 // intron // 0 // --- // --- // --- // --- /// ENST00000354581 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1997408	atcaacctgttatgcc[C/T]gacactcctttctgta	C	T	ENST00000356894 // intron // 0 // --- // --- // --- // --- /// ENST00000354581 // intron // 0 // --- // --- // --- // ---	-	q31.1
SNP_A-1930223	ttcattctctacctga[C/T]agaacttcaccttaag	C	T	NM_147180 // upstream // 193342 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 1194931 // Hs.3232 // CYLC2 //	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m ,q31.1
SNP_A-2193324	catctctccaggttgc[C/T]aggtattataattcac	C	T	NM_147180 // upstream // 280855 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 1107418 // Hs.3232 // CYLC2 //	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m ,q31.1
SNP_A-1888719	tgagggaatggggaaa[A/G]tgagacaagaaatgga	A	G	NM_147180 // upstream // 447860 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 940413 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m ,q31.1
SNP_A-1706599	tgttatttttttctcctactggca[A/G]aacgttagacaatatttcaacttag	A	G	NM_001340 // downstream // 979069 // Hs.3232 // CYLC2 // 1539 // cylicin, basic protein of sperm head cytoskeleton 2 /// NM_006444 // upstream // 96768 // Hs.119023 // SMC2L1 // 10592 // SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	CYLC2	CYLC2 , rs515821, cylicin, basic protein of sperm head cytoskeleton 2 ,q31.1
SNP_A-2148963	atggttataaattcca[A/G]gggaacactctaaacc	A	G	NM_147180 // upstream // 728660 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 659613 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-1910082	tgtcatatgtatgtga[C/T]taattcaatgccttcc	C	T	NM_147180 // upstream // 939173 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 449100 // Hs.3232 // CYLC2 // 1	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-1816331	gttagaattgcagatg[C/T]acactatagtttaggg	C	T	NM_147180 // upstream // 1145925 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 242348 // Hs.3232 // CYLC2 //	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1997429	ccatggatgaggatag[C/T]atatgtaactgctcac	C	T	NM_147180 // upstream // 1171779 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 216494 // Hs.3232 // CYLC2 //	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m q31.1
SNP_A-2079041	acccagaaaatgggaa[A/G]taaaggtgagccaaat	A	G	NM_147180 // upstream // 1218760 // Hs.151167 // PPP3R2 // 5535 // Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m /// NM_001340 // upstream // 169513 // Hs.3232 // CYLC2 //	PPP3R2	PPP3R2, Homo sapiens protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, beta isoform (calcineurin B, type II) (PPP3R2), m ,q31.1
SNP_A-1667618	tatagtttcacgttaatctccagat[C/T]ctgttaagccactaaatac cagttt	C	T	NM_006444 // downstream // 464534 // Hs.119023 // SMC2L1 // 10592 // SMC2 structural maintenance of chromosomes 2-like 1 (yeast) /// NM_015469 // upstream // 143498 // Hs.24608 // NIPSNAP3A // 25934 // nipsnap homolog 3A (C. elegans)	SMC2L1	SMC2L1 , rs956193, SMC2 structural maintenance of chromosomes 2-like 1 (yeast) ,q31.1
SNP_A-2040366	aaccagactaagccca[G/T]ctttatcagttagcag	G	T	NM_001340 // downstream // 96787 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 991794 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1832383	tacaaaacaattaaaa[A/G]ttagctaagcatggtg	A	G	NM_001340 // downstream // 171121 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 917460 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2048095	aagcaattggttccac[A/C]cctgagtttctgattg	A	C	NM_001340 // downstream // 172478 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 916103 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2251691	cttcagtatctcttac[A/G]catgcaaataatacgc	A	G	NM_001340 // downstream // 271433 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 817148 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2102639	agatttaagaagtagc[A/T]gagaatttcaaatata	A	T	NM_001340 // downstream // 313671 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 774910 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2293574	gcagcatccggataaa[C/T]gacacctagtggttag	C	T	NM_001340 // downstream // 314503 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 774078 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2189079	cagttaacaccgacta[C/T]taaagctcctgtttct	C	T	NM_001340 // downstream // 315008 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 773573 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2266272	gaagggttaggaatta[A/C]aaagattggtggataa	A	C	NM_001340 // downstream // 323676 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 764905 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2097132	agactacctgacata[C/T]gagactacctccttg	C	T	NM_001340 // downstream // 335192 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 753389 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1856155	tcacaaatactacaaa[A/G]tttcagaattactatt	A	G	NM_001340 // downstream // 336918 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 751663 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1997442	ccttgtttacacaa[G/T]tgatgcagtaatagg	G	T	NM_001340 // downstream // 468264 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 620317 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-1744891	cagctagtttccttccttatctaaaa[C/T]tgtggtcaatagcaacaga ttattt	C	T	NM_022109 // intron // 0 // Hs.414728 // CDW92 // 23446 // CDW92 antigen /// NM_080546 // intron // 0 // Hs.414728 // CDW92 // 23446 // CDW92 antigen	CDW92	CDW92 , rs7040751, CDW92 antigen .q31.1
SNP_A-1869280	tcctgggctgtgcaga[A/G]aaaagatgccttgat	A	G	NM_001340 // downstream // 762668 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 325913 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2146283	atgctactgttgccat[A/G]aagtatttttagtctg	A	G	NM_001340 // downstream // 868251 // Hs.3232 // CYLC2 // 1539 // Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /// NM_006444 // upstream // 220330 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenanc	CYLC2	CYLC2, Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), q31.1
SNP_A-2029238	aaagaagctaaactga[C/G]agagaaaacttaaatgc	C	G	NM_006444 // intron // 0 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// ENST00000286398 // intron // 0 // — // — // — // — /// ENST00000259347 // intron // 0 // — /	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-1953137	tttctttacttgaaaa[A/C]tcaccattaagtcaag	A	C	NM_006444 // intron // 0 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// ENST00000286398 // intron // 0 // — // — // — // — /// ENST00000259347 // intron // 0 // — /	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2269066	gaattgaaagcttcat[A/G]agttaaaagagctaca	A	G	NM_006444 // intron // 0 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// ENST00000286398 // intron // 0 // — // — // — // — /// ENST00000259347 // intron // 0 // — /	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-1896462	tgctacacttgatagc[A/G]cagtacgtagtcaaca	A	G	NM_006444 // downstream // 264840 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 98014 // — // OR13F1 // 138805 // Homo sapiens olfactory recept	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2035289	aaatggaatgatttga[C/T]ggtattctagaaaact	C	T	NM_006444 // downstream // 276996 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 85858 // — // OR13F1 // 138805 // Homo sapiens olfactory recept	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1813888	gtgtattggttctgctt[A/G]aagacttcatttgtt	A	G	NM_006444 // downstream // 308645 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 54209 // — // OR13F1 // 138805 // Homo sapiens olfactory recept	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-2014432	tgtgtctactcctagc[C/G]cccaggaaagaatctg	C	G	NM_006444 // downstream // 332456 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 30398 // — // OR13F1 // 138805 // Homo sapiens olfactory recept	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-1997477	ttctttaactgtcaa[A/G]tactgaataaactcat	A	G	NM_006444 // downstream // 342714 // Hs.119023 // SMC2L1 // 10592 // Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA. /// NM_001004485 // upstream // 20140 // — // OR13F1 // 138805 // Homo sapiens olfactory recept	SMC2L1	SMC2L1, Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), q31.1
SNP_A-1846423	tatatgtgggggatga[G/T]aaaatatctgtgtgtg	G	T	NM_001004485 // downstream // 929 // — // OR13F1 // 138805 // Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), mRNA. /// ENST00000334726 // downstream // 929 // — // — // — // — /// ENST00000277216 // downstream // 201	OR13F1	OR13F1, Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), q31.1
SNP_A-1875463	tctctggagctataga[A/G]attgaggccaatgtg	A	G	NM_001004485 // downstream // 1322 // — // OR13F1 // 138805 // Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), mRNA. /// ENST00000334726 // downstream // 1322 // — // — // — // — /// ENST00000277216 // downstream // 1	OR13F1	OR13F1, Homo sapiens olfactory receptor, family 13, subfamily F, member 1 (OR13F1), q31.1
SNP_A-2139760	atctaaaataacaaga[A/G]aagtcacagtaaaaat	A	G	NM_001004483 // downstream // 26761 // — // OR13C8 // 138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 7780 // — // OR13C2 // 392376 // Homo sapiens olfactory receptor, famil	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-2303094	gctatacatttgcaca[G/T]atacttctttttgttc	G	T	NM_001004483 // downstream // 27391 // — // OR13C8 // 138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 7150 // — // OR13C2 // 392376 // Homo sapiens olfactory receptor, famil	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-1813649	gtgtacaagctcaaaa[G/T]agactcatcactatat	G	T	NM_001004483 // downstream // 27555 // — // OR13C8 // 138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 6986 // — // OR13C2 // 392376 // Homo sapiens olfactory receptor, famil	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-1957211	ttttactcccctcttta[A/G]ctgtaagacagagca	A	G	NM_001004483 // downstream // 29299 // — // OR13C8 // 138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 5242 // — // OR13C2 // 392376 // Homo sapiens olfactory receptor, famil	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-1997482	gttaaagacaagcata[C/T]acacctggctattctt	C	T	NM_001004483 // downstream // 32010 // — // OR13C8 // 138802 // Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), mRNA. /// NM_001004481 // downstream // 2531 // — // OR13C2 // 392376 // Homo sapiens olfactory receptor, famil	OR13C8	OR13C8, Homo sapiens olfactory receptor, family 13, subfamily C, member 8 (OR13C8), q31.1
SNP_A-1859979	tcaggttggggtttgaa[A/G]tgatcctgaggagact	A	G	NM_001004481 // upstream // 4670 // — // OR13C2 // 392376 // Homo sapiens olfactory receptor, family 13, subfamily C, member 2 (OR13C2), mRNA. /// NM_001004482 // upstream // 4670 // — // OR13C5 // 138799 // Homo sapiens olfactory receptor, family 13,	OR13C2	OR13C2, Homo sapiens olfactory receptor, family 13, subfamily C, member 2 (OR13C2), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2271022	gacataaagtaattca[C/T]aaggctgggcaaatt	C	T	NM_001004481 // upstream // 6233 // --- // OR13C2 // 392376 // Homo sapiens olfactory receptor, family 13, subfamily C, member 2 (OR13C2), mRNA. /// NM_001004482 // upstream // 6233 // --- // OR13C5 // 138799 // Homo sapiens olfactory receptor, family 13,	OR13C2	OR13C2, Homo sapiens olfactory receptor, family 13, subfamily C, member 2 (OR13C2), q31.1
SNP_A-2100682	agatacttactaaag[A/G]atggaaaaacatcatc	A	G	NM_001001956 // upstream // 1435 // --- // OR13C9 // 286362 // Homo sapiens olfactory receptor, family 13, subfamily C, member 9 (OR13C9), mRNA. /// NM_001004484 // upstream // 74879 // --- // OR13D1 // 286365 // Homo sapiens olfactory receptor, family 13	OR13C9	OR13C9, Homo sapiens olfactory receptor, family 13, subfamily C, member 9 (OR13C9), q31.1
SNP_A-1917494	tgttttaggctgttc[A/G]acaaaattttctgtga	A	G	NM_001001956 // upstream // 3909 // --- // OR13C9 // 286362 // Homo sapiens olfactory receptor, family 13, subfamily C, member 9 (OR13C9), mRNA. /// NM_001004484 // upstream // 72405 // --- // OR13D1 // 286365 // Homo sapiens olfactory receptor, family 13	OR13C9	OR13C9, Homo sapiens olfactory receptor, family 13, subfamily C, member 9 (OR13C9), q31.1
SNP_A-2072988	acaggactggacacca[A/G]aaataatgtcaaggta	A	G	NM_005502 // CDS // 0 // Hs.429294 // ABCA1 // 19 // Homo sapiens ATP binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// ENST00000297693 // CDS // 0 // --- // --- // ---	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-2071924	acagagattactctga[C/T]acatttgtcaacatgt	C	T	NM_005502 // intron // 0 // Hs.429294 // ABCA1 // 19 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// ENST00000297693 // intron // 0 // --- // --- // ---	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-1997494	attaaggcagcattaa[C/G]acaaaaacaatcttaa	C	G	NM_005502 // upstream // 124033 // Hs.429294 // ABCA1 // 19 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /// NM_022109 // upstream // 192642 // Hs.494700 // CDW92 // 23446 // Homo sapiens CDW92 antigen (CDW92), mRNA.	ABCA1	ABCA1, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), q31.1
SNP_A-2170020	caagggagaagggctg[A/G]atttgcctgtaaag	A	G	NM_022109 // intron // 0 // Hs.494700 // CDW92 // 23446 // Homo sapiens CDW92 antigen (CDW92), mRNA. /// NM_080546 // intron // 0 // Hs.494700 // CDW92 // 23446 // Homo sapiens CDW92 antigen (CDW92), mRNA. /// ENST00000185520 // intron // 0 // --- // --	CDW92	CDW92, Homo sapiens CDW92 antigen (CDW92), q31.1
SNP_A-1828231	taagaggcttctggga[A/G]atagatgttcaaacc	A	G	ENST00000343170 // intron // 0 // --- // --- // ---	-	q31.1
SNP_A-1873775	tctcagcacccttcaaa[A/T]tcacctgatgaaatatt	A	T	ENST00000343170 // intron // 0 // --- // --- // ---	-	q31.1
SNP_A-1807300	gtctcttcaattaggg[A/G]cagacataacacatac	A	G	ENST00000343170 // intron // 0 // --- // --- // ---	-	q31.1
SNP_A-2219701	ccttaactgattaacc[A/G]actttgcagcattcca	A	G	ENST00000343170 // intron // 0 // --- // --- // ---	-	q31.1
SNP_A-2222786	cgattactgaatagta[C/T]ggtaaaagtgttaa	C	T	NM_006731 // intron // 0 // Hs.55777 // FCMD // 2218 // Homo sapiens Fukuyama type congenital muscular dystrophy (fukutin) (FCMD), mRNA. /// ENST00000357998 // intron // 0 // --- // --- // ---	FCMD	FCMD, Homo sapiens Fukuyama type congenital muscular dystrophy (fukutin) (FCMD), q31.2
SNP_A-2119381	agtataagttatgcac[A/G]actggctttgtccta	A	G	NM_005421 // downstream // 5140 // Hs.247978 // TAL2 // 6887 // Homo sapiens T-cell acute lymphocytic leukemia 2 (TAL2), mRNA. /// NM_018112 // upstream // 26581 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87)	TAL2	TAL2, Homo sapiens T-cell acute lymphocytic leukemia 2 (TAL2), q31.2
SNP_A-2014443	aagataaaatttgaag[C/G]ctctcttatcaagaa	C	G	NM_018112 // downstream // 520003 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 // downstream // 520003 // --- // --- // --- /// ENST00000324126 // downstream // 564779 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1914654	tgttaatctgtttcta[C/T]gaaagttcatcaacca	C	T	NM_018112 // downstream // 530117 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA. /// ENST00000262559 // downstream // 530117 // --- // --- // --- /// ENST00000324126 // downstream // 554665 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2191516	catatgatactggaga[A/C]cttccccctttctgc	A	C	NM_018112 // downstream // 534631 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 534631 // — // — // — /// ENST00000324126 // downstream // 550151 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1922175	ttacttcagaactgga[C/T]catttagttgccactg	C	T	NM_018112 // downstream // 535187 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 535187 // — // — // — /// ENST00000324126 // downstream // 549595 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2048670	aagccaccgcatcgag[C/T]ccaatatcacatttac	C	T	NM_018112 // downstream // 571561 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 571561 // — // — // — /// ENST00000324126 // downstream // 513221 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2222177	cgacaaaatgagtgaa[C/T]gtaaatttagtccaaa	C	T	NM_018112 // downstream // 577371 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 577371 // — // — // — /// ENST00000324126 // downstream // 507411 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2128793	ataatcgtctcactaa[A/G]atgtcatgcttggct	A	G	NM_018112 // downstream // 600577 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 600577 // — // — // — /// ENST00000324126 // downstream // 484205 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2196178	catgtggcaagttata[C/T]ggtattaggctagta	C	T	NM_018112 // downstream // 606170 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 606170 // — // — // — /// ENST00000324126 // downstream // 478612 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1666320	cagtggagagctactaagtggcaa[A/G]agactgagtttcctct gtgattgt	A	G	NM_004235 // upstream // 648188 // Hs.376206 // KLF4 // 9314 // Kruppel-like factor 4 (gut) /// NM_006686 // downstream // 716756 // Hs.31323 // IKBKAP // 8518 // inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated pr	KLF4	KLF4 , rs1836459, Kruppel-like factor 4 (gut), q31.2
SNP_A-2263964	gaactatgttggttcc[C/T]agaacttaagtgtcag	C	T	NM_018112 // downstream // 885758 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 885758 // — // — // — /// ENST00000324126 // downstream // 199024 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1865225	tccatagagactcatc[A/G]acacatttcttcagt	A	G	NM_018112 // downstream // 930815 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 930815 // — // — // — /// ENST00000324126 // downstream // 153967 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-1925308	ttatctaagcaatgac[C/T]gagcgacttcaaatt	C	T	NM_018112 // downstream // 951315 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 951315 // — // — // — /// ENST00000324126 // downstream // 133467 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2
SNP_A-2184085	cagccccctgacatgcc[A/G]actcttgtgtgacata	A	G	NM_018112 // downstream // 998712 // Hs.411925 // TMEM38B // 55151 // Homo sapiens chromosome 9 open reading frame 87 (C9orf87), mRNA /// ENST00000262559 // downstream // 998712 // — // — // — /// ENST00000324126 // downstream // 86070 // -	TMEM38B	TMEM38B, Homo sapiens chromosome 9 open reading frame 87 (C9orf87), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1868689	tcctctgtcaaatagg[A/G]acaacaggttttttgt	A	G	NM_021224 // downstream // 116487 // Hs.370379 // ZNF462 // 58499 // Homo sapiens zinc finger protein 462 (ZNF462), mRNA. /// NM_002874 // upstream // 155310 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. //	ZNF462	ZNF462, Homo sapiens zinc finger protein 462 (ZNF462), q31.2
SNP_A-2185269	caggaagctttccata[C/T]aaaaccttgtagag	C	T	NM_021224 // downstream // 207012 // Hs.370379 // ZNF462 // 58499 // Homo sapiens zinc finger protein 462 (ZNF462), mRNA. /// NM_002874 // upstream // 64785 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. ///	ZNF462	ZNF462, Homo sapiens zinc finger protein 462 (ZNF462), q31.2
SNP_A-1997537	atacagcttatttatc[C/T]gagttttttgtagttca	C	T	NM_002874 // intron // 0 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// ENST00000262560 // intron // 0 // --- // --- // --- /// ENST00000358015 // intron // 0 // --- // --- // ---	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2294784	gcagttgcacaaataa[A/G]cataacctaggatctg	A	G	NM_002874 // downstream // 51389 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 51515 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2144368	atgataaagtaacttc[A/C]acctgacacagtaaaa	A	C	NM_002874 // downstream // 52027 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 52153 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2244380	ctggaatgagaatgcc[A/G]cgtccaggctgtgtta	A	G	NM_002874 // downstream // 52082 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 52208 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2179926	cacttttcttacttaaa[G/T]tcttccaatgacttc	G	T	NM_002874 // downstream // 53479 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 53605 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2253020	cttctcctggcttttta[G/T]gaaatctcactgttg	G	T	NM_002874 // downstream // 54148 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 54274 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-1821868	gttttagtgacattcc[A/G]caaagcctacctgtgt	A	G	NM_002874 // downstream // 54203 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 54329 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-1791736	gggtctgggatgtctc[A/G]caagtcctggaaactc	A	G	NM_002874 // downstream // 55257 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 55383 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-1943105	ttggtattcgcacagc[C/T]ctttaaagttttaag	C	T	NM_002874 // downstream // 58369 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 58495 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2230792	ctatgatattagctgg[G/T]attctcaatgctcatt	G	T	NM_002874 // downstream // 61122 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 61248 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2125476	agtttataaactagga[G/T]gacatactaagagctt	G	T	NM_002874 // downstream // 72141 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA. /// NM_002874 // downstream // 72267 // Hs.521640 // RAD23B // 5887 // Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), m	RAD23B	RAD23B, Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), q31.2
SNP_A-2177307	cacctgttatgttcca[A/G]gtgtctgaggagctag	A	G	NM_004235 // upstream // 120653 // Hs.376206 // KLF4 // 9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 120653 // — // — // — // — /// ENST00000316479 // upstream // 120653 // — // — // — //	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-1997549	tggcctggaaagaaca[G/T]ctacagtatggccaca	G	T	NM_004235 // upstream // 130362 // Hs.376206 // KLF4 // 9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 130362 // — // — // — // — /// ENST00000316479 // upstream // 130362 // — // — // — //	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-1795814	ggtggcaggcataagc[A/G]aggcagttcctgcatt	A	G	NM_004235 // upstream // 146125 // Hs.376206 // KLF4 // 9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 146125 // — // — // — // — /// ENST00000316479 // upstream // 146125 // — // — // — //	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-2253197	cttctgataacccctc[C/T]aatctatgtatgtgtt	C	T	NM_004235 // upstream // 172982 // Hs.376206 // KLF4 // 9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 172982 // — // — // — // — /// ENST00000316479 // upstream // 172982 // — // — // — //	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-2044031	aacttgcagccagtca[A/G]gaaagtcaagagaaga	A	G	NM_004235 // upstream // 246196 // Hs.376206 // KLF4 // 9314 // Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /// ENST00000259349 // upstream // 246196 // — // — // — // — /// ENST00000316479 // upstream // 246196 // — // — // — //	KLF4	KLF4, Homo sapiens Kruppel-like factor 4 (gut) (KLF4), q31.2
SNP_A-1997554	ccaaaaagcccaaact[C/G]aatgaatctactgctc	C	G	ENST00000297812 // upstream // 7609 // — // — // — // — /// ENST00000333948 // upstream // 784394 // — // — // — // —	-	q31.2
SNP_A-2241246	ctgaggcagaggggat[A/G]aatgggtagaaagtga	A	G	ENST00000297812 // upstream // 105672 // — // — // — // — /// ENST00000333948 // upstream // 686331 // — // — // — // —	-	q31.2
SNP_A-2183294	cagcacacttgctgca[C/T]agaggtagatttacag	C	T	ENST00000297812 // upstream // 298524 // — // — // — // — /// ENST00000333948 // upstream // 493479 // — // — // — // —	-	q31.2
SNP_A-1832381	tacaaaacaagactgg[A/G]cattggacatattttg	A	G	ENST00000297812 // upstream // 303282 // — // — // — // — /// ENST00000333948 // upstream // 488721 // — // — // — // —	-	q31.2
SNP_A-1852236	tattgtgaaaaatcaa[A/T]tgagatgatgtaaaat	A	T	ENST00000297812 // upstream // 305186 // — // — // — // — /// ENST00000333948 // upstream // 486817 // — // — // — // —	-	q31.2
SNP_A-2211214	ccctaaagaactacac[A/G]agtagaaagggtatca	A	G	ENST00000297812 // upstream // 307418 // — // — // — // — /// ENST00000333948 // upstream // 484585 // — // — // — // —	-	q31.2
SNP_A-2313009	ggactttgtataatgc[C/T]cttcactcctcccctt	C	T	ENST00000297812 // upstream // 318124 // — // — // — // — /// ENST00000333948 // upstream // 473879 // — // — // — // —	-	q31.2
SNP_A-2246600	ctgtaagagttcacat[A/G]atagctgagtggcgag	A	G	ENST00000297812 // upstream // 320517 // — // — // — // — /// ENST00000333948 // upstream // 471486 // — // — // — // —	-	q31.2
SNP_A-1856656	tcacataaattaccat[A/G]aagatgaaatgtcaga	A	G	ENST00000297812 // upstream // 348186 // — // — // — // — /// ENST00000333948 // upstream // 443817 // — // — // — // —	-	q31.2
SNP_A-2259289	gaaaaagaccagtaaa[A/T]ggactctccctagagc	A	T	ENST00000297812 // upstream // 350951 // — // — // — // — /// ENST00000333948 // upstream // 441052 // — // — // — // —	-	q31.2
SNP_A-1922611	ttagacccttgggtgc[A/G]acagcatttatagggt	A	G	ENST00000297812 // upstream // 388691 // — // — // — // — /// ENST00000333948 // upstream // 403312 // — // — // — // —	-	q31.2
SNP_A-1997580	tgatgacaggtagatg[A/T]cagaacggagcaaagt	A	T	ENST00000297812 // upstream // 467488 // — // — // — // — /// ENST00000333948 // upstream // 324515 // — // — // — // —	-	q31.2
SNP_A-1806741	gtctagagcttaggaa[A/G]tatgtcacctgctctg	A	G	ENST00000297812 // upstream // 563150 // — // — // — // — /// ENST00000333948 // upstream // 228853 // — // — // — // —	-	q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897208	tgctctcctgaaatga[A/T]cacattaaaacaaaca	A	T	NM_003640 // intron // 0 // Hs.494738 // IKBKAP // 8518 // Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA. /// ENST00000262535 // intron // 0 // — // — // — // —	IKBKAP	IKBKAP, Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), q31.3
SNP_A-1913693	tgtgtataaaacaca[C/T]ggagaaccacctaact	C	T	NM_032012 // upstream // 11804 // Hs.308074 // C9orf5 // 23731 // Homo sapiens chromosome 9 open reading frame 5 (C9orf5), mRNA. /// ENST00000223608 // upstream // 11804 // — // — // — // — /// ENST00000259327 // downstream // 5706 // — // — // —	C9orf5	C9orf5, Homo sapiens chromosome 9 open reading frame 5 (C9orf5), q31.3
SNP_A-1849136	tatgcgacttttggata[A/G]ggaagttcattgcat	A	G	NM_019114 // intron // 0 // Hs.269180 // EPB41L4B // 54566 // Homo sapiens erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), mRNA. /// ENST00000262536 // intron // 0 // — // — // — // —	EPB41L4B	EPB41L4B, Homo sapiens erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), q31.3
SNP_A-1802282	gtatatgtagcccaca[C/G]agtagactcacagcta	C	G	NM_019114 // intron // 0 // Hs.269180 // EPB41L4B // 54566 // Homo sapiens erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), mRNA. /// ENST00000262536 // intron // 0 // — // — // — // —	EPB41L4B	EPB41L4B, Homo sapiens erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), q31.3
SNP_A-2136753	atcacttgcaaaaact[A/G]aaaaggtcaataatgc	A	G	NM_019114 // intron // 0 // Hs.269180 // EPB41L4B // 54566 // Homo sapiens erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), mRNA. /// NM_018424 // intron // 0 // Hs.269180 // EPB41L4B // 54566 // Homo sapiens erythrocyte membrane protein band 4.1	EPB41L4B	EPB41L4B, Homo sapiens erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), q31.3
SNP_A-1915637	tgttctctcttgcca[C/T]agttattgttgtaagg	C	T	NM_147150 // upstream // 175470 // Hs.259461 // PALM2-AKAP2 // 445815 // Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, mRNA. /// NM_001004065 // upstream // 175470 // Hs.259461 // AKAP2 // 11217 // Homo sapiens A kinase (PRKA) anch	PALM2-AKAP2	PALM2-AKAP2, Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, q31.3
SNP_A-2145382	atgcagagctactcaa[A/G]gcatggaattctaag	A	G	NM_147150 // upstream // 100666 // Hs.259461 // PALM2-AKAP2 // 445815 // Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, mRNA. /// NM_001004065 // upstream // 100666 // Hs.259461 // AKAP2 // 11217 // Homo sapiens A kinase (PRKA) anch	PALM2-AKAP2	PALM2-AKAP2, Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, q31.3
SNP_A-2014459	ttactcctacgaaagt[A/G]aaatggcaaaagtgta	A	G	NM_147150 // upstream // 11111 // Hs.259461 // PALM2-AKAP2 // 445815 // Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, mRNA. /// NM_001004065 // upstream // 11111 // Hs.259461 // AKAP2 // 11217 // Homo sapiens A kinase (PRKA) anchor	PALM2-AKAP2	PALM2-AKAP2, Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, q31.3
SNP_A-2032199	aaagtgtaccttgaa[C/T]cggagaagtcgggccg	C	T	NM_147150 // intron // 0 // Hs.259461 // PALM2-AKAP2 // 445815 // Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, mRNA. /// NM_001004065 // intron // 0 // Hs.259461 // AKAP2 // 11217 // Homo sapiens A kinase (PRKA) anchor protein 2 (	PALM2-AKAP2	PALM2-AKAP2, Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, q31.3
SNP_A-2201154	ccaagtgcccgactag[A/C]agcaggtctgaaacag	A	C	NM_147150 // intron // 0 // Hs.259461 // PALM2-AKAP2 // 445815 // Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, mRNA. /// NM_001004065 // intron // 0 // Hs.259461 // AKAP2 // 11217 // Homo sapiens A kinase (PRKA) anchor protein 2 (	PALM2-AKAP2	PALM2-AKAP2, Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, q31.3
SNP_A-2014466	tggctgctcagagtca[C/T]gtgtcagccttctccc	C	T	NM_147150 // intron // 0 // Hs.259461 // PALM2-AKAP2 // 445815 // Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, mRNA. /// NM_001004065 // intron // 0 // Hs.259461 // AKAP2 // 11217 // Homo sapiens A kinase (PRKA) anchor protein 2 (	PALM2-AKAP2	PALM2-AKAP2, Homo sapiens PALM2-AKAP2 protein (PALM2-AKAP2), transcript variant 2, q31.3
SNP_A-1755492	attagagcataaaaaaaatgaaattat[C/T]ggtactgaaaagtatg atttctaaa	C	T	NM_003358 // downstream // 12477 // Hs.432605 // UGCG // 7357 // UDP-glucose ceramide glucosyltransferase /// NM_022486 // downstream // 95157 // Hs.28564 // SUSD1 // 64420 // sushi domain containing 1	UGCG	UGCG, rs1037182, UDP-glucose ceramide glucosyltransferase, q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1673330	ccagaaagaacaagttattgacaaa[A/G]gaaagggagttaga ccatcgctgga	A	G	NM_003358 // downstream // 12900 // Hs.432605 // UGCG // 7357 // UDP-glucose ceramide glucosyltransferase /// NM_022486 // downstream // 94734 // Hs.28564 // SUSD1 // 64420 // sushi domain containing 1	UGCG	UGCG , rs10513152, UDP-glucose ceramide glucosyltransferase ,q31.3
SNP_A-2067670	acaacaatagtaaaaag[G/T]ttatcactagcagatg	G	T	NM_003329 // upstream // 50171 // Hs.435136 // TXN // 7295 // Homo sapiens thioredoxin (TXN), mRNA. /// ENST00000259332 // upstream // 50171 // — // — // — /// ENST00000297826 // downstream // 59612 // — // — // —	TXN	TXN, Homo sapiens thioredoxin (TXN), q31.3
SNP_A-2288827	gattgttttatttacj[C/G]cacctgctcatccata	C	G	ENST00000297826 // intron // 0 // — // — // —	-	q31.3
SNP_A-1863310	tcatttaataagtca[A/G]tcatagtccacttgta	A	G	NM_005592 // upstream // 52350 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// ENST00000302728 // upstream // 66455 // — // — // — /// ENST00000189978 // upstream // 52350 // — // –	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-1852305	tattgttctctgtaatt[A/T]atgtcaccaggcctgc	A	T	NM_005592 // upstream // 27932 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// ENST00000302728 // upstream // 90873 // — // — // — /// ENST00000189978 // upstream // 27932 // — // –	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-1903934	tgggattcctctttcaa[C/T]ctggttgcaacacttc	C	T	NM_005592 // intron // 0 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// ENST00000189978 // intron // 0 // — // — // —	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2210671	ccccctaatgtaagc[C/T]gctcccccattctacca	C	T	NM_005592 // intron // 0 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// ENST00000189978 // intron // 0 // — // — // —	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-1997660	agccagggagttctgt[A/G]aaattatcttgtgttg	A	G	NM_005592 // downstream // 28559 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream // 43707 // Hs.126667 // EDG2 // 1902 // Homo sapiens endothelial differentiation, lysophosp	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2156877	attcttccaaattcta[C/T]gtccttgactacctat	C	T	NM_005592 // downstream // 30621 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream // 41645 // Hs.126667 // EDG2 // 1902 // Homo sapiens endothelial differentiation, lysophosp	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-1951404	tttctacattgaaca[A/T]ctgttatacttgtaat	A	T	NM_005592 // downstream // 58186 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream // 14080 // Hs.126667 // EDG2 // 1902 // Homo sapiens endothelial differentiation, lysophosp	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-2265471	gaagccataaagaaag[C/G]attgatgtgtatctaa	C	G	NM_005592 // downstream // 58935 // Hs.521653 // MUSK // 4593 // Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), mRNA. /// NM_001401 // downstream // 13331 // Hs.126667 // EDG2 // 1902 // Homo sapiens endothelial differentiation, lysophosp	MUSK	MUSK, Homo sapiens muscle, skeletal, receptor tyrosine kinase (MUSK), q31.3
SNP_A-1690061	atgccatgagtttccttctgtac[C/T]aagacctagcacagttctg agagg	C	T	NM_003408 // downstream // 103050 // Hs.150406 // ZFP37 // 7539 // zinc finger protein 37 homolog (mouse) /// NM_033051 // upstream // 48079 // Hs.512668 // TSCOT // 57864 // thymic stromal co-transporter	ZFP37	ZFP37 , rs20225543, zinc finger protein 37 homolog (mouse) ,q32
SNP_A-2065733	aatttatttttaaatgc[A/T]aaagtagtggcctta	A	T	ENST00000259335 // intron // 0 // — // — // —	-	q31.3
SNP_A-1923603	ttaggtttgtatcca[A/G]tgctgcgggagggacc	A	G	NM_012212 // downstream // 6342 // Hs.546348 // LTB4DH // 22949 // Homo sapiens leukotriene B4 12-hydroxydehydrogenase (LTB4DH), mRNA. /// NM_012212 // downstream // 6490 // Hs.546348 // LTB4DH // 22949 // Homo sapiens leukotriene B4 12-hydroxydehydrogena	LTB4DH	LTB4DH, Homo sapiens leukotriene B4 12-hydroxydehydrogenase (LTB4DH), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2233372	ctcaggtctttgtctat[C/T]gttagcaagagccttc	C	T	NM_004125 // intron // 0 // Hs.534196 // GNG10 // 2790 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 10 (GNG10), mRNA. /// ENST00000313480 // intron // 0 // --- // --- // ---	GNG10	GNG10, Homo sapiens guanine nucleotide binding protein (G protein), gamma 10 (GNG10), q31.3
SNP_A-1921715	ttacgtagccaaaatta[C/T]catttctttctata	C	T	NM_173521 // upstream // 11393 // Hs.428209 // C9orf84 // 158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 90430 // Hs.304249 // UGCG // 7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-2036622	aaattggaagtttaag[C/G]ccgagcactgtggctc	C	G	NM_173521 // upstream // 32880 // Hs.428209 // C9orf84 // 158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 68943 // Hs.304249 // UGCG // 7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-1895540	tgcctagtaaaggtca[C/T]gattgctcatctttca	C	T	NM_173521 // upstream // 49726 // Hs.428209 // C9orf84 // 158401 // Homo sapiens chromosome 9 open reading frame 84 (C9orf84), mRNA. /// NM_003358 // upstream // 52097 // Hs.304249 // UGCG // 7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (	C9orf84	C9orf84, Homo sapiens chromosome 9 open reading frame 84 (C9orf84), q31.3
SNP_A-2140604	atctctaagcaaagcg[C/T]aatagacctgaatca	C	T	NM_003358 // downstream // 11618 // Hs.304249 // UGCG // 7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), mRNA. /// NM_022486 // downstream // 96092 // Hs.494827 // SUSD1 // 64420 // Homo sapiens sushi domain containing 1 (SUSD1), mRN	UGCG	UGCG, Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), q31.3
SNP_A-1881347	tctttcagtatctgg[G/T]gcaaattctgttccaa	G	T	NM_003358 // downstream // 29610 // Hs.304249 // UGCG // 7357 // Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), mRNA. /// NM_022486 // downstream // 78100 // Hs.494827 // SUSD1 // 64420 // Homo sapiens sushi domain containing 1 (SUSD1), mRN	UGCG	UGCG, Homo sapiens UDP-glucose ceramide glucosyltransferase (UGCG), q31.3
SNP_A-2210787	cccctggctgatcata[C/T]gttaagttgttatagc	C	T	NM_032303 // intron // 0 // Hs.59486 // HSDL2 // 84263 // Homo sapiens chromosome 9 open reading frame 99 (C9orf99), mRNA. /// ENST00000338786 // intron // 0 // --- // --- // --- /// ENST00000262542 // intron // 0 // --- // --- // ---	HSDL2	HSDL2, Homo sapiens chromosome 9 open reading frame 99 (C9orf99), q32
SNP_A-2184860	cagctgtaagaagaaa[G/T]gaagtactgatagata	G	T	ENST00000356558 // intron // 0 // --- // --- // --- // --- /// ENST00000337530 // intron // 0 // --- // --- // ---	-	q32
SNP_A-2272744	gacgtgtcctcataaa[C/T]ggagggaaatctgtg	C	T	NM_021106 // intron // 0 // Hs.494875 // RGS3 // 5998 // Homo sapiens regulator of G-protein signalling 3 (RGS3), transcript variant 2, mRNA. /// NM_134427 // intron // 0 // Hs.494875 // RGS3 // 5998 // Homo sapiens regulator of G-protein signalling 3 (RG	RGS3	RGS3, Homo sapiens regulator of G-protein signalling 3 (RGS3), transcript variant 2, q32
SNP_A-1997724	tctactcattgataaa[C/T]ctgaagccatagga	C	T	ENST00000317885 // upstream // 149174 // --- // --- // --- // --- /// ENST00000288466 // upstream // 110446 // --- // --- // --- // --- /// ENST00000307730 // upstream // 262018 // --- // --- // --- // ---	-	q32
SNP_A-1883562	tgaacctcgttgatac[A/G]gacctcagtcatgaat	A	G	ENST00000288466 // intron // 0 // --- // --- // ---	-	q32
SNP_A-2286797	gatgggaaaagagccc[A/G]gagaaggaaagcaaca	A	G	ENST00000288466 // intron // 0 // --- // --- // ---	-	q32
SNP_A-2262550	gaaatgttagctgtga[C/T]cttatacctagtgcct	C	T	NM_032888 // intron // 0 // Hs.494892 // COL27A1 // 85301 // Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), mRNA. /// ENST00000357257 // intron // 0 // --- // --- // --- /// ENST00000359387 // intron // 0 // --- // --- // --- /// ENST	COL27A1	COL27A1, Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), q32
SNP_A-2218188	cctgctaaggaaaata[C/G]aaactgagccgggagg	C	G	NM_032888 // intron // 0 // Hs.494892 // COL27A1 // 85301 // Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), mRNA. /// ENST00000357257 // intron // 0 // --- // --- // --- /// ENST00000359387 // intron // 0 // --- // --- // --- /// ENST	COL27A1	COL27A1, Homo sapiens collagen, type XXVII, alpha 1 (COL27A1), q32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2233348	ctcaggggccagagaa[C/G]gttgctgtcttgccca	C	G	NM_004888 // upstream // 77587 // Hs.388654 // ATP6V1G1 // 9550 // Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), mRNA. /// ENST00000277323 // upstream // 4734 // — // — // — // — /// ENST00000265134 // u	ATP6V1G1	ATP6V1G1, Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), q32
SNP_A-1716301	catctagatctaaaaacaacactca[C/T]tgaggtaggaaataa aaagtaacaa	C	T	NM_014010 // intron // 0 // - // - // - // -	-	-, rs7040792, -,q33.1
SNP_A-1698805	tccttaaacttctcaatgtctccat[G/T]tttcttttttgttacaaggagtt aac	G	T	NM_014010 // intron // 0 // - // - // - // -	-	-, rs1885234, -,q33.1
SNP_A-1783277	ggcagtcctccttctc[C/T]aggttacatgaggcag	C	T	NM_001244 // 3UTR // 0 // Hs.494901 // TNFSF8 // 944 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8), mRNA. /// ENST00000223795 // 3UTR // 0 // — // — // — // —	TNFSF8	TNFSF8, Homo sapiens tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8), q32
SNP_A-1676476	gaaatgtgttggtaggtatggtcta[C/T]gtgttatggtgtccagaag aggagc	C	T	NM_014010 // intron // 0 // - // - // - // -	-	-, rs10491578, -,q33.1
SNP_A-2232780	ctcactggaatcccaa[A/G]gactttataaaaatgc	A	G	NM_002160 // intron // 0 // Hs.143250 // TNC // 3371 // Homo sapiens tenascin C (hexabrachion) (TNC), mRNA. /// ENST00000350763 // intron // 0 // — // — // — // — /// ENST00000345230 // intron // 0 // — // — // — // — /// ENST00000346706 /	TNC	TNC, Homo sapiens tenascin C (hexabrachion) (TNC), q33.1
SNP_A-2152461	attaactgtggcttat[A/G]aattgctgcttcagcc	A	G	NM_002160 // upstream // 256760 // Hs.143250 // TNC // 3371 // Homo sapiens tenascin C (hexabrachion) (TNC), mRNA. /// NM_017418 // upstream // 1783 // Hs.148841 // DEC1 // 50514 // Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA. /// ENST0000035	TNC	TNC, Homo sapiens tenascin C (hexabrachion) (TNC), q33.1
SNP_A-2150104	atgtcctaagaactta[A/G]taagcctttgttcaag	A	G	NM_017418 // downstream // 150263 // Hs.148841 // DEC1 // 50514 // Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA. /// NM_002581 // upstream // 601404 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysi	DEC1	DEC1, Homo sapiens deleted in esophageal cancer 1 (DEC1), q33.1
SNP_A-1713772	taacacgcaatattaccattttcaa[A/T]ctgtgttttcagaacagaa ttgttt	A	T	AB014534 // intron // 0 // Hs.30898 // ASTN2 // 23245 // astrotactin 2	ASTN2	ASTN2 , rs10513299, astrotactin 2,q33.1
SNP_A-2267453	gaatatagcaagtcct[A/C]aaaagatgacagttat	A	C	NM_017418 // downstream // 454899 // Hs.148841 // DEC1 // 50514 // Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA. /// NM_002581 // upstream // 296768 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysi	DEC1	DEC1, Homo sapiens deleted in esophageal cancer 1 (DEC1), q33.1
SNP_A-1842656	tagtaaaaactacagc[C/T]gataggaacccaggat	C	T	NM_017418 // downstream // 509617 // Hs.148841 // DEC1 // 50514 // Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA. /// NM_002581 // upstream // 242050 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysi	DEC1	DEC1, Homo sapiens deleted in esophageal cancer 1 (DEC1), q33.1
SNP_A-2263825	gaacgctggagctcat[A/C]aaactggagttcgtgt	A	C	NM_017418 // downstream // 545714 // Hs.148841 // DEC1 // 50514 // Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA. /// NM_002581 // upstream // 205953 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysi	DEC1	DEC1, Homo sapiens deleted in esophageal cancer 1 (DEC1), q33.1
SNP_A-1866100	tcccagatgtgtgggt[C/G]aaatcgtcactgacac	C	G	NM_002581 // downstream // 12307 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // downstream // 18011 // — // — // 0 // Human pregnancy-associated plasma protein-A preprofor	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098929	agagcttagattgtga[C/G]agattgagaagcttcc	C	G	NM_002581 // downstream // 21368 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // downstream // 27092 // --- // --- // 0 // Human pregnancy-associated plasma protein-A preprotor	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1
SNP_A-1997779	agtgatacctaaaccc[A/G]aaggatgagtagaaat	A	G	NM_002581 // downstream // 22621 // Hs.494928 // PAPPA // 5069 // Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA. /// U28727 // downstream // 28325 // --- // --- // 0 // Human pregnancy-associated plasma protein-A preprotor	PAPPA	PAPPA, Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), q33.1
SNP_A-2046910	aagaggtgagggaggg[C/T]caccacatactaatttt	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2310915	ggaaggagccaataga[C/T]ggtggaggcagaaac	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2056848	aatagggaaagagaaa[C/G]gattgtgaaagatgga	C	G	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2039568	aacatctcgctttcaa[C/T]ggcaaattataggcga	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2156608	attctgattatgttta[C/T]gatcctcaaaaggctt	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2260686	gaaacctagtaaaatt[G/T]aatggaagcatgaaga	G	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2031791	aaagtatcatcagtca[G/T]cagtgttaactggact	G	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2155511	attcatttaatttgta[C/G]agcaacaccatgaatt	C	G	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2113270	aggccgtcactggagd[A/G]agttcacagagcagta	A	G	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2254283	ctgcaaattcactta[C/G]gttaggaaatcagttg	C	G	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2173690	cacacaa[gaaaggta[A/T]attttgagccttctc	A	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2257603	ctttgcatttgcata[C/T]ggaaaaactgatctta	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1938457	ttgactgaatatcac[A/G]catctccctagctgt	A	G	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1997786	gtaatagcattttgag[A/G]aagttagaatatcgca	A	G	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1997787	aaagcctcaccacagg[A/T]cagaatggaaaccgtc	A	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1859031	tcagcattggctcaaa[C/T]tgggctaagacattta	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1708899	gtgagtgaaacaataacatggaatc[A/G]gaaacctttggccca gatttcgttt	A	G	NM_003266 // downstream // 813691 // Hs.174312 // TLR4 // 7099 // toll-like receptor 4 /// NM_014618 // downstream // 637164 // Hs.6090 // DBC1 // 1620 // deleted in bladder cancer 1 /// NM_138554 // downstream // 813691 // Hs.174312 // TLR4 // 7099 // t	TLR4	TLR4, rs7037164, toll-like receptor 4 ,q33.1
SNP_A-1757645	acccattgttgatcttcagtttag[C/G]ccatgttctactgttaactg ctgcg	C	G	NM_003266 // downstream // 822057 // Hs.174312 // TLR4 // 7099 // toll-like receptor 4 /// NM_014618 // downstream // 628798 // Hs.6090 // DBC1 // 1620 // deleted in bladder cancer 1 /// NM_138554 // downstream // 822057 // Hs.174312 // TLR4 // 7099 // t	TLR4	TLR4, rs4412426, toll-like receptor 4 ,q33.1
SNP_A-1714853	gatgtgcatgaatactgggagataa[C/T]attgttggtagtaaaact aagggct	C	T	NM_003266 // downstream // 822780 // Hs.174312 // TLR4 // 7099 // toll-like receptor 4 /// NM_014618 // downstream // 628075 // Hs.6090 // DBC1 // 1620 // deleted in bladder cancer 1 /// NM_138554 // downstream // 822780 // Hs.174312 // TLR4 // 7099 // t	TLR4	TLR4, rs10513334, toll-like receptor 4 ,q33.1
SNP_A-2294459	gcagtacttatcacac[C/T]gtggcatgtgtttagc	C	T	NM_198186 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // intron // 0 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 3, mRNA. /// E	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1644902	tgcacactctgaagaattgtagac[G/T]cagttcagaagaggact ttattctg	G	T	NM_014618 // intron // 0 // Hs.6090 // DBC1 // 1620 // deleted in bladder cancer 1	DBC1	DBC1, rs4144592, deleted in bladder cancer 1,q33.1
SNP_A-2276801	gagatacaatgatagat[C/G]gaagttgaaccaatt	C	G	NM_198186 // upstream // 100167 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 100167 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1789199	gggcatagcaaaaaag[C/G]cataacagaggaagc	C	G	NM_198186 // upstream // 106854 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 106854 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2147487	atggataaggtaatca[A/G]tgagttgtcaatgtac	A	G	NM_198186 // upstream // 123561 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 123561 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1853020	tatttgattattctta[A/G]caattcacacttctca	A	G	NM_198186 // upstream // 127821 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 127821 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2194017	catgaatgctgtcaga[A/G]cctttgtttttcctca	A	G	NM_198186 // upstream // 134662 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 134662 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-2279565	gaggcaaaagtgaaag[C/G]cagattatggtgagct	C	G	NM_198186 // upstream // 238693 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, mRNA. /// NM_198187 // upstream // 238693 // Hs.546352 // ASTN2 // 23245 // Homo sapiens astrotactin 2 (ASTN2), transcript variant	ASTN2	ASTN2, Homo sapiens astrotactin 2 (ASTN2), transcript variant 2, q33.1
SNP_A-1697380	aggtactatctcatctaatccttac[C/T]caaagcacaaggggga atagctgac	C	T	NM_014618 // upstream // 45092 // Hs.6090 // DBC1 // 1620 // deleted in bladder cancer 1 /// NM_018249 // downstream // 974360 // Hs.437967 // CDK5RAP2 // 55755 // CDK5 regulatory subunit associated protein 2	DBC1	DBC1 , rs10491527, deleted in bladder cancer 1 ,q33.1
SNP_A-1921392	ttaccagagatcaaga[A/G]ctcactttcaatttca	A	G	NM_138557 // downstream // 69031 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 68205 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcrip	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-2159448	atttacaaagagaaaa[C/T]tagttcacctgaatga	C	T	NM_138557 // downstream // 92968 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 92142 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcrip	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-2157502	attgatcgcagaaagc[G/T]caatagattgtgaaga	G	T	NM_138557 // downstream // 133403 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 132577 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcr	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-2152897	attacacaactggtaa[A/G]gtagcaataaagaaat	A	G	NM_138557 // downstream // 136787 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 135961 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcr	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-2279598	gaggcaataggcagaa[C/T]cacagaaggcagtcag	C	T	NM_138557 // downstream // 140696 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, mRNA. /// NM_138556 // downstream // 139870 // Hs.174312 // TLR4 // 7099 // Homo sapiens toll-like receptor 4 (TLR4), transcr	TLR4	TLR4, Homo sapiens toll-like receptor 4 (TLR4), transcript variant 4, q33.1
SNP_A-1700576	tgtctgctttcttgttcattcaata[A/T]tgcctgtttttgaccactccatc ac	A	T	NM_014618 // upstream // 526286 // Hs.6090 // DBC1 // 1620 // deleted in bladder cancer 1 /// NM_018249 // downstream // 493166 // Hs.437967 // CDK5RAP2 // 55755 // CDK5 regulatory subunit associated protein 2	DBC1	DBC1 , rs2151642, deleted in bladder cancer 1 ,q33.2
SNP_A-1881167	tctttagacactccaa[A/T]cttgtcatgggaaatt	A	T	NM_014618 // downstream // 633948 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 449402 // --- // --- // --- // --- /// ENST00000265922 // downstream // 633948 // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1833009	tacacacagatgggaa[C/T]gaaggtatagaggact	C	T	NM_014618 // downstream // 632240 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 451110 // --- // --- // --- // --- /// ENST00000265922 // downstream // 632240 // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2033224	aaatactgcaaagtta[A/G]gaatctgagcaatacg	A	G	NM_014618 // downstream // 627188 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 456162 // --- // --- // --- // --- /// ENST00000265922 // downstream // 627188 // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1814778	gtgtgtctgtgagaga[A/C]agtttgtatatgtgtc	A	C	NM_014618 // downstream // 182641 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 900709 // --- // --- // --- // --- /// ENST00000265922 // downstream // 182641 // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1839251	tagaggtaggtagagg[C/T]caggtggagagagata	C	T	NM_014618 // downstream // 12052 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000332944 // upstream // 1071298 // --- // --- // --- // --- /// ENST00000265922 // downstream // 12052 // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2227867	ctaccctcaaccttga[C/T]gagcaaacccdgcctt	C	T	NM_014618 // intron // 0 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1807587	gtctggcgttccacca[G/T]tagcaggtcactcaat	G	T	NM_014618 // intron // 0 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1997869	ttcctgtccacgttc[A/G]cccagctagatcaaat	A	G	NM_014618 // intron // 0 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2030812	aaaggaaaacaaaacat[A/G]agcatagaatggaatc	A	G	NM_014618 // intron // 0 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-1892562	tgcaatgactaacctat[G/T]cccaagacaatagaga	G	T	NM_014618 // intron // 0 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2146104	atgccttcagctggtg[G/T]ataaaggaaatggcaat	G	T	NM_014618 // intron // 0 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// ENST00000265922 // intron // 0 // --- // --- // --- // ---	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2162556	attttcctgaacacta[C/T]ggaaggaggggccgatt	C	T	NM_014618 // upstream // 35540 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 983913 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2110936	aggacttgttcaaaaa[C/T]gtattcctggcctgct	C	T	NM_014618 // upstream // 49829 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 969624 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2262369	gaaatgatgtccaaga[C/T]ggatatgaagggtta	C	T	NM_014618 // upstream // 145950 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 873503 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259490	gaaaacaacatgaaaa[C/T]acagttaggattaaga	C	T	NM_014618 // upstream // 329523 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 689930 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2170407	caagtcaaagtcctac[A/G]aaatgaccagcacatt	A	G	NM_014618 // upstream // 352731 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 666722 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2120767	agtcctgcctgagcga[C/G]agataatgcaaagagc	C	G	NM_014618 // upstream // 367451 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 652002 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.1
SNP_A-2037602	aacaagaaagctgtga[A/C]agtttttgactcaaag	A	C	NM_014618 // upstream // 388786 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 630667 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-1997886	cagttaattccagatg[G/T]atgttgttaccagtgt	G	T	NM_014618 // upstream // 395073 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 624380 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2299794	gcctaacgtatcctgc[A/G]gacccaagttagaagc	A	G	NM_014618 // upstream // 526478 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 492975 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2081763	accttctcaaggtcac[A/C]aagtgcatccggtata	A	C	NM_014618 // upstream // 528353 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 491100 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2197400	cattccaggaactgtc[A/G]aaagggcaatgtgatt	A	G	NM_014618 // upstream // 537921 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 481532 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2152323	attaaatttgaagacc[A/G]caatgaagagagaaat	A	G	NM_014618 // upstream // 538750 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 480703 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-1997894	tgctcaaaagaaggca[A/G]tcaaatcttctggtaa	A	G	NM_014618 // upstream // 541468 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 477985 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2308979	gcttttcacatattgc[A/C]ccctggaaaatggtcc	A	C	NM_014618 // upstream // 701767 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 317686 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2281305	gagtatgaaaagtgag[A/C]ataattgtgggaggca	A	C	NM_014618 // upstream // 964545 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 54908 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-1869561	tccttaaaagtgaaga[A/C]ggaggcggaagagaag	A	C	NM_014618 // upstream // 974273 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 45180 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-2138844	atccctattcataatc[C/T]caacctgcccctgtgt	C	T	NM_014618 // upstream // 1007523 // Hs.532316 // DBC1 // 1620 // Homo sapiens deleted in bladder cancer 1 (DBC1), mRNA. /// NM_018249 // downstream // 11930 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CD	DBC1	DBC1, Homo sapiens deleted in bladder cancer 1 (DBC1), q33.2
SNP_A-1854315	tcaaagtgctttcaaa[A/G]acatagtttggtcagt	A	G	NM_018249 // intron // 0 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), mRNA. /// ENST00000359309 // intron // 0 // — // — // — // — /// ENST00000360822 // intron // 0 // — // — // –	CDK5RAP2	CDK5RAP2, Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), q33.2
SNP_A-1997908	tggtcagaccacacaa[C/G]cctgagcagtttggga	C	G	NM_018249 // intron // 0 // Hs.269560 // CDK5RAP2 // 55755 // Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), mRNA. /// ENST00000359309 // intron // 0 // — // — // — // — /// ENST00000360822 // intron // 0 // — // — // –	CDK5RAP2	CDK5RAP2, Homo sapiens CDK5 regulatory subunit associated protein 2 (CDK5RAP2), q33.2
SNP_A-1944050	ttgtcaaaacaatcca[A/G]atctatttcaacagct	A	G	NM_001735 // intron // 0 // Hs.494997 // C5 // 727 // Homo sapiens complement component 5 (C5), mRNA. /// ENST00000223642 // intron // 0 // — // — // — // —	C5	C5, Homo sapiens complement component 5 (C5), q33.2
SNP_A-2176211	caccactggcctatga[A/T]aaccttacagttcatc	A	T	NM_007018 // intron // 0 // Hs.246344 // CEP1 // 11064 // Homo sapiens centrosomal protein 1 (CEP1), mRNA. /// ENST00000238341 // intron // 0 // — // — // — // —	CEP1	CEP1, Homo sapiens centrosomal protein 1 (CEP1), q33.2
SNP_A-2258456	cttttcgggtgcaggg[A/G]cacgttttgactttct	A	G	NM_016322 // upstream // 809 // Hs.371563 // RAB14 // 51552 // Homo sapiens RAB14, member RAS oncogene family (RAB14), mRNA. /// NM_198252 // upstream // 65506 // Hs.522373 // GSN // 2934 // Homo sapiens gelsolin (amyloidosis, Finnish type) (GSN), transcr	RAB14	RAB14, Homo sapiens RAB14, member RAS oncogene family (RAB14), q33.2
SNP_A-2055683	aataatgtatgctaca[A/G]cacaaagcatttatat	A	G	NM_198194 // upstream // 236129 // Hs.253903 // STOM // 2040 // Homo sapiens stomatin (STOM), transcript variant 2, mRNA. /// NM_004099 // upstream // 236129 // Hs.253903 // STOM // 2040 // Homo sapiens stomatin (STOM), transcript variant 1, mRNA. /// NM_	STOM	STOM, Homo sapiens stomatin (STOM), transcript variant 2, q33.2
SNP_A-2202593	ccacctcctgagctta[C/G]agaccattggaactcg	C	G	NM_198194 // upstream // 293330 // Hs.253903 // STOM // 2040 // Homo sapiens stomatin (STOM), transcript variant 2, mRNA. /// NM_004099 // upstream // 293330 // Hs.253903 // STOM // 2040 // Homo sapiens stomatin (STOM), transcript variant 1, mRNA. /// NM_	STOM	STOM, Homo sapiens stomatin (STOM), transcript variant 2, q33.2
SNP_A-2309057	gcttttggaggatgga[A/C]ggagattgtaaattga	A	C	NM_194252 // intron // 0 // Hs.546505 // C9orf20 // 158135 // Homo sapiens chromosome 9 open reading frame 20 (C9orf20), mRNA. /// ENST00000321582 // intron // 0 // — // — // — // —	C9orf20	C9orf20, Homo sapiens chromosome 9 open reading frame 20 (C9orf20), q33.2
SNP_A-2188927	cagtgtcatataagga[A/C]cccgttcaaaaccacc	A	C	NM_194252 // intron // 0 // Hs.546505 // C9orf20 // 158135 // Homo sapiens chromosome 9 open reading frame 20 (C9orf20), mRNA. /// ENST00000321582 // intron // 0 // — // — // — // —	C9orf20	C9orf20, Homo sapiens chromosome 9 open reading frame 20 (C9orf20), q33.2
SNP_A-2032115	aaagtgctattaaccc[A/G]atgataaagattatga	A	G	NM_194252 // intron // 0 // Hs.546505 // C9orf20 // 158135 // Homo sapiens chromosome 9 open reading frame 20 (C9orf20), mRNA. /// ENST00000321582 // intron // 0 // — // — // — // — /// ENST00000336217 // intron // 0 // — // — // — // —	C9orf20	C9orf20, Homo sapiens chromosome 9 open reading frame 20 (C9orf20), q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2195582	catggtcagaagaggg[A/G]catttcctctacttca	A	G	NM_199177 // downstream // 30990 // Hs.368011 // MRRF // 92399 // Homo sapiens mitochondrial ribosome recycling factor (MRRF), nuclear gene encoding mitochondrial protein, transcript variant 2, /// NM_199176 // downstream // 68624 // Hs.368011 // MRRF //	MRRF	MRRF, Homo sapiens mitochondrial ribosome recycling factor (MRRF), nuclear gene encoding mitochondrial protein, transcript variant 2, q33.2
SNP_A-1875903	tctgaaaggtgttgaa[C/T]gtaattaacttgtccc	C	T	X64989 // intron // 0 // Hs.460145 // OR1J2 // 26740 // H.sapiens mRNA HTPCRX15 for olfactory receptor. /// ENST00000335302 // intron // 0 // — // — // —	OR1J2	OR1J2, H.sapiens HTPCRX15 for olfactory receptor. q33.2
SNP_A-2133625	atatcagataagggact[A/G]atgacgctgaggtggc	A	G	NM_001004457 // intron // 0 // Hs.533921 // OR1N2 // 138882 // Homo sapiens olfactory receptor, family 1, subfamily N, member 2 (OR1N2), mRNA. /// ENST00000304873 // intron // 0 // — // — // —	OR1N2	OR1N2, Homo sapiens olfactory receptor, family 1, subfamily N, member 2 (OR1N2), q33.2
SNP_A-2197705	cattcttatagactag[A/C]aggagcataggacaag	A	C	NM_012197 // intron // 0 // Hs.271341 // RABGAP1 // 23637 // Homo sapiens RAB GTPase activating protein 1 (RABGAP1), mRNA. /// ENST00000343851 // intron // 0 // — // — // —	RABGAP1	RABGAP1, Homo sapiens RAB GTPase activating protein 1 (RABGAP1), q33.2
SNP_A-2257879	cttgtaaattccaca[C/T]gaaaaagttcaaaagc	C	T	NM_012197 // intron // 0 // Hs.271341 // RABGAP1 // 23637 // Homo sapiens RAB GTPase activating protein 1 (RABGAP1), mRNA. /// ENST00000343851 // intron // 0 // — // — // —	RABGAP1	RABGAP1, Homo sapiens RAB GTPase activating protein 1 (RABGAP1), q33.3
SNP_A-1857060	tcaccctcctggtat[A/T]cacagtcaccattgtc	A	T	ENST00000277300 // intron // 0 // — // — // —	-	q33.3
SNP_A-2308419	gcttgtttagttttct[A/G]ctactagctgtgtgac	A	G	ENST00000326805 // intron // 0 // — // — // — /// ENST00000309058 // intron // 0 // — // — // — /// —	-	q33.3
SNP_A-1886649	tgactcctgtcttaca[C/G]cgtcaacctctccggc	C	G	NM_173689 // downstream // 600739 // — // CRB2 // 286204 // Homo sapiens crumbs homolog 2 (Drosophila) (CRB2), mRNA. /// NM_004789 // upstream // 36772 // Hs.445265 // LHX2 // 9355 // Homo sapiens LIM homeobox 2 (LHX2), mRNA. /// ENST00000359999 // down	CRB2	CRB2, Homo sapiens crumbs homolog 2 (Drosophila) (CRB2), q33.3
SNP_A-2087164	actgatgatttctcc[A/G]agaagctctcctttc	A	G	NM_004789 // downstream // 6160 // Hs.445265 // LHX2 // 9355 // Homo sapiens LIM homeobox 2 (LHX2), mRNA. /// NM_014397 // upstream // 218290 // Hs.197071 // NEK6 // 10783 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 6 (NEK6), mRNA. /// N	LHX2	LHX2, Homo sapiens LIM homeobox 2 (LHX2), q33.3
SNP_A-2079071	acccagactctgacc[A/G]gcaaaaaccgcgagat	A	G	NM_004789 // downstream // 65074 // Hs.445265 // LHX2 // 9355 // Homo sapiens LIM homeobox 2 (LHX2), mRNA. /// NM_014397 // upstream // 159376 // Hs.197071 // NEK6 // 10783 // Homo sapiens NIMA (never in mitosis gene a)-related kinase 6 (NEK6), mRNA. ///	LHX2	LHX2, Homo sapiens LIM homeobox 2 (LHX2), q33.3
SNP_A-1688074	ataaaaatcactgagcagtttgt[C/T]aaaacccgttctgatt ggcata	C	T	NM_032293 // intron // 0 // Hs.201800 // GARNL3 // 84253 // GTPase activating RANGAP domain-like 3	GARNL3	GARNL3 , rs10513480, GTPase activating RANGAP domain-like 3,q33.3
SNP_A-1927284	ttcaaagctattcag[A/G]accgtggcaaccgcta	A	G	NM_024117 // intron // 0 // Hs.495138 // MAPKAP1 // 79109 // Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), mRNA. /// BC003044 // intron // 0 // Hs.495138 // MAPKAP1 // 79109 // Homo sapiens mitogen-activated protein kinase	MAPKAP1	MAPKAP1, Homo sapiens mitogen-activated protein kinase associated protein 1 (MAPKAP1), q33.3
SNP_A-2275751	gagacccacaggccca[A/G]catgagaggctagtg	A	G	NM_006195 // downstream // 54614 // Hs.428027 // PBX3 // 5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream // 54614 // — // — // — // — // — /// ENST00000342287 // downstream // 55779 // —	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-2222736	cgatgccacattccca[A/G]tggaagaagatgctaa	A	G	NM_006195 // downstream // 150567 // Hs.428027 // PBX3 // 5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream // 150567 // — // — // — // — // — /// ENST00000342287 // downstream // 151732 //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2046167	aagactgtgaaaggta[C/T]gattccagaaaagaag	C	T	NM_006195 // downstream // 221885 // Hs.428027 // PBX3 // 5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream // 221885 // --- // --- // --- /// ENST00000342287 // downstream // 223050 //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-2062664	aatgtcgtctgcccag[C/G]aatgcagagtgtagat	C	G	NM_006195 // downstream // 265495 // Hs.428027 // PBX3 // 5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream // 265495 // --- // --- // --- /// ENST00000342287 // downstream // 266660 //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-1953336	ttgaaacgaagtctct[C/T]ctctactgccgaggct	C	T	NM_006195 // downstream // 307409 // Hs.428027 // PBX3 // 5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream // 307409 // --- // --- // --- /// ENST00000342287 // downstream // 308574 //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-1809561	gtgagagtctgtttcaa[A/G]ataaagaagtgccagg	A	G	NM_006195 // downstream // 308019 // Hs.428027 // PBX3 // 5090 // Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA. /// ENST00000300401 // downstream // 308019 // --- // --- // --- /// ENST00000342287 // downstream // 309184 //	PBX3	PBX3, Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), q33.3
SNP_A-2201499	ccaatgtcaaactaca[G/T]gatagccgcctccaga	G	T	ENST00000357220 // intron // 0 // --- // --- // --- /// ENST00000360044 // intron // 0 // --- // - -// --- // —	-	q33.3
SNP_A-1932825	ttccttgtgggcttca[C/T]gtcctacttacagag	C	T	NM_002316 // upstream // 51015 // Hs.133709 // LMX1B // 4010 // Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), mRNA. /// AF057135 // upstream // 51015 // Hs.133709 // LMX1B // 4010 // Homo sapiens LIM homeodomain protein LMX1B mRNA, compl	LMX1B	LMX1B, Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), q33.3
SNP_A-1788120	gggagatgcccagtgaa[C/T]gggtctgccagggatc	C	T	NM_002316 // intron // 0 // Hs.133709 // LMX1B // 4010 // Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), mRNA. /// AF057135 // intron // 0 // Hs.133709 // LMX1B // 4010 // Homo sapiens LIM homeodomain protein LMX1B mRNA, complete cds. ///	LMX1B	LMX1B, Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), q33.3
SNP_A-2159200	atttaaagaaatgcaa[C/G]atgaattcacacacac	C	G	NM_002316 // downstream // 22076 // Hs.133709 // LMX1B // 4010 // Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), mRNA. /// AF057135 // downstream // 22076 // Hs.133709 // LMX1B // 4010 // Homo sapiens LIM homeodomain protein LMX1B mRNA, c	LMX1B	LMX1B, Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), q33.3
SNP_A-2151751	atgtttaatttctgtta[C/T]ggcacctgctcctteg	C	T	AB082524 // downstream // 26835 // Hs.177633 // ZBTB34 // 403341 // Homo sapiens mRNA for KIAA1993 protein. /// NM_012098 // downstream // 179600 // Hs.521731 // ANGPTL2 // 23452 // Homo sapiens angiopoietin-like 2 (ANGPTL2), mRNA. /// ENST00000319119 //	ZBTB34	ZBTB34, Homo sapiens for KIAA1993 protein. q33.3
SNP_A-1956335	tttgttaaggaaacta[C/T]gaattccctgacaaaa	C	T	ENST00000259351 // intron // 0 // --- // --- // --- /// ENST00000303578 // intron // 0 // --- // --- // --- /// ENST00000300410 // intron // 0 // --- // - -// --- // —	-	q33.3
SNP_A-2074389	acatacgaagtaggaa[A/G]taagcagaaagatttc	A	G	NM_012098 // upstream // 135520 // Hs.521731 // ANGPTL2 // 23452 // Homo sapiens angiopoietin-like 2 (ANGPTL2), mRNA. /// NM_032293 // upstream // 6582 // Hs.29304 // GARNL3 // 84253 // Homo sapiens GTPase activating Rap/RanGAP domain-like 3 (GARNL3), mRN	ANGPTL2	ANGPTL2, Homo sapiens angiopoietin-like 2 (ANGPTL2), q33.3
SNP_A-1998008	agatgtcagtttcccc[A/G]catgactgatgtcact	A	G	NM_032293 // intron // 0 // Hs.29304 // GARNL3 // 84253 // Homo sapiens GTPase activating Rap/RanGAP domain-like 3 (GARNL3), mRNA. /// ENST00000314904 // intron // 0 // --- // --- // --- /// ENST00000338940 // intron // 0 // --- // --- // -	GARNL3	GARNL3, Homo sapiens GTPase activating Rap

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2240907	ctgagacgtacgctca[C/G]acatcatgcatgagaa	C	G	NM_014580 // downstream // 13323 // Hs.179522 // SLC2A8 // 29988 // Homo sapiens solute carrier family 2, (facilitated glucose transporter) member 8 (SLC2A8), mRNA. /// NM_007135 // upstream // 3175 // Hs.522399 // ZNF79 // 7633 // Homo sapiens zinc finge	SLC2A8	SLC2A8, Homo sapiens solute carrier family 2, (facilitated glucose transporter) member 8 (SLC2A8), q33.3
SNP_A-2142459	atgaaatgaacagtcc[A/G]actggcctacttgctc	A	G	NM_007135 // intron // 0 // Hs.522399 // ZNF79 // 7633 // Homo sapiens zinc finger protein 79 (pT7) (ZNF79), mRNA. /// ENST00000357834 // intron // 0 // — // — // — // —	ZNF79	ZNF79, Homo sapiens zinc finger protein 79 (pT7) (ZNF79), q33.3
SNP_A-2149230	atgtaagcagaaacta[C/T]gtcttcatccccactc	C	T	NM_007135 // intron // 0 // Hs.522399 // ZNF79 // 7633 // Homo sapiens zinc finger protein 79 (pT7) (ZNF79), mRNA. /// ENST00000357834 // intron // 0 // — // — // — // —	ZNF79	ZNF79, Homo sapiens zinc finger protein 79 (pT7) (ZNF79), q33.3
SNP_A-1889200	tgagtctggcaaccat[C/T]aaggtactgggccctc	C	T	NM_138361 // CDS // 0 // Hs.495188 // LRSAM1 // 90678 // Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, mRNA. /// ENST00000300417 // CDS // 0 // — // — // — // — /// ENST00000356168 // CDS //	LRSAM1	LRSAM1, Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, q33.3
SNP_A-2243265	ctgcctggtctcacta[A/G]ggccatccgaggtggg	A	G	NM_138361 // intron // 0 // Hs.495188 // LRSAM1 // 90678 // Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, mRNA. /// ENST00000300417 // intron // 0 // — // — // — // — /// ENST00000356168 // i	LRSAM1	LRSAM1, Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, q34.11
SNP_A-2273757	gactgctttgagagag[A/G]aggattaggatgctgg	A	G	NM_001261 // downstream // 8753 // Hs.150423 // CDK9 // 1025 // Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA. /// NM_004957 // upstream // 4059 // Hs.335084 // FPGS // 2356 // Homo sapiens folylpolyglutamate synthase (FPGS), m	CDK9	CDK9, Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), q34.11
SNP_A-2208513	cccacgaatctccaca[C/T]cagcaatggcaagact	C	T	NM_173492 // upstream // 2163 // Hs.445486 // PIP5KL1 // 138429 // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase-like 1 (PIP5KL1), mRNA. /// NM_152690 // downstream // 5445 // Hs.108973 // DPM2 // 8818 // Homo sapiens dolichyl-phosphate mannosylt	PIP5KL1	PIP5KL1, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase-like 1 (PIP5KL1), q34.11
SNP_A-1820595	gtttcaacctctgtca[C/T]cagggaattactcaaa	C	T	NM_197956 // downstream // 90685 // Hs.373606 // C9orf90 // 203245 // Homo sapiens chromosome 9 open reading frame 90 (C9orf90), mRNA. /// ENST00000291841 // upstream // 4221 // — // — // — // — /// ENST00000304792 // downstream // 90685 // — //	C9orf90	C9orf90, Homo sapiens chromosome 9 open reading frame 90 (C9orf90), q34.11
SNP_A-2026887	aaacacgtgagaggaa[A/G]cacaggccgggtgtga	A	G	NM_197956 // downstream // 7534 // Hs.373606 // C9orf90 // 203245 // Homo sapiens chromosome 9 open reading frame 90 (C9orf90), mRNA. /// ENST00000291841 // upstream // 87372 // — // — // — // — /// ENST00000304792 // downstream // 7534 // — //	C9orf90	C9orf90, Homo sapiens chromosome 9 open reading frame 90 (C9orf90), q34.11
SNP_A-1864886	tccaggctccaagctc[A/G]ctattggcaggcactg	A	G	NM_052901 // 3UTR // 0 // Hs.5476 // SLC25A25 // 114789 // Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 (SLC25A25), mRNA. /// ENST00000277470 // 3UTR // 0 // --- // — // — // — /// ENST00000344324 // 3U	SLC25A25	SLC25A25, Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 (SLC25A25), q34.11
SNP_A-1740845	taaaaataaaagaccaagaacacat[A/G]agctggaatgattaa tatgttaaac	A	G	NM_020960 // intron // 0 // Hs.442329 // GPR107 // 57720 // G protein-coupled receptor 107	GPR107	GPR107 , rs1407568, G protein-coupled receptor 107,q34.11
SNP_A-2115893	agggtgtgggtagtaa[A/G]ctgcaggaaactgaca	A	G	NM_203434 // upstream // 70139 // Hs.529857 // IER5L // 389792 // Homo sapiens immediate early response 5-like (IER5L), mRNA. /// ENST00000339671 // upstream // 70139 // — // — // — // — /// ENST00000316786 // upstream // 72825 // — // — // –	IER5L	IER5L, Homo sapiens immediate early response 5-like (IER5L), q34.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2191089	catagtaggtgctcaa[C/T]gaactcagattgaact	C	T	NM_203434 // upstream // 82435 // Hs.529857 // IER5L // 389792 // Homo sapiens immediate early response 5-like (IER5L), mRNA. /// ENST00000339671 // upstream // 82435 // — // — // — // — /// ENST00000316786 // upstream // 60529 // — // — // –	IER5L	IER5L, Homo sapiens immediate early response 5-like (IER5L), q34.11
SNP_A-2312538	ggacctcatgctaaga[C/T]gcgcaacaaaattagg	C	T	NM_199350 // downstream // 132645 // Hs.124223 // LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 // downstream // 141287 // — // — // — // — /// ENST00000316717 // downstream // 132645 //	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-1933770	ttctatccaggatcca[A/G]aagtttctcctgatgg	A	G	NM_199350 // downstream // 40761 // Hs.124223 // LOC375759 // 375759 // Homo sapiens hypothetical protein LOC375759 (LOC375759), mRNA. /// ENST00000355781 // downstream // 233171 // — // — // — // — /// ENST00000316717 // downstream // 40761 // –	LOC375759	LOC375759, Homo sapiens hypothetical protein LOC375759 (LOC375759), q34.11
SNP_A-2192832	catcctcctcacgtaa[C/G]tctctacggaaaagcc	C	G	NM_014064 // intron // 0 // Hs.522433 // AD-003 // 28989 // Homo sapiens AD-003 protein (AD-003), mRNA. /// ENST00000340583 // intron // 0 // — // — // — // —	AD-003	AD-003, Homo sapiens AD-003 protein (AD-003), q34.11
SNP_A-2051996	aaggtgttcagaccca[A/G]ggtactgcatctcttc	A	G	NM_014064 // intron // 0 // Hs.522433 // AD-003 // 28989 // Homo sapiens AD-003 protein (AD-003), mRNA. /// ENST00000340583 // intron // 0 // — // — // — // —	AD-003	AD-003, Homo sapiens AD-003 protein (AD-003), q34.11
SNP_A-2301995	gcgtcttcgtacatca[A/G]tctctgtgcacagcgg	A	G	NM_016307 // downstream // 9624 // Hs.546395 // PRRX2 // 51450 // Homo sapiens paired related homeobox 2 (PRRX2), mRNA. /// NM_198797 // downstream // 6037 // Hs.146688 // PTGES // 9536 // Homo sapiens prostaglandin E synthase (PTGES), transcript variant	PRRX2	PRRX2, Homo sapiens paired related homeobox 2 (PRRX2), q34.11
SNP_A-1938856	ttgaggccacctgtgg[A/G]aatggaagactgtgga	A	G	NM_015033 // intron // 0 // Hs.189409 // FNBP1 // 23048 // Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // — // — // — // —	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-2284843	gatccaacagacaccc[C/T]ccaagatttaatattt	C	T	NM_015033 // intron // 0 // Hs.189409 // FNBP1 // 23048 // Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // — // — // — // —	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-1938449	ttgacttctatagtta[A/G]gttggcatttttataa	A	G	NM_015033 // intron // 0 // Hs.189409 // FNBP1 // 23048 // Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // — // — // — // —	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-1882905	tgaaaggtatctatta[C/T]agtcctactggtgttt	C	T	NM_015033 // intron // 0 // Hs.189409 // FNBP1 // 23048 // Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // — // — // — // —	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-1795264	ggtgagtggaggaaaa[C/T]ctaggtcgtggaaatg	C	T	NM_015033 // intron // 0 // Hs.189409 // FNBP1 // 23048 // Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // — // — // — // — /// ENST00000355681 // intron // 0 // — // — // — // —	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-2249672	cttaagttgtgaggca[C/T]tcggtacatagattga	C	T	NM_015033 // intron // 0 // Hs.189409 // FNBP1 // 23048 // Homo sapiens formin binding protein 1 (FNBP1), mRNA. /// ENST00000335141 // intron // 0 // — // — // — // —	FNBP1	FNBP1, Homo sapiens formin binding protein 1 (FNBP1), q34.11
SNP_A-1802559	gtatctccattgcttg[C/T]atctggtattgttatc	C	T	NM_020960 // intron // 0 // Hs.512461 // GPR107 // 57720 // Homo sapiens G protein-coupled receptor 107 (GPR107), mRNA. /// ENST00000291972 // intron // 0 // — // — // — // — /// ENST00000338106 // intron // 0 // — // — // — // — /// ENST0	GPR107	GPR107, Homo sapiens G protein-coupled receptor 107 (GPR107), q34.11
SNP_A-2122712	agtggagaagccaata[C/G]gcaaacccaagtccac	C	G	ENST00000291972 // intron // 0 // — // — // — // — /// ENST00000347136 // intron // 0 // — // — // — // —	-	q34.11
SNP_A-2107434	agctacgacagattga[A/T]tagagctggcatccaa	A	T	NM_014286 // intron // 0 // Hs.301760 // FREQ // 23413 // Homo sapiens frequenin homolog (Drosophila) (FREQ), mRNA. /// ENST00000223979 // intron // 0 // — // — // — // —	FREQ	FREQ, Homo sapiens frequenin homolog (Drosophila) (FREQ), q34.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2032504	aaataaaaattaaaag[A/G]attcagcctgcccagt	A	G	NM_014286 // intron // 0 // Hs.301760 // FREQ // 23413 // Homo sapiens frequenin homolog (Drosophila) (FREQ), mRNA. /// ENST00000223979 // intron // 0 // — // — // — // —	FREQ	FREQ, Homo sapiens frequenin homolog (Drosophila) (FREQ), q34.11
SNP_A-1819860	gttgtggtatcttttc[A/C]aatcaaccctaagcaa	A	C	NM_000050 // intron // 0 // Hs.160786 // ASS // 445 // Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, mRNA. /// NM_054012 // intron // 0 // Hs.160786 // ASS // 445 // Homo sapiens argininosuccinate synthetase (ASS), transcript vari	ASS	ASS, Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, q34.11
SNP_A-1915415	tgttccccttgtacac[A/C]gagatacggacaatag	A	C	NM_000050 // intron // 0 // Hs.160786 // ASS // 445 // Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, mRNA. /// NM_054012 // intron // 0 // Hs.160786 // ASS // 445 // Homo sapiens argininosuccinate synthetase (ASS), transcript vari	ASS	ASS, Homo sapiens argininosuccinate synthetase (ASS), transcript variant 1, q34.11
SNP_A-1647108	acctgccagaggaaaaaggctctag[C/G]tattattaacagcagt tgtactatg	C	G	NM_007344 // upstream // 171068 // Hs.54780 // TTF1 // 7270 // transcription termination factor, RNA polymerase I /// NM_020064 // upstream // 4716 // Hs.283809 // BARHL1 // 56751 // BarH-like 1 (Drosophila)	TTF1	TTF1 , rs578802, transcription termination factor, RNA polymerase I ,q34.13
SNP_A-2314793	ggagtgagcagcatcc[A/G]accgccgcctctgaca	A	G	NM_007313 // downstream // 4690 // Hs.431048 // ABL1 // 25 // Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1 (ABL1), transcript variant b, mRNA. /// NM_005157 // downstream // 4690 // Hs.431048 // ABL1 // 25 // Homo sapiens v-abl Abel	ABL1	ABL1, Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1 (ABL1), transcript variant b, q34.12
SNP_A-1710714	cctcagttatagactacatgcatca[C/T]tattgagtactgattatta agctat	C	T	NM_022779 // intron // 0 // Hs.133082 // DDX31 // 64794 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 /// NM_138620 // intron // 0 // Hs.133082 // DDX31 // 64794 // DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	DDX31	DDX31 , rs10512415, DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 ,q34.13
SNP_A-1914173	tgtgtgtgtgccttca[A/G]aggtcctcaggtcagg	A	G	ENST00000292015 // downstream // 26129 // — // — // — // — /// ENST00000357304 // upstream // 371 // — // — // — // — /// ENST00000320547 // upstream // 11692 // — // — // — // —	-	q34.13
SNP_A-2268244	gaatgagccagagttc[A/G]aatgcaagatgaaacg	A	G	NM_005312 // upstream // 59989 // Hs.127897 // RAPGEF1 // 2889 // Homo sapiens Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1), transcript variant 1, mRNA. /// NM_198679 // upstream // 59989 // Hs.127897 // RAPGEF1 // 2889 // Homo sapiens Rap gua	RAPGEF1	RAPGEF1, Homo sapiens Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1), transcript variant 1, q34.13
SNP_A-1795986	ggtggtattttgtgcc[C/T]ctcaccagctttccct	C	T	NM_004269 // downstream // 75327 // Hs.374262 // CRSP8 // 9442 // Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa (CRSP8), mRNA. /// ENST00000330174 // upstream // 2012 // — // — // — // — /// ENST00000292035 //	CRSP8	CRSP8, Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa (CRSP8), q34.13
SNP_A-1865012	tccagtcaaccactac[A/G]gagaggaaaaacattc	A	G	NM_004269 // intron // 0 // Hs.374262 // CRSP8 // 9442 // Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa (CRSP8), mRNA. /// ENST00000292035 // intron // 0 // — // — // — // — /// ENST00000357028 // intron // 0	CRSP8	CRSP8, Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa (CRSP8), q34.13
SNP_A-2195914	catgtcagactgtcca[C/G]gtgcaaattctggatt	C	G	NM_032536 // intron // 0 // Hs.163642 // NTNG2 // 84628 // Homo sapiens netrin G2 (NTNG2), mRNA. /// ENST00000356598 // intron // 0 // — // — // — // — /// ENST00000360670 // intron // 0 // — // — // — // —	NTNG2	NTNG2, Homo sapiens netrin G2 (NTNG2), q34.13
SNP_A-2213902	cctaaatttccctaca[C/T]gtcagacttcccagtt	C	T	NM_015046 // intron // 0 // Hs.460317 // ALS4 // 23064 // Homo sapiens senataxin (KIAA0625), mRNA. /// ENST00000224140 // intron // 0 // — // — // — // —	ALS4	ALS4, Homo sapiens senataxin (KIAA0625), q34.13
SNP_A-2195768	catgtaccatcataca[G/T]agctatttttttgtat	G	T	NM_207417 // intron // 0 // Hs.201709 // FLJ46082 // 389799 // Homo sapiens FLJ46082 protein (FLJ46082), mRNA. /// ENST00000343036 // intron // 0 // — // — // — // —	FLJ46082	FLJ46082, Homo sapiens FLJ46082 protein (FLJ46082), q34.13
SNP_A-2305756	gctgcctcctacttca[C/T]gagctggcatttagca	C	T	NM_207417 // intron // 0 // Hs.201709 // FLJ46082 // 389799 // Homo sapiens FLJ46082 protein (FLJ46082), mRNA. /// ENST00000343036 // intron // 0 // — // — // — // —	FLJ46082	FLJ46082, Homo sapiens FLJ46082 protein (FLJ46082), q34.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1786974	gggaaaagcgcttcca[A/G]aaaagttgagcctgtc	A	G	NM_207417 // intron // 0 // Hs.201709 // FLJ46082 // 389799 // Homo sapiens FLJ46082 protein (FLJ46082), mRNA. /// ENST00000343036 // intron // 0 // — // — // — // —	FLJ46082	FLJ46082, Homo sapiens FLJ46082 protein (FLJ46082), q34.13
SNP_A-1998055	cttattttaagatctc[A/G]caatgccagcaacggc	A	G	NM_138620 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA. /// NM_022779 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box p	DDX31	DDX31, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, q34.13
SNP_A-1814587	gtgtggacttttagaa[A/G]tgatactgctctgggt	A	G	NM_138620 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA. /// NM_022779 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box p	DDX31	DDX31, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, q34.13
SNP_A-2224992	cgtgggtataaccgga[C/T]gaaacctgtgtgtgca	C	T	NM_138620 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA. /// NM_022779 // intron // 0 // Hs.495410 // DDX31 // 64794 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box p	DDX31	DDX31, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, q34.13
SNP_A-2086102	actctctccagttcta[A/C]gactcctctctacatc	A	C	NM_000368 // intron // 0 // Hs.370854 // TSC1 // 7248 // Homo sapiens tuberous sclerosis 1 (TSC1), mRNA. /// ENST00000298552 // intron // 0 // — // — // — // —	TSC1	TSC1, Homo sapiens tuberous sclerosis 1 (TSC1), q34.13
SNP_A-1998060	aggtagctgccctggc[A/G]tatttaacaacatcag	A	G	NM_000368 // CDS // 0 // Hs.370854 // TSC1 // 7248 // Homo sapiens tuberous sclerosis 1 (TSC1), mRNA. /// ENST00000298552 // CDS // 0 // — // — // — // —	TSC1	TSC1, Homo sapiens tuberous sclerosis 1 (TSC1), q34.13
SNP_A-1791270	gggtaagactgagcga[A/G]ggagataaaggaaatt	A	G	NM_000368 // intron // 0 // Hs.370854 // TSC1 // 7248 // Homo sapiens tuberous sclerosis 1 (TSC1), mRNA. /// ENST00000298552 // intron // 0 // — // — // — // —	TSC1	TSC1, Homo sapiens tuberous sclerosis 1 (TSC1), q34.13
SNP_A-2034174	aaatccaacactgtca[C/T]gataagagcactcaat	C	T	NM_021996 // upstream // 19630 // Hs.495419 // GBGT1 // 26301 // Homo sapiens globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (GBGT1), mRNA. /// NM_014581 // downstream // 21736 // Hs.449629 // OBP2B // 29989 // Homo sapiens odorant binding protei	GBGT1	GBGT1, Homo sapiens globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (GBGT1), q34.2
SNP_A-2272080	gaccctgtaacggcca[A/G]cgttgcagtctgaggt	A	G	NM_020469 // intron // 0 // Hs.495420 // ABO // 28 // Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra /// ENST00000319878 // intron // 0 // — // — // — // —	ABO	ABO, Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra q34.2
SNP_A-2051988	aaggtgtggataaggg[A/C]actactgtacgtgact	A	C	NM_020469 // intron // 0 // Hs.495420 // ABO // 28 // Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra /// ENST00000319878 // intron // 0 // — // — // — // —	ABO	ABO, Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra ,q34.2
SNP_A-2201226	ccaagtttgggaaacc[A/G]gcaaggtgagtattgg	A	G	NM_020469 // upstream // 2876 // Hs.495420 // ABO // 28 // Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra /// NM_006753 // downstream // 44072 // Hs.274430 // SURF6 // 6838	ABO	ABO, Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra ,q34.2
SNP_A-2300435	gcctcttcttataata[A/G]ggacaccagtcacatt	A	G	NM_020469 // upstream // 41182 // Hs.495420 // ABO // 28 // Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra /// NM_006753 // downstream // 5766 // Hs.274430 // SURF6 // 6838	ABO	ABO, Homo sapiens ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltra ,q34.2
SNP_A-1819662	gttgtatctgtgaaaa[G/T]ttaaagtattcacact	G	T	ENST00000358558 // intron // 0 // — // — // — // — /// ENST00000356943 // intron // 0 // — // — // — // —	-	q34.2
SNP_A-1926126	ttatgttttaacgaga[C/G]aagatcagcttgtgta	C	G	ENST00000344942 // intron // 0 // — // — // — // —	-	q34.2
SNP_A-2178453	cactcccctcctgtaa[C/T]gtgctgagctctgacc	C	T	ENST00000344942 // intron // 0 // — // — // — // —	-	q34.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102698	agatttccagttcccc[C/T]ctgagttctggcccat	C	T	NM_017588 // downstream // 229321 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream // 229321 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcrip	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-1824332	taaacctcctttaccaa[C/T]acaaactcgagtgtct	C	T	NM_017588 // downstream // 242400 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream // 242400 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcrip	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-2098900	agagctgggttcgaa[A/G]ctagcatttcaggcac	A	G	NM_017588 // downstream // 263440 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream // 263440 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcrip	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-2221638	cctttggacaaacctt[C/T]aaaatctgtctctgga	C	T	NM_017588 // downstream // 296759 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, mRNA. /// NM_052821 // downstream // 296759 // Hs.397638 // WDR5 // 11091 // Homo sapiens WD repeat domain 5 (WDR5), transcrip	WDR5	WDR5, Homo sapiens WD repeat domain 5 (WDR5), transcript variant 1, q34.2
SNP_A-2293633	gcagccatgtggtgga[A/C]ggggatggaactcagt	A	C	NM_000093 // upstream // 164452 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 37263 // — // — // — /// ENST00000328009 // upstream // 164452 // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2
SNP_A-2212479	ccctgttgtaaggacc[C/T]gattaattacactgga	C	T	NM_000093 // upstream // 106315 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 95400 // — // — // — /// ENST00000328009 // upstream // 106315 // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2
SNP_A-1945676	ttgttgatatgtgaaa[C/T]gtggtctgtgatgtcc	C	T	NM_000093 // upstream // 96469 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000356384 // downstream // 105246 // — // — // — // — /// ENST00000328009 // upstream // 96469 // — // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.2
SNP_A-1809297	gtgactcccagaggta[C/T]taaggaaaggagaaag	C	T	NM_000093 // intron // 0 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // — // — // — /// ENST00000355306 // intron // 0 // — // — // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-1782591	ggcacctgcccaattc[A/G]cctggcagattcaggc	A	G	NM_000093 // intron // 0 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // — // — // — /// ENST00000355306 // intron // 0 // — // — // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2223760	cggccatgtgctacac[A/G]ctacgcaaggctcctc	A	G	NM_000093 // intron // 0 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // — // — // — /// ENST00000355306 // intron // 0 // — // — // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2277324	gagattgtaggctttc[C/T]atcacgttgtattga	C	T	NM_000093 // intron // 0 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // — // — // — /// ENST00000355306 // intron // 0 // — // — // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2270282	gacacgtaacatggcc[A/G]gaagttatcggcagaa	A	G	NM_000093 // intron // 0 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // — // — // — /// ENST00000355306 // intron // 0 // — // — // — // — // —	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2174894	cacaggctacttcatc[C/T]agaccagaaaggactc	C	T	NM_000093 // intron // 0 // Hs.210283 // COL5A1 // 1289 // Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA. /// ENST00000328009 // intron // 0 // --- // --- // --- /// ENST00000355306 // intron // 0 // --- // --- // --- // ---	COL5A1	COL5A1, Homo sapiens collagen, type V, alpha 1 (COL5A1), q34.3
SNP_A-2145334	atgcactgtggcctca[C/T]gcttcagccattcact	C	T	NM_015837 // downstream // 1457 // Hs.54517 // FCN2 // 2220 // Homo sapiens ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2), transcript variant SV1, mRNA. /// NM_004108 // downstream // 1457 // Hs.54517 // FCN2 // 2220 // Homo sa	FCN2	FCN2, Homo sapiens ficolin (collagen q34.3
SNP_A-2053067	aagtcgtgccagtagc[C/T]gagcaaagctggtatt	C	T	NM_002003 // intron // 0 // Hs.440898 // FCN1 // 2219 // Homo sapiens ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA. /// ENST00000223427 // intron // 0 // --- // --- // --- /// ENST00000308299 // intron // 0 // --- // --- //	FCN1	FCN1, Homo sapiens ficolin (collagen,q34.3
SNP_A-2301332	gcctttccaagactca[C/T]agaacgtgcggtagag	C	T	NM_014811 // upstream // 9030 // Hs.533260 // KIAA0649 // 9858 // Homo sapiens KIAA0649 (KIAA0649), mRNA. /// ENST00000320778 // downstream // 127093 // --- // --- // --- /// ENST00000356818 // upstream // 9030 // --- // --- // --- /// ENST0	KIAA0649	KIAA0649, Homo sapiens KIAA0649 (KIAA0649), q34.3
SNP_A-1895200	tgcccgttagatcaa[C/T]cagatgcactccagag	C	T	NM_144654 // upstream // 12139 // Hs.414028 // C9orf116 // 138162 // Homo sapiens chromosome 9 open reading frame 116 (C9orf116), mRNA. /// NM_016034 // downstream // 9203 // Hs.382044 // MRPS2 // 51116 // Homo sapiens mitochondrial ribosomal protein S2 (	C9orf116	C9orf116, Homo sapiens chromosome 9 open reading frame 116 (C9orf116), q34.3
SNP_A-2199452	cattttatcctcaga[A/G]atgaccatactcatta	A	G	NM_002571 // downstream // 1823 // Hs.532325 // PAEP // 5047 // Homo sapiens progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin /// NM_001001676 // upstream // 94723 // Hs.532679 // LCN9 //	PAEP	PAEP, Homo sapiens progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, q34.3
SNP_A-1853902	tcaaaaggccagaaaaa[A/G]tccaggagtcaggaag	A	G	NM_001001676 // downstream // 25053 // Hs.532679 // LCN9 // 392399 // Homo sapiens lipocalin 9 (LCN9), mRNA. /// ENST00000277526 // downstream // 25053 // --- // --- // --- /// ENST00000298466 // downstream // 2611 // --- // --- // ---	LCN9	LCN9, Homo sapiens lipocalin 9 (LCN9), q34.3
SNP_A-2304994	gctgaaaccgcagctg[A/T]aaaagaaatcatgttt	A	T	ENST00000298480 // intron // 0 // --- // --- // --- /// ENST00000263604 // intron // 0 // --- // --- // ---	-	q34.3
SNP_A-2099689	agaggtggcgacaaca[C/T]gaagcccattggtgga	C	T	NM_015447 // upstream // 42200 // Hs.522493 // CAMSAP1 // 157922 // Homo sapiens calmodulin regulated spectrin-associated protein 1 (CAMSAP1), mRNA. /// NM_016172 // downstream // 7869 // Hs.9194 // UBADC1 // 10422 // Homo sapiens ubiquitin associated dom	CAMSAP1	CAMSAP1, Homo sapiens calmodulin regulated spectrin-associated protein 1 (CAMSAP1), q34.3
SNP_A-2250167	cttactgaggtcatca[A/G]tcagctatttttcaaat	A	G	NM_144653 // upstream // 64346 // Hs.112895 // BTBD14A // 138151 // Homo sapiens BTB (POZ) domain containing 14A (BTBD14A), mRNA. /// NM_014564 // downstream // 36621 // Hs.148427 // LHX3 // 8022 // Homo sapiens LIM homeobox 3 (LHX3), transcript variant 2	BTBD14A	BTBD14A, Homo sapiens BTB (POZ) domain containing 14A (BTBD14A), q34.3
SNP_A-2079520	accctgcacaactca[G/T]ctgatggaaccaagtg	G	T	NM_201446 // upstream // 97096 // Hs.91481 // EGFL7 // 51162 // Homo sapiens EGF-like-domain, multiple 7 (EGFL7), transcript variant 2, mRNA. /// NM_016215 // upstream // 97096 // Hs.91481 // EGFL7 // 51162 // Homo sapiens EGF-like-domain, multiple 7 (EGF	EGFL7	EGFL7, Homo sapiens EGF-like-domain, multiple 7 (EGFL7), transcript variant 2, q34.3
SNP_A-1902298	tggccatccaagttcg[A/G]aggcgacgtggtaggg	A	G	NM_032874 // 5UTR // 0 // Hs.370555 // KIAA1984 // 84960 // Homo sapiens KIAA1984 (KIAA1984), mRNA. /// ENST00000338005 // CDS // 0 // --- // --- // --- /// ENST00000322866 // 5UTR // 0 // --- // --- // --- // ---	KIAA1984	KIAA1984, Homo sapiens KIAA1984 (KIAA1984), q34.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893590	tgcagggaacgataa[C/T]gccccagacatgggtt	C	T	NM_007230 // intron // 0 // --- // --- // 0 // --- /// NM_016219 // intron // 0 // Hs.279881 // MAN1B1 // 11253 // Homo sapiens mannosidase, alpha, class 1B, member 1 (MAN1B1), mRNA. /// ENST00000320452 // intron // 0 // --- // --- // ---	-	q34.3
SNP_A-2186204	caggccttgggtaatc[A/G]catcactatttggat	A	G	NM_138778 // intron // 0 // Hs.292570 // C9orf112 // 92715 // Homo sapiens chromosome 9 open reading frame 112 (C9orf112), mRNA. /// ENST00000359347 // intron // 0 // --- // --- // --- /// ENST00000277540 // intron // 0 // --- // --- // ---	C9orf112	C9orf112, Homo sapiens chromosome 9 open reading frame 112 (C9orf112), q34.3
SNP_A-1810274	gtgatgcagttaaccc[C/G]atcttctactagtgtc	C	G	NM_024757 // intron // 0 // Hs.495511 // EHMT1 // 79813 // Homo sapiens euchromatic histone methyltransferase 1 (EHMT1), mRNA. /// ENST00000359347 // intron // 0 // --- // --- // --- /// ENST00000358074 // intron // 0 // --- // --- // --- // ---	EHMT1	EHMT1, Homo sapiens euchromatic histone methyltransferase 1 (EHMT1), q34.3
SNP_A-2053965	aagttaagcataaaat[C/T]actgtacgacccagca	C	T	NM_014974 // intron // 0 // Hs.432397 // KIAA0934 // 22982 // Homo sapiens KIAA0934 (KIAA0934), mRNA. /// ENST00000280886 // intron // 0 // --- // --- // ---	KIAA0934	KIAA0934, Homo sapiens KIAA0934 (KIAA0934), p15.3
SNP_A-1735146	acatataaatatctgatgaatagga[C/T]acaaaatgtgaaatcat ctgagtaa	C	T	AB023151 // upstream // 68115 // Hs.116204 // KIAA0934 // 22982 // KIAA0934 /// BC003381 // downstream // 51763 // Hs.192881 // KIAA0217 // 23185 // KIAA0217	KIAA0934	KIAA0934, rs2790381, KIAA0934, p15.3
SNP_A-2237871	ctctgaatcagaaacc[G/T]ggaaagaaaaagaatg	G	T	ENST00000263154 // upstream // 12941 // --- // --- // --- // --- /// ENST00000354890 // upstream // 33434 // --- // --- // --- // ---	-	p15.3
SNP_A-1675820	ctgctgtgaatctattaccgtaac[C/T]ggtcctgtctcctctaagc ctgtt	C	T	NM_018702 // intron // 0 // Hs.192731 // ADARB2 // 105 // adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)	ADARB2	ADARB2, rs1112787, adenosine deaminase, RNA-specific, B2 (RED2 homolog rat),p15.3
SNP_A-1901878	tggcagcaaaatgcca[A/G]tcttccatcaagatg	A	G	NM_018702 // intron // 0 // Hs.369716 // ADARB2 // 105 // Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), mRNA. /// ENST00000329223 // intron // 0 // --- // --- // --- // ---	ADARB2	ADARB2, Homo sapiens adenosine deaminase, RNA-specific, B2 (RED2 homolog rat) (ADARB2), p15.3
SNP_A-2104227	agcagatcaagcagca[C/G]atcagcttgcacgaag	C	G	NM_033261 // upstream // 906171 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 887839 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame 1	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1928292	ttcacattatcttaa[A/C]catatgtctggctt	A	C	NM_033261 // upstream // 937012 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 918680 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame 1	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1863176	tcatttcataaattcc[C/T]gaagacagtgaaaggc	C	T	NM_033261 // upstream // 1045738 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1027406 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2049238	aagctatggcttta[C/G]agatcataaaaccagt	C	G	NM_033261 // upstream // 1083704 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1065372 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2269413	gaatttgtgtatgca[C/T]gtatcttaattaacac	C	T	NM_033261 // upstream // 1164888 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1146556 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2199895	ccaaagaagcttcacc[A/T]aatttagcacatatat	A	T	NM_033261 // upstream // 1198649 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1180317 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1814282	gtgtctgactgaaaa[A/C]gaaacgaatgattta	A	C	NM_033261 // upstream // 1214696 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1196364 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2138571	atccatttcacacagc[A/G]acatagagagagttct	A	G	NM_033261 // upstream // 1218445 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1200113 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1992230	cttacctgtgagctta[A/G]ggaacaggagttaaat	A	G	NM_033261 // upstream // 1238374 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1220042 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2281750	gagtgaagcaaattac[A/C]aaagcacacagcatgc	A	C	NM_033261 // upstream // 1247677 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1229345 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2000899	ccaatggagcaagtac[A/G]aacatttactgccgat	A	G	NM_033261 // upstream // 1249953 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1231621 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2290451	gcaacgagatctctga[C/T]agtaatgggtaaccct	C	T	NM_033261 // upstream // 1254330 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1235998 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2282276	gagttactggtttgca[C/T]gaacagcctggtgga	C	T	NM_033261 // upstream // 1259190 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1240858 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1992241	tgtttgatatgaaaga[A/G]gagattttaaccaga	A	G	NM_033261 // upstream // 1269923 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1251591 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1892744	tgcacagaaggaaagc[A/G]aagggtgcatgcggct	A	G	NM_033261 // upstream // 1272469 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1254137 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1700083	cgtagatggtgattctaaggagaac[A/G]ctgtctctttttatataat ctcc	A	G	NM_002627 // upstream // 665117 // Hs.26010 // PFKP // 5214 // phosphofructokinase, platelet /// NM_018702 // upstream // 664925 // Hs.192731 // ADARB2 // 105 // adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)	PFKP	PFKP , rs826487, phosphofructokinase, platelet ,p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2105646	agccactaggaaccga[C/T]gtagaaattatagaaa	C	T	NM_033261 // upstream // 1378438 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1360106 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-2288438	gattcttgaaatacag[A/G]agactgattattaagg	A	G	NM_033261 // upstream // 1441269 // Hs.9270 // IDI2 // 91734 // Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), mRNA. /// NM_018470 // downstream // 1422937 // Hs.534466 // C10orf110 // 55853 // Homo sapiens chromosome 10 open reading frame	IDI2	IDI2, Homo sapiens isopentenyl-diphosphate delta isomerase 2 (IDI2), p15.3
SNP_A-1916835	tgtttctatctttcac[A/G]aagcttacataatctt	A	G	NM_002627 // upstream // 469980 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 75190 // — // — // — /// ENST00000263145 // upstream // 469980 // — // — // — 1	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1947259	ttaaattgtattgata[A/G]gaaatctgaggagaaa	A	G	NM_002627 // upstream // 468217 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 76953 // — // — // — /// ENST00000263145 // upstream // 468217 // — // — // — 1	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1992352	actgctgaaaaaaacta[A/G]ctgcaaatttattgaa	A	G	NM_002627 // upstream // 463807 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 81363 // — // — // — /// ENST00000263145 // upstream // 463807 // — // — // — 1	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-2109938	aggaactgtggcatcc[A/G]agaagtttttcaaagca	A	G	NM_002627 // upstream // 452585 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 92585 // — // — // — /// ENST00000263145 // upstream // 452585 // — // — // — 1	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-2233585	ctcataaaagtcgcca[A/G]ataaatgaaaattcga	A	G	NM_002627 // upstream // 442878 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 102292 // — // — // — /// ENST00000263145 // upstream // 442878 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-2053828	aagtgctttgaccag[A/G]atagtaacttgcaaat	A	G	NM_002627 // upstream // 440402 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 104768 // — // — // — /// ENST00000263145 // upstream // 440402 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1992361	gtgactgtggaaaaca[A/G]accagatattcaagtt	A	G	NM_002627 // upstream // 428648 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 116522 // — // — // — /// ENST00000263145 // upstream // 428648 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1890887	tgatgctcttcactcaa[C/T]taagtaaatttgagtt	C	T	NM_002627 // upstream // 414554 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 130616 // — // — // — /// ENST00000263145 // upstream // 414554 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-2122138	agtgattcaaccaaaat[A/G]atgccaaaatcccaga	A	G	NM_002627 // upstream // 386219 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 158951 // — // — // — /// ENST00000263145 // upstream // 386219 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1895539	tgcctaggtttttcaa[G/T]tcctctccaggacag	G	T	NM_002627 // upstream // 338136 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 207034 // — // — // — /// ENST00000263145 // upstream // 338136 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3
SNP_A-1948712	tttatagattccagca[A/G]gagagcgacattctca	A	G	NM_002627 // upstream // 117938 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 427232 // — // — // — /// ENST00000263145 // upstream // 117938 // — // — // —	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1830878	taatcttgggggtcta[C/T]agcgtgctggtcattc	C	T	NM_002627 // upstream // 93261 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 451909 // — // — // — // /// ENST00000263145 // upstream // 93261 // — // — // — //	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.2
SNP_A-2043224	aactgcctatcctaa[A/T]attgcaatccaaagg	A	T	NM_002627 // upstream // 73640 // Hs.26010 // PFKP // 5214 // Homo sapiens phosphofructokinase, platelet (PFKP), mRNA. /// ENST00000355844 // downstream // 471530 // — // — // — // /// ENST00000263145 // upstream // 73640 // — // — // — //	PFKP	PFKP, Homo sapiens phosphofructokinase, platelet (PFKP), p15.2
SNP_A-2144073	atgaggactaaacgca[A/G]cagtggtatgaaggg	A	G	NM_014889 // upstream // 89871 // Hs.528300 // PITRM1 // 10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 516367 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB).	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-1839076	tagagattcataaagc[A/G]agtgaaataatgtat	A	G	NM_014889 // upstream // 100104 // Hs.528300 // PITRM1 // 10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 506134 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB)	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-1814362	gtgtgacacccggtaa[C/T]gtgtccagttgagaaa	C	T	NM_014889 // upstream // 123180 // Hs.528300 // PITRM1 // 10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 483058 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB)	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2220584	ccttcttctgctctta[C/T]ctaaatgcgttccgag	C	T	NM_014889 // upstream // 134489 // Hs.528300 // PITRM1 // 10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 471749 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB)	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2121111	agtctcttcctctgtc[A/G]catgagagttaatctt	A	G	NM_014889 // upstream // 160663 // Hs.528300 // PITRM1 // 10531 // Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA. /// NM_001300 // downstream // 445575 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB)	PITRM1	PITRM1, Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), p15.2
SNP_A-2089880	acttctacccaaaag[A/C]atctgctatttctct	A	C	NM_001300 // upstream // 357180 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 683791 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1789943	gggcttgcagactgga[A/G]cagccatgctaaagaa	A	G	NM_001300 // upstream // 376125 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 664846 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1652194	gtccaaattatttgtccaacagcac[A/G]tagttaatatgaagtaga gctagat	A	G	NM_001300 // upstream // 684249 // Hs.285313 // COPEB // 1316 // core promoter element binding protein /// NM_031436 // upstream // 356855 // Hs.250469 // AKR1CL2 // 83592 // aldo-keto reductase family 1, member C4-like 2	COPEB	COPEB , rs2077668, core promoter element binding protein ,p15.1
SNP_A-2192665	catccattgagttgca[A/G]ataatccagtaaccat	A	G	NM_001300 // upstream // 711340 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 329631 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209700	cccattagactcaaaa[C/T]ggtcccgcttatatat	C	T	NM_001300 // upstream // 737098 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 303873 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2163367	atttttgaaaattgg[C/T]acgtgcataaatatatg	C	T	NM_001300 // upstream // 789407 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 251564 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2044217	aacttcatttttga[A/T]gatgtgagggccaaga	A	T	NM_001300 // upstream // 847544 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 193427 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1865224	tccatagactgcatc[A/G]agagaaagaaggagagg	A	G	NM_001300 // upstream // 995797 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 45174 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-2098430	agagcaacagctacca[A/C]cacaaaatgaaaagctc	A	C	NM_001300 // upstream // 1007722 // Hs.285313 // KLF6 // 1316 // Homo sapiens core promoter element binding protein (COPEB), mRNA. /// NM_031436 // upstream // 33249 // Hs.537121 // AKR1CL2 // 83592 // Homo sapiens aldo-keto reductase family 1, member C4	KLF6	KLF6, Homo sapiens core promoter element binding protein (COPEB), p15.1
SNP_A-1855550	tcaagttctgcttcc[A/G]aaaccagaaagaaagta	A	G	NM_001353 // upstream // 60637 // Hs.460260 // AKR1C1 // 1645 // Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogena /// ENST00000281339 // upstream // 10649 // --- // --- // ---	AKR1C1	AKR1C1, Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogena p15.1
SNP_A-2145576	atgcatatgaacaagg[A/G]ccaataatttaaacgt	A	G	NM_205845 // upstream // 45510 // Hs.498513 // AKR1C2 // 1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 45510 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste .p15.1
SNP_A-2298533	gcccacaatcttcct[G/T]aaactatgtattcctt	G	T	NM_205845 // upstream // 58278 // Hs.498513 // AKR1C2 // 1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 58278 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste .p15.1
SNP_A-2000927	gagaactactgttaca[G/T]catctatttaagtgt	G	T	NM_205845 // upstream // 72115 // Hs.498513 // AKR1C2 // 1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 72115 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste .p15.1
SNP_A-2192903	catcctgtgtaaataq[C/G]cacttaaggaactga	C	G	NM_205845 // upstream // 77062 // Hs.498513 // AKR1C2 // 1646 // Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste /// NM_001354 // upstream // 77062 // Hs.498513 // AKR1C2 //	AKR1C2	AKR1C2, Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxyste .p15.1
SNP_A-2156603	attctgatgatctgaa[C/T]tgtgtttgagagaaat	C	T	NM_001818 // intron // 0 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// ENST00000305623 // intron // 0 // --- // --- // --- ///	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd .p15.1
SNP_A-2237088	ctctcaacgatattca[A/G]aagtaaactctgttc	A	G	ENST00000305623 // intron // 0 // --- // --- // ---	-	p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1830831	taatctgctgtagaaa[C/T]tgtcagcttcttct	C	T	NM_001818 // downstream // 79404 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 66660 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-2116591	aggtcagaaaggtgga[A/G]agaaaggagacaaagga	A	G	NM_001818 // downstream // 96416 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 49648 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd p15.1
SNP_A-1800948	gtagataaaagacaga[C/G]gattccattcaccaaa	C	G	NM_001818 // downstream // 123803 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 22261 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-2094861	agaatcttcacgagagt[C/T]caaccctgcagttatg	C	T	NM_001818 // downstream // 125155 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 20909 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-2000931	caatggacctaaatc[G/T]cagtcttgttaatgct	G	T	NM_001818 // downstream // 127237 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 18827 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-2314859	ggagtgggaccttcta[A/G]cacgttcccaatggtg	A	G	NM_001818 // downstream // 129847 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 16217 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-1866569	tcccccaccagatgcg[G/T]cattcaagttgtaaag	G	T	NM_001818 // downstream // 143349 // Hs.498514 // AKR1C4 // 1109 // Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd /// NM_053049 // upstream // 2715 // Hs.511775 // UCN3 //	AKR1C4	AKR1C4, Homo sapiens aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihyd ,p15.1
SNP_A-2289824	gcaaacagcagactcc[A/G]agaccactggaggcct	A	G	NM_005185 // downstream // 126814 // Hs.239600 // CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 35798 // Hs.445899 // ASB13 // 79754 // Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA.	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1
SNP_A-2139608	atcgagtgtaggaaaaa[C/T]gaaagacaggtgcagg	C	T	NM_005185 // downstream // 128859 // Hs.239600 // CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 33753 // Hs.445899 // ASB13 // 79754 // Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA.	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1
SNP_A-2070290	acaccaaggaagttca[A/G]gcatctggttgattt	A	G	NM_005185 // downstream // 131974 // Hs.239600 // CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 30638 // Hs.445899 // ASB13 // 79754 // Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA.	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1
SNP_A-2211720	ccctcctagatatgaa[C/T]gaagacacatgtggcc	C	T	NM_005185 // downstream // 133359 // Hs.239600 // CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 29253 // Hs.445899 // ASB13 // 79754 // Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA.	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181218	cagacattgactgcad[C/G]gaaaagcctctggg	C	G	NM_005185 // downstream // 134018 // Hs.239600 // CALML3 // 810 // Homo sapiens calmodulin-like 3 (CALML3), mRNA. /// NM_024701 // downstream // 28594 // Hs.445899 // ASB13 // 79754 // Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA.	CALML3	CALML3, Homo sapiens calmodulin-like 3 (CALML3), p15.1
SNP_A-1714533	atcaaaacaaagagttccctgatga[A/G]gaatgacaggagata aggctggaaa	A	G	NM_178150 // intron // 0 // Hs.387099 // FBXO18 // 84893 // F-box only protein, helicase, 18	FBXO18	FBXO18 , rs591878, F-box only protein, helicase, 18,p15.1
SNP_A-1727595	actgcagcctgtttattatcatga[C/T]gtttgcttctagttatgtgctt tt	C	T	NM_032807 // intron // 0 // Hs.387099 // FBXO18 // 84893 // F-box only protein, helicase, 18 /// NM_178150 // intron // 0 // Hs.387099 // FBXO18 // 84893 // F-box only protein, helicase, 18	FBXO18	FBXO18 , rs6602330, F-box only protein, helicase, 18 ,p15.1
SNP_A-2242652	ctgcatacagtcgggg[G/T]agaaaaaacaatcaaca	G	T	ENST00000191063 // intron // 0 // — // — // — /// ENST00000256878 // intron // 0 // — // — // —	-	p15.1
SNP_A-2256389	ctttatccataaatgc[A/G]gatggcacggtgcctg	A	G	NM_032807 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, mRNA. /// NM_178150 // intron // 0 // Hs.498543 // FBXO18 // 84893 // Homo sapiens F-box protein, helicase, 18 (FBXO18), t	FBXO18	FBXO18, Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 1, p15.1
SNP_A-1710808	cctactctttctctctctttgctta[A/T]gtcaatgaatggcaccccat ccttc	A	T	NM_000417 // intron // 0 // Hs.130058 // IL2RA // 3559 // interleukin 2 receptor, alpha	IL2RA	IL2RA , rs791590, interleukin 2 receptor, alpha,p15.1
SNP_A-1834045	tacatatggttgataa[A/G]gtgaagaattacaaaa	A	G	NM_000417 // intron // 0 // Hs.231367 // IL2RA // 3559 // Homo sapiens interleukin 2 receptor, alpha (IL2RA), mRNA. /// ENST00000281359 // intron // 0 // — // — // —	IL2RA	IL2RA, Homo sapiens interleukin 2 receptor, alpha (IL2RA), p15.1
SNP_A-1920176	ttaatctccctgaaa[A/G]cacctgtcgtgatgcc	A	G	NM_000417 // intron // 0 // Hs.231367 // IL2RA // 3559 // Homo sapiens interleukin 2 receptor, alpha (IL2RA), mRNA. /// ENST00000281359 // intron // 0 // — // — // —	IL2RA	IL2RA, Homo sapiens interleukin 2 receptor, alpha (IL2RA), p15.1
SNP_A-1863724	tccaagaccactcaga[C/T]ccttggataaagtcacc	C	T	NM_000417 // intron // 0 // Hs.231367 // IL2RA // 3559 // Homo sapiens interleukin 2 receptor, alpha (IL2RA), mRNA. /// ENST00000281359 // intron // 0 // — // — // —	IL2RA	IL2RA, Homo sapiens interleukin 2 receptor, alpha (IL2RA), p15.1
SNP_A-1827333	taacgtgttggaagtc[C/T]ccataaggcacatgag	C	T	NM_000417 // upstream // 19223 // Hs.231367 // IL2RA // 3559 // Homo sapiens interleukin 2 receptor, alpha (IL2RA), mRNA. /// NM_032905 // upstream // 7512 // Hs.498548 // RBM17 // 84991 // Homo sapiens RNA binding motif protein 17 (RBM17), mRNA. /// ENST	IL2RA	IL2RA, Homo sapiens interleukin 2 receptor, alpha (IL2RA), p15.1
SNP_A-2238358	ctctgggacgttgca[C/T]gaggaacattccgaac	C	T	ENST00000360521 // intron // 0 // — // — // —	-	p15.1
SNP_A-2190478	catacatgcagacaaa[A/G]gcttataaagaaagtt	A	G	NM_004566 // downstream // 16956 // Hs.195471 // PFKFB3 // 5209 // Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA. /// ENST00000360521 // downstream // 35179 // — // — - // — // — /// ENST00000359346 // downstream	PFKFB3	PFKFB3, Homo sapiens 6-phosphofructo-2-kinase,p15.1
SNP_A-2105391	agccaaacacttact[A/G]agaaaaaacatccaa	A	G	NM_006257 // downstream // 33986 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // downstream // 34007 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// ENST00000031	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1
SNP_A-2116933	aggtgaaaaatattca[C/G]ctcaggcccttcaca	C	G	NM_006257 // downstream // 33948 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// NM_006257 // downstream // 33969 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// ENST00000031	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1
SNP_A-1906357	tggtgcagttcaaatc[C/T]aggttcatcaagggtc	C	T	NM_006257 // intron // 0 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA. /// ENST00000357287 // intron // 0 // — // — // — /// ENST00000263125 // intron // 0 // — // — // — // —	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1993470	cgtccaatgagaatca[C/T]gtgaaagcattgaaag	C	T	NM_006257 // intron // 0 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// ENST00000357287 // intron // 0 // — // — // — /// ENST00000263125 // intron // 0 // — // — // — // —	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1
SNP_A-2155816	attccgaggtcctggg[A/G]agtagtttaggaacag	A	G	NM_006257 // intron // 0 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// ENST00000357287 // intron // 0 // — // — // — /// ENST00000263125 // intron // 0 // — // — // — // —	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1
SNP_A-2171816	caatgacggtcacaaag[C/T]ggccagccctctact	C	T	NM_006257 // intron // 0 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// ENST00000357287 // intron // 0 // — // — // — /// ENST00000263125 // intron // 0 // — // — // — // —	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p15.1
SNP_A-1681172	acaaaatcttgatttatttttggtca[C/T]atatctaatcattgagttggctt	C	T	AB046837 // downstream // 460652 // Hs.29299 // SFMBT2 // 57713 // Scm-like with four mbt domains 2 /// AK093639 // upstream // 174425 // - // - // - // Homo sapiens cDNA FLJ36320 fis, clone THYMU2005480.	SFMBT2	SFMBT2 , rs1327689, Scm-like with four mbt domains 2 ,p14
SNP_A-1993560	actctttggtgtagac[A/G]ggaggagtcctaata	A	G	NM_006257 // upstream // 109138 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// NM_006257 // upstream // 174096 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// ENST00000003572	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-1884875	tgaatcttcagggaac[A/T]ccatttttgcagggc	A	T	NM_006257 // upstream // 109680 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// NM_006257 // upstream // 174638 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// ENST00000003572	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-1790566	ggggccgtcgccacaga[A/C]aaatagaaaatgata	A	C	NM_006257 // upstream // 159100 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// NM_006257 // upstream // 224058 // Hs.498570 // PRKCQ // 5588 // Homo sapiens protein kinase C, theta (PRKCQ), mRNA /// ENST00000003572	PRKCQ	PRKCQ, Homo sapiens protein kinase C, theta (PRKCQ), p14
SNP_A-1781256	ggatgtaacctgaaa[C/T]gtctggacaggtctc	C	T	ENST00000356312 // upstream // 90881 // — // — // — // — /// ENST00000357074 // downstream // 244208 // — // — // — // — /// ENST00000358765 // downstream // 244208 // — // — // — // —	-	p14
SNP_A-1993689	tgtgctgaagtttca[A/G]cgcagtgcctaagcct	A	G	ENST00000356312 // upstream // 100656 // — // — // — // — /// ENST00000357074 // downstream // 234433 // — // — // — // — /// ENST00000358765 // downstream // 234433 // — // — // — // —	-	p14
SNP_A-2000943	gcccactacagaaggg[A/G]caaagaacacatttta	A	G	ENST00000356312 // upstream // 108742 // — // — // — // — /// ENST00000357074 // downstream // 226347 // — // — // — // — /// ENST00000358765 // downstream // 226347 // — // — // — // —	-	p14
SNP_A-1752999	tacattctaaacagtttgaaaagac[A/G]agtctcaaagagggac ctctacgtg	A	G	AB046837 // downstream // 185368 // Hs.29299 // SFMBT2 // 57713 // Scm-like with four mbt domains 2 /// AK093639 // upstream // 449709 // - // - // - // Homo sapiens cDNA FLJ36320 fis, clone THYMU2005480.	SFMBT2	SFMBT2 , rs1417031, Scm-like with four mbt domains 2 ,p14
SNP_A-2044315	aacttttaacctacca[C/T]tgcatttagaataact	C	T	ENST00000356312 // upstream // 138011 // — // — // — // — /// ENST00000357074 // downstream // 197078 // — // — // — // — /// ENST00000358765 // downstream // 197078 // — // — // — // —	-	p14
SNP_A-2187478	caggtttatcagtga[A/G]taagttgccatgaagg	A	G	ENST00000356312 // upstream // 147538 // — // — // — // — /// ENST00000357074 // downstream // 187551 // — // — // — // — /// ENST00000358765 // downstream // 187551 // — // — // — // —	-	p14
SNP_A-1993717	cttccactggacaaga[A/T]ggcagatgttgtcact	A	T	ENST00000356312 // upstream // 148195 // — // — // — // — /// ENST00000357074 // downstream // 186894 // — // — // — // — /// ENST00000358765 // downstream // 186894 // — // — // — // —	-	p14
SNP_A-1898490	tgcttctgtacaacttt[C/T]aaggcgttgtctgggat	C	T	ENST00000356312 // upstream // 159563 // — // — // — // — /// ENST00000357074 // downstream // 175526 // — // — // — // — /// ENST00000358765 // downstream // 175526 // — // — // — // —	-	p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2294732	gcagttaagtacgcta[A/G]caagtctaactctgac	A	G	ENST00000356312 // upstream // 167583 // --- // --- // --- // --- /// ENST00000357074 // downstream // 167506 // --- // --- // --- // --- /// ENST00000358765 // downstream // 167506 // --- // --- // --- // ---	-	p14
SNP_A-2171669	caatctgacattgtca[C/T]gttcggacaaaaaagt	C	T	ENST00000356312 // upstream // 168425 // --- // --- // --- // --- /// ENST00000357074 // downstream // 166664 // --- // --- // --- // --- /// ENST00000358765 // downstream // 166664 // --- // --- // --- // ---	-	p14
SNP_A-1781037	ggatgcagctctgaaa[A/C]cattcctggtccttgt	A	C	ENST00000356312 // upstream // 171765 // --- // --- // --- // --- /// ENST00000357074 // downstream // 163324 // --- // --- // --- // --- /// ENST00000358765 // downstream // 163324 // --- // --- // --- // ---	-	p14
SNP_A-2246993	ctgtatgtctcaaggt[C/G]aatcaggtagaaaggt	C	G	ENST00000356312 // upstream // 186856 // --- // --- // --- // --- /// ENST00000357074 // downstream // 148233 // --- // --- // --- // --- /// ENST00000358765 // downstream // 148233 // --- // --- // --- // ---	-	p14
SNP_A-1993771	gctacgggaatttagc[A/G]gagaacgaagtcacct	A	G	ENST00000356312 // upstream // 276517 // --- // --- // --- // --- /// ENST00000357074 // downstream // 58572 // --- // --- // --- // --- /// ENST00000358765 // downstream // 58572 // --- // --- // --- // ---	-	p14
SNP_A-1993776	gaaacgcttccaaaaa[C/G]tgcaggaatgatttct	C	G	ENST00000356312 // upstream // 292475 // --- // --- // --- // --- /// ENST00000357074 // downstream // 42614 // --- // --- // --- // --- /// ENST00000358765 // downstream // 42614 // --- // --- // --- // ---	-	p14
SNP_A-2099792	agagtaagggctaaac[A/C]cctggcttatggagtc	A	C	NM_030569 // downstream // 90462 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // downstream // 90462 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globu	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-2298816	gcccatgcctgaaacc[C/T]ggcaagcactcagttt	C	T	NM_030569 // intron // 0 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-1993941	taagttttgcaacaga[A/G]aaaagtcaatataatg	A	G	NM_030569 // intron // 0 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-1801559	gtaggtgacacgctgg[A/T]cagggatgaagatttc	A	T	NM_030569 // intron // 0 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, mRNA. /// NM_032817 // intron // 0 // Hs.498586 // ITIH5 // 80760 // Homo sapiens inter-alpha (globulin) inhibitor H	ITIH5	ITIH5, Homo sapiens inter-alpha (globulin) inhibitor H5 (ITIH5), transcript variant 1, p14
SNP_A-1696214	cacccgtcttgggccaatccttca[C/G]caacgcccgtgatctc catgctggc	C	G	NM_002216 // CDS // 0 // Hs.75285 // ITIH2 // 3698 // inter-alpha (globulin) inhibitor, H2 polypeptide	ITIH2	ITIH2 , rs3740217, inter-alpha (globulin) inhibitor, H2 polypeptide,p14
SNP_A-2212865	ccctttctcagtcaga[C/T]cagtaacatcaaaagt	C	T	ENST00000298453 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-2101428	agatctttataagtca[G/T]tgaaccagtattttcc	G	T	ENST00000344293 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-2234210	ctcatttcatttaatc[A/C]ctgtaaaacaacctct	A	C	ENST00000344293 // intron // 0 // --- // --- // --- // ---	-	p14
SNP_A-1851151	tattcaagcttaccaa[A/G]aacttttcacatttgt	A	G	NM_002051 // downstream // 108237 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 108237 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1677016	actgttaaacttttggactagtcac[G/T]cttgtggtccttagtaagct ggtaa	G	T	NM_002051 // downstream // 156810 // Hs.169946 // GATA3 // 2625 // GATA binding protein 3 /// NM_006561 // upstream // 2786407 // Hs.211610 // CUGBP2 // 10659 // CUG triplet repeat, RNA binding protein 2	GATA3	GATA3 , rs4747760, GATA binding protein 3 ,p14
SNP_A-1994158	catatttgtaaggtac[A/G]aggcgtataaaggttt	A	G	NM_002051 // downstream // 129311 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 129311 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2258028	ctttgtgtgggcagaaa[A/G]gtttattattattat	A	G	NM_002051 // downstream // 163029 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 163029 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2141423	atctgtttaggactg[A/C]aattacaagactattt	A	C	NM_002051 // downstream // 206883 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 206883 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2048507	aagcatgagcttagga[G/T]tatctgtgatcacctt	G	T	NM_002051 // downstream // 209390 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 209390 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1870075	tccttgggcatcatgta[C/T]cattgtaatcttctt	C	T	NM_002051 // downstream // 368532 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 368532 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2120057	agtcactaaggaaaaa[A/G]tcagagatactaggag	A	G	NM_002051 // downstream // 395193 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 395193 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1684472	ggctagcttggaatgggaaaagca[C/T]gaagctcgaaagtg gtaaagaaaa	C	T	NM_002051 // downstream // 446993 // Hs.169946 // GATA3 // 2625 // GATA binding protein 3 /// NM_006561 // upstream // 2496224 // Hs.211610 // CUGBP2 // 10659 // CUG triplet repeat, RNA binding protein 2	GATA3	GATA3 , rs10508356, GATA binding protein 3 ,p14
SNP_A-2204375	ccagcgcagtagccaa[C/T]caaagaatacgtatat	C	T	NM_002051 // downstream // 434518 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 434518 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1785774	ggctctgtccttaag[A/C]aaatctagtgtgtgtc	A	C	NM_002051 // downstream // 435032 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 435032 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1727515	atccctatttaaatcgtgttacaca[A/C]aaaaaaatgaatttaaaa accatg	A	C	NM_002051 // downstream // 480679 // Hs.169946 // GATA3 // 2625 // GATA binding protein 3 /// NM_006561 // upstream // 2462538 // Hs.211610 // CUGBP2 // 10659 // CUG triplet repeat, RNA binding protein 2	GATA3	GATA3 , rs1325886, GATA binding protein 3 ,p14
SNP_A-1994303	ctatagtttgattcca[C/T]gagagagtgggtgagg	C	T	NM_002051 // downstream // 445261 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 445261 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1994306	ccaagatcacaagtta[C/G]atgttagctccccta t	C	G	NM_002051 // downstream // 445394 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 445394 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800851	gtagagacggttccaa[C/T]gtgtcttcagtaacca	C	T	NM_002051 // downstream // 446045 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 446045 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1867266	tccctgtccttagaa[A/C]aacaggagcagaagat	A	C	NM_002051 // downstream // 456962 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 456962 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2288479	gattgaagaaggttaa[C/G]aaatcccagatattag	C	G	NM_002051 // downstream // 473386 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 473386 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1994325	acttccaatctggaga[A/G]gatcaaatgaggctgc	A	G	NM_002051 // downstream // 475657 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 475657 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1994332	gcaattggtgttcctc[A/G]aaaaggtgtctgtgg	A	G	NM_002051 // downstream // 480824 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 480824 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1854660	tcaacactgggactta[C/T]gttaccaaagtaaggg	C	T	NM_002051 // downstream // 520258 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 520258 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2153351	attagaagcaacaaag[A/G]ccagagaagggttgtca	A	G	NM_002051 // downstream // 521071 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 521071 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-1905619	tggtaggtacttttgaa[C/T]catttttgtgccaatta	C	T	NM_002051 // downstream // 653700 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 653700 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2246605	ctgtaagattcaatga[C/T]gtctctggtgcagcag	C	T	NM_002051 // downstream // 920109 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 920109 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2106939	agccttggaggaactc[C/T]gaggaatggttaaaag	C	T	NM_002051 // 1252367 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, mRNA. /// NM_001002295 // downstream // 1252367 // Hs.524134 // GATA3 // 2625 // Homo sapiens GATA binding protein 3 (GA	GATA3	GATA3, Homo sapiens GATA binding protein 3 (GATA3), transcript variant 2, p14
SNP_A-2024313	aaaagccattgatagc[A/G]aagtaaagtgagattg	A	G	ENST00000334127 // downstream // 95057 // --- // --- // --- /// ENST00000242916 // upstream // 670886 // --- // --- // ---	-	p14
SNP_A-2109711	aggaaagtaacaatat[C/G]ataactggatgtgttc	C	G	ENST00000334127 // downstream // 327778 // --- // --- // --- /// ENST00000242916 // upstream // 438165 // --- // --- // ---	-	p14
SNP_A-2231299	ctattcctaaaactga[A/G]ggatgagatattatcc	A	G	ENST00000334127 // downstream // 353180 // --- // --- // --- /// ENST00000242916 // upstream // 412763 // --- // --- // ---	-	p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1842302	taggtagaattgtccc[C/T]atttaccatcatatatcc	C	T	ENST00000334127 // downstream // 399973 // — // — // — /// ENST00000242916 // upstream // 365970 // — // — // — ///	-	p14
SNP_A-1994775	tcgtgttaacactcct[C/T]aacttctgtgtcata	C	T	ENST00000334127 // downstream // 417658 // — // — // — /// ENST00000242916 // upstream // 348285 // — // — // — ///	-	p14
SNP_A-1813740	gtgtagccttcagaac[A/G]ctaatttacaggatgt	A	G	ENST00000334127 // downstream // 459491 // — // — // — /// ENST00000242916 // upstream // 306452 // — // — // — ///	-	p14
SNP_A-1816787	gttatcttaggccaa[A/T]ctgatcctgctatgag	A	T	ENST00000334127 // downstream // 485435 // — // — // — /// ENST00000242916 // upstream // 280508 // — // — // — ///	-	p14
SNP_A-1832092	taatttagcatgcaag[A/G]cagagtgcagcactgg	A	G	ENST00000334127 // downstream // 496408 // — // — // — /// ENST00000242916 // upstream // 269535 // — // — // — ///	-	p14
SNP_A-1994811	aggagatcaatgggaa[A/G]gcgttacagtgactc	A	G	ENST00000334127 // downstream // 512951 // — // — // — /// ENST00000242916 // upstream // 252992 // — // — // — ///	-	p14
SNP_A-1748617	tcacttgctgtaagaataaatcac[A/G]agaaaatgtgcaacttg gaggttct	A	G	NM_002051 // downstream // 1950324 // Hs.169946 // GATA3 // 2625 // GATA binding protein 3 /// NM_006561 // upstream // 992893 // Hs.211610 // CUGBP2 // 10659 // CUG triplet repeat, RNA binding protein 2	GATA3	GATA3 , rs10508377, GATA binding protein 3 ,p14
SNP_A-1895067	tgcccagggaccagtc[C/T]agaagattacaagagg	C	T	ENST00000334127 // downstream // 644587 // — // — // — /// ENST00000242916 // upstream // 121356 // — // — // — ///	-	p14
SNP_A-1915165	tgttcaccgatatact[A/G]gagtgtttataaacc	A	G	ENST00000334127 // downstream // 714059 // — // — // — /// ENST00000242916 // upstream // 51884 // — // — // — ///	-	p14
SNP_A-2000956	cttccactctccaaca[C/T]gacaaggtcaatcaaa	C	T	ENST00000334127 // downstream // 721392 // — // — // — /// ENST00000242916 // upstream // 44551 // — // — // — ///	-	p14
SNP_A-2086650	actgaaggaatagggaa[C/T]gcttctatttatcaaa	C	T	NM_006561 // upstream // 791424 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream // 938459 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding p	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2177225	cacctggaatgagaga[C/G]ccaatttctcctttta	C	G	NM_006561 // upstream // 784172 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream // 931207 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding p	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1889725	tgataataatgatgtc[G/T]cacaaaatttaggct	G	T	NM_006561 // upstream // 473473 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream // 620508 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding p	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1924548	ttatacctgactgca[A/C]tgacttcaatccgt	A	C	NM_006561 // upstream // 444690 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream // 591725 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding p	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2288935	gatttataactataaa[A/G]tgtcttgaacaaaatg	A	G	NM_006561 // upstream // 283021 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // upstream // 430056 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding p	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2297373	gccactcctgtagtca[C/G]cagttgttcatcagtt	C	G	NM_006561 // intron // 0 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// ENST00000354440 // intron // 0 // — // — // — /// ENST00000315874 // intron // 0 // — // — // — // –	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2275805	gagacctggaggtta[C/T]cttcttctctttccta	C	T	NM_006561 // downstream // 28802 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // downstream // 29587 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2147976	atggctgcaatgaatc[A/G]aaaatctgcaagagat	A	G	NM_006561 // downstream // 44839 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // downstream // 45624 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-1873283	tctattttggtatctc[C/T]atttgggtctgtcaaa	C	T	NM_006561 // downstream // 61961 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA. /// NM_006561 // downstream // 62746 // Hs.309288 // CUGBP2 // 10659 // Homo sapiens CUG triplet repeat, RNA binding	CUGBP2	CUGBP2, Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), p14
SNP_A-2262929	gaacaactccatatcc[G/T]caaaagcatttttaat	G	T	D13644 // intron // 0 // Hs.498661 // USP6NL // 9712 // Homo sapiens mRNA for KIAA0019 protein, partial cds. /// ENST00000277575 // intron // 0 // — // — // — // —	USP6NL	USP6NL, Homo sapiens for KIAA0019 protein, partial cds. p14
SNP_A-1796657	ggttaggggattataa[A/C]aaatgatgattaaccc	A	C	D13644 // upstream // 11694 // Hs.498661 // USP6NL // 9712 // Homo sapiens mRNA for KIAA0019 protein, partial cds. /// NM_024693 // upstream // 119052 // Hs.22242 // ECHDC3 // 79746 // Homo sapiens enoyl Coenzyme A hydratase domain containing 3 (ECHDC3),	USP6NL	USP6NL, Homo sapiens for KIAA0019 protein, partial cds. p14
SNP_A-2222780	cgatgttgacagctac[A/C]gactgattaccaattt	A	C	D13644 // upstream // 59661 // Hs.498661 // USP6NL // 9712 // Homo sapiens mRNA for KIAA0019 protein, partial cds. /// NM_024693 // upstream // 71085 // Hs.22242 // ECHDC3 // 79746 // Homo sapiens enoyl Coenzyme A hydratase domain containing 3 (ECHDC3), m	USP6NL	USP6NL, Homo sapiens for KIAA0019 protein, partial cds. p14
SNP_A-1708791	ctgtaaatgtgtaaggcaaaatacc[A/G]cctggtccctgctgccc cctgagct	A	G	NM_015542 // downstream // 42158 // Hs.3862 // UPF2 // 26019 // UPF2 regulator of nonsense transcripts homolog (yeast) /// NM_080599 // downstream // 42158 // Hs.3862 // UPF2 // 26019 // UPF2 regulator of nonsense transcripts homolog (yeast) /// NM_15325	UPF2	UPF2 , rs717799, UPF2 regulator of nonsense transcripts homolog (yeast) ,p14
SNP_A-2084109	actagcctacacaata[C/T]ggcgagactctgtctc	C	T	NM_015542 // intron // 0 // Hs.370689 // UPF2 // 26019 // Homo sapiens UPF2 regulator of nonsense transcripts homolog (yeast) (UPF2), transcript variant 2, mRNA. /// NM_080599 // intron // 0 // Hs.370689 // UPF2 // 26019 // Homo sapiens UPF2 regulator of	UPF2	UPF2, Homo sapiens UPF2 regulator of nonsense transcripts homolog (yeast) (UPF2), transcript variant 2, p14
SNP_A-1878776	tctgttgcctcatcca[C/T]gcagttactgtttacc	C	T	NM_020397 // intron // 0 // Hs.156723 // CAMK1D // 57118 // Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 // Hs.156723 // CAMK1D // 57118 // Homo sapiens calcium/calmodulin-dependent protein kinas	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-1811664	gtgctgggatgctgta[C/T]gtaaacctggactttg	C	T	NM_020397 // intron // 0 // Hs.156723 // CAMK1D // 57118 // Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // intron // 0 // Hs.156723 // CAMK1D // 57118 // Homo sapiens calcium/calmodulin-dependent protein kinas	CAMK1D	CAMK1D, Homo sapiens calcium,p13
SNP_A-2134920	atattatttcatcccc[C/G]aggtactaagccttgt	C	G	NM_020397 // downstream // 57934 // Hs.156723 // CAMK1D // 57118 // Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA. /// NM_153498 // downstream // 54772 // Hs.156723 // CAMK1D // 57118 // Homo sapiens calcium/calmodulin-depende	CAMK1D	CAMK1D, Homo sapiens calcium p13
SNP_A-2218021	cctgccaccaaagcct[A/C]aatcttcctgccatac	A	C	NM_031455 // upstream // 49658 // Hs.498720 // CCDC3 // 83643 // Homo sapiens coiled-coil domain containing 3 (CCDC3), mRNA. /// NM_021980 // upstream // 48087 // Hs.332706 // OPTN // 10133 // Homo sapiens optineurin (OPTN), mRNA. /// NM_021980 // upstrea	CCDC3	CCDC3, Homo sapiens coiled-coil domain containing 3 (CCDC3), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2170593	caagtggcaaaataac[A/G]gtatcaacgagtcaca	A	G	NM_021980 // intron // 0 // Hs.332706 // OPTN // 10133 // Homo sapiens optineurin (OPTN), mRNA. /// ENST00000263036 // intron // 0 // — // — // — /// ENST00000336241 // intron // 0 // — // — // — // —	OPTN	OPTN, Homo sapiens optineurin (OPTN), p13
SNP_A-1950769	tttcatttccagttaa[A/C]gttgaatgtttatcct	A	C	NM_021980 // downstream // 5011 // Hs.332706 // OPTN // 10133 // Homo sapiens optineurin (OPTN), mRNA. /// NM_021980 // downstream // 4655 // Hs.332706 // OPTN // 10133 // Homo sapiens optineurin (OPTN), mRNA. /// ENST00000263036 // downstream // 5011 //	OPTN	OPTN, Homo sapiens optineurin (OPTN), p13
SNP_A-1951677	tttccttgaaacagag[A/T]aacagaaaactgccag	A	T	NM_018518 // intron // 0 // Hs.198363 // MCM10 // 55388 // Homo sapiens MCM10 minichromosome maintenance deficient 10 (S. cerevisiae) (MCM10), transcript variant 2, mRNA. /// NM_182751 // intron // 0 // Hs.198363 // MCM10 // 55388 // Homo sapiens MCM10 mi	MCM10	MCM10, Homo sapiens MCM10 minichromosome maintenance deficient 10 (S. cerevisiae) (MCM10), transcript variant 2, p13
SNP_A-1995852	gaggctgtgcatttcc[C/G]atgactccggagcttc	C	G	NM_006214 // downstream // 39433 // Hs.498732 // PHYH // 5264 // Homo sapiens phytanoyl-CoA hydroxylase (Refsum disease) (PHYH), mRNA. /// ENST00000298442 // upstream // 4036 // — // — // — // — /// ENST00000263038 // downstream // 39433 // — //	PHYH	PHYH, Homo sapiens phytanoyl-CoA hydroxylase (Refsum disease) (PHYH), p13
SNP_A-1803604	gtcaaaagggaaaagg[C/T]agctgatgaggttaca	C	T	NM_018027 // 3UTR // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // 3UTR // 0 // — // — // — /// ENST00000357447 // 3UTR // 0 // — // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1863762	tccaagcacactcacc[A/G]gatattaggaaagtta	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — /// ENST000003	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2300481	gcctgaagccacacag[C/T]cagtaaggagctccca	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — /// ENST000003	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2224905	cgtgcgtgaagagtac[A/G]acacaaaactgtaaac	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — /// ENST000003	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1996055	tatgtggctcaccca[C/T]cactgagggcagatcc	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — /// ENST000003	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2187521	cagtaaaggcagtaac[A/G]atctttgatggtagtc	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — /// ENST000003	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2285357	gatctggctcaaatcc[C/T]ctgtttatatgatcc	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1949192	tttatgggaggatgaa[A/T]tcagtataaagatagc	A	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835998	tactaataataatgac[C/T]gtaaagagttatggca	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2188157	cagtcccatctgataa[C/T]tccacactgttggtga	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1996169	ggctactgcctgcac[A/G]ctgcaggtataggcaa	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1893140	tgcagaaggcaacaca[A/G]aagttagcatccatgt	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1996201	gtactagctctcctta[C/G]gcttagggtggtagat	C	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2264946	gaagagggaatgattg[A/G]ataatgagtttggcag	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1818578	gttgaaagagattgat[C/T]aactgtttagagtaa	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2160775	atttctatagaaacac[A/G]gaagaggaaggagcaca	A	G	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1996279	ctggacaatcagctaa[C/T]gcttttagaaaaacag	C	T	NM_018027 // intron // 0 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// ENST00000358621 // intron // 0 // — // — // — /// ENST00000357447 // intron // 0 // — // — // —	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2254220	cttgatggttgccttc[C/T]agcccctgaatagctt	C	T	NM_018027 // upstream // 67176 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_018027 // upstream // 67140 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_03	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1835842	tacgtaccagagaaata[G/T]ggcagcttaggaaaaa	G	T	NM_018027 // upstream // 72516 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_018027 // upstream // 72480 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_03	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2304330	gctccttctgcctgga[G/T]ccctatttttcccaga	G	T	NM_018027 // upstream // 93009 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_018027 // upstream // 92973 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_03	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2231219	ctattatggccatgtg[A/G]caagaacccagctctt	A	G	NM_018027 // upstream // 93405 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_018027 // upstream // 93369 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_03	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909287	tgtatgtaatgtcaga[C/T]agtgttaagtgccatg	C	T	NM_018027 // upstream // 93496 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_018027 // upstream // 93460 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_03	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-2270140	gacacagtattggcac[A/C]aggagggcccagtgaa	A	C	NM_018027 // upstream // 137706 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_018027 // upstream // 137670 // Hs.439488 // FRMD4A // 55691 // Homo sapiens FERM domain containing 4A (FRMD4A), mRNA. /// NM_	FRMD4A	FRMD4A, Homo sapiens FERM domain containing 4A (FRMD4A), p13
SNP_A-1826056	taaatgtcctatgcca[A/G]cctacagcttaaaaa	A	G	NM_031453 // intron // 0 // Hs.446315 // C10orf45 // 83641 // Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // — // — // —	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-1871153	tcgtctttagccaca[C/G]atttggccactggacg	C	G	NM_031453 // intron // 0 // Hs.446315 // C10orf45 // 83641 // Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // — // — // —	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-2037501	aacaacattcgttgca[C/T]ggtggaaatttcagaa	C	T	NM_031453 // intron // 0 // Hs.446315 // C10orf45 // 83641 // Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // — // — // —	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-2109670	aggaaagcaatcattg[C/T]aaactggaaatgcta	C	T	NM_031453 // intron // 0 // Hs.446315 // C10orf45 // 83641 // Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // — // — // —	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-1898210	tgcttaagagccagta[C/T]aagaacagcttaagac	C	T	NM_031453 // intron // 0 // Hs.446315 // C10orf45 // 83641 // Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // — // — // —	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-2088863	actgttgcatggaaag[C/G]ctatgtccacatagaa	C	G	NM_031453 // intron // 0 // Hs.446315 // C10orf45 // 83641 // Homo sapiens chromosome 10 open reading frame 45 (C10orf45), mRNA. /// ENST00000181796 // intron // 0 // — // — // —	C10orf45	C10orf45, Homo sapiens chromosome 10 open reading frame 45 (C10orf45), p13
SNP_A-1933521	ttctacttcagctgga[C/T]gctatttttgtcaattg	C	T	NM_022487 // intron // 0 // Hs.524156 // DCLRE1C // 64421 // Homo sapiens DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae) (DCLRE1C), mRNA. /// ENST00000357283 // intron // 0 // — // — // — /// ENST00000298913 // intron // 0 // — // -	DCLRE1C	DCLRE1C, Homo sapiens DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae) (DCLRE1C), p13
SNP_A-2256281	cttagggcatcccaa[A/G]ctaagcagggtat	A	G	ENST00000355828 // intron // 0 // — // — // —	-	p13
SNP_A-1996456	tagaagtcaacaagca[A/T]aggagcaactagctg	A	T	ENST00000355828 // intron // 0 // — // — // —	-	p13
SNP_A-2055882	aatacaatggtaatgg[A/G]atcccacagtaatttg	A	G	NM_018324 // upstream // 25669 // Hs.24309 // THEDC1 // 55301 // Homo sapiens thioesterase domain containing 1 (THEDC1), mRNA. /// ENST00000357670 // upstream // 18323 // — // — // — /// ENST00000356299 // upstream // 25669 // — // — // -	THEDC1	THEDC1, Homo sapiens thioesterase domain containing 1 (THEDC1), p13
SNP_A-1882245	tgaaaaagagtttaac[A/G]atagtcatctgattta	A	G	ENST00000324851 // intron // 0 // — // — // — /// ENST00000344513 // intron // 0 // — // — // —	-	p13
SNP_A-1877711	tctgggaatctgtgta[C/T]agttagcagttgcatg	C	T	NM_003638 // downstream // 54497 // Hs.171311 // ITGA8 // 8516 // Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000324851 // upstream // 91533 // — // — // — /// E	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-2091126	acttggcatctcaaa[C/T]gaagccatcaaggtgg	C	T	NM_003638 // intron // 0 // Hs.171311 // ITGA8 // 8516 // Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // — // — // —	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101011	agatcaaaactcaaaa[C/T]tcaaagtatgattatt	C	T	NM_003638 // intron // 0 // Hs.171311 // ITGA8 // 8516 // Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // — // — // —	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-1996602	gtaactgtgaagtctg[A/C]aatctcatgtgaccac	A	C	NM_003638 // intron // 0 // Hs.171311 // ITGA8 // 8516 // Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// ENST00000265937 // intron // 0 // — // — // —	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-2167007	caacaacatcctttcaa[C/T]ggccaaaaagcatcca	C	T	NM_003638 // upstream // 37000 // Hs.171311 // ITGA8 // 8516 // Homo sapiens integrin, alpha 8 (ITGA8), mRNA. /// NM_024948 // downstream // 21399 // Hs.158870 // C10orf97 // 80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. ///	ITGA8	ITGA8, Homo sapiens integrin, alpha 8 (ITGA8), p13
SNP_A-1732015	ctggcaagaactataatctattaaa[A/C]ccctcaataatgtgtaa acatacat	A	C	NM_024948 // upstream // 339336 // Hs.285107 // C10orf97 // 80013 // chromosome 10 open reading frame 97 /// NM_030664 // upstream // 237112 // Hs.397381 // PTER // 9317 // phosphotriesterase related	C10orf97	C10orf97 , rs10508502, chromosome 10 open reading frame 97 ,p13
SNP_A-2306067	gctggaatttaaatgg[A/G]acatatagatgctaat	A	G	NM_024948 // upstream // 401358 // Hs.158870 // C10orf97 // 80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// NM_030664 // upstream // 175094 // Hs.444321 // PTER // 9317 // Homo sapiens phosphotriesterase related (PTER), tra	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-1841075	tagcttatccattgaa[A/T]acttaacagcactcag	A	T	NM_024948 // upstream // 421012 // Hs.158870 // C10orf97 // 80013 // Homo sapiens chromosome 10 open reading frame 97 (C10orf97), mRNA. /// NM_030664 // upstream // 155440 // Hs.444321 // PTER // 9317 // Homo sapiens phosphotriesterase related (PTER), tra	C10orf97	C10orf97, Homo sapiens chromosome 10 open reading frame 97 (C10orf97), p13
SNP_A-1723140	tctctatgggggaaggccatgaata[A/G]cctctgccgtatgttg agaagag	A	G	NM_030664 // intron // 0 // Hs.397381 // PTER // 9317 // phosphotriesterase related	PTER	PTER , rs902073, phosphotriesterase related,p13
SNP_A-1996678	gggtaggactttccag[A/G]actctatttaccgt	A	G	NM_030664 // intron // 0 // Hs.444321 // PTER // 9317 // Homo sapiens phosphotriesterase related (PTER), transcript variant 2, mRNA. /// NM_001001484 // intron // 0 // Hs.444321 // PTER // 9317 // Homo sapiens phosphotriesterase related (PTER), transcript	PTER	PTER, Homo sapiens phosphotriesterase related (PTER), transcript variant 2, p13
SNP_A-1881410	tctttccctgcttca[C/T]gatgggcctatgtgtc	C	T	NM_152724 // intron // 0 // Hs.524161 // RSU1 // 6251 // Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, mRNA. /// NM_012425 // intron // 0 // Hs.524161 // RSU1 // 6251 // Homo sapiens Ras suppressor protein 1 (RSU1), transcript varian	RSU1	RSU1, Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, p13
SNP_A-1827147	taaccctcaatatctct[A/G]gaatgtgactatttgg	A	G	NM_152724 // intron // 0 // Hs.524161 // RSU1 // 6251 // Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, mRNA. /// NM_012425 // intron // 0 // Hs.524161 // RSU1 // 6251 // Homo sapiens Ras suppressor protein 1 (RSU1), transcript varian	RSU1	RSU1, Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 2, p13
SNP_A-2066225	aatttacttcactcaa[C/T]atcactggcgtcaact	C	T	NM_001081 // intron // 0 // Hs.166206 // CUBN // 8029 // Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // — // — // —	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-1843661	tagtggtctgattcaa[C/T]gtgacctgctccctct	C	T	NM_001081 // intron // 0 // Hs.166206 // CUBN // 8029 // Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // — // — // —	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-1865891	tcccaaggcaaagcta[A/G]caaatgatattactat	A	G	NM_001081 // intron // 0 // Hs.166206 // CUBN // 8029 // Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // — // — // —	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-2087601	actgctcaacactcca[A/G]aaatcctgagaccat	A	G	NM_001081 // intron // 0 // Hs.166206 // CUBN // 8029 // Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // — // — // —	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1877968	tctggtttgttacaga[C/G]agcctcagaattcagg	C	G	NM_001081 // intron // 0 // Hs.166206 // CUBN // 8029 // Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), mRNA. /// ENST00000265929 // intron // 0 // --- // --- // ---	CUBN	CUBN, Homo sapiens cubilin (intrinsic factor-cobalamin receptor) (CUBN), p13
SNP_A-1842301	taggtagaaggggttga[A/G]aattgtagatgaagt	A	G	ENST00000359417 // intron // 0 // --- // --- // --- /// ENST00000360278 // intron // 0 // --- // --- // ---	-	p12.33
SNP_A-2206269	ccatcccagaaacaca[C/T]tgtgcatcccacctgt	C	T	NM_201593 // intron // 0 // Hs.59093 // CACNB2 // 783 // Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, mRNA. /// NM_201572 // intron // 0 // Hs.59093 // CACNB2 // 783 // Homo sapiens calcium channel, volta	CACNB2	CACNB2, Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, p12.33
SNP_A-1997092	atgaaggacctccaag[A/C]caggatatatatgaag	A	C	NM_201593 // intron // 0 // Hs.59093 // CACNB2 // 783 // Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, mRNA. /// NM_201572 // intron // 0 // Hs.59093 // CACNB2 // 783 // Homo sapiens calcium channel, volta	CACNB2	CACNB2, Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, p12.33
SNP_A-2184901	cagctgtggtctctaa[C/T]gcaaaaataagatact	C	T	NM_201593 // intron // 0 // Hs.59093 // CACNB2 // 783 // Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, mRNA. /// NM_201572 // intron // 0 // Hs.59093 // CACNB2 // 783 // Homo sapiens calcium channel, volta	CACNB2	CACNB2, Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2), transcript variant 5, p12.32
SNP_A-2030670	aaagctgaactcataa[A/T]aacagagagttagaat	A	T	NM_178815 // downstream // 339238 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 799194 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1729296	ggacttgaagtttgaaatctttaa[C/T]aggcatacaaatggctgc accactt	C	T	NM_032812 // upstream // 638560 // Hs.444997 // PLXDC2 // 84898 // plexin domain containing 2 /// NM_178815 // downstream // 500500 // Hs.25362 // ARL8 // 221079 // ADP-ribosylation factor-like 8	PLXDC2	PLXDC2 , rs4748559, plexin domain containing 2 ,p12.31
SNP_A-1905018	tgggtccctgagtaaa[C/T]tcaatagaaaagccgc	C	T	NM_178815 // downstream // 801767 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 336665 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2313295	ggagacattaaactgal[C/G]acagcaatcacaccct	C	G	NM_178815 // downstream // 865107 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 273325 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1705573	aaaattggagtttgcctagtcctgc[A/G]aagttctgttccaaaaggg aaataa	A	G	NM_032812 // upstream // 2196?0 // Hs.444997 // PLXDC2 // 84898 // plexin domain containing 2 /// NM_178815 // downstream // 919390 // Hs.25362 // ARL8 // 221079 // ADP-ribosylation factor-like 8	PLXDC2	PLXDC2 , rs14097?7, plexin domain containing 2 ,p12.31
SNP_A-2045927	aagaccagtccaagaa[C/G]caaaatatcaaaacct	C	G	NM_178815 // downstream // 900746 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 237686 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2084774	actatttcaaagtga[A/T]aactgcagctagtcg	A	T	NM_178815 // downstream // 902693 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 235739 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1719555	gcaaaacagtccagttattatga[C/G]gattttgttagtccttagc acttg	C	G	NM_032812 // upstream // 191104 // Hs.444997 // PLXDC2 // 84898 // plexin domain containing 2 /// NM_178815 // downstream // 947956 // Hs.25362 // ARL8 // 221079 // ADP-ribosylation factor-like 8	PLXDC2	PLXDC2 , rs10508588, plexin domain containing 2 ,p12.31
SNP_A-2279081	gaggaataggaataga[C/T]gagtaaagtgaccagt	C	T	NM_178815 // downstream // 969471 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 168961 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2260873	gaaactgccaacaggg[A/C]cagcgagggtgaccat	A	C	NM_178815 // downstream // 974068 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 164364 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-2271167	gacatctctgagagggt[G/T]ataatttgagttaaga	G	T	NM_178815 // downstream // 996063 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 142369 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1951366	tttccggtgacagata[C/T]acctctatccaaatctt	C	T	NM_178815 // downstream // 996126 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 142306 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1794818	ggtctgtatcctaaa[A/G]gtaaagatgagttagc	A	G	NM_178815 // downstream // 997973 // Hs.25362 // ARL8 // 221079 // Homo sapiens ADP-ribosylation factor-like 8 (ARL8), mRNA. /// NM_032812 // upstream // 140459 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. ///	ARL8	ARL8, Homo sapiens ADP-ribosylation factor-like 8 (ARL8), p12.31
SNP_A-1997693	ttcttggaagttgtag[A/T]ccaaagatactattca	A	T	NM_032812 // intron // 0 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // intron // 0 // — // — // — /// ENST00000298012 // intron // 0 // — // — // —	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-1736857	cctgacccaggctaggagcagttga[G/T]gccttcatagaataac cacatgttc	G	T	NM_032812 // intron // 0 // Hs.444997 // PLXDC2 // 84898 // plexin domain containing 2	PLXDC2	PLXDC2 , rs10508606, plexin domain containing 2,p12.31
SNP_A-2261322	gaaagcagaggaaaa[C/T]tagctaagtaggtaaa	C	T	NM_032812 // intron // 0 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // intron // 0 // — // — // — /// ENST00000298012 // intron // 0 // — // — // —	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-1872018	tctacccctggacccc[A/G]caaggtcatgccctc	A	G	NM_032812 // downstream // 104799 // Hs.148200 // PLXDC2 // 84898 // Homo sapiens plexin domain containing 2 (PLXDC2), mRNA. /// ENST00000277585 // downstream // 104799 // — // — // — /// ENST00000298012 // downstream // 104795 // — // —	PLXDC2	PLXDC2, Homo sapiens plexin domain containing 2 (PLXDC2), p12.31
SNP_A-2293193	gcagagataacattga[C/T]ctgaacttgtatcta	C	T	ENST00000356111 // intron // 0 // — // — // —	-	p12.31
SNP_A-2133611	atatcacttttgctttc[A/G]ccctattccatccat	A	G	NM_006393 // downstream // 92935 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 97443 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// E	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-2091533	agaaaaagctacctga[C/T]gccaagaaagaaacac	C	T	NM_006393 // downstream // 52879 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 57387 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// E	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1998001	ggacaagtaggaactg[C/T]actttgcacaaatca	C	T	NM_006393 // downstream // 11174 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // downstream // 15682 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// E	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-1901804	tggcactggctactca[C/G]ggtatttccaattaaa	C	G	NM_006393 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// ENST00000311749 ///	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-2190133	cataaggcccacatagat[C/T]gcagctaggggagat	C	T	NM_006393 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 1, mRNA. /// NM_213569 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// ENST00000311749 ///	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 1, p12.31
SNP_A-2263780	gaaccttccggaagac[A/G]gtcatcaaaacaaaaa	A	G	NM_213569 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// ENST00000311725 // intron // 0 // — // — // — // —	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 2, p12.31
SNP_A-2235419	ctcccttgacttatgat[A/C]cctccaataagctaaa	A	C	NM_213569 // intron // 0 // Hs.5025 // NEBL // 10529 // Homo sapiens nebulette (NEBL), transcript variant 2, mRNA. /// ENST00000311725 // intron // 0 // — // — // — // —	NEBL	NEBL, Homo sapiens nebulette (NEBL), transcript variant 2, p12.31
SNP_A-2159361	atttaatatatcttaa[C/T]gtttggttctgatgtc	C	T	NM_022365 // upstream // 190541 // Hs.499000 // DNAJC1 // 64215 // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 1 (DNAJC1), mRNA. /// NM_018029 // downstream // 15251 // Hs.534462 // FLJ10213 // 55096 // Homo sapiens hypothetical protein FLJ1021	DNAJC1	DNAJC1, Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 1 (DNAJC1), p12.31
SNP_A-2126213	ataaaaacatgacatc[G/T]acatattaccctcccca	G	T	NM_172242 // intron // 0 // Hs.527698 // SPAG6 // 9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, mRNA. /// NM_012443 // intron // 0 // Hs.527698 // SPAG6 // 9576 // Homo sapiens sperm associated antigen 6 (SPAG6), transcrip	SPAG6	SPAG6, Homo sapiens sperm associated antigen 6 (SPAG6), transcript variant 2, p12.2
SNP_A-2046662	aagagcctaattcctat[A/C]cttgaaggttgtttg	A	C	NM_005028 // intron // 0 // Hs.499029 // PIP5K2A // 5305 // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), mRNA. /// ENST00000280452 // intron // 0 // — // — // — // —	PIP5K2A	PIP5K2A, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), p12.2
SNP_A-2092810	agaaatgtttaaaaa[C/G]tgagagccattgcact	C	G	NM_005028 // intron // 0 // Hs.499029 // PIP5K2A // 5305 // Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), mRNA. /// ENST00000280452 // intron // 0 // — // — // — // —	PIP5K2A	PIP5K2A, Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A), p12.2
SNP_A-2196584	cattaaactacagaaa[A/C]atccttccattaccct	A	C	NM_173081 // intron // 0 // Hs.137270 // ARMC3 // 219681 // Homo sapiens armadillo repeat containing 3 (ARMC3), mRNA. /// ENST00000298032 // intron // 0 // — // — // — // —	ARMC3	ARMC3, Homo sapiens armadillo repeat containing 3 (ARMC3), p12.2
SNP_A-2172014	caatgcttggctcaaa[A/G]ttaaagagaagcatgg	A	G	NM_019590 // upstream // 628386 // Hs.445885 // KIAA1217 // 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000298035 // downstream // 139875 // — // — // — // — /// ENST00000323059 // upstream // 628386 // — // — // — // — ///	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.2
SNP_A-2159269	atttaacatattaaaac[C/T]gagtgctagagccaag	C	T	NM_019590 // upstream // 608884 // Hs.445885 // KIAA1217 // 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000298035 // downstream // 159377 // — // — // — // — /// ENST00000323059 // upstream // 608884 // — // — // — // — ///	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.2
SNP_A-1946190	tttaaaaaagctcaag[A/C]aaaatgcatctaattg	A	C	NM_019590 // upstream // 561881 // Hs.445885 // KIAA1217 // 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000298035 // downstream // 206380 // — // — // — // — /// ENST00000323059 // upstream // 561881 // — // — // — // — ///	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1855632	tcaataatttantca[A/G]gatgaggatatgagcc	A	G	NM_019590 // upstream // 163165 // Hs.445885 // KIAA1217 // 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000298035 // downstream // 605096 // --- // --- // --- // --- /// ENST00000323059 // upstream // 163165 // --- // --- // --- // --- ///	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.2
SNP_A-2167478	caacatcctttgcta[C/T]agagttttttta	C	T	NM_019590 // upstream // 89695 // Hs.445885 // KIAA1217 // 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000298035 // downstream // 678566 // --- // --- // --- // --- /// ENST00000323059 // upstream // 89695 // --- // --- // --- // --- /// EN	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.2
SNP_A-1951932	tttctacttattgctg[G/T]aggtaatcacattcca	G	T	NM_019590 // intron // 0 // Hs.445885 // KIAA1217 // 56243 // Homo sapiens KIAA1217 (KIAA1217), mRNA. /// ENST00000323059 // intron // 0 // --- // --- // ---	KIAA1217	KIAA1217, Homo sapiens KIAA1217 (KIAA1217), p12.1
SNP_A-2175498	cacatctcacatcaac[C/G]agtgattggaaaacga	C	G	NM_020200 // intron // 0 // Hs.405619 // PRTFDC1 // 56952 // Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA. /// ENST00000358336 // intron // 0 // --- // --- // --- /// ENST00000320152 // intron // 0 // --- // --- // --	PRTFDC1	PRTFDC1, Homo sapiens phosphoribosyl transferase domain containing 1 (PRTFDC1), p12.1
SNP_A-2021743	aaaaacagcaagctgg[A/G]aacttaagcagaaac	A	G	NM_145010 // intron // 0 // Hs.534486 // C10orf63 // 219670 // Homo sapiens chromosome 10 open reading frame 63 (C10orf63), mRNA. /// ENST00000331161 // intron // 0 // --- // --- // --- /// ENST00000280623 // intron // 0 // --- // --- // --	C10orf63	C10orf63, Homo sapiens chromosome 10 open reading frame 63 (C10orf63), p12.1
SNP_A-1792891	ggtaattaacaaacac[C/T]gatcatttgaaggagt	C	T	NM_024838 // downstream // 86114 // Hs.546436 // THNSL1 // 79896 // Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), mRNA. /// NM_020752 // upstream // 62585 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR15	THNSL1	THNSL1, Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), p12.1
SNP_A-1998720	gaagatgaaagagagt[A/C]aatgcaggaacaggtg	A	C	NM_024838 // downstream // 122271 // Hs.546436 // THNSL1 // 79896 // Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), mRNA. /// NM_020752 // upstream // 26428 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR1	THNSL1	THNSL1, Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), p12.1
SNP_A-1906744	tggttaatccatttca[A/G]tgaaaacaaccttgat	A	G	NM_024838 // downstream // 139159 // Hs.546436 // THNSL1 // 79896 // Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), mRNA. /// NM_020752 // upstream // 9540 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR15	THNSL1	THNSL1, Homo sapiens threonine synthase-like 1 (bacterial) (THNSL1), p12.1
SNP_A-1906944	tggttctgaggccttc[A/G]aatttagactgaacca	A	G	NM_020752 // intron // 0 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// ENST00000280625 // intron // 0 // --- // --- // ---	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-1998777	ccattgcctgggagc[C/T]atcgcaatgaggccag	C	T	NM_020752 // intron // 0 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// ENST00000280625 // intron // 0 // --- // --- // ---	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-2283734	gataggaaaaccaaata[A/G]caatgtcaaacctagc	A	G	NM_020752 // intron // 0 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// ENST00000280625 // intron // 0 // --- // --- // ---	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-1874924	tctctaccagtgttc[C/T]caatgagtagtgatca	C	T	NM_020752 // downstream // 75422 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// NM_017433 // upstream // 259267 // Hs.131367 // MYO3A // 53904 // Homo sapiens myosin IIIA (MYO3A), mRNA. /// ENST00000280	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-2247438	ctgtctatcgtgatcc[A/T]catttttgtttaaaaa	A	T	NM_020752 // downstream // 181707 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// NM_017433 // upstream // 152982 // Hs.131367 // MYO3A // 53904 // Homo sapiens myosin IIIA (MYO3A), mRNA. /// ENST00000280	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1886396	tgacctttatcactta[C/T]gagaatatgcttgcta	C	T	NM_020752 // downstream // 205374 // Hs.499108 // GPR158 // 57512 // Homo sapiens G protein-coupled receptor 158 (GPR158), mRNA. /// NM_017433 // upstream // 129315 // Hs.131367 // MYO3A // 53904 // Homo sapiens myosin IIIA (MYO3A), mRNA. /// ENST00000280	GPR158	GPR158, Homo sapiens G protein-coupled receptor 158 (GPR158), p12.1
SNP_A-2001057	gatgccttggttattg[C/T]caacactcctgcagat	C	T	NM_005470 // intron // 0 // Hs.508148 // ABI1 // 10006 // Homo sapiens abl-interactor 1 (ABI1), mRNA. /// ENST00000346832 // intron // 0 // — // — // — // — /// ENST00000359188 // intron // 0 // — // — // --- // --- /// ENST00000357225 // intr	ABI1	ABI1, Homo sapiens abl-interactor 1 (ABI1), p12.1
SNP_A-1741009	agaaacaaattaggatacatccata[A/C]aatagaacactactta gcggtaaca	A	C	NM_005470 // intron // 0 // Hs.42710 // ABI1 // 10006 // abl-interactor 1	ABI1	ABI1 , rs2182294, abl-interactor 1,p12.1
SNP_A-2223283	cgcggcctgcatcttc[A/G]cagtctgcatgctggt	A	G	NM_005470 // upstream // 76038 // Hs.508148 // ABI1 // 10006 // Homo sapiens abl-interactor 1 (ABI1), mRNA. /// ENST00000346832 // upstream // 76046 // — // — // — // — /// ENST00000359188 // upstream // 76037 // — // — // --- // — /// ENST0	ABI1	ABI1, Homo sapiens abl-interactor 1 (ABI1), p12.1
SNP_A-1957717	ttttatgtcaaagagg[A/C]attttaggatgatatg	A	C	NM_032844 // downstream // 2017 // Hs.276905 // MASTL // 84930 // Homo sapiens microtubule associated serine/threonine kinase-like (MASTL), mRNA. /// NM_145698 // downstream // 7882 // Hs.530597 // ACBD5 // 91452 // Homo sapiens acyl-Coenzyme A binding do	MASTL	MASTL, Homo sapiens microtubule associated serine,p12.1
SNP_A-2130806	atacttgcagagctag[A/G]agtgaatcaggggaat	A	G	ENST00000340021 // upstream // 78397 // — // — // — // — /// ENST00000340878 // downstream // 7977 // --- // --- // ---	-	p12.1
SNP_A-1902156	tggcattttggttcta[A/T]attttggtagcctttc	A	T	NM_021252 // intron // 0 // Hs.406799 // RAB18 // 22931 // Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA. /// ENST00000265946 // intron // 0 // — // — // — // --- /// ENST00000356940 // intron // 0 // — // — // — // —	RAB18	RAB18, Homo sapiens RAB18, member RAS oncogene family (RAB18), p12.1
SNP_A-2041904	aactaacttgacgtac[A/G]agcacctctgtaaata	A	G	NM_021252 // downstream // 2161 // Hs.406799 // RAB18 // 22931 // Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA. /// NM_173576 // downstream // 130553 // Hs.128193 // C10orf48 // 283078 // Homo sapiens chromosome 10 open reading frame 48 (C	RAB18	RAB18, Homo sapiens RAB18, member RAS oncogene family (RAB18), p12.1
SNP_A-2036184	aaattatggcctataa[C/T]catcctttccaaaaat	C	T	NM_173496 // intron // 0 // Hs.499159 // MPP7 // 143098 // Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), mRNA. /// ENST00000337532 // intron // 0 // — // — // — // — /// ENST00000355519 // intron // 0 // —	MPP7	MPP7, Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), p12.1
SNP_A-1943303	ttggtgtattgaagtc[A/G]gaatacctgtgcctgc	A	G	NM_173496 // intron // 0 // Hs.499159 // MPP7 // 143098 // Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), mRNA. /// ENST00000337532 // intron // 0 // — // — // — // — /// ENST00000355519 // intron // 0 // —	MPP7	MPP7, Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), p12.1
SNP_A-2139442	atccttcaggcactcc[C/T]ccctaaatattgcttc	C	T	NM_173496 // intron // 0 // Hs.499159 // MPP7 // 143098 // Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), mRNA. /// ENST00000337532 // intron // 0 // — // — // — // — /// ENST00000355519 // intron // 0 // —	MPP7	MPP7, Homo sapiens membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (MPP7), p12.1
SNP_A-1710976	aggtaaaaaaaaacactttaccag[A/G]caggacattgcaagg ccacagagat	A	G	NM_012342 // downstream // 63177 // Hs.348802 // BAMBI // 25805 // BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) /// NM_173577 // upstream // 100464 // Hs.375078 // C10orf126 // 283080 // chromosome 10 open reading frame 126	BAMBI	BAMBI , rs787116, BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) ,p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1871618	tctaagtatctgggac[A/T]ctagttggtacaaaac	A	T	NM_012342 // downstream // 128188 // Hs.533336 // BAMBI // 25805 // Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI), mRNA. /// ENST00000224324 // downstream // 128188 // — // — // — /// ENST00000320125 /	BAMBI	BAMBI, Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI), p12.1
SNP_A-2072359	acagcaaggctgaaac[G/T]atcagaatgtgggaga	G	T	ENST00000354953 // upstream // 16180 // — // — // — /// ENST00000277685 // downstream // 35128 // — // — // — // —	-	p12.1
SNP_A-2121635	agtgaatcaagttaat[A/G]atctacagccttcctt	A	G	ENST00000354953 // upstream // 33939 // — // — // — /// ENST00000277685 // downstream // 17369 // — // — // — // —	-	p12.1
SNP_A-2052388	aagtacctaagtaaaa[C/T]tccacttagccagaat	C	T	NM_183058 // upstream // 277744 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 277744 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstrea	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2123189	agtggttcttgctccaa[A/T]tgaattgttttgcac	A	T	NM_183058 // upstream // 274743 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 274743 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstrea	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2053493	aagtgcatacctccca[C/T]aaggaatctacaacag	C	T	NM_183058 // upstream // 234199 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 234199 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstrea	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p12.1
SNP_A-2170053	caagggcctacctaaa[C/T]tcaagggagggaaca	C	T	NM_183058 // upstream // 151932 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 151932 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstrea	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2197169	cattcaaggacattta[C/T]ggtttaccccaatagg	C	T	NM_183058 // upstream // 140184 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 140184 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstrea	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2049368	aagctgaaagagcgac[C/T]ggcagttcagaatttc	C	T	NM_183058 // upstream // 58794 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 58794 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstream	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2285434	gatcttcaggcagaaac[C/G]aagaggagttgcatgt	C	G	NM_183058 // upstream // 49964 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 49964 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstream	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2036230	aaattcaaacacaaaa[C/G]aggcaccaactatatc	C	G	NM_183058 // upstream // 6595 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // upstream // 6595 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000277685 // upstream //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2095859	agacagagtctggcta[C/T]ggagtcccgttatggg	C	T	NM_183058 // intron // 0 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // intron // 0 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000239738 // intron // 0 // — //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2203430	ccagaaatacatatga[A/G]cacagcattgaggata	A	G	NM_183058 // intron // 0 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // intron // 0 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000239738 // intron // 0 // --- //	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-1999714	accagatatggcttca[G/T]aggagggaacagtgca	G	T	NM_183058 // downstream // 57119 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // downstream // 57119 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000239738 // downs	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-1904990	tgggtcagcaactcta[C/T]taagacttataaatag	C	T	NM_183058 // downstream // 109732 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// NM_032517 // downstream // 109732 // Hs.117530 // LYZL1 // 84569 // Homo sapiens lysozyme-like 1 (LYZL1), mRNA. /// ENST00000239738 // dow	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-2061378	aatgccgcagggagga[A/T]cttgcagcatttcttg	A	T	NM_021738 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /// ENST0000035	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-2272767	gacgttttaaccgagc[A/G]ctgatggtggtgtatt	A	G	NM_021738 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /// ENST0000035	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-1654683	catccatgttttagcatatgtcagc[A/C]ctacaatccttttttaaacctgaata	A	C	NM_003174 // intron // 0 // Hs.163111 // SVIL // 6840 // supervillin	SVIL	SVIL , rs1265446, supervillin,p11.23
SNP_A-2201675	ccacaaagggacaact[A/G]agaaaataagaaatgg	A	G	NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /// ENST00000356412 // intron // 0 // --- // --- // --- // --- /// ENST00000354659 // intron // 0 // --- // --- // --- // ---	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 1, p11.23
SNP_A-2247114	ctgtcacatgtgtgag[C/G]caagttagaagcaatg	C	G	NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /// ENST00000356412 // intron // 0 // --- // --- // --- // --- /// ENST00000354659 // intron // 0 // --- // --- // --- // ---	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 1, p11.23
SNP_A-2270445	gacagaacgcctatga[A/G]aacatgtgccagtctg	A	G	NM_003174 // intron // 0 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /// ENST00000356412 // intron // 0 // --- // --- // --- // --- /// ENST00000354659 // intron // 0 // --- // --- // --- // ---	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 1, p11.23
SNP_A-2046576	aagagattctaacagc[A/C]aaaagctcactactct	A	C	NM_021738 // upstream // 343068 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 2, mRNA. /// NM_003174 // upstream // 242239 // Hs.499209 // SVIL // 6840 // Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /	SVIL	SVIL, Homo sapiens supervillin (SVIL), transcript variant 2, p11.23
SNP_A-1999737	tagggagggactgaga[C/T]gtgaccagcagctgga	C	T	ENST00000298635 // intron // 0 // --- // --- // --- // ---	-	p11.23
SNP_A-2132731	atataaacttccctta[C/T]gcagcttttcagcaac	C	T	NM_018109 // downstream // 114361 // Hs.173946 // PAPD1 // 55149 // Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA. /// ENST00000298635 // upstream // 82976 // --- // --- // --- // --- /// ENST00000263063 // downstream // 114361 // --- // -	PAPD1	PAPD1, Homo sapiens PAP associated domain containing 1 (PAPD1), p11.23
SNP_A-1924366	ttataactgagaaaat[G/T]atgacggtgaaagaga	G	T	NM_018109 // downstream // 101632 // Hs.173946 // PAPD1 // 55149 // Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA. /// ENST00000298635 // upstream // 95705 // --- // --- // --- // --- /// ENST00000263063 // downstream // 101632 // --- // -	PAPD1	PAPD1, Homo sapiens PAP associated domain containing 1 (PAPD1), p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1756799	ttacctagaaattgaaattaacatt[C/T]aacctcaggatctccaagtccaaaag	C	T	AB040895 // upstream // 219171 // Hs.192726 // KIAA1462 // 57608 // KIAA1462 /// NM_018109 // downstream // 65187 // Hs.173946 // PAPD1 // 55149 // PAP associated domain containing 1	KIAA1462	KIAA1462 , rs533049, KIAA1462 ,p11.23
SNP_A-2079300	accccaaaagatgtga[A/C]aggactgttacgtaa	A	C	NM_018109 // downstream // 13086 // Hs.173946 // PAPD1 // 55149 // Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA. /// ENST00000298635 // upstream // 184251 // — // — // — /// ENST00000263063 // downstream // 13086 // — // -	PAPD1	PAPD1, Homo sapiens PAP associated domain containing 1 (PAPD1), p11.23
SNP_A-2100739	agatagcatttgtacc[C/T]caaggtcagtggccca	C	T	NM_183058 // upstream // 32072 // Hs.522610 // LYZL2 // 119180 // Homo sapiens lysozyme-like 2 (LYZL2), mRNA. /// ENST00000260633 // upstream // 32072 // — // — // — /// ENST00000340836 // upstream // 41747 // — // — // —	LYZL2	LYZL2, Homo sapiens lysozyme-like 2 (LYZL2), p11.23
SNP_A-1947181	ttaatgctgagttta[A/G]aactggaattcagcaa	A	G	NM_182755 // upstream // 113124 // Hs.128037 // LOC220929 // 220929 // Homo sapiens hypothetical protein LOC220929 (LOC220929), mRNA. /// NM_030751 // upstream // 221666 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interl	LOC220929	LOC220929, Homo sapiens hypothetical protein LOC220929 (LOC220929), p11.22
SNP_A-1809818	gtgagggaggtcacat[C/T]gaaacagaagttagg	C	T	NM_182755 // upstream // 174624 // Hs.128037 // LOC220929 // 220929 // Homo sapiens hypothetical protein LOC220929 (LOC220929), mRNA. /// NM_030751 // upstream // 160166 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interl	LOC220929	LOC220929, Homo sapiens hypothetical protein LOC220929 (LOC220929), p11.22
SNP_A-1683792	cagacaagaggttctgatttctgaga[G/T]gtgtagactcccttgggacttagg	G	T	AK094743 // downstream // 161891 // Hs.499254 // - // - // CDNA FLJ37424 fis, clone BRAWH2001492 /// NM_030751 // upstream // 119677 // Hs.232068 // TCF8 // 6935 // transcription factor 8 (represses interleukin 2 expression) /// NM_182755 // upstream //	-	-, rs2797894, CDNA FLJ37424 fis, clone BRAWH2001492 ,p11.22
SNP_A-2026805	aaacacagatctctaa[A/G]caactcaactaaatca	A	G	NM_182755 // upstream // 180604 // Hs.128037 // LOC220929 // 220929 // Homo sapiens hypothetical protein LOC220929 (LOC220929), mRNA. /// NM_030751 // upstream // 154186 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interl	LOC220929	LOC220929, Homo sapiens hypothetical protein LOC220929 (LOC220929), p11.22
SNP_A-2290963	gcaagtccaaaattca[C/T]aggaccggctggcagg	C	T	NM_182755 // upstream // 192222 // Hs.128037 // LOC220929 // 220929 // Homo sapiens hypothetical protein LOC220929 (LOC220929), mRNA. /// NM_030751 // upstream // 142568 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interl	LOC220929	LOC220929, Homo sapiens hypothetical protein LOC220929 (LOC220929), p11.22
SNP_A-2241183	ctgaggaaagttaggat[A/G]aggaaagctggccaaa	A	G	NM_182755 // upstream // 275052 // Hs.128037 // LOC220929 // 220929 // Homo sapiens hypothetical protein LOC220929 (LOC220929), mRNA. /// NM_030751 // upstream // 59738 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interle	LOC220929	LOC220929, Homo sapiens hypothetical protein LOC220929 (LOC220929), p11.22
SNP_A-2036589	aaattgcctggcaaaa[C/T]gttaactctcaaatct	C	T	NM_030751 // intron // 0 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA. /// ENST00000360572 // intron // 0 // — // — // — /// ENST00000357723 // intron // 0 // — // —	TCF8	TCF8, Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), p11.22
SNP_A-1732902	atattatgctgtaatacactgttca[A/C]atattatgagattctaatggt taaa	A	C	NM_030751 // intron // 0 // Hs.232068 // TCF8 // 6935 // transcription factor 8 (represses interleukin 2 expression)	TCF8	TCF8, rs161273, transcription factor 8 (represses interleukin 2 expression),p11.22
SNP_A-1999760	ttcattatgtgcaaag[C/G]ctcctgactgaaaatc	C	G	NM_030751 // intron // 0 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA. /// ENST00000360572 // intron // 0 // — // — // — /// ENST00000357723 // intron // 0 // — // —	TCF8	TCF8, Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1809907	gtgagtcctattgaac[C/G]ctgcagacaaacccct	C	G	NM_030751 // downstream // 68516 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA. /// NM_018287 // downstream // 208591 // Hs.499264 // ARHGAP12 // 94134 // Homo sapiens Rho GTPase acti	TCF8	TCF8, Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), p11.22
SNP_A-2099564	agagggtgtaatgtta[C/T]ggaggccaagagaaga	C	T	NM_030751 // downstream // 70313 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA. /// NM_018287 // downstream // 206794 // Hs.499264 // ARHGAP12 // 94134 // Homo sapiens Rho GTPase acti	TCF8	TCF8, Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), p11.22
SNP_A-2296486	gcatttgatgactgca[C/T]taatctttgtaattcc	C	T	NM_030751 // downstream // 211646 // Hs.124503 // TCF8 // 6935 // Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA. /// NM_018287 // downstream // 65461 // Hs.499264 // ARHGAP12 // 94134 // Homo sapiens Rho GTPase acti	TCF8	TCF8, Homo sapiens transcription factor 8 (represses interleukin 2 expression) (TCF8), p11.22
SNP_A-1748375	ttaagccaacaagattttgcttaca[A/T]ccctagtaggaaagtaaccttgaaa	A	T	NM_004521 // upstream // 146877 // Hs.149436 // KIF5B // 3799 // kinesin family member 5B /// NM_025209 // downstream // 65767 // Hs.443721 // EPC1 // 80314 // enhancer of polycomb homolog 1 (Drosophila)	KIF5B	KIF5B , rs10508771, kinesin family member 5B ,p11.22
SNP_A-2286699	gatggatttgaacagg[C/G]acccaagactatactg	C	G	NM_024688 // intron // 0 // Hs.436242 // C10orf68 // 79741 // Homo sapiens chromosome 10 open reading frame 68 (C10orf68), mRNA. /// ENST00000302316 // intron // 0 // — // — // — // —	C10orf68	C10orf68, Homo sapiens chromosome 10 open reading frame 68 (C10orf68), p11.22
SNP_A-1913865	tgtgtctcagtgtaaa[C/T]ttcttaagattcaacc	C	T	NM_024688 // intron // 0 // Hs.436242 // C10orf68 // 79741 // Homo sapiens chromosome 10 open reading frame 68 (C10orf68), mRNA. /// ENST00000302316 // intron // 0 // — // — // — // —	C10orf68	C10orf68, Homo sapiens chromosome 10 open reading frame 68 (C10orf68), p11.22
SNP_A-1693355	gtggtagcagcaggaggttggttta[A/G]agtagcttaattgtattgtctgccc	A	G	NM_002211 // upstream // 164237 // Hs.287797 // ITGB1 // 3688 // integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) /// NM_003873 // downstream // 57569 // Hs.173548 // NRP1 // 8829 // neuropilin 1 /// NM_033666	ITGB1	ITGB1 , rs2070302, integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) ,p11.22
SNP_A-2131223	atagagcaaactgtca[A/G]gcagtacttaactcac	A	G	NM_003873 // downstream // 64043 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000277647 // upstream // 55048 // — // — // — // — /// ENST00000265371 // downstream // 64043 // — // — // — // — /// ENST00	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1728277	catgaccacaggttccatgatgcta[C/T]gtctctatgtaggcgtatttcagt	C	T	NM_002211 // upstream // 191369 // Hs.287797 // ITGB1 // 3688 // integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) /// NM_003873 // downstream // 30437 // Hs.173548 // NRP1 // 8829 // neuropilin 1 /// NM_033666	ITGB1	ITGB1 , rs2180562, integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) ,p11.22
SNP_A-1686518	tttagttcatctgttctttcgttca[A/G]cccttagagaggtcatgtagtagca	A	G	NM_002211 // upstream // 192034 // Hs.287797 // ITGB1 // 3688 // integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) /// NM_003873 // downstream // 29772 // Hs.173548 // NRP1 // 8829 // neuropilin 1 /// NM_033666	ITGB1	ITGB1 , rs10508780, integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) ,p11.22
SNP_A-2257663	ctttgctgaaactcgc[C/T]cagtgttggaaaactc	C	T	NM_003873 // downstream // 47562 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000277647 // upstream // 71529 // — // — // — // — /// ENST00000265371 // downstream // 47562 // — // — // — // — /// ENST00	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1867990	tcctaggccatctagt[C/G]aggagcggtgcaagag	C	G	NM_003873 // downstream // 40195 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000277647 // upstream // 78896 // --- // --- // --- /// ENST00000265371 // downstream // 40195 // --- // --- // --- /// ENST00	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1888285	tgagctctccattgat[A/G]agaatcttcccatctc	A	G	NM_003873 // downstream // 33891 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000277647 // upstream // 85200 // --- // --- // --- /// ENST00000265371 // downstream // 33891 // --- // --- // --- /// ENST00	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1738014	aatgacaaaatgtccaacacttcaa[G/T]atttttctttagaaact gtacatc	G	T	NM_003873 // intron // 0 // Hs.173548 // NRP1 // 8829 // neuropilin 1	NRP1	NRP1 , rs2254826, neuropilin 1,p11.22
SNP_A-2153082	attacccacaaacaga[A/G]cacttggagtccagat	A	G	NM_003873 // intron // 0 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000265371 // intron // 0 // --- // --- // ---	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2158123	attggagggaggccag[A/G]atacattagcgttctg	A	G	NM_003873 // intron // 0 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000265371 // intron // 0 // --- // --- // --- /// ENST00000309510 // intron // 0 // --- // --- // ---	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2112725	aggcagccaaatttta[C/T]gttggagcgtgtgta	C	T	NM_003873 // intron // 0 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000265371 // intron // 0 // --- // --- // --- /// ENST00000309510 // intron // 0 // --- // --- // ---	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1999791	tttgctaattctggca[C/T]aggttttgctgtcagg	C	T	NM_003873 // intron // 0 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// ENST00000265371 // intron // 0 // --- // --- // --- /// ENST00000309510 // intron // 0 // --- // --- // ---	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2262976	gaacaagtaccaaaga[G/T]caagtgcttattggagt	G	T	NM_003873 // upstream // 33740 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 741279 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2055276	aataagaggcaggaag[A/C]aaactaaagaatgagg	A	C	NM_003873 // upstream // 33894 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 741125 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2200759	ccaagagaggtcagaaa[G/T]aattcaatcgatgtg	G	T	NM_003873 // upstream // 64185 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 710834 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1842702	tagtaacctccctttc[C/T]ccctttgcactggttt	C	T	NM_003873 // upstream // 67111 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 707908 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2249435	cttaaatcaccacgcc[A/G]atcttgccagtgcgaa	A	G	NM_003873 // upstream // 76203 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 698816 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2261756	gaaagtgtatgacaaa[C/G]gaaagctggaataaat	C	G	NM_003873 // upstream // 78561 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 696458 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1909258	tgtatggaagaggagtt[C/T]aactatccgagagaca	C	T	NM_003873 // upstream // 148166 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 626853 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1999808	gctgtatcctcccatc[A/C]aatggaaattagtgg	A	C	NM_003873 // upstream // 172010 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 603009 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2293296	gcagaggtggaaacag[A/G]acgggaactactgaa	A	G	NM_003873 // upstream // 239257 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 535762 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2071346	acactttagatgtggg[A/C]atgaaataaaataggac	A	C	NM_003873 // upstream // 405292 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 369727 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2089649	acttcatgtctatcac[A/G]aatgcatcatcaccca	A	G	NM_003873 // upstream // 405438 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 369581 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2116122	aggtaacatgacaac[A/G]gacagaaaccatgcac	A	G	NM_003873 // upstream // 420987 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 354032 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1999814	gtcctaatcccccatac[C/T]catgtaagtgacctta	C	T	NM_003873 // upstream // 449678 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 325341 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2115276	aggggaatttggttc[C/G]atttgtgtcttgtgt	C	G	NM_003873 // upstream // 746878 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 28141 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA.	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-2232622	ctcacctgtcctttgg[A/G]aaagatggtctccact	A	G	NM_003873 // upstream // 773593 // Hs.131704 // NRP1 // 8829 // Homo sapiens neuropilin 1 (NRP1), mRNA. /// NM_019619 // downstream // 1426 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /	NRP1	NRP1, Homo sapiens neuropilin 1 (NRP1), p11.22
SNP_A-1934706	ttctctgtacatatgc[A/G]actctctaataaaaggc	A	G	NM_019619 // 3UTR // 0 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// ENST00000354496 // 3UTR // 0 // — // — // —	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1793387	ggtagggatgaaacacg[G/T]ccctagtctcctgcag	G	T	NM_019619 // intron // 0 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// ENST00000354496 // intron // 0 // — // — // — /// ENST00000351738 // intron // 0 // — // — // -	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.21
SNP_A-2169220	caagattgttgacccct[C/T]aaatgttgccaagagct	C	T	NM_019619 // intron // 0 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// ENST00000354496 // intron // 0 // — // — // — /// ENST00000351738 // intron // 0 // — // — // -	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.21
SNP_A-1821931	gtttattgctctgcaa[C/T]gtgtgtcacatttaa	C	T	NM_019619 // upstream // 31275 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA. /// NM_019619 // upstream // 31486 // Hs.131489 // PARD3 // 56288 // Homo sapiens par-3 partitioning defective	PARD3	PARD3, Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), p11.21
SNP_A-2139139	atcctcatcctatcat[C/T]agggactgtcaagagc	C	T	NM_182718 // downstream // 65242 // Hs.200250 // CREM // 1390 // Homo sapiens cAMP responsive element modulator (CREM), transcript variant 5, mRNA. /// NM_001881 // downstream // 65242 // Hs.200250 // CREM // 1390 // Homo sapiens cAMP responsive element m	CREM	CREM, Homo sapiens cAMP responsive element modulator (CREM), transcript variant 5, p11.21
SNP_A-1648008	gtccttaagcgcaaggtccaaataa[C/T]gttgacctttgtatccc agcatcc	C	T	NM_145012 // intron // 0 // Hs.6820 // C10orf9 // 219771 // chromosome 10 open reading frame 9 /// NM_181698 // intron // 0 // Hs.6820 // C10orf9 // 219771 // chromosome 10 open reading frame 9	C10orf9	C10orf9 , rs2474519, chromosome 10 open reading frame 9 , p11.21
SNP_A-1753053	ctgagtgaactcactgccaagatcc[A/G]cgtaagaatatttaaa gtcacagat	A	G	NM_145012 // intron // 0 // Hs.6820 // C10orf9 // 219771 // chromosome 10 open reading frame 9 /// NM_181698 // intron // 0 // Hs.6820 // C10orf9 // 219771 // chromosome 10 open reading frame 9	C10orf9	C10orf9 , rs2504371, chromosome 10 open reading frame 9 , p11.21
SNP_A-2027073	aaacagcatcatctca[C/T]cagttttgttttgag	C	T	NM_181698 // intron // 0 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA. /// NM_145012 // intron // 0 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA.	C10orf9	C10orf9, Homo sapiens chromosome 10 open reading frame 9 (C10orf9), p11.21
SNP_A-2162228	atttagagacttgca[C/T]attgacaaatggta	C	T	NM_181698 // intron // 0 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA. /// NM_145012 // intron // 0 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA.	C10orf9	C10orf9, Homo sapiens chromosome 10 open reading frame 9 (C10orf9), p11.21
SNP_A-1891805	tgatttcctttatcg[A/G]atctttccaaagcgtc	A	G	NM_181698 // intron // 0 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA. /// NM_145012 // intron // 0 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA.	C10orf9	C10orf9, Homo sapiens chromosome 10 open reading frame 9 (C10orf9), p11.21
SNP_A-1999879	tagacagtgtccagct[C/G]aatatttgttgaagga	C	G	NM_181698 // downstream // 5237 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA. /// NM_181698 // downstream // 3665 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C	C10orf9	C10orf9, Homo sapiens chromosome 10 open reading frame 9 (C10orf9), p11.21
SNP_A-1915842	tgttgaattaccaaga[C/T]gtttcctcacctgtaa	C	T	NM_181698 // downstream // 19644 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9 (C10orf9), mRNA. /// NM_181698 // downstream // 18072 // Hs.14745 // C10orf9 // 219771 // Homo sapiens chromosome 10 open reading frame 9	C10orf9	C10orf9, Homo sapiens chromosome 10 open reading frame 9 (C10orf9), p11.21
SNP_A-2146454	atgctctactatgaac[A/C]aggacattctcaggac	A	C	NM_031866 // upstream // 106423 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 106423 // — // — // — /// ENST00000279434 // downstream // 774964 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1956638	tttgttttgcttgagaa[A/G]acacaaattgctgctat	A	G	NM_031866 // upstream // 107918 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 107918 // — // — // — // — /// ENST00000279434 // downstream // 773469 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2314449	ggagggcttattctaa[C/T]gattgttccaggctcct	C	T	NM_031866 // upstream // 129952 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 129952 // — // — // — // — /// ENST00000279434 // downstream // 751435 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2269315	gaatttgaatatggca[C/T]aatgatttgtcattta	C	T	NM_031866 // upstream // 179533 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 179533 // — // — // — // — /// ENST00000279434 // downstream // 701854 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-1952337	tttctctctttctcaa[C/T]gcagggaacagcattg	C	T	NM_031866 // upstream // 287024 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 287024 // — // — // — // — /// ENST00000279434 // downstream // 594363 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-1904091	tgggcatcactaaagg[C/T]ataaggtatttttcagt	C	T	NM_031866 // upstream // 287656 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 287656 // — // — // — // — /// ENST00000279434 // downstream // 593731 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-1999930	gtcgtgcaggttgcac[A/G]ggaaatctgcgattcc	A	G	NM_031866 // upstream // 407858 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 407858 // — // — // — // — /// ENST00000279434 // downstream // 473529 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-1886127	tgaccagttgaacaga[A/T]tagggatgtcaaaaac	A	T	NM_031866 // upstream // 480814 // Hs.302634 // FZD8 // 8325 // Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA. /// ENST00000321644 // upstream // 480814 // — // — // — // — /// ENST00000279434 // downstream // 400573 // — // — // -	FZD8	FZD8, Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), p11.21
SNP_A-2187590	cagtaagcacaggtta[G/T]agttctagcaatcact	G	T	ENST00000279434 // upstream // 71741 // — // — // — // — /// ENST00000277669 // upstream // 529879 // — // — // — // — /// ENST00000338499 // upstream // 620352 // — // — // — // —	-	p11.21
SNP_A-2117745	aggttcttgagatccc[A/G]ataaaataaacaaatc	A	G	ENST00000277669 // downstream // 313239 // — // — // — // — /// ENST00000338499 // downstream // 324350 // — // — // — // — /// ENST00000340140 // downstream // 273080 // — // — // —	-	p11.21
SNP_A-2000063	aatctgcgagctgccc[A/G]aaagtaccttgatgtt	A	G	X69115 // downstream // 42659 // Hs.292575 // ZNF37A // 7587 // H.sapiens ZNF37A mRNA for zinc finger protein. /// ENST00000351773 // downstream // 42659 // — // — // — /// ENST00000361085 // downstream // 42659 // — // — // — // — // —	ZNF37A	ZNF37A, H.sapiens ZNF37A for zinc finger protein. p11.21
SNP_A-1693319	tttccagtgcactagatgaaaaata[C/G]caatgaagagtagaat aaagacaaa	C	G	AF165514 // upstream // 100386 // Hs.380900 // LOC158160 // 158160 // hypothetical protein LOC158160 /// AJ492195 // downstream // 132657 // Hs.446382 // ZNF37A // 7587 // zinc finger protein 37a (KOX 21)	LOC158160	LOC158160, rs10508864, hypothetical protein LOC158160, p11.1
SNP_A-2309568	ggaaactcgaatcttc[C/T]agtatcggcaaaggga	C	T	ENST00000355536 // downstream // 2722184 // — // — // — // — /// ENST00000357051 // downstream // 397994 // — // — // — // —	-	q11.1
SNP_A-1932502	ttcctggatgcgggac[A/G]agaactcaggacttgc	A	G	NM_006955 // upstream // 133905 // Hs.499453 // ZNF11B // 7558 // Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), mRNA. /// NM_014753 // upstream // 10362 // Hs.10848 // BMS1L // 9790 // Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BM	ZNF11B	ZNF11B, Homo sapiens zinc finger protein 11b (KOX 2) (ZNF11B), q11.21
SNP_A-2274708	gagaaagaccatatct[C/T]aaagagagagagag	C	T	NM_014753 // intron // 0 // Hs.10848 // BMS1L // 9790 // Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), mRNA. /// ENST00000298600 // intron // 0 // — // — // —	BMS1L	BMS1L, Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2217964	cctgcatacagtgctc[A/G]cctgcatgggtgctc	A	G	NM_014753 // downstream // 46351 // Hs.10848 // BMS1L // 9790 // Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), mRNA. /// NM_020630 // upstream // 199327 // Hs.350321 // RET // 5979 // Homo sapiens ret proto-oncogene (multiple endocrin	BMS1L	BMS1L, Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), q11.21
SNP_A-2247102	ctgtcacacaaactca[A/T]ccctgctgttacagcg	A	T	NM_014753 // downstream // 80650 // Hs.10848 // BMS1L // 9790 // Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), mRNA. /// NM_020630 // upstream // 165028 // Hs.350321 // RET // 5979 // Homo sapiens ret proto-oncogene (multiple endocrin	BMS1L	BMS1L, Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), q11.21
SNP_A-1877905	tctggtgttggtgcta[C/T]aggagaatgcataagt	C	T	NM_014753 // downstream // 98579 // Hs.10848 // BMS1L // 9790 // Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), mRNA. /// NM_020630 // upstream // 147099 // Hs.350321 // RET // 5979 // Homo sapiens ret proto-oncogene (multiple endocrin	BMS1L	BMS1L, Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), q11.21
SNP_A-1781273	ggatgtagtgctggaa[A/G]aagtgaaatgcaatc	A	G	NM_018590 // downstream // 2850 // Hs.180758 // GALNACT-2 // 55454 // Homo sapiens chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA. /// ENST00000307209 // downstream // 2850 // --- // --- // --- /// ENST00000360619 // downstream // 6384 // --- // -	GALNACT-2	GALNACT-2, Homo sapiens chondroitin sulfate GalNAcT-2 (GALNACT-2), q11.21
SNP_A-1875751	tctcttaaacttaca[A/G]gatcataaccttga	A	G	ENST00000360619 // intron // 0 // --- // --- // --- /// ENST00000356121 // intron // 0 // --- // --- // ---	-	q11.21
SNP_A-1878422	tctgtgaccacaataa[A/G]ataacagaagtcaacg	A	G	ENST00000360619 // intron // 0 // --- // --- // --- /// ENST00000356121 // intron // 0 // --- // --- // ---	-	q11.21
SNP_A-2113213	aggcccctagagaagc[C/T]gcaagagggtttccag	C	T	NM_173160 // upstream // 88104 // Hs.130497 // FXYD4 // 53828 // Homo sapiens FXYD domain containing ion transport regulator 4 (FXYD4), mRNA. /// ENST00000360619 // upstream // 18724 // --- // --- // --- /// ENST00000356121 // upstream // 18720 //	FXYD4	FXYD4, Homo sapiens FXYD domain containing ion transport regulator 4 (FXYD4), q11.21
SNP_A-1735308	gagccatgtcatggttaccaagctat[A/C]agtttttgttcattatgtat cttca	A	C	AK097743 // upstream // 33818 // Hs.407619 // - // - // CDNA FLJ40424 fis, clone TESTI2039026 /// NM_005758 // downstream // 81796 // - // - // - // -	-	-, rs951259, CDNA FLJ40424 fis, clone TESTI2039026, q11.21
SNP_A-2000209	ttgtgaactgaccttt[C/T]ccattcctgagttcct	C	T	NM_199168 // downstream // 671541 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 671541 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2202815	ccactaacaaggtccc[A/G]agaataccgagagtga	A	G	NM_199168 // downstream // 663170 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 663170 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1754844	aaattggcctacttatatatggaca[A/G]ctgatttgcaaccaacgt gcacaga	A	G	AK097743 // upstream // 91061 // Hs.407619 // - // - // CDNA FLJ40424 fis, clone TESTI2039026 /// NM_005758 // downstream // 24553 // - // - // -	-	-, rs7477243, CDNA FLJ40424 fis, clone TESTI2039026, q11.21
SNP_A-1700356	atgaaaaggtaattaaaaaattcaca[A/C]ggaaatgtaaaggac ataaactagc	A	C	AK097743 // upstream // 91235 // Hs.407619 // - // - // CDNA FLJ40424 fis, clone TESTI2039026 /// NM_005758 // downstream // 24379 // - // - // -	-	-, rs994358, CDNA FLJ40424 fis, clone TESTI2039026, q11.21
SNP_A-2138605	atcccaaggaacctgc[A/G]agacccctctagaaac	A	G	NM_199168 // downstream // 641610 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 641610 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2224171	cggtcgagctgtttcc[A/G]atcttaggaactggc	A	G	NM_199168 // downstream // 641484 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 641484 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2275662	gagacagtgatttaa[A/T]cagggtagtcgggata	A	T	NM_199168 // downstream // 634160 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 634160 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2097667	agagaatttgttggac[A/C]aggaagttgagctaag	A	C	NM_199168 // downstream // 619715 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 619715 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2176717	cacccggccggctggt[A/G]aatttctagctcaac	A	G	NM_199168 // downstream // 619693 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 619693 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2182632	cagatctaacaaaagc[A/G]aaaggaagcaactcat	A	G	NM_199168 // downstream // 575618 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 575618 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1871440	tctaacatagctcgtc[C/T]cttgaattgtcactga	C	T	NM_199168 // downstream // 491199 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 491199 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2133169	atataggatgaaatac[A/T]ccaagatttgtccaaa	A	T	NM_199168 // downstream // 486557 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 486557 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1936190	ttcttcactagaggga[A/G]catttagccaaggaaa	A	G	NM_199168 // downstream // 322625 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // downstream // 322625 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemoki	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2176734	caccctagcatgcaaa[C/G]gttgatgtggacgca	C	G	NM_199168 // upstream // 33839 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 33839 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2197955	caltgcatcataaaaa[A/G]aaacaaccagtgtata	A	G	NM_199168 // upstream // 85731 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 85731 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1875813	tctcttttacaggctg[C/G]actaggaaatcctcag	C	G	NM_199168 // upstream // 266741 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 266741 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1901032	tggatatgtcatctaa[C/T]ataaatggaatcataa	C	T	NM_199168 // upstream // 357036 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 357036 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2174428	cacagaatagctccgg[C/T]tgtttaaccaatagca	C	T	NM_199168 // upstream // 454405 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 454405 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2100102	agagtggcattcaa[A/G]aagcccagattaatg	A	G	NM_199168 // upstream // 486362 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 486362 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-1927005	ttattgagcaatgcaj[C/G]taggcactgactgggg	C	G	NM_199168 // upstream // 486683 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA. /// NM_000609 // upstream // 486683 // Hs.522891 // CXCL12 // 6387 // Homo sapiens chemokine (	CXCL12	CXCL12, Homo sapiens chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), q11.21
SNP_A-2286956	gatggtcattacccggg[A/G]atggaaggagggttga	A	G	NM_000698 // intron // 0 // Hs.89499 // ALOX5 // 240 // Homo sapiens arachidonate 5-lipoxygenase (ALOX5), mRNA. /// ENST00000265455 // intron // 0 // — // — // —	ALOX5	ALOX5, Homo sapiens arachidonate 5-lipoxygenase (ALOX5), q11.21
SNP_A-2035224	aaatgctgataaaatac[A/G]aactgaactcacttct	A	G	ENST00000358313 // downstream // 270149 // — // — // — /// ENST00000342900 // downstream // 270149 // — // — // — /// ENST00000321814 // upstream // 15474 // — // — // —	-	q11.22
SNP_A-1934300	ttctcccaatacagga[A/G]ctttggaggtcactt	A	G	ENST00000358313 // downstream // 270301 // — // — // — /// ENST00000342900 // downstream // 270301 // — // — // — /// ENST00000321814 // upstream // 15322 // — // — // —	-	q11.22
SNP_A-2239270	ctcttgtggcccctcc[A/G]aaggtcctgtgcctcc	A	G	ENST00000358313 // downstream // 274541 // — // — // — /// ENST00000342900 // downstream // 274541 // — // — // — /// ENST00000321814 // upstream // 11082 // — // — // —	-	q11.22
SNP_A-2122357	agtgcccaatcctctca[A/T]gtcatgttggctgct	A	T	ENST00000358313 // downstream // 274978 // — // — // — /// ENST00000342900 // downstream // 274978 // — // — // — /// ENST00000321814 // upstream // 10645 // — // — // —	-	q11.22
SNP_A-1909516	tgtatttcacctctaa[C/T]gaagaaatcttaag	C	T	ENST00000358313 // downstream // 276814 // — // — // — /// ENST00000342900 // downstream // 276814 // — // — // — /// ENST00000321814 // upstream // 8809 // — // — // —	-	q11.22
SNP_A-2125249	agttgtatctcctga[C/G]gctttcattggcattt	C	G	ENST00000354871 // intron // 0 // — // — // —	-	q11.22
SNP_A-1709179	aagtagtttatttttttaatttca[A/G]gtgatgtaatttaaaacctaag ttg	A	G	NM_002750 // downstream // 43 // Hs.445864 // MAPK8 // 5599 // mitogen-activated protein kinase 8 /// NM_021226 // downstream // 10854 // Hs.435063 // ARHGAP22 // 58504 // Rho GTPase activating protein 22 /// NM_139046 // downstream // 43 // Hs.445864 //	MAPK8	MAPK8 , rs10622225, mitogen-activated protein kinase 8 ,q11.22
SNP_A-2000415	gctacctgtgtatac[C/G]atgatgtataactcca	C	G	NM_152428 // intron // 0 // Hs.532437 // FRMPD2 // 143162 // Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), mRNA. /// ENST00000305531 // intron // 0 // — // — // —	FRMPD2	FRMPD2, Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), q11.22
SNP_A-1870781	tcgcttcctggttgaa[C/T]gatgaaaaatgattgt	C	T	NM_152428 // intron // 0 // Hs.532437 // FRMPD2 // 143162 // Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), mRNA. /// ENST00000305531 // intron // 0 // — // — // —	FRMPD2	FRMPD2, Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), q11.22
SNP_A-2301137	gccttcctgacctgga[A/G]agaggtgttggtcttc	A	G	NM_152428 // intron // 0 // Hs.532437 // FRMPD2 // 143162 // Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), mRNA. /// ENST00000305531 // intron // 0 // — // — // —	FRMPD2	FRMPD2, Homo sapiens FERM and PDZ domain containing 2 (FRMPD2), q11.22
SNP_A-1679310	cctagtaatggggttactatggtgat[A/G]aggaattaggataatgga gatggcgc	A	G	AY324801 // intron // 0 // Hs.435063 // ARHGAP22 // 58504 // Rho GTPase activating protein 22	ARHGAP22	ARHGAP22, rs1345107, Rho GTPase activating protein 22,q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932607	ttcctgttgcactgaa[A/G]gctctaagtaagatga	A	G	NM_021226 // intron // 0 // Hs.435063 // ARHGAP22 // 58504 // Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), mRNA. /// ENST00000249601 // intron // 0 // — // — // — // —	ARHGAP22	ARHGAP22, Homo sapiens Rho GTPase activating protein 22 (ARHGAP22), q11.22
SNP_A-2070010	acacagtgtgctattc[A/G]atgccgtctgctctgg	A	G	NM_173524 // intron // 0 // — // C10orf64 // 159491 // Homo sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// ENST00000360890 // intron // 0 // — // — // — // — /// ENST00000325239 // intron // 0 // — // — // — // —	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-1873127	tctattacattctgac[G/T]gactaataaaaccctg	G	T	NM_173524 // intron // 0 // — // C10orf64 // 159491 // Homo sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// ENST00000360890 // intron // 0 // — // — // — // — /// ENST00000325239 // intron // 0 // — // — // — // —	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-2059024	aatcccagaaatagaa[C/T]gttgactggaaaaagc	C	T	NM_173524 // intron // 0 // — // C10orf64 // 159491 // Homo sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// ENST00000360890 // intron // 0 // — // — // — // — /// ENST00000325239 // intron // 0 // — // — // — // —	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-1702775	ttttcaccaaggtctactggcacat[A/G]aaaataagtaagtcagg ctccaacc	A	G	BC029839 // upstream // 44834 // Hs.374708 // C10orf73 // 170370 // chromosome 10 open reading frame 73	C10orf73	C10orf73 , rs10508912, chromosome 10 open reading frame 73,q11.23
SNP_A-1815332	gtgtttatgaagtaag[A/G]ccattcaaaatcaaat	A	G	ENST00000312002 // intron // 0 // — // — // — // — /// ENST00000265453 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2044920	aagaacagaagaactc[A/G]aatgaagccagtgagg	A	G	ENST00000312002 // intron // 0 // — // — // — // — /// ENST00000265453 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2217995	cctgcattgagctaca[A/G]gacaagactggggcct	A	G	ENST00000312002 // intron // 0 // — // — // — // — /// ENST00000265453 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2000504	actcactccatccagt[A/G]accagagtctactcca	A	G	NM_173524 // downstream // 176789 // — // C10orf64 // 159491 // Homo sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// NM_144984 // downstream // 117165 // Hs.522928 // C10orf72 // 196740 // Homo sapiens chromosome 10 open reading frame	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-1785112	ggcgtggggcctgcca[A/G]atgtcttgagcctgct	A	G	NM_173524 // downstream // 178145 // — // C10orf64 // 159491 // Homo sapiens chromosome 10 open reading frame 64 (C10orf64), mRNA. /// NM_144984 // downstream // 115809 // Hs.522928 // C10orf72 // 196740 // Homo sapiens chromosome 10 open reading frame	C10orf64	C10orf64, Homo sapiens chromosome 10 open reading frame 64 (C10orf64), q11.23
SNP_A-1852546	tatttaggatagaaag[A/C]aacaagctctccctaa	A	C	ENST00000332853 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-1829592	taagtgttttattggc[A/G]gaataatttgcaaaca	A	G	ENST00000311787 // upstream // 111868 // — // — // — // — /// ENST00000323868 // upstream // 53305 // — // — // — // —	-	q11.23
SNP_A-2000541	atacatcaattttccc[A/G]caggacgggtctccaa	A	G	ENST00000323868 // downstream // 27979 // — // — // — // — /// ENST00000298420 // downstream // 10650 // — // — // — // —	-	q11.23
SNP_A-1798223	gtaaacttaattggca[A/C]atctgagcagatgaaa	A	C	NM_000124 // intron // 0 // Hs.133444 // ERCC6 // 2074 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), mRNA. /// ENST00000265899 // intron // 0 // — // — // — // — /// ENST00000355832	ERCC6	ERCC6, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), q11.23
SNP_A-1956441	tttgttctgtttcgaa[C/T]tggtcttacaaaatgc	C	T	NM_000124 // intron // 0 // Hs.133444 // ERCC6 // 2074 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), mRNA. /// NM_170753 // CDS // 0 // Hs.133444 // PGBD3 // 267004 // Homo sapiens piggyBac	ERCC6	ERCC6, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), q11.23
SNP_A-2121086	agtctctctcattgca[C/T]caaggtaacaaacctg	C	T	NM_000124 // upstream // 57506 // Hs.133444 // ERCC6 // 2074 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), mRNA. /// NM_000124 // upstream // 56990 // Hs.133444 // ERCC6 // 2074 // Homo sapi	ERCC6	ERCC6, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2310809	ggaagccttcattaac[A/G]aggacggatggcaggg	A	G	NM_000124 // upstream // 58911 // Hs.133444 // ERCC6 // 2074 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), mRNA. /// NM_000124 // upstream // 58395 // Hs.133444 // ERCC6 // 2074 // Homo sapi	ERCC6	ERCC6, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 6 (ERCC6), q11.23
SNP_A-1812524	gtggccggaatgcaga[A/G]atgaagcactgagcac	A	G	NM_020986 // intron // 0 // Hs.302002 // CHAT // 1103 // Homo sapiens choline acetyltransferase (CHAT), transcript variant N2, mRNA. /// NM_020984 // intron // 0 // Hs.302002 // CHAT // 1103 // Homo sapiens choline acetyltransferase (CHAT), transcript var	CHAT	CHAT, Homo sapiens choline acetyltransferase (CHAT), transcript variant N2, q11.23
SNP_A-2042036	aactacctctactaac[C/T]accatctaagcatgga	C	T	NM_182554 // intron // 0 // Hs.131287 // C10orf53 // 282966 // Homo sapiens chromosome 10 open reading frame 53 (C10orf53), mRNA. /// ENST00000319744 // intron // 0 // — // — // — // —	C10orf53	C10orf53, Homo sapiens chromosome 10 open reading frame 53 (C10orf53), q11.23
SNP_A-2292780	gcacttgtgcttgata[A/G]aggcagagtaagttga	A	G	NM_182554 // intron // 0 // Hs.131287 // C10orf53 // 282966 // Homo sapiens chromosome 10 open reading frame 53 (C10orf53), mRNA. /// ENST00000319744 // intron // 0 // — // — // — // —	C10orf53	C10orf53, Homo sapiens chromosome 10 open reading frame 53 (C10orf53), q11.23
SNP_A-2214306	cctacatggctatcca[C/T]agaaaactggctaaat	C	T	NM_018245 // intron // 0 // Hs.17860 // OGDHL // 55753 // Homo sapiens oxoglutarate dehydrogenase-like (OGDHL), mRNA. /// ENST00000355036 // intron // 0 // — // — // — // —	OGDHL	OGDHL, Homo sapiens oxoglutarate dehydrogenase-like (OGDHL), q11.23
SNP_A-2184173	cagcctatactctatg[C/T]agcctcacagtgaact	C	T	NM_138634 // intron // 0 // Hs.255462 // MSMB // 4477 // Homo sapiens microseminoprotein, beta- (MSMB), transcript variant PSP57, mRNA. /// NM_002443 // intron // 0 // Hs.255462 // MSMB // 4477 // Homo sapiens microseminoprotein, beta- (MSMB), transcript	MSMB	MSMB, Homo sapiens microseminoprotein, beta- (MSMB), transcript variant PSP57, q11.23
SNP_A-2055414	aataagtccctcgatc[A/G]attcatcatgcctgtg	A	G	NM_019893 // upstream // 24523 // Hs.512645 // ASAH2 // 56624 // Homo sapiens N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2 (ASAH2), mRNA. /// ENST00000341534 // upstream // 24523 // — // — // — // — /// ENST00000359012 // downstre	ASAH2	ASAH2, Homo sapiens N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2 (ASAH2), q11.23
SNP_A-2000631	gtaatgaattgattga[C/T]ggatatttgttttcaa	C	T	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2272813	gactaaccagttacaa[C/T]agaatgggtgcctata	C	T	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-1795415	ggtgcacatggatata[A/C]agatgcgaacaacaga	A	C	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2046220	aagacttggagtacat[C/T]agagcatctcataagt	C	T	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2119569	agtatgaatctataaa[A/C]caccagcaagtggagc	A	C	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2000650	ataaacagtggtagca[C/T]atcacaaaattatacc	C	T	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-1950431	tttcagtccccaggtc[C/T]ctaacatcaaatgtat	C	T	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2171128	caatagcatgataagg[C/T]aggcactaatctcatc	C	T	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2103178	agcaaccattcctgca[A/G]ggtttttttggttatt	A	G	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2000658	aaagtagaatgtgatc[A/G]aaaaaactctcagttg	A	G	ENST00000359012 // intron // 0 // — // — // — // — /// ENST00000358195 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-2254893	cttggattagccactg[C/G]atatgaagcttcccca	C	G	ENST00000331308 // upstream // 5968 // — // — // — // — /// ENST00000340638 // upstream // 10924 // — // — // — // — /// ENST00000341207 // upstream // 13198 // — // — // — // — /// ENST00000342531 // upstream // 13198 // — // –	-	q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2152279	attaaatgaaggttta[G/T]aattggctaccttgt	G	T	NM_138932 // upstream // 64548 // Hs.499643 // ACF // 29974 // Homo sapiens apobec-1 complementation factor (ACF), transcript variant 2, mRNA. /// NM_138933 // upstream // 64548 // Hs.499643 // ACF // 29974 // Homo sapiens apobec-1 complementation factor	ACF	ACF, Homo sapiens apobec-1 complementation factor (ACF), transcript variant 2, q11.23
SNP_A-2301861	gcgggcatgaaggcac[G/T]cctaatggaatattca	G	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// ENST00000332193 // intron // 0 // — // — // —	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q11.23
SNP_A-1862335	tcatgtacaggttaac[C/T]aaaaaatgtcacatttc	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q11.23
SNP_A-1816782	gttactctgctcctca[G/T]gtggtagcacttgtca	G	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q11.23
SNP_A-2133691	atatccaaattctgag[A/G]atccgaaagtggacat	A	G	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q11.23
SNP_A-1860308	tcagtgagatatgaca[C/T]aaaaagttctcatctc	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q11.23
SNP_A-2211985	ccctgagcacctaca[G/T]aacatagcaattcctt	G	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-1918686	ttaaatttccatctac[C/T]gacactctgctgaagc	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-2000707	ctaatgttcttatc[C/T]gaaagttactgtgcat	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-2288343	gattctcacaggaaca[C/T]gaactctactgtcaac	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-1934793	ttctctgtactagac[C/T]aggaatcagcaagtat	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2000760	ccactaattctatgg[C/T]atgcctatatccacaa	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-1870196	tccttatgtaggtaa[C/T]gtgttcaaacataagt	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-2177559	cacgcagttggtcaca[C/T]aaagtagcaacacggc	C	T	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-2072144	acagatattgtaagtt[A/C]aaatcagatagtgtat	A	C	D45864 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens mRNA for cGMP-dependent protein kinase type I alpha, complete cds. /// NM_006258 // intron // 0 // Hs.2689 // PRKG1 // 5592 // Homo sapiens protein kinase, cGMP-dependent, type I (PRKG1), m	PRKG1	PRKG1, Homo sapiens for cGMP-dependent protein kinase type I alpha, complete cds, q21.1
SNP_A-2104880	agcatagtttaaaca[G/T]ctgagaggttagtcc	G	T	NM_012242 // downstream // 116684 // Hs.40499 // DKK1 // 22943 // Homo sapiens dickkopf homolog 1 (Xenopus laevis) (DKK1), mRNA. /// NM_000242 // downstream // 331325 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, solub	DKK1	DKK1, Homo sapiens dickkopf homolog 1 (Xenopus laevis) (DKK1), q21.1
SNP_A-1726000	ggcccaggtaaaatatgttgaac[A/G]agttgtttgtcttacctca caatt	A	G	NM_000242 // upstream // 370734 // Hs.2314 // MBL2 // 4153 // mannose-binding lectin (protein C) 2, soluble (opsonic defect) /// NM_033056 // downstream // 678666 // Hs.232819 // PCDH15 // 65217 // protocadherin 15	MBL2	MBL2, rs10508989, mannose-binding lectin (protein C) 2, soluble (opsonic defect), q21.1
SNP_A-2058326	aatcaataatgaaaa[A/C]gttgtgaacaaatggt	A	C	NM_000242 // upstream // 119483 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 929917 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2231256	ctattcactacaaatc[A/G]ccaaagttatctctta	A	G	NM_000242 // upstream // 126377 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 923023 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1834468	tacatttttacaggac[A/G]attgggaaatctcc	A	G	NM_000242 // upstream // 138388 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 911012 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2240262	ctgaatgcaggagata[C/T]cagtttggtgtgtga	C	T	NM_000242 // upstream // 162490 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 886910 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2212968	ccctttttttcttatga[A/G]tagctctccactgact	A	G	NM_000242 // upstream // 351900 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 697500 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1847798	tatctcatgcaactca[C/G]tacttatgtcttata	C	G	NM_000242 // upstream // 353390 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 696010 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2091569	agaaaaatcatgttaa[C/T]ggttgttgtctctagt	C	T	NM_000242 // upstream // 353976 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 695424 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1821587	gtttgtccagcaaaaa[A/G]caagatatgtatctaa	A	G	NM_000242 // upstream // 369542 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 679858 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2000913	tatgagctttttcttc[C/T]aattgcacagcttctg	C	T	NM_000242 // upstream // 370682 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 678718 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2146208	atgctaaaaccataag[C/T]caacacagaagaaaga	C	T	NM_000242 // upstream // 371339 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 678061 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2152816	attaatttacttgtga[C/T]atctggcttagaagta	C	T	NM_000242 // upstream // 372526 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 676874 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1813143	gtggtagttagctttc[C/T]attcctgtgtaattca	C	T	NM_000242 // upstream // 373445 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 675955 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2152600	attaagttaggatttc[A/G]aatgattacaagagat	A	G	NM_000242 // upstream // 379746 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 669654 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-1957598	tttatccaacactta[C/T]agagatcctgatgtt	C	T	NM_000242 // upstream // 390439 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 658961 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2057928	aatattgaacttttcc[A/G]ctgacatagtttgaat	A	G	NM_000242 // upstream // 390539 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 658861 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2124430	agttcacgttgtatca[A/T]atagaacattgacacg	A	T	NM_000242 // upstream // 614069 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 435331 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2127318	ataaattagaatcaca[A/T]tagtagttatgattgt	A	T	NM_000242 // upstream // 637272 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 412128 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2179222	cactgggtgcatagaa[G/T]attttctgactgtcaaa	G	T	NM_000242 // upstream // 704613 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 344787 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2043492	aactgtagccctagaa[C/T]ggcattggctgtacgt	C	T	NM_000242 // upstream // 825207 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 224193 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2000963	caagcagggggcttaca[A/G]tatatcaaaccataag	A	G	NM_000242 // upstream // 862672 // Hs.499674 // MBL2 // 4153 // Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), mRNA. /// NM_033056 // downstream // 186728 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 1	MBL2	MBL2, Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic defect) (MBL2), q21.1
SNP_A-2100300	agagtttgaacctcaa[C/T]tcaggtaactcctgtg	C	T	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2278731	gagcttaaaaaagaaa[C/T]gtgaacacaggagtta	C	T	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2143116	atgaattaagttcac[C/T]gataaatctgaaatta	C	T	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2309252	ggaaaactgaggtaca[A/G]aaggttatgtcatgta	A	G	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2001032	ttttgtcgataaggaa[A/G]atatcagagtgggat	A	G	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1846224	tatatcgtggaataca[A/G]aatactgaaatacaaa	A	G	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1794184	ggtcatacctaatag[A/G]actggtggttagaaaa	A	G	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2250049	ctcacctctggtgaaa[A/G]gagaatgccatttgtt	A	G	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2198160	cattgtaagagtacaa[C/G]agcaagaccaaacatt	C	G	NM_033056 // intron // 0 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// ENST00000320301 // intron // 0 // — // — // — // —	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1819910	gttgttaatttcatac[C/T]accaacctactgtcta	C	T	NM_033056 // upstream // 65502 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 1490646 // Hs.42650 // ZWNT // 11130 // Homo sapiens ZW10 interactor (ZWNT), transcript variant 1, mRNA. /// N	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1743949	ccctcacaatttattactcataag[C/G]catttatatcatttgcttccc tgta	C	G	NM_007057 // downstream // 694767 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_032997 // downstream // 694767 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_033056 // upstream // 861389 // Hs.232819 // PCDH15 // 65217 // protocadherin	ZWINT	ZWINT , rs10509037, ZW10 interactor ,q21.1
SNP_A-2117794	aggttgccaaaaactа[C/T]gaaacaattcttgaca	C	T	NM_033056 // upstream // 895849 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 660299 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// N	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1912083	tgtgaggacactaaaa[A/C]agccttacgaagattt	A	C	NM_033056 // upstream // 922602 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 633546 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// N	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1906624	tggtgtccgtaacaaa[C/T]gtcatttgaagtcat	C	T	NM_033056 // upstream // 940003 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 616145 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// N	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-2149817	atgtatttttcaaatata[C/G]gttacccaatccaaaaa	C	G	NM_033056 // upstream // 941027 // Hs.232819 // PCDH15 // 65217 // Homo sapiens protocadherin 15 (PCDH15), mRNA. /// NM_007057 // downstream // 615121 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// N	PCDH15	PCDH15, Homo sapiens protocadherin 15 (PCDH15), q21.1
SNP_A-1751103	ataatgcatgcatatgaatcacctа[C/T]gaagatttgtgtcagac atttcata	C	T	NM_007057 // upstream // 245247 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_032997 // upstream // 245247 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_152230 // downstream // 1589577 // Hs.156306 // IMPK // 253430 // inositol polyph	ZWINT	ZWINT , rs10509050, ZW10 interactor ,q21.1
SNP_A-1704337	tgtgatgatggaatttcagttataa[G/T]gctgaatgaatttgggaaa aataatt	G	T	NM_007057 // upstream // 246123 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_032997 // upstream // 246123 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_152230 // downstream // 1588701 // Hs.156306 // IMPK // 253430 // inositol polyph	ZWINT	ZWINT , rs10509051, ZW10 interactor ,q21.1
SNP_A-1718927	gatttaggaggtacctgaaaaacta[C/T]gttaaatgaaaaactaa aatcagcg	C	T	NM_007057 // upstream // 249360 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_032997 // upstream // 249360 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_152230 // downstream // 1585464 // Hs.156306 // IMPK // 253430 // inositol polyph	ZWINT	ZWINT , rs10509052, ZW10 interactor ,q21.1
SNP_A-1713217	tttaaaaatagtggcaaggaagat[A/T]aattactttaaatggcttt ctatg	A	T	NM_007057 // upstream // 252258 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_032997 // upstream // 252258 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_152230 // downstream // 1582566 // Hs.156306 // IMPK // 253430 // inositol polyph	ZWINT	ZWINT , rs10509053, ZW10 interactor ,q21.1
SNP_A-2269447	gacaaaaatatctgct[A/G]acacttatgaacacat	A	G	NM_007057 // upstream // 266587 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 266587 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript varian	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2243294	ctgccttatatcccctc[A/G]aatggcagagactatg	A	G	NM_007057 // upstream // 485639 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 485639 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript varian	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932963	ttcgacagagtcaagga[A/G]ccaagacagatacacg	A	G	NM_007057 // upstream // 1160859 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1160859 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1923190	ttagctcacctcaata[A/G]gccacaaactatggtc	A	G	NM_007057 // upstream // 1212051 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1212051 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2166324	caaatctagcatatca[C/T]ctgttttataaagct	C	T	NM_007057 // upstream // 1212290 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1212290 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1911161	tgtctgatttatgtag[C/G]ctaacagaattggttca	C	G	NM_007057 // upstream // 1219710 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1219710 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2108547	agctggatttccaaacta[A/C]agcggtctctcaggta	A	C	NM_007057 // upstream // 1231347 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1231347 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2221832	cctttgaatgaaaga[G/T]cacactcaatggtcag	G	T	NM_007057 // upstream // 1235595 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1235595 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1715875	tggatctagcatttcaacccaggtc[C/G]atctacttttaatgatagaacaca	C	G	NM_007057 // upstream // 1785028 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_032997 // upstream // 1785028 // Hs.42650 // ZWINT // 11130 // ZW10 interactor /// NM_152230 // downstream // 49796 // Hs.156306 // IMPK // 253430 // inositol polyph	ZWINT	ZWINT , rs1875592, ZW10 interactor ,q21.1
SNP_A-1828396	taagatttctgaggaaa[C/T]tgtaagcaaaactcat	C	T	NM_007057 // upstream // 1642405 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1642405 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2278158	gagcctactttgcccaa[C/T]ttctgagatattatcg	C	T	NM_007057 // upstream // 1696077 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1696077 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1796536	ggttacacaaatgaa[C/T]atctgaactgatctct	C	T	NM_007057 // upstream // 1705471 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1705471 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-1854913	tcaactcaatgagttg[A/G]aaaaaagtaataagac	A	G	NM_007057 // upstream // 1809829 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1809829 // Hs.42650 // ZWINT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2276248	gagagagtgctggcaa[C/T]agaaaaggaaatgggc	C	T	NM_007057 // upstream // 1829214 // Hs.42650 // ZWNT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, mRNA. /// NM_032997 // upstream // 1829214 // Hs.42650 // ZWNT // 11130 // Homo sapiens ZW10 interactor (ZWINT), transcript vari	ZWINT	ZWINT, Homo sapiens ZW10 interactor (ZWINT), transcript variant 1, q21.1
SNP_A-2001415	taagagatgcctgta[A/G]aagtcacatttgaaca	A	G	NM_003201 // downstream // 353446 // Hs.75133 // TFAM // 7019 // Homo sapiens transcription factor A, mitochondrial (TFAM), mRNA. /// NM_012251 // downstream // 353446 // Hs.75133 // TFAM // 7019 // Homo sapiens transcription factor A, mitochondrial (TFAM	TFAM	TFAM, Homo sapiens transcription factor A, mitochondrial (TFAM), q21.1
SNP_A-1844622	tataaccttctctaca[G/T]tatacctcactatgat	G	T	NM_003201 // downstream // 355862 // Hs.75133 // TFAM // 7019 // Homo sapiens transcription factor A, mitochondrial (TFAM), mRNA. /// NM_012251 // downstream // 355862 // Hs.75133 // TFAM // 7019 // Homo sapiens transcription factor A, mitochondrial (TFAM	TFAM	TFAM, Homo sapiens transcription factor A, mitochondrial (TFAM), q21.1
SNP_A-2051500	aagggtccacaaaaaga[C/T]gtcaccatttggaaaga	C	T	NM_032439 // upstream // 331464 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 401011 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with seq	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1954737	ttgctctgttgtatc[A/G]actctgttccttttgtc	A	G	NM_032439 // upstream // 326894 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 396441 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with seq	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-2175853	cacatttccctttaga[C/T]gcttattgatgccatt	C	T	NM_032439 // upstream // 319024 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 388571 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with seq	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1961001	tttttggcaccataaat[C/G]ataatcttctccatct	C	G	NM_032439 // upstream // 249927 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 319474 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with seq	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1915129	tgttatttcaactaaa[A/G]tgatatctccgttag	A	G	NM_032439 // upstream // 196821 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 266368 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with seq	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1835110	taccctatgcttatac[A/G]actgacccagcccct	A	G	NM_032439 // upstream // 40940 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // downstream // 110487 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with sequ	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.1
SNP_A-1872254	tctagaaagagtagca[C/T]cttaattaatcatt	C	T	NM_032439 // downstream // 279854 // Hs.499704 // PHYHIPL // 84457 // Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), mRNA. /// NM_001001971 // upstream // 164552 // Hs.499705 // FAM113C1 // 220965 // Homo sapiens family with seq	PHYHIPL	PHYHIPL, Homo sapiens phytanoyl-CoA hydroxylase interacting protein-like (PHYHIPL), q21.2
SNP_A-2001530	acaccatgtcttggca[A/G]catcttattattct	A	G	NM_194298 // upstream // 11254 // Hs.499709 // SLC16A9 // 220963 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), mRNA. /// NM_005436 // downstream // 41508 // Hs.327068 // CCDC6 // 8030 // Homo sapiens coil	SLC16A9	SLC16A9, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2217580	cctgagagataccagg[A/G]tatggctggtgatatg	A	G	NM_194298 // upstream // 42883 // Hs.499709 // SLC16A9 // 220963 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), mRNA. /// NM_005436 // downstream // 9879 // Hs.327068 // CCDC6 // 8030 // Homo sapiens coile	SLC16A9	SLC16A9, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 9 (SLC16A9), q21.2
SNP_A-2287569	gattaaaatttatgaa[C/T]caattgtcatccaaaa	C	T	NM_001149 // downstream // 44367 // Hs.499725 // ANK3 // 288 // Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, mRNA. /// NM_020987 // downstream // 44367 // Hs.499725 // ANK3 // 288 // Homo sapiens ankyrin 3, node of Ran	ANK3	ANK3, Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 2, q21.2
SNP_A-2165125	caaacttgtcattca[A/G]acctgatttttttg	A	G	NM_020987 // intron // 0 // Hs.499725 // ANK3 // 288 // Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA. /// ENST00000280772 // intron // 0 // — // — // — /// ENST00000280771 // intron // 0 // — // —	ANK3	ANK3, Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, q21.2
SNP_A-1928103	ttcacaaatggtttct[C/T]aaacatggctatgtgt	C	T	NM_020987 // intron // 0 // Hs.499725 // ANK3 // 288 // Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA. /// ENST00000280772 // intron // 0 // — // — // — /// ENST00000280771 // intron // 0 // — // —	ANK3	ANK3, Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, q21.2
SNP_A-1698123	tcttcctctctggctctaggcacca[A/G]aactataagacaataaat tcctgtt	A	G	NM_001786 // downstream // 50932 // Hs.334562 // CDC2 // 983 // cell division cycle 2, G1 to S and G2 to M /// NM_014836 // downstream // 25699 // Hs.15099 // RHOBTB1 // 9886 // Rho-related BTB domain containing 1 /// NM_033379 // downstream // 50932 //	CDC2	CDC2 , rs2393702, cell division cycle 2, G1 to S and G2 to M ,q21.2
SNP_A-1820900	gtttctaatggcctg[C/T]atggaacttcttcacc	C	T	NM_033379 // upstream // 37636 // Hs.334562 // CDC2 // 983 // Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 2, mRNA. /// NM_001786 // upstream // 37636 // Hs.334562 // CDC2 // 983 // Homo sapiens cell division cycle 2,	CDC2	CDC2, Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 2, q21.2
SNP_A-2200814	ccaagatactggctta[C/T]gtttactctcaaattt	C	T	NM_198225 // upstream // 202310 // Hs.148670 // RHOBTB1 // 9886 // Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, mRNA. /// NM_014836 // upstream // 202310 // Hs.148670 // RHOBTB1 // 9886 // Homo sapiens Rho-related BTB	RHOBTB1	RHOBTB1, Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, q21.2
SNP_A-2001189	tactcatcagtaaaact[A/G]gagctggtgatacttc	A	G	NM_198225 // upstream // 359529 // Hs.148670 // RHOBTB1 // 9886 // Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, mRNA. /// NM_014836 // upstream // 359529 // Hs.148670 // RHOBTB1 // 9886 // Homo sapiens Rho-related BTB	RHOBTB1	RHOBTB1, Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, q21.2
SNP_A-2085345	actcatggcaaacttg[A/C]aaaatctgtcttggt	A	C	NM_198225 // upstream // 442558 // Hs.148670 // RHOBTB1 // 9886 // Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, mRNA. /// NM_014836 // upstream // 442558 // Hs.148670 // RHOBTB1 // 9886 // Homo sapiens Rho-related BTB	RHOBTB1	RHOBTB1, Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 2, q21.2
SNP_A-1789524	gggcctgctatcagcc[C/G]ctgtgattagagcat	C	G	NM_178505 // upstream // 67050 // Hs.302714 // TMEM26 // 219623 // Homo sapiens transmembrane protein 26 (TMEM26), mRNA. /// NM_173554 // upstream // 142673 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf10	TMEM26	TMEM26, Homo sapiens transmembrane protein 26 (TMEM26), q21.2
SNP_A-2227591	ctacagttagttgtta[C/T]gatcagatgtctgtaa	C	T	NM_178505 // upstream // 87510 // Hs.302714 // TMEM26 // 219623 // Homo sapiens transmembrane protein 26 (TMEM26), mRNA. /// NM_173554 // upstream // 122213 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf10	TMEM26	TMEM26, Homo sapiens transmembrane protein 26 (TMEM26), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2227790	ctaccagttgtacga[C/T]agatgactcctctgg	C	T	NM_178505 // upstream // 94135 // Hs.302714 // TMEM26 // 219623 // Homo sapiens transmembrane protein 26 (TMEM26), mRNA. /// NM_173554 // upstream // 115588 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf10	TMEM26	TMEM26, Homo sapiens transmembrane protein 26 (TMEM26), q21.2
SNP_A-1819347	gttggcaaacaaagaa[C/T]agtcaacaacttctt	C	T	NM_178505 // upstream // 123406 // Hs.302714 // TMEM26 // 219623 // Homo sapiens transmembrane protein 26 (TMEM26), mRNA. /// NM_173554 // upstream // 86317 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf10	TMEM26	TMEM26, Homo sapiens transmembrane protein 26 (TMEM26), q21.2
SNP_A-2054682	aataaaagaccccaga[C/T]tcaagtaacacttttt	C	T	NM_178505 // upstream // 134524 // Hs.302714 // TMEM26 // 219623 // Homo sapiens transmembrane protein 26 (TMEM26), mRNA. /// NM_173554 // upstream // 75199 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf10	TMEM26	TMEM26, Homo sapiens transmembrane protein 26 (TMEM26), q21.2
SNP_A-2159634	atttacttttagcagca[A/C]aaccttatgttaaatg	A	C	NM_178505 // upstream // 139846 // Hs.302714 // TMEM26 // 219623 // Homo sapiens transmembrane protein 26 (TMEM26), mRNA. /// NM_173554 // upstream // 69877 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf10	TMEM26	TMEM26, Homo sapiens transmembrane protein 26 (TMEM26), q21.2
SNP_A-1833996	tacatagtacttaaca[C/G]aagagtgagaaggtgt	C	G	NM_173554 // downstream // 120010 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf107), mRNA. /// BX641020 // upstream // 15360 // Hs.535297 // ARID5B // 84159 // Homo sapiens mRNA; cDNA DKFZp686G23148 (from	C10orf107	C10orf107, Homo sapiens chromosome 10 open reading frame 107 (C10orf107), q21.2
SNP_A-2235650	ctcctatggataggaa[C/T]gttagctagttagccc	C	T	NM_173554 // downstream // 120521 // Hs.252954 // C10orf107 // 219621 // Homo sapiens chromosome 10 open reading frame 107 (C10orf107), mRNA. /// BX641020 // upstream // 14849 // Hs.535297 // ARID5B // 84159 // Homo sapiens mRNA; cDNA DKFZp686G23148 (from	C10orf107	C10orf107, Homo sapiens chromosome 10 open reading frame 107 (C10orf107), q21.2
SNP_A-1898567	tgcttgccatgacaac[A/G]aaatttaatagaaata	A	G	NM_145307 // upstream // 99667 // Hs.58559 // PLEKHK1 // 219790 // Homo sapiens pleckstrin homology domain containing, family K member 1 (PLEKHK1), mRNA. /// NM_199450 // upstream // 5818 // Hs.22653 // ZNF365 // 22891 // Homo sapiens zinc finger protein	PLEKHK1	PLEKHK1, Homo sapiens pleckstrin homology domain containing, family K member 1 (PLEKHK1), q21.2
SNP_A-1801228	gtagctgaaccaaaaca[C/T]ggcattagcaaattga	C	T	NM_199450 // intron // 0 // Hs.22653 // ZNF365 // 22891 // Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, mRNA. /// NM_199451 // intron // 0 // Hs.22653 // ZNF365 // 22891 // Homo sapiens zinc finger protein 365 (ZNF365), transcript	ZNF365	ZNF365, Homo sapiens zinc finger protein 365 (ZNF365), transcript variant B, q21.2
SNP_A-1668100	gccaatatataagaaagtgttaag[C/G]aagataaaacgcaaagtacatttta	C	G	NM_013266 // downstream // 1926522 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 2933268 // Hs.499861 // LRRTM3 // 347731 // leucine rich repeat transmembrane neuronal 3	CTNNA3	CTNNA3 , rs2251417, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1660395	ataatcttccttttcccataaagac[A/G]agcataatcaccaggagtgatattc	A	G	NM_013266 // downstream // 1926349 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 2933095 // Hs.499861 // LRRTM3 // 347731 // leucine rich repeat transmembrane neuronal 3	CTNNA3	CTNNA3 , rs2251513, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-2001902	ttgcctgttccaatca[A/G]taaagctactaaaatg	A	G	NM_013266 // downstream // 2207191 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 88562 // --- // --- // --- /// ENST00000330298 // downstream // 2	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2001905	atcttaatcctttcaa[A/C]taatgctctctcaat	A	C	NM_013266 // downstream // 2156722 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 139031 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1846122	tatatattacagcctaj[C/G]agggggataggatataa	C	G	NM_013266 // downstream // 2121327 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 174426 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2273983	gactgtgtgacataaa[C/T]cctgacttgagtccag	C	T	NM_013266 // downstream // 2121102 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 174651 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1909095	tgtatcatcctctaaa[A/C]gtgaaatatttcatca	A	C	NM_013266 // downstream // 2120125 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 175628 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2290694	gcaagaggcaatgagg[A/G]cctggattaagtaagt	A	G	NM_013266 // downstream // 2117613 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 178140 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2139530	atcctttctatttttc[A/C]aacgtatatctcaccc	A	C	NM_013266 // downstream // 2117552 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 178201 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1825728	taaatccaagtataa[C/T]gccggctacatacaga	C	T	NM_013266 // downstream // 2059925 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 235828 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1923976	ttagtgcagaacatct[G/T]aacactttggactt	G	T	NM_013266 // downstream // 2046188 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 249565 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2001920	tctgctatcagatagt[C/G]aaagacaaaacagcca	C	G	NM_013266 // downstream // 2009255 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 286498 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1866546	tccccatgttttgtc[A/G]ctttagctgttctctc	A	G	NM_013266 // downstream // 2009200 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 286553 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1843117	tagtcacattgctgta[C/T]cttagggctccagaac	C	T	NM_013266 // downstream // 2006337 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 289416 // --- //, --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2127462	ataacacataaggaatc[C/T]gactgctttgtccat	C	T	NM_013266 // downstream // 2005133 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 290620 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2001930	agctcagaagattgca[A/T]agttaagtagaaatga	A	T	NM_013266 // downstream // 1979921 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 315832 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2206591	ccatgaacaattttga[A/G]cagccaatgtgacatc	A	G	NM_013266 // downstream // 1961120 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 334633 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1943973	ttgtatgtagaaacat[A/G]aggacctgcaagcaca	A	G	NM_013266 // downstream // 1942009 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 353744 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1858305	tcagaatgatagtagg[A/G]agagaggcatttccaa	A	G	NM_013266 // downstream // 1941905 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 353848 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2122103	agtgatggctattcac[A/G]ggggacagtggtcact	A	G	NM_013266 // downstream // 1941505 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 354248 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2206365	ccatcctttctgagta[C/T]gaatgtgtggagataa	C	T	NM_013266 // downstream // 1940234 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 355519 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2001202	tatatacgttgtgtcca[C/T]gatctgtcctggctga	C	T	NM_013266 // downstream // 1934872 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 360881 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1882757	tgaaagaattgtaagc[A/C]aacaaaggacaagatt	A	C	NM_013266 // downstream // 1928974 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 366779 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2212182	ccctgcttggacgctat[C/T]accaaagtacacacag	C	T	NM_013266 // downstream // 1907414 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 388339 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1886312	tgacctcctgatattc[A/G]catgactttctcactt	A	G	NM_013266 // downstream // 1846344 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 449409 // --- // --- // --- /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2179788	cactggctataccta[C/G]ctgcccagggaaactga	C	G	NM_013266 // downstream // 1702808 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 592945 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1668442	aactccacataagatactgtggaca[C/T]atatttaaaacaaagtttttgttt	C	T	NM_013266 // downstream // 1042654 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_178011 // upstream // 2049400 // Hs.499861 // LRRTM3 // 347731 // leucine rich repeat transmembrane neuronal 3	CTNNA3	CTNNA3 , rs2339575, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-1936468	ttcttgaaaaaccatg[A/C]aaagtgcggccctagg	A	C	NM_013266 // downstream // 1213924 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 1081829 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1795705	ggtggacaagtatgat[A/C]aaaatttctgggtata	A	C	NM_013266 // downstream // 1182894 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 1112859 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1907402	tgtaaaatttgaagca[A/T]agtcaaagtcatatga	A	T	NM_013266 // downstream // 556783 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 1738970 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2180665	cagaaggccaggaaatc[A/G]cctctgctctaagccc	A	G	NM_013266 // downstream // 542710 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 1753043 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2001991	caaattttagagaaaga[A/G]gttaagggcaagatga	A	G	NM_013266 // downstream // 535698 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 1760055 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2001992	tgtgtagcttaaaga[C/T]ggtatttttggactag	C	T	NM_013266 // downstream // 535667 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 1760086 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1875752	tctcttaaaggcctg[C/G]agttcagatgcttgca	C	G	NM_013266 // downstream // 234378 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 2061375 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1688472	cctacctgtacccttttcggcttca[A/C]aaactcctcagaaatgca	A	C	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs3858138, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-1645178	tactgtggctttaactacacca[C/T]gactgaatttttagttgttatag	C	T	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs10509251, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-2024994	aaaataagattatgac[G/T]ccctaaggtgttgtgg	G	T	NM_013266 // downstream // 150132 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000326531 // downstream // 2145621 // — // — // — /// ENST00000330298 // downstream //	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1661053	cttaatttgctgtatgaagtacaac[C/T]gaggatgcctcacttcatgctgtat	C	T	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs10509247, catenin (cadherin-associated protein), alpha 3,q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1797015	ggttctgaactctaaa[A/G]atgctgtgcttaagt	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1855545	tcaagttaagcaaaa[C/T]atgctgtctctatcaa	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1924849	ttatatcttccaacag[G/T]attcaggctaggcaa	G	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2002056	ttatgtgttgttaaac[G/T]gttaaatgttcaatct	G	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1718329	agctcaattatcttactacttcctgg[A/G]aaatacagtatctctcac gtggga	A	G	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3, rs10509262, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-1789536	gggcctgtactcagaa[A/G]gaatcccatcaagaca	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2150212	atgctataaatgagc[A/G]caaaaggaaattaaaa	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2039811	aacattatgagaatca[A/T]aaccgtaccctat	A	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2289806	gcaaacaatcccattg[A/G]aaagtggacatgaaca	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2001210	ggtgttgtacctaaaa[C/T]gtctttgccaaagctg	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1734498	agcaaatagacaaaaaatatgcttaa[C/T]gttgttcataataattaa aattact	C	T	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs1911355, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-2216600	cctctatctccacgaa[C/T]tcaattgatttaattt	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2063990	aattatgaagtcaaat[A/G]agtatcatgcatgagg	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2257246	ctttctaaatcacta[C/T]aacctacaatcaacac	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2262450	gaaatggcaaagctac[A/G]ggaacaataaaattcc	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2064049	aattattacaaagctta[C/T]cgtatgggaaggcagt	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1684398	aacttgacatttgctcggtctacat[C/G]tgatcctaagggttccag ataagat	C	G	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs1925633, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-2267266	gaatactcatttgcaa[C/T]tgtatgtgagaaaaa	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1654205	acattaggtaggaaatattgatggta[A/C]gatatccgtatatggcct catcag	A	C	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs7073720, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-2182910	cagattagattgtaaaa[C/T]gccacaagtgtggaaa	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1893352	tgcagcacgaatatca[G/T]agcttccatattgag	G	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1806397	gtccttgagaatttc[C/T]atacattgtacaagtt	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2149099	atgtaaaactaggaaa[C/T]ccaaatgcaacaagtg	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2002129	acagaaataatgcaca[C/T]tccataatctcaaaca	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2084845	actcaaatactgatga[C/T]cgctataaagacacat	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2044928	aagaacagagtaatc[A/T]cactcatttctagat	A	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2198561	catttattgcctatac[A/G]agagcctgaaacgatg	A	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2067101	acaaagaaatataaaga[C/G]acagtttctgtttca	C	G	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000359463 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1649534	catagcccagagccaatctgtgcaa[C/T]aggatatgtcctcagt gtatagcc	C	T	NM_013266 // intron // 0 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3	CTNNA3	CTNNA3 , rs1582573, catenin (cadherin-associated protein), alpha 3,q21.3
SNP_A-2263836	gaacggatgaatgtaa[A/C]gatttccacaggaatt	A	C	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — /// ENST00000327748 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1722630	aagatataaagcaataataaaacca[G/T]agtacacatttcttttg gcaccttc	G	T	NM_013266 // upstream // 95538 // Hs.257051 // CTNNA3 // 29119 // catenin (cadherin-associated protein), alpha 3 /// NM_021800 // downstream // 4963 // Hs.260720 // DNAJC12 // 56521 // DnaJ (Hsp40) homolog, subfamily C, member 12 /// NM_178011 // downstr	CTNNA3	CTNNA3 , rs1969735, catenin (cadherin-associated protein), alpha 3 ,q21.3
SNP_A-2286145	gatgcactaggatcga[C/T]gccaggttcagagaat	C	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // — /// ENST00000327748 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2114179	agggaaatggagatac[A/T]caattatcaaacagtc	A	T	NM_013266 // intron // 0 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// ENST00000330298 // intron // 0 // — // — // — // — /// ENST00000327748 // intron // 0 // — // — // —	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-1830163	taatagcaaagaataa[C/T]taaaatcccaaactta	C	T	NM_013266 // upstream // 37716 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// NM_021800 // downstream // 111441 // Hs.260720 // DNAJC12 // 56521 // Homo sapiens DnaJ (Hsp40) homolog, subf	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2128660	ataatatttagagaaa[A/G]accatagctacagaag	A	G	NM_013266 // upstream // 46070 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// NM_021800 // downstream // 103087 // Hs.260720 // DNAJC12 // 56521 // Homo sapiens DnaJ (Hsp40) homolog, subf	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2289538	gatttttctttgctca[C/T]catggagagagctaaa	C	T	NM_013266 // upstream // 121714 // Hs.325275 // CTNNA3 // 29119 // Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA. /// NM_021800 // downstream // 27443 // Hs.260720 // DNAJC12 // 56521 // Homo sapiens DnaJ (Hsp40) homolog, subf	CTNNA3	CTNNA3, Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), q21.3
SNP_A-2303551	gctcaatattgctaca[A/G]cgttgatgagaaaaat	A	G	NM_030625 // intron // 0 // Hs.156905 // CXXC6 // 80312 // Homo sapiens CXXC finger 6 (CXXC6). mRNA. /// ENST00000260906 // intron // 0 // — // — // — // —	CXXC6	CXXC6, Homo sapiens CXXC finger 6 (CXXC6), q21.3
SNP_A-2193246	catctcatggtaatta[C/G]aaactctgattggctg	C	G	ENST00000359886 // intron // 0 // — // — // — // — /// ENST00000360690 // intron // 0 // — // — // — // —	-	q22.1
SNP_A-1700500	ttgaataaataccaaggagtgtgct[A/T]gctagattgtatgttaagt gtatgt	A	T	NM_020999 // upstream // 38292 // - // - // - // - /// NM_145306 // upstream // 18600 // Hs.421107 // C10orf35 // 219738 // chromosome 10 open reading frame 35	-	- , rs1599710, - ,q22.1
SNP_A-1909955	tgtcagctctgacatc[A/G]attattccagggttct	A	G	NM_033498 // intron // 0 // Hs.370365 // HK1 // 3098 // Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA. /// NM_033497 // intron // 0 // Hs.370365 // HK1 // 3098 // Homo sapiens hexokinase 1 (HK1),	HK1	HK1, Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, q22.1
SNP_A-1785158	ggctaaatgggggtac[A/G]gatgagaaagtgaaag	A	G	NM_033498 // intron // 0 // Hs.370365 // HK1 // 3098 // Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA. /// NM_033497 // intron // 0 // Hs.370365 // HK1 // 3098 // Homo sapiens hexokinase 1 (HK1),	HK1	HK1, Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, transcript variant 4, q22.1
SNP_A-1960517	tttttcacataagagc[C/G]ctgagacctccccagg	C	G	NM_001057 // upstream // 7755 // Hs.88372 // TACR2 // 6865 // Homo sapiens tachykinin receptor 2 (TACR2), mRNA. /// NM_012339 // upstream // 26874 // Hs.499941 // TM4SF15 // 23555 // Homo sapiens transmembrane 4 superfamily member 15 (TM4SF15), mRNA. ///	TACR2	TACR2, Homo sapiens tachykinin receptor 2 (TACR2), q22.1
SNP_A-1924016	ttagtggctggccagg[A/C]agacgagttttggttg	A	C	NM_012339 // intron // 0 // Hs.499941 // TM4SF15 // 23555 // Homo sapiens transmembrane 4 superfamily member 15 (TM4SF15), mRNA. /// ENST00000263561 // intron // 0 // — // — // — // —	TM4SF15	TM4SF15, Homo sapiens transmembrane 4 superfamily member 15 (TM4SF15), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1751683	tgccctaatccagctagctatagaa[A/T]ataaggtcttacaattat agggtca	A	T	NM_005203 // intron // 0 // Hs.211933 // COL13A1 // 1305 // collagen, type XIII, alpha 1 /// NM_080798 // intron // 0 // Hs.211933 // COL13A1 // 1305 // collagen, type XIII, alpha 1 /// NM_080799 // intron // 0 // Hs.211933 // COL13A1 // 1305 // collagen	COL13A1	COL13A1 , rs10509315, collagen, type XIII, alpha 1 ,q22.1
SNP_A-1880767	tcttggctcactgcaa[A/C]cttagctcactgcaac	A	C	NM_145306 // downstream // 93828 // Hs.522992 // C10orf35 // 219738 // Homo sapiens chromosome 10 open reading frame 35 (C10orf35), mRNA. /// NM_080806 // upstream // 74469 // Hs.211933 // COL13A1 // 1305 // Homo sapiens collagen, type XIII, alpha 1 (COL1	C10orf35	C10orf35, Homo sapiens chromosome 10 open reading frame 35 (C10orf35), q22.1
SNP_A-1952311	tttctctcaattacca[C/T]gtcccaattctagaga	C	T	NM_080806 // intron // 0 // Hs.211933 // COL13A1 // 1305 // Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, mRNA. /// NM_080810 // intron // 0 // Hs.211933 // COL13A1 // 1305 // Homo sapiens collagen, type XIII, alpha 1 (COL13A	COL13A1	COL13A1, Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, q22.1
SNP_A-2249805	cttaattatgtcgagg[C/T]ccaacaacacatggta	C	T	NM_080806 // intron // 0 // Hs.211933 // COL13A1 // 1305 // Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, mRNA. /// NM_080810 // intron // 0 // Hs.211933 // COL13A1 // 1305 // Homo sapiens collagen, type XIII, alpha 1 (COL13A	COL13A1	COL13A1, Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, q22.1
SNP_A-2130070	ataccagtgtttctcc[A/G]gaagcaaatggagcac	A	G	NM_032797 // intron // 0 // Hs.117062 // AMID // 84883 // Homo sapiens apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death (AMID), mRNA. /// ENST00000354601 // intron // 0 // — // — // — // –	AMID	AMID, Homo sapiens apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death (AMID), q22.1
SNP_A-2298798	gcccatcctactgtca[C/G]ggtgacctcatctgtc	C	G	NM_020150 // upstream // 23212 // Hs.499960 // SARA1 // 56681 // Homo sapiens SAR1a gene homolog 1 (S. cerevisiae) (SARA1), mRNA. /// NM_021129 // downstream // 9106 // Hs.437403 // PP // 5464 // Homo sapiens pyrophosphatase (inorganic) (PP), mRNA. /// EN	SARA1	SARA1, Homo sapiens SAR1a gene homolog 1 (S. cerevisiae) (SARA1), q22.1
SNP_A-1920712	ttacaaatcttactac[C/T]atgctatctgtccaac	C	T	NM_021129 // intron // 0 // Hs.437403 // PP // 5464 // Homo sapiens pyrophosphatase (inorganic) (PP), mRNA. /// ENST00000321141 // intron // 0 // — // — // — // —	PP	PP, Homo sapiens pyrophosphatase (inorganic) (PP), q22.1
SNP_A-1903154	tggcttcaccgggttc[A/G]aggatgaaaatttcac	A	G	NM_022146 // upstream // 4422 // Hs.302026 // GPR147 // 64106 // Homo sapiens G protein-coupled receptor 147 (GPR147), mRNA. /// NM_207119 // downstream // 28153 // Hs.7778 // LRRC20 // 55222 // Homo sapiens leucine rich repeat containing 20 (LRRC20), tra	GPR147	GPR147, Homo sapiens G protein-coupled receptor 147 (GPR147), q22.1
SNP_A-2207220	ccattcaagttaataa[A/G]cgcagggctgggcatg	A	G	NM_207119 // intron // 0 // Hs.7778 // LRRC20 // 55222 // Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 1, mRNA. /// NM_018205 // intron // 0 // Hs.7778 // LRRC20 // 55222 // Homo sapiens leucine rich repeat containing 20 (LR	LRRC20	LRRC20, Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 1, q22.1
SNP_A-1789332	gggccagaaattgtca[C/G]gctcccaagcttgcac	C	G	NM_014431 // intron // 0 // Hs.202351 // KIAA1274 // 27143 // Homo sapiens paladin (PALD), mRNA. /// ENST00000263563 // intron // 0 // — // — // — // —	KIAA1274	KIAA1274, Homo sapiens paladin (PALD), q22.1
SNP_A-1906175	tggtgaagctgggatc[A/G]gaacctgtttagactt	A	G	NM_005041 // upstream // 1282 // Hs.2200 // PRF1 // 5551 // Homo sapiens perforin 1 (pore forming protein) (PRF1), mRNA. /// NM_139155 // upstream // 68763 // Hs.352156 // ADAMTS14 // 140766 // Homo sapiens a disintegrin-like and metalloprotease (reprolys	PRF1	PRF1, Homo sapiens perforin 1 (pore forming protein) (PRF1), q22.1
SNP_A-1877876	tctggtgcacatagta[C/G]gagttgcgcttggcac	C	G	NM_139155 // CDS // 0 // Hs.352156 // ADAMTS14 // 140766 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 14 (ADAMTS14), transcrip /// NM_080722 // CDS // 0 // Hs.352156 // ADAMTS14 // 140766 // Ho	ADAMTS14	ADAMTS14, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 14 (ADAMTS14), transcrip ,q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2254426	cttgccagccatgcta[C/T]gatgcacacagatgtg	C	T	NM_139155 // intron // 0 // Hs.352156 // ADAMTS14 // 140766 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 14 (ADAMTS14), transcrip /// NM_080722 // intron // 0 // Hs.352156 // ADAMTS14 // 140766	ADAMTS14	ADAMTS14, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 14 (ADAMTS14), transcrip ,q22.1
SNP_A-2191434	catatctcctgtctcc[A/G]aaggccctccagtgtg	A	G	NM_000281 // upstream // 40310 // Hs.3192 // PCBD1 // 5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) (PCBD), tran /// NM_001001939 // upstream // 40310 // Hs.3192 // PCBD1 // 509	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase q22.1
SNP_A-1923761	ttagtaattaggactc[A/G]ctttcagggccagtcc	A	G	NM_000281 // upstream // 67324 // Hs.3192 // PCBD1 // 5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) (PCBD), tran /// NM_001001939 // upstream // 67324 // Hs.3192 // PCBD1 // 509	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase,q22.1
SNP_A-2029902	aaagatatcacactga[A/T]ccattacactgatgac	A	T	NM_000281 // upstream // 131359 // Hs.3192 // PCBD1 // 5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) (PCBD), tran /// NM_001001939 // upstream // 131359 // Hs.3192 // PCBD1 // 5	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase,q22.1
SNP_A-2281664	gagtctggattctgtc[G/T]ctttctgggcatatct	G	T	NM_000281 // upstream // 143585 // Hs.3192 // PCBD1 // 5092 // Homo sapiens 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) (PCBD), tran /// NM_001001939 // upstream // 143585 // Hs.3192 // PCBD1 // 5	PCBD1	PCBD1, Homo sapiens 6-pyruvoyl-tetrahydropterin synthase,q22.1
SNP_A-1685750	ggtggctacagagggaatagctaac[A/C]gagtttcaggtgaca gaaggaggag	A	C	NM_022124 // intron // 0 // Hs.310897 // CDH23 // 64072 // cadherin related 23	CDH23	CDH23 , rs1234888, cadherin related 23,q22.1
SNP_A-2192516	catccaacaagtggcc[A/G]ccacactgctgggaca	A	G	NM_022124 // intron // 0 // Hs.546421 // CDH23 // 64072 // Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, mRNA. /// NM_052836 // intron // 0 // Hs.546421 // CDH23 // 64072 // Homo sapiens cadherin-like 23 (CDH23), transcript variant 2, mRNA.	CDH23	CDH23, Homo sapiens cadherin-like 23 (CDH23), transcript variant 1, q22.1
SNP_A-2002516	ctagtaggtgctcaaa[A/G]aagccattcactcttt	A	G	NM_002778 // upstream // 45973 // Hs.523004 // PSAP // 5660 // Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA. /// NM_004273 // upstream // 67138 // Hs.158304 // CHST3 // 9469 // Homo sapiens carboh	PSAP	PSAP, Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), q22.1
SNP_A-1806550	gtcgtgtgtacaggcc[A/G]agccccagtggcgtag	A	G	NM_002778 // upstream // 56339 // Hs.523004 // PSAP // 5660 // Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA. /// NM_004273 // upstream // 56772 // Hs.158304 // CHST3 // 9469 // Homo sapiens carboh	PSAP	PSAP, Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), q22.1
SNP_A-2116521	aggtcaaatgccagaa[A/C]tgtgtcaccatcaaat	A	C	NM_002778 // upstream // 97257 // Hs.523004 // PSAP // 5660 // Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA. /// NM_004273 // upstream // 15854 // Hs.158304 // CHST3 // 9469 // Homo sapiens carboh	PSAP	PSAP, Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), q22.1
SNP_A-2243483	ctgctaatgtggacag[C/T]agactttatccctcct	C	T	NM_004273 // 3UTR // 0 // Hs.158304 // CHST3 // 9469 // Homo sapiens carbohydrate (chondroitin 6) sulfotransferase 3 (CHST3), mRNA. /// ENST00000242466 // 3UTR // 0 // — // — // — // —	CHST3	CHST3, Homo sapiens carbohydrate (chondroitin 6) sulfotransferase 3 (CHST3), q22.1
SNP_A-1781061	ggatgccacagtgtta[A/G]gtagagcagtgatacg	A	G	NM_015947 // intron // 0 // Hs.500007 // ASCC1 // 51008 // Homo sapiens activating signal cointegrator 1 complex subunit 1 (ASCC1), mRNA. /// AY013290 // intron // 0 // Hs.500007 // ASCC1 // 51008 // Homo sapiens ASC-1 complex subunit P50 mRNA, complete c	ASCC1	ASCC1, Homo sapiens activating signal cointegrator 1 complex subunit 1 (ASCC1), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2140867	atctgaatgtgtgtca[C/T]ggtatttttgtggaa	C	T	NM_138357 // intron // 0 // Hs.128021 // C10orf42 // 90550 // Homo sapiens chromosome 10 open reading frame 42 (C10orf42), mRNA. /// ENST00000342180 // intron // 0 // — // — // — /// ENST00000357157 // intron // 0 // — // — // — // —	C10orf42	C10orf42, Homo sapiens chromosome 10 open reading frame 42 (C10orf42), q22.1
SNP_A-1782331	ggcaatgagtcagtaa[C/T]gtggtgcagtggtcca	C	T	NM_152586 // upstream // 9348 // Hs.434502 // USP54 // 159195 // Homo sapiens ubiquitin specific protease 54 (USP54), mRNA. /// NM_021245 // downstream // 46716 // Hs.238756 // MYOZ1 // 58529 // Homo sapiens myozenin 1 (MYOZ1), mRNA. /// ENST00000339859 /	USP54	USP54, Homo sapiens ubiquitin specific protease 54 (USP54), q22.2
SNP_A-2290543	gcaactgtagtcccac[A/G]cttgcttcttgtgctt	A	G	NM_172169 // intron // 0 // Hs.523045 // CAMK2G // 818 // Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma (CAMK2G), transcript variant 2, mRNA. /// NM_172172 // intron // 0 // Hs.523045 // CAMK2G // 818 // Homo sapiens calci	CAMK2G	CAMK2G, Homo sapiens calcium,q22.2
SNP_A-1796367	ggtgttctacgttca[C/T]gttgtccttatgtaac	C	T	NM_172169 // intron // 0 // Hs.523045 // CAMK2G // 818 // Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma (CAMK2G), transcript variant 2, mRNA. /// NM_172172 // intron // 0 // Hs.523045 // CAMK2G // 818 // Homo sapiens calci	CAMK2G	CAMK2G, Homo sapiens calcium,q22.2
SNP_A-1946936	tttaaggtcagcatac[C/T]catacggctgcaatat	C	T	NM_012095 // intron // 0 // Hs.500104 // AP3M1 // 26985 // Homo sapiens adaptor-related protein complex 3, mu 1 subunit (AP3M1), transcript variant 2, mRNA. /// NM_207012 // intron // 0 // Hs.500104 // AP3M1 // 26985 // Homo sapiens adaptor-related protei	AP3M1	AP3M1, Homo sapiens adaptor-related protein complex 3, mu 1 subunit (AP3M1), transcript variant 2, q22.2
SNP_A-2290449	gcaacgaacttgataa[C/G]tgggtttagaagtag	C	G	NM_006721 // intron // 0 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, mRNA. /// NM_001123 // intron // 0 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-short, mR	ADK	ADK, Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, q22.2
SNP_A-2097184	agacttctaagctagc[A/G]attaagtgtatttct	A	G	NM_006721 // intron // 0 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, mRNA. /// NM_001123 // intron // 0 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-short, mR	ADK	ADK, Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, q22.2
SNP_A-2169351	caagcagtctgactta[C/T]gcacttaaccacagtt	C	T	NM_006721 // intron // 0 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, mRNA. /// NM_001123 // intron // 0 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-short, mR	ADK	ADK, Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, q22.2
SNP_A-2044843	aagaaattcactgtga[A/C]caaacacacacacaca	A	C	NM_006721 // downstream // 37873 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, mRNA. /// NM_001123 // downstream // 37873 // Hs.500118 // ADK // 132 // Homo sapiens adenosine kinase (ADK), transcript varia	ADK	ADK, Homo sapiens adenosine kinase (ADK), transcript variant ADK-long, q22.2
SNP_A-2293108	gcagaccctgcaaaca[A/G]ctatctcggagacag	A	G	NM_032024 // intron // 0 // Hs.118161 // C10orf11 // 83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // intron // 0 // — // — // — // —	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.2
SNP_A-2024872	aaaagtttctagggaa[C/T]gtaatgtccatgagat	C	T	NM_032024 // intron // 0 // Hs.118161 // C10orf11 // 83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // intron // 0 // — // — // — // —	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2038332	aacacgagtcacaatc[A/G]gaacttatatatttac	A	G	NM_032024 // downstream // 206513 // Hs.118161 // C10orf11 // 83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // downstream // 206513 // --- // --- // --- // --- /// ENST00000331566 // downstream // 113938 /	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.3
SNP_A-2002763	cctatgagagggtaca[C/T]gctaggaatttgagaa	C	T	NM_032024 // downstream // 232011 // Hs.118161 // C10orf11 // 83938 // Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA. /// ENST00000277847 // downstream // 232011 // --- // --- // --- // --- /// ENST00000331566 // downstream // 88440 //	C10orf11	C10orf11, Homo sapiens chromosome 10 open reading frame 11 (C10orf11), q22.3
SNP_A-1837537	tacttgcttgaatgta[C/T]agggatgatttatcga	C	T	NM_002247 // intron // 0 // Hs.144795 // KCNMA1 // 3778 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 // 3778 // Homo sapiens large condu	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-1794415	ggtccctatgggctac[C/G]acaggacaagaagaac	C	G	NM_002247 // intron // 0 // Hs.144795 // KCNMA1 // 3778 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 // 3778 // Homo sapiens large condu	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2136502	atcaccatgatgtaca[A/G]taatagatgtcttgaa	A	G	NM_002247 // intron // 0 // Hs.144795 // KCNMA1 // 3778 // Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA. /// U11058 // intron // 0 // Hs.144795 // KCNMA1 // 3778 // Homo sapiens large condu	KCNMA1	KCNMA1, Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), q22.3
SNP_A-2207658	ccatttgttgaaaaga[A/C]cattcttcctgcattt	A	C	NM_004747 // downstream // 38002 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream // 19982 // --- // --- // --- // --- /// ENST00000320511 // downstream // 38002 // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1836520	tactcgctgcaagaaa[A/G]agagaagcaaaatagt	A	G	NM_004747 // downstream // 21018 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream // 36966 // --- // --- // --- // --- /// ENST00000320511 // downstream // 21018 // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2114920	agggcagtgagcctca[C/T]gtggattctgtttcta	C	T	NM_004747 // downstream // 18990 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream // 38994 // --- // --- // --- // --- /// ENST00000320511 // downstream // 18990 // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2002867	tcttaatgaggctact[C/T]aaaagcaggagaaaca	C	T	NM_004747 // downstream // 18575 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream // 39409 // --- // --- // --- // --- /// ENST00000320511 // downstream // 18575 // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2125481	agtttatagataagga[C/T]atcaggaccgtcaatt	C	T	NM_004747 // downstream // 6476 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream // 51508 // --- // --- // --- // --- /// ENST00000320511 // downstream // 6476 // --- // --- /	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2001276	aatgtaatccaaatgc[C/T]cagttatgggaaacta	C	T	NM_004747 // downstream // 6369 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000341821 // downstream // 51615 // --- // --- // --- // --- /// ENST00000320511 // downstream // 6369 // --- // --- /	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1885095	tgaatgttaagctcac[C/T]gatcttggcctcaggt	C	T	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800324	gtactaactacactaa[C/T]gcaaaatgccaaaatt	C	T	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2002872	ccattctccigtataa[C/T]aaccccaatgccatca	C	T	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2002873	ttgtgttatttggacg[C/T]ccatttggaagaccat	C	T	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2002877	agctgcttatatcacc[A/G]gaagaaaagtttaca	A	G	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2106932	agcctgctagaaagc[A/G]cgaggttggcacatct	A	G	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2147898	atggcggtgctgtgtc[A/G]aaacaaagctcccagg	A	G	NM_004747 // intron // 0 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// ENST00000320511 // intron // 0 // --- // --- // ---	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-1912965	tgtggaatggtggtac[C/T]gcaatggctacatgga	C	T	NM_004747 // upstream // 70335 // Hs.500245 // DLG5 // 9231 // Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA. /// NM_007055 // downstream // 36618 // Hs.436896 // POLR3A // 11128 // Homo sapiens polymerase (RNA) III (DNA directed) polypept	DLG5	DLG5, Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), q22.3
SNP_A-2002925	ttagggactgtgcatc[A/G]cacctattcagtact	A	G	NM_033022 // downstream // 420526 // Hs.356794 // RPS24 // 6229 // mRNA. /// NM_033022 // downstream // 420525 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), t	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2168947	caagagcactcaagtg[A/C]agaacacaaggcaagt	A	C	NM_033022 // downstream // 503659 // Hs.356794 // RPS24 // 6229 // mRNA. /// NM_033022 // downstream // 503658 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), t	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-1797024	ggttctgatgatttgc[C/T]atctgcagttatctgg	C	T	NM_033022 // downstream // 516450 // Hs.356794 // RPS24 // 6229 // mRNA. /// NM_033022 // downstream // 516449 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), t	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-1870672	tcgccacatcctgaga[A/G]tagccaacgtgtgggg	A	G	NM_033022 // downstream // 734072 // Hs.356794 // RPS24 // 6229 // mRNA. /// NM_033022 // downstream // 734071 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), t	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2303256	gctatgccagctatga[A/G]gtgccatgcagtcatc	A	G	NM_033022 // downstream // 977108 // Hs.356794 // RPS24 // 6229 // mRNA. /// NM_033022 // downstream // 977107 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), t	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2285154	gatctagcttcaacaa[C/T]aatttataaggcacac	C	T	NM_033022 // downstream // 1000604 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream // 1000603 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24),	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2189271	cagttccctgattgaa[C/T]tgtcacattgtcttaa	C	T	NM_033022 // downstream // 1024990 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream // 1024989 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24),	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2003003	gatctaaggacatttc[C/G]ccgaaaccaggcaaaa	C	G	NM_033022 // downstream // 1072024 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream // 1072023 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24),	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-1781889	ggcaaaaagactctac[A/G]cctgtaatagatgaaa	A	G	NM_033022 // downstream // 1076631 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, mRNA. /// NM_033022 // downstream // 1076630 // Hs.356794 // RPS24 // 6229 // Homo sapiens ribosomal protein S24 (RPS24),	RPS24	RPS24, Homo sapiens ribosomal protein S24 (RPS24), transcript variant 1, q22.3
SNP_A-2218725	cctggctgactcacca[C/T]actaactgccctactc	C	T	NM_020338 // intron // 0 // Hs.193118 // RAI17 // 57178 // Homo sapiens retinoic acid induced 17 (RAI17), mRNA. /// ENST00000334512 // intron // 0 // — // — // — // —	RAI17	RAI17, Homo sapiens retinoic acid induced 17 (RAI17), q22.3
SNP_A-2217619	cctgagcctgctgaaa[C/T]gatagaaaatgcaatc	C	T	NM_020338 // intron // 0 // Hs.193118 // RAI17 // 57178 // Homo sapiens retinoic acid induced 17 (RAI17), mRNA. /// ENST00000334512 // intron // 0 // — // — // — // —	RAI17	RAI17, Homo sapiens retinoic acid induced 17 (RAI17), q22.3
SNP_A-1804075	gtcacactactgacaa[C/G]tgccaggatttgaatc	C	G	NM_020338 // intron // 0 // Hs.193118 // RAI17 // 57178 // Homo sapiens retinoic acid induced 17 (RAI17), mRNA. /// ENST00000334512 // intron // 0 // — // — // — // —	RAI17	RAI17, Homo sapiens retinoic acid induced 17 (RAI17), q22.3
SNP_A-1861788	tcatcttcagtttccc[C/T]ggacttagcagaggga	C	T	NM_020338 // intron // 0 // Hs.193118 // RAI17 // 57178 // Homo sapiens retinoic acid induced 17 (RAI17), mRNA. /// ENST00000334512 // intron // 0 // — // — // — // —	RAI17	RAI17, Homo sapiens retinoic acid induced 17 (RAI17), q22.3
SNP_A-1924599	ttatagaagataccag[C/T]cctggtcgcacacacc	C	T	NM_020338 // intron // 0 // Hs.193118 // RAI17 // 57178 // Homo sapiens retinoic acid induced 17 (RAI17), mRNA. /// ENST00000334512 // intron // 0 // — // — // — // — /// ENST00000360331 // intron // 0 // — // — // — // —	RAI17	RAI17, Homo sapiens retinoic acid induced 17 (RAI17), q22.3
SNP_A-2003029	gagaccaggtgacagc[A/G]gcacttgaccattaca	A	G	NM_005729 // downstream // 14955 // Hs.381072 // PPIF // 10105 // Homo sapiens peptidylprolyl isomerase F (cyclophilin F) (PPIF), nuclear gene encoding mitochondrial protein, mRNA. /// NM_153367 // downstream // 12049 // Hs.523080 // C10orf56 // 219654 //	PPIF	PPIF, Homo sapiens peptidylprolyl isomerase F (cyclophilin F) (PPIF), nuclear gene encoding mitochondrial protein, q22.3
SNP_A-2180486	cagaactatctgaaga[C/G]agtctgatgtaattct	C	G	NM_003019 // upstream // 58476 // Hs.253495 // SFTPD // 6441 // Homo sapiens surfactant, pulmonary-associated protein D (SFTPD), mRNA. /// NM_025125 // upstream // 71089 // Hs.169982 // C10orf57 // 80195 // Homo sapiens chromosome 10 open reading frame 57	SFTPD	SFTPD, Homo sapiens surfactant, pulmonary-associated protein D (SFTPD), q22.3
SNP_A-2156927	attcttgcctctgaaa[C/T]atagtgatgagcccag	C	T	NM_003019 // upstream // 107028 // Hs.253495 // SFTPD // 6441 // Homo sapiens surfactant, pulmonary-associated protein D (SFTPD), mRNA. /// NM_025125 // upstream // 22537 // Hs.169982 // C10orf57 // 80195 // Homo sapiens chromosome 10 open reading frame 5	SFTPD	SFTPD, Homo sapiens surfactant, pulmonary-associated protein D (SFTPD), q22.3
SNP_A-2109989	aggaagaatgacatcc[A/G]aagggtgtggagcagc	A	G	NM_001157 // downstream // 1319 // Hs.530291 // ANXA11 // 311 // Homo sapiens annexin A11 (ANXA11), transcript variant a, mRNA. /// NM_145869 // downstream // 1319 // Hs.530291 // ANXA11 // 311 // Homo sapiens annexin A11 (ANXA11), transcript variant c, m	ANXA11	ANXA11, Homo sapiens annexin A11 (ANXA11), transcript variant a, q22.3
SNP_A-1656871	aatgaaaatcagcagtctctaaata[A/G]cttcaccagaaccca atccaaccag	A	G	AK091518 // upstream // 57992 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_030927 // downstream // 65376 // Hs.509050 // DC-TM4F2 // 81619 // tetraspanin similar to TM4SF9	FLJ41984	FLJ41984 , rs1913759, FLJ41984 protein ,q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1741293	agggacagcgcgcattaacttagaa[C/T]ctgctaagtgtacatat taaatcgt	C	T	AK091518 // upstream // 17711 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_030927 // downstream // 105657 // Hs.509050 // DC-TM4F2 // 81619 // tetraspanin similar to TM4SF9	FLJ41984	FLJ41984 , rs9325452, FLJ41984 protein ,q22.3
SNP_A-1897358	tgctgaaacaggaaga[A/G]atcagattcaacaga	A	G	NM_032372 // CDS // 0 // Hs.512782 // MGC16186 // 84332 // Homo sapiens hypothetical protein MGC16186 (MGC16186), mRNA. /// ENST00000316132 // CDS // 0 // — // — // — /// ENST00000256039 // CDS // 0 // — // — // —	MGC16186	MGC16186, Homo sapiens hypotheticl protein MGC16186 (MGC16186), q22.3
SNP_A-1783648	ggcatgtctgaagca[C/T]gtactactgtgacttg	C	T	NM_032333 // intron // 0 // Hs.500333 // C10orf58 // 84293 // Homo sapiens chromosome 10 open reading frame 58 (C10orf58), mRNA. /// ENST00000344718 // intron // 0 // — // — // —	C10orf58	C10orf58, Homo sapiens chromosome 10 open reading frame 58 (C10orf58), q22.3
SNP_A-2087972	actggcatgtttctga[C/T]gttgctaggtgtgttt	C	T	NM_032333 // intron // 0 // Hs.500333 // C10orf58 // 84293 // Homo sapiens chromosome 10 open reading frame 58 (C10orf58), mRNA. /// ENST00000344718 // intron // 0 // — // — // —	C10orf58	C10orf58, Homo sapiens chromosome 10 open reading frame 58 (C10orf58), q22.3
SNP_A-2003143	gttagctgttcctttg[C/T]ttggctacgtccatgt	C	T	NM_207372 // intron // 0 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // intron // 0 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2001291	ccctctctctccaaaaa[A/T]gaaagtacacctaagg	A	T	NM_207372 // intron // 0 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // intron // 0 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1880929	tcttgtcgcagcttca[A/G]agccctccaggtgtgc	A	G	NM_207372 // downstream // 8403 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 8403 // — // — // — /// ENST00000313455 // downstream // 8403 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1876715	tctgcagaaaggcaaaa[C/T]cataagtgtgatgac	C	T	NM_207372 // downstream // 293175 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 293175 // — // — // — /// ENST00000313455 // downstream // 293175 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2112299	aggcaaaaaatctgctc[C/T]ataggttggactatcc	C	T	NM_207372 // downstream // 418106 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 418106 // — // — // — /// ENST00000313455 // downstream // 418106 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2133643	atatcaggctagagga[C/T]aataatttggagggtc	C	T	NM_207372 // downstream // 423482 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 423482 // — // — // — /// ENST00000313455 // downstream // 423482 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-2104875	agcatagtggcataaag[C/T]aacaaaccatttgcag	C	T	NM_207372 // downstream // 479659 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 479659 // — // — // — /// ENST00000313455 // downstream // 479659 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1939886	ttgcacatagctaaga[C/G]aatgactgcccttatt	C	G	NM_207372 // downstream // 500461 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 500461 // — // — // — /// ENST00000313455 // downstream // 500461 // — // — // —	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q22.3
SNP_A-1747143	tcatctagaagcatcttattaaaaa[G/T]gatcagaatttaatacag caggatt	G	T	AK091518 // downstream // 829498 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 2663446 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs10490925, FLJ41984 protein ,q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2072689	acagcctgcatatta[C/T]ggcctacagatcaaca	C	T	NM_207372 // downstream // 580370 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 580370 // — // — // — /// ENST00000313455 // downstream // 580370 // — // — /	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q23.1
SNP_A-1921474	ttaccccaggacttcc[A/G]aattgggagatcttgc	A	G	NM_207372 // downstream // 1186127 // Hs.147643 // SH2D4B // 387694 // Homo sapiens SH2 domain containing 4B (SH2D4B), mRNA. /// ENST00000339284 // downstream // 1186127 // — // — // — /// ENST00000313455 // downstream // 1186127 // — // –	SH2D4B	SH2D4B, Homo sapiens SH2 domain containing 4B (SH2D4B), q23.1
SNP_A-2274960	gagaaccaaagcactc[A/G]ctattacaaagggcc	A	G	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-1690245	tgtaaacatctagacacacaaatgta[C/T]gctaaatgtactacttta atttctt	C	T	AK091518 // downstream // 2179394 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 1313550 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs478982, FLJ41984 protein ,q23.1
SNP_A-2003301	atactaacgttaaag[A/G]atgatcctctacttat	A	G	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-1787361	gggaagcttggatcaa[C/T]gaactggcagcctta	C	T	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-2003325	aagatgcaaagaaaca[A/G]agtgcgaatcgaagtc	A	G	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-1863059	tcatttaacctttaca[A/G]gataaaagtagctatta	A	G	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-1919472	ttaagccctatcatg[C/T]attgtagccaaaacct	C	T	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-2242548	ctgcaggacataagga[A/G]agaatagcaactgata	A	G	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-2292237	gcacctacttatatc[A/T]gacattgtgttggatg	A	T	ENST00000332738 // intron // 0 // — // — // —	-	q23.1
SNP_A-1737878	ccccatgatcttctcattaaaca[C/T]tatttctggcaattaaactt att	C	T	AK091518 // downstream // 2533565 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 959379 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs2348884, FLJ41984 protein ,q23.1
SNP_A-1716991	ctacactgatctgggagaaaattaa[C/T]gaagtagcatcagtaa tgtataaa	C	T	AK091518 // downstream // 2535290 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 957654 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs2348886, FLJ41984 protein ,q23.1
SNP_A-1645688	atatgtgcatgcgctcacacataca[A/T]gcataaaatatttgggct ctgtttc	A	T	AK091518 // downstream // 2536287 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 956657 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs1339837, FLJ41984 protein ,q23.1
SNP_A-1739877	aagtaatgggtcctggcaataacta[C/T]ggatttatttcttgttgg tctt	C	T	AK091518 // downstream // 2807051 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 685893 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs10509475, FLJ41984 protein ,q23.1
SNP_A-2003352	gtaatgtcaggctgta[A/G]catctgtgactgctgc	A	G	NM_014394 // upstream // 997239 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 997239 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2031512	aaaggtgcaaatcata[A/C]aagagaaaatgataaa	A	C	NM_014394 // upstream // 968834 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 968834 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2003357	ctgggttggaccaca[G/T]actgcttaagtcatct	G	T	NM_014394 // upstream // 951786 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 951786 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113900	aggctgttagtaagag[A/G]ccttatattaatctgt	A	G	NM_014394 // upstream // 939874 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 939874 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2003359	ttccccgtactgtaga[A/C]aactcatcagctcaga	A	C	NM_014394 // upstream // 929615 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 929615 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1890056	tgatatcaggtaaaca[C/T]actgcttgatttta	C	T	NM_014394 // upstream // 792600 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 792600 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1798275	gtaaagatggatttaa[A/G]ccactgtcatctcctg	A	G	NM_014394 // upstream // 774075 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 774075 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1653186	cactggccattactgtttgtgggta[G/T]cttccccaaggcttctgaagagaag	G	T	AK091518 // downstream // 3071201 // Hs.371620 // FLJ41984 // 387694 // FLJ41984 protein /// NM_014394 // upstream // 421743 // Hs.352656 // GHITM // 27069 // growth hormone inducible transmembrane protein	FLJ41984	FLJ41984 , rs10509480, FLJ41984 protein ,q23.1
SNP_A-1825514	taaatactgataataa[A/G]catgaatggcaagagt	A	G	NM_014394 // upstream // 725109 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 725109 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2077746	accacttggtgcagca[C/G]gaaaatgttctagttc	C	G	NM_014394 // upstream // 685237 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 685237 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2304607	gctctctttgatac[A/T]ctattgcctttctt	A	T	NM_014394 // upstream // 671042 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 671042 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1835233	tacctaactggtttga[A/G]aactcacaaaaaacta	A	G	NM_014394 // upstream // 666364 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 666364 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2003387	gcaattgcagacttta[A/T]accagtttcagcagcg	A	T	NM_014394 // upstream // 439274 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 439274 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2076849	accaaacattgtcga[A/C]tattgaattaacactt	A	C	NM_014394 // upstream // 370768 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 370768 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA: cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251450	ctcacaattgacattg[A/G]aggatgtgatgactat	A	G	NM_014394 // upstream // 350014 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 350014 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1940028	ttgcagcactaitcgc[A/G]atggcagagacagaat	A	G	NM_014394 // upstream // 341376 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 341376 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-1806265	gtccigtgtgatacac[G/T]gtcttccttagtcttt	G	T	NM_014394 // upstream // 317879 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 317879 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2115097	agggctccacagaaaa[A/G]ctgaggaagccaaagg	A	G	NM_014394 // upstream // 226307 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 226307 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2230493	ctatccacgcctgggal[A/G]aatgacctccaacttg	A	G	NM_014394 // upstream // 207440 // Hs.352656 // GHITM // 27069 // Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA. /// AL136713 // upstream // 207440 // Hs.352656 // GHITM // 27069 // Homo sapiens mRNA; cDNA DKFZp566K113 (from cl	GHITM	GHITM, Homo sapiens growth hormone inducible transmembrane protein (GHITM), q23.1
SNP_A-2195920	catgtcagcttggctal[A/G]gtggaagcagatttcc	A	G	NM_002921 // downstream // 29041 // Hs.1544 // RGR // 5995 // Homo sapiens retinal G protein coupled receptor (RGR), mRNA. /// NM_018999 // upstream // 82960 // Hs.461988 // KIAA1128 // 54462 // Homo sapiens KIAA1128 (KIAA1128), mRNA. /// ENST00000277780	RGR	RGR, Homo sapiens retinal G protein coupled receptor (RGR), q23.1
SNP_A-2003429	ccactgtgaaccttag[A/G]ccatcatgcccatgtt	A	G	ENST00000359979 // intron // 0 // — // — // —	-	q23.1
SNP_A-1673848	ggctatttcacaggaacctcagata[A/C]aatactttccctaaag cctgctct	A	C	NM_018999 // downstream // 172586 // Hs.81897 // KIAA1128 // 54462 // KIAA1128 protein	KIAA1128	KIAA1128 , rs6585876, KIAA1128 protein,q23.1
SNP_A-1670153	cttctagatctgtagaaacacatca[A/G]agcttttttaaatcccctat agccat	A	G	NM_018999 // downstream // 174588 // Hs.81897 // KIAA1128 // 54462 // KIAA1128 protein	KIAA1128	KIAA1128 , rs4131709, KIAA1128 protein,q23.1
SNP_A-2182243	cagagtaggatgctta[A/C]acaaagaaacagcttg	A	C	AB033046 // downstream // 1009735 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 28558 // — // — // — // — /// ENST00000327946 // downstream // 1009735 // — // — // —	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-1816556	gttagtctacaccaaa[C/T]aaattctgacccccaa	C	T	AB033046 // downstream // 932703 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 105590 // — // — // — // — /// ENST00000327946 // downstream // 932703 // — // — // —	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.1
SNP_A-1744011	ttctctcctggccaccagcagaaaac[C/T]gagtagagaataaact ctcaggcta	C	T	NM_018999 // downstream // 911177 // Hs.81897 // KIAA1128 // 54462 // KIAA1128 protein	KIAA1128	KIAA1128 , rs10509521, KIAA1128 protein,q23.2
SNP_A-1745017	ggtttaaatttcagtaagatttcal[A/G]ggcagaatgagacttccg gcaacta	A	G	NM_018999 // downstream // 993899 // Hs.81897 // KIAA1128 // 54462 // KIAA1128 protein	KIAA1128	KIAA1128 , rs1876895, KIAA1128 protein,q23.2
SNP_A-1668302	atgtttctctcctgagctaaaggta[C/T]ccactgaggaaaggaat ttgtggt	C	T	NM_018999 // downstream // 1017533 // Hs.81897 // KIAA1128 // 54462 // KIAA1128 protein	KIAA1128	KIAA1128 , rs869466, KIAA1128 protein,q23.2
SNP_A-1794313	ggtccacttgaacac[A/G]atgaaaacaggacaag	A	G	AB033046 // downstream // 180001 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 858292 // — // — // — // — /// ENST00000327946 // downstream // 180001 // — // — // —	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2273821	gactggcaggataatc[A/C]agaactagttagaatc	A	C	AB033046 // downstream // 179610 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 858683 // --- // --- // --- // --- /// ENST00000327946 // downstream // 179610 // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-1817044	gttattttatctggtc[C/T]acaaaacaaaccaaca	C	T	AB033046 // downstream // 175829 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000199026 // downstream // 862464 // --- // --- // --- // --- /// ENST00000327946 // downstream // 175829 // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-1758384	cttcccagagagacgaattcaggga[A/T]gttgctccacggtggc tccgaccca	A	T	AB033046 // intron // 0 // Hs.125988 // GRID1 // 2894 // glutamate receptor, ionotropic, delta 1	GRID1	GRID1 , rs10509529, glutamate receptor, ionotropic, delta 1,q23.2
SNP_A-2241003	ctgagattcttaccag[A/G]aaacccagagaagccc	A	G	AB033046 // intron // 0 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-2243878	ctgctggtccaggagc[A/G]cacttggagaaccact	A	G	AB033046 // intron // 0 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-2098891	agagctggcacaacca[C/G]agcacctctctaccca	C	G	AB033046 // intron // 0 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. ,q23.2
SNP_A-1786713	ggcttgtgaggaaggc[C/T]aaccataccatgaaag	C	T	AB033046 // intron // 0 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-1945052	ttgtgtagagtaggta[A/T]cattgcatccattttc	A	T	AB033046 // intron // 0 // Hs.530653 // GRID1 // 2894 // Homo sapiens mRNA for KIAA1220 protein, partial cds. /// ENST00000327946 // intron // 0 // --- // --- // --- // ---	GRID1	GRID1, Homo sapiens for KIAA1220 protein, partial cds. q23.2
SNP_A-2154667	attatttttgaagta[C/T]gtcaatggagtatttt	C	T	NM_015045 // intron // 0 // Hs.203099 // KIAA0261 // 23063 // Homo sapiens KIAA0261 (KIAA0261), mRNA. /// ENST00000342368 // intron // 0 // --- // --- // --- // --- /// ENST00000298767 // intron // 0 // --- // --- // --- // --- /// ENST00000263070 // intr	KIAA0261	KIAA0261, Homo sapiens KIAA0261 (KIAA0261), q23.2
SNP_A-2003648	gcccattccagtggaa[A/C]agaagtgctactttgg	A	C	NM_004897 // downstream // 105586 // Hs.121260 // MINPP1 // 9562 // Homo sapiens multiple inositol polyphosphate histidine phosphatase, 1 (MINPP1), mRNA. /// NM_004670 // upstream // 898 // Hs.524491 // PAPSS2 // 9060 // Homo sapiens 3'-phosphoadenosine 5	MINPP1	MINPP1, Homo sapiens multiple inositol polyphosphate histidine phosphatase, 1 (MINPP1), q23.31
SNP_A-1843225	tagtcctagagtagaa[C/T]catgctgtaaaataga	C	T	NM_152427 // downstream // 8062 // Hs.369431 // --- // 0 // Homo sapiens cofilin pseudogene 1 (CFLP1), mRNA. /// NM_000314 // upstream // 11366 // Hs.500466 // PTEN // 5728 // Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cance	-	-, Homo sapiens cofilin pseudogene 1 (CFLP1), q23.31
SNP_A-2050080	aaggaattttagctta[C/T]gaaagcaatcagagaa	C	T	NM_000314 // downstream // 198334 // Hs.500466 // PTEN // 5728 // Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /// NM_018363 // downstream // 110869 // Hs.149849 // C10orf59 // 55328 // Homo sapiens ch	PTEN	PTEN, Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), q23.31
SNP_A-2200276	ccaacaatgctgtgga[C/T]ctaacaagagaagaag	C	T	NM_000314 // downstream // 288706 // Hs.500466 // PTEN // 5728 // Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /// NM_018363 // downstream // 20497 // Hs.149849 // C10orf59 // 55328 // Homo sapiens chr	PTEN	PTEN, Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), q23.31
SNP_A-2043219	aactgccctctagcca[C/T]gagagttactacaatt	C	T	NM_018363 // intron // 0 // Hs.149849 // C10orf59 // 55328 // Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // --- // --- // --- // --- /// ENST00000331772 // intron // 0 // --- // --- // --- // ---	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1750357	actgaatatgttatagggatagaaa[A/C]taatgacagagaaaa aacaaaatta	A	C	NM_004190 // downstream // 8880 // Hs.159177 // LIPF // 8513 // lipase, gastric /// NM_144590 // downstream // 134884 // Hs.217484 // MGC22805 // 118932 // hypothetical protein MGC22805	LIPF	LIPF , rs303519, lipase, gastric ,q23.31
SNP_A-1880291	tctctctgttctgaaa[C/T]gccataaagagccagc	C	T	NM_018363 // intron // 0 // Hs.149849 // C10orf59 // 55328 // Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // — // — // — // — /// ENST00000331772 // intron // 0 // — // — // — // —	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-2241727	ctgatcataatttccc[A/G]aatctctcgctccatt	A	G	NM_018363 // intron // 0 // Hs.149849 // C10orf59 // 55328 // Homo sapiens chromosome 10 open reading frame 59 (C10orf59), mRNA. /// ENST00000328997 // intron // 0 // — // — // — // — /// ENST00000331772 // intron // 0 // — // — // — // —	C10orf59	C10orf59, Homo sapiens chromosome 10 open reading frame 59 (C10orf59), q23.31
SNP_A-2003716	aacactaggccataa[C/T]tagtattcataaatgt	C	T	ENST00000298799 // intron // 0 // — // — // —	-	q23.31
SNP_A-2003721	ccagtgaagagtgaca[G/T]caaaaatcatagctga	G	T	NM_004190 // upstream // 6716 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// NM_004190 // upstream // 6717 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// ENST00000298799 // downstream // 5076	LIPF	LIPF, Homo sapiens lipase, gastric (LIPF), q23.31
SNP_A-2304227	gctcctagaactcttg[A/G]aacactttcatgcctt	A	G	NM_004190 // intron // 0 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// ENST00000355843 // intron // 0 // — // — // — // — /// ENST00000238983 // intron // 0 // — // — // — // —	LIPF	LIPF, Homo sapiens lipase, gastric (LIPF), q23.31
SNP_A-1671274	ttaagattaaataaaaggactttcta[C/G]taatcaagagtgattggtt ttctt	C	G	NM_000043 // intron // 0 // Hs.82359 // TNFRSF6 // 355 // tumor necrosis factor receptor superfamily, member 6 /// NM_152871 // intron // 0 // Hs.82359 // TNFRSF6 // 355 // tumor necrosis factor receptor superfamily, member 6 /// NM_152872 // intron // 0	TNFRSF6	TNFRSF6 , rs2296600, tumor necrosis factor receptor superfamily, member 6 ,q23.31
SNP_A-1758047	ccaaacagcacatgattattcgtca[A/G]acagtttcgtattccag atactgga	A	G	NM_000043 // downstream // 215 // Hs.82359 // TNFRSF6 // 355 // tumor necrosis factor receptor superfamily, member 6 /// NM_003956 // downstream // 189938 // Hs.47357 // CH25H // 9023 // cholesterol 25-hydroxylase /// NM_152871 // downstream // 215 // Hs	TNFRSF6	TNFRSF6 , rs9325604, tumor necrosis factor receptor superfamily, member 6 ,q23.31
SNP_A-2003727	atggacgttatcaaggt[A/T]cagctgccggccatct	A	T	NM_004190 // downstream // 78585 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// NM_004190 // downstream // 78588 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// ENST00000355843 // downstream /	LIPF	LIPF, Homo sapiens lipase, gastric (LIPF), q23.31
SNP_A-2107365	agctacaaatttcca[A/G]agaatgtctacatgta	A	G	NM_004190 // downstream // 128713 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// NM_004190 // downstream // 128716 // Hs.523130 // LIPF // 8513 // Homo sapiens lipase, gastric (LIPF), mRNA. /// ENST00000355843 // downstream	LIPF	LIPF, Homo sapiens lipase, gastric (LIPF), q23.31
SNP_A-1844186	tagtttccacttatgc[A/G]aggcactgtacctaaa	A	G	NM_144590 // intron // 0 // Hs.217484 // ANKRD22 // 118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// ENST00000282676 // intron // 0 // — // — // — // —	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31
SNP_A-1932556	ttcctgtaagcaagaa[C/T]ggcaagtaacaattc	C	T	NM_144590 // intron // 0 // Hs.217484 // ANKRD22 // 118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// ENST00000282676 // intron // 0 // — // — // — // —	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31
SNP_A-1800605	gtacttagcgatatc[C/G]atgagacatctaggtg	C	G	NM_144590 // intron // 0 // Hs.217484 // ANKRD22 // 118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// ENST00000282676 // intron // 0 // — // — // — // —	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31
SNP_A-2236873	ctctagattgggaca[C/T]agggttatcatttttc	C	T	NM_144590 // intron // 0 // Hs.217484 // ANKRD22 // 118932 // Homo sapiens ankyrin repeat domain 22 (ANKRD22), mRNA. /// ENST00000282676 // intron // 0 // — // — // — // —	ANKRD22	ANKRD22, Homo sapiens ankyrin repeat domain 22 (ANKRD22), q23.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1642519	attccagtagagtaaattcataaca[A/G]tgtaagcagccttatcc agaaacag	A	G	NM_000043 // downstream // 170267 // Hs.82359 // TNFRSF6 // 355 // tumor necrosis factor receptor superfamily, member 6 /// NM_003956 // downstream // 19886 // Hs.47357 // CH25H // 9023 // cholesterol 25-hydroxylase /// NM_152871 // downstream // 170267	TNFRSF6	TNFRSF6 , rs10788637, tumor necrosis factor receptor superfamily, member 6 ,q23.31
SNP_A-2003747	tctgtagaaagctata[A/G]aagaagtcaaggtaag	A	G	NM_020799 // intron // 0 // Hs.16229 // AMSH-LP // 57559 // Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), mRNA. /// ENST00000307717 // intron // 0 // --- // --- // --- // --- /// ENST00000315250 // intron // 0	AMSH-LP	AMSH-LP, Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), q23.31
SNP_A-2060865	aatgatatgactcatg[A/G]aaagtgattagttcac	A	G	NM_020799 // intron // 0 // Hs.16229 // AMSH-LP // 57559 // Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), mRNA. /// ENST00000307717 // intron // 0 // --- // --- // --- // --- /// ENST00000315250 // intron // 0	AMSH-LP	AMSH-LP, Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), q23.31
SNP_A-2067557	acaaattagtagacaa[A/G]gctaatgcaccaaaaa	A	G	ENST00000307717 // intron // 0 // --- // --- // --- // ---	-	q23.31
SNP_A-2003752	tcttaagtgtctgcta[C/T]gatcttaatatgtctc	C	T	ENST00000307717 // intron // 0 // --- // --- // --- // ---	-	q23.31
SNP_A-2153613	attaggaatgagactc[A/G]agccatataaagtcaa	A	G	NM_020799 // downstream // 57259 // Hs.16229 // AMSH-LP // 57559 // Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), mRNA. /// NM_001613 // upstream // 27990 // Hs.500483 // ACTA2 // 59 // Homo sapiens actin, alp	AMSH-LP	AMSH-LP, Homo sapiens associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP), q23.31
SNP_A-2261360	gaaagccagcctacaa[A/G]gtcagcatgaaatcac	A	G	NM_152876 // downstream // 3777 // Hs.244139 // FAS // 355 // Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, mRNA. /// NM_152877 // downstream // 3777 // Hs.244139 // FAS // 355 // Homo sapiens tumor nec	FAS	FAS, Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, q23.31
SNP_A-2096813	agactattttgtcata[G/T]agttggtaaggcttat	G	T	NM_152876 // downstream // 73530 // Hs.244139 // FAS // 355 // Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, mRNA. /// NM_152877 // downstream // 73530 // Hs.244139 // FAS // 355 // Homo sapiens tumor n	FAS	FAS, Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, q23.31
SNP_A-2288185	gattccaaagtgacct[A/G]aaggaaattcgaattt	A	G	NM_152876 // downstream // 76278 // Hs.244139 // FAS // 355 // Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, mRNA. /// NM_152877 // downstream // 76278 // Hs.244139 // FAS // 355 // Homo sapiens tumor n	FAS	FAS, Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, q23.31
SNP_A-2170886	caataacaacaacaca[A/G]tcccaatggcattttc	A	G	NM_152876 // downstream // 97616 // Hs.244139 // FAS // 355 // Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, mRNA. /// NM_152877 // downstream // 97616 // Hs.244139 // FAS // 355 // Homo sapiens tumor n	FAS	FAS, Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, q23.31
SNP_A-1881289	tctttcaaaagttgag[A/G]acacaagaatgcagca	A	G	NM_152876 // downstream // 105385 // Hs.244139 // FAS // 355 // Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, mRNA. /// NM_152877 // downstream // 105385 // Hs.244139 // FAS // 355 // Homo sapiens tumor	FAS	FAS, Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, q23.31
SNP_A-1860237	tcagtctaactcctac[A/T]cattctttaaggattc	A	T	NM_152876 // downstream // 109731 // Hs.244139 // FAS // 355 // Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, mRNA. /// NM_152877 // downstream // 109731 // Hs.244139 // FAS // 355 // Homo sapiens tumor	FAS	FAS, Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), transcript variant 6, q23.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1688530	taatggttccgtatgtaccaacttg[C/G]aaaaagcggaaaatctattcatgga	C	G	NM_012420 // downstream // 83536 // Hs.252839 // IFIT5 // 24138 // interferon-induced protein with tetratricopeptide repeats 5 /// NM_138316 // downstream // 78460 // Hs.116122 // PANK1 // 53354 // pantothenate kinase 1 /// NM_148977 // downstream // 784	IFIT5	IFIT5 , rs10509574, interferon-induced protein with tetratricopeptide repeats 5 ,q23.31
SNP_A-1752681	aacctaaagcatatgtagttaaata[C/T]attagaagtcaagccctgattaatt	C	T	NM_138316 // intron // 0 // Hs.116122 // PANK1 // 53354 // pantothenate kinase 1 /// NM_148977 // intron // 0 // Hs.116122 // PANK1 // 53354 // pantothenate kinase 1 /// NM_148978 // intron // 0 // Hs.116122 // PANK1 // 53354 // pantothenate kinase 1	PANK1	PANK1 , rs727427, pantothenate kinase 1 ,q23.31
SNP_A-1743725	cataaaaatacaggttaattaaaca[A/G]aaatggtcagtgagggagtgaatgg	A	G	NM_016195 // intron // 0 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs10509579, M-phase phosphoprotein 1,q23.31
SNP_A-1755246	gacactgcatgataacttacgaatt[A/G]tatattgcaagttatggatgataac	A	G	NM_016195 // intron // 0 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs2077946, M-phase phosphoprotein 1,q23.31
SNP_A-1659018	catatcccatctcattccaaaaatc[A/G]gcttactggtaacttctttcaatac	A	G	NM_016195 // intron // 0 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs2026550, M-phase phosphoprotein 1,q23.31
SNP_A-2273291	gactccagaagaaggg[C/T]agcagctgttggagat	C	T	NM_148978 // upstream // 24756 // Hs.465933 // PANK1 // 53354 // Homo sapiens pantothenate kinase 1 (PANK1), transcript variant beta, mRNA. /// NM_148977 // upstream // 23075 // Hs.465933 // PANK1 // 53354 // Homo sapiens pantothenate kinase 1 (PANK1), tr	PANK1	PANK1, Homo sapiens pantothenate kinase 1 (PANK1), transcript variant beta, q23.31
SNP_A-1940599	ttgcctattgctaata[G/T]agtaaaagccacaata	G	T	NM_016195 // intron // 0 // Hs.240 // MPHOSPH1 // 9585 // Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA. /// ENST00000260753 // intron // 0 // — // — // — // — /// ENST00000360148 // intron // 0 // — // — // — // —	MPHOSPH1	MPHOSPH1, Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), q23.31
SNP_A-1896838	tgctcaatctcaggga[A/T]ctgtcaaatggttctg	A	T	NM_016195 // CDS // 0 // Hs.240 // MPHOSPH1 // 9585 // Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA. /// ENST00000260753 // CDS // 0 // — // — // — // — /// ENST00000360148 // CDS // 0 // — // — // — // —	MPHOSPH1	MPHOSPH1, Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), q23.31
SNP_A-1956832	ttttaacacaggtgga[A/G]tatcagaaaaatgtag	A	G	NM_016195 // intron // 0 // Hs.240 // MPHOSPH1 // 9585 // Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA. /// ENST00000260753 // intron // 0 // — // — // — // — /// ENST00000360148 // intron // 0 // — // — // — // —	MPHOSPH1	MPHOSPH1, Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), q23.31
SNP_A-1749359	tatgagccccactgtggatctgtac[A/G]tttccttagggcattggagcttcag	A	G	NM_016195 // downstream // 495535 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs2209672, M-phase phosphoprotein 1,q23.31
SNP_A-2247576	ctgtcttaattactca[A/G]tgactgttcaaagaaa	A	G	ENST00000277860 // downstream // 86017 // — // — // — // — /// ENST00000356117 // downstream // 631188 // — // — // — // —	-	q23.31
SNP_A-2101655	agatgatgcatttctc[A/G]gaatgtgtccccacat	A	G	ENST00000277860 // downstream // 189362 // — // — // — // — /// ENST00000356117 // downstream // 527843 // — // — // — // —	-	q23.31
SNP_A-1837765	tacttttagcagtcac[A/G]gaccccaagcccaaac	A	G	ENST00000277860 // downstream // 190305 // — // — // — // — /// ENST00000356117 // downstream // 526900 // — // — // — // —	-	q23.31
SNP_A-1749663	agatcgcataatttagtttagaata[A/C]agagatcttgtcacctttcctctaa	A	C	NM_016195 // downstream // 728687 // Hs.240 // MPHOSPH1 // 9585 // M-phase phosphoprotein 1	MPHOSPH1	MPHOSPH1 , rs10509603, M-phase phosphoprotein 1,q23.31
SNP_A-2029907	aaagatatgtacatca[A/G]cattggataactgggc	A	G	ENST00000277860 // downstream // 218101 // — // — // — // — /// ENST00000356117 // downstream // 499104 // — // — // — // —	-	q23.31
SNP_A-1926400	ttattatttgacagta[C/T]agtatggagactacag	C	T	ENST00000277860 // downstream // 277647 // — // — // — // — /// ENST00000356117 // downstream // 439558 // — // — // — // —	-	q23.31
SNP_A-2202995	ccactctggtttataa[A/G]atacctgaaatacctg	A	G	ENST00000277860 // downstream // 327562 // — // — // — // — /// ENST00000356117 // downstream // 389643 // — // — // — // —	-	q23.31
SNP_A-2281156	gagtactattacaaag[A/G]aagtgaccagatttga	A	G	ENST00000277860 // downstream // 379819 // — // — // — // — /// ENST00000356117 // downstream // 337386 // — // — // — // —	-	q23.31
SNP_A-1746278	ctctacatgtagatataggtattaa[C/T]ataagcatatgtgtaacatatatgt	C	T	AK025278 // upstream // 8676 // - // - // - // Homo sapiens cDNA: FLJ21625 fis, clone COL08015. /// NM_000872 // downstream // 34489 // Hs.73739 // HTR7 // 3363 // 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) /// NM_019859 // do	-	- , rs1936572, Homo sapiens cDNA: FLJ21625 fis, clone COL08015. ,q23.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2269867	gacaatacggcatttta[C/T]ctaccacaggcaatga	C	T	ENST00000277860 // downstream // 624267 // --- // --- // --- /// ENST00000356117 // downstream // 92938 // --- // --- // ---	-	q23.31
SNP_A-1798689	gtaaccacaagcctaa[A/C]ctgcatatgaagagca	A	C	ENST00000277860 // downstream // 635999 // --- // --- // --- /// ENST00000356117 // downstream // 81206 // --- // --- // ---	-	q23.31
SNP_A-2001342	attgtattatattaaag[C/T]caaaggtgtatattgt	C	T	ENST00000277860 // downstream // 645581 // --- // --- // --- /// ENST00000356117 // downstream // 71624 // --- // --- // ---	-	q23.31
SNP_A-2188383	cagtctttctctgtaa[A/C]tctctatacggagtgc	A	C	ENST00000277860 // downstream // 688240 // --- // --- // --- /// ENST00000356117 // downstream // 28965 // --- // --- // ---	-	q23.31
SNP_A-2051296	aagggcagacatttta[C/T]gtgtttgctaaaatcc	C	T	NM_000872 // downstream // 59 // Hs.73739 // HTR7 // 3363 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, mRNA. /// NM_019860 // downstream // 59 // Hs.73739 // HTR7 // 3363 // Homo sapi	HTR7	HTR7, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, q23.31
SNP_A-2176826	caccctacaggaaga[C/T]cttaatgacagaacat	C	T	NM_000872 // intron // 0 // Hs.73739 // HTR7 // 3363 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, mRNA. /// NM_019860 // intron // 0 // Hs.73739 // HTR7 // 3363 // Homo sapi	HTR7	HTR7, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled) (HTR7), transcript variant a, q23.31
SNP_A-2281100	gagtaattgaaatcac[A/G]ggaatgatgagactc	A	G	NM_006413 // intron // 0 // Hs.139120 // RPP30 // 10556 // Homo sapiens ribonuclease P/MRP 30kDa subunit (RPP30), mRNA. /// ENST00000277882 // intron // 0 // --- // --- // ---	RPP30	RPP30, Homo sapiens ribonuclease P,q23.31
SNP_A-2225527	ctaaaagctcgtagccc[A/G]gcaatttccctgccaa	A	G	NM_014391 // upstream // 130757 // Hs.448589 // ANKRD1 // 27063 // Homo sapiens ankyrin repeat domain 1 (cardiac muscle) (ANKRD1), mRNA. /// ENST00000277871 // upstream // 130757 // --- // --- // --- /// ENST00000333970 // upstream // 1019 // --- /	ANKRD1	ANKRD1, Homo sapiens ankyrin repeat domain 1 (cardiac muscle) (ANKRD1), q23.31
SNP_A-1780911	ggatgaatagtctaca[A/T]agcaaactccttccat	A	T	ENST00000333970 // downstream // 3711 // --- // --- // --- /// ENST00000318847 // downstream // 95494 // --- // --- // ---	-	q23.31
SNP_A-2190743	catagaaccaattgaa[A/G]tcagtctgcttttat	A	G	ENST00000333970 // downstream // 14809 // --- // --- // --- /// ENST00000318847 // downstream // 84396 // --- // --- // ---	-	q23.31
SNP_A-2030969	aaaggactagagataa[C/T]gcaagtaaatctgaca	C	T	ENST00000333970 // downstream // 20579 // --- // --- // --- /// ENST00000318847 // downstream // 78626 // --- // --- // ---	-	q23.31
SNP_A-2293809	gcagcctatctgag[A/G]ctaggactggtgagat	A	G	ENST00000333970 // downstream // 77885 // --- // --- // --- /// ENST00000318847 // downstream // 21320 // --- // --- // ---	-	q23.31
SNP_A-1714374	ttatctccaatctccacttcgtac[A/G]ccacatatacataagagtttcaaa	A	G	NM_000783 // downstream // 77974 // Hs.150595 // CYP26A1 // 1592 // cytochrome P450, family 26, subfamily A, polypeptide 1 /// NM_013451 // downstream // 150572 // Hs.362731 // FER1L3 // 26509 // fer-1-like 3, myoferlin (C. elegans) /// NM_057157 // down	CYP26A1	CYP26A1 , rs1339822, cytochrome P450, family 26, subfamily A, polypeptide 1 ,q23.33
SNP_A-1649152	ctccttcaatgtctgtagaagaaag[C/G]ctgaagggtgagctaagtccatca	C	G	NM_000783 // downstream // 177912 // Hs.150595 // CYP26A1 // 1592 // cytochrome P450, family 26, subfamily A, polypeptide 1 /// NM_013451 // downstream // 50634 // Hs.362731 // FER1L3 // 26509 // fer-1-like 3, myoferlin (C. elegans) /// NM_057157 // down	CYP26A1	CYP26A1 , rs1418754, cytochrome P450, family 26, subfamily A, polypeptide 1 ,q23.33
SNP_A-1741425	ggtttctgacttttgcaagttgcctc[C/G]atcttctccaagactgttttggaat	C	G	NM_013451 // intron // 0 // Hs.362731 // FER1L3 // 26509 // fer-1-like 3, myoferlin (C. elegans) /// NM_133337 // intron // 0 // Hs.362731 // FER1L3 // 26509 // fer-1-like 3, myoferlin (C. elegans)	FER1L3	FER1L3 , rs7867663, fer-1-like 3, myoferlin (C. elegans), q23.33
SNP_A-2083019	acgtggtgattgtcca[C/G]gacatggcaaagtggt	C	G	NM_019053 // intron // 0 // Hs.292097 // SEC15L1 // 54536 // Homo sapiens SEC15-like 1 (S. cerevisiae) (SEC15L1), mRNA. /// ENST00000260762 // intron // 0 // --- // --- // --- /// ENST00000334657 // intron // 0 // --- // --- // --- /// ENST0	SEC15L1	SEC15L1, Homo sapiens SEC15-like 1 (S. cerevisiae) (SEC15L1), q23.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1787811	gggacctgcaagagaa[C/T]gatctgtgctggcac	C	T	NM_057157 // downstream // 2435 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 2429 // Hs.150595 // CYP26A1 // 1592 // Homo sapie	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2110412	aggaattcagcccaga[A/G]aagagtcagtcagaaa	A	G	NM_057157 // downstream // 37482 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 37476 // Hs.150595 // CYP26A1 // 1592 // Homo sap	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-1943217	ttggtgaagtattatc[C/T]gaagtcaaaaagcagg	C	T	NM_057157 // downstream // 65123 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 65117 // Hs.150595 // CYP26A1 // 1592 // Homo sap	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2228854	ctagagtgtgtctgca[C/T]taagatcactggagcc	C	T	NM_057157 // downstream // 100587 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 100581 // Hs.150595 // CYP26A1 // 1592 // Homo s	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-1812579	gtggctaaaaatcaca[A/G]tgtctttgatgtactt	A	G	NM_057157 // downstream // 113391 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 113385 // Hs.150595 // CYP26A1 // 1592 // Homo s	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2059453	aatctagttcacaatg[C/T]atgagctttctctgc	C	T	NM_057157 // downstream // 115617 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 115611 // Hs.150595 // CYP26A1 // 1592 // Homo s	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-1961386	ttttttgctacccaaa[C/T]gactgtggattaagag	C	T	NM_057157 // downstream // 121245 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 121239 // Hs.150595 // CYP26A1 // 1592 // Homo s	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2047522	aagatgctggcatca[A/T]ccaaagtgaccaatga	A	T	NM_057157 // downstream // 123679 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 123673 // Hs.150595 // CYP26A1 // 1592 // Homo s	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2306827	gctgtgcagccttgga[A/G]aagttgcataacctct	A	G	NM_057157 // downstream // 125470 // Hs.150595 // CYP26A1 // 1592 // Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, mRNA. /// NM_000783 // downstream // 125464 // Hs.150595 // CYP26A1 // 1592 // Homo s	CYP26A1	CYP26A1, Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1), transcript variant 2, q23.33
SNP_A-2032417	aaagtttatttgcca[A/G]tcttaactacctat	A	G	NM_133337 // downstream // 13925 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // downstream // 13925 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3.	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-1662598	ggtccctggacggagaatccagtat[C/T]ggtggcccactggctc ctgctggcc	C	T	NM_006204 // intron // 0 // Hs.93173 // PDE6C // 5146 // phosphodiesterase 6C, cGMP-specific, cone, alpha prime	PDE6C	PDE6C , rs2077733, phosphodiesterase 6C, cGMP-specific, cone, alpha prime,q23.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1941749	ttggaatggtcaaaaa[C/G]tagaagcccaggtggt	C	G	NM_133337 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3, myoferlin (C. el	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-2004035	ccagtaatcttccttc[A/G]aattcatgaaacactg	A	G	NM_133337 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, mRNA. /// NM_013451 // intron // 0 // Hs.500572 // FER1L3 // 26509 // Homo sapiens fer-1-like 3, myoferlin (C. el	FER1L3	FER1L3, Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), transcript variant 2, q23.33
SNP_A-2029005	aaagaaaatctgtcta[C/G]agtgctgaagcagcta	C	G	NM_018131 // intron // 0 // Hs.14559 // C10orf3 // 55165 // Homo sapiens chromosome 10 open reading frame 3 (C10orf3), mRNA. /// ENST00000347778 // intron // 0 // — // — // — // — /// ENST00000358339 // intron // 0 // — // — // — // — ///	C10orf3	C10orf3, Homo sapiens chromosome 10 open reading frame 3 (C10orf3), q23.33
SNP_A-2004073	tgatattcctgcccag[A/G]aacttaagaactgccc	A	G	ENST00000347778 // intron // 0 // — // — // — // —	-	q23.33
SNP_A-2004076	acattcttaaaagcca[A/G]tgctacagtgggaatg	A	G	ENST00000347778 // intron // 0 // — // — // — // —	-	q23.33
SNP_A-2069741	acacactgggactacc[A/G]ctgctctgtgagacaa	A	G	ENST00000347778 // intron // 0 // — // — // — // —	-	q23.33
SNP_A-1866073	tcccagacctccacac[C/T]attagtccacgtgaat	C	T	NM_005097 // intron // 0 // Hs.533670 // LGI1 // 9211 // Homo sapiens leucine-rich, glioma inactivated 1 (LGI1), mRNA. /// ENST00000347778 // intron // 0 // — // — // — // — /// ENST00000265991 // intron // 0 // — // — // — // —	LGI1	LGI1, Homo sapiens leucine-rich, glioma inactivated 1 (LGI1), q23.33
SNP_A-1749549	agatggcactcctctagtcatctca[C/T]atcccaagtcttctcagaccccacc	C	T	NM_006434 // intron // 0 // Hs.108924 // SORBS1 // 10580 // sorbin and SH3 domain containing 1 /// NM_015385 // intron // 0 // Hs.108924 // SORBS1 // 10580 // sorbin and SH3 domain containing 1	SORBS1	SORBS1 , rs7085635, sorbin and SH3 domain containing 1 ,q24.1
SNP_A-1802666	gtatgaccagagctga[A/G]aacagattatgtgaaa	A	G	NM_000770 // intron // 0 // Hs.282871 // CYP2C8 // 1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// ENST00000285985 // intron // 0 // — // — // — // —	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-1897316	tgctcttgatcatgga[C/T]aaatagcaattctacc	C	T	NM_000770 // intron // 0 // Hs.282871 // CYP2C8 // 1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// ENST00000285985 // intron // 0 // — // — // — // —	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-2211529	ccctcaaggtcataaa[G/T]tcccaactggtcatta	G	T	NM_000770 // upstream // 275 // Hs.282871 // CYP2C8 // 1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // upstream // 347 // Hs.282871 // CYP2C8 // 1558 // Homo sapiens cyt	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-2004147	tacccagcctttacc[A/G]ctatgcaatataggca	A	G	NM_000770 // upstream // 113331 // Hs.282871 // CYP2C8 // 1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // upstream // 113403 // Hs.282871 // CYP2C8 // 1558 // Homo sapie	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-2164062	caaaagcacgggtaac[C/G]aatgcaaaaattgata	C	G	NM_000770 // upstream // 116281 // Hs.282871 // CYP2C8 // 1558 // Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA. /// NM_030878 // upstream // 116353 // Hs.282871 // CYP2C8 // 1558 // Homo sapie	CYP2C8	CYP2C8, Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 8 (CYP2C8), transcript variant Hp1-1, q23.33
SNP_A-1886811	tgactggaatcaatta[C/T]ctagcaaacaatttgg	C	T	NM_015385 // intron // 0 // Hs.38621 // SORBS1 // 10580 // Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), mRNA. /// NM_006434 // intron // 0 // Hs.38621 // SORBS1 // 10580 // Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), mRNA. /// A	SORBS1	SORBS1, Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2004168	tcaaaatcacttaccc[A/G]atattgatcagactct	A	G	NM_015385 // intron // 0 // Hs.38621 // SORBS1 // 10580 // Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), mRNA. /// NM_006434 // intron // 0 // Hs.38621 // SORBS1 // 10580 // Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), mRNA. /// A	SORBS1	SORBS1, Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), q24.1
SNP_A-2239781	ctgaaatccaggcttc[C/T]agacttttcctgcct	C	T	NM_015385 // upstream // 18795 // Hs.38621 // SORBS1 // 10580 // Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), mRNA. /// NM_006434 // upstream // 18795 // Hs.38621 // SORBS1 // 10580 // Homo sapiens sorbin and SH3 domain containing 1 (SORBS1).	SORBS1	SORBS1, Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), q24.1
SNP_A-1797348	ggtgtggagaaaaaa[C/G]aacgcttatacacaat	C	G	NM_001776 // intron // 0 // Hs.523173 // ENTPD1 // 953 // Homo sapiens ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), mRNA. /// ENST00000260756 // intron // 0 // --- // --- // ---	ENTPD1	ENTPD1, Homo sapiens ectonucleoside triphosphate diphosphohydrolase 1 (ENTPD1), q24.1
SNP_A-2275488	gagaatttgcaaagaa[C/T]gggagacaccttatt	C	T	NM_013314 // intron // 0 // Hs.444049 // BLNK // 29760 // Homo sapiens B-cell linker (BLNK), mRNA. /// ENST00000314967 // intron // 0 // --- // --- // --- /// ENST00000224337 // intron // 0 // --- // --- // ---	BLNK	BLNK, Homo sapiens B-cell linker (BLNK), q24.1
SNP_A-2132399	atagtccagaagggaa[A/G]atagattattgtatta	A	G	NM_013314 // intron // 0 // Hs.444049 // BLNK // 29760 // Homo sapiens B-cell linker (BLNK), mRNA. /// ENST00000314967 // intron // 0 // --- // --- // --- /// ENST00000224337 // intron // 0 // --- // --- // ---	BLNK	BLNK, Homo sapiens B-cell linker (BLNK), q24.1
SNP_A-2004243	aacaaacaaacaaaaaa[C/T]ctgatcttgcaatttg	C	T	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2004244	agctagttgaagaata[C/T]gattgccttacaaatg	C	T	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2236279	ctccttttcattaaaa[A/T]tggcccagcagggact	A	T	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2122521	agtgctgaagtgctga[C/G]tagcggtgttcctaat	C	G	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2232899	ctcagaaggcaagcca[G/T]acttcattaggtcatag	G	T	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2090725	acttacttaagctct[A/T]actaaaggaagcatct	A	T	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2110333	aggaatctgacaagga[C/T]gagagaattctggctt	C	T	NM_012465 // intron // 0 // Hs.154296 // TLL2 // 7093 // Homo sapiens tolloid-like 2 (TLL2), mRNA. /// ENST00000265996 // intron // 0 // --- // --- // --- /// ENST00000357947 // intron // 0 // --- // --- // ---	TLL2	TLL2, Homo sapiens tolloid-like 2 (TLL2), q24.1
SNP_A-2156921	attcttgagagacgac[C/T]ccaggaaaaggtcaat	C	T	NM_152309 // intron // 0 // Hs.310456 // PIK3AP1 // 118788 // Homo sapiens phosphoinositide-3-kinase adaptor protein 1 (PIK3AP1), mRNA. /// ENST00000339364 // intron // 0 // --- // --- // --- /// ENST00000318798 // intron // 0 // --- // ---	PIK3AP1	PIK3AP1, Homo sapiens phosphoinositide-3-kinase adaptor protein 1 (PIK3AP1), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1935229	ttctgcccaaccattc[A/G]cttatctgtccgcaca	A	G	NM_152309 // intron // 0 // Hs.310456 // PIK3AP1 // 118788 // Homo sapiens phosphoinositide-3-kinase adaptor protein 1 (PIK3AP1), mRNA. /// ENST00000339364 // intron // 0 // --- // --- // --- /// ENST00000318798 // intron // 0 // --- // --- // ---	PIK3AP1	PIK3AP1, Homo sapiens phosphoinositide-3-kinase adaptor protein 1 (PIK3AP1), q24.1
SNP_A-1649298	gatccaattaagactggatcccct[G/T]agataatgagtggaag agtgtggtg	G	T	NM_012083 // upstream // 21251 // Hs.140720 // FRAT2 // 23401 // frequently rearranged in advanced T-cell lymphomas 2 /// NM_015179 // downstream // 750 // Hs.434251 // KIAA0690 // 23223 // KIAA0690	FRAT2	FRAT2, rs10509713, frequently rearranged in advanced T-cell lymphomas 2, q24.1
SNP_A-1795873	ggtggctttctaacc[A/C]gggggaatagcttcag	A	C	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2315009	ggagtttctaaaagtc[A/C]aaatgcacaaagaga	A	C	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2180223	cagaaagacaaccata[C/T]ccggaatctggtccgg	C	T	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-1806468	gtcgctgcagatgtgg[C/T]atttctctcccaaaga	C	T	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2237952	ctctgagctatcagtc[A/G]caatgcaagaggggagc	A	G	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2261611	gaaaggtctttgagaa[C/T]aggaattggtccatga	C	T	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2213511	ccggttctgtcccacc[A/G]aaactattagatgtca	A	G	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-1945587	ttgtctctgtggcccg[C/G]agtatgtacctccctg	C	G	NM_003061 // intron // 0 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// ENST00000266058 // intron // 0 // --- // --- // --- /// ENST00000314867 // intron // 0 // --- // --- // ---	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2100588	agatacaggaaacccca[A/G]tgaacccaaagcacag	A	G	NM_003061 // upstream // 4794 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// NM_032900 // downstream // 31462 // Hs.80305 // ARHGAP19 // 84986 // Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), mRNA.	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2052712	aagtatttttgggaaga[A/G]atggcaaatccatatc	A	G	NM_003061 // upstream // 23385 // Hs.500712 // SLIT1 // 6585 // Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA. /// NM_032900 // downstream // 12871 // Hs.80305 // ARHGAP19 // 84986 // Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), mRNA	SLIT1	SLIT1, Homo sapiens slit homolog 1 (Drosophila) (SLIT1), q24.1
SNP_A-2046742	aagaggaaaaattgata[C/T]actgtcatctgttta	C	T	NM_032900 // intron // 0 // Hs.80305 // ARHGAP19 // 84986 // Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), mRNA. /// ENST00000355366 // intron // 0 // --- // --- // --- /// ENST00000355695 // intron // 0 // --- // --- // ---	ARHGAP19	ARHGAP19, Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2253486	ctcttcacagtttca[C/T]agatagatttattctt	C	T	NM_032900 // intron // 0 // Hs.80305 // ARHGAP19 // 84986 // Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), mRNA. /// ENST00000355366 // intron // 0 // --- // --- // --- /// ENST00000355695 // intron // 0 // --- // --- // --- ///	ARHGAP19	ARHGAP19, Homo sapiens Rho GTPase activating protein 19 (ARHGAP19), q24.1
SNP_A-2238697	ctctgtttctctgggc[A/G]agcagaaagcaaaagg	A	G	NM_015179 // intron // 0 // Hs.434251 // KIAA0690 // 23223 // Homo sapiens KIAA0690 (KIAA0690), mRNA. /// ENST00000315563 // intron // 0 // --- // --- // --- /// ENST00000266051 // intron // 0 // --- // --- // --- ///	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-1809890	gtgagatagcattga[A/T]gttctaaacagcccta	A	T	NM_015179 // intron // 0 // Hs.434251 // KIAA0690 // 23223 // Homo sapiens KIAA0690 (KIAA0690), mRNA. /// ENST00000315563 // intron // 0 // --- // --- // --- /// ENST00000266051 // intron // 0 // --- // --- // --- ///	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-2001365	agttttatccattca[A/C]acccccctcaatctggc	A	C	NM_015179 // intron // 0 // Hs.434251 // KIAA0690 // 23223 // Homo sapiens KIAA0690 (KIAA0690), mRNA. /// ENST00000315563 // intron // 0 // --- // --- // --- /// ENST00000266051 // intron // 0 // --- // --- // --- ///	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-2263380	gaacatctcctctgct[G/T]aagtactgaggtag	G	T	NM_015179 // intron // 0 // Hs.434251 // KIAA0690 // 23223 // Homo sapiens KIAA0690 (KIAA0690), mRNA. /// ENST00000315563 // intron // 0 // --- // --- // --- /// ENST00000266051 // intron // 0 // --- // --- // --- ///	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-1935638	ttctgtatctgctaaa[C/T]tggaaggactgccct	C	T	NM_015179 // intron // 0 // Hs.434251 // KIAA0690 // 23223 // Homo sapiens KIAA0690 (KIAA0690), mRNA. /// ENST00000315563 // intron // 0 // --- // --- // --- /// ENST00000266051 // intron // 0 // --- // --- // --- ///	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-2218881	cctgggtaccgggtg[A/G]aagagattgtgctcag	A	G	NM_015179 // upstream // 6339 // Hs.434251 // KIAA0690 // 23223 // Homo sapiens KIAA0690 (KIAA0690), mRNA. /// NM_002629 // upstream // 18591 // Hs.447492 // PGAM1 // 5223 // Homo sapiens phosphoglycerate mutase 1 (brain) (PGAM1), mRNA. /// ENST00000031556	KIAA0690	KIAA0690, Homo sapiens KIAA0690 (KIAA0690), q24.1
SNP_A-1848726	tatgagtcatgcctac[C/T]ggcccgaggctgcctc	C	T	NM_024954 // intron // 0 // Hs.500724 // UBTD1 // 80019 // Homo sapiens ubiquitin domain containing 1 (UBTD1), mRNA. /// ENST00000298807 // intron // 0 // --- // --- // ---	UBTD1	UBTD1, Homo sapiens ubiquitin domain containing 1 (UBTD1), q24.1
SNP_A-2281954	gagtgctcaattgcgc[A/G]ccatatttatatattg	A	G	NM_021732 // intron // 0 // Hs.23918 // AVPI1 // 60370 // Homo sapiens arginine vasopressin-induced 1 (AVPI1), mRNA. /// ENST00000239046 // intron // 0 // --- // --- // ---	AVPI1	AVPI1, Homo sapiens arginine vasopressin-induced 1 (AVPI1), q24.2
SNP_A-1809493	gtgagacagcaatgaa[C/G]agaacaggcaaggtcc	C	G	NM_003015 // upstream // 30474 // Hs.279565 // SFRP5 // 6425 // Homo sapiens secreted frizzled-related protein 5 (SFRP5), mRNA. /// ENST00000266066 // upstream // 30474 // --- // --- // --- /// ENST00000285621 // upstream // 57001 // --- // --- //	SFRP5	SFRP5, Homo sapiens secreted frizzled-related protein 5 (SFRP5), q24.2
SNP_A-2181903	cagagcctcagagtgg[A/G]aggtgttggtattgc	A	G	NM_018058 // intron // 0 // Hs.500741 // CRTAC1 // 55118 // Homo sapiens cartilage acidic protein 1 (CRTAC1), mRNA. /// ENST00000210816 // intron // 0 // --- // --- // --- /// ENST00000298819 // intron // 0 // --- // --- // --- /// ENST00000	CRTAC1	CRTAC1, Homo sapiens cartilage acidic protein 1 (CRTAC1), q24.2
SNP_A-1744845	ttgttatctctggtagcaggatta[C/T]agagcatttctttttaagaa tatt	C	T	NM_021828 // intron // 0 // Hs.302018 // HPSE2 // 60495 // heparanase 2	HPSE2	HPSE2, rs716838, heparanase 2,q24.2
SNP_A-2288926	gattagtgcccatga[C/T]gatgatgaattattag	C	T	NM_014472 // downstream // 633 // Hs.419800 // C10orf28 // 27291 // Homo sapiens chromosome 10 open reading frame 28 (C10orf28), mRNA. /// NM_032211 // downstream // 2168 // Hs.306814 // LOXL4 // 84171 // Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA. /	C10orf28	C10orf28, Homo sapiens chromosome 10 open reading frame 28 (C10orf28), q24.2
SNP_A-2237599	ctctctccagctaaaa[G/T]atcaggaaaagggcag	G	T	NM_032211 // upstream // 14430 // Hs.306814 // LOXL4 // 84171 // Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA. /// NM_032709 // downstream // 100886 // Hs.238303 // C10orf33 // 84795 // Homo sapiens chromosome 10 open reading frame 33 (C10orf33), mRNA.	LOXL4	LOXL4, Homo sapiens lysyl oxidase-like 4 (LOXL4), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2236562	ctcgttctttttcacg[G/T]ccatgtagattccata	G	T	NM_032211 // upstream // 19968 // Hs.306814 // LOXL4 // 84171 // Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA. /// NM_032709 // downstream // 95348 // Hs.238303 // C10orf33 // 84795 // Homo sapiens chromosome 10 open reading frame 33 (C10orf33), mRNA.	LOXL4	LOXL4, Homo sapiens lysyl oxidase-like 4 (LOXL4), q24.2
SNP_A-2021545	aaaaaatcaaacctga[A/G]tataatgacatctgta	A	G	NM_032211 // upstream // 88190 // Hs.306814 // LOXL4 // 84171 // Homo sapiens lysyl oxidase-like 4 (LOXL4), mRNA. /// NM_032709 // downstream // 27126 // Hs.238303 // C10orf33 // 84795 // Homo sapiens chromosome 10 open reading frame 33 (C10orf33), mRNA.	LOXL4	LOXL4, Homo sapiens lysyl oxidase-like 4 (LOXL4), q24.2
SNP_A-2124244	agttatattgagaata[C/G]agaacactgttcatac	C	G	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2175938	caccaaaatgcctcat[A/G]acgtttactaaatagt	A	G	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2268242	gaatgagcagaataaa[C/G]cacctgaagtataaaa	C	G	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2040816	aaccccacaatattaa[A/C]tcaatgtaattcacca	A	C	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2074129	acataaaatatgctaa[A/C]aataatgacagttgat	A	C	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-1810541	gtgcaaaacagtatcg[A/T]atgttgcatgcaaatc	A	T	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-2309656	ggaaagagttggacca[A/C]gtatctaatactccaa	A	C	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-1939184	ttgatatcactgagtc[C/T]ctgtggcacaactcat	C	T	NM_021828 // intron // 0 // Hs.500750 // HPSE2 // 60495 // Homo sapiens heparanase 2 (HPSE2), mRNA. /// ENST00000347890 // intron // 0 // — // — // — // — /// ENST00000329594 // intron // 0 // — // — // — // — /// ENST00000308616 // intron	HPSE2	HPSE2, Homo sapiens heparanase 2 (HPSE2), q24.2
SNP_A-1837505	tacttgatcctggtta[C/T]gaatagtcagcttgtt	C	T	NM_002079 // upstream // 22934 // Hs.500756 // GOT1 // 2805 // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA. /// NM_145285 // upstream // 79430 // Hs.243272 // NKX2-3 // 159296 // Homo sapiens NK2 t	GOT1	GOT1, Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), q24.2
SNP_A-2076032	acattatgaggaagaa[G/T]atgaaactcaaaggta	G	T	NM_002079 // upstream // 39836 // Hs.500756 // GOT1 // 2805 // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA. /// NM_145285 // upstream // 62528 // Hs.243272 // NKX2-3 // 159296 // Homo sapiens NK2 t	GOT1	GOT1, Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1788529	gggataggctagatca[A/G]agatgccagggagaga	A	G	NM_002079 // upstream // 67445 // Hs.500756 // GOT1 // 2805 // Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA. /// NM_145285 // upstream // 34919 // Hs.243272 // NKX2-3 // 159296 // Homo sapiens NK2 t	GOT1	GOT1, Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), q24.2
SNP_A-2262045	gaaatagtctataaaa[C/T]gaagcggcagtaggag	C	T	NM_015960 // intron // 0 // Hs.16606 // CUTC // 51076 // Homo sapiens cutC copper transporter homolog (E.coli) (CUTC), mRNA. /// ENST00000312750 // intron // 0 // --- // --- // --- // ---	CUTC	CUTC, Homo sapiens cutC copper transporter homolog (E.coli) (CUTC), q24.2
SNP_A-1642093	agaaagagggaattatctcctggag[C/T]agttcgtaaagcatac tgttttatg	C	T	NM_006459 // intron // 0 // Hs.285818 // C10orf69 // 10613 // chromosome 10 open reading frame 69	C10orf69	C10orf69 , rs10509741, chromosome 10 open reading frame 69,q24.2
SNP_A-2154553	attattgtccaaagaa[A/T]ataccagcatgatgca	A	T	NM_001278 // intron // 0 // Hs.198998 // CHUK // 1147 // Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), mRNA. /// ENST00000266054 // intron // 0 // --- // --- // --- // ---	CHUK	CHUK, Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), q24.31
SNP_A-1821987	gttttcagtgacatcc[A/G]gaggctgttttaccag	A	G	NM_018294 // CDS // 0 // Hs.215502 // CWF19L1 // 55280 // Homo sapiens CWF19-like 1, cell cycle control (S. pombe) (CWF19L1), mRNA. /// ENST00000354105 // CDS // 0 // --- // --- // --- // --- /// ENST00000338048 // 5UTR // 0 // --- // --- // --- // ---	CWF19L1	CWF19L1, Homo sapiens CWF19-like 1, cell cycle control (S. pombe) (CWF19L1), q24.31
SNP_A-2004502	gtaggaggatcaagca[A/G]tgaacttggtagtgaa	A	G	NM_018294 // intron // 0 // Hs.215502 // CWF19L1 // 55280 // Homo sapiens CWF19-like 1, cell cycle control (S. pombe) (CWF19L1), mRNA. /// ENST00000354105 // intron // 0 // --- // --- // --- // --- /// ENST00000338048 // intron // 0 // --- // --- // --- /	CWF19L1	CWF19L1, Homo sapiens CWF19-like 1, cell cycle control (S. pombe) (CWF19L1), q24.31
SNP_A-2157322	attgagaaactaggcc[G/T]atctattgtgagcagc	G	T	NM_016112 // CDS // 0 // Hs.159241 // PKD2L1 // 9033 // Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), mRNA. /// ENST00000318222 // CDS // 0 // --- // --- // --- // --- /// ENST00000353274 // CDS // 0 // --- // --- // --- // --- /// ENST00000033	PKD2L1	PKD2L1, Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), q24.31
SNP_A-1819383	gttggcctctagtaaa[C/T]acctcatccatcaagc	C	T	NM_016112 // intron // 0 // Hs.159241 // PKD2L1 // 9033 // Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), mRNA. /// ENST00000318222 // intron // 0 // --- // --- // --- // --- /// ENST00000353274 // intron // 0 // --- // --- // --- // --- /// EN	PKD2L1	PKD2L1, Homo sapiens polycystic kidney disease 2-like 1 (PKD2L1), q24.31
SNP_A-2288133	gattcaggccagtaat[C/T]agaatgaagtttgggg	C	T	NM_003393 // intron // 0 // Hs.421281 // WNT8B // 7479 // Homo sapiens wingless-type MMTV integration site family, member 8B (WNT8B), mRNA. /// ENST00000343737 // intron // 0 // --- // --- // --- // ---	WNT8B	WNT8B, Homo sapiens wingless-type MMTV integration site family, member 8B (WNT8B), q24.31
SNP_A-1819637	gttgtaggtgtcatta[C/T]gtgtgactgtcatagt	C	T	NM_017902 // downstream // 19654 // Hs.500788 // HIF1AN // 55662 // Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), mRNA. /// NM_003987 // upstream // 175923 // Hs.155644 // PAX2 // 5076 // Homo sapiens paired box gene 2 (PAX2),	HIF1AN	HIF1AN, Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), q24.31
SNP_A-2243223	ctgcctgaaacccagc[A/G]ctaggtagtgtagcca	A	G	NM_017902 // downstream // 81985 // Hs.500788 // HIF1AN // 55662 // Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), mRNA. /// NM_003987 // upstream // 113592 // Hs.155644 // PAX2 // 5076 // Homo sapiens paired box gene 2 (PAX2),	HIF1AN	HIF1AN, Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), q24.31
SNP_A-2208483	cccacctgcaatgccc[A/G]aatgagcagcggctcc	A	G	NM_030971 // intron // 0 // Hs.283844 // SFXN3 // 81855 // Homo sapiens similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA. /// ENST00000224807 // intron // 0 // --- // --- // --- // ---	SFXN3	SFXN3, Homo sapiens similar to rat tricarboxylate carrier-like protein (BA108L7.2), q24.31
SNP_A-2137569	atcatcggaagtacac[A/G]cagtctcagacacaaa	A	G	NM_030929 // downstream // 5059 // Hs.512762 // KAZALD1 // 81621 // Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), mRNA. /// ENST00000224809 // downstream // 5059 // --- // --- // --- // --- /// ENST00000313664 // downstream // 5115	KAZALD1	KAZALD1, Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), q24.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2139274	atcctgaggttctccc[C/T]atcctacaccatgtcc	C	T	NM_030929 // downstream // 17375 // Hs.512762 // KAZALD1 // 81621 // Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), mRNA. /// ENST00000224809 // downstream // 17375 // — // — // — // — /// ENST00000313664 // downstream // 17	KAZALD1	KAZALD1, Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), q24.31
SNP_A-1907183	tggtttctagtcctct[C/T]aacccatcaaggtgga	C	T	NM_030929 // downstream // 22425 // Hs.512762 // KAZALD1 // 81621 // Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), mRNA. /// ENST00000224809 // downstream // 22425 // — // — // — // — /// ENST00000313664 // downstream // 22	KAZALD1	KAZALD1, Homo sapiens Kazal-type serine protease inhibitor domain 1 (KAZALD1), q24.31
SNP_A-2116626	aggtcaggaaccctgc[A/G]acatactctcttctcc	A	G	NM_022039 // upstream // 32355 // Hs.500822 // SHFM3 // 6468 // Homo sapiens split hand/foot malformation (ectrodactyly) type 3 (SHFM3), mRNA. /// NM_033165 // downstream // 42516 // Hs.57710 // FGF8 // 2253 // Homo sapiens fibroblast growth factor 8 (and	SHFM3	SHFM3, Homo sapiens split hand,q24.32
SNP_A-2024878	aaaagttgacactgat[A/G]acaataaagcttttct	A	G	NM_024541 // intron // 0 // Hs.16004 // C10orf76 // 79591 // Homo sapiens chromosome 10 open reading frame 76 (C10orf76), mRNA. /// ENST00000263485 // intron // 0 // — // — // — // —	C10orf76	C10orf76, Homo sapiens chromosome 10 open reading frame 76 (C10orf76), q24.32
SNP_A-2001395	tcacaggaccaagcac[A/G]atgccttgcacaaagc	A	G	NM_178858 // downstream // 26429 // Hs.44070 // SFXN2 // 118980 // Homo sapiens sideroflexin 2 (SFXN2), mRNA. /// NM_017787 // upstream // 10635 // Hs.500897 // C10orf26 // 54838 // Homo sapiens chromosome 10 open reading frame 26 (C10orf26), mRNA. /// EN	SFXN2	SFXN2, Homo sapiens sideroflexin 2 (SFXN2), q24.32
SNP_A-2256545	ctttatttttttatcc[A/G]cagtgtacatcatata	A	G	NM_012229 // intron // 0 // Hs.158209 // NT5C2 // 22978 // Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), mRNA. /// ENST00000343289 // intron // 0 // — // — // — // —	NT5C2	NT5C2, Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), q24.33
SNP_A-1755552	tcagttgttctttttctgtcttccc[C/T]attatcagcagctgttataagccct	C	T	NM_014631 // upstream // 20098 // - // - // - // - /// NM_024928 // downstream // 168823 // Hs.273387 // OBFC1 // 79991 // oligonucleotide/oligosaccharide-binding fold containing 1	-	- , rs7895096, - ,q24.33
SNP_A-2176141	caccacattctcagtg[C/T]accgtgacttccttcc	C	T	NM_024928 // downstream // 54924 // Hs.134491 // OBFC1 // 79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. /// ENST00000315994 // upstream // 154104 // — // — // — // — /// ENST00000224947 // upstream	OBFC1	OBFC1, Homo sapiens oligonucleotide,q24.33
SNP_A-2313642	ggagatggctacacaa[A/G]tgtgaaaggatggttg	A	G	NM_024928 // downstream // 1324 // Hs.134491 // OBFC1 // 79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. /// ENST00000315994 // upstream // 207704 // — // — // — // — /// ENST00000224947 // upstream /	OBFC1	OBFC1, Homo sapiens oligonucleotide,q24.33
SNP_A-2004674	ctccaccagaaaccac[A/G]aaggctaatgttctag	A	G	NM_024928 // intron // 0 // Hs.134491 // OBFC1 // 79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. /// ENST00000224950 // intron // 0 // — // — // — // —	OBFC1	OBFC1, Homo sapiens oligonucleotide q24.33
SNP_A-1959098	ttttgaagactgtttc[A/T]ctcacatggttgccac	A	T	NM_024928 // intron // 0 // Hs.134491 // OBFC1 // 79991 // Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 1 (OBFC1), mRNA. /// ENST00000224950 // intron // 0 // — // — // — // —	OBFC1	OBFC1, Homo sapiens oligonucleotide,q24.33
SNP_A-2080042	accgagtgagccttcc[G/T]gcaattgactaatgtg	G	T	NM_000494 // intron // 0 // Hs.117938 // COL17A1 // 1308 // Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, mRNA. /// NM_130778 // intron // 0 // Hs.117938 // COL17A1 // 1308 // Homo sapiens collagen, type XVII, alpha 1 (COL1	COL17A1	COL17A1, Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2129641	atacagattataaggat[A/C]agcaataagtaatgtg	A	C	NM_000494 // intron // 0 // Hs.117938 // COL17A1 // 1308 // Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, mRNA. /// NM_130778 // intron // 0 // Hs.117938 // COL17A1 // 1308 // Homo sapiens collagen, type XVII, alpha 1 (COL1	COL17A1	COL17A1, Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, q25.1
SNP_A-1843828	tagttacaggtccaac[A/G]gagttcactctaagac	A	G	NM_000494 // upstream // 18928 // Hs.117938 // COL17A1 // 1308 // Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, mRNA. /// NM_130778 // upstream // 18928 // Hs.117938 // COL17A1 // 1308 // Homo sapiens collagen, type XVII, a	COL17A1	COL17A1, Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, q25.1
SNP_A-1953189	tttctttctcggtgac[A/C]gtaggagtggaaatga	A	C	NM_033397 // intron // 0 // Hs.523252 // KIAA1754 // 85450 // Homo sapiens KIAA1754 (KIAA1754), mRNA. /// ENST00000337478 // intron // 0 // — // — // — /// ENST00000278071 // intron // 0 // — // — // — // — /// ENST00000358187 // intr	KIAA1754	KIAA1754, Homo sapiens KIAA1754 (KIAA1754), q25.1
SNP_A-1915213	tgttcacctctttaac[C/T]gcaactgaatggatca	C	T	ENST00000357719 // intron // 0 // — // — // — // — /// ENST00000312902 // intron // 0 // — // — // — /// ENST00000239104 // intron // 0 // — // — // — // — // —	-	q25.1
SNP_A-2092138	agaaactgttacaac[A/C]aattagagactgggta	A	C	ENST00000357719 // intron // 0 // — // — // — /// ENST00000239104 // intron // 0 // — // — // —	-	q25.1
SNP_A-2203115	ccactgctgtaaataa[C/T]agtgaagtgaataccc	C	T	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2222930	cgcactgacagcctcc[A/G]cgatgggaagatcaca	A	G	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1715397	aggtactaggagggtcagagagaaa[C/T]gcctgcttacctcta ggaattggtc	C	T	NM_014978 // intron // 0 // Hs.348526 // SORCS3 // 22986 // sortilin-related VPS10 domain containing receptor 3	SORCS3	SORCS3, rs697192, sortilin-related VPS10 domain containing receptor 3, q25.1
SNP_A-1934629	ttctctgaaccccaga[C/T]tcatttatccagctca	C	T	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2310976	ggaaggaaatcatac[A/G]gctctaggctctaact	A	G	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1842080	tagggcagtggtcttat[A/C]aagggaatttgccaga	A	C	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2004791	cgcatcctgatattcc[A/T]acagagtcctgacttc	A	T	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2091212	acttgtttctctgta[A/T]attcccaaccaatatg	A	T	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2171309	caatatgtaagtaaat[C/G]agtacagttgcgtgcc	C	G	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2179865	cactttagaaaaccgg[C/T]agtgtctcctaaagct	C	T	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2124579	agttcctactctctag[A/G]catggcttcttctcc	A	G	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1809122	gtgacatattgagtc[A/T]acctgaatattcagaa	A	T	NM_014978 // intron // 0 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// ENST00000286935 // intron // 0 // — // — // — // —	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1716845	acaggtttaggtagagaagaaagg[C/T]aaaatgcaagcagat ttatgtcat	C	T	NM_014978 // downstream // 965689 // Hs.346526 // SORCS3 // 22986 // sortilin-related VPS10 domain containing receptor 3 /// NM_052918 // downstream // 342739 // Hs.348923 // SORCS1 // 114815 // sortilin-related VPS10 domain containing receptor 1	SORCS3	SORCS3, rs7068381, sortilin-related VPS10 domain containing receptor 3, q25.1
SNP_A-1901498	tggatttctatagaac[A/T]gcataatgccatgctt	A	T	NM_014978 // downstream // 659099 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 651190 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1956401	ttgttatttttttgat[C/T]gctacttcctaatttt	C	T	NM_014978 // downstream // 681868 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 628421 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2126236	ataaaaagcagtgata[A/C]ccaggttgtgtactgt	A	C	NM_014978 // downstream // 747487 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 562802 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1925730	ttatgcatctggtatc[A/G]aataaaaaattggaaag	A	G	NM_014978 // downstream // 762884 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 547405 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1923237	ttagctggctttgaac[A/G]agttcctcttggaat	A	G	NM_014978 // downstream // 798166 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 512123 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2038634	aacagacaccaggacc[A/G]ccataccacacactgc	A	G	NM_014978 // downstream // 921810 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 388479 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-2001411	aaacacatagatggta[A/C]ataaaggagataaggt	A	C	NM_014978 // downstream // 956009 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 354280 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related V	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1
SNP_A-1953093	tttcttggtctagcaa[A/G]aaatcattggtggaga	A	G	NM_014978 // downstream // 1010818 // Hs.546349 // SORCS3 // 22986 // Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), mRNA. /// NM_052918 // downstream // 299471 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related	SORCS3	SORCS3, Homo sapiens sortilin-related VPS10 domain containing receptor 3 (SORCS3), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1658992	ttgtagcacatggagagccctcgtg[A/G]agagcaaaaaactttttgtaaattt	A	G	NM_052918 // intron // 0 // Hs.348923 // SORCS1 // 114815 // sortilin-related VPS10 domain containing receptor 1	SORCS1	SORCS1, rs1023024, sortilin-related VPS10 domain containing receptor 1,q25.1
SNP_A-2001417	ggtggatcctctgtaa[G/T]gcagagcaacatgatt	G	T	NM_052918 // intron // 0 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron // 0 // — // — // — /// ENST00000344440 // intron // 0 // — // — /	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2302271	gctaacaacctaagat[C/G]aacccaagacccaaga	C	G	NM_052918 // intron // 0 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron // 0 // — // — // — /// ENST00000344440 // intron // 0 // — // — /	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2191429	catatctagtggatag[C/T]agagtcggcaattaac	C	T	NM_052918 // intron // 0 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// ENST00000263054 // intron // 0 // — // — // — /// ENST00000344440 // intron // 0 // — // — /	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1818586	gttgaaataaggagca[C/T]aggccttatccaca	C	T	NM_052918 // upstream // 3921 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 2696319 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopeptida	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1839798	tagattagatgatccc[C/T]caatgtccctttcaac	C	T	NM_052918 // upstream // 259436 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 2440804 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2269392	gaattttccagtgaag[C/G]acaggtctatctaaga	C	G	NM_052918 // upstream // 264078 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 2436162 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2182050	cagaggatgacttga[A/G]acctgaggctcagct	A	G	NM_052918 // upstream // 287851 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 2412389 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2076341	acattgccctggttgc[C/T]ctccggtttgaaacaa	C	T	NM_052918 // upstream // 288496 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 2411744 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1833560	tacagcatttgatacaa[C/T]aatatggatttctcct	C	T	NM_052918 // upstream // 291768 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 2408472 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1688316	tgctgttcatctcatgcccataaat[G/T]aataaaccggtgatcagcaaatcag	G	T	NM_020383 // downstream // 1489919 // Hs.390623 // XPNPEP1 // 7511 // X-prolyl aminopeptidase (aminopeptidase P) 1, soluble /// NM_052918 // upstream // 1210313 // Hs.348923 // SORCS1 // 114815 // sortilin-related VPS10 domain containing receptor 1	XPNPEP1	XPNPEP1, rs10491022, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble ,q25.1
SNP_A-1789860	gggctgtagaaggtta[C/G]aggtccaacttctgta	C	G	NM_052918 // upstream // 946888 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1753352 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1693144	tatattatgtcctgcl[C/T]gattgagtataitatcat	C	T	NM_020383 // downstream // 1417241 // Hs.390623 // XPNPEP1 // 7511 // X-prolyl aminopeptidase (aminopeptidase P) 1, soluble /// NM_052918 // upstream // 1282991 // Hs.348923 // SORCS1 // 114815 // sortilin-related VPS10 domain containing receptor 1	XPNPEP1	XPNPEP1, rs1928449, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble, q25.1
SNP_A-1750151	agaacaaatgaaggcactcaggta[A/G]cgagttcagtgtagt cagaggcaaa	A	G	NM_020383 // downstream // 1382488 // Hs.390623 // XPNPEP1 // 7511 // X-prolyl aminopeptidase (aminopeptidase P) 1, soluble /// NM_052918 // upstream // 1317744 // Hs.348923 // SORCS1 // 114815 // sortilin-related VPS10 domain containing receptor 1	XPNPEP1	XPNPEP1, rs10509872, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble, q25.1
SNP_A-2183396	cagcactcttgagga[C/T]agttagatagtatttg	C	T	NM_052918 // upstream // 1234463 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1465777 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2158595	attgtagtccccaaaa[A/T]ttctgatcaaccaaat	A	T	NM_052918 // upstream // 1244088 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1456152 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2207504	ccatttagacaagcgc[A/G]attctgaaaatgatgc	A	G	NM_052918 // upstream // 1250553 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1449687 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2201014	ccaaggctatattgaa[A/G]ctctttggtccagtt	A	G	NM_052918 // upstream // 1256340 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1443900 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1838490	tagaatgaacgaatga[A/T]ccctcgctaaaaccag	A	T	NM_052918 // upstream // 1264108 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1436132 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1795687	ggtggaaggcagatag[C/T]agtggactaaagaggt	C	T	NM_052918 // upstream // 1272536 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1427704 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1833724	tacaggtacatataaa[A/T]tgatttacaggtatct	A	T	NM_052918 // upstream // 1303364 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1396876 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2277733	gagcaggcttcctgta[G/T]gtcatcaaactcaaag	G	T	NM_052918 // upstream // 1309957 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1390283 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2103483	agcaatgctctattc[A/G]cacttttttaagttag	A	G	NM_052918 // upstream // 1337142 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1363098 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246788	ctgtagatagttgag[A/G]attatgaaatgtgact	A	G	NM_052918 // upstream // 1339018 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1361222 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2276749	gagataaaatacagaa[A/T]ccttaacatgataaaac	A	T	NM_052918 // upstream // 1339114 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1361126 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1942432	ttggctatattgtata[C/T]gactgagttccacatt	C	T	NM_052918 // upstream // 1353631 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1346609 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2269855	gacaagtttgtataaa[G/T]caatcgttcatctttt	G	T	NM_052918 // upstream // 1385559 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1314681 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2049636	aagcttcctaataacat[A/G]taggctaggattaacc	A	G	NM_052918 // upstream // 1461683 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1238557 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2118998	agtagaatggacacca[C/T]aaaatataaagagcca	C	T	NM_052918 // upstream // 1595663 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 1104577 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopept	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1939142	ttgatacttttgtcc[A/G]ccttgtgctcatttttc	A	G	NM_052918 // upstream // 1823439 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 876801 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1806414	gtcctttatcatttc[C/T]ctgaggctagctgaaa	C	T	NM_052918 // upstream // 2069747 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 630493 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2055151	aataaccgagagcaaa[G/T]tgttcaatccagcccc	G	T	NM_052918 // upstream // 2104500 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 595740 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2196676	cattaagtggccaaga[C/T]agaatgcaaacctttt	C	T	NM_052918 // upstream // 2213864 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 486376 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1682256	acaatttttcttaagagctaaatga[A/C]cctcgttaggtggatttttcctct	A	C	NM_020383 // downstream // 80854 // Hs.390623 // XPNPEP1 // 7511 // X-prolyl aminopeptidase (aminopeptidase P) 1, soluble /// NM_052918 // upstream // 2619378 // Hs.348923 // SORCS1 // 114815 // sortilin-related VPS10 domain containing receptor 1	XPNPEP1	XPNPEP1, rs2145940, X-prolyl aminopeptidase (aminopeptidase P) 1, soluble, q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1934220	ttctccaacaaccaaat[C/T]aacagatgtcttgaat	C	T	NM_052918 // upstream // 2311083 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 389157 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2045037	aagaactggtgtaatg[A/C]aactcaatctggtgc	A	C	NM_052918 // upstream // 2328475 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 371765 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1935115	ttctgatttataagat[A/C]actgttaatacctа	A	C	NM_052918 // upstream // 2352680 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 347560 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2106079	agcccagatctcacd[A/G]ctcagggccaaattt	A	G	NM_052918 // upstream // 2464175 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 236065 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1910938	tgtctattcctaacd[A/G]gactgaggatatcaat	A	G	NM_052918 // upstream // 2464401 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 235839 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopepti	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-2267387	gaatagggctgcttaf[C/T]gaatccaggagttaat	C	T	NM_052918 // upstream // 2621984 // Hs.145675 // SORCS1 // 114815 // Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), mRNA. /// NM_020383 // downstream // 78256 // Hs.390623 // XPNPEP1 // 7511 // Homo sapiens X-prolyl aminopeptid	SORCS1	SORCS1, Homo sapiens sortilin-related VPS10 domain containing receptor 1 (SORCS1), q25.1
SNP_A-1659506	tattcccacccagagcccagtgtaa[C/T]tgctttattgtatcaaatt atgtc	C	T	NM_005962 // intron // 0 // Hs.118630 // MXI1 // 4601 // MAX interacting protein 1 /// NM_130439 // intron // 0 // Hs.118630 // MXI1 // 4601 // MAX interacting protein 1	MXI1	MXI1, rs1935465, MAX interacting protein 1, q25.2
SNP_A-1803707	gtcaaatgaaatcccaa[A/G]gccgtccaaatccgag	A	G	NM_019903 // downstream // 71521 // Hs.501012 // ADD3 // 120 // Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /// NM_016824 // downstream // 71528 // Hs.501012 // ADD3 // 120 // Homo sapiens adducin 3 (gamma) (ADD3), transcript varian	ADD3	ADD3, Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, q25.2
SNP_A-1955756	tttgtacttccgtta[C/T]gtcagatatgtgtgta	C	T	NM_130439 // intron // 0 // Hs.501023 // MXI1 // 4601 // Homo sapiens MAX interactor 1 (MXI1), transcript variant 2, mRNA. /// L07648 // intron // 0 // — // — // 0 // Human MXI1 mRNA, complete cds. /// ENST00000307319 // intron // 0 // — // -	MXI1	MXI1, Homo sapiens MAX interactor 1 (MXI1), transcript variant 2, q25.2
SNP_A-2118083	agtaaaagttcaaca[A/T]catccgctaggggcttg	A	T	NM_005871 // upstream // 66785 // Hs.79968 // SMNDC1 // 10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream // 126194 // Hs.2128 // DUSP5 // 1847 // Homo sapiens dual specificity phosphatase 5 (DUSP5),	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-1867343	tccctccaacaaca[C/T]gtgaagcacagagctc	C	T	NM_005871 // upstream // 83907 // Hs.79968 // SMNDC1 // 10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream // 109072 // Hs.2128 // DUSP5 // 1847 // Homo sapiens dual specificity phosphatase 5 (DUSP5),	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1889613	tgataaacctcacagt[G/T]aatgatccagctgccg	G	T	NM_005871 // upstream // 83954 // Hs.79968 // SMNDC1 // 10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream // 109025 // Hs.2128 // DUSP5 // 1847 // Homo sapiens dual specificity phosphatase 5 (DUSP5),	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-1846752	tatcaacgtgtgcatc[A/G]aggcaactcatttcct	A	G	NM_005871 // upstream // 89413 // Hs.79968 // SMNDC1 // 10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream // 103566 // Hs.2128 // DUSP5 // 1847 // Homo sapiens dual specificity phosphatase 5 (DUSP5),	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-1660049	atacctcgaatcttactacaacagt[A/G]aacttaacacaaaaaaggacatttt	A	G	AK097703 // downstream // 137886 // Hs.293219 // - // - // CDNA FLJ40384 fis, clone TESTI2035796 /// BC009366 // upstream // 87891 // Hs.336954 // - // - // CDNA clone IMAGE:4110850, partial cds	-	- , rs2419577, CDNA FLJ40384 fis, clone TESTI2035796 ,q25.2
SNP_A-1641855	ttcactgctctgtctccagcagtta[C/G]ggttcattcttaggttctgaaatca	C	G	AK097703 // downstream // 137218 // Hs.293219 // - // - // CDNA FLJ40384 fis, clone TESTI2035796 /// BC009366 // upstream // 88559 // Hs.336954 // - // - // CDNA clone IMAGE:4110850, partial cds	-	- , rs10509929, CDNA FLJ40384 fis, clone TESTI2035796 ,q25.2
SNP_A-2272383	gacctgcttgttggaa[C/G]ggtgcaaatggaaact	C	G	NM_005871 // upstream // 169522 // Hs.79968 // SMNDC1 // 10285 // Homo sapiens survival motor neuron domain containing 1 (SMNDC1), mRNA. /// NM_004419 // upstream // 23457 // Hs.2128 // DUSP5 // 1847 // Homo sapiens dual specificity phosphatase 5 (DUSP5),	SMNDC1	SMNDC1, Homo sapiens survival motor neuron domain containing 1 (SMNDC1), q25.2
SNP_A-1924853	ttatatgaagattgag[A/G]aagtatagaggaaaaa	A	G	NM_145341 // upstream // 257024 // Hs.232543 // PDCD4 // 27250 // Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA. /// NM_014456 // upstream // 260503 // Hs.232543 // PDCD4 // 27250 // Homo sa	PDCD4	PDCD4, Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, q25.2
SNP_A-2138903	atccctgtagccttgc[A/G]attatgtggctgttat	A	G	NM_145341 // upstream // 256781 // Hs.232543 // PDCD4 // 27250 // Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA. /// NM_014456 // upstream // 260260 // Hs.232543 // PDCD4 // 27250 // Homo sa	PDCD4	PDCD4, Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, q25.2
SNP_A-2165115	caaactttccacacat[A/G]acttaagagaagaaga	A	G	NM_145341 // upstream // 125975 // Hs.232543 // PDCD4 // 27250 // Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA. /// NM_014456 // upstream // 129454 // Hs.232543 // PDCD4 // 27250 // Homo sa	PDCD4	PDCD4, Homo sapiens programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, q25.2
SNP_A-1929860	ttcatctctgcagagt[C/G]acaatggagttgctga	C	G	NM_000681 // downstream // 46901 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 1022153 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-1957670	ttttatgagtcccaga[C/G]gtttgctccaagtggt	C	G	NM_000681 // downstream // 61584 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 1007470 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2256275	ctttaggcttgctata[C/T]ctttcactgaaaagca	C	T	NM_000681 // downstream // 86082 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 982972 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitocho	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187679	cagtacatatagcttc[A/G]cataaagatcagccat	A	G	NM_000681 // downstream // 242394 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 826660 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2086538	actgaaactactcaaaa[C/T]tgggaagtcgtgcagg	C	T	NM_000681 // downstream // 261468 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 807586 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-1882171	tctttttggtgtttg[C/T]acagctaaggatgcag	C	T	NM_000681 // downstream // 268884 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 800170 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2005307	tccttcctgctttaa[C/T]tgattgatctcatcat	C	T	NM_000681 // downstream // 279934 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 789120 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-1881740	tcttgggatagtgt[C/G]aatagagttgatttgc	C	G	NM_000681 // downstream // 325926 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 743128 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2075545	acatgcagcaaagata[C/G]ccttctcaaaataaaa	C	G	NM_000681 // downstream // 326144 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 742910 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2286586	gatggactcctaaacc[A/G]atcttatctaactgt	A	G	NM_000681 // downstream // 343299 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 725755 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2274752	gagaaagctattgcaa[A/G]ggatgatgttgaatac	A	G	NM_000681 // downstream // 481472 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 587582 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2146797	atgcttgcagatgatc[A/G]atgtgcctggattg	A	G	NM_000681 // downstream // 514508 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 554546 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2303506	gctcaactcctgaaat[G/T]atgaaggaaatctt	G	T	NM_000681 // downstream // 549686 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 519368 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2208410	cccaccatgcgtagaa[A/G]ggatatgtttccaag	A	G	NM_000681 // downstream // 572169 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 496885 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2078759	accatttcaaagctat[A/T]ctctttcaaatacca	A	T	NM_000681 // downstream // 582581 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 486473 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-1935048	ttctgatactaccttc[A/T]caatttattaaaatct	A	T	NM_000681 // downstream // 611682 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 457372 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2005359	tctcagcaaggatcac[A/C]atgacagcgtccactg	A	C	NM_000681 // downstream // 754223 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 314831 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2059868	aatcttaaaaacagaa[A/G]ctaaacatcagtgtct	A	G	NM_000681 // downstream // 756629 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 312425 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2005361	agatgacttgtctcaa[C/T]gtgcaaaatggctgc	C	T	NM_000681 // downstream // 774527 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 294527 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2005362	tccttctcctggtgca[C/T]tgatccatcttaactc	C	T	NM_000681 // downstream // 775685 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 293369 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2074705	acataigagtagttg[C/T]ataacccataacaatt	C	T	NM_000681 // downstream // 819123 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 249931 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2188446	cagtgaataggtctcc[A/G]aaggacagagtctgca	A	G	NM_000681 // downstream // 858613 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 210441 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2090562	actigtgaacccctcg[A/G]acattcagtcgccaca	A	G	NM_000681 // downstream // 872041 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 197013 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2195876	catgtattcaattgcc[A/G]cagggtcttttccaaa	A	G	NM_000681 // downstream // 875532 // Hs.249159 // ADRA2A // 150 // Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA. /// NM_020918 // downstream // 193522 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitoch	ADRA2A	ADRA2A, Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), q25.2
SNP_A-2176701	caccccttaattaca[C/T]gatcttagtgctttc	C	T	NM_020918 // upstream // 89136 // Hs.42586 // GPAM // 57678 // Homo sapiens glycerol-3-phosphate acyltransferase, mitochondrial (GPAM), mRNA. /// NM_058222 // upstream // 10839 // Hs.348615 // TECTB // 6975 // Homo sapiens tectorin beta (TECTB), mRNA. ///	GPAM	GPAM, Homo sapiens glycerol-3-phosphate acyltransferase, mitochondrial (GPAM), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1704799	gacagagtgagactctgtctaaaaa[A/G]taaataaatgagacttgtcagctc	A	G	NM_024880 // upstream // 289183 // - // - // - // - /// NM_030756 // upstream // 168593 // Hs.214039 // TCF7L2 // 6934 // transcription factor 7-like 2 (T-cell specific, HMG-box) /// NM_145206 // downstream // 44086 // Hs.189575 // VTI1A // 143187 // yes	-	-, rs1815239, -, q25.2
SNP_A-1833712	tacagggtctgtgaccf[A/G]aatacattgagaaact	A	G	NM_145206 // intron // 0 // Hs.194554 // VTI1A // 143187 // Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// ENST00000281221 // intron // 0 // — // — // — // —	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-1874886	tctctaaccagatcgaf[C/G]gctacagttgtgaga	C	G	NM_145206 // intron // 0 // Hs.194554 // VTI1A // 143187 // Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// ENST00000281221 // intron // 0 // — // — // — // —	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2221374	ccttcatcaagggccf[A/G]agatcccagctacag	A	G	NM_145206 // downstream // 11758 // Hs.194554 // VTI1A // 143187 // Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// NM_030756 // upstream // 200921 // Hs.501080 // TCF7L2 // 6934 // Homo sapiens trans	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-1818799	gttgagattaggaagaf[A/G]aactacaaaacagca	A	G	NM_145206 // downstream // 121488 // Hs.194554 // VTI1A // 143187 // Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), mRNA. /// NM_030756 // upstream // 91191 // Hs.501080 // TCF7L2 // 6934 // Homo sapiens trans	VTI1A	VTI1A, Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), q25.2
SNP_A-2198429	catttactgaaatctaf[C/G]gccctttgtgtgatc	C	G	NM_030756 // downstream // 12656 // Hs.501080 // TCF7L2 // 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // downstream // 12656 // Hs.501080 // TCF7L2 // 6934 // Homo sapiens mRNA for hTCF-4. ///	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-2204978	ccagggtagcagatacf[A/G]acacccatgtgccaca	A	G	NM_030756 // downstream // 149082 // Hs.501080 // TCF7L2 // 6934 // Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA. /// Y11306 // downstream // 149082 // Hs.501080 // TCF7L2 // 6934 // Homo sapiens mRNA for hTCF-4. //	TCF7L2	TCF7L2, Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), q25.3
SNP_A-1751151	tgacaggtgtgaggtccaggtacacf[C/T]cggtcagattctctctc attggat	C	T	NM_032550 // CDS // 0 // Hs.353196 // KIAA1914 // 84632 // KIAA1914	KIAA1914	KIAA1914, rs2286396, KIAA1914,q25.3
SNP_A-1953186	ttctcttctcaaaaccf[A/G]caatcactccgagcat	A	G	NM_000684 // upstream // 19974 // Hs.99913 // ADRB1 // 153 // Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA. /// ENST00000358967 // downstream // 106884 // — // — // — // — /// ENST00000046967 // upstream // 19974 // — // — // — // —	ADRB1	ADRB1, Homo sapiens adrenergic, beta-1-, receptor (ADRB1), q25.3
SNP_A-1871490	tctaactcaacactgcf[C/G]atgatgccctgagtaa	C	G	NM_000684 // downstream // 18217 // Hs.99913 // ADRB1 // 153 // Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA. /// NM_018017 // downstream // 58229 // Hs.159066 // C10orf118 // 55088 // Homo sapiens chromosome 10 open reading frame 118 (C10orf1	ADRB1	ADRB1, Homo sapiens adrenergic, beta-1-, receptor (ADRB1), q25.3
SNP_A-1729085	cctccagcagccttcaacacatgcf[A/G]ctgcacacatgccccc atgtgtctc	A	G	NM_002313 // intron // 0 // Hs.442540 // ABLIM1 // 3983 // actin binding LIM protein 1 /// NM_006719 // intron // 0 // Hs.442540 // ABLIM1 // 3983 // actin binding LIM protein 1 /// NM_006720 // intron // 0 // Hs.442540 // ABLIM1 // 3983 // actin binding	ABLIM1	ABLIM1, rs727532, actin binding LIM protein 1 ,q25.3
SNP_A-1718311	aagatgaggaaggtaaatgaaaatc[C/T]catgtttataaagatct aggatgcc	C	T	NM_002313 // intron // 0 // Hs.442540 // ABLIM1 // 3983 // actin binding LIM protein 1 /// NM_006719 // intron // 0 // Hs.442540 // ABLIM1 // 3983 // actin binding LIM protein 1	ABLIM1	ABLIM1, rs7923449, actin binding LIM protein 1 ,q25.3
SNP_A-2021567	aaaaaatccaaccaaaa[C/G]aaagcagcagaacaaa	C	G	NM_198496 // intron // 0 // Hs.197741 // AMACO // 340706 // Homo sapiens A-domain containing protein similar to matrilin and collagen (AMACO), mRNA. /// ENST00000298715 // intron // 0 // — // — // — // —	AMACO	AMACO, Homo sapiens A-domain containing protein similar to matrilin and collagen (AMACO), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1848642	tatgagataaagacaa[A/G]agggaaatgtaggag	A	G	NM_001001936 // upstream // 7971 // Hs.501106 // KIAA1914 // 84632 // Homo sapiens KIAA1914 (KIAA1914), transcript variant 1, mRNA. /// NM_032550 // upstream // 7971 // Hs.501106 // KIAA1914 // 84632 // Homo sapiens KIAA1914 (KIAA1914), transcript variant	KIAA1914	KIAA1914, Homo sapiens KIAA1914 (KIAA1914), transcript variant 1, q25.3
SNP_A-2101272	agatcctgctgtata[A/G]gaacaggaatacagct	A	G	NM_001003408 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1).	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-1866847	tcctaaaaaatttcg[A/T]aaatcatcctagtctt	A	T	NM_001003408 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1).	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-1912220	tgtgatcatcaattaa[A/G]ggctctaattcctt	A	G	NM_001003408 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1).	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-1780917	ggatgaatggaaagga[A/C]atattcaaggggggag	A	C	NM_001003408 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // intron // 0 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1).	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-2298741	gcccagtctaaagaa[A/C]atgaaaacaccctc	A	C	NM_001003408 // upstream // 48597 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, mRNA. /// NM_002313 // upstream // 48597 // Hs.438236 // ABLIM1 // 3983 // Homo sapiens actin binding LIM protein	ABLIM1	ABLIM1, Homo sapiens actin binding LIM protein 1 (ABLIM1), transcript variant 3, q25.3
SNP_A-1845912	tataaaccctgcac[C/T]acacatttgaaaact	C	T	NM_207303 // intron // 0 // Hs.501127 // ATRNL1 // 26033 // Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// ENST00000355044 // intron // 0 // — // — // — /// ENST00000303745 // intron // 0 // — // — // —	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2134055	atatgaaattgtgtca[C/T]taatcagtctttattt	C	T	NM_207303 // intron // 0 // Hs.501127 // ATRNL1 // 26033 // Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// ENST00000355044 // intron // 0 // — // — // — /// ENST00000303745 // intron // 0 // — // — // —	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2256760	ctttcattaggctcaa[C/T]ctccaacgatgggtat	C	T	NM_005264 // intron // 0 // Hs.444372 // GFRA1 // 2674 // GDNF family receptor alpha 1 /// NM_145793 // intron // 0 // Hs.444372 // GFRA1 // 2674 // GDNF family receptor alpha 1	GFRA1	GFRA1, rs10510015, GDNF family receptor alpha 1, q25.3
SNP_A-2196515	catgtttaagagaac[C/G]actctggctgctaag	C	G	NM_207303 // downstream // 19224 // Hs.501127 // ATRNL1 // 26033 // Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// NM_145793 // downstream // 96144 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2184120	cagcccttcgttaata[A/G]ccactctctttcaga	A	G	NM_207303 // downstream // 24475 // Hs.501127 // ATRNL1 // 26033 // Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// NM_145793 // downstream // 90893 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2312628	ggacgtatgtgtacaq[A/C]aaaacttgatcacaag	A	C	NM_207303 // downstream // 24919 // Hs.501127 // ATRNL1 // 26033 // Homo sapiens attractin-like 1 (ATRNL1), mRNA. /// NM_145793 // downstream // 90449 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2	ATRNL1	ATRNL1, Homo sapiens attractin-like 1 (ATRNL1), q25.3
SNP_A-2005734	caatgggcattcatca[A/G]actcccaaaagcacggt	A	G	NM_145793 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), trans	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-1654307	atactgtatgttttttgaataatga[C/T]aaaagcatgtaacataacacaaaca	C	T	BC044830 // downstream // 39392 // Hs.233407 // C10orf96 // 374355 // chromosome 10 open reading frame 96 /// NM_000936 // upstream // 126527 // Hs.102876 // PNLIP // 5406 // pancreatic lipase	C10orf96	C10orf96 , rs7907051, chromosome 10 open reading frame 96 ,q25.3
SNP_A-1644098	aagatgaatgtgtataatggtctta[A/C]aggaatggagagtcaatatgggaa	A	C	BC044830 // downstream // 53592 // Hs.233407 // C10orf96 // 374355 // chromosome 10 open reading frame 96 /// NM_000936 // upstream // 112327 // Hs.102876 // PNLIP // 5406 // pancreatic lipase	C10orf96	C10orf96 , rs1431486, chromosome 10 open reading frame 96 ,q25.3
SNP_A-2072639	acagcctactatttgaa[A/C]gaaagatcgtaaaaga	A	C	NM_145793 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), trans	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-1869492	tcctgttaacagaaga[A/G]ggagatataaaacatca	A	G	NM_145793 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), trans	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-2202824	ccactaaggagtttac[C/T]atatgccagagtaaat	C	T	NM_145793 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // intron // 0 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), trans	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-2005751	attgcaaaggcagtaa[A/G]agcacaccaagaaat	A	G	NM_145793 // upstream // 15875 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // upstream // 15875 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (G	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-1860546	tcagttgaaatgagtc[A/G]aatctgaaaaccctg	A	G	NM_145793 // upstream // 27548 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // upstream // 27548 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (G	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-1854939	tcaactcttatttac[A/G]actagcacaacatgc	A	G	NM_145793 // upstream // 40706 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, mRNA. /// NM_005264 // upstream // 40706 // Hs.109425 // GFRA1 // 2674 // Homo sapiens GDNF family receptor alpha 1 (G	GFRA1	GFRA1, Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 2, q25.3
SNP_A-2183405	cagcactgcttactc[C/T]atgacattaatgcatt	C	T	ENST00000333254 // intron // 0 // --- // --- // ---	-	q25.3
SNP_A-1939855	ttgcaattgacagatc[A/G]ctagataaaagagttt	A	G	ENST00000333254 // downstream // 31476 // --- // --- // --- // --- /// ENST00000277891 // upstream // 16363 // --- // --- // --- // --- /// ENST00000333401 // downstream // 28224 // --- // --- // --- // ---	-	q25.3
SNP_A-2257181	ctttctgccagtgttaa[C/T]atggacaaaattagta	C	T	ENST00000333254 // downstream // 33225 // --- // --- // --- // --- /// ENST00000277891 // upstream // 14614 // --- // --- // --- // --- /// ENST00000333401 // downstream // 26475 // --- // --- // --- // ---	-	q25.3
SNP_A-2068845	acaatccaaattccaa[A/G]catctaagctgatttt	A	G	ENST00000277891 // CDS // 0 // --- // --- // ---	-	q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2302615	gctacatggtcattag[A/G]acatcccttcctctac	A	G	ENST00000277891 // intron // 0 // — // — // — // —	-	q25.3
SNP_A-1889184	tgagtctcagatgaga[A/C]ctttgactttgagctt	A	C	ENST00000277891 // intron // 0 // — // — // — // —	-	q25.3
SNP_A-2104368	agcagctactagagac[A/G]caacttcagttaaaaa	A	G	AB007877 // intron // 0 // Hs.524617 // HSPA12A // 259217 // Homo sapiens KIAA0417 mRNA, complete cds. /// ENST00000298777 // intron // 0 // — // — // — // —	HSPA12A	HSPA12A, Homo sapiens KIAA0417 complete cds. ,q25.3
SNP_A-1728559	gaaatattttaaaggaggactccga[C/T]caccgagctttggtgtt gatactga	C	T	NM_181840 // intron // 0 // Hs.449650 // TRIK // 338567 // TWIK-related spinal cord K+ channe	TRIK	TRIK , rs363306, TWIK-related spinal cord K+ channe,q26.11
SNP_A-1735082	tcttgggtcagagccctcaccagga[G/T]cgtggcccatcactca gccctgcc	G	T	NM_181840 // intron // 0 // Hs.449650 // TRIK // 338567 // TWIK-related spinal cord K+ channe	TRIK	TRIK , rs363307, TWIK-related spinal cord K+ channe,q26.11
SNP_A-1807068	gtctccatcagcagga[A/G]gaagcgtttgggggaa	A	G	NM_018330 // upstream // 119463 // Hs.501140 // KIAA1598 // 57698 // Homo sapiens KIAA1598 (KIAA1598), mRNA. /// NM_199131 // downstream // 29724 // Hs.441536 // VAX1 // 11023 // Homo sapiens ventral anterior homeobox 1 (VAX1), mRNA. /// ENST00000355371 /	KIAA1598	KIAA1598, Homo sapiens KIAA1598 (KIAA1598), q26.11
SNP_A-2252823	cttctagaaaggactc[A/G]ctgtgcagctttgatg	A	G	NM_199131 // upstream // 57752 // Hs.441536 // VAX1 // 11023 // Homo sapiens ventral anterior homeobox 1 (VAX1), mRNA. /// NM_181840 // upstream // 1436 // Hs.449650 // KCNK18 // 338567 // Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), mRNA.	VAX1	VAX1, Homo sapiens ventral anterior homeobox 1 (VAX1), q26.11
SNP_A-2005823	gaattgatgcttgccc[A/G]ctccagaagatctagc	A	G	NM_181840 // intron // 0 // Hs.449650 // KCNK18 // 338567 // Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), mRNA. /// ENST00000334549 // intron // 0 // — // — // — // —	KCNK18	KCNK18, Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), q26.11
SNP_A-1903639	tgggagaagatgtaaa[A/C]aagtcagtatgtgaac	A	C	NM_181840 // downstream // 3335 // Hs.449650 // KCNK18 // 338567 // Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), mRNA. /// NM_003054 // upstream // 27459 // Hs.369009 // SLC18A2 // 6571 // Homo sapiens solute carrier family 18 (vesicular mo	KCNK18	KCNK18, Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), q26.11
SNP_A-2122182	agtgatttttgcaaga[C/T]tcaagcaagatctagt	C	T	NM_181840 // downstream // 3746 // Hs.449650 // KCNK18 // 338567 // Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), mRNA. /// NM_003054 // upstream // 27048 // Hs.369009 // SLC18A2 // 6571 // Homo sapiens solute carrier family 18 (vesicular mo	KCNK18	KCNK18, Homo sapiens TWIK-related spinal cord K+ channel (TRESK-2), q26.11
SNP_A-2235515	ctccgtggtagttaga[C/T]gagcacagaggatggc	C	T	NM_003054 // intron // 0 // Hs.369009 // SLC18A2 // 6571 // Homo sapiens solute carrier family 18 (vesicular monoamine), member 2 (SLC18A2), mRNA. /// ENST00000298472 // intron // 0 // — // — // — // —	SLC18A2	SLC18A2, Homo sapiens solute carrier family 18 (vesicular monoamine), member 2 (SLC18A2), q26.11
SNP_A-1829801	taataaatctctgaaa[A/G]gataagtgagaaacca	A	G	NM_173791 // intron // 0 // Hs.501149 // PDZK8 // 118987 // Homo sapiens PDZ domain containing 8 (PDZK8), mRNA. /// ENST00000298474 // intron // 0 // — // — // — // — /// ENST00000334464 // intron // 0 // — // — // — // —	PDZK8	PDZK8, Homo sapiens PDZ domain containing 8 (PDZK8), q26.11
SNP_A-1852917	tatttcttacctttta[G/T]cctcaaaacaaaggct	G	T	NM_173791 // upstream // 22548 // Hs.501149 // PDZK8 // 118987 // Homo sapiens PDZ domain containing 8 (PDZK8), mRNA. /// NM_004098 // upstream // 144471 // Hs.202095 // EMX2 // 2018 // Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), mRNA. ///	PDZK8	PDZK8, Homo sapiens PDZ domain containing 8 (PDZK8), q26.11
SNP_A-2302580	gctacagcaaccccaa[C/T]ccccacggtcacgtgc	C	T	NM_004098 // downstream // 7027 // Hs.202095 // EMX2 // 2018 // Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), mRNA. /// NM_014904 // downstream // 448349 // Hs.173656 // RAB11FIP2 // 22841 // Homo sapiens RAB11 family interacting protein 2 (	EMX2	EMX2, Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), q26.11
SNP_A-2179764	cacttgccttgttcac[A/G]caatatgtcatgcata	A	G	NM_004098 // downstream // 18268 // Hs.202095 // EMX2 // 2018 // Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), mRNA. /// NM_014904 // downstream // 437108 // Hs.173656 // RAB11FIP2 // 22841 // Homo sapiens RAB11 family interacting protein 2	EMX2	EMX2, Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), q26.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2052869	aagtcagtggaaaacg[A/G]actcttcatcctatga	A	G	NM_178816 // downstream // 24806 // Hs.89387 // CASC2 // 255082 // Homo sapiens cancer susceptibility candidate 2 (CASC2), mRNA. /// NM_201377 // downstream // 27136 // Hs.89387 // CASC2 // 255082 // Homo sapiens cancer susceptibility candidate 2 (CASC2),	CASC2	CASC2, Homo sapiens cancer susceptibility candidate 2 (CASC2), q26.11
SNP_A-1853413	tatttttctatgttcccc[C/T]aagcacccccttctgg	C	T	NM_022063 // upstream // 586 // Hs.372309 // C10orf84 // 63877 // Homo sapiens chromosome 10 open reading frame 84 (C10orf84), mRNA. /// NM_004248 // downstream // 251226 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10),	C10orf84	C10orf84, Homo sapiens chromosome 10 open reading frame 84 (C10orf84), q26.11
SNP_A-1939731	ttgcaaagcactaaat[A/G]aatggagagatgcgcc	A	G	NM_022063 // upstream // 60736 // Hs.372309 // C10orf84 // 63877 // Homo sapiens chromosome 10 open reading frame 84 (C10orf84), mRNA. /// NM_004248 // downstream // 191076 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10	C10orf84	C10orf84, Homo sapiens chromosome 10 open reading frame 84 (C10orf84), q26.11
SNP_A-2244177	ctgcttttctaagaga[A/C]cccaaatacagagtag	A	C	NM_004248 // upstream // 12149 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 77164 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-2271258	gacatggcggcttaca[C/T]gttaatagglagattc	C	T	NM_004248 // upstream // 30915 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 58398 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-2112119	aggatgttaacagcta[C/T]taatttaagtggtgac	C	T	NM_004248 // upstream // 36742 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 52571 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-1948213	tttagcctgttaatag[A/G]aagcgaacatctaccc	A	G	NM_004248 // upstream // 74025 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 15288 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-2278652	gagctggatgctgtca[C/T]atcatctttccgggt	C	T	NM_004248 // upstream // 74798 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 14515 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-1817628	gttccagctttctcaa[C/T]ggaaaatgaggctgtt	C	T	NM_004248 // upstream // 78036 // Hs.248119 // GPR10 // 2834 // Homo sapiens G protein-coupled receptor 10 (GPR10), mRNA. /// NM_153810 // downstream // 111277 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46	GPR10	GPR10, Homo sapiens G protein-coupled receptor 10 (GPR10), q26.11
SNP_A-2026554	aaacaacagaaaccaa[C/T]gccagttaactaaagt	C	T	NM_153810 // upstream // 8848 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// NM_199461 // upstream // 265666 // Hs.351851 // NANOS1 // 340719 // Homo sapiens nanos homolog 1 (Drosophila) (NANOS	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11
SNP_A-2157492	attgatcattgttaaa[C/G]cttgatgatggaaaca	C	G	NM_153810 // upstream // 95038 // Hs.420024 // C10orf46 // 143384 // Homo sapiens chromosome 10 open reading frame 46 (C10orf46), mRNA. /// NM_199461 // upstream // 179476 // Hs.351851 // NANOS1 // 340719 // Homo sapiens nanos homolog 1 (Drosophila) (NANO	C10orf46	C10orf46, Homo sapiens chromosome 10 open reading frame 46 (C10orf46), q26.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2081761	accttctagcatctac[A/G]cacctaaagcagggtt	A	G	ENST00000355736 // intron // 0 // — // — // — // — /// ENST00000357356 // intron // 0 // — // — // — // —	-	q26.11
SNP_A-1809736	gtgaggaagcaggtga[C/T]ggcctgaccactgtac	C	T	ENST00000355736 // intron // 0 // — // — // — // — /// ENST00000357356 // intron // 0 // — // — // — // —	-	q26.11
SNP_A-1664690	tagcacttaccacgttgtaatgtaa[C/T]ttaactcttcacagggttct tgact	C	T	NM_003252 // upstream // 45010 // Hs.335786 // TIAL1 // 7073 // TIA1 cytotoxic granule-associated RNA binding protein-like 1 /// NM_004281 // upstream // 9850 // Hs.15259 // BAG3 // 9531 // BCL2-associated athanogene 3 /// NM_022333 // upstream // 45077	TIAL1	TIAL1 , rs196278, TIA1 cytotoxic granule-associated RNA binding protein-like 1 ,q26.11
SNP_A-2114861	agggcacctgctggag[A/G]acatcgctggcagctg	A	G	ENST00000355736 // intron // 0 // — // — // — // — /// ENST00000357356 // intron // 0 // — // — // — // —	-	q26.11
SNP_A-2133522	atatcaaagagttacc[A/C]ccattacagtatttac	A	C	ENST00000355736 // intron // 0 // — // — // — // — /// ENST00000357356 // intron // 0 // — // — // — // —	-	q26.11
SNP_A-1915304	tgttcatgcactcaac[A/G]ctatgtggtttcctgg	A	G	ENST00000355736 // intron // 0 // — // — // — // — /// ENST00000357356 // intron // 0 // — // — // — // —	-	q26.11
SNP_A-1843172	tagtcatcgcattgga[A/G]ctattcctctaccttc	A	G	ENST00000355736 // intron // 0 // — // — // — // — /// ENST00000357356 // intron // 0 // — // — // — // —	-	q26.11
SNP_A-1869510	tcctgttccttctggc[A/T]catgcattgctttgtg	A	T	ENST00000313060 // CDS // 0 // — // — // — // —	-	q26.11
SNP_A-2163419	atttttttttcaccaga[C/T]gttcactgacttcgtg	C	T	ENST00000313060 // 3UTR // 0 // — // — // — // —	-	q26.11
SNP_A-2292817	gcacttttaaaagacc[C/T]attgaattgtttgtga	C	T	NM_002925 // downstream // 20550 // Hs.501200 // RGS10 // 6001 // Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, mRNA. /// ENST00000313060 // downstream // 19650 // — // — // — // — /// ENST00000278155 // downstre	RGS10	RGS10, Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, q26.11
SNP_A-2047901	aagcaaagaaagtcac[A/G]gaaagaaaccagagtg	A	G	NM_002925 // downstream // 20510 // Hs.501200 // RGS10 // 6001 // Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, mRNA. /// ENST00000313060 // downstream // 19690 // — // — // — // — /// ENST00000278155 // downstre	RGS10	RGS10, Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, q26.11
SNP_A-2240071	ctgaaggagagcccaa[C/T]accaagttctaataat	C	T	NM_002925 // downstream // 19878 // Hs.501200 // RGS10 // 6001 // Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, mRNA. /// ENST00000313060 // downstream // 20322 // — // — // — // — /// ENST00000278155 // downstre	RGS10	RGS10, Homo sapiens regulator of G-protein signalling 10 (RGS10), transcript variant 2, q26.11
SNP_A-1906086	tggtctgaggcagttt[A/C]aaaattgagagacagt	A	C	NM_004281 // downstream // 12681 // Hs.523309 // BAG3 // 9531 // Homo sapiens BCL2-associated athanogene 3 (BAG3), mRNA. /// ENST00000281679 // downstream // 12681 // — // — // — // — /// ENST00000360241 // upstream // 35601 // — // — // — // —	BAG3	BAG3, Homo sapiens BCL2-associated athanogene 3 (BAG3), q26.11
SNP_A-2034660	aaatgaaagttgatca[A/G]tacttggggaataaat	A	G	ENST00000360241 // intron // 0 // — // — // — // — /// ENST00000354225 // intron // 0 // — // — // — // —	-	q26.12
SNP_A-2005978	gaccagcttgcttaac[C/T]gatgttgggaagttgt	C	T	ENST00000360241 // intron // 0 // — // — // — // — /// ENST00000354225 // intron // 0 // — // — // — // —	-	q26.12
SNP_A-1816298	gttagaaaattgccaa[A/C]aaagtaataactgatt	A	C	NM_024834 // intron // 0 // Hs.124246 // C10orf119 // 79892 // Homo sapiens chromosome 10 open reading frame 119 (C10orf119), mRNA. /// ENST00000360003 // intron // 0 // — // — // — // — /// ENST00000357741 // intron // 0 // — // — // — // -	C10orf119	C10orf119, Homo sapiens chromosome 10 open reading frame 119 (C10orf119), q26.12
SNP_A-2180204	cagaaactgaatgcaa[A/G]tctgaaagctacactt	A	G	NM_007190 // downstream // 72548 // Hs.435004 // SEC23IP // 11196 // Homo sapiens SEC23 interacting protein (SEC23IP), mRNA. /// NM_000982 // downstream // 340008 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST0	SEC23IP	SEC23IP, Homo sapiens SEC23 interacting protein (SEC23IP), q26.12
SNP_A-1643824	actaacacatgactactaaaatcag[C/G]ctttttttcatttctgctgta actca	C	G	AK094721 // upstream // 92442 // Hs.196578 // - // - // CDNA FLJ37402 fis, clone BRAMY2028072 /// NM_007190 // downstream // 564034 // Hs.300208 // SEC23IP // 11196 // SEC23 interacting protein	-	- , rs966157, CDNA FLJ37402 fis, clone BRAMY2028072 ,q26.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1660265	actcaaatattctataaatcctaga[A/T]ataaaggaagcagtgtg tgtgtaat	A	T	AK094721 // upstream // 92396 // Hs.196578 // - // - // CDNA FLJ37402 fis, clone BRAMY2028072 /// NM_007190 // downstream // 564080 // Hs.300208 // SEC23IP // 11196 // SEC23 interacting protein	-	- , rs966158, CDNA FLJ37402 fis, clone BRAMY2028072 ,q26.12
SNP_A-1701861	gccccaggttggcctctctggtcta[C/G]gacatgggaaagagat ctctagagg	C	G	AK094721 // upstream // 77982 // Hs.196578 // - // - // CDNA FLJ37402 fis, clone BRAMY2028072 /// NM_007190 // downstream // 578494 // Hs.300208 // SEC23IP // 11196 // SEC23 interacting protein	-	- , rs10510071, CDNA FLJ37402 fis, clone BRAMY2028072 ,q26.12
SNP_A-2124689	agttctcccaaagcac[A/G]catagttttctcatt	A	G	NM_000982 // upstream // 24109 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 24109 // --- // --- // --- // --- /// ENST00000322663 // upstream // 218917 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2099351	agaggcgagcaatgga[C/G]gaaaggagggaaaatc	C	G	NM_000982 // upstream // 24340 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 24340 // --- // --- // --- // --- /// ENST00000322663 // upstream // 218686 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2238420	ctctggtcatttgcag[A/G]atcaaatccaaactcc	A	G	NM_000982 // upstream // 40429 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 40429 // --- // --- // --- // --- /// ENST00000322663 // upstream // 202597 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2197067	cattatgttaactacc[A/G]ctgttttaaatcattt	A	G	NM_000982 // upstream // 47099 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 47099 // --- // --- // --- // --- /// ENST00000322663 // upstream // 195927 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2163643	caaaaagtataccaaa[A/G]agcaacaactaatacc	A	G	NM_000982 // upstream // 151919 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 151919 // --- // --- // --- // --- /// ENST00000322663 // upstream // 91107 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2124253	agttatccgaagcaga[A/G]agaatgggagggacac	A	G	NM_000982 // upstream // 162516 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 162516 // --- // --- // --- // --- /// ENST00000322663 // upstream // 80510 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-1940912	ttgctagggaagtcta[C/T]gccagaagaagagaag	C	T	NM_000982 // upstream // 189747 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 189747 // --- // --- // --- // --- /// ENST00000322663 // upstream // 53279 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2006018	attttattcagtacaa[C/T]gtgaaacttcttgacc	C	T	NM_000982 // upstream // 192406 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 192406 // --- // --- // --- // --- /// ENST00000322663 // upstream // 50620 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-2232256	ctcaatgccaatacac[A/C]agcaactttaagagac	A	C	NM_000982 // upstream // 218734 // Hs.381123 // RPL21 // 6144 // Homo sapiens ribosomal protein L21 (RPL21), mRNA. /// ENST00000330207 // upstream // 218734 // --- // --- // --- // --- /// ENST00000322663 // upstream // 24292 // --- // --- // --- // ---	RPL21	RPL21, Homo sapiens ribosomal protein L21 (RPL21), q26.12
SNP_A-1726810	attttaccaaactgtgtatagggac[A/G]gcgagtgtgaccaatct gtctgcag	A	G	NM_000141 // downstream // 511491 // Hs.404081 // FGFR2 // 2263 // fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, /// NM_018117 // downstream // 57329 // Hs.16677 // WDR11 /	FGFR2	FGFR2 , rs10510084, fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, ,q26.12
SNP_A-2067877	acaacctacagaatga[C/G]ataaaagttttgcaat	C	G	NM_022976 // downstream // 47490 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // downstream // 47490 // Hs.533683 // FGFR2 /	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2235377	ctccctggtttggaaa[C/T]agccctgctcacagaa	C	T	NM_022976 // downstream // 45190 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // downstream // 45190 // Hs.533683 // FGFR2 /	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2006038	tggaaggtctcaataaa[C/T]ggtattcaaatgactg	C	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2167042	caacaagcatggctga[A/C]taacttctgggctca	A	C	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2117854	aggttgtgtatgctgc[A/G]aatggcggtgaagctt	A	G	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-1909351	tgtattaaattatgcc[A/G]catagtctcgcatgtg	A	G	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d .q26.12
SNP_A-1698685	tagataccctagaaactagttctcc[C/T]actggtgtaaaaaggatgctaagaa	C	T	NM_000141 // downstream // 359606 // Hs.404081 // FGFR2 // 2263 // fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, /// NM_018117 // downstream // 209214 // Hs.16677 // WDR11	FGFR2	FGFR2 , rs2250945, fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, q26.12
SNP_A-1798498	gtaaatggctatatgc[A/G]ctgcaaattatgattg	A	G	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-1827691	taactgttgaagagaaa[A/C]ggagatggcttcccca	A	C	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2235924	ctcctgcaaagggtga[C/T]gttgcatcagacacc	C	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2264605	gaagaatacttttgcta[C/T]gtaggtgaatttaaaa	C	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.12
SNP_A-2077605	accacctgcaacatgc[C/T]aagctactttggtgt	C	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d .q26.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209390	cccatacaggtctgd[A/C]caattattagttgaaa	A	C	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-2234867	ctccaatctccagagaa[A/G]tgcagttccccgtcc	A	G	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-2142462	atgaaatgagaaaaaaa[C/T]gctgggaagacgcacc	C	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-1945093	ttgtgtccaggcaaac[G/T]aaggcggttccaacac	G	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-2210841	ccccttagctttaaaa[C/T]gtttgactgaaatcta	C	T	NM_022976 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // intron // 0 // Hs.533683 // FGFR2 // 2263 // Homo s	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-2116863	aggtctgatcggccca[C/T]gcttgatgaagagag	C	T	NM_022976 // upstream // 41930 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // upstream // 41930 // Hs.533683 // FGFR2 // 22	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial d ,q26.13
SNP_A-2166029	caaataatcatagccc[A/G]cagtctacagccacaa	A	G	NM_022976 // upstream // 105816 // Hs.533683 // FGFR2 // 2263 // Homo sapiens fibroblast growth factor receptor 2 (bactena-expressed kinase, keratinocyte growth factor receptor, craniofacial d /// NM_022974 // upstream // 105816 // Hs.533683 // FGFR2 //	FGFR2	FGFR2, Homo sapiens fibroblast growth factor receptor 2 (bactena-expressed kinase, keratinocyte growth factor receptor, craniofacial d q26.13
SNP_A-1742487	taagagaattaaggcagagaagaga[C/T]gggagccacttagc agagggccatc	C	T	AF528099 // intron // 0 // Hs.23196 // TACC2 // 10579 // transforming, acidic coiled-coil containing protein 2	TACC2	TACC2 , rs2420994, transforming, acidic coiled-coil containing protein 2,q26.13
SNP_A-1650326	aatgaaaccaactaggtcaagcaat[A/G]tatcctctttaigtca ctgaatt	A	G	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // chromosome 10 open reading frame 87	C10orf87	C10orf87 , rs3905303, chromosome 10 open reading frame 87,q26.13
SNP_A-2181276	cagaccctgtaacac[C/T]attagactttctattt	C	T	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2006169	tgattccagttgtgat[C/G]agcatatttgccccatg	C	G	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2170584	caagtggaaagagcac[C/T]gcagattgaggagtcc	C	T	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006182	aggctagcctaagatg[A/G]caaagttggatagaaa	A	G	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-1932851	ttccttattgaaaaa[A/T]ccaggtggccggatg	A	T	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2184343	cagcgaacctctaccc[C/T]agttatcaatactaga	C	T	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2006187	agaagctaacctgac[A/G]gaaatagctccgtgtt	A	G	NM_206861 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // intron // 0 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, ac	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2171507	caatcattttctctaa[C/T]cttcatagtagttgca	C	T	NM_206861 // downstream // 3368 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // downstream // 3368 // Hs.501252 // TACC2 // 10579 // Homo sapiens tr	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2006189	aacaactcatgttaaa[C/G]agtacagtaggaccgc	C	G	NM_206861 // downstream // 14505 // Hs.501252 // TACC2 // 10579 // Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, mRNA. /// NM_206862 // downstream // 14505 // Hs.501252 // TACC2 // 10579 // Homo sapiens	TACC2	TACC2, Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), transcript variant 2, q26.13
SNP_A-2006193	ctaaggaactcggcaa[C/T]ggaaaagtgttggcca	C	T	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // — // — // —	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2089800	acttccttgcgagtac[C/T]ctaatcttttgtgcc	C	T	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // — // — // —	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2183713	cagcatcccgcaccca[A/G]gcattgcaatggacc	A	G	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // — // — // —	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2206600	ccatgaactcaactac[C/T]ctcacaaacatcagtg	C	T	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // — // — // —	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2257697	ctttggaaaatatggc[A/G]caggtccatgaactc	A	G	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // — // — // —	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2172202	caatgtcctcgttcca[C/T]gaagcttttcctcatt	C	T	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // — // — // —	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2006195	atctgtttgagacca[C/G]ggtcactctagcagtc	C	G	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // --- // --- // ---	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2180715	cagaagtcagaagaga[A/G]gcacttaaaactgaa	A	G	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // --- // --- // ---	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2142787	atgaaggatctattca[C/T]gaacacataccgtgt	C	T	NM_144587 // intron // 0 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// ENST00000260723 // intron // 0 // --- // --- // ---	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2001527	tctgagatgtctgtta[C/G]actcagggtgtcaga	C	G	NM_144587 // downstream // 12244 // Hs.422466 // C10orf87 // 118663 // Homo sapiens chromosome 10 open reading frame 87 (C10orf87), mRNA. /// NM_001001974 // upstream // 24300 // Hs.287830 // PLEKHA1 // 59338 // Homo sapiens pleckstrin homology domain con	C10orf87	C10orf87, Homo sapiens chromosome 10 open reading frame 87 (C10orf87), q26.13
SNP_A-2127043	ataaataacgcaagta[A/G]agaactcctgtagat	A	G	NM_022034 // upstream // 34831 // Hs.114648 // CUZD1 // 50624 // Homo sapiens CUB and zona pellucida-like domains 1 (CUZD1), mRNA. /// NM_152644 // upstream // 6063 // Hs.114648 // FAM24B // 196792 // Homo sapiens family with sequence similarity 24, membe	CUZD1	CUZD1, Homo sapiens CUB and zona pellucida-like domains 1 (CUZD1), q26.13
SNP_A-1703737	aaatgccatgatgtaaatttgtatg[A/C]aagttgtgtgaacattaaggaattt	A	C	NM_004725 // downstream // 209864 // Hs.418533 // BUB3 // 9184 // BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) /// NM_153442 // upstream // 291128 // Hs.12751 // GPR26 // 2849 // G protein-coupled receptor 26	BUB3	BUB3 , rs4980285, BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast), q26.13
SNP_A-2173712	cacacacacaacttgc[C/T]attggatttaaatgt	C	T	NM_004725 // upstream // 1816 // Hs.418533 // BUB3 // 9184 // Homo sapiens BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), mRNA. /// ENST00000342742 // downstream // 2476 // --- // --- // --- /// ENST00000284670 // upstream //	BUB3	BUB3, Homo sapiens BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), q26.13
SNP_A-2006276	gtgctttactagtgcc[A/G]gcgcagtagtgcttag	A	G	NM_004725 // downstream // 329 // Hs.418533 // BUB3 // 9184 // Homo sapiens BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), mRNA. /// ENST00000284670 // downstream // 329 // --- // --- // --- /// ENST00000339577 // downstream /	BUB3	BUB3, Homo sapiens BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), q26.13
SNP_A-2308221	gcttggactggaagat[A/G]agccactaggaaaat	A	G	NM_153442 // upstream // 191379 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 303106 // --- // --- // --- /// ENST00000284674 // upstream // 191379 // --- // --- // ---	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1814317	gtgtgaaaggagaagc[G/T]aattctggcagatgaa	G	T	NM_153442 // upstream // 186619 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 307866 // --- // --- // --- /// ENST00000284674 // upstream // 186619 // --- // --- // ---	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-2045381	aagaataaattcagca[A/G]gagagctgcggtgag	A	G	NM_153442 // upstream // 176107 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 318378 // --- // --- // --- /// ENST00000284674 // upstream // 176107 // --- // --- // ---	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-2305645	gctgcatgcctgtcc[A/G]ctggtttggagaacag	A	G	NM_153442 // upstream // 173778 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 320707 // --- // --- // --- /// ENST00000284674 // upstream // 173778 // --- // --- // ---	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1881784	tctttgtctctccaat[A/G]atcacaaagttaagct	A	G	NM_153442 // upstream // 172634 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 321851 // --- // --- // --- /// ENST00000284674 // upstream // 172634 // --- // --- // ---	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101956	agatgggtttggtgag[A/G]atgaaaacaacactta	A	G	NM_153442 // upstream // 170798 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 323687 // — // — // — // — /// ENST00000284674 // upstream // 170798 // — // — // —	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1947688	tttactagctcaaacc[G/T]ctgaagctcagaatga	G	T	NM_153442 // upstream // 166255 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 328230 // — // — // — // — /// ENST00000284674 // upstream // 166255 // — // — // —	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-2034021	aaatcagactaatacg[G/T]cctgagaggaaattta	G	T	NM_153442 // upstream // 87141 // Hs.12751 // GPR26 // 2849 // Homo sapiens G protein-coupled receptor 26 (GPR26), mRNA. /// ENST00000339577 // upstream // 407344 // — // — // — // — /// ENST00000284674 // upstream // 87141 // — // — // — //	GPR26	GPR26, Homo sapiens G protein-coupled receptor 26 (GPR26), q26.13
SNP_A-1920010	ttaatagtaaccaaac[C/T]ctctgctctaacaacc	C	T	ENST00000313360 // 5UTR // 0 // — // — // — // —	-	q26.13
SNP_A-1878368	tctgtcttcactctga[C/T]tcaatcaccaggggat	C	T	NM_198148 // downstream // 41581 // Hs.307574 // CPXM2 // 119587 // Homo sapiens carboxypeptidase X (M14 family), member 2 (CPXM2), mRNA. /// ENST00000313360 // downstream // 6660 // — // — // — // — /// ENST00000241305 // downstream // 41581 // -	CPXM2	CPXM2, Homo sapiens carboxypeptidase X (M14 family), member 2 (CPXM2), q26.13
SNP_A-1878205	tctgtcaatgggctaa[A/G]tggacctaacttacta	A	G	NM_198148 // intron // 0 // Hs.307574 // CPXM2 // 119587 // Homo sapiens carboxypeptidase X (M14 family), member 2 (CPXM2), mRNA. /// ENST00000241305 // intron // 0 // — // — // — // —	CPXM2	CPXM2, Homo sapiens carboxypeptidase X (M14 family), member 2 (CPXM2), q26.13
SNP_A-2176646	caccccagcagactag[A/G]accaaactggaaccca	A	G	NM_015892 // upstream // 11209 // Hs.287537 // GALNAC4S-6ST // 51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// NM_000274 // downstream // 222762 // Hs.523332 // OAT // 4942 // Homo sapiens ornithine aminotransferase (gyrate a	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-1864666	tccagcagcatatgcc[A/C]acaaggactgcaaaca	A	C	NM_015892 // upstream // 11304 // Hs.287537 // GALNAC4S-6ST // 51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// NM_000274 // downstream // 222667 // Hs.523332 // OAT // 4942 // Homo sapiens ornithine aminotransferase (gyrate a	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-2132622	atagttgaagaggcaa[A/G]gaatcaaatattaata	A	G	NM_015892 // upstream // 13219 // Hs.287537 // GALNAC4S-6ST // 51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// NM_000274 // downstream // 220752 // Hs.523332 // OAT // 4942 // Homo sapiens ornithine aminotransferase (gyrate a	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-1960557	tttttcataaacccac[C/T]cattaacagccatgag	C	T	NM_015892 // upstream // 72687 // Hs.287537 // GALNAC4S-6ST // 51363 // Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), mRNA. /// NM_000274 // downstream // 161284 // Hs.523332 // OAT // 4942 // Homo sapiens ornithine aminotransferase (gyrate a	GALNAC4S-6ST	GALNAC4S-6ST, Homo sapiens B cell RAG associated protein (GALNAC4S-6ST), q26.13
SNP_A-2006360	tttaggaatgttaaac[A/G]ctaattcttaattcaa	A	G	NM_000274 // 3UTR // 0 // Hs.523332 // OAT // 4942 // Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000224242 // 3UTR // 0 // — // — // — // —	OAT	OAT, Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, q26.13
SNP_A-2236836	ctctagaaaattacca[A/T]gtaggaagtgttaata	A	T	NM_000274 // upstream // 9737 // Hs.523332 // OAT // 4942 // Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000224242 // upstream // 9737 // — // — // — // — /// ENST000	OAT	OAT, Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, q26.13
SNP_A-2305568	gctgcacgtaggtcca[A/T]tcttggatggtgcctt	A	T	NM_032182 // downstream // 50613 // Hs.280695 // KIAA0157 // 23172 // Homo sapiens KIAA0157 (KIAA0157), mRNA. /// NM_017580 // upstream // 54843 // Hs.546399 // ZRANB1 // 54764 // Homo sapiens zinc finger, RAN-binding domain containing 1 (ZRANB1), mRNA. /	KIAA0157	KIAA0157, Homo sapiens KIAA0157 (KIAA0157), q26.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2039528	aacatcctctacaggg[A/C]aaagaagtatgctgat	A	C	NM_032182 // downstream // 84411 // Hs.280695 // KIAA0157 // 23172 // Homo sapiens KIAA0157 (KIAA0157), mRNA. /// NM_017580 // upstream // 21045 // Hs.546399 // ZRANB1 // 54764 // Homo sapiens zinc finger, RAN-binding domain containing 1 (ZRANB1), mRNA. /	KIAA0157	KIAA0157, Homo sapiens KIAA0157 (KIAA0157), q26.13
SNP_A-2268940	gaattcagaagatcaa[A/G]caacgtctattttatc	A	G	NM_032182 // downstream // 105321 // Hs.280695 // KIAA0157 // 23172 // Homo sapiens KIAA0157 (KIAA0157), mRNA. /// NM_017580 // upstream // 135 // Hs.546399 // ZRANB1 // 54764 // Homo sapiens zinc finger, RAN-binding domain containing 1 (ZRANB1), mRNA. //	KIAA0157	KIAA0157, Homo sapiens KIAA0157 (KIAA0157), q26.13
SNP_A-2128949	ataatgtatagcaaca[C/T]tatgaatcccatttttt	C	T	NM_001329 // intron // 0 // Hs.501345 // CTBP2 // 1488 // Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA. /// ENST00000337195 // intron // 0 // — // — // — // — /// ENST00000309022 // intron // 0 // — // — // —	CTBP2	CTBP2, Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, q26.13
SNP_A-1824920	taaagccaggattctg[C/G]acagattgctgcccct	C	G	NM_001329 // intron // 0 // Hs.501345 // CTBP2 // 1488 // Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA. /// ENST00000337195 // intron // 0 // — // — // — // — /// ENST00000309022 // intron // 0 // — // — // —	CTBP2	CTBP2, Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, q26.13
SNP_A-2074011	acagttgctaagctaa[C/T]gagaaaacactaatca	C	T	NM_207424 // upstream // 141841 // Hs.531501 // — // 0 // Homo sapiens FLJ40536 protein (FLJ40536), mRNA. /// ENST00000316750 // upstream // 141841 // — // — // — // — /// ENST00000308945 // downstream // 286607 // — // — // — // —	-	-, Homo sapiens FLJ40536 protein (FLJ40536), q26.13
SNP_A-1815896	gttaatcttggtgcaa[C/T]ctggacattttatatc	C	T	NM_207424 // upstream // 246564 // Hs.531501 // — // 0 // Homo sapiens FLJ40536 protein (FLJ40536), mRNA. /// ENST00000316750 // upstream // 246564 // — // — // — // — /// ENST00000308945 // downstream // 181884 // — // — // — // —	-	-, Homo sapiens FLJ40536 protein (FLJ40536), q26.13
SNP_A-2006465	catacacaaatacaaa[C/T]aggctatgctcccaga	C	T	NM_000375 // intron // 0 // Hs.501376 // UROS // 7390 // Homo sapiens uroporphyrinogen III synthase (congenital erythropoietic porphyria) (UROS), mRNA. /// ENST00000342958 // intron // 0 // — // — // — // —	UROS	UROS, Homo sapiens uroporphyrinogen III synthase (congenital erythropoietic porphyria) (UROS), q26.2
SNP_A-1654981	attttaaagttcatgtaggtgttga[C/T]aatgatttccctttcaagccagaac	C	T	NM_003474 // intron // 0 // Hs.8850 // ADAM12 // 8038 // a disintegrin and metalloproteinase domain 12 (meltrin alpha) /// NM_021641 // intron // 0 // Hs.8850 // ADAM12 // 8038 // a disintegrin and metalloproteinase domain 12 (meltrin alpha)	ADAM12	ADAM12 , rs10510152, a disintegrin and metalloproteinase domain 12 (meltrin alpha) ,q26.2
SNP_A-1660751	acatttttttaaataattgattgga[C/T]tcaagaagcaccacaaggccagaaa	C	T	NM_003474 // intron // 0 // Hs.8850 // ADAM12 // 8038 // a disintegrin and metalloproteinase domain 12 (meltrin alpha) /// NM_021641 // intron // 0 // Hs.8850 // ADAM12 // 8038 // a disintegrin and metalloproteinase domain 12 (meltrin alpha)	ADAM12	ADAM12 , rs4357606, a disintegrin and metalloproteinase domain 12 (meltrin alpha) ,q26.2
SNP_A-2129127	ataattgaagctgggt[A/G]acagatacaagaggat	A	G	NM_078468 // downstream // 131001 // Hs.370292 // BCCIP // 56647 // Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant B, mRNA. /// NM_016567 // downstream // 113965 // Hs.370292 // BCCIP // 56647 // Homo sapiens BRCA2 and CDKN1	BCCIP	BCCIP, Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant B, q26.2
SNP_A-2144822	atgatgtgggaggaca[C/T]gtgacaactggtgagt	C	T	NM_003474 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disin	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-1791811	gggtgacaggcataca[C/T]ctactgcactaaagaa	C	T	NM_003474 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disin	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2026559	aaacaacagtgaaaaa[C/T]aagtcattctgcatct	C	T	NM_003474 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disin	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-1912159	tgtgagtttgcaagtct[C/T]acgtggcacagagaca	C	T	NM_003474 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disin	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-2058097	aatatttttgataaggg[A/G]aaatccatgaatgaat	A	G	NM_003474 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, mRNA. /// NM_021641 // intron // 0 // Hs.386283 // ADAM12 // 8038 // Homo sapiens a disin	ADAM12	ADAM12, Homo sapiens a disintegrin and metalloproteinase domain 12 (meltrin alpha) (ADAM12), transcript variant 1, q26.2
SNP_A-1665240	catgggtgtttataaacagtgaa[C/T]atgcaacaacaaggaa aggctttcc	C	T	NM_001380 // upstream // 125513 // Hs.437620 // DOCK1 // 1793 // dedicator of cytokinesis 1	DOCK1	DOCK1, rs7894577, dedicator of cytokinesis 1,q26.2
SNP_A-1881002	tcttgttattaggaaaa[C/T]ggcatgagtgtgtgc	C	T	NM_001004298 // intron // 0 // Hs.44939 // C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// ENST00000356858 // intron // 0 // — // — // — /// ENST00000284694 // intron // 0 // — // — // — // -	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-2287029	gatggttttgggatga[C/T]tcaaatgcattacact	C	T	NM_001004298 // upstream // 191775 // Hs.44939 // C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 // upstream // 192238 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1)	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-1739475	ttaactagctttcaacacttaaa[C/T]atagaaatgattcaccgtg acttg	C	T	NM_001380 // intron // 0 // Hs.437620 // DOCK1 // 1793 // dedicator of cytokinesis 1	DOCK1	DOCK1, rs1770390, dedicator of cytokinesis 1,q26.2
SNP_A-2249694	cttaatacgcaagtgc[A/G]ctgtaacctttcaga	A	G	NM_001004298 // upstream // 219924 // Hs.44939 // C10orf90 // 118611 // Homo sapiens chromosome 10 open reading frame 90 (C10orf90), mRNA. /// NM_001380 // upstream // 164089 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1)	C10orf90	C10orf90, Homo sapiens chromosome 10 open reading frame 90 (C10orf90), q26.2
SNP_A-2096929	agactctgtgaattca[A/G]tatgttacatggcaaa	A	G	NM_001380 // intron // 0 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// ENST00000280333 // intron // 0 // — // — // —	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-2204065	ccagcaactgtgcttct[C/T]aaacataggatcttct	C	T	NM_001380 // intron // 0 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// ENST00000280333 // intron // 0 // — // — // —	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-1825726	taaatccaagctttac[A/T]gagattataaatttgt	A	T	NM_001380 // intron // 0 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// ENST00000280333 // intron // 0 // — // — // —	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-2279782	gaggccatatgagaaac[C/G]atcatgcaagagacca	C	G	NM_001380 // intron // 0 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// ENST00000280333 // intron // 0 // — // — // —	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-2209302	cccagtggctctgggga[A/G]cttctgtaaatcttac	A	G	NM_001380 // intron // 0 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// ENST00000280333 // intron // 0 // — // — // —	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2
SNP_A-2059289	aatcgacaccagaaac[A/C]actgaactgacgagag	A	C	NM_001380 // downstream // 240280 // Hs.159195 // DOCK1 // 1793 // Homo sapiens dedicator of cytokinesis 1 (DOCK1), mRNA. /// NM_207426 // upstream // 45771 // Hs.449674 // FLJ46831 // 399823 // Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// ENST0000	DOCK1	DOCK1, Homo sapiens dedicator of cytokinesis 1 (DOCK1), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169238	caagcaaaattcaaac[A/C]actttgaactcgttt	A	C	NM_207426 // downstream // 14443 // Hs.449674 // FLJ46831 // 399823 /// Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 124442 // Hs.242014 // MGC32871 // 119467 // Homo sapiens hypothetical protein MGC32871 (MGC32871), mRNA.	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-2282680	gagttgttctatc[A/T]cagtataaactcat	A	T	NM_207426 // downstream // 66742 // Hs.449674 // FLJ46831 // 399823 /// Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 72143 // Hs.242014 // MGC32871 // 119467 // Homo sapiens hypothetical protein MGC32871 (MGC32871), mRNA.	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-2192411	catcatgccagcatga[A/T]ctgtggcaaaacatg	A	T	NM_207426 // downstream // 79910 // Hs.449674 // FLJ46831 // 399823 /// Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 58975 // Hs.242014 // MGC32871 // 119467 // Homo sapiens hypothetical protein MGC32871 (MGC32871), mRNA.	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-2067376	acaaatactcttccq[A/G]gctgactttgctcaga	A	G	NM_207426 // downstream // 87553 // Hs.449674 // FLJ46831 // 399823 /// Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 51332 // Hs.242014 // MGC32871 // 119467 // Homo sapiens hypothetical protein MGC32871 (MGC32871), mRNA.	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-2089696	acttccagccttgatg[A/G]aaatgttctgttacct	A	G	NM_207426 // downstream // 88128 // Hs.449674 // FLJ46831 // 399823 /// Homo sapiens FLJ46831 protein (FLJ46831), mRNA. /// NM_152311 // downstream // 50757 // Hs.242014 // MGC32871 // 119467 // Homo sapiens hypothetical protein MGC32871 (MGC32871), mRNA.	FLJ46831	FLJ46831, Homo sapiens FLJ46831 protein (FLJ46831), q26.2
SNP_A-1815129	gtgttctctctgga[C/T]cttcatagtggtgtg	C	T	NM_006504 // intron // 0 // Hs.127022 // PTPRE // 5791 // Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA. /// ENST00000254667 // intron // 0 // — // — // — // ///, ENST00000360287 // intron // 0 //	PTPRE	PTPRE, Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, q26.2
SNP_A-2089813	acttcgatgatgacgt[G/T]aagttgtctgcaaatc	G	T	NM_006504 // intron // 0 // Hs.127022 // PTPRE // 5791 // Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA. /// ENST00000254667 // intron // 0 // — // — // — // ///, ENST00000360287 // intron // 0 //	PTPRE	PTPRE, Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, q26.2
SNP_A-2082888	acgtcccttgttcttc[C/T]gaaagactcaaaattg	C	T	NM_006504 // intron // 0 // Hs.127022 // PTPRE // 5791 // Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA. /// ENST00000254667 // intron // 0 // — // — // — // ///, ENST00000360287 // intron // 0 //	PTPRE	PTPRE, Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, q26.2
SNP_A-2063714	aattagaaccccccaga[C/T]attgctggtaagaatt	C	T	NM_006504 // intron // 0 // Hs.127022 // PTPRE // 5791 // Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA. /// ENST00000254667 // intron // 0 // — // — // — // ///, ENST00000360287 // intron // 0 //	PTPRE	PTPRE, Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, q26.2
SNP_A-2088859	actgttgagggagtag[A/G]atatacaacctgctt	A	G	NM_006504 // intron // 0 // Hs.127022 // PTPRE // 5791 // Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA. /// ENST00000254667 // intron // 0 // — // — // — // ///, ENST00000360287 // intron // 0 //	PTPRE	PTPRE, Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, q26.2
SNP_A-1877094	tctgctctaagaaggc[A/G]agatcggagtttgtg	A	G	NM_002417 // upstream // 20686 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 20686 // — // — // — // — /// ENST00000344483 // upstream // 21223 // —	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2159816	atttagttctcatctg[C/G]acctatccacatccagt	C	G	NM_002417 // upstream // 242829 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 242829 // — // — // — // — /// ENST00000344483 // upstream // 243366 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2217957	cctgcagtctgcctct[C/T]actaaatgtctggtt	C	T	NM_002417 // upstream // 365051 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 365051 // --- // --- // --- /// ENST00000344483 // upstream // 365588 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2195091	catggaataaaccaaa[C/G]gatgggacaaactag	C	G	NM_002417 // upstream // 367069 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 367069 // --- // --- // --- /// ENST00000344483 // upstream // 367606 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2298953	gccccatgcactgtga[C/T]ggaggttatttctctg	C	T	NM_002417 // upstream // 393749 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 393749 // --- // --- // --- /// ENST00000344483 // upstream // 394286 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1786353	ggctgttggcccatc[C/T]aacaaaaggcaatgtg	C	T	NM_002417 // upstream // 393990 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 393990 // --- // --- // --- /// ENST00000344483 // upstream // 394527 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1834724	taccagaaatagaaaag[C/G]aacattgcagaatgat	C	G	NM_002417 // upstream // 511153 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 511153 // --- // --- // --- /// ENST00000344483 // upstream // 511690 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1787948	gggactttcaggtac[C/T]agcacttaaaggcaga	C	T	NM_002417 // upstream // 532586 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 532586 // --- // --- // --- /// ENST00000344483 // upstream // 533123 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2110800	aggactacaccttcca[C/T]gaatgttctgctaacc	C	T	NM_002417 // upstream // 587427 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 587427 // --- // --- // --- /// ENST00000344483 // upstream // 587964 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-1952869	tttctactagattctt[A/C]acagcttactggcatt	A	C	NM_002417 // upstream // 588455 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 588455 // --- // --- // --- /// ENST00000344483 // upstream // 588992 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2259756	gaaaagagcccgtttct[A/G]caggtgcaggtgtttg	A	G	NM_002417 // upstream // 661284 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 661284 // --- // --- // --- /// ENST00000344483 // upstream // 661821 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.2
SNP_A-2234217	ctcatttcccttaggt[C/T]acaggatatcagcggg	C	T	NM_002417 // upstream // 694899 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 694899 // --- // --- // --- /// ENST00000344483 // upstream // 695436 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.3
SNP_A-1900031	tggacctatctattaa[G/T]tctccatactccact	G	T	NM_002417 // upstream // 751049 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 751049 // --- // --- // --- /// ENST00000344483 // upstream // 751586 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.3
SNP_A-2300701	gcctgctttcagtgaa[C/T]gctcagctaccggccc	C	T	NM_002417 // upstream // 783697 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 783697 // --- // --- // --- /// ENST00000344483 // upstream // 784234 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.3
SNP_A-2001584	tctttcttctgcccac[C/T]acagcaaattcaggtc	C	T	NM_002417 // upstream // 786455 // Hs.80976 // MKI67 // 4288 // Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA. /// ENST00000277994 // upstream // 786455 // --- // --- // --- /// ENST00000344483 // upstream // 786992 //	MKI67	MKI67, Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), q26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884818	tgaatccagtggta[A/G]gaatcctctgaatccc	A	G	NM_002412 // upstream // 519150 // Hs.501522 // MGMT // 4255 // Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), mRNA. /// ENST00000248179 // downstream // 32936 // — // — // — /// ENST00000306010 // upstream // 519150 // — // -	MGMT	MGMT, Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), q26.3
SNP_A-1935353	ttctggaaatcagtct[A/G]acatatcaagagacta	A	G	ENST00000318084 // downstream // 41135 // — // — // — /// ENST00000355311 // downstream // 6024 // — // — // — /// ENST00000318060 // downstream // 7503 // — // — // —	-	q26.3
SNP_A-1818375	gttcttaccacgtaaa[A/G]tagccaaaaatgata	A	G	ENST00000355311 // intron // 0 // — // — // — /// ENST00000318060 // intron // 0 // — // — // —	-	q26.3
SNP_A-2006682	cactgttcaacacca[C/T]gaagttacagaaggtg	C	T	ENST00000355311 // intron // 0 // — // — // — /// ENST00000318060 // intron // 0 // — // — // —	-	q26.3
SNP_A-2310333	ggaacgttctgcatcc[C/T]gactttatcaacatgg	C	T	ENST00000355311 // upstream // 36436 // — // — // — /// ENST00000318060 // upstream // 35930 // — // — // — /// ENST00000316929 // upstream // 105805 // — // — // —	-	q26.3
SNP_A-1863447	tccaaaaggctttaa[A/T]caccacagtagtgctg	A	T	NM_006541 // upstream // 1969 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// ENST00000316929 // downstream // 25601 // — // — // — /// ENST00000225000 // upstream // 1969 // — // — // —	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2213374	ccggcactggccaag[A/C]ctcacaacagcctggg	A	C	NM_006541 // downstream // 38801 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 873215 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L), m	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2213367	ccggcaaggatggagg[A/C]agcactgttgttgga	A	C	NM_006541 // downstream // 124043 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 787973 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L).	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1902255	tggccagcatgtgagg[C/T]cccgggctccgggttt	C	T	NM_006541 // downstream // 320305 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 591711 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L).	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2114577	agggaggccaagccta[C/T]aacctgtgactagcag	C	T	NM_006541 // downstream // 332869 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 579147 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L).	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2266138	gaaggctttggtccag[A/T]aagtcctgcttctctt	A	T	NM_006541 // downstream // 336328 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 575688 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L).	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1743551	gcatggcagagggtacaggacctaa[A/T]atggttttctgtgtccc cacccaa	A	T	NM_006541 // downstream // 764111 // Hs.42644 // TXNL2 // 10539 // thioredoxin-like 2 /// NM_174937 // downstream // 143761 // Hs.7621 // TCERG1L // 256536 // transcription elongation regulator 1-like	TXNL2	TXNL2, rs1368665, thioredoxin-like 2 ,q26.3
SNP_A-1952065	tttctattgtgaataa[A/G]tgtgaaagtcagaaacc	A	G	NM_006541 // downstream // 429485 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 482531 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L).	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2202713	ccacgactctgggacc[C/T]caatacttagtgtgtc	C	T	NM_006541 // downstream // 587529 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 324487 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1863491	tccaaacccattttca[A/G]agatgcattgtccttg	A	G	NM_006541 // downstream // 591671 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 320345 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2306823	gctgtgcacattcagc[A/G]agtgccttacgctttc	A	G	NM_006541 // downstream // 756437 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 155579 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1887355	tgagaatcggacaccg[C/T]agtgcggcagcgctgt	C	T	NM_006541 // downstream // 757879 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 154137 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1792235	gggttcaattttggta[C/T]gctgtattttcctgga	C	T	NM_006541 // downstream // 760117 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 151899 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1827649	taactggttatagctg[C/T]agcacctctttctatt	C	T	NM_006541 // downstream // 762168 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 149848 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2284031	gatatattttggtgaa[A/T]cgaatatcaattttca	A	T	NM_006541 // downstream // 768759 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 143257 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-2267973	gaatctccatgaagaa[A/T]cctttgcagtaacaac	A	T	NM_006541 // downstream // 773278 // Hs.42644 // TXNL2 // 10539 // Homo sapiens thioredoxin-like 2 (TXNL2), mRNA. /// NM_174937 // downstream // 138738 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L),	TXNL2	TXNL2, Homo sapiens thioredoxin-like 2 (TXNL2), q26.3
SNP_A-1883400	tgaacagaagccatgc[A/G]ctattaaaacagtggc	A	G	NM_174937 // intron // 0 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L), mRNA. /// ENST00000315848 // intron // 0 // — // — // — // —	TCERG1L	TCERG1L, Homo sapiens transcription elongation regulator 1-like (TCERG1L), q26.3
SNP_A-2187092	caggtcaaaggtagat[A/G]agagaggaatggttgc	A	G	NM_174937 // intron // 0 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L), mRNA. /// ENST00000315848 // intron // 0 // — // — // — // —	TCERG1L	TCERG1L, Homo sapiens transcription elongation regulator 1-like (TCERG1L), q26.3
SNP_A-1922068	ttactgtaaatggata[A/G]gtaaatgactggtaaa	A	G	NM_174937 // upstream // 53405 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L), mRNA. /// NM_001001677 // downstream // 401343 // Hs.523353 // FLJ46300 // 399827 // Homo sapiens FLJ46300 protein (FLJ46	TCERG1L	TCERG1L, Homo sapiens transcription elongation regulator 1-like (TCERG1L), q26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181151	cagacaggtggaggga[G/T]actggccagagctggc	G	T	NM_174937 // upstream // 389313 // Hs.126575 // TCERG1L // 256536 // Homo sapiens transcription elongation regulator 1-like (TCERG1L), mRNA. /// NM_001001677 // downstream // 65435 // Hs.523353 // FLJ46300 // 399827 // Homo sapiens FLJ46300 protein (FLJ46	TCERG1L	TCERG1L, Homo sapiens transcription elongation regulator 1-like (TCERG1L), q26.3
SNP_A-1916368	tgttgtgtttctagaa[A/C]tcgtcagctgggaggt	A	C	NM_001001677 // upstream // 121793 // Hs.523353 // FLJ46300 // 399827 // Homo sapiens FLJ46300 protein (FLJ46300), mRNA. /// NM_018461 // upstream // 3627 // Hs.380372 // PPP2R2D // 55844 // Homo sapiens protein phosphatase 2, regulatory subunit B, delta	FLJ46300	FLJ46300, Homo sapiens FLJ46300 protein (FLJ46300), q26.3
SNP_A-1931617	ttcccggtcacggcac[C/T]gcctttcactgatgc	C	T	NM_018461 // intron // 0 // Hs.380372 // PPP2R2D // 55844 // Homo sapiens protein phosphatase 2, regulatory subunit B, delta isoform (PPP2R2D), transcript variant 1, mRNA. /// NM_001003656 // intron // 0 // Hs.380372 // PPP2R2D // 55844 // Homo sapiens pr	PPP2R2D	PPP2R2D, Homo sapiens protein phosphatase 2, regulatory subunit B, delta isoform (PPP2R2D), transcript variant 1, q26.3
SNP_A-1826977	taacatttatgaaacc[A/G]gctaaaactcaaaacc	A	G	NM_018461 // intron // 0 // Hs.380372 // PPP2R2D // 55844 // Homo sapiens protein phosphatase 2, regulatory subunit B, delta isoform (PPP2R2D), transcript variant 1, mRNA. /// NM_001003656 // intron // 0 // Hs.380372 // PPP2R2D // 55844 // Homo sapiens pr	PPP2R2D	PPP2R2D, Homo sapiens protein phosphatase 2, regulatory subunit B, delta isoform (PPP2R2D), transcript variant 1, q26.3
SNP_A-1829987	taatacaaaggcaagc[C/G]agggtctgtctcggag	C	G	NM_004052 // intron // 0 // — // BNIP3 // 664 // Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000313081 // intron // 0 // — // — // —	BNIP3	BNIP3, Homo sapiens BCL2,q26.3
SNP_A-1784663	ggcctcttctaatga[C/T]aaaaggcgtttgct	C	T	NM_004052 // upstream // 3203 // — // BNIP3 // 664 // Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000313081 // upstream // 3203 // — // — // — /// ENST00	BNIP3	BNIP3, Homo sapiens BCL2,q26.3
SNP_A-2264641	gaagaatgttgctaa[C/T]agaggaatttcctcatc	C	T	ENST00000298622 // intron // 0 // — // — // —	-	q26.3
SNP_A-2299148	gcccgtagggagtatc[A/G]cttgacggagagtgag	A	G	NM_173575 // intron // 0 // Hs.469002 // STK32C // 282974 // Homo sapiens serine/threonine kinase 32C (STK32C), mRNA. /// ENST00000298630 // intron // 0 // — // — // —	STK32C	STK32C, Homo sapiens serine q26.3
SNP_A-2298983	gccccctccgagagac[C/T]ggaaaatatgttggtac	C	T	NM_173572 // upstream // 45014 // Hs.375837 // C10orf93 // 255352 // Homo sapiens chromosome 10 open reading frame 93 (C10orf93), mRNA. /// NM_032422 // upstream // 122246 // Hs.435183 // GPR123 // 84435 // Homo sapiens G protein-coupled receptor 123 (GPR	C10orf93	C10orf93, Homo sapiens chromosome 10 open reading frame 93 (C10orf93), q26.3
SNP_A-2036059	aaattacctcaaaatg[C/G]accataggtttaaatg	C	G	NM_173572 // upstream // 56334 // Hs.375837 // C10orf93 // 255352 // Homo sapiens chromosome 10 open reading frame 93 (C10orf93), mRNA. /// NM_032422 // upstream // 110926 // Hs.435183 // GPR123 // 84435 // Homo sapiens G protein-coupled receptor 123 (GPR	C10orf93	C10orf93, Homo sapiens chromosome 10 open reading frame 93 (C10orf93), q26.3
SNP_A-1703733	atgctgcaaaccagagagcaaggac[A/C]acatggaagatgc agaggaaggct	A	C	NM_000773 // upstream // 65509 // Hs.75183 // CYP2E1 // 1571 // cytochrome P450, family 2, subfamily E, polypeptide 1 /// NM_138384 // downstream // 40535 // Hs.449641 // Spm // 92170 // shadow of prion protein	CYP2E1	CYP2E1, rs2252728, cytochrome P450, family 2, subfamily E, polypeptide 1, q26.3
SNP_A-1928678	ttcagaaaaggaaaaca[C/T]caaaggcgctggagct	C	T	NM_032422 // intron // 0 // Hs.435183 // GPR123 // 84435 // Homo sapiens G protein-coupled receptor 123 (GPR123), mRNA. /// ENST00000359673 // intron // 0 // — // — // — // — /// ENST00000360949 // intron // 0 // — // — // — // —	GPR123	GPR123, Homo sapiens G protein-coupled receptor 123 (GPR123), q26.3
SNP_A-2259588	gaaaacctgctataaa[A/C]ggtaatgatgacaaa	A	C	NM_033404 // intron // 0 // Hs.530685 // KNDC1 // 85442 // Homo sapiens kinase non-catalytic C-lobe domain (KIND) containing 1 (KNDC1), transcript variant 2, mRNA. /// NM_152643 // intron // 0 // Hs.530685 // KNDC1 // 85442 // Homo sapiens kinase non-cata	KNDC1	KNDC1, Homo sapiens kinase non-catalytic C-lobe domain (KIND) containing 1 (KNDC1), transcript variant 2, q26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2269324	gaatttgataaaagtc[A/G]acacttatgataaaaa	A	G	ENST00000298743 // intron // 0 // — // — // — // —	-	q26.3
SNP_A-2188173	cagtcccttctggttg[A/G]aatatttgcatcatgt	A	G	NM_021034 // upstream // 45660 // Hs.374650 // IFITM3 // 10410 // Homo sapiens interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA. /// NM_178537 // upstream // 3094 // Hs.148074 // Beta4GalNAc-T4 // 338707 // Homo sapiens beta1,4-N-acetylgal	IFITM3	IFITM3, Homo sapiens interferon induced transmembrane protein 3 (1-8U) (IFITM3), p15.5
SNP_A-2258027	ctttgtgtgctccaga[A/G]aaaggggcagcacca	A	G	NM_003475 // downstream // 1822 // Hs.72925 // C11orf13 // 8045 // Homo sapiens chromosome 11 open reading frame 13 (C11orf13), mRNA. /// ENST00000344375 // downstream // 1822 // — // — // — // — /// ENST00000264555 // upstream // 10646 // — //	C11orf13	C11orf13, Homo sapiens chromosome 11 open reading frame 13 (C11orf13), p15.5
SNP_A-1926594	ttattcttgtattcac[C/T]atctgctgtatcagct	C	T	ENST00000264555 // intron // 0 // — // — // — // —	-	p15.5
SNP_A-1887974	tgagcacctcttagaa[C/T]agcagccggagccagg	C	T	ENST00000264555 // intron // 0 // — // — // — // —	-	p15.5
SNP_A-1786205	ggctggtcctgggaag[C/T]aggtagtcggagaagg	C	T	NM_000797 // downstream // 1288 // Hs.99922 // DRD4 // 1815 // Homo sapiens dopamine receptor D4 (DRD4), mRNA. /// NM_021008 // downstream // 2234 // Hs.243994 // DEAF1 // 10522 // Homo sapiens deformed epidermal autoregulatory factor 1 (Drosophila) (DEAF	DRD4	DRD4, Homo sapiens dopamine receptor D4 (DRD4), p15.5
SNP_A-2100287	agagtttccaacagac[C/T]gagttggccgccacag	C	T	NM_021008 // intron // 0 // Hs.243994 // DEAF1 // 10522 // Homo sapiens deformed epidermal autoregulatory factor 1 (Drosophila) (DEAF1), mRNA. /// ENST00000317330 // intron // 0 // — // — // — // — /// ENST00000338675 // intron // 0 // — // —	DEAF1	DEAF1, Homo sapiens deformed epidermal autoregulatory factor 1 (Drosophila) (DEAF1), p15.5
SNP_A-1797583	ggtttctacatgctaa[A/G]gagcaacacggagcgg	A	G	NM_022772 // downstream // 5346 // Hs.55016 // EPS8L2 // 64787 // Homo sapiens EPS8-like 2 (EPS8L2), mRNA. /// NM_006755 // upstream // 14360 // Hs.438678 // TALDO1 // 6888 // Homo sapiens transaldolase 1 (TALDO1), mRNA. /// ENST00000318562 // downstream	EPS8L2	EPS8L2, Homo sapiens EPS8-like 2 (EPS8L2), p15.5
SNP_A-2070005	acacagtggacacgct[A/G]aaggttggcaggctgc	A	G	AF086604 // CDS // 0 // Hs.523395 // MUC5B // 4587 // Homo sapiens mucin (MUC5B) mRNA, partial cds. /// ENST00000349637 // CDS // 0 // — // — // — // —	MUC5B	MUC5B, Homo sapiens mucin (MUC5B) partial cds. ,p15.5
SNP_A-2265433	gaagccaaagttcatg[A/G]atgacattttgttgtt	A	G	NM_019009 // upstream // 49925 // Hs.368527 // TOLLIP // 54472 // Homo sapiens toll interacting protein (TOLLIP), mRNA. /// NM_003957 // upstream // 30367 // Hs.170819 // BRSK2 // 9024 // Homo sapiens serine/threonine kinase 29 (STK29), mRNA. /// NM_05300	TOLLIP	TOLLIP, Homo sapiens toll interacting protein (TOLLIP), p15.5
SNP_A-1928363	ttcacccaaattattc[C/T]actcaccaaatcagcc	C	T	NM_019009 // upstream // 59077 // Hs.368527 // TOLLIP // 54472 // Homo sapiens toll interacting protein (TOLLIP), mRNA. /// NM_003957 // upstream // 21215 // Hs.170819 // BRSK2 // 9024 // Homo sapiens serine/threonine kinase 29 (STK29), mRNA. /// NM_05300	TOLLIP	TOLLIP, Homo sapiens toll interacting protein (TOLLIP), p15.5
SNP_A-2209133	cccaggctgaccaccc[G/T]cgagtgctgcccgcac	G	T	ENST00000359211 // intron // 0 // — // — // — // — /// ENST00000354699 // intron // 0 // — // — // — // —	-	p15.5
SNP_A-1854634	tcaacacaggaaagat[G/T]agagcacgtgggcaga	G	T	NM_207427 // 3UTR // 0 // Hs.501648 // — // 0 // Homo sapiens hypothetical gene supported by AY129010 (LOC399851), mRNA. /// ENST00000331756 // 3UTR // 0 // — // — // — // —	-	-, Homo sapiens hypothetical gene supported by AY129010 (LOC399851), p15.5
SNP_A-2178686	cactcttcctaatcac[C/T]gactcgaactgtaatg	C	T	ENST00000328953 // upstream // 2664 // — // — // — // — /// ENST00000359229 // upstream // 5105 // — // — // — // —	-	p15.5
SNP_A-2304052	gctccagcatacacgg[C/G]aagagtcaccgagtgc	C	G	ENST00000328953 // upstream // 6585 // — // — // — // — /// ENST00000359229 // upstream // 1184 // — // — // — // —	-	p15.5
SNP_A-2194872	catgctagatagaccc[C/T]ctggagtcatttccac	C	T	NM_021134 // intron // 0 // Hs.3254 // MRPL23 // 6150 // Homo sapiens mitochondrial ribosomal protein L23 (MRPL23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000228013 // intron // 0 // — // — // — // —	MRPL23	MRPL23, Homo sapiens mitochondrial ribosomal protein L23 (MRPL23), nuclear gene encoding mitochondrial protein, p15.5

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1847365	tatcccaggatagaaaa[C/T]ctgaacgcatccctga	C	T	NM_006757 // downstream // 25193 // Hs.73454 // TNNT3 // 7140 // Homo sapiens troponin T3, skeletal, fast (TNNT3), mRNA. /// NM_021134 // downstream // 7300 // Hs.3254 // MRPL23 // 6150 // Homo sapiens mitochondrial ribosomal protein L23 (MRPL23), nuclear	TNNT3	TNNT3, Homo sapiens troponin T3, skeletal, fast (TNNT3), p15.5
SNP_A-1930704	ttccacccactggtca[C/T]gttgcagccgggtgag	C	T	ENST00000252900 // upstream // 9071 // — // — // — /// ENST00000329678 // downstream // 122470 // — // — // —	-	p15.5
SNP_A-2100090	agagtggaatatggac[A/G]atggtaggtgtatgaa	A	G	ENST00000252900 // upstream // 68148 // — // — // — /// ENST00000329678 // downstream // 63393 // — // — // —	-	p15.5
SNP_A-2122448	agtgcggagggaacag[A/G]atcatttaggagcaca	A	G	NM_139024 // downstream // 2302 // Hs.271954 // PHEMX // 10077 // Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, mRNA. /// NM_005705 // downstream // 2302 // Hs.271954 // PHEMX // 10077 // Homo sapiens pan-hematopoietic expressio	PHEMX	PHEMX, Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, p15.5
SNP_A-2283063	gataaggagattagta[C/T]ggtagaaggaggtca	C	T	NM_139024 // downstream // 9348 // Hs.271954 // PHEMX // 10077 // Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, mRNA. /// NM_005705 // downstream // 9348 // Hs.271954 // PHEMX // 10077 // Homo sapiens pan-hematopoietic expressio	PHEMX	PHEMX, Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 3, p15.5
SNP_A-2279707	gaggcataaatgttta[C/T]aatggttatctgtaac	C	T	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-2096384	agacccatctctagta[C/T]cagctacgtgggaggt	C	T	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-1859784	tcagggcatcttggaa[A/G]aactgaatttgctaac	A	G	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-2222217	cgacatcttggagaa[A/C]acaacaacaaaggctg	A	C	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-1942229	ttggcactgccttgcc[C/G]aaaacctcctagagac	C	G	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-2186983	caggtaagcccgtgc[C/T]gagccttcctgccctc	C	T	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-1752733	tagccacctttcacacaacttcctg[C/T]ggaaacactgtgaattc ctaagcc	C	T	NM_000218 // intron // 0 // Hs.367809 // KCNQ1 // 3784 // potassium voltage-gated channel, KQT-like subfamily, member 1 /// NM_181797 // intron // 0 // Hs.367809 // KCNQ1 // 3784 // potassium voltage-gated channel, KQT-like subfamily, member 1 /// NM_181	KCNQ1	KCNQ1, rs63934, potassium voltage-gated channel, KQT-like subfamily, member 1, p15.5

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2176134	caccacagtcagatac[A/G]atgctgacagggacgg	A	G	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-2203798	ccagagctcaaggact[A/G]aagttccaaagagcc	A	G	NM_000218 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, mRNA. /// NM_181798 // intron // 0 // Hs.95162 // KCNQ1 // 3784 // Homo sapiens potassium vo	KCNQ1	KCNQ1, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 1 (KCNQ1), transcript variant 1, p15.5
SNP_A-2006973	gatgcaagctaccacc[A/G]ggcggtcagcttgcc	A	G	NM_007105 // intron // 0 // Hs.300076 // SLC22A1LS // 5003 // Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like antisense (SLC22A1LS), mRNA. /// ENST00000315745 // intron // 0 // — // — // —	SLC22A1LS	SLC22A1LS, Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like antisense (SLC22A1LS), p15.4
SNP_A-1932693	ttccttccaaaactcc[C/T]cagcttggtaaca	C	T	ENST00000328126 // downstream // 12101 // — // — // — /// ENST00000333132 // upstream // 1818 // — // — // —	-	p15.4
SNP_A-2304243	gctcctcagagtataa[A/G]gaaaagccagcagcaga	A	G	NM_014489 // intron // 0 // Hs.133968 // FRAG1 // 27315 // Homo sapiens FGF receptor activating protein 1 (FRAG1), mRNA. /// ENST00000350451 // intron // 0 // — // — // — // — /// ENST00000300730 // intron // 0 // — // — // — // — /// ENST	FRAG1	FRAG1, Homo sapiens FGF receptor activating protein 1 (FRAG1), p15.4
SNP_A-2213893	cctaaatggtattaaa[C/G]aactatgagcaacatg	C	G	NM_001665 // upstream // 3602 // Hs.501728 // RHOG // 391 // Homo sapiens ras homolog gene family, member G (rho G) (RHOG), mRNA. /// NM_003156 // upstream // 11147 // Hs.501735 // STIM1 // 6786 // Homo sapiens stromal interaction molecule 1 (STIM1), mRNA	RHOG	RHOG, Homo sapiens ras homolog gene family, member G (rho G) (RHOG), p15.4
SNP_A-1823892	taaaatgtgtctcta[C/T]gaacagcatataattg	C	T	NM_003156 // intron // 0 // Hs.501735 // STIM1 // 6786 // Homo sapiens stromal interaction molecule 1 (STIM1), mRNA. /// ENST00000300737 // intron // 0 // — // — // — // —	STIM1	STIM1, Homo sapiens stromal interaction molecule 1 (STIM1), p15.4
SNP_A-1920464	ttaattatttttagta[C/T]agttgacaagcaaaaa	C	T	ENST00000334059 // upstream // 16488 // — // — // — // — /// ENST00000334468 // upstream // 25303 // — // — // — // —	-	p15.4
SNP_A-2007105	gccatgaaccctttta[C/T]gcctatactctagtgt	C	T	NM_001005172 // upstream // 14615 // — // OR52K2 // 119774 // Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), mRNA. /// ENST00000307648 // upstream // 2496 // — // — // — // — /// ENST00000325719 // upstream // 14615	OR52K2	OR52K2, Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), p15.4
SNP_A-2040870	aacccgatcactttttc[C/T]cccaaacaattacatt	C	T	NM_001005172 // downstream // 12164 // — // OR52K2 // 119774 // Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), mRNA. /// NM_001005171 // upstream // 26453 // — // OR52K1 // 390036 // Homo sapiens olfactory receptor, family	OR52K2	OR52K2, Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), p15.4
SNP_A-1781381	ggatgttgcattctgat[C/G]atatgggtggcacaag	C	G	NM_001005172 // downstream // 19794 // — // OR52K2 // 119774 // Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), mRNA. /// NM_001005171 // upstream // 18823 // — // OR52K1 // 390036 // Homo sapiens olfactory receptor, family	OR52K2	OR52K2, Homo sapiens olfactory receptor, family 52, subfamily K, member 2 (OR52K2), p15.4
SNP_A-1738461	cattctggctgatgtagaaaaagct[C/G]aaggcaattatagttta cataact	C	G	NM_144663 // downstream // 59538 // Hs.350556 // NOV1 // 143501 // NOV1	NOV1	NOV1, rs10500604, NOV1,p15.4
SNP_A-1741951	ctacaatgtgagtctgggtgaag[C/T]caaaagttgagtgtgta gcaagga	C	T	NM_144663 // downstream // 49801 // Hs.350556 // NOV1 // 143501 // NOV1	NOV1	NOV1, rs10500605, NOV1,p15.4
SNP_A-2144275	atgagtgatcatctta[C/T]aataaacttttgtgcc	C	T	NM_018073 // upstream // 10611 // Hs.523438 // TRIM68 // 55128 // Homo sapiens ring finger protein 137 (RNF137), mRNA. /// NM_001004751 // upstream // 20959 // — // OR51D1 // 390038 // Homo sapiens olfactory receptor, family 51, subfamily D, member 1 (O	TRIM68	TRIM68, Homo sapiens ring finger protein 137 (RNF137), p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1887585	tgagagatctgatggg[C/T]agatgctgcttattgt	C	T	NM_018073 // upstream // 30407 // Hs.523438 // TRIM68 // 55128 // Homo sapiens ring finger protein 137 (RNF137), mRNA. /// NM_001004751 // upstream // 1163 // --- // OR51D1 // 390038 // Homo sapiens olfactory receptor, family 51, subfamily D, member 1 (OR	TRIM68	TRIM68, Homo sapiens ring finger protein 137 (RNF137), p15.4
SNP_A-2007169	atatcgttgtagcgtt[C/T]aaaatagttattccaa	C	T	ENST00000357170 // intron // 0 // --- // --- // ---	-	p15.4
SNP_A-1782463	ggcacactcttagtta[C/T]agaaatgtgccatctt	C	T	NM_001004755 // downstream // 8297 // --- // OR51L1 // 119682 // Homo sapiens olfactory receptor, family 51, subfamily L, member 1 (OR51L1), mRNA. /// ENST00000321543 // downstream // 8297 // --- // --- // --- /// ENST00000321534 // upstream // 382	OR51L1	OR51L1, Homo sapiens olfactory receptor, family 51, subfamily L, member 1 (OR51L1), p15.4
SNP_A-2231482	ctatttaaagaacaaaa[C/T]tttccacattgttgat	C	T	NM_001004755 // downstream // 32630 // --- // OR51L1 // 119682 // Homo sapiens olfactory receptor, family 51, subfamily L, member 1 (OR51L1), mRNA. /// ENST00000321543 // downstream // 32630 // --- // --- // --- /// ENST00000321534 // upstream // 1	OR51L1	OR51L1, Homo sapiens olfactory receptor, family 51, subfamily L, member 1 (OR51L1), p15.4
SNP_A-2133327	atatatcaaaagtaag[C/T]cctcagatgtcatact	C	T	NM_001004757 // upstream // 3144 // Hs.528592 // OR51Q1 // 390061 // Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), mRNA. /// ENST00000332043 // downstream // 15510 // --- // --- // --- /// ENST00000300778 // upstream /	OR51Q1	OR51Q1, Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), p15.4
SNP_A-2311709	ggaattcaaagtattg[C/T]aacaggcttgaatctg	C	T	NM_001004757 // downstream // 7377 // Hs.528592 // OR51Q1 // 390061 // Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), mRNA. /// NM_001005288 // downstream // 10039 // --- // OR5I1 // 390063 // Homo sapiens olfactory receptor,	OR51Q1	OR51Q1, Homo sapiens olfactory receptor, family 51, subfamily Q, member 1 (OR51Q1), p15.4
SNP_A-1720225	gttaatctaaatgaataaaattaacaa[C/T]gataaacgtacctttctg ctctga	C	T	NM_017481 // downstream // 58956 // Hs.189184 // UBQLN3 // 50613 // ubiquilin 3 /// NM_033180 // upstream // 124049 // - // - // - // -	UBQLN3	UBQLN3 , rs10500641, ubiquilin 3, p15.4
SNP_A-1865964	tcccacattgcatca[C/T]ctggttttctacatc	C	T	NM_001005163 // CDS // 0 // --- // OR52D1 // 390066 // Homo sapiens olfactory receptor, family 52, subfamily D, member 1 (OR52D1), mRNA. /// ENST00000322641 // CDS // 0 // --- // --- // ---	OR52D1	OR52D1, Homo sapiens olfactory receptor, family 52, subfamily D, member 1 (OR52D1), p15.4
SNP_A-2007311	atgacagacgtgatcc[A/T]cattgctgtcctctac	A	T	NM_001005289 // upstream // 6440 // --- // OR52H1 // 390067 // Homo sapiens olfactory receptor, family 52, subfamily H, member 1 (OR52H1), mRNA. /// NM_001005162 // upstream // 28977 // --- // OR52B6 // 340980 // Homo sapiens olfactory receptor, family 52	OR52H1	OR52H1, Homo sapiens olfactory receptor, family 52, subfamily H, member 1 (OR52H1), p15.4
SNP_A-2199591	ccaaaacacacatcctca[A/G]taltaaaatcaccaaa	A	G	NM_033092 // intron // 0 // Hs.370515 // TRIM5 // 85363 // Homo sapiens tripartite motif-containing 5 (TRIM5), transcript variant gamma, mRNA. /// NM_033093 // intron // 0 // Hs.370515 // TRIM5 // 85363 // Homo sapiens tripartite motif-containing 5 (TRIM5	TRIM5	TRIM5, Homo sapiens tripartite motif-containing 5 (TRIM5), transcript variant gamma, p15.4
SNP_A-2091939	agaaacaccagtggaa[C/T]gaccatgtacaagctc	C	T	ENST00000316998 // CDS // 0 // --- // --- // ---	-	p15.4
SNP_A-1950734	ttcattctctctcat[G/T]acttctctgcagatc	G	T	NM_001005168 // downstream // 9977 // --- // OR52E8 // 390079 // Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), mRNA. /// NM_001005167 // downstream // 9977 // Hs.534693 // OR52E6 // 390078 // Homo sapiens olfactory receptor,	OR52E8	OR52E8, Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), p15.4
SNP_A-1825504	taaatacgctcaaaaa[C/T]acctcgacacagaaat	C	T	NM_001005168 // upstream // 17992 // --- // OR52E8 // 390079 // Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), mRNA. /// NM_001005167 // upstream // 17992 // Hs.534693 // OR52E6 // 390078 // Homo sapiens olfactory receptor, fa	OR52E8	OR52E8, Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2241115	ctgagctaaggagtta[C/T]atctagcatggtgttt	C	T	NM_001005168 // upstream // 22766 // --- // OR52E8 // 390079 // Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), mRNA. /// NM_001005167 // upstream // 22766 // Hs.534693 // OR52E6 // 390078 // Homo sapiens olfactory receptor, fa	OR52E8	OR52E8, Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), p15.4
SNP_A-2152938	attacagaggtaagaa[C/T]gcttgtgcaggagaag	C	T	NM_001005168 // upstream // 23065 // --- // OR52E8 // 390079 // Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), mRNA. /// NM_001005167 // upstream // 23065 // Hs.534693 // OR52E6 // 390078 // Homo sapiens olfactory receptor, fa	OR52E8	OR52E8, Homo sapiens olfactory receptor, family 52, subfamily E, member 8 (OR52E8), p15.4
SNP_A-2254987	cttggctataatgcag[A/G]cccaaagaactgcttt	A	G	NM_001001916 // downstream // 14260 // --- // OR52J3 // 119679 // Homo sapiens olfactory receptor, family 52, subfamily J, member 3 (OR52J3), mRNA. /// NM_001005165 // downstream // 14260 // --- // OR52E4 // 390081 // Homo sapiens olfactory receptor, fami	OR52J3	OR52J3, Homo sapiens olfactory receptor, family 52, subfamily J, member 3 (OR52J3), p15.4
SNP_A-1867414	tccctttattccttac[C/T]gaagcaaatacatcag	C	T	ENST00000340110 // intron // 0 // --- // --- // --- // ---	-	p15.4
SNP_A-2169691	caaggaagaagaagca[G/T]gatgacgaaccaggaa	G	T	NM_000543 // downstream // 33180 // Hs.498173 // SMPD1 // 6609 // Homo sapiens sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1), mRNA. /// NM_001164 // upstream // 9105 // Hs.372840 // APBB1 // 322 // Homo sapiens amyloid	SMPD1	SMPD1, Homo sapiens sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1), p15.4
SNP_A-1927350	ttcaaacattgaaaac[G/T]gatttttctagagcac	G	T	ENST00000299468 // intron // 0 // --- // --- // ---	-	p15.4
SNP_A-1658606	acaatgtctctgagtttgctatttc[C/T]acttcataatatttttaacaagata	C	T	BC014538 // intron // 0 // Hs.161427 // ZNF215 // 7762 // zinc finger protein 215	ZNF215	ZNF215 , rs762854, zinc finger protein 215,p15.4
SNP_A-2104866	agcataggagagctac[A/G]gtaatactatttttaa	A	G	NM_013250 // downstream // 34998 // Hs.523457 // ZNF215 // 7762 // Homo sapiens zinc finger protein 215 (ZNF215), mRNA. /// NM_013249 // downstream // 6483 // Hs.445849 // ZNF214 // 7761 // Homo sapiens zinc finger protein 214 (ZNF214), mRNA. /// ENST0000	ZNF215	ZNF215, Homo sapiens zinc finger protein 215 (ZNF215), p15.4
SNP_A-2139489	atccttgcattcctat[A/C]ataaactgtctgatca	A	C	NM_013249 // intron // 0 // Hs.445849 // ZNF214 // 7761 // Homo sapiens zinc finger protein 214 (ZNF214), mRNA. /// ENST00000278314 // intron // 0 // --- // --- // --- // ---	ZNF214	ZNF214, Homo sapiens zinc finger protein 214 (ZNF214), p15.4
SNP_A-2244719	ctggagttcccacaga[A/G]acaattctccatagta	A	G	NM_176822 // downstream // 9039 // Hs.449637 // NALP14 // 338323 // Homo sapiens NACHT, leucine rich repeat and PYD containing 14 (NALP14), mRNA. /// NM_014469 // upstream // 8539 // Hs.121605 // HNRNPG-T // 27288 // Homo sapiens testes-specific heterogen	NALP14	NALP14, Homo sapiens NACHT, leucine rich repeat and PYD containing 14 (NALP14), p15.4
SNP_A-1846824	tatcaatgtttcccaa[A/G]gtaaggttcacttgcc	A	G	NM_014469 // downstream // 155086 // Hs.121605 // HNRNPG-T // 27288 // Homo sapiens testes-specific heterogenous nuclear ribonucleoprotein G-T (HNRNPG-T), mRNA. /// NM_175733 // upstream // 6201 // Hs.177193 // SYT9 // 143425 // Homo sapiens synaptotagmin	HNRNPG-T	HNRNPG-T, Homo sapiens testes-specific heterogenous nuclear ribonucleoprotein G-T (HNRNPG-T), p15.4
SNP_A-1807148	gtctccttctattcca[A/G]gtttgctggagcttct	A	G	NM_175733 // intron // 0 // Hs.177193 // SYT9 // 143425 // Homo sapiens synaptotagmin IX (SYT9), mRNA. /// ENST00000318881 // intron // 0 // --- // --- // --- // --- /// ENST00000306843 // intron // 0 // --- // --- // --- // --- /// ENST00000359657 // int	SYT9	SYT9, Homo sapiens synaptotagmin IX (SYT9), p15.4
SNP_A-1825105	taaagggtaggtttcc[C/T]cagatccaatgggcca	C	T	BC021714 // intron // 0 // Hs.16019 // PPFIBP2 // 8495 // Homo sapiens PTPRF interacting protein, binding protein 2 (liprin beta 2), mRNA (cDNA clone MGC:26737 IMAGE:4826610), complete c /// ENST00000299492 // intron // 0 // --- // --- // --- // ---	PPFIBP2	PPFIBP2, Homo sapiens PTPRF interacting protein, binding protein 2 (liprin beta 2), (cDNA clone MGC:26737 IMAGE:4826610), complete c ,p15.4
SNP_A-2145562	atgcatagatatgcca[C/G]aacagacattcgggct	C	G	NM_003320 // intron // 0 // Hs.231850 // TUB // 7275 // Homo sapiens tubby homolog (mouse) (TUB), transcript variant 1, mRNA. /// ENST00000305253 // intron // 0 // --- // --- // --- // ---	TUB	TUB, Homo sapiens tubby homolog (mouse) (TUB), transcript variant 1, p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308431	gctttaaagagtcaaa[A/G]tatcagagaaacgttta	A	G	NM_003320 // intron // 0 // Hs.231850 // TUB // 7275 // Homo sapiens tubby homolog (mouse) (TUB), transcript variant 1, mRNA. /// ENST00000305253 // intron // 0 // --- // --- // ---	TUB	TUB, Homo sapiens tubby homolog (mouse) (TUB), transcript variant 1, p15.4
SNP_A-2211548	ccctcacatgcagaaa[A/G]gcactcaagaatccag	A	G	NM_003320 // intron // 0 // Hs.231850 // TUB // 7275 // Homo sapiens tubby homolog (mouse) (TUB), transcript variant 1, mRNA. /// NM_177972 // intron // 0 // Hs.231850 // TUB // 7275 // Homo sapiens tubby homolog (mouse) (TUB), transcript variant 2, mRNA.	TUB	TUB, Homo sapiens tubby homolog (mouse) (TUB), transcript variant 1, p15.4
SNP_A-2292502	gcactcagcctaaaaa[C/T]gtatgttctctaga	C	T	NM_024557 // intron // 0 // Hs.458375 // RIC3 // 79608 // Homo sapiens RIC3 protein (RIC3), mRNA. /// ENST00000335425 // intron // 0 // --- // --- // --- /// ENST00000343202 // intron // 0 // --- // --- // ---	RIC3	RIC3, Homo sapiens RIC3 protein (RIC3), p15.4
SNP_A-2115021	agggcctacactaccc[C/G]acctctctcacaagc	C	G	NM_002315 // intron // 0 // Hs.1149 // LMO1 // 4004 // Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// ENST00000332914 // intron // 0 // --- // --- // --- /// ENST00000335790 // intron // 0 // --- // --- // ---	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-1787224	gggaacaggtttgaga[C/T]gggtgcatcacggttt	C	T	NM_002315 // upstream // 30958 // Hs.1149 // LMO1 // 4004 // Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// NM_030906 // downstream // 97054 // Hs.501833 // STK33 // 65975 // Homo sapiens serine/threonine kinase 33 (STK33), mRNA. /// NM_03	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-2256230	ctttagcagtcactgta[A/G]agtccaccacaaggac	A	G	NM_002315 // upstream // 119095 // Hs.1149 // LMO1 // 4004 // Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), mRNA. /// NM_030906 // downstream // 8917 // Hs.501833 // STK33 // 65975 // Homo sapiens serine/threonine kinase 33 (STK33), mRNA. /// NM_03	LMO1	LMO1, Homo sapiens LIM domain only 1 (rhombotin 1) (LMO1), p15.4
SNP_A-2068702	acaatactataacaaa[G/T]aggtttcagtcaagg	G	T	NM_030906 // intron // 0 // Hs.501833 // STK33 // 65975 // Homo sapiens serine/threonine kinase 33 (STK33), mRNA. /// ENST00000315204 // intron // 0 // --- // --- // --- /// ENST00000358872 // intron // 0 // --- // --- // ---	STK33	STK33, Homo sapiens serine p15.4
SNP_A-2001689	aagcatattgaagca[G/T]aaagacatggaaatat	G	T	NM_030906 // intron // 0 // Hs.501833 // STK33 // 65975 // Homo sapiens serine/threonine kinase 33 (STK33), mRNA. /// ENST00000315204 // intron // 0 // --- // --- // --- /// ENST00000358872 // intron // 0 // --- // --- // ---	STK33	STK33, Homo sapiens serine,p15.4
SNP_A-1688160	ggatgcattgtttgccaggacagac[A/G]gaacttcagtaaagatt atctggca	A	G	NM_030906 // intron // 0 // Hs.148135 // STK33 // 65975 // serine/threonine kinase 33	STK33	STK33, , rs10500704, serine,p15.4
SNP_A-1768462	gggagttatcaggggtc[A/C]acatcttagttcata	A	C	AB002296 // intron // 0 // Hs.130836 // TRIM66 // 9866 // Homo sapiens mRNA for KIAA0298 protein, partial cds. /// ENST00000299550 // intron // 0 // --- // --- // ---	TRIM66	TRIM66, Homo sapiens for KIAA0298 protein, partial cds, p15.4
SNP_A-2296830	gccaacttgcagccaa[A/G]caaaagggcagcaccc	A	G	AB002296 // intron // 0 // Hs.130836 // TRIM66 // 9866 // Homo sapiens mRNA for KIAA0298 protein, partial cds. /// ENST00000299550 // intron // 0 // --- // --- // ---	TRIM66	TRIM66, Homo sapiens for KIAA0298 protein, partial cds, p15.4
SNP_A-1794181	ggtcataaggagctac[C/T]gaacttttgatcaag	C	T	AB002296 // upstream // 21453 // Hs.130836 // TRIM66 // 9866 // Homo sapiens mRNA for KIAA0298 protein, partial cds. /// NM_000990 // upstream // 2503 // Hs.523463 // RPL27A // 6157 // Homo sapiens ribosomal protein L27a (RPL27A), mRNA. /// NM_000990 // u	TRIM66	TRIM66, Homo sapiens for KIAA0298 protein, partial cds, p15.4
SNP_A-1897250	tgctctgctccctccc[C/G]actcggacttgccagg	C	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803538	gtatttttaacctgca[A/G]acaatgctgggtata	A	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-1836872	tactgccagcaaaaaa[C/T]gaaagcagaggctaaa	C	T	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-1870889	tcgggagcagaggtcc[A/G]gaagactggttccatc	A	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2235240	ctcccgagccaatcct[A/G]aaaggtttctgacagc	A	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-1937829	ttgaatacgaggctga[C/G]aagaaccccaagagta	C	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // CDS // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2216161	cctccctatgtaaaac[A/G]gcaactcatctctact	A	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2038733	aacagatacttcaccat[C/G]agaggatacccaaaca	C	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-1793836	ggtatttcgtgcaga[A/T]cttcacccagaaagcc	A	T	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2295568	gcatctgtttaaagac[A/G]agcacatacctggaaa	A	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2007586	agccaataaaataggc[A/G]agtttcctcccactcc	A	G	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4
SNP_A-2229526	ctagggttcagtctcc[C/T]ttccagaaagtagaa	C	T	NM_139157 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA. /// NM_213618 // intron // 0 // Hs.117715 // ST5 // 6764 // Homo sapiens suppression of tumorigenicity 5 (ST5), transcr	ST5	ST5, Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944722	ttgtgatgacatatca[C/G]attgctgtttcatttga	C	G	NM_003442 // intron // 0 // Hs.523471 // ZNF143 // 7702 // Homo sapiens zinc finger protein 143 (clone pHZ-1) (ZNF143), mRNA. /// ENST00000299606 // intron // 0 // — // — // —	ZNF143	ZNF143, Homo sapiens zinc finger protein 143 (clone pHZ-1) (ZNF143), p15.4
SNP_A-1799812	gtacaatggagaaggga[A/G]gaaggattatctgtt	A	G	NM_003390 // downstream // 11962 // Hs.249441 // WEE1 // 7465 // Homo sapiens WEE1 homolog (S. pombe) (WEE1), mRNA. /// ENST00000299613 // downstream // 11962 // — // — // — // — /// ENST00000309192 // upstream // 59874 // — // — // — // —	WEE1	WEE1, Homo sapiens WEE1 homolog (S. pombe) (WEE1), p15.4
SNP_A-1816906	gttattaggtgtggcaa[A/G]agcatagtgtgtttca	A	G	NM_003390 // downstream // 12265 // Hs.249441 // WEE1 // 7465 // Homo sapiens WEE1 homolog (S. pombe) (WEE1), mRNA. /// ENST00000299613 // downstream // 12265 // — // — // — // — /// ENST00000309192 // upstream // 59571 // — // — // — // —	WEE1	WEE1, Homo sapiens WEE1 homolog (S. pombe) (WEE1), p15.4
SNP_A-1785642	ggctccgaagaggaca[A/G]cattgcaatggtgaca	A	G	NM_003390 // downstream // 12528 // Hs.249441 // WEE1 // 7465 // Homo sapiens WEE1 homolog (S. pombe) (WEE1), mRNA. /// ENST00000299613 // downstream // 12528 // — // — // — // — /// ENST00000309192 // upstream // 59308 // — // — // — // —	WEE1	WEE1, Homo sapiens WEE1 homolog (S. pombe) (WEE1), p15.4
SNP_A-2114893	agggcagcatcatccc[A/G]agagtgtaggaggagc	A	G	NM_003390 // downstream // 18653 // Hs.249441 // WEE1 // 7465 // Homo sapiens WEE1 homolog (S. pombe) (WEE1), mRNA. /// ENST00000299613 // downstream // 18653 // — // — // — // — /// ENST00000309192 // upstream // 53183 // — // — // — // —	WEE1	WEE1, Homo sapiens WEE1 homolog (S. pombe) (WEE1), p15.4
SNP_A-2224939	cgtggaccacggatgat[C/G]tatggagggaagatc	C	G	NM_003390 // downstream // 20820 // Hs.249441 // WEE1 // 7465 // Homo sapiens WEE1 homolog (S. pombe) (WEE1), mRNA. /// ENST00000299613 // downstream // 20820 // — // — // — // — /// ENST00000309192 // upstream // 51016 // — // — // — // —	WEE1	WEE1, Homo sapiens WEE1 homolog (S. pombe) (WEE1), p15.4
SNP_A-2254429	cttgccagtgttcgtat[G/T]aattgaaaatatttaa	G	T	NM_015055 // intron // 0 // Hs.153026 // SWAP70 // 23075 // Homo sapiens SWAP-70 protein (SWAP70), mRNA. /// ENST00000355139 // intron // 0 // — // — // — // — /// ENST00000318950 // intron // 0 // — // — // — // —	SWAP70	SWAP70, Homo sapiens SWAP-70 protein (SWAP70), p15.4
SNP_A-2141602	atcttcaagagaccca[A/G]atccaggttgtctta	A	G	NM_015055 // intron // 0 // Hs.153026 // SWAP70 // 23075 // Homo sapiens SWAP-70 protein (SWAP70), mRNA. /// ENST00000355139 // intron // 0 // — // — // — // — /// ENST00000318950 // intron // 0 // — // — // — // —	SWAP70	SWAP70, Homo sapiens SWAP-70 protein (SWAP70), p15.4
SNP_A-2242016	ctgattcgtataataa[A/G]tcacagcaaaataacc	A	G	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2086340	actcttacaagtcata[C/T]gcacacacaagacagc	C	T	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1676924	actaaggaaagaagagacatactat[A/G]aaactgtaatttcagta gtactgtga	A	G	NM_030962 // intron // 0 // Hs.438794 // CMT4B2 // 81846 // Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding)	CMT4B2	CMT4B2 , rs7929338, Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding),p15.4
SNP_A-2173547	cacaatggctctcccta[C/G]acaagaggttcatgag	C	G	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1662486	ttgtcaacaatcatagacagtatac[A/G]cggaaagaaaaaagcc agtaatttg	A	G	NM_030962 // intron // 0 // Hs.438794 // CMT4B2 // 81846 // Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding)	CMT4B2	CMT4B2 , rs10500716, Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding),p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2126682	ataaacatataacatc[C/G]agaaaaaagaatgtgag	C	G	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2259179	gaaaaaataccctgca[A/G]actaattataagttta	A	G	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2199659	ccaaaaggagcaattc[A/G]cacttgaggaaatgag	A	G	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1936747	ttctttaggaccttga[A/G]gtttagtactgtagtt	A	G	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1725718	ggtatgcaggggctagtattctcgaa[A/G]ccaatttacatatgact agcagct	A	G	NM_030962 // intron // 0 // Hs.438794 // CMT4B2 // 81846 // Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding)	CMT4B2	CMT4B2 , rs7110312, Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding),p15.4
SNP_A-1647414	gaatctatcattgctaaaatatcaa[A/G]aaggctataaatttaaag taatat	A	G	NM_030962 // intron // 0 // Hs.438794 // CMT4B2 // 81846 // Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding)	CMT4B2	CMT4B2 , rs10500719, Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding),p15.4
SNP_A-1754314	actgtcactttctcttggtttcc[C/T]aaatctaacttaatacaaatttt c	C	T	NM_030962 // intron // 0 // Hs.438794 // CMT4B2 // 81846 // Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding)	CMT4B2	CMT4B2 , rs10500720, Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding),p15.4
SNP_A-2227395	ctacacaaccaaagaga[A/T]actgaggtgtccagct	A	T	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-2143109	atgaatgttatgacca[C/T]gtttctaggtaacatc	C	T	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1879716	tcttcatatttgacaa[C/T]cagctggctactgaca	C	T	NM_030962 // intron // 0 // Hs.438794 // SBF2 // 81846 // Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), mRNA. /// ENST00000256190 // intron // 0 // — // — // — // —	SBF2	SBF2, Homo sapiens Charcot-Marie-Tooth neuropathy 4B2 (autosomal recessive, with myelin outfolding) (CMT4B2), p15.4
SNP_A-1818598	gttgaaattggcactt[A/C]ataacatttccagcag	A	C	NM_001124 // downstream // 40417 // Hs.441047 // ADM // 133 // Homo sapiens adrenomedullin (ADM), mRNA. /// NM_000480 // upstream // 102884 // Hs.501890 // AMPD3 // 272 // Homo sapiens adenosine monophosphate deaminase (isoform E) (AMPD3), mRNA. /// D12775	ADM	ADM, Homo sapiens adrenomedullin (ADM), p15.4
SNP_A-1721570	tgcaaattcgtaacattctacctac[A/T]aaccictttctcagctctcc ctgcc	A	T	NM_000480 // upstream // 102131 // Hs.83918 // AMPD3 // 272 // adenosine monophosphate deaminase (isoform E) /// NM_001124 // downstream // 41170 // Hs.441047 // ADM // 133 // adrenomedullin	AMPD3	AMPD3 , rs1597450, adenosine monophosphate deaminase (isoform E) ,p15.4
SNP_A-2169257	caagcaagaatccaga[C/G]accacagattaagaca	C	G	NM_001124 // downstream // 68120 // Hs.441047 // ADM // 133 // Homo sapiens adrenomedullin (ADM), mRNA. /// NM_000480 // upstream // 75181 // Hs.501890 // AMPD3 // 272 // Homo sapiens adenosine monophosphate deaminase (isoform E) (AMPD3), mRNA. /// D12775	ADM	ADM, Homo sapiens adrenomedullin (ADM), p15.4
SNP_A-2084730	actattgttcttttttc[A/C]aaatgttctggctag	A	C	NM_001124 // downstream // 74616 // Hs.441047 // ADM // 133 // Homo sapiens adrenomedullin (ADM), mRNA. /// NM_000480 // upstream // 68685 // Hs.501890 // AMPD3 // 272 // Homo sapiens adenosine monophosphate deaminase (isoform E) (AMPD3), mRNA. /// D12775	ADM	ADM, Homo sapiens adrenomedullin (ADM), p15.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2218434	cctggaaggttcttca[C/T]acttgccttctaatgt	C	T	NM_006069 // intron // 0 // Hs.501898 // MRVI1 // 10335 // Homo sapiens murine retrovirus integration site 1 homolog (MRVI1), transcript variant 1, mRNA. /// NM_130385 // intron // 0 // Hs.501898 // MRVI1 // 10335 // Homo sapiens murine retrovirus integra	MRVI1	MRVI1, Homo sapiens murine retrovirus integration site 1 homolog (MRVI1), transcript variant 1, p15.4
SNP_A-2218109	cctgcctcatctctgt[A/G]aagctggttacttcct	A	G	NM_006691 // upstream // 169491 // Hs.246769 // XLKD1 // 10894 // Homo sapiens extracellular link domain containing 1 (XLKD1), mRNA. /// NM_006069 // upstream // 85978 // Hs.501898 // MRVI1 // 10335 // Homo sapiens murine retrovirus integration site 1 hom	XLKD1	XLKD1, Homo sapiens extracellular link domain containing 1 (XLKD1), p15.3
SNP_A-2223278	cgcgcttgaagagcaa[A/G]ggatttgtcattgcg	A	G	NM_021211 // upstream // 1460 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 411347 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2210240	ccccatctcctccacc[G/T]ctacctctgagttcta	G	T	NM_021211 // upstream // 80659 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 332148 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2239349	ctctttcagtgatgca[A/G]gctactcaccctaca	A	G	NM_021211 // upstream // 131410 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 281397 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acety	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-1957489	tttataagaataccc[C/G]acatattggattgggt	C	G	NM_021211 // upstream // 145168 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 267639 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acety	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-1879638	tcttcagaaagtccgc[G/T]cttaaatctgggggag	G	T	NM_021211 // upstream // 236411 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 176396 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acety	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2279385	gaggagtaagctatgc[A/G]cattcaagccaagagc	A	G	NM_021211 // upstream // 290194 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 122613 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acety	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-1814241	gtgtctggtagaggaa[A/G]gttgctttatgcacc	A	G	NM_021211 // upstream // 299345 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 113462 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acety	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-1838461	tagaatcattgctagt[G/T]aaagttgagagaagga	G	T	NM_021211 // upstream // 391237 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 21570 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3
SNP_A-2186665	cagggcatagcacttа[A/C]gagtaggtgacccctt	A	C	NM_021211 // upstream // 406691 // Hs.25726 // LOC58486 // 58486 // Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), mRNA. /// NM_198516 // downstream // 6116 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-	LOC58486	LOC58486, Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486), p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2302797	gctagaaattaacacc[C/T]ccagaaagcaactctc	C	T	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2143792	atgagagaaaatcctga[G/T]aatcatattgacacaa	G	T	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2034906	aaatgagggctggaac[A/G]cctgtctacttgcctg	A	G	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2312187	ggacagccgccacatg[A/C]actaaaatggcaggtc	A	C	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2244265	ctggaaatttggatac[C/T]gaggctctgggaacgc	C	T	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2099013	agaggaaatgatgtgc[A/G]aatgagaaaatttaa	A	G	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2198203	cattgtcacccttaca[C/T]gggaaaagagctgct	C	T	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-2077278	accaatgagtctgcaa[C/T]aggtgtctcagcagc	C	T	NM_198516 // intron // 0 // Hs.501911 // GALNTL4 // 374378 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), mRNA. /// ENST00000227756 // intron // 0 // — // — // —	GALNTL4	GALNTL4, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 (GALNTL4), p15.3
SNP_A-1738214	gtaaaggaagtatttggtagtaaata[C/T]agcctgaacaccaaatc agagatagg	C	T	AF116621 // downstream // 28685 // - // - // Homo sapiens PRO1084 mRNA, complete cds. /// NM_017944 // upstream // 86648 // Hs.441028 // USP47 // 55031 // ubiquitin specific protease 47	-	-, rs7117834, Homo sapiens PRO1084 mRNA, complete cds. p15.3
SNP_A-1915505	tgttcgcagtcgcata[A/T]tacaaccatgtttcac	A	T	NM_013253 // 3UTR // 0 // Hs.292156 // DKK3 // 27122 // Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA. /// NM_015881 // 3UTR // 0 // Hs.292156 // DKK3 // 27122 // Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA. /// ENST00000	DKK3	DKK3, Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), p15.3
SNP_A-2188470	cagtgacacctatgtg[A/G]agtgctaattgggaa	A	G	NM_013253 // upstream // 19735 // Hs.292156 // DKK3 // 27122 // Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA. /// NM_015881 // upstream // 19735 // Hs.292156 // DKK3 // 27122 // Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRN	DKK3	DKK3, Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), p15.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897994	tgctgtattgcacaaa[A/C]tcaccgggaaccttt	A	C	NM_014632 // intron // 0 // Hs.501928 // MICAL2 // 9645 // Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), mRNA. /// ENST00000256194 // intron // 0 // --- // --- // --- /// ENST00000342902 // intron // 0 // --- // --- // ---	MICAL2	MICAL2, Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), p15.3
SNP_A-2043420	aactgggggcacttt[d/C]agccaaaactcccagc	A	C	NM_014632 // downstream // 9282 // Hs.501928 // MICAL2 // 9645 // Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), mRNA. /// NM_032867 // upstream // 20761 // Hs.128196 // FLJ14966 // 84953 // Homo sapiens hypothetical protein FLJ14966 (FLJ14966)	MICAL2	MICAL2, Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), p15.3
SNP_A-1705797	ctccatttcccctccaattgccaga[C/T]ggttttaggcaactacaagaaaaa	C	T	NM_014632 // downstream // 18665 // Hs.309674 // MICAL2 // 9645 // flavoprotein oxidoreductase MICAL2 /// NM_032867 // upstream // 11370 // Hs.128196 // FLJ14966 // 84953 // hypothetical protein FLJ14966	MICAL2	MICAL2 , rs10500754, flavoprotein oxidoreductase MICAL2 .p15.3
SNP_A-1845730	tataggtgctggggtc[A/G]cttgttataccggt	A	G	NM_032867 // intron // 0 // Hs.128196 // FLJ14966 // 84953 // Homo sapiens hypothetical protein FLJ14966 (FLJ14966), mRNA. /// ENST00000256186 // intron // 0 // --- // --- // ---	FLJ14966	FLJ14966, Homo sapiens hypothetical protein FLJ14966 (FLJ14966), p15.3
SNP_A-1935315	ttctgctgttaagtaa[A/G]aggccaccactaaagc	A	G	NM_032867 // downstream // 16943 // Hs.128196 // FLJ14966 // 84953 // Homo sapiens hypothetical protein FLJ14966 (FLJ14966), mRNA. /// NM_018222 // upstream // 1469 // Hs.436319 // PARVA // 55742 // Homo sapiens parvin, alpha (PARVA), mRNA. /// ENST000002	FLJ14966	FLJ14966, Homo sapiens hypothetical protein FLJ14966 (FLJ14966), p15.3
SNP_A-1795391	ggtgcaaaaaggccctc[C/T]aatcacaaaacacttc	C	T	NM_018222 // intron // 0 // Hs.436319 // PARVA // 55742 // Homo sapiens parvin, alpha (PARVA), mRNA. /// ENST00000334956 // intron // 0 // --- // --- // ---	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.3
SNP_A-1945482	ttgttcaggaacctgc[A/G]atgagtcccatcctt	A	G	NM_018222 // intron // 0 // Hs.436319 // PARVA // 55742 // Homo sapiens parvin, alpha (PARVA), mRNA. /// ENST00000334956 // intron // 0 // --- // --- // ---	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.3
SNP_A-2069162	acaattcccaggatag[C/G]catttgaggcaagg	C	G	NM_018222 // downstream // 16781 // Hs.436319 // PARVA // 55742 // Homo sapiens parvin, alpha (PARVA), mRNA. /// NM_021961 // upstream // 197469 // Hs.546308 // TEAD1 // 7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.3
SNP_A-2147121	atggaatctccaggat[C/G]aagctcaggatttctg	C	G	NM_018222 // downstream // 18108 // Hs.436319 // PARVA // 55742 // Homo sapiens parvin, alpha (PARVA), mRNA. /// NM_021961 // upstream // 196142 // Hs.546308 // TEAD1 // 7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor	PARVA	PARVA, Homo sapiens parvin, alpha (PARVA), p15.3
SNP_A-2275134	gagaagatggttggaa[A/G]gatacaaggggtgact	A	G	ENST00000358412 // intron // 0 // --- // --- // ---	-	p15.2
SNP_A-1923557	ttagggctgatggagc[A/G]gagaattaatcaggga	A	G	NM_021961 // intron // 0 // Hs.546308 // TEAD1 // 7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- /// ENST00000334310 // intron // 0 // –	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2232050	ctcaagagactcacttt[A/G]aaagcttttctgggcc	A	G	NM_021961 // intron // 0 // Hs.546308 // TEAD1 // 7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- /// ENST00000334310 // intron // 0 // –	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2098878	agagctgcggataaaa[A/C]aagcaaaagctgagcc	A	C	NM_021961 // intron // 0 // Hs.546308 // TEAD1 // 7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- /// ENST00000334310 // intron // 0 // –	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2
SNP_A-2215851	cctcattgttaagcaa[C/G]tcatcactgtatatca	C	G	NM_021961 // intron // 0 // Hs.546308 // TEAD1 // 7003 // Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA. /// ENST00000358412 // intron // 0 // --- // --- // --- /// ENST00000334310 // intron // 0 // –	TEAD1	TEAD1, Homo sapiens TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2106777	agcctgggagacttcca[A/G]tagccagtttgtgctg	A	G	NM_001178 // upstream // 208906 // Hs.65734 // ARNTL // 406 // Homo sapiens aryl hydrocarbon receptor nuclear translocator-like (ARNTL). /// mRNA. /// ENST00000340761 // downstream // 57797 // --- // --- // --- /// ENST00000339779 // downstream // 5823	ARNTL	ARNTL, Homo sapiens aryl hydrocarbon receptor nuclear translocator-like (ARNTL), p15.2
SNP_A-2038500	aacactgtgtgtctat[A/G]atttacagatgcttg	A	G	NM_000315 // upstream // 142230 // Hs.37045 // PTH // 5741 // Homo sapiens parathyroid hormone (PTH), mRNA. /// NM_032228 // upstream // 30474 // Hs.501991 // MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// ENST00000	PTH	PTH, Homo sapiens parathyroid hormone (PTH), p15.2
SNP_A-2171374	caatatttttttcaa[C/T]ctggagtagatacaga	C	T	NM_000315 // upstream // 151634 // Hs.37045 // PTH // 5741 // Homo sapiens parathyroid hormone (PTH), mRNA. /// NM_032228 // upstream // 21070 // Hs.501991 // MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// ENST00000	PTH	PTH, Homo sapiens parathyroid hormone (PTH), p15.2
SNP_A-1899839	tggaatttggaggaaaa[C/T]gtaaaatgtcagccag	C	T	NM_032228 // intron // 0 // Hs.501991 // MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// ENST00000355107 // intron // 0 // --- // --- // --- /// ENST00000354817 // intron // 0 // --- // --- // --- /// E	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-1667952	acacagatatcagctattaactagc[C/T]gatttgcaaaaacgtca gataaaac	C	T	NM_006108 // upstream // 219943 // Hs.5378 // SPON1 // 10418 // spondin 1, extracellular matrix protein /// NM_032228 // downstream // 13862 // Hs.288368 // MLSTD2 // 84188 // male sterility domain containing 2	SPON1	SPON1, rs723789, spondin 1, extracellular matrix protein, p15.3
SNP_A-1924510	ttatacagtagccaaa[C/T]tccacgtagcttttag	C	T	NM_032228 // downstream // 52121 // Hs.501991 // MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream // 178226 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-1909649	tgtcaacctttcac[A/G]agctacatttccctt	A	G	NM_032228 // downstream // 56736 // Hs.501991 // MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream // 173611 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-2107883	agctccaggatttcag[C/T]ctacagaggaaaacag	C	T	NM_032228 // downstream // 199513 // Hs.501991 // MLSTD2 // 84188 // Homo sapiens male sterility domain containing 2 (MLSTD2), mRNA. /// NM_006108 // upstream // 30834 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein	MLSTD2	MLSTD2, Homo sapiens male sterility domain containing 2 (MLSTD2), p15.2
SNP_A-2093078	agaacaggagtcagta[A/T]actttttctataaagg	A	T	NM_006108 // intron // 0 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-2007947	actttcctttcaaaga[A/T]tacccctgtacaagtc	A	T	NM_006108 // intron // 0 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-2308102	gcttgagtctggtac[A/C]aaatggtgcaataagg	A	C	NM_006108 // intron // 0 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-1929755	ttcatcaggacttata[A/G]catattggatctaagg	A	G	NM_006108 // intron // 0 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-1956682	ttttaaaaatattccc[A/G]aagtcatgctgcttat	A	G	NM_006108 // intron // 0 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2
SNP_A-1940474	ttgcccagtctcca[A/G]atagatacacacagga	A	G	NM_006108 // intron // 0 // Hs.445818 // SPON1 // 10418 // Homo sapiens spondin 1, extracellular matrix protein (SPON1), mRNA. /// ENST00000310358 // intron // 0 // --- // --- // ---	SPON1	SPON1, Homo sapiens spondin 1, extracellular matrix protein (SPON1), p15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1740661	gctaggaaggcaataaaggataaga[C/T]gtgtttgagaaatag caagaatttt	C	T	NM_148976 // intron // 0 // Hs.82159 // PSMA1 // 5682 // proteasome (prosome, macropain) subunit, alpha type, 1	PSMA1	PSMA1 , rs1375953, proteasome (prosome, macropain) subunit, alpha type, 1,p15.2
SNP_A-2007978	taggataaattcacaga[C/T]gtaatgtgcccattac	C	T	NM_000728 // downstream // 80746 // Hs.534305 // CALCB // 797 // Homo sapiens calcitonin-related polypeptide, beta (CALCB), mRNA. /// ENST00000324229 // downstream // 80746 // — // — // — /// ENST00000344052 // upstream // 17749 // — // —	CALCB	CALCB, Homo sapiens calcitonin-related polypeptide, beta (CALCB), p15.2
SNP_A-1854208	tcaaaatgaaaggcc[G/T]atgatctcaagttcat	G	T	NM_033326 // downstream // 111436 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // downstream // 111436 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// NM_033326 //	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.2
SNP_A-1925449	ttatctgttgcaacaa[A/T]ctaccactctgttat	A	T	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-1960351	tttttaggactatgta[C/T]attgggcacataagac	C	T	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-1911773	tgtgaatcaaaatggc[A/G]caatggctaaaatttc	A	G	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2112859	aggcatagcaaaaaga[C/T]cattgaacacaataaa	G	T	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-1700372	ttagtccataaagaaagatagagca[A/G]aaaatacctacaagt aggcaagtaa	A	G	NM_033326 // intron // 0 // Hs.326876 // SOX6 // 55553 // SRY (sex determining region Y)-box 6	SOX6	SOX6 , rs957476, SRY (sex determining region Y)-box 6,p15.2
SNP_A-2119580	agtatgacatttaga[A/G]gatccactacctct	A	G	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2056373	aatacttaaatgtca[A/G]ctagtaattggatggg	A	G	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2049001	aagcctgtataatgag[C/T]aaatttgatgtatgaa	C	T	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1
SNP_A-2122478	agtgctaggtcctgta[C/T]aaaatctccacaaatt	C	T	NM_033326 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), mRNA. /// AF309034 // intron // 0 // Hs.368226 // SOX6 // 55553 // Homo sapiens SOX6 mRNA, complete cds. /// ENST00000336941 // intron // 0	SOX6	SOX6, Homo sapiens SRY (sex determining region Y)-box 6 (SOX6), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2289036	gatttccaacaacttc[A/G]acaatgtacccatttt	A	G	NM_005013 /// intron // 0 // Hs.128686 // NUCB2 // 4925 // Homo sapiens nucleobindin 2 (NUCB2), mRNA. /// ENST00000323688 // intron // 0 // --- // --- // ---	NUCB2	NUCB2, Homo sapiens nucleobindin 2 (NUCB2), p15.1
SNP_A-1923750	ttagtaataaaatttca[C/G]taagtcagctaaacca	C	G	NM_005013 // downstream // 4933 // Hs.128686 // NUCB2 // 4925 // Homo sapiens nucleobindin 2 (NUCB2), mRNA. /// ENST00000323688 // downstream // 4933 // --- // --- // --- /// ENST00000338965 // upstream // 15848 // --- // --- // ---	NUCB2	NUCB2, Homo sapiens nucleobindin 2 (NUCB2), p15.1
SNP_A-2205287	ccagtcagtaagggtc[A/G]cccgaacttaggctct	A	G	AB006955 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens mRNA for AIE-75, complete cds. /// ENST00000344020 // intron // 0 // --- // --- // --- /// ENST00000358979 // intron // 0 // --- // --- // ---	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-2313742	ggagcacatggagaaac[A/G]accacattgtgtccca	A	G	AB006955 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens mRNA for AIE-75, complete cds. /// NM_153676 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens Usher syndrome 1C (autosomal recessive, severe) (USH1C), transcript variant b	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-1915190	tgttcaatgtcagaca[A/T]cttgtaactgatagta	A	T	AB006955 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens mRNA for AIE-75, complete cds. /// NM_153676 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens Usher syndrome 1C (autosomal recessive, severe) (USH1C), transcript variant b	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-2188320	cagtctggaccaaaag[A/G]aatattgtaactgaca	A	G	AB006955 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens mRNA for AIE-75, complete cds. /// NM_153676 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens Usher syndrome 1C (autosomal recessive, severe) (USH1C), transcript variant b	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-1839419	tagataaaggcattaa[C/G]ctctgtcaggaaaaat	C	G	AB006955 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens mRNA for AIE-75, complete cds. /// NM_153676 // intron // 0 // Hs.502072 // USH1C // 10083 // Homo sapiens Usher syndrome 1C (autosomal recessive, severe) (USH1C), transcript variant b	USH1C	USH1C, Homo sapiens for AIE-75, complete cds. ,p15.1
SNP_A-2122260	agtgcagccagcatta[C/T]ggattgtaagcaaacc	C	T	ENST00000344891 // intron // 0 // --- // --- // --- /// ENST00000342528 // intron // 0 // --- // --- // --- /// ENST00000341823 // intron // 0 // --- // --- // ---	-	p15.1
SNP_A-1823960	taaaattggacagagcd[A/G]cagagagttcctatat	A	G	NM_002478 // upstream // 18127 // Hs.181768 // MYOD1 // 4654 // Homo sapiens myogenic factor 3 (MYOD1), mRNA. /// ENST00000344891 // downstream // 55541 // --- // --- // --- /// ENST00000342528 // downstream // 62551 // --- // --- // --- /// ---	MYOD1	MYOD1, Homo sapiens myogenic factor 3 (MYOD1), p15.1
SNP_A-2280235	gagggcagttagatga[C/T]gacactcacactgtgg	C	T	NM_005316 // intron // 0 // Hs.523510 // GTF2H1 // 2965 // Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA. /// ENST00000265963 // intron // 0 // --- // --- // ---	GTF2H1	GTF2H1, Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), p15.1
SNP_A-1816199	gttactataaccagaaa[A/G]attgagaaggaaagaa	A	G	NM_005316 // intron // 0 // Hs.523510 // GTF2H1 // 2965 // Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA. /// ENST00000265963 // intron // 0 // --- // --- // ---	GTF2H1	GTF2H1, Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), p15.1
SNP_A-2105240	agcattcagtgtatca[A/G]caagcctcgtacaata	A	G	NM_005316 // intron // 0 // Hs.523510 // GTF2H1 // 2965 // Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA. /// ENST00000265963 // intron // 0 // --- // --- // ---	GTF2H1	GTF2H1, Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), p15.1
SNP_A-1825477	taaatacaatgctaaa[A/C]atgctggcataaagt	A	C	NM_005316 // intron // 0 // Hs.523510 // GTF2H1 // 2965 // Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA. /// ENST00000265963 // intron // 0 // --- // --- // ---	GTF2H1	GTF2H1, Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2249830	cttaatttatcatct[C/G]acaaagaaaatggatc	C	G	NM_005316 // downstream // 5269 // Hs.523510 // GTF2H1 // 2965 // Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), mRNA. /// NM_005566 // upstream // 22262 // Hs.2795 // LDHA // 3939 // Homo sapiens lactate dehydrogena	GTF2H1	GTF2H1, Homo sapiens general transcription factor IIH, polypeptide 1 (62kD subunit) (GTF2H1), p15.1
SNP_A-2302343	gctaagatatggaagtg[A/G]acctaaatatttatca	A	G	NM_006292 // intron // 0 // Hs.523512 // TSG101 // 7251 // Homo sapiens tumor susceptibility gene 101 (TSG101), mRNA. /// ENST00000357193 // intron // 0 // — // — // — /// ENST00000251968 // intron // 0 // — // — // — // —	TSG101	TSG101, Homo sapiens tumor susceptibility gene 101 (TSG101), p15.1
SNP_A-2154941	attcacagaacactat[G/T]aatacttacgtgttc	G	T	NM_006292 // intron // 0 // Hs.523512 // TSG101 // 7251 // Homo sapiens tumor susceptibility gene 101 (TSG101), mRNA. /// ENST00000357193 // intron // 0 // — // — // — /// ENST00000251968 // intron // 0 // — // — // — // —	TSG101	TSG101, Homo sapiens tumor susceptibility gene 101 (TSG101), p15.1
SNP_A-1787707	gggacagtccagagta[C/T]agtttcgcaaaatgtg	C	T	NM_006292 // intron // 0 // Hs.523512 // TSG101 // 7251 // Homo sapiens tumor susceptibility gene 101 (TSG101), mRNA. /// ENST00000357193 // intron // 0 // — // — // — /// ENST00000251968 // intron // 0 // — // — // — // —	TSG101	TSG101, Homo sapiens tumor susceptibility gene 101 (TSG101), p15.1
SNP_A-2189189	cagttatgtttaaca[C/T]tggcattatgtgtgtc	C	T	NM_018314 // intron // 0 // Hs.407991 // UEV3 // 55293 // Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA. /// ENST00000320750 // intron // 0 // — // — // —	UEV3	UEV3, Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), p15.1
SNP_A-2194745	catgcccagccaataa[C/G]tatattccttcgttta	C	G	NM_018314 // intron // 0 // Hs.407991 // UEV3 // 55293 // Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA. /// ENST00000320750 // intron // 0 // — // — // — /// ENST00000300038 // intron // 0 // — // — // —	UEV3	UEV3, Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), p15.1
SNP_A-2237778	ctctcttgtttccaa[C/G]tattgttcacctgga	C	G	NM_018314 // upstream // 605 // Hs.407991 // UEV3 // 55293 // Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA. /// NM_194285 // downstream // 17395 // Hs.268668 // FLJ39441 // 144108 // Homo sapiens hypothetical protein FLJ39441 (FLJ39441),	UEV3	UEV3, Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), p15.1
SNP_A-1859551	tcaggatcatgctttc[A/G]cctggagcaacgtgaa	A	G	NM_018314 // upstream // 6932 // Hs.407991 // UEV3 // 55293 // Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA. /// NM_194285 // downstream // 11068 // Hs.268668 // FLJ39441 // 144108 // Homo sapiens hypothetical protein FLJ39441 (FLJ39441)	UEV3	UEV3, Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), p15.1
SNP_A-2083990	actagaagtcccccata[C/T]atgccactggcagcca	C	T	NM_018314 // upstream // 8148 // Hs.407991 // UEV3 // 55293 // Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA. /// NM_194285 // downstream // 9852 // Hs.268668 // FLJ39441 // 144108 // Homo sapiens hypothetical protein FLJ39441 (FLJ39441),	UEV3	UEV3, Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), p15.1
SNP_A-2080316	acctacaatgagagaa[A/G]agtacatcaaaaggaa	A	G	AK090923 // intron // 0 // Hs.79092 // PTPN5 // 84867 // Homo sapiens cDNA FLJ33604 fis, clone BRAMY2015251, highly similar to PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.4 /// NM_032781 // intron // 0 // Hs.79092 // PTPN5 // 84867 // Homo sa	PTPN5	PTPN5, Homo sapiens cDNA FLJ33604 fis, clone BRAMY2015251, highly similar to PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.4 ,p15.1
SNP_A-2307424	gcttatcactagacac[A/G]gaaaataaaactatg	A	G	NM_054030 // upstream // 39232 // Hs.350566 // MRGX2 // 117194 // Homo sapiens G protein-coupled receptor MRGX2 (MRGX2), mRNA. /// NM_001001483 // upstream // 17232 // Hs.188569 // ZDHHC13 // 54503 // Homo sapiens zinc finger, DHHC domain containing 13 (Z	MRGX2	MRGX2, Homo sapiens G protein-coupled receptor MRGX2 (MRGX2), p15.1
SNP_A-2123467	agtgtgaaccacccata[C/T]ccggcaaaagatgcta	C	T	NM_024680 // upstream // 91427 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 380978 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. //	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2218068	cctgccccaagctcta[C/T]gcaaatgctgttcccc	C	T	NM_024680 // upstream // 279611 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 192794 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2303737	gctcagatttcaggaa[G/T]ggggaacaggaagatg	G	T	NM_024680 // upstream // 279765 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 192640 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1885982	tgacattgggaattaa[A/C]agtgacaattctaag	A	C	NM_024680 // upstream // 281857 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 190548 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2280219	gagggcactgttccac[A/G]atgtgataggtatttc	A	G	NM_024680 // upstream // 284761 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 187644 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-2008250	ttgacctttttgcagg[A/G]acactccattcccatg	A	G	NM_024680 // upstream // 291910 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 180495 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1901666	tggcaagggaatcata[A/G]caacgcacatggctc	A	G	NM_024680 // upstream // 300289 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 172116 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1875066	tctctcaagtgggtca[A/G]aaagataaggggcctc	A	G	NM_024680 // upstream // 300668 // Hs.523526 // FLJ23311 // 79733 // Homo sapiens FLJ23311 protein (FLJ23311), mRNA. /// NM_145117 // upstream // 171737 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /	FLJ23311	FLJ23311, Homo sapiens FLJ23311 protein (FLJ23311), p15.1
SNP_A-1752565	gaaggatccctggtaggtccaataa[C/T]gcagccaagctgtga cacatctcta	C	T	AB063115 // intron // 0 // Hs.407934 // NAV2 // 89797 // neuron navigator 2	NAV2	NAV2 , rs10500854, neuron navigator 2,p15.1
SNP_A-1687130	catcaaaaccgagtgattgaaggag[A/C]atgagaacgagatg gactttggtctc	A	C	AB063115 // intron // 0 // Hs.407934 // NAV2 // 89797 // neuron navigator 2	NAV2	NAV2 , rs717195, neuron navigator 2,p15.1
SNP_A-1823992	taaaatttgatatgtc[A/T]catcactccattctct	A	T	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1804100	gtcacagctcacataa[C/T]actctcacaggtacct	C	T	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-1959075	ttttgaaatggaaatc[A/G]atacaaatgatatcac	A	G	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2310271	ggaaccagctgttaaa[A/G]tagaactccgcaaaac	A	G	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-2023307	aaaaccagcaagtgaa[A/C]aacgcatgcttggcag	A	C	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-2243501	ctgctactgagcttga[C/T]gtagtgtacacttgct	C	T	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-2141069	atctgctagcagtgac[C/T]gagtacgtagaaggaa	C	T	NM_145117 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, mRNA. /// NM_182964 // intron // 0 // Hs.502116 // NAV2 // 89797 // Homo sapiens neuron navigator 2 (NAV2), transcript variant 1, mRNA.	NAV2	NAV2, Homo sapiens neuron navigator 2 (NAV2), transcript variant 2, p15.1
SNP_A-2074706	acatatgagtgaatga[C/T]gataataagtcacaaa	C	T	NM_006410 // upstream // 55633 // Hs.90753 // HTATIP2 // 10553 // Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), mRNA. /// ENST00000227256 // upstream // 147845 // — // — // — // — /// ENST00000338653 // upstream // 55633 // — //	HTATIP2	HTATIP2, Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), p15.1
SNP_A-2174456	cacagacaccagaaga[A/G]aagaccacgtgaagac	A	G	NM_006410 // upstream // 7303 // Hs.90753 // HTATIP2 // 10553 // Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), mRNA. /// ENST00000227256 // upstream // 196175 // — // — // — // — /// ENST00000338653 // upstream // 7303 // — // -	HTATIP2	HTATIP2, Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), p15.1
SNP_A-2278020	gagccatcagaagtgg[A/G]aagagggaagggagca	A	G	NM_006410 // upstream // 7224 // Hs.90753 // HTATIP2 // 10553 // Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), mRNA. /// ENST00000227256 // upstream // 196254 // — // — // — // — /// ENST00000338653 // upstream // 7224 // — // -	HTATIP2	HTATIP2, Homo sapiens HIV-1 Tat interactive protein 2, 30kDa (HTATIP2), p15.1
SNP_A-2190610	catactatacctatgc[A/G]cagaatcatggatata	A	G	NM_005788 // downstream // 40866 // Hs.152337 // HRMT1L3 // 10196 // Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), mRNA. /// NM_004211 // upstream // 49305 // Hs.136557 // SLC6A5 // 9152 // Homo sapiens solute carrier family	HRMT1L3	HRMT1L3, Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), p15.1
SNP_A-1883591	tgaacgagatatttaa[A/T]cccttgtgagatgctt	A	T	NM_004211 // intron // 0 // Hs.136557 // SLC6A5 // 9152 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 5 (SLC6A5), mRNA. /// ENST00000298923 // intron // 0 // — // — // — // —	SLC6A5	SLC6A5, Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 5 (SLC6A5), p15.1
SNP_A-2231019	ctatgtatcttttcga[A/G]gagtgtttgttcacgt	A	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // — // — // — // —	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1925099	ttatcaggatggttga[C/T]tacccactcaatttcc	C	T	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // — // — // — // —	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2008346	ggccacttgcagatac[C/G]aaaatctgaaaatctt	C	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // — // — // — // —	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1959426	ttttgccagacaaata[C/G]ggagaaaaaaggatgc	C	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // — // — // — // —	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2156335	atctcaatcatatca[A/T]catttacaggtccct	A	T	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2061012	aatgattgccacaaac[C/T]gcctaacacaaagctt	C	T	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2163647	caaaaagtcagagagt[C/G]acgtgaaaggtaactg	C	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2178727	cactgaaaattgctta[A/C]ggtgctattaataact	A	C	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1924141	ttagttgaagttccca[A/G]atacatgatagcctgc	A	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- /// ENST00000325319 // intron // 0 // --- // --- // --- /// ENST00000357134 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1801109	gtagcagttgaagaag[A/T]accaacatatgaagtc	A	T	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- /// ENST00000325319 // intron // 0 // --- // --- // --- /// ENST00000357134 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-2055677	aataatggtcttcaag[C/G]atgattgatgttagta	C	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- /// ENST00000325319 // intron // 0 // --- // --- // --- /// ENST00000357134 //	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1873134	tctattagatgttgcaj[A/G]aatgttcttaacctct	A	G	NM_006157 // intron // 0 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// ENST00000298925 // intron // 0 // --- // --- // --- /// ENST00000325319 // intron // 0 // --- // --- // ---	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p15.1
SNP_A-1925743	ttatgccagactataa[A/G]gcaatatttaggaatt	A	G	NM_006157 // downstream // 325900 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 291590 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2228278	ctactgaagtctttgal[A/G]aattacgtatcagga	A	G	NM_006157 // downstream // 356056 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 261434 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2223058	cgcattaaagtacatc[A/C]ccttaactcactctg	A	C	NM_006157 // downstream // 356295 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 261195 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2274266	gacttgatctaacata[C/G]cattatcacggtgaa	C	G	NM_006157 // downstream // 384455 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 233035 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2155885	attcctatttaactc[C/T]ctgcaaaaataaac	C	T	NM_006157 // downstream // 386220 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 231270 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1931311	ttcccaagtgataagc[A/G]ataatgacaaggttaa	A	G	NM_006157 // downstream // 386851 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 230639 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1924781	ttatatacgacttttа[C/G]attcttcacacttttc	C	G	NM_006157 // downstream // 401376 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 216114 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2157359	attgagatgcattttg[A/G]aaacacagaaatccag	A	G	NM_006157 // downstream // 409153 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 208337 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2188333	cagtctgtatcctctc[C/T]gaagcaatgattttcc	C	T	NM_006157 // downstream // 409801 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 207689 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1958431	ttttcctcacccccac[A/G]atgaatccagtagcaa	A	G	NM_006157 // downstream // 428545 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 188945 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-2057239	aatataggtggaatcc[C/T]ggaatataaagaaggc	C	T	NM_006157 // downstream // 458824 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 158666 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1662284	caagaatacttaaagttccagagta[C/T]atatgcagttaacaata tagtctca	C	T	NM_006157 // downstream // 470530 // Hs.376489 // NELL1 // 4745 // NEL-like 1 (chicken) /// NM_020346 // upstream // 292131 // Hs.242821 // SLC17A6 // 57084 // solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	NELL1	NELL1 , rs10500921, NEL-like 1 (chicken) ,p14.3
SNP_A-2090697	actttacagagctaca[A/G]aatactcacagagtga	A	G	NM_006157 // downstream // 543944 // Hs.502145 // NELL1 // 4745 // Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA. /// NM_213599 // upstream // 73546 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST000	NELL1	NELL1, Homo sapiens NEL-like 1 (chicken) (NELL1), p14.3
SNP_A-1826397	taaatttttgtaaaca[C/G]gcaaatgatctgaata	C	G	NM_213599 // intron // 0 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00000324559 // intron // 0 // — // — // — // —	TMEM16E	TMEM16E, Homo sapiens transmembrane protein 16E (TMEM16E), p14.3
SNP_A-2001808	cctccaatatacacac[A/G]atttcatagtgccact	A	G	NM_213599 // intron // 0 // Hs.154329 // TMEM16E // 203859 // Homo sapiens transmembrane protein 16E (TMEM16E), mRNA. /// ENST00000324559 // intron // 0 // — // — // — // —	TMEM16E	TMEM16E, Homo sapiens transmembrane protein 16E (TMEM16E), p14.3
SNP_A-1808346	gtctttttagacataa[C/T]gctattgtacacttaa	C	T	NM_020346 // downstream // 175048 // Hs.242821 // SLC17A6 // 57084 // Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), mRNA. /// NM_022725 // downstream // 70141 // Hs.523543 // FANCF // 2188	SLC17A6	SLC17A6, Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (SLC17A6), p14.3
SNP_A-1665498	gggttgtttcttaaaaaaaattcac[A/G]caactgacaggaggaat tgtcttta	A	G	NM_022725 // 3UTR // 0 // Hs.65328 // FANCF // 2188 // Fanconi anemia, complementation group F	FANCF	FANCF , rs10500938, Fanconi anemia, complementation group F,p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2088702	actgtggcctgtgtacf[A/G]atgtcaaaagagtagg	A	G	NM_005256 // intron // 0 // Hs.135665 // GAS2 // 2620 // Homo sapiens growth arrest-specific 2 (GAS2), transcript variant 1, mRNA. /// NM_177553 // intron // 0 // Hs.135665 // GAS2 // 2620 // Homo sapiens growth arrest-specific 2 (GAS2), transcript varian	GAS2	GAS2, Homo sapiens growth arrest-specific 2 (GAS2), transcript variant 1, p14.3
SNP_A-2095375	agaatttccactgaa[C/T]agctgtgatatatgga	C	T	NM_005256 // intron // 0 // Hs.135665 // GAS2 // 2620 // Homo sapiens growth arrest-specific 2 (GAS2), transcript variant 1, mRNA. /// NM_177553 // intron // 0 // Hs.135665 // GAS2 // 2620 // Homo sapiens growth arrest-specific 2 (GAS2), transcript varian	GAS2	GAS2, Homo sapiens growth arrest-specific 2 (GAS2), transcript variant 1, p14.3
SNP_A-2194006	catgaatcatcctctac[C/G]tacctttaacttttc	C	G	ENST00000354193 // upstream // 9639 // — // — // — /// ENST00000336930 // upstream // 1657582 // — // — // —	-	p14.3
SNP_A-2193651	catcttcctcatgac[C/G]aacatttcatgtctg	C	G	ENST00000354193 // upstream // 12140 // — // — // — /// ENST00000336930 // upstream // 1655081 // — // — // —	-	p14.3
SNP_A-2279216	gaggactggaggggtga[C/G]tattgtggtttcctg	C	G	ENST00000354193 // upstream // 12272 // — // — // — /// ENST00000336930 // upstream // 1654949 // — // — // —	-	p14.3
SNP_A-2222481	cgaggaagtcatttctg[C/T]caaccatcgtcttcat	C	T	ENST00000354193 // upstream // 153484 // — // — // — /// ENST00000336930 // upstream // 1513737 // — // — // —	-	p14.3
SNP_A-1818117	gttctccatgcctgtg[A/G]agcaacctggaaggaa	A	G	ENST00000354193 // upstream // 188625 // — // — // — /// ENST00000336930 // upstream // 1478596 // — // — // —	-	p14.3
SNP_A-2275219	gagaaggcagaaaaga[A/C]gacgaagaaagaagca	A	C	ENST00000354193 // upstream // 191235 // — // — // — /// ENST00000336930 // upstream // 1475986 // — // — // —	-	p14.3
SNP_A-2146909	atggaaaaattcctca[A/G]catccaggtacagtcc	A	G	ENST00000354193 // upstream // 460808 // — // — // — /// ENST00000336930 // upstream // 1206413 // — // — // —	-	p14.3
SNP_A-1904937	tgggtagctagtcagga[C/T]acgaacagggcaggag	C	T	ENST00000354193 // upstream // 475524 // — // — // — /// ENST00000336930 // upstream // 1191697 // — // — // —	-	p14.3
SNP_A-2272770	gacgtttgataaagaa[C/G]attagtatgaatagaa	C	G	ENST00000354193 // upstream // 521641 // — // — // — /// ENST00000336930 // upstream // 1145580 // — // — // —	-	p14.3
SNP_A-2228075	ctactaaaattaaaca[C/T]tgggagacctccag	C	T	ENST00000354193 // upstream // 545741 // — // — // — /// ENST00000336930 // upstream // 1121480 // — // — // —	-	p14.3
SNP_A-1803640	gtcaaactcaggaaat[C/G]agaggatagaatggta	C	G	ENST00000354193 // upstream // 566797 // — // — // — /// ENST00000336930 // upstream // 1100424 // — // — // —	-	p14.3
SNP_A-1874399	tctccattcctactct[C/T]ataatcaaagcataca	C	T	ENST00000354193 // upstream // 570032 // — // — // — /// ENST00000336930 // upstream // 1097189 // — // — // —	-	p14.3
SNP_A-2044667	aagaaagactatgcaa[A/G]accactgtaatagaga	A	G	ENST00000354193 // upstream // 644196 // — // — // — /// ENST00000336930 // upstream // 1023025 // — // — // —	-	p14.3
SNP_A-1905388	tggtaagagaaaatgat[A/G]gaatgaaagagtagtc	A	G	ENST00000354193 // upstream // 667019 // — // — // — /// ENST00000336930 // upstream // 1000202 // — // — // —	-	p14.3
SNP_A-2169855	caaggcaaactggatc[A/G]cactgaagctcaagaa	A	G	ENST00000354193 // upstream // 668563 // — // — // — /// ENST00000336930 // upstream // 998658 // — // — // —	-	p14.3
SNP_A-2028497	aaactgaactccttctc[A/C]ctatggtggatttta	A	C	ENST00000354193 // upstream // 668899 // — // — // — /// ENST00000336930 // upstream // 998322 // — // — // —	-	p14.3
SNP_A-2306231	gctggcccaagtttac[C/G]caaacaccaggagaga	C	G	ENST00000354193 // upstream // 679679 // — // — // — /// ENST00000336930 // upstream // 987542 // — // — // —	-	p14.3
SNP_A-1702275	gaaatcatataagcaatgatga[C/G]acaaaattataaagc atcacacaaa	C	G	AL832641 // upstream // 993708 // Hs.194765 // LOC338645 // 338645 // hypothetical protein LOC338645	LOC338645	LOC338645 , rs10500959, hypothetical protein LOC338645,p14.3
SNP_A-2112861	aggcataggaaagaca[A/G]atagcacgtattctta	A	G	ENST00000354193 // upstream // 732981 // — // — // — /// ENST00000336930 // upstream // 934240 // — // — // —	-	p14.3
SNP_A-1863110	tcatttagctgaaaaa[C/T]cataatgatagcattg	C	T	ENST00000354193 // upstream // 760877 // — // — // — /// ENST00000336930 // upstream // 906344 // — // — // —	-	p14.3
SNP_A-1933238	ttctaaatgactactt[A/G]aaaaggcgagagtgat	A	G	ENST00000354193 // upstream // 1150907 // — // — // — /// ENST00000336930 // upstream // 516314 // — // — // —	-	p14.3
SNP_A-1725138	tgaataaagcgctaaaatattatgat[A/G]caagtaaacacatttta aggcctc	A	G	AL832641 // upstream // 519373 // Hs.194765 // LOC338645 // 338645 // hypothetical protein LOC338645	LOC338645	LOC338645 , rs10500971, hypothetical protein LOC338645,p14.3
SNP_A-1688716	atttctagatagtagcaaggaaatgat[A/C]tacattaaaatttttaaat atgttg	A	C	AL832641 // upstream // 518866 // Hs.194765 // LOC338645 // 338645 // hypothetical protein LOC338645	LOC338645	LOC338645 , rs10500972, hypothetical protein LOC338645,p14.3
SNP_A-1825179	taaagtactcacgata[C/G]tatttctctcaaaag	C	G	ENST00000354193 // upstream // 1267747 // — // — // — /// ENST00000336930 // upstream // 399474 // — // — // —	-	p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1831310	taatggtcagagaaa[A/T]tcaatttgtgtgttt	A	T	ENST00000354193 // upstream // 1290548 // --- // --- // --- /// ENST00000336930 // upstream // 376673 // --- // --- // ---	-	p14.3
SNP_A-1799588	gtaattattgagttga[A/T]catttaagcatatcag	A	T	ENST00000354193 // upstream // 1290886 // --- // --- // --- /// ENST00000336930 // upstream // 376335 // --- // --- // ---	-	p14.3
SNP_A-2008662	aaggcagtacttatta[C/G]agagaaaagacagtttt	C	G	ENST00000354193 // upstream // 1308187 // --- // --- // --- /// ENST00000336930 // upstream // 359034 // --- // --- // ---	-	p14.3
SNP_A-2008663	tgcctaaacttcttgc[A/C]aaggaaaataagctgaa	A	C	ENST00000354193 // upstream // 1308893 // --- // --- // --- /// ENST00000336930 // upstream // 358328 // --- // --- // ---	-	p14.3
SNP_A-1663578	aaatcagaacctgggtcatatcaag[A/G]actagcaataatgag cactgaaata	A	G	AL832641 // upstream // 358909 // Hs.194765 // LOC338645 // 338645 // hypothetical protein LOC338645	LOC338645	LOC338645 , rs2947734, hypothetical protein LOC338645,p14.3
SNP_A-2190565	cataccctttttgcccc[A/G]cagactctgctaaca	A	G	ENST00000354193 // upstream // 1320646 // --- // --- // --- /// ENST00000336930 // upstream // 346575 // --- // --- // ---	-	p14.3
SNP_A-2305329	gctgaggtttcactgcd[A/G]agtaaaatatggccagg	A	G	ENST00000354193 // upstream // 1320712 // --- // --- // --- /// ENST00000336930 // upstream // 346509 // --- // --- // ---	-	p14.3
SNP_A-2008712	atgtactgagtccaaa[G/T]atattcattcaaataa	G	T	ENST00000336930 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-2058363	aatcacactgggtggc[A/G]atctactctggaactt	A	G	ENST00000336930 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-1937238	ttgaaaatctgggata[C/G]agaacatgcaggtttg	C	G	ENST00000336930 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-1827102	taaccattcaagcaaa[A/G]gttagtagttaaaatt	A	G	ENST00000336930 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-2045964	aagaccctgtgggtc[C/G]aggatcaaagggattt	C	G	ENST00000336930 // intron // 0 // --- // --- // ---	-	p14.3
SNP_A-1814158	gtgtctacttgacag[A/C]caggattaaaagtagg	A	C	ENST00000278194 // downstream // 16241 // --- // --- // --- /// ENST00000278194 // downstream // 489601 // --- // --- // ---	-	p14.3
SNP_A-2082099	acgaactgctacaatt[G/T]aaatggatgagttagg	G	T	ENST00000336930 // downstream // 16355 // --- // --- // --- /// ENST00000278194 // downstream // 489487 // --- // --- // ---	-	p14.3
SNP_A-1728237	tacataataatatatgggaaaataa[A/G]atcagtgcaaacttatta gtagata	A	G	NM_031418 // upstream // 1230880 // Hs.91791 // TMEM16C // 63982 // transmembrane protein 16C /// NM_145650 // downstream // 1460247 // Hs.24139 // MUC15 // 143662 // mucin 15	TMEM16C	TMEM16C , rs1900210, transmembrane protein 16C ,p14.3
SNP_A-2153715	attagtaaaatttgaa[A/T]gaggcctgtagatgtg	A	T	ENST00000336930 // downstream // 29889 // --- // --- // --- /// ENST00000278194 // downstream // 475953 // --- // --- // ---	-	p14.3
SNP_A-2254119	ctgagtggatggttc[C/T]aagaggaggctttcctg	C	T	NM_031418 // upstream // 615099 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 842708 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1857236	tcaccttcaaatggaa[C/T]gccatcaagctaacag	C	T	NM_031418 // upstream // 603526 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 831135 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1913347	tgtgggtgtccatata[G/T]gtagtattctggaggt	G	T	NM_031418 // upstream // 601893 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 829502 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1781423	ggattaagagaaagcc[A/G]ccttttagatagctct	A	G	NM_031418 // upstream // 595185 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 822794 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1922318	ttacttttacaactca[A/G]agttctgtgtactatc	A	G	NM_031418 // upstream // 594150 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 821759 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1646988	acacatttccdggcctatagttac[C/T]gggcacaataaaggtgt gaaaaca	C	T	NM_031418 // upstream // 597150 // Hs.91791 // TMEM16C // 63982 // transmembrane protein 16C /// NM_145650 // downstream // 826517 // Hs.24139 // MUC15 // 143662 // mucin 15	TMEM16C	TMEM16C , rs10501022, transmembrane protein 16C ,p14.3
SNP_A-1850526	tattaacatggatgac[G/T]gaacaaatcaatgaaa	G	T	NM_031418 // upstream // 581762 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 809371 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2142432	atgaaatagtgttcag[A/C]agtagatacacataia	A	C	NM_031418 // upstream // 581719 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 809328 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2154028	attatattcatggtcc[C/T]agccaatccataaat	C	T	NM_031418 // upstream // 580526 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 808135 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2098524	agagcaggaactatca[C/T]aaaatcttggcacaaa	C	T	NM_031418 // upstream // 575880 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 803489 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1817399	gttcaggctatgcta[A/G]aaattagtaggccaaa	A	G	NM_031418 // upstream // 566119 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 793728 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2221701	ccttgtgtatatctgc[A/G]caatggtctagtttt	A	G	NM_031418 // upstream // 551923 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 779532 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1952600	tttctgctatcttcaa[C/T]ctgaatttaagaaaat	C	T	NM_031418 // upstream // 546147 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 773756 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-1740489	taaagtttcaatttagatcttgcct[A/G]aaaacttcaatagcaaga agacac	A	G	NM_031418 // upstream // 553318 // Hs.91791 // TMEM16C // 63982 // transmembrane protein 16C /// NM_145650 // downstream // 782685 // Hs.24139 // MUC15 // 143662 // mucin 15	TMEM16C	TMEM16C , rs1038931, transmembrane protein 16C ,p14.3
SNP_A-2008893	aaagcattccaaataat[A/G]gaactctccagtagt	A	G	NM_031418 // upstream // 403166 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 630775 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3
SNP_A-2065677	aatttatatcaattac[A/G]atgttactggcaggtc	A	G	NM_031418 // upstream // 325696 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 553305 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932754	ttcctctttttggd[C/T]gaatattattcatata	C	T	NM_031418 // upstream // 305519 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 533128 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2071639	acagaataatatacagaaa[G/T]gttgggtgacaaattt	G	T	NM_031418 // upstream // 304202 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 531811 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1918568	ttaaatgccaatgctc[A/G]gaatatttaacctgca	A	G	NM_031418 // upstream // 303476 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 531085 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1822859	taaaaagatgttatca[A/G]tgaagtaaactgttct	A	G	NM_031418 // upstream // 299366 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 526975 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1958018	ttttcactcagcttaa[A/T]tcctgaagtttcatc	A	T	NM_031418 // upstream // 299107 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 526716 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1852687	tatttcaaagtaacac[A/G]gtagctccatgtttag	A	G	NM_031418 // upstream // 298862 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 526471 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2008910	acatccaaacactata[A/T]gcctaggacatctaaa	A	T	NM_031418 // upstream // 292327 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 519936 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-1647462	tacatttagctgacagatgtttgca[A/G]taatcataattaatgttcca atcat	A	G	NM_031418 // upstream // 296356 // Hs.91791 // TMEM16C // 63982 // transmembrane protein 16C /// NM_145650 // downstream // 525723 // Hs.24139 // MUC15 // 143662 // mucin 15	TMEM16C	TMEM16C , rs725853, transmembrane protein 16C ,p14.3
SNP_A-1709693	tgttgtctgtcatcaatgacaaca[C/T]tcactcaatgggtccaga gtcacta	C	T	NM_031418 // upstream // 296171 // Hs.91791 // TMEM16C // 63982 // transmembrane protein 16C /// NM_145650 // downstream // 525538 // Hs.24139 // MUC15 // 143662 // mucin 15	TMEM16C	TMEM16C , rs725854, transmembrane protein 16C ,p14.3
SNP_A-2300683	gcctgctgaagaagcc[A/G]aattgtttgccacag	A	G	NM_031418 // upstream // 282910 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 510519 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2
SNP_A-2099712	agaggttaagttactg[A/C]aggcaagtgccatgga	A	C	NM_031418 // upstream // 269519 // Hs.91791 // TMEM16C // 63982 // Homo sapiens transmembrane protein 16C (TMEM16C), mRNA. /// NM_145650 // downstream // 497128 // Hs.407152 // MUC15 // 143662 // Homo sapiens mucin 15 (MUC15), mRNA. /// ENST00000278194 //	TMEM16C	TMEM16C, Homo sapiens transmembrane protein 16C (TMEM16C), p14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2029025	aaagaaacagaaactc[A/C]agatactatagacaga	A	C	NM_178498 // intron // 0 // Hs.148907 // SLC5A12 // 159963 // Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 12 (SLC5A12), mRNA. /// ENST00000340797 // intron // 0 // — // — /// ENST00000280467 // intron // 0	SLC5A12	SLC5A12, Homo sapiens solute carrier family 5 (sodium,p14.2
SNP_A-2112226	aggatttacaattaca[G/T]acagtgctttattgag	G	T	NM_178498 // upstream // 67130 // Hs.148907 // SLC5A12 // 159963 // Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 12 (SLC5A12), mRNA. /// NM_203371 // upstream // 204952 // Hs.32478 // LOC387758 // 387758 // Homo sapiens simi	SLC5A12	SLC5A12, Homo sapiens solute carrier family 5 (sodium,p14.2
SNP_A-1922709	ttagagcacaaaaagc[A/G]atgtgtaaaaattgt	A	G	NM_178498 // upstream // 99746 // Hs.148907 // SLC5A12 // 159963 // Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 12 (SLC5A12), mRNA. /// NM_203371 // upstream // 172336 // Hs.32478 // LOC387758 // 387758 // Homo sapiens simi	SLC5A12	SLC5A12, Homo sapiens solute carrier family 5 (sodium,p14.2
SNP_A-2171613	caatctacaggtttaa[C/T]gtaattccatcaaag	C	T	NM_178498 // upstream // 152359 // Hs.148907 // SLC5A12 // 159963 // Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 12 (SLC5A12), mRNA. /// NM_203371 // upstream // 119723 // Hs.32478 // LOC387758 // 387758 // Homo sapiens sim	SLC5A12	SLC5A12, Homo sapiens solute carrier family 5 (sodium,p14.2
SNP_A-2048246	aagcagaaataaagcat[A/G]agagccaattaattgt	A	G	NM_003986 // intron // 0 // Hs.144845 // BBOX1 // 8424 // Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA. /// ENST00000263182 // intron // 0 // — // — // —	BBOX1	BBOX1, Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), p14.2
SNP_A-2222009	cgaacactatcaaaaa[A/T]ctccagcccagccatg	A	T	NM_003986 // downstream // 46514 // Hs.144845 // BBOX1 // 8424 // Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA. /// ENST00000263182 // downstream // 46514 // — // — // — ///	BBOX1	BBOX1, Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), p14.2
SNP_A-2297564	gccagagccagcaatc[A/G]atgtgaggaaggtgct	A	G	NM_003986 // downstream // 59548 // Hs.144845 // BBOX1 // 8424 // Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA. /// ENST00000263182 // downstream // 59548 // — // — // — ///	BBOX1	BBOX1, Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), p14.2
SNP_A-2009040	ccaatgaaatttataa[C/T]gccttgtcaaatttt	C	T	NM_003986 // downstream // 85210 // Hs.144845 // BBOX1 // 8424 // Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA. /// ENST00000263182 // downstream // 85210 // — // — // — ///	BBOX1	BBOX1, Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), p14.2
SNP_A-2300936	gccgtgctctataga[C/T]gaaatacaaagccta	C	T	NM_031217 // downstream // 25546 // Hs.301052 // KIF18A // 81930 // Homo sapiens kinesin family member 18A (KIF18A), mRNA. /// ENST00000314102 // upstream // 104040 // — // — // — /// ENST00000263181 // downstream // 25546 // — // — // –	KIF18A	KIF18A, Homo sapiens kinesin family member 18A (KIF18A), p14.1
SNP_A-2292540	gcactctggattcaca[A/T]aatttacattctatct	A	T	NM_031217 // downstream // 20767 // Hs.301052 // KIF18A // 81930 // Homo sapiens kinesin family member 18A (KIF18A), mRNA. /// ENST00000314102 // upstream // 108819 // — // — // — /// ENST00000263181 // downstream // 20767 // — // — // –	KIF18A	KIF18A, Homo sapiens kinesin family member 18A (KIF18A), p14.1
SNP_A-1689114	agattatagtcaaaagtggctttca[G/T]acctgattcagctataatt ttttaa	G	T	NM_031217 // intron // 0 // Hs.301052 // DKFZP434G2226 // 81930 // kinesin family member 18A	DKFZP434G226	DKFZP434G2226, rs10501094, kinesin family member 18A,p14.1
SNP_A-1947958	ttagaagtaacattg[A/G]aaacattaaacttctt	A	G	NM_152636 // intron // 0 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// ENST00000342303 // intron // 0 // — // — // — /// ENST00000303459 // intron // 0 // — // — // —	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2009127	tattaagaaaatagcc[A/C]aagtattgaaagtatc	A	C	NM_152636 // intron // 0 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// ENST00000342303 // intron // 0 // — // — // — // — /// ENST00000303459 // intron // 0 // — // — // — // —	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1866949	tccctatgttgtgata[C/T]gacctgttaacttggc	C	T	NM_152636 // intron // 0 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// ENST00000342303 // intron // 0 // — // — // — // — /// ENST00000303459 // intron // 0 // — // — // — // —	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1785636	ggctccctcatgctcc[A/G]cttctggttgggtttg	A	G	NM_152636 // downstream // 188256 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream // 1489065 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shak	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1887365	tgagaatgaaaactgg[C/T]acagccattatggaca	C	T	NM_152636 // downstream // 679264 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream // 998057 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shake	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1947705	tttactattctatgca[A/G]tcaaagtagaaaattt	A	G	NM_152636 // downstream // 840789 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream // 836532 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shake	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-1665386	catatactctaatagtaatttttga[A/G]agaaagtgaaaacaagactaatttt	A	G	NM_002233 // downstream // 815251 // Hs.458267 // KCNA4 // 3739 // potassium voltage-gated channel, shaker-related subfamily, member 4 /// NM_152636 // downstream // 861571 // Hs.366407 // FLJ33979 // 196074 // hypothetical protein FLJ33979	KCNA4	KCNA4 , rs10501114, potassium voltage-gated channel, shaker-related subfamily, member 4 ,p14.1
SNP_A-2042274	aactatgaagttcagt[C/T]aataataatgtatata	C	T	NM_152636 // downstream // 1078514 // Hs.243326 // FLJ33979 // 196074 // Homo sapiens hypothetical protein FLJ33979 (FLJ33979), mRNA. /// NM_002233 // downstream // 598807 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shak	FLJ33979	FLJ33979, Homo sapiens hypothetical protein FLJ33979 (FLJ33979), p14.1
SNP_A-2009274	aagaactttgtcaatt[C/G]aatcagatgaaatata	C	G	NM_002233 // upstream // 60589 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 158636 // Hs.36975 // FSHB // 2488 // Homo sapiens follicle stimul	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-1667666	ggcagtgcaaccatttaggatttac[A/C]gcctggaatatcacgtttagcaat	A	C	NM_000510 // upstream // 62361 // Hs.36975 // FSHB // 2488 // follicle stimulating hormone, beta polypeptide /// NM_002233 // upstream // 152601 // Hs.458267 // KCNA4 // 3739 // potassium voltage-gated channel, shaker-related subfamily, member 4	FSHB	FSHB , rs4506622, follicle stimulating hormone, beta polypeptide ,p14.1
SNP_A-2195756	catgtacaggataaaa[C/T]gcaatgaaagcccact	C	T	NM_002233 // upstream // 200169 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 19056 // Hs.36975 // FSHB // 2488 // Homo sapiens follicle stimul	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-2040371	aaccagagcccttaca[C/T]tggtctacaagttcca	C	T	NM_002233 // upstream // 217400 // Hs.458267 // KCNA4 // 3739 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), mRNA. /// NM_000510 // upstream // 1825 // Hs.36975 // FSHB // 2488 // Homo sapiens follicle stimula	KCNA4	KCNA4, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 4 (KCNA4), p14.1
SNP_A-1855291	tcaaggaactggtata[C/T]gaaacagtgagagtgc	C	T	NM_000510 // CDS // 0 // Hs.36975 // FSHB // 2488 // Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), mRNA. /// ENST00000254122 // CDS // 0 // — // — // — // —	FSHB	FSHB, Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), p14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2091792	agaaaatactggaaga[C/G]gatgtttgaggtaagc	C	G	NM_000510 // downstream // 520 // Hs.36975 // FSHB // 2488 // Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), mRNA. /// NM_152316 // upstream // 88789 // Hs.502208 // FLJ38968 // 120534 // Homo sapiens hypothetical protein FLJ38968 (FL	FSHB	FSHB, Homo sapiens follicle stimulating hormone, beta polypeptide (FSHB), p14.1
SNP_A-2258101	ctttaaaaaaatgaca[A/T]gacacaaaaatatgaca	A	T	NM_001585 // upstream // 137646 // Hs.159538 // C22orf1 // 758 // Homo sapiens chromosome 22 open reading frame 1 (C22orf1), mRNA. /// NM_001584 // upstream // 137646 // Hs.289795 // C11orf8 // 744 // Homo sapiens chromosome 11 open reading frame 8 (C11or	C22orf1	C22orf1, Homo sapiens chromosome 22 open reading frame 1 (C22orf1), p14.1
SNP_A-2009379	cttccacttaagcca[C/G]attctaacttgacact	C	G	NM_001585 // upstream // 161556 // Hs.159538 // C22orf1 // 758 // Homo sapiens chromosome 22 open reading frame 1 (C22orf1), mRNA. /// NM_001584 // upstream // 161556 // Hs.289795 // C11orf8 // 744 // Homo sapiens chromosome 11 open reading frame 8 (C11or	C22orf1	C22orf1, Homo sapiens chromosome 22 open reading frame 1 (C22orf1), p14.1
SNP_A-2025860	aaaatgggtgatatga[C/T]aaatgaaataggagtc	C	T	NM_002901 // downstream // 69860 // Hs.97887 // RCN1 // 5954 // Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA. /// NM_000378 // downstream // 212391 // Hs.408453 // WT1 // 7490 // Homo sapiens Wilms tumor 1 (WT1), transcript v	RCN1	RCN1, Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), p13
SNP_A-2166900	caaattttggagttaa[C/T]ggcctccacaattatg	C	T	NM_015855 // downstream // 42924 // Hs.546393 // WT-1 // 51352 // Homo sapiens Wilms tumor associated protein (WT-1), mRNA. /// NM_006360 // upstream // 100817 // Hs.502244 // GA17 // 10480 // Homo sapiens dendritic cell protein (GA17), mRNA. /// ENST00	WT-1	WT-1, Homo sapiens Wilms tumor associated protein (WT-1), p13
SNP_A-1945347	ttgttagacgctaacc[A/G]ggggaaagagtgcaga	A	G	NM_015855 // downstream // 45315 // Hs.546393 // WT-1 // 51352 // Homo sapiens Wilms tumor associated protein (WT-1), mRNA. /// NM_006360 // upstream // 98426 // Hs.502244 // GA17 // 10480 // Homo sapiens dendritic cell protein (GA17), mRNA. /// ENST000	WT-1	WT-1, Homo sapiens Wilms tumor associated protein (WT-1), p13
SNP_A-2162433	atttcacattgtcga[C/T]tcacttttttggtcac	C	T	NM_015855 // downstream // 80166 // Hs.546393 // WT-1 // 51352 // Homo sapiens Wilms tumor associated protein (WT-1), mRNA. /// NM_006360 // upstream // 63575 // Hs.502244 // GA17 // 10480 // Homo sapiens dendritic cell protein (GA17), mRNA. /// ENST000	WT-1	WT-1, Homo sapiens Wilms tumor associated protein (WT-1), p13
SNP_A-1849327	tatggaacagtaaaga[A/T]gttaatggttgggt	A	T	NM_018393 // downstream // 141717 // Hs.533701 // FLJ11336 // 55346 // Homo sapiens hypothetical protein FLJ11336 (FLJ11336), mRNA. /// NM_001326 // upstream // 53588 // Hs.44402 // CSTF3 // 1479 // Homo sapiens cleavage stimulation factor, 3' pre-RNA, su	FLJ11336	FLJ11336, Homo sapiens hypothetical protein FLJ11336 (FLJ11336), p13
SNP_A-2142682	atgaagagaggaatgg[A/C]aaaaagtgaatcggag	A	C	NM_005734 // intron // 0 // Hs.201918 // HIPK3 // 10114 // Homo sapiens homeodomain interacting protein kinase 3 (HIPK3), mRNA. /// ENST00000303296 // intron // 0 // --- // --- // ---	HIPK3	HIPK3, Homo sapiens homeodomain interacting protein kinase 3 (HIPK3), p13
SNP_A-2182849	cagatgtgcaaatgaa[A/C]agagccaatcagacag	A	C	NM_005734 // downstream // 38009 // Hs.201918 // HIPK3 // 10114 // Homo sapiens homeodomain interacting protein kinase 3 (HIPK3), mRNA. /// ENST00000303296 // downstream // 38009 // --- // --- // --- /// ENST00000265654 // upstream // 151353 // ---	HIPK3	HIPK3, Homo sapiens homeodomain interacting protein kinase 3 (HIPK3), p13
SNP_A-1934067	ttctcagagctcagtc[C/T]acaacagcctgctgag	C	T	ENST00000265654 // intron // 0 // --- // --- // ---	-	p13
SNP_A-2301446	gccttttgattaca[C/T]gtgtttatttatgagt	C	T	NM_005574 // upstream // 1165 // Hs.34560 // LMO2 // 4005 // Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), mRNA. /// Z48042 // upstream // 158171 // Hs.471818 // M11S1 // 4076 // H.sapiens mRNA encoding GPI-anchored protein p137. /// NM_203364	LMO2	LMO2, Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1905252	tgggttgcccacattc[A/G]cctcaatatatctaac	A	G	NM_005574 // upstream // 104120 // Hs.34560 // LMO2 // 4005 // Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), mRNA. /// Z48042 // upstream // 55216 // Hs.471818 // M11S1 // 4076 // H.sapiens mRNA encoding GPI-anchored protein p137. /// NM_20336	LMO2	LMO2, Homo sapiens LIM domain only 2 (rhombotin like 1) (LMO2), p13
SNP_A-1839830	tagattcatgctcatg[A/C]catatctcaagtgttg	A	C	NM_005574 // upstream // 157097 // Hs.34560 // LMO2 // 4005 // Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), mRNA. /// Z48042 // upstream // 2239 // Hs.471818 // M11S1 // 4076 // H.sapiens mRNA encoding GPI-anchored protein p137. /// NM_203364	LMO2	LMO2, Homo sapiens LIM domain only 2 (rhombotin like 1) (LMO2), p13
SNP_A-2075882	acattaaagagcataa[C/T]ctccatgcagtccacc	C	T	NM_145804 // intron // 0 // Hs.23361 // ABTB2 // 25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// ENST00000298992 // intron // 0 // --- // --- // ---	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-2240973	ctgagatactccccatg[C/T]aggtggctttaattcc	C	T	NM_145804 // intron // 0 // Hs.23361 // ABTB2 // 25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// ENST00000298992 // intron // 0 // --- // --- // ---	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-1801948	gtataaagattaaggc[A/T]ccagaggcaggtagga	A	T	NM_145804 // upstream // 25580 // Hs.23361 // ABTB2 // 25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// NM_001752 // upstream // 56111 // Hs.502302 // CAT // 847 // Homo sapiens catalase (CAT), mRNA. /// ENST0000002	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-2080003	accgaaataatatctg[A/G]caattacctggtttt	A	G	NM_145804 // upstream // 42128 // Hs.23361 // ABTB2 // 25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// NM_001752 // upstream // 39563 // Hs.502302 // CAT // 847 // Homo sapiens catalase (CAT), mRNA. /// ENST0000002	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-2072993	acaggactgtttaa[C/G]caacatacaggcctgt	C	G	NM_145804 // upstream // 68691 // Hs.23361 // ABTB2 // 25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// NM_001752 // upstream // 13000 // Hs.502302 // CAT // 847 // Homo sapiens catalase (CAT), mRNA. /// ENST0000002	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-2135870	atcaacacattcatta[C/T]ggactgagagcacaca	C	T	NM_145804 // upstream // 76507 // Hs.23361 // ABTB2 // 25841 // Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA. /// NM_001752 // upstream // 5184 // Hs.502302 // CAT // 847 // Homo sapiens catalase (CAT), mRNA. /// ENST0000029	ABTB2	ABTB2, Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), p13
SNP_A-1756395	attgcaaagctatg[acccgtgaca[A/G]gtaaatgaaaggtttg attgtgct	A	G	NM_001752 // intron // 0 // Hs.395771 // CAT // 847 // catalase	CAT	CAT , rs769218, catalase,p13
SNP_A-2238106	ctctgcatttgccaa[G/T]agttggagaagttggg	G	T	NM_001752 // intron // 0 // Hs.502302 // CAT // 847 // Homo sapiens catalase (CAT), mRNA. /// ENST00000241052 // intron // 0 // --- // --- // ---	CAT	CAT, Homo sapiens catalase (CAT), p13
SNP_A-2001886	ttgatttcttctcata[A/C]gagtgggtgagattaa	A	C	NM_001422 // intron // 0 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // intron // 0 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor 5 (ets do	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13
SNP_A-2245214	ctggctaagtagccaa[C/G]gtctttgtggagagc	C	G	NM_001422 // intron // 0 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // intron // 0 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor 5 (ets do	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2009686	aigttatcaagctgca[C/T]gtggatcattcacac	C	T	NM_001422 // upstream // 7303 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // upstream // 7303 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13
SNP_A-1719125	ttagaaagaccattttgcagagtgca[G/T]tacacagaatgtttcag gacaccc	G	T	NM_001422 // upstream // 26919 // Hs.11713 // ELF5 // 2001 // E74-like factor 5 (ets domain transcription factor) /// NM_012153 // upstream // 80374 // Hs.200228 // EHF // 26298 // ets homologous factor /// NM_172233 // upstream // 80374 // Hs.200228 //	ELF5	ELF5, rs836124, E74-like factor 5 (ets domain transcription factor), p13
SNP_A-2212224	ccctggatctattgat[A/C]gccttctgttttagct	A	C	NM_001422 // upstream // 40471 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, mRNA. /// NM_198381 // upstream // 40471 // Hs.11713 // ELF5 // 2001 // Homo sapiens E74-like fact	ELF5	ELF5, Homo sapiens E74-like factor 5 (ets domain transcription factor) (ELF5), transcript variant 2, p13
SNP_A-2310588	ggaagagaaaacacca[A/G]tacacaccatatatca	A	G	NM_012153 // downstream // 208649 // Hs.502306 // EHF // 26298 // Homo sapiens ets homologous factor (EHF), mRNA. /// NM_015957 // downstream // 12115 // Hs.447794 // MMRP19 // 51074 // Homo sapiens likely ortholog of mouse monocyte macrophage 19 (MMRP19)	EHF	EHF, Homo sapiens ets homologous factor (EHF), p13
SNP_A-2009781	catgtcagctgaaacc[C/T]aatattagctatatct	C	T	NM_003477 // downstream // 113843 // Hs.502315 // PDHX // 8050 // Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), mRNA. /// NM_001001392 // upstream // 29058 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Hn	PDHX	PDHX, Homo sapiens pyruvate dehydrogenase complex, component X (PDHX), p13
SNP_A-1688400	caagatgctggtgacaccactgagal[C/T]gtgagagagaagca catgggtgcagg	C	T	NM_000610 // upstream // 13230 // Hs.306278 // CD44 // 960 // CD44 antigen (homing function and Indian blood group system) /// NM_003477 // downstream // 129982 // Hs.329817 // PDHX // 8050 // pyruvate dehydrogenase complex, component X	CD44	CD44 , rs2785175, CD44 antigen (homing function and Indian blood group system), p13
SNP_A-1689026	taaaagtcttttaatcatccaatggt[A/G]aattaatggacaccttct gtatgc	A	G	NM_000610 // upstream // 7357 // Hs.306278 // CD44 // 960 // CD44 antigen (homing function and Indian blood group system) /// NM_003477 // downstream // 135855 // Hs.329817 // PDHX // 8050 // pyruvate dehydrogenase complex, component X	CD44	CD44 , rs10488808, CD44 antigen (homing function and Indian blood group system), p13
SNP_A-2009785	ggactctggacaacca[C/T]gaggaaacttggaaa	C	T	NM_001001392 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antig	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-2009786	aggagctgtgatctga[C/T]gaaggacattcagtga	C	T	NM_001001392 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antig	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-2009791	ttgcttgcagctgtta[A/T]ctctaatccctataac	A	T	NM_001001392 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antig	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-1817109	gttcaaatagactcaa[A/C]actgctgaacacaaat	A	C	NM_001001392 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antig	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2205809	ccatacctgtaagaga[A/G]aaacaacaggatattg	A	G	NM_001001392 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // intron // 0 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antig	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-1745400	tcagatatggactccagtcatagta[C/T]aacgcttcagcctactg caaatcca	C	T	NM_000610 // CDS // 0 // Hs.306278 // CD44 // 960 // CD44 antigen (homing function and Indian blood group system)	CD44	CD44 , rs1467558, CD44 antigen (homing function and Indian blood group system),p13
SNP_A-2260006	gaaaataaaaagtaaa[G/T]ctctcactgaactcta	G	T	NM_001001392 // downstream // 5254 // Hs.502328 // CD44 // 960 // Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, mRNA. /// NM_001001391 // downstream // 5254 // Hs.502328 // CD44 // 960 // Homo sapi	CD44	CD44, Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 5, p13
SNP_A-1696342	ctagtaagagtgtcaaaatgagtag[A/G]agaaaatggtttatgtc atacaggt	A	G	NM_000610 // downstream // 9801 // Hs.306278 // CD44 // 960 // CD44 antigen (homing function and Indian blood group system)	CD44	CD44 , rs10488812, CD44 antigen (homing function and Indian blood group system),p13
SNP_A-1933934	ttctcaaatctaagga[C/T]acttctggaattgctg	C	T	NM_004171 // intron // 0 // Hs.502338 // SLC1A2 // 6506 // Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // --- // ---	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-2283973	gatataggaaacatca[A/G]tcagggaatggagaaa	A	G	NM_004171 // intron // 0 // Hs.502338 // SLC1A2 // 6506 // Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // --- // ---	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-1841482	taggagcagattttac[A/G]acacggcttcaaactc	A	G	NM_004171 // intron // 0 // Hs.502338 // SLC1A2 // 6506 // Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), mRNA. /// ENST00000278379 // intron // 0 // --- // --- // --- // ---	SLC1A2	SLC1A2, Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), p13
SNP_A-1660023	gaacctagaaaaaaggcctgaaata[C/G]aaacatacatttgg gagttatcagg	C	G	NM_004171 // intron // 0 // Hs.349088 // SLC1A2 // 6506 // solute carrier family 1 (glial high affinity glutamate transporter), member 2	SLC1A2	SLC1A2 , rs3945930, solute carrier family 1 (glial high affinity glutamate transporter), member 2,p13
SNP_A-2009828	cagaagtatgcttaac[A/G]ctcctatagtctgaag	A	G	NM_015430 // intron // 0 // Hs.55044 // DKFZP586H2123 // 25891 // Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, mRNA. /// NM_001001991 // intron // 0 // Hs.55044 // DKFZP586H2123 // 25891 // Homo sapiens regen	DKFZP586H2123	DKFZP586H2123, Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, p13
SNP_A-1814680	gtgtggtcaagaatta[C/T]atttgttacttggtct	C	T	NM_015430 // upstream // 41023 // Hs.55044 // DKFZP586H2123 // 25891 // Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, mRNA. /// NM_001001991 // upstream // 41023 // Hs.55044 // DKFZP586H2123 // 25891 // Homo s	DKFZP586H2123	DKFZP586H2123, Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, p13
SNP_A-1782684	ggcactggattcaaaa[C/T]gggatggtgcttggga	C	T	NM_015430 // upstream // 55795 // Hs.55044 // DKFZP586H2123 // 25891 // Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, mRNA. /// NM_001001991 // upstream // 55795 // Hs.55044 // DKFZP586H2123 // 25891 // Homo s	DKFZP586H2123	DKFZP586H2123, Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, p13
SNP_A-2060017	aatctttcctcttgtc[A/G]acttggcaagcctggg	A	G	NM_015430 // upstream // 64852 // Hs.55044 // DKFZP586H2123 // 25891 // Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, mRNA. /// NM_001001991 // upstream // 64852 // Hs.55044 // DKFZP586H2123 // 25891 // Homo s	DKFZP586H2123	DKFZP586H2123, Homo sapiens regeneration associated muscle protease (DKFZP586H2123), transcript variant 1, p13
SNP_A-2043805	aacttcaatgaaaaga[C/T]ggactggtttataaaa	C	T	NM_017583 // intron // 0 // Hs.192103 // TRIM44 // 54765 // Homo sapiens tripartite motif-containing 44 (TRIM44), mRNA. /// ENST00000299413 // intron // 0 // --- // --- // --- // ---	TRIM44	TRIM44, Homo sapiens tripartite motif-containing 44 (TRIM44), p13
SNP_A-1749595	gcagtcattctgcaattacgttcac[C/T]cttcttcaagctggctcca agtata	C	T	NM_017583 // intron // 0 // Hs.14512 // TRIM44 // 54765 // tripartite motif-containing 44	TRIM44	TRIM44 , rs963811, tripartite motif-containing 44,p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1882280	tgaaaaattctacaga[A/G]gttccaagtgtggtgt	A	G	NM_017583 // intron // 0 // Hs.192103 // TRIM44 // 54765 // Homo sapiens tripartite motif-containing 44 (TRIM44), mRNA. /// ENST00000299413 // intron // 0 // — // — // — // —	TRIM44	TRIM44, Homo sapiens tripartite motif-containing 44 (TRIM44), p13
SNP_A-2225436	ctaaaaagcaacctca[A/G]gaattccaaaagctaa	A	G	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1818422	gttcttccccgtcca[C/T]gacaaagattctctcc	C	T	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-2160355	atttcaggctagaatc[A/G]ccaagatttgatgaca	A	G	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-2158061	attggaacctcagtca[A/G]taaaaaggcatctcct	A	G	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-2136624	atcactatctgtggag[C/T]agaaaatattctggtg	C	T	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1683948	ttgttaaggggaaaaaattaactta[C/T]ggtgtagtgattagagg gaaacgtc	C	T	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // hypothetical protein LOC143458	LOC143458	LOC143458 , rs10501144, hypothetical protein LOC143458,p13
SNP_A-2224050	cggggtttttggtcaa[C/T]taagttcaggaaacac	C	T	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1948745	tttatagttaagtctc[A/G]aaatgaggtagtgtgt	A	G	NM_174902 // intron // 0 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// ENST00000315571 // intron // 0 // — // — // — // —	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-2127169	ataaatccagaggtcc[C/T]gatgagattgtgttga	C	T	NM_174902 // downstream // 14935 // Hs.205865 // LOC143458 // 143458 // Homo sapiens hypothetical protein LOC143458 (LOC143458), mRNA. /// NM_207428 // downstream // 22213 // Hs.502363 // FLJ45212 // 399879 // Homo sapiens FLJ45212 protein (FLJ45212), mRN	LOC143458	LOC143458, Homo sapiens hypothetical protein LOC143458 (LOC143458), p13
SNP_A-1832990	tacacaatagaaagga[C/T]ggacagttttcttgcc	C	T	NM_138787 // intron // 0 // Hs.406726 // LOC119710 // 119710 // Homo sapiens hypothetical protein BC009561 (LOC119710), mRNA. /// ENST00000347206 // intron // 0 // — // — // — // — /// ENST00000334307 // intron // 0 // — // — // — // —	LOC119710	LOC119710, Homo sapiens hypothetical protein BC009561 (LOC119710), p12
SNP_A-2305546	gctgcaatttgctaca[A/G]tggcccctctccaatg	A	G	NM_000448 // downstream // 107139 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 130473 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. ///	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2052439	aagtagaaaagtaaac[G/T]ccaaggtaagattgtc	G	T	NM_000448 // downstream // 1316524 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1339858 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2184112	cagccctgtgaaggga[C/G]gtatgccacactccaa	C	G	NM_000448 // downstream // 1527069 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1550403 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1844250	tagtttggtcaggtac[C/T]gggcaaagtaattttc	C	T	NM_000448 // downstream // 1565006 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1588340 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2039108	aacaggtggaaacaaa[C/T]gtggatttcctaagaca	C	T	NM_000448 // downstream // 1789941 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1813275 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1688120	ttcagccaagagaccaattaataa[C/T]gcaagaaaaaaggtttattaaggac	C	T	NM_000448 // downstream // 1831950 // Hs.73958 // RAG1 // 5896 // recombination activating gene 1 /// NM_000536 // upstream // 1813459 // Hs.159376 // RAG2 // 5897 // recombination activating gene 2 /// NM_138787 // downstream // 1752425 // Hs.406726 //	RAG1	RAG1 , rs10501198, recombination activating gene 1, p12
SNP_A-2010110	tgtcacataaggtatc[A/G]ctcaacattaagtagc	A	G	NM_000448 // downstream // 1811301 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1834635 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2067666	acaacaagtgccatga[C/T]gaggatctcatgaga	C	T	NM_000448 // downstream // 1814976 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1838310 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2089240	acttactgtatggaaa[A/G]tgctgtggtcaaatta	A	G	NM_000448 // downstream // 1816679 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1840013 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1908555	tgtagcaactggaaaa[C/T]gagacaaggaaacatg	C	T	NM_000448 // downstream // 1932763 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1956097 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2123609	agtgtgtgtatttcc[A/G]acaatttccaaggta	A	G	NM_000448 // downstream // 1945150 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1968484 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2010118	aattagtttctcttta[C/G]tctgttgaaacgcg	C	G	NM_000448 // downstream // 1945659 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 1968993 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2010120	gtactatgagtttgca[A/T]atgtaggaatacaac	A	T	NM_000448 // downstream // 1992320 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2015654 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2046143	aagactgcaaagcaac[C/T]agctaaaaacaccaag	C	T	NM_000448 // downstream // 2204532 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2227866 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2234230	ctcatttgaccctatc[A/G]ccaaaggcagtcatat	A	G	NM_000448 // downstream // 2735128 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 2758462 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102400	agattccacctcaaaaa[A/G]accaatttcattgctc	A	G	NM_000448 // downstream // 3132719 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 3156053 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-1926949	ttatttccttgtataa[C/T]acacatgtttgatcca	C	T	NM_000448 // downstream // 3346345 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 3369679 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2263498	gaaccaattggtgata[C/T]attgaaaaaacagttt	C	T	NM_000448 // downstream // 3349279 // Hs.73958 // RAG1 // 5896 // Homo sapiens recombination activating gene 1 (RAG1), mRNA. /// NM_000536 // upstream // 3372613 // Hs.159376 // RAG2 // 5897 // Homo sapiens recombination activating gene 2 (RAG2), mRNA. //	RAG1	RAG1, Homo sapiens recombination activating gene 1 (RAG1), p12
SNP_A-2010275	gaaagactagttagagt[A/G]caatctaggagagaaa	A	G	NM_020929 // intron // 0 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// ENST00000278198 // intron // 0 // — // — // —	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2010276	gtgactatagctggtg[C/T]aatcattagcaaacag	C	T	NM_020929 // upstream // 2953 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 3014916 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // upstr	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1677962	tcctaatcacataatacatttttca[C/T]gctctagcgaagtaaatac aattag	C	T	NM_006595 // upstream // 2976477 // Hs.444340 // API5 // 8539 // apoptosis inhibitor 5	API5	API5, rs10501229, apoptosis inhibitor 5,p12
SNP_A-1696336	attctcttcgagataggcaccctta[C/T]aaaaagtgaagtcttcca tgatgta	C	T	NM_006595 // upstream // 2976300 // Hs.444340 // API5 // 8539 // apoptosis inhibitor 5	API5	API5, rs10501230, apoptosis inhibitor 5,p12
SNP_A-2290260	gcaacaactggtcata[G/T]ctctccctttctggg	G	T	NM_020929 // upstream // 53893 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2963976 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // upst	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2010315	atgtatttaaaaca[A/T]ctgtgccagttctaa	A	T	NM_020929 // upstream // 240276 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2777593 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2036807	aaatttcagatcttag[C/G]acagccaggaaacaat	C	G	NM_020929 // upstream // 323248 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2694621 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1869355	tcctgtaagcctttca[A/G]aatctttcatctcc	A	G	NM_020929 // upstream // 706187 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 2311682 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2298567	gcccacatgtaacatg[G/T]aattgctcccgttt	G	T	NM_020929 // upstream // 1533729 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1484140 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // up	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1898293	tgctataaatttgta[G/T]gaagtttctgcctgc	G	T	NM_020929 // upstream // 1558033 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1459836 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // up	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1892296	tgcaacggacgtgtca[A/G]atagcctacctggg	A	G	NM_020929 // upstream // 1577941 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1439928 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // up	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1861094	tcatataaataatgta[A/C]gtttccctctgattg	A	C	NM_020929 // upstream // 1856019 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 1161850 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // up	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2113797	aggctgctacaggtca[A/C]ctgaatcaccaacccc	A	C	NM_020929 // upstream // 2060237 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 957632 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1857243	tcaccttccacacctc[A/G]aaagaaaagctgagtt	A	G	NM_020929 // upstream // 2111562 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 906307 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2010573	tgattaaataaatcaa[C/T]gaattccagcatcaaa	C	T	NM_020929 // upstream // 2119181 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 898688 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2190490	catacattattaactc[A/G]gacaagtcatttaaca	A	G	NM_020929 // upstream // 2340478 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 677391 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2065788	aatttcagtttccag[C/G]agctaggtatccccctg	C	G	NM_020929 // upstream // 2383796 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 634073 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2068412	acaaggcagctcatgg[G/T]aaactaatcactcaga	G	T	NM_020929 // upstream // 2429870 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 587999 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2216713	cctctctaatctataa[C/T]cttgtgtctctagaag	C	T	NM_020929 // upstream // 2435638 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 582231 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-2038407	aacactgaaagttcac[G/T]aagtatcgggcattgc	G	T	NM_020929 // upstream // 2436312 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 581557 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1690685	ataatctgttcagtgaggagtataa[A/G]cttgagtattacagtctggttcagg	A	G	NM_006595 // upstream // 465976 // Hs.444340 // API5 // 8539 // apoptosis inhibitor 5	API5	API5 , rs4132365, apoptosis inhibitor 5,p12
SNP_A-2162944	attttgtcagccaata[A/G]aacaccacttgggtgt	A	G	NM_020929 // upstream // 2881014 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 136855 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1930422	ttcatttttctttca[A/T]gtctgtgtagtattcc	A	T	NM_020929 // upstream // 2896765 // Hs.135736 // NGL-1 // 57689 // Homo sapiens netrin-G1 ligand (NGL-1), mRNA. /// NM_006595 // upstream // 121104 // Hs.435771 // API5 // 8539 // Homo sapiens apoptosis inhibitor 5 (API5), mRNA. /// ENST00000278198 // ups	NGL-1	NGL-1, Homo sapiens netrin-G1 ligand (NGL-1), p12
SNP_A-1675952	accccattcaaacatcacaataaca[C/T]ccccatttttccaacaggaaatta	C	T	BC031305 // downstream // 102073 // Hs.130481 // - // 143970 // CDNA clone IMAGE:5272580, partial cds /// NM_016142 // upstream // 8289 // Hs.132513 // HSD17B12 // 51144 // hydroxysteroid (17-beta) dehydrogenase 12	-	- , rs10501303, CDNA clone IMAGE:5272580, partial cds ,p11.2
SNP_A-2010642	gatgtatagcacttga[A/G]gtttcagaagaaggag	A	G	NM_016142 // intron // 0 // Hs.132513 // HSD17B12 // 51144 // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), mRNA. /// ENST00000278353 // intron // 0 // — // — // — // —	HSD17B12	HSD17B12, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), p11.2
SNP_A-2166435	caaatgaggactccaa[C/T]tcctaagggatctcaa	C	T	NM_139178 // intron // 0 // Hs.368920 // DEPC-1 // 221120 // Homo sapiens prostate cancer antigen-1 (DEPC-1), mRNA. /// ENST00000302708 // intron // 0 // — // — // — // — /// ENST00000342800 // intron // 0 // — // — // — // —	DEPC-1	DEPC-1, Homo sapiens prostate cancer antigen-1 (DEPC-1), p11.2
SNP_A-1811071	gtgccatattgcttcc[G/T]actatgtcatgtgagt	G	T	NM_032592 // upstream // 94690 // Hs.126706 // PHACS // 84680 // Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), mRNA. /// ENST00000339446 // downstream // 27696 // — // — // — // — /// ENST00000263776 // upstream // 94690 // —	PHACS	PHACS, Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), p11.2
SNP_A-2089223	acttactcaggggcaa[C/T]cttgggaaattccctc	C	T	NM_032592 // upstream // 34321 // Hs.126706 // PHACS // 84680 // Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), mRNA. /// ENST00000339446 // downstream // 88065 // — // — // — // — /// ENST00000263776 // upstream // 34321 // —	PHACS	PHACS, Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), p11.2
SNP_A-1922367	ttagaaaagttgaata[A/G]cctactagccatgtga	A	G	NM_032592 // upstream // 16548 // Hs.126706 // PHACS // 84680 // Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), mRNA. /// ENST00000339446 // downstream // 105838 // — // — // — // — /// ENST00000263776 // upstream // 16548 // —	PHACS	PHACS, Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), p11.2
SNP_A-1821502	gtttgggtttgtagag[A/G]cagcaatccttaaccc	A	G	NM_032592 // intron // 0 // Hs.126706 // PHACS // 84680 // Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), mRNA. /// ENST00000263776 // intron // 0 // — // — // — // —	PHACS	PHACS, Homo sapiens 1-aminocyclopropane-1-carboxylate synthase (PHACS), p11.2
SNP_A-2034967	aaatgatgattctctt[C/T]aaatcctacacaacca	C	T	NM_207122 // intron // 0 // Hs.368404 // EXT2 // 2132 // Homo sapiens exostoses (multiple) 2 (EXT2), transcript variant 2, mRNA. /// NM_000401 // intron // 0 // Hs.368404 // EXT2 // 2132 // Homo sapiens exostoses (multiple) 2 (EXT2), transcript variant 1,	EXT2	EXT2, Homo sapiens exostoses (multiple) 2 (EXT2), transcript variant 2, p11.2
SNP_A-1842119	tagggctcaacccaga[A/G]gtctgacgcacatgaa	A	G	AB058691 // intron // 0 // Hs.436055 // ALX4 // 60529 // Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // intron // 0 // Hs.436055 // ALX4 // 60529 // Homo sapiens aristaless-like homeobox 4 (ALX4), mRNA. /// ENST00000329255 // intron	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds. ,p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187026	caggtacttgcagcta[C/T]gaggacagctccagga	C	T	AB058691 // upstream // 36762 // Hs.436055 // ALX4 // 60529 // Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // upstream // 36640 // Hs.436055 // ALX4 // 60529 // Homo sapiens aristaless-like homeobox 4 (ALX4), mRNA. /// NM_002231 //	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds, p11.2
SNP_A-2280377	gagggatcttgggagc[A/G]ccagttgcccttctttt	A	G	AB058691 // upstream // 38415 // Hs.436055 // ALX4 // 60529 // Homo sapiens mRNA for KIAA1788 protein, partial cds. /// NM_021926 // upstream // 38293 // Hs.436055 // ALX4 // 60529 // Homo sapiens aristaless-like homeobox 4 (ALX4), mRNA. /// NM_002231 //	ALX4	ALX4, Homo sapiens for KIAA1788 protein, partial cds, p11.2
SNP_A-2184599	cagcctcagtacaaaccg[A/G]ggctcagtacaaacag	A	G	NM_002231 // downstream // 127719 // Hs.527778 // KAI1 // 3732 // Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocl /// NM_130783 // upstream // 112843 // Hs.385634 // LOC90139	KAI1	KAI1, Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocl, p11.2
SNP_A-1845884	tatataaacagtcatg[G/T]cttagaatccacggag	G	T	NM_002231 // downstream // 152130 // Hs.527778 // KAI1 // 3732 // Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocl /// NM_130783 // upstream // 88432 // Hs.385634 // LOC90139	KAI1	KAI1, Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monocl, p11.2
SNP_A-2082305	acgatctgacagttcc[A/G]ctcccaattatttct	A	G	NM_020826 // upstream // 111243 // Hs.436643 // SYT13 // 57586 // Homo sapiens synaptotagmin XIII (SYT13), mRNA. /// NM_003654 // downstream // 251314 // Hs.104576 // CHST1 // 8534 // Homo sapiens carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (C	SYT13	SYT13, Homo sapiens synaptotagmin XIII (SYT13), p11.2
SNP_A-2079250	acccatgataaaccaaa[C/T]agcaaaatttaagta	C	T	NM_003654 // upstream // 82489 // Hs.104576 // CHST1 // 8534 // Homo sapiens carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), mRNA. /// NM_018389 // upstream // 56980 // Hs.12211 // SLC35C1 // 55343 // Homo sapiens solute carrier family 35	CHST1	CHST1, Homo sapiens carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1), p11.2
SNP_A-1733614	gccagaaggtaaggaaggcacaaac[A/G]aacatccaattca cagtaataggag	A	G	NM_016621 // upstream // 36869 // Hs.104888 // BHC80 // 51317 // BRAF35/HDAC2 complex (80 kDa) /// NM_052854 // upstream // 119706 // Hs.405961 // CREB3L1 // 90993 // cAMP responsive element binding protein 3-like 1	BHC80	BHC80, rs2029483, BRAF35,p11.2
SNP_A-2188620	cagtgcacagagttct[G/T]agaaagcattgggct	G	T	NM_017749 // intron // 0 // Hs.546404 // FLJ20294 // 55626 // Homo sapiens hypothetical protein FLJ20294 (FLJ20294), mRNA. /// ENST00000314845 // intron // 0 // — // — // — // — /// ENST00000298834 // intron // 0 // — // — // —	FLJ20294	FLJ20294, Homo sapiens hypothetical protein FLJ20294 (FLJ20294), p11.2
SNP_A-1789601	gggcgtgccttcctc[C/T]gaaataatatgttca	C	T	NM_014342 // intron // 0 // Hs.269944 // MTCH2 // 23788 // Homo sapiens mitochondrial carrier homolog 2 (C. elegans) (MTCH2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000302503 // intron // 0 // — // — // —	MTCH2	MTCH2, Homo sapiens mitochondrial carrier homolog 2 (C. elegans) (MTCH2), nuclear gene encoding mitochondrial protein, p11.2
SNP_A-2234941	ctccatcccacaaga[C/T]aatttatggcagttat	C	T	NM_002843 // intron // 0 // Hs.318547 // PTPRJ // 5795 // Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 // intron // 0 // — // — // —	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2
SNP_A-1807260	gtctctgccttttgga[C/T]gggagataggcaccc	C	T	NM_002843 // intron // 0 // Hs.318547 // PTPRJ // 5795 // Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 // intron // 0 // — // — // —	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2
SNP_A-2167347	caacaggcaacttgaa[C/T]ggacaaggccctagaa	C	T	NM_002843 // intron // 0 // Hs.318547 // PTPRJ // 5795 // Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 // intron // 0 // — // — // —	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2
SNP_A-2102161	agatgttgcaatgtga[A/C]aagtttgctcaacg	A	C	NM_002843 // intron // 0 // Hs.318547 // PTPRJ // 5795 // Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA. /// ENST00000278456 // intron // 0 // — // — // —	PTPRJ	PTPRJ, Homo sapiens protein tyrosine phosphatase, receptor type, J (PTPRJ), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2286118	gatgcaacaagagtaa[A/G]gagcccagaatgatgc	A	G	ENST00000243148 // upstream // 384726 // --- // --- // --- /// ENST00000332682 // downstream // 13973 // --- // --- // --- /// ENST00000356225 // downstream // 13979 // --- // --- // --- /// ENST00000335614 // downstream // 13985 // -	-	p11.12
SNP_A-2084440	actatcactctgctaa[A/G]tgtggaatctcatcta	A	G	NM_001005270 // intron // 0 // --- // OR4C12 // 283093 // Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// ENST00000335238 // intron // 0 // --- // --- // ---	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12
SNP_A-2048701	aagccagaggaatata[A/T]ccaacatatctactca	A	T	NM_001005270 // intron // 0 // --- // OR4C12 // 283093 // Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// ENST00000335238 // intron // 0 // --- // --- // ---	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12
SNP_A-1808646	gtgaaccccccattcaq[A/C]atcacctcaagagaa	A	C	NM_001005270 // intron // 0 // --- // OR4C12 // 283093 // Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// ENST00000335238 // intron // 0 // --- // --- // ---	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12
SNP_A-2139755	atctaaaactgcagaa[C/T]atgattacctgcttt	C	T	NM_001005270 // upstream // 4760 // --- // OR4C12 // 283093 // Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// NM_001004703 // upstream // 98127 // --- // OR4C46 // 119749 // Homo sapiens olfactory receptor, family 4,	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12
SNP_A-2258536	cttttctggaccaaga[C/T]gtgagtatttgaaacc	C	T	NM_001005270 // upstream // 18282 // --- // OR4C12 // 283093 // Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), mRNA. /// NM_001004703 // upstream // 84605 // --- // OR4C46 // 119749 // Homo sapiens olfactory receptor, family 4	OR4C12	OR4C12, Homo sapiens olfactory receptor, family 4, subfamily C, member 12 (OR4C12), p11.12
SNP_A-2260264	gaaaatgtgagagaaa[G/T]gtgagaagagcatgag	G	T	NM_001005275 // downstream // 31315 // --- // OR4A15 // 81328 // Homo sapiens olfactory receptor, family 4, subfamily A, member 15 (OR4A15), mRNA. /// ENST00000314706 // downstream // 31315 // --- // --- // --- /// ENST00000314689 // upstream // 66	OR4A15	OR4A15, Homo sapiens olfactory receptor, family 4, subfamily A, member 15 (OR4A15), q11
SNP_A-2168418	caacttcctgacggtc[C/T]ctttacatctttgtt	C	T	ENST00000328673 // CDS // 0 // --- // --- // ---	-	q11
SNP_A-1902304	tggccatctgtaaccc[C/T]ctgctgtacatggtga	C	T	ENST00000334016 // CDS // 0 // --- // --- // ---	-	q11
SNP_A-2192757	catcctggagactat[G/T]agcatcggttacagtg	G	T	ENST00000334020 // downstream // 14112 // --- // --- // --- /// ENST00000344048 // downstream // 2172 // --- // --- // ---	-	q11
SNP_A-2011103	ttttttcattaaaatca[A/G]aatgtgaagaacaata	A	G	NM_001001960 // upstream // 737 // --- // OR5W2 // 390148 // Homo sapiens olfactory receptor, family 5, subfamily W, member 2 (OR5W2), mRNA. /// NM_006637 // downstream // 20137 // Hs.533706 // OR5I1 // 10798 // Homo sapiens olfactory receptor, family 5,	OR5W2	OR5W2, Homo sapiens olfactory receptor, family 5, subfamily W, member 2 (OR5W2), q11
SNP_A-1840321	tagcatcgactgtccaj[A/G]agaaatcacttcttag	A	G	NM_006637 // upstream // 11319 // Hs.533706 // OR5I1 // 10798 // Homo sapiens olfactory receptor, family 5, subfamily I, member 1 (OR5I1), mRNA. /// ENST00000301532 // upstream // 11319 // --- // --- // --- /// ENST00000312345 // downstream // 1983	OR5I1	OR5I1, Homo sapiens olfactory receptor, family 5, subfamily I, member 1 (OR5I1), q11
SNP_A-1948860	ttatcaatttctacc[A/G]cataatgttgcttcag	A	G	NM_001004746 // downstream // 19304 // --- // OR5T2 // 219464 // Homo sapiens olfactory receptor, family 5, subfamily T, member 2 (OR5T2), mRNA. /// ENST00000313276 // upstream // 1222 // --- // --- // --- /// ENST00000313264 // downstream // 19304	OR5T2	OR5T2, Homo sapiens olfactory receptor, family 5, subfamily T, member 2 (OR5T2), q11
SNP_A-1909331	tgtatgttacactgag[A/G]ccctctagaagtgaaa	A	G	NM_001004740 // downstream // 10705 // --- // OR5M1 // 390168 // Homo sapiens olfactory receptor, family 5, subfamily M, member 1 (OR5M1), mRNA. /// NM_001004741 // downstream // 10705 // --- // OR5M10 // 390167 // Homo sapiens olfactory receptor, family	OR5M1	OR5M1, Homo sapiens olfactory receptor, family 5, subfamily M, member 1 (OR5M1), q11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2087681	actgctgtgggtgaaa[C/T]gtggcatgccctggaa	C	T	NM_001004740 // downstream // 348 // — // OR5M1 // 390168 // Homo sapiens olfactory receptor, family 5, subfamily M, member 1 (OR5M1), mRNA. /// NM_001004741 // downstream // 348 // — // OR5M10 // 390167 // Homo sapiens olfactory receptor, family 5, s	OR5M1	OR5M1, Homo sapiens olfactory receptor, family 5, subfamily M, member 1 (OR5M1), q11
SNP_A-2110663	aggacatttttaccaa[C/T]ggtggtgcatcacaga	C	T	NM_001005284 // CDS // 0 // — // OR9G4 // 283189 // Homo sapiens olfactory receptor, family 9, subfamily G, member 4 (OR9G4), mRNA. /// ENST00000302957 // CDS // 0 // — // — // — // —	OR9G4	OR9G4, Homo sapiens olfactory receptor, family 9, subfamily G, member 4 (OR9G4), q11
SNP_A-2206577	ccatgaaacattgtaa[A/G]aaattattggttgatc	A	G	ENST00000326910 // upstream // 82604 // — // — // — // — /// ENST00000329786 // upstream // 32160 // — // — // — // —	-	q11
SNP_A-1817599	gttccaccattaaaat[A/G]actgtgtgatattggg	A	G	ENST00000326910 // upstream // 100039 // — // — // — // — /// ENST00000329786 // upstream // 14725 // — // — // — // —	-	q11
SNP_A-2275718	gagaccacagaagtaa[A/G]tgattgctttgagttt	A	G	ENST00000326910 // upstream // 109158 // — // — // — // — /// ENST00000329786 // upstream // 5606 // — // — // — // —	-	q11
SNP_A-2150560	atgtgagccttcaacc[A/G]ccttaaaaataactga	A	G	ENST00000329786 // intron // 0 // — // — // — // —	-	q11
SNP_A-2292252	gcacctcacaaatcaa[C/T]gaatagccgcaaaata	C	T	NM_004811 // intron // 0 // Hs.125474 // LPXN // 9404 // Homo sapiens leupaxin (LPXN), mRNA. /// ENST00000263845 // intron // 0 // — // — // — // —	LPXN	LPXN, Homo sapiens leupaxin (LPXN), q12.1
SNP_A-2296679	gccaaagcacaatttc[A/C]attcactgatctatgt	A	C	NM_053023 // downstream // 18560 // Hs.524920 // ZFP91 // 80829 // Homo sapiens zinc finger protein 91 homolog (mouse) (ZFP91), transcript variant 1, mRNA. /// NM_170768 // downstream // 18560 // Hs.524920 // ZFP91 // 80829 // Homo sapiens zinc finger pro	ZFP91	ZFP91, Homo sapiens zinc finger protein 91 homolog (mouse) (ZFP91), transcript variant 1, q12.1
SNP_A-2226652	ctaagtattatgctaa[A/G]cacttcctagtcactt	A	G	NM_005838 // intron // 0 // Hs.145384 // GLYAT // 10249 // Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // intron // 0 // Hs.145384 // GLYAT // 10249 // Homo sapiens	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-1819665	gttgtatgcatgctaa[C/T]ttaaggcattctccct	C	T	NM_005838 // intron // 0 // Hs.145384 // GLYAT // 10249 // Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // intron // 0 // Hs.145384 // GLYAT // 10249 // Homo sapiens	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-2034429	aaatctcagagttcgc[A/T]actaaaaaactcattc	A	T	NM_005838 // upstream // 34612 // Hs.145384 // GLYAT // 10249 // Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_201648 // upstream // 34612 // Hs.145384 // GLYAT // 10249 //	GLYAT	GLYAT, Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, transcript variant 2, q12.1
SNP_A-2011303	caaattcaaaaggata[C/T]gcactggctttttctg	C	T	NM_145016 // intron // 0 // Hs.254271 // BXMAS2-10 // 219970 // Homo sapiens BXMAS2-10 (BXMAS2-10), mRNA. /// ENST00000287275 // intron // 0 // — // — // — // —	BXMAS2-10	BXMAS2-10, Homo sapiens BXMAS2-10 (BXMAS2-10), q12.1
SNP_A-2011309	aaacaatatactaaga[A/G]gtttgaatgtacctgg	A	G	NM_145016 // upstream // 7696 // Hs.254271 // BXMAS2-10 // 219970 // Homo sapiens BXMAS2-10 (BXMAS2-10), mRNA. /// NM_080661 // upstream // 90517 // Hs.38085 // MGC15937 // 92292 // Homo sapiens similar to RIKEN cDNA 0610008P16 gene (MGC15937), mRNA. ///	BXMAS2-10	BXMAS2-10, Homo sapiens BXMAS2-10 (BXMAS2-10), q12.1
SNP_A-2268725	gaatgtttgaatactc[A/G]aggaaattttagtaaa	A	G	NM_145016 // upstream // 35974 // Hs.254271 // BXMAS2-10 // 219970 // Homo sapiens BXMAS2-10 (BXMAS2-10), mRNA. /// NM_080661 // upstream // 62239 // Hs.38085 // MGC15937 // 92292 // Homo sapiens similar to RIKEN cDNA 0610008P16 gene (MGC15937), mRNA. ///	BXMAS2-10	BXMAS2-10, Homo sapiens BXMAS2-10 (BXMAS2-10), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802104	gtatactatggaatca[C/G]actagtatgaatgtatt	C	G	NM_145016 // upstream // 42526 // Hs.254271 // BXMAS2-10 // 219970 // Homo sapiens BXMAS2-10 (BXMAS2-10), mRNA. /// NM_080661 // upstream // 55687 // Hs.38085 // MGC15937 // 92292 // Homo sapiens similar to RIKEN cDNA 0610008P16 gene (MGC15937), mRNA. ///	BXMAS2-10	BXMAS2-10, Homo sapiens BXMAS2-10 (BXMAS2-10), q12.1
SNP_A-1946817	ttaagaattggagag[G/T]aattgcatttgcttt	G	T	NM_001004729 // upstream // 109264 // — // OR5AN1 // 390195 // Homo sapiens olfactory receptor, family 5, subfamily AN, member 1 (OR5AN1), mRNA. /// ENST00000361050 // upstream // 42327 // — // — // — /// ENST00000313940 // upstream // 1092	OR5AN1	OR5AN1, Homo sapiens olfactory receptor, family 5, subfamily AN, member 1 (OR5AN1), q12.1
SNP_A-2222846	cgcaaaagaagatgta[C/T]gatcagccaaaaaaca	C	T	NM_001005324 // upstream // 10355 // Hs.530733 // OR10V1 // 390201 // Homo sapiens olfactory receptor, family 10, subfamily V, member 1 (OR10V1), mRNA. /// NM_004177 // upstream // 30859 // Hs.530733 // STX3A // 6809 // Homo sapiens syntaxin 3A (STX3A), m	OR10V1	OR10V1, Homo sapiens olfactory receptor, family 10, subfamily V, member 1 (OR10V1), q12.1
SNP_A-1768564	gggatatttaactcca[A/G]tgttctgtcctgggttt	A	G	NM_004177 // intron // 0 // Hs.530733 // STX3A // 6809 // Homo sapiens syntaxin 3A (STX3A), mRNA. /// ENST00000337979 // intron // 0 // — // — // — /// ENST00000300150 // intron // 0 // — // — // —	STX3A	STX3A, Homo sapiens syntaxin 3A (STX3A), q12.1
SNP_A-1658828	cattcatttacagaaaagaattactg[A/T]aactcaaacagctaaaataaattgt	A	T	NM_001062 // upstream // 131722 // Hs.2012 // TCN1 // 6947 // transcobalamin I (vitamin B12 binding protein, R binder family) /// NM_173801 // upstream // 42142 // Hs.132310 // FLJ36198 // 219990 // hypothetical protein FLJ36198	TCN1	TCN1, rs481560, transcobalamin I (vitamin B12 binding protein, R binder family), q12.1
SNP_A-1959016	ttttctttcaagatc[A/T]catgaaaaccagctt	A	T	ENST00000360247 // intron // 0 // — // — // — // —	-	q12.1
SNP_A-1787968	gggagaaagaggttac[A/G]ggctccagacaagaaa	A	G	NM_024021 // downstream // 25277 // Hs.325960 // MS4A4A // 51338 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4A), transcript variant 1, mRNA. /// NM_148975 // downstream // 25277 // Hs.325960 // MS4A4A // 51338 // Homo sapiens	MS4A4A	MS4A4A, Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4A), transcript variant 1, q12.2
SNP_A-2011420	agatcctgtgttgcct[A/G]ttgatttcaagtctgg	A	G	NM_206938 // intron // 0 // Hs.530735 // MS4A7 // 58475 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 7 (MS4A7), transcript variant 2, mRNA. /// NM_206940 // intron // 0 // Hs.530735 // MS4A7 // 58475 // Homo sapiens membrane-spanning 4	MS4A7	MS4A7, Homo sapiens membrane-spanning 4-domains, subfamily A, member 7 (MS4A7), transcript variant 2, q12.2
SNP_A-2231169	ctattactatgaagta[A/G]gataatcaactatcct	A	G	NM_021950 // downstream // 1852 // Hs.438040 // MS4A1 // 931 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 1 (MS4A1), transcript variant 3, mRNA. /// NM_152866 // downstream // 1852 // Hs.438040 // MS4A1 // 931 // Homo sapiens membrane-	MS4A1	MS4A1, Homo sapiens membrane-spanning 4-domains, subfamily A, member 1 (MS4A1), transcript variant 3, q12.2
SNP_A-2198511	catttatcatttatca[A/C]tatgaaccagtgcat	A	C	NM_017716 // downstream // 15328 // Hs.272789 // MS4A12 // 54860 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), mRNA. /// NM_174939 // upstream // 98321 // Hs.372650 // MGC39681 // 283197 // Homo sapiens hypothetical protein	MS4A12	MS4A12, Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), q12.2
SNP_A-2090185	actgatcaaattggc[G/T]aggtaatctcgtgcc	G	T	NM_017716 // downstream // 44294 // Hs.272789 // MS4A12 // 54860 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), mRNA. /// NM_174939 // upstream // 69355 // Hs.372650 // MGC39681 // 283197 // Homo sapiens hypothetical protein	MS4A12	MS4A12, Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), q12.2
SNP_A-2085848	actccttgggaaaaaaq[A/G]gcgaaggcaccactca	A	G	NM_017716 // downstream // 58671 // Hs.272789 // MS4A12 // 54860 // Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), mRNA. /// NM_174939 // upstream // 54978 // Hs.372650 // MGC39681 // 283197 // Homo sapiens hypothetical protein	MS4A12	MS4A12, Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 (MS4A12), q12.2
SNP_A-1722734	gctcagccacatgggcttccactca[A/C]caaggctgacttggct acagtcact	A	C	NM_174939 // intron // 0 // Hs.372650 // MGC39681 // 283197 // hypothetical protein MGC39681	MGC39681	MGC39681, rs10807719, hypothetical protein MGC39681.q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2212159	ccctgctgcagtctta[C/T]gctccatgcagtccct	C	T	NM_006725 // downstream // 42521 // Hs.502710 // CD6 // 923 // Homo sapiens CD6 antigen (CD6), mRNA. /// NM_014207 // upstream // 39600 // Hs.58685 // CD5 // 921 // Homo sapiens CD5 antigen (p56-62) (CD5), mRNA. /// ENST00000313421 // downstream // 42521	CD6	CD6, Homo sapiens CD6 antigen (CD6), q12.2
SNP_A-2222644	cgatacaacttcactc[A/G]agagctcgccgcttcc	A	G	NM_006725 // downstream // 45778 // Hs.502710 // CD6 // 923 // Homo sapiens CD6 antigen (CD6), mRNA. /// NM_014207 // upstream // 36343 // Hs.58685 // CD5 // 921 // Homo sapiens CD5 antigen (p56-62) (CD5), mRNA. /// ENST00000313421 // downstream // 45778	CD6	CD6, Homo sapiens CD6 antigen (CD6), q12.2
SNP_A-2157518	attgatgacttcaggt[C/T]acacgatacaggaatg	C	T	NM_006725 // downstream // 46197 // Hs.502710 // CD6 // 923 // Homo sapiens CD6 antigen (CD6), mRNA. /// NM_014207 // upstream // 35924 // Hs.58685 // CD5 // 921 // Homo sapiens CD5 antigen (p56-62) (CD5), mRNA. /// ENST00000313421 // downstream // 46197	CD6	CD6, Homo sapiens CD6 antigen (CD6), q12.2
SNP_A-1837647	tactttatatcttgac[A/T]aaatcgatcccacagg	A	T	ENST00000301765 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-1856207	tcacaagaatctgatc[C/T]atactaagcagctgcc	C	T	NM_017841 // downstream // 6740 // Hs.313247 // FLJ20487 // 54949 // Homo sapiens hypothetical protein FLJ20487 (FLJ20487), mRNA. /// NM_145017 // upstream // 27627 // Hs.502726 // FLJ32771 // 220004 // Homo sapiens IIIG9 protein (FLJ32771), mRNA. /// ENS	FLJ20487	FLJ20487, Homo sapiens hypothetical protein FLJ20487 (FLJ20487), q12.2
SNP_A-1790027	ggggaaactaaggtac[A/G]aagagttaagagactt	A	G	NM_004200 // intron // 0 // Hs.502730 // SYT7 // 9066 // Homo sapiens synaptotagmin VII (SYT7), mRNA. /// ENST00000263846 // intron // 0 // --- // --- // --- // ---	SYT7	SYT7, Homo sapiens synaptotagmin VII (SYT7), q12.2
SNP_A-2234693	ctccagctctgtaaca[C/T]atggtggaacttcttt	C	T	NM_004200 // intron // 0 // Hs.502730 // SYT7 // 9066 // Homo sapiens synaptotagmin VII (SYT7), mRNA. /// ENST00000263846 // intron // 0 // --- // --- // --- // ---	SYT7	SYT7, Homo sapiens synaptotagmin VII (SYT7), q12.2
SNP_A-1859001	tcagcatcatcctgga[C/T]tatgttcttccaagaa	C	T	NM_004200 // intron // 0 // Hs.502730 // SYT7 // 9066 // Homo sapiens synaptotagmin VII (SYT7), mRNA. /// ENST00000263846 // intron // 0 // --- // --- // --- // ---	SYT7	SYT7, Homo sapiens synaptotagmin VII (SYT7), q12.2
SNP_A-2097352	agagaaactgaggcac[C/T]ggaagacctgcttctc	C	T	ENST00000244906 // intron // 0 // --- // --- // --- // --- /// ENST00000278836 // intron // 0 // --- // --- // --- // ---	-	q12.2
SNP_A-2204695	ccaggagtgttgctca[C/T]gttactcccttaggcc	C	T	NM_004265 // intron // 0 // Hs.502745 // FADS2 // 9415 // Homo sapiens fatty acid desaturase 2 (FADS2), mRNA. /// ENST00000337189 // intron // 0 // --- // --- // --- // --- /// ENST00000257261 // intron // 0 // --- // --- // --- // --- /// ENST00000278840	FADS2	FADS2, Homo sapiens fatty acid desaturase 2 (FADS2), q12.2
SNP_A-1901243	tggatgctctcaataa[A/C]aataacaaggcccagt	A	C	NM_020238 // upstream // 110107 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000357097 // downstream // 44401 // --- // --- // --- // --- /// ENST00000278849 // upstream // 110107 //	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-2248239	ctgtggttaccaagaa[A/G]gtagccaatgtcaggg	A	G	NM_020238 // upstream // 108822 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000357097 // downstream // 45686 // --- // --- // --- // --- /// ENST00000278849 // upstream // 108822 //	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-1958000	ttttcacattgctacc[A/G]aatatatcctaaaatg	A	G	NM_020238 // upstream // 90658 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000357097 // downstream // 63850 // --- // --- // --- // --- /// ENST00000278849 // upstream // 90658 // -	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2011509	gttctagtcccagcaa[C/T]gcctccaacagggtgt	C	T	NM_020238 // upstream // 61541 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000357097 // downstream // 92967 // --- // --- // --- // --- /// ENST00000278849 // upstream // 61541 // -	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-2030806	aaagctttttgagtac[C/T]aatgtgaccctcaaag	C	T	NM_020238 // upstream // 45484 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000357097 // downstream // 109024 // --- // --- // --- // --- /// ENST00000278849 // upstream // 45484 //	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-2116745	aggtccctgagaacaa[C/T]ggaaataactcgtggc	C	T	NM_020238 // CDS // 0 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000278849 // CDS // 0 // --- // --- // --- // ---	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-1795709	ggtggaccataacagc[A/C]attgtatagaactctt	A	C	NM_020238 // intron // 0 // Hs.142179 // INCENP // 3619 // Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), mRNA. /// ENST00000278849 // intron // 0 // --- // --- // --- // ---	INCENP	INCENP, Homo sapiens inner centromere protein antigens 135,q12.3
SNP_A-1867231	tccctgggacatccca[C/T]agtgaccgtgtccact	C	T	NM_206998 // intron // 0 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// ENST00000358585 // intron // 0 // --- // --- // --- // ---	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2247650	ctgtctttgtagaaca[C/T]gcaggttagcccacca	C	T	NM_206998 // upstream // 13506 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 24878 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-1913302	tgtgggcaggaggtag[A/G]aagcacaagggataga	A	G	NM_206998 // upstream // 14156 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 24228 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2228817	ctagagcttttcttgc[C/T]gaggaaaagaatcatc	C	T	NM_206998 // upstream // 14321 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 24063 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2185031	cagcttgtaactgcca[C/T]gatgtcaaagccatgg	C	T	NM_206998 // upstream // 17372 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 21012 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-1784038	ggccagattctatact[A/G]aactctgaggctataa	A	G	NM_206998 // upstream // 17467 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 20917 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2309704	ggaaagctctttctga[C/T]gagaggacgtttaggt	C	T	NM_206998 // upstream // 19537 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 18847 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3
SNP_A-2188817	cagtgggagctataaa[C/G]gtcagtgttgccttag	C	G	NM_206998 // upstream // 22211 // Hs.473247 // SCGB1D4 // 404552 // Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), mRNA. /// NM_025080 // upstream // 16173 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// E	SCGB1D4	SCGB1D4, Homo sapiens secretoglobin family 1D member 4 (SCGB1D4), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1756028	tcctaattactttccagtgtactac[C/T]accaacaattcatcaacg agcattt	C	T	NM_002411 // downstream // 42914 // Hs.46452 // SCGB2A2 // 4250 // secretoglobin, family 2A, member 2 /// NM_025080 // upstream // 21423 // Hs.433197 // ASRGL1 // 80150 // asparaginase like 1	SCGB2A2	SCGB2A2 , rs953169, secretogtobin, family 2A, member 2 ,q12.3
SNP_A-2134827	atattagaagtcggac[A/G]ctacatgaaagttaaa	A	G	NM_025080 // intron // 0 // Hs.535326 // ASRGL1 // 80150 // Homo sapiens asparaginase like 1 (ASRGL1), mRNA. /// ENST00000301776 // intron // 0 // — // — // — // —	ASRGL1	ASRGL1, Homo sapiens asparaginase like 1 (ASRGL1), q12.3
SNP_A-1858446	tcagagaagtatggga[A/T]gatagttgaagggaga	A	T	NM_080866 // upstream // 122854 // Hs.502772 // SLC22A9 // 114571 // Homo sapiens solute carrier family 22 (organic anion/cation transporter), member 9 (SLC22A9), mRNA. /// NM_199352 // upstream // 122854 // Hs.332119 // LOC387601 // 387601 // Homo sapien	SLC22A9	SLC22A9, Homo sapiens solute carrier family 22 (organic anion q12.3
SNP_A-1938157	ttgacataataagcca[C/T]tggaaaacggaaagat	C	T	ENST00000356525 // intron // 0 // — // — // — // — /// ENST00000358198 // intron // 0 // — // — // — // —	-	q12.3
SNP_A-2311635	ggaatgtcgttccttc[C/T]ccatctttgcagacgc	C	T	NM_014067 // intron // 0 // Hs.502814 // LRP16 // 28992 // Homo sapiens LRP16 protein (LRP16), mRNA. /// ENST00000255681 // intron // 0 // — // — // — // —	LRP16	LRP16, Homo sapiens LRP16 protein (LRP16), q13.1
SNP_A-2141608	atcttcaattgactac[C/T]gcaaagaccctaaccc	C	T	NM_018484 // upstream // 85977 // Hs.220844 // SLC22A11 // 55867 // Homo sapiens solute carrier family 22 (organic anion/cation transporter), member 11 (SLC22A11), mRNA. /// ENST00000316124 // downstream // 17995 // — // — // — // — /// ENST000003	SLC22A11	SLC22A11, Homo sapiens solute carrier family 22 (organic anion,q13.1
SNP_A-1682342	gaggaatggcttattttctgatgac[C/T]acatgtgggactatttcaa ccgcca	C	T	NM_004927 // downstream // 47029 // Hs.75859 // MRPL49 // 740 // mitochondrial ribosomal protein L49 /// NM_005186 // upstream // 7473 // Hs.356181 // CAPN1 // 823 // calpain 1, (mu/I) large subunit /// NM_032431 // upstream // 39867 // Hs.321535 // HRD1	MRPL49	MRPL49 , rs1195963, mitochondrial ribosomal protein L49 ,q13.1
SNP_A-2270108	gacacagcaatgaaaa[C/T]aactgcttctccactc	C	T	NM_001004326 // intron // 0 // Hs.525920 // FLJ16331 // 440044 // Homo sapiens FLJ16331 protein (FLJ16331), mRNA. /// NM_152760 // intron // 0 // Hs.533600 // FLJ30934 // 254122 // Homo sapiens hypothetical protein FLJ30934 (FLJ30934), mRNA. /// ENST00000	FLJ16331	FLJ16331, Homo sapiens FLJ16331 protein (FLJ16331), q13.1
SNP_A-1793920	ggtcaagtgactccga[A/G]atcaattttacttaga	A	G	NM_018026 // intron // 0 // Hs.536275 // PACS1 // 55690 // Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), mRNA. /// ENST00000320580 // intron // 0 // — // — // — // —	PACS1	PACS1, Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), q13.2
SNP_A-1794733	ggtctctgttcttcaa[C/T]acattagcgcaatgtg	C	T	NM_018026 // intron // 0 // Hs.536275 // PACS1 // 55690 // Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), mRNA. /// ENST00000320580 // intron // 0 // — // — // — // —	PACS1	PACS1, Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), q13.2
SNP_A-2249572	cttaagaatgttctta[A/G]gaaagcagtaaaacgt	A	G	NM_018026 // intron // 0 // Hs.536275 // PACS1 // 55690 // Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), mRNA. /// ENST00000320580 // intron // 0 // — // — // — // —	PACS1	PACS1, Homo sapiens phosphofurin acidic cluster sorting protein 1 (PACS1), q13.2
SNP_A-1797549	ggtttccagagggtga[C/T]gctcaacctttgccag	C	T	NM_000920 // intron // 0 // Hs.89890 // PC // 5091 // Homo sapiens pyruvate carboxylase (PC), nuclear gene encoding mitochondrial protein, transcript variant A, mRNA. /// NM_022172 // intron // 0 // Hs.89890 // PC // 5091 // Homo sapiens pyruvate carboxyl	PC	PC, Homo sapiens pyruvate carboxylase (PC), nuclear gene encoding mitochondrial protein, transcript variant A, q13.2
SNP_A-1887896	tgagatttgaacccag[A/G]cggttggctccagtcg	A	G	NM_005851 // upstream // 367 // Hs.523835 // DOC-1R // 10263 // Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R), mRNA. /// NM_031204 // downstream // 9949 // Hs.278984 // CABP2 // 51475 // Homo sapiens calcium binding protein 2 (CA	DOC-1R	DOC-1R, Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R), q13.2
SNP_A-2096061	agacatactgccaaca[C/T]gcatggggatgctcga	C	T	NM_080658 // intron // 0 // Hs.126265 // ACY3 // 91703 // Homo sapiens aspartoacylase (aminocyclase) 3 (ACY3), mRNA. /// ENST00000255082 // intron // 0 // — // — // — // —	ACY3	ACY3, Homo sapiens aspartoacylase (aminocyclase) 3 (ACY3), q13.2
SNP_A-1866287	tcccatctcagcctgg[A/G]agtaatcccaaagtgc	A	G	ENST00000339095 // intron // 0 // — // — // — // —	-	q13.2
SNP_A-2042083	aactagaagatctcca[A/T]ctagctattaaaaatt	A	T	ENST00000339095 // intron // 0 // — // — // — // —	-	q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2011794	gtgccaagtctataaa[C/T]gtgtctggaattggtg	C	T	ENST00000339095 // intron // 0 // — // — // — // —	-	q13.2
SNP_A-2011805	agcataaacgtgcaag[A/C]agagccaatacgtctt	A	C	NM_002335 // intron // 0 // Hs.6347 // LRP5 // 4041 // Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), mRNA. /// ENST00000294304 // intron // 0 // — // — // — // —	LRP5	LRP5, Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), q13.2
SNP_A-1950649	tttcatgccaaaagca[A/G]gagaactgagtggtta	A	G	NM_002335 // intron // 0 // Hs.6347 // LRP5 // 4041 // Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), mRNA. /// ENST00000294304 // intron // 0 // — // — // — // —	LRP5	LRP5, Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), q13.2
SNP_A-1815297	gtgtttaaagaggcaa[A/C]aatgaggagacattgc	A	C	NM_001876 // intron // 0 // Hs.503043 // CPT1A // 1374 // Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000265641 // intron // 0 // — // — // — // —	CPT1A	CPT1A, Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A), nuclear gene encoding mitochondrial protein, q13.3
SNP_A-1800197	gtacctaatttgcttc[A/T]agctttgtttttgggt	A	T	NM_181515 // intron // 0 // Hs.503047 // MRPL21 // 219927 // Homo sapiens mitochondrial ribosomal protein L21 (MRPL21), nuclear gene encoding mitochondrial protein, transcript variant 1, mR /// NM_181513 // intron // 0 // Hs.503047 // MRPL21 // 219927 //	MRPL21	MRPL21, Homo sapiens mitochondrial ribosomal protein L21 (MRPL21), nuclear gene encoding mitochondrial protein, transcript variant 1, mR ,q13.3
SNP_A-1911521	tgtctttctctcctaa[C/T]gcgtgagtctgtactt	C	T	NM_181515 // intron // 0 // Hs.503047 // MRPL21 // 219927 // Homo sapiens mitochondrial ribosomal protein L21 (MRPL21), nuclear gene encoding mitochondrial protein, transcript variant 1, mR /// NM_181513 // intron // 0 // Hs.503047 // MRPL21 // 219927 //	MRPL21	MRPL21, Homo sapiens mitochondrial ribosomal protein L21 (MRPL21), nuclear gene encoding mitochondrial protein, transcript variant 1, mR ,q13.3
SNP_A-2280874	gaggttatggcatgca[C/G]aattagaacatccatg	C	G	NM_002180 // downstream // 23610 // Hs.503048 // IGHMBP2 // 3508 // Homo sapiens immunoglobulin mu binding protein 2 (IGHMBP2), mRNA. /// NM_198923 // downstream // 15813 // Hs.527802 // MRGPRD // 116512 // Homo sapiens MAS-related GPR, member D (MRGPRD),	IGHMBP2	IGHMBP2, Homo sapiens immunoglobulin mu binding protein 2 (IGHMBP2), q13.3
SNP_A-2212122	ccctgcctgctggcca[C/T]gtacctagacagccac	C	T	NM_138768 // downstream // 118094 // Hs.523848 // MYEOV // 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 225631 // Hs.523852 // CCND1 // 595 // Homo sapien	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-1899547	tggaaggaataaggag[A/C]agcactagatgagggc	A	C	NM_138768 // downstream // 155359 // Hs.523848 // MYEOV // 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 188366 // Hs.523852 // CCND1 // 595 // Homo sapien	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-2202384	ccaccatccagactat[A/G]acacagaaccatccta	A	G	NM_138768 // downstream // 157620 // Hs.523848 // MYEOV // 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 186105 // Hs.523852 // CCND1 // 595 // Homo sapien	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-2305571	gctgcactctctcagg[A/T]cccgtgtgattgagca	A	T	NM_138768 // downstream // 204789 // Hs.523848 // MYEOV // 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 138936 // Hs.523852 // CCND1 // 595 // Homo sapien	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3
SNP_A-2172095	caatgggagtatgaca[C/T]gattagagttttgaat	C	T	NM_138768 // downstream // 322124 // Hs.523848 // MYEOV // 26579 // Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), mRNA. /// NM_053056 // upstream // 21601 // Hs.523852 // CCND1 // 595 // Homo sapiens	MYEOV	MYEOV, Homo sapiens myeloma overexpressed gene (in a subset of t(11;14) positive multiple myelomas) (MYEOV), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1661564	actgcgacccactcgtgcaccgtac[C/T]ggagtttgtggatgact ctagcaga	C	T	NM_053056 // upstream // 34880 // Hs.371468 // CCND1 // 595 // cyclin D1 (PRAD1: parathyroid adenomatosis 1) /// NM_138768 // downstream // 353810 // Hs.436000 // MYEOV // 26579 // myeloma overexpressed gene (in a subset of t(11;14) positive multiple mye	CCND1	CCND1 , rs633485, cyclin D1 (PRAD1: parathyroid adenomatosis 1) ,q13.3
SNP_A-2122104	agtgatgggcaagtac[A/C]agttgtgaacagaacc	A	C	NM_005247 // upstream // 172170 // Hs.37092 // FGF3 // 2248 // Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream // 86995 // Hs.503074 // TMEM16A // 551	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-1905147	tgggtgggtagatgaa[C/T]ggatgatggatggata	C	T	NM_005247 // upstream // 172794 // Hs.37092 // FGF3 // 2248 // Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream // 86371 // Hs.503074 // TMEM16A // 551	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-2061853	aatggatggatggaca[A/G]ctggatagatgaatgg	A	G	NM_005247 // upstream // 172905 // Hs.37092 // FGF3 // 2248 // Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream // 86260 // Hs.503074 // TMEM16A // 551	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-2177062	cacctccaacagtggg[A/G]acgacatttcgatatg	A	G	NM_005247 // upstream // 180039 // Hs.37092 // FGF3 // 2248 // Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream // 79126 // Hs.503074 // TMEM16A // 551	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-1876237	tctgagaacataacag[C/G]attctaatgtgttggc	C	G	NM_005247 // upstream // 180204 // Hs.37092 // FGF3 // 2248 // Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), mRNA. /// NM_018043 // upstream // 78961 // Hs.503074 // TMEM16A // 551	FGF3	FGF3, Homo sapiens fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog) (FGF3), q13.3
SNP_A-1953737	tttgactttctggata[C/T]gctgaacttatgcgca	C	T	NM_018043 // intron // 0 // Hs.503074 // TMEM16A // 55107 // Homo sapiens transmembrane protein 16A (TMEM16A), mRNA. /// ENST00000356134 // intron // 0 // — // — // — // — /// ENST00000355303 // intron // 0 // — // — // — // — /// ENST0000	TMEM16A	TMEM16A, Homo sapiens transmembrane protein 16A (TMEM16A), q13.3
SNP_A-2114971	agggccacggagggta[C/T]gagtagtcagttgagg	C	T	NM_018043 // intron // 0 // Hs.503074 // TMEM16A // 55107 // Homo sapiens transmembrane protein 16A (TMEM16A), mRNA. /// ENST00000356134 // intron // 0 // — // — // — // — /// ENST00000355303 // intron // 0 // — // — // — // — /// ENST0000	TMEM16A	TMEM16A, Homo sapiens transmembrane protein 16A (TMEM16A), q13.3
SNP_A-2106138	agcccatgtcaaatttt[A/T]aaaaaatcatcgccaa	A	T	NM_018043 // intron // 0 // Hs.503074 // TMEM16A // 55107 // Homo sapiens transmembrane protein 16A (TMEM16A), mRNA. /// ENST00000356134 // intron // 0 // — // — // — // — /// ENST00000355303 // intron // 0 // — // — // — // —	TMEM16A	TMEM16A, Homo sapiens transmembrane protein 16A (TMEM16A), q13.3
SNP_A-2093690	agaagacctgagtgaa[C/T]gtttggagatggcgag	C	T	NM_003626 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), /// NM_177423 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo	PPFIA1	PPFIA1, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), q13.3
SNP_A-2273731	gactgctcttgctata[A/T]ctttttcctggatgtt	A	T	NM_003626 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), /// NM_177423 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo	PPFIA1	PPFIA1, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1868005	tcctagtctcctctaa[A/G]ccagtgtcttcctcat	A	G	NM_003626 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), /// NM_177423 // intron // 0 // Hs.530749 // PPFIA1 // 8500 // Homo	PPFIA1	PPFIA1, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), q13.3
SNP_A-2217783	cctgattccgtttata[A/C]gaaatgctcagaatag	A	C	NM_005231 // downstream // 25120 // Hs.206500 // CTTN // 2017 // Homo sapiens cortactin (CTTN), transcript variant 1, mRNA. /// NM_138565 // downstream // 25111 // Hs.206500 // CTTN // 2017 // Homo sapiens cortactin (CTTN), transcript variant 2, mRNA. ///	CTTN	CTTN, Homo sapiens cortactin (CTTN), transcript variant 1, q13.3
SNP_A-1893862	tgcatacacgcttctg[G/T]actgtaccattgtata	G	T	NM_012309 // upstream // 156346 // Hs.268726 // SHANK2 // 22941 // Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, mRNA. /// NM_133266 // upstream // 156346 // Hs.268726 // SHANK2 // 22941 // Homo sapiens SH3 and mul	SHANK2	SHANK2, Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, q13.4
SNP_A-1951786	tttcgtggctggaacc[A/G]acaccaaccctagcac	A	G	NM_012309 // upstream // 157649 // Hs.268726 // SHANK2 // 22941 // Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, mRNA. /// NM_133266 // upstream // 157649 // Hs.268726 // SHANK2 // 22941 // Homo sapiens SH3 and mul	SHANK2	SHANK2, Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, q13.4
SNP_A-2222950	cgcagaccccggggac[A/G]atcaagatgccagctc	A	G	ENST00000338508 // upstream // 11887 // — // — // — // — /// ENST00000331301 // downstream // 251757 // — // — // — // —	-	q13.4
SNP_A-1940464	ttgcccaagaggaaga[C/T]gacaggaaaggtgggg	C	T	ENST00000338508 // upstream // 16958 // — // — // — // — /// ENST00000331301 // downstream // 246686 // — // — // — // —	-	q13.4
SNP_A-2230015	ctataaatgattgtta[C/T]gaaaagttcaagtaat	C	T	ENST00000338508 // upstream // 26072 // — // — // — // — /// ENST00000331301 // downstream // 237572 // — // — // — // —	-	q13.4
SNP_A-1844275	tagttttcagttttga[A/G]gcaactggtttctatt	A	G	ENST00000338508 // upstream // 41985 // — // — // — // — /// ENST00000331301 // downstream // 221659 // — // — // — // —	-	q13.4
SNP_A-2041419	aaccttaattggccag[C/T]agaggtttgcatgaag	C	T	ENST00000338508 // upstream // 61041 // — // — // — // — /// ENST00000331301 // downstream // 202603 // — // — // — // —	-	q13.4
SNP_A-1846336	tatatgcattaaaaat[A/G]aaatcccttcgctgct	A	G	ENST00000338508 // upstream // 62061 // — // — // — // — /// ENST00000331301 // downstream // 201583 // — // — // — // —	-	q13.4
SNP_A-1895245	tgcccggagaatggga[A/G]cagcactgtcagcaga	A	G	ENST00000338508 // upstream // 164317 // — // — // — // — /// ENST00000331301 // downstream // 99327 // — // — // — // —	-	q13.4
SNP_A-2263654	gaacccgcaagccaga[A/G]cgtattcccatgacct	A	G	NM_001360 // intron // 0 // Hs.503134 // DHCR7 // 1717 // Homo sapiens 7-dehydrocholesterol reductase (DHCR7), mRNA. /// ENST00000352170 // intron // 0 // — // — // — // — /// ENST00000355527 // intron // 0 // — // — // — // —	DHCR7	DHCR7, Homo sapiens 7-dehydrocholesterol reductase (DHCR7), q13.4
SNP_A-2268493	gaatggctaagaagaa[A/G]taaatcaaagtttagc	A	G	ENST00000358061 // downstream // 26331 // — // — // — // — /// ENST00000357176 // downstream // 26331 // — // — // — // — /// ENST00000329336 // upstream // 15666 // — // — // — // —	-	q13.4
SNP_A-1794508	ggtcctggggctctaa[A/C]ggtagtaggggctcta	A	C	NM_030813 // upstream // 105823 // Hs.523877 // SKD3 // 81570 // Homo sapiens suppressor of potassium transport defect 3 (SKD3), mRNA. /// NM_002599 // downstream // 35795 // Hs.503163 // PDE2A // 5138 // Homo sapiens phosphodiesterase 2A, cGMP-stimulated	SKD3	SKD3, Homo sapiens suppressor of potassium transport defect 3 (SKD3), q13.4
SNP_A-1784157	ggccatcatttcctga[A/G]ggatgtaaactctctt	A	G	NM_002599 // intron // 0 // Hs.503163 // PDE2A // 5138 // Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA. /// ENST00000334456 // intron // 0 // — // — // — // —	PDE2A	PDE2A, Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), q13.4
SNP_A-1818456	gttcttgcctcttgaa[G/T]ctggaggcatttggct	G	T	NM_002564 // intron // 0 // Hs.339 // P2RY2 // 5029 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 2, mRNA. /// NM_176071 // intron // 0 // Hs.339 // P2RY2 // 5029 // Homo sapiens purinergic receptor P2Y, G-prote	P2RY2	P2RY2, Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 2, q13.4

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2177487	cacgaatcctaccata[C/T]attgttgagccatgtt	C	T	NM_002564 // intron // 0 // Hs.339 // P2RY2 // 5029 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 2, mRNA. /// NM_176071 // intron // 0 // Hs.339 // P2RY2 // 5029 // Homo sapiens purinergic receptor P2Y, G-prote	P2RY2	P2RY2, Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 2, q13.4
SNP_A-2165431	caaagcaattgtaaaai[C/T]gtgggggaggaaatta	C	T	NM_002564 // downstream // 5950 // Hs.339 // P2RY2 // 5029 // Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 2, mRNA. /// NM_176071 // downstream // 5950 // Hs.339 // P2RY2 // 5029 // Homo sapiens purinergic recepto	P2RY2	P2RY2, Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 2, q13.4
SNP_A-1892402	tgcaagcttgaagtgg[A/G]ccaactcttttagga	A	G	NM_004154 // intron // 0 // Hs.16362 // P2RY6 // 5031 // Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 4, mRNA. /// NM_176798 // intron // 0 // Hs.16362 // P2RY6 // 5031 // Homo sapiens pyrimidinergic receptor	P2RY6	P2RY6, Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 4, q13.4
SNP_A-2304148	gctccccagaaaacccd[A/G]gagttcttcaaatccc	A	G	NM_004154 // intron // 0 // Hs.16362 // P2RY6 // 5031 // Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 4, mRNA. /// NM_176798 // intron // 0 // Hs.16362 // P2RY6 // 5031 // Homo sapiens pyrimidinergic receptor	P2RY6	P2RY6, Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 4, q13.4
SNP_A-1904221	tgggcggatcctgaag[A/G]cactaactgtggccat	A	G	NM_004154 // intron // 0 // Hs.16362 // P2RY6 // 5031 // Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 4, mRNA. /// NM_176798 // intron // 0 // Hs.16362 // P2RY6 // 5031 // Homo sapiens pyrimidinergic receptor	P2RY6	P2RY6, Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 4, q13.4
SNP_A-2301639	gcgcagggagatgcaa[C/T]gaggaagcgttcctt	C	T	NM_003356 // intron // 0 // Hs.101337 // UCP3 // 7352 // Homo sapiens uncoupling protein 3 (mitochondrial, proton carrier) (UCP3), nuclear gene encoding mitochondrial protein, transcrip /// NM_022803 // intron // 0 // Hs.101337 // UCP3 // 7352 // Homo sap	UCP3	UCP3, Homo sapiens uncoupling protein 3 (mitochondrial, proton carrier) (UCP3), nuclear gene encoding mitochondrial protein, transcrip, q13.4
SNP_A-2012015	gtaaaatgtgaaata[C/T]atgtaagtgtttatgt	C	T	NM_016147 // intron // 0 // Hs.503251 // PME-1 // 51400 // Homo sapiens protein phosphatase methylesterase-1 (PME-1), mRNA. /// ENST00000327431 // intron // 0 // — // — // — /// ENST00000328257 // intron // 0 // — // — // — // —	PME-1	PME-1, Homo sapiens protein phosphatase methylesterase-1 (PME-1), q13.4
SNP_A-1926383	ttattattagggaaaaa[G/T]ttggaaacagtgtgag	G	T	NM_173582 // upstream // 28089 // Hs.26612 // PGM2L1 // 283209 // Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), mRNA. /// NM_005472 // downstream // 28607 // Hs.523899 // KCNE3 // 10008 // Homo sapiens potassium voltage-gated channel, Isk-related fam	PGM2L1	PGM2L1, Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), q13.4
SNP_A-2012022	taggagctggaaatca[C/T]agaatctctcaccctt	C	T	NM_173582 // upstream // 43546 // Hs.26612 // PGM2L1 // 283209 // Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), mRNA. /// NM_005472 // downstream // 13150 // Hs.523899 // KCNE3 // 10008 // Homo sapiens potassium voltage-gated channel, Isk-related fam	PGM2L1	PGM2L1, Homo sapiens phosphoglucomutase 2-like 1 (PGM2L1), q13.4
SNP_A-2106764	agcctggcattggcta[C/T]acccacttctggttag	C	T	NM_007256 // intron // 0 // Hs.7884 // SLCO2B1 // 11309 // Homo sapiens solute carrier organic anion transporter family, member 2B1 (SLCO2B1), mRNA. /// ENST00000289575 // intron // 0 // — // — // — // — /// ENST00000341411 // intron // 0 // — /	SLCO2B1	SLCO2B1, Homo sapiens solute carrier organic anion transporter family, member 2B1 (SLCO2B1), q13.4
SNP_A-1788339	gggaggggcttggata[A/G]cagagagaggaattg	A	G	NM_033063 // intron // 0 // Hs.239444 // MAP6 // 4135 // Homo sapiens microtubule-associated protein 6 (MAP6), transcript variant 1, mRNA. /// NM_207577 // intron // 0 // Hs.239444 // MAP6 // 4135 // Homo sapiens microtubule-associated protein 6 (MAP6), t	MAP6	MAP6, Homo sapiens microtubule-associated protein 6 (MAP6), transcript variant 1, q13.5

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2124325	agttattcactgttta[G/T]ctgaaattcacatttg	G	T	NM_004626 // upstream // 84679 // Hs.108219 // WNT11 // 7481 // Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), mRNA. /// NM_004705 // downstream // 58751 // Hs.503315 // PRKRIR // 5612 // Homo sapiens protein-kinase, interfero	WNT11	WNT11, Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), q13.5
SNP_A-1936546	ttcttgcattgctgta[A/G]agaactacctgagact	A	G	NM_004626 // upstream // 129691 // Hs.108219 // WNT11 // 7481 // Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), mRNA. /// NM_004705 // downstream // 13739 // Hs.503315 // PRKRIR // 5612 // Homo sapiens protein-kinase, interfer	WNT11	WNT11, Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), q13.5
SNP_A-1866479	tccccagccagggtaa[C/G]agcttgatcagatgtg	C	G	NM_020193 // upstream // 34154 // Hs.352588 // C11orf30 // 56946 // Homo sapiens chromosome 11 open reading frame 30 (C11orf30), mRNA. /// ENST00000321844 // downstream // 29008 // — // — // — // — /// ENST00000343878 // upstream // 32274 // — /	C11orf30	C11orf30, Homo sapiens chromosome 11 open reading frame 30 (C11orf30), q13.5
SNP_A-2074969	acatcatgctggttca[C/T]tatattgatgtcattt	C	T	NM_005512 // upstream // 57280 // Hs.151641 // GARP // 2615 // Homo sapiens glycoprotein A repetitions predominant (GARP), mRNA. /// NM_015516 // upstream // 55304 // Hs.8361 // TSK // 25987 // Homo sapiens likely ortholog of chicken tsukushi (TSK), mRNA.	GARP	GARP, Homo sapiens glycoprotein A repetitions predominant (GARP), q13.5
SNP_A-2173246	cacaactaccttccca[C/T]tggcctctggactcca	C	T	NM_005512 // upstream // 93941 // Hs.151641 // GARP // 2615 // Homo sapiens glycoprotein A repetitions predominant (GARP), mRNA. /// NM_015516 // upstream // 18643 // Hs.8361 // TSK // 25987 // Homo sapiens likely ortholog of chicken tsukushi (TSK), mRNA.	GARP	GARP, Homo sapiens glycoprotein A repetitions predominant (GARP), q13.5
SNP_A-2260575	gaaacatgggcataca[A/G]ctttattccttcctgc	A	G	NM_018367 // intron // 0 // Hs.23862 // PHCA // 55331 // Homo sapiens phytoceramidase, alkaline (PHCA), mRNA. /// ENST00000278544 // intron // 0 // — // — // — // — // —	PHCA	PHCA, Homo sapiens phytoceramidase, alkaline (PHCA), q13.5
SNP_A-2021843	aaaaacctttgaatta[C/T]gtagatttatgccgct	C	T	NM_138706 // intron // 0 // Hs.352622 // B3Gn-T6 // 192134 // Homo sapiens beta-1,3-N-acetylglucosaminyltransferase protein (IMAGE:4907098), mRNA. /// ENST00000354301 // intron // 0 // — // — // — // —	B3Gn-T6	B3Gn-T6, Homo sapiens beta-1,3-N-acetylglucosaminyltransferase protein (IMAGE:4907098), q13.5
SNP_A-2226502	ctaagccaattaatgc[A/G]gaatggaaagtcaaac	A	G	NM_002576 // upstream // 49078 // Hs.435714 // PAK1 // 5058 // Homo sapiens p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast) (PAK1), mRNA. /// NM_002576 // upstream // 111014 // Hs.435714 // PAK1 // 5058 // Homo sapiens p21/Cdc42/Rac1-activated ki	PAK1	PAK1, Homo sapiens p21,q13.5
SNP_A-2200137	ccaaatgaaataaaga[A/C]ataaagcgacacatta	A	C	NM_173039 // intron // 0 // Hs.503345 // AQP11 // 282679 // Homo sapiens aquaporin 11 (AQP11), mRNA. /// ENST00000313578 // intron // 0 // — // — // — // —	AQP11	AQP11, Homo sapiens aquaporin 11 (AQP11), q13.5
SNP_A-1863154	tcatttatttaagagc[C/T]ctttccgattgcctcc	C	T	NM_001293 // intron // 0 // Hs.430733 // CLNS1A // 1207 // Homo sapiens chloride channel, nucleotide-sensitive, 1A (CLNS1A), mRNA. /// ENST00000263309 // intron // 0 // — // — // — // —	CLNS1A	CLNS1A, Homo sapiens chloride channel, nucleotide sensitive, 1A (CLNS1A), q13.5
SNP_A-2093403	agaactctgaagatga[C/T]gagctagctaaagaat	C	T	NM_016578 // CDS // 0 // Hs.420229 // HBXAP // 51773 // Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000360355 // CDS // 0 // — // — // — // — /// ENST00000308488 // CDS // 0 // — // — // — // —	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-2204809	ccaggccctgggcaga[A/G]taattgacttggggac	A	G	NM_016578 // intron // 0 // Hs.420229 // HBXAP // 51773 // Homo sapiens hepatitis B virus x associated protein (HBXAP), mRNA. /// ENST00000308488 // intron // 0 // — // — // — // —	HBXAP	HBXAP, Homo sapiens hepatitis B virus x associated protein (HBXAP), q13.5
SNP_A-1872400	tctagatgttctgacc[C/T]aaagatgtagtctaca	C	T	NM_023930 // 3UTR // 0 // Hs.17296 // KCTD14 // 65987 // Homo sapiens potassium channel tetramerisation domain containing 14 (KCTD14), mRNA. /// ENST00000353172 // 3UTR // 0 // — // — // — // —	KCTD14	KCTD14, Homo sapiens potassium channel tetramerisation domain containing 14 (KCTD14), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1924670	ttatagctgatgaaaac[A/G]aacttgaaaaaattaa	A	G	NM_024079 // upstream // 15581 // Hs.503368 // ALG8 // 79053 // Homo sapiens asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase) (ALG8), mRNA. /// ENST00000299626 // upstream // 15581 // — // — // — // — /// ENST000003	ALG8	ALG8, Homo sapiens asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase) (ALG8), q14.1
SNP_A-2012324	tagattctagtcacca[C/T]gctaatgtctcacaca	C	T	NM_001031 // upstream // 3583504 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 8216 // — // — // — // — /// ENST00000357859 // upstream // 3583504 // — // — // — // –	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2002065	caaaggtgtgatccat[C/G]aataaaagcatcatta	C	G	NM_001031 // upstream // 3583260 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 8460 // — // — // — // — /// ENST00000357859 // upstream // 3583260 // — // — // — // –	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2115177	agggcttcagtgtctc[C/T]aagtgtaatgcaaaga	C	T	NM_001031 // upstream // 3583103 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 8617 // — // — // — // — /// ENST00000357859 // upstream // 3583103 // — // — // — // –	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2012336	agcggacacccagtaa[A/T]gtatgcaattttgctt	A	T	NM_001031 // upstream // 3416628 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 175092 // — // — // — // — /// ENST00000357859 // upstream // 3416628 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2046222	aagacttgggaaactt[G/T]aacaagtctgcagtgg	G	T	NM_001031 // upstream // 3413843 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 177877 // — // — // — // — /// ENST00000357859 // upstream // 3413843 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2012375	ctgtttgaaggccagg[A/C]agaatggtatttggag	A	C	NM_001031 // upstream // 3094838 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 496882 // — // — // — // — /// ENST00000357859 // upstream // 3094838 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2083909	actactgccaaaagta[C/T]gatttcttgtgaattt	C	T	NM_001031 // upstream // 2809614 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 782106 // — // — // — // — /// ENST00000357859 // upstream // 2809614 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2002073	acaggtgttgaactaa[C/T]gtgtaacgatttgata	C	T	NM_001031 // upstream // 2735524 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 856196 // — // — // — // — /// ENST00000357859 // upstream // 2735524 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1736571	ttcttgtttccaatattatgggaca[C/T]gaaatctttgagattctagaaagtt	C	T	AF009227 // upstream // 841094 // - // - // - // Homo sapiens gamma-heregulin mRNA, complete cds. /// NM_175885 // downstream // 2674997 // Hs.448218 // MGC33846 // 220382 // hypothetical protein MGC33846 /// NM_175891 // downstream // 2672932 // - // -	-	- , rs1893814, Homo sapiens gamma-heregulin mRNA, complete cds. ,q14.1
SNP_A-2032669	aaataaatgaggaaga[A/G]aagttagaataagacc	A	G	NM_001031 // upstream // 2537008 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1054712 // — // — // — // — /// ENST00000357859 // upstream // 2537008 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2076222	acattctcttagacag[A/T]cacccacctgattatg	A	T	NM_001031 // upstream // 2433419 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1158301 // — // — // — // — /// ENST00000357859 // upstream // 2433419 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2090922	actttcctaagcaaac[A/G]caaactgagcgagttt	A	G	NM_001031 // upstream // 2417261 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1174459 // — // — // — // — /// ENST00000357859 // upstream // 2417261 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175847	cacatttcaaaataaa[C/T]tgtgccttcgcagtag	C	T	NM_001031 // upstream // 2385191 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1206629 // — // — // — // /// ENST00000357859 // upstream // 2385191 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2032172	aaagtgggaatcagg[A/G]acttaggttaaataat	A	G	NM_001031 // upstream // 2379309 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1212411 // — // — // — // /// ENST00000357859 // upstream // 2379309 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2239151	ctcttgagtcaacccc[C/T]agagacaaactcctcag	C	T	NM_001031 // upstream // 1743211 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 1848509 // — // — // — // /// ENST00000357859 // upstream // 1743211 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1754604	gaagtttcacacatggtcaaata[A/C]aagaaaaacaatcagattgtttagg	A	C	AF009227 // upstream // 1698431 // - // - // - // Homo sapiens gamma-heregulin mRNA, complete cds. /// NM_175885 // downstream // 1817660 // Hs.448218 // MGC33846 // 220382 // hypothetical protein MGC33846 /// NM_175891 // downstream // 1815595 // - // -	-	- , rs1909138, Homo sapiens gamma-heregulin mRNA, complete cds. , q14.1
SNP_A-1663574	ttagtagtgatttctaatttgtttcca[C/T]agataaaactagggaatttcaaga	C	T	AF009227 // upstream // 1791298 // - // - // - // Homo sapiens gamma-heregulin mRNA, complete cds. /// NM_175885 // downstream // 1724793 // Hs.448218 // MGC33846 // 220382 // hypothetical protein MGC33846 /// NM_175891 // downstream // 1722728 // - // -	-	- , rs1566241, Homo sapiens gamma-heregulin mRNA, complete cds. , q14.1
SNP_A-2275759	gagaccccaaggaggaa[A/G]gaattgagctatact	A	G	NM_001031 // 1485091 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2106629 // — // — // — // /// ENST00000357859 // upstream // 1485091 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2241662	ctgatagtggcctcta[C/T]gataaatttaaacca	C	T	NM_001031 // upstream // 1405769 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2185951 // — // — // — // /// ENST00000357859 // upstream // 1405769 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2099106	agaggacatttgccat[C/T]gatgtaagtgtttaa	C	T	NM_001031 // upstream // 1366432 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2225288 // — // — // — // /// ENST00000357859 // upstream // 1366432 // — // — // — //	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1717243	gtctaggcttccaggcctgtatga[G/T]aaggctgccatgaagatctctgac	G	T	AF009227 // upstream // 2514835 // - // - // - // Homo sapiens gamma-heregulin mRNA, complete cds. /// NM_175885 // downstream // 1001256 // Hs.448218 // MGC33846 // 220382 // hypothetical protein MGC33846 /// NM_175891 // downstream // 999191 // - // -	-	- , rs11114556, Homo sapiens gamma-heregulin mRNA, complete cds. , q14.1
SNP_A-2095529	agacaagccttagaag[A/G]agctgtacagaaccat	A	G	NM_001031 // upstream // 907516 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2684204 // — // — // — // /// ENST00000357859 // upstream // 907516 // — // — // — // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2156622	attctgcataaactaa[A/G]aagctgtggatatttt	A	G	NM_001031 // upstream // 874364 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2717356 // — // — // — // /// ENST00000357859 // upstream // 874364 // — // — // — // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1882256	tgaaaaagtatgagat[A/G]agtctggttcatttta	A	G	NM_001031 // upstream // 601232 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 2990488 // — // — // — // /// ENST00000357859 // upstream // 601232 // — // — // — // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2111373	aggaggaaatagctca[C/T]gccaaatcattgggat	C	T	NM_001031 // upstream // 204534 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3387186 // — // — // — // /// ENST00000357859 // upstream // 204534 // — // — // — // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1720857	ccacattggctctatgttcagagag[C/T]gtctaccctcaagtttcaagattg	C	T	AF009227 // upstream // 3239235 // - // - // - // Homo sapiens gamma-heregulin mRNA, complete cds. /// NM_175885 // downstream // 276856 // Hs.448218 // MGC33846 // 220382 // hypothetical protein MGC33846 /// NM_175891 // downstream // 274791 // - // - /	-	-, rs972560, Homo sapiens gamma-heregulin mRNA, complete cds., q14.1
SNP_A-2002089	cacttactgaacaat[A/G]aagaaggtgagagaga	A	G	NM_001031 // upstream // 182390 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3409330 // --- // --- // --- /// ENST00000357859 // upstream // 182390 // --- // --- // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2099612	agaggtagggcacaa[C/T]ggtgaaaataaatat	C	T	NM_001031 // upstream // 179423 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3412297 // --- // --- // --- /// ENST00000357859 // upstream // 179423 // --- // --- // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2178688	cactcttcctcctgaa[G/T]tcttatggccttttcc	G	T	NM_001031 // upstream // 175836 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3415884 // --- // --- // --- /// ENST00000357859 // upstream // 175836 // --- // --- // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1939927	ttgcactagcttcctc[A/G]acattacttagagaag	A	G	NM_001031 // upstream // 175702 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3416018 // --- // --- // --- /// ENST00000357859 // upstream // 175702 // --- // --- // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1798401	gtaaataggagttaga[C/G]gcagaatggaacacat	C	G	NM_001031 // upstream // 122846 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3468874 // --- // --- // --- /// ENST00000357859 // upstream // 122846 // --- // --- // -	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-1833324	tacacttttttttcca[C/T]gctaatcgagaaaagc	C	T	NM_001031 // upstream // 82374 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3509346 // --- // --- // --- /// ENST00000357859 // upstream // 82374 // --- // --- // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2104867	agcataggattataaa[A/G]tgtgggttagccatca	A	G	NM_001031 // upstream // 78964 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3512756 // --- // --- // --- /// ENST00000357859 // upstream // 78964 // --- // --- // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2169283	caagcacaaaagaata[C/T]cagcccttgaatgaga	C	T	NM_001031 // upstream // 69167 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3522553 // --- // --- // --- /// ENST00000357859 // upstream // 69167 // --- // --- // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2120486	agtccaatagtaacaa[C/T]gtgatttacagtaggt	C	T	NM_001031 // upstream // 68503 // Hs.546293 // RPS28 // 6234 // Homo sapiens ribosomal protein S28 (RPS28), mRNA. /// ENST00000355278 // downstream // 3523217 // --- // --- // --- /// ENST00000357859 // upstream // 68503 // --- // --- // ---	RPS28	RPS28, Homo sapiens ribosomal protein S28 (RPS28), q14.1
SNP_A-2075290	acatctgagagcaaa[C/T]aaatcacatttggac	C	T	NM_014488 // upstream // 8329 // Hs.40758 // RAB30 // 27314 // Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA. /// NM_015885 // upstream // 76972 // Hs.128959 // PCF11 // 51585 // Homo sapiens pre-mRNA cleavage complex II protein Pcf11 (PCF1	RAB30	RAB30, Homo sapiens RAB30, member RAS oncogene family (RAB30), q14.1
SNP_A-2294375	gcaggtggactatttc[C/T]acatttgtcttctata	C	T	NM_014488 // upstream // 31063 // Hs.40758 // RAB30 // 27314 // Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA. /// NM_015885 // upstream // 54238 // Hs.128959 // PCF11 // 51585 // Homo sapiens pre-mRNA cleavage complex II protein Pcf11 (PCF	RAB30	RAB30, Homo sapiens RAB30, member RAS oncogene family (RAB30), q14.1
SNP_A-1886401	tgaccttgtctgaaa[C/T]gctggacaaaatttca	C	T	NM_021825 // upstream // 164378 // Hs.368866 // MDS025 // 60492 // Homo sapiens hypothetical protein MDS025 (MDS025), mRNA. /// NM_001364 // downstream // 8334 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (	MDS025	MDS025, Homo sapiens hypothetical protein MDS025 (MDS025), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209553	cccatctggcattcca[C/T]aggagaaaggtctactg	C	T	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1800544	gtacttacgggaaatat[A/G]aagctaatgagatgtg	A	G	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1912350	tgtgattgtccctta[A/C]acagcttatcagtgac	A	C	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1816942	gttatttagactcaa[C/G]gaaccctagacattt	C	G	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2284326	gatatttactcaagca[C/T]gtcaagaggtaagagg	C	T	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2083263	actaaagaaaatcctca[A/G]tgaagctgctttgaca	A	G	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2066379	aatttttgcatatttga[C/T]gtatgttgctgtatac	C	T	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// ENST00000280241 // intron // 0 // — // — // —	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2090843	actttcaccagaatta[C/T]atttcaaggattaa	C	T	NM_001364 // upstream // 288057 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream // 805842 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1720399	gaaaaaatataatacatcttctaac[A/T]atcttaactgatgcctca caactct	A	T	NM_001364 // intron // 0 // Hs.215839 // DLG2 // 1740 // discs, large homolog 2, chapsyn-110 (Drosophila)	DLG2	DLG2, rs10501573, discs, large homolog 2, chapsyn-110 (Drosophila),q14.1
SNP_A-2026858	aaacaccttaccca[C/T]ggcttctgacctagg	C	T	NM_001364 // upstream // 396389 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream // 697510 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2029333	aaagaatggactatca[A/G]tacaatcaacaaatta	A	G	NM_001364 // upstream // 456325 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream // 637574 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1785255	ggctacttcagagcaa[C/T]cagaagtctaatgtt	C	T	NM_001364 // upstream // 478630 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream // 615269 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2295775	gcatgctattatgcta[C/T]caaaagcttaaaatat	C	T	NM_001364 // upstream // 479159 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA. /// NM_018480 // upstream // 614740 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2051638	aaggtacattttgta[A/G]cttcgccactcatacc	A	G	NM_001364 // upstream // 489221 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 604678 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1644586	gttagatgctttctgtaatggaaaa[C/G]tgattggctttaaaaataa gaaaaa	C	G	NM_001364 // upstream // 54090 // Hs.215839 // DLG2 // 1740 // discs, large homolog 2, chapsyn-110 (Drosophila) /// NM_018480 // upstream // 651134 // Hs.476335 // HT007 // 55863 // uncharacterized hypothalamus protein HT007	DLG2	DLG2 . rs651661, discs, large homolog 2, chapsyn-110 (Drosophila), q14.1
SNP_A-2012868	acatggcatcactctt[A/G]aaatttgagacaggtt	A	G	NM_001364 // upstream // 541780 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 552119 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2012871	ttacccattagggaaa[C/G]tgcatttctaccaagc	C	G	NM_001364 // upstream // 555529 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 538370 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2115422	agggggctatagagat[C/G]aggtaattcatggagc	C	G	NM_001364 // upstream // 624494 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 469405 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2012881	gaaatttgcagggtaa[A/G]atactagatatgagag	A	G	NM_001364 // upstream // 697303 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 396596 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2121609	agtgaaggtaagaccc[A/G]gctaataacaaaactt	A	G	NM_001364 // upstream // 825736 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 268163 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-1911383	tgtctattatgcaga[C/T]agagttccctagataa	C	T	NM_001364 // upstream // 1021019 // Hs.215839 // DLG2 // 1740 // Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2). mRNA. /// NM_018480 // upstream // 72880 // Hs.525063 // HT007 // 55863 // Homo sapiens uncharacterized hypothalamus pro	DLG2	DLG2, Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), q14.1
SNP_A-2125991	agttttccttttgtaac[C/T]ggtgccaaagataggt	C	T	NM_206928 // upstream // 102106 // Hs.369520 // SYTL2 // 54843 // Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, mRNA. /// NM_032379 // upstream // 102106 // Hs.369520 // SYTL2 // 54843 // Homo sapiens synaptotagmin-like 2 (SYTL2), trans	SYTL2	SYTL2, Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant d, q14.1
SNP_A-2089471	acttattgtagaaaac[G/T]gggggcaagacaagta	G	T	NM_173556 // intron // 0 // Hs.129284 // MGC34732 // 220047 // Homo sapiens hypothetical protein MGC34732 (MGC34732), mRNA. /// ENST00000342404 // intron // 0 // — // — // — /// ENST00000280245 // intron // 0 // — // — // —	MGC34732	MGC34732, Homo sapiens hypothetical protein MGC34732 (MGC34732), q14.1
SNP_A-2134386	atatggaagaaaccag[A/G]aatagtgaaatttggg	A	G	NM_173556 // downstream // 11712 // Hs.129284 // MGC34732 // 220047 // Homo sapiens hypothetical protein MGC34732 (MGC34732), mRNA. /// NM_007166 // downstream // 25723 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin a	MGC34732	MGC34732, Homo sapiens hypothetical protein MGC34732 (MGC34732), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1822377	gtttigttgattgtca[C/T]ggataaaggtacaact	C	T	NM_173556 // downstream // 25123 // Hs.129284 // MGC34732 // 220047 // Homo sapiens hypothetical protein MGC34732 (MGC34732), mRNA. /// NM_007166 // downstream // 12312 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin a	MGC34732	MGC34732, Homo sapiens hypothetical protein MGC34732 (MGC34732), q14.2
SNP_A-1829668	taagttgcttacttta[C/G]gccaaaaattagctag	C	G	NM_173556 // downstream // 26850 // Hs.129284 // MGC34732 // 220047 // Homo sapiens hypothetical protein MGC34732 (MGC34732), mRNA. /// NM_007166 // downstream // 10585 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin a	MGC34732	MGC34732, Homo sapiens hypothetical protein MGC34732 (MGC34732), q14.2
SNP_A-1652856	ttgctgttagatttacaaataagta[C/T]gttgttattactgacatgca aaatc	C	T	NM_173556 // intron // 0 // Hs.129284 // MGC34732 // 220047 // hypothetical protein MGC34732	MGC34732	MGC34732, rs10501600, hypothetical protein MGC34732,q14.2
SNP_A-1828975	taaggcctatttctca[G/T]aagtcacatttigttg	G	T	NM_173556 // downstream // 36037 // Hs.129284 // MGC34732 // 220047 // Homo sapiens hypothetical protein MGC34732 (MGC34732), mRNA. /// NM_007166 // downstream // 1398 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin as	MGC34732	MGC34732, Homo sapiens hypothetical protein MGC34732 (MGC34732), q14.2
SNP_A-1828445	taagcaactggattca[A/C]cgtaccactaatggcc	A	C	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1951610	ttccctgtgacaatga[A/T]attacagtacaaaaa	A	T	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1914271	tgtgttatagtgggaa[A/G]aagactggattcagag	A	G	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2252365	cttcccttatctcta[A/T]cttatcactaatctat	A	T	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1934857	ttctgaaacaggtata[C/T]gttacttcacacagg	C	T	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1944914	ttgtggatttgtaagt[C/G]aaacaaaggctcattt	C	G	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1875020	tctctatcctcataca[C/T]ctcataaccatacacc	C	T	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2012947	gacaatacgcaaacta[A/G]gcacccataagatatt	A	G	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2012948	caaaagaattaacaca[A/G]tgtcaggacaaactgt	A	G	NM_007166 // intron // 0 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// ENST00000341783 // intron // 0 // — // — /// ENST00000356360 // intron // 0 // — // — ///	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287895	gattatagagttcaca[A/G]ggtatttcaaagccat	A	G	NM_007166 // upstream // 7924 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 167991 // Hs.503510 // EED // 8726 // Homo sapiens embryonic ectoderm developm	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2242412	ctgcactggctactaa[C/T]gtgaccataaatttcc	C	T	NM_007166 // upstream // 8451 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 167464 // Hs.503510 // EED // 8726 // Homo sapiens embryonic ectoderm developm	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1749555	ctatcaaataaaatgtgagccagaag[A/G]ttttaatgggagaaat taacttta	A	G	NM_007166 // intron // 0 // Hs.39252 // PICALM // 8301 // phosphatidylinositol binding clathrin assembly protein	PICALM	PICALM , rs1941375, phosphatidylinositol binding clathrin assembly protein, q14.2
SNP_A-1705057	aatggtatttgtgtagctaaacata[G/T]atctaaacatagaacag atacagta	G	T	AF116656 // downstream // 28418 // - // - // Homo sapiens PRO1167 mRNA, complete cds. /// NM_003797 // upstream // 170836 // Hs.512812 // EED // 8726 // embryonic ectoderm development /// NM_007166 // upstream // 5008 // Hs.39252 // PICALM // 8301 /	-	- , rs638509, Homo sapiens PRO1167 mRNA, complete cds, q14.2
SNP_A-1816650	gttatactgtggaatg[C/T]atctgaagatcacct	C	T	NM_007166 // upstream // 58184 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 117731 // Hs.503510 // EED // 8726 // Homo sapiens embryonic ectoderm develop	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1893645	tgcaggtttgattcc[A/G]cagatctggtgggac	A	G	NM_007166 // upstream // 81519 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 94396 // Hs.503510 // EED // 8726 // Homo sapiens embryonic ectoderm developm	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2050001	aaggaagtacctcctta[C/T]gatatgcaagacaaaa	C	T	NM_007166 // upstream // 89837 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 86078 // Hs.503510 // EED // 8726 // Homo sapiens embryonic ectoderm developm	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-2068521	acaagtattaactgtg[C/T]attgctttgagcttag	C	T	NM_007166 // upstream // 147533 // Hs.163893 // PICALM // 8301 // Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), mRNA. /// NM_152991 // upstream // 28382 // Hs.503510 // EED // 8726 // Homo sapiens embryonic ectoderm develop	PICALM	PICALM, Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), q14.2
SNP_A-1680600	aagtaacaaatgattatagcaatta[C/T]agtgggtgagtgcaatg agagggga	C	T	NM_006680 // intron // 0 // Hs.376590 // ME3 // 10873 // malic enzyme 3, NADP(+)-dependent, mitochondrial	ME3	ME3 , rs10501620, malic enzyme 3, NADP(+)-dependent, mitochondrial, q14.2
SNP_A-1714901	aggtatctactagataagcgcaca[A/G]aagagttctttactaga catgatga	A	G	NM_006680 // intron // 0 // Hs.376590 // ME3 // 10873 // malic enzyme 3, NADP(+)-dependent, mitochondrial	ME3	ME3 , rs10501621, malic enzyme 3, NADP(+)-dependent, mitochondrial, q14.2
SNP_A-2243708	ctgctcttcgtactga[C/T]cctgctttctgcagg	C	T	NM_006680 // upstream // 86746 // Hs.199743 // ME3 // 10873 // Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006680 // upstream // 86630 // Hs.199743 // ME3 // 10873 // Homo	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-1904771	tgggtacacaaaaaa[G/T]aaatctgaaacagac	G	T	NM_006680 // upstream // 115174 // Hs.199743 // ME3 // 10873 // Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006680 // upstream // 115058 // Hs.199743 // ME3 // 10873 // Hom	ME3	ME3, Homo sapiens malic enzyme 3, NADP(+)-dependent, mitochondrial (ME3), nuclear gene encoding mitochondrial protein, q14.2
SNP_A-1833802	tacagtcacattgggg[A/G]agattaagacatgaga	A	G	NM_012193 // upstream // 4409 // Hs.19545 // FZD4 // 8322 // Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), mRNA. /// NM_022918 // upstream // 78223 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. //	FZD4	FZD4, Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1738705	aagctcagttgccctgatagtagcat[C/T]gtttctgtttctgatgtacc tttt	C	T	NM_012193 // 3UTR // 0 // Hs.19545 // FZD4 // 8322 // frizzled homolog 4 (Drosophila)	FZD4	FZD4 , rs713065, frizzled homolog 4 (Drosophila),q14.2
SNP_A-1876645	tctgcaaccagaacct[A/C]aggtgacttatagttg	A	C	NM_022918 // intron // 0 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// ENST00000340353 // intron // 0 // — // — // — /// ENST00000305494 // intron // 0 // — // — // — /// EN	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2100994	agatatttctcaacca[C/T]gctaccagaactaca	C	T	NM_022918 // intron // 0 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// ENST00000340353 // intron // 0 // — // — // — /// ENST00000305494 // intron // 0 // — // — // —	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2013071	agggatgctgagtcta[A/G]gcaaggcagataaagc	A	G	NM_022918 // downstream // 2727 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 771121 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB38	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-1932536	ttccrggtatataaca[A/G]attctcaattaataca	A	G	NM_022918 // downstream // 152738 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 621110 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2161518	atttgcttattctacc[A/G]attctcagttctaac	A	G	NM_022918 // downstream // 172662 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 601186 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-1942676	ttgggagggcatgtaa[A/G]cttcaaaaccctcca	A	G	NM_022918 // downstream // 203587 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 570261 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-1815092	gtgttccctcctatac[A/C]caagcacagaaaatgc	A	C	NM_022918 // downstream // 252036 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 521812 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-1823666	taaaatagtcactacg[C/T]caatgtaccatatttg	C	T	NM_022918 // downstream // 260751 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 513097 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2227035	ctaatggtgtttgaa[C/T]aagcatttagaaaatt	C	T	NM_022918 // downstream // 271834 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 502014 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2013089	ccaaactcctctgcta[C/T]ctgttatctactag	C	T	NM_022918 // downstream // 302642 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 471206 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-1881504	tctttctcttacatca[C/T]acttccttatacatg	C	T	NM_022918 // downstream // 566080 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 207768 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2147890	atggcgaaaaaccata[C/T]ataaaccagtgcattc	C	T	NM_022918 // downstream // 592571 // Hs.188591 // FLJ22104 // 65084 // Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA. /// NM_022337 // downstream // 181277 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB	FLJ22104	FLJ22104, Homo sapiens hypothetical protein FLJ22104 (FLJ22104), q14.2
SNP_A-2075847	acatgtgttggggtca[C/T]agaaccatcagtagac	C	T	NM_022337 // intron // 0 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // — // — // — // —	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-1800995	gtagatctaagagtgc[A/G]acctcagaaatcccac	A	G	NM_022337 // intron // 0 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // — // — // — // —	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-2146612	atgctgggatatgcac[C/T]gagatttgtctaacta	C	T	NM_022337 // intron // 0 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // — // — // — // —	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-2266881	gaagttgacaaaacct[C/G]aaggctagtgtgatgt	C	G	NM_022337 // intron // 0 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// ENST00000243662 // intron // 0 // — // — // — // —	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-2241972	ctgattaccagttgaa[C/T]gggtgtgaaagtgctc	C	T	NM_022337 // upstream // 592 // Hs.283148 // RAB38 // 23682 // Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /// NM_001814 // downstream // 117567 // Hs.128065 // CTSC // 1075 // Homo sapiens cathepsin C (CTSC), transcript variant 1, mRNA.	RAB38	RAB38, Homo sapiens RAB38, member RAS oncogene family (RAB38), q14.2
SNP_A-1729346	gagacttgatgcagtttaacacaac[C/T]atggaataaatggaag gagtagaga	C	T	NM_022337 // intron // 0 // Hs.108923 // RAB38 // 23682 // RAB38, member RAS oncogene family	RAB38	RAB38 , rs10501659, RAB38, member RAS oncogene family,q14.2
SNP_A-1747631	aaagttaatataatggctgcgggaa[C/G]tatttagataatctcac agcagaag	C	G	NM_022337 // intron // 0 // Hs.108923 // RAB38 // 23682 // RAB38, member RAS oncogene family	RAB38	RAB38 , rs10501660, RAB38, member RAS oncogene family,q14.2
SNP_A-1702765	ctactaaaactatttcaaaaaatca[A/G]gaagcgtctcctcccta actcattc	A	G	NM_022337 // intron // 0 // Hs.108923 // RAB38 // 23682 // RAB38, member RAS oncogene family	RAB38	RAB38 , rs2386577, RAB38, member RAS oncogene family,q14.2
SNP_A-2204633	ccaggagaaaaagaaa[C/T]gtgagagatcgtataa	C	T	NM_000842 // intron // 0 // Hs.147361 // GRM5 // 2915 // Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915 // Human mRNA for metabotropic glutamate receptor subtype 5b, complete cds. /// E	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-2291127	gcaatagctgttggca[C/T]tcaaaaatatgagaga	C	T	NM_000842 // intron // 0 // Hs.147361 // GRM5 // 2915 // Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA. /// D28539 // intron // 0 // Hs.147361 // GRM5 // 2915 // Human mRNA for metabotropic glutamate receptor subtype 5b, complete cds. /// E	GRM5	GRM5, Homo sapiens glutamate receptor, metabotropic 5 (GRM5), q14.3
SNP_A-2112970	aggcattcaggtttaa[C/T]taccatgttttggtag	C	T	NM_005467 // upstream // 32576 // Hs.503560 // NAALAD2 // 10003 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), mRNA. /// ENST00000332005 // downstream // 15712 // — // — // — // — /// ENST00000321955 // upstream // 32576	NAALAD2	NAALAD2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), q14.3
SNP_A-2221870	ccttttgtcagattta[G/T]ccacaaacatttcata	G	T	NM_005467 // intron // 0 // Hs.503560 // NAALAD2 // 10003 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), mRNA. /// ENST00000321955 // intron // 0 // — // — // — // —	NAALAD2	NAALAD2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), q14.3
SNP_A-2036132	aaattatagcaaggaa[C/G]atgaattctcagacat	C	G	NM_005467 // 3UTR // 0 // Hs.503560 // NAALAD2 // 10003 // Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), mRNA. /// ENST00000321955 // 3UTR // 0 // — // — // — // —	NAALAD2	NAALAD2, Homo sapiens N-acetylated alpha-linked acidic dipeptidase 2 (NAALAD2), q14.3
SNP_A-2277353	gagatttccttatata[A/C]cctgagtgaataagct	A	C	NM_012124 // upstream // 7176 // Hs.22857 // CHORDC1 // 26973 // Homo sapiens cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1), mRNA. /// ENST00000320585 // upstream // 7176 // — // — // — // — /// ENST000003	CHORDC1	CHORDC1, Homo sapiens cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1689911	tgctctcagcaatttgcaagatgga[A/G]tactatatttttaaaaatcaggtaa	A	G	NM_012124 // intron // 0 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1 , rs10501713, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3
SNP_A-1650734	taccaaataaatgctcagtttcacc[A/G]gctctcttacactaatgtgaacact	A	G	NM_012124 // upstream // 227839 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1 , rs10501719, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3
SNP_A-2116695	aggtcatttttgcta[G/T]gatgataaaataaagga	G	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1901078	tggatcataatctggc[C/T]gaatttctgtgctgtg	C	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2103418	agcaataagatatcca[A/G]ctctaatctgactcca	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2094780	agaatccaaaataaaa[C/T]ggtgctgtttatgaga	C	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2084343	actataatttgaaggc[A/G]cctaatttgccttgag	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2052547	aagtagtcaaaaccaa[C/T]tcatggctagagtata	C	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1801842	gtagttatcggtagtc[A/T]atctagttgcagagac	A	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1655077	acaccatgaagtttattctctagca[A/T]aattgatgattgtacttctaacaga	A	T	NM_012124 // upstream // 275557 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1 , rs565481, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3
SNP_A-2013400	aactatttaactagag[A/T]acccttatcatgcttt	A	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2013401	ggaaaggaattaacaa[A/G]gagcatgaaggtatct	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1652838	ttcccttcaaattcagaaattttac[C/G]aaggcatttataggcttgaagcttc	C	G	NM_012124 // upstream // 281641 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1 , rs570090, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3
SNP_A-2013403	tgaaaatacactctaa[A/G]ccatatcttaaccaat	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2013406	agagcaaaatttggca[C/G]tgaatcattgttcaaa	C	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2283940	gatatacaagcaagaa[A/G]gtaaagtcataataac	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1823075	taaaaattttcaccac[C/T]gaatcccataaattaa	C	T	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2013409	tagagtatcatctgac[A/G]cataggaataattaac	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1958352	ttttcccatcaaaaga[A/G]aggaggatttagatga	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2116382	aggtagtaacagggat[A/G]agaatagcctcctgcc	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2134634	atatgtggtttttaaa[A/G]tgttgttgaatcggcc	A	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2013480	tacattctgcattgta[C/G]ctttcttgaccttatg	C	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1730481	cagatcttcttcctcctacacagaa[C/T]tatttttgctaagtctttgcaaaa	C	T	NM_012124 // upstream // 684060 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1 , rs10501744, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3
SNP_A-2134960	atattcaccatatact[C/G]aggccacagagttaaa	C	G	ENST00000318973 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2260283	gaaaattaataaggac[A/G]catttttacagccat	A	G	ENST00000318973 // downstream // 29314 // — // — // — // — /// ENST00000329885 // downstream // 725988 // — // — // — // —	-	q14.3
SNP_A-2205754	ccataatctatttggc[C/T]agaaaggttgattcat	C	T	ENST00000318973 // downstream // 47193 // — // — // — // — /// ENST00000329885 // downstream // 708109 // — // — // — // —	-	q14.3
SNP_A-2235719	ctcctccaacaaagaa[A/G]ctagtcagttggataa	A	G	ENST00000318973 // downstream // 49798 // — // — // — // — /// ENST00000329885 // downstream // 705504 // — // — // — // —	-	q14.3
SNP_A-1781852	ggattttgagaataac[A/G]gcagaaacaaacctac	A	G	ENST00000318973 // downstream // 134951 // — // — // — // — /// ENST00000329885 // downstream // 620351 // — // — // — // —	-	q14.3
SNP_A-1831538	taattaacattcagcc[A/T]ctaaaccaggaccaaa	A	T	ENST00000318973 // downstream // 581359 // — // — // — // — /// ENST00000329885 // downstream // 173943 // — // — // — // —	-	q14.3
SNP_A-1819129	gttgctagcgaacata[C/T]atttaggctgtgggcc	C	T	ENST00000318973 // downstream // 584165 // — // — // — // — /// ENST00000329885 // downstream // 171137 // — // — // — // —	-	q14.3
SNP_A-1846588	tatatttagaccaaaa[A/G]tttatcaaggatggca	A	G	ENST00000318973 // downstream // 590587 // — // — // — // — /// ENST00000329885 // downstream // 164715 // — // — // — // —	-	q14.3
SNP_A-2013552	catcatcatgactgga[A/G]ataatgcctgaaattg	A	G	ENST00000318973 // downstream // 591308 // — // — // — // — /// ENST00000329885 // downstream // 163994 // — // — // — // —	-	q14.3
SNP_A-1688962	tcactgatgattcatatataagcca[C/T]gtggactcaaataaattctcatcct	C	T	NM_012124 // upstream // 1577928 // Hs.22857 // CHORDC1 // 26973 // cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	CHORDC1	CHORDC1 , rs6483154, cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1,q14.3
SNP_A-1863775	tccaagctaaaaaaaa[A/C]cgcatatattattgaa	A	C	ENST00000318973 // downstream // 663093 // — // — // — // — /// ENST00000329885 // downstream // 92209 // — // — // — // —	-	q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2051597	aaggtaacaatataaa[C/G]caccaacacaatgcct	C	G	ENST00000329885 // upstream // 100598 // — // — // — /// ENST00000359050 // upstream // 304601 // — // — // — /// ENST00000339373 // downstream // 447589 // — // — // —	-	q14.3
SNP_A-1864379	tccactgagaaattac[A/G]gcttccatttatcaca	A	G	ENST00000329885 // upstream // 141242 // — // — // — /// ENST00000359050 // upstream // 263957 // — // — // — /// ENST00000339373 // downstream // 406945 // — // — // —	-	q14.3
SNP_A-2199483	catttttctgtggtag[A/C]caatatgctagatgtc	A	C	ENST00000329885 // upstream // 149633 // — // — // — /// ENST00000359050 // upstream // 255566 // — // — // — /// ENST00000339373 // downstream // 398554 // — // — // —	-	q14.3
SNP_A-1868441	tcctccccctgtgtctc[A/C]gaaaccacacaaaatt	A	C	ENST00000329885 // upstream // 160378 // — // — // — /// ENST00000359050 // upstream // 244821 // — // — // — /// ENST00000339373 // downstream // 387809 // — // — // —	-	q14.3
SNP_A-1813141	gtggtagtgtccttca[G/T]atgctcacaggaaggt	G	T	ENST00000359050 // intron // 0 // — // — // —	-	q14.3
SNP_A-1803484	gtatttttagaaatagc[A/T]aaacataacaaagtga	A	T	NM_005959 // upstream // 50516 // Hs.147853 // MTNR1B // 4544 // Homo sapiens melatonin receptor 1B (MTNR1B), mRNA. /// ENST00000298049 // downstream // 2545 // — // — // — /// ENST00000257068 // upstream // 50516 // — // — // —	MTNR1B	MTNR1B, Homo sapiens melatonin receptor 1B (MTNR1B), q21
SNP_A-1935553	ttctggtctgaaaatac[A/G]ctaaaagtgaggagca	A	G	NM_020179 // upstream // 93040 // Hs.438064 // FN5 // 56935 // Homo sapiens FN5 protein (FN5), mRNA. /// NM_024116 // downstream // 93783 // Hs.355750 // MGC5306 // 79101 // Homo sapiens hypothetical protein MGC5306 (MGC5306), mRNA. /// ENST00000298966 //	FN5	FN5, Homo sapiens FN5 protein (FN5), q21
SNP_A-2233250	ctcaggaatggtgggga[A/T]tcagcaatgtgttgtg	A	T	ENST00000279835 // upstream // 55639 // — // — // — /// ENST00000315765 // upstream // 115255 // — // — // — /// ENST00000334665 // upstream // 139701 // — // — // — /// ENST00000345073 // upstream // 158210 // — // —	-	q21
SNP_A-2132759	atataaataaactcca[A/G]atatttacacaacaca	A	G	ENST00000279835 // upstream // 55663 // — // — // — /// ENST00000315765 // upstream // 115231 // — // — // — /// ENST00000334665 // upstream // 139677 // — // — // — /// ENST00000345073 // upstream // 158186 // — // —	-	q21
SNP_A-2091551	agaaaaagtgtccgtc[A/G]aagcccttgctcacct	A	G	ENST00000279835 // upstream // 120973 // — // — // — /// ENST00000315765 // upstream // 49921 // — // — // — /// ENST00000334665 // upstream // 74367 // — // — // — /// ENST00000345073 // upstream // 92876 // — // —	-	q21
SNP_A-2013809	gtaatggaatcataaa[C/T]ccaaaatcatagagcc	C	T	ENST00000279835 // upstream // 131282 // — // — // — /// ENST00000315765 // upstream // 39612 // — // — // — /// ENST00000334665 // upstream // 64058 // — // — // — /// ENST00000345073 // upstream // 82567 // — // —	-	q21
SNP_A-2013810	tcttgctttgttcata[C/T]gtagcacagttgaaat	C	T	ENST00000279835 // upstream // 133512 // — // — // — /// ENST00000315765 // upstream // 37382 // — // — // — /// ENST00000334665 // upstream // 61828 // — // — // — /// ENST00000345073 // upstream // 80337 // — // —	-	q21
SNP_A-2013819	gcagcggcatgctaa[A/G]tgtgtcatcctagaac	A	G	ENST00000315765 // intron // 0 // — // — // —	-	q21
SNP_A-1754938	ttccttgagtctactagaattagc[G/T]ctttcactggtaaaaagttattcc	G	T	NM_004268 // downstream // 208778 // Hs.226630 // CRSP6 // 9440 // cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa /// NM_015368 // upstream // 106863 // Hs.32163 // PANX1 // 24145 // pannexin 1	CRSP6	CRSP6 , rs2949865, cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa, q21
SNP_A-2056555	aatagagttacccaca[A/C]gaaactggaaatcgag	A	C	NM_016540 // downstream // 40467 // Hs.272385 // GPR83 // 10888 // Homo sapiens G protein-coupled receptor 83 (GPR83), mRNA. /// ENST00000328458 // downstream // 29167 // — // — // — /// ENST00000333405 // downstream // 29235 // — // — // —	GPR83	GPR83, Homo sapiens G protein-coupled receptor 83 (GPR83), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2093864	agaagatttagggatc[A/T]ataagcaaggacttta	A	T	NM_005590 // intron // 0 // Hs.192649 // MRE11A // 4361 // Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 2, mRNA. /// NM_005591 // intron // 0 // Hs.192649 // MRE11A // 4361 // Homo sapiens MRE11 meioti	MRE11A	MRE11A, Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 2, q21
SNP_A-1792275	gggttctcagaggcaa[A/G]ttcagaccgtgttgtt	A	G	NM_005591 // intron // 0 // Hs.192649 // MRE11A // 4361 // Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 1, mRNA. /// ENST00000323929 // intron // 0 // — // — // — // —	MRE11A	MRE11A, Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 1, q21
SNP_A-2264919	gaagaggaagaaagca[A/C]aatcatcctatctga	A	C	NM_152431 // intron // 0 // Hs.58248 // PIWIL4 // 143689 // Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// ENST00000299001 // intron // 0 // — // — // —	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-1803476	gtattgttgcaaaag[A/G]atgctatcccaagtca	A	G	NM_152431 // intron // 0 // Hs.58248 // PIWIL4 // 143689 // Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// ENST00000299001 // intron // 0 // — // — // — // —	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-1911669	tgtgaacctcataatt[G/T]aagtatttcagcaaa	G	T	NM_152431 // downstream // 56 // Hs.58248 // PIWIL4 // 143689 // Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// NM_130847 // upstream // 146899 // Hs.503594 // AMOTL1 // 154810 // Homo sapiens angiomotin like 1 (AMOTL1), mRNA. /// ENST00002990	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-2116159	aggtaaggatgctcaa[C/T]aaagggaatttgacta	C	T	NM_152431 // downstream // 14163 // Hs.58248 // PIWIL4 // 143689 // Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), mRNA. /// NM_130847 // upstream // 132792 // Hs.503594 // AMOTL1 // 154810 // Homo sapiens angiomotin like 1 (AMOTL1), mRNA. /// ENST000002	PIWIL4	PIWIL4, Homo sapiens piwi-like 4 (Drosophila) (PIWIL4), q21
SNP_A-2241438	ctgagtcatgcaattg[A/G]agggaatccaatttc	A	G	NM_018039 // downstream // 26812 // Hs.503598 // JMJD2D // 55693 // Homo sapiens jumonji domain containing 2D (JMJD2D), mRNA. /// AB020637 // upstream // 63529 // Hs.167115 // KIAA0830 // 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// E	JMJD2D	JMJD2D, Homo sapiens jumonji domain containing 2D (JMJD2D), q21
SNP_A-1789796	gggctgagtttgtgac[A/G]agagggaaaacacaaa	A	G	NM_018039 // downstream // 75763 // Hs.503598 // JMJD2D // 55693 // Homo sapiens jumonji domain containing 2D (JMJD2D), mRNA. /// AB020637 // upstream // 14578 // Hs.167115 // KIAA0830 // 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// E	JMJD2D	JMJD2D, Homo sapiens jumonji domain containing 2D (JMJD2D), q21
SNP_A-2143347	atgacatgatctagg[C/T]ctagagaagttgagaa	C	T	AB020637 // intron // 0 // Hs.167115 // KIAA0830 // 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// ENST00000278505 // intron // 0 // — // — // — // —	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds, q21
SNP_A-2002150	ccagtagcatcccaag[C/T]atctgaatgaggaggg	C	T	AB020637 // intron // 0 // Hs.167115 // KIAA0830 // 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// ENST00000278505 // intron // 0 // — // — // — // —	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds, q21
SNP_A-1748563	ctgctgttatctagtgtttataa[C/G]aagggatccaagtcaacttgttg	C	G	AB020637 // intron // 0 // Hs.167115 // KIAA0830 // 23052 // KIAA0830 protein	KIAA0830	KIAA0830 , rs641937, KIAA0830 protein,q21
SNP_A-2133425	atatatgtttaaagtc[C/T]gaactggaatgtctgg	C	T	AB020637 // downstream // 23507 // Hs.167115 // KIAA0830 // 23052 // Homo sapiens mRNA for KIAA0830 protein, partial cds. /// NM_144665 // downstream // 16819 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// ENST00000278505 //	KIAA0830	KIAA0830, Homo sapiens for KIAA0830 protein, partial cds, q21
SNP_A-1656715	tgatcaaggtaggatctaaacatca[A/G]ctcttcataaatccagaatctcaatt	A	G	NM_144664 // downstream // 490474 // Hs.288304 // MGC33371 // 143684 // hypothetical protein MGC33371 /// NM_144665 // upstream // 47399 // Hs.271953 // SESN3 // 143686 // sestrin 3	MGC33371	MGC33371 , rs976337, hypothetical protein MGC33371, q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2125234	agttgtactgaggtta[A/G]gggatggactcaaggc	A	G	NM_144665 // upstream // 98636 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 439235 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1688982	tacactcactaagatggaagaaggct[A/G]ctggatcctggaacaagggaagga	A	G	NM_144664 // downstream // 361834 // Hs.288304 // MGC33371 // 143684 // hypothetical protein MGC33371 /// NM_144665 // upstream // 176039 // Hs.271953 // SESN3 // 143686 // sestrin 3	MGC33371	MGC33371 , rs4121863, hypothetical protein MGC33371 , q21
SNP_A-1899338	tggaaccacagaggct[A/G]aaagattggtctgtta	A	G	NM_144665 // upstream // 228216 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 309655 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2039857	aacatttctagctaaga[A/G]cccatcaataacacaa	A	G	NM_144665 // upstream // 260743 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 277128 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1871890	tctacagaaccataaa[C/T]gctcttgaactcatca	C	T	NM_144665 // upstream // 265155 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 272716 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1867959	tcctagcataatcacc[A/G]catgaagcaatttcc	A	G	NM_144665 // upstream // 271490 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 266381 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2013996	aatttccagtctcta[C/T]catgaagcaaggacc	C	T	NM_144665 // upstream // 277833 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 260038 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1826876	taacatatccctgaggt[C/T]aaaaccctgcaacttc	C	T	NM_144665 // upstream // 313661 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 224210 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-2243164	ctgcctatggcttatg[A/G]atatctgtttgcatt	A	G	NM_144665 // upstream // 385389 // Hs.120633 // SESN3 // 143686 // Homo sapiens sestrin 3 (SESN3), mRNA. /// NM_144664 // downstream // 152482 // Hs.288304 // MGC33371 // 143684 // Homo sapiens hypothetical protein MGC33371 (MGC33371), mRNA. /// NM_144664	SESN3	SESN3, Homo sapiens sestrin 3 (SESN3), q21
SNP_A-1644920	attcagtaaaagatgcagtcactac[C/T]attctaaaaaccttaataagtaat	C	T	NM_016156 // upstream // 33586 // Hs.181326 // MTMR2 // 8898 // myotubularin related protein 2 /// NM_032427 // downstream // 20395 // Hs.112472 // MAML2 // 84441 // mastermind-like 2 (Drosophila)	MTMR2	MTMR2 , rs10501833, myotubularin related protein 2 ,q21
SNP_A-2124929	agttgagcaacaagaa[A/T]gtgaaaggaaatttag	A	T	NM_032427 // intron // 0 // Hs.428214 // MAML2 // 84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// intron // 0 // --- // --- // ---	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-1876365	tctgaggtggccctaa[A/G]aatccggatttctaac	A	G	NM_032427 // upstream // 35862 // Hs.428214 // MAML2 // 84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 223395 // Hs.525088 // FLJ23518 // 79780 // Homo sapiens hypothetical protein FLJ23518 (FLJ23518), m	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1931288	ttcccaacagcataac[A/G]agtgtaatttatggg	A	G	NM_032427 // upstream // 158618 // Hs.428214 // MAML2 // 84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 100639 // Hs.525088 // FLJ23518 // 79780 // Homo sapiens hypothetical protein FLJ23518 (FLJ23518).	MAML2	MAML2, Homo sapiens mastermind-like 2 ((Drosophila) (MAML2), q21
SNP_A-1735504	attattctttgaactgaaagtcag[G/T]agaccttgatttagactca ctcca	G	T	NM_032427 // intron // 0 // Hs.112472 // MAML2 // 84441 // mastermind-like 2 (Drosophila)	MAML2	MAML2 , rs2186584, mastermind-like 2 (Drosophila),q21
SNP_A-1895939	tgccttagaagagtccj[A/C]atgcattcacatagca	A	C	NM_032427 // upstream // 217336 // Hs.428214 // MAML2 // 84441 // Homo sapiens mastermind-like 2 (Drosophila) (MAML2), mRNA. /// NM_024725 // downstream // 41921 // Hs.525088 // FLJ23518 // 79780 // Homo sapiens hypothetical protein FLJ23518 (FLJ23518). m	MAML2	MAML2, Homo sapiens mastermind-like 2 (Drosophila) (MAML2), q21
SNP_A-1669885	tagctagaaattattgaaaacccaa[C/T]atatgcaagattctagg ccctttctt	C	T	NM_032427 // intron // 0 // Hs.112472 // MAML2 // 84441 // mastermind-like 2 (Drosophila)	MAML2	MAML2 , rs557277, mastermind-like 2 (Drosophila),q21
SNP_A-1658586	cctattgtagtaaatttgtaatcc[A/G]gataattatataaagcac agttat	A	G	NM_032427 // intron // 0 // Hs.112472 // MAML2 // 84441 // mastermind-like 2 (Drosophila)	MAML2	MAML2 , rs502822, mastermind-like 2 (Drosophila),q21
SNP_A-1712663	gagatacagttacctcttcaatcca[A/G]tagagaccacttgattta ccactct	A	G	NM_032427 // intron // 0 // Hs.112472 // MAML2 // 84441 // mastermind-like 2 (Drosophila)	MAML2	MAML2 , rs483905, mastermind-like 2 (Drosophila),q21
SNP_A-1927397	ttcaaagagctatttc[A/T]cctattcccgtgcctc	A	T	NM_003772 // downstream // 78054 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 78054 // — // — // — // — /// ENST00000334937 // downstream // 2096536 // — // — // —	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2139953	atctaccatgtgatca[A/G]gtttaacatcatcgtg	A	G	NM_003772 // downstream // 508354 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 508354 // — // — // — // — /// ENST00000334937 // downstream // 1666236 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2311984	ggacaatgtgcaataa[A/G]gtttttcatgtcctct	A	G	NM_003772 // downstream // 578524 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 578524 // — // — // — // — /// ENST00000334937 // downstream // 1596066 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q21
SNP_A-2297690	gccagctcattactac[C/G]aggttagctctcaggt	C	G	NM_003772 // downstream // 697342 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 697342 // — // — // — // — /// ENST00000334937 // downstream // 1477248 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2014197	ggagttgagtttagga[C/T]acctgctatatgatc	C	T	NM_003772 // downstream // 732683 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 732683 // — // — // — // — /// ENST00000334937 // downstream // 1441907 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2014214	gtactttggtgtagtta[C/T]aggaagagcactgaaa	C	T	NM_003772 // downstream // 953843 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 953843 // — // — // — // — /// ENST00000334937 // downstream // 1220747 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1934428	ttctcctgaaacagat[C/T]gtaaaaatttgaaatt	C	T	NM_003772 // downstream // 1139780 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1139780 // — // — // — // — /// ENST00000334937 // downstream // 1034810 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1708675	agtcagtttaatacgaagcaaaaaa[C/G]ttctctcatttgtgcagc cggatgg	C	G	NM_003772 // downstream // 1521658 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 1093050 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 1093050 // Hs.234790 // CNTN5 // 53942 // contac	JRKL	JRKL , rs1986446, jerky homolog-like (mouse) ,q22.1
SNP_A-2286954	gatggtcatgatcagt[G/T]aacttgccagtatct	G	T	NM_003772 // downstream // 1656179 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1656179 // — // — // — // — /// ENST00000334937 // downstream // 518411 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1745448	tcttcctaaaagttagcttatgtct[C/T]ttggaaatggaaatggaag tggtgg	C	T	NM_003772 // downstream // 1643746 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 970962 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 970962 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs561146, jerky homolog-like (mouse) ,q22.1
SNP_A-1740049	ccagcctacttctgctatatcccca[A/T]tggccagaaatgtgttata ttcgtta	A	T	NM_003772 // downstream // 1643838 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 970870 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 970870 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs624607, jerky homolog-like (mouse) ,q22.1
SNP_A-1673690	atggttttttaaagaaaagatacca[C/T]gctgcaaagtctctgaa aatggga	C	T	NM_003772 // downstream // 1644081 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 970627 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 970627 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs625569, jerky homolog-like (mouse) ,q22.1
SNP_A-1706859	tcactaccatgaaaaaaatgcacct[A/G]aaaattaagataaaat ttcatcatg	A	G	NM_003772 // downstream // 1644886 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 969822 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 969822 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs482657, jerky homolog-like (mouse) ,q22.1
SNP_A-1737563	taaaaagggcaaagtgctttactac[A/T]caaatatcttactgcact ttgaaca	A	T	NM_003772 // downstream // 1644980 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 969728 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 969728 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs639755, jerky homolog-like (mouse) ,q22.1
SNP_A-2014247	agaattctgcatttta[C/T]gtgaaaaacagcttgt	C	T	NM_003772 // downstream // 1707816 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1707816 // — // — // — // — /// ENST00000334937 // downstream // 466774 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2014248	gtgtgaattcagaaat[A/G]aagttggatttacatt	A	G	NM_003772 // downstream // 1707986 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1707986 // — // — // — // — /// ENST00000334937 // downstream // 466604 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1655071	ttttctctgtaacctaatcagaa[A/G]taatctgtcaagcagtcaat ttatc	A	G	NM_003772 // downstream // 1689599 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 925109 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 925109 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs546136, jerky homolog-like (mouse) ,q22.1
SNP_A-1661592	acaaagcttgttacctaatgaaga[C/T]attttatcacttgtctatta atat	C	T	NM_003772 // downstream // 1692308 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 922400 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 922400 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs10501878, jerky homolog-like (mouse) ,q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1744607	caaattaaaatagctattataaaaa[A/G]gacgagatatatgtag gcaaaggtg	A	G	NM_003772 // downstream // 1695396 // Hs.105940 // JRKL // 8690 // jerky homolog-like (mouse) /// NM_014361 // upstream // 919312 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // upstream // 919312 // Hs.234790 // CNTN5 // 53942 // contacti	JRKL	JRKL , rs2509867, jerky homolog-like (mouse) q22.1
SNP_A-1943999	ttgtattcccggtgta[C/T]cagaaattgtgcttg	C	T	NM_003772 // downstream // 1752402 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1752402 // — // — // — // — /// ENST00000334937 // downstream // 422188 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2014255	cctttatatggaataa[C/T]gagaggtctgagaaaa	C	T	NM_003772 // downstream // 1843440 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1843440 // — // — // — // — /// ENST00000334937 // downstream // 331150 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2028741	aaacttagctattgaa[C/G]gttagagttaggccat	C	G	NM_003772 // downstream // 1852014 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1852014 // — // — // — // — /// ENST00000334937 // downstream // 322576 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1939724	ttgcaaactgtacata[C/T]ggcaaaggtctaatat	C	T	NM_003772 // downstream // 1864239 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1864239 // — // — // — // — /// ENST00000334937 // downstream // 310351 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1919664	ttaaggtgtgcaaata[G/T]cttatccaaacaaaca	G	T	NM_003772 // downstream // 1880535 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 1880535 // — // — // — // — /// ENST00000334937 // downstream // 294055 // — // — //	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-1914587	tgttaactatttgaaa[G/T]ggttgagaagtctcct	G	T	NM_003772 // downstream // 2155211 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 2155211 // — // — // — // — /// ENST00000334937 // downstream // 19379 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2295743	gcatgattgtcaaaca[C/T]gtgatagaggtagt	C	T	NM_003772 // downstream // 2168223 // Hs.105940 // JRKL // 8690 // Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA. /// ENST00000332349 // downstream // 2168223 // — // — // — // — /// ENST00000334937 // downstream // 6367 // — // — // -	JRKL	JRKL, Homo sapiens jerky homolog-like (mouse) (JRKL), q22.1
SNP_A-2187411	caggttctggaggtca[A/G]gattgattatcagctg	A	G	NM_014361 // upstream // 1247266 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1247266 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2.	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2061672	aatggaaagccagtaa[C/G]gaggctagggggcttgg	C	G	NM_014361 // upstream // 1222196 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1222196 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2.	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1945188	ttgtgttcagcatttaa[C/T]ggtatattggagagta	C	T	NM_014361 // upstream // 1187070 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 1187070 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2.	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2237538	ctctctacaagggcaa[A/C]acagagaggaaatatg	A	C	NM_014361 // upstream // 1126146 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 1126146 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2,	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2036083	aaattagagatgaagt[A/C]aagtatcaaatagaca	A	C	NM_014361 // upstream // 1111125 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 1111125 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2,	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1830798	taatctcigccttaa[A/T]tagtgactcaaagtag	A	T	NM_014361 // upstream // 1111018 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 1111018 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2,	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2131258	atagaggcacacgata[C/G]aggatcaacatataaa	C	G	NM_014361 // upstream // 1091721 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 1091721 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2,	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1947015	tttaataaaaaatcac[A/G]aaacctgcaaagaaac	A	G	NM_014361 // upstream // 1085132 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 1085132 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2,	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1894290	tgcattgctggattc[G/T]acacttgaagtccata	G	T	NM_014361 // upstream // 1036544 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 1036544 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2,	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2014309	gatttggcccactcq[A/G]acttcattcgtatta	A	G	NM_014361 // upstream // 987416 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 987416 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1840373	tagcattctgacagag[A/G]acttaagcagagatgt	A	G	NM_014361 // upstream // 757100 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 757100 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1943347	ttggttataaattctg[A/C]actttcgtgaattatt	A	C	NM_014361 // upstream // 744447 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 744447 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2014336	gagttgtcagtcgacat[C/T]taaatgaaaagaagga	C	T	NM_014361 // upstream // 743861 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 743861 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2101116	agatcagcaaacctaa[A/C]ctcaggccaaagaa	A	C	NM_014361 // upstream // 736896 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA /// NM_175566 // upstream // 736896 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1662090	tccacacttataaatgcagtagtta[C/T]aggcttggtaatgagat catgaat	C	T	NM_014361 // intron // 0 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // intron // 0 // Hs.234790 // CNTN5 // 53942 // contactin 5	CNTN5	CNTN5, , rs1940484, contactin 5 ,q22.1
SNP_A-1650620	ccctgccacctgttttttcttctcc[C/T]gaatgcatttactgtgttact ctg	C	T	NM_014361 // intron // 0 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // intron // 0 // Hs.234790 // CNTN5 // 53942 // contactin 5	CNTN5	CNTN5, , rs726533, contactin 5 ,q22.1
SNP_A-1683272	gtgtcctctcttctaagctccaaaa[C/T]aactgtagtctcaagatg aagttac	C	T	NM_014361 // intron // 0 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_175566 // intron // 0 // Hs.234790 // CNTN5 // 53942 // contactin 5	CNTN5	CNTN5, , rs4600174, contactin 5 ,q22.1
SNP_A-1837328	tacttcaacaatgtga[A/G]ctctagctgccgccaa	A	G	NM_014361 // upstream // 351043 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 351043 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2253674	cttcttttagtaggca[A/G]gttatcctgaaaatta	A	G	NM_014361 // upstream // 197788 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 197788 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2014404	aataaaatctttccta[C/G]agtttggcacaatca	C	G	NM_014361 // upstream // 197090 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 197090 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1940049	ttgcagctgaaaaagc[A/G]caaagtagaggaactc	A	G	NM_014361 // upstream // 144888 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 144888 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1956230	tttgtgtactacacac[A/T]ctcgttgcaactact	A	T	NM_014361 // upstream // 125161 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // upstream // 125161 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, m	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1944354	ttgtcctttttgttc[C/G]actgatgtcctattca	C	G	NM_014361 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, mRNA. /// ENST0	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1946376	tttaaacacctctcac[A/G]caaaatttaataataa	A	G	NM_014361 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, mRNA. /// ENST0	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-1856312	tcacacaatgctggaa[A/C]tcctctaatatttttat	A	C	NM_014361 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, mRNA. /// ENST0	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1
SNP_A-2014481	tgagcctcactaccag[C/G]atttctgggtcaccag	C	G	NM_014361 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA. /// NM_175566 // intron // 0 // Hs.268707 // CNTN5 // 53942 // Homo sapiens contactin 5 (CNTN5), transcript variant 2, mRNA. /// ENST0	CNTN5	CNTN5, Homo sapiens contactin 5 (CNTN5), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1688832	acatatattgaacaccatggcatca[C/G]agtgatatatctccaatttc agtctaa	C	G	NM_014361 // downstream // 232318 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_152432 // upstream // 370790 // - // - // - /// NM_175566 // downstream // 232318 // Hs.234790 // CNTN5 // 53942 // contactin 5	CNTN5	CNTN5 , rs661134, contactin 5 ,q22.1
SNP_A-2014541	acaggatctgctatga[A/G]agaaatggaaaggagt	A	G	ENST00000298824 // intron // 0 // --- // --- // ---	-	q22.1
SNP_A-1682724	aacctgtcctttgacgctttgaagc[C/T]aaacattgacttctttctc tagct	C	T	NM_014361 // downstream // 510511 // Hs.234790 // CNTN5 // 53942 // contactin 5 /// NM_152432 // upstream // 92597 // - // - // - /// NM_175566 // downstream // 510511 // Hs.234790 // CNTN5 // 53942 // contactin 5	CNTN5	CNTN5 , rs1074544, contactin 5 ,q22.1
SNP_A-2303441	gctatttttctgaaac[A/G]cacaccatttttataat	A	G	ENST00000298824 // downstream // 15452 // --- // --- // --- /// ENST00000298815 // upstream // 8067 // --- // --- // ---	-	q22.1
SNP_A-2149882	atgtcacaccagctgg[C/T]aaaggagaaaatgtttt	C	T	NM_032021 // downstream // 9783 // Hs.44004 // AD031 // 83935 // Homo sapiens AD031 protein (AD031), mRNA. /// NM_000926 // downstream // 34655 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// ENST00000303130 // downstrea	AD031	AD031, Homo sapiens AD031 protein (AD031), q22.1
SNP_A-1684032	aggtctaaaatgtgtacatttataa[A/G]tcatatactaatgagtcac atctca	A	G	NM_000926 // downstream // 28397 // Hs.2905 // PGR // 5241 // progesterone receptor /// NM_032021 // downstream // 16041 // Hs.44004 // AD031 // 83935 // AD031 protein	PGR	PGR , rs521744, progesterone receptor ,q22.1
SNP_A-2029133	aaagaacaaaacacctca[A/G]agaagatttaacaacc	A	G	NM_000926 // intron // 0 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// ENST00000325455 // intron // 0 // --- // --- // --- /// ENST00000263463 // intron // 0 // --- // --- // --- /// ENST00000309109 // in	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-1841952	tagggaaaggaggaatat[C/T]acaaacgtttggaaga	C	T	NM_000926 // upstream // 51556 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 269556 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, mem	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2014580	aatagaggaaattaa[A/G]agagtgaatatttgca	A	G	NM_000926 // upstream // 96865 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 224247 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, mem	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-1921085	ttacagtaggtattaa[C/T]tgttcagcatcttaag	C	T	NM_000926 // upstream // 113264 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 207848 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, me	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2230729	ctatgacaatatctga[A/G]agaatgaatggatacc	A	G	NM_000926 // upstream // 144408 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 176704 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, me	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-1896255	tgcgtcttggtttcta[A/C]tacaggaagtgacatt	A	C	NM_000926 // upstream // 170421 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 150691 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, me	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-1646346	ccctgtaaatgtaattgcctaacaa[G/T]attagttgccattagtaa atgagc	G	T	NM_000926 // upstream // 147632 // Hs.2905 // PGR // 5241 // progesterone receptor /// NM_004621 // downstream // 173486 // Hs.159003 // TRPC6 // 7225 // transient receptor potential cation channel, subfamily C, member 6	PGR	PGR , rs10501976, progesterone receptor ,q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805864	gtccctgacttccaga[C/T]ggtatctctggaccag	C	T	NM_000926 // upstream // 189911 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 131201 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, me	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2087519	actgcctgcagatgcat[C/T]tcattacttcctacct	C	T	NM_000926 // upstream // 193619 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 127493 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, me	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2014591	ttaaataagggaagaat[C/T]agctcaagatgagatg	C	T	NM_000926 // upstream // 207775 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 113337 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, me	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2308403	gcttgttcctgttaga[A/T]aattacatatatcagg	A	T	NM_000926 // upstream // 233942 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 87170 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, mem	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2281542	gagtccatgttcaaca[A/G]cctcattttggtcaga	A	G	NM_000926 // upstream // 242389 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 78723 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, mem	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-1733876	agaatttaaaaggaacacatgacaa[C/T]atattgaggcatcaa atgtagata	C	T	NM_000926 // upstream // 224989 // Hs.2905 // PGR // 5241 // progesterone receptor /// NM_004621 // downstream // 96129 // Hs.159003 // TRPC6 // 7225 // transient receptor potential cation channel, subfamily C, member 6	PGR	PGR , rs10501978, progesterone receptor , q22.1
SNP_A-2072827	acagctggcttctcca[A/C]catcctgggttcctta	A	C	NM_000926 // upstream // 298932 // Hs.368072 // PGR // 5241 // Homo sapiens progesterone receptor (PGR), mRNA. /// NM_004621 // downstream // 22180 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, mem	PGR	PGR, Homo sapiens progesterone receptor (PGR), q22.1
SNP_A-2312203	ggacagcttttccggt[A/G]caaagaaagcagaaaa	A	G	NM_004621 // upstream // 37971 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), mRNA. /// ENST00000344327 // upstream // 37971 // — // — // — /// ENST00000360497 // upst	TRPC6	TRPC6, Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), q22.1
SNP_A-2276875	gagatatcttggtata[C/T]gccctttcaacctctc	C	T	NM_004621 // upstream // 42737 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), mRNA. /// ENST00000344327 // upstream // 42737 // — // — // — /// ENST00000360497 // upst	TRPC6	TRPC6, Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), q22.1
SNP_A-2014625	gaataatatagatggt[C/G]atttaggtaaagaagt	C	G	NM_004621 // upstream // 85025 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), mRNA. /// ENST00000344327 // upstream // 85025 // — // — // — /// ENST00000360497 // upst	TRPC6	TRPC6, Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), q22.1
SNP_A-1884817	tgaatccacgaccaca[A/C]agaaaaacgcagaact	A	C	NM_004621 // upstream // 109874 // Hs.159003 // TRPC6 // 7225 // Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), mRNA. /// ENST00000344327 // upstream // 109874 // — // — // — /// ENST00000360497 // up	TRPC6	TRPC6, Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2155134	attcagatactgagaa[A/C]cttagagaaaatccc	A	C	NM_002423 // intron // 0 // Hs.2256 // MMP7 // 4316 // Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA. /// ENST00000260227 // intron // 0 // --- // --- // ---	MMP7	MMP7, Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), q22.2
SNP_A-1888621	tgaggcattgtactga[C/G]agagtggtgtagcaag	C	G	NM_022122 // upstream // 3940 // Hs.534479 // MMP27 // 64066 // Homo sapiens matrix metalloproteinase 27 (MMP27), mRNA. /// NM_002424 // downstream // 2981 // Hs.161839 // MMP8 // 4317 // Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (M	MMP27	MMP27, Homo sapiens matrix metalloproteinase 27 (MMP27), q22.2
SNP_A-2198859	catttgaaatttttgc[A/T]acctcatgatactaag	A	T	NM_002424 // intron // 0 // Hs.161839 // MMP8 // 4317 // Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), mRNA. /// ENST00000236826 // intron // 0 // --- // --- // ---	MMP8	MMP8, Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), q22.2
SNP_A-2234223	ctcatttctaagcaaa[G/T]tcatcgcccaaacaaa	G	T	ENST00000299828 // intron // 0 // --- // --- // ---	-	q22.3
SNP_A-1864385	tccactgatttttcagd[A/G]aagtatatatttggaa	A	G	NM_033135 // downstream // 693083 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 693083 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1704095	ctagcatgtaggaaaactccaccc[G/T]aatttgaattgtcccat gtaacag	G	T	AK093336 // upstream // 503732 // Hs.146775 // - // - // Hypothetical protein mRNA, complete cds /// NM_024606 // downstream // 53243 // - // // - // - /// NM_025208 // downstream // 374325 // Hs.112885 // PDGFD // 80310 // platelet derived growth fact	-	-, rs1007349, Hypothetical protein mRNA, complete cds, q22.3
SNP_A-1862535	tcattaagcccatcca[C/T]aactttataactcagt	C	T	NM_033135 // downstream // 246793 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 246793 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1897141	tgctcgcaggttatag[A/G]agagacataagtaggc	A	G	NM_033135 // downstream // 223041 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 223041 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1797311	ggttgtaggatgtggg[A/G]aataggtgagtctaca	A	G	NM_033135 // downstream // 222863 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 222863 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2124141	agttagcatattatca[A/T]tccacagtgcaggaaa	A	T	NM_033135 // downstream // 203558 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 203558 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1744285	gacctgaaaccataaagacataga[A/C]gataacatcagaaa aaaccctag	A	C	AK093336 // upstream // 349663 // Hs.146775 // - // - // Hypothetical protein mRNA, complete cds /// NM_024606 // downstream // 207312 // - // - // - /// NM_025208 // downstream // 220256 // Hs.112885 // PDGFD // 80310 // platelet derived growth fac	-	-, rs1917450, Hypothetical protein mRNA, complete cds, q22.3
SNP_A-2063893	aattatacataacacd[C/T]tgtagcccgtggct	C	T	NM_033135 // downstream // 169540 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 169540 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123055	agtgggtggctatg[A/G]aaaggaaaaatgagtc	A	G	NM_033135 // downstream // 113862 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 113862 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived gr	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1860136	tcagtatctcatgta[C/G]aaagcagtagtcatat	C	G	NM_033135 // downstream // 82985 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 82985 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived grow	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2014857	gtatgtgttctaaaaa[A/G]aatgaatgtatccatg	A	G	NM_033135 // downstream // 64389 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // downstream // 64389 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived grow	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2014884	actggcctgaaattcg[A/G]aagactcagtagtttg	A	G	NM_033135 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDG	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2036040	aaattacacagcaaca[A/T]cgaggacaacaggcaa	A	T	NM_033135 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDG	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2224865	cgtgcactcagaaatc[A/G]atgtataacatttgac	A	G	NM_033135 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDG	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2014888	ggtattattgtctatg[C/T]ataccaatgtggctga	C	T	NM_033135 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // intron // 0 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDG	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-1716749	aaacgattcaagggcagttttcac[A/G]gcaccttgatgaaggtg gaacaaag	A	G	NM_025208 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D /// NM_033135 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D	PDGFD	PDGFD, rs361262, platelet derived growth factor D ,q22.3
SNP_A-1655769	aataatgctacagatccctagaac[A/G]gactagaaaatgtattc agcatttt	A	G	NM_025208 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D /// NM_033135 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D	PDGFD	PDGFD, rs361263, platelet derived growth factor D ,q22.3
SNP_A-1684296	tatattagtggcatgtcagttccca[C/T]gattgtacacatagttca aacatc	C	T	NM_025208 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D /// NM_033135 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D	PDGFD	PDGFD, rs361266, platelet derived growth factor D q22.3
SNP_A-1658652	gcgagtttgcagttacatgctgag[A/G]actgcatatttttctgttttgt tta	A	G	NM_025208 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D /// NM_033135 // intron // 0 // Hs.112885 // PDGFD // 80310 // platelet derived growth factor D	PDGFD	PDGFD, rs361308, platelet derived growth factor D q22.3
SNP_A-1834112	tacatcctagacctaa[G/T]gtacaagctgaaacta	G	T	NM_033135 // upstream // 105638 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // upstream // 105638 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864215	tccaccctatatttccq[C/T]gctttctctctgacca	C	T	NM_033135 // upstream // 159394 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // upstream // 159394 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2241026	ctgagcaactggctaa[A/C]ctctatctgcacccgg	A	C	NM_033135 // upstream // 687283 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, mRNA. /// NM_025208 // upstream // 687283 // Hs.352298 // PDGFD // 80310 // Homo sapiens platelet derived growth	PDGFD	PDGFD, Homo sapiens platelet derived growth factor D (PDGFD), transcript variant 2, q22.3
SNP_A-2036712	aaattgttcaaacctc[A/T]ctatacaaaataaact	A	T	NM_004347 // intron // 0 // Hs.213327 // CASP5 // 838 // Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), mRNA. /// ENST00000260315 // intron // 0 // — // — // —	CASP5	CASP5, Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), q22.3
SNP_A-2014985	tgtgtgagaaaactcq[A/G]gaaatttctaaatgca	A	G	NM_004347 // upstream // 13858 // Hs.213327 // CASP5 // 838 // Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), mRNA. /// NM_033295 // downstream // 2682 // Hs.2490 // CASP1 // 834 // Homo sapiens caspase 1, apoptosis-related cysteine	CASP5	CASP5, Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), q22.3
SNP_A-2235382	ctcccgtcatcttac[C/G]cttgattggagacag	C	G	NM_004347 // upstream // 15498 // Hs.213327 // CASP5 // 838 // Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), mRNA. /// NM_033295 // downstream // 1042 // Hs.2490 // CASP1 // 834 // Homo sapiens caspase 1, apoptosis-related cysteine	CASP5	CASP5, Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), q22.3
SNP_A-2136349	atcacactacactgtc[A/G]ctgtcataaactagctg	A	G	NM_004347 // upstream // 16177 // Hs.213327 // CASP5 // 838 // Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), mRNA. /// NM_033295 // downstream // 363 // Hs.2490 // CASP1 // 834 // Homo sapiens caspase 1, apoptosis-related cysteine p	CASP5	CASP5, Homo sapiens caspase 5, apoptosis-related cysteine protease (CASP5), q22.3
SNP_A-2258770	ctttgtccagccaca[G/T]ggttctttagcacatt	G	T	NM_052889 // intron // 0 // Hs.348365 // COPI // 114769 // Homo sapiens CARD only protein (COP), mRNA. /// NM_033293 // intron // 0 // Hs.2490 // CASP1 // 834 // Homo sapiens caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	COPI	COPI, Homo sapiens CARD only protein (COP), q22.3
SNP_A-1679210	cactgcctgaagagctgcaagagac[A/C]aggaaatatcatgaa cagtggtatcc	A	C	NM_001223 // intron // 0 // Hs.2490 // CASP1 // 834 // caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) /// NM_033292 // intron // 0 // Hs.2490 // CASP1 // 834 // caspase 1, apoptosis-related cysteine protease (interleukin	CASP1	CASP1 , rs1503391, caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) q22.3
SNP_A-1693214	tctatttttatattattctagtttat[C/T]gtattcaatatctctgtcctcccat	C	T	NM_001223 // intron // 0 // Hs.2490 // CASP1 // 834 // caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) /// NM_033292 // intron // 0 // Hs.2490 // CASP1 // 834 // caspase 1, apoptosis-related cysteine protease (interleukin	CASP1	CASP1 , rs6922897, caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) q22.3
SNP_A-1737267	aaactagaataaatataaaatagaa[C/T]gatgaatgctaaaatc atggtgtgc	C	T	NM_001223 // intron // 0 // Hs.2490 // CASP1 // 834 // caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) /// NM_033292 // intron // 0 // Hs.2490 // CASP1 // 834 // caspase 1, apoptosis-related cysteine protease (interleukin	CASP1	CASP1 , rs6922914, caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) q22.3
SNP_A-1952635	tttctggagaagtgca[A/C]atggatcgctcttcat	A	C	NM_021571 // upstream // 8114 // Hs.56279 // ICEBERG // 59082 // Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), mRNA. /// NM_000829 // upstream // 462883 // Hs.503743 // GRIA4 // 2893 // Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4), m	ICEBERG	ICEBERG, Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839644	tagatgacaaataaaaa[A/G]tgtgctgtatctgaat	A	G	NM_021571 // upstream // 262455 // Hs.56279 // ICEBERG // 59082 // Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), mRNA. /// NM_000829 // upstream // 208542 // Hs.503743 // GRIA4 // 2893 // Homo sapiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4),	ICEBERG	ICEBERG, Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), q22.3
SNP_A-2127359	ataaattgtctttta[A/C]atgtcagaactaggaa	A	C	NM_021571 // upstream // 331815 // Hs.56279 // ICEBERG // 59082 // Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), mRNA. /// NM_000829 // upstream // 139182 // Hs.503743 // GRIA4 // 2893 // Homo sapiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4),	ICEBERG	ICEBERG, Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), q22.3
SNP_A-2090353	acttggaacagtcaaa[C/T]gaaattatacttagct	C	T	NM_021571 // upstream // 431613 // Hs.56279 // ICEBERG // 59082 // Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), mRNA. /// NM_000829 // upstream // 39384 // Hs.503743 // GRIA4 // 2893 // Homo sapiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4),	ICEBERG	ICEBERG, Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), q22.3
SNP_A-1836288	tactattgccttaa[C/T]attggagcaatcgaca	C	T	NM_021571 // upstream // 450233 // Hs.56279 // ICEBERG // 59082 // Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), mRNA. /// NM_000829 // upstream // 20764 // Hs.503743 // GRIA4 // 2893 // Homo sapiens glutamate receptor, ionotrophic, AMPA 4 (GRIA4),	ICEBERG	ICEBERG, Homo sapiens ICEBERG caspase-1 inhibitor (ICEBERG), q22.3
SNP_A-2163821	caaaacactatacata[C/G]aaatagtaaacgcata	C	G	NM_015423 // downstream // 2055 // Hs.524009 // AASDHPPT // 60496 // Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), mRNA. /// NM_000855 // downstream // 586436 // Hs.503756 // GUCY1A2 // 2977 // Homo sapie	AASDHPPT	AASDHPPT, Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), q22.3
SNP_A-2015089	aaagaccaagacaaac[C/T]catcttcacagagaaa	C	T	NM_015423 // downstream // 292978 // Hs.524009 // AASDHPPT // 60496 // Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), mRNA. /// NM_000855 // downstream // 295513 // Hs.503756 // GUCY1A2 // 2977 // Homo sap	AASDHPPT	AASDHPPT, Homo sapiens aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT), q22.3
SNP_A-2242201	ctgcaaatttaggcta[C/T]ctgatacagcctagtc	C	T	NM_000855 // intron // 0 // Hs.503756 // GUCY1A2 // 2977 // Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// ENST00000347596 // intron // 0 // — // — // — /// ENST00000282249 // intron // 0 // — // — // — // —	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2314039	ggagcttgtgattctc[A/T]aataagcttctgagat	A	T	NM_000855 // intron // 0 // Hs.503756 // GUCY1A2 // 2977 // Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// ENST00000347596 // intron // 0 // — // — // — /// ENST00000282249 // intron // 0 // — // — // — // —	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2015115	aaagaaactcgttcca[A/G]catttcacagcttt	A	G	NM_000855 // intron // 0 // Hs.503756 // GUCY1A2 // 2977 // Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// ENST00000347596 // intron // 0 // — // — // — /// ENST00000282249 // intron // 0 // — // — // — // —	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2301044	gccttatagatgaaag[C/T]accaggtatcagtagg	C	T	NM_000855 // intron // 0 // Hs.503756 // GUCY1A2 // 2977 // Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// ENST00000347596 // intron // 0 // — // — // — /// ENST00000282249 // intron // 0 // — // — // — // —	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-1704505	cagtcctatccatgatattaacaca[A/G]caatgcttattctggcaa aaaaaaa	A	G	NM_000855 // intron // 0 // Hs.178295 // GUCY1A2 // 2977 // guanylate cyclase 1, soluble, alpha 2	GUCY1A2	GUCY1A2, rs3133355, guanylate cyclase 1, soluble, alpha 2 q22.3
SNP_A-1740623	ctgaatgcccctgttattattaaca[A/C]cttattctacacttgaaggagctg	A	C	NM_000855 // upstream // 253966 // Hs.178295 // GUCY1A2 // 2977 // guanylate cyclase 1, soluble, alpha 2 /// NM_152434 // downstream // 53946 // Hs.24380 // CWF19L2 // 143884 // CWF19-like 2, cell cycle control (S. pombe)	GUCY1A2	GUCY1A2, rs1388171, guanylate cyclase 1, soluble, alpha 2 q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2269477	gacaaaaggatcaaaac[C/T]gttccaagtcactta	C	T	NM_000855 /// upstream /// 304012 /// Hs.503756 /// GUCY1A2 /// 2977 /// Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), mRNA. /// NM_152434 /// downstream /// 3900 /// Hs.212140 /// CWF19L2 /// 143884 /// Homo sapiens CWF19-like 2, cell cycle control (	GUCY1A2	GUCY1A2, Homo sapiens guanylate cyclase 1, soluble, alpha 2 (GUCY1A2), q22.3
SNP_A-2166098	caaatagaattaggg[A/G]gtcttctgtacaaata	A	G	NM_138775 /// intron /// 0 /// Hs.503763 /// LOC91801 /// 91801 /// Homo sapiens hypothetical protein BC015183 (LOC91801), mRNA. /// ENST00000260318 /// intron /// 0 /// --- /// --- /// ---	LOC91801	LOC91801, Homo sapiens hypothetical protein BC015183 (LOC91801), q22.3
SNP_A-1727090	aaaattgtagatggacctctaaatta[C/T]atttatctttccaggga gagcaa	C	T	NM_138775 /// intron /// 0 /// Hs.91559 /// LOC91801 /// 91801 /// hypothetical protein BC015183	LOC91801	LOC91801 , rs10502094, hypothetical protein BC015183,q22.3
SNP_A-2176765	caccctccgaaggttd[A/G]aggctatttgtgttcg	A	G	NM_017515 /// downstream /// 78833 /// Hs.524014 /// SLC35F2 /// 54733 /// Homo sapiens solute carrier family 35, member F2 (SLC35F2), mRNA. /// ENST00000305991 /// upstream /// 103 /// --- /// --- /// --- /// ENST00000354413 /// upstream /// 60244 /// --- /// -	SLC35F2	SLC35F2, Homo sapiens solute carrier family 35, member F2 (SLC35F2), q22.3
SNP_A-2048689	aagccactttcatgal[C/T]gtagcatagacttcct	C	T	NM_015065 /// upstream /// 31181 /// Hs.269591 /// SLAC2-B /// 23086 /// Homo sapiens SLAC2-B (SLAC2-B), mRNA. /// NM_015065 /// upstream /// 31076 /// Hs.269591 /// SLAC2-B /// 23086 /// Homo sapiens SLAC2-B (SLAC2-B), mRNA. /// NM_004398 /// upstream /// 40275 /// Hs.	SLAC2-B	SLAC2-B, Homo sapiens SLAC2-B (SLAC2-B), q22.3
SNP_A-1685650	tagtttataaattgtaatcctaatc[C/T]ataatgtgatgaaaatggtc aatga	C	T	NM_004398 /// intron /// 0 /// Hs.41706 /// DDX10 /// 1662 /// DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	DDX10	DDX10 , rs8998972, DEAD (Asp-Glu-Ala-Asp) box polypeptide 10,q22.3
SNP_A-2233438	ctcagtagtcaaaata[C/T]ctgtagtaggaagcca	C	T	NM_004398 /// intron /// 0 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// ENST00000322536 /// intron /// 0 /// --- /// --- /// ---	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2021751	aaaaacaggacaacaa[A/T]aagtcaccatagcctt	A	T	NM_004398 /// downstream /// 78289 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 /// upstream /// 402991 /// Hs.172982 /// LOC399947 /// 399947 /// Homo sapiens similar to expressed sequence A	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1890873	tgatgcgtatccaaca[A/T]acacttgcaaatgtac	A	T	NM_004398 /// downstream /// 152753 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 /// upstream /// 328527 /// Hs.172982 /// LOC399947 /// 399947 /// Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1813328	gtggtggaaagagcac[C/T]acactgagattacaaa	C	T	NM_004398 /// downstream /// 191890 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 /// upstream /// 289390 /// Hs.172982 /// LOC399947 /// 399947 /// Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2259737	gaaaagaccattatca[A/T]caagaagctgggaag	A	T	NM_004398 /// downstream /// 231028 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 /// upstream /// 250252 /// Hs.172982 /// LOC399947 /// 399947 /// Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1818466	gttcttggcttcatca[C/T]ggaaagaattcaaagg	C	T	NM_004398 /// downstream /// 243284 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 /// upstream /// 237996 /// Hs.172982 /// LOC399947 /// 399947 /// Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2218037	cctgccaggagtaacc[A/G]aggaagccaaccctga	A	G	NM_004398 /// downstream /// 307653 /// Hs.525115 /// DDX10 /// 1662 /// Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 /// upstream /// 173627 /// Hs.172982 /// LOC399947 /// 399947 /// Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246661	ctgtaatggtctctga[G/T]taggcatttctgctag	G	T	NM_004398 // downstream // 323336 // Hs.525115 // DDX10 // 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream // 157944 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-1818410	gttcttcattacagac[A/C]ctggcaacaagcctaa	A	C	NM_004398 // downstream // 323491 // Hs.525115 // DDX10 // 1662 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA. /// NM_207645 // upstream // 157789 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence	DDX10	DDX10, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), q22.3
SNP_A-2035972	aaattaacagaggttal[A/C]actgaggaagagaaat	A	C	NM_207645 // downstream // 179140 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 179140 // --- // --- // --- /// ENST00000278590 // upstream // 5310	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-2092951	agaacaatgtgaaaca[A/G]gaagtgctagagatg	A	G	NM_207645 // downstream // 336972 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 336972 // --- // --- // --- /// ENST00000278590 // upstream // 3731	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-2016768	caatcatcaccaatc[A/G]acaaatttgacctgaa	A	G	NM_207645 // downstream // 573641 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 573641 // --- // --- // --- /// ENST00000278590 // upstream // 1365	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-2083466	actaaggaaacttata[C/T]agagtgctgcagcaat	C	T	NM_207645 // downstream // 618958 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 618958 // --- // --- // --- /// ENST00000278590 // upstream // 9120	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-1958512	ttttcgaaatggtaga[C/T]gaacactgaactcaaa	C	T	NM_207645 // downstream // 675808 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 675808 // --- // --- // --- /// ENST00000278590 // upstream // 3435	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-1896663	tgctataacaaaactc[A/G]aagcatctaacaattc	A	G	NM_207645 // downstream // 683525 // Hs.172982 // LOC399947 // 399947 // Homo sapiens similar to expressed sequence AI593442 (LOC399947), mRNA. /// ENST00000327419 // downstream // 683525 // --- // --- // --- /// ENST00000278590 // upstream // 2663	LOC399947	LOC399947, Homo sapiens similar to expressed sequence AI593442 (LOC399947), q22.3
SNP_A-2054115	aagttcatacagcttc[A/C]caaagattagatataa	A	C	ENST00000278590 // intron // 0 /// --- /// --- /// ---	-	q22.3
SNP_A-1655211	gaaggaattggaaagcaataaaaac[C/T]gaactagtccaaga aggctttatgg	C	T	AB051513 // upstream // 28360 // Hs.376289 // KIAA1726 // 85463 // KIAA1726 protein /// BC035798 // downstream // 698864 // Hs.172982 // LOC399947 // 399947 // similar to expressed sequence AI593442	KIAA1726	KIAA1726 , rs1789369, KIAA1726 protein ,q22.3
SNP_A-1751767	taaaatccatccaaatgacttaaaa[A/G]aggaagtagaaatgg aataaactta	A	G	AB051513 // upstream // 27703 // Hs.376289 // KIAA1726 // 85463 // KIAA1726 protein /// BC035798 // downstream // 699521 // Hs.172982 // LOC399947 // 399947 // similar to expressed sequence AI593442	KIAA1726	KIAA1726 , rs746463, KIAA1726 protein ,q22.3
SNP_A-2107142	agcggtcctgcaggat[C/G]aaagtagactaaagca	C	G	NM_020809 // upstream // 27423 // Hs.6136 // ARHGAP20 // 57569 // Homo sapiens Rho GTPase activating protein 20 (ARHGAP20), mRNA. /// ENST00000260283 // upstream // 27423 // --- // --- // --- /// ENST00000357139 // upstream // 26962 // --- // ---	ARHGAP20	ARHGAP20, Homo sapiens Rho GTPase activating protein 20 (ARHGAP20), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044911	aagaacactccattta[C/T]caaagcaataaccaat	C	T	NM_020809 // upstream // 28362 // Hs.6136 // ARHGAP20 // 57569 // Homo sapiens Rho GTPase activating protein 20 (ARHGAP20), mRNA. /// ENST00000260283 // upstream // 28362 // — // — // — /// ENST00000357139 // upstream // 27901 // — // — // —	ARHGAP20	ARHGAP20, Homo sapiens Rho GTPase activating protein 20 (ARHGAP20), q23.1
SNP_A-1791275	gggtaagctactgcta[C/T]ctatttctgaggttat	C	T	NM_198498 // upstream // 306341 // Hs.298685 // MGC50104 // 341032 // Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), mRNA. /// ENST00000354861 // upstream // 160666 // — // — // — /// ENST00000280325 // upstream // 306341 // -	MGC50104	MGC50104, Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), q23.1
SNP_A-2174957	cacagggtgaccatgc[A/G]ctctgtggcttccctg	A	G	NM_198498 // upstream // 236312 // Hs.298685 // MGC50104 // 341032 // Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), mRNA. /// ENST00000354861 // upstream // 230695 // — // — // — /// ENST00000280325 // upstream // 236312 // -	MGC50104	MGC50104, Homo sapiens Similar to RIKEN cDNA 1810046K07 gene (MGC50104), q23.1
SNP_A-1708040	agggtcaatcatgatgtttctggt[A/G]tagggaagagtttggaat gcatcct	A	G	AB037812 // upstream // 541523 // Hs.6136 // ARHGAP20 // 57569 // Rho GTPase activating protein 20	ARHGAP20	ARHGAP20 , rs1986684, Rho GTPase activating protein 20,q23.1
SNP_A-2018065	tggacagagaatcccc[C/T]cggttaattcaattca	C	T	NM_207429 // upstream // 50743 // Hs.125166 // FLJ45803 // 399948 // Homo sapiens FLJ45803 protein (FLJ45803), mRNA. /// NM_006235 // downstream // 1703 // Hs.2407 // POU2AF1 // 5450 // Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRN	FLJ45803	FLJ45803, Homo sapiens FLJ45803 protein (FLJ45803), q23.1
SNP_A-2002240	taaatatcttctgcc[A/G]ctaatccaccctttat	A	G	NM_006235 // upstream // 50940 // Hs.2407 // POU2AF1 // 5450 // Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRNA. /// NM_017589 // downstream // 40002 // Hs.128180 // BTG4 // 54766 // Homo sapiens B-cell translocation gene 4 (BTG4).	POU2AF1	POU2AF1, Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), q23.1
SNP_A-2194050	catgacaatgcaccat[A/C]agcgttactattatg	A	C	NM_006235 // upstream // 53469 // Hs.2407 // POU2AF1 // 5450 // Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), mRNA. /// NM_017589 // downstream // 37473 // Hs.128180 // BTG4 // 54766 // Homo sapiens B-cell translocation gene 4 (BTG4).	POU2AF1	POU2AF1, Homo sapiens POU domain, class 2, associating factor 1 (POU2AF1), q23.1
SNP_A-1691974	gatgaagatatcatctttcaaacag[A/G]gaatcagaatcaccac ctgaggaag	A	G	NM_017589 // intron // 0 // Hs.128180 // BTG4 // 54766 // B-cell translocation gene 4	BTG4	BTG4, rs1113851, B-cell translocation gene 4,q23.1
SNP_A-2002241	cagtaaggtccccaac[C/T]atatacagtgttctaa	C	T	NM_207430 // intron // 0 // Hs.411600 // FLJ46266 // 399949 // Homo sapiens FLJ46266 protein (FLJ46266), mRNA. /// ENST00000332814 // intron // 0 // — // — // —	FLJ46266	FLJ46266, Homo sapiens FLJ46266 protein (FLJ46266), q23.1
SNP_A-1856645	tcacagtttaacatac[C/G]aagactttcactatct	C	G	NM_207430 // intron // 0 // Hs.411600 // FLJ46266 // 399949 // Homo sapiens FLJ46266 protein (FLJ46266), mRNA. /// ENST00000332814 // intron // 0 // — // — // —	FLJ46266	FLJ46266, Homo sapiens FLJ46266 protein (FLJ46266), q23.1
SNP_A-1756617	aaaaacagtattgttgtctcagtac[A/T]attagattaaaagagtac aggacta	A	T	AL136764 // upstream // 36296 // Hs.306864 // SIK2 // 23235 // salt-inducible serine/threonine kinase 2 /// NM_178834 // downstream // 5108 // Hs.317614 // LOC143903 // 143903 // layilin	SIK2	SIK2 , rs659529, salt-inducible serine,q23.1
SNP_A-1926089	ttatgttattgtttcca[A/G]ggtaactttttctctt	A	G	NM_015191 // upstream // 36296 // Hs.306864 // SIK2 // 23235 // salt-inducible serine/threonine kinase 2 /// NM_178834 // downstream // 5108 // Hs.317614 // LOC143903 // 143903 // layilin	SIK2	SIK2, rs659529, salt-inducible serine,q23.1
SNP_A-2128121	ataagctcccatatga[C/T]cggaaactgaagacat	C	T	NM_015191 // intron // 0 // Hs.269128 // SNF1LK2 // 23235 // Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // — // — // —	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine,q23.1
SNP_A-2187995	cagtcaagagataccc[G/T]aacagctggccttgg	G	T	NM_015191 // intron // 0 // Hs.269128 // SNF1LK2 // 23235 // Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // — // — // —	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine,q23.1
SNP_A-1850662	tattacagatttacca[C/T]gtgcgagctctattc	C	T	NM_015191 // intron // 0 // Hs.269128 // SNF1LK2 // 23235 // Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // — // — // —	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine,q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1903297	tggctttttctctgc[C/G]caagtgtggagagaaa	C	G	NM_015191 // intron // 0 // Hs.269128 // SNF1LK2 // 23235 // Homo sapiens salt-inducible serine/threonine kinase 2 (SIK2), mRNA. /// ENST00000304987 // intron // 0 // --- // --- // ---	SNF1LK2	SNF1LK2, Homo sapiens salt-inducible serine,q23.1
SNP_A-2267063	gaataacaatgttgca[C/T]attaacacatcttccc	C	T	NM_002716 // intron // 0 // Hs.546276 // PPP2R1B // 5519 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (PPP2R1B), transcript variant 1, mR /// NM_181699 // intron // 0 // Hs.546276 // PPP2R1B // 5519 // Ho	PPP2R1B	PPP2R1B, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (PPP2R1B), transcript variant 1, mR ,q23.1
SNP_A-1921781	ttactaatggattaga[C/T]gtgtggaacaaggcac	C	T	NM_002716 // intron // 0 // Hs.546276 // PPP2R1B // 5519 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (PPP2R1B), transcript variant 1, mR /// NM_181699 // intron // 0 // Hs.546276 // PPP2R1B // 5519 // Ho	PPP2R1B	PPP2R1B, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (PPP2R1B), transcript variant 1, mR ,q23.1
SNP_A-1718183	gaaaaattatgtccgtaactaaccaa[A/G]gggtgaattgtccatca cagcagtg	A	G	NM_002716 // upstream // 10829 // Hs.431156 // PPP2R1B // 5519 // protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /// NM_024740 // downstream // 9012 // Hs.120824 // DIBD1 // 79796 // disrupted in bipolar affective disorde	PPP2R1B	PPP2R1B , rs105502148, protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform ,q23.1
SNP_A-2308277	gctgggggaatgtgta[C/T]gagtctgctggtgctg	C	T	M17409 // upstream // 812323 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 812323 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2238739	ctcttaaggccttac[A/G]aggttggcagaagagt	A	G	M17409 // upstream // 625204 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 625204 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2285454	gatcttctgtttaagc[C/T]gaagcctgggaaaga	C	T	M17409 // upstream // 617271 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 617271 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2266734	gaagtgcttccttaaa[A/G]agttcaatatgaattg	A	G	M17409 // upstream // 615464 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 615464 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2019298	tcacctccaattccta[C/G]accaactacatagaat	C	G	M17409 // upstream // 226998 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 226998 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2019302	tagaatttttcacaaa[A/G]ctgaatggtattcatc	A	G	M17409 // upstream // 226963 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 226963 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-2139990	atctactgtgaatatc[A/T]ctagaacacaaaatag	A	T	M17409 // upstream // 226384 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 226384 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247894	ctgtgcaatattaagat[A/G]aatagctttcacaaac	A	G	M17409 // upstream // 226294 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 226294 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-2268149	gaatgaataaaggcta[C/T]ctacaagggctcaga	C	T	M17409 // upstream // 220151 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 220151 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-1668292	gtgtgtgtttgaattagtggtat[C/G]agaggctattgacttaat ttg	C	G	NM_000615 // intron // 0 // Hs.78792 // NCAM1 // 4684 // neural cell adhesion molecule 1	NCAM1	NCAM1, , rs7944570, neural cell adhesion molecule 1,q23.1
SNP_A-2030349	aaagcatgggctgaa[A/T]ggtttggagtcaaaat	A	T	M17409 // upstream // 194550 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 194550 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-1841583	taggatcctggttccc[C/T]gatcacatggtgaaac	C	T	M17409 // upstream // 179603 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 179603 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-2081900	accttgtggctcaaca[C/T]ggctgctacactccag	C	T	M17409 // upstream // 179536 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 179536 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-2019407	atatttgcataaacag[C/T]atagtatctagcagtt	C	T	M17409 // upstream // 179241 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 179241 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-2189086	cagttaagatttttcac[C/T]ggctactttgctccc	C	T	M17409 // upstream // 176024 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 176024 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-1814603	gtgtggatttgactca[C/T]actaaaccaaatctat	C	T	M17409 // upstream // 173883 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 173883 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1
SNP_A-1812077	gtggactctggaaaac[A/T]caagaaatatccattt	A	T	M17409 // upstream // 172754 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 172754 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. ,q23.1
SNP_A-1934006	ttctcacattagaagc[A/G]ctggcaagagatgttt	A	G	M17409 // upstream // 161049 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 161049 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end. q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2090194	acttgatgcgaaccaat[C/T]ggtagacccgctcatc	C	T	M17409 // upstream // 160794 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // upstream // 160794 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (NC	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end, q23.1
SNP_A-2019872	aacctctataatttca[C/T]gatctcagtatcaaat	C	T	M17409 // downstream // 46555 // Hs.503878 // NCAM1 // 4684 // Human neural cell adhesion molecule (N-CAM) mRNA, clone lambda-9.5, 3' end. /// NM_000615 // downstream // 32747 // Hs.503878 // NCAM1 // 4684 // Homo sapiens neural cell adhesion molecule 1 (	NCAM1	NCAM1, Human neural cell adhesion molecule (N-CAM) clone lambda-9.5, 3' end, q23.1
SNP_A-2203826	ccagaggctgcagaga[C/G]agtaacatggagaatt	C	G	NM_016574 // intron // 0 // Hs.73893 // DRD2 // 1813 // Homo sapiens dopamine receptor D2 (DRD2), transcript variant 2, mRNA. /// NM_000795 // intron // 0 // Hs.73893 // DRD2 // 1813 // Homo sapiens dopamine receptor D2 (DRD2), transcript variant 1, mRNA.	DRD2	DRD2, Homo sapiens dopamine receptor D2 (DRD2), transcript variant 2, q23.2
SNP_A-2314663	ggagtatataagagaa[A/G]aacattgctttgtgtg	A	G	NM_016574 // intron // 0 // Hs.73893 // DRD2 // 1813 // Homo sapiens dopamine receptor D2 (DRD2), transcript variant 2, mRNA. /// NM_000795 // intron // 0 // Hs.73893 // DRD2 // 1813 // Homo sapiens dopamine receptor D2 (DRD2), transcript variant 1, mRNA.	DRD2	DRD2, Homo sapiens dopamine receptor D2 (DRD2), transcript variant 2, q23.2
SNP_A-2020465	cacaggaaatgcataa[C/T]accagtgactcgaggc	C	T	NM_006006 // intron // 0 // Hs.171299 // ZBTB16 // 7704 // Homo sapiens zinc finger and BTB domain containing 16 (ZBTB16), mRNA. /// ENST00000335953 // intron // 0 // — // — /// ENST00000310883 // intron // 0 // — // — // —	ZBTB16	ZBTB16, Homo sapiens zinc finger and BTB domain containing 16 (ZBTB16), q23.2
SNP_A-1867761	tcctaagaaccaggga[A/G]atgaggagagcttcgg	A	G	NM_006006 // intron // 0 // Hs.171299 // ZBTB16 // 7704 // Homo sapiens zinc finger and BTB domain containing 16 (ZBTB16), mRNA. /// ENST00000335953 // intron // 0 // — // — /// ENST00000310883 // intron // 0 // — // — // —	ZBTB16	ZBTB16, Homo sapiens zinc finger and BTB domain containing 16 (ZBTB16), q23.2
SNP_A-2307129	gcttaaaattggatgc[A/G]gacccagaagattgta	A	G	NM_006006 // intron // 0 // Hs.171299 // ZBTB16 // 7704 // Homo sapiens zinc finger and BTB domain containing 16 (ZBTB16), mRNA. /// ENST00000335953 // intron // 0 // — // — /// ENST00000310883 // intron // 0 // — // — // —	ZBTB16	ZBTB16, Homo sapiens zinc finger and BTB domain containing 16 (ZBTB16), q23.2
SNP_A-1906593	tggtgtacagactgaa[C/G]accagatccagaaagt	C	G	NM_006169 // intron // 0 // Hs.503911 // NNMT // 4837 // Homo sapiens nicotinamide N-methyltransferase (NNMT), mRNA. /// ENST00000299964 // intron // 0 // — // — // —	NNMT	NNMT, Homo sapiens nicotinamide N-methyltransferase (NNMT), q23.2
SNP_A-1822598	gttttttctggttcaa[C/T]ggggggaaaattggtt	C	T	NM_006169 // intron // 0 // Hs.503911 // NNMT // 4837 // Homo sapiens nicotinamide N-methyltransferase (NNMT), mRNA. /// ENST00000299964 // intron // 0 // — // — // —	NNMT	NNMT, Homo sapiens nicotinamide N-methyltransferase (NNMT), q23.2
SNP_A-2186132	caggccatccaagtca[C/T]ataaggtggagtaatg	C	T	NM_016090 // downstream // 7570 // Hs.533736 // RBM7 // 10179 // Homo sapiens RNA binding motif protein 7 (RBM7), mRNA. /// NM_015523 // upstream // 22936 // Hs.7527 // DKFZP566E144 // 25996 // Homo sapiens small fragment nuclease (DKFZP566E144), mRNA. //	RBM7	RBM7, Homo sapiens RNA binding motif protein 7 (RBM7), q23.2
SNP_A-1693198	ggatggatatgaagagatactagaa[A/G]gtggaaatagtgagcc agcaatagtg	A	G	NM_016090 // intron // 0 // Hs.124177 // RBM7 // 10179 // RNA binding motif protein 7	RBM7	RBM7, rs536179, RNA binding motif protein 7, q23.2
SNP_A-1815484	gtgttttagggtgta[C/T]ataagtggaatgatta	C	T	NM_015523 // downstream // 15189 // Hs.7527 // DKFZP566E144 // 25996 // Homo sapiens small fragment nuclease (DKFZP566E144), mRNA. /// NM_152315 // downstream // 56248 // Hs.374720 // FAM55A // 120400 // Homo sapiens hypothetical protein MGC34290 (MGC3429	DKFZP566E144	DKFZP566E144, Homo sapiens small fragment nuclease (DKFZP566E144), q23.2
SNP_A-2234596	ctccagaaacttgcca[A/G]ctacccataaaggct	A	G	NM_017678 // upstream // 142636 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 435917 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946919	tttaaggatgtatcta[C/T]gccactctgaccttca	C	T	NM_017678 // upstream // 148565 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 429988 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2059044	aatccccaaggctgta[A/T]caagtatctctgctac	A	T	NM_017678 // upstream // 220417 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 358136 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2125623	agtttcctgtctggac[A/G]ctagaaataacaacaa	A	G	NM_017678 // upstream // 301794 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 276759 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2174658	cacagcactatgctca[C/T]tctccagtctttgccc	C	T	NM_017678 // upstream // 353131 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 225422 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2243636	ctgctccctgccacca[C/T]tctgagactactctcg	C	T	NM_017678 // upstream // 376937 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 201616 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.2
SNP_A-2084998	actcacagtgcgttaa[A/G]gatccaactgtgaaca	A	G	NM_017678 // upstream // 571936 // Hs.179100 // C11orf33 // 54827 // Homo sapiens chromosome 11 open reading frame 33 (C11orf33), mRNA. /// NM_014333 // downstream // 6617 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4	C11orf33	C11orf33, Homo sapiens chromosome 11 open reading frame 33 (C11orf33), q23.3
SNP_A-2002263	gccagaattaaccaga[A/G]gtctgaaaggccaatg	A	G	NM_014333 // intron // 0 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // intron // 0 // --- // --- // --- // --- /// ENST00000328158 // intron // 0 // --- // --- // --- // ---	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2020830	tggaccatgttaatca[A/G]atcagtttgttccaac	A	G	NM_014333 // upstream // 41740 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 41740 // --- // --- // --- // --- /// ENST00000328158 // upstream // 41740 // --- // --- /	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1907770	tgtaaggataggttaa[A/G]ctgccattcctaagca	A	G	NM_014333 // upstream // 57867 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 57867 // --- // --- // --- // --- /// ENST00000328158 // upstream // 57867 // --- // --- /	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1863136	tcatttatccaggcaa[A/T]gttactagggctatag	A	T	NM_014333 // upstream // 387065 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 387065 // --- // --- // --- // --- /// ENST00000328158 // upstream // 387065 // --- // –	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2020847	acttctgtgtgtttttc[A/G]aaagttcaggcgtgca	A	G	NM_014333 // upstream // 423552 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 423552 // --- // --- // --- // --- /// ENST00000328158 // upstream // 423552 // --- // –	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2143125	atgaattcaatacaag[A/G]agttaaacttacacaa	A	G	NM_014333 // upstream // 630358 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 630358 // -- // -- // -- /// ENST00000328158 // upstream // 630358 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1887739	tgagatactgggtgtg[A/G]aagtgttcttaagaa	A	G	NM_014333 // upstream // 782653 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 782653 // -- // -- // -- /// ENST00000328158 // upstream // 782653 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2091270	actttatttagata[C/T]gcgtgtacatatgcag	C	T	NM_014333 // upstream // 794034 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 794034 // -- // -- // -- /// ENST00000328158 // upstream // 794034 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2020863	attgaagcacataacd[A/G]aagtcatcagcacagg	A	G	NM_014333 // upstream // 929871 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 929871 // -- // -- // -- /// ENST00000328158 // upstream // 929871 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1802449	gtatccacattgtcta[C/T]actacctgcctgttag	C	T	NM_014333 // upstream // 939401 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 939401 // -- // -- // -- /// ENST00000328158 // upstream // 939401 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-1859678	tcaggctctcaaacaa[C/G]agtttcagaaaaaagt	C	G	NM_014333 // upstream // 961172 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 961172 // -- // -- // -- /// ENST00000328158 // upstream // 961172 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2020864	gcctgctagagtggta[C/T]agtcctgcagtgtcca	C	T	NM_014333 // upstream // 980748 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 980748 // -- // -- // -- /// ENST00000328158 // upstream // 980748 // -- // -	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2264225	gaactgtgggaaataa[C/T]cattgttaagtcatc	C	T	NM_014333 // upstream // 1130328 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 1130328 // -- // -- // -- /// ENST00000328158 // upstream // 1130328 // -- //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2283293	gatacaacccccataggt[A/T]atagacagcatgtact	A	T	NM_014333 // upstream // 1156367 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 1156367 // -- // -- // -- /// ENST00000328158 // upstream // 1156367 // -- //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2268472	gaatggcacctgttgc[A/G]cctaaggtcatgtgg	A	G	NM_014333 // upstream // 1185213 // Hs.370510 // IGSF4 // 23705 // Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), mRNA. /// ENST00000331581 // upstream // 1185213 // -- // -- // -- /// ENST00000328158 // upstream // 1185213 // -- //	IGSF4	IGSF4, Homo sapiens immunoglobulin superfamily, member 4 (IGSF4), q23.3
SNP_A-2020877	ctgtttcaggaactcad[A/G]cagtatcccagggtt	A	G	NM_032725 // downstream // 19067 // Hs.437341 // MGC13125 // 84811 // Homo sapiens hypothetical protein MGC13125 (MGC13125), mRNA. /// ENST00000357928 // downstream // 12859 // -- // -- // -- /// ENST00000260210 // downstream // 19067 // -- //	MGC13125	MGC13125, Homo sapiens hypothetical protein MGC13125 (MGC13125), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920968	ttacagacctgtaata[A/T]gctttccaacttccca	A	T	NM_032725 // downstream // 17182 // Hs.437341 // MGC13125 // 84811 // Homo sapiens hypothetical protein MGC13125 (MGC13125), mRNA. /// ENST00000357928 // downstream // 14744 // --- // --- // --- /// ENST00000260210 // downstream // 17182 // --- //	MGC13125	MGC13125, Homo sapiens hypothetical protein MGC13125 (MGC13125), q23.3
SNP_A-1650860	ataaaggatatctacaaaaaaccta[C/T]acagctacaacacatt taataaatg	C	T	NM_032725 // intron // 0 // Hs.39143 // MGC13125 // 84811 // hypothetical protein MGC13125	MGC13125	MGC13125, rs180324, hypothetical protein MGC13125,q23.3
SNP_A-2020887	ggctgccaacacattg[C/T]aatttgagaagcatcc	C	T	NM_025164 // intron // 0 // Hs.167451 // KIAA0999 // 23387 // Homo sapiens KIAA0999 protein (KIAA0999), mRNA. /// ENST00000292055 // intron // 0 // --- // --- // ---	KIAA0999	KIAA0999, Homo sapiens KIAA0999 protein (KIAA0999), q23.3
SNP_A-2020889	aatggttacaagcaa[C/T]aatggatcacctccaa	C	T	NM_025164 // intron // 0 // Hs.167451 // KIAA0999 // 23387 // Homo sapiens KIAA0999 protein (KIAA0999), mRNA. /// ENST00000292055 // intron // 0 // --- // --- // --- // ---	KIAA0999	KIAA0999, Homo sapiens KIAA0999 protein (KIAA0999), q23.3
SNP_A-1648206	aatgatttcagaagtcatttcaag[A/G]aatacgtccttaactggt agatta	A	G	AB023216 // intron // 0 // Hs.444909 // KIAA0999 // 23387 // KIAA0999 protein	KIAA0999	KIAA0999, rs10502222, KIAA0999 protein,q23.3
SNP_A-2002274	aaataaaattagggagac[A/G]gattctcatgttggtt	A	G	NM_002572 // downstream // 4484 // Hs.188501 // PAFAH1B2 // 5049 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa (PAFAH1B2), mRNA. /// NM_015996 // upstream // 6998 // Hs.410977 // SIDT2 // 51092 // Homo sapiens	PAFAH1B2	PAFAH1B2, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30kDa (PAFAH1B2), q23.3
SNP_A-2169941	caaggcgcacttttc[C/T]aggaagctttcctgga	C	T	NM_015996 // intron // 0 // Hs.410977 // SIDT2 // 51092 // Homo sapiens SID1 transmembrane family, member 2 (SIDT2), mRNA. /// ENST00000324225 // intron // 0 // --- // --- // --- // ENST00000278951 // intron // 0 // --- // --- // ---	SIDT2	SIDT2, Homo sapiens SID1 transmembrane family, member 2 (SIDT2), q23.3
SNP_A-1939006	ttgagtcttcagaacat[A/G]ggaatcaggaagtctt	A	G	NM_014956 // intron // 0 // Hs.504009 // Cep164 // 22897 // Homo sapiens KIAA1052 protein (Cep164), mRNA. /// ENST00000278935 // intron // 0 // - // --- // ---	Cep164	Cep164, Homo sapiens KIAA1052 protein (Cep164), q23.3
SNP_A-1868430	tcctcccacctcaaca[C/T]cggaaagttctgggtt	C	T	NM_020693 // intron // 0 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // --- // --- // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1856505	tcatcagatgcagagaa[G/T]cccacagagtgcatca	G	T	NM_020693 // intron // 0 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // --- // --- // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1694773	cccacacatggcagctgaggtaga[G/T]gctaagctttatagat tatctttgg	G	T	NM_020693 // intron // 0 // Hs.397966 // DSCAML1 // 57453 // Down syndrome cell adhesion molecule like 1	DSCAML1	DSCAML1, rs10502226, Down syndrome cell adhesion molecule like 1,q23.3
SNP_A-2232246	ctcaatgaattcaagc[G/T]gctggtggtagtgata	G	T	NM_020693 // intron // 0 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // --- // --- // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1861394	tcatcaggcttgtagat[C/T]ggtatgcagatgagc	C	T	NM_020693 // intron // 0 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // --- // --- // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1865665	tccattcagcaggtac[A/G]gagaatctgctttgag	A	G	NM_020693 // intron // 0 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // --- // --- // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-2077529	accacacactcagctcc[A/G]gattattgcagagctg	A	G	NM_020693 // intron // 0 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// ENST00000321322 // intron // 0 // --- // --- // ---	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2166493	caaatgcctggccagcc[A/G]gagatcaggaggcaaat	A	G	NM_020693 // upstream // 19146 // Hs.137183 // DSCAML1 // 57453 // Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), mRNA. /// NM_001680 // downstream // 3670 // Hs.413137 // FXYD2 // 486 // Homo sapiens FXYD domain containing ion transp	DSCAML1	DSCAML1, Homo sapiens Down syndrome cell adhesion molecule like 1 (DSCAML1), q23.3
SNP_A-1903169	tggcttccaaatgtcc[A/G]aacaggtttctctcc	A	G	NM_001558 // downstream // 3961 // Hs.504035 // IL10RA // 3587 // Homo sapiens interleukin 10 receptor, alpha (IL10RA), mRNA. /// NM_183247 // upstream // 71611 // Hs.161985 // TMPRSS4 // 56649 // Homo sapiens transmembrane protease, serine 4 (TMPRSS4), t	IL10RA	IL10RA, Homo sapiens interleukin 10 receptor, alpha (IL10RA), q23.3
SNP_A-2119668	agtattaaagaacagc[A/G]ctacactggatgtgac	A	G	NM_001558 // downstream // 36907 // Hs.504035 // IL10RA // 3587 // Homo sapiens interleukin 10 receptor, alpha (IL10RA), mRNA. /// NM_183247 // upstream // 38665 // Hs.161985 // TMPRSS4 // 56649 // Homo sapiens transmembrane protease, serine 4 (TMPRSS4),	IL10RA	IL10RA, Homo sapiens interleukin 10 receptor, alpha (IL10RA), q23.3
SNP_A-2302783	gctacttggtagcaca[C/T]agacttgggcctgagc	C	T	NM_183247 // intron // 0 // Hs.161985 // TMPRSS4 // 56649 // Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, mRNA. /// NM_019894 // intron // 0 // Hs.161985 // TMPRSS4 // 56649 // Homo sapiens transmembrane protease, serine	TMPRSS4	TMPRSS4, Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, q23.3
SNP_A-1872758	tctataagtgattaca[C/T]aaattttggaacgact	C	T	NM_183247 // intron // 0 // Hs.161985 // TMPRSS4 // 56649 // Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, mRNA. /// NM_019894 // intron // 0 // Hs.161985 // TMPRSS4 // 56649 // Homo sapiens transmembrane protease, serine	TMPRSS4	TMPRSS4, Homo sapiens transmembrane protease, serine 4 (TMPRSS4), transcript variant 2, q23.3
SNP_A-1938639	ttgagagtctcctca[C/T]ggtcaagaaaaaggga	C	T	NM_174934 // upstream // 8449 // Hs.65239 // SCN4B // 6330 // Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), mRNA. /// NM_004588 // downstream // 4218 // Hs.129783 // SCN2B // 6327 // Homo sapiens sodium channel, voltage-gated, type II	SCN4B	SCN4B, Homo sapiens sodium channel, voltage-gated, type IV, beta (SCN4B), q23.3
SNP_A-2226334	ctaagaagcctataca[A/G]tcatacttcagagata	A	G	NM_144765 // upstream // 22993 // Hs.116651 // EVA1 // 10205 // Homo sapiens epithelial V-like antigen 1 (EVA1), transcript variant 2, mRNA. /// NM_005797 // upstream // 22993 // Hs.116651 // EVA1 // 10205 // Homo sapiens epithelial V-like antigen 1 (EVA1	EVA1	EVA1, Homo sapiens epithelial V-like antigen 1 (EVA1), transcript variant 2, q23.3
SNP_A-1828181	taagaggaggagaagag[A/C]aaacggtcaggaggca	A	C	NM_000732 // intron // 0 // Hs.504048 // CD3D // 915 // Homo sapiens CD3D antigen, delta polypeptide (TiT3 complex) (CD3D), mRNA. /// ENST00000300692 // intron // 0 // — // — // —	CD3D	CD3D, Homo sapiens CD3D antigen, delta polypeptide (TiT3 complex) (CD3D), q23.3
SNP_A-1871988	tctaccaggatgacaa[A/G]cagtttggacatgc	A	G	NM_007180 // CDS // 0 // Hs.129712 // TREH // 11181 // Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), mRNA. /// ENST00000264029 // CDS // 0 // — // — // —	TREH	TREH, Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), q23.3
SNP_A-1910838	tgtctaccattgggac[C/T]ggagacacatctgta	C	T	NM_007180 // upstream // 29365 // Hs.129712 // TREH // 11181 // Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), mRNA. /// ENST00000264029 // upstream // 29365 // — // — // — // — /// ENST00000358732 // downstream // 14204 // –	TREH	TREH, Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), q23.3
SNP_A-2311076	ggaagtagaaaataaa[A/G]ggtacaggtcagtgt	A	G	NM_203285 // intron // 0 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // intron // 0 // Hs.334846 // PVRL1 // 5818 // Homo sapiens pol	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944791	ttgtgccctatcacc[C/T]gcaagctctgagatgc	C	T	NM_203285 // upstream // 44925 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 44925 // Hs.334846 // PVRL1 // 5818 // Homo	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-1794349	ggtccatctgatcaca[C/G]actagtgtcgttagcc	C	G	NM_203285 // upstream // 61882 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 61882 // Hs.334846 // PVRL1 // 5818 // Homo	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2204161	ccagcagcatgacctc[C/G]cttgacttctctgagc	C	G	NM_203285 // upstream // 74287 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 74287 // Hs.334846 // PVRL1 // 5818 // Homo	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2084691	actattctagtaggaa[A/C]ctgacicttaaaaact	A	C	NM_203285 // upstream // 84172 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 84172 // Hs.334846 // PVRL1 // 5818 // Homo	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2057714	aatatgtacttctcaa[C/T]gtattaccatgtaggc	C	T	NM_203285 // upstream // 172313 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 172313 // Hs.334846 // PVRL1 // 5818 // Ho	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2137176	atcaggtggaatggtc[C/T]ctcctcttctgacctc	C	T	NM_203285 // upstream // 250393 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 250393 // Hs.334846 // PVRL1 // 5818 // Ho	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2002300	cctgcctgccatagac[C/T]gagtgtgtgtcttccc	C	T	NM_203285 // upstream // 335499 // Hs.334846 // PVRL1 // 5818 // Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, mRNA. /// NM_002855 // upstream // 335499 // Hs.334846 // PVRL1 // 5818 // Ho	PVRL1	PVRL1, Homo sapiens poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin) (PVRL1), transcript variant 2, q23.3
SNP_A-2002305	cagtacaaagagtaac[A/C]ccaggcctacctggac	A	C	NM_014619 // upstream // 135799 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000359034 // downstream // 32486 // — // — // — // — /// ENST00000278723 // upstream // 135799 // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2115772	agggtgaactgaggag[A/G]ccacacttatatcagc	A	G	NM_014619 // upstream // 81012 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000359034 // downstream // 87273 // — // — // — // — /// ENST00000278723 // upstream // 81012 // — // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-1787843	gggacgttcgcatctc[A/G]ctttccctagagatgg	A	G	NM_014619 // upstream // 25400 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000359034 // downstream // 142885 // — // — // — // — /// ENST00000278723 // upstream // 25400 // — // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-1885224	tgaattgaaaacagta[C/G]atgccgagataaaatg	C	G	NM_014619 // intron // 0 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000278723 // intron // 0 // — // — // — // — // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2158049	attggaaatagactga[A/C]ggacaggacagagaac	A	C	NM_014619 // intron // 0 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000278723 // intron // 0 // — // — // — // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1812638	gtggctgctcagtgga[C/T]gatggaccttccaggg	C	T	NM_014619 // intron // 0 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000278723 // intron // 0 // — // — // — // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-1834490	taccaaaataactgca[A/G]cgtggtgtgtaagtgg	A	G	NM_014619 // intron // 0 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// ENST00000278723 // intron // 0 // — // — // — // —	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2024492	aaaaggagagaatgga[C/T]gttgaactaaactgag	C	T	NM_014619 // downstream // 33854 // Hs.533740 // GRIK4 // 2900 // Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), mRNA. /// NM_152715 // upstream // 4002 // Hs.504136 // MGC10233 // 219899 // Homo sapiens hypothetical protein MGC10233 (MGC	GRIK4	GRIK4, Homo sapiens glutamate receptor, ionotropic, kainate 4 (GRIK4), q23.3
SNP_A-2193363	catctcttctattcct[C/G]aaatatcatacaagtg	C	G	NM_005422 // downstream // 76114 // Hs.248162 // TECTA // 7007 // Homo sapiens tectorin alpha (TECTA), mRNA. /// NM_006918 // upstream // 25869 // Hs.287749 // SC5DL // 6309 // Homo sapiens sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-li	TECTA	TECTA, Homo sapiens tectorin alpha (TECTA), q23.3
SNP_A-1850162	tatgtgggggcagcag[A/G]cacatggatactctct	A	G	NM_006918 // downstream // 25254 // Hs.287749 // SC5DL // 6309 // Homo sapiens sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like (SC5DL), mRNA. /// ENST00000264027 // downstream // 25254 // — // — // — // — /// ENST00000329573 //	SC5DL	SC5DL, Homo sapiens sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like (SC5DL), q23.3
SNP_A-1851501	tattcctttgaaaaac[C/T]aggtaaatagcaagat	C	T	NM_003105 // downstream // 180091 // Hs.368592 // SORL1 // 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 305826 // Hs.533964 // BRCC2 // 414899 // Homo sapiens BRCC2 mRNA	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q23.3
SNP_A-2122656	agtggaagagtagaga[A/C]aggagcctgactgcag	A	C	NM_003105 // downstream // 274462 // Hs.368592 // SORL1 // 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 211455 // Hs.533964 // BRCC2 // 414899 // Homo sapiens BRCC2 mRNA	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-2108761	agctgtgcctggaacc[A/G]agagataaatgcataa	A	G	NM_003105 // downstream // 279277 // Hs.368592 // SORL1 // 6653 // Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /// NM_001001786 // downstream // 206640 // Hs.533964 // BRCC2 // 414899 // Homo sapiens BRCC2 mRNA	SORL1	SORL1, Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), q24.1
SNP_A-1693553	taaggcccaattctttcatccttct[A/G]aattataaagaatgacac agggatg	A	G	NM_003105 // downstream // 319215 // Hs.438159 // SORL1 // 6653 // sortilin-related receptor, L(DLR class) A repeats-containing	SORL1	SORL1 , rs1219425, sortilin-related receptor, L(DLR class) A repeats-containing,q24.1
SNP_A-2151865	atgtttgataacatag[C/G]cacctctttctgactt	C	G	NM_001001786 // upstream // 25608 // Hs.533964 // BRCC2 // 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 514206 // Hs.444075 // STS-1 // 84959 // Homo sapiens Cbl-interacting protein Sts-1 (STS-1), mRNA. /// ENST00000329163	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-1914908	tgttaggcaatctcac[A/G]gacctggggctttgct	A	G	NM_001001786 // upstream // 36297 // Hs.533964 // BRCC2 // 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 503517 // Hs.444075 // STS-1 // 84959 // Homo sapiens Cbl-interacting protein Sts-1 (STS-1), mRNA. /// ENST00000329163	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-1667076	tgtcatttctattcacgaggcaaaa[C/T]ctgtatctcagtttggtga atagtt	C	T	NM_032873 // upstream // 532864 // Hs.55067 // KIAA1959 // 84959 // nm23-phosphorylated unknown substrate	KIAA1959	KIAA1959 , rs511514, nm23-phosphorylated unknown substrate,q24.1
SNP_A-1690723	aacttgctttcaacccagtgatacc[C/G]atttccaacttctggactc tagacc	C	G	NM_032873 // upstream // 259108 // Hs.55067 // KIAA1959 // 84959 // nm23-phosphorylated unknown substrate	KIAA1959	KIAA1959 , rs655283, nm23-phosphorylated unknown substrate,q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2021311	tccaaagcctgtggta[C/T]gtaaagacttgtgagg	C	T	NM_001001786 // upstream // 416833 // Hs.533964 // BRCC2 // 414899 // Homo sapiens BRCC2 mRNA (BRCC2), mRNA. /// NM_032873 // upstream // 122981 // Hs.444075 // STS-1 // 84959 // Homo sapiens Cbl-interacting protein Sts-1 (STS-1), mRNA. /// ENST0000032916	BRCC2	BRCC2, Homo sapiens BRCC2 (BRCC2), q24.1
SNP_A-1869364	tcctgtacttactacc[C/T]ctatgacacttgtgtt	C	T	NM_019604 // downstream // 7675 // Hs.159523 // CRTAM // 56253 // Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM), mRNA. /// NM_199124 // upstream // 2378 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ235	CRTAM	CRTAM, Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM), q24.1
SNP_A-2152636	attaataatcagaaga[A/T]ggccaattaaaaccac	A	T	NM_019604 // downstream // 9842 // Hs.159523 // CRTAM // 56253 // Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM), mRNA. /// NM_199124 // upstream // 211 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ2355	CRTAM	CRTAM, Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM), q24.1
SNP_A-1786008	ggctgcctcgccgccc[C/G]gacttcccagcgccgg	C	G	NM_199124 // 5UTR // 0 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, mRNA. /// ENST00000307257 // 5UTR // 0 // — // — // — // —	FLJ23554	FLJ23554, Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, q24.1
SNP_A-2244820	ctggatggatatgaca[A/G]taacaatgacatcact	A	G	NM_199124 // intron // 0 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, mRNA. /// NM_024806 // intron // 0 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ23554 (	FLJ23554	FLJ23554, Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, q24.1
SNP_A-1879360	tcttagttcaaaagca[C/T]aattgtaaaatcccaa	C	T	NM_199124 // intron // 0 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, mRNA. /// NM_024806 // intron // 0 // Hs.164705 // FLJ23554 // 79864 // Homo sapiens hypothetical protein FLJ23554 (	FLJ23554	FLJ23554, Homo sapiens hypothetical protein FLJ23554 (FLJ23554), transcript variant 2, q24.1
SNP_A-2048514	aagcatgattgggggtt[A/G]aacatctgccaccatc	A	G	NM_024769 // intron // 0 // Hs.504187 // ASAM // 79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000299322 // intron // 0 // — // — // — // —	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1850611	tattaatgccagcaaa[C/G]agtctttataggatga	C	G	NM_024769 // intron // 0 // Hs.504187 // ASAM // 79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000299322 // intron // 0 // — // — // — // —	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1904638	tggggctgaaagatga[A/C]gtaaatgtaacccaaa	A	C	NM_024769 // intron // 0 // Hs.504187 // ASAM // 79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000299322 // intron // 0 // — // — // — // —	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2184435	cagctaaacagattag[A/G]aaaggcttcatgaaga	A	G	NM_024769 // upstream // 26236 // Hs.504187 // ASAM // 79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 105064 // — // — // — // — /// ENST00000299322 // upstream // 26236 // — // — //	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1781459	ggattagaagaaccta[C/T]gtatcagccgggcgca	C	T	NM_024769 // upstream // 238643 // Hs.504187 // ASAM // 79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 317471 // — // — // — // — /// ENST00000299322 // upstream // 238643 // — // —	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-2157462	attgatactaacagga[A/G]agattgcctcagttgc	A	G	NM_024769 // upstream // 279513 // Hs.504187 // ASAM // 79827 // Homo sapiens adipocyte-specific adhesion molecule (ASAM), mRNA. /// ENST00000358727 // upstream // 358341 // — // — // — // — /// ENST00000299322 // upstream // 279513 // — // —	ASAM	ASAM, Homo sapiens adipocyte-specific adhesion molecule (ASAM), q24.1
SNP_A-1665430	acctatctatctatctatctgataa[A/G]ctctttaattgcctggcagtacttg	A	G	NM_003455 // upstream // 25130 // Hs.112556 // ZNF202 // 7753 // zinc finger protein 202 /// NM_014622 // upstream // 359398 // Hs.152944 // LOH11CR2A // 4013 // loss of heterozygosity, 11, chromosomal region 2, gene A	ZNF202	ZNF202 , rs10502268, zinc finger protein 202 ,q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1742789	atgcagagggaggtgggagtgtctc[A/G]agttagcaggtaaaagcaaatgttca	A	G	NM_003455 // upstream // 26062 // Hs.112556 // ZNF202 // 7753 // zinc finger protein 202 /// NM_014622 // upstream // 358466 // Hs.152944 // LOH11CR2A // 4013 // loss of heterozygosity, 11, chromosomal region 2, gene A	ZNF202	ZNF202 , rs10502270, zinc finger protein 202 q24.1
SNP_A-1714304	cccgcagctgttagagggctattccc[C/T]aaagagtttctaggagttga agtttct	C	T	NM_003455 // upstream // 47816 // Hs.112556 // ZNF202 // 7753 // zinc finger protein 202 /// NM_014622 // upstream // 336712 // Hs.152944 // LOH11CR2A // 4013 // loss of heterozygosity, 11, chromosomal region 2, gene A	ZNF202	ZNF202 , rs10502271, zinc finger protein 202 q24.1
SNP_A-1758277	gcagtatagcaagacccccatctcta[C/T]caatatttttgaaaaaactagccagg	C	T	NM_003455 // upstream // 78965 // Hs.112556 // ZNF202 // 7753 // zinc finger protein 202 /// NM_014622 // upstream // 305563 // Hs.152944 // LOH11CR2A // 4013 // loss of heterozygosity, 11, chromosomal region 2, gene A	ZNF202	ZNF202 , rs724467, zinc finger protein 202 q24.1
SNP_A-2313312	ggagaccataaaggaa[A/G]atggaatgattactaa	A	G	NM_001005325 // upstream // 91284 // Hs.537122 // OR6M1 // 390261 // Homo sapiens olfactory receptor, family 6, subfamily M, member 1 (OR6M1), mRNA. /// NM_001005197 // upstream // 8798 // Hs.449688 // OR8D4 // 338662 // Homo sapiens olfactory receptor, f	OR6M1	OR6M1, Homo sapiens olfactory receptor, family 6, subfamily M, member 1 (OR6M1), q24.1
SNP_A-2021862	cagaactataaggctcc[C/T]catctcagagttgg	C	T	NM_001004464 // upstream // 16055 // — // OR10G8 // 219869 // Homo sapiens olfactory receptor, family 10, subfamily G, member 8 (OR10G8), mRNA. /// ENST00000307002 // upstream // 4359 // — // — // — // — /// ENST00000306983 // upstream // 16055	OR10G8	OR10G8, Homo sapiens olfactory receptor, family 10, subfamily G, member 8 (OR10G8), q24.1
SNP_A-1847651	tatctaatgtcttttc[C/T]catttacctcccctgga	C	T	NM_001001953 // upstream // 41373 // — // OR10G9 // 219870 // Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), mRNA. /// NM_001004462 // upstream // 41373 // — // OR10G4 // 390264 // Homo sapiens olfactory receptor, family 1	OR10G9	OR10G9, Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), q24.1
SNP_A-1791391	gggtagctgcctaatat[A/T]agcatcaggagattga	A	T	NM_001001953 // upstream // 43860 // — // OR10G9 // 219870 // Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), mRNA. /// NM_001004462 // upstream // 43860 // — // OR10G4 // 390264 // Homo sapiens olfactory receptor, family 1	OR10G9	OR10G9, Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), q24.1
SNP_A-2150591	atgtgataacgtacgc[C/T]gagggagcctaatcag	C	T	NM_001001953 // upstream // 47449 // — // OR10G9 // 219870 // Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), mRNA. /// NM_001004462 // upstream // 47449 // — // OR10G4 // 390264 // Homo sapiens olfactory receptor, family 1	OR10G9	OR10G9, Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), q24.1
SNP_A-2160656	atttcctaacaaaaa[C/T]tcagattgctattaac	C	T	ENST00000355343 // downstream // 21129 // — // — // — // — /// ENST00000318666 // upstream // 5046 // — // — // — // —	-	q24.1
SNP_A-2134551	atatgtatatcctgaa[A/T]cacataaaagttgttt	A	T	NM_001002905 // downstream // 29128 // Hs.448172 // OR8G1P // 26494 // Homo sapiens olfactory receptor, family 8, subfamily G, member 1 (OR8G1P), mRNA. /// NM_001005198 // downstream // 29128 // Hs.448172 // OR8G5 // 219865 // Homo sapiens olfactory recep	OR8G1P	OR8G1P, Homo sapiens olfactory receptor, family 8, subfamily G, member 1 (OR8G1P), q24.1
SNP_A-2022035	ttttaaagtgttac[C/T]ctacctctgccgattc	C	T	NM_001002918 // upstream // 2263 // Hs.504212 // OR8D2 // 283160 // Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), mRNA. /// ENST00000357438 // upstream // 2263 // — // — // — // — /// ENST00000354597 // downstream // 73	OR8D2	OR8D2, Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), q24.1
SNP_A-2288794	gattgtgttcagttca[C/T]actttcatgcacccat	C	T	NM_001002918 // upstream // 5431 // Hs.504212 // OR8D2 // 283160 // Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), mRNA. /// ENST00000357438 // upstream // 5431 // — // — // — // — /// ENST00000354597 // downstream // 70	OR8D2	OR8D2, Homo sapiens olfactory receptor, family 8, subfamily D, member 2 (OR8D2), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1956943	ttttaagggatgtaaa[A/G]atgttgggtggaggtg	A	G	NM_012378 // upstream // 74475 // Hs.351822 // OR8B8 // 26493 // Homo sapiens olfactory receptor, family 8, subfamily B, member 8 (OR8B8), mRNA. /// NM_001005195 // downstream // 27162 // --- // OR8B12 // 219858 // Homo sapiens olfactory receptor, family	OR8B8	OR8B8, Homo sapiens olfactory receptor, family 8, subfamily B, member 8 (OR8B8), q24.2
SNP_A-2214952	cctatctgaaatttac[G/T]cagtgtcagggtgata	G	T	NM_001005195 // upstream // 25867 // --- // OR8B12 // 219858 // Homo sapiens olfactory receptor, family 8, subfamily B, member 12 (OR8B12), mRNA. /// NM_001005194 // upstream // 599 // Hs.339298 // OR8A1 // 390275 // Homo sapiens olfactory receptor, famil	OR8B12	OR8B12, Homo sapiens olfactory receptor, family 8, subfamily B, member 12 (OR8B12), q24.2
SNP_A-1947967	tttagaatagcaatta[C/T]cagttccaatatcccc	C	T	NM_022062 // intron // 0 // Hs.278564 // PKNOX2 // 63876 // Homo sapiens PBX/knotted 1 homeobox 2 (PKNOX2), mRNA. /// ENST00000298282 // intron // 0 // --- // --- // --- // ---	PKNOX2	PKNOX2, Homo sapiens PBX q24.2
SNP_A-2277049	gagatgagctagccga[C/T]ggtgacaaagccagtt	C	T	NM_022062 // intron // 0 // Hs.278564 // PKNOX2 // 63876 // Homo sapiens PBX/knotted 1 homeobox 2 (PKNOX2), mRNA. /// ENST00000298282 // intron // 0 // --- // --- // --- // ---	PKNOX2	PKNOX2, Homo sapiens PBX,q24.2
SNP_A-1959843	ttttgtattaccatca[C/T]acgagataggtgtgtt	C	T	NM_022062 // intron // 0 // Hs.278564 // PKNOX2 // 63876 // Homo sapiens PBX/knotted 1 homeobox 2 (PKNOX2), mRNA. /// ENST00000298282 // intron // 0 // --- // --- // --- // ---	PKNOX2	PKNOX2, Homo sapiens PBX,q24.2
SNP_A-1782393	ggcaatttggaaaacc[C/T]gaaaggcaggagacct	C	T	NM_022062 // intron // 0 // Hs.278564 // PKNOX2 // 63876 // Homo sapiens PBX/knotted 1 homeobox 2 (PKNOX2), mRNA. /// ENST00000298282 // intron // 0 // --- // --- // --- // ---	PKNOX2	PKNOX2, Homo sapiens PBX,q24.2
SNP_A-1943632	ttgtaatgcttacagg[C/T]atgatgcttagtactt	C	T	NM_005103 // intron // 0 // Hs.224008 // FEZ1 // 9638 // Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA. /// NM_022549 // intron // 0 // Hs.224008 // FEZ1 // 9638 // Homo sapiens fasciculation and elo	FEZ1	FEZ1, Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, q24.2
SNP_A-2151500	atgttctcagggttga[A/G]gtgagggcagctgagc	A	G	NM_004879 // intron // 0 // Hs.343911 // EI24 // 9538 // Homo sapiens etoposide induced 2.4 mRNA (EI24), mRNA. /// ENST00000278903 // intron // 0 // --- // --- // --- // ---	EI24	EI24, Homo sapiens etoposide induced 2.4 (EI24), q24.2
SNP_A-1923810	ttagtagtaagtgttc[C/G]atgtaattttacttta	C	G	NM_004879 // downstream // 6976 // Hs.343911 // EI24 // 9538 // Homo sapiens etoposide induced 2.4 mRNA (EI24), mRNA. /// NM_152713 // upstream // 1256 // Hs.504237 // ITM1 // 3703 // Homo sapiens integral membrane protein 1 (ITM1), mRNA. /// NM_152713 //	EI24	EI24, Homo sapiens etoposide induced 2.4 (EI24), q24.2
SNP_A-1870656	tcgcatctaccccata[A/G]gagcttaggacagtca	A	G	NM_001274 // intron // 0 // Hs.24529 // CHEK1 // 1111 // Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA. /// ENST00000278916 // intron // 0 // --- // --- // --- // ---	CHEK1	CHEK1, Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), q24.2
SNP_A-1758078	agaaatacaggcagctgtctatatc[C/T]gataggctacagttctg gaagtgtg	C	T	NM_152713 // intron // 0 // Hs.287850 // ITM1 // 3703 // integral membrane protein 1	ITM1	ITM1 , rs477961, integral membrane protein 1,q24.2
SNP_A-2056324	aatactgtcagcagaa[G/T]gttatctccaagataa	G	T	NM_001274 // downstream // 13565 // Hs.24529 // CHEK1 // 1111 // Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA. /// NM_020115 // downstream // 3028 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript	CHEK1	CHEK1, Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), q24.2
SNP_A-2240388	ctgacaatataagaaa[C/G]gagtgggcaactgatg	C	G	NM_020115 // intron // 0 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // intron // 0 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2
SNP_A-2251699	cttcagtctatcaaaa[A/G]cacatcaagtacacag	A	G	NM_020115 // upstream // 16186 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // upstream // 16186 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1)	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1896936	tgctcagtcttaaaca[C/T]aatttgggaccgaggg	C	T	NM_020115 // upstream // 48924 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // upstream // 48924 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1)	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2
SNP_A-2180762	cagaataagatgactt[A/C]aacacagtaggaaagg	A	C	NM_020115 // upstream // 52593 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // upstream // 52593 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1)	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2
SNP_A-2084360	actatactgtactgtat[A/G]agaatgcaaggataa	A	G	NM_020115 // upstream // 64971 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, mRNA. /// NM_020113 // upstream // 64971 // Hs.169222 // ACRV1 // 56 // Homo sapiens acrosomal vesicle protein 1 (ACRV1)	ACRV1	ACRV1, Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 11, q24.2
SNP_A-2280207	gagggcaaaagaacac[C/T]actgtttctcagggat	C	T	NM_212555 // intron // 0 // 369185 // UNQ3112 // 399967 // Homo sapiens LVLF3112 (UNQ3112), mRNA. /// ENST00000358524 // intron // 0 // — // — // —	UNQ3112	UNQ3112, Homo sapiens LVLF3112 (UNQ3112), q24.2
SNP_A-2022433	gtttctccatgttggc[C/T]agtttgtttatgacca	C	T	NM_013264 // intron // 0 // Hs.420263 // DDX25 // 29118 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), mRNA. /// ENST00000263576 // intron // 0 // — // — // — // —	DDX25	DDX25, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), q24.2
SNP_A-1930133	ttcattagtattatta[C/T]agacattatgtcaggt	C	T	NM_013264 // intron // 0 // Hs.420263 // DDX25 // 29118 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), mRNA. /// ENST00000263576 // intron // 0 // — // — // — // —	DDX25	DDX25, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), q24.2
SNP_A-2267750	gaatcatcccagttca[C/G]gtgtgtttctgtatt	C	G	NM_013264 // downstream // 4100 // Hs.420263 // DDX25 // 29118 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), mRNA. /// NM_016952 // downstream // 33471 // Hs.530804 // CDON // 50937 // Homo sapiens cell adhesion molecule-related/down-	DDX25	DDX25, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), q24.2
SNP_A-2115016	agggcccgggctggcccc[A/G]acagcacacatggaga	A	G	NM_013264 // downstream // 18676 // Hs.420263 // DDX25 // 29118 // Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), mRNA. /// NM_016952 // downstream // 18895 // Hs.530804 // CDON // 50937 // Homo sapiens cell adhesion molecule-related/down	DDX25	DDX25, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), q24.2
SNP_A-2241083	ctgagccaggctctaa[A/G]tgctttccatggctta	A	G	NM_016952 // intron // 0 // Hs.530804 // CDON // 50937 // Homo sapiens cell adhesion molecule-related/down-regulated by oncogenes (CDON), mRNA. /// ENST00000263577 // intron // 0 // — // — // — // —	CDON	CDON, Homo sapiens cell adhesion molecule-related q24.2
SNP_A-2038078	aacacacctgtcttca[C/T]ccagagatggtatctc	C	T	NM_032795 // downstream // 119176 // Hs.150458 // RPUSD4 // 84881 // Homo sapiens hypothetical protein FLJ14494 (FLJ14494), mRNA. /// ENST00000333615 // downstream // 14638 // — // — // — // — /// ENST00000298317 // downstream // 119176 // — //	RPUSD4	RPUSD4, Homo sapiens hypothetical protein FLJ14494 (FLJ14494), q24.2
SNP_A-2212744	ccctgcattcgtccca[A/G]aagaaggcaggacccc	A	G	NM_014026 // intron // 0 // Hs.504249 // DCPS // 28960 // Homo sapiens mRNA decapping enzyme (DCPS), mRNA. /// ENST00000263579 // intron // 0 // — // — // — // —	DCPS	DCPS, Homo sapiens decapping enzyme (DCPS), q24.2
SNP_A-1886178	tgacccactgactgac[G/T]gataaaaatggatttt	G	T	NM_032531 // intron // 0 // Hs.302350 // KIRREL3 // 84623 // Homo sapiens kin of IRRE like 3 (Drosophila) (KIRREL3), mRNA. /// ENST00000278934 // intron // 0 // — // — // — // —	KIRREL3	KIRREL3, Homo sapiens kin of IRRE like 3 (Drosophila) (KIRREL3), q24.2
SNP_A-2071323	acacttggccactaag[C/T]aggaagtcctggcagg	C	T	NM_006278 // downstream // 177227 // Hs.504251 // ST3GAL4 // 6484 // Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), mRNA. /// X74570 // downstream // 177227 // Hs.504251 // ST3GAL4 // 6484 // H.sapiens mRNA for	ST3GAL4	ST3GAL4, Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1817866	gttcctgttgcaaaa[C/G]ggcaagtacaataatg	C	G	NM_006278 // downstream // 509875 // Hs.504251 // ST3GAL4 // 6484 // Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), mRNA. /// X74570 // downstream // 509875 // Hs.504251 // ST3GAL4 // 6484 // H.sapiens mRNA for	ST3GAL4	ST3GAL4, Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), q24.2
SNP_A-2250137	cttactcctgaaaaa[G/T]aagtgagtgagcctaa	G	T	NM_006278 // downstream // 518671 // Hs.504251 // ST3GAL4 // 6484 // Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), mRNA. /// X74570 // downstream // 518671 // Hs.504251 // ST3GAL4 // 6484 // H.sapiens mRNA for	ST3GAL4	ST3GAL4, Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), q24.2
SNP_A-2040156	aaccaagattcagtta[C/G]gacacaataaaataat	C	G	NM_006278 // downstream // 566318 // Hs.504251 // ST3GAL4 // 6484 // Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), mRNA. /// X74570 // downstream // 566318 // Hs.504251 // ST3GAL4 // 6484 // H.sapiens mRNA for	ST3GAL4	ST3GAL4, Homo sapiens sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4C), q24.2
SNP_A-2285596	gatgaacacctctct[C/G]aagaaaggaaggacca	C	G	NM_173579 // downstream // 4348 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 330557 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000031980	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1870358	tcctttaagctaaa[C/G]caatagaaaagcccatt	C	G	NM_173579 // downstream // 4589 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 930316 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000031980	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2072104	acagataaattactaag[A/G]acagactgtgccattg	A	G	NM_173579 // downstream // 25526 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 909379 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000031980	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1887313	tgagaagtaatcatca[A/G]gtagcagtgaatcagg	A	G	NM_173579 // downstream // 107507 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 827398 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000319	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1945477	ttgttcagagtcaaaa[C/T]gtaggacctagatctg	C	T	NM_173579 // downstream // 112941 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 821964 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000319	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2173170	cacaacaataaaacga[C/T]gctgtataaaagtgct	C	T	NM_173579 // downstream // 115387 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 819518 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000319	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-1906209	tggtgacatcttcata[C/T]agtgtaagtggtcaa	C	T	NM_173579 // downstream // 116551 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 818354 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000319	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2090000	actcttaacctttcccc[C/T]gctccagtctagtctt	C	T	NM_173579 // downstream // 116743 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 818162 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000319	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2183273	cagcaattgcttaata[A/G]atgtataacccaaata	A	G	NM_173579 // downstream // 247870 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 687035 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST00000319	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2052500	aagtagctgccaataa[C/T]gagtacccagccttga	C	T	NM_173579 // downstream // 923494 // --- // FLJ40224 // 283165 // Homo sapiens hypothetical protein FLJ40224 (FLJ40224), mRNA. /// NM_001001394 // downstream // 11411 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// ENST000003198	FLJ40224	FLJ40224, Homo sapiens hypothetical protein FLJ40224 (FLJ40224), q24.2
SNP_A-2073100	acaggcaaataaggaa[A/G]ttatggtgtgggctac	A	G	NM_001001394 // upstream // 154221 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 362891 // Hs.369438 // ETS1 // 2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1)	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.2
SNP_A-1907217	tggtttgctggttagc[G/T]gcagaaatttgcactt	G	T	NM_001001394 // upstream // 213553 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 303559 // Hs.369438 // ETS1 // 2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1)	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.3
SNP_A-1799297	gtaataattaacaagc[G/T]gaataggcaacctaca	G	T	NM_001001394 // upstream // 311709 // Hs.546397 // HCG3 // 414061 // Homo sapiens HCG3 gene (HCG3), mRNA. /// NM_005238 // downstream // 205403 // Hs.369438 // ETS1 // 2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1)	HCG3	HCG3, Homo sapiens HCG3 gene (HCG3), q24.3
SNP_A-1824109	taaacactactcctcc[C/T]caagttattaagaatc	C	T	NM_005238 // intron // 0 // Hs.369438 // ETS1 // 2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// ENST00000319397 // intron // 0 // --- // --- // --- // --- /// ENST00000345075 // intron // 0 // --- // ---	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3
SNP_A-2272241	gacctcagaatgacaa[A/G]acatcagtatggttgt	A	G	NM_005238 // intron // 0 // Hs.369438 // ETS1 // 2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// ENST00000319397 // intron // 0 // --- // --- // --- // --- /// ENST00000345075 // intron // 0 // --- // ---	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3
SNP_A-2092976	agaacacactgaagga[G/T]tatagatgaactcatc	G	T	NM_005238 // upstream // 58058 // Hs.369438 // ETS1 // 2113 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA. /// NM_002017 // upstream // 113810 // Hs.504281 // FLI1 // 2313 // Homo sapiens Friend leukemia virus in	ETS1	ETS1, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), q24.3
SNP_A-2298810	gcccatgagccaagca[A/G]tctcaaattttatacc	A	G	NM_002017 // intron // 0 // Hs.504281 // FLI1 // 2313 // Homo sapiens Friend leukemia virus integration 1 (FLI1), mRNA. /// ENST00000344954 // intron // 0 // --- // --- // --- // ---	FLI1	FLI1, Homo sapiens Friend leukemia virus integration 1 (FLI1), q24.3
SNP_A-2023487	tcacctatgtgaggac[G/T]gtagcattgattggga	G	T	NM_002017 // intron // 0 // Hs.504281 // FLI1 // 2313 // Homo sapiens Friend leukemia virus integration 1 (FLI1), mRNA. /// ENST00000344954 // intron // 0 // --- // --- // --- // --- /// ENST00000281428 // intron // 0 // --- // --- // --- // ---	FLI1	FLI1, Homo sapiens Friend leukemia virus integration 1 (FLI1), q24.3
SNP_A-2190445	catacagtcaacattc[A/G]ctaactgagtaggtgt	A	G	NM_153766 // upstream // 46253 // Hs.527830 // KCNJ1 // 3758 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 1 (KCNJ1), transcript variant rom-k4, mRNA. /// NM_153767 // upstream // 46253 // Hs.527830 // KCNJ1 // 3758 // Homo sa	KCNJ1	KCNJ1, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 1 (KCNJ1), transcript variant rom-k4, q24.3
SNP_A-2054760	aataaaattgggtata[C/T]ggtacagccccagtag	C	T	NM_000890 // intron // 0 // Hs.444595 // KCNJ5 // 3762 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), mRNA. /// ENST00000338350 // intron // 0 // --- // --- // --- // ---	KCNJ5	KCNJ5, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213504	ccggtggtcctaacta[A/G]ccctgtctcctgcca	A	G	NM_000890 // intron // 0 // Hs.444595 // KCNJ5 // 3762 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), mRNA. /// NM_145013 // CDS // 0 // Hs.351133 // MGC35558 // 219833 // Homo sapiens hypothetical protein MGC35558 (	KCNJ5	KCNJ5, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), q24.3
SNP_A-2311187	ggaagtgtcatgtagat[A/C]atggctcagctgcag	A	C	NM_000890 // downstream // 16840 // Hs.444595 // KCNJ5 // 3762 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), mRNA. /// NM_145013 // upstream // 29197 // Hs.351133 // MGC35558 // 219833 // Homo sapiens hypothetical p	KCNJ5	KCNJ5, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 5 (KCNJ5), q24.3
SNP_A-1951061	ttccataactgaaaa[C/G]gaggcaagattatta	C	G	ENST00000323401 // intron // 0 // --- // --- // --- /// ENST00000356092 // intron // 0 // --- // --- // ---	-	q24.3
SNP_A-1910745	tgtcgatcttaaaccc[A/G]aagcatagagaaatgg	A	G	ENST00000356886 // upstream // 49742 // --- // --- // --- /// ENST00000299101 // downstream // 8405 // --- // --- // ---	-	q24.3
SNP_A-2077800	accagaagcaaatttta[A/G]gtgttattgcacttt	A	G	NM_003658 // intron // 0 // Hs.167218 // BARX2 // 8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// ENST00000281437 // intron // 0 // --- // --- // ---	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2134432	atatggctaagtatta[C/T]gatgtgaagaaacttg	C	T	NM_003658 // intron // 0 // Hs.167218 // BARX2 // 8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// ENST00000281437 // intron // 0 // --- // --- // ---	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-1796105	ggtgtagcaatgagtg[C/T]agcaatgtgtaggt	C	T	NM_003658 // intron // 0 // Hs.167218 // BARX2 // 8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// ENST00000281437 // intron // 0 // --- // --- // ---	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2257639	ctttgctaaaagaatg[A/G]aacttctgagcaggt	A	G	NM_003658 // downstream // 160360 // Hs.167218 // BARX2 // 8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// NM_138788 // upstream // 203566 // Hs.504301 // TMEM45B // 120224 // Homo sapiens hypothetical protein BC016153 (LOC120224), mRNA. ///	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2282590	gagtttatccatctcc[A/G]ctagatttttctagttt	A	G	NM_003658 // downstream // 349236 // Hs.167218 // BARX2 // 8538 // Homo sapiens BarH-like homeobox 2 (BARX2), mRNA. /// NM_138788 // upstream // 14690 // Hs.504301 // TMEM45B // 120224 // Homo sapiens hypothetical protein BC016153 (LOC120224), mRNA. /// E	BARX2	BARX2, Homo sapiens BarH-like homeobox 2 (BARX2), q24.3
SNP_A-2235204	ctccccttattgca[C/T]gaatagtgtaccagca	C	T	NM_138788 // intron // 0 // Hs.504301 // TMEM45B // 120224 // Homo sapiens hypothetical protein BC016153 (LOC120224), mRNA. /// ENST00000281441 // intron // 0 // --- // --- // ---	TMEM45B	TMEM45B, Homo sapiens hypothetical protein BC016153 (LOC120224), q24.3
SNP_A-2055354	aataaggagctaaatc[C/G]aaaatatacaagaaac	C	G	NM_138788 // intron // 0 // Hs.504301 // TMEM45B // 120224 // Homo sapiens hypothetical protein BC016153 (LOC120224), mRNA. /// ENST00000281441 // intron // 0 // --- // --- // ---	TMEM45B	TMEM45B, Homo sapiens hypothetical protein BC016153 (LOC120224), q24.3
SNP_A-2187928	cagtatgtgttatgat[C/G]gccaattatcacatct	C	G	NM_199439 // intron // 0 // Hs.275086 // PRDM10 // 56980 // Homo sapiens PR domain containing 10 (PRDM10), transcript variant 4, mRNA. /// NM_199438 // intron // 0 // Hs.275086 // PRDM10 // 56980 // Homo sapiens PR domain containing 10 (PRDM10), transcrip	PRDM10	PRDM10, Homo sapiens PR domain containing 10 (PRDM10), transcript variant 4, q24.3
SNP_A-2295623	gcatgaacagaatgccd[A/G]cacaggtgaagactgg	A	G	NM_199438 // CDS // 0 // Hs.275086 // PRDM10 // 56980 // Homo sapiens PR domain containing 10 (PRDM10), transcript variant 3, mRNA. /// NM_020228 // CDS // 0 // Hs.275086 // PRDM10 // 56980 // Homo sapiens PR domain containing 10 (PRDM10), transcript vari	PRDM10	PRDM10, Homo sapiens PR domain containing 10 (PRDM10), transcript variant 3, q24.3
SNP_A-1958317	ttttccatatcaaggc[C/T]ctgctttggcatcgaa	C	T	NM_001642 // upstream // 7475 // Hs.370247 // APLP2 // 334 // Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA. /// ENST00000334139 // upstream // 29211 // --- // --- // --- /// ENST00000263574 // upstream // 7475 // --- // ---	APLP2	APLP2, Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2234400	ctccaaggtacaatta[C/G]acatctcccataccac	C	G	NM_001642 // intron // 0 // Hs.370247 // APLP2 // 334 // Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA. /// ENST00000263574 // intron // 0 // — // — // — // — /// ENST00000345598 // intron // 0 // — // — // — // — /	APLP2	APLP2, Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), q24.3
SNP_A-1781887	ggcaaaaaatgcagta[A/G]taaagcaaatgtgact	A	G	NM_001642 // intron // 0 // Hs.370247 // APLP2 // 334 // Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA. /// ENST00000263574 // intron // 0 // — // — // — // — /// ENST00000345598 // intron // 0 // — // — // — // — /	APLP2	APLP2, Homo sapiens amyloid beta (A4) precursor-like protein 2 (APLP2), q24.3
SNP_A-2156008	attccttaggatctac[A/G]caaccttggatctgga	A	G	NM_007037 // intron // 0 // Hs.271605 // ADAMTS8 // 11095 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8 (ADAMTS8), mRNA. /// ENST00000257359 // intron // 0 // — // — // — // —	ADAMTS8	ADAMTS8, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8 (ADAMTS8), q24.3
SNP_A-2138972	atccggctgagcaata[C/T]gctttcactcccactt	C	T	NM_007037 // upstream // 9991 // Hs.271605 // ADAMTS8 // 11095 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8 (ADAMTS8), mRNA. /// NM_139055 // upstream // 9990 // Hs.534221 // ADAMTS15 // 1706	ADAMTS8	ADAMTS8, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8 (ADAMTS8), q24.3
SNP_A-2210085	ccccagatgtagcacc[A/G]ccactgttctcctcag	A	G	NM_139055 // downstream // 44042 // Hs.534221 // ADAMTS15 // 170689 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 (ADAMTS15), mRNA. /// NM_173580 // upstream // 155116 // — // FLJ39058 // 2	ADAMTS15	ADAMTS15, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 15 (ADAMTS15), q24.3
SNP_A-1825746	taaatccgaggcaata[C/G]aggttctcaactccca	C	G	NM_173580 // intron // 0 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // intron // 0 // — // — // — // —	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-2176885	caccggcctagtgtca[C/T]gctccaagagaccaca	C	T	NM_173580 // intron // 0 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // intron // 0 // — // — // — // —	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-1883186	tgaaatggtcctgaaa[A/G]ttaggtatcatgtttt	A	G	NM_173580 // downstream // 140 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream // 140 // — // — // — // — /// ENST00000316996 // downstream // 129856 // — // — // -	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-1852861	tatttctattttgtgg[C/T]ccaagacagtggctcc	C	T	NM_173580 // downstream // 1723 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream // 1723 // — // — // — // — /// ENST00000316996 // downstream // 128273 // — // — //	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-2155564	attccaagctaccctc[A/G]aaggactaaggcttgc	A	G	NM_173580 // downstream // 13489 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream // 13489 // — // — // — // — /// ENST00000316996 // downstream // 116507 // — // —	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-2033632	aaatatcctgaaaacc[A/G]aaagattataccaata	A	G	NM_173580 // downstream // 19955 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream // 19955 // — // — // — // — /// ENST00000316996 // downstream // 110041 // — // —	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-1868127	tcctattacctagtca[A/G]attctgaggaaatggg	A	G	NM_173580 // downstream // 31809 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream // 31809 // — // — // — // — /// ENST00000316996 // downstream // 98187 // — // — /	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3
SNP_A-1827315	taacggacagaagccc[A/G]aaaatggatgaggctc	A	G	NM_173580 // downstream // 55586 // — // FLJ39058 // 283171 // Homo sapiens hypothetical protein FLJ39058 (FLJ39058), mRNA. /// ENST00000317019 // downstream // 55586 // — // — // — // — /// ENST00000316996 // downstream // 74410 // — // — /	FLJ39058	FLJ39058, Homo sapiens hypothetical protein FLJ39058 (FLJ39058), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1841722	taggcaggaggttaga[C/T]gagaaacttccaaaaa	C	T	D87443 // downstream // 4700 // Hs.444024 // SNX19 // 399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// ENST00000316996 // upstream // 9070 // — // — // — /// ENST00000265909 // downstream // 4700 // — // — // —	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds, q24.3
SNP_A-2123593	agtgtgtccgccatcat[C/T]ccaaatctgaatacat	C	T	D87443 // upstream // 122627 // Hs.444024 // SNX19 // 399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 621148 // Hs.299419 // FLJ45436 // 399980 // Homo sapiens FLJ45436 protein (FLJ45436), mRNA. /// ENST00000265909	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds, q25
SNP_A-2258139	ctttaagcatctgaa[C/T]ggtggaagaggctgaa	C	T	D87443 // upstream // 291077 // Hs.444024 // SNX19 // 399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 452698 // Hs.299419 // FLJ45436 // 399980 // Homo sapiens FLJ45436 protein (FLJ45436), mRNA. /// ENST00000265909	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds, q25
SNP_A-2272062	gaccctgatttctaaa[C/G]acaaaaatctcagagga	C	G	D87443 // upstream // 298748 // Hs.444024 // SNX19 // 399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 445027 // Hs.299419 // FLJ45436 // 399980 // Homo sapiens FLJ45436 protein (FLJ45436), mRNA. /// ENST00000265909	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds, q25
SNP_A-2032281	aaagttaatctctat[G/T]agtcaggtctccagag	G	T	D87443 // upstream // 325951 // Hs.444024 // SNX19 // 399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 417824 // Hs.299419 // FLJ45436 // 399980 // Homo sapiens FLJ45436 protein (FLJ45436), mRNA. /// ENST00000265909	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds, q25
SNP_A-1932975	ttcgaggagattactc[A/C]agttagcagcagaact	A	C	D87443 // upstream // 612172 // Hs.444024 // SNX19 // 399979 // Homo sapiens mRNA for KIAA0254 gene, partial cds. /// NM_207432 // downstream // 131603 // Hs.299419 // FLJ45436 // 399980 // Homo sapiens FLJ45436 protein (FLJ45436), mRNA. /// ENST00000265909	SNX19	SNX19, Homo sapiens for KIAA0254 gene, partial cds, q25
SNP_A-2024665	tcaagtggaccagaaa[A/C]aaagtcaaggaggtgc	A	C	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2217705	cctgatacagttctccc[A/C]aatctgctgcaaatac	A	C	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2049950	aaggaagagcacacac[A/G]atggtaatggttaaac	A	G	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2002418	gggtagctgatggcaa[A/G]tgggaatgaaggtaat	A	G	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-1786927	ggctttttcagatgta[C/G]aatatgctcggtttgg	C	G	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-1879610	tcttcaccacctgcat[A/G]aaatagagcttccaac	A	G	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2126408	ataaaagagagagaaa[A/G]acaacttgcagcttg	A	G	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-2024797	agtgattgagtattca[C/T]ctgtaagatagtgaca	C	T	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25
SNP_A-1801665	gtagtagtagttcaca[C/G]acagtgagtgacacgt	C	G	NM_016522 // intron // 0 // Hs.504352 // HNT // 50863 // Homo sapiens neurotrimin (HNT), mRNA. /// ENST00000333299 // intron // 0 // — // — // —	HNT	HNT, Homo sapiens neurotrimin (HNT), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1847547	tatccttagtttacf[A/G]cttctcagcctagaat	A	G	NM_002545 // intron // 0 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // intron // 0 // --- // --- // ---	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-2024803	aaaagtgattggacac[A/G]aattgaaaaatatctt	A	G	NM_002545 // intron // 0 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // intron // 0 // --- // --- // ---	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-2229937	ctagtttccttgtat[C/G]agaaccagactcatgg	C	G	NM_002545 // intron // 0 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // intron // 0 // --- // --- // ---	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-1829332	taagtcaccgtacacc[C/T]cgaaattcacagcgga	C	T	NM_002545 // upstream // 37748 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // upstream // 37748 // --- // --- // --- /// ENST00000358513 // downstream // 31795 //	OPCML	OPCML, Homo sapiens opioid binding protein,q25
SNP_A-2190389	catacacagttcatca[C/T]gatccaaacgtcgtt	C	T	NM_002545 // upstream // 38030 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // upstream // 38030 // --- // --- // --- /// ENST00000358513 // downstream // 31513 //	OPCML	OPCML, Homo sapiens opioid binding protein,q25
SNP_A-2219168	cctgtcaatgtctaga[A/G]atgatccgaacacata	A	G	NM_002545 // upstream // 50695 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000331898 // upstream // 50695 // --- // --- // --- /// ENST00000358513 // downstream // 18848 //	OPCML	OPCML, Homo sapiens opioid binding protein,q25
SNP_A-2196148	catgtgctaactattc[A/C]aaatgtctatgcctgc	A	C	NM_002545 // upstream // 64683 // Hs.4817 // OPCML // 4978 // Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA. /// ENST00000358513 // upstream // 64683 // --- // --- // --- /// ENST00000331898 // upstream // 4860 //	OPCML	OPCML, Homo sapiens opioid binding protein q25
SNP_A-2002432	gagcttaaatgtcccc[C/T]gatgccaacgattgag	C	T	ENST00000358513 // upstream // 9122 // --- // --- // --- /// ENST00000360103 // upstream // 4094 // --- // --- // ---	-	q25
SNP_A-2311062	ggaagtaatctcaaata[C/G]gtaagagttataagaa	C	G	NM_174927 // downstream // 803345 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 11284 // --- // --- // --- /// ENST00000299140 // downstream // 803345 // --- // --- // ---	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2276332	gagagcactgccttga[A/G]gttggccgcgtgtgcc	A	G	NM_174927 // downstream // 775036 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 39593 // --- // --- // --- /// ENST00000299140 // downstream // 775036 // --- // --- // ---	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-1913731	tgtgtatgttgaagca[C/T]gaactgtgaatctta	C	T	NM_174927 // downstream // 641197 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 173432 // --- // --- // --- /// ENST00000299140 // downstream // 641197 // --- // --- // ---	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-1815339	gtgtttcaaacagaga[A/T]aatttagtgaggagaa	A	T	NM_174927 // downstream // 462842 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 351787 // --- // --- // --- /// ENST00000299140 // downstream // 462842 // --- // --- // ---	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2045955	aagaccctagaacttac[C/T]gctaacaaatggtaaa	C	T	NM_174927 // downstream // 458773 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 355856 // --- // --- // --- /// ENST00000299140 // downstream // 458773 // --- // --- // ---	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2049413	aagctgagttacagag[C/G]acttcacataccaggc	C	G	NM_174927 // downstream // 287020 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000360103 // downstream // 527609 // — // — // — // — /// ENST00000299140 // downstream // 287020 // — // — // — // —	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-2182130	cagagggaatttctca[C/T]ctttcagacagaagaa	C	T	NM_174927 // intron // 0 // Hs.97541 // SPAS1 // 219938 // Homo sapiens spergen-1 (SPAS1), mRNA. /// ENST00000299140 // intron // 0 // — // — // — // —	SPAS1	SPAS1, Homo sapiens spergen-1 (SPAS1), q25
SNP_A-1683552	gggccacttgaagttagggtgcaca[A/G]taccaatgcaagctg ctatcacaat	A	G	NM_002545 // upstream // 883547 // Hs.4817 // OPCML // 4978 // opioid binding protein/cell adhesion molecule-like /// NM_174927 // downstream // 13933 // Hs.97541 // SPAS1 // 219938 // spergen-1	OPCML	OPCML , rs715797, opioid binding protein,q25
SNP_A-1746440	caaacccttttgcgaactgcgcaca[C/T]gagggatctaagttgc acgctcctt	C	T	NM_032801 // upstream // 6168 // Hs.419149 // JAM3 // 83700 // junctional adhesion molecule 3	JAM3	JAM3 , rs661820, junctional adhesion molecule 3,q25
SNP_A-1784772	ggcctggagtgggctc[C/T]aagtaatacccagcaa	C	T	NM_032801 // intron // 0 // Hs.150718 // JAM3 // 83700 // Homo sapiens junctional adhesion molecule 3 (JAM3), mRNA. /// ENST00000299106 // intron // 0 // — // — // — // —	JAM3	JAM3, Homo sapiens junctional adhesion molecule 3 (JAM3), q25
SNP_A-2224259	cggttacatgatcaca[A/G]gtctcctgttcatgcc	A	G	NM_014384 // intron // 0 // Hs.14791 // ACAD8 // 27034 // Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA. /// ENST00000281182 // intron // 0 // — // — // — // —	ACAD8	ACAD8, Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), q25
SNP_A-2180694	cagaaggtgagagagc[A/G]gagaaaatatctaata	A	G	NM_138416 // intron // 0 // Hs.270778 // LOC112937 // 112937 // Homo sapiens hypothetical protein BC011001 (LOC112937), mRNA. /// ENST00000281180 // intron // 0 // — // — // — // —	LOC112937	LOC112937, Homo sapiens hypothetical protein BC011001 (LOC112937), q25
SNP_A-2064225	aattcacacataacag[A/G]aggggtggcataaact	A	G	NM_018644 // upstream // 88621 // Hs.381050 // B3GAT1 // 27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 88621 // Hs.381050 // B3GAT1 // 27087 // Homo sa	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-2064235	aattcacatagaaaaa[C/T]gagcaagtaagaattg	C	T	NM_018644 // upstream // 94991 // Hs.381050 // B3GAT1 // 27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 94991 // Hs.381050 // B3GAT1 // 27087 // Homo sa	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-2179389	cactgtgtggtccctc[A/G]atgcagtaagaggaaa	A	G	NM_018644 // upstream // 130102 // Hs.381050 // B3GAT1 // 27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 130102 // Hs.381050 // B3GAT1 // 27087 // Homo	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-1831169	taatgcgttagcggac[A/G]ataaagaataacccta	A	G	NM_018644 // upstream // 184844 // Hs.381050 // B3GAT1 // 27087 // Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, mRNA. /// NM_054025 // upstream // 184844 // Hs.381050 // B3GAT1 // 27087 // Homo	B3GAT1	B3GAT1, Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), transcript variant 1, q25
SNP_A-2086215	actctgcttgtcaaga[A/G]gatggctctggcctcc	A	G	ENST00000360397 // intron // 0 // — // — // — // —	-	q25
SNP_A-2178981	cactgcatcctcttca[C/T]cccagatccagttgtc	C	T	ENST00000360397 // intron // 0 // — // — // — // —	-	q25
SNP_A-2256845	ctttccatttgcttaa[C/T]tctctgaggacctccc	C	T	ENST00000326261 // intron // 0 // — // — // — // —	-	p13.33
SNP_A-1882811	tgaaagcaagtttcaa[C/T]aggaggttcatgggag	C	T	NM_173593 // intron // 0 // Hs.504416 // B4GalNac-T3 // 283358 // Homo sapiens beta 1,4-N-acetylgalactosaminyltransferase-transferase-III (B4GalNac-T3), mRNA. /// ENST00000266383 // intron // 0 // — // — // — // —	B4GalNac-T3	B4GalNac-T3, Homo sapiens beta 1,4-N-acetylgalactosaminyltransferase-transferase-III (B4GalNac-T3), p13.33
SNP_A-1945411	ttgttattagattctc[A/G]ctgtataaatgagtta	A	G	NM_173593 // intron // 0 // Hs.504416 // B4GalNac-T3 // 283358 // Homo sapiens beta 1,4-N-acetylgalactosaminyltransferase-transferase-III (B4GalNac-T3), mRNA. /// ENST00000266383 // intron // 0 // — // — // — // —	B4GalNac-T3	B4GalNac-T3, Homo sapiens beta 1,4-N-acetylgalactosaminyltransferase-transferase-III (B4GalNac-T3), p13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181396	cagactattacacaca[A/G]gcgagaaataaacttc	A	G	NM_016533 // intron // 0 // Hs.504422 // NINJ2 // 4815 // Homo sapiens ninjurin 2 (NINJ2), mRNA. /// ENST00000305108 // intron // 0 // --- // --- // --- // ---	NINJ2	NINJ2, Homo sapiens ninjurin 2 (NINJ2), p13.33
SNP_A-2270115	gacacagcgttcttta[C/T]attctaattctagctc	C	T	NM_016533 // intron // 0 // Hs.504422 // NINJ2 // 4815 // Homo sapiens ninjurin 2 (NINJ2), mRNA. /// ENST00000305108 // intron // 0 // --- // --- // --- // ---	NINJ2	NINJ2, Homo sapiens ninjurin 2 (NINJ2), p13.33
SNP_A-2065115	aattgctatttcagct[C/G]accttccccaaaactt	C	G	NM_016533 // intron // 0 // Hs.504422 // NINJ2 // 4815 // Homo sapiens ninjurin 2 (NINJ2), mRNA. /// ENST00000305108 // intron // 0 // --- // --- // --- // ---	NINJ2	NINJ2, Homo sapiens ninjurin 2 (NINJ2), p13.33
SNP_A-2002467	aggccttaattcctca[A/G]cgaaaactgcaaccat	A	G	NM_016533 // upstream // 13483 // Hs.504422 // NINJ2 // 4815 // Homo sapiens ninjurin 2 (NINJ2), mRNA. /// NM_018979 // upstream // 76494 // Hs.504432 // WNK1 // 65125 // Homo sapiens protein kinase, lysine deficient 1 (PRKWNK1), mRNA. /// ENST00000305108	NINJ2	NINJ2, Homo sapiens ninjurin 2 (NINJ2), p13.33
SNP_A-2118804	agtaccctgtctctca[A/G]attcccatatcaactc	A	G	NM_018979 // CDS // 0 // Hs.504432 // WNK1 // 65125 // Homo sapiens protein kinase, lysine deficient 1 (PRKWNK1), mRNA. /// ENST00000252477 // intron // 0 // --- // --- // --- // --- /// ENST00000315939 // CDS // 0 // --- // --- // --- // --- /// ENST0000	WNK1	WNK1, Homo sapiens protein kinase, lysine deficient 1 (PRKWNK1), p13.33
SNP_A-2260355	gaaacaaaagcttcca[C/T]cacgactgtaacaggt	C	T	NM_015064 // downstream // 56818 // Hs.400431 // RAB6IP2 // 23085 // Homo sapiens Rab6-interacting protein 2 (ELKS), transcript variant alpha, mRNA. /// NM_178037 // downstream // 53664 // Hs.400431 // RAB6IP2 // 23085 // Homo sapiens Rab6-interacting pro	RAB6IP2	RAB6IP2, Homo sapiens Rab6-interacting protein 2 (ELKS), transcript variant alpha, p13.33
SNP_A-1793701	ggtatgtgccaaaaac[G/T]gtataaatgaaactat	G	T	NM_024551 // intron // 0 // Hs.371642 // ADIPOR2 // 79602 // Homo sapiens adiponectin receptor 2 (ADIPOR2), mRNA. /// ENST00000357103 // intron // 0 // --- // --- // --- // --- /// ENST00000005924 // intron // 0 // --- // --- // --- // ---	ADIPOR2	ADIPOR2, Homo sapiens adiponectin receptor 2 (ADIPOR2), p13.33
SNP_A-2130465	atactcaaactttcct[A/G]agaaatttcaactgga	A	G	NM_021953 // intron // 0 // Hs.239 // FOXM1 // 2305 // Homo sapiens forkhead box M1 (FOXM1), transcript variant 2, mRNA. /// NM_202002 // intron // 0 // Hs.239 // FOXM1 // 2305 // Homo sapiens forkhead box M1 (FOXM1), transcript variant 1, mRNA. /// ENST0	FOXM1	FOXM1, Homo sapiens forkhead box M1 (FOXM1), transcript variant 2, p13.33
SNP_A-2232770	ctcactgcctcaggca[C/T]gggcacgaagaagaga	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.33
SNP_A-2300655	gcctgccctgtcgtcc[A/G]catgacaacctgggag	A	G	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.33
SNP_A-2217171	cctctttacaaaatga[C/T]gaggtttttaccccac	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.33
SNP_A-2186521	cagggaccaggtgtcc[A/G]gagcttcccagcagtc	A	G	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2101130	agatcagggaacaacc[G/T]agtgactgggcaaagt	G	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2255556	cttgtgcatggtgaga[C/G]gacaaggggcaatcaa	C	G	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // --- // --- // --- // ---	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1652876	gaggcaccatcactgggtatcagc[C/T]atctcatctcaggatc ccaccttaa	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // transmembrane 4 superfamily member tetraspan NET-5	NET-5	NET-5, rs10491967, transmembrane 4 superfamily member tetraspan NET-5,p13.32
SNP_A-2027267	aagctacagagaaccca[A/G]gtgactcttcatcca	A	G	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // — // — // —	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-1801339	gtaggaccctgtctca[C/T]gatctgtgtggta	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // — // — // —	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-1932131	ttcctcagaatataaa[C/T]gctgtacaaggtgtta	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // — // — // —	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-1910348	tgtccagtacctccta[C/T]gtatttgttacgcact	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // — // — // —	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-1859255	tcagctcctttatgtc[C/T]ctgtcctagctatctg	C	T	NM_006675 // intron // 0 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// ENST00000011898 // intron // 0 // — // — // —	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2164214	caaaagttgataccta[C/T]ccttcatgagactgcc	C	T	NM_006675 // downstream // 10178 // Hs.129826 // NET-5 // 10867 // Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA. /// NM_001030 // upstream // 84819 // Hs.546291 // RPS27 // 6232 // Homo sapiens ribosomal protein S27 (metal	NET-5	NET-5, Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), p13.32
SNP_A-2304795	gctctgtggttctgad[A/G]cttttcacatccactc	A	G	NM_032680 // intron // 0 // Hs.504534 // MGC4266 // 84766 // Homo sapiens hypothetical protein MGC4266 (MGC4266), mRNA. /// ENST00000333750 // intron // 0 // — // — // — /// ENST00000252322 // intron // 0 // — // — // —	MGC4266	MGC4266, Homo sapiens hypothetical protein MGC4266 (MGC4266), p13.32
SNP_A-2106546	agcctcaatcacctaa[A/C]tgaattgtgcagttca	A	C	NM_032680 // intron // 0 // Hs.504534 // MGC4266 // 84766 // Homo sapiens hypothetical protein MGC4266 (MGC4266), mRNA. /// ENST00000252322 // intron // 0 // — // — // —	MGC4266	MGC4266, Homo sapiens hypothetical protein MGC4266 (MGC4266), p13.32
SNP_A-1881344	tctttcaggttctgag[C/G]acactgtggtgagtga	C	G	NM_032680 // upstream // 22775 // Hs.504534 // MGC4266 // 84766 // Homo sapiens hypothetical protein MGC4266 (MGC4266), mRNA. /// NM_020367 // downstream // 36097 // Hs.504538 // PARP11 // 57097 // Homo sapiens poly (ADP-ribose) polymerase family, member	MGC4266	MGC4266, Homo sapiens hypothetical protein MGC4266 (MGC4266), p13.32
SNP_A-2122896	agtggctacaggatga[A/G]ctgggactcaaacaca	A	G	NM_020367 // upstream // 376591 // Hs.504538 // PARP11 // 57097 // Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), mRNA. /// NM_001759 // upstream // 23807 // Hs.376071 // CCND2 // 894 // Homo sapiens cyclin D2 (CCND2), mRNA. /// ENS	PARP11	PARP11, Homo sapiens poly (ADP-ribose) polymerase family, member 11 (PARP11), p13.32
SNP_A-1899148	tggaaaggctgccatg[A/G]caaaaataagctggaa	A	G	NM_020638 // upstream // 6193 // Hs.287370 // FGF23 // 8074 // Homo sapiens fibroblast growth factor 23 (FGF23), mRNA. /// NM_020996 // downstream // 48221 // Hs.166015 // FGF6 // 2251 // Homo sapiens fibroblast growth factor 6 (FGF6), mRNA. /// ENST00000	FGF23	FGF23, Homo sapiens fibroblast growth factor 23 (FGF23), p13.32
SNP_A-1863295	tcatttgtctataggaa[C/T]gattggactgtagatg	C	T	NM_020638 // upstream // 44711 // Hs.287370 // FGF23 // 8074 // Homo sapiens fibroblast growth factor 23 (FGF23), mRNA. /// NM_020996 // downstream // 9703 // Hs.166015 // FGF6 // 2251 // Homo sapiens fibroblast growth factor 6 (FGF6), mRNA. /// ENST00000	FGF23	FGF23, Homo sapiens fibroblast growth factor 23 (FGF23), p13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082639	acggcatgcactacaa[C/T]cagtgggtctcccaca	C	T	NM_020996 // intron // 0 // Hs.166015 // FGF6 // 2251 // Homo sapiens fibroblast growth factor 6 (FGF6), mRNA. /// ENST00000228837 // intron // 0 // --- // --- // --- // ---	FGF6	FGF6, Homo sapiens fibroblast growth factor 6 (FGF6), p13.32
SNP_A-2108568	agctggccagcactta[C/G]aactcccattacacca	C	G	NM_003845 // intron // 0 // Hs.439530 // DYRK4 // 8798 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4), mRNA. /// ENST00000010132 // intron // 0 // --- // --- // --- // ---	DYRK4	DYRK4, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4), p13.32
SNP_A-1828422	taagcaaaaaggaacc[A/G]gaacctgaagatttgg	A	G	NM_005002 // intron // 0 // Hs.75227 // NDUFA9 // 4704 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), mRNA. /// ENST00000266544 // intron // 0 // --- // --- // --- // ---	NDUFA9	NDUFA9, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), p13.32
SNP_A-1919671	ttaaggttctagttaa[A/C]cactgagaaactggcc	A	C	NM_005002 // downstream // 10156 // Hs.75227 // NDUFA9 // 4704 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), mRNA. /// NM_017417 // upstream // 23199 // Hs.511985 // GALNT8 // 26290 // Homo sapiens UDP-N-acetyl-alp	NDUFA9	NDUFA9, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), p13.32
SNP_A-1820024	gttgtttgaatgacag[A/G]agagaagcagttcagt	A	G	NM_017417 // intron // 0 // Hs.511985 // GALNT8 // 26290 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA. /// ENST00000252318 // intron // 0 // --- // --- // --- // ---	GALNT8	GALNT8, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), p13.32
SNP_A-1755156	tatttccagtgtggaggtcagagag[C/T]caaacctttgaggtgga ggctcccc	C	T	NM_000217 // downstream // 14783 // Hs.60843 // KCNA1 // 3736 // potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) /// NM_002234 // upstream // 116270 // Hs.150208 // KCNA5 // 3741 // potassium voltage-ga	KCNA1	KCNA1 , rs10492062, potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) ,p13.32
SNP_A-2224501	cgtatcagggacccaa[A/C]ggaataactaggacac	A	C	NM_000217 // downstream // 41865 // Hs.60843 // KCNA1 // 3736 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), mRNA. /// ENST00000228858 // downstream // 41865 // --- // --- // –	KCNA1	KCNA1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), p13.32
SNP_A-1900302	tggagacctaagctaa[C/G]cgtccttttctcctcc	C	G	NM_000217 // downstream // 69889 // Hs.60843 // KCNA1 // 3736 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), mRNA. /// ENST00000228858 // downstream // 69889 // --- // --- // –	KCNA1	KCNA1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), p13.32
SNP_A-2048444	aagcataatccagcca[C/T]gattacaataggagag	C	T	NM_000217 // downstream // 74809 // Hs.60843 // KCNA1 // 3736 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), mRNA. /// ENST00000228858 // downstream // 74809 // --- // --- // –	KCNA1	KCNA1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), p13.32
SNP_A-1812170	gtggaggaaagagagc[A/G]aagtgaccgccagttt	A	G	NM_000217 // downstream // 91510 // Hs.60843 // KCNA1 // 3736 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), mRNA. /// ENST00000228858 // downstream // 91510 // --- // --- // –	KCNA1	KCNA1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), p13.32
SNP_A-1890462	tgatctcctagttagc[C/T]cctcaggtccaggtac	C	T	NM_000217 // downstream // 108322 // Hs.60843 // KCNA1 // 3736 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), mRNA. /// ENST00000228858 // downstream // 108322 // --- // --- // ---	KCNA1	KCNA1, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia) (KCNA1), p13.32
SNP_A-2301777	gcggactgttcctaat[C/T]atacagccagcaggag	C	T	NM_002234 // downstream // 167013 // Hs.150208 // KCNA5 // 3741 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), mRNA. /// NM_207433 // downstream // 152948 // Hs.525253 // --- // 0 // Homo sapiens FLJ44874 prot	KCNA5	KCNA5, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), p13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2211820	ccctctgaacgatagc[A/G]caagactgtatctttt	A	G	NM_002234 // downstream // 288191 // Hs.150208 // KCNA5 // 3741 // Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), mRNA. /// NM_207433 // downstream // 31770 // Hs.525253 // --- // 0 // Homo sapiens FLJ44874 prote	KCNA5	KCNA5, Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), p13.31
SNP_A-2028977	aatccagaaagatgac[A/G]aggaatgggtcacagg	A	G	NM_207433 // upstream // 1724 // Hs.525253 // --- // 0 // Homo sapiens FLJ44874 protein (FLJ44874), mRNA. /// NM_002527 // upstream // 125153 // Hs.99171 // NTF3 // 4908 // Homo sapiens neurotrophin 3 (NTF3), mRNA. /// ENST00000358037 // upstream // 1724	-	-, Homo sapiens FLJ44874 protein (FLJ44874), p13.31
SNP_A-1714911	ctggattcgagttaaaatcatctcc[G/T]ctgtagttctcctgattaccatcat	G	T	NM_002234 // downstream // 322199 // Hs.150208 // KCNA5 // 3741 // potassium voltage-gated channel, shaker-related subfamily, member 5 /// NM_002527 // upstream // 125118 // Hs.99171 // NTF3 // 4908 // neurotrophin 3	KCNA5	KCNA5 , rs10492094, potassium voltage-gated channel, shaker-related subfamily, member 5 ,p13.31
SNP_A-2029004	agctcacaacacctaa[A/C]ccaggcagtcatgggt	A	C	NM_207433 // upstream // 88152 // Hs.525253 // --- // 0 // Homo sapiens FLJ44874 protein (FLJ44874), mRNA. /// NM_002527 // upstream // 38725 // Hs.99171 // NTF3 // 4908 // Homo sapiens neurotrophin 3 (NTF3), mRNA. /// ENST00000358037 // upstream // 88152	-	-, Homo sapiens FLJ44874 protein (FLJ44874), p13.31
SNP_A-2238270	ctctggacaataacaa[C/T]ggtggccaatgttcat	C	T	NM_020373 // intron // 0 // Hs.148970 // TMEM16B // 57101 // Homo sapiens transmembrane protein 16B (TMEM16B), mRNA. /// ENST00000327087 // intron // 0 // --- // --- // --- // ---	TMEM16B	TMEM16B, Homo sapiens transmembrane protein 16B (TMEM16B), p13.31
SNP_A-2299181	gccctacagtgtacaa[C/T]gacttccatattccca	C	T	NM_000552 // intron // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-1886588	tgactcaatgataagg[A/C]aacaccctagaatagt	A	C	NM_000552 // intron // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2293510	gcagcagaatgatgta[C/T]cggccagactccacca	C	T	NM_000552 // CDS // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // CDS // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2025642	aaaatgactaaatcca[C/T]tgaggaatcaccaggc	C	T	NM_000552 // intron // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-1883139	tgaaatgagcgcctaa[C/T]aggatagccacagcct	C	T	NM_000552 // intron // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2028077	aaacgtgccagaacta[C/T]gacctggagtgcatga	C	T	NM_000552 // CDS // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // CDS // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2203853	ccagaggtttatttca[A/C]atagtgagtgtcgcta	A	C	NM_000552 // intron // 0 // Hs.440848 // VWF // 7450 // Homo sapiens von Willebrand factor (VWF), mRNA. /// ENST00000261405 // intron // 0 // --- // --- // --- // ---	VWF	VWF, Homo sapiens von Willebrand factor (VWF), p13.31
SNP_A-2213286	ccgctctgtcaaagat[A/G]aactaggaaagacgcc	A	G	NM_001038 // upstream // 3735 // Hs.130989 // SCNN1A // 6337 // Homo sapiens sodium channel, nonvoltage-gated 1 alpha (SCNN1A), mRNA. /// NM_002342 // upstream // 4878 // Hs.1116 // LTBR // 4055 // Homo sapiens lymphotoxin beta receptor (TNFR superfamily,	SCNN1A	SCNN1A, Homo sapiens sodium channel, nonvoltage-gated 1 alpha (SCNN1A), p13.31
SNP_A-2078815	acccaaacaagacaag[A/G]ccagacatttcatttc	A	G	NM_002342 // downstream // 44802 // Hs.1116 // LTBR // 4055 // Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), mRNA. /// NM_001242 // upstream // 8535 // Hs.355307 // TNFRSF7 // 939 // Homo sapiens tumor necrosis factor recepto	LTBR	LTBR, Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), p13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2139106	atcctcaagcagatga[A/G]gactcagtcaagaggt	A	G	NM_002342 // downstream // 44882 // Hs.1116 // LTBR // 4055 // Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), mRNA. /// NM_001242 // upstream // 8455 // Hs.355307 // TNFRSF7 // 939 // Homo sapiens tumor necrosis factor recepto	LTBR	LTBR, Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), p13.31
SNP_A-1888566	tgaggatgggggatcat[A/C]accagaacaggccaca	A	C	NM_020400 // upstream // 1932 // Hs.155538 // GPR92 // 57121 // Homo sapiens G protein-coupled receptor 92 (GPR92), mRNA. /// NM_032489 // downstream // 23 // Hs.123239 // ACRBP // 84519 // Homo sapiens acrosin binding protein (ACRBP), mRNA. /// ENST00000	GPR92	GPR92, Homo sapiens G protein-coupled receptor 92 (GPR92), p13.31
SNP_A-1801300	gtaggaaagctgttga[C/G]agtcatggccgtatac	C	G	NM_003481 // intron // 0 // Hs.3759 // USP5 // 8078 // Homo sapiens ubiquitin specific protease 5 (isopeptidase T) (USP5), mRNA. /// ENST00000229268 // intron // 0 // --- // --- // ---	USP5	USP5, Homo sapiens ubiquitin specific protease 5 (isopeptidase T) (USP5), p13.31
SNP_A-2146759	atgcttccctgccacd[C/G]aggagtctgagcaaat	C	G	NM_015509 // downstream // 11292 // Hs.527839 // NECAP1 // 25977 // Homo sapiens DKFZP566B183 protein (DKFZP566B183), mRNA. /// NM_016184 // upstream // 14576 // Hs.504657 // CLEC4A // 50856 // Homo sapiens C-type (calcium dependent, carbohydrate-recognit	NECAP1	NECAP1, Homo sapiens DKFZP566B183 protein (DKFZP566B183), p13.31
SNP_A-1733340	cggccctaatgtatacctattaac[A/G]gccaggtacgatgactc acgcctga	A	G	NM_015509 // downstream // 18630 // Hs.527839 // DKFZP566B183 // 25977 // DKFZP566B183 protein /// NM_016184 // upstream // 7237 // Hs.115515 // CLECSF6 // 50856 // C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6	DKFZP566B183	DKFZP566B183, rs2110067, DKFZP566B183 protein ,p13.31
SNP_A-2144446	atgatactgttaccag[C/T]agaagagattccagtt	C	T	NM_016184 // downstream // 29090 // Hs.504657 // CLEC4A // 50856 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6 (CLECSF6), transcript vari /// NM_194448 // downstream // 29090 // Hs.504657 // CLEC4	CLEC4A	CLEC4A, Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6 (CLECSF6), transcript vari p13.31
SNP_A-2290970	gcaagtcccttcccaa[A/C]aagcgcaagggacagt	A	C	ENST00000352293 // upstream // 45275 // --- // --- // --- /// ENST00000307147 // upstream // 45275 // --- // --- // --- /// ENST00000340787 // upstream // 45275 // --- // --- // --- /// ENST00000315287 // downstream // 88147 // --- //	-	p13.31
SNP_A-2002511	gcaataaaacagacac[C/T]gagaagtaagatgaaa	C	T	NM_080387 // CDS // 0 // Hs.351811 // CLEC4D // 338339 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 8 (CLECSF8), mRNA. /// ENST00000299665 // CDS // 0 // --- // --- // ---	CLEC4D	CLEC4D, Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 8 (CLECSF8), p13.31
SNP_A-1922472	ttagaagaagcaaggt[A/G]aacaaggaatattgct	A	G	NM_020661 // upstream // 22290 // Hs.149342 // AICDA // 57379 // Homo sapiens activation-induced cytidine deaminase (AICDA), mRNA. /// ENST00000229335 // upstream // 22290 // --- // --- // --- /// ENST00000318527 // upstream // 6135 // --- // --- /	AICDA	AICDA, Homo sapiens activation-induced cytidine deaminase (AICDA), p13.31
SNP_A-1791795	gggtgaatcagcaatt[C/G]aagtgtgtctttcta	C	G	NM_144670 // intron // 0 // Hs.334306 // FLJ25179 // 144568 // Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // --- /// ENST00000299698 // intron // 0 // --- // --- // --- E	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31
SNP_A-2051589	aaggtaaagtccaaac[A/G]caggcctggagctcag	A	G	NM_144670 // intron // 0 // Hs.334306 // FLJ25179 // 144568 // Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // --- /// ENST00000299698 // intron // 0 // --- // --- // --- E	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31
SNP_A-2002513	cctcttttgtgtccd[C/T]caaacactgatttcca	C	T	NM_144670 // intron // 0 // Hs.334306 // FLJ25179 // 144568 // Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // --- /// ENST00000299698 // intron // 0 // --- // --- // --- E	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2054409	aagttacctattggt[G/T]cactattctaggcacg	G	T	NM_144670 // intron // 0 // Hs.334306 // FLJ25179 // 144568 // Homo sapiens hypothetical protein FLJ25179 (FLJ25179), mRNA. /// ENST00000338538 // intron // 0 // --- // --- // --- // --- /// ENST00000299698 // intron // 0 // --- // --- // --- /// E	FLJ25179	FLJ25179, Homo sapiens hypothetical protein FLJ25179 (FLJ25179), p13.31
SNP_A-1708394	aaacatttatgggctctgctcttaa[C/T]gtctctttgcctactggac cctg	C	T	NM_005810 // intron // 0 // Hs.146322 // KLRG1 // 10219 // killer cell lectin-like receptor subfamily G, member 1	KLRG1	KLRG1, rs3026252, killer cell lectin-like receptor subfamily G, member 1,p13.31
SNP_A-1742553	attgcacaagggactacagaaccca[C/T]ggtgttgtggagaag aatgccactt	C	T	NM_000014 // upstream // 18314 // Hs.74561 // A2M // 2 // alpha-2-macroglobulin /// NM_002864 // downstream // 14636 // Hs.480143 // PZP // 5858 // pregnancy-zone protein	A2M	A2M , rs2889717, alpha-2-macroglobulin ,p13.31
SNP_A-2308409	gcttgttgtggaatta[C/T]actatgcctgttactc	C	T	ENST00000324717 // upstream // 13155 // --- // --- // --- // --- /// ENST00000341155 // upstream // 40997 // --- // --- // --- // ---	-	p13.31
SNP_A-2235187	ctccccccattctccat[C/T]agctccttttccagct	C	T	ENST00000341155 // downstream // 65667 // --- // --- // --- // --- /// ENST00000334227 // downstream // 18986 // --- // --- // --- // ---	-	p13.31
SNP_A-1908235	tgtacctcagtctcgaat[C/T]gattagtttccctg	C	T	NM_002258 // upstream // 54300 // Hs.169824 // KLRB1 // 3820 // Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLR1). mRNA. /// NM_013269 // upstream // 7424 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell recept	KLRB1	KLRB1, Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), p13.31
SNP_A-2305852	gctgctatggctgcta[C/T]aacaactttcaaaaa	C	T	NM_002258 // upstream // 61299 // Hs.169824 // KLRB1 // 3820 // Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1). mRNA. /// NM_013269 // upstream // 425 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell recepto	KLRB1	KLRB1, Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), p13.31
SNP_A-2102167	agatgttggaactatc[C/T]gacaaacagtttaaag	C	T	NM_013269 // intron // 0 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, mRNA. /// NM_001004420 // intron // 0 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell receptor (OCIL).	CLEC2D	CLEC2D, Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, p13.31
SNP_A-1822608	gtttttgatataaga[C/G]aagtctactggcaaca	C	G	NM_013269 // intron // 0 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, mRNA. /// NM_001004420 // intron // 0 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell receptor (OCIL).	CLEC2D	CLEC2D, Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, p13.31
SNP_A-2031467	actatgagccaaatca[A/T]ggatggaattaggaat	A	T	NM_013269 // downstream // 25413 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1. mRNA. /// NM_001004420 // downstream // 25413 // Hs.268326 // CLEC2D // 29121 // Homo sapiens lectin-like NK cell r	CLEC2D	CLEC2D, Homo sapiens lectin-like NK cell receptor (OCIL), transcript variant 1, p13.31
SNP_A-2244522	ctggacttctgagcta[C/T]agaaaccgcaagataa	C	T	NM_172004 // upstream // 13649 // Hs.434223 // DCAL1 // 160365 // Homo sapiens dendritic cell-associated lectin-1 (DCAL1), mRNA. /// NM_001781 // downstream // 5575 // Hs.208854 // CD69 // 969 // Homo sapiens CD69 antigen (p60, early T-cell activation ant	DCAL1	DCAL1, Homo sapiens dendritic cell-associated lectin-1 (DCAL1), p13.31
SNP_A-2279446	gaggatatacatagga[A/G]taggtttgttgggcca	A	G	NM_001781 // intron // 0 // Hs.208854 // CD69 // 969 // Homo sapiens CD69 antigen (p60, early T-cell activation antigen) (CD69), mRNA. /// ENST00000228434 // intron // 0 // --- // --- // ---	CD69	CD69, Homo sapiens CD69 antigen (p60, early T-cell activation antigen) (CD69), p13.31
SNP_A-1959413	tttgcatttcaatca[G/T]caaagaatgaaagtcc	G	T	NM_001781 // upstream // 39305 // Hs.208854 // CD69 // 969 // Homo sapiens CD69 antigen (p60, early T-cell activation antigen) (CD69), mRNA. /// NM_016523 // upstream // 27275 // Hs.183125 // KLRF1 // 51348 // Homo sapiens killer cell lectin-like receptor	CD69	CD69, Homo sapiens CD69 antigen (p60, early T-cell activation antigen) (CD69), p13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2031750	ctttatcatttgcaga[A/G]gtagtataaagattaa	A	G	NM_201623 // intron // 0 // Hs.190519 // CLEC12A // 160364 // Homo sapiens myeloid inhibitory C-type lectin-like receptor (MICL), transcript variant 2, mRNA. /// NM_138337 // intron // 0 // Hs.190519 // CLEC12A // 160364 // Homo sapiens myeloid inhibitory	CLEC12A	CLEC12A, Homo sapiens myeloid inhibitory C-type lectin-like receptor (MICL), transcript variant 2, p13.31
SNP_A-1702595	tggttattagcattttcagtaagga[C/G]gtatgtttagtaaacagcc ctcatc	C	G	NM_005042 // downstream // 4608 // Hs.73952 // PRH2 // 5555 // proline-rich protein HaeIII subfamily 2 /// NM_023922 // downstream // 1328 // Hs.278469 // TAS2R14 // 50840 // taste receptor, type 2, member 14	PRH2	PRH2 , rs10492104, proline-rich protein HaeIII subfamily 2 ,p13.2
SNP_A-1825378	taaataaactaagttc[A/G]atgcagctaatagagc	A	G	NM_176889 // upstream // 16494 // Hs.504733 // TAS2R49 // 259295 // Homo sapiens taste receptor, type 2, member 49 (TAS2R49), mRNA. /// NM_176888 // downstream // 7303 // Hs.534594 // TAS2R48 // 259294 // Homo sapiens taste receptor, type 2, member 48 (TA	TAS2R49	TAS2R49, Homo sapiens taste receptor, type 2, member 49 (TAS2R49), p13.2
SNP_A-1734858	gctgaattatggctttttctttttcc[A/C]ataggatttacatgtacactc atct	A	C	NM_001987 // intron // 0 // Hs.171262 // ETV6 // 2120 // ets variant gene 6 (TEL oncogene)	ETV6	ETV6 , rs2900208, ets variant gene 6 (TEL oncogene),p13.2
SNP_A-1683928	tcattgctaggaattatctgcaaca[A/G]taatgaatatctccttgttc tttta	A	G	NM_001987 // intron // 0 // Hs.171262 // ETV6 // 2120 // ets variant gene 6 (TEL oncogene)	ETV6	ETV6 , rs2856338, ets variant gene 6 (TEL oncogene),p13.2
SNP_A-2034823	aaatgactgagaagtg[A/G]aagcgttctgcctatg	A	G	NM_001987 // downstream // 160257 // Hs.504765 // ETV6 // 2120 // Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), mRNA. /// NM_138722 // upstream // 15300 // Hs.504794 // BCL2L14 // 79370 // Homo sapiens BCL2-like 14 (apoptosis facilitator) (BCL2L1	ETV6	ETV6, Homo sapiens ets variant gene 6 (TEL oncogene) (ETV6), p13.2
SNP_A-1903577	tgggacccttcatgga[C/G]cttcttaatgtgcaag	C	G	NM_138722 // intron // 0 // Hs.504794 // BCL2L14 // 79370 // Homo sapiens BCL2-like 14 (apoptosis facilitator) (BCL2L14), transcript variant 1, mRNA. /// NM_138723 // intron // 0 // Hs.504794 // BCL2L14 // 79370 // Homo sapiens BCL2-like 14 (apoptosis fac	BCL2L14	BCL2L14, Homo sapiens BCL2-like 14 (apoptosis facilitator) (BCL2L14), transcript variant 1, p13.2
SNP_A-2298260	gccatgggaagtttca[C/T]gcaaagccagtttctc	C	T	NM_030640 // upstream // 20802 // Hs.536535 // DUSP16 // 80824 // Homo sapiens dual specificity phosphatase 16 (DUSP16), mRNA. /// NM_001310 // upstream // 28712 // Hs.13313 // CREBL2 // 1389 // Homo sapiens cAMP responsive element binding protein-like 2	DUSP16	DUSP16, Homo sapiens dual specificity phosphatase 16 (DUSP16), p13.2
SNP_A-2090535	acttgtcagagttcag[A/G]aaccactggtagaaat	A	G	NM_001310 // intron // 0 // Hs.13313 // CREBL2 // 1389 // Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2), mRNA. /// ENST00000228865 // intron // 0 // — // — // — // —	CREBL2	CREBL2, Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2), p13.2
SNP_A-2033745	ttctcagctgtaaacc[C/T]gggtcactccagccat	C	T	NM_018654 // upstream // 1682 // Hs.546402 // GPRC5D // 55507 // Homo sapiens G protein-coupled receptor, family C, group 5, member D (GPRC5D), mRNA. /// NM_015987 // downstream // 22804 // Hs.294133 // HEBP1 // 50865 // Homo sapiens heme binding protein	GPRC5D	GPRC5D, Homo sapiens G protein-coupled receptor, family C, group 5, member D (GPRC5D), p13.1
SNP_A-1899477	tggaagagtgtgcaaa[A/C]ctttcgagactcctca	A	C	NM_015987 // upstream // 2119 // Hs.294133 // HEBP1 // 50865 // Homo sapiens heme binding protein 1 (HEBP1), mRNA. /// ENST00000014930 // upstream // 2119 // — // — // — // — /// ENST00000331998 // downstream // 162 // — // — // — // — ///	HEBP1	HEBP1, Homo sapiens heme binding protein 1 (HEBP1), p13.1
SNP_A-2125388	agtttaagtaattagc[C/G]gatgtggtttggctct	C	G	ENST00000197268 // intron // 0 // — // — // — // —	-	p13.1
SNP_A-1748491	cgttggctgatctttcaacttccaa[A/C]ttctttacaacttccaacatt ttat	A	C	NM_001423 // downstream // 7232 // Hs.306692 // EMP1 // 2012 // epithelial membrane protein 1 /// NM_182558 // downstream // 147084 // Hs.448717 // FLJ33810 // 283422 // hypothetical protein FLJ33810	EMP1	EMP1 , rs10505773, epithelial membrane protein 1 ,p13.1
SNP_A-2195300	catggccccctatgca[G/T]gaagtgtctcttaaga	G	T	NM_001423 // downstream // 78250 // Hs.436298 // EMP1 // 2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 76066 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRN	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2044423	aagaaaaaggaaagta[C/G]gggcatatgaagggat	C	G	NM_001423 // downstream // 109694 // Hs.436298 // EMP1 // 2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 44622 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mR	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-2236554	ctcctatgtttttctg[A/G]cacctaattctccttg	A	G	NM_001423 // downstream // 109778 // Hs.436298 // EMP1 // 2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 44538 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mR	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-2033954	atactgatttcttcaj[C/T]agtcccaatactttcct	C	T	NM_001423 // downstream // 116722 // Hs.436298 // EMP1 // 2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 37594 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mR	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-2033975	tcactttcacttagat[A/G]gaacagagctttttgga	A	G	NM_001423 // downstream // 141389 // Hs.436298 // EMP1 // 2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 12927 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mR	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-1728319	tgacacaataatgaagcaaccttc[C/T]aatacattcaagaagct ggaaactg	C	T	NM_001423 // downstream // 142653 // Hs.306692 // EMP1 // 2012 // epithelial membrane protein 1 /// NM_182558 // downstream // 11663 // Hs.448717 // FLJ33810 // 283422 // hypothetical protein FLJ33810	EMP1	EMP1 , rs10492121, epithelial membrane protein 1 ,p13.1
SNP_A-1641841	aactgaaaaggctacctttataaa[C/T]ctcaaaactggctagg taggaatc	C	T	NM_001423 // downstream // 143767 // Hs.306692 // EMP1 // 2012 // epithelial membrane protein 1 /// NM_182558 // downstream // 10549 // Hs.448717 // FLJ33810 // 283422 // hypothetical protein FLJ33810	EMP1	EMP1 , rs1993510, epithelial membrane protein 1 ,p13.1
SNP_A-1730725	aaagaattaaatttatatatgaag[A/G]aacctacggtgtaccttg aaaattt	A	G	NM_001423 // downstream // 144362 // Hs.306692 // EMP1 // 2012 // epithelial membrane protein 1 /// NM_182558 // downstream // 9954 // Hs.448717 // FLJ33810 // 283422 // hypothetical protein FLJ33810	EMP1	EMP1 , -, epithelial membrane protein 1 ,p13.1
SNP_A-2178562	cactctagcctggtac[A/C]aacacctgagaaaggc	A	C	NM_001423 // downstream // 153042 // Hs.436298 // EMP1 // 2012 // Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /// NM_182558 // downstream // 1274 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRN	EMP1	EMP1, Homo sapiens epithelial membrane protein 1 (EMP1), p13.1
SNP_A-2302854	gctagagtgttgtcac[A/C]agaatgtctgtctgc	A	C	NM_182558 // upstream // 30003 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 154777 // Hs.445066 // GRIN2B // 2904 // Homo sapiens glutamate receptor, ionotropic, N-methyl	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-1888150	tgagccgaagctcgag[A/G]ataggagcaccaccaaa	A	G	NM_182558 // upstream // 41928 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 142852 // Hs.445066 // GRIN2B // 2904 // Homo sapiens glutamate receptor, ionotropic, N-methyl	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-2083275	actaaagcatttccatg[A/C]attaagaagctagtcc	A	C	NM_182558 // upstream // 56153 // Hs.448717 // FLJ33810 // 283422 // Homo sapiens hypothetical protein FLJ33810 (FLJ33810), mRNA. /// NM_000834 // downstream // 128627 // Hs.445066 // GRIN2B // 2904 // Homo sapiens glutamate receptor, ionotropic, N-methyl	FLJ33810	FLJ33810, Homo sapiens hypothetical protein FLJ33810 (FLJ33810), p13.1
SNP_A-1656425	tgggagaattccagtgtttattaa[C/T]tgctggtgatcctctctcta ggat	C	T	NM_000834 // intron // 0 // Hs.1198 // GRIN2B // 2904 // glutamate receptor, ionotropic, N-methyl D-aspartate 2B	GRIN2B	GRIN2B , rs2160734, glutamate receptor, ionotropic, N-methyl D-aspartate 2B,p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1834111	tacatcccagcattat[A/C]aaaagctcaacccat	A	C	NM_000834 // upstream // 31428 // Hs.445066 // GRIN2B // 2904 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), mRNA. /// NM_018179 // upstream // 354136 // Hs.546406 // ATF7IP // 55729 // Homo sapiens activating transcript	GRIN2B	GRIN2B, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), p13.1
SNP_A-1785845	ggctgaattagcacat[C/G]aggctgaagttggcca	C	G	NM_000834 // upstream // 72221 // Hs.445066 // GRIN2B // 2904 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), mRNA. /// NM_018179 // upstream // 313343 // Hs.546406 // ATF7IP // 55729 // Homo sapiens activating transcript	GRIN2B	GRIN2B, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B), p13.1
SNP_A-2138103	atccaagccattatgal[A/G]aatccaaaaggaattg	A	G	NM_175874 // intron // 0 // Hs.534555 // MGC47869 // 144608 // Homo sapiens hypothetical protein MGC47869 (MGC47869), mRNA. /// ENST00000330828 // intron // 0 // — // — // — // —	MGC47869	MGC47869, Homo sapiens hypothetical protein MGC47869 (MGC47869), p12.3
SNP_A-1797723	gtttggctagagtaa[A/C]tgaaaggatggaggtg	A	C	NM_021071 // intron // 0 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// ENST00000228936 // intron // 0 // — // — // —	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-2297490	gccagaaaagatttggg[C/T]atatgttagtagctag	C	T	NM_021071 // intron // 0 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// ENST00000228936 // intron // 0 // — // — // —	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-1699879	ttaaggaccttctgatgttcctt c[A/G]cttactgattgagagaaaa acaaag	A	G	NM_021071 // intron // 0 // Hs.512584 // DO // 420 // Dombrock blood group	DO	DO, rs1001096, Dombrock blood group,p12.3
SNP_A-2260864	gaaactgatgtagtaa[C/G]tgttattgatatgtt	C	G	NM_021071 // upstream // 6359 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 32322 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 635	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-2152512	attaagatattagcag[A/G]attatgttcaaacc	A	G	NM_021071 // upstream // 7162 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 31519 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 716	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-2035191	atggagttgagtcaa[G/T]ctagtcagtagttgag	G	T	NM_021071 // upstream // 8394 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 30287 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 839	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-2035198	caacctaggctaccaa[A/C]tcgtaaagacgttctt	A	C	NM_021071 // upstream // 29919 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 8762 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 299	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-2035199	tgcagggatataaaca[C/G]ctagccctcttcccct	C	G	NM_021071 // upstream // 33297 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 5384 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 332	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-2035204	tctaggaataatcaga[C/T]ggctagcaatgtctgg	C	T	NM_021071 // upstream // 34558 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 4123 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 345	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-1803311	gtattgtattaacta[C/T]tactatggtctggata	C	T	NM_021071 // upstream // 35222 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 3459 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 352	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2120851	agtcgctgtgtttttc[C/T]agaactctcaactcca	C	T	NM_021071 // upstream // 36615 // Hs.13776 // DO // 420 // Homo sapiens Dombrock blood group (DO), mRNA. /// NM_000900 // downstream // 2066 // Hs.365706 // MGP // 4256 // Homo sapiens matrix Gla protein (MGP), mRNA. /// ENST00000228936 // upstream // 366	DO	DO, Homo sapiens Dombrock blood group (DO), p12.3
SNP_A-1916271	tgttgtaggttgtggg[A/T]aatttaatgacattca	A	T	NM_001175 // intron // 0 // Hs.504877 // ARHGDIB // 397 // Homo sapiens Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB), mRNA. /// ENST00000228945 // intron // 0 // — // — // — // —	ARHGDIB	ARHGDIB, Homo sapiens Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB), p12.3
SNP_A-2204779	ccaggcatcctgaaca[C/T]caaaggattatgagga	C	T	NM_032918 // upstream // 32881 // Hs.199487 // RERG // 85004 // Homo sapiens RAS-like, estrogen-regulated, growth inhibitor (RERG), mRNA. /// NM_002848 // upstream // 68302 // Hs.160871 // PTPRO // 5800 // Homo sapiens protein tyrosine phosphatase, recept	RERG	RERG, Homo sapiens RAS-like, estrogen-regulated, growth inhibitor (RERG), p12.3
SNP_A-2035525	agatagcttaggatga[A/G]gaaaccacagtgtcct	A	G	NM_002848 // intron // 0 // Hs.160871 // PTPRO // 5800 // Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, mRNA. /// NM_030668 // intron // 0 // Hs.160871 // PTPRO // 5800 // Homo sapiens protein tyrosine phosphat	PTPRO	PTPRO, Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 2, p12.3
SNP_A-2035786	tctttgcttcttccga[C/T]ggctagctctgttact	C	T	NM_007178 // intron // 0 // Hs.504895 // STRAP // 11171 // Homo sapiens serine/threonine kinase receptor associated protein (STRAP), mRNA. /// ENST00000025399 // intron // 0 // — // — // — // —	STRAP	STRAP, Homo sapiens serine p12.3
SNP_A-1694637	caactatgctacacagaagtttaga[A/T]atgaaggagataattgttccatgag	A	T	NM_015954 // downstream // 35941 // Hs.3727 // STRAP // 11171 // serine/threonine kinase receptor associated protein /// NM_020300 // upstream // 274427 // Hs.389700 // MGST1 // 4257 // microsomal glutathione S-transferase 1 /// NM_145764 // upstream //	STRAP	STRAP , rs10505790, serine.p12.3
SNP_A-2117480	aggtgtggccttggga[A/G]aacttaagagacaaag	A	G	NM_020300 // upstream // 23207 // Hs.389700 // MGST1 // 4257 // Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 1b, mRNA. /// NM_145792 // upstream // 23207 // Hs.389700 // MGST1 // 4257 // Homo sapiens microsomal glutathio	MGST1	MGST1, Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 1b, p12.3
SNP_A-2135391	atatttccaaataaga[A/C]caccttctgacatgag	A	C	NM_020300 // downstream // 89522 // Hs.389700 // MGST1 // 4257 // Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 1b, mRNA. /// NM_145792 // downstream // 89522 // Hs.389700 // MGST1 // 4257 // Homo sapiens microsomal gluta	MGST1	MGST1, Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 1b, p12.3
SNP_A-1705655	accctaggagcctattttctttgta[C/G]actatgttataatttatttgaagac	C	G	NM_018640 // upstream // 119806 // Hs.301914 // DAT1 // 55885 // neuronal specific transcription factor DAT1 /// NM_024730 // downstream // 1354567 // Hs.115497 // FLJ22655 // 79785 // hypothetical protein FLJ22655	DAT1	DAT1 , rs10492193, neuronal specific transcription factor DAT1 ,p12.3
SNP_A-2074336	acatacagaaagaaaa[A/G]agttcattgtggcctt	A	G	NM_001001395 // upstream // 175796 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 175796 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2186673	cagggccaagagaaaa[A/G]gtagtcagagtgaggg	A	G	NM_001001395 // upstream // 193109 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 193109 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1894580	tgccaccagattccct[C/T]actcttcagcttgcag	C	T	NM_001001395 // upstream // 483361 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 483361 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1898435	tgcttccttcactacc[A/G]acaagtttatgagaa	A	G	NM_001001395 // upstream // 736866 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 736866 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1793162	ggtagaatagcaagaaa[G/T]ggtgctttttctctt	G	T	NM_001001395 // upstream // 758279 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 758279 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2158436	attggttccaagcacc[C/T]gcctacctacatcaca	C	T	NM_001001395 // upstream // 908765 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 908765 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1820206	gtttacaagagtgtta[A/G]gtaagattctggagag	A	G	NM_001001395 // upstream // 922493 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 922493 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1878971	tcttaaaggcttactg[A/C]atttgttagaacaaa	A	C	NM_001001395 // upstream // 923651 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 923651 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2021081	aaaaaaaacagtgaga[A/G]acagtggtaggtgtg	A	G	NM_001001395 // upstream // 1000198 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1000198 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2137258	atcagtgacttgatg[C/T]aagtagcttcaataaa	C	T	NM_001001395 // upstream // 1073530 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1073530 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2249819	cttaattggctgaaa[A/C]aaatacagggctggaa	A	C	NM_001001395 // upstream // 1203279 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1203279 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-2229679	ctagtatatttgagca[C/T]tgaaattatttcctgg	C	T	NM_001001395 // upstream // 1414558 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA. /// NM_018640 // upstream // 1414558 // Hs.504908 // LMO3 // 55885 // Homo sapiens LIM domain only 3	LMO3	LMO3, Homo sapiens LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, p12.3
SNP_A-1798819	gtaacttaattattg[A/G]aaaagatcctgatgta	A	G	NM_024730 // upstream // 63366 // Hs.115497 // FLJ22655 // 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 107994 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma p	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-2174602	cacagatcaaaactc[A/G]ctgcaaacatgaaaac	A	G	NM_024730 // upstream // 72835 // Hs.115497 // FLJ22655 // 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 98525 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma po	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1859716	tcagggaaagctattc[A/G]aaagcaggccaagtca	A	G	NM_024730 // upstream // 73879 // Hs.115497 // FLJ22655 // 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 97481 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma po	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-2282459	gagttgaagagttaag[C/T]ccctactcaccatcat	C	T	NM_024730 // upstream // 78340 // Hs.115497 // FLJ22655 // 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 93020 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma po	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-2120944	agtctagggtgagaaa[C/G]cagttagtgatcatgc	C	G	NM_024730 // upstream // 103583 // Hs.115497 // FLJ22655 // 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 67777 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma p	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-2089794	acttcctcactgata[C/T]gcctttcaattgtct	C	T	NM_024730 // upstream // 126582 // Hs.115497 // FLJ22655 // 79785 // Homo sapiens hypothetical protein FLJ22655 (FLJ22655), mRNA. /// NM_004570 // upstream // 44778 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma p	FLJ22655	FLJ22655, Homo sapiens hypothetical protein FLJ22655 (FLJ22655), p12.3
SNP_A-1815054	gtgttcaccagaaaaaa[C/T]gtctacattctagat	C	T	NM_004570 // intron // 0 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // — // — // —	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-2223529	cggaacctagttgtga[C/T]atagaagtgttagcct	C	T	NM_004570 // intron // 0 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // — // — // —	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-2037071	tacaaaggagaaaaca[C/T]ggagctggaacaata	C	T	NM_004570 // intron // 0 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // — // — // —	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-1872679	tctagtgagctagcaa[A/T]gcgagttaaacagaca	A	T	NM_004570 // intron // 0 // Hs.22500 // PIK3C2G // 5288 // Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), mRNA. /// ENST00000266497 // intron // 0 // — // — // —	PIK3C2G	PIK3C2G, Homo sapiens phosphoinositide-3-kinase, class 2, gamma polypeptide (PIK3C2G), p12.3
SNP_A-1814483	gtgtgcatacagagaaa[A/G]tatgattattagggac	A	G	NM_033328 // downstream // 72445 // Hs.131288 // CAPZA3 // 93661 // Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA. /// NM_019012 // upstream // 318162 // Hs.188614 // PLEKHA5 // 54477 // Homo sapiens pleckstrin homolo	CAPZA3	CAPZA3, Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), p12.3
SNP_A-1914878	tgttagcattcctttc[G/T]aagtccaaacaaaata	G	T	NM_033328 // downstream // 211839 // Hs.131288 // CAPZA3 // 93661 // Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA. /// NM_019012 // upstream // 178768 // Hs.188614 // PLEKHA5 // 54477 // Homo sapiens pleckstrin homol	CAPZA3	CAPZA3, Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), p12.3
SNP_A-1954913	ttgctttttcctttc[A/G]atttaacacatagag	A	G	NM_019012 // intron // 0 // Hs.188614 // PLEKHA5 // 54477 // Homo sapiens pleckstrin homology domain containing, family A member 5 (PLEKHA5), mRNA. /// ENST00000299275 // intron // 0 // — // — // — /// ENST00000317589 // intron // 0 // — //	PLEKHA5	PLEKHA5, Homo sapiens pleckstrin homology domain containing, family A member 5 (PLEKHA5), p12.3
SNP_A-2191904	catcaactcaccagga[G/T]agtgagcactaagaac	G	T	NM_019012 // downstream // 2666 // Hs.188614 // PLEKHA5 // 54477 // Homo sapiens pleckstrin homology domain containing, family A member 5 (PLEKHA5), mRNA. /// NM_153207 // upstream // 60627 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protei	PLEKHA5	PLEKHA5, Homo sapiens pleckstrin homology domain containing, family A member 5 (PLEKHA5), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1790556	ggggccctcgctacc[A/G]acagttcctctccatg	A	G	NM_153207 // downstream // 160994 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 160573 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.3
SNP_A-1943106	ttggtattgcagagtat[A/C]attgaagccagtataa	A	C	NM_153207 // downstream // 348621 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 348200 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-2039395	aacatagccaaattcc[A/G]aatcttgggggagatg	A	G	NM_153207 // downstream // 365262 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 364841 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-1678262	tctatttttaatctgaggaaccttc[A/C]taatgctttctgtagtagctg cacc	A	C	NM_000921 // upstream // 441687 // Hs.386791 // PDE3A // 5139 // phosphodiesterase 3A, cGMP-inhibited /// NM_153207 // downstream // 406954 // Hs.528315 // AEBP2 // 121536 // AE binding protein 2	PDE3A	PDE3A , rs1527260, phosphodiesterase 3A, cGMP-inhibited ,p12.2
SNP_A-2188450	cagtgaatgaggagaga[G/T]aggttcctgatgtgaa	G	T	NM_153207 // downstream // 415642 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 415221 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-2076704	acatttcttttaggtc[A/T]ccatttattgatggac	A	T	NM_153207 // downstream // 482691 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 482270 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-1870424	tccttttttaatatcc[A/G]gcatctgacttattag	A	G	NM_153207 // downstream // 484326 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 483905 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-2021051	aaaaaaaaaaggcatag[A/G]catttgcaaagcatt	A	G	NM_153207 // downstream // 513233 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 512812 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-1918744	ttaacaagcttagaaa[C/T]ctcctaagtgcagggc	C	T	NM_153207 // downstream // 603356 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 602935 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-2038104	gcatagcaatattatc[A/G]ctatccttccaattc	A	G	NM_153207 // downstream // 605273 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 604852 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-1915038	tgttatgagatgggaa[C/G]atatacacagcctctcc	C	G	NM_153207 // downstream // 610758 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 610337 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1798365	gtaaagttggagtta[C/T]acaacacttggtaac	C	T	NM_153207 // downstream // 723096 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_153207 // downstream // 722675 // Hs.504943 // AEBP2 // 121536 // Homo sapiens AE binding protein 2 (AEBP2), mRNA. /// NM_000921 /	AEBP2	AEBP2, Homo sapiens AE binding protein 2 (AEBP2), p12.2
SNP_A-2178769	cactgaatacacataa[A/T]caacagagagcaatgt	A	T	NM_000921 // intron // 0 // Hs.386791 // PDE3A // 5139 // Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), mRNA. /// U36798 // intron // 0 // Hs.386791 // PDE3A // 5139 // Homo sapiens platelet cGI-PDE mRNA, complete cds. /// ENST00000325802 //	PDE3A	PDE3A, Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), p12.2
SNP_A-1861195	tcatatgttgcccc[A/G]gaaggaaaaacttgtg	A	G	NM_000921 // intron // 0 // Hs.386791 // PDE3A // 5139 // Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), mRNA. /// U36798 // intron // 0 // Hs.386791 // PDE3A // 5139 // Homo sapiens platelet cGI-PDE mRNA, complete cds. /// ENST00000325802 //	PDE3A	PDE3A, Homo sapiens phosphodiesterase 3A, cGMP-inhibited (PDE3A), p12.2
SNP_A-1711754	atggaaaaatgtctccaatctga[A/G]aaatcttttatcatcattc aggca	A	G	NM_006446 // upstream // 112272 // Hs.137425 // SLCO1B1 // 10599 // solute carrier organic anion transporter family, member 1B1 /// NM_019844 // downstream // 102210 // Hs.422811 // SLCO1B3 // 28234 // solute carrier organic anion transporter family, mem	SLCO1B1	SLCO1B1, rs1995409, solute carrier organic anion transporter family, member 1B1 ,p12.2
SNP_A-1853259	tatttaatacaggtc[G/T]cattgaattagataa	G	T	NM_006446 // intron // 0 // Hs.137425 // SLCO1B1 // 10599 // Homo sapiens solute carrier organic anion transporter family, member 1B1 (SLCO1B1), mRNA. /// ENST00000256958 // intron // 0 // --- // --- // --- // ---	SLCO1B1	SLCO1B1, Homo sapiens solute carrier organic anion transporter family, member 1B1 (SLCO1B1), p12.1
SNP_A-2237613	ctctctcttaatcca[C/T]cataccagaaacctat	C	T	NM_021094 // intron // 0 // Hs.46440 // SLCO1A2 // 6579 // Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, mRNA. /// NM_134431 // intron // 0 // Hs.46440 // SLCO1A2 // 6579 // Homo sapiens solute c	SLCO1A2	SLCO1A2, Homo sapiens solute carrier organic anion transporter family, member 1A2 (SLCO1A2), transcript variant 2, p12.1
SNP_A-1861520	tcatcccagcaaagaa[G/T]cagtttgttaactcct	G	T	NM_002907 // intron // 0 // Hs.235069 // RECQL // 5965 // Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, mRNA. /// NM_032941 // intron // 0 // Hs.235069 // RECQL // 5965 // Homo sapiens RecQ protein-like (DNA helicase	RECQL	RECQL, Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, p12.1
SNP_A-1814125	gtgtccttgagtttca[C/T]gtaaccaaacaccttt	C	T	NM_016072 // intron // 0 // Hs.62275 // GOLT1B // 51026 // Homo sapiens CGI-141 protein (CGI-141), mRNA. /// ENST00000229314 // intron // 0 // --- // --- // ---	GOLT1B	GOLT1B, Homo sapiens CGI-141 protein (CGI-141), p12.1
SNP_A-1653524	caataataagtaaacagaaaacaata[C/T]gtgcaactccaagtc tcttaagact	C	T	NM_005691 // intron // 0 // Hs.137418 // ABCC9 // 10060 // ATP-binding cassette, sub-family C (CFTR/MRP), member 9 /// NM_020297 // intron // 0 // Hs.137418 // ABCC9 // 10060 // ATP-binding cassette, sub-family C (CFTR/MRP), member 9 /// NM_020298 // int	ABCC9	ABCC9, rs829080, ATP-binding cassette, sub-family C (CFTR,p12.1
SNP_A-2297026	gccaatgttaacctca[A/G]ctgatgaagccatgtg	A	G	NM_020297 // upstream // 10053 // Hs.446050 // ABCC9 // 10060 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B, mRNA. /// NM_020298 // upstream // 10053 // Hs.446050 // ABCC9 // 10060 // Homo sapien	ABCC9	ABCC9, Homo sapiens ATP-binding cassette, sub-family C (CFTR p12.1
SNP_A-1802600	gtatctgttccaatca[A/G]ctaataggaaggtgct	A	G	NM_018638 // downstream // 75948 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 770641 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1807839	gtcttacattgattgaj[A/C]agatctgtatacata	A	C	NM_018638 // downstream // 149742 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 696847 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcrip	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2242170	ctgcaaagattgctac[A/C]atttactcataaagtc	A	C	NM_018638 // downstream // 153898 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 692691 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcrip	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2043767	aacttatggtctcacaj[A/C]aaaatcgatcaaggt	A	C	NM_018638 // downstream // 154003 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 692586 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcrip	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2238985	ctcttcctgtgtcttc[A/T]ccttattctgttaggg	A	T	NM_018638 // downstream // 154135 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 692454 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcrip	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-1851655	tattcgtcaggatac[C/T]gtaagctccataaaga	C	T	NM_018638 // downstream // 511147 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 335442 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcrip	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-2090148	acttgagcacctggat[A/C]agcaacctgattcatc	A	C	NM_018638 // downstream // 786991 // Hs.240056 // ETNK1 // 55500 // Homo sapiens ethanolamine kinase 1 (ETNK1), mRNA. /// NM_152989 // downstream // 59598 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript	ETNK1	ETNK1, Homo sapiens ethanolamine kinase 1 (ETNK1), p12.1
SNP_A-1931764	ttcccttaagattgaa[A/G]cctggattagttctcc	A	G	NM_152989 // intron // 0 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // intron // 0 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-2055370	aataaggctttagaa[A/T]cagacaagtcggaatg	A	T	NM_152989 // intron // 0 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // intron // 0 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-1874579	tctcctaatgtttca[C/T]gccaagaaagaaccat	C	T	NM_152989 // upstream // 40899 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // upstream // 40899 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining regio	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-2289987	gcaaaggatcactccca[C/T]tgaatttgtattactt	C	T	NM_152989 // upstream // 311655 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, mRNA. /// NM_006940 // upstream // 311655 // Hs.505007 // SOX5 // 6660 // Homo sapiens SRY (sex determining reg	SOX5	SOX5, Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcript variant 2, p12.1
SNP_A-2058050	aatatttgctcctttaj[C/G]atgaacatataattta	C	G	NM_144667 // upstream // 3251 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 223991 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosoli	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027365	aaacatggctagaat[A/G]aaagtctttaaaacac	A	G	NM_144667 // upstream // 8484 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 218758 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosoli	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-2041291	gcctggaatgatagtat[A/G]cttattgctgattg	A	G	NM_144667 // upstream // 42804 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 184438 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosol	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-2270083	gacacagaaattaaca[A/G]catttttcctgcctga	A	G	NM_144667 // upstream // 59921 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 167321 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosol	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-2041308	tctaagaatttgtgga[A/C]atcaaaagaggatttg	A	C	NM_144667 // upstream // 61893 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 165349 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosol	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-2041321	gacaggcagaglactg[C/G]aaaggagttaagccaa	C	G	NM_144667 // upstream // 83678 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 143564 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosol	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-1859050	tcagccaagttaactal[C/T]ctgccaaagcaaagca	C	T	NM_144667 // upstream // 86454 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 140788 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosol	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-2030202	aaagcacacttaagccl[A/G]aaagctctggtttgtt	A	G	NM_144667 // upstream // 161732 // Hs.350668 // FLJ32894 // 144360 // Homo sapiens hypothetical protein FLJ32894 (FLJ32894), mRNA. /// NM_005504 // downstream // 65510 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosol	FLJ32894	FLJ32894, Homo sapiens hypothetical protein FLJ32894 (FLJ32894), p12.1
SNP_A-2051329	aagggcccagtcctag[A/C]agaattcaacacctgc	A	C	NM_005504 // upstream // 11643 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// NM_006152 // upstream // 91366 // Hs.124922 // LRMP // 4033 // Homo sapiens lymphoid-restricted membrane protein (L	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2039316	aacataagaattacag[A/C]agattctcagtgtaaa	A	C	NM_005504 // upstream // 15251 // Hs.438993 // BCAT1 // 586 // Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /// NM_006152 // upstream // 87758 // Hs.124922 // LRMP // 4033 // Homo sapiens lymphoid-restricted membrane protein (L	BCAT1	BCAT1, Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), p12.1
SNP_A-2041909	taccaaaagaggatac[A/G]attgtcacaaaacaat	A	G	NM_006152 // downstream // 214951 // Hs.124922 // LRMP // 4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /// NM_006152 // downstream // 215225 // Hs.124922 // LRMP // 4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP	LRMP	LRMP, Homo sapiens lymphoid-restricted membrane protein (LRMP), p12.1
SNP_A-2223938	cgggcacatttctac[A/C]cgttcgctgagaagcc	A	C	NM_006152 // downstream // 361084 // Hs.124922 // LRMP // 4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA. /// NM_006152 // downstream // 361358 // Hs.124922 // LRMP // 4033 // Homo sapiens lymphoid-restricted membrane protein (LRMP	LRMP	LRMP, Homo sapiens lymphoid-restricted membrane protein (LRMP), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2152783	attaattcacigttaa[A/C]gctactgctctattca	A	C	NM_152590 // upstream // 221752 // Hs.44647 // FLJ36004 // 160492 // Homo sapiens hypothetical protein FLJ36004 (FLJ36004), mRNA. /// NM_007211 // upstream // 184061 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12o	FLJ36004	FLJ36004, Homo sapiens hypothetical protein FLJ36004 (FLJ36004), p12.1
SNP_A-1883939	tgaagagtaacaaaag[A/C]cttagaaaatgattcc	A	C	NM_152590 // upstream // 266345 // Hs.44647 // FLJ36004 // 160492 // Homo sapiens hypothetical protein FLJ36004 (FLJ36004), mRNA. /// NM_007211 // upstream // 139468 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12o	FLJ36004	FLJ36004, Homo sapiens hypothetical protein FLJ36004 (FLJ36004), p12.1
SNP_A-2224552	cgtatttagtattca[A/G]ctattcatgcagcta	A	G	NM_152590 // upstream // 293742 // Hs.44647 // FLJ36004 // 160492 // Homo sapiens hypothetical protein FLJ36004 (FLJ36004), mRNA. /// NM_007211 // upstream // 112071 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12o	FLJ36004	FLJ36004, Homo sapiens hypothetical protein FLJ36004 (FLJ36004), p12.1
SNP_A-2297806	gccagcttatctctc[C/G]acctcaaatgatccgc	C	G	NM_007211 // intron // 0 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12orf2), mRNA. /// ENST00000282884 // intron // 0 // — // — // —	C12orf2	C12orf2, Homo sapiens chromosome 12 open reading frame 2 (C12orf2), p12.1
SNP_A-2268642	gaatgtgaatgccaaa[C/G]tacggaagcaacctaa	C	G	NM_007211 // downstream // 19574 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12orf2), mRNA. /// NM_030762 // downstream // 21381 // Hs.177841 // BHLHB3 // 79365 // Homo sapiens basic helix-loop-helix domain contai	C12orf2	C12orf2, Homo sapiens chromosome 12 open reading frame 2 (C12orf2), p12.1
SNP_A-2234339	ctccaaatttagccca[C/T]gcacagagtcagggga	C	T	NM_007211 // downstream // 30131 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12orf2), mRNA. /// NM_030762 // downstream // 10824 // Hs.177841 // BHLHB3 // 79365 // Homo sapiens basic helix-loop-helix domain contai	C12orf2	C12orf2, Homo sapiens chromosome 12 open reading frame 2 (C12orf2), p12.1
SNP_A-2288652	gattggagagagagga[A/G]aagcatttaggttg	A	G	NM_007211 // downstream // 35642 // Hs.269941 // C12orf2 // 11228 // Homo sapiens chromosome 12 open reading frame 2 (C12orf2), mRNA. /// NM_030762 // downstream // 5313 // Hs.177841 // BHLHB3 // 79365 // Homo sapiens basic helix-loop-helix domain contain	C12orf2	C12orf2, Homo sapiens chromosome 12 open reading frame 2 (C12orf2), p12.1
SNP_A-1699339	aatcactacagttctcagatttaca[C/G]cttttttgtcattggcttga tgt	C	G	NM_030762 // 3UTR // 0 // Hs.437282 // BHLHB3 // 79365 // basic helix-loop-helix domain containing, class B, 3	BHLHB3	BHLHB3 , rs1048155, basic helix-loop-helix domain containing, class B, 3,p12.1
SNP_A-2021679	aaaaacactgagtag[A/G]atgccacttaaaagcg	A	G	NM_005086 // intron // 0 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // intron // 0 // — // — // —	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p12.1
SNP_A-1939513	ttgattagtgacccag[A/G]aaaccaattctgaaat	A	G	NM_005086 // downstream // 211945 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 211945 // — // — // — /// ENST00000242737 // downstream // 276408 // -	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-2168667	caagaagctcacaatg[A/T]agtgtatataaaagga	A	T	NM_005086 // downstream // 236231 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 236231 // — // — // — /// ENST00000242737 // downstream // 252122 // -	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-2300169	gcctccaggtcttaaa[C/T]gatgctagctggagt	C	T	NM_005086 // downstream // 289000 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 289000 // — // — // — /// ENST00000242737 // downstream // 199353 // -	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2261548	gaaaggcttgacaccc[A/T]ccttgtgatcacggtc	A	T	NM_005086 // downstream // 309260 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 309260 // — // — // — // — /// ENST00000242737 // downstream // 179093 // -	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-2089399	acttatcaattgttcc[A/G]gcaagtggtgattact	A	G	NM_005086 // downstream // 315239 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 315239 // — // — // — // — /// ENST00000242737 // downstream // 173114 // -	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-1712757	cagatttataaaaggtattcaaagg[C/G]cacataatgtttggttgagttaggt	C	G	NM_002223 // intron // 0 // Hs.512235 // ITPR2 // 3709 // inositol 1,4,5-triphosphate receptor, type 2	ITPR2	ITPR2 , rs10506003, inositol 1,4,5-triphosphate receptor, type 2,p11.23
SNP_A-1834080	tacatcactggcctaa[G/T]ctacaaaaccctgaat	G	T	NM_005086 // downstream // 373159 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 373159 // — // — // — // — /// ENST00000242737 // downstream // 115194 // -	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-1875755	tctctttaatatgacc[C/T]gaaaaataacttccag	C	T	NM_005086 // downstream // 408336 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 408336 // — // — // — // — /// ENST00000242737 // downstream // 80017 // –	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-2043299	gctgggaagtgctaag[C/T]ccagaaatcgagtttt	C	T	NM_005086 // downstream // 412698 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 412698 // — // — // — // — /// ENST00000242737 // downstream // 75655 // –	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-2242048	ctgattggtactatga[C/T]gtttaaagatttcctt	C	T	NM_005086 // downstream // 423670 // Hs.183428 // SSPN // 8082 // Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA. /// ENST00000242729 // downstream // 423670 // — // — // — // — /// ENST00000242737 // downstream // 64683 // –	SSPN	SSPN, Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), p11.23
SNP_A-1827354	taactaaagcctagaa[C/T]gatttcaggagctgcc	C	T	NM_018164 // intron // 0 // Hs.505077 // C12orf11 // 55726 // Homo sapiens hypothetical protein FLJ10637 (FLJ10637), mRNA. /// ENST00000335745 // intron // 0 // — // — // — // — /// ENST00000261191 // intron // 0 // — // — // — // —	C12orf11	C12orf11, Homo sapiens hypothetical protein FLJ10637 (FLJ10637), p11.23
SNP_A-1823140	taaaacactctttgta[C/T]gcagcaaggaaagaat	C	T	NM_015000 // upstream // 110489 // Hs.184523 // STK38L // 23012 // Homo sapiens serine/threonine kinase 38 like (STK38L), mRNA. /// ENST00000330397 // upstream // 51180 // — // — // — // — /// ENST00000282893 // upstream // 110489 // — // — //	STK38L	STK38L, Homo sapiens serine,p11.23
SNP_A-1845306	tatactccattcatga[C/G]acatgatacaaatgca	C	G	NM_015000 // upstream // 53893 // Hs.184523 // STK38L // 23012 // Homo sapiens serine/threonine kinase 38 like (STK38L), mRNA. /// ENST00000330397 // upstream // 107776 // — // — // — // — // — /// ENST00000282893 // upstream // 53893 // — // — //	STK38L	STK38L, Homo sapiens serine,p11.23
SNP_A-2092696	agaaatgaaaggcaac[A/G]gtgaacagtgtttgct	A	G	NM_015000 // intron // 0 // Hs.184523 // STK38L // 23012 // Homo sapiens serine/threonine kinase 38 like (STK38L), mRNA. /// ENST00000282893 // intron // 0 // — // — // — // —	STK38L	STK38L, Homo sapiens serine,p11.23
SNP_A-1800506	gtactgtaaatgtcca[C/T]ctgattttatttatga	C	T	NM_015000 // intron // 0 // Hs.184523 // STK38L // 23012 // Homo sapiens serine/threonine kinase 38 like (STK38L), mRNA. /// ENST00000282893 // intron // 0 // — // — // — // —	STK38L	STK38L, Homo sapiens serine,p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1928237	ttcacagtatcagaac[C/G]actcatcacccaaccc	C	G	NM_020183 // downstream // 36981 // Hs.434269 // ARNTL2 // 56938 // Homo sapiens aryl hydrocarbon receptor nuclear translocator-like 2 (ARNTL2), mRNA. /// ENST00000261178 // downstream // 36981 // --- // --- // --- // --- /// ENST00000311001 // downstream	ARNTL2	ARNTL2, Homo sapiens aryl hydrocarbon receptor nuclear translocator-like 2 (ARNTL2), p11.23
SNP_A-1724906	tgtggctagtagctactgtatcaaa[C/T]agtgtagagaacattttc atcaaca	C	T	NM_003622 // upstream // 55485 // Hs.389023 // PPFIBP1 // 8496 // PTPRF interacting protein, binding protein 1 (liprin beta 1) /// NM_020183 // downstream // 48094 // Hs.434269 // ARNTL2 // 56938 // aryl hydrocarbon receptor nuclear translocator-like 2 /	PPFIBP1	PPFIBP1 , rs306640, PTPRF interacting protein, binding protein 1 (liprin beta 1) ,p11.23
SNP_A-2135975	atcaagaagaaacacc[C/T]gaattgcaacctgttg	C	T	NM_198964 // upstream // 13095 // Hs.89626 // PTHLH // 5744 // Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3, mRNA. /// NM_002820 // upstream // 13095 // Hs.89626 // PTHLH // 5744 // Homo sapiens parathyroid hormone-like horm	PTHLH	PTHLH, Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3, p11.22
SNP_A-2247019	ctgtattctcaccttc[C/T]ctgggcttatccatat	C	T	NM_198964 // upstream // 87704 // Hs.89626 // PTHLH // 5744 // Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3, mRNA. /// NM_002820 // upstream // 87704 // Hs.89626 // PTHLH // 5744 // Homo sapiens parathyroid hormone-like horm	PTHLH	PTHLH, Homo sapiens parathyroid hormone-like hormone (PTHLH), transcript variant 3, p11.22
SNP_A-2281778	gagtgacattaggaga[A/T]aaagtgacttgcttgt	A	T	NM_018318 // downstream // 22766 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 577243 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA.	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1841264	taggaacaatggatta[G/T]gtttcattctgattct	G	T	NM_018318 // downstream // 42798 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 557211 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA.	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2153978	attatataatgctcaa[G/T]aggtcaattcagtgaa	G	T	NM_018318 // downstream // 66494 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 533515 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA.	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2044783	tttttctttgagtggc[A/G]taggaattatgatatt	A	G	NM_018318 // downstream // 247078 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 352931 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1872286	tctagaagttaaaaac[A/C]aattagcgatctttac	A	C	NM_018318 // downstream // 247201 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 352808 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2267615	gaatcaaattataaac[A/C]aagcacagaaaatgat	A	C	NM_018318 // downstream // 247232 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 352777 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1725758	attaaaaaagaaaataattaacgga[C/T]gatagtgtttatcaacc tactgtga	C	T	NM_018099 // upstream // 364615 // Hs.134497 // MLSTD1 // 55711 // male sterility domain containing 1 /// NM_018318 // downstream // 309869 // Hs.406485 // FLJ11088 // 55297 // GGA binding partner	MLSTD1	MLSTD1 , rs1480640, male sterility domain containing 1 ,p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2154527	attattgccccagacc[C/T]ggcctggaatgaatac	C	T	NM_018318 // downstream // 321173 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 278836 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1913738	tgtgtattctctccca[C/G]actggtacaaaattg	C	G	NM_018318 // downstream // 322243 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 277766 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1805294	gtcatttgcatgatta[C/G]agaaagaaaaagtcac	C	G	NM_018318 // downstream // 329372 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 270637 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2085838	actcctctttctgaa[C/T]aagtgtgtgtcctatg	C	T	NM_018318 // downstream // 330375 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 269634 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2096864	agactcatttcttgac[C/T]aaacctattctttgtc	C	T	NM_018318 // downstream // 334323 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 265686 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-1729242	tagaatatacattatttcatctacf[A/G]aatggaacaatctgtaaga ttgacc	A	G	NM_018099 // upstream // 306019 // Hs.134497 // MLSTD1 // 55711 // male sterility domain containing 1 /// NM_018318 // downstream // 368465 // Hs.406485 // FLJ11088 // 55297 // GGA binding partner	MLSTD1	MLSTD1 , rs1601981, male sterility domain containing 1 , p11.22
SNP_A-1813123	gtggtagaatgcatga[C/T]taccagatatactgag	C	T	NM_018318 // downstream // 391400 // Hs.129278 // FLJ11088 // 55297 // Homo sapiens GGA binding partner (FLJ11088), mRNA. /// NM_018099 // upstream // 208609 // Hs.298851 // MLSTD1 // 55711 // Homo sapiens male sterility domain containing 1 (MLSTD1), mRNA	FLJ11088	FLJ11088, Homo sapiens GGA binding partner (FLJ11088), p11.22
SNP_A-2022266	aaaaagtcaaactatt[C/G]aaacagcaatattcaa	C	G	NM_175861 // intron // 0 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// ENST00000256062 // intron // 0 // --- // --- // ---	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1865281	tccatattctgattccf[A/G]atcatactacatatact	A	G	NM_175861 // intron // 0 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// ENST00000256062 // intron // 0 // --- // --- // ---	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1803457	gtatttgggcaaaag[C/G]ctagatatctaaaaac	C	G	NM_175861 // intron // 0 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// ENST00000256062 // intron // 0 // --- // --- // ---	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1847457	tatcctatttgatggc[C/T]caatctcatgttactg	C	T	NM_031920 // upstream // 357077 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 233205 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 6128	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2257718	ctttggacctcatgta[C/T]gctataggcttccctg	C	T	NM_031920 // upstream // 361392 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 237520 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 6085	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2290103	gcaaatatattgttccd[C/T]gaaaacttcattagtt	C	T	NM_031920 // upstream // 403600 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 279728 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 5663	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1874496	tctcccctcacgttcca[A/G]tatcaaattcctgta	A	G	NM_031920 // upstream // 414647 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 290775 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 5552	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1931185	ttccattacttgacat[C/T]gatcaggcattcccccg	C	T	NM_031920 // upstream // 542395 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 418523 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 4275	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2255480	ctgctctgggtctacat[G/T]atgtggtaaaagctg	G	T	NM_031920 // upstream // 566721 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 442849 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 4031	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2176357	caccataagttaggag[G/T]cacgtgcaaagaggat	G	T	NM_031920 // upstream // 569202 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 445330 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 4007	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2098224	agagataggaccccctc[A/G]agatcattatcctcc	A	G	NM_031920 // upstream // 570932 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 447060 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3989	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2046287	gtggatccacatttta[A/C]aagtgggaagaagat	A	C	NM_031920 // upstream // 577401 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 453529 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3925	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2177063	cacctccacctgaact[A/C]acaatgtctgctat	A	C	NM_031920 // upstream // 608415 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 484543 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3614	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1726374	ttctactgagaaattaaatgtaaa[A/C]ttaaggattatccctttcc aaaaa	A	C	NM_006390 // downstream // 360678 // Hs.316977 // IPO8 // 10526 // importin 8 /// NM_031920 // upstream // 525135 // Hs.528689 // ARG99 // 83857 // ARG99 protein /// NM_175861 // upstream // 485364 // Hs.528689 // ARG99 // 83857 // ARG99 protein	IPO8	IPO8 , rs2700047, importin 8 ,p11.22
SNP_A-2293915	gcagctttcttggaaa[C/T]agttcaggcccagtct	C	T	NM_031920 // upstream // 622465 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 498593 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3474	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1890201	tgatcacaagacctta[A/C]aaactatgtgagaaaa	A	C	NM_031920 // upstream // 647631 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 523759 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3222	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1695783	agtgcagtggtgggattataattca[C/T]ggtagcttaaattcctggctcaa	C	T	NM_006390 // downstream // 321754 // Hs.316977 // IPO8 // 10526 // importin 8 /// NM_031920 // upstream // 564059 // Hs.528689 // ARG99 // 83857 // ARG99 protein /// NM_175861 // upstream // 524288 // Hs.528689 // ARG99 // 83857 // ARG99 protein	IPO8	IPO8 , rs1320925, importin 8 ,p11.22
SNP_A-1877400	tctggagcggactgaa[A/G]gaaaagatagattggg	A	G	NM_031920 // upstream // 659673 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 535801 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3102	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1908015	tgtaatttggtcatca[C/T]cagaagactgtgacat	C	T	NM_031920 // upstream // 661063 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 537191 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3088	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2108176	agctctttcacacaga[C/T]tatgtaatttggtcat	C	T	NM_031920 // upstream // 661082 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 537210 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3088	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2110274	aggaatacaaacatca[C/T]aatgcgagggagaaaa	C	T	NM_031920 // upstream // 661570 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 537698 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 3083	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2126752	ataaactctgttcacc[C/T]gaagataggaaaaaag	C	T	NM_031920 // upstream // 670397 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 546525 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2995	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1871453	tctaacattgctataa[C/T]aaaacgaggaggactg	C	T	NM_031920 // upstream // 671103 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 547231 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2988	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2178021	cactactgaagcaaaa[C/T]ctttctaagtacttttg	C	T	NM_031920 // upstream // 672373 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 548501 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2975	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2046541	gtgcctaaacatcata[A/G]gagtaagacctgaaaa	A	G	NM_031920 // upstream // 672443 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 548571 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2974	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2308905	gcttgttccatgcaa[C/T]gagttacttgaaaca	C	T	NM_031920 // upstream // 672484 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 548612 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2974	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2107012	agcgacatataagatc[C/T]catttgaaacaccta	C	T	NM_031920 // upstream // 675011 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 551139 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2949	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2089142	acttaatttggaata[C/T]gccggctttcgacaaa	C	T	NM_031920 // upstream // 678736 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 554864 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2911	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2046564	ctccaagaaatagcac[A/G]agagggtgatgatggc	A	G	NM_031920 // upstream // 682799 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 558927 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2871	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2265482	gaagccatggacagtg[C/G]caactttcccagcaat	C	G	NM_031920 // upstream // 683309 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 559437 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2866	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2046567	ggtagagtaacatcta[C/T]accacatctacttct	C	T	NM_031920 // upstream // 683804 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 559932 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2861	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2046573	caattcagtccatgta[C/T]ctgttaaaaacagctt	C	T	NM_031920 // upstream // 684198 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 560326 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2857	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1854614	tcaacaaggaaaagtgc[C/T]gagatagaaggccaga	C	T	NM_031920 // upstream // 685072 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 561200 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2848	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1866987	tccctcaggcataaatg[C/G]aatgatgtggctaggt	C	G	NM_031920 // upstream // 685567 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 561695 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2843	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2154303	attatggctttaagt[C/T]aaccaaagatatttc	C	T	NM_031920 // upstream // 686051 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 562179 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2838	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1914479	tgtgtttctaggaag[C/G]cattactcattataa	C	G	NM_031920 // upstream // 686098 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 562226 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2838	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2074245	acataaggtaaaaaaa[G/T]gtcaatcttgaagtca	G	T	NM_031920 // upstream // 690115 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 566243 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2797	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1928063	ttcaattcttagtaaaa[A/G]gctccattgtagtcag	A	G	NM_031920 // upstream // 691090 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 567218 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2788	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2199423	catttttgttcaacaga[C/G]ataaaagaagatggca	C	G	NM_031920 // upstream // 691716 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 567844 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2781	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1889548	tgagtttcttgccaaa[A/G]tgaaattggatgctaa	A	G	NM_031920 // upstream // 697921 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 574049 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2719	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2279485	gaggatgagatgccag[A/T]atgtctatgcatggtg	A	T	NM_031920 // upstream // 698912 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 575040 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2710	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2053938	aagttaaacttggaaa[C/T]gaatcacatacaaaa	C	T	NM_031920 // upstream // 704287 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 580415 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2656	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2274703	gagaaagaagtttaag[C/T]ataaggctgcctcaag	C	T	NM_031920 // upstream // 704717 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 580845 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2651	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2240310	ctgaattccagtaaaa[C/G]agataatgccaaccat	C	G	NM_031920 // upstream // 704916 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 581044 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2649	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1880397	tcttgacaatattggg[C/T]catcttatgcatggac	C	T	NM_031920 // upstream // 720718 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 596846 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2491	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2299409	gccctgtaaaaataac[C/G]aatcctccaactgtg	C	G	NM_031920 // upstream // 741248 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 617376 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 2286	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2213728	ccgttctatagcggta[A/G]gttcctccttgttct	A	G	NM_031920 // upstream // 818378 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 694506 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 1515	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-1847524	tatccttatgtgggca[C/T]agtgcaaggcgttact	C	T	NM_031920 // upstream // 835178 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 711306 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 1347	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2289212	gatttgcccctataaa[C/G]atgccaaaaaatgaga	C	G	NM_031920 // upstream // 844823 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 720951 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 1250	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100621	agataccatcttacaa[C/T]catcgaaatggctatt	C	T	NM_031920 // upstream // 894364 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 770492 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 7555	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.22
SNP_A-2172881	caatttggatctcta[C/T]ggcatactgaaggctt	C	T	NM_031920 // upstream // 898001 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 774129 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 7191	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.21
SNP_A-2104335	agcagccagtgacata[C/G]aacgatggtagatt	C	G	NM_031920 // upstream // 905448 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 781576 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 6446	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.21
SNP_A-1788441	gggagtggtaagaaga[A/G]gtcaaattcaagatct	A	G	NM_031920 // upstream // 906058 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 782186 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 6385	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.21
SNP_A-2039950	aacatttcacacacaa[A/G]agttcagaatcctggg	A	G	NM_031920 // upstream // 968092 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 844220 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 1822	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.21
SNP_A-1799475	gtaatgcacattaata[C/T]ctctttccctttaata	C	T	NM_031920 // upstream // 968256 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_175861 // upstream // 844384 // Hs.401954 // ARG99 // 83857 // Homo sapiens ARG99 protein (ARG99), mRNA. /// NM_006390 // downstream // 1658	ARG99	ARG99, Homo sapiens ARG99 protein (ARG99), p11.21
SNP_A-2263039	gaacacaacttcaac[A/G]ctattccaatgggcaa	A	G	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // --- // --- // --- //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2052370	aagtacagttctgtta[C/T]agcgtactagttgggc	C	T	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // --- // --- // --- //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2232100	ctcaagctgtttctca[A/G]agtagcctgataattt	A	G	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // --- // --- // --- //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-1893661	tgcagtactggaataa[C/G]aacagataagtacata	C	G	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // --- // --- // --- //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2110630	aggacatcaaaaatt[A/G]aagtgattaitgcttct	A	G	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // --- // --- // --- //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2089196	acttacccatacaaat[C/G]acgatgcaaaccagca	C	G	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // --- // --- // --- //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2112328	aggcaaactacgttca[C/T]gttcttcataaagctg	C	T	NM_006390 // intron // 0 // Hs.505136 // IPO8 // 10526 // Homo sapiens importin 8 (IPO8), mRNA. /// NM_006391 // intron // 0 // Hs.523470 // IPO7 // 10527 // Homo sapiens importin 7 (IPO7), mRNA. /// ENST00000256079 // intron // 0 // — // — // — //	IPO8	IPO8, Homo sapiens importin 8 (IPO8), p11.21
SNP_A-2002635	agtgatttgtctaata[A/G]atccgggcaaagtaaa	A	G	NM_032156 // intron // 0 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // intron // 0 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transc	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-1908717	tgtagggctttgtaga[C/T]acactaaggacatttt	C	T	NM_032156 // intron // 0 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // intron // 0 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transc	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-1855894	tcaatggaagtgtata[C/T]agagagaagtggacag	C	T	NM_032156 // upstream // 11701 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 11701 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1Q	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2186032	caggcagtatctagta[C/T]caagcacattgctttc	C	T	NM_032156 // upstream // 25836 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 25836 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1Q	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2220742	ccttgagcttaacctc[C/T]gagaatctgccaaaaa	C	T	NM_032156 // upstream // 124897 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 124897 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2127551	ataacattgtagggca[A/G]tacattactcatgtgt	A	G	NM_032156 // upstream // 128328 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 128328 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2181716	cagagaggaagctggc[A/G]atctctgtcaattctg	A	G	NM_032156 // upstream // 130433 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 130433 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2281842	gagtgatactttgagg[A/T]catgtgactaaccccg	A	T	NM_032156 // upstream // 147696 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 147696 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-2105658	agccactctttcttca[A/C]cccatggagacatctt	A	C	NM_032156 // upstream // 180684 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, mRNA. /// NM_001002259 // upstream // 180684 // Hs.234355 // C1QDC1 // 65981 // Homo sapiens C1q domain containing 1 (C	C1QDC1	C1QDC1, Homo sapiens C1q domain containing 1 (C1QDC1), transcript variant 3, p11.21
SNP_A-1872396	tctagatggtgcttag[C/T]cctggagtgggaaggg	C	T	ENST00000261177 // intron // 0 // — // — // — // —	-	p11.21
SNP_A-2263803	gaacgactggtttaga[C/T]gcttggtcactatacc	C	T	NM_030655 // upstream // 78148 // Hs.443960 // DDX11 // 1663 // Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11), transcript var /// NM_030653 // upstream // 78152 // Hs.443960 // DDX11 // 16	DDX11	DDX11, Homo sapiens DEAD,p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2208140	cccaagtttgaagtta[C/T]ggtcaatgcaccacaa	C	T	ENST00000354978 // intron // 0 // --- // --- // --- // --- /// ENST00000313826 // CDS // 0 // --- // --- // --- // --- /// ENST00000327800 // intron // 0 // --- // --- // --- // --- /// ENST00000266524 // CDS // 0 // --- // --- // --- // --- /// ENST00000	-	p11.21
SNP_A-2175905	cacattttcttcattc[A/G]atctatcattgatgga	A	G	ENST00000354978 // intron // 0 // --- // --- // --- // --- /// ENST00000313826 // intron // 0 // --- // --- // --- // --- /// ENST00000327800 // intron // 0 // --- // --- // --- // --- /// ENST00000266524 // intron // 0 // --- // --- // --- // --- /// ENS	-	p11.21
SNP_A-2186365	caggctgttagggaat[C/G]acagtaataagagtaa	C	G	NM_021238 // downstream // 40065 // Hs.505154 // C12orf14 // 58516 // Homo sapiens chromosome 12 open reading frame 14 (C12orf14), mRNA. /// ENST00000354978 // upstream // 39290 // --- // --- // --- // --- /// ENST00000327497 // upstream // 110693 // ---	C12orf14	C12orf14, Homo sapiens chromosome 12 open reading frame 14 (C12orf14), p11.21
SNP_A-1876978	tctgcctgaatcaaac[C/T]acaaaaatagccagat	C	T	NM_144973 // intron // 0 // Hs.118166 // MGC24039 // 160518 // Homo sapiens hypothetical protein MGC24039 (MGC24039), mRNA. /// ENST00000306833 // intron // 0 // --- // --- // --- // --- /// ENST00000354285 // intron // 0 // --- // --- // --- // ---	MGC24039	MGC24039, Homo sapiens hypothetical protein MGC24039 (MGC24039), p11.21
SNP_A-1655671	tgcccagaggtcaagtcttctgcac[A/G]cgcttcagcctcacctc ttgcagct	A	G	NM_018169 // upstream // 211615 // Hs.236844 // FLJ10652 // 55196 // hypothetical protein FLJ10652	FLJ10652	FLJ10652 , rs1259633, hypothetical protein FLJ10652,p11.21
SNP_A-2048285	agacattaaatcctaa[C/T]ggacactaagccctcc	C	T	NM_018169 // upstream // 31543 // Hs.445129 // FLJ10652 // 55196 // Homo sapiens hypothetical protein FLJ10652 (FLJ10652), mRNA. /// ENST00000340398 // upstream // 161349 // --- // --- // --- // --- /// ENST00000312561 // upstream // 31543 // --- // --- /	FLJ10652	FLJ10652, Homo sapiens hypothetical protein FLJ10652 (FLJ10652), p11.21
SNP_A-1887656	tgagaggctcctgata[A/G]taacttttaatgattt	A	G	NM_001714 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BI	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2272734	gacgtggatttgagaa[A/T]catcagcacgcaagga	A	T	NM_001714 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BI	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2122884	agtggcccttccttcc[C/T]gattcctacactcctc	C	T	NM_001714 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BI	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2178563	cactctagcggcccta[A/C]acaaagttcttacctg	A	C	NM_001714 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BI	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2232555	ctcaccccacacctaa[C/T]gaatccgaatctgccc	C	T	NM_001714 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, mRNA. /// NM_001003398 // intron // 0 // Hs.505202 // BICD1 // 636 // Homo sapiens Bicaudal D homolog 1 (Drosophila) (BI	BICD1	BICD1, Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), transcript variant 1, p11.21
SNP_A-2144733	atgatgctcattattc[A/G]agtattcagacataac	A	G	NM_004572 // intron // 0 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // intron // 0 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a, mRNA. /// EN	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1947574	tttaccctaatgctcat[C/T]ggcagtggccagtttt	C	T	NM_004572 // upstream // 215804 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 215913 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.21
SNP_A-1680892	gaagaacttggaagttgtgggtga[C/T]gaatacttggttctata gaagaaa	C	T	NM_004572 // upstream // 221222 // Hs.25051 // PKP2 // 5318 // plakophilin 2 /// NM_032834 // upstream // 907960 // Hs.102971 // ALG10 // 84920 // asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase)	PKP2	PKP2, rs7303471, plakophilin 2, p11.21
SNP_A-1832077	taatttaatccatgc[A/C]actaaagataatgtta	A	C	NM_004572 // upstream // 330151 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 330260 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.1
SNP_A-2028776	aaacttcatcgtaatg[C/T]atccagtctttttc	C	T	NM_004572 // upstream // 349279 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 349388 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.1
SNP_A-1823804	taaaatgactgtaaga[C/T]actagaaatgtgaga	C	T	NM_004572 // upstream // 349971 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 350080 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.1
SNP_A-2049377	acataattgccttaac[C/T]agacctcctcctgcag	C	T	NM_004572 // upstream // 460643 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 460752 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.1
SNP_A-1875833	tctcttttaggctta[C/T]ggaatgacttaaagt	C	T	NM_004572 // upstream // 462143 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, mRNA. /// NM_001005242 // upstream // 462252 // Hs.164384 // PKP2 // 5318 // Homo sapiens plakophilin 2 (PKP2), transcript variant 2a	PKP2	PKP2, Homo sapiens plakophilin 2 (PKP2), transcript variant 2b, p11.1
SNP_A-1909277	tgtatggtataagtga[A/T]ccatcattcatttat	A	T	NM_198992 // upstream // 92904 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 489558 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-g	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-2168340	caactgtcccctggac[C/G]attcccagagacca	C	G	NM_198992 // upstream // 97095 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 485367 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-g	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-1810006	gtgataacatgagcta[C/G]ggtagtgttataataa	C	G	NM_198992 // upstream // 161904 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 420558 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-2023900	aaaagaagtctgtttc[A/G]aaaactcaggcaggcc	A	G	NM_198992 // upstream // 181866 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 400596 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936215	ttcttcaggaaattga[C/T]cagagtcatcaaaata	C	T	NM_198992 // upstream // 199785 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 382677 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-2270886	gacagtactttcaaat[C/T]atcatgagttttgttt	C	T	NM_198992 // upstream // 232323 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 350139 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-2049695	tttatccttcatttgc[A/G]ctcatgctctttgttt	A	G	NM_198992 // upstream // 236586 // Hs.118703 // SYT10 // 341359 // Homo sapiens synaptotagmin X (SYT10), mRNA. /// NM_032834 // upstream // 345876 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-	SYT10	SYT10, Homo sapiens synaptotagmin X (SYT10), p11.1
SNP_A-2121217	agtctgggacccccgc[A/G]gaagacagtgccttcc	A	G	NM_032834 // downstream // 301699 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), mRNA. /// ENST00000266483 // downstream // 301699 // — // — // — // — /// E	ALG10	ALG10, Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), p11.1
SNP_A-2046054	aagactacatttgggga[A/C]aaagggagccaaagca	A	C	NM_032834 // downstream // 2868998 // Hs.102971 // ALG10 // 84920 // Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), mRNA. /// ENST00000266483 // downstream // 2868998 // — // — // — // — ///	ALG10	ALG10, Homo sapiens asparagine-linked glycosylation 10 homolog (yeast, alpha-1,2-glucosyltransferase) (ALG10), q12
SNP_A-2197255	cattcagatgagaaca[C/T]attttgcaaggaaaaa	C	T	NM_153634 // downstream // 309673 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000308742 // downstream // 21063 // — // — // — // — /// ENST00000331366 // downstream // 309673 // — // — // — // — ///	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2079990	acccttgccctttta[C/T]aatttggcttttatgt	C	T	NM_153634 // downstream // 265931 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000308742 // downstream // 64805 // — // — // — // — /// ENST00000331366 // downstream // 265931 // — // — // — // — ///	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2025855	aaaatggggatctatc[A/G]aaaaatggtaattatg	A	G	NM_153634 // downstream // 157770 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000308742 // downstream // 172966 // — // — // — // — /// ENST00000331366 // downstream // 157770 // — // — // — // — ///	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2137292	atcagtgtgcaaaaac[A/C]acagtcattcctatac	A	C	NM_153634 // downstream // 152573 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000308742 // downstream // 178163 // — // — // — // — /// ENST00000331366 // downstream // 152573 // — // — // — // — ///	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2295654	gcatgacaaatttgcc[A/C]atgtctaaattacagt	A	C	NM_153634 // downstream // 3580 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000308742 // downstream // 327156 // — // — // — // — /// ENST00000331366 // downstream // 3580 // — // — // — // — /// ENS	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-1884923	tgaatgaattctggta[C/T]aaaaagaacattagtg	C	T	NM_153634 // intron // 0 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000331366 // intron // 0 // — // — // — // — /// ENST00000360449 // intron // 0 // — // — // — // —	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2236851	ctctagacttttcccta[C/T]cagtctccaatattc	C	T	NM_153634 // upstream // 56248 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000331366 // upstream // 56248 // — // — // — // — /// ENST00000360449 // upstream // 54449 // — // — // — // — /// ENST0000	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-1786809	ggctttctcaatttga[C/T]atgaattctgtgagaa	C	T	NM_153634 // upstream // 266325 // Hs.40910 // CPNE8 // 144402 // Homo sapiens copine VIII (CPNE8), mRNA. /// ENST00000331366 // upstream // 266325 // — // — // — // — /// ENST00000360449 // upstream // 264526 // — // — // — // — /// ENST0	CPNE8	CPNE8, Homo sapiens copine VIII (CPNE8), q12
SNP_A-2051181	ccagaatgtccaaaata[C/T]acagtttgataggcc	C	T	ENST00000341813 // intron // 0 // — // — // — // — /// ENST00000313553 // intron // 0 // — // — // — // —	-	q12
SNP_A-2118568	agtaatgaaaagaaaa[C/T]ggataacttattgagt	C	T	NM_052885 // intron // 0 // Hs.524341 // SLC2A13 // 114134 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), mRNA. /// ENST00000280871 // intron // 0 // — // — // — // —	SLC2A13	SLC2A13, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), q12
SNP_A-2169869	caaggcaccaatcacg[G/T]atgcattggcaatcag	G	T	NM_052885 // intron // 0 // Hs.524341 // SLC2A13 // 114134 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), mRNA. /// ENST00000280871 // intron // 0 // — // — // — // —	SLC2A13	SLC2A13, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), q12
SNP_A-1736979	tgctcaatactaaactcttccaaac[A/C]gttggaatctatcactggaattctga	A	C	NM_052885 // intron // 0 // Hs.528311 // SLC2A13 // 114134 // solute carrier family 2 (facilitated glucose transporter), member 13	SLC2A13	SLC2A13, rs10506144, solute carrier family 2 (facilitated glucose transporter), member 13,q12
SNP_A-2201179	ccaagtgttcaccata[C/T]agtcagtaattgattc	C	T	NM_175038 // upstream // 131876 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 212018 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRN	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2189491	cagttgttcagtgttt[A/T]aaaagtttgaaccgt	A	T	NM_175038 // upstream // 109134 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 189276 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRN	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-1836886	tactgcctcaaaagcaa[C/T]atcatgacaagatacc	C	T	NM_175038 // upstream // 50260 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 130402 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2052230	tggtcactctagtcaa[C/G]aatttgcatctgacg	C	G	NM_175038 // upstream // 19217 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 99359 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA.	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-2286393	gatgtcttgtagtac[A/G]aatggtgtatcctagt	A	G	NM_175038 // upstream // 3545 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA. /// NM_175038 // upstream // 83687 // Hs.143434 // CNTN1 // 1272 // Homo sapiens contactin 1 (CNTN1), transcript variant 2, mRNA.	CNTN1	CNTN1, Homo sapiens contactin 1 (CNTN1), transcript variant 2, q12
SNP_A-1858104	tcagaaaatagagcaa[A/G]aaaaagtagcataatg	A	G	NM_013377 // downstream // 70057 // Hs.380044 // PDZRN4 // 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 // downstream // 70057 // — // — // — // — /// ENST00000280876 // downstream // 442605 // —	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2285652	gatgaagtaggcagtg[C/T]agtttttgccctacca	C	T	NM_013377 // downstream // 213221 // Hs.380044 // PDZRN4 // 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 // downstream // 213221 // --- // --- // --- // --- /// ENST00000280876 // downstream // 299441 // --	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12
SNP_A-2053569	ttacatttacatttac[C/T]actaattccctgagct	C	T	NM_013377 // downstream // 394177 // Hs.380044 // PDZRN4 // 29951 // Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), mRNA. /// ENST00000298919 // downstream // 394177 // --- // --- // --- // --- /// ENST00000280876 // downstream // 118485 // --	PDZRN4	PDZRN4, Homo sapiens PDZ domain containing RING finger 4 (PDZRN4), q12
SNP_A-2209630	cccatggatcaggtcc[C/T]agattctcttatctgt	C	T	NM_153026 // upstream // 32486 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 732048 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2092679	agaaatctcaacagga[A/T]gcctctaaataatctt	A	T	NM_153026 // upstream // 49526 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 715008 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-1701167	gatgttttgtttttctctataggca[A/C]ctcataagttacaatgccaaagtct	A	C	NM_025003 // downstream // 681989 // Hs.287554 // ADAMTS20 // 80070 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 /// NM_153026 // upstream // 82545 // Hs.6786 // PRICKLE1 // 144165 // prickle-like 1 (Dr	ADAMTS20	ADAMTS20 , rs4480597, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 ,q12
SNP_A-1709335	gttacttttttgattcagataaaaca[C/T]gcttgggaaaaagtacctggaggca	C	T	NM_025003 // downstream // 681920 // Hs.287554 // ADAMTS20 // 80070 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 /// NM_153026 // upstream // 82614 // Hs.6786 // PRICKLE1 // 144165 // prickle-like 1 (Dr	ADAMTS20	ADAMTS20 , rs4131406, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 ,q12
SNP_A-2220789	ccttgatctgcttaaa[A/G]ttacagtaatatcact	A	G	NM_153026 // upstream // 84780 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 679754 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-1821359	gtttgctggaccaaac[C/T]gaacagactgcagtac	C	T	NM_153026 // upstream // 150713 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 613821 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2054342	gagtctgagatgtccc[A/G]ccctaacaccaaatga	A	G	NM_153026 // upstream // 264425 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 500109 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2090872	actttcatctgtttaa[C/T]atattgccaaaatatc	C	T	NM_153026 // upstream // 266879 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 497655 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2240540	ctgaccatacaaccaa[A/G]caatccctggctagac	A	G	NM_153026 // upstream // 324358 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 440176 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2268825	gaattagaaaaaacta[C/T]gctgaatttcatatgc	C	T	NM_153026 // upstream // 350330 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 414204 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-1797444	ggtttacttttgtttc[C/G]atgtgagcatatgcgt	C	G	NM_153026 // upstream // 698305 // Hs.524348 // PRICKLE1 // 144165 // Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), mRNA. /// NM_175851 // downstream // 66229 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease	PRICKLE1	PRICKLE1, Homo sapiens prickle-like 1 (Drosophila) (PRICKLE1), q12
SNP_A-2145000	atgatttgcaatgtgg[G/T]actacaagcggccctc	G	T	NM_175851 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip /// NM_025003 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 /	ADAMTS20	ADAMTS20, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip q12
SNP_A-2281982	gagtgctttttctgt[C/G]aagcgtaattagtgca	C	G	NM_175851 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip /// NM_025003 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 /	ADAMTS20	ADAMTS20, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip q12
SNP_A-2054825	aaaagacattgtttg[A/C]aacctgagtacatgga	A	C	NM_175851 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip /// NM_025003 // intron // 0 // Hs.287554 // ADAMTS20 // 80070 /	ADAMTS20	ADAMTS20, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 20 (ADAMTS20), transcrip q12
SNP_A-2300367	gcctctgatttcacca[C/T]gctgcactgtatccat	C	T	NM_032256 // intron // 0 // Hs.444668 // DKFZp434K2435 // 84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// ENST00000266534 // intron // 0 // --- // --- // ---	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-2055079	agtgtaaaaatatgac[A/G]tacatacgtatgaaa	A	G	NM_032256 // intron // 0 // Hs.444668 // DKFZp434K2435 // 84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// ENST00000266534 // intron // 0 // --- // --- // ---	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-2266401	gaaggttataaaggaa[C/G]agtggctgaaatgtt	C	G	NM_032256 // intron // 0 // Hs.444668 // DKFZp434K2435 // 84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// ENST00000266534 // intron // 0 // --- // --- // ---	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-2209891	ccccaactgtctttca[C/T]cttagtctttccttc	C	T	NM_032256 // downstream // 18087 // Hs.444668 // DKFZp434K2435 // 84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// NM_006159 // downstream // 100438 // Hs.505326 // NELL2 // 4753 // Homo sapiens NEL-like 2 (chicken) (NEL	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-1804754	gtcaggttactgccac[G/T]aaataaaaactatgga	G	T	NM_032256 // downstream // 30243 // Hs.444668 // DKFZp434K2435 // 84216 // Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA. /// NM_006159 // downstream // 88282 // Hs.505326 // NELL2 // 4753 // Homo sapiens NEL-like 2 (chicken) (NELL	DKFZp434K2435	DKFZp434K2435, Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), q12
SNP_A-2055427	catgccatagaaacat[A/G]agaggactactgcagt	A	G	NM_006159 // intron // 0 // Hs.505326 // NELL2 // 4753 // Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2055436	atgtaaagtatagtac[A/C]gcagttccctcttacc	A	C	NM_006159 // intron // 0 // Hs.505326 // NELL2 // 4753 // Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2261906	gaaataagtgtttac[C/T]accaaatatctttct	C	T	NM_006159 // intron // 0 // Hs.505326 // NELL2 // 4753 // Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // --- // --- // ---	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2055586	aagtattgcgaattca[A/G]cattagcagagacac	A	G	NM_006159 // intron // 0 // Hs.505326 // NELL2 // 4753 // Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA. /// ENST00000333837 // intron // 0 // — // — // —	NELL2	NELL2, Homo sapiens NEL-like 2 (chicken) (NELL2), q12
SNP_A-2029451	aaagacagttttaac[A/G]atgcccattaaaatg	A	G	NM_001004329 // upstream // 53496 // Hs.302764 // FLJ16139 // 440097 // Homo sapiens FLJ16139 protein (FLJ16139), mRNA. /// NM_015899 // downstream // 68767 // Hs.334649 // PLEKHA9 // 51054 // Homo sapiens pleckstrin homology domain containing, family A (	FLJ16139	FLJ16139, Homo sapiens FLJ16139 protein (FLJ16139), q12
SNP_A-2055886	tccacaatgattttca[A/C]ctctctgggtattca	A	C	ENST00000320560 // downstream // 65573 // — // — // — /// ENST00000338636 // upstream // 231793 // — // — // — /// ENST00000334344 // upstream // 319783 // — // — // —	-	q12
SNP_A-1923216	ttagcttcttcaaggga[A/T]tcctatgctgtttccc	A	T	NM_004719 // upstream // 86365 // Hs.210367 // SFRS2IP // 9169 // Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA. /// NM_004719 // upstream // 25785 // Hs.210367 // SFRS2IP // 9169 // Homo sapiens splicing factor	SFRS2IP	SFRS2IP, Homo sapiens splicing factor, arginine q13.11
SNP_A-2175567	cacatgacccgctaac[A/G]attctctatctttta	A	G	NM_004719 // upstream // 191141 // Hs.210367 // SFRS2IP // 9169 // Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA. /// NM_004719 // upstream // 130541 // Hs.210367 // SFRS2IP // 9169 // Homo sapiens splicing fact	SFRS2IP	SFRS2IP, Homo sapiens splicing factor, arginine q13.11
SNP_A-2098188	agagagtttgtagctg[A/C]aaaagaatagggatag	A	C	NM_004719 // upstream // 257561 // Hs.210367 // SFRS2IP // 9169 // Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA. /// NM_004719 // upstream // 196961 // Hs.210367 // SFRS2IP // 9169 // Homo sapiens splicing fact	SFRS2IP	SFRS2IP, Homo sapiens splicing factor, arginine q13.11
SNP_A-1927773	ttcaagcctactctct[G/T]aatcctatactacact	G	T	NM_030674 // upstream // 79940 // Hs.533770 // SLC38A1 // 81539 // Homo sapiens solute carrier family 38, member 1 (SLC38A1), mRNA. /// NM_018976 // downstream // 9237 // Hs.221847 // SLC38A2 // 54407 // Homo sapiens solute carrier family 38, member 2 (SL	SLC38A1	SLC38A1, Homo sapiens solute carrier family 38, member 1 (SLC38A1), q13.11
SNP_A-2056307	aagtgatttgtggca[C/G]tgaaatccctttttca	C	G	NM_030674 // upstream // 86170 // Hs.533770 // SLC38A1 // 81539 // Homo sapiens solute carrier family 38, member 1 (SLC38A1), mRNA. /// NM_018976 // downstream // 3007 // Hs.221847 // SLC38A2 // 54407 // Homo sapiens solute carrier family 38, member 2 (SL	SLC38A1	SLC38A1, Homo sapiens solute carrier family 38, member 1 (SLC38A1), q13.11
SNP_A-2053135	aagtctcttaaggccc[A/G]gacctagaagtcacag	A	G	NM_018976 // upstream // 32343 // Hs.221847 // SLC38A2 // 54407 // Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA. /// ENST00000256689 // upstream // 32343 // — // — // — // — /// ENST00000314053 // downstream // 116821 // — //	SLC38A2	SLC38A2, Homo sapiens solute carrier family 38, member 2 (SLC38A2), q13.11
SNP_A-2002696	ctacactcagctggtc[C/G]atgttacttcctacc	C	G	NM_018976 // upstream // 97648 // Hs.221847 // SLC38A2 // 54407 // Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA. /// ENST00000256689 // upstream // 97648 // — // — // — // — /// ENST00000314053 // downstream // 51516 // — // -	SLC38A2	SLC38A2, Homo sapiens solute carrier family 38, member 2 (SLC38A2), q13.11
SNP_A-1908431	tgtagaagcaagtcct[A/G]actttgaacttggc	A	G	NM_018976 // upstream // 114213 // Hs.221847 // SLC38A2 // 54407 // Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA. /// ENST00000256689 // upstream // 114213 // — // — // — // — /// ENST00000314053 // downstream // 34951 // — //	SLC38A2	SLC38A2, Homo sapiens solute carrier family 38, member 2 (SLC38A2), q13.11
SNP_A-2154446	attattcaaagcagag[A/T]aaattgctgcctgaag	A	T	NM_018018 // downstream // 226836 // Hs.446077 // SLC38A4 // 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// ENST00000314053 // upstream // 15738 // — // — // — // — /// ENST00000266579 // downstream // 226836 // —	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2064300	aattcaggcaactcca[A/G]agacatggatatggaa	A	G	NM_018018 // intron // 0 // Hs.446077 // SLC38A4 // 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// ENST00000266579 // intron // 0 // — // — // — /// ENST00000354644 // intron // 0 // — // — // —	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-1859502	tcaggagagttggtta[C/T]gtgaaaagaatgtgca	C	T	NM_018018 // upstream // 131331 // Hs.446077 // SLC38A4 // 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 118424 // Hs.121520 // AMIGO2 // 347902 // Homo sapiens amphoterin induced gene 2 (AMIGO2),	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-2039118	aacaggttctataaaa[C/T]aatgagagagtgtaat	C	T	NM_018018 // upstream // 187662 // Hs.446077 // SLC38A4 // 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 82093 // Hs.121520 // AMIGO2 // 347902 // Homo sapiens amphoterin induced gene 2 (AMIGO2).	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-2186972	caggtaacaataacac[A/G]gaacaaaataatagaa	A	G	NM_018018 // upstream // 220761 // Hs.446077 // SLC38A4 // 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 28994 // Hs.121520 // AMIGO2 // 347902 // Homo sapiens amphoterin induced gene 2 (AMIGO2).	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-2116960	aggtgaagacaactat[A/G]aaagatgacactgggc	A	G	NM_018018 // upstream // 241448 // Hs.446077 // SLC38A4 // 55089 // Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA. /// NM_181847 // downstream // 8307 // Hs.121520 // AMIGO2 // 347902 // Homo sapiens amphoterin induced gene 2 (AMIGO2), m	SLC38A4	SLC38A4, Homo sapiens solute carrier family 38, member 4 (SLC38A4), q13.11
SNP_A-1794537	ggtcctttcctctca[A/G]agagttctcagtgagc	A	G	NM_138371 // downstream // 36206 // Hs.258002 // MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 // downstream // 390430 // Hs.437855 // FLJ21908 // 79657 // Homo sapiens hypothetical protein FLJ21908 (FLJ21	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-2076292	acattgacaaagtaca[A/G]gttagaaatacaaac	A	G	NM_138371 // downstream // 76073 // Hs.258002 // MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 // downstream // 350563 // Hs.437855 // FLJ21908 // 79657 // Homo sapiens hypothetical protein FLJ21908 (FLJ21	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-2113786	aggctgccatctatg[C/T]agacttacagaaaaag	C	T	NM_138371 // downstream // 140393 // Hs.258002 // MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 // downstream // 286243 // Hs.437855 // FLJ21908 // 79657 // Homo sapiens hypothetical protein FLJ21908 (FLJ2	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-2263476	gaaccaagaagttaag[A/T]cacaacacagagtttc	A	T	NM_138371 // downstream // 142776 // Hs.258002 // MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 // downstream // 283860 // Hs.437855 // FLJ21908 // 79657 // Homo sapiens hypothetical protein FLJ21908 (FLJ2	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-1904852	tgggttgttgtatta[A/G]atgaactaatgtatgc	A	G	NM_138371 // downstream // 310280 // Hs.258002 // MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 // downstream // 116356 // Hs.437855 // FLJ21908 // 79657 // Homo sapiens hypothetical protein FLJ21908 (FLJ2	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11
SNP_A-2213006	ccgaaggctggctgat[C/T]ggatagtgaatagtaa	C	T	NM_138371 // downstream // 316354 // Hs.258002 // MGC16044 // 91523 // Homo sapiens hypothetical protein MGC16044 (MGC16044), mRNA. /// NM_024604 // downstream // 110282 // Hs.437855 // FLJ21908 // 79657 // Homo sapiens hypothetical protein FLJ21908 (FLJ2	MGC16044	MGC16044, Homo sapiens hypothetical protein MGC16044 (MGC16044), q13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864469	tccagaaactggcaca[C/T]ccaatcagtccttgcc	C	T	NM_017842 // intron // 0 // Hs.438867 // FLJ20489 // 55652 // Homo sapiens hypothetical protein FLJ20489 (FLJ20489), mRNA. /// ENST00000282438 // intron // 0 // — // — // — // —	FLJ20489	FLJ20489, Homo sapiens hypothetical protein FLJ20489 (FLJ20489), q13.11
SNP_A-2299372	gccctgccttttcctc[A/G]ccattgttcagacaag	A	G	NM_000376 // intron // 0 // Hs.524368 // VDR // 7421 // Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA. /// ENST00000229022 // intron // 0 // — // — // — // —	VDR	VDR, Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), q13.11
SNP_A-2137567	atcatcgccatctctg[C/T]agtccttgtaatgtga	C	T	NM_001004134 // upstream // 80920 // Hs.446790 // OR10AD1 // 121275 // Homo sapiens olfactory receptor, family 10, subfamily AD, member 1 (OR10AD1), mRNA. /// NM_181788 // upstream // 44768 // Hs.155833 // LOC341567 // 341567 // Homo sapiens HANP1 (LOC341	OR10AD1	OR10AD1, Homo sapiens olfactory receptor, family 10, subfamily AD, member 1 (OR10AD1), q13.11
SNP_A-1669567	tctgttattaagcctctctcgctcc[A/G]ctccttggtagcaattttcctaata	A	G	NM_002289 // intron // 0 // Hs.72938 // LALBA // 3906 // lactalbumin, alpha-	LALBA	LALBA , rs2071380, lactalbumin, alpha-,q13.11
SNP_A-2119201	agtaggatttgaatca[G/T]gttacgttattttcta	G	T	NM_024902 // downstream // 3265 // Hs.170298 // FLJ13236 // 79962 // Homo sapiens hypothetical protein FLJ13236 (FLJ13236), mRNA. /// NM_024902 // downstream // 3092 // Hs.170298 // FLJ13236 // 79962 // Homo sapiens hypothetical protein FLJ13236 (FLJ13236	FLJ13236	FLJ13236, Homo sapiens hypothetical protein FLJ13236 (FLJ13236), q13.12
SNP_A-1735136	ttaagtgaaggggacagccgaggga[C/T]atattttaccatgacagccttgtag	C	T	NM_023071 // upstream // 8642 // Hs.152982 // SPATS2 // 65244 // spermatogenesis associated, serine-rich 2 /// NM_024902 // downstream // 6968 // Hs.204907 // FLJ13236 // 79962 // hypothetical protein FLJ13236	SPATS2	SPATS2 , rs10506284, spermatogenesis associated, serine-rich 2 ,q13.12
SNP_A-1883157	tgaaatgcagcagaaa[A/G]gaaaaggaataaacat	A	G	NM_012272 // intron // 0 // Hs.33104 // HYPC // 25766 // Homo sapiens Huntingtin interacting protein C (HYPC), mRNA. /// ENST00000261897 // intron // 0 // — // — // — // — /// ENST00000341308 // intron // 0 // — // — // — // — /// ENST0000	HYPC	HYPC, Homo sapiens Huntingtin interacting protein C (HYPC), q13.12
SNP_A-2065549	aatttaataggctaga[C/G]caacagtaaagtaact	C	G	NM_012306 // intron // 0 // Hs.182859 // FAIM2 // 23017 // Homo sapiens Fas apoptotic inhibitory molecule 2 (FAIM2), mRNA. /// ENST00000320634 // intron // 0 // — // — // — // —	FAIM2	FAIM2, Homo sapiens Fas apoptotic inhibitory molecule 2 (FAIM2), q13.12
SNP_A-2058114	agcacagtactgataa[C/T]cttcaatcatatatgg	C	T	NM_012306 // upstream // 8040 // Hs.182859 // FAIM2 // 23017 // Homo sapiens Fas apoptotic inhibitory molecule 2 (FAIM2), mRNA. /// NM_000486 // upstream // 38769 // Hs.130730 // AQP2 // 359 // Homo sapiens aquaporin 2 (collecting duct) (AQP2), mRNA. ///	FAIM2	FAIM2, Homo sapiens Fas apoptotic inhibitory molecule 2 (FAIM2), q13.12
SNP_A-2147315	atggagagaactagga[A/G]agtgaggagaacccca	A	G	NM_001095 // intron // 0 // Hs.274361 // ACCN2 // 41 // Homo sapiens amiloride-sensitive cation channel 2, neuronal (ACCN2), transcript variant 2, mRNA. /// NM_020039 // intron // 0 // Hs.274361 // ACCN2 // 41 // Homo sapiens amiloride-sensitive cation ch	ACCN2	ACCN2, Homo sapiens amiloride-sensitive cation channel 2, neuronal (ACCN2), transcript variant 2, q13.12
SNP_A-2262683	gaaattcttgggtttg[C/T]aggatggtagataaga	C	T	NM_004858 // intron // 0 // Hs.370636 // SLC4A8 // 9498 // Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8), mRNA. /// ENST00000358657 // intron // 0 // — // — // — // — /// ENST00000319957 // intron // 0 /	SLC4A8	SLC4A8, Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 8 (SLC4A8), q13.13
SNP_A-1835864	tacgtctcactccacc[A/C]aatttacccaaagctg	A	C	NM_014191 // upstream // 36725 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000316708 // downstream // 131671 // — // — // — // — /// ENST00000357961 // upstream // 36725 //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-2024821	aaaagtggattttgaa[A/G]agtggattaaattgct	A	G	NM_014191 // upstream // 26813 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000316708 // downstream // 141583 // — // — // — // — /// ENST00000357961 // upstream // 26813 //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2198765	catttctcagaacgta[C/T]ccccatcgttaagtga	C	T	NM_014191 // upstream // 15279 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000316708 // downstream // 153117 // — // — // — // — /// ENST00000357961 // upstream // 15279 //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-2092350	agaaagctggagctct[A/G]agacttaaagaatggg	A	G	NM_014191 // intron // 0 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000357961 // intron // 0 // — // — // — // — /// ENST00000355133 // intron // 0 // — // — // — //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-2058949	tcaccaaagtggatta[C/T]caactttataacaaaa	C	T	NM_014191 // intron // 0 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000357961 // intron // 0 // — // — // — // — /// ENST00000355133 // intron // 0 // — // — // — //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-1666152	attatgttgtcttgtcacacattct[C/G]aaacactggtgagagagg cagtgaa	C	G	NM_014191 // intron // 0 // Hs.124189 // SCN8A // 6334 // sodium channel, voltage gated, type VIII, alpha	SCN8A	SCN8A , rs10506303, sodium channel, voltage gated, type VIII, alpha,q13.13
SNP_A-2058954	ctccctttataggcac[C/T]gtctaatgactgactc	C	T	NM_014191 // intron // 0 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000355133 // intron // 0 // — // — // — // — /// ENST00000354534 // intron // 0 // — // — // — //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-2058957	ggtggtattttcgcca[C/T]gtacatccttaccttc	C	T	NM_014191 // intron // 0 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000355133 // intron // 0 // — // — // — // — /// ENST00000354534 // intron // 0 // — // — // — //	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-1729524	tctttccttttcatctctgttgctc[A/G]actgcactctctgacctacctg ctt	A	G	NM_014191 // intron // 0 // Hs.124189 // SCN8A // 6334 // sodium channel, voltage gated, type VIII, alpha	SCN8A	SCN8A , rs303816, sodium channel, voltage gated, type VIII, alpha,q13.13
SNP_A-1956896	ttttaagaactcaaag[A/G]attgtagccggtatgg	A	G	NM_014191 // 3UTR // 0 // Hs.124189 // SCN8A // 6334 // Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA. /// ENST00000355133 // 3UTR // 0 // — // — // — // — /// ENST00000354534 // 3UTR // 0 // — // — // — // —	SCN8A	SCN8A, Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), q13.13
SNP_A-2267338	gaatagatgagactga[A/G]gaagttagctgtgata	A	G	NM_000020 // downstream // 1070 // Hs.410104 // ACVRL1 // 94 // Homo sapiens activin A receptor type II-like 1 (ACVRL1), mRNA. /// NM_004302 // upstream // 29563 // Hs.438918 // ACVR1B // 91 // Homo sapiens activin A receptor, type IB (ACVR1B), transcript	ACVRL1	ACVRL1, Homo sapiens activin A receptor type II-like 1 (ACVRL1), q13.13
SNP_A-1874330	tctccaggtacgagaa[C/G]tgtaatttcgaccctg	C	G	NM_000020 // downstream // 2204 // Hs.410104 // ACVRL1 // 94 // Homo sapiens activin A receptor type II-like 1 (ACVRL1), mRNA. /// NM_004302 // upstream // 28429 // Hs.438918 // ACVR1B // 91 // Homo sapiens activin A receptor, type IB (ACVR1B), transcript	ACVRL1	ACVRL1, Homo sapiens activin A receptor type II-like 1 (ACVRL1), q13.13
SNP_A-1665700	tctatctagacatcttcttcaaac[C/T]gtcagaagactgaataga gaaacag	C	T	NM_000020 // downstream // 4398 // Hs.410104 // ACVRL1 // 94 // activin A receptor type II-like 1 /// NM_004302 // upstream // 26235 // Hs.371974 // ACVR1B // 91 // activin A receptor, type IB /// NM_020327 // upstream // 26235 // Hs.371974 // ACVR1B //	ACVRL1	ACVRL1 , rs706824, activin A receptor type II-like 1 ,q13.13
SNP_A-2190223	cataatcatctaaaaa[C/G]gttcttagaggaaaat	C	G	NM_004302 // intron // 0 // Hs.438918 // ACVR1B // 91 // Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, mRNA. /// NM_020328 // intron // 0 // Hs.438918 // ACVR1B // 91 // Homo sapiens activin A receptor, type IB (ACVR1B), transcr	ACVR1B	ACVR1B, Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, q13.13
SNP_A-2252988	cttctccagagcaaga[A/T]cccaaaaggaaacgaa	A	T	NM_004302 // intron // 0 // Hs.438918 // ACVR1B // 91 // Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, mRNA. /// NM_020328 // intron // 0 // Hs.438918 // ACVR1B // 91 // Homo sapiens activin A receptor, type IB (ACVR1B), transcr	ACVR1B	ACVR1B, Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 1, q13.13
SNP_A-1936609	ttcttggcgcactacc[A/G]gacactgggggacaca	A	G	NM_021934 // downstream // 87897 // Hs.9911 // FLJ11773 // 60673 // Homo sapiens hypothetical protein FLJ11773 (FLJ11773), mRNA. /// NM_182507 // downstream // 3617 // Hs.140978 // LOC144501 // 144501 // Homo sapiens hypothetical protein LOC144501 (LOC144	FLJ11773	FLJ11773, Homo sapiens hypothetical protein FLJ11773 (FLJ11773), q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2210202	ccccataacagtcaca[A/C]tctaccctgacgtggg	A	C	NM_182507 // intron // 0 // Hs.140978 // LOC144501 // 144501 // Homo sapiens hypothetical protein LOC144501 (LOC144501), mRNA. /// ENST00000301446 // intron // 0 // — // — // — // —	LOC144501	LOC144501, Homo sapiens hypothetical protein LOC144501 (LOC144501), q13.13
SNP_A-1843739	tagtgtgtgtatagaa[C/T]ttccagttacaaagtg	C	T	NM_182507 // intron // 0 // Hs.140978 // LOC144501 // 144501 // Homo sapiens hypothetical protein LOC144501 (LOC144501), mRNA. /// ENST00000301446 // intron // 0 // — // — // — // —	LOC144501	LOC144501, Homo sapiens hypothetical protein LOC144501 (LOC144501), q13.13
SNP_A-2302502	gctaattcctgcaaag[A/C]atctgggacatatctg	A	C	NM_182507 // upstream // 8036 // Hs.140978 // LOC144501 // 144501 // Homo sapiens hypothetical protein LOC144501 (LOC144501), mRNA. /// NM_005556 // upstream // 39436 // Hs.411501 // KRT7 // 3855 // Homo sapiens keratin 7 (KRT7), mRNA. /// ENST00000301446	LOC144501	LOC144501, Homo sapiens hypothetical protein LOC144501 (LOC144501), q13.13
SNP_A-2083741	actacagtttgaggaa[C/T]gtttgttgaactaaac	C	T	NM_182507 // upstream // 11938 // Hs.140978 // LOC144501 // 144501 // Homo sapiens hypothetical protein LOC144501 (LOC144501), mRNA. /// NM_005556 // upstream // 35534 // Hs.411501 // KRT7 // 3855 // Homo sapiens keratin 7 (KRT7), mRNA. /// ENST00000030144	LOC144501	LOC144501, Homo sapiens hypothetical protein LOC144501 (LOC144501), q13.13
SNP_A-1797041	ggttctgggcaggcaa[A/G]cttttcttagagctt	A	G	NM_005556 // downstream // 3045 // Hs.411501 // KRT7 // 3855 // Homo sapiens keratin 7 (KRT7), mRNA. /// ENST00000331817 // downstream // 3045 // — // — // — // — /// ENST00000257935 // downstream // 288 // — // — // — // —	KRT7	KRT7, Homo sapiens keratin 7 (KRT7), q13.13
SNP_A-1934678	ttctctgcttctgcca[C/T]gactgaactgctgcca	C	T	NM_002283 // upstream // 5254 // Hs.182507 // KRTHB5 // 3891 // Homo sapiens keratin, hair, basic, 5 (KRTHB5), mRNA. /// NM_033045 // downstream // 4469 // Hs.272336 // KRTHB4 // 3890 // Homo sapiens keratin, hair, basic, 4 (KRTHB4), mRNA. /// ENST0000025	KRTHB5	KRTHB5, Homo sapiens keratin, hair, basic, 5 (KRTHB5), q13.13
SNP_A-1855331	tcaaggattgttaaca[A/C]cttcttcgctttctga	A	C	NM_004693 // upstream // 2778 // Hs.145949 // K6HF // 9119 // Homo sapiens cytokeratin type II (K6HF), mRNA. /// NM_173086 // downstream // 9553 // Hs.446417 // KRT6E // 286887 // Homo sapiens keratin 6E (KRT6E), mRNA. /// NM_005554 // downstream // 9553	K6HF	K6HF, Homo sapiens cytokeratin type II (K6HF), q13.13
SNP_A-1833853	tacagtgtaaagactc[A/T]actcctctgtccctct	A	T	NM_173086 // upstream // 20051 // Hs.446417 // KRT6E // 286887 // Homo sapiens keratin 6E (KRT6E), mRNA. /// NM_005554 // upstream // 20051 // Hs.367762 // KRT6A // 3853 // Homo sapiens keratin 6A (KRT6A), mRNA. /// NM_005555 // upstream // 20051 // Hs.52	KRT6E	KRT6E, Homo sapiens keratin 6E (KRT6E), q13.13
SNP_A-2206711	ccatgatagatacaga[C/T]gttagagcttcctcat	C	T	NM_175053 // upstream // 11498 // Hs.56255 // K6IRS4 // 121391 // Homo sapiens keratin 6 irs4 (K6IRS4), mRNA. /// NM_080747 // downstream // 266 // Hs.147040 // K6IRS2 // 140807 // Homo sapiens keratin protein K6irs (K6IRS2), mRNA. /// ENST00000305620 //	K6IRS4	K6IRS4, Homo sapiens keratin 6 irs4 (K6IRS4), q13.13
SNP_A-2273282	gactccaattttcatc[C/T]cactttccccacataa	C	T	NM_080747 // intron // 0 // Hs.147040 // K6IRS2 // 140807 // Homo sapiens keratin protein K6irs (K6IRS2), mRNA. /// ENST00000293745 // intron // 0 // — // — // — // —	K6IRS2	K6IRS2, Homo sapiens keratin protein K6irs (K6IRS2), q13.13
SNP_A-1944166	ttgtcagtcaatcctа[C/T]gtaaaaattctcctct	C	T	NM_080747 // upstream // 1741 // Hs.147040 // K6IRS2 // 140807 // Homo sapiens keratin protein K6irs (K6IRS2), mRNA. /// NM_175068 // downstream // 4322 // Hs.55410 // K6IRS3 // 319101 // Homo sapiens keratin 6 irs3 (K6IRS3), mRNA. /// ENST00000293745 //	K6IRS2	K6IRS2, Homo sapiens keratin protein K6irs (K6IRS2), q13.13
SNP_A-2168017	caactaaggactctcc[A/G]aggttttaaagctggg	A	G	NM_175068 // upstream // 25073 // Hs.55410 // K6IRS3 // 319101 // Homo sapiens keratin 6 irs3 (K6IRS3), mRNA. /// NM_000423 // downstream // 927 // Hs.707 // KRT2A // 3849 // Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), mRNA.	K6IRS3	K6IRS3, Homo sapiens keratin 6 irs3 (K6IRS3), q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2214247	cctacacatgtggtt[A/G]aacaagacagctgct	A	G	NM_000423 // upstream // 3876 // Hs.707 // KRT2A // 3849 // Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), mRNA. /// NM_006121 // downstream // 18624 // Hs.80828 // KRT1 // 3848 // Homo sapiens keratin 1 (epidermolytic hyperker	KRT2A	KRT2A, Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), q13.13
SNP_A-2158002	attgcttgagatcaac[C/T]atggtaggtatattta	C	T	NM_000423 // upstream // 12043 // Hs.707 // KRT2A // 3849 // Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), mRNA. /// NM_006121 // downstream // 10457 // Hs.80828 // KRT1 // 3848 // Homo sapiens keratin 1 (epidermolytic hyperke	KRT2A	KRT2A, Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), q13.13
SNP_A-1947110	tttaatcatcctgttc[C/T]atatttggtgacctta	C	T	NM_000423 // upstream // 12660 // Hs.707 // KRT2A // 3849 // Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), mRNA. /// NM_006121 // downstream // 9840 // Hs.80828 // KRT1 // 3848 // Homo sapiens keratin 1 (epidermolytic hyperker	KRT2A	KRT2A, Homo sapiens keratin 2A (epidermal ichthyosis bullosa of Siemens) (KRT2A), q13.13
SNP_A-1896855	tgctcacatatgggcc[G/T]gatcctgactccaaaa	G	T	NM_175078 // upstream // 20446 // Hs.334989 // KRT11B // 374454 // Homo sapiens keratin 1B (KRT1B), mRNA. /// ENST00000341809 // upstream // 20446 // — // — // — /// ENST00000321887 // upstream // 6940 // — // — // —	KRT1B	KRT1B, Homo sapiens keratin 1B (KRT1B), q13.13
SNP_A-2114503	agggagataaccatta[A/G]atctgactgcccgaga	A	G	NM_015848 // downstream // 6595 // Hs.512601 // HUMCYT2A // 51350 // Homo sapiens cytokeratin 2 (HUMCYT2A), mRNA. /// ENST00000321887 // downstream // 28765 // — // — // — /// ENST00000332411 // downstream // 6595 // — // — // —	HUMCYT2A	HUMCYT2A, Homo sapiens cytokeratin 2 (HUMCYT2A), q13.13
SNP_A-2256237	ctttagcatttgataa[A/C]cactgctaagacttt	A	C	NM_015848 // intron // 0 // Hs.512601 // HUMCYT2A // 51350 // Homo sapiens cytokeratin 2 (HUMCYT2A), mRNA. /// ENST00000332411 // intron // 0 // — // — // —	HUMCYT2A	HUMCYT2A, Homo sapiens cytokeratin 2 (HUMCYT2A), q13.13
SNP_A-2084616	actatgtcaatgtat[G/T]aggaaagttcttggc	G	T	NM_015848 // intron // 0 // Hs.512601 // HUMCYT2A // 51350 // Homo sapiens cytokeratin 2 (HUMCYT2A), mRNA. /// ENST00000332411 // intron // 0 // — // — // —	HUMCYT2A	HUMCYT2A, Homo sapiens cytokeratin 2 (HUMCYT2A), q13.13
SNP_A-1910345	tgtccaggtccaggga[A/G]cgattattgtccatgg	A	G	NM_057088 // CDS // 0 // Hs.410397 // KRT3 // 3850 // Homo sapiens keratin 3 (KRT3), mRNA. /// ENST00000309505 // CDS // 0 // — // — // — // —	KRT3	KRT3, Homo sapiens keratin 3 (KRT3), q13.13
SNP_A-1747305	ctcccagcccctctagtggaataac[A/G]agatgactgttcagacc ctaccatc	A	G	NM_002272 // downstream // 2886 // Hs.371139 // KRT4 // 3851 // keratin 4 /// NM_057088 // upstream // 7622 // Hs.410397 // KRT3 // 3850 // keratin 3	KRT4	KRT4 , rs7965628, keratin 4 ,q13.13
SNP_A-2041957	aactaatctcaaacaa[C/T]gtttcccaaactgcct	C	T	NM_199187 // downstream // 23411 // Hs.406013 // KRT18 // 3875 // Homo sapiens keratin 18 (KRT18), transcript variant 2, mRNA. /// NM_000224 // downstream // 23411 // Hs.406013 // KRT18 // 3875 // Homo sapiens keratin 18 (KRT18), transcript variant 1, mRN	KRT18	KRT18, Homo sapiens keratin 18 (KRT18), transcript variant 2, q13.13
SNP_A-2002740	ttcctgaaaagatgaa[C/T]gagattgagaaacctt	C	T	NM_199187 // downstream // 44817 // Hs.406013 // KRT18 // 3875 // Homo sapiens keratin 18 (KRT18), transcript variant 2, mRNA. /// NM_000224 // downstream // 44817 // Hs.406013 // KRT18 // 3875 // Homo sapiens keratin 18 (KRT18), transcript variant 1, mRN	KRT18	KRT18, Homo sapiens keratin 18 (KRT18), transcript variant 2, q13.13
SNP_A-2093222	agaacccacaagccca[A/G]acaatcacctagccc	A	G	NM_138473 // CDS // 0 // Hs.524461 // SP1 // 6667 // Homo sapiens Sp1 transcription factor (SP1), mRNA. /// ENST00000327443 // CDS // 0 // — // — // —	SP1	SP1, Homo sapiens Sp1 transcription factor (SP1), q13.13
SNP_A-2084274	actagtgattccaaag[A/C]aaccagcctctctctt	A	C	NM_001002031 // intron // 0 // Hs.524464 // ATP5G2 // 517 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (ATP5G2), nuclear gene en /// NM_005176 // intron // 0 // Hs.524464 // ATP5G2 // 517 // Hom	ATP5G2	ATP5G2, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (ATP5G2), nuclear gene en ,q13.13
SNP_A-1685406	ccatcagcacccaaggcagatatag[C/G]aaggcagtcagcc attcctcctaga	C	G	NM_017410 // upstream // 119985 // Hs.118608 // HOXC13 // 3229 // homeo box C13 /// NM_020898 // upstream // 91372 // Hs.156667 // KIAA1536 // 57658 // KIAA1536 protein	HOXC13	HOXC13 , rs3910926, homeo box C13 ,q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2032872	aaataagtgcaaataa[A/T]acaatgttgaggaact	A	T	NM_020898 // upstream // 135957 // Hs.156667 // KIAA1536 // 57658 // Homo sapiens KIAA1536 protein (KIAA1536), mRNA. /// NM_017410 // upstream // 75400 // Hs.118608 // HOXC13 // 3229 // Homo sapiens homeo box C13 (HOXC13), mRNA. /// ENST00000262059 // ups	KIAA1536	KIAA1536, Homo sapiens KIAA1536 protein (KIAA1536), q13.13
SNP_A-2060776	ctcttcttatcactgg[C/T]agcatcttatcacaat	C	T	NM_020898 // upstream // 140248 // Hs.156667 // KIAA1536 // 57658 // Homo sapiens KIAA1536 protein (KIAA1536), mRNA. /// NM_017410 // upstream // 71109 // Hs.118608 // HOXC13 // 3229 // Homo sapiens homeo box C13 (HOXC13), mRNA. /// ENST00000262059 // ups	KIAA1536	KIAA1536, Homo sapiens KIAA1536 protein (KIAA1536), q13.13
SNP_A-2310150	ggaacactcaccaacc[A/G]gatttgtgcatgtgtg	A	G	NM_020898 // upstream // 179825 // Hs.156667 // KIAA1536 // 57658 // Homo sapiens KIAA1536 protein (KIAA1536), mRNA. /// NM_017410 // upstream // 31532 // Hs.118608 // HOXC13 // 3229 // Homo sapiens homeo box C13 (HOXC13), mRNA. /// ENST00000262059 // ups	KIAA1536	KIAA1536, Homo sapiens KIAA1536 protein (KIAA1536), q13.13
SNP_A-2291976	gcacatgaaatacagc[A/G]gatggcaggctgaca	A	G	NM_014620 // intron // 0 // Hs.820 // HOXC4 // 3221 // Homo sapiens homeo box C4 (HOXC4), transcript variant 1, mRNA. /// NM_153633 // intron // 0 // Hs.820 // HOXC4 // 3221 // Homo sapiens homeo box C4 (HOXC4), transcript variant 2, mRNA. /// ENST00000030	HOXC4	HOXC4, Homo sapiens homeo box C4 (HOXC4), transcript variant 1, q13.13
SNP_A-2195830	catgtagtcgttgtca[C/T]gcatcagatcatttaa	C	T	NM_014311 // upstream // 18274 // Hs.5212 // SMUG1 // 23583 // Homo sapiens single-strand selective monofunctional uracil DNA glycosylase (SMUG1), mRNA. /// NM_012117 // downstream // 34380 // Hs.349283 // CBX5 // 23468 // Homo sapiens chromobox homolog 5	SMUG1	SMUG1, Homo sapiens single-strand selective monofunctional uracil DNA glycosylase (SMUG1), q13.13
SNP_A-1903315	tgggaaacaggagtta[A/G]agtggaagcaacatta	A	G	NM_002205 // intron // 0 // Hs.505654 // ITGA5 // 3678 // Homo sapiens integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5), mRNA. /// ENST00000293379 // intron // 0 // — // — // — // —	ITGA5	ITGA5, Homo sapiens integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5), q13.13
SNP_A-1813704	gtgtacttccgggcga[C/T]agtgatgccaaaataa	C	T	NM_053283 // upstream // 37036 // Hs.350570 // DCD // 117159 // Homo sapiens dermcidin (DCD), mRNA. /// NM_058173 // upstream // 169146 // Hs.348419 // LOC118430 // 118430 // Homo sapiens small breast epithelial mucin (LOC118430), mRNA. /// ENST00000029337	DCD	DCD, Homo sapiens dermcidin (DCD), q13.2
SNP_A-2275303	gagaagttcttctgaa[A/T]tgcagtataaaagata	A	T	NM_053283 // upstream // 56850 // Hs.350570 // DCD // 117159 // Homo sapiens dermcidin (DCD), mRNA. /// NM_058173 // upstream // 149332 // Hs.348419 // LOC118430 // 118430 // Homo sapiens small breast epithelial mucin (LOC118430), mRNA. /// ENST00000029337	DCD	DCD, Homo sapiens dermcidin (DCD), q13.2
SNP_A-2093439	agaactggtcagactc[A/C]aggtggctcctctgca	A	C	NM_079423 // intron // 0 // Hs.505705 // MYL6 // 4637 // Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 2, mRNA. /// NM_079425 // intron // 0 // Hs.505705 // MYL6 // 4637 // Homo sapiens myosin, l	MYL6	MYL6, Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 2, q13.2
SNP_A-2059788	aatctggctaatgata[A/T]gctggcaaaaaattg	A	T	NM_003725 // downstream // 92510 // Hs.524513 // RODH // 8630 // Homo sapiens 3-hydroxysteroid epimerase (RODH), mRNA. /// NM_148897 // downstream // 42854 // Hs.380178 // SDR-O // 121214 // Homo sapiens orphan short-chain dehydrogenase / reductase (SDR-O	RODH	RODH, Homo sapiens 3-hydroxysteroid epimerase (RODH), q13.3
SNP_A-1820745	gtttccaatatttagc[A/G]atcattcacagcactg	A	G	NM_003725 // downstream // 107094 // Hs.524513 // RODH // 8630 // Homo sapiens 3-hydroxysteroid epimerase (RODH), mRNA. /// NM_148897 // downstream // 28270 // Hs.380178 // SDR-O // 121214 // Homo sapiens orphan short-chain dehydrogenase / reductase (SDR-	RODH	RODH, Homo sapiens 3-hydroxysteroid epimerase (RODH), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932314	ttcctcttcaaaataa[C/T]gagaggttcagattag	C	T	NM_003708 // upstream // 24172 // Hs.134958 // RODH-4 // 8608 // Homo sapiens microsomal NAD+-dependent retinol dehydrogenase 4 (RODH-4), mRNA. /// NM_007264 // upstream // 12676 // Hs.483909 // ADMR // 11318 // Homo sapiens adrenomedullin receptor (ADMR)	RODH-4	RODH-4, Homo sapiens microsomal NAD+-dependent retinol dehydrogenase 4 (RODH-4), q13.3
SNP_A-2026563	aaacaacatatttgta[A/G]ggcacctttatgtac	A	G	NM_013251 // intron // 0 // Hs.9730 // TAC3 // 6866 // Homo sapiens tachykinin 3 (neuromedin K, neurokinin beta) (TAC3), mRNA. /// ENST00000300108 // intron // 0 // — // — // --- // --- /// ENST00000357616 // intron // 0 // — // — // --- // —	TAC3	TAC3, Homo sapiens tachykinin 3 (neuromedin K, neurokinin beta) (TAC3), q13.3
SNP_A-1918233	ttaaagagaagaaaga[A/C]atgctcatgtgaccag	A	C	NM_003153 // intron // 0 // Hs.524518 // STAT6 // 6778 // Homo sapiens signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA. /// ENST00000300134 // intron // 0 // --- // — // — // —	STAT6	STAT6, Homo sapiens signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), q13.3
SNP_A-1810411	gtgattatgatgatca[A/T]cctggtttaggaccca	A	T	X82272 // upstream // 29530 // — // — // 0 // Human endogenous retrovirus env mRNA. /// NM_153377 // downstream // 512148 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST000	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-1932269	ttcctctcccatttac[C/T]agcgataggagtggag	C	T	X82272 // upstream // 38995 // — // --- // 0 // Human endogenous retrovirus env mRNA. /// NM_153377 // downstream // 502683 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST000	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2151903	atgtttggttaaggaa[C/T]gaacaggagacctagc	C	T	X82272 // upstream // 47318 // --- // — // 0 // Human endogenous retrovirus env mRNA. /// NM_153377 // downstream // 494360 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST000	-	-, Human endogenous retrovirus env q14.1
SNP_A-2064600	aattctaccccgacaa[C/T]ctcagcttctgcctat	C	T	X82272 // upstream // 85764 // — // --- // 0 // Human endogenous retrovirus env mRNA. /// NM_153377 // downstream // 455914 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST000	-	-, Human endogenous retrovirus env q14.1
SNP_A-1930392	ttcattttccagcaat[G/T]atgcctactttgcagt	G	T	X82272 // upstream // 250464 // — // — // 0 // Human endogenous retrovirus env mRNA. /// NM_153377 // downstream // 291214 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2063830	caaggaaatggaagta[A/T]aagtattgttccagtc	A	T	X82272 // upstream // 279222 // — // --- // 0 // Human endogenous retrovirus env mRNA. /// NM_153377 // downstream // 262456 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00	-	-, Human endogenous retrovirus env ,q14.1
SNP_A-2209528	cccatctcaaagataa[A/G]ctcagctaaacatatc	A	G	NM_153377 // intron // 0 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron // 0 // --- // — // — // ---	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2307787	gcttcctgttgaataa[G/T]gtatatctgtcaatag	G	T	NM_153377 // intron // 0 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron // 0 // --- // — // — // —	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-1668889	gggaatgagaatttaacccaggaga[A/G]gggaatgctttaagaaaatctcata	A	G	NM_004731 // upstream // 787673 // Hs.439643 // SLC16A7 // 9194 // solute carrier family 16 (monocarboxylic acid transporters), member 7 /// NM_153377 // upstream // 15794 // Hs.19669 // FLJ90440 // 121227 // hypothetical protein FLJ90440	SLC16A7	SLC16A7 , rs1020031, solute carrier family 16 (monocarboxylic acid transporters), member 7 ,q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2268065	gaatcttgccatccca[A/G]tcatgaaaagaaactg	A	G	NM_153377 // intron // 0 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron // 0 // --- // --- // ---	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-1913380	tgtgggttcaggataaa[A/G]tatcggtaatacaaga	A	G	NM_153377 // intron // 0 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// ENST00000320743 // intron // 0 // --- // --- // ---	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2227889	ctacctaatatctttta[C/T]atccttacctcaaaac	C	T	NM_153377 // upstream // 20306 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// NM_004731 // upstream // 655280 // Hs.439643 // SLC16A7 // 9194 // Homo sapiens solute carrier family	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2293399	gcagatggatgttaa[A/C]actttcaaagtagtt	A	C	NM_153377 // upstream // 206068 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// NM_004731 // upstream // 469518 // Hs.439643 // SLC16A7 // 9194 // Homo sapiens solute carrier family	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2166749	caaattctagctctc[A/G]acatttgacaatactg	A	G	NM_153377 // upstream // 221374 // Hs.253736 // LRIG3 // 121227 // Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), mRNA. /// NM_004731 // upstream // 454212 // Hs.439643 // SLC16A7 // 9194 // Homo sapiens solute carrier family	LRIG3	LRIG3, Homo sapiens leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3), q14.1
SNP_A-2275280	gagaagtgaagaaaaag[C/G]agatttcactcagtct	C	G	ENST00000343378 // downstream // 34465 // --- // --- // --- /// ENST00000354800 // downstream // 717108 // --- // --- // ---	-	q14.1
SNP_A-2044678	aagaaagatttgatga[C/T]gttaactttctagga	C	T	ENST00000343378 // downstream // 64181 // --- // --- // --- /// ENST00000354800 // downstream // 687392 // --- // --- // ---	-	q14.1
SNP_A-2083178	actaaaaagttttcat[C/T]tcctgagaatcctca	C	T	ENST00000343378 // downstream // 96472 // --- // --- // --- /// ENST00000354800 // downstream // 655101 // --- // --- // ---	-	q14.1
SNP_A-2064823	tttcagaattcacaaa[C/G]cctttaatactgcag	C	G	ENST00000343378 // downstream // 127052 // --- // --- // --- /// ENST00000354800 // downstream // 624521 // --- // --- // ---	-	q14.1
SNP_A-1860300	tcagtgacaaaaagaa[C/T]attggtgctttacac	C	T	ENST00000343378 // downstream // 146910 // --- // --- // --- /// ENST00000354800 // downstream // 604663 // --- // --- // ---	-	q14.1
SNP_A-1693437	tccttcattatattcaagtttta[A/G]atacatagctaagggaatatg ctgt	A	G	NM_004731 // downstream // 470412 // Hs.439643 // SLC16A7 // 9194 // solute carrier family 16 (monocarboxylic acid transporters), member 7 /// NM_178539 // downstream // 1456237 // Hs.269745 // TAFA2 // 338811 // TAFA2 protein	SLC16A7	SLC16A7 , rs7304826, solute carrier family 16 (monocarboxylic acid transporters), member 7 ,q14.1
SNP_A-2217565	cctgagacaccctcaj[C/T]agtcgtgctacaggaa	C	T	NM_178539 // downstream // 1061309 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream // 254 // --- // --- // --- /// ENST00000358343 // downstream // 1061309 // --- // --- // --- /	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-1820320	gtttagattcagtagt[A/T]atgtgtataggtgtat	A	T	NM_178539 // downstream // 1034342 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream // 27221 // --- // --- // --- /// ENST00000358343 // downstream // 1034342 // --- // --- // ---	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-1835185	taccgatgtgttgta[A/T]aaaacaatctcagaag	A	T	NM_178539 // downstream // 891499 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream // 170064 // --- // --- // --- /// ENST00000358343 // downstream // 891499 // --- // --- // ---	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2271615	gaccacataaaaaga[A/G]gtttacacgctaaa	A	G	NM_178539 // downstream // 357077 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream // 704486 // --- // --- // --- /// ENST00000358343 // downstream // 357077 // --- // --- // ---	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1932801	ttccttggcaaaacac[C/T]caagttgaaaacctca	C	T	NM_178539 // downstream // 107860 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream // 953703 // — // — // — // — /// ENST00000358343 // downstream // 107860 // — // — // — // —	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2066088	gggggatctctttttta[C/G]tgaggtatactgtggg	C	G	NM_178539 // downstream // 41951 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000360644 // upstream // 1019612 // — // — // — // — /// ENST00000358343 // downstream // 41951 // — // — // — // — //	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-1943315	ttggtgtgtgatgcta[C/T]gtaaactctgttaacc	C	T	NM_178539 // intron // 0 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // — // — // — // — /// ENST00000356036 // intron // 0 // — // — // — // —	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2153439	attagataacttcaaa[C/T]agtgacaaccttgcag	C	T	NM_178539 // intron // 0 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // — // — // — // — /// ENST00000356036 // intron // 0 // — // — // — // —	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-2130304	atacggattccaggta[C/G]gctcaaaaaaacacaa	C	G	NM_178539 // intron // 0 // Hs.269745 // FAM19A2 // 338811 // Homo sapiens TAFA2 protein (TAFA2), mRNA. /// ENST00000358343 // intron // 0 // — // — // — // — /// ENST00000356036 // intron // 0 // — // — // — // —	FAM19A2	FAM19A2, Homo sapiens TAFA2 protein (TAFA2), q14.1
SNP_A-1929611	ttcatagctccctgta[C/T]gtttacttcacagcac	C	T	AF106069 // intron // 0 // Hs.434951 // USP15 // 9958 // Homo sapiens deubiquitinating enzyme (UNPH4) mRNA, complete cds. /// NM_006313 // intron // 0 // Hs.434951 // USP15 // 9958 // Homo sapiens ubiquitin specific protease 15 (USP15), mRNA. /// ENST0000	USP15	USP15, Homo sapiens deubiquitinating enzyme (UNPH4) complete cds. q14.1
SNP_A-2282778	gataaaatactagaac[A/G]gaatcaacagattaca	A	G	AF106069 // intron // 0 // Hs.434951 // USP15 // 9958 // Homo sapiens deubiquitinating enzyme (UNPH4) mRNA, complete cds. /// NM_006313 // intron // 0 // Hs.434951 // USP15 // 9958 // Homo sapiens ubiquitin specific protease 15 (USP15), mRNA. /// ENST0000	USP15	USP15, Homo sapiens deubiquitinating enzyme (UNPH4) complete cds. q14.1
SNP_A-1941508	ttgctttggccacaga[A/G]atcatgatgagtataa	A	G	ENST00000280379 // intron // 0 // — // — // — // —	-	q14.1
SNP_A-2066589	aaggtaaaggctgcca[A/G]tagttggtgggaaata	A	G	ENST00000228705 // intron // 0 // — // — // — // —	-	q14.1
SNP_A-2270627	gacagatttgcttcag[A/G]atggtggtttggctct	A	G	ENST00000228705 // intron // 0 // — // — // — // —	-	q14.2
SNP_A-2207266	ccattccatgcagaga[C/T]cctcagagtatccctg	C	T	ENST00000228705 // intron // 0 // — // — // — // —	-	q14.2
SNP_A-1816297	gttagaaaaaatatca[A/C]aacataataggccaag	A	C	ENST00000228705 // intron // 0 // — // — // — // —	-	q14.2
SNP_A-1923085	ttagccacatagtcat[C/G]ataagtgattacattt	C	G	NM_003973 // downstream // 135889 // Hs.446522 // RPL14 // 9045 // Homo sapiens ribosomal protein L14 (RPL14), mRNA. /// NM_000706 // downstream // 44533 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// ENST	RPL14	RPL14, Homo sapiens ribosomal protein L14 (RPL14), q14.2
SNP_A-1643413	caagtataatataataagctaatag[A/T]atacgaatatagaggaagatatctg	A	T	AB032983 // upstream // 288968 // Hs.21894 // PPM1H // 57460 // protein phosphatase 1H (PP2C domain containing) /// NM_000706 // downstream // 25202 // Hs.2131 // AVPR1A // 552 // arginine vasopressin receptor 1A	PPM1H	PPM1H , rs1495028, protein phosphatase 1H (PP2C domain containing) ,q14.2
SNP_A-1792379	gggttgtctcattaca[A/C]acttatccctcctccc	A	C	NM_003973 // downstream // 156882 // Hs.446522 // RPL14 // 9045 // Homo sapiens ribosomal protein L14 (RPL14), mRNA. /// NM_000706 // downstream // 23540 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// ENST	RPL14	RPL14, Homo sapiens ribosomal protein L14 (RPL14), q14.2
SNP_A-2074766	acatattattggtcaa[G/T]aaaagcatgaaaactg	G	T	NM_000706 // 3UTR // 0 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// ENST00000299178 // 3UTR // 0 // — // — // — // —	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2098606	agagccaaactatctc[A/C]atatcaaaacaggtag	A	C	NM_000706 // upstream // 42831 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 363272 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2154306	attatggagaattaa[A/G]catcttatgctcta	A	G	NM_000706 // upstream // 61308 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 344795 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2279927	gaggctctcactagac[A/G]cattctcaatactgtc	A	G	NM_000706 // upstream // 76563 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 329540 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-1884762	tgaatcaacaactgag[C/T]gtataaaactatgctt	C	T	NM_000706 // upstream // 145905 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 260198 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2074545	acataggatttaatca[C/T]ccttgcccataaact	C	T	NM_000706 // upstream // 224422 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 181681 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2287668	gattaatatatgtgt[A/G]aaggccaagcaactcc	A	G	NM_000706 // upstream // 235060 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 171043 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2067186	tacacttactaaaaga[C/T]attccacacgctaga	C	T	NM_000706 // upstream // 294595 // Hs.2131 // AVPR1A // 552 // Homo sapiens arginine vasopressin receptor 1A (AVPR1A), mRNA. /// NM_173812 // downstream // 111508 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949),	AVPR1A	AVPR1A, Homo sapiens arginine vasopressin receptor 1A (AVPR1A), q14.2
SNP_A-2246618	ctgtaagtataatgca[A/C]attcccaaatctgaga	A	C	NM_173812 // upstream // 55574 // Hs.533644 // FLJ32949 // 283417 // Homo sapiens hypothetical protein FLJ32949 (FLJ32949), mRNA. /// NM_014254 // upstream // 55788 // Hs.216386 // TMEM5 // 10329 // Homo sapiens transmembrane protein 5 (TMEM5), mRNA. ///	FLJ32949	FLJ32949, Homo sapiens hypothetical protein FLJ32949 (FLJ32949), q14.2
SNP_A-1942652	ttgggagacagaaggt[A/G]aaccatatgtggagaa	A	G	NM_020762 // intron // 0 // Hs.450763 // SRGAP1 // 57522 // Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), mRNA. /// ENST00000355086 // intron // 0 // — // — // — // — /// ENST00000357825 // intron // 0 // — // — // — // — // –	SRGAP1	SRGAP1, Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), q14.2
SNP_A-1894000	tgcatcagtgacgac[C/T]attgagtcatttta	C	T	NM_020762 // intron // 0 // Hs.450763 // SRGAP1 // 57522 // Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), mRNA. /// ENST00000355086 // intron // 0 // — // — // — // — /// ENST00000357825 // intron // 0 // — // — // — // –	SRGAP1	SRGAP1, Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), q14.2
SNP_A-2267955	gaatctcacacttaac[A/G]acaaggcttaaacatc	A	G	NM_020762 // intron // 0 // Hs.450763 // SRGAP1 // 57522 // Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), mRNA. /// ENST00000355086 // intron // 0 // — // — // — // — /// ENST00000357825 // intron // 0 // — // — // — // –	SRGAP1	SRGAP1, Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), q14.2
SNP_A-1882837	tgaaagccgattacac[A/G]aagtcatttggtttg	A	G	NM_020762 // intron // 0 // Hs.450763 // SRGAP1 // 57522 // Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), mRNA. /// ENST00000355086 // intron // 0 // — // — // — // — /// ENST00000357825 // intron // 0 // — // — // — // –	SRGAP1	SRGAP1, Homo sapiens SLIT-ROBO Rho GTPase activating protein 1 (SRGAP1), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783256	ggcagtactaccaatc[A/G]cataaagaagtattca	A	G	ENST00000333722 // intron // 0 // — // — // — // —	-	q14.2
SNP_A-1861636	tcatctatcagcccta[C/T]ggtgtccccacagccc	C	T	ENST00000229088 // CDS // 0 // — // — // — // —	-	q14.3
SNP_A-2274048	gacttagacattaaga[A/T]gatccctagctggaaa	A	T	NM_007191 // upstream // 17629 // Hs.284122 // WIF1 // 11197 // Homo sapiens WNT inhibitory factor 1 (WIF1), mRNA. /// NM_014319 // upstream // 30626 // Hs.505905 // LEMD3 // 23592 // Homo sapiens integral inner nuclear membrane protein (MAN1), mRNA. ///	WIF1	WIF1, Homo sapiens WNT inhibitory factor 1 (WIF1), q14.3
SNP_A-1835044	taccccacattctaaa[A/G]taagaggacaatgaga	A	G	NM_198080 // intron // 0 // Hs.339024 // MSRB3 // 253827 // Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // — // — // — // — /// ENST00000308259 // intron // 0 // — // — // — // —	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-2068449	ccgtccaatcaacaac[C/T]gagtgtcttcaacctc	C	T	NM_198080 // intron // 0 // Hs.339024 // MSRB3 // 253827 // Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // — // — // — // — /// ENST00000308259 // intron // 0 // — // — // — // —	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-1793265	ggtagatttccagata[C/G]acagtcatgcatctca	C	G	NM_198080 // intron // 0 // Hs.339024 // MSRB3 // 253827 // Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // — // — // — // — /// ENST00000308259 // intron // 0 // — // — // — // —	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-2294513	gcagtcacataatcta[C/G]agaaaggacaagttaa	C	G	NM_198080 // intron // 0 // Hs.339024 // MSRB3 // 253827 // Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // — // — // — // — /// ENST00000308259 // intron // 0 // — // — // — // —	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-2134640	atatgtgtcttgaaaa[A/G]tagggaatttacaata	A	G	NM_198080 // intron // 0 // Hs.339024 // MSRB3 // 253827 // Homo sapiens hypothetical protein LOC253827 (LOC253827), mRNA. /// ENST00000355192 // intron // 0 // — // — // — // — /// ENST00000308259 // intron // 0 // — // — // — // —	MSRB3	MSRB3, Homo sapiens hypothetical protein LOC253827 (LOC253827), q14.3
SNP_A-2203258	ccacttccactcaatg[A/G]acaagtgaatatattt	A	G	ENST00000356215 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2068645	acaaggctacaaacac[A/G]gataatacaattgctg	A	G	ENST00000356215 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-2002808	aatcagtcccttccac[A/G]gccattgaacttttgg	A	G	NM_007199 // intron // 0 // Hs.369265 // IRAK3 // 11213 // Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), mRNA. /// ENST00000261233 // intron // 0 // — // — // — // —	IRAK3	IRAK3, Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), q14.3
SNP_A-1856376	tcacaccctcatttgg[A/T]caaaggagctgttggc	A	T	AJ133439 // intron // 0 // Hs.505946 // GRIP1 // 23426 // Homo sapiens mRNA for GRIP1 protein. /// ENST00000286445 // intron // 0 // — // — // — // — /// ENST00000359742 // intron // 0 // — // — // — // —	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. ,q14.3
SNP_A-1879771	tcttcatttgcaaaac[A/G]gtaaaaatcatttcta	A	G	AJ133439 // upstream // 4911 // Hs.505946 // GRIP1 // 23426 // Homo sapiens mRNA for GRIP1 protein. /// NM_018448 // upstream // 585313 // Hs.546407 // TIP120A // 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// ENST00000286445 // upstre	GRIP1	GRIP1, Homo sapiens for GRIP1 protein. ,q14.3
SNP_A-2280744	gaggtgagctctaacc[A/G]gaggatatagggggga	A	G	NM_018448 // downstream // 126144 // Hs.546407 // TIP120A // 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// NM_003583 // upstream // 208690 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation reg	TIP120A	TIP120A, Homo sapiens TBP-interacting protein (TIP120A), q15
SNP_A-1938138	ttgacaggcgaaagaa[A/T]tgggattatggcactt	A	T	NM_018448 // downstream // 221329 // Hs.546407 // TIP120A // 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// NM_003583 // upstream // 113505 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation reg	TIP120A	TIP120A, Homo sapiens TBP-interacting protein (TIP120A), q15
SNP_A-2229108	ctagcctcattcttgg[A/T]atttacatccccagga	A	T	NM_018448 // downstream // 284024 // Hs.546407 // TIP120A // 55832 // Homo sapiens TBP-interacting protein (TIP120A), mRNA. /// NM_003583 // upstream // 50810 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regu	TIP120A	TIP120A, Homo sapiens TBP-interacting protein (TIP120A), q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2002822	ctgcaccatacataag[A/C]aggacttggaaggaaa	A	C	NM_003583 // downstream // 77533 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 77533 // Hs.173135 // DYRK2 // 8445 // Homo	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-1827628	taactggatgactctg[C/T]agtagctctcttccaa	C	T	NM_003583 // downstream // 151237 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 151237 // Hs.173135 // DYRK2 // 8445 // Ho	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-2176244	caccagacaggagaaa[C/G]acaatgagaatggagg	C	G	NM_003583 // downstream // 151348 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 151348 // Hs.173135 // DYRK2 // 8445 // Ho	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-2191882	catcaaatggcccaac[A/G]aactgcaagtaatgat	A	G	NM_003583 // downstream // 151461 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 151461 // Hs.173135 // DYRK2 // 8445 // Ho	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-2313242	ggagacaaagcctaac[C/T]atatcattccacttat	C	T	NM_003583 // downstream // 307838 // Hs.173135 // DYRK2 // 8445 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA. /// NM_006482 // downstream // 307838 // Hs.173135 // DYRK2 // 8445 // Ho	DYRK2	DYRK2, Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, q15
SNP_A-1703047	atatccattatttgcatagcaacaa[C/T]taggaaatagcctacat gtccaaat	C	T	NM_000619 // downstream // 78907 // Hs.856 // IFNG // 3458 // interferon, gamma /// NM_003583 // downstream // 415499 // Hs.173135 // DYRK2 // 8445 // dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 /// NM_006482 // downstream // 415499	IFNG	IFNG , rs7316231, interferon, gamma ,q15
SNP_A-1667786	cactatacttgcctaggtaactaac[A/G]catggattatacattttaa tgtgtg	A	G	NM_000619 // downstream // 54721 // Hs.856 // IFNG // 3458 // interferon, gamma /// NM_003583 // downstream // 439685 // Hs.173135 // DYRK2 // 8445 // dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 /// NM_006482 // downstream // 439685	IFNG	IFNG , rs10492198, interferon, gamma ,q15
SNP_A-1910663	tgtcctggtgcctacc[A/G]catagggtttcttcct	A	G	NM_198320 // upstream // 195029 // Hs.334873 // CPM // 1368 // Homo sapiens carboxypeptidase M (CPM), transcript variant 2, mRNA. /// NM_001874 // upstream // 195029 // Hs.334873 // CPM // 1368 // Homo sapiens carboxypeptidase M (CPM), transcript variant	CPM	CPM, Homo sapiens carboxypeptidase M (CPM), transcript variant 2, q15
SNP_A-2164115	caaaaggaaaaaaagt[C/G]acaggctaagagaggt	C	G	NM_198320 // upstream // 214838 // Hs.334873 // CPM // 1368 // Homo sapiens carboxypeptidase M (CPM), transcript variant 2, mRNA. /// NM_001874 // upstream // 214838 // Hs.334873 // CPM // 1368 // Homo sapiens carboxypeptidase M (CPM), transcript variant	CPM	CPM, Homo sapiens carboxypeptidase M (CPM), transcript variant 2, q15
SNP_A-2091547	agaaaaagtctagtga[C/T]gctagagggagattaa	C	T	NM_198320 // upstream // 254725 // Hs.334873 // CPM // 1368 // Homo sapiens carboxypeptidase M (CPM), transcript variant 2, mRNA. /// NM_001874 // upstream // 254725 // Hs.334873 // CPM // 1368 // Homo sapiens carboxypeptidase M (CPM), transcript variant	CPM	CPM, Homo sapiens carboxypeptidase M (CPM), transcript variant 2, q15
SNP_A-1908007	tgtaatttccgcacaa[A/G]aacttttacacacatg	A	G	NM_007007 // downstream // 42291 // Hs.369606 // CPSF6 // 11052 // Homo sapiens cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA. /// NM_000239 // upstream // 34820 // Hs.524579 // LYZ // 4069 // Homo sapiens lysozyme (renal amyloidosis	CPSF6	CPSF6, Homo sapiens cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2068102	acaagaaccacggccaa[A/G]agccacactcacatt	A	G	NM_175624 // intron // 0 // Hs.258209 // RAB3IP // 117177 // Homo sapiens RAB3A interacting protein (rabin3) (RAB3IP), transcript variant beta 1, mRNA. /// NM_022456 // intron // 0 // Hs.258209 // RAB3IP // 117177 // Homo sapiens RAB3A interacting protein	RAB3IP	RAB3IP, Homo sapiens RAB3A interacting protein (rabin3) (RAB3IP), transcript variant beta 1, q15
SNP_A-1676722	ttgttaaaaagatgcaacatttcta[C/T]ctccaagaagttgaaat atataaa	C	T	NM_002837 // downstream // 83608 // Hs.434375 // PTPRB // 5787 // protein tyrosine phosphatase, receptor type, B /// NM_014505 // downstream // 6378 // Hs.348361 // KCNMB4 // 27345 // potassium large conductance calcium-activated channel, subfamily M, be	PTPRB	PTPRB , rs438847, protein tyrosine phosphatase, receptor type, B, q15
SNP_A-1920994	ttacagatgaggaaaag[A/T]acagttcagaaagctt	A	T	NM_002837 // intron // 0 // Hs.434375 // PTPRB // 5787 // Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-2056156	aatacctgaactaccc[A/G]aaagttaaatgcacca	A	G	NM_002837 // intron // 0 // Hs.434375 // PTPRB // 5787 // Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // --- // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-2305100	gctgaatgatgttagc[A/G]ccaagtgagacttact	A	G	NM_002837 // intron // 0 // Hs.434375 // PTPRB // 5787 // Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-2141534	atcttagcaaaggaaa[C/T]gaatgttcagtccaat	C	T	NM_002837 // intron // 0 // Hs.434375 // PTPRB // 5787 // Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // --- // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-1929018	ttcagctacttattag[G/T]cagcctagaaaaaataa	G	T	NM_002837 // intron // 0 // Hs.434375 // PTPRB // 5787 // Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA. /// ENST00000261266 // intron // 0 // --- // --- // --- // --- /// ENST00000334414 // intron // 0 // --- // --- // ---	PTPRB	PTPRB, Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), q15
SNP_A-2072690	attaggctgccatggat[A/G]tacctgtatgttggcc	A	G	ENST00000334414 // intron // 0 // --- // --- // --- // ---	-	q15
SNP_A-2129113	ataattcctgagatca[C/T]aacaagaggtctactt	C	T	NM_002849 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA. /// NM_130846 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphat	PTPRR	PTPRR, Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, q15
SNP_A-2185181	caggaaattatcgtcc[A/G]aatcctctttttaag	A	G	NM_002849 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA. /// NM_130846 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphat	PTPRR	PTPRR, Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, q15
SNP_A-2072738	catagtagaaaacaaa[C/G]agggaagatacggtta	C	G	NM_002849 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA. /// NM_130846 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphat	PTPRR	PTPRR, Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, q15
SNP_A-1732097	ctccttcaaattcaccctatccag[C/G]atgcacttggcctcaggg catcacc	C	G	NM_002849 // intron // 0 // Hs.198288 // PTPRR // 5801 // protein tyrosine phosphatase, receptor type, R /// NM_130846 // intron // 0 // Hs.198288 // PTPRR // 5801 // protein tyrosine phosphatase, receptor type, R	PTPRR	PTPRR , rs4283028, protein tyrosine phosphatase, receptor type, R, q15
SNP_A-2082183	acgactagtcttaaa[A/G]tacatatttggatatg	A	G	NM_002849 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA. /// NM_130846 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphat	PTPRR	PTPRR, Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, q15

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2265486	gaagccatttttagg[G/T]attcactcagaagata	G	T	NM_002849 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA. /// NM_130846 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphat	PTPRR	PTPRR, Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, q15
SNP_A-1820055	gttgtttttcccctcc[C/T]catatagccgaacatt	C	T	NM_002849 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA. /// NM_130846 // intron // 0 // Hs.506076 // PTPRR // 5801 // Homo sapiens protein tyrosine phosphat	PTPRR	PTPRR, Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, q15
SNP_A-2099164	agaggagcattaaaaa[A/T]ttggggcatttcatct	A	T	NM_004616 // intron // 0 // Hs.170563 // TM4SF3 // 7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// ENST00000247829 // intron // 0 // — // — // — // —	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-2261641	gaaagtaatgttctaa[A/G]gtctttggaagtcagt	A	G	NM_004616 // upstream // 75798 // Hs.170563 // TM4SF3 // 7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// NM_003667 // upstream // 206236 // Hs.172176 // LGR5 // 8549 // Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-2002840	ataccttgccaggtac[A/T]caagagcttaaaattt	A	T	NM_004616 // upstream // 151207 // Hs.170563 // TM4SF3 // 7103 // Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA. /// NM_003667 // upstream // 130827 // Hs.172176 // LGR5 // 8549 // Homo sapiens G protein-coupled receptor 49 (GPR49), mRN	TM4SF3	TM4SF3, Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), q15
SNP_A-1831215	taatgctttaaataca[C/T]ataccacaaatactac	C	T	NM_003667 // intron // 0 // Hs.172176 // LGR5 // 8549 // Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA. /// ENST00000266674 // intron // 0 // — // — // — // —	LGR5	LGR5, Homo sapiens G protein-coupled receptor 49 (GPR49), q21.1
SNP_A-2181535	cagagaaacactttca[G/T]gcaaaccttgaagact	G	T	NM_003667 // intron // 0 // Hs.172176 // LGR5 // 8549 // Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA. /// ENST00000266674 // intron // 0 // — // — // — // —	LGR5	LGR5, Homo sapiens G protein-coupled receptor 49 (GPR49), q21.1
SNP_A-1814428	gtgtgatcgatctatc[C/T]cttagctgaacaaatt	C	T	NM_003667 // downstream // 106 // Hs.172176 // LGR5 // 8549 // Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA. /// NM_144982 // downstream // 24750 // Hs.527874 // MGC23401 // 196441 // Homo sapiens hypothetical protein MGC23401 (MGC23401), mRNA	LGR5	LGR5, Homo sapiens G protein-coupled receptor 49 (GPR49), q21.1
SNP_A-1858543	tcagaggatccaggaa[C/T]ctcactgtatgcaaag	C	T	NM_022771 // downstream // 2334 // Hs.284630 // TBC1D15 // 64786 // Homo sapiens TBC1 domain family, member 15 (TBC1D15), mRNA. /// NM_173353 // upstream // 12195 // Hs.376337 // TPH2 // 121278 // Homo sapiens tryptophan hydroxylase 2 (TPH2), mRNA. /// EN	TBC1D15	TBC1D15, Homo sapiens TBC1 domain family, member 15 (TBC1D15), q21.1
SNP_A-2100044	agagtgactcatcttc[A/G]caaaaagatacattaa	A	G	NM_173353 // intron // 0 // Hs.376337 // TPH2 // 121278 // Homo sapiens tryptophan hydroxylase 2 (TPH2), mRNA. /// ENST00000333850 // intron // 0 // — // — // — // — /// ENST00000266669 // intron // 0 // — // — // — // —	TPH2	TPH2, Homo sapiens tryptophan hydroxylase 2 (TPH2), q21.1
SNP_A-1833579	tacagcctggagctaa[A/T]tcctaaaggtgcccat	A	T	NM_173353 // downstream // 75194 // Hs.376337 // TPH2 // 121278 // Homo sapiens tryptophan hydroxylase 2 (TPH2), mRNA. /// NM_013381 // upstream // 165048 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (T	TPH2	TPH2, Homo sapiens tryptophan hydroxylase 2 (TPH2), q21.1
SNP_A-2075428	acatgactgttaaata[C/T]atttctgaacaatttg	C	T	NM_013381 // downstream // 127879 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 2246596 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2131203	atagagagagcacaaa[G/T]ttaagaaacacaagaa	G	T	NM_013381 // downstream // 258631 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 2115844 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2298062	gccatattgacttaa[A/G]aaatcccatgcaggcc	A	G	NM_013381 // downstream // 284321 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 2090154 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2198466	catttaggcagaaga[A/G]atagctcataaaaagg	A	G	NM_013381 // downstream // 357842 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 2016633 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1714795	tgaataacttttgtaaaaccaagca[C/T]ataatttctacaatatcc ctattag	C	T	NM_013381 // downstream // 381689 // Hs.6510 // TRHDE // 29953 // thyrotropin-releasing hormone degrading ectoenzyme /// NM_032662 // downstream // 1244985 // - // - // - // -	TRHDE	TRHDE , rs952394, thyrotropin-releasing hormone degrading ectoenzyme ,q21.1
SNP_A-1726546	ttctagcagttatgtttaattaag[A/G]atgtagctattgtttgaatgtg tca	A	G	NM_013381 // downstream // 385088 // Hs.6510 // TRHDE // 29953 // thyrotropin-releasing hormone degrading ectoenzyme /// NM_032662 // downstream // 1241586 // - // - // - // -	TRHDE	TRHDE , rs10506711, thyrotropin-releasing hormone degrading ectoenzyme ,q21.1
SNP_A-2269762	gacaagatattaagg[A/G]atcaaggaaaagtgaa	A	G	NM_013381 // downstream // 461759 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1912716 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1959979	tttggtgtgccttc[A/G]atttttaaatatagta	A	G	NM_013381 // downstream // 477476 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1896999 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1792696	ggtaactagttagaaa[A/C]tgcctaatatggacaa	A	C	NM_013381 // downstream // 508028 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1866447 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1822061	gtttccctggatcgtc[G/T]caatgcttgtggattt	G	T	NM_013381 // downstream // 513824 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1860651 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2136828	atcagaagactggtta[C/T]gagagtgctgcaatca	C	T	NM_013381 // downstream // 542043 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1832432 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2121348	agtctctgataccca[A/G]gctctcaactctcatc	A	G	NM_013381 // downstream // 542065 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1832410 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-2101383	agatctgattacctc[A/G]cttactaatcaaccacc	A	G	NM_013381 // downstream // 1114753 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1259722 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1650924	agtttcagacaggtacactacctta[C/T]gcaataatacacagcc agtatcctg	C	T	NM_013381 // downstream // 1151719 // Hs.6510 // TRHDE // 29953 // thyrotropin-releasing hormone degrading ectoenzyme /// NM_032662 // downstream // 474955 // - // - // - // -	TRHDE	TRHDE , rs2033862, thyrotropin-releasing hormone degrading ectoenzyme, q21.1
SNP_A-1808246	gtctttgaaattctca[A/T]gaaaaaitatttgaca	A	T	NM_013381 // downstream // 1253464 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 1121011 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1821741	gttttaaatgcggatc[C/T]acataagtcccaaatc	C	T	NM_013381 // downstream // 2032337 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 342138 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1865799	tcccaaaacagtatca[A/C]aactctgccctctt	A	C	NM_013381 // downstream // 2050380 // Hs.199814 // TRHDE // 29953 // Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA. /// NM_153748 // downstream // 324095 // Hs.27214 // KCNC2 // 3747 // Homo sapiens potassium voltage-gated	TRHDE	TRHDE, Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), q21.1
SNP_A-1709675	aatgtgtcccctacctgcaggaagat[A/G]tgacctcccattcctag cagaaatg	A	G	NM_139136 // downstream // 8005 // Hs.345757 // KCNC2 // 3747 // potassium voltage-gated channel, Shaw-related subfamily, member 2 /// NM_139137 // downstream // 10987 // Hs.345757 // KCNC2 // 3747 // potassium voltage-gated channel, Shaw-related subfami	KCNC2	KCNC2 , rs1589968, potassium voltage-gated channel, Shaw-related subfamily, member 2, q21.1
SNP_A-1881272	gtagcaattggctacctttaagtac[C/G]aacttcagtaattcttgc cacttt	C	G	NM_006851 // downstream // 105712 // Hs.511765 // GLIPR1 // 11010 // GLI pathogenesis-related 1 (glioma) /// NM_007043 // upstream // 93211 // Hs.269857 // HRB2 // 11103 // HIV-1 rev binding protein 2 /// NM_007350 // downstream // 425246 // Hs.82101 //	GLIPR1	GLIPR1 , rs1542570, GLI pathogenesis-related 1 (glioma), q21.2
SNP_A-2303101	gctatactctaaagaa[C/T]ggggaggcttaagttt	C	T	NM_006851 // downstream // 160527 // Hs.205558 // GLIPR1 // 11010 // Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), mRNA. /// NM_007043 // upstream // 148026 // Hs.269857 // HRB2 // 11103 // Homo sapiens HIV-1 rev binding protein 2 (HRB2), mRN	GLIPR1	GLIPR1, Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), q21.2
SNP_A-1741369	cagctaccactcagattaccgat[A/G]agcacttgtgtattattg cacttt	A	G	NM_006851 // downstream // 314550 // Hs.511765 // GLIPR1 // 11010 // GLI pathogenesis-related 1 (glioma) /// NM_007043 // upstream // 302049 // Hs.269857 // HRB2 // 11103 // HIV-1 rev binding protein 2 /// NM_007350 // downstream // 216408 // Hs.82101 //	GLIPR1	GLIPR1, Homo sapiens GLI pathogenesis-related 1 (glioma), q21.2
SNP_A-2076223	aggctttattaggta[C/T]gaagatgagtgtcaca	C	T	NM_006851 // downstream // 319693 // Hs.205558 // GLIPR1 // 11010 // Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), mRNA. /// NM_007043 // upstream // 307192 // Hs.269857 // HRB2 // 11103 // Homo sapiens HIV-1 rev binding protein 2 (HRB2), mRN	GLIPR1	GLIPR1, Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), q21.2
SNP_A-1908064	tgtacaattctctccc[C/T]gcatgcctgagtgta	C	T	NM_006851 // downstream // 327105 // Hs.205558 // GLIPR1 // 11010 // Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), mRNA. /// NM_007043 // upstream // 314604 // Hs.269857 // HRB2 // 11103 // Homo sapiens HIV-1 rev binding protein 2 (HRB2), mRN	GLIPR1	GLIPR1, Homo sapiens GLI pathogenesis-related 1 (glioma) (GLIPR1), q21.2
SNP_A-2170109	caagggtccaaaaaaa[C/T]agactggtacttataa	C	T	NM_005969 // intron // 0 // Hs.501684 // NAP1L4 // 4676 // Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), mRNA. /// NM_139207 // intron // 0 // Hs.524599 // NAP1L1 // 4673 // Homo sapiens nucleosome assembly protein 1-like 1 (NAP1L1), transcr	NAP1L4	NAP1L4, Homo sapiens nucleosome assembly protein 1-like 4 (NAP1L4), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2132043	atagggaagatcgttat[C/T]gtgctaaaatacagct	C	T	NM_015336 // intron // 0 // Hs.4014 // ZDHHC17 // 23390 // Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), mRNA. /// ENST00000334822 // intron // 0 // — // — // — /// ENST00000359019 // intron // 0 // — // — // —	ZDHHC17	ZDHHC17, Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), q21.2
SNP_A-1824387	taaacgttagcaggtat[A/G]ggacattaaaacagtt	A	G	NM_015336 // downstream // 1483 // Hs.4014 // ZDHHC17 // 23390 // Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), mRNA. /// NM_001321 // downstream // 3539 // Hs.530904 // CSRP2 // 1466 // Homo sapiens cysteine and glycine-rich protein 2 (C	ZDHHC17	ZDHHC17, Homo sapiens zinc finger, DHHC domain containing 17 (ZDHHC17), q21.2
SNP_A-2233752	ctcatcagagccgtat[C/G]ataatcaagagctgac	C	G	NM_001321 // intron // 0 // Hs.530904 // CSRP2 // 1466 // Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA. /// ENST00000311083 // intron // 0 // — // — // —	CSRP2	CSRP2, Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), q21.2
SNP_A-2198297	cattgttccatttggc[C/T]agacattgtattatct	C	T	NM_001321 // upstream // 69004 // Hs.530904 // CSRP2 // 1466 // Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA. /// NM_203394 // downstream // 73230 // Hs.416375 // E2F7 // 144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. //	CSRP2	CSRP2, Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), q21.2
SNP_A-2076896	atcaacattttctca[A/T]cttataatgccatctc	A	T	NM_203394 // upstream // 22356 // Hs.416375 // E2F7 // 144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 743494 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000322886 /	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-1722976	aaccctgaactcgtgggtattttgta[C/T]attcaggtagtagttgcgt ccctat	C	T	AJ488202 // downstream // 180116 // - // - // - // Homo sapiens partial mRNA for steerin3 protein (STEERIN3 gene), alternative exon 1b. /// NM_014903 // upstream // 79035 // Hs.306322 // NAV3 // 89795 // neuron navigator 3	-	- , rs10506759, Homo sapiens partial mRNA for steerin3 protein (STEERIN3 gene), alternative exon 1b. ,q21.2
SNP_A-1660985	ggtggatgggtgcagcaaacaatta[C/T]gacacttgtctacctat gtaacaaa	C	T	AJ488202 // downstream // 190094 // - // - // - // Homo sapiens partial mRNA for steerin3 protein (STEERIN3 gene), alternative exon 1b. /// NM_014903 // upstream // 69057 // Hs.306322 // NAV3 // 89795 // neuron navigator 3	-	- , rs1402319, Homo sapiens partial mRNA for steerin3 protein (STEERIN3 gene), alternative exon 1b. ,q21.2
SNP_A-2272181	gacctacctgtggata[A/G]gttctactggactcct	A	G	NM_203394 // upstream // 702527 // Hs.416375 // E2F7 // 144455 // Homo sapiens E2F transcription factor 7 (E2F7), mRNA. /// NM_014903 // upstream // 63323 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000322886 /	E2F7	E2F7, Homo sapiens E2F transcription factor 7 (E2F7), q21.2
SNP_A-2089445	acttattagaaaagta[A/G]gcagaaaacctgaatg	A	G	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-1822938	taaaaaataaggttata[A/G]aaagagtctgagcgaa	A	G	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2262069	gaaatatcaactggaa[A/G]aatgaaaaagtgatca	A	G	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2077988	taacttctgagttac[A/G]cctagagtacatggaa	A	G	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2149971	atgtcataggtttctg[G/T]aaaagacagacacaga	G	T	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2103384	agcaagtgcctttata[C/G]agttcatgaagcata	C	G	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2086411	actcttctgggctaa[C/T]atgagtcaaaataata	C	T	NM_014903 // intron // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // intron // 0 // - // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215206	cctcaaagcacattcc[A/G]caaactgacacagaag	A	G	NM_014903 // CDS // 0 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// ENST00000228327 // CDS // 0 // — // — // — /// ENST00000266692 // CDS // 0 // — // — // —	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-1726082	gtttaaagagcaatctttgtaataaa[A/C]taagctcatgatgttggg atcaga	A	C	NM_005639 // upstream // 882556 // Hs.154679 // SYT1 // 6857 // synaptotagmin I /// NM_014903 // downstream // 122787 // Hs.306322 // NAV3 // 89795 // neuron navigator 3	SYT1	SYT1 , rs10506781, synaptotagmin I ,q21.2
SNP_A-1910270	tgtccaagatctctcc[A/C]agtcaactttctaaaa	A	C	NM_014903 // downstream // 176972 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// NM_005639 // upstream // 474861 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// NM_005639 // upstream // 47	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2153041	attaccaaatgatata[C/G]gatttttctacatggc	C	G	NM_014903 // downstream // 198567 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// NM_005639 // upstream // 453266 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// NM_005639 // upstream // 45	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-1896369	tgctaagcaatggtgg[A/G]aaatatctttttcaa	A	G	NM_014903 // downstream // 282100 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// NM_005639 // upstream // 369733 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// NM_005639 // upstream // 37	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-2283745	gataggaaggtagat[C/G]acaactgccttgttca	C	G	NM_014903 // downstream // 457836 // Hs.306322 // NAV3 // 89795 // Homo sapiens neuron navigator 3 (NAV3), mRNA. /// NM_005639 // upstream // 193997 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// NM_005639 // upstream // 19	NAV3	NAV3, Homo sapiens neuron navigator 3 (NAV3), q21.2
SNP_A-1918639	ttaaattcaaactgac[A/G]cctccaaaatcaacac	A	G	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — /// ENST00000261205 // intron // 0 // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-2226683	ctaagtgagaactgct[C/G]acactgtctatagcaa	C	G	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — /// ENST00000261205 // intron // 0 // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-1827803	taacttagttcagaat[A/C]agaaaggtgttaaaat	A	C	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — /// ENST00000261205 // intron // 0 // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-1659820	aaatctgaaatttgagcaacacagat[A/G]ctttgggggtttgccac cttttag	A	G	NM_005639 // upstream // 55278 // Hs.154679 // SYT1 // 6857 // synaptotagmin I /// NM_014903 // downstream // 950065 // Hs.306322 // NAV3 // 89795 // neuron navigator 3	SYT1	SYT1 , rs9610173, synaptotagmin I ,q21.2
SNP_A-2114569	agggaggcaaattacc[G/T]aagctgcaatttcctg	G	T	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — /// ENST00000261205 // intron // 0 // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-1807372	gtctgacatgtgagga[C/T]atggtgaaaagaccat	C	T	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — /// ENST00000261205 // intron // 0 // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-1951702	ttccttctcatcta[A/G]catgtttaattgtcc	A	G	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — /// ENST00000261205 // intron // 0 // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2247472	ctgtctccactttcca[A/G]cacattcctttctttg	A	G	NM_005639 // intron // 0 // Hs.310545 // SYT1 // 6857 // Homo sapiens synaptotagmin I (SYT1), mRNA. /// ENST00000357425 // intron // 0 // — // — // — // — /// ENST00000261205 // intron // 0 // — // — // — // —	SYT1	SYT1, Homo sapiens synaptotagmin I (SYT1), q21.2
SNP_A-1942817	ttggggaagacaagct[C/T]acaagtagtttcatta	C	T	ENST00000328569 // intron // 0 // — // — // — // —	-	q21.31
SNP_A-2117199	aggtgcgcaacaagaa[A/G]gtacagcctttggagg	A	G	NM_002469 // downstream // 1099 // Hs.35937 // MYF6 // 4618 // Homo sapiens myogenic factor 6 (herculin) (MYF6), mRNA. /// NM_005593 // upstream // 6451 // Hs.178023 // MYF5 // 4617 // Homo sapiens myogenic factor 5 (MYF5), mRNA. /// ENST00000228641 // do	MYF6	MYF6, Homo sapiens myogenic factor 6 (herculin) (MYF6), q21.31
SNP_A-2193551	catctgtggatcatgc[A/C]ctacgctaatatctaa	A	C	NM_005593 // intron // 0 // Hs.178023 // MYF5 // 4617 // Homo sapiens myogenic factor 5 (MYF5), mRNA. /// ENST00000228644 // intron // 0 // — // — // — // —	MYF5	MYF5, Homo sapiens myogenic factor 5 (MYF5), q21.31
SNP_A-2079711	tagctttgcactcaac[A/G]aaactccaaatcctaa	A	G	NM_005593 // downstream // 26837 // Hs.178023 // MYF5 // 4617 // Homo sapiens myogenic factor 5 (MYF5), mRNA. /// NM_004664 // downstream // 50891 // Hs.144333 // LIN7A // 8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// ENST0000022864	MYF5	MYF5, Homo sapiens myogenic factor 5 (MYF5), q21.31
SNP_A-1914049	tgtgtggaaaagaagg[G/T]acagtcgttgggaata	G	T	NM_004664 // intron // 0 // Hs.144333 // LIN7A // 8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// ENST00000261203 // intron // 0 // — // — // — // —	LIN7A	LIN7A, Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), q21.31
SNP_A-2235354	ctccctgccatcaaac[A/C]atatacactttggtga	A	C	NM_004664 // intron // 0 // Hs.144333 // LIN7A // 8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// ENST00000261203 // intron // 0 // — // — // — // —	LIN7A	LIN7A, Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), q21.31
SNP_A-1937977	ttgaattagaaagtgg[G/T]atattcaaggagcaat	G	T	NM_004664 // intron // 0 // Hs.144333 // LIN7A // 8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// ENST00000261203 // intron // 0 // — // — // — // —	LIN7A	LIN7A, Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), q21.31
SNP_A-2081658	accttattagactgaa[A/G]gtagaaaatgtctatt	A	G	NM_004664 // intron // 0 // Hs.144333 // LIN7A // 8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// ENST00000261203 // intron // 0 // — // — // — // —	LIN7A	LIN7A, Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), q21.31
SNP_A-1876710	tctgcactgcacttga[C/T]gtgtatgtactgacta	C	T	NM_004664 // upstream // 5764 // Hs.144333 // LIN7A // 8825 // Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA. /// NM_024560 // upstream // 134351 // Hs.259559 // FLJ21963 // 79611 // Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST000002	LIN7A	LIN7A, Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), q21.31
SNP_A-2079971	ggaacaacaaagtgga[A/T]gtttctggttattttc	A	T	NM_024560 // intron // 0 // Hs.259559 // FLJ21963 // 79611 // Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST00000261206 // intron // 0 // — // — // — // —	FLJ21963	FLJ21963, Homo sapiens FLJ21963 protein (FLJ21963), q21.31
SNP_A-1934254	ttctccactctcaaaa[C/T]gaagactggtttgcaa	C	T	NM_024560 // intron // 0 // Hs.259559 // FLJ21963 // 79611 // Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST00000261206 // intron // 0 // — // — // — // —	FLJ21963	FLJ21963, Homo sapiens FLJ21963 protein (FLJ21963), q21.31
SNP_A-2178223	cactatttgggtgaca[A/G]gtaccctaaaagtcca	A	G	NM_024560 // intron // 0 // Hs.259559 // FLJ21963 // 79611 // Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST00000261206 // intron // 0 // — // — // — // —	FLJ21963	FLJ21963, Homo sapiens FLJ21963 protein (FLJ21963), q21.31
SNP_A-2203986	ccagatggtttgtcca[C/T]aaatcagctttcttgt	C	T	NM_024560 // intron // 0 // Hs.259559 // FLJ21963 // 79611 // Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST00000261206 // intron // 0 // — // — // — // —	FLJ21963	FLJ21963, Homo sapiens FLJ21963 protein (FLJ21963), q21.31
SNP_A-2080032	tgaagacaagtaaact[C/T]acagattgtcataaat	C	T	NM_024560 // intron // 0 // Hs.259559 // FLJ21963 // 79611 // Homo sapiens FLJ21963 protein (FLJ21963), mRNA. /// ENST00000261206 // intron // 0 // — // — // — // —	FLJ21963	FLJ21963, Homo sapiens FLJ21963 protein (FLJ21963), q21.31
SNP_A-2034099	aaatcatcactaaaac[A/G]acattgatacacatat	A	G	NM_003625 // intron // 0 // Hs.506216 // PPFIA2 // 8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// ENST00000333447 // intron // 0 // — // — // — // —	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909893	tgtcactttgtgatag[A/G]aatttttcagttgcat	A	G	NM_003625 // intron // 0 // Hs.506216 // PPFIA2 // 8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// ENST00000333447 // intron // 0 // — // — // — // —	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-1845513	tatagaggatgaagca[C/G]gtttaaaaattggaca	C	G	NM_003625 // upstream // 23755 // Hs.506216 // PPFIA2 // 8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// NM_014167 // downstream // 574865 // Hs.90527 // HSPC128	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-1861901	tcatgaagttcaagga[A/C]gggcttgattagaacg	A	C	NM_003625 // upstream // 34545 // Hs.506216 // PPFIA2 // 8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// NM_014167 // downstream // 564075 // Hs.90527 // HSPC128	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-1753659	aaaacattgtggtcactcctaaaag[A/G]aacctagcacccatta gcagtctct	A	G	NM_003625 // upstream // 48893 // Hs.30881 // PPFIA2 // 8499 // protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 /// NM_014167 // downstream // 544618 // Hs.90527 // HSPC128 // 29080 // HSPC128 pro	PPFIA2	PPFIA2 , rs1922558, protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 ,q21.31
SNP_A-2213967	cctaaccttgtgttca[C/T]gcgtaggtgtttagtt	C	T	NM_003625 // upstream // 85424 // Hs.506216 // PPFIA2 // 8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// NM_014167 // downstream // 513196 // Hs.90527 // HSPC128	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-2080636	tatagcaggaaacttc[C/T]acatttttgttactga	C	T	NM_003625 // upstream // 473185 // Hs.506216 // PPFIA2 // 8499 // Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), /// NM_014167 // downstream // 125435 // Hs.90527 // HSPC128	PPFIA2	PPFIA2, Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 (PPFIA2), q21.31
SNP_A-1885516	tgacaatatgtggatg[C/T]acaatcttgcttcttt	C	T	NM_032230 // intron // 0 // Hs.506222 // FLJ22789 // 84190 // Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// ENST00000248306 // intron // 0 // — // — // — // —	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-1907808	tgtaagtatgagcaaa[A/C]acttgtaaaattaaaa	A	C	NM_032230 // intron // 0 // Hs.506222 // FLJ22789 // 84190 // Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// ENST00000248306 // intron // 0 // — // — // — // —	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-2080697	atgatctgtaccaggc[A/G]atgcttccattccaat	A	G	NM_032230 // intron // 0 // Hs.506222 // FLJ22789 // 84190 // Homo sapiens hypothetical protein FLJ22789 (FLJ22789), mRNA. /// ENST00000248306 // intron // 0 // — // — // — // —	FLJ22789	FLJ22789, Homo sapiens hypothetical protein FLJ22789 (FLJ22789), q21.31
SNP_A-1646386	aatatatcaggaaccaccgatattc[A/G]tgagatatgccatatatt tttattt	A	G	NM_152588 // intron // 0 // Hs.387753 // DKFZp762A217 // 160335 // hypothetical protein DKFZp762A217	DKFZp762A217	DKFZp762A217 , rs1369035, hypothetical protein DKFZp762A217,q21.31
SNP_A-2080974	gtccagtccggcgata[C/T]gcttgtcgcttgtatt	C	T	NM_152588 // intron // 0 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// ENST00000321196 // intron // 0 // — // — // — // —	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2241000	ctgagattcacttata[C/T]atactcgaactattca	C	T	NM_152588 // downstream // 333421 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1392946 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2058147	aatcaaacaccactta[G/T]gtcatataaatctttt	G	T	NM_152588 // downstream // 334071 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1392296 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074605	acatagttggtcatta[A/T]gcacttacaaaaaaag	A	T	NM_152588 // downstream // 345808 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1380559 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1654465	ttttccctatttttaaatgtgatta[C/T]ggtgattacctaagaccattag tgg	C	T	NM_018057 // downstream // 1399252 // Hs.44424 // SLC6A15 // 55117 // solute carrier family 6 (neurotransmitter transporter), member 15 /// NM_152588 // downstream // 348851 // Hs.387753 // DKFZp762A217 // 160335 // hypothetical protein DKFZp762A217	SLC6A15	SLC6A15 , rs3112097, solute carrier family 6 (neurotransmitter transporter), member 15 ,q21.31
SNP_A-2200799	ccaagagtcactctta[C/T]gttgacttctaacatc	C	T	NM_152588 // downstream // 382488 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1343879 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2293538	gcagcaggaaggttaa[C/G]gactgaaagggctctc	C	G	NM_152588 // downstream // 403930 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1322437 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2081369	aaaatcacctgtgtcc[A/G]ccaatgaatgagtgga	A	G	NM_152588 // downstream // 502724 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1223643 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1747085	atcaatacatgaaaatgaggactg[C/T]gtatcaacaaatttagc tcaagtgc	C	T	NM_018057 // downstream // 1215323 // Hs.44424 // SLC6A15 // 55117 // solute carrier family 6 (neurotransmitter transporter), member 15 /// NM_152588 // downstream // 532780 // Hs.387753 // DKFZp762A217 // 160335 // hypothetical protein DKFZp762A217	SLC6A15	SLC6A15 , rs1391072, solute carrier family 6 (neurotransmitter transporter), member 15 ,q21.31
SNP_A-1735985	aaataaatatattaatctaagacttc[A/G]gaaagaaacaaaccca caaataata	A	G	NM_018057 // downstream // 1142192 // Hs.44424 // SLC6A15 // 55117 // solute carrier family 6 (neurotransmitter transporter), member 15 /// NM_152588 // downstream // 605911 // Hs.387753 // DKFZp762A217 // 160335 // hypothetical protein DKFZp762A217	SLC6A15	SLC6A15 , rs717997, solute carrier family 6 (neurotransmitter transporter), member 15 ,q21.31
SNP_A-2205779	ccatacaacaaaaatgg[A/C]aagaagtgtgatggtg	A	C	NM_152588 // downstream // 621089 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 1105278 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2036709	aaattgttaccaggaa[A/G]gaaggcaggaagaaga	A	G	NM_152588 // downstream // 1310593 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 415774 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2110290	aggaatagtgagagtg[C/G]agttggagtgtgaga	C	G	NM_152588 // downstream // 1315879 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 410488 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2249748	cttaatcttgtctctc[A/C]aacattactgacatc	A	C	NM_152588 // downstream // 1353578 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 372789 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1953438	tttgaacttcctgcta[C/T]ataacataactaccca	C	T	NM_152588 // downstream // 1365051 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 361316 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1861091	tcatagttttctttgg[C/T]cattcctagagaattg	C	T	NM_152588 // downstream // 1365666 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 360701 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2219709	ccttaagcagtcacag[C/T]aatgatgtcatattga	C	T	NM_152588 // downstream // 1412282 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 314085 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2243651	ctgctcgtaatatcag[C/G]attagagcaagtagga	C	G	NM_152588 // downstream // 1451984 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 274383 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-2211578	ccctcacttgagtgaa[A/T]ctgcaaattatcacta	A	T	NM_152588 // downstream // 1468261 // Hs.444240 // DKFZp762A217 // 160335 // Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA. /// NM_182767 // downstream // 258106 // Hs.44424 // SLC6A15 // 55117 // Homo sapiens solute carrier family 6	DKFZp762A217	DKFZp762A217, Homo sapiens hypothetical protein DKFZp762A217 (DKFZp762A217), q21.31
SNP_A-1745390	gttgcctcatactctctcctcacag[A/G]aaaaggcagattgaggc tgctgggt	A	G	NM_018057 // downstream // 254639 // Hs.44424 // SLC6A15 // 55117 // solute carrier family 6 (neurotransmitter transporter), member 15 /// NM_152588 // downstream // 1493464 // Hs.387753 // DKFZp762A217 // 160335 // hypothetical protein DKFZp762A217	SLC6A15	SLC6A15 , rs10506909, solute carrier family 6 (neurotransmitter transporter), member 15 ,q21.31
SNP_A-2082245	agctctgcagacctga[C/T]agatgtggcaaataca	C	T	NM_032165 // intron // 0 // Hs.531254 // LRRIQ1 // 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// ENST00000256007 // intron // 0 // — // — // — // —	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-1847094	tatcatcagctacacc[A/G]aacactcaagtgtagc	A	G	NM_032165 // intron // 0 // Hs.531254 // LRRIQ1 // 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// ENST00000256007 // intron // 0 // — // — // — // —	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-2284283	gatattgaatggtttc[C/T]aatcttccatattacc	C	T	NM_032165 // intron // 0 // Hs.531254 // LRRIQ1 // 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// ENST00000256007 // intron // 0 // — // — // — // —	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-1942328	ttggccagcaatgaac[A/G]aatgattttgcctcac	A	G	NM_032165 // downstream // 38152 // Hs.531254 // LRRIQ1 // 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// NM_006982 // upstream // 117097 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeopr	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31
SNP_A-1832537	tacaaataggacatca[C/T]gaaaactgcatcaaat	C	T	NM_032165 // downstream // 58365 // Hs.531254 // LRRIQ1 // 84125 // Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), mRNA. /// NM_006982 // upstream // 96884 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeopro	LRRIQ1	LRRIQ1, Homo sapiens leucine-rich repeats and IQ motif containing 1 (LRRIQ1), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1959158	ttttgacattgcaaacC/Ggaaaaattcacttcta	C	G	NM_006982 // downstream // 40918 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 531598 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2085837	actccttctggaaacaA/Gctgcttcttatccttc	A	G	NM_006982 // downstream // 41699 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 530817 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1828149	taagacttttacttgaC/Tgttgaaattacagtca	C	T	NM_006982 // downstream // 61126 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 511390 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1901068	tggatcactacagtgaA/Cgtattacagttgtaca	A	C	NM_006982 // downstream // 106566 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 465950 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1927062	ttatttgtgagccataA/Taatgaagtagtaaaat	A	T	NM_006982 // downstream // 258676 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 313840 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1938988	ttgagtccacactataC/Tgtcaggctgtactagc	C	T	NM_006982 // downstream // 286088 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 286428 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2034868	aaatgagatatagaaaA/Ttgttccagactgcac	A	T	NM_006982 // downstream // 315196 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 257320 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1947230	tttaattcatgtgctaC/Tctatggagtctttaa	C	T	NM_006982 // downstream // 321354 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 251162 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2084370	actatagccacgggagA/Taagatattagaattgg	A	T	NM_006982 // downstream // 322060 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 250456 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2169335	caagcagcataggacC/Tgtagttgaagcaagag	C	T	NM_006982 // downstream // 373983 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 198533 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-2195042	catggaaaacaggttaC/Tagtggcaaggatagaa	C	T	NM_006982 // downstream // 399920 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 172596 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1685752	ggtttatagagttatactcagttaq[C/T]gacagatctaaaatgaac ttcttcc	C	T	NM_005447 // downstream // 100187 // Hs.159396 // PAMCI // 9182 // peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor /// NM_006982 // downstream // 402585 // Hs.41683 // CART1 // 8092 // cartilage paired-class homeoprotein 1	PAMCI	PAMCI, rs10506924, peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor, q21.31
SNP_A-2082467	tagatatgagtaggagg[C/T]atccaggttagacata	C	T	NM_006982 // downstream // 402681 // Hs.41683 // CART1 // 8092 // Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA. /// NM_006183 // upstream // 169835 // Hs.80962 // NTS // 4922 // Homo sapiens neurotensin (NTS), mRNA. /// ENST00000316824	CART1	CART1, Homo sapiens cartilage paired-class homeoprotein 1 (CART1), q21.31
SNP_A-1823733	taaaatcactgaagaa[A/T]tattccactattatg	A	T	NM_013244 // upstream // 295269 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1635032 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2299687	gccgggcagtaaccta[C/T]aagtatttaccagttc	C	T	NM_013244 // upstream // 547459 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1382842 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1947672	tttactaagtttaca[A/C]atcaggcaaacctcat	A	C	NM_013244 // upstream // 558061 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 1372240 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1908293	tgtactagcagaatta[C/T]taaagaagttacagat	C	T	NM_013244 // upstream // 1016397 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 913904 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1939321	ttgatcttgccagtaa[A/G]cgagatatttgatgat	A	G	NM_013244 // upstream // 1044387 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 885914 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2069210	acaattggatttggaa[A/C]attgacctaatgtcag	A	C	NM_013244 // upstream // 1160377 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 769924 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2194882	catgctatatggcaca[A/C]caaaacttaaatgaaa	A	C	NM_013244 // upstream // 1226698 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 703603 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2002905	caagcacacctaatgc[A/G]caagtctgattcta	A	G	NM_013244 // upstream // 1319923 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 610378 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1917303	tgttttcatgaatcaa[A/G]ttacacttttgttcac	A	G	NM_013244 // upstream // 1571011 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 359290 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2288212	gattccattatcataa[A/G]tgcagaggctgagagg	A	G	NM_013244 // upstream // 1590271 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 340030 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2257814	ctttgggatttcagga[A/T]attaaccgatttataa	A	T	NM_013244 // upstream // 1593978 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 336323 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1673210	ccctctggatctcttaattagccta[C/T]gttttcttaaataaaaatttatttt	C	T	NM_013244 // upstream // 962284 // Hs.422827 // HGNT-IV-H // 25834 // UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog /// NM_152589 // downstream // 178887 // Hs.112930 // FLJ35821 // 160419 // hypothetical p	HGNT-IV-H	HGNT-IV-H , rs1436178, UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog_q21.32
SNP_A-1646486	gctttaagatttgagttaaaaata[G/T]actgattgaaaaaataaattttta	G	T	NM_013244 // upstream // 962320 // Hs.422827 // HGNT-IV-H // 25834 // UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog /// NM_152589 // downstream // 178851 // Hs.112930 // FLJ35821 // 160419 // hypothetical p	HGNT-IV-H	HGNT-IV-H , rs1436179, UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog_q21.32
SNP_A-2083419	tgtctctgactaaata[C/T]gagtaatgtgcactact	C	T	NM_013244 // upstream // 1751579 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 178722 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1826778	taacaggagatttatca[C/T]ggtgttcttatgttc	C	T	NM_013244 // upstream // 1757396 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 172905 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1801681	gtagtatcttttaaac[C/G]aagacagtaagattta	C	G	NM_013244 // upstream // 1775532 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 154769 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1688046	tgacccattatattaacaaacaacca[C/T]gtcctgtgctgaagttatggaagt	C	T	NM_013244 // upstream // 988337 // Hs.422827 // HGNT-IV-H // 25834 // UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog /// NM_152589 // downstream // 152834 // Hs.112930 // FLJ35821 // 160419 // hypothetical p	HGNT-IV-H	HGNT-IV-H , rs39111720, UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homolog_q21.32
SNP_A-1831604	taattactgattgtg[C/T]agtaggaaggctcaa	C	T	NM_013244 // upstream // 1780170 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 150131 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-1958748	ttttctgactctaatc[A/G]ccaatcaataagcac	A	G	NM_013244 // upstream // 1801286 // Hs.126195 // HGNT-IV-H // 25834 // Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), mRNA. /// NM_152589 // downstream // 129015 // Hs.112930 // FLJ35821 //	HGNT-IV-H	HGNT-IV-H, Homo sapiens UDP-N-acetylglucosamine:a-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV (HGNT-IV-H), q21.32
SNP_A-2094314	agaagtatagtgaggt[A/G]aataagaaaacaggct	A	G	NM_003994 // upstream // 97789 // Hs.1048 // KITLG // 4254 // Homo sapiens KIT ligand (KITLG), transcript variant a, mRNA. /// NM_000899 // upstream // 97789 // Hs.1048 // KITLG // 4254 // Homo sapiens KIT ligand (KITLG), transcript variant b, mRNA. /// N	KITLG	KITLG, Homo sapiens KIT ligand (KITLG), transcript variant a, q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1842231	tagggtggaagcctat[A/G]aatacgaaggaaaaat	A	G	NM_003994 /// upstream /// 189720 /// Hs.1048 /// KITLG /// 4254 /// Homo sapiens KIT ligand (KITLG), transcript variant a, mRNA. /// NM_000899 /// upstream /// 189720 /// Hs.1048 /// KITLG /// 4254 /// Homo sapiens KIT ligand (KITLG), transcript variant b, mRNA. ///	KITLG	KITLG, Homo sapiens KIT ligand (KITLG), transcript variant a, q21.33
SNP_A-2039159	aacagtaggctggagta[C/T]ccaacactgatcataa	C	T	NM_001682 /// upstream /// 97590 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 /// upstream /// 97590 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, Ca+	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1849541	tatgggatatcaagaa[A/G]aaaagtaaacatcacc	A	G	NM_001682 /// upstream /// 112090 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 /// upstream /// 112090 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, C	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1868368	tcctcatttccacccaa[C/G]tcatacacttaaacat	C	G	NM_001682 /// upstream /// 125230 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 /// upstream /// 125230 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, C	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-2161612	atttggcccatttttc[C/T]catgctcatggccact	C	T	NM_001682 /// upstream /// 173358 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, mRNA. /// NM_001001323 /// upstream /// 173358 /// Hs.506276 /// ATP2B1 /// 490 /// Homo sapiens ATPase, C	ATP2B1	ATP2B1, Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1), transcript variant 2, q21.33
SNP_A-1754758	gagagtgattactatgtttaattgc[A/G]aagtcttacaaaaatttca aaccag	A	G	NM_001682 /// upstream /// 1113134 /// Hs.20952 /// ATP2B1 /// 490 /// ATPase, Ca++ transporting, plasma membrane 1 /// NM_152768 /// upstream /// 148822 /// Hs.350600 /// FLJ25378 /// 255055 /// hypothetical protein FLJ25378	ATP2B1	ATP2B1 , rs10506991, ATPase, Ca++ transporting, plasma membrane 1 ,q21.33
SNP_A-2085265	agtcactatgtagaa[C/G]agttaaactatcaaaa	C	G	ENST00000359455 /// 3UTR /// 0 /// --- /// --- /// ---	-	q21.33
SNP_A-2126692	ataatcactattccaa[A/G]tcacaaatcagagaag	A	G	NM_152638 /// upstream /// 6613 /// Hs.128574 /// MGC26598 /// 196477 /// Homo sapiens hypothetical protein MGC26598 (MGC26598), mRNA. /// NM_004950 /// downstream /// 2334 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRN	MGC26598	MGC26598, Homo sapiens hypothetical protein MGC26598 (MGC26598), q21.33
SNP_A-2268724	gaatgtttgaataacc[A/G]gaaggcaggaatctca	A	G	NM_152638 /// upstream /// 7504 /// Hs.128574 /// MGC26598 /// 196477 /// Homo sapiens hypothetical protein MGC26598 (MGC26598), mRNA. /// NM_004950 /// downstream /// 1443 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRN	MGC26598	MGC26598, Homo sapiens hypothetical protein MGC26598 (MGC26598), q21.33
SNP_A-1946680	ttaacagtacctaga[A/C]gaatgttgaataacc	A	C	NM_152638 /// upstream /// 7521 /// Hs.128574 /// MGC26598 /// 196477 /// Homo sapiens hypothetical protein MGC26598 (MGC26598), mRNA. /// NM_004950 /// downstream /// 1426 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRN	MGC26598	MGC26598, Homo sapiens hypothetical protein MGC26598 (MGC26598), q21.33
SNP_A-1930399	ttcattttcttcaaca[C/G]gtgaaacttcagtgg	C	G	NM_004950 /// intron /// 0 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 /// intron /// 0 /// --- /// --- /// ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2174813	cacaggaagatagaca[A/T]agaaacaaatttgag	A	T	NM_004950 /// intron /// 0 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 /// intron /// 0 /// --- /// --- /// ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-1799544	gtaatgttgtcaagtc[C/T]aataaatcactattca	C	T	NM_004950 /// intron /// 0 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 /// intron /// 0 /// --- /// --- /// ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-1892574	tgcaatgcagcatcaa[G/T]tgccagaaagataggt	G	T	NM_004950 /// intron /// 0 /// Hs.435680 /// DSPG3 /// 1833 /// Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 /// intron /// 0 /// --- /// --- /// ---	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2150445	atgtgaacccaagcac[A/G]atggggttagccttca	A	G	NM_004950 // intron // 0 // Hs.435680 // DSPG3 // 1833 // Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 // intron // 0 // — // — // — // —	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2196455	catgtttaaaaggcac[C/T]atttggtaagattccc	C	T	NM_004950 // intron // 0 // Hs.435680 // DSPG3 // 1833 // Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// ENST00000261172 // intron // 0 // — // — // — // —	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2085329	tcctccttctacgtaa[A/G]gtatcccatgcttcta	A	G	NM_004950 // upstream // 3905 // Hs.435680 // DSPG3 // 1833 // Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// NM_007035 // downstream // 41559 // Hs.125750 // KERA // 11081 // Homo sapiens keratocan (KERA), mRNA. /// ENST00000261172 // up	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-1801093	gtagcagatgaaaatg[C/T]agacttcaagggccat	C	T	NM_004950 // upstream // 4201 // Hs.435680 // DSPG3 // 1833 // Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// NM_007035 // downstream // 41263 // Hs.125750 // KERA // 11081 // Homo sapiens keratocan (KERA), mRNA. /// ENST00000261172 // up	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-1665100	tttctttctctttttttgtggtctt[C/T]agtaagttgtatgttgtaagtactt	C	T	NM_004950 // upstream // 29163 // Hs.435680 // DSPG3 // 1833 // dermatan sulfate proteoglycan 3 /// NM_007035 // downstream // 16301 // Hs.125750 // KERA // 11081 // keratocan	DSPG3	DSPG3 , rs1920780, dermatan sulfate proteoglycan 3 ,q21.33
SNP_A-1701171	tatatatggcagaataaatggttac[G/T]aagtttgagaatatgtgaattttaa	G	T	NM_004950 // upstream // 29885 // Hs.435680 // DSPG3 // 1833 // dermatan sulfate proteoglycan 3 /// NM_007035 // downstream // 15579 // Hs.125750 // KERA // 11081 // keratocan	DSPG3	DSPG3 , rs887921, dermatan sulfate proteoglycan 3 ,q21.33
SNP_A-1849018	tatgcatcattgatta[A/G]aagagaaattagcaag	A	G	NM_004950 // upstream // 31984 // Hs.435680 // DSPG3 // 1833 // Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA. /// NM_007035 // downstream // 13480 // Hs.125750 // KERA // 11081 // Homo sapiens keratocan (KERA), mRNA. /// ENST00000261172 // u	DSPG3	DSPG3, Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), q21.33
SNP_A-2108961	agcttatggagtatta[C/T]gtgtgtagtatagacc	C	T	NM_007035 // intron // 0 // Hs.125750 // KERA // 11081 // Homo sapiens keratocan (KERA), mRNA. /// ENST00000266719 // intron // 0 // — // — // — // —	KERA	KERA, Homo sapiens keratocan (KERA), q21.33
SNP_A-1912176	tgtgataagtggtcca[C/T]gaaactatcagactcc	C	T	NM_007035 // upstream // 8794 // Hs.125750 // KERA // 11081 // Homo sapiens keratocan (KERA), mRNA. /// NM_002345 // downstream // 36408 // Hs.406475 // LUM // 4060 // Homo sapiens lumican (LUM), mRNA. /// ENST00000266719 // upstream // 8794 // — // —	KERA	KERA, Homo sapiens keratocan (KERA), q21.33
SNP_A-1683986	gtgagttttcaatttatgaagccaa[C/T]aggttaaggccattttcagcagttg	C	T	NM_002345 // downstream // 29823 // Hs.406475 // LUM // 4060 // lumican /// NM_007035 // upstream // 15374 // Hs.125750 // KERA // 11081 // keratocan	LUM	LUM , rs1920731, lumican ,q21.33
SNP_A-1819903	gttgttaagcattggc[C/T]gatgaaataaaacaag	C	T	NM_007035 // upstream // 22291 // Hs.125750 // KERA // 11081 // Homo sapiens keratocan (KERA), mRNA. /// NM_002345 // downstream // 22911 // Hs.406475 // LUM // 4060 // Homo sapiens lumican (LUM), mRNA. /// ENST00000266719 // upstream // 22291 // — // -	KERA	KERA, Homo sapiens keratocan (KERA), q21.33
SNP_A-1837704	tactttcttcatgcca[A/C]aatcgaagatgccatg	A	C	NM_002345 // intron // 0 // Hs.406475 // LUM // 4060 // Homo sapiens lumican (LUM), mRNA. /// ENST00000266718 // intron // 0 // — // — // — // —	LUM	LUM, Homo sapiens lumican (LUM), q21.33
SNP_A-2198892	catttgaggtctgtta[C/T]aaataccacaacacat	C	T	NM_002345 // upstream // 1489 // Hs.406475 // LUM // 4060 // Homo sapiens lumican (LUM), mRNA. /// NM_133506 // downstream // 32253 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // downstream // 32253	LUM	LUM, Homo sapiens lumican (LUM), q21.33
SNP_A-2053784	aagtgtaggcttatca[A/G]accttaaagcatctga	A	G	NM_002345 // upstream // 3855 // Hs.406475 // LUM // 4060 // Homo sapiens lumican (LUM), mRNA. /// NM_133506 // downstream // 29887 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // downstream // 29887	LUM	LUM, Homo sapiens lumican (LUM), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2047444	aagatgactaatgaag[A/G]aattagaaagcactgag	A	G	NM_133506 // upstream // 38551 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 38551 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504 /	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1805983	gtcctaagagatcaga[C/T]agctttctgcaattaa	C	T	NM_133506 // upstream // 57826 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 57826 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504 /	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2044983	aagaacctaagaatttc[A/G]ccctgatattgcaaa	A	G	NM_133506 // upstream // 73666 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 73666 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504 /	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2059778	aatctggaagacttca[A/G]taagttgtaaagattt	A	G	NM_133506 // upstream // 201881 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 201881 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2002924	ctgaagcccagaaaga[C/T]gtgcaattacccaaga	C	T	NM_133506 // upstream // 423062 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 423062 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2111113	aggagaggagaagaatg[C/G]aatcaaacttacagac	C	G	NM_133506 // upstream // 473460 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 473460 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2273674	gactgcaagaaatttat[C/T]ggtatagcgtcactag	C	T	NM_133506 // upstream // 544449 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 544449 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2158611	attgtatcacttaaca[A/G]tagagcctaaacagta	A	G	NM_133506 // upstream // 559668 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 559668 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1799571	gtaattacttaaggga[A/C]tagaaatgttttgag	A	C	NM_133506 // upstream // 587870 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 587870 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1849205	tatgctctttgccgtc[A/G]aactgctaaatattgt	A	G	NM_133506 // upstream // 591973 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 591973 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1930633	ttccaatttggtaaca[C/T]gaagggaacagtggtt	C	T	NM_133506 // upstream // 689255 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 689255 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2105195	agcattaaatgagata[C/T]tacactatgacagagt	C	T	NM_133506 // upstream // 711306 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 711306 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2002932	cagtacagccttgcta[A/G]gaagcccacaaaagca	A	G	NM_133506 // upstream // 812329 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 812329 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-2279726	gaggcatgaaaataca[C/T]tggaaagcaggctcat	C	T	NM_133506 // upstream // 847470 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant D, mRNA. /// NM_133505 // upstream // 847470 // Hs.156316 // DCN // 1634 // Homo sapiens decorin (DCN), transcript variant C, mRNA. /// NM_133504	DCN	DCN, Homo sapiens decorin (DCN), transcript variant D, q21.33
SNP_A-1729810	atcaaacactatgtataatttcaaa[C/T]tgtagcattaataggagatacttca	C	T	NM_001731 // downstream // 3514 // Hs.255935 // BTG1 // 694 // B-cell translocation gene 1, anti-proliferative /// NM_001920 // upstream // 956792 // Hs.156316 // DCN // 1634 // decorin /// NM_133503 // upstream // 960168 // Hs.156316 // DCN // 1634 // d	BTG1	BTG1 , rs1836681, B-cell translocation gene 1, anti-proliferative ,q21.33
SNP_A-1810312	gtgatggcagtccatg[A/G]ataatttgcacttgtt	A	G	NM_001731 // upstream // 308939 // Hs.255935 // BTG1 // 694 // Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), mRNA. /// NM_001004330 // upstream // 281752 // Hs.403150 // FLJ46688 // 440107 // Homo sapiens FLJ46688 protein (FLJ46688)	BTG1	BTG1, Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), q22
SNP_A-2261308	gaaagcaatcacagac[A/G]atatataggtgaatat	A	G	NM_001731 // upstream // 315472 // Hs.255935 // BTG1 // 694 // Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), mRNA. /// NM_001004330 // upstream // 275219 // Hs.403150 // FLJ46688 // 440107 // Homo sapiens FLJ46688 protein (FLJ46688)	BTG1	BTG1, Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), q22
SNP_A-2068560	acaagtgactaagtta[A/C]agagagttatgaataa	A	C	NM_001731 // upstream // 333238 // Hs.255935 // BTG1 // 694 // Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), mRNA. /// NM_001004330 // upstream // 257453 // Hs.403150 // FLJ46688 // 440107 // Homo sapiens FLJ46688 protein (FLJ46688)	BTG1	BTG1, Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), q22
SNP_A-2313441	ggagagcactcaggta[A/G]caacacaatagatctg	A	G	NM_001731 // upstream // 416570 // Hs.255935 // BTG1 // 694 // Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), mRNA. /// NM_001004330 // upstream // 174121 // Hs.403150 // FLJ46688 // 440107 // Homo sapiens FLJ46688 protein (FLJ46688)	BTG1	BTG1, Homo sapiens B-cell translocation gene 1, anti-proliferative (BTG1), q22
SNP_A-2086942	ctaattatccagcttg[G/T]aagagtccctgacatc	G	T	NM_003877 // downstream // 8526 // Hs.485572 // SOCS2 // 8835 // Homo sapiens suppressor of cytokine signaling 2 (SOCS2), mRNA. /// NM_002629 // downstream // 56094 // Hs.447492 // PGAM1 // 5223 // Homo sapiens phosphoglycerate mutase 1 (brain) (PGAM1), m	SOCS2	SOCS2, Homo sapiens suppressor of cytokine signaling 2 (SOCS2), q22
SNP_A-2254177	cttgatctaaacagga[A/G]gttcagtcaatcacta	A	G	NM_003805 // intron // 0 // Hs.38533 // CRADD // 8738 // Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// ENST00000332896 // intron // 0 // — // — // — // — /// ENST00000306632 // intron // 0 // — // –	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-2253998	cttgagaatttccaag[A/T]ctaggtaagagcaaca	A	T	NM_003805 // downstream // 86020 // Hs.38533 // CRADD // 8738 // Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// NM_003805 // downstream // 86002 // Hs.38533 // CRADD // 8738 // Homo sapiens CASP2 and RIPK1 doma	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1854755	tcaacatgaggacaat[A/G]aagttgaagaccttta	A	G	NM_003805 // downstream // 244379 // Hs.38533 // CRADD // 8738 // Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), mRNA. /// NM_003805 // downstream // 244361 // Hs.38533 // CRADD // 8738 // Homo sapiens CASP2 and RIPK1 do	CRADD	CRADD, Homo sapiens CASP2 and RIPK1 domain containing adaptor with death domain (CRADD), q22
SNP_A-2087558	gcatattggtaggcaa[C/T]gggtatttctacaatg	C	T	NM_005761 // intron // 0 // Hs.286229 // PLXNC1 // 10154 // Homo sapiens plexin C1 (PLXNC1), mRNA. /// ENST00000258526 // intron // 0 // --- // --- // --- // ---	PLXNC1	PLXNC1, Homo sapiens plexin C1 (PLXNC1), q22
SNP_A-2285378	gatctgtaacctggac[A/G]actaaaacatggtttc	A	G	NM_016122 // intron // 0 // Hs.279209 // NY-REN-58 // 51134 // Homo sapiens NY-REN-58 antigen (NY-REN-58), mRNA. /// ENST00000339839 // intron // 0 // — // — // — // —	NY-REN-58	NY-REN-58, Homo sapiens NY-REN-58 antigen (NY-REN-58), q22
SNP_A-2066734	acaaaagacagcaaac[A/G]agtggaacaacttgct	A	G	NM_016122 // CDS // 0 // Hs.279209 // NY-REN-58 // 51134 // Homo sapiens NY-REN-58 antigen (NY-REN-58), mRNA. /// ENST00000339839 // CDS // 0 // — // — // — // —	NY-REN-58	NY-REN-58, Homo sapiens NY-REN-58 antigen (NY-REN-58), q22
SNP_A-1780456	ggatagaagacattac[A/G]gggtagactcacattt	A	G	NM_016122 // intron // 0 // Hs.279209 // NY-REN-58 // 51134 // Homo sapiens NY-REN-58 antigen (NY-REN-58), mRNA. /// ENST00000339839 // intron // 0 // — // — // — // —	NY-REN-58	NY-REN-58, Homo sapiens NY-REN-58 antigen (NY-REN-58), q22
SNP_A-2215834	cctcattatcttgact[C/T]aaacctgtctctgtcc	C	T	NM_020698 // intron // 0 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // intron // 0 // --- // --- // --- // ---	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2044897	aagaacaagttcctcc[G/T]cgctcacatatgtagt	G	T	NM_020698 // intron // 0 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // intron // 0 // — // — // — // —	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-1914774	tgttacctctcatcaa[A/G]ttcgacttaatgttat	A	G	NM_020698 // intron // 0 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // intron // 0 // — // — // — // —	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2037185	aacaaacaaaaccact[G/T]accaaattgatgcata	G	T	NM_020698 // upstream // 116281 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // upstream // 116281 // — // — // — // — /// ENST00000341598 // upstream // 67627 // — // — // — // —	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2114561	agggaggacaccgagg[A/C]atatatgatgcagatt	A	C	NM_020698 // upstream // 150969 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // upstream // 150969 // — // — // — // — /// ENST00000341598 // upstream // 32939 // — // — // — // —	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2087982	ccattcataaatgtaa[C/T]gccagggagtgccaca	C	T	NM_020698 // upstream // 158815 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // upstream // 158815 // — // — // — // — /// ENST00000341598 // upstream // 25093 // --- // --- // --- // —	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2281917	gagtgccacagctatg[A/C]ataaaagtcaagcagg	A	C	NM_020698 // upstream // 158838 // Hs.370410 // TMCC3 // 57458 // Homo sapiens KIAA1145 protein (KIAA1145), mRNA. /// ENST00000261226 // upstream // 158838 // — // — // — // — /// ENST00000341598 // upstream // 25070 // — // — // — // —	TMCC3	TMCC3, Homo sapiens KIAA1145 protein (KIAA1145), q22
SNP_A-2252437	cttcctattctgacca[C/T]ccagttatgctgtgat	C	T	ENST00000343958 // intron // 0 // — // — // — // — /// ENST00000325276 // intron // 0 // — // — // — // — /// ENST00000360036 // intron // 0 // — // — // — // — // ---	-	q22
SNP_A-2248921	ctgttggtcattcagt[A/G]aatatttatggagcac	A	G	AF216644 // intron // 0 // Hs.24135 // VEZATIN // 55591 // Homo sapiens clone A34.1 transmembrane protein vezatin mRNA, complete cds. /// NM_017599 // intron // 0 // Hs.24135 // VEZATIN // 55591 // Homo sapiens transmembrane protein vezatin (VEZATIN), mRN	VEZATIN	VEZATIN, Homo sapiens clone A34.1 transmembrane protein vezatin complete cds. q22
SNP_A-2258170	cttttacactagaaaa[C/T]ctcacaaagtagtcaa	C	T	NM_021229 // upstream // 53867 // Hs.201034 // NTN4 // 59277 // Homo sapiens netrin 4 (NTN4), mRNA. /// NM_003095 // upstream // 14462 // Hs.105465 // SNRPF // 6636 // Homo sapiens small nuclear ribonucleoprotein polypeptide F (SNRPF), mRNA. /// ENST00000	NTN4	NTN4, Homo sapiens netrin 4 (NTN4), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1954023	tttgatcactctaa[C/T]aatttactgctgatt	C	T	NM_000895 // upstream // 8189 // Hs.524648 // LTA4H // 4048 // Homo sapiens leukotriene A4 hydrolase (LTA4H), mRNA. /// NM_005230 // upstream // 150653 // Hs.46523 // ELK3 // 2004 // Homo sapiens ELK3, ETS-domain protein (SRF accessory protein 2) (ELK3).	LTA4H	LTA4H, Homo sapiens leukotriene A4 hydrolase (LTA4H), q23.1
SNP_A-2089700	acttccaggttctaaa[A/G]tgtaatggttaaaaga	A	G	NM_002595 // intron // 0 // Hs.506415 // PCTK2 // 5128 // Homo sapiens PCTAIRE protein kinase 2 (PCTK2), mRNA. /// ENST00000261211 // intron // 0 // — // — // — // —	PCTK2	PCTK2, Homo sapiens PCTAIRE protein kinase 2 (PCTK2), q23.1
SNP_A-2180067	cagaaaaatgaatgac[C/T]aatgtgaaaggtaaag	C	T	NM_002595 // upstream // 67147 // Hs.506415 // PCTK2 // 5128 // Homo sapiens PCTAIRE protein kinase 2 (PCTK2), mRNA. /// ENST00000261211 // upstream // 67147 // — // — // — /// ENST00000298953 // upstream // 22015 // — // — // — // —	PCTK2	PCTK2, Homo sapiens PCTAIRE protein kinase 2 (PCTK2), q23.1
SNP_A-2089067	ctacataaacttggag[A/G]aaggacaagactatca	A	G	NM_198520 // intron // 0 // Hs.436197 // FLJ44112 // 374467 // Homo sapiens FLJ44112 protein (FLJ44112), mRNA. /// ENST00000342887 // intron // 0 // — // — // — // —	FLJ44112	FLJ44112, Homo sapiens FLJ44112 protein (FLJ44112), q23.1
SNP_A-2031737	aaagtaggcaagaaaa[C/G]gagttgtagataatat	C	G	NM_152905 // downstream // 112465 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 112465 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1857171	tcacctcctcatttta[C/G]agttaaaaatactgag	C	G	NM_152905 // downstream // 125331 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 125331 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2059198	aatcctgccaaaaaaa[A/C]caattgagcatgtc	A	C	NM_152905 // downstream // 131287 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 131287 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1821186	gtttgaccaaacaacc[A/G]agcaccataatctagc	A	G	NM_152905 // downstream // 176506 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 176506 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1853483	tattttgcgatacaaa[C/T]ttaatcacttaggtgt	C	T	NM_152905 // downstream // 194404 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 194404 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1910233	tgtcattttaatagtc[A/G]ccaaggaagaaaaat	A	G	NM_152905 // downstream // 205978 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 205978 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2191774	catatttcaataggtt[A/G]aaacagtcgaccagat	A	G	NM_152905 // downstream // 267469 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 267469 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2050215	aaggacttgagcccaa[A/C]tgtcccgcaaatcct	A	C	NM_152905 // downstream // 363318 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 363318 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141848	atcttgctccacattc[A/G]cagttgtaagtgcctt	A	G	NM_152905 // downstream // 368476 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 368476 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2196565	cattaaaatatctcac[A/G]aaaaggttcttaattc	A	G	NM_152905 // downstream // 382154 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 382154 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2191393	catatccacatatact[A/T]acacaaatggatgttt	A	T	NM_152905 // downstream // 437267 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 437267 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2126965	ataaagtcgatcaaca[C/T]acaccatttatttcc	C	T	NM_152905 // downstream // 568741 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 568741 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1895538	tgcctaggtttaagcat[C/G]agttctatctgaaca	C	G	NM_152905 // downstream // 902505 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 902505 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2090411	actcaggagctaggaa[A/G]ggtattctgatactgc	A	G	NM_152905 // downstream // 1032271 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1032271 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2211257	ccctaagctgacttta[C/G]agattcttcatttgtt	C	G	NM_152905 // downstream // 1238820 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1238820 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1901349	tggatgttctaatca[C/T]ctacaaggaatccatg	C	T	NM_152905 // downstream // 1239519 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1239519 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1816614	gttataacctctgggg[A/G]cactcaccgttagcca	A	G	NM_152905 // downstream // 1245438 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1245438 // — // — // — // — /// ENST00000341716	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1738869	taatctcctctcatgtggtaagtta[C/T]gatagaaattattaaaaaat tgctg	C	T	NM_003276 // upstream // 300923 // Hs.11355 // TMPO // 7112 // thymopoietin /// NM_152905 // downstream // 1262480 // Hs.14456 // NEDD1 // 121441 // neural precursor cell expressed, developmentally down-regulated 1	TMPO	TMPO , rs1383132, thymopoietin q23.1
SNP_A-2211389	ccctagataacacac[A/C]gcagcgcaaccctaat	A	C	NM_152905 // downstream // 1274235 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1274235 // — // — // — // — /// ENST00000341171	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1793010	ggtacccacgttgtag[C/G]actgttgttaagatta	C	G	NM_152905 // downstream // 1322192 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1322192 // — // — // — // — /// ENST0000034171	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1860218	tcagtcctcactggac[A/G]ccccgcatctatacct	A	G	NM_152905 // downstream // 1339374 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1339374 // — // — // — // — /// ENST0000034171	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2293710	gcagccttgaggaaag[A/G]agtcacaactcaaaga	A	G	NM_152905 // downstream // 1341167 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1341167 // — // — // — // — /// ENST0000034171	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1870295	tcctttgatgcaacca[C/T]cagtgccaagctttga	C	T	NM_152905 // downstream // 1351544 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1351544 // — // — // — // — /// ENST0000034171	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-1746977	gctggcaacgtcttccatcttttca[C/T]aagcagaacacaggcatcgcagatg	C	T	NM_003276 // upstream // 197768 // Hs.11355 // TMPO // 7112 // thymopoietin /// NM_152905 // downstream // 1365635 // Hs.14456 // NEDD1 // 121441 // neural precursor cell expressed, developmentally down-regulated 1	TMPO	TMPO , rs10507105, thymopoietin ,q23.1
SNP_A-1758301	atggcctttataaataatcccacta[C/T]gtatcttcttttttcagtctgtgaga	C	T	NM_003276 // upstream // 197447 // Hs.11355 // TMPO // 7112 // thymopoietin /// NM_152905 // downstream // 1365956 // Hs.14456 // NEDD1 // 121441 // neural precursor cell expressed, developmentally down-regulated 1	TMPO	TMPO , rs1351343, thymopoietin ,q23.1
SNP_A-1700305	tatagtcattttagttcaaagtctg[A/C]aattaaaactgcaaagtaatttcct	A	C	NM_003276 // upstream // 162842 // Hs.11355 // TMPO // 7112 // thymopoietin /// NM_152905 // downstream // 1400561 // Hs.14456 // NEDD1 // 121441 // neural precursor cell expressed, developmentally down-regulated 1	TMPO	TMPO , rs10492288, thymopoietin ,q23.1
SNP_A-2175552	cacatgaaccaagtcc[A/G]cagagagtcatcagtg	A	G	NM_152905 // downstream // 1452241 // Hs.270084 // NEDD1 // 121441 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA. /// ENST00000266742 // downstream // 1452241 // — // — // — // — /// ENST0000034171	NEDD1	NEDD1, Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), q23.1
SNP_A-2090804	gaggatttgattttca[G/T]cagtctttatgagacc	G	T	BC053675 // upstream // 49190 // Hs.11355 // TMPO // 7112 // Homo sapiens thymopoietin, mRNA (cDNA clone MGC:61508 IMAGE:6170639), complete cds. /// NM_003276 // upstream // 49227 // Hs.11355 // TMPO // 7112 // Homo sapiens thymopoietin (TMPO), mRNA. ///	TMPO	TMPO, Homo sapiens thymopoietin, (cDNA clone MGC:61508 IMAGE:6170639), complete cds. ,q23.1
SNP_A-2027348	aaacatgataatacac[C/T]gctttatacagacata	C	T	BC053675 // intron // 0 // Hs.11355 // TMPO // 7112 // Homo sapiens thymopoietin, mRNA (cDNA clone MGC:61508 IMAGE:6170639), complete cds. /// ENST00000343315 // intron // 0 // — // — // — // — /// ENST00000261210 // intron // 0 // — // — // -	TMPO	TMPO, Homo sapiens thymopoietin, (cDNA clone MGC:61508 IMAGE:6170639), complete cds. q23.1
SNP_A-2022926	aaaacaagttactgaa[A/C]gcgagatctacttaaa	A	C	NM_020140 // intron // 0 // Hs.506458 // EB-1 // 56899 // Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 // Hs.506458 // EB-1 // 56899 // Homo sapiens E2a-Pbx1-associated protein (EB-1), transcrip	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1877018	tctgcgaattaagaac[C/T]gctacattagaggagc	C	T	NM_020140 // intron // 0 // Hs.506458 // EB-1 // 56899 // Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, mRNA. /// NM_152788 // intron // 0 // Hs.506458 // EB-1 // 56899 // Homo sapiens E2a-Pbx1-associated protein (EB-1), transcrip	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 3, q23.1
SNP_A-1890782	tgatgattagagcaaa[A/T]ttgtcagttaaaaaat	A	T	NM_152788 // intron // 0 // Hs.506458 // EB-1 // 56899 // Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, mRNA. /// ENST00000329257 // intron // 0 // — // — // — // —	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, q23.1
SNP_A-1814324	gtgtgaaatcaactgc[A/T]aatcagttatgtgttt	A	T	NM_152788 // intron // 0 // Hs.506458 // EB-1 // 56899 // Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, mRNA. /// ENST00000329257 // intron // 0 // — // — // — // —	EB-1	EB-1, Homo sapiens E2a-Pbx1-associated protein (EB-1), transcript variant 1, q23.1
SNP_A-1959371	ttttgcaccttcctca[C/T]taaattgggtccttaa	C	T	ENST00000279907 // intron // 0 // — // — // — // —	-	q23.1
SNP_A-1821615	gtttgtgagagtaatc[A/C]acattgacacttatag	A	C	NM_017600 // upstream // 34507 // Hs.524660 // DKFZp434M0331 // 55592 // Homo sapiens hypothetical protein DKFZp434M0331 (DKFZp434M0331), mRNA. /// NM_022496 // upstream // 2752 // Hs.115088 // ACTR6 // 64431 // Homo sapiens ARP6 actin-related protein 6 h	DKFZp434M0331	DKFZp434M0331, Homo sapiens hypothetical protein DKFZp434M0331 (DKFZp434M0331), q23.1
SNP_A-1702445	catagctcgtttatatcaataatgc[A/G]gattaaaatatttgctaatgaactc	A	G	NM_174942 // downstream // 113516 // Hs.20575 // LOC283431 // 283431 // hypothetical protein LOC283431 /// NM_178826 // upstream // 56386 // Hs.58785 // TMEM16D // 121601 // transmembrane protein 16D	LOC283431	LOC283431 , rs1877882, hypothetical protein LOC283431 ,q23.1
SNP_A-1733670	attggggatagaaggagatagactc[A/G]acaggcttaccacctggatgtgagg	A	G	NM_174942 // downstream // 132301 // Hs.20575 // LOC283431 // 283431 // hypothetical protein LOC283431 /// NM_178826 // upstream // 37601 // Hs.58785 // TMEM16D // 121601 // transmembrane protein 16D	LOC283431	LOC283431 , rs952464, hypothetical protein LOC283431 ,q23.1
SNP_A-2091662	tgttagaatgggggta[C/T]taaactaagaagtaat	C	T	NM_178826 // intron // 0 // Hs.58785 // TMEM16D // 121601 // Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // — // — // — // —	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2091692	tacagtatagggtcaa[A/C]ttctgtagccagctgg	A	C	NM_178826 // intron // 0 // Hs.58785 // TMEM16D // 121601 // Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // — // — // — // —	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-1695203	tgtgtttcctgatagaagcatttct[A/G]cattaaacatgaggacttccaaggt	A	G	NM_178826 // intron // 0 // Hs.58785 // TMEM16D // 121601 // transmembrane protein 16D	TMEM16D	TMEM16D , rs938335, transmembrane protein 16D,q23.1
SNP_A-2234776	ctccagtgattccaca[C/G]gttcactcaatcacta	C	G	NM_178826 // intron // 0 // Hs.58785 // TMEM16D // 121601 // Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // — // — // — // —	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-1703073	gccatcttactaaggtaatcagaat[A/G]agaaaaaactgaaaattgatgtcat	A	G	NM_178826 // intron // 0 // Hs.58785 // TMEM16D // 121601 // transmembrane protein 16D	TMEM16D	TMEM16D , rs612640, transmembrane protein 16D,q23.1
SNP_A-2080797	acctcctgctatcatg[A/G]aagacaaattatatttt	A	G	NM_178826 // intron // 0 // Hs.58785 // TMEM16D // 121601 // Homo sapiens transmembrane protein 16D (TMEM16D), mRNA. /// ENST00000281268 // intron // 0 // — // — // — // —	TMEM16D	TMEM16D, Homo sapiens transmembrane protein 16D (TMEM16D), q23.1
SNP_A-2168218	caactgaacgttacac[C/T]gcaatcctgggcttgg	C	T	NM_152323 // downstream // 12955 // Hs.511791 // SPIC // 121599 // Homo sapiens Spi-C transcription factor (Spi-1/PU.1 related) (SPIC), mRNA. /// NM_206821 // upstream // 95021 // Hs.506502 // MYBPC1 // 4604 // Homo sapiens myosin binding protein C, slow	SPIC	SPIC, Homo sapiens Spi-C transcription factor (Spi-1,q23.2
SNP_A-2210799	cccctggtccttagta[C/G]agcagacgagtcccct	C	G	NM_152323 // downstream // 74964 // Hs.511791 // SPIC // 121599 // Homo sapiens Spi-C transcription factor (Spi-1/PU.1 related) (SPIC), mRNA. /// NM_206821 // upstream // 33012 // Hs.506502 // MYBPC1 // 4604 // Homo sapiens myosin binding protein C, slow	SPIC	SPIC, Homo sapiens Spi-C transcription factor (Spi-1,q23.2
SNP_A-1670141	attgaaaataaagaagttgtatgaa[C/T]gaatgccatcatattttttcctcct	C	T	NM_002465 // intron // 0 // Hs.169849 // MYBPC1 // 4604 // myosin binding protein C, slow type	MYBPC1	MYBPC1 , rs6538998, myosin binding protein C, slow type,q23.2
SNP_A-1747023	tgatgggacctaaaagtttactctg[A/G]aaatgtacgttaaagcccataaata	A	G	NM_002465 // intron // 0 // Hs.169849 // MYBPC1 // 4604 // myosin binding protein C, slow type	MYBPC1	MYBPC1 , rs1697485, myosin binding protein C, slow type,q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800840	gtagagaacatggcaa[A/G]tgtcacatagacttta	A	G	NM_206821 // intron // 0 // Hs.506502 // MYBPC1 // 4604 // Homo sapiens myosin binding protein C, slow type (MYBPC1), transcript variant 4, mRNA. /// NM_206820 // intron // 0 // Hs.506502 // MYBPC1 // 4604 // Homo sapiens myosin binding protein C, slow ty	MYBPC1	MYBPC1, Homo sapiens myosin binding protein C, slow type (MYBPC1), transcript variant 4, q23.2
SNP_A-1688240	aactgtttttccctatcttcaacaa[C/T]gtcgttctctgcttcccatgtgtga	C	T	NM_002465 // intron // 0 // Hs.169849 // MYBPC1 // 4604 // myosin binding protein C, slow type	MYBPC1	MYBPC1 , rs3794282, myosin binding protein C, slow type,q23.2
SNP_A-2092407	acctccaaagagtcca[C/T]tgattactgatttgtt	C	T	NM_024312 // intron // 0 // Hs.46850 // MGC4170 // 79158 // Homo sapiens MGC4170 protein (MGC4170), mRNA. /// ENST00000299314 // intron // 0 // --- // --- // --- // ---	MGC4170	MGC4170, Homo sapiens MGC4170 protein (MGC4170), q23.2
SNP_A-2133547	atatcaagtgtttata[C/T]ggaaaggatagcaata	C	T	NM_018370 // downstream // 83676 // Hs.525634 // FLJ11259 // 55332 // Homo sapiens hypothetical protein FLJ11259 (FLJ11259), mRNA. /// NM_016053 // downstream // 5655 // Hs.405692 // CGI-116 // 51019 // Homo sapiens CGI-116 protein (CGI-116), mRNA. /// EN	FLJ11259	FLJ11259, Homo sapiens hypothetical protein FLJ11259 (FLJ11259), q23.2
SNP_A-1845389	tatactttaagactca[C/T]gttctcaaacttcaga	C	T	NM_017915 // intron // 0 // Hs.330663 // FLJ20641 // 55010 // Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA. /// ENST00000327680 // intron // 0 // --- // --- // --- // --- /// ENST00000358383 // intron // 0 // --- // --- // --- // ---	FLJ20641	FLJ20641, Homo sapiens hypothetical protein FLJ20641 (FLJ20641), q23.2
SNP_A-2132241	atagtaagctcctaca[A/C]ctttatgatgtttagt	A	C	NM_017915 // downstream // 44230 // Hs.330663 // FLJ20641 // 55010 // Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA. /// NM_002674 // upstream // 43910 // Hs.2182 // PMCH // 5367 // Homo sapiens pro-melanin-concentrating hormone (PMCH), mRNA	FLJ20641	FLJ20641, Homo sapiens hypothetical protein FLJ20641 (FLJ20641), q23.2
SNP_A-2077859	accagagctttgttaa[A/T]tacaacctagactatg	A	T	NM_000618 // intron // 0 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // intron // 0 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to mRNA. /// ENST0	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-2071907	acagagataaaaaata[C/T]gtggttcctgtctcca	C	T	NM_000618 // upstream // 93975 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 94140 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to mRN	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-1891954	tgattttggtttcata[C/T]gagctactgttgcaat	C	T	NM_000618 // upstream // 96952 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 97117 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to mRN	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-1948587	tttataaaatcagtaa[A/C]aggaaagctccaaaac	A	C	NM_000618 // upstream // 100782 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 100947 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to m	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-1818877	gttgataatactttgc[C/T]gaacttattccctggg	C	T	NM_000618 // upstream // 117353 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 117518 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to m	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-2081673	accttcaaagactgca[C/T]ccttttcgatcttgga	C	T	NM_000618 // upstream // 121423 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 121588 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to m	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2151087	atgtgtcttctctgtat[C/T]cttccactgttacat	C	T	NM_000618 // upstream // 143876 // Hs.160562 // IGF1 // 3479 // Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), mRNA. /// M11568 // upstream // 144041 // Hs.160562 // IGF1 // 3479 // Human insulin-like growth factor IB (IGF-IB) cDNA to m	IGF1	IGF1, Homo sapiens insulin-like growth factor 1 (somatomedin C) (IGF1), q23.2
SNP_A-2120729	agtcctagctggtgaa[A/G]atgactccctttggaa	A	G	NM_004316 // downstream // 20642 // Hs.524672 // ASCL1 // 429 // Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), mRNA. /// ENST00000266744 // downstream // 20642 // — // — // — // — /// ENST00000356833 // upstream // 199664 // —	ASCL1	ASCL1, Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), q23.2
SNP_A-1894209	tgcattaagaagcaaa[G/T]gttcaagccttgaaa	G	T	NM_004316 // downstream // 111679 // Hs.524672 // ASCL1 // 429 // Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), mRNA. /// ENST00000266744 // downstream // 111679 // — // — // — // — /// ENST00000356833 // upstream // 108627 // –	ASCL1	ASCL1, Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), q23.2
SNP_A-1661019	ttattccacttgatttcaaaacaa[C/G]ttaatgatgtaggtattgtta ttct	C	G	NM_004316 // downstream // 206655 // Hs.1619 // ASCL1 // 429 // achaete-scute complex-like 1 (Drosophila)	ASCL1	ASCL1, rs10507158, achaete-scute complex-like 1 (Drosophila),q23.2
SNP_A-2267001	gaataaaattcagaatt[A/G]acggatttggtggtgc	A	G	NM_004316 // downstream // 219288 // Hs.524672 // ASCL1 // 429 // Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), mRNA. /// ENST00000266744 // downstream // 219288 // — // — // — // — /// ENST00000356833 // upstream // 1018 // —	ASCL1	ASCL1, Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), q23.2
SNP_A-2050365	aaggaggctaataaaa[A/G]cacacatagtattgag	A	G	NM_198521 // downstream // 119734 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream // 1323 // — // — // — /// ENST00000315192 // downstream // 119734 // — // — // —	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-1911471	tgtcttgtagtagac[A/G]ccaaattgtagctaat	A	G	NM_198521 // downstream // 115631 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream // 5426 // — // — // — /// ENST00000315192 // downstream // 115631 // — // — // —	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-1866094	tcccagagtttgggg[A/G]aagataatgtttcttt	A	G	NM_198521 // downstream // 113736 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream // 7321 // — // — // — // — /// ENST00000315192 // downstream // 113736 // — // — // —	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-2230879	ctatgctgactgatac[A/G]gagccctaacagggga	A	G	NM_198521 // downstream // 94630 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream // 26427 // — // — // — // — /// ENST00000315192 // downstream // 94630 // — // — // — // — /	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-1725772	tgtttcaggatagccaaattggata[A/G]gtagtaaggacaagtgt tttttag	A	G	NM_004316 // downstream // 252995 // Hs.1619 // ASCL1 // 429 // achaete-scute complex-like 1 (Drosophila)	ASCL1	ASCL1, rs1401994, achaete-scute complex-like 1 (Drosophila),q23.2
SNP_A-2275349	gagaatatctgctc[A/G]agaggaaatgttgcata	A	G	NM_198521 // downstream // 86954 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000356833 // downstream // 34103 // — // — // — // — /// ENST00000315192 // downstream // 86954 // — // — // — /	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-1792667	ggtaacagaattcaga[A/G]gaaagacatcaaatgc	A	G	NM_198521 // intron // 0 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000315192 // intron // 0 // — // — // — // —	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2
SNP_A-1658038	caatgatgatgagctttctcata[A/T]gattgttggccgcatagat gtcttc	A	T	AK058052 // intron // 0 // Hs.126519 // FLJ25323 // 374470 // FLJ25323 protein	FLJ25323	FLJ25323 , rs4015536, FLJ25323 protein,q23.2
SNP_A-2093599	ccatacttaacctaaa[C/G]agccaacagaggtcaa	C	G	NM_198521 // intron // 0 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// ENST00000315192 // intron // 0 // — // — // — // —	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2182521	cagatatatgtctaga[A/G]atggactgcctaaact	A	G	NM_198521 // upstream // 43291 // Hs.534649 // FLJ25323 // 374470 // Homo sapiens FLJ25323 protein (FLJ25323), mRNA. /// NM_017564 // upstream // 134709 // Hs.408249 // STAB2 // 55576 // Homo sapiens stabilin 2 (STAB2), mRNA. /// ENST00000315192 // upstre	FLJ25323	FLJ25323, Homo sapiens FLJ25323 protein (FLJ25323), q23.3
SNP_A-1857602	tcactctagtttgtca[A/G]tatccctttgaaagtg	A	G	NM_016575 // intron // 0 // Hs.48428 // TU12B1-TY // 51559 // Homo sapiens TU12B1-TY protein (TU12B1-TY), mRNA. /// ENST00000339146 // intron // 0 // — // — // — // —	TU12B1-TY	TU12B1-TY, Homo sapiens TU12B1-TY protein (TU12B1-TY), q23.3
SNP_A-1808179	gtctttaagtacttta[C/T]accttgtaatgcatat	C	T	ENST00000344460 // intron // 0 // — // — // — // —	-	q23.3
SNP_A-2003002	agctcatggtccaaga[C/T]ggctgctccagttcta	C	T	NM_031302 // intron // 0 // Hs.159993 // GLT8D2 // 83468 // Homo sapiens gycosyltransferase (LOC83468), mRNA. /// ENST00000360814 // intron // 0 // — // — // — // —	GLT8D2	GLT8D2, Homo sapiens gycosyltransferase (LOC83468), q23.3
SNP_A-2177081	cacctcctacctcata[A/T]gcagaccgtcgaaatc	A	T	NM_003330 // downstream // 11188 // Hs.434367 // TXNRD1 // 7296 // Homo sapiens thioredoxin reductase 1 (TXNRD1), transcript variant 1, mRNA. /// NM_182729 // downstream // 11188 // Hs.434367 // TXNRD1 // 7296 // Homo sapiens thioredoxin reductase 1 (TXNR	TXNRD1	TXNRD1, Homo sapiens thioredoxin reductase 1 (TXNRD1), transcript variant 1, q23.3
SNP_A-2022887	aaaacaacagcaccaa[A/G]taagatgagttgacag	A	G	NM_018413 // intron // 0 // Hs.546386 // CHST11 // 50515 // Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // — // — // — // —	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2096278	agaccagacgaattcc[G/T]agtgtgtggcttggta	G	T	NM_018413 // intron // 0 // Hs.546386 // CHST11 // 50515 // Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // — // — // — // —	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2263924	gaactactctaaacag[A/C]agattgacaaggtttt	A	C	NM_018413 // intron // 0 // Hs.546386 // CHST11 // 50515 // Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), mRNA. /// ENST00000303694 // intron // 0 // — // — // — // —	CHST11	CHST11, Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 11 (CHST11), q23.3
SNP_A-2094636	agggcttaaagtacaa[A/C]ctctctctgacagatg	A	C	NM_032148 // intron // 0 // Hs.306448 // SLC41A2 // 84102 // Homo sapiens solute carrier family 41, member 2 (SLC41A2), mRNA. /// ENST00000258538 // intron // 0 // — // — // — // —	SLC41A2	SLC41A2, Homo sapiens solute carrier family 41, member 2 (SLC41A2), q23.3
SNP_A-1900627	tggaggcaggacaggg[A/G]cagactggagctggat	A	G	NM_018171 // intron // 0 // Hs.506603 // DIP13B // 55198 // Homo sapiens DIP13 beta (DIP13B), mRNA. /// ENST00000258530 // intron // 0 // — // — // — // — /// ENST00000311166 // intron // 0 // — // — // — // —	DIP13B	DIP13B, Homo sapiens DIP13 beta (DIP13B), q23.3
SNP_A-2093152	agaacatgtattcacc[A/G]atttggaccaggttta	A	G	NM_207376 // intron // 0 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// ENST00000310995 // intron // 0 // — // — // — // —	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1922535	ttagaatcgattttaa[C/G]tggtattagccagtgg	C	G	NM_207376 // intron // 0 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// ENST00000310995 // intron // 0 // — // — // — // —	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2094963	aacactatgcaattta[C/T]aacacctttccacata	C	T	NM_207376 // downstream // 121061 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 570769 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1856189	tcacaaccactttgga[A/G]cccatcggagagcctc	A	G	NM_207376 // downstream // 168025 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 523805 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116202	aggtaattcagcaaga[C/T]ctaaaggcacctcct	C	T	NM_207376 // downstream // 191553 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 500277 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2306153	gctggagtgatgataa[A/G]cttatggagaagtggt	A	G	NM_207376 // downstream // 192379 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 499451 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1667040	atagacccaacacgagcattc[C/T]ctattcgattttccatc ttctgtg	C	T	NM_014840 // downstream // 484870 // - // - // -	-	-, rs2888856, -,q23.3
SNP_A-2087195	actgattaacgtgaaaa[C/T]ggcatccaaatggta	C	T	NM_207376 // downstream // 213606 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 478224 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2161944	atttgtattgaaaga[G/T]aatttgaaggtggtt	G	T	NM_207376 // downstream // 218020 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 473810 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2255377	ctgtcaaacatattc[A/G]cataaacgcttctcat	A	G	NM_207376 // downstream // 270149 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 421681 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1876271	tctgagagtgaaaaga[C/T]ggagctgaaacttaag	C	T	NM_207376 // downstream // 270197 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 421633 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2137218	atcagtatcatttttg[C/G]attatcttctataaat	C	G	NM_207376 // downstream // 277811 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 414019 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1850144	tatgtggagcactatg[A/G]aaagagaaaggagata	A	G	NM_207376 // downstream // 278172 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 413658 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2199347	catttgagacagtta[C/T]ggttggaaaatttct	C	T	NM_207376 // downstream // 278736 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 413094 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2124005	agttacaattgtgcaa[C/T]agaggaccgagagaca	C	T	NM_207376 // downstream // 283056 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA /// NM_014840 // downstream // 408774 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784561	ggcctactagagcaag[A/G]caggctttctcagtcc	A	G	NM_207376 // downstream // 301294 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 390536 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2152374	attaacattatgttca[A/G]ccaatcactttgaga	A	G	NM_207376 // downstream // 352430 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 339400 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2294102	gcaggcaagtttgcta[C/T]ggctgtttcatttctg	C	T	NM_207376 // downstream // 370647 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 321183 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2221515	ccttttctcgcttatc[A/G]atctcctagcatgcag	A	G	NM_207376 // downstream // 373711 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 318119 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1940165	ttgcatatattatcca[A/G]gtttagagatgggaaa	A	G	NM_207376 // downstream // 378263 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 313567 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2238432	ctctggtgagttccaa[C/T]agtcctacagggtttc	C	T	NM_207376 // downstream // 380157 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 311673 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2239156	ctctgataactacaa[C/T]tcgattgctacatttt	C	T	NM_207376 // downstream // 380231 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 311599 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2097220	agacttggcattagta[A/G]gtttctgttcaagttc	A	G	NM_207376 // downstream // 396647 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 295183 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1722642	tagatgctttactggtccctttca[G/T]tcctaaaattatatgatctcta aaca	G	T	NM_014840 // downstream // 294720 // - // - // - // -	-	- , rs4600310, - ,q23.3
SNP_A-1836482	tactcccagaggttga[G/T]cgataggtgaatggtc	G	T	NM_207376 // downstream // 402875 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 288955 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2095211	tgtttgatattcaaga[C/T]ggtatttgtcatttgg	C	T	NM_207376 // downstream // 441710 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 250120 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1822282	gttttgctttacttc[A/G]ctggttgctaccactt	A	G	NM_207376 // downstream // 534147 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 157683 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2073022	acaggaggcacacaaa[G/T]tcctattggattgtgg	G	T	NM_207376 // downstream // 542393 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 149437 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1642865	ttctcttgagtgaagattcccataa[A/G]gttgctttgtaaatgtgtcc aggg	A	G	NM_014840 // downstream // 142422 // - // - // -	-	- , rs10507204, - , q23.3
SNP_A-2309574	ggaaactgagaggcag[A/G]aaagaattgtccgtgc	A	G	NM_207376 // downstream // 560315 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 131515 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-1852394	tatttaagcacttaag[A/G]aatctcaggcatttta	A	G	NM_207376 // downstream // 662134 // Hs.525657 // LOC387882 // 387882 // Homo sapiens hypothetical protein (LOC387882), mRNA. /// NM_014840 // downstream // 29696 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (A	LOC387882	LOC387882, Homo sapiens hypothetical protein (LOC387882), q23.3
SNP_A-2238623	ctctgtgtaaatacaa[A/G]cgtaactggcttctaa	A	G	NM_014840 // intron // 0 // Hs.524692 // ARK5 // 9891 // Homo sapiens AMP-activated protein kinase family member 5 (ARK5), mRNA. /// ENST00000261402 // intron // 0 // — // — // — /// ENST00000359413 // intron // 0 // — // — // — // —	ARK5	ARK5, Homo sapiens AMP-activated protein kinase family member 5 (ARK5), q23.3
SNP_A-2225220	cgttcctagaagagac[A/G]gagagcgctgactgaa	A	G	NM_018082 // downstream // 10348 // Hs.62696 // POLR3B // 55703 // Homo sapiens polymerase (RNA) III (DNA directed) polypeptide B (POLR3B), mRNA. /// NM_213594 // upstream // 62710 // Hs.388827 // RFX4 // 5992 // Homo sapiens regulatory factor X, 4 (influ	POLR3B	POLR3B, Homo sapiens polymerase (RNA) III (DNA directed) polypeptide B (POLR3B), q23.3
SNP_A-2221715	ccttttgtccgcacac[C/T]gagccagtaatatatt	C	T	NM_213594 // intron // 0 // Hs.388827 // RFX4 // 5992 // Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 3, mRNA. /// ENST00000357881 // intron // 0 // — // — // — // —	RFX4	RFX4, Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 3, q23.3
SNP_A-2120338	agtcatccaaattcca[C/T]gctgggttgacctac	C	T	NM_213594 // intron // 0 // Hs.388827 // RFX4 // 5992 // Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 3, mRNA. /// NM_002920 // intron // 0 // Hs.388827 // RFX4 // 5992 // Homo sapiens regulatory fact	RFX4	RFX4, Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 3, q23.3
SNP_A-2239441	ctctttgctgagctac[C/T]gtaaacatacaccatg	C	T	NM_004075 // upstream // 284122 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 239636 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2235331	ctccctctgtctttgg[A/G]actaagaatggatctt	A	G	NM_004075 // upstream // 285217 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 238541 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1900709	tggaggtagtttgtta[A/T]gctgcatatgcacaat	A	T	NM_004075 // upstream // 417770 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 105988 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2124610	agttccttccatcaac[A/G]gtctatttgcccatcc	A	G	NM_004075 // upstream // 418166 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 105592 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2096300	tgccctctggaactc[A/G]cagtataaccatatgt	A	G	NM_004075 // upstream // 419000 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 104758 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1819146	gttgctcaatatgtga[A/G]gcaacatttaaaaca	A	G	NM_004075 // upstream // 421689 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 102069 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2155639	attccagcctctgcaa[C/G]ttcgtccgcagtttt	C	G	NM_004075 // upstream // 444264 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 79494 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2073403	acaggtctaaagtgct[A/G]agaattatctgcaca	A	G	NM_004075 // upstream // 444854 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 78904 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1818320	gttctgtcattggaca[A/T]gaaatttagtcaaaag	A	T	NM_004075 // upstream // 459045 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 64713 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-1942324	ttggccacttaagcaa[C/T]ggtcagaagtccaggc	C	T	NM_004075 // upstream // 476287 // Hs.151573 // CRY1 // 1407 // Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA. /// NM_152322 // upstream // 47471 // Hs.271272 // BTBD11 // 121551 // Homo sapiens BTB (POZ) domain containing 11 (BTBD11), mRNA.	CRY1	CRY1, Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), q23.3
SNP_A-2204201	ccagcatattctatcc[A/G]caacatttctcagtag	A	G	NM_203436 // downstream // 97236 // Hs.149910 // ASCL4 // 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 // downstream // 97236 // — // — // — /// ENST00000332082 // upstream // 255860 // -	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2003021	cagtgacagatttaac[A/G]gattaaaatttcctgt	A	G	NM_203436 // downstream // 133687 // Hs.149910 // ASCL4 // 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 // downstream // 133687 // — // — // — /// ENST00000332082 // upstream // 219409 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2210442	ccccccagaggtatga[C/T]cacagctcaactaag	C	T	NM_203436 // downstream // 223430 // Hs.149910 // ASCL4 // 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 // downstream // 223430 // — // — // — /// ENST00000332082 // upstream // 129666 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3
SNP_A-2174962	cacagggttgctaaaat[A/C]aaaaagacaggattct	A	C	NM_203436 // downstream // 254290 // Hs.149910 // ASCL4 // 121549 // Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), mRNA. /// ENST00000342331 // downstream // 254290 // — // — // — /// ENST00000332082 // upstream // 98806 //	ASCL4	ASCL4, Homo sapiens achaete-scute complex-like 4 (Drosophila) (ASCL4), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1930604	ttccaatctgtacac[A/G]gggaaagatgaagaa	A	G	NM_004072 // upstream // 139327 // Hs.506659 // CMKLR1 // 1240 // Homo sapiens chemokine-like receptor 1 (CMKLR1), mRNA. /// ENST00000312143 // upstream // 139327 // --- // --- // --- /// ENST00000357208 // upstream // 82988 // --- // --- // ---	CMKLR1	CMKLR1, Homo sapiens chemokine-like receptor 1 (CMKLR1), q23.3
SNP_A-2213970	cctaactaatacaaca[A/T]ctaaatcatctatgt	A	T	NM_004072 // upstream // 173959 // Hs.506659 // CMKLR1 // 1240 // Homo sapiens chemokine-like receptor 1 (CMKLR1), mRNA. /// ENST00000312143 // upstream // 173959 // --- // --- // --- /// ENST00000357208 // upstream // 48356 // --- // --- // ---	CMKLR1	CMKLR1, Homo sapiens chemokine-like receptor 1 (CMKLR1), q23.3
SNP_A-2181269	cagaccccaaaaagcca[C/T]catattataggattcc	C	T	NM_004072 // upstream // 214699 // Hs.506659 // CMKLR1 // 1240 // Homo sapiens chemokine-like receptor 1 (CMKLR1), mRNA. /// ENST00000312143 // upstream // 214699 // --- // --- // --- /// ENST00000357208 // upstream // 7616 // --- // --- // ---	CMKLR1	CMKLR1, Homo sapiens chemokine-like receptor 1 (CMKLR1), q23.3
SNP_A-1642227	ggctcacctgtgccttgaacattca[A/G]tgaagaagctgaacca acacaggtt	A	G	NM_014301 // downstream // 1939 // Hs.350702 // ISCU // 23479 // iron-sulfur cluster assembly enzyme /// NM_181724 // downstream // 18545 // Hs.449718 // LOC338773 // 338773 // hypothetical protein LOC338773	ISCU	ISCU , rs10492251, iron-sulfur cluster assembly enzyme ,q23.3
SNP_A-1810088	gtgatatctgcttgct[A/G]aaaaggatctggtgat	A	G	NM_018711 // intron // 0 // Hs.4221 // DKFZp761H039 // 55530 // Homo sapiens hypothetical protein DKFZp761H039 (DKFZp761H039), mRNA. /// ENST00000299134 // intron // 0 // --- // --- // ---	DKFZp761H039	DKFZp761H039, Homo sapiens hypothetical protein DKFZp761H039 (DKFZp761H039), q24.11
SNP_A-1911754	tgtgaagtttctggg[G/T]agagcacccaaggcca	G	T	NM_001093 // intron // 0 // Hs.234898 // ACACB // 32 // Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA. /// ENST00000338432 // intron // 0 // --- // --- // ---	ACACB	ACACB, Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), q24.11
SNP_A-2231536	ctatttattaaccaa[A/C]ccctatgtgaagtgt	A	C	NM_213596 // intron // 0 // Hs.528316 // FOXN4 // 121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// AF425596 // intron // 0 // Hs.528316 // FOXN4 // 121643 // Homo sapiens clone 12 forkhead/winged helix transcription factor FOXN4 (FOXN4), mRNA, par	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2148341	atgggaagtcttggg[A/C]agataactcaatgccc	A	C	NM_213596 // intron // 0 // Hs.528316 // FOXN4 // 121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// ENST00000355216 // intron // 0 // --- // --- // ---	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2092457	agaaagtagtcagata[C/T]gctaagttctcagcca	C	T	NM_213596 // intron // 0 // Hs.528316 // FOXN4 // 121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// ENST00000355216 // intron // 0 // --- // --- // ---	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2161814	atttgtcagttgatgag[A/G]aatctgagtggtttct	A	G	NM_213596 // upstream // 25950 // Hs.528316 // FOXN4 // 121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// AF425596 // upstream // 44918 // Hs.528316 // FOXN4 // 121643 // Homo sapiens clone 12 forkhead/winged helix transcription factor FOXN4 (FOXN	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2248454	ctgtgttcatatgaaat[C/T]gtccatgatagggcaa	C	T	NM_213596 // upstream // 36665 // Hs.528316 // FOXN4 // 121643 // Homo sapiens forkhead box N4 (FOXN4), mRNA. /// AF425596 // upstream // 55633 // Hs.528316 // FOXN4 // 121643 // Homo sapiens clone 12 forkhead/winged helix transcription factor FOXN4 (FOXN	FOXN4	FOXN4, Homo sapiens forkhead box N4 (FOXN4), q24.11
SNP_A-2097327	ttagccagtttgtcct[C/G]aacattgagctccgtg	C	G	ENST00000341410 // intron // 0 // --- // --- // ---	-	q24.11
SNP_A-1795707	ggtggacacatacgta[A/G]aaattcatgggdat	A	G	ENST00000341410 // intron // 0 // --- // --- // ---	-	q24.11
SNP_A-2230842	ctatgcatatttatac[A/G]acagcatcatcaggatt	A	G	ENST00000341410 // intron // 0 // --- // --- // ---	-	q24.11
SNP_A-2003030	gagggaaccagaggggg[C/G]cacctaacgtccggtgt	C	G	ENST00000341410 // intron // 0 // --- // --- // ---	-	q24.11
SNP_A-2097344	ctactgggacctagac[A/G]atgtgagatcatctgt	A	G	ENST00000341410 // intron // 0 // --- // --- // ---	-	q24.11
SNP_A-2097359	cacagggaaatcacc[A/G]catactaattctgtgt	A	G	NM_031954 // intron // 0 // Hs.524731 // KCTD10 // 83892 // Homo sapiens potassium channel tetramerisation domain containing 10 (KCTD10), mRNA. /// ENST00000228495 // intron // 0 // --- // --- // ---	KCTD10	KCTD10, Homo sapiens potassium channel tetramerisation domain containing 10 (KCTD10), q24.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1952610	tttctgctgccacgtc[A/G]agggtttatttttgag	A	G	NM_031954 // intron // 0 // Hs.524731 // KCTD10 // 83892 // Homo sapiens potassium channel tetramerisation domain containing 10 (KCTD10), mRNA. /// ENST00000228495 // intron // 0 // — // — // — // —	KCTD10	KCTD10, Homo sapiens potassium channel tetramerisation domain containing 10 (KCTD10), q24.11
SNP_A-2191042	cataggtacctgataa[A/G]catcatcacatttagt	A	G	NM_130466 // intron // 0 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // intron // 0 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), tra	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-2304092	gctccatgagcgtaga[C/G]atcttgcccgtcctgt	C	G	NM_130466 // intron // 0 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // intron // 0 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), tra	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-1713544	agaaaaaacattgataaggtccata[A/G]ctgaatggaaggaac aaaatacaaa	A	G	NM_130466 // intron // 0 // Hs.305834 // UBE3B // 89910 // ubiquitin protein ligase E3B	UBE3B	UBE3B , rs7311187, ubiquitin protein ligase E3B,q24.11
SNP_A-2003031	ccgaagggccttttaa[A/G]tctaaggagctttgtc	A	G	NM_130466 // intron // 0 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // intron // 0 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), tra	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-1862239	tcatggctgtgataac[G/T]gtcattattttgttcc	G	T	NM_130466 // downstream // 2958 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // downstream // 2958 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-2289014	gatttcagacttaaca[A/G]cttctagaattgtgag	A	G	NM_130466 // downstream // 6113 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // downstream // 6113 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-2097430	aggaaaaactagccca[C/T]agccagagatggtacc	C	T	NM_130466 // downstream // 7172 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // downstream // 7172 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-2097433	atgaaagtcctagaga[C/G]gtgtgtaccttacagt	C	G	NM_130466 // downstream // 13070 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA. /// NM_183415 // downstream // 13070 // Hs.374067 // UBE3B // 89910 // Homo sapiens ubiquitin protein ligase	UBE3B	UBE3B, Homo sapiens ubiquitin protein ligase E3B (UBE3B), transcript variant 1, q24.11
SNP_A-2055975	aatacagccgtggcac[C/G]gatctcagaggcataa	C	G	NM_052845 // 3UTR // 0 // Hs.12106 // MMAB // 326625 // Homo sapiens methylmalonic aciduria (cobalamin deficiency) type B (MMAB), mRNA. /// ENST00000266839 // 3UTR // 0 // — // — // — // —	MMAB	MMAB, Homo sapiens methylmalonic aciduria (cobalamin deficiency) type B (MMAB), q24.11
SNP_A-2236546	ctcgtgtgccatccat[C/T]aagtgcaagatggctg	C	T	NM_052845 // intron // 0 // Hs.12106 // MMAB // 326625 // Homo sapiens methylmalonic aciduria (cobalamin deficiency) type B (MMAB), mRNA. /// ENST00000266839 // intron // 0 // — // — // — // —	MMAB	MMAB, Homo sapiens methylmalonic aciduria (cobalamin deficiency) type B (MMAB), q24.11
SNP_A-1787126	gggaaagtggacctca[A/G]cttacccaacattggt	A	G	NM_000431 // CDS // 0 // Hs.130607 // MVK // 4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// ENST00000228510 // CDS // 0 // — // — // — // — // —	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11
SNP_A-2072838	acagctgttccatctc[A/G]attacaaagctctgaa	A	G	NM_000431 // intron // 0 // Hs.130607 // MVK // 4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// ENST00000228510 // intron // 0 // — // — // — // — // —	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2223137	cgcccagcctgagctat[C/T]gtttagatgtgcatt	C	T	NM_000431 // downstream // 7281 // Hs.130607 // MVK // 4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// NM_032829 // upstream // 109842 // Hs.144655 // FLJ14721 // 84915 // Homo sapiens hypothetical protein FLJ14721 (FLJ14721).	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11
SNP_A-2085738	actcctccataaaaac[A/G]cttctccaaatttctg	A	G	NM_000431 // downstream // 19977 // Hs.130607 // MVK // 4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// NM_032829 // upstream // 97146 // Hs.144655 // FLJ14721 // 84915 // Homo sapiens hypothetical protein FLJ14721 (FLJ14721).	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11
SNP_A-1783830	ggccaactctgaggac[A/G]gcactccaaagggtgg	A	G	NM_000431 // downstream // 40202 // Hs.130607 // MVK // 4598 // Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), mRNA. /// NM_032829 // upstream // 76921 // Hs.144655 // FLJ14721 // 84915 // Homo sapiens hypothetical protein FLJ14721 (FLJ14721).	MVK	MVK, Homo sapiens mevalonate kinase (mevalonic aciduria) (MVK), q24.11
SNP_A-1811132	gtgccccgtgcagtga[C/G]agccgctttcctgcag	C	G	NM_032829 // intron // 0 // Hs.144655 // FLJ14721 // 84915 // Homo sapiens hypothetical protein FLJ14721 (FLJ14721), mRNA. /// ENST00000358906 // intron // 0 // — // — // — /// ENST00000266849 // intron // 0 // — // — // —	FLJ14721	FLJ14721, Homo sapiens hypothetical protein FLJ14721 (FLJ14721), q24.11
SNP_A-2035751	aaatgtgcttgacaga[C/T]atttcaagtacaaaaa	C	T	NM_033121 // intron // 0 // Hs.528703 // ANKRD13 // 88455 // Homo sapiens ankyrin repeat domain 13 (ANKRD13), mRNA. /// ENST00000261739 // intron // 0 // — // — // — /// ENST00000334689 // intron // 0 // — // — // —	ANKRD13	ANKRD13, Homo sapiens ankyrin repeat domain 13 (ANKRD13), q24.11
SNP_A-2308733	gctttctttttcatttta[C/T]ctaatttcatcaattg	C	T	NM_139283 // upstream // 63417 // Hs.13854 // TA-PP2C // 160760 // Homo sapiens T-cell activation protein phosphatase 2C (TA-PP2C), mRNA. /// NM_032369 // downstream // 2045 // Hs.334637 // MGC15619 // 84329 // Homo sapiens hypothetical protein MGC15619 (.	TA-PP2C	TA-PP2C, Homo sapiens T-cell activation protein phosphatase 2C (TA-PP2C), q24.11
SNP_A-2185989	caggcagagaagaaaa[A/G]ttggaggttgggggcg	A	G	NM_152591 // intron // 0 // Hs.437141 // FLJ35843 // 160762 // Homo sapiens hypothetical protein FLJ35843 (FLJ35843), mRNA. /// ENST00000308208 // intron // 0 // — // — // —	FLJ35843	FLJ35843, Homo sapiens hypothetical protein FLJ35843 (FLJ35843), q24.11
SNP_A-1832759	tacaaggcacaggacg[A/G]ccctgcaatgagaaat	A	G	AB006631 // intron // 0 // Hs.124953 // CUTL2 // 23316 // Homo sapiens mRNA for KIAA0293 gene, partial cds. /// ENST00000261726 // intron // 0 // — // — // —	CUTL2	CUTL2, Homo sapiens for KIAA0293 gene, partial cds, q24.11
SNP_A-2272317	gaccttcttgattaagt[G/T]acaccattattatgaa	G	T	NM_138341 // intron // 0 // Hs.506815 // LOC89894 // 89894 // Homo sapiens hypothetical protein BC000282 (LOC89894), mRNA. /// ENST00000330904 // intron // 0 // — // — // — /// ENST00000355445 // intron // 0 // — // — // — /// EN	LOC89894	LOC89894, Homo sapiens hypothetical protein BC000282 (LOC89894), q24.13
SNP_A-1893604	tgcaggtgttgtagaa[A/G]gaaccaatgagttaat	A	G	NM_014954 // intron // 0 // Hs.21239 // RPH3A // 22895 // Homo sapiens rabphilin 3A homolog (mouse) (RPH3A), mRNA. /// ENST00000261730 // intron // 0 // — // — // — // —	RPH3A	RPH3A, Homo sapiens rabphilin 3A homolog (mouse) (RPH3A), q24.13
SNP_A-2090402	acttggcacccattca[A/G]tcatacatgtctcaga	A	G	NM_006187 // 3UTR // 0 // Hs.528634 // OAS3 // 4940 // Homo sapiens 2'-5'-oligoadenylate synthetase 3, 100kDa (OAS3), mRNA. /// ENST00000228928 // 3UTR // 0 // — // — // —	OAS3	OAS3, Homo sapiens 2'-5'-oligoadenylate synthetase 3, 100kDa (OAS3), q24.13
SNP_A-1950644	tttcatgcaaaccacca[C/T]gacctggctctaagcct	C	T	NM_138432 // downstream // 8043 // Hs.337594 // SDSL // 113675 // Homo sapiens serine dehydratase-like (SDSL), mRNA. /// NM_022363 // downstream // 16571 // Hs.302029 // LHX5 // 64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// ENST00000345635 // dow	SDSL	SDSL, Homo sapiens serine dehydratase-like (SDSL), q24.13
SNP_A-2098888	aatcagtgctcttctc[A/G]aacttaaatgattctc	A	G	NM_022363 // upstream // 169938 // Hs.302029 // LHX5 // 64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 174732 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// ENST00000261731 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1783482	ggcatccaggcttgta[C/T]cttgacagtctgacttc	C	T	NM_022363 // upstream // 196300 // Hs.302029 // LHX5 // 64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 148370 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// ENST00000261731 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-1856526	tcacagccaggtcacc[A/G]gaaacttcccacagat	A	G	NM_022363 // upstream // 224280 // Hs.302029 // LHX5 // 64211 // Homo sapiens LIM homeobox 5 (LHX5), mRNA. /// NM_016196 // downstream // 120390 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// ENST00000261731 //	LHX5	LHX5, Homo sapiens LIM homeobox 5 (LHX5), q24.13
SNP_A-1812908	gtggggaagggattca[C/T]ggtctcaccttcgcat	C	T	NM_016196 // intron // 0 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// ENST00000261741 // intron // 0 // — // — // — // —	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.13
SNP_A-2250040	cttacctaactgcccat[A/G]ctaagattccctgta	A	G	NM_016196 // intron // 0 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// ENST00000261741 // intron // 0 // — // — // — // —	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-1846353	tatatgcttaaacttc[C/T]agtccaccttgaatat	C	T	NM_016196 // upstream // 115926 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 271699 // Hs.381715 // TBX5 // 6910 // Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA. /// NM_0	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2099348	cctgcttttcacgtc[A/T]agggagtgcttgctc	A	T	NM_016196 // upstream // 124174 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 263451 // Hs.381715 // TBX5 // 6910 // Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA. /// NM_0	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2099349	gaaggccatgttgtaa[A/C]ctactgaatagaacat	A	C	NM_016196 // upstream // 124394 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 263231 // Hs.381715 // TBX5 // 6910 // Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA. /// NM_0	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2110920	aggacttgacccttcc[A/C]acagtatctctctacc	A	C	NM_016196 // upstream // 126392 // Hs.7482 // RBM19 // 9904 // Homo sapiens RNA binding motif protein 19 (RBM19), mRNA. /// NM_080718 // downstream // 261233 // Hs.381715 // TBX5 // 6910 // Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA. /// NM_0	RBM19	RBM19, Homo sapiens RNA binding motif protein 19 (RBM19), q24.21
SNP_A-2182563	cagatcaagaaccaacc[A/G]gcccatgtgttacttt	A	G	NM_005996 // downstream // 223679 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // downstream // 223679 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary s	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2224245	cggtgtctcacacaaa[A/T]cctcagtggtggttat	A	T	NM_005996 // downstream // 160238 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // downstream // 160238 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary s	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1857231	tcaccttatagtatca[C/T]aatcagaagttttgct	C	T	NM_005996 // downstream // 83822 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // downstream // 83822 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syn	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2236759	ctctacattgctgat[A/G]actctgagcttcattt	A	G	NM_005996 // upstream // 112677 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 112677 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1865355	tccatccaggaaagaac[A/G]gtagcacctgaaaatc	A	G	NM_005996 // upstream // 264715 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 264715 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1818967	gttgcaaagattaaac[C/G]agtgattcttaacccc	C	G	NM_005996 // upstream // 404593 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 404593 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2230647	ctatctgtttcattta[C/T]gtattgttgcataacc	C	T	NM_005996 // upstream // 470055 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 470055 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1810303	gtgatggagcccccaa[C/T]agttgcctgagtcttg	C	T	NM_005996 // upstream // 569456 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 569456 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1796493	ggttaagagaaagtat[A/G]agttaacacgggtgag	A	G	NM_005996 // upstream // 680347 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 680347 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2047549	aagatggcaacagaga[C/G]agtctactgcaagac	C	G	NM_005996 // upstream // 712977 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 712977 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2185449	caggacctctataccaa[C/G]ctaagaaacattctta	C	G	NM_005996 // upstream // 734160 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 734160 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2196978	cattatatctggcacc[C/T]gccttcatctgtagcc	C	T	NM_005996 // upstream // 737227 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 737227 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2137128	atcaggcatttactat[C/G]agctagatttttggct	C	G	NM_005996 // upstream // 751221 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 751221 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2286469	gatgcttgcacccagt[C/G]aaccatcagtacccag	C	G	NM_005996 // upstream // 806471 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 806471 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1866238	tcccagttaagaggaa[A/T]tactctgctacaccc	A	T	NM_005996 // upstream // 807222 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 807222 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1795588	ggtgctctatccagga[G/T]tcagcacaatattaca	G	T	NM_005996 // upstream // 809976 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 809976 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1900751	tggagtaaagtctaag[G/T]atcttaccccagaatt	G	T	NM_005996 // upstream // 810303 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 810303 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1936521	ttcttgatcgtcctt[A/G]cctgacatcatggtaa	A	G	NM_005996 // upstream // 810658 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 810658 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2243643	ctgctcctgcaaccac[G/T]actaaaaccctggctt	G	T	NM_005996 // upstream // 810692 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 810692 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2107150	agcggttgccctgac[A/G]ctcaactctcactagg	A	G	NM_005996 // upstream // 812031 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 812031 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2166019	caaataaggccgatga[C/T]aggaggtaagaggtca	C	T	NM_005996 // upstream // 828730 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 828730 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2076015	acattatcagttgaaa[A/C]aatcgctctaggata	A	C	NM_005996 // upstream // 829269 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 829269 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2193564	catctgttgtttttca[A/G]tatccgttccaccttc	A	G	NM_005996 // upstream // 837095 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 837095 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2077642	accacggaaaccgatc[A/G]aaaagtatcagccatg	A	G	NM_005996 // upstream // 838440 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 838440 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1802393	gtatcagccatgatga[A/T]gaatgtagaacactcg	A	T	NM_005996 // upstream // 838461 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 838461 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2040771	aacccagtgagcattt[C/G]aaaaccctgtaagtct	C	G	NM_005996 // upstream // 841824 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 841824 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1808141	gtcttggtcaaactta[C/T]tccctctgccctgtat	C	T	NM_005996 // upstream // 892288 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 892288 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1867101	tccctcttattcactg[A/T]acctgatggtagtttt	A	T	NM_005996 // upstream // 893136 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 893136 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2161148	atttgaataacgagaa[A/G]gaggcagagaccagca	A	G	NM_005996 // upstream // 917374 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 917374 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2226716	ctaagtgtggttcatg[C/G]acaggtaatatcagcg	C	G	NM_005996 // upstream // 922673 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 922673 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1902146	tggcatttctgaacat[A/G]aggtgctgaagtgaag	A	G	NM_005996 // upstream // 925141 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 925141 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2295424	gcatccgtaggcgtca[C/T]gctcttctccaaggc	C	T	NM_005996 // upstream // 946097 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 946097 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2135963	atcaacttgattgaca[A/G]ctcagtgtaaagtggt	A	G	NM_005996 // upstream // 953082 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 953082 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndr	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2284805	gatcattgcaaggaaa[A/C]gtagaagtactagata	A	C	NM_005996 // upstream // 1078355 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 1078355 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syn	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-1813131	gtggtagcttccagga[A/G]tcaagagtcaagatga	A	G	NM_005996 // upstream // 1111041 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 1111041 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syn	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2101132	gaaactggacatgtac[A/G]gaagggctgcccgat	A	G	NM_005996 // upstream // 1174849 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 1174849 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syn	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21
SNP_A-2129384	atacaagccacaatac[G/T]gatgaatctcaaaaac	G	T	NM_005996 // upstream // 1189933 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA. /// NM_016569 // upstream // 1189933 // Hs.129895 // TBX3 // 6926 // Homo sapiens T-box 3 (ulnar mammary syn	TBX3	TBX3, Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, q24.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2101195	tgcatcactatcagta[A/T]agttaagcctgtgtcg	A	T	NM_015335 // intron // 0 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// ENST00000281928 // intron // 0 // — // — // — // —	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-1920627	ttaattttagtaacta[C/T]catgtcctgaaggtta	C	T	NM_015335 // intron // 0 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// ENST00000281928 // intron // 0 // — // — // — // —	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-2059920	aatcttcagtgggata[C/G]gatgggctataaagaa	C	G	NM_015335 // intron // 0 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// ENST00000281928 // intron // 0 // — // — // — // —	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-2102244	agattacaacaaaaca[A/G]ggataaatgcacttcc	A	G	NM_015335 // intron // 0 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// ENST00000281928 // intron // 0 // — // — // — // —	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-1891609	tgattgatggtagaga[C/T]ggggtcttgatgtgtg	C	T	NM_015335 // upstream // 34594 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// NM_207436 // upstream // 221490 // Hs.441601 // FLJ42957 // 400077 // Homo sapiens FLJ42957 protein (FLJ42957)	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-2101356	taaaatgccagtctca[C/G]aaggttgttgtttaag	C	G	NM_015335 // upstream // 115256 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// NM_207436 // upstream // 140828 // Hs.441601 // FLJ42957 // 400077 // Homo sapiens FLJ42957 protein (FLJ42957	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-1843676	tagtggttgccttgga[A/G]attacaagtaacatct	A	G	NM_015335 // upstream // 120531 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// NM_207436 // upstream // 135553 // Hs.441601 // FLJ42957 // 400077 // Homo sapiens FLJ42957 protein (FLJ42957	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.21
SNP_A-2260452	gaaacaccggcattag[C/T]agattgcagagttcta	C	T	NM_015335 // upstream // 153942 // Hs.159799 // THRAP2 // 23389 // Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), mRNA. /// NM_207436 // upstream // 102142 // Hs.441601 // FLJ42957 // 400077 // Homo sapiens FLJ42957 protein (FLJ42957	THRAP2	THRAP2, Homo sapiens thyroid hormone receptor associated protein 2 (THRAP2), q24.22
SNP_A-1789748	gggctctctggaacaa[A/G]tggtgtccctcctgac	A	G	NM_024738 // downstream // 114286 // Hs.528681 // FLJ21415 // 79794 // Homo sapiens hypothetical protein FLJ21415 (FLJ21415), mRNA. /// ENST00000306985 // downstream // 25185 // — // — // — // — /// ENST00000261318 // downstream // 114286 // — /	FLJ21415	FLJ21415, Homo sapiens hypothetical protein FLJ21415 (FLJ21415), q24.22
SNP_A-2106109	agcccagtccctttac[A/G]ccgcagacattcagct	A	G	NM_032814 // intron // 0 // Hs.437195 // FLJ14627 // 84900 // Homo sapiens hypothetical protein FLJ14627 (FLJ14627), mRNA. /// ENST00000319176 // intron // 0 // — // — // — // — /// ENST00000257575 // intron // 0 // — // — // — // —	FLJ14627	FLJ14627, Homo sapiens hypothetical protein FLJ14627 (FLJ14627), q24.22
SNP_A-2024446	aaaaggaaatccatca[A/G]tagtgtctactaacat	A	G	NM_153348 // intron // 0 // Hs.435466 // FBXW8 // 26259 // Homo sapiens F-box and WD-40 domain protein 8 (FBXW8), transcript variant 1, mRNA. /// NM_012174 // intron // 0 // Hs.435466 // FBXW8 // 26259 // Homo sapiens F-box and WD-40 domain protein 8 (FBX	FBXW8	FBXW8, Homo sapiens F-box and WD-40 domain protein 8 (FBXW8), transcript variant 1, q24.22
SNP_A-1784177	ggccatgagaaaagaa[A/G]acagacagggacaaca	A	G	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // — // — // — // — /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-1680834	aaaactgtcttaaaagaaaatctat[C/T]ccatgctctatctttcagagaccta	C	T	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // kinase suppressor of Ras-2	KSR2	KSR2 , rs1878420, kinase suppressor of Ras-2,q24.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102264	ggtacaaggatgaaca[C/T]gtcattgaacaattac	C	T	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // — // — // — // — /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2102265	agagtcagggttcaaa[G/T]ataggcgtgtctgacc	G	T	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // — // — // — // — /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2077876	accagataatctgaca[A/G]taatcagtgtgttagt	A	G	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // — // — // — // — /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-1930226	ttcattctctctttta[A/G]gcaaatgtcatggtta	A	G	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000302438 // intron // 0 // — // — // — // — /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.22
SNP_A-2235699	ctcctcagccgcacca[C/T]ccttccttgtcactca	C	T	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.23
SNP_A-2278881	gaggaaaatagaggaa[A/G]acttgctaagcatgag	A	G	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.23
SNP_A-2305235	gctgagacttgaatga[C/T]aagaaagcatcagaca	C	T	NM_173598 // intron // 0 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// ENST00000339824 // intron // 0 // — // — // — // —	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.23
SNP_A-1898641	tgcttgtcccaccggc[G/T]agagctcttctgtcag	G	T	NM_173598 // upstream // 20152 // Hs.375836 // KSR2 // 283455 // Homo sapiens kinase suppressor of Ras-2 (KSR2), mRNA. /// NM_007370 // upstream // 141017 // Hs.506989 // RFC5 // 5985 // Homo sapiens replication factor C (activator 1) 5, 36.5kDa (RFC5), t	KSR2	KSR2, Homo sapiens kinase suppressor of Ras-2 (KSR2), q24.23
SNP_A-2287413	gatgttaccctcttaa[A/G]agatcaaagccaactt	A	G	NM_016281 // intron // 0 // Hs.368304 // TAOK3 // 51347 // Homo sapiens TAO kinase 3 (TAOK3), mRNA. /// ENST00000257545 // intron // 0 // — // — // — // — /// ENST00000359166 // intron // 0 // — // — // — // — /// ENST00000359811 // intron	TAOK3	TAOK3, Homo sapiens TAO kinase 3 (TAOK3), q24.23
SNP_A-1836220	tactatctctaaatac[A/G]aacacagatgtttaca	A	G	NM_016281 // intron // 0 // Hs.368304 // TAOK3 // 51347 // Homo sapiens TAO kinase 3 (TAOK3), mRNA. /// ENST00000257545 // intron // 0 // — // — // — // — /// ENST00000359166 // intron // 0 // — // — // — // —	TAOK3	TAOK3, Homo sapiens TAO kinase 3 (TAOK3), q24.23
SNP_A-1805946	gtccggagtcctaaca[A/G]gaaggcatagcaataa	A	G	NM_194286 // upstream // 530200 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 33673 // — // — // — // — /// ENST00000267260 // upstream // 530200 // — // — // — // -	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2252052	cttccaccaggctacc[A/C]gatttttaaatgatct	A	C	NM_194286 // upstream // 529908 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 33965 // — // — // — // — /// ENST00000267260 // upstream // 529908 // — // — // — // -	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1892719	tgcacacccccacta[C/T]acacacaagttctgtt	C	T	NM_194286 // upstream // 469569 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 94304 // — // — // — // — /// ENST00000267260 // upstream // 469569 // — // — // — // -	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1710956	acacctctttctcttcatcacaaac[A/G]ccctagttcaatccacca tcattgc	A	G	AK024460 // downstream // 209329 // Hs.416630 // SDS3 // 64426 // likely ortholog of mouse Sds3 /// AY130006 // upstream // 529478 // Hs.530641 // KIAA1853 // 84530 // KIAA1853 protein	SDS3	SDS3 , rs4126012, likely ortholog of mouse Sds3 ,q24.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116964	aggtgaagctgtcctd[A/G]cagggataacaagaat	A	G	NM_194286 // upstream // 370812 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 193061 // — // — // — // — /// ENST00000267260 // upstream // 370812 // — // — // — // —	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1940179	ttgcatcaggtgaggg[A/G]aaaagagagagagag	A	G	NM_194286 // upstream // 304827 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 259046 // — // — // — // — /// ENST00000267260 // upstream // 304827 // — // — // — // —	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-1810321	gtgatggaaactgga[A/C]attgagaggcctctg	A	C	NM_194286 // upstream // 62931 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000251152 // downstream // 500942 // — // — // — // — /// ENST00000267260 // upstream // 62931 // — // — // — // -	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2107232	agcgtttctctatga[C/T]ggtttgcttaagaga	C	T	NM_194286 // intron // 0 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // intron // 0 // — // — // —	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2039487	aacatcaggaaattag[C/T]ccaaagcatctcaaaa	C	T	NM_194286 // intron // 0 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // intron // 0 // — // — // —	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2026598	aaacaacttgacgaga[A/G]aggtggatggaggga	A	G	NM_194286 // intron // 0 // Hs.112577 // KIAA1853 // 84530 // Homo sapiens KIAA1853 protein (KIAA1853), mRNA. /// ENST00000267260 // intron // 0 // — // — // —	KIAA1853	KIAA1853, Homo sapiens KIAA1853 protein (KIAA1853), q24.23
SNP_A-2227254	ctacaaaatgcattaa[C/T]ggtgatgcaagcacta	C	T	NM_014365 // intron // 0 // Hs.400095 // HSPB8 // 26353 // Homo sapiens heat shock 22kDa protein 8 (HSPB8), mRNA. /// ENST00000281938 // intron // 0 // — // — // — // —	HSPB8	HSPB8, Homo sapiens heat shock 22kDa protein 8 (HSPB8), q24.23
SNP_A-2003064	tgagtaatatttacc[A/G]aggtcaatccagctt	A	G	NM_178499 // upstream // 124645 // Hs.98188 // MGC39827 // 160777 // Homo sapiens hypothetical protein MGC39827 (MGC39827), mRNA. /// ENST00000326763 // downstream // 14700 // — // — // — // — /// ENST00000327554 // upstream // 124645 // — // -	MGC39827	MGC39827, Homo sapiens hypothetical protein MGC39827 (MGC39827), q24.23
SNP_A-2245526	ctgggatagagagaga[C/G]cgtggtgggcatgga	C	G	NM_178499 // intron // 0 // Hs.98188 // MGC39827 // 160777 // Homo sapiens hypothetical protein MGC39827 (MGC39827), mRNA. /// ENST00000327554 // intron // 0 // — // — // —	MGC39827	MGC39827, Homo sapiens hypothetical protein MGC39827 (MGC39827), q24.23
SNP_A-2205265	ccagtcaaggatttag[C/T]cattaatctggatgg	C	T	NM_012240 // upstream // 5458 // Hs.50861 // SIRT4 // 23409 // Homo sapiens sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae) (SIRT4), mRNA. /// ENST00000242630 // downstream // 14186 // — // — // — /// ENST00000	SIRT4	SIRT4, Homo sapiens sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae) (SIRT4), q24.23
SNP_A-1954725	tttgctctatctgtcc[C/T]gatggtttgatttttc	C	T	NM_015918 // upstream // 51773 // Hs.279913 // POP5 // 51367 // Homo sapiens processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae) (POP5), transcript variant 1, mRNA. /// NM_198202 // upstream // 51772 // Hs.279913 // POP5 // 51367 // Homo	POP5	POP5, Homo sapiens processing of precursor 5, ribonuclease P q24.31
SNP_A-2201719	ccacaagagtgggaaa[A/G]ccagaatgagcagaag	A	G	NM_014730 // intron // 0 // Hs.507074 // KIAA0152 // 9761 // Homo sapiens KIAA0152 gene product (KIAA0152), mRNA. /// ENST00000228506 // intron // 0 // — // — // — // —	KIAA0152	KIAA0152, Homo sapiens KIAA0152 gene product (KIAA0152), q24.31
SNP_A-2267625	gaatcaagagtgggaat[C/T]gtctaaggaccgaagt	C	T	NM_139015 // intron // 0 // Hs.507087 // SPPL3 // 121665 // Homo sapiens signal peptide peptidase 3 (SPPL3), mRNA. /// ENST00000353487 // intron // 0 // — // — // — // —	SPPL3	SPPL3, Homo sapiens signal peptide peptidase 3 (SPPL3), q24.31
SNP_A-2195910	catgtcactttgaaa[C/T]gaaaatgccacacga	C	T	NM_139015 // upstream // 3051 // Hs.507087 // SPPL3 // 121665 // Homo sapiens signal peptide peptidase 3 (SPPL3), mRNA. /// ENST00000353487 // upstream // 3051 // — // — // — // — /// ENST00000308819 // upstream // 7029 // — // — // — // —	SPPL3	SPPL3, Homo sapiens signal peptide peptidase 3 (SPPL3), q24.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2262364	gaaatgatagatttgc[C/T]aggaggtgaaagatgg	C	T	NM_002562 // intron // 0 // Hs.507102 // P2RX7 // 5027 // Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7), transcript variant 1, mRNA. /// NM_177427 // intron // 0 // Hs.507102 // P2RX7 // 5027 // Homo sapiens purinergic receptor	P2RX7	P2RX7, Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7), transcript variant 1, q24.31
SNP_A-2234337	ctccaaattaaacaca[C/T]acaggtaaccagaacc	C	T	NM_153499 // intron // 0 // Hs.297343 // CAMKK2 // 10645 // Homo sapiens calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 2, mRNA. /// NM_172226 // intron // 0 // Hs.297343 // CAMKK2 // 10645 // Homo sapiens calcium/	CAMKK2	CAMKK2, Homo sapiens calcium,q24.31
SNP_A-1932819	ttccttgttagcaa[A/C]tcctactccattgcct	A	C	NM_019034 // intron // 0 // Hs.223617 // RHOF // 54509 // Homo sapiens ras homolog gene family, member F (in filopodia) (RHOF), mRNA. /// ENST00000356560 // intron // 0 // — // — // — /// ENST00000267205 // intron // 0 // — // — // — //	RHOF	RHOF, Homo sapiens ras homolog gene family, member F (in filopodia) (RHOF), q24.31
SNP_A-2148745	atggtctgaatctgtc[C/T]cctcttcctcccaaat	C	T	NM_014708 // downstream // 56650 // Hs.300559 // KNTC1 // 9735 // Homo sapiens kinetochore associated 1 (KNTC1), mRNA. /// NM_006018 // downstream // 20830 // Hs.458425 // GPR109B // 8843 // Homo sapiens G protein-coupled receptor 109B (GPR109B), mRNA. //	KNTC1	KNTC1, Homo sapiens kinetochore associated 1 (KNTC1), q24.31
SNP_A-2300162	gcctccaggaggagat[A/G]acaggtgagccagata	A	G	ENST00000330860 // CDS // 0 // — // — // —	-	q24.31
SNP_A-2122086	agtgatgcatgcccaa[C/T]tgatggcgaaataggt	C	T	ENST00000280562 // intron // 0 // — // — // —	-	q24.31
SNP_A-2095738	agacacgtttcaaatat[C/G]gaattgcattatcatt	C	G	X98258 // intron // 0 // Hs.507175 // MPHOSPH9 // 10198 // H.sapiens mRNA for M-phase phosphoprotein, mpp9. /// ENST00000356855 // intron // 0 // — // — // — /// ENST00000302349 // intron // 0 // — // — // —	MPHOSPH9	MPHOSPH9, H.sapiens for M-phase phosphoprotein, mpp9. q24.31
SNP_A-2003081	ttgtccacattctgcct[A/G]agtgaacgtgaacaat	A	G	X98258 // 5UTR // 0 // Hs.507175 // MPHOSPH9 // 10198 // H.sapiens mRNA for M-phase phosphoprotein, mpp9. /// NM_022782 // intron // 0 // Hs.507175 // MPHOSPH9 // 10198 // Homo sapiens M-phase phosphoprotein 9 (MPHOSPH9), mRNA. /// ENST00000356855 // intr	MPHOSPH9	MPHOSPH9, H.sapiens for M-phase phosphoprotein, mpp9. q24.31
SNP_A-1806768	gtctaggctctaaaca[C/T]aaaacttgggctta	C	T	X98258 // intron // 0 // Hs.507175 // MPHOSPH9 // 10198 // H.sapiens mRNA for M-phase phosphoprotein, mpp9. /// NM_022782 // intron // 0 // Hs.507175 // MPHOSPH9 // 10198 // Homo sapiens M-phase phosphoprotein 9 (MPHOSPH9), mRNA. /// ENST00000356855 // in	MPHOSPH9	MPHOSPH9, H.sapiens for M-phase phosphoprotein, mpp9. q24.31
SNP_A-2038087	aacacactggcacaca[C/T]tgtctttcagcttaca	C	T	NM_018183 // intron // 0 // Hs.144055 // SBNO1 // 55206 // Homo sapiens sno, strawberry notch homolog 1 (Drosophila) (SBNO1), mRNA. /// ENST00000267176 // intron // 0 // — // — // — // —	SBNO1	SBNO1, Homo sapiens sno, strawberry notch homolog 1 (Drosophila) (SBNO1), q24.31
SNP_A-1857110	tcaccgaggatgctaa[C/T]aagcagcacaggtgag	C	T	NM_012463 // intron // 0 // Hs.201939 // ATP6V0A2 // 23545 // Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), mRNA. /// ENST00000330342 // intron // 0 // — // — // — // — - /// ENST00000357745 // intron // 0 // —	ATP6V0A2	ATP6V0A2, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), q24.31
SNP_A-2047865	aagcaaaaatccgtaa[A/G]gcaaatcattgagtca	A	G	NM_012463 // intron // 0 // Hs.201939 // ATP6V0A2 // 23545 // Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), mRNA. /// ENST00000330342 // intron // 0 // — // — // — // — - /// ENST00000357745 // intron // 0 // —	ATP6V0A2	ATP6V0A2, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), q24.31
SNP_A-2269761	gacaagagttgaacac[A/G]gtctcacatctgtcag	A	G	NM_012463 // intron // 0 // Hs.201939 // ATP6V0A2 // 23545 // Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), mRNA. /// ENST00000330342 // intron // 0 // — // — // — // — - /// ENST00000357745 // intron // 0 // —	ATP6V0A2	ATP6V0A2, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), q24.31
SNP_A-2046385	aagagacagggactat[A/G]agcagtaagaggtggg	A	G	NM_012463 // intron // 0 // Hs.201939 // ATP6V0A2 // 23545 // Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), mRNA. /// ENST00000330342 // intron // 0 // — // — // — // — -	ATP6V0A2	ATP6V0A2, Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 (ATP6V0A2), q24.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2237795	ctctcttttgtttgtg[A/G]agctacaatattttcc	A	G	NM_152437 // downstream // 64577 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 214662 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC144347	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-1914460	tgtgtttgtgtagcta[C/T]catgagatttgtggtc	C	T	NM_152437 // downstream // 102947 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 176292 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC14434	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2269332	gaatttgcctgctcac[C/T]gaaatgcatctataac	C	T	NM_152437 // downstream // 169086 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 110153 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC14434	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2068799	acaatatttcatccac[C/T]gatcaatgcataacct	C	T	NM_152437 // downstream // 169528 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 109711 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC14434	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2211067	cccggaggcctgaaga[C/T]ggtgcagatgcgctgt	C	T	NM_152437 // downstream // 209290 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 69949 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC144347	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2277740	gagcagggtctggaaa[C/T]gaaggtgtgctccgct	C	T	NM_152437 // downstream // 249757 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 29482 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC144347	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2310127	ggaacacacacaggga[C/G]aaatgacaggcaaata	C	G	NM_152437 // downstream // 256462 // Hs.524828 // ZFOC1 // 144348 // Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), mRNA. /// NM_181709 // upstream // 22777 // Hs.432901 // LOC144347 // 144347 // Homo sapiens hypothetical protein LOC144347	ZFOC1	ZFOC1, Homo sapiens hypothetical protein DKFZp761B128 (DKFZp761B128), q24.31
SNP_A-2198120	cattggtaatccatcc[C/T]atcactcttgtccact	C	T	NM_006312 // upstream // 91846 // Hs.137510 // NCOR2 // 9612 // Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /// NM_005505 // downstream // 190533 // Hs.298813 // SCARB1 // 949 // Homo sapiens scavenger receptor class B, member 1 (SCARB1),	NCOR2	NCOR2, Homo sapiens nuclear receptor co-repressor 2 (NCOR2), q24.31
SNP_A-2174482	cacagacgttggagcc[A/G]gatgacctgggttcac	A	G	NM_006312 // upstream // 176103 // Hs.137510 // NCOR2 // 9612 // Homo sapiens nuclear receptor co-repressor 2 (NCOR2), mRNA. /// NM_005505 // downstream // 106276 // Hs.298813 // SCARB1 // 949 // Homo sapiens scavenger receptor class B, member 1 (SCARB1),	NCOR2	NCOR2, Homo sapiens nuclear receptor co-repressor 2 (NCOR2), q24.31
SNP_A-1821793	gttttacagatgagga[A/C]gcgactctcagttaag	A	C	NM_005505 // intron // 0 // Hs.298813 // SCARB1 // 949 // Homo sapiens scavenger receptor class B, member 1 (SCARB1), mRNA. /// ENST00000261693 // intron // 0 // — // — // — // — /// ENST00000339570 // intron // 0 // — // — // — // —	SCARB1	SCARB1, Homo sapiens scavenger receptor class B, member 1 (SCARB1), q24.31
SNP_A-1917503	tgttttatggcctac[C/T]catgctgagacatatt	C	T	NM_005505 // intron // 0 // Hs.298813 // SCARB1 // 949 // Homo sapiens scavenger receptor class B, member 1 (SCARB1), mRNA. /// ENST00000261693 // intron // 0 // — // — // — // — /// ENST00000339570 // intron // 0 // — // — // — // —	SCARB1	SCARB1, Homo sapiens scavenger receptor class B, member 1 (SCARB1), q24.31
SNP_A-2312468	ggacccacagctgaga[A/G]ggaacaagcctcccca	A	G	NM_032656 // intron // 0 // Hs.107382 // DHX37 // 57647 // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 37 (DHX37), mRNA. /// ENST00000308736 // intron // 0 // — // — // — // —	DHX37	DHX37, Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 37 (DHX37), q24.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1781153	ggatgaaggcacagc[A/G]aatggcaggaggatgg	A	G	NM_032656 // intron // 0 // Hs.107382 // DHX37 // 57647 // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 37 (DHX37), mRNA. /// ENST00000308736 // intron // 0 // — // — // — // —	DHX37	DHX37, Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 37 (DHX37), q24.31
SNP_A-2126623	ataaacaacatatgccd[A/C]attaacagacaaaggc	A	C	ENST00002999308 // intron // 0 // — // — // — // —	-	q24.31
SNP_A-2312304	ggacatctgaactagc[A/G]gcgtttgtggaatttgg	A	G	ENST00000266765 // downstream // 46500 // — // — // — // — /// ENST00000345111 // upstream // 1043509 // — // — // — // —	-	q24.31
SNP_A-1726620	aattgtgaaccatcagaatatgaaac[A/G]atgcaatactaaacattatgagat	A	G	AB067493 // downstream // 448464 // Hs.6496 // KIAA1906 // 114795 // KIAA1906 protein	KIAA1906	KIAA1906, rs10492041, KIAA1906 protein,q24.31
SNP_A-1959711	tttggtacaataaca[G/T]aattacttcatcttca	G	T	ENST00000345111 // upstream // 766804 // — // — // — // — /// ENST00000266765 // downstream // 323205 // — // — // — // — ///	-	q24.31
SNP_A-1827271	taacctccagtcatc[A/G]gaattgtgggccaaat	A	G	ENST00000266765 // downstream // 324199 // — // — // — // — /// ENST00000345111 // upstream // 765810 // — // — // — // —	-	q24.31
SNP_A-2034718	aaatgaagcccttggal[C/T]ggtcagtgacgaccct	C	T	ENST00000266765 // downstream // 507956 // — // — // — // — /// ENST00000345111 // upstream // 582053 // — // — // — // —	-	q24.31
SNP_A-2205281	ccagtcacttcctgat[A/G]aatatcctgcataaac	A	G	ENST00000266765 // downstream // 511803 // — // — // — // — /// ENST00000345111 // upstream // 578206 // — // — // — // —	-	q24.31
SNP_A-2003092	tgccagacatttcaga[A/G]gtaaacatggcttatt	A	G	ENST00000266765 // downstream // 581549 // — // — // — // — /// ENST00000345111 // upstream // 508460 // — // — // — // —	-	q24.31
SNP_A-2106242	ctttatgtgtcagtca[C/T]agtgtatattgatt	C	T	ENST00000266765 // downstream // 584720 // — // — // — // — /// ENST00000345111 // upstream // 505289 // — // — // — // —	-	q24.31
SNP_A-1897881	tgctgggggaagacca[C/T]taacagaaggcgtgta	C	T	ENST00000266765 // downstream // 1006092 // — // — // — // — /// ENST00000345111 // upstream // 83917 // — // — // — // —	-	q24.32
SNP_A-1961443	ttttttaaccactgal[G/T]atgttttgaggcatt	G	T	ENST00000345111 // downstream // 44410 // — // — // — // — /// ENST00000355517 // downstream // 1095079 // — // — // — // —	-	q24.32
SNP_A-2121261	agtctgttatgtatal[C/T]gaaacacttcccaggg	C	T	ENST00000345111 // downstream // 49684 // — // — // — // — /// ENST00000355517 // downstream // 1089805 // — // — // — // —	-	q24.32
SNP_A-1886719	tgactgaaaatcatca[C/T]atgagcattggctgt	C	T	ENST00000345111 // downstream // 160912 // — // — // — // — /// ENST00000355517 // downstream // 978577 // — // — // — // —	-	q24.32
SNP_A-1798753	gtaactacctaaaac[C/T]gcaactgtgcaaaac	C	T	ENST00000345111 // downstream // 194081 // — // — // — // — /// ENST00000355517 // downstream // 945408 // — // — // — // —	-	q24.32
SNP_A-1941865	ttggagagaataaag[C/T]cgatacattcacatat	C	T	ENST00000345111 // downstream // 200021 // — // — // — // — /// ENST00000355517 // downstream // 939468 // — // — // — // —	-	q24.32
SNP_A-2261071	gaaagaattcaaggaa[A/G]tccataaagtaaaagc	A	G	ENST00000345111 // downstream // 208630 // — // — // — // — /// ENST00000355517 // downstream // 930859 // — // — // — // —	-	q24.32
SNP_A-2293161	gcagagaaagcataaa[C/T]gcccttgacaaaacgg	C	T	ENST00000345111 // downstream // 651553 // — // — // — // — /// ENST00000355517 // downstream // 487936 // — // — // — // —	-	q24.32
SNP_A-2119686	agtattactgaaatgc[A/C]gaactcacaaatgtgc	A	C	ENST00000345111 // downstream // 725309 // — // — // — // — /// ENST00000355517 // downstream // 414180 // — // — // — // —	-	q24.32
SNP_A-2113402	aggcgaaaagttaaac[A/G]atcagccagtgaaact	A	G	ENST00000345111 // downstream // 729439 // — // — // — // — /// ENST00000355517 // downstream // 410050 // — // — // — // —	-	q24.32
SNP_A-1882091	tcttttatctggaga[A/G]tagccctttgttgtgg	A	G	ENST00000345111 // downstream // 1067908 // — // — // — // — /// ENST00000355517 // downstream // 71581 // — // — // — // —	-	q24.32
SNP_A-2206775	ccatgcataagccatg[C/T]agtttataatatttgg	C	T	ENST00000345111 // downstream // 1070828 // — // — // — // — /// ENST00000355517 // downstream // 68661 // — // — // — // —	-	q24.32
SNP_A-2067485	acaaatgattatttga[A/G]ggcttaagcaagtgta	A	G	ENST00000345111 // upstream // 177511 // — // — // — // — /// ENST00000355517 // upstream // 553546 // — // — // — // — /// ENST00000315208 // upstream // 494893 // — // — // — // — ///	-	q24.32
SNP_A-1909798	tgtcacagttctgcca[C/T]tgaagagccaaagaac	C	T	ENST00000315208 // upstream // 236164 // — // — // — // — /// ENST00000345111 // upstream // 520349 // — // — // — // — /// ENST00000355517 // upstream // 210708 // — // — // — // —	-	q24.32
SNP_A-2257092	ctttctcatatggttg[A/T]acaggcgatttgcgc	A	T	ENST00000315208 // upstream // 532244 // — // — // — // — /// ENST00000355517 // upstream // 198813 // — // — // — // —	-	q24.32
SNP_A-2121075	agtctctagcgtctac[C/G]agggtgagcatgagcc	C	G	ENST00000315208 // upstream // 198813 // — // — // — // —	-	q24.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255403	cttgtcagtgttctgc[C/T]gagctactttatctg	C	T	NM_145648 // downstream // 41077 // Hs.507260 // SLC15A4 // 121260 // Homo sapiens solute carrier family 15, member 4 (SLC15A4), mRNA. /// ENST00000315208 // downstream // 44234 // — // — // — /// ENST00000266771 // downstream // 41077 // —	SLC15A4	SLC15A4, Homo sapiens solute carrier family 15, member 4 (SLC15A4), q24.32
SNP_A-1647362	gtgaggacacaacccagaagaataa[A/G]atcagaggactgacgtgactcaagt	A	G	NM_007197 // upstream // 1064374 // Hs.31664 // FZD10 // 11211 // frizzled homolog 10 (Drosophila)	FZD10	FZD10 , rs1386212, frizzled homolog 10 (Drosophila), q24.33
SNP_A-1818129	gttctcctggctgaac[A/G]cttggtcaacaatgct	A	G	NM_144669 // intron // 0 // Hs.12381 // FLJ31978 // 144423 // Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// ENST00000355128 // intron // 0 // — // — // — /// ENST00000281703 // intron // 0 // — // — // —	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-2105188	agcatgtttcatgtgc[A/G]cctctaagctctgcca	A	G	NM_144669 // intron // 0 // Hs.12381 // FLJ31978 // 144423 // Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// ENST00000355128 // intron // 0 // — // — // — /// ENST00000281703 // intron // 0 // — // — // —	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-1835134	tacctcgcatttccaa[A/G]attccctgcagctag	A	G	NM_144669 // downstream // 4658 // Hs.12381 // FLJ31978 // 144423 // Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// NM_133448 // downstream // 82104 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. //	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-1865014	tccagtcacaaccagc[C/T]gagcatgactaggtc	C	T	NM_144669 // downstream // 25265 // Hs.12381 // FLJ31978 // 144423 // Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// NM_133448 // downstream // 61497 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-2100727	agatagatgcctccaa[A/G]atgatcacgcaagcc	A	G	NM_144669 // downstream // 60858 // Hs.12381 // FLJ31978 // 144423 // Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// NM_133448 // downstream // 25904 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-2003117	ctgccccaggggacat[A/G]atggagacaacgttg	A	G	NM_144669 // downstream // 67003 // Hs.12381 // FLJ31978 // 144423 // Homo sapiens hypothetical protein FLJ31978 (FLJ31978), mRNA. /// NM_133448 // downstream // 19759 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /	FLJ31978	FLJ31978, Homo sapiens hypothetical protein FLJ31978 (FLJ31978), q24.32
SNP_A-1785903	ggctgaggcagcgac[A/G]acctacaaagcaatag	A	G	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-1899964	tggacatcgagaaaaac[A/G]gaaccctcatctggcc	A	G	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-2117616	aggttaggacttaaga[A/G]gcatctcaagggacag	A	G	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-1783588	ggcatgccagactcaa[A/G]cgtgtcottgaacata	A	G	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.32
SNP_A-2130328	atacgttaaaggcact[A/C]aagagagatgaagtgc	A	C	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2107967	atccgctagtgagcgat[C/T]ggctaggtctggagat	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1930176	ttcattcaggctcaca[A/G]tgctagccatgtcatc	A	G	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2218321	cctgcttacataattc[A/C]aaagaggtataactgc	A	C	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1818521	gttctttgaagcttct[C/T]attggttacaattcca	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2267634	gaatcaataagttcaa[A/C]ggcttgaaacaaagtc	A	C	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2307558	gcttcaccaatgctag[A/C]aggtccttgaaactag	A	C	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2094153	agaaggcgaagaacac[C/T]gaacatcttctggag	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1814042	gtgtccagaatcccaa[C/T]ccagagacagaggact	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1841152	tagctttatctgggtc[C/T]cttttcaaatgttacc	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2225808	ctaaagtggaagtata[C/G]gcagagcctgtgtgtct	C	G	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1870453	tcgaaattgtagttga[C/T]atacatctagaggtct	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2069933	acacaggatgggacaa[C/T]gtgaccacagtggatg	C	T	NM_133448 // intron // 0 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// ENST00000299038 // intron // 0 // — // — // —	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1852034	tattgctcaactaagq[A/T]acttcggtaatcatgc	A	T	NM_133448 // upstream // 38066 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 221054 // Hs.31664 // FZD10 // 11211 // Homo sapiens frizzled homolog 10 (Drosophila) (FZD10), mRNA. /// ENST	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2076876	accaaagactgaaaga[C/T]gcaatagtcctctggg	C	T	NM_133448 // upstream // 78048 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 181072 // Hs.31664 // FZD10 // 11211 // Homo sapiens frizzled homolog 10 (Drosophila) (FZD10), mRNA. /// ENST	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-1896514	tgctaccttttacata[C/T]gcagctctctaccc	C	T	NM_133448 // upstream // 93251 // Hs.252489 // KIAA1944 // 121256 // Homo sapiens KIAA1944 protein (KIAA1944), mRNA. /// NM_007197 // upstream // 165869 // Hs.31664 // FZD10 // 11211 // Homo sapiens frizzled homolog 10 (Drosophila) (FZD10), mRNA. /// ENST	KIAA1944	KIAA1944, Homo sapiens KIAA1944 protein (KIAA1944), q24.33
SNP_A-2073012	acaggagcaaatgttc[C/T]gaaaagaggacacaat	C	T	NM_015347 // intron // 0 // Hs.225014 // KIAA0318 // 23504 // Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // — // — // — // —	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-2151730	atgttgttttctgai[C/T]gtgcaatgtgaggcag	C	T	NM_015347 // intron // 0 // Hs.225014 // KIAA0318 // 23504 // Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // — // — // — // — // — // — // — // ENST00000359212 // intron // 0 // — // — // —	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-2176905	caccgtggaaggacc[A/G]gcaagtgagaccatgc	A	G	NM_015347 // intron // 0 // Hs.225014 // KIAA0318 // 23504 // Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// ENST00000261655 // intron // 0 // — // — // —	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2267298	gaatagaaactctctc[C/T]ccgtgtctccaggttt	C	T	NM_015347 // upstream // 67871 // Hs.225014 // KIAA0318 // 23504 // Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// NM_015347 // upstream // 155696 // Hs.225014 // KIAA0318 // 23504 // Homo sapiens RIM binding protein 2 (KIAA0318), mRNA. /// NM_0	KIAA0318	KIAA0318, Homo sapiens RIM binding protein 2 (KIAA0318), q24.33
SNP_A-2283153	gataatcacataccaa[G/T]atacaaatgttgcata	G	T	NM_198827 // intron // 0 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// ENST00000261654 // intron // 0 // — // — // — // — /// ENST00000335486 // intron // 0 // — // — // — // —	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2223583	cggacatcaggaaggc[A/G]cagtgaacatgaaaca	A	G	NM_198827 // intron // 0 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// ENST00000261654 // intron // 0 // — // — // — // — /// ENST00000335486 // intron // 0 // — // — // — // —	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2299747	gccgtgtgtatttcaa[A/G]tctactttccgtttat	A	G	NM_198827 // downstream // 319063 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream // 394089 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (su	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-1897941	tgctggtttatgtcat[C/T]aataaaatgctgcaat	C	T	NM_198827 // downstream // 339398 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream // 373754 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (su	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-1913289	tgtgggcaaagggcaa[C/T]gtctctcctgtgcaca	C	T	NM_198827 // downstream // 599355 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream // 113797 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (su	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-1840218	tagcagctgatgcaaa[A/G]tggtagcactatacat	A	G	NM_198827 // downstream // 655269 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream // 57883 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (sup	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2098671	agagccccccaccccaa[C/T]ggacgatggaggctcg	C	T	NM_198827 // downstream // 695229 // Hs.435168 // GPR133 // 283383 // Homo sapiens G protein-coupled receptor 133 (GPR133), mRNA. /// NM_152235 // upstream // 17923 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (sup	GPR133	GPR133, Homo sapiens G protein-coupled receptor 133 (GPR133), q24.33
SNP_A-2204371	ccagcctttatgaagc[A/C]cttactgtgtaccaga	A	C	NM_152235 // intron // 0 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila) (SFRS8), transcript varia /// NM_004592 // intron // 0 // Hs.308171 // SFRS8 // 6433 // Homo s	SFRS8	SFRS8, Homo sapiens splicing factor, arginine,q24.33
SNP_A-2236989	ctctatgaagcaaata[C/T]agttgttgccagatgt	C	T	NM_152235 // intron // 0 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila) (SFRS8), transcript varia /// NM_004592 // intron // 0 // Hs.308171 // SFRS8 // 6433 // Homo s	SFRS8	SFRS8, Homo sapiens splicing factor, arginine,q24.33
SNP_A-2064227	aattcacacgagatta[A/C]gatcatgcagagatac	A	C	NM_152235 // intron // 0 // Hs.308171 // SFRS8 // 6433 // Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila) (SFRS8), transcript varia /// NM_004592 // intron // 0 // Hs.308171 // SFRS8 // 6433 // Homo s	SFRS8	SFRS8, Homo sapiens splicing factor, arginine,q24.33
SNP_A-2202205	ccacattaagaagtga[C/G]gaccatctatcagctc	C	G	ENST00000261673 // intron // 0 // — // — // — // —	-	q24.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2104594	agcaggtgcttcgaga[A/C]agtgtatccacagctg	A	C	NM_006231 // intron // 0 // Hs.524871 // POLE // 5426 // Homo sapiens polymerase (DNA directed), epsilon (POLE), mRNA. /// ENST00000320574 // intron // 0 // — // — // — // —	POLE	POLE, Homo sapiens polymerase (DNA directed), epsilon (POLE), q24.33
SNP_A-2286226	gatgccacacccatga[C/T]gagtcgaagcaaaggg	C	T	NM_018223 // intron // 0 // Hs.507336 // CHFR // 55743 // Homo sapiens checkpoint with forkhead and ring finger domains (CHFR), mRNA. /// BC012072 // intron // 0 // Hs.507336 // CHFR // 55743 // Homo sapiens checkpoint with forkhead and ring finger domain	CHFR	CHFR, Homo sapiens checkpoint with forkhead and ring finger domains (CHFR), q24.33
SNP_A-1727052	cttagtagagaaagatttctttaaa[C/T]ggatacaaaaagcacaaaacataaa	C	T	NM_006001 // downstream // 296477 // Hs.349695 // TUBA2 // 7278 // tubulin, alpha 2 /// NM_079836 // downstream // 296477 // Hs.349695 // TUBA2 // 7278 // tubulin, alpha 2	TUBA2	TUBA2 , rs1855637, tubulin, alpha 2 ,q11
SNP_A-1698981	atcagcctaagaaagaaaagtatcc[C/G]aacttcttcctatgtatgaagttcc	C	G	NM_006001 // downstream // 296126 // Hs.349695 // TUBA2 // 7278 // tubulin, alpha 2 /// NM_079836 // downstream // 296126 // Hs.349695 // TUBA2 // 7278 // tubulin, alpha 2	TUBA2	TUBA2 , rs2801744, tubulin, alpha 2 ,q11
SNP_A-2313899	ggagcctgccagaagg[G/T]agtgagcttgtgctga	G	T	ENST00000344538 // intron // 0 // — // — // — // — // — /// ENST00000343130 // intron // 0 // — // — // — // — // — /// ENST00000338506 // intron // 0 // — // — // — // — // — /// ENST00000344439 // intron // 0 // — // — // — // — // —	-	q12.11
SNP_A-1667208	attggcagtgacttgttacaacagc[A/G]cagacaactcacagagatggcaaag	A	G	NM_003453 // downstream // 27264 // Hs.315241 // ZNF198 // 7750 // zinc finger protein 198 /// NM_021954 // downstream // 27970 // - // - // - // - /// NM_138474 // downstream // 68961 // - // - // - // -	ZNF198	ZNF198 , rs2313626, zinc finger protein 198 ,q12.11
SNP_A-1668134	ctcatgagctccatgaaattgttta[C/T]aaaagtctatgtcaggtcgggcatg	C	T	NM_006783 // upstream // 31963 // Hs.48956 // GJB6 // 10804 // gap junction protein, beta 6 (connexin 30) /// NM_015974 // downstream // 148231 // Hs.108896 // CRYL1 // 51084 // crystallin, lambda 1	GJB6	GJB6 , rs10492508, gap junction protein, beta 6 (connexin 30) ,q12.11
SNP_A-2303588	gctcacaagttcgaga[C/G]cacactggacaacatg	C	G	NM_079836 // upstream // 217041 // Hs.349695 // TUBA2 // 7278 // Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, mRNA. /// NM_006001 // upstream // 217041 // Hs.349695 // TUBA2 // 7278 // Homo sapiens tubulin, alpha 2 (TUBA2), transcript vari	TUBA2	TUBA2, Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, q12.11
SNP_A-1818747	gttgactccataacta[A/C]attccatagtcataaa	A	C	NM_021954 // downstream // 78980 // Hs.533967 // GJA3 // 2700 // Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), mRNA. /// ENST00000360875 // downstream // 17951 // — // — // — // — /// ENST00000241125 // downstream // 7898	GJA3	GJA3, Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), q12.11
SNP_A-2100981	agatattgtcggattc[A/G]atttttttaaaggcaa	A	G	NM_021954 // downstream // 61510 // Hs.533967 // GJA3 // 2700 // Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), mRNA. /// ENST00000360875 // downstream // 35421 // — // — // — // — /// ENST00000241125 // downstream // 6151	GJA3	GJA3, Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), q12.11
SNP_A-2077733	accactgttctggaca[C/T]cacgttattgctcaag	C	T	NM_021954 // upstream // 40896 // Hs.533967 // GJA3 // 2700 // Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), mRNA. /// NM_004004 // downstream // 3291 // Hs.524894 // GJB2 // 2706 // Homo sapiens gap junction protein, beta 2, 26k	GJA3	GJA3, Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), q12.11
SNP_A-1876129	tctgacagtcaagcag[C/T]agtaactgtgctggga	C	T	NM_021954 // upstream // 41033 // Hs.533967 // GJA3 // 2700 // Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), mRNA. /// NM_004004 // downstream // 3154 // Hs.524894 // GJB2 // 2706 // Homo sapiens gap junction protein, beta 2, 26k	GJA3	GJA3, Homo sapiens gap junction protein, alpha 3, 46kDa (connexin 46) (GJA3), q12.11
SNP_A-2145765	atgccactccacttac[C/G]cattcaacaataaact	C	G	NM_006783 // upstream // 56123 // Hs.511757 // GJB6 // 10804 // Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), mRNA. /// NM_006783 // upstream // 55544 // Hs.511757 // GJB6 // 10804 // Homo sapiens gap junction protein, beta 6 (connexin 3	GJB6	GJB6, Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), q12.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2286760	gatggccttgcctttta[C/T]aatgctcagggtttgg	C	T	NM_006783 // upstream // 119468 // Hs.511757 // GJB6 // 10804 // Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), mRNA. /// NM_006783 // upstream // 118889 // Hs.511757 // GJB6 // 10804 // Homo sapiens gap junction protein, beta 6 (connexin	GJB6	GJB6, Homo sapiens gap junction protein, beta 6 (connexin 30) (GJB6), q12.11
SNP_A-2106668	agcctgaacaaaaatc[C/G]agcctaagcaaaaaga	C	G	NM_015974 // intron // 0 // Hs.370703 // CRYL1 // 51084 // Homo sapiens crystallin, lambda 1 (CRYL1), mRNA. /// ENST00000340808 // intron // 0 // — // — // — // — /// ENST00000298248 // intron // 0 // — // — // — // —	CRYL1	CRYL1, Homo sapiens crystallin, lambda 1 (CRYL1), q12.11
SNP_A-2160113	atttatttcgtgaaca[C/T]tgggggttgctttttc	C	T	NM_006531 // intron // 0 // Hs.187376 // TTC10 // 8100 // Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, mRNA. /// NM_175605 // intron // 0 // Hs.187376 // TTC10 // 8100 // Homo sapiens tetratricopeptide repeat domain 10 (T	TTC10	TTC10, Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, q12.11
SNP_A-1784405	ggccctaatcaaggaa[C/T]attcgtttttctcaga	C	T	NM_006531 // intron // 0 // Hs.187376 // TTC10 // 8100 // Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, mRNA. /// NM_175605 // intron // 0 // Hs.187376 // TTC10 // 8100 // Homo sapiens tetratricopeptide repeat domain 10 (T	TTC10	TTC10, Homo sapiens tetratricopeptide repeat domain 10 (TTC10), transcript variant 2, q12.11
SNP_A-2129433	atacaatgcatagtaa[A/G]cctttctcccatataa	A	G	ENST00000255305 // intron // 0 // — // — // — // —	-	q12.11
SNP_A-1723018	ggagagaagacgtttcaagtcccag[C/T]atagaaaacgccagtcctactgctc	C	T	NM_000231 // upstream // 1215547 // Hs.37167 // SGCG // 6445 // sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) /// NM_002010 // downstream // 263360 // Hs.111 // FGF9 // 2254 // fibroblast growth factor 9 (glia-activating factor)	SGCG	SGCG , rs717265, sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) ,q12.11
SNP_A-2150392	atgtctttggtaccaa[C/T]gtattcatatttctgt	C	T	NM_145061 // intron // 0 // Hs.88523 // C13orf3 // 221150 // Homo sapiens chromosome 13 open reading frame 3 (C13orf3), mRNA. /// ENST00000298260 // intron // 0 // — // — // — // — /// ENST00000314759 // intron // 0 // — // — // — // —	C13orf3	C13orf3, Homo sapiens chromosome 13 open reading frame 3 (C13orf3), q12.11
SNP_A-1664008	aactttctcaactggataacgaata[C/T]ctacaaaagaacttatagctaacac	C	T	NM_000231 // upstream // 764414 // Hs.37167 // SGCG // 6445 // sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) /// NM_002010 // downstream // 714493 // Hs.111 // FGF9 // 2254 // fibroblast growth factor 9 (glia-activating factor)	SGCG	SGCG , rs1577359, sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) ,q12.11
SNP_A-2150111	atgtcctagctaaaat[C/T]atagtttcctccacgt	C	T	NM_153251 // intron // 0 // Hs.24283 // FLJ25952 // 253832 // Homo sapiens hypothetical protein FLJ25952 (FLJ25952), mRNA. /// ENST00000320220 // intron // 0 // — // — // — // —	FLJ25952	FLJ25952, Homo sapiens hypothetical protein FLJ25952 (FLJ25952), q12.11
SNP_A-1925306	ttatctaagaaagcac[G/T]gactacaatgtattta	G	T	NM_152726 // intron // 0 // Hs.412103 // EFHA1 // 221154 // Homo sapiens EF hand domain family A1 (EFHA1), mRNA. /// ENST00000298285 // intron // 0 // — // — // — // —	EFHA1	EFHA1, Homo sapiens EF hand domain family A1 (EFHA1), q12.11
SNP_A-2214052	cctaagggactttaac[C/T]agaattcttctttttt	C	T	NM_003868 // downstream // 71986 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 71986 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor) (F	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1856629	tcacagtgtggattaa[A/G]gaggaagtgcccacgt	A	G	NM_003868 // downstream // 79581 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 79581 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor) (F	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1882768	tgaaagacttttgaag[A/G]cccaacaaaattgttg	A	G	NM_003868 // downstream // 123845 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 123845 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2112682	gcaatatttttacaaat[A/G]ccagaaatgcgacctttc	A	G	NM_003868 // downstream // 139987 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 139987 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1690015	ctaaaaccatcagtaagacggatca[C/T]gctaagatgaaggct ttttgctcaga	C	T	NM_000231 // upstream // 51537 // Hs.37167 // SGCG // 6445 // sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) /// NM_002010 // downstream // 1427370 // Hs.111 // FGF9 // 2254 // fibroblast growth factor 9 (glia-activating factor)	SGCG	SGCG , rs9317499, sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) ,q12.12
SNP_A-1719037	ttggtatttctcgttatcaagcatag[G/T]gtggtatagtagcagaagt caaaaa	G	T	NM_000231 // upstream // 37438 // Hs.37167 // SGCG // 6445 // sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) /// NM_002010 // downstream // 1441469 // Hs.111 // FGF9 // 2254 // fibroblast growth factor 9 (glia-activating factor)	SGCG	SGCG , rs10507325, sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) ,q12.12
SNP_A-1749271	cgatcaagtaatttttgagtgaaaa[C/T]atcaagtagataaaaat cccaagaa	C	T	NM_000231 // upstream // 36511 // Hs.37167 // SGCG // 6445 // sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) /// NM_002010 // downstream // 1442396 // Hs.111 // FGF9 // 2254 // fibroblast growth factor 9 (glia-activating factor)	SGCG	SGCG , rs7983559, sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) ,q12.12
SNP_A-2112919	tgcatacagatgcata[C/T]aagtgttaaacaata	C	T	NM_003868 // downstream // 371189 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 371189 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1918103	ttaaacccagtaagga[C/T]ctgaacagtagacat	C	T	NM_003868 // downstream // 413940 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 413940 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1780830	ggatctggctcttga[A/G]caaatgttagaagttt	A	G	NM_003868 // downstream // 509353 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 509353 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2151120	atgtgtgtaaagatgct[C/T]atttagtgagtttgct	C	T	NM_003868 // downstream // 593396 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 593396 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2249791	cttaatgtttaatata[C/T]gtataatgcactatgt	C	T	NM_003868 // downstream // 693004 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 693004 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2041605	aacgatttcagctacc[A/G]ggaaaagattaccctgc	A	G	NM_003868 // downstream // 813500 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 813500 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2055340	aataagctcgtggata[A/G]gaaacacgttatgcct	A	G	NM_003868 // downstream // 946903 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 946903 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor)	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113392	tgtgcaaatctgtcga[C/T]aacttcttctactc	C	T	NM_003868 // downstream // 1003067 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1003067 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2113395	tatttataaaatcttc[A/G]atggcctctgtgcaaa	A	G	NM_003868 // downstream // 1003092 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1003092 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2113398	cttgaaattgactcag[A/G]caaatggtagactgta	A	G	NM_003868 // downstream // 1005524 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1005524 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-1903832	tgggatcacaatggaa[A/G]gaagtaacagtagaaa	A	G	NM_003868 // downstream // 1017527 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1017527 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.11
SNP_A-2166671	caagaaggagattaaa[A/G]atatgcagcccaagg	A	G	NM_003868 // downstream // 1052875 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1052875 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-1871447	tctaacattcctggtat[A/G]cacggtcacagcaaac	A	G	NM_003868 // downstream // 1052994 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1052994 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-1820648	gtttcactctgttcct[C/G]actcttccttcagcgc	C	G	NM_003868 // downstream // 1074154 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1074154 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-1936059	ttcttagtgtagtaa[A/G]ccagtattccaatcca	A	G	NM_003868 // downstream // 1074322 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1074322 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2122876	agtggccataaaactc[A/G]acatttacacattat	A	G	NM_003868 // downstream // 1112941 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1112941 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2053212	aagtcttcgagggtac[A/C]aaacaaggaactatgg	A	C	NM_003868 // downstream // 1120139 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1120139 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2083870	actactagggcagatc[C/T]caactgattagagatg	C	T	NM_003868 // downstream // 1173384 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1173384 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2061360	aatgccccagctcttc[C/G]caatttcctaacatac	C	G	NM_003868 // downstream // 1398916 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1398916 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-2179056	cactgctgcacatcta[A/G]gatatattctctaaca	A	G	NM_003868 // downstream // 1471068 // Hs.534376 // FGF16 // 8823 // Homo sapiens fibroblast growth factor 16 (FGF16), mRNA. /// NM_002010 // downstream // 1471068 // Hs.111 // FGF9 // 2254 // Homo sapiens fibroblast growth factor 9 (glia-activating factor	FGF16	FGF16, Homo sapiens fibroblast growth factor 16 (FGF16), q12.12
SNP_A-1843285	tagtctcaacatagac[A/G]acttagaggtcattga	A	G	NM_000231 // intron // 0 // Hs.37167 // SGCG // 6445 // Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), mRNA. /// ENST00000218867 // intron // 0 // — // — // — // —	SGCG	SGCG, Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), q12.12
SNP_A-2241730	ctgatcatctttcaac[C/G]gatgctcccacagcct	C	G	NM_000231 // intron // 0 // Hs.37167 // SGCG // 6445 // Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), mRNA. /// ENST00000218867 // intron // 0 // — // — // — // —	SGCG	SGCG, Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), q12.12
SNP_A-2273929	gactgtcaaaagccac[A/G]atggacagcattcata	A	G	NM_000231 // intron // 0 // Hs.37167 // SGCG // 6445 // Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), mRNA. /// ENST00000218867 // intron // 0 // — // — // — // —	SGCG	SGCG, Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), q12.12
SNP_A-1809345	gtgactgtaaatgcgc[A/G]caactcagaaggggag	A	G	NM_000231 // CDS // 0 // Hs.37167 // SGCG // 6445 // Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), mRNA. /// ENST00000218867 // CDS // 0 // — // — // — // —	SGCG	SGCG, Homo sapiens sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG), q12.12
SNP_A-2021576	aaaaaatctacctatc[A/G]caggcaatctctaggg	A	G	NM_014363 // upstream // 148833 // Hs.159492 // SACS // 26278 // Homo sapiens spastic ataxia of Charlevoix-Saguenay (sacsin) (SACS), mRNA. /// NM_148957 // upstream // 53264 // Hs.149168 // TNFRSF19 // 55504 // Homo sapiens tumor necrosis factor receptor	SACS	SACS, Homo sapiens spastic ataxia of Charlevoix-Saguenay (sacsin) (SACS), q12.12
SNP_A-2250477	cttaggccaatgccta[A/G]cacttactaaatagcc	A	G	NM_148957 // intron // 0 // Hs.149168 // TNFRSF19 // 55504 // Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 2, mRNA. /// ENST00000248484 // intron // 0 // — // — // — // —	TNFRSF19	TNFRSF19, Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 2, q12.12
SNP_A-2195024	catgcttgtggaatac[A/G]gtaaaccaggcatcat	A	G	NM_148957 // intron // 0 // Hs.149168 // TNFRSF19 // 55504 // Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 2, mRNA. /// NM_018647 // intron // 0 // Hs.149168 // TNFRSF19 // 55504 // Homo sapiens tumor n	TNFRSF19	TNFRSF19, Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 2, q12.12
SNP_A-2139409	atccttaacagccttc[A/G]atgttgtctgtgttct	A	G	NM_148957 // intron // 0 // Hs.149168 // TNFRSF19 // 55504 // Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 2, mRNA. /// NM_018647 // intron // 0 // Hs.149168 // TNFRSF19 // 55504 // Homo sapiens tumor n	TNFRSF19	TNFRSF19, Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 2, q12.12
SNP_A-2024685	aaaagtacataataaa[C/G]gtataagactgagatg	C	G	NM_005932 // intron // 0 // Hs.507498 // MIPEP // 4285 // Homo sapiens mitochondrial intermediate peptidase (MIPEP), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000028585 // intron // 0 // — // — // — // —	MIPEP	MIPEP, Homo sapiens mitochondrial intermediate peptidase (MIPEP), nuclear gene encoding mitochondrial protein, q12.12
SNP_A-2265996	gaaggatggaagataa[A/C]aaatgcatgtggacac	A	C	NM_207439 // upstream // 115991 // Hs.524916 // FLJ46358 // 400110 // Homo sapiens FLJ46358 protein (FLJ46358), mRNA. /// NM_153023 // upstream // 97975 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// N	FLJ46358	FLJ46358, Homo sapiens FLJ46358 protein (FLJ46358), q12.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2114730	gcccaagtcccaactc[A/G]gaggtcctaagtagac	A	G	NM_207439 // upstream // 206299 // Hs.524916 // FLJ46358 // 400110 // Homo sapiens FLJ46358 protein (FLJ46358), mRNA. /// NM_153023 // upstream // 7667 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// NM	FLJ46358	FLJ46358, Homo sapiens FLJ46358 protein (FLJ46358), q12.12
SNP_A-2276238	gagagaggtgaagaaa[A/G]gtttgaagctagtaga	A	G	NM_153023 // intron // 0 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// ENST00000360220 // intron // 0 // — // — // — /// ENST00000266929 // intron // 0 // — // — // —	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2185923	caggcaagaatcagga[C/T]agggtaatttctgggg	C	T	NM_153023 // intron // 0 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// ENST00000360220 // intron // 0 // — // — // — /// ENST00000266929 // intron // 0 // — // — // —	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2248249	ctgtggtttctcccaa[C/T]ggcagcaacttcaggg	C	T	NM_153023 // intron // 0 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// ENST00000360220 // intron // 0 // — // — // — /// ENST00000266929 // intron // 0 // — // — // —	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-1915745	tgttctgatgggttc[C/T]attttattttgcccct	C	T	NM_153023 // intron // 0 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// ENST00000360220 // intron // 0 // — // — // — /// ENST00000266929 // intron // 0 // — // — // —	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2245170	ctggcctttcatgccd[A/G]acgagattctcatgta	A	G	NM_153023 // downstream // 53939 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// NM_178540 // downstream // 36075 // Hs.362854 // MGC48915 // 338872 // Homo sapiens hypothetical protein MGC48915 (MGC489	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2311238	ggaataaaatatctgtct[A/G]ctcacaaccccctgagt	A	G	NM_153023 // downstream // 83104 // Hs.131017 // SPATA13 // 221178 // Homo sapiens spermatogenesis associated 13 (SPATA13), mRNA. /// NM_178540 // downstream // 65240 // Hs.362854 // MGC48915 // 338872 // Homo sapiens hypothetical protein MGC48915 (MGC489	SPATA13	SPATA13, Homo sapiens spermatogenesis associated 13 (SPATA13), q12.12
SNP_A-2115063	tacttccagaaagcac[A/G]ggatactgtcatctt	A	G	NM_006437 // CDS // 0 // Hs.117825 // PARP4 // 143 // Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA. /// ENST00000218883 // CDS // 0 // — // — // —	PARP4	PARP4, Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), q12.12
SNP_A-2078463	accatctatgtaacct[A/C]aaatctgtcatctgta	A	C	NM_006437 // upstream // 25428 // Hs.117825 // PARP4 // 143 // Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA. /// NM_001676 // upstream // 142313 // Hs.147111 // ATP12A // 479 // Homo sapiens ATPase, H+/K+ transporting, nongastr	PARP4	PARP4, Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), q12.12
SNP_A-2091851	agaaaatgccagaata[C/G]aacacgaatgcctatt	C	G	NM_006437 // upstream // 30889 // Hs.117825 // PARP4 // 143 // Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), mRNA. /// NM_001676 // upstream // 136852 // Hs.147111 // ATP12A // 479 // Homo sapiens ATPase, H+/K+ transporting, nongastr	PARP4	PARP4, Homo sapiens poly (ADP-ribose) polymerase family, member 4 (PARP4), q12.12
SNP_A-2184785	cagctgcctggaggat[C/T]aggagagacttcccca	C	T	NM_001676 // intron // 0 // Hs.147111 // ATP12A // 479 // Homo sapiens ATPase, H+/K+ transporting, nongastric, alpha polypeptide (ATP12A), mRNA. /// ENST00000218548 // intron // 0 // — // — // —	ATP12A	ATP12A, Homo sapiens ATPase, H+ q12.12
SNP_A-2299447	gcccttaaaatcacca[C/T]gccaggtaagtgtcc	C	T	AL390129 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// ENST00000281620 // intron // 0 // — // — // —	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912), q12.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2116047	ccatctgtagcctaaa[A/G]acaatgttgccaaggg	A	G	AL390129 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // intron // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase, aminophospholipid transporter-like, Class I.	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912), q12.13
SNP_A-1818724	gttgaccaccccgatat[G/T]agaatttgtgattic	G	T	AL390129 // 3UTR // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // 3UTR // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912), q12.13
SNP_A-1913193	tgtggctaaggagttc[A/C]aataaatgttctcagg	A	C	AL390129 // 3UTR // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens mRNA; cDNA DKFZp761K0912 (from clone DKFZp761K0912). /// NM_016529 // 3UTR // 0 // Hs.444957 // ATP8A2 // 51761 // Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type	ATP8A2	ATP8A2, Homo sapiens cDNA DKFZp761K0912 (from clone DKFZp761K0912), q12.13
SNP_A-2267875	gaatcctagcttcctat[A/G]atagttggtaaaatgt	A	G	NM_001260 // downstream // 66560 // Hs.382306 // CDK8 // 1024 // Homo sapiens cyclin-dependent kinase 8 (CDK8), mRNA. /// NM_006646 // upstream // 86758 // Hs.82318 // WASF3 // 10810 // Homo sapiens WAS protein family, member 3 (WASF3), mRNA. /// ENST0000	CDK8	CDK8, Homo sapiens cyclin-dependent kinase 8 (CDK8), q12.13
SNP_A-2296181	gcattctatatcgtaa[A/G]ctctgcaaacctccac	A	G	NM_001260 // downstream // 67370 // Hs.382306 // CDK8 // 1024 // Homo sapiens cyclin-dependent kinase 8 (CDK8), mRNA. /// NM_006646 // upstream // 85948 // Hs.82318 // WASF3 // 10810 // Homo sapiens WAS protein family, member 3 (WASF3), mRNA. /// ENST0000	CDK8	CDK8, Homo sapiens cyclin-dependent kinase 8 (CDK8), q12.13
SNP_A-2117182	atcttgaagaagaaaaa[C/T]gtctttcaaaatatta	C	T	NM_006646 // intron // 0 // Hs.82318 // WASF3 // 10810 // Homo sapiens WAS protein family, member 3 (WASF3), mRNA. /// ENST00000361042 // intron // 0 // — // — // ENST00000335327 // intron // 0 // — // — // — // —	WASF3	WASF3, Homo sapiens WAS protein family, member 3 (WASF3), q12.13
SNP_A-2066319	aattttctaatgatta[C/G]gataggaaaaatagca	C	G	NM_006646 // downstream // 22742 // Hs.82318 // WASF3 // 10810 // Homo sapiens WAS protein family, member 3 (WASF3), mRNA. /// NM_005288 // downstream // 47155 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. ///	WASF3	WASF3, Homo sapiens WAS protein family, member 3 (WASF3), q12.13
SNP_A-2220083	ccttcacaaaacttac[A/T]gcaatcacaattgttg	A	T	NM_005288 // upstream // 24816 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 24816 // — // — // — // — /// ENST00000359449 // downstream // 232908 // — // — // —	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-2195066	catggaaatgtcctaa[C/T]agtcctgtctcagag	C	T	NM_005288 // upstream // 82287 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 82287 // — // — // — // — /// ENST00000359449 // downstream // 175437 // — // — // —	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-2087368	actgcagcttccatta[A/G]atgtaaatactctt	A	G	NM_005288 // upstream // 143142 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 143142 // — // — // — // — /// ENST00000359449 // downstream // 114582 // — // — // -	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-2260930	gaaacttctgtgacac[A/G]gctccaaaaggtgcct	A	G	NM_005288 // upstream // 146237 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 146237 // — // — // — // — /// ENST00000359449 // downstream // 111487 // — // — // -	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-2088803	actgttactgttcaca[G/T]agcaagttagtttagt	G	T	NM_005288 // upstream // 177938 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 177938 // — // — // — // — /// ENST00000359449 // downstream // 79786 // — // — // —	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1799853	gtacaccatagtggga[C/T]agggtgccaggagacc	C	T	NM_005288 // upstream // 231598 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 231598 // --- // --- // --- /// ENST00000359449 // downstream // 26126 // --- // --- // --	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-1944024	ttgtatttcctagctc[C/G]atccactgaaagagct	C	G	NM_005288 // upstream // 250338 // Hs.123034 // GPR12 // 2835 // Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA. /// ENST00000255329 // upstream // 250338 // --- // --- // --- /// ENST00000359449 // downstream // 7386 // --- // --- // --	GPR12	GPR12, Homo sapiens G protein-coupled receptor 12 (GPR12), q12.13
SNP_A-1901566	tggcaaaatttccca[A/G]ctcctctttgtttcaa	A	G	NM_206827 // downstream // 21451 // Hs.192131 // RASL11A // 387496 // Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA. /// NM_002097 // upstream // 129403 // Hs.445977 // GTF3A // 2971 // Homo sapiens general transcription factor IIIA (GTF3A),	RASL11A	RASL11A, Homo sapiens RAS-like, family 11, member A (RASL11A), q12.2
SNP_A-2265182	gaagattataatgaag[C/T]agaaaaagtcctactg	C	T	NM_206827 // downstream // 52850 // Hs.192131 // RASL11A // 387496 // Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA. /// NM_002097 // upstream // 98004 // Hs.445977 // GTF3A // 2971 // Homo sapiens general transcription factor IIIA (GTF3A), m	RASL11A	RASL11A, Homo sapiens RAS-like, family 11, member A (RASL11A), q12.2
SNP_A-2168309	caactgggataaaatac[A/G]acagaagtgagcgcag	A	G	NM_206827 // downstream // 100148 // Hs.192131 // RASL11A // 387496 // Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA. /// NM_002097 // upstream // 50706 // Hs.445977 // GTF3A // 2971 // Homo sapiens general transcription factor IIIA (GTF3A),	RASL11A	RASL11A, Homo sapiens RAS-like, family 11, member A (RASL11A), q12.2
SNP_A-2139197	atcctctaggcttcgg[A/G]atttttgtaaagctctc	A	G	NM_206827 // downstream // 150534 // Hs.192131 // RASL11A // 387496 // Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA. /// NM_002097 // upstream // 320 // Hs.445977 // GTF3A // 2971 // Homo sapiens general transcription factor IIIA (GTF3A), mR	RASL11A	RASL11A, Homo sapiens RAS-like, family 11, member A (RASL11A), q12.2
SNP_A-1902355	tggcccatcacactaa[C/G]aaccagaagatctgca	C	G	NM_145657 // downstream // 108551 // Hs.351785 // GSH1 // 219409 // Homo sapiens GS homeobox 1 (GSH1), mRNA. /// NM_000209 // upstream // 17537 // Hs.32938 // IPF1 // 3651 // Homo sapiens insulin promoter factor 1, homeodomain transcription factor (IPF1),	GSH1	GSH1, Homo sapiens GS homeobox 1 (GSH1), q12.2
SNP_A-2083484	actaagggctggaag[A/G]catcaagaaaggctgt	A	G	NM_145657 // downstream // 111596 // Hs.351785 // GSH1 // 219409 // Homo sapiens GS homeobox 1 (GSH1), mRNA. /// NM_000209 // upstream // 14492 // Hs.32938 // IPF1 // 3651 // Homo sapiens insulin promoter factor 1, homeodomain transcription factor (IPF1),	GSH1	GSH1, Homo sapiens GS homeobox 1 (GSH1), q12.2
SNP_A-1804463	gtcagacaactggaga[A/G]gaaacttaatgcaaca	A	G	NM_145657 // downstream // 112267 // Hs.351785 // GSH1 // 219409 // Homo sapiens GS homeobox 1 (GSH1), mRNA. /// NM_000209 // upstream // 13821 // Hs.32938 // IPF1 // 3651 // Homo sapiens insulin promoter factor 1, homeodomain transcription factor (IPF1),	GSH1	GSH1, Homo sapiens GS homeobox 1 (GSH1), q12.2
SNP_A-2281620	gagtctcaagactcca[A/G]tgcaaatgatgaaggc	A	G	NM_145657 // downstream // 116870 // Hs.351785 // GSH1 // 219409 // Homo sapiens GS homeobox 1 (GSH1), mRNA. /// NM_000209 // upstream // 9218 // Hs.32938 // IPF1 // 3651 // Homo sapiens insulin promoter factor 1, homeodomain transcription factor (IPF1),	GSH1	GSH1, Homo sapiens GS homeobox 1 (GSH1), q12.2
SNP_A-2043321	aactggaattccatac[A/G]ctgcgagtgggaacat	A	G	NM_004119 // intron // 0 // Hs.507590 // FLT3 // 2322 // Homo sapiens fms-related tyrosine kinase 3 (FLT3), mRNA. /// ENST00000241453 // intron // 0 // --- // --- // --- // ---	FLT3	FLT3, Homo sapiens fms-related tyrosine kinase 3 (FLT3), q12.2
SNP_A-2134371	atatggaaaatgaaga[G/T]cacaaaaataaacctt	G	T	NM_175854 // intron // 0 // Hs.369984 // PAN3 // 255967 // Homo sapiens PABP1-dependent poly A-specific ribonuclease subunit PAN3 (PAN3), mRNA. /// ENST00000282391 // intron // 0 // --- // --- // --- // ---	PAN3	PAN3, Homo sapiens PABP1-dependent poly A-specific ribonuclease subunit PAN3 (PAN3), q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2045000	aagaacgtgttcgccc[A/G]gaggttaggcgatttg	A	G	NM_002019 // upstream // 69266 // Hs.507621 // FLT1 // 2321 // Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mR /// NM_015932 // upstream // 94753 // Hs.268742 // C13orf12 //	FLT1	FLT1, Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factor,q12.3
SNP_A-1805022	gtcatctacagtgaaa[A/T]gtcaaaggagaattaa	A	T	NM_181785 // upstream // 17356 // Hs.117167 // LOC283537 // 283537 // Homo sapiens hypothetical protein LOC283537 (LOC283537), mRNA. /// ENST00000266943 // upstream // 17356 // — // — // — // — /// ENST00000255289 // upstream // 288984 // — // -	LOC283537	LOC283537, Homo sapiens hypothetical protein LOC283537 (LOC283537), q12.3
SNP_A-2208617	cccactgattacaaac[A/G]atggaacttaaacaag	A	G	NM_181785 // upstream // 246340 // Hs.117167 // LOC283537 // 283537 // Homo sapiens hypothetical protein LOC283537 (LOC283537), mRNA. /// ENST00000266943 // upstream // 246340 // — // — // — // — /// ENST00000255289 // upstream // 60000 // — //	LOC283537	LOC283537, Homo sapiens hypothetical protein LOC283537 (LOC283537), q12.3
SNP_A-2238147	ctctgcctacagataa[C/T]gcttttacatctctag	C	T	ENST00000255289 // intron // 0 // — // — // — // —	-	q12.3
SNP_A-1950171	tttcactgtgcattca[A/G]caaacaaaattgtcct	A	G	ENST00000255289 // intron // 0 // — // — // — // —	-	q12.3
SNP_A-2160434	atttcattaatttgcc[C/T]aaagtcacaggtgata	C	T	ENST00000255289 // intron // 0 // — // — // --- // ---	-	q12.3
SNP_A-2258387	cttttccaaatgtaaa[C/T]gtcagctataacaact	C	T	ENST00000255289 // intron // 0 // — // — // — // —	-	q12.3
SNP_A-2188488	cagtgacctgctgaaa[A/G]tcactctgtctctact	A	G	NM_003045 // upstream // 11782 // Hs.14846 // SLC7A1 // 6541 // Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// NM_007106 // downstream // 157142 // Hs.145575 // UBL3 // 5412 // Homo sapiens	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-2103064	agcaaatcagcagtta[C/T]attgactattacatca	C	T	NM_003045 // upstream // 17387 // Hs.14846 // SLC7A1 // 6541 // Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// NM_007106 // downstream // 151537 // Hs.145575 // UBL3 // 5412 // Homo sapiens	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-2077847	accagagacttaggtc[C/T]gaagcaaagagctgtg	C	T	NM_003045 // upstream // 29407 // Hs.14846 // SLC7A1 // 6541 // Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA. /// NM_007106 // downstream // 139517 // Hs.145575 // UBL3 // 5412 // Homo sapiens	SLC7A1	SLC7A1, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), q12.3
SNP_A-2166720	caaattcatattctta[A/C]caattccttttggta	A	C	NM_007106 // intron // 0 // Hs.145575 // UBL3 // 5412 // Homo sapiens ubiquitin-like 3 (UBL3), mRNA. /// ENST00000241470 // intron // 0 // --- // - - // — // —	UBL3	UBL3, Homo sapiens ubiquitin-like 3 (UBL3), q12.3
SNP_A-2157364	attgagcaactactac[A/G]agctgaaccctgatga	A	G	NM_007106 // upstream // 15134 // Hs.145575 // UBL3 // 5412 // Homo sapiens ubiquitin-like 3 (UBL3), mRNA. /// ENST00000241470 // upstream // 15134 // — // — // — // — /// ENST00000241471 // upstream // 72646 // — // — // — // ---	UBL3	UBL3, Homo sapiens ubiquitin-like 3 (UBL3), q12.3
SNP_A-2122874	agtggccagcagagca[A/C]ggatttttttctagaag	A	C	ENST00000241471 // intron // 0 // --- // --- // --- // ---	-	q12.3
SNP_A-2052899	aagtcatctacttaac[A/C]ctcagttctagaattg	A	C	NM_032116 // downstream // 87004 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000241471 // downstream // 171111 // — // — // — // — /// ENST00000261628 // downstream // 87004 // — // –	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-2216648	cctctcagcgctttcc[A/G]catctcttcaggggct	A	G	NM_032116 // downstream // 83425 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000241471 // downstream // 174690 // — // — // — // — /// ENST00000261628 // downstream // 83425 // — // –	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2176299	caccaggataagtagg[C/G]cacttttctgagcatc	C	G	NM_032116 // downstream // 83281 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000241471 // downstream // 174834 // — // — // — // — /// ENST00000261628 // downstream // 83281 // — // –	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-1905145	tgggtgggctctaatc[C/G]aacatgactggtgtcc	C	G	NM_032116 // intron // 0 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000261628 // intron // 0 // --- // — // — // —	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-1810911	gtgcatcagctcaagg[C/T]aactggtgtggctctg	C	T	NM_032116 // upstream // 61371 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000261628 // upstream // 61371 // — // — // — // — /// ENST00000302464 // upstream // 59173 // --- // — // –	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-1899380	tggaactccacagcca[A/G]aagattagacgttgtt	A	G	NM_032116 // upstream // 64707 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000261628 // upstream // 64707 // — // — // — // — /// ENST00000302464 // upstream // 55837 // — // — // –	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-1881529	tctttctggtagagga[G/T]cctatttgggaaacaa	G	T	NM_032116 // upstream // 95261 // Hs.119672 // KATNAL1 // 84056 // Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), mRNA. /// ENST00000261628 // upstream // 95261 // — // — // — // — /// ENST00000302464 // upstream // 25283 // — // — // –	KATNAL1	KATNAL1, Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), q12.3
SNP_A-1866887	tccctacattaaggaa[A/G]tacgacaaacacgagg	A	G	NM_002128 // intron // 0 // Hs.434102 // HMGB1 // 3146 // Homo sapiens high-mobility group box 1 (HMGB1), mRNA. /// ENST00000341423 // intron // 0 // — // — // — // —	HMGB1	HMGB1, Homo sapiens high-mobility group box 1 (HMGB1), q12.3
SNP_A-2268282	gaatgataggtagtta[C/T]acagagagaatcccta	C	T	NM_002128 // intron // 0 // Hs.434102 // HMGB1 // 3146 // Homo sapiens high-mobility group box 1 (HMGB1), mRNA. /// ENST00000341423 // intron // 0 // — // — // — // —	HMGB1	HMGB1, Homo sapiens high-mobility group box 1 (HMGB1), q12.3
SNP_A-2133511	atatcaaaatctgcat[A/G]agcagcccaggtgaga	A	G	NM_002128 // intron // 0 // Hs.434102 // HMGB1 // 3146 // Homo sapiens high-mobility group box 1 (HMGB1), mRNA. /// ENST00000341423 // intron // 0 // — // — // — // —	HMGB1	HMGB1, Homo sapiens high-mobility group box 1 (HMGB1), q12.3
SNP_A-2223477	cgcttctgaagattta[A/T]gagagagcggtcacat	A	T	NM_005800 // downstream // 48009 // Hs.533831 // C13orf22 // 10208 // Homo sapiens chromosome 13 open reading frame 22 (C13orf22), mRNA. /// NM_001629 // upstream // 27974 // Hs.507658 // ALOX5AP // 241 // Homo sapiens arachidonate 5-lipoxygenase-activati	C13orf22	C13orf22, Homo sapiens chromosome 13 open reading frame 22 (C13orf22), q12.3
SNP_A-1738625	atctggctacccacacctggattta[G/T]gttcccatggcccacaa ctgaaaag	G	T	NM_145293 // intron // 0 // Hs.352186 // LOC196549 // 196549 // similar to hypothetical protein FLJ20897	LOC196549	LOC196549 , rs9315149, similar to hypothetical protein FLJ20897,q13.1
SNP_A-1910754	tgtcgcctttgtttca[A/G]cgccttcagtctcccc	A	G	NM_001629 // downstream // 107334 // Hs.507658 // ALOX5AP // 241 // Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA. /// NM_032849 // upstream // 34438 // Hs.62905 // FLJ14834 // 84935 // Homo sapiens hypothetical protein FLJ14	ALOX5AP	ALOX5AP, Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), q12.3
SNP_A-2077392	accacacttagtcaca[A/G]aaatctttaaaagaat	A	G	NM_152325 // intron // 0 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// ENST00000320096 // intron // 0 // --- // --- // --- // —	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-1838653	tagacaccaccagtcc[C/T]gagctgggcaaccctg	C	T	NM_152325 // intron // 0 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// ENST00000320096 // intron // 0 // — // — // — // —	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2120939	gaggattttagaagaa[C/T]gatggtgtttacagtc	C	T	NM_152325 // intron // 0 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// ENST00000320096 // intron // 0 // --- // --- // --- // —	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1915533	tgttctacatccacct[C/G]aagtgtgcaggccttt	C	G	NM_152325 // downstream // 69508 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 // downstream // 92106 // Hs.36927 // HSPH1 // 10808 // Homo sapiens heat shock 105kDa/110kDa protein 1 (HSPH	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2121021	gcatggacttaccaa[A/G]ctgatctcaggtcaaa	A	G	NM_152325 // downstream // 93004 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 // downstream // 68610 // Hs.36927 // HSPH1 // 10808 // Homo sapiens heat shock 105kDa/110kDa protein 1 (HSPH	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2121027	ggctcaggagacaatga[C/T]gattcagctaacctag	C	T	NM_152325 // downstream // 93707 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 // downstream // 67907 // Hs.36927 // HSPH1 // 10808 // Homo sapiens heat shock 105kDa/110kDa protein 1 (HSPH	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-2288870	gatttacacaccaatc[A/G]caagaaatgactggca	A	G	NM_152325 // downstream // 112926 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 // downstream // 48688 // Hs.36927 // HSPH1 // 10808 // Homo sapiens heat shock 105kDa/110kDa protein 1 (HSP	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-1882083	tcttttttactactac[C/T]ccaacccctcagagc	C	T	NM_152325 // downstream // 134241 // Hs.124463 // MGC40178 // 122046 // Homo sapiens hypothetical protein MGC40178 (MGC40178), mRNA. /// NM_006644 // downstream // 27373 // Hs.36927 // HSPH1 // 10808 // Homo sapiens heat shock 105kDa/110kDa protein 1 (HSP	MGC40178	MGC40178, Homo sapiens hypothetical protein MGC40178 (MGC40178), q12.3
SNP_A-1724424	attccaggccaatatttctttactc[C/T]caattcctctatatatac cacc	C	T	NM_014887 // intron // 0 // Hs.131727 // PFAAP5 // 10443 // phosphonoformate immuno-associated protein 5	PFAAP5	PFAAP5 , rs1952994, phosphonoformate immuno-associated protein 5,q13.1
SNP_A-1841968	tagggaaggaagctac[A/T]ctcctagtataccaga	A	T	NM_194318 // downstream // 191348 // Hs.13205 // B3GTL // 145173 // Homo sapiens beta 3-glycosyltransferase-like (B3GTL), mRNA. /// NM_130806 // upstream // 216669 // Hs.531002 // LGR8 // 122042 // Homo sapiens leucine-rich repeat-containing G protein-cou	B3GTL	B3GTL, Homo sapiens beta 3-glycosyltransferase-like (B3GTL), q12.3
SNP_A-1835553	tacctgttacagac[C/T]atggcttagattc	C	T	NM_194318 // downstream // 257246 // Hs.13205 // B3GTL // 145173 // Homo sapiens beta 3-glycosyltransferase-like (B3GTL), mRNA. /// NM_130806 // upstream // 150771 // Hs.531002 // LGR8 // 122042 // Homo sapiens leucine-rich repeat-containing G protein-cou	B3GTL	B3GTL, Homo sapiens beta 3-glycosyltransferase-like (B3GTL), q12.3
SNP_A-1758319	tccacaatcaattctcattgtatga[G/T]acctaatgtttgaaggtgc tatgct	G	T	NM_004795 // upstream // 117888 // Hs.171062 // KL // 9365 // klotho /// NM_015032 // downstream // 120526 // Hs.168625 // APRIN // 23047 // androgen-induced proliferation inhibitor /// NM_015928 // downstream // 122637 // Hs.168625 // APRIN // 23047 //	KL	KL , -, klotho ,q13.1
SNP_A-1754240	tataatcgcgtgtcttgcatttattc[G/T]cagtgaacttacccccctctc ttcc	G	T	NM_004795 // upstream // 17517 // Hs.171062 // KL // 9365 // klotho /// NM_015032 // downstream // 220897 // Hs.168625 // APRIN // 23047 // androgen-induced proliferation inhibitor /// NM_015928 // downstream // 223008 // Hs.168625 // APRIN // 23047 // a	KL	KL , rs797709, klotho ,q13.1
SNP_A-1946684	tttaacatactgtca[C/T]gagagggtaatactt	C	T	NM_145293 // downstream // 37930 // Hs.507667 // LOC196549 // 196549 // Homo sapiens similar to hypothetical protein FLJ20897 (LOC196549), mRNA. /// NM_023037 // upstream // 202735 // Hs.507669 // 13CDNA73 // 10129 // Homo sapiens hypothetical protein CG0	LOC196549	LOC196549, Homo sapiens similar to hypothetical protein FLJ20897 (LOC196549), q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074397	acatacggcatttaag[A/G]aaatttgtggttagt	A	G	NM_145293 // downstream // 61881 // Hs.507667 // LOC196549 // 196549 // Homo sapiens similar to hypothetical protein FLJ20897 (LOC196549), mRNA. /// NM_023037 // upstream // 178784 // Hs.507669 // 13CDNA73 // 10129 // Homo sapiens hypothetical protein CG0	LOC196549	LOC196549, Homo sapiens similar to hypothetical protein FLJ20897 (LOC196549), q13.1
SNP_A-1870093	tcctgtagagaccac[C/T]gcctgtataatgaatc	C	T	NM_145293 // downstream // 74192 // Hs.507667 // LOC196549 // 196549 // Homo sapiens similar to hypothetical protein FLJ20897 (LOC196549), mRNA. /// NM_023037 // upstream // 166473 // Hs.507669 // 13CDNA73 // 10129 // Homo sapiens hypothetical protein CG0	LOC196549	LOC196549, Homo sapiens similar to hypothetical protein FLJ20897 (LOC196549), q13.1
SNP_A-2290477	gcaactaatagtgcca[A/T]aagtaaaaactacaa	A	T	ENST00000318671 // intron // 0 // — // — // —	-	q13.1
SNP_A-2086688	actgaatagtattgc[C/T]gaagatcgtttaaaa	C	T	ENST00000318671 // intron // 0 // — // — // —	-	q13.1
SNP_A-1930187	ttcattcattcaaaaa[A/C]catgtactgtccatga	A	G	ENST00000318671 // intron // 0 // — // — // —	-	q13.1
SNP_A-1890859	tgatgcctattgatta[C/T]gaatatggttgtcctt	C	T	ENST00000318671 // intron // 0 // — // — // —	-	q13.1
SNP_A-2249097	ctgtttctacgccaca[A/G]taataaacacatcgga	A	G	NM_033111 // intron // 0 // Hs.507680 // LOC88523 // 88523 // Homo sapiens CG016 (LOC88523), mRNA. /// NM_052818 // 5UTR // 0 // Hs.161220 // CG018 // 90634 // Homo sapiens hypothetical gene CG018 (CG018), mRNA. /// ENST00000357505 // intron // 0 // — /	LOC88523	LOC88523, Homo sapiens CG016 (LOC88523), q13.1
SNP_A-2195923	catgtcagggtgctaa[A/G]ccttatccctagaga	A	G	NM_015032 // downstream // 94776 // Hs.369263 // APRIN // 23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream // 94776 // Hs.369263 // APRIN // 23047 // Homo sapiens androgen-induced proliferation inhi	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-2122817	tggagttgatttcaac[C/T]ggactaagccaatttc	C	T	NM_015032 // downstream // 129636 // Hs.369263 // APRIN // 23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream // 129636 // Hs.369263 // APRIN // 23047 // Homo sapiens androgen-induced proliferation in	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-2122835	ttaagctgctacatga[A/C]atgcaaaatcattaag	A	C	NM_015032 // downstream // 133319 // Hs.369263 // APRIN // 23047 // Homo sapiens androgen-induced proliferation inhibitor (APRIN), mRNA. /// NM_015928 // downstream // 133319 // Hs.369263 // APRIN // 23047 // Homo sapiens androgen-induced proliferation in	APRIN	APRIN, Homo sapiens androgen-induced proliferation inhibitor (APRIN), q13.1
SNP_A-2276849	gagatagcaatataaa[C/G]tcagcagcttgcagac	C	G	NM_052851 // upstream // 288323 // Hs.507704 // STARD13 // 90627 // Homo sapiens START domain containing 13 (STARD13), transcript variant gamma. mRNA. /// NM_178007 // upstream // 288323 // Hs.507704 // STARD13 // 90627 // Homo sapiens START domain contai	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.2
SNP_A-2054802	aataaacctgcttcaa[A/C]cttcatcaatcattgt	A	C	NM_052851 // upstream // 440952 // Hs.507704 // STARD13 // 90627 // Homo sapiens START domain containing 13 (STARD13), transcript variant gamma. mRNA. /// NM_178007 // upstream // 440952 // Hs.507704 // STARD13 // 90627 // Homo sapiens START domain contai	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.2
SNP_A-2003226	tccctgtgttacaga[A/C]cttacagaatcatcag	A	C	NM_052851 // upstream // 471355 // Hs.507704 // STARD13 // 90627 // Homo sapiens START domain containing 13 (STARD13), transcript variant gamma. mRNA. /// NM_178007 // upstream // 471355 // Hs.507704 // STARD13 // 90627 // Homo sapiens START domain contai	STARD13	STARD13, Homo sapiens START domain containing 13 (STARD13), transcript variant gamma, q13.2
SNP_A-2235723	ctcctccacccattg[C/T]atataagcctggaggt	C	T	NM_181558 // downstream // 35657 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 35657 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication fac	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1904434	tgggaatctacctac[G/T]catctacatttcctag	G	T	NM_181558 // downstream // 278878 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 278878 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication f	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-2124312	tctggacatatactgta[A/G]ggcttaaccttgaata	A	G	NM_181558 // downstream // 348795 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 348795 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication f	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-2182350	cagagttagagataaa[A/C]gtcacataatgcttag	A	C	NM_181558 // downstream // 857088 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 857088 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication f	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-1936993	ttcttttaacaaagga[C/T]ggcttatttcttatc	C	T	NM_181558 // downstream // 882327 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 882327 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication f	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-2042051	aactactatttactga[A/C]ctagagagaaaaggac	A	C	NM_181558 // downstream // 1037800 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA. /// NM_002915 // downstream // 1037800 // Hs.115474 // RFC3 // 5983 // Homo sapiens replication	RFC3	RFC3, Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, q13.2
SNP_A-2247742	ctgtgacccttgcaa[C/T]gaaccttcaccctgc	C	T	NM_015678 // downstream // 40991 // Hs.491172 // NBEA // 26960 // Homo sapiens neurobeachin (NBEA), mRNA. /// NM_005584 // upstream // 237588 // Hs.532575 // MAB21L1 // 4081 // Homo sapiens mab-21-like 1 (C. elegans) (MAB21L1), mRNA. /// AB002367 // downs	NBEA	NBEA, Homo sapiens neurobeachin (NBEA), q13.3
SNP_A-2125812	tgattaaattatgctc[A/C]caagatcagttcctag	A	C	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-2087122	actgatcagcctgaag[A/T]atcttatagtgccaaa	A	T	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-1823731	taaaatcacatagaaa[G/T]tgccacacaaatgtta	G	T	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-1942290	ttgcatgcctctct[A/G]atcaatatatctttac	A	G	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-2095872	agacagatccgcacct[G/T]aattactatgcctaaa	G	T	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1840827	tagctatttcctcagt[C/T]acaaagaatagtgtgt	C	T	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-1915295	tgttcatcagatctgc[A/G]ctattagagatgagtc	A	G	AB002367 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // intron // 0 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// ENST00000003606	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-2183026	cagatttgatatagcc[A/G]aagaaaagatttagtaa	A	G	AB002367 // upstream // 9113 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens mRNA for KIAA0369 gene, partial cds. /// NM_004734 // upstream // 9113 // Hs.507755 // DCAMKL1 // 9201 // Homo sapiens doublecortin and CaM kinase-like 1 (DCAMKL1), mRNA. /// NM_	DCAMKL1	DCAMKL1, Homo sapiens for KIAA0369 gene, partial cds, q13.3
SNP_A-2052791	aagtcaccccttccta[C/T]gatgcaactgctgtaa	C	T	NM_017826 // CDS // 0 // Hs.124519 // FLJ20449 // 54937 // Homo sapiens hypothetical protein FLJ20449 (FLJ20449), mRNA. /// ENST00000218554 // CDS // 0 // — // — // — // —	FLJ20449	FLJ20449, Homo sapiens hypothetical protein FLJ20449 (FLJ20449), q13.3
SNP_A-1666626	atttgaaaatatacagccagaggaa[A/G]ataagaaaaaaaga ataaaaaaaga	A	G	NM_006475 // downstream // 138065 // Hs.136348 // POSTN // 10631 // periostin, osteoblast specific factor /// NM_145203 // upstream // 318913 // Hs.512897 // CSNK1A1L // 122011 // casein kinase 1, alpha 1-like	POSTN	POSTN , rs1853326, periostin, osteoblast specific factor ,q13.3
SNP_A-2022830	aaaacaaaccaaagaa[A/C]cagatcagttcacaaa	A	C	NM_003914 // upstream // 58807 // Hs.417050 // CCNA1 // 8900 // Homo sapiens cyclin A1 (CCNA1), mRNA. /// ENST00000239854 // downstream // 5465 // — // — // — // — /// ENST00000255465 // upstream // 58807 // — // — // — // —	CCNA1	CCNA1, Homo sapiens cyclin A1 (CCNA1), q13.3
SNP_A-1655265	ctttcttcttgggagtgagagta[C/T]ggactttgtatcaggcag acgtgg	C	T	NM_006475 // downstream // 49634 // Hs.136348 // POSTN // 10631 // periostin, osteoblast specific factor /// NM_145203 // upstream // 407344 // Hs.512897 // CSNK1A1L // 122011 // casein kinase 1, alpha 1-like	POSTN	POSTN, rs9315495, periostin, osteoblast specific factor ,q13.3
SNP_A-1723260	tatcaagaataactaaagccttca[A/T]gtacactatgcaatcc ctagcca	A	T	NM_006475 // upstream // 942 // Hs.136348 // POSTN // 10631 // periostin, osteoblast specific factor /// NM_016179 // downstream // 36979 // Hs.262960 // TRPC4 // 7223 // transient receptor potential cation channel, subfamily C, member 4	POSTN	POSTN , rs1028728, periostin, osteoblast specific factor ,q13.3
SNP_A-1643521	attttaatgctgacacacagagtaa[C/T]aatcccatggcccagc actacgtca	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // transient receptor potential cation channel, subfamily C, member 4	TRPC4	TRPC4, rs7332871, transient receptor potential cation channel, subfamily C, member 4,q13.3
SNP_A-1693913	atctctctatctattgtaaaaa[A/T]gagattagattcaatagtttc ata	A	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // transient receptor potential cation channel, subfamily C, member 4	TRPC4	TRPC4, rs9315508, transient receptor potential cation channel, subfamily C, member 4,q13.3
SNP_A-1698669	gttggcactacaatttagctgttc[A/G]aaataactcatattagcac taatt	A	G	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // transient receptor potential cation channel, subfamily C, member 4	TRPC4	TRPC4, rs1570607, transient receptor potential cation channel, subfamily C, member 4,q13.3
SNP_A-1703483	aacaaaaacttgggccatggtgga[A/T]tcaatctaaaatatatcct ttttgcc	A	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // transient receptor potential cation channel, subfamily C, member 4	TRPC4	TRPC4, rs10507459, transient receptor potential cation channel, subfamily C, member 4,q13.3
SNP_A-2251932	ctccaacattgtgca[C/G]taagtcatttggaatc	C	G	NM_000538 // downstream // 3752 // Hs.24422 // RFXAP // 5994 // Homo sapiens regulatory factor X-associated protein (RFXAP), mRNA. /// NM_005905 // downstream // 14715 // Hs.528630 // SMAD9 // 4093 // Homo sapiens SMAD, mothers against DPP homolog 9 (Dros	RFXAP	RFXAP, Homo sapiens regulatory factor X-associated protein (RFXAP), q13.3
SNP_A-1708506	ttgtaaaactgtccctttcctcad[A/G]tattgtggtatgacatttct cacc	A	G	NM_016179 // upstream // 138243 // Hs.262960 // TRPC4 // 7223 // transient receptor potential cation channel, subfamily C, member 4 /// NM_016617 // upstream // 341840 // Hs.367646 // Utm1 // 51569 // ubiquitin-fold modifier 1	TRPC4	TRPC4, rs2250286, transient receptor potential cation channel, subfamily C, member 4 ,q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2126784	tgacctagatggtccaa[G/T]aaattaagatcactca	G	T	NM_145203 // upstream // 123446 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 123446 // — // — // — /// ENST00000356619 // upstream // 306238 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2024461	aaaaggaaattataaag[C/G]cttcaagcatttttgg	C	G	NM_145203 // upstream // 221825 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 221825 // — // — // — /// ENST00000356619 // upstream // 207859 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2306347	gctgggcactgggctg[C/T]caattctgtggatcag	C	T	NM_145203 // upstream // 236409 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 236409 // — // — // — /// ENST00000356619 // upstream // 193275 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1873183	tctattctctgacttat[C/T]tgctttttttgtatga	C	T	NM_145203 // upstream // 269086 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 269086 // — // — // — /// ENST00000356619 // upstream // 160598 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2124742	agttctgctgcatgag[A/T]ctagagcaccaggtag	A	T	NM_145203 // upstream // 318326 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 318326 // — // — // — /// ENST00000356619 // upstream // 111358 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1952178	tttctcattaatttac[C/T]ggtcattcaggagcat	C	T	NM_145203 // upstream // 321318 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 321318 // — // — // — /// ENST00000356619 // upstream // 108366 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1803441	gtatttgataactgag[A/T]agtcattagcaatctg	A	T	NM_145203 // upstream // 324668 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 324668 // — // — // — /// ENST00000356619 // upstream // 105016 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2111264	aggagcagtcacagta[C/G]agcagtgggtttgaat	C	G	NM_145203 // upstream // 324703 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 324703 // — // — // — /// ENST00000356619 // upstream // 104981 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1785430	ggctcaaacatagaca[A/C]aaactgtcgagtcctg	A	C	NM_145203 // upstream // 328616 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 328616 // — // — // — /// ENST00000356619 // upstream // 101068 // — // –	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2075671	acatggcaaggaacat[C/T]agtggttatgactgat	C	T	NM_145203 // upstream // 360446 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 360446 // — // — // — /// ENST00000356619 // upstream // 69238 // — // —	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1948456	ttagtcatttccacac[C/T]cctttgtagccttct	C	T	NM_145203 // upstream // 360644 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 360644 // — // — // — /// ENST00000356619 // upstream // 69040 // — // —	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2138832	atccctaagtaaggac[A/C]agtgcttgggaattaa	A	C	NM_145203 // upstream // 380854 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 380854 // — // — // — // — /// ENST00000356619 // upstream // 48830 // — // —	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2127077	gcactggaaaagatga[C/T]gacaattgtctaattc	C	T	NM_145203 // upstream // 415268 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 415268 // — // — // — // — /// ENST00000356619 // upstream // 14416 // — // —	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-1816944	gttattctcatacata[C/T]ggagttcacaaaattt	C	T	NM_145203 // upstream // 421414 // Hs.512897 // CSNK1A1L // 122011 // Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), mRNA. /// ENST00000325213 // upstream // 421414 // — // — // — // — /// ENST00000356619 // upstream // 8270 // — // —	CSNK1A1L	CSNK1A1L, Homo sapiens casein kinase 1, alpha 1-like (CSNK1A1L), q13.3
SNP_A-2106002	agcccaaaccctaaga[C/T]tatggagaaccaaaga	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2308568	gctttcaaagaggcta[C/T]cttagggtttatacta	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-1874774	tctcctttaacaatcc[C/T]attaatgtgtaggacg	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2086846	actgactgtctactca[C/T]aggactaagtgaccttt	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-1651846	gtgggcctatcttttactaagagga[A/G]aagaatgtgcagtccca cccacagc	A	G	BX538304 // 3UTR // 0 // Hs.253994 // DKFZp686J0811 // 341640 // hypothetical protein DKFZp686J0811	DKFZp686J0811	DKFZp686J0811 , rs7337135, hypothetical protein DKFZp686J0811,q13.3
SNP_A-1693260	tttaatgttgactttggagttggca[C/T]actggaaaagaattagag gtaagat	C	T	BX538304 // 3UTR // 0 // Hs.253994 // DKFZp686J0811 // 341640 // hypothetical protein DKFZp686J0811	DKFZp686J0811	DKFZp686J0811 , rs2184141, hypothetical protein DKFZp686J0811,q13.3
SNP_A-2214712	cctaggcacactgcca[C/T]gttcttcgtctatgtt	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2067646	acaacaacaacaacta[C/T]gggataaggatataaa	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2273590	gactgactgtgttcca[C/T]agcttaataatgctct	C	T	NM_016179 // intron // 0 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// ENST00000340120 // intron // 0 // — // — // — // — /// ENST00000338947 // intron // 0 // -	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-1922361	ttagaaaagaacaata[A/C]ctaacaataccctaac	A	C	NM_016179 // upstream // 231876 // Hs.262960 // TRPC4 // 7223 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA. /// NM_016617 // upstream // 248173 // Hs.524969 // Ufm1 // 51569 // Homo sapiens ubiquitin-fol	TRPC4	TRPC4, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), q13.3
SNP_A-2228434	ctacttcacaccttgg[A/G]aacatcgtgaacatca	A	G	NM_016617 // downstream // 263689 // Hs.524969 // Ufm1 // 51569 // Homo sapiens ubiquitin-fold modifier 1 (Ufm1), mRNA. /// ENST00000239878 // downstream // 263689 // — // — // — // — /// ENST00000298350 // upstream // 264729 // — // — // —	Ufm1	Ufm1, Homo sapiens ubiquitin-fold modifier 1 (Ufm1), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2165765	caaaggtggtcacaga[A/T]ctatactgcaagtacc	A	T	NM_207361 // intron // 0 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// ENST00000280481 // intron // 0 // — // — // —	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2162501	attttcattcaaccta[A/G]ggaaggatcttaagaa	A	G	NM_207361 // intron // 0 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// ENST00000280481 // intron // 0 // — // — // —	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2187621	cagtaatagctcctaj[A/G]acactcagtatcttttc	A	G	NM_207361 // 3UTR // 0 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// ENST00000280481 // 3UTR // 0 // — // — // —	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-1787030	gggaaaccatgggtaa[A/C]cctttcattgtggtgt	A	C	NM_207361 // downstream // 2473 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 77518 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STOM	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-1644952	atacaggagaaaagctgaggttcaca[A/C]aagtagatttctctcc gacatcct	A	C	AB032960 // downstream // 206268 // Hs.512905 // COG6 // 57511 // component of oligomeric golgi complex 6	COG6	COG6 , rs276420, component of oligomeric golgi complex 6,q14.11
SNP_A-2040458	aaccagggaggactccc[C/T]ctcgcaccaggatctc	C	T	NM_207361 // downstream // 35472 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 44519 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STO	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2185521	caggagaaactgcaga[A/G]ccctcttcatcccaaa	A	G	NM_207361 // downstream // 35704 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 44287 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STO	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2303516	gctcagagagatcaa[A/C]gtacttactctcatga	A	C	NM_207361 // downstream // 56453 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 23538 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STO	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2305872	gctgctcctcattctct[A/G]caaactctgtggatag	A	G	NM_207361 // downstream // 59097 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 20894 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STO	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2128394	tgtcaatatgatgtgg[C/G]agtcgaaaaggtgaaa	C	G	NM_207361 // downstream // 65267 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 14724 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STO	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2288366	gattctctgccttaga[C/T]gagtgttcaggagagc	C	T	NM_207361 // downstream // 66156 // Hs.253994 // FREM2 // 341640 // Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), mRNA. /// NM_145286 // downstream // 13835 // Hs.327794 // STOML3 /// 161003 // Homo sapiens stomatin (EPB72)-like 3 (STO	FREM2	FREM2, Homo sapiens Fras1 related extracellular matrix protein 2 (FREM2), q13.3
SNP_A-2180375	cagaaattgtcattcc[C/T]cttgtcactcagaaga	C	T	NM_005780 // downstream // 236041 // Hs.507798 // LHFP // 10186 // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /// ENST00000344021 // downstream // 57790 // — // — // — // — /// ENST00000328577 // downstream // 236041 // — // — // -	LHFP	LHFP, Homo sapiens lipoma HMGIC fusion partner (LHFP), q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2083147	acgtttgagagatttа[A/G]ggaggaaaaagcaaca	A	G	NM_005780 // downstream // 213886 // Hs.507798 // LHFP // 10186 // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /// ENST00000344021 // downstream // 79945 // — // — // — /// ENST00000328577 // downstream // 213886 // — // — // -	LHFP	LHFP, Homo sapiens lipoma HMGIC fusion partner (LHFP), q13.3
SNP_A-2084326	actataaccgtttgat[A/G]catcacatctcaggta	A	G	NM_005780 // downstream // 130738 // Hs.507798 // LHFP // 10186 // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /// ENST00000344021 // downstream // 163093 // — // — // — /// ENST00000328577 // downstream // 130738 // — // — //	LHFP	LHFP, Homo sapiens lipoma HMGIC fusion partner (LHFP), q13.3
SNP_A-2112792	aggcaggtcctgctaa[A/T]caagtgatcccatgaa	A	T	NM_005780 // downstream // 86459 // Hs.507798 // LHFP // 10186 // Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /// ENST00000344021 // downstream // 207372 // — // — // — /// ENST00000328577 // downstream // 86459 // — // — // —	LHFP	LHFP, Homo sapiens lipoma HMGIC fusion partner (LHFP), q13.3
SNP_A-1758212	tgtttatctagttgctaaatac[A/G]acttatggttcaaagagaaa atgca	A	G	AY116216 // intron // 0 // Hs.287664 // - // - // CDNA: FLJ21437 fis, clone COL04285	-	-, rs1319281, CDNA: FLJ21437 fis, clone COL04285,q14.11
SNP_A-1783932	ggccacatgacacttc[A/G]ctgagtatctacagca	A	G	NM_020751 // intron // 0 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// ENST00000255468 // intron // 0 // — // — // — /// ENST00000356576 // intron // 0 // — // — // —	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-1697735	ggagaaatagtgtacgtgttggaga[G/T]actcagacagggtact aggaaaaat	G	T	NM_172373 // intron // 0 // Hs.124030 // ELF1 // 1997 // E74-like factor 1 (ets domain transcription factor)	ELF1	ELF1, rs9315797, E74-like factor 1 (ets domain transcription factor),q14.11
SNP_A-1856401	tcacactcatacaata[A/G]gcagcaatgccacatc	A	G	NM_020751 // downstream // 173785 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 629403 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-1851907	tatgatatttatttа[C/T]acagcggctattcatt	C	T	NM_020751 // downstream // 315991 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 487197 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2115691	agggtcagatgttaaaa[C/T]ggagacagctggagcc	C	T	NM_020751 // downstream // 412704 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 390484 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2129288	aaggacagggtcacca[C/T]aatttctttcataaga	C	T	NM_020751 // downstream // 415278 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 387910 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-1933203	ttctaaacatgacttа[C/T]agagttttctctggg	C	T	NM_020751 // downstream // 614097 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 189091 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2223670	cggatgcagcaagaaa[C/G]gaagtcaggatgggag	C	G	NM_020751 // downstream // 652337 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 150851 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1878860	tctgtttccttttatta[C/T]catgtaagcttatga	C	T	NM_020751 // downstream // 653390 // Hs.507805 // COG6 // 57511 // Homo sapiens component of oligomeric golgi complex 6 (COG6), mRNA. /// NM_002015 // downstream // 149798 // Hs.370666 // FOXO1A // 2308 // Homo sapiens forkhead box O1A (rhabdomyosarcoma)	COG6	COG6, Homo sapiens component of oligomeric golgi complex 6 (COG6), q14.11
SNP_A-2084665	actattattatctccc[A/G]agtttactatatcata	A	G	NM_172373 // upstream // 6368 // Hs.135646 // ELF1 // 1997 // Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1), mRNA. /// NM_007187 // upstream // 72876 // Hs.411300 // WBP4 // 11193 // Homo sapiens WW domain binding protein 4 (form	ELF1	ELF1, Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1), q14.11
SNP_A-1801106	gtagcagtggcatgtg[A/C]aaaattctgttttaa	A	C	NM_172373 // upstream // 75826 // Hs.135646 // ELF1 // 1997 // Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1), mRNA. /// NM_007187 // upstream // 3418 // Hs.411300 // WBP4 // 11193 // Homo sapiens WW domain binding protein 4 (form	ELF1	ELF1, Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1), q14.11
SNP_A-1700107	agcatctatatgaacgttcaaggat[A/C]ataaaagtaaggtaaa agctttc	A	C	NM_152910 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta /// NM_178009 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta	DGKH	DGKH , rs9315894, diacylglycerol kinase, eta ,q14.11
SNP_A-1675710	tgtcctgtgcctcaggatctctac[C/T]catagttgtattgttttcattt t	C	T	NM_152910 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta /// NM_178009 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta	DGKH	DGKH , rs10492443, diacylglycerol kinase, eta ,q14.11
SNP_A-1665548	ctgcttttctgcagtaatcccata[A/G]ctttctattcacatttctttatg a	A	G	NM_152910 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta /// NM_178009 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta	DGKH	DGKH , rs9315897, diacylglycerol kinase, eta ,q14.11
SNP_A-1727351	aagtgaccttcatccgagtctgaj[A/G]ggaagagtgagaaaag gagcaattt	A	G	NM_152910 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta /// NM_178009 // intron // 0 // Hs.378969 // DGKH // 160851 // diacylglycerol kinase, eta	DGKH	DGKH , rs347413, diacylglycerol kinase, eta ,q14.11
SNP_A-1900081	tggactatgcattggat[A/G]ctaggtggtctttatc	A	G	NM_024561 // downstream // 33580 // Hs.512914 // NARG1L // 79612 // Homo sapiens hypothetical protein FLJ22054 (FLJ22054), transcript variant 1, mRNA. /// NM_018527 // downstream // 33576 // Hs.512914 // NARG1L // 79612 // Homo sapiens hypothetical protei	NARG1L	NARG1L, Homo sapiens hypothetical protein FLJ22054 (FLJ22054), transcript variant 1, q14.11
SNP_A-2242790	ctgcatttccaactga[C/G]gtaccaggccatctta	C	G	NM_014059 // downstream // 69913 // Hs.507866 // RGC32 // 28984 // Homo sapiens response gene to complement 32 (RGC32), mRNA. /// ENST00000341475 // downstream // 69913 // — // — // — /// ENST00000353805 // downstream // 69913 // — // — /	RGC32	RGC32, Homo sapiens response gene to complement 32 (RGC32), q14.11
SNP_A-2053440	aagtgattcattccaa[A/G]catctgatggttccc	A	G	NM_014059 // downstream // 94511 // Hs.507866 // RGC32 // 28984 // Homo sapiens response gene to complement 32 (RGC32), mRNA. /// ENST00000341475 // downstream // 94511 // — // — // — /// ENST00000353805 // downstream // 94511 // — // — /	RGC32	RGC32, Homo sapiens response gene to complement 32 (RGC32), q14.11
SNP_A-1658838	gcagccaagattcaatgcttggaaa[G/T]gaagttaaagttggag gacaaacaa	G	T	NM_003701 // downstream // 143270 // Hs.333791 // TNFSF11 // 8600 // tumor necrosis factor (ligand) superfamily, member 11 /// NM_033012 // downstream // 143270 // Hs.333791 // TNFSF11 // 8600 // tumor necrosis factor (ligand) superfamily, member 11 ///	TNFSF11	TNFSF11 , rs727227, tumor necrosis factor (ligand) superfamily, member 11 ,q14.11
SNP_A-2156955	attctgttctcaaaat[A/G]cttacattctgatcca	A	G	ENST00000251030 // intron // 0 // — // — // —	-	q14.11
SNP_A-2130183	agatgatttcttgtta[C/T]gaagcttacactcatt	C	T	ENST00000251030 // intron // 0 // — // — // —	-	q14.11
SNP_A-1735943	acaacactgtcagttgctgtcctgat[A/G]gaaggtggccaggag ctctagaagg	A	G	AF305819 // upstream // 111584 // - // - // Homo sapiens PRO0777 mRNA, complete cds. /// NM_033255 // downstream // 76359 // Hs.343800 // EPST11 // 94240 // epithelial stromal interaction 1 (breast) /// NM_182508 // downstream // 20080 // Hs.16970 /	-	-, rs7987618, Homo sapiens PRO0777 mRNA, complete cds, q14.11
SNP_A-1845068	tatacacatatgtgac[C/G]ttccactctctggc	C	G	ENST00000251030 // intron // 0 // — // — // — /// ENST00000281496 // intron // 0 // — // — // —	-	q14.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2260796	gaaactatgacagagg[A/G]aaagtaagtgtttaa	A	G	ENST00000251030 // intron // 0 // --- // --- // --- /// ENST00000281496 // intron // 0 // --- // --- // ---	-	q14.11
SNP_A-1925458	ttatctagtttaccaa[C/G]tgaggaggcatctgttc	C	G	ENST00000281496 // intron // 0 // --- // --- // ---	-	q14.11
SNP_A-2172177	caatgtatgaaaatgc[C/T]atttccctgaaactat	C	T	ENST00000281496 // intron // 0 // --- // --- // ---	-	q14.11
SNP_A-2095058	agaatgtcaaattccaa[C/T]ctacctccatgttcat	C	T	NM_152910 // upstream // 51753 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // upstream // 51753 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2201592	ccaattgttggccttc[A/G]acaccagggcaggga	A	G	NM_152910 // upstream // 18648 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // upstream // 18648 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2292835	gcagaaaaggaatcgg[G/T]agtcaaggaaggctgga	G	T	NM_152910 // upstream // 18595 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // upstream // 18595 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2091933	agaaacacaagcagga[A/C]aggatgaaatcagccg	A	C	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2153420	attaggaggagcccaaa[C/T]aaggcaatagcaaga	C	T	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2268643	gaatgtgacatggttc[C/T]ccgccctcaagaatt	C	T	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2130462	gactcaaaggtaactc[A/G]cgagaatactagttc	A	G	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2130516	tgaacctggtagcata[C/G]gcatctcatgatgaca	C	G	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2308450	gctttaagagacactat[C/T]caaatcgtttgtgaga	C	T	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-2288567	gattgcaaagtcctac[C/T]aaccagaaacgtgcaa	C	T	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2020973	aaaaaaaaaaaaaatc[A/G]atgattgccaggagta	A	G	NM_152910 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, mRNA. /// NM_178009 // intron // 0 // Hs.527910 // DGKH // 160851 // Homo sapiens diacylglycerol kinase, eta (DGKH), transcrip	DGKH	DGKH, Homo sapiens diacylglycerol kinase, eta (DGKH), transcript variant 1, q14.11
SNP_A-1892026	tgcaaaagttgagcta[C/T]gattgttatgaacctc	C	T	NM_033012 // upstream // 146472 // Hs.333791 // TNFSF11 // 8600 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, mRNA. /// NM_033012 // upstream // 155395 // Hs.333791 // TNFSF11 // 8600 // Homo sapien	TNFSF11	TNFSF11, Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, q14.11
SNP_A-2167043	caacaagcatttgtaa[A/G]gagaaccagttagcaa	A	G	NM_033012 // downstream // 140167 // Hs.333791 // TNFSF11 // 8600 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, mRNA. /// NM_033012 // downstream // 139327 // Hs.333791 // TNFSF11 // 8600 // Homo sa	TNFSF11	TNFSF11, Homo sapiens tumor necrosis factor (ligand) superfamily, member 11 (TNFSF11), transcript variant 2, q14.11
SNP_A-2131274	tcagagtcttagagat[A/G]gtatcccaggtgactt	A	G	NM_182508 // downstream // 2853 // Hs.16970 // FLJ40919 // 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 91989 // Hs.546467 // EPSTI1 // 94240 // Homo sapiens epithelial stromal interaction 1 (breast	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-1920149	ttaatcctcacccttc[A/G]cagtccagaggctgcc	A	G	NM_182508 // downstream // 5676 // Hs.16970 // FLJ40919 // 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 89166 // Hs.546467 // EPSTI1 // 94240 // Homo sapiens epithelial stromal interaction 1 (breast	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-1918679	ttaaattgttcattga[C/T]gtcccaaacctgaagc	C	T	NM_182508 // downstream // 13817 // Hs.16970 // FLJ40919 // 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 81025 // Hs.546467 // EPSTI1 // 94240 // Homo sapiens epithelial stromal interaction 1 (breas	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-2081576	accttaactccactga[A/G]gatcatgaacaatgct	A	G	NM_182508 // downstream // 13991 // Hs.16970 // FLJ40919 // 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 80851 // Hs.546467 // EPSTI1 // 94240 // Homo sapiens epithelial stromal interaction 1 (breas	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-1953642	tttgaccaatacgtac[C/T]cttaatcggccatctg	C	T	NM_182508 // downstream // 33562 // Hs.16970 // FLJ40919 // 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 61280 // Hs.546467 // EPSTI1 // 94240 // Homo sapiens epithelial stromal interaction 1 (breas	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-1836447	tactcattttagctca[A/C]ctatggtttctaaaac	A	C	NM_182508 // downstream // 92207 // Hs.16970 // FLJ40919 // 144809 // Homo sapiens hypothetical protein FLJ40919 (FLJ40919), mRNA. /// NM_033255 // downstream // 2635 // Hs.546467 // EPSTI1 // 94240 // Homo sapiens epithelial stromal interaction 1 (breast	FLJ40919	FLJ40919, Homo sapiens hypothetical protein FLJ40919 (FLJ40919), q14.11
SNP_A-2232370	ctcacaatttttctac[C/T]atccatatgttaatga	C	T	NM_017993 // intron // 0 // Hs.128258 // FLJ10094 // 55068 // Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /// ENST00000261488 // intron // 0 // --- // --- // --- // ---	FLJ10094	FLJ10094, Homo sapiens hypothetical protein FLJ10094 (FLJ10094), q14.11
SNP_A-2257638	ctttgcgtgctggaac[A/G]accacgaaactgagca	A	G	NM_017993 // upstream // 26636 // Hs.128258 // FLJ10094 // 55068 // Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA. /// NM_144974 // downstream // 42896 // --- // FLJ31846 // 160857 // Homo sapiens hypothetical protein FLJ31846 (FLJ31846), mR	FLJ10094	FLJ10094, Homo sapiens hypothetical protein FLJ10094 (FLJ10094), q14.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2233381	ctcaggtggtcctcac[C/G]agaatctgacaggcag	C	G	NM_153218 // downstream // 43179 // Hs.210586 // FLJ38725 // 144811 // Homo sapiens hypothetical protein FLJ38725 (FLJ38725), mRNA. /// ENST00000325686 // downstream // 43179 // — // — // — /// ENST00000267129 // downstream // 225218 // — /	FLJ38725	FLJ38725, Homo sapiens hypothetical protein FLJ38725 (FLJ38725), q14.11
SNP_A-1783785	ggccaaaatgccatcc[A/G]atagcctcatttatct	A	G	NM_153218 // downstream // 198636 // Hs.210586 // FLJ38725 // 144811 // Homo sapiens hypothetical protein FLJ38725 (FLJ38725), mRNA. /// ENST00000325686 // downstream // 198636 // — // — // — /// ENST00000267129 // downstream // 69761 // —	FLJ38725	FLJ38725, Homo sapiens hypothetical protein FLJ38725 (FLJ38725), q14.11
SNP_A-2132736	ctgaatcgcatctgaa[C/T]tacatgcccaggattg	C	T	ENST00000267129 // upstream // 176565 // — // — // — /// ENST00000281516 // upstream // 36422 // — // — // —	-	q14.11
SNP_A-1957443	ttttagtgatgtgtca[A/G]cgcacaatgaggaaaa	A	G	NM_183422 // upstream // 153714 // Hs.507916 // TGFB1I4 // 8848 // Homo sapiens transforming growth factor beta 1 induced transcript 4 (TGFB1I4), transcript variant 1, mRNA. /// NM_006022 // upstream // 293436 // Hs.507916 // TGFB1I4 // 8848 // Homo sapie	TGFB1I4	TGFB1I4, Homo sapiens transforming growth factor beta 1 induced transcript 4 (TGFB1I4), transcript variant 1, q14.12
SNP_A-1890926	tgatggaacatcgcaa[A/G]tccagctcggaggaat	A	G	NM_183422 // upstream // 177754 // Hs.507916 // TGFB1I4 // 8848 // Homo sapiens transforming growth factor beta 1 induced transcript 4 (TGFB1I4), transcript variant 1, mRNA. /// NM_006022 // upstream // 317476 // Hs.507916 // TGFB1I4 // 8848 // Homo sapie	TGFB1I4	TGFB1I4, Homo sapiens transforming growth factor beta 1 induced transcript 4 (TGFB1I4), transcript variant 1, q14.12
SNP_A-2121455	agtctttggaaagat[G/T]aaggaaatgatcagaa	G	T	NM_012345 // intron // 0 // Hs.525006 // NUFIP1 // 26747 // Homo sapiens nuclear fragile X mental retardation protein interacting protein 1 (NUFIP1), mRNA. /// ENST00000218567 // intron // 0 // — // — // —	NUFIP1	NUFIP1, Homo sapiens nuclear fragile X mental retardation protein interacting protein 1 (NUFIP1), q14.12
SNP_A-2275903	gagactctgtgagcaa[A/G]tgacttcctaatactt	A	G	NM_021631 // upstream // 10127 // Hs.302015 // FKSG2 // 59347 // Homo sapiens apoptosis inhibitor (FKSG2), mRNA. /// NM_003295 // upstream // 10127 // Hs.374596 // TPT1 // 7178 // Homo sapiens tumor protein, translationally-controlled 1 (TPT1), mRNA. ///	FKSG2	FKSG2, Homo sapiens apoptosis inhibitor (FKSG2), q14.13
SNP_A-2286575	gatggacattcaattc[A/C]ataagcccagcgtgtg	A	C	NM_021631 // upstream // 17925 // Hs.302015 // FKSG2 // 59347 // Homo sapiens apoptosis inhibitor (FKSG2), mRNA. /// NM_003295 // upstream // 17925 // Hs.374596 // TPT1 // 7178 // Homo sapiens tumor protein, translationally-controlled 1 (TPT1), mRNA. ///	FKSG2	FKSG2, Homo sapiens apoptosis inhibitor (FKSG2), q14.13
SNP_A-1872070	tctacgaaacgcttcg[C/T]atatgttacctcattt	C	T	NM_021631 // upstream // 32155 // Hs.302015 // FKSG2 // 59347 // Homo sapiens apoptosis inhibitor (FKSG2), mRNA. /// NM_003295 // upstream // 32155 // Hs.374596 // TPT1 // 7178 // Homo sapiens tumor protein, translationally-controlled 1 (TPT1), mRNA. ///	FKSG2	FKSG2, Homo sapiens apoptosis inhibitor (FKSG2), q14.13
SNP_A-2242196	ctgcaaatggtgaaga[A/G]agaaggaggctagccta	A	G	NM_152719 // downstream // 54536 // Hs.186363 // NURIT // 220082 // Homo sapiens testis-specific leucine zipper protein nurit (NURIT), mRNA. /// NM_198849 // downstream // 11191 // Hs.368483 // LOC283514 // 283514 // Homo sapiens similar to seven in absen	NURIT	NURIT, Homo sapiens testis-specific leucine zipper protein nurit (NURIT), q14.13
SNP_A-1729818	ggcataaccttgacattgctctcaa[C/T]cctgaatttctttttgag catg	C	T	NM_000821 // upstream // 428706 // Hs.424980 // HTR2A // 3356 // 5-hydroxytryptamine (serotonin) receptor 2A /// NM_003850 // downstream // 617913 // Hs.182217 // SUCLA2 // 8803 // succinate-CoA ligase, ADP-forming, beta subunit	HTR2A	HTR2A, rs1417205, 5-hydroxytryptamine (serotonin) receptor 2A ,q14.2
SNP_A-1818455	gttcttgcctcacaga[A/G]aggaatagtatccagt	A	G	ENST00000309963 // downstream // 20933 // — // — // — /// ENST00000322896 // downstream // 45237 // — // — // —	-	q14.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869235	tcctggcccagcggcct[A/G]agatacctgacctgtt	A	G	NM_015116 // upstream // 73254 // Hs.507971 // LRCH1 // 23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000322896 // upstream // 41724 // — // — // — /// ENST00000258643 // up	LRCH1	LRCH1. Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.13
SNP_A-2166651	caaattaacccaagtc[A/G]atacctgtgcagttcc	A	G	NM_015116 // upstream // 25820 // Hs.507971 // LRCH1 // 23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000322896 // upstream // 89158 // — // — // — /// ENST00000258643 // up	LRCH1	LRCH1. Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.13
SNP_A-2070802	acactaccatctctcat[C/T]gtgttttgagccaaa	C	T	NM_015116 // intron // 0 // Hs.507971 // LRCH1 // 23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000258643 // intron // 0 // — // — // — /// ENST00000311191 // intron // 0 //	LRCH1	LRCH1. Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.13
SNP_A-2081091	acctgagatgtttgag[A/G]aagttactcaatttc	A	G	NM_015116 // intron // 0 // Hs.507971 // LRCH1 // 23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000258643 // intron // 0 // — // — // — /// ENST00000311191 // intron // 0 //	LRCH1	LRCH1. Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.13
SNP_A-1661131	gagaacaacttgacacatctatttc[C/T]agccagagcagcagtg actggcagg	C	T	NM_000621 // upstream // 901037 // Hs.424980 // HTR2A // 3356 // 5-hydroxytryptamine (serotonin) receptor 2A /// NM_003850 // downstream // 145582 // Hs.182217 // SUCLA2 // 8803 // succinate-CoA ligase, ADP-forming, beta subunit	HTR2A	HTR2A , rs1172484, 5-hydroxytryptamine (serotonin) receptor 2A, q14.2
SNP_A-1883199	tgaaatgtgatttcaj[C/T]aaaactagtatttca	C	T	NM_015116 // intron // 0 // Hs.507971 // LRCH1 // 23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// ENST00000258643 // intron // 0 // — // — // — /// ENST00000311191 // intron // 0 //	LRCH1	LRCH1. Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.2
SNP_A-1744675	tttggttgagttgccatctgtct[A/G]aaagcattaggaacttcatt gcttg	A	G	NM_000621 // upstream // 958342 // Hs.424980 // HTR2A // 3356 // 5-hydroxytryptamine (serotonin) receptor 2A /// NM_003850 // downstream // 88277 // Hs.182217 // SUCLA2 // 8803 // succinate-CoA ligase, ADP-forming, beta subunit	HTR2A	HTR2A , rs4414373, 5-hydroxytryptamine (serotonin) receptor 2A, q14.2
SNP_A-2112120	aggatgttatgttggc[A/G]ctccttctatcctagt	A	G	NM_015116 // downstream // 18595 // Hs.507971 // LRCH1 // 23143 // Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), mRNA. /// NM_001984 // downstream // 9067 // Hs.432491 // ESD // 2098 // Homo sapiens esterase D/f	LRCH1	LRCH1. Homo sapiens leucine-rich repeats and calponin homology (CH) domain containing 1 (LRCH1), q14.2
SNP_A-2155003	attcacgtagtgctta[A/G]aatgctgcttctacca	A	G	NM_001984 // intron // 0 // Hs.432491 // ESD // 2098 // Homo sapiens esterase D/formylglutathione hydrolase (ESD), mRNA. /// ENST00000267160 // intron // 0 // — // — // —	ESD	ESD. Homo sapiens esterase D,q14.2
SNP_A-2208478	cccaccttaaacacc[A/T]acacattagagattaa	A	T	NM_001984 // upstream // 4971 // Hs.432491 // ESD // 2098 // Homo sapiens esterase D/formylglutathione hydrolase (ESD), mRNA. /// NM_000621 // downstream // 31175 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (H	ESD	ESD. Homo sapiens esterase D q14.2
SNP_A-1908220	tgtaccccttctgtta[C/T]gaccaatagcctaatc	C	T	NM_000621 // upstream // 137782 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 908835 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1806886	gtctcaaaagctgtca[C/T]tccttcaggtacctga	C	T	NM_000621 // upstream // 172464 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 874153 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1953971	ttgataagaatatca[C/T]ggaatctgtaaaatgc	C	T	NM_000621 // upstream // 181190 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 865427 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2075034	acatccatgcacatga[A/T]cacttttctaatatt	A	T	NM_000621 // upstream // 182967 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 863650 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1903724	tgggaggagagcgcta[C/T]ggatacatactttgtc	C	T	NM_000621 // upstream // 185548 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 861069 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2141758	atcttcttcacagagc[A/G]gaacatattcacacca	A	G	NM_000621 // upstream // 371294 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 675323 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2192557	catccaccattacatc[A/G]aaaacttgggaaacc	A	G	NM_000621 // upstream // 371440 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 675177 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2264792	gaagacttgagacaaa[A/G]ttaatgagtgttaaag	A	G	NM_000621 // upstream // 383907 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 662710 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1812480	gtggccactatgcttc[A/C]ctgtttacgtttat	A	C	NM_000621 // upstream // 392712 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 653905 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2231492	ctatttaatcaactaa[A/G]ctcagttcccaatatg	A	G	NM_000621 // upstream // 395060 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 651557 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2096264	agaccacccttcagaa[A/G]tggacaatttgatcgg	A	G	NM_000621 // upstream // 502968 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 543649 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1814741	gtgtgtagtatttcaa[C/T]agctttggagtgtaa	C	T	NM_000621 // upstream // 515429 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 531188 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1866640	tccccgttcatccatc[C/T]aagaccacagtggtaa	C	T	NM_000621 // upstream // 588225 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 458392 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2161266	atttgataataggtga[A/G]gctagtttgcagattg	A	G	NM_000621 // upstream // 633343 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 413274 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-2223317	cgctagactattctac[A/G]ctctatagaaacaaat	A	G	NM_000621 // upstream // 932075 // Hs.424980 // HTR2A // 3356 // Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /// NM_003850 // downstream // 114542 // Hs.546323 // SUCLA2 // 8803 // Homo sapiens succinate-CoA ligase, ADP-forming	HTR2A	HTR2A, Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), q14.2
SNP_A-1906274	tggtgagttttagcaa[A/T]atttggatataagaga	A	T	NM_014166 // upstream // 28250 // Hs.181112 // MED4 // 29079 // Homo sapiens vitamin D receptor interacting protein (VDRIP), mRNA. /// ENST00000258648 // upstream // 28250 // --- // --- // --- // --- /// ENST00000310929 // downstream // 11004 // --- // ---	MED4	MED4, Homo sapiens vitamin D receptor interacting protein (VDRIP), q14.2
SNP_A-1826773	taacaggacactctcc[A/G]gatttggacccagaac	A	G	NM_001268 // upstream // 56879 // Hs.25447 // CHC1L // 1102 // Homo sapiens chromosome condensation 1-like (CHC1L), mRNA. /// NM_020377 // upstream // 116496 // Hs.253706 // CYSLTR2 // 57105 // Homo sapiens cysteinyl leukotriene receptor 2 (CYSLTR2), mRNA	CHC1L	CHC1L, Homo sapiens chromosome condensation 1-like (CHC1L), q14.2
SNP_A-1830856	taatcttagaccaaaa[A/G]gaacctctggggtgat	A	G	NM_001268 // upstream // 146203 // Hs.25447 // CHC1L // 1102 // Homo sapiens chromosome condensation 1-like (CHC1L), mRNA. /// NM_020377 // upstream // 27172 // Hs.253706 // CYSLTR2 // 57105 // Homo sapiens cysteinyl leukotriene receptor 2 (CYSLTR2), mRNA	CHC1L	CHC1L, Homo sapiens chromosome condensation 1-like (CHC1L), q14.2
SNP_A-2055077	aataacaaaatggaaa[C/G]taaaatcagcacctac	C	G	NM_014923 // upstream // 166013 // Hs.508010 // FNDC3A // 22862 // Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// NM_014923 // upstream // 300463 // Hs.508010 // FNDC3A // 22862 // Homo sapiens fibronectin type III domain contain	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-2311769	ggaattgctgggccat[A/G]agataactatatgttt	A	G	NM_014923 // upstream // 32910 // Hs.508010 // FNDC3A // 22862 // Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// NM_014923 // upstream // 167360 // Hs.508010 // FNDC3A // 22862 // Homo sapiens fibronectin type III domain containi	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-2243481	ctgctaatgaggttta[A/G]caatattctcataagc	A	G	NM_014923 // upstream // 18508 // Hs.508010 // FNDC3A // 22862 // Homo sapiens fibronectin type III domain containing 3 (FNDC3), mRNA. /// NM_014923 // upstream // 152958 // Hs.508010 // FNDC3A // 22862 // Homo sapiens fibronectin type III domain containi	FNDC3A	FNDC3A, Homo sapiens fibronectin type III domain containing 3 (FNDC3), q14.2
SNP_A-2220315	ccttccgaatagacgc[A/G]atctcttgaggggaga	A	G	NM_018191 // CDS // 0 // Hs.508021 // RCBTB1 // 55213 // Homo sapiens regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1), mRNA. /// ENST00000258646 // CDS // 0 // --- // --- // --- // ---	RCBTB1	RCBTB1, Homo sapiens regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1 (RCBTB1), q14.2
SNP_A-2075777	acatggtttaggaaat[A/C]aaaatctgtttctaat	A	C	NM_005798 // downstream // 3730 // Hs.436922 // RFP2 // 10206 // Homo sapiens ret finger protein 2 (RFP2), transcript variant 1, mRNA. /// NM_052811 // downstream // 3730 // Hs.436922 // RFP2 // 10206 // Homo sapiens ret finger protein 2 (RFP2), transcrip	RFP2	RFP2, Homo sapiens ret finger protein 2 (RFP2), transcript variant 1, q14.2
SNP_A-2195098	catggaatcacattac[A/G]gaaaatcatcagaggc	A	G	NM_153290 // downstream // 231903 // --- // --- // 0 // --- /// NM_198989 // downstream // 437660 // Hs.285829 // DLEU7 // 220107 // Homo sapiens deleted in lymphocytic leukemia 7 (DLEU7), mRNA. /// ENST00000327170 // downstream // 231903 // --- // --- // ---	-	q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282942	gataacaggaatttga[C/T]ggttagtgatggtaac	C	T	NM_004129 // upstream // 18770 // Hs.411573 // GUCY1B2 // 2974 // Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), mRNA. /// NM_145019 // upstream // 137643 // Hs.292590 // FLJ30707 // 220108 // Homo sapiens hypothetical protein FLJ30707 (FLJ3	GUCY1B2	GUCY1B2, Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), q14.3
SNP_A-2270404	gacactttctttagcc[C/T]gagcacatttttaact	C	T	NM_004129 // upstream // 46024 // Hs.411573 // GUCY1B2 // 2974 // Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), mRNA. /// NM_145019 // upstream // 110389 // Hs.292590 // FLJ30707 // 220108 // Homo sapiens hypothetical protein FLJ30707 (FLJ3	GUCY1B2	GUCY1B2, Homo sapiens guanylate cyclase 1, soluble, beta 2 (GUCY1B2), q14.3
SNP_A-1657582	tccttagctcctcataactaaagca[A/C]agtcagcctcgaccag agaagaggt	A	C	NM_002590 // downstream // 15726 // Hs.19492 // PCDH8 // 5100 // protocadherin 8 /// NM_007015 // upstream // 88549 // Hs.421391 // LECT1 // 11061 // leukocyte cell derived chemotaxin 1 /// NM_032949 // downstream // 15726 // Hs.19492 // PCDH8 // 5100 //	PCDH8	PCDH8 , rs640428, protocadherin 8 ,q14.3
SNP_A-1818669	gttgaatctgttcatc[A/G]atttgggaaatattgc	A	G	ENST00000356159 // intron // 0 // — // — // — // —	-	q14.3
SNP_A-1671656	aaggattgatgcattcatttttttc[A/G]cttatttggtgctttcaaaacc aat	A	G	AK097615 // upstream // 3669084 // Hs.525056 // FLJ40296 // 122183 // FLJ40296 protein /// NM_006418 // downstream // 419782 // Hs.273321 // GW112 // 10562 // differentially expressed in hematopoietic lineages	FLJ40296	FLJ40296 , rs2408930, FLJ40296 protein ,q14.3
SNP_A-2112447	aggcaatctaatgtag[C/T]atctctgtaccgtaaa	C	T	NM_006704 // intron // 0 // Hs.281902 // SUGT1 // 10910 // Homo sapiens SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) (SUGT1), mRNA. /// ENST00000310528 // intron // 0 // — // — // — // — /// ENST00000298172 // intron // 0 // — // — //	SUGT1	SUGT1, Homo sapiens SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) (SUGT1), q14.3
SNP_A-1871690	tctaatattgaaagta[G/T]gaactgtctggatcta	G	T	NM_032949 // downstream // 18909 // Hs.19492 // PCDH8 // 5100 // Homo sapiens protocadherin 8 (PCDH8), transcript variant 2, mRNA. /// NM_002590 // downstream // 18909 // Hs.19492 // PCDH8 // 5100 // Homo sapiens protocadherin 8 (PCDH8), transcript varian	PCDH8	PCDH8, Homo sapiens protocadherin 8 (PCDH8), transcript variant 2, q14.3
SNP_A-2169754	caaggactgtttttc[A/G]actttcattaaaatcc	A	G	NM_006418 // intron // 0 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // intron // 0 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2158666	attgtcacaatgtgta[C/G]aatcaagtgggacaag	C	G	NM_006418 // intron // 0 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // intron // 0 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2158892	attgtggtagccttta[C/T]atgactatacacttgt	C	T	NM_006418 // downstream // 1168 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 1168 // — // — // — // — /// ENST00000258651 // downstream // 1387485 // --- // --- // --- // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2246888	ctgtagtgatttagca[C/T]gggtgtttgtctttca	C	T	NM_006418 // downstream // 9094 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 9094 // — // — // — // — /// ENST00000258651 // downstream // 1379559 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2098661	agagccatttgcaaag[A/G]aaatagatacaaatat	A	G	NM_006418 // downstream // 14076 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 14076 // — // — // — // — /// ENST00000258651 // downstream // 1374577 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2147346	atggagcacaaaggaa[A/T]tctcataaccagttag	A	T	NM_006418 // downstream // 19747 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 19747 // — // --- // --- // --- /// ENST00000258651 // downstream // 1368906 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2157317	attgactttcccataa[A/G]tgtgtggttttgagtg	A	G	NM_006418 // downstream // 19952 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 19952 // — // — // — // — /// ENST00000258651 // downstream // 1368701 // — // — // — // ---	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2191577	catatgggcatgatgc[G/T]gagttttgatgatcca	G	T	NM_006418 // downstream // 570582 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 570582 // — // — // — // — /// ENST00000258651 // downstream // 818071 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2061218	aatgcataatgaaaaa[C/T]tgagtaatacattagt	C	T	NM_006418 // downstream // 737725 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 737725 // — // — // — // — /// ENST00000258651 // downstream // 650928 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1901965	tggcagtactggctac[A/C]gatcttgggtaatcca	A	C	NM_006418 // downstream // 917330 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 917330 // — // — // — // — /// ENST00000258651 // downstream // 471323 // — // — // — // —	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1857526	tcactcaggaggaata[C/T]agatgagcggtttatt	C	T	NM_006418 // downstream // 1033126 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 1033126 // — // — // — // — /// ENST00000258651 // downstream // 355527 // — // — // — // –	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-2250234	cttactttcagcaatg[A/G]acagagcatccagaca	A	G	NM_006418 // downstream // 1247176 // Hs.508113 // OLFM4 // 10562 // Homo sapiens olfactomedin 4 (OLFM4), mRNA. /// ENST00000219022 // downstream // 1247176 // — // — // — // — /// ENST00000258651 // downstream // 141477 // — // — // — // –	OLFM4	OLFM4, Homo sapiens olfactomedin 4 (OLFM4), q14.3
SNP_A-1678984	acaaatggctagcacatagtacgtg[A/G]atatagccttacttccaaagtgaca	A	G	AK097615 // upstream // 1565674 // Hs.525056 // FLJ40296 // 122183 // FLJ40296 protein /// NM_006418 // downstream // 2523192 // Hs.273321 // GW112 // 10562 // differentially expressed in hematopoietic lineages	FLJ40296	FLJ40296 , rs10507601, FLJ40296 protein ,q21.1
SNP_A-2067815	acaacatttttaagca[C/T]gggccttagtgataaa	C	T	NM_014459 // upstream // 3062190 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 128304 // — // — // — // — /// ENST00000237807 // upstream // 3062190 // — // — // — // —	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q14.3
SNP_A-1644578	aaaagagttaatagagatggaaaga[C/T]caatagaagatgctaacaagaaggt	C	T	AK097615 // upstream // 109328 // Hs.525056 // FLJ40296 // 122183 // FLJ40296 protein /// NM_006418 // downstream // 3979538 // Hs.273321 // GW112 // 10562 // differentially expressed in hematopoietic lineages	FLJ40296	FLJ40296 , rs9285210, FLJ40296 protein ,q21.1
SNP_A-1666468	gacaaacaatcaattatagccataa[A/C]cttagtgtaaagaattataatataa	A	C	AK097615 // upstream // 109225 // Hs.525056 // FLJ40296 // 122183 // FLJ40296 protein /// NM_006418 // downstream // 3979641 // Hs.273321 // GW112 // 10562 // differentially expressed in hematopoietic lineages	FLJ40296	FLJ40296 , rs9285211, FLJ40296 protein ,q21.1
SNP_A-1668560	tattcagtctgaaaaaatgatacac[A/T]accctattagccactcaactttggc	A	T	AK097615 // upstream // 19207 // Hs.525056 // FLJ40296 // 122183 // FLJ40296 protein /// NM_006418 // downstream // 4069659 // Hs.273321 // GW112 // 10562 // differentially expressed in hematopoietic lineages	FLJ40296	FLJ40296 , rs479855, FLJ40296 protein ,q21.1
SNP_A-1667204	aatttaactgggcacatttatcctg[C/T]atatttcgtggcaaagttaactaaa	C	T	AK097615 // downstream // 151614 // Hs.525056 // FLJ40296 // 122183 // FLJ40296 protein /// NM_014459 // upstream // 309978 // Hs.106511 // PCDH17 // 27253 // protocadherin 17	FLJ40296	FLJ40296 , rs1936755, FLJ40296 protein ,q21.1
SNP_A-1819931	gttgttatttttagca[C/G]agatgtagactacatt	C	G	NM_014459 // upstream // 645250 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2545244 // — // — // — // — /// ENST00000237807 // upstream // 645250 // — // — // — // —	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2310515	ggaagaactcacttcc[A/G]atttgacacagttttg	A	G	NM_014459 // upstream // 617057 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2573437 // — // — // — // — /// ENST00000237807 // upstream // 617057 // — // — // — // —	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2141149	actctattaacacaca[C/T]tgggctgttgatgatc	C	T	NM_014459 // upstream // 603794 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2586700 // — // — // — // — /// ENST00000237807 // upstream // 603794 // — // — // — // —	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2141173	ttatgtgaatttatta[C/T]ggcaatcctagaaaac	C	T	NM_014459 // upstream // 576186 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2614308 // --- // --- // --- /// ENST00000237807 // upstream // 576186 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1917455	tgttttgtgaggtctt[A/C]aaagcgaaatatttgg	A	C	NM_014459 // upstream // 569887 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2620607 // --- // --- // --- /// ENST00000237807 // upstream // 569887 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1853690	tatttttcatgctga[C/T]cctgtgtaagtcttg	C	T	NM_014459 // upstream // 569250 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2621244 // --- // --- // --- /// ENST00000237807 // upstream // 569250 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2238096	ctctgcatatagcata[A/C]ggagcacagtgcagct	A	C	NM_014459 // upstream // 545551 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2644943 // --- // --- // --- /// ENST00000237807 // upstream // 545551 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2293045	gcagacaaaaatgccat[C/G]agaattcaagcaagaa	C	G	NM_014459 // upstream // 545495 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2644999 // --- // --- // --- /// ENST00000237807 // upstream // 545495 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1809442	gtgagaacggtcacta[A/C]aaaatttcccacaaac	A	C	NM_014459 // upstream // 502925 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2687569 // --- // --- // --- /// ENST00000237807 // upstream // 502925 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2141329	agaaaaaactctgaaa[A/T]tgctgtaaaaagccct	A	T	NM_014459 // upstream // 402759 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2787735 // --- // --- // --- /// ENST00000237807 // upstream // 402759 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2113653	agcctcagtgtcattd[A/G]aggcaatatttcaaa	A	G	NM_014459 // upstream // 377865 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2812629 // --- // --- // --- /// ENST00000237807 // upstream // 377865 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2083514	actaagttctattgccd[C/T]ctgggactaagttcaa	C	T	NM_014459 // upstream // 279061 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2911433 // --- // --- // --- /// ENST00000237807 // upstream // 279061 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2215779	cctcatcttgaaccac[C/G]ctttccctaatgtgc	C	G	NM_014459 // upstream // 261643 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2928851 // --- // --- // --- /// ENST00000237807 // upstream // 261643 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-2177392	cacctgaattgtaat[A/G]atcctaacgtgtcatg	A	G	NM_014459 // upstream // 253537 // Hs.106511 // PCDH17 // 27253 // Homo sapiens protocadherin 17 (PCDH17), mRNA. /// ENST00000258651 // upstream // 2936957 // --- // --- // --- /// ENST00000237807 // upstream // 253537 // --- // --- // ---	PCDH17	PCDH17, Homo sapiens protocadherin 17 (PCDH17), q21.1
SNP_A-1726094	gcctctgtggacttgagagatgacc[A/G]aatagcaaagaaagt atcataagg	A	G	BC034915 // upstream // 1000637 // Hs.381993 // --- // --- // CDNA clone IMAGE:5277680, partial cds /// NM_030932 // downstream // 326436 // Hs.122164 // DIAPH3 // 81624 // diaphanous homolog 3 (Drosophila)	-	- , rs9317079, CDNA clone IMAGE:5277680, partial cds ,q21.2
SNP_A-1845880	tatataaaatgagatc[C/G]aaccacttatacagat	C	G	NM_030932 // downstream // 1124619 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 371269 // --- // --- // --- /// ENST00000267214 // downstream // 1124619 // ---	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287050	gatgtaacttgaccac[A/G]ctaaagtagatcagag	A	G	NM_030932 // downstream // 1124312 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 371576 // — // — // — /// ENST00000267214 // downstream // 1124312 // —	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2142486	ggtgagtggatgaggc[A/G]aacatcttcccagctc	A	G	NM_030932 // downstream // 1056921 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 438967 // — // — // — /// ENST00000267214 // downstream // 1056921 // —	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2096785	agactatattatctaa[A/C]ctcgcccaaacctcaat	A	C	NM_030932 // downstream // 1013564 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 482324 // — // — // — /// ENST00000267214 // downstream // 1013564 // —	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2181153	cagacagtacaaataa[A/T]aaacgaacacaacttc	A	T	NM_030932 // downstream // 929805 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 566083 // — // — // — /// ENST00000267214 // downstream // 929805 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2142784	tgtgcatgattgagga[C/T]atctctgttaatt	C	T	NM_030932 // downstream // 802753 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 693135 // — // — // — /// ENST00000267214 // downstream // 802753 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2142823	gaatgagtggattcac[A/G]aaagtctatataaacc	A	G	NM_030932 // downstream // 778172 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 717716 // — // — // — /// ENST00000267214 // downstream // 778172 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.1
SNP_A-2120434	agtcattgcaaaatca[A/G]tactcctaccctgaat	A	G	NM_030932 // downstream // 719947 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 775941 // — // — // — /// ENST00000267214 // downstream // 719947 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1873254	tctatttcttgtgcc[A/G]ccaataccatgatcga	A	G	NM_030932 // downstream // 680462 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 815426 // — // — // — /// ENST00000267214 // downstream // 680462 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2234176	ctcattgtggtttgga[A/G]tacctaatgactaat	A	G	NM_030932 // downstream // 470466 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1025422 // — // — // — /// ENST00000267214 // downstream // 470466 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2210896	ccccttggcagtatta[C/T]ggtggctgtcccag	C	T	NM_030932 // downstream // 420511 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1075377 // — // — // — /// ENST00000267214 // downstream // 420511 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2201098	ccaagtcattaaagca[A/G]agccggatagttgaaa	A	G	NM_030932 // downstream // 409329 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1086559 // — // — // — /// ENST00000267214 // downstream // 409329 // — //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2158735	attgtctattgtcttc[C/G]atgttcccatgcctag	C	G	NM_030932 // downstream // 407889 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1087999 // — // — // — // — /// ENST00000267214 // downstream // 407889 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1827551	taactgaacaatacaa[A/G]cccagatggattgggt	A	G	NM_030932 // downstream // 406501 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1089387 // — // — // — // — /// ENST00000267214 // downstream // 406501 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2173189	cacaacagtactaaaa[C/T]ggtaggtagatattat	C	T	NM_030932 // downstream // 382744 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1113144 // — // — // — // — /// ENST00000267214 // downstream // 382744 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1804808	gtcagtctttccatta[C/T]gtagctaaagcaacta	C	T	NM_030932 // downstream // 374722 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1121166 // — // — // — // — /// ENST00000267214 // downstream // 374722 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1935699	ttctgtctttggatgc[A/C]cctaactgctcagaag	A	C	NM_030932 // downstream // 318043 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1177845 // — // — // — // — /// ENST00000267214 // downstream // 318043 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1797541	ggtttcatttagagca[G/T]taataaatacctggca	G	T	NM_030932 // downstream // 317829 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1178059 // — // — // — // — /// ENST00000267214 // downstream // 317829 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2003342	tgtgcgtcagttctag[C/T]aatgccaaaaagagga	C	T	NM_030932 // downstream // 310575 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1185313 // — // — // — // — /// ENST00000267214 // downstream // 310575 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2143397	taccaaaacctgcatc[C/T]gaaataacttctaaga	C	T	NM_030932 // downstream // 292168 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// ENST00000359909 // upstream // 1203720 // — // — // — // — /// ENST00000267214 // downstream // 292168 // — /	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-1702763	agaatgatgttcaccaatagctagg[C/G]atgattaatattgagtaaagatttg	C	G	NM_022843 // downstream // 648902 // Hs.391781 // PCDH20 // 64881 // protocadherin 20 /// NM_030794 // downstream // 186908 // Hs.112707 // TDRD3 // 81550 // tudor domain containing 3	PCDH20	PCDH20 , rs1999518, protocadherin 20 ,q21.2
SNP_A-1719091	ttgttttaaatgttatcttagtgtc[C/T]cattggtctgaggtttttcctcttg	C	T	NM_022843 // downstream // 547271 // Hs.391781 // PCDH20 // 64881 // protocadherin 20 /// NM_030794 // downstream // 288539 // Hs.112707 // TDRD3 // 81550 // tudor domain containing 3	PCDH20	PCDH20 , rs167272, protocadherin 20 ,q21.2
SNP_A-1720669	actttatccttccagccgcaactca[A/G]atgacccaaagtcagacatcacatc	A	G	NM_022843 // downstream // 273255 // Hs.391781 // PCDH20 // 64881 // protocadherin 20 /// NM_030794 // downstream // 562555 // Hs.112707 // TDRD3 // 81550 // tudor domain containing 3	PCDH20	PCDH20 , rs2137986, protocadherin 20 ,q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2003347	agtaatctgtttaaag[A/G]caaattggatcctta	A	G	NM_030932 // upstream // 300242 // Hs.508141 // DIAPH3 // 81624 // Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA. /// NM_030794 // upstream // 83002 // Hs.525061 // TDRD3 // 81550 // Homo sapiens tudor domain containing 3 (TDRD3), mRNA. //	DIAPH3	DIAPH3, Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), q21.2
SNP_A-2209708	cccattatcgataaagc[A/G]cctggtttgatttcat	A	G	NM_022843 // downstream // 638215 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 639596 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1798135	gtaaacaatgataaacd[A/G]caagaaacgatctcat	A	G	NM_022843 // downstream // 625625 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 627006 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2030240	aaagcactgttacatat[C/G]agaaatccctcaaaa	C	G	NM_022843 // downstream // 596074 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 597455 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2144560	cacatttattctaaacd[C/G]acacatgaaccgagaa	C	G	NM_022843 // downstream // 571458 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 572839 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2144575	aatttcagaaaagcat[A/G]agtgctagacctcctt	A	G	NM_022843 // downstream // 564002 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 565383 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1846483	tatattattgaatgac[A/T]aatcactttcataaac	A	T	NM_022843 // downstream // 560663 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 562044 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2305660	gctgcatttcatgtca[C/T]tcgttcttttcactcat	C	T	NM_022843 // downstream // 548713 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 550094 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2144613	ttgtctttccatgata[G/T]caataactttaacat	G	T	NM_022843 // downstream // 547398 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 548779 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1945053	ttgtgtagatatttaa[G/T]ggctcaatttgaatc	G	T	NM_022843 // downstream // 502050 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 503431 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2144980	atgtgttgatttctca[C/T]gtcaatactttactac	C	T	NM_022843 // downstream // 273493 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 274874 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2267126	gaataagtgagtcgta[G/T]ccatgttattctgaaa	G	T	NM_022843 // downstream // 219138 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 220519 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-2145044	aagtagcatggaaaaa[C/G]ttgttatgtgaaaat	C	G	NM_022843 // downstream // 197274 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // downstream // 198655 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000331773 /	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.2
SNP_A-1741445	ttcattggtgaggtatttaaagac[C/T]gagtagcttaatatttaac cacaag	C	T	NM_022843 // upstream // 957452 // Hs.391781 // PCDH20 // 64881 // protocadherin 20 /// NM_173604 // downstream // 1456247 // Hs.166754 // FLJ25694 // 283492 // hypothetical protein FLJ25694	PCDH20	PCDH20 , rs2590492, protocadherin 20 ,q21.31
SNP_A-1650102	atttattgaatactgtatattatgt[C/T]aaaattgtgatgatttttgtacc agg	C	T	NM_022843 // upstream // 1179985 // Hs.391781 // PCDH20 // 64881 // protocadherin 20 /// NM_173604 // downstream // 1233714 // Hs.166754 // FLJ25694 // 283492 // hypothetical protein FLJ25694	PCDH20	PCDH20 , rs10507678, protocadherin 20 ,q21.31
SNP_A-2116914	aggtctttagacgtag[A/G]aatcagaatgatataa	A	G	NM_022843 // upstream // 326432 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 339121 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000358674 // up	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-1933651	ttctaggtgaagtggc[A/G]agacagaaatggggctg	A	G	NM_022843 // upstream // 632559 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 645248 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000358674 // up	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-1735787	aagccccactgaagtaattggtagaa[A/G]aatgagtaacatgata [redacted] aacacctgg	A	G	NM_022843 // upstream // 1832217 // Hs.391781 // PCDH20 // 64881 // protocadherin 20 /// NM_173604 // downstream // 581482 // Hs.166754 // FLJ25694 // 283492 // hypothetical protein FLJ25694	PCDH20	PCDH20 , rs9317297, protocadherin 20 ,q21.31
SNP_A-1906893	tggttccagacttttgg[C/T]aacaactgaaatatcc	C	T	NM_022843 // upstream // 873415 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 886104 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000358674 // up	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-1798820	gtaacttagactaaaa[C/G]tgttgtccacaagatt	C	G	NM_022843 // upstream // 1098599 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 1111288 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000358674 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-2146930	tggacttccatgtgag[C/T]atttatctccctacgt	C	T	NM_022843 // upstream // 1845356 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// NM_022843 // upstream // 1858045 // Hs.391781 // PCDH20 // 64881 // Homo sapiens protocadherin 20 (PCDH20), mRNA. /// ENST00000358674 //	PCDH20	PCDH20, Homo sapiens protocadherin 20 (PCDH20), q21.31
SNP_A-1669245	cccatatctaatctgtttttatccaj[C/T]attgtattctattattgcttaact [redacted] g	C	T	NM_020403 // downstream // 1787022 // Hs.492696 // PCDH9 // 5101 // protocadherin 9 /// NM_173604 // upstream // 6716871 // Hs.166754 // FLJ25694 // 283492 // hypothetical protein FLJ25694	PCDH9	PCDH9 , rs1953643, protocadherin 9 ,q21.31
SNP_A-1899830	tggaatttcaaccccat[A/G]aatttaactcaattat	A	G	ENST00000324792 // upstream // 15590 // — // — // — // — /// ENST00000355561 // upstream // 949418 // — // — // — // —	-	q21.31
SNP_A-2196981	cattatatttcaagctct[A/G]cctgccattagccaaa	A	G	ENST00000324792 // upstream // 562582 // — // — // — // — /// ENST00000355561 // upstream // 402426 // — // — // — // —	-	q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137397	atcatacctattcaa[A/G]actgtgtaaaacaagt	A	G	ENST00000324792 // upstream // 640125 /// ENST00000355561 // upstream // 324883 ///	-	q21.31
SNP_A-2205071	ccaggtgaatgtcaaa[A/C]cacctacatgtagaac	A	C	ENST00000324792 // upstream // 647954 /// ENST00000355561 // upstream // 317054 ///	-	q21.31
SNP_A-2154513	attattgaatgccatg[A/T]atatagtaatgaggag	A	T	ENST00000324792 // upstream // 655233 /// ENST00000355561 // upstream // 309775 ///	-	q21.31
SNP_A-1956645	tttgttttgtgtttaa[C/G]tatagtcaccatgctg	C	G	NM_020403 // downstream // 1337473 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // downstream // 1337473 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.31
SNP_A-2149059	cttctactctacagcc[A/G]gatttatttcagaaga	A	G	NM_020403 // downstream // 1080484 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // downstream // 1080484 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-1937541	ttgaactaatttgcac[G/T]cttagcaacagtgtaa	G	T	NM_020403 // downstream // 841737 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // downstream // 841737 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript va	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-1702973	tgcaaacaatttgtttttggcattg[A/C]atgtaaagactatcatcatttactt	A	C	NM_020403 // intron // 0 // Hs.492696 // PCDH9 // 5101 // protocadherin 9	PCDH9	PCDH9 , rs10492473, protocadherin 9,q21.32
SNP_A-1667672	caatttgatgttctgtgtagaagac[A/G]attggtgaaggcttctattcagcca	A	G	NM_020403 // intron // 0 // Hs.492696 // PCDH9 // 5101 // protocadherin 9	PCDH9	PCDH9 , rs964381, protocadherin 9,q21.32
SNP_A-1735901	ccactgagcacatagcaattatgaca[G/T]aactatttcctgagacatgggagat	G	T	NM_020403 // intron // 0 // Hs.492696 // PCDH9 // 5101 // protocadherin 9	PCDH9	PCDH9 , rs9317651, protocadherin 9,q21.32
SNP_A-2090770	actttatagaacataaa[C/G]tattgcatataacaag	C	G	NM_020403 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 1, mRNA. ///	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-1913737	tgtgtattctgaaaca[C/T]caattatctggagaga	C	T	NM_020403 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 1, mRNA. ///	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2150712	tccttacatttctgaa[A/G]tatatccatgtaacca	A	G	NM_020403 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 1, mRNA. ///	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2151084	gagaaattggaaaaaa[A/C]ctgtgtcatatgctta	A	C	NM_020403 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // intron // 0 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 1, mRNA. ///	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-1897530	tgctgatgagattcaa[A/G]ctatgagaaggcattt	A	G	NM_020403 // upstream // 27278 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 27278 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2151248	tgatccatcatgagag[G/T]cagtaatgtgttttcc	G	T	NM_020403 // upstream // 160875 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 160875 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript varian	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2097120	agacttaacactttcc[A/T]cgtgggcaaagagagt	A	T	NM_020403 // upstream // 384243 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 384243 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript varian	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2125059	agtgctctgcattag[A/G]caatgtgtggtaactt	A	G	NM_020403 // upstream // 518850 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 518850 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript varian	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2028249	aaactatattgtttgg[G/T]agggtaacagcgaatg	G	T	NM_020403 // upstream // 533177 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 533177 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript varian	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-2151550	aattctctcaaacttt[C/G]aaacagctgcctttt	C	G	NM_020403 // upstream // 559082 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 559082 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript varian	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.32
SNP_A-1658752	ttactctcaggagtgttcatgccaa[C/T]acagagtggttttttgaca cagttt	C	T	NM_020403 // upstream // 1679043 // Hs.492696 // PCDH9 // 5101 // protocadherin 9 /// NM_020866 // downstream // 792993 // Hs.106808 // KLHL1 // 57626 // kelch-like 1 (Drosophila)	PCDH9	PCDH9 , rs1438650, protocadherin 9 ,q21.33
SNP_A-1664508	gtggaaaggaaatagtgatcaatacc[C/T]acatgaactaacttat aacacagtg	C	T	NM_020403 // upstream // 2017246 // Hs.492696 // PCDH9 // 5101 // protocadherin 9 /// NM_020866 // downstream // 454790 // Hs.106808 // KLHL1 // 57626 // kelch-like 1 (Drosophila)	PCDH9	PCDH9 , rs1119008, protocadherin 9 ,q21.33
SNP_A-2204724	ccaggattcaaatgta[A/G]caatgcaaagttatt	A	G	NM_020403 // upstream // 975237 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 975237 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript varian	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2219561	cctgttggctctctaa[C/T]tcatggacaaaatcaa	C	T	NM_020403 // upstream // 1016695 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1016695 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1954709	ttlgctcattgtcttc[C/T]aaacataaaattgctc	C	T	NM_020403 // upstream // 1397024 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1397024 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2143178	atgacaaaacttaata[C/T]gtcctactgtaattga	C	T	NM_020403 // upstream // 1625162 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1625162 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2066854	acaaaatctgctgaca[C/T]gagtacatagcactag	C	T	NM_020403 // upstream // 1637298 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1637298 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2074504	acatagcactagaaaa[C/G]aagctttctgacaccc	C	G	NM_020403 // upstream // 1637319 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1637319 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1719117	ctttgatgaaagtggccaaatttta[A/T]cataacagaatgaaaaa tagtcatt	A	T	NM_020866 // intron // 0 // Hs.106808 // KLHL1 // 57626 // kelch-like 1 (Drosophila)	KLHL1	KLHL1 , rs9317874, kelch-like 1 (Drosophila),q21.33
SNP_A-1865250	tccatataacatgctct[A/G]agacctacatataa	A	G	NM_020403 // upstream // 1787797 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1787797 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2214885	cctatattatgaagtg[A/G]aaaaccagtctttga	A	G	NM_020403 // upstream // 1794237 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1794237 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2056738	aatagctattctgatc[A/G]atgttaaatggtaact	A	G	NM_020403 // upstream // 1833410 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1833410 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2288072	gattcaatttcccaag[C/G]aacaataacagactat	C	G	NM_020403 // upstream // 1834553 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1834553 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1841958	tagggaaccgaaatca[C/T]ctgctactgtgatgtt	C	T	NM_020403 // upstream // 1864487 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1864487 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1851937	tattgatttccaccca[A/G]aagtatgactcaaga	A	G	NM_020403 // upstream // 1887986 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 1887986 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-2250073	cttacgcaggcatcggt[A/G]ccaaccccacctgaaga	A	G	NM_020403 // upstream // 2116303 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, mRNA. /// NM_203487 // upstream // 2116303 // Hs.407643 // PCDH9 // 5101 // Homo sapiens protocadherin 9 (PCDH9), transcript vari	PCDH9	PCDH9, Homo sapiens protocadherin 9 (PCDH9), transcript variant 2, q21.33
SNP_A-1724412	taaaagaatctattaatgggccct a[A/T]aaaattagctatgtacat tattttc	A	T	NM_004392 // downstream // 989547 // Hs.63931 // DACH1 // 1602 // dachshund homolog 1 (Drosophila) /// NM_020866 // upstream // 340092 // Hs.106808 // KLHL1 // 57626 // kelch-like 1 (Drosophila) /// NM_080759 // downstream // 989547 // Hs.63931 // DACH1	DACH1	DACH1, rs9317931, dachshund homolog 1 (Drosophila) ,q21.33
SNP_A-1711334	ttcattgcatttagtaataatct[C/G]aacattcatgatacataaga gtat	C	G	NM_004392 // downstream // 726432 // Hs.63931 // DACH1 // 1602 // dachshund homolog 1 (Drosophila) /// NM_020866 // upstream // 603207 // Hs.106808 // KLHL1 // 57626 // kelch-like 1 (Drosophila) /// NM_080759 // downstream // 726432 // Hs.63931 // DACH1	DACH1	DACH1, rs10492733, dachshund homolog 1 (Drosophila) ,q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1655437	tcacttatcatgaagctattggg[A/G]gttatataagataaaagctgatga	A	G	NM_004392 // downstream // 562822 // Hs.63931 // DACH1 // 1602 // dachshund homolog 1 (Drosophila) /// NM_020866 // upstream // 766817 // Hs.106808 // KLHL1 // 57626 // kelch-like 1 (Drosophila) /// NM_080759 // downstream // 562822 // Hs.63931 // DACH1	DACH1	DACH1 , rs7990294, dachshund homolog 1 (Drosophila), q21.33
SNP_A-2079642	accctaattagtaaa[A/G]gagccatcaaaatact	A	G	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1951778	tttcgtctctgacaac[A/T]ctaatgacttcatcta	A	T	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2290591	gcaagaaaggatgatc[C/T]agaaactactgtaaa	C	T	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2066936	acaaacaagaaaaagaa[G/T]gtgaaccctgtac	G	T	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1924992	ttatcaaaggtgccga[C/T]aatatacaatgggag	C	T	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2127543	ataacattaagagaac[A/G]aagtcctgtactccag	A	G	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2037124	aacaaaagcatgaaaa[C/G]tgaatatgttgaaatg	C	G	NM_020866 // intron // 0 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// ENST00000279889 // intron // 0 // — // — // — // —	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2126862	ataaagcaagcttcca[C/T]atccatacagagctt	C	T	NM_020866 // upstream // 12106 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 1317401 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2153873	tacatgaaactctcaa[A/G]cagactgacacacatt	A	G	NM_020866 // upstream // 97689 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 1231818 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1834523	taccaaatggatggaa[G/T]aatgaaataactgatt	G	T	NM_020866 // upstream // 331161 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 998346 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-1842362	taggtattgtctttta[C/G]gtcaaccatttacttt	C	G	NM_020866 // upstream // 340190 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 989317 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2027804	aaacccttgaccatg[A/G]agacttgaacaatcac	A	G	NM_020866 // upstream // 340920 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 988587 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2151742	atgtttaacatttcaa[A/G]ggtgcataatccaact	A	G	NM_020866 // upstream // 385027 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 944480 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1917159	tgttgtttgcaata[C/T]acctcaatttaaatt	C	T	NM_020866 // upstream // 385183 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 944324 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2188866	cagtggtgtataattа[C/T]gagaaaattctatttt	C	T	NM_020866 // upstream // 429041 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 900466 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2218044	cctgccataaaacttcg[G/T]cacacaatggagtcta	G	T	NM_020866 // upstream // 658058 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 671449 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2154718	tttagccaggctttccg[A/G]ctctcacctccaaata	A	G	NM_020866 // upstream // 902523 // Hs.508201 // KLHL1 // 57626 // Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA. /// NM_080759 // downstream // 426984 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcrip	KLHL1	KLHL1, Homo sapiens kelch-like 1 (Drosophila) (KLHL1), q21.33
SNP_A-2094541	agaataaggactgaga[C/T]gatctggcaatgaaga	C	T	NM_080759 // intron // 0 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // intron // 0 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-2155430	ttgactcagttctca[C/T]ctctaagttgagttga	C	T	NM_080759 // intron // 0 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // intron // 0 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-2224585	cgtcactcctagtcc[A/G]gataaccagatccagt	A	G	NM_080759 // upstream // 234991 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // upstream // 235414 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Dros	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-2112555	aggcacgacctggaaa[G/T]ctcaattaaaatcaca	G	T	NM_080759 // upstream // 439008 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // upstream // 439431 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Dros	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q21.33
SNP_A-1668698	cttactctgtctaaaaggaagttta[C/T]attatgaggacaaaggagatggat	C	T	NM_001730 // downstream // 484323 // Hs.84728 // KLF5 // 688 // Kruppel like factor 5 (intestinal) /// NM_007249 // downstream // 124151 // Hs.164467 // KLF12 // 11278 // Kruppel-like factor 12 /// NM_016285 // downstream // 250708 // Hs.164467 // KLF12	KLF5	KLF5 , rs9318191, Kruppel-like factor 5 (intestinal) ,q22.1
SNP_A-1649786	aaataaataaatctaacttaagatg[C/T]aattttgagggtctgcttgggtt	C	T	NM_001730 // downstream // 544041 // Hs.84728 // KLF5 // 688 // Kruppel like factor 5 (intestinal) /// NM_007249 // downstream // 64433 // Hs.164467 // KLF12 // 11278 // Kruppel-like factor 12 /// NM_016285 // downstream // 190990 // Hs.164467 // KLF12 /	KLF5	KLF5 , rs10492702, Kruppel-like factor 5 (intestinal) ,q22.1
SNP_A-2034742	aaatgaatcaataatc[C/T]gagctaggaagttag	C	T	NM_080759 // upstream // 830345 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, mRNA. /// NM_004392 // upstream // 830768 // Hs.129452 // DACH1 // 1602 // Homo sapiens dachshund homolog 1 (Dros	DACH1	DACH1, Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2302927	gctaggaagaggtgct[C/T]acactcagctcactgg	C	T	NM_024808 // downstream // 136109 // Hs.209715 // FLJ22624 // 79866 // Homo sapiens FLJ22624 protein (FLJ22624), mRNA. /// NM_014953 // upstream // 242570 // Hs.531029 // KIAA1008 // 22894 // Homo sapiens KIAA1008 (KIAA1008), mRNA. /// AF330044 // upstrea	FLJ22624	FLJ22624, Homo sapiens FLJ22624 protein (FLJ22624), q22.1
SNP_A-1883316	tgaacaacacagaata[A/C]atactcataccttttt	A	C	NM_016285 // downstream // 442880 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 442880 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-1934058	ttctcagaatccttcc[A/G]gcatccagtataaagtg	A	G	NM_016285 // downstream // 362084 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 362084 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-1916467	tgtttaaagtgatggaa[A/G]aatagacagatggaaa	A	G	NM_016285 // downstream // 342524 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 342524 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2159013	attgttcctggagac[C/G]agtgacattgataggg	C	G	NM_016285 // downstream // 319423 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 319423 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2242750	ctgcatgttcagacaa[A/G]gagtggttgaggaaga	A	G	NM_016285 // downstream // 256125 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 256125 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2246043	ctggtatctggatgag[A/G]atggcaaccgctcttc	A	G	NM_016285 // downstream // 133615 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 133615 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2203492	ccagaagacacgtgac[A/G]ggggttctcagtataa	A	G	NM_016285 // downstream // 133297 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 133297 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2117168	aggtgccaagccataa[A/G]cttcagtgtaattcac	A	G	NM_016285 // downstream // 31236 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // downstream // 31236 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12).	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2157746	cctcaggctgcaa[C/T]gtagagggcctgaac	C	T	NM_016285 // intron // 0 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // intron // 0 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript vari	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-2157939	caatccaacacagtag[G/T]ttcactatcaccatt	G	T	NM_016285 // upstream // 133223 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // upstream // 133223 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), t	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2157942	cacctgactgtgctaa[A/C]actagagcctatttct	A	C	NM_016285 // upstream // 133755 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, mRNA. /// NM_007249 // upstream // 133755 // Hs.373857 // KLF12 // 11278 // Homo sapiens Kruppel-like factor 12 (KLF12), t	KLF12	KLF12, Homo sapiens Kruppel-like factor 12 (KLF12), transcript variant 2, q22.1
SNP_A-1809279	gtgactatcctactaa[A/G]tatcttactcaacgaa	A	G	ENST00000325811 // upstream // 32399 // — // — // — // — /// ENST00000325796 // downstream // 786424 // — // — // — // —	-	q22.1
SNP_A-1654171	cttaaacttatttatgaaatcgtcc[C/T]aattgatgtaaagagccatttattg	C	T	AF330045 // intron // 0 // Hs.5978 // LMO7 // 4008 // LIM domain only 7	LMO7	LMO7 , rs9318370, LIM domain only 7,q22.2
SNP_A-1806339	gtccttctgaatatcg[A/G]atagagaaggaaacca	A	G	ENST00000325811 // upstream // 222952 // — // — // — // — /// ENST00000325796 // downstream // 595871 // — // — // — // —	-	q22.1
SNP_A-2291123	gcaatagctagataac[A/C]agcatacatacccaca	A	C	ENST00000325811 // upstream // 223432 // — // — // — // — /// ENST00000325796 // downstream // 595391 // — // — // — // —	-	q22.1
SNP_A-2266981	gaataaaaatgcaaga[A/G]agatctgtcttagcct	A	G	ENST00000325811 // upstream // 225190 // — // — // — // — /// ENST00000325796 // downstream // 593633 // — // — // — // —	-	q22.1
SNP_A-2158445	atgatgtagtatagaa[A/G]tgggaaaataggctct	A	G	ENST00000325811 // upstream // 235021 // — // — // — // — /// ENST00000325796 // downstream // 583802 // — // — // — // —	-	q22.1
SNP_A-1951318	tttccctggttgatga[A/G]gtgttaggtacgttag	A	G	ENST00000325811 // upstream // 237136 // — // — // — // — /// ENST00000325796 // downstream // 581687 // — // — // — // —	-	q22.1
SNP_A-2178594	cactctccacataaaa[A/T]tattcaaataggctgg	A	T	ENST00000325811 // upstream // 241413 // — // — // — // — /// ENST00000325796 // downstream // 577410 // — // — // — // —	-	q22.1
SNP_A-1678588	agttgttgaaggaatggtgatatac[C/T]ggctgacacaagtcttta cttactg	C	T	NM_138444 // downstream // 846465 // Hs.109438 // KCTD12 // 115207 // potassium channel tetramerisation domain containing 12	KCTD12	KCTD12 , rs10507846, potassium channel tetramerisation domain containing 12,q22.2
SNP_A-1720307	aatttgatccttttaagctgtgtta[C/T]gtaggccggtactgcattca gtcta	C	T	NM_138444 // downstream // 457181 // Hs.109438 // KCTD12 // 115207 // potassium channel tetramerisation domain containing 12	KCTD12	KCTD12 , rs1576867, potassium channel tetramerisation domain containing 12,q22.2
SNP_A-1744763	gagtccccaagctggaaattgttaa[C/T]tattgaccaaattagaa ataaatat	C	T	NM_138444 // downstream // 437482 // Hs.109438 // KCTD12 // 115207 // potassium channel tetramerisation domain containing 12	KCTD12	KCTD12 , rs10507856, potassium channel tetramerisation domain containing 12,q22.2
SNP_A-1688206	cttaattcaattttcttcagtccta[G/T]aatagtcagcacatgcagtt atttt	G	T	NM_138444 // downstream // 376222 // Hs.109438 // KCTD12 // 115207 // potassium channel tetramerisation domain containing 12	KCTD12	KCTD12 , rs283966, potassium channel tetramerisation domain containing 12,q22.2
SNP_A-2042546	aactcatgtatttgta[C/T]gggtggtgtattagtc	C	T	NM_005358 // intron // 0 // Hs.207631 // LMO7 // 4008 // Homo sapiens LIM domain 7 (LMO7), mRNA. /// AF330045 // intron // 0 // Hs.207631 // LMO7 // 4008 // Homo sapiens LIM domain only 7 (LMO7) mRNA, complete cds. /// ENST00000321813 // intron // 0 // –	LMO7	LMO7, Homo sapiens LIM domain 7 (LMO7), q22.2
SNP_A-2254183	cttgatctctacttta[C/T]cgatgagaaaataagg	C	T	NM_005358 // intron // 0 // Hs.207631 // LMO7 // 4008 // Homo sapiens LIM domain 7 (LMO7), mRNA. /// AF330045 // intron // 0 // Hs.207631 // LMO7 // 4008 // Homo sapiens LIM domain only 7 (LMO7) mRNA, complete cds. /// ENST00000321813 // intron // 0 // –	LMO7	LMO7, Homo sapiens LIM domain 7 (LMO7), q22.2
SNP_A-1711578	agtaatactaccttagatgtgaaaa[C/T]actaatattagcaccag acttcagg	C	T	NM_001208 // downstream // 44956 // - // - // - // - /// NM_006493 // upstream // 17004 // Hs.30213 // CLN5 // 1203 // ceroid-lipofuscinosis, neuronal 5	-	- , rs679090, - ,q22.3
SNP_A-1795604	ggtgctgccaaaattc[C/T]agttattggaccaaaa	C	T	NM_138444 // downstream // 486856 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 511894 // — // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2267115	gaataaggagaatgta[A/T]gcacaaagaacaagat	A	T	NM_138444 // downstream // 482757 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 515993 // — // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043391	aactggctcataaatc[G/T]atagtcatgagaaatt	G	T	NM_138444 // downstream // 476186 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 522564 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-1942637	ttgggacctcaagaag[A/C]agatattgaatgggat	A	C	NM_138444 // downstream // 468294 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 530456 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-1802715	gtatgatggacccaga[A/G]cttaaatttttgttagt	A	G	NM_138444 // downstream // 466537 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 532213 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2226365	ctaagacatcagctaa[A/G]gaaagtatatgacacg	A	G	NM_138444 // downstream // 455325 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 543425 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2036218	aaattatttctccaaa[A/C]aaagacagggtgtatc	A	C	NM_138444 // downstream // 447385 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 551365 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2231199	ctattataattgaata[C/T]ggtcacgtgccacata	C	T	NM_138444 // downstream // 445563 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 553187 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-1794139	ggtcagtaatgtgtta[C/T]gctttgacattatcat	C	T	NM_138444 // downstream // 445434 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 553316 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-1938264	ttgacctcagtgacta[A/G]aacaggagaagaacgtc	A	G	NM_138444 // downstream // 441497 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 557253 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2150524	atgtgactcaatggtc[C/T]caagatactgccagtc	C	T	NM_138444 // downstream // 423594 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 575156 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2271764	gaccagtggttcagc[A/G]ataagctgatgtagcc	A	G	NM_138444 // downstream // 423431 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 575319 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2214126	cctaatctttgctaa[C/G]tggactttccatata	C	G	NM_138444 // downstream // 422289 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 576461 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1718141	gttgcactattcatatttataaga[C/G]cgaatcatactcagttttgttcct	C	G	NM_003843 // intron // 0 // Hs.115166 // SCEL // 8796 // sciellin /// NM_144777 // intron // 0 // Hs.115166 // SCEL // 8796 // sciellin	SCEL	SCEL, rs10507870, sciellin, q22.3
SNP_A-2256847	ctttccatttggata[A/C]atcttcacactac	A	C	NM_138444 // downstream // 384416 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 614334 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2160393	ccaatagaagtaatac[A/T]acaggttcagaatcca	A	T	NM_138444 // downstream // 379202 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 619548 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2160395	gcttgagtctttgatat[C/T]aggggtgacagagata	C	T	NM_138444 // downstream // 379170 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 619580 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.2
SNP_A-2276472	gagaggcaaaaagaga[A/G]gaattcaaccttgaac	A	G	NM_138444 // downstream // 155774 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000318245 // downstream // 842976 // — // — // — /// ENST00000317765 // downst	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.3
SNP_A-1894244	tgcattattgtctccaj[A/G]atattccaaaccctcc	A	G	NM_138444 // upstream // 39085 // Hs.109438 // KCTD12 // 115207 // Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), mRNA. /// ENST00000317765 // upstream // 39085 // — // — // — /// ENST00000237763 // upstream //	KCTD12	KCTD12, Homo sapiens potassium channel tetramerisation domain containing 12 (KCTD12), q22.3
SNP_A-2155808	attcccttagggagaaa[C/T]aaccaaagatgctgct	C	T	NM_006493 // upstream // 25010 // Hs.30213 // CLN5 // 1203 // Homo sapiens ceroid-lipofuscinosis, neuronal 5 (CLN5), mRNA. /// ENST00000218979 // downstream // 7677 // — // — // — /// ENST00000218990 // upstream // 25010 // — // — // —	CLN5	CLN5, Homo sapiens ceroid-lipofuscinosis, neuronal 5 (CLN5), q22.3
SNP_A-2161969	atttgttcttgaattc[C/G]aggccaaccagggtcc	C	G	NM_012158 // intron // 0 // Hs.508284 // FBXL3 // 26224 // Homo sapiens F-box and leucine-rich repeat protein 3 (FBXL3), mRNA. /// ENST00000281993 // intron // 0 // — // — // — /// ENST00000355619 // intron // 0 // — // — // —	FBXL3	FBXL3, Homo sapiens F-box and leucine-rich repeat protein 3 (FBXL3), q22.3
SNP_A-1842392	taggtccacacttgac[A/G]gtacactctcatgagg	A	G	NM_012158 // upstream // 13158 // Hs.508284 // FBXL3 // 26224 // Homo sapiens F-box and leucine-rich repeat protein 3 (FBXL3), mRNA. /// NM_012158 // upstream // 13156 // Hs.508284 // FBXL3 // 26224 // Homo sapiens F-box and leucine-rich repeat protein 3	FBXL3	FBXL3, Homo sapiens F-box and leucine-rich repeat protein 3 (FBXL3), q22.3
SNP_A-2156578	attctgacgagtaatc[A/C]acacagtgggaggg	A	C	NM_015057 // intron // 0 // Hs.151411 // MYCBP2 // 23077 // Homo sapiens MYC binding protein 2 (MYCBP2), mRNA. /// ENST00000357337 // intron // 0 // — // — // — // — /// ENST00000360084 // intron // 0 // — // — // — // —	MYCBP2	MYCBP2, Homo sapiens MYC binding protein 2 (MYCBP2), q22.3
SNP_A-1893243	tgcagaggacacagaa[A/G]tgttaggacatggac	A	G	NM_003843 // intron // 0 // Hs.115166 // SCEL // 8796 // Homo sapiens sciellin (SCEL), transcript variant 1, mRNA. /// ENST00000348770 // intron // 0 // — // — // — // —	SCEL	SCEL, Homo sapiens sciellin (SCEL), transcript variant 1, q22.3
SNP_A-1807858	gtcttagcaacagaaaa[A/G]ctcttagatagtaggc	A	G	NM_003843 // intron // 0 // Hs.115166 // SCEL // 8796 // Homo sapiens sciellin (SCEL), transcript variant 1, mRNA. /// ENST00000348770 // intron // 0 // — // — // — // —	SCEL	SCEL, Homo sapiens sciellin (SCEL), transcript variant 1, q22.3
SNP_A-1817834	gttcctggtcccactg[C/T]aggttctggccatgcc	C	T	NM_144595 // upstream // 57013 // Hs.349955 // FLJ30046 // 122060 // Homo sapiens hypothetical protein FLJ30046 (FLJ30046), mRNA. /// NM_144595 // upstream // 78769 // Hs.349955 // FLJ30046 // 122060 // Homo sapiens hypothetical protein FLJ30046 (FLJ30046	FLJ30046	FLJ30046, Homo sapiens hypothetical protein FLJ30046 (FLJ30046), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2161451	ccccctttcgtggga[C/T]gagagcagagggagat	C	T	NM_144595 // upstream // 40406 // Hs.349955 // FLJ30046 // 122060 // Homo sapiens hypothetical protein FLJ30046 (FLJ30046), mRNA. /// NM_144595 // upstream // 62162 // Hs.349955 // FLJ30046 // 122060 // Homo sapiens hypothetical protein FLJ30046 (FLJ30046	FLJ30046	FLJ30046, Homo sapiens hypothetical protein FLJ30046 (FLJ30046), q22.3
SNP_A-1921110	ttacagttaaaaaacg[G/T]cagcctggactaagag	G	T	NM_000115 // upstream // 357307 // Hs.82002 // EDNRB // 1910 // Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, mRNA. /// NM_003991 // upstream // 357307 // Hs.82002 // EDNRB // 1910 // Homo sapiens endothelin receptor type B (EDNRB	EDNRB	EDNRB, Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, q22.3
SNP_A-1878195	tctgtcaagaaacaaac[A/C]acgacgtcacatttat	A	C	NM_000115 // upstream // 516185 // Hs.82002 // EDNRB // 1910 // Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, mRNA. /// NM_003991 // upstream // 516185 // Hs.82002 // EDNRB // 1910 // Homo sapiens endothelin receptor type B (EDNRB	EDNRB	EDNRB, Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, q31.1
SNP_A-2219158	cctgtcaaaaaaaaga[A/G]cactcaattctgttt	A	G	NM_000115 // upstream // 617786 // Hs.82002 // EDNRB // 1910 // Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, mRNA. /// NM_003991 // upstream // 617786 // Hs.82002 // EDNRB // 1910 // Homo sapiens endothelin receptor type B (EDNRB	EDNRB	EDNRB, Homo sapiens endothelin receptor type B (EDNRB), transcript variant 1, q31.1
SNP_A-1727849	ttttctctccctggcagtgtgtaca[A/G]aagcgaagactacaggc tgaaattc	A	G	NM_005842 // downstream // 618420 // Hs.18676 // SPRY2 // 10253 // sprouty homolog 2 (Drosophila)	SPRY2	SPRY2 , rs3908811, sprouty homolog 2 (Drosophila),q31.1
SNP_A-1738983	ttagtctttctagggatgactacta[A/G]aactccaaatagtatggc cttattt	A	G	NM_005842 // downstream // 566581 // Hs.18676 // SPRY2 // 10253 // sprouty homolog 2 (Drosophila)	SPRY2	SPRY2 , rs10507900, sprouty homolog 2 (Drosophila),q31.1
SNP_A-1645576	ctcttaagggtagagatttcaaaga[C/T]gtaacttccaccacaa cagatggg	C	T	NM_005842 // downstream // 504027 // Hs.18676 // SPRY2 // 10253 // sprouty homolog 2 (Drosophila)	SPRY2	SPRY2 , rs2152227, sprouty homolog 2 (Drosophila),q31.1
SNP_A-1733248	ccagagttccagctctggtaaatcat[C/T]agctttaggtggtctca agtcca	C	T	NM_005842 // downstream // 291199 // Hs.18676 // SPRY2 // 10253 // sprouty homolog 2 (Drosophila)	SPRY2	SPRY2 , rs10507903, sprouty homolog 2 (Drosophila),q31.1
SNP_A-1934971	ttctgacttgaggta[C/T]gctactaggctgatta	C	T	NM_024546 // upstream // 331702 // Hs.93956 // C13orf7 // 79596 // Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA. /// NM_022118 // downstream // 329090 // Hs.131715 // C13orf10 // 64062 // Homo sapiens chromosome 13 open reading frame 10	C13orf7	C13orf7, Homo sapiens chromosome 13 open reading frame 7 (C13orf7), q31.1
SNP_A-2120720	agtcctacactaaatc[C/T]agtctcatacccttgc	C	T	NM_024546 // upstream // 539775 // Hs.93956 // C13orf7 // 79596 // Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA. /// NM_022118 // downstream // 121017 // Hs.131715 // C13orf10 // 64062 // Homo sapiens chromosome 13 open reading frame 10	C13orf7	C13orf7, Homo sapiens chromosome 13 open reading frame 7 (C13orf7), q31.1
SNP_A-2092599	agaaatagccttctaa[A/G]acagcactaataaaaa	A	G	NM_022118 // upstream // 67449 // Hs.131715 // C13orf10 // 64062 // Homo sapiens chromosome 13 open reading frame 10 (C13orf10), mRNA. /// ENST00000327303 // upstream // 104253 // — // — // — /// ENST00000267229 // upstream // 67449 // — //	C13orf10	C13orf10, Homo sapiens chromosome 13 open reading frame 10 (C13orf10), q31.1
SNP_A-1847004	tatcaggaataaggac[A/G]gagtttcaaagaacat	A	G	ENST00000216652 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2178270	cactcacaactcatta[G/T]cacagccttgatccca	G	T	NM_005842 // downstream // 686582 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000216652 // downstream // 95311 // — // — // — // — /// ENST00000258661 // downstream // 686582 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2239158	ctctgataattccac[A/G]ctcctaaggcatcagg	A	G	NM_005842 // downstream // 669180 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000216652 // downstream // 112713 // — // — // — // — /// ENST00000258661 // downstream // 669180 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920015	ttaatagtgcaatctc[A/G]acaagtgcgtatgagt	A	G	NM_005842 // downstream // 662344 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 119549 // --- // --- // --- /// ENST00000258661 // downstream // 662344 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2210642	cccctcatttagtaga[C/T]gcttgctaaatattat	C	T	NM_005842 // downstream // 658868 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 123025 // --- // --- // --- /// ENST00000258661 // downstream // 658868 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1874268	tctccactggaaaaag[A/G]ataaatgtcttctaag	A	G	NM_005842 // downstream // 643323 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 138570 // --- // --- // --- /// ENST00000258661 // downstream // 643323 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2115326	agggatagggtaca[A/G]catttcagagaggagg	A	G	NM_005842 // downstream // 620998 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 160895 // --- // --- // --- /// ENST00000258661 // downstream // 620998 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1953798	tttgagagttgtcaaa[A/G]tatatgttacttaagg	A	G	NM_005842 // downstream // 614846 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 167047 // --- // --- // --- /// ENST00000258661 // downstream // 614846 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2028623	aaactggcacataaac[A/G]ctagatcttcaactga	A	G	NM_005842 // downstream // 598509 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 183384 // --- // --- // --- /// ENST00000258661 // downstream // 598509 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1832926	tacaattcaaggtaaa[C/T]gtgtaaatggaaattt	C	T	NM_005842 // downstream // 588950 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 192943 // --- // --- // --- /// ENST00000258661 // downstream // 588950 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2190615	catactcaatagttaa[C/T]agactgcattttgcat	C	T	NM_005842 // downstream // 567802 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 214091 // --- // --- // --- /// ENST00000258661 // downstream // 567802 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2052574	aagtagtttagcaga[A/G]caaagaagtcaagttc	A	G	NM_005842 // downstream // 549714 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 232179 // --- // --- // --- /// ENST00000258661 // downstream // 549714 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1830936	taatgaatagaactaa[A/G]taatcatcccttaca	A	G	NM_005842 // downstream // 484454 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 297439 // --- // --- // --- /// ENST00000258661 // downstream // 484454 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2122211	agtgcaagtttattga[C/G]acctacaaatgtcaca	C	G	NM_005842 // downstream // 482107 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 299786 // --- // --- // --- /// ENST00000258661 // downstream // 482107 // --- // ---	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1915880	tgttgagagcttccta[C/T]gtgtcaagtctgtga	C	T	NM_005842 // downstream // 482003 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 299890 // — // — // — /// ENST00000258661 // downstream // 482003 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1907549	tgtaaattactaacac[C/T]gtcaactgagagtaga	C	T	NM_005842 // downstream // 463827 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 318066 // — // — // — /// ENST00000258661 // downstream // 463827 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2062680	aatgtctattgtgacc[C/T]cattattcatttctgt	C	T	NM_005842 // downstream // 463410 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 318483 // — // — // — /// ENST00000258661 // downstream // 463410 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2213013	ccgaagtcctgctttc[A/C]attctaggttcctgcc	A	C	NM_005842 // downstream // 298974 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 482919 // — // — // — /// ENST00000258661 // downstream // 298974 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2104844	agcatactgcttagta[C/T]gctgagagaagaaagcgc	C	T	NM_005842 // downstream // 186117 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 595776 // — // — // — /// ENST00000258661 // downstream // 186117 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2238972	ctcttcctagcctcca[C/T]gtaacattataaatat	C	T	NM_005842 // downstream // 153247 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // downstream // 628646 // — // — // — /// ENST00000258661 // downstream // 153247 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2085570	actccatcttccagta[C/T]gctttaactccatctt	C	T	NM_005842 // upstream // 39942 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000218652 // upstream // 39942 // — // — // — /// ENST00000314900 // downstream // 2538189 // — // — // -	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1683218	cacaacaatttcttatctagaaaa[A/T]gtaattgctttgacctac cttga	A	T	BC016673 // downstream // 1335946 // - // - // Homo sapiens cDNA clone MGC:21889 IMAGE:4345550, complete cds. /// NM_005842 // upstream // 1241997 // Hs.18676 // SPRY2 // 10253 // sprouty homolog 2 (Drosophila)	-	- , rs1855547, Homo sapiens cDNA clone MGC:21889 IMAGE:4345550, complete cds. , q31.1
SNP_A-2290931	gcaaggttttcacca[A/G]ccaacaaacatgcgaa	A	G	NM_005842 // upstream // 171146 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream // 171146 // — // — // — /// ENST00000314900 // downstream // 2406985 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1812282	gtggatgaacaaaatac[C/T]aagaggaaaacttcaag	C	T	NM_005842 // upstream // 375291 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream // 375291 // — // — // — /// ENST00000314900 // downstream // 2202840 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2230118	ctatacacacagtgta[A/C]gtagtaacatgactga	A	C	NM_005842 // upstream // 734208 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream // 734208 // — // — // — /// ENST00000314900 // downstream // 1843923 // — // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2164509	ccatatataataaacac[G/T]ggaatcttcataaatg	G	T	NM_005842 // upstream // 1381890 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream // 1381890 // — // — // — /// ENST00000314900 // downstream // 1196241 // — // —	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-2039615	aacatgaactgtacca[C/T]ccacttacgttgcat	C	T	NM_005842 // upstream // 1881821 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream // 1881821 // — // — // — /// ENST00000314900 // downstream // 696310 // — // — /	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1674399	atattcatagtgtatcatatgctaa[C/T]gaaatgcaaataacatca attctgg	C	T	AB067497 // downstream // 389244 // Hs.415478 // SLITRK1 // 114798 // SLIT and NTRK-like family, member 1 /// BC016873 // upstream // 567641 // - // - // Homo sapiens cDNA clone MGC:21889 IMAGE:4345550, complete cds.	SLITRK1	SLITRK1 , rs9318946, SLIT and NTRK-like family, member 1 ,q31.1
SNP_A-2048853	aagccctcaactgtga[A/G]aagggaccctgaaagt	A	G	NM_005842 // upstream // 2314870 // Hs.18676 // SPRY2 // 10253 // Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA. /// ENST00000258661 // upstream // 2314870 // — // — // — /// ENST00000314900 // downstream // 263261 // — // — /	SPRY2	SPRY2, Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), q31.1
SNP_A-1650250	ccatttgtatttatactatatttgc[C/G]cttttgatacttttctcttctttagtt	C	G	AB067497 // upstream // 75143 // Hs.415478 // SLITRK1 // 114798 // SLIT and NTRK-like family, member 1 /// NM_032229 // downstream // 1836330 // Hs.120910 // SLITRK6 // 84189 // SLIT and NTRK-like family, member 6	SLITRK1	SLITRK1 , rs9319006, SLIT and NTRK-like family, member 1 ,q31.1
SNP_A-1746296	tgcgggaggtgtgccttatcatca[A/G]actcagtagctttcccctg agtactt	A	G	AB067497 // upstream // 168384 // Hs.415478 // SLITRK1 // 114798 // SLIT and NTRK-like family, member 1 /// NM_032229 // downstream // 1743089 // Hs.120910 // SLITRK6 // 84189 // SLIT and NTRK-like family, member 6	SLITRK1	SLITRK1 , rs9319013, SLIT and NTRK-like family, member 1 ,q31.1
SNP_A-1905023	tgggtcctaacaaacc[A/G]atgtgagctcatgaaa	A	G	ENST00000314900 // upstream // 183938 // — // — // — /// ENST00000357497 // downstream // 508177 // — // — // — /// ENST00000359402 // downstream // 508230 // — // — // —	-	q31.1
SNP_A-2119054	agtagaggaagtagtg[A/G]agtaaaatgcttttta	A	G	ENST00000314900 // upstream // 607552 // — // — // — /// ENST00000357497 // downstream // 84563 // — // — // — /// ENST00000359402 // downstream // 84616 // — // — // —	-	q31.1
SNP_A-1834535	taccaacaacaattgta[C/G]ctgagctgtttcactc	C	G	ENST00000314900 // upstream // 615790 // — // — // — /// ENST00000357497 // downstream // 76325 // — // — // — /// ENST00000359402 // downstream // 76378 // — // — // —	-	q31.1
SNP_A-2156681	attctggatcagaaggg[A/T]aaacttacgtgtatt	A	T	ENST00000314900 // upstream // 162836 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000357497 // upstream // 73538 // — // — // — /// ENST00000359402 // upstream // 104499 // —	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-2166397	aacctgtaggtcctc[C/T]agtgcaggatgtactt	C	T	NM_052910 // upstream // 288965 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream // 288965 // — // — // — /// ENST00000355692 // downstream // 529014 // —	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-1848524	tatgaatttttacttta[A/G]cgatcacacagctaaa	A	G	NM_052910 // upstream // 318408 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream // 318408 // — // — // — /// ENST00000355692 // downstream // 499571 // —	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-1858993	tcagcataatgtttct[C/G]ctctcagatcttgaag	C	G	NM_052910 // upstream // 322066 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream // 322066 // — // — // — /// ENST00000355692 // downstream // 495913 // —	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796431	ggtgtttgttatgctg[C/T]acaatttgtcaaatac	C	T	NM_052910 // upstream // 473227 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream // 473227 // — // — // — // — /// ENST00000355692 // downstream // 344752 // —	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-1948072	tttagagtccacttac[A/G]cttgacttatatgtga	A	G	NM_052910 // upstream // 661025 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream // 661025 // — // — // — // — /// ENST00000355692 // downstream // 156954 // —	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-1957476	ttttataaatgatgaa[A/G]ccaattcaggtatatt	A	G	NM_052910 // upstream // 810791 // Hs.415478 // SLITRK1 // 114798 // Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), mRNA. /// ENST00000314878 // upstream // 810791 // — // — // — // — /// ENST00000355692 // downstream // 7188 // — /	SLITRK1	SLITRK1, Homo sapiens SLIT and NTRK-like family, member 1 (SLITRK1), q31.1
SNP_A-2053928	aagttaaaaacctaga[C/T]caattataggctgctg	C	T	NM_032229 // downstream // 1081248 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 9171 // — // — // — // — /// ENST00000332380 // downstream // 1081248 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2235098	ctcccagttttgctga[A/G]taagtgtgaagtgtca	A	G	NM_032229 // downstream // 1074428 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 15991 // — // — // — // — /// ENST00000332380 // downstream // 1074428 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2022848	aaaacaaacacaaaaa[C/T]attactcatacttgac	C	T	NM_032229 // downstream // 871430 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 218989 // — // — // — // — /// ENST00000332380 // downstream // 871430 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1890995	tgatgggagaggcatc[C/T]ctgaaggtttctgaca	C	T	NM_032229 // downstream // 572404 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 518015 // — // — // — // — /// ENST00000332380 // downstream // 572404 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1824283	taaaccatcttccaaa[G/T]tgaatgtaccattttg	G	T	NM_032229 // downstream // 556421 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 533998 // — // — // — // — /// ENST00000332380 // downstream // 556421 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1688518	tgaccaaagatttaaatcacaatac[A/G]acattccctttggatac attgaaag	A	G	NM_032229 // upstream // 554985 // Hs.120910 // SLITRK6 // 84189 // SLIT and NTRK-like family, member 6	SLITRK6	SLITRK6 , rs4523806, SLIT and NTRK-like family, member 6,q31.1
SNP_A-1932760	ttccttgaatcagaca[A/G]atctgtgtcaatacccc	A	G	NM_032229 // downstream // 476579 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 613840 // — // — // — // — /// ENST00000332380 // downstream // 476579 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-2289107	gatttctctgtctcat[A/T]aatatataaaacctga	A	T	NM_032229 // downstream // 184782 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000357014 // downstream // 905637 // — // — // — // — /// ENST00000332380 // downstream // 184782 //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2298545	gcccaggaaaaagg[G/T]aaactgacccaatgga	G	T	NM_032229 // upstream // 291522 // Hs.525105 // SLITRK6 // 84189 // Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), mRNA. /// ENST00000332380 // upstream // 291522 // --- // --- // --- /// ENST00000313206 // upstream // 294419 // --- //	SLITRK6	SLITRK6, Homo sapiens SLIT and NTRK-like family, member 6 (SLITRK6), q31.1
SNP_A-1889274	tgagtgcacttaccat[A/T]aaagtgttagattaag	A	T	NM_015567 // upstream // 1291999 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 103382 // --- // --- // --- // --- /// ENST00000298025 // upstream // 1291999 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-2158726	attgtctacttaact[G/T]actactgcaaagacta	G	T	NM_015567 // upstream // 1127147 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 268234 // --- // --- // --- // --- /// ENST00000298025 // upstream // 1127147 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-1812689	gtggctttatgctgcc[C/T]ccatgtaatttagtt	C	T	NM_015567 // upstream // 1063613 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 331768 // --- // --- // --- // --- /// ENST00000298025 // upstream // 1063613 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-2110358	aggaatgtctttgca[A/G]tgaaagtcagctggac	A	G	NM_015567 // upstream // 1047755 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 347626 // --- // --- // --- // --- /// ENST00000298025 // upstream // 1047755 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-2038350	aacacggcagaataa[A/C]agggtgtaatgtcagt	A	C	NM_015567 // upstream // 1004414 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 390967 // --- // --- // --- // --- /// ENST00000298025 // upstream // 1004414 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-2276782	gagataagttgagggtg[C/T]cacataggaagaatat	C	T	NM_015567 // upstream // 914102 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 481279 // --- // --- // --- // --- /// ENST00000298025 // upstream // 914102 // --- /	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.1
SNP_A-2168825	ttcacaacctgttatt[C/T]aaagtccaccgtatt	C	T	NM_015567 // upstream // 610180 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 785201 // --- // --- // --- // --- /// ENST00000298025 // upstream // 610180 // --- /	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2129813	atacatatacacgata[A/G]aaatatacacatacat	A	G	NM_015567 // upstream // 541353 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 854028 // --- // --- // --- // --- /// ENST00000298025 // upstream // 541353 // --- /	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2156746	attctgtctttctgc[A/G]cagttcaaataagggc	A	G	NM_015567 // upstream // 374552 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 1020829 // --- // --- // --- // --- /// ENST00000298025 // upstream // 374552 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1782095	ggcaacattgacgaat[A/G]acagttacatttattt	A	G	NM_015567 // upstream // 347834 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000330224 // downstream // 1047547 // --- // --- // --- // --- /// ENST00000298025 // upstream // 347834 // ---	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2162270	atttataaggaattg[A/G]aagtcattgaaaatat	A	G	NM_015567 // downstream // 143998 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 143998 // — // — // — // — /// ENST00000298437 // downstream // 1537711 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1830363	taatatgccaagttaa[A/T]caaaaccatttaatg	A	T	NM_015567 // downstream // 340459 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 340459 // — // — // — // — /// ENST00000298437 // downstream // 1341250 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1810981	gtgcatttttcctagag[A/T]ctcaggatgagaagaa	A	T	NM_015567 // downstream // 444536 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 444536 // — // — // — // — /// ENST00000298437 // downstream // 1237173 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1722662	ttgcagaaccattagaccaaaagcc[A/G]aagtaagtgtgtgaa ctcacaatag	A	G	AB020725 // downstream // 1566632 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 2152720 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs314565, SLIT and NTRK-like family, member 5 ,q31.2
SNP_A-1747857	caattatcccaaagcttcatggtgt[A/C]aacttgcaaacgtttgct acttgtc	A	C	AB020725 // downstream // 1576457 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 2142895 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs3114578, SLIT and NTRK-like family, member 5 ,q31.2
SNP_A-2100571	agatacaactcctgtg[A/G]acaacttcatggatc	A	G	NM_015567 // downstream // 662089 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 662089 // — // — // — // — /// ENST00000298437 // downstream // 1019620 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2140621	atcttagagatataa[C/T]cacatttactcaagaa	C	T	NM_015567 // downstream // 682994 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 682994 // — // — // — // — /// ENST00000298437 // downstream // 998715 // -	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2279294	gaggagatgtaaattc[A/G]caggcacttccagcta	A	G	NM_015567 // downstream // 730520 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 730520 // — // — // — // — /// ENST00000298437 // downstream // 951189 // -	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1915675	tgttctggaaggaaat[C/T]gaaggtcatagccgaa	C	T	NM_015567 // downstream // 860452 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 860452 // — // — // — // — /// ENST00000298437 // downstream // 821257 // -	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1922246	ttactgtaaacctcc[A/G]aaattgaggcaagtta	A	G	NM_015567 // downstream // 861350 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 861350 // — // — // — // — /// ENST00000298437 // downstream // 820359 // -	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1793004	ggtaccatattgtca[C/T]gtggattgaaatctta	C	T	NM_015567 // downstream // 865022 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 865022 // — // — // — // — /// ENST00000298437 // downstream // 816687 // -	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2199610	ccaaaacctaatata[A/T]ctctcacggtcggact	A	T	NM_015567 // downstream // 1024574 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 1024574 // — // — // — // — /// ENST00000298437 // downstream // 657135 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2024948	aaaataaagtaaggag[C/T]atcaaggccaaaatct	C	T	NM_015567 // downstream // 1228075 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 1228075 // — // — // — // — /// ENST00000298437 // downstream // 453634 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2170323	aatcaggattacctca[A/G]gagatagaagttaaga	A	G	NM_015567 // downstream // 1501489 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 1501489 // — // — // — // — /// ENST00000298437 // downstream // 180220 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2170355	ccatttgttaactcca[G/T]tgaattgtctgtgcaa	G	T	NM_015567 // downstream // 1534085 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 1534085 // — // — // — // — /// ENST00000298437 // downstream // 147624 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1810874	gtgcagtgcaaggcta[C/T]actcaggagcagagtg	C	T	NM_015567 // downstream // 1599901 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 1599901 // — // — // — // — /// ENST00000298437 // downstream // 81808 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-1848674	tatgagcctgtaagaa[C/T]cacagaattactgggc	C	T	NM_015567 // downstream // 1614460 // Hs.58009 // SLITRK5 // 26050 // Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), mRNA. /// ENST00000298025 // downstream // 1614460 // — // — // — // — /// ENST00000298437 // downstream // 67249 //	SLITRK5	SLITRK5, Homo sapiens SLIT and NTRK-like family, member 5 (SLITRK5), q31.2
SNP_A-2170545	gatgagaaacacttac[C/T]cttcctgttatggtga	C	T	ENST00000298437 // upstream // 50913 // — // — // — // — /// ENST00000330770 // downstream // 419461 // — // — // — // —	-	q31.3
SNP_A-2294640	gcagtgcagtcataat[A/G]aaggtcttactcaatt	A	G	ENST00000298437 // upstream // 214867 // — // — // — // — /// ENST00000330770 // downstream // 255507 // — // — // — // —	-	q31.3
SNP_A-1701229	tctttagggtagtaataaagactaa[A/G]taagtagtgtctgaatct atggcag	A	G	AB020725 // downstream // 3036178 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 683174 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs729270, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-2095918	agacaggaaagaaata[A/G]ctgcccatgaaaagga	A	G	ENST00000298437 // upstream // 304125 // — // — // — // — /// ENST00000330770 // downstream // 166249 // — // — // — // —	-	q31.3
SNP_A-1690057	aaatgagatattttgtatttagtaa[A/G]aaggcctcagctacatata agtgta	A	G	AB020725 // downstream // 3178066 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 541286 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs10507985, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1715719	agtcaatattagtttgcaatgataa[C/T]gatgataattttcatgaac aagtta	C	T	AB020725 // downstream // 3197265 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 522087 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs10507986, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1694279	ggggggataattttacacataactc[A/G]tagggttttcatgataattt aaaag	A	G	AB020725 // downstream // 3206785 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 512567 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs1414291, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1721750	tatggaagctctttttttgcaccc[A/G]ccagacacttcttccctgaa caaat	A	G	AB020725 // downstream // 3236426 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 482926 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs10507989, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1755240	atgctcaccattttcatagcagaaa[A/G]ctagttatactaaattgtt ctaatt	A	G	AB020725 // downstream // 3263369 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 455983 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs3928092, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-2040184	aaccaatacatggcac[A/G]agaagagacaaaaatt	A	G	NM_213724 // upstream // 1492386 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 1492386 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosom	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1858033	tcacttctctctctg[A/T]cacatctctgaagcag	A	T	NM_213724 // upstream // 1490836 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 1490836 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosom	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1729500	atagtccagatcctaactagaggatg[A/G]aaatgtgaattgtgtctg cctgatct	A	G	AB020725 // downstream // 3313385 // Hs.58009 // SLITRK5 // 26050 // SLIT and NTRK-like family, member 5 /// NM_004466 // upstream // 405967 // Hs.450919 // GPC5 // 2262 // glypican 5	SLITRK5	SLITRK5 , rs9284262, SLIT and NTRK-like family, member 5 ,q31.3
SNP_A-1914256	tgtgttacttgcaaaa[C/T]atcctggcttaagaa	C	T	NM_213724 // upstream // 1052545 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 1052545 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosom	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2151727	atgttgttttatgcaa[C/T]gaattttgaacagaaa	C	T	NM_213724 // upstream // 588046 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 588046 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2092678	agaaatctcaaagtca[A/C]atgaatggcaatattt	A	C	NM_213724 // upstream // 491618 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 491618 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2037395	aacaaatgtttgtgaa[A/G]aagcggcttgaaaat	A	G	NM_213724 // upstream // 485831 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 485831 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2298589	gcccactaacatctgg[G/T]caatttccaatgcaa	G	T	NM_213724 // upstream // 477767 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 477767 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1917775	ttaaaaccattgctag[A/T]cacagcttggatgtat	A	T	NM_213724 // upstream // 467206 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 467206 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2050743	aaggcagtaaaacatc[A/G]caatttaacttttata	A	G	NM_213724 // upstream // 463812 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 463812 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2136614	atcactagaaattggat[A/G]gttcatgaaaatgca	A	G	NM_213724 // upstream // 460339 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 460339 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2171950	gaaggagaacttagtc[C/T]gagtaaaggtcacaag	C	T	NM_213724 // upstream // 457477 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 457477 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2027697	aaaccatttcaatcaa[A/G]taattcagaataaagc	A	G	NM_213724 // upstream // 433497 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 433497 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2144403	atgataaatagtacttc[A/G]ctacatcttgatcct	A	G	NM_213724 // upstream // 418462 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 418462 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2218739	cctggctgtatatgaa[A/G]gaggatcaaacacaaa	A	G	NM_213724 // upstream // 396139 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 396139 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1831242	taatggagaaaaattc[C/T]actgagctaaatatat	C	T	NM_213724 // upstream // 392754 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 392754 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2096556	agacctgtcaatgtgt[A/T]aaaatattatctagaa	A	T	NM_213724 // upstream // 385570 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 385570 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1780828	ggatctggcattgcac[A/G]acaggtgaaaataagg	A	G	NM_213724 // upstream // 315669 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 315669 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-2172119	tgtaaatcacctctcc[A/G]ctactccttaggctcc	A	G	NM_213724 // upstream // 287111 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 287111 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1820221	gtttacactgtagtca[C/T]tgaaatcaatctacgc	C	T	NM_213724 // upstream // 210583 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA. /// NM_213723 // upstream // 210583 // Hs.24115 // C13orf25 // 407975 // Homo sapiens chromosome	C13orf25	C13orf25, Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, q31.3
SNP_A-1724684	taatgtccctttacaatgtatagca[A/G]ggatactgattagagagc catcatt	A	G	NM_004466 // intron // 0 // Hs.450919 // GPC5 // 2262 // glypican 5	GPC5	GPC5, rs6492611, glypican 5,q31.3
SNP_A-1674409	taacagaaaaaagaaaaaagaagaac[A/G]acagataagatat ttgtggtatctg	A	G	NM_004466 // intron // 0 // Hs.450919 // GPC5 // 2262 // glypican 5	GPC5	GPC5, rs1333674, glypican 5,q31.3
SNP_A-1677620	atataatgatcgtatgtaaataagc[A/G]cagcataacttactgaa aagagaaa	A	G	NM_004466 // intron // 0 // Hs.450919 // GPC5 // 2262 // glypican 5	GPC5	GPC5, rs1413191, glypican 5,q31.3
SNP_A-2172770	ccacagtgtcctggac[C/T]catttagatcaattgt	C	T	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2120366	agtcatgagagaagac[C/T]gaatgctaaaggaacc	C	T	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2273595	gactgagaaaggagaaa[C/T]ggggaagtatgaagg	C	T	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1926227	ttattacatcaagaac[A/G]agataggtgccacaac	A	G	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1822745	taaaaaatatgttatc[G/T]ctagcttcagcgtcct	G	T	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1722256	tgaaatcctaatcctctaggagg[G/T]aattattaacttgaatttg atgttt	G	T	NM_005708 // intron // 0 // Hs.508411 // GPC6 // 10082 // glypican 6	GPC6	GPC6 , rs7333716, glypican 6,q31.3
SNP_A-2176366	caccatataacaagca[G/T]aacctactgagatgga	G	T	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1788581	gggatcaggtagaagga[A/C]gttacagcggacaacc	A	C	NM_004466 // intron // 0 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// ENST00000319143 // intron // 0 // — // — // —	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1733554	ggatatttgagctcatggtacatta[C/T]aaaggagtatgtcaacat agagcac	C	T	NM_005708 // intron // 0 // Hs.508411 // GPC6 // 10082 // glypican 6	GPC6	GPC6 , rs7981536, glypican 6,q31.3
SNP_A-2308649	gctttccattacttca[C/T]gtctgagtccagttc	C	T	NM_004466 // downstream // 56588 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 304430 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000319143 // downstream // 56588 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2173734	aacactgtgactatca[G/T]acgatgtgaatgactc	G	T	NM_004466 // downstream // 66416 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 294602 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000319143 // downstream // 66416 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1653940	aattctatgaattctgggccagtct[C/G]tccacccagaatgtagta ttctaaa	C	G	NM_005708 // intron // 0 // Hs.508411 // GPC6 // 10082 // glypican 6	GPC6	GPC6 , rs1410747, glypican 6,q31.3
SNP_A-1929001	ttcagcctggcttaggt[C/T]agatagtaaatatttt	C	T	NM_004466 // downstream // 116514 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 244504 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000319143 // downstream // 116514	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2173784	gagtgaagaggaaccca[C/G]aagttctaagcactaa	C	G	NM_004466 // downstream // 281685 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 79333 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000319143 // downstream // 281685 /	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-2297023	gccaatgtgatttatg[A/G]agatttctgaaaaaa	A	G	NM_004466 // downstream // 356611 // Hs.546254 // GPC5 // 2262 // Homo sapiens glypican 5 (GPC5), mRNA. /// NM_005708 // upstream // 4407 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000319143 // downstream // 356611 //	GPC5	GPC5, Homo sapiens glypican 5 (GPC5), q31.3
SNP_A-1816303	gttagaaagcccagac[C/T]cttgaaaaactaccaa	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-1933234	ttctaaatcaatgacat[C/T]ctgttcacatgttaag	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-1824522	taaactgttttttcca[C/T]gaatgagagaaaggaa	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2143848	atgagataccacttta[C/T]gaccactgcgatgact	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1872106	tctactagccagtaaa[C/T]gtctgaatgtgtggct	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2303178	gctatcattcacttcaf[C/T]ggaggacacaaatgc	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2036775	aaatttatcctctac[A/G]ctcatctactgtgac	A	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2253467	cttctatcagtgtga[A/T]gatctttgataacagt	A	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2256403	cttatctgacctaaa[G/T]aaacttcatcatcctt	G	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2312224	ggacagggccctaaac[C/T]atgcatcgtggctgtt	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2174621	agataatttgccaca[C/T]gtatcttgtctttt	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2069948	acacagggaagtataa[A/G]atatccacgcaaaatc	A	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2174655	ctttacttagacaga[C/G]attaacatcagaaggc	C	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-1747393	gaaagacaaggctcaggttgccaaag[C/T]gccaccctccattg aaaaatggag	C	T	NM_005845 // intron // 0 // Hs.307915 // ABCC4 // 10257 // ATP-binding cassette, sub-family C (CFTR/MRP), member 4	ABCC4	ABCC4 , rs2009772, ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-1937786	ttgaagtgtgagataaa[A/G]atataaagacaggccca	A	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-1736701	gatttctctatccaaatagccagca[A/G]atactactcacctgattg acagact	A	G	NM_005845 // intron // 0 // Hs.307915 // ABCC4 // 10257 // ATP-binding cassette, sub-family C (CFTR/MRP), member 4	ABCC4	ABCC4 , rs1564351, ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-1689012	gaccagagtgcggaaacctcattca[C/T]atatcattaacacacc tggcatacg	C	T	NM_005845 // intron // 0 // Hs.307915 // ABCC4 // 10257 // ATP-binding cassette, sub-family C (CFTR/MRP), member 4	ABCC4	ABCC4 , rs1926657, ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-1818331	gttctgtgaagtttct[C/G]atgttctacttcttg	C	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2209928	ccccaatggctatata[A/C]atgagaaaaccaatat	A	C	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2089468	acttattgcttactg[A/G]acatcataagattgc	A	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2174929	ttgtgacagtaaatga[C/T]ggaacacttatcaat	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2174942	tctaggaagtattgaa[C/T]ctgtctaagaaaccct	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3
SNP_A-2034641	aaatgaaacaacaatc[C/T]ccacgaagcagtctta	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939350	ttgatgaatttctcac[A/G]agatactcatgcaata	A	G	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q32.1
SNP_A-2241693	ctgatattagtccata[C/T]gcaatttcttacaaaa	C	T	NM_005708 // intron // 0 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// ENST00000330809 // intron // 0 // — // — // — // —	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q32.1
SNP_A-2108039	agctctcaggatttgc[C/T]agtaagtagtttgtag	C	T	NM_005708 // downstream // 13665 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// NM_001922 // downstream // 22707 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related p	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q32.1
SNP_A-2122424	agtgcctgtcattaga[C/T]ggggtggtttaaacaa	C	T	NM_005708 // downstream // 28306 // Hs.444329 // GPC6 // 10082 // Homo sapiens glypican 6 (GPC6), mRNA. /// NM_001922 // downstream // 8066 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related pr	GPC6	GPC6, Homo sapiens glypican 6 (GPC6), q32.1
SNP_A-1782830	ggcagagaattacctc[A/G]aattaagttcaaattt	A	G	NM_001922 // intron // 0 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// ENST00000218564 // intron // 0 // — // — // — // —	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-1708176	cttgagacagcaatgaagggatgaa[A/G]gaatgaatgagtttat atttcaatt	A	G	-		, rs723576, ,q32.1
SNP_A-2098383	agagatttccgtcatc[A/G]agtaaatttagagaag	A	G	NM_001922 // intron // 0 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// ENST00000218564 // intron // 0 // — // — // — // —	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-2062935	aatgtgtctaggaaac[C/T]ctctagtgcttagtcc	C	T	NM_001922 // intron // 0 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// ENST00000218564 // intron // 0 // — // — // — // —	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-2291878	gcacagtcctaggcca[C/T]gctcaaattttattat	C	T	NM_001922 // upstream // 32627 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 61759 // Hs.12393 // TGDS // 23483 // Homo sapiens TDP-g	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-2288430	gattcttcctgatata[A/C]ctgagaagaaaccagc	A	C	NM_001922 // upstream // 45370 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 49016 // Hs.12393 // TGDS // 23483 // Homo sapiens TDP-g	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-2175204	tgaattggtaattggc[A/G]gatcaagtaaaatgtt	A	G	NM_001922 // upstream // 57478 // Hs.301865 // DCT // 1638 // Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), mRNA. /// NM_014305 // downstream // 36908 // Hs.12393 // TGDS // 23483 // Homo sapiens TDP-g	DCT	DCT, Homo sapiens dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT), q32.1
SNP_A-1710313	cctggcaatcagtaattacctatgt[C/G]ttttctgcattttctttacca ataa	C	G	-		, rs3901894, ,q32.1
SNP_A-2003487	agagtgtgctcaagtg[A/T]aatcgacaaccagtaa	A	T	NM_180989 // downstream // 74790 // Hs.159422 // ITR // 160897 // Homo sapiens intimal thickness-related receptor (ITR), mRNA. /// NM_007084 // downstream // 6741 // Hs.187577 // SOX21 // 11166 // Homo sapiens SRY (sex determining region Y)-box 21 (SOX21)	ITR	ITR, Homo sapiens intimal thickness-related receptor (ITR), q32.1
SNP_A-1754628	aacaatcctcttccagatatttgac[A/G]tggcttcctccttcaccttc tttgg	A	G	NM_020121 // intron // 0 // Hs.308242 // UGCGL2 // 55757 // UDP-glucose ceramide glucosyltransferase-like 2	UGCGL2	UGCGL2 , rs2389530, UDP-glucose ceramide glucosyltransferase-like 2,q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1954266	tttgcaatgtagtgac[A/T]aggtcctttcacc	A	T	NM_005845 // downstream // 189683 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000340968 // upstream // 71227 // — // — // — /// ENST00000261295 // downstream	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2162525	atttccagtttgat[A/C]aaatgaaaccacaggg	A	C	NM_005845 // downstream // 178294 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000340968 // upstream // 82616 // — // — // — /// ENST00000261295 // downstream	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-1664222	atttggaatcttccagtaatgtcca[A/C]gtaatcaacatgagacca ggtgaaa	A	C	NM_020121 // intron // 0 // Hs.308242 // UGCGL2 // 55757 // UDP-glucose ceramide glucosyltransferase-like 2	UGCGL2	UGCGL2 , rs544080, UDP-glucose ceramide glucosyltransferase-like 2,q32.1
SNP_A-1643399	accatctctggctggccctggaatg[A/G]cattacagtttctgaca caatgca	A	G	NM_020121 // intron // 0 // Hs.308242 // UGCGL2 // 55757 // UDP-glucose ceramide glucosyltransferase-like 2	UGCGL2	UGCGL2 , rs7983589, UDP-glucose ceramide glucosyltransferase-like 2,q32.1
SNP_A-2063814	aattaggacaagagaa[C/T]gaagtcatagaaggg	C	T	NM_005845 // downstream // 75820 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000340968 // upstream // 185090 // — // — // — /// ENST00000261295 // downstream	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-2091577	agaaaaatgtcacaga[A/C]cacatacatattatat	A	C	NM_005845 // downstream // 38014 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000340968 // upstream // 222896 // — // — // — /// ENST00000261295 // downstream	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-2122096	agtgatggaatgggac[G/T]gaaacccaagtctgcc	G	T	NM_005845 // intron // 0 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000261295 // intron // 0 // — // — // —	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-1835501	tacctggcacaggaca[G/T]gtactcagtaagtgag	G	T	NM_005845 // intron // 0 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000261295 // intron // 0 // — // — // —	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q32.1
SNP_A-2183876	cagccaatcaggtac[A/G]ggaacacccaaatatg	A	G	NM_005845 // intron // 0 // Hs.508423 // ABCC4 // 10257 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA. /// ENST00000261295 // intron // 0 // — // — // —	ABCC4	ABCC4, Homo sapiens ATP-binding cassette, sub-family C (CFTR q32.1
SNP_A-1751961	tggtagttctgtatcccaagccaaa[C/T]tcaaaatccgaaattatc tgttaca	C	T	NM_153456 // intron // 0 // Hs.508459 // HS6ST3 // 266722 // heparan sulfate 6-O-sulfotransferase 3	HS6ST3	HS6ST3 , rs1327634, heparan sulfate 6-O-sulfotransferase 3,q32.1
SNP_A-2052538	aagtaggttctaccat[A/G]attatcccaagaaca	A	G	NM_182848 // intron // 0 // Hs.534377 // CLDN10 // 9071 // Homo sapiens claudin 10 (CLDN10), transcript variant 1, mRNA. /// ENST00000257311 // intron // 0 // — // — // —	CLDN10	CLDN10, Homo sapiens claudin 10 (CLDN10), transcript variant 1, q32.1
SNP_A-1642557	cacagagcagtcacagaccaaatga[C/T]ggataattaagcatt ctggtacca	C	T	NM_153456 // intron // 0 // Hs.508459 // HS6ST3 // 266722 // heparan sulfate 6-O-sulfotransferase 3	HS6ST3	HS6ST3 , rs6491307, heparan sulfate 6-O-sulfotransferase 3,q32.1
SNP_A-2186352	caggctgggttaga[G/T]ctattggagaaggta	G	T	NM_006260 // intron // 0 // Hs.59214 // DNAJC3 // 5611 // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 3 (DNAJC3), mRNA. /// ENST00000218763 // intron // 0 // — // — // — /// ENST00000360638 // intron // 0 // — // — // —	DNAJC3	DNAJC3, Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 3 (DNAJC3), q32.1
SNP_A-2070808	acactacgtacagaaa[C/T]gaaccaccaccacctt	C	T	NM_006260 // intron // 0 // Hs.59214 // DNAJC3 // 5611 // Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 3 (DNAJC3), mRNA. /// ENST00000218763 // intron // 0 // — // — // —	DNAJC3	DNAJC3, Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 3 (DNAJC3), q32.1
SNP_A-1799432	gtaatctgtaggtaaa[A/C]catactgtcacactg	A	C	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3, Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1961140	tttttaaaaaccgtc[A/G]aagctatacagtagtt	A	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2096283	agaccagataaagaaga[G/T]agatttgagtaggagg	G	T	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2176226	tggattagtgcaagct[A/G]aagtgtcatcatatat	A	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2116113	aggtaacaagatcagc[A/G]aatgctaacagcagct	A	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2157406	attgaggtcttataga[C/T]atgaaatagctgcaga	C	T	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-1833775	tacagtacctaaaatat[C/G]taagcactcaaaaaag	C	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-1878436	tctgtgagatgtccaa[C/T]gaacgtgtcaggctaa	C	T	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-1940444	ttgccattccacaaat[A/G]actatgaaagtgcatg	A	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2064069	aattattccaaatatca[C/T]gtatcaccctgcatgc	C	T	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2054387	aagtttaagaaaatga[C/G]aaatcagccttagaaa	C	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2256916	ctttcctatctctaca[C/T]ctgctctttcctcagc	C	T	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2181299	cagacctcccctaatgc[A/G]attattgtaccaata	A	G	NM_153456 // intron // 0 // Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// ENST00000329068 // intron // 0 // — // — // —	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1
SNP_A-2031174	aaaggcataacaaggg[A/G]ccttcattacttcaaac	A	G	ENST00000326161 // 5UTR // 0 // — // — // —	-	q32.1
SNP_A-2306458	gctggtattgtgctga[C/T]ctacgaggtttccaaa	C	T	NM_153456 // downstream // 25887 /// Hs.171001 // HS6ST3 // 266722 // Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3), mRNA. /// NM_080818 // downstream // 126634 // Hs.352218 // OXGR1 // 27199 // Homo sapiens oxoglutarate (alpha-ketoglutarate	HS6ST3	HS6ST3. Homo sapiens heparan sulfate 6-O-sulfotransferase 3 (HS6ST3). q32.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2176741	acatgaatagtatgaa[C/T]gaaaacaatcctgt	C	T	NM_080818 // upstream // 171910 // Hs.352218 // OXGR1 // 27199 // Homo sapiens oxoglutarate (alpha-ketoglutarate) receptor 1 (OXGR1), mRNA. /// NM_207304 // upstream // 56060 // Hs.125715 // MBNL2 // 10150 // Homo sapiens muscleblind-like 2 (Drosophila) (	OXGR1	OXGR1, Homo sapiens oxoglutarate (alpha-ketoglutarate) receptor 1 (OXGR1), q32.1
SNP_A-1720465	ctgctcacccactcatgagaacaca[C/G]ctaaaagaatgtattt aacagtgtt	C	G	NM_005073 // intron // 0 // Hs.489180 // SLC15A1 // 6564 // solute carrier family 15 (oligopeptide transporter), member 1	SLC15A1	SLC15A1 , rs4772122, solute carrier family 15 (oligopeptide transporter), member 1,q32.3
SNP_A-1800665	gtagaaagttaatgag[C/T]caagagcccttataat	C	T	NM_021033 // downstream // 385388 // Hs.508480 // RAP2A // 5911 // Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA. /// NM_002271 // upstream // 100318 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. //	RAP2A	RAP2A, Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), q32.2
SNP_A-2299307	gccctctgtattctgat[C/T]ggtgaagtttgtggtt	C	T	NM_021033 // downstream // 388636 // Hs.508480 // RAP2A // 5911 // Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA. /// NM_002271 // upstream // 97070 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. ///	RAP2A	RAP2A, Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), q32.2
SNP_A-2277649	gagcagaactattaaa[C/T]aacaaggtctatatgg	C	T	NM_021033 // downstream // 463138 // Hs.508480 // RAP2A // 5911 // Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA. /// NM_002271 // upstream // 22568 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. ///	RAP2A	RAP2A, Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), q32.2
SNP_A-2309785	ggaaagtaggtcacgat[C/T]ataaaggtcaaataa	C	T	NM_002271 // downstream // 39034 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_002271 // downstream // 36620 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_005766 /	RANBP5	RANBP5, Homo sapiens RAN binding protein 5 (RANBP5), q32.2
SNP_A-1788140	gggagattggtcaagc[A/G]aagtggttcacactg	A	G	NM_002271 // downstream // 67178 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_002271 // downstream // 64764 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_005766 /	RANBP5	RANBP5, Homo sapiens RAN binding protein 5 (RANBP5), q32.2
SNP_A-2177322	tgagtctatcctgagc[C/T]atctgtaactagcaat	C	T	NM_002271 // downstream // 112397 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_002271 // downstream // 109983 // Hs.513057 // RANBP5 // 3843 // Homo sapiens RAN binding protein 5 (RANBP5), mRNA. /// NM_005766	RANBP5	RANBP5, Homo sapiens RAN binding protein 5 (RANBP5), q32.2
SNP_A-1886028	tgaccaaatgagaagg[A/G]atgggcttaacacatg	A	G	NM_005766 // intron // 0 // Hs.525135 // FARP1 // 10160 // Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // — // — // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-2249923	cttacagctcccattc[C/T]ctaatttaagaaaat	C	T	NM_005766 // intron // 0 // Hs.525135 // FARP1 // 10160 // Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // — // — // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-1935437	ttctggcagatttgc[G/T]gacaaggctcaattta	G	T	NM_005766 // intron // 0 // Hs.525135 // FARP1 // 10160 // Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // — // — // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-2189403	cagttgatttaaataa[A/G]gttggagaggccatac	A	G	NM_005766 // intron // 0 // Hs.525135 // FARP1 // 10160 // Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // — // — // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950693	tttcatgttcttgata[A/C]tacagtgacctttag	A	C	NM_005766 // intron // 0 // Hs.525135 // FARP1 // 10160 // Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // — // — // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-2209060	cccaggacacaaaaaac[C/T]gagttgcttcttca	C	T	NM_005766 // intron // 0 // Hs.525135 // FARP1 // 10160 // Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, mRNA. /// ENST00000319562 // intron // 0 // — // — // — // —	FARP1	FARP1, Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), transcript variant 1, q32.2
SNP_A-2103383	agcaagtgcaaagccaa[A/G]tgagaactgagtgtaa	A	G	NM_005073 // downstream // 37247 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 109564 // — // — // — /// ENST00000356773 // do	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2217001	cctctgttccaaag[A/C]ccttcaatataattc	A	C	NM_005073 // downstream // 25658 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 121153 // — // — // — /// ENST00000356773 // do	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2252504	cttcctcttacttcc[A/G]aatgccctactctgt	A	G	NM_005073 // downstream // 20263 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 126548 // — // — // — /// ENST00000356773 // do	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2182271	cagagtcaggagattg[A/G]ataataacactcttct	A	G	NM_005073 // downstream // 16555 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 130256 // — // — // — /// ENST00000356773 // do	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-1789584	gggcgcgtgtcttaa[A/G]tcccaccggcttctcc	A	G	NM_005073 // downstream // 13304 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000313290 // upstream // 133507 // — // — // — /// ENST00000356773 // do	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2177757	atattatggtaaaag[A/G]aaacatagactcaatc	A	G	NM_005073 // intron // 0 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000356773 // intron // 0 // — // — // — // — /// ENST00000354311 // intron // 0 // –	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2177760	gcaagttatagatacg[C/T]acatgttgacaagaac	C	T	NM_005073 // intron // 0 // Hs.436893 // SLC15A1 // 6564 // Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), mRNA. /// ENST00000356773 // intron // 0 // — // — // — // — /// ENST00000354311 // intron // 0 // –	SLC15A1	SLC15A1, Homo sapiens solute carrier family 15 (oligopeptide transporter), member 1 (SLC15A1), q32.2
SNP_A-2293651	gcagccccttggtga[C/T]ggtctacaaagaacgc	C	T	NM_015296 // intron // 0 // Hs.314413 // DOCK9 // 23348 // Homo sapiens dedicator of cytokinesis 9 (DOCK9), mRNA. /// ENST00000357329 // intron // 0 // — // — // — // — /// ENST00000339416 // intron // 0 // — // — // — // —	DOCK9	DOCK9, Homo sapiens dedicator of cytokinesis 9 (DOCK9), q32.3
SNP_A-2178048	agtgtaatcacaggat[C/T]cctataagagaagact	C	T	NM_015296 // upstream // 45008 // Hs.314413 // DOCK9 // 23348 // Homo sapiens dedicator of cytokinesis 9 (DOCK9), mRNA. /// ENST00000340449 // upstream // 282824 // — // — // — // — /// ENST00000357329 // upstream // 45008 // — // — // — // —	DOCK9	DOCK9, Homo sapiens dedicator of cytokinesis 9 (DOCK9), q32.3
SNP_A-2141512	atctacctaagagag[A/G]agcatataatccattc	A	G	NM_177967 // intron // 0 // Hs.508545 // PHGDHL1 // 337867 // Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), mRNA. /// ENST00000355700 // intron // 0 // — // — // — // — /// ENST00000325028 // intron // 0 // — // — // — // –	PHGDHL1	PHGDHL1, Homo sapiens phosphoglycerate dehydrogenase like 1 (PHGDHL1), q32.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1692438	ttttccctcaactattttagcaca[G/T]ggagttcacaactcattcca gctac	G	T	NM_032813 // upstream // 270230 // Hs.172963 // FLJ14624 // 84899 // hypothetical protein FLJ14624 /// NM_052867 // downstream // 142883 // Hs.391323 // VGCNL1 // 259232 // voltage gated channel like 1	FLJ14624	FLJ14624 , rs10508050, hypothetical protein FLJ14624 ,q32.3
SNP_A-2051423	aaggggctattttctc[C/G]agtggccacaggattg	C	G	NM_032813 // upstream // 108099 // Hs.190983 // FLJ14624 // 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA. /// NM_032813 // upstream // 108069 // Hs.190983 // FLJ14624 // 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624	FLJ14624	FLJ14624, Homo sapiens hypothetical protein FLJ14624 (FLJ14624), q32.3
SNP_A-1927244	ttcaaaaacagtctgc[A/C]actttacacaaacgtt	A	C	NM_032813 // upstream // 275901 // Hs.190983 // FLJ14624 // 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA. /// NM_032813 // upstream // 275871 // Hs.190983 // FLJ14624 // 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624	FLJ14624	FLJ14624, Homo sapiens hypothetical protein FLJ14624 (FLJ14624), q32.3
SNP_A-2129239	ataattttatgggacc[G/T]ccatcatttatgcagt	G	T	NM_032813 // upstream // 339822 // Hs.190983 // FLJ14624 // 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624), mRNA. /// NM_032813 // upstream // 339792 // Hs.190983 // FLJ14624 // 84899 // Homo sapiens hypothetical protein FLJ14624 (FLJ14624	FLJ14624	FLJ14624, Homo sapiens hypothetical protein FLJ14624 (FLJ14624), q32.3
SNP_A-1864915	tccaggggagtactgt[A/G]aataacagagatgtta	A	G	NM_052867 // intron // 0 // Hs.525146 // VGCNL1 // 259232 // Homo sapiens voltage gated channel like 1 (VGCNL1), mRNA. /// ENST00000343647 // intron // 0 // — // — // — // — /// ENST00000325793 // intron // 0 // — // — // — // —	VGCNL1	VGCNL1, Homo sapiens voltage gated channel like 1 (VGCNL1), q33.1
SNP_A-1682570	gaattaatatattatcaatcataac[C/T]gtatctatatatatttaaaa aaaga	C	T	NM_003291 // upstream // 103623 // Hs.432424 // TPP2 // 7174 // tripeptidyl peptidase II /// NM_004115 // upstream // 576755 // Hs.223851 // FGF14 // 2259 // fibroblast growth factor 14 /// NM_175929 // upstream // 91626 // Hs.223851 // FGF14 // 2259 //	TPP2	TPP2 , rs1927384, tripeptidyl peptidase II ,q33.1
SNP_A-2180037	cacttttgatgcaaa[C/T]ttctctttaaaagaca	C	T	NM_004791 // intron // 0 // Hs.508597 // ITGBL1 // 9358 // Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), mRNA. /// ENST00000355866 // intron // 0 // — // — // — // —	ITGBL1	ITGBL1, Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), q33.1
SNP_A-2281092	gagtaatgctaatcca[A/G]gactgctggtttttca	A	G	NM_004791 // intron // 0 // Hs.508597 // ITGBL1 // 9358 // Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), mRNA. /// ENST00000355866 // intron // 0 // — // — // — // —	ITGBL1	ITGBL1, Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), q33.1
SNP_A-1877391	tctggagatgaagtct[A/C]aaactgctcagttaaa	A	C	NM_175929 // intron // 0 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // — // — // — // —	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-2089435	acttatggtggttact[C/T]aactttgcatcagttc	C	T	NM_175929 // intron // 0 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // — // — // — // —	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-1817770	gttcctactttaccga[A/T]agcccaggggcctctt	A	T	NM_175929 // intron // 0 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, mRNA. /// ENST00000339527 // intron // 0 // — // — // — // —	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 2, q33.1
SNP_A-2152104	attaaaaggtcataaa[C/T]tattgtgaagaacagc	C	T	NM_004115 // upstream // 511057 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, mRNA. /// NM_175929 // upstream // 26024 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FG	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, q33.1
SNP_A-2289401	gattttcagattcaga[G/T]ggaattgcaaggggat	G	T	NM_004115 // upstream // 567303 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, mRNA. /// NM_175929 // upstream // 82270 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FG	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1938804	ttgaggaaagagaatc[A/T]ccataactggcatatt	A	T	NM_004115 // upstream // 601392 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, mRNA. /// NM_175929 // upstream // 116359 // Hs.508616 // FGF14 // 2259 // Homo sapiens fibroblast growth factor 14 (F	FGF14	FGF14, Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, q33.1
SNP_A-1709667	atcaatgttctctgttgtaatacca[C/G]atatggtgagattatttctac agag	C	G	NM_000452 // upstream // 1059186 // Hs.194783 // SLC10A2 // 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 // downstream // 1333026 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 //	SLC10A2	SLC10A2, rs10508128, solute carrier family 10 (sodium,q33.1
SNP_A-1654417	taatattaggtaatgtaaatgatga[C/T]aaatgagagatagcttat acccagt	C	T	NM_000452 // upstream // 1060347 // Hs.194783 // SLC10A2 // 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 // downstream // 1331865 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 //	SLC10A2	SLC10A2, rs10508129, solute carrier family 10 (sodium,q33.1
SNP_A-1755076	atcatgttaatggtaaaatttttaa[C/T]gtcaagagcagtataaaa caggtca	C	T	NM_000452 // upstream // 1061189 // Hs.194783 // SLC10A2 // 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 // downstream // 1331023 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 //	SLC10A2	SLC10A2, rs10508130, solute carrier family 10 (sodium,q33.1
SNP_A-1674793	aggctacctaataaaaggatgaaac[A/G]gatgcaaattccgag aagtgtgcag	A	G	NM_000452 // upstream // 1112196 // Hs.194783 // SLC10A2 // 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 // downstream // 1280016 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 //	SLC10A2	SLC10A2, rs9300901, solute carrier family 10 (sodium,q33.1
SNP_A-1791176	ggggttccaaagaaa[A/G]gcatcaacatcacctg	A	G	NM_000452 // upstream // 109618 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 109618 // — // — // — /// ENST00000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1
SNP_A-1755200	gaagagccctgggccttaagggaa[C/T]attgttgtaggctggc agtactcc	C	T	NM_000452 // upstream // 1296027 // Hs.194783 // SLC10A2 // 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 // downstream // 1096185 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 //	SLC10A2	SLC10A2, rs1590919, solute carrier family 10 (sodium,q33.2
SNP_A-2144909	atgattcgagacccaa[C/T]agaaatgtcacatagg	C	T	NM_000452 // upstream // 324779 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 324779 // — // — // — /// ENST00000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1
SNP_A-1750919	ggattaccccaaatgaacaaatacaa[A/G]ctttaaaagtgatca ctttgcac	A	G	NM_000452 // upstream // 1547859 // Hs.194783 // SLC10A2 // 6555 // solute carrier family 10 (sodium/bile acid cotransporter family), member 2 /// NM_172368 // downstream // 844353 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 // u	SLC10A2	SLC10A2, rs10508148, solute carrier family 10 (sodium,q33.2
SNP_A-2182318	atgcaggagattacaa[C/T]aatagctacagtacct	C	T	NM_000452 // upstream // 473217 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 473217 // — // — // — /// ENST00000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2043899	aactctagaccataa[C/T]actgtgagatagtaaa	C	T	NM_000452 // upstream // 480379 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 480379 // — // — // — /// ENST00000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium,q33.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2154974	attcacatttctacat[A/T]aaggccagcaatgaat	A	T	NM_000452 // upstream // 490533 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 490533 /// — /// — /// — /// ENST00000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2035985	aaattaactacattc[A/G]aatctgaaagtcaatg	A	G	NM_000452 // upstream // 849181 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 849181 /// — /// — /// — /// ENST00000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2190453	catacagttgttgagat[C/T]aatcttacacacttag	C	T	NM_000452 // upstream // 1071346 // Hs.194783 // SLC10A2 // 6555 // Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 2 (SLC10A2), mRNA. /// ENST00000245312 // upstream // 1071346 /// — /// — /// — /// ENST000	SLC10A2	SLC10A2, Homo sapiens solute carrier family 10 (sodium q33.1
SNP_A-2157362	attgagattccagaaa[C/T]atagctaacccaaatt	C	T	NM_172370 // upstream // 1032685 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 88131 // — // — // — // — /// ENST00000332759 // upstream // 1032685 // — // — // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1897366	tgctgaaagcaatttat[C/T]ggactcaaagctattt	C	T	NM_172370 // upstream // 1012874 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 107942 // — // — // — // — /// ENST00000332759 // upstream // 1012874 // — // — //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2130119	atacccacttgtggc[A/G]ccgattttctgtatta	A	G	NM_172370 // upstream // 1001937 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 118879 // — // — // — // — /// ENST00000332759 // upstream // 1001937 // — // — //	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1889963	tgataggtaaacaaga[G/T]cattggtgtgttagga	G	T	NM_172370 // upstream // 997692 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 123124 // — // — // — // — /// ENST00000332759 // upstream // 997692 // — // — // —	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2085441	actccaagactatgta[C/T]gcaaatatcctacaa	C	T	NM_172370 // upstream // 978019 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 142797 // — // — // — // — /// ENST00000332759 // upstream // 978019 // — // — // –	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1953046	ttcttgagaggacaa[A/G]tgctgtatcctcac	A	G	NM_172370 // upstream // 976146 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 144670 // — // — // — // — /// ENST00000332759 // upstream // 976146 // — // — // –	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1887984	tgagcactttgtagctat[C/T]ctttgaaaatagcatg	C	T	NM_172370 // upstream // 956499 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 164317 // — // — // — // — /// ENST00000332759 // upstream // 956499 // — // — // –	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2111597	aggagtagcaaaatcc[A/G]attgaaaaaattctat	A	G	NM_172370 // upstream // 956465 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 164351 // — // — // — // — /// ENST00000332759 // upstream // 956465 // — // — // –	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2183774	cagcatgccttgtca[G/T]gtatctggccatgtgc	G	T	NM_172370 // upstream // 956183 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 164633 // -- // -- // -- /// ENST00000332759 // upstream // 956183 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2196461	catgtttaccaatgag[A/G]aattcatcataatttt	A	G	NM_172370 // upstream // 871552 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 249264 // -- // -- // -- /// ENST00000332759 // upstream // 871552 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1643377	atcttagtggccaagggcacttct[C/G]acccatttaaacactcc agctaaga	C	G	NM_004093 // downstream // 671467 // Hs.30942 // EFNB2 // 1948 // ephrin-B2 /// NM_172368 // upstream // 327502 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 // downstream // 328645 // Hs.381382 // DAOA // 267012 // D-amino acid ox	EFNB2	EFNB2 , rs10508167, ephrin-B2, q33.2
SNP_A-1713019	tttcagcatacttacacccgataac[C/T]aatttcctaacttggacct ccgtc	C	T	NM_004093 // downstream // 594615 // Hs.30942 // EFNB2 // 1948 // ephrin-B2 /// NM_172368 // upstream // 404354 // Hs.406746 // G30 // 282706 // putative protein LG30 /// NM_172370 // downstream // 405497 // Hs.381382 // DAOA // 267012 // D-amino acid ox	EFNB2	EFNB2 , rs7991198, ephrin-B2, q33.2
SNP_A-1796567	ggttaccaactatatc[A/G]atcactggtttgcaac	A	G	NM_172370 // upstream // 550552 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 570264 // -- // -- // -- /// ENST00000332759 // upstream // 550552 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2083368	actaacattgaatact[A/G]acactgaatgtaaatg	A	G	NM_172370 // upstream // 544483 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 576333 // -- // -- // -- /// ENST00000332759 // upstream // 544483 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1920228	ttaatgacaaaaatca[C/G]aattacatttgtatca	C	G	NM_172370 // upstream // 376339 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 744477 // -- // -- // -- /// ENST00000332759 // upstream // 376339 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1828443	taagcaactagtctgat[C/G]agaaacattttattgg	C	G	NM_172370 // upstream // 177580 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 943236 // -- // -- // -- /// ENST00000332759 // upstream // 177580 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2184172	tatccttttctctaac[A/G]cttgcaaaatctttca	A	G	NM_172370 // upstream // 159941 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 960875 // -- // -- // -- /// ENST00000332759 // upstream // 159941 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2184216	agcatatttgacacca[A/C]cgtagatcactcctta	A	C	NM_172370 // upstream // 119396 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 1001420 // -- // -- // -- /// ENST00000332759 // upstream // 119396 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1864778	tccagctggctggaa[A/T]atgtgtaccgtgtggt	A	T	NM_172370 // upstream // 117684 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000355321 // upstream // 1003132 // -- // -- // -- /// ENST00000332759 // upstream // 117684 // -- // -- // -	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1737171	ctaacttaagtgtggatcccca[A/T]atcattgttgtctttcaaa agtt	A	T	NM_004093 // intron // 0 // Hs.30942 // EFNB2 // 1948 // ephrin-B2	EFNB2	EFNB2 , rs10508176, ephrin-B2,q33.3
SNP_A-2184273	ggtgctaaaatggttc[C/T]cttgtcagaggagtta	C	T	NM_172370 // intron // 0 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// ENST00000332759 // intron // 0 // — // — // — /// ENST00000331510 // intron // 0 // — // — // — /// ENST0000	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1690519	ctgtaatccctaagaagcatgttc[A/G]agaaaataatttaggttcc cacatag	A	G	AF144054 // downstream // 93087 // - // - // Homo sapiens apoptosis related protein APR-4 mRNA, partial cds. /// NM_018011 // upstream // 280699 // Hs.406114 // FLJ10154 // 55082 // hypothetical protein FLJ10154	-	-, rs288740, Homo sapiens apoptosis related protein APR-4 mRNA, partial cds., q33.3
SNP_A-2003557	gtgcctcagcgccaaa[C/T]aggatccaggcctccg	C	T	NM_172370 // downstream // 348256 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 651412 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1898953	tggaaaaaaacataag[A/C]atgcatacatgggtgc	A	C	NM_172370 // downstream // 374024 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 625644 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2178849	cactgaggcttggcac[C/T]atttgagagatgccaa	C	T	NM_172370 // downstream // 410116 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 589552 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-1802343	gtatcaaacgataatg[A/C]agtaagaactgatccc	A	C	NM_172370 // downstream // 411828 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 587840 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2034011	aaatcactagccata[A/G]catcttccaattgaga	A	G	NM_172370 // downstream // 412114 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 587554 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2083008	acgtggagcagtgaa[A/G]ggaaccaatttcaaa	A	G	NM_172370 // downstream // 551597 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 448071 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2139884	atctaatgctgaggcc[A/G]acaaggaagacacaa	A	G	NM_172370 // downstream // 567185 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 432483 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2171228	caatatatagttgta[A/T]attcaacgctttccc	A	T	NM_172370 // downstream // 713736 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 285932 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.2
SNP_A-2081728	accttccccgtgtggal[C/T]acgagagaacacgagc	C	T	NM_172370 // downstream // 899640 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 100028 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2185514	ctgcattcctttacaj[C/T]atagaaggtgcttac	C	T	NM_172370 // downstream // 912064 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 87604 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759 /	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3
SNP_A-1829799	taataaatcctattccd[A/G]cacggtgttatgaac	A	G	NM_172370 // downstream // 929369 // Hs.381382 // DAOA // 267012 // Homo sapiens D-amino acid oxidase activator (DAOA), mRNA. /// NM_004093 // downstream // 70299 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000332759 /	DAOA	DAOA, Homo sapiens D-amino acid oxidase activator (DAOA), q33.3
SNP_A-2185612	aagtcagcctcagatat[C/T]gacccaaggatacgt	C	T	NM_004093 // intron // 0 // Hs.149239 // EFNB2 // 1948 // Homo sapiens ephrin-B2 (EFNB2), mRNA. /// ENST00000245323 // intron // 0 // --- // --- // --- // ---	EFNB2	EFNB2, Homo sapiens ephrin-B2 (EFNB2), q33.3
SNP_A-2098045	agagagctcagactca[C/T]tctgttttagtgact	C	T	NM_018011 // upstream // 53757 // Hs.508644 // FLJ10154 // 55082 // Homo sapiens hypothetical protein FLJ10154 (FLJ10154), mRNA. /// ENST00000360629 // upstream // 53757 // --- // --- // --- // --- ENST00000257322 // upstream // 53730 // --- // --- //	FLJ10154	FLJ10154, Homo sapiens hypothetical protein FLJ10154 (FLJ10154), q33.3
SNP_A-2185663	atttgaccttgagaaa[A/T]taaatcttcatgccat	A	T	NM_018011 // upstream // 80935 // Hs.508644 // FLJ10154 // 55082 // Homo sapiens hypothetical protein FLJ10154 (FLJ10154), mRNA. /// ENST00000360629 // upstream // 80935 // --- // --- // --- // --- ENST00000257322 // upstream // 80908 // --- // --- //	FLJ10154	FLJ10154, Homo sapiens hypothetical protein FLJ10154 (FLJ10154), q33.3
SNP_A-2067480	acaaatgatattaaca[C/T]agagagcgagggtgaa	C	T	ENST00000322426 // downstream // 44239 // --- // --- // --- // --- ENST00000310543 // downstream // 155763 // --- // --- // --- // ---	-	q33.3
SNP_A-1828064	taagacaatcagtcaa[A/T]caaatgctattgagta	A	T	ENST00000322426 // downstream // 193026 // --- // --- // --- // --- ENST00000310543 // downstream // 6976 // --- // --- // --- // ---	-	q33.3
SNP_A-1698125	ctcagaagccatttttaatttggj[C/T]atcgttcggcatgtggaga gttgag	C	T	AF144054 // upstream // 1180253 // - // - // Homo sapiens apoptosis related protein APR-4 mRNA, partial cds. /// NM_002312 // downstream // 85403 // Hs.166091 // LIG4 // 3981 // ligase IV, DNA, ATP-dependent	-	- , rs1223978, Homo sapiens apoptosis related protein APR-4 mRNA, partial cds. , q33.3
SNP_A-1923771	ttagtacagacgcaac[A/C]aatcatctttttttt	A	C	NM_206937 // downstream // 1113828 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 1113828 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcrip	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2185997	cttccggaaatgccac[C/T]gggacttgtttatcc	C	T	NM_206937 // downstream // 990148 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 990148 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2279199	gaggactaagagggac[A/G]ccaggataaaacaagt	A	G	NM_206937 // downstream // 990128 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 990128 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1898091	tgctgtggccgggaac[C/T]gtgactcttgccaac	C	T	NM_206937 // downstream // 955173 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 955173 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1902995	tggctggagaaaccaaa[G/T]acaaggtagagaggaa	G	T	NM_206937 // downstream // 953756 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 953756 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2188973	cagtgtgagaatgagg[C/T]cattatttttgtgtta	C	T	NM_206937 // downstream // 943319 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 943319 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2053460	aagtgcaacatgagaat[C/G]gtgaaaaaatgcatta	C	G	NM_206937 // downstream // 921965 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 921965 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1859149	tcagcctggaaacaga[A/G]cgacatattgatacat	A	G	NM_206937 // downstream // 920730 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 920730 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2259139	gaaaaaaatgtaaaa[C/T]ttggagagactctcag	C	T	NM_206937 // downstream // 908517 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 908517 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2046082	aagactatggtagagc[A/G]catttcctgaactcaa	A	G	NM_206937 // downstream // 631292 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 631292 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1793705	ggtatgtggtaatggc[A/C]gaaaaaataaacacaa	A	C	NM_206937 // downstream // 621666 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 621666 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2186230	taccaagtcactatta[C/T]agagccaatccagatg	C	T	NM_206937 // downstream // 531646 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 531646 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2031276	aaaggggaagagaaaaa[G/T]gtaagtcaggtcatta	G	T	NM_206937 // downstream // 436625 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 436625 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2124317	agttattcaaattcct[C/T]aatctggattagtaca	C	T	NM_206937 // downstream // 382841 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 382841 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2244237	ctggaaactgcagaag[A/G]attgtgatctatttga	A	G	NM_206937 // downstream // 367201 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 367201 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2040298	aaccactaagtatgaa[A/G]tagatgtctgtctc	A	G	NM_206937 // downstream // 325891 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 325891 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2197739	cattcttgtcttggtc[A/G]cagaaggaacggcaca	A	G	NM_206937 // downstream // 232863 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 232863 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1870206	tcctttcacagtaata[C/T]agattcgtttcaatga	C	T	NM_206937 // downstream // 165618 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 165618 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1739959	gcatgacttacttttattggaacaa[C/G]gagacactgcttaactcccgatttg	C	G	AB020672 // intron // 0 // Hs.175411 // MYR8 // 23026 // myosin heavy chain Myr 8	MYR8	MYR8 , rs2038707, myosin heavy chain Myr 8,q33.3
SNP_A-2084553	actatgcccatgtaca[A/C]gaactatgtagatgaa	A	C	NM_206937 // downstream // 93698 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 93698 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript va	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1868555	tcctctatatcaaaca[C/T]tggacttccaggaaat	C	T	NM_206937 // downstream // 84837 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 84837 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript va	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1959898	ttttgtctgacagata[C/T]ctctagagtgccacat	C	T	NM_206937 // downstream // 84771 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 84771 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript va	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1670027	aaagccaaacctcttatttctcata[A/G]cttgctgtggtcagcagataggcat	A	G	NM_003749 // downstream // 555208 // Hs.143648 // IRS2 // 8660 // insulin receptor substrate 2	IRS2	IRS2 , rs592398, insulin receptor substrate 2,q33.3
SNP_A-1851766	tattgaaatgtgtcac[G/T]gcctgtgagaacaaca	G	T	NM_206937 // downstream // 80339 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 80339 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript va	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2235385	ctccctgtccccctttc[A/T]atattggtcactggac	A	T	NM_206937 // downstream // 52625 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 52625 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript va	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-1924102	ttagttatcagactta[C/T]gtttcagagtgtggga	C	T	NM_206937 // downstream // 51207 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 51207 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript va	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2048551	aagcattagtgattct[G/T]actgatagacatcatg	G	T	NM_206937 // downstream // 3011 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA. /// NM_002312 // downstream // 3011 // Hs.166091 // LIG4 // 3981 // Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), transcript vari	LIG4	LIG4, Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), q33.3
SNP_A-2305513	gctgcaacatgcatga[A/C]cattcaaaacatgcca	A	C	NM_032859 // downstream // 16506 // Hs.183528 // C13orf6 // 84945 // Homo sapiens chromosome 13 open reading frame 6 (C13orf6), mRNA. /// NM_006573 // upstream // 18869 // Hs.525157 // TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) super	C13orf6	C13orf6, Homo sapiens chromosome 13 open reading frame 6 (C13orf6), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2251502	cttcactcctgcctga[A/G]attttaaatattcccc	A	G	NM_006573 // downstream // 42993 // Hs.525157 // TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 42993 // — // — // — // — /// ENST00000251041 // upstr	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-2231750	ctcaaaatagcctatg[A/G]atgttccctgattaac	A	G	NM_006573 // downstream // 119853 // Hs.525157 // TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 119853 // — // — // — // — /// ENST00000251041 // ups	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-1712181	gtgttttcactctcttgcattttct[C/T]caatgaaaagctaagtacaggagtg	C	T	NM_003749 // downstream // 236271 // Hs.143648 // IRS2 // 8660 // insulin receptor substrate 2	IRS2	IRS2 , rs1410425, insulin receptor substrate 2,q33.3
SNP_A-1857152	tcacctatgtggaaaa[A/G]catataacgaaataat	A	G	NM_006573 // downstream // 145174 // Hs.525157 // TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 145174 // — // — // — // — /// ENST00000251041 // ups	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-2222099	cgaagtgctggaatga[C/T]gaatgataataatttg	C	T	NM_006573 // downstream // 276652 // Hs.525157 // TNFSF13B // 10673 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), mRNA. /// ENST00000218706 // downstream // 276652 // — // — // — // — /// ENST00000251041 // ups	TNFSF13B	TNFSF13B, Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), q33.3
SNP_A-1822012	gttttcatttaaaacc[C/T]atttggacaatgtaaa	C	T	ENST00000251041 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-2262011	gaaatagcaaagggaa[A/T]ctttcaggctgaaatg	A	T	ENST00000251041 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-1799728	gtacaaacacaggtaa[A/C]caatccttgctgttag	A	C	ENST00000251041 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-2187337	tcaaagatcttgccaa[A/C]aatctctctctttgaa	A	C	ENST00000251041 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-1877447	tctggatctctaggaa[A/G]tctcacattggcttaa	A	G	ENST00000251041 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-2187508	cttgtttccaaaataa[A/G]gaataatgtccaaaac	A	G	ENST00000358401 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-1904101	tgggcatgaataaaac[C/T]ggctgtgagatacgac	C	T	ENST00000358401 // intron // 0 // — // — // — // —	-	q33.3
SNP_A-2206829	ccatgctatggacata[A/G]taggcacttaatgatc	A	G	NM_003749 // downstream // 544945 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 2055 // — // — // — // — /// ENST00000331375 // downstream // 544945 // — // — // –	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-1933331	ttctaagttctcaaaa[A/C]tcctctgcatacacct	A	C	NM_003749 // downstream // 519757 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 27243 // — // — // — // — /// ENST00000331375 // downstream // 519757 // — // — // -	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-1867738	tcctaacatcagtgga[A/C]tattcaatccgataag	A	C	NM_003749 // downstream // 424458 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 122542 // — // — // — // — /// ENST00000331375 // downstream // 424458 // — // — //	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-1829341	taagtcagaggcttcc[A/G]ctgatttcactgggag	A	G	NM_003749 // downstream // 379490 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 167510 // — // — // — // — // — /// ENST00000331375 // downstream // 379490 // — // — //	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-2092217	agaaagaatatttaac[A/C]acaactgcagcccagg	A	C	NM_003749 // downstream // 339060 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 207940 // — // — // — // — // — /// ENST00000331375 // downstream // 339060 // — // — //	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284850	gatccaagatttgtcc[A/G]attatgaagttcccaa	A	G	NM_003749 // downstream // 322286 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 224714 // --- // --- // --- /// ENST00000331375 // downstream // 322286 // --- // -- //	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q33.3
SNP_A-2266524	gaagtatattattcaa[C/G]attgatttttccttcc	C	G	NM_003749 // downstream // 63965 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// ENST00000358401 // downstream // 483035 // --- // --- // --- /// ENST00000331375 // downstream // 63965 // --- // --- // -	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-1918907	ttaacatttcttcaca[G/T]agtccagcatattct	G	T	NM_003749 // upstream // 116125 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 246271 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-1901907	tggcagctctcttcag[A/T]atatgcggcgctgtgg	A	T	NM_003749 // upstream // 350571 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 11825 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST0	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-2100019	agagtgaaaaagtgca[C/T]ggaaagagccagcata	C	T	NM_003749 // upstream // 354162 // Hs.442344 // IRS2 // 8660 // Homo sapiens insulin receptor substrate 2 (IRS2), mRNA. /// NM_001845 // downstream // 8234 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00	IRS2	IRS2, Homo sapiens insulin receptor substrate 2 (IRS2), q34
SNP_A-2188212	atatcagggagagatca[G/T]gaatagggagggatttg	G	T	NM_001845 // intron // 0 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00000340079 // intron // 0 // --- // --- // --- // ---	COL4A1	COL4A1, Homo sapiens collagen, type IV, alpha 1 (COL4A1), q34
SNP_A-2280186	gagggatcaaaaactа[C/T]gtaacaggtagaagcgt	C	T	NM_001845 // intron // 0 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00000340079 // intron // 0 // --- // --- // --- // ---	COL4A1	COL4A1, Homo sapiens collagen, type IV, alpha 1 (COL4A1), q34
SNP_A-1875068	tctctcaatgacatac[A/G]ctggtatttgaacagt	A	G	NM_001845 // intron // 0 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00000340079 // intron // 0 // --- // --- // --- // ---	COL4A1	COL4A1, Homo sapiens collagen, type IV, alpha 1 (COL4A1), q34
SNP_A-1806911	gtctcaagagttgcga[C/T]ggttttataaatggga	C	T	NM_001845 // intron // 0 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00000340079 // intron // 0 // --- // --- // --- // ---	COL4A1	COL4A1, Homo sapiens collagen, type IV, alpha 1 (COL4A1), q34
SNP_A-1798088	gtaaaatcatctccaa[A/C]tcaacattaatgcgtt	A	C	NM_001845 // intron // 0 // Hs.17441 // COL4A1 // 1282 // Homo sapiens collagen, type IV, alpha 1 (COL4A1), mRNA. /// ENST00000340079 // intron // 0 // --- // --- // --- // ---	COL4A1	COL4A1, Homo sapiens collagen, type IV, alpha 1 (COL4A1), q34
SNP_A-2287034	gatgtaaaacaacag[A/G]attcaaatgaaatcat	A	G	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1861888	tcatgaactctgaaaa[A/G]aaaggctaagatgac	A	G	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2182036	cagaggagcaaggaaga[A/C]attggctgtagaggagt	A	C	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1810849	gtgcaggtcacagttg[C/T]accaccccagcacaaat	C	T	ENST00000298721 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1867443	tccctttttaccttttca[C/T]agtcctgagacattcc	C	T	ENST00000298721 // intron // 0 // --- // --- // --- // --- /// ENST00000257309 // intron // 0 // --- // --- // --- // --- /// ENST00000358169 // intron // 0 // --- // --- // --- // --- /// ENST00000360467 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2240526	ctgaccactgtccaca[C/G]atatcaggatcagagt	C	G	ENST00000298721 // intron // 0 // --- // --- // --- // --- /// ENST00000257309 // intron // 0 // --- // --- // --- // --- /// ENST00000360467 // intron // 0 // --- // --- // --- // --- /// ENST00000354467 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-2229981	ctataaacattcatac[C/T]gaggcttttgtacttg	C	T	NM_017817 // upstream // 23180 // Hs.508720 // RAB20 // 55647 // Homo sapiens RAB20, member RAS oncogene family (RAB20), mRNA. /// NM_018210 // upstream // 30748 // Hs.408324 // FLJ10769 // 55739 // Homo sapiens hypothetical protein FLJ10769 (FLJ10769), m	RAB20	RAB20, Homo sapiens RAB20, member RAS oncogene family (RAB20), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2311361	ggaatatctataggc[A/G]agagggagaaccagaa	A	G	NM_145735 // intron // 0 // Hs.508738 // ARHGEF7 // 8874 // Homo sapiens Rho guanine nucleotide exchange factor (GEF) 7 (ARHGEF7), transcript variant 2, mRNA. /// NM_003899 // intron // 0 // Hs.508738 // ARHGEF7 // 8874 // Homo sapiens Rho guanine nucleot	ARHGEF7	ARHGEF7, Homo sapiens Rho guanine nucleotide exchange factor (GEF) 7 (ARHGEF7), transcript variant 2, q34
SNP_A-1913637	tgtgtagaaactaagal[C/G]agaaaagtttatctac	C	G	NM_152324 // downstream // 45728 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 929591 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2265697	gaagctgcctacaggal[G/T]aaggtatttctgtt	G	T	NM_152324 // downstream // 62419 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 912900 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2088011	actggctagagaaactc[A/G]gaaagagagaaatcctg	A	G	NM_152324 // downstream // 62737 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 912582 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-1849575	tatgggggccagaaaaa[A/C]ctgaagtcaagagatg	A	C	NM_152324 // downstream // 149600 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 825719 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2234659	ctccagcaacgtctaa[C/T]caaatccagtctttga	C	T	NM_152324 // downstream // 150073 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 825246 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2142709	atgaagatctggaaata[A/G]tgagttgaacctggc	A	G	NM_152324 // downstream // 230764 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 744555 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2312241	ggacagtcatacccccd[A/G]ccacagtgagcgagtg	A	G	NM_152324 // downstream // 245123 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 730196 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-1691760	actaataggtgacttacgctataaa[C/T]gtgcaagagatgttcca gataacat	C	T	NM_006322 // downstream // 44667 // Hs.9884 // TUBGCP3 // 10426 // tubulin, gamma complex associated protein 3 /// NM_145248 // downstream // 5660 // Hs.97592 // LOC122258 // 122258 // LOC122258	TUBGCP3	TUBGCP3, rs2317438, tubulin, gamma complex associated protein 3 ,q34
SNP_A-1794411	ggtccctaagccgccca[C/T]ggccatttcaaagctg	C	T	NM_152324 // downstream // 876259 // Hs.210677 // MGC35169 // 121793 // Homo sapiens hypothetical protein MGC35169 (MGC35169), mRNA. /// NM_005986 // upstream // 99060 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1	MGC35169	MGC35169, Homo sapiens hypothetical protein MGC35169 (MGC35169), q34
SNP_A-2263468	gaaccaaccagaagaa[C/T]gaaactacgaacacgt	C	T	NM_005986 // downstream // 168237 // Hs.202526 // SOX1 // 6656 // Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA. /// NM_145248 // upstream // 136394 // Hs.97592 // LOC122258 // 122258 // Homo sapiens LOC122258 (LOC122258), mRNA. /// ENST0	SOX1	SOX1, Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), q34
SNP_A-1659218	aagaagggtggaggtatctgtaaa[A/G]ctatttctttccctttgt aatgaa	A	G	NM_017905 // intron // 0 // Hs.27337 // C13orf11 // 55002 // chromosome 13 open reading frame 11	C13orf11	C13orf11, rs2260111, chromosome 13 open reading frame 11,q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1913855	tgtgtctactaaaccaa[C/T]gctgcagcctctctat	C	T	NM_145248 // downstream // 1232 // Hs.97592 // LOC122258 // 122258 // Homo sapiens LOC122258 (LOC122258), mRNA. /// NM_006322 // downstream // 49092 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mR	LOC122258	LOC122258, Homo sapiens LOC122258 (LOC122258), q34
SNP_A-1917607	ttaaaaaaagattgag[A/G]ccgtactgagaggat	A	G	NM_006322 // intron // 0 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // — // — // — /// ENST00000357915 // intron // 0 // — // — // — /	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1810989	gtgccaacatttttat[C/G]accatagggaagaggc	C	G	NM_006322 // intron // 0 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // — // — // — /// ENST00000357915 // intron // 0 // — // — // — /	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1830472	taatcaaatcattatc[C/T]aacgtgtagaatctaa	C	T	NM_006322 // intron // 0 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // — // — // — /// ENST00000357915 // intron // 0 // — // — // — /	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1937255	ttgaaacaaattgcaa[A/G]agtcatcatgtgtgac	A	G	NM_006322 // intron // 0 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // — // — // — /// ENST00000357915 // intron // 0 // — // — // — /	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-1902949	tggctgcaagtttgga[C/T]ggaaacagactcctgg	C	T	NM_006322 // intron // 0 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// ENST00000261965 // intron // 0 // — // — // — /// ENST00000357915 // intron // 0 // — // — // — /	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-2142164	atctttttctgagcag[C/T]agacctaataggagg	C	T	ENST00000357915 // intron // 0 // — // — // — /	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-2154772	attcaacctgcctaaa[C/G]tggaagctgtatgatt	C	G	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-2167957	caacggattgaaacttt[C/G]aaccaggctttgaaaa	C	G	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-2221772	cctttttcaggcctata[A/C]aacctctcaaagcct	A	C	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-2217182	ccictcttccggattca[C/T]ctgctctaaaatatt	C	T	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-1794732	ggtctctgttagcacc[A/G]cttattgcatcccac	A	G	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-2050889	aaggcctgagttaaca[C/T]ggagtaggagctcaga	C	T	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-1811394	gtgctaatttgaaaaa[A/C]ctcagtgcaccgtggg	A	C	ENST00000359749 // intron // 0 // — // — // —	-	q34
SNP_A-1916943	tgtttgaagctataca[C/T]ggacggcagaacaaga	C	T	NM_006322 // upstream // 182714 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// NM_207440 // downstream // 86384 // Hs.374200 // FLJ26443 // 400165 // Homo sapiens FLJ26443 protein (FLJ2644	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-2276500	gagaggctcaaggggd[A/G]agacgctgcgtttcag	A	G	NM_006322 // upstream // 188844 // Hs.224152 // TUBGCP3 // 10426 // Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA. /// NM_207440 // downstream // 92514 // Hs.374200 // FLJ26443 // 400165 // Homo sapiens FLJ26443 protein (FLJ2644	TUBGCP3	TUBGCP3, Homo sapiens tubulin, gamma complex associated protein 3 (TUBGCP3), q34
SNP_A-2095073	agaatgtgtaaattat[C/G]ctctaagtagttaatt	C	G	AB028944 // intron // 0 // Hs.29189 // ATP11A // 23250 // Homo sapiens mRNA for KIAA1021 protein, partial cds. /// ENST00000261962 // intron // 0 // — // — // — /// ENST00000283558 // intron // 0 // — // — // —	ATP11A	ATP11A, Homo sapiens for KIAA1021 protein, partial cds., q34
SNP_A-2110390	aggaatgttactgaa[C/T]ctgcacgtgttaaca	C	T	AB028944 // downstream // 42014 // Hs.29189 // ATP11A // 23250 // Homo sapiens mRNA for KIAA1021 protein, partial cds. /// AB002360 // upstream // 40374 // Hs.170422 // MCF2L // 23263 // Human mRNA for KIAA0362 gene, partial cds. /// NM_024979 // upstream	ATP11A	ATP11A, Homo sapiens for KIAA1021 protein, partial cds., q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2109606	aggaaaccagatgaaa[A/G]gatattccataaagca	A	G	AB002360 // intron // 0 // Hs.170422 // MCF2L // 23263 // Human mRNA for KIAA0362 gene, partial cds. /// NM_024979 // intron // 0 // Hs.170422 // MCF2L // 23263 // Homo sapiens MCF.2 cell line derived transforming sequence-like (MCF2L), mRNA. /// ENST0000	MCF2L	MCF2L, Human for KIAA0362 gene, partial cds, q34
SNP_A-2212663	cccttcgttcaaactc[C/T]cacctgttttaggcac	C	T	NM_138430 // upstream // 1543 // Hs.98669 // ADPRHL1 // 113622 // Homo sapiens ADP-ribosylhydrolase like 1 (ADPRHL1), transcript variant 1, mRNA. /// NM_199162 // upstream // 1543 // Hs.98669 // ADPRHL1 // 113622 // Homo sapiens ADP-ribosylhydrolase like	ADPRHL1	ADPRHL1, Homo sapiens ADP-ribosylhydrolase like 1 (ADPRHL1), transcript variant 1, q34
SNP_A-2202726	ccacgcccgagaaaaa[A/C]caatttaatgcttctg	A	C	ENST00000332592 // 3UTR // 0 // --- // --- // --- // ---	-	q34
SNP_A-1801904	gtagtttgccgacccc[A/G]atctagattctagagg	A	G	NM_018185 // intron // 0 // Hs.369453 // C13orf17 // 55208 // Homo sapiens chromosome 13 open reading frame 17 (C13orf17), mRNA. /// ENST00000332592 // intron // 0 // --- // --- // --- // --- /// ENST00000279933 // intron // 0 // — // — // — // —	C13orf17	C13orf17, Homo sapiens chromosome 13 open reading frame 17 (C13orf17), q34
SNP_A-1948093	tttagatagtagctcc[A/G]cattcaggtctcacat	A	G	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // — // --- // — // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-1820450	gtttatccatgcttga[C/T]gagattcttgaagatg	C	T	NM_017905 // CDS // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // CDS // 0 // — // — // — // —	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-2163263	atttttggagaatgaa[C/T]gctaaacagaagaatg	C	T	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // — // — // — // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-2247668	ctgtgaaactccttgc[C/T]gacatctgattgagtg	C	T	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // --- // --- // --- // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-2176794	caccctgagctcaaga[C/T]gaccattttccccact	C	T	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // — // --- // — // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-2111340	aggagctgagttcaca[A/G]ggacaccatttccttg	A	G	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // — // --- // — // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-2088897	actgtttagtggaagc[C/T]gacttgctcagagcct	C	T	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // --- // --- // --- // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-2190443	atgaagtagaagggaa[C/T]gtctgaacacttggca	C	T	NM_017905 // intron // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // intron // 0 // — // --- // — // ---	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-1887692	tgagagtcggcatgac[A/G]gccatgaagagcccga	A	G	NM_017905 // CDS // 0 // Hs.317593 // C13orf11 // 55002 // Homo sapiens chromosome 13 open reading frame 11 (C13orf11), mRNA. /// ENST00000279934 // CDS // 0 // — // — // — // —	C13orf11	C13orf11, Homo sapiens chromosome 13 open reading frame 11 (C13orf11), q34
SNP_A-1960213	tttttaagtagaaaaa[C/T]gcgagaatgtggagtg	C	T	ENST00000357860 // intron // 0 // — // --- // — // ---	-	q34
SNP_A-2184222	cagcctctttccttaa[C/T]gccttcagtggagagg	C	T	NM_182614 // intron // 0 // Hs.280805 // MGC20579 // 348013 // Homo sapiens hypothetical protein MGC20579 (MGC20579), mRNA. /// ENST00000357860 // intron // 0 // — // --- // — // --- /// ENST00000357630 // intron // 0 // — // --- // — // --- /// E	MGC20579	MGC20579, Homo sapiens hypothetical protein MGC20579 (MGC20579), q34

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2212973	ccgaaaagactctagc[A/G]cggccatgtagtggaa	A	G	ENST00000357860 // intron // 0 // --- // --- // --- // --- /// ENST00000360383 // intron // 0 // --- // --- // --- // ---	-	q34
SNP_A-1851948	tattgcaaagttctga[A/G]aaatgattttgaaaaa	A	G	NM_007111 // downstream // 719861 // Hs.79353 // TFDP1 // 7027 // Homo sapiens transcription factor Dp-1 (TFDP1), mRNA. /// NM_000705 // upstream // 702847 // Hs.434202 // ATP4B // 496 // Homo sapiens ATPase, H+/K+ exchanging, beta polypeptide (ATP4B), mR	TFDP1	TFDP1, Homo sapiens transcription factor Dp-1 (TFDP1), q34
SNP_A-2216525	cctctaagataacaaa[A/G]tagtgcccaattatat	A	G	NM_001004063 // downstream // 14936 // --- // OR4K1 // 79544 // Homo sapiens olfactory receptor, family 4, subfamily K, member 1 (OR4K1), mRNA. /// ENST00000285600 // downstream // 14936 // --- // --- // --- // --- /// ENST00000305051 // upstream // 24053	OR4K1	OR4K1, Homo sapiens olfactory receptor, family 4, subfamily K, member 1 (OR4K1), q11.2
SNP_A-2079512	acccctcttatgaaag[G/T]aattaaccgagactca	G	T	NM_001004714 // upstream // 19652 // --- // OR4K13 // 390433 // Homo sapiens olfactory receptor, family 4, subfamily K, member 13 (OR4K13), mRNA. /// NM_001004717 // upstream // 5635 // --- // OR4L1 // 122742 // Homo sapiens olfactory receptor, family 4,	OR4K13	OR4K13, Homo sapiens olfactory receptor, family 4, subfamily K, member 13 (OR4K13), q11.2
SNP_A-2191584	aagtggttcatcagta[C/T]cttacacttatttta	C	T	NM_007110 // intron // 0 // Hs.508835 // TEP1 // 7011 // Homo sapiens telomerase-associated protein 1 (TEP1), mRNA. /// ENST00000354718 // intron // 0 // --- // --- // --- // --- /// ENST00000262715 // intron // 0 // --- // --- // --- // --- /// ENST00000	TEP1	TEP1, Homo sapiens telomerase-associated protein 1 (TEP1), q11.2
SNP_A-1644352	ctcaagaagtttaaaaagcatagga[C/T]tcaaggggagacgct tacaaaaagt	C	T	NM_019852 // intron // 0 // Hs.168799 // METTL3 // 56339 // methyltransferase like 3	METTL3	METTL3 , rs719785, methyltransferase like 3,q11.2
SNP_A-2181529	cagagaaaagctggga[C/T]gcacggaaaacattaa	C	T	ENST00000344581 // intron // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-1955851	tttgtattaaaattac[C/T]gacaaagatgtgatgt	C	T	NM_002937 // intron // 0 // Hs.283749 // RNASE4 // 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, mRNA. /// NM_194431 // intron // 0 // Hs.283749 // RNASE4 // 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNAS	RNASE4	RNASE4, Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, q11.2
SNP_A-2245322	ctggctgtatgaaatc[A/G]atggaataacgtgctt	A	G	NM_002937 // intron // 0 // Hs.283749 // RNASE4 // 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, mRNA. /// NM_194431 // intron // 0 // Hs.283749 // RNASE4 // 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNAS	RNASE4	RNASE4, Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, q11.2
SNP_A-1708849	aaaagatagaacagaattccgaggc[C/T]ctgaacattcagga gggtaaaacgg	C	T	BC035680 // intron // 0 // - // - // - // Homo sapiens cDNA clone MGC:46252 IMAGE:5748161, complete cds.	-	- , rs2075486, Homo sapiens cDNA clone MGC:46252 IMAGE:5748161, complete cds.,q11.2
SNP_A-2250534	cttagtacttggatta[C/T]agcttcagcagatcaa	C	T	NM_002937 // intron // 0 // Hs.283749 // RNASE4 // 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, mRNA. /// NM_194431 // intron // 0 // Hs.283749 // RNASE4 // 6038 // Homo sapiens ribonuclease, RNase A family, 4 (RNAS	RNASE4	RNASE4, Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), transcript variant 2, q11.2
SNP_A-1739057	aaaaaaaaaaagtaatctcattgta[A/G]aggaaagcagctgttc acaagagca	A	G	BC035680 // intron // 0 // - // - // - // Homo sapiens cDNA clone MGC:46252 IMAGE:5748161, complete cds.	-	- , rs8022648, Homo sapiens cDNA clone MGC:46252 IMAGE:5748161, complete cds.,q11.2
SNP_A-1947165	tttaatgagaaaacga[C/T]aggctttgtctttcaa	C	T	NM_002935 // downstream // 3713 // Hs.73839 // RNASE3 // 6037 // Homo sapiens ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3), mRNA. /// ENST00000304639 // downstream // 3713 // --- // --- // --- // --- /// ENST00000258817 // upstre	RNASE3	RNASE3, Homo sapiens ribonuclease, RNase A family, 3 (eosinophil cationic protein) (RNASE3), q11.2
SNP_A-1658732	cagaatttccaaacagagggaaaaa[C/T]taggtggacttgaaa tagtaactca	C	T	BC035680 // intron // 0 // - // - // - // Homo sapiens cDNA clone MGC:46252 IMAGE:5748161, complete cds.	-	- , rs10483267, Homo sapiens cDNA clone MGC:46252 IMAGE:5748161, complete cds.,q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920958	ttacagaatggcccca[A/G]tcattaatgcctccta	A	G	NM_002934 // downstream // 8748 // Hs.728 // RNASE2 // 6036 // Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA. /// ENST00000304625 // downstream // 8748 // --- // --- // --- // --- /// ENST00000327351 //	RNASE2	RNASE2, Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), q11.2
SNP_A-2003610	gaagataaatccaatg[C/G]atatggagcagtggaa	C	G	NM_022734 // upstream // 4766 // Hs.512693 // FLJ20859 // 64745 // Homo sapiens FLJ20859 gene (FLJ20859), mRNA. /// ENST00000327351 // upstream // 148 // --- // --- // --- // --- /// ENST00000349375 // upstream // 4766 // --- // --- // --- // --- /// ENST	FLJ20859	FLJ20859, Homo sapiens FLJ20859 gene (FLJ20859), q11.2
SNP_A-2192345	acccacaattaaggta[A/C]aatctggtcacataac	A	C	NM_001004731 // upstream // 47246 // --- // OR5AU1 // 390445 // Homo sapiens olfactory receptor, family 5, subfamily AU, member 1 (OR5AU1), mRNA. /// NM_004500 // downstream // 7438 // Hs.508848 // HNRPC // 3183 // Homo sapiens heterogeneous nuclear ribon	OR5AU1	OR5AU1, Homo sapiens olfactory receptor, family 5, subfamily AU, member 1 (OR5AU1), q11.2
SNP_A-1940588	ttgcctagcaatcata[C/T]ctgttccttaaaagga	C	T	NM_004500 // intron // 0 // Hs.508848 // HNRPC // 3183 // Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 2, mRNA. /// NM_031314 // intron // 0 // Hs.508848 // HNRPC // 3183 // Homo sapiens heterogeneous nuclear	HNRPC	HNRPC, Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1 q11.2
SNP_A-2192430	cgcaggaagccaacgg[C/T]acttaccaatcagtgt	C	T	NM_020366 // intron // 0 // Hs.126035 // RPGRIP1 // 57096 // Homo sapiens retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1), mRNA. /// ENST00000206660 // intron // 0 // --- // --- // --- // --- /// ENST00000307974 // intron // 0 // ---	RPGRIP1	RPGRIP1, Homo sapiens retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1), q11.2
SNP_A-2247517	ctgtctgaaattttgg[G/T]attagtcagaagcaga	G	T	AB046784 // intron // 0 // Hs.530698 // CHD8 // 57680 // Homo sapiens mRNA for KIAA1564 protein, partial cds. /// ENST00000262707 // intron // 0 // --- // --- // --- // ---	CHD8	CHD8, Homo sapiens for KIAA1564 protein, partial cds. ,q11.2
SNP_A-1738258	ctaaacagtggtaaaa[C/T]gagattatgtacaggt	C	T	-		, rs227026, ,q11.2
SNP_A-1838226	tagaagaaaatggcaa[C/T]taagagtgcaaagcac	C	T	NM_014828 // intron // 0 // Hs.194035 // C14orf92 // 9878 // Homo sapiens chromosome 14 open reading frame 92 (C14orf92), mRNA. /// ENST00000262709 // intron // 0 // --- // --- // --- // ---	C14orf92	C14orf92, Homo sapiens chromosome 14 open reading frame 92 (C14orf92), q11.2
SNP_A-1831356	taatgtagtcattaag[C/T]ccttcccctacaatcc	C	T	NM_005407 // upstream // 13573 // Hs.416358 // SALL2 // 6297 // Homo sapiens sal-like 2 (Drosophila) (SALL2), mRNA. /// ENST00000317492 // upstream // 24555 // --- // --- // --- // --- /// ENST00000327430 // upstream // 13573 // --- // --- // --- // --- /	SALL2	SALL2, Homo sapiens sal-like 2 (Drosophila) (SALL2), q11.2
SNP_A-1932945	ttcgaaaagataaaga[C/T]gatacaacatgagaaa	C	T	NM_005407 // upstream // 16780 // Hs.416358 // SALL2 // 6297 // Homo sapiens sal-like 2 (Drosophila) (SALL2), mRNA. /// ENST00000317492 // upstream // 27762 // --- // --- // --- // --- /// ENST00000327430 // upstream // 16780 // --- // --- // --- // --- /	SALL2	SALL2, Homo sapiens sal-like 2 (Drosophila) (SALL2), q11.2
SNP_A-2144744	atgatggaggagatgc[C/T]catatcaatgactgag	C	T	ENST00000303532 // CDS // 0 // --- // --- // --- // ---	-	q11.2
SNP_A-1907047	tggttggcaatcaatc[A/G]aactcattataccacg	A	G	ENST00000303532 // upstream // 11638 // --- // --- // --- // --- /// ENST00000312058 // downstream // 51553 // --- // --- // --- // ---	-	q11.2
SNP_A-2239789	ctgaaatcttttctca[A/T]ccaggtttgctaatcc	A	T	ENST00000303532 // upstream // 14942 // --- // --- // --- // --- /// ENST00000312058 // downstream // 48249 // --- // --- // --- // ---	-	q11.2
SNP_A-2054940	aataaataattttcca[C/T]cgatattggacatgag	C	T	ENST00000303532 // upstream // 14988 // --- // --- // --- // --- /// ENST00000312058 // downstream // 48203 // --- // --- // --- // ---	-	q11.2
SNP_A-2144457	atgatagagccattca[A/T]ggtgtctcaatagctc	A	T	NM_001001912 // downstream // 126946 // Hs.547982 // OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 // upstream // 59425 // Hs.454581 // MGC40069 // 348035 // Homo sapiens hypothetical prote	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936108	ttcttatctgtttaac[A/T]ctgccataaattaagtg	A	T	NM_001001912 // downstream // 134030 // Hs.547982 // OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 // upstream // 52341 // Hs.454581 // MGC40069 // 348035 // Homo sapiens hypothetical prote	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-2066700	acaaaactaaacatac[C/T]attgccatacagtcca	C	T	NM_001001912 // downstream // 151798 // Hs.547982 // OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 // upstream // 34573 // Hs.454581 // MGC40069 // 348035 // Homo sapiens hypothetical prote	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-1907907	tgtaatctgaatgaaac[C/T]gagcaaaactaaaca	C	T	NM_001001912 // downstream // 166987 // Hs.547982 // OR4E2 // 26686 // Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA. /// NM_182615 // upstream // 19384 // Hs.454581 // MGC40069 // 348035 // Homo sapiens hypothetical prote	OR4E2	OR4E2, Homo sapiens olfactory receptor, family 4, subfamily E, member 2 (OR4E2), q11.2
SNP_A-1719751	cacgttctcgttgtagccacattac[A/G]ccttgcattactctttgcc actg	A	G	NM_017815 // intron // 0 // Hs.442782 // C14orf94 // 54930 // chromosome 14 open reading frame 94	C14orf94	C14orf94 , rs712486, chromosome 14 open reading frame 94.q11.2
SNP_A-1956763	ttttaaagatccattc[C/T]attttacctgacccac	C	T	ENST00000206681 // downstream // 20788 // --- // --- // --- /// ENST00000339800 // upstream // 41753 // --- // --- // ---	-	q11.2
SNP_A-2228380	ctactgtcaatagtaa[C/T]ggcaaaggcctattat	C	T	M15565 // upstream // 69146 // Hs.508893 // --- // 0 // Human T-cell receptor rearranged alpha-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000339800 // downstream // 22569 // --- // --- // --- /// ENST00000250499 // upstream // 69146 // -	-	-, Human T-cell receptor rearranged alpha-chain V-region (V-D-J) complete cds. q11.2
SNP_A-2189356	cagttctttccaaaag[C/G]caaggtgaatcctctg	C	G	M15565 // downstream // 223921 // Hs.508893 // --- // 0 // Human T-cell receptor rearranged alpha-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000250499 // downstream // 223921 // --- // --- // --- /// ENST00000299064 // upstream // 35771 /	-	-, Human T-cell receptor rearranged alpha-chain V-region (V-D-J) complete cds. q11.2
SNP_A-2003619	ctgggtgtgggagtga[A/G]ggcatcccttgtttat	A	G	M15565 // downstream // 227105 // Hs.508893 // --- // 0 // Human T-cell receptor rearranged alpha-chain V-region (V-D-J) mRNA, complete cds. /// ENST00000250499 // downstream // 227105 // --- // --- // --- /// ENST00000299064 // upstream // 32587 /	-	-, Human T-cell receptor rearranged alpha-chain V-region (V-D-J) complete cds. q11.2
SNP_A-1915564	tgtctatatgattta[C/T]ggacataacagcccac	C	T	ENST00000299064 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-2032293	aaagttacctttggaa[C/T]ggaacaaagctccaa	C	T	ENST00000299064 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-1888184	tgagccttaaattcca[G/T]agggaagagagccaa	G	T	NM_001344 // downstream // 4528 // Hs.82890 // DAD1 // 1603 // Homo sapiens defender against cell death 1 (DAD1), mRNA. /// ENST00000299064 // downstream // 8189 // --- // --- // --- // --- /// ENST00000339338 // downstream // 95965 // --- // --- // --- /	DAD1	DAD1, Homo sapiens defender against cell death 1 (DAD1), q11.2
SNP_A-1952707	tttctgtagcacttaa[C/T]tcatggtaagcaaaaa	C	T	NM_001344 // downstream // 4465 // Hs.82890 // DAD1 // 1603 // Homo sapiens defender against cell death 1 (DAD1), mRNA. /// ENST00000299064 // downstream // 8252 // --- // --- // --- // --- /// ENST00000339338 // downstream // 96028 // --- // --- // --- /	DAD1	DAD1, Homo sapiens defender against cell death 1 (DAD1), q11.2
SNP_A-2193900	accaaagatgctcaat[A/T]aaagcagcagctga	A	T	ENST00000312039 // upstream // 16913 // --- // --- // --- /// ENST00000357217 // downstream // 112565 // --- // --- // ---	-	q11.2
SNP_A-1848573	tatgacgtatgcagcaa[A/G]gttaatcacggccagg	A	G	AL834198 // intron // 0 // Hs.4997 // RBM23 // 55147 // Homo sapiens mRNA; cDNA DKFZp547I166 (from clone DKFZp547I166). /// NM_018107 // intron // 0 // Hs.4997 // RBM23 // 55147 // Homo sapiens RNA binding motif protein 23 (RBM23), mRNA. /// ENST00000003598	RBM23	RBM23, Homo sapiens cDNA DKFZp547I166 (from clone DKFZp547I166), q11.2
SNP_A-1863596	tccaaatcttactaaa[A/G]ctcagaaagcagtgga	A	G	NM_006109 // intron // 0 // Hs.367854 // SKB1 // 10419 // Homo sapiens SKB1 homolog (S. pombe) (SKB1), mRNA. /// ENST00000324366 // intron // 0 // --- // --- // --- /// ENST00000216350 // intron // 0 // --- // --- // ---	SKB1	SKB1, Homo sapiens SKB1 homolog (S. pombe) (SKB1), q11.2
SNP_A-1808136	gtcttgggtatgaccc[A/G]caatctgtccaaaaaa	A	G	NM_012244 // intron // 0 // Hs.22891 // SLC7A8 // 23428 // Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), transcript variant 1, mRNA /// NM_182728 // intron // 0 // Hs.22891 // SLC7A8 // 23428 // Homo	SLC7A8	SLC7A8, Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), transcript variant 1, q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1900984	tggatacttaacatct[A/T]aactgaggcagttaat	A	T	NM_005794 // downstream // 21206 // Hs.272499 // DHRS2 // 10202 // Homo sapiens dehydrogenase/reductase (SDR family) member 2 (DHRS2), transcript variant 2, mRNA. /// NM_182908 // downstream // 21206 // Hs.272499 // DHRS2 // 10202 // Homo sapiens dehydrog	DHRS2	DHRS2, Homo sapiens dehydrogenase q11.2
SNP_A-1834917	taccatttattagaccc[A/G]accactctcaaattgc	A	G	NM_005794 // downstream // 39197 // Hs.272499 // DHRS2 // 10202 // Homo sapiens dehydrogenase/reductase (SDR family) member 2 (DHRS2), transcript variant 2, mRNA. /// NM_182908 // downstream // 39197 // Hs.272499 // DHRS2 // 10202 // Homo sapiens dehydrog	DHRS2	DHRS2, Homo sapiens dehydrogenase q11.2
SNP_A-2161075	atttcttttgtgcac[C/T]ggatgtcctataatgt	C	T	NM_005794 // downstream // 196239 // Hs.272499 // DHRS2 // 10202 // Homo sapiens dehydrogenase/reductase (SDR family) member 2 (DHRS2), transcript variant 2, mRNA. /// NM_182908 // downstream // 196239 // Hs.272499 // DHRS2 // 10202 // Homo sapiens dehydr	DHRS2	DHRS2, Homo sapiens dehydrogenase q11.2
SNP_A-1690369	ctagaagataaagataacaatggtaa[A/T]attgacagaggataa ccgttatct	A	T	NM_014178 // intron // 0 // Hs.99291 // STXBP6 // 29091 // syntaxin binding protein 6 (amisyn)	STXBP6	STXBP6 , rs10483291, syntaxin binding protein 6 (amisyn),q12
SNP_A-1710588	tagaggattttcagattgcaagggt[C/T]aacaaataacagttaaa atggaatg	C	T	NM_002515 // downstream // 1202790 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_006489 // downstream // 1202790 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_006491 // downstream // 1227024 //	NOVA1	NOVA1 , rs1461549, neuro-oncological ventral antigen 1 ,q12
SNP_A-1675263	ataaattacagttattgatggatg[A/G]agatctgtgctaagactt gggctc	A	G	NM_002515 // downstream // 1194058 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_006489 // downstream // 1194058 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_006491 // downstream // 1218292 //	NOVA1	NOVA1 , rs1349878, neuro-oncological ventral antigen 1 ,q12
SNP_A-2301561	gcgagtactgaaccag[C/G]cgtattcaccttgaa	C	G	NM_020195 // upstream // 39071 // Hs.283111 // C14orf124 // 56948 // Homo sapiens chromosome 14 open reading frame 124 (C14orf124), mRNA. /// NM_001836 // downstream // 23888 // Hs.135626 // CMA1 // 1215 // Homo sapiens chymase 1, mast cell (CMA1), mRNA.	C14orf124	C14orf124, Homo sapiens chromosome 14 open reading frame 124 (C14orf124), q11.2
SNP_A-2238044	ctctgcaaacttacca[A/G]gaggcttatggtggat	A	G	NM_004131 // intron // 0 // Hs.1051 // GZMB // 3002 // Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA. /// ENST00000216341 // intron // 0 // -- // -- // -- // --	GZMB	GZMB, Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), q11.2
SNP_A-2250845	cttatctgaccacaaat[G/T]tatgattcagaaaga	G	T	NM_004131 // upstream // 143945 // Hs.1051 // GZMB // 3002 // Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA. /// NM_014178 // downstream // 31491 // Hs.508958 // STXBP6 // 29091 // Homo sapiens synt	GZMB	GZMB, Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), q12
SNP_A-1894098	tgcatgaataggttat[C/G]aaaagtaccatcaagt	C	G	NM_004131 // upstream // 163702 // Hs.1051 // GZMB // 3002 // Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA. /// NM_014178 // downstream // 11734 // Hs.508958 // STXBP6 // 29091 // Homo sapiens synt	GZMB	GZMB, Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), q12
SNP_A-2195977	tgcaccaggataatca[G/T]atggaagaagcctac	G	T	NM_014178 // intron // 0 // Hs.508958 // STXBP6 // 29091 // Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), mRNA. /// ENST00000323944 // intron // 0 // -- // -- // -- /// ENST00000303411 // intron // 0 // -- // -- // -- ///	STXBP6	STXBP6, Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), q12
SNP_A-2281480	gagtcatgaatgttgg[C/T]atagcaggaaaaacct	C	T	NM_014178 // intron // 0 // Hs.508958 // STXBP6 // 29091 // Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), mRNA. /// ENST00000323944 // intron // 0 // -- // -- // -- /// ENST00000303411 // intron // 0 // -- // -- // -- ///	STXBP6	STXBP6, Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1658394	gtgacgtgacatcacttgaaaacaq[G/T]aaagcctcatcatttac caggttgg	G	T	NM_002515 // downstream // 332111 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_006489 // downstream // 332111 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_006491 // downstream // 356345 // Hs.	NOVA1	NOVA1 , rs10483307, neuro-oncological ventral antigen 1 ,q12
SNP_A-2281835	gagtgagtcactgtca[C/T]ggttattggtccaatc	C	T	NM_014178 // upstream // 72433 // Hs.508958 // STXBP6 // 29091 // Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), mRNA. /// NM_014178 // upstream // 72267 // Hs.508958 // STXBP6 // 29091 // Homo sapiens syntaxin binding protein 6 (amisyn) (STXB	STXBP6	STXBP6, Homo sapiens syntaxin binding protein 6 (amisyn) (STXBP6), q12
SNP_A-2143233	atgacaatgatttcaa[C/T]atacagttaagaaaaa	C	T	NM_006489 // downstream // 1140552 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 1140552 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncologica	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1795835	ggtggccgttgctgta[A/T]aattgctcgtatattg	A	T	NM_006489 // downstream // 417418 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 417418 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2197479	ctctgctgtgaaatca[A/G]taaagaatagtgataa	A	G	NM_006489 // downstream // 335256 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 335256 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2264238	gaacttaaaagttac[A/G]aaaggccatattaatg	A	G	NM_006489 // downstream // 329428 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 329428 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2022798	aaaaatttctgactga[C/T]gtgttattagctcatt	C	T	NM_006489 // downstream // 326825 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 326825 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1807016	gtctcatggctgacac[C/T]gatcaaaacaaaggaa	C	T	NM_006489 // downstream // 276231 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 276231 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1664724	ataattctacaggtggtgagagtga[C/T]gaaatagaatacaatttt gttatga	C	T	NM_002515 // upstream // 666283 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral antigen 1 /// NM_004052 // upstream // 1000570 // - // - // - /// NM_006489 // upstream // 666283 // Hs.292511 // NOVA1 // 4857 // neuro-oncological ventral a	NOVA1	NOVA1, rs202970, neuro-oncological ventral antigen 1 ,q12
SNP_A-2298011	gccatacaattgatac[C/T]gaaattaaccagacaa	C	T	NM_006489 // downstream // 201904 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 201904 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2197788	aatggatagattgaat[A/G]agcgtctgaaattcta	A	G	NM_006489 // downstream // 41358 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // downstream // 41358 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ve	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2075341	acatgaaatacacacc[A/G]aggaacactacaaagc	A	G	NM_006489 // upstream // 28095 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 28042 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventra	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1816848	gttatgtagccctag[C/T]aaacaaatatgcttac	C	T	NM_006489 // upstream // 109602 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 109549 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2198236	tgctaggaagcaggca[C/T]tcatttcaggacttca	C	T	NM_006489 // upstream // 236004 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 235951 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1906783	tggttagcctctgata[A/C]aaattgtctctagca	A	C	NM_006489 // upstream // 264389 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 264336 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2118092	agtaaaatataggaaac[A/G]gaaagcacattagtgt	A	G	NM_006489 // upstream // 312821 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 312768 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1793076	ggtactgacttttgaac[A/G]atagacaatacttca	A	G	NM_006489 // upstream // 416758 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 416705 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2003642	tgtcagaaaacagtgat[A/T]agaaatttttattcag	A	T	NM_006489 // upstream // 477176 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 477123 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1831325	taatgttgccagtaa[C/T]tctcttctccctcaat	C	T	NM_006489 // upstream // 657158 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 657105 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological vent	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1927482	ttcaaatcaccataca[A/C]caggaatcaatacaaa	A	C	NM_006489 // upstream // 1681505 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1681452 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ve	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-2194380	catgatgactgacctta[C/T]cgtatttccaaagaca	C	T	NM_006489 // upstream // 1953323 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1953270 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ve	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1882604	tgaaacagcttccaag[C/T]agtgagctaaacaagt	C	T	NM_006489 // upstream // 1968556 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1968503 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ve	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2283784	gataggctataattac[A/G]aagattgatcatatcg	A	G	NM_006489 // upstream // 1982902 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, mRNA. /// NM_002515 // upstream // 1982849 // Hs.211225 // NOVA1 // 4857 // Homo sapiens neuro-oncological ve	NOVA1	NOVA1, Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), transcript variant 2, q12
SNP_A-1657149	taaacacgtgccatggtgatttgct[A/G]tatagatcaacctgtcactaggta	A	G	NM_002742 // intron // 0 // Hs.2891 // PRKCM // 5587 // protein kinase C, mu	PRKCM	PRKCM , rs2225899, protein kinase C, mu,q12
SNP_A-1645186	aaaaaaataataaggaacatagttga[A/G]gattgaactttgaggaactccaaca	A	G	NM_002742 // intron // 0 // Hs.2891 // PRKCM // 5587 // protein kinase C, mu	PRKCM	PRKCM , rs226001, protein kinase C, mu,q12
SNP_A-1723938	aatatcattttattctgctatatga[G/T]gtataaaatttcattctgggcttaa	G	T	NM_002742 // intron // 0 // Hs.2891 // PRKCM // 5587 // protein kinase C, mu	PRKCM	PRKCM , rs225998, protein kinase C, mu,q12
SNP_A-2200242	tctttatggggtcacc[A/G]gagtaccatatttcca	A	G	NM_002742 // downstream // 555843 // Hs.508999 // PRKD1 // 5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000335192 // downstream // 228226 // — // — // — // — /// ENST00000331968 // downstream // 555843 // — // — // — //	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2173503	cacaatcctgacttct[A/C]acatggattaatttaa	A	C	NM_002742 // downstream // 506336 // Hs.508999 // PRKD1 // 5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000335192 // downstream // 277733 // — // — // — // — /// ENST00000331968 // downstream // 506336 // — // — // — //	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2200329	aaattttccaagtgat[A/G]agaaataataccacac	A	G	NM_002742 // downstream // 444432 // Hs.508999 // PRKD1 // 5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000335192 // downstream // 339637 // — // — // — // — /// ENST00000331968 // downstream // 444432 // — // — // — //	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-1646996	ggagattggcattgaacccaagaca[A/T]ccttaatttctcaatatctctataa	A	T	NM_002742 // upstream // 26778 // Hs.2891 // PRKCM // 5587 // protein kinase C, mu /// NM_017769 // upstream // 254693 // Hs.79828 // KIAA1333 // 55632 // KIAA1333	PRKCM	PRKCM , rs10483377, protein kinase C, mu ,q12
SNP_A-1736719	taccatgactgcatttgtcaaggaa[G/T]aaatgggttaatgttaggaagccag	G	T	NM_002742 // upstream // 27651 // Hs.2891 // PRKCM // 5587 // protein kinase C, mu /// NM_017769 // upstream // 253820 // Hs.79828 // KIAA1333 // 55632 // KIAA1333	PRKCM	PRKCM , rs2025052, protein kinase C, mu ,q12
SNP_A-1675702	tttcaatattagcctccattttgcc[A/G]aaaccttctcaaaggggcaggtgaa	A	G	NM_002742 // upstream // 50892 // Hs.2891 // PRKCM // 5587 // protein kinase C, mu /// NM_017769 // upstream // 230579 // Hs.79828 // KIAA1333 // 55632 // KIAA1333	PRKCM	PRKCM , rs10483376, protein kinase C, mu ,q12
SNP_A-2201001	catagtgattacacta[C/T]gtttttctaaccactt	C	T	NM_002742 // upstream // 92905 // Hs.508999 // PRKD1 // 5587 // Homo sapiens protein kinase C, mu (PRKCM), mRNA. /// ENST00000331968 // upstream // 92905 // — // — // — // — /// ENST00000354501 // upstream // 27977 // — // — // — // —	PRKD1	PRKD1, Homo sapiens protein kinase C, mu (PRKCM), q12
SNP_A-2303270	gctatggcagtcatca[A/G]atcattcctctattgt	A	G	NM_017769 // upstream // 263190 // Hs.509008 // KIAA1333 // 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 247264 // — // — // — // — /// ENST00000206595 // upstream // 263190 // — // — // — // — ///	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12
SNP_A-1814193	gtgtctcctcatgcta[A/G]cctatgtccttttatc	A	G	NM_017769 // upstream // 185757 // Hs.509008 // KIAA1333 // 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 324697 // — // — // — // — /// ENST00000206595 // upstream // 185757 // — // — // — // — ///	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12
SNP_A-1799854	gtacaccatatcacca[A/G]tgaagtgttcttgtca	A	G	NM_017769 // upstream // 179887 // Hs.509008 // KIAA1333 // 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 330567 // — // — // — // — /// ENST00000206595 // upstream // 179887 // — // — // — // — ///	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12
SNP_A-2260130	gaaaatcatacatata[C/T]gccaaccttccttgtt	C	T	NM_017769 // upstream // 179225 // Hs.509008 // KIAA1333 // 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 331229 // — // — // — // — /// ENST00000206595 // upstream // 179225 // — // — // — // — ///	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12
SNP_A-2201354	gtacatgcaaatacag[C/T]ctaagcccatctccct	C	T	NM_017769 // upstream // 169988 // Hs.509008 // KIAA1333 // 55632 // Homo sapiens KIAA1333 (KIAA1333), mRNA. /// ENST00000354501 // downstream // 340466 // — // — // — // — /// ENST00000206595 // upstream // 169988 // — // — // — // — ///	KIAA1333	KIAA1333, Homo sapiens KIAA1333 (KIAA1333), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134053	atatgaaattaatacа[A/T]gctttatgtgtttga	A	T	NM_014574 // intron // 0 // Hs.401843 // STRN3 // 29966 // Homo sapiens striatin, calmodulin binding protein 3 (STRN3), mRNA. /// U17989 // intron // 0 // Hs.401843 // STRN3 // 29966 // Homo sapiens nuclear autoantigen GS2NA mRNA, complete cds. /// ENST00	STRN3	STRN3, Homo sapiens striatin, calmodulin binding protein 3 (STRN3), q12
SNP_A-1679548	ttttaggtaaaactttcaataa[A/G]cacagtcattataccgttaa aaaaa	A	G	NM_004274 // 3UTR // 0 // Hs.419136 // AKAP6 // 9472 // A kinase (PRKA) anchor protein 6	AKAP6	AKAP6, rs42614436, A kinase (PRKA) anchor protein 6,q12
SNP_A-2301889	gcggtcagagcaccaa[A/T]cttacgagccttgtga	A	T	NM_001173 // downstream // 46820 // Hs.525287 // ARHGAP5 // 394 // Homo sapiens Rho GTPase activating protein 5 (ARHGAP5), mRNA. /// ENST00000216743 // downstream // 46820 // — // — // — /// ENST00000307425 // downstream // 69955 // — // –	ARHGAP5	ARHGAP5, Homo sapiens Rho GTPase activating protein 5 (ARHGAP5), q12
SNP_A-1934121	ttctcagtgcctaatg[C/T]agtggcagatgcatct	C	T	NM_001173 // downstream // 69890 // Hs.525287 // ARHGAP5 // 394 // Homo sapiens Rho GTPase activating protein 5 (ARHGAP5), mRNA. /// ENST00000216743 // downstream // 69890 // — // — // — /// ENST00000307425 // downstream // 46885 // — // –	ARHGAP5	ARHGAP5, Homo sapiens Rho GTPase activating protein 5 (ARHGAP5), q12
SNP_A-1691530	agaggtgctcaacatgtagtataaq[C/T]gtctttctgttccacatta atctcc	C	T	NM_022123 // intron // 0 // Hs.243209 // NPAS3 // 64067 // neuronal PAS domain protein 3	NPAS3	NPAS3, rs1315148, neuronal PAS domain protein 3,q13.1
SNP_A-2144456	atgatagacatcctag[A/G]ataaaatgaacatagg	A	G	NM_004274 // intron // 0 // Hs.509083 // AKAP6 // 9472 // Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA. /// ENST00000280979 // intron // 0 // — // — // — // —	AKAP6	AKAP6, Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), q12
SNP_A-1690735	catgagaatcacaatttcccttttgtg[C/G]atctctgagaaatggaaga ataagat	C	G	NM_022073 // downstream // 36101 // Hs.443906 // EGLN3 // 112399 // egl nine homolog 3 (C. elegans) /// NM_022123 // downstream // 86370 // Hs.243209 // NPAS3 // 64067 // neuronal PAS domain protein 3 /// NM_033344 // downstream // 37101 // - // - // -	EGLN3	EGLN3, rs1632578, egl nine homolog 3 (C. elegans), q13.1
SNP_A-2203376	atcaacacaatgcaca[A/G]ggcagaacattagaaa	A	G	NM_004274 // downstream // 60663 // Hs.509083 // AKAP6 // 9472 // Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA. /// AF164438 // upstream // 45592 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA,	AKAP6	AKAP6, Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), q13.1
SNP_A-1665166	agagcagaagaggtcagcatggac[A/G]aacatcggagcag gaagaccaggaa	A	G	NM_022073 // upstream // 37811 // Hs.443906 // EGLN3 // 112399 // egl nine homolog 3 (C. elegans) /// NM_033344 // upstream // 37857 // - // - // - // - /// NM_138288 // downstream // 445271 // Hs.353161 // C14orf147 // 171546 // chromosome 14 open readi	EGLN3	EGLN3, rs958721, egl nine homolog 3 (C. elegans) q13.1
SNP_A-1949060	tttatgaatcttcaaa[A/G]atagaacagacatgaa	A	G	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2269612	gacaaatgacatatca[G/T]ccaatcttcaatgagc	G	T	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. .q13.1
SNP_A-2099711	agaggttaagtgattc[C/G]aagtatttcacacagc	C	G	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2071941	acagagcacagaactc[A/G]cgctaagaaatgtctg	A	G	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-1935774	ttctgtgtcttccact[C/T]agaataaaggctgctg	C	T	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2052725	aagtcaaacaaagtgtc[G/T]attcgggttccagagt	G	T	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2300591	gcctgattgtagaacc[C/T]gaactcttgtcat	C	T	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2189854	cataaagcaccaaaga[A/C]gactttcaaagttgt	A	C	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2233796	ctcatccctgaaaaaa[A/T]cattgttcacacac	A	T	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-1944776	ttgtgcagttgactca[C/T]gaaaggcaaaggaag	C	T	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2048313	aagcagatggaaacg[A/C]aatcttagaagaaaca	A	C	AF164438 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // intron // 0 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (NPAS3), mRNA. /	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-1908535	tgtagatgtaggtagt[C/T]aagatcaggtcatgct	C	T	AF164438 // downstream // 6863 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // downstream // 6863 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3 (N	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2204580	gtcttgaaacaggca[C/G]aacatcttcatgcct	C	G	AF164438 // downstream // 13874 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // downstream // 13874 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2290535	gcaactggatagacac[A/G]ggactttaaacgcaca	A	G	AF164438 // downstream // 50443 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // downstream // 50443 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2283958	gatatacttaactcta[C/T]ggcagataactatttg	C	T	AF164438 // downstream // 61062 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // downstream // 61062 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. q13.1
SNP_A-2147884	atggccttgctcttac[A/T]cactactctttatcta	A	T	AF164438 // downstream // 96355 // Hs.509113 // NPAS3 // 64067 // Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) mRNA, complete cds. /// NM_022123 // downstream // 96355 // Hs.509113 // NPAS3 // 64067 // Homo sapiens neuronal PAS domain protein 3	NPAS3	NPAS3, Homo sapiens basic-helix-loop-helix-PAS protein (MOP6) complete cds. ,q13.1
SNP_A-1872308	tctagacaatcttgac[A/C]aaaaatcttcattctc	A	C	NM_022073 // intron // 0 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// ENST00000250457 // intron // 0 // --- // --- // --- // ---	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-1914227	tgtgttaaacttgcgt[A/C]aacttcaaatattaat	A	C	NM_022073 // intron // 0 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// ENST00000250457 // intron // 0 // --- // --- // --- // ---	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2204640	aattacagcaacattg[C/T]cttccagtgtgcatct	C	T	NM_022073 // upstream // 3392 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 478476 // Hs.269909 // C14orf147 // 171546 // Homo sapiens chromosome 14 open reading frame 147 (C1	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-1831232	taatggaatcatataa[C/T]ctgtgacctttgtga	C	T	NM_022073 // upstream // 3901 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 477967 // Hs.269909 // C14orf147 // 171546 // Homo sapiens chromosome 14 open reading frame 147 (C1	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-1793297	ggtagccacaatagca[A/G]atatagaacatttcca	A	G	NM_022073 // upstream // 31670 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 450198 // Hs.269909 // C14orf147 // 171546 // Homo sapiens chromosome 14 open reading frame 147 (C	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2204694	ccttctttccacgtct[C/T]tcagtttctgtgtcaa	C	T	NM_022073 // upstream // 60228 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 421640 // Hs.269909 // C14orf147 // 171546 // Homo sapiens chromosome 14 open reading frame 147 (C	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2303936	gctcatggtttgttta[C/T]accactccccactccc	C	T	NM_022073 // upstream // 86007 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 395861 // Hs.269909 // C14orf147 // 171546 // Homo sapiens chromosome 14 open reading frame 147 (C	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-2119206	agtaggcaacagaaac[C/T]ctgaaatggtgggaca	C	T	NM_022073 // upstream // 307841 // Hs.135507 // EGLN3 // 112399 // Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA. /// NM_138288 // downstream // 174027 // Hs.269909 // C14orf147 // 171546 // Homo sapiens chromosome 14 open reading frame 147 (	EGLN3	EGLN3, Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), q13.1
SNP_A-1820928	gtttctattaaggatc[A/G]aggtacagagggtaga	A	G	NM_003136 // upstream // 7141 // Hs.167535 // SRP54 // 6729 // Homo sapiens signal recognition particle 54kDa (SRP54), mRNA. /// ENST00000330704 // downstream // 35549 // --- // --- // --- // --- /// ENST00000216774 // upstream // 7141 // --- // --- // –	SRP54	SRP54, Homo sapiens signal recognition particle 54kDa (SRP54), q13.2
SNP_A-2205288	ggcaggagagttaggc[A/G]aatacagcatctttga	A	G	AB002389 // intron // 0 // Hs.458487 // KIAA0391 // 9692 // Homo sapiens mRNA for KIAA0391 gene, partial cds. /// ENST00000250377 // intron // 0 // --- // --- // --- // --- /// ENST00000321130 // intron // 0 // --- // --- // --- // --- // ---	KIAA0391	KIAA0391, Homo sapiens for KIAA0391 gene, partial cds. ,q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1797428	ggtttacaaatggcta[C/T]ccataaaaaatacaac	C	T	AB002389 // intron // 0 // Hs.458487 // KIAA0391 // 9692 // Homo sapiens mRNA for KIAA0391 gene, partial cds. /// ENST00000250377 // intron // 0 // — // — // — // — /// ENST00000321130 // intron // 0 // — // — // — // —	KIAA0391	KIAA0391, Homo sapiens for KIAA0391 gene, partial cds. q13.2
SNP_A-1919467	ttaagcccatctaaaa[A/G]gctaatgcaaattccc	A	G	AB002389 // 3UTR // 0 // Hs.458487 // KIAA0391 // 9692 // Homo sapiens mRNA for KIAA0391 gene, partial cds. /// ENST00000321130 // 3UTR // 0 // — // — // — // —	KIAA0391	KIAA0391, Homo sapiens for KIAA0391 gene, partial cds. q13.2
SNP_A-1711422	ggtagtgggaaaagacatagttcccj[A/G]aattcttctggagtctat agtgtaa	A	G	NM_003317 // upstream // 50727 // Hs.94367 // TITF1 // 7080 // thyroid transcription factor 1 /// NM_014360 // downstream // 9587 // Hs.234763 // NKX2-8 // 26257 // NK2 transcription factor related, locus 8 (Drosophila)	TITF1	TITF1, rs381858, thyroid transcription factor 1 q13.3
SNP_A-2164373	caaaatcttcacaata[C/T]ggtcaacttcctttcc	C	T	NM_020529 // upstream // 99502 // Hs.81328 // NFKBIA // 4792 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA. /// NM_032594 // upstream // 29794 // Hs.62813 // INSM2 // 84684 // Homo sapie	NFKBIA	NFKBIA, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), q13.2
SNP_A-2088555	actgtctagcacagaa[C/G]caaacaatgaaatgtt	C	G	NM_020529 // upstream // 105151 // Hs.81328 // NFKBIA // 4792 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA. /// NM_032594 // upstream // 24145 // Hs.62813 // INSM2 // 84684 // Homo sapi	NFKBIA	NFKBIA, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), q13.2
SNP_A-1716385	ttgaataatggtctataacctctaa[C/T]tgccagacatttgccatac cagttt	C	T	NM_006194 // intron // 0 // Hs.132576 // PAX9 // 5083 // paired box gene 9	PAX9	PAX9, rs8004187, paired box gene 9 q13.3
SNP_A-1752273	atataacctaggaatgacoctaaaa[C/T]gaagagaaaataatc ttacttttg	C	T	NM_030631 // intron // 0 // Hs.55080 // SLC25A21 // 89874 // solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	SLC25A21	SLC25A21, rs1179966, solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 q13.3
SNP_A-2100085	agagtgctcatatcacj[A/G]gaggcacgtaagtcat	A	G	NM_032352 // downstream // 186840 // Hs.525299 // BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 // downstream // 241058 // Hs.368647 // MBIP // 51562 // Homo sapiens MAP3K12 binding inhibitory pro	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.2
SNP_A-2227856	ctaccctatcaatagj[A/G]aatcaggtatgctggc	A	G	NM_032352 // downstream // 201263 // Hs.525299 // BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 // downstream // 226635 // Hs.368647 // MBIP // 51562 // Homo sapiens MAP3K12 binding inhibitory pro	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.3
SNP_A-2146606	atgctggcggacgta[C/G]agtaatttaaccagag	C	G	NM_032352 // downstream // 201288 // Hs.525299 // BRMS1L // 84312 // Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), mRNA. /// NM_016586 // downstream // 226610 // Hs.368647 // MBIP // 51562 // Homo sapiens MAP3K12 binding inhibitory pro	BRMS1L	BRMS1L, Homo sapiens breast cancer metastasis-suppressor 1-like (BRMS1L), q13.3
SNP_A-2206193	tcttacactaaagcaa[C/G]tgttgctgatttggg	C	G	NM_003317 // downstream // 97074 // Hs.94367 // TITF1 // 7080 // Homo sapiens thyroid transcription factor 1 (TITF1), mRNA. /// NM_003317 // downstream // 97925 // Hs.94367 // TITF1 // 7080 // Homo sapiens thyroid transcription factor 1 (TITF1), mRNA. ///	TITF1	TITF1, Homo sapiens thyroid transcription factor 1 (TITF1), q13.3
SNP_A-1845879	tatataaaatgagaaa[C/G]atgagttcatatatcc	C	G	NM_003317 // downstream // 44464 // Hs.94367 // TITF1 // 7080 // Homo sapiens thyroid transcription factor 1 (TITF1), mRNA. /// NM_003317 // downstream // 45315 // Hs.94367 // TITF1 // 7080 // Homo sapiens thyroid transcription factor 1 (TITF1), mRNA. ///	TITF1	TITF1, Homo sapiens thyroid transcription factor 1 (TITF1), q13.3
SNP_A-2206383	ctgagacacaatttccc[A/G]ctgacagcaaacaaa	A	G	NM_014360 // upstream // 15458 // Hs.234763 // NKX2-8 // 26257 // Homo sapiens NK2 transcription factor related, locus 8 (Drosophila) (NKX2-8), mRNA. /// ENST00000258829 // upstream // 15458 // — // — // — // — /// ENST00000358631 // upstream // 2	NKX2-8	NKX2-8, Homo sapiens NK2 transcription factor related, locus 8 (Drosophila) (NKX2-8), q13.3
SNP_A-2168522	caagaaaagaaggtga[A/G]aagcatcactcagtta	A	G	ENST00000358001 // intron // 0 // — // — // — // —	-	q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2306441	gctggtacttcacaat[C/G]ataccctgttgtaaca	C	G	NM_207441 // upstream // 1399 // Hs.440174 // --- // 0 // Homo sapiens FLJ42220 protein (FLJ42220), mRNA. /// ENST00000358001 // upstream // 12322 // --- // --- // --- // --- /// ENST00000344665 // upstream // 1399 // --- // --- // --- // ---	-	-, Homo sapiens FLJ42220 protein (FLJ42220), q13.3
SNP_A-1834650	taccacatcaggtgaa[A/T]catccaaacaagagaa	A	T	NM_207441 // upstream // 1247 // Hs.440174 // --- // 0 // Homo sapiens FLJ42220 protein (FLJ42220), mRNA. /// ENST00000358001 // upstream // 12474 // --- // --- // --- // --- /// ENST00000344665 // upstream // 1247 // --- // --- // --- // ---	-	-, Homo sapiens FLJ42220 protein (FLJ42220), q13.3
SNP_A-1739891	ttggcaggtcggtctaagggtcctc[A/G]atagtagatgctagtggtggctatt	A	G	BC038110 // downstream // 138538 // Hs.249986 // C14orf25 // 319089 // chromosome 14 open reading frame 25 /// NM_001049 // upstream // 102264 // Hs.248160 // SSTR1 // 6751 // somatostatin receptor 1	C14orf25	C14orf25 , rs2001398, chromosome 14 open reading frame 25 ,q21.1
SNP_A-1676678	tttaaacttagtatacaagaaata[C/T]cactaggttgtgttaagatgtaagt	C	T	BC038110 // downstream // 172919 // Hs.249986 // C14orf25 // 319089 // chromosome 14 open reading frame 25 /// NM_001049 // upstream // 67883 // Hs.248160 // SSTR1 // 6751 // somatostatin receptor 1	C14orf25	C14orf25 , rs2415451, chromosome 14 open reading frame 25 ,q21.1
SNP_A-1747481	ctattgtaagtctactctttctata[G/T]aattcctggaaattatacaatgtct	G	T	NM_006364 // downstream // 649815 // Hs.528298 // SEC23A // 10484 // Sec23 homolog A (S. cerevisiae) /// NM_175060 // upstream // 126766 // Hs.257913 // C14orf27 // 161198 // chromosome 14 open reading frame 27	SEC23A	SEC23A , rs10484116, Sec23 homolog A (S. cerevisiae) ,q21.1
SNP_A-2298602	gcccactgaaacagac[A/T]aaaaacaacaggaaat	A	T	NM_138731 // intron // 0 // Hs.145251 // MIPOL1 // 145282 // Homo sapiens mirror-image polydactyly 1 (MIPOL1), mRNA. /// ENST00000327441 // intron // 0 // --- // --- // --- // ---	MIPOL1	MIPOL1, Homo sapiens mirror-image polydactyly 1 (MIPOL1), q13.3
SNP_A-1869204	tcctggagtctcaagg[A/G]aatgaaggctgctgac	A	G	BX161415 // intron // 0 // Hs.209293 // TTC6 // 115669 // human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). /// ENST00000332415 // intron // 0 // --- // --- // --- // --- /// ENST00000267368 // intron // 0 // --- // --- // ---	TTC6	TTC6, human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). q21.1
SNP_A-2258363	cttttcaggctcttcc[C/T]aaaccataaacaacat	C	T	BX161415 // downstream // 156703 // Hs.209293 // TTC6 // 115669 // human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). /// NM_001049 // upstream // 208611 // Hs.248160 // SSTR1 // 6751 // Homo sapiens somatostatin receptor	TTC6	TTC6, human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). ,q21.1
SNP_A-2259050	ctttttgaataaatg[A/T]actgaactgaaaaaga	A	T	BX161415 // downstream // 226770 // Hs.209293 // TTC6 // 115669 // human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). /// NM_001049 // upstream // 138544 // Hs.248160 // SSTR1 // 6751 // Homo sapiens somatostatin receptor	TTC6	TTC6, human full-length cDNA clone CS0DD003YF17 of Neuroblastoma of Homo sapiens (human). ,q21.1
SNP_A-1659108	gctattaaggaactagagttgataa[A/G]taaatgtgtataggttcctttgca	A	G	NM_177452 // intron // 0 // Hs.13303 // TRAPPC6B // 122553 // trafficking protein particle complex 6B	TRAPPC6B	TRAPPC6B , rs10483542, trafficking protein particle complex 6B,q21.1
SNP_A-1890645	tgatgaatacatacaa[A/G]ctaatttgctaaaact	A	G	NM_001049 // downstream // 28230 // Hs.248160 // SSTR1 // 6751 // Homo sapiens somatostatin receptor 1 (SSTR1), mRNA. /// NM_175060 // downstream // 13257 // Hs.525307 // CLEC14A // 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mR	SSTR1	SSTR1, Homo sapiens somatostatin receptor 1 (SSTR1), q21.1
SNP_A-2236544	ctcgtgtaattttcac[A/C]agaatctccctcattt	A	C	NM_175060 // upstream // 136273 // Hs.525307 // CLEC14A // 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream // 639623 // Hs.272927 // SEC23A // 10484 // Homo sapiens Sec23 homolog A (S. cerevisiae) (	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2208251	gtttcctaagacaaag[C/G]ccatgaaactagaaac	C	G	NM_175060 // upstream // 452651 // Hs.525307 // CLEC14A // 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream // 323245 // Hs.272927 // SEC23A // 10484 // Homo sapiens Sec23 homolog A (S. cerevisiae) (	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2208433	aggagagaatcttgaa[A/T]tgacagactatttatt	A	T	NM_175060 // upstream // 715305 // Hs.525307 // CLEC14A // 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream // 60591 // Hs.272927 // SEC23A // 10484 // Homo sapiens Sec23 homolog A (S. cerevisiae) (S	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2208440	agggtatgtgatctgc[C/T]gaacaatcagtaattt	C	T	NM_175060 // upstream // 746710 // Hs.525307 // CLEC14A // 161198 // Homo sapiens chromosome 14 open reading frame 27 (C14orf27), mRNA. /// NM_006364 // downstream // 29186 // Hs.272927 // SEC23A // 10484 // Homo sapiens Sec23 homolog A (S. cerevisiae) (S	CLEC14A	CLEC14A, Homo sapiens chromosome 14 open reading frame 27 (C14orf27), q21.1
SNP_A-2066453	aatttttacaaagtga[A/T]caaacccatgtaacaa	A	T	NM_203301 // upstream // 187550 // Hs.324342 // FBXO33 // 254170 // Homo sapiens F-box protein 33 (FBXO33), mRNA. /// ENST00000298097 // upstream // 187550 // — // — // — // — /// ENST00000357299 // downstream // 784924 // — // — // — // —	FBXO33	FBXO33, Homo sapiens F-box protein 33 (FBXO33), q21.1
SNP_A-2234369	ctccaacttaaaaacc[A/C]gatctttgtcttactc	A	C	NM_203301 // upstream // 315260 // Hs.324342 // FBXO33 // 254170 // Homo sapiens F-box protein 33 (FBXO33), mRNA. /// ENST00000298097 // upstream // 315260 // — // — // — // — /// ENST00000357299 // downstream // 657214 // — // — // — // —	FBXO33	FBXO33, Homo sapiens F-box protein 33 (FBXO33), q21.1
SNP_A-1813792	gtgtagttctgctaga[C/T]atgagttgacagacct	C	T	NM_203301 // upstream // 600367 // Hs.324342 // FBXO33 // 254170 // Homo sapiens F-box protein 33 (FBXO33), mRNA. /// ENST00000298097 // upstream // 600367 // — // — // — // — /// ENST00000357299 // downstream // 372107 // — // — // — // —	FBXO33	FBXO33, Homo sapiens F-box protein 33 (FBXO33), q21.1
SNP_A-2209139	ctggcaacagctctca[A/G]catttaaggactcaat	A	G	NM_203301 // upstream // 631545 // Hs.324342 // FBXO33 // 254170 // Homo sapiens F-box protein 33 (FBXO33), mRNA. /// ENST00000298097 // upstream // 631545 // — // — // — // — /// ENST00000357299 // downstream // 340929 // — // — // — // —	FBXO33	FBXO33, Homo sapiens F-box protein 33 (FBXO33), q21.1
SNP_A-1668578	caacaaaaatcttaatgggtaattc[C/T]aatgtacaactaagttttaatatca	C	T	NM_152447 // upstream // 273156 // Hs.31522 // LRFN5 // 145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs8022809, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1748175	atatttcagcacaacacaaccggac[A/G]gctaactaagattatgttttgacct	A	G	NM_152447 // upstream // 231388 // Hs.31522 // LRFN5 // 145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs3910110, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1721401	ttcctagatcaagccatactcacaa[A/C]gactaagacactgtgacagagacta	A	C	NM_152447 // upstream // 192896 // Hs.31522 // LRFN5 // 145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs10483528, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-2285978	gatgataccatttaga[A/G]tatcccatgagaagtg	A	G	NM_152447 // upstream // 1180665 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 3554 // — // — // — // — /// ENST00000298119 // ups	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1665434	aaccagctgaggctagcccaaattg[C/T]tgacccataaaatcataaacaaata	C	T	NM_152447 // intron // 0 // Hs.31522 // LRFN5 // 145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs2010155, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1648178	gcaatgtggtcatatgttcctaaga[A/T]gcacaattattgaaaacttaatta	A	T	NM_152447 // intron // 0 // Hs.31522 // LRFN5 // 145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs10483523, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-1643746	cctccacacacaaacaggaagtaca[C/T]ctgcctgcttaccgtacacagacag	C	T	NM_152447 // intron // 0 // Hs.31522 // LRFN5 // 145581 // leucine rich repeat and fibronectin type III domain containing 5	LRFN5	LRFN5 , rs10483522, leucine rich repeat and fibronectin type III domain containing 5,q21.1
SNP_A-2209996	catatacctatttata[A/C]gctaaatctgactcac	A	C	NM_152447 // upstream // 573548 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 610671 // — // — // — // — /// ENST00000298119 // up	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2174332	cacactgtatctgccd[A/G]caaaagcctcacaatg	A	G	NM_152447 // upstream // 323576 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 860643 // — // — // — // /// ENST00000298119 // up	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2175127	cacagtgccctttgal[A/G]ctgaaaagaaggagga	A	G	NM_152447 // upstream // 229519 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 954700 // — // — // — // /// ENST00000298119 // up	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1867160	tccctgattccctgacf[A/G]catatttaccatgct	A	G	NM_152447 // upstream // 208699 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 975520 // — // — // — // /// ENST00000298119 // up	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2098996	agaggaaactcattgal[C/T]atacaggagaccaca	C	T	NM_152447 // upstream // 196046 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 988173 // — // — // — // /// ENST00000298119 // up	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1846461	tatattacagcatcta[C/T]gagtcgataaatttat	C	T	NM_152447 // upstream // 116359 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000357299 // upstream // 1067860 // — // — // — // /// ENST00000298119 // u	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2210293	tggcatccttcaatca[C/T]gaggactatttagaa	C	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1954557	ttgcctatgtatgta[A/T]ccttccagaaaatgta	A	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2288564	gattgcaaaatacaaat[C/T]atcgcttgccaatagg	C	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2141105	atctggaaattgaggal[A/T]gtcttatggtggagaa	A	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2127598	ataaccaataaaaaaa[C/T]ctgctaacaaaagtgc	C	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2030774	aaagcttgatcattaa[A/T]aaaacggcctaatttc	A	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2174939	cacaggcttcaaaaa[C/T]gtctatgctatccttc	C	T	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2234500	ctccaccaggcttta[A/C]ctccttgacggaaacg	A	C	NM_152447 // intron // 0 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// ENST00000298119 // intron // 0 // — // — // —	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2210464	gacattaatcacacag[G/T]atgcatagaggaataa	G	T	NM_152447 // downstream // 90272 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 2509693 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chro	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2221749	cctttataacatcaa[A/G]atggtccagaattca	A	G	NM_152447 // downstream // 281527 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 2318438 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chr	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-1877915	tctggttagcccgac[C/T]gatacagcagttacag	C	T	NM_152447 // downstream // 458150 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 2141815 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chr	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.1
SNP_A-2240423	ctgacacctcaatcat[G/T]actggatctgctgggt	G	T	NM_152447 // downstream // 1379053 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 1220912 // Hs.307086 // C14orf155 // 84075 // Homo sapiens ch	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-2083908	actactgcattatccc[A/C]agaaattctctatatc	A	C	NM_152447 // downstream // 1418189 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 1181776 // Hs.307086 // C14orf155 // 84075 // Homo sapiens ch	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-1920414	ttaattaacatgtgtc[C/T]agtatttttgagaaa	C	T	NM_152447 // downstream // 1493337 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 1106628 // Hs.307086 // C14orf155 // 84075 // Homo sapiens ch	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-2152522	attaagcaatctctgg[A/G]atgtttctcttttt	A	G	NM_152447 // downstream // 1650086 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 949879 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chr	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-1724386	tcaactgaacagatatttattgaga[A/C]cctagtgtgtacaaagta tgctgcc	A	C	NM_032135 // upstream // 253085 // Hs.307086 // DKFZP434F1017 // 84075 // hypothetical protein DKFZp434F1017	DKFZP434F1017	DKFZP434F1017, rs229712, hypothetical protein DKFZp434F1017.q21.2
SNP_A-2066852	acaaaatcgatttgca[C/T]aaattactagcattcc	C	T	NM_152447 // downstream // 2052925 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 547040 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chr	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-1807137	gtctcctggataataa[C/G]agatagtgattggctc	C	G	NM_152447 // downstream // 2192565 // Hs.136893 // LRFN5 // 145581 // Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), mRNA. /// NM_032135 // downstream // 407400 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chr	LRFN5	LRFN5, Homo sapiens leucine rich repeat and fibronectin type III domain containing 5 (LRFN5), q21.2
SNP_A-1653258	tcaggaaaacatgagctaccaaaac[A/G]tactaaatgaggtac cattgaccaa	A	G	NM_018353 // upstream // 329049 // Hs.437941 // C14orf106 // 55320 // chromosome 14 open reading frame 106 /// NM_080746 // downstream // 1068768 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	C14orf106	C14orf106, rs7494280, chromosome 14 open reading frame 106.q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1720921	tacaaggaatatatggtagctgatga[C/T]cttcaccttaggatcc accacaac	C	T	NM_018353 // upstream // 337414 // Hs.437941 // C14orf106 // 55320 // chromosome 14 open reading frame 106 /// NM_080746 // downstream // 1060403 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	C14orf106	C14orf106 , rs2415902, chromosome 14 open reading frame 106 ,q21.2
SNP_A-1840763	tagctactccttggc[C/T]gcatcgttcagaagt	C	T	NM_032135 // upstream // 105397 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 // upstream // 105397 // — // — // — // — /// ENST00000332097 // downstream // 248094 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-2123831	agttaaagtaagaaaa[G/T]gcaccaccaattataa	G	T	NM_032135 // upstream // 113415 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 // upstream // 113415 // — // — // — // — /// ENST00000332097 // downstream // 240076 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-1838048	tagaaatcacctaaga[C/T]ggcagagattgagctg	C	T	NM_032135 // upstream // 193212 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 // upstream // 193212 // — // — // — // — /// ENST00000332097 // downstream // 160279 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-1716685	gtgaatatacaaagtgatagaatta[A/G]accaactgtaagaatg aacagatct	A	G	NM_080746 // downstream // 746656 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like /// NM_018353 // upstream // 651161 // Hs.437941 // C14orf106 // 55320 // chromosome 14 open reading frame 106	RPL10L	RPL10L , rs10483586, ribosomal protein L10-like ,q21.2
SNP_A-1689763	ctttttttacactatgaagcaaca[A/G]tgttctctaaatagcagggt gcttt	A	G	NM_018353 // upstream // 651214 // Hs.437941 // C14orf106 // 55320 // chromosome 14 open reading frame 106 /// NM_080746 // downstream // 746603 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	C14orf106	C14orf106 , rs10483587, chromosome 14 open reading frame 106 ,q21.2
SNP_A-2288463	gattgaaaagagatag[A/C]aagaatgtgtggcaag	A	C	NM_032135 // upstream // 334198 // Hs.307086 // C14orf155 // 84075 // Homo sapiens chromosome 14 open reading frame 155 (C14orf155), mRNA. /// ENST00000340446 // upstream // 334198 // — // — // — // — /// ENST00000332097 // downstream // 19293 //	C14orf155	C14orf155, Homo sapiens chromosome 14 open reading frame 155 (C14orf155), q21.2
SNP_A-2212098	ggaagctcaatttaa[C/T]ctcatcatagaactct	C	T	ENST00000332097 // upstream // 732 // — // — // — // — /// ENST00000325192 // upstream // 36033 // — // — // — // —	-	q21.2
SNP_A-2296469	gcatttctttcacccf[A/G]gacacttgctttcaaa	A	G	NM_017658 // downstream // 17754 // Hs.174682 // BTBD5 // 54813 // Homo sapiens BTB (POZ) domain containing 5 (BTBD5), mRNA. /// NM_017658 // downstream // 17769 // Hs.174682 // BTBD5 // 54813 // Homo sapiens BTB (POZ) domain containing 5 (BTBD5), mRNA. /	BTBD5	BTBD5, Homo sapiens BTB (POZ) domain containing 5 (BTBD5), q21.2
SNP_A-2025978	aaaatgttagtgattatta[C/T]gccaatgttaacatcc	C	T	NM_017658 // downstream // 853 // Hs.174682 // BTBD5 // 54813 // Homo sapiens BTB (POZ) domain containing 5 (BTBD5), mRNA. /// NM_017658 // downstream // 868 // Hs.174682 // BTBD5 // 54813 // Homo sapiens BTB (POZ) domain containing 5 (BTBD5), mRNA. /// E	BTBD5	BTBD5, Homo sapiens BTB (POZ) domain containing 5 (BTBD5), q21.2
SNP_A-2003717	gccagatgattctgtc[C/T]aagcgtaggctaatgt	C	T	ENST00000261241 // intron // 0 // — // — // —	-	q21.2
SNP_A-2230204	ctatagaatagtgcaa[A/G]tgagcaggacttttct	A	G	ENST00000261241 // 3UTR // 0 // — // — // —	-	q21.2
SNP_A-1737315	ttttccaacacagcacttatgaag[G/T]agaactggagcattaag ataaaata	G	T	NM_018353 // upstream // 963359 // Hs.437941 // C14orf106 // 55320 // chromosome 14 open reading frame 106 /// NM_080746 // downstream // 434458 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	C14orf106	C14orf106 , rs8660855, chromosome 14 open reading frame 106 ,q21.2
SNP_A-1715817	tgtctggtatcctagagcagatcca[C/G]gttgccatttgaaatcatt gatgta	C	G	NM_018353 // upstream // 1143758 // Hs.437941 // C14orf106 // 55320 // chromosome 14 open reading frame 106 /// NM_080746 // downstream // 254059 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	C14orf106	C14orf106 , rs10498397, chromosome 14 open reading frame 106 ,q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2212415	ttgtgtgttttgat[C/G]agacagcttgtaggga	C	G	NM_201260 // downstream // 442990 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 442990 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1749459	atggtatgtttacattccaaggcat[A/G]aacttgttaaaattacaattaatct	A	G	NM_001032 // downstream // 2604175 // Hs.539 // RPS29 // 6235 // ribosomal protein S29 /// NM_080746 // upstream // 325100 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	RPS29	RPS29 , rs2050966, ribosomal protein S29 ,q21.3
SNP_A-2212638	tatttaagtccaagt[A/G]aacctcctggaaaaga	A	G	NM_201260 // downstream // 607089 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 607089 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1942990	ttgggtgtggactta[C/T]ctgggggcagttactt	C	T	NM_201260 // downstream // 628690 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 628690 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2103534	agcaattgcactcaca[A/G]taacatcaaaaattta	A	G	NM_201260 // downstream // 632964 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 632964 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1854587	tcaacaaatacgccag[A/G]aaagctactatctcat	A	G	NM_201260 // downstream // 662168 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 662168 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1948412	ttagtacaaggttga[C/T]ggaaatgtgagttagc	C	T	NM_201260 // downstream // 692206 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 692206 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2234252	ctcatttatcttgc[A/G]gaaactccttgcagta	A	G	NM_201260 // downstream // 793994 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 793994 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-1843884	tagttatacagttgg[A/C]attctaatcccaagtt	A	C	NM_201260 // downstream // 803453 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 803453 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2102940	agcaaacaacaatata[C/G]agcctagcaacattat	C	G	NM_201260 // downstream // 982589 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 982589 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2
SNP_A-2109785	aggaaatgtaaaagga[C/G]acagtgcaatacagtc	C	G	NM_201260 // downstream // 1144872 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, mRNA. /// NM_201261 // downstream // 1144872 // Hs.230601 // TIM14 // 131118 // Homo sapiens homolog of yeast TIM14 (T	TIM14	TIM14, Homo sapiens homolog of yeast TIM14 (TIM14), transcript variant 3, q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2215363	cctcacaatgaatcaa[C/G]gaaatggaaaattaaaa	C	G	NM_182830 // intron // 0 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // — // — // — /// ENST00000357362 // intron // 0 // — // — // —	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1679202	atttcatttcattctccagtttacaj[C/T]gattagaaataagaagtcctg aagac	C	T	NM_001032 // downstream // 1563255 // Hs.539 // RPS29 // 6235 // ribosomal protein S29 /// NM_080746 // upstream // 1346020 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	RPS29	RPS29 , rs698305, ribosomal protein S29 ,q21.3
SNP_A-1692048	ttgtcattcacatacacttgcaatg[C/T]caaataaatgtatgttgaa gagaag	C	T	NM_001032 // downstream // 1583170 // Hs.539 // RPS29 // 6235 // ribosomal protein S29 /// NM_080746 // upstream // 1346105 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	RPS29	RPS29 , rs712450, ribosomal protein S29 ,q21.3
SNP_A-2118330	agtaactagtatactat[C/T]agtgctcacagaccac	C	T	NM_182830 // intron // 0 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // — // — // — /// ENST00000357362 // intron // 0 // — // — // —	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2066000	aatttgataccaaata[C/T]gccctagtagtcccg	C	T	NM_182830 // intron // 0 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // — // — // — /// ENST00000357362 // intron // 0 // — // — // —	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1889728	tgataatagctagtac[A/G]aaggatgcacaaagtg	A	G	NM_182830 // intron // 0 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // — // — // — /// ENST00000357362 // intron // 0 // — // — // —	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1830350	taatatgaacaacaaa[G/T]ggctaagttgaaagg	G	T	NM_182830 // intron // 0 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // — // — // — /// ENST00000357362 // intron // 0 // — // — // —	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1723020	acctctaaagaatgtataagagagg[C/T]aattaaatagtaatggt agggaaaa	C	T	NM_001032 // downstream // 1308575 // Hs.539 // RPS29 // 6235 // ribosomal protein S29 /// NM_080746 // upstream // 1620700 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	RPS29	RPS29 , rs2416153, ribosomal protein S29 ,q21.3
SNP_A-1800655	gtagaaactgtagaa[C/T]gtgggatttgctgaga	C	T	NM_182830 // intron // 0 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// ENST00000333599 // intron // 0 // — // — // — /// ENST00000357362 // intron // 0 // — // — // —	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1723638	caatcaagaaccctggacacaaatga[C/T]ggtctttgcatatcatttt tagcctt	C	T	NM_001032 // downstream // 808089 // Hs.539 // RPS29 // 6235 // ribosomal protein S29 /// NM_080746 // upstream // 2121186 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	RPS29	RPS29 , rs2261151, ribosomal protein S29 ,q21.3
SNP_A-1715537	caggtaccttttcattcatcttcatc[A/G]atatcccttagtatctaccct cttgt	A	G	NM_001032 // downstream // 798285 // Hs.539 // RPS29 // 6235 // ribosomal protein S29 /// NM_080746 // upstream // 2130990 // Hs.308332 // RPL10L // 140801 // ribosomal protein L10-like	RPS29	RPS29 , rs2816724, ribosomal protein S29 ,q21.3
SNP_A-1936795	ttctttcagaagatgc[A/G]agagtttattcatact	A	G	NM_182830 // upstream // 548618 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 217221 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_00	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2099619	agaggtatgagagcag[C/G]atagttcattcctgat	C	G	NM_182830 // upstream // 655699 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 324302 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_00	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950428	tttcagtcagagagaa[C/T]aggacaccgaaagtaa	C	T	NM_182830 // upstream // 893642 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 562245 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_00	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2279881	gaggctaaaaagtaaa[A/G]tatggtgggatagaca	A	G	NM_182830 // upstream // 1165800 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 834403 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_0	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2229955	ctataaaaatctagac[A/G]aaaacatggaagaaat	A	G	NM_182830 // upstream // 1197879 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 866482 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_0	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1863234	tcatttctgtatctgg[A/G]agaaaatagatgcatt	A	G	NM_182830 // upstream // 1250792 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 919395 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_0	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1853097	tatttggatagtaaaa[G/T]taatgcataacaaata	G	T	NM_182830 // upstream // 1261435 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 930038 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_0	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2086351	actcttacttgcttaa[A/G]tagaacttttgctgga	A	G	NM_182830 // upstream // 1262720 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 931323 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_0	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2003731	atacctacaactagaa[C/T]tgctgagtaagagtag	C	T	NM_182830 // upstream // 1369821 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1038424 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2256294	ctttagtaactaagca[A/G]gcataagtcagagtta	A	G	NM_182830 // upstream // 1772325 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1440928 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-2081181	acctgcataagttaac[A/G]gtaaaatcaactcttt	A	G	NM_182830 // upstream // 1963272 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1631875 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1785527	ggctcagctacaaaga[A/T]cagtaagtcttgcttt	A	T	NM_182830 // upstream // 2093930 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1762533 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1922919	ttagattgattctaga[A/T]actcacagatgtaata	A	T	NM_182830 // upstream // 2103150 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1771753 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897888	tgctgggtttcagcaa[A/G]aacttacttgtcagtt	A	G	NM_182830 // upstream // 2138251 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_182830 // upstream // 1806854 // Hs.436380 // MAMDC1 // 161357 // Homo sapiens MAM domain containing 1 (MAMDC1), mRNA. /// NM_	MAMDC1	MAMDC1, Homo sapiens MAM domain containing 1 (MAMDC1), q21.3
SNP_A-1835986	tactaaggtctagttg[G/T]actgttccagtaggat	G	T	NM_002692 // CDS // 0 // Hs.162777 // POLE2 // 5427 // Homo sapiens polymerase (DNA directed), epsilon 2 (p59 subunit) (POLE2), mRNA. /// ENST00000216367 // CDS // 0 // --- // --- // --- // ---	POLE2	POLE2, Homo sapiens polymerase (DNA directed), epsilon 2 (p59 subunit) (POLE2), q21.3
SNP_A-2193251	catctcattcatgaca[C/G]aagagccctcgtgact	C	G	NM_004713 // intron // 0 // Hs.388584 // SDCCAG1 // 9147 // Homo sapiens serologically defined colon cancer antigen 1 (SDCCAG1), mRNA. /// ENST00000298310 // intron // 0 // --- // --- // --- // ---	SDCCAG1	SDCCAG1, Homo sapiens serologically defined colon cancer antigen 1 (SDCCAG1), q21.3
SNP_A-2214608	cctagatattcagtga[A/T]attggaagagttagat	A	T	NM_006939 // intron // 0 // Hs.291533 // SOS2 // 6655 // Homo sapiens son of sevenless homolog 2 (Drosophila) (SOS2), mRNA. /// ENST00000216373 // intron // 0 // --- // --- // --- // --- /// ENST00000354238 // intron // 0 // --- // --- // --- // ---	SOS2	SOS2, Homo sapiens son of sevenless homolog 2 (Drosophila) (SOS2), q21.3
SNP_A-2129948	atacattcttataaga[G/T]tcatctccaatgtgca	G	T	NM_006575 // intron // 0 // Hs.130491 // MAP4K5 // 11183 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 1, mRNA. /// NM_198794 // intron // 0 // Hs.130491 // MAP4K5 // 11183 // Homo sapiens mitogen-act	MAP4K5	MAP4K5, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 1, q21.3
SNP_A-2092571	agaaataccataaata[C/T]gaagacgtggcaaaaa	C	T	NM_006575 // intron // 0 // Hs.130491 // MAP4K5 // 11183 // Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 1, mRNA. /// NM_198794 // intron // 0 // Hs.130491 // MAP4K5 // 11183 // Homo sapiens mitogen-act	MAP4K5	MAP4K5, Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), transcript variant 1, q21.3
SNP_A-2116016	agggtttcctaacata[A/T]ccaatcagcttgcaat	A	T	NM_020921 // intron // 0 // Hs.310429 // NIN // 51199 // Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, mRNA. /// NM_182945 // intron // 0 // Hs.310429 // NIN // 51199 // Homo sapiens ninein (GSK3B interacting protein) (NIN),	NIN	NIN, Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, q22.1
SNP_A-2266171	gaagggacgaggaaga[A/C]caatgacacttctctg	A	C	NM_020921 // intron // 0 // Hs.310429 // NIN // 51199 // Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, mRNA. /// NM_182945 // intron // 0 // Hs.310429 // NIN // 51199 // Homo sapiens ninein (GSK3B interacting protein) (NIN),	NIN	NIN, Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, q22.1
SNP_A-1868051	tcctatagccagtaaa[A/T]agtagtatgtggtggt	A	T	NM_020921 // intron // 0 // Hs.310429 // NIN // 51199 // Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, mRNA. /// NM_182945 // intron // 0 // Hs.310429 // NIN // 51199 // Homo sapiens ninein (GSK3B interacting protein) (NIN),	NIN	NIN, Homo sapiens ninein (GSK3B interacting protein) (NIN), transcript variant 2, q22.1
SNP_A-1739485	gaggttatttggcatattccactca[C/T]ctaaaagcatttttccttcatacaa	C	T	BC020774 // intron // 0 // Hs.112928 // GNG2 // 54331 // guanine nucleotide binding protein (G protein), gamma 2	GNG2	GNG2 , rs10498438, guanine nucleotide binding protein (G protein), gamma 2,q22.1
SNP_A-1677522	atctgatttagctaagatgctttac[C/T]gacaggatatcctgtatctagttaa	C	T	BC020774 // intron // 0 // Hs.112928 // GNG2 // 54331 // guanine nucleotide binding protein (G protein), gamma 2	GNG2	GNG2 , rs7154422, guanine nucleotide binding protein (G protein), gamma 2,q22.1
SNP_A-2196597	cattaaatattaatcg[A/T]atgaatgagtgtgttg	A	T	NM_002863 // upstream // 21598 // Hs.282417 // PYGL // 5836 // Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA. /// NM_015163 // downstream // 9156 // Hs.368928 // TRIM9 // 114088 // Homo sapiens t	PYGL	PYGL, Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), q22.1
SNP_A-1793768	ggtattctgtggcata[A/T]taacacgtgtcacaca	A	T	NM_015163 // upstream // 84861 // Hs.368928 // TRIM9 // 114088 // Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 1, mRNA. /// NM_052978 // upstream // 84861 // Hs.368928 // TRIM9 // 114088 // Homo sapiens tripartite motif-containin	TRIM9	TRIM9, Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1707235	tggataagagactggacccattcgat[C/G]gcaatcagagagcat ctcctggaga	C	G	NM_000953 // intron // 0 // Hs.306831 // PTGDR // 5729 // prostaglandin D2 receptor (DP)	PTGDR	PTGDR , rs10498445, prostaglandin D2 receptor (DP),q22.1
SNP_A-1645824	ccttgatgatgtgagtgacttcag[A/G]agacctggtgcactcac ttggcaca	A	G	NM_000956 // downstream // 14617 // Hs.2090 // PTGER2 // 5732 // prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	PTGER2 , rs708511, prostaglandin E receptor 2 (subtype EP2), 53kDa,q22.1
SNP_A-1734426	gtaacaagaaccagctgctaggaaaa[C/T]aggtcccagttatgt atgaaactcc	C	T	NM_000956 // downstream // 84006 // Hs.2090 // PTGER2 // 5732 // prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	PTGER2 , rs781354, prostaglandin E receptor 2 (subtype EP2), 53kDa,q22.1
SNP_A-1676272	ggttcttgttaccaggatgtaaat[A/G]atgaaaataaaatttttgc ctttg	A	G	NM_000956 // downstream // 84045 // Hs.2090 // PTGER2 // 5732 // prostaglandin E receptor 2 (subtype EP2), 53kDa	PTGER2	PTGER2 , rs897968, prostaglandin E receptor 2 (subtype EP2), 53kDa,q22.1
SNP_A-2111461	aggaggcattattgat[C/T]agcggtgtaggtattc	C	T	NM_030755 // downstream // 85644 // Hs.125221 // TXNDC // 81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA /// NM_152330 // upstream // 147452 // Hs.434914 // C14orf31 // 122786 // Homo sapiens chromosome 14 open reading frame 31 (C14orf	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-1788330	gggagggagttacgtat[C/T]gggaacaatgacagga	C	T	NM_030755 // downstream // 104806 // Hs.125221 // TXNDC // 81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA /// NM_152330 // upstream // 128290 // Hs.434914 // C14orf31 // 122786 // Homo sapiens chromosome 14 open reading frame 31 (C14or	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-1668727	atggacaaaaggaggactgaattaca[A/C]aagccggaagaaa agagaatgttga	A	C	AB037765 // intron // 0 // Hs.292164 // KIAA1344 // 57544 // KIAA1344	KIAA1344	KIAA1344 , rs781381, KIAA1344,q22.1
SNP_A-2047641	aagatgttcaacctag[A/G]aaattggctaaataaa	A	G	NM_030755 // downstream // 144848 // Hs.125221 // TXNDC // 81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA /// NM_152330 // upstream // 88248 // Hs.434914 // C14orf31 // 122786 // Homo sapiens chromosome 14 open reading frame 31 (C14orf	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-2298534	gcccacacatcaggaa[C/G]agtcccacagcatgag	C	G	NM_030755 // downstream // 165787 // Hs.125221 // TXNDC // 81542 // Homo sapiens thioredoxin domain containing (TXNDC), mRNA /// NM_152330 // upstream // 67309 // Hs.434914 // C14orf31 // 122786 // Homo sapiens chromosome 14 open reading frame 31 (C14orf	TXNDC	TXNDC, Homo sapiens thioredoxin domain containing (TXNDC), q22.1
SNP_A-2068665	acaataataacagcaa[C/T]gatggcttctgcttat	C	T	NM_152330 // intron // 0 // Hs.434914 // C14orf31 // 122786 // Homo sapiens chromosome 14 open reading frame 31 (C14orf31), mRNA /// ENST00000356218 // intron // 0 // — // — // —	C14orf31	C14orf31, Homo sapiens chromosome 14 open reading frame 31 (C14orf31), q22.1
SNP_A-2070975	acactctcctgtgaaa[A/G]ttctacctaatgggta	A	G	BC060856 // upstream // 45201 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000325284 // downstream // 44261 // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-1796097	ggtgtaccttcaggca[A/G]aggtaggcttcaacaa	A	C	BC060856 // upstream // 19429 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000325284 // downstream // 70033 // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-2216326	tgattgttatggccca[A/G]cattaatcataggtgc	A	G	BC060856 // intron // 0 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-2050414	aaggagttctcaaaca[C/T]aaicttcttcgacaga	C	T	BC060856 // intron // 0 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-2274200	gacttctgaaggaaga[C/T]gataagccaacccatt	C	T	BC060856 // intron // 0 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1816792	gttatgaacacaggaa[A/G]tcatttaaaactgaga	A	G	BC060856 // intron // 0 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // — // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-2023219	aaaacatgattctaag[A/T]aggagaccataggctt	A	T	BC060856 // intron // 0 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // — // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-1893175	tgcagacacctcaaca[C/T]tgcatttctgttcatc	C	T	BC060856 // intron // 0 // Hs.187772 // GNG2 // 54331 // Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, mRNA (cDNA clone MGC:71780 IMAGE:5276390), complete cds. /// ENST00000335281 // intron // 0 // — // — // — // —	GNG2	GNG2, Homo sapiens guanine nucleotide binding protein (G protein), gamma 2, (cDNA clone MGC:71780 IMAGE:5276390), complete cds. q22.1
SNP_A-2081084	acctgagataggccaa[C/T]ggtaatcgagaaaggg	C	T	NM_007361 // upstream // 5516 // Hs.369840 // NID2 // 22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 192969 // Hs.306831 // PTGDR // 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// ENST0000	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-2150316	atgtctggaagttaga[A/T]caggactataccaaat	A	T	NM_007361 // upstream // 5697 // Hs.369840 // NID2 // 22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 192788 // Hs.306831 // PTGDR // 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// ENST0000	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-2141536	atcttagcaatgatga[A/G]ctacttcaaggtcacc	A	G	NM_007361 // upstream // 6193 // Hs.369840 // NID2 // 22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 192292 // Hs.306831 // PTGDR // 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// ENST0000	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-2259038	ctttttccttatgcc[C/T]gcttatctactcagtt	C	T	NM_007361 // upstream // 6523 // Hs.369840 // NID2 // 22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 191962 // Hs.306831 // PTGDR // 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// ENST0000	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-1838583	tagaattgtttggtac[A/G]cagacattggtaacat	A	G	NM_007361 // upstream // 95105 // Hs.369840 // NID2 // 22795 // Homo sapiens nidogen 2 (osteonidogen) (NID2), mRNA. /// NM_000953 // upstream // 103380 // Hs.306831 // PTGDR // 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// ENST000	NID2	NID2, Homo sapiens nidogen 2 (osteonidogen) (NID2), q22.1
SNP_A-1960761	tttttctggctgtacc[C/T]ctaatactttgtctgg	C	T	NM_000953 // downstream // 11480 // Hs.306831 // PTGDR // 5729 // Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), mRNA. /// NM_000956 // upstream // 26192 // Hs.2090 // PTGER2 // 5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (P	PTGDR	PTGDR, Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), q22.1
SNP_A-1689823	accttttttcatgtcagcaaacaca[A/G]attttcatcatttttaatgttg aaa	A	G	AB051492 // upstream // 327006 // - // - // - // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// NM_001202 // downstream // 529069 // Hs.68879 // BMP4 // 652 // bone morphogenetic protein 4 /// NM_130850 // downstream // 529069 // Hs.68879 // BM	-	- , rs1954331, Homo sapiens mRNA for KIAA1705 protein, partial cds. ,q22.1
SNP_A-2296218	gcattctttcagaggc[A/G]ataggagaaattctat	A	G	NM_000956 // downstream // 21596 // Hs.2090 // PTGER2 // 5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // downstream // 21596 // — // - // — // — /// ENST00000281741 // downstream // 80393	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2188434	cagtgaagattagagc[A/G]agttttcctggctag	A	G	NM_000956 // downstream // 63111 // Hs.2090 // PTGER2 // 5732 // Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA. /// ENST00000245457 // downstream // 63111 // — // — /// ENST00000281741 // downstream // 38878	PTGER2	PTGER2, Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), q22.1
SNP_A-1925746	ttatgccattaaaaaa[A/G]ttgttacagtgggagc	A	G	ENST00000281741 // intron // 0 // — // — // —	-	q22.1
SNP_A-1822676	taaaaaaatgaagata[C/T]tgtatagcaaagaaca	C	T	ENST00000281741 // intron // 0 // — // — // —	-	q22.1
SNP_A-1919188	ttaacttcgagtaga[C/G]ggattaagtgacttct	C	G	ENST00000281741 // intron // 0 // — // — // —	-	q22.1
SNP_A-1884056	tgaagcagggcaggc[A/G]atacaagaacaagga	A	G	ENST00000281741 // intron // 0 // — // — // —	-	q22.1
SNP_A-2103784	agcaccagattccca[A/G]aggaaatagatctaat	A	G	ENST00000321662 // intron // 0 // — // — // —	-	q22.1
SNP_A-2050479	aaggatcatgtgaaga[A/C]aagaatcggtacagg	A	C	ENST00000321662 // intron // 0 // — // — // —	-	q22.1
SNP_A-2217101	agcagagaaatgccac[A/G]attagatcagagttag	A	G	NM_014584 // intron // 0 // Hs.525339 // ERO1L // 30001 // Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), mRNA. /// ENST00000359133 // intron // 0 // — // — // — /// ENST00000354459 // intron // 0 // — // — // —	ERO1L	ERO1L, Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), q22.1
SNP_A-2217115	ttgttactaatgataa[A/G]tggtttctaagcacca	A	G	NM_014584 // intron // 0 // Hs.525339 // ERO1L // 30001 // Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), mRNA. /// ENST00000359133 // intron // 0 // — // — // — /// ENST00000354459 // intron // 0 // — // — // —	ERO1L	ERO1L, Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), q22.1
SNP_A-2278077	gagcccatagcggaga[A/G]tcagagtgaaaacagg	A	G	NM_030637 // downstream // 21525 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // downstream // 22118 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000032392	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-1932622	ttccgtttgtgaca[C/T]gtatttctgtaggctg	C	T	NM_030637 // downstream // 18625 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // downstream // 19218 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000032392	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2186542	caggagagaaaacggt[A/G]aatgtgttttccttg	A	G	NM_030637 // downstream // 16958 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // downstream // 17551 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000032392	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-1832983	tacacaagaaatgagc[A/C]aagagttcctggagaa	A	C	NM_030637 // downstream // 6856 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // downstream // 7449 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000323920	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-1866877	tccctaatgttacaaa[C/G]gtgaagacaggttaaa	C	G	NM_030637 // upstream // 3664 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // upstream // 3848 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000357758 // u	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2123641	agtgttaccttaataa[C/T]gcaaatagcatcatcg	C	T	NM_030637 // upstream // 176527 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // upstream // 176711 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000357758	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2127431	ataacaacttaattta[C/G]atcacgtagaaaaact	C	G	NM_030637 // upstream // 269410 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // upstream // 269594 // — // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000357758	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041007	aaccgaaattggaagc[A/G]aaagcagtcaggaact	A	G	NM_030637 // upstream // 380297 // Hs.513260 // DDHD1 // 80821 // Homo sapiens DDHD domain containing 1 (DDHD1), mRNA. /// AB051492 // upstream // 380481 // --- // DDHD1 // 80821 // Homo sapiens mRNA for KIAA1705 protein, partial cds. /// ENST00000357758	DDHD1	DDHD1, Homo sapiens DDHD domain containing 1 (DDHD1), q22.1
SNP_A-2260156	gaaaatctgagttaaa[C/T]gaactttgtgggggtt	C	T	NM_001202 // downstream // 268015 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // downstream // 268015 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BM	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.1
SNP_A-1943261	ttggtgctgtcatgaa[C/T]ggtcccagggtaattt	C	T	NM_001202 // downstream // 267516 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // downstream // 267516 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BM	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.1
SNP_A-1896776	tgctatttattatttc[C/G]aaccatcttatttcag	C	G	NM_001202 // upstream // 177670 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 177670 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2163361	atttttcctgtgaat[A/G]atagagtggaggtgtc	A	G	NM_001202 // upstream // 200930 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 200930 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-1866621	tccccctttggaatta[C/T]ggcaaaaaggtgaact	C	T	NM_001202 // upstream // 225457 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 225457 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2078676	accattatgttaggga[C/T]gcttactcatcaattc	C	T	NM_001202 // upstream // 226643 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 226643 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2113043	aggccacaagttgttg[C/G]atttggtgtaaaccag	C	G	NM_001202 // upstream // 387114 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 387114 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2218388	aggaaagagttggtgg[A/G]actagcttatcatgga	A	G	NM_001202 // upstream // 391408 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 391408 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-1944531	ttgtctttacttgtat[A/G]aggcatcccaccagtg	A	G	NM_001202 // upstream // 396863 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA. /// NM_130850 // upstream // 396863 // Hs.68879 // BMP4 // 652 // Homo sapiens bone morphogenetic protein 4 (BMP4),	BMP4	BMP4, Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1, q22.2
SNP_A-2194854	catgctaactagaaag[C/G]agggaggtagacactg	C	G	NM_015589 // intron // 0 // Hs.98259 // SAMD4 // 23034 // Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // --- // --- // --- // --- /// ENST00000305831 // intron // 0 // --- // --- // --- // ---	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2069873	acacagcaggaagtag[A/G]acatcaaataaacaac	A	G	NM_015589 // intron // 0 // Hs.98259 // SAMD4 // 23034 // Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // — // — // — // — /// ENST00000305831 // intron // 0 // — // — // — // —	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2
SNP_A-2079683	accctatgtatactca[C/G]cgcttgtcctattgct	C	G	NM_015589 // intron // 0 // Hs.98259 // SAMD4 // 23034 // Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // — // — // — // — /// ENST00000305831 // intron // 0 // — // — // — // —	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2
SNP_A-1801245	gtagctggaggactca[C/T]gatttctgtctcatgg	C	T	NM_015589 // intron // 0 // Hs.98259 // SAMD4 // 23034 // Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // — // — // — // — /// ENST00000305831 // intron // 0 // — // — // — // — ///	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2
SNP_A-2110089	aggaagcgtcaggcca[A/G]agtttcggggctgccg	A	G	NM_015589 // intron // 0 // Hs.98259 // SAMD4 // 23034 // Homo sapiens sterile alpha motif domain containing 4 (SAMD4), mRNA. /// ENST00000357634 // intron // 0 // — // — // — // — /// ENST00000305831 // intron // 0 // — // — // — // — ///	SAMD4	SAMD4, Homo sapiens sterile alpha motif domain containing 4 (SAMD4), q22.2
SNP_A-1847615	tatctaaaagctacca[C/T]ctgtaggtaataagaa	C	T	NM_000161 // intron // 0 // Hs.86724 // GCH1 // 2643 // Homo sapiens GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA. /// ENST00000254299 // intron // 0 // — // — // — // — /// ENST00000359663 // intron // 0 // — // — // — // –	GCH1	GCH1, Homo sapiens GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), q22.2
SNP_A-2218842	cagttgcaaagtcctt[C/G]aaaacaaagggagtac	C	G	NM_144578 // intron // 0 // Hs.437831 // C14orf32 // 93487 // Homo sapiens chromosome 14 open reading frame 32 (C14orf32), mRNA. /// ENST00000305778 // intron // 0 // — // — // — // —	C14orf32	C14orf32, Homo sapiens chromosome 14 open reading frame 32 (C14orf32), q22.3
SNP_A-1955919	tttgtcatatggaaaa[A/G]tgattggtttcaaagt	A	G	NM_017943 // intron // 0 // Hs.525348 // FBXO34 // 55030 // Homo sapiens F-box protein 34 (FBXO34), mRNA. /// ENST00000313833 // intron // 0 // — // — // — // —	FBXO34	FBXO34, Homo sapiens F-box protein 34 (FBXO34), q22.3
SNP_A-1941876	ttggagaatttggaaa[C/T]ccagaaaaacatgatt	C	T	NM_199047 // intron // 0 // Hs.528278 // TBPL2 // 387332 // Homo sapiens TATA box binding protein like 2 (TBPL2), mRNA. /// ENST00000247219 // intron // 0 // — // — // — // —	TBPL2	TBPL2, Homo sapiens TATA box binding protein like 2 (TBPL2), q22.3
SNP_A-2162943	attttgtatgcttttа[C/T]gaactgctgaagttaa	C	T	NM_199047 // intron // 0 // Hs.528278 // TBPL2 // 387332 // Homo sapiens TATA box binding protein like 2 (TBPL2), mRNA. /// ENST00000247219 // intron // 0 // — // — // — // —	TBPL2	TBPL2, Homo sapiens TATA box binding protein like 2 (TBPL2), q22.3
SNP_A-1896563	tgctagaagtacctgg[A/G]aaatccctctgagccc	A	G	NM_182926 // downstream // 57951 // Hs.509414 // KTN1 // 3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 375958 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. ///	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-2294521	gcagtcaggtagatac[A/G]cttcagccactgtctt	A	G	NM_182926 // downstream // 144197 // Hs.509414 // KTN1 // 3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 289712 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. ///	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-1782065	ggcaacacaagaataa[C/T]gcacataataaataca	C	T	NM_182926 // downstream // 185351 // Hs.509414 // KTN1 // 3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 248558 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. ///	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3
SNP_A-1939143	ttgatagaaaaagttc[A/G]caggccctggcttaag	A	G	NM_182926 // downstream // 316398 // Hs.509414 // KTN1 // 3895 // Homo sapiens kinectin 1 (kinesin receptor) (KTN1), mRNA. /// NM_021255 // upstream // 117511 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. ///	KTN1	KTN1, Homo sapiens kinectin 1 (kinesin receptor) (KTN1), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2053721	aagtgggtaaagagtg[A/G]acagaggagttgaggt	A	G	NM_021255 // downstream // 30479 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 248012 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-1904173	tgggccctacctctca[A/G]gtgtctggttcggcag	A	G	NM_021255 // downstream // 37419 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 241072 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2116561	aggtcacacagacagc[A/G]aaagtatctccagtgg	A	G	NM_021255 // downstream // 39082 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 239409 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-1874939	tctctactagatgagc[A/G]aaatactttccctgg	A	G	NM_021255 // downstream // 39697 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 238794 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2217637	cctgaggagaaaagaaa[A/T]cagaaatcggtagat	A	T	NM_021255 // downstream // 48989 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 229502 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-1852215	tattgtcatatttcaa[C/G]aatgagcaaactgaag	C	G	NM_021255 // downstream // 194846 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 83645 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2220305	ttaaagtctctgctta[G/T]gatactgagaaaaaa	G	T	NM_021255 // downstream // 226214 // Hs.105103 // PELI2 // 57161 // Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA. /// BC045556 // upstream // 52277 // Hs.497253 // C14orf101 // 54916 // Homo sapiens chromosome 14 open reading frame 101, mRNA	PELI2	PELI2, Homo sapiens pellino homolog 2 (Drosophila) (PELI2), q22.3
SNP_A-2152338	attaacaaggcagtga[A/G]ttaaagctacctatt	A	G	NM_172337 // upstream // 24493 // Hs.288655 // OTX2 // 5015 // Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), transcript variant 2, mRNA. /// NM_021728 // upstream // 24493 // Hs.288655 // OTX2 // 5015 // Homo sapiens orthodenticle homolog 2 (D	OTX2	OTX2, Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), transcript variant 2, q22.3
SNP_A-1827239	taacctgctttcctca[A/C]attgtattccttcc	A	C	ENST00000339762 // intron // 0 // — // — // —	-	q22.3
SNP_A-2285132	gatctcactggaaaa[A/G]ttgtagccaaaatatag	A	G	ENST00000339762 // intron // 0 // — // — // —	-	q23.1
SNP_A-2075326	acatgaaaagttgcaa[C/T]gtcaagcaaaactgta	C	T	ENST00000339762 // intron // 0 // — // — // —	-	q23.1
SNP_A-2052242	aagtaagaaaagctat[C/G]aatcagtttctccta	C	G	ENST00000339762 // intron // 0 // — // — // —	-	q23.1
SNP_A-1921462	ttacccactttgaaa[C/T]gtagctgccttgatct	C	T	NM_001001872 // downstream // 66705 // Hs.535420 // C14orf37 // 145407 // Homo sapiens chromosome 14 open reading frame 37 (C14orf37), mRNA. /// ENST00000281555 // upstream // 347933 // — // — // — /// ENST00000339762 // upstream // 71560 //	C14orf37	C14orf37, Homo sapiens chromosome 14 open reading frame 37 (C14orf37), q23.1
SNP_A-1868624	tcctctctcctcagga[C/T]gtgtttacctctgtggc	C	T	NM_001001872 // downstream // 42702 // Hs.535420 // C14orf37 // 145407 // Homo sapiens chromosome 14 open reading frame 37 (C14orf37), mRNA. /// ENST00000281555 // upstream // 371936 // — // — // — /// ENST00000339762 // upstream // 95563 //	C14orf37	C14orf37, Homo sapiens chromosome 14 open reading frame 37 (C14orf37), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2282207	gagtgtttacatggcc[A/G]caggtaattcattcag	A	G	NM_001001872 // downstream // 9766 // Hs.535420 // C14orf37 // 145407 // Homo sapiens chromosome 14 open reading frame 37 (C14orf37), mRNA. /// ENST00000281555 // upstream // 404872 // --- // --- // --- /// ENST00000339762 // upstream // 128499 //	C14orf37	C14orf37, Homo sapiens chromosome 14 open reading frame 37 (C14orf37), q23.1
SNP_A-2003771	ggcttgaacataggcc[A/C]aaggtaaatagaagat	A	C	NM_001001872 // intron // 0 // Hs.535420 // C14orf37 // 145407 // Homo sapiens chromosome 14 open reading frame 37 (C14orf37), mRNA. /// ENST00000267485 // intron // 0 // --- // --- // ---	C14orf37	C14orf37, Homo sapiens chromosome 14 open reading frame 37 (C14orf37), q23.1
SNP_A-1652520	atgtagctgaacttgatgttctaaa[C/T]gtgactttcaaaataaaa taattt	C	T	NM_014992 // intron // 0 // Hs.356537 // DAAM1 // 23002 // dishevelled associated activator of morphogenesis 1	DAAM1	DAAM1 , rs10483714, dishevelled associated activator of morphogenesis 1, q23.1
SNP_A-2284554	gatcacctctttggccg[G/T]cgagaaaaagatgttcc	G	T	NM_016651 // downstream // 119005 // Hs.48950 // DACT1 // 51339 // Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), mRNA. /// NM_014992 // upstream // 421358 // Hs.19156 // DAAM1 // 23002 // Homo sapiens dishevelled associated	DACT1	DACT1, Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), q23.1
SNP_A-1866339	tcccattcactttggat[C/T]aaatttcagagatttc	C	T	NM_016651 // downstream // 136497 // Hs.48950 // DACT1 // 51339 // Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), mRNA. /// NM_014992 // upstream // 403866 // Hs.19156 // DAAM1 // 23002 // Homo sapiens dishevelled associated	DACT1	DACT1, Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), q23.1
SNP_A-1816729	gttatcatgttagagat[A/T]aataacctgagttact	A	T	NM_016651 // downstream // 228113 // Hs.48950 // DACT1 // 51339 // Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), mRNA. /// NM_014992 // upstream // 312250 // Hs.19156 // DAAM1 // 23002 // Homo sapiens dishevelled associated	DACT1	DACT1, Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1), q23.1
SNP_A-2224870	cgtgcaggctgatca[C/T]cactttaactggagt	C	T	NM_014992 // intron // 0 // Hs.19156 // DAAM1 // 23002 // Homo sapiens dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA. /// ENST00000360909 // intron // 0 // --- // --- // --- /// ENST00000351081 // intron // 0 // --- // --- // --	DAAM1	DAAM1, Homo sapiens dishevelled associated activator of morphogenesis 1 (DAAM1), q23.1
SNP_A-2111423	aggaggaggaaggagat[A/G]agtatgaagagcacag	A	G	NM_014992 // downstream // 6935 // Hs.19156 // DAAM1 // 23002 // Homo sapiens dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA. /// NM_022571 // downstream // 87054 // Hs.512691 // GPR135 // 64582 // Homo sapiens G protein-coupled recepto	DAAM1	DAAM1, Homo sapiens dishevelled associated activator of morphogenesis 1 (DAAM1), q23.1
SNP_A-2190564	catacctctgtatgag[A/G]attatgtctctctgc	A	G	AF529304 // intron // 0 // Hs.446850 // C14orf100 // 51528 // Homo sapiens medulloblastoma antigen MU-MB-50.4 mRNA, complete cds. /// NM_016475 // intron // 0 // Hs.446850 // C14orf100 // 51528 // Homo sapiens chromosome 14 open reading frame 100 (C14orf1	C14orf100	C14orf100, Homo sapiens medulloblastoma antigen MU-MB-50.4 complete cds, q23.1
SNP_A-1929322	ttcagtcatgagttgat[C/T]ggacatttaggttttt	C	T	NM_206852 // upstream // 253181 // Hs.368626 // RTN1 // 6252 // Homo sapiens reticulon 1 (RTN1), transcript variant 3, mRNA. /// NM_206857 // upstream // 13144 // Hs.368626 // RTN1 // 6252 // Homo sapiens reticulon 1 (RTN1), transcript variant 2, mRNA. //	RTN1	RTN1, Homo sapiens reticulon 1 (RTN1), transcript variant 3, q23.1
SNP_A-2136871	atcagaccttactccat[C/T]ccagaatggccattat	C	T	NM_005982 // upstream // 47850 // Hs.54416 // SIX1 // 6495 // Homo sapiens sine oculis homeobox homolog 1 (Drosophila) (SIX1), mRNA. /// NM_017420 // downstream // 16095 // Hs.279004 // SIX4 // 51804 // Homo sapiens sine oculis homeobox homolog 4 (Drosoph	SIX1	SIX1, Homo sapiens sine oculis homeobox homolog 1 (Drosophila) (SIX1), q23.1
SNP_A-1663180	agcgttgctgacaaagtctctaat[G/T]atctcaggaccagtcag ggtaattt	G	T	NM_003082 // downstream // 141128 // Hs.179312 // SNAPC1 // 6617 // small nuclear RNA activating complex, polypeptide 1, 43kDa /// NM_031914 // upstream // 58465 // Hs.404139 // SYT14L // 83851 // synaptotagmin XIV-like	SNAPC1	SNAPC1, rs217690, small nuclear RNA activating complex, polypeptide 1, 43kDa, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1811546	gtgctctgaaatttta[G/T]gagtgttcatattagc	G	T	NM_002431 // intron // 0 // Hs.509523 // MNAT1 // 4331 // Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), mRNA. /// ENST00000261245 // intron // 0 // — // — // — // —	MNAT1	MNAT1, Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), q23.1
SNP_A-1734684	ctctcatgttaatgagaaaggatcg[C/T]atcatgtagctatattatta taatg	C	T	NM_139318 // downstream // 531536 // Hs.27043 // KCNH5 // 27133 // potassium voltage-gated channel, subfamily H (eag-related), member 5 /// NM_172375 // downstream // 531536 // Hs.27043 // KCNH5 // 27133 // potassium voltage-gated channel, subfamily H (e	KCNH5	KCNH5 , rs1467163, potassium voltage-gated channel, subfamily H (eag-related), member 5 ,q23.2
SNP_A-2288081	gattcacactgaatta[C/T]agcattggatgtgtag	C	T	NM_006255 // intron // 0 // Hs.333907 // PRKCH // 5583 // Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// ENST00000332981 // intron // 0 // — // — // — // —	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-2223795	cctactcctgtcatg[C/T]atggatctgttgtat	C	T	NM_006255 // intron // 0 // Hs.333907 // PRKCH // 5583 // Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// ENST00000332981 // intron // 0 // — // — // — // —	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-1957981	tttttcacaatatttg[A/G]aattgcaagtgattga	A	G	NM_006255 // intron // 0 // Hs.333907 // PRKCH // 5583 // Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// ENST00000332981 // intron // 0 // — // — // — // —	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-2223910	gaggccagaggaggat[A/G]aataccatgaaacaga	A	G	NM_006255 // intron // 0 // Hs.333907 // PRKCH // 5583 // Homo sapiens protein kinase C, eta (PRKCH), mRNA. /// ENST00000332981 // intron // 0 // — // — // — // —	PRKCH	PRKCH, Homo sapiens protein kinase C, eta (PRKCH), q23.1
SNP_A-1661622	aatttaaaaaccagaaatcaggctat[C/T]ggttccagctacacatt tattggta	C	T	NM_139318 // intron // 0 // Hs.27043 // KCNH5 // 27133 // potassium voltage-gated channel, subfamily H (eag-related), member 5 /// NM_172375 // intron // 0 // Hs.27043 // KCNH5 // 27133 // potassium voltage-gated channel, subfamily H (eag-related), membe	KCNH5	KCNH5 , rs21011551, potassium voltage-gated channel, subfamily H (eag-related), member 5 ,q23.2
SNP_A-2032205	aaagtgtagggagtgat[A/G]caaatcttaaaacag	A	G	NM_003082 // downstream // 44235 // Hs.179312 // SNAPC1 // 6617 // Homo sapiens small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), mRNA. /// NM_031914 // upstream // 155161 // Hs.404139 // SYT14L // 83851 // Homo sapiens synaptotagmin XI	SNAPC1	SNAPC1, Homo sapiens small nuclear RNA activating complex, polypeptide 1, 43kDa (SNAPC1), q23.2
SNP_A-2135251	atattgtataatgcaa[C/T]gtgtaaatttgtaaa	C	T	NM_031914 // intron // 0 // Hs.404139 // SYT14L // 83851 // Homo sapiens synaptotagmin XIV-like (SYT14L), mRNA. /// ENST00000267487 // intron // 0 // — // — // — // — /// ENST00000358254 // intron // 0 // — // — // — // —	SYT14L	SYT14L, Homo sapiens synaptotagmin XIV-like (SYT14L), q23.2
SNP_A-2290330	gcaacagcattactaa[A/G]gttgtttgtggtggct	A	G	NM_172375 // downstream // 539367 // Hs.27043 // KCNH5 // 27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 539367 // Hs.527656 // KCNH1 // 3756 /	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2034896	aaatgaggaccctgag[A/G]aattgagtgtttaccc	A	G	NM_172375 // downstream // 526481 // Hs.27043 // KCNH5 // 27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // downstream // 526481 // Hs.527656 // KCNH1 // 3756 /	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-1658254	tattaaagatattccagtggaaaaa[C/T]ggcgaagctccaacc tgtggtgac	C	T	NM_030791 // downstream // 46521 // Hs.24678 // SGPP1 // 81537 // sphingosine-1-phosphate phosphatase 1 /// NM_080666 // upstream // 38710 // Hs.497301 // LOC112840 // 112840 // similar to RIKEN cDNA 2600001A11 gene	SGPP1	SGPP1, rs10498509, sphingosine-1-phosphate phosphatase 1 ,q23.2
SNP_A-2230519	ctatccgagtttcac[A/G]gagtccaggagaaagt	A	G	NM_172375 // intron // 0 // Hs.27043 // KCNH5 // 27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 // 3756 // Homo sapiens pot	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2129241	ataattttcagagccc[A/G]atgcaagattaaaaag	A	G	NM_172375 // intron // 0 // Hs.27043 // KCNH5 // 27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 // 3756 // Homo sapiens pot	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-1863705	tccaacttgtctaaaa[C/T]tgcaagaataagcttt	C	T	NM_172375 // intron // 0 // Hs.27043 // KCNH5 // 27133 // Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, mRNA. /// NM_002238 // intron // 0 // Hs.527656 // KCNH1 // 3756 // Homo sapiens pot	KCNH5	KCNH5, Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 5 (KCNH5), transcript variant 3, q23.2
SNP_A-2070710	acacggtatggtggaa[A/G]tagttctaaaataacc	A	G	NM_020663 // intron // 0 // Hs.525389 // RHOJ // 57381 // Homo sapiens ras homolog gene family, member J (RHOJ), mRNA. /// ENST00000316754 // intron // 0 // — // — // — // —	RHOJ	RHOJ, Homo sapiens ras homolog gene family, member J (RHOJ), q23.2
SNP_A-2023473	aaaactaacagcttga[A/G]tacagtttgtcacact	A	G	NM_006246 // intron // 0 // Hs.334868 // PPP2R5E // 5529 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /// ENST00000337537 // intron // 0 // — // — // — // —	PPP2R5E	PPP2R5E, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), q23.2
SNP_A-2061625	aatgctttcctctcta[A/G]accacgcggctcactt	A	G	NM_006246 // intron // 0 // Hs.334868 // PPP2R5E // 5529 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /// ENST00000337537 // intron // 0 // — // — // — // —	PPP2R5E	PPP2R5E, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), q23.2
SNP_A-2296791	gccaaccactattcag[A/G]cagtttacccacaatg	A	G	NM_006246 // intron // 0 // Hs.334868 // PPP2R5E // 5529 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /// ENST00000337537 // intron // 0 // — // — // — // —	PPP2R5E	PPP2R5E, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), q23.2
SNP_A-2090945	actttctaagacatac[A/G]agaggagttgaaatta	A	G	NM_006246 // upstream // 19702 // Hs.334868 // PPP2R5E // 5529 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /// NM_080666 // downstream // 35716 // Hs.497301 // C14orf150 // 112840 // Homo sapiens chr	PPP2R5E	PPP2R5E, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), q23.2
SNP_A-2293899	gcagcttgctataaaa[C/G]tatgcaaaagattaag	C	G	NM_006246 // upstream // 28648 // Hs.334868 // PPP2R5E // 5529 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /// NM_080666 // downstream // 26770 // Hs.497301 // C14orf150 // 112840 // Homo sapiens chr	PPP2R5E	PPP2R5E, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), q23.2
SNP_A-2178554	cactctacatactcta[C/T]ggaatggccactcttc	C	T	NM_015180 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat contain	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2
SNP_A-2025286	aaaatatgtaaaacaa[C/T]gtgaaatgcctatgga	C	T	NM_015180 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat contain	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2
SNP_A-2216783	cctctctttcttctta[C/G]agccttcctggatctt	C	G	NM_015180 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat contain	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2
SNP_A-1911163	tgtctgcaaaacttta[C/T]cttgtgttccacttca	C	T	NM_015180 // CDS // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // CDS // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, n	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2179442	cacttaaaaattttcc[C/T]aagtagcactgtttct	C	T	NM_015180 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat contain	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2
SNP_A-2156387	attctcatctggtcta[A/T]attgacttctaaaagg	A	T	NM_015180 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat contain	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2
SNP_A-1829991	taatacaagcagcagc[A/C]agaatttcaagtgcat	A	C	NM_015180 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, mRNA. /// NM_182912 // intron // 0 // Hs.525392 // SYNE2 // 23224 // Homo sapiens spectrin repeat contain	SYNE2	SYNE2, Homo sapiens spectrin repeat containing, nuclear envelope 2 (SYNE2), transcript variant 1, q23.2
SNP_A-1820813	gtttccgtttggatct[C/T]aatgtgaacacagctg	C	T	NM_172365 // downstream // 65194 // Hs.144696 // C14orf50 // 145376 // Homo sapiens chromosome 14 open reading frame 50 (C14orf50), mRNA. /// ENST00000298705 // downstream // 65194 // — // — // — // — /// ENST00000356612 // upstream // 49864 // –	C14orf50	C14orf50, Homo sapiens chromosome 14 open reading frame 50 (C14orf50), q23.3
SNP_A-2256790	ctttccaacaaaccca[G/T]gaaggaggtactatta	G	T	NM_000347 // intron // 0 // Hs.417303 // SPTB // 6710 // Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type I) (SPTB), mRNA. /// ENST00000284159 // intron // 0 // — // — // — // — /// ENST00000335612 // intron // 0 //	SPTB	SPTB, Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type I) (SPTB), q23.3
SNP_A-2003798	gcgacatctgagaaga[G/T]atctgaggaatgagaa	G	T	NM_000347 // intron // 0 // Hs.417303 // SPTB // 6710 // Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type I) (SPTB), mRNA. /// ENST00000335612 // intron // 0 // — // — // — // —	SPTB	SPTB, Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type I) (SPTB), q23.3
SNP_A-2091173	actttgtcatttcaca[C/T]tatacacaaacattaa	C	T	NM_178156 // upstream // 164421 // Hs.118722 // FUT8 // 2530 // Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 3, mRNA. /// NM_178154 // upstream // 164421 // Hs.118722 // FUT8 // 2530 // Homo sapiens fucosyl	FUT8	FUT8, Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 3, q23.3
SNP_A-2045694	aagacaataggcaaac[A/C]actgtgtggaagcagg	A	C	NM_178156 // upstream // 152093 // Hs.118722 // FUT8 // 2530 // Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 3, mRNA. /// NM_178154 // upstream // 152093 // Hs.118722 // FUT8 // 2530 // Homo sapiens fucosyl	FUT8	FUT8, Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 3, q23.3
SNP_A-2063831	aattagggatctaggc[C/T]acctctatcttatagt	C	T	ENST00000344386 // intron // 0 // — // — // — // —	-	q23.3
SNP_A-1793527	ggtataacacagcaga[A/G]cccaattctaaaacct	A	G	NM_178156 // intron // 0 // Hs.118722 // FUT8 // 2530 // Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 3, mRNA. /// NM_178154 // intron // 0 // Hs.118722 // FUT8 // 2530 // Homo sapiens fucosyltransferase 8	FUT8	FUT8, Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), transcript variant 3, q23.3
SNP_A-1917076	tgtttggataacctca[C/G]tcaataaatatcgtca	C	G	ENST00000340589 // upstream // 71323 // — // — // — // — /// ENST00000310149 // downstream // 60449 // — // — // — // —	-	q23.3
SNP_A-2169051	caagagtgatgaacag[A/G]aaagtgctaaagccag	A	G	ENST00000340589 // upstream // 80862 // — // — // — // — /// ENST00000310149 // downstream // 50910 // — // — // — // —	-	q23.3
SNP_A-1932185	ttcctccacatatatc[C/T]gaacctcattttattt	C	T	ENST00000340589 // upstream // 84785 // — // — // — // — /// ENST00000310149 // downstream // 46987 // — // — // — // —	-	q23.3
SNP_A-2169500	caagccttgtgaaaac[A/C]cactgttcctacccat	A	C	ENST00000340589 // upstream // 85195 // — // — // — // — /// ENST00000310149 // downstream // 46577 // — // — // — // —	-	q23.3
SNP_A-2071055	acactgatgtagcaat[G/T]aagcaaaacagtaaag	G	T	ENST00000340589 // upstream // 105398 // — // — // — // — /// ENST00000310149 // downstream // 26374 // — // — // — // —	-	q23.3
SNP_A-2183853	cagccaaacctaaatg[C/T]aaaccatgctgccaac	C	T	ENST00000340589 // upstream // 120985 // — // — // — // — /// ENST00000310149 // downstream // 10787 // — // — // — // —	-	q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1878008	tctgtaaggtttgttd[A/G]cacaatgtccttctg	A	G	ENST00000340589 // upstream // 121524 // --- // --- // --- /// ENST00000310149 // downstream // 10248 // --- // --- // ---	-	q23.3
SNP_A-2021857	aaaaactaaaaaaacac[A/G]gtcagacaataggcaa	A	G	AF272663 // intron // 0 // Hs.208765 // GPHN // 10243 // Homo sapiens gephyrin mRNA, complete cds. /// NM_020806 // intron // 0 // Hs.208765 // GPHN // 10243 // Homo sapiens gephyrin (GPHN), mRNA. /// ENST00000315266 // intron // 0 // --- // --- //	GPHN	GPHN, Homo sapiens gephyrin complete cds. q23.3
SNP_A-1961289	ttttttccatttttgt[A/G]aaacctcagagacatc	A	G	AF272663 // intron // 0 // Hs.208765 // GPHN // 10243 // Homo sapiens gephyrin mRNA, complete cds. /// NM_020806 // intron // 0 // Hs.208765 // GPHN // 10243 // Homo sapiens gephyrin (GPHN), mRNA. /// ENST00000315266 // intron // 0 // --- // --- //	GPHN	GPHN, Homo sapiens gephyrin complete cds. q23.3
SNP_A-2104601	agcaggttcagttcac[A/G]atgatttttcaaattca	A	G	AF272663 // intron // 0 // Hs.208765 // GPHN // 10243 // Homo sapiens gephyrin mRNA, complete cds. /// NM_020806 // intron // 0 // Hs.208765 // GPHN // 10243 // Homo sapiens gephyrin (GPHN), mRNA. /// ENST00000315266 // intron // 0 // --- // --- //	GPHN	GPHN, Homo sapiens gephyrin complete cds. q23.3
SNP_A-1796085	ggtgtaagtgcaaagc[G/T]aagatttgaatttctaa	G	T	NM_004094 // intron // 0 // Hs.151777 // EIF2S1 // 1965 // Homo sapiens eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1), mRNA. /// ENST00000256383 // intron // 0 // --- // --- // ---	EIF2S1	EIF2S1, Homo sapiens eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1), q23.3
SNP_A-2258032	cttgtgtttacatac[A/G]atcctaggtgcccc	A	G	NM_016445 // upstream // 18810 // Hs.170473 // PLEK2 // 26499 // Homo sapiens pleckstrin 2 (PLEK2), mRNA. /// NM_182526 // downstream // 42466 // Hs.509707 // FLJ33387 // 161145 // Homo sapiens hypothetical protein FLJ33387 (FLJ33387), mRNA. /// ENST00000	PLEK2	PLEK2, Homo sapiens pleckstrin 2 (PLEK2), q23.3
SNP_A-2209865	ccccaacaacctggca[A/G]agagtccctattctc	A	G	NM_016445 // upstream // 18839 // Hs.170473 // PLEK2 // 26499 // Homo sapiens pleckstrin 2 (PLEK2), mRNA. /// NM_182526 // downstream // 42437 // Hs.509707 // FLJ33387 // 161145 // Homo sapiens hypothetical protein FLJ33387 (FLJ33387), mRNA. /// ENST00000	PLEK2	PLEK2, Homo sapiens pleckstrin 2 (PLEK2), q23.3
SNP_A-1794783	ggtctggaaatatacaa[A/G]ctctcccagctctcat	A	G	NM_016445 // upstream // 33931 // Hs.170473 // PLEK2 // 26499 // Homo sapiens pleckstrin 2 (PLEK2), mRNA. /// NM_182526 // downstream // 27345 // Hs.509707 // FLJ33387 // 161145 // Homo sapiens hypothetical protein FLJ33387 (FLJ33387), mRNA. /// ENST00000	PLEK2	PLEK2, Homo sapiens pleckstrin 2 (PLEK2), q23.3
SNP_A-1692920	catagcacgtccataacacaaatag[A/C]cctcaggaggaatcg tgacatccag	A	C	BX248061 // intron // 0 // Hs.509754 // RAD51L1 // 5890 // RAD51-like 1 (S. cerevisiae)	RAD51L1	RAD51L1, rs761951, RAD51-like 1 (S. cerevisiae),q24.1
SNP_A-1792986	ggtacatttttaggatg[A/G]acagaaaatgctgact	A	G	ENST00000329153 // intron // 0 // --- // --- // ---	-	q24.1
SNP_A-2103643	agcacagaatgaatccc[A/G]atgctctgaaaatgtgc	A	G	NM_133510 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-2033085	aaatacagcaccacaa[A/C]gttgtttaagccctg	A	C	NM_133510 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-2227900	actgttcatcagcttc[A/G]agtaacaaacataccа	A	G	NM_133510 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2243363	ctgcgaattcctgtca[C/T]aaatggagttttcctc	C	T	NM_133510 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-2227964	aatgctggtttcttta[G/T]gccctaatagctgctg	G	T	NM_133510 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-2034555	aaatcttactcttccc[G/T]atgacttggctgagtg	G	T	NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// NM_133509 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-2228125	atgataatgctaatac[A/G]agaatctccttgaaga	A	G	NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// NM_133509 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-2270716	gacagctggaacattc[A/G]cagtgctgtttcctta	A	G	NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// ENST00000342389 // intron // 0 // --- // --- // --- // ---	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-1863335	tcattttcatgtcggc[C/T]atagtttccatgccta	C	T	NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// ENST00000342389 // intron // 0 // --- // --- // --- // ---	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-1854037	tcaaacactacaacat[C/T]agatcccagcttcccc	C	T	NM_002877 // intron // 0 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, mRNA. /// ENST00000342389 // intron // 0 // --- // --- // --- // ---	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 1, q24.1
SNP_A-2048033	aagcaagtgagggtca[A/G]acttaggttgtgtgag	A	G	NM_133510 // downstream // 211719 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // downstream // 211719 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. ce	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-2307178	gcttaacttttaagga[A/G]gtaccaaaatgttttc	A	G	NM_133510 // downstream // 242073 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA. /// NM_002877 // downstream // 242073 // Hs.172587 // RAD51L1 // 5890 // Homo sapiens RAD51-like 1 (S. ce	RAD51L1	RAD51L1, Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, q24.1
SNP_A-1679150	aaaggtttatttataaattaggcac[A/G]gtatagatgaacaataataactaat	A	G	NM_022137 // intron // 0 // Hs.14144 // SMOC1 // 64093 // SPARC related modular calcium binding 1	SMOC1	SMOC1 , rs227438, SPARC related modular calcium binding 1,q24.2
SNP_A-1943500	ttgtaaagaggagaca[A/C]tattttcatcattgaa	A	C	NM_001102 // intron // 0 // Hs.509765 // ACTN1 // 87 // Homo sapiens actinin, alpha 1 (ACTN1), mRNA. /// ENST00000193403 // intron // 0 // --- // --- // --- // ---	ACTN1	ACTN1, Homo sapiens actinin, alpha 1 (ACTN1), q24.1
SNP_A-2086558	actgaaagtagcaaac[C/T]ggatgcccgcagggga	C	T	AB032956 // intron // 0 // Hs.21035 // GALNTL1 // 57452 // Homo sapiens mRNA for KIAA1130 protein, partial cds. /// ENST00000360173 // intron // 0 // --- // --- // --- // --- /// ENST00000337827 // intron // 0 // --- // --- // --- // ---	GALNTL1	GALNTL1, Homo sapiens for KIAA1130 protein, partial cds. q24.1
SNP_A-2132179	ataggtgttatgtaca[A/G]ataaaacgggacaacg	A	G	AB032956 // downstream // 11540 // Hs.21035 // GALNTL1 // 57452 // Homo sapiens mRNA for KIAA1130 protein, partial cds. /// NM_004450 // downstream // 14130 // Hs.509791 // ERH // 2079 // Homo sapiens enhancer of rudimentary homolog (Drosophila) (ERH), mR	GALNTL1	GALNTL1, Homo sapiens for KIAA1130 protein, partial cds. ,q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1782127	ggcaactcctccaacc[A/G]caggtttccacattat	A	G	AB032956 // downstream // 21099 // Hs.21035 // GALNTL1 // 57452 // Homo sapiens mRNA for KIAA1130 protein, partial cds. /// NM_004450 // downstream // 4571 // Hs.509791 // ERH // 2079 // Homo sapiens enhancer of rudimentary homolog (Drosophila) (ERH), mRN	GALNTL1	GALNTL1, Homo sapiens for KIAA1130 protein, partial cds. ,q24.1
SNP_A-2310278	ggaaccatatctaaga[A/C]gtgctgcagaagctgt	A	C	NM_018375 // downstream // 20089 // Hs.432690 // SLC39A9 // 55334 // Homo sapiens solute carrier family 39 (zinc transporter), member 9 (SLC39A9), mRNA. /// NM_018375 // downstream // 21919 // Hs.432690 // SLC39A9 // 55334 // Homo sapiens solute carrier f	SLC39A9	SLC39A9, Homo sapiens solute carrier family 39 (zinc transporter), member 9 (SLC39A9), q24.1
SNP_A-1646172	cttaggcggttagggtgtgatctta[C/T]gaaaagaattggcaggc cttctgag	C	T	D86980 // intron // 0 // Hs.79170 // TTC9 // 23508 // tetratricopeptide repeat domain 9	TTC9	TTC9 , rs1205238, tetratricopeptide repeat domain 9,q24.2
SNP_A-2221018	ccttgggtttaaatta[C/T]gcaagtcctgactagc	C	T	NM_014734 // intron // 0 // Hs.440025 // KIAA0247 // 9766 // Homo sapiens KIAA0247 (KIAA0247), mRNA. /// ENST00000342745 // intron // 0 // — // — // — // —	KIAA0247	KIAA0247, Homo sapiens KIAA0247 (KIAA0247), q24.1
SNP_A-1678830	tatagattcattaaagggtcttaaa[A/C]taggagctaggctgtgct gcaggct	A	C	NM_014982 // upstream // 79121 // Hs.55947 // PCNX // 22990 // pecanex homolog (Drosophila)	PCNX	PCNX , rs7144786, pecanex homolog (Drosophila),q24.2
SNP_A-1876268	tctgagaggttaaaga[G/T]tagccagctcaaagat	G	T	NM_182936 // intron // 0 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // intron // 0 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute c	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-2298785	gcccatatttctggtg[C/G]ataatttctagagatc	C	G	NM_182936 // intron // 0 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // intron // 0 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute c	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-1848886	tatgatttctggcccc[A/T]cgatggtcatagtcta	A	T	NM_182936 // intron // 0 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // intron // 0 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute c	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-2219952	ccttatcatctcagtc[C/T]gaaactccttaagctg	C	T	NM_182936 // upstream // 27402 // Hs.337696 // SLC8A3 // 6547 // Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, mRNA. /// NM_058240 // upstream // 27402 // Hs.337696 // SLC8A3 // 6547 // Homo sapi	SLC8A3	SLC8A3, Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant f, q24.2
SNP_A-1961053	tttttgtactccctcc[A/G]aagtatgcaacatact	A	G	D86980 // intron // 0 // Hs.79170 // TTC9 // 23508 // Human mRNA for KIAA0227 gene, partial cds. /// ENST00000256367 // intron // 0 // — // — // — // —	TTC9	TTC9, Human for KIAA0227 gene, partial cds. ,q24.2
SNP_A-2229802	tttggagaaatgtcca[C/G]tcaatcctttgcccat	C	G	NM_033141 // intron // 0 // Hs.437214 // MAP3K9 // 4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// ENST00000005198 // intron // 0 // — // — // — // —	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2292003	gcacattatgaggaag[C/G]ctggtgctttgggttg	C	G	NM_033141 // intron // 0 // Hs.437214 // MAP3K9 // 4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// ENST00000005198 // intron // 0 // — // — // — // —	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2146713	atgcttacacttattc[C/G]aatgtacatttaatta	C	G	NM_033141 // upstream // 22536 // Hs.437214 // MAP3K9 // 4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 // upstream // 75108 // Hs.158722 // PCNX // 22990 // Homo sapiens pecanex homolog (Drosophila) (P	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944375	ttgtctaagtttagcc[C/T]gaggccccctaacag	C	T	NM_033141 // upstream // 22735 // Hs.437214 // MAP3K9 // 4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 // upstream // 74909 // Hs.158722 // PCNX // 22990 // Homo sapiens pecanex homolog (Drosophila) (P	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2137991	atcatttttttgtata[C/T]gttggaagcgctcgtg	C	T	NM_033141 // upstream // 24121 // Hs.437214 // MAP3K9 // 4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 // upstream // 73523 // Hs.158722 // PCNX // 22990 // Homo sapiens pecanex homolog (Drosophila) (P	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-2063685	aattactgtatgttaa[A/G]gtaggagcttacgcct	A	G	NM_033141 // upstream // 24854 // Hs.437214 // MAP3K9 // 4293 // Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), mRNA. /// NM_014982 // upstream // 72790 // Hs.158722 // PCNX // 22990 // Homo sapiens pecanex homolog (Drosophila) (P	MAP3K9	MAP3K9, Homo sapiens mitogen-activated protein kinase kinase kinase 9 (MAP3K9), q24.2
SNP_A-1751285	aaaaaaaaggttaatgggactcag[C/T]aattagtgaaacatac agaataaata	C	T	NM_004296 // intron // 0 // Hs.435678 // RGS6 // 9628 // regulator of G-protein signalling 6	RGS6	RGS6 , rs728497, regulator of G-protein signalling 6,q24.2
SNP_A-2125104	agttggaagttgaccc[A/T]acatgagctatggcac	A	T	NM_014982 // downstream // 69600 // Hs.158722 // PCNX // 22990 // Homo sapiens pecanex homolog (Drosophila) (PCNX), mRNA. /// ENST00000304743 // downstream // 69600 // — // — // — /// ENST00000238570 // downstream // 69600 // — // — // –	PCNX	PCNX, Homo sapiens pecanex homolog (Drosophila) (PCNX), q24.2
SNP_A-1782598	ggcaccttccgcatga[C/T]gttttaatttgatgtt	C	T	NM_014982 // downstream // 92496 // Hs.158722 // PCNX // 22990 // Homo sapiens pecanex homolog (Drosophila) (PCNX), mRNA. /// ENST00000304743 // downstream // 92496 // — // — // — /// ENST00000238570 // downstream // 92496 // — // — // –	PCNX	PCNX, Homo sapiens pecanex homolog (Drosophila) (PCNX), q24.2
SNP_A-2264240	gaacttaacaagcttc[C/T]ccaacaaaggaaaatg	C	T	NM_015556 // downstream // 130151 // Hs.208846 // SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 95240 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein sig	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2
SNP_A-2229524	ctagggtggtctgaga[C/T]ggctttaactataagg	C	T	NM_015556 // downstream // 205737 // Hs.208846 // SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 19654 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein sig	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2
SNP_A-2235755	ctcctcctgccagaaa[C/G]gttttaaggacctca	C	G	NM_015556 // downstream // 207427 // Hs.208846 // SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 17964 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein sig	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2
SNP_A-2063058	aatgttcaatgacaga[C/T]agagtgtccgtttcag	C	T	NM_015556 // downstream // 219701 // Hs.208846 // SIPA1L1 // 26037 // Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), mRNA. /// NM_004296 // upstream // 5690 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein sign	SIPA1L1	SIPA1L1, Homo sapiens signal-induced proliferation-associated 1 like 1 (SIPA1L1), q24.2
SNP_A-1912815	tgtgctggagaactca[C/T]ggaatctgcacttgga	C	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2230560	gctttggcagtgtca[C/T]agagtttaaaggacaa	C	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2230561	ggtcatggcctcacaa[A/G]ctcttactgtcttggt	A	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2135862	atcaacaaagctctca[C/G]gataaggatggtgttg	C	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2251009	cttatgttttcacag[A/G]cctttacaaatataa	A	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2140208	atctatgtgtataaac[C/T]atggccacatttctg	C	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2028189	aaactacttcaccat[C/G]atacttctgatttctc	C	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2146331	atgctatccaaaggact[C/T]cttcaaatgaaataga	C	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2240827	ctgagaaattcacata[A/C]aaattggtcctggact	A	C	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1904293	tgggctctggagaaat[A/G]tggctccatcagcaga	A	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2264435	gaagaaactgaaccac[A/G]cctacatcttgtcta	A	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1941698	ttggaagtggtgtcct[C/T]aatggagaggcggatc	C	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2231124	atcaaaaactccagaa[G/T]aaattctcatgcagtt	G	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2309494	ggaaacagtaaaatta[C/G]atgggcatacatattt	C	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2053991	aagttacataaataaaa[C/G]tcagaggctttgtaaa	C	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1793092	ggtactggtcggaaggt[C/G]aaatttattgtattag	C	G	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-1815100	gtgttcctctatagca[G/T]gtctgacgcctcttg	G	T	NM_004296 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA. /// AF156932 // intron // 0 // Hs.509872 // RGS6 // 9628 // Homo sapiens G protein signaling 6 regulator (RGS6) mRNA, complete cds. ///	RGS6	RGS6, Homo sapiens regulator of G-protein signalling 6 (RGS6), q24.2
SNP_A-2281465	gagtcataacagacca[C/G]agcagagagtcttcct	C	G	NM_152331 // downstream // 25766 // Hs.49433 // PTE2B // 122970 // Homo sapiens peroxisomal acyl-CoA thioesterase 2B (PTE2B), mRNA. /// NM_031427 // upstream // 23468 // Hs.525445 // C14orf168 // 83544 // Homo sapiens chromosome 14 open reading frame 168	PTE2B	PTE2B, Homo sapiens peroxisomal acyl-CoA thioesterase 2B (PTE2B), q24.3
SNP_A-2174759	cacagctagtaggaaaa[A/T]atggaaataagctctc	A	T	NM_152444 // intron // 0 // Hs.98365 // ZADH1 // 145482 // Homo sapiens zinc binding alcohol dehydrogenase, domain containing 1 (ZADH1). mRNA. /// ENST00000267568 // intron // 0 // — // — // — // —	ZADH1	ZADH1, Homo sapiens zinc binding alcohol dehydrogenase, domain containing 1 (ZADH1), q24.3
SNP_A-1758029	atgaaccagcaaaagagactgtgaa[A/G]gaacagctagaga aataggaagaaa	A	G	NM_014381 // intron // 0 // Hs.279843 // MLH3 // 27030 // mutL homolog 3 (E. coli)	MLH3	MLH3 , rs175072, mutL homolog 3 (E. coli),q24.3
SNP_A-2232156	ttcaatccaaatcccat[A/G]gtaactgtaaaataca	A	G	NM_001249 // CDS // 0 // Hs.131555 // ENTPD5 // 957 // Homo sapiens ectonucleoside triphosphate diphosphohydrolase 5 (ENTPD5), mRNA. /// ENST00000334696 // CDS // 0 // — // — // —	ENTPD5	ENTPD5, Homo sapiens ectonucleoside triphosphate diphosphohydrolase 5 (ENTPD5), q24.3
SNP_A-1667044	cgtgctgcagctggccagaataacd[A/T]atctcattcaaggcat cacgacgtt	A	T	NM_001107 // intron // 0 // Hs.18573 // ACYP1 // 97 // acylphosphatase 1, erythrocyte (common) type /// NM_033116 // CDS // 0 // Hs.7200 // NEK9 // 91754 // NIMA (never in mitosis gene a)- related kinase 9	ACYP1	ACYP1 , rs175449, acylphosphatase 1, erythrocyte (common) type ,q24.3
SNP_A-2160067	atttattgaaaccaca[A/G]tgcaaacaattaaaaa	A	G	NM_025057 // downstream // 116336 // Hs.260555 // C14orf45 // 80127 // Homo sapiens chromosome 14 open reading frame 45 (C14orf45). mRNA. /// NM_005589 // upstream // 97933 // Hs.293970 // ALDH6A1 // 4329 // Homo sapiens aldehyde dehydrogenase 6 family, m	C14orf45	C14orf45, Homo sapiens chromosome 14 open reading frame 45 (C14orf45), q24.3
SNP_A-2062875	aatgtggctttcacat[C/T]agttttaaaatttga	C	T	L40400 // intron // 0 // Hs.531111 // YLPM1 // 56252 // Homo sapiens (clone zap113) mRNA, 3' end of cds. /// ENST00000238571 // intron // 0 // — // — // — /// ENST00000325680 // intron // 0 // — // — // — // —	YLPM1	YLPM1, Homo sapiens (clone zap113) 3' end of cds, q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082174	acgaccctgaggcta[C/G]agaacagaataaatag	C	G	L40400 // intron // 0 // Hs.531111 // YLPM1 // 56252 // Homo sapiens (clone zap113) mRNA, 3' end of cds. /// ENST00000238571 // intron // 0 // — // — // — /// ENST00000325680 // intron // 0 // — // — // — /// ENST00000309760	YLPM1	YLPM1, Homo sapiens (clone zap113) 3' end of cds., q24.3
SNP_A-2140046	atctagcagccatttta[C/T]ctgttccaacttact	C	T	// intron // 0 // — // — // —	-	q24.3
SNP_A-2232629	gtaaatctgtggctca[A/G]agagacttcggtattc	A	G	ENST00000238583 // intron // 0 // — // — // — /// ENST00000315338 // intron // 0 // — // — // —	-	q24.3
SNP_A-1840871	tagctccaatcaagta[A/G]cgaatgtctactgggt	A	G	NM_001933 // intron // 0 // Hs.525459 // DLST // 1743 // Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), mRNA. /// ENST00000334220 // intron // 0 // — // — // — /// ENST00000238671 // intr	DLST	DLST, Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), q24.3
SNP_A-2070646	acacgaactgcccca[C/G]tcttatctagtgctg	C	G	NM_001933 // intron // 0 // Hs.525459 // DLST // 1743 // Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), mRNA. /// ENST00000334220 // intron // 0 // — // — // — /// ENST00000238671 // intr	DLST	DLST, Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), q24.3
SNP_A-2232670	gccactgctgtcaaggt[G/T]aaggatgaagcaacag	G	T	NM_031464 // upstream // 2035 // Hs.414481 // RPS6KL1 // 83694 // Homo sapiens ribosomal protein S6 kinase-like 1 (RPS6KL1), mRNA. /// NM_002632 // downstream // 17628 // Hs.252820 // PGF // 5228 // Homo sapiens placental growth factor, vascular endotheli	RPS6KL1	RPS6KL1, Homo sapiens ribosomal protein S6 kinase-like 1 (RPS6KL1), q24.3
SNP_A-2232734	gatgtaaggaagggggc[A/G]aatcatatagtgagtc	A	G	NM_014381 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo sapiens mutL homolog 3 (E. coli) (MLH3), mRNA. /// AF195657 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo sapiens DNA mismatch repair protein (MLH3) mRNA, complete cds. /// ENST00000238	MLH3	MLH3, Homo sapiens mutL homolog 3 (E. coli) (MLH3), q24.3
SNP_A-2232735	agccaactgctggaaa[A/G]aattatcaggaaact	A	G	NM_014381 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo sapiens mutL homolog 3 (E. coli) (MLH3), mRNA. /// AF195657 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo sapiens DNA mismatch repair protein (MLH3) mRNA, complete cds. /// ENST00000238	MLH3	MLH3, Homo sapiens mutL homolog 3 (E. coli) (MLH3), q24.3
SNP_A-1832156	taatttctaaaagggc[A/T]ctgttgcacacttaag	A	T	NM_014381 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo sapiens mutL homolog 3 (E. coli) (MLH3), mRNA. /// AF195657 // intron // 0 // Hs.279843 // MLH3 // 27030 // Homo sapiens DNA mismatch repair protein (MLH3) mRNA, complete cds. /// ENST00000238	MLH3	MLH3, Homo sapiens mutL homolog 3 (E. coli) (MLH3), q24.3
SNP_A-2097492	agagaactggaatgga[A/C]ctgaatttgttgaga	A	C	NM_024643 // 3UTR // 0 // Hs.48642 // C14orf140 // 79696 // Homo sapiens chromosome 14 open reading frame 140 (C14orf140), mRNA. /// ENST00000238686 // 3UTR // 0 // — // — // —	C14orf140	C14orf140, Homo sapiens chromosome 14 open reading frame 140 (C14orf140), q24.3
SNP_A-1850255	tatgttaagaaagaaa[A/C]ctccatttagctgtt	A	C	NM_024643 // downstream // 429 // Hs.48642 // C14orf140 // 79696 // Homo sapiens chromosome 14 open reading frame 140 (C14orf140), mRNA. /// NM_033116 // downstream // 3602 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- relate	C14orf140	C14orf140, Homo sapiens chromosome 14 open reading frame 140 (C14orf140), q24.3
SNP_A-1815928	gttaatgtctgcgaga[A/G]tattatcagttcagat	A	G	NM_024643 // downstream // 894 // Hs.48642 // C14orf140 // 79696 // Homo sapiens chromosome 14 open reading frame 140 (C14orf140), mRNA. /// NM_033116 // downstream // 3137 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- relate	C14orf140	C14orf140, Homo sapiens chromosome 14 open reading frame 140 (C14orf140), q24.3
SNP_A-1951897	tttctacagttgacca[C/T]cagatgaaatattaat	C	T	NM_033116 // intron // 0 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA. /// ENST00000238616 // intron // 0 // — // — // —	NEK9	NEK9, Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1910107	tgtcatcctgagtaa[G/T]atgtgacttcacaatg	G	T	NM_033116 // intron // 0 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA. /// ENST00000238616 // intron // 0 // — // — // —	NEK9	NEK9, Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), q24.3
SNP_A-2077479	accacatgacacctga[C/T]ggatagctttgccttg	C	T	NM_033116 // CDS // 0 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA. /// ENST00000238616 // CDS // 0 // — // — // —	NEK9	NEK9, Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), q24.3
SNP_A-2148970	atggttcacttttca[A/G]gcagtaggaattggaa	A	G	NM_033116 // intron // 0 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA. /// ENST00000238616 // intron // 0 // — // — // —	NEK9	NEK9, Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), q24.3
SNP_A-2209369	cccataagataccaca[A/C]ctcttcaactatcact	A	C	NM_033116 // intron // 0 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA. /// ENST00000238616 // intron // 0 // — // — // —	NEK9	NEK9, Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), q24.3
SNP_A-2302218	gctaaagtgtaagttat[C/T]agttgcaggtgggatg	C	T	NM_033116 // intron // 0 // Hs.7200 // NEK9 // 91754 // Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA. /// ENST00000238616 // intron // 0 // — // — // —	NEK9	NEK9, Homo sapiens NIMA (never in mitosis gene a)- related kinase 9 (NEK9), q24.3
SNP_A-1895046	tgcccagccaggataa[C/T]gaacttaaaaagaaaa	C	T	NM_006827 // intron // 0 // Hs.74137 // TMP21 // 10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// ENST00000303575 // intron // 0 // — // — // —	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2308527	gctttatatcacagta[C/G]aaaaagctaaaaaatc	C	G	NM_006827 // intron // 0 // Hs.74137 // TMP21 // 10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// ENST00000303575 // intron // 0 // — // — // —	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2022306	aaaaagttaatctagc[G/T]aatgctccaagttaca	G	T	NM_006827 // intron // 0 // Hs.74137 // TMP21 // 10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// ENST00000303575 // intron // 0 // — // — // —	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2026513	aaacaaatcaatgccc[A/G]aaccaatctgaattgg	A	G	NM_006827 // intron // 0 // Hs.74137 // TMP21 // 10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// ENST00000303575 // intron // 0 // — // — // —	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-2081607	accttacctaagcaga[C/T]tctcttttgaagctc	C	T	NM_006827 // upstream // 43566 // Hs.74137 // TMP21 // 10972 // Homo sapiens transmembrane trafficking protein (TMP21), mRNA. /// NM_005252 // upstream // 58673 // Hs.25647 // FOS // 2353 // Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolo	TMP21	TMP21, Homo sapiens transmembrane trafficking protein (TMP21), q24.3
SNP_A-1785554	ggctcatatacattta[C/T]gagaggcgtgtgtgtg	C	T	NM_130469 // upstream // 27754 // Hs.196482 // JDP2 // 122953 // Homo sapiens jun dimerization protein 2 (JDP2), mRNA. /// NM_130469 // upstream // 31531 // Hs.196482 // JDP2 // 122953 // Homo sapiens jun dimerization protein 2 (JDP2), mRNA. /// ENST00000	JDP2	JDP2, Homo sapiens jun dimerization protein 2 (JDP2), q24.3
SNP_A-2192591	catccagttccttcaa[A/G]ctatactaacctgtt	A	G	NM_130469 // downstream // 12473 // Hs.196482 // JDP2 // 122953 // Homo sapiens jun dimerization protein 2 (JDP2), mRNA. /// NM_006399 // upstream // 39159 // Hs.509964 // BATF // 10538 // Homo sapiens basic leucine zipper transcription factor, ATF-like (	JDP2	JDP2, Homo sapiens jun dimerization protein 2 (JDP2), q24.3
SNP_A-2108483	agctgcttaggatggc[A/G]aaacagaaacaagcac	A	G	NM_052873 // downstream // 37756 // Hs.532626 // MGC16028 // 112752 // Homo sapiens MGC16028 similar to RIKEN cDNA 1700019E19 gene (MGC16028), mRNA. /// NM_017972 // upstream // 30414 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chromosome 14 open r	MGC16028	MGC16028, Homo sapiens MGC16028 similar to RIKEN cDNA 1700019E19 gene (MGC16028), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2118270	agtaacaacaaggata[A/G]agagtctgaacttccc	A	G	NM_017972 // intron // 0 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // intron // 0 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chromosome 14 open re	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-1855667	tcaataggaagccgaa[A/G]ctgtagcagttgcctt	A	G	NM_017972 // intron // 0 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // intron // 0 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chromosome 14 open re	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-2225238	cgttctgtgggttgca[C/T]ctgtaataagtcagac	C	T	NM_017972 // downstream // 25746 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, mRNA. /// NM_017926 // downstream // 25746 // Hs.410231 // C14orf118 // 55668 // Homo sapiens chrom	C14orf118	C14orf118, Homo sapiens chromosome 14 open reading frame 118 (C14orf118), transcript variant 2, q24.3
SNP_A-1731871	cactaccccatcaaagcaacagtaa[C/T]ggagaatcagaaattttgccactga	C	T	NM_022067 // intron // 0 // Hs.16157 // C14orf133 // 63894 // chromosome 14 open reading frame 133	C14orf133	C14orf133 , rs10483882, chromosome 14 open reading frame 133.q24.3
SNP_A-2243076	ctgcctggaaattac[C/T]ggggacttctggaagt	C	T	NM_004452 // downstream // 52341 // Hs.435845 // ESRRB // 2103 // Homo sapiens estrogen-related receptor beta (ESRRB), mRNA. /// NM_014909 // upstream // 209966 // Hs.525479 // KIAA1036 // 22846 // Homo sapiens KIAA1036 (KIAA1036), mRNA. /// ENST00000002615	ESRRB	ESRRB, Homo sapiens estrogen-related receptor beta (ESRRB), q24.3
SNP_A-1856757	tcacatgatctttaa[A/T]tcactccccggcttct	A	T	NM_004452 // downstream // 154292 // Hs.435845 // ESRRB // 2103 // Homo sapiens estrogen-related receptor beta (ESRRB), mRNA. /// NM_014909 // upstream // 108015 // Hs.525479 // KIAA1036 // 22846 // Homo sapiens KIAA1036 (KIAA1036), mRNA. /// ENST00000000261	ESRRB	ESRRB, Homo sapiens estrogen-related receptor beta (ESRRB), q24.3
SNP_A-1790465	gggcgcagaacactggg[A/G]agccaggtatagagag	A	G	NM_014909 // 3UTR // 0 // Hs.525479 // KIAA1036 // 22846 // Homo sapiens KIAA1036 (KIAA1036), mRNA. /// ENST00000167106 // 3UTR // 0 // — // — // —	KIAA1036	KIAA1036, Homo sapiens KIAA1036 (KIAA1036), q24.3
SNP_A-2301800	gcggcaatgtttcagc[A/C]gagtctggcaagacgg	A	C	NM_194287 // intron // 0 // Hs.147276 // C14orf166B // 145497 // Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), mRNA. /// ENST00000216453 // intron // 0 // — // — // — // — /// ENST00000216450 // intron // 0 // — // — // —	C14orf166B	C14orf166B, Homo sapiens chromosome 14 open reading frame 166B (C14orf166B), q24.3
SNP_A-1722274	ctggactccaattctgattgacagaa[C/T]gaaatggcaaaggtaagaggtagac	C	T	AJ316284 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs880373, neurexin 3.q24.3
SNP_A-2053457	aagtgcaaatcattca[A/G]ccgagattcagggcct	A	G	ENST00000298351 // intron // 0 // — // — // —	-	q24.3
SNP_A-2234125	ttgtttttctgtgttc[A/G]cctgctgtctgcttgt	A	G	NM_013382 // intron // 0 // Hs.132989 // POMT2 // 29954 // Homo sapiens protein-O-mannosyltransferase 2 (POMT2), mRNA. /// ENST00000261534 // intron // 0 // — // — // — // —	POMT2	POMT2, Homo sapiens protein-O-mannosyltransferase 2 (POMT2), q24.3
SNP_A-2272128	gaccggacagcgactct[C/T]acccgctacgcactc	C	T	NM_145871 // intron // 0 // Hs.26403 // GSTZ1 // 2954 // Homo sapiens glutathione transferase zeta 1 (maleylacetoacetate isomerase) (GSTZ1), transcript variant 2, mRNA. /// NM_001513 // intron // 0 // Hs.26403 // GSTZ1 // 2954 // Homo sapiens glutathione	GSTZ1	GSTZ1, Homo sapiens glutathione transferase zeta 1 (maleylacetoacetate isomerase) (GSTZ1), transcript variant 2, q24.3
SNP_A-2025644	aaaatgactgtgaaa[A/G]gaagtcaagccagtag	A	G	NM_213601 // intron // 0 // Hs.200413 // TMED8 // 283578 // Homo sapiens hypothetical protein LOC283578 (LOC283578), mRNA. /// ENST00000216468 // intron // 0 // — // — // —	TMED8	TMED8, Homo sapiens hypothetical protein LOC283578 (LOC283578), q24.3
SNP_A-1833024	tacacacgaatgtg[a/c]ggaacactttaattt	C	G	ENST00000216471 // intron // 0 // — // — // —	-	q24.3
SNP_A-1933068	ttcgggcattggaaa[A/G]agaatcagggtactt	A	G	ENST00000216471 // intron // 0 // — // — // —	-	q24.3
SNP_A-1940995	ttgctcaggatcttag[G/T]atcattacaagtcttc	G	T	NM_138791 // upstream // 3562 // Hs.97556 // C14orf148 // 122945 // Homo sapiens chromosome 14 open reading frame 148 (C14orf148), mRNA. /// NM_022067 // downstream // 57 // Hs.16157 // C14orf133 // 63894 // Homo sapiens chromosome 14 open reading frame 1	C14orf148	C14orf148, Homo sapiens chromosome 14 open reading frame 148 (C14orf148), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829562	taagtgtaggtaatta[A/C]gaggcacagagcctgc	A	C	NM_012111 // downstream // 133 // Hs.204041 // AHSA1 // 10598 // Homo sapiens AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) (AHSA1), mRNA. /// NM_199265 // downstream // 4800 // Hs.29742 // THSD3 // 145501 // Homo sapiens thrombospo	AHSA1	AHSA1, Homo sapiens AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) (AHSA1), q24.3
SNP_A-2235932	ctcctgcagctacagc[G/T]atttccttcgtctgtt	G	T	NM_012111 // downstream // 1162 // Hs.204041 // AHSA1 // 10598 // Homo sapiens AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) (AHSA1), mRNA. /// NM_199265 // downstream // 3771 // Hs.29742 // THSD3 // 145501 // Homo sapiens thrombosp	AHSA1	AHSA1, Homo sapiens AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast) (AHSA1), q24.3
SNP_A-1712993	ctgcagaaagctcaaggggcaaacc[C/T]aatgttagacagag aggggctcctt	C	T	NM_004796 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs10483914, neurexin 3,q24.3
SNP_A-2234458	agggtggagatgcaac[A/G]acattgactagtgatt	A	G	NM_004863 // upstream // 41687 // Hs.435661 // SPTLC2 // 9517 // Homo sapiens serine palmitoyltransferase, long chain base subunit 2 (SPTLC2), mRNA. /// BC025787 // downstream // 14593 // Hs.94542 // ALKBH // 8846 // Homo sapiens alkB, alkylation repair h	SPTLC2	SPTLC2, Homo sapiens serine palmitoyltransferase, long chain base subunit 2 (SPTLC2), q24.3
SNP_A-2234476	cttcctgaaacgtgta[C/G]taaaatgatcagaaaa	C	G	BC025787 // intron // 0 // Hs.94542 // ALKBH // 8846 // Homo sapiens alkB, alkylation repair homolog (E. coli), mRNA (cDNA clone MGC:34444 IMAGE:5229152), complete cds. /// NM_006020 // intron // 0 // Hs.94542 // ALKBH // 8846 // Homo sapiens alkB, alkyla	ALKBH	ALKBH, Homo sapiens alkB, alkylation repair homolog (E. coli), (cDNA clone MGC:34444 IMAGE:5229152), complete cds. ,q24.3
SNP_A-2060261	aatgaagagccacaac[A/C]aactgggcagagaaag	A	C	NM_020421 // downstream // 88250 // Hs.413208 // ADCK1 // 57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 220893 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha,	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-2021281	aaaaaaattcaatccc[A/C]agagcgattagatttg	A	C	NM_020421 // downstream // 95904 // Hs.413208 // ADCK1 // 57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 213239 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha,	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-2094584	agaataccctgcaaaa[C/T]ggtgatacagagcaga	C	T	NM_020421 // downstream // 148020 // Hs.413208 // ADCK1 // 57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 161123 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha,	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-1807237	gtctctcttactccca[A/G]tgctcttctagtacct	A	G	NM_020421 // downstream // 155744 // Hs.413208 // ADCK1 // 57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 153399 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha,	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-2179498	cacttactgtaaggaa[A/C]ggaaacaaaattgaag	A	C	NM_020421 // downstream // 189580 // Hs.413208 // ADCK1 // 57143 // Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA. /// NM_004801 // upstream // 119563 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha,	ADCK1	ADCK1, Homo sapiens aarF domain containing kinase 1 (ADCK1), q24.3
SNP_A-1867872	tcctacctattgcaca[A/G]aacaacggtaaaagga	A	G	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// ENST00000332068 // intron // 0 // — // — // — // — /// ENST00000330071 // intron // 0 // — // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2229864	ctagttcacattgacc[C/T]aaatgccactggagta	C	T	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// ENST00000332068 // intron // 0 // — // — // — // — /// ENST00000330071 // intron // 0 // — // — // — // —	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1732598	aatctctgtcttatgttcactataa[A/G]tgtttaagtcaacataatgctagc	A	G	NM_004796 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3 /// NM_138970 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs10483924, neurexin 3 .q31.1
SNP_A-1664872	ataaaccctagagattaggcaagtg[A/G]aaagaattatgaaataaaacaaagc	A	G	NM_004796 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3 /// NM_138970 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs2216901, neurexin 3 .q31.1
SNP_A-1731937	aaaatacaatctatagaacactata[A/C]taaaagagatatgtaataactcaca	A	C	NM_004796 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3 /// NM_138970 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs221418, neurexin 3 .q31.1
SNP_A-1714633	attttccttgctttggcagttac[A/G]atctatcagtgttatttgtaaaatg	A	G	NM_004796 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3 /// NM_138970 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs7158064, neurexin 3 .q31.1
SNP_A-1720109	gaaaaatacaacaaatttggccaaaa[A/G]caccctgatcactgtggaggaaaca	A	G	NM_004796 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3 /// NM_138970 // intron // 0 // Hs.247837 // NRXN3 // 9369 // neurexin 3	NRXN3	NRXN3 , rs10483933, neurexin 3 .q31.1
SNP_A-2235320	attgtagtccctgccaa[C/T]ccttactccaacacat	C	T	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// E	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q24.3
SNP_A-2048140	aagcacatagcccaaa[A/G]tcaacagctattaaaa	A	G	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// E	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2038907	aacagctactaagtga[C/T]gatgccaaggatttaa	C	T	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-1678854	tgtagcccttcaaataatttatgaj[C/T]gttttgccctatctgtagaattgt	C	T	NM_152446 // intron // 0 // - // - // - // -	-	-, rs17519, -.q31.1
SNP_A-1741661	agtaaattgaattgaatacttgtta[C/T]caagattaagtagtatgatgatgtg	C	T	NM_152446 // intron // 0 // - // - // - // -	-	-, rs8016670, -.q31.1
SNP_A-2235989	ttcaaggaactcagtc[A/G]ataattacaagctaat	A	G	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2256868	ctttcagagaaaaccc[A/G]gatacagggcatgaga	A	G	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2055638	aataatgagttgccta[C/T]taagaaccagggaat	C	T	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2133584	atatcacatggttcta[C/T]gatgacacacagattt	C	T	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1837384	tacttccattgaagga[C/G]agctaagtggaaacta	C	G	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-1906827	tggttattagtgttca[A/G]tgaaagacacaagcaa	A	G	NM_004801 // intron // 0 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // intron // 0 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant alpha, mRNA. /// N	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2266148	gaagggaacttagaga[A/G]catctacaatccacag	A	G	NM_004801 // downstream // 141110 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // downstream // 141110 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2215717	cctcataatttagaaa[A/G]caatcttactctgagt	A	G	NM_004801 // downstream // 359572 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // downstream // 359572 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2251568	cttcagagccatcata[C/T]caatttagttccagca	C	T	NM_004801 // downstream // 528368 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // downstream // 528368 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2236712	gatttttatagcagac[A/G]cttagcccaagtaaga	A	G	NM_004801 // downstream // 620886 // Hs.468505 // NRXN1 // 9378 // Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, mRNA. /// NM_004796 // downstream // 620886 // Hs.368307 // NRXN3 // 9369 // Homo sapiens neurexin 3 (NRXN3), transcript variant	NRXN1	NRXN1, Homo sapiens neurexin 1 (NRXN1), transcript variant alpha, q31.1
SNP_A-2236799	ttaacgctgtcaccga[A/G]gtagaatagatattca	A	G	ENST00000281129 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1917702	ttaaaaatagtatccc[A/G]cccaaagtactgataa	A	G	ENST00000281129 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2301481	gcgaagattacatgag[A/G]aagtctccaaaagcaa	A	G	ENST00000281129 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-1808157	gtcttgtctgtggcaa[C/G]tgttgtgagactgttc	C	G	ENST00000216517 // intron // 0 // — // — // — // — /// ENST00000331280 // intron // 0 // — // — // — // —	-	q31.1
SNP_A-2146624	atgctggtctcattta[C/T]gggctgcctaagaaat	C	T	NM_005065 // upstream // 37661 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 3958694 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmemb	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-1856477	tcacagagaaggaaag[C/T]acactcaatctgtcat	C	T	NM_005065 // upstream // 444142 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 3552213 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmem	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-2279221	gaggacttcccagcca[C/T]gaaaaactaagtcaat	C	T	NM_005065 // upstream // 559439 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 3436916 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmem	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-1725226	cttaatatctttctaaaagcaataa[A/G]ctcatttgcaacagaacttggagaa	A	G	BX248253 // downstream // 2332754 // Hs.497484 // - // - // Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human) /// NM_005065 // upstream // 1658590 // Hs.181300 // SEL1L // 6400 // sel-1 suppressor of lin-12-like (C. elegans	-	- , rs1350280, Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human) ,q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2259426	gaaaaatgccagaaag[C/T]caataatacatgcatg	C	T	NM_005065 // upstream // 706346 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 3290009 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmem	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.1
SNP_A-1658028	ttttcagctgctgatttcaaattca[C/T]gtaatacacgagttacag gtaaat	C	T	BX248253 // downstream // 2077551 // Hs.497484 // - // - // Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human) /// NM_005065 // upstream // 1913793 // Hs.181300 // SEL1L // 6400 // sel-1 suppressor of lin-12-like (C. elegans	-	-, rs229809, Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human), q31.2
SNP_A-2093925	agaagcagtgaggata[C/G]agaagctgcaaattga	C	G	NM_005065 // upstream // 1304345 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2692010 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2166780	caaattgaattaatga[C/T]agaaagtgtagcaaag	C	T	NM_005065 // upstream // 1304370 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2691985 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1824779	taaagatactttctag[A/G]attacacctgtgcttc	A	G	NM_005065 // upstream // 1304539 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2691816 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1749379	aatcaattaggataaactactacac[G/T]aaagaggctgatatttt ctcagcag	G	T	BX248253 // downstream // 1491128 // Hs.497484 // - // - // Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human) /// NM_005065 // upstream // 2500216 // Hs.181300 // SEL1L // 6400 // sel-1 suppressor of lin-12-like (C. elegans	-	-, rs10484124, Human full-length cDNA clone CS0DF017YB20 of Fetal brain of Homo sapiens (human), q31.3
SNP_A-1953570	ttgaatttaaccaat[A/G]agaagcactggtaggg	A	G	NM_005065 // upstream // 1480487 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2515868 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2032813	aaataagcactattga[C/T]acagagcaggttctg	C	T	NM_005065 // upstream // 1524509 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2471846 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2117738	aggttcttatactaat[C/T]aaatgctgaacatata	C	T	NM_005065 // upstream // 1531393 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2464962 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1879023	tcttaactctgaagac[G/T]agctttgaattctgtc	G	T	NM_005065 // upstream // 1541540 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2454815 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1846457	tatattaagcaaatcg[C/T]agtacttcaaaacaaa	C	T	NM_005065 // upstream // 1541634 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2454721 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2192505	catccaaaaacctaga[A/G]gagctggattaattac	A	G	NM_005065 // upstream // 1779045 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2217310 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2045005	aagaactaaatgtaca[A/G]tgaaatttgggactaa	A	G	NM_005065 // upstream // 1790019 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2206336 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2239785	tatgtgagatctgtga[A/G]ctatgtaatgcctttc	A	G	NM_005065 // upstream // 1937041 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 2059314 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-1837322	tacttcaaaattgcta[A/G]gagaagattttaggtg	A	G	NM_005065 // upstream // 2166685 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1829670 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2303300	gctatgtagagaaacta[A/G]gaaaatgaatcaagta	A	G	NM_005065 // upstream // 2184823 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1811532 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.2
SNP_A-2059394	aatctaatcaaagtca[C/T]actggatcggaaaagg	C	T	NM_005065 // upstream // 2405428 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1590927 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2028681	aaactgtccgctgaac[A/C]agggcgcttacatta	A	C	NM_005065 // upstream // 2422258 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1574097 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-1936811	ttctttcatttttcaca[G/T]atttcactgcagaaac	G	T	NM_005065 // upstream // 2465713 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1530642 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2261084	gaaagacaatgaagcat[C/T]gtaggtactcaggatc	C	T	NM_005065 // upstream // 2586519 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1409836 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2093785	agaagagggaagagg[C/G]acaatgccgtggact	C	G	NM_005065 // upstream // 2694356 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1301999 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-2067949	acaactagcaaaatga[A/C]aggagttaagtcctta	A	C	NM_005065 // upstream // 2883310 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 1113045 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transme	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1867488	tccgagccctacttac[A/G]atttgtcgtttactt	A	G	NM_005065 // upstream // 3563627 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 432728 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmem	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-1954771	ttlgctgcggacttaa[A/G]cttacaaggtaattg	A	G	NM_005065 // upstream // 3590939 // Hs.181300 // SEL1L // 6400 // Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA. /// NM_013231 // upstream // 405416 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmem	SEL1L	SEL1L, Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), q31.3
SNP_A-1683166	agatcaagaagtacagtctatactat[C/T]gaaattaaagttactag cacagtat	C	T	BC034577 // upstream // 496286 // Hs.381998 // LOC283585 // 283585 // hypothetical protein LOC283585 /// NM_013231 // downstream // 781576 // Hs.48998 // FLRT2 // 23768 // fibronectin leucine rich transmembrane protein 2	LOC283585	LOC283585 , rs2022641, hypothetical protein LOC283585 ,q31.3
SNP_A-1725692	aagagacttggtacattgaccaca[A/T]ccatatatatatagtca cataatca	A	T	BC034577 // upstream // 449584 // Hs.381998 // LOC283585 // 283585 // hypothetical protein LOC283585 /// NM_013231 // downstream // 828278 // Hs.48998 // FLRT2 // 23768 // fibronectin leucine rich transmembrane protein 2	LOC283585	LOC283585 , rs8023222, hypothetical protein LOC283585 ,q31.3
SNP_A-1737657	taattgcagcagttcaggctagaga[C/T]ggtgatattggtggagg tacaacgt	C	T	BC034577 // upstream // 52003 // Hs.381998 // LOC283585 // 283585 // hypothetical protein LOC283585 /// NM_013231 // downstream // 1225859 // Hs.48998 // FLRT2 // 23768 // fibronectin leucine rich transmembrane protein 2	LOC283585	LOC283585 , rs7159769, hypothetical protein LOC283585 ,q31.3
SNP_A-1731179	ccagtcagtgcaggttattaaactc[A/G]agcaaaagttcactga agcaaagac	A	G	NM_000153 // downstream // 681878 // Hs.408273 // GALC // 2581 // galactosylceramidase (Krabbe disease)	GALC	GALC , rs10498613, galactosylceramidase (Krabbe disease),q31.3
SNP_A-2297942	gccagtgggtatccta[C/T]gagtaaatatccccag	C	T	NM_013231 // downstream // 629506 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 629506 // --- // --- // --- /// ENST00000360002 // upstream // 652	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1878683	tctgttataaaaacca[A/C]cagagtaatcaatatt	A	C	NM_013231 // downstream // 629610 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 629610 // --- // --- // --- /// ENST00000360002 // upstream // 652	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1891555	tgattctgttcctgaa[C/T]tggcattgatacagta	C	T	NM_013231 // downstream // 758384 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 758384 // --- // --- // --- /// ENST00000360002 // upstream // 523	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2242583	gggccatgtctatcaa[C/T]accaacaggttgtgct	C	T	NM_013231 // downstream // 769393 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 769393 // --- // --- // --- /// ENST00000360002 // upstream // 512	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2242587	acactcacacagatccg[G/T]caatcaattggcaaac	G	T	NM_013231 // downstream // 769622 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 769622 // --- // --- // --- /// ENST00000360002 // upstream // 512	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1700638	aaataaaaggcatatataaaatcca[A/G]tgcaaagcacaaaa gccaagaacag	A	G	NM_000153 // downstream // 450487 // Hs.408273 // GALC // 2581 // galactosylceramidase (Krabbe disease)	GALC	GALC , rs10483999, galactosylceramidase (Krabbe disease),q31.3
SNP_A-2046068	aagactaggctgccaa[C/T]agctaggaaaagaagtg	C	T	NM_013231 // downstream // 821483 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 821483 // --- // --- // --- /// ENST00000360002 // upstream // 460	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1754108	ccagaagtaagccatatagccaccc[A/G]caggtttgaggaatt ctagaaaata	A	G	NM_000153 // downstream // 234150 // Hs.408273 // GALC // 2581 // galactosylceramidase (Krabbe disease)	GALC	GALC , rs1959715, galactosylceramidase (Krabbe disease),q31.3
SNP_A-1818233	gttctgcaaatttcac[A/G]cttgccagcaattgag	A	G	NM_013231 // downstream // 1158527 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 1158527 // — // — // — // — /// ENST00000360002 // upstream // 1	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2243020	tgtgtatctgtaatcg[C/T]tgtatcacattgagc	C	T	NM_013231 // downstream // 1208959 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 1208959 // — // — // — // — /// ENST00000360002 // upstream // 7	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-2144836	atgatgttgcataaaca[A/G]atgatttccaaaattt	A	G	NM_013231 // downstream // 1223833 // Hs.533710 // FLRT2 // 23768 // Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA. /// ENST00000330753 // downstream // 1223833 // — // — // — // — /// ENST00000360002 // upstream // 5	FLRT2	FLRT2, Homo sapiens fibronectin leucine rich transmembrane protein 2 (FLRT2), q31.3
SNP_A-1918962	ttaaccctaaaatcagc[A/G]attacaatgtgaatat	A	G	NM_000153 // downstream // 1013738 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 13303 // — // — // — // — /// ENST00000261304 // downstream // 1013738 // —	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2105261	agcattctaggcctgat[C/T]gttataaaggtgtgt	C	T	NM_000153 // downstream // 291937 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 735104 // — // — // — // — /// ENST00000261304 // downstream // 291937 // — /	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-1865084	tccagtggaaatccgat[C/T]ctgggcaatttatgac	C	T	NM_000153 // downstream // 290730 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 736311 // — // — // — // — /// ENST00000261304 // downstream // 290730 // — /	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-1829506	taagtgcctcatttc[G/T]aatcaaattctcccc	G	T	NM_000153 // downstream // 238500 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 788541 // — // — // — // — /// ENST00000261304 // downstream // 238500 // — /	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2243628	tgggacatttcctaac[A/G]cttaaacagctactc	A	G	NM_000153 // downstream // 218502 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 808539 // — // — // — // — /// ENST00000261304 // downstream // 218502 // — /	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-1814876	gtgtgttataatctcc[A/G]ctgtatttctgtctgc	A	G	NM_000153 // downstream // 182330 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 844711 // — // — // — // — /// ENST00000261304 // downstream // 182330 // — /	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3
SNP_A-2069015	acaatgctatgaacca[C/T]aaagctgaagttcaac	C	T	NM_000153 // downstream // 51840 // Hs.513439 // GALC // 2581 // Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA. /// ENST00000360002 // downstream // 975201 // — // — // — // — /// ENST00000261304 // downstream // 51840 // — //	GALC	GALC, Homo sapiens galactosylceramidase (Krabbe disease) (GALC), q31.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2244155	gcttaatgtacccca[A/G]agatgcccacaaaatg	A	G	NM_003608 // downstream // 124311 // Hs.513440 // GPR65 // 8477 // Homo sapiens G protein-coupled receptor 65 (GPR65), mRNA. /// NM_138317 // downstream // 48531 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium channel, subfamily K, member 10 (KC	GPR65	GPR65, Homo sapiens G protein-coupled receptor 65 (GPR65), q31.3
SNP_A-1878778	tctgttgctacacaga[A/G]ctacctgagaatgggt	A	G	NM_138317 // upstream // 15219 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 67433 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium cha	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-1942590	ttggaaccactctta[C/T]gaagcacagtgattat	C	T	NM_138317 // upstream // 19532 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 71746 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium cha	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-2214947	cctatctccattaaaac[A/G]aaacctaaccaaacac	A	G	NM_138317 // upstream // 19604 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 71818 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium cha	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-2039307	aacataaccattcaaa[A/G]ctaacttctggtcct	A	G	NM_138317 // upstream // 28677 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, mRNA. /// NM_138318 // upstream // 80891 // Hs.365690 // KCNK10 // 54207 // Homo sapiens potassium cha	KCNK10	KCNK10, Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript variant 2, q31.3
SNP_A-1651854	ggagttcttcgaagatccatatta[C/T]gaagaggtaaaaagtga aattgtag	C	T	NM_005197 // intron // 0 // Hs.211773 // C14orf116 // 55453 // chromosome 14 open reading frame 116	C14orf116	C14orf116, , rs394499, chromosome 14 open reading frame 116.q32.11
SNP_A-2244524	aaggaagccaggtagg[A/T]gcctcaagtttccatg	A	T	NM_007039 // intron // 0 // Hs.437040 // PTPN21 // 11099 // Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA. /// ENST00000328736 // intron // 0 // — // — // — // —	PTPN21	PTPN21, Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), q31.3
SNP_A-1672070	ttctgtaaattacacatttcaaggag[A/G]ctttatgcaagaatgcat caagac	A	G	NM_018319 // intron // 0 // Hs.131252 // TDP1 // 55775 // tyrosyl-DNA phosphodiesterase 1	TDP1	TDP1, , rs8015271, tyrosyl-DNA phosphodiesterase 1.q32.11
SNP_A-2201222	ccaagtttccttttcac[C/T]ggcatcgaccctggaa	C	T	U68723 // intron // 0 // Hs.434286 // CHES1 // 1112 // Human checkpoint suppressor 1 mRNA, complete cds. /// NM_005197 // intron // 0 // Hs.434286 // CHES1 // 1112 // Homo sapiens checkpoint suppressor 1 (CHES1), mRNA. /// ENST00000354324 // intron // 0 /	CHES1	CHES1, Human checkpoint suppressor 1 complete cds. q32.11
SNP_A-2213243	ccgcgtcactgttca[C/T]attctggaagtgttcg	C	T	U68723 // intron // 0 // Hs.434286 // CHES1 // 1112 // Human checkpoint suppressor 1 mRNA, complete cds. /// NM_005197 // intron // 0 // Hs.434286 // CHES1 // 1112 // Homo sapiens checkpoint suppressor 1 (CHES1), mRNA. /// ENST00000354324 // intron // 0 /	CHES1	CHES1, Human checkpoint suppressor 1 complete cds. q32.11
SNP_A-1723658	ataaaccatccacgccgagaaaccc[A/G]ctgaccgtactatct gcatattaa	A	G	BX248275 // intron // 0 // Hs.400383 // TTC7L1 // 145567 // tetratricopeptide repeat domain 7 like 1	TTC7L1	TTC7L1, , rs1014527, tetratricopeptide repeat domain 7 like 1.q32.11
SNP_A-2075503	acatgatgaaacaaaa[C/T]agcaagcgactcttga	C	T	NM_145231 // downstream // 45026 // Hs.123232 // C14orf143 // 90141 // Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000327820 // upstream // 12207 // — // — // — // — /// ENST00000316738 // downstream // 45026 //	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-2027853	aaacctagagctcaga[C/G]ctgaaaggccaggggt	C	G	NM_145231 // downstream // 13336 // Hs.123232 // C14orf143 // 90141 // Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000327820 // upstream // 43897 // — // — // — // — /// ENST00000316738 // downstream // 13336 //	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2256677	cttcagattagcacc[A/G]acttacttctgtatc	A	G	NM_145231 // downstream // 11511 // Hs.123232 // C14orf143 // 90141 // Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000327820 // upstream // 45722 // — // — // — /// ENST00000316738 // downstream // 11511 //	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-1826166	taaattagaatcgccc[A/G]taaatctgttgatca	A	G	NM_145231 // downstream // 9255 // Hs.123232 // C14orf143 // 90141 // Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000327820 // upstream // 47978 // — // — // — /// ENST00000316738 // downstream // 9255 // –	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-1811877	gtggaaaaaaatggag[A/G]cagatatgggtggtag	A	G	NM_145231 // intron // 0 // Hs.123232 // C14orf143 // 90141 // Homo sapiens chromosome 14 open reading frame 143 (C14orf143), mRNA. /// ENST00000316738 // intron // 0 // — // — // — /// ENST00000267544 // intron // 0 // — // — // -	C14orf143	C14orf143, Homo sapiens chromosome 14 open reading frame 143 (C14orf143), q32.11
SNP_A-1712323	aactggctgatctcttgtcctcaag[A/G]tttcaaaagctaaaaga ggtccatt	A	G	NM_004755 // intron // 0 // Hs.109058 // RPS6KA5 // 9252 // ribosomal protein S6 kinase, 90kDa, polypeptide 5 /// NM_182398 // intron // 0 // Hs.109058 // RPS6KA5 // 9252 // ribosomal protein S6 kinase, 90kDa, polypeptide 5	RPS6KA5	RPS6KA5, rs1951454, ribosomal protein S6 kinase, 90kDa, polypeptide 5, q32.11
SNP_A-1789372	gggccatctgcctaca[C/T]cagtgaggaaggatga	C	T	NM_199043 // upstream // 23796 // Hs.528131 // C14orf102 // 55051 // Homo sapiens chromosome 14 open reading frame 102 (C14orf102), transcript variant 2, mRNA. /// NM_017970 // upstream // 23796 // Hs.528131 // C14orf102 // 55051 // Homo sapiens chromosom	C14orf102	C14orf102, Homo sapiens chromosome 14 open reading frame 102 (C14orf102), transcript variant 2, q32.11
SNP_A-2228345	ctactggaaattctaggc[C/T]cttggtcattctctc	C	T	NM_001743 // downstream // 58203 // Hs.468442 // CALM2 // 805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // downstream // 58203 // Hs.282410 // CALM1 // 801 // Homo sapiens calmodulin 1 (phosphorylase kinase, d	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q32.12
SNP_A-1937081	ttctttgcactaggc[G/T]agcacatttaagcct	G	T	NM_001743 // downstream // 63345 // Hs.468442 // CALM2 // 805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // downstream // 63345 // Hs.282410 // CALM1 // 801 // Homo sapiens calmodulin 1 (phosphorylase kinase, d	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q32.12
SNP_A-2206369	ccatcgaagaggaggta[A/G]agacttccctgtttgg	A	G	NM_001743 // downstream // 97032 // Hs.468442 // CALM2 // 805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // downstream // 97032 // Hs.282410 // CALM1 // 801 // Homo sapiens calmodulin 1 (phosphorylase kinase, d	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q32.12
SNP_A-2169653	caaggaaaagaatttc[C/T]ctactggctcctgccc	C	T	NM_004755 // intron // 0 // Hs.510225 // RPS6KA5 // 9252 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA. /// NM_182398 // intron // 0 // Hs.510225 // RPS6KA5 // 9252 // Homo sapiens ribosomal protei	RPS6KA5	RPS6KA5, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, q32.12
SNP_A-1934078	ttctcagatgcaatcc[A/G]ccaaaaatacccagga	A	G	NM_004755 // upstream // 28554 // Hs.510225 // RPS6KA5 // 9252 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA. /// NM_182398 // upstream // 28554 // Hs.510225 // RPS6KA5 // 9252 // Homo sapiens ribo	RPS6KA5	RPS6KA5, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, q32.12
SNP_A-1834618	taccacaaaaaattcca[C/T]gatgaacccagtacca	C	T	NM_004755 // upstream // 47628 // Hs.510225 // RPS6KA5 // 9252 // Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, mRNA. /// NM_182398 // upstream // 47628 // Hs.510225 // RPS6KA5 // 9252 // Homo sapiens ribo	RPS6KA5	RPS6KA5, Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5), transcript variant 1, q32.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2080443	acctagcgcgtcagta[C/T]gacagtttcccaaac	C	T	NM_024952 // intron // 0 // Hs.309849 // C14orf159 // 80017 // Homo sapiens chromosome 14 open reading frame 159 (C14orf159), mRNA. /// ENST00000359852 // intron // 0 // — // — // — // — /// ENST00000336843 // intron // 0 // — // — // -	C14orf159	C14orf159, Homo sapiens chromosome 14 open reading frame 159 (C14orf159), q32.12
SNP_A-2089965	acttctgccctgcaaa[C/T]gacaagttaagagaa	C	T	NM_024952 // intron // 0 // Hs.309849 // C14orf159 // 80017 // Homo sapiens chromosome 14 open reading frame 159 (C14orf159), mRNA. /// ENST00000359852 // intron // 0 // — // — // — // — /// ENST00000336843 // intron // 0 // — // — // — // -	C14orf159	C14orf159, Homo sapiens chromosome 14 open reading frame 159 (C14orf159), q32.12
SNP_A-1849163	tatgctaggcctgacc[A/G]attaaagctgagagca	A	G	NM_017936 // upstream // 16154 // Hs.533887 // KIAA2010 // 55671 // Homo sapiens KIAA2010 (KIAA2010), transcript variant 2, mRNA. /// NM_032560 // upstream // 16154 // Hs.533887 // KIAA2010 // 55671 // Homo sapiens KIAA2010 (KIAA2010), transcript variant	KIAA2010	KIAA2010, Homo sapiens KIAA2010 (KIAA2010), transcript variant 2, q32.12
SNP_A-2246223	attcaggagtgataga[C/T]gttctaatcttagaa	C	T	NM_024764 // intron // 0 // Hs.131755 // C14orf161 // 79820 // Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // — // — // — // —	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2003928	tgatgtaacagaagtc[A/G]aaaaacttaatatca	A	G	NM_024764 // intron // 0 // Hs.131755 // C14orf161 // 79820 // Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // — // — // — // —	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2236992	ctctatgaattaaatc[C/G]acacaacagatttctt	C	G	NM_024764 // intron // 0 // Hs.131755 // C14orf161 // 79820 // Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // — // — // — // —	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2099602	agaggtagacaaaaaa[C/G]agttcttgacacttca	C	G	NM_024764 // intron // 0 // Hs.131755 // C14orf161 // 79820 // Homo sapiens chromosome 14 open reading frame 161 (C14orf161), mRNA. /// ENST00000256343 // intron // 0 // — // — // — // —	C14orf161	C14orf161, Homo sapiens chromosome 14 open reading frame 161 (C14orf161), q32.12
SNP_A-2146875	atgctttctggtgta[C/T]ggacagagccttctt	C	T	NM_006329 // intron // 0 // Hs.332708 // FBLN5 // 10516 // Homo sapiens fibulin 5 (FBLN5), mRNA. /// ENST00000342058 // intron // 0 // — // — // — // - /// ENST00000267620 // intron // 0 // — // — // — // —	FBLN5	FBLN5, Homo sapiens fibulin 5 (FBLN5), q32.12
SNP_A-2229521	ctagggtgatggtcaa[A/G]acacagacagttgaa	A	G	NM_004239 // intron // 0 // Hs.546327 // TRIP11 // 9321 // Homo sapiens thyroid hormone receptor interactor 11 (TRIP11), mRNA. /// ENST00000267622 // intron // 0 // — // — // — // —	TRIP11	TRIP11, Homo sapiens thyroid hormone receptor interactor 11 (TRIP11), q32.12
SNP_A-2003932	taatttaatcagaatg[C/T]catgtttcctggctgg	C	T	NM_153648 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (SLC24A4), transcript variant 3, mRNA. /// NM_153647 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Hom	SLC24A4	SLC24A4, Homo sapiens solute carrier family 24 (sodium,q32.12
SNP_A-2128728	ataatccaactgatac[A/T]cattaaagctagaaat	A	T	NM_153648 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (SLC24A4), transcript variant 3, mRNA. /// NM_153647 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Hom	SLC24A4	SLC24A4, Homo sapiens solute carrier family 24 (sodium,q32.12
SNP_A-2201363	ccaatcccgtgctaga[C/T]aaaccctcctgctgt	C	T	NM_153648 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (SLC24A4), transcript variant 3, mRNA. /// NM_153647 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Hom	SLC24A4	SLC24A4, Homo sapiens solute carrier family 24 (sodium,q32.12
SNP_A-2207407	ccattgcctttgcaca[A/G]tagttttaagttcttc	A	G	NM_153648 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (SLC24A4), transcript variant 3, mRNA. /// NM_153647 // intron // 0 // Hs.510281 // SLC24A4 // 123041 // Hom	SLC24A4	SLC24A4, Homo sapiens solute carrier family 24 (sodium q32.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2080230	acctaaatgtccatca[A/G]taagggaccagggaaa	A	G	NM_024832 // intron // 0 // Hs.326822 // RIN3 // 79890 // Homo sapiens Ras and Rab interactor 3 (RIN3), mRNA. /// ENST00000354637 // intron // 0 // — // — // — /// ENST00000216487 // intron // 0 // — // — // — // —	RIN3	RIN3, Homo sapiens Ras and Rab interactor 3 (RIN3), q32.12
SNP_A-2236203	ctcctgctaggaaaaa[C/G]tcccaaggaggcaact	C	G	NM_024832 // intron // 0 // Hs.326822 // RIN3 // 79890 // Homo sapiens Ras and Rab interactor 3 (RIN3), mRNA. /// ENST00000354637 // intron // 0 // — // — // — /// ENST00000216487 // intron // 0 // — // — // — // —	RIN3	RIN3, Homo sapiens Ras and Rab interactor 3 (RIN3), q32.12
SNP_A-2305668	gctgccaaagtacgag[C/G]cctgtcctgcgccag	C	G	NM_024832 // CDS // 0 // Hs.326822 // RIN3 // 79890 // Homo sapiens Ras and Rab interactor 3 (RIN3), mRNA. /// ENST00000354637 // intron // 0 // — // — // — /// ENST00000216487 // CDS // 0 // — // — // — // — // -	RIN3	RIN3, Homo sapiens Ras and Rab interactor 3 (RIN3), q32.12
SNP_A-2247241	tggacttattataga[A/G]ccctctgtatctata	A	G	NM_005113 // intron // 0 // Hs.104320 // GOLGA5 // 9950 // Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA. /// ENST00000163416 // intron // 0 // — // — // — // — /// ENST00000355976 // intron // 0 // — // — // — // —	GOLGA5	GOLGA5, Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), q32.12
SNP_A-2234523	ctccacctcattcccc[A/G]ctttacacagaaga	A	G	NM_014216 // intron // 0 // Hs.308122 // ITPK1 // 3705 // Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA. /// ENST00000311458 // intron // 0 // — // — // — // — /// ENST00000354313 // intron // 0 // — // — // — // — ///	ITPK1	ITPK1, Homo sapiens inositol 1,3,4-triphosphate 5 q32.13
SNP_A-1833637	tacaggaggattctgd[A/C]cttacctgtcacatat	A	C	NM_001002860 // intron // 0 // Hs.525549 // BTBD7 // 55727 // Homo sapiens BTB (POZ) domain containing 7 (BTBD7), transcript variant 1, mRNA. /// ENST00000335125 // intron // 0 // — // — // — // — /// ENST00000334746 // intron // 0 // — // — /	BTBD7	BTBD7, Homo sapiens BTB (POZ) domain containing 7 (BTBD7), transcript variant 1, q32.13
SNP_A-1745644	tggcaagacttgaaacattggaaag[A/C]attactccagaaaga ctctcagaa	A	C	BX248259 // downstream // 18606 // Hs.145890 // LOC256394 // 256394 // antiproteinase-like 2 /// NM_000295 // upstream // 35102 // Hs.297681 // SERPINA1 // 5265 // serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),	LOC256394	LOC256394 , rs7145288, antiproteinase-like 2 q32.13
SNP_A-1663862	actaatgccctggccagttacagcc[A/G]atatgaacacacaggt ccaagtaat	A	G	BX248259 // downstream // 3429 // Hs.145890 // LOC256394 // 256394 // antiproteinase-like 2 /// NM_000295 // upstream // 50279 // Hs.297681 // SERPINA1 // 5265 // serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), m	LOC256394	LOC256394 , rs1989296, antiproteinase-like 2 q32.13
SNP_A-1810156	gtgatcccagcagcta[C/T]ggatgttaatgacaat	C	T	NM_178013 // intron // 0 // Hs.432401 // PRIMA1 // 145270 // Homo sapiens proline rich membrane anchor 1 (PRIMA1), mRNA. /// ENST00000316227 // intron // 0 // — // — // — // — /// ENST00000343423 // intron // 0 // — // — // — // —	PRIMA1	PRIMA1, Homo sapiens proline rich membrane anchor 1 (PRIMA1), q32.13
SNP_A-1931164	ttccatgggtaaatca[A/C]ggcaaagacaggccct	A	C	NM_178013 // upstream // 58229 // Hs.432401 // PRIMA1 // 145270 // Homo sapiens proline rich membrane anchor 1 (PRIMA1), mRNA. /// NM_138344 // upstream // 72924 // Hs.525550 // C14orf152 // 90050 // Homo sapiens chromosome 14 open reading frame 152 (C14o	PRIMA1	PRIMA1, Homo sapiens proline rich membrane anchor 1 (PRIMA1), q32.13
SNP_A-1932867	ttcctttctcataataa[A/G]ctgtaaatgcaggca	A	G	NM_178013 // upstream // 65055 // Hs.432401 // PRIMA1 // 145270 // Homo sapiens proline rich membrane anchor 1 (PRIMA1), mRNA. /// NM_138344 // upstream // 66098 // Hs.525550 // C14orf152 // 90050 // Homo sapiens chromosome 14 open reading frame 152 (C14o	PRIMA1	PRIMA1, Homo sapiens proline rich membrane anchor 1 (PRIMA1), q32.13
SNP_A-1895153	tgccccagaaacttta[A/T]caaaggcttcaattca	A	T	NM_016150 // intron // 0 // Hs.510327 // ASB2 // 51676 // Homo sapiens ankyrin repeat and SOCS box-containing 2 (ASB2), mRNA. /// ENST00000315988 // intron // 0 // — // — // — // —	ASB2	ASB2, Homo sapiens ankyrin repeat and SOCS box-containing 2 (ASB2), q32.13
SNP_A-1896450	tgctacaagtagaaaaa[C/T]tccccatctgacctca	C	T	NM_020958 // intron // 0 // Hs.259599 // KIAA1622 // 57718 // Homo sapiens KIAA1622 (KIAA1622), transcript variant 2, mRNA. /// NM_058237 // intron // 0 // Hs.259599 // KIAA1622 // 57718 // Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, mRNA. ///	KIAA1622	KIAA1622, Homo sapiens KIAA1622 (KIAA1622), transcript variant 2, q32.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2126949	ataaagtaacttgcca[C/T]cgctttattgaataaa	C	T	NM_058237 // intron // 0 // Hs.259599 // KIAA1622 // 57718 // Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, mRNA. /// ENST00000304338 // intron // 0 // — // — // — // —	KIAA1622	KIAA1622, Homo sapiens KIAA1622 (KIAA1622), transcript variant 1, q32.13
SNP_A-2197305	cattcatagaaaatca[C/T]gtagcgttaatcatat	C	T	NM_016186 // intron // 0 // Hs.118620 // SERPINA10 // 51156 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 (SERPINA10), mR /// ENST00000261994 // intron // 0 // — // — // — // —	SERPINA10	SERPINA10, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 (SERPINA10), mR ,q32.13
SNP_A-1844462	tataaaggaaggcagc[A/G]gagtatattgggaaga	A	G	NM_016186 // upstream // 1813 // Hs.118620 // SERPINA10 // 51156 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 (SERPINA10), mR /// NM_001756 // downstream // 9165 // Hs.532635 // SERPIN	SERPINA10	SERPINA10, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 (SERPINA10), mR ,q32.13
SNP_A-2248224	tctatggattgctcag[C/T]caaaattcttggttct	C	T	NM_001756 // intron // 0 // Hs.532635 // SERPINA6 // 866 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 (SERPINA6), mRNA /// ENST00000341584 // intron // 0 // — // — // — // —	SERPINA6	SERPINA6, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 (SERPINA6), q32.13
SNP_A-1737591	ggcagcccctgggtgagcaatttct[G/T]gcaggcatccagcccataaagtgtt	G	T	NM_024633 // downstream // 12093 // Hs.41502 // C14orf139 // 79686 // chromosome 14 open reading frame 139 /// NM_024734 // upstream // 75311 // Hs.301478 // CLMN // 79789 // calmin (calponin-like, transmembrane)	C14orf139	C14orf139 , rs1074925, chromosome 14 open reading frame 139 ,q32.13
SNP_A-1836637	tactcttcctaacttc[C/T]ctgttttcatcctccc	C	T	NM_000295 // upstream // 30774 // Hs.525557 // SERPINA1 // 5265 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran /// NM_001002236 // upstream // 30774 // Hs.525557 // SERPI	SERPINA1	SERPINA1, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), tran ,q32.13
SNP_A-1812300	gtggatggatggatgc[A/G]aatgtaacttagaaag	A	G	NM_175739 // intron // 0 // Hs.317970 // SERPINA9 // 327657 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 (SERPINA9), mRNA /// ENST00000298845 // intron // 0 // — // — // — // —	SERPINA9	SERPINA9, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9 (SERPINA9), q32.13
SNP_A-2165860	caaagtctccctaata[C/T]agacgcacccaatgca	C	T	NM_006215 // intron // 0 // Hs.159628 // SERPINA4 // 5267 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4 (SERPINA4), mRNA /// ENST00000298841 // intron // 0 // — // — // — // — //	SERPINA4	SERPINA4, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4 (SERPINA4), q32.13
SNP_A-2093005	agaacacctagaattt[A/T]aaaaaagcaatagata	A	T	NM_207378 // downstream // 29177 // Hs.527795 // SERPINA13 // 388007 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 13 (SERPINA13), mR /// ENST00000338704 // downstream // 29177 // — // -	SERPINA13	SERPINA13, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 13 (SERPINA13), mR ,q32.13
SNP_A-2210145	ccccagggtgcacacc[A/G]ctacgtctgccataag	A	G	NM_207378 // downstream // 33979 // Hs.527795 // SERPINA13 // 388007 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 13 (SERPINA13), mR /// ENST00000338704 // downstream // 33979 // — // -	SERPINA13	SERPINA13, Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 13 (SERPINA13), mR q32.13
SNP_A-2208600	cccactctctgctgta[C/T]cagaaccaacccagga	C	T	NM_173849 // upstream // 43652 // Hs.440438 // GSC // 145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 272415 // Hs.87889 // DICER1 // 23405 // Homo sapiens Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 2, mRN	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-1695325	ccaagaataggacttagtatttaca[C/T]tacagtccaggggctgacctctgc	C	T	BX247990 // downstream // 157535 // Hs.136572 // - // - // Human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human) /// NM_020215 // upstream // 176115 // Hs.6434 // C14orf132 // 56967 // chromosome 14 open reading f	-	- , rs2145632, Human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human) ,q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1670876	ggtcaccacagtatgccatgacttaj[C/T]gatgctacaaaatcac attgctccc	C	T	BX247990 // downstream // 157613 // Hs.136572 // - // - // Human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human) /// NM_020215 // upstream // 176037 // Hs.6434 // C14orf132 // 56967 // chromosome 14 open reading f	-	-, rs2180895, Human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human) ,q32.2
SNP_A-2219721	ccttaaggtgcaataaa[A/C]aacttaaactttgtga	A	C	NM_173849 // upstream // 90707 // Hs.440438 // GSC // 145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 225360 // Hs.87889 // DICER1 // 23405 // Homo sapiens Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 2, mRN	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2034419	aaatctattgtctaccc[C/T]atctgtttctttttat	C	T	NM_173849 // upstream // 90850 // Hs.440438 // GSC // 145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 225217 // Hs.87889 // DICER1 // 23405 // Homo sapiens Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 2, mRN	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-1672332	acctcatgatccagcagtaaaggt[C/G]agcagctgaggggga tctcccaga	C	G	BX247990 // downstream // 267494 // Hs.136572 // - // - // Human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human) /// NM_020215 // upstream // 66156 // Hs.6434 // C14orf132 // 56967 // chromosome 14 open reading fr	-	-, rs1951801, Human full-length cDNA clone CS0DG006YJ19 of B cells (Ramos cell line) of Homo sapiens (human) ,q32.2
SNP_A-1904564	tggggcaaggagtgca[A/G]atagttgggagatggg	A	G	NM_173849 // upstream // 211274 // Hs.440438 // GSC // 145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 104793 // Hs.87889 // DICER1 // 23405 // Homo sapiens Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 2, mR	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2192181	catcagcaatgataa[C/T]gaaggttccgtcctag	C	T	NM_173849 // upstream // 261688 // Hs.440438 // GSC // 145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 54379 // Hs.87889 // DICER1 // 23405 // Homo sapiens Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 2, mRN	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-1961028	ttttggtaatcacac[C/T]gtgggatgggagaga	C	T	NM_173849 // upstream // 274288 // Hs.440438 // GSC // 145258 // Homo sapiens goosecoid (GSC), mRNA. /// NM_030621 // downstream // 41779 // Hs.87889 // DICER1 // 23405 // Homo sapiens Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 2, mRN	GSC	GSC, Homo sapiens goosecoid (GSC), q32.13
SNP_A-2222057	cgaagaggatcgtgta[A/G]cttttactaggaccc	A	G	NM_016417 // downstream // 77704 // Hs.532683 // C14orf87 // 51218 // Homo sapiens chromosome 14 open reading frame 87 (C14orf87), mRNA. /// NM_020553 // upstream // 40184 // Hs.510368 // TCL6 // 27004 // Homo sapiens T-cell leukemia/lymphoma 6 (TCL6), tr	C14orf87	C14orf87, Homo sapiens chromosome 14 open reading frame 87 (C14orf87), q32.13
SNP_A-2044728	aagaaagtcatgcaca[A/T]tgaaaaacatgtgaaa	A	T	NM_021966 // upstream // 912 // Hs.2484 // TCL1A // 8115 // Homo sapiens T-cell leukemia/lymphoma 1A (TCL1A), mRNA. /// ENST00000216612 // upstream // 912 // — // — // — // — /// ENST00000334154 // upstream // 41181 // — // — // — // — // —	TCL1A	TCL1A, Homo sapiens T-cell leukemia,q32.13
SNP_A-2209433	cccatatcaatctgcc[A/G]ctggcccacaggtcact	A	G	NM_020215 // upstream // 224528 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 58346 // — // — // — // — /// ENST00000329809 // upstream // 224528 // -	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.13
SNP_A-2194235	catgaggaagacagaa[A/C]ggccagctaggaggg	A	C	NM_020215 // upstream // 164304 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 118570 // — // — // — // — /// ENST00000329809 // upstream // 164304 // -	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897306	tgctcttcctggcttg[A/G]agaactactgctggcc	A	G	NM_020215 // upstream // 129425 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 153449 // --- // --- // --- // --- /// ENST00000329809 // upstream // 129425 // -	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-2107140	agcggtcatgtaccgc[A/G]agagttgggaagaaca	A	G	NM_020215 // upstream // 115251 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 167623 // --- // --- // --- // --- /// ENST00000329809 // upstream // 115251 // -	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-1875120	tctctcattgttgcaa[C/T]cttctttacaaatgca	C	T	NM_020215 // upstream // 90568 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 192306 // --- // --- // --- // --- /// ENST00000329809 // upstream // 90568 // ---	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-2163924	caaaactagagcctaa[C/T]catggatgccgaggat	C	T	NM_020215 // upstream // 52067 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 230807 // --- // --- // --- // --- /// ENST00000329809 // upstream // 52067 // ---	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-2038616	aacagaatgcaacaaa[A/T]catgttcaaccaaaca	A	T	NM_020215 // upstream // 15454 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// ENST00000334154 // downstream // 267420 // --- // --- // --- // --- /// ENST00000329809 // upstream // 15454 // ---	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-2039335	aacataatggcatctc[A/G]agtcatattcttttgg	A	G	NM_020215 // downstream // 27035 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// NM_000623 // upstream // 84029 // Hs.546240 // BDKRB2 // 624 // Homo sapiens bradykinin receptor B2 (BDKRB2), mRN	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-2288132	gattcaggcaagagga[C/T]atgtggagaacacata	C	T	NM_020215 // downstream // 32758 // Hs.6434 // C14orf132 // 56967 // Homo sapiens chromosome 14 open reading frame 132 (C14orf132), mRNA. /// NM_000623 // upstream // 78306 // Hs.546240 // BDKRB2 // 624 // Homo sapiens bradykinin receptor B2 (BDKRB2), mRN	C14orf132	C14orf132, Homo sapiens chromosome 14 open reading frame 132 (C14orf132), q32.2
SNP_A-2096884	agactcccggaagata[C/T]ggcccagaccacttgc	C	T	NM_000623 // intron // 0 // Hs.546240 // BDKRB2 // 624 // Homo sapiens bradykinin receptor B2 (BDKRB2), mRNA. /// ENST00000306005 // intron // 0 // --- // --- // --- // ---	BDKRB2	BDKRB2, Homo sapiens bradykinin receptor B2 (BDKRB2), q32.2
SNP_A-2123469	agtgtgaacttacacc[A/G]ctgatatgtctagaaa	A	G	NM_032632 // downstream // 24554 // Hs.253726 // PAPOLA // 10914 // Homo sapiens poly(A) polymerase alpha (PAPOLA), mRNA. /// NM_020144 // downstream // 24554 // Hs.487409 // PAPOLB // 56903 // Homo sapiens poly(A) polymerase beta (testis specific) (PAPOL	PAPOLA	PAPOLA, Homo sapiens poly(A) polymerase alpha (PAPOLA), q32.2
SNP_A-2251511	atcatcatggttagaa[A/G]gaaaagcaatacacca	A	G	NM_003384 // downstream // 540643 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 540643 // --- // --- // --- // --- /// ENST00000355909 // downstream // 211317 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2251519	cttccaactgcaaggc[C/T]gagactcataattcct	C	T	NM_003384 // downstream // 547335 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 547335 // --- // --- // --- // --- /// ENST00000355909 // downstream // 204625 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2081283	acctggacaatgacca[C/T]cgtttagtaaactgat	C	T	NM_003384 // downstream // 549129 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 549129 // --- // --- // --- // --- /// ENST00000355909 // downstream // 202831 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1880611	tcttgcctacagaaag[A/C]caggagatgcggcttt	A	C	NM_003384 // downstream // 581264 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 581264 // --- // --- // --- /// ENST00000355909 // downstream // 170696 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2121109	agtcttatgaaaac[C/T]ggtaggagacaggcgta	C	T	NM_003384 // downstream // 596573 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 596573 // --- // --- // --- /// ENST00000355909 // downstream // 155387 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2251584	taggcagtaggcaaat[A/G]ataattgaggaaacca	A	G	NM_003384 // downstream // 646150 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 646150 // --- // --- // --- /// ENST00000355909 // downstream // 105810 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-1842312	taggtagcatggcaag[G/T]ctgcttaaacaaca	G	T	NM_003384 // downstream // 650486 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 650486 // --- // --- // --- /// ENST00000355909 // downstream // 101474 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2251623	actaggctgtgttata[C/T]gacactcgagtctttt	C	T	NM_003384 // downstream // 703902 // Hs.422662 // VRK1 // 7443 // Homo sapiens vaccinia related kinase 1 (VRK1), mRNA. /// ENST00000216639 // downstream // 703902 // --- // --- // --- /// ENST00000355909 // downstream // 48058 // --- // --- // ---	VRK1	VRK1, Homo sapiens vaccinia related kinase 1 (VRK1), q32.2
SNP_A-2295575	gcatcttattctatca[C/T]actcacctatttttgga	C	T	NM_182560 // upstream // 429632 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream // 635703 // --- // --- // --- /// ENST00000325812 // upstream // 429632 // --- // --	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2252680	agatttgtgtctggaa[C/T]ccagatgagcctaaag	C	T	NM_182560 // upstream // 171225 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream // 894110 // --- // --- // --- /// ENST00000325812 // upstream // 171225 // --- // --	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2114131	agggaaacttggaaaaa[C/T]gaggctaaccattctc	C	T	NM_182560 // upstream // 121627 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream // 943708 // --- // --- // --- /// ENST00000325812 // upstream // 121627 // --- // --	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2226760	ctaataaagtgctaa[A/T]ggagcttaggactaag	A	T	NM_182560 // upstream // 106121 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream // 959214 // --- // --- // --- /// ENST00000325812 // upstream // 106121 // --- // --	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2206454	ccatctcttcaaattc[C/G]ctgtctaacctcattt	C	G	NM_182560 // upstream // 98899 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000355909 // upstream // 966436 // --- // --- // --- /// ENST00000325812 // upstream // 98899 // --- // --	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2159330	atttaaggtcctctct[G/T]acactgggatttggg	G	T	NM_182560 // downstream // 32614 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 32614 // --- // --- // --- /// ENST00000357187 // upstream // 239536 // --- //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2063194	aatgttctattccac[C/T]gtcagtattaacattg	C	T	NM_182560 // downstream // 84860 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 84860 // --- // --- // --- /// ENST00000357187 // upstream // 187290 // --- //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2100448	agataaactaattcta[C/T]gaggctattactaatg	C	T	NM_182560 // downstream // 192021 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 192021 // — // — // — /// ENST00000357187 // upstream // 80129 // — //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-1849499	tatggctactgaaggat[C/T]ggatttggtttgcca	C	T	NM_182560 // downstream // 192132 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 192132 // — // — // — /// ENST00000357187 // upstream // 80018 // — //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2158081	attggaatattcctaa[C/T]gtcagagagcttcata	C	T	NM_182560 // downstream // 192286 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 192286 // — // — // — /// ENST00000357187 // upstream // 79864 // — //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2253360	ttctcttatattttca[G/T]ggacccaaaccatgtc	G	T	NM_182560 // downstream // 201510 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 201510 // — // — // — /// ENST00000357187 // upstream // 70640 // — //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2253371	taagaacaagatgcta[C/T]gtaaaaggaacaatca	C	T	NM_182560 // downstream // 204282 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 204282 // — // — // — /// ENST00000357187 // upstream // 67868 // — //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-1944260	ttgtccagggcaaaaa[A/G]cctgaacttggagct	A	G	NM_182560 // downstream // 213899 // Hs.448754 // FLJ25773 // 283598 // Homo sapiens hypothetical protein FLJ25773 (FLJ25773), mRNA. /// ENST00000325812 // downstream // 213899 // — // — // — /// ENST00000357187 // upstream // 58251 // — //	FLJ25773	FLJ25773, Homo sapiens hypothetical protein FLJ25773 (FLJ25773), q32.2
SNP_A-2284889	gatccagcagaagaca[C/T]ggcatgcgagatcttg	C	T	NM_022898 // intron // 0 // Hs.510396 // BCL11B // 64919 // Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 2, mRNA. /// NM_138576 // intron // 0 // Hs.510396 // BCL11B // 64919 // Homo sapiens B-cell CLL/lymphoma 1	BCL11B	BCL11B, Homo sapiens B-cell CLL,q32.2
SNP_A-2205016	ccaggtaactcagttq[C/T]cccatgaaagagcccc	C	T	NM_022898 // intron // 0 // Hs.510396 // BCL11B // 64919 // Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 2, mRNA. /// NM_138576 // intron // 0 // Hs.510396 // BCL11B // 64919 // Homo sapiens B-cell CLL/lymphoma 1	BCL11B	BCL11B, Homo sapiens B-cell CLL,q32.2
SNP_A-2186455	cagggaacagtattcc[C/T]aatgtgcactgagaag	C	T	NM_022898 // upstream // 87350 // Hs.510396 // BCL11B // 64919 // Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 2, mRNA. /// NM_138576 // upstream // 87350 // Hs.510396 // BCL11B // 64919 // Homo sapiens B-cell CL	BCL11B	BCL11B, Homo sapiens B-cell CLL,q32.2
SNP_A-1793364	ggtaggatatccaccc[C/T]aaaatgccacagtggt	C	T	ENST00000330710 // intron // 0 // — // — // — // —	-	q32.2
SNP_A-1869456	tcctgtgctgcctcc[A/G]ctctatcgggcgtgt	A	G	NM_006668 // downstream // 19672 // Hs.25121 // CYP46A1 // 10858 // Homo sapiens cytochrome P450, family 46, subfamily A, polypeptide 1 (CYP46A1), mRNA. /// NM_004434 // upstream // 46484 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule	CYP46A1	CYP46A1, Homo sapiens cytochrome P450, family 46, subfamily A, polypeptide 1 (CYP46A1), q32.2
SNP_A-1732648	ttgatgttccaaagccaagataaca[A/C]ctctatcatttgataaag atcaagt	A	C	AF422192 // upstream // 29556 // - // - // Homo sapiens esophagus cancer-related gene-2 interaction susceptibility protein mRNA, partial cds. /// AK055725 // downstream // 2354 // Hs.418271 // MEG3 // 55384 // maternally expressed 3	-	-, rs721910, Homo sapiens esophagus cancer-related gene-2 interaction susceptibility protein mRNA, partial cds, q32.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1855297	tcaaggaatcaaagca[C/T]ggtgttacaaaatcaa	C	T	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // — // — // — // — /// ENST00000262233 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-1861009	tcatagcaaaaggcca[A/G]gtttaaagcatagtg	A	G	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // — // — // — // — /// ENST00000262233 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2254294	agcccctacatcacccc[C/G]cagtttcagaagcaaa	C	G	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // — // — // — // — /// ENST00000262233 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2094766	agaatcatagcaacaa[A/G]aagtagagaggtggtt	A	G	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // — // — // — // — /// ENST00000262233 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-1801859	gtagttctcagtgtat[A/G]agtcttctaactcctt	A	G	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // — // — // — // — /// ENST00000262233 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-1902141	tggcatttatgtcaaa[A/G]ttatacactacactca	A	G	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000334192 // intron // 0 // — // — // — // — /// ENST00000262233 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2289968	gcaaagcttatggaaa[A/C]gaggcctgttgtttct	A	C	NM_004434 // intron // 0 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// ENST00000262233 // intron // 0 // — // — // — // — /// ENST00000327921 // intron // 0 // — // — // — // -	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-2053011	aagtccgagatcaaga[C/T]gccaggcagttcagtt	C	T	NM_004434 // downstream // 111378 // Hs.12451 // EML1 // 2009 // Homo sapiens echinoderm microtubule associated protein like 1 (EML1), mRNA. /// NM_016337 // upstream // 12499 // Hs.125867 // EVL // 51466 // Homo sapiens Enah/Vasp-like (EVL), mRNA. /// EN	EML1	EML1, Homo sapiens echinoderm microtubule associated protein like 1 (EML1), q32.2
SNP_A-1859164	tcagcctctctctca[C/T]aacagcctgggatggg	C	T	NM_016337 // intron // 0 // Hs.125867 // EVL // 51466 // Homo sapiens Enah/Vasp-like (EVL), mRNA. /// ENST00000358288 // intron // 0 // — // — // — // — /// ENST00000355449 // intron // 0 // — // — // — // —	EVL	EVL, Homo sapiens Enah,q32.2
SNP_A-2314406	ggagggagctgggaaga[C/T]agaggtgcccaagtg	C	T	NM_024515 // intron // 0 // Hs.395306 // MGC4645 // 79446 // Homo sapiens pre-mRNA splicing factor-like (MGC4645), mRNA. /// ENST00000335290 // intron // 0 // — // — // — // —	MGC4645	MGC4645, Homo sapiens pre- splicing factor-like (MGC4645), q32.2
SNP_A-2254739	cttggaaacagtatcc[A/G]atctcaattcacgaag	A	G	ENST00000357290 // intron // 0 // — // — // — // — /// ENST00000334896 // 5UTR // 0 // — // — // — // —	-	q32.2
SNP_A-1927066	ttatttgtgtaacgac[A/G]ggctctattcttgag	A	G	ENST00000357290 // intron // 0 // — // — // — // — /// ENST00000334896 // intron // 0 // — // — // — // —	-	q32.2
SNP_A-2163176	attttccttggctat[C/G]actgtttcagtacata	C	G	NM_001362 // upstream // 572888 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 94154 // — // — // — // — /// ENST00000359323 // upstream // 572888 // — // — // —	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2096367	agacccacggagctca[C/T]ggtcgtcagggtcct	C	T	NM_001362 // upstream // 491387 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 175655 // — // — // — // — /// ENST00000359323 // upstream // 491387 // — // — // -	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-1809645	gtgagcaggtaggcac[A/T]agtaagcctgaattca	A	T	NM_001362 // upstream // 347280 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 319762 // — // — // — // — /// ENST00000359323 // upstream // 347280 // — // -	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1795413	ggtgcacagatgtcaa[C/G]gattgaagttcagaa	C	G	NM_001362 // upstream // 265647 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 401395 // --- // --- // --- /// ENST00000359323 // upstream // 265647 // --- // ---	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2120244	agtcaggttgtcccaa[A/C]gtctgctcgagtctgg	A	C	NM_001362 // upstream // 212331 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 454711 // --- // --- // --- /// ENST00000359323 // upstream // 212331 // --- // ---	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2207081	ccatgtttcttttaaa[C/T]gccgctatcccatctt	C	T	NM_001362 // upstream // 209108 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 457934 // --- // --- // --- /// ENST00000359323 // upstream // 209108 // --- // ---	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2265018	gaagataaataaacta[C/G]agctacatgaagcaac	C	G	NM_001362 // upstream // 180943 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 486099 // --- // --- // --- /// ENST00000359323 // upstream // 180943 // --- // ---	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2117815	aggttggagacatctg[A/G]aaaaggtagcaaatga	A	G	NM_001362 // upstream // 153339 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// ENST00000357288 // downstream // 513703 // --- // --- // --- /// ENST00000359323 // upstream // 153339 // --- // ---	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-1887059	tgacttctcgaatggg[A/G]ccaatgtacatcctac	A	G	NM_001362 // downstream // 121509 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// NM_178588 // upstream // 124876 // Hs.368264 // PPP2R5C // 5527 // Homo sapiens protein phosphatase 2, regulatory subunit B	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2255285	tgtgctctaaccatc[A/G]cattaggccacctctc	A	G	NM_001362 // downstream // 131810 // Hs.49322 // DIO3 // 1735 // Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA. /// NM_178588 // upstream // 114575 // Hs.368264 // PPP2R5C // 5527 // Homo sapiens protein phosphatase 2, regulatory subunit B	DIO3	DIO3, Homo sapiens deiodinase, iodothyronine, type III (DIO3), q32.31
SNP_A-2255311	gcgttataaacactgc[A/T]cagtaactgatactca	A	T	NM_178588 // intron // 0 // Hs.368264 // PPP2R5C // 5527 // Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), transcript variant 4, mRNA. /// NM_178587 // intron // 0 // Hs.368264 // PPP2R5C // 5527 // Homo sapiens p	PPP2R5C	PPP2R5C, Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), transcript variant 4, q32.31
SNP_A-1864349	tccacttcctgcttcac[A/C]gcctttctgtccagc	A	C	NM_005348 // intron // 0 // Hs.525600 // HSPCA // 3320 // Homo sapiens heat shock 90kDa protein 1, alpha (HSPCA), mRNA. /// ENST00000216281 // intron // 0 // --- // --- // ---	HSPCA	HSPCA, Homo sapiens heat shock 90kDa protein 1, alpha (HSPCA), q32.32
SNP_A-1908218	tgtaccccccagagag[A/T]caacttcaaggactcc	A	T	NM_181308 // intron // 0 // Hs.36859 // WDR20 // 91833 // Homo sapiens WD repeat domain 20 (WDR20), transcript variant 3, mRNA. /// NM_144574 // intron // 0 // Hs.36859 // WDR20 // 91833 // Homo sapiens WD repeat domain 20 (WDR20), transcript variant 2, m	WDR20	WDR20, Homo sapiens WD repeat domain 20 (WDR20), transcript variant 3, q32.32
SNP_A-2113547	aggctacaggtagtaa[G/T]ccttctagaagagcct	G	T	ENST00000193029 // intron // 0 // --- // --- // --- /// ENST00000356835 // intron // 0 // --- // --- // --- /// ENST00000358648 // intron // 0 // --- // --- // --- /// ENST00000360114 // intron // 0 // --- // --- // --- /// ENST00000193029 // intron // 0 // --- // --- // --- /// ENST00000358648 // intron // 0 // --- // --- // --- /// ENST00000360114 // intron // 0 // --- // --- // ---	-	q32.32
SNP_A-2125578	agtttcagtcaataac[A/G]gcaacttaatattagg	A	G		-	q32.32
SNP_A-2003988	cttgttcacaggtc[A/C]caggaatatgctgggt	A	C	NM_152326 // upstream // 49233 // Hs.432945 // ANKRD9 // 122416 // Homo sapiens ankyrin repeat domain 9 (ANKRD9), mRNA. /// NM_015156 // upstream // 34846 // Hs.510521 // RCOR1 // 23186 // Homo sapiens REST corepressor 1 (RCOR1), mRNA. /// ENST00000286918	ANKRD9	ANKRD9, Homo sapiens ankyrin repeat domain 9 (ANKRD9), q32.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2051747	aaggtcacgttcatgq[A/C]gatgatggaagacctc	A	C	ENST00000359628 // intron // 0 // — // — // — /// ENST00000359398 // intron // 0 // — // — // —	-	q32.32
SNP_A-1888141	tgagcccgtctctgaa[C/T]acaaaccagacctcct	C	T	NM_006291 // downstream // 446 // Hs.525607 // TNFAIP2 // 7127 // Homo sapiens tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), mRNA. /// ENST00000333007 // downstream // 446 // — // — // — /// ENST00000311549 // upstream // 10712 //	TNFAIP2	TNFAIP2, Homo sapiens tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), q32.32
SNP_A-2081758	acctctgtctaac[C/T]acatgaatcctggctt	C	T	ENST00000311549 // intron // 0 // — // — // —	-	q32.32
SNP_A-2132923	atataatttttctcc[A/G]caaagaacagaaacac	A	G	ENST00000311549 // intron // 0 // — // — // —	-	q32.32
SNP_A-2237403	ctctccctggaggtca[A/G]gtaggactgaaggttc	A	G	ENST00000311549 // intron // 0 // — // — // —	-	q32.32
SNP_A-2222431	cgagccaccgtatcca[A/G]cctacaaatatttaa	A	G	NM_032374 // intron // 0 // Hs.116029 // C14orf153 // 84334 // Homo sapiens chromosome 14 open reading frame 153 (C14orf153), mRNA. /// ENST00000247618 // intron // 0 // — // — // —	C14orf153	C14orf153, Homo sapiens chromosome 14 open reading frame 153 (C14orf153), q32.33
SNP_A-2286792	gatggcttctaagaca[C/T]ccaaatacaaatgct	C	T	NM_015316 // upstream // 59199 // Hs.546353 // PPP1R13B // 23368 // Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 13B (PPP1R13B), mRNA. /// NM_004894 // downstream // 5528 // Hs.109052 // C14orf2 // 9556 // Homo sapiens chromosome 14	PPP1R13B	PPP1R13B, Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 13B (PPP1R13B), q32.33
SNP_A-2053109	aagtctcaaagcaaat[G/T]agttacttctagata	G	T	NM_153046 // intron // 0 // Hs.21454 // TDRD9 // 122402 // Homo sapiens tudor domain containing 9 (TDRD9), mRNA. /// ENST00000339063 // intron // 0 // — // — // — /// ENST00000286956 // intron // 0 // — // — // — /// ENST00000334	TDRD9	TDRD9, Homo sapiens tudor domain containing 9 (TDRD9), q32.33
SNP_A-2170891	caataacacaaaggaa[A/G]catcttgcagacttcg	A	G	NM_153046 // intron // 0 // Hs.21454 // TDRD9 // 122402 // Homo sapiens tudor domain containing 9 (TDRD9), mRNA. /// ENST00000339063 // intron // 0 // — // — // — /// ENST00000286956 // intron // 0 // — // — // — /// ENST00000334	TDRD9	TDRD9, Homo sapiens tudor domain containing 9 (TDRD9), q32.33
SNP_A-2243346	ctgccttccagcac[A/C]aggaaacatccacagc	A	C	ENST00000342537 // intron // 0 // — // — // —	-	q32.33
SNP_A-1782397	ggcacaaaacaataqc[C/T]ccaatccaactgcatt	C	T	ENST00000342537 // intron // 0 // — // — // —	-	q32.33
SNP_A-2181959	cagagctggccagaca[C/T]atcgttggaggaaga	C	T	NM_138790 // upstream // 9184 // Hs.407101 // C14orf175 // 122618 // Homo sapiens hypothetical protein BC015003 (LOC122618), mRNA. /// ENST00000251181 // downstream // 18927 // — // — // — /// ENST00000299538 // upstream // 9184 // — // —	C14orf175	C14orf175, Homo sapiens hypothetical protein BC015003 (LOC122618), q32.33
SNP_A-1864462	tccagaaaatgacatc[A/G]cctgaggtataaccag	A	G	J00231 // intron // 0 // Hs.525646 // IGHG3 // 3502 // Human Ig gamma3 heavy chain disease OMM protein mRNA. /// X17115 // intron // 0 // Hs.525648 // IGHM // 3507 // Human mRNA for IgM heavy chain complete sequence. /// ENST00000300887 // intron // 0 //	IGHG3	IGHG3, Human Ig gamma3 heavy chain disease OMM protein q32.33
SNP_A-2257903	tgtacttatttgttga[C/T]aaacattgatactata	C	T	X17115 // intron // 0 // Hs.525648 // IGHM // 3507 // Human mRNA for IgM heavy chain complete sequence. /// ENST00000359542 // intron // 0 // — // — // — /// ENST00000321645 // intron // 0 // — // — // — /// ENST00000359196 // in	IGHM	IGHM, Human for IgM heavy chain complete sequence. q32.33
SNP_A-2257905	agtaatgtggactccg[A/G]gctctgacaatttgta	A	G	X17115 // intron // 0 // Hs.525648 // IGHM // 3507 // Human mRNA for IgM heavy chain complete sequence. /// ENST00000359542 // intron // 0 // — // — // — /// ENST00000321645 // intron // 0 // — // — // — /// ENST00000359196 // in	IGHM	IGHM, Human for IgM heavy chain complete sequence. q32.33
SNP_A-2263762	gaacctgtaaaaatca[C/T]ggaaatacaagtgctg	C	T	X17115 // intron // 0 // Hs.525648 // IGHM // 3507 // Human mRNA for IgM heavy chain complete sequence. /// ENST00000359542 // intron // 0 // — // — // — /// ENST00000321645 // intron // 0 // — // — // — /// ENST00000359196 // in	IGHM	IGHM, Human for IgM heavy chain complete sequence. q32.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123278	agtgtagagtttcaga[C/G]accaggccattcactt	C	G	ENST00000334963 // upstream // 137088 // --- // --- // --- /// ENST00000324413 // downstream // 171194 // --- // --- // --- // ---	-	q11.2
SNP_A-2240618	ctgaccttgactgcag[C/T]agggttttatgagtgg	C	T	ENST00000334963 // upstream // 271069 // --- // --- // --- /// ENST00000324413 // downstream // 37213 // --- // --- // --- // ---	-	q11.2
SNP_A-2004012	ctcttcaccaatgatat[C/T]gatcttatgcctagaa	C	T	NM_207355 // intron // 0 // Hs.449801 // POTE15 // 339010 // Homo sapiens protein expressed in prostate, ovary, testis, and placenta 15 (POTE15), mRNA. /// ENST00000327822 // intron // 0 // --- // --- // --- // ---	POTE15	POTE15, Homo sapiens protein expressed in prostate, ovary, testis, and placenta 15 (POTE15), q11.2
SNP_A-2214629	cctagatttcaaagga[C/T]atgtggaaatgcctga	C	T	NM_014376 // intron // 0 // Hs.519702 // CYFIP2 // 26999 // Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), mRNA. /// NM_014608 // intron // 0 // Hs.26704 // CYFIP1 // 23191 // Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), mR	CYFIP2	CYFIP2, Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), q11.2
SNP_A-1786714	ggctgtgcatgggaa[C/T]ggcacttcgtctccag	C	T	NM_014376 // intron // 0 // Hs.519702 // CYFIP2 // 26999 // Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), mRNA. /// NM_014608 // intron // 0 // Hs.26704 // CYFIP1 // 23191 // Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), mR	CYFIP2	CYFIP2, Homo sapiens cytoplasmic FMR1 interacting protein 2 (CYFIP2), q11.2
SNP_A-2106958	agcctttcagtgaaaa[A/T]gaatgtttgggcaga	A	T	NM_182561 // downstream // 30396 // Hs.372394 // FLJ36144 // 283685 // Homo sapiens hypothetical protein FLJ36144 (FLJ36144), mRNA. /// ENST00000328919 // downstream // 208832 // --- // --- // --- // --- ENST00000358142 // downstream // 44274 // --- // ---	FLJ36144	FLJ36144, Homo sapiens hypothetical protein FLJ36144 (FLJ36144), q11.2
SNP_A-2069309	acacaaaaatgggaaa[A/T]atgtggagactgcctc	A	T	NM_005664 // downstream // 31253 // Hs.72964 // MKRN3 // 7681 // Homo sapiens makorin, ring finger protein, 3 (MKRN3), mRNA. /// NM_002487 // downstream // 86560 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// ENST000003	MKRN3	MKRN3, Homo sapiens makorin, ring finger protein, 3 (MKRN3), q11.2
SNP_A-2120351	agtcatctccttgaa[A/G]tgctgtatccagggtg	A	G	NM_005664 // downstream // 52360 // Hs.72964 // MKRN3 // 7681 // Homo sapiens makorin, ring finger protein, 3 (MKRN3), mRNA. /// NM_002487 // downstream // 65453 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// ENST000003	MKRN3	MKRN3, Homo sapiens makorin, ring finger protein, 3 (MKRN3), q11.2
SNP_A-2178626	cactctgaaaacacta[C/T]gtactgcacaatccaa	C	T	NM_002487 // upstream // 76924 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 911727 // Hs.451286 // C15orf2 // 23742 // Homo sapiens chromosome 15 open reading frame 2 (C15orf2), mRNA. /// ENST	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-1857420	tcactactaagcgacc[A/C]atactgacatgattgt	A	C	NM_002487 // upstream // 95168 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 893483 // Hs.451286 // C15orf2 // 23742 // Homo sapiens chromosome 15 open reading frame 2 (C15orf2), mRNA. /// ENST	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-1905167	tgggtgtgcatagggа[C/G]agaagggccaacctag	C	G	NM_002487 // upstream // 106609 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 882042 // Hs.451286 // C15orf2 // 23742 // Homo sapiens chromosome 15 open reading frame 2 (C15orf2), mRNA. /// ENS	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-2030354	aaagcattagctttgc[A/G]gagaaaaaatctggca	A	G	NM_002487 // upstream // 139245 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 849406 // Hs.451286 // C15orf2 // 23742 // Homo sapiens chromosome 15 open reading frame 2 (C15orf2), mRNA. /// ENS	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2216137	cctcccctatctgctg[C/G]acgtactgctccccac	C	G	NM_002487 // upstream // 209948 // Hs.50130 // NDN // 4692 // Homo sapiens necdin homolog (mouse) (NDN), mRNA. /// NM_018958 // upstream // 778703 // Hs.451286 // C15orf2 // 23742 // Homo sapiens chromosome 15 open reading frame 2 (C15orf2), mRNA. /// ENS	NDN	NDN, Homo sapiens necdin homolog (mouse) (NDN), q11.2
SNP_A-1820487	gtttatggagcataaa[C/T]gtgtcgaatgttacct	C	T	NM_018958 // downstream // 115843 // Hs.451286 // C15orf2 // 23742 // Homo sapiens chromosome 15 open reading frame 2 (C15orf2), mRNA. /// NM_003097 // upstream // 28466 // Hs.525700 // SNRPN // 6638 // Homo sapiens small nuclear ribonucleoprotein polypep	C15orf2	C15orf2, Homo sapiens chromosome 15 open reading frame 2 (C15orf2), q11.2
SNP_A-1805941	gtccgcgttttcacaa[C/G]atcatttcaatctgc	C	G	NM_000462 // upstream // 123462 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 123462 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2004033	attaagtgaaagaagc[A/G]caaatctgtctaacac	A	G	NM_000462 // upstream // 127880 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 127880 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2261968	caagaatttggtctca[G/T]gatagctctgacccac	G	T	NM_000462 // upstream // 134063 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 134063 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-1899161	tggaaagtccaaataa[C/G]gtccagaaaaatagtt	C	G	NM_000462 // upstream // 169139 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 169139 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2191895	catcaaccagcggcaa[C/T]tgtgaatgtaaacaaa	C	T	NM_000462 // upstream // 204062 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 204062 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-1802649	gtatgaagcacatata[C/T]gagacagcaaaggttc	C	T	NM_000462 // upstream // 314084 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 314084 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2004037	tgagcaggagatgtac[A/G]gagaccacgtagcaag	A	G	NM_000462 // upstream // 318964 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 318964 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2262261	atgggatgacagacc[C/T]ggaactgataacagga	C	T	NM_000462 // upstream // 484220 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 484220 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-1753381	tacccaccaaattatcttaaaaac[A/G]ctaatcctgaatgctca gggaggc	A	G	NM_000814 // downstream // 587628 // Hs.302352 // GABRB3 // 2562 // gamma-aminobutyric acid (GABA) A receptor, beta 3 /// NM_021912 // downstream // 587628 // Hs.302352 // GABRB3 // 2562 // gamma-aminobutyric acid (GABA) A receptor, beta 3 /// NM_024490	GABRB3	GABRB3, rs2175462, gamma-aminobutyric acid (GABA) A receptor, beta 3 q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1935033	ttctgagttaggtaga[A/C]cttcaatatggccaga	A	C	NM_000462 // upstream // 575819 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 575819 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v q12
SNP_A-2193934	catgaagaagagtata[C/T]ctgtaacaaaaacact	C	T	NM_000462 // upstream // 792933 // Hs.22543 // UBE3A // 7337 // Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v /// NM_130838 // upstream // 792933 // Hs.22543 // UBE3A // 73	UBE3A	UBE3A, Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), transcript v .q12
SNP_A-2258152	cttttaatggtttgaa[A/G]ttagagaacatacttc	A	G	NM_000814 // upstream // 10455 // Hs.302352 // GABRB3 // 2562 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, mRNA /// NM_021912 // upstream // 9747 // Hs.302352 // GABRB3 // 2562 // Homo sapiens gamma-am	GABRB3	GABRB3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 3 (GABRB3), transcript variant 1, q12
SNP_A-2263149	gtaacattgtgaggta[C/G]atcaacttgtcttca	C	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2259651	gaaaactggatcatgc[A/G]agcctcagacatagca	A	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2148671	atggtatttgagtctg[A/G]actgaaagaatcaaca	A	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-1755362	gagtgtcgcagaggagtttaatttg[C/T]aaaagtgcagtatgcaaatttgagg	C	T	NM_033223 // intron // 0 // Hs.104133 // GABRG3 // 2567 // gamma-aminobutyric acid (GABA) A receptor, gamma 3	GABRG3	GABRG3 , rs10519588, gamma-aminobutyric acid (GABA) A receptor, gamma 3,q12
SNP_A-2306670	gctgtcaaatgacaaa[C/T]gattactggcttttct	C	T	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-1938029	ttgaatttctttaggc[C/T]ctccggtatttcata	C	T	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2030332	aaagcatcattaaaaa[C/G]tgtatgcagacattgta	C	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2263223	acttaacaaacattga[C/T]ctcctatgatgtacca	C	T	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2004049	actaaatggtggtaa[C/T]tgtatttgacataac	C	T	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-1855736	tcaatcacacatctta[A/G]cgaagccaaagtctgt	A	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // — // — // — // —	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2166573	caaatggtgtcacaga[A/G]taagtgcaaagtaatg	A	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2004050	acaacacagtcctgtc[A/G]ctgaatgcctggtttg	A	G	NM_033223 // intron // 0 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// ENST00000333743 // intron // 0 // --- // --- // --- // ---	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2263533	gtgtatataatttttta[C/G]ctcctcagctatgatc	C	G	NM_033223 // downstream // 133922 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// NM_000275 // downstream // 88084 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism I	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2240124	ctgaagtctgagtgga[C/T]acttgtagtcaagcca	C	T	NM_033223 // downstream // 156476 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// NM_000275 // downstream // 65530 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism I	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2205501	ccagtgtcttgaacta[C/T]gcatctcttccaacct	C	T	NM_033223 // downstream // 197465 // Hs.156855 // GABRG3 // 2567 // Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), mRNA. /// NM_000275 // downstream // 24541 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism I	GABRG3	GABRG3, Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 3 (GABRG3), q12
SNP_A-2263685	gtggcagacagaaaaa[A/T]ttaaaactaatgaatg	A	T	NM_000275 // intron // 0 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA. /// ENST00000353809 // intron // 0 // --- // --- // --- // --- /// ENST00000354638 // intron // 0 // --- // -	OCA2	OCA2, Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), q13.1
SNP_A-2263687	gcacggctctgaaggc[A/G]agagtgtgaaaccagg	A	G	NM_000275 // intron // 0 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA. /// ENST00000353809 // intron // 0 // --- // --- // --- // --- /// ENST00000354638 // intron // 0 // --- // -	OCA2	OCA2, Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), q13.1
SNP_A-2242571	ctgcaggggtctcatc[C/T]gaacacttactccaag	C	T	NM_000275 // intron // 0 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA. /// ENST00000353809 // intron // 0 // --- // --- // --- // --- /// ENST00000354638 // intron // 0 // --- // -	OCA2	OCA2, Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), q13.1
SNP_A-2076436	acatttaaaagaatga[C/T]gggatgcctttgttta	C	T	NM_000275 // intron // 0 // Hs.130937 // OCA2 // 4948 // Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA. /// ENST00000353809 // intron // 0 // --- // --- // --- // --- /// ENST00000354638 // intron // 0 // --- // -	OCA2	OCA2, Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), q13.1
SNP_A-2085340	actcatgctttcatcc[A/G]agtgttcagtatcata	A	G	ENST00000329523 // upstream // 241016 // --- // --- // --- // --- /// ENST00000328146 // upstream // 22190 // --- // --- // --- // ---	-	q13.1
SNP_A-2246409	ctggttgatactccct[A/G]aatcacaggtcgcctt	A	G	NM_005503 // intron // 0 // Hs.525718 // APBA2 // 321 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2298122	gccatcctctattttg[C/T]acgctcagtcacccca	C	T	NM_005503 // intron // 0 // Hs.525718 // APBA2 // 321 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2106666	agcctctttcctcaaa[C/T]agcaagagtctagact	C	T	NM_005503 // intron // 0 // Hs.525718 // APBA2 // 321 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // ---	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2085780	actcctgccaccttg[A/G]agaaaattatcctgaa	A	G	NM_005503 // intron // 0 // Hs.525718 // APBA2 // 321 // Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), mRNA. /// ENST00000219865 // intron // 0 // --- // --- // --- // --	APBA2	APBA2, Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like) (APBA2), q13.1
SNP_A-2233356	ctcaggttcattagc[A/C]aatcaaaaatgcacag	A	C	AB011146 // intron // 0 // Hs.383564 // KIAA0574 // 23359 // Homo sapiens mRNA for KIAA0574 protein, partial cds. /// ENST00000261275 // intron // 0 // --- // --- // --	KIAA0574	KIAA0574, Homo sapiens for KIAA0574 protein, partial cds., q13.1
SNP_A-2196563	cattaaaagttgctaa[A/C]atcacagagaacacca	A	C	NM_138704 // upstream // 27892 // Hs.94011 // NDNL2 // 56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 27892 // --- // --- // --- // ENST00000327892 // upstream // 314973 // --- // --- // --- // --	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1
SNP_A-2179299	cactgtcgaggtcata[A/C]gaagtgaggaaagtct	A	C	NM_138704 // upstream // 60891 // Hs.94011 // NDNL2 // 56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 60891 // --- // --- // --- // ENST00000327892 // upstream // 281974 // --- // --- // --- // --	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1
SNP_A-1885751	tgacagcctgtccac[A/T]cgctctgtctccacc	A	T	NM_138704 // upstream // 114735 // Hs.94011 // NDNL2 // 56160 // Homo sapiens necdin-like 2 (NDNL2), mRNA. /// ENST00000332303 // upstream // 114735 // --- // --- // --- // ENST00000327892 // upstream // 228130 // --- // --- // --- // --	NDNL2	NDNL2, Homo sapiens necdin-like 2 (NDNL2), q13.1
SNP_A-2264617	agtagtagtaaaagca[A/G]agcacctgtgtattat	A	G	NM_175610 // intron // 0 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // intron // 0 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.1
SNP_A-1858352	tcagacagatgctggt[A/G]aacaggaaatgaacta	A	G	NM_003257 // intron // 0 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 1, mRNA. /// ENST00000356107 // intron // 0 // --- // --- // --	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 1, q13.1
SNP_A-2264770	ctagaagatgtttcaa[C/T]gatcggataactagca	C	T	NM_175610 // upstream // 142533 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // upstream // 98956 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction pro	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.1
SNP_A-2243630	ctgctccatttagtta[G/T]agctggctttagcaag	G	T	NM_175610 // upstream // 216757 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // upstream // 173180 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction pr	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.2
SNP_A-2286695	gatggattgggtgac[C/T]attttagaaaggacc	C	T	NM_175610 // upstream // 220132 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // upstream // 176555 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction pr	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.2
SNP_A-2173887	cacacagctaataaaa[A/G]tcactgccaaaatcca	A	G	NM_175610 // upstream // 259034 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, mRNA. /// NM_003257 // upstream // 215457 // Hs.510833 // TJP1 // 7082 // Homo sapiens tight junction pr	TJP1	TJP1, Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1), transcript variant 2, q13.2
SNP_A-2250987	ctatgtgaatgctca[C/T]caaaggataaacaatt	C	T	ENST00000220192 // intron // 0 // --- // --- // --	-	q13.2
SNP_A-1918456	ttaaatagtgaattgc[C/T]agaggaaatactataaa	C	T	ENST00000220192 // intron // 0 // --- // --- // --	-	q13.2
SNP_A-1645424	tggagctgacgcttcctcaatcata[C/G]ggtgaaccgtcccaggg gtagctggg	C	G	NM_002420 // intron // 0 // Hs.155942 // TRPM1 // 4308 // transient receptor potential cation channel, subfamily M, member 1	TRPM1	TRPM1 , rs10519727, transient receptor potential cation channel, subfamily M, member 1 q13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2255988	ctttaagtatgcaaag[C/T]cgctgcatcaagtcaa	C	T	NM_002420 // intron // 0 // Hs.155942 // TRPM1 // 4308 // Homo sapiens transient receptor potential cation channel, subfamily M, member 1 (TRPM1), mRNA. /// ENST00000220192 // intron // 0 // -- // -- // -- /// ENST00000256552 // intron // 0 // -	TRPM1	TRPM1, Homo sapiens transient receptor potential cation channel, subfamily M, member 1 (TRPM1), q13.3
SNP_A-1902927	tggctgagatgccgac[C/T]gcagcgatgagctcgc	C	T	NM_015995 // intron // 0 // Hs.525752 // KLF13 // 51621 // Homo sapiens Kruppel-like factor 13 (KLF13), mRNA. /// ENST00000220192 // intron // 0 // -- // -- // -- /// ENST00000307145 // intron // 0 // -- // -- // --	KLF13	KLF13, Homo sapiens Kruppel-like factor 13 (KLF13), q13.3
SNP_A-2265947	atttgcatttcaggaa[C/T]gtgcaggccgggagga	C	T	NM_130901 // upstream // 140340 // Hs.355236 // C15orf16 // 161725 // Homo sapiens chromosome 15 open reading frame 16 (C15orf16), mRNA. /// ENST00000307050 // upstream // 140340 // -- // -- // -- /// ENST00000323993 // upstream // 179701 // --	C15orf16	C15orf16, Homo sapiens chromosome 15 open reading frame 16 (C15orf16), q13.3
SNP_A-2266023	ttctgggacagccat[G/T]aaggacagtagtgaag	G	T	NM_130901 // upstream // 281910 // Hs.355236 // C15orf16 // 161725 // Homo sapiens chromosome 15 open reading frame 16 (C15orf16), mRNA. /// ENST00000307050 // upstream // 281910 // -- // -- // -- /// ENST00000323993 // upstream // 38131 // --	C15orf16	C15orf16, Homo sapiens chromosome 15 open reading frame 16 (C15orf16), q13.3
SNP_A-2297273	gccaccgtgcaggccd[A/G]aaagtctttattaat	A	G	NM_000746 // intron // 0 // Hs.511772 // CHRNA7 // 1139 // Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 7 (CHRNA7), mRNA. /// NM_148911 // intron // 0 // Hs.510853 // CHRFAM7A // 89832 // Homo sapiens CHRNA7 (cholinergic receptor, nicot	CHRNA7	CHRNA7, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 7 (CHRNA7), q13.3
SNP_A-2309962	ggaaatgaagaacctd[A/G]aaatgagtggcca	A	G	NM_000746 // intron // 0 // Hs.511772 // CHRNA7 // 1139 // Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 7 (CHRNA7), mRNA. /// NM_148911 // intron // 0 // Hs.510853 // CHRFAM7A // 89832 // Homo sapiens CHRNA7 (cholinergic receptor, nicot	CHRNA7	CHRNA7, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 7 (CHRNA7), q13.3
SNP_A-2116124	aggtaaccaggagaca[C/T]cactgtaaattgaaat	C	T	NM_013372 // downstream // 16589 // Hs.40098 // GREM1 // 26585 // Homo sapiens gremlin 1 homolog, cysteine knot superfamily (Xenopus laevis) (GREM1), mRNA. /// ENST00000300177 // downstream // 16589 // -- // -- // -- /// ENST00000322805 // downs	GREM1	GREM1, Homo sapiens gremlin 1 homolog, cysteine knot superfamily (Xenopus laevis) (GREM1), q13.3
SNP_A-1909244	tgtatgccactgagct[A/G]aatgttgggacaaat	A	G	ENST00000334528 // intron // 0 // -- // -- // -- /// ENST00000320930 // intron // 0 // -- // -- // -- /// ENST00000329131 // intron // 0 // -- // -- // --	-	q13.3
SNP_A-1689194	agcctgggaagcctgaccacaaaccd[A/G]gcatctccaaggca tgaataaattag	A	G	NM_001036 // upstream // 156027 // Hs.427717 // RYR3 // 6263 // ryanodine receptor 3 /// NM_013372 // downstream // 420284 // Hs.40098 // CKTSF1B1 // 26585 // cysteine knot superfamily 1, BMP antagonist 1	RYR3	RYR3 , rs1399079, ryanodine receptor 3 ,q13.3
SNP_A-2104915	agcatattgtatcat[C/G]acaaaagatttgcagc	C	G	ENST00000300172 // upstream // 6346 // -- // -- // -- // -- /// ENST00000355802 // upstream // 58726 // -- // -- // -- // -- /// ENST00000358682 // upstream // 58742 // -- // -- // -- // --	-	q13.3
SNP_A-1935514	ttctgggcactccga[C/T]aaggtgcatggaagg	C	T	ENST00000355802 // intron // 0 // -- // -- // -- // -- /// ENST00000358682 // intron // 0 // -- // -- // --	-	q14
SNP_A-2267274	ttaacttgttagggcc[C/T]attgtctacgtctgtc	C	T	ENST00000355802 // intron // 0 // -- // -- // -- /// ENST00000358682 // intron // 0 // -- // -- // --	-	q14
SNP_A-2032190	aaagtggttgctacta[A/G]ggaataacagcagctg	A	G	ENST00000355802 // intron // 0 // -- // -- // -- /// ENST00000358682 // intron // 0 // -- // -- // --	-	q14
SNP_A-2286670	gatggatgaataggaa[C/T]gcaaaaaggtggcttt	C	T	ENST00000355802 // intron // 0 // -- // -- // -- /// ENST00000358682 // intron // 0 // -- // -- // --	-	q14
SNP_A-2144300	atgagtgttctggaaa[C/G]atcatccaagcatgag	C	G	ENST00000355802 // intron // 0 // -- // -- // -- /// ENST00000358682 // intron // 0 // -- // -- // --	-	q14
SNP_A-1785734	ggctctctataaaca[C/T]gtgcatgcagaaagac	C	T	ENST00000355802 // intron // 0 // -- // -- // -- /// ENST00000358682 // intron // 0 // -- // -- // --	-	q14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2195431	catggatctgaaatc[A/G]cttttccaaatgcagc	A	G	ENST00000355802 // intron // 0 // — // — // — /// ENST00000358682 // intron // 0 // — // — // —	-	q14
SNP_A-1902834	tggctccggtatgaat[G/T]aactaatgtgcacata	G	T	ENST00000355802 // intron // 0 // — // — // — /// ENST00000358682 // intron // 0 // — // — // —	-	q14
SNP_A-2273969	gactgtgccttttgcaf[A/G]atttttctcaaacc	A	G	ENST00000355802 // intron // 0 // — // — // — /// ENST00000358682 // intron // 0 // — // — // —	-	q14
SNP_A-2194309	catgagtttgcatcaa[A/C]taccgtctctgaaaa	A	C	ENST00000355802 // intron // 0 // — // — // — /// ENST00000358682 // intron // 0 // — // — // —	-	q14
SNP_A-1883674	tgaactgagaaaaaga[C/G]agtgctaacttctagg	C	G	ENST00000355802 // intron // 0 // — // — // — /// ENST00000358682 // intron // 0 // — // — // —	-	q14
SNP_A-2301399	gccttgtttcagtcc[C/G]aaccagagcagaagta	C	G	NM_152595 // downstream // 4179 // Hs.156317 // PGBD4 // 161779 // Homo sapiens piggyBac transposable element derived 4 (PGBD4), mRNA. /// NM_024713 // downstream // 32191 // Hs.510938 // C15orf29 // 79768 // Homo sapiens chromosome 15 open reading frame	PGBD4	PGBD4, Homo sapiens piggyBac transposable element derived 4 (PGBD4), q14
SNP_A-2191004	cataggcatgtttggc[C/T]ctacatttcactact	C	T	AF477977 // intron // 0 // Hs.4876 // SLC12A6 // 9990 // Homo sapiens K-Cl cotransporter KCC3 variant isoform mRNA, complete cds. /// NM_005135 // intron // 0 // Hs.4876 // SLC12A6 // 9990 // Homo sapiens solute carrier family 12 (potassium/chloride trans	SLC12A6	SLC12A6, Homo sapiens K-Cl cotransporter KCC3 variant isoform, complete cds., q14
SNP_A-1853240	tatttaaagaaaaaga[C/T]agccagacaaggctgg	C	T	AF477977 // intron // 0 // Hs.4876 // SLC12A6 // 9990 // Homo sapiens K-Cl cotransporter KCC3 variant isoform mRNA, complete cds. /// NM_005135 // intron // 0 // Hs.4876 // SLC12A6 // 9990 // Homo sapiens solute carrier family 12 (potassium/chloride trans	SLC12A6	SLC12A6, Homo sapiens K-Cl cotransporter KCC3 variant isoform, complete cds., q14
SNP_A-2064534	aattcctgcacacaga[A/G]gaaaggatcagtgaaa	A	G	NM_015003 // upstream // 291433 // Hs.182982 // GOLGIN-67 // 23015 // Homo sapiens golgin-67 (GOLGIN-67), transcript variant 1, mRNA. /// NM_181076 // upstream // 291433 // Hs.182982 // GOLGIN-67 // 23015 // Homo sapiens golgin-67 (GOLGIN-67), transcript	GOLGIN-67	GOLGIN-67, Homo sapiens golgin-67 (GOLGIN-67), transcript variant 1, q14
SNP_A-1648072	aactgcaggaagcacaatttagtca[C/G]aattagcaataaaaa aaataacact	C	G	AB011132 // downstream // 56612 // Hs.129952 // AQR // 9716 // likely ortholog of mouse aquarius /// NM_005159 // upstream // 4129 // - // - // - // -	AQR	AQR, rs475786, likely ortholog of mouse aquarius, q14
SNP_A-2143973	atgagcctaggccaga[C/T]atgatggctcatgcct	C	T	NM_015003 // upstream // 353811 // Hs.182982 // GOLGIN-67 // 23015 // Homo sapiens golgin-67 (GOLGIN-67), transcript variant 1, mRNA. /// NM_181076 // upstream // 353811 // Hs.182982 // GOLGIN-67 // 23015 // Homo sapiens golgin-67 (GOLGIN-67), transcript	GOLGIN-67	GOLGIN-67, Homo sapiens golgin-67 (GOLGIN-67), transcript variant 1, q14
SNP_A-1862955	tcattgcttggtggta[G/T]agcgaatggtgtgggg	G	T	NM_020660 // upstream // 7094 // Hs.283816 // CX36 // 57369 // Homo sapiens connexin-36 (CX36), mRNA. /// NM_005159 // downstream // 28649 // Hs.118127 // ACTC // 70 // Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA. /// NM_001100 // downstream //	CX36	CX36, Homo sapiens connexin-36 (CX36), q14
SNP_A-2161357	attgcaatcataaag[C/T]attggacatcagcta	C	T	NM_005159 // upstream // 31859 // Hs.118127 // ACTC // 70 // Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA. /// NM_001100 // upstream // 31859 // Hs.1288 // ACTA1 // 58 // Homo sapiens actin, alpha 1, skeletal muscle (ACTA1), mRNA. /// NM_014691	ACTC	ACTC, Homo sapiens actin, alpha, cardiac muscle (ACTC), q14
SNP_A-1944398	ttgtctatgtttcaca[G/T]tggaacagcaccatat	G	T	NM_080650 // upstream // 166241 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 310824 // — // — // — /// ENST00000256538 // upstream // 166241 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1939491	ttgattaaatggagta[A/G]gagccttctatctaat	A	G	NM_080650 // upstream // 366147 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 510730 // — // — // — /// ENST00000256538 // upstream // 366147 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2229550	ctaggtatatatcccc[C/T]caaattgaaagcaagg	C	T	NM_080650 // upstream // 371976 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 516559 // — // — // — /// ENST00000256538 // upstream // 371976 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2263977	gaactcaaataatctc[C/T]gacctgctaacagatg	C	T	NM_080650 // upstream // 381613 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 526196 // — // — // — /// ENST00000256538 // upstream // 381613 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2269829	gtttgttagtgctat[C/T]atcctcagtacatgga	C	T	NM_080650 // upstream // 465876 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 610459 // — // — // — /// ENST00000256538 // upstream // 465876 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-2066038	aatttgctactcaga[A/G]atgatggaacaacttt	A	G	NM_080650 // upstream // 612188 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 756771 // — // — // — /// ENST00000256538 // upstream // 612188 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-1861329	tcatcacagttggaaat[C/T]gtttaagccaaatcat	C	T	NM_080650 // upstream // 810956 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 955539 // — // — // — /// ENST00000256538 // upstream // 810956 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-1815509	gttaaaaagccaacta[G/T]ggtactatgctcagg	G	T	NM_080650 // upstream // 863588 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 1008171 // — // — // — /// ENST00000256538 // upstream // 863588 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-1723080	atcactacaatcttacattgtcaat[C/T]aaacatcaccaaacctat aatgcac	C	T	BC028192 // downstream // 306551 // Hs.367962 // - // 390575 // Similar to casein kinase 1, alpha 1 (LOC390575), mRNA /// NM_032499 // upstream // 87294 // Hs.48348 // HH114 // 84529 // hypothetical protein HH114 /// NM_080650 // upstream // 946405 // Hs	-	- , rs10518884, Similar to casein kinase 1, alpha 1 (LOC390575), mRNA ,q14
SNP_A-1827874	taagaaaatgagattt[A/T]aaaaacgtgagcagtt	A	T	NM_080650 // upstream // 881362 // Hs.107196 // MGC14798 // 89978 // Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA. /// ENST00000311061 // downstream // 1025945 // — // — // — /// ENST00000256538 // upstream // 881362 //	MGC14798	MGC14798, Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), q14
SNP_A-1940053	ttgcagctgtgggaac[A/G]attggccggcagcagg	A	G	NM_032499 // upstream // 74621 // Hs.546456 // HH114 // 84529 // Homo sapiens hypothetical protein HH114 (HH114), mRNA. /// ENST00000267752 // downstream // 44854 // — // — // — /// ENST00000338183 // upstream // 74621 // — // — // — //	HH114	HH114, Homo sapiens hypothetical protein HH114 (HH114), q14
SNP_A-1686326	gcattagaaattaagcctcaaagga[A/C]atacatataalaagtg atcacaga	A	C	NM_032499 // intron // 0 // Hs.48348 // HH114 // 84529 // hypothetical protein HH114	HH114	HH114 , rs2045014, hypothetical protein HH114,q14
SNP_A-1929713	ttcatatttctgcca[G/T]cattcattggtttaa	G	T	NM_032499 // intron // 0 // Hs.546456 // HH114 // 84529 // Homo sapiens hypothetical protein HH114 (HH114), mRNA. /// ENST00000338183 // intron // 0 // — // — // —	HH114	HH114, Homo sapiens hypothetical protein HH114 (HH114), q14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2131769	atagctcaagtatcaa[C/G]agttctaaagctaac	C	G	NM_032499 // downstream // 66829 // Hs.546456 // HH114 // 84529 // Homo sapiens hypothetical protein HH114 (HH114), mRNA. /// NM_170677 // downstream // 13956 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1	HH114	HH114, Homo sapiens hypothetical protein HH114 (HH114), q14
SNP_A-1646010	ccaatataaatttggctcatcttc[A/G]cattaatacatttgggttc aggtt	A	G	NM_002399 // intron // 0 // Hs.362805 // MEIS2 // 4212 // Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) /// NM_020149 // intron // 0 // Hs.362805 // MEIS2 // 4212 // Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse	MEIS2	MEIS2, rs10518924, Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse), q14
SNP_A-1886526	tgactagaagtccacа[C/G]gagtatgcaaggaaat	C	G	NM_170677 // intron // 0 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // intron // 0 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2145324	atgcactcttccttcaa[G/T]gccatttcctcacga	G	T	NM_170677 // intron // 0 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // intron // 0 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2270956	tgcagttcttaaaag[C/T]atcatgctctcttgc	C	T	NM_170677 // upstream // 102037 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 102037 // Hs.510989 // MEIS2 // 4212 // Hom	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-1816326	gttagaatcatcataa[A/G]ctgtttcctctaagt	A	G	NM_170677 // upstream // 154830 // Hs.510989 // MEIS2 // 4212 // Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, mRNA. /// NM_172315 // upstream // 154830 // Hs.510989 // MEIS2 // 4212 // Hom	MEIS2	MEIS2, Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), transcript variant a, q14
SNP_A-2284310	gatattgtatttagcc[A/G]aaaatgctgttctaa	A	G	NM_152453 // downstream // 160808 // Hs.179646 // MGC35118 // 145942 // Homo sapiens hypothetical protein MGC35118 (MGC35118), mRNA. /// NM_152594 // upstream // 140091 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containi	MGC35118	MGC35118, Homo sapiens hypothetical protein MGC35118 (MGC35118), q14
SNP_A-1731483	actaaaccctctgtgcctcaaacttа[C/T]gtgtgaaataacagcac tcacttat	C	T	NM_152594 // intron // 0 // Hs.132804 // SPRED1 // 161742 // sprouty-related, EVH1 domain containing 1	SPRED1	SPRED1, rs7179433, sprouty-related, EVH1 domain containing 1,q14
SNP_A-1681994	gaaccctgtagacttacagactcag[G/T]aaacataatactcttt aaaaaaaa	G	T	NM_152594 // intron // 0 // Hs.132804 // SPRED1 // 161742 // sprouty-related, EVH1 domain containing 1	SPRED1	SPRED1, rs1916151, sprouty-related, EVH1 domain containing 1,q14
SNP_A-1649030	ctactaaagtgcactgtttattcac[C/T]gagaaggcttttaaagga aagctac	C	T	NM_152594 // intron // 0 // Hs.132804 // SPRED1 // 161742 // sprouty-related, EVH1 domain containing 1	SPRED1	SPRED1, rs10520054, sprouty-related, EVH1 domain containing 1,q14
SNP_A-1649598	atactaaacttcttataaagttac[A/C]ataattagaagagtgtacat gcata	A	C	NM_152594 // intron // 0 // Hs.132804 // SPRED1 // 161742 // sprouty-related, EVH1 domain containing 1	SPRED1	SPRED1, rs13573382, sprouty-related, EVH1 domain containing 1,q14
SNP_A-1816870	gttatggtgtatct[A/G]aagacccgtgttatat	A	G	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2271664	ctgcagtataaaatca[C/T]ggaatctgctgctgtt	C	T	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-1898267	tgcttagagtctacttt[A/T]agagatcacagtgacag	A	T	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2271709	ctctgaatgatacaca[A/G]ctgagaaaagtctgt	A	G	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2234861	ctccatttccacatta[C/T]cttgtcactctaagt	C	T	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2187897	cagtatctacagttcc[C/T]atatccaataaaccc	C	T	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2265620	gaagctagataaataga[A/C]ccatggtgattcataa	A	C	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2092234	agaaagacaccaggga[A/T]gtacgggcagaggaaa	A	T	NM_152594 // intron // 0 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// ENST00000299084 // intron // 0 // — // — // —	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2151223	atgttaagcttccaag[A/T]aaacaaaaatcttgta	A	T	NM_152594 // downstream // 70406 // Hs.525781 // SPRED1 // 161742 // Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA. /// NM_173611 // upstream // 29708 // — // FLJ38426 // 283742 // Homo sapiens hypothetical protein FLJ38426 (FLJ3	SPRED1	SPRED1, Homo sapiens sprouty-related, EVH1 domain containing 1 (SPRED1), q14
SNP_A-2294680	gcagtgggagaaaaca[A/G]agaggaattggtaact	A	G	NM_207444 // downstream // 308 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 308 // — // — // — /// ENST00000358555 // downstream // 336353 // — // — // — // -	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-1859554	tcaggatctaactcaa[A/G]tctggcttctatgact	A	G	NM_207444 // downstream // 11170 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 11170 // — // — // — /// ENST00000358555 // downstream // 325491 // — // — // —	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2048127	aagcacagagactgca[C/G]ggtacaaaggagcaag	C	G	NM_207444 // downstream // 11570 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 11570 // — // — // — /// ENST00000358555 // downstream // 325091 // — // — // —	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2235577	ctcctaccacttcagg[A/G]atgttacttgtagttg	A	G	NM_207444 // downstream // 37327 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 37327 // — // — // — /// ENST00000358555 // downstream // 299334 // — // — // —	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2163672	caaaaatagattgaaa[G/T]gtagaggctttaaat	G	T	NM_207444 // downstream // 44894 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 44894 // — // — // — /// ENST00000358555 // downstream // 291767 // — // — // —	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2285773	gatgactaagtggcta[A/G]aatgtcactcagagtc	A	G	NM_207444 // downstream // 45783 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 45783 // — // — // — /// ENST00000358555 // downstream // 290878 // — // — // —	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2139398	atccgttggaaaaca[A/G]tccttccttcagttg	A	G	NM_207444 // downstream // 167110 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 167110 // — // — // — /// ENST00000358555 // downstream // 169551 // — // — // -	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2136678	atcactgagtcagaaa[C/T]tggtgctgaagactc	C	T	NM_207444 // downstream // 220903 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 220903 // — // — // — /// ENST00000358555 // downstream // 115758 // — // — // –	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2110236	aggaagtgtagtagag[C/T]caaagtcgaagtggt	C	T	NM_207444 // downstream // 236232 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 236232 // — // — // — /// ENST00000358555 // downstream // 100429 // — // — // –	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-1904850	tggggttgtgctagcat[C/T]cgggcagtgagcagag	C	T	NM_207444 // downstream // 242066 // Hs.448785 // FLJ35695 // 400359 // Homo sapiens FLJ35695 protein (FLJ35695), mRNA. /// ENST00000318792 // downstream // 242066 // — // — // — /// ENST00000358555 // downstream // 94595 // — // — // –	FLJ35695	FLJ35695, Homo sapiens FLJ35695 protein (FLJ35695), q14
SNP_A-2079217	acccatagatgtagaa[A/G]tgttgaacgtacaaca	A	G	NM_207445 // upstream // 177471 // Hs.376109 // FLJ39531 // 400360 // Homo sapiens FLJ39531 protein (FLJ39531), mRNA. /// ENST00000358555 // upstream // 35630 // — // — // — /// ENST00000318578 // upstream // 177471 // — // — // — // –	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ39531), q14
SNP_A-2172571	caattctgcttttcct[C/T]agatgcaaacatttta	C	T	NM_207445 // upstream // 164303 // Hs.376109 // FLJ39531 // 400360 // Homo sapiens FLJ39531 protein (FLJ39531), mRNA. /// ENST00000358555 // upstream // 48798 // — // — // — /// ENST00000318578 // upstream // 164303 // — // — // — // –	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ39531), q14
SNP_A-2043097	aactgatatgctaaga[A/C]tatgagtactaatgtt	A	C	NM_207445 // upstream // 16202 // Hs.376109 // FLJ39531 // 400360 // Homo sapiens FLJ39531 protein (FLJ39531), mRNA. /// ENST00000358555 // upstream // 196899 // — // — // — /// ENST00000318578 // upstream // 16202 // — // — // — // –	FLJ39531	FLJ39531, Homo sapiens FLJ39531 protein (FLJ39531), q14
SNP_A-2058366	aatcacagaaatgctc[A/G]ccttatatataaact	A	G	NM_130468 // downstream // 9 // Hs.442449 // D4ST1 // 113189 // Homo sapiens dermatan 4 sulfotransferase 1 (D4ST1), mRNA. /// NM_052849 // downstream // 58180 // Hs.146520 // MGC20481 // 90416 // Homo sapiens hypothetical protein MGC20481 (MGC20481), mRNA	D4ST1	D4ST1, Homo sapiens dermatan 4 sulfotransferase 1 (D4ST1), q15.1
SNP_A-1642269	gatagtagaagtcccatggagaaga[A/G]atcaaatgatgaga ctgaaaggtt	A	G	NM_020380 // intron // 0 // Hs.438982 // AF15Q14 // 57082 // AF15q14 protein /// NM_144508 // intron // 0 // Hs.438982 // AF15Q14 // 57082 // AF15q14 protein /// NM_170589 // intron // 0 // Hs.438982 // AF15Q14 // 57082 // AF15q14 protein	AF15Q14	AF15Q14, rs10518697, AF15q14 protein, q15.1
SNP_A-2300137	gcctcatttataaaac[A/G]ctggtacggccaaact	A	G	NM_020380 // intron // 0 // Hs.181855 // AF15Q14 // 57082 // Homo sapiens AF15q14 protein (AF15Q14), mRNA. /// NM_144508 // intron // 0 // Hs.181855 // AF15Q14 // 57082 // Homo sapiens AF15q14 protein (AF15Q14), mRNA. /// NM_170589 // intron // 0 // Hs.18	AF15Q14	AF15Q14, Homo sapiens AF15q14 protein (AF15Q14), q15.1
SNP_A-1864449	tccacttttcctaaattc[A/G]gcgcactctaggtacg	A	G	NM_152596 // intron // 0 // Hs.307999 // MGC33637 // 161829 // Homo sapiens hypothetical protein MGC33637 (MGC33637), mRNA. /// ENST00000314982 // intron // 0 // — // — // — // —	MGC33637	MGC33637, Homo sapiens hypothetical protein MGC33637 (MGC33637), q15.1
SNP_A-1659606	tcagaacccatactctgcgggcctt[A/G]aaatggaaaatctctcc tctagaca	A	G	NM_007280 // intron // 0 // Hs.191583 // OIP5 // 11339 // Opa-interacting protein 5	OIP5	OIP5, rs10518718, Opa-interacting protein 5, q15.1
SNP_A-2024482	aaaaggactatacgcc[A/T]aaagagctgcaagaac	A	T	NM_016013 // upstream // 10399 // Hs.106529 // NDUFAF1 // 51103 // Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (NDUFAF1), mRNA. /// NM_015138 // upstream // 4297 // Hs.511096 // KIAA0252 // 23168 // Homo sapiens KIAA	NDUFAF1	NDUFAF1, Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1 (NDUFAF1), q15.1
SNP_A-2201137	ccaagtgacttctaca[C/T]cagggaattgtattga	C	T	NM_015138 // intron // 0 // Hs.511096 // KIAA0252 // 23168 // Homo sapiens KIAA0252 (KIAA0252), mRNA. /// ENST00000260373 // intron // 0 // — // — // —	KIAA0252	KIAA0252, Homo sapiens KIAA0252 (KIAA0252), q15.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1812134	gtggagaggttgctta[C/T]ctgcaagtgcgtccaa	C	T	NM_015138 // downstream // 1514 // Hs.511096 // KIAA0252 // 23168 // Homo sapiens KIAA0252 (KIAA0252), mRNA. /// NM_002220 // upstream // 9381 // Hs.2722 // ITPKA // 3706 // Homo sapiens inositol 1,4,5-trisphosphate 3-kinase A (ITPKA), mRNA. /// ENST00000	KIAA0252	KIAA0252, Homo sapiens KIAA0252 (KIAA0252), q15.1
SNP_A-1673030	atgcatattgctggaggaagtaata[A/C]caatgatgcaaatttgc ctggaaac	A	C	BC038449 // upstream // 16909 // Hs.435961 // MGA // 23269 // MAX gene associated /// NM_006293 // downstream // 25329 // Hs.381282 // TYRO3 // 7301 // TYRO3 protein tyrosine kinase	MGA	MGA , rs4072386, MAX gene associated ,q15.1
SNP_A-1877560	tctggccttttcacta[A/G]aatacaacaaagatta	A	G	NM_006293 // downstream // 23049 // Hs.381282 // TYRO3 // 7301 // Homo sapiens TYRO3 protein tyrosine kinase (TYRO3), mRNA. /// ENST00000263798 // downstream // 23049 // — // — // — // — /// ENST00000219905 // upstream // 58069 // — // — // —	TYRO3	TYRO3, Homo sapiens TYRO3 protein tyrosine kinase (TYRO3), q15.1
SNP_A-1871385	tctaaatgcttgatac[A/G]ggagcagaaattattt	A	G	ENST00000219905 // intron // 0 // — // — // — // —	-	q15.1
SNP_A-2274082	gtttgaataaacatag[A/C]cccaatttcaaacctt	A	C	ENST00000360498 // intron // 0 // — // — // — // — /// ENST00000260357 // intron // 0 // — // — // — // —	-	q15.1
SNP_A-2305760	gctgcctctcctcttc[A/G]cgttttccccacagcg	A	G	NM_005090 // intron // 0 // Hs.546320 // PLA2G4B // 8681 // Homo sapiens phospholipase A2, group IVB (cytosolic) (PLA2G4B), mRNA. /// ENST00000335032 // intron // 0 // — // — // — // — /// ENST00000342159 // intron // 0 // — // — // — // —	PLA2G4B	PLA2G4B, Homo sapiens phospholipase A2, group IVB (cytosolic) (PLA2G4B), q15.1
SNP_A-2125066	agttgctgagggctac[A/G]aggcagatactacagg	A	G	NM_198442 // upstream // 36539 // Hs.148725 // FLJ45651 // 123745 // Homo sapiens FLJ45651 protein (FLJ45651), mRNA. /// NM_178034 // downstream // 33622 // Hs.380225 // PLA2G4D // 283748 // Homo sapiens phospholipase A2, group IVD (cytosolic) (PLA2G4D),	FLJ45651	FLJ45651, Homo sapiens FLJ45651 protein (FLJ45651), q15.1
SNP_A-1833630	tacaggacttgggaca[C/G]actggatatggaagga	C	G	NM_198442 // upstream // 48517 // Hs.148725 // FLJ45651 // 123745 // Homo sapiens FLJ45651 protein (FLJ45651), mRNA. /// NM_178034 // downstream // 21644 // Hs.380225 // PLA2G4D // 283748 // Homo sapiens phospholipase A2, group IVD (cytosolic) (PLA2G4D),	FLJ45651	FLJ45651, Homo sapiens FLJ45651 protein (FLJ45651), q15.1
SNP_A-2274656	ccctcgacactggagc[C/G]aaatgtcaattgagaa	C	G	NM_173090 // intron // 0 // Hs.143261 // CAPN3 // 825 // Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 6, mRNA. /// NM_173089 // intron // 0 // Hs.143261 // CAPN3 // 825 // Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 5, mRNA. ///	CAPN3	CAPN3, Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 6, q15.1
SNP_A-2147455	atggagtgggtatgaa[A/G]agataaagaactgaag	A	G	NM_173090 // intron // 0 // Hs.143261 // CAPN3 // 825 // Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 6, mRNA. /// NM_173089 // intron // 0 // Hs.143261 // CAPN3 // 825 // Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 5, mRNA. ///	CAPN3	CAPN3, Homo sapiens calpain 3, (p94) (CAPN3), transcript variant 6, q15.1
SNP_A-1838249	tagaagaccacagtca[A/G]atattggtgagtgcca	A	G	NM_022473 // upstream // 35407 // Hs.511143 // ZFP106 // 64397 // Homo sapiens SH3-domain binding protein 3 (SH3BP3), mRNA. /// NM_130798 // upstream // 2698 // Hs.511149 // SNAP23 // 8773 // Homo sapiens synaptosomal-associated protein, 23kDa (SNAP23), t	ZFP106	ZFP106, Homo sapiens SH3-domain binding protein 3 (SH3BP3), q15.1
SNP_A-2175473	cacatcctggatgttg[A/G]ataatgtgataaggag	A	G	NM_173500 // intron // 0 // Hs.511837 // TTBK2 // 146057 // Homo sapiens tau tubulin kinase 2 (TTBK2), mRNA. /// ENST00000263802 // intron // 0 // — // — // — // — /// ENST00000267890 // intron // 0 // — // — // — // —	TTBK2	TTBK2, Homo sapiens tau tubulin kinase 2 (TTBK2), q15.2
SNP_A-1807239	gtctctgaaaatgcca[C/T]gctcacagttccctaa	C	T	NM_174916 // intron // 0 // Hs.145209 // UBR1 // 197131 // Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), mRNA. /// ENST00000326693 // intron // 0 // — // — // — // — /// ENST00000290650 // intron // 0 // — // — // —	UBR1	UBR1, Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), q15.2
SNP_A-1895119	tgcccattattttggg[A/G]acaaattggaaaatac	A	G	NM_174916 // intron // 0 // Hs.145209 // UBR1 // 197131 // Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), mRNA. /// ENST00000326693 // intron // 0 // — // — // — // — /// ENST00000290650 // intron // 0 // — // — // —	UBR1	UBR1, Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), q15.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2274843	aaaatacaagtgttgc[C/T]aagtgcaaaaaacaga	C	T	NM_174916 // intron // 0 // Hs.145209 // UBR1 // 197131 // Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), mRNA. /// ENST00000326693 // intron // 0 // — // — // — /// ENST00000290650 // intron // 0 // — // — // —	UBR1	UBR1, Homo sapiens ubiquitin protein ligase E3 component n-recognin 1 (UBR1), q15.2
SNP_A-2081101	acctgagcttcaaacc[A/G]gcaagttttaattaa	A	G	ENST00000326693 // intron // 0 // — // — // — // —	-	q15.2
SNP_A-1908419	tgtagaacaaatactgc[C/T]gatttatcacaccaga	C	T	NM_004245 // intron // 0 // Hs.129719 // TGM5 // 9333 // Homo sapiens transglutaminase 5 (TGM5), transcript variant 2, mRNA. /// NM_201631 // intron // 0 // Hs.129719 // TGM5 // 9333 // Homo sapiens transglutaminase 5 (TGM5), transcript variant 1, mRNA. /	TGM5	TGM5, Homo sapiens transglutaminase 5 (TGM5), transcript variant 2, q15.2
SNP_A-1660101	gtatcagaatttagaacaaaaact[C/T]caaaagtgaaatggag aagcaagaa	C	T	NM_014793 // downstream // 2483 // Hs.200596 // LCMT2 // 9836 // leucine carboxyl methyltransferase 2 /// NM_052955 // upstream // 23040 // Hs.164661 // TGM7 // 116179 // transglutaminase 7	LCMT2	LCMT2, rs956391, leucine carboxyl methyltransferase 2, q15.3
SNP_A-1699303	tgccagggccccccatggtcatgca[A/G]atatgagactttcccttа gatccctc	A	G	NM_002373 // intron // 0 // Hs.194301 // MAP1A // 4130 // microtubule-associated protein 1A	MAP1A	MAP1A, rs694985, microtubule-associated protein 1A,q15.3
SNP_A-1836923	tactgctgggttttaat[A/G]tctgcctctgcccttt	A	G	NM_014659 // intron // 0 // Hs.156814 // KIAA0377 // 9677 // Homo sapiens KIAA0377 gene product (KIAA0377), mRNA. /// NM_153700 // intron // 0 // Hs.253260 // STRC // 161497 // Homo sapiens stereocilin (STRC), mRNA. /// ENST00000348806 // intron // 0 // -	KIAA0377	KIAA0377, Homo sapiens KIAA0377 gene product (KIAA0377), q15.3
SNP_A-1670271	gaaccatgccaccgggggatatctta[C/T]gtgctgaacatgggggg gaaactctt	C	T	BC001926 // intron // 0 // Hs.153998 // CKMT1 // 1159 // creatine kinase, mitochondrial 1 (ubiquitous)	CKMT1	CKMT1, rs2467426, creatine kinase, mitochondrial 1 (ubiquitous),q15.3
SNP_A-2275229	tgctgttgtacagcttgtaagagca[A/G]gctaacaagagggcc agtcttatt	A	G	NM_014659 // intron // 0 // Hs.156814 // KIAA0377 // 9677 // Homo sapiens KIAA0377 gene product (KIAA0377), mRNA. /// NM_172096 // intron // 0 // Hs.389181 // CATSPER2 // 117155 // Homo sapiens cation channel, sperm associated 2 (CATSPER2), transcript var	KIAA0377	KIAA0377, Homo sapiens KIAA0377 gene product (KIAA0377), q15.3
SNP_A-1720995	aaaaccaatggagtta[C/T]gctatacttattcta	C	T	NM_032892 // intron // 0 // Hs.161134 // MGC14161 // 84978 // hypothetical protein MGC14161	MGC14161	MGC14161, rs2412822, hypothetical protein MGC14161,q15.3
SNP_A-2088192	actggtaactggtaaaa[C/T]gggaacttgagggaac	C	T	NM_032892 // intron // 0 // Hs.368399 // MGC14161 // 84978 // Homo sapiens hypothetical protein MGC14161 (MGC14161), mRNA. /// ENST00000351529 // intron // 0 // — // — // — /// ENST00000340861 // intron // 0 // — // — // —	MGC14161	MGC14161, Homo sapiens hypothetical protein MGC14161 (MGC14161), q15.3
SNP_A-2134468	atatggtaagtgctat[A/G]agtcccccaggcact	A	G	NM_032892 // intron // 0 // Hs.368399 // MGC14161 // 84978 // Homo sapiens hypothetical protein MGC14161 (MGC14161), mRNA. /// ENST00000351529 // intron // 0 // — // — // — /// ENST00000340861 // intron // 0 // — // — // —	MGC14161	MGC14161, Homo sapiens hypothetical protein MGC14161 (MGC14161), q15.3
SNP_A-1780940	ggatgactgacaatac[A/G]gacactccacttatt	A	G	NM_032892 // intron // 0 // Hs.368399 // MGC14161 // 84978 // Homo sapiens hypothetical protein MGC14161 (MGC14161), mRNA. /// ENST00000351529 // intron // 0 // — // — // — /// ENST00000340861 // intron // 0 // — // — // —	MGC14161	MGC14161, Homo sapiens hypothetical protein MGC14161 (MGC14161), q15.3
SNP_A-2275472	gcctcctagaagaaaa[C/T]gaaactctagggcact	C	T	ENST00000333616 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-1957983	ttttcacaattcttgta[A/G]cgagacaagaactatg	A	G	NM_182985 // intron // 0 // Hs.169810 // RNF36 // 140691 // Homo sapiens ring finger protein 36 (RNF36), transcript variant a, mRNA. /// NM_080745 // intron // 0 // Hs.169810 // RNF36 // 140691 // Homo sapiens ring finger protein 36 (RNF36), transcript va	RNF36	RNF36, Homo sapiens ring finger protein 36 (RNF36), transcript variant a, q21.1
SNP_A-1886386	tgaccttgaccaatca[A/G]agaaaagcagccctcaa	A	G	NM_014080 // intron // 0 // Hs.71377 // DUOX2 // 50506 // Homo sapiens dual oxidase 2 (DUOX2), mRNA. /// ENST00000267837 // intron // 0 // — // — // — // —	DUOX2	DUOX2, Homo sapiens dual oxidase 2 (DUOX2), q21.1
SNP_A-2244743	ctggataccccgttaaac[C/T]agccagggtctggctc	C	T	NM_144565 // intron // 0 // Hs.356664 // NIP // 90527 // Homo sapiens homolog of Drosophila Numb-interacting protein (NIP), mRNA. /// ENST00000322839 // intron // 0 // — // — // — // — /// ENST00000267803 // intron // 0 // — // — // — // —	NIP	NIP, Homo sapiens homolog of Drosophila Numb-interacting protein (NIP), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207982	cccaaccctacagcaa[A/G]tgtggtggttccgaag	A	G	ENST00000290894 // intron // 0 // — // — // — // — /// ENST00000318390 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-2034939	aaatgatagataatga[A/G]caagctacaactaagt	A	G	NM_021199 // intron // 0 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// ENST00000260324 // intron // 0 // — // — // — // —	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2143454	atgaccttcttactaa[C/T]tgaaattctgactacc	C	T	NM_021199 // intron // 0 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// ENST00000260324 // intron // 0 // — // — // — // —	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2276872	acgcaaaaacagctaa[C/T]ggccaggtgctgcatt	C	T	NM_021199 // downstream // 954931 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 1072277 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2276947	ctatgaagaccgtcta[C/T]acacactgaaggaact	C	T	NM_021199 // downstream // 1049145 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 978063 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1690437	tagataaattattggcaagactaac[A/C]agaaataatatgcaaat taacaaaa	A	C	NM_020858 // upstream // 893590 // Hs.191098 // SEMA6D // 80031 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D /// NM_021199 // downstream // 1133618 // Hs.435468 // SQRDL // 58472 // sulfide quinone reductase-like (ye	SEMA6D	SEMA6D , rs10519083, sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D ,q21.1
SNP_A-2277288	tgaaaattgccgtgac[A/G]ctttcttgcttcatgt	A	G	NM_021199 // downstream // 1464544 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 562664 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1857244	tcaccttcctctcatc[A/G]gaaaagagataacaag	A	G	NM_021199 // downstream // 1521458 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 505750 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2229402	ctaggcactttcaaca[C/T]tattcatttaaacctg	C	T	NM_021199 // downstream // 1696248 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 330960 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1869640	tccttagagtgaagca[A/G]ctttttctctgaatgt	A	G	NM_021199 // downstream // 1763006 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 264202 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2195883	catgtatttctcccaa[G/T]aagctcaaagaacttc	G	T	NM_021199 // downstream // 1828577 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 198631 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2256929	ctttcctcatgcagcc[A/G]atcatccaagttcttt	A	G	NM_021199 // downstream // 1828718 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 198490 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2231400	ctattgccaccgatac[A/G]aactggcttcagtgta	A	G	NM_021199 // downstream // 1832841 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 194367 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2293386	gcagatgagtagtcgga[C/T]agcaattatattagaa	C	T	NM_021199 // downstream // 1834362 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 192846 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-1788498	gggataaactgctta[A/T]atacgttctaggca	A	T	NM_021199 // downstream // 1918969 // Hs.511251 // SQRDL // 58472 // Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), mRNA. /// NM_024966 // upstream // 108239 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (	SQRDL	SQRDL, Homo sapiens sulfide quinone reductase-like (yeast) (SQRDL), q21.1
SNP_A-2277959	aagcatccgtagctctca[A/C]gggtaccigtagaaca	A	C	NM_024966 // intron // 0 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // intron // 0 // Hs.511265 // SEMA6D // 80031 // Ho	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN q21.1
SNP_A-2234163	ctcattggtctgggta[C/T]gatcagtgaataiaga	C	T	NM_024966 // downstream // 143299 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 143299 // Hs.511265 // SEM	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN q21.1
SNP_A-1744393	cagcaaaaaaggagcagctgcacttc[A/G]atttctgatgtctttct ccaggct	A	G	NM_016132 // downstream // 57336 // Hs.447521 // MYEF2 // 50804 // Hs.191098 // SEMA6D // 80031 // sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D /// NM_	MYEF2	MYEF2 , rs10519163, myelin expression factor 2 q21.1
SNP_A-2157283	attgacgcgctgagag[A/G]caacataacatcagtt	A	G	NM_024966 // downstream // 285479 // Hs.511265 // SEMA6D // 80031 // Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN /// NM_153619 // downstream // 285479 // Hs.511265 // SEM	SEMA6D	SEMA6D, Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D (SEMA6D), transcript variant 6, mRN q21.1
SNP_A-2300839	gcctggtcaaagcaga[C/G]ggttttattgagatgt	C	G	NM_000138 // intron // 0 // Hs.146447 // FBN1 // 2200 // Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1), mRNA. /// ENST00000316623 // intron // 0 // — // — // —	FBN1	FBN1, Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1), q21.1
SNP_A-1832508	tacaaaggttattgata[C/T]agaaacaagcaaataa	C	T	ENST00000325747 // intron // 0 // — // — // —	-	q21.1
SNP_A-1930461	ttccaaacctctctca[A/G]ctatccttggtattt	A	G	NM_203349 // intron // 0 // Hs.207589 // RaLP // 399694 // Homo sapiens rai-like protein (RaLP), mRNA. /// ENST00000332408 // intron // 0 // — // — - // — // —	RaLP	RaLP, Homo sapiens rai-like protein (RaLP), q21.1
SNP_A-2278899	ccttgagtccctaga[A/C]gcattgggtaaataag	A	C	NM_203349 // intron // 0 // Hs.207589 // RaLP // 399694 // Homo sapiens rai-like protein (RaLP), mRNA. /// ENST00000332408 // intron // 0 // — // — - // — // —	RaLP	RaLP, Homo sapiens rai-like protein (RaLP), q21.1
SNP_A-2092162	agaaacttctctaat[C/T]atctcaaatggaaggt	C	T	NM_203349 // intron // 0 // Hs.207589 // RaLP // 399694 // Homo sapiens rai-like protein (RaLP), mRNA. /// ENST00000332408 // intron // 0 // — // — - // — // —	RaLP	RaLP, Homo sapiens rai-like protein (RaLP), q21.1
SNP_A-1879158	tcttaccatcttttc[C/T]agccacatagaaggtt	C	T	NM_014701 // intron // 0 // Hs.9997 // KIAA0256 // 9728 // Homo sapiens KIAA0256 gene product (KIAA0256), mRNA. /// ENST00000261847 // intron // 0 // — // — // — // —	KIAA0256	KIAA0256, Homo sapiens KIAA0256 gene product (KIAA0256), q21.1
SNP_A-1668859	caatttctatgagtgatgagaaagc[A/G]aatacctttattccacata gcattt	A	G	D87445 // upstream // 49591 // Hs.372033 // KIAA0256 // 9728 // KIAA0256 gene product /// NM_004236 // downstream // 31293 // Hs.30212 // TRIP15 // 9318 // thyroid receptor interacting protein 15	KIAA0256	KIAA0256 , rs10519208, KIAA0256 gene product q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2278928	tgagggaatgatatgc[A/G]cagaattcagaataga	A	G	NM_014701 // intron // 0 // Hs.9997 // KIAA0256 // 9728 // Homo sapiens KIAA0256 gene product (KIAA0256), mRNA. /// ENST00000261847 // intron // 0 // — // — // —	KIAA0256	KIAA0256, Homo sapiens KIAA0256 gene product (KIAA0256), q21.1
SNP_A-1833433	tacagagaagctatgt[C/T]attgctgacagacata	C	T	NM_152647 // intron // 0 // Hs.410609 // FLJ32800 // 196951 // Homo sapiens hypothetical protein FLJ32800 (FLJ32800), mRNA. /// NM_002009 // intron // 0 // Hs.122006 // FGF7 // 2252 // Homo sapiens fibroblast growth factor 7 (keratinocyte growth factor) (	FLJ32800	FLJ32800, Homo sapiens hypothetical protein FLJ32800 (FLJ32800), q21.2
SNP_A-2279561	tccatttgttcatctct[C/T]gacacggacgaagcca	C	T	NM_024837 // intron // 0 // Hs.511311 // ATP8B4 // 79895 // Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), mRNA. /// ENST00000284509 // intron // 0 // — // — // —	ATP8B4	ATP8B4, Homo sapiens ATPase, Class I, type 8B, member 4 (ATP8B4), q21.2
SNP_A-1729029	cagtgaggtaatgttagcagaagga[C/T]gttgcataaagtcaag gacacatt	C	T	AK090830 // upstream // 48098 // Hs.152818 // USP8 // 9101 // ubiquitin specific protease 8 /// NM_005154 // downstream // 43155 // Hs.152818 // USP8 // 9101 // ubiquitin specific protease 8 /// NM_017672 // downstream // 17365 // Hs.143619 // TRPM7 // 5	USP8	USP8 , rs2135452, ubiquitin specific protease 8 q21.2
SNP_A-2279824	caagaatgtctcagtc[G/T]cggtaatttccggcc	G	T	NM_203494 // intron // 0 // Hs.498027 // USP50 // 373509 // Homo sapiens ubiquitin specific protease 50 (USP50), mRNA. /// ENST00000306479 // intron // 0 // — // — // —	USP50	USP50, Homo sapiens ubiquitin specific protease 50 (USP50), q21.2
SNP_A-2190609	catactagtttcttccc[C/T]atcctttcatgactca	C	T	NM_032802 // upstream // 119737 // Hs.401537 // SPPL2A // 84888 // Homo sapiens putative intramembrane cleaving protease (SPPL2A), mRNA. /// NM_007347 // upstream // 23310 // Hs.413366 // AP4E1 // 23431 // Homo sapiens adaptor-related protein complex 4, e	SPPL2A	SPPL2A, Homo sapiens putative intramembrane cleaving protease (SPPL2A), q21.2
SNP_A-1753777	attcactaccacaataattcaagccc[C/T]ggaactaatagccatttt taaactc	C	T	NM_007347 // intron // 0 // Hs.413366 // AP4E1 // 23431 // adaptor-related protein complex 4, epsilon 1 subunit	AP4E1	AP4E1, rs2306335, adaptor-related protein complex 4, epsilon 1 subunit,q21.2
SNP_A-2260707	gaaacctgcagtgaaa[A/G]cgtaaggtgatggagc	A	G	NM_007347 // intron // 0 // Hs.413366 // AP4E1 // 23431 // Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA. /// ENST00000261842 // intron // 0 // — // — // —	AP4E1	AP4E1, Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), q21.2
SNP_A-1810914	gtgcatcatgaaagaa[A/G]ctcgtcgaagaaagga	A	G	NM_007347 // intron // 0 // Hs.413366 // AP4E1 // 23431 // Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA. /// ENST00000261842 // intron // 0 // — // — // —	AP4E1	AP4E1, Homo sapiens adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), q21.2
SNP_A-2186681	cagtgctaagaggaaat[A/G]aacactcattgtgcag	A	G	NM_207381 // upstream // 1608 // Hs.306343 // FLJ41287 // 388121 // Homo sapiens FLJ41287 protein (FLJ41287), mRNA. /// NM_031226 // downstream // 149423 // Hs.511367 // CYP19A1 // 1588 // Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide	FLJ41287	FLJ41287, Homo sapiens FLJ41287 protein (FLJ41287), q21.2
SNP_A-2279977	ggtcttgctctgaata[C/T]gatcctgcaaggaggc	C	T	NM_207381 // upstream // 5285 // Hs.306343 // FLJ41287 // 388121 // Homo sapiens FLJ41287 protein (FLJ41287), mRNA. /// NM_031226 // downstream // 145746 // Hs.511367 // CYP19A1 // 1588 // Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide	FLJ41287	FLJ41287, Homo sapiens FLJ41287 protein (FLJ41287), q21.2
SNP_A-2236427	ctcggaactgccaggg[A/T]acaaacaattgaagcc	A	T	NM_207381 // upstream // 19099 // Hs.306343 // FLJ41287 // 388121 // Homo sapiens FLJ41287 protein (FLJ41287), mRNA. /// NM_031226 // downstream // 131932 // Hs.511367 // CYP19A1 // 1588 // Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide	FLJ41287	FLJ41287, Homo sapiens FLJ41287 protein (FLJ41287), q21.2
SNP_A-2004152	ccattataaaactgaa[A/G]aatcataagttgaatc	A	G	NM_031226 // upstream // 2181 // Hs.511367 // CYP19A1 // 1588 // Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide 1 (CYP19A1), transcript variant 2, mRNA. /// NM_000103 // upstream // 2181 // Hs.511367 // CYP19A1 // 1588 // Homo sapiens c	CYP19A1	CYP19A1, Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide 1 (CYP19A1), transcript variant 2, q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2041193	aacctcagctttgaca[C/G]tgcattttaagaaaaa	C	G	NM_181789 // intron // 0 // Hs.526441 // COLM // 342035 // Homo sapiens collomin (COLM), mRNA. /// ENST00000358542 // intron // 0 // — // — // — // —	COLM	COLM, Homo sapiens collomin (COLM), q21.2
SNP_A-2180644	cagaagcttttaaata[A/C]cttacatgagctgaaa	A	C	NM_181789 // intron // 0 // Hs.526441 // COLM // 342035 // Homo sapiens collomin (COLM), mRNA. /// ENST00000358542 // intron // 0 // — // — // — // —	COLM	COLM, Homo sapiens collomin (COLM), q21.2
SNP_A-2034303	aaatcctcagctttta[C/T]aacatttggaaataac	C	T	NM_181789 // intron // 0 // Hs.526441 // COLM // 342035 // Homo sapiens collomin (COLM), mRNA. /// ENST00000358542 // intron // 0 // — // — // — // —	COLM	COLM, Homo sapiens collomin (COLM), q21.2
SNP_A-2125997	agttttctaagagata[A/T]ggaatttaagttacaa	A	T	NM_181789 // intron // 0 // Hs.526441 // COLM // 342035 // Homo sapiens collomin (COLM), mRNA. /// ENST00000358542 // intron // 0 // — // — // — // —	COLM	COLM, Homo sapiens collomin (COLM), q21.2
SNP_A-2115650	agggtatatgggcaca[C/T]tgctgtaactgctgtg	C	T	NM_018728 // intron // 0 // Hs.487036 // MYO5C // 55930 // Homo sapiens myosin VC (MYO5C), mRNA. /// ENST00000261839 // intron // 0 // — // — // — // —	MYO5C	MYO5C, Homo sapiens myosin VC (MYO5C), q21.2
SNP_A-2259747	gaaaagagaaatgtag[A/G]cataaggccacataat	A	G	NM_000259 // intron // 0 // Hs.21213 // MYO5A // 4644 // Homo sapiens myosin VA (heavy polypeptide 12, myoxin) (MYO5A), mRNA. /// ENST00000358212 // intron // 0 // — // — // — // — /// ENST00000356338 // intron // 0 // — // — // — // — ///	MYO5A	MYO5A, Homo sapiens myosin VA (heavy polypeptide 12, myoxin) (MYO5A), q21.2
SNP_A-1823561	taaaagtggatctatc[C/T]cagaaaaaatctaggc	C	T	NM_006628 // downstream // 23048 // Hs.512908 // ARPP-19 // 10776 // Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), mRNA. /// ENST00000312528 // downstream // 18135 // — // — // — // — /// ENST00000249822 // downstream // 23048 // — //	ARPP-19	ARPP-19, Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), q21.2
SNP_A-1949830	tttcaacaaatattgg[A/G]agctatcatatgccag	A	G	NM_006628 // downstream // 15526 // Hs.512908 // ARPP-19 // 10776 // Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), mRNA. /// ENST00000312528 // downstream // 25657 // — // — // — // — /// ENST00000249822 // downstream // 15526 // — //	ARPP-19	ARPP-19, Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), q21.2
SNP_A-2163391	attttttaagagaac[A/C]aaatgcagcaaatgcc	A	C	NM_006628 // downstream // 4167 // Hs.512908 // ARPP-19 // 10776 // Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), mRNA. /// ENST00000312528 // downstream // 37016 // — // — // — // — /// ENST00000249822 // downstream // 4167 // — // -	ARPP-19	ARPP-19, Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), q21.2
SNP_A-2163482	caaaaaacaaggtatc[C/T]ctagatggcagtttag	C	T	NM_006628 // upstream // 2775 // Hs.512908 // ARPP-19 // 10776 // Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), mRNA. /// ENST00000249822 // upstream // 2775 // — // — // — // — /// ENST00000261844 // downstream // 9381 // — // — //	ARPP-19	ARPP-19, Homo sapiens cyclic AMP phosphoprotein, 19 kD (ARPP-19), q21.2
SNP_A-1873658	tctcactcccaagtaa[C/T]cactattctcatttcc	C	T	NM_004498 // downstream // 51210 // Hs.439486 // ONECUT1 // 3175 // Homo sapiens one cut domain, family member 1 (ONECUT1), mRNA. /// ENST00000261844 // upstream // 27145 // — // — // — // — /// ENST00000305901 // downstream // 51210 // — // —	ONECUT1	ONECUT1, Homo sapiens one cut domain, family member 1 (ONECUT1), q21.3
SNP_A-2281020	ttttacagctacagat[A/C]aacttgtatgatttgg	A	C	NM_182758 // downstream // 580606 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 // downstream // 48089 // — // — // — // — /// ENST00000338242 // downstream // 580606 // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1813950	gtgtcaccccaccaga[C/T]gttgatgagatttgat	C	T	NM_182758 // downstream // 502276 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 // downstream // 126419 // — // — // — // — /// ENST00000338242 // downstream // 502276 // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909306	tgtatgtcctgaaaat[A/G]aaaggagaatatgtcc	A	G	NM_182758 // downstream // 499700 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 // downstream // 128995 // — // — // — // — /// ENST00000338242 // downstream // 499700 // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1750821	agcatgatctctgggagcagaagac[C/G]aagatgctaaatgctggccctccat	C	G	NM_004498 // upstream // 376126 // Hs.439486 // ONECUT1 // 3175 // one cut domain, family member 1 /// NM_182758 // downstream // 349030 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	ONECUT1	ONECUT1 , rs10518710, one cut domain, family member 1 ,q21.3
SNP_A-2281257	ggcaaaaaattgaatg[A/G]agattgacagaatcag	A	G	NM_182758 // downstream // 395844 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 // downstream // 232851 // — // — // — // — /// ENST00000338242 // downstream // 395844 // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1758399	ggatacaaattcactatggtattac[A/G]gagatcaatttattagctaccacgc	A	G	NM_004498 // upstream // 543535 // Hs.439486 // ONECUT1 // 3175 // one cut domain, family member 1 /// NM_182758 // downstream // 181621 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	ONECUT1	ONECUT1 , rs1386169, one cut domain, family member 1 ,q21.3
SNP_A-1828180	taagagaggagaaccc[A/G]ggaatgaaggtcttgt	A	G	NM_182758 // downstream // 120744 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000360618 // downstream // 507951 // — // — // — // — /// ENST00000338242 // downstream // 120744 // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1749069	ggcaactgaatagaataaaccactg[C/T]agtaccagaccaaagccaaacaaaa	C	T	NM_182758 // intron // 0 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	FLJ38736	FLJ38736 , rs1906417, hypothetical protein FLJ38736,q21.3
SNP_A-2187940	cagtattcacttttaa[A/C]tgttgtggctctgagt	A	C	NM_182758 // intron // 0 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000338242 // intron // 0 // — // — // — // — /// ENST00000360509 // intron // 0 // — // — // — // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1695115	atgctttatttcactgaacttaaac[C/T]acatattctgaaaatcacaatgcat	C	T	NM_182758 // intron // 0 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	FLJ38736	FLJ38736 , rs475377, hypothetical protein FLJ38736,q21.3
SNP_A-1653968	ttcagatctttgcccatagtgatct[A/G]actccaaaagagaaactaggggtta	A	G	NM_182758 // intron // 0 // Hs.208067 // FLJ38736 // 256764 // hypothetical protein FLJ38736	FLJ38736	FLJ38736 , rs956553, hypothetical protein FLJ38736,q21.3
SNP_A-2284627	gatcagatctcataac[C/T]ggtacatcacaaagtg	C	T	NM_182758 // intron // 0 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000338242 // intron // 0 // — // — // — // — /// ENST00000360509 // intron // 0 // — // — // — // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2282151	ctgcctaatatgtgaa[A/T]atcctgcttatccctg	A	T	NM_182758 // intron // 0 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// ENST00000338242 // intron // 0 // — // — // — // — /// ENST00000360509 // intron // 0 // — // — // — // —	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2282567	tgcattagtaaatcaa[C/T]cagacaaatcatttac	C	T	NM_182758 // upstream // 224692 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 221476 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ387	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-2282568	atcatacactgtctta[C/T]gagatttcttctttgg	C	T	NM_182758 // upstream // 224724 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 221508 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ387	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3
SNP_A-1867058	tccctctaatgtcaag[A/G]cctattcacctgaacc	A	G	NM_182758 // upstream // 458298 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ38736), mRNA. /// NM_182758 // upstream // 455082 // Hs.208067 // FLJ38736 // 256764 // Homo sapiens hypothetical protein FLJ38736 (FLJ387	FLJ38736	FLJ38736, Homo sapiens hypothetical protein FLJ38736 (FLJ38736), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1910334	tgtccaggaggattga[A/C]aacaatatggtatcca	A	C	ENST00000311590 // intron // 0 // --- // --- // --- /// ENST00000260323 // intron // 0 // --- // --- // ---	-	q21.3
SNP_A-1667052	tctcaatatcctcctgaagcctgaaa[A/T]ctttggttagcatccatg cctctc	A	T	NM_016304 // downstream // 517455 // Hs.274772 // C15orf15 // 51187 // chromosome 15 open reading frame 15	C15orf15	C15orf15 , rs10518775, chromosome 15 open reading frame 15,q21.3
SNP_A-1959526	tttgctggatactct[C/T]aattttcctctccaga	C	T	NM_016304 // downstream // 516805 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 117710 // --- // --- // --- /// ENST00000260323 // downstream // 35906 //	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2004172	ctttacaacaatagta[C/T]gaaaatgatgctttt	C	T	NM_016304 // downstream // 484693 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 149822 // --- // --- // --- /// ENST00000260323 // downstream // 68018 //	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-1890139	tgatattgggcaaaa[A/G]cagggaaatgcaccat	A	G	NM_016304 // downstream // 336758 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 297757 // --- // --- // --- /// ENST00000260323 // downstream // 215953 /	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2032173	aaagtgggagttgtgg[A/G]aagcccaacttgtagc	A	G	NM_016304 // downstream // 336343 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 298172 // --- // --- // --- /// ENST00000260323 // downstream // 216368 /	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-2283613	ctaaatatcacacttta[A/C]ctgagaaaagttctt	A	C	NM_016304 // downstream // 274036 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 360479 // --- // --- // --- /// ENST00000260323 // downstream // 278675 /	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-1866900	tccctactgacagcca[C/T]ctggtattcagactg	C	T	NM_016304 // downstream // 265409 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 369106 // --- // --- // --- /// ENST00000260323 // downstream // 287302 /	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-1948381	tttaggtgcaactagc[A/G]gaaaaaaatacgcatt	A	G	NM_016304 // downstream // 216095 // Hs.274772 // C15orf15 // 51187 // Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA. /// ENST00000311590 // downstream // 418420 // --- // --- // --- /// ENST00000260323 // downstream // 336616 /	C15orf15	C15orf15, Homo sapiens chromosome 15 open reading frame 15 (C15orf15), q21.3
SNP_A-1859427	tcaggaatcatttcaa[C/T]gccctcttgtttcctaa	C	T	NM_004580 // intron // 0 // Hs.298651 // RAB27A // 5873 // Homo sapiens RAB27A, member RAS oncogene family (RAB27A), transcript variant 1, mRNA. /// NM_183235 // intron // 0 // Hs.298651 // RAB27A // 5873 // Homo sapiens RAB27A, member RAS oncogene family	RAB27A	RAB27A, Homo sapiens RAB27A, member RAS oncogene family (RAB27A), transcript variant 1, q21.3
SNP_A-2038929	aacagctgaacaatgc[C/T]agggagagtcaggtga	C	T	NM_004855 // intron // 0 // Hs.126115 // PIGB // 9488 // Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA. /// ENST00000164305 // intron // 0 // --- // --- // ---	PIGB	PIGB, Homo sapiens phosphatidylinositol glycan, class B (PIGB), q21.3
SNP_A-2079413	acccccattgacagata[A/G]gttgtataatgccac	A	G	NM_198400 // intron // 0 // Hs.1565 // NEDD4 // 4734 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 4 (NEDD4), mRNA. /// NM_006154 // intron // 0 // Hs.1565 // NEDD4 // 4734 // Homo sapiens neural precursor cell expressed.	NEDD4	NEDD4, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4 (NEDD4), q21.3
SNP_A-1743233	tcccctgaaatcctgttaaacctgg[G/T]aaatggagagtaagga ggaattgga	G	T	D42055 // upstream // 60820 // Hs.1565 // NEDD4 // 4734 // neural precursor cell expressed, developmentally down-regulated 4 /// NM_022841 // downstream // 38093 // Hs.21767 // FLJ12994 // 64864 // hypothetical protein FLJ12994	NEDD4	NEDD4, rs10518835, neural precursor cell expressed, developmentally down-regulated 4, q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2068631	acaataaagctcctta[C/T]agtggtggagaagagc	C	T	NM_207038 // intron // 0 // Hs.511504 // TCF12 // 6938 // Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // intron // 0 // Hs.511504 // TCF12 // 6938 // Homo sapiens	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-2285086	tcttctctactgaca[C/G]atcggctactctcaaa	C	G	NM_207038 // intron // 0 // Hs.511504 // TCF12 // 6938 // Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA. /// NM_003205 // intron // 0 // Hs.511504 // TCF12 // 6938 // Homo sapiens	TCF12	TCF12, Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, q21.3
SNP_A-2240052	ctgaagctaacaacta[C/T]cacctttctccactt	C	T	NM_032866 // downstream // 21300 // Hs.148989 // CGNL1 // 84952 // Homo sapiens likely ortholog of mouse junction-associated coiled-coil protein (JACOP), mRNA. /// NM_152451 // upstream // 20018 // Hs.50841 // Gup1 // 145781 // Homo sapiens GRINL1A comple	CGNL1	CGNL1, Homo sapiens likely ortholog of mouse junction-associated coiled-coil protein (JACOP), q21.3
SNP_A-2285635	gtaaccatgatgaaga[C/G]ctaaatgcctaccag	C	G	NM_152451 // intron // 0 // Hs.50841 // Gup1 // 145781 // Homo sapiens GRINL1A complex upstream protein (Gup1), mRNA. /// ENST00000267853 // intron // 0 // — // — // —	Gup1	Gup1, Homo sapiens GRINL1A complex upstream protein (Gup1), q21.3
SNP_A-2259132	gaaaaaaatccgag[C/T]attctggtcatagtt	C	T	NM_152451 // downstream // 42669 // Hs.50841 // Gup1 // 145781 // Homo sapiens GRINL1A complex upstream protein (Gup1), mRNA. /// NM_015532 // downstream // 32070 // Hs.437256 // GRINL1A // 81488 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-	Gup1	Gup1, Homo sapiens GRINL1A complex upstream protein (Gup1), q21.3
SNP_A-1783131	ggcaggagaagagacc[C/T]gagtaggcaattggta	C	T	NM_152451 // downstream // 53875 // Hs.50841 // Gup1 // 145781 // Homo sapiens GRINL1A complex upstream protein (Gup1), mRNA. /// NM_015532 // downstream // 43276 // Hs.437256 // GRINL1A // 81488 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-	Gup1	Gup1, Homo sapiens GRINL1A complex upstream protein (Gup1), q21.3
SNP_A-2162744	atttttgacccagacta[C/T]ctgagctttcatgttg	C	T	NM_152451 // downstream // 54596 // Hs.50841 // Gup1 // 145781 // Homo sapiens GRINL1A complex upstream protein (Gup1), mRNA. /// NM_015532 // downstream // 43997 // Hs.437256 // GRINL1A // 81488 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-	Gup1	Gup1, Homo sapiens GRINL1A complex upstream protein (Gup1), q21.3
SNP_A-2037660	aacaagattgcagaggt[A/G]catttttagactattg	A	G	NM_020980 // downstream // 239319 // Hs.104624 // AQP9 // 366 // Homo sapiens aquaporin 9 (AQP9), mRNA. /// NM_000236 // upstream // 6747 // Hs.188630 // LIPC // 3990 // Homo sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000219319 // downstream // 23931	AQP9	AQP9, Homo sapiens aquaporin 9 (AQP9), q21.3
SNP_A-2063731	aattagacaacccccaa[C/T]ccgacagagcatttca	C	T	NM_000236 // intron // 0 // Hs.188630 // LIPC // 3990 // Homo sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // — // — // —	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2185611	caggagcacataacag[A/G]agcttaatatgaatct	A	G	NM_000236 // intron // 0 // Hs.188630 // LIPC // 3990 // Homo sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // — // — // —	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2286756	ctgcatggttaatcca[A/G]tcaaagcccaacctgc	A	G	NM_000236 // intron // 0 // Hs.188630 // LIPC // 3990 // Homo sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // — // — // —	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-1756088	tattttgccaaggttaaagacatta[C/T]cgtgacacagcctcagg aggtcctg	C	T	NM_000236 // intron // 0 // Hs.9994 // LIPC // 3990 // lipase, hepatic	LIPC	LIPC, rs1869129, lipase, hepatic,q21.3
SNP_A-2286850	ttagaataagtaccaa[C/T]ggagcatctagcatc	C	T	NM_000236 // intron // 0 // Hs.188630 // LIPC // 3990 // Homo sapiens lipase, hepatic (LIPC), mRNA. /// ENST00000299022 // intron // 0 // — // — // —	LIPC	LIPC, Homo sapiens lipase, hepatic (LIPC), q21.3
SNP_A-2287165	ttattgaatgagaac[C/T]ataaatgaataagtga	C	T	NM_017610 // intron // 0 // Hs.404423 // RNF111 // 54778 // Homo sapiens ring finger protein 111 (RNF111), mRNA. /// ENST00000348370 // intron // 0 // — // — // — // —	RNF111	RNF111, Homo sapiens ring finger protein 111 (RNF111), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287545	ggaaaaggcagggtta[C/T]agctgatgagtttgat	C	T	NM_004998 // upstream // 45509 // Hs.370392 // MYO1E // 4643 // Homo sapiens myosin IE (MYO1E), mRNA. /// NM_033195 // downstream // 209877 // Hs.307052 // LDHAL6B // 92483 // Homo sapiens lactate dehydrogenase A-like 6B (LDHAL6B), mRNA. /// NM_152450 //	MYO1E	MYO1E, Homo sapiens myosin IE (MYO1E), q22.2
SNP_A-2086785	actgacattttagaca[A/G]aagagcagaaattcgg	A	G	NM_004998 // upstream // 48662 // Hs.370392 // MYO1E // 4643 // Homo sapiens myosin IE (MYO1E), mRNA. /// NM_033195 // downstream // 213030 // Hs.307052 // LDHAL6B // 92483 // Homo sapiens lactate dehydrogenase A-like 6B (LDHAL6B), mRNA. /// NM_152450 //	MYO1E	MYO1E, Homo sapiens myosin IE (MYO1E), q22.2
SNP_A-2193139	catctagttcttcaca[C/T]gccaaatgagcagctg	C	T	NM_152450 // intron // 0 // Hs.531168 // MGC26690 // 145773 // Homo sapiens hypothetical protein MGC26690 (MGC26690), mRNA. /// ENST00000288228 // intron // 0 // — // — // — // —	MGC26690	MGC26690, Homo sapiens hypothetical protein MGC26690 (MGC26690), q22.2
SNP_A-2049379	aagctgaagaaggata[A/T]gaacactatacaatgt	A	T	NM_152450 // intron // 0 // Hs.531168 // MGC26690 // 145773 // Homo sapiens hypothetical protein MGC26690 (MGC26690), mRNA. /// ENST00000288228 // intron // 0 // — // — // — // —	MGC26690	MGC26690, Homo sapiens hypothetical protein MGC26690 (MGC26690), q22.2
SNP_A-2264135	gaactgatgagaatga[A/G]aggctttcccaaaat	A	G	NM_152450 // intron // 0 // Hs.531168 // MGC26690 // 145773 // Homo sapiens hypothetical protein MGC26690 (MGC26690), mRNA. /// ENST00000288228 // intron // 0 // — // — // — // —	MGC26690	MGC26690, Homo sapiens hypothetical protein MGC26690 (MGC26690), q22.2
SNP_A-2287551	atcaattgccttaaaa[C/T]aatgaatgcctactaa	C	T	NM_152450 // intron // 0 // Hs.531168 // MGC26690 // 145773 // Homo sapiens hypothetical protein MGC26690 (MGC26690), mRNA. /// ENST00000288228 // intron // 0 // — // — // — // —	MGC26690	MGC26690, Homo sapiens hypothetical protein MGC26690 (MGC26690), q22.2
SNP_A-2094597	agaatagaaaatggca[C/T]gataactccaagttt	C	T	NM_182777 // downstream // 201258 // Hs.356572 // RPS3A // 6189 // Homo sapiens ribosomal protein S3A (RPS3A), mRNA. /// NM_001006 // downstream // 201258 // Hs.356572 // RPS3A // 6189 // Homo sapiens ribosomal protein S3A (RPS3A), mRNA. /// NM_012182 //	RPS3A	RPS3A, Homo sapiens ribosomal protein S3A (RPS3A), q22.2
SNP_A-1730803	ttgtggccttatgaatgtctttca[A/G]tctgaccagagctgcaact ccttct	A	G	NM_004039 // downstream // 87172 // Hs.462864 // ANXA2 // 302 // annexin A2 /// NM_012182 // downstream // 254222 // Hs.247756 // FOXB1 // 27023 // forkhead box B1	ANXA2	ANXA2 , rs10519008, annexin A2 q22.2
SNP_A-1713273	cacttacatgatatggaatcctcaa[C/T]gaaagttcagcagaga gaatttttg	C	T	NM_004039 // downstream // 66045 // Hs.462864 // ANXA2 // 302 // annexin A2 /// NM_012182 // downstream // 275349 // Hs.247756 // FOXB1 // 27023 // forkhead box B1	ANXA2	ANXA2 , rs1509804, annexin A2 q22.2
SNP_A-2261256	gaaagatgacaggcac[A/G]atgtagggaaggccaga	A	G	NM_012182 // downstream // 223163 // Hs.247756 // FOXB1 // 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 118046 // Hs.511605 // ANXA2 // 302 // Homo sapiens annexin A2 (ANXA2), transcript variant 1, mRNA. /// NM_00	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2103696	agcacagtcataggaa[A/G]taaaaccatatcaagg	A	G	NM_012182 // downstream // 279557 // Hs.247756 // FOXB1 // 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 61652 // Hs.511605 // ANXA2 // 302 // Homo sapiens annexin A2 (ANXA2), transcript variant 1, mRNA. /// NM_004	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-1807560	gtctggatctactccc[C/T]aagaccgaccaggcag	C	T	NM_012182 // downstream // 281199 // Hs.247756 // FOXB1 // 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 60010 // Hs.511605 // ANXA2 // 302 // Homo sapiens annexin A2 (ANXA2), transcript variant 1, mRNA. /// NM_004	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2239557	ctgaaaaaaattgacc[A/G]gatttcataaaattga	A	G	NM_012182 // downstream // 282191 // Hs.247756 // FOXB1 // 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 59018 // Hs.511605 // ANXA2 // 302 // Homo sapiens annexin A2 (ANXA2), transcript variant 1, mRNA. /// NM_004	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181512	cagactgtgtaggcc[C/T]gataaccccttgttt	C	T	NM_012182 // downstream // 288871 // Hs.247756 // FOXB1 // 27023 // Homo sapiens forkhead box B1 (FOXB1), mRNA. /// NM_001002858 // downstream // 52338 // Hs.511605 // ANXA2 // 302 // Homo sapiens annexin A2 (ANXA2), transcript variant 1, mRNA. /// NM_004	FOXB1	FOXB1, Homo sapiens forkhead box B1 (FOXB1), q22.2
SNP_A-2076875	accaaagactaaaacc[C/T]gctacaatgtggaaaa	C	T	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2178571	cactctatcatgcttc[A/G]ccaatcttgtccttta	A	G	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2288989	gcagaacacaaaaatg[A/G]acagaaacgtacaggt	A	G	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2021339	aaaaaacgtttcaaca[A/G]cttctatcatcagctc	A	G	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2232457	ctcacataaaactaag[A/G]caggcttgaggaagg	A	G	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2187453	caggtttatcttcata[A/T]gctggcaaggagattc	A	T	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2244111	ctgcttgtttctaata[C/T]gcccatcaaccaaagc	C	T	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2268685	gaatgtgtatagcttal[C/T]cctcaaatctcaaaac	C	T	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1950072	tttcacatgacaagag[G/T]aactcagcctaacac	G	T	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2223200	cgcctcacctgttgcc[A/G]ctagcatttgcacact	A	G	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2030856	aaaggaaaatctgaaca[G/T]gaatttgagatacctа	G	T	NM_134261 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // intron // 0 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcr	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2254707	cttgcttggacagtca[G/T]aagcactgagttattc	G	T	NM_134261 // upstream // 92428 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 92428 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RO	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2094809	agaatcctgttaccta[C/T]gtttaaaatgatggat	C	T	NM_134261 // upstream // 92604 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 92604 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RO	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1785022	ggcggaagaatcaagga[A/G]ggtcaatgggctatg	A	G	NM_134261 // upstream // 95274 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 95274 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RO	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2173494	cacaatccaggccaga[C/G]gtgataatggcctaaa	C	G	NM_134261 // upstream // 173226 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 173226 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2221922	ccttttttcatttccc[A/G]gatatttccaatatt	A	G	NM_134261 // upstream // 234326 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 234326 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1908907	tgtataaaattacaca[C/T]tgagaaaaggaggacat	C	T	NM_134261 // upstream // 358147 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 358147 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2289582	aagctaatgaacaa[C/T]gctagagaaccagagg	C	T	NM_134261 // upstream // 439603 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 439603 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1653440	caatggcttctccttatgaatctt[A/T]cttaatttctcccccagctgc tca	A	T	NM_002943 // upstream // 1139859 // Hs.528666 // RORA // 6095 // RAR-related orphan receptor A /// NM_017684 // downstream // 84997 // Hs.328109 // VPS13C // 54832 // vacuolar protein sorting 13C (yeast) /// NM_134260 // upstream // 1139859 // Hs.528666	RORA	RORA , rs2414749, RAR-related orphan receptor A q22.2
SNP_A-1827317	taacggatgggaaaaa[A/T]ggtttgtagatggag	A	T	NM_134261 // upstream // 525477 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 525477 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1892204	tgcaaatgggcacgta[A/G]ccttcaacaagtgtcc	A	G	NM_134261 // upstream // 528419 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 528419 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2171431	caatcacatcatacct[A/G]acattcaggccgcaca	A	G	NM_134261 // upstream // 534336 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 534336 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1812874	gtgggctatggtacaa[C/T]atcagttcatatttcg	C	T	NM_134261 // upstream // 547819 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 547819 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-1909736	tgtcaatgttatttaa[C/T]ccgaataagaacatta	C	T	NM_134261 // upstream // 555264 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, mRNA. /// NM_134262 // upstream // 555264 // Hs.200050 // RORA // 6095 // Homo sapiens RAR-related orphan receptor A (	RORA	RORA, Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 1, q22.2
SNP_A-2031691	aaagtacctgacatca[A/T]acattgtctcacctgt	A	T	NM_207322 // downstream // 67506 // Hs.202656 // NLF1 // 145741 // Homo sapiens hypothetical LOC145741 (LOC145741), mRNA. /// ENST00000355522 // downstream // 67506 // — // — // — // — /// ENST00000358850 // downstream // 66818 // — // — // –	NLF1	NLF1, Homo sapiens hypothetical LOC145741 (LOC145741), q22.2
SNP_A-1797263	ggttggcgggtccata[C/G]aagtgtctgctgcctt	C	G	NM_207322 // downstream // 78354 // Hs.202656 // NLF1 // 145741 // Homo sapiens hypothetical LOC145741 (LOC145741), mRNA. /// ENST00000355522 // downstream // 78354 // — // — // — // — /// ENST00000358850 // downstream // 55970 // — // — // –	NLF1	NLF1, Homo sapiens hypothetical LOC145741 (LOC145741), q22.2
SNP_A-1835809	tacgggagaattggaa[C/T]gaactctctttgctct	C	T	NM_173805 // upstream // 6926 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 391590 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-1795396	ggtgcaaagacacaga[C/G]atatagacatggtgaa	C	G	NM_173805 // upstream // 27627 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 370889 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-1780875	ggatgaaacttgaaga[C/T]gttaaatgaaataagc	C	T	NM_173805 // upstream // 55226 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 343290 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2290236	gacttaagggaactcg[C/T]cattggatgtagtgac	C	T	NM_173805 // upstream // 221601 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 176915 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 /	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-1925714	ttatgcagcacctaca[A/G]taagtaacagacctta	A	G	NM_173805 // upstream // 241272 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 157244 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 /	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-1858267	tcagaaggagtagatg[A/G]aaccaccatgaacttt	A	G	NM_173805 // upstream // 275808 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 122708 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 /	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2221588	ccttgcaaatcacaa[C/G]tgaatctcctaaatcc	C	G	NM_173805 // upstream // 290220 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 108296 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 /	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2279900	gaggctagcttcaagat[C/T]agctgctgcagtataa	C	T	NM_173805 // upstream // 348667 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 49849 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-1924493	ttatacacagacgcaa[A/G]ctaccatcctgtagc	A	G	NM_173805 // upstream // 356035 // Hs.370479 // FLJ38723 // 255180 // Homo sapiens hypothetical protein FLJ38723 (FLJ38723), mRNA. /// NM_006289 // upstream // 42481 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000299125 //	FLJ38723	FLJ38723, Homo sapiens hypothetical protein FLJ38723 (FLJ38723), q22.2
SNP_A-2108501	agctgcttccagtcc[A/G]cagaggatgctccda	A	G	NM_006289 // intron // 0 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000306829 // intron // 0 // — // — // — // —	TLN1	TLN1, Homo sapiens talin 1 (TLN1), q22.2
SNP_A-2144573	atgatccatggtggga[C/T]acatcctcaacaac	C	T	NM_006289 // intron // 0 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000306829 // intron // 0 // — // — // — // —	TLN1	TLN1, Homo sapiens talin 1 (TLN1), q22.2
SNP_A-2124811	agttcttgaccactgc[A/G]gacaaggcagatgcag	A	G	NM_006289 // intron // 0 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000306829 // intron // 0 // — // — // — // —	TLN1	TLN1, Homo sapiens talin 1 (TLN1), q22.2
SNP_A-2193979	catgaagtactatttg[A/T]aggagaataaaatatcc	A	T	NM_006289 // intron // 0 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// ENST00000306829 // intron // 0 // — // — // — // —	TLN1	TLN1, Homo sapiens talin 1 (TLN1), q22.2
SNP_A-2299655	gccgcttcctctccaa[A/C]attcacataggcgaaa	A	C	NM_006289 // downstream // 190200 // Hs.375001 // TLN1 // 7094 // Homo sapiens talin 1 (TLN1), mRNA. /// NM_000366 // upstream // 11008 // Hs.133892 // TPM1 // 7168 // Homo sapiens tropomyosin 1 (alpha) (TPM1), mRNA. /// ENST00000306829 // downstream // 1	TLN1	TLN1, Homo sapiens talin 1 (TLN1), q22.2
SNP_A-2070541	acacctcatggttctc[C/T]aaatggtgaccatctc	C	T	NM_000366 // downstream // 7991 // Hs.133892 // TPM1 // 7168 // Homo sapiens tropomyosin 1 (alpha) (TPM1), mRNA. /// NM_032857 // upstream // 47737 // Hs.410388 // LACTB // 114294 // Homo sapiens lactamase, beta (LACTB), nuclear gene encoding mitochondria	TPM1	TPM1, Homo sapiens tropomyosin 1 (alpha) (TPM1), q22.2
SNP_A-1925910	ttatggtatagacaca[C/T]ggtagaatactataca	C	T	NM_031301 // intron // 0 // Hs.511703 // APH1B // 83464 // Homo sapiens anterior pharynx defective 1B-like (PSFL), mRNA. /// ENST00000261879 // intron // 0 // — // — // — // —	APH1B	APH1B, Homo sapiens anterior pharynx defective 1B-like (PSFL), q22.2
SNP_A-1923115	ttagccgtgctgtgga[C/T]gagacgtgaaaaaggt	C	T	NM_206925 // upstream // 18822 // Hs.210995 // CA12 // 771 // Homo sapiens carbonic anhydrase XII (CA12), transcript variant 2, mRNA. /// NM_001218 // upstream // 18822 // Hs.210995 // CA12 // 771 // Homo sapiens carbonic anhydrase XII (CA12), transcript	CA12	CA12, Homo sapiens carbonic anhydrase XII (CA12), transcript variant 2, q22.2
SNP_A-2158185	attggcagagaatatat[C/T]ggagatccgggagaaa	C	T	NM_003922 // intron // 0 // Hs.210385 // HERC1 // 8925 // Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA. /// ENST00000261887 // intron // 0 // — // — // — // —	HERC1	HERC1, Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), q22.31
SNP_A-2267688	gaatcagacagcaaaa[G/T]aatgtggacaagat	G	T	NM_003922 // upstream // 23602 // Hs.210385 // HERC1 // 8925 // Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA. /// NM_014326 // downstream // 49544 // Hs.237886 // DAPK2 // 2	HERC1	HERC1, Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1910242	tgtccaaaaggactca[C/T]ggagaaagcgcctcct	C	T	NM_003922 // upstream // 63211 // Hs.210385 // HERC1 // 8925 // Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA. /// NM_014326 // downstream // 9935 // Hs.237886 // DAPK2 // 23	HERC1	HERC1, Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), q22.31
SNP_A-2291296	ctgagcagctctgaca[C/G]ggattcactggtgtcc	C	G	NM_014326 // intron // 0 // Hs.237886 // DAPK2 // 23604 // Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // — // — // — // —	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-2273677	gactgcacaaggtaat[C/G]agccctaaagaaaccc	C	G	NM_014326 // intron // 0 // Hs.237886 // DAPK2 // 23604 // Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // — // — // — // —	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-1949997	tttcaatttactgata[C/T]gaacatttgttgaagg	C	T	NM_014326 // intron // 0 // Hs.237886 // DAPK2 // 23604 // Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // — // — // — // —	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-2291815	gcacagcatttgttcc[G/T]ctttgtcatctgtctt	G	T	NM_014326 // intron // 0 // Hs.237886 // DAPK2 // 23604 // Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // — // — // — // —	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-1952070	tttctatttcacactt[A/T]aagaaacaaaggctca	A	T	NM_014326 // intron // 0 // Hs.237886 // DAPK2 // 23604 // Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA. /// ENST00000261891 // intron // 0 // — // — // — // —	DAPK2	DAPK2, Homo sapiens death-associated protein kinase 2 (DAPK2), q22.31
SNP_A-2273353	gactcctgaagaccaa[C/T]agaaaacaaacgaaca	C	T	NM_152826 // intron // 0 // Hs.188634 // SNX1 // 6642 // Homo sapiens sorting nexin 1 (SNX1), transcript variant 3, mRNA. /// NM_003100 // intron // 0 // Hs.134822 // SNX2 // 6643 // Homo sapiens sorting nexin 2 (SNX2), mRNA. /// NM_148955 // intron // 0	SNX1	SNX1, Homo sapiens sorting nexin 1 (SNX1), transcript variant 3, q22.31
SNP_A-2162761	attttgagcagccaga[C/G]aggtgaagtatacaat	C	G	NM_182703 // intron // 0 // Hs.207157 // LOC348094 // 348094 // Homo sapiens hypothetical protein LOC348094 (LOC348094), mRNA. /// ENST00000319580 // intron // 0 // — // — // — // —	LOC348094	LOC348094, Homo sapiens hypothetical protein LOC348094 (LOC348094), q22.31
SNP_A-1807508	gtctgctataagtcta[A/G]taatagtcacgccttt	A	G	NM_005848 // upstream // 52098 // Hs.513817 // MYCPBP // 10260 // Homo sapiens c-myc promoter binding protein (MYCPBP), mRNA. /// NM_004663 // upstream // 25112 // Hs.321541 // RAB11A // 8766 // Homo sapiens RAB11A, member RAS oncogene family (RAB11A), mR	MYCPBP	MYCPBP, Homo sapiens c-myc promoter binding protein (MYCPBP), q22.31
SNP_A-2004241	tttagcttaattcaac[C/T]aagtgtcttaaaatgg	C	T	NM_032445 // intron // 0 // Hs.438250 // MEGF11 // 84465 // Homo sapiens MEGF11 protein (MEGF11), mRNA. /// ENST00000288745 // intron // 0 // — // — // — // —	MEGF11	MEGF11, Homo sapiens MEGF11 protein (MEGF11), q22.31
SNP_A-1746424	tgagtccaagcagtacccttcctca[A/G]taattctcaaataggcct ctgaagt	A	G	NM_005585 // upstream // 66201 // Hs.153863 // MADH6 // 4091 // MAD, mothers against decapentaplegic homolog 6 (Drosophila) /// NM_017975 // downstream // 86997 // Hs.21331 // FLJ10036 // 55055 // hypothetical protein FLJ10036	MADH6	MADH6 , rs893912, MAD, mothers against decapentaplegic homolog 6 (Drosophila) ,q22.31
SNP_A-2004246	gaaaggtaaacagccc[C/T]gatgtccagccatagg	C	T	NM_000968 // upstream // 74150 // Hs.432898 // RPL4 // 6124 // Homo sapiens ribosomal protein L4 (RPL4), mRNA. /// NM_000968 // upstream // 54464 // Hs.432898 // RPL4 // 6124 // Homo sapiens ribosomal protein L4 (RPL4), mRNA. /// NM_017975 // downstream /	RPL4	RPL4, Homo sapiens ribosomal protein L4 (RPL4), q22.31
SNP_A-2069866	acacagcacattgctg[A/G]acatcaataaatattt	A	G	NM_000968 // upstream // 87791 // Hs.432898 // RPL4 // 6124 // Homo sapiens ribosomal protein L4 (RPL4), mRNA. /// NM_000968 // upstream // 68105 // Hs.432898 // RPL4 // 6124 // Homo sapiens ribosomal protein L4 (RPL4), mRNA. /// NM_017975 // downstream /	RPL4	RPL4, Homo sapiens ribosomal protein L4 (RPL4), q22.31
SNP_A-1828362	taagatgtaaatagaa[A/G]catcgtgtgagacttc	A	G	NM_000968 // upstream // 184145 // Hs.432898 // RPL4 // 6124 // Homo sapiens ribosomal protein L4 (RPL4), mRNA. /// NM_000968 // upstream // 164459 // Hs.432898 // RPL4 // 6124 // Homo sapiens ribosomal protein L4 (RPL4), mRNA. /// NM_017975 // downstream	RPL4	RPL4, Homo sapiens ribosomal protein L4 (RPL4), q22.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1899293	tggaacacggaactct[C/T]agagtctgttagatga	C	T	NM_005585 // intron // 0 // Hs.153863 // SMAD6 // 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// ENST00000288840 // intron // 0 // — // — // — // — /// ENST00000338426 // intron // 0 // — // — // — // —	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.31
SNP_A-2186932	cagggtgtgtggttca[G/T]tccattcagtgtgttc	G	T	NM_005585 // intron // 0 // Hs.153863 // SMAD6 // 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// ENST00000288840 // intron // 0 // --- // --- // --- // --- /// ENST00000338426 // intron // 0 // — // — // — // —	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.31
SNP_A-1801107	gtagcagtggtgaaaa[C/T]gcttgcatgggtgcgc	C	T	NM_005585 // downstream // 80744 // Hs.153863 // SMAD6 // 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 // upstream // 203208 // Hs.288261 // SMAD3 // 4088 // Homo sapiens SMAD, mothers against DPP homo	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.32
SNP_A-2296968	gccaataacagtagct[A/C]aaagaatgcttactgt	A	C	NM_005585 // downstream // 139783 // Hs.153863 // SMAD6 // 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 // upstream // 144169 // Hs.288261 // SMAD3 // 4088 // Homo sapiens SMAD, mothers against DPP hom	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.33
SNP_A-1817699	gttcccagttgtgtca[C/G]attctcaccacctacc	C	G	NM_005585 // downstream // 141813 // Hs.153863 // SMAD6 // 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 // upstream // 142139 // Hs.288261 // SMAD3 // 4088 // Homo sapiens SMAD, mothers against DPP hom	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.33
SNP_A-1941151	ttgctgagaaacaaag[G/T]catttttctgtctcttt	G	T	NM_005585 // downstream // 257058 // Hs.153863 // SMAD6 // 4091 // Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), mRNA. /// NM_005902 // upstream // 26894 // Hs.288261 // SMAD3 // 4088 // Homo sapiens SMAD, mothers against DPP homo	SMAD6	SMAD6, Homo sapiens SMAD, mothers against DPP homolog 6 (Drosophila) (SMAD6), q22.33
SNP_A-1830873	taatcttgccacatga[A/T]atttaccaaaacagaa	A	T	NM_005902 // intron // 0 // Hs.288261 // SMAD3 // 4088 // Homo sapiens SMAD, mothers against DPP homolog 3 (Drosophila) (SMAD3), mRNA. /// ENST00000327367 // intron // 0 // — // — // — // —	SMAD3	SMAD3, Homo sapiens SMAD, mothers against DPP homolog 3 (Drosophila) (SMAD3), q22.33
SNP_A-2226062	ctaacaggccgcacac[C/G]ggtatcagtccacggc	C	G	NM_005902 // intron // 0 // Hs.288261 // SMAD3 // 4088 // Homo sapiens SMAD, mothers against DPP homolog 3 (Drosophila) (SMAD3), mRNA. /// ENST00000327367 // intron // 0 // — // — // — // —	SMAD3	SMAD3, Homo sapiens SMAD, mothers against DPP homolog 3 (Drosophila) (SMAD3), q22.33
SNP_A-1888515	tgaggagcgctggtct[C/T]acctatgatcccaaag	C	T	NM_002757 // downstream // 12740 // Hs.114198 // MAP2K5 // 5607 // Homo sapiens mitogen-activated protein kinase kinase 5 (MAP2K5), transcript variant B, mRNA. /// NM_145161 // downstream // 12586 // Hs.114198 // MAP2K5 // 5607 // Homo sapiens mitogen-act	MAP2K5	MAP2K5, Homo sapiens mitogen-activated protein kinase kinase 5 (MAP2K5), transcript variant B, q23
SNP_A-1866161	tcccaggatgttccga[C/G]ggctaagaccagagcg	C	G	NM_016166 // upstream // 218451 // Hs.162458 // PIAS1 // 8554 // Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), mRNA. /// ENST00000341418 // downstream // 1943 // --- // — // — // — /// ENST00000249636 // upstream // 218451 // — // -	PIAS1	PIAS1, Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), q23
SNP_A-1794406	ggtcccggaggctccc[A/G]ctgtccacatctgcat	A	G	NM_001004439 // intron // 0 // Hs.436416 // ITGA11 // 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, mRNA. /// NM_012211 // intron // 0 // Hs.436416 // ITGA11 // 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transcript varia	ITGA11	ITGA11, Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, q23
SNP_A-2076746	acatttttctcactaa[C/T]gctcagcagagaaaaa	C	T	NM_001004439 // upstream // 9512 // Hs.436416 // ITGA11 // 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, mRNA. /// NM_012211 // upstream // 9512 // Hs.436416 // ITGA11 // 22801 // Homo sapiens integrin, alpha 11 (ITGA11), transc	ITGA11	ITGA11, Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 1, q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1863258	tcatttgcagttgaga[A/G]aaatgtaaacaaatgt	A	G	NM_006091 // intron // 0 // Hs.24907 // CORO2B // 10391 // Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA. /// ENST00000261861 // intron // 0 // --- // --- // --- // ---	CORO2B	CORO2B, Homo sapiens coronin, actin binding protein, 2B (CORO2B), q23
SNP_A-1802477	gtatccctacccatca[C/T]atttaaggcctcgaat	C	T	NM_006091 // intron // 0 // Hs.24907 // CORO2B // 10391 // Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA. /// ENST00000261861 // intron // 0 // --- // --- // --- // ---	CORO2B	CORO2B, Homo sapiens coronin, actin binding protein, 2B (CORO2B), q23
SNP_A-1863982	tccacaaatacatgga[A/C]actctgaacgtcctct	A	C	NM_006091 // downstream // 22360 // Hs.24907 // CORO2B // 10391 // Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA. /// NM_006305 // downstream // 29707 // Hs.458747 // ANP32A // 8125 // Homo sapiens acidic (leucine-rich) nuclear phosphopro	CORO2B	CORO2B, Homo sapiens coronin, actin binding protein, 2B (CORO2B), q23
SNP_A-2293727	ggttaattaatgaagc[C/T]gccgtaacttttttgt	C	T	NM_145658 // upstream // 16538 // Hs.128105 // SPESP1 // 246777 // Homo sapiens sperm equatorial segment protein 1 (SPESP1), mRNA. /// ENST00000321952 // downstream // 79230 // — // — // — // — /// ENST00000310673 // upstream // 16538 // — // –	SPESP1	SPESP1, Homo sapiens sperm equatorial segment protein 1 (SPESP1), q23
SNP_A-1652954	aaagaatgagagtgtggccctagaa[C/T]atttgtcatgcagtgtg ctcagagc	C	T	BC031958 // upstream // 154615 // Hs.369937 // - // - // MRNA similar to LOC145836 (cDNA clone MGC:42951 IMAGE:4837541), complete cds /// NM_001003 // downstream // 225074 // Hs.356502 // RPLP1 // 6176 // ribosomal protein, large, P1	-	- , rs10518826, MRNA similar to LOC145836 (cDNA clone MGC:42951 IMAGE:4837541), complete cds ,q23
SNP_A-1696830	catgttggtatggcactctctatgt[C/T]acagcacagagacctcta ctttgcc	C	T	BC031958 // upstream // 55368 // Hs.369937 // - // - // MRNA similar to LOC145836 (cDNA clone MGC:42951 IMAGE:4837541), complete cds /// NM_001003 // downstream // 324321 // Hs.356502 // RPLP1 // 6176 // ribosomal protein, large, P1	-	- , rs186248, MRNA similar to LOC145836 (cDNA clone MGC:42951 IMAGE:4837541), complete cds ,q23
SNP_A-2286395	gatgctctttagctga[C/T]ggaggtaaggtctccc	C	T	NM_213725 // downstream // 280949 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 // downstream // 280949 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large,	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-2308990	gcttttccaatttaca[A/G]tgatcaggaacccacg	A	G	NM_213725 // downstream // 284910 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 // downstream // 284910 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large,	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-2286643	gatggagtgtggaaaa[G/T]tctgaatgacagccaa	G	T	NM_213725 // downstream // 286204 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 // downstream // 286204 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large,	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-2294204	gaatctcagaattttg[C/G]aagtgcttcaggccgg	C	G	NM_213725 // downstream // 324244 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, mRNA. /// NM_001003 // downstream // 324244 // Hs.356502 // RPLP1 // 6176 // Homo sapiens ribosomal protein, large,	RPLP1	RPLP1, Homo sapiens ribosomal protein, large, P1 (RPLP1), transcript variant 2, q23
SNP_A-2294285	tagagaattgggagaa[A/T]gaactgtttgggagcc	A	T	NM_005078 // downstream // 185168 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// ENST00000318987 // downstream // 20998 // — // — // — // — /// ENST00000317509 // dow	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-1703665	cctattcctaagccccttccacca[C/G]gacatctttgatcctaa gcaagat	C	G	NM_005078 // downstream // 90643 // Hs.287362 // TLE3 // 7090 // transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	TLE3	TLE3 , rs2415068, transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila),q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1930990	ttccagtcacacagca[C/T]agacctgacaccaaag	C	T	NM_005078 // downstream // 153412 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// ENST00000318987 // downstream // 52754 // — // — // — /// ENST00000317509 // dow	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2089657	acttcatttcacaaggt[C/T]attggccagaactatt	C	T	NM_005078 // upstream // 30802 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 528232 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantige	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2257835	ctttggttagtcatc[C/T]aaatacctctgggtcc	C	T	NM_005078 // upstream // 90725 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 468309 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantige	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2175798	cacattgcagacataa[C/G]acaggaaggctgttc	C	G	NM_005078 // upstream // 94875 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 464159 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantige	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2306996	gctgttctagaaagct[A/G]aagatccaattctaag	A	G	NM_005078 // upstream // 94901 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 464133 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantige	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2294548	gtatgtgtgaaaataa[C/G]tagcaggcttgggggga	C	G	NM_005078 // upstream // 105252 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 453782 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantig	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-1674050	taaaggcagaggcccagcaccacctta[A/G]agaagagagactgca aaaggaatcat	A	G	NM_005078 // upstream // 368816 // Hs.287362 // TLE3 // 7090 // transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) /// NM_018003 // downstream // 191299 // Hs.49753 // UACA // 55075 // uveal autoantigen with coiled-coil domains and ankyrin	TLE3	TLE3, rs10518906, transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila), q23
SNP_A-1726662	aaacaatgaataacttttgtgcactt[A/G]acccatctgtagaaaac catctgtg	A	G	NM_005078 // upstream // 369744 // Hs.287362 // TLE3 // 7090 // transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) /// NM_018003 // downstream // 190371 // Hs.49753 // UACA // 55075 // uveal autoantigen with coiled-coil domains and ankyrin	TLE3	TLE3, rs952960, transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila), q23
SNP_A-1837082	tactgtatctatcaa[C/G]tgtaagacacgtttca	C	G	NM_005078 // upstream // 332365 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 226669 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantig	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2268241	gaatgagcacagtgaa[G/T]atccaattagtgagtt	G	T	NM_005078 // upstream // 437112 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 121922 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantig	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23
SNP_A-2047491	aagatgcacggcagca[A/C]agcattatatagtatt	A	C	NM_005078 // upstream // 543492 // Hs.287362 // TLE3 // 7090 // Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA. /// NM_018003 // downstream // 15542 // Hs.108049 // UACA // 55075 // Homo sapiens uveal autoantige	TLE3	TLE3, Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2104861	agcatagccacctct[A/T]aagactgtagcaccag	A	T	NM_024817 // intron // 0 // Hs.387057 // FLJ13710 // 79875 // Homo sapiens hypothetical protein FLJ13710 (FLJ13710), mRNA. /// ENST00000357769 // intron // 0 // — // — // — // — /// ENST00000345002 // intron // 0 // — // — // — // — /// EN	FLJ13710	FLJ13710, Homo sapiens hypothetical protein FLJ13710 (FLJ13710), q23
SNP_A-2136232	atcaattccacaltac[A/G]gccagttaaagaacaa	A	G	NM_024817 // 3UTR // 0 // Hs.387057 // FLJ13710 // 79875 // Homo sapiens hypothetical protein FLJ13710 (FLJ13710), mRNA. /// ENST00000345002 // intron // 0 // — // — // — // — /// ENST00000261862 // 3UTR // 0 // — // — // — // —	FLJ13710	FLJ13710, Homo sapiens hypothetical protein FLJ13710 (FLJ13710), q23
SNP_A-1904057	tgggcagatcactccag[A/G]agttcgaaagtagcct	A	G	NM_024817 // downstream // 7395 // Hs.387057 // FLJ13710 // 79875 // Homo sapiens hypothetical protein FLJ13710 (FLJ13710), mRNA. /// NM_024817 // downstream // 4772 // Hs.387057 // FLJ13710 // 79875 // Homo sapiens hypothetical protein FLJ13710 (FLJ13710	FLJ13710	FLJ13710, Homo sapiens hypothetical protein FLJ13710 (FLJ13710), q23
SNP_A-2295567	tcatttacacaactgal[A/G]tactccacagctcata	A	G	NM_006901 // intron // 0 // Hs.546268 // MYO9A // 4649 // Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // — // — // — // — /// ENST00000354477 // intron // 0 // — // — // — // —	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-1890316	tgatccacatttggtc[A/G]cagatgtagatcccc	A	G	NM_006901 // intron // 0 // Hs.546268 // MYO9A // 4649 // Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // — // — // — // — /// ENST00000354477 // intron // 0 // — // — // — // —	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2303776	gctcaggagttaaagal[C/T]caggttggacaacaca	C	T	NM_006901 // intron // 0 // Hs.546268 // MYO9A // 4649 // Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // — // — // — // — /// ENST00000354477 // intron // 0 // — // — // — // —	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2032236	aaagtgtgtcacctta[C/T]agaaaagagcaaggtct	C	T	NM_006901 // intron // 0 // Hs.546268 // MYO9A // 4649 // Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // — // — // — // — /// ENST00000354477 // intron // 0 // — // — // — // —	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2077031	accaacctatgaagac[A/T]gtctccacagctcaag	A	T	NM_006901 // intron // 0 // Hs.546268 // MYO9A // 4649 // Homo sapiens myosin IXA (MYO9A), mRNA. /// ENST00000356056 // intron // 0 // — // — // — // — /// ENST00000354477 // intron // 0 // — // — // — // —	MYO9A	MYO9A, Homo sapiens myosin IXA (MYO9A), q23
SNP_A-2025762	aaaatgctaatccaaa[C/T]aagggcaggttggaga	C	T	NM_145204 // downstream // 14808 // Hs.513002 // SENP8 // 123228 // Homo sapiens SUMO/sentrin specific protease family member 8 (SENP8), mRNA. /// ENST00000340912 // downstream // 14808 // — // — // — // — /// ENST00000309731 // downstream // 4037	SENP8	SENP8, Homo sapiens SUMO,q23
SNP_A-2062756	aatgtgacctccagca[A/G]ctttctcagcccag	A	G	NM_002654 // upstream // 5425 // Hs.198281 // PKM2 // 5315 // Homo sapiens pyruvate kinase, muscle (PKM2), transcript variant 1, mRNA. /// NM_182470 // upstream // 5425 // Hs.198281 // PKM2 // 5315 // Homo sapiens pyruvate kinase, muscle (PKM2), transcrip	PKM2	PKM2, Homo sapiens pyruvate kinase, muscle (PKM2), transcript variant 1, q23
SNP_A-2225820	ctaaataagaaaaagtc[C/T]aagttgagtctataaa	C	T	NM_020213 // intron // 0 // Hs.270244 // PARP6 // 56965 // Homo sapiens poly (ADP-ribose) polymerase family, member 6 (PARP6), mRNA. /// NM_020214 // intron // 0 // Hs.270244 // PARP6 // 56965 // Homo sapiens poly (ADP-ribose) polymerase family, member 6	PARP6	PARP6, Homo sapiens poly (ADP-ribose) polymerase family, member 6 (PARP6), q23
SNP_A-2092616	agaaatatctgtgtaa[C/T]acaactgctaaattat	C	T	NM_052840 // intron // 0 // Hs.348342 // BRUNOL6 // 60677 // Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), mRNA. /// ENST00000287202 // intron // 0 // — // — // — // —	BRUNOL6	BRUNOL6, Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), q23
SNP_A-2138555	atccattcttaaggca[C/T]gaacacaaatagtgag	C	T	NM_052840 // intron // 0 // Hs.348342 // BRUNOL6 // 60677 // Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), mRNA. /// ENST00000287202 // intron // 0 // — // — // — // —	BRUNOL6	BRUNOL6, Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1927972	ttcaatcctggctcta[C/T]cacttgcttctctaag	C	T	NM_052840 // intron // 0 // Hs.348342 // BRUNOL6 // 60677 // Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), mRNA. /// ENST00000287202 // intron // 0 // — // — // — // —	BRUNOL6	BRUNOL6, Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), q23
SNP_A-1787505	gggaatcatgatctta[A/C]cttgcagcgttgtgat	A	C	NM_052840 // intron // 0 // Hs.348342 // BRUNOL6 // 60677 // Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), mRNA. /// ENST00000287202 // intron // 0 // — // — // — // —	BRUNOL6	BRUNOL6, Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), q23
SNP_A-2076462	acatttacacaaagaa[A/G]tgggtattgtgaaaga	A	G	ENST00000341689 // intron // 0 // — // — // — // —	-	q24.1
SNP_A-1799611	gtaattctgccataac[A/G]aaactcacctgattgg	A	G	NM_005744 // upstream // 64890 // Hs.268787 // ARIH1 // 25820 // Homo sapiens ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) (ARIH1), mRNA. /// ENST00000341689 // downstream // 1407 // — // — // — // — /// ENST000	ARIH1	ARIH1, Homo sapiens ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) (ARIH1), q24.1
SNP_A-1742203	ccattgtacaacagtattctaggcc[A/G]ccaacaaaagtgtgac agacacact	A	G	AJ009771 // 3UTR // 0 // Hs.181461 // ARIH1 // 25820 // ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	ARIH1	ARIH1 , rs4777517, ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila),q24.1
SNP_A-1661143	catcctagggagaatttcaatcata[C/T]gtaagtgcagacagaa ttaggtact	C	T	NM_033028 // intron // 0 // Hs.26471 // BBS4 // 585 // Bardet-Biedl syndrome 4	BBS4	BBS4 , rs4777529, Bardet-Biedl syndrome 4,q24.1
SNP_A-1781527	ggattcactctgaaga[A/G]catggattaagtttga	A	G	NM_033028 // intron // 0 // Hs.208681 // BBS4 // 585 // Homo sapiens Bardet-Biedl syndrome 4 (BBS4), mRNA. /// ENST00000268057 // intron // 0 // — // — // — // —	BBS4	BBS4, Homo sapiens Bardet-Biedl syndrome 4 (BBS4), q24.1
SNP_A-2300279	gcctctaaggcaaaga[C/G]gatgtttcctatctcc	C	G	NM_031284 // intron // 0 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// ENST00000311669 // intron // 0 // — // — // — // —	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-1831630	taattagcgatcttac[C/T]gcattttgcaaatagg	C	T	NM_031284 // intron // 0 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// ENST00000311669 // intron // 0 // — // — // — // —	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2295862	tgttgtagcccttgta[A/G]catctgctgtagtgat	A	G	NM_031284 // upstream // 3432 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 265393 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST00000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2073821	acagtgcctggactag[A/G]agcagctaacatccca	A	G	NM_031284 // upstream // 11294 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 257531 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-1834328	tacattcacctttgca[C/T]atatcttctgctggtc	C	T	NM_031284 // upstream // 28186 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 240639 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2295890	tatgttgatccaaaga[C/T]tcaggaattaaaaagt	C	T	NM_031284 // upstream // 45901 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 222924 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2176559	cacccagcatgttgta[C/T]gtccacgtgtttttgt	C	T	NM_031284 // upstream // 76387 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 192438 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2295907	cttgtgtagaaaaagc[A/G]aacagactgctcacaa	A	G	NM_031284 // upstream // 82086 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 186739 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2217316	cctgaacccctttcac[C/T]gtctatttggatagaa	C	T	NM_031284 // upstream // 83942 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 184883 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-1815971	gttaatttattcagc[A/G]acagtttcatagta	A	G	NM_031284 // upstream // 182738 // Hs.513013 // ADPGK // 83440 // Homo sapiens ADP-dependent glucokinase (ADPGK), mRNA. /// NM_002499 // upstream // 86087 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST0000	ADPGK	ADPGK, Homo sapiens ADP-dependent glucokinase (ADPGK), q24.1
SNP_A-2187651	cagtacaaaaaggagaa[C/T]agaaccccagtcaagc	C	T	NM_002499 // intron // 0 // Hs.388613 // NEO1 // 4756 // Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA. /// ENST00000261908 // intron // 0 // — // — // — /// ENST00000339362 // intron // 0 // — // — // — // —	NEO1	NEO1, Homo sapiens neogenin homolog 1 (chicken) (NEO1), q24.1
SNP_A-1952577	tttctgccctaagaga[C/G]cacagaaatagctgtaa	C	G	NM_005477 // upstream // 10340 // Hs.225671 // HCN4 // 10021 // Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4), mRNA. /// ENST00000261917 // upstream // 10340 // — // — // — // — /// ENST00000331090 //	HCN4	HCN4, Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4), q24.1
SNP_A-2127766	ataactggtatttctc[C/T]aggaactctctgtaac	C	T	ENST00000331090 // intron // 0 // — // — // — /// —	-	q24.1
SNP_A-2023607	aaaactgaggaaggaa[C/G]aggagccacacatgtc	C	G	ENST00000287226 // intron // 0 // — // — // —	-	q24.1
SNP_A-2273164	gactcacacagaaatc[A/G]cttggagaggaagaac	A	G	NM_025240 // intron // 0 // Hs.77873 // B7H3 // 80381 // Homo sapiens B7 homolog 3 (B7H3), mRNA. /// ENST00000287226 // intron // 0 // — // — // — // — // — /// ENST00000318424 // intron // 0 // — // — // — // — // — /// ENST00000318443 // intron //	B7H3	B7H3, Homo sapiens B7 homolog 3 (B7H3), q24.1
SNP_A-2095116	agaatgtttgacatga[C/T]acaaagctgcccgaag	C	T	NM_025240 // intron // 0 // Hs.77873 // B7H3 // 80381 // Homo sapiens B7 homolog 3 (B7H3), mRNA. /// ENST00000318424 // intron // 0 // — // — // — // — // — /// ENST00000318443 // intron // 0 // — // — // — // —	B7H3	B7H3, Homo sapiens B7 homolog 3 (B7H3), q24.1
SNP_A-2145469	atgcaggctacttcca[C/T]tcaagctctagaagga	C	T	NM_025240 // intron // 0 // Hs.77873 // B7H3 // 80381 // Homo sapiens B7 homolog 3 (B7H3), mRNA. /// ENST00000318424 // intron // 0 // — // — // — // — // — /// ENST00000318443 // intron // 0 // — // — // — // —	B7H3	B7H3, Homo sapiens B7 homolog 3 (B7H3), q24.1
SNP_A-1809565	gtgagagttagaaaatg[A/G]acaatggagttctgtg	A	G	NM_017455 // upstream // 130579 // Hs.187866 // SDFR1 // 27020 // Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, mRNA. /// NM_012428 // upstream // 130629 // Hs.187866 // SDFR1 // 27020 // Homo sapiens stromal cell	SDFR1	SDFR1, Homo sapiens stromal cell derived factor receptor 1 (SDFR1), transcript variant alpha, q24.1
SNP_A-1887562	tgagagactgtttgtg[C/T]aagaaggagcgagagg	C	T	NM_033246 // intron // 0 // Hs.526464 // PML // 5371 // Homo sapiens promyelocytic leukemia (PML), transcript variant 7, mRNA. /// NM_002675 // intron // 0 // Hs.526464 // PML // 5371 // Homo sapiens promyelocytic leukemia (PML), transcript variant 6, mRN	PML	PML, Homo sapiens promyelocytic leukemia (PML), transcript variant 7, q24.1
SNP_A-2212466	ccctgttcactcttcc[A/T]caaagaacccttcccc	A	T	NM_182791 // intron // 0 // Hs.383206 // FLJ32855 // 80125 // Homo sapiens hypothetical protein FLJ32855 (FLJ32855), mRNA. /// ENST00000321288 // intron // 0 // — // — // — // — /// ENST00000321374 // intron // 0 // — // — // — // — /// EN	FLJ32855	FLJ32855, Homo sapiens hypothetical protein FLJ32855 (FLJ32855), q24.1
SNP_A-1905125	tgggtgctgtgggtaa[A/G]gtctgagggggacagtg	A	G	NM_182791 // intron // 0 // Hs.383206 // FLJ32855 // 80125 // Homo sapiens hypothetical protein FLJ32855 (FLJ32855), mRNA. /// ENST00000321288 // intron // 0 // — // — // — // — /// ENST00000321374 // intron // 0 // — // — // — // — /// EN	FLJ32855	FLJ32855, Homo sapiens hypothetical protein FLJ32855 (FLJ32855), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2201375	ccaatcgagagaaaaa[A/T]tcatgcctgcccatgt	A	T	NM_182791 // intron // 0 // Hs.383206 // FLJ32855 // 80125 // Homo sapiens hypothetical protein FLJ32855 (FLJ32855), mRNA. /// ENST00000321288 // intron // 0 // — // — // — // — /// ENST00000321374 // intron // 0 // — // — // — // — /// EN	FLJ32855	FLJ32855, Homo sapiens hypothetical protein FLJ32855 (FLJ32855), q24.1
SNP_A-2312470	ggacccactgactttc[A/C]agtgtagatgtggatg	A	C	NM_182791 // intron // 0 // Hs.383206 // FLJ32855 // 80125 // Homo sapiens hypothetical protein FLJ32855 (FLJ32855), mRNA. /// ENST00000321288 // intron // 0 // — // — // — // — /// ENST00000321374 // intron // 0 // — // — // — // — /// EN	FLJ32855	FLJ32855, Homo sapiens hypothetical protein FLJ32855 (FLJ32855), q24.1
SNP_A-1804274	gtcacgtatcattgtg[A/G]aatactccattaagcc	A	G	NM_182791 // downstream // 410 // Hs.383206 // FLJ32855 // 80125 // Homo sapiens hypothetical protein FLJ32855 (FLJ32855), mRNA. /// NM_000781 // downstream // 1213 // Hs.303980 // CYP11A1 // 1583 // Homo sapiens cytochrome P450, family 11, subfamily A, p	FLJ32855	FLJ32855, Homo sapiens hypothetical protein FLJ32855 (FLJ32855), q24.1
SNP_A-1813132	gtggtaggagactgac[A/G]aagaaattgattagtc	A	G	NM_000781 // intron // 0 // Hs.303980 // CYP11A1 // 1583 // Homo sapiens cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1), nuclear gene encoding mitochondrial protein, mRNA /// ENST00000268053 // intron // 0 // — // — // — // —	CYP11A1	CYP11A1, Homo sapiens cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1), nuclear gene encoding mitochondrial protein, q24.1
SNP_A-2296941	gccaagtgcaatctta[C/G]aggaatgacccatgta	C	G	NM_000126 // intron // 0 // Hs.39925 // ETFA // 2108 // Homo sapiens electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) (ETFA), nuclear gene encoding mitochondria /// ENST00000267950 // intron // 0 // — // — // — // —	ETFA	ETFA, Homo sapiens electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) (ETFA), nuclear gene encoding mitochondria q24.2
SNP_A-1674323	gaacaaagaggaaagatggccaaga[C/T]gaccacttgaattc ctatgaaatga	C	T	NM_020843 // intron // 0 // Hs.285848 // ZNF291 // 49855 // zinc finger protein 291	ZNF291	ZNF291 , rs3743175, zinc finger protein 291,q24.3
SNP_A-2300138	gcctcatttcctatac[A/G]aaacagtcactaaaca	A	G	NM_020843 // intron // 0 // Hs.458986 // ZNF291 // 49855 // Homo sapiens zinc finger protein 291 (ZNF291), mRNA. /// ENST00000324767 // intron // 0 // — // — // — // — /// ENST00000303521 // intron // 0 // — // — // — // —	ZNF291	ZNF291, Homo sapiens zinc finger protein 291 (ZNF291), q24.3
SNP_A-1913675	tgtgtagtacagtgtt[C/G]aaaagtttgttctcaa	C	G	NM_020843 // intron // 0 // Hs.458986 // ZNF291 // 49855 // Homo sapiens zinc finger protein 291 (ZNF291), mRNA. /// ENST00000324767 // intron // 0 // — // — // — // — /// ENST00000303521 // intron // 0 // — // — // — // —	ZNF291	ZNF291, Homo sapiens zinc finger protein 291 (ZNF291), q24.3
SNP_A-2150641	atgtgattcatgtata[A/T]caaagaggatcaggaa	A	T	ENST00000312493 // 3UTR // 0 // — // — // — // —	-	q24.3
SNP_A-2232802	ctcactgtgtctggca[C/T]tcaccccaattattac	C	T	ENST00000312493 // intron // 0 // — // — // — // —	-	q24.3
SNP_A-2303700	gctcagaaaattaaag[A/T]agaaaattcagagctg	A	T	ENST00000312493 // intron // 0 // — // — // — // —	-	q24.3
SNP_A-2052708	aagtattttatactta[C/T]ggcatatcgtcactgg	C	T	NM_018200 // downstream // 108965 // Hs.69594 // HMG20A // 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 18505 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-2027421	aaacattgacgctttc[A/G]atatcatgttaatttc	A	G	NM_018200 // downstream // 114041 // Hs.69594 // HMG20A // 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 13429 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-1833217	tacacgcgacactctc[A/G]cccttgcattcacacg	A	G	NM_018200 // downstream // 119298 // Hs.69594 // HMG20A // 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 8172 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. //	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-1912099	tgtgaggctgtacata[C/T]gtgagctcctccgtgt	C	T	NM_018200 // downstream // 119447 // Hs.69594 // HMG20A // 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 8023 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. //	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2113643	aggctcagagagggaa[A/G]gtaacctgcctagagt	A	G	NM_018200 // downstream // 124394 // Hs.69594 // HMG20A // 10363 // Homo sapiens high-mobility group 20A (HMG20A), mRNA. /// NM_032808 // downstream // 3076 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. //	HMG20A	HMG20A, Homo sapiens high-mobility group 20A (HMG20A), q24.3
SNP_A-1871919	tctacaggcatctcac[A/C]atttacgtgtccactg	A	C	NM_032808 // intron // 0 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// ENST00000355300 // intron // 0 // — // — // — // —	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-1942859	ttggggcctacgccta[A/C]attcgagggcctgaac	A	C	NM_032808 // intron // 0 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// ENST00000355300 // intron // 0 // — // — // — // —	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-2096639	agacggcctcggctgc[A/G]atggcgcctggaaagt	A	G	NM_032808 // upstream // 154194 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// NM_032808 // upstream // 90428 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mR	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-2051946	aaggtggattaccaca[A/G]tgctccccaagcacac	A	G	NM_032808 // upstream // 165107 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// NM_032808 // upstream // 101341 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), m	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-2096294	agaccagcccctatca[A/T]gctccctggcacacag	A	T	NM_032808 // upstream // 206974 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), mRNA. /// NM_032808 // upstream // 143208 // Hs.132344 // LRRN6A // 84894 // Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), m	LRRN6A	LRRN6A, Homo sapiens leucine rich repeat neuronal 6A (LRRN6A), q24.3
SNP_A-1674613	gctgactgaaacttagcccttcatg[G/T]acttaaacttgtttccttttaaact	G	T	NM_015079 // intron // 0 // Hs.438702 // KIAA1055 // 23102 // KIAA1055 protein	KIAA1055	KIAA1055 , rs10519182, KIAA1055 protein,q25.1
SNP_A-2078884	acccaacttggacctg[A/T]agagtcaaggtcaaag	A	T	NM_006383 // intron // 0 // Hs.129867 // CIB2 // 10518 // Homo sapiens calcium and integrin binding family member 2 (CIB2), mRNA. /// ENST00000258930 // intron // 0 // — // — // — // —	CIB2	CIB2, Homo sapiens calcium and integrin binding family member 2 (CIB2), q25.1
SNP_A-2268228	gaatgagacctgaagc[C/T]gctggacatcagggca	C	T	NM_006383 // intron // 0 // Hs.129867 // CIB2 // 10518 // Homo sapiens calcium and integrin binding family member 2 (CIB2), mRNA. /// ENST00000258930 // intron // 0 // — // — // — // —	CIB2	CIB2, Homo sapiens calcium and integrin binding family member 2 (CIB2), q25.1
SNP_A-2229445	ctaggctctggcaaag[A/G]atcagaacataacact	A	G	NM_006383 // intron // 0 // Hs.129867 // CIB2 // 10518 // Homo sapiens calcium and integrin binding family member 2 (CIB2), mRNA. /// ENST00000258930 // intron // 0 // — // — // — // —	CIB2	CIB2, Homo sapiens calcium and integrin binding family member 2 (CIB2), q25.1
SNP_A-2113084	aggccagatctaaaaa[C/T]gtactgtcaagaaaca	C	T	NM_005530 // 3UTR // 0 // Hs.546262 // IDH3A // 3419 // Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, mRNA. /// NM_015162 // 3UTR // 0 // Hs.250616 // BG1 // 23205 // Homo sapiens lipidosin (BG1	IDH3A	IDH3A, Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, q25.1
SNP_A-2141208	atctggtatataggag[C/T]ctacaatggctatcac	C	T	NM_025234 // intron // 0 // Hs.513055 // REC14 // 80349 // Homo sapiens recombination protein REC14 (REC14), mRNA. /// ENST00000267973 // intron // 0 // — // — // — // — // —	REC14	REC14, Homo sapiens recombination protein REC14 (REC14), q25.1
SNP_A-1806124	gtcctctccctggtac[C/T]atctgttagtccactc	C	T	NM_004378 // downstream // 47779 // Hs.346950 // CRABP1 // 1381 // Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), mRNA. /// NM_004136 // upstream // 42282 // Hs.436031 // IREB2 // 3658 // Homo sapiens iron-responsive element binding prote	CRABP1	CRABP1, Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), q25.1
SNP_A-2278357	gagctaattaaaccaa[C/T]gtggacccaagtgcct	C	T	NM_004378 // downstream // 49104 // Hs.346950 // CRABP1 // 1381 // Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), mRNA. /// NM_004136 // upstream // 40957 // Hs.436031 // IREB2 // 3658 // Homo sapiens iron-responsive element binding prote	CRABP1	CRABP1, Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2312841	ggactgctttccacac[A/C]cttgtaatttcatccc	A	C	NM_004378 // downstream // 71238 // Hs.346950 // CRABP1 // 1381 // Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), mRNA. /// NM_004136 // upstream // 18823 // Hs.436031 // IREB2 // 3658 // Homo sapiens iron-responsive element binding prote	CRABP1	CRABP1, Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), q25.1
SNP_A-1924563	ttatactcactactca[C/T]attcattttacaccaa	C	T	NM_004136 // intron // 0 // Hs.436031 // IREB2 // 3658 // Homo sapiens iron-responsive element binding protein 2 (IREB2), mRNA. /// ENST00000258886 // intron // 0 // — // — // — // —	IREB2	IREB2, Homo sapiens iron-responsive element binding protein 2 (IREB2), q25.1
SNP_A-2257371	ctttgaaatgcaaacc[C/T]catcatgacatgcctt	C	T	NM_014272 // intron // 0 // Hs.16441 // ADAMTS7 // 11173 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 (ADAMTS7), mRNA. /// ENST00000258883 // intron // 0 // — // — // — // —	ADAMTS7	ADAMTS7, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 (ADAMTS7), q25.1
SNP_A-2298539	ttctacttgttgataa[A/G]gcatggaactgaatgg	A	G	NM_002891 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras pro	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-2205781	ccatacacagcaagca[C/T]ggggatgtggaggaag	C	T	NM_002891 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras pro	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-2250290	cttagaatgtgtaaac[G/T]gcagctgctcaggaaa	G	T	NM_002891 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras pro	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-1906819	tggttatctttgggaa[A/G]cagaactatgcttgat	A	G	NM_002891 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras pro	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-1796985	ggttctcaatttttct[G/T]aaatggatgtgtatac	G	T	NM_002891 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // intron // 0 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras pro	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-2217591	cctgagagttgagtga[A/G]aatgaataaaaattag	A	G	NM_002891 // upstream // 105487 // Hs.459035 // RASGRF1 // 5923 // Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, mRNA. /// NM_153815 // upstream // 105487 // Hs.459035 // RASGRF1 // 5923 // Homo s	RASGRF1	RASGRF1, Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), transcript variant 1, q25.1
SNP_A-1688104	gataggtctagcagtagagatcaac[C/G]aaggtgatgcaccca ggagacatct	C	G	AK097337 // downstream // 310906 // - // - // - // Homo sapiens cDNA FLJ40018 fis, clone STOMA2006398. /// NM_002891 // upstream // 206334 // Hs.221811 // RASGRF1 // 5923 // Ras protein-specific guanine nucleotide-releasing factor 1 /// NM_007364 // upst	-	- , rs1434464, Homo sapiens cDNA FLJ40018 fis, clone STOMA2006398. ,q25.1
SNP_A-2092428	agaaagggatgtatgc[A/G]aaccagtttagaggca	A	G	NM_007364 // intron // 0 // Hs.513058 // TMED3 // 23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// ENST00000299705 // intron // 0 // — // — // — // —	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-1941659	ttggaactggcaattc[A/G]acagcttttatttgct	A	G	NM_007364 // downstream // 4932 // Hs.513058 // TMED3 // 23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 104740 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cd	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1816510	gttaggtgaaaaacaa[A/G]aggtgcataccataat	A	G	NM_007364 // downstream // 25767 // Hs.513058 // TMED3 // 23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 83905 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cd	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-2004301	aaaaacaactcaggga[C/T]gtatgttaggatgttg	C	T	NM_007364 // downstream // 45238 // Hs.513058 // TMED3 // 23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 64434 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cd	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-2271539	gaccaagacaaaaaaca[A/T]gactactccataatta	A	T	NM_007364 // downstream // 46854 // Hs.513058 // TMED3 // 23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 62818 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cd	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-2218201	cctgctacctccttac[C/T]gctccagaggacctt	C	T	NM_007364 // downstream // 58625 // Hs.513058 // TMED3 // 23423 // Homo sapiens chromosome 15 open reading frame 22 (C15orf22), mRNA. /// AB028947 // upstream // 51047 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cd	TMED3	TMED3, Homo sapiens chromosome 15 open reading frame 22 (C15orf22), q25.1
SNP_A-2042430	aactcacctacatcac[A/G]caaccagtaagtttca	A	G	AB028947 // downstream // 122411 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 250267 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2298947	tgcttccttcacctag[A/T]aacatacctgtgtcct	A	T	AB028947 // downstream // 142459 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 230219 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2298949	tgaggtctcataaaaa[A/G]agtgtgtatcataagg	A	G	AB028947 // downstream // 143001 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 229677 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2077872	accagagtcatcttttc[A/G]aaaatacagatcagaa	A	G	AB028947 // downstream // 190111 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 182567 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2148563	atggtaagaacaaaac[A/C]gtatgtgagagacagc	A	C	AB028947 // downstream // 206348 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 166330 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2283436	gatacciggacatgga[C/T]gggctaaaaggaatca	C	T	AB028947 // downstream // 208413 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 164265 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2251069	cttattccttaatctg[G/T]accaagtaacacggtg	G	T	AB028947 // downstream // 208992 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 163686 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-for	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1651840	aacaactgaccaaggactctggctg[C/T]ctttgaaatatattatcatgtttga	C	T	NM_006441 // downstream // 40449 // Hs.118131 // MTHFS // 10588 // 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	MTHFS	MTHFS , rs1380642, 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase),q25.1
SNP_A-1675203	cttgaatttattctcttatagttcc[A/G]aaggccagaaatctgaaatcagttt	A	G	NM_006441 // downstream // 37743 // Hs.118131 // MTHFS // 10588 // 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	MTHFS	MTHFS , rs724721, 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase),q25.1
SNP_A-1956444	tttgttcttatgactc[C/T]atgattctgtgtcaag	C	T	AB028947 // downstream // 315665 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 57013 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-form	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-2071956	acagagccaactatac[C/T]atcccaatttgcataa	C	T	AB028947 // downstream // 346996 // Hs.301654 // KIAA1024 // 23251 // Homo sapiens mRNA for KIAA1024 protein, partial cds. /// NM_006441 // downstream // 25682 // Hs.459049 // MTHFS // 10588 // Homo sapiens 5,10-methenyltetrahydrofolate synthetase (5-form	KIAA1024	KIAA1024, Homo sapiens for KIAA1024 protein, partial cds. q25.1
SNP_A-1733496	attcaaggtgagagaggcctttgga[A/G]catactaatgaaacttgatttta	A	G	NM_019006 // intron // 0 // Hs.83954 // AWP1 // 54469 // protein associated with PRK1	AWP1	AWP1 , rs10519280, protein associated with PRK1,q25.1
SNP_A-2037820	aacaataccgtgaatg[C/G]aaaaacctcttccaaa	C	G	NM_000137 // downstream // 45542 // Hs.73875 // FAH // 2184 // Homo sapiens fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA. /// NM_014862 // upstream // 172513 // Hs.459070 // ARNT2 // 9915 // Homo sapiens aryl-hydrocarbon receptor nuclea	FAH	FAH, Homo sapiens fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), q25.1
SNP_A-1793131	ggtagaaacagaccac[G/T]aatgattccacaatta	G	T	NM_000137 // downstream // 73781 // Hs.73875 // FAH // 2184 // Homo sapiens fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA. /// NM_014862 // upstream // 144274 // Hs.459070 // ARNT2 // 9915 // Homo sapiens aryl-hydrocarbon receptor nuclea	FAH	FAH, Homo sapiens fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), q25.1
SNP_A-1869628	tccttactgctaaatc[C/T]aaaacacgtttttcct	C	T	NM_014862 // intron // 0 // Hs.459070 // ARNT2 // 9915 // Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 // ARNT2 // 9915 // Homo sapiens mRNA for KIAA0307 gene, partial cds. /// ENST0	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2091089	actttgccaatcatca[C/T]tctccatctcatcagc	C	T	NM_014862 // intron // 0 // Hs.459070 // ARNT2 // 9915 // Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 // ARNT2 // 9915 // Homo sapiens mRNA for KIAA0307 gene, partial cds. /// ENST0	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-2042655	aactcctgaacacaga[A/G]cttagaacacagcagg	A	G	NM_014862 // intron // 0 // Hs.459070 // ARNT2 // 9915 // Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA. /// AB002305 // intron // 0 // Hs.459070 // ARNT2 // 9915 // Homo sapiens mRNA for KIAA0307 gene, partial cds. /// ENST0	ARNT2	ARNT2, Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), q25.1
SNP_A-1715159	aaatgatgagcatgagccagattta[A/G]gaggaatgctgactcttttttaaa	A	G	AL390079 // intron // 0 // Hs.26765 // LOC58489 // 58489 // hypothetical protein from EUROIMAGE 588495	LOC58489	LOC58489 , rs960170, hypothetical protein from EUROIMAGE 588495,q25.1
SNP_A-1675269	agcagttctcacttattactaggac[A/C]aaggaacagtaagtcttttcctttc	A	C	AB033025 // upstream // 119180 // Hs.212584 // KIAA1199 // 57214 // KIAA1199 protein /// AL390079 // downstream // 14752 // Hs.26765 // LOC58489 // 58489 // hypothetical protein from EUROIMAGE 588495	KIAA1199	KIAA1199 , rs2660992, KIAA1199 protein ,q25.1
SNP_A-2068708	acaatactgcgttgta[C/T]acttaaaaattaacca	C	T	ENST00000258884 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2119755	agtattgttaatcata[G/T]gctctatactgtacgg	G	T	ENST00000258884 // intron // 0 // --- // --- // --- // ---	-	q25.1
SNP_A-2061630	aatgctttctgataac[A/G]gcgttcagtgaaaaga	A	G	ENST00000258884 // intron // 0 // --- // --- // --- // ---	-	q25.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2148606	atggtagaacttcttc[C/T]gaaattggagtcaatc	C	T	NM_022566 // downstream // 124305 // Hs.513071 // MESDC1 // 59274 // Homo sapiens mesoderm development candidate 1 (MESDC1), mRNA. /// NM_173528 // upstream // 5994 // — // C15orf26 // 161502 // Homo sapiens chromosome 15 open reading frame 26 (C15orf26	MESDC1	MESDC1, Homo sapiens mesoderm development candidate 1 (MESDC1), q25.1
SNP_A-2299664	tggggtttcccttgac[C/T]gtatgatgactgacac	C	T	NM_173528 // intron // 0 // — // C15orf26 // 161502 // Homo sapiens chromosome 15 open reading frame 26 (C15orf26), mRNA. /// ENST00000286732 // intron // 0 // — // — // — // —	C15orf26	C15orf26, Homo sapiens chromosome 15 open reading frame 26 (C15orf26), q25.1
SNP_A-2158176	attggcaacatttgac[A/T]ggtatcagatggttat	A	T	NM_173528 // intron // 0 // — // C15orf26 // 161502 // Homo sapiens chromosome 15 open reading frame 26 (C15orf26), mRNA. /// ENST00000286732 // intron // 0 // — // — // — // —	C15orf26	C15orf26, Homo sapiens chromosome 15 open reading frame 26 (C15orf26), q25.1
SNP_A-2031572	aaaggttgttcctaaa[A/G]taagggcagagtcaca	A	G	NM_004513 // 3UTR // 0 // Hs.459095 // IL16 // 3603 // Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), transcript variant 1, mRNA. /// ENST00000355368 // 3UTR // 0 // — // — // — // —	IL16	IL16, Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), transcript variant 1, q25.1
SNP_A-2299703	caaggtaagcaagcca[C/G]gttgatagctctaagg	C	G	NM_181841 // upstream // 145081 // — // — // 0 // — /// NM_181841 // upstream // 145002 // — // — // 0 // — /// NM_032246 // downstream // 522629 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mR	-	q25.2
SNP_A-1860456	tcagtgtttatttcca[A/G]tctaacggagagctca	A	G	NM_032246 // upstream // 49415 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 34795 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domai	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2094520	agaataacatgaaccc[A/G]agcagaatcatgtttt	A	G	NM_032246 // upstream // 55644 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 28566 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domai	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-1809436	gtgagaaattgagaac[A/G]aaagagaggcactgtt	A	G	NM_032246 // upstream // 56024 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 28186 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domai	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2195867	catgtatgtgattctc[A/G]gaaaccagcaaaggag	A	G	NM_032246 // upstream // 71366 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 12844 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domai	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2151444	atgttccagtgtaaaa[A/G]ttgtcaaagtggaatt	A	G	NM_032246 // upstream // 71556 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 12654 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domai	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2138641	atcccactaagtggcc[G/T]ctgtttattacccagt	G	T	NM_032246 // upstream // 74935 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 9275 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domain	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2288576	gattgcactttgagaa[C/T]cctgctttataacttg	C	T	NM_032246 // upstream // 76996 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 7214 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domain	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1916298	tgttgtcagtccacaa[A/G]tagaagtgagagtgtt	A	G	NM_032246 // upstream // 82676 // Hs.104744 // RKHD3 // 84206 // Homo sapiens ring finger and KH domain containing 3 (RKHD3), mRNA. /// NM_024580 // downstream // 1534 // Hs.459114 // EFTUD1 // 79631 // Homo sapiens elongation factor Tu GTP binding domain	RKHD3	RKHD3, Homo sapiens ring finger and KH domain containing 3 (RKHD3), q25.2
SNP_A-2226999	ctaatgcaagctcgaa[A/G]ccatttagagaactac	A	G	NM_207517 // intron // 0 // Hs.459162 // ADAMTSL3 // 57188 // Homo sapiens ADAMTS-like 3 (ADAMTSL3), mRNA. /// ENST00000286744 // intron // 0 // — // — // — /// ENST00000286745 // intron // 0 // — // — // — // —	ADAMTSL3	ADAMTSL3, Homo sapiens ADAMTS-like 3 (ADAMTSL3), q25.2
SNP_A-2300640	gtccctgaatcatcac[A/G]ctgagtggtctttttc	A	G	NM_207517 // intron // 0 // Hs.459162 // ADAMTSL3 // 57188 // Homo sapiens ADAMTS-like 3 (ADAMTSL3), mRNA. /// ENST00000286744 // intron // 0 // — // — // — /// ENST00000286745 // intron // 0 // — // — // — // —	ADAMTSL3	ADAMTSL3, Homo sapiens ADAMTS-like 3 (ADAMTSL3), q25.2
SNP_A-1680724	tgtttctttttgcaggagactgca[C/T]agacacaactcactactgt atgttt	C	T	AB033059 // CDS // 0 // Hs.18705 // ADAMTSL3 // 57188 // ADAMTS-like 3	ADAMTSL3	ADAMTSL3 , rs950169, ADAMTS-like 3,q25.2
SNP_A-1891451	tgattcatggacaaca[G/T]taacatttttttctg	G	T	NM_207517 // intron // 0 // Hs.459162 // ADAMTSL3 // 57188 // Homo sapiens ADAMTS-like 3 (ADAMTSL3), mRNA. /// ENST00000286744 // intron // 0 // — // — // —	ADAMTSL3	ADAMTSL3, Homo sapiens ADAMTS-like 3 (ADAMTSL3), q25.2
SNP_A-1665876	ggaggaactttctaaaaactggtat[A/G]aaatgagtaaaaaag catagaacca	A	G	AB033059 // downstream // 20798 // Hs.18705 // ADAMTSL3 // 57188 // ADAMTS-like 3	ADAMTSL3	ADAMTSL3 , rs10520569, ADAMTS-like 3,q25.2
SNP_A-2178305	cactcacttgaacct[C/G]aaaaactgacctggt	C	G	NM_201651 // downstream // 72938 // Hs.459187 // SLC28A1 // 9154 // Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (SLC28A1), mRNA. /// NM_004213 // downstream // 23176 // Hs.459187 // SLC28A1 // 9154 // Homo sapie	SLC28A1	SLC28A1, Homo sapiens solute carrier family 28 (sodium-coupled nucleoside transporter), member 1 (SLC28A1), q25.3
SNP_A-2075378	acatgaagttctggaa[C/T]gggcagtttacgtact	C	T	U03634 // intron // 0 // — // — // 0 // Human P47 LBC oncogene mRNA, complete cds. /// ENST00000348841 // intron // 0 // — // — // — // — /// ENST00000352462 // intron // 0 // — // — // — // — /// ENST00000258877 // intron // 0 // —	-	-, Human P47 LBC oncogene complete cds, q25.3
SNP_A-2301474	aatttagtgctttaaa[A/G]aagtcaggcttacc	A	G	U03634 // intron // 0 // — // — // 0 // Human P47 LBC oncogene mRNA, complete cds. /// ENST00000348841 // intron // 0 // — // — // — // — /// ENST00000352462 // intron // 0 // — // — // — // — /// ENST00000258877 // intron // 0 // —	-	-, Human P47 LBC oncogene complete cds, q25.3
SNP_A-2230701	ctatgaacttgttttc[C/T]ccttcattgaaagataa	C	T	U03634 // intron // 0 // — // — // 0 // Human P47 LBC oncogene mRNA, complete cds. /// ENST00000348841 // intron // 0 // — // — // — // — /// ENST00000352462 // intron // 0 // — // — // — // — /// ENST00000258877 // intron // 0 // —	-	-, Human P47 LBC oncogene complete cds, q25.3
SNP_A-1960875	tttttgacaggctctc[A/G]ctcaattgttcaggct	A	G	NM_022480 // upstream // 27700 // Hs.498371 // ENC2 // 64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 27657 // Hs.498371 // ENC2 // 64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-1890728	tgatgagtcactttca[C/T]tccataacacaatctt	C	T	NM_022480 // upstream // 167949 // Hs.498371 // ENC2 // 64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 167906 // Hs.498371 // ENC2 // 64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA.	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-2070277	acaccaacattagatc[A/G]ataactcctccgaatg	A	G	NM_022480 // upstream // 219373 // Hs.498371 // ENC2 // 64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA. /// NM_022480 // upstream // 219330 // Hs.498371 // ENC2 // 64410 // Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA.	ENC2	ENC2, Homo sapiens hypothetical protein FLJ12587 (FLJ12587), q25.3
SNP_A-1715501	tatatggacaatttaaagttcattat[C/T]aacttgcaggataaactg atgaaa	C	T	NM_152336 // intron // 0 // Hs.350741 // FLJ32310 // 123624 // hypothetical protein FLJ32310	FLJ32310	FLJ32310 , rs8025054, hypothetical protein FLJ32310,q25.3
SNP_A-1757831	aaatagtttggagactatttgatga[C/T]gattggccctacagagta gtcagcc	C	T	NM_152336 // intron // 0 // Hs.350741 // FLJ32310 // 123624 // hypothetical protein FLJ32310	FLJ32310	FLJ32310 , rs1039116, hypothetical protein FLJ32310,q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2302251	gctaaatggtgtttaa[A/G]tggtcttagggtttaa	A	G	NM_152336 // downstream // 27429 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 1254058 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ3	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2301852	tagatgacagatgcta[A/C]taaggacgtcatcatt	A	C	NM_152336 // downstream // 166083 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 1115404 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2293604	gcagccaagctactaa[C/T]gataaagccctctgat	C	T	NM_152336 // downstream // 210905 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 1070582 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-1722566	attctgagactcatttcaagggtat[G/T]aagttaatgaaaagtattg tgttg	G	T	NM_152336 // downstream // 356471 // Hs.350741 // FLJ32310 // 123624 // hypothetical protein FLJ32310 /// NM_152454 // upstream // 925023 // Hs.350808 // FLJ31461 // 145978 // hypothetical protein FLJ31461	FLJ32310	FLJ32310 , rs2246309, hypothetical protein FLJ32310 ,q25.3
SNP_A-1856520	tcacagcatatgatga[C/G]taagattctcaacatg	C	G	NM_152336 // downstream // 457764 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 823723 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ3	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2302318	tcaagatttgaccta[A/G]gttgcttctcttcat	A	G	NM_152336 // downstream // 779147 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 502340 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ3	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-1694573	caaggcatgtgataggagttctcaa[C/T]aaatataaacccatgt ccttcatgg	C	T	NM_152336 // downstream // 881265 // Hs.350741 // FLJ32310 // 123624 // hypothetical protein FLJ32310 /// NM_152454 // upstream // 400229 // Hs.350808 // FLJ31461 // 145978 // hypothetical protein FLJ31461	FLJ32310	FLJ32310 , rs3844975, hypothetical protein FLJ32310 ,q25.3
SNP_A-2162034	atttaaaagcaggac[A/G]aggagcaggaaagcta	A	G	NM_152336 // downstream // 914218 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 367269 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ3	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2302497	tcagaaagttccagaa[A/C]tacaattgtcagaag	A	C	NM_152336 // downstream // 922233 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 359254 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ3	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2227274	ctacaaataatcatca[C/T]gtgaaacaaagaacaa	C	T	NM_152336 // downstream // 924002 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 357485 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ3	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2080237	acctaacacaaatgga[A/G]ggaaaaaggagacaaa	A	G	NM_152336 // downstream // 1008967 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 272520 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2023067	aaaacagacatgaaga[A/G]ctacaattgattggg	A	G	NM_152336 // downstream // 1021655 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 259832 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2134973	atattcagacactgcg[A/G]aactatgtagggtgaa	A	G	NM_152336 // downstream // 1023363 // Hs.350741 // FLJ32310 // 123624 // Homo sapiens hypothetical protein FLJ32310 (FLJ32310), mRNA. /// NM_152454 // upstream // 258124 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ	FLJ32310	FLJ32310, Homo sapiens hypothetical protein FLJ32310 (FLJ32310), q25.3
SNP_A-2004337	ctgttcaaccttaaca[A/T]aaaggagaataaatca	A	T	NM_152454 // downstream // 19098 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 278034 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor,	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-2302917	cgcagcatggacttaa[A/T]agctttaacctacct	A	T	NM_152454 // downstream // 35438 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 261694 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor,	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-2187413	caggttcttgattgca[G/T]gagtcagtggggaaia	G	T	NM_152454 // downstream // 184636 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 112496 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-2222988	cgcagggacctggcac[A/G]agagtcagagcctagt	A	G	NM_152454 // downstream // 185252 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 111880 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-2283203	gataatgggatctgtc[A/G]catacactctagaggg	A	G	NM_152454 // downstream // 206613 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 90519 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor,	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-1835172	taccgaaaatatacaa[A/G]caactacaaatcaata	A	G	NM_152454 // downstream // 207340 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 89792 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor,	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-2302959	ggtcgtggtcatctac[C/G]atggctggatatgact	C	G	NM_152454 // downstream // 237366 // Hs.350808 // FLJ31461 // 145978 // Homo sapiens hypothetical protein FLJ31461 (FLJ31461), mRNA. /// NM_002530 // downstream // 59766 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor.	FLJ31461	FLJ31461, Homo sapiens hypothetical protein FLJ31461 (FLJ31461), q25.3
SNP_A-1868732	tcctcttctctatacc[A/G]atgagctccaggagga	A	G	NM_002530 // intron // 0 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), mRNA. /// U05012 // intron // 0 // Hs.410969 // NTRK3 // 4916 // Human receptor tyrosine kinase TrkC (NTRK3) mRNA, complete cds.	NTRK3	NTRK3, Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), q25.3
SNP_A-2282959	gataaccagagcataa[C/G]aggtttctgtaggaag	C	G	NM_002530 // intron // 0 // Hs.410969 // NTRK3 // 4916 // Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), mRNA. /// U05012 // intron // 0 // Hs.410969 // NTRK3 // 4916 // Human receptor tyrosine kinase TrkC (NTRK3) mRNA, complete cds.	NTRK3	NTRK3, Homo sapiens neurotrophic tyrosine kinase, receptor, type 3 (NTRK3), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1682678	gaaatactgctaaacctcaatct[C/T]cctgttatagaaagtggg aatcata	C	T	NM_002530 // upstream // 65252 // Hs.26776 // NTRK3 // 4916 // neurotrophic tyrosine kinase, receptor, type 3 /// NM_022163 // downstream // 137803 // Hs.424264 // MRPL46 // 26589 // mitochondrial ribosomal protein L46	NTRK3	NTRK3 , rs1372600, neurotrophic tyrosine kinase, receptor, type 3, q25.3
SNP_A-2249899	cttacactacatttac[G/T]agacaccgataatttt	G	T	NM_022163 // intron // 0 // Hs.534261 // MRPL46 // 26589 // Homo sapiens mitochondrial ribosomal protein L46 (MRPL46), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000312475 // intron // 0 // — // — // —	MRPL46	MRPL46, Homo sapiens mitochondrial ribosomal protein L46 (MRPL46), nuclear gene encoding mitochondrial protein, q25.3
SNP_A-2004348	gtctgagaaaaaccaa[G/T]aagttctttgtggaa	G	T	NM_017996 // upstream // 78796 // Hs.42140 // DET1 // 55070 // Homo sapiens de-etiolated 1 (DET1), mRNA. /// NM_022767 // upstream // 10845 // Hs.436102 // FLJ12484 // 64782 // Homo sapiens hypothetical protein FLJ12484 (FLJ12484), mRNA. /// ENST00000 2681	DET1	DET1, Homo sapiens de-etiolated 1 (DET1), q26.1
SNP_A-2101110	agatcagatgaataat[A/G]aatgtgaagcccaaca	A	G	NM_022767 // intron // 0 // Hs.436102 // FLJ12484 // 64782 // Homo sapiens hypothetical protein FLJ12484 (FLJ12484), mRNA. /// ENST00000332810 // intron // 0 // — // — // —	FLJ12484	FLJ12484, Homo sapiens hypothetical protein FLJ12484 (FLJ12484), q26.1
SNP_A-1931246	ttccatttctcaagca[C/T]gtggtttctgtagacc	C	T	NM_002201 // downstream // 66440 // Hs.459265 // ISG20 // 3669 // Homo sapiens interferon stimulated gene 20kDa (ISG20), mRNA. /// NM_013227 // upstream // 81386 // Hs.2159 // AGC1 // 176 // Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, lar	ISG20	ISG20, Homo sapiens interferon stimulated gene 20kDa (ISG20), q26.1
SNP_A-1698383	aaacagccacctcccccaacagatgc[G/T]tccatcccagcttctc cggaatgga	G	T	NM_001135 // CDS // 0 // Hs.2159 // AGC1 // 176 // aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) /// NM_013227 // CDS // 0 // Hs.2159 // AGC1 // 176 // aggrecan 1 (chondro	AGC1	AGC1, rs698621, aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) q26.1
SNP_A-1820618	gtttcaattcaagtcc[A/T]aagggaagaaaaagca	A	T	NM_013227 // intron // 0 // Hs.2159 // AGC1 // 176 // Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an /// ENST00000268134 // intron // 0 // — // — // — // —	AGC1	AGC1, Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal an q26.1
SNP_A-1949660	ttatttttctcaatga[A/G]gcagacattcactcca	A	G	NM_005928 // upstream // 103005 // Hs.3745 // MFGE8 // 4240 // Homo sapiens milk fat globule-EGF factor 8 protein (MFGE8), mRNA. /// NM_007011 // upstream // 72008 // Hs.122337 // ABHD2 // 11057 // Homo sapiens abhydrolase domain containing 2 (ABHD2), tra	MFGE8	MFGE8, Homo sapiens milk fat globule-EGF factor 8 protein (MFGE8), q26.1
SNP_A-1787202	gggaacaaggatccaa[C/T]tgctgccctgctaga	C	T	NM_000326 // upstream // 6017 // Hs.1933 // RLBP1 // 6017 // Homo sapiens retinaldehyde binding protein 1 (RLBP1), mRNA. /// ENST00000268125 // intron // 0 // — // — // — // —	RLBP1	RLBP1, Homo sapiens retinaldehyde binding protein 1 (RLBP1), q26.1
SNP_A-2272116	gaccgcagaaactgt[C/G]aaaagagatgagccag	C	G	NM_000326 // upstream // 21499 // Hs.1933 // RLBP1 // 6017 // Homo sapiens retinaldehyde binding protein 1 (RLBP1), mRNA. /// NM_018193 // upstream // 20247 // Hs.513126 // FLJ10719 // 55215 // Homo sapiens hypothetical protein FLJ10719 (FLJ10719), mRNA.	RLBP1	RLBP1, Homo sapiens retinaldehyde binding protein 1 (RLBP1), q26.1
SNP_A-2303828	gtgatatgatgtttca[A/G]aaatgaaggcagcaga	A	G	NM_002693 // intron // 0 // Hs.440902 // POLG // 5428 // Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA. /// ENST00000268124 // intron // 0 // — // — // — // —	POLG	POLG, Homo sapiens polymerase (DNA directed), gamma (POLG), q26.1
SNP_A-1833580	tacagcctgggctatc[A/G]aggtgttgctaggcc	A	G	NM_002693 // intron // 0 // Hs.440902 // POLG // 5428 // Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA. /// ENST00000268124 // intron // 0 // — // — // — // —	POLG	POLG, Homo sapiens polymerase (DNA directed), gamma (POLG), q26.1
SNP_A-2156106	attcgtaatggtgcca[A/G]cttgccaaattgccc	A	G	NM_018193 // downstream // 129839 // Hs.513126 // FLJ10719 // 55215 // Homo sapiens hypothetical protein FLJ10719 (FLJ10719), mRNA. /// NM_018193 // downstream // 129152 // Hs.513126 // FLJ10719 // 55215 // Homo sapiens hypothetical protein FLJ10719 (FLJ1	FLJ10719	FLJ10719, Homo sapiens hypothetical protein FLJ10719 (FLJ10719), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2137165	atcaggtagatctgac[A/T]aacgtgggcaactgag	A	T	NM_018193 // downstream // 146024 // Hs.513126 // FLJ10719 // 55215 // Homo sapiens hypothetical protein FLJ10719 (FLJ10719), mRNA. /// NM_018193 // downstream // 145337 // Hs.513126 // FLJ10719 // 55215 // Homo sapiens hypothetical protein FLJ10719 (FLJ1	FLJ10719	FLJ10719, Homo sapiens hypothetical protein FLJ10719 (FLJ10719), q26.1
SNP_A-1895452	tgccgttttgtagac[A/G]ctgttatctttttcc	A	G	AF180519 // downstream // 41314 // Hs.546646 // GABARAPL3 // 23766 // Homo sapiens GABA-A receptor-associated protein mRNA, complete cds. /// ENST00000330739 // downstream // 12681 // — // — // — /// ENST00000312365 // downstream // 41314 //	GABARAPL3	GABARAPL3, Homo sapiens GABA-A receptor-associated protein complete cds, q26.1
SNP_A-1644574	gctgatagatcagaatcctttcaa[C/T]gtagaagctgaggaac cactcccaa	C	T	NM_003870 // intron // 0 // Hs.1742 // IQGAP1 // 8826 // IQ motif containing GTPase activating protein 1	IQGAP1	IQGAP1, rs10520689, IQ motif containing GTPase activating protein 1,q26.1
SNP_A-1657844	ggtaggaaaaaggaatttcagtgtta[C/T]ggtgataagagcttggg gtaatttt	C	T	NM_003870 // intron // 0 // Hs.1742 // IQGAP1 // 8826 // IQ motif containing GTPase activating protein 1	IQGAP1	IQGAP1, rs10520688, IQ motif containing GTPase activating protein 1,q26.1
SNP_A-2251609	cttcagccaccataca[A/C]gtagcaaactggaatc	A	C	NM_003870 // intron // 0 // Hs.430551 // IQGAP1 // 8826 // Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA. /// ENST00000268182 // intron // 0 // — // — // —	IQGAP1	IQGAP1, Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), q26.1
SNP_A-2132753	atataaagtagttaaa[C/T]acataagtgggtgagt	C	T	NM_003870 // intron // 0 // Hs.430551 // IQGAP1 // 8826 // Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA. /// ENST00000268182 // intron // 0 // — // — // —	IQGAP1	IQGAP1, Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), q26.1
SNP_A-2256283	ctttaggtttcaaga[C/G]ggcatttttaaggtcc	C	G	NM_000057 // intron // 0 // Hs.169348 // BLM // 641 // Homo sapiens Bloom syndrome (BLM), mRNA. /// ENST00000355112 // intron // 0 // — // — // — /// ENST00000357307 // intron // 0 // — // — // —	BLM	BLM, Homo sapiens Bloom syndrome (BLM), q26.1
SNP_A-2281604	gagtctaataacatag[C/T]cattccagagacattg	C	T	NM_014848 // intron // 0 // Hs.8071 // SV2B // 9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// ENST00000330276 // intron // 0 // — // — // —	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2305032	caggtatggaatcttat[C/G]gtttgtactaatcgaa	C	G	NM_014848 // downstream // 35773 // Hs.8071 // SV2B // 9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 522663 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter family	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-1882336	tgaaaaccatcttagat[A/T]atgcctgcagactccc	A	T	NM_014848 // downstream // 43864 // Hs.8071 // SV2B // 9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 514572 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter family	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2270784	gacaggatgtgattta[C/T]gtgtttgaaaggaaac	C	T	NM_014848 // downstream // 316490 // Hs.8071 // SV2B // 9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 241946 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter famil	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-1936636	ttcttggtctctaca[A/G]tctttcctgtgaagag	A	G	NM_014848 // downstream // 324586 // Hs.8071 // SV2B // 9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 233850 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter famil	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1
SNP_A-2088267	actggtgtggattca[A/G]aattcaagtcagcctg	A	G	NM_014848 // downstream // 329087 // Hs.8071 // SV2B // 9899 // Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), mRNA. /// NM_013272 // upstream // 229349 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter famil	SV2B	SV2B, Homo sapiens synaptic vesicle glycoprotein 2B (SV2B), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1825655	taaatattggtggaa[A/G]gctcatcgttagcag	A	G	NM_013272 // intron // 0 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), mRNA. /// ENST00000318445 // intron // 0 // — // — // —	SLCO3A1	SLCO3A1, Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), q26.1
SNP_A-2299468	gcccttcacggctagc[G/T]gagctctaaagttcac	G	T	NM_013272 // downstream // 109408 // Hs.311187 // SLCO3A1 // 28232 // Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), mRNA. /// ENST00000318445 // downstream // 109408 // — // — // — /// ENST00000333792 //	SLCO3A1	SLCO3A1, Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), q26.1
SNP_A-1663620	caatttttttcagcgtgttctata[C/T]gcccattactgagctggtccc tggg	C	T	NM_153040 // downstream // 72124 // Hs.367879 // FLJ32831 // 145858 // hypothetical protein FLJ32831	FLJ32831	FLJ32831, rs285702, hypothetical protein FLJ32831,q26.1
SNP_A-1824562	taaactttaatgacc[A/T]ctctatctcgtatctg	A	T	NM_153040 // downstream // 76732 // Hs.367879 // FLJ32831 // 145858 // Homo sapiens hypothetical protein FLJ32831 (FLJ32831), mRNA. /// NM_207446 // downstream // 39602 // Hs.27373 // LOC400451 // 400451 // Homo sapiens hypothetical gene supported by AK07	FLJ32831	FLJ32831, Homo sapiens hypothetical protein FLJ32831 (FLJ32831), q26.1
SNP_A-1877688	tctgggccaaagagat[A/C]aggtcatatgttccaa	A	C	NM_153040 // downstream // 113172 // Hs.367879 // FLJ32831 // 145858 // Homo sapiens hypothetical protein FLJ32831 (FLJ32831), mRNA. /// NM_207446 // downstream // 3162 // Hs.27373 // LOC400451 // 400451 // Homo sapiens hypothetical gene supported by AK07	FLJ32831	FLJ32831, Homo sapiens hypothetical protein FLJ32831 (FLJ32831), q26.1
SNP_A-2141064	atctgcgctataggaa[C/T]gcacctcttggttac	C	T	NM_153040 // downstream // 113748 // Hs.367879 // FLJ32831 // 145858 // Homo sapiens hypothetical protein FLJ32831 (FLJ32831), mRNA. /// NM_207446 // downstream // 2586 // Hs.27373 // LOC400451 // 400451 // Homo sapiens hypothetical gene supported by AK07	FLJ32831	FLJ32831, Homo sapiens hypothetical protein FLJ32831 (FLJ32831), q26.1
SNP_A-1823080	taaaacaaaaaaaccac[C/T]atgatctcgtattctc	C	T	NM_001271 // intron // 0 // Hs.546244 // CHD2 // 1106 // Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2), mRNA. /// ENST00000309818 // intron // 0 // — // — // —	CHD2	CHD2, Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2), q26.1
SNP_A-2306155	gatatgtagatttgcc[A/G]agggagaggtaaaat	A	G	NM_020211 // upstream // 18347 // Hs.271277 // RGMA // 56963 // Homo sapiens RGM domain family, member A (RGMA), mRNA. /// NM_207447 // upstream // 114571 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000329082 // u	RGMA	RGMA, Homo sapiens RGM domain family, member A (RGMA), q26.1
SNP_A-1782403	ggcacaaagcaggaag[G/T]actggttggaagtg	G	T	NM_020211 // upstream // 62544 // Hs.271277 // RGMA // 56963 // Homo sapiens RGM domain family, member A (RGMA), mRNA. /// NM_207447 // upstream // 70374 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000329082 // up	RGMA	RGMA, Homo sapiens RGM domain family, member A (RGMA), q26.1
SNP_A-2302525	gctacaaaaagacaaa[A/C]ggaggtatagtgattg	A	C	NM_020211 // upstream // 120568 // Hs.271277 // RGMA // 56963 // Homo sapiens RGM domain family, member A (RGMA), mRNA. /// NM_207447 // upstream // 12350 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000329082 // u	RGMA	RGMA, Homo sapiens RGM domain family, member A (RGMA), q26.1
SNP_A-1856971	tcaccagttacttcta[C/G]gtacatttgctttat	C	G	NM_207447 // downstream // 198866 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 198866 // — // — // — /// ENST00000333325 // upstream // 566574 // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1834267	tacatgtaagaaacac[C/G]aagagcagcatgtggc	C	G	NM_207447 // downstream // 200874 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 200874 // — // — // — /// ENST00000333325 // upstream // 564566 // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1944214	ttgtcattcaatctca[C/T]atacccaatttccta	C	T	NM_207447 // downstream // 201414 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 201414 // — // — // — /// ENST00000333325 // upstream // 564026 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2282955	gataaccactccaaca[A/C]gatcattcaaggtca	A	C	NM_207447 // downstream // 217011 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 217011 // — // — // — // — /// ENST00000333325 // upstream // 548429 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2286155	gatgcagactgggact[C/T]aagacgctggctccc	C	T	NM_207447 // downstream // 241693 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 241693 // — // — // — // — /// ENST00000333325 // upstream // 523747 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2306382	ttaaacgttctgtgc[A/G]attcttctttcttt	A	G	NM_207447 // downstream // 278339 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 278339 // — // — // — // — /// ENST00000333325 // upstream // 487101 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-2255649	cttgttaagtgattgcc[C/T]cccttccccaaataaa	C	T	NM_207447 // downstream // 465320 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 465320 // — // — // — // — /// ENST00000333325 // upstream // 300120 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1914421	tgtgtttccaaccaga[C/T]ggctatgaagtgaacc	C	T	NM_207447 // downstream // 481675 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 481675 // — // — // — // — /// ENST00000333325 // upstream // 283765 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1908474	tgtagagactacacaa[C/T]gatggcgagtaagaca	C	T	NM_207447 // downstream // 482133 // Hs.531264 // UNQ9370 // 400454 // Homo sapiens IFMQ9370 (UNQ9370), mRNA. /// ENST00000358863 // downstream // 482133 // — // — // — // — /// ENST00000333325 // upstream // 283307 // — // — // — // —	UNQ9370	UNQ9370, Homo sapiens IFMQ9370 (UNQ9370), q26.1
SNP_A-1730507	tcctgaaaattatactttttataaa[A/G]acctctgagaacaaatgct ggttta	A	G	NM_020211 // upstream // 722777 // Hs.271277 // RGMA // 56963 // RGMA domain family, member A	RGMA	RGMA, rs1935634, RGM domain family, member A,q26.2
SNP_A-1956431	tttgttcgggacacca[A/G]gaacctgcaactgagt	A	G	NM_018349 // upstream // 247519 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 314063 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with tw	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1817114	gttcaaatctaaccac[C/T]ggataggcaaactgg	C	T	NM_018349 // upstream // 238501 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 305045 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with tw	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2269981	gacaatttctaaagat[A/C]acacttgtcaatggcc	A	C	NM_018349 // upstream // 237637 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 304181 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with tw	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2230205	ctatagaatgcctaaa[A/G]aggaaattattgtcc	A	G	NM_018349 // upstream // 234170 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 300714 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with tw	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2193575	catcttaacgatttga[G/T]cctcatgttttcttct	G	T	NM_018349 // upstream // 200943 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 267487 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with tw	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2127844	ataagaaagattgaga[A/G]atggaaaaataaaaag	A	G	NM_018349 // upstream // 158835 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // upstream // 225379 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with tw	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2042048	aactactacatagaaa[A/G]gaaatagttacacaag	A	G	NM_018349 // intron // 0 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // — // — // —	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2144312	atgagttactctcgat[A/T]aaaaagatactgcaac	A	T	NM_018349 // intron // 0 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // — // — // —	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1715565	aaaaggcaagatacccaaaatatctg[A/G]aaaacatagggaaagagaaagacc	A	G	NM_018349 // intron // 0 // Hs.33368 // FLJ11175 // 55784 // hypothetical protein FLJ11175	FLJ11175	FLJ11175, rs3784647, hypothetical protein FLJ11175,q26.2
SNP_A-2265984	gaaggatctggtttgt[A/G]aaaagcattagcatag	A	G	NM_018349 // intron // 0 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // — // — // — /// ENST00000310362 // intron // 0 // — // -	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2313002	ggacttgctttgaa[C/T]atacctttctctcatt	C	T	NM_018349 // intron // 0 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// ENST00000357742 // intron // 0 // — // — // — /// ENST00000310362 // intron // 0 // — // -	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2186179	caggcctgaagtatca[A/T]ggagagaaggcgaaag	A	T	NM_018349 // downstream // 104718 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 106087 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2085832	actcctccctgttac[A/G]agttctgctcctgtg	A	G	NM_018349 // downstream // 182740 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 184109 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2204483	ccagctggagagcacc[A/G]agatgtattgcaagt	A	G	NM_018349 // downstream // 236161 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 237530 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2135310	atatttaatttaaaaa[A/G]cctgtctatcagctag	A	G	NM_018349 // downstream // 236539 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 237908 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1950347	tttcagctgactggat[A/G]aaataaggaaatacaa	A	G	NM_018349 // downstream // 387473 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 388842 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2307540	gaggctcagtgcatca[A/T]ctgcctgcagaaaata	A	T	NM_018349 // downstream // 401597 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 402966 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2307745	agagggaagagtacaa[A/G]ttaaaatgtcagagat	A	G	NM_018349 // downstream // 666856 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 668225 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2143200	atgacaacaccttcac[A/G]ccttgatacaccagga	A	G	NM_018349 // downstream // 771883 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 773252 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2110243	aggaagtttatcatca[C/G]agcagaatttctgat	C	G	NM_018349 // downstream // 783070 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 784439 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1784302	ggcccagttagaaatg[A/G]agctggcattgagaat	A	G	NM_018349 // downstream // 864839 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 866208 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2026012	aaaattaaaacaaccc[A/G]gcattgtgaccacat	A	G	NM_018349 // downstream // 945442 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 946811 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains wit	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2247523	ctgtctgatagatcaa[C/T]taccaaatgaacctct	C	T	NM_018349 // downstream // 1029090 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1030459 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1656963	aattatttccactaacggtgaaac[A/G]ctaaatggacgacttctt atttatt	A	G	NM_018349 // downstream // 1549983 // Hs.33368 // FLJ11175 // 55784 // hypothetical protein FLJ11175 /// NM_021005 // upstream // 300439 // Hs.347991 // NR2F2 // 7026 // nuclear receptor subfamily 2, group F, member 2	FLJ11175	FLJ11175 , rs4417514, hypothetical protein FLJ11175 .q26.2
SNP_A-1756673	ctactagaaatggaaacaaacaaa[A/G]gcttactctacaaaa aggaggaaaa	A	G	NM_018349 // downstream // 1551520 // Hs.33368 // FLJ11175 // 55784 // hypothetical protein FLJ11175 /// NM_021005 // upstream // 298902 // Hs.347991 // NR2F2 // 7026 // nuclear receptor subfamily 2, group F, member 2	FLJ11175	FLJ11175 , rs10520806, hypothetical protein FLJ11175 .q26.2
SNP_A-2308560	gcattccaaatgtctc[A/G]cctcaagcaagcactt	A	G	NM_018349 // downstream // 1522130 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1523499 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2308565	taccacatcttctggt[A/G]aacaactcagcctatc	A	G	NM_018349 // downstream // 1528620 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1529989 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2308638	gctcctctactggg c[A/G]aaaaggaagcttctc	A	G	NM_018349 // downstream // 1568722 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1570091 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2181374	cagactaatacagtaa[A/G]gaagtacaattgctgg	A	G	NM_018349 // downstream // 1580541 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1581910 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2151425	atgttcatccactatc[A/G]ccagcaattgtacttc	A	G	NM_018349 // downstream // 1580558 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1581927 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-1847177	tatcattctattgatg[A/G]aaaatggaccacacatt	A	G	NM_018349 // downstream // 1582589 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1583958 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2065789	aatttcataacaatca[A/G]atcatgtgcttatttt	A	G	NM_018349 // downstream // 1585327 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1586696 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2147062	atggaagctaagaaac[C/G]agtaagtaagcaagaa	C	G	NM_018349 // downstream // 1697122 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1698491 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2243124	ctgccgtgttcacca[C/T]gctaaatccgagaaat	C	T	NM_018349 // downstream // 1787235 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), mRNA. /// NM_018349 // downstream // 1788604 // Hs.33368 // MCTP2 // 55784 // Homo sapiens multiple C2-domains w	MCTP2	MCTP2, Homo sapiens multiple C2-domains with two transmembrane regions 2 (MCTP2), q26.2
SNP_A-2052203	aagtaacacatggaaa[A/G]gttttaattctcacga	A	G	ENST00000327469 // downstream // 50095 // — // — // — // — /// ENST00000344738 // upstream // 345534 // — // — // — // —	-	q26.2
SNP_A-2024627	aaaaggctgaactta[A/C]taaactataaatttgtc	A	C	ENST00000344738 // upstream // 2083 // — // — // — // —	-	q26.2
SNP_A-2069546	acacacaatatggtaa[C/T]cgtggctgagaactgg	C	T	NM_173499 // downstream // 121198 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 1053901 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4)	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1642495	aacagcatatatatgcaagattaga[C/T]ctccccgtgaaaggag gtagctggg	C	T	BC028704 // upstream // 941046 // Hs.6093 // ARRDC4 // 91947 // arrestin domain containing 4 /// NM_173499 // downstream // 234058 // - // - // -	ARRDC4	ARRDC4 , rs1828770, arrestin domain containing 4 ,q26.2
SNP_A-1758230	gtgccccttctgggggagataa[A/G]ggaagtaggatcact cagttttca	A	G	BC028704 // upstream // 940670 // Hs.6093 // ARRDC4 // 91947 // arrestin domain containing 4 /// NM_173499 // downstream // 234434 // - // - // -	ARRDC4	ARRDC4 , rs1849648, arrestin domain containing 4 ,q26.2
SNP_A-2309096	agagctggatctggga[G/T]gtaagagagagaaagc	G	T	NM_173499 // downstream // 217865 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 957234 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4).	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1840589	tagccggaatgttttat[C/T]ggagcatcaaaggaca	C	T	NM_173499 // downstream // 227631 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 947468 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4).	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1925234	ttatccctggaagttg[C/T]aaatgcagttgtagta	C	T	NM_173499 // downstream // 227854 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 947245 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4).	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1788144	gggagcaaatcctaaa[C/T]ctcagaccactcactc	C	T	NM_173499 // downstream // 586792 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 588307 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4).	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-2240329	ctgaattgagataaca[C/T]gaagatttttatgct	C	T	NM_173499 // downstream // 817270 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 357829 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4).	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-1786765	gggattagatgagaca[C/G]tatctgtgaaagctct	C	G	NM_173499 // downstream // 1022532 // Hs.326528 // SPATA8 // 145946 // Homo sapiens spermatogenesis-related protein 8 (MGC44294), mRNA. /// NM_183376 // upstream // 152567 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4)	SPATA8	SPATA8, Homo sapiens spermatogenesis-related protein 8 (MGC44294), q26.2
SNP_A-2258159	cttttaattgggatca[C/T]gccaggggattagacc	C	T	NM_183376 // downstream // 144685 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA. /// NM_182562 // downstream // 337638 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743).	ARRDC4	ARRDC4, Homo sapiens arrestin domain containing 4 (ARRDC4), q26.3
SNP_A-2289485	gattttgttaccaac[A/G]gtcaactgttccaa	A	G	NM_183376 // downstream // 191888 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA. /// NM_182562 // downstream // 290435 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743).	ARRDC4	ARRDC4, Homo sapiens arrestin domain containing 4 (ARRDC4), q26.3
SNP_A-2166181	caaatattccttagtc[A/G]cataccactaccatgg	A	G	NM_183376 // downstream // 301918 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA. /// NM_182562 // downstream // 180405 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743).	ARRDC4	ARRDC4, Homo sapiens arrestin domain containing 4 (ARRDC4), q26.3
SNP_A-2291860	gcacaggtcactctaa[C/T]gaatgacagctgtaat	C	T	NM_183376 // downstream // 363832 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA. /// NM_182562 // downstream // 118491 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743).	ARRDC4	ARRDC4, Homo sapiens arrestin domain containing 4 (ARRDC4), q26.3
SNP_A-1927444	ttcaagtcttgtcag[C/T]ctcagaattctagtcc	C	T	NM_183376 // downstream // 393540 // Hs.6093 // ARRDC4 // 91947 // Homo sapiens arrestin domain containing 4 (ARRDC4), mRNA. /// NM_182562 // downstream // 88783 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743).	ARRDC4	ARRDC4, Homo sapiens arrestin domain containing 4 (ARRDC4), q26.3
SNP_A-1798218	gtaaactggaaaactc[G/T]atgcaaatgtcaggtt	G	T	NM_182562 // upstream // 49821 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743), mRNA. /// NM_000875 // upstream // 118949 // Hs.20573 // IGF1R // 3480 // Homo sapiens insulin-like growth factor 1 receptor (IGF1R	FLJ39743	FLJ39743, Homo sapiens hypothetical protein FLJ39743 (FLJ39743), q26.3
SNP_A-1846874	tatcacaggaatacaa[A/G]tgttcacaggtactct	A	G	NM_182562 // upstream // 96143 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743), mRNA. /// NM_000875 // upstream // 72627 // Hs.20573 // IGF1R // 3480 // Homo sapiens insulin-like growth factor 1 receptor (IGF1R)	FLJ39743	FLJ39743, Homo sapiens hypothetical protein FLJ39743 (FLJ39743), q26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2106742	agcctgcttttctcac[C/T]gtattgttactcgttg	C	T	NM_182562 // upstream // 146487 // Hs.155488 // FLJ39743 // 283777 // Homo sapiens hypothetical protein FLJ39743 (FLJ39743), mRNA. /// NM_000875 // upstream // 22283 // Hs.20573 // IGF1R // 3480 // Homo sapiens insulin-like growth factor 1 receptor (IGF1R	FLJ39743	FLJ39743, Homo sapiens hypothetical protein FLJ39743 (FLJ39743), q26.3
SNP_A-2177198	cacctgccaagacaaa[A/G]agacacgaatgagtac	A	G	NM_000875 // intron // 0 // Hs.20573 // IGF1R // 3480 // Homo sapiens insulin-like growth factor 1 receptor (IGF1R), mRNA. /// ENST00000268035 // intron // 0 // — // — // — // — // —	IGF1R	IGF1R, Homo sapiens insulin-like growth factor 1 receptor (IGF1R), q26.3
SNP_A-2090307	acttgctccaacaggt[C/G]aacgtgattgaaaatt	C	G	NM_000875 // intron // 0 // Hs.20573 // IGF1R // 3480 // Homo sapiens insulin-like growth factor 1 receptor (IGF1R), mRNA. /// ENST00000268035 // intron // 0 // — // — // — // — // —	IGF1R	IGF1R, Homo sapiens insulin-like growth factor 1 receptor (IGF1R), q26.3
SNP_A-2146299	atgctagctagtgtta[C/G]gaagcgagcataaaca	C	G	NM_144598 // downstream // 121464 // Hs.459507 // LRRC28 // 123355 // Homo sapiens leucine rich repeat containing 28 (LRRC28), mRNA. /// NM_005587 // upstream // 58255 // Hs.268675 // MEF2A // 4205 // Homo sapiens MADS box transcription enhancer factor 2,	LRRC28	LRRC28, Homo sapiens leucine rich repeat containing 28 (LRRC28), q26.3
SNP_A-2155234	attcaggtgctcccca[A/G]atgcagagccaccaac	A	G	NM_139057 // intron // 0 // Hs.459524 // ADAMTS17 // 170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // — // — // — // — // —	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-2132147	ataggtccgtgcagaa[A/G]cttgtacgtgaataat	A	G	NM_139057 // intron // 0 // Hs.459524 // ADAMTS17 // 170691 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), mRNA. /// ENST00000268070 // intron // 0 // — // — // — // — // —	ADAMTS17	ADAMTS17, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 17 (ADAMTS17), q26.3
SNP_A-1804277	gtcacgtggccagaga[A/T]aagaaagcatcaaacc	A	T	NM_207383 // upstream // 4050 // Hs.136982 // FLJ42289 // 388182 // Homo sapiens FLJ42289 protein (FLJ42289), mRNA. /// NM_178842 // downstream // 46204 // Hs.416099 // LASS3 // 204219 // Homo sapiens LAG1 longevity assurance homolog 3 (S. cerevisiae) (LA	FLJ42289	FLJ42289, Homo sapiens FLJ42289 protein (FLJ42289), q26.3
SNP_A-1833166	tacacccaccacagaa[A/C]tctctattccctcctc	A	C	NM_024708 // downstream // 162560 // Hs.31845 // ASB7 // 140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 143322 // Hs.31845 // ASB7 // 140460 // Homo sapiens ankyrin repeat	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3
SNP_A-1833514	tacagattcaagagca[C/G]agtgaaccccaaatag	C	G	NM_024708 // downstream // 192856 // Hs.31845 // ASB7 // 140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 173618 // Hs.31845 // ASB7 // 140460 // Homo sapiens ankyrin repeat	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3
SNP_A-2176650	caccccaggactcaca[G/T]catggcaaaaatccaa	G	T	NM_024708 // downstream // 243754 // Hs.31845 // ASB7 // 140460 // Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, mRNA. /// NM_024708 // downstream // 224516 // Hs.31845 // ASB7 // 140460 // Homo sapiens ankyrin repeat	ASB7	ASB7, Homo sapiens ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 1, q26.3
SNP_A-1828658	taagcgtctccatggc[A/G]cgttctggacacacag	A	G	NM_000693 // downstream // 8087 // Hs.459538 // ALDH1A3 // 220 // Homo sapiens aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), mRNA. /// ENST00000346623 // downstream // 8087 // — // - - // — // — /// ENST00000329841 // downstream // 8087 // -	ALDH1A3	ALDH1A3, Homo sapiens aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), q26.3
SNP_A-1854184	tcaaagagatccagta[C/T]ggctaccgccgggtga	C	T	NM_014918 // CDS // 0 // Hs.110488 // CHSY1 // 22856 // Homo sapiens carbohydrate (chondroitin) synthase 1 (CHSY1), mRNA. /// ENST00000254190 // CDS // 0 // — // — // — // — // —	CHSY1	CHSY1, Homo sapiens carbohydrate (chondroitin) synthase 1 (CHSY1), q26.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2311037	gggcaaccatgatgtt[C/T]gtgttgcaatttgtac	C	T	NM_002570 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subt	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-1899972	tggacatggctcacaa[A/G]cagttgttgatttgact	A	G	NM_002570 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subt	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-2296998	gccaatgaaaaaagaa[C/T]gcctggttgcgacgta	C	T	NM_002570 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subt	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-1838771	tagacctggaaatgac[A/G]ctgtgaatagacagga	A	G	NM_002570 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // intron // 0 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subt	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin q26.3
SNP_A-2114786	agggattctttctgag[A/G]ccaaaaaccctttccc	A	G	NM_002570 // upstream // 90631 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein convertase subtilisin/kexin type 6 (PCSK6), transcript variant 1, mRNA. /// NM_138322 // upstream // 90631 // Hs.498494 // PCSK6 // 5046 // Homo sapiens proprotein con	PCSK6	PCSK6, Homo sapiens proprotein convertase subtilisin,q26.3
SNP_A-2131890	ataggaagttgtacac[A/G]ggtatctacagtatga	A	G	ENST00000354222 // intron // 0 // — // — // — /// ENST00000355919 // intron // 0 // — // — // — /// ENST00000331055 // intron // 0 // — // - // — // —	-	p13.3
SNP_A-2243694	ctgctctggctccac[A/G]cagattgtccgaacgc	A	G	NM_032039 // intron // 0 // Hs.513225 // C16orf9 // 83986 // Homo sapiens hypothetical protein DKFZp761D0211 (DKFZP761D0211), mRNA. /// ENST00000354222 // intron // 0 // — // — // — /// ENST00000355919 // intron // 0 // — // — // -	C16orf9	C16orf9, Homo sapiens hypothetical protein DKFZp761D0211 (DKFZP761D0211), p13.3
SNP_A-1902380	tggcccgggggtccagal[C/G]agaaaacagggagaccc	C	G	NM_001053 // upstream // 8923 // Hs.449840 // SSTR5 // 6755 // Homo sapiens somatostatin receptor 5 (SSTR5), mRNA. /// ENST00000301702 // upstream // 19789 // — // — // — /// ENST00000293897 // upstream // 8923 // — // — // — // —	SSTR5	SSTR5, Homo sapiens somatostatin receptor 5 (SSTR5), p13.3
SNP_A-1877518	tctggcatcccagggal[A/C]atcctcaaggcctctg	A	C	NM_206835 // downstream // 95940 // Hs.334479 // TRAF7 // 84231 // Homo sapiens TNF receptor-associated factor 7 (TRAF7), transcript variant 2, mRNA. /// NM_032271 // downstream // 95940 // Hs.334479 // TRAF7 // 84231 // Homo sapiens TNF receptor-associat	TRAF7	TRAF7, Homo sapiens TNF receptor-associated factor 7 (TRAF7), transcript variant 2, p13.3
SNP_A-1805926	gtcccttctcactgt[A/G]agctacctgggtcaca	A	G	NM_001089 // intron // 0 // Hs.26630 // ABCA3 // 21 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA. /// ENST00000301732 // intron // 0 // — // — // — /// ENST00000358568 // intron // 0 // — // — // — /	ABCA3	ABCA3, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), p13.3
SNP_A-2195090	catggaagttctgcac[C/T]gcttttcacacactt	C	T	NM_001089 // upstream // 50320 // Hs.26630 // ABCA3 // 21 // Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA. /// NM_001761 // upstream // 49264 // Hs.1973 // CCNF // 899 // Homo sapiens cyclin F (CCNF), mRNA. /// ENST000003	ABCA3	ABCA3, Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), p13.3
SNP_A-1911478	tgtctgtgctagtag[G/T]cactcagtgtgtatgt	G	T	NM_022468 // intron // 0 // Hs.528670 // MMP25 // 64386 // Homo sapiens matrix metalloproteinase 25 (MMP25), transcript variant 1, mRNA. /// NM_022718 // intron // 0 // Hs.528670 // MMP25 // 64386 // Homo sapiens matrix metalloproteinase 25 (MMP25), trans	MMP25	MMP25, Homo sapiens matrix metalloproteinase 25 (MMP25), transcript variant 1, p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1943214	ttggtgaaagaagaaa[C/G]tcaagcagaagattta	C	G	NM_004220 // downstream // 37668 // Hs.115284 // ZNF213 // 7760 // Homo sapiens zinc finger protein 213 (ZNF213), mRNA. /// NM_012360 // upstream // 23775 // Hs.278464 // OR1F1 // 4992 // Homo sapiens olfactory receptor, family 1, subfamily F, member 1 (O	ZNF213	ZNF213, Homo sapiens zinc finger protein 213 (ZNF213), p13.3
SNP_A-2170979	caataattaaacaagc[A/G]gacaaaaatgacaagt	A	G	NM_004220 // downstream // 58687 // Hs.115284 // ZNF213 // 7760 // Homo sapiens zinc finger protein 213 (ZNF213), mRNA. /// NM_012360 // upstream // 2756 // Hs.278464 // OR1F1 // 4992 // Homo sapiens olfactory receptor, family 1, subfamily F, member 1 (OR	ZNF213	ZNF213, Homo sapiens zinc finger protein 213 (ZNF213), p13.3
SNP_A-1938127	ttgacagattcaaata[C/T]gtacaaaaggctgggg	C	T	NM_198088 // intron // 0 // Hs.513288 // ZNF200 // 7752 // Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /// NM_198087 // intron // 0 // Hs.513288 // ZNF200 // 7752 // Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /// NM_003454 // intron //	ZNF200	ZNF200, Homo sapiens zinc finger protein 200 (ZNF200), p13.3
SNP_A-2313838	tgttttattcaatgta[G/T]cagagccttgccacag	G	T	NM_198088 // intron // 0 // Hs.513288 // ZNF200 // 7752 // Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /// NM_198087 // intron // 0 // Hs.513288 // ZNF200 // 7752 // Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /// NM_003454 // intron //	ZNF200	ZNF200, Homo sapiens zinc finger protein 200 (ZNF200), p13.3
SNP_A-1948303	tttaggcaaagtacac[A/G]cattatcagatttggg	A	G	NM_153028 // downstream // 3907 // Hs.513292 // ZNF75A // 7627 // Homo sapiens zinc finger protein 75a (ZNF75A), mRNA. /// ENST00000293995 // downstream // 3907 // — // — // — // — /// ENST00000343567 // downstream // 866 // — // — // — // -	ZNF75A	ZNF75A, Homo sapiens zinc finger protein 75a (ZNF75A), p13.3
SNP_A-2298910	gccccagataatacaa[A/C]aaaatggccaacgttt	A	C	NM_015041 // intron // 0 // Hs.155995 // CLUAP1 // 23059 // Homo sapiens clusterin associated protein 1 (CLUAP1), mRNA. /// NM_024793 // intron // 0 // Hs.155995 // CLUAP1 // 23059 // Homo sapiens clusterin associated protein 1 (CLUAP1), mRNA. /// ENST000	CLUAP1	CLUAP1, Homo sapiens clusterin associated protein 1 (CLUAP1), p13.3
SNP_A-2314153	ggtgaagtctccataa[C/T]gcagttcttaaaaaaa	C	T	NM_004380 // intron // 0 // Hs.459759 // CREBBP // 1387 // Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), mRNA. /// ENST00000262367 // intron // 0 // — // — // — // —	CREBBP	CREBBP, Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), p13.3
SNP_A-2093425	agaactgcaagtctcc[A/G]cgtcgggtggcacaga	A	G	ENST00000330063 // CDS // 0 // — // — // — // —	-	p13.3
SNP_A-1884010	tgaagattggctccca[A/G]tgataggaaactgctg	A	G	NM_016936 // intron // 0 // Hs.440219 // UBN1 // 29855 // Homo sapiens ubinuclein 1 (UBN1), mRNA. /// NM_016936 // 5UTR // 0 // Hs.440219 // UBN1 // 29855 // Homo sapiens ubinuclein 1 (UBN1), mRNA. /// ENST00000262376 // intron // 0 // — // — // — // -	UBN1	UBN1, Homo sapiens ubinuclein 1 (UBN1), p13.3
SNP_A-1862315	tcatgtaaatattcag[C/T]aatgtgcttcctgtga	C	T	ENST00000251170 // intron // 0 // — // — // — // —	-	p13.3
SNP_A-2099901	agagtcaaattaccga[C/G]cacttgtgcgggaaaa	C	G	ENST00000340054 // upstream // 18166 // — // — // — // — /// ENST00000314100 // upstream // 199079 // — // — // — // —	-	p13.3
SNP_A-2233380	ctcaggtgggctttgc[A/G]agggggtagatactga	A	G	ENST00000340054 // upstream // 156531 // — // — // — // — /// ENST00000314100 // upstream // 60714 // — // — // — // —	-	p13.3
SNP_A-1798208	gtaaactccagcaaaa[C/T]gctaaactcactcatc	C	T	ENST00000340054 // upstream // 171858 // — // — // — // — /// ENST00000314100 // upstream // 45387 // — // — // — // —	-	p13.3
SNP_A-1880295	tcttctttaatcctcc[A/G]gcaagactaggtctcc	A	G	ENST00000340054 // upstream // 173983 // — // — // — // — /// ENST00000314100 // upstream // 43262 // — // — // — // —	-	p13.3
SNP_A-2109097	agcttctctcctggag[G/T]caagtgcttcagtgta	G	T	ENST00000340054 // upstream // 185042 // — // — // — // — /// ENST00000314100 // upstream // 32203 // — // — // — // —	-	p13.3
SNP_A-2260526	gaaacagggaaaggac[C/T]caaaaatgcaaaatgc	C	T	ENST00000340054 // upstream // 194046 // — // — // — // — /// ENST00000314100 // upstream // 23199 // — // — // — // —	-	p13.3
SNP_A-2208318	cccacaggagaccgga[C/T]gcgagcaagcgcacag	C	T	ENST00000340054 // upstream // 205262 // — // — // — // — /// ENST00000314100 // upstream // 11983 // — // — // — // —	-	p13.3
SNP_A-2004493	gtatcaaaacacatac[A/C]aaggatgaataagatg	A	C	ENST00000340054 // upstream // 210361 // — // — // — // — /// ENST00000314100 // upstream // 6884 // — // — // — // —	-	p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169928	caaggccgagcacctа[C/G]agaaggtcaagttgca	C	G	ENST00000314100 // downstream // 123750 // --- // --- // --- /// ENST00000314071 // upstream // 887323 // --- // --- // ---	-	p13.3
SNP_A-2158747	attgtctgagcgcata[C/T]ctgtgaattgtcata	C	T	ENST00000314100 // downstream // 241486 // --- // --- // --- /// ENST00000314071 // upstream // 769587 // --- // --- // ---	-	p13.3
SNP_A-1744063	ggtgcatcactaagcacattata[A/G]acattagcttgctaagc ccacaaca	A	G	NM_018723 // upstream // 381629 // Hs.57937 // A2BP1 // 54715 // ataxin 2-binding protein 1 /// NM_019109 // downstream // 551918 // Hs.406461 // ALG1 // 56052 // asparagine-linked glycosylation 1 homolog (yeast, beta 1,4-mannosyltransferase) /// NM_1458	A2BP1	A2BP1, rs881006, ataxin 2-binding protein 1, p13.3
SNP_A-2120150	agtcagagcgacagca[A/G]aggaaacgggttcaag	A	G	ENST00000314071 // upstream // 377621 // --- // --- // --- /// ENST00000314071 // upstream // 633452 // --- // --- // ---	-	p13.3
SNP_A-2304525	gctctcagtataggta[C/T]gtgctagagacttgta	C	T	ENST00000314100 // downstream // 403269 // --- // --- // --- /// ENST00000314071 // upstream // 607804 // --- // --- // ---	-	p13.3
SNP_A-1824441	taaactcaagagtgca[G/T]aagaggtacctgagga	G	T	ENST00000314100 // downstream // 405765 // --- // --- // --- /// ENST00000314071 // upstream // 605308 // --- // --- // ---	-	p13.3
SNP_A-2276023	gagagaaaaggtcaca[G/T]gctataggacttcaatg	G	T	ENST00000314100 // downstream // 553174 // --- // --- // --- /// ENST00000314071 // upstream // 457899 // --- // --- // ---	-	p13.3
SNP_A-2268981	gaattccagggatttg[C/T]agattactccagagta	C	T	ENST00000314100 // downstream // 648589 // --- // --- // --- /// ENST00000314071 // upstream // 362484 // --- // --- // ---	-	p13.3
SNP_A-2216531	cctctaatattggccca[A/G]ctttcactacctttt	A	G	ENST00000314100 // downstream // 723058 // --- // --- // --- /// ENST00000314071 // upstream // 288015 // --- // --- // ---	-	p13.3
SNP_A-2136398	atcacaggttattgta[C/T]ggatttactagatacа	C	T	ENST00000314071 // downstream // 22183 // --- // --- // --- /// ENST00000314058 // upstream // 302019 // --- // --- // ---	-	p13.2
SNP_A-1824793	taaagatccagaactc[A/G]ccctgatgaaaatttc	A	G	ENST00000314071 // downstream // 28761 // --- // --- // --- /// ENST00000314058 // upstream // 295441 // --- // --- // ---	-	p13.2
SNP_A-2251034	cttattagagtgtcta[A/T]gaagtgtcctctgttc	A	T	ENST00000314071 // downstream // 28916 // --- // --- // --- /// ENST00000314058 // upstream // 295286 // --- // --- // ---	-	p13.2
SNP_A-1875494	tctctggtgagattca[C/T]gtttctaactcgtata	C	T	ENST00000314071 // downstream // 32549 // --- // --- // --- /// ENST00000314058 // upstream // 291653 // --- // --- // ---	-	p13.2
SNP_A-1891942	tgatttttgcatcatga[A/T]cctagtcacagtatcc	A	T	ENST00000314071 // downstream // 109304 // --- // --- // --- /// ENST00000314058 // upstream // 214898 // --- // --- // ---	-	p13.2
SNP_A-1789828	gggctggaaaaaagca[C/T]gtcccaggaagaagcc	C	T	ENST00000314071 // downstream // 253393 // --- // --- // --- /// ENST00000314058 // upstream // 70809 // --- // --- // ---	-	p13.2
SNP_A-2040757	aacccagctgagaaaa[C/G]atgatatcttcctgt	C	G	ENST00000314058 // downstream // 8354 // --- // --- // --- /// ENST00000359349 // upstream // 403849 // --- // --- // ---	-	p13.2
SNP_A-2276663	gagegtcttccagcta[C/T]gtactcaagatcttag	C	T	ENST00000314058 // downstream // 18254 // --- // --- // --- /// ENST00000359349 // upstream // 393949 // --- // --- // ---	-	p13.2
SNP_A-1943534	ttgtaaatgggacctg[C/G]acagattgctaagtct	C	G	ENST00000314058 // downstream // 250587 // --- // --- // --- /// ENST00000359349 // upstream // 161616 // --- // --- // ---	-	p13.2
SNP_A-2162314	atttttatgacatatta[C/G]aaacattggatacatt	C	G	ENST00000314058 // downstream // 337029 // --- // --- // --- /// ENST00000359349 // upstream // 75174 // --- // --- // ---	-	p13.2
SNP_A-1782332	agtagggcacccataaa[A/G]aattcctaagttact	A	G	NM_145893 // upstream // 169650 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA /// NM_145891 // upstream // 169652 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1782335	attgatgaaattcct[C/T]aactgtgtgccatttt	C	T	NM_145893 // upstream // 169357 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA /// NM_145891 // upstream // 169359 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1839760	tagatgtggtgagcta[A/C]cttattcacctcagt	A	C	NM_145893 // upstream // 109632 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA /// NM_145891 // upstream // 109634 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1808658	gtgaacgatagtagtc[C/G]attcctgattcattct	C	G	NM_145893 // upstream // 101421 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 101423 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2149525	atgtagccatttttag[C/T]agtccaggaaagcagg	C	T	NM_145893 // upstream // 99735 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 99737 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1784758	ggcctgctgctactcca[C/T]gtattgtgttcaacag	C	T	NM_145893 // upstream // 99277 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 99279 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2037870	aacaatcggatgtcca[C/G]aatgcaaactatacat	C	G	NM_145893 // upstream // 99127 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 99129 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1803834	gtcaagccagtcaaga[C/T]ggaaatttgtccattg	C	T	NM_145893 // upstream // 98813 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 98815 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1802650	gtatgaagcatttaac[C/G]atgaagtcttctgttg	C	G	NM_145893 // upstream // 98197 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 98199 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2189330	cagttctgccatccac[C/G]agacaggaaaggttata	C	G	NM_145893 // upstream // 85865 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 85867 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1874863	tctcgttgggaactca[G/T]actttaccctaaggac	G	T	NM_145893 // upstream // 79304 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 79306 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1958621	tttctcaaaggtaga[C/G]gtgatcactagtttga	C	G	NM_145893 // upstream // 73714 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 73716 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2265496	gaagccccagaatttc[A/G]atgttctcaggaatca	A	G	NM_145893 // upstream // 69393 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 69395 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2128214	ataaggaaggtaccat[C/T]tgggcagtttcagacc	C	T	NM_145893 // upstream // 62234 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // upstream // 62236 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1715195	aacctagtcttgctgaggacaagga[C/T]atgtgacaaacccagg cacaagga	C	T	NM_018723 /// intron /// 0 /// Hs.57937 /// A2BP1 /// 54715 /// ataxin 2-binding protein 1	A2BP1	A2BP1 , rs1922585, ataxin 2-binding protein 1,p13.2
SNP_A-2254301	cttgcaataacggctc[C/T]gacattccctaaact	C	T	NM_145893 /// upstream /// 31280 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// upstream /// 31282 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2208093	cccaaggaaacaccct[A/G]agaaaagacagagagta	A	G	NM_145893 /// upstream /// 27491 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// upstream /// 27493 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2B	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1782551	taattgaattctctgc[C/G]aaccctgtccgccgt	C	G	NM_145893 /// upstream /// 1643 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// upstream /// 1645 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1840508	tagccatctagctatc[A/G]atccatacagccatcc	A	G	NM_145893 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcr	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2201818	ccacacatccctgaat[C/G]acttgttaaaacctag	C	G	NM_145893 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcr	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2297932	gccagtggaaatggga[C/T]agtaagcactgagtaa	C	T	NM_145893 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcr	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2191750	catatttaaggacaag[C/G]acaaagaactcttagt	C	G	NM_145893 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcr	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1783059	atatttcttaaactta[C/T]ggtcatcaaagacctc	C	T	NM_145893 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcr	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2023331	aaaaccattggatctc[A/G]aaggtagaggtcaccc	A	G	NM_145893 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// intron /// 0 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcr	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1689426	cagatattgagaaagaataacctttt[G/T]atagaagacacgttag ggaaaat	G	T	NM_018723 /// intron /// 0 /// Hs.57937 /// A2BP1 /// 54715 /// ataxin 2-binding protein 1 /// NM_145891 /// intron /// 0 /// Hs.57937 /// A2BP1 /// 54715 /// ataxin 2-binding p	A2BP1	A2BP1 , rs763650, ataxin 2-binding protein 1 ,p13.2
SNP_A-2285576	gatgaaatgtgaaatc[G/T]aaccgttcagactaaa	G	T	NM_145893 /// downstream /// 227073 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 /// downstream /// 225799 /// Hs.527984 /// A2BP1 /// 54715 /// Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1838468	tagaatccagctttcc[C/T]gacttgaagtacaaat	C	T	NM_145893 // downstream // 248129 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 246855 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1804896	gtcataagactttcaj[C/T]gagaaatggctgagat	C	T	NM_145893 // downstream // 337139 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 335865 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1891422	tgattcaatctgtgca[C/T]tcagaatccactgaat	C	T	NM_145893 // downstream // 351339 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 350065 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2246507	ctgtaaaatgggaaaa[C/G]tgtagccgtacttgct	C	G	NM_145893 // downstream // 416895 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 415621 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2255307	cttgtacatatccacc[A/G]gaactcttgggtgatt	A	G	NM_145893 // downstream // 444653 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 443379 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1796821	ggttcagactgtaaga[A/G]acatcctgcccatctg	A	G	NM_145893 // downstream // 576578 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 575304 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2241863	ctgatgctaatctctc[C/G]caaaaacaccatccgt	C	G	NM_145893 // downstream // 609527 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 608253 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-1857393	tcactaatcaagttga[C/T]gaggtcagcaacagtc	C	T	NM_145893 // downstream // 657327 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 656053 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2182119	cagaggctttctgaaa[C/T]ctgcaggcaagaaaa	C	T	NM_145893 // downstream // 921049 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, mRNA. /// NM_145891 // downstream // 919775 // Hs.527984 // A2BP1 // 54715 // Homo sapiens ataxin 2-binding protein	A2BP1	A2BP1, Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 3, p13.2
SNP_A-2283547	gatacttgtgaagaaa[A/G]ctgtcagcatgtggaa	A	G	NM_024109 // downstream // 24351 // Hs.306380 // MGC2654 // 79091 // Homo sapiens hypothetical protein MGC2654 (MGC2654), mRNA. /// NM_000663 // upstream // 4017 // Hs.336768 // ABAT // 18 // Homo sapiens 4-aminobutyrate aminotransferase (ABAT), nuclear g	MGC2654	MGC2654, Homo sapiens hypothetical protein MGC2654 (MGC2654), p13.2
SNP_A-2151476	atgttcgtagcacaaa[C/T]gcatcaatggcaaccg	C	T	NM_000663 // intron // 0 // Hs.336768 // ABAT // 18 // Homo sapiens 4-aminobutyrate aminotransferase (ABAT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA. /// NM_020686 // intron // 0 // Hs.336768 // ABAT // 18 // Homo sapiens 4	ABAT	ABAT, Homo sapiens 4-aminobutyrate aminotransferase (ABAT), nuclear gene encoding mitochondrial protein, transcript variant 2, p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1898544	tgcttgagtgcactga[C/T]agccaaattacccaaa	C	T	NM_000303 // intron // 0 // Hs.459855 // PMM2 // 5373 // Homo sapiens phosphomannomutase 2 (PMM2), mRNA. /// ENST00000268261 // intron // 0 // --- // --- // --- // ---	PMM2	PMM2, Homo sapiens phosphomannomutase 2 (PMM2), p13.2
SNP_A-2111104	aggagagaagcttgga[C/T]atgtgtgcagggtgat	C	T	NM_003470 // intron // 0 // Hs.386939 // USP7 // 7874 // Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA. /// ENST00000344836 // intron // 0 // --- // --- // --- // ---	USP7	USP7, Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), p13.2
SNP_A-2177472	cacgaaacaacgtgta[C/T]aagacaagcaatctgg	C	T	NM_003470 // intron // 0 // Hs.386939 // USP7 // 7874 // Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA. /// ENST00000344836 // intron // 0 // --- // --- // --- // ---	USP7	USP7, Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), p13.2
SNP_A-1781452	ggattacttacagtaa[A/G]tgaaaaccaagacttg	A	G	NM_003470 // upstream // 45047 // Hs.386939 // USP7 // 7874 // Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA. /// NM_014117 // upstream // 83149 // Hs.221497 // PRO0149 // 29035 // Homo sapiens PRO0149 protein (PRO0149)	USP7	USP7, Homo sapiens ubiquitin specific protease 7 (herpes virus-associated) (USP7), p13.2
SNP_A-2066157	aatttgttaattaaga[A/G]tagatggtgagctgtc	A	G	NM_000833 // downstream // 597316 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 8952 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2148240	atgggcaaaggccaga[A/G]gcaggaaccaaaggag	A	G	NM_000833 // downstream // 577336 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 28932 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2099165	agaggagccaatgcca[C/G]aaagaagcaacatcca	C	G	NM_000833 // downstream // 556698 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 49570 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2248054	ctgtggaaacaggaag[A/T]ctgagacctagagaag	A	T	NM_000833 // downstream // 554925 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 51343 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1784199	gctttttggcagcatc[C/G]aacccatagcaaagcc	C	G	NM_000833 // downstream // 526114 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 80154 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1844208	tagtttctgtgtctcc[C/G]cccttcaacaattttc	C	G	NM_000833 // downstream // 522799 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 83469 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2140599	atctctaaattcatca[A/G]gttgcatacattaaat	A	G	NM_000833 // downstream // 520750 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 85518 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1919534	ttaaggaagacccccc[C/T]aaattgtataagcctc	C	T	NM_000833 // downstream // 520388 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 85880 // --- // --- // --- // --- /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2277597	gagcacctgagttcaa[C/T]ctactgttctgcattt	C	T	NM_000833 // downstream // 510219 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 96049 // — // — /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2023233	aaaacattaaattaag[A/G]aattcatcaccacatt	A	G	NM_000833 // downstream // 507727 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 98541 // — // — /// ENST00000330684 // downstream	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2004531	tatcagtgaagaaaca[C/G]tgagatattaaacagt	C	G	NM_000833 // downstream // 506186 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 100082 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1784259	atgtagcaaacctgtc[C/T]aagtctgcgtgtccga	C	T	NM_000833 // downstream // 466971 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 139297 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2268649	gaatgtgatatagata[C/T]gtagtagccacatttt	C	T	NM_000833 // downstream // 455836 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 150432 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2022459	aaaaatattcgcttga[C/T]gcacagtgggattata	C	T	NM_000833 // downstream // 443653 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 162615 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1784336	ttgagcaatggccctc[G/T]ttaatttatcagata	G	T	NM_000833 // downstream // 418314 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 187954 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1802960	gtatgttatttacac[A/G]caaaagacagagtgtt	A	G	NM_000833 // downstream // 396820 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 209448 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2096063	agacatagaagcaaag[G/T]aatagcacagggagtc	G	T	NM_000833 // downstream // 341604 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 264664 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2053559	aagtgctctttcccga[C/T]aactgaacactaaa	C	T	NM_000833 // downstream // 339552 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 266716 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2182983	cagattgcttggtata[C/T]atcgtactgagtgggga	C	T	NM_000833 // downstream // 294482 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 311786 // — // — // — /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2263525	gaaccagaaaacgtaga[C/T]ggttttgcaaatgaac	C	T	NM_000833 // downstream // 230270 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 375998 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1934550	ttcctcagaagtgga[C/T]gccaagaaggaatttg	C	T	NM_000833 // downstream // 211616 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 394652 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2203489	ccagaagaagaattga[A/G]aatagagacatacaaa	A	G	NM_000833 // downstream // 211582 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 394686 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1957977	ttttcaattgagaaag[C/T]aatcttcagtgcaaag	C	T	NM_000833 // downstream // 211329 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 394939 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2141905	atcttgtcttcttctta[C/T]gcactaattgtgtctt	C	T	NM_000833 // downstream // 206193 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 400075 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1866469	tccccagagcccaata[G/T]agtgaatgcatgcagt	G	T	NM_000833 // downstream // 203038 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 403230 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2208135	cccaagttctcacatc[A/G]ctcaaacaatggaggt	A	G	NM_000833 // downstream // 171592 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000333457 // upstream // 434676 // --- // --- // --- /// ENST00000330684 // downstrea	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1718057	tatatatgtatatatttattttgcat[A/G]ttgtggttcacccctctagact gt	A	G	NM_000833 // downstream // 201366 // Hs.125338 // GRIN2A // 2903 // glutamate receptor, ionotropic, N-methyl D-aspartate 2A /// NM_014117 // upstream // 465635 // Hs.406602 // PRO0149 // 29035 // PRO0149 protein	GRIN2A	GRIN2A , rs1074042, glutamate receptor, ionotropic, N-methyl D-aspartate 2A ,p13.2
SNP_A-2234525	ctccacctctcacca[A/G]taccaatctcccaag	A	G	NM_000833 // intron // 0 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000330684 // intron // 0 // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2246713	ctgtacattaataccc[C/T]aagaggcaatgtaagg	C	T	NM_000833 // intron // 0 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000330684 // intron // 0 // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-1785004	agtcctgcgctacaga[A/C]acggttaaacttatt	A	C	NM_000833 // intron // 0 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// ENST00000330684 // intron // 0 // --- // --- // ---	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2
SNP_A-2062818	aatgtgcctgtatcca[A/C]aagaaatgaaacctgc	A	C	NM_000833 // upstream // 83133 // Hs.411472 // GRIN2A // 2903 // Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), mRNA. /// NM_024997 // upstream // 167055 // Hs.513343 // ATF7IP2 // 80063 // Homo sapiens activating transcrip	GRIN2A	GRIN2A, Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2270421	gacagaaaagtcctac[A/G]aggaggctgtcagcac	A	G	ENST00000261657 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-1937303	ttgaaagacccacaga[A/G]gagtttgcataagagc	A	G	ENST00000261657 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2082932	acgtgaaggatttgca[C/T]aggccattcacagatg	C	T	ENST00000261657 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2075824	acatgtgagtgctcta[C/T]gtatcgtagtgtcat	C	T	ENST00000261657 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2115786	aggtgactgacccca[A/C]aaaccatgaacaaagg	A	C	ENST00000261657 // downstream // 12390 // --- // --- // --- // --- // ENST00000340704 // upstream // 48082 // --- // --- // --- // ---	-	p13.13
SNP_A-2173401	cacaagggattgatca[A/G]agaggttgcctcaggc	A	G	NM_002761 // upstream // 31988 // Hs.2909 // PRM1 // 5619 // Homo sapiens protamine 1 (PRM1), mRNA. /// NM_152308 // upstream // 32128 // Hs.347524 // MGC24665 // 116028 // Homo sapiens hypothetical protein MGC24665 (MGC24665), mRNA. /// ENST00000312511 /	PRM1	PRM1, Homo sapiens protamine 1 (PRM1), p13.13
SNP_A-1879324	tcttagggacataata[A/G]agtcacaaacttacag	A	G	NM_015914 // intron // 0 // Hs.313847 // TXNDC11 // 51061 // Homo sapiens hypothetical protein LOC51061 (LOC51061), mRNA. /// ENST00000283033 // intron // 0 // --- // --- // --- // --- // ENST00000356957 // intron // 0 // --- // --- // ---	TXNDC11	TXNDC11, Homo sapiens hypothetical protein LOC51061 (LOC51061), p13.13
SNP_A-2225432	ctaaaaagaaacaggc[A/G]gacaaaggatcactga	A	G	NM_015914 // intron // 0 // Hs.313847 // TXNDC11 // 51061 // Homo sapiens hypothetical protein LOC51061 (LOC51061), mRNA. /// ENST00000283033 // intron // 0 // --- // --- // --- // --- // ENST00000356957 // intron // 0 // --- // --- // ---	TXNDC11	TXNDC11, Homo sapiens hypothetical protein LOC51061 (LOC51061), p13.13
SNP_A-1892148	tgcaaagtgaacatac[A/T]cattaagagagaagt	A	T	NM_014153 // upstream // 17646 // Hs.371856 // ZC3HDC7 // 29066 // Homo sapiens zinc finger CCCH type domain containing 7 (ZC3HDC7), mRNA. /// NM_014153 // upstream // 3047 // Hs.371856 // ZC3HDC7 // 29066 // Homo sapiens zinc finger CCCH type domain cont	ZC3HDC7	ZC3HDC7, Homo sapiens zinc finger CCCH type domain containing 7 (ZC3HDC7), p13.13
SNP_A-2276971	gagatctctcacgaaa[C/G]aaacaagatcaaggat	C	G	NM_015659 // upstream // 17795 // Hs.528354 // RSL1D1 // 26156 // Homo sapiens DKFZP564M182 protein (DKFZP564M182), mRNA. /// NM_002094 // downstream // 3349 // Hs.528780 // GSPT1 // 2935 // Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA. /// ENST0	RSL1D1	RSL1D1, Homo sapiens DKFZP564M182 protein (DKFZP564M182), p13.13
SNP_A-1786093	tcgtccatcctagtac[C/T]atgcgtcatttctttt	C	T	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2254212	cttgatggacgcgagt[A/G]aaagagatgtagtcct	A	G	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2238675	ctctgttggctgagta[C/T]agtagctcatgcttgt	C	T	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2195742	catgtaatttggagc[G/T]ataaaggcctaattag	G	T	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2279890	gaggctaagtcttggt[A/G]agaggaggagaattaa	A	G	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-1813297	gtggtgatgataagta[C/T]ataaacccatgcctg	C	T	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.13
SNP_A-2211610	ccctcagtggagggca[A/C]ctgttgctcacttgtc	A	C	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // ---	-	p13.12
SNP_A-1851576	tattctcattcgctca[A/G]ctcgccagccctggct	A	G	ENST00000306030 // intron // 0 // --- // --- // --- // --- // ENST00000323433 // intron // 0 // --- // --- // --- // ENST00000219090 // intron // 0 // --- // --- - // --- // ---	-	p13.12
SNP_A-1684304	gctcagtggcactgtagtttgaa[C/T]acctggatgccaaaaac agaaaaca	C	T	AK074072 // intron // 0 // Hs.145047 // LOC92017 // 92017 // similar to RIKEN cDNA 4933437K13	LOC92017	LOC92017, rs10492794, similar to RIKEN cDNA 4933437K13,p13.12
SNP_A-2082689	acgggctcccaggctat[C/T]gtgtctcaagtccgcc	C	T	NM_005236 // upstream // 1017235 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 303 // --- // --- // --- // --- // EN	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2272577	gacgaggacccagtca[A/T]aaatttctctcatatc	A	T	NM_005236 // upstream // 745222 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 272316 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1958191	tttcattagagaaaa[C/G]agtgaacatgttaagt	C	G	NM_005236 // upstream // 685503 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 332035 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1787250	aagtctccggagtca[C/G]cttcttcttcattata	C	G	NM_005236 // upstream // 677579 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 339959 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1787259	actaggacccctctgag[A/G]agctggaagaaatcac	A	G	NM_005236 // upstream // 668573 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 348965 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1719857	ttagatatgagtatcctcaggagtct[A/G]aaacatctcttgccttaa gttctgt	A	G	NM_005236 // upstream // 658274 // Hs.511917 // ERCC4 // 2072 // excision repair cross-complementing rodent repair deficiency, complementation group 4 /// NM_018340 // upstream // 458025 // Hs.200481 // FLJ11151 // 55313 // hypothetical protein FLJ11151	ERCC4	ERCC4 , rs10521098, excision repair cross-complementing rodent repair deficiency, complementation group 4, p13.12
SNP_A-2182331	cagagtggatccgaac[A/G]cttacagaaattgga	A	G	NM_005236 // upstream // 436813 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 580725 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1793434	ggtagtaagtacttag[C/G]agatactcaaagaggt	C	G	NM_005236 // upstream // 376029 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 641509 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1787029	gggaaaccatgacaat[A/G]aaggaagaacttgcac	A	G	NM_005236 // upstream // 260639 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 756899 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1804532	gtcagatcagctgagt[C/G]aaacctggcagttcca	C	G	NM_005236 // upstream // 222558 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000299958 // downstream // 794980 // — // — // — // — ///	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-1704757	aagtgaaaggctctgacacactcta[C/T]ggtggaaaacacattc atcattgca	C	T	NM_005236 // upstream // 263329 // Hs.511917 // ERCC4 // 2072 // excision repair cross-complementing rodent repair deficiency, complementation group 4 /// NM_018340 // upstream // 852970 // Hs.200481 // FLJ11151 // 55313 // hypothetical protein FLJ11151	ERCC4	ERCC4 , rs7185124, excision repair cross-complementing rodent repair deficiency, complementation group 4, p13.12
SNP_A-1788012	actctgcatgttccaf[A/G]aaaggctctctcct	A	G	NM_005236 // intron // 0 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000311895 // intron // 0 // — // — // — // —	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1788025	attttcagggtaatca[C/T]aaataggggtggttaa	C	T	NM_005236 // intron // 0 // Hs.460019 // ERCC4 // 2072 // Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA. /// ENST00000311895 // intron // 0 // — // — // — // —	ERCC4	ERCC4, Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), p13.12
SNP_A-2314721	ggagtcctctaccaca[C/T]gtgaatcttgaatatt	C	T	NM_014048 // intron // 0 // Hs.49143 // MKL2 // 57496 // Homo sapiens MKL/myocardin-like 2 (MKL2), mRNA. /// ENST00000318282 // intron // 0 // — // — // — // —	MKL2	MKL2, Homo sapiens MKL,p13.12
SNP_A-2256746	ctttcatgctaacatg[C/G]aaagaaaggtacctgc	C	G	NM_014048 // intron // 0 // Hs.49143 // MKL2 // 57496 // Homo sapiens MKL/myocardin-like 2 (MKL2), mRNA. /// AB033069 // intron // 0 // Hs.49143 // MKL2 // 57496 // Homo sapiens mRNA for KIAA1243 protein, partial cds. /// ENST00000318282 // intron // 0 //	MKL2	MKL2, Homo sapiens MKL,p13.12
SNP_A-2087455	actgccagcatctcta[A/G]ccatctgattaggttt	A	G	NM_033201 // intron // 0 // Hs.460095 // C16orf45 // 89927 // Homo sapiens hypothetical gene BC008967 (BC008967), mRNA. /// ENST00000300006 // intron // 0 // — // — // — // — /// ENST00000356470 // intron // 0 // — // — // — // — /// ENST0	C16orf45	C16orf45, Homo sapiens hypothetical gene BC008967 (BC008967), p13.11
SNP_A-2314840	ggagtgcttctcaatc[A/G]agggcaactgtcccac	A	G	NM_002474 // intron // 0 // Hs.460109 // MYH11 // 4629 // Homo sapiens myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM1, mRNA. /// NM_022844 // intron // 0 // Hs.460109 // MYH11 // 4629 // Homo sapiens myosin, heavy polypeptide	MYH11	MYH11, Homo sapiens myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM1, p13.11
SNP_A-2004568	cagaattggtggttaa[A/G]tacatggaaaacaaga	A	G	NM_002474 // intron // 0 // Hs.460109 // MYH11 // 4629 // Homo sapiens myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM1, mRNA. /// NM_022844 // intron // 0 // Hs.460109 // MYH11 // 4629 // Homo sapiens myosin, heavy polypeptide	MYH11	MYH11, Homo sapiens myosin, heavy polypeptide 11, smooth muscle (MYH11), transcript variant SM1, p13.11
SNP_A-2082426	acgccaaatgaggtac[A/G]gggaagggactttaca	A	G	NM_019899 // intron // 0 // Hs.391464 // ABCC1 // 4363 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 4, mRNA. /// NM_019900 // intron // 0 // Hs.391464 // ABCC1 // 4363 // Homo sapiens ATP-binding cass	ABCC1	ABCC1, Homo sapiens ATP-binding cassette, sub-family C (CFTR p13.11
SNP_A-2211595	ccctcagctcttctac[A/G]agtggacgtggaatga	A	G	NM_019899 // intron // 0 // Hs.391464 // ABCC1 // 4363 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 4, mRNA. /// NM_019900 // intron // 0 // Hs.391464 // ABCC1 // 4363 // Homo sapiens ATP-binding cass	ABCC1	ABCC1, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p13.11
SNP_A-2077638	accacgcagacctcac[C/T]ggttctcccgctgtgc	C	T	NM_001171 // intron // 0 // Hs.442182 // ABCC6 // 368 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA. /// ENST00000205557 // intron // 0 // — // — // — // —	ABCC6	ABCC6, Homo sapiens ATP-binding cassette, sub-family C (CFTR,p13.11
SNP_A-2080496	acctatattagaatgc[C/T]gaaaaataacaaaaac	C	T	NM_022166 // downstream // 341538 // Hs.302736 // XYLT1 // 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000327792 // downstream // 415364 // — // — // — // — /// ENST00000261381 // downstream // 341538 // — // — // — // —	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2107529	agctagtatttttgc[G/T]agtagatatgtacatt	G	T	NM_022166 // intron // 0 // Hs.302736 // XYLT1 // 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // intron // 0 // — // — // — // —	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2004578	atagctctcacttttta[A/G]gacatctcatctgatc	A	G	NM_022166 // intron // 0 // Hs.302736 // XYLT1 // 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // intron // 0 // — // — // — // —	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-1876243	tctgagaaggtatcca[C/T]gagctccatctgactg	C	T	NM_022166 // upstream // 131684 // Hs.302736 // XYLT1 // 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // upstream // 131684 // — // — // — // — /// ENST00000339124 // upstream // 330172 // — // — // — // —	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2043638	aactgttttttgaagc[A/G]aagaatgcagaactag	A	G	NM_022166 // upstream // 347288 // Hs.302736 // XYLT1 // 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // upstream // 347288 // — // — // — // — /// ENST00000339124 // upstream // 114568 // — // — // — // —	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-2144282	atgagtgcttcactgc[C/T]cttttacttgcatctt	C	T	NM_022166 // upstream // 385358 // Hs.302736 // XYLT1 // 64131 // Homo sapiens xylosyltransferase I (XYLT1), mRNA. /// ENST00000261381 // upstream // 385358 // — // — // — // — /// ENST00000339124 // upstream // 76498 // — // — // — // —	XYLT1	XYLT1, Homo sapiens xylosyltransferase I (XYLT1), p12.3
SNP_A-1899713	tggaatccagggtgac[C/G]aaggcatgacaagggt	C	G	NM_001004067 // upstream // 33181 // Hs.460141 // NOMO3 // 408050 // Homo sapiens nodal modulator 3 (NOMO3), mRNA. /// NM_014287 // upstream // 33181 // Hs.209113 // NOMO1 // 23420 // Homo sapiens nodal modulator 1 (NOMO1), mRNA. /// NM_173614 // upstream	NOMO3	NOMO3, Homo sapiens nodal modulator 3 (NOMO3), p12.3
SNP_A-1861336	tcatcaccacaggcga[C/G]ataactgaagctcaaa	C	G	NM_001004067 // upstream // 206040 // Hs.460141 // NOMO3 // 408050 // Homo sapiens nodal modulator 3 (NOMO3), mRNA. /// NM_014287 // upstream // 206040 // Hs.209113 // NOMO1 // 23420 // Homo sapiens nodal modulator 1 (NOMO1), mRNA. /// NM_173614 // upstre	NOMO3	NOMO3, Homo sapiens nodal modulator 3 (NOMO3), p12.3
SNP_A-1797245	ggttggaccaaagaaa[A/G]accatctgcaagcctg	A	G	NM_016138 // downstream // 31393 // Hs.157113 // COQ7 // 10229 // Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), mRNA. /// NM_016524 // upstream // 56895 // Hs.258326 // LOC51760 // 51760 // Homo sapiens B/K protein (LOC51760), mRNA. /// ENS	COQ7	COQ7, Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), p12.3
SNP_A-1789817	tcccagctgcaaaata[C/T]acccaacctggtgata	C	T	NM_016138 // downstream // 37425 // Hs.157113 // COQ7 // 10229 // Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), mRNA. /// NM_016524 // upstream // 50863 // Hs.258326 // LOC51760 // 51760 // Homo sapiens B/K protein (LOC51760), mRNA. /// ENS	COQ7	COQ7, Homo sapiens coenzyme Q7 homolog, ubiquinone (yeast) (COQ7), p12.3
SNP_A-1857732	tcactgccatgtacta[C/T]gctaagcgctttacat	C	T	NM_016524 // intron // 0 // Hs.258326 // LOC51760 // 51760 // Homo sapiens B/K protein (LOC51760), mRNA. /// ENST00000261375 // intron // 0 // — // — // — // — /// ENST00000355377 // intron // 0 // — // — // — // —	LOC51760	LOC51760, Homo sapiens B p12.3
SNP_A-2180888	cagaatggtgttccca[C/G]ggtgctgttgtttaag	C	G	NM_020314 // intron // 0 // Hs.546412 // MGC16824 // 57020 // Homo sapiens esophageal cancer associated protein (MGC16824), mRNA. /// ENST00000251143 // intron // 0 // — // — // — // — /// ENST00000306146 // intron // 0 // — // — // — // —	MGC16824	MGC16824, Homo sapiens esophageal cancer associated protein (MGC16824), p12.3
SNP_A-2051736	aaggtcaattaggcac[A/G]ccattagagactattc	A	G	NM_016235 // upstream // 182663 // Hs.148685 // GPRC5B // 51704 // Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA. /// NM_001502 // downstream // 242083 // Hs.53985 // GP2 // 2813 // Homo sapiens glycoprotein 2 (zymoge	GPRC5B	GPRC5B, Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), p12.3
SNP_A-2037295	aacaaaggaccgatat[C/G]aagaatatattaagaa	C	G	NM_017888 // intron // 0 // Hs.122939 // FLJ20581 // 54988 // Homo sapiens hypothetical protein FLJ20581 (FLJ20581), mRNA. /// ENST00000331849 // intron // 0 // — // — // — // — /// ENST00000355494 // intron // 0 // — // — // — // —	FLJ20581	FLJ20581, Homo sapiens hypothetical protein FLJ20581 (FLJ20581), p12.3
SNP_A-2004610	ccgaatggctgggtga[A/G]agtctgacctagaaga	A	G	NM_182617 // upstream // 38802 // Hs.298252 // HXMA // 348158 // Homo sapiens xenobiotic/medium-chain fatty acid:CoA ligase (HXMA), nuclear gene encoding mitochondrial protein, mRNA. /// NM_052956 // downstream // 8242 // Hs.306812 // BUCS1 // 116285 // H	HXMA	HXMA, Homo sapiens xenobiotic,p12.3
SNP_A-2192673	catcccaaaagttcca[G/T]gtgggttcagacagga	G	T	NM_052956 // intron // 0 // Hs.306812 // BUCS1 // 116285 // Homo sapiens butyryl Coenzyme A synthetase 1 (BUCS1), mRNA. /// ENST00000219151 // intron // 0 // — // — // — // — /// ENST00000307493 // intron // 0 // — // — // — // —	BUCS1	BUCS1, Homo sapiens butyryl Coenzyme A synthetase 1 (BUCS1), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2187087	caggtatttggtctaa[A/T]ctcaccaaaaggacag	A	T	NM_017736 // intron // 0 // Hs.460232 // THUMPD1 // 55623 // Homo sapiens THUMP domain containing 1 (THUMPD1), mRNA. /// ENST00000173569 // intron // 0 // — // — // — // —	THUMPD1	THUMPD1, Homo sapiens THUMP domain containing 1 (THUMPD1), p12.3
SNP_A-2262688	gaaattgaagaaatac[C/T]caaattcttgctgaag	C	T	NM_202000 // intron // 0 // Hs.160976 // SAH // 6296 // Homo sapiens SA hypertension-associated homolog (rat) (SAH), transcript variant 2, mRNA. /// NM_005622 // intron // 0 // Hs.160976 // SAH // 6296 // Homo sapiens SA hypertension-associated homolog (r	SAH	SAH, Homo sapiens SA hypertension-associated homolog (rat) (SAH), transcript variant 2, p12.3
SNP_A-2178664	cactctgtacctcaca[A/T]gaatgaactggaaaat	A	T	NM_144672 // intron // 0 // Hs.408336 // OTOA // 146183 // Homo sapiens otoancorin (OTOA), mRNA. /// NM_170664 // intron // 0 // Hs.408336 // OTOA // 146183 // Homo sapiens otoancorin (OTOA), mRNA. /// ENST00000324089 // intron // 0 // — // — // — // —	OTOA	OTOA, Homo sapiens otoancorin (OTOA), p12.2
SNP_A-2113822	aggctggatgatgtcc[C/T]gctgatctattgctgt	C	T	NM_144672 // intron // 0 // Hs.408336 // OTOA // 146183 // Homo sapiens otoancorin (OTOA), mRNA. /// NM_170664 // intron // 0 // Hs.408336 // OTOA // 146183 // Homo sapiens otoancorin (OTOA), mRNA. /// ENST00000324089 // intron // 0 // — // — // — // —	OTOA	OTOA, Homo sapiens otoancorin (OTOA), p12.2
SNP_A-1823659	taaaatagcccttgca[C/T]gatgacagttttatat	C	T	NM_013302 // intron // 0 // Hs.498892 // EEF2K // 29904 // Homo sapiens eukaryotic elongation factor-2 kinase (EEF2K), mRNA. /// ENST00000263026 // intron // 0 // — // — // — // — // —	EEF2K	EEF2K, Homo sapiens eukaryotic elongation factor-2 kinase (EEF2K), p12.1
SNP_A-2308056	gcttgaatacaagtac[A/G]cctggttccaggaact	A	G	D86974 // downstream // 258603 // Hs.460313 // KIAA0220 // 283846 // Homo sapiens mRNA for KIAA0220 gene, partial cds. /// NM_006043 // upstream // 19181 // Hs.115830 // HS3ST2 // 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (	KIAA0220	KIAA0220, Homo sapiens for KIAA0220 gene, partial cds. ,p12.1
SNP_A-2238837	ctcttatcatcttccc[A/G]caaaactgaaaaatct	A	G	D86974 // downstream // 259119 // Hs.460313 // KIAA0220 // 283846 // Homo sapiens mRNA for KIAA0220 gene, partial cds. /// NM_006043 // upstream // 18665 // Hs.115830 // HS3ST2 // 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (	KIAA0220	KIAA0220, Homo sapiens for KIAA0220 gene, partial cds. ,p12.1
SNP_A-1868394	tcctccacctcaataa[C/G]acgtttgcagtttaca	C	G	D86974 // downstream // 262558 // Hs.460313 // KIAA0220 // 283846 // Homo sapiens mRNA for KIAA0220 gene, partial cds. /// NM_006043 // upstream // 15226 // Hs.115830 // HS3ST2 // 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (	KIAA0220	KIAA0220, Homo sapiens for KIAA0220 gene, partial cds. ,p12.1
SNP_A-1821398	gtttggaaggttctcc[A/G]ctctatctgaaagccc	A	G	NM_006043 // intron // 0 // Hs.115830 // HS3ST2 // 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// ENST00000261374 // intron // 0 // — // — // — // —	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2149749	atgtatgtttacacgc[C/T]ctggttgcctgctcat	C	T	NM_006043 // downstream // 27905 // Hs.115830 // HS3ST2 // 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 123391 // Hs.183817 // USP31 // 57478 // Homo sapiens ubiquitin specific pr	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2179238	cactggtgggaagcat[C/G]agaagatgtgaagagc	C	G	NM_006043 // downstream // 52687 // Hs.115830 // HS3ST2 // 9956 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /// NM_020718 // downstream // 98609 // Hs.183817 // USP31 // 57478 // Homo sapiens ubiquitin specific pro	HS3ST2	HS3ST2, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), p12.1
SNP_A-2047852	aagatttttaagcagc[A/G]gagtaacatggttcag	A	G	NM_153603 // intron // 0 // Hs.185807 // COG7 // 91949 // Homo sapiens component of oligomeric golgi complex 7 (COG7), mRNA. /// ENST00000307149 // intron // 0 // — // — // — // —	COG7	COG7, Homo sapiens component of oligomeric golgi complex 7 (COG7), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1791977	taaacctgcctcaaad[A/G]gagatttctcttttggt	A	G	NM_022097 // downstream // 3808 // Hs.178589 // LOC63928 // 63928 // Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA. /// NM_212535 // upstream // 73258 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB	LOC63928	LOC63928, Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), p12.1
SNP_A-2245767	ctgggggaagaataga[A/T]acatgcaataggtct	A	T	NM_022097 // downstream // 28676 // Hs.178589 // LOC63928 // 63928 // Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA. /// NM_212535 // upstream // 48390 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKC	LOC63928	LOC63928, Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), p12.1
SNP_A-2032580	aaataaacataatcaa[C/T]aaaggaaagcggcttg	C	T	NM_022097 // downstream // 40112 // Hs.178589 // LOC63928 // 63928 // Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA. /// NM_212535 // upstream // 36954 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKC	LOC63928	LOC63928, Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), p12.1
SNP_A-1829353	taagtcataaaggatg[G/T]atagcacacaaaagac	G	T	NM_022097 // downstream // 50167 // Hs.178589 // LOC63928 // 63928 // Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA. /// NM_212535 // upstream // 26899 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKC	LOC63928	LOC63928, Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), p12.1
SNP_A-1950983	tttccagaggtttggat[C/T]gattatgcggggagca	C	T	NM_022097 // downstream // 54629 // Hs.178589 // LOC63928 // 63928 // Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA. /// NM_212535 // upstream // 22437 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKC	LOC63928	LOC63928, Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), p12.1
SNP_A-1785710	ggctctaggaggaggaat[A/G]aagagtggtcaagtgc	A	G	NM_212535 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcrip	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1
SNP_A-1860175	tcagtcagtgttgctat[C/T]aaatctaggcacctgt	C	T	NM_212535 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcrip	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1
SNP_A-2140826	atctgaaatgtgtgaa[A/C]aaatagtaaatattta	A	C	NM_212535 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcrip	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1
SNP_A-2112564	aggcactagctcatca[G/T]aaatattagctattac	G	T	NM_212535 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcrip	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1
SNP_A-2238056	ctctgcaatgattagal[A/T]tcccaagaaaaggtca	A	T	NM_212535 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcrip	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1
SNP_A-1886429	tgacgctattgtgtta[A/T]ctgccaggttcctctt	A	T	NM_212535 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, mRNA. /// NM_002738 // intron // 0 // Hs.460355 // PRKCB1 // 5579 // Homo sapiens protein kinase C, beta 1 (PRKCB1), transcrip	PRKCB1	PRKCB1, Homo sapiens protein kinase C, beta 1 (PRKCB1), transcript variant 1, p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2123442	agtgtctggtaatgag[A/G]cataagttaaatgcca	A	G	NM_006539 // intron // 0 // Hs.7235 // CACNG3 // 10368 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA. /// ENST00000005284 // intron // 0 // --- // --- // --- // ---	CACNG3	CACNG3, Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), p12.1
SNP_A-1850989	tattatctgagaataa[A/G]gatgccttacaacagt	A	G	NM_006539 // intron // 0 // Hs.7235 // CACNG3 // 10368 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA. /// ENST00000005284 // intron // 0 // --- // --- // --- // ---	CACNG3	CACNG3, Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), p12.1
SNP_A-2313384	ggagagaagattgtac[C/T]aatagttcgtctctgg	C	T	NM_006539 // intron // 0 // Hs.7235 // CACNG3 // 10368 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA. /// ENST00000005284 // intron // 0 // --- // --- // --- // ---	CACNG3	CACNG3, Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), p12.1
SNP_A-2253651	cttctttgcacttatc[C/T]atttctagggacagat	C	T	NM_006539 // intron // 0 // Hs.7235 // CACNG3 // 10368 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA. /// ENST00000005284 // intron // 0 // --- // --- // --- // ---	CACNG3	CACNG3, Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), p12.1
SNP_A-1682460	gccttgcccctctacttgacagcca[A/G]tgaagagcacagacttgggagccac	A	G	NM_006539 // intron // 0 // Hs.7235 // CACNG3 // 10368 // calcium channel, voltage-dependent, gamma subunit 3	CACNG3	CACNG3 , rs723722, calcium channel, voltage-dependent, gamma subunit 3,p12.1
SNP_A-1889420	tgagttatgagtccac[C/T]accacctccaaaactt	C	T	NM_006539 // downstream // 43799 // Hs.7235 // CACNG3 // 10368 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA. /// NM_018703 // upstream // 133372 // Hs.188553 // RBBP6 // 5930 // Homo sapiens retinoblastoma binding pro	CACNG3	CACNG3, Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), p12.1
SNP_A-2132532	atagtggtgacaaaga[C/T]gtttgattcacaaaga	C	T	NM_207448 // upstream // 12957 // Hs.532558 // FLJ45256 // 400511 // Homo sapiens FLJ45256 protein (FLJ45256), mRNA. /// NM_014494 // upstream // 46230 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// NM	FLJ45256	FLJ45256, Homo sapiens FLJ45256 protein (FLJ45256), p12.1
SNP_A-2309660	ggaaagatagcgaaaa[A/G]gttgttactatcacac	A	G	NM_014494 // intron // 0 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// NM_020847 // intron // 0 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// ENS	TNRC6A	TNRC6A, Homo sapiens trinucleotide repeat containing 6 (TNRC6), p12.1
SNP_A-1792436	acgccatgagaattta[C/T]gcttggcttagtgttc	C	T	NM_014494 // intron // 0 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// NM_020847 // intron // 0 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// ENS	TNRC6A	TNRC6A, Homo sapiens trinucleotide repeat containing 6 (TNRC6), p12.1
SNP_A-1792439	gccaaggcagagacaa[C/T]tggcgagctcgctcag	C	T	NM_014494 // intron // 0 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// NM_020847 // intron // 0 // Hs.407740 // TNRC6A // 27327 // Homo sapiens trinucleotide repeat containing 6 (TNRC6), mRNA. /// ENS	TNRC6A	TNRC6A, Homo sapiens trinucleotide repeat containing 6 (TNRC6), p12.1
SNP_A-2293654	gcagccctacaagagg[A/G]aaagagtcagtcctgg	A	G	NM_052944 // intron // 0 // Hs.164118 // SLC5A11 // 115584 // Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 11 (SLC5A11), mRNA. /// ENST00000347898 // intron // 0 // --- // --- // --- // ---	SLC5A11	SLC5A11, Homo sapiens solute carrier family 5 (sodium,p12.1
SNP_A-1929701	ttcatatttaaagccc[A/G]gattcaaagaaccaaa	A	G	ENST00000329698 // downstream // 19202 // --- // --- // --- // --- /// ENST00000360895 // upstream // 12909 // --- // --- // --- // ---	-	p12.1
SNP_A-2263609	gaacccaccaatttcg[A/G]acacaacttcactcct	A	G	ENST00000329698 // downstream // 25454 // --- // --- // --- // --- /// ENST00000360895 // upstream // 6657 // --- // --- // --- // ---	-	p12.1
SNP_A-2198000	cattgctaagcccccca[C/T]aggaccgtggaagggg	C	T	NM_001169 // intron // 0 // Hs.176658 // AQP8 // 343 // Homo sapiens aquaporin 8 (AQP8), mRNA. /// ENST00000219660 // intron // 0 // --- // --- // --- // ---	AQP8	AQP8, Homo sapiens aquaporin 8 (AQP8), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1793057	cctgatgtctttgaaa[A/G]gtgttctgggcaagct	A	G	NM_006040 // upstream // 74380 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000335078 // upstream // 163391 // --- // --- // --- /// ENST00000331351 // upstream // 743	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-1856119	tcacaaaaccagaatc[C/T]cattgaacttccgcaa	C	T	NM_006040 // intron // 0 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2307950	gcttctgtctccctaa[C/T]tcagtgcaggccacaa	C	T	NM_006040 // intron // 0 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2101139	agatcagtgcctgaca[C/T]atgtggacattccat	C	T	NM_006040 // intron // 0 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2314120	ggaggacctcatgatc[A/G]ctaactggaggagatg	A	G	NM_006040 // intron // 0 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2265826	gaaggaagaccagtaa[C/T]gctggagggcagtgag	C	T	NM_006040 // intron // 0 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// ENST00000331351 // intron // 0 // --- // --- // ---	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2293122	gcagacctttttgtc[A/G]ctcacatatacattaa	A	G	NM_006040 // downstream // 342 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 930117 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA. /	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-1912940	tgtggaagacagggac[A/G]ggtcagctggccaag	A	G	NM_006040 // downstream // 303874 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 626585 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-1868959	tcctgagttctttccaa[C/G]aggaccgcgcatcccaa	C	G	NM_006040 // downstream // 354766 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 575693 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-1736913	aatcagccataggttccaaggaat[A/G]aaattgataggaaaa gctatctaga	A	G	AF105378 // downstream // 355684 // Hs.8040 // HS3ST4 // 9951 // heparan sulfate (glucosamine) 3-O-sulfotransferase 4 /// BC031257 // upstream // 573555 // Hs.120831 // TNT // 162083 // TNT protein	HS3ST4	HS3ST4 , rs7206138, heparan sulfate (glucosamine) 3-O-sulfotransferase 4 ,p12.1
SNP_A-2122492	agtgctcacgaaaaga[C/T]gaacacacataagcac	C	T	NM_006040 // downstream // 490688 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 439771 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2071365	acacttttcctgaaaca[C/T]ctgcttggctgttcc	C	T	NM_006040 // downstream // 599425 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 331034 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2212223	ccctggatctggaaag[C/T]agacagcccaggtgct	C	T	NM_006040 // downstream // 686270 // Hs.510835 // HS3ST4 // 9951 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), mRNA. /// NM_182831 // upstream // 244189 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA	HS3ST4	HS3ST4, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4), p12.1
SNP_A-2004659	gatggagggcagtgga[A/G]tagcggagagtagtgg	A	G	NM_182831 // downstream // 112205 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA. /// NM_024773 // upstream // 22125 // Hs.145717 // FLJ13798 // 79831 // Homo sapiens hypothetical protein FLJ13798 (FLJ13798), mRNA. /// ENST000003311	TNT	TNT, Homo sapiens TNT protein (TNT), p12.1
SNP_A-1794254	ccatcccatctaccaa[A/G]cccctcaagtcccagg	A	G	NM_182831 // downstream // 112233 // Hs.120831 // TNT // 162083 // Homo sapiens TNT protein (TNT), mRNA. /// NM_024773 // upstream // 22097 // Hs.145717 // FLJ13798 // 79831 // Homo sapiens hypothetical protein FLJ13798 (FLJ13798), mRNA. /// ENST000003311	TNT	TNT, Homo sapiens TNT protein (TNT), p12.1
SNP_A-1952272	tttctccttgacagca[A/T]gaaaatgttctaaaac	A	T	NM_145080 // upstream // 26561 // Hs.284295 // NSMCE1 // 197370 // Homo sapiens non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA. /// NM_000418 // upstream // 44860 // Hs.513457 // IL4R // 3566 // Homo sapiens interleukin 4 r	NSMCE1	NSMCE1, Homo sapiens non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), p12.1
SNP_A-2131810	atagctgggtactcac[C/T]agggcccatcttttt	C	T	NM_021798 // intron // 0 // Hs.210546 // IL21R // 50615 // Homo sapiens interleukin 21 receptor (IL21R), transcript variant 1, mRNA. /// NM_181079 // intron // 0 // Hs.210546 // IL21R // 50615 // Homo sapiens interleukin 21 receptor (IL21R), transcript va	IL21R	IL21R, Homo sapiens interleukin 21 receptor (IL21R), transcript variant 1, p12.1
SNP_A-2100189	agagttagtgacatgc[A/T]catagaaaaccaagca	A	T	NM_001520 // intron // 0 // Hs.371718 // GTF3C1 // 2975 // Homo sapiens general transcription factor IIIC, polypeptide 1, alpha 220kDa (GTF3C1), mRNA. /// ENST00000170629 // intron // 0 // --- // --- // --- // --- /// ENST00000356183 // intron // 0 // ---	GTF3C1	GTF3C1, Homo sapiens general transcription factor IIIC, polypeptide 1, alpha 220kDa (GTF3C1), p12.1
SNP_A-2025441	aaaatccaggcttctc[A/G]atatgatctagcccct	A	G	ENST00000261588 // intron // 0 // --- // --- // --- // ---	-	p11.2
SNP_A-2148778	atggtgacaacagtaa[C/T]aataatatggtgataa	C	T	NM_144675 // intron // 0 // Hs.91910 // MGC18079 // 146395 // Homo sapiens hypothetical protein MGC18079 (MGC18079), mRNA. /// ENST00000304678 // intron // 0 // --- // --- // --- // ---	MGC18079	MGC18079, Homo sapiens hypothetical protein MGC18079 (MGC18079), p11.2
SNP_A-1817486	gttcatccacttggta[G/T]ctttttctagtgtaa	G	T	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2116403	aggtataaaatttgcc[A/G]caggagactgatctta	A	G	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1885352	tgaattttcccacaga[C/T]gttgcagattttatta	C	T	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1887512	tgagactgcgtcgttg[C/G]atttagcttaagttgt	C	G	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2183423	cagcacttctcagtac[C/G]aattacagaggctgaa	C	G	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2228023	ctacgcacccaacaaa[C/T]gtttatttccttcact	C	T	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2254335	cttgcagacagttaca[A/G]aggtcacatatatagc	A	G	NM_015171 // intron // 0 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // intron // 0 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2048251	aagcagaaccaacgaa[C/G]agagagaaactgaatt	C	G	NM_015171 // upstream // 5927 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 5927 // --- // --- // --- // --- /// ENST00000357856 // upstream // 46879 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2219037	cctggttttgattata[C/T]gccctgccccttggct	C	T	NM_015171 // upstream // 17231 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 17231 // --- // --- // --- // --- /// ENST00000357856 // upstream // 35575 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2242031	ctgattgaccagagtc[C/T]gaatccaaagtctccc	C	T	NM_015171 // upstream // 20585 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 20585 // --- // --- // --- // --- /// ENST00000357856 // upstream // 32221 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2264073	gaactctgaaccacac[A/G]gatgcaagaccatttc	A	G	NM_015171 // upstream // 23964 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 23964 // --- // --- // --- // --- /// ENST00000357856 // upstream // 28842 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1946508	tttaaagtatactgca[C/T]agattattttcaaata	C	T	NM_015171 // upstream // 27829 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 27829 // --- // --- // --- // --- /// ENST00000357856 // upstream // 24977 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2290151	gcaaatgattttaaaa[C/G]tgcgtaatgcaaagga	C	G	NM_015171 // upstream // 35680 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 35680 // --- // --- // --- // --- /// ENST00000357856 // upstream // 17126 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-1751811	atatccggtgtgttacaacacatgc[C/G]attagcaaagatattcaaactcatg	C	G	AY026388 // intron // 0 // Hs.150684 // XPO6 // 23214 // exportin 6	XPO6	XPO6 , rs3922800, exportin 6,p12.1
SNP_A-1897355	tgctgaaaaaaagtaa[A/C]tcgtgtgcatgaattc	A	C	NM_015171 // upstream // 40808 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 40808 // --- // --- // --- // --- /// ENST00000357856 // upstream // 11998 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2175910	cacattttggtcctca[A/G]gaaggaagaaagatgg	A	G	NM_015171 // upstream // 41968 // Hs.460468 // XPO6 // 23214 // Homo sapiens exportin 6 (XPO6), mRNA. /// ENST00000304658 // upstream // 41968 // --- // --- // --- // --- /// ENST00000357856 // upstream // 10838 // --- // --- // --- // ---	XPO6	XPO6, Homo sapiens exportin 6 (XPO6), p11.2
SNP_A-2211105	cccgggtgccactgac[A/G]gggccggtgaaggaaa	A	G	NM_004320 // CDS // 0 // Hs.546237 // ATP2A1 // 487 // Homo sapiens ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 (ATP2A1), transcript variant b, mRNA. /// NM_173201 // CDS // 0 // Hs.546237 // ATP2A1 // 487 // Homo sapiens ATPase, Ca++ transpo	ATP2A1	ATP2A1, Homo sapiens ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 (ATP2A1), transcript variant b, p11.2
SNP_A-1818137	gttctcgtcgcccagc[C/T]aggtgccattggggta	C	T	ENST00000327307 // downstream // 227658 // --- // --- // --- // --- /// ENST00000310908 // downstream // 208209 // --- // --- // --- // --- /// ENST00000319583 // downstream // 190441 // --- // --- // --- // --- /// ENST00000289484 // upstream // 26 // ---	-	p11.2
SNP_A-2148299	atgggctaactactta[C/T]ggtgcactcaggctaa	C	T	NM_000887 // downstream // 4148 // Hs.248472 // ITGAX // 3687 // Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), mRNA. /// U37028 // upstream // 6131 // Hs.513528 // ITGAD // 3681 // Human leukointegrin alpha d chain mRNA	ITGAX	ITGAX, Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide) (ITGAX), p11.2
SNP_A-2051792	aaggtcctattatgca[C/G]ggttggtttccagtaa	C	G	NM_001004300 // downstream // 165570 // Hs.528826 // LOC124411 // 124411 // Homo sapiens hypothetical protein LOC124411 (LOC124411), mRNA. /// NM_003414 // downstream // 9833 // Hs.460645 // ZNF267 // 10308 // Homo sapiens zinc finger protein 267 (ZNF267)	LOC124411	LOC124411, Homo sapiens hypothetical protein LOC124411 (LOC124411), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1797773	aggaaaacaaaccaca[C/T]tgatacaaagaccaag	C	T	NM_018206 // intron // 0 // Hs.454528 // VPS35 // 55737 // Homo sapiens vacuolar protein sorting 35 (yeast) (VPS35), mRNA. /// ENST00000354740 // intron // 0 // — // — // — // — /// ENST00000299138 // intron // 0 // — // — // — // —	VPS35	VPS35, Homo sapiens vacuolar protein sorting 35 (yeast) (VPS35), q11.2
SNP_A-1926582	ttattctgtgaactca[C/G]cttatctggttctttc	C	G	NM_145186 // intron // 0 // Hs.335891 // ABCC11 // 85320 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 11 (ABCC11), transcript variant 3, mRNA. /// NM_033151 // intron // 0 // Hs.335891 // ABCC11 // 85320 // Homo sapiens ATP-bindin	ABCC11	ABCC11, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q12.1
SNP_A-2298476	gcccaactactcaacc[A/C]accacctagcacaacc	A	C	NM_153029 // upstream // 536416 // Hs.511839 // N4BP1 // 9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 132165 // Hs.458423 // CBLN1 // 869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// ENST000002623	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-2242458	ctgcagactggtaacg[C/T]acacttggcagggtgc	C	T	NM_153029 // upstream // 537776 // Hs.511839 // N4BP1 // 9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 130805 // Hs.458423 // CBLN1 // 869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// ENST000002623	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-1918993	ttaacctgcatatata[A/C]ctatcactgtaatact	A	C	NM_153029 // upstream // 562175 // Hs.511839 // N4BP1 // 9683 // Homo sapiens Nedd4 binding protein 1 (N4BP1), mRNA. /// NM_004352 // downstream // 106406 // Hs.458423 // CBLN1 // 869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// ENST000002623	N4BP1	N4BP1, Homo sapiens Nedd4 binding protein 1 (N4BP1), q12.1
SNP_A-1898319	tgcttatgttgtacca[A/G]gttatatgatgttgcc	A	G	NM_004352 // upstream // 11389 // Hs.458423 // CBLN1 // 869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// NM_207449 // upstream // 51448 // Hs.514338 // FLJ44674 // 400535 // Homo sapiens FLJ44674 protein (FLJ44674), mRNA. /// ENST00000219197	CBLN1	CBLN1, Homo sapiens cerebellin 1 precursor (CBLN1), q12.1
SNP_A-2286727	gatggcagcaggaata[C/G]agaggtaggcaaggta	C	G	NM_004352 // upstream // 22390 // Hs.458423 // CBLN1 // 869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// NM_207449 // upstream // 40447 // Hs.514338 // FLJ44674 // 400535 // Homo sapiens FLJ44674 protein (FLJ44674), mRNA. /// ENST00000219197	CBLN1	CBLN1, Homo sapiens cerebellin 1 precursor (CBLN1), q12.1
SNP_A-2208962	cccagccgatctggca[A/G]acttctcatccttcaa	A	G	NM_004352 // upstream // 22808 // Hs.458423 // CBLN1 // 869 // Homo sapiens cerebellin 1 precursor (CBLN1), mRNA. /// NM_207449 // upstream // 40029 // Hs.514338 // FLJ44674 // 400535 // Homo sapiens FLJ44674 protein (FLJ44674), mRNA. /// ENST00000219197	CBLN1	CBLN1, Homo sapiens cerebellin 1 precursor (CBLN1), q12.1
SNP_A-2072879	acagctttatcaggta[A/T]aatatccttggttggc	A	T	NM_144602 // intron // 0 // Hs.125875 // MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// ENST00000299191 // intron // 0 // — // — // — // —	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-2029634	aaagagagaaaggcac[A/G]agtcaggatttgggtt	A	G	NM_144602 // downstream // 4723 // Hs.125875 // MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// NM_015069 // downstream // 86482 // Hs.530930 // ZNF423 // 23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA.	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-1783909	ggccacacacagtgga[A/C]gaagggtagtttctga	A	C	NM_144602 // downstream // 10652 // Hs.125875 // MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// NM_015069 // downstream // 80553 // Hs.530930 // ZNF423 // 23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284693	gatcagtgaagcctca[A/G]ctaccccacgggttct	A	G	NM_144602 // downstream // 18770 // Hs.125875 // MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// NM_015069 // downstream // 72435 // Hs.530930 // ZNF423 // 23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-2230938	ctatggcgaccaatag[C/T]aataggaccacaccta	C	T	NM_144602 // downstream // 87991 // Hs.125875 // MGC33367 // 123970 // Homo sapiens hypothetical protein MGC32905 (MGC33367), mRNA. /// NM_015069 // downstream // 3214 // Hs.530930 // ZNF423 // 23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA.	MGC33367	MGC33367, Homo sapiens hypothetical protein MGC32905 (MGC33367), q12.1
SNP_A-2223770	cggcccctggccagca[C/G]acgaatcagaaggaaa	C	G	NM_015069 // intron // 0 // Hs.530930 // ZNF423 // 23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA. /// ENST00000262383 // intron // 0 // --- // --- // --- // ---	ZNF423	ZNF423, Homo sapiens zinc finger protein 423 (ZNF423), q12.1
SNP_A-1906880	tggttcatcctattaa[C/T]gggagcagtacaaaac	C	T	NM_015069 // upstream // 53127 // Hs.530930 // ZNF423 // 23090 // Homo sapiens zinc finger protein 423 (ZNF423), mRNA. /// NM_017939 // upstream // 185856 // Hs.313917 // FLJ20718 // 55027 // Homo sapiens hypothetical protein FLJ20718 (FLJ20718), mRNA. //	ZNF423	ZNF423, Homo sapiens zinc finger protein 423 (ZNF423), q12.1
SNP_A-1799471	ttattccagttgctcc[G/T]ctcattgtgaatatgg	G	T	NM_017939 // downstream // 81798 // Hs.313917 // FLJ20718 // 55027 // Homo sapiens hypothetical protein FLJ20718 (FLJ20718), mRNA. /// NM_182922 // downstream // 82720 // Hs.313917 // FLJ20718 // 55027 // Homo sapiens hypothetical protein FLJ20718 (FLJ207	FLJ20718	FLJ20718, Homo sapiens hypothetical protein FLJ20718 (FLJ20718), q12.1
SNP_A-2077095	accaagacacagagga[C/T]agaagtaacttgttca	C	T	NM_013263 // upstream // 38374 // Hs.437894 // BRD7 // 29117 // Homo sapiens bromodomain containing 7 (BRD7), mRNA. /// NM_033119 // upstream // 141062 // Hs.298434 // NKD1 // 85407 // Homo sapiens naked cuticle homolog 1 (Drosophila) (NKD1), mRNA. /// EN	BRD7	BRD7, Homo sapiens bromodomain containing 7 (BRD7), q12.1
SNP_A-1927822	ttcaaggggacataac[A/C]gtaggtggccgtgcca	A	C	NM_013263 // upstream // 38403 // Hs.437894 // BRD7 // 29117 // Homo sapiens bromodomain containing 7 (BRD7), mRNA. /// NM_033119 // upstream // 141033 // Hs.298434 // NKD1 // 85407 // Homo sapiens naked cuticle homolog 1 (Drosophila) (NKD1), mRNA. /// EN	BRD7	BRD7, Homo sapiens bromodomain containing 7 (BRD7), q12.1
SNP_A-2176598	cacccatgaacccatc[A/G]ctcaactcaagaacta	A	G	NM_013263 // upstream // 129366 // Hs.437894 // BRD7 // 29117 // Homo sapiens bromodomain containing 7 (BRD7), mRNA. /// NM_033119 // upstream // 50070 // Hs.298434 // NKD1 // 85407 // Homo sapiens naked cuticle homolog 1 (Drosophila) (NKD1), mRNA. /// EN	BRD7	BRD7, Homo sapiens bromodomain containing 7 (BRD7), q12.1
SNP_A-1668342	atgaattttatttaatccttgagga[A/C]atggttcttttctcacacacataaa	A	C	NM_004352 // upstream // 8733 // Hs.458423 // CBLN1 // 869 // cerebellin 1 precursor /// NM_144602 // upstream // 83392 // Hs.125875 // MGC33367 // 123970 // hypothetical protein MGC32905	CBLN1	CBLN1 , rs1858274, cerebellin 1 precursor ,q12.1
SNP_A-2281659	gagtctgctaccttcc[A/T]accctgagtctgtatg	A	T	NM_013263 // upstream // 160842 // Hs.437894 // BRD7 // 29117 // Homo sapiens bromodomain containing 7 (BRD7), mRNA. /// NM_033119 // upstream // 18594 // Hs.298434 // NKD1 // 85407 // Homo sapiens naked cuticle homolog 1 (Drosophila) (NKD1), mRNA. /// EN	BRD7	BRD7, Homo sapiens bromodomain containing 7 (BRD7), q12.1
SNP_A-2230131	ctatacaggaccattc[C/T]cgtgaaaagttgaaag	C	T	NM_015247 // downstream // 50526 // Hs.432993 // CYLD // 1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream // 50529 // Hs.432993 // CYLD // 1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1835691	tacctttagacttg[C/T]aggaaataacagtaca	C	T	NM_015247 // downstream // 144627 // Hs.432993 // CYLD // 1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream // 144630 // Hs.432993 // CYLD // 1540 // Homo sapiens cylindromatosis (turban tumor syndrome)	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-2295582	gcatcttcctcgcaga[A/C]aagtcactcccattat	A	C	NM_015247 // downstream // 217460 // Hs.432993 // CYLD // 1540 // Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA. /// NM_015247 // downstream // 217463 // Hs.432993 // CYLD // 1540 // Homo sapiens cylindromatosis (turban tumor syndrome)	CYLD	CYLD, Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), q12.1
SNP_A-1941663	ttggaacttgctacct[A/T]acctcacagtccctca	A	T	NM_002968 // upstream // 194416 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 300133 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tr	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-2185512	caggacttttgttggg[G/T]agcgtgttaagttagc	G	T	NM_002968 // upstream // 208396 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 286153 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tr	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1800283	tcacattacaaaatcc[A/G]gaaccatttaacctag	A	G	NM_002968 // upstream // 231174 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 263375 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tr	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1888319	tgagctggcaaatcaa[A/G]tctcatatgcatgagt	A	G	NM_002968 // upstream // 233257 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 261292 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tr	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1902746	tggctatcataacata[C/G]aagtcctagagctctg	C	G	NM_002968 // upstream // 234013 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 260536 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tr	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1854816	tcaccaggagtaaag[C/T]ctcttagcaactaag	C	T	NM_002968 // upstream // 268971 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 225578 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tr	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-2276002	gagagaaaactggaga[A/G]attagaataacgggtt	A	G	NM_002968 // upstream // 404839 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 89710 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1941618	ttggaaatgctggaaa[C/T]cacaatggcagaacca	C	T	NM_002968 // upstream // 411885 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 82664 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1790254	ggggagatgggtttgat[A/G]tacataggcaacagca	A	G	NM_002968 // upstream // 413717 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 80832 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2134548	atatgtatagtagcac[G/T]ggacaaatagtaaata	G	T	NM_002968 // upstream // 414108 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 80441 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1781436	ggattacaggaaaata[C/T]aggacctatgccctgt	C	T	NM_002968 // upstream // 419990 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 74559 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-2094671	agaatatcacacatca[A/G]aaggttgtcagcctag	A	G	NM_002968 // upstream // 425409 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 69140 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1958357	ttttcccatgagagcc[A/G]aacactgcatccaaaa	A	G	NM_002968 // upstream // 427073 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 67476 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-2235542	ctcctaaggaaaccaa[A/G]ctcacaatagtaatac	A	G	NM_002968 // upstream // 438283 // Hs.135787 // SALL1 // 6299 // Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA. /// NM_002136 // upstream // 56266 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), tra	SALL1	SALL1, Homo sapiens sal-like 1 (Drosophila) (SALL1), q12.1
SNP_A-1800678	tgtgattcacatgaca[C/G]tatgatgtaagctttt	C	G	NM_002136 // downstream // 80572 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 80572 // — // — // — // — /// ENST00000219746 //	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2168131	caactcatccagtaac[A/G]cagatttttatctgga	A	G	NM_002136 // downstream // 202361 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 202361 // — // — // — // — /// ENST00000219746 /	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2247649	ctgtctttggccacca[C/T]ggattgcctgagcaaa	C	T	NM_002136 // downstream // 705429 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 705429 // — // — // — // — /// ENST00000219746 /	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-1940659	ttgcctgcattcctta[G/T]cttcctgtttcaaggc	G	T	NM_002136 // downstream // 772540 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 772540 // — // — // — // — /// ENST00000219746 /	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-2228401	ctactgtgtcatcaaa[G/T]cttagcaattagcctc	G	T	NM_002136 // downstream // 782660 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 782660 // — // — // — // — /// ENST00000219746 /	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1
SNP_A-1848576	tatgactacttctcac[A/G]ctgagctcacatactc	A	G	NM_002136 // downstream // 783556 // Hs.546261 // HNRPA1 // 3178 // Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, mRNA. /// ENST00000357495 // downstream // 783556 // — // — // — // — /// ENST00000219746 /	HNRPA1	HNRPA1, Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 1, q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1801456	acatttccatcttcca[A/G]tgcttctattgatggc	A	G	NM_025134 // upstream // 472347 // Hs.530936 // CHD9 // 80205 // Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), mRNA. /// AF150735 // downstream // 524537 // --- // --- // 0 // Homo sapiens proteinx0008 (AD013) mRNA, complete cds. /// EN	CHD9	CHD9, Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), q12.2
SNP_A-2098356	agagattcggatgtaa[A/G]gaattagagaggcccct	A	G	NM_025134 // upstream // 396317 // Hs.530936 // CHD9 // 80205 // Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), mRNA. /// AF150735 // downstream // 448507 // --- // --- // 0 // Homo sapiens proteinx0008 (AD013) mRNA, complete cds. /// EN	CHD9	CHD9, Homo sapiens chromodomain helicase DNA binding protein 9 (CHD9), q12.2
SNP_A-1863482	tccaaacatttaggaa[A/G]ggagttaaatgcagtc	A	G	ENST00000355606 // intron // 0 // --- // --- // --- /// ENST00000315547 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2287349	gatgttaagttacaa[A/G]acaaaaatgcatctt	A	G	NM_005611 // upstream // 59899 // Hs.513609 // RBL2 // 5934 // Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA. /// ENST00000333556 // upstream // 3580 // --- // --- // --- /// ENST00000262133 // upstream // 59899 // --- // --- // ---	RBL2	RBL2, Homo sapiens retinoblastoma-like 2 (p130) (RBL2), q12.2
SNP_A-1921742	ttactaaaattcacaa[C/T]tcagctaaaacatga	C	T	NM_005611 // intron // 0 // Hs.513609 // RBL2 // 5934 // Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA. /// ENST00000262133 // intron // 0 // --- // --- // --- // ---	RBL2	RBL2, Homo sapiens retinoblastoma-like 2 (p130) (RBL2), q12.2
SNP_A-2066673	acaaaaacagataaaaaa[C/T]cctagaaaatgagacat	C	T	NM_005611 // intron // 0 // Hs.513609 // RBL2 // 5934 // Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA. /// ENST00000262133 // intron // 0 // --- // --- // --- // ---	RBL2	RBL2, Homo sapiens retinoblastoma-like 2 (p130) (RBL2), q12.2
SNP_A-2172181	caatgtattgatcagc[A/G]caatgaaacataaattt	A	G	NM_005611 // intron // 0 // Hs.513609 // RBL2 // 5934 // Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA. /// ENST00000262133 // intron // 0 // --- // --- // --- // ---	RBL2	RBL2, Homo sapiens retinoblastoma-like 2 (p130) (RBL2), q12.2
SNP_A-2004713	gtggttagtccgtccca[A/G]tctcggcactccactt	A	G	NM_022476 // upstream // 1006 // Hs.380897 // FTS // 64400 // Homo sapiens fused toes homolog (mouse) (FTS), mRNA. /// ENST00000300245 // upstream // 1006 // --- // --- // --- /// ENST00000262135 // downstream // 96443 // --- // --- // --- // ---	FTS	FTS, Homo sapiens fused toes homolog (mouse) (FTS), q12.2
SNP_A-1819739	gttgtcctatagttaa[C/T]aatgatcctcagacaa	C	T	NM_022476 // upstream // 4239 // Hs.380897 // FTS // 64400 // Homo sapiens fused toes homolog (mouse) (FTS), mRNA. /// ENST00000300245 // upstream // 4239 // --- // --- // --- /// ENST00000262135 // downstream // 93210 // --- // --- // --- // ---	FTS	FTS, Homo sapiens fused toes homolog (mouse) (FTS), q12.2
SNP_A-1724214	ttcagagactaagtgtccagtaa[C/G]acaaggtgcatttggttc ctttgaa	C	G	BC034401 // upstream // 288819 // Hs.126652 // - // - // CDNA clone IMAGE:5172086, partial cds /// U80736 // downstream // 64089 // Hs.110826 // TNRC9 // 27324 // tnnucleotide repeat containing 9	-	-, rs1124390, CDNA clone IMAGE:5172086, partial cds, q12.1
SNP_A-1880261	tcttcttctgagagac[C/G]tcatatgacccactga	C	G	ENST00000262135 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2103911	agcactgaaacactca[C/T]tcatggttggaagccc	C	T	ENST00000262135 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-1833662	tacaggcatatttcac[A/G]gaatacatagtagaaa	A	G	ENST00000262135 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-1865177	tccataaagaaatccca[C/T]agtggctgggtacagc	C	T	ENST00000262135 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2175099	cacagtgaagatgtga[C/G]gtgttggtaagtaccc	C	G	ENST00000268349 // intron // 0 // --- // --- // --- /// ENST00000355787 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-1781198	ggatggctgccaagtc[A/G]caagcatttacaaca	A	G	ENST00000268349 // intron // 0 // --- // --- // --- /// ENST00000355787 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-1922921	ttagatttactgataa[C/G]aacaagcctaaatact	C	G	ENST00000268349 // intron // 0 // --- // --- // --- /// ENST00000355787 // intron // 0 // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2004715	ccccatgcttggagga[A/G]ctcattgacattgtcg	A	G	ENST00000268349 // intron // 0 // --- // --- // --- /// ENST00000355787 // intron // 0 // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-1805866	gtcctgaggctggaa[C/T]gggcttaatgtcgtgg	C	T	ENST00000268349 // intron // 0 // --- // --- // --- /// ENST00000355787 // intron // 0 // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // ---	-	q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172261	caatgttaactcacag[A/G]acagactataagacac	A	G	ENST00000268349 // intron // 0 // --- // --- // --- /// ENST00000355787 // intron // 0 // --- // --- // --- /// ENST00000360126 // intron // 0 // --- // --- // ---	-	q12.2
SNP_A-2296169	gcattcgtctttgctc[A/G]aacaatgcccccatcaa	A	G	NM_024336 // downstream // 14860 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// ENST00000357652 // upstream // 143071 // --- // --- // --- /// ENST00000329734 // downstream // 14860 // --- // --- // ---	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1917478	tgttttaaatcagat[C/T]acaccctgaggttctg	C	T	NM_024336 // upstream // 8196 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 636537 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST00000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1660977	atggataactgagaggcataccgcaa[A/G]gtgcggcaatcagttctagtatcag	A	G	AF150735 // downstream // 127630 // - // - // - // Homo sapiens proteinx0008 (AD013) mRNA, complete cds. /// U80736 // upstream // 634185 // Hs.110826 // TNRC9 // 27324 // trinucleotide repeat containing 9	-	-, rs4784289, Homo sapiens proteinx0008 (AD013) mRNA, complete cds., q12.2
SNP_A-2218898	cctgggtctatgtgca[C/T]gccgctatgctcgggt	C	T	NM_024336 // upstream // 22691 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 622042 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST0000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2206536	ccatcttctctgtcaa[A/G]gttgactaagttaaca	A	G	NM_024336 // upstream // 104593 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 540140 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1782036	ggcaaatgaaaaagag[A/G]aaaatcatcagggata	A	G	NM_024336 // upstream // 122500 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 522233 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2226007	ctaacaaggaataata[A/C]ctggccttgttata	A	C	NM_024336 // upstream // 122708 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 522025 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2119829	agtcaaacccttttcc[A/G]ctattaacatgatatt	A	G	NM_024336 // upstream // 122845 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 521888 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1802749	cttttgcaaaaaatct[A/T]aagcaaggaggcagaaa	A	T	NM_024336 // upstream // 200403 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 444330 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-2279638	gaggcactgctgtgta[A/C]gtggtattgttattac	A	C	NM_024336 // upstream // 567543 // Hs.499205 // IRX3 // 79191 // Homo sapiens iroquois homeobox protein 3 (IRX3), mRNA. /// NM_005853 // upstream // 77190 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// ENST0000	IRX3	IRX3, Homo sapiens iroquois homeobox protein 3 (IRX3), q12.2
SNP_A-1795427	ggtgcactgtgaaagc[C/T]gaggaaatcaggagat	C	T	NM_005853 // downstream // 50503 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 338772 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST00	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2071024	acactgacagtgagtc[A/C]atatctcagctgatat	A	C	NM_005853 // downstream // 141545 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 247730 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST0	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1875186	tctctccttgagaggc[C/T]atgcggcaacgtgctc	C	T	NM_005853 // downstream // 169641 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 219634 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST0	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1803186	gttagttgcaattgtg[A/T]caagagaagggcatgg	A	T	NM_005853 // downstream // 174794 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 214481 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST0	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-2258853	cttttagctgttaag[G/T]agggatgccaatcact	G	T	NM_005853 // downstream // 185616 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 203659 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST0	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1839095	tagagcaaattgaaca[C/G]agagaatagtgcaaaa	C	G	NM_005853 // downstream // 237693 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 151582 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST0	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1861589	tcatcgggtcttccca[A/G]taacctctaaggtagt	A	G	NM_005853 // downstream // 272499 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 116776 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST0	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1883696	tgaactggtcaggtac[C/T]gattcatctatgatat	C	T	NM_005853 // downstream // 360864 // Hs.435730 // IRX5 // 10265 // Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA. /// NM_024335 // upstream // 28411 // Hs.369907 // IRX6 // 79190 // Homo sapiens iroquois homeobox protein 6 (IRX6), mRNA. /// ENST00	IRX5	IRX5, Homo sapiens iroquois homeobox protein 5 (IRX5), q12.2
SNP_A-1679038	ccacigtctttcaccagagatgaaa[G/T]taacaatgtactcaatg tcatctag	G	T	AB051539 // downstream // 143095 // Hs.284741 // FTO // 79068 // fatso	FTO	FTO , rs10521301, fatso,q12.2
SNP_A-1787253	gggaactagataaccct[A/G]agaacctgctggccac	A	G	NM_017839 // downstream // 5931 // Hs.460857 // FLJ20481 // 54947 // Homo sapiens hypothetical protein FLJ20481 (FLJ20481), mRNA. /// NM_001043 // upstream // 67353 // Hs.78036 // SLC6A2 // 6530 // Homo sapiens solute carrier family 6 (neurotransmitter tr	FLJ20481	FLJ20481, Homo sapiens hypothetical protein FLJ20481 (FLJ20481), q12.2
SNP_A-2219495	cctgttcactccagta[C/T]ctattctgtctcagg	C	T	NM_017839 // downstream // 47610 // Hs.460857 // FLJ20481 // 54947 // Homo sapiens hypothetical protein FLJ20481 (FLJ20481), mRNA. /// NM_001043 // upstream // 25674 // Hs.78036 // SLC6A2 // 6530 // Homo sapiens solute carrier family 6 (neurotransmitter t	FLJ20481	FLJ20481, Homo sapiens hypothetical protein FLJ20481 (FLJ20481), q12.2
SNP_A-1808163	gtctgtggtctgcaa[C/T]gcctaaggtccatgca	C	T	NM_017839 // downstream // 57171 // Hs.460857 // FLJ20481 // 54947 // Homo sapiens hypothetical protein FLJ20481 (FLJ20481), mRNA. /// NM_001043 // upstream // 16113 // Hs.78036 // SLC6A2 // 6530 // Homo sapiens solute carrier family 6 (neurotransmitter t	FLJ20481	FLJ20481, Homo sapiens hypothetical protein FLJ20481 (FLJ20481), q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1803968	tacactatattccac[A/G]aagagaacaacttta	A	G	NM_001043 // downstream // 3396 // Hs.78036 // SLC6A2 // 6530 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // downstream // 3396 // — // — // — /// ENST0000	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-1730383	tcagagccttcacatttatccgtta[C/T]actactttcccaactcaatg tgctat	C	T	NM_005853 // upstream // 444900 // Hs.25351 // IRX5 // 10265 // iroquois homeobox protein 5	IRX5	IRX5 , rs933516, iroquois homeobox protein 5,q12.2
SNP_A-1934319	ttcccccagccctc[C/T]catcgcagggaataat	C	T	NM_001043 // downstream // 48764 // Hs.78036 // SLC6A2 // 6530 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), mRNA. /// ENST00000219833 // downstream // 48764 // — // — // — /// ENST00	SLC6A2	SLC6A2, Homo sapiens solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2 (SLC6A2), q12.2
SNP_A-1881005	tctgttcattatagg[C/T]caaaatggttaaaacc	C	T	NM_145024 // intron // 0 // Hs.350800 // FLJ31547 // 221223 // Homo sapiens hypothetical protein FLJ31547 (FLJ31547), mRNA. /// ENST00000319165 // intron // 0 // — // — // — /// ENST00000290567 // intron // 0 // — // — // —	FLJ31547	FLJ31547, Homo sapiens hypothetical protein FLJ31547 (FLJ31547), q12.2
SNP_A-1668032	ttggccagctcttgagtgccttt[A/G]aagatttccggcttctctcat ccgg	A	G	NM_005853 // downstream // 246112 // Hs.25351 // IRX5 // 10265 // iroquois homeobox protein 5 /// U90305 // upstream // 144817 // - // - // - // Human iroquois-dass homeodomain protein IRX-3 mRNA, partial cds.	IRX5	IRX5 , rs728571, iroquois homeobox protein 5 q12.2
SNP_A-2062295	aatggttctacctctc[C/T]actggagaaaacagaa	C	T	NM_138958 // intron // 0 // Hs.295137 // AMFR // 267 // Homo sapiens autocrine motility factor receptor (AMFR), transcript variant 2, mRNA. /// NM_001144 // intron // 0 // Hs.295137 // AMFR // 267 // Homo sapiens autocrine motility factor receptor (AMFR),	AMFR	AMFR, Homo sapiens autocrine motility factor receptor (AMFR), transcript variant 2, q12.2
SNP_A-2292450	gcactacctggcatac[A/G]ataggtacataataaa	A	G	NM_031885 // intron // 0 // Hs.333738 // BBS2 // 583 // Homo sapiens Bardet-Biedl syndrome 2 (BBS2), mRNA. /// ENST00000245157 // intron // 0 // — // — // —	BBS2	BBS2, Homo sapiens Bardet-Biedl syndrome 2 (BBS2), q12.2
SNP_A-1804616	ctttcctgctggaaac[G/T]gacttgatacacagac	G	T	NM_031885 // upstream // 7299 // Hs.333738 // BBS2 // 583 // Homo sapiens Bardet-Biedl syndrome 2 (BBS2), mRNA. /// NM_032935 // upstream // 37547 // Hs.194762 // MT4 // 84560 // Homo sapiens metallothionein IV (MT4), mRNA. /// ENST00000245157 // upstream	BBS2	BBS2, Homo sapiens Bardet-Biedl syndrome 2 (BBS2), q12.2
SNP_A-1743595	tcttccacactgaaggtacagatcc[G/T]gcacttgccaggccag gacactgaa	G	T	NM_004530 // upstream // 141382 // Hs.367877 // MMP2 // 4313 // matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) /// U90305 // downstream // 10052 // - // - // - // Human iroquois-dass homeodomain protein IRX-3 mRNA	MMP2	MMP2 , rs10521326, matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) ,q12.2
SNP_A-2314533	ggaggtcatatttggc[C/G]atctgagctgaagagg	C	G	NM_005949 // intron // 0 // Hs.513626 // MT1F // 4494 // Homo sapiens metallothionein 1F (functional) (MT1F), mRNA. /// NM_176870 // intron // 0 // Hs.188518 // MT1K // 4499 // Homo sapiens metallothionein 1K (MT1K), mRNA. /// NM_005951 // intron // 0 //	MT1F	MT1F, Homo sapiens metallothionein 1F (functional) (MT1F), q12.2
SNP_A-1859880	tcaggtaagacctgcg[A/G]aagaactgaggaagc	A	G	ENST00000258193 // intron // 0 // — // — // —	-	q12.2
SNP_A-2251626	cttcagcttatgagac[C/G]aaaatgctgccagctg	C	G	ENST00000258193 // intron // 0 // — // — // —	-	q13
SNP_A-2045445	aagaatattcaaaagc[A/G]caattcaaccagacga	A	G	ENST00000258193 // intron // 0 // — // — // —	-	q13
SNP_A-2081648	accttatcattatica[A/G]aaggtagagttctgga	A	G	NM_014669 // intron // 0 // Hs.276878 // NUP93 // 9688 // Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000258193 // intron // 0 // — // — // — /// ENST00000308159 // intron // 0 // — // — // —	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-1793291	ggtagcatagtagata[C/T]catatggttattgtt	C	T	NM_014669 // intron // 0 // Hs.276878 // NUP93 // 9688 // Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // — // — // —	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-1820053	gttgttttaaggagc[A/C]atttacaggcagaagg	A	C	NM_014669 // intron // 0 // Hs.276878 // NUP93 // 9688 // Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // — // — // —	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1880497	tcttgatatgacatta[G/T]aaatgctgccaagaaa	G	T	NM_014669 // intron // 0 // Hs.276878 // NUP93 // 9688 // Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // — // — // —	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-1942114	ttggattatgtttca[C/T]tcaaagaccagcatat	C	T	NM_014669 // intron // 0 // Hs.276878 // NUP93 // 9688 // Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // — // — // —	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-1810870	gtgcagtgaccggga[C/G]aagctatcaccccat	C	G	NM_014669 // intron // 0 // Hs.276878 // NUP93 // 9688 // Homo sapiens nucleoporin 93kDa (NUP93), mRNA. /// ENST00000308159 // intron // 0 // — // — // —	NUP93	NUP93, Homo sapiens nucleoporin 93kDa (NUP93), q13
SNP_A-1804292	gtcactacctgatgaa[A/C]gagtgagattacttt	A	C	NM_005946 // downstream // 203923 // Hs.440939 // MT1A // 4489 // Homo sapiens metallothionein 1A (functional) (MT1A), mRNA. /// NM_176870 // downstream // 203923 // Hs.188518 // MT1K // 4499 // Homo sapiens metallothionein 1K (MT1K), mRNA. /// NM_005947	MT1A	MT1A, Homo sapiens metallothionein 1A (functional) (MT1A), q13
SNP_A-2072813	acagctgcaggtcaga[A/G]aatgcgggggaggagac	A	G	NM_000339 // intron // 0 // Hs.369271 // SLC12A3 // 6559 // Homo sapiens solute carrier family 12 (sodium/chloride transporters), member 3 (SLC12A3), mRNA. /// ENST00000262502 // intron // 0 // — // — // — // —	SLC12A3	SLC12A3, Homo sapiens solute carrier family 12 (sodium,q13
SNP_A-1933956	ttctcaagatttagga[A/T]tcacctgacactaaac	A	T	NM_002694 // intron // 0 // Hs.79402 // POLR2C // 5432 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant alpha, mRNA. /// NM_032940 // intron // 0 // Hs.79402 // POLR2C // 5432 // Homo sapiens polymerase	POLR2C	POLR2C, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant alpha, q13
SNP_A-2242851	ctgccacagctctgccd[A/G]cgggagaaaggccctg	A	G	NM_018110 // intron // 0 // Hs.279832 // DOK4 // 55715 // Homo sapiens docking protein 4 (DOK4), mRNA. /// ENST00000340099 // intron // 0 // — // — // —	DOK4	DOK4, Homo sapiens docking protein 4 (DOK4), q13
SNP_A-1944186	ttgtcatcacttttaccc[A/G]ggctgtcaggagcatc	A	G	NM_002694 // downstream // 33601 // Hs.79402 // POLR2C // 5432 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant alpha, mRNA. /// NM_032940 // downstream // 33601 // Hs.79402 // POLR2C // 5432 // Homo sap	POLR2C	POLR2C, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide C, 33kDa (POLR2C), transcript variant alpha, q13
SNP_A-1913883	tgtgtctgctatagag[C/T]caaatgacccaataag	C	T	NM_153837 // downstream // 17473 // Hs.187884 // GPR114 // 221188 // Homo sapiens G protein-coupled receptor 114 (GPR114), mRNA. /// AK160368 // downstream // 2978 // Hs.187884 // GPR114 // 221188 // Homo sapiens mRNA for FLJ00270 protein. /// NM_170776 /	GPR114	GPR114, Homo sapiens G protein-coupled receptor 114 (GPR114), q13
SNP_A-2246673	ctgtaatggtaagaa[C/T]ttctggtgggcaccc	C	T	NM_001297 // intron // 0 // Hs.147062 // CNGB1 // 1258 // Homo sapiens cyclic nucleotide gated channel beta 1 (CNGB1), mRNA. /// ENST00000251102 // intron // 0 // — // — // — // —	CNGB1	CNGB1, Homo sapiens cyclic nucleotide gated channel beta 1 (CNGB1), q13
SNP_A-2004755	agtgaaagaaaacaac[A/G]atggcttagacaagag	A	G	ENST00000360226 // intron // 0 // — // — // — // — /// ENST00000219301 // intron // 0 // — // — // — // —	-	q21
SNP_A-2229294	ctaggactggttaaca[A/G]tggtaaagaaaatgca	A	G	NM_022770 // downstream // 18991 // Hs.47125 // FLJ13912 // 64785 // Homo sapiens hypothetical protein FLJ13912 (FLJ13912), mRNA. /// NM_022910 // upstream // 38579 // Hs.322430 // NDRG4 // 65009 // Homo sapiens NDRG family member 4 (NDRG4), mRNA. /// NM_	FLJ13912	FLJ13912, Homo sapiens hypothetical protein FLJ13912 (FLJ13912), q21
SNP_A-1792372	gggttgtaggtacttat[C/T]ggcattgagagctctg	C	T	NM_022770 // downstream // 27806 // Hs.47125 // FLJ13912 // 64785 // Homo sapiens hypothetical protein FLJ13912 (FLJ13912), mRNA. /// NM_022910 // upstream // 29764 // Hs.322430 // NDRG4 // 65009 // Homo sapiens NDRG family member 4 (NDRG4), mRNA. /// NM_	FLJ13912	FLJ13912, Homo sapiens hypothetical protein FLJ13912 (FLJ13912), q21
SNP_A-1870732	tcgctacggatccagg[C/T]cattcctggtgagcc	C	T	NM_022910 // 3UTR // 0 // Hs.322430 // NDRG4 // 65009 // Homo sapiens NDRG family member 4 (NDRG4), mRNA. /// NM_020465 // 3UTR // 0 // Hs.322430 // NDRG4 // 65009 // Homo sapiens NDRG family member 4 (NDRG4), mRNA. /// AB021172 // 3UTR // 0 // Hs.322430	NDRG4	NDRG4, Homo sapiens NDRG family member 4 (NDRG4), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2102286	agattagcccctgaaa[C/T]gttgtattattcaaag	C	T	NM_002080 // upstream // 217094 // Hs.460929 // GOT2 // 2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 217094 // --- // --- // --- /// ENST0000	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-2047416	aagatgaaccaagaaa[A/G]taatctacctgctttt	A	G	NM_002080 // upstream // 224308 // Hs.460929 // GOT2 // 2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 224308 // --- // --- // --- /// ENST0000	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1920614	ttaatttggcagaagc[A/G]agaagatcatttcagc	A	G	NM_002080 // upstream // 435790 // Hs.460929 // GOT2 // 2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 435790 // --- // --- // --- /// ENST0000	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1790339	ggggataactcgagac[C/T]atggagatgagaata	C	T	NM_002080 // upstream // 613249 // Hs.460929 // GOT2 // 2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 613249 // --- // --- // --- /// ENST0000	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-2309860	ggaaatacatttcata[A/G]gatgatagctcccaaa	A	G	NM_002080 // upstream // 680083 // Hs.460929 // GOT2 // 2806 // Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), mRNA. /// ENST00000245206 // upstream // 680083 // --- // --- // --- /// ENST0000	GOT2	GOT2, Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), q21
SNP_A-1782636	ggcactcaatgactca[C/T]ggaataataaagtatc	C	T	NM_001796 // downstream // 2146292 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 59582 // --- // --- // --- /// ENST00000299345 // downstream // 2146292 // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1806619	ctaaccataaatcctg[A/G]ataaagaagaactgca	A	G	NM_001796 // downstream // 2094448 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 111426 // --- // --- // --- /// ENST00000299345 // downstream // 2094448 // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1721816	agtgggtgcttatagcaatactcca[A/G]tgcaattcaaccatcat atgataag	A	G	NM_001896 // intron // 0 // Hs.82201 // CSNK2A2 // 1459 // casein kinase 2, alpha prime polypeptide	CSNK2A2	CSNK2A2 , rs1107277, casein kinase 2, alpha prime polypeptide,q21
SNP_A-1919070	ttaactcaggtttaa[C/T]gttgaaagataga atg	C	T	NM_001796 // downstream // 1953532 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 252342 // --- // --- // --- /// ENST00000299345 // downstream // 1953532 // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1842219	tagggtgaaattgta[A/T]ataatgatagggatg	A	T	NM_001796 // downstream // 1826564 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 379310 // --- // --- // --- /// ENST00000299345 // downstream // 1826564 // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2148410	atgggggtttctatta[C/G]agggctctactcttg	C	G	NM_001796 // downstream // 1757839 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 448035 // --- // --- // --- /// ENST00000299345 // downstream // 1757839 // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2232372	ctcacacacaaatacc[C/T]ataccctgtttccacc	C	T	NM_001796 // downstream // 1306489 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 899385 // --- // --- // --- /// ENST00000299345 // downstream // 1306489 // --- // --- // ---	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1712749	tgatgtgatcatatggtgattacaa[C/T]tgatgatttaaaccagc cctgca	C	T	NM_001796 // downstream // 2278700 // Hs.388928 // CDH8 // 1006 // cadherin 8, type 2 /// NM_002080 // upstream // 640202 // Hs.314658 // GOT2 // 2806 // glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	CDH8	CDH8 , rs725517, cadherin 8, type 2 ,q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2087968	actggcatgaaacaaa[A/T]ttgtgattagaattct	A	T	NM_001796 // downstream // 579825 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 1626049 // — // — // — /// ENST00000299345 // downstream // 579825 // — // — // — // —	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2167988	caacgttattagcagc[A/G]gaaaaaaacatgtgtc	A	G	NM_001796 // downstream // 579701 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// ENST00000360198 // upstream // 1626173 // — // — // — // — /// ENST00000299345 // downstream // 579701 // — // — // — // —	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2238925	ctcttcatttccagat[A/G]aatttagaagcagct	A	G	NM_001796 // upstream // 157998 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2751948 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1909503	tgtatttagatattcca[C/T]gttttctgacagaaac	C	T	NM_001796 // upstream // 212756 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2697190 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1808468	tcttaagccctcata[A/G]agactccacaccctgg	A	G	NM_001796 // upstream // 277459 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2632487 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1839855	tagattgagattatgc[A/G]acaccaatgtgtaaaa	A	G	NM_001796 // upstream // 546478 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2363468 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2152384	attaaccactgataga[A/C]acttaggttgattctg	A	C	NM_001796 // upstream // 582078 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2327868 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1788677	gggatgcgcataaatga[C/T]atagtgatgaattcaa	C	T	NM_001796 // upstream // 596513 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2313433 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1844864	tataatcaggctataa[C/G]tagatatattccagaa	C	G	NM_001796 // upstream // 679283 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2230663 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2054124	aagttcattccccaca[A/G]tcacagcttctccagc	A	G	NM_001796 // upstream // 731626 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2178320 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1808877	gtagaccgagggaaca[C/T]aatagagaaaccagaa	C	T	NM_001796 // upstream // 738210 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2171736 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796983	ggttctcaagcttagd[A/G]acacaatcatatcatc	A	G	NM_001796 // upstream // 800982 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 2108964 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1809196	tattccggctgtact[C/G]aattactagaacaact	C	G	NM_001796 // upstream // 1053924 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1856022 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), tran	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2155497	attcattgcaatcaca[A/G]tcaaaatgtcgtcagg	A	G	NM_001796 // upstream // 1091505 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1818441 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), tran	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1912551	tgtgccaaaccttac[A/G]cacttatattgcttt	A	G	NM_001796 // upstream // 1282045 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1627901 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), tran	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2027615	aaaccagtcagataga[C/T]atggatgattagtgtc	C	T	NM_001796 // upstream // 1532842 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1377104 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), tran	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1899731	tggaatctggaatgga[A/T]atgatgtgacccaatg	A	T	NM_001796 // upstream // 1554750 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1355196 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), tran	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2181329	cagacctttcatattc[C/G]ccttcagccttcatca	C	G	NM_001796 // upstream // 1729354 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 1180592 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), tran	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1863682	tccaactattcaaaca[A/C]aactgagatgcttgta	A	C	NM_001796 // upstream // 1980034 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 929912 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1825690	taaatcagaaatctgc[A/G]aatagaagatgtgttt	A	G	NM_001796 // upstream // 2100444 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 809502 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2129003	ataatgtttgtacac[A/C]agctgagttctaaagc	A	C	NM_001796 // upstream // 2142667 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 767279 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1874814	tctcgagagcatgaaa[C/G]ggggagagactgctc	C	G	NM_001796 // upstream // 2591783 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 318163 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1786702	ggcttggtttggaaaat[A/G]aatccatcacgagatg	A	G	NM_001796 // upstream // 2801488 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 108458 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), trans	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1934049	ttctcactttctgtc[C/T]cgggagaatgaaattt	C	T	NM_001796 // upstream // 2811753 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 98193 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transc	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-2284002	gatatatagtggtcat[A/T]acaaacactgtactcat	A	T	NM_001796 // upstream // 2832708 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 77238 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transc	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1810664	ttacagagcttttgta[A/T]aaattgcaatcctatg	A	T	NM_001796 // upstream // 2871605 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 38341 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transc	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1795551	ggtgctaaccaaaaccc[G/T]cctttctctctact	G	T	NM_001796 // upstream // 2884425 // Hs.368322 // CDH8 // 1006 // Homo sapiens cadherin 8, type 2 (CDH8), mRNA. /// NM_001797 // downstream // 25521 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transc	CDH8	CDH8, Homo sapiens cadherin 8, type 2 (CDH8), q21
SNP_A-1932106	ttcctcaaggagttta[C/T]ggtcaggtaactgcat	C	T	NM_001797 // intron // 0 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// ENST00000268603 // intron // 0 // --- // --- // ---	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q21
SNP_A-2254074	ctgaggccaagctaa[A/G]cattgctactggcctt	A	G	NM_001797 // upstream // 62768 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 179761 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q21
SNP_A-2061367	aatgccctcaaagtac[C/G]gacagcaccatcttgc	C	G	NM_001797 // upstream // 195382 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 312375 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1811086	tccactaggtgtaaga[A/C]actttataagccaca	A	C	NM_001797 // upstream // 247302 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 364295 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2141131	atctggaggttaggtc[A/G]atgcagctaggtctgc	A	G	NM_001797 // upstream // 536562 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 653555 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2158131	attggagttggaagtc[C/T]gaagatgggagagaag	C	T	NM_001797 // upstream // 597131 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 714124 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1811316	agtccctgttccctga[C/T]gatttatgggctgta	C	T	NM_001797 // upstream // 622766 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 739759 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1690709	aaaatatttgcattgtaaagatc[A/G]aaaacataaaggcttactgacaaa	A	G	NM_001796 // upstream // 2538419 // Hs.388928 // CDH8 // 1006 // cadherin 8, type 2 /// NM_001797 // downstream // 372155 // Hs.443435 // CDH11 // 1009 // cadherin 11, type 2, OB-cadherin (osteoblast) /// NM_033664 // downstream // 372155 // Hs.443435 //	CDH8	CDH8 , rs4303504, cadherin 8, type 2, q21
SNP_A-1907175	tgtttcctgccac[A/G]agtgtgaatacgagac	A	G	NM_001797 // upstream // 829011 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 946004 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1811665	tgaataatatggaaaa[C/T]gacctagtttgaaaa	C	T	NM_001797 // upstream // 876818 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 993811 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11,	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1813192	gtggtcacatcacatc[A/G]aatgtgcctcctcatg	A	G	NM_001797 // upstream // 928868 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1045861 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1811763	tctactgtgatttaat[A/G]atggacttaacatac	A	G	NM_001797 // upstream // 960793 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1077786 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2066604	acaaaaagccaggaac[C/G]agggcaagtccatgga	C	G	NM_001797 // upstream // 991654 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1108647 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1822134	gttttctgtttaaagc[A/G]gaatgtttcgagagcc	A	G	NM_001797 // upstream // 1056586 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1173579 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 1	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1818773	gttgagaaggaggcaa[A/C]ataatcagtcatcagg	A	C	NM_001797 // upstream // 1068661 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1185654 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 1	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1834123	tacatcgttgcagata[A/C]ctatagggggtgtgtc	A	C	NM_001797 // upstream // 1113976 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1230969 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 1	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2217414	cctgaatgtgcttgac[A/G]atgctcagagagtttt	A	G	NM_001797 // upstream // 1128860 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1245853 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 1	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1840878	tagctccccgcacatc[A/G]attcccttctgatgct	A	G	NM_001797 // upstream // 1138845 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1255838 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 1	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-2139083	atcctatgcacaactc[A/G]catggaatcccaag	A	G	NM_001797 // upstream // 1208834 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA. /// NM_033664 // upstream // 1325827 // Hs.116471 // CDH11 // 1009 // Homo sapiens cadherin 1	CDH11	CDH11, Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, q22.1
SNP_A-1703419	actgattgaggctccactgtgtgaa[C/T]aactgtacttaacacac aatagag	C	T	NM_001795 // upstream // 1095294 // Hs.76206 // CDH5 // 1003 // cadherin 5, type 2, VE-cadherin (vascular epithelium) /// NM_001797 // upstream // 150531 // Hs.443435 // CDH11 // 1009 // cadherin 11, type 2, OB-cadherin (osteoblast) /// NM_033664 // upst	CDH5	CDH5, rs9302570, cadherin 5, type 2, VE-cadherin (vascular epithelium), q21
SNP_A-2261162	gaaagagcaaggaaac[C/T]agcgtaactggactgg	C	T	NM_016951 // intron // 0 // Hs.15159 // CKLF // 51192 // Homo sapiens chemokine-like factor (CKLF), transcript variant 1, mRNA. /// NM_181640 // intron // 0 // Hs.15159 // CKLF // 51192 // Homo sapiens chemokine-like factor (CKLF), transcript variant 2, m	CKLF	CKLF, Homo sapiens chemokine-like factor (CKLF), transcript variant 1, q22.1
SNP_A-2032712	aaataacacactgtac[C/T]gatgagttacaaatgt	C	T	NM_178818 // intron // 0 // Hs.325825 // CKLFSF4 // 146223 // Homo sapiens chemokine-like factor super family 4 (CKLFSF4), transcript variant 1, mRNA. /// NM_181521 // intron // 0 // Hs.325825 // CKLFSF4 // 146223 // Homo sapiens chemokine-like factor sup	CKLFSF4	CKLFSF4, Homo sapiens chemokine-like factor super family 4 (CKLFSF4), transcript variant 1, q22.1
SNP_A-1895683	tgcctctccatcctg[A/C]agcactactcaaccac	A	C	NM_006141 // intron // 0 // Hs.369068 // DNCLI2 // 1783 // Homo sapiens dynein, cytoplasmic, light intermediate polypeptide 2 (DNCLI2), mRNA. /// ENST00000258198 // intron // 0 // — // — // —	DNCLI2	DNCLI2, Homo sapiens dynein, cytoplasmic, light intermediate polypeptide 2 (DNCLI2), q22.1
SNP_A-1672072	tctcagcagtttcctgagagtacc[A/G]ccaaagtctcatcatattt gagagg	A	G	NM_001795 // upstream // 125302 // Hs.76206 // CDH5 // 1003 // cadherin 5, type 2, VE-cadherin (vascular epithelium) /// NM_001797 // upstream // 1120523 // Hs.443435 // CDH11 // 1009 // cadherin 11, type 2, OB-cadherin (osteoblast) /// NM_033664 // upst	CDH5	CDH5, rs163417, cadherin 5, type 2, VE-cadherin (vascular epithelium), q22.1
SNP_A-1729794	tgatagtcccctgtttctttagtacg[C/T]tccctgtctcactggtttgga ggca	C	T	NM_004614 // intron // 0 // Hs.274701 // TK2 // 7084 // thymidine kinase 2, mitochondrial	TK2	TK2, rs28171, thymidine kinase 2, mitochondrial,q22.1
SNP_A-2217770	cctgatgtctcctttta[C/T]tgttctctcatcatt	C	T	NM_018667 // intron // 0 // Hs.368421 // SMPD3 // 55512 // Homo sapiens sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II) (SMPD3), mRNA. /// ENST00000219334 // intron // 0 // — // — // —	SMPD3	SMPD3, Homo sapiens sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II) (SMPD3), q22.1
SNP_A-2065656	aatttagtgtcttagcf[A/G]atcggtacatgatggt	A	G	ENST00000261778 // intron // 0 // — // — // —	-	q22.1
SNP_A-2125886	agtttgttagcagaac[A/G]agaagaaagttaaagt	A	G	NM_032830 // intron // 0 // Hs.461113 // CIRH1A // 84916 // Homo sapiens cirrhosis, autosomal recessive 1A (cirhin) (CIRH1A), mRNA. /// ENST00000314423 // intron // 0 // — // — // — /// ENST00000352319 // intron // 0 // — // — // -	CIRH1A	CIRH1A, Homo sapiens cirrhosis, autosomal recessive 1A (cirhin) (CIRH1A), q22.1
SNP_A-1924611	ttatagacagctgtaa[A/G]acaaaagtcagaataa	A	G	NM_006750 // intron // 0 // Hs.461117 // SNTB2 // 6645 // Homo sapiens syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), transcript variant 1, mRNA /// NM_130845 // intron // 0 // Hs.461117 // SNTB2 // 6645 // Homo s	SNTB2	SNTB2, Homo sapiens syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), transcript variant 1, q22.1
SNP_A-2236835	ctctagaaaatagtca[G/T]cctgatatacgatctg	G	T	NM_006750 // intron // 0 // Hs.461117 // SNTB2 // 6645 // Homo sapiens syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), transcript variant 1, mRNA /// NM_130845 // intron // 0 // Hs.461117 // SNTB2 // 6645 // Homo s	SNTB2	SNTB2, Homo sapiens syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), transcript variant 1, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2197617	cattctcctcttccac[A/G]gacagaattcgttctt	A	G	NM_199424 // intron // 0 // Hs.408458 // WWP2 // 11060 // Homo sapiens WW domain containing E3 ubiquitin protein ligase 2 (WWP2), transcript variant 2, mRNA. /// NM_007014 // intron // 0 // Hs.408458 // WWP2 // 11060 // Homo sapiens WW domain containing E	WWP2	WWP2, Homo sapiens WW domain containing E3 ubiquitin protein ligase 2 (WWP2), transcript variant 2, q22.1
SNP_A-2195311	catggcctcttggaga[G/T]caggaacgttttgtt	G	T	NM_017990 // upstream // 23181 // Hs.546400 // PDPR // 55066 // Homo sapiens pyruvate dehydrogenase phosphatase regulatory subunit (PDPR), mRNA. /// ENST00000331116 // upstream // 51470 // — // — // — // — /// ENST00000288050 // upstream // 23181	PDPR	PDPR, Homo sapiens pyruvate dehydrogenase phosphatase regulatory subunit (PDPR), q22.1
SNP_A-1734894	ccagaaatatttctgagaatttcag[G/T]aggacagacaaattag gactgtaaa	G	T	NM_006750 // intron // 0 // Hs.42219 // SNTB2 // 6645 // syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) /// NM_130845 // intron // 0 // Hs.42219 // SNTB2 // 6645 // syntrophin, beta 2 (dystrophin-associated protein A1, 59	SNTB2	SNTB2 , rs10500549, syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2), q22.1
SNP_A-2114519	agggagcagagctaggt[A/G]ccagtgtacccagaat	A	G	NM_145818 // intron // 0 // Hs.208680 // COG4 // 25839 // Homo sapiens component of oligomeric golgi complex 4 (COG4), transcript variant Cog4S, mRNA. /// NM_015386 // intron // 0 // Hs.208680 // COG4 // 25839 // Homo sapiens component of oligomeric golgi	COG4	COG4, Homo sapiens component of oligomeric golgi complex 4 (COG4), transcript variant Cog4S, q22.1
SNP_A-2231822	ctcaaagcaggaccaaa[G/T]aaaatatgacatgcctc	G	T	NM_145818 // intron // 0 // Hs.208680 // COG4 // 25839 // Homo sapiens component of oligomeric golgi complex 4 (COG4), transcript variant Cog4S, mRNA. /// NM_015386 // intron // 0 // Hs.208680 // COG4 // 25839 // Homo sapiens component of oligomeric golgi	COG4	COG4, Homo sapiens component of oligomeric golgi complex 4 (COG4), transcript variant Cog4S, q22.1
SNP_A-2147239	atggactctctaag[A/G]aactcgctactctcca	A	G	NM_012426 // intron // 0 // Hs.514435 // SF3B3 // 23450 // Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA. /// ENST00000310750 // intron // 0 // — // — // — // — /// ENST00000302516 // intron // 0 // — // — // — // —	SF3B3	SF3B3, Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), q22.1
SNP_A-1894735	tgccagctttacaagc[C/G]acagaatcaccaaaac	C	G	NM_012426 // downstream // 66532 // Hs.514435 // SF3B3 // 23450 // Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA. /// NM_152456 // upstream // 7516 // Hs.461214 // MGC34647 // 146433 // Homo sapiens hypothetical protein MGC34647 (MGC346	SF3B3	SF3B3, Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), q22.1
SNP_A-2180508	cagaactgtgagacga[C/T]acattcctgttgctct	C	T	NM_152456 // intron // 0 // Hs.461214 // MGC34647 // 146433 // Homo sapiens hypothetical protein MGC34647 (MGC34647), mRNA. /// ENST00000288098 // intron // 0 // — // — // — // —	MGC34647	MGC34647, Homo sapiens hypothetical protein MGC34647 (MGC34647), q22.1
SNP_A-1841506	taggaggacacagctc[C/T]acaatctgggatagga	C	T	ENST00000302830 // upstream // 16587 // — // — // — // — /// ENST00000309900 // downstream // 22708 // — // — // — // —	-	q22.2
SNP_A-2158902	atgtggttgcaattc[A/G]catttccctggtgacc	A	G	NM_017558 // upstream // 19624 // Hs.461229 // HYDIN // 54768 // Homo sapiens hydrocephalus inducing (HYDIN), mRNA. /// NM_018348 // downstream // 32013 // Hs.72782 // FLJ11171 // 55783 // Homo sapiens hypothetical protein FLJ11171 (FLJ11171), mRNA. /// E	HYDIN	HYDIN, Homo sapiens hydrocephalus inducing (HYDIN), q22.2
SNP_A-2056103	aataccagctgttaaa[C/T]gtaatgagaaaatgta	C	T	NM_017558 // upstream // 24120 // Hs.461229 // HYDIN // 54768 // Homo sapiens hydrocephalus inducing (HYDIN), mRNA. /// NM_018348 // downstream // 27517 // Hs.72782 // FLJ11171 // 55783 // Homo sapiens hypothetical protein FLJ11171 (FLJ11171), mRNA. /// E	HYDIN	HYDIN, Homo sapiens hydrocephalus inducing (HYDIN), q22.2
SNP_A-2246412	ctgattgatttagaa[A/C]atagcacctatctt	A	C	NM_018348 // upstream // 6787 // Hs.72782 // FLJ11171 // 55783 // Homo sapiens hypothetical protein FLJ11171 (FLJ11171), mRNA. /// NM_007088 // upstream // 62321 // Hs.106857 // CALB2 // 794 // Homo sapiens calbindin 2, 29kDa (calretinin) (CALB2), transcr	FLJ11171	FLJ11171, Homo sapiens hypothetical protein FLJ11171 (FLJ11171), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1940702	ttgccttcatcattca[C/T]tctgagccagtgactg	C	T	NM_018348 // upstream // 50786 // Hs.72782 // FLJ11171 // 55783 // Homo sapiens hypothetical protein FLJ11171 (FLJ11171), mRNA. /// NM_007088 // upstream // 18322 // Hs.106857 // CALB2 // 794 // Homo sapiens calbindin 2, 29kDa (calretinin) (CALB2), transc	FLJ11171	FLJ11171, Homo sapiens hypothetical protein FLJ11171 (FLJ11171), q22.2
SNP_A-2209063	cccaggacagagctga[A/C]gccatccagagaccct	A	C	NM_007088 // downstream // 11819 // Hs.106857 // CALB2 // 794 // Homo sapiens calbindin 2, 29kDa (calretinin) (CALB2), transcript variant CALB2c, mRNA. /// NM_007087 // downstream // 11819 // Hs.106857 // CALB2 // 794 // Homo sapiens calbindin 2, 29kDa (c	CALB2	CALB2, Homo sapiens calbindin 2, 29kDa (calretinin) (CALB2), transcript variant CALB2c, q22.2
SNP_A-2269774	gacaagcaatgcagac[A/G]caggcagaaggagaca	A	G	NM_007088 // downstream // 12064 // Hs.106857 // CALB2 // 794 // Homo sapiens calbindin 2, 29kDa (calretinin) (CALB2), transcript variant CALB2c, mRNA. /// NM_007087 // downstream // 12064 // Hs.106857 // CALB2 // 794 // Homo sapiens calbindin 2, 29kDa (c	CALB2	CALB2, Homo sapiens calbindin 2, 29kDa (calretinin) (CALB2), transcript variant CALB2c, q22.2
SNP_A-1815236	gtgttggcataaagca[A/G]acactcaacaggttat	A	G	NM_181536 // intron // 0 // Hs.461263 // PKD1L3 // 342372 // Homo sapiens polycystic kidney disease 1-like 3 (PKD1L3), mRNA. /// ENST00000335106 // intron // 0 // — // — // — // —	PKD1L3	PKD1L3, Homo sapiens polycystic kidney disease 1-like 3 (PKD1L3), q22.2
SNP_A-2135197	atattgctgcttccta[C/T]cctctgtgtctttcct	C	T	NM_181536 // intron // 0 // Hs.461263 // PKD1L3 // 342372 // Homo sapiens polycystic kidney disease 1-like 3 (PKD1L3), mRNA. /// ENST00000335106 // intron // 0 // — // — // — // —	PKD1L3	PKD1L3, Homo sapiens polycystic kidney disease 1-like 3 (PKD1L3), q22.2
SNP_A-2227101	ctaattacatgacata[A/C]aataataatgctcaga	A	C	NM_001361 // intron // 0 // Hs.405639 // DHODH // 1723 // Homo sapiens dihydroorotate dehydrogenase (DHODH), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000219240 // intron // 0 // — // — // — // —	DHODH	DHODH, Homo sapiens dihydroorotate dehydrogenase (DHODH), nuclear gene encoding mitochondrial protein, q22.2
SNP_A-1815914	cattgggtcgtaacca[C/T]agtcagaggttttgtt	C	T	NM_006885 // upstream // 69130 // Hs.461285 // ATBF1 // 463 // Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA. /// NM_207385 // downstream // 9133 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST	ATBF1	ATBF1, Homo sapiens AT-binding transcription factor 1 (ATBF1), q22.3
SNP_A-1865033	tccagtcctaagaaca[C/T]ggcacctctcagcctt	C	T	NM_207385 // upstream // 215102 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 215102 // — // — // — // — /// ENST00000332289 // downstream // 581643 // — // — // — //	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-2228606	ctagaacctagaaaaa[A/G]agctcaccacagcaac	A	G	NM_207385 // upstream // 223984 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 223984 // — // — // — // — /// ENST00000332289 // downstream // 572761 // — // — // — //	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-1824857	taaagcacacagactc[A/G]aagtaacttgcccagg	A	G	NM_207385 // upstream // 266442 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 266442 // — // — // — // — /// ENST00000332289 // downstream // 530303 // — // — // — //	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-2273633	gactgaggttctaaag[A/T]cggaaattcacatcag	A	T	NM_207385 // upstream // 266760 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 266760 // — // — // — // — /// ENST00000332289 // downstream // 529985 // — // — // — //	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-1830682	taatccctgaaatcta[C/T]gaatgtgttacgttac	C	T	NM_207385 // upstream // 625609 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 625609 // — // — // — // — /// ENST00000332289 // downstream // 171136 // — // — // — //	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-2142689	atgaagagcttcccca[A/G]tgaacacatggcgtgc	A	G	NM_207385 // upstream // 721006 // Hs.371893 // C16orf47 // 388289 // Homo sapiens FLJ26184 protein (FLJ26184), mRNA. /// ENST00000358463 // upstream // 721006 // — // — // — // — /// ENST00000332289 // downstream // 75739 // — // — // — //	C16orf47	C16orf47, Homo sapiens FLJ26184 protein (FLJ26184), q22.3
SNP_A-2054240	aagttgatagaaattc[A/G]atttggggaagctagg	A	G	ENST00000332289 // upstream // 86913 // — // — // — // — /// ENST00000328558 // upstream // 192559 // — // — // — // —	-	q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1799514	gtaatggttgaatgta[C/T]cgtgaacaaatttta	C	T	ENST00000332289 // upstream // 134401 // — // — // — /// ENST00000328558 // upstream // 145071 // — // — // — // —	-	q22.3
SNP_A-2179398	cactgttaaaggttct[C/G]accatcctggcatcca	C	G	NM_002811 // intron // 0 // Hs.440604 // PSMD7 // 5713 // Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7), mRNA. /// ENST00000219313 // intron // 0 // — // — // — // —	PSMD7	PSMD7, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7), q22.3
SNP_A-2296440	gcatttccttaaaaa[C/T]cggagcactgacttg	C	T	NM_024306 // upstream // 98668 // Hs.461329 // FA2H // 79152 // Homo sapiens fatty acid 2-hydroxylase (FA2H), mRNA. /// ENST00000219368 // upstream // 98668 // — // — // — /// ENST00000205064 // downstream // 83 // — // — // — // —	FA2H	FA2H, Homo sapiens fatty acid 2-hydroxylase (FA2H), q22.3
SNP_A-1827749	taacttcccaaatcaa[C/T]gactcccagttaaca	C	T	ENST00000205064 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2265109	gaagatgaagcaagga[A/G]gagtattaggaggtgg	A	G	ENST00000205064 // intron // 0 // — // — // — // — /// ENST00000262144 // intron // 0 // — // — // —	-	q22.3
SNP_A-2231240	ctattcaacattcact[C/G]aacacaaatctagcta	C	G	ENST00000262144 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2217051	cctcttataactgagc[A/C]aataaggacaaaagct	A	C	NM_153688 // downstream // 14030 // Hs.388813 // ZFP1 // 162239 // Homo sapiens zinc finger protein 1 homolog (mouse) (ZFP1), mRNA. /// NM_001906 // downstream // 17989 // Hs.7402 // CTRB1 // 1504 // Homo sapiens chymotrypsinogen B1 (CTRB1), mRNA. /// EN	ZFP1	ZFP1, Homo sapiens zinc finger protein 1 homolog (mouse) (ZFP1), q22.3
SNP_A-1858642	tcagataaagagagaaa[A/G]gagaaatgtttaatcc	A	G	NM_006324 // intron // 0 // Hs.461361 // CFDP1 // 10428 // Homo sapiens craniofacial development protein 1 (CFDP1), mRNA. /// ENST00000283882 // intron // 0 // — // — // — // —	CFDP1	CFDP1, Homo sapiens craniofacial development protein 1 (CFDP1), q23.1
SNP_A-1857755	tcactggaggtcaaaa[A/C]ggttcacaagaggcag	A	C	NM_007285 // downstream // 11215 // Hs.461379 // GABARAPL2 // 11345 // Homo sapiens GABA(A) receptor-associated protein-like 2 (GABARAPL2), mRNA. /// NM_012091 // downstream // 10005 // Hs.188661 // ADAT1 // 23536 // Homo sapiens adenosine deaminase, tRNA	GABARAPL2	GABARAPL2, Homo sapiens GABA(A) receptor-associated protein-like 2 (GABARAPL2), q23.1
SNP_A-1933585	ttctagattgtctacat[G/T]tggcctccaaaacatt	G	T	ENST00000332413 // upstream // 311265 // — // — // — // — /// ENST00000332049 // upstream // 311265 // — // — // — // — /// ENST00000355617 // upstream // 311265 // — // — // — // — /// ENST00000358420 // downstream // 52468 // —	-	q23.1
SNP_A-1859096	tcagccctagattca[C/G]ctcctatccgtgtaat	C	G	NM_033401 // upstream // 95027 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 95027 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2233107	ctcagcaggattagtat[C/G]ctttagatgcatgtg	C	G	NM_033401 // upstream // 74542 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 74542 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2114095	agggaaaaaaaaactcc[A/G]gcagacaaaactgtaa	A	G	NM_033401 // upstream // 74389 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 74389 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2144157	atgagggcagggatc[A/C]attgtttcatttctc	A	C	NM_033401 // upstream // 50015 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 50015 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1956587	tttgtttgcatcatta[C/T]gtaaggattctatgac	C	T	NM_033401 // upstream // 49969 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 49969 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2076127	acattcattcattcaa[C/T]ggctatcttttgagac	C	T	NM_033401 // upstream // 46651 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 46651 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2283307	gatacaattcgttttc[C/T]cagattttacctatta	C	T	NM_033401 // upstream // 42657 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // upstream // 42657 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associ	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2174036	cacaccacaactctca[A/T]cattgcacccatggct	A	T	NM_033401 // intron // 0 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // intron // 0 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2058212	aatcaaccacttcaca[A/C]gatacgatagagacac	A	C	NM_033401 // downstream // 17735 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 17735 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin as	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1918249	ttaaagataatggaag[A/G]caaagagaaatgtttg	A	G	NM_033401 // downstream // 349840 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 349840 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1818727	aacatatttggaagac[A/G]agaaaatgaacccaga	A	G	NM_033401 // downstream // 361046 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 361046 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1928792	ttcagactactactga[C/G]acaatcatttttttgat	C	G	NM_033401 // downstream // 429739 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 429739 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1818835	ttgaagctgaatgtga[C/T]atttgaactcaaatcc	C	T	NM_033401 // downstream // 438365 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 438365 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2282130	gagtgtcatctttatc[A/G]aagtcaaaagtccagg	A	G	NM_033401 // downstream // 457334 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 457334 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2297559	gccagagcaaatgaaa[C/T]gacaaatgaaaaaccg	C	T	NM_033401 // downstream // 482639 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 482639 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2112164	aggattcaaggaagaa[A/C]tcagagtggctagaat	A	C	NM_033401 // downstream // 493075 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 493075 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2088427	actgtagtataacgtg[C/T]aactcatttgctccgt	C	T	NM_033401 // downstream // 494141 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 494141 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2294085	gcaggattcaacatgga[A/T]ggaaagtttgaatatt	A	T	NM_033401 // downstream // 503227 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 503227 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2197440	cattcccatgctagaa[C/G]gaaaaaatccaactcc	C	G	NM_033401 // downstream // 504836 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 504836 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1943267	ttggtggaataaaagc[A/G]catgatcttgggacgc	A	G	NM_033401 // downstream // 507972 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 507972 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2072080	acagagttctccacac[A/G]tgtgaatagctccgaga	A	G	NM_033401 // downstream // 518929 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 518929 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-1831686	taattatgaacaaaac[A/G]cagtagaataaacaca	A	G	NM_033401 // downstream // 519259 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, mRNA. /// NM_138994 // downstream // 519259 // Hs.461389 // CNTNAP4 // 85445 // Homo sapiens contactin	CNTNAP4	CNTNAP4, Homo sapiens contactin associated protein-like 4 (CNTNAP4), transcript variant 1, q23.1
SNP_A-2194644	catgcatcccatcttc[A/G]accaggcgccggcagg	A	G	NM_014940 // CDS // 0 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// ENST00000248248 // CDS // 0 // — // — // — /// ENST00000320859 // intron // 0 // — // — // — // —	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2202467	ccacccgtctcaaaca[C/T]tccaaaacacgtgtcc	C	T	NM_014940 // downstream // 13765 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 69122 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2300834	gcctggtacccagcag[A/G]caatcggcaaatgcct	A	G	NM_014940 // downstream // 13962 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 68925 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2046979	aagagtccacaaacta[C/T]agcctacaggtcaaat	C	T	NM_014940 // downstream // 20425 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 62462 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2149432	atgtactggcttaaa[C/T]gagggatttcctgct	C	T	NM_014940 // downstream // 20945 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 61942 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2028971	aaagaaaactctgaag[A/C]atacagaaagagccga	A	C	NM_014940 // downstream // 24092 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 58795 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2021748	aaaaacagctcaaata[A/G]gtcaaaggaggcccac	A	G	NM_014940 // downstream // 30176 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 52711 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2285182	gatctcaaacaacctа[A/G]acctcagatgaacta	A	G	NM_014940 // downstream // 60708 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 22179 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-1819160	taacatttgggaaaa[C/T]gattggctaatcaaaa	C	T	NM_014940 // downstream // 63652 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 19235 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2273129	gactattttcctgaaa[A/T]aaaacaggcacacaac	A	T	NM_014940 // downstream // 68815 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 14072 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-1888625	tgaggccaaaaaataa[A/G]ataggaagtgcttgga	A	G	NM_014940 // downstream // 77751 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 5136 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2056004	aatacagtcactacaa[A/C]tggtttacaaaactca	A	C	NM_014940 // downstream // 79411 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 3476 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-2134289	atatgcataaggattc[C/G]atgctttgtctgtttt	C	G	NM_014940 // downstream // 80443 // Hs.436089 // HSRG1 // 22879 // Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA. /// NM_139054 // downstream // 2444 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (	HSRG1	HSRG1, Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), q23.1
SNP_A-1803882	gtcaagtcagtgtgga[G/T]tcaactctattttat	G	T	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-2308363	gcttgtgacagtaaac[C/G]cagaacttgaggccag	C	G	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip .q23.1
SNP_A-1915694	tgtctgtgcaaaagc[G/T]caacatgaacctatat	G	T	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip .q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1819356	tagcatggtataaaaa[A/C]ttctctccaactatga	A	C	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-2057422	aatatcatgactatca[C/T]tgaagcttggagtagc	C	T	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // intron // 0 // Hs.188746 // ADAMTS18 // 170692	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip ,q23.1
SNP_A-1725504	ttcgtggggagaaagacatgtaata[C/T]ggaaaacagaaggg cacacaggagg	C	T	NM_138994 // intron // 0 // Hs.156829 // CASPR4 // 85445 // cell recognition protein CASPR4	CASPR4	CASPR4 , -, cell recognition protein CASPR4,q23.1
SNP_A-1819688	taatcataaagcagca[C/T]atttccaagctctgaa	C	T	NM_139054 // upstream // 104451 // Hs.188746 // ADAMTS18 // 170692 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip /// NM_199355 // upstream // 104451 // Hs.188746 // ADAM	ADAMTS18	ADAMTS18, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 (ADAMTS18), transcrip q23.1
SNP_A-1934780	ttctcttgcctacttc[C/G]agtcccagagaatggg	C	G	ENST00000268533 // intron // 0 // — // — // — // —	-	q23.1
SNP_A-1880355	tcttgaacactcacca[C/G]cgactgcaaatatgtc	C	G	ENST00000268533 // intron // 0 // — // — // — // —	-	q23.1
SNP_A-1894398	tgccaaaaacatcaaa[A/C]aatagtagacttagga	A	C	NM_020927 // intron // 0 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // — // — // — // —	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-2033338	aaatagatgttccagt[G/T]aaagaagctgttttat	G	T	NM_020927 // intron // 0 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // — // — // — // —	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-2052451	aagtagaatgctaaga[A/C]gttcgtaagtttttaa	A	C	NM_020927 // intron // 0 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // — // — // — // —	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1832901	tacaatggtctgaaga[C/T]gacaaaaaaatgcttg	C	T	NM_020927 // intron // 0 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // — // — // — // —	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-2125830	agtttggggtgcagta[C/T]ctgttttggatgcttg	C	T	NM_020927 // intron // 0 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// ENST00000302536 // intron // 0 // — // — // — // —	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1926279	ttattagagttgtcga[C/T]gaaaaaaatctaactt	C	T	NM_020927 // downstream // 11491 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// NM_005752 // upstream // 30997 // Hs.177936 // CLEC3A // 10143 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition do	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1930216	ttcattctcaagatca[A/G]cttttccttgtccctt	A	G	NM_020927 // downstream // 11578 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// NM_005752 // upstream // 30910 // Hs.177936 // CLEC3A // 10143 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition do	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-1800309	gtacgtgagttctagc[A/G]agatgccagagaatcc	A	G	NM_020927 // downstream // 15117 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// NM_005752 // upstream // 27371 // Hs.177936 // CLEC3A // 10143 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition do	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1
SNP_A-2104362	agcagctaaatatgaa[A/G]agagagcagaagacac	A	G	NM_020927 // downstream // 19205 // Hs.461405 // KIAA1576 // 57687 // Homo sapiens KIAA1576 protein (KIAA1576), mRNA. /// NM_005752 // upstream // 23283 // Hs.177936 // CLEC3A // 10143 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition do	KIAA1576	KIAA1576, Homo sapiens KIAA1576 protein (KIAA1576), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1946727	tttaacctcctgcta[A/G]aatcaatgtgattca	A	G	NM_005752 // downstream // 62320 // Hs.177936 // CLEC3A // 10143 // Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECS /// NM_130790 // upstream // 5237 // Hs.461453 // WWOX //	CLEC3A	CLEC3A, Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECS ,q23.1
SNP_A-2142931	atgaatagaaaaaatca[A/G]actgctagaacctcca	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2027197	aaacagtctaggtaca[C/T]gaagaaaacacatct	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2004880	ccaggaccaatggaca[A/G]aatctgcaaggaggca	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2290850	gcaaggatgttcctg[A/G]ataatgtgcactgagc	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1869547	tcctgtttcaagatg[C/G]agtggacictcttta	C	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1707649	aaggtctatgttctgaaaggaataa[C/T]aggatacttgttaagtg aatggtg	C	T	NM_014940 // upstream // 150755 // Hs.436089 // HSRG1 // 22879 // HSV-1 stimulation-related gene 1 /// NM_033401 // downstream // 481417 // Hs.156829 // CASPR4 // 85445 // cell recognition protein CASPR4 /// NM_138994 // downstream // 545282 // Hs.156829	HSRG1	HSRG1 , rs1502431, HSV-1 stimulation-related gene 1, q23.1
SNP_A-1857468	tcactatctttggaat[C/T]tactgtgacagagga	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2139854	atctaagcatgaagga[C/G]accctagaattgcac	C	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2037509	aacaaccagaagatca[C/T]gagctaaaccaataaa	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2025375	aaaatcagaacatata[A/C]ctctaaggaaaaagg	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2214567	cctagagaaacctgca[A/C]acttgtgtctcacct	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1847897	tatctcttgaccatgc[C/T]attgattagttatgtg	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1945721	ttgtgctgtatccca[C/T]tccaactcattgatc	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1805186	gtcattatggatctta[C/T]ataaacaagaaataaa	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1923676	ttaggtgttatgatgc[C/T]aatttgcccacatatt	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2259917	gaaaaggggggctggga[C/T]acgttggtgatttttt	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2147446	atggagtctccatcc[A/G]ctggtaaaatctggaa	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1820937	atttttcaagaatcctc[A/G]tacaaattgtccaggg	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1832167	taatttcttcatcctc[A/C]aactctagctcctagc	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1732656	tgtacatttaatctcttattgccaa[A/G]gtctcctaaaactgtgtatgaaaca	A	G	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18	ADAMTS18	ADAMTS18 , rs10514412, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18 q23.1
SNP_A-2187106	caggtcagccagttgg[A/G]aacagagagttgacggag	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2093293	agaacgagagctcata[C/T]ggcatccacgcgtgtc	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1720899	aaatatcttcccacgatttctact[C/T]agcttcaaactctcagtgg gtctat	C	T	NM_139054 // intron // 0 // Hs.188746 // ADAMTS18 // 170692 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18	ADAMTS18	ADAMTS18 , rs166673, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18,q23.1
SNP_A-1860438	tcagtgtggcccagat[A/C]aacctgtcctctctt	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2132478	atagtgatcaccataa[C/G]tcaaggaaaatccaga	C	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2274168	gactctcctgccacc[A/G]gaataaaggaatagag	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2216272	cctcctcaattccata[A/C]gcagagattcggagtg	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2264852	gaagagaggaagggaa[C/T]gttggaaccaatgctg	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2179016	cactgcctggtcagta[C/T]aagaagcacttctctg	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2265013	gaagataaaagagttac[C/T]cagaactgagcagaga	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2100007	agagtctgtgctttgc[A/G]cttctggctttgtga	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1930554	ttccaagcctaagaca[C/T]gtgctgtttctatgct	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1904756	tgggggttcgttacat[C/G]aagtgtgggtctgt	C	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1822076	tcagcatctttgtta[C/T]acccgaagtgcatcc	C	T	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2088531	actgtcctcatttttca[A/G]gctgaagaaccaagct	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1887349	tgagaatatttttcacc[A/C]cggaaattggcacatg	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1945383	ttgttatagattgaat[A/C]atgtcccgaagaaat	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1822200	gatgctgttcctctca[A/C]gtgggaaaaatttggt	A	C	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1753485	gtagtgtatattaatacatagtc[A/G]ccaatatgccaattggctc gcagac	A	G	NM_020927 // intron // 0 // Hs.22975 // KIAA1576 // 57687 // KIAA1576 protein	KIAA1576	KIAA1576 , rs416461, KIAA1576 protein,q23.1
SNP_A-1741671	ctgcccagttcatccagtccatacc[C/T]atgtttccttagggctca tcctgc	C	T	NM_020927 // intron // 0 // Hs.22975 // KIAA1576 // 57687 // KIAA1576 protein	KIAA1576	KIAA1576 , rs8062335, KIAA1576 protein,q23.1
SNP_A-1822223	atagaatgcaaaacttt[A/G]aaaaagacatacctttt	A	G	NM_130790 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // intron // 0 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1787986	gggagaaggtaagtca[C/T]ggaggattcgagccag	C	T	NM_130790 // downstream // 47051 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 47051 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2135909	atcaacatttataga[A/C]aggaaccagtggcttc	A	C	NM_130790 // downstream // 66987 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 66987 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2267344	gaatagatttttcagaa[A/G]agagaaacgcagatga	A	G	NM_130790 // downstream // 114772 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 114772 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2069005	acaatgccactgaaca[A/G]ctttcattgtctatgt	A	G	NM_130790 // downstream // 193343 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 193343 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2209843	ccccaaaggatttgaa[A/T]cttcccaggcatgggg	A	T	NM_130790 // downstream // 256578 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 256578 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1787741	gggaccaaagactatg[A/G]aaagtgaacctggctg	A	G	NM_130790 // downstream // 272378 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 272378 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1822641	atttgggggtgatgac[A/G]gaacattttaatcac	A	G	NM_130790 // downstream // 334856 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 334856 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1906063	tggtctctcatgtgtc[A/G]acatttaccaagcctt	A	G	NM_130790 // downstream // 340710 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 340710 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1866687	tcccctctacacctga[A/G]agtctggaaaattctg	A	G	NM_130790 // downstream // 345248 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 345248 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2192894	catcctgtaggccaaa[C/T]gtagtggttcaaatc	C	T	NM_130790 // downstream // 359514 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 359514 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-2094618	agaatagcattgatgt[C/T]aatgaagaactaggaa	C	T	NM_130790 // downstream // 362661 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, mRNA. /// NM_130844 // downstream // 362661 // Hs.461453 // WWOX // 51741 // Homo sapiens WW domain containin	WWOX	WWOX, Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, q23.1
SNP_A-1815488	gtgtttttgctgaaag[A/T]cttgttagtttccttc	A	T	NM_005360 // upstream // 206481 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 733762 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic.	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-2290208	gcaaattcaagagaaa[C/T]gtaatgatgggctaca	C	T	NM_005360 // upstream // 232875 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 707368 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic.	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-1800030	gtacatgatttattga[C/G]gatgtgcgttcagtag	C	G	NM_005360 // upstream // 235214 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 705029 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic.	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1881744	tcttgggttctaaca[C/T]cttggtacatgtgaa	C	T	NM_005360 // upstream // 242633 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 697610 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-1844947	tataattaaaccccacd[A/G]atacgtaagagataaa	A	G	NM_005360 // upstream // 271595 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 668648 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.1
SNP_A-1822852	ggacttaattatcaaa[A/G]gaagcgagctgagcat	A	G	NM_005360 // upstream // 334512 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 605731 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-2072002	acagaggatgaccata[C/T]gaagaggcagcaaggg	C	T	NM_005360 // upstream // 341611 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 598632 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-1843873	tagttagtccaattgt[C/T]aagtggcaaaaattag	C	T	NM_005360 // upstream // 530024 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 410219 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-2132386	atagtcagtacctcaa[C/G]gtcacagagccagccg	C	G	NM_005360 // upstream // 558419 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 381824 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-2078281	accataaggaaacgga[A/G]tacaaagaggcaaatt	A	G	NM_005360 // upstream // 713620 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 226623 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-2161617	atttggctaatgagaa[A/G]acagatacttaaagag	A	G	NM_005360 // upstream // 715712 // Hs.134859 // MAF // 4094 // Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA. /// NM_130897 // upstream // 224531 // Hs.98849 // DNCL2B // 83657 // Homo sapiens dynein, cytoplasmic,	MAF	MAF, Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), q23.2
SNP_A-1710660	tagcttgtagttctgcacccaaaa[C/T]cattcctcaggcgata aaatact	C	T	AF116601 // upstream // 729520 // - /// - /// Homo sapiens PRO0128 mRNA, complete cds. /// NM_005360 // downstream // 311523 // Hs.134859 // MAF // 4094 // v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) /// NM_016373 // downstream // 7	-	-, rs10514450, Homo sapiens PRO0128 mRNA, complete cds, q23.1
SNP_A-1705525	ggccttaccacaaaatttgcattc[A/C]cgacaatcacttaggca tgtctct	A	C	AF116601 // upstream // 790332 // - /// - /// Homo sapiens PRO0128 mRNA, complete cds. /// NM_005360 // downstream // 250711 // Hs.134859 // MAF // 4094 // v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) /// NM_016373 // downstream // 1	-	-, rs10514452, Homo sapiens PRO0128 mRNA, complete cds, q23.1
SNP_A-1874537	tctccctttcttcaaa[C/T]actgcaaatccactaa	C	T	NM_152342 // intron // 0 // Hs.373908 // CDYL2 // 124359 // Homo sapiens chromodomain protein, Y-like 2 (CDYL2), mRNA. /// ENST00000299564 // intron // 0 // — // — // —	CDYL2	CDYL2, Homo sapiens chromodomain protein, Y-like 2 (CDYL2), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2286750	gatggcccccatgtgat[A/C]aagaaccatgcaacag	A	C	NM_052892 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-li	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-2305712	gctgcccagagtaagaa[A/G]taggtgtagcactgtg	A	G	NM_052892 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-li	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-1913207	tgtggctcatttaccc[A/T]agaacacagaagagag	A	T	NM_052892 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // intron // 0 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-li	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-2190359	catacaagagctggac[A/G]agatgactcacaccta	A	G	NM_052892 // upstream // 1886 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, mRNA. /// NM_182740 // upstream // 1886 // Hs.413525 // PKD1L2 // 114780 // Homo sapiens polycystic kidney di	PKD1L2	PKD1L2, Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2), transcript variant 1, q23.2
SNP_A-2181970	cagagctgtcaagggc[C/T]agaagaatataattaa	C	T	NM_022041 // intron // 0 // Hs.112569 // GAN // 8139 // Homo sapiens giant axonal neuropathy (gigaxonin) (GAN), mRNA. /// ENST00000248272 // intron // 0 // — // — // —	GAN	GAN, Homo sapiens giant axonal neuropathy (gigaxonin) (GAN), q23.2
SNP_A-2245289	ctggctgagaagcaga[A/G]aaatgaaaaaacattt	A	G	NM_030629 // intron // 0 // Hs.461510 // CMIP // 80790 // Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, mRNA. /// NM_198390 // intron // 0 // Hs.461510 // CMIP // 80790 // Homo sapiens c-Maf-inducing protein (CMIP), transcript var	CMIP	CMIP, Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, q23.2
SNP_A-2243407	ctgcggctgcccctaa[A/G]aggacagattgttgct	A	G	NM_030629 // downstream // 29805 // Hs.461510 // CMIP // 80790 // Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, mRNA. /// NM_198390 // downstream // 29805 // Hs.461510 // CMIP // 80790 // Homo sapiens c-Maf-inducing protein (CMIP)	CMIP	CMIP, Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, q23.2
SNP_A-2127470	ataacaccttcaatta[A/G]acagaaaaccaggacaa	A	G	NM_002661 // intron // 0 // Hs.413111 // PLCG2 // 5336 // Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // — // — // — /// ENST00000359376 // intron // 0 // — // —	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-1802064	gtatacatagaattca[C/T]ccattgtatgcagcat	C	T	NM_002661 // intron // 0 // Hs.413111 // PLCG2 // 5336 // Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // — // — // — /// ENST00000359376 // intron // 0 // — // —	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-2188133	cagtccaggctacaaa[A/G]agtagaagaatgccc	A	G	NM_002661 // intron // 0 // Hs.413111 // PLCG2 // 5336 // Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // — // — // — /// ENST00000359376 // intron // 0 // — // —	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-2225221	cgttcctagcctgac[G/T]ctgtaacagatttctt	G	T	NM_002661 // intron // 0 // Hs.413111 // PLCG2 // 5336 // Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // — // — // — /// ENST00000359376 // intron // 0 // — // —	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2
SNP_A-2128538	ataatacgacaactta[A/G]gagaaactatttactt	A	G	NM_002661 // intron // 0 // Hs.413111 // PLCG2 // 5336 // Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), mRNA. /// ENST00000357974 // intron // 0 // — // — // — /// ENST00000359376 // intron // 0 // — // —	PLCG2	PLCG2, Homo sapiens phospholipase C, gamma 2 (phosphatidylinositol-specific) (PLCG2), q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1909241	tgtatgcataagtaga[A/T]gtgtctatctctgtat	A	T	NM_145168 // upstream // 17712 // Hs.87779 // HSPC105 // 93517 // Homo sapiens NAD(P) dependent steroid dehydrogenase-like (HSPC105), mRNA. /// NM_002153 // upstream // 6081 // Hs.162795 // HSD17B2 // 3294 // Homo sapiens hydroxysteroid (17-beta) dehydrog	HSPC105	HSPC105, Homo sapiens NAD(P) dependent steroid dehydrogenase-like (HSPC105), q23.3
SNP_A-2161300	atttgatgagctctct[C/G]aaggcaagaaagcccaa	C	G	NM_002153 // intron // 0 // Hs.162795 // HSD17B2 // 3294 // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// ENST00000199936 // intron // 0 // — // — // —	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-1842058	tagggatttttgaa[A/C]ctaccattaaagctac	A	C	NM_002153 // downstream // 39582 // Hs.162795 // HSD17B2 // 3294 // Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA. /// NM_005792 // downstream // 10053 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPH	HSD17B2	HSD17B2, Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), q23.3
SNP_A-1824689	aattaaagaaagtcaa[A/G]ccgagaccagcatata	A	G	NM_005792 // intron // 0 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// ENST00000258169 // intron // 0 // — // — // — // —	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2283846	gatagtcactatacta[C/G]ccacaacagcaatgcc	C	G	NM_005792 // upstream // 4470 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 683672 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. ///	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1883057	tgaaatatttgtgtc[A/C]gaaaccatgctaggca	A	C	NM_005792 // upstream // 309246 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 378896 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1807448	gtctgcacacctgga[C/G]gtttctgaggctcctc	C	G	NM_005792 // upstream // 336994 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 351148 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1825312	gcttttcagagtgttc[A/G]aggatcagggagcatg	A	G	NM_005792 // upstream // 412824 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 275318 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2248939	ctgttgtaattgtcac[C/G]catcttgacaaggtgg	C	G	NM_005792 // upstream // 496690 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 191452 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1825525	tgaccaatatatggca[A/G]atgagagtctttggg	A	G	NM_005792 // upstream // 578775 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 109367 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1825554	taaatagggaactgga[A/T]agatgctcaggaagag	A	T	NM_005792 // upstream // 580875 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 107267 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1670632	ccagggtctttgcacaggatttttc[A/G]cacacagtacaagtctg ggtctctgg	A	G	NM_030629 // intron // 0 // Hs.19597 // CMIP // 80790 // c-Maf-inducing protein	CMIP	CMIP , rs9319570, c-Maf-inducing protein,q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2210009	ccccacgagccaaaag[C/G]agtggatctagagtga	C	G	NM_005792 // upstream // 597718 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 90424 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2234137	ctcattgaacaagcaag[C/T]tccatttagttccgtg	C	T	NM_005792 // upstream // 613439 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 74703 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-2089961	acttctgcattctggct[C/T]gacaggaatgtcaacg	C	T	NM_005792 // upstream // 614073 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 74069 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1825587	cacttggttcctaga[G/T]gcattcctactagttt	G	T	NM_005792 // upstream // 617940 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 70202 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1808960	gtgaatgtgcatcccc[C/T]caaagacaggcagtaa	C	T	NM_005792 // upstream // 652201 // Hs.344400 // MPHOSPH6 // 10200 // Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA. /// NM_001257 // upstream // 35941 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. //	MPHOSPH6	MPHOSPH6, Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), q23.3
SNP_A-1873771	tctcagcaaagcgaga[A/G]agggtcctgcttgcag	A	G	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2237239	ctctcatctcgggaaa[A/T]ctttagagttgttgt	A	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1879482	tcttattccaaggaaa[A/C]gagtggaagatgaaaa	A	C	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1837441	tacttctgagtgtttat[C/T]agtttcagtgattctg	C	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2082866	acgtcaatgcatagaa[C/T]ggcctccacagcaaag	C	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1839458	tagatacagtaaaaaa[A/T]ctagtggctcatgcct	A	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1889700	tgataaggggtgtcaga[A/T]aatgggtctccctccc	A	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1729848	acaaaacctcaagaattattaagaa[A/G]attctgctgtagtgtcc ctggtctt	A	G	NM_001257 // upstream // 357012 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart) /// NM_005792 // upstream // 99754 // Hs.344400 // MPHOSPH6 // 10200 // M-phase phosphoprotein 6	CDH13	CDH13 , rs2967321, cadherin 13, H-cadherin (heart) q23.3
SNP_A-2167357	caacagggagtcatgc[A/G]aggttgtagagaagtg	A	G	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1826501	aggagcactggatgag[C/G]agttgtttgaggtaag	C	G	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2067087	acaaactgcgttgaa[A/T]caaagtgacccttaag	A	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1955604	ttlggtttlaccctlg[A/C]atgttttctggcaac	A	C	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2062801	aatgtgcaagaaagga[C/T]ccaacaaggcagcttt	C	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2085866	actcgagggctctaca[A/G]ccatttgccgggcggg	A	G	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2106922	agccttgcaaaggaga[C/T]gatagtgagactgaag	C	T	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-2266782	gaagtgtcccactgt[A/G]aaactagaaaaatcta	A	G	NM_001257 // intron // 0 // Hs.436040 // CDH13 // 1012 // Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA. /// ENST00000268613 // intron // 0 // — // — // — // —	CDH13	CDH13, Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), q23.3
SNP_A-1658626	tacagccaccaagaaaaaataagcca[C/T]gttatgtaaaaaga gaagttgtaga	C	T	NM_001257 // upstream // 39773 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart) /// NM_005792 // upstream // 416993 // Hs.344400 // MPHOSPH6 // 10200 // M-phase phosphoprotein 6	CDH13	CDH13 , rs10514546, cadherin 13, H-cadherin (heart), q23.3
SNP_A-1703009	attctgccgggtttctgagtcac[C/T]gagcatatgggcctcag gttggac	C	T	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs3852734, cadherin 13, H-cadherin (heart), q23.3
SNP_A-1648478	ccataaacccacacttccttctaca[C/T]gtgagctttaattaatccc agaatt	C	T	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs10514551, cadherin 13, H-cadherin (heart), q23.3
SNP_A-1812228	gtggagttctgtggag[C/G]acaggcctagttgag	C	G	NM_012213 // downstream // 21110 // Hs.461571 // MLYCD // 23417 // Homo sapiens malonyl-CoA decarboxylase (MLYCD), mRNA. /// NM_182980 // upstream // 11777 // Hs.528383 // OKL38 // 29948 // Homo sapiens pregnancy-induced growth inhibitor (OKL38), mRNA. //	MLYCD	MLYCD, Homo sapiens malonyl-CoA decarboxylase (MLYCD), q23.3
SNP_A-1664262	aatgcatctgggaaggctagcattg[C/T]gtctgacatgtaacag ccccttgcaa	C	T	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs1462035, cadherin 13, H-cadherin (heart), q23.3
SNP_A-1901722	tggcacaacattgtga[A/G]tacttaaagccactgg	A	G	NM_003791 // downstream // 5575 // Hs.75890 // MBTPS1 // 8720 // Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, mRNA. /// NM_201268 // downstream // 5890 // Hs.75890 // MBTPS1 // 8720 // Homo sapiens memb	MBTPS1	MBTPS1, Homo sapiens membrane-bound transcription factor protease, site 1 (MBTPS1), transcript variant 1, q23.3
SNP_A-1827804	taacttttataagctac[A/G]gatgttaaatggtgag	A	G	NM_031463 // intron // 0 // Hs.546450 // HSDL1 // 83693 // Homo sapiens steroid dehydrogenase-like (LOC83693), mRNA. /// ENST00000219439 // intron // 0 // — // — // — // —	HSDL1	HSDL1, Homo sapiens steroid dehydrogenase-like (LOC83693), q24.1
SNP_A-1900824	tggagtgagattgtga[A/G]acttggagctgtgca	A	G	NM_139174 // downstream // 14624 // Hs.8977 // LOC161931 // 161931 // Homo sapiens testis nuclear RNA-binding protein-like (LOC161931), mRNA. /// NM_133490 // downstream // 10427 // Hs.335877 // KCNG4 // 93107 // Homo sapiens potassium voltage-gated chann	LOC161931	LOC161931, Homo sapiens testis nuclear RNA-binding protein-like (LOC161931), q24.1
SNP_A-2242959	ctgccatgatcataaa[A/C]gaccagttcccaggat	A	C	NM_133490 // upstream // 20811 // Hs.335877 // KCNG4 // 93107 // Homo sapiens potassium voltage-gated channel, subfamily G, member 4 (KCNG4), transcript variant 2, mRNA. /// NM_172347 // upstream // 20811 // Hs.335877 // KCNG4 // 93107 // Homo sapiens pot	KCNG4	KCNG4, Homo sapiens potassium voltage-gated channel, subfamily G, member 4 (KCNG4), transcript variant 2, q24.1
SNP_A-2123173	agtggttatttatga[G/T]aatagtgacaagcctt	G	T	NM_021197 // intron // 0 // Hs.36688 // WFDC1 // 58189 // Homo sapiens WAP four-disulfide core domain 1 (WFDC1), mRNA. /// ENST00000219454 // intron // 0 // — // — // — // —	WFDC1	WFDC1, Homo sapiens WAP four-disulfide core domain 1 (WFDC1), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1912451	tgtgcagaactgtgt[C/T]attttttctagggaga	C	T	NM_014861 // intron // 0 // Hs.6168 // KIAA0703 // 9914 // Homo sapiens KIAA0703 gene product (KIAA0703), mRNA. /// ENST00000262429 // intron // 0 // — // — // —	KIAA0703	KIAA0703, Homo sapiens KIAA0703 gene product (KIAA0703), q24.1
SNP_A-1668318	ggaggttcccatatattctccagccd[G/T]ctcctgtagttatgctggg gccaca	G	T	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs889713, cadherin 13, H-cadherin (heart),q23.3
SNP_A-1828442	aaagtgaaaagtgcac[C/T]gtatttcaagtctgaa	C	T	NM_005153 // intron // 0 // Hs.136778 // USP10 // 9100 // Homo sapiens ubiquitin specific protease 10 (USP10), mRNA. /// ENST00000219473 // intron // 0 // — // — // —	USP10	USP10, Homo sapiens ubiquitin specific protease 10 (USP10), q24.1
SNP_A-1755602	ttggaagtggatgtgagcatagaag[A/G]aaacttcaggaatggg gttaggttca	A	G	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs10514591, cadherin 13, H-cadherin (heart),q23.3
SNP_A-2085892	actcggcttagaccc[C/T]agttctgcgacttagc	C	T	NM_031476 // downstream // 40128 // Hs.513779 // LCRISP2 // 83716 // Homo sapiens hypothetical protein DKFZp434B044 (DKFZP434B044), mRNA. /// NM_017740 // downstream // 24837 // Hs.461610 // ZDHHC7 // 55625 // Homo sapiens zinc finger, DHHC domain contain	LCRISP2	LCRISP2, Homo sapiens hypothetical protein DKFZp434B044 (DKFZP434B044), q24.1
SNP_A-1684846	tgtcctttacattctgctaatag[C/T]ggttaattaagcagaaagc aatggt	C	T	NM_001257 // intron // 0 // Hs.63984 // CDH13 // 1012 // cadherin 13, H-cadherin (heart)	CDH13	CDH13 , rs10514600, cadherin 13, H-cadherin (heart),q23.3
SNP_A-2299809	gcctaaggtatctaca[A/T]ctggtccttcacaga	A	T	NM_198491 // upstream // 96095 // Hs.125713 // FLJ44299 // 339145 // Homo sapiens FLJ44299 protein (FLJ44299), mRNA. /// NM_153238 // upstream // 74355 // Hs.375058 // MGC22001 // 197196 // Homo sapiens hypothetical protein MGC22001 (MGC22001), mRNA. ///	FLJ44299	FLJ44299, Homo sapiens FLJ44299 protein (FLJ44299), q24.1
SNP_A-2304648	gctctgacactgagaa[C/T]gggcacttcccgctc	C	T	NM_153238 // downstream // 2884 // Hs.375058 // MGC22001 // 197196 // Homo sapiens hypothetical protein MGC22001 (MGC22001), mRNA. /// ENST00000316859 // downstream // 2884 // — // — // — // — /// ENST00000338693 // downstream // 115082 // — //	MGC22001	MGC22001, Homo sapiens hypothetical protein MGC22001 (MGC22001), q24.1
SNP_A-2099146	agaggagacagcagaa[A/C]aagccgcaggacagag	A	C	NM_153238 // downstream // 15972 // Hs.375058 // MGC22001 // 197196 // Homo sapiens hypothetical protein MGC22001 (MGC22001), mRNA. /// ENST00000316859 // downstream // 15972 // — // — // — // — /// ENST00000338693 // downstream // 101994 // — /	MGC22001	MGC22001, Homo sapiens hypothetical protein MGC22001 (MGC22001), q24.1
SNP_A-2177031	cacctcaagcacgctaa[C/T]ggaaatggaatcacac	C	T	NM_153238 // downstream // 55205 // Hs.375058 // MGC22001 // 197196 // Homo sapiens hypothetical protein MGC22001 (MGC22001), mRNA. /// ENST00000316859 // downstream // 55205 // — // — // — // — /// ENST00000338693 // downstream // 62761 // — //	MGC22001	MGC22001, Homo sapiens hypothetical protein MGC22001 (MGC22001), q24.1
SNP_A-2293507	gcagcagaaagagccaa[C/T]gtgcatgggattcca	C	T	NM_006067 // intron // 0 // Hs.173162 // NOC4 // 10328 // Homo sapiens neighbor of COX4 (NOC4), mRNA. /// ENST00000253457 // intron // 0 // — - // — // — // —	NOC4	NOC4, Homo sapiens neighbor of COX4 (NOC4), q24.1
SNP_A-2200227	ccaaatttagagcaag[C/G]ccctttgatagtgtat	C	G	NM_006067 // intron // 0 // Hs.173162 // NOC4 // 10328 // Homo sapiens neighbor of COX4 (NOC4), mRNA. /// ENST00000253457 // intron // 0 // — - // — // — // —	NOC4	NOC4, Homo sapiens neighbor of COX4 (NOC4), q24.1
SNP_A-1912808	tgtgctgccgtgacag[A/G]ctccaattcttcaggga	A	G	NM_001861 // intron // 0 // Hs.433419 // COX4I1 // 1327 // Homo sapiens cytochrome c oxidase subunit IV isoform 1 (COX4I1), mRNA. /// ENST00000253452 // intron // 0 // — // — // — // —	COX4I1	COX4I1, Homo sapiens cytochrome c oxidase subunit IV isoform 1 (COX4I1), q24.1
SNP_A-2202352	ccaccaggatggctaa[A/C]acataaacgactgaaa	A	C	NM_002163 // downstream // 11428 // Hs.137427 // IRF8 // 3394 // Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /// ENST00000268638 // downstream // 11428 // — // — // — // — /// ENST00000342604 // upstream // 40353 /	IRF8	IRF8, Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), q24.1
SNP_A-2152772	attaattaccaggtca[A/G]atcacttggagagaga	A	G	NM_002163 // downstream // 38035 // Hs.137427 // IRF8 // 3394 // Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /// ENST00000268638 // downstream // 38035 // — // — // — // — /// ENST00000342604 // upstream // 13746 /	IRF8	IRF8, Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2305741	gctgcctaaattcaca[A/G]gaaagagccctgacaa	A	G	NM_002163 // downstream // 47959 // Hs.137427 // IRF8 // 3394 // Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /// ENST00000268638 // downstream // 47959 // --- // --- // --- // --- /// ENST00000342604 // upstream // 3822 //	IRF8	IRF8, Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), q24.1
SNP_A-2293459	gcagcaagatgactga[C/T]ggagcccagacaaaat	C	T	ENST00000342604 // downstream // 11175 // --- // --- // --- // --- /// ENST00000326395 // upstream // 50662 // --- // --- // --- // ---	-	q24.1
SNP_A-1834825	taccataaaacccgtg[A/G]aataacagcagaggca	A	G	ENST00000342604 // downstream // 42312 // --- // --- // --- // --- /// ENST00000326395 // upstream // 19525 // --- // --- // --- // ---	-	q24.1
SNP_A-1944534	ttgtctttatttgtag[A/G]aagtccagtattgcat	A	G	ENST00000342604 // downstream // 45576 // --- // --- // --- // --- /// ENST00000326395 // upstream // 16261 // --- // --- // --- // ---	-	q24.1
SNP_A-1736479	taatagagccatcgatgaaaaaaat[C/G]ataaactcattgtgag atgtaatca	C	G	NM_031476 // intron // 0 // Hs.262958 // DKFZP434B044 // 83716 // hypothetical protein DKFZp434B044	DKFZP434B044	DKFZP434B044 , rs721004, hypothetical protein DKFZp434B044,q24.1
SNP_A-2223731	cggcaggctgcttagg[A/C]atctcgggacttaagg	A	C	ENST00000326395 // downstream // 220791 // --- // --- // --- // --- /// ENST00000304488 // downstream // 78558 // --- // --- // --- // ---	-	q24.1
SNP_A-2240887	ctgagacaatgtcctc[C/T]ctgttgctacctctat	C	T	NM_001451 // upstream // 149039 // Hs.155591 // FOXF1 // 2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 22679 // --- // --- // --- // --- /// ENST00000262426 // upstream // 149039 // --- // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-2197984	cattgcccctagagtc[A/C]aacagaatctgttcat	A	C	NM_001451 // upstream // 147902 // Hs.155591 // FOXF1 // 2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 23816 // --- // --- // --- // --- /// ENST00000262426 // upstream // 147902 // --- // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-1830306	atgaggggaatgagac[A/G]agccagacttggacct	A	G	NM_001451 // upstream // 134054 // Hs.155591 // FOXF1 // 2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 37664 // --- // --- // --- // --- /// ENST00000262426 // upstream // 134054 // --- // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-1828708	taagctcttgaaagga[C/G]aagaaaaggaatttgt	C	G	NM_001451 // upstream // 100740 // Hs.155591 // FOXF1 // 2294 // Homo sapiens forkhead box F1 (FOXF1), mRNA. /// ENST00000304488 // upstream // 70978 // --- // --- // --- // --- /// ENST00000262426 // upstream // 100740 // --- // --- // --- // ---	FOXF1	FOXF1, Homo sapiens forkhead box F1 (FOXF1), q24.1
SNP_A-2179615	cacttccacatttcca[C/T]tctaacggcccctgcg	C	T	NM_022764 // intron // 0 // Hs.343627 // FLJ12998 // 64779 // Homo sapiens hypothetical protein FLJ12998 (FLJ12998), mRNA. /// ENST00000360900 // intron // 0 // --- // --- // --- // --- /// ENST00000322911 // intron // 0 // --- // --- // --- // ---	FLJ12998	FLJ12998, Homo sapiens hypothetical protein FLJ12998 (FLJ12998), q24.1
SNP_A-1883514	tgaaccagtgagttgg[A/G]aaacactctatgaaag	A	G	NM_005250 // downstream // 112434 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 112434 // --- // --- // --- // --- /// ENST00000253461 // downstream // 610622 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2282875	gataaatacttcaaaa[G/T]ggtgttccaggacaag	G	T	NM_005250 // downstream // 122206 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 122206 // --- // --- // --- // --- /// ENST00000253461 // downstream // 600850 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2199886	ccaaagaaatcaaaac[A/G]aaggaggaagtcaaga	A	G	NM_005250 // downstream // 186307 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 186307 // --- // --- // --- // --- /// ENST00000253461 // downstream // 536749 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2029543	aaagactcaagagtgg[A/C]aacgttaagaaaaagc	A	C	NM_005250 // downstream // 206570 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 206570 // --- // --- // --- // --- /// ENST00000253461 // downstream // 516486 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1791480	gggtatgggagacaga[A/G]atccaatcacttccct	A	G	NM_005250 // downstream // 206969 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 206969 // --- // --- // --- // --- /// ENST00000253461 // downstream // 516087 // --- // --- // --- // ---	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2004984	caacccaccacacta[C/T]gtttctcttctctag	C	T	NM_005250 // downstream // 237535 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 237535 // — // — // — /// ENST00000253461 // downstream // 485521 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1830938	cctcaaatgtaaacta[A/C]ggatggcatccctcct	A	C	NM_005250 // downstream // 241337 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 241337 // — // — // — /// ENST00000253461 // downstream // 481719 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1906886	tggttccaaagaagaa[G/T]cgtggttgtgagttgc	G	T	NM_005250 // downstream // 244574 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 244574 // — // — // — /// ENST00000253461 // downstream // 478482 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2096624	agacgcgctttggaata[A/G]tcatttccctcaggcc	A	G	NM_005250 // downstream // 254028 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 254028 // — // — // — /// ENST00000253461 // downstream // 469028 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1903238	tggcttgtcatgggaa[A/C]atcacatgtaaccacc	A	C	NM_005250 // downstream // 341118 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 341118 // — // — // — /// ENST00000253461 // downstream // 381938 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-2004986	aagccagaagagcaca[A/G]tgagttgggagcttct	A	G	NM_005250 // downstream // 363847 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 363847 // — // — // — /// ENST00000253461 // downstream // 359209 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.1
SNP_A-1665132	aaacaggttgttttgtctttatc[G/T]ttgttagagttatagatttatg at	G	T	AF384996 // upstream // 113929 // - // - // - // Homo sapiens MUSP1 (MUSP1) mRNA, complete cds. /// NM_002163 // downstream // 210 // Hs.14453 // ICSBP1 // 3394 // interferon consensus sequence binding protein 1	-	-, rs1568391, Homo sapiens MUSP1 (MUSP1) mRNA, complete cds, q24.1
SNP_A-2087060	actgagttccagtgaa[A/G]ttcaccgcaacaggca	A	G	NM_005250 // downstream // 593095 // Hs.533830 // FOXL1 // 2300 // Homo sapiens forkhead box L1 (FOXL1), mRNA. /// ENST00000320241 // downstream // 593095 // — // — // — /// ENST00000253461 // downstream // 129961 // — // — // — /// —	FOXL1	FOXL1, Homo sapiens forkhead box L1 (FOXL1), q24.2
SNP_A-1758475	ctctatttgctattgataaaagcaa[C/T]gtaactgaaattactctgt acctca	C	T	AF384996 // upstream // 69241 // - // - // - // Homo sapiens MUSP1 (MUSP1) mRNA, complete cds. /// NM_002163 // downstream // 44898 // Hs.14453 // ICSBP1 // 3394 // interferon consensus sequence binding protein 1	-	-, rs9308979, Homo sapiens MUSP1 (MUSP1) mRNA, complete cds, q24.1
SNP_A-1733270	cttttcttcgcacaaaagccctgg[C/T]agttagctcacaaccccc taggcct	C	T	AF384996 // upstream // 59753 // - // - // - // Homo sapiens MUSP1 (MUSP1) mRNA, complete cds. /// NM_002163 // downstream // 54386 // Hs.14453 // ICSBP1 // 3394 // interferon consensus sequence binding protein 1	-	-, rs9308365, Homo sapiens MUSP1 (MUSP1) mRNA, complete cds, q24.1
SNP_A-1693701	gcgaagaaaaaggttctacaag[A/G]cagctcacagcttgg acttagccc	A	G	AF384996 // upstream // 59714 // - // - // - // Homo sapiens MUSP1 (MUSP1) mRNA, complete cds. /// NM_002163 // downstream // 54425 // Hs.14453 // ICSBP1 // 3394 // interferon consensus sequence binding protein 1	-	-, rs9308366, Homo sapiens MUSP1 (MUSP1) mRNA, complete cds, q24.1
SNP_A-1826064	taaatgtctggttga[C/T]ggtgcaacagttgact	C	T	NM_015144 // upstream // 89060 // Hs.156231 // ZCCHC14 // 23174 // Homo sapiens zinc finger, CCHC domain containing 14 (ZCCHC14), mRNA. /// NM_020655 // upstream // 21974 // Hs.123450 // JPH3 // 57338 // Homo sapiens junctophilin 3 (JPH3), mRNA. /// ENST0 — — — —	ZCCHC14	ZCCHC14, Homo sapiens zinc finger, CCHC domain containing 14 (ZCCHC14), q24.2
SNP_A-2247423	ctgctagccatggaa[C/G]tagttcgcactgaaac	C	G	NM_017566 // upstream // 8832 // Hs.461688 // KLHDC4 // 54758 // Homo sapiens kelch domain containing 4 (KLHDC4), mRNA. /// NM_003486 // downstream // 55243 // Hs.513797 // SLC7A5 // 8140 // Homo sapiens solute carrier family 7 (cationic amino acid transp	KLHDC4	KLHDC4, Homo sapiens kelch domain containing 4 (KLHDC4), q24.2
SNP_A-1691954	tgtaaatggaaaaatgagaacaacg[A/T]ccctattacaaagaa agcccagggt	A	T	NM_005250 // downstream // 210484 // Hs.381273 // FOXL1 // 2300 // forkhead box L1	FOXL1	FOXL1, rs6539977, forkhead box L1 q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2301947	gcgtatccgagaacca[C/T]aagcgtctcccctacc	C	T	NM_004933 // CDS // 0 // Hs.148090 // CDH15 // 1013 // Homo sapiens cadherin 15, M-cadherin (myotubule) (CDH15), mRNA. /// ENST00000289746 // CDS // 0 // --- // --- // ---	CDH15	CDH15, Homo sapiens cadherin 15, M-cadherin (myotubule) (CDH15), q24.3
SNP_A-2272182	gacctactatctatct[C/G]acagcacaatagggta	C	G	NM_013275 // intron // 0 // Hs.335003 // ANKRD11 // 29123 // Homo sapiens ankyrin repeat domain 11 (ANKRD11), mRNA. /// ENST00000301030 // intron // 0 // --- // --- // ---	ANKRD11	ANKRD11, Homo sapiens ankyrin repeat domain 11 (ANKRD11), q24.3
SNP_A-2116615	aggtcagatgtgacga[C/G]agcaggcccatcaagg	C	G	ENST00000305699 // 3UTR // 0 // --- // --- // ---	-	q24.3
SNP_A-1879141	tcttacataacaacca[C/G]agttaccaaaatcgag	C	G	NM_018289 // intron // 0 // Hs.461819 // FLJ10979 // 55275 // Homo sapiens hypothetical protein FLJ10979 (FLJ10979), mRNA. /// ENST00000321906 // intron // 0 // --- // --- // --- /// ENST00000291074 // intron // 0 // --- // --- // --- /// EN	FLJ10979	FLJ10979, Homo sapiens hypothetical protein FLJ10979 (FLJ10979), p13.3
SNP_A-1882409	tgaaaagcagtagaag[A/G]aacagtcagagatgcc	A	G	NM_001092 // 3UTR // 0 // Hs.159306 // ABR // 29 // Homo sapiens active BCR-related gene (ABR), transcript variant 2, mRNA. /// NM_021962 // 3UTR // 0 // Hs.159306 // ABR // 29 // Homo sapiens active BCR-related gene (ABR), transcript variant 1, mRNA. ///	ABR	ABR, Homo sapiens active BCR-related gene (ABR), transcript variant 2, p13.3
SNP_A-2242026	ctgattctaaatgta[C/T]gcggaaatgcaaaaac	C	T	NM_006761 // downstream // 6645 // Hs.513851 // YWHAE // 7531 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide (YWHAE), mRNA. /// ENST00000333813 // downstream // 36912 // --- // --- // ---	YWHAE	YWHAE, Homo sapiens tyrosine 3-monooxygenase p13.3
SNP_A-1843989	tagttctactcaatta[A/G]gatgagcaaaaggctg	A	G	NM_006761 // intron // 0 // Hs.513851 // YWHAE // 7531 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide (YWHAE), mRNA. /// ENST00000264335 // intron // 0 // --- // --- // ---	YWHAE	YWHAE, Homo sapiens tyrosine 3-monooxygenase p13.3
SNP_A-1781411	ggattaaatgagatgat[C/T]ccatacaaaggcagtc	C	T	NM_005206 // upstream // 3783 // Hs.461896 // CRK // 1398 // Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian) (CRK), transcript variant I, mRNA. /// NM_016823 // upstream // 3783 // Hs.461896 // CRK // 1398 // Homo sapiens v-crk sarcoma viru	CRK	CRK, Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian) (CRK), transcript variant I, p13.3
SNP_A-2215873	cctcattttgcaaaaa[A/G]ctatgtaagggaagtt	A	G	ENST00000355065 // intron // 0 // --- // --- // ---	-	p13.3
SNP_A-1914204	tgtgttatcttcta[A/C]gccagttttctgatt	A	C	NM_152348 // intron // 0 // Hs.234572 // FLJ33817 // 124997 // Homo sapiens hypothetical protein FLJ33817 (FLJ33817), mRNA. /// ENST00000355065 // intron // 0 // --- // --- // --- /// ENST00000309182 // intron // 0 // --- // --- // --- /// E	FLJ33817	FLJ33817, Homo sapiens hypothetical protein FLJ33817 (FLJ33817), p13.3
SNP_A-1835807	tacgggaaagagacct[C/T]agatcaattggatgcc	C	T	NM_000934 // intron // 0 // Hs.159509 // SERPINF2 // 5345 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member /// ENST00000324015 // intron // 0 // --- // --- // ---	SERPINF2	SERPINF2, Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member. p13.3
SNP_A-2111908	aggatcctgagaacag[A/G]aggcaaatctcaaagc	A	G	NM_052928 // intron // 0 // Hs.514602 // SMYD4 // 114826 // Homo sapiens SET and MYND domain containing 4 (SMYD4), mRNA. /// ENST00000305513 // intron // 0 // --- // --- // ---	SMYD4	SMYD4, Homo sapiens SET and MYND domain containing 4 (SMYD4), p13.3
SNP_A-1903520	tgggaatttattgct[C/G]aagtcagtcattgaaa	C	G	NM_052928 // intron // 0 // Hs.514602 // SMYD4 // 114826 // Homo sapiens SET and MYND domain containing 4 (SMYD4), mRNA. /// ENST00000305513 // intron // 0 // --- // --- // ---	SMYD4	SMYD4, Homo sapiens SET and MYND domain containing 4 (SMYD4), p13.3
SNP_A-2216935	cctctggctaagtgaa[A/G]gttatcaggtggactt	A	G	NM_052928 // intron // 0 // Hs.514602 // SMYD4 // 114826 // Homo sapiens SET and MYND domain containing 4 (SMYD4), mRNA. /// ENST00000305513 // intron // 0 // --- // --- // ---	SMYD4	SMYD4, Homo sapiens SET and MYND domain containing 4 (SMYD4), p13.3
SNP_A-2242060	ctgatttgttgctttca[C/G]gtaaacagatgtcctt	C	G	NM_052928 // CDS // 0 // Hs.514602 // SMYD4 // 114826 // Homo sapiens SET and MYND domain containing 4 (SMYD4), mRNA. /// ENST00000305513 // CDS // 0 // --- // --- // ---	SMYD4	SMYD4, Homo sapiens SET and MYND domain containing 4 (SMYD4), p13.3
SNP_A-2169813	caaggatagcttcagc[A/G]gacttcctggaaacaag	A	G	NM_002945 // CDS // 0 // Hs.461925 // RPA1 // 6117 // Homo sapiens replication protein A1, 70kDa (RPA1), mRNA. /// ENST00000254719 // CDS // 0 // --- // --- // ---	RPA1	RPA1, Homo sapiens replication protein A1, 70kDa (RPA1), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805868	gtcccgattcaaaaa[A/C]tgttaagcaccactca	A	C	NM_178568 // upstream // 33038 // Hs.22917 // RTN4RL1 // 146760 // Homo sapiens reticulon 4 receptor-like 1 (RTN4RL1), mRNA. /// NM_001383 // upstream // 59253 // Hs.513856 // DPH2L1 // 1801 // Homo sapiens DPH2-like 1 (S. cerevisiae) (DPH2L1), mRNA. ///	RTN4RL1	RTN4RL1, Homo sapiens reticulon 4 receptor-like 1 (RTN4RL1), p13.3
SNP_A-1816766	gttatctctggaatgcf[A/G]agtttaagcatgaaag	A	G	NM_025023 // intron // 0 // Hs.448342 // — // 0 // Homo sapiens hypothetical protein FLJ14069 (FLJ14069), mRNA. /// NM_017575 // intron // 0 // Hs.448342 // C17orf31 // 23293 // Homo sapiens chromosome 17 open reading frame 31 (C17orf31), mRNA. /// ENST	-	-, Homo sapiens hypothetical protein FLJ14069 (FLJ14069), p13.3
SNP_A-2215503	cctcacttaccttcc[C/T]caatgacatcaggtct	C	T	NM_024086 // upstream // 30724 // Hs.513862 // MGC3329 // 79066 // Homo sapiens hypothetical protein MGC3329 (MGC3329), mRNA. /// NM_000430 // upstream // 51032 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, is	MGC3329	MGC3329, Homo sapiens hypothetical protein MGC3329 (MGC3329), p13.3
SNP_A-2157227	attgacaaatgatacc[A/G]gaaaaaatgactaaaa	A	G	NM_024086 // upstream // 59749 // Hs.513862 // MGC3329 // 79066 // Homo sapiens hypothetical protein MGC3329 (MGC3329), mRNA. /// NM_000430 // upstream // 22007 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, is	MGC3329	MGC3329, Homo sapiens hypothetical protein MGC3329 (MGC3329), p13.3
SNP_A-2161243	atttgaggttggagag[A/G]cacgtctgagccagat	A	G	NM_000430 // intron // 0 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // — // — // —	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-1947071	tttaataggttggttc[A/G]cttcagaactaacttg	A	G	NM_000430 // intron // 0 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // — // — // —	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-1948812	tttatattatgtgctat[C/G]tgtattgtcttaaataa	C	G	NM_000430 // intron // 0 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // — // — // —	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-2035058	aaatgcacacttaaaa[A/G]tatttccagccatatt	A	G	NM_000430 // intron // 0 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // — // — // —	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-1828665	taagctaacagacata[A/T]cattaaggagctaata	A	T	NM_000430 // intron // 0 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // intron // 0 // — // — // —	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-2259682	gaaaagaaaaaaattc[C/T]atccctgagtctgtca	C	T	NM_000430 // downstream // 3143 // Hs.77318 // PAFAH1B1 // 5048 // Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA. /// ENST00000006951 // downstream // 3143 // — // — // — /// ENST000	PAFAH1B1	PAFAH1B1, Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), p13.3
SNP_A-2236528	ctcgtcttgcagggac[A/G]gaactcatcttcctcc	A	G	ENST00000322335 // intron // 0 // — // — // — // —	-	p13.3
SNP_A-1853339	tatttattgtagtac[A/G]acttgctcgaagctg	A	G	NM_015085 // intron // 0 // Hs.499659 // GARNL4 // 23108 // Homo sapiens GTPase activating Rap/RanGAP domain-like 4 (GARNL4), mRNA. /// ENST00000254695 // intron // 0 // — // — // — // —	GARNL4	GARNL4, Homo sapiens GTPase activating Rap p13.3
SNP_A-2038774	aacagatgtgtttcca[C/T]tgacggcaatcaggtt	C	T	NM_015085 // intron // 0 // Hs.499659 // GARNL4 // 23108 // Homo sapiens GTPase activating Rap/RanGAP domain-like 4 (GARNL4), mRNA. /// ENST00000254695 // intron // 0 // — // — // — // —	GARNL4	GARNL4, Homo sapiens GTPase activating Rap,p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2148411	atggggtaaatgaaca[A/G]gaagaggatgtagaag	A	G	NM_014565 // CDS // 0 // Hs.532688 // OR1A1 // 8383 // Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), mRNA. /// ENST00000304094 // CDS // 0 // --- // --- // --- // ---	OR1A1	OR1A1, Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), p13.3
SNP_A-1645058	tgcattgggtgtgctttcgaaatta[C/T]aaagcagatcacgtagc gtccctgt	C	T	NM_002551 // downstream // 15618 // Hs.272377 // OR3A2 // 4995 // olfactory receptor, family 3, subfamily A, member 2 /// NM_014565 // downstream // 45802 // - // - // -	OR3A2	OR3A2 , rs9303166, olfactory receptor, family 3, subfamily A, member 2 ,p13.2
SNP_A-2052769	aagtcaatgagaataa[C/T]ggaggctgccccattc	C	T	NM_015113 // intron // 0 // Hs.277624 // ZZEF1 // 23140 // Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // --- // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-1834018	gaggaagtattctagc[A/G]caacaaaaaatgaatt	A	G	NM_015113 // intron // 0 // Hs.277624 // ZZEF1 // 23140 // Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // --- // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-1794153	ggtcagtgatggtgca[C/T]agagagctcatgactt	C	T	NM_015113 // CDS // 0 // Hs.277624 // ZZEF1 // 23140 // Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // CDS // 0 // --- // --- // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-2277341	gagatttagacaactg[A/G]cagagaatctgggact	A	G	NM_015113 // intron // 0 // Hs.277624 // ZZEF1 // 23140 // Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), mRNA. /// ENST00000263089 // intron // 0 // --- // --- // --- // ---	ZZEF1	ZZEF1, Homo sapiens zinc finger, ZZ-type with EF hand domain 1 (ZZEF1), p13.2
SNP_A-2237404	ctctccctggctgggc[A/G]aacgtgtggaagttga	A	G	NM_144611 // downstream // 5234 // Hs.513871 // MGC32124 // 124936 // Homo sapiens hypothetical protein MGC32124 (MGC32124), mRNA. /// NM_020740 // downstream // 978 // Hs.513875 // ANKFY1 // 51479 // Homo sapiens ankyrin repeat and FYVE domain containing	MGC32124	MGC32124, Homo sapiens hypothetical protein MGC32124 (MGC32124), p13.2
SNP_A-2313225	ggagaattacctcaac[C/T]gtctcttgaccatgtc	C	T	NM_002663 // CDS // 0 // Hs.104519 // PLD2 // 5338 // Homo sapiens phospholipase D2 (PLD2), mRNA. /// ENST00000263088 // CDS // 0 // --- // --- // --- // ---	PLD2	PLD2, Homo sapiens phospholipase D2 (PLD2), p13.2
SNP_A-2128078	ataagcatggtgggtt[A/G]aacatggaggcccatt	A	G	NM_014922 // upstream // 113585 // Hs.513902 // NALP1 // 22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 113585 // Hs.513902 // NALP1 // 22861 // Homo sapiens NACHT, l	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-2068822	acaatcacagggcgtg[C/G]aaacctaaagtcaagg	C	G	NM_014922 // upstream // 275979 // Hs.513902 // NALP1 // 22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 275979 // Hs.513902 // NALP1 // 22861 // Homo sapiens NACHT, l	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-1835133	catgggagagcaccac[A/G]gattctgcaaagtggt	A	G	NM_014922 // upstream // 377292 // Hs.513902 // NALP1 // 22861 // Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, mRNA. /// NM_033006 // upstream // 377292 // Hs.513902 // NALP1 // 22861 // Homo sapiens NACHT, l	NALP1	NALP1, Homo sapiens NACHT, leucine rich repeat and PYD containing 1 (NALP1), transcript variant 2, p13.2
SNP_A-2296886	gccaagcctctccaaa[A/G]tctccggagctcttcc	A	G	NM_014336 // downstream // 289131 // Hs.279887 // AIPL1 // 23746 // Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA. /// ENST00000317744 // downstream // 14151 // --- // --- // --- // --- /// ENST00000356513 // downstream /	AIPL1	AIPL1, Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), p13.2
SNP_A-1686614	aatgaaaatcccagaggtatgcagg[C/T]ttcaggcacagtttga tccagtagt	C	T	NM_014922 // upstream // 377716 // Hs.511937 // NALP1 // 22861 // NACHT, leucine rich repeat and PYD containing 1 /// NM_021730 // upstream // 461210 // - // - // - // - /// NM_033004 // upstream // 378238 // Hs.511937 // NALP1 // 22861 // NACHT, leucine	NALP1	NALP1 , rs723656, NACHT, leucine rich repeat and PYD containing 1 ,p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2242315	ctgcacactcatatgc[A/G]cacacacatattggac	A	G	NM_014336 // downstream // 191063 // Hs.279887 // AIPL1 // 23746 // Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA. /// ENST00000317744 // downstream // 112219 // --- // --- // --- /// ENST00000356513 // downstream	AIPL1	AIPL1, Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), p13.2
SNP_A-1864711	tccagccctgctgaca[A/G]attggtctttggtgaa	A	G	NM_014336 // downstream // 169015 // Hs.279887 // AIPL1 // 23746 // Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA. /// ENST00000317744 // downstream // 134267 // --- // --- // --- /// ENST00000356513 // downstream	AIPL1	AIPL1, Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), p13.2
SNP_A-2262707	gaaattgcctgagtaa[C/G]tgctgacttgctgaac	C	G	NM_014336 // downstream // 167147 // Hs.279887 // AIPL1 // 23746 // Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA. /// ENST00000317744 // downstream // 136135 // --- // --- // --- /// ENST00000356513 // downstream	AIPL1	AIPL1, Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), p13.2
SNP_A-2314844	ggagtggaaagtgtaa[C/G]agagggatgtctggtc	C	G	NM_014336 // downstream // 165876 // Hs.279887 // AIPL1 // 23746 // Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA. /// ENST00000317744 // downstream // 137406 // --- // --- // --- /// ENST00000356513 // downstream	AIPL1	AIPL1, Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), p13.2
SNP_A-1835574	gcccagaggacacata[C/T]cattttcttctgttcc	C	T	NM_031220 // intron // 0 // Hs.183983 // PITPNM3 // 83394 // Homo sapiens PITPNM family member 3 (PITPNM3), mRNA. /// ENST00000262483 // intron // 0 // --- // --- // --- // ---	PITPNM3	PITPNM3, Homo sapiens PITPNM family member 3 (PITPNM3), p13.2
SNP_A-1785276	ggctagatagtgacca[A/G]cagcgtgaatgaagcc	A	G	NM_053285 // intron // 0 // Hs.462108 // TEKT1 // 83659 // Homo sapiens tektin 1 (TEKT1), mRNA. /// ENST00000338694 // intron // 0 // --- // --- // --- // ---	TEKT1	TEKT1, Homo sapiens tektin 1 (TEKT1), p13.1
SNP_A-2194103	catgaccttacaaaaa[A/G]gattagagtaggtgag	A	G	NM_053285 // intron // 0 // Hs.462108 // TEKT1 // 83659 // Homo sapiens tektin 1 (TEKT1), mRNA. /// ENST00000338694 // intron // 0 // --- // --- // --- // ---	TEKT1	TEKT1, Homo sapiens tektin 1 (TEKT1), p13.1
SNP_A-1664416	tggtggaatgaattcggtggcctaa[A/G]tgtaccttcctcaaatgc cacggct	A	G	NM_016060 // upstream // 3631 // Hs.43566 // CGI-125 // 51003 // CGI-125 protein /// NM_177550 // downstream // 29484 // Hs.399496 // SLC13A5 // 284111 // solute carrier family 13 (sodium-dependent citrate transporter), member 5	CGI-125	CGI-125 , rs10491083, CGI-125 protein ,p13.1
SNP_A-2301920	gcgtaatcctattccc[A/G]gacagaattacaagtg	A	G	NM_000697 // intron // 0 // Hs.422967 // ALOX12 // 239 // Homo sapiens arachidonate 12-lipoxygenase (ALOX12), mRNA. /// ENST00000251535 // intron // 0 // --- // --- // --- // ---	ALOX12	ALOX12, Homo sapiens arachidonate 12-lipoxygenase (ALOX12), p13.1
SNP_A-2130977	atagaaccagcttcta[A/G]gttcaggaaggaaacc	A	G	NM_153357 // upstream // 15030 // Hs.336564 // SLC16A11 // 162515 // Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 11 (SLC16A11), mRNA. /// NM_006344 // downstream // 15585 // Hs.54403 // CLEC10A // 10462 // Homo sapiens	SLC16A11	SLC16A11, Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 11 (SLC16A11), p13.1
SNP_A-2293252	gcagaggaagcttcta[C/T]gcgctagagaggatca	C	T	NM_003985 // 3UTR // 0 // Hs.203420 // TNK1 // 8711 // Homo sapiens tyrosine kinase, non-receptor, 1 (TNK1), mRNA. /// ENST00000311668 // 3UTR // 0 // --- // --- // --- // --- /// ENST00000360316 // 3UTR // 0 // --- // --- // --- // ---	TNK1	TNK1, Homo sapiens tyrosine kinase, non-receptor, 1 (TNK1), p13.1
SNP_A-2168155	caactcggggaaacca[G/T]caaggagtggggatat	G	T	NM_175734 // downstream // 5171 // Hs.380704 // LOC201243 // 201243 // Homo sapiens hypothetical protein LOC201243 (LOC201243), mRNA. /// NM_178518 // upstream // 2707 // Hs.355497 // FLJ36878 // 284114 // Homo sapiens hypothetical protein FLJ36878 (FLJ36	LOC201243	LOC201243, Homo sapiens hypothetical protein LOC201243 (LOC201243), p13.1
SNP_A-2294500	gcagtattgatgaaga[C/G]agtatgggatctgtga	C	G	NM_000747 // intron // 0 // Hs.330386 // CHRNB1 // 1140 // Homo sapiens cholinergic receptor, nicotinic, beta polypeptide 1 (muscle) (CHRNB1), mRNA. /// ENST00000306071 // intron // 0 // --- // --- // --- // ---	CHRNB1	CHRNB1, Homo sapiens cholinergic receptor, nicotinic, beta polypeptide 1 (muscle) (CHRNB1), p13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1836151	gagggaatggtaaaga[C/T]gccagagctcctcagc	C	T	NM_020899 // intron // 0 // Hs.35096 // ZBTB4 // 57659 // Homo sapiens zinc finger and BTB domain containing 4 (ZBTB4), mRNA. /// ENST00000311403 // intron // 0 // — // — // — // —	ZBTB4	ZBTB4, Homo sapiens zinc finger and BTB domain containing 4 (ZBTB4), p13.1
SNP_A-1906353	tggtgcagctgcgcta[C/T]ggcgaagacggcctgg	C	T	NM_000937 // CDS // 0 // Hs.270017 // POLR2A // 5430 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA. /// ENST00000322644 // CDS // 0 // — // — // — // —	POLR2A	POLR2A, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), p13.1
SNP_A-2265993	gaaggatgctgaaagg[C/T]aagctctagtgcaaga	C	T	NM_000937 // intron // 0 // Hs.270017 // POLR2A // 5430 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA. /// ENST00000322644 // intron // 0 // — // — // — // —	POLR2A	POLR2A, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), p13.1
SNP_A-2199580	ccaaaaatagaaaaat[G/T]aagtgtggtgctacat	G	T	NM_000937 // intron // 0 // Hs.270017 // POLR2A // 5430 // Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA. /// ENST00000322644 // intron // 0 // — // — // — // —	POLR2A	POLR2A, Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), p13.1
SNP_A-1836389	gccctccacatagtca[C/T]gtcagggagctttagg	C	T	NM_030808 // upstream // 41711 // Hs.372123 // NDEL1 // 81565 // Homo sapiens nudE nuclear distribution gene E homolog like 1 (A. nidulans) (NDEL1), mRNA. /// NM_005964 // downstream // 80064 // Hs.16355 // MYH10 // 4628 // Homo sapiens myosin, heavy poly	NDEL1	NDEL1, Homo sapiens nudE nuclear distribution gene E homolog like 1 (A. nidulans) (NDEL1), p13.1
SNP_A-2056328	aatactgttaagaaca[A/G]aacagagagaccactg	A	G	NM_005964 // intron // 0 // Hs.16355 // MYH10 // 4628 // Homo sapiens myosin, heavy polypeptide 10, non-muscle (MYH10), mRNA. /// ENST00000269243 // intron // 0 // — // — // — // —	MYH10	MYH10, Homo sapiens myosin, heavy polypeptide 10, non-muscle (MYH10), p13.1
SNP_A-2178502	cactcctgtcgaagcc[C/T]acgtgtatcatcacca	C	T	NM_030808 // downstream // 191516 // Hs.372123 // NDEL1 // 81565 // Homo sapiens nudE nuclear distribution gene E homolog like 1 (A. nidulans) (NDEL1), mRNA. /// NM_005964 // upstream // 28960 // Hs.16355 // MYH10 // 4628 // Homo sapiens myosin, heavy pol	NDEL1	NDEL1, Homo sapiens nudE nuclear distribution gene E homolog like 1 (A. nidulans) (NDEL1), p13.1
SNP_A-1805874	gtccctgcgcttaacc[A/G]ctaatctctgctgctc	A	G	NM_014308 // downstream // 6570 // Hs.278901 // PIK3R5 // 23533 // Homo sapiens phosphoinositide-3-kinase, regulatory subunit 5, p101 (PIK3R5), mRNA. /// ENST00000311434 // upstream // 5845 // — // — // — // — /// ENST00000269300 // downstream //	PIK3R5	PIK3R5, Homo sapiens phosphoinositide-3-kinase, regulatory subunit 5, p101 (PIK3R5), p13.1
SNP_A-1681554	tcttgtcttactgcattggatagaa[C/T]gtcaaagtaatggtatatat aataa	C	T	NM_004822 // intron // 0 // Hs.309918 // NTN1 // 9423 // netrin 1	NTN1	NTN1 , rs8076457, netrin 1,p13.1
SNP_A-1837079	actgttggctcacaga[A/C]agagtggagttctgag	A	C	NM_004853 // intron // 0 // Hs.431109 // STX8 // 9482 // Homo sapiens syntaxin 8 (STX8), mRNA. /// ENST00000306357 // intron // 0 // — // — // — // —	STX8	STX8, Homo sapiens syntaxin 8 (STX8), p13.1
SNP_A-1919100	ttaactctgtacgaga[A/G]caagagcttactatga	A	G	NM_004246 // intron // 0 // Hs.248202 // GLP2R // 9340 // Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA. /// ENST00000262441 // intron // 0 // — // — // — // —	GLP2R	GLP2R, Homo sapiens glucagon-like peptide 2 receptor (GLP2R), p13.1
SNP_A-1801157	gtagcctcagggaacc[C/T]agattaaaggggagag	C	T	NM_003644 // intron // 0 // Hs.462214 // GAS7 // 8522 // Homo sapiens growth arrest-specific 7 (GAS7), transcript variant a, mRNA. /// NM_201432 // intron // 0 // Hs.462214 // GAS7 // 8522 // Homo sapiens growth arrest-specific 7 (GAS7), transcript varian	GAS7	GAS7, Homo sapiens growth arrest-specific 7 (GAS7), transcript variant a, p13.1
SNP_A-2283409	gatacccaccgagcta[C/T]atctcccaatgtcagt	C	T	NM_207386 // upstream // 250439 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000342036 // upstream // 187277 // — // — // — // — /// ENST00000343478 // upstream // 250439 // — // — // — // -	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-2040568	aaccatcgcagtatga[A/G]gctcatcattccaaac	A	G	NM_207386 // upstream // 249782 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000342036 // upstream // 187934 // — // — // — // — /// ENST00000343478 // upstream // 249782 // — // — // — // -	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1863318	tcattttacttgcaca[C/G]agaggaccttagtctt	C	G	NM_207386 // upstream // 139979 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000342036 // upstream // 297737 // — // — // — // — /// ENST00000343478 // upstream // 139979 // — // — // — // -	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-1644366	gagaactgtgtgcctggctgcgcat[A/G]agattgtgggattatca agaaaagt	A	G	NM_020233 // downstream // 283912 // Hs.47668 // MDS006 // 56985 // x 006 protein /// NM_175903 // upstream // 566621 // Hs.30875 // LOC284033 // 284033 // hypothetical protein LOC284033	MDS006	MDS006 , rs758112, x 006 protein .p12
SNP_A-2240695	ctgactctgcaccata[A/C]atgtcaaacaccaggt	A	C	NM_207386 // intron // 0 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000343478 // intron // 0 // — // — // — // —	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-1835339	tacctcaataaatgcc[C/G]agatatcttcttaaag	C	G	NM_207386 // intron // 0 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000343478 // intron // 0 // — // — // — // —	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-1783642	ggcatgtagatggaca[A/G]tataggcagtgcagtg	A	G	NM_207386 // intron // 0 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000343478 // intron // 0 // — // — // — // —	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-2161127	atttgaacatctacgg[C/T]caaacctcaatccttc	C	T	NM_207386 // intron // 0 // Hs.441035 // FLJ45455 // 388336 // Homo sapiens FLJ45455 protein (FLJ45455), mRNA. /// ENST00000343478 // intron // 0 // — // — // — // —	FLJ45455	FLJ45455, Homo sapiens FLJ45455 protein (FLJ45455), p12
SNP_A-1865253	tccatatagtcatcca[A/G]ctctttctgatatgaa	A	G	NM_004662 // intron // 0 // Hs.526552 // DNAH9 // 1770 // Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, mRNA. /// NM_001372 // intron // 0 // Hs.526552 // DNAH9 // 1770 // Homo sapiens dynein, axonemal, heavy polypeptid	DNAH9	DNAH9, Homo sapiens dynein, axonemal, heavy polypeptide 9 (DNAH9), transcript variant 1, p12
SNP_A-1751577	gactttgtgttctgtggattcccta[C/T]attgctaacctctcccttacc acct	C	T	NM_001372 // intron // 0 // Hs.409174 // DNAH9 // 1770 // dynein, axonemal, heavy polypeptide 9	DNAH9	DNAH9 , rs10521189, dynein, axonemal, heavy polypeptide 9,p12
SNP_A-1653452	ctgaatccgtatcttctctatcctc[A/G]ctaccactggttttgccttctt ttg	A	G	NM_001372 // intron // 0 // Hs.409174 // DNAH9 // 1770 // dynein, axonemal, heavy polypeptide 9	DNAH9	DNAH9 , rs10521190, dynein, axonemal, heavy polypeptide 9,p12
SNP_A-1693218	aaagtaagtaacagcatgagaatga[C/T]gtgccattaaatacta ctattggac	C	T	NM_001372 // intron // 0 // Hs.409174 // DNAH9 // 1770 // dynein, axonemal, heavy polypeptide 9	DNAH9	DNAH9 , rs10521191, dynein, axonemal, heavy polypeptide 9,p12
SNP_A-2146686	atgctgtttggataaa[C/T]catcatccaagtttga	C	T	NM_003010 // intron // 0 // Hs.514681 // MAP2K4 // 6416 // Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /// ENST00000353533 // intron // 0 // — // — // — // —	MAP2K4	MAP2K4, Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), p12
SNP_A-1839297	aaatggctggctattc[A/G]ctatattttgcagaac	A	G	NM_003010 // downstream // 136852 // Hs.514681 // MAP2K4 // 6416 // Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /// ENST00000353533 // downstream // 136852 // — // — // — // — /// ENST00000313495 // upstream // 269287 //	MAP2K4	MAP2K4, Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), p12
SNP_A-2102034	agatgtatgccacatc[A/G]aagtgtcttgcttaca	A	G	NM_003010 // downstream // 143010 // Hs.514681 // MAP2K4 // 6416 // Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /// ENST00000353533 // downstream // 143010 // — // — // — // — /// ENST00000313495 // upstream // 263129 //	MAP2K4	MAP2K4, Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), p12
SNP_A-2250822	cttatcgtcagacacc[A/G]cattatggaaatctac	A	G	ENST00000313495 // intron // 0 // — // — // — // —	-	p12
SNP_A-2253906	cttgacacatacgggg[C/T]agagctatttcatcac	C	T	ENST00000313495 // intron // 0 // — // — // — // —	-	p12
SNP_A-2111477	aggaggcgcattttca[C/T]attctacttcatggtt	C	T	NM_153604 // intron // 0 // Hs.462257 // MYOCD // 93649 // Homo sapiens myocardin (MYOCD), mRNA. /// ENST00000356106 // intron // 0 // — // — // — // — /// ENST00000343344 // intron // 0 // — // — // — // —	MYOCD	MYOCD, Homo sapiens myocardin (MYOCD), p12
SNP_A-1653568	catgagattacaatatttcttgtaa[A/G]agttcttaatgttatgttcaa agga	A	G	NM_153604 // intron // 0 // Hs.42128 // MYOCD // 93649 // myocardin	MYOCD	MYOCD , rs10491101, myocardin,p12
SNP_A-2060705	aatgagcttaaaacaa[C/T]gtcaagtctctaataa	C	T	NM_014859 // intron // 0 // Hs.499758 // KIAA0672 // 9912 // Homo sapiens KIAA0672 gene product (KIAA0672), mRNA. /// ENST00000340825 // intron // 0 // — // — // — // — /// ENST00000262444 // intron // 0 // — // — // — // —	KIAA0672	KIAA0672, Homo sapiens KIAA0672 gene product (KIAA0672), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1688808	cagtatacaacaagcagaagtttgcd[C/T]cttgaaaaactgtagt gtagttagt	C	T	NM_153604 // intron // 0 // Hs.42128 // MYOCD // 93649 // myocardin	MYOCD	MYOCD, rs10521197, myocardin,p12
SNP_A-1870147	tccttaactcacaca[A/G]caaagcggtaagtgat	A	G	NM_018127 // upstream // 110422 // Hs.434232 // ELAC2 // 60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 367260 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferas	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-2257415	cttgaatgttggaa[A/G]gatttgttctggct	A	G	NM_018127 // upstream // 113574 // Hs.434232 // ELAC2 // 60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 364108 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferas	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-2146955	atggaaaggcttaaat[C/T]actctcaaataaaaa	C	T	NM_018127 // upstream // 203725 // Hs.434232 // ELAC2 // 60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 273957 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferas	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-1937280	ttgaaacctgtggcag[A/G]atgtgttaggaccgtt	A	G	NM_018127 // upstream // 239324 // Hs.434232 // ELAC2 // 60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 238358 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferas	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-1789279	gggcatttgctgtgcgc[A/G]ctgagtgaatagttct	A	G	NM_018127 // upstream // 439150 // Hs.434232 // ELAC2 // 60528 // Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA. /// NM_006042 // downstream // 38532 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase	ELAC2	ELAC2, Homo sapiens elaC homolog 2 (E. coli) (ELAC2), p12
SNP_A-2228787	ctagagatgaggacaa[C/T]ttacatgctccctctc	C	T	NM_006042 // intron // 0 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// ENST00000284110 // intron // 0 // — // — // — // -	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12
SNP_A-2137989	atcatttttactaccg[C/G]attggcatgatttat	C	G	NM_006042 // upstream // 52148 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// NM_001303 // upstream // 415327 // Hs.462278 // COX10 // 1352 // Homo sapiens COX10 homolog, cytoc	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12
SNP_A-2043217	aactgccctaacgggg[C/T]gccagaatcccagac	C	T	NM_006042 // upstream // 320846 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// NM_001303 // upstream // 146629 // Hs.462278 // COX10 // 1352 // Homo sapiens COX10 homolog, cyto	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12
SNP_A-2273972	gactgtgcttagaagg[A/G]ccttaataaataacat	A	G	NM_006042 // upstream // 344378 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// NM_001303 // upstream // 123097 // Hs.462278 // COX10 // 1352 // Homo sapiens COX10 homolog, cyto	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12
SNP_A-1954408	tttgcatctaagcctac[C/T]gttgatgggatcaatg	C	T	NM_006042 // upstream // 375173 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// NM_001303 // upstream // 92302 // Hs.462278 // COX10 // 1352 // Homo sapiens COX10 homolog, cytoc	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12
SNP_A-1957268	ttttagaaacgcttccg[A/G]ctctgttaagatttaa	A	G	NM_006042 // upstream // 387347 // Hs.462270 // HS3ST3A1 // 9955 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA. /// NM_001303 // upstream // 80128 // Hs.462278 // COX10 // 1352 // Homo sapiens COX10 homolog, cytoc	HS3ST3A1	HS3ST3A1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1840919	aggttcggataaagat[C/T]acaggaagatgagcag	C	T	NM_001303 // intron // 0 // Hs.462278 // COX10 // 1352 // Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene enc /// ENST00000261843 // intron // 0 // — // — // —	COX10	COX10, Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene enc p12
SNP_A-1841026	cactcattgcccctgc[A/G]gaatccacacacccc	A	G	NM_006041 // intron // 0 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// ENST00000245519 // intron // 0 // — // — // — /// ENST00000360954 // intron // 0 // — // -	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-1895159	tgcccagctagggat[A/G]actttcaggtgtgacc	A	G	NM_006041 // downstream // 44607 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 44349 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-2165450	caaagcactgtgcatg[A/G]attaactccttaatc	A	G	NM_006041 // downstream // 70912 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 70654 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-1838914	tagagaaattgaggccc[A/G]gattgcattcttcaaa	A	G	NM_006041 // downstream // 89022 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 88764 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-1958023	ttttcactgaaaataa[A/G]gttactaagagttac	A	G	NM_006041 // downstream // 178430 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), mRNA. /// NM_006041 // downstream // 178172 // Hs.48384 // HS3ST3B1 // 9953 // Homo sapiens heparan sulfat	HS3ST3B1	HS3ST3B1, Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), p12
SNP_A-2193863	catgaaataaggtggat[C/T]ctgtgtagccaacagg	C	T	NM_000304 // downstream // 452997 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 // downstream // 452997 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-1828874	taaggaggacttagca[C/T]gaggctgctttctctg	C	T	NM_000304 // downstream // 116798 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 // downstream // 116798 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2092801	agaaaatgttcaata[C/T]acaacattagagaat	C	T	NM_000304 // downstream // 38917 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 // downstream // 38917 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein 2	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2166416	caaatgactatttcta[C/T]gtgtagaccccagggc	C	T	NM_000304 // downstream // 16078 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA. /// NM_153321 // downstream // 16078 // Hs.372031 // PMP22 // 5376 // Homo sapiens peripheral myelin protein 2	PMP22	PMP22, Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, p12
SNP_A-2283145	gataaatatccaacctat[C/T]cggcaactttcgactt	C	T	NM_031898 // upstream // 63784 // Hs.414648 // TEKT3 // 64518 // Homo sapiens tektin 3 (TEKT3), mRNA. /// NM_173622 // downstream // 32407 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000003386	TEKT3	TEKT3, Homo sapiens tektin 3 (TEKT3), p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2071387	acactttccagtgga[C/T]gtgaaatgtatgata	C	T	NM_031898 // upstream // 63945 // Hs.414648 // TEKT3 // 64518 // Homo sapiens tektin 3 (TEKT3), mRNA. /// NM_173622 // downstream // 32246 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000033869	TEKT3	TEKT3, Homo sapiens tektin 3 (TEKT3), p12
SNP_A-2249125	ctgttgcaagggcta[A/C]agactagaaacaatct	A	C	NM_031898 // upstream // 79769 // Hs.414648 // TEKT3 // 64518 // Homo sapiens tektin 3 (TEKT3), mRNA. /// NM_173622 // downstream // 16422 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000033869	TEKT3	TEKT3, Homo sapiens tektin 3 (TEKT3), p12
SNP_A-2117630	aggttatatttgggaa[A/G]gtatggattacagaga	A	G	NM_031898 // upstream // 94384 // Hs.414648 // TEKT3 // 64518 // Homo sapiens tektin 3 (TEKT3), mRNA. /// NM_173622 // downstream // 1807 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000033869	TEKT3	TEKT3, Homo sapiens tektin 3 (TEKT3), p12
SNP_A-1788024	gggagacatagccggaa[A/G]gtttagtcactgtgc	A	G	NM_173622 // intron // 0 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000312177 // intron // 0 // — // — // —	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-1877504	tctggcagagtccaaa[C/T]tcaaacgcctggagca	C	T	NM_173622 // intron // 0 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// ENST00000312177 // intron // 0 // — // — // —	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-2042233	aactatagtccgatac[A/G]gtataagtgtgtcaaa	A	G	NM_173622 // upstream // 6448 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// NM_145301 // downstream // 28206 // Hs.528884 // LOC201158 // 201158 // Homo sapiens similar to CGI-148 protein (LOC201158	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-2156450	attctccttggcaagc[C/T]aggctcatccacttac	C	T	NM_173622 // upstream // 12745 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// NM_145301 // downstream // 21909 // Hs.528884 // LOC201158 // 201158 // Homo sapiens similar to CGI-148 protein (LOC20115	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-1944177	ttgtcatacatcatggt[C/T]atagctttgcagtt	C	T	NM_173622 // upstream // 19057 // Hs.164595 // FLJ36674 // 284040 // Homo sapiens hypothetical protein FLJ36674 (FLJ36674), mRNA. /// NM_145301 // downstream // 15597 // Hs.528884 // LOC201158 // 201158 // Homo sapiens similar to CGI-148 protein (LOC20115	FLJ36674	FLJ36674, Homo sapiens hypothetical protein FLJ36674 (FLJ36674), p12
SNP_A-1944606	ttgtgaaggaaatcta[A/G]ggacttggtaacgga	A	G	NM_145301 // intron // 0 // Hs.528884 // LOC201158 // 201158 // Homo sapiens similar to CGI-148 protein (LOC201158), mRNA. /// ENST00000225576 // intron // 0 // — // — // — // —	LOC201158	LOC201158, Homo sapiens similar to CGI-148 protein (LOC201158), p12
SNP_A-1723088	ttacacttgctgttgataaactcga[C/T]aactgtcctgtttaggtct cacc	C	T	NM_031898 // upstream // 92182 // Hs.414648 // TEKT3 // 64518 // tektin 3 /// NM_173622 // downstream // 2257 // Hs.164595 // FLJ36674 // 284040 // hypothetical protein FLJ36674	TEKT3	TEKT3, rs2954750, tektin 3 ,p12
SNP_A-1842652	atttctgattttacs[G/T]attgcaaacctagat	G	T	NM_020652 // downstream // 29792 // Hs.333150 // ZNF286 // 57335 // Homo sapiens zinc finger protein 286 (ZNF286), mRNA. /// NM_178571 // downstream // 30116 // Hs.513965 // MGC51025 // 353149 // Homo sapiens hypothetical protein MGC51025 (MGC51025), mRNA	ZNF286	ZNF286, Homo sapiens zinc finger protein 286 (ZNF286), p12
SNP_A-1748133	ttgcggaggagccgtcattacaaca[A/G]tcggtctgagactag gagcaacg		G	BC053514 // intron // 0 // Hs.241305 // TRIM16 // 10626 // tripartite motif-containing 16	TRIM16	TRIM16 , rs10521309, tripartite motif-containing 16,p12
SNP_A-1722556	tactcaggctaaaagtcagtaaaaa[C/T]acataaactcacttgtg ccattacc	C	T	NM_000676 // upstream // 168630 // Hs.45743 // ADORA2B // 136 // adenosine A2b receptor /// NM_020652 // downstream // 58363 // Hs.333150 // ZNF286 // 57335 // zinc finger protein 286 /// NM_178571 // downstream // 31835 // Hs.382193 // MGC51025 // 35314	ADORA2B	ADORA2B , rs2324027, adenosine A2b receptor p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1731341	aataatataaaagagtaagaatgaca[A/G]ctaactatcagtcag gagaggttag	A	G	AK093015 // upstream // 30530 // Hs.25425 // FLJ35696 // 388341 // FLJ35696 protein /// NM_020653 // downstream // 29017 // Hs.99724 // ZNF287 // 57336 // zinc finger protein 287 /// NM_152350 // downstream // 80356 // Hs.270232 // MGC40157 // 125144 //	FLJ35696	FLJ35696 , rs7218218, FLJ35696 protein ,p11.2
SNP_A-1865299	tccatcaaggaacctc[C/T]agtgttgcaggcaaga	C	T	ENST00000304654 // intron // 0 // — // — // — // —	-	p11.2
SNP_A-2252808	cttctacgaatgtcta[C/G]aggaacaaagggaaac	C	G	NM_182568 // downstream // 283528 // Hs.448012 // FLJ36492 // 284047 // Homo sapiens hypothetical protein FLJ36492 (FLJ36492), mRNA. /// NM_001004306 // downstream // 339632 // Hs.220574 // MGC87631 // 339184 // Homo sapiens similar to hypothetical protei	FLJ36492	FLJ36492, Homo sapiens hypothetical protein FLJ36492 (FLJ36492), p11.2
SNP_A-2089623	acttcatacctgtcag[C/G]atggctagaattaaaa	C	G	NM_182568 // downstream // 283791 // Hs.448012 // FLJ36492 // 284047 // Homo sapiens hypothetical protein FLJ36492 (FLJ36492), mRNA. /// NM_001004306 // downstream // 339895 // Hs.220574 // MGC87631 // 339184 // Homo sapiens similar to hypothetical protei	FLJ36492	FLJ36492, Homo sapiens hypothetical protein FLJ36492 (FLJ36492), p11.2
SNP_A-2261313	gaaagcacagatacca[A/G]taatgttcaacaattc	A	G	NM_003653 // downstream // 7245 // Hs.6076 // COPS3 // 8533 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) (COPS3), mRNA. /// ENST00000330153 // upstream // 3649 // — // — // — // — /// ENST00000268717 // downst	COPS3	COPS3, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) (COPS3), p11.2
SNP_A-1824374	taaacggactgtgagc[C/T]gatgagtagcatttac	C	T	NM_003653 // downstream // 3922 // Hs.6076 // COPS3 // 8533 // Homo sapiens COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) (COPS3), mRNA. /// ENST00000330153 // upstream // 6972 // — // — // — // — /// ENST00000268717 // downst	COPS3	COPS3, Homo sapiens COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) (COPS3), p11.2
SNP_A-2175123	cacagtgcaagacatc[A/G]agacctcgagtttagc	A	G	NM_018019 // upstream // 720 // Hs.244595 // MED9 // 55090 // Homo sapiens mediator subunit 25 (MED25), mRNA. /// ENST00000328591 // upstream // 92254 // — // — // — // — /// ENST00000268711 // upstream // 720 // — // — // — // —	MED9	MED9, Homo sapiens mediator subunit 25 (MED25), p11.2
SNP_A-2173899	cacacaggaaattttg[A/G]aagggacacatggcag	A	G	NM_016084 // upstream // 4167 // Hs.25829 // RASD1 // 51655 // Homo sapiens RAS, dexamethasone-induced 1 (RASD1), mRNA. /// NM_007169 // downstream // 5005 // Hs.287717 // PEMT // 10400 // Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT),	RASD1	RASD1, Homo sapiens RAS, dexamethasone-induced 1 (RASD1), p11.2
SNP_A-1902670	tggctaagcctctgcc[A/G]actacactggcttcta	A	G	NM_016084 // upstream // 4817 // Hs.25829 // RASD1 // 51655 // Homo sapiens RAS, dexamethasone-induced 1 (RASD1), mRNA. /// NM_007169 // downstream // 4355 // Hs.287717 // PEMT // 10400 // Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT),	RASD1	RASD1, Homo sapiens RAS, dexamethasone-induced 1 (RASD1), p11.2
SNP_A-1843751	caagtgcatatatgaa[C/T]aggcggctctccgagg	C	T	NM_007169 // intron // 0 // Hs.287717 // PEMT // 10400 // Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT), nuclear gene encoding mitochondrial protein, transcript varian /// NM_148173 // intron // 0 // Hs.287717 // PEMT // 10400 // Homo s	PEMT	PEMT, Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT), nuclear gene encoding mitochondrial protein, transcript varian ,p11.2
SNP_A-2187008	caggtacccagcaaac[C/T]ggatgctcagccaagg	C	T	NM_007169 // intron // 0 // Hs.287717 // PEMT // 10400 // Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT), nuclear gene encoding mitochondrial protein, transcript varian /// NM_148173 // intron // 0 // Hs.287717 // PEMT // 10400 // Homo s	PEMT	PEMT, Homo sapiens phosphatidylethanolamine N-methyltransferase (PEMT), nuclear gene encoding mitochondrial protein, transcript varian p11.2
SNP_A-2259966	gaaaagtgaatactgc[C/T]cggagctccggagaca	C	T	NM_031294 // intron // 0 // Hs.528889 // DKFZP586M1120 // 83450 // Homo sapiens hypothetical protein DKFZp586M1120 (DKFZP586M1120), mRNA. /// NM_144678 // intron // 0 // Hs.462379 // TOM1L2 // 146691 // Homo sapiens target of myb1-like 2 (chicken) (TOM1L2	DKFZP586M1120	DKFZP586M1120, Homo sapiens hypothetical protein DKFZp586M1120 (DKFZP586M1120), p11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2144058	atgaggaaggctgcag[A/G]cagagcaaattgagga	A	G	NM_016239 // intron // 0 // Hs.462390 // MYO15A // 51168 // Homo sapiens myosin XVA (MYO15A), mRNA. /// ENST00000205890 // intron // 0 // — // — // —	MYO15A	MYO15A, Homo sapiens myosin XVA (MYO15A), p11.2
SNP_A-2005103	attgatgtttacgtg[A/C]acataacctgaatctt	A	C	ENST00000348256 // downstream // 497 // — // — // — /// ENST00000339799 // downstream // 497 // — // — // — // — /// ENST00000338234 // downstream // 11710 // — // — // — // — /// ENST00000340898 // downstream // 16247 // —	-	p11.2
SNP_A-1866779	tcccgactctgtttca[C/T]cagtcgctccccagg	C	T	NM_002756 // intron // 0 // Hs.514012 // MAP2K3 // 5606 // Homo sapiens mitogen-activated protein kinase kinase 3 (MAP2K3), transcript variant A, mRNA. /// NM_145109 // intron // 0 // Hs.514012 // MAP2K3 // 5606 // Homo sapiens mitogen-activated protein k	MAP2K3	MAP2K3, Homo sapiens mitogen-activated protein kinase kinase 3 (MAP2K3), transcript variant A, p11.2
SNP_A-2065148	aattgctttattgaag[C/T]atagttgtctaaggtt	C	T	NM_021012 // downstream // 67265 // Hs.2363 // KCNJ12 // 3768 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 12 (KCNJ12), mRNA. /// ENST00000331718 // downstream // 67265 // — // — // — /// ENST00000358213 // downs	KCNJ12	KCNJ12, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 12 (KCNJ12), p11.2
SNP_A-1926698	ttattgccttttctca[G/T]gttatttttgaaattta	G	T	NM_134265 // upstream // 32816 // Hs.446017 // WSB1 // 26118 // Homo sapiens WD repeat and SOCS box-containing 1 (WSB1), transcript variant 2, mRNA. /// NM_015626 // upstream // 32816 // Hs.446017 // WSB1 // 26118 // Homo sapiens WD repeat and SOCS box-co	WSB1	WSB1, Homo sapiens WD repeat and SOCS box-containing 1 (WSB1), transcript variant 2, q11.1
SNP_A-1846014	tcctgatggtcctcgc[A/C]acttctgagtcactcc	A	C	NM_134265 // downstream // 95473 // Hs.446017 // WSB1 // 26118 // Homo sapiens WD repeat and SOCS box-containing 1 (WSB1), transcript variant 2, mRNA. /// NM_015626 // downstream // 95473 // Hs.446017 // WSB1 // 26118 // Homo sapiens WD repeat and SOCS bo	WSB1	WSB1, Homo sapiens WD repeat and SOCS box-containing 1 (WSB1), transcript variant 2, q11.1
SNP_A-2304493	gctctattcagaaaggt[C/G]actgtgacatggccct	C	G	NM_000625 // upstream // 20729 // Hs.462525 // NOS2A // 4843 // Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, mRNA. /// NM_153292 // upstream // 20729 // Hs.462525 // NOS2A // 4843 // Homo sapiens nitric oxi	NOS2A	NOS2A, Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, q11.2
SNP_A-2261441	gaaaggaaaagaatca[C/G]tagttgcaaaagtca	C	G	NM_000625 // upstream // 36939 // Hs.462525 // NOS2A // 4843 // Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, mRNA. /// NM_153292 // upstream // 36939 // Hs.462525 // NOS2A // 4843 // Homo sapiens nitric oxi	NOS2A	NOS2A, Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), transcript variant 1, q11.2
SNP_A-2170055	caagggcctggtatga[C/T]gttgtggcaatctcat	C	T	NM_033198 // intron // 0 // Hs.462550 // PIGS // 94005 // Homo sapiens phosphatidylinositol glycan, class S (PIGS), mRNA. /// ENST00000268758 // intron // 0 // — // — // — /// ENST00000355715 // intron // 0 // — // — // — /// ENS	PIGS	PIGS, Homo sapiens phosphatidylinositol glycan, class S (PIGS), q11.2
SNP_A-1846058	tctcccaacactgaaa[C/T]gtgcctgcctggctt	C	T	NM_006461 // intron // 0 // Hs.514033 // SPAG5 // 10615 // Homo sapiens sperm associated antigen 5 (SPAG5), mRNA. /// ENST00000321765 // intron // 0 // — // — // —	SPAG5	SPAG5, Homo sapiens sperm associated antigen 5 (SPAG5), q11.2
SNP_A-2060669	aatgagatggtatttg[C/T]aaagtggttagtacac	C	T	NM_018182 // intron // 0 // Hs.232197 // FLJ10700 // 55731 // Homo sapiens hypothetical protein FLJ10700 (FLJ10700), mRNA. /// ENST00000341217 // intron // 0 // — // — // —	FLJ10700	FLJ10700, Homo sapiens hypothetical protein FLJ10700 (FLJ10700), q11.2
SNP_A-2262118	gaaatatttccatccc[A/C]aatagctaaactaaa	A	C	NM_020791 // intron // 0 // Hs.462606 // TAOK1 // 57551 // Homo sapiens TAO kinase 1 (TAOK1), mRNA. /// ENST00000261716 // intron // 0 // — // — // —	TAOK1	TAOK1, Homo sapiens TAO kinase 1 (TAOK1), q11.2
SNP_A-2248447	ctgtgttaggtcacgg[A/G]agaagtgagggtgaca	A	G	NM_001045 // intron // 0 // Hs.448453 // SLC6A4 // 6532 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), mRNA. /// ENST00000261707 // intron // 0 // — // — // — // —	SLC6A4	SLC6A4, Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2090611	actgttatcagcaca[A/G]gaaaatacaagaagt	A	G	NM_001045 // intron // 0 // Hs.448453 // SLC6A4 // 6532 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), mRNA. /// ENST00000261707 // intron // 0 // — // — // — // —	SLC6A4	SLC6A4, Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), q11.2
SNP_A-1795240	ggtgaggttatggaga[C/T]cgctcttgtcagaatt	C	T	NM_001045 // intron // 0 // Hs.448453 // SLC6A4 // 6532 // Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), mRNA. /// ENST00000261707 // intron // 0 // — // — // — // —	SLC6A4	SLC6A4, Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), q11.2
SNP_A-1736507	ttctctgagagtttcccaaattatt[C/T]gtcattggcagagcgccctc catgga	C	T	U43586 // intron // 0 // Hs.276238 // KSR // 8844 // kinase suppressor of ras	KSR	KSR, rs1382047, kinase suppressor of ras,q11.1
SNP_A-2261357	gaaagccaatcactga[C/G]acaccaagtattgcca	C	G	NM_032932 // downstream // 112274 // Hs.406788 // RAB11FIP4 // 84440 // Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), mRNA. /// NM_018405 // downstream // 204331 // Hs.462729 // HSA272196 // 55352 // Homo sapiens hypothetical pro	RAB11FIP4	RAB11FIP4, Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), q11.2
SNP_A-2265276	gaagcaatgcgccccc[C/T]aaccagtgtgatggag	C	T	NM_032932 // downstream // 259473 // Hs.406788 // RAB11FIP4 // 84440 // Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), mRNA. /// NM_018405 // downstream // 57132 // Hs.462729 // HSA272196 // 55352 // Homo sapiens hypothetical prot	RAB11FIP4	RAB11FIP4, Homo sapiens RAB11 family interacting protein 4 (class II) (RAB11FIP4), q11.2
SNP_A-1708643	taaatttcacctcagctaagatagc[C/T]cctccacctcctagaag gataatat	C	T	NM_020772 // upstream // 75294 // Hs.355608 // 182-FIP // 57532 // 82-kD FMRP Interacting Protein	182-FIP	182-FIP, rs1400790, 82-kD FMRP Interacting Protein,q11.2
SNP_A-1941496	ttgctttctcactcct[C/T]aaatactgcttcatct	C	T	NM_015194 // intron // 0 // Hs.462777 // MYO1D // 4642 // Homo sapiens myosin ID (MYO1D), mRNA. /// ENST00000318217 // intron // 0 // — // — // —	MYO1D	MYO1D, Homo sapiens myosin ID (MYO1D), q11.2
SNP_A-2193502	catctgggaatcagca[C/T]agctggccgagttta	C	T	NM_015194 // intron // 0 // Hs.462777 // MYO1D // 4642 // Homo sapiens myosin ID (MYO1D), mRNA. /// ENST00000318217 // intron // 0 // — // — // —	MYO1D	MYO1D, Homo sapiens myosin ID (MYO1D), q11.2
SNP_A-2192286	catcagtcttctaagct[A/T]aggagaacctttttaa	A	T	NM_015194 // intron // 0 // Hs.462777 // MYO1D // 4642 // Homo sapiens myosin ID (MYO1D), mRNA. /// ENST00000318217 // intron // 0 // — // — // — /// ENST00000355978 // intron // 0 // — // — // —	MYO1D	MYO1D, Homo sapiens myosin ID (MYO1D), q11.2
SNP_A-1892188	tgcaaatctctgtgaa[C/T]gttaccagctttaagt	C	T	NM_015194 // intron // 0 // Hs.462777 // MYO1D // 4642 // Homo sapiens myosin ID (MYO1D), mRNA. /// ENST00000318217 // intron // 0 // — // — // — /// ENST00000355978 // intron // 0 // — // — // —	MYO1D	MYO1D, Homo sapiens myosin ID (MYO1D), q11.2
SNP_A-2177444	caccttttcccaacctta[C/G]ccatagctcgaaagtc	C	G	NM_015194 // intron // 0 // Hs.462777 // MYO1D // 4642 // Homo sapiens myosin ID (MYO1D), mRNA. /// ENST00000318217 // intron // 0 // — // — // — /// ENST00000355978 // intron // 0 // — // — // —	MYO1D	MYO1D, Homo sapiens myosin ID (MYO1D), q11.2
SNP_A-2311754	ggaattgagaatgaccf[A/G]cagacttgactagctg	A	G	NM_183377 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, mRNA. /// NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensiti	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, q11.2
SNP_A-1847738	tctatgttcaaaccag[A/C]atcagagagaatagaa	A	C	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-2026942	aaacactgtggttaaa[G/T]aaagatttgagtcct	G	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2272305	gacctctgccttcaat[A/G]aacttaacaaccagtta	A	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-1903166	tggcttcattgctagaa[C/T]aactgagtgcttgctt	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-2213963	cctaacctcttttgta[C/T]ctcttcttgaagctatc	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-2131394	atagatgcagaatggat[C/T]taggtgtgcgataaat	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q11.2
SNP_A-1819036	gttgcatgtcaagata[A/G]tactgttaggaagtac	A	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1882698	tgaaactctgcagtca[C/T]tatctatgctgaaaga	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2273624	gactgaggcacagaca[A/G]ggaacacaatcgcctc	A	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2059386	aatctaagtagaggcc[A/C]cgatacctccacagct	A	C	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2178169	cactatctgttgaagg[C/T]cacactgtgcccaca	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1931045	ttccataaggaactgc[C/T]aaacttcttccaaag	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2227719	ctacatttatgggac[A/G]attggtacctggagtg	A	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-2299529	gccctttggcatctc[A/G]ctaatctgaatcctct	A	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1784058	ggccagctgtcagcac[C/T]gagatgggggtagtga	C	T	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1856626	tcacagtgtaaggtag[A/G]cattgacaatcttcct	A	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // — // — // —	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2005138	atttattcaatggaca[C/G]agaacaagtattaag	C	G	NM_001094 // intron // 0 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, mRNA. /// ENST00000359872 // intron // 0 // --- // --- // ---	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 2, q12
SNP_A-1939923	ttgcactaatggcttct[A/G]acataattgctagtag	A	G	NM_183377 // upstream // 876671 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, mRNA. /// NM_001094 // upstream // 13126 // Hs.368417 // ACCN1 // 40 // Homo sapiens amil	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, q12
SNP_A-1848744	acttgcttaggcccgal[C/T]taacatttgcactcac	C	T	NM_183377 // upstream // 881768 // Hs.368417 // ACCN1 // 40 // Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, mRNA. /// NM_001094 // upstream // 18223 // Hs.368417 // ACCN1 // 40 // Homo sapiens amil	ACCN1	ACCN1, Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), transcript variant 1, q12
SNP_A-1848955	tggagacatgtagaaa[G/T]gaaagtgagggcagg	G	T	NM_005408 // downstream // 582 // Hs.414629 // CCL13 // 6357 // Homo sapiens chemokine (C-C motif) ligand 13 (CCL13), mRNA. /// NM_002981 // downstream // 1189 // Hs.72918 // CCL1 // 6346 // Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), mRNA. /// EN	CCL13	CCL13, Homo sapiens chemokine (C-C motif) ligand 13 (CCL13), q12
SNP_A-2005141	ccccctgaattgctgcaa[A/T]ctctctttagccctca	A	T	NM_005408 // downstream // 1333 // Hs.414629 // CCL13 // 6357 // Homo sapiens chemokine (C-C motif) ligand 13 (CCL13), mRNA. /// NM_002981 // downstream // 438 // Hs.72918 // CCL1 // 6346 // Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), mRNA. /// EN	CCL13	CCL13, Homo sapiens chemokine (C-C motif) ligand 13 (CCL13), q12
SNP_A-1871557	tctaagatcaaccagal[G/T]agtaagagatagagtt	G	T	NM_002981 // intron // 0 // Hs.72918 // CCL1 // 6346 // Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), mRNA. /// ENST00000225842 // intron // 0 // --- // --- // ---	CCL1	CCL1, Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), q12
SNP_A-1849314	aaattaatttcaagct[A/G]agagtgcacaggtttg	A	G	NM_002981 // upstream // 149988 // Hs.72918 // CCL1 // 6346 // Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), mRNA. /// NM_207454 // downstream // 60902 // Hs.514090 // FLJ44815 // 400591 // Homo sapiens FLJ44815 protein (FLJ44815), mRNA. /// ENST000	CCL1	CCL1, Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), q12
SNP_A-1902406	tggccctgtacttcaa[C/T]atgaccacacttttaga	C	T	NM_207313 // downstream // 43984 // Hs.310482 // LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 // downstream // 244630 // Hs.73072 // CCT6B // 10693 // Homo sapiens chaperonin containing TCP1, subunit 6	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-2071556	acagaacttcaccaaa[C/T]ggacttctcaaagatc	C	T	NM_207313 // downstream // 57747 // Hs.310482 // LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 // downstream // 230867 // Hs.73072 // CCT6B // 10693 // Homo sapiens chaperonin containing TCP1, subunit 6	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-1849444	tatggattctctcaaa[C/G]accaagaaaagaaatg	C	G	NM_207313 // downstream // 62031 // Hs.310482 // LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 // downstream // 226583 // Hs.73072 // CCT6B // 10693 // Homo sapiens chaperonin containing TCP1, subunit 6	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-2053315	aagtgaatttgacaca[A/G]tccctccctcaaaga	A	G	NM_207313 // downstream // 63300 // Hs.310482 // LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 // downstream // 225314 // Hs.73072 // CCT6B // 10693 // Homo sapiens chaperonin containing TCP1, subunit 6	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2307488	gcttattgccttttcc[A/G]gaagtagggagcagca	A	G	NM_207313 // downstream // 63437 // Hs.310482 // LOC124842 // 124842 // Homo sapiens hypothetical protein LOC124842 (LOC124842), mRNA. /// BC027591 // downstream // 225177 // Hs.73072 // CCT6B // 10693 // Homo sapiens chaperonin containing TCP1, subunit 6	LOC124842	LOC124842, Homo sapiens hypothetical protein LOC124842 (LOC124842), q12
SNP_A-2115669	agggtattttaaagca[A/C]atcctaagcaacatat	A	C	NM_152462 // upstream // 29193 // Hs.514814 // AMAC1 // 146861 // Homo sapiens transmembrane protein 21A (TMEM21A), mRNA. /// NM_144975 // upstream // 19571 // Hs.546510 // MGC19764 // 162394 // Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA.	AMAC1	AMAC1, Homo sapiens transmembrane protein 21A (TMEM21A), q12
SNP_A-2307676	gcttccaacttcccta[C/T]gacaacacccttgaat	C	T	NM_144975 // intron // 0 // Hs.546510 // MGC19764 // 162394 // Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA. /// ENST00000299977 // intron // 0 // — // — // — // —	MGC19764	MGC19764, Homo sapiens hypothetical protein MGC19764 (MGC19764), q12
SNP_A-1860401	tcagtgggaaatgtaa[A/C]tatgggggagctcagg	A	C	NM_144975 // intron // 0 // Hs.546510 // MGC19764 // 162394 // Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA. /// ENST00000299977 // intron // 0 // — // — // — // —	MGC19764	MGC19764, Homo sapiens hypothetical protein MGC19764 (MGC19764), q12
SNP_A-1805692	gtcccactgtacccaa[G/T]ttctccctctctgaac	G	T	NM_144975 // downstream // 1434 // Hs.546510 // MGC19764 // 162394 // Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA. /// NM_152270 // downstream // 81490 // Hs.462829 // FLJ34922 // 91607 // Homo sapiens hypothetical protein FLJ34922 (FLJ349	MGC19764	MGC19764, Homo sapiens hypothetical protein MGC19764 (MGC19764), q12
SNP_A-2005146	gttggtggtcttgtta[C/T]cagaagaaagttacta	C	T	NM_144682 // upstream // 71528 // Hs.462833 // FLJ31952 // 146857 // Homo sapiens hypothetical protein FLJ31952 (FLJ31952), mRNA. /// ENST00000360502 // upstream // 74615 // — // — // — // — /// ENST00000285013 // upstream // 71528 // — // — /	FLJ31952	FLJ31952, Homo sapiens hypothetical protein FLJ31952 (FLJ31952), q12
SNP_A-1923829	ttagtatctctgacag[C/G]actgtgtttagtgtga	C	G	ENST00000361112 // intron // 0 // — // — // — // —	-	q12
SNP_A-2140832	atctgaacaccttgca[A/G]tcgttgcggacaaaca	A	G	NM_152781 // intron // 0 // Hs.514820 // FLJ32830 // 256957 // Homo sapiens hypothetical protein FLJ32830 (FLJ32830), mRNA. /// ENST00000311880 // intron // 0 // — // — // — // — // —	FLJ32830	FLJ32830, Homo sapiens hypothetical protein FLJ32830 (FLJ32830), q12
SNP_A-1903674	tgggagatggcaggaa[A/C]aaaagcctaaagtaat	A	C	NM_020426 // upstream // 20914 // Hs.97477 // LYZL6 // 57151 // Homo sapiens lysozyme-like 6 (LYZL6), mRNA. /// NM_004590 // downstream // 11950 // Hs.10458 // CCL16 // 6360 // Homo sapiens chemokine (C-C motif) ligand 16 (CCL16), mRNA. /// ENST00000029327	LYZL6	LYZL6, Homo sapiens lysozyme-like 6 (LYZL6), q12
SNP_A-1938590	ttgagactctgtacaa[A/G]ttcctaccttccccat	A	G	NM_005064 // upstream // 10773 // Hs.169191 // CCL23 // 6368 // Homo sapiens chemokine (C-C motif) ligand 23 (CCL23), transcript variant CKbeta8-1, mRNA. /// NM_145898 // upstream // 10773 // Hs.169191 // CCL23 // 6368 // Homo sapiens chemokine (C-C motif	CCL23	CCL23, Homo sapiens chemokine (C-C motif) ligand 23 (CCL23), transcript variant CKbeta8-1, q12
SNP_A-2128694	ataatcactgttgtaa[C/T]aagaagagcaagatat	C	T	NM_005064 // upstream // 11228 // Hs.169191 // CCL23 // 6368 // Homo sapiens chemokine (C-C motif) ligand 23 (CCL23), transcript variant CKbeta8-1, mRNA. /// NM_145898 // upstream // 11228 // Hs.169191 // CCL23 // 6368 // Homo sapiens chemokine (C-C motif	CCL23	CCL23, Homo sapiens chemokine (C-C motif) ligand 23 (CCL23), transcript variant CKbeta8-1, q12
SNP_A-2181947	cagagctgagagagaa[A/C]cccttgagttgtgttg	A	C	NM_005064 // upstream // 27813 // Hs.169191 // CCL23 // 6368 // Homo sapiens chemokine (C-C motif) ligand 23 (CCL23), transcript variant CKbeta8-1, mRNA. /// NM_145898 // upstream // 27813 // Hs.169191 // CCL23 // 6368 // Homo sapiens chemokine (C-C motif	CCL23	CCL23, Homo sapiens chemokine (C-C motif) ligand 23 (CCL23), transcript variant CKbeta8-1, q12
SNP_A-2071763	acagacattattagca[A/G]gagttttaaacaagtc	A	G	NM_002988 // downstream // 48562 // Hs.143961 // CCL18 // 6362 // Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), mRNA. /// NM_002983 // upstream // 29915 // Hs.514107 // CCL3 // 6348 // Homo sapiens chemokine (C	CCL18	CCL18, Homo sapiens chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (CCL18), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1690089	gcaggagaggccagcagcaaggata[A/G]gaaaaaggagtat tagaaaggagcat	A	G	NM_001094 // intron // 0 // Hs.6517 // ACCN1 // 40 // amiloride-sensitive cation channel 1, neuronal (degenerin)	ACCN1	ACCN1 , rs63954, amiloride-sensitive cation channel 1, neuronal (degenerin),q11.2
SNP_A-1732021	tggcagtcaccctcagagcccagaa[C/T]agcagaaataaaca gaaaacaggaa	C	T	NM_001094 // intron // 0 // Hs.6517 // ACCN1 // 40 // amiloride-sensitive cation channel 1, neuronal (degenerin)	ACCN1	ACCN1 , rs727206, amiloride-sensitive cation channel 1, neuronal (degenerin),q11.2
SNP_A-1794015	ggtcacgtgggaagac[A/G]gtcaaccagctgcagt	A	G	NM_024835 // downstream // 89277 // Hs.514116 // ZNF403 // 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 78324 // Hs.462859 // MGC4172 // 79154 // Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA. //	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-2131595	atagcatctgctttta[A/G]aaggagctgacatttt	A	G	NM_024835 // downstream // 129983 // Hs.514116 // ZNF403 // 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 119030 // Hs.462859 // MGC4172 // 79154 // Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA.	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-1931880	ttccgtatatcttgtaj[A/G]agggcctgtgttgttc	A	G	NM_024835 // downstream // 229058 // Hs.514116 // ZNF403 // 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 218105 // Hs.462859 // MGC4172 // 79154 // Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA.	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-2229279	ctaggacaaagcaggt[A/C]aaatatctgggacga	A	C	NM_024835 // downstream // 280787 // Hs.514116 // ZNF403 // 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 269834 // Hs.462859 // MGC4172 // 79154 // Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA.	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-1850991	aatgctccaagtgaa[A/G]gctaatcagagcacgg	A	G	NM_024835 // downstream // 302132 // Hs.514116 // ZNF403 // 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 291179 // Hs.462859 // MGC4172 // 79154 // Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA.	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-1850995	aggttgcctttgcatg[C/G]agaacagggtacaaga	C	G	NM_024835 // downstream // 303222 // Hs.514116 // ZNF403 // 79893 // Homo sapiens zinc finger protein 403 (ZNF403), mRNA. /// NM_024308 // downstream // 292269 // Hs.462859 // MGC4172 // 79154 // Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA.	ZNF403	ZNF403, Homo sapiens zinc finger protein 403 (ZNF403), q12
SNP_A-1676082	gtctggcattggttcaatggttgcac[C/T]acctcaacaacctgtct agaaggg	C	T	NM_001094 // intron // 0 // Hs.6517 // ACCN1 // 40 // amiloride-sensitive cation channel 1, neuronal (degenerin)	ACCN1	ACCN1 , rs317343, amiloride-sensitive cation channel 1, neuronal (degenerin),q11.2
SNP_A-2239233	ctcttggtccagaact[A/G]aggcctacatgcatcc	A	G	NM_198839 // intron // 0 // Hs.160556 // ACACA // 31 // Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), transcript variant 2, mRNA. /// NM_198834 // intron // 0 // Hs.160556 // ACACA // 31 // Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACA	ACACA	ACACA, Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), transcript variant 2, q12
SNP_A-1904571	tggggcacagtgggggt[A/C]agaatgcacagacact	A	C	NM_133439 // intron // 0 // Hs.500066 // TADA2L // 6871 // Homo sapiens transcriptional adaptor 2 (ADA2 homolog, yeast)-like (TADA2L), transcript variant 2, mRNA. /// NM_001488 // intron // 0 // Hs.500066 // TADA2L // 6871 // Homo sapiens transcriptional	TADA2L	TADA2L, Homo sapiens transcriptional adaptor 2 (ADA2 homolog, yeast)-like (TADA2L), transcript variant 2, q12
SNP_A-2291882	gcacagtgaagtaaaa[C/T]gagggtaaaggtgctg	C	T	NM_006481 // intron // 0 // Hs.191144 // TCF2 // 6928 // Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), transcript variant b, mRNA. /// NM_000458 // intron // 0 // Hs.191144 // TCF2 // 6928 // Homo sapiens tran	TCF2	TCF2, Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), transcript variant b, q12
SNP_A-1678844	ccattattccctcatcagtgcccag[A/G]acgatgtaccccctttat cattcc	A	G	NM_006584 // downstream // 37740 // Hs.73072 // CCT6B // 10693 // chaperonin containing TCP1, subunit 6B (zeta 2)	CCT6B	CCT6B , rs4796013, chaperonin containing TCP1, subunit 6B (zeta 2),q11.2
SNP_A-2266094	gaaggcctggtttcc[C/G]agagcccaaccctaag	C	G	ENST00000300901 // intron // 0 // — // — // —	-	q12
SNP_A-2228020	ctacgattcataatga[C/T]atccgtgtgcacacca	C	T	ENST00000300901 // intron // 0 // — // — // —	-	q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1851660	ctggactccagtcccc[A/G]agtgtaaccagaggca	A	G	NM_025248 // upstream // 41770 // Hs.448872 // SNIP // 80725 // Homo sapiens SNAP25-interacting protein (SNIP), mRNA. /// AK126665 // upstream // 56600 // Hs.448872 // SNIP // 80725 // Homo sapiens cDNA FLJ44709 fis, clone BRACE3019570, highly similar to	SNIP	SNIP, Homo sapiens SNAP25-interacting protein (SNIP), q12
SNP_A-1894857	tgccatcccgtcacta[A/C]aagatgcctagcctta	A	C	NM_020405 // intron // 0 // Hs.125036 // PLXDC1 // 57125 // Homo sapiens plexin domain containing 1 (PLXDC1), mRNA. /// ENST00000315392 // intron // 0 // — // — // — // —	PLXDC1	PLXDC1, Homo sapiens plexin domain containing 1 (PLXDC1), q12
SNP_A-2066216	aattttacacagcttc[A/G]agtggttcatgaactc	A	G	NM_198993 // upstream // 4925 // Hs.145068 // STAC2 // 342667 // Homo sapiens SH3 and cysteine rich domain 2 (STAC2), mRNA. /// NM_032875 // downstream // 29949 // Hs.462946 // FBXL20 // 84961 // Homo sapiens F-box and leucine-rich repeat protein 20 (FBXL	STAC2	STAC2, Homo sapiens SH3 and cysteine rich domain 2 (STAC2), q12
SNP_A-2178191	cactatgggaatttga[G/T]gggtgcattaaagtag	G	T	NM_183231 // intron // 0 // Hs.444388 // ZNFN1A3 // 22806 // Homo sapiens zinc finger protein, subfamily 1A, 3 (Aiolos) (ZNFN1A3), transcript variant 5, mRNA. /// NM_183232 // intron // 0 // Hs.444388 // ZNFN1A3 // 22806 // Homo sapiens zinc finger protei	ZNFN1A3	ZNFN1A3, Homo sapiens zinc finger protein, subfamily 1A, 3 (Aiolos) (ZNFN1A3), transcript variant 5, q21.1
SNP_A-2311893	ggacaaagatgagata[C/T]gagtgtttattcaacc	C	T	NM_019010 // upstream // 15903 // Hs.84905 // KRT20 // 54474 // Homo sapiens keratin 20 (KRT20), mRNA. /// NM_173213 // downstream // 21570 // Hs.9029 // KRT23 // 25984 // Homo sapiens keratin 23 (histone deacetylase inducible) (KRT23), transcript variant	KRT20	KRT20, Homo sapiens keratin 20 (KRT20), q21.2
SNP_A-2285691	gatgaattaaggtatc[A/G]aaggatggagacaaga	A	G	NM_031958 // upstream // 16398 // Hs.534500 // KRTAP3-1 // 83896 // Homo sapiens keratin associated protein 3-1 (KRTAP3-1), mRNA. /// ENST00000360088 // upstream // 16398 // — // — // — // — /// ENST00000357851 // downstream // 1159 // — // —	KRTAP3-1	KRTAP3-1, Homo sapiens keratin associated protein 3-1 (KRTAP3-1), q21.2
SNP_A-2029489	aaagaccagggataca[C/T]ctcttgtccaatagct	C	T	NM_033184 // upstream // 2108 // Hs.406714 // KRTAP2-4 // 85294 // Homo sapiens keratin associated protein 2-4 (KRTAP2-4), mRNA. /// ENST00000328878 // upstream // 2108 // — // — // — // — /// ENST00000332991 // upstream // 22049 // — // — //	KRTAP2-4	KRTAP2-4, Homo sapiens keratin associated protein 2-4 (KRTAP2-4), q21.2
SNP_A-2075906	acattaagttccagga[A/G]acctcaagagtatgag	A	G	NM_021013 // intron // 0 // Hs.296942 // KRTHA4 // 3885 // Homo sapiens keratin, hair, acidic, 4 (KRTHA4), mRNA. /// ENST00000251648 // intron // 0 // — // — // — // — // —	KRTHA4	KRTHA4, Homo sapiens keratin, hair, acidic, 4 (KRTHA4), q21.2
SNP_A-1954686	tttgctattaaacttc[A/G]cttctgcagcagaatg	A	G	NM_002277 // upstream // 8628 // Hs.41696 // KRTHA1 // 3881 // Homo sapiens keratin, hair, acidic, 1 (KRTHA1), mRNA. /// NM_003770 // downstream // 14337 // Hs.159403 // KRTHA7 // 8688 // Homo sapiens keratin, hair, acidic, 7 (KRTHA7), mRNA. /// ENST00000	KRTHA1	KRTHA1, Homo sapiens keratin, hair, acidic, 1 (KRTHA1), q21.2
SNP_A-1801769	gtagtgagacctccaa[A/G]ataaaatgctactagg	A	G	NM_006771 // intron // 0 // Hs.248188 // KRTHA8 // 8687 // Homo sapiens keratin, hair, acidic, 8 (KRTHA8), mRNA. /// ENST00000246646 // intron // 0 // — // — // — // —	KRTHA8	KRTHA8, Homo sapiens keratin, hair, acidic, 8 (KRTHA8), q21.2
SNP_A-2246210	ctggtgaggtgtacaa[C/T]gagccctcctcagatg	C	T	NM_002278 // upstream // 8702 // Hs.41752 // KRTHA2 // 3882 // Homo sapiens keratin, hair, acidic, 2 (KRTHA2), mRNA. /// NM_002280 // downstream // 601 // Hs.73082 // KRTHA5 // 3886 // Homo sapiens keratin, hair, acidic, 5 (KRTHA5), mRNA. /// NM_182497 //	KRTHA2	KRTHA2, Homo sapiens keratin, hair, acidic, 2 (KRTHA2), q21.2
SNP_A-2309497	ggaaacagttcagact[A/C]aaataaacaaatcatt	A	C	ENST00000357284 // intron // 0 // — // — // — // — // — /// ENST00000359615 // intron // 0 // — // — // — // —	-	q21.31
SNP_A-2223843	cggctgcccacccttc[A/G]acactattacccatcg	A	G	NM_005440 // downstream // 7645 // Hs.436395 // RND2 // 8153 // Homo sapiens ras homolog gene family, member N (ARHN), mRNA. /// NM_007305 // downstream // 7976 // Hs.194143 // BRCA1 // 672 // Homo sapiens breast cancer 1, early onset (BRCA1), transcript	RND2	RND2, Homo sapiens ras homolog gene family, member N (ARHN), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1853728	tacctcaagtactcac[C/T]atgaccccatcaacag	C	T	NM_007305 // intron // 0 // Hs.194143 // BRCA1 // 672 // Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-delta9-10-11b, mRNA. /// NM_007295 // intron // 0 // Hs.194143 // BRCA1 // 672 // Homo sapiens breast cancer 1, early onse	BRCA1	BRCA1, Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-delta9-10-11b, q21.31
SNP_A-2070053	acacatacctagaaca[C/G]agcctaaaaaagcatc	C	G	ENST00000341011 // intron // 0 // — // — // — // —	-	q21.31
SNP_A-2185453	caggacgacatggaca[A/G]tagcgtcttctccagg	A	G	NM_002722 // upstream // 472 // Hs.184604 // PPY // 5539 // Homo sapiens pancreatic polypeptide (PPY), mRNA. /// NM_004160 // downstream // 10617 // Hs.169249 // PYY // 5697 // Homo sapiens peptide YY (PYY), mRNA. /// ENST00000225992 // upstream // 472 //	PPY	PPY, Homo sapiens pancreatic polypeptide (PPY), q21.31
SNP_A-1903654	tgggagacgtcgttaa[A/G]tgatgttgccagggta	A	G	NM_004160 // intron // 0 // Hs.169249 // PYY // 5697 // Homo sapiens peptide YY (PYY), mRNA. /// ENST00000360085 // intron // 0 // — // — // - - // — /// ENST00000253409 // intron // 0 // — // — // — // —	PYY	PYY, Homo sapiens peptide YY (PYY), q21.31
SNP_A-1663046	cactgattgatacatctttcagtaa[A/G]tgaattcggcacatccac agtgtcc	A	G	NM_030966 // downstream // 4340 // Hs.247935 // KRTAP1-3 // 81850 // keratin associated protein 1-3 /// NM_030967 // downstream // 11013 // Hs.247934 // KRTAP1-1 // 81851 // keratin associated protein 1-1 /// NM_031957 // upstream // 2344 // Hs.307030 //	KRTAP1-3	KRTAP1-3 , rs8072687, keratin associated protein 1-3 ,q21.2
SNP_A-2202594	ccacctcctggacaga[C/T]aaggatgaagttcact	C	T	NM_002087 // intron // 0 // Hs.514220 // GRN // 2896 // Homo sapiens granulin (GRN), mRNA. /// ENST00000053867 // intron // 0 // — // — // — // — /// ENST00000357351 // intron // 0 // — // — // — // —	GRN	GRN, Homo sapiens granulin (GRN), q21.31
SNP_A-1694463	atcagaactttctggcaaagtcgga[A/G]aggaggctttggtaaa acaagattg	A	G	NM_030975 // downstream // 58016 // - // - // - // - /// NM_031962 // downstream // 80926 // Hs.307012 // KRTAP9-3 // 83900 // keratin associated protein 9-3 /// NM_031964 // downstream // 540 // Hs.307009 // KRTAP17-1 // 83902 // keratin associated prot	-	- , rs10512485, - ,q21.2
SNP_A-1879785	tcttccaagtgaggac[A/C]atgcggcttgcctttg	A	C	NM_152466 // downstream // 74205 // Hs.128813 // FLJ25168 // 147081 // Homo sapiens hypothetical protein FLJ25168 (FLJ25168), mRNA. /// NM_004382 // upstream // 90940 // Hs.417628 // CRHR1 // 1394 // Homo sapiens corticotropin releasing hormone receptor 1	FLJ25168	FLJ25168, Homo sapiens hypothetical protein FLJ25168 (FLJ25168), q21.31
SNP_A-1855153	ctgcaggcatagaaag[C/T]aactggactgcacctg	C	T	NM_152466 // downstream // 87703 // Hs.128813 // FLJ25168 // 147081 // Homo sapiens hypothetical protein FLJ25168 (FLJ25168), mRNA. /// NM_004382 // upstream // 77442 // Hs.417628 // CRHR1 // 1394 // Homo sapiens corticotropin releasing hormone receptor 1	FLJ25168	FLJ25168, Homo sapiens hypothetical protein FLJ25168 (FLJ25168), q21.31
SNP_A-2210239	ccccatctagtcccaa[C/T]gcaacaacctatgcaa	C	T	NM_016841 // intron // 0 // Hs.101174 // MAPT // 4137 // Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 4, mRNA. /// NM_016834 // intron // 0 // Hs.101174 // MAPT // 4137 // Homo sapiens microtubule-associated protein tau (MAPT	MAPT	MAPT, Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 4, q21.31
SNP_A-2199736	ccaaaatgtgtgatca[A/T]caagaatggagtcttt	A	T	NM_016841 // intron // 0 // Hs.101174 // MAPT // 4137 // Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 4, mRNA. /// NM_016834 // intron // 0 // Hs.101174 // MAPT // 4137 // Homo sapiens microtubule-associated protein tau (MAPT	MAPT	MAPT, Homo sapiens microtubule-associated protein tau (MAPT), transcript variant 4, q21.31
SNP_A-1849442	tatggattaccaaaag[C/T]cctgcgctaggtccct	C	T	NM_004287 // intron // 0 // Hs.463278 // GOSR2 // 9570 // Homo sapiens golgi SNAP receptor complex member 2 (GOSR2), transcript variant A, mRNA. /// NM_054022 // intron // 0 // Hs.463278 // GOSR2 // 9570 // Homo sapiens golgi SNAP receptor complex member	GOSR2	GOSR2, Homo sapiens golgi SNAP receptor complex member 2 (GOSR2), transcript variant A, q21.32
SNP_A-2307825	gcttctaagtacagca[A/G]gcctaaggcagtgtgt	A	G	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32
SNP_A-1916012	tgttgcaggagagtaa[A/G]gaaagcacttttgttat	A	G	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2279876	gaggcggtgaggaaga[A/G]catcagaagagatggc	A	G	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32
SNP_A-2122477	agtgctagggaatcac[A/G]gtgaaagccagtccct	A	G	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32
SNP_A-2278461	gagctcagtctggaga[A/G]gaagacaagtaaagaa	A	G	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32
SNP_A-2034805	aaatgacccttcagta[G/T]gtcattttctcactga	G	T	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32
SNP_A-1855586	tcaataaatctgccta[A/T]aatgttcaaaaattac	A	T	ENST00000341671 // intron // 0 // — // — // — // —	-	q21.32
SNP_A-1952332	tttctctctgccatgc[A/G]aggccacttcaagaag	A	G	NM_001256 // downstream // 18302 // Hs.463295 // CDC27 // 996 // Homo sapiens cell division cycle 27 (CDC27), mRNA. /// ENST00000309965 // downstream // 51514 // — // — // — // — /// ENST00000066544 // downstream // 18302 // — // — // — // -	CDC27	CDC27, Homo sapiens cell division cycle 27 (CDC27), q21.32
SNP_A-2100061	agagtgatatttattg[A/G]aaacttactacctgaa	A	G	NM_001256 // intron // 0 // Hs.463295 // CDC27 // 996 // Homo sapiens cell division cycle 27 (CDC27), mRNA. /// ENST00000066544 // intron // 0 // — // — // — // —	CDC27	CDC27, Homo sapiens cell division cycle 27 (CDC27), q21.32
SNP_A-2087283	actgcaagctggcact[A/C]aagaggattagactta	A	C	NM_001256 // intron // 0 // Hs.463295 // CDC27 // 996 // Homo sapiens cell division cycle 27 (CDC27), mRNA. /// ENST00000066544 // intron // 0 // — // — // — // —	CDC27	CDC27, Homo sapiens cell division cycle 27 (CDC27), q21.32
SNP_A-1957904	ttttcaaagttggaca[A/T]aaaatacaggagtaat	A	T	NM_013351 // downstream // 22458 // Hs.272409 // TBX21 // 30009 // Homo sapiens T-box 21 (TBX21), mRNA. /// NM_145798 // downstream // 38790 // Hs.463320 // OSBPL7 // 114881 // Homo sapiens oxysterol binding protein-like 7 (OSBPL7), transcript variant 1,	TBX21	TBX21, Homo sapiens T-box 21 (TBX21), q21.32
SNP_A-1856885	tggattcttcttctac[A/G]atatcctttggctctt	A	G	NM_003726 // intron // 0 // Hs.316931 // SCAP1 // 8631 // Homo sapiens src family associated phosphoprotein 1 (SCAP1), mRNA. /// ENST00000336915 // intron // 0 // — // — // — // —	SCAP1	SCAP1, Homo sapiens src family associated phosphoprotein 1 (SCAP1), q21.32
SNP_A-1791817	gggtgacgctgaagag[A/G]aagagttgagtctgtc	A	G	NM_018952 // intron // 0 // Hs.98428 // HOXB6 // 3216 // Homo sapiens homeo box B6 (HOXB6), transcript variant 2, mRNA. /// NM_156037 // intron // 0 // Hs.98428 // HOXB6 // 3216 // Homo sapiens homeo box B6 (HOXB6), transcript variant 1, mRNA. /// NM_1560	HOXB6	HOXB6, Homo sapiens homeo box B6 (HOXB6), transcript variant 2, q21.32
SNP_A-2034029	aaatcagagtgcaaaa[A/G]ccataacggtacagct	A	G	NM_018952 // upstream // 296 // Hs.98428 // HOXB6 // 3216 // Homo sapiens homeo box B6 (HOXB6), transcript variant 2, mRNA. /// NM_156037 // upstream // 296 // Hs.98428 // HOXB6 // 3216 // Homo sapiens homeo box B6 (HOXB6), transcript variant 1, mRNA. ///	HOXB6	HOXB6, Homo sapiens homeo box B6 (HOXB6), transcript variant 2, q21.32
SNP_A-1787597	gggacaaaaatgtgcc[A/T]cttgaaactgagttta	A	T	NM_024016 // upstream // 5457 // Hs.514292 // HOXB8 // 3218 // Homo sapiens homeo box B8 (HOXB8), mRNA. /// NM_024017 // downstream // 768 // Hs.463350 // HOXB9 // 3219 // Homo sapiens homeo box B9 (HOXB9), mRNA. /// ENST00000239144 // upstream // 5457 //	HOXB8	HOXB8, Homo sapiens homeo box B8 (HOXB8), q21.32
SNP_A-2083875	actactatccaattcc[A/G]gaacctgtgcctgtgt	A	G	NM_024017 // upstream // 49826 // Hs.463350 // HOXB9 // 3219 // Homo sapiens homeo box B9 (HOXB9), mRNA. /// NM_032391 // downstream // 45541 // Hs.116467 // PRAC // 84366 // Homo sapiens small nuclear protein PRAC (PRAC), mRNA. /// ENST00000311177 // ups	HOXB9	HOXB9, Homo sapiens homeo box B9 (HOXB9), q21.32
SNP_A-2137220	atcagtatgttcacaa[A/G]ataaattgagtaaacc	A	G	NM_024017 // upstream // 53328 // Hs.463350 // HOXB9 // 3219 // Homo sapiens homeo box B9 (HOXB9), mRNA. /// NM_032391 // downstream // 42039 // Hs.116467 // PRAC // 84366 // Homo sapiens small nuclear protein PRAC (PRAC), mRNA. /// ENST00000311177 // ups	HOXB9	HOXB9, Homo sapiens homeo box B9 (HOXB9), q21.32
SNP_A-2053738	aagtggtcagattgaa[G/T]aacatgattgattaca	G	T	NM_024017 // upstream // 88084 // Hs.463350 // HOXB9 // 3219 // Homo sapiens homeo box B9 (HOXB9), mRNA. /// NM_032391 // downstream // 7283 // Hs.116467 // PRAC // 84366 // Homo sapiens small nuclear protein PRAC (PRAC), mRNA. /// ENST00000311177 // upst	HOXB9	HOXB9, Homo sapiens homeo box B9 (HOXB9), q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2208045	ccaagaatggaaata[A/G]gagtcaaaacagcctc	A	G	NM_006361 // upstream // 24980 // Hs.66731 // HOXB13 // 10481 // Homo sapiens homeo box B13 (HOXB13), mRNA. /// NM_173623 // downstream // 8577 // Hs.91930 // FLJ35808 // 284076 // Homo sapiens hypothetical protein FLJ35808 (FLJ35808), mRNA. /// ENST00000	HOXB13	HOXB13, Homo sapiens homeo box B13 (HOXB13), q21.32
SNP_A-1887882	tgagattgctgctcag[A/G]acttaggagagccatc	A	G	NM_173623 // upstream // 36542 // Hs.91930 // FLJ35808 // 284076 // Homo sapiens hypothetical protein FLJ35808 (FLJ35808), mRNA. /// NM_005831 // upstream // 144 // Hs.514920 // NDP52 // 10241 // Homo sapiens nuclear domain 10 protein (NDP52), mRNA. /// E	FLJ35808	FLJ35808, Homo sapiens hypothetical protein FLJ35808 (FLJ35808), q21.32
SNP_A-1875670	tctcttctgaaatcaa[C/T]agtccccctagtagct	C	T	NM_006546 // downstream // 65994 // Hs.144936 // IMP-1 // 10642 // Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1), mRNA. /// NM_153446 // upstream // 17188 // Hs.374679 // GALGT2 // 124872 // Homo sapiens UDP-GalNAc:Neu5Acalpha2-3Galbeta-R beta1,4-N-a	IMP-1	IMP-1, Homo sapiens IGF-II binding protein 1 (IMP-1), q21.32
SNP_A-2230412	ctatcaatgaggttta[A/T]aaaaacaacaacgaag	A	T	NM_002634 // upstream // 46780 // Hs.514303 // PHB // 5245 // Homo sapiens prohibitin (PHB), mRNA. /// NM_002507 // upstream // 33633 // Hs.415768 // NGFR // 4804 // Homo sapiens nerve growth factor receptor (TNFR superfamily, member 16) (NGFR), mRNA. ///	PHB	PHB, Homo sapiens prohibitin (PHB), q21.32
SNP_A-2289811	gcaaacatataggaaac[C/T]acatagtaaaagagtg	C	T	NM_002634 // upstream // 48979 // Hs.514303 // PHB // 5245 // Homo sapiens prohibitin (PHB), mRNA. /// NM_002507 // upstream // 31434 // Hs.415768 // NGFR // 4804 // Homo sapiens nerve growth factor receptor (TNFR superfamily, member 16) (NGFR), mRNA. ///	PHB	PHB, Homo sapiens prohibitin (PHB), q21.32
SNP_A-1877203	tctgcttcccaacttc[C/T]acttccaggcaggcc	C	T	NM_002634 // upstream // 51911 // Hs.514303 // PHB // 5245 // Homo sapiens prohibitin (PHB), mRNA. /// NM_002507 // upstream // 28502 // Hs.415768 // NGFR // 4804 // Homo sapiens nerve growth factor receptor (TNFR superfamily, member 16) (NGFR), mRNA. ///	PHB	PHB, Homo sapiens prohibitin (PHB), q21.32
SNP_A-1857671	atggaaacaggaagtc[A/G]cttaggcttgaagca	A	G	NM_170685 // upstream // 53607 // Hs.434138 // TAC4 // 255061 // Homo sapiens tachykinin 4 (hemokinin) (TAC4), mRNA. /// NM_001934 // upstream // 67576 // Hs.172648 // DLX4 // 1748 // Homo sapiens distal-less homeobox 4 (DLX4), transcript variant 2, mRNA.	TAC4	TAC4, Homo sapiens tachykinin 4 (hemokinin) (TAC4), q21.33
SNP_A-1860618	tcagtttctgatctg[G/T]aaaaggaatgataac	G	T	NM_170685 // upstream // 74767 // Hs.434138 // TAC4 // 255061 // Homo sapiens tachykinin 4 (hemokinin) (TAC4), mRNA. /// NM_001934 // upstream // 46416 // Hs.172648 // DLX4 // 1748 // Homo sapiens distal-less homeobox 4 (DLX4), transcript variant 2, mRNA.	TAC4	TAC4, Homo sapiens tachykinin 4 (hemokinin) (TAC4), q21.33
SNP_A-2314203	ggaggatatctgaaat[A/G]agaagtgaaggatgtg	A	G	NM_005220 // upstream // 3847 // Hs.134194 // DLX3 // 1747 // Homo sapiens distal-less homeo box 3 (DLX3), mRNA. /// NM_005501 // upstream // 57296 // Hs.265829 // ITGA3 // 3675 // Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 re	DLX3	DLX3, Homo sapiens distal-less homeo box 3 (DLX3), q21.33
SNP_A-1885218	tgaattctggaaagga[A/G]atgcaggtttaagtat	A	G	NM_005501 // intron // 0 // Hs.265829 // ITGA3 // 3675 // Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA. /// NM_002204 // intron // 0 // Hs.265829 // ITGA3 // 3675 // Homo sapiens int	ITGA3	ITGA3, Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, q21.33
SNP_A-1668166	gcctctgagctctcgggaggtc[A/G]aatctctctgacccagc aggagac	A	G	BC006271 // intron // 0 // Hs.43141 // LOC284058 // 284058 // hypothetical protein LOC284058	LOC284058	LOC284058, rs3883305, hypothetical protein LOC284058,q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2111149	aggagaggacccagaa[A/T]cttttatgctccttg	A	T	NM_000088 // upstream // 18776 // Hs.172928 // COL1A1 // 1277 // Homo sapiens collagen, type I, alpha 1 (COL1A1), mRNA. /// NM_153229 // upstream // 54064 // Hs.224630 // FLJ33318 // 162461 // Homo sapiens hypothetical protein FLJ33318 (FLJ33318), mRNA. /	COL1A1	COL1A1, Homo sapiens collagen, type I, alpha 1 (COL1A1), q21.33
SNP_A-2257119	ctttctcgaaagagtc[A/G]atcgatgtagcaaact	A	G	NM_000088 // upstream // 49420 // Hs.172928 // COL1A1 // 1277 // Homo sapiens collagen, type I, alpha 1 (COL1A1), mRNA. /// NM_153229 // upstream // 23420 // Hs.224630 // FLJ33318 // 162461 // Homo sapiens hypothetical protein FLJ33318 (FLJ33318), mRNA. /	COL1A1	COL1A1, Homo sapiens collagen, type I, alpha 1 (COL1A1), q21.33
SNP_A-1857916	aagttaccctcggccc[A/G]gacgttgccttccttt	A	G	NM_153229 // 3UTR // 0 // Hs.224630 // FLJ33318 // 162461 // Homo sapiens hypothetical protein FLJ33318 (FLJ33318), mRNA. /// ENST00000300433 // 3UTR // 0 // --- // --- // --- // ---	FLJ33318	FLJ33318, Homo sapiens hypothetical protein FLJ33318 (FLJ33318), q21.33
SNP_A-2162567	attttcctttcagggc[C/T]atatagactgttcgtc	C	T	NM_153229 // downstream // 56349 // Hs.224630 // FLJ33318 // 162461 // Homo sapiens hypothetical protein FLJ33318 (FLJ33318), mRNA. /// NM_022167 // upstream // 8200 // Hs.463416 // XYLT2 // 64132 // Homo sapiens xylosyltransferase II (XYLT2), mRNA. /// E	FLJ33318	FLJ33318, Homo sapiens hypothetical protein FLJ33318 (FLJ33318), q21.33
SNP_A-2097932	agagagaccttcacaa[A/G]taataagacccaagaa	A	G	NM_152463 // 3UTR // 0 // Hs.514330 // EME1 // 146956 // Homo sapiens essential meiotic endonuclease 1 homolog 1 (S. pombe) (EME1), mRNA. /// ENST00000338165 // 3UTR // 0 // --- // --- // --- // ---	EME1	EME1, Homo sapiens essential meiotic endonuclease 1 homolog 1 (S. pombe) (EME1), q21.33
SNP_A-2055306	aataagcaagagccct[C/G]acttgtccatgaaatt	C	G	NM_025149 // intron // 0 // Hs.288959 // FLJ20920 // 80221 // Homo sapiens hypothetical protein FLJ20920 (FLJ20920), mRNA. /// ENST00000300441 // intron // 0 // --- // --- // --- // ---	FLJ20920	FLJ20920, Homo sapiens hypothetical protein FLJ20920 (FLJ20920), q21.33
SNP_A-2248903	ctgttggctgtggatc[A/G]atctgggccctctcac	A	G	NM_175575 // intron // 0 // Hs.211475 // WFIKKN2 // 124857 // Homo sapiens WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (WFIKKN2), mRNA. /// ENST00000311378 // intron // 0 // --- // --- // --- // ---	WFIKKN2	WFIKKN2, Homo sapiens WAP, follistatin q21.33
SNP_A-1926190	ttattaagtctctcaa[A/T]taaaatgccagacatg	A	T	NM_175575 // downstream // 16532 // Hs.211475 // WFIKKN2 // 124857 // Homo sapiens WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (WFIKKN2), mRNA. /// NM_005749 // downstream // 4102 // Hs.531550 // TOB1 // 10140 // Homo sap	WFIKKN2	WFIKKN2, Homo sapiens WAP, follistatin q21.33
SNP_A-2111204	aggagatgtaaagaat[G/T]aggaagttaagcttta	G	T	NM_016001 // downstream // 21583 // Hs.463465 // WDR50 // 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 310801 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // downstre	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33
SNP_A-1911533	tgtctttgctattttg[A/G]atagtgctacaatgaa	A	G	NM_016001 // downstream // 147100 // Hs.463465 // WDR50 // 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 185284 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // downstr	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33
SNP_A-2276481	gagaggcatcagacta[C/T]gctgcaggtttggccc	C	T	NM_016001 // downstream // 213972 // Hs.463465 // WDR50 // 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 118412 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // downstr	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33
SNP_A-1858694	aactcccactaccta[A/G]acaaagccattagaga	A	G	NM_016001 // downstream // 217962 // Hs.463465 // WDR50 // 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 114422 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // downstr	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1858741	tgtctgacattgatgc[A/G]aaaagtaaagtaaaag	A	G	NM_016001 // downstream // 331961 // Hs.463465 // WDR50 // 51096 // Homo sapiens CGI-48 protein (CGI-48), mRNA. /// NM_020178 // downstream // 423 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // downstream	WDR50	WDR50, Homo sapiens CGI-48 protein (CGI-48), q21.33
SNP_A-2231759	ctcaaaatgacatacc[A/G]atgaccaataggtata	A	G	NM_020178 // intron // 0 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // — // — // — /// ENST00000340813 // intron // 0 // — // — // —	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-2047061	aagagttgtcatcatc[C/T]actgttcagctgtgg	C	T	NM_020178 // intron // 0 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // — // — // — /// ENST00000340813 // intron // 0 // — // — // —	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-1859055	aatgggcaagagaata[G/T]ccagactagctaggac	G	T	NM_020178 // intron // 0 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // — // — // — /// ENST00000340813 // intron // 0 // — // — // —	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-1959097	tttgaagactaacca[A/T]ggtttctttgaagtga	A	T	NM_020178 // intron // 0 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // — // — // — /// ENST00000340813 // intron // 0 // — // — // —	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-1795725	ggtggagaaagaaaac[C/T]gtagagcaagccaact	C	T	NM_020178 // intron // 0 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // — // — // — /// ENST00000340813 // intron // 0 // — // — // —	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-2260854	gaaactgaggccaagt[A/C]aatagttcacagggc	A	C	NM_020178 // intron // 0 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// ENST00000285273 // intron // 0 // — // — // — /// ENST00000340813 // intron // 0 // — // — // —	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q21.33
SNP_A-1859402	gtaaatctctcagaca[A/G]tagagagacgaaggat	A	G	NM_020178 // upstream // 33369 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 33782 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstream /	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-1859421	tcatgtcaccaaatta[A/G]gaagaggcactaggaa	A	G	NM_020178 // upstream // 62441 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 62854 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstream /	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-1859433	tatgcttgagtaacta[C/T]attccgggtctatat	C	T	NM_020178 // upstream // 66951 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 67364 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstream /	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-1859447	catgcttctcaatca[A/G]gcaagtacatgtttta	A	G	NM_020178 // upstream // 72877 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 73290 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstream /	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-2118556	agtaatcgatggcta[C/G]atgaggtagaagtgt	C	G	NM_020178 // upstream // 76243 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 76656 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstream /	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1923289	ttaggaaaqtcgctgc[A/G]aactggtactataaat	A	G	NM_020178 // upstream // 346215 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 346628 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstream	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-2040111	aaccaaatttgcgttat[C/T]catataaaacccatgagc	C	T	NM_020178 // upstream // 1307529 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 1307942 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstre	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-2312081	ggacacgattatacca[A/C]aagatgaactgcatga	A	C	NM_020178 // upstream // 1466116 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 1466529 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstre	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-1952002	tttctagtttgggggat[A/T]aaattgtcacttgaat	A	T	NM_020178 // upstream // 1474149 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_020178 // upstream // 1474562 // Hs.463466 // CA10 // 56934 // Homo sapiens carbonic anhydrase X (CA10), mRNA. /// NM_032559 // upstre	CA10	CA10, Homo sapiens carbonic anhydrase X (CA10), q22
SNP_A-1852340	taittaaaacctgaaa[C/T]ggaagactgtacaaat	C	T	NM_032559 // downstream // 823701 // Hs.226805 // KIF2B // 84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 251930 // Hs.153504 // TOM1L1 // 10040 // Homo sapiens target of myb1-like 1 (chicken) (TOM1L1), mRNA. /// NM_0	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2005201	tgtccaaaagactcag[A/G]agtgatatatttagat	A	G	NM_032559 // downstream // 976088 // Hs.226805 // KIF2B // 84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 99543 // Hs.153504 // TOM1L1 // 10040 // Homo sapiens target of myb1-like 1 (chicken) (TOM1L1), mRNA. /// NM_00	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2137666	atcatgagtttaacc[A/G]cttcacacctgcagtt	A	G	NM_032559 // downstream // 976354 // Hs.226805 // KIF2B // 84643 // Homo sapiens kinesin protein (LOC84643), mRNA. /// NM_005486 // upstream // 99277 // Hs.153504 // TOM1L1 // 10040 // Homo sapiens target of myb1-like 1 (chicken) (TOM1L1), mRNA. /// NM_00	KIF2B	KIF2B, Homo sapiens kinesin protein (LOC84643), q22
SNP_A-2057223	aatatagccatgtatg[A/C]aaatttaatctagaa	A	C	NM_178509 // intron // 0 // Hs.35199 // STXBP4 // 252983 // Homo sapiens syntaxin binding protein 4 (STXBP4), mRNA. /// ENST00000299341 // intron // 0 // --- // --- // --- // ---	STXBP4	STXBP4, Homo sapiens syntaxin binding protein 4 (STXBP4), q22
SNP_A-1793125	ggtagaaaaagatacc[A/G]aaatgtcatggtgata	A	G	NM_178509 // downstream // 189115 // Hs.35199 // STXBP4 // 252983 // Homo sapiens syntaxin binding protein 4 (STXBP4), mRNA. /// NM_002126 // upstream // 31119 // Hs.196952 // HLF // 3131 // Homo sapiens hepatic leukemia factor (HLF), mRNA. /// ENST000002	STXBP4	STXBP4, Homo sapiens syntaxin binding protein 4 (STXBP4), q22
SNP_A-1754394	agaaataatgtggctgctttcaca[C/T]tcctcttaagtaaaaatc cctgcc	C	T	NM_020178 // upstream // 67191 // Hs.283110 // CA10 // 56934 // carbonic anhydrase X /// NM_032559 // upstream // 1595706 // Hs.226805 // LOC84643 // 84643 // kinesin protein	CA10	CA10 , rs10515000, carbonic anhydrase X, q22
SNP_A-2094994	agaatggataagaata[C/T]atatggatgctagtga	C	T	NM_198403 // upstream // 63943 // Hs.379190 // MMD2 // 221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 // upstream // 63943 // Hs.463483 // MMD // 23531 // Homo sapiens monocyte to macrophage differen	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-2213481	ccgctatatacaccag[A/G]ccaagacaatataagg	A	G	NM_198403 // upstream // 109448 // Hs.379190 // MMD2 // 221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 // upstream // 109448 // Hs.463483 // MMD // 23531 // Homo sapiens monocyte to macrophage differ	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2032995	aaataaatttcacctca[C/G]cagatttgtcctttca	C	G	NM_198403 // upstream // 196610 // Hs.379190 // MMD2 // 221938 // Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), mRNA. /// NM_012329 // upstream // 196610 // Hs.463483 // MMD // 23531 // Homo sapiens monocyte to macrophage differ	MMD2	MMD2, Homo sapiens monocyte to macrophage differentiation-associated 2 (MMD2), q23.1
SNP_A-1823219	taaaaccatgtatgca[A/G]atcactaaacgtagag	A	G	NM_021213 // downstream // 247224 // Hs.285218 // PCTP // 58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 128884 // Hs.463493 // FLJ38335 // 162282 // Homo sapiens hypothetical protein FLJ38335 (FLJ383	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2
SNP_A-2092341	agaaagctaaatcagc[A/G]gccacaagaatagtat	A	G	NM_021213 // downstream // 252554 // Hs.285218 // PCTP // 58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 123554 // Hs.463493 // FLJ38335 // 162282 // Homo sapiens hypothetical protein FLJ38335 (FLJ383	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2
SNP_A-1916303	tgttgtcatttgctgta[A/G]atggtgtcctcgcaa	A	G	NM_021213 // downstream // 253523 // Hs.285218 // PCTP // 58488 // Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA. /// NM_153228 // upstream // 122585 // Hs.463493 // FLJ38335 // 162282 // Homo sapiens hypothetical protein FLJ38335 (FLJ383	PCTP	PCTP, Homo sapiens phosphatidylcholine transfer protein (PCTP), q23.2
SNP_A-2162946	atttgtcattgtccc[A/G]ccttgggtcttttcca	A	G	NM_005450 // upstream // 65203 // Hs.248201 // NOG // 9241 // Homo sapiens noggin (NOG), mRNA. /// ENST00000338778 // downstream // 17442 // — // — // — /// ENST00000332822 // upstream // 65203 // — // — // —	NOG	NOG, Homo sapiens noggin (NOG), q23.2
SNP_A-1847197	tatcatttctaggtc[A/G]aattctcaaggaaga	A	G	NM_005450 // downstream // 108316 // Hs.248201 // NOG // 9241 // Homo sapiens noggin (NOG), mRNA. /// NM_003647 // upstream // 130690 // Hs.546318 // DGKE // 8526 // Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), mRNA. /// ENST00000332822 // do	NOG	NOG, Homo sapiens noggin (NOG), q23.2
SNP_A-2255577	cttgtggaaggaggag[C/T]cagaataaaaggagaa	C	T	NM_005450 // downstream // 136895 // Hs.248201 // NOG // 9241 // Homo sapiens noggin (NOG), mRNA. /// NM_003647 // upstream // 102111 // Hs.546318 // DGKE // 8526 // Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), mRNA. /// ENST00000332822 // do	NOG	NOG, Homo sapiens noggin (NOG), q23.2
SNP_A-1753933	tctataaagcagatatttccatca[C/T]gagatttcaaatctg aaaaa	C	T	NM_020178 // upstream // 1456366 // Hs.283110 // CA10 // 56934 // carbonic anhydrase X /// NM_032559 // upstream // 206531 // Hs.226805 // LOC84643 // 84643 // kinesin protein	CA10	CA10, rs1876697, carbonic anhydrase X, q22
SNP_A-1924572	ttatactgccactttc[C/T]ctagtctctgtagctc	C	T	NM_003647 // intron // 0 // Hs.546318 // DGKE // 8526 // Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), mRNA. /// ENST00000284061 // intron // 0 // — // — // — // —	DGKE	DGKE, Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), q23.2
SNP_A-2142915	atgaatatatatatgaa[A/G]ccctcacactccatc	A	G	NM_003647 // downstream // 25009 // Hs.546318 // DGKE // 8526 // Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), mRNA. /// NM_005082 // downstream // 2637 // Hs.528952 // TRIM25 // 7706 // Homo sapiens tripartite motif-containing 25 (TRIM25), mR	DGKE	DGKE, Homo sapiens diacylglycerol kinase, epsilon 64kDa (DGKE), q23.2
SNP_A-1944636	ttgtgacacggagtac[A/C]ctgatgacctcagagc	A	C	NM_005082 // intron // 0 // Hs.528952 // TRIM25 // 7706 // Homo sapiens tripartite motif-containing 25 (TRIM25), mRNA. /// ENST00000316881 // intron // 0 // — // — // — // —	TRIM25	TRIM25, Homo sapiens tripartite motif-containing 25 (TRIM25), q23.2
SNP_A-2071227	acacttaactcacttc[A/C]atcttctaaatacgtg	A	C	NM_138962 // intron // 0 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), t	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1890866	tgatgcctgccactca[A/G]tagatgctagttctc	A	G	NM_138962 // intron // 0 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), t	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-2213652	ccgtggaaatttctta[C/T]gggctggtgctgttcc	C	T	NM_138962 // intron // 0 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // intron // 0 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), t	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-2079157	acccaggctactcata[C/G]actcatgagaaataat	C	G	NM_138962 // downstream // 52219 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // downstream // 98975 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Droso	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-1727303	ctcagggcatgtcttctacaatatt[C/T]tatgtcatctagaccatttc aaatc	C	T	NM_004375 // downstream // 331694 // Hs.436988 // COX11 // 1353 // COX11 homolog, cytochrome c oxidase assembly protein (yeast) /// NM_005486 // upstream // 280631 // Hs.153504 // TOM1L1 // 10040 // target of myb1-like 1 (chicken) /// NM_032559 // downst	COX11	COX11, rs1373155, COX11 homolog, cytochrome c oxidase assembly protein (yeast), q22
SNP_A-2046112	aagactctcttcaaaa[A/G]aacaaaaaaagcagct	A	G	NM_138962 // downstream // 63100 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, mRNA. /// NM_170721 // downstream // 109856 // Hs.134470 // MSI2 // 124540 // Homo sapiens musashi homolog 2 (Dros	MSI2	MSI2, Homo sapiens musashi homolog 2 (Drosophila) (MSI2), transcript variant 1, q23.2
SNP_A-1833072	tacacaggctgagaaa[C/T]ccatgatccctggcct	C	T	NM_016070 // downstream // 91893 // Hs.5836 // MRPS23 // 51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 2316 // — // — // — /// ENST000	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-1793465	ggtagtggaatcaaga[A/G]gttgctgttttgcta	A	G	NM_016070 // downstream // 91724 // Hs.5836 // MRPS23 // 51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 2485 // — // — // — /// ENST000	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-2194239	catgaggaggctgtaa[C/T]cactgaaataggccag	C	T	NM_016070 // downstream // 91017 // Hs.5836 // MRPS23 // 51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 3192 // — // — // — /// ENST000	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-1706083	tacaggcacaaaattatactcgac[A/G]cagaatgagttggtgct ttccagag	A	G	NM_004375 // downstream // 271375 // Hs.436988 // COX11 // 1353 // COX11 homolog, cytochrome c oxidase assembly protein (yeast) /// NM_005486 // upstream // 220312 // Hs.153504 // TOM1L1 // 10040 // target of myb1-like 1 (chicken) /// NM_032559 // downst	COX11	COX11, rs10515075, COX11 homolog, cytochrome c oxidase assembly protein (yeast), q22
SNP_A-1841972	tagggaagtgcttaca[C/T]atcaatctgtacatgt	C	T	NM_016070 // downstream // 27216 // Hs.5836 // MRPS23 // 51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 66993 // — // — // — /// ENST00	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-1864522	tgggctttccactac[C/T]gctcaaaatagtaata	C	T	NM_016070 // downstream // 3872 // Hs.5836 // MRPS23 // 51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 90337 // — // — // — /// ENST000	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086345	actcttaccacaaagc[G/T]caagtcagcttggcct	G	T	NM_016070 // downstream // 201 // Hs.5836 // MRPS23 // 51649 // Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000299415 // upstream // 94008 // — // — // — // — /// ENST0000	MRPS23	MRPS23, Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, q23.2
SNP_A-1895041	tgcccagcaggatacc[C/T]cattcttcacgatgtg	C	T	NM_006151 // intron // 0 // Hs.234742 // LPO // 4025 // Homo sapiens lactoperoxidase (LPO), mRNA. /// ENST00000262290 // intron // 0 // — // — // — // —	LPO	LPO, Homo sapiens lactoperoxidase (LPO), q23.2
SNP_A-1866191	tcccaggtgctcccag[A/G]acatttaatttgtagt	A	G	NM_016261 // intron // 0 // Hs.463638 // TUBD1 // 51174 // Homo sapiens tubulin, delta 1 (TUBD1), mRNA. /// ENST00000346141 // intron // 0 // — // — // — // — /// ENST00000325752 // intron // 0 // — // — // — // — /// ENST00000340993 // in	TUBD1	TUBD1, Homo sapiens tubulin, delta 1 (TUBD1), q23.2
SNP_A-2256145	ctttactctgtggatc[C/T]aatctttcacttttttt	C	T	NM_003161 // intron // 0 // Hs.463642 // RPS6KB1 // 6198 // Homo sapiens ribosomal protein S6 kinase, 70kDa, polypeptide 1 (RPS6KB1), mRNA. /// ENST00000225577 // intron // 0 // — // — // — // —	RPS6KB1	RPS6KB1, Homo sapiens ribosomal protein S6 kinase, 70kDa, polypeptide 1 (RPS6KB1), q23.2
SNP_A-1860907	tcatacctcttactac[C/T]ggcttcagtatcaaaa	C	T	NM_006380 // intron // 0 // Hs.84084 // APPBP2 // 10513 // Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA. /// ENST00000083182 // intron // 0 // — // — // — // —	APPBP2	APPBP2, Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), q23.2
SNP_A-1729692	actgagcccagctctaattctaaaa[A/C]ctttaatatgactttcaa gatttta	A	C	NM_016070 // downstream // 143036 // Hs.5836 // MRPS23 // 51649 // mitochondrial ribosomal protein S23 /// NM_024846 // downstream // 416428 // - // - // - // - /// NM_138962 // downstream // 16507 // Hs.185084 // MSI2 // 124540 // musashi homolog 2 (Dro	MRPS23	MRPS23 , rs1544508, mitochondrial ribosomal protein S23 ,q23.2
SNP_A-1896556	tgctagaaaactgcta[C/G]acaaacatcatcagta	C	G	NM_017679 // intron // 0 // Hs.463702 // BCAS3 // 54828 // Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), mRNA. /// AK025510 // intron // 0 // Hs.463702 // BCAS3 // 54828 // Homo sapiens cDNA: FLJ21857 fis, clone HEP02294. /// ENST00000269133	BCAS3	BCAS3, Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), q23.2
SNP_A-1911170	tgtctgcaatagagac[A/G]cagagacgatgaattc	A	G	NM_017679 // intron // 0 // Hs.463702 // BCAS3 // 54828 // Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), mRNA. /// AK025510 // intron // 0 // Hs.463702 // BCAS3 // 54828 // Homo sapiens cDNA: FLJ21857 fis, clone HEP02294. /// ENST00000269133	BCAS3	BCAS3, Homo sapiens breast carcinoma amplified sequence 3 (BCAS3), q23.2
SNP_A-2169970	caaggctggtctttcc[C/T]ctaccttgagttccca	C	T	NM_005994 // intron // 0 // Hs.531085 // TBX2 // 6909 // Homo sapiens T-box 2 (TBX2), mRNA. /// ENST00000240328 // intron // 0 // — // — // — // —	TBX2	TBX2, Homo sapiens T-box 2 (TBX2), q23.2
SNP_A-1892630	tgcaattgctgaacca[C/T]gtggtaactctatgtt	C	T	NM_203425 // downstream // 9692 // Hs.434459 // LOC388407 // 388407 // Homo sapiens hypothetical gene supported by BC046200 (LOC388407), mRNA. /// NM_018488 // upstream // 33474 // Hs.143907 // TBX4 // 9496 // Homo sapiens T-box 4 (TBX4), mRNA. /// ENST00	LOC388407	LOC388407, Homo sapiens hypothetical gene supported by BC046200 (LOC388407), q23.2
SNP_A-2210429	cccccattgaccagag[A/G]aaaaaatagctgctgg	A	G	NM_018488 // intron // 0 // Hs.143907 // TBX4 // 9496 // Homo sapiens T-box 4 (TBX4), mRNA. /// ENST00000240335 // intron // 0 // — // — // — // —	TBX4	TBX4, Homo sapiens T-box 4 (TBX4), q23.2
SNP_A-2148393	atgggggaggataata[C/T]gaatgaaggtctaggg	C	T	NM_018488 // downstream // 22901 // Hs.143907 // TBX4 // 9496 // Homo sapiens T-box 4 (TBX4), mRNA. /// NM_199290 // downstream // 83329 // Hs.512195 // MGC71999 // 342538 // Homo sapiens alpha-NAC protein (MGC71999), mRNA. /// ENST00000240335 // downstre	TBX4	TBX4, Homo sapiens T-box 4 (TBX4), q23.2
SNP_A-2135651	atcaaaaatcatctca[C/G]tagggtcagaggggc	C	G	NM_152598 // intron // 0 // Hs.446268 // FLJ35757 // 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // intron // 0 // — // — // — // —	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1897003	tgctcattgaacagaa[A/G]gatctcaaggctgggt	A	G	NM_152598 // upstream // 106651 // Hs.446268 // FLJ35757 // 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // upstream // 106651 // — // — // — /// ENST00000339479 // upstream // 94565 // — // —	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-1833531	tacagcaattaatgctct[C/T]cgagtctcatttccca	C	T	NM_152598 // upstream // 113347 // Hs.446268 // FLJ35757 // 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // upstream // 113347 // — // — // — /// ENST00000339479 // upstream // 87869 // — // —	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-2170839	caataaactggaagga[A/G]gaaaaactatcactgc	A	G	NM_152598 // upstream // 148676 // Hs.446268 // FLJ35757 // 162333 // Homo sapiens hypothetical protein FLJ35757 (FLJ35757), mRNA. /// ENST00000311269 // upstream // 148676 // — // — // — /// ENST00000339479 // upstream // 52540 // — // —	FLJ35757	FLJ35757, Homo sapiens hypothetical protein FLJ35757 (FLJ35757), q23.3
SNP_A-2091532	agaaaaagcccaaaca[C/T]gtgaacataagaggtc	C	T	NM_152831 // intron // 0 // Hs.298469 // ACE // 1636 // Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 (ACE), transcript variant 3, mRNA. /// ENST00000290863 // intron // 0 // — // — // — // —	ACE	ACE, Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 (ACE), transcript variant 3, q23.3
SNP_A-1932521	ttcctgggaaaaaaaa[A/G]catcttgtaatgtatg	A	G	NM_018469 // intron // 0 // Hs.175414 // HT008 // 55852 // Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), mRNA. /// ENST00000258991 // intron // 0 // — // — // — // —	HT008	HT008, Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), q23.3
SNP_A-1864796	tccagcttgtggacaa[A/G]agacctaatggttccc	A	G	NM_003835 // intron // 0 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// ENST00000262406 // intron // 0 // — // — // — // —	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2231301	ctatttcctagactctat[A/T]cctagttctcataact	A	T	NM_003835 // intron // 0 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// ENST00000262406 // intron // 0 // — // — // — // —	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2313104	ggagaaattactctcta[A/T]cctatctttttcaatt	A	T	NM_003835 // downstream // 8979 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 292857 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. ///	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2175696	cacattaaggcttcca[C/T]agtctcagagtttcta	C	T	NM_003835 // downstream // 38021 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 263815 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. ///	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2186104	caggccaattgtcttat[C/T]actgactgataaaagc	C	T	NM_003835 // downstream // 46782 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 255054 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. ///	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2246032	ctggtagtttgcagaa[A/G]agatgagagtcaggaa	A	G	NM_003835 // downstream // 64840 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 236996 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. ///	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-1927748	ttcaagatgcactgac[A/G]cattgcattatccccc	A	G	NM_003835 // downstream // 73313 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 228523 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. ///	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1869655	tccttagggtagccaa[C/T]gaagcaaatgatgat	C	T	NM_003835 // downstream // 127821 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 174015 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2240488	ctgacatcagagaaagg[G/T]caggcttactcctt	G	T	NM_003835 // downstream // 161984 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 139852 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-1867960	atggcatcttataa[C/T]gagtatgagttgaaat	C	T	NM_003835 // downstream // 188049 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 113787 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2036834	aaatttcgacttccttg[A/T]aggatttcaatctatt	A	T	NM_003835 // downstream // 198569 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 103267 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-1908633	tgtagctgttgttcac[C/G]aagagatagccccict	C	G	NM_003835 // downstream // 199162 // Hs.132327 // RGS9 // 8787 // Homo sapiens regulator of G-protein signalling 9 (RGS9), mRNA. /// NM_004655 // downstream // 102674 // Hs.156527 // AXIN2 // 8313 // Homo sapiens axin 2 (conductin, axil) (AXIN2), mRNA. //	RGS9	RGS9, Homo sapiens regulator of G-protein signalling 9 (RGS9), q24.1
SNP_A-2169540	caagctatgcagcctct[G/T]aagtgcaagggctagg	G	T	NM_145036 // intron // 0 // Hs.408676 // MGC33887 // 201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// ENST00000284400 // intron // 0 // — // — // — // —	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-2073701	acagtccgggctttaa[C/T]agggagcctggaaca	C	T	NM_145036 // intron // 0 // Hs.408676 // MGC33887 // 201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// ENST00000284400 // intron // 0 // — // — // — // —	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-1840566	tagcccctggcaatcat[C/T]cactctacttgttta	C	T	NM_145036 // intron // 0 // Hs.408676 // MGC33887 // 201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// ENST00000284400 // intron // 0 // — // — // — // —	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-1669681	ctagcccigtgtggccatatgcagta[A/G]cactgaatagattaaagtaattg	A	G	NM_015623 // upstream // 496416 // - // - // - /// NM_025185 // upstream // 463954 // - // - // - /// NM_030658 // upstream // 429690 // - // - // - /// NM_152598 // upstream // 117031 // Hs.146197 // FLJ35757 // 162333 // hypothetical pro	-	-, rs10491166, -, q23.3
SNP_A-1890732	tgatgagttaaaggag[C/T]aagtctcaaaataata	C	T	NM_145036 // upstream // 99906 // Hs.408676 // MGC33887 // 201134 // Homo sapiens hypothetical protein MGC33887 (MGC33887), mRNA. /// NM_000042 // downstream // 49039 // Hs.445358 // APOH // 350 // Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (AP	MGC33887	MGC33887, Homo sapiens hypothetical protein MGC33887 (MGC33887), q24.1
SNP_A-1948164	tttagcagacgaaaac[A/C]actttggtagtgccag	A	C	NM_000042 // upstream // 1 // Hs.445358 // APOH // 350 // Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH), mRNA. /// NM_002737 // upstream // 73397 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST0	APOH	APOH, Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH), q24.2
SNP_A-2115417	agggggctggtttgata[C/T]cttgtggtctcctgc	C	T	NM_002737 // intron // 0 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // — // — // — // —	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1873918	tctcagttatgctaggl[A/C]agaaaaggagctctgt	A	C	NM_002737 // intron // 0 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // — // — // — // —	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1804756	gtcaggttctggtcac[A/G]ctgtcattctggctgc	A	G	NM_002737 // intron // 0 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1867144	ttacagaaagagaaggt[C/T]cattgcttgcaaacaa	C	T	NM_002737 // intron // 0 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1867048	tagttacacagataca[C/T]gcacctttttattat	C	T	NM_002737 // intron // 0 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1883468	tgaacatggcagctaa[A/G]cattggcacaagtctt	A	G	NM_002737 // intron // 0 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// ENST00000284384 // intron // 0 // --- // --- // --- // ---	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-1867009	cttcagtcactgggaa[G/T]cagcgcctctgcctac	G	T	NM_002737 // downstream // 14499 // Hs.531704 // PRKCA // 5578 // Homo sapiens protein kinase C, alpha (PRKCA), mRNA. /// NM_014404 // upstream // 52090 // Hs.278907 // CACNG5 // 27091 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 5 (C	PRKCA	PRKCA, Homo sapiens protein kinase C, alpha (PRKCA), q24.2
SNP_A-2118291	agtaacagccatgaaa[C/G]caacaaaccgcatcac	C	G	NM_014405 // intron // 0 // Hs.514423 // CACNG4 // 27092 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), mRNA. /// ENST00000262138 // intron // 0 // --- // --- // --- // ---	CACNG4	CACNG4, Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), q24.2
SNP_A-2182510	cagatagttaggcta[A/G]caatgtgattgatggt	A	G	NM_014405 // downstream // 5697 // Hs.514423 // CACNG4 // 27092 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), mRNA. /// NM_000727 // upstream // 5491 // Hs.147989 // CACNG1 // 786 // Homo sapiens calcium channel, voltage-de	CACNG4	CACNG4, Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), q24.2
SNP_A-2163055	attttacttttcaca[A/G]tctctaacatgacc	A	G	ENST00000356004 // intron // 0 // --- // --- // --- // --- /// ENST00000358691 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1827686	taactgttaaatttggt[A/G]caccatcgttgttca	A	G	ENST00000356004 // intron // 0 // --- // --- // --- // --- /// ENST00000358691 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1866813	tgactgatttggatga[G/T]gacattcccactgagc	G	T	ENST00000356004 // intron // 0 // --- // --- // --- // --- /// ENST00000358691 // intron // 0 // --- // --- // --- // ---	-	q24.2
SNP_A-1866807	tgtcattctggttttta[C/T]acgccagtggatggat	C	T	NM_174871 // downstream // 24218 // Hs.4295 // PSMD12 // 5718 // Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, mRNA. /// NM_002816 // downstream // 24218 // Hs.4295 // PSMD12 // 5718 // Homo sapie	PSMD12	PSMD12, Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), transcript variant 2, q24.2
SNP_A-1752365	ataaagagatccggtttctaagca[A/G]agtctcccagatcatac gcccacct	A	G	BC040521 // intron // 0 // Hs.16206 // HT008 // 55852 // uncharacterized hypothalamus protein HT008	HT008	HT008 , rs10512501, uncharacterized hypothalamus protein HT008.q23.3
SNP_A-1868611	aaagcatactgacaaaa[C/T]ctttgagactgtaaat	C	T	ENST00000284414 // upstream // 8853 // --- // --- // --- // --- /// ENST00000340441 // downstream // 13568 // --- // --- // --- // ---	-	q24.2
SNP_A-1668969	cgccccctgtacagtagattctttta[A/G]caccacctcagaacaca ctgaacag	A	G	NM_003835 // downstream // 55994 // Hs.117149 // RGS9 // 8787 // regulator of G-protein signalling 9 /// NM_004655 // downstream // 245846 // Hs.127337 // AXIN2 // 8313 // axin 2 (conductin, axil)	RGS9	RGS9 , rs718597, regulator of G-protein signalling 9 .q24.1
SNP_A-1803295	gtattggcaagagaacq[C/T]gagtttcaggccggtg	C	T	NM_014960 // intron // 0 // Hs.437249 // KIAA1001 // 22901 // Homo sapiens Arylsulfatase G (KIAA1001), mRNA. /// ENST00000355179 // intron // 0 // --- // --- // --- // --- /// ENST00000269079 // intron // 0 // --- // --- // --- // ---	KIAA1001	KIAA1001, Homo sapiens Arylsulfatase G (KIAA1001), q24.2
SNP_A-2059554	aatctcatctgccaca[A/G]gagactaaatctagcc	A	G	NM_017565 // upstream // 92750 // Hs.268874 // FAM20A // 54757 // Homo sapiens family with sequence similarity 20, member A (FAM20A), mRNA. /// NM_007168 // downstream // 173588 // Hs.58351 // ABCA8 // 10351 // Homo sapiens ATP-binding cassette, sub-famil	FAM20A	FAM20A, Homo sapiens family with sequence similarity 20, member A (FAM20A), q24.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920380	ttaatggattgtta[C/T]agtcaggcaattatcc	C	T	NM_017565 // upstream // 152936 // Hs.268874 // FAM20A // 54757 // Homo sapiens family with sequence similarity 20, member A (FAM20A), mRNA. /// NM_007168 // downstream // 113402 // Hs.58351 // ABCA8 // 10351 // Homo sapiens ATP-binding cassette, sub-fami	FAM20A	FAM20A, Homo sapiens family with sequence similarity 20, member A (FAM20A), q24.2
SNP_A-1662054	tacttatgcatggtctaatgaattc[C/T]ctttcttcttgttgtgcaatggct	C	T	NM_000042 // upstream // 44906 // Hs.1252 // APOH // 350 // apolipoprotein H (beta-2-glycoprotein I) /// NM_002737 // upstream // 28511 // Hs.349611 // PRKCA // 5578 // protein kinase C, alpha	APOH	APOH , rs1558358, apolipoprotein H (beta-2-glycoprotein I), q24.2
SNP_A-1872806	tctatagcacctcad[A/G]gatatcagccaggccc	A	G	NM_002758 // intron // 0 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // intron // 0 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein k	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1869581	gtagtagcccagaaga[C/T]gagaaaaaaggagttc	C	T	NM_002758 // downstream // 218032 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 218032 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2309672	ggaaagcaagaggtaa[A/C]tacaggtcaaatcaaa	A	C	NM_002758 // downstream // 219336 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 219336 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1922300	ttactttgctttctca[C/T]ccatccgattcaaaat	C	T	NM_002758 // downstream // 219511 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 219511 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1780986	ggatgagtgggggaata[C/G]agtgagtgcttgatat	C	G	NM_002758 // downstream // 337655 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 337655 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2144772	atgatggtatttaaggt[A/T]cactactgatgttctt	A	T	NM_002758 // downstream // 344081 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 344081 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1869702	ttctcattcaggtctc[C/T]caacaatagtgcaaag	C	T	NM_002758 // downstream // 359261 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 359261 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2179674	cacttctctgcaaata[C/G]taaaaggaatggca	C	G	NM_002758 // downstream // 418240 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 418240 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-1796008	ggtggtcttgcattga[C/G]taaggaggtaagtgga	C	G	NM_002758 // downstream // 497802 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 497802 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1895847	tgcctgggaagaagca[A/G]gagtaagttcatgaaa	A	G	NM_002758 // downstream // 513479 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA. /// NM_031988 // downstream // 513479 // Hs.463978 // MAP2K6 // 5608 // Homo sapiens mitogen-a	MAP2K6	MAP2K6, Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, q24.3
SNP_A-2308462	gctttacaaaatatgc[C/T]gcaccggagagtgga	C	T	NM_000891 // downstream // 3605 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 3605 // — // — // — /// ENST00000334565 // upstream /	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1870202	gcagcaaccttccaag[C/T]cttcgagtgctattgc	C	T	NM_000891 // downstream // 90325 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 90325 // — // — // — /// ENST00000334565 // upstream	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1870275	cctgtcctctctttaa[A/C]tgctccaaatatgctt	A	C	NM_000891 // downstream // 119060 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 119060 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1955319	tttgggcatacaggcc[A/G]gatatacacacacagg	A	G	NM_000891 // downstream // 490802 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 490802 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1875234	tctctcctctaaca[A/G]tgatggtactggtata	A	G	NM_000891 // downstream // 585644 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 585644 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2062892	aatgtggtagaagtaa[A/G]gttataagagtctag	A	G	NM_000891 // downstream // 722209 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 722209 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2217044	cctcttagctatgtgc[C/T]cttgaaaattaaact	C	T	NM_000891 // downstream // 822095 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 822095 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1850146	tatgtggagtttcaag[A/C]aatggtagaacattta	A	C	NM_000891 // downstream // 846086 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 846086 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1870864	aaagcatctgctcatc[A/G]aaagacactgaaaaaa	A	G	NM_000891 // downstream // 867669 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 867669 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1870903	gacaggataacaatac[A/C]atatctggactgtctg	A	C	NM_000891 // downstream // 945239 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 945239 // — // — // — /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2127828	ataacttggttccaa[G/T]atttgatttctaat	G	T	NM_000891 // downstream // 988681 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 988681 // — // — // — // /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2157830	attgccttggtagaaaa[A/G]gagtatggtgggcacc	A	G	NM_000891 // downstream // 990107 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 990107 // — // — // — // /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1819702	gttgtcacagccagaa[C/T]atttacaacagtgtg	C	T	NM_000891 // downstream // 996917 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 996917 // — // — // — // /// ENST00000334565 // upstre	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2184029	cagcccaactaaaccat[C/T]caactccaagactcac	C	T	NM_000891 // downstream // 1003311 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1003311 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1789719	gggctcatgaactgaa[C/T]agagggaatccagaaa	C	T	NM_000891 // downstream // 1019060 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1019060 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1924667	ttatagctatcataaa[A/G]gtgaagaaaaacatcc	A	G	NM_000891 // downstream // 1054836 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1054836 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2282931	gataacaatccaacac[A/C]gtgcttatggagcatg	A	C	NM_000891 // downstream // 1064691 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1064691 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2128838	ataatgacggagcacc[C/T]acaagaaacatccaag	C	T	NM_000891 // downstream // 1065866 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1065866 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-1905693	tggtatgatctgaatt[C/T]aagagtcctttctggc	C	T	NM_000891 // downstream // 1066751 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1066751 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2280656	gaggtccacgcttagc[A/G]gaatttgtagaatgga	A	G	NM_000891 // downstream // 1071744 // Hs.1547 // KCNJ2 // 3759 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), mRNA. /// ENST00000243457 // downstream // 1071744 // — // — // — // /// ENST00000334565 // upst	KCNJ2	KCNJ2, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 2 (KCNJ2), q24.3
SNP_A-2067136	acaaagatccatattat[C/T]cagcctctaaataca	C	T	ENST00000334565 // downstream // 59960 // — // — // — // — /// ENST00000355158 // upstream // 357371 // — // — // — // —	-	q24.3
SNP_A-2285141	gatctacttggctcca[A/C]attccacactgtcttc	A	C	ENST00000334565 // downstream // 217570 // — // — // — // — /// ENST00000355156 // upstream // 199761 // — // — // — // —	-	q24.3
SNP_A-2021177	aaaaaaagaaaggcaa[A/T]cagaggaagggata	A	T	ENST00000334565 // downstream // 281192 // — // — // — // — /// ENST00000355156 // upstream // 136139 // — // — // — // —	-	q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1913415	tgtggtataagagaag[G/T]agctaaacagagaaat	G	T	ENST00000334565 // downstream // 293527 /// --- /// --- /// --- /// ENST00000355156 // upstream // 123804 /// --- /// --- /// ---	-	q24.3
SNP_A-1828171	taagagacttgcaatg[A/G]atgtaataactggatg	A	G	NM_000346 // upstream // 46370 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// ENST00000356078 // downstream // 34174 /// --- /// --- /// --- /// ENST0000	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-2125366	agttgtttgggaaaaa[C/T]atgtccactagacct	C	T	NM_000346 // downstream // 73081 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 446456 // Hs.221127 // SLC39A11 // 201266 // Homo	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-2083102	acgttctctctaga[C/T]ggtctcatggttggcc	C	T	NM_000346 // downstream // 183348 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 336189 // Hs.221127 // SLC39A11 // 201266 // Homo	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-2294903	gcataacctggtgggat[A/G]atggtggtaccgccgc	A	G	NM_000346 // downstream // 183748 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 335789 // Hs.221127 // SLC39A11 // 201266 // Homo	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-1915470	tgttcctgctttggga[C/T]gcttctgcatgacat	C	T	NM_000346 // downstream // 183866 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 335671 // Hs.221127 // SLC39A11 // 201266 // Homo	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-1916098	tgttgcttagtactta[C/T]gactgagacttacacc	C	T	NM_000346 // downstream // 301049 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 218488 // Hs.221127 // SLC39A11 // 201266 // Homo	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-1871848	atttcttactattca[C/T]ctatgcattgtgtatt	C	T	NM_000346 // downstream // 360501 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 159036 // Hs.221127 // SLC39A11 // 201266 // Homo	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-2210137	ccccaggcttgcccca[C/T]gtttccactttccct	C	T	NM_000346 // downstream // 511512 // Hs.2316 // SOX9 // 6662 // Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA. /// NM_139177 // downstream // 8025 // Hs.221127 // SLC39A11 // 201266 // Homo s	SOX9	SOX9, Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), q24.3
SNP_A-1646978	gagaatgttaagtcttgcagtattg[C/T]ttaaccctgaaggagtttg tgttag	C	T	NM_002758 // downstream // 97386 // Hs.256924 // MAP2K6 // 5608 // mitogen-activated protein kinase kinase 6 /// NM_018658 // upstream // 434568 // Hs.414021 // KCNJ16 // 3773 // potassium inwardly-rectifying channel, subfamily J, member 16 /// NM_031988	MAP2K6	MAP2K6 , rs763698, mitogen-activated protein kinase kinase 6 q24.3
SNP_A-2117661	aggttcacctgattccg[C/T]cgacccatctggcttg	C	T	NM_139177 // intron // 0 // Hs.221127 // SLC39A11 // 201266 // Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- /// ENST00000356155 // intron // 0 //	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-1872026	ttcctaacttgtatac[A/G]ccaaccggaacattct	A	G	NM_139177 // intron // 0 // Hs.221127 // SLC39A11 // 201266 // Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // --- // --- // --- // --- /// ENST00000356155 // intron // 0 //	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2058876	aatccaatggcagga[C/T]gagaaaaacacatgga	C	T	NM_139177 // intron // 0 // Hs.221127 // SLC39A11 // 201266 // Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), mRNA. /// ENST00000255559 // intron // 0 // — // — // — // - /// ENST00000356155 // intron // 0 //	SLC39A11	SLC39A11, Homo sapiens solute carrier family 39 (metal ion transporter), member 11 (SLC39A11), q24.3
SNP_A-2221972	cgaaaggatttggtc[A/G]agggagtacaagaccc	A	G	NM_019064 // upstream // 58515 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 253835 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-1825122	taaaggtacgtccatc[C/G]gaacaaatggagaaac	C	G	NM_019064 // upstream // 65186 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 247164 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-2308894	gctttgtggcgtgtaa[C/T]aaagaactgccgagcag	C	T	NM_019064 // upstream // 81846 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 230504 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-2112947	aggcatggcacagaac[A/G]agggacgaaacaattg	A	G	NM_019064 // upstream // 203614 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 108736 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRN	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-1928645	ttcactgtcttctta[A/G]ctgtggtacctccagc	A	G	NM_019064 // upstream // 241346 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 71004 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-1933001	ttcgcaaatctctgcc[A/G]cacaaaatcatgagca	A	G	NM_019064 // upstream // 266750 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 45600 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-2106262	agcccgttctcttctc[G/T]ccttgccagctgtctg	G	T	NM_019064 // upstream // 277543 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 34807 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-1812304	gtggatgggcaagtga[C/T]agatgtgtggaaactc	C	T	NM_019064 // upstream // 291419 // Hs.435719 // SDK2 // 54549 // Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA. /// NM_182564 // downstream // 20931 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA	SDK2	SDK2, Homo sapiens sidekick homolog 2 (chicken) (SDK2), q25.1
SNP_A-1895533	tgcctagctcaaggccd[A/G]ataaccatgttgaacc	A	G	NM_182564 // upstream // 30465 // Hs.464079 // FLJ40319 // 283982 // Homo sapiens hypothetical protein FLJ40319 (FLJ40319), mRNA. /// NM_000999 // upstream // 349393 // Hs.380953 // RPL38 // 6169 // Homo sapiens ribosomal protein L38 (RPL38), mRNA. /// EN	FLJ40319	FLJ40319, Homo sapiens hypothetical protein FLJ40319 (FLJ40319), q25.1
SNP_A-1724538	ttcttattgggtgctggtatatctc[A/G]tcatttagagaggtctgagag aaga	A	G	BC034818 // upstream // 1112413 // Hs.381996 // - // - // Clone IMAGE:4825217, mRNA, partial cds /// NM_000891 // downstream // 779860 // Hs.1547 // KCNJ2 // 3759 // potassium inwardly-rectifying channel, subfamily J, member 2	-	-, rs1073572, Clone IMAGE:4825217, mRNA, partial cds ,q24.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082403	acgcagctgcacctgg[G/T]acagcagacacagctg	G	T	NM_152460 // downstream // 9693 // Hs.350775 // FLJ31882 // 146723 // Homo sapiens hypothetical protein FLJ31882 (FLJ31882), mRNA. /// NM_181449 // downstream // 5985 // Hs.158954 // IREM2 // 342510 // Homo sapiens immune receptor expressed on myeloid cel	FLJ31882	FLJ31882, Homo sapiens hypothetical protein FLJ31882 (FLJ31882), q25.1
SNP_A-1910973	tgtctcaggtctacac[A/G]agacaggagtgggag	A	G	NM_181449 // upstream // 2594 // Hs.158954 // IREM2 // 342510 // Homo sapiens immune receptor expressed on myeloid cells 2 (IREM2), mRNA. /// NM_175738 // upstream // 44244 // Hs.351413 // RAB37 // 326624 // Homo sapiens RAB37, member RAS oncogene family	IREM2	IREM2, Homo sapiens immune receptor expressed on myeloid cells 2 (IREM2), q25.1
SNP_A-1808721	gtgaagaggaatcaa[A/G]tgtgcaaggtttac	A	G	NM_175738 // intron // 0 // Hs.351413 // RAB37 // 326624 // Homo sapiens RAB37, member RAS oncogene family (RAB37), mRNA. /// ENST00000340415 // intron // 0 // — // — // — // — /// ENST00000318752 // intron // 0 // — // — // —	RAB37	RAB37, Homo sapiens RAB37, member RAS oncogene family (RAB37), q25.1
SNP_A-1873244	ttggaagctgcagtcc[A/G]ctccgtctcttccag	A	G	NM_017728 // intron // 0 // Hs.370262 // FLJ20255 // 54868 // Homo sapiens hypothetical protein FLJ20255 (FLJ20255), mRNA. /// ENST00000335464 // intron // 0 // — // — // —	FLJ20255	FLJ20255, Homo sapiens hypothetical protein FLJ20255 (FLJ20255), q25.1
SNP_A-1873248	gccagctaatttataa[C/T]gtcatatggctagac	C	T	NM_017728 // intron // 0 // Hs.370262 // FLJ20255 // 54868 // Homo sapiens hypothetical protein FLJ20255 (FLJ20255), mRNA. /// ENST00000335464 // intron // 0 // — // — // —	FLJ20255	FLJ20255, Homo sapiens hypothetical protein FLJ20255 (FLJ20255), q25.1
SNP_A-2305912	gctgctgcagtctgaa[C/T]ggtgacggtggcccct	C	T	NM_024585 // intron // 0 // Hs.413047 // ARMC7 // 79637 // Homo sapiens armadillo repeat containing 7 (ARMC7), mRNA. /// ENST00000245543 // intron // 0 // — // — // —	ARMC7	ARMC7, Homo sapiens armadillo repeat containing 7 (ARMC7), q25.1
SNP_A-1878403	tctgtgaagatgtggt[C/T]aagtcacaagtgatac	C	T	NM_001002032 // upstream // 5721 // Hs.532803 // HN1 // 51155 // Homo sapiens hematological and neurological expressed 1 (HN1), transcript variant 2, mRNA. /// NM_016185 // upstream // 5718 // Hs.532803 // HN1 // 51155 // Homo sapiens hematological and ne	HN1	HN1, Homo sapiens hematological and neurological expressed 1 (HN1), transcript variant 2, q25.1
SNP_A-1751539	ttatctttaaacacctttgaaata[C/T]tactcttcctggtgtctgaatt aga	C	T	NM_000346 // downstream // 302586 // Hs.2316 // SOX9 // 6662 // SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) /// NM_139177 // downstream // 216942 // Hs.3402 // SLC39A11 // 201266 // solute carrier family 39 (metal	SOX9	SOX9 , rs4793448, SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal), q24.3
SNP_A-1714497	gcaagctttttctgtaaaggaccac[A/G]gagtaaacatttcaact ttgtggg	A	G	NM_000346 // downstream // 340284 // Hs.2316 // SOX9 // 6662 // SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) /// NM_139177 // downstream // 179244 // Hs.3402 // SLC39A11 // 201266 // solute carrier family 39 (metal	SOX9	SOX9 , rs1035076, SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal), q24.3
SNP_A-2196165	catgtgctttaaaca[C/G]gtcttcaaagatcac	C	G	ENST00000325720 // intron // 0 // — // — // — /// ENST00000293201 // intron // 0 // — // — // —	-	q25.1
SNP_A-2293351	gcagatataatgactc[G/T]aatacctgtagccatc	G	T	NM_144677 // intron // 0 // Hs.144531 // MGAT5B // 146664 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari /// NM_198955 // intron // 0 // Hs.144531 // MGAT5B // 146664 //	MGAT5B	MGAT5B, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari .q25.2
SNP_A-2285040	gatcctgcccactctat[C/T]aaatgaggacacccagg	C	T	NM_144677 // intron // 0 // Hs.144531 // MGAT5B // 146664 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari /// NM_198955 // intron // 0 // Hs.144531 // MGAT5B // 146664 //	MGAT5B	MGAT5B, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari .q25.2
SNP_A-1818398	gttcttcaatttgaga[C/T]gaggccagactggatt	C	T	NM_144677 // downstream // 7184 // Hs.144531 // MGAT5B // 146664 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari /// NM_198955 // downstream // 7184 // Hs.144531 // MGAT5B	MGAT5B	MGAT5B, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari .q25.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1794161	ggtcagtggtcattgg[A/G]attcaagctaagtctt	A	G	NM_144677 // downstream // 42373 // Hs.144531 // MGAT5B // 146664 // Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript var /// NM_198955 // downstream // 42373 // Hs.144531 // MGAT	MGAT5B	MGAT5B, Homo sapiens mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isoenzyme B (MGAT5B), transcript vari ,q25.2
SNP_A-1671996	acgttcagcacttttgcaaactagaa[C/T]atgccccagaggctcc gggtgcaac	C	T	NM_139018 // intron // 0 // Hs.235768 // NKIR // 146722 // NK inhibitory receptor precursor /// NM_175738 // intron // 0 // Hs.351413 // RAB37 // 326624 // RAB37, member RAS oncogene family	NKIR	NKIR , rs10512597, NK inhibitory receptor precursor ,q25.1
SNP_A-2223146	cgcccccatccatgagc[A/G]agccaagggtagtatc	A	G	NM_006640 // downstream // 382167 // Hs.440932 // SEPT9 // 10801 // Homo sapiens MLL septin-like fusion (MSF), mRNA. /// NM_018996 // upstream // 166153 // Hs.80618 // TNRC6C // 57690 // Homo sapiens KIAA1582 protein (KIAA1582), mRNA. /// ENST00000329047	SEPT9	SEPT9, Homo sapiens MLL septin-like fusion (MSF), q25.3
SNP_A-2179348	cactgtgcaaggtagat[C/G]agtaacttttaaata	C	G	NM_006640 // downstream // 501562 // Hs.440932 // SEPT9 // 10801 // Homo sapiens MLL septin-like fusion (MSF), mRNA. /// NM_018996 // upstream // 46758 // Hs.80618 // TNRC6C // 57690 // Homo sapiens KIAA1582 protein (KIAA1582), mRNA. /// ENST00000329047 /	SEPT9	SEPT9, Homo sapiens MLL septin-like fusion (MSF), q25.3
SNP_A-2038678	aacagagagcgcccca[A/T]ctgtgtatccacaggg	A	T	NM_003955 // downstream // 37437 // Hs.527973 // SOCS3 // 9021 // Homo sapiens suppressor of cytokine signaling 3 (SOCS3), mRNA. /// ENST00000331036 // upstream // 65018 // — // — // — // — /// ENST00000327710 // upstream // 65018 // — // — //	SOCS3	SOCS3, Homo sapiens suppressor of cytokine signaling 3 (SOCS3), q25.3
SNP_A-2005322	tgccacgcaaaaccccd[A/T]agcacttttgtaggcat	A	T	NM_003955 // downstream // 30835 // Hs.527973 // SOCS3 // 9021 // Homo sapiens suppressor of cytokine signaling 3 (SOCS3), mRNA. /// ENST00000331036 // upstream // 71620 // — // — // — // — /// ENST00000327710 // upstream // 71620 // — // — //	SOCS3	SOCS3, Homo sapiens suppressor of cytokine signaling 3 (SOCS3), q25.3
SNP_A-2203601	ccagacaactgaagac[A/G]gcctatagcccagagc	A	G	NM_173628 // downstream // 9544 // — // FLJ40457 // 284176 // Homo sapiens hypothetical protein FLJ40457 (FLJ40457), mRNA. /// ENST00000300671 // upstream // 33820 // — // — // — // — /// ENST00000313223 // downstream // 9544 // — // — // -	FLJ40457	FLJ40457, Homo sapiens hypothetical protein FLJ40457 (FLJ40457), q25.3
SNP_A-2252473	cttcctcccaaaggaa[A/T]cctccatctctagttg	A	T	NM_173628 // downstream // 3625 // — // FLJ40457 // 284176 // Homo sapiens hypothetical protein FLJ40457 (FLJ40457), mRNA. /// ENST00000300671 // upstream // 39739 // — // — // — // — /// ENST00000313223 // downstream // 3625 // — // — // -	FLJ40457	FLJ40457, Homo sapiens hypothetical protein FLJ40457 (FLJ40457), q25.3
SNP_A-1836614	tactctgtacccagaa[A/C]ctcaccttctctggg	A	C	NM_003255 // intron // 0 // Hs.104839 // TIMP2 // 7077 // Homo sapiens tissue inhibitor of metalloproteinase 2 (TIMP2), mRNA. /// ENST00000262768 // intron // 0 // — // — // — // —	TIMP2	TIMP2, Homo sapiens tissue inhibitor of metalloproteinase 2 (TIMP2), q25.3
SNP_A-2297482	gccagaaaagagaaac[A/C]aggctacacgcaggac	A	C	NM_198594 // intron // 0 // Hs.201398 // C1QTNF1 // 114897 // Homo sapiens C1q and tumor necrosis factor related protein 1 (C1QTNF1), mRNA. /// NM_198593 // intron // 0 // Hs.201398 // C1QTNF1 // 114897 // Homo sapiens C1q and tumor necrosis factor relate	C1QTNF1	C1QTNF1, Homo sapiens C1q and tumor necrosis factor related protein 1 (C1QTNF1), q25.3
SNP_A-1839322	tagagtccaggtccac[A/G]gaagtagttaaggtt	A	G	NM_178543 // downstream // 7567 // Hs.114084 // ENPP7 // 339221 // Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 7 (ENPP7), mRNA. /// NM_032647 // upstream // 28409 // Hs.368410 // MGC10661 // 84733 // Homo sapiens hypothetical protein MGC	ENPP7	ENPP7, Homo sapiens ectonucleotide pyrophosphatase,q25.3
SNP_A-2254520	ctgcctgggacacc[A/G]atactcagctgacagc	A	G	ENST00000269336 // intron // 0 // — // — // — // —	-	q25.3
SNP_A-1956154	ttgtggaaagcaaca[A/G]tacatatcagtcaatg	A	G	NM_000152 // intron // 0 // Hs.1437 // GAA // 2548 // Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), mRNA. /// ENST00000302262 // intron // 0 // — // — // — // — /// ENST00000354343 // intron // 0 //	GAA	GAA, Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), q25.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1796490	ggttaagaagcaggaa[C/T]gtttgtcttgaggcca	C	T	NM_000152 // downstream // 2408 // Hs.1437 // GAA // 2548 // Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), mRNA. /// NM_000152 // downstream // 2412 // Hs.1437 // GAA // 2548 // Homo sapiens glucosidase, al	GAA	GAA, Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), q25.3
SNP_A-2097284	agagaaaaaagctcag[C/T]attagcagagaagacg	C	T	NM_000152 // downstream // 4842 // Hs.1437 // GAA // 2548 // Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), mRNA. /// NM_000152 // downstream // 4846 // Hs.1437 // GAA // 2548 // Homo sapiens glucosidase, al	GAA	GAA, Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), q25.3
SNP_A-2299110	gcccgccaagatctac[G/T]gaatcggacaccctgg	G	T	NM_000199 // intron // 0 // Hs.31074 // SGSH // 6448 // Homo sapiens N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH), mRNA. /// ENST00000326317 // intron // 0 // — // — // — // —	SGSH	SGSH, Homo sapiens N-sulfoglucosamine sulfohydrolase (sulfamidase) (SGSH), q25.3
SNP_A-1909842	tgtcacgaggaaggta[C/T]gaggaaggctgtcccc	C	T	NM_020761 // intron // 0 // Hs.133044 // raptor // 57521 // Homo sapiens raptor (raptor), mRNA. /// ENST00000306801 // intron // 0 // — // — // — // — /// ENST00000355313 // intron // 0 // — // — // — // —	raptor	raptor, Homo sapiens raptor (raptor), q25.3
SNP_A-2290564	gcaacttgcagttccg[A/G]agagcgctggctgctt	A	G	NM_017450 // downstream // 25597 // Hs.128316 // BAIAP2 // 10458 // Homo sapiens BAI1-associated protein 2 (BAIAP2), transcript variant 1, mRNA. /// NM_006340 // downstream // 19885 // Hs.128316 // BAIAP2 // 10458 // Homo sapiens BAI1-associated protein 2	BAIAP2	BAIAP2, Homo sapiens BAI1-associated protein 2 (BAIAP2), transcript variant 1, q25.3
SNP_A-2202198	ccacatggggcctcgc[A/G]ctcgcgttacccttcc	A	G	ENST00000333655 // upstream // 35616 // — // — // — // — /// ENST00000307745 // upstream // 21601 // — // — // — // — /// ENST00000288425 // upstream // 39696 // — // — // — // —	-	q25.3
SNP_A-2289629	gcaaaaatcaaatcca[A/G]tcaaactaaatcacca	A	G	NM_017921 // intron // 0 // Hs.464333 // NPL4 // 55666 // Homo sapiens nuclear protein localization 4 (NPL4), mRNA. /// ENST00000331134 // intron // 0 // — // — // — // —	NPL4	NPL4, Homo sapiens nuclear protein localization 4 (NPL4), q25.3
SNP_A-2213990	cctaactgtaacatca[A/G]gggaaagtgataggaa	A	G	NM_017921 // intron // 0 // Hs.464333 // NPL4 // 55666 // Homo sapiens nuclear protein localization 4 (NPL4), mRNA. /// ENST00000331134 // intron // 0 // — // — // — // —	NPL4	NPL4, Homo sapiens nuclear protein localization 4 (NPL4), q25.3
SNP_A-1910482	tgtccctgaacaccaa[A/C]taccgagacagctgat	A	C	ENST00000329214 // 3UTR // 0 // — // — // — // —	-	q25.3
SNP_A-2093288	agaacctttcacacgc[A/G]atctcagaatttacaa	A	G	NM_012140 // downstream // 5095 // Hs.511841 // SLC25A10 // 1468 // Homo sapiens solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (SLC25A10), mRNA. /// ENST00000350690 // downstream // 5095 // — // — // — // —	SLC25A10	SLC25A10, Homo sapiens solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (SLC25A10), q25.3
SNP_A-1955499	tttggtctctttggga[A/G]gaagttatacaaaaag	A	G	NM_001893 // intron // 0 // Hs.477070 // CSNK1D // 1453 // Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 1, mRNA. /// NM_139062 // intron // 0 // Hs.477070 // CSNK1D // 1453 // Homo sapiens casein kinase 1, delta (CSNK1D), transcript va	CSNK1D	CSNK1D, Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 1, q25.3
SNP_A-1717593	tggatcgtttcagtagcttatctga[A/G]gagcctctgcctagctga aggtcac	A	G	AB046860 // intron // 0 // Hs.512624 // FLJ20753 // 55036 // hypothetical protein FLJ20753	FLJ20753	FLJ20753 , rs2361701, hypothetical protein FLJ20753,q25.3
SNP_A-1916270	tgttgtaggcaatgtg[C/T]aattcctgaaaggctg	C	T	NM_005151 // intron // 0 // Hs.464416 // USP14 // 9097 // Homo sapiens ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), mRNA. /// ENST00000261601 // intron // 0 // — // — // — // —	USP14	USP14, Homo sapiens ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), p11.32
SNP_A-2074095	acagttttgaacacag[A/C]attaactaggtcttga	A	C	NM_005131 // upstream // 19656 // Hs.1540 // THOC1 // 9984 // Homo sapiens THO complex 1 (THOC1), mRNA. /// NM_030781 // downstream // 31651 // Hs.464422 // COLEC12 // 81035 // Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant II,	THOC1	THOC1, Homo sapiens THO complex 1 (THOC1), p11.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1737373	aaaatgtttaaaattccagattaa[G/T]tgcacattacttcttttttttct	G	T	NM_005131 // upstream // 27023 // Hs.1540 // THOC1 // 9984 // THO complex 1 /// NM_030781 // downstream // 24310 // Hs.29423 // COLEC12 // 81035 // collectin sub-family member 12 /// NM_130386 // downstream // 24310 // Hs.29423 // COLEC12 // 81035 // col	THOC1	THOC1, rs585955, THO complex 1, p11.32
SNP_A-2048660	aagccacagtacaaac[A/G]agtgagttgggttttt	A	G	NM_030781 // intron // 0 // Hs.464422 // COLEC12 // 81035 // Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant II, mRNA. /// NM_130386 // intron // 0 // Hs.464422 // COLEC12 // 81035 // Homo sapiens collectin sub-family member 12 (	COLEC12	COLEC12, Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant II, p11.32
SNP_A-2122370	agtgcccggcacatta[C/T]acatgcttaatagaca	C	T	NM_030781 // upstream // 28987 // Hs.464422 // COLEC12 // 81035 // Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant II, mRNA. /// NM_130386 // upstream // 28987 // Hs.464422 // COLEC12 // 81035 // Homo sapiens collectin sub-family	COLEC12	COLEC12, Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant II, p11.32
SNP_A-1876616	gtcccatttatcactc[A/T]cagtcctgaatttggt	A	T	NM_202758 // intron // 0 // Hs.475848 // — // 0 // Homo sapiens rTS beta protein (HSRTSBETA), transcript variant 1, mRNA. /// NM_017512 // intron // 0 // Hs.475848 // ENOSF1 // 55556 // Homo sapiens rTS beta protein (HSRTSBETA), transcript variant 2, mR	-	-, Homo sapiens rTS beta protein (HSRTSBETA), transcript variant 1, p11.32
SNP_A-1677586	gtaggagagccatcccgggcagcca[A/C]tagtatgtgcaaacgcttgcaaaca	A	C	NM_001117 // downstream // 17140 // Hs.68137 // ADCYAP1 // 116 // adenylate cyclase activating polypeptide 1 (pituitary) /// NM_031416 // downstream // 326200 // Hs.326788 // C18orf2 // 56651 // chromosome 18 open reading frame 2	ADCYAP1	ADCYAP1, rs10502291, adenylate cyclase activating polypeptide 1 (pituitary), p11.32
SNP_A-1876783	caaaatgaaatgttcc[C/G]caaacaaatattcagaa	C	G	NM_001117 // downstream // 21455 // Hs.531719 // ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 339936 // Hs.464442 // C18orf2 // 56651 // Homo sapiens chromosome 18 op	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-1656189	ttgggataagatgagcctcctggga[C/T]gcaaacactcctgaattagagtcat	C	T	NM_001117 // downstream // 21519 // Hs.68137 // ADCYAP1 // 116 // adenylate cyclase activating polypeptide 1 (pituitary) /// NM_031416 // downstream // 321821 // Hs.326788 // C18orf2 // 56651 // chromosome 18 open reading frame 2	ADCYAP1	ADCYAP1, rs4798774, adenylate cyclase activating polypeptide 1 (pituitary), p11.32
SNP_A-1654703	ataggctggtgttaactggcccaag[A/G]actgacattaaaagctggttagaa	A	G	NM_001117 // downstream // 21729 // Hs.68137 // ADCYAP1 // 116 // adenylate cyclase activating polypeptide 1 (pituitary) /// NM_031416 // downstream // 321611 // Hs.326788 // C18orf2 // 56651 // chromosome 18 open reading frame 2	ADCYAP1	ADCYAP1, rs4797355, adenylate cyclase activating polypeptide 1 (pituitary), p11.32
SNP_A-1876791	ctcctctactccca[G/T]actgtgatcaactgta	G	T	NM_001117 // downstream // 22849 // Hs.531719 // ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 338542 // Hs.464442 // C18orf2 // 56651 // Homo sapiens chromosome 18 op	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-2094604	agaatagacttcaaca[A/G]ggagcctgtggtatga	A	G	NM_001117 // downstream // 34680 // Hs.531719 // ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 326711 // Hs.464442 // C18orf2 // 56651 // Homo sapiens chromosome 18 op	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-1901681	tggcaataaatttacg[C/T]atttctctggctcta	C	T	NM_001117 // downstream // 106539 // Hs.531719 // ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 254852 // Hs.464442 // C18orf2 // 56651 // Homo sapiens chromosome 18 o	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1876908	ttcactgtgccttat[C/T]aattgcatttgttcac	C	T	NM_001117 // downstream // 142204 // Hs.531719 // ADCYAP1 // 116 // Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), mRNA. /// NM_031416 // downstream // 219187 // Hs.464442 // C18orf2 // 56651 // Homo sapiens chromosome 18 o	ADCYAP1	ADCYAP1, Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1), p11.32
SNP_A-2091928	agaaacaatggaagtc[C/T]aaacctgtaaaataat	C	T	NM_031416 // upstream // 80691 // Hs.464442 // C18orf2 // 56651 // Homo sapiens chromosome 18 open reading frame 2 (C18orf2), mRNA. /// ENST00000269201 // upstream // 80691 // — // — // — // — /// ENST00000334697 // upstream // 83238 // — // —	C18orf2	C18orf2, Homo sapiens chromosome 18 open reading frame 2 (C18orf2), p11.32
SNP_A-1676668	aaaattaacacaggacaaatctata[A/C]gacttgagtttggtgat aagatat	A	C	NM_022840 // downstream // 841867 // Hs.122546 // METTL4 // 64863 // methyltransferase like 4 /// NM_031416 // upstream // 426418 // Hs.326788 // C18orf2 // 56651 // chromosome 18 open reading frame 2	METTL4	METTL4 , rs718714, methyltransferase like 4 ,p11.32
SNP_A-1877867	ttcacctaatcctac[C/T]gggggcttagctgtat	C	T	NM_022840 // downstream // 508480 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 665176 // — // — // — // — /// ENST00000308448 // upstream // 665206 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1848526	tatgaatttggttca[A/C]cttccatagctgtact	A	C	NM_022840 // downstream // 442956 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 730700 // — // — // — // — /// ENST00000308448 // upstream // 730730 // — // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-2105568	agccacaggtaaccac[G/T]gatctcagaacaaaga	G	T	NM_022840 // downstream // 367443 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 806213 // — // — // — // — /// ENST00000308448 // upstream // 806243 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-2249088	ctgttccttcacaa[C/T]cacctcttgcacactg	C	T	NM_022840 // downstream // 363939 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 809717 // — // — // — // — /// ENST00000308448 // upstream // 809747 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1873712	tctcagaagcccttga[A/G]actactgtgcctgaat	A	G	NM_022840 // downstream // 270553 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 903103 // — // — // — // — /// ENST00000308448 // upstream // 903133 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1660493	taatatatagatgtgtttaataata[C/T]gttttcagaaaggcagttttttt	C	T	NM_022840 // downstream // 265640 // Hs.122546 // METTL4 // 64863 // methyltransferase like 4 /// NM_031416 // upstream // 1002645 // Hs.326788 // C18orf2 // 56651 // chromosome 18 open reading frame 2	METTL4	METTL4 , rs621949, methyltransferase like 4 ,p11.32
SNP_A-2037746	aacaagtacaatacac[C/T]ggaatgggacgcaaag	C	T	NM_022840 // downstream // 44596 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 1129060 // — // — // — // — /// ENST00000308448 // upstream // 1129090 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1899595	tggaagtaggagtagg[A/G]agaggagagtgtcccc	A	G	NM_022840 // downstream // 19632 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 1154024 // — // — // — // — /// ENST00000308448 // upstream // 1154054 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32
SNP_A-1878357	aggctgaaaactgcat[A/G]agctcagctgtcccat	A	G	NM_022840 // downstream // 16219 // Hs.126888 // METTL4 // 64863 // Homo sapiens methyltransferase like 4 (METTL4), mRNA. /// ENST00000328142 // upstream // 1157437 // — // — // — // — /// ENST00000308448 // upstream // 1157467 // — // — // —	METTL4	METTL4, Homo sapiens methyltransferase like 4 (METTL4), p11.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1649012	ttgttgttgtttgtgataccgta[C/G]attagtttttattgctgctgtaac	C	G	NM_003803 // upstream // 44654 // Hs.451604 // MYOM1 // 8736 // myomesin 1 (skelemin) 185kDa /// NM_006471 // upstream // 8922 // Hs.233936 // MRCL3 // 10627 // myosin regulatory light chain MRCL3	MYOM1	MYOM1 , rs2165807, myomesin 1 (skelemin) 185kDa_p11.31
SNP_A-2145434	atgcagcggtaaaaaa[G/T]taataaggatgatctc	G	T	NM_173211 // upstream // 20710 // Hs.373550 // TGIF // 7050 // Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, mRNA. /// NM_174886 // upstream // 20710 // Hs.373550 // TGIF // 7050 // Homo sapiens TGFB-induced factor	TGIF	TGIF, Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, p11.31
SNP_A-2300253	gcctcgccagcttaa[C/T]aaccgtttggatatga	C	T	NM_173211 // 5UTR // 0 // Hs.373550 // TGIF // 7050 // Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, mRNA. /// NM_174886 // 5UTR // 0 // Hs.373550 // TGIF // 7050 // Homo sapiens TGFB-induced factor (TALE family hom	TGIF	TGIF, Homo sapiens TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 7, p11.31
SNP_A-1903079	tggctgttacagtgaa[C/T]attaaagacttaaaat	C	T	NM_001003809 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, lar	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1682496	ctctttttgaaaagtctagggtata[C/T]acagtagcattgctttgaagaggaa	C	T	NM_004746 // intron // 0 // Hs.290270 // DLGAP1 // 9229 // discs, large (Drosophila) homolog-associated protein 1	DLGAP1	DLGAP1 , rs918174, discs, large (Drosophila) homolog-associated protein 1,p11.31
SNP_A-2145452	atgcaggaagcaataa[C/G]atgtggcactattgtc	C	G	NM_001003809 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, lar	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2063012	aatgttaattgctctc[G/T]aatgtcatcagatctt	G	T	NM_001003809 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, lar	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2047085	aagataaaaagctgga[C/T]ggaaagttgaacttac	C	T	NM_001003809 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // intron // 0 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, lar	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1787802	gggacctccttgggca[A/G]aaatcatccgtagctc	A	G	NM_001003809 // upstream // 74197 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 39358 // Hs.19872 // DLGAP1 // 9229 // Homo sapien	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1834826	taccataaagacccac[A/G]catgcaaacgttcatt	A	G	NM_001003809 // upstream // 340458 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 305619 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1810701	gtgcaccigctacac[A/G]agagtactaaggatcc	A	G	NM_001003809 // upstream // 404097 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 369258 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2285844	gatgagatactgtctc[A/G]cagatgtcagaatgtc	A	G	NM_001003809 // upstream // 481009 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 446170 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1850933	tattatagcggaccttt[A/C]aaaaatacgttatttg	A	C	NM_001003809 // upstream // 493598 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 458759 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1816579	gttagttaataacaaa[A/G]ctgtggtcatttctcc	A	G	NM_001003809 // upstream // 622455 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 587616 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1898719	tgctttatgccttctc[A/G]atcataaaaggaagat	A	G	NM_001003809 // upstream // 643638 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 608799 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2160148	atttcaaacctacccc[C/T]gatgcctcaaacctac	C	T	NM_001003809 // upstream // 653006 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 618167 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1911233	tgtctggatttgtcca[A/C]agcacccagaacaatg	A	C	NM_001003809 // upstream // 783854 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 749015 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1812940	gtggggcctaatggga[A/G]gtttagatcatgagga	A	G	NM_001003809 // upstream // 925911 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 891072 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1827531	taactctgcttataaa[A/G]ggggtgtattctccct	A	G	NM_001003809 // upstream // 935324 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 900485 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2277396	gagcaaaaataactga[C/G]acttgcaaaggaatgc	C	G	NM_001003809 // upstream // 964366 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 929527 // Hs.19872 // DLGAP1 // 9229 // Homo sapi	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-2083158	acgttttagctcctca[A/C]attaattctgaagcat	A	C	NM_001003809 // upstream // 1125210 // Hs.19872 // DLGAP1 // 9229 // Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, mRNA. /// NM_004746 // upstream // 1090371 // Hs.19872 // DLGAP1 // 9229 // Homo sa	DLGAP1	DLGAP1, Homo sapiens discs, large (Drosophila) homolog-associated protein 1 (DLGAP1), transcript variant beta, p11.31
SNP_A-1846804	tatcaatatctcacaa[C/T]cttacaaagttgaaat	C	T	NM_012307 // upstream // 110303 // Hs.213394 // EPB41L3 // 23136 // Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// NM_173464 // downstream // 377825 // Hs.128279 // L3MBTL4 // 91133 // Homo sapiens l(3)mbt-like 4 (Drosophil	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1661488	tgaaggatcccigggagtgattgtg[C/T]acctgagctgtggctttt gtctaag	C	T	NM_012307 // upstream // 111395 // Hs.103839 // EPB41L3 // 23136 // erythrocyte membrane protein band 4.1-like 3 /// NM_173464 // downstream // 374008 // Hs.95111 // FLJ35936 // 91133 // hypothetical protein FLJ35936	EPB41L3	EPB41L3 , rs7243271, erythrocyte membrane protein band 4.1-like 3 ,p11.31
SNP_A-2100674	agatacttcagagaac[A/G]atgaaaatgcacatcc	A	G	NM_012307 // upstream // 180204 // Hs.213394 // EPB41L3 // 23136 // Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// NM_173464 // downstream // 307924 // Hs.128279 // L3MBTL4 // 91133 // Homo sapiens l(3)mbt-like 4 (Drosophi	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-1951832	tttctaacacagagga[A/G]ccaacaaatgtgatgt	A	G	NM_012307 // upstream // 180682 // Hs.213394 // EPB41L3 // 23136 // Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// NM_173464 // downstream // 307446 // Hs.128279 // L3MBTL4 // 91133 // Homo sapiens l(3)mbt-like 4 (Drosophil	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-1758489	ttttctcatccaaggaaaacaaac[C/G]cttgctatcatttctctat cctc	C	G	NM_012307 // upstream // 360937 // Hs.103839 // EPB41L3 // 23136 // erythrocyte membrane protein band 4.1-like 3 /// NM_173464 // downstream // 124466 // Hs.95111 // FLJ35936 // 91133 // hypothetical protein FLJ35936	EPB41L3	EPB41L3, rs10502337, erythrocyte membrane protein band 4.1-like 3 ,p11.31
SNP_A-1945392	ttgttatcactctgac[C/T]ggtgtcttgtttttg	C	T	NM_012307 // upstream // 403888 // Hs.213394 // EPB41L3 // 23136 // Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA. /// NM_173464 // downstream // 84240 // Hs.128279 // L3MBTL4 // 91133 // Homo sapiens l(3)mbt-like 4 (Drosophila	EPB41L3	EPB41L3, Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), p11.31
SNP_A-2129402	atacaagtagcaagaa[A/C]tgaaatatagctggct	A	C	ENST00000317931 // intron // 0 // --- // --- // ---	-	p11.31
SNP_A-1936339	ttcttcctttctcac[A/C]agggcataatcgtgtc	A	C	ENST00000317931 // intron // 0 // --- // --- // ---	-	p11.31
SNP_A-2211702	ccctcccgcatggaa[G/T]tgactaaatagcagca	G	T	ENST00000317931 // intron // 0 // --- // --- // ---	-	p11.31
SNP_A-2221415	cctttcccacggctca[C/T]ctctcttggagttc	C	T	NM_173464 // intron // 0 // Hs.128279 // L3MBTL4 // 91133 // Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA. /// ENST00000317931 // intron // 0 // --- // --- // --- /// ENST00000284898: // intron // 0 // --- // --- // ---	L3MBTL4	L3MBTL4, Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), p11.31
SNP_A-1831885	taattgaaagtgataa[C/T]gtagaggactgatagc	C	T	NM_173464 // upstream // 3837 // Hs.128279 // L3MBTL4 // 91133 // Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), mRNA. /// ENST00000317931 // upstream // 3837 // --- // --- // --- // --- ENST00000284898 // upstream // 3837 // --- // --- // --- // --- //	L3MBTL4	L3MBTL4, Homo sapiens l(3)mbt-like 4 (Drosophila) (L3MBTL4), p11.31
SNP_A-1920645	ttaatttttgatata[C/G]gtgtttacagctataa	C	G	ENST00000340697 // upstream // 55465 // --- // --- // --- // --- /// ENST00000262227 // upstream // 270879 // --- // --- // --- // --- /// ENST00000314319 // upstream // 319358 // --- // --- // --- // ---	-	p11.31
SNP_A-2302752	gctactgcaaagatac[C/T]ggctttaactctgaat	C	T	ENST00000340697 // upstream // 61878 // --- // --- // --- // --- /// ENST00000262227 // upstream // 264466 // --- // --- // --- // --- /// ENST00000314319 // upstream // 312945 // --- // --- // --- // ---	-	p11.31
SNP_A-1803831	gtcaagcatggttgaa[C/T]tcactggcataaaacc	C	T	ENST00000340697 // upstream // 83810 // --- // --- // --- // --- /// ENST00000262227 // upstream // 242534 // --- // --- // --- // --- /// ENST00000314319 // upstream // 291013 // --- // --- // --- // ---	-	p11.31
SNP_A-2213030	ccgaattgtcaccagc[C/T]gatctgatgtccctcc	C	T	ENST00000340697 // upstream // 213370 // --- // --- // --- // --- /// ENST00000262227 // upstream // 112974 // --- // --- // --- // --- /// ENST00000314319 // upstream // 161453 // --- // --- // --- // ---	-	p11.31
SNP_A-2280561	gaggtaggagttaccl[A/G]aatttggagaaagcag	A	G	ENST00000340697 // upstream // 262589 // --- // --- // --- // --- /// ENST00000262227 // upstream // 63755 // --- // --- // --- // --- /// ENST00000314319 // upstream // 112234 // --- // --- // --- // ---	-	p11.31
SNP_A-2085202	actcaggtaatataaa[C/T]gaggccggaaatgag	C	T	ENST00000340697 // upstream // 304688 // --- // --- // --- // --- /// ENST00000262227 // upstream // 21656 // --- // --- // --- // --- /// ENST00000314319 // upstream // 70135 // --- // --- // --- // ---	-	p11.31
SNP_A-2229527	ctaggttgatggaga[A/G]aatcgtgttgtacgag	A	G	ENST00000217725 // intron // 0 // --- // --- // --- /// ENST00000344342 // intron // 0 // --- // --- // ---	-	p11.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1845075	tatacacgtacgcata[G/T]ataaatgtgaaataaa	G	T	NM_002845 // upstream // 134298 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000217725 // upstream // 460404 // --- // --- // --- /// ENST00000344342 // upstream // 353486 // -	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1882569	atagtgaccatcaata[C/T]ctggagggtagagga	C	T	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1841225	taggaaacttgcaaaa[A/G]agagttagttcactta	A	G	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1915575	tgttctatttttcaaq[G/T]ggcacatatcagtatt	G	T	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-2164357	caaaatctcaatagca[C/T]caaggttaagaaaccc	C	T	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1783281	ggcagtctggtcccig[A/G]aataagacctgctgtt	A	G	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1828676	taagctactcttggac[A/G]caggctctgctcactt	A	G	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-2246461	ctggttgctctacaf[C/G]cactggcaatgcctlc	C	G	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1830576	taatcataactgacaa[G/T]ctattaagggtacttg	G	T	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-2150585	atgtgagttgtagagc[A/C]agcatcaaatcatggt	A	C	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1781267	ggatgtagcctattgc[C/T]gaaaacaatgataaaa	C	T	NM_002845 // intron // 0 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // intron // 0 // --- // --- // ---	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-1674881	gtcccagttcatctcttgaggaaa[C/T]aaagggctaggggtg aaggaagg	C	T	NM_002845 // intron // 0 // Hs.154151 // PTPRM // 5797 // protein tyrosine phosphatase, receptor type, M	PTPRM	PTPRM , rs2242148, protein tyrosine phosphatase, receptor type, M,p11.23
SNP_A-1871712	tctaatctctgtatct[G/T]aattcctgcatctgat	G	T	NM_002845 // downstream // 18388 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // downstream // 18388 // --- // --- // --- /// ENST00000354369 // upstream // 556953 //	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23
SNP_A-2083016	acgtggtatcagtctat[C/T]ggagaggctaagctca	C	T	NM_002845 // downstream // 69256 // Hs.49774 // PTPRM // 5797 // Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA. /// ENST00000332175 // downstream // 69256 // --- // --- // --- /// ENST00000354369 // upstream // 607821 //	PTPRM	PTPRM, Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2050435	aaggataaggttaaat[C/G]acaccctacaaaccat	C	G	ENST00000327621 // downstream // 5437 // — // — // — // — /// ENST00000329286 // upstream // 57673 // — // — // — // —	-	p11.22
SNP_A-2198916	catttgatttttccta[C/T]gaagtctttgaaatca	C	T	ENST00000327621 // downstream // 16865 // — // — // — // — /// ENST00000329286 // upstream // 46245 // — // — // — // —	-	p11.22
SNP_A-1883215	ttattctatctcaaag[A/C]ctcaagacttggacta	A	C	ENST00000327621 // downstream // 21352 // — // — // — // — /// ENST00000329286 // upstream // 41758 // — // — // — // —	-	p11.22
SNP_A-1702745	tttcccagtttggtgatacaacaac[A/G]cttggagaattcaaagc ctcttatt	A	G	AB018345 // upstream // 155729 // Hs.434101 // KIAA0802 // 23255 // KIAA0802 /// NM_002845 // downstream // 221105 // Hs.154151 // PTPRM // 5797 // protein tyrosine phosphatase, receptor type, M /// NM_024976 // downstream // 610377 // - // - // - // -	KIAA0802	KIAA0802 , rs7505175, KIAA0802 ,p11.22
SNP_A-1883315	gttttgaaaaataggc[A/G]aaaaagtgtaggagaa	A	G	NM_015210 // upstream // 30016 // Hs.464563 // KIAA0802 // 23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000357520 // downstream // 35821 // — // — // — // — /// ENST00000306329 // upstream // 30016 // — // — // — // — /// ENS	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1883344	tggttacgagttcaca[A/C]cattttcagtgttaag	A	C	NM_015210 // upstream // 1279 // Hs.464563 // KIAA0802 // 23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000357520 // downstream // 64558 // — // — // — // — /// ENST00000306329 // upstream // 1279 // — // — // — // — /// ENST0	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1883346	tatcccatcaagagaa[C/T]gagctactcacttgac	C	T	NM_015210 // upstream // 1048 // Hs.464563 // KIAA0802 // 23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000357520 // downstream // 64789 // — // — // — // — /// ENST00000306329 // upstream // 1048 // — // — // — // — /// ENST0	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-2309761	ggaaagggcacagata[C/T]ggcaactcatccccca	C	T	NM_015210 // upstream // 980 // Hs.464563 // KIAA0802 // 23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000357520 // downstream // 64857 // — // — // — // — /// ENST00000306329 // upstream // 980 // — // — // — // — /// ENST000	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1814528	gtgtgctcacaatgca[A/G]cttttacactcagaga	A	G	NM_015210 // intron // 0 // Hs.464563 // KIAA0802 // 23255 // Homo sapiens KIAA0802 (KIAA0802), mRNA. /// ENST00000306329 // intron // 0 // — // — // — // — /// ENST00000359865 // intron // 0 // — // — // — // —	KIAA0802	KIAA0802, Homo sapiens KIAA0802 (KIAA0802), p11.22
SNP_A-1671450	gaaatggtgactagccccagcataa[C/T]gtttcttcaatttttaaa aaccac	C	T	AB018345 // downstream // 192327 // Hs.434101 // KIAA0802 // 23255 // KIAA0802 /// NM_021074 // upstream // 77623 // Hs.51299 // NDUFV2 // 4729 // NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	KIAA0802	KIAA0802 , rs987850, KIAA0802 ,p11.22
SNP_A-1916100	tgttgcttcaaataac[A/G]agatttcattcttttt	A	G	NM_021074 // upstream // 16505 // Hs.464572 // NDUFV2 // 4729 // Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), mRNA. /// ENST00000333526 // downstream // 65448 // — // - // — // — /// ENST00000318388 // upstream // 1	NDUFV2	NDUFV2, Homo sapiens NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), p11.22
SNP_A-2206380	ccatcgctttccttaa[A/T]atagatatcatgaaaa	A	T	NM_015208 // intron // 0 // Hs.464585 // ANKRD12 // 23253 // Homo sapiens ankyrin repeat domain 12 (ANKRD12), mRNA. /// ENST00000262126 // intron // 0 // — // — // — // —	ANKRD12	ANKRD12, Homo sapiens ankyrin repeat domain 12 (ANKRD12), p11.22
SNP_A-2308956	gcttttagtgtattta[C/T]caagatgttccaccat	C	T	NM_015208 // intron // 0 // Hs.464585 // ANKRD12 // 23253 // Homo sapiens ankyrin repeat domain 12 (ANKRD12), mRNA. /// ENST00000262126 // intron // 0 // — // — // — // —	ANKRD12	ANKRD12, Homo sapiens ankyrin repeat domain 12 (ANKRD12), p11.22
SNP_A-1898123	tgctgtgtgtttactc[C/T]agaacgccctgctcac	C	T	NM_020648 // downstream // 26008 // Hs.514685 // TWSG1 // 57045 // Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), mRNA. /// NM_006788 // upstream // 47110 // Hs.528993 // RALBP1 // 10928 // Homo sapiens ralA binding protein 1 (RALBP1),	TWSG1	TWSG1, Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2309934	ggaaatcattgcatag[A/G]cctctccctgacaata	A	G	NM_020648 // downstream // 55526 // Hs.514685 // TWSG1 // 57045 // Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), mRNA. /// NM_006788 // upstream // 17592 // Hs.528993 // RALBP1 // 10928 // Homo sapiens ralA binding protein 1 (RALBP1),	TWSG1	TWSG1, Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), p11.22
SNP_A-1834301	tacattacatatcctg[A/G]agcgcacgtgtaaaag	A	G	NM_006788 // intron // 0 // Hs.528993 // RALBP1 // 10928 // Homo sapiens ralA binding protein 1 (RALBP1), mRNA. /// ENST00000019317 // intron // 0 // --- // --- // --- // ---	RALBP1	RALBP1, Homo sapiens ralA binding protein 1 (RALBP1), p11.22
SNP_A-1730893	acaaatataaaaagaactagtcagcc[C/T]atatgtaacacatatt caacaaatc	C	T	NM_006788 // intron // 0 // Hs.75447 // RALBP1 // 10928 // ralA binding protein 1	RALBP1	RALBP1 , rs7240572, ralA binding protein 1,p11.22
SNP_A-1883892	aggcagaggcttcagc[A/G]taagatcccacagctt	A	G	NM_006788 // downstream // 428 // Hs.528993 // RALBP1 // 10928 // Homo sapiens ralA binding protein 1 (RALBP1), mRNA. /// NM_005134 // downstream // 8310 // Hs.464595 // PPP4R1 // 9989 // Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1),	RALBP1	RALBP1, Homo sapiens ralA binding protein 1 (RALBP1), p11.22
SNP_A-2005449	atgttggtaattcttg[G/T]actagttcaatctttt	G	T	NM_005134 // intron // 0 // Hs.464595 // PPP4R1 // 9989 // Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA. /// ENST00000285124 // intron // 0 // --- // --- // --- // ---	PPP4R1	PPP4R1, Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), p11.22
SNP_A-2128984	ataatgttaacttaaa[A/G]tatgtcacaaagatct	A	G	NM_005134 // intron // 0 // Hs.464595 // PPP4R1 // 9989 // Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA. /// ENST00000285124 // intron // 0 // --- // --- // --- // ---	PPP4R1	PPP4R1, Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), p11.22
SNP_A-2005450	ctgttcttgcaactaa[C/T]gagcatggattggagc	C	T	NM_005134 // upstream // 24476 // Hs.464595 // PPP4R1 // 9989 // Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), mRNA. /// NM_006868 // upstream // 69228 // Hs.99528 // RAB31 // 11031 // Homo sapiens RAB31, member RAS oncogene family (R	PPP4R1	PPP4R1, Homo sapiens protein phosphatase 4, regulatory subunit 1 (PPP4R1), p11.22
SNP_A-1810185	gtgatctgactctaca[A/G]cctcagcacctaattt	A	G	NM_006868 // intron // 0 // Hs.99528 // RAB31 // 11031 // Homo sapiens RAB31, member RAS oncogene family (RAB31), mRNA. /// ENST00000306096 // intron // 0 // --- // --- // --- // ---	RAB31	RAB31, Homo sapiens RAB31, member RAS oncogene family (RAB31), p11.22
SNP_A-1884103	gatgcacttggcaccg[C/G]atagtttttctcgggc	C	G	NM_006868 // intron // 0 // Hs.99528 // RAB31 // 11031 // Homo sapiens RAB31, member RAS oncogene family (RAB31), mRNA. /// ENST00000306096 // intron // 0 // --- // --- // --- // ---	RAB31	RAB31, Homo sapiens RAB31, member RAS oncogene family (RAB31), p11.22
SNP_A-1666674	catcgaagtctcaaatgtagtgtcc[A/C]agatgagaaatgtcatt caggaatt	A	C	NM_003574 // upstream // 23738 // Hs.165195 // VAPA // 9218 // VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa /// NM_032243 // downstream // 2358 // Hs.98712 // TXNDC2 // 84203 // thioredoxin domain containing 2 (spermatozoa)	VAPA	VAPA , rs10513878, VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa ,p11.22
SNP_A-2128559	ataatagacaagaata[A/G]gcaggaaaagtctcaa	A	G	NM_032243 // downstream // 4445 // Hs.98712 // TXNDC2 // 84203 // Homo sapiens thioredoxin domain containing 2 (spermatozoa) (TXNDC2), mRNA. /// NM_194434 // upstream // 21389 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane	TXNDC2	TXNDC2, Homo sapiens thioredoxin domain containing 2 (spermatozoa) (TXNDC2), p11.22
SNP_A-1824253	taaaccaaggtttccc[A/T]ggattgtctaacttag	A	T	NM_194434 // downstream // 79262 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 79262 // Hs.165195 // VAPA // 9218 // H	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2287215	gatgtctgtggccgca[A/G]tatcagaacgttataa	A	G	NM_194434 // downstream // 87947 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 87947 // Hs.165195 // VAPA // 9218 // H	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2277408	gagcaaaatgtcaaga[A/G]atctagaggtggtgta	A	G	NM_194434 // downstream // 89418 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 89418 // Hs.165195 // VAPA // 9218 // H	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-1797710	ggtttggacaaagaac[C/T]gttctgtcatgttt	C	T	NM_194434 // downstream // 92850 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 92850 // Hs.165195 // VAPA // 9218 // H	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2246918	ctgtatacgatatata[C/T]tactcaggtgataggt	C	T	NM_194434 // downstream // 96426 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 96426 // Hs.165195 // VAPA // 9218 // H	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2022539	aaaaatctggaaaata[A/G]taatgactcaataaat	A	G	NM_194434 // downstream // 179182 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 179182 // Hs.165195 // VAPA // 9218 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2298999	gccccggataacccca[C/G]agaatatagccagaga	C	G	NM_194434 // downstream // 190691 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 190691 // Hs.165195 // VAPA // 9218 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2172212	caatgtctcctcccca[C/T]ggatttttcacctcaa	C	T	NM_194434 // downstream // 258482 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 258482 // Hs.165195 // VAPA // 9218 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2038200	aacacatggaaaaggg[C/T]agtgtagacagatca	C	T	NM_194434 // downstream // 313245 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 313245 // Hs.165195 // VAPA // 9218 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2124296	agttatgtagcatgaa[C/T]gtggaataacccatca	C	T	NM_194434 // downstream // 464263 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 464263 // Hs.165195 // VAPA // 9218 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-1800360	gtactaggaagaaccc[A/T]cactttgatctcaat	A	T	NM_194434 // downstream // 475791 // Hs.165195 // VAPA // 9218 // Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, mRNA. /// NM_003574 // downstream // 475791 // Hs.165195 // VAPA // 9218 //	VAPA	VAPA, Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 2, p11.22
SNP_A-2139993	atctacttacatctta[A/C]agcatttgaggtcaat	A	C	NM_003826 // downstream // 4646 // Hs.464622 // NAPG // 8774 // Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG), mRNA. /// NM_022068 // downstream // 115852 // Hs.293907 // FAM38B // 63895 // Homo sapiens family with sequen	NAPG	NAPG, Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG), p11.22
SNP_A-1698925	ggtgtagattgttccacttcttgaa[C/T]gtaaagcccaacctctag aaaggg	C	T	NM_003826 // downstream // 7299 // Hs.370431 // NAPG // 8774 // N-ethylmaleimide-sensitive factor attachment protein, gamma /// NM_022068 // downstream // 113194 // Hs.293907 // FLJ23403 // 63895 // hypothetical protein FLJ23403	NAPG	NAPG, rs10502394, N-ethylmaleimide-sensitive factor attachment protein, gamma ,p11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1955303	tttgggagtcagaata[C/T]ggatcgaggtgagtca	C	T	NM_003826 // downstream // 16215 // Hs.464622 // NAPG // 8774 // Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG), mRNA. /// NM_022068 // downstream // 104283 // Hs.293907 // FAM38B // 63895 // Homo sapiens family with seque	NAPG	NAPG, Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG), p11.22
SNP_A-2310943	ggaaggcaagtcagga[C/T]tcatatcggtacagat	C	T	NM_207347 // intron // 0 // Hs.434163 // --- // 0 // Homo sapiens chromosome 18 open reading frame 30 (C18orf30), mRNA. /// ENST00000310146 // intron // 0 // --- // --- // --- // ---	-	-, Homo sapiens chromosome 18 open reading frame 30 (C18orf30), p11.22
SNP_A-2097312	agagaaaagcgtgcaa[A/G]taagtgctccgtgagg	A	G	ENST00000302079 // intron // 0 // --- // --- // --- // ---	-	p11.22
SNP_A-1886851	tgactgtcactgataa[C/T]aagaccgataagcaga	C	T	ENST00000302079 // upstream // 78452 // --- // --- // --- // --- /// ENST00000321719 // upstream // 659730 // --- // --- // --- // ---	-	p11.21
SNP_A-2227223	ctaattttgagttcat[A/T]aaatggtgctttttgt	A	T	ENST00000302079 // upstream // 434661 // --- // --- // --- // --- /// ENST00000321719 // upstream // 303521 // --- // --- // --- // ---	-	p11.21
SNP_A-2266425	gaaggttttatttcaa[C/T]ttcgaaggtgtcatca	C	T	ENST00000302079 // upstream // 436280 // --- // --- // --- // --- /// ENST00000321719 // upstream // 301902 // --- // --- // --- // ---	-	p11.21
SNP_A-1935145	ttctgcacagggttca[C/T]agtatttcataggaca	C	T	ENST00000302079 // upstream // 438699 // --- // --- // --- // --- /// ENST00000321719 // upstream // 299483 // --- // --- // --- // ---	-	p11.21
SNP_A-2142137	atcttttcttaccaaa[A/C]gtctcacaaaaccagt	A	C	ENST00000302079 // upstream // 449869 // --- // --- // --- // --- /// ENST00000321719 // upstream // 288313 // --- // --- // --- // ---	-	p11.21
SNP_A-1652048	cctgccgttgatggtctgttgaacc[A/G]ctccccgtctcactattccatgagt	A	G	NM_002071 // upstream // 235370 // Hs.136295 // GNAL // 2774 // guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type /// NM_020412 // upstream // 334641 // Hs.136295 // GNAL // 2774 // guanine nucleotide b	GNAL	GNAL , rs1004322, guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type ,p11.21
SNP_A-1947876	tttactttccatctca[C/T]tcctcaaaatatcctc	C	T	NM_182978 // upstream // 23717 // Hs.136295 // GNAL // 2774 // Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans /// NM_002071 // upstream // 86633 // Hs.136295 // GNAL // 2774	GNAL	GNAL, Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans ,p11.21
SNP_A-1831149	taatgccatgaaggga[A/G]aaaacaggattctcag	A	G	NM_182978 // upstream // 1694 // Hs.136295 // GNAL // 2774 // Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans /// NM_002071 // upstream // 64610 // Hs.136295 // GNAL // 2774	GNAL	GNAL, Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans ,p11.21
SNP_A-1708018	agaactgatgcttcaagaagatgaa[C/G]aaagtttgagcaacagtgtgcagtg	C	G	AK090868 // intron // 0 // Hs.136295 // GNAL // 2774 // guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	GNAL	GNAL , rs10502413, guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type,p11.21
SNP_A-1750333	ccttgctcgtagtagctgcctttca[C/T]agactacattccctgtgtcattcac	C	T	AK090868 // intron // 0 // Hs.136295 // GNAL // 2774 // guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	GNAL	GNAL , rs9303743, guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type,p11.21
SNP_A-2148660	atggtattaactttga[C/T]gtaatttgcattttgg	C	T	NM_182978 // intron // 0 // Hs.136295 // GNAL // 2774 // Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans /// NM_002071 // intron // 0 // Hs.136295 // GNAL // 2774 // Homo sap	GNAL	GNAL, Homo sapiens guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), trans p11.21
SNP_A-1844811	tataataagcaaaaca[C/T]tgtgacaactaaggtg	C	T	NM_138608 // intron // 0 // Hs.288147 // MPPE1 // 65258 // Homo sapiens metallophosphoesterase 1 (MPPE1), mRNA. /// NM_023075 // intron // 0 // Hs.288147 // MPPE1 // 65258 // Homo sapiens metallophosphoesterase 1 (MPPE1), mRNA. /// ENST00000317235 // intr	MPPE1	MPPE1, Homo sapiens metallophosphoesterase 1 (MPPE1), p11.21
SNP_A-2070968	acactctcactccacc[A/G]gcaatgagttaggtat	A	G	NM_014214 // intron // 0 // Hs.367992 // IMPA2 // 3613 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // intron // 0 // --- // --- // --- // ---	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2292842	gcagaaaatgatccaa[C/T]ggcttcccgctgctca	C	T	NM_014214 // intron // 0 // Hs.367992 // IMPA2 // 3613 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // intron // 0 // --- // --- // --- // ---	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1859954	tcaggtggcaggtgta[G/T]ctcttattcggtgagaa	G	T	NM_014214 // downstream // 5117 // Hs.367992 // IMPA2 // 3613 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // downstream // 5117 // — // — // — /// ENST00000331584 // downstream // 21011 // — // — ///	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2147909	atggctaaagtaagga[C/T]atgcaataaaaattta	C	T	NM_014214 // downstream // 8537 // Hs.367992 // IMPA2 // 3613 // Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA. /// ENST00000269159 // downstream // 8537 // — // — // — // — /// ENST00000331584 // downstream // 17591 // — // — ///	IMPA2	IMPA2, Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), p11.21
SNP_A-2215121	cctattggatagttcc[A/G]acatctgggccaggcc	A	G	NM_001279 // downstream // 23257 // Hs.249129 // CIDEA // 1149 // Homo sapiens cell death-inducing DFFA-like effector a (CIDEA), transcript variant 1, mRNA. /// NM_198289 // downstream // 23257 // Hs.249129 // CIDEA // 1149 // Homo sapiens cell death-indu	CIDEA	CIDEA, Homo sapiens cell death-inducing DFFA-like effector a (CIDEA), transcript variant 1, p11.21
SNP_A-2229699	ctagtcaagagtagaa[C/T]tgatgtaaggctaaag	C	T	NM_006796 // upstream // 22287 // Hs.528996 // AFG3L2 // 10939 // Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000269143 // intron // 0 // — // — // — // —	AFG3L2	AFG3L2, Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, p11.21
SNP_A-1886633	cttcttcctccctaac[A/G]gaacctgactttgtg	A	G	NM_006796 // intron // 0 // Hs.528996 // AFG3L2 // 10939 // Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, mRNA. /// NM_006553 // upstream // 8447 // Hs.514718 // C18orf43 // 10650 // Hom	AFG3L2	AFG3L2, Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, p11.21
SNP_A-1930561	ttccaaggcaattgac[C/T]acttagttatccctc	C	T	ENST00000309836 // intron // 0 // — // — // —	-	p11.21
SNP_A-2146125	atgccttggttcgggc[G/T]cttcctgagatctca	G	T	NM_024899 // upstream // 77244 // Hs.236940 // C18orf9 // 79959 // Homo sapiens chromosome 18 open reading frame 9 (C18orf9), mRNA. /// NM_020232 // downstream // 54210 // Hs.464652 // TNFSF5IP1 // 56984 // Homo sapiens tumor necrosis factor superfamily,	C18orf9	C18orf9, Homo sapiens chromosome 18 open reading frame 9 (C18orf9), p11.21
SNP_A-1692528	ggttttgattacctatgactgacac[C/T]ggcccaaatgactggtatggacag	C	T	NM_002828 // intron // 0 // Hs.446126 // PTPN2 // 5771 // protein tyrosine phosphatase, non-receptor type 2 /// NM_080422 // intron // 0 // Hs.446126 // PTPN2 // 5771 // protein tyrosine phosphatase, non-receptor type 2 /// NM_080423 // intron // 0 // Hs	PTPN2	PTPN2, rs10502415, protein tyrosine phosphatase, non-receptor type 2, p11.21
SNP_A-1782372	ggcaattcagaactaa[C/T]gttgtaagatctctag	C	T	NM_080423 // intron // 0 // Hs.123352 // PTPN2 // 5771 // Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, mRNA. /// NM_080422 // intron // 0 // Hs.123352 // PTPN2 // 5771 // Homo sapiens protein tyrosine phosp	PTPN2	PTPN2, Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, p11.21
SNP_A-2199153	catttaagcacattta[C/T]acctgagtgattgttg	C	T	NM_080423 // intron // 0 // Hs.123352 // PTPN2 // 5771 // Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, mRNA. /// NM_080422 // intron // 0 // Hs.123352 // PTPN2 // 5771 // Homo sapiens protein tyrosine phosp	PTPN2	PTPN2, Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, p11.21
SNP_A-2294450	gcagtacatatcaaag[G/T]cctcttgactcagata	G	T	NM_018069 // intron // 0 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, mRNA. /// NM_032142 // intron // 0 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), t	Cep192	Cep192, Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, p11.21
SNP_A-1832577	tacaaatgttacagtt[A/T]aaagtatatgcaccttt	A	T	NM_018069 // intron // 0 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, mRNA. /// NM_032142 // intron // 0 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), t	Cep192	Cep192, Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1672692	caatttaaaaacagttaaatgcata[A/G]aacaaagcagtagca caaataaaac	A	G	NM_032142 // intron // 0 // - // - // -	-	-, rs1787013, -,p11.21
SNP_A-1724620	ttggttaaaaatgacaaaaagactt[A/C]aaatggacttgtcagga gtgtgcta	A	C	NM_032142 // intron // 0 // - // - // -	-	-, rs571002, -,p11.21
SNP_A-2187401	caggttcctcacagcc[C/T]gcttttctgtagccc	C	T	NM_018069 // intron // 0 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, mRNA /// NM_032142 // intron // 0 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), t	Cep192	Cep192, Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, p11.21
SNP_A-2105729	agccagattctgctta[C/T]gttttggtgccccat	C	T	NM_018069 // downstream // 5634 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, mRNA /// NM_032142 // downstream // 5634 // Hs.100914 // Cep192 // 55125 // Homo sapiens centrosomal protein 192 k	Cep192	Cep192, Homo sapiens centrosomal protein 192 kDa (Cep192), transcript variant 2, p11.21
SNP_A-2079769	accctgaactacatta[C/T]gctgaacaagtaacca	C	T	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-2094768	agaatcatcctcttcaj[C/T]gttgtttaggatgta	C	T	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-2313982	ggagctctgtttcaaaa[C/T]acgttaatttctgttg	C	T	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1883931	tgaagaggagcagaga[C/T]gacttggccacccact	C	T	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1872038	tctacctatcagaaaa[A/C]gattacagaattcatg	A	C	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-2240083	ctgaaggcaattgcag[A/G]agccgtccaccgcatg	A	G	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1857954	tcacttgataggcccaa[A/T]attcatggcaggtcag	A	T	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1843458	tagtgaggtcattaat[A/G]aacagctggtgaatg	A	G	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2232557	ctcaccccacatgcta[C/T]ggagaacatttcagg	C	T	NM_181482 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, mRNA. /// NM_001003675 // intron // 0 // Hs.464697 // C18orf1 // 753 // Homo sapiens chromosome 18 open reading fr	C18orf1	C18orf1, Homo sapiens chromosome 18 open reading frame 1 (C18orf1), transcript variant a2, p11.21
SNP_A-1887468	gctgttatttggacgat[C/T]aggtttcccatccatt	C	T	NM_003799 // downstream // 46452 // Hs.8086 // RNMT // 8731 // Homo sapiens RNA (guanine-7-) methyltransferase (RNMT), mRNA. /// NM_005913 // upstream // 14758 // Hs.248145 // MC5R // 4161 // Homo sapiens melanocortin 5 receptor (MC5R), mRNA. /// ENST0000	RNMT	RNMT, Homo sapiens RNA (guanine-7-) methyltransferase (RNMT), p11.21
SNP_A-2266903	gaattatttcaccaca[A/T]cctttctggaaattgt	A	T	NM_145287 // downstream // 157122 // Hs.352635 // ZNF519 // 162655 // Homo sapiens zinc finger protein 519 (ZNF519), mRNA. /// ENST00000329784 // upstream // 27680 // --- // --- // --- /// ENST00000309305 // downstream // 157122 // --- // --- // --	ZNF519	ZNF519, Homo sapiens zinc finger protein 519 (ZNF519), p11.21
SNP_A-1693455	atcaaacatacagaacaggttgtgat[C/T]agtttttatgtctgcttg ctgtgg	C	T	NM_000529 // upstream // 98132 // Hs.248144 // MC2R // 4158 // melanocortin 2 receptor (adrenocorticotropic hormone) /// NM_145287 // downstream // 121075 // Hs.352635 // ZNF519 // 162655 // zinc finger protein 519	MC2R	MC2R , rs10502426, melanocortin 2 receptor (adrenocorticotropic hormone) ,p11.21
SNP_A-2204091	ccagcaatttggaag[A/C]cgaaccaggaggatca	A	C	ENST00000341645 // upstream // 183075 // --- // --- // --- // --- /// ENST00000358087 // upstream // 183462 // --- // --- // --- // --- /// ENST00000344409 // upstream // 183143 // --- // --- // --- // --- /// ENST00000320584 // upstream // 21675 // --- // -	-	p11.21
SNP_A-1877999	tctgtaacgatacttat[C/T]aaaatgcaagtgata	C	T	ENST00000341645 // upstream // 183435 // --- // --- // --- // --- /// ENST00000358087 // upstream // 183822 // --- // --- // --- // --- /// ENST00000344409 // upstream // 183503 // --- // --- // --- // --- /// ENST00000320584 // upstream // 21315 // --- // -	-	p11.21
SNP_A-1954238	tttgcaactactctca[C/T]taagttaccaagattt	C	T	ENST00000341645 // upstream // 193442 // --- // --- // --- // --- /// ENST00000358087 // upstream // 193829 // --- // --- // --- // --- /// ENST00000344409 // upstream // 193510 // --- // --- // --- // --- /// ENST00000320584 // upstream // 11308 // --- // -	-	p11.21
SNP_A-1882577	tgaaacaacctaaaca[C/T]taatgccgagtaatga	C	T	ENST00000341645 // upstream // 193603 // --- // --- // --- // --- /// ENST00000358087 // upstream // 193990 // --- // --- // --- // --- /// ENST00000344409 // upstream // 193671 // --- // --- // --- // --- /// ENST00000320584 // upstream // 11147 // --- // -	-	p11.21
SNP_A-2215835	cctcattattgaacac[A/T]gtcttacctaatttttc	A	T	ENST00000341645 // upstream // 196030 // --- // --- // --- // --- /// ENST00000358087 // upstream // 196417 // --- // --- // --- // --- /// ENST00000344409 // upstream // 196098 // --- // --- // --- // --- /// ENST00000320584 // upstream // 8720 // --- // -	-	p11.21
SNP_A-2280344	gaggggcccaacatta[A/G]taatgattccatacca	A	G	ENST00000341645 // upstream // 201111 // --- // --- // --- // --- /// ENST00000358087 // upstream // 201498 // --- // --- // --- // --- /// ENST00000344409 // upstream // 201179 // --- // --- // --- // --- /// ENST00000320584 // upstream // 3639 // --- // -	-	p11.21
SNP_A-2255984	ctttaaggtaitggac[A/G]aatagtcaaatgttct	A	G	NM_024935 // intron // 0 // Hs.54838 // KIAA1772 // 80000 // Homo sapiens KIAA1772 (KIAA1772), mRNA. /// ENST00000269218 // intron // 0 // --- // --- // ---	KIAA1772	KIAA1772, Homo sapiens KIAA1772 (KIAA1772), q11.1
SNP_A-2175435	cacatcatgatggcta[C/T]aaaatatgttgtaga	C	T	NM_138340 // intron // 0 // Hs.397978 // ABHD3 // 171586 // Homo sapiens abhydrolase domain containing 3 (ABHD3), mRNA. /// ENST00000289119 // intron // 0 // --- // --- // ---	ABHD3	ABHD3, Homo sapiens abhydrolase domain containing 3 (ABHD3), q11.2
SNP_A-2084637	actattaacatatatca[C/T]ctactgtgctatcca	C	T	NM_020774 // downstream // 250468 // Hs.140903 // MIB1 // 57534 // Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), mRNA. /// NM_005257 // upstream // 50170 // Hs.514746 // GATA6 // 2627 // Homo sapiens GATA binding protein 6 (GATA6), mRNA. /// ENST00	MIB1	MIB1, Homo sapiens mindbomb homolog 1 (Drosophila) (MIB1), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2303811	gctcagtacatcataa[A/C]tatttggcaaatgtta	A	C	NM_005257 // downstream // 148358 // Hs.514746 // GATA6 // 2627 // Homo sapiens GATA binding protein 6 (GATA6), mRNA. /// NM_022663 // downstream // 64008 // Hs.406709 // CTAGE1 // 64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAG	GATA6	GATA6, Homo sapiens GATA binding protein 6 (GATA6), q11.2
SNP_A-1892048	tgcaaacaaataaaag[G/T]catcattaccattgct	G	T	NM_005257 // downstream // 167892 // Hs.514746 // GATA6 // 2627 // Homo sapiens GATA binding protein 6 (GATA6), mRNA. /// NM_022663 // downstream // 44474 // Hs.406709 // CTAGE1 // 64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAG	GATA6	GATA6, Homo sapiens GATA binding protein 6 (GATA6), q11.2
SNP_A-1836464	tactccagcaattccc[A/G]gcagtctttttaaac	A	G	NM_022663 // upstream // 150562 // Hs.406709 // CTAGE1 // 64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 367916 // Hs.546282 // RBBP8 // 5932 // Homo sapiens retinobl	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-1934771	ttctcttgaactccat[A/G]agctgtagtaatcaac	A	G	NM_022663 // upstream // 165325 // Hs.406709 // CTAGE1 // 64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 353153 // Hs.546282 // RBBP8 // 5932 // Homo sapiens retinobl	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-1889774	tggctcccagcaaaga[C/T]gactccaggctttctt	C	T	NM_022663 // upstream // 279065 // Hs.406709 // CTAGE1 // 64693 // Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, mRNA. /// NM_203292 // upstream // 239413 // Hs.546282 // RBBP8 // 5932 // Homo sapiens retinobl	CTAGE1	CTAGE1, Homo sapiens cutaneous T-cell lymphoma-associated antigen 1 (CTAGE1), transcript variant 2, q11.2
SNP_A-1916200	tgttgggctctgggaa[A/G]gtgcatgtaggaagcc	A	G	NM_138375 // intron // 0 // Hs.11108 // CABLES1 // 91768 // Homo sapiens Cdk5 and Abl enzyme substrate 1 (CABLES1), mRNA. /// ENST00000256925 // intron // 0 // — // — // — // — /// ENST00000322369 // intron // 0 // — // — // — // —	CABLES1	CABLES1, Homo sapiens Cdk5 and Abl enzyme substrate 1 (CABLES1), q11.2
SNP_A-1863212	tcatttctcaaccatc[G/T]attttcctgcttccaa	G	T	NM_003831 // intron // 0 // Hs.445511 // RIOK3 // 8780 // Homo sapiens RIO kinase 3 (yeast) (RIOK3), transcript variant 1, mRNA. /// NM_145906 // intron // 0 // Hs.445511 // RIOK3 // 8780 // Homo sapiens RIO kinase 3 (yeast) (RIOK3), transcript variant 2,	RIOK3	RIOK3, Homo sapiens RIO kinase 3 (yeast) (RIOK3), transcript variant 1, q11.2
SNP_A-1940869	ttgctacagagaagaa[A/C]ttcctgtgctaagcat	A	C	NM_198129 // intron // 0 // Hs.436367 // LAMA3 // 3909 // Homo sapiens laminin, alpha 3 (LAMA3), transcript variant 1, mRNA. /// ENST00000313654 // intron // 0 // — // — // — // —	LAMA3	LAMA3, Homo sapiens laminin, alpha 3 (LAMA3), transcript variant 1, q11.2
SNP_A-2266428	gaagtaaaaatgagaa[A/G]tgaggggtgtgatatt	A	G	NM_198129 // intron // 0 // Hs.436367 // LAMA3 // 3909 // Homo sapiens laminin, alpha 3 (LAMA3), transcript variant 1, mRNA. /// ENST00000313654 // intron // 0 // — // — // — // —	LAMA3	LAMA3, Homo sapiens laminin, alpha 3 (LAMA3), transcript variant 1, q11.2
SNP_A-1813779	gtgtagtactgcagtc[C/T]gaactgtaagcatgaa	C	T	NM_153211 // intron // 0 // Hs.546474 // C18orf17 // 125488 // Homo sapiens chromosome 18 open reading frame 17 (C18orf17), mRNA. /// ENST00000304621 // intron // 0 // — // — // — // —	C18orf17	C18orf17, Homo sapiens chromosome 18 open reading frame 17 (C18orf17), q11.2
SNP_A-2309070	gcttttgtctcattaa[C/T]tatacctggacacact	C	T	NM_153211 // intron // 0 // Hs.546474 // C18orf17 // 125488 // Homo sapiens chromosome 18 open reading frame 17 (C18orf17), mRNA. /// ENST00000304621 // intron // 0 // — // — // — // —	C18orf17	C18orf17, Homo sapiens chromosome 18 open reading frame 17 (C18orf17), q11.2
SNP_A-1807039	gtctccaacttcctaa[A/C]caccagttactaataa	A	C	NM_138643 // intron // 0 // Hs.511983 // CABYR // 26256 // Homo sapiens calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2) (CABYR), transcript variant 5, mRNA. /// NM_138644 // intron // 0 // Hs.511983 // CABYR // 26256 // Homo sapi	CABYR	CABYR, Homo sapiens calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2) (CABYR), transcript variant 5, q11.2
SNP_A-2145817	atgccataacatttac[C/T]ccacaactactgctct	C	T	ENST00000340580 // intron // 0 // — // — // — // — /// ENST00000344172 // intron // 0 // — // — // — // —	-	q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2198390	cattttaatgttgaa[A/T]gaaacagaccaccaac	A	T	ENST00000340580 // upstream // 94319 // --- // --- /// ENST00000359604 // upstream // 184579 // --- // --- // --- /// ENST00000344172 // upstream // 95322 // --- // --- // --- /// ENST00000357293 // downstream // 253492 // ---	-	q11.2
SNP_A-2106364	agcccttctctggctc[A/G]ctgtttggcctgctgt	A	G	ENST00000340580 // upstream // 183815 // --- // --- // --- /// ENST00000359604 // upstream // 274075 // --- // --- // --- /// ENST00000344172 // upstream // 184818 // --- // --- // --- /// ENST00000357293 // downstream // 163996 // ---	-	q11.2
SNP_A-2090521	actgtatacacccaa[C/T]catcgaaccaataatt	C	T	ENST00000340580 // upstream // 196954 // --- // --- // --- /// ENST00000359604 // upstream // 287214 // --- // --- // --- /// ENST00000344172 // upstream // 197957 // --- // --- // --- /// ENST00000357293 // downstream // 150857 // ---	-	q11.2
SNP_A-1824274	taaaccaggctggaaa[A/G]agtgctcctagagtat	A	G	ENST00000340580 // upstream // 199804 // --- // --- // --- /// ENST00000359604 // upstream // 290064 // --- // --- // --- /// ENST00000344172 // upstream // 200807 // --- // --- // --- /// ENST00000357293 // downstream // 148007 // ---	-	q11.2
SNP_A-1891388	tacatgggacttgaaa[C/T]ggatgtacatgggtgt	C	T	ENST00000340580 // upstream // 267673 // --- // --- // --- /// ENST00000359604 // upstream // 357933 // --- // --- // --- /// ENST00000344172 // upstream // 268676 // --- // --- // --- /// ENST00000357293 // downstream // 80138 // ---	-	q11.2
SNP_A-2166583	caaatgtaaccagcta[C/T]gtgcgggtgtctggat	C	T	ENST00000340580 // upstream // 277318 // --- // --- // --- /// ENST00000359604 // upstream // 367578 // --- // --- // --- /// ENST00000344172 // upstream // 278321 // --- // --- // --- /// ENST00000357293 // downstream // 70493 // ---	-	q11.2
SNP_A-1694227	ttcctccatggagctacaacttac[C/G]atatcttcctccccatttc tctga	C	G	NM_015461 // downstream // 58849 // Hs.280305 // ZNF521 // 25925 // zinc finger protein 521 /// NM_021624 // downstream // 523122 // Hs.287388 // HRH4 // 59340 // histamine receptor H4	ZNF521	ZNF521 , rs1941616, zinc finger protein 521 , q11.2
SNP_A-1870392	tcctttgccttaat[C/T]aagtgagatttggctt	C	T	ENST00000340580 // upstream // 294077 // --- // --- // --- /// ENST00000359604 // upstream // 384337 // --- // --- // --- /// ENST00000344172 // upstream // 295080 // --- // --- // --- /// ENST00000357293 // downstream // 53734 // ---	-	q11.2
SNP_A-2256617	ctttcacagttgtata[C/T]gcagctagcaagaaaa	C	T	ENST00000357293 // intron // 0 // --- // --- // --- /// ENST00000355656 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-1905754	tggtattattggagc[C/T]gaatttcacctgtatt	C	T	ENST00000357293 // intron // 0 // --- // --- // --- /// ENST00000355656 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-2301414	gcctttcaggctgcc[A/G]aaaattcatgttggcg	A	G	ENST00000357293 // intron // 0 // --- // --- // --- /// ENST00000355656 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-2125449	agtttagagtatcttat[C/T]caggcaagtggctaga	C	T	ENST00000357293 // intron // 0 // --- // --- // --- /// ENST00000355656 // intron // 0 // --- // --- // ---	-	q11.2
SNP_A-2301150	gccttcgtgccaaact[C/T]actaggccctgaggat	C	T	Y09321 // intron // 0 // Hs.369519 // TAF4B // 6875 // H.sapiens TAFII105 mRNA, partial. /// ENST00000269142 // intron // 0 // --- // --- // ---	TAF4B	TAF4B, H.sapiens TAFII105 partial, q11.2
SNP_A-2235168	ctccccatcctcaaac[C/G]caggtaaaatgtttcg	C	G	Y09321 // intron // 0 // Hs.369519 // TAF4B // 6875 // H.sapiens TAFII105 mRNA, partial. /// ENST00000269142 // intron // 0 // --- // --- // ---	TAF4B	TAF4B, H.sapiens TAFII105 partial, q11.2
SNP_A-1892100	acaacagaagtttcta[C/G]gaacttgcacacaca	C	G	Y09321 // downstream // 47948 // Hs.369519 // TAF4B // 6875 // H.sapiens TAFII105 mRNA, partial. /// NM_198991 // downstream // 16950 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. ///	TAF4B	TAF4B, H.sapiens TAFII105 partial, q11.2
SNP_A-1785975	ggctgcagttattaca[C/G]ctctctatttcttg	C	G	NM_198991 // intron // 0 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // --- // --- // ---	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1894707	tgccagcatccaatcc[A/G]agaaccaatgaatcac	A	G	NM_198991 // intron // 0 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // — // — // — // —	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-2232276	ctcaatgtagtacaaaa[A/C]aaagaatggtgatttct	A	C	NM_198991 // intron // 0 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // — // — // — // —	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-2312578	ggaccttgagtgataa[C/T]agtgtgtcaatgttc	C	T	NM_198991 // intron // 0 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // — // — // — // —	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-2161309	attgatggttttgt[C/T]aactgagcaagtattt	C	T	NM_198991 // intron // 0 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // — // — // — // —	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-1871013	tcgtcaagtacctgtc[A/G]aaacgcaacccctct	A	G	NM_198991 // intron // 0 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// ENST00000317932 // intron // 0 // — // — // — // —	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-2057564	aatatgaagagcgtac[C/T]gtaatggcttaaac	C	T	NM_198991 // upstream // 149313 // Hs.526630 // KCTD1 // 284252 // Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), mRNA. /// NM_001650 // downstream // 73491 // Hs.315369 // AQP4 // 361 // Homo sapiens aquaporin 4 (AQP4), trans	KCTD1	KCTD1, Homo sapiens potassium channel tetramerisation domain containing 1 (KCTD1), q11.2
SNP_A-1659192	tctcccattgttagcaattaggcaa[A/G]gacattagtgacagagg ggcatcca	A	G	NM_031422 // intron // 0 // Hs.231943 // CHST9 // 83539 // carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	CHST9	CHST9, rs335920, carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9,q11.2
SNP_A-2046379	aagagacaatgtcatg[A/G]aaaaggggagaacaga	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-2005536	gtcagtgtatcattat[C/T]atttctggtcatcca	C	T	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-2005537	actgtgggcaatttta[A/G]gcacccaaccatggta	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1892840	agaatgaaacaacata[C/T]ctacgtagctagcaag	C	T	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-2038036	aacacaagttttaga[A/G]cacactgcatcagtga	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1892862	ccttggtaacatcaa[A/C]ccttggaaaagttgg	A	C	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1841860	taggctatatcttgca[C/T]gttattgactcctatt	C	T	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2040007	aacattttaagaggac[A/G]ctgaacatttcctag	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1892894	ggatgtggaaggatac[A/G]aaaacagagataaagg	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1836972	tactggatcacgtctat[A/G]gaaaatttaaaatatgc	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1950457	tttcagttaaataatc[A/G]gacaatgtatatgatt	A	G	NM_031422 // intron // 0 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// ENST00000284224 // intron // 0 // — // — // —	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-2157512	attgatcttctcttta[C/T]gccagatttaacagcg	C	T	NM_031422 // upstream // 36020 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 286972 // Hs.546489 // C18orf16 // 147429 // Homo sapiens chromosome 18	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1656687	ccttccttatagaatgaatttgaa[A/T]gagtagttaacaaatacgt aaatgc	A	T	NM_001650 // upstream // 378798 // Hs.315369 // AQP4 // 361 // aquaporin 4 /// NM_001792 // downstream // 706446 // Hs.334131 // CDH2 // 1000 // cadherin 2, type 1, N-cadherin (neuronal) /// NM_004028 // upstream // 381955 // Hs.315369 // AQP4 // 361 //	AQP4	AQP4, rs10502487, aquaporin 4 ,q11.2
SNP_A-1716057	gaaatttttcctggagttataggc[C/T]gattatattagtctgttctca cact	C	T	NM_001650 // upstream // 379065 // Hs.315369 // AQP4 // 361 // aquaporin 4 /// NM_001792 // downstream // 706179 // Hs.334131 // CDH2 // 1000 // cadherin 2, type 1, N-cadherin (neuronal) /// NM_004028 // upstream // 382222 // Hs.315369 // AQP4 // 361 //	AQP4	AQP4, rs10502488, aquaporin 4 ,q11.2
SNP_A-1893078	gaacctagtggcacca[A/T]caggattgtcagagcc	A	T	NM_031422 // upstream // 170383 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 421335 // Hs.546489 // C18orf16 // 147429 // Homo sapiens chromosome 18	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q11.2
SNP_A-1694647	tctgggaaactgaaaaataaataata[A/C]gccatgaatacctctat ttttatgt	A	C	NM_001650 // upstream // 492225 // Hs.315369 // AQP4 // 361 // aquaporin 4 /// NM_001792 // downstream // 593019 // Hs.334131 // CDH2 // 1000 // cadherin 2, type 1, N-cadherin (neuronal) /// NM_004028 // upstream // 495382 // Hs.315369 // AQP4 // 361 //	AQP4	AQP4, rs7242201, aquaporin 4 ,q11.2
SNP_A-2239438	ctctttgcctttcaccf[A/G]ctctggaaaacatcct	A	G	NM_031422 // upstream // 293558 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 544510 // Hs.546489 // C18orf16 // 147429 // Homo sapiens chromosome 18	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q12.1
SNP_A-2212502	ccctaagtaactcgc[A/G]cacgcgggacctgttc	A	G	NM_031422 // upstream // 383644 // Hs.44584 // CHST9 // 83539 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), mRNA. /// NM_153010 // downstream // 634596 // Hs.546489 // C18orf16 // 147429 // Homo sapiens chromosome 18	CHST9	CHST9, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (CHST9), q12.1
SNP_A-2298614	gcccactggaattaa[A/C]agagtaccaattcca	A	C	NM_001792 // intron // 0 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // — // — // —	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1893615	aactgccgatggttgc[G/T]atatggctatttccaa	G	T	NM_001792 // intron // 0 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // — // — // —	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2241432	ctgagtcagattaaaa[A/G]tggactggcttccata	A	G	NM_001792 // intron // 0 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // — // — // —	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1950057	ttcacagttattatc[A/T]catctgaaccatatta	A	T	NM_001792 // intron // 0 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // — // — // —	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1834553	taccaactgtcaataa[C/T]gtcacataaattacat	C	T	NM_001792 // intron // 0 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // — // — // —	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1940630	ttgcctcttacctcag[A/G]aaaggacaccatatgg	A	G	NM_001792 // intron // 0 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// ENST00000269141 // intron // 0 // — // — // —	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2256584	ctttcaagggtaacca[A/G]cttctcaacatgaaaa	A	G	NM_001792 // upstream // 145863 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 2667977 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1792816	ggtaataacatctaag[A/C]aatggctttctctaa	A	C	NM_001792 // upstream // 764934 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 2048906 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2074663	acatatcaaactcaaa[A/C]ctcaaagctcatatat	A	C	NM_001792 // upstream // 846682 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 1967158 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1853561	tatttttaactgttcc[A/T]gaatatgtataggata	A	T	NM_001792 // upstream // 1219682 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 1593958 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript vana	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1830019	taatacatacactaaa[A/G]cagttaggcgagggca	A	G	NM_001792 // upstream // 1454051 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 1359789 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript vana	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2149129	atgtaaactatgctta[A/G]agaaaatcagaaagtc	A	G	NM_001792 // upstream // 1516267 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 1297573 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript vana	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-2005549	tgcatatacaaataca[A/G]tgcacccatgaaatga	A	G	NM_001792 // upstream // 1586369 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 1227471 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript vana	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1929531	ttcataatcatttcca[A/G]catttccaaagaactg	A	G	NM_001792 // upstream // 2431940 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 381900 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1895606	cacacatttttcatagc[C/T]cacttttgtctaccaga	C	T	NM_001792 // upstream // 2703456 // Hs.464829 // CDH2 // 1000 // Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA. /// NM_001941 // downstream // 110384 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript varian	CDH2	CDH2, Homo sapiens cadherin 2, type 1, N-cadherin (neuronal) (CDH2), q12.1
SNP_A-1675259	tgtgaaaaacacataggcaagataa[C/G]tagcccaatctaggg aatttgacag	C	G	NM_001941 // downstream // 103172 // Hs.41690 // DSC3 // 1825 // desmocollin 3 /// NM_024423 // downstream // 103172 // Hs.41690 // DSC3 // 1825 // desmocollin 3	DSC3	DSC3 , rs10502551, desmocollin 3 ,q12.1
SNP_A-1895669	gagaggtataatcaag[A/C]agcgtgaagctgagtc	A	C	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-1895670	tccgaaatcctagtg[C/T]agcatttagaagtcct	C	T	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-1822058	gttttcctcttcttta[A/G]ctattctcaccgtctc	A	G	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-1957367	ttttagctgttgatcc[C/T]gatgaacctgtccatg	C	T	NM_001941 // CDS // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // CDS // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// ENST000	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2107357	agctaatttgaaatga[C/G]attgctactgataat	C	G	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2048608	aagccaaataaaggca[A/C]cttcccatactcagat	A	C	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2103211	agcaactgctggcaat[C/G]agaaatggatggaaat	C	G	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2263014	gaacaattaaactcag[G/T]gcaataggaaaaattc	G	T	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2120219	agtcaggcatatcaat[A/T]aaagtcctacatcaaa	A	T	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086099	actctctcaccttcta[C/G]agcacaactggatttt	C	G	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-2172934	cacaaaaccccaaatg[C/T]atgcttgtaaactgaa	C	T	NM_001941 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, mRNA. /// NM_024423 // intron // 0 // Hs.41690 // DSC3 // 1825 // Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3b, mRNA. /// E	DSC3	DSC3, Homo sapiens desmocollin 3 (DSC3), transcript variant Dsc3a, q12.1
SNP_A-1853049	tattgcatttctaaa[A/G]cttgatatacttcct	A	G	NM_024421 // upstream // 46196 // Hs.348436 // DSC1 // 1823 // Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, mRNA. /// NM_004948 // upstream // 46196 // Hs.348436 // DSC1 // 1823 // Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1	DSC1	DSC1, Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, q12.1
SNP_A-1895946	ccctggaaagaaagaat[A/G]gagccagaattctgt	A	G	NM_024421 // upstream // 84078 // Hs.348436 // DSC1 // 1823 // Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, mRNA. /// NM_004948 // upstream // 84078 // Hs.348436 // DSC1 // 1823 // Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1	DSC1	DSC1, Homo sapiens desmocollin 1 (DSC1), transcript variant Dsc1a, q12.1
SNP_A-1824512	taaactgtctagctag[C/T]cctttggtatatgag	C	T	NM_014939 // intron // 0 // Hs.202001 // KIAA1012 // 22878 // Homo sapiens KIAA1012 (KIAA1012), mRNA. /// ENST00000283351 // intron // 0 // — // — // — /// ENST00000355989 // intron // 0 // — // — // — // —	KIAA1012	KIAA1012, Homo sapiens KIAA1012 (KIAA1012), q12.1
SNP_A-1679908	aaatactttctaataaatttgtga[A/G]tgaatgatctaatgcctatta tt	A	G	NM_005925 // intron // 0 // Hs.194777 // MEP1B // 4225 // meprin A, beta	MEP1B	MEP1B , rs10502585, meprin A, beta q12.1
SNP_A-2052424	aagtactgtttgaga[A/G]gactgaattggtgccc	A	G	NM_005925 // downstream // 20796 // Hs.194777 // MEP1B // 4225 // Homo sapiens meprin A, beta (MEP1B), mRNA. /// NM_022751 // downstream // 26319 // Hs.444314 // C18orf11 // 64762 // Homo sapiens chromosome 18 open reading frame 11 (C18orf11), mRNA. /// E	MEP1B	MEP1B, Homo sapiens meprin A, beta (MEP1B), q12.1
SNP_A-1710878	gtacacagatactgaaaatgcacac[A/G]ctgcactcggcatctt cagcgcctc	A	G	AB037805 // downstream // 196119 // Hs.88442 // KIAA1384 // 57565 // KIAA1384 protein /// NM_022751 // upstream // 6068 // Hs.12727 // C18orf11 // 64762 // chromosome 18 open reading frame 11	KIAA1384	KIAA1384 , rs10502603, KIAA1384 protein, q12.1
SNP_A-1683030	atgaaagaatttaaggcaaattcaa[C/T]gctgataatgaacatta atgtacat	C	T	AB037805 // downstream // 184989 // Hs.88442 // KIAA1384 // 57565 // KIAA1384 protein /// NM_022751 // upstream // 17198 // Hs.12727 // C18orf11 // 64762 // chromosome 18 open reading frame 11	KIAA1384	KIAA1384 , rs10502604, KIAA1384 protein, q12.1
SNP_A-2308068	gcttgacagaagtgga[C/T]ataaggaaagttgagg	C	T	NM_022751 // upstream // 48741 // Hs.444314 // C18orf11 // 64762 // Homo sapiens chromosome 18 open reading frame 11 (C18orf11), mRNA. /// AB037805 // downstream // 153502 // Hs.446164 // KLHL14 // 57565 // Homo sapiens mRNA for KIAA1384 protein, partial	C18orf11	C18orf11, Homo sapiens chromosome 18 open reading frame 11 (C18orf11), q12.1
SNP_A-1934268	ttctccaggcttctcc[C/T]ggaatattcatggcaa	C	T	AB037805 // intron // 0 // Hs.446164 // KLHL14 // 57565 // Homo sapiens mRNA for KIAA1384 protein, partial cds. /// ENST00000359358 // intron // 0 // — // — // — /// ENST00000358095 // intron // 0 // — // — // — // — /// ENST00000003556	KLHL14	KLHL14, Homo sapiens for KIAA1384 protein, partial cds. ,q12.1
SNP_A-2304066	gctccaggtaaaaca[C/G]agcatggatcttcaaa	C	G	AB037805 // upstream // 137377 // Hs.446164 // KLHL14 // 57565 // Homo sapiens mRNA for KIAA1384 protein, partial cds. /// NM_198995 // downstream // 29691 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34).	KLHL14	KLHL14, Homo sapiens for KIAA1384 protein, partial cds. q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2005562	aacaggcttaacttaa[C/T]gtggcaaatgattgag	C	T	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2143811	atgagagcctaatgca[A/G]aaggtgtctgtaagga	A	G	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2213218	ccgcatttagagtcca[A/T]ccaaatcactataaag	A	T	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2064423	aattccaatagattca[A/G]cctcgaaggtcttct	A	G	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1943627	ttgtaatcttcataaa[A/G]gaacctgtaaaatttt	A	G	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1916267	tgttgtagctattgca[A/G]atgagatctttcatt	A	G	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1884498	tgaagttactcacaaa[C/G]agacttggagccccgct	C	G	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1726904	caaatattatagccacacagaatga[A/T]ctttaaaatatggggct gagcaggg	A	T	AB051500 // upstream // 635233 // Hs.307003 // KIAA1713 // 80816 // KIAA1713 protein	KIAA1713	KIAA1713 , rs273024, KIAA1713 protein,q12.1
SNP_A-2037455	aacaacaatttatgca[A/C]ctgctgtccataaat	A	C	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1830997	taatgagaggtagttc[G/T]aaaatacaggcaatcc	G	T	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1879121	tcttacaagatagaaa[C/G]acctaaatgtgtacat	C	G	NM_198995 // intron // 0 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // intron // 0 // — // — // —	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-2025201	aaaataggccattata[C/G]ggaaataccagtaata	C	G	NM_198995 // upstream // 4564 // Hs.115461 // C18orf34 // 374864 // Homo sapiens chromosome 18 open reading frame 34 (C18orf34), mRNA. /// ENST00000300227 // upstream // 4564 // — // — // — /// ENST00000269197 // upstream // 294545 // — //	C18orf34	C18orf34, Homo sapiens chromosome 18 open reading frame 34 (C18orf34), q12.1
SNP_A-1700193	gaatcaaattaaaatgttggaaata[C/T]agtcatcattaacatttt aaatgc	C	T	AB051500 // upstream // 275897 // Hs.307003 // KIAA1713 // 80816 // KIAA1713 protein	KIAA1713	KIAA1713 , rs9304121, KIAA1713 protein,q12.1
SNP_A-1748091	aacataattcagcataaccagtta[A/G]gtttctttctatgtttcttg tct	A	G	AB051500 // upstream // 76244 // Hs.307003 // KIAA1713 // 80816 // KIAA1713 protein	KIAA1713	KIAA1713 , rs1981360, KIAA1713 protein,q12.1
SNP_A-2074610	acatataaaatgcttcc[A/G]gatttaaagtggctt	A	G	NM_003787 // intron // 0 // Hs.546322 // NOL4 // 8715 // Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // - // — // — /// ENST00000261592 // intron // 0 // — // — // — // —	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2294448	gcagtacatacagcaa[A/G]tcgccaaatgaaaata	A	G	NM_003787 // intron // 0 // Hs.546322 // NOL4 // 8715 // Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // – - // — // — /// ENST00000261592 // intron // 0 // — // — // —	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-1898353	ttatatggttgaattg[A/G]atgagagttaatatgg	A	G	NM_003787 // intron // 0 // Hs.546322 // NOL4 // 8715 // Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // – - // — // — /// ENST00000261592 // intron // 0 // — // — // —	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-2005569	ctggagtatttctgg[A/G]atttcctcaaccact	A	G	NM_003787 // intron // 0 // Hs.546322 // NOL4 // 8715 // Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // – - // — // — /// ENST00000261592 // intron // 0 // — // — // —	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-2102616	agattggttgtagal[A/T]aaggaagaattcacag	A	T	NM_003787 // intron // 0 // Hs.546322 // NOL4 // 8715 // Homo sapiens nucleolar protein 4 (NOL4), mRNA. /// ENST00000269185 // intron // 0 // – - // — // — /// ENST00000261592 // intron // 0 // — // — // —	NOL4	NOL4, Homo sapiens nucleolar protein 4 (NOL4), q12.1
SNP_A-1898453	gccagtctacactgcd[A/G]aagtgtttcacttagc	A	G	NM_001390 // intron // 0 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, mRNA. /// ENST00000283365 // intron // 0 // — // — // —	DTNA	DTNA, Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, q12.1
SNP_A-1930088	ttcattaaaccccaaga[A/G]gacctctatctccaat	A	G	NM_001390 // intron // 0 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, mRNA. /// NM_032975 // intron // 0 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 2, mRNA. /	DTNA	DTNA, Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, q12.1
SNP_A-2005574	taagtcacttaatgtc[C/T]caaagctcatatttttt	C	T	NM_001390 // intron // 0 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, mRNA. /// NM_032975 // intron // 0 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 2, mRNA. /	DTNA	DTNA, Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, q12.1
SNP_A-1695525	tctctggcctaagttctaagagaaa[A/C]atgattgtgctataagct agggact	A	C	NM_001390 // downstream // 147798 // Hs.255526 // DTNA // 1837 // dystrobrevin, alpha /// NM_001391 // downstream // 165238 // Hs.255526 // DTNA // 1837 // dystrobrevin, alpha /// NM_001392 // downstream // 203246 // Hs.255526 // DTNA // 1837 // dystrobr	DTNA	DTNA , rs920799, dystrobrevin, alpha, q12.1
SNP_A-2107243	agctaaaatgtgtttg[C/T]acgtatgactgtggat	C	T	NM_001390 // downstream // 146243 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, mRNA. /// NM_032975 // downstream // 146243 // Hs.58919 // DTNA // 1837 // Homo sapiens dystrobrevin, alpha (DTNA), transcript	DTNA	DTNA, Homo sapiens dystrobrevin, alpha (DTNA), transcript variant 1, q12.1
SNP_A-2128200	ataaggctaagagaga[C/G]agactgaaaggttaga	C	G	NM_006965 // intron // 0 // Hs.514802 // ZNF24 // 7572 // Homo sapiens zinc finger protein 24 (KOX 17) (ZNF24), mRNA. /// ENST00000261332 // intron // 0 // — // — // —	ZNF24	ZNF24, Homo sapiens zinc finger protein 24 (KOX 17) (ZNF24), q12.2
SNP_A-1863252	tcatttgataaaaggg[C/T]catgctacttaaaca	C	T	NM_145756 // intron // 0 // Hs.351005 // ZNF396 // 252884 // Homo sapiens zinc finger protein 396 (ZNF396), mRNA. /// ENST00000306346 // intron // 0 // — // — // —	ZNF396	ZNF396, Homo sapiens zinc finger protein 396 (ZNF396), q12.2
SNP_A-1822257	gtttgcctcccttca[A/G]atctatcctgtgtt	A	G	NM_145756 // upstream // 2096 // Hs.351005 // ZNF396 // 252884 // Homo sapiens zinc finger protein 396 (ZNF396), mRNA. /// ENST00000306346 // upstream // 2096 // — // — // — /// ENST00000357689 // upstream // 679 // — // — // —	ZNF396	ZNF396, Homo sapiens zinc finger protein 396 (ZNF396), q12.2
SNP_A-1846252	tatatctgattgcagc[A/G]gcaaaggctatcccc	A	G	NM_194281 // downstream // 84502 // Hs.464903 // C18orf37 // 125476 // Homo sapiens chromosome 18 open reading frame 37 (C18orf37), mRNA. /// ENST00000357689 // downstream // 479 // — // — // — /// ENST00000283410 // downstream // 70990 // –	C18orf37	C18orf37, Homo sapiens chromosome 18 open reading frame 37 (C18orf37), q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2224672	cgtcgtgtgatttttc[A/G]catgcttccgtgtaga	A	G	NM_194281 // upstream // 74700 // Hs.464903 // C18orf37 // 125476 // Homo sapiens chromosome 18 open reading frame 37 (C18orf37), mRNA. /// NM_020474 // upstream // 81980 // Hs.514806 // GALNT1 // 2589 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:po	C18orf37	C18orf37, Homo sapiens chromosome 18 open reading frame 37 (C18orf37), q12.2
SNP_A-2265445	gaagccaataatacat[C/G]aaggcccatgaaaaag	C	G	NM_020474 // downstream // 97144 // Hs.514806 // GALNT1 // 2589 // Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA. /// NM_031446 // upstream // 163791 // Hs.37883 // C18orf21 // 8	GALNT1	GALNT1, Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), q12.2
SNP_A-1958672	tttctctcctagctca[C/T]cacgggcaaatacaa	C	T	NM_017947 // intron // 0 // Hs.405028 // MOCOS // 55034 // Homo sapiens molybdenum cofactor sulfurase (MOCOS), mRNA. /// ENST00000261326 // intron // 0 // — // — // —	MOCOS	MOCOS, Homo sapiens molybdenum cofactor sulfurase (MOCOS), q12.2
SNP_A-2120216	agtcaggcaagaatga[A/G]gtaactcccatgctga	A	G	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-1854689	tcaacaggatgatcta[C/T]gctcttttgattagag	C	T	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2130861	atacttttggttatgta[C/T]agaaaatggaatgtgt	C	T	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2288561	gattgatttctcacca[A/T]aatggaaaagagcaact	A	T	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2186113	caggccaagacttgtga[A/G]aggaaagtatttatgc	A	G	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2250235	cttactttcctctaag[A/G]caatctgtgaaccaca	A	G	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2177276	cacctgtaatccgtaa[A/G]tgaatccaactggaa	A	G	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2108841	agctgttgtagtct[C/G]aatgatttgttccatt	C	G	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2073076	acaggatctcctaagg[A/G]agctttcaaattgcaa	A	G	ENST00000359247 // intron // 0 // — // — // —	-	q12.2
SNP_A-2211134	cccgtcagatggagaa[C/T]gtgaccatgctttcct	C	T	ENST00000359247 // intron // 0 // — // — // — /// ENST00000257209 // intron // 0 // — // — // —	-	q12.2
SNP_A-1953912	tttgagtacacataat[C/T]agttctcgaggaaagg	C	T	ENST00000280022 // upstream // 136485 // — // — // — /// ENST00000334919 // upstream // 136514 // — // — // — /// ENST00000322194 // downstream // 1632635 // — // — // —	-	q12.2
SNP_A-1880343	tcttgaaagctgattt[A/T]aaaacacacacccact	A	T	ENST00000280022 // upstream // 466722 // — // — // — /// ENST00000334919 // upstream // 466751 // — // — // — /// ENST00000322194 // downstream // 1302398 // — // — // —	-	q12.2
SNP_A-1900948	actctattcaagagca[A/G]gacgttgttgtgcacc	A	G	ENST00000280022 // upstream // 557111 // — // — // — /// ENST00000334919 // upstream // 557140 // — // — // — /// ENST00000322194 // downstream // 1212009 // — // — // —	-	q12.2
SNP_A-1822098	gttttctcatttggag[A/C]cctgagataaaatgta	A	C	ENST00000280022 // upstream // 674648 // — // — // — /// ENST00000334919 // upstream // 674677 // — // — // — /// ENST00000322194 // downstream // 1094472 // — // — // —	-	q12.2
SNP_A-1901062	actcatgcagtcaaac[G/T]ccctctgggttccag	G	T	ENST00000280022 // upstream // 726003 // — // — // — /// ENST00000334919 // upstream // 726032 // — // — // — /// ENST00000322194 // downstream // 1043117 // — // — // —	-	q12.2
SNP_A-1901189	ggtatggttgctgata[C/T]aaactcaaaatacaaa	C	T	ENST00000280022 // upstream // 834812 // — // — // — /// ENST00000334919 // upstream // 834841 // — // — // — /// ENST00000322194 // downstream // 934308 // — // — // —	-	q12.2
SNP_A-1750387	aaaaaatttccagtgttgtttct[C/T]acccactgttgtgatgatgat tcat	C	T	NM_002647 // upstream // 3549451 // Hs.418150 // PIK3C3 // 5269 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 840155 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3, rs11965582, phosphoinositide-3-kinase, class 3, q12.2
SNP_A-1901370	tggctataaaagtcaa[A/G]atcaacaatgcactat	A	G	ENST00000280022 // upstream // 937411 // — // — // — /// ENST00000334919 // upstream // 937440 // — // — // — /// ENST00000322194 // downstream // 831709 // — // — // —	-	q12.2
SNP_A-2256014	ctttaaatattcactgaa[A/G]ggcaatagtaatttct	A	G	ENST00000280022 // upstream // 1016866 // — // — // — /// ENST00000334919 // upstream // 1016895 // — // — // — /// ENST00000322194 // downstream // 752254 // — // — // —	-	q12.2
SNP_A-1901476	atatctgttgttgccc[C/T]gctagactttataaca	C	T	ENST00000280022 // upstream // 1021877 // — // — // — /// ENST00000334919 // upstream // 1021906 // — // — // — /// ENST00000322194 // downstream // 747243 // — // — // —	-	q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960058	ttttgtttaaacataa[A/G]ggcaaagaggaacttg	A	G	ENST00000280022 // upstream // 1036724 // --- // --- // --- /// ENST00000334919 // upstream // 1036753 // --- // --- // --- /// ENST00000322194 // downstream // 732396 // --- // --- // ---	-	q12.2
SNP_A-1686434	atcatccccaatcctcacaaaaaa[G/T]aagtctaactataaa acatagacc	G	T	NM_002647 // upstream // 3301006 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 1088600 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs4627439, phosphoinositide-3-kinase, class 3 ,q12.2
SNP_A-2230004	ctataaataataaaaa[A/G]ttgatggcactgttta	A	G	ENST00000280022 // upstream // 1357164 // --- // --- // --- /// ENST00000334919 // upstream // 1357193 // --- // --- // --- /// ENST00000322194 // downstream // 411956 // --- // --- // ---	-	q12.2
SNP_A-1715343	aaaagggggctacatttgaggcatg[C/T]acaatactctgatcaa gatttcctg	C	T	NM_002647 // upstream // 2908233 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 1481373 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs10502719, phosphoinositide-3-kinase, class 3 ,q12.2
SNP_A-2088907	actgttctctcccca[A/G]atgcattattagt	A	G	ENST00000280022 // upstream // 1677275 // --- // --- // --- /// ENST00000334919 // upstream // 1677304 // --- // --- // --- /// ENST00000322194 // downstream // 91845 // --- // --- // ---	-	q12.2
SNP_A-1743491	ttatgaagaaatggacttagccat[C/T]gaccttaggctacgtgtc ttagtc	C	T	NM_002647 // upstream // 2674554 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 1715052 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs10502721, phosphoinositide-3-kinase, class 3 ,q12.2
SNP_A-1901968	tttcatgaagatcata[C/T]actttgccaagtggcag	C	T	ENST00000280022 // upstream // 1714431 // --- // --- // --- /// ENST00000334919 // upstream // 1714460 // --- // --- // --- /// ENST00000322194 // downstream // 54689 // --- // --- // ---	-	q12.2
SNP_A-1943113	ttggtatttgattct[C/T]actaggctcccctgca	C	T	ENST00000280022 // upstream // 1728786 // --- // --- // --- /// ENST00000334919 // upstream // 1728815 // --- // --- // --- /// ENST00000322194 // downstream // 40334 // --- // --- // ---	-	q12.2
SNP_A-1655345	ttttggagctggatcctggtcca[A/C]aggaaaaataatgaga acattaaga	A	C	NM_002647 // upstream // 2636838 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 1752768 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs10502723, phosphoinositide-3-kinase, class 3 ,q12.2
SNP_A-2190488	catacattagttccaa[C/T]tcccagttctaccact	C	T	NM_002647 // upstream // 2109536 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 510024 // --- // --- // --- /// ENST00000262039 // upstream // 2109536 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1902325	ctttttttcacaatttct[A/T]cagatactgactcatt	A	T	NM_002647 // upstream // 2109300 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 510260 // --- // --- // --- /// ENST00000262039 // upstream // 2109300 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1892288	tgcaacctcttggaac[A/G]atgacggatcaggca	A	G	NM_002647 // upstream // 2107165 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 512395 // --- // --- // --- /// ENST00000262039 // upstream // 2107165 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1933221	ttctaagggatctac[A/G]ggtgaagctatctaaa	A	G	NM_002647 // upstream // 2104676 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 514884 // --- // --- // --- /// ENST00000262039 // upstream // 2104676 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1902368	acctatttataggata[A/C]ctgtccatggattatc	A	C	NM_002647 // upstream // 2034886 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 584674 // --- // --- // --- /// ENST00000262039 // upstream // 2034886 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1902370	ttgtatgctcactac[A/G]atggctttgcatagca	A	G	NM_002647 // upstream // 2034319 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 585241 // — // — // — /// ENST00000262039 // upstream // 2034319 // — // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1948085	ttagataaqtatggg[C/T]aaaaacgtatcaacac	C	T	NM_002647 // upstream // 2033924 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 585636 // — // — // — /// ENST00000262039 // upstream // 2033924 // — // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2152767	attaatgtttaatca[A/T]gaagtggaacagaaac	A	T	NM_002647 // upstream // 2012693 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 606867 // — // — // — /// ENST00000262039 // upstream // 2012693 // — // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2188304	cagtctgaaaactaaa[A/G]tgatgccagtgaagca	A	G	NM_002647 // upstream // 1979769 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 639791 // — // — // — /// ENST00000262039 // upstream // 1979769 // — // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1902438	ttgaacatattctgac[A/C]catgaatctgggacag	A	C	NM_002647 // upstream // 1961522 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 658038 // — // — // — /// ENST00000262039 // upstream // 1961522 // — // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1902463	tgcagagactgaaaaa[C/T]gttggccaagtaatt	C	T	NM_002647 // upstream // 1947969 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 671591 // — // — // — /// ENST00000262039 // upstream // 1947969 // — // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2269541	gacaaagaggaggacaa[C/T]gcagtgaagaaataaa	C	T	NM_002647 // upstream // 1533842 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1085718 // — // — // — /// ENST00000262039 // upstream // 1533842 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2290552	gcaacttcaagagaca[A/G]gtattatcagctatg	A	G	NM_002647 // upstream // 1392255 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1227305 // — // — // — /// ENST00000262039 // upstream // 1392255 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2199954	ccaaagcaagggatca[C/T]gaagcaggcctcccac	C	T	NM_002647 // upstream // 1392159 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1227401 // — // — // — /// ENST00000262039 // upstream // 1392159 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2282388	gagttccatttgtggc[C/T]aggacagttctgccaa	C	T	NM_002647 // upstream // 1378555 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1241005 // — // — // — /// ENST00000262039 // upstream // 1378555 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2151987	atgttttgcaaggatc[C/T]atattatctttaaagc	C	T	NM_002647 // upstream // 1341715 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1277845 // — // — // — /// ENST00000262039 // upstream // 1341715 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1902979	ctatcgtttactgaca[A/T]tacaaatcctgaataa	A	T	NM_002647 // upstream // 1325317 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1294243 // — // — // — // — /// ENST00000262039 // upstream // 1325317 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1884770	cttaattatatctaggtctaataca[A/G]gcatggctagagtttaagt gggcaa	A	G	NM_002647 // upstream // 1315357 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 3074249 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs1545112, phosphoinositide-3-kinase, class 3 q12.3
SNP_A-1864108	tccacagttacatctc[G/T]agttatcatgttc	G	T	NM_002647 // upstream // 1303258 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1316302 // — // — // — // — /// ENST00000262039 // upstream // 1303258 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2230107	ctataatttgtagga[C/T]gcatagttggccaata	C	T	NM_002647 // upstream // 1298921 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1320639 // — // — // — // — /// ENST00000262039 // upstream // 1298921 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1857843	tcactgttggtgggaa[A/C]gtaggttgattccatg	A	C	NM_002647 // upstream // 1298449 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1321111 // — // — // — // — /// ENST00000262039 // upstream // 1298449 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1914188	tgtgtgtgtttccc[G/T]ctggcctgctccctcc	G	T	NM_002647 // upstream // 1292096 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1327464 // — // — // — // — /// ENST00000262039 // upstream // 1292096 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1890000	tgatagttgcctaata[A/T]cttcctgtaaaaactc	A	T	NM_002647 // upstream // 1287510 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1332050 // — // — // — // — /// ENST00000262039 // upstream // 1287510 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2250036	cttacccttgagcaa[A/G]tacagtattcatactt	A	G	NM_002647 // upstream // 1282150 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1337410 // — // — // — // — /// ENST00000262039 // upstream // 1282150 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1903064	tgtctctgtctctcaa[C/T]tagataattcctactg	C	T	NM_002647 // upstream // 1277969 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1341591 // — // — // — // — /// ENST00000262039 // upstream // 1277969 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1829989	taatacaactcacaga[A/C]gctttactccaaatga	A	C	NM_002647 // upstream // 1265127 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1354433 // — // — // — // — /// ENST00000262039 // upstream // 1265127 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2005607	gactcctaacataaca[A/C]ccatctgcagccatag	A	C	NM_002647 // upstream // 1258799 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1360761 // — // — // — // — /// ENST00000262039 // upstream // 1258799 // — //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1729606	actgaggttggtcagagagattata[C/T]cgtccttgatttaaaata ataacca	C	T	NM_002647 // upstream // 1217800 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 3171806 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs10502742, phosphoinositide-3-kinase, class 3 ,q12.3
SNP_A-1865757	tccatttccataccta[C/T]caggatacaaccagac	C	T	NM_002647 // upstream // 1095495 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1524065 // --- // --- // --- /// ENST00000262039 // upstream // 1095495 // --- //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1923435	ttaggcaaagacttta[C/T]ggtaaagatttctaa	C	T	NM_002647 // upstream // 985713 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1633847 // --- // --- // --- /// ENST00000262039 // upstream // 985713 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2163062	attttagatattaac[C/G]ctgatcatcggtatg	C	G	NM_002647 // upstream // 969064 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1650496 // --- // --- // --- /// ENST00000262039 // upstream // 969064 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2270317	gacactattcccctgc[A/G]catggtcatatctgt	A	G	NM_002647 // upstream // 890181 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 1729379 // --- // --- // --- /// ENST00000262039 // upstream // 890181 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1960516	ttttcacagcttaca[C/T]gaaacttggcttca	C	T	NM_002647 // upstream // 576358 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2043202 // --- // --- // --- /// ENST00000262039 // upstream // 576358 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1732848	gcctttaggaggtccatccttccaa[C/T]gcctgagcaataaatttca gaagata	C	T	NM_002647 // upstream // 413722 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 3975884 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs10502766, phosphoinositide-3-kinase, class 3 ,q12.3
SNP_A-2036778	aaatttatgaaagaaa[G/T]ccatttgggggtgtga	G	T	NM_002647 // upstream // 404291 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2215269 // --- // --- // --- /// ENST00000262039 // upstream // 404291 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1905981	tggtcttaaaaatga[A/G]gaagtttgaatgagat	A	G	NM_002647 // upstream // 399848 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2219712 // --- // --- // --- /// ENST00000262039 // upstream // 399848 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1700081	tattgtttcagagtgctatcaagaaa[C/T]gtatatgaattaggagtaa ttgtta	C	T	NM_002647 // upstream // 372138 // Hs.418150 // PIK3C3 // 5289 // phosphoinositide-3-kinase, class 3 /// NM_020180 // upstream // 4017468 // Hs.435976 // BRUNOL4 // 56853 // bruno-like 4, RNA binding protein (Drosophila)	PIK3C3	PIK3C3 , rs10502770, phosphoinositide-3-kinase, class 3 ,q12.3
SNP_A-1903752	aatatgagatgaattat[C/G]agtgcaccttgccggg	C	G	NM_002647 // upstream // 371177 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2248383 // --- // --- // --- /// ENST00000262039 // upstream // 371177 // --- // -	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2025942	aaaatgtgaaattagat[C/T]gcctggaatataccag	C	T	NM_002647 // upstream // 351826 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2267734 // — // — // — /// ENST00000262039 // upstream // 351826 // — // –	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1805176	gtcattagtgtcttca[G/T]aaaaactgagattaaa	G	T	NM_002647 // upstream // 106784 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2512776 // — // — // — /// ENST00000262039 // upstream // 106784 // — // –	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1903951	cctgggtgatgctttg[A/G]aaaaaatctgtttacc	A	G	NM_002647 // upstream // 102521 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2517039 // — // — // — /// ENST00000262039 // upstream // 102521 // — // –	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1918531	ttaaatgaaatgataa[A/G]tgagatgatacaggta	A	G	NM_002647 // upstream // 36966 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// ENST00000322194 // upstream // 2582594 // — // — // — /// ENST00000262039 // upstream // 36966 // — // –	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1710359	gcacaagtgaaactgccattgcaaa[A/G]tttactactgagacag tgaaagtga	A	G	BC021928 // intron // 0 // Hs.514832 // C22orf1 // 758 // chromosome 22 open reading frame 1	C22orf1	C22orf1 , rs898783, chromosome 22 open reading frame 1,q12.3
SNP_A-2100808	agatagtttttgagaa[G/T]catgaaagaccaaaaa	G	T	NM_002647 // downstream // 374779 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 286970 // Hs.464985 // RIT2 // 6014 // Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA. //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2082795	acgtaaaatgctatgc[A/G]actaagccaaagtctt	A	G	NM_002647 // downstream // 503102 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 158647 // Hs.464985 // RIT2 // 6014 // Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA. //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-2133193	atatagtaggagttaa[C/G]aaatgatgatgtacta	C	G	NM_002647 // downstream // 503323 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 158426 // Hs.464985 // RIT2 // 6014 // Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA. //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1853840	tcaaaacctgagtata[A/C]gtactgtaggagctaa	A	C	NM_002647 // downstream // 503493 // Hs.464971 // PIK3C3 // 5289 // Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA. /// NM_002930 // downstream // 158256 // Hs.464985 // RIT2 // 6014 // Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA. //	PIK3C3	PIK3C3, Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), q12.3
SNP_A-1744315	gaataaattgggcaaagttttcattta[A/C]aacctgatggatgatctgt aaaaga	A	C	NM_002930 // upstream // 1683 // Hs.464985 // RIT2 // 6014 // Ras-like without CAAX 2 /// NM_020783 // downstream // 150519 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	RIT2	RIT2 , rs4890428, Ras-like without CAAX 2 ,q12.3
SNP_A-1958977	tttctttacatttat[A/G]agtggtatcaagatag	A	G	NM_020783 // downstream // 120883 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// ENST00000354821 // downstream // 6635 // — // — // — /// ENST00000255224 // downstream // 120883 // — // — // –	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1691598	caagctctctttccctacctta[C/T]aaacatgactcctctttttctct tc	C	T	NM_002930 // upstream // 37521 // Hs.464985 // RIT2 // 6014 // Ras-like without CAAX 2 /// NM_020783 // downstream // 114681 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	RIT2	RIT2 , rs1518148, Ras-like without CAAX 2 ,q12.3
SNP_A-1862655	tcattatgttaggtga[A/G]ataagatagagaacaa	A	G	NM_020783 // downstream // 88478 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// ENST00000354821 // downstream // 39040 // — // — // — /// ENST00000255224 // downstream // 88478 // — // — // — // –	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1650372	ctctggaaagcaaattcactacaaa[A/G]gattgaagcaaaaag gaagagttac	A	G	NM_015559 // upstream // 1358648 // Hs.201369 // SETBP1 // 26040 // SET binding protein 1 /// NM_020783 // upstream // 65477 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs627966, SET binding protein 1 ,q12.3
SNP_A-2086461	acictttcctagtgtg[G/T]acattaatcaaagttt	G	T	NM_020783 // upstream // 74574 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1349463 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2035006	aaatgattgactcccc[A/C]gattgattaacccag	A	C	NM_020783 // upstream // 76134 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1347903 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1893253	tgcagaggtctgatta[C/T]ggtatggtgtcagttc	C	T	NM_020783 // upstream // 77168 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1346869 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2209295	cccagtggccatgaaa[C/G]accacaaggctgtcat	C	G	NM_020783 // upstream // 77543 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1346494 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1794226	ggtcatgacagctttc[C/T]gaaaatacaccaatgc	C	T	NM_020783 // upstream // 77772 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1346265 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2005622	cagaagactgcaaaac[A/C]atgtagtaataatgca	A	C	NM_020783 // upstream // 95701 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1328336 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1758137	tttaaacigttagtcaggcctaaaa[A/C]gttgaaaatgttcattctg aaatta	A	C	NM_015559 // upstream // 1292133 // Hs.201369 // SETBP1 // 26040 // SET binding protein 1 /// NM_020783 // upstream // 131992 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs687483, SET binding protein 1 ,q12.3
SNP_A-2075507	acatgatgctactggaa[A/G]gaataatcagaagtca	A	G	NM_020783 // upstream // 132945 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1291092 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // ups	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1715177	tagaaatttgtgcataatctgccac[A/G]aattaaaagtaggtata aatatga	A	G	NM_015559 // upstream // 1282842 // Hs.201369 // SETBP1 // 26040 // SET binding protein 1 /// NM_020783 // upstream // 141283 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs1144613, SET binding protein 1 ,q12.3
SNP_A-1668811	tgaaaatatttggatataattgaaa[C/G]taaaaaggaaatcccat gaccactg	C	G	NM_015559 // upstream // 1266987 // Hs.201369 // SETBP1 // 26040 // SET binding protein 1 /// NM_020783 // upstream // 157138 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs604693, SET binding protein 1 ,q12.3
SNP_A-2074477	acatagagacaatctat[A/G]aagaactaatgtttct	A	G	NM_020783 // upstream // 194803 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1229234 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // ups	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1840988	tagctgctagagtgaa[A/C]gaaaaaccttgtggca	A	C	NM_020783 // upstream // 202029 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 1222008 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // ups	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-1653938	ttttttttacttcctctgaatttgc[C/T]gatttcattcatttctcaaactcc c	C	T	NM_015559 // upstream // 1183213 // Hs.201369 // SETBP1 // 26040 // SET binding protein 1 /// NM_020783 // upstream // 240912 // Hs.8059 // SYT4 // 6860 // synaptotagmin IV	SETBP1	SETBP1 , rs8096082, SET binding protein 1 ,q12.3
SNP_A-1872899	tctatcagtaacttaa[A/C]aaagaggtgcaggaag	A	C	NM_020783 // upstream // 485686 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 938351 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2025061	aaaatacacaaacaca[A/C]atttatttagctcata	A	C	NM_020783 // upstream // 917428 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 506609 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // upst	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2314182	ggaggaggcagattga[C/G]ggtgacgggtacctgc	C	G	NM_020783 // upstream // 1176011 // Hs.8059 // SYT4 // 6860 // Homo sapiens synaptotagmin IV (SYT4), mRNA. /// NM_015559 // upstream // 248026 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000255224 // ups	SYT4	SYT4, Homo sapiens synaptotagmin IV (SYT4), q12.3
SNP_A-2130623	atactgcacatttacc[A/T]caaccttggtgttatt	A	T	NM_015559 // intron // 0 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// ENST00000282030 // intron // 0 // — // — // — // —	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1906520	tcctgggagataatag[A/G]ataaactcatggagga	A	G	NM_015559 // downstream // 80889 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 478968 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1852966	tatttgaaccactctg[A/G]aacaagaagaaaattg	A	G	NM_015559 // downstream // 91172 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 468685 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1804555	gtcagcaacaagctaa[C/T]caatgggactgaacaa	C	T	NM_015559 // downstream // 91701 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 468156 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2121169	agtctgcaggacagga[A/G]aacaatctaccaagat	A	G	NM_015559 // downstream // 92095 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 467762 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1816399	gttagattggcaggaa[C/T]ggccctgagtatttat	C	T	NM_015559 // downstream // 92511 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 467346 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2297694	gccagctccttgacgg[A/G]attctttcatgaacag	A	G	NM_015559 // downstream // 95230 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 464627 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1884571	tgaataacatggtaaa[A/G]tcttggttcgataagt	A	G	NM_015559 // downstream // 95318 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 464539 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2027316	aaacatctactccagc[C/T]acttaggtgtactgaa	C	T	NM_015559 // downstream // 139505 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 420352 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2035714	aaatgtgaacaatgga[A/G]tattagtgccaggtca	A	G	NM_015559 // downstream // 157608 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 402249 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2085107	actcagacatactcat[C/G]acacaatgaaatgaag	C	G	NM_015559 // downstream // 180249 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 379608 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2121270	agtctgttttcaaata[G/T]gttagaggcaatcagg	G	T	NM_015559 // downstream // 371428 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 188429 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-2209962	ccccacagctccttga[C/T]gaattcttatatggac	C	T	NM_015559 // downstream // 374011 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 185846 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1695967	tgcatcttctagaagactgtgaaga[C/G]attgcactgggccaac catacttgt	C	G	NM_007163 // upstream // 135598 // Hs.193377 // SLC14A2 // 8170 // solute carrier family 14 (urea transporter), member 2 /// NM_015559 // downstream // 424225 // Hs.201369 // SETBP1 // 26040 // SET binding protein 1	SLC14A2	SLC14A2 , rs10502865, solute carrier family 14 (urea transporter), member 2 ,q12.3
SNP_A-2313725	ggagcaatctatactc[C/T]catcaccaggtttttt	C	T	NM_015559 // downstream // 458498 // Hs.435458 // SETBP1 // 26040 // Homo sapiens SET binding protein 1 (SETBP1), mRNA. /// NM_007163 // upstream // 101359 // Hs.135642 // SLC14A2 // 8170 // Homo sapiens solute carrier family 14 (urea transporter), member	SETBP1	SETBP1, Homo sapiens SET binding protein 1 (SETBP1), q12.3
SNP_A-1826844	taacataaagttttca[A/G]ggttcatttatgttgt	A	G	ENST00000360459 // intron // 0 // — // — // — // —	-	q12.3
SNP_A-2278396	gagctaggcactggac[A/C]aaggtctgtctatctc	A	C	NM_144612 // intron // 0 // Hs.345877 // LOXHD1 // 125336 // Homo sapiens lipoxygenase homology domains 1 (LOXHD1), mRNA. /// ENST00000300591 // intron // 0 // — // — // — // — /// ENST00000335730 // intron // 0 // — // — // — // —	LOXHD1	LOXHD1, Homo sapiens lipoxygenase homology domains 1 (LOXHD1), q21.1
SNP_A-2164705	caaacaggatggacaa[A/C]aagaacctcaaatatc	A	C	NM_144612 // upstream // 53531 // Hs.345877 // LOXHD1 // 125336 // Homo sapiens lipoxygenase homology domains 1 (LOXHD1), mRNA. /// NM_013305 // downstream // 24047 // Hs.465025 // ST8SIA5 // 29906 // Homo sapiens sialyltransferase 8E (alpha-2, 8-polysial	LOXHD1	LOXHD1, Homo sapiens lipoxygenase homology domains 1 (LOXHD1), q21.1
SNP_A-1935616	ttctgtacccagtaca[A/T]ccaacaagcaggactc	A	T	NM_144612 // upstream // 62170 // Hs.345877 // LOXHD1 // 125336 // Homo sapiens lipoxygenase homology domains 1 (LOXHD1), mRNA. /// NM_013305 // downstream // 15408 // Hs.465025 // ST8SIA5 // 29906 // Homo sapiens sialyltransferase 8E (alpha-2, 8-polysial	LOXHD1	LOXHD1, Homo sapiens lipoxygenase homology domains 1 (LOXHD1), q21.1
SNP_A-1739975	ccaggcaaaacttgtatagggctga[C/T]cctggaagcgtgcctg tagataagg	C	T	NM_013305 // intron // 0 // Hs.22985 // SIAT8E // 29906 // sialyltransferase 8E (alpha-2, 8-polysialyltransferase)	SIAT8E	SIAT8E , rs4449041, sialyltransferase 8E (alpha-2, 8-polysialyltransferase),q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1833296	tacactgttgtaagaa[A/C]ttcccatagaacgcag	A	C	NM_016097 // upstream // 149013 // Hs.130917 // IER3IP1 // 51124 // Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), mRNA. /// ENST00000256433 // upstream // 149013 // — // — // — /// ENST00000256421 // downstream // 1	IER3IP1	IER3IP1, Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), q21.1
SNP_A-2005641	gacaaaaggcagccac[A/G]aatgaaagttgaagtc	A	G	NM_016097 // upstream // 536553 // Hs.130917 // IER3IP1 // 51124 // Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), mRNA. /// ENST00000256433 // upstream // 536553 // — // — // — /// ENST00000256421 // downstream // 5	IER3IP1	IER3IP1, Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), q21.1
SNP_A-2094957	agaatgcctggcaca[G/T]ccgctcactatggtca	G	T	NM_016097 // upstream // 596666 // Hs.130917 // IER3IP1 // 51124 // Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), mRNA. /// ENST00000256433 // upstream // 596666 // — // — // — /// ENST00000256421 // downstream // 6	IER3IP1	IER3IP1, Homo sapiens immediate early response 3 interacting protein 1 (IER3IP1), q21.1
SNP_A-2238336	ctctggctagccgtca[G/T]attggaaagcattca	G	T	NM_005901 // upstream // 9384 // Hs.465061 // SMAD2 // 4087 // Homo sapiens SMAD, mothers against DPP homolog 2 (Drosophila) (SMAD2), transcript variant 1, mRNA. /// NM_001003652 // upstream // 9384 // Hs.465061 // SMAD2 // 4087 // Homo sapiens SMAD, moth	SMAD2	SMAD2, Homo sapiens SMAD, mothers against DPP homolog 2 (Drosophila) (SMAD2), transcript variant 1, q21.1
SNP_A-2047403	aagatcttatttttgt[G/T]aagcctctgtagtagg	G	T	NM_005901 // upstream // 26367 // Hs.465061 // SMAD2 // 4087 // Homo sapiens SMAD, mothers against DPP homolog 2 (Drosophila) (SMAD2), transcript variant 1, mRNA. /// NM_001003652 // upstream // 26367 // Hs.465061 // SMAD2 // 4087 // Homo sapiens SMAD, mo	SMAD2	SMAD2, Homo sapiens SMAD, mothers against DPP homolog 2 (Drosophila) (SMAD2), transcript variant 1, q21.1
SNP_A-2240153	ctgaagttttttccag[A/C]actggcttatcatgag	A	C	ENST00000332053 // intron // 0 // — // — // —	-	q21.1
SNP_A-1911702	tgtgaagagtagaaaag[A/C]attttgttgggcagag	A	C	ENST00000332053 // upstream // 7162 // — // — // — /// ENST00000324663 // upstream // 204032 // — // — // —	-	q21.1
SNP_A-2161173	atttgacagatgagga[A/G]actaaagtgaaggtga	A	G	ENST00000332053 // upstream // 10459 // — // — // — /// ENST00000324663 // upstream // 200735 // — // — // —	-	q21.1
SNP_A-1938257	ttgaccctgcagttgc[A/C]ccctagcaaactgaaa	A	C	ENST00000332053 // upstream // 10650 // — // — // — /// ENST00000324663 // upstream // 200544 // — // — // —	-	q21.1
SNP_A-2226788	ctaataatacggcaca[C/T]gatctatgtcggctt	C	T	ENST00000332053 // upstream // 91889 // — // — // — /// ENST00000324663 // upstream // 119305 // — // — // —	-	q21.1
SNP_A-2005645	ccacctggccccaca[A/G]ccaatgtgtttcaggg	A	G	ENST00000332053 // upstream // 155859 // — // — // — /// ENST00000324663 // upstream // 55335 // — // — // —	-	q21.1
SNP_A-2213835	cctaaagacaagaccac[C/T]gcctctgaggaccaa	C	T	ENST00000332053 // upstream // 163529 // — // — // — /// ENST00000324663 // upstream // 47665 // — // — // —	-	q21.1
SNP_A-1674044	accctcattatacctgcctggcta[A/T]actttattctctctgtctctct ga	A	T	NM_005901 // upstream // 277539 // Hs.110741 // MADH2 // 4087 // MAD, mothers against decapentaplegic homolog 2 (Drosophila) /// NM_032362 // upstream // 44207 // - // - // - // -	MADH2	MADH2 , rs953570, MAD, mothers against decapentaplegic homolog 2 (Drosophila), q21.1
SNP_A-2299856	gcctacctgagatcac[A/G]aacatatattccag	A	G	ENST00000332053 // upstream // 165660 // — // — // — /// ENST00000324663 // upstream // 45514 // — // — // —	-	q21.1
SNP_A-2045729	aagacaccagtgaaggt[C/T]catgttcgccataaga	C	T	ENST00000324663 // downstream // 7914 // — // — // — /// ENST00000332560 // upstream // 217810 // — // — // —	-	q21.1
SNP_A-1792038	gggtgggagtgttaca[C/T]actgttaggagttgat	C	T	ENST00000324663 // downstream // 95353 // — // — // — /// ENST00000332560 // upstream // 130371 // — // — // —	-	q21.1
SNP_A-1725164	tgataaaaacaaagaactggatcaa[A/C]actggaaaggagaa cgctcagagga	A	C	NM_014772 // upstream // 149318 // Hs.64096 // KIAA0427 // 9811 // KIAA0427 /// NM_032362 // downstream // 136901 // - // - // - // -	KIAA0427	KIAA0427 , rs10502892, KIAA0427 ,q21.1
SNP_A-1850594	taltaatactcaccaa[A/T]atttcttccaatgta	A	T	ENST00000324663 // downstream // 164795 // — // — // — /// ENST00000332560 // upstream // 60929 // — // — // —	-	q21.1
SNP_A-1912425	tgtgcacacatcttcc[G/T]ctgctttcccagctca	G	T	NM_014772 // intron // 0 // Hs.145230 // KIAA0427 // 9811 // Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // — // — // —	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1896045	tgcctttcctgacata[G/T]gtatgacttgaagaaa	G	T	NM_014772 // intron // 0 // Hs.145230 // KIAA0427 // 9811 // Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-2029641	aaagagagagcaacta[C/T]gtagagaaggtcatgg	C	T	NM_014772 // intron // 0 // Hs.145230 // KIAA0427 // 9811 // Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-1909328	ggccacccggcgcaac[C/T]gactttctgctctctg	C	T	NM_014772 // intron // 0 // Hs.145230 // KIAA0427 // 9811 // Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-2236534	ctcgtgcccctagaac[C/T]gttaaggcatgagaga	C	T	NM_014772 // intron // 0 // Hs.145230 // KIAA0427 // 9811 // Homo sapiens KIAA0427 (KIAA0427), mRNA. /// ENST00000256413 // intron // 0 // --- // --- // --- // ---	KIAA0427	KIAA0427, Homo sapiens KIAA0427 (KIAA0427), q21.1
SNP_A-1789579	gggcgcagtcaggtga[A/G]aaaggacgtgcctaaa	A	G	NM_017653 // intron // 0 // Hs.162996 // DYM // 54808 // Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-1815697	gttaactaaatataca[A/G]ctccttaatgaagaca	A	G	NM_017653 // intron // 0 // Hs.162996 // DYM // 54808 // Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-1850750	tattactgtatataga[A/G]tcaatgcacaggttat	A	G	NM_017653 // intron // 0 // Hs.162996 // DYM // 54808 // Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-1699911	gatggtttggactaatctgactctc[G/T]cgtgcatgttgttttcatcctctac	G	T	NM_017653 // intron // 0 // Hs.501125 // FLJ20071 // 54808 // dymeclin	FLJ20071	FLJ20071 , rs7240563, dymeclin,q21.1
SNP_A-1932439	ttcctgcattccacaa[A/G]tgttccctctgggttc	A	G	NM_017653 // intron // 0 // Hs.162996 // DYM // 54808 // Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-2265185	gaagattatgttaata[A/C]aaggtcaggtatgtgc	A	C	NM_017653 // intron // 0 // Hs.162996 // DYM // 54808 // Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-2026714	aaacaatgccttttca[C/T]gttgatgatcacttta	C	T	NM_017653 // intron // 0 // Hs.162996 // DYM // 54808 // Homo sapiens dymeclin (FLJ20071), mRNA. /// ENST00000269445 // intron // 0 // --- // --- // --- // ---	DYM	DYM, Homo sapiens dymeclin (FLJ20071), q21.1
SNP_A-1898706	tgctttagctctttgc[A/G]catatttaagacttttt	A	G	NM_006033 // downstream // 13190 // Hs.465102 // LIPG // 9388 // Homo sapiens lipase, endothelial (LIPG), mRNA. /// NM_006111 // downstream // 177411 // Hs.200136 // ACAA2 // 10449 // Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoac	LIPG	LIPG, Homo sapiens lipase, endothelial (LIPG), q21.1
SNP_A-1851313	tattcatgagagtata[A/T]aaatttatgtgattac	A	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- /// ENST00000356732 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. ,q21.1
SNP_A-2005649	gctttattacatgacc[A/C]gagtgtagaaggcagt	A	C	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- /// ENST00000356732 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2213553	ccgtattcccattcaa[C/T]cacaggaagccccata	C	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // --- /// ENST00000356732 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. ,q21.1
SNP_A-2241215	ctgaggactttgagaa[G/T]actcgacaagccttca	G	T	AB032945 // CDS // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // CDS // 0 // --- // --- // --- // --- /// ENST00000356732 // 3UTR // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1800660	gtagaaagcatttccc[A/G]gacctcaacataagc	A	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // — /// ENST00000356732 // intron // 0 // — // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2234668	ctccagccagattaaa[C/T]gctaaagcacagtcc	C	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // — /// ENST00000356732 // intron // 0 // — // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2206092	ccatcaacatcagaca[A/G]aaagaccagatgacat	A	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // — /// ENST00000356732 // intron // 0 // — // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2103551	agcaatttcaaactta[C/G]ggaaaaggctatgaaa	C	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2021542	aaaaaatatttgctca[A/G]tacctgtagtcagcat	A	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1648934	cacatggaagtgaaaggatataaa[C/T]tcaagtggatgacag ccatacatta	C	T	AB032945 // intron // 0 // Hs.512590 // MYO5B // 4645 // myosin VB	MYO5B	MYO5B , rs7237077, myosin VB.q21.1
SNP_A-2158756	attgtctggtgtttta[C/T]gtgtagcaggcttcca	C	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2104089	agcagaagtcttcaga[A/C]accaagcccacccctga	A	C	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1934815	ttctcttctcaaggg[C/T]actatgctgcacacct agaggaccacctgccaaatctcac[C/G]taagtcactgctta	C	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1649556	atgcagggct	C	G	AB032945 // intron // 0 // Hs.512590 // MYO5B // 4645 // myosin VB	MYO5B	MYO5B , rs868973, myosin VB.q21.1
SNP_A-1717091	aaatctaacatcttcggtagcata[C/G]aagaccgttcctgagc ctggcccca	C	G	AB032945 // intron // 0 // Hs.512590 // MYO5B // 4645 // myosin VB	MYO5B	MYO5B , rs10502906, myosin VB.q21.1
SNP_A-1740081	caggaggcagaaactgttaccagca[C/T]tagcggatgtgaaa aatggggcagt	C	T	AB032945 // intron // 0 // Hs.512590 // MYO5B // 4645 // myosin VB	MYO5B	MYO5B , rs11985467, myosin VB.q21.1
SNP_A-2192354	catcatcagatgctca[A/G]cagctttccacaatgt	A	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1892928	tgcaccttctcaacta[C/G]gtctgttatttttcag	C	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2193247	catctcattaacgaca[A/G]atccaagatgtgccag	A	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1910474	agtctctaatccaa[C/T]ggttcatttgtcgtat	C	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-2077113	accaagatcagagaag[G/T]atcgagtccatgtgca	G	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1780312	ggataacctaattgccc[C/T]gattaatcattatac	C	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1815161	gtgttctgcccaaaa[G/T]tcacaacctccatgta	G	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // — // — // —	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2209042	cccaggaaaggctgaa[A/G]agaagcatggaggttg	A	G	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds, q21.1
SNP_A-1724544	gcaagaccaaacatcaaatttatga[C/T]gaagtgtggagagaagaattgtgaa	C	T	AB032945 // intron // 0 // Hs.512590 // MYO5B // 4645 // myosin VB	MYO5B	MYO5B , rs1790440, myosin VB,q21.1
SNP_A-1786733	ggctttaaattttcca[A/T]tcccaaaaatgtataa	A	T	AB032945 // intron // 0 // Hs.445218 // MYO5B // 4645 // Homo sapiens mRNA for KIAA1119 protein, partial cds. /// ENST00000285039 // intron // 0 // --- // --- // --- // ---	MYO5B	MYO5B, Homo sapiens for KIAA1119 protein, partial cds. q21.1
SNP_A-1675720	aaacaaacttatccctgaactaaaa[A/C]ctgggcatggactcactgaccctga	A	C	L29143 // upstream // 198571 // - // - // - // Homo sapiens myosin mRNA, partial cds. /// NM_145020 // downstream // 27267 // Hs.371212 // FLJ32743 // 220136 // hypothetical protein FLJ32743	-	- , rs1662897, Homo sapiens myosin mRNA, partial cds. ,q21.1
SNP_A-1660557	cagtttcaggctaggttcttgccct[A/G]tatgtgtgacttcaggttggcttt	A	G	L29143 // upstream // 218125 // - // - // - // Homo sapiens myosin mRNA, partial cds. /// NM_145020 // downstream // 7713 // Hs.371212 // FLJ32743 // 220136 // hypothetical protein FLJ32743	-	- , rs1373185, Homo sapiens myosin mRNA, partial cds. ,q21.1
SNP_A-2100074	agagtgcaggttagaa[C/T]gcattggtatggtcct	C	T	NM_145020 // intron // 0 // Hs.132701 // CCDC11 // 220136 // Homo sapiens hypothetical protein FLJ32743 (FLJ32743), mRNA. /// ENST00000303601 // intron // 0 // --- // --- // --- // ---	CCDC11	CCDC11, Homo sapiens hypothetical protein FLJ32743 (FLJ32743), q21.1
SNP_A-2273494	gactcttatgaataaa[G/T]ctacgatgaatagaca	G	T	NM_145020 // intron // 0 // Hs.132701 // CCDC11 // 220136 // Homo sapiens hypothetical protein FLJ32743 (FLJ32743), mRNA. /// ENST00000303601 // intron // 0 // --- // --- // --- // ---	CCDC11	CCDC11, Homo sapiens hypothetical protein FLJ32743 (FLJ32743), q21.1
SNP_A-2064363	aattcatctaactagc[A/G]aaaactcagtcataca	A	G	NM_145020 // intron // 0 // Hs.132701 // CCDC11 // 220136 // Homo sapiens hypothetical protein FLJ32743 (FLJ32743), mRNA. /// ENST00000303601 // intron // 0 // --- // --- // --- // ---	CCDC11	CCDC11, Homo sapiens hypothetical protein FLJ32743 (FLJ32743), q21.1
SNP_A-2190544	catacctctgtctcc[G/T]cattagggatactctc	G	T	NM_014593 // intron // 0 // Hs.180933 // CXXC1 // 30827 // Homo sapiens CXXC finger 1 (PHD domain) (CXXC1), mRNA. /// ENST00000285106 // intron // 0 // --- // --- // --- // ---	CXXC1	CXXC1, Homo sapiens CXXC finger 1 (PHD domain) (CXXC1), q21.1
SNP_A-1869933	tccttcttagatgcgg[A/G]acaagaaaacacaact	A	G	NM_031939 // upstream // 27930 // Hs.131072 // MRO // 83876 // Homo sapiens maestro (MRO), mRNA. /// NM_031939 // upstream // 22565 // Hs.131072 // MRO // 83876 // Homo sapiens maestro (MRO), mRNA. /// NM_002396 // upstream // 31192 // Hs.233119 // ME2 //	MRO	MRO, Homo sapiens maestro (MRO), q21.1
SNP_A-1942752	ttgggcatcctcttaa[C/T]gagttagcaattaaat	C	T	NM_005359 // downstream // 23772 // Hs.75862 // SMAD4 // 4089 // Homo sapiens SMAD, mothers against DPP homolog 4 (Drosophila) (SMAD4), mRNA. /// NM_016626 // downstream // 71009 // Hs.465144 // RKHD2 // 51320 // Homo sapiens ring finger and KH domain con	SMAD4	SMAD4, Homo sapiens SMAD, mothers against DPP homolog 4 (Drosophila) (SMAD4), q21.1
SNP_A-1896039	tgcctttcaagcttcc[A/G]gattagttattaaaaa	A	G	NM_016626 // upstream // 413084 // Hs.465144 // RKHD2 // 51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 730692 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRN	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-1911798	gtcttgcgcttctgga[C/T]gaatgcagctcatgat	C	T	NM_016626 // upstream // 560600 // Hs.465144 // RKHD2 // 51320 // Homo sapiens ring finger and KH domain containing 2 (RKHD2), mRNA. /// NM_005215 // upstream // 583176 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRN	RKHD2	RKHD2, Homo sapiens ring finger and KH domain containing 2 (RKHD2), q21.1
SNP_A-1844371	tataaaatatgatcac[A/T]accatgtggataataa	A	T	NM_005215 // intron // 0 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1793994	ggtcaccccaacctag[A/T]atgtaaatggactttc	A	T	NM_005215 // intron // 0 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1913667	gctgtcctaccaggag[A/G]cctgcttctacacaaa	A	G	NM_005215 // intron // 0 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// ENST00000304775 // intron // 0 // --- // --- // ---	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-2250997	cttatgtgtctctggc[A/C]atactcttgttctga	A	C	NM_005215 // downstream // 394677 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 228875 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transc	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1757113	aaactgcgtggaggtcatcgaata[A/G]ggtacctgaccacag cgtggtaaac	A	G	NM_003927 // downstream // 218867 // Hs.25674 // MBD2 // 8932 // methyl-CpG binding domain protein 2 /// NM_005215 // downstream // 404420 // Hs.172562 // DCC // 1630 // deleted in colorectal carcinoma /// NM_015832 // downstream // 218867 // Hs.25674 // ---	MBD2	MBD2 , rs10515967 , methyl-CpG binding domain protein 2 , q21.2
SNP_A-2184022	cagccatttgcagtgg[A/G]atttcctacctgagcc	A	G	NM_005215 // downstream // 420659 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 202893 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transc	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1956637	ttgttttgcactgca[C/T]agttgtttgggagaca	C	T	NM_005215 // downstream // 440656 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 182896 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transc	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-2244241	ctggaaagacagagtc[A/G]ctaacaactgaaaaat	A	G	NM_005215 // downstream // 451254 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 172298 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transc	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1888348	tgagcttattcagtga[A/C]gtggtacatattatgt	A	C	NM_005215 // downstream // 499509 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 124043 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transc	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1826532	taacaagtgaaaaaaa[A/G]ttgcctgaggatgtgt	A	G	NM_005215 // downstream // 530441 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 93111 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcr	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-2059055	aatccccgtatgccaa[A/G]gttgctaagatctgtg	A	G	NM_005215 // downstream // 578401 // Hs.172562 // DCC // 1630 // Homo sapiens deleted in colorectal carcinoma (DCC), mRNA. /// NM_003927 // downstream // 45151 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcr	DCC	DCC, Homo sapiens deleted in colorectal carcinoma (DCC), q21.2
SNP_A-1956038	tttgtcttacagtga[C/T]gatggaagaatgtaca	C	T	NM_003927 // 3UTR // 0 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcript variant 1, mRNA. /// ENST00000256429 // 3UTR // 0 // --- // --- // ---	MBD2	MBD2, Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcript variant 1, q21.2
SNP_A-1915421	tgttccctcagtgaac[A/C]cccaaaattcaaaata	A	C	NM_003927 // upstream // 29250 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcript variant 1, mRNA. /// NM_015832 // upstream // 29250 // Hs.25674 // MBD2 // 8932 // Homo sapiens methyl-CpG binding domain pro	MBD2	MBD2, Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcript variant 1, q21.2
SNP_A-1914593	tgttaactgctttccc[C/T]cccaaatatgtatcac	C	T	NM_007195 // intron // 0 // Hs.438533 // POLI // 11201 // Homo sapiens polymerase (DNA directed) iota (POLI), mRNA. /// ENST00000217800 // intron // 0 // --- // --- // ---	POLI	POLI, Homo sapiens polymerase (DNA directed) iota (POLI), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1914579	ttttaaacaaaaatga[C/T]gactggtgacagaaaa	C	T	NM_173529 // downstream // 1933 // Hs.208701 // C18orf54 // 162681 // Homo sapiens hypothetical protein MGC33382 (MGC33382), mRNA. /// NM_173629 // upstream // 245076 // — // C18orf26 // 284254 // Homo sapiens chromosome 18 open reading frame 26 (C18orf	C18orf54	C18orf54, Homo sapiens hypothetical protein MGC33382 (MGC33382), q21.2
SNP_A-1741971	gtgtttagttaccaggcaagcaggga[A/C]gccacaatggtgactc agtgtgtga	A	C	NM_173529 // downstream // 10564 // Hs.208701 // MGC33382 // 162681 // hypothetical protein MGC33382 /// NM_173629 // upstream // 240109 // Hs.376146 // FLJ39106 // 284254 // hypothetical protein FLJ39106	MGC33382	MGC33382 , rs940310, hypothetical protein MGC33382 , q21.2
SNP_A-1943078	ttggtataataaggac[A/G]ctccaaattcataaaa	A	G	NM_173529 // downstream // 27621 // Hs.208701 // C18orf54 // 162681 // Homo sapiens hypothetical protein MGC33382 (MGC33382), mRNA. /// NM_173629 // upstream // 219388 // — // C18orf26 // 284254 // Homo sapiens chromosome 18 open reading frame 26 (C18or	C18orf54	C18orf54, Homo sapiens hypothetical protein MGC33382 (MGC33382), q21.2
SNP_A-1877389	tctggagagttaaaga[C/T]ggtgatcaataatttc	C	T	NM_173529 // downstream // 38484 // Hs.208701 // C18orf54 // 162681 // Homo sapiens hypothetical protein MGC33382 (MGC33382), mRNA. /// NM_173629 // upstream // 208525 // — // C18orf26 // 284254 // Homo sapiens chromosome 18 open reading frame 26 (C18or	C18orf54	C18orf54, Homo sapiens hypothetical protein MGC33382 (MGC33382), q21.2
SNP_A-2282479	gagttgcaggcatcca[A/G]gctgtaagtagtagca	A	G	NM_173529 // downstream // 214233 // Hs.208701 // C18orf54 // 162681 // Homo sapiens hypothetical protein MGC33382 (MGC33382), mRNA. /// NM_173629 // upstream // 32776 // — // C18orf26 // 284254 // Homo sapiens chromosome 18 open reading frame 26 (C18or	C18orf54	C18orf54, Homo sapiens hypothetical protein MGC33382 (MGC33382), q21.2
SNP_A-1858631	tcagagttctctcaaa[C/T]acatgtcagccaacaa	C	T	NM_173529 // downstream // 245112 // Hs.208701 // C18orf54 // 162681 // Homo sapiens hypothetical protein MGC33382 (MGC33382), mRNA. /// NM_173629 // upstream // 1897 // — // C18orf26 // 284254 // Homo sapiens chromosome 18 open reading frame 26 (C18orf	C18orf54	C18orf54, Homo sapiens hypothetical protein MGC33382 (MGC33382), q21.2
SNP_A-1848933	tatgcaataaaacactt[C/T]aactataggccagttc	C	T	NM_004163 // intron // 0 // Hs.25318 // RAB27B // 5874 // Homo sapiens RAB27B, member RAS oncogene family (RAB27B), mRNA. /// ENST00000262094 // intron // 0 // — // — // — // —	RAB27B	RAB27B, Homo sapiens RAB27B, member RAS oncogene family (RAB27B), q21.2
SNP_A-1861954	tcatgagaaagtgaac[C/T]agaaggagtgattacg	C	T	NM_004163 // downstream // 6815 // Hs.25318 // RAB27B // 5874 // Homo sapiens RAB27B, member RAS oncogene family (RAB27B), mRNA. /// NM_025214 // downstream // 4853 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA.	RAB27B	RAB27B, Homo sapiens RAB27B, member RAS oncogene family (RAB27B), q21.2
SNP_A-2040293	aaccacggcacatagc[A/G]aagtctaccatttct	A	G	NM_025214 // intron // 0 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// ENST00000337363 // intron // 0 // — // — // — // —	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-1883893	tgaagactgagcaata[C/T]ggcggtcactgtgcc	C	T	NM_025214 // upstream // 16212 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 252246 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST000003	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-1898175	tgctgtttggcatta[A/G]ggaacaaaaatctct	A	G	NM_025214 // upstream // 48565 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 219893 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST000003	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-1915239	cacattttacgctgac[A/C]aacccaatctaagatg	A	C	NM_025214 // upstream // 86494 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 181964 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST000003	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805277	gtcatttcagtggcaa[A/G]gagaagaacagacatc	A	G	NM_025214 // upstream // 228641 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 39817 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST0000003	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-1694051	cagcccaaggaactaaggcataacag[A/T]cattaccatggccaaactgctttt	A	T	NM_003199 // downstream // 30984 // Hs.359289 // TCF4 // 6925 // transcription factor 4 /// NM_025214 // upstream // 237348 // Hs.30315 // SE57-1 // 80323 // CTCL tumor antigen se57-1	TCF4	TCF4, rs1526173, transcription factor 4, q21.2
SNP_A-2308283	gctgggtgatgggaa[A/G]gtgatgcaaatgagaa	A	G	NM_025214 // upstream // 259799 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 8659 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST0000033	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-2178963	cactgcagctgcttcc[A/G]gaaaaatgggatatt	A	G	NM_025214 // upstream // 259974 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 8484 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST0000033	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-1855785	tcaatctacttgcaa[A/G]attggaggctattc	A	G	NM_025214 // upstream // 263330 // Hs.120790 // SE57-1 // 80323 // Homo sapiens CTCL tumor antigen se57-1 (SE57-1), mRNA. /// NM_003199 // downstream // 5128 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST0000033	SE57-1	SE57-1, Homo sapiens CTCL tumor antigen se57-1 (SE57-1), q21.2
SNP_A-2284356	gatatttggtttctc[A/G]cagacattaacccaa	A	G	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1871354	tctaaatagcctgtta[C/G]agaatttcagcgaagc	C	G	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1960471	ttttattttgtgtac[A/T]gatataacaaaggta	A	T	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2181168	cagacatacacggtaa[C/T]tgggaatgtcacagcta	C	T	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1680142	gagaaatagtgttaactagtatcttg[C/T]agaaaaataatggcattgtatctatt	C	T	NM_003199 // intron // 0 // Hs.359289 // TCF4 // 6925 // transcription factor 4	TCF4	TCF4, rs10515970, transcription factor 4, q21.2
SNP_A-1915497	ttatgtaaataataaac[A/C]aaattgtcatggctta	A	C	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2041483	aacctggtgggcaaa[A/C]ctcctgcctgggaaa	A	C	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2005674	tcactgtacctactca[A/T]agagatgcttggagaa	A	T	NM_003199 // intron // 0 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// ENST00000356073 // intron // 0 // — // — // — /// ENST00000354452 // intron // 0 // — // — // —	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1720587	ttaaaaagcataacaccacgtgcat[C/G]ataagctctcaataaatacaggctg	C	G	NM_003199 // intron // 0 // Hs.359289 // TCF4 // 6925 // transcription factor 4	TCF4	TCF4, rs10503003, transcription factor 4, q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1784010	ggccagacatcaaacc[C/T]ctacttcggcctaitg	C	T	NM_003199 // upstream // 144974 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 869221 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1929294	ttcagtatcattgatg[C/T]aactaccttatgactc	C	T	NM_003199 // upstream // 178262 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 835933 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1916039	tgcatcgatgtactaa[A/G]cacttcaataatcatc	A	G	NM_003199 // upstream // 372439 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 641756 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2217435	cctgacaacttgttct[A/G]actgtagaaactaggg	A	G	NM_003199 // upstream // 559275 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 454920 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2084780	actattttcgttcct[C/T]agctttcagactcaga	C	T	NM_003199 // upstream // 794833 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 219362 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2040548	aaccatcacaatagag[A/G]agtcttaaattccgtc	A	G	NM_003199 // upstream // 795110 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 219085 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2274150	gacttcatgtggacaa[C/T]ggctaacagtgccatt	C	T	NM_003199 // upstream // 861234 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 152961 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2021115	aaaaaaaagtccacca[C/T]gaatacatcagaaca	C	T	NM_003199 // upstream // 861659 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 152536 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2162671	atttcttatactgca[A/T]caaagctagcacattt	A	T	NM_003199 // upstream // 865769 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 148426 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-1822048	gtttccctttgtgtg[A/C]aataatgtaagtaagt	A	C	NM_003199 // upstream // 885931 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 128264 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2
SNP_A-2085200	actcaggtaaaactac[C/T]gctagccggtaaagt	C	T	NM_003199 // upstream // 890255 // Hs.200285 // TCF4 // 6925 // Homo sapiens transcription factor 4 (TCF4), mRNA. /// NM_004786 // downstream // 123940 // Hs.114412 // TXNL1 // 9352 // Homo sapiens thioredoxin-like 1 (TXNL1), mRNA. /// ENST00000356073 //	TCF4	TCF4, Homo sapiens transcription factor 4 (TCF4), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1831560	taattaatatgtgaaa[A/G]gaacaacattaggttt	A	G	NM_052834 // intron // 0 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // intron // 0 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 1, mRNA.	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1915677	tgttctggccagtggg[C/T]atatcaggtaaaaagc	C	T	NM_052834 // downstream // 66807 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 66807 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2005681	gagactgaagcagaaa[C/G]ataatttgagcccagg	C	G	NM_052834 // downstream // 142726 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 142726 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1793714	ggtatgttgccaaaaa[G/T]ctcagtttaaaagagt	G	T	NM_052834 // downstream // 150284 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 150284 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2169449	caagcccaactgctaa[A/G]gacgagggaaagcctc	A	G	NM_052834 // downstream // 159126 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 159126 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1917261	gtgctctttaacccac[A/C]aactgcaacacaaatc	A	C	NM_052834 // downstream // 164926 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 164926 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1737581	tgttttgcagccatgaaaaatgaca[C/T]ctctgaaagatatttaac aacatga	C	T	NM_015879 // upstream // 152420 // Hs.298923 // SIAT8C // 51046 // sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase) /// NM_175906 // downstream // 49777 // Hs.127882 // MGC33608 // 284257 // hypothetical protein MGC33608	SIAT8C	SIAT8C , rs1468885, sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase) ,q21.31
SNP_A-1935248	ttctgcctgaaaattc[C/T]agtatttcctctgtac	C	T	NM_052834 // downstream // 176619 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 176619 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2131580	atagcatagagcctaa[C/T]acatcaccagatggca	C	T	NM_052834 // downstream // 193542 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 193542 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2091678	agaaaagagaggtca[A/T]ctttcctttttataga	A	T	NM_052834 // downstream // 236541 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 236541 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1744341	ctttcaaagcatcatggaattagg[A/G]aatactaaactggaaa gggttgttt	A	G	NM_015879 // upstream // 74369 // Hs.298923 // SIAT8C // 51046 // sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase) /// NM_175906 // downstream // 127828 // Hs.127882 // MGC33608 // 284257 // hypothetical protein MGC33608	SIAT8C	SIAT8C , rs1943394, sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase) ,q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2276424	gagaggaaattaccaa[C/G]ctgcataatggagaca	C	G	NM_052834 // downstream // 249397 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 249397 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2295066	gcatagcatgaggtca[A/G]acagcaatatgcagag	A	G	NM_052834 // downstream // 249504 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 249504 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1917362	tctttgctgcagtcaa[A/G]ctctacttgttacatt	A	G	NM_052834 // downstream // 258759 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 258759 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-1917365	cagggccctgttcaac[C/G]atcacttcctccctca	C	G	NM_052834 // downstream // 258906 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, mRNA. /// NM_015285 // downstream // 258906 // Hs.465213 // WDR7 // 23335 // Homo sapiens WD repeat domain 7 (WDR7), transcrip	WDR7	WDR7, Homo sapiens WD repeat domain 7 (WDR7), transcript variant 2, q21.31
SNP_A-2103753	agcacattcttggaaa[G/T]gcactttgtttgtcct	G	T	NM_004852 // intron // 0 // Hs.194725 // ONECUT2 // 9480 // Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// ENST00000262095 // intron // 0 // --- // --- // --- // ---	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-2197227	cattcactggtaaata[C/T]gcacattgtgacctttt	C	T	NM_004852 // downstream // 1443 // Hs.194725 // ONECUT2 // 9480 // Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// NM_000140 // downstream // 71235 // Hs.465221 // FECH // 2235 // Homo sapiens ferrochelatase (protoporphyria) (FECH), mRNA	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-1903227	tggcttgctttgaaca[A/C]ccccacgtggccccac	A	C	NM_004852 // downstream // 1483 // Hs.194725 // ONECUT2 // 9480 // Homo sapiens one cut domain, family member 2 (ONECUT2), mRNA. /// NM_000140 // downstream // 71195 // Hs.465221 // FECH // 2235 // Homo sapiens ferrochelatase (protoporphyria) (FECH), mRNA	ONECUT2	ONECUT2, Homo sapiens one cut domain, family member 2 (ONECUT2), q21.31
SNP_A-1758623	gtttcatatttgcattgctcatgaa[C/T]gtaaacaaaatgtcgatatgtgtga	C	T	NM_000140 // downstream // 4967 // Hs.443610 // FECH // 2235 // ferrochelatase (protoporphyria) /// NM_004852 // downstream // 67773 // Hs.194725 // ONECUT2 // 9480 // one cut domain, family member 2	FECH	FECH , rs1037829, ferrochelatase (protoporphyria) ,q21.31
SNP_A-2096937	agactcttcttggacc[A/G]agacctcatgacactt	A	G	NM_000140 // CDS // 0 // Hs.465221 // FECH // 2235 // Homo sapiens ferrochelatase (protoporphyria) (FECH), mRNA. /// ENST00000262093 // CDS // 0 // --- // --- // --- // ---	FECH	FECH, Homo sapiens ferrochelatase (protoporphyria) (FECH), q21.31
SNP_A-2116254	aggtacgtaatggaaa[A/G]taaactagagctggct	A	G	NM_005603 // intron // 0 // Hs.216623 // ATP8B1 // 5205 // Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA. /// ENST00000357493 // intron // 0 // --- // --- // --- // --- /// ENST00000283684 // intron // 0 // --- // --- // --- // ---	ATP8B1	ATP8B1, Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), q21.31
SNP_A-1787919	gggacttatgtatgcc[G/T]cactgactgaagtaaa	G	T	NM_005603 // intron // 0 // Hs.216623 // ATP8B1 // 5205 // Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA. /// ENST00000357493 // intron // 0 // --- // --- // --- // --- /// ENST00000283684 // intron // 0 // --- // --- // --- // ---	ATP8B1	ATP8B1, Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), q21.31
SNP_A-2229934	ctagttttcagtctca[C/T]gatttccgctctctgt	C	T	NM_005603 // intron // 0 // Hs.216623 // ATP8B1 // 5205 // Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA. /// ENST00000357493 // intron // 0 // --- // --- // --- // --- /// ENST00000283684 // intron // 0 // --- // --- // --- // ---	ATP8B1	ATP8B1, Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), q21.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1917696	gaggaagatcccaaac[G/T]ggatggaggcaaagtg	G	T	NM_005603 // upstream // 38671 // Hs.216623 // ATP8B1 // 5205 // Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA. /// ENST00000357493 // downstream // 38739 // — // — // — // — /// ENST00000283684 // upstream // 38671 // — // —	ATP8B1	ATP8B1, Homo sapiens ATPase, Class I, type 8B, member 1 (ATP8B1), q21.31
SNP_A-1917749	ctttaagtgattctga[A/T]gagaaactggttagga	A	T	ENST00000269477 // downstream // 29923 // — // — // — // — /// ENST00000303758 // downstream // 149911 // — // — // — // —	-	q21.31
SNP_A-2005696	tgtaaaaagccagata[C/T]taagtagttgaggctt	C	T	NM_015277 // intron // 0 // Hs.185677 // NEDD4L // 23327 // Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), mRNA. /// ENST00000256830 // intron // 0 // — // — // — // — /// ENST00000356462 // intron //	NEDD4L	NEDD4L, Homo sapiens neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), q21.31
SNP_A-1725094	attgtctggctttagtagatgctca[C/G]ctcttgatgatcacacaat agagag	C	G	NM_018181 // downstream // 123379 // Hs.368756 // ZNF532 // 55205 // zinc finger protein 532 /// NM_033280 // upstream // 31673 // Hs.45107 // LOC90701 // 90701 // similar to signal peptidase complex (18kD)	ZNF532	ZNF532 , rs1563712, zinc finger protein 532 ,q21.32
SNP_A-1693711	atagggctgataagaaagtcatcct[C/T]aatgttctattgcaccat atgcatc	C	T	AB075863 // intron // 0 // Hs.443699 // FLJ30681 // 147372 // KIAA1983 protein	FLJ30681	FLJ30681 , rs10503029, KIAA1983 protein,q21.32
SNP_A-1859265	tcagctctccttttaa[A/C]tacaggtgactgtagc	A	C	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-2114085	aggcttttgagaggtc[A/G]aagaggctccttgtca	A	G	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-1833884	tacagttcggacattc[A/G]agcatcgcgatttctc	A	G	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-1918935	caagaggaaagtctaa[A/G]ggcatcacagaatctc	A	G	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-2208869	cccagatgtgattaac[A/T]caagttccaaagtaag	A	T	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-2175357	cacatattacaaacca[A/G]tgaggaaggaagtatt	A	G	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-2051968	aaggtggtggttctga[A/C]gtaatggtaagtgtga	A	C	NM_133459 // intron // 0 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // intron // 0 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-2252965	cttctcatgagaaaaa[A/G]taaggtgataagtgct	A	G	NM_133459 // upstream // 18053 // Hs.34333 // CCBE1 // 147372 // Homo sapiens KIAA1983 protein (FLJ30681), mRNA. /// ENST00000333570 // upstream // 18053 // — // — // — // — /// ENST00000299756 // upstream // 46127 // — // — // — // —	CCBE1	CCBE1, Homo sapiens KIAA1983 protein (FLJ30681), q21.32
SNP_A-2296024	gcattacagaaagaat[A/G]aactccaagtcgttta	A	G	NM_021127 // upstream // 47019 // Hs.96 // PMAIP1 // 5366 // Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. /// ENST00000330674 // downstream // 27935 // — // — // — // — /// ENST00000316660 // upstream // 47019 //	PMAIP1	PMAIP1, Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), q21.32
SNP_A-2295804	gcatggagacaagtgc[A/C]aatcactttacatgag	A	C	NM_021127 // downstream // 7582 // Hs.96 // PMAIP1 // 5366 // Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. /// ENST00000316660 // downstream // 7582 // — // — // — // — /// ENST00000269518 // downstream // 8358 //	PMAIP1	PMAIP1, Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), q21.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2082823	acgtactgaatcccgg[C/T]acaagaaatgcagagt	C	T	NM_021127 // downstream // 76738 // Hs.96 // PMAIP1 // 5366 // Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. /// ENST00000316660 // downstream // 76738 // — // — // — /// ENST00000269518 // downstream // 77514	PMAIP1	PMAIP1, Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), q21.32
SNP_A-1911265	tgtctggtgtgaacca[C/T]ggggtttagaggaat	C	T	NM_021127 // downstream // 87216 // Hs.96 // PMAIP1 // 5366 // Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. /// ENST00000316660 // downstream // 87216 // — // — // — /// ENST00000269518 // downstream // 87992	PMAIP1	PMAIP1, Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), q21.32
SNP_A-1786651	ggcttgatgactgtga[C/G]agtgaaggagagacaa	C	G	NM_021127 // downstream // 91159 // Hs.96 // PMAIP1 // 5366 // Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA. /// ENST00000316660 // downstream // 91159 // — // — // — /// ENST00000269518 // downstream // 91935	PMAIP1	PMAIP1, Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), q21.32
SNP_A-2272330	gacctgaatacagccc[A/G]gatgctagcagaaac	A	G	NM_005912 // downstream // 303727 // Hs.532833 // MC4R // 4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 56482 // — // — // — /// ENST00000299766 // downstream // 303727 // — // — // -	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1919330	taggtccgatgtgttta[C/T]agcatttagtgtaaga	C	T	NM_005912 // downstream // 262900 // Hs.532833 // MC4R // 4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 97309 // — // — // — /// ENST00000299766 // downstream // 262900 // — // — // -	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1751769	aggagtgattatgcattggtttatg[C/T]caagtaaaataaagaat aagatga	C	T	NM_005912 // downstream // 179782 // - // - // - /// NM_021127 // downstream // 287265 // Hs.96 // PMAIP1 // 5366 // phorbol-12-myristate-13-acetate-induced protein 1	-	- , rs492443, - , q21.32
SNP_A-2044305	aacttgtctgctgaa[C/T]ctaaagaataaggaga	C	T	NM_005912 // downstream // 153968 // Hs.532833 // MC4R // 4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 206241 // — // — // — /// ENST00000299766 // downstream // 153968 // — // — // —	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-2176228	caccacttctccag[A/C]ccccaaagtcaagtag	A	C	NM_005912 // downstream // 140367 // Hs.532833 // MC4R // 4160 // Homo sapiens melanocortin 4 receptor (MC4R), mRNA. /// ENST00000341108 // upstream // 219842 // — // — // — /// ENST00000299766 // downstream // 140367 // — // — // —	MC4R	MC4R, Homo sapiens melanocortin 4 receptor (MC4R), q21.32
SNP_A-1749753	gtactggctgcccttggtcagaa[A/G]aaatgaaataaaggaa gttctccag	A	G	NM_005912 // upstream // 20352 // - // - // - /// NM_031891 // upstream // 1097841 // Hs.302138 // CDH20 // 28316 // cadherin 20, type 2	-	- , rs1943228, - , q21.32
SNP_A-1920407	tgacatagctaatgca[A/G]cgttttttcaggcagccc	A	G	NM_031891 // upstream // 375955 // Hs.147340 // CDH20 // 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 319671 // — // — // — /// ENST00000262717 // upstream // 375955 // — // — // —	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.32
SNP_A-2165714	caaaggaatgactgc[C/T]ctgagcttacaaattc	C	T	NM_031891 // upstream // 362859 // Hs.147340 // CDH20 // 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000328480 // upstream // 332767 // — // — // — /// ENST00000262717 // upstream // 362859 // — // — // —	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.32
SNP_A-1842605	taggtttactcataacc[C/T]gtcagaaattggaaaa	C	T	NM_031891 // intron // 0 // Hs.147340 // CDH20 // 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// ENST00000262717 // intron // 0 // — // — // —	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.33
SNP_A-2259398	gaaaaatcagaatacaa[C/G]aagcctcgctaagttc	C	G	NM_031891 // downstream // 47541 // Hs.147340 // CDH20 // 28316 // Homo sapiens cadherin 20, type 2 (CDH20), mRNA. /// NM_173557 // downstream // 210697 // Hs.465316 // RNF152 // 220441 // Homo sapiens ring finger protein 152 (RNF152), mRNA. /// ENST00000	CDH20	CDH20, Homo sapiens cadherin 20, type 2 (CDH20), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287906	gattatatatagcaga[A/G]tagtgcagtggcttaa	A	G	NM_173557 // upstream // 18905 // Hs.465316 // RNF152 // 220441 // Homo sapiens ring finger protein 152 (RNF152), mRNA. /// NM_012327 // downstream // 132251 // Hs.157031 // PIGN // 23556 // Homo sapiens phosphatidylinositol glycan, class N (PIGN), transc	RNF152	RNF152, Homo sapiens ring finger protein 152 (RNF152), q21.33
SNP_A-1921097	ggagagcctgttgata[C/T]catcatttggtaggca	C	T	NM_012327 // intron // 0 // Hs.157031 // PIGN // 23556 // Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, mRNA. /// NM_176787 // intron // 0 // Hs.157031 // PIGN // 23556 // Homo sapiens phosphatidylinositol glycan, class N	PIGN	PIGN, Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, q21.33
SNP_A-1712707	ttaggaaaactagttagcataatga[A/G]gaataggaaaggatactggaatgca	A	G	NM_012327 // intron // 0 // Hs.157031 // PIGN // 23556 // phosphatidylinositol glycan, class N /// NM_176787 // intron // 0 // Hs.157031 // PIGN // 23556 // phosphatidylinositol glycan, class N	PIGN	PIGN , rs4274523, phosphatidylinositol glycan, class N ,q21.33
SNP_A-2045232	aagaagctggaaaata[C/T]ggaaaactgaggaaat	C	T	NM_012327 // intron // 0 // Hs.157031 // PIGN // 23556 // Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, mRNA. /// NM_176787 // intron // 0 // Hs.157031 // PIGN // 23556 // Homo sapiens phosphatidylinositol glycan, class N	PIGN	PIGN, Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2, q21.33
SNP_A-2142367	atgaaagcagcgtcat[G/T]acatcttctaagaatc	G	T	NM_020854 // CDS // 0 // Hs.465323 // KIAA1468 // 57614 // Homo sapiens KIAA1468 (KIAA1468), mRNA. /// ENST00000299783 // CDS // 0 // — // — // — // — /// ENST00000256858 // CDS // 0 // — // — // — // —	KIAA1468	KIAA1468, Homo sapiens KIAA1468 (KIAA1468), q21.33
SNP_A-1925644	ttatgaggctttaggg[A/G]aatgtcaaccctcaaa	A	G	NM_017742 // intron // 0 // Hs.114191 // ZCCHC2 // 54877 // Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), mRNA. /// ENST00000269499 // intron // 0 // — // — // — // —	ZCCHC2	ZCCHC2, Homo sapiens zinc finger, CCHC domain containing 2 (ZCCHC2), q21.33
SNP_A-1921634	cttgtgcagaatggga[C/G]atgtgaatcactgtgt	C	G	NM_194449 // intron // 0 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // — // — // — // — // —	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-2046868	aagaggggtgttacca[G/T]ggcattacttatgctt	G	T	NM_194449 // intron // 0 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // — // — // — // — // —	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-2270897	gacagtcaaagcctca[C/T]tctactcctcactgca	C	T	NM_194449 // intron // 0 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // — // — // — // — // —	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-1921670	agttctatagatgtac[A/G]cactgaagagatcagt	A	G	NM_194449 // intron // 0 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // — // — // — // — // —	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-1845177	tataccaaaatgctca[A/C]tatcattccttttgct	A	C	NM_194449 // intron // 0 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// ENST00000262719 // intron // 0 // — // — // — // — // —	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-2079173	acccaggtctctcaaa[C/T]ttcacagctccatgca	C	T	NM_194449 // downstream // 58523 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// NM_000633 // downstream // 84391 // Hs.150749 // BCL2 // 596 // Hom	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2005730	aaagaatatagaagaaa[A/G]acatcagtagagaaga	A	G	NM_194449 // downstream // 61061 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// NM_000633 // downstream // 81853 // Hs.150749 // BCL2 // 596 // Hom	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-1905500	tggtaccagcacgtaa[A/G]ggagtcaagcgcagca	A	G	NM_194449 // downstream // 117349 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// NM_000633 // downstream // 25565 // Hs.150749 // BCL2 // 596 // Ho	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-1921840	ggagatgacgtgatg[A/G]aatagtgactaagttc	A	G	NM_194449 // downstream // 132534 // Hs.465337 // PLEKHE1 // 23239 // Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), mRNA. /// NM_000633 // downstream // 10380 // Hs.150749 // BCL2 // 596 // Ho	PLEKHE1	PLEKHE1, Homo sapiens pleckstrin homology domain containing, family E (with leucine rich repeats) member 1 (PLEKHE1), q21.33
SNP_A-1946800	tttagaaaggtgcca[C/G]attgcagaacaggga	C	G	NM_002035 // intron // 0 // Hs.74050 // FVT1 // 2531 // Homo sapiens follicular lymphoma variant translocation 1 (FVT1), mRNA. /// ENST00000326575 // intron // 0 // — // — // — /// ENST00000342313 // intron // 0 // — // — // —	FVT1	FVT1, Homo sapiens follicular lymphoma variant translocation 1 (FVT1), q21.33
SNP_A-1795239	ggtgaggtgtgtttcc[A/G]aatctgaaatctcagc	A	G	NM_004869 // intron // 0 // Hs.126550 // VPS4B // 9525 // Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA. /// ENST00000238497 // intron // 0 // — // — // —	VPS4B	VPS4B, Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), q21.33
SNP_A-2070029	acacataaaaacacat[A/G]aggacaagtaaaactg	A	G	NM_004869 // intron // 0 // Hs.126550 // VPS4B // 9525 // Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA. /// ENST00000238497 // intron // 0 // — // — // —	VPS4B	VPS4B, Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), q21.33
SNP_A-1941811	ttggaccttgaattgc[C/T]cttaaatcacacatgc	C	T	NM_004869 // upstream // 4681 // Hs.126550 // VPS4B // 9525 // Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA. /// NM_080474 // upstream // 129019 // Hs.348541 // SERPINB12 // 89777 // Homo sapiens serine (or cysteine) proteinase inhibitor	VPS4B	VPS4B, Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), q21.33
SNP_A-1922105	gcctagataagaaaaag[A/G]agtggcagccactgtg	A	G	NM_004869 // upstream // 35638 // Hs.126550 // VPS4B // 9525 // Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA. /// NM_080474 // upstream // 98062 // Hs.348541 // SERPINB12 // 89777 // Homo sapiens serine (or cysteine) proteinase inhibitor	VPS4B	VPS4B, Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), q21.33
SNP_A-1875225	tctctctctaatactat[C/T]agcagaagcaggttac	C	T	NM_012397 // downstream // 17640 // Hs.241407 // SERPINB13 // 5275 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), mRNA. /// NM_002974 // downstream // 22184 // Hs.123035 // SERPINB4 // 6318 // Homo s	SERPINB13	SERPINB13, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), q21.33
SNP_A-2297269	gccaccgctgtagtag[C/G]attcggatcatcacct	C	G	NM_006919 // CDS // 0 // Hs.227948 // SERPINB3 // 6317 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3 (SERPINB3), mRNA. /// ENST00000360996 // intron // 0 // — /// — // — /// ENST00000345651 // intron	SERPINB3	SERPINB3, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3 (SERPINB3), q21.33
SNP_A-1922373	ttccgagtttggtgtc[G/T]aattctctcaaatcaa	G	T	NM_002974 // upstream // 68348 // Hs.123035 // SERPINB4 // 6318 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA. /// NM_006919 // upstream // 50711 // Hs.227948 // SERPINB3 // 6317 // Homo sapiens	SERPINB4	SERPINB4, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), q21.33
SNP_A-2164814	caaaccagattcttag[C/T]cacagggcaccagtgg	C	T	NM_002974 // upstream // 92817 // Hs.123035 // SERPINB4 // 6318 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), mRNA. /// NM_006919 // upstream // 75180 // Hs.227948 // SERPINB3 // 6317 // Homo sapiens	SERPINB4	SERPINB4, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 (SERPINB4), q21.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1956970	ttttaagttgggagat[A/C]ataagtcatcttgttt	A	C	NM_003784 // intron // 0 // Hs.138202 // SERPINB7 // 8710 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), mRNA. /// ENST00000336429 // intron // 0 // --- // --- // --- // ---	SERPINB7	SERPINB7, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), q21.33
SNP_A-1959708	ttttggtaaaaagcaa[A/G]gcaactagttacataa	A	G	NM_003784 // intron // 0 // Hs.138202 // SERPINB7 // 8710 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), mRNA. /// ENST00000336429 // intron // 0 // --- // --- // --- // ---	SERPINB7	SERPINB7, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), q21.33
SNP_A-1896437	tgctaatttttattta[A/T]gtgtcacctgatgaaa	A	T	NM_003784 // intron // 0 // Hs.138202 // SERPINB7 // 8710 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), mRNA. /// ENST00000336429 // intron // 0 // --- // --- // --- // --- /// ENST00000238484 // intr	SERPINB7	SERPINB7, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), q21.33
SNP_A-1868346	tcctcatgaatgtcca[A/G]tgatattacatctgat	A	G	NM_003784 // intron // 0 // Hs.138202 // SERPINB7 // 8710 // Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), mRNA. /// ENST00000336429 // intron // 0 // --- // --- // --- // --- /// ENST00000238484 // intr	SERPINB7	SERPINB7, Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), q21.33
SNP_A-1891264	tgatgtttgggtagac[C/T]gagtaaaagctgagaa	C	T	NM_152728 // upstream // 88099 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 88099 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1434976 // ---	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2044309	aactttgttctgtaca[C/T]ggactaaatattgtct	C	T	NM_152728 // upstream // 120712 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 120712 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1402363 // --	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1809051	gtgacaagtgacagga[A/G]gacacagttaaccgtc	A	G	NM_152728 // upstream // 121376 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 121376 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1401699 // --	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2163214	atttttctttatcttg[A/C]agaaaagcaccaagtg	A	C	NM_152728 // upstream // 121709 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 121709 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1401366 // --	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2084025	actagagcacacccaa[C/T]tagaatgcagatctgg	C	T	NM_152728 // upstream // 122218 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 122218 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1400857 // --	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2113066	aggccactgcgatcaa[C/T]gccccaataacatatt	C	T	NM_152728 // upstream // 142903 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 142903 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1380172 // --	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1923170	gtccagagaagtaagt[C/G]aatgttctgaagacat	C	G	NM_152728 // upstream // 181444 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 181444 // --- // --- // --- // --- /// ENST00000359723 // upstream // 1341631 // --	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1690009	aggctgggcactaggaaataacca[C/T]tgggtctctgagttcct ctcaaagc	C	T	NM_004361 // upstream // 1407909 // Hs.272211 // CDH7 // 1005 // cadherin 7, type 2 /// NM_033646 // upstream // 1407240 // Hs.272211 // CDH7 // 1005 // cadherin 7, type 2 /// NM_152728 // upstream // 193984 // Hs.416763 // MGC39571 // 221241 // hypothet	CDH7	CDH7 , rs10503090, cadherin 7, type 2 , q22.1
SNP_A-1923219	aacattgattctgaaaa[A/G]gtaagcctgctccctt	A	G	NM_152728 // upstream // 203460 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 203460 // — // — // — // — /// ENST00000359723 // upstream // 1319615 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1955266	tttggctttctggaaa[C/G]ttcattgacgtgcaac	C	G	NM_152728 // upstream // 214703 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 214703 // — // — // — // — /// ENST00000359723 // upstream // 1308372 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1846372	tatatggctcagtggg[G/T]aactacctgttaaaca	G	T	NM_152728 // upstream // 636183 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 636183 // — // — // — // — /// ENST00000359723 // upstream // 886892 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1856295	tcacaattttaagtc[A/C]acacctggaatttgga	A	C	NM_152728 // upstream // 659871 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 659871 // — // — // — // — /// ENST00000359723 // upstream // 863204 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2152862	attacacacatagac[A/G]aactaagtatgttgta	A	G	NM_152728 // upstream // 1464561 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 1464561 // — // — // — // — /// ENST00000359723 // upstream // 58514 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1804766	gtcagtaactatgtta[A/G]attctgagatactaaa	A	G	NM_152728 // upstream // 1489242 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 1489242 // — // — // — // — /// ENST00000359723 // upstream // 33833 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-1848489	tatgaatcacatggtat[A/G]atttccgttacatcag	A	G	NM_152728 // upstream // 1502078 // Hs.416763 // C18orf20 // 221241 // Homo sapiens chromosome 18 open reading frame 20 (C18orf20), mRNA. /// ENST00000323355 // upstream // 1502078 // — // — // — // — /// ENST00000359723 // upstream // 20997 // —	C18orf20	C18orf20, Homo sapiens chromosome 18 open reading frame 20 (C18orf20), q22.1
SNP_A-2057807	aatattaatttctaaac[C/T]atgtaagcgcatataa	C	T	NM_004361 // intron // 0 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // intron // 0 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant a, mRNA. /	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1852430	tatttaatggtgtta[C/T]gctcttgcaaaaattt	C	T	NM_004361 // downstream // 49108 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 49108 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript va	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2179878	cacttatctcaaccaa[C/G]atttgctaggcttttt	C	G	NM_004361 // downstream // 131936 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 131936 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2065351	aattgtcaattatttg[C/T]acggtgatgaatgaag	C	T	NM_004361 // downstream // 143211 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 143211 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2070579	acacctgcttttacac[C/T]aaaattagccttgcaa	C	T	NM_004361 // downstream // 143250 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 143250 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2204153	ccagcagatcataaag[A/T]attgagaacagggaac	A	T	NM_004361 // downstream // 146309 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 146309 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1707117	tcagtcctatttatttttatacacta[A/G]taccagatagcacttcctaaaatac	A	G	NM_004361 // downstream // 153069 // Hs.272211 // CDH7 // 1005 // cadherin 7, type 2 /// NM_021153 // downstream // 470078 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2 /// NM_033646 // downstream // 153068 // Hs.272211 // CDH7 // 1005 // cadherin	CDH7	CDH7 , rs2541771, cadherin 7, type 2 ,q22.1
SNP_A-1719003	ctgattactttgctaatttatttga[C/T]gtatcctgcttcttcttcaagctca	C	T	NM_004361 // downstream // 154641 // Hs.272211 // CDH7 // 1005 // cadherin 7, type 2 /// NM_021153 // downstream // 468506 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2 /// NM_033646 // downstream // 154640 // Hs.272211 // CDH7 // 1005 // cadherin	CDH7	CDH7 , rs2706624, cadherin 7, type 2 ,q22.1
SNP_A-2163748	caaaaattacaacgaa[A/G]tgatcttgccctgaag	A	G	NM_004361 // downstream // 168657 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 168657 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1924940	ggtacctttggatgta[C/T]gtaagagtgagcattt	C	T	NM_004361 // downstream // 199345 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 199345 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1924944	tctatgactctcccat[G/T]actataattgctatta	G	T	NM_004361 // downstream // 199838 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 199838 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1924945	aatgaagaaaagtaca[A/G]ggaaggttgacattat	A	G	NM_004361 // downstream // 200602 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 200602 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1868536	tcctctaaggtgcacc[A/G]gaaaggaagtgttcac	A	G	NM_004361 // downstream // 202250 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 202250 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2189825	cataaactgacggcaa[C/T]tggagtttaaatagtc	C	T	NM_004361 // downstream // 202862 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 202862 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1691174	caaaggcgacatatttcaattgtaa[A/T]gtttcagaaataaatgat taacaac	A	T	NM_004361 // downstream // 210553 // Hs.272211 // CDH7 // 1005 // cadherin 7, type 2 /// NM_021153 // downstream // 412594 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2 /// NM_033646 // downstream // 210552 // Hs.272211 // CDH7 // 1005 // cadherin	CDH7	CDH7 , rs2193295, cadherin 7, type 2 ,q22.1
SNP_A-2204077	ccagcaaataatacata[C/T]caatgtctgaagagca	C	T	NM_004361 // downstream // 208990 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 208990 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1895426	tgccggtaatatcaag[A/G]cattggagcaggagct	A	G	NM_004361 // downstream // 209069 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 209069 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1905980	tggtcctgtaaaccca[C/T]gtcagtttgaagtgtc	C	T	NM_004361 // downstream // 253526 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 253526 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2285708	gatgaatttttgtttgc[C/T]attgttcattaggaat	C	T	NM_004361 // downstream // 288704 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 288704 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2130241	atacctagtttctca[A/T]caaatcatatatattt	A	T	NM_004361 // downstream // 294760 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 294760 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2043656	aacttaacgagttat[C/G]acaactttgcatttg	C	G	NM_004361 // downstream // 331918 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 331918 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1921771	ttactaataagttcaa[A/G]gtggttgctatttctt	A	G	NM_004361 // downstream // 354075 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 354075 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2170768	caagtttatatatcaa[A/G]gtaaccatcacatcca	A	G	NM_004361 // downstream // 364553 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 364553 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1899735	tggaatcttgaaaag[A/T]atcgagagcccaaaag	A	T	NM_004361 // downstream // 365202 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA /// NM_033646 // downstream // 365202 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1713239	ctctgcttgcagtttcacttcct[A/G]tggagtcttttgtgaacag aagt	A	G	NM_004361 // downstream // 374442 // Hs.272211 // CDH7 // 1005 // cadherin 7, type 2 /// NM_021153 // downstream // 248705 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2 /// NM_033646 // downstream // 374441 // Hs.272211 // CDH7 // 1005 // cadherin	CDH7	CDH7 , rs1388177, cadherin 7, type 2 ,q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1819093	gttgcctgcagaatta[C/G]cttgaatatgtagatt	C	G	NM_004361 // downstream // 524935 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 524935 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2182392	cagagttttagaaata[C/G]tatacagcagcattaa	C	G	NM_004361 // downstream // 527601 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 527601 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-1920154	ttaatcctgatttccc[C/T]gacatttagttcaata	C	T	NM_004361 // downstream // 594638 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, mRNA. /// NM_033646 // downstream // 594638 // Hs.130306 // CDH7 // 1005 // Homo sapiens cadherin 7, type 2 (CDH7), transcript	CDH7	CDH7, Homo sapiens cadherin 7, type 2 (CDH7), transcript variant b, q22.1
SNP_A-2046009	aagacgaaatttctga[C/T]gagaagacaactaaaa	C	T	NM_021153 // intron // 0 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // intron // 0 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2198756	catttctatatactga[G/T]aacgtccatgctgaga	G	T	NM_021153 // intron // 0 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // intron // 0 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1932254	ttcctctaaccgtaca[C/G]tccagagcctgatcct	C	G	NM_021153 // upstream // 57081 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 57081 // — // — // — // — /// ENST00000319884 // downstream // 823349 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1670882	aagaaggagcagcagacatgccaaa[C/T]atgtaggcaaatat ttttaaatata	C	T	AL831865 // downstream // 759829 // Hs.389019 // - // - // MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217) /// NM_021153 // upstream // 117987 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2	-	- , rs923416, MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217) ,q22.1
SNP_A-1695375	tgctctagagattacattgtgcctt[G/T]tcaacatattagtctgctta aagtt	G	T	AL831865 // downstream // 759628 // Hs.389019 // - // - // MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217) /// NM_021153 // upstream // 118188 // Hs.42771 // CDH19 // 28513 // cadherin 19, type 2	-	- , rs923415, MRNA; cDNA DKFZp761N2217 (from clone DKFZp761N2217) ,q22.1
SNP_A-2262956	gaacaagcctagagta[C/T]gaaaatgacaataaat	C	T	NM_021153 // upstream // 219831 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 219831 // — // — // — // — /// ENST00000319884 // downstream // 660599 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2026721	aaacaatgtattcttc[G/T]aaagcgtgtatccatt	G	T	NM_021153 // upstream // 270361 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 270361 // — // — // — // — /// ENST00000319884 // downstream // 610069 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1953424	tttgaacctttggtc[A/G]agtttcatattccagc	A	G	NM_021153 // upstream // 282049 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 282049 // — // — // — // — /// ENST00000319884 // downstream // 598381 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-2281189	gagtagaggagagaag[A/T]aggcgtacctataaaa	A	T	NM_021153 // upstream // 446528 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 446528 // — // — // — // — /// ENST00000319884 // downstream // 433902 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1956997	ttttaatatgaggaca[C/T]ggaagaaagaaaacag	C	T	NM_021153 // upstream // 538644 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 538644 // — // — // — // — /// ENST00000319884 // downstream // 341786 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1906055	tggtctccgtatttta[C/T]ggcaaatttcttgtat	C	T	NM_021153 // upstream // 689533 // Hs.42771 // CDH19 // 28513 // Homo sapiens cadherin 19, type 2 (CDH19), mRNA. /// ENST00000262150 // upstream // 689533 // — // — // — /// ENST00000319884 // downstream // 190897 // — // — // — // —	CDH19	CDH19, Homo sapiens cadherin 19, type 2 (CDH19), q22.1
SNP_A-1897784	tgctggagaaaggcgtc[C/T]actcacagattgttct	C	T	NM_032160 // downstream // 2559 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// ENST00000319884 // upstream // 23565 // — // — // — /// ENST00000310045 // downstream // 2559 // — // -	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2226128	ctaaccattcacagaa[C/T]catgttaggtccta	C	T	NM_032160 // upstream // 91567 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 1067485 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1926076	catatttgtgacata[C/T]agtgtgagtgctgaga	C	T	NM_032160 // upstream // 108777 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 1050275 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1926077	atgttctgtttaatga[G/T]agtgatgcagtagggt	G	T	NM_032160 // upstream // 108839 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 1050213 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1926181	taggatggtgaaacta[C/T]gcctgggacttttat	C	T	NM_032160 // upstream // 199111 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 959941 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2083194	actaaaactattagca[C/G]aggtttggcatgaac	C	G	NM_032160 // upstream // 213676 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 945376 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2165753	caaaggtaatgagcta[C/T]aataacatttgaaaac	C	T	NM_032160 // upstream // 253368 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 905684 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2070770	acactaacaacttag[A/G]atctgctgatgaagca	A	G	NM_032160 // upstream // 275105 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 883947 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1868774	tcctcttttataagca[A/T]atcatttggtagtta	A	T	NM_032160 // upstream // 308203 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 850849 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1851846	tattgacttgtagcaa[C/T]ggagcaatgtacttca	C	T	NM_032160 // upstream // 404808 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 754244 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1702523	tgatttcaaataaaagtacagataa[A/G]atcatctttagagatat gttgtca	A	G	NM_019022 // downstream // 746121 // Hs.440534 // FLJ20793 // 54495 // FLJ20793 protein /// NM_032160 // upstream // 411632 // Hs.124673 // NCAG1 // 92126 // NCAG1	FLJ20793	FLJ20793 , rs1350744, FLJ20793 protein ,q22.1
SNP_A-1808519	gtgaaatacacaaaag[A/T]cttcaacatttggca	A	T	NM_032160 // upstream // 415470 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 743582 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2203199	ccactgtcttcttagata[C/T]attcaatgccatcaac	C	T	NM_032160 // upstream // 415695 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 743357 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1807004	gtctcatactgtcgcc[C/T]agttgcagtgcaatg	C	T	NM_032160 // upstream // 428994 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 730058 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2133109	atatagagaccataaa[A/G]tattggaggagagat	A	G	NM_032160 // upstream // 529897 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 629155 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2236750	ctctacagtttctgat[A/G]aaaagttcattgtcat	A	G	NM_032160 // upstream // 550722 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 608330 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2135966	atcaacttgactgta[A/C]cttagaaattatacag	A	C	NM_032160 // upstream // 674450 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 484602 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-2271268	gacatgtaatggtgcc[A/G]attttgatccacttg	A	G	NM_032160 // upstream // 766731 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 392321 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1954105	ttgatgtgacaattc[A/G]acccttgtgccattg	A	G	NM_032160 // upstream // 766862 // Hs.124673 // C18orf4 // 92126 // Homo sapiens chromosome 18 open reading frame 4 (C18orf4), mRNA. /// NM_019022 // downstream // 392190 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA.	C18orf4	C18orf4, Homo sapiens chromosome 18 open reading frame 4 (C18orf4), q22.1
SNP_A-1877578	tctggctattctgtac[C/T]attcaaataacaactt	C	T	NM_019022 // upstream // 109586 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA. /// NM_024781 // upstream // 13991 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA.	TXNDC10	TXNDC10, Homo sapiens FLJ20793 protein (FLJ20793), q22.1
SNP_A-2038523	aacagaaaacatttcc[A/G]aagacttataatatca	A	G	NM_019022 // upstream // 109625 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA. /// NM_024781 // upstream // 13952 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA.	TXNDC10	TXNDC10, Homo sapiens FLJ20793 protein (FLJ20793), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1839818	tagattattggcttgat[G/T]taccttacttctaatg	G	T	NM_019022 // upstream // 113510 // Hs.440534 // TXNDC10 // 54495 // Homo sapiens FLJ20793 protein (FLJ20793), mRNA. /// NM_024781 // upstream // 10067 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA.	TXNDC10	TXNDC10, Homo sapiens FLJ20793 protein (FLJ20793), q22.1
SNP_A-1927561	ctctttagaaatacc[A/G]cacagagtgagagat	A	G	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // — // — // — /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1849017	tatgcatcagataccaa[A/C]ctaaatatttcagttt	A	C	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // — // — // — /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-2098059	agagaggaaagcggaa[A/G]aataagtcttgtggac	A	G	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // — // — // — /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1798720	gtaacctgttcctatg[C/G]agcaaagagatggtgc	C	G	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // — // — // — /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1842781	tagtacacttcctgca[G/T]gtgatatctccagaa	G	T	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // — // — // — /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-2099267	agaggcacatcaattc[A/G]aattatgtcatattt	A	G	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000360242 // intron // 0 // — // — // — /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1810409	gtgattatctccacaa[C/T]gaatctcagtatatat	C	T	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1884937	tgaatgagaagtaacaa[A/G]attatccaacattatt	A	G	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1927644	gggcacagatgtctta[A/C]aaaatctaacaagaat	A	C	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-2215793	cctcatgcaatgcaga[A/C]ccttacaagaaataa	A	C	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1664970	gttaaattacctaaacttcttata[C/T]cctcttcaatatttgatgtgct	C	T	NM_024781 // intron // 0 // Hs.146025 // FLJ23594 // 79839 // hypothetical protein FLJ23594	FLJ23594	FLJ23594, rs10503140, hypothetical protein FLJ23594,q22.1
SNP_A-1709349	ggaactgtaaaatttataaacaac[A/C]acatgtcagcataaac ttgataaag	A	C	NM_024781 // intron // 0 // Hs.146025 // FLJ23594 // 79839 // hypothetical protein FLJ23594	FLJ23594	FLJ23594, rs10516009, hypothetical protein FLJ23594,q22.1
SNP_A-1927659	gaaaagcaaatgcctg[A/G]aaagttcctgccatta	A	G	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1927668	tctactgtcagtagga[C/T]gtcttgctttatgaca	C	T	NM_024781 // intron // 0 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// ENST00000319445 // intron // 0 // — // — // —	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1697977	gaggacaaaggagaccacagtgaaa[C/G]attactgtagatga gtcttagctgt	C	G	NM_024781 // intron // 0 // Hs.146025 // FLJ23594 // 79839 // hypothetical protein FLJ23594	FLJ23594	FLJ23594, rs9319771, hypothetical protein FLJ23594, q22.1
SNP_A-2060058	aatctttgaagtctc[A/G]atgttctcaactgtaa	A	G	NM_024781 // downstream // 9291 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 798478 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. /// E	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.1
SNP_A-1861846	tcatcttggatgctc[A/C]aactgtcaacagctca	A	C	NM_024781 // downstream // 186725 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 621044 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-1944161	ttgtcagtaattccag[A/G]aaataaaatgccctat	A	G	NM_024781 // downstream // 439389 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 368380 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-1912321	tgtgattatacattgc[C/T]ccataccaatatattt	C	T	NM_024781 // downstream // 439509 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 368260 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-1803656	gtcaaagattgctgaa[C/T]ccaagagtattatgt	C	T	NM_024781 // downstream // 450925 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 356844 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2160231	atttcacagtgcctga[C/T]gatgttcaaaatgtgt	C	T	NM_024781 // downstream // 668535 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 139234 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2263731	gaaccctctagtttta[C/T]gtggccttgaacgacc	C	T	NM_024781 // downstream // 701415 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 106354 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2154151	attatctctgaaggga[C/T]gattagcaaattgat	C	T	NM_024781 // downstream // 737659 // Hs.280781 // C18orf14 // 79839 // Homo sapiens chromosome 18 open reading frame 14 (C18orf14), mRNA. /// NM_006566 // downstream // 70110 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. ///	C18orf14	C18orf14, Homo sapiens chromosome 18 open reading frame 14 (C18orf14), q22.2
SNP_A-2098431	agagcaactgaacacc[A/G]gcatccttctccaaa	A	G	NM_006566 // intron // 0 // Hs.369661 // CD226 // 10666 // Homo sapiens CD226 antigen (CD226), mRNA. /// ENST00000280200 // intron // 0 // — // — // —	CD226	CD226, Homo sapiens CD226 antigen (CD226), q22.2
SNP_A-2182947	cagattccctggagaa[C/T]ggtcttctgatctctt	C	T	NM_173630 // intron // 0 // Hs.31931 // RTTN // 25914 // Homo sapiens rotatin (RTTN), mRNA. /// ENST00000255674 // intron // 0 // — // — // — // —	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-2277259	gagattattcgaaata[C/G]gttacttgaaattta	C	G	NM_173630 // intron // 0 // Hs.31931 // RTTN // 25914 // Homo sapiens rotatin (RTTN), mRNA. /// ENST00000255674 // intron // 0 // — // — // — // —	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1852400	tatttaaggcctgaac[A/G]cacttatcttataa	A	G	NM_173630 // intron // 0 // Hs.31931 // RTTN // 25914 // Homo sapiens rotatin (RTTN), mRNA. /// ENST00000025674 // intron // 0 // --- // --- // --- // ---	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-1960859	ttttgaacttagtca[A/C]agaaggccttctaaa	A	C	NM_173630 // upstream // 12094 // Hs.31931 // RTTN // 25914 // Homo sapiens rotatin (RTTN), mRNA. /// NM_004232 // upstream // 71205 // Hs.44439 // SOCS6 // 9306 // Homo sapiens suppressor of cytokine signaling 6 (SOCS6), mRNA. /// ENST00000025674 // upst	RTTN	RTTN, Homo sapiens rotatin (RTTN), q22.2
SNP_A-1797833	ggttttcatgttgtta[C/T]ctacacttaaaggca	C	T	NM_004232 // intron // 0 // Hs.44439 // SOCS6 // 9306 // Homo sapiens suppressor of cytokine signaling 6 (SOCS6), mRNA. /// ENST00000302056 // intron // 0 // --- // --- // ---	SOCS6	SOCS6, Homo sapiens suppressor of cytokine signaling 6 (SOCS6), q22.2
SNP_A-2313933	ggagctaactgcctaa[A/C]ctctgtcctgttccct	A	C	NM_004232 // downstream // 35342 // Hs.44439 // SOCS6 // 9306 // Homo sapiens suppressor of cytokine signaling 6 (SOCS6), mRNA. /// ENST00000302056 // downstream // 35342 // --- // --- // --- // --- /// ENST00000333967 // downstream // 268106 // --- // -	SOCS6	SOCS6, Homo sapiens suppressor of cytokine signaling 6 (SOCS6), q22.2
SNP_A-2025786	aaaatggaaaaatacc[C/T]gctgcattagtggaat	C	T	NM_004232 // downstream // 276791 // Hs.44439 // SOCS6 // 9306 // Homo sapiens suppressor of cytokine signaling 6 (SOCS6), mRNA. /// ENST00000302056 // downstream // 276791 // --- // --- // --- // --- /// ENST00000333967 // downstream // 26657 // --- // -	SOCS6	SOCS6, Homo sapiens suppressor of cytokine signaling 6 (SOCS6), q22.2
SNP_A-1874266	tctccactcactgctc[G/T]ataaggacctgaccca	G	T	ENST00000333967 // upstream // 42050 // --- // --- // --- // --- /// ENST00000357663 // downstream // 400283 // --- // --- // --- // -	-	q22.2
SNP_A-2261317	gaaagcactcccagaa[C/G]agcatccccagaggg	C	G	ENST00000333967 // upstream // 112924 // --- // --- // --- // --- /// ENST00000357663 // downstream // 329409 // --- // --- // --- // -	-	q22.2
SNP_A-2100209	agagttcctgcatgac[C/T]gagttcctccttctg	C	T	NM_182511 // downstream // 1410264 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 29165 // --- // --- // --- // --- /// ENST00000269503 // downstream // 1410264 // --- // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2216044	cctccattgtcacaag[G/T]cccttctatatgtat	G	T	NM_182511 // downstream // 1386947 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 52482 // --- // --- // --- // --- /// ENST00000269503 // downstream // 1386947 // --- // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1865776	tccatttgttatttg[C/T]agtagttgtcatctga	C	T	NM_182511 // downstream // 1386204 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 53225 // --- // --- // --- // --- /// ENST00000269503 // downstream // 1386204 // --- // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1939404	ttgatgctcaacacaa[A/T]ttcattggagacaatg	A	T	NM_182511 // downstream // 1298560 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 140869 // --- // --- // --- // --- /// ENST00000269503 // downstream // 1298560 // --- // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2114761	agggatgtggagtaac[C/T]agagctcacacttac	C	T	NM_182511 // downstream // 872748 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 566681 // --- // --- // --- // --- /// ENST00000269503 // downstream // 872748 // --- // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2034109	aaatcatctggataaa[A/G]ctaacattcaggaatt	A	G	NM_182511 // downstream // 864167 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 575262 // --- // --- // --- // --- /// ENST00000269503 // downstream // 864167 // --- // --- // -	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2029235	aaagaagcagtgagaa[C/T]agcataaagaattagg	C	T	NM_182511 // downstream // 247326 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 1192103 // --- // --- // --- /// ENST00000269503 // downstream // 247326 // --- // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2159540	attiacccagtaccaa[A/G]gtaatttccacatttt	A	G	NM_182511 // downstream // 129592 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 1309837 // --- // --- // --- // --- /// ENST00000269503 // downstream // 129592 // --- // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2040867	aacccgagactgcaag[A/G]cttcaaatttgtcttc	A	G	NM_182511 // downstream // 98384 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// ENST00000360395 // upstream // 1341045 // --- // --- // --- // --- /// ENST00000269503 // downstream // 98384 // --- // --- // --- // ---	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1641755	actttatatatatttttgtcagcta[C/T]gaaaacattaaacgctctct actaa	C	T	NM_178506 // upstream // 1852348 // - // - // - /// NM_182511 // downstream // 41610 // Hs.131596 // CBLN2 // 147381 // cerebellin 2 precursor	-	- , rs1432071, - ,q22.3
SNP_A-2119325	agtagttgcactgcta[C/T]aatcatatctctttt	C	T	NM_182511 // upstream // 35733 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// NM_138966 // downstream // 162256 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), tr	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-1887179	tgagaaatcaaagaca[A/G]tggtgatacttcagag	A	G	NM_182511 // upstream // 99679 // Hs.514946 // CBLN2 // 147381 // Homo sapiens cerebellin 2 precursor (CBLN2), mRNA. /// NM_138966 // downstream // 98310 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), tra	CBLN2	CBLN2, Homo sapiens cerebellin 2 precursor (CBLN2), q22.3
SNP_A-2144521	atgatattgtggaaaa[C/T]gtcaaagaggcctgaa	C	T	NM_138966 // upstream // 39913 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 41789 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP)	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1793008	ggtacccaagttgcaa[A/G]atgagatcccctctct	A	G	NM_138966 // upstream // 52038 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 53914 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP)	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2042907	aactctttaattgcc[G/T]gaaagagcatctcgaa	G	T	NM_138966 // upstream // 80941 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 82817 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP)	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2032137	aaagtggaacttgaga[A/C]aagaaagtaatattag	A	C	NM_138966 // upstream // 81094 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 82970 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP)	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1862250	tcatgggaattgtcct[A/G]aaatccgagttcccag	A	G	NM_138966 // upstream // 85126 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 87002 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP)	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1931786	gtgtcatacctgatgg[C/T]gtaccacagagcttct	C	T	NM_138966 // upstream // 129120 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 130996 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2271682	gaccagaatctgtctat[C/T]gaggcagcctctgctgt	C	T	NM_138966 // upstream // 268335 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 270211 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2152932	attacagactcatcaa[C/T]gacaccgtatttccca	C	T	NM_138966 // upstream // 295424 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 297300 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2080472	acctagtcatcactga[C/T]agttccctgggatat	C	T	NM_138966 // upstream // 307796 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 309672 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2152901	attacacatatggctc[A/G]ctctaaatgcctgttc	A	G	NM_138966 // upstream // 308200 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 310076 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1883905	tgaagagaacaaagta[C/T]gaaaacagtgaaaatt	C	T	NM_138966 // upstream // 319536 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 321412 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2270553	gacagagatgccttaa[A/C]ctactgacttttcccc	A	C	NM_138966 // upstream // 322596 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 324472 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2066059	aatttggaatttgttca[A/T]agacacaaaagctcaa	A	T	NM_138966 // upstream // 330491 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 332367 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2080698	acctcatgtgcctctg[A/G]actgaacattgtatct	A	G	NM_138966 // upstream // 332097 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 333973 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2203491	ccagaagacacagatg[C/G]cactaactcatatggg	C	G	NM_138966 // upstream // 340961 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 342837 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1718963	gtacctctaattctgctctctcaa[A/C]cctttaggccataggatgg atctaa	A	C	BC034583 // intron // 0 // Hs.397449 // - // 400655 // Clone IMAGE:4825594, mRNA	-	- , rs9319865. Clone IMAGE:4825594, mRNA,q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1936242	ttcttcatgagctaaa[A/G]attgtaatcacigttg	A	G	NM_138966 // upstream // 469788 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 471664 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2251535	cttcagaaacaggaaa[C/T]gatgtgaaataaatta	C	T	NM_138966 // upstream // 540769 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 542645 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1950351	ttcagcttatatgta[A/G]ctagcattattcaagg	A	G	NM_138966 // upstream // 555634 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 557510 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2303040	gctagttccaacaacc[C/G]aggtgaccacattcca	C	G	NM_138966 // upstream // 558920 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 560796 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1863262	tcatttgcctcctctg[A/G]attgattgcaacaaag	A	G	NM_138966 // upstream // 569228 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 571104 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2046807	aagaggatcaactata[A/G]ataagagagaagctat	A	G	NM_138966 // upstream // 573843 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 575719 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1796530	ggttaattttggtcaa[A/G]gaatgtgtatgtggaa	A	G	NM_138966 // upstream // 597048 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 598924 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-2142038	atcttcttatgttga[C/T]gtcacttgttacttgc	C	T	NM_138966 // upstream // 692077 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, mRNA. /// NM_138999 // upstream // 693953 // Hs.465407 // NETO1 // 81832 // Homo sapiens neuropilin (NR	NETO1	NETO1, Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 1 (NETO1), transcript variant 3, q22.3
SNP_A-1680408	gtgcttgccctctcttcagaagtaa[C/T]gcttagaatacactgtaa actttc	C	T	NM_152676 // intron // 0 // Hs.170668 // FBXO15 // 201456 // F-box only protein 15	FBXO15	FBXO15, rs10514110, F-box only protein 15,q22.3
SNP_A-1933163	agaaatagtgtaaccaa[G/T]catggctctccggt	G	T	NM_152676 // intron // 0 // Hs.465411 // FBXO15 // 201456 // Homo sapiens F-box protein 15 (FBXO15), mRNA. /// ENST00000269500 // intron // 0 // — // — // — /// ENST00000344331 // intron // 0 // — // — // — // —	FBXO15	FBXO15, Homo sapiens F-box protein 15 (FBXO15), q22.3
SNP_A-2045997	aagaccttcaccaaca[A/G]atttgtaatctatg	A	G	NM_152676 // intron // 0 // Hs.465411 // FBXO15 // 201456 // Homo sapiens F-box protein 15 (FBXO15), mRNA. /// ENST00000269500 // intron // 0 // — // — // — /// ENST00000344331 // intron // 0 // — // — // — // —	FBXO15	FBXO15, Homo sapiens F-box protein 15 (FBXO15), q22.3
SNP_A-1815633	gttaaatgtttagccf[A/G]aagataggggcatatc	A	G	NM_152676 // intron // 0 // Hs.465411 // FBXO15 // 201456 // Homo sapiens F-box protein 15 (FBXO15), mRNA. /// ENST00000269500 // intron // 0 // — // — // — /// ENST00000344331 // intron // 0 // — // — // — // —	FBXO15	FBXO15, Homo sapiens F-box protein 15 (FBXO15), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2231405	ctattgctaagctgaa[C/T]tatttaccattatg	C	T	NM_014177 // downstream // 86817 // Hs.532835 // C18orf55 // 29090 // Homo sapiens HSPC154 protein (HSPC154), mRNA. /// NM_001914 // downstream // 7695 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // downstream //	C18orf55	C18orf55, Homo sapiens HSPC154 protein (HSPC154), q22.3
SNP_A-2115012	agggccgaaagagtag[A/C]cgagggctggtggtct	A	C	NM_014177 // downstream // 89156 // Hs.532835 // C18orf55 // 29090 // Homo sapiens HSPC154 protein (HSPC154), mRNA. /// NM_001914 // downstream // 5356 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // downstream //	C18orf55	C18orf55, Homo sapiens HSPC154 protein (HSPC154), q22.3
SNP_A-1825994	taaatgggaagtaaga[G/T]gactgaatcagcccct	G	T	NM_014177 // downstream // 93569 // Hs.532835 // C18orf55 // 29090 // Homo sapiens HSPC154 protein (HSPC154), mRNA. /// NM_001914 // downstream // 943 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // downstream //	C18orf55	C18orf55, Homo sapiens HSPC154 protein (HSPC154), q22.3
SNP_A-2234085	ctcattcagagagtag[A/G]attgtttgtaaactct	A	G	NM_014177 // downstream // 93735 // Hs.532835 // C18orf55 // 29090 // Homo sapiens HSPC154 protein (HSPC154), mRNA. /// NM_001914 // downstream // 777 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // downstream //	C18orf55	C18orf55, Homo sapiens HSPC154 protein (HSPC154), q22.3
SNP_A-1864346	tccactccatagctaa[C/T]gcacactccagcgtaa	C	T	NM_001914 // intron // 0 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // intron // 0 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// ENST00000299438 // intron // 0 // — // — // -	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-2210673	cccctctagactacgc[A/C]agcatgatcctttccc	A	C	NM_001914 // intron // 0 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // intron // 0 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// ENST00000299438 // intron // 0 // — // — // -	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-1959454	ttttgccgttgcacct[A/G]aaactgcagagttat	A	G	NM_001914 // upstream // 11978 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // upstream // 11914 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// ENST00000299438 // upstream // 11978	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-2021377	aaaaaagaaatcaaac[A/G]gaattagaacgtgtt	A	G	NM_001914 // upstream // 33391 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // upstream // 33327 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// ENST00000299438 // upstream // 33391	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-2189219	cagttcacaacatatc[C/G]gacatcaggcaacaaa	C	G	NM_001914 // upstream // 34842 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // upstream // 34778 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// ENST00000299438 // upstream // 34842	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-2276610	gagagtaaaggtaaga[C/T]gctcctgaagtgtctg	C	T	NM_001914 // upstream // 94649 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// NM_148923 // upstream // 94585 // Hs.465413 // CYB5 // 1528 // Homo sapiens cytochrome b-5 (CYB5), mRNA. /// ENST00000299438 // upstream // 94649	CYB5	CYB5, Homo sapiens cytochrome b-5 (CYB5), q22.3
SNP_A-1886322	tgacctctgaaaatgal[C/T]gaaataacaactttt	C	T	ENST00000333971 // upstream // 15576 // — // — // — /// ENST00000343998 // downstream // 29844 // — // — // — // —	-	q22.3
SNP_A-2063170	aatgtttagtcaataa[A/G]aaaagtccaggttgt	A	G	ENST00000333971 // upstream // 15785 // — // — // — // — /// ENST00000343998 // downstream // 29635 // — // — // — // —	-	q22.3
SNP_A-1785987	ggctgccaaacatgca[A/G]atagaagcaaacctg	A	G	ENST00000333971 // upstream // 15844 // — // — // — // — /// ENST00000343998 // downstream // 29576 // — // — // — // —	-	q22.3
SNP_A-1911788	tgtgaatgagtggtaa[A/C]ctccaatactgttgca	A	C	ENST00000333971 // upstream // 29057 // — // — // — // — /// ENST00000343998 // downstream // 16363 // — // — // — // —	-	q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2030894	aaaggaagcacaaata[A/G]ctctcaaactaagaaa	A	G	ENST00000343998 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2155792	attccctcaacaatta[C/G]agcaccttctgggtcc	C	G	ENST00000343998 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2287057	gatgtaatcagccaaa[C/T]agccaatgaggcagca	C	T	NM_018235 // intron // 0 // Hs.149185 // CNDP2 // 55748 // Homo sapiens CNDP dipeptidase 2 (metallopeptidase M20 family) (CNDP2), mRNA. /// ENST00000324262 // intron // 0 // — // — // — // — /// ENST00000324301 // intron // 0 // — // — // —	CNDP2	CNDP2, Homo sapiens CNDP dipeptidase 2 (metallopeptidase M20 family) (CNDP2), q22.3
SNP_A-2065746	aatttcaactctgaaa[A/G]ttacataatcacaaag	A	G	NM_032649 // intron // 0 // Hs.400613 // CNDP1 // 84735 // Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), mRNA. /// ENST00000323246 // intron // 0 // — // — // — // — /// ENST00000358821 // intron // 0 // — // — //	CNDP1	CNDP1, Homo sapiens carnosine dipeptidase 1 (metallopeptidase M20 family) (CNDP1), q22.3
SNP_A-2236510	ctcgtatcctgactac[G/T]agaagaacgaagcagg	G	T	NM_017757 // intron // 0 // Hs.536490 // ZNF407 // 55628 // Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // — // — // — // — /// ENST00000309902 // intron // 0 // — // — // — // —	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1933825	ggaattaaaatacaca[A/C]acagatgtgcttggta	A	C	NM_017757 // intron // 0 // Hs.536490 // ZNF407 // 55628 // Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // — // — // — // — /// ENST00000309902 // intron // 0 // — // — // — // —	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1925892	ttatgggtaagcagta[A/T]aaatagacgtagaatg	A	T	NM_017757 // intron // 0 // Hs.536490 // ZNF407 // 55628 // Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // intron // 0 // — // — // — // —	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-1691836	attaagaactacaagggaaggaaaa[C/T]gctgacccatagac taaagcagagg	C	T	AB051490 // intron // 0 // Hs.465430 // ZNF407 // 55628 // zinc finger protein 407	ZNF407	ZNF407 , rs2404483, zinc finger protein 407,q22.3
SNP_A-1934103	cgtttcattgcagaaa[G/T]aaaacgaatacaagca	G	T	NM_017757 // downstream // 38807 // Hs.536490 // ZNF407 // 55628 // Homo sapiens zinc finger protein 407 (ZNF407), mRNA. /// ENST00000299687 // downstream // 38807 // — // — // — // — /// ENST00000309902 // downstream // 299852 // — // — // —	ZNF407	ZNF407, Homo sapiens zinc finger protein 407 (ZNF407), q22.3
SNP_A-2102104	agatgtgcgattataa[C/T]gaataacacagagcaa	C	T	NM_175907 // downstream // 82628 // Hs.465433 // ZADH2 // 284273 // Homo sapiens zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), mRNA. /// ENST00000322371 // upstream // 9653 // — // — // — // — /// ENST00000322342 // downstream /	ZADH2	ZADH2, Homo sapiens zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), q22.3
SNP_A-2256749	ctttcatggtcagaac[C/T]gtgatacttctactgg	C	T	NM_175907 // downstream // 3211 // Hs.465433 // ZADH2 // 284273 // Homo sapiens zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), mRNA. /// ENST00000322371 // upstream // 89070 // — // — // — // — /// ENST00000322342 // downstream /	ZADH2	ZADH2, Homo sapiens zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2), q22.3
SNP_A-2158351	attgggtttgtagacc[C/T]ggagtcatcagactgc	C	T	NM_005786 // intron // 0 // Hs.284217 // SDCCAG33 // 10194 // Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), mRNA. /// ENST00000322038 // intron // 0 // — // — // — // —	SDCCAG33	SDCCAG33, Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), q22.3
SNP_A-1944198	ttgtcatgatgatgcc[A/G]agttgaaggaccattc	A	G	NM_005786 // downstream // 68960 // Hs.284217 // SDCCAG33 // 10194 // Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), mRNA. /// ENST00000322038 // downstream // 68960 // — // — // — // — /// ENST00000328731 // upstream // 71	SDCCAG33	SDCCAG33, Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), q22.3
SNP_A-1902819	tggctccagggaaccc[A/G]aagtaacatcacagcc	A	G	D86975 // downstream // 785121 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 142771 // — // — // — // — /// ENST00000217537 // downstream // 785121 // — // — // — //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds. ,q23
SNP_A-2107445	agctactcagctctgg[A/G]aaagttcagtataatg	A	G	D86975 // downstream // 773325 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 154567 // — // — // — // — /// ENST00000217537 // downstream // 773325 // — // — // — //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds. q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2211242	ccctaacctcctccatc[A/G]actacctgaatacgtg	A	G	D86975 // downstream // 718519 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 209373 // --- // --- // --- /// ENST00000217537 // downstream // 718519 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-1914663	tgttaatgagtgttca[A/G]tcagcattagtgaatt	A	G	D86975 // downstream // 560137 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 367755 // --- // --- // --- /// ENST00000217537 // downstream // 560137 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-2087415	actgcatgaggtaata[A/C]atgttgtcgtttat	A	C	D86975 // downstream // 527128 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 400764 // --- // --- // --- /// ENST00000217537 // downstream // 527128 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-1856842	tcacatttgctaagtc[C/G]ctttgctgtgtaatg	C	G	D86975 // downstream // 523122 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 404770 // --- // --- // --- /// ENST00000217537 // downstream // 523122 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-1658974	aataaattaaggtaaacacacatgta[C/T]taatgctcatattagctg	C	T	NM_014643 // downstream // 472162 // - // - // - // -	-	-, rs10514191, -q23
SNP_A-1642267	aagtccctctcttagataaatca[C/T]agttagtgcagagaaattt ctctaat	C	T	NM_014643 // downstream // 471983 // - // - // - // -	-	-, rs10514192, -q23
SNP_A-1853891	tcaaaaggacacagtg[A/C]agtcattaaaaaccag	A	C	D86975 // downstream // 458964 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 468928 // --- // --- // --- /// ENST00000217537 // downstream // 458964 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-1654959	taactaaacagaatgtatatgtgcc[G/T]caatcaattaaataaggg aactttat	G	T	NM_014643 // downstream // 392132 // - // - // - // -	-	-, rs10514196, -q23
SNP_A-1694957	ctgtggttttaaatgtttgtaaata[C/G]ctgcaatgcacttgacgttc agtg	C	G	NM_014643 // downstream // 392058 // - // - // - // -	-	-, rs10514197, -q23
SNP_A-2276756	gagataaaactttcaga[C/T]gctgaagccccagaga	C	T	D86975 // downstream // 286730 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 641162 // --- // --- // --- /// ENST00000217537 // downstream // 286730 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-2041320	aacctgcatgggttcc[C/G]gaaggtggcacagtct	C	G	D86975 // downstream // 230210 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000328731 // downstream // 697682 // --- // --- // --- /// ENST00000217537 // downstream // 230210 // --- // --- // -- //	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-1732736	atgggtttattaagaaaggcagaaa[A/G]ctaattatttaaaacctg taataaa	A	G	NM_014643 // intron // 0 // - // - // -	-	-, rs690378, -q23
SNP_A-2205629	ccagtttctcagtcac[A/G]aatctagcccagagct	A	G	D86975 // intron // 0 // Hs.436973 // ZNF516 // 9658 // Homo sapiens mRNA for KIAA0222 gene, partial cds. /// ENST00000217537 // intron // 0 // --- // --- // ---	ZNF516	ZNF516, Homo sapiens for KIAA0222 gene, partial cds, q23
SNP_A-2099614	agaggtagtatcacga[C/T]gggcaaagaccgattc	C	T	NM_207460 // downstream // 59849 // Hs.451549 // FLJ44313 // 400658 // Homo sapiens FLJ44313 protein (FLJ44313), mRNA. /// NM_207461 // upstream // 132247 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// ENST000003	FLJ44313	FLJ44313, Homo sapiens FLJ44313 protein (FLJ44313), q23
SNP_A-1800247	gtacctgtccatgaaa[C/T]gtctctgtagtagctg	C	T	NM_207461 // downstream // 13553 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 118477 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236), mR	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23
SNP_A-1909808	tgtcacatggtatctc[A/G]atgttacttttttc	A	G	NM_207461 // downstream // 29859 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 102171 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236), mR	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1875897	tctgaaagcaaagaac[C/T]gtcaatctgaaatttt	C	T	NM_207461 // downstream // 38882 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 93148 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) mRN	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23
SNP_A-2122715	agtggagagaatacca[G/T]agtcctccgccagtcc	G	T	NM_207461 // downstream // 42491 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 89539 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) mRN	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23
SNP_A-2255819	cttgtttcctgctc[A/G]agatatgccctgggtt	A	G	NM_207461 // downstream // 47350 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 84680 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) mRN	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23
SNP_A-2160961	atttcigttcttctat[C/T]attacccggtctcaga	C	T	NM_207461 // downstream // 88879 // Hs.514963 // FLJ44881 // 400661 // Homo sapiens FLJ44881 protein (FLJ44881), mRNA. /// AF085243 // upstream // 43151 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) mRN	FLJ44881	FLJ44881, Homo sapiens FLJ44881 protein (FLJ44881), q23
SNP_A-2235948	ctcctgccgcttccaaa[A/G]gataaaagtctggcagg	A	G	AF085243 // intron // 0 // Hs.189826 // ZNF236 // 7776 // Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) mRNA, complete cds. /// NM_007345 // intron // 0 // Hs.189826 // ZNF236 // 7776 // Homo sapiens zinc finger protein 236 (ZNF236), mR	ZNF236	ZNF236, Homo sapiens C2H2 type Kruppel-like zinc finger protein (ZNF236) complete cds. q23
SNP_A-1845692	tataggcattcctctc[A/G]aagtctcattactctg	A	G	NM_002385 // intron // 0 // Hs.501262 // MBP // 4155 // Homo sapiens myelin basic protein (MBP), mRNA. /// BC008749 // intron // 0 // Hs.501262 // MBP // 4155 // Homo sapiens myelin basic protein, mRNA (cDNA clone IMAGE:3346521), partial cds. /// ENST0000	MBP	MBP, Homo sapiens myelin basic protein (MBP), q23
SNP_A-1936393	accagtgaaaagaggc[A/G]cacttctagtcatca	A	G	BC008749 // intron // 0 // Hs.501262 // MBP // 4155 // Homo sapiens myelin basic protein, mRNA (cDNA clone IMAGE:3346521), partial cds. /// ENST0000035594 // intron // 0 // — // — // — /// ENST0000035454 2 // intron // 0 // — // — // —	MBP	MBP, Homo sapiens myelin basic protein, (cDNA clone IMAGE:3346521), partial cds. q23
SNP_A-2043418	aactgggatttgaaa[A/T]gtagaagacgcagcgc	A	T	NM_002385 // upstream // 152649 // Hs.501262 // MBP // 4155 // Homo sapiens myelin basic protein (MBP), mRNA. /// BC008749 // upstream // 103319 // Hs.501262 // MBP // 4155 // Homo sapiens myelin basic protein, mRNA (cDNA clone IMAGE:3346521), partial cds	MBP	MBP, Homo sapiens myelin basic protein (MBP), q23
SNP_A-1929739	ttcatcacctacagga[G/T]ctggcaacctatggat	G	T	NM_001480 // downstream // 366361 // Hs.272191 // GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1363821 // Hs.514980 // SALL3 // 27164 // Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST0000029972	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2272111	gaccgacacacctgca[A/G]aaacgtaattccttg	A	G	NM_001480 // downstream // 487630 // Hs.272191 // GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 1242552 // Hs.514980 // SALL3 // 27164 // Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST0000029972	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-1821831	gtttagaatgcgacat[A/G]ggtttaatcctgtc	A	G	NM_001480 // downstream // 998073 // Hs.272191 // GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 732109 // Hs.514980 // SALL3 // 27164 // Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST0000029727	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2243069	ctgccctgagcatcta[C/T]attacagtacttgctg	C	T	NM_001480 // downstream // 1052434 // Hs.272191 // GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 677748 // Hs.514980 // SALL3 // 27164 // Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST00000029972	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2259435	gaaaaatggcatgaaa[C/G]gagaaggagaaaatgt	C	G	NM_001480 // downstream // 1513119 // Hs.272191 // GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 217063 // Hs.514980 // SALL3 // 27164 // Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST00000029972	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-2223172	cgccctgatcttggc[A/G]acttgtgtctttgcac	A	G	NM_001480 // downstream // 1612845 // Hs.272191 // GALR1 // 2587 // Homo sapiens galanin receptor 1 (GALR1), mRNA. /// NM_171999 // upstream // 117337 // Hs.514980 // SALL3 // 27164 // Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA. /// ENST00000029972	GALR1	GALR1, Homo sapiens galanin receptor 1 (GALR1), q23
SNP_A-1931824	ttccctttgtggctac[C/T]atacatcaaaaacagg	C	T	NM_198531 // intron // 0 // Hs.465475 // ATP9B // 374868 // Homo sapiens ATPase, Class II, type 9B (ATP9B), mRNA. /// AK097757 // intron // 0 // Hs.465475 // ATP9B // 374868 // Homo sapiens cDNA FLJ40438 fis, clone TESTI2039776, highly similar to POTENTIA	ATP9B	ATP9B, Homo sapiens ATPase, Class II, type 9B (ATP9B), q23
SNP_A-1795481	ggtgccagcacagaag[A/G]cttagtacctgcatgg	A	G	NM_198531 // intron // 0 // Hs.465475 // ATP9B // 374868 // Homo sapiens ATPase, Class II, type 9B (ATP9B), mRNA. /// AK097757 // intron // 0 // Hs.465475 // ATP9B // 374868 // Homo sapiens cDNA FLJ40438 fis, clone TESTI2039776, highly similar to POTENTIA	ATP9B	ATP9B, Homo sapiens ATPase, Class II, type 9B (ATP9B), q23
SNP_A-2095831	agatcagacttttcta[A/G]atgtccaaagagctga	A	G	NM_172388 // downstream // 96655 // Hs.534074 // NFATC1 // 4772 // Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1), transcript variant 4, mRNA. /// NM_006162 // downstream // 96655 // Hs.534074 // NFATC1 //	NFATC1	NFATC1, Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1), transcript variant 4, q23
SNP_A-2216868	cctctgccactgaaaa[A/C]gtgtggtttgatggag	A	C	NM_004715 // downstream // 25263 // Hs.465490 // CTDP1 // 9150 // Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), transcript variant /// NM_048368 // downstream // 25263 // Hs.465490 // CTDP1 //	CTDP1	CTDP1, Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), transcript variant ,q23
SNP_A-2243575	ctgctcaacaacctc[A/G]agtccagaatgcccca	A	G	NM_006701 // upstream // 16688 // Hs.465498 // TXNL4A // 10907 // Homo sapiens thioredoxin-like 4A (TXNL4A), mRNA. /// NM_024805 // upstream // 29138 // Hs.532987 // C18orf22 // 79863 // Homo sapiens chromosome 18 open reading frame 22 (C18orf22), mRNA. /	TXNL4A	TXNL4A, Homo sapiens thioredoxin-like 4A (TXNL4A), q23
SNP_A-2111507	aggagggcaaaaatca[C/T]ctggtgaccattggac	C	T	NM_006701 // upstream // 19403 // Hs.465498 // TXNL4A // 10907 // Homo sapiens thioredoxin-like 4A (TXNL4A), mRNA. /// NM_024805 // upstream // 26423 // Hs.532987 // C18orf22 // 79863 // Homo sapiens chromosome 18 open reading frame 22 (C18orf22), mRNA. /	TXNL4A	TXNL4A, Homo sapiens thioredoxin-like 4A (TXNL4A), q23
SNP_A-2146029	atgcctgagagcttgc[A/G]ccgggtggaggtagc	A	G	NM_032510 // intron // 0 // Hs.436554 // PARD6G // 84552 // Homo sapiens par-6 partitioning defective 6 homolog gamma (C. elegans) (PARD6G), mRNA. /// ENST00000353265 // intron // 0 // — // — // —	PARD6G	PARD6G, Homo sapiens par-6 partitioning defective 6 homolog gamma (C. elegans) (PARD6G), q23
SNP_A-1848123	tatcttagatattcca[A/G]tcaaatccaatctccc	A	G	ENST00000356848 // intron // 0 // — // — // —	-	p13.3
SNP_A-2109351	agctttgcagatgtag[A/G]cggttgaggtcacact	A	G	NM_033513 // intron // 0 // Hs.369613 // C19orf20 // 91978 // Homo sapiens chromosome 19 open reading frame 20 (C19orf20), mRNA. /// ENST00000339938 // intron // 0 // — // — // — /// ENST00000317255 // intron // 0 // — // — // —	C19orf20	C19orf20, Homo sapiens chromosome 19 open reading frame 20 (C19orf20), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2204107	ccagcaccagggccac[A/G]ctgttcctcgggcctc	A	G	NM_002085 // downstream // 382 // Hs.433951 // GPX4 // 2879 // Homo sapiens glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), mRNA. /// ENST00000354171 // downstream // 382 // — // — // — // — /// ENST00000250872 // downstream // 481	GPX4	GPX4, Homo sapiens glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), p13.3
SNP_A-1894698	tgccagcaagccctcc[G/T]cggatgtttgttgaat	G	T	NM_001405 // downstream // 10192 // Hs.532655 // EFNA2 // 1943 // Homo sapiens ephrin-A2 (EFNA2), mRNA. /// NM_032853 // upstream // 44874 // Hs.515016 // MUM1 // 84939 // Homo sapiens melanoma associated antigen (mutated) 1 (MUM1), mRNA. /// ENST00000215	EFNA2	EFNA2, Homo sapiens ephrin-A2 (EFNA2), p13.3
SNP_A-2073300	acaggggtctcaggaa[C/T]gttcatgggatacaat	C	T	NM_001405 // downstream // 10593 // Hs.532655 // EFNA2 // 1943 // Homo sapiens ephrin-A2 (EFNA2), mRNA. /// NM_032853 // upstream // 44473 // Hs.515016 // MUM1 // 84939 // Homo sapiens melanoma associated antigen (mutated) 1 (MUM1), mRNA. /// ENST00000215	EFNA2	EFNA2, Homo sapiens ephrin-A2 (EFNA2), p13.3
SNP_A-1833487	tacagataggaagaaa[C/T]ctggcttgtgaggacg	C	T	NM_017797 // intron // 0 // Hs.465543 // BTBD2 // 55643 // Homo sapiens BTB (POZ) domain containing 2 (BTBD2), mRNA. /// ENST00000255608 // intron // 0 // — // — // — // —	BTBD2	BTBD2, Homo sapiens BTB (POZ) domain containing 2 (BTBD2), p13.3
SNP_A-2301175	gccttctggctgtaac[C/T]ggggttttcttctctg	C	T	NM_016199 // downstream // 3342 // Hs.512610 // LSM7 // 51690 // Homo sapiens LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM7), mRNA. /// NM_020172 // upstream // 10500 // Hs.330742 // SPPL2B // 56928 // Homo sapiens SPPL2b (SPPL2B), m	LSM7	LSM7, Homo sapiens LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM7), p13.3
SNP_A-2096585	agaccttgttacatca[A/G]cttacatcatcttaca	A	G	NM_173480 // downstream // 28685 // Hs.374945 // LOC126295 // 126295 // Homo sapiens hypothetical protein LOC126295 (LOC126295), mRNA. /// NM_021217 // upstream // 2221 // Hs.38004 // ZNF77 // 58492 // Homo sapiens zinc finger protein 77 (pT1) (ZNF77), mR	LOC126295	LOC126295, Homo sapiens hypothetical protein LOC126295 (LOC126295), p13.3
SNP_A-2095578	agacaatctttccaga[A/T]gtgctttacaacagtg	A	T	NM_002068 // intron // 0 // Hs.73797 // GNA15 // 2769 // Homo sapiens guanine nucleotide binding protein (G protein), alpha 15 (Gq class) (GNA15), mRNA. /// ENST00000262958 // intron // 0 // — // — // — // —	GNA15	GNA15, Homo sapiens guanine nucleotide binding protein (G protein), alpha 15 (Gq class) (GNA15), p13.3
SNP_A-1809031	gtgacaaccacagata[G/T]cccaacactggcaagt	G	T	ENST00000318934 // intron // 0 // — // — // — // — /// ENST00000262969 // intron // 0 // — // — // — // —	-	p13.3
SNP_A-2064926	aattgagaatgagctc[A/C]ccatcgctggaggtat	A	C	NM_020209 // intron // 0 // Hs.7423 // SHD // 56961 // Homo sapiens src homology 2 domain-containing transforming protein D (SHD), mRNA. /// ENST00000221852 // intron // 0 // — // — // — // —	SHD	SHD, Homo sapiens src homology 2 domain-containing transforming protein D (SHD), p13.3
SNP_A-2080682	acctcatctcgcactc[A/G]caggctgttattaggg	A	G	NM_003025 // intron // 0 // Hs.97616 // SH3GL1 // 6455 // Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA. /// ENST00000269886 // intron // 0 // — // — // — // —	SH3GL1	SH3GL1, Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), p13.3
SNP_A-2223279	cgcggaatctgggctg[C/T]acgtgtgttctgtttg	C	T	NM_139159 // intron // 0 // Hs.515081 // DPP9 // 91039 // Homo sapiens dipeptidylpeptidase 9 (DPP9), mRNA. /// ENST00000301296 // intron // 0 // — // — // — // — /// ENST00000357909 // intron // 0 // — // — // — // — /// ENST00000262960 //	DPP9	DPP9, Homo sapiens dipeptidylpeptidase 9 (DPP9), p13.3
SNP_A-1874553	tctccggccccctcca[A/C]tctatctcaagccttg	A	C	NM_005817 // intron // 0 // Hs.140452 // M6PRBP1 // 10226 // Homo sapiens mannose-6-phosphate receptor binding protein 1 (M6PRBP1), mRNA. /// ENST00000221957 // intron // 0 // — // — // — // —	M6PRBP1	M6PRBP1, Homo sapiens mannose-6-phosphate receptor binding protein 1 (M6PRBP1), p13.3
SNP_A-1781361	ggatgttaaataaaga[C/T]gaggagcccacttgac	C	T	NM_015015 // intron // 0 // Hs.371013 // JMJD2B // 23030 // Homo sapiens jumonji domain containing 2B (JMJD2B), mRNA. /// ENST00000159111 // intron // 0 // — // — // — // —	JMJD2B	JMJD2B, Homo sapiens jumonji domain containing 2B (JMJD2B), p13.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2291708	gcacacctacgccata[C/T]ggtatgcttgagagcc	C	T	NM_181710 // downstream // 12241 // Hs.126496 // ZNRF4 // 148066 // Homo sapiens zinc and ring finger 4 (ZNRF4), mRNA. /// NM_153375 // downstream // 89078 // Hs.515575 // PLAC2 // 257000 // Homo sapiens placenta-specific 2 (PLAC2), mRNA. /// ENST00000222	ZNRF4	ZNRF4, Homo sapiens zinc and ring finger 4 (ZNRF4), p13.3
SNP_A-1941065	gcaattaggagctgtg[C/G]actttaaacacaatga	C	G	NM_181710 // downstream // 13544 // Hs.126496 // ZNRF4 // 148066 // Homo sapiens zinc and ring finger 4 (ZNRF4), mRNA. /// NM_153375 // downstream // 87775 // Hs.515575 // PLAC2 // 257000 // Homo sapiens placenta-specific 2 (PLAC2), mRNA. /// ENST00000222	ZNRF4	ZNRF4, Homo sapiens zinc and ring finger 4 (ZNRF4), p13.3
SNP_A-2107076	agcgcatcggcacacc[A/G]gatgagggtctctctc	A	G	NM_004558 // downstream // 1968 // Hs.234775 // NRTN // 4902 // Homo sapiens neurturin (NRTN), mRNA. /// NM_000150 // downstream // 496 // Hs.32956 // FUT6 // 2528 // Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), mRNA. /// ENS	NRTN	NRTN, Homo sapiens neurturin (NRTN), p13.3
SNP_A-2116181	aggtaatataagagct[C/T]accagatagagtagac	C	T	NM_000150 // intron // 0 // Hs.32956 // FUT6 // 2528 // Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), mRNA. /// ENST00000286955 // intron // 0 // --- // --- // --- // ---	FUT6	FUT6, Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), p13.3
SNP_A-1820156	gtttaaggtcatcctc[C/T]ctcaaaaccagtattc	C	T	NM_000150 // upstream // 18 // Hs.32956 // FUT6 // 2528 // Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), mRNA. /// NM_000149 // downstream // 3156 // Hs.169238 // FUT3 // 2525 // Homo sapiens fucosyltransferase 3 (galactoside	FUT6	FUT6, Homo sapiens fucosyltransferase 6 (alpha (1,3) fucosyltransferase) (FUT6), p13.3
SNP_A-1882412	tgaaaagcccgctgtc[C/G]ctgcacgtcccacact	C	G	NM_003624 // intron // 0 // Hs.531752 // RANBP3 // 8498 // Homo sapiens RAN binding protein 3 (RANBP3), transcript variant RANBP3-a, mRNA. /// NM_007322 // intron // 0 // Hs.531752 // RANBP3 // 8498 // Homo sapiens RAN binding protein 3 (RANBP3), transcri	RANBP3	RANBP3, Homo sapiens RAN binding protein 3 (RANBP3), transcript variant RANBP3-a, p13.3
SNP_A-2263138	gaacacttagaacacc[A/G]catttatagatgaga	A	G	NM_030924 // intron // 0 // Hs.465720 // BGR // 81616 // Homo sapiens bubblegum related protein (BGR), mRNA. /// ENST00000252669 // intron // 0 // --- // --- // --- // ---	BGR	BGR, Homo sapiens bubblegum related protein (BGR), p13.3
SNP_A-2108678	agctgtaccagggtta[C/T]ggatagttgtaggaag	C	T	NM_001252 // upstream // 67450 // Hs.501497 // TNFSF7 // 970 // Homo sapiens tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7), mRNA. /// NM_003807 // downstream // 5955 // Hs.129708 // TNFSF14 // 8740 // Homo sapiens tumor necrosis factor (li	TNFSF7	TNFSF7, Homo sapiens tumor necrosis factor (ligand) superfamily, member 7 (TNFSF7), p13.3
SNP_A-2268186	gaatgacacaaagtaa[C/G]tgtgagctatgatgat	C	G	NM_000064 // intron // 0 // Hs.529053 // C3 // 718 // Homo sapiens complement component 3 (C3), mRNA. /// ENST00000245907 // intron // 0 // --- // --- // --- // ---	C3	C3, Homo sapiens complement component 3 (C3), p13.3
SNP_A-2050926	aaggcgtttaggaagc[A/G]atgagtttgagtgttt	A	G	NM_000064 // intron // 0 // Hs.529053 // C3 // 718 // Homo sapiens complement component 3 (C3), mRNA. /// ENST00000245907 // intron // 0 // --- // --- // --- // ---	C3	C3, Homo sapiens complement component 3 (C3), p13.3
SNP_A-2094614	agaatagatgttttac[A/G]agaccacaggctgaga	A	G	NM_005490 // CDS // 0 // Hs.439645 // SH2D3A // 10045 // Homo sapiens SH2 domain containing 3A (SH2D3A), mRNA. /// ENST00000245908 // CDS // 0 // --- // --- // --- // ---	SH2D3A	SH2D3A, Homo sapiens SH2 domain containing 3A (SH2D3A), p13.3
SNP_A-1929565	ttcatacatcttgtta[A/G]agtttgctcatgttat	A	G	NM_024341 // 3UTR // 0 // Hs.250821 // ZNF557 // 79230 // Homo sapiens zinc finger protein 557 (ZNF557), mRNA. /// ENST00000252840 // 3UTR // 0 // --- // --- // --- // ---	ZNF557	ZNF557, Homo sapiens zinc finger protein 557 (ZNF557), p13.2
SNP_A-1783341	ggcagtttctggattg[A/G]aatatcagtcatgcat	A	G	NM_000208 // intron // 0 // Hs.465744 // INSR // 3643 // Homo sapiens insulin receptor (INSR), mRNA. /// ENST00000302850 // intron // 0 // --- // --- // --- /// ENST00000341500 // intron // 0 // --- // --- // --- // ---	INSR	INSR, Homo sapiens insulin receptor (INSR), p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308168	gcttgcgacacttcac[A/G]ggctatcgcatcgagc	A	G	NM_000208 // CDS // 0 // Hs.465744 // INSR // 3643 // Homo sapiens insulin receptor (INSR), mRNA. /// ENST00000302850 // CDS // 0 // — // — // — /// ENST00000341500 // CDS // 0 // — // — // —	INSR	INSR, Homo sapiens insulin receptor (INSR), p13.2
SNP_A-1805882	gtcccttggagtaagca[A/G]acttccttatacctat	A	G	NM_000208 // intron // 0 // Hs.465744 // INSR // 3643 // Homo sapiens insulin receptor (INSR), mRNA. /// ENST00000302850 // intron // 0 // — // — // — /// ENST00000341500 // intron // 0 // — // — // —	INSR	INSR, Homo sapiens insulin receptor (INSR), p13.2
SNP_A-2038703	aacagaggcgtgcagc[A/G]aagtaaacacgggaag	A	G	NM_000208 // intron // 0 // Hs.465744 // INSR // 3643 // Homo sapiens insulin receptor (INSR), mRNA. /// ENST00000302850 // intron // 0 // — // — // — /// ENST00000341500 // intron // 0 // — // — // —	INSR	INSR, Homo sapiens insulin receptor (INSR), p13.2
SNP_A-2231338	ctattcgatctattc[C/T]attggctagcttag	C	T	NM_001419 // intron // 0 // Hs.184492 // ELAVL1 // 1994 // Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), mRNA. /// NM_032447 // intron // 0 // Hs.370362 // FBN3 // 84467 // Homo sapiens fibrillin 3 (FBN3	ELAVL1	ELAVL1, Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (ELAVL1), p13.2
SNP_A-1880113	tcttctctagtccatg[A/T]atatgtatacgtacat	A	T	NM_031203 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, mRNA. /// NM_005968 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucl	HNRPM	HNRPM, Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, p13.2
SNP_A-1881085	tcttaactgaagagc[C/T]gatcttattctggga	C	T	NM_031203 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, mRNA. /// NM_005968 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucl	HNRPM	HNRPM, Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, p13.2
SNP_A-2209272	cccagtgatgactgcc[A/G]gaaacatttttgttctg	A	G	NM_031203 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, mRNA. /// NM_005968 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucl	HNRPM	HNRPM, Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, p13.2
SNP_A-1903187	tggcttctaggtggca[A/G]ggctaaataaatacat	A	G	NM_031203 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, mRNA. /// NM_005968 // intron // 0 // Hs.465808 // HNRPM // 4670 // Homo sapiens heterogeneous nuclear ribonucl	HNRPM	HNRPM, Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 2, p13.2
SNP_A-1942895	ctattgctgtctgcaa[A/C]ctacttcaaaatgcaa	A	C	NM_144693 // downstream // 5553 // Hs.349444 // ZNF558 // 148156 // Homo sapiens zinc finger protein 558 (ZNF558), mRNA. /// ENST00000342205 // upstream // 53594 // — // — // — /// ENST00000301475 // downstream // 5553 // — // — // — //	ZNF558	ZNF558, Homo sapiens zinc finger protein 558 (ZNF558), p13.2
SNP_A-2202077	ccacagtctacctgat[C/T]attggagttttctgag	C	T	ENST00000331986 // CDS // 0 // — // — // —	-	p13.2
SNP_A-1856431	tcacacttccatgact[G/T]acacagagaagaagtga	G	T	ENST00000331986 // CDS // 0 // — // — // —	-	p13.2
SNP_A-1877049	tctgctacttttctggat[C/T]aaataaggaaaccctct	C	T	NM_001004456 // upstream // 101606 // — // OR1M1 // 125963 // Homo sapiens olfactory receptor, family 1, subfamily M, member 1 (OR1M1), mRNA. /// ENST00000331986 // upstream // 10501 // — // — // — /// ENST00000305465 // upstream // 101606	OR1M1	OR1M1, Homo sapiens olfactory receptor, family 1, subfamily M, member 1 (OR1M1), p13.2
SNP_A-2262555	gaaatgttcaatgtgc[A/C]agcttctataaactc	A	C	ENST00000344049 // downstream // 1774 // — // — // — /// ENST00000344844 // upstream // 13359 // — // — // —	-	p13.2
SNP_A-2069455	acacaagtaaatgcac[A/G]ctcaaatataggagct	A	G	ENST00000344844 // downstream // 14859 // — // — // — /// ENST00000308650 // downstream // 27353 // — // — // —	-	p13.2
SNP_A-2051287	aagggcacagataaggt[C/T]actaggcatagaatct	C	T	ENST00000301496 // intron // 0 // — // — // — /// ENST00000333905 // intron // 0 // — // — // — /// ENST00000356596 // intron // 0 // — // — // — /// ENST00000356382 // intron // 0 // — // — // — /// ENS	-	p13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1790539	ggggccagcacgtctg[C/G]agcctttatgggcac	C	G	NM_203500 // upstream // 7727 // Hs.465870 // KEAP1 // 9817 // Homo sapiens kelch-like ECH-associated protein 1 (KEAP1), transcript variant 1, mRNA. /// NM_012289 // upstream // 7727 // Hs.465870 // KEAP1 // 9817 // Homo sapiens kelch-like ECH-associated	KEAP1	KEAP1, Homo sapiens kelch-like ECH-associated protein 1 (KEAP1), transcript variant 1, p13.2
SNP_A-2167965	caacgggccagaccac[A/G]ggaaggacggtgttg	A	G	NM_020428 // 3UTR // 0 // Hs.515134 // CTL2 // 57153 // Homo sapiens CTL2 gene (CTL2), mRNA. /// ENST00000359378 // 5UTR // 0 // — // — // — /// ENST00000335757 // 3UTR // 0 // — // — // —	CTL2	CTL2, Homo sapiens CTL2 gene (CTL2), p13.2
SNP_A-1784780	ggcctggctgaccaga[A/G]attggaaacccgacg	A	G	NM_153464 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, mRNA. /// NM_004516 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin enhancer binding f	ILF3	ILF3, Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, p13.2
SNP_A-2246120	ctggtcctgcgtgagat[C/G]atctacaaacctcc	C	G	NM_153464 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, mRNA. /// NM_004516 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin enhancer binding f	ILF3	ILF3, Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, p13.2
SNP_A-2115816	agggtgcaactgccaa[A/G]aactggtcctgcgtga	A	G	NM_153464 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, mRNA. /// NM_004516 // intron // 0 // Hs.465885 // ILF3 // 3609 // Homo sapiens interleukin enhancer binding f	ILF3	ILF3, Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 3, p13.2
SNP_A-1943740	cccatttcatctggta[C/T]ctaacaggtctgtgc	C	T	NM_004945 // intron // 0 // Hs.211463 // DNM2 // 1785 // Homo sapiens dynamin 2 (DNM2), mRNA. /// ENST00000359692 // intron // 0 // — // — // — /// ENST00000355667 // intron // 0 // — // — // — // —	DNM2	DNM2, Homo sapiens dynamin 2 (DNM2), p13.2
SNP_A-2150556	atgtgagccacagcga[C/T]aggaactattaccaat	C	T	NM_138783 // intron // 0 // Hs.465928 // ZNF653 // 115950 // Homo sapiens zinc finger protein Zip67 (ZIP67), mRNA. /// ENST00000293771 // intron // 0 // — // — // — // —	ZNF653	ZNF653, Homo sapiens zinc finger protein Zip67 (ZIP67), p13.2
SNP_A-1960960	tttttgctcaggttac[G/T]caaatatgaagacaacc	G	T	ENST00000342073 // upstream // 16846 // — // — // — // — /// ENST00000344893 // upstream // 1351 // — // — // — // —	-	p13.2
SNP_A-1730831	atacggctacctacctagtacacat[C/T]atctacaatataacatttt ctttt	C	T	NM_145295 // downstream // 67364 // Hs.14831 // ZNF627 // 199692 // zinc finger protein 627	ZNF627	ZNF627 , rs286300, zinc finger protein 627,p13.2
SNP_A-2091244	actttacccctagttc[C/G]agatgacagactgaac	C	G	NM_152357 // CDS // 0 // Hs.418192 // ZNF440 // 126070 // Homo sapiens zinc finger protein 440 (ZNF440), mRNA. /// ENST00000304060 // CDS // 0 // — // — // — // —	ZNF440	ZNF440, Homo sapiens zinc finger protein 440 (ZNF440), p13.2
SNP_A-2045570	aagaaatagtgcaggg[A/T]caattacaaaagggac	A	T	NM_005815 // upstream // 20542 // Hs.142150 // ZNF443 // 10224 // Homo sapiens zinc finger protein 443 (ZNF443), mRNA. /// NM_152601 // downstream // 7813 // Hs.306478 // FLJ38281 // 163051 // Homo sapiens hypothetical protein FLJ38281 (FLJ38281), mRNA. /	ZNF443	ZNF443, Homo sapiens zinc finger protein 443 (ZNF443), p13.2
SNP_A-2297176	gccacatcgttttgtc[A/G]actttttgttttgtt	A	G	NM_144976 // intron // 0 // Hs.534574 // ZNF564 // 163050 // Homo sapiens zinc finger protein 564 (ZNF564), mRNA. /// ENST00000339282 // intron // 0 // — // — // — // —	ZNF564	ZNF564, Homo sapiens zinc finger protein 564 (ZNF564), p13.2
SNP_A-2206838	ccatgctctgcttctc[A/G]acctgtgttttcacct	A	G	NM_002501 // intron // 0 // Hs.257970 // NFIX // 4784 // Homo sapiens nuclear factor I/X (CCAAT-binding transcription factor) (NFIX), mRNA. /// L31881 // intron // 0 // — // NFIX // 4784 // Human nuclear factor I-X mRNA, complete cds. /// ENST00000026482	NFIX	NFIX, Homo sapiens nuclear factor I,p13.13
SNP_A-2272934	gactactcagatgatgt[A/G]aaaactattgtatata	A	G	NM_023035 // upstream // 27681 // Hs.408449 // CACNA1A // 773 // Homo sapiens calcium channel, voltage-dependent, P/Q type, alpha 1A subunit (CACNA1A), transcript variant 2, mRNA. /// NM_000068 // upstream // 27681 // Hs.408449 // CACNA1A // 773 // Homo s	CACNA1A	CACNA1A, Homo sapiens calcium channel, voltage-dependent, P p13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1698751	ttttttatcaaaagcaaccaactca[A/G]attgctaatccaacagtt actaag	A	G	NM_032571 // intron // 0 // Hs.438468 // EMR3 // 84658 // egf-like module containing, mucin-like, hormone receptor-like 3 /// NM_152939 // intron // 0 // Hs.438468 // EMR3 // 84658 // egf-like module containing, mucin-like, hormone receptor-like 3	EMR3	EMR3 , -, egf-like module containing, mucin-like, hormone receptor-like 3, p13.12
SNP_A-1796023	ggtggtgcccttcaggaa[C/T]tcctcgtgtgtcaatg	C	T	NM_152918 // CDS // 0 // Hs.531619 // EMR2 // 30817 // Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 2 (EMR2), transcript variant 4, mRNA. /// NM_152917 // CDS // 0 // Hs.531619 // EMR2 // 30817 // Homo sapiens egf-like module	EMR2	EMR2, Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 2 (EMR2), transcript variant 4, p13.12
SNP_A-1704341	aaacaaggaaaggaaggcacatccctca[A/G]agttttgtactgcca ttcctcctg	A	G	NM_017506 // upstream // 725 // Hs.137573 // OR7A5 // 26659 // olfactory receptor, family 7, subfamily A, member 5 /// NM_030901 // downstream // 51237 // Hs.247717 // OR7A17 // 26333 // olfactory receptor, family 7, subfamily A, member 17	OR7A5	OR7A5, rs8101893, olfactory receptor, family 7, subfamily A, member 5 ,p13.12
SNP_A-2030858	aaaggaaatggcatca[A/G]tatgtcaaggagatat	A	G	NM_005071 // upstream // 27776 // Hs.515217 // SLC1A6 // 6511 // Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA. /// NM_005071 // upstream // 21001 // Hs.515217 // SLC1A6 // 6511 // Homo sapie	SLC1A6	SLC1A6, Homo sapiens solute carrier family 1 (high affinity aspartate p13.12
SNP_A-2247957	ctgtgcccagcctaca[A/C]gtctcatttctgtaat	A	C	NM_014299 // upstream // 62156 // Hs.187763 // BRD4 // 23476 // Homo sapiens bromodomain containing 4 (BRD4), transcript variant short, mRNA. /// NM_058243 // upstream // 62156 // Hs.187763 // BRD4 // 23476 // Homo sapiens bromodomain containing 4 (BRD4).	BRD4	BRD4, Homo sapiens bromodomain containing 4 (BRD4), transcript variant short, p13.12
SNP_A-1943237	ttggtgagtatgtgaa[A/G]aaatcaggaccttat	A	G	NM_014371 // intron // 0 // Hs.399800 // AKAP8L // 26993 // Homo sapiens A kinase (PRKA) anchor protein 8-like (AKAP8L), mRNA. /// ENST00000263378 // intron // 0 /// --- /// --- /// ---	AKAP8L	AKAP8L, Homo sapiens A kinase (PRKA) anchor protein 8-like (AKAP8L), p13.12
SNP_A-2210536	ccccgcacggtactgaa[C/T]cacctaaaaatatatc	C	T	NM_014371 // intron // 0 // Hs.399800 // AKAP8L // 26993 // Homo sapiens A kinase (PRKA) anchor protein 8-like (AKAP8L), mRNA. /// ENST00000263378 // intron // 0 // --- // --- // ---	AKAP8L	AKAP8L, Homo sapiens A kinase (PRKA) anchor protein 8-like (AKAP8L), p13.12
SNP_A-2159430	atttaatttaatgttc[A/G]ctttgacttcaacag	A	G	NM_052890 // upstream // 32813 // Hs.282244 // PGLYRP2 // 114770 // Homo sapiens peptidoglycan recognition protein 2 (PGLYRP2), mRNA. /// AK055882 // upstream // 32813 // Hs.282244 // PGLYRP2 // 114770 // Homo sapiens cDNA FLJ31320 fis, clone LIVER1000542	PGLYRP2	PGLYRP2, Homo sapiens peptidoglycan recognition protein 2 (PGLYRP2), p13.12
SNP_A-2151516	atgttctgcaacacct[A/G]agcatagctcaacgct	A	G	NM_173483 // downstream // 20994 // --- // FLJ39501 // 126410 // Homo sapiens hypothetical protein FLJ39501 (FLJ39501), mRNA. /// ENST00000269703 // downstream // 20994 // --- // --- // --- /// ENST00000333997 // upstream // 38346 // --- // --- //	FLJ39501	FLJ39501, Homo sapiens hypothetical protein FLJ39501 (FLJ39501), p13.12
SNP_A-2221574	ccttgagtctgtgct[A/G]acctaagcctggtga	A	G	NM_021187 // intron // 0 // Hs.187393 // CYP4F11 // 57834 // Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 11 (CYP4F11), mRNA. /// ENST00000248041 // intron // 0 // --- // --- // --- /// ENST00000326742 // intron // 0 // --- // -	CYP4F11	CYP4F11, Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 11 (CYP4F11), p13.12
SNP_A-1782242	ggcaagtaggaagtag[A/G]atggcccagaccactt	A	G	NM_021235 // intron // 0 // Hs.292072 // EPS15L1 // 58513 // Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), mRNA. /// ENST00000248070 // intron // 0 // --- // --- // ---	EPS15L1	EPS15L1, Homo sapiens epidermal growth factor receptor pathway substrate 15-like 1 (EPS15L1), p13.11
SNP_A-2191600	catatgtataccatga[C/T]gacttgtgtgggtgca	C	T	NM_015692 // intron // 0 // Hs.529075 // CPAMD8 // 27151 // Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), mRNA. /// ENST00000291440 // intron // 0 // --- // --- // ---	CPAMD8	CPAMD8, Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), p13.11
SNP_A-2280749	gaggtgagtagtaggg[C/T]gacaatcaaaacttca	C	T	NM_015692 // intron // 0 // Hs.529075 // CPAMD8 // 27151 // Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), mRNA. /// ENST00000291440 // intron // 0 // --- // --- // ---	CPAMD8	CPAMD8, Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), p13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2217198	cctctttgccaaatcc[A/G]agggcatgaaggtcta	A	G	NM_015692 // intron // 0 // Hs.529075 // CPAMD8 // 27151 // Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), mRNA. /// ENST00000291440 // intron // 0 // --- // --- // --- // ---	CPAMD8	CPAMD8, Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), p13.11
SNP_A-2222324	cgactttgaaccaagg[A/G]ccgaacttctctgagc	A	G	NM_015692 // intron // 0 // Hs.529075 // CPAMD8 // 27151 // Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), mRNA. /// ENST00000291440 // intron // 0 // --- // --- // --- // ---	CPAMD8	CPAMD8, Homo sapiens C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (CPAMD8), p13.11
SNP_A-1788009	gggagacacagagagt[A/G]aagaatccagctggac	A	G	NM_024578 // downstream // 377 // Hs.422676 // FLJ22709 // 79629 // Homo sapiens hypothetical protein FLJ22709 (FLJ22709), mRNA. /// NM_005234 // downstream // 2294 // Hs.466148 // NR2F6 // 2063 // Homo sapiens nuclear receptor subfamily 2, group F, membe	FLJ22709	FLJ22709, Homo sapiens hypothetical protein FLJ22709 (FLJ22709), p13.11
SNP_A-2303508	gctcaactgagacctg[A/G]aaggattgagcccagc	A	G	NM_012088 // intron // 0 // Hs.466165 // PGLS // 25796 // Homo sapiens 6-phosphogluconolactonase (PGLS), mRNA. /// ENST00000252603 // intron // 0 // --- // --- // --- // ---	PGLS	PGLS, Homo sapiens 6-phosphogluconolactonase (PGLS), p13.11
SNP_A-2173507	cacaatctatgcacgt[A/G]acaaaattacacttgt	A	G	NM_024656 // intron // 0 // Hs.418795 // GLT25D1 // 79709 // Homo sapiens glycosyltransferase 25 domain containing 1 (GLT25D1), mRNA. /// ENST00000252599 // intron // 0 // --- // --- // --- // ---	GLT25D1	GLT25D1, Homo sapiens glycosyltransferase 25 domain containing 1 (GLT25D1), p13.11
SNP_A-1907738	tgtaagataaagcaga[C/G]actatgaggaactaga	C	G	NM_015122 // intron // 0 // Hs.96485 // FCHO1 // 23149 // Homo sapiens FCH domain only 1 (FCHO1), mRNA. /// ENST00000252771 // intron // 0 // --- // --- // --- // ---	FCHO1	FCHO1, Homo sapiens FCH domain only 1 (FCHO1), p13.11
SNP_A-2263566	gaaccatcacaaccga[A/C]ctggctatttacgatg	A	C	NM_015683 // downstream // 1301 // Hs.515249 // ARRDC2 // 27106 // Homo sapiens arrestin domain containing 2 (ARRDC2), mRNA. /// NM_005535 // downstream // 43600 // Hs.223894 // IL12RB1 // 3594 // Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), tr	ARRDC2	ARRDC2, Homo sapiens arrestin domain containing 2 (ARRDC2), p13.11
SNP_A-2247674	ctgtgaaataaggcaa[A/G]tgagggactctccagg	A	G	NM_005535 // intron // 0 // Hs.223894 // IL12RB1 // 3594 // Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), transcript variant 1, mRNA. /// ENST00000221270 // intron // 0 // --- // --- // --- // ---	IL12RB1	IL12RB1, Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), transcript variant 1, p13.11
SNP_A-2188132	cagtccaggcaagaca[A/T]attcatcctgtaccct	A	T	ENST00000357416 // 5UTR // 0 // --- // --- // --- // --- /// ENST00000359737 // intron // 0 // --- // --- // --- // --- /// ENST00000358422 // intron // 0 // --- // --- // --- // --- /// ENST00000252814 // intron // 0 // --- // --- // --- // --- /// ENST0	-	p13.11
SNP_A-1873437	tctcaagatgcattga[A/T]gagatgagacaccatg	A	T	NM_014884 // intron // 0 // Hs.515271 // SFRS14 // 10147 // Homo sapiens splicing factor, arginine/serine-rich 14 (SFRS14), mRNA. /// ENST00000330854 // intron // 0 // --- // --- // --- // ---	SFRS14	SFRS14, Homo sapiens splicing factor, arginine p13.11
SNP_A-1748399	gcagtcagttgaactcaactgttta[A/G]caagaaggaatttttcatctcagtc	A	G	NM_025245 // intron // 0 // Hs.118388 // PBX4 // 80714 // pre-B-cell leukemia transcription factor 4	PBX4	PBX4 , rs10500212, pre-B-cell leukemia transcription factor 4,p13.11
SNP_A-1799640	gtaattggggccttga[A/G]cctgatccagctttga	A	G	NM_016573 // upstream // 525 // Hs.49427 // GMIP // 51291 // Homo sapiens GEM interacting protein (GMIP), mRNA. /// ENST00000203556 // upstream // 525 // --- // --- // --- // --- /// ENST00000291503 // downstream // 1070 // --- // --- // --- // --- /// EN	GMIP	GMIP, Homo sapiens GEM interacting protein (GMIP), p13.11
SNP_A-1937361	ttgaaagtctacactc[C/T]atgcttcaggtggtcc	C	T	NM_031218 // upstream // 55975 // Hs.301059 // ZNF505 // 81931 // Homo sapiens zinc finger protein 505 (ZNF505), transcript variant 1, mRNA. /// NM_001004126 // upstream // 55975 // Hs.301059 // ZNF505 // 81931 // Homo sapiens zinc finger protein 505 (ZNF	ZNF505	ZNF505, Homo sapiens zinc finger protein 505 (ZNF505), transcript variant 1, p12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2005912	catgtaaaaatgatac[C/G]ctttggctttggctta	C	G	NM_033196 // upstream // 43508 // Hs.306298 // LOC91120 // 91120 // Homo sapiens hypothetical ZNF-like protein (LOC91120), mRNA. /// NM_033196 // upstream // 36770 // Hs.306298 // LOC91120 // 91120 // Homo sapiens hypothetical ZNF-like protein (LOC91120),	LOC91120	LOC91120, Homo sapiens hypothetical ZNF-like protein (LOC91120), p12
SNP_A-2118345	agtaactgaggaagaa[C/T]tggtatctctgtaaaa	C	T	NM_145297 // upstream // 172754 // Hs.50158 // ZNF626 // 199777 // Homo sapiens zinc finger protein 626 (ZNF626), mRNA. /// NM_003429 // upstream // 114864 // Hs.37138 // ZNF85 // 7639 // Homo sapiens zinc finger protein 85 (HPF4, HTF1) (ZNF85), mRNA. ///	ZNF626	ZNF626, Homo sapiens zinc finger protein 626 (ZNF626), p12
SNP_A-1902759	tggctattcttcacct[A/G]acttttaaaatagtat	A	G	NM_001001415 // downstream // 135713 // Hs.310336 // ZNF429 // 353088 // Homo sapiens zinc finger protein 429 (ZNF429), mRNA. /// NM_173531 // downstream // 52404 // Hs.365142 // ZNF100 // 163227 // Homo sapiens zinc finger protein 100 (ZNF100), mRNA. ///	ZNF429	ZNF429, Homo sapiens zinc finger protein 429 (ZNF429), p12
SNP_A-2047379	aagatctgaaaagctt[C/G]aagagccacactctca	C	G	NM_173531 // intron // 0 // Hs.365142 // ZNF100 // 163227 // Homo sapiens zinc finger protein 100 (ZNF100), mRNA. /// ENST00000358296 // intron // 0 // — // — // — // —	ZNF100	ZNF100, Homo sapiens zinc finger protein 100 (ZNF100), p12
SNP_A-2136770	atcactttcaggtaca[C/G]gtatcaaatgtagatt	C	G	NM_003423 // upstream // 133970 // Hs.534365 // ZNF43 // 7594 // Homo sapiens zinc finger protein 43 (HTF6) (ZNF43), mRNA. /// NM_178523 // upstream // 119611 // Hs.148374 // ZNF616 // 90317 // Homo sapiens zinc finger protein 616 (ZNF616), mRNA. /// NM_0	ZNF43	ZNF43, Homo sapiens zinc finger protein 43 (HTF6) (ZNF43), p12
SNP_A-2086748	actgacaactaataac[C/T]gagtgtgcccagaatc	C	T	NM_001001411 // intron // 0 // Hs.531759 // LOC163223 // 163223 // Homo sapiens similar to Zinc finger protein 208 (LOC163223), mRNA. /// NM_178523 // intron // 0 // Hs.148374 // ZNF616 // 90317 // Homo sapiens zinc finger protein 616 (ZNF616), mRNA. ///	LOC163223	LOC163223, Homo sapiens similar to Zinc finger protein 208 (LOC163223), p12
SNP_A-2218643	cctggccaggcaacca[A/G]gtgatatgactctctg	A	G	ENST00000359111 // intron // 0 // — // — // — // — /// ENST00000339567 // intron // 0 // — // — // — // — /// ENST00000343332 // intron // 0 // — // — // — // — /// ENST00000360532 // intron // 0 // — // — // — // — /// ENS	-	p12
SNP_A-1736537	acccaacagacagcatacatggtca[A/C]cactatccaggactc tccataataa	A	C	NM_138286 // upstream // 109660 // Hs.187337 // LOC148213 // 148213 // hypothetical protein FLJ31526	LOC148213	LOC148213 , rs251750, hypothetical protein FLJ31526,p12
SNP_A-1805426	gtccacagaacttttg[C/T]aggaatggatatgaat	C	T	ENST00000359111 // intron // 0 // — // — // — // — /// ENST00000339567 // intron // 0 // — // — // — // — /// ENST00000343332 // intron // 0 // — // — // — // — /// ENST00000360532 // intron // 0 // — // — // — // — /// ENS	-	p12
SNP_A-1950917	aggcattatcctcaaa[A/G]cctaaagctgctctca	A	G	NM_001001411 // upstream // 734456 // Hs.531759 // LOC163223 // 163223 // Homo sapiens similar to Zinc finger protein 208 (LOC163223), mRNA. /// NM_178523 // upstream // 734441 // Hs.148374 // ZNF616 // 90317 // Homo sapiens zinc finger protein 616 (ZNF61	LOC163223	LOC163223, Homo sapiens similar to Zinc finger protein 208 (LOC163223), p12
SNP_A-2138758	atccccaggatcagaa[C/T]atcttccactccttcc	C	T	X82272 // upstream // 253157 // — // — // 0 // Human endogenous retrovirus env mRNA. /// ENST00000355833 // upstream // 253157 // — // — // — // — /// ENST00000329394 // upstream // 43143 // — // — // — // — /// ENST00000360285 // upst	-	-, Human endogenous retrovirus env ,q12
SNP_A-1951484	cctgacatccagctca[C/T]tcatgcacatcccttg	C	T	X82272 // upstream // 293211 // — // — // 0 // Human endogenous retrovirus env mRNA. /// ENST00000355833 // upstream // 293211 // — // — // — // — /// ENST00000329394 // upstream // 3089 // — // — // — // — /// ENST00000360285 // upstr	-	-, Human endogenous retrovirus env q12
SNP_A-2236127	ctccttcaactctagg[A/C]actcagaagcctttta	A	C	ENST00000329394 // intron // 0 // — // — // — // — /// ENST00000360285 // intron // 0 // — // — // — // — /// ENST00000339882 // intron // 0 // — // — // — // —	-	q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2201357	ccaatccagctttccc[C/T]ccagcatcatctatct	C	T	ENST00000329394 // intron // 0 // — // — // — /// ENST00000360285 // intron // 0 // — // — // — /// ENST00000339882 // intron // 0 // — // — -// — // —	-	q12
SNP_A-1795676	ggtggaactggaacga[C/T]taaaacactaccatat	G	T	ENST00000329394 // intron // 0 // — // — // — /// ENST00000360285 // intron // 0 // — // — // — /// ENST00000339882 // intron // 0 // — // — -// — // —	-	q12
SNP_A-1752089	gtagagtacgcccagaatctatcaa[C/G]ttaaggattaaacttaa atctactc	C	G	NM_004876 // downstream // 9068288 // Hs.434406 // ZNF539 // 399655 // zinc finger protein 539 /// NM_006003 // downstream // 1218697 // Hs.355735 // UQCRFS1 // 7386 // ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	ZNF539	ZNF539 , rs9304858, zinc finger protein 539 ,q12
SNP_A-1951569	gtggaaaagacaaagc[A/G]attttctacaagaa	A	G	ENST00000329394 // downstream // 5497 // — // — // — /// ENST00000360285 // downstream // 5497 // — // — // — /// ENST00000339882 // downstream // 5497 // — // — // — /// ENST00000327999 // downstream // 694000 // -	-	q12
SNP_A-1920106	ttaatcagggccagga[A/T]tactcacgcaggaaat	A	T	ENST00000329394 // downstream // 330398 // — // — // — /// ENST00000360285 // downstream // 330398 // — // — // — /// ENST00000339882 // downstream // 330398 // — // — // — /// ENST00000327999 // downstream // 369099	-	q12
SNP_A-1823769	taaaatctcaaatcgc[A/G]atgtccctagcaatct	A	G	ENST00000329394 // downstream // 378337 // — // — // — /// ENST00000360285 // downstream // 378337 // — // — // — /// ENST00000339882 // downstream // 378337 // — // — // — /// ENST00000327999 // downstream // 321160	-	q12
SNP_A-2199256	catttcacagcagca[A/G]aaggtcatcaggagat	A	G	ENST00000329394 // downstream // 414722 // — // — // — /// ENST00000360285 // downstream // 414722 // — // — // — /// ENST00000339882 // downstream // 414722 // — // — // — /// ENST00000327999 // downstream // 284775	-	q12
SNP_A-1809839	gtgaggtacaatccca[A/G]tgccatctatctgctc	A	G	ENST00000329394 // downstream // 416478 // — // — // — /// ENST00000360285 // downstream // 416478 // — // — // — /// ENST00000339882 // downstream // 416478 // — // — // — /// ENST00000327999 // downstream // 283019	-	q12
SNP_A-2150953	atgtggtacacgaata[C/T]gacagaatattattca	C	T	ENST00000329394 // downstream // 424075 // — // — // — /// ENST00000360285 // downstream // 424075 // — // — // — /// ENST00000339882 // downstream // 424075 // — // — // — /// ENST00000327999 // downstream // 275422	-	q12
SNP_A-2005940	tggatctcactctatc[A/G]ctgttatatgttacgt	A	G	ENST00000329394 // downstream // 500880 // — // — // — /// ENST00000360285 // downstream // 500880 // — // — // — /// ENST00000339882 // downstream // 500880 // — // — // — /// ENST00000327999 // downstream // 198617	-	q12
SNP_A-1952167	tgtcaccatattgtta[A/G]ctggttttatgtaga	A	G	NM_006003 // downstream // 450884 // Hs.170107 // UQCRFS1 // 7386 // Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), mRNA. /// ENST00000327999 // upstream // 48303 // — // — // — /// ENST00000304863	UQCRFS1	UQCRFS1, Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), q12
SNP_A-2101042	agatcaagtgtaaaga[C/T]aagtaaatggtagttg	C	T	NM_006003 // upstream // 154524 // Hs.170107 // UQCRFS1 // 7386 // Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), mRNA. /// ENST00000304863 // upstream // 154524 // — // — // — /// ENST00000335523 /	UQCRFS1	UQCRFS1, Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), q12
SNP_A-1782763	ggcagaagattgcaca[A/G]cctccctggacccttа	A	G	NM_006003 // upstream // 264243 // Hs.170107 // UQCRFS1 // 7386 // Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), mRNA. /// ENST00000304863 // upstream // 264243 // — // — // — /// ENST00000335523 /	UQCRFS1	UQCRFS1, Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1953027	agcagaatctttttgc[A/G]ccatgcatgacattcc	A	G	NM_006627 // upstream // 29348 // Hs.412870 // POP4 // 10775 // Homo sapiens processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae) (POP4), mRNA. /// ENST00000335523 // downstream // 46804 // — // — // — // — /// ENST00000335517 //	POP4	POP4, Homo sapiens processing of precursor 4, ribonuclease P,q12
SNP_A-1787801	gggacctcccataaac[A/G]gaatcacagagtcacc	A	G	NM_031448 // upstream // 89521 // Hs.529094 // C19orf12 // 83636 // Homo sapiens chromosome 19 open reading frame 12 (C19orf12), mRNA. /// NM_031448 // upstream // 89484 // Hs.529094 // C19orf12 // 83636 // Homo sapiens chromosome 19 open reading frame 12	C19orf12	C19orf12, Homo sapiens chromosome 19 open reading frame 12 (C19orf12), q12
SNP_A-2228690	ctagacaactgagaaa[C/G]cattcccattttgcaa	C	G	NM_001238 // downstream // 44010 // Hs.244723 // CCNE1 // 898 // Homo sapiens cyclin E1 (CCNE1), transcript variant 1, mRNA. /// NM_057182 // downstream // 44010 // Hs.244723 // CCNE1 // 898 // Homo sapiens cyclin E1 (CCNE1), transcript variant 2, mRNA. /	CCNE1	CCNE1, Homo sapiens cyclin E1 (CCNE1), transcript variant 1, q12
SNP_A-1815473	gtgttttgtagttttc[A/G]atgtacaaacttgctc	A	G	ENST00000360605 // intron // 0 // — // — // — // —	-	q12
SNP_A-1953771	gaggctttgttttata[A/G]atgggaaccacagaaa	A	G	ENST00000355537 // downstream // 32765 // — // — // — // — /// ENST00000354623 // downstream // 32765 // — // — // — // — /// ENST00000283950 // upstream // 558631 // — // — // — // —	-	q12
SNP_A-2299457	gcccttaggcaaatca[C/T]caatgacccatgttca	C	T	ENST00000355537 // downstream // 113156 // — // — // — // — /// ENST00000354623 // downstream // 113156 // — // — // — // — /// ENST00000283950 // upstream // 478240 // — // — // — // —	-	q12
SNP_A-2005947	cagctatcaccctgag[C/T]caccgaacttccttcc	C	T	ENST00000355537 // downstream // 119894 // — // — // — // — /// ENST00000354623 // downstream // 119894 // — // — // — // — /// ENST00000283950 // upstream // 471502 // — // — // — // —	-	q12
SNP_A-2005948	ttttgtgtgttcagga[C/T]gcagactggagtgggt	C	T	ENST00000355537 // downstream // 318101 // — // — // — // — /// ENST00000354623 // downstream // 318101 // — // — // — // — /// ENST00000283950 // upstream // 273295 // — // — // — // —	-	q12
SNP_A-1721229	ggtattgttttgtcctagcattact[C/G]agaccatcctcatttctatccaggc	C	G	AL137518 // upstream // 247989 // Hs.220597 // DKFZp566F0947 // 94023 // hypothetical gene DKFZp566F0947 /// NM_014717 // downstream // 343407 // - // - // - // -	DKFZp566F0947	DKFZp566F0947 , rs278215, hypothetical gene DKFZp566F0947 ,q12
SNP_A-1954080	cctgtattatcaacca[C/T]gcaagatcacatcttg	C	T	NM_020856 // downstream // 107868 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000283950 // downstream // 14377 // — // — // — // — /// ENST00000240587 // downstream // 107868 // — // — // -	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-2203497	ccagaagagatataca[A/G]tgatgctgataatttc	A	G	NM_020856 // intron // 0 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // intron // 0 // — // — // — // —	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-2005955	ttggcttggggtgaaa[C/G]gtggacatgggagttc	C	G	NM_020856 // upstream // 372852 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 372852 // — // — // — // — /// ENST00000355898 // upstream // 623557 // — // — // — //	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-2142527	atgaacacctatacac[A/G]aaattctccaaaattc	A	G	NM_020856 // upstream // 406522 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 406522 // — // — // — // — /// ENST00000355898 // upstream // 589887 // — // — // — //	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12
SNP_A-1814883	gtgtgttctgacagta[A/T]cccatatggaactggg	A	T	NM_020856 // upstream // 424110 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 424110 // — // — // — // — /// ENST00000355898 // upstream // 572299 // — // — // — //	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1864872	tccaggcatggcatcc[A/G]ctgctgtagagaagtt	A	G	NM_020856 // upstream // 835263 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 835263 // — // — // — // — /// ENST00000355898 // upstream // 161146 // — // — // — //	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q13.11
SNP_A-1956500	tttgttgtcattgcca[C/G]ggaaaccttttattat	C	G	NM_020856 // upstream // 970085 // Hs.278436 // ZNF537 // 57616 // Homo sapiens zinc finger protein 537 (ZNF537), mRNA. /// ENST00000240587 // upstream // 970085 // — // — // — // — /// ENST00000355898 // upstream // 26324 // — // — // — //	ZNF537	ZNF537, Homo sapiens zinc finger protein 537 (ZNF537), q13.11
SNP_A-2063475	aattaataactttaca[A/T]tagcctctaagcgtcg	A	T	NM_153220 // intron // 0 // Hs.194392 // MGC35440 // 147990 // Homo sapiens hypothetical protein MGC35440 (MGC35440), mRNA. /// NM_207325 // intron // 0 // Hs.194392 // LOC147991 // 147991 // Homo sapiens hypothetical protein LOC147991 (LOC147991), mRNA.	MGC35440	MGC35440, Homo sapiens hypothetical protein MGC35440 (MGC35440), q13.11
SNP_A-2036389	aaattctaatgcattc[A/G]cataacctttttcaag	A	G	NM_032139 // intron // 0 // Hs.59236 // ANKRD27 // 84079 // Homo sapiens ankyrin repeat domain 27 (VPS9 domain) (ANKRD27), mRNA. /// ENST00000306065 // intron // 0 // — // — // — // —	ANKRD27	ANKRD27, Homo sapiens ankyrin repeat domain 27 (VPS9 domain) (ANKRD27), q13.11
SNP_A-2214587	cctagaggacctggga[C/T]caagctgctagaccac	C	T	NM_032816 // intron // 0 // Hs.317590 // FLJ14640 // 84902 // Homo sapiens hypothetical protein FLJ14640 (FLJ14640), mRNA. /// ENST00000305768 // intron // 0 // — // — // — // —	FLJ14640	FLJ14640, Homo sapiens hypothetical protein FLJ14640 (FLJ14640), q13.11
SNP_A-1955626	ggttgtttctaggaac[A/G]ctaccatcaaagatat	A	G	NM_019849 // upstream // 132021 // Hs.58679 // SLC7A10 // 56301 // Homo sapiens solute carrier family 7, (neutral amino acid transporter, y+ system) member 10 (SLC7A10), mRNA. /// NM_001806 // upstream // 15832 // Hs.429666 // CEBPG // 1054 // Homo sapien	SLC7A10	SLC7A10, Homo sapiens solute carrier family 7, (neutral amino acid transporter, y+ system) member 10 (SLC7A10), q13.11
SNP_A-2111453	aggaggcacaaaataa[C/G]tgttttctagtgtgtc	C	G	NM_019849 // upstream // 141457 // Hs.58679 // SLC7A10 // 56301 // Homo sapiens solute carrier family 7, (neutral amino acid transporter, y+ system) member 10 (SLC7A10), mRNA. /// NM_001806 // upstream // 6396 // Hs.429666 // CEBPG // 1054 // Homo sapiens	SLC7A10	SLC7A10, Homo sapiens solute carrier family 7, (neutral amino acid transporter, y+ system) member 10 (SLC7A10), q13.11
SNP_A-1955663	ggtgatttggaactga[A/G]attggcttttatttta	A	G	NM_001806 // downstream // 2803 // Hs.429666 // CEBPG // 1054 // Homo sapiens CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG), mRNA. /// NM_000285 // downstream // 1471 // Hs.36473 // PEPD // 5184 // Homo sapiens peptidase D (PEPD), mRNA. /// ENST00	CEBPG	CEBPG, Homo sapiens CCAAT,q13.11
SNP_A-1870933	tcggtaattaaacacg[A/G]aacagctgtcactctg	A	G	NM_000285 // upstream // 35608 // Hs.36473 // PEPD // 5184 // Homo sapiens peptidase D (PEPD), mRNA. /// ENST00000244137 // upstream // 35608 // — // — // — // — /// ENST00000310822 // downstream // 31804 // — // — // — // —	PEPD	PEPD, Homo sapiens peptidase D (PEPD), q13.11
SNP_A-2201920	ccacagaacagtatgc[A/G]cacttgctaaaaatct	A	G	NM_022467 // intron // 0 // Hs.165724 // CHST8 // 64377 // Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (CHST8), mRNA. /// ENST00000262622 // intron // 0 // — // — // — // —	CHST8	CHST8, Homo sapiens carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (CHST8), q13.11
SNP_A-2076339	acattgccaagtgtaa[G/T]gacgtttacttctgt	G	T	NM_024076 // downstream // 175767 // Hs.221873 // KCTD15 // 79047 // Homo sapiens potassium channel tetramerisation domain containing 15 (KCTD15), mRNA. /// ENST00000284006 // downstream // 175767 // — // — // — // — /// ENST00000334591 // downstr	KCTD15	KCTD15, Homo sapiens potassium channel tetramerisation domain containing 15 (KCTD15), q13.11
SNP_A-2289052	gatttccctataaaca[A/G]ataatgcaccatgaac	A	G	NM_015578 // upstream // 71716 // Hs.407368 // C19orf13 // 26065 // Homo sapiens chromosome 19 open reading frame 13 (C19orf13), mRNA. /// ENST00000334591 // upstream // 7540 // — // — // — // — /// ENST00000356258 // upstream // 71688 // — // -	C19orf13	C19orf13, Homo sapiens chromosome 19 open reading frame 13 (C19orf13), q13.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2193656	catcttctagcacggal[A/G]taattaaattcaagtt	A	G	NM_015578 // intron // 0 // Hs.407368 // C19orf13 // 26065 // Homo sapiens chromosome 19 open reading frame 13 (C19orf13), mRNA. /// ENST00000356258 // intron // 0 // — // — // — // — /// ENST00000324222 // intron // 0 // — // — // —	C19orf13	C19orf13, Homo sapiens chromosome 19 open reading frame 13 (C19orf13), q13.11
SNP_A-2089112	actaatccatcaata[A/C]taactgagcatcctta	A	C	NM_005499 // intron // 0 // Hs.511739 // UBA2 // 10054 // Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA. /// ENST00000246548 // intron // 0 // — // — // —	UBA2	UBA2, Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), q13.11
SNP_A-2082516	acgctgaagccactgal[A/G]atcctgaccagttic	A	G	NM_005499 // intron // 0 // Hs.511739 // UBA2 // 10054 // Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA. /// ENST00000246548 // intron // 0 // — // — // —	UBA2	UBA2, Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), q13.11
SNP_A-2150906	atgtgggacagtacac[A/G]cagagtgttgccaatc	A	G	NM_144779 // downstream // 3058 // Hs.333418 // FXYD5 // 53827 // Homo sapiens FXYD domain containing ion transport regulator 5 (FXYD5), transcript variant 1, mRNA. /// NM_014164 // downstream // 3058 // Hs.333418 // FXYD5 // 53827 // Homo sapiens FXYD do	FXYD5	FXYD5, Homo sapiens FXYD domain containing ion transport regulator 5 (FXYD5), transcript variant 1, q13.12
SNP_A-2072047	acagagtatgatacac[A/G]gtactctctaagctic	A	G	NM_014364 // intron // 0 // Hs.248017 // GAPDS // 26330 // Homo sapiens glyceraldehyde-3-phosphate dehydrogenase, spermatogenic (GAPDS), mRNA. /// ENST00000222286 // intron // 0 // — // — // — // —	GAPDS	GAPDS, Homo sapiens glyceraldehyde-3-phosphate dehydrogenase, spermatogenic (GAPDS), q13.12
SNP_A-1910055	tgtcataaatatcccca[C/T]gcctatctccatata	C	T	NM_032825 // intron // 0 // Hs.138297 // ZNF382 // 84911 // Homo sapiens zinc finger protein 382 (ZNF382), mRNA. /// ENST00000292928 // intron // 0 // — // — // —	ZNF382	ZNF382, Homo sapiens zinc finger protein 382 (ZNF382), q13.12
SNP_A-1803192	gtatcggccttctat[A/C]aggtggctagctggtt	A	C	NM_198539 // downstream // 12762 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 112977 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-1957588	ctgtcatcctcacaaa[A/G]aaatgcaggtgacctt	A	G	NM_198539 // downstream // 21532 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 104207 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-2236764	ctctaccatttttaac[C/T]gcgtaactttgaggcg	C	T	NM_198539 // downstream // 23869 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 101870 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-2185095	cagcttgttcttaa[C/T]gagagtattagtcat	C	T	NM_198539 // downstream // 31476 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 94263 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA.	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-1906169	tggtgaaccaagaaag[C/T]cgtaaatacatggata	C	T	NM_198539 // downstream // 31843 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 93896 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA.	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-1653730	aaaagagattatgcagaatgcaatt[A/C]aaaaagacaaatga gcagatgtaca	A	C	AK093123 // downstream // 34189 // Hs.404220 // ZNF568 // 374900 // zinc finger protein 568 /// NM_144689 // upstream // 93354 // Hs.133437 // FLJ32191 // 147923 // hypothetical protein FLJ32191	ZNF568	ZNF568 , rs1644669, zinc finger protein 568 ,q13.12
SNP_A-1744991	tctgaagagaaaaattactggactg[A/C]aaggtataaaaagag attatgcaga	A	C	AK093123 // downstream // 34223 // Hs.404220 // ZNF568 // 374900 // zinc finger protein 568 /// NM_144689 // upstream // 93320 // Hs.133437 // FLJ32191 // 147923 // hypothetical protein FLJ32191	ZNF568	ZNF568 , rs1644670, zinc finger protein 568 ,q13.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2236221	ctccttgttccttagc[C/T]accagaactgatggag	C	T	NM_198539 // downstream // 37510 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 88229 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA.	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-2103645	agcacagacattaaga[A/C]aaccaggtagcaacag	A	C	NM_198539 // downstream // 72731 // Hs.404220 // ZNF568 // 374900 // Homo sapiens zinc finger protein 568 (ZNF568), mRNA. /// NM_144689 // upstream // 53008 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA.	ZNF568	ZNF568, Homo sapiens zinc finger protein 568 (ZNF568), q13.12
SNP_A-1694765	tagaaacagctgcctttaatgacag[C/G]aagatgtaagacaag tgtttattaa	C	G	AK093123 // downstream // 89893 // Hs.404220 // ZNF568 // 374900 // zinc finger protein 568 /// NM_144689 // upstream // 37650 // Hs.133437 // FLJ32191 // 147923 // hypothetical protein FLJ32191	ZNF568	ZNF568 , rs7246739, zinc finger protein 568 ,q13.13
SNP_A-1758587	tgcatctctctgatccagctgggaa[A/G]gtgttgggaaaaagctg agggttag	A	G	AK093123 // downstream // 114480 // Hs.404220 // ZNF568 // 374900 // zinc finger protein 568 /// NM_144689 // upstream // 13063 // Hs.133437 // FLJ32191 // 147923 // hypothetical protein FLJ32191	ZNF568	ZNF568 , rs1818748, zinc finger protein 568 ,q13.13
SNP_A-1810530	gtgattttccaaccta[C/G]atgataactttattcc	C	G	NM_144689 // intron // 0 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA. /// ENST00000304239 // intron // 0 // — // — // — // — /// ENST00000337995 // intron // 0 // — // — // — // — /// E	FLJ32191	FLJ32191, Homo sapiens hypothetical protein FLJ32191 (FLJ32191), q13.12
SNP_A-2283380	gatacatataacaaaa[A/T]gatcaactagtagagc	A	T	NM_144689 // 3UTR // 0 // Hs.444992 // FLJ32191 // 147923 // Homo sapiens hypothetical protein FLJ32191 (FLJ32191), mRNA. /// ENST00000304239 // intron // 0 // — // — // — // — /// ENST00000337995 // 3UTR // 0 // — // — // — // — /// ENST0	FLJ32191	FLJ32191, Homo sapiens hypothetical protein FLJ32191 (FLJ32191), q13.12
SNP_A-2098459	agagcaatggaattaa[C/T]gtggatgacatcataa	C	T	NM_152279 // upstream // 15971 // Hs.466589 // ZNF585B // 92285 // Homo sapiens zinc finger protein 585B (ZNF585B), mRNA. /// NM_152604 // upstream // 9 // Hs.359656 // ZNF383 // 163087 // Homo sapiens zinc finger protein 383 (ZNF383), mRNA. /// ENST00000	ZNF585B	ZNF585B, Homo sapiens zinc finger protein 585B (ZNF585B), q13.12
SNP_A-2123175	agtggttcagatttac[A/G]agggtaactcaggtga	A	G	NM_152604 // downstream // 89237 // Hs.359656 // ZNF383 // 163087 // Homo sapiens zinc finger protein 383 (ZNF383), mRNA. /// AB013897 // upstream // 1757 // Hs.129165 // HKR1 // 284459 // Homo sapiens mRNA for HKR1, partial cds. /// NM_181786 // upstream	ZNF383	ZNF383, Homo sapiens zinc finger protein 383 (ZNF383), q13.12
SNP_A-2218564	cctggattaaatgtca[A/G]ctgtagctagtgagga	A	G	AB011117 // intron // 0 // Hs.157259 // SIPA1L3 // 23094 // Homo sapiens mRNA for KIAA0545 protein, partial cds. /// ENST00000222345 // intron // 0 // — // — // — // —	SIPA1L3	SIPA1L3, Homo sapiens for KIAA0545 protein, partial cds. ,q13.13
SNP_A-1818757	gttgactggctagtga[C/T]ccttcatgccccagga	C	T	AB011117 // intron // 0 // Hs.157259 // SIPA1L3 // 23094 // Homo sapiens mRNA for KIAA0545 protein, partial cds. /// ENST00000222345 // intron // 0 // — // — // — // —	SIPA1L3	SIPA1L3, Homo sapiens for KIAA0545 protein, partial cds. ,q13.13
SNP_A-2091651	agaaaagaaaagcagg[A/C]attggcgagccagcag	A	C	AB011117 // intron // 0 // Hs.157259 // SIPA1L3 // 23094 // Homo sapiens mRNA for KIAA0545 protein, partial cds. /// ENST00000222345 // intron // 0 // — // — // — // —	SIPA1L3	SIPA1L3, Homo sapiens for KIAA0545 protein, partial cds. ,q13.13
SNP_A-2260999	gaaagaaatgactcta[C/G]acaatgacctgagtca	C	G	AB011117 // intron // 0 // Hs.157259 // SIPA1L3 // 23094 // Homo sapiens mRNA for KIAA0545 protein, partial cds. /// ENST00000222345 // intron // 0 // — // — // — // —	SIPA1L3	SIPA1L3, Homo sapiens for KIAA0545 protein, partial cds. ,q13.13
SNP_A-2216295	cctcctcgaggtgggc[A/G]aagatcacagccggca	A	G	NM_004823 // CDS // 0 // Hs.240395 // KCNK6 // 9424 // Homo sapiens potassium channel, subfamily K, member 6 (KCNK6), mRNA. /// ENST00000263372 // CDS // 0 // — // — // — // —	KCNK6	KCNK6, Homo sapiens potassium channel, subfamily K, member 6 (KCNK6), q13.2
SNP_A-1847752	tatctatttgattagg[C/T]catgaatttaggcgag	C	T	NM_000540 // intron // 0 // Hs.466664 // RYR1 // 6261 // Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA. /// ENST00000359596 // intron // 0 // — // — // — // — /// ENST00000360985 // intron // 0 // — // — // — // — /// ENST00000	RYR1	RYR1, Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2213574	ccgtccaggaatggad[A/G]attcgcttccctgca	A	G	NM_004924 // intron // 0 // Hs.270291 // ACTN4 // 81 // Homo sapiens actinin, alpha 4 (ACTN4), mRNA. /// ENST00000252699 // intron // 0 // --- // --- // ---	ACTN4	ACTN4, Homo sapiens actinin, alpha 4 (ACTN4), q13.2
SNP_A-2041658	aacggaacttaaaaga[A/G]catgtgacccaggaa	A	G	NM_002307 // downstream // 3872 // Hs.99923 // LGALS7 // 3963 // Homo sapiens lectin, galactoside-binding, soluble, 7 (galectin 7) (LGALS7), mRNA. /// NM_006149 // downstream // 6051 // Hs.5302 // LGALS4 // 3960 // Homo sapiens lectin, galactoside-binding	LGALS7	LGALS7, Homo sapiens lectin, galactoside-binding, soluble, 7 (galectin 7) (LGALS7), q13.2
SNP_A-2138153	atccaattctcaatca[A/T]ctgggccctgagtgga	A	T	NM_002503 // intron // 0 // Hs.9731 // NFKBIB // 4793 // Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta (NFKBIB), transcript variant 1, /// NM_001001716 // intron // 0 // Hs.9731 // NFKBIB // 4793 // Homo s	NFKBIB	NFKBIB, Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta (NFKBIB), transcript variant 1, q13.2
SNP_A-1958959	ccigtcgggatgacta[C/T]caaatcctggaaaatt	C	T	NM_153232 // upstream // 56108 // Hs.18949 // CRI2 // 163126 // Homo sapiens CREBBP/EP300 inhibitor 2 (CRI2), mRNA. /// NM_013268 // upstream // 6523 // Hs.23671 // LGALS13 // 29124 // Homo sapiens lectin, galactoside-binding, soluble, 13 (galectin 13) (L	CRI2	CRI2, Homo sapiens CREBBP q13.2
SNP_A-2061127	aatgcacagataaaga[C/T]gatggagtgaggatga	C	T	NM_001828 // intron // 0 // Hs.889 // CLC // 1178 // Homo sapiens Charcot-Leyden crystal protein (CLC), mRNA. /// ENST00000221804 // intron // 0 // --- // --- // ---	CLC	CLC, Homo sapiens Charcot-Leyden crystal protein (CLC), q13.2
SNP_A-1786217	ggctgtgggaacaaa[A/G]atatctcaggcat	A	G	NM_000767 // upstream // 14462 // Hs.1360 // CYP2B6 // 1555 // Homo sapiens cytochrome P450, family 2, subfamily B, polypeptide 6 (CYP2B6), mRNA. /// ENST00000330446 // downstream // 26179 // --- // --- // --- /// ENST00000324071 // upstream // 144	CYP2B6	CYP2B6, Homo sapiens cytochrome P450, family 2, subfamily B, polypeptide 6 (CYP2B6), q13.2
SNP_A-2196426	catgttgatgccatcg[C/T]caagtcctgatcaggt	C	T	NM_018035 // upstream // 7620 // Hs.351099 // FLJ10241 // 55101 // Homo sapiens hypothetical protein FLJ10241 (FLJ10241), mRNA. /// ENST00000221943 // upstream // 7620 // --- // --- // --- /// ENST00000301183 // upstream // 7615 // --- // --- // ---	FLJ10241	FLJ10241, Homo sapiens hypothetical protein FLJ10241 (FLJ10241), q13.2
SNP_A-1784922	ggccttgtggcccaa[C/T]ggtcagtgcctagcga	C	T	NM_002698 // upstream // 39901 // Hs.515429 // POU2F2 // 5452 // Homo sapiens POU domain, class 2, transcription factor 2 (POU2F2), mRNA. /// NM_133328 // downstream // 26271 // Hs.515432 // DEDD2 // 162989 // Homo sapiens death effector domain containing	POU2F2	POU2F2, Homo sapiens POU domain, class 2, transcription factor 2 (POU2F2), q13.2
SNP_A-2152123	attaaaatctttctcc[A/G]actacagaccaccatt	A	G	NM_002784 // intron // 0 // Hs.502092 // PSG9 // 5678 // Homo sapiens pregnancy specific beta-1-glycoprotein 9 (PSG9), mRNA. /// ENST00000291752 // intron // 0 // --- // --- // --- /// ENST00000270077 // intron // 0 // --- // --- // --- ///	PSG9	PSG9, Homo sapiens pregnancy specific beta-1-glycoprotein 9 (PSG9), q13.31
SNP_A-2255154	cttgggttttcaatg[C/G]agattgctaacatgaa	C	G	NM_006297 // intron // 0 // Hs.98493 // XRCC1 // 7515 // Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1), mRNA. /// ENST00000262887 // intron // 0 // --- // --- // --- // ---	XRCC1	XRCC1, Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1), q13.31
SNP_A-2005986	tccacatggccctaga[A/T]acatttcttccttttt	A	T	NM_002659 // intron // 0 // Hs.466871 // PLAUR // 5329 // Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 1, mRNA. /// ENST00000339082 // intron // 0 // --- // --- // --- /// ENST00000221264 // intron // 0 // ---	PLAUR	PLAUR, Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 1, q13.31
SNP_A-2025585	aaaatgaaaacacaaa[G/T]ctcaccattgccaac	G	T	NM_002659 // intron // 0 // Hs.466871 // PLAUR // 5329 // Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 1, mRNA. /// ENST00000339082 // intron // 0 // --- // --- // --- /// ENST00000221264 // intron // 0 // ---	PLAUR	PLAUR, Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 1, q13.31
SNP_A-2068276	acaagcacctcctaaa[C/T]ctcatctttgtctcta	C	T	NM_019108 // intron // 0 // Hs.466875 // FLJ12886 // 56006 // Homo sapiens hypothetical protein FLJ12886 (FLJ12886), mRNA. /// ENST00000222379 // intron // 0 // --- // --- // --- /// ENST00000270066 // intron // 0 // --- // --- // ---	FLJ12886	FLJ12886, Homo sapiens hypothetical protein FLJ12886 (FLJ12886), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1957171	ttttacctcttcagta[A/G]acataaataccatgaaa	A	G	NM_013362 // intron // 0 // Hs.279567 // ZNF225 // 7768 // Homo sapiens zinc finger protein 225 (ZNF225), mRNA. /// ENST00000262894 // intron // 0 // --- // --- // --- // ---	ZNF225	ZNF225, Homo sapiens zinc finger protein 225 (ZNF225), q13.31
SNP_A-2027641	aaaccatatcaatgga[C/T]gaaacaactgagtcac	C	T	NM_152354 // intron // 0 // Hs.515454 // ZNF285 // 26974 // Homo sapiens zinc finger protein 285 (ZNF285), mRNA. /// ENST00000330997 // intron // 0 // --- // --- // --- // ---	ZNF285	ZNF285, Homo sapiens zinc finger protein 285 (ZNF285), q13.31
SNP_A-1877275	tctggaaaatatgaaa[A/C]cttgctcaaccctacc	A	C	X52336 // downstream // 23949 // Hs.381285 // ZNF13 // 7560 // Human Kox5 mRNA for zinc finger protein, partial. /// NM_013256 // upstream // 37961 // Hs.130683 // ZNF180 // 7733 // Homo sapiens zinc finger protein 180 (HHZ168) (ZNF180), mRNA. /// NM_1984	ZNF13	ZNF13, Human Kox5 for zinc finger protein, partial. ,q13.31
SNP_A-2144795	atgatgtcagagactc[A/G]agaatgcgcggctggt	A	G	NM_198541 // downstream // 48077 // Hs.546554 // IGFL1 // 374918 // Homo sapiens insulin growth factor-like family member 1 (IGFL1), mRNA. /// NM_152795 // upstream // 17737 // Hs.420830 // HIF3A // 64344 // Homo sapiens hypoxia inducible factor 3, alpha	IGFL1	IGFL1, Homo sapiens insulin growth factor-like family member 1 (IGFL1), q13.32
SNP_A-2210864	ccccttccttaccctc[A/T]cactaagaacagtggc	A	T	NM_152795 // intron // 0 // Hs.420830 // HIF3A // 64344 // Homo sapiens hypoxia inducible factor 3, alpha subunit (HIF3A), transcript variant 3, mRNA. /// NM_152796 // intron // 0 // Hs.420830 // HIF3A // 64344 // Homo sapiens hypoxia inducible factor 3,	HIF3A	HIF3A, Homo sapiens hypoxia inducible factor 3, alpha subunit (HIF3A), transcript variant 3, q13.32
SNP_A-2033659	aaatatcttccgctac[C/T]cgggagaccccgcggg	C	T	NM_032040 // upstream // 14080 // Hs.97876 // CCDC8 // 83987 // Homo sapiens coiled-coil domain containing 8 (CCDC8), mRNA. /// NM_018215 // downstream // 23257 // Hs.8395 // FLJ10781 // 55228 // Homo sapiens hypothetical protein FLJ10781 (FLJ10781), mRNA	CCDC8	CCDC8, Homo sapiens coiled-coil domain containing 8 (CCDC8), q13.32
SNP_A-1903527	tgggacaactgccaac[A/G]gagtgtcgtaggcgcg	A	G	NM_032040 // upstream // 15995 // Hs.97876 // CCDC8 // 83987 // Homo sapiens coiled-coil domain containing 8 (CCDC8), mRNA. /// NM_018215 // downstream // 21342 // Hs.8395 // FLJ10781 // 55228 // Homo sapiens hypothetical protein FLJ10781 (FLJ10781), mRNA	CCDC8	CCDC8, Homo sapiens coiled-coil domain containing 8 (CCDC8), q13.32
SNP_A-2089221	acttactattacctgg[A/G]catttttccagcctc	A	G	NM_001743 // upstream // 84044 // Hs.468442 // CALM2 // 805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // upstream // 84044 // Hs.282410 // CALM1 // 801 // Homo sapiens calmodulin 1 (phosphorylase kinase, delta	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q13.32
SNP_A-1961665	gagcagatctgtctgg[A/C]aggcatattctcaatc	A	C	NM_001743 // upstream // 69588 // Hs.468442 // CALM2 // 805 // Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA. /// NM_006888 // upstream // 69588 // Hs.282410 // CALM1 // 801 // Homo sapiens calmodulin 1 (phosphorylase kinase, delta	CALM2	CALM2, Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), q13.32
SNP_A-2243557	ctgctattaccgcatc[A/G]ctatgtcagttgaggc	A	G	AB029010 // intron // 0 // Hs.172884 // SLC8A2 // 6543 // Homo sapiens mRNA for KIAA1087 protein, partial cds. /// ENST00000236877 // intron // 0 // --- // --- // --- // ---	SLC8A2	SLC8A2, Homo sapiens for KIAA1087 protein, partial cds. ,q13.32
SNP_A-2173016	cacaaaccttgcccat[C/T]agtcggaatcaatttc	C	T	NM_032255 // upstream // 44753 // Hs.14161 // ZNF541 // 84215 // Homo sapiens zinc finger protein 541 (ZNF541), mRNA. /// NM_015711 // upstream // 89312 // Hs.97244 // GLTSCR1 // 29998 // Homo sapiens glioma tumor suppressor candidate region gene 1 (GLTSC	ZNF541	ZNF541, Homo sapiens zinc finger protein 541 (ZNF541), q13.32
SNP_A-2254533	cttgcgcgtctctctc[A/G]ctgcttattcttcata	A	G	NM_032255 // upstream // 92154 // Hs.14161 // ZNF541 // 84215 // Homo sapiens zinc finger protein 541 (ZNF541), mRNA. /// NM_015711 // upstream // 41911 // Hs.97244 // GLTSCR1 // 29998 // Homo sapiens glioma tumor suppressor candidate region gene 1 (GLTSC	ZNF541	ZNF541, Homo sapiens zinc finger protein 541 (ZNF541), q13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2163944	caaaactcttgattga[C/T]accttgtttcccgtct	C	T	NM_000554 // intron // 0 // Hs.249186 // CRX // 1406 // Homo sapiens cone-rod homeobox (CRX), mRNA. /// ENST00000221996 // intron // 0 // - // — // — // —	CRX	CRX, Homo sapiens cone-rod homeobox (CRX), q13.32
SNP_A-2291073	gcaataagacaaaaaa[A/G]gctgacagcatgccat	A	G	NM_000554 // intron // 0 // Hs.249186 // CRX // 1406 // Homo sapiens cone-rod homeobox (CRX), mRNA. /// ENST00000221996 // intron // 0 // - // — // — // —	CRX	CRX, Homo sapiens cone-rod homeobox (CRX), q13.32
SNP_A-1961674	tatttcctaatctcaa[C/G]ctctttcctcagctcc	C	G	NM_022142 // downstream // 3135 // Hs.104894 // ELSPBP1 // 64100 // Homo sapiens epididymal sperm binding protein 1 (ELSPBP1), mRNA. /// NM_019855 // downstream // 1673 // Hs.117694 // CABP5 // 56344 // Homo sapiens calcium binding protein 5 (CABP5), mRNA	ELSPBP1	ELSPBP1, Homo sapiens epididymal sperm binding protein 1 (ELSPBP1), q13.32
SNP_A-1872159	tctactgaccaagggc[C/T]gccaaactattgccag	C	T	NM_019855 // upstream // 2644 // Hs.117694 // CABP5 // 56344 // Homo sapiens calcium binding protein 5 (CABP5), mRNA. /// NM_003706 // downstream // 1156 // Hs.18858 // PLA2G4C // 8605 // Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-indepe	CABP5	CABP5, Homo sapiens calcium binding protein 5 (CABP5), q13.32
SNP_A-1961676	gtgggtgagtcacgca[C/T]ccttcccacgacttgg	C	T	NM_003706 // intron // 0 // Hs.18858 // PLA2G4C // 8605 // Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA. /// ENST00000354276 // intron // 0 // — // — // — // — /// ENST00000222105 // intron // 0 // —	PLA2G4C	PLA2G4C, Homo sapiens phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), q13.32
SNP_A-1725920	agatgaaggaacccattcaacttga[A/G]attactgaaaaaaga catgggactt	A	G	NM_014959 // CDS // 0 // Hs.446146 // CARD8 // 22900 // caspase recruitment domain family, member 8	CARD8	CARD8 , rs10500299, caspase recruitment domain family, member 8,q13.33
SNP_A-1844258	tagttttaacagcatg[C/G]acctggtctctacaac	C	G	NM_019113 // downstream // 27079 // Hs.283015 // FGF21 // 26291 // Homo sapiens fibroblast growth factor 21 (FGF21), mRNA. /// NM_001190 // downstream // 9660 // Hs.512670 // BCAT2 // 587 // Homo sapiens branched chain aminotransferase 2, mitochondrial (B	FGF21	FGF21, Homo sapiens fibroblast growth factor 21 (FGF21), q13.33
SNP_A-2301476	gcgaactcactcatga[C/T]tacgagaacagcatgg	C	T	NM_019113 // downstream // 27305 // Hs.283015 // FGF21 // 26291 // Homo sapiens fibroblast growth factor 21 (FGF21), mRNA. /// NM_001190 // downstream // 9434 // Hs.512670 // BCAT2 // 587 // Homo sapiens branched chain aminotransferase 2, mitochondrial (B	FGF21	FGF21, Homo sapiens fibroblast growth factor 21 (FGF21), q13.33
SNP_A-1645260	cgtgtcagggtccgcaatcaggtgg[C/T]gaacatcccgtccttc attgtccgc	C	T	NM_021733 // downstream // 20097 // Hs.224210 // TSKS // 60385 // testis-specific kinase substrate /// NM_152359 // downstream // 5926 // Hs.112195 // CPT1C // 126129 // carnitine palmitoyltransferase 1C	TSKS	TSKS , rs3810261, testis-specific kinase substrate ,q13.33
SNP_A-2285102	gatcgtgagtcataaa[A/G]ggcctgcaaatttcat	A	G	NM_032375 // intron // 0 // Hs.515542 // AKT1S1 // 84335 // Homo sapiens AKT1 substrate 1 (proline-rich) (AKT1S1), mRNA. /// ENST00000308692 // intron // 0 // — // — // — // —	AKT1S1	AKT1S1, Homo sapiens AKT1 substrate 1 (proline-rich) (AKT1S1), q13.33
SNP_A-2291356	gcaatggtcaaaaaga[A/G]tccaactgtgcaggct	A	G	NM_004533 // intron // 0 // Hs.85937 // MYBPC2 // 4606 // Homo sapiens myosin binding protein C, fast type (MYBPC2), mRNA. /// ENST00000357701 // intron // 0 // — // — // — // — /// ENST00000270620 // intron // 0 // — // — // — // —	MYBPC2	MYBPC2, Homo sapiens myosin binding protein C, fast type (MYBPC2), q13.33
SNP_A-1854878	tcaacgcgattcgtaa[C/T]gcttcctaattcgtag	C	T	NM_032298 // downstream // 84820 // Hs.515554 // SYT3 // 84258 // Homo sapiens synaptotagmin III (SYT3), mRNA. /// NM_016148 // downstream // 124668 // Hs.274255 // SHANK1 // 50944 // Homo sapiens SH3 and multiple ankyrin repeat domains 1 (SHANK1), mRNA.	SYT3	SYT3, Homo sapiens synaptotagmin III (SYT3), q13.33
SNP_A-2138586	atcccaaactcatccg[A/G]agcacaattttacccc	A	G	NM_023006 // upstream // 20902 // Hs.250770 // KLK15 // 55554 // Homo sapiens kallikrein 15 (KLK15), transcript variant 1, mRNA. /// NM_138564 // upstream // 20902 // Hs.250770 // KLK15 // 55554 // Homo sapiens kallikrein 15 (KLK15), transcript variant 3,	KLK15	KLK15, Homo sapiens kallikrein 15 (KLK15), transcript variant 1, q13.41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1687924	tggaaaagactttctttcctaatga[A/G]gagagctctgccaacag agtctctc	A	G	NM_004917 // upstream // 28705 // Hs.218366 // KLK4 // 9622 // kallikrein 4 (prostase, enamel matrix, prostate) /// NM_012427 // downstream // 3862 // Hs.50915 // KLK5 // 25818 // kallikrein 5	KLK4	KLK4 , rs268914, kallikrein 4 (prostase, enamel matrix, prostate) ,q13.41
SNP_A-2275689	gagacatggaggagca[C/T]gtgggtagctagcatt	C	T	NM_005046 // intron // 0 // Hs.151254 // KLK7 // 5650 // Homo sapiens kallikrein 7 (chymotryptic, stratum corneum) (KLK7), transcript variant 1, mRNA. /// NM_139277 // intron // 0 // Hs.151254 // KLK7 // 5650 // Homo sapiens kallikrein 7 (chymotryptic, st	KLK7	KLK7, Homo sapiens kallikrein 7 (chymotryptic, stratum corneum) (KLK7), transcript variant 1, q13.41
SNP_A-2231258	ctattcagacaattta[C/G]agcatcacggaaccta	C	G	NM_144507 // intron // 0 // Hs.104570 // KLK8 // 11202 // Homo sapiens kallikrein 8 (neuropsin/ovasin) (KLK8), transcript variant 4, mRNA. /// NM_144506 // intron // 0 // Hs.104570 // KLK8 // 11202 // Homo sapiens kallikrein 8 (neuropsin/ovasin) (KLK8), t	KLK8	KLK8, Homo sapiens kallikrein 8 (neuropsin,q13.41
SNP_A-2309731	ggaaaggatacaatac[A/G]cctgacccagctgctc	A	G	NM_145894 // upstream // 4794 // Hs.411572 // KLK12 // 43849 // Homo sapiens kallikrein 12 (KLK12), transcript variant 2, mRNA. /// NM_145895 // upstream // 4794 // Hs.411572 // KLK12 // 43849 // Homo sapiens kallikrein 12 (KLK12), transcript variant 3, m	KLK12	KLK12, Homo sapiens kallikrein 12 (KLK12), transcript variant 2, q13.41
SNP_A-2137120	atcaggattctagatc[A/G]aacctggattatgact	A	G	NM_022046 // intron // 0 // Hs.283925 // KLK14 // 43847 // Homo sapiens kallikrein 14 (KLK14), mRNA. /// ENST00000156499 // intron // 0 // — // — // — // —	KLK14	KLK14, Homo sapiens kallikrein 14 (KLK14), q13.41
SNP_A-2071755	acagacatataagtac[C/T]agttgccaccagaatc	C	T	NM_014441 // downstream // 192 // Hs.245828 // SIGLEC9 // 27180 // Homo sapiens sialic acid binding Ig-like lectin 9 (SIGLEC9), mRNA. /// NM_016543 // upstream // 11806 // Hs.274470 // SIGLEC7 // 27036 // Homo sapiens sialic acid binding Ig-like lectin 7	SIGLEC9	SIGLEC9, Homo sapiens sialic acid binding Ig-like lectin 9 (SIGLEC9), q13.41
SNP_A-2193228	catctcaggtccataa[A/G]aaacacgggagagtcc	A	G	NM_016543 // downstream // 817 // Hs.274470 // SIGLEC7 // 27036 // Homo sapiens sialic acid binding Ig-like lectin 7 (SIGLEC7), mRNA. /// NM_014385 // downstream // 817 // Hs.274470 // SIGLEC7 // 27036 // Homo sapiens sialic acid binding Ig-like lectin 7	SIGLEC7	SIGLEC7, Homo sapiens sialic acid binding Ig-like lectin 7 (SIGLEC7), q13.41
SNP_A-1801609	gtaggtttttctctca[C/T]gtttggagacgaggga	C	T	ENST00000305812 // intron // 0 // — // — // — // — /// ENST00000341811 // intron // 0 // — // — // — // —	-	q13.41
SNP_A-1816512	gttaggtgctgactca[C/T]gagagtgaaaaccaaa	C	T	NM_001772 // downstream // 6319 // Hs.83731 // CD33 // 945 // Homo sapiens CD33 antigen (gp67) (CD33), mRNA. /// NM_173635 // upstream // 17738 // Hs.381087 // FLJ40235 // 284369 // Homo sapiens hypothetical protein FLJ40235 (FLJ40235), mRNA. /// ENST0000	CD33	CD33, Homo sapiens CD33 antigen (gp67) (CD33), q13.41
SNP_A-2135272	atattgtgtccaacta[C/T]ggaagagttcccctac	C	T	NM_001772 // downstream // 19311 // Hs.83731 // CD33 // 945 // Homo sapiens CD33 antigen (gp67) (CD33), mRNA. /// NM_173635 // upstream // 4746 // Hs.381087 // FLJ40235 // 284369 // Homo sapiens hypothetical protein FLJ40235 (FLJ40235), mRNA. /// ENST0000	CD33	CD33, Homo sapiens CD33 antigen (gp67) (CD33), q13.41
SNP_A-1951607	tttcctgtctgaaaac[A/G]cttgctctacaaaaac	A	G	NM_173635 // downstream // 24448 // Hs.381087 // FLJ40235 // 284369 // Homo sapiens hypothetical protein FLJ40235 (FLJ40235), mRNA. /// ENST00000316401 // downstream // 24448 // — // — // — // — /// ENST00000270642 // upstream // 18854 // — // -	FLJ40235	FLJ40235, Homo sapiens hypothetical protein FLJ40235 (FLJ40235), q13.41
SNP_A-2153437	attagagtttacataa[C/T]agccgagctgagaaaa	C	T	NM_033130 // upstream // 26413 // Hs.284813 // SIGLEC10 // 89790 // Homo sapiens sialic acid binding Ig-like lectin 10 (SIGLEC10), mRNA. /// NM_014442 // downstream // 6968 // Hs.447899 // SIGLEC8 // 27181 // Homo sapiens sialic acid binding Ig-like lecti	SIGLEC10	SIGLEC10, Homo sapiens sialic acid binding Ig-like lectin 10 (SIGLEC10), q13.41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2114241	agggaagaggatagaa[A/G]tgtgcataatcatgtg	A	G	NM_001245 // upstream // 29432 // Hs.397255 // SIGLEC6 // 946 // Homo sapiens sialic acid binding Ig-like lectin 6 (SIGLEC6), transcript variant 1, mRNA. /// NM_198846 // upstream // 29478 // Hs.397255 // SIGLEC6 // 946 // Homo sapiens sialic acid binding	SIGLEC6	SIGLEC6, Homo sapiens sialic acid binding Ig-like lectin 6 (SIGLEC6), transcript variant 1, q13.41
SNP_A-2165729	caaagggccaaattac[A/G]agacaaatgaggttcc	A	G	ENST00000360844 // upstream // 45468 // --- // --- // --- // --- /// ENST00000358133 // upstream // 45462 // --- // --- // --- // --- /// ENST00000358634 // upstream // 11842 // --- // --- // --- // ---	-	q13.41
SNP_A-2205467	ccagtggcttagtaaa[C/T]ggagtcacattaaatg	C	T	NM_024840 // downstream // 4757 // Hs.183390 // ZNF613 // 79898 // Homo sapiens zinc finger protein 613 (ZNF613), mRNA. /// NM_021632 // downstream // 13832 // Hs.407694 // ZNF350 // 59348 // Homo sapiens zinc finger protein 350 (ZNF350), mRNA. /// ENST00	ZNF613	ZNF613, Homo sapiens zinc finger protein 613 (ZNF613), q13.41
SNP_A-1922626	ttagacgccccaata[G/T]acagactattttcttt	G	T	NM_024840 // downstream // 8774 // Hs.183390 // ZNF613 // 79898 // Homo sapiens zinc finger protein 613 (ZNF613), mRNA. /// NM_021632 // downstream // 9815 // Hs.407694 // ZNF350 // 59348 // Homo sapiens zinc finger protein 350 (ZNF350), mRNA. /// ENST000	ZNF613	ZNF613, Homo sapiens zinc finger protein 613 (ZNF613), q13.41
SNP_A-1961707	aagcaagattgtgata[C/T]gtttgacttacatgaa	C	T	NM_198480 // CDS // 0 // Hs.368355 // ZNF615 // 284370 // Homo sapiens zinc finger protein 615 (ZNF615), mRNA. /// ENST00000354939 // CDS // 0 // --- // --- // --- // ---	ZNF615	ZNF615, Homo sapiens zinc finger protein 615 (ZNF615), q13.41
SNP_A-2185724	caggagtgggctgata[A/C]aactttgccgtggcag	A	C	NM_025040 // upstream // 1688 // Hs.292336 // ZNF614 // 80110 // Homo sapiens zinc finger protein 614 (ZNF614), mRNA. /// NM_014650 // downstream // 1327 // Hs.178471 // ZNF432 // 9668 // Homo sapiens zinc finger protein 432 (ZNF432), mRNA. /// NM_014650	ZNF614	ZNF614, Homo sapiens zinc finger protein 614 (ZNF614), q13.41
SNP_A-1818699	gttgacaatctatatc[A/G]atttgacagctttcta	A	G	NM_014650 // intron // 0 // Hs.178471 // ZNF432 // 9668 // Homo sapiens zinc finger protein 432 (ZNF432), mRNA. /// ENST00000221315 // intron // 0 // --- // --- // --- // --- /// ENST00000301097 // intron // 0 // --- // --- // --- // ---	ZNF432	ZNF432, Homo sapiens zinc finger protein 432 (ZNF432), q13.41
SNP_A-2101385	agatctgtgaaaagtc[A/C]atttctgctgtttaaa	A	C	ENST00000359973 // upstream // 3610 // --- // --- // --- // --- /// ENST00000328244 // downstream // 43866 // --- // --- // --- // ---	-	q13.41
SNP_A-1899164	tggaaagtgacgatca[A/G]agaggtaaagacacct	A	G	NM_014225 // intron // 0 // Hs.467192 // PPP2R1A // 5518 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA. /// ENST00000322088 // intron // 0 // --- // --- // --- // ---	PPP2R1A	PPP2R1A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), q13.41
SNP_A-2191746	catatttaaatcgccc[A/G]atagaatggaatcaag	A	G	NM_014225 // intron // 0 // Hs.467192 // PPP2R1A // 5518 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA. /// ENST00000322088 // intron // 0 // --- // --- // --- // --- /// ENST00000361107 /	PPP2R1A	PPP2R1A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), q13.41
SNP_A-1862491	tcatgtttagatatga[A/T]aatgaacatatttaaa	A	T	NM_014225 // downstream // 41708 // Hs.467192 // PPP2R1A // 5518 // Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA. /// ENST00000322088 // downstream // 41708 // --- // --- // --- // --- /// E	PPP2R1A	PPP2R1A, Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), q13.41
SNP_A-1912671	tgtgccttaaatgaga[A/G]gaaatcgatctgatgt	A	G	NM_173530 // downstream // 3598 // Hs.357663 // ZNF610 // 162963 // Homo sapiens zinc finger protein 610 (ZNF610), mRNA. /// NM_032423 // upstream // 27503 // Hs.531612 // ZNF528 // 84436 // Homo sapiens zinc finger protein 528 (ZNF528), mRNA. /// ENST000	ZNF610	ZNF610, Homo sapiens zinc finger protein 610 (ZNF610), q13.41
SNP_A-1909519	tgtatttcagttctta[C/T]agtgtgtgctgatttt	C	T	NM_032423 // downstream // 71964 // Hs.531612 // ZNF528 // 84436 // Homo sapiens zinc finger protein 528 (ZNF528), mRNA. /// NM_152472 // upstream // 20593 // Hs.502318 // ZNF578 // 147660 // Homo sapiens zinc finger protein 578 (ZNF578), mRNA. /// ENST00	ZNF528	ZNF528, Homo sapiens zinc finger protein 528 (ZNF528), q13.41

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175658	cacatggtgtgttttg[A/C]acatttttctgggagt	A	C	NM_032423 // downstream // 79643 // Hs.531612 // ZNF528 // 84436 // Homo sapiens zinc finger protein 528 (ZNF528), mRNA. /// NM_152472 // upstream // 12914 // Hs.502318 // ZNF578 // 147660 // Homo sapiens zinc finger protein 578 (ZNF578), mRNA. /// ENST00	ZNF528	ZNF528, Homo sapiens zinc finger protein 528 (ZNF528), q13.41
SNP_A-1961716	ctcagctcaatgcaaa[A/C]cttggcctcctgggtt	A	C	ENST00000360272 // upstream // 1535 // — // — // — // — /// ENST00000331416 // downstream // 73040 // — // — // — // —	-	q13.41
SNP_A-1876091	tctgaatttcaatggc[C/T]aagaatagtccaacag	C	T	NM_024924 // upstream // 32178 // Hs.270435 // FLJ12985 // 79986 // Homo sapiens hypothetical protein FLJ12985 (FLJ12985), mRNA. /// NM_207394 // upstream // 6788 // Hs.515586 // FLJ45949 // 388560 // Homo sapiens FLJ45949 protein (FLJ45949), mRNA. /// EN	FLJ12985	FLJ12985, Homo sapiens hypothetical protein FLJ12985 (FLJ12985), q13.41
SNP_A-1961720	acactgaaaacacata[G/T]caggccaatgctgtgt	G	T	NM_024924 // upstream // 34878 // Hs.270435 // FLJ12985 // 79986 // Homo sapiens hypothetical protein FLJ12985 (FLJ12985), mRNA. /// NM_207394 // upstream // 4088 // Hs.515586 // FLJ45949 // 388560 // Homo sapiens FLJ45949 protein (FLJ45949), mRNA. /// EN	FLJ12985	FLJ12985, Homo sapiens hypothetical protein FLJ12985 (FLJ12985), q13.41
SNP_A-2247575	ctgtcttaaggcctgc[A/G]atctcaactcaggagg	A	G	NM_024733 // intron // 0 // Hs.117270 // FLJ14345 // 79788 // Homo sapiens hypothetical protein FLJ14345 (FLJ14345), mRNA. /// ENST00000357130 // intron // 0 // — // — // — // — /// ENST00000360729 // intron // 0 // — // — // — // —	FLJ14345	FLJ14345, Homo sapiens hypothetical protein FLJ14345 (FLJ14345), q13.42
SNP_A-1816994	gttatttaatcaaata[C/T]tagtatggaatgaggc	C	T	ENST00000324257 // downstream // 4686 // — // — // — // — /// ENST00000355509 // upstream // 9196 // — // — // — // —	-	q13.42
SNP_A-2006041	aaaaagttgacaggta[G/T]tacagaacgatatgat	G	T	NM_001004301 // CDS // 0 // Hs.515897 // FLJ16542 // 126017 // Homo sapiens FLJ16542 protein (FLJ16542), mRNA. /// ENST00000334095 // CDS // 0 // — // — // — // —	FLJ16542	FLJ16542, Homo sapiens FLJ16542 protein (FLJ16542), q13.42
SNP_A-1910764	tgtcggattttaggag[C/G]ctcactacagagggca	C	G	NM_001004301 // downstream // 9488 // Hs.515897 // FLJ16542 // 126017 // Homo sapiens FLJ16542 protein (FLJ16542), mRNA. /// NM_138372 // upstream // 20393 // Hs.190394 // LOC91661 // 91661 // Homo sapiens hypothetical protein BC001610 (LOC91661), mRNA. /	FLJ16542	FLJ16542, Homo sapiens FLJ16542 protein (FLJ16542), q13.42
SNP_A-2078672	accattagtccaaaga[C/T]gctaaacccaaggact	C	T	NM_033297 // downstream // 165219 // Hs.367965 // NALP12 // 91662 // Homo sapiens NACHT, leucine rich repeat and PYD containing 12 (NALP12), mRNA. /// NM_144687 // downstream // 165219 // Hs.367965 // NALP12 // 91662 // Homo sapiens NACHT, leucine rich re	NALP12	NALP12, Homo sapiens NACHT, leucine rich repeat and PYD containing 12 (NALP12), q13.42
SNP_A-1885577	tgacacagcagggtca[C/T]gttctctcctgaggcc	C	T	NM_006864 // CDS // 0 // Hs.515601 // LILRB3 // 11025 // Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA. /// ENST00000245620 // CDS // 0 // — // — // — // — /// ENST00000346401	LILRB3	LILRB3, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), q13.42
SNP_A-1821561	gtttgtaggatgtaaa[A/G]taagagagtgagagag	A	G	NM_006864 // intron // 0 // Hs.515601 // LILRB3 // 11025 // Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA. /// ENST00000245620 // intron // 0 // — // — // — // —	LILRB3	LILRB3, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), q13.42
SNP_A-1871847	tctacaataaaaccat[C/G]aatctcaaatcattgg	C	G	NM_006865 // upstream // 10828 // Hs.113277 // LILRA3 // 11026 // Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3 (LILRA3), mRNA. /// NM_181985 // downstream // 3260 // Hs.512233 // LIR9 // 353514 // Homo sap	LILRA3	LILRA3, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3 (LILRA3), q13.42
SNP_A-1938983	ttgagtcatagctaaa[A/G]tgtggtttcagataaa	A	G	NM_033206 // downstream // 12917 // Hs.288520 // FLJ00060 // 90011 // Homo sapiens hypothetical gene FLJ00060 (FLJ00060), mRNA. /// NM_006866 // upstream // 17405 // Hs.546340 // LILRA2 // 11027 // Homo sapiens leukocyte immunoglobulin-like receptor, subf	FLJ00060	FLJ00060, Homo sapiens hypothetical gene FLJ00060 (FLJ00060), q13.42

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1902362	tggcccattcttaaggt[C/T]cagcaattaagctcca	C	T	NM_006669 // downstream // 17742 // Hs.149924 // LILRB1 // 10859 // Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 (LILRB1), mRNA. /// NM_006847 // upstream // 7731 // Hs.67846 // LILRB4 // 11006 // H	LILRB1	LILRB1, Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1 (LILRB1), q13.42
SNP_A-1861897	tcatgaaggtgatgaa[A/G]gctacaaatatgtttt	A	G	NM_003180 // intron // 0 // Hs.23179 // SYT5 // 6861 // Homo sapiens synaptotagmin V (SYT5), mRNA. /// ENST00000336739 // intron // 0 // --- // --- // --- /// ENST00000354308 // intron // 0 // --- // --- // ---	SYT5	SYT5, Homo sapiens synaptotagmin V (SYT5), q13.42
SNP_A-2220764	ccttgagtaggtatcc[C/T]ctcacctatggaggcc	C	T	NM_145007 // downstream // 531 // Hs.375039 // NALP11 // 204801 // Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), mRNA. /// ENST00000341750 // downstream // 11712 // --- // --- // --- /// ENST00000360133 // downstream // 53	NALP11	NALP11, Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), q13.42
SNP_A-1723992	gtcttctccagagaaagaaaaaga[C/T]cacgttatcctagg ggaacctct	C	T	NM_145007 // intron // 0 // Hs.375039 // NALP11 // 204801 // NACHT, leucine rich repeat and PYD containing 11	NALP11	NALP11, rs7254875, NACHT, leucine rich repeat and PYD containing 11,q13.42
SNP_A-1712609	cactcagatgtgtctatcagaata[C/T]ggaatcaccagctacttt aatggat	C	T	NM_145007 // intron // 0 // Hs.375039 // NALP11 // 204801 // NACHT, leucine rich repeat and PYD containing 11	NALP11	NALP11, rs10500321, NACHT, leucine rich repeat and PYD containing 11,q13.42
SNP_A-1946070	ttgttttccactgggat[A/G]cagtcatgtaagtac	A	G	NM_145007 // intron // 0 // Hs.375039 // NALP11 // 204801 // Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), mRNA. /// ENST00000360133 // intron // 0 // --- // --- // --- /// ENST00000308725 // intron // 0 // --- // --- // -	NALP11	NALP11, Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), q13.43
SNP_A-2234909	ctccatggtgaccctt[C/T]aaatgtcagtagcagg	C	T	NM_145007 // intron // 0 // Hs.375039 // NALP11 // 204801 // Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), mRNA. /// ENST00000360133 // intron // 0 // --- // --- // --- /// ENST00000308725 // intron // 0 // --- // --- // -	NALP11	NALP11, Homo sapiens NACHT, leucine rich repeat and PYD containing 11 (NALP11), q13.43
SNP_A-2255596	cttgtggtccttgaat[A/G]atcactgtacgtggct	A	G	NM_134444 // CDS // 0 // Hs.351637 // NALP4 // 147945 // Homo sapiens NACHT, leucine rich repeat and PYD containing 4 (NALP4), mRNA. /// ENST00000301295 // CDS // 0 // --- // --- // --- /// ENST00000346986 // CDS // 0 // --- // --- // ---	NALP4	NALP4, Homo sapiens NACHT, leucine rich repeat and PYD containing 4 (NALP4), q13.43
SNP_A-1893355	tgcagcagaaatagaa[C/T]gtgtacaggaacctat	C	T	NM_134444 // CDS // 0 // Hs.351637 // NALP4 // 147945 // Homo sapiens NACHT, leucine rich repeat and PYD containing 4 (NALP4), mRNA. /// ENST00000301295 // CDS // 0 // --- // --- // --- /// ENST00000346986 // CDS // 0 // --- // --- // ---	NALP4	NALP4, Homo sapiens NACHT, leucine rich repeat and PYD containing 4 (NALP4), q13.43
SNP_A-2170994	caatacaaaagctgct[A/G]acacaagtaaacagtg	A	G	NM_176810 // intron // 0 // Hs.446924 // NALP13 // 126204 // Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), mRNA. /// ENST00000342929 // intron // 0 // --- // --- // ---	NALP13	NALP13, Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), q13.43
SNP_A-1961745	ccagccatgcagggga[C/T]gataaaagctcagcag	C	T	NM_176810 // intron // 0 // Hs.446924 // NALP13 // 126204 // Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), mRNA. /// ENST00000342929 // intron // 0 // --- // --- // ---	NALP13	NALP13, Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), q13.43
SNP_A-1910786	tgtcgtctaagccac[C/G]aaattcatggtaaatt	C	G	NM_176810 // upstream // 11211 // Hs.446924 // NALP13 // 126204 // Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), mRNA. /// NM_176811 // upstream // 4310 // Hs.446925 // NALP8 // 126205 // Homo sapiens NACHT, leucine rich repeat a	NALP13	NALP13, Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), q13.43
SNP_A-2306136	gctggaggcttgtaca[C/T]tgggtcatgaaagac	C	T	NM_176810 // upstream // 11770 // Hs.446924 // NALP13 // 126204 // Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), mRNA. /// NM_176811 // upstream // 3751 // Hs.446925 // NALP8 // 126205 // Homo sapiens NACHT, leucine rich repeat a	NALP13	NALP13, Homo sapiens NACHT, leucine rich repeat and PYD containing 13 (NALP13), q13.43
SNP_A-2125148	agttggcccaatttta[C/T]gcatggattatgagga	C	T	NM_021216 // downstream // 30805 // Hs.301431 // ZNF71 // 58491 // Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), mRNA. /// ENST00000328070 // downstream // 30805 // --- // --- // --- /// ENST00000342088 // downstream // 10023 // --- // ---	ZNF71	ZNF71, Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), q13.43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2105445	agccaacagtacttgc[C/T]gatgtcttgaatgtgg	C	T	NM_021216 // downstream // 31801 // Hs.301431 // ZNF71 // 58491 // Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), mRNA. /// ENST00000328070 // downstream // 31801 // — // — // — // — /// ENST00000342088 // downstream // 9027 // — // — //	ZNF71	ZNF71, Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), q13.43
SNP_A-2272174	gacctaatttcattga[C/T]gacagaagtatccact	C	T	NM_021216 // downstream // 36077 // Hs.301431 // ZNF71 // 58491 // Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), mRNA. /// ENST00000328070 // downstream // 36077 // — // — // — // — /// ENST00000342088 // downstream // 4751 // — // — //	ZNF71	ZNF71, Homo sapiens zinc finger protein 71 (Cos26) (ZNF71), q13.43
SNP_A-1961760	tgtttcttcatttgtc[C/T]atgcattaaccattga	C	T	NM_015363 // upstream // 133453 // Hs.201776 // ZIM2 // 23619 // Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /// NM_006210 // upstream // 133464 // Hs.201776 // PEG3 // 5178 // Homo sapiens paternally expressed 3 (PEG3), mRNA. /// NM_020903 // ups	ZIM2	ZIM2, Homo sapiens zinc finger, imprinted 2 (ZIM2), q13.43
SNP_A-1850395	tatgtttgcagattca[G/T]aaagtgcaaggtgcag	G	T	NM_015363 // upstream // 181098 // Hs.201776 // ZIM2 // 23619 // Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /// NM_006210 // upstream // 181109 // Hs.201776 // PEG3 // 5178 // Homo sapiens paternally expressed 3 (PEG3), mRNA. /// NM_020903 // ups	ZIM2	ZIM2, Homo sapiens zinc finger, imprinted 2 (ZIM2), q13.43
SNP_A-2022445	aaaaatatcttcatga[C/T]gttggaataggcaaat	C	T	NM_015363 // upstream // 188786 // Hs.201776 // ZIM2 // 23619 // Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /// NM_006210 // upstream // 188797 // Hs.201776 // PEG3 // 5178 // Homo sapiens paternally expressed 3 (PEG3), mRNA. /// NM_020903 // ups	ZIM2	ZIM2, Homo sapiens zinc finger, imprinted 2 (ZIM2), q13.43
SNP_A-2021972	aaaaagaacaaaaaaa[A/G]ttgctattctggccct	A	G	NM_015363 // upstream // 261523 // Hs.201776 // ZIM2 // 23619 // Homo sapiens zinc finger, imprinted 2 (ZIM2), mRNA. /// NM_006210 // upstream // 261534 // Hs.201776 // PEG3 // 5178 // Homo sapiens paternally expressed 3 (PEG3), mRNA. /// NM_020903 // ups	ZIM2	ZIM2, Homo sapiens zinc finger, imprinted 2 (ZIM2), q13.43
SNP_A-1837997	tagaaagcccagaaaa[C/T]ctagctaaccgaatc	C	T	NM_020633 // downstream // 5574 // Hs.534474 // VN1R1 // 57191 // Homo sapiens vomeronasal 1 receptor 1 (VN1R1), mRNA. /// ENST00000334181 // downstream // 4366 // — // — // — // — /// ENST00000321039 // downstream // 5574 // — // — // — //	VN1R1	VN1R1, Homo sapiens vomeronasal 1 receptor 1 (VN1R1), q13.43
SNP_A-2066738	acaaaagacatctcca[A/T]tgattgcacagcacag	A	T	ENST00000356584 // CDS // 0 // — // — // — // — /// ENST00000291809 // CDS // 0 // — // — // — // —	-	q13.43
SNP_A-1844431	tataaactgtcagtaa[G/T]gtgaagaaatggaaaa	G	T	NM_024691 // downstream // 191 // Hs.98593 // ZNF419 // 79744 // Homo sapiens hypothetical protein FLJ23233 (FLJ23233), mRNA. /// NM_198542 // downstream // 191 // Hs.230260 // MGC4728 // 374928 // Homo sapiens similar to hypothetical protein FLJ23233 (MG	ZNF419	ZNF419, Homo sapiens hypothetical protein FLJ23233 (FLJ23233), q13.43
SNP_A-1902561	tggccttgtgttgtcg[C/G]ataggatcagaacctg	C	G	NM_153231 // intron // 0 // Hs.180257 // ZNF550 // 162972 // Homo sapiens zinc finger protein 550 (ZNF550), mRNA. /// ENST00000325134 // intron // 0 // — // — // — // — /// ENST00000344222 // intron // 0 // — // — // — // —	ZNF550	ZNF550, Homo sapiens zinc finger protein 550 (ZNF550), q13.43
SNP_A-2293249	gcagagcttgaggaag[G/T]ataattattgttgttt	G	T	NM_021089 // intron // 0 // Hs.2077 // ZNF8 // 7554 // Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), mRNA. /// ENST00000355486 // intron // 0 // — // — // — // — /// ENST00000196548 // intron // 0 // — // — // — // —	ZNF8	ZNF8, Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), q13.43
SNP_A-1893575	tgcaggctttgaagac[A/G]ggcaaagggccatgag	A	G	NM_021089 // intron // 0 // Hs.2077 // ZNF8 // 7554 // Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), mRNA. /// ENST00000355486 // intron // 0 // — // — // — // — /// ENST00000196548 // intron // 0 // — // — // — // —	ZNF8	ZNF8, Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), q13.43
SNP_A-2006075	agggctcctgttttac[A/G]agaaaaatgcttcttt	A	G	NM_021089 // intron // 0 // Hs.2077 // ZNF8 // 7554 // Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), mRNA. /// ENST00000355486 // intron // 0 // — // — // — // — /// ENST00000196548 // intron // 0 // — // — // — // —	ZNF8	ZNF8, Homo sapiens zinc finger protein 8 (clone HF.18) (ZNF8), q13.43

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2286176	gatgcaggggggcggca[A/G]ggttcgtgacagaata	A	G	NM_005762 // CDS // 0 // Hs.467408 // TRIM28 // 10155 // Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA. /// ENST00000253024 // CDS // 0 // — // — // — /// ENST00000341753 // CDS // 0 // — // — // — ///	TRIM28	TRIM28, Homo sapiens tripartite motif-containing 28 (TRIM28), q13.43
SNP_A-1967425	ggtcaccagtaatatc[A/G]agacttctatagcttc	A	G	NM_080831 // downstream // 10230 // Hs.112087 // DEFB129 // 140881 // Homo sapiens defensin, beta 129 (DEFB129), mRNA. /// NM_207469 // upstream // 17620 // Hs.516819 // DEFB32 // 400830 // Homo sapiens KFLL827 (UNQ827), mRNA. /// ENST00000246105 // downs	DEFB129	DEFB129, Homo sapiens defensin, beta 129 (DEFB129), p13
SNP_A-1822233	gtttgcaaaagcttc[A/G]gaaagaaattatggct	A	G	NM_144628 // upstream // 10264 // Hs.203514 // TBC1D20 // 128637 // Homo sapiens chromosome 20 open reading frame 140 (C20orf140), mRNA. /// NM_177560 // downstream // 9879 // Hs.446484 // CSNK2A1 // 1457 // Homo sapiens casein kinase 2, alpha 1 polypepti	TBC1D20	TBC1D20, Homo sapiens chromosome 20 open reading frame 140 (C20orf140), p13
SNP_A-1655167	tggacacaatttaagg[A/G]agaaaaatagtgaagca	A	G	NM_031424 // intron // 0 // Hs.19002 // C20orf55 // 83541 // chromosome 20 open reading frame 55	C20orf55	C20orf55, rs1114734, chromosome 20 open reading frame 55,p13
SNP_A-1967436	catgagctcatactga[C/T]caaacaaaccacccaa	C	T	NM_033409 // upstream // 57747 // Hs.283865 // C20orf54 // 113278 // Homo sapiens chromosome 20 open reading frame 54 (C20orf54), mRNA. /// ENST00000217256 // upstream // 57747 // — // — // — /// ENST00000217256 // downstream // 13212 // —	C20orf54	C20orf54, Homo sapiens chromosome 20 open reading frame 54 (C20orf54), p13
SNP_A-2292168	gcacccatctctacaga[C/T]gaaaccgtgaagggac	C	T	NM_015985 // intron // 0 // Hs.278973 // ANGPT4 // 51378 // Homo sapiens angiopoietin 4 (ANGPT4), mRNA. /// ENST00000262924 // intron // 0 // — // — // — // —	ANGPT4	ANGPT4, Homo sapiens angiopoietin 4 (ANGPT4), p13
SNP_A-2121949	agtgagtagctacaac[A/G]ctatgctgagtcccat	A	G	NM_015985 // intron // 0 // Hs.278973 // ANGPT4 // 51378 // Homo sapiens angiopoietin 4 (ANGPT4), mRNA. /// ENST00000262924 // intron // 0 // — // — // — // —	ANGPT4	ANGPT4, Homo sapiens angiopoietin 4 (ANGPT4), p13
SNP_A-1929897	ttcatctttaaaaccc[A/G]atgactgcaatttccaa	A	G	NM_018354 // upstream // 14120 // Hs.516834 // C20orf46 // 55321 // Homo sapiens chromosome 20 open reading frame 46 (C20orf46), mRNA. /// ENST00000246097 // upstream // 14120 // — // — // — // — /// ENST00000246108 // upstream // 29861 // — //	C20orf46	C20orf46, Homo sapiens chromosome 20 open reading frame 46 (C20orf46), p13
SNP_A-1886630	tgactccatcgtgaaa[C/T]aagcaagacccattcc	C	T	NM_018354 // upstream // 30415 // Hs.516834 // C20orf46 // 55321 // Homo sapiens chromosome 20 open reading frame 46 (C20orf46), mRNA. /// ENST00000246097 // upstream // 30415 // — // — // — // — /// ENST00000246108 // upstream // 13566 // — //	C20orf46	C20orf46, Homo sapiens chromosome 20 open reading frame 46 (C20orf46), p13
SNP_A-2265819	gaaggaacttcacccat[A/T]ctgcaggaggtaactg	A	T	NM_178460 // downstream // 13692 // Hs.339789 // PTPNS1L2 // 128646 // Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), mRNA. /// ENST00000359801 // upstream // 29169 // — // — // — // — /// ENST00000002461	PTPNS1L2	PTPNS1L2, Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), p13
SNP_A-2176172	caccaccttgaaaca[C/T]gcttctaaactcacc	C	T	NM_178460 // downstream // 13510 // Hs.339789 // PTPNS1L2 // 128646 // Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), mRNA. /// ENST00000359801 // upstream // 29351 // — // — // — // — /// ENST00000002461	PTPNS1L2	PTPNS1L2, Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), p13
SNP_A-2167454	caacatatagcagaga[G/T]aagtcattctgtacc	G	T	NM_178460 // intron // 0 // Hs.339789 // PTPNS1L2 // 128646 // Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), mRNA. /// ENST00000246102 // intron // 0 // — // — // — // —	PTPNS1L2	PTPNS1L2, Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), p13
SNP_A-2228180	ctactcaaacagcaaa[G/T]cctatagttgggttgc	G	T	NM_178460 // upstream // 3920 // Hs.339789 // PTPNS1L2 // 128646 // Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), mRNA. /// NM_006065 // downstream // 1621 // Hs.134565 // SIRPB1 // 10326 // Homo sapiens signa	PTPNS1L2	PTPNS1L2, Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1-like 2 (PTPNS1L2), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1726910	ggcagacacagttctggcaactgag[A/G]atacagataatcctc ccccaccccc	A	G	NM_006065 // downstream // 502 // Hs.194784 // SIRPB1 // 10326 // signal-regulatory protein beta 1 /// NM_178460 // upstream // 4723 // Hs.339789 // PTPNS1L2 // 128646 // protein tyrosine phosphatase, non-receptor type substrate 1-like 2	SIRPB1	SIRPB1 , rs3848788, signal-regulatory protein beta 1 ,p13
SNP_A-2259273	gaaaaagaaatttgca[A/T]ggaaatgtgatgactt	A	T	NM_006065 // upstream // 1564 // Hs.134565 // SIRPB1 // 10326 // Homo sapiens signal-regulatory protein beta 1 (SIRPB1), mRNA. /// NM_080816 // downstream // 7592 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), tr	SIRPB1	SIRPB1, Homo sapiens signal-regulatory protein beta 1 (SIRPB1), p13
SNP_A-1754312	acatggagagattgctgaatatcga[A/C]ccatcctacattcctg ggataaat	A	C	NM_018556 // upstream // 24597 // Hs.50716 // SIRPB2 // 55423 // signal-regulatory protein beta 2 /// NM_080792 // upstream // 212426 // Hs.156114 // PTPNS1 // 140885 // protein tyrosine phosphatase, non-receptor type substrate 1 /// NM_080816 // upstrea	SIRPB2	SIRPB2 , rs202548, signal-regulatory protein beta 2 ,p13
SNP_A-1679304	gaatcactctaagatggtcatgaaa[A/T]tttcacttggaaaggca tgtggaat	A	T	NM_018556 // upstream // 43207 // Hs.50716 // SIRPB2 // 55423 // signal-regulatory protein beta 2 /// NM_080792 // upstream // 193816 // Hs.156114 // PTPNS1 // 140885 // protein tyrosine phosphatase, non-receptor type substrate 1 /// NM_080816 // upstrea	SIRPB2	SIRPB2 , rs1438101, signal-regulatory protein beta 2 ,p13
SNP_A-1791966	gggtggaaaatgttca[A/G]tcatctgaaggaccta	A	G	NM_080816 // upstream // 201006 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 // upstream // 201006 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory prot	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-1897821	tgctggcatgagic[C/T]ctgcttgagggtttat	C	T	NM_080816 // upstream // 206378 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 // upstream // 206378 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory prot	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-2115287	aggggactcaggtggg[A/G]cattaagagcatctgc	A	G	NM_080816 // upstream // 206456 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 // upstream // 206456 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory prot	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-1903006	tggctggctgaataaa[C/T]gctcggatgctcttca	C	T	NM_080816 // upstream // 218131 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA. /// NM_018556 // upstream // 218131 // Hs.50716 // SIRPB2 // 55423 // Homo sapiens signal-regulatory prot	SIRPB2	SIRPB2, Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, p13
SNP_A-2124065	agttactaaattgtga[C/T]atggaagacagcaaaa	C	T	NM_080792 // downstream // 19613 // Hs.128846 // PTPNS1 // 140885 // Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA. /// NM_024411 // downstream // 19258 // Hs.22584 // PDYN // 5173 // Homo sapiens prodynorphin (PD	PTPNS1	PTPNS1, Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), p13
SNP_A-2210610	cccctattaaatcccat[A/G]tcaggttgtgagaag	A	G	NM_024411 // upstream // 13323 // Hs.22584 // PDYN // 5173 // Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 95494 // Hs.100057 // STK35 // 140901 // Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// ENST00000217305 // upstr	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13
SNP_A-2136057	atcaaggtctggttaa[C/T]tgcagagcctgctccc	C	T	NM_024411 // upstream // 13680 // Hs.22584 // PDYN // 5173 // Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 95137 // Hs.100057 // STK35 // 140901 // Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// ENST00000217305 // upstr	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1804657	gtcaggaccccccttа[C/T]atgctgttagagaacc	C	T	NM_024411 // upstream // 14681 // Hs.22584 // PDYN // 5173 // Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 94136 // Hs.100057 // STK35 // 140901 // Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// ENST00000217305 // upstr	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13
SNP_A-2181460	cagactggtaatata[A/G]ggagactctacttcta	A	G	NM_024411 // upstream // 18350 // Hs.22584 // PDYN // 5173 // Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 90467 // Hs.100057 // STK35 // 140901 // Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// ENST00000217305 // upstr	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13
SNP_A-2099519	agagggctcgctgtaa[C/T]gttacactgcttagc	C	T	NM_024411 // upstream // 102754 // Hs.22584 // PDYN // 5173 // Homo sapiens prodynorphin (PDYN), mRNA. /// NM_080836 // upstream // 6063 // Hs.100057 // STK35 // 140901 // Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// ENST00000217305 // upstr	PDYN	PDYN, Homo sapiens prodynorphin (PDYN), p13
SNP_A-2060360	aatgaatgaataaaca[C/G]tgcaaatgcataaata	C	G	NM_080836 // downstream // 63320 // Hs.100057 // STK35 // 140901 // Homo sapiens serine/threonine kinase 35 (STK35), mRNA. /// NM_003245 // upstream // 84159 // Hs.2022 // TGM3 // 7053 // Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-g	STK35	STK35, Homo sapiens serine,p13
SNP_A-1667302	tgccaatatttatacgtatactaa[A/G]taacagccccagtgctgg agagtgg	A	G	NM_003245 // upstream // 105045 // Hs.2022 // TGM3 // 7053 // transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) /// NM_080836 // downstream // 73606 // Hs.100057 // STK35 // 140901 // serine/threonine kinase 35	TGM3	TGM3, rs6132407, transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase), p13
SNP_A-1869490	tcctgttaaaccatccf[C/T]agacatatgcagtcat	C	T	NM_198994 // intron // 0 // Hs.452039 // TGM6 // 343641 // Homo sapiens transglutaminase 6 (TGM6), mRNA. /// ENST00000202625 // intron // 0 // – // — // — // —	TGM6	TGM6, Homo sapiens transglutaminase 6 (TGM6), p13
SNP_A-2166254	caaatcatgtattgaa[C/T]ggataaagcactctca	C	T	NM_198994 // intron // 0 // Hs.452039 // TGM6 // 343641 // Homo sapiens transglutaminase 6 (TGM6), mRNA. /// ENST00000202625 // intron // 0 // – // — // — // —	TGM6	TGM6, Homo sapiens transglutaminase 6 (TGM6), p13
SNP_A-1904978	tgggtcaaaagcctca[G/T]ataaataatgatagcta	G	T	NM_198994 // intron // 0 // Hs.452039 // TGM6 // 343641 // Homo sapiens transglutaminase 6 (TGM6), mRNA. /// ENST00000202625 // intron // 0 // – // — // — // —	TGM6	TGM6, Homo sapiens transglutaminase 6 (TGM6), p13
SNP_A-2175830	cacatttaagcactta[A/G]taaacatctctggcct	A	G	NM_198994 // intron // 0 // Hs.452039 // TGM6 // 343641 // Homo sapiens transglutaminase 6 (TGM6), mRNA. /// ENST00000202625 // intron // 0 // – // — // — // —	TGM6	TGM6, Homo sapiens transglutaminase 6 (TGM6), p13
SNP_A-1710836	ataggcatgactgattaaatcatag[A/G]ccttaggtgataaactc aatcttca	A	G	NM_003091 // downstream // 51401 // Hs.83753 // SNRPB // 6628 // small nuclear ribonucleoprotein polypeptides B and B1 /// NM_003245 // downstream // 69156 // Hs.2022 // TGM3 // 7053 // transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamylt	SNRPB	SNRPB, rs4053458, small nuclear ribonucleoprotein polypeptides B and B1, p13
SNP_A-2007208	aggatgatatacagat[C/G]aaatgccaggtgattt	C	G	NM_198216 // intron // 0 // Hs.83753 // SNRPB // 6628 // Homo sapiens small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB), transcript variant 1, mRNA. /// NM_003091 // intron // 0 // Hs.83753 // SNRPB // 6628 // Homo sapiens small nuclear ribonu	SNRPB	SNRPB, Homo sapiens small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB), transcript variant 1, p13
SNP_A-1929846	ttcatctccaaagata[C/T]tacacttgtacagggt	C	T	NM_024325 // intron // 0 // Hs.516846 // ZNF343 // 79175 // Homo sapiens novel C2H2 type zinc finger protein (MGC10715), mRNA. /// ENST00000278772 // intron // 0 // — // — // — // ENST00000358413 // intron // 0 // — // — // — // —	ZNF343	ZNF343, Homo sapiens novel C2H2 type zinc finger protein (MGC10715), p13
SNP_A-1744973	agaaactatttctatgtaaacaca[G/T]ataagagggtgttgac ttctgct	G	T	NM_003091 // upstream // 6405 // Hs.83753 // SNRPB // 6628 // small nuclear ribonucleoprotein polypeptides B and B1 /// NM_024325 // downstream // 4679 // Hs.317169 // MGC10715 // 79175 // novel C2H2 type zinc finger protein	SNRPB	SNRPB, rs4446127, small nuclear ribonucleoprotein polypeptides B and B1, p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1873677	tctcactgtttttca[A/G]atcctcagtgtttca	A	G	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2159273	atttaaccagaatatc[A/G]atcatcaagccagaac	A	G	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2247112	ctgtcacaggaggggaa[C/T]ggtaaacactgtagg	C	T	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1918035	ttaaacaacaataacg[A/G]caacaattataacaac	A	G	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1785300	ggctaggccatccata[A/G]ctgcctcaatagagcc	A	G	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2245826	ctgggttatgacctg[A/G]actgtactacacagga	A	G	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1792473	gggttttagagtccag[C/T]ccccattggctcacta	C	T	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1808840	gtgaagttgagaagag[C/T]cacaaatctgtaaaag	C	T	NM_080751 // CDS // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // CDS // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /// ENS	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2039195	aacagtctgatttcac[A/G]ctgtttcataggctct	A	G	NM_080751 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // intron // 0 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, complete cds. /	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2126046	agtttgcaaaaggta[C/T]aatgcagagcgttgtc	C	T	NM_080751 // downstream // 761 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 761 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, com	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1910080	tgtcatatgccttccc[C/G]caagctaacctacctg	C	G	NM_080751 // downstream // 1442 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 1442 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, c	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2293593	gcagcattagatgaca[C/T]atacattccgtcacat	C	T	NM_080751 // downstream // 1720 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 1720 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, c	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-2136690	atcactgccaaaaaaaa[C/G]acaaggaatgctgggc	C	G	NM_080751 // downstream // 5067 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 5067 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, c	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1853468	tatttgatgtattca[C/T]gacggttaaaataatt	C	T	NM_080751 // downstream // 9580 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like 2 (TMC2), mRNA. /// AF417580 // downstream // 9580 // Hs.352626 // TMC2 // 117532 // Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA, c	TMC2	TMC2, Homo sapiens transmembrane channel-like 2 (TMC2), p13
SNP_A-1682092	atcatttttccataacagaccttgg[A/G]attcttagagagtgagtag gtgctg	A	G	U49283 // intron // 0 // - // - // Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete	-	-, rs6115686, Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete,p13
SNP_A-1838204	tagaactggtactcaa[A/G]atgtccacagttaacc	A	G	NM_030811 // downstream // 10220 // Hs.18946 // MRPS26 // 64949 // Homo sapiens mitochondrial ribosomal protein S26 (MRPS26), nuclear gene encoding mitochondrial protein, mRNA. /// NM_000915 // upstream // 13151 // Hs.113216 // OXT // 5020 // Homo sapiens	MRPS26	MRPS26, Homo sapiens mitochondrial ribosomal protein S26 (MRPS26), nuclear gene encoding mitochondrial protein, p13
SNP_A-2036787	aaatttcaactgatgg[A/C]aactataagacaaatg	A	C	ENST00000252031 // intron // 0 // --- // --- // ---	-	p13
SNP_A-1967488	agaggcgctgggctcg[C/G]agcctgtttccaagaa	C	G	NM_012070 // 3UTR // 0 // Hs.276252 // ATRN // 8455 // Homo sapiens attractin (ATRN), transcript variant 3, mRNA. /// NM_139321 // 3UTR // 0 // Hs.276252 // ATRN // 8455 // Homo sapiens attractin (ATRN), transcript variant 1, mRNA. /// NM_139322 // 3UTR /	ATRN	ATRN, Homo sapiens attractin (ATRN), transcript variant 3, p13
SNP_A-2115402	agggcgcgggcgagga[A/C]ccaagctaagagaaca	A	C	ENST00000305989 // downstream // 35689 // --- // --- // ---

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2308727	gcttctttatcttgcd[C/T]atcgatgctccctaat	C	T	NM_000678 // upstream // 427358 // Hs.557 // ADRA1D // 146 // Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), mRNA. /// NM_000311 // upstream // 10052 // Hs.472010 // PRNP // 5621 // Homo sapiens prion protein (p27-30) (Creutzfeld-Jakob disease, Ge	ADRA1D	ADRA1D, Homo sapiens adrenergic, alpha-1D-, receptor (ADRA1D), p13
SNP_A-2133421	atatatgttacagttat[C/T]gttcactgtgaatatg	C	T	NM_000311 // 3UTR // 0 // Hs.472010 // PRNP // 5621 // Homo sapiens prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia) /// NM_183079 // 3UTR // 0 // Hs.472010 // PRNP // 5621 // Homo sapiens	PRNP	PRNP, Homo sapiens prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia), p13
SNP_A-2062006	aatggctttcttcccc[C/G]actccaacacaatgag	C	G	NM_177549 // upstream // 8475 // Hs.126516 // LOC149830 // 149830 // Homo sapiens M8 protein (LOC149830), mRNA. /// NM_014737 // downstream // 30881 // Hs.379970 // RASSF2 // 9770 // Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), tra	LOC149830	LOC149830, Homo sapiens M8 protein (LOC149830), p13
SNP_A-2234933	ctccattagatttccat[C/G]ggatggcttttgggg	C	G	NM_177549 // upstream // 9245 // Hs.126516 // LOC149830 // 149830 // Homo sapiens M8 protein (LOC149830), mRNA. /// NM_014737 // downstream // 30111 // Hs.379970 // RASSF2 // 9770 // Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), tra	LOC149830	LOC149830, Homo sapiens M8 protein (LOC149830), p13
SNP_A-1857345	tccctttcccgcattat[C/T]gtgacaagctcctct	C	T	NM_177549 // upstream // 9708 // Hs.126516 // LOC149830 // 149830 // Homo sapiens M8 protein (LOC149830), mRNA. /// NM_014737 // downstream // 29648 // Hs.379970 // RASSF2 // 9770 // Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), tra	LOC149830	LOC149830, Homo sapiens M8 protein (LOC149830), p13
SNP_A-1864456	tccacttttgaaccgg[G/T]atccaaaaatccactt	G	T	NM_177549 // upstream // 27975 // Hs.126516 // LOC149830 // 149830 // Homo sapiens M8 protein (LOC149830), mRNA. /// NM_014737 // downstream // 11381 // Hs.379970 // RASSF2 // 9770 // Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), tr	LOC149830	LOC149830, Homo sapiens M8 protein (LOC149830), p13
SNP_A-1796957	ggttcgtattctcatc[C/T]gaggtagcagaagcac	C	T	NM_014737 // upstream // 16312 // Hs.379970 // RASSF2 // 9770 // Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), transcript variant 1, mRNA. /// NM_170774 // upstream // 16312 // Hs.379970 // RASSF2 // 9770 // Homo sapiens Ras associa	RASSF2	RASSF2, Homo sapiens Ras association (RalGDS,p13
SNP_A-1908512	tgtagataaaggttgat[C/T]ggatttcattctttt	C	T	NM_003818 // intron // 0 // Hs.472027 // CDS2 // 8760 // Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 (CDS2), mRNA. /// ENST00000217268 // intron // 0 // — // — // — // —	CDS2	CDS2, Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 (CDS2), p12.3
SNP_A-1806140	gtcctctgtgtaccca[C/T]ccagtgtactctct	C	T	NM_003818 // downstream // 79112 // Hs.472027 // CDS2 // 8760 // Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 (CDS2), mRNA. /// ENST00000217268 // downstream // 79112 // — // — // — // — /// ENST00000278654 // do	CDS2	CDS2, Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 (CDS2), p12.3
SNP_A-1722190	caaatttcccattgctagcctaag[C/T]aaagaatggagcattg gattaaag	C	T	AK090863 // downstream // 42640 // Hs.528510 // - // 388785 // LOC388785 (LOC388785), mRNA /// NM_175877 // upstream // 110844 // Hs.431161 // MGC35023 // 149836 // hypothetical protein MGC35023	-	-, rs4813744, LOC388785 (LOC388785), mRNA, p12.3
SNP_A-1967537	ggcgttggcttcaac[A/G]aactgtggtcaagga	A	G	NM_152504 // intron // 0 // Hs.529340 // FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// ENST00000354847 // intron // 0 // — // — // — /// ENST00000303142 // intron // 0 // — // — // —	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3
SNP_A-2293429	gcagatttgcatttta[C/T]aacttgtcatgtcaaa	C	T	NM_152504 // intron // 0 // Hs.529340 // FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// ENST00000354847 // intron // 0 // — // — // — /// ENST00000303142 // intron // 0 // — // — // —	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1960119	tttttaaaagaatttg[A/C]attgtggctgcagggt	A	C	NM_152504 // downstream // 3325 // Hs.529340 // FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// NM_001819 // upstream // 44287 // Hs.516874 // CHGB // 1114 // Homo sapiens chromogranin B (secretogranin 1) (CHGB), mRN	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3
SNP_A-1895360	tgcccttgatgtacca[A/G]agcagtgtttaccagg	A	G	NM_152504 // downstream // 20392 // Hs.529340 // FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// NM_001819 // upstream // 27220 // Hs.516874 // CHGB // 1114 // Homo sapiens chromogranin B (secretogranin 1) (CHGB), mR	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3
SNP_A-2283838	gatagtaggtggctaa[C/T]agaattgacaggatgg	C	T	NM_152504 // downstream // 20864 // Hs.529340 // FLJ25067 // 149840 // Homo sapiens hypothetical protein FLJ25067 (FLJ25067), mRNA. /// NM_001819 // upstream // 26748 // Hs.516874 // CHGB // 1114 // Homo sapiens chromogranin B (secretogranin 1) (CHGB), mR	FLJ25067	FLJ25067, Homo sapiens hypothetical protein FLJ25067 (FLJ25067), p12.3
SNP_A-1909116	tgtatccataagacca[C/T]agaggggggaaaagaca	C	T	NM_001819 // downstream // 12470 // Hs.516874 // CHGB // 1114 // Homo sapiens chromogranin B (secretogranin 1) (CHGB), mRNA. /// NM_015939 // downstream // 13 // Hs.128791 // CGI-09 // 51605 // Homo sapiens CGI-09 protein (CGI-09), mRNA. /// ENST000002030	CHGB	CHGB, Homo sapiens chromogranin B (secretogranin 1) (CHGB), p12.3
SNP_A-1710047	gttgtttataaggaagttgcaaata[C/T]acaagaaagcctatata ctataaaa	C	T	NM_015939 // intron // 0 // Hs.128791 // CGI-09 // 51605 // CGI-09 protein	CGI-09	CGI-09 , rs6117011, CGI-09 protein,p12.3
SNP_A-2264352	gaactttatttttctca[G/T]gtatagattgatagga	G	T	NM_017671 // upstream // 62297 // Hs.472054 // C20orf42 // 55612 // Homo sapiens chromosome 20 open reading frame 42 (C20orf42), mRNA. /// ENST00000217289 // upstream // 62297 // — // — // — // — /// ENST00000358795 // upstream // 62811 // — //	C20orf42	C20orf42, Homo sapiens chromosome 20 open reading frame 42 (C20orf42), p12.3
SNP_A-2067717	acaacactctcatcca[C/T]gcaactatcaaatgcc	C	T	NM_001200 // upstream // 473166 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// ENST00000341547 // upstream // 92741 // — // — // — // — /// ENST00000323644 // upstream // 92741 // — // — // — // —	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1898324	tgcttattccaaacaa[A/G]gttgtagtatgaatta	A	G	NM_001200 // upstream // 177339 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// ENST00000341547 // upstream // 388568 // — // — // — // — /// ENST00000323644 // upstream // 388568 // — // — // — // -	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2157915	attgctctaactaacc[A/C]ctgtccaacagaaaca	A	C	NM_001200 // downstream // 10361 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 1093487 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1967583	attggatggagggtaa[A/C]gttttaaagtcagcac	A	C	NM_001200 // downstream // 36161 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 1067687 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2249184	ctgttttccaatggac[A/G]gaaacttttgtaaac	A	G	NM_001200 // downstream // 262474 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 841374 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1929644	ttcatataggctacaa[A/G]aaaatgtttaatatat	A	G	NM_001200 // downstream // 290322 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 813526 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2313109	ggagaacacacttaac[A/T]cttgaattagtaaatc	A	T	NM_001200 // downstream // 828816 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 275032 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-2038722	aacagagttctcaaca[C/T]ggcaaaatttttttat	C	T	NM_001200 // downstream // 831813 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 272035 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1949452	ttattctgtctcaa[C/T]agtggcatggatggtc	C	T	NM_001200 // downstream // 866203 // Hs.73853 // BMP2 // 650 // Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /// NM_017545 // downstream // 237645 // Hs.193640 // HAO1 // 54363 // Homo sapiens hydroxyacid oxidase (glycolate oxidase) 1 (HAO1), m	BMP2	BMP2, Homo sapiens bone morphogenetic protein 2 (BMP2), p12.3
SNP_A-1753921	gttgtaaacagatgtgctgccattc[A/G]gactgttgtttatttataga gcac	A	G	NM_017545 // intron // 0 // Hs.193640 // HAO1 // 54363 // hydroxyacid oxidase (glycolate oxidase) 1	HAO1	HAO1 , rs2223276, hydroxyacid oxidase (glycolate oxidase) 1,p12.3
SNP_A-1822153	gttttcttctctgtga[A/G]gttatcaatcagcaga	A	G	NM_182734 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, b	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-2119967	agtcacaagcactctt[A/T]aaaggataacacaaac	A	T	NM_182734 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, b	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-1800898	gtagaggaattgtggc[A/C]gattgaataggaagtt	A	C	NM_182734 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, b	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-1946999	tttaagttcttgaaag[A/G]caatgctctgatggac	A	G	NM_182734 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, b	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-2132345	atagtatgccactaccc[A/G]cccaactcacattaaa	A	G	NM_182734 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA. /// NM_015192 // intron // 0 // Hs.310537 // PLCB1 // 23236 // Homo sapiens phospholipase C, b	PLCB1	PLCB1, Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, p12.3
SNP_A-1693881	gtggaatttcccagccctaggcataj[C/T]caaaagatccttgagc tttgaagg	C	T	NM_000933 // upstream // 297886 // Hs.151408 // PLCB4 // 5332 // phospholipase C, beta 4 /// NM_015192 // downstream // 191190 // Hs.429643 // PLCB1 // 23236 // phospholipase C, beta 1 (phosphoinositide-specific)	PLCB4	PLCB4 , rs724088, phospholipase C, beta 4 ,p12.3
SNP_A-2149132	atgtaaagaaaggacc[A/G]atttactgccctcag	A	G	NM_182797 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript vari	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2
SNP_A-1967677	aataaaatattgtagca[C/T]gaacttgaggaaacat	C	T	NM_182797 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript vari	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2030829	aaaggaaaacaggaaca[G/T]gaatcttgatggagga	G	T	NM_182797 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript vari	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2
SNP_A-1900491	tggagcccactactca[A/G]ggaaacaaggagctcc	A	G	NM_182797 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript vari	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2
SNP_A-2045386	aagaataacatttgaa[C/T]gagagagtctgaaat	C	T	NM_182797 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, mRNA. /// NM_000933 // intron // 0 // Hs.472101 // PLCB4 // 5332 // Homo sapiens phospholipase C, beta 4 (PLCB4), transcript vari	PLCB4	PLCB4, Homo sapiens phospholipase C, beta 4 (PLCB4), transcript variant 2, p12.2
SNP_A-1784559	ggcctacagcaaatga[A/G]gaaatgccacaagttc	A	G	NM_020341 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), trans	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-1906443	tggtggaacttttgag[A/G]ccttaccatttggaga	A	G	NM_020341 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), trans	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-1967698	attggaatgttcctaa[C/T]gtaagaaataataaa	C	T	NM_020341 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), trans	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-1791433	gggtataaggtagaga[C/T]ctaaacacatggaaa	C	T	NM_020341 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, mRNA. /// NM_177990 // intron // 0 // Hs.32539 // PAK7 // 57144 // Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), trans	PAK7	PAK7, Homo sapiens p21(CDKN1A)-activated kinase 7 (PAK7), transcript variant 1, p12.2
SNP_A-2007339	gggcagtagtacaaaa[A/C]gtttcttatccagcct	A	C	NM_198798 // downstream // 21765 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, mRNA. /// NM_022096 // downstream // 21765 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKR	ANKRD5	ANKRD5, Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, p12.2
SNP_A-2222329	cgagaaagaccatcag[A/G]aattctgaaacaaa	A	G	NM_198798 // downstream // 34443 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, mRNA. /// NM_022096 // downstream // 34443 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKR	ANKRD5	ANKRD5, Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, p12.2
SNP_A-2068008	acaactgctgtactaa[A/G]ctactccatttttagg	A	G	NM_198798 // downstream // 49825 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, mRNA. /// NM_022096 // downstream // 49825 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKR	ANKRD5	ANKRD5, Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, p12.2
SNP_A-2198847	catttcttttgctttccc[A/G]agctctggatttagagg	A	G	NM_198798 // downstream // 53359 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, mRNA. /// NM_022096 // downstream // 53359 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKR	ANKRD5	ANKRD5, Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2307421	gcttatcaacctatta[A/C]ctctgtattaagccct	A	C	NM_198798 // downstream // 66346 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, mRNA. /// NM_022096 // downstream // 66346 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKR	ANKRD5	ANKRD5, Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, p12.2
SNP_A-1913493	tgtggttaacaagtta[A/G]agaaaaacacattgcca	A	G	NM_198798 // downstream // 112259 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, mRNA. /// NM_022096 // downstream // 112259 // Hs.70903 // ANKRD5 // 63926 // Homo sapiens ankyrin repeat domain 5 (AN	ANKRD5	ANKRD5, Homo sapiens ankyrin repeat domain 5 (ANKRD5), transcript variant 2, p12.2
SNP_A-1714585	tttaccctctaaaaggcatatttg[C/T]atctctaaaggaatcttcac gtctt	C	T	NM_003081 // upstream // 87558 // Hs.221974 // SNAP25 // 6616 // synaptosomal-associated protein, 25kDa /// NM_022096 // downstream // 75450 // Hs.70903 // ANKRD5 // 63926 // ankyrin repeat domain 5 /// NM_130811 // upstream // 87558 // Hs.221974 // SNAP	SNAP25	SNAP25 , rs491244, synaptosomal-associated protein, 25kDa .p12.2
SNP_A-2154193	attatctttctaccat[C/G]agatatatcatttgct	C	G	NM_130811 // intron // 0 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // intron // 0 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-associated protei	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-1839192	tagaggaatcaacaaa[C/T]cactgaatcaggaaaa	C	T	NM_130811 // intron // 0 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // intron // 0 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-associated protei	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-1856474	tcacagagaaagagac[C/T]gaacattaaacaccat	C	T	NM_130811 // downstream // 63093 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // downstream // 63093 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-a	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-2069014	acaatgctatctctta[C/T]cccacgtgctctctt	C	T	NM_130811 // downstream // 69110 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, mRNA. /// NM_003081 // downstream // 69110 // Hs.167317 // SNAP25 // 6616 // Homo sapiens synaptosomal-a	SNAP25	SNAP25, Homo sapiens synaptosomal-associated protein, 25kDa (SNAP25), transcript variant 2, p12.2
SNP_A-2307674	gcttccaacctcctca[C/T]gaagtctgtaaagcac	C	T	ENST00000334534 // intron // 0 // — // — // —	-	p12.2
SNP_A-2156300	attctatgaagcaaaa[A/G]ctaaagggaaatcag	A	G	NM_000214 // downstream // 3914 // Hs.224012 // JAG1 // 182 // Homo sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA. /// ENST00000334534 // downstream // 10393 // — // — // — /// ENST00000246083 // upstream // 19578 // — // — // — //	JAG1	JAG1, Homo sapiens jagged 1 (Alagille syndrome) (JAG1), p12.2
SNP_A-2218996	cctggtggtaatgaaa[C/T]acactgtttatctgaa	C	T	NM_000214 // upstream // 237162 // Hs.224012 // JAG1 // 182 // Homo sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA. /// ENST00000254958 // upstream // 237162 // — // — // — /// ENST00000246101 // upstream // 117013 // — // — // — //	JAG1	JAG1, Homo sapiens jagged 1 (Alagille syndrome) (JAG1), p12.2
SNP_A-2133354	atatatctaggcctcca[A/G]tctcctctctgtaac	A	G	NM_000214 // upstream // 301435 // Hs.224012 // JAG1 // 182 // Homo sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA. /// ENST00000254958 // upstream // 301435 // — // — // — /// ENST00000246101 // upstream // 52740 // — // — // — // -	JAG1	JAG1, Homo sapiens jagged 1 (Alagille syndrome) (JAG1), p12.2
SNP_A-2091490	agaaaaacaaatagga[A/T]agaacaagaacatca	A	T	NM_000214 // upstream // 302915 // Hs.224012 // JAG1 // 182 // Homo sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA. /// ENST00000254958 // upstream // 302915 // — // — // — // ENST00000246101 // upstream // 51260 // — // — // — // -	JAG1	JAG1, Homo sapiens jagged 1 (Alagille syndrome) (JAG1), p12.2
SNP_A-2075470	acatgagtgatgaaat[A/G]aaatatgcaacaaacc	A	G	ENST00000246101 // downstream // 633158 // — // — // — // — /// ENST00000358396 // downstream // 148786 // — // — // — // —	-	p12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1710135	acacttctctactgccgaattttcc[C/T]gaatgtgacttagccacc agggagt	C	T	NM_014962 // downstream // 156909 // Hs.7935 // BTBD3 // 22903 // BTB (POZ) domain containing 3 /// NM_018327 // upstream // 925695 // Hs.272242 // C20orf38 // 55304 // chromosome 20 open reading frame 38 /// NM_181443 // downstream // 156909 // Hs.7935	BTBD3	BTBD3 , rs7261415, BTB (POZ) domain containing 3 ,p12.1
SNP_A-2189151	cagttagcctttgatg[C/T]attataattgtcacaa	C	T	NM_181443 // downstream // 230156 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 // downstream // 230156 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain conta	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1967787	agtgatgtccgttaga[A/G]attttctgcactgtcc	A	G	NM_181443 // downstream // 287055 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 // downstream // 287055 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain conta	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1825840	taaatgaaatcaatta[G/T]gtaaaaagcattgtaa	G	T	NM_181443 // downstream // 298698 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 // downstream // 298698 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain conta	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1967793	aatatggaagcagaaa[G/T]gttaaacgatttggcc	G	T	NM_181443 // downstream // 366494 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 // downstream // 366494 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain conta	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1874088	tctcattaaatacaca[A/C]tgcagtccgacagctc	A	C	NM_181443 // downstream // 428157 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 // downstream // 428157 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain conta	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-2112499	aggcacacctctaggc[A/G]cttggtggctgcccag	A	G	NM_181443 // downstream // 431377 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, mRNA. /// NM_014962 // downstream // 431377 // Hs.244590 // BTBD3 // 22903 // Homo sapiens BTB (POZ) domain conta	BTBD3	BTBD3, Homo sapiens BTB (POZ) domain containing 3 (BTBD3), transcript variant 2, p12.1
SNP_A-1904644	tggggctggctacaag[A/G]aagaccaagtgattag	A	G	NM_018327 // upstream // 619092 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 9172 // — // — // — // — /// ENST00000304791 // upstream // 619092 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1842599	taggttgtgcttttca[C/T]gtcaatttatttggca	C	T	NM_018327 // upstream // 609380 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 18884 // — // — // — // — /// ENST00000304791 // upstream // 609380 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2300716	gcctggaagtgacaca[G/T]tgctgcttcagctcat	G	T	NM_018327 // upstream // 607530 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 20734 // — // — // — // — /// ENST00000304791 // upstream // 607530 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2135183	atattgccctgttttg[A/G]atctccgtattttgtc	A	G	NM_018327 // upstream // 606911 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 21353 // — // — // — // — /// ENST00000304791 // upstream // 606911 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1844241	tagtttgctgagtttcd[A/G]attatcctgggcata	A	G	NM_018327 // upstream // 594921 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 33343 // — // — // — /// ENST00000304791 // upstream // 594921 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1967799	gctgcaacagctcccaa[A/G]cttccccagtgagac	A	G	NM_018327 // upstream // 580647 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 47617 // — // — // — /// ENST00000304791 // upstream // 580647 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2177601	cacgctttgcatcata[C/G]cacctggaaggaaatt	C	G	NM_018327 // upstream // 575363 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 52901 // — // — // — /// ENST00000304791 // upstream // 575363 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1945907	ttgtttcacagttgggt[A/G]catctagcaacagttg	A	G	NM_018327 // upstream // 571761 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 56503 // — // — // — /// ENST00000304791 // upstream // 571761 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1869446	tcctgtgccaaaaaaa[A/T]atctcatttctcaatc	A	T	NM_018327 // upstream // 566425 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 61839 // — // — // — /// ENST00000304791 // upstream // 566425 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1653106	aggtcaaacttcctctctatatggc[C/T]aaaccctatggtagatgct tggtaa	C	T	NM_014962 // downstream // 652278 // Hs.7935 // BTBD3 // 22903 // BTB (POZ) domain containing 3 /// NM_018327 // upstream // 430326 // Hs.272242 // C20orf38 // 55304 // chromosome 20 open reading frame 38 /// NM_181443 // downstream // 652278 // Hs.7935	BTBD3	BTBD3 , rs6109480, BTB (POZ) domain containing 3 ,p12.1
SNP_A-1897497	tgctgaggttcgaaca[C/G]tgctggttagagaact	C	G	NM_018327 // upstream // 356084 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 272180 // — // — // — /// ENST00000304791 // upstream // 356084 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2007388	tgataagaaactaaga[C/T]actatgttactatatag	C	T	NM_018327 // upstream // 113934 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 514330 // — // — // — /// ENST00000304791 // upstream // 113934 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1967819	acaatttctggaagc[C/T]cagatgtaggaggagt	C	T	NM_018327 // upstream // 84723 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000338690 // downstream // 543541 // — // — // — /// ENST00000304791 // upstream // 84723 // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-1948385	tttaggtggattaa[A/G]agaaaatgtcttctg	A	G	NM_018327 // intron // 0 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000304791 // intron // 0 // — // — // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2167937	caacgcagctgtggaa[A/C]gaaaaggaacaaaaagt	A	C	NM_018327 // CDS // 0 // Hs.272242 // C20orf38 // 55304 // Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA. /// ENST00000304791 // CDS // 0 // — // — // — // —	C20orf38	C20orf38, Homo sapiens chromosome 20 open reading frame 38 (C20orf38), p12.1
SNP_A-2115361	agggcacttccatgga[A/G]agattatttggaacag	A	G	ENST00000217206 // intron // 0 // — // — // — // —	-	p12.1
SNP_A-1967835	tgagtagcgttttata[G/T]gtacaaattccacctc	G	T	ENST00000217206 // intron // 0 // — // — // — // —	-	p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1950024	tttcacaatcacaagc[A/T]caagtagtagacttaa	A	T	ENST00000217204 // downstream // 104666 // --- // --- // --- /// ENST00000217206 // downstream // 17774 // --- // --- // --- // --- /// ENST00000262487 // upstream // 86051 // --- // --- // --- // ---	-	p12.1
SNP_A-2185139	caggaaaccagatctg[C/T]caacttggagtttga	C	T	ENST00000262487 // intron // 0 // --- // --- // ---	-	p12.1
SNP_A-1967837	cagaacgttgtttcta[C/T]gagtagagctcagaca	C	T	ENST00000262487 // intron // 0 // --- // --- // ---	-	p12.1
SNP_A-1850150	tatgtggcagattcaa[C/T]ttactagatataggca	C	T	NM_017714 // downstream // 80905 // Hs.369932 // C20orf13 // 55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// NM_017714 // downstream // 81366 // Hs.369932 // C20orf13 // 55617 // Homo sapiens chromosome 20 open reading fram	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-1967840	gccatttaaaattgcg[C/T]caagcatagtactgaa	C	T	NM_017714 // downstream // 80905 // Hs.369932 // C20orf13 // 55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// ENST00000337743 // intron // 0 // --- // --- // --- /// ENST00000355975 // intron // 0 // --- // --- // ---	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-2118988	agtagaagtgggacaa[A/G]aagaaacatgactgag	A	G	NM_017714 // intron // 0 // Hs.369932 // C20orf13 // 55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// ENST00000337743 // intron // 0 // --- // --- // --- /// ENST00000355975 // intron // 0 // --- // --- // ---	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-2007394	gaaaagcagcaccgaa[A/C]accctgcttatttcaa	A	C	NM_017714 // intron // 0 // Hs.369932 // C20orf13 // 55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// ENST00000337743 // intron // 0 // --- // --- // --- /// ENST00000355975 // intron // 0 // --- // --- // ---	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-1931348	ttcccactggttaaaa[A/C]attgtgagctaaaaat	A	C	NM_017714 // intron // 0 // Hs.369932 // C20orf13 // 55617 // Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA. /// ENST00000337743 // intron // 0 // --- // --- // --- /// ENST00000355975 // intron // 0 // --- // --- // ---	C20orf13	C20orf13, Homo sapiens chromosome 20 open reading frame 13 (C20orf13), p12.1
SNP_A-2229238	ctaggaaataatatgc[A/G]gaaattaaggagtgca	A	G	NM_199052 // intron // 0 // Hs.472165 // C20orf7 // 79133 // Homo sapiens chromosome 20 open reading frame 7 (C20orf7), transcript variant 2, mRNA. /// NM_024120 // intron // 0 // Hs.472165 // C20orf7 // 79133 // Homo sapiens chromosome 20 open reading fr	C20orf7	C20orf7, Homo sapiens chromosome 20 open reading frame 7 (C20orf7), transcript variant 2, p12.1
SNP_A-2251522	cttcacttgaatatcd[A/G]actccacatatccaaa	A	G	NM_198391 // upstream // 107136 // Hs.41296 // FLRT3 // 23767 // Homo sapiens fibronectin leucine rich transmembrane protein 3 (FLRT3), transcript variant 2, mRNA. /// NM_013281 // upstream // 107136 // Hs.41296 // FLRT3 // 23767 // Homo sapiens fibronect	FLRT3	FLRT3, Homo sapiens fibronectin leucine rich transmembrane protein 3 (FLRT3), transcript variant 2, p12.1
SNP_A-1796818	ggttcagaaatttgac[A/G]ccagacctatttaaatt	A	G	ENST00000217246 // downstream // 24566 // --- // --- // --- /// ENST00000333788 // upstream // 48024 // --- // --- // ---	-	p12.1
SNP_A-1867906	tcctacttatccttca[C/G]atcaacacacctctaat	C	G	ENST00000217246 // downstream // 29760 // --- // --- // --- /// ENST00000333788 // upstream // 42830 // --- // --- // ---	-	p12.1
SNP_A-2054591	aagttttttcccacca[A/G]aatgcaaggatgaac	A	G	ENST00000333788 // downstream // 168959 // --- // --- // --- /// ENST00000299455 // upstream // 302927 // --- // --- // ---	-	p12.1
SNP_A-1884871	tgaatctgtgacacaa[C/T]ataaatcactgtgtaa	C	T	ENST00000333788 // downstream // 269028 // --- // --- // --- /// ENST00000299455 // upstream // 202858 // --- // --- // ---	-	p12.1
SNP_A-2128070	ataagcataaatacttaa[G/T]cacaattcctggcagt	G	T	ENST00000333788 // downstream // 441479 // --- // --- // --- /// ENST00000299455 // upstream // 30407 // --- // --- // ---	-	p12.1
SNP_A-1967883	agttaaagttttttca[A/G]gatctcataatcctaa	A	G	ENST00000299455 // downstream // 8329 // --- // --- // --- /// ENST00000340000 // upstream // 748677 // --- // --- // ---	-	p12.1
SNP_A-1967885	tataatggatcaagaa[A/G]gacactacatcactgc	A	G	ENST00000299455 // downstream // 12071 // --- // --- // --- /// ENST00000340000 // upstream // 744935 // --- // --- // ---	-	p12.1
SNP_A-1967887	gctgagatgattgttt[A/C]aaaatggttccaagtt	A	C	ENST00000299455 // downstream // 12958 // --- // --- // --- /// ENST00000340000 // upstream // 744048 // --- // --- // ---	-	p12.1
SNP_A-2113766	aggctgcacccaggaa[C/G]gaatgtgatcttggaa	C	G	ENST00000299455 // downstream // 13041 // --- // --- // --- /// ENST00000340000 // upstream // 743965 // --- // --- // ---	-	p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1645088	aaaaatccctcttgcaactccattg[A/C]attgtacataaacaagtcaagaaag	A	C	NM_017683 // downstream // 1032748 // - // - // - /// NM_024704 // downstream // 1032748 // Hs.101774 // C20orf23 // 55614 // chromosome 20 open reading frame 23	-	- , rs175304, - , p12.1
SNP_A-1793935	ggtcaatgaggctgaa[A/C]aagccatgaataaattt	A	C	ENST00000299455 // downstream // 264963 // — // — // — // — /// ENST00000340000 // upstream // 492043 // — // — // — // —	-	p12.1
SNP_A-2123067	agtggtaactggcttta[C/G]agcttaacctcactgc	C	G	ENST00000299455 // downstream // 650479 // — // — // — // — /// ENST00000340000 // upstream // 106527 // — // — // — // —	-	p12.1
SNP_A-1924127	ttagttctataaaccc[A/G]ggactgagtttcaa	A	G	ENST00000299455 // downstream // 675468 // — // — // — // — /// ENST00000340000 // upstream // 81538 // — // — // — // —	-	p12.1
SNP_A-1967922	ctgcagtctgccttac[A/G]ggtagtgtgcctatc	A	G	ENST00000299455 // downstream // 688696 // — // — // — // — /// ENST00000340000 // upstream // 68310 // — // — // — // —	-	p12.1
SNP_A-1967923	tcatgatacgtgctaa[C/T]gaagggaaatgtaggt	C	T	ENST00000299455 // downstream // 691595 // — // — // — // — /// ENST00000340000 // upstream // 65411 // — // — // — // —	-	p12.1
SNP_A-2201428	ccaatgacggacaggat[A/G]ggggcgaacaaatacc	A	G	ENST00000299455 // downstream // 691926 // — // — // — // — /// ENST00000340000 // upstream // 65080 // — // — // — // —	-	p12.1
SNP_A-1967924	tttatatattccacac[C/T]gtagattataaattga	C	T	ENST00000299455 // downstream // 703875 // — // — // — // — /// ENST00000340000 // upstream // 53131 // — // — // — // —	-	p12.1
SNP_A-1708556	cagatcatagtagtggtagtcctta[C/T]gcattatggtaaatgcttccacgt	C	T	NM_017683 // downstream // 357529 // - // - // - /// NM_024704 // downstream // 357529 // Hs.101774 // C20orf23 // 55614 // chromosome 20 open reading frame 23	-	- , rs722337, - , p12.1
SNP_A-1724022	ttccttcttctcctacatatatccca[A/G]atcctcatggtttcttttctaatca	A	G	NM_017683 // downstream // 351943 // - // - // - /// NM_024704 // downstream // 351943 // Hs.101774 // C20orf23 // 55614 // chromosome 20 open reading frame 23	-	- , rs6105492, - , p12.1
SNP_A-1646334	tggacaatgaacaatgcagtaataaa[A/T]gtgggcgttcatagccacatgtaat	A	T	NM_017683 // downstream // 349039 // - // - // - /// NM_024704 // downstream // 349039 // Hs.101774 // C20orf23 // 55614 // chromosome 20 open reading frame 23	-	- , rs6043620, - , p12.1
SNP_A-1655649	aaaatgcttggaataaagatttgg[C/T]cagattcaaggtttaaactccacac	C	T	NM_017683 // downstream // 216083 // - // - // - /// NM_024704 // downstream // 216083 // Hs.101774 // C20orf23 // 55614 // chromosome 20 open reading frame 23	-	- , rs10485545, - , p12.1
SNP_A-2204279	ccagccatcccagagg[A/C]aagagccaacctgtta	A	C	NM_024704 // downstream // 162993 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA /// ENST00000340000 // downstream // 59236 // — // — // — // — /// ENST00000355755 // downstream // 162993 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2070893	acactcagagcaaaat[A/G]aaacataaaccataat	A	G	NM_024704 // downstream // 141722 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA /// ENST00000340000 // downstream // 80507 // — // — // — // — /// ENST00000355755 // downstream // 141722 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2042462	aactcagattgcaccat[C/T]aagagtctgctatcca	C	T	NM_024704 // downstream // 139426 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA /// ENST00000340000 // downstream // 82803 // — // — // — // — /// ENST00000355755 // downstream // 139426 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2314665	ggagtatatgttggaa[A/T]cagtggcaattgcttta	A	T	NM_024704 // downstream // 136342 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA /// ENST00000340000 // downstream // 85887 // — // — // — // — /// ENST00000355755 // downstream // 136342 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1871807	tctaatttatccaaa[C/G]agccattagaagttct	C	G	NM_024704 // downstream // 114319 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA /// ENST00000340000 // downstream // 107910 // — // — // — // — /// ENST00000355755 // downstream // 114319 //	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1920096	ttaatcacttgggtaa[C/T]ggagaaaatcatttga	C	T	NM_024704 // downstream // 113742 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000340000 // downstream // 108487 // — // — // — /// ENST00000355755 // downstream // 113742 /	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1721427	acagcactgttagcaatgttatccaa[C/T]gtgcttaaaattaaaacac aaccccct	C	T	NM_017683 // downstream // 76546 // - // - // - /// NM_024704 // downstream // 76546 // Hs.101774 // C20orf23 // 55614 // chromosome 20 open reading frame 23	-	- , rs10485547, - , p12.1
SNP_A-2155175	attcagccagactcga[A/G]aagacaatgacctgcc	A	G	NM_024704 // intron // 0 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000355755 // intron // 0 // — // — // — /// ENST00000354981 // intron // 0 // — // — // —	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1937608	ttgaagaatgagaaaaa[C/T]tttgtgttttttg	C	T	NM_024704 // intron // 0 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// ENST00000355755 // intron // 0 // — // — // — /// ENST00000354981 // intron // 0 // — // — // —	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2192404	catcatgataaacatc[C/T]ctctcgaaaataagca	C	T	NM_024704 // upstream // 16521 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 140030 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polyp	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2261762	gaaagtgtctcttcc[C/T]cttctcctcttctta	C	T	NM_024704 // upstream // 31664 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 124887 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polyp	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2307304	gcttacttatctcaa[C/T]acaatttgttcatgg	C	T	NM_024704 // upstream // 69015 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 87536 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polype	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2062969	aatgtgttgaaaaacc[A/G]ggtgcattaggtgcct	A	G	NM_024704 // upstream // 75523 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 81028 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polype	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2034009	aaatcactgtcccttc[A/T]ctttacccacaaacgt	A	T	NM_024704 // upstream // 89027 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 67524 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polype	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1858528	tcagagcttggctgaa[A/G]tctgaaccccagctgc	A	G	NM_024704 // upstream // 89294 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 67257 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polype	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2111734	aggataaatttgtgga[C/G]aagtgacaggacaaat	C	G	NM_024704 // upstream // 89856 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 66695 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polype	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-2295313	gcatcaggaaacagag[A/G]agcataagacggtaga	A	G	NM_024704 // upstream // 96372 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 60179 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polype	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1732061	tctacactgcctgcaagaatgttcg[A/T]ccctagcagctgagggtgacactga	A	T	NM_003092 // upstream // 105803 // Hs.280378 // SNRPB2 // 6629 // small nuclear ribonucleoprotein polypeptide B" /// NM_017683 // upstream // 50775 // - // - // - // - /// NM_024704 // upstream // 50776 // Hs.101774 // C20orf23 // 55614 // chromosome 20	SNRPB2	SNRPB2 , rs6080334, small nuclear ribonucleoprotein polypeptide B" ,p12.1
SNP_A-1917743	ttaaaacaacagcaaa[C/T]atttatttagctcatg	C	T	NM_024704 // upstream // 101061 // Hs.101774 // C20orf23 // 55614 // Homo sapiens chromosome 20 open reading frame 23 (C20orf23), mRNA. /// NM_003092 // upstream // 55490 // Hs.280378 // SNRPB2 // 6629 // Homo sapiens small nuclear ribonucleoprotein polyp	C20orf23	C20orf23, Homo sapiens chromosome 20 open reading frame 23 (C20orf23), p12.1
SNP_A-1738048	atgaacatgtttttcaaatacaaat[C/T]gacaatccagagcctatacctcagc	C	T	NM_003092 // upstream // 56502 // Hs.280378 // SNRPB2 // 6629 // small nuclear ribonucleoprotein polypeptide B" /// NM_017683 // upstream // 100076 // - // - // - // - /// NM_024704 // upstream // 100077 // Hs.101774 // C20orf23 // 55614 // chromosome 2	SNRPB2	SNRPB2 , rs2328024, small nuclear ribonucleoprotein polypeptide B" ,p12.1
SNP_A-1678008	tctaagggccgctgtcatcataccc[A/G]gacatggttgcctttactgcactag	A	G	NM_002594 // upstream // 394530 // Hs.315186 // PCSK2 // 5126 // proprotein convertase subtilisin/kexin type 2 /// NM_020157 // downstream // 80292 // Hs.41119 // OTOR // 56914 // otoraplin	PCSK2	PCSK2 , rs10485563, proprotein convertase subtilisin,p12.1
SNP_A-1721754	ccccgaagtcacaaggtgtttttgc[A/G]tagcttgtcccatttgccggaaaac	A	G	NM_002594 // upstream // 222030 // Hs.315186 // PCSK2 // 5126 // proprotein convertase subtilisin/kexin type 2 /// NM_020157 // downstream // 252792 // Hs.41119 // OTOR // 56914 // otoraplin	PCSK2	PCSK2 , rs724053, proprotein convertase subtilisin,p12.1
SNP_A-1753913	agctctgcaatttgtgtttcaatga[C/G]aactctagggcaggagcctccaacc	C	G	NM_002594 // upstream // 203066 // Hs.315186 // PCSK2 // 5126 // proprotein convertase subtilisin/kexin type 2 /// NM_020157 // downstream // 271756 // Hs.41119 // OTOR // 56914 // otoraplin	PCSK2	PCSK2 , rs763406, proprotein convertase subtilisin,p12.1
SNP_A-1955062	tttggaggtatgtgga[A/T]gacttttaatccttc	A	T	NM_020157 // downstream // 355978 // Hs.41119 // OTOR // 56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 118844 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST0	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-2264314	gaacttgatacgcagc[C/T]ccccccaaactttggag	C	T	NM_020157 // downstream // 401451 // Hs.41119 // OTOR // 56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 73371 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-2152587	attaagtgaaataagc[C/T]agcaacagaaagacaa	C	T	NM_020157 // downstream // 403549 // Hs.41119 // OTOR // 56914 // Homo sapiens otoraplin (OTOR), mRNA. /// NM_002594 // upstream // 71273 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00	OTOR	OTOR, Homo sapiens otoraplin (OTOR), p12.1
SNP_A-1925930	ttatggtggactgtgc[A/G]aaaatggccacaatac	A	G	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-2095443	agacaaataacactga[C/T]gactgaattcctcaga	C	T	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-2242760	ctgcattaattccata[C/T]ctgccccctgaacagc	C	T	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1
SNP_A-2252697	cttcgctaatgcacaa[C/T]gaaccctcacttccaa	C	T	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1911887	tgtgacatttcaatc[A/G]cttctaacagcactgg	A	G	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-2067421	acaaatcaaattgcca[A/G]gctggtgttcagaac	A	G	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-2267604	gaatcaaaacctctga[A/G]cctggacatcatttt	A	G	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-1908077	tgtacacatttggtca[A/G]atatgcctaggaaa	A	G	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin p12.1
SNP_A-1820192	gtttaatgtgtactta[C/T]agctttctcattgct	C	T	NM_002594 // intron // 0 // Hs.315186 // PCSK2 // 5126 // Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA. /// ENST00000262545 // intron // 0 // — // — // —	PCSK2	PCSK2, Homo sapiens proprotein convertase subtilisin,p12.1
SNP_A-2223548	cggaagtacaacaacc[A/G]gatcagaagtgtaaaa	A	G	NM_001195 // upstream // 29856 // Hs.129702 // BFSP1 // 631 // Homo sapiens beaded filament structural protein 1, filensin (BFSP1), mRNA. /// NM_006870 // upstream // 8930 // Hs.304192 // DSTN // 11034 // Homo sapiens destrin (actin depolymerizing factor)	BFSP1	BFSP1, Homo sapiens beaded filament structural protein 1, filensin (BFSP1), p12.1
SNP_A-1834971	tacccaccacatttag[C/T]atctgttacagccaac	C	T	NM_178477 // downstream // 205061 // Hs.115366 // C20orf179 // 140836 // Homo sapiens chromosome 20 open reading frame 179 (C20orf179), mRNA. /// NM_178477 // downstream // 205055 // Hs.115366 // C20orf179 // 140836 // Homo sapiens chromosome 20 open read	C20orf179	C20orf179, Homo sapiens chromosome 20 open reading frame 179 (C20orf179), p11.23
SNP_A-2239433	ctctttgccgaagtga[A/T]atactgcatatgaaac	A	T	NM_052865 // downstream // 1732 // Hs.320823 // C20orf72 // 92667 // Homo sapiens chromosome 20 open reading frame 72 (C20orf72), mRNA. /// NM_021220 // downstream // 24596 // Hs.546418 // ZNF339 // 58495 // Homo sapiens zinc finger protein 339 (ZNF339),	C20orf72	C20orf72, Homo sapiens chromosome 20 open reading frame 72 (C20orf72), p11.23
SNP_A-1875411	tctctgcctctctcaa[C/T]atttaggaagtatctct	C	T	NM_021220 // upstream // 44204 // Hs.546418 // ZNF339 // 58495 // Homo sapiens zinc finger protein 339 (ZNF339), mRNA. /// NM_020536 // upstream // 35802 // Hs.488051 // CSRP2BP // 57325 // Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant	ZNF339	ZNF339, Homo sapiens zinc finger protein 339 (ZNF339), p11.23
SNP_A-1968011	gctagaagttggtagct[A/G]ccaggtttgaagcag	A	G	NM_020536 // intron // 0 // Hs.488051 // CSRP2BP // 57325 // Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, mRNA. /// NM_177926 // intron // 0 // Hs.488051 // CSRP2BP // 57325 // Homo sapiens CSRP2 binding protein (CSRP2BP), transcrip	CSRP2BP	CSRP2BP, Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, p11.23
SNP_A-1859197	tcagcgtgtgtaaaaa[C/T]ggttgtggtggcttta	C	T	NM_153328 // upstream // 9619 // Hs.69330 // RBBP9 // 10741 // Homo sapiens retinoblastoma binding protein 9 (RBBP9), transcript variant 2, mRNA. /// NM_006606 // upstream // 9619 // Hs.69330 // RBBP9 // 10741 // Homo sapiens retinoblastoma binding protei	RBBP9	RBBP9, Homo sapiens retinoblastoma binding protein 9 (RBBP9), transcript variant 2, p11.23
SNP_A-2038251	aacaccacctctccga[A/G]tatagtcatcagtgag	A	G	NM_006363 // intron // 0 // Hs.369373 // SEC23B // 10483 // Homo sapiens Sec23 homolog B (S. cerevisiae) (SEC23B), transcript variant 1, mRNA. /// NM_032986 // intron // 0 // Hs.369373 // SEC23B // 10483 // Homo sapiens Sec23 homolog B (S. cerevisiae) (SE	SEC23B	SEC23B, Homo sapiens Sec23 homolog B (S. cerevisiae) (SEC23B), transcript variant 1, p11.23
SNP_A-1882504	tgaaaatgaccttaaa[C/T]tacagactgatcctga	C	T	NM_080820 // downstream // 20416 // Hs.434207 // HARS2 // 92675 // Homo sapiens histidyl-tRNA synthetase 2 (HARS2), mRNA. /// ENST00000262550 // downstream // 20416 // — // — // — /// ENST00000359848 // downstream // 2223 // — // — // —	HARS2	HARS2, Homo sapiens histidyl-tRNA synthetase 2 (HARS2), p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2207713	ccatttgcggtggac[C/T]attgatctgaagaatg	C	T	NM_178483 // CDS // 0 // Hs.112794 // C20orf79 // 140856 // Homo sapiens chromosome 20 open reading frame 79 (C20orf79), mRNA. /// ENST00000278779 // intron // 0 // --- // --- // --- /// ENST00000254968 // CDS // 0 // --- // --- // ---	C20orf79	C20orf79, Homo sapiens chromosome 20 open reading frame 79 (C20orf79), p11.23
SNP_A-2064994	aattgatgcactacaa[C/T]gcttttactgcttca	C	T	NM_178483 // intron // 0 // Hs.112794 // C20orf79 // 140856 // Homo sapiens chromosome 20 open reading frame 79 (C20orf79), mRNA. /// ENST00000278779 // intron // 0 // --- // --- // --- /// ENST00000254968 // intron // 0 // --- // --- // ---	C20orf79	C20orf79, Homo sapiens chromosome 20 open reading frame 79 (C20orf79), p11.23
SNP_A-1872763	tctataatagaaaaag[C/T]ctggatgcacatagga	G	T	NM_178483 // downstream // 144546 // Hs.112794 // C20orf79 // 140856 // Homo sapiens chromosome 20 open reading frame 79 (C20orf79), mRNA. /// NM_020689 // upstream // 165761 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodiu	C20orf79	C20orf79, Homo sapiens chromosome 20 open reading frame 79 (C20orf79), p11.23
SNP_A-1968055	ttctcatttctcaagc[C/T]ctcattcagagcctta	C	T	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium p11.23
SNP_A-2182133	cagagggagacggcac[A/G]aggttgagcatctaag	A	G	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium p11.23
SNP_A-2021429	aaaaaagcaaagaaga[C/T]gtatgcgggtttctgc	C	T	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium,p11.23
SNP_A-1968068	aagggaacattcaagc[C/T]gcgatgttcagaaagt	C	T	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium,p11.23
SNP_A-1968070	tgcatggtggtgacaa[G/T]tattgacatggcaaag	G	T	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium,p11.23
SNP_A-1901127	tggatctgactcataaa[C/T]ggtcaacctcagaatg	C	T	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium,p11.23
SNP_A-2007497	acagaggcttaggaca[A/G]cagaaaagacttaccca	A	G	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium p11.23
SNP_A-2007499	taacaacgaagaagaa[A/T]agttgattgtgctttt	A	T	NM_020689 // intron // 0 // Hs.211252 // SLC24A3 // 57419 // Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA. /// ENST00000328041 // intron // 0 // --- // ---	SLC24A3	SLC24A3, Homo sapiens solute carrier family 24 (sodium,p11.23
SNP_A-1673134	tataagcaataactataaattattg[A/G]tgagtaaagagaaatca tcttagag	A	G	NM_020689 // intron // 0 // Hs.439909 // SLC24A3 // 57419 // solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	SLC24A3	SLC24A3 , rs722850, solute carrier family 24 (sodium,p11.23
SNP_A-2110730	aggacctacacttgta[A/G]caatgactctgtaata	A	G	ENST00000318350 // upstream // 14859 // --- // --- // --- /// ENST00000246019 // downstream // 50552 // --- // --- // ---	-	p11.23
SNP_A-2208406	cccaccataggtgctc[A/G]cttaagctgagccctt	A	G	NM_018993 // upstream // 109502 // Hs.472270 // RIN2 // 54453 // Homo sapiens Ras and Rab interactor 2 (RIN2), mRNA. /// ENST00000246019 // upstream // 1654 // --- // --- // --- /// ENST00000255006 // upstream // 109502 // --- // --- // ---	RIN2	RIN2, Homo sapiens Ras and Rab interactor 2 (RIN2), p11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2155098	attcagaatgaggcta[C/T]ggaaagtgaagatgtc	C	T	NM_018993 // intron // 0 // Hs.472270 // RIN2 // 54453 // Homo sapiens Ras and Rab interactor 2 (RIN2), mRNA. /// ENST00000255006 // intron // 0 // --- // --- // ---	RIN2	RIN2, Homo sapiens Ras and Rab interactor 2 (RIN2), p11.23
SNP_A-2027584	aaaccagatgagaaaa[G/T]gcacaagacgctgtac	G	T	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000340348 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1800966	gtagatagcaaatcac[C/T]ataaccacggtcatgg	C	T	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000340348 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-2120548	agtccagtaccagccaa[A/G]tgacaagataaacatg	A	G	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000340348 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-2305257	gctgagcaaagtagtg[C/T]aatatgacaatgtttt	C	T	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000343997 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-2269124	gaattgctagcaaccg[C/T]caggaagtaggaagag	C	T	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000343997 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1893906	tgcatagcaggcaaat[A/G]ataaaacaaaatgaga	A	G	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000343997 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1968095	caagtgaaataggaaa[A/G]tgtacaccacgctgga	A	G	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000343997 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-2220562	cctctgtggcctcct[A/G]agaacagaagagatca	A	G	NM_015585 // intron // 0 // Hs.176013 // C20orf26 // 26074 // Homo sapiens chromosome 20 open reading frame 26 (C20orf26), mRNA. /// ENST00000245957 // intron // 0 // --- // --- // --- /// ENST00000343997 // intron // 0 // --- // --- // ---	C20orf26	C20orf26, Homo sapiens chromosome 20 open reading frame 26 (C20orf26), p11.23
SNP_A-1897926	tgctggtggcaggagc[A/G]acatctatctgttcc	A	G	ENST00000334386 // intron // 0 // --- // --- // ---	-	p11.23
SNP_A-2227114	ctaattataatggagg[G/T]acagcatatcccagta	G	T	NM_021104 // downstream // 533160 // Hs.381172 // RPL41 // 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 533160 // --- // --- // --- /// ENST00000338741 // downstream // 111549 // --- // --- // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-1905544	tggtagaaagcagggat[A/G]agagggagacagggta	A	G	NM_021104 // downstream // 558542 // Hs.381172 // RPL41 // 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 558542 // --- // --- // --- /// ENST00000338741 // downstream // 86167 // --- // --- // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-2023708	aaaacttcgtggataa[C/T]atgaaagtcaaagat	C	T	NM_021104 // downstream // 581338 // Hs.381172 // RPL41 // 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 581338 // --- // --- // --- /// ENST00000338741 // downstream // 63371 // --- // --- // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-1968136	ccactcatcttgctca[C/G]cggatgtcgctataaa	C	G	NM_021104 // downstream // 586083 // Hs.381172 // RPL41 // 6171 // Homo sapiens ribosomal protein L41 (RPL41), mRNA. /// ENST00000321137 // downstream // 586083 // --- // --- // --- /// ENST00000338741 // downstream // 58626 // --- // --- // ---	RPL41	RPL41, Homo sapiens ribosomal protein L41 (RPL41), p11.22
SNP_A-1912247	tgtgatgaaatctccj[A/G]gcaaggcctcttgagg	A	G	ENST00000338741 // upstream // 39843 // --- // --- // --- /// ENST00000304952 // downstream // 104597 // --- // --- // ---	-	p11.21
SNP_A-2213706	ccgttaacgaagaccca[A/T]catcactgtcttcaga	A	T	ENST00000338741 // upstream // 113641 // --- // --- // --- /// ENST00000304952 // downstream // 30599 // --- // --- // ---	-	p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2130976	ategaaccagcattca[A/G]aatagtgattgttcct	A	G	NM_021784 // upstream // 32102 // Hs.155651 // FOXA2 // 3170 // Homo sapiens forkhead box A2 (FOXA2), transcript variant 1, mRNA. /// NM_153675 // upstream // 32102 // Hs.155651 // FOXA2 // 3170 // Homo sapiens forkhead box A2 (FOXA2), transcript variant	FOXA2	FOXA2, Homo sapiens forkhead box A2 (FOXA2), transcript variant 1, p11.21
SNP_A-2307999	gcttcttgttcaaaaa[C/T]gagaaatgtgtaaaac	C	T	NM_012072 // upstream // 174790 // Hs.97199 // C1QR1 // 22918 // Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), mRNA. /// NM_013248 // upstream // 89606 // Hs.516933 // NXT1 // 29107 // Homo sapiens NTF2-like export factor 1 (NXT	C1QR1	C1QR1, Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), p11.21
SNP_A-2076872	accaaagacaacttaa[C/T]ggggaaagctgcagca	C	T	NM_013248 // downstream // 853 // Hs.516933 // NXT1 // 29107 // Homo sapiens NTF2-like export factor 1 (NXT1), mRNA. /// NM_022482 // upstream // 6558 // Hs.28921 // ZNF336 // 64412 // Homo sapiens zinc finger protein 336 (ZNF336), mRNA. /// NM_022482 //	NXT1	NXT1, Homo sapiens NTF2-like export factor 1 (NXT1), p11.21
SNP_A-2212996	ccgaactgagtagtta[C/G]agagaccacatggcca	C	G	NM_080830 // intron // 0 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 2, mRNA. /// NM_130794 // intron // 0 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 1, mRNA. /// ENS	CST11	CST11, Homo sapiens cystatin 11 (CST11), transcript variant 2, p11.21
SNP_A-2299881	gcctatgatttgaagg[C/T]aagttgctccctataa	C	T	NM_080830 // upstream // 12115 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 2, mRNA. /// NM_130794 // upstream // 12115 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 1, m	CST11	CST11, Homo sapiens cystatin 11 (CST11), transcript variant 2, p11.21
SNP_A-1968174	ggctgcatgaatcaca[A/G]tgatgtcttctccaga	A	G	NM_080830 // upstream // 27600 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 2, mRNA. /// NM_130794 // upstream // 27600 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 1, m	CST11	CST11, Homo sapiens cystatin 11 (CST11), transcript variant 2, p11.21
SNP_A-1968175	gtggctgtgctgtccf[A/G]gaacagtaggcatggg	A	G	NM_080830 // upstream // 28296 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 2, mRNA. /// NM_130794 // upstream // 28296 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 1, m	CST11	CST11, Homo sapiens cystatin 11 (CST11), transcript variant 2, p11.21
SNP_A-1968177	acacctgaggactcca[A/T]gtatttatgatttagg	A	T	NM_080830 // upstream // 28540 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 2, mRNA. /// NM_130794 // upstream // 28540 // Hs.128100 // CST11 // 140880 // Homo sapiens cystatin 11 (CST11), transcript variant 1, m	CST11	CST11, Homo sapiens cystatin 11 (CST11), transcript variant 2, p11.21
SNP_A-2026840	aaacacatctgtctaj[A/G]ggtgggtcatcagga	A	G	NM_005492 // downstream // 21552 // Hs.121602 // CST8 // 10047 // Homo sapiens cystatin 8 (cystatin-related epididymal specific) (CST8), mRNA. /// NM_080610 // downstream // 47168 // Hs.121554 // CST9L // 128821 // Homo sapiens cystatin 9-like (mouse) (CS	CST8	CST8, Homo sapiens cystatin 8 (cystatin-related epididymal specific) (CST8), p11.21
SNP_A-1816659	gttatagatgccaccc[A/G]ggattatcctatctc	A	G	NM_001898 // CDS // 0 // Hs.123114 // CST1 // 1469 // Homo sapiens cystatin SN (CST1), mRNA. /// ENST00000304749 // CDS // 0 // — // — // —	CST1	CST1, Homo sapiens cystatin SN (CST1), p11.21
SNP_A-1825538	taaatagatagcgatc[A/G]atgtggttctttcc	A	G	NM_001898 // upstream // 71874 // Hs.123114 // CST1 // 1469 // Homo sapiens cystatin SN (CST1), mRNA. /// NM_001322 // downstream // 958 // Hs.516939 // CST2 // 1470 // Homo sapiens cystatin SA (CST2), mRNA. /// ENST00000304749 // upstream // 71874 // —	CST1	CST1, Homo sapiens cystatin SN (CST1), p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2007544	gtcagttctgggtgga[A/G]gccgtggtccagagtg	A	G	NM_001900 // upstream // 58728 // Hs.121489 // CST5 // 1473 // Homo sapiens cystatin D (CST5), mRNA. /// NM_080920 // downstream // 46586 // Hs.355394 // GGTLA4 // 92086 // Homo sapiens gamma-glutamyltransferase-like activity 4 (GGTLA4), transcript varian	CST5	CST5, Homo sapiens cystatin D (CST5), p11.21
SNP_A-1935191	ttctgcatctgttgaa[C/T]gtaaggggaggtagc	C	T	NM_001900 // upstream // 73246 // Hs.121489 // CST5 // 1473 // Homo sapiens cystatin D (CST5), mRNA. /// NM_080920 // downstream // 32068 // Hs.355394 // GGTLA4 // 92086 // Homo sapiens gamma-glutamyltransferase-like activity 4 (GGTLA4), transcript varian	CST5	CST5, Homo sapiens cystatin D (CST5), p11.21
SNP_A-1856809	tcacattcccctgtta[C/T]gagctgagccctggag	C	T	NM_024893 // upstream // 461272 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream // 13796 // — // — // — /// ENST00000262490 // upstream // 461272 // —	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1683786	tcattaagtagtgaaatcacatctg[A/G]tacagaagctgcaattggagtcaac	A	G	NM_024893 // upstream // 275807 // Hs.233634 // C20orf39 // 79953 // chromosome 20 open reading frame 39 /// NM_080920 // upstream // 206516 // Hs.355394 // GGTLA4 // 92086 // gamma-glutamyltransferase-like activity 4 /// NM_178311 // upstream // 204612	C20orf39	C20orf39 , rs1580754, chromosome 20 open reading frame 39 ,p11.21
SNP_A-2045177	aagaagatcctctca[A/T]atgttgtgtcattcat	A	T	NM_024893 // upstream // 167725 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream // 307343 // — // — // — /// ENST00000262490 // upstream // 167725 // -	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-2007552	ctgattttcttccata[A/G]cgctgttcctacctc	A	G	NM_024893 // upstream // 88167 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream // 386901 // — // — // — /// ENST00000262490 // upstream // 88167 // —	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-2171572	caatcctcagtgttga[C/T]agaagtgctagaaggc	C	T	NM_024893 // upstream // 55065 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream // 420003 // — // — // — /// ENST00000262490 // upstream // 55065 // —	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1968204	aagaggaataccagat[A/G]actaggaaatgctaac	A	G	NM_024893 // upstream // 18746 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000319850 // downstream // 456322 // — // — // — /// ENST00000262490 // upstream // 18746 // —	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1680974	ggtccctgctgtgtctcggcactga[C/T]ggcaatgtgtacaaagcaacaagtg	C	T	NM_024893 // upstream // 24386 // Hs.233634 // C20orf39 // 79953 // chromosome 20 open reading frame 39 /// NM_080920 // upstream // 457937 // Hs.355394 // GGTLA4 // 92086 // gamma-glutamyltransferase-like activity 4 /// NM_178311 // upstream // 456033 /	C20orf39	C20orf39 , rs10485833, chromosome 20 open reading frame 39 ,p11.21
SNP_A-2141235	atctgtaaaatggcac[C/T]gataaaaagatccta	C	T	NM_024893 // downstream // 164301 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000262490 // downstream // 164301 // — // — // — /// ENST00000342726 // upstream // 99927 // -	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-2256252	ctttagcttctctggg[A/G]aaccaaacatttcctg	A	G	NM_024893 // downstream // 164887 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000262490 // downstream // 164887 // — // — // — /// ENST00000342726 // upstream // 99341 // -	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2060963	aatgatggggaattgc[G/T]agtggacgatgacaga	G	T	NM_024893 // downstream // 165995 // Hs.124638 // C20orf39 // 79953 // Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA. /// ENST00000262490 // downstream // 165995 // --- // --- // --- // --- /// ENST00000342726 // upstream // 98233 // -	C20orf39	C20orf39, Homo sapiens chromosome 20 open reading frame 39 (C20orf39), p11.21
SNP_A-1791035	ggggtccctttctcc[A/G]ctccaaagataccaca	A	G	NM_014588 // intron // 0 // Hs.274264 // VSX1 // 30813 // Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, mRNA. /// NM_199425 // CDS // 0 // Hs.274264 // VSX1 // 30813 // Homo sapiens visual system homeo	VSX1	VSX1, Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, p11.21
SNP_A-1867001	tccctccaaggcatcc[A/G]ccacaattgcaaccgt	A	G	NM_014588 // upstream // 8687 // Hs.274264 // VSX1 // 30813 // Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, mRNA. /// NM_199425 // upstream // 8687 // Hs.274264 // VSX1 // 30813 // Homo sapiens visual	VSX1	VSX1, Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), transcript variant 1, p11.21
SNP_A-2254265	cttgattttgagtgct[C/T]acacctcgatcttgaa	C	T	NM_025176 // upstream // 14854 // Hs.472347 // KIAA0980 // 22981 // Homo sapiens KIAA0980 protein (KIAA0980), mRNA. /// NM_152667 // downstream // 12616 // Hs.143137 // HDHD4 // 140838 // Homo sapiens haloacid dehalogenase-like hydrolase domain containing	KIAA0980	KIAA0980, Homo sapiens KIAA0980 protein (KIAA0980), p11.21
SNP_A-2223333	cgctcaaacacacgca[A/C]aagctttggtctcaat	A	C	NM_207470 // upstream // 19416 // Hs.516959 // FLJ45832 // 400841 // Homo sapiens FLJ45832 protein (FLJ45832), mRNA. /// NM_207350 // upstream // 71525 // Hs.529357 // MGC72104 // 284802 // Homo sapiens similar to FRG1 protein (FSHD region gene 1 protein)	FLJ45832	FLJ45832, Homo sapiens FLJ45832 protein (FLJ45832), q11.1
SNP_A-2276843	gagatagatccacgta[C/T]gcatggtcaattgaat	C	T	ENST00000252021 // intron // 0 // --- // --- // --- // ---	-	q11.21
SNP_A-2179376	cactgtgggccaaaca[C/T]ggaccgagggctttcc	C	T	ENST00000201961 // upstream // 5232 // --- // --- // --- // --- /// ENST00000341639 // upstream // 60911 // --- // --- // --- // --- // ---	-	q11.21
SNP_A-2116583	aggtcacgttggttgg[C/T]aaaggtgtctgagcct	C	T	NM_182584 // upstream // 344 // Hs.482274 // FLJ33706 // 284805 // Homo sapiens hypothetical protein FLJ33706 (FLJ33706), mRNA. /// ENST00000360785 // upstream // 344 // --- // --- // --- // --- /// ENST00000360170 // downstream // 38684 // --- // --- //	FLJ33706	FLJ33706, Homo sapiens hypothetical protein FLJ33706 (FLJ33706), q11.21
SNP_A-1870553	tcgagggtgagatgaa[C/G]taaaagactggaatgt	C	G	NM_182584 // upstream // 23469 // Hs.482274 // FLJ33706 // 284805 // Homo sapiens hypothetical protein FLJ33706 (FLJ33706), mRNA. /// ENST00000360785 // upstream // 23469 // --- // --- // --- // --- /// ENST00000360170 // downstream // 15559 // --- // ---	FLJ33706	FLJ33706, Homo sapiens hypothetical protein FLJ33706 (FLJ33706), q11.21
SNP_A-1900027	tggaccgtgggcttca[A/G]gtgtgttattaacccc	A	G	NM_182584 // upstream // 23966 // Hs.482274 // FLJ33706 // 284805 // Homo sapiens hypothetical protein FLJ33706 (FLJ33706), mRNA. /// ENST00000360785 // upstream // 23966 // --- // --- // --- // --- /// ENST00000360170 // downstream // 15062 // --- // ---	FLJ33706	FLJ33706, Homo sapiens hypothetical protein FLJ33706 (FLJ33706), q11.21
SNP_A-1928059	ttcaattcgctctgca[C/T]gtactgagcacctgct	C	T	NM_053041 // intron // 0 // Hs.408427 // COMMD7 // 149951 // Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // --- // --- // --- // ---	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21
SNP_A-2281772	gagtgacagaacaaga[A/T]cctagctcaaaaaata	A	T	NM_053041 // intron // 0 // Hs.408427 // COMMD7 // 149951 // Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // --- // --- // --- // ---	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21
SNP_A-1932435	ttcctgcatgactgat[A/G]ataggatacactgggg	A	G	NM_053041 // intron // 0 // Hs.408427 // COMMD7 // 149951 // Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // --- // --- // --- // ---	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21
SNP_A-1905607	tggtaggacttaggaa[G/T]atttgatggtcaaggc	G	T	NM_053041 // intron // 0 // Hs.408427 // COMMD7 // 149951 // Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // --- // --- // --- // ---	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2097432	agagaaatggccaaa[C/T]gactcaggtaagttgc	C	T	NM_053041 // intron // 0 // Hs.408427 // COMMD7 // 149951 // Homo sapiens COMM domain containing 7 (COMMD7), mRNA. /// ENST00000278980 // intron // 0 // — // — // —	COMMD7	COMMD7, Homo sapiens COMM domain containing 7 (COMMD7), q11.21
SNP_A-2239741	ctgaaagtatgtttca[A/G]agtcagttaacatgat	A	G	NM_012325 // downstream // 999 // Hs.472437 // MAPRE1 // 22919 // Homo sapiens microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA. /// NM_080675 // downstream // 1323?2 // Hs.375186 // SPAG4L // 140732 // Homo sapiens sperm associated a	MAPRE1	MAPRE1, Homo sapiens microtubule-associated protein, RP,q11.21
SNP_A-1853520	tatttgtaagataaa[C/T]gtctttcaccaggaga	C	T	NM_012325 // downstream // 9158 // Hs.472437 // MAPRE1 // 22919 // Homo sapiens microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA. /// NM_080675 // downstream // 124213 // Hs.375186 // SPAG4L // 140732 // Homo sapiens sperm associated	MAPRE1	MAPRE1, Homo sapiens microtubule-associated protein, RP q11.21
SNP_A-2271377	gacattggagccttgc[C/T]ccgccaccgagctgcg	C	T	NM_174897 // CDS // 0 // Hs.375090 // BPIL3 // 128859 // Homo sapiens bactericidal/permeability-increasing protein-like 3 (BPIL3), mRNA. /// ENST00000349552 // CDS // 0 // — // — // — // —	BPIL3	BPIL3, Homo sapiens bactericidal q11.21
SNP_A-2088379	actgtaccaggaatta[C/T]acttgctcatgatac	C	T	NM_176812 // intron // 0 // Hs.472471 // C20orf178 // 128866 // Homo sapiens chromosome 20 open reading frame 178 (C20orf178), mRNA. /// ENST00000217402 // intron // 0 // — // — // — // —	C20orf178	C20orf178, Homo sapiens chromosome 20 open reading frame 178 (C20orf178), q11.22
SNP_A-2127028	ataaataaataaaatt[A/T]aaatacgccacttata	A	T	NM_003908 // upstream // 91466 // Hs.429180 // EIF2S2 // 8894 // Homo sapiens eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), mRNA. /// NM_001672 // upstream // 56651 // Hs.432400 // ASIP // 434 // Homo sapiens agouti signaling	EIF2S2	EIF2S2, Homo sapiens eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), q11.22
SNP_A-1968259	gagaagcaattagaac[C/T]gtaacaatggaagtaa	C	T	NM_139274 // intron // 0 // Hs.517034 // ACAS2 // 55902 // Homo sapiens acetyl-Coenzyme A synthetase 2 (ADP forming) (ACAS2), transcript variant 2, mRNA. /// NM_018677 // intron // 0 // Hs.517034 // ACAS2 // 55902 // Homo sapiens acetyl-Coenzyme A synthet	ACAS2	ACAS2, Homo sapiens acetyl-Coenzyme A synthetase 2 (ADP forming) (ACAS2), transcript variant 2, q11.22
SNP_A-2223650	cggagtcacctggggal[C/T]aatggtcagaggtcag	C	T	ENST00000262873 // intron // 0 // — // — // — // — /// ENST00000291303 // intron // 0 // — // — // — // —	-	q11.22
SNP_A-1793643	ggtatgaaggaagttal[A/G]ggaaactagctggtaa	A	G	NM_199368 // intron // 0 // Hs.168073 // TRPC4AP // 26133 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 associated protein (TRPC4AP), transcript variant /// NM_016638 // intron // 0 // Hs.168073 // TRPC4AP // 26133 //	TRPC4AP	TRPC4AP, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 associated protein (TRPC4AP), transcript variant q11.22
SNP_A-2072958	acaggaattaattgga[A/G]aggactaccaatggtc	A	G	NM_199368 // upstream // 8690 // Hs.168073 // TRPC4AP // 26133 // Homo sapiens transient receptor potential cation channel, subfamily C, member 4 associated protein (TRPC4AP), transcript variant /// NM_015638 // upstream // 8690 // Hs.168073 // TRPC4AP //	TRPC4AP	TRPC4AP, Homo sapiens transient receptor potential cation channel, subfamily C, member 4 associated protein (TRPC4AP), transcript variant q11.22
SNP_A-1744647	acctaaacacgtggctgactctc[G/T]gagactactgtttctc agcatct	G	T	NM_007367 // upstream // 126272 // Hs.389101 // RALY // 22913 // RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) /// NM_016732 // upstream // 126272 // Hs.389101 // RALY // 22913 // RNA binding protein (autoantigenic, hnRNP-assoc	RALY	RALY , rs718404, RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) q11.22
SNP_A-1904378	tgggctgtgacttac[C/T]atggcggccacagcca	C	T	NM_199513 // intron // 0 // Hs.18128 // C20orf44 // 55245 // Homo sapiens chromosome 20 open reading frame 44 (C20orf44), transcript variant 3, mRNA. /// NM_018244 // intron // 0 // Hs.18128 // C20orf44 // 55245 // Homo sapiens chromosome 20 open reading	C20orf44	C20orf44, Homo sapiens chromosome 20 open reading frame 44 (C20orf44), transcript variant 3, q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1655629	ttgatggagcaaacatgatgttctt[A/G]ttccaatccatcatgattct tacaa	A	G	NM_001672 // upstream // 2135 // Hs.361642 // ASIP // 434 // agouti signaling protein, nonagouti homolog (mouse) /// NM_003908 // upstream // 145982 // Hs.429180 // EIF2S2 // 8894 // eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	ASIP	ASIP , rs2378132, agouti signaling protein, nonagouti homolog (mouse), q11.22
SNP_A-1646626	gctatttgctggctccccaggcaa[A/C]aagaaggcataataat tgtcaatat	A	C	NM_000687 // downstream // 6249 // Hs.388004 // AHCY // 191 // S-adenosylhomocysteine hydrolase /// NM_001672 // downstream // 4679 // Hs.361642 // ASIP // 434 // agouti signaling protein, nonagouti homolog (mouse)	AHCY	AHCY , rs819145, S-adenosylhomocysteine hydrolase, q11.22
SNP_A-1649210	actatgtcagtgaataaaagttcct[C/G]aatgccaagcaatggct tacacctg	C	G	NM_015638 // intron // 0 // Hs.168073 // TRPC4AP // 26133 // transient receptor potential cation channel, subfamily C, member 4 associated protein	TRPC4AP	TRPC4AP , rs717593, transient receptor potential cation channel, subfamily C, member 4 associated protein,q11.22
SNP_A-2221160	ccttgttcctggcacat[A/G]tgcttaatgtcctaaa	A	G	NM_199484 // intron // 0 // Hs.184062 // C20orf24 // 55969 // Homo sapiens chromosome 20 open reading frame 24 (C20orf24), transcript variant 3, mRNA. /// NM_199485 // intron // 0 // Hs.184062 // C20orf24 // 55969 // Homo sapiens chromosome 20 open readin	C20orf24	C20orf24, Homo sapiens chromosome 20 open reading frame 24 (C20orf24), transcript variant 3, q11.23
SNP_A-1934278	ttctccatctgtgaaat[C/T]gactggagatcagca	C	T	NM_006698 // upstream // 49483 // Hs.472651 // BLCAP // 10904 // Homo sapiens bladder cancer associated protein (BLCAP), mRNA. /// NM_181689 // downstream // 53670 // Hs.504703 // NNAT // 4826 // Homo sapiens neuronatin (NNAT), transcript variant 2, mRNA.	BLCAP	BLCAP, Homo sapiens bladder cancer associated protein (BLCAP), q11.23
SNP_A-2286074	gatgattccggatgat[C/T]taaagcacattacatt	C	T	NM_006698 // upstream // 50132 // Hs.472651 // BLCAP // 10904 // Homo sapiens bladder cancer associated protein (BLCAP), mRNA. /// NM_181689 // downstream // 54319 // Hs.504703 // NNAT // 4826 // Homo sapiens neuronatin (NNAT), transcript variant 2, mRNA.	BLCAP	BLCAP, Homo sapiens bladder cancer associated protein (BLCAP), q11.23
SNP_A-2289676	gcaaaactcttcccc[A/G]gaagtgacagctatat	A	G	NM_006698 // upstream // 72552 // Hs.472651 // BLCAP // 10904 // Homo sapiens bladder cancer associated protein (BLCAP), mRNA. /// NM_181689 // downstream // 76739 // Hs.504703 // NNAT // 4826 // Homo sapiens neuronatin (NNAT), transcript variant 2, mRNA.	BLCAP	BLCAP, Homo sapiens bladder cancer associated protein (BLCAP), q11.23
SNP_A-2146673	atgctgttagccacat[C/T]ataactggtggtagaa	C	T	NM_001725 // intron // 0 // Hs.529019 // BPI // 671 // Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA. /// ENST00000262865 // intron // 0 // — // — // —	BPI	BPI, Homo sapiens bactericidal,q11.23
SNP_A-2007605	gaagcctgtggtttaa[A/C]tcctatattctagcta	A	C	NM_001725 // intron // 0 // Hs.529019 // BPI // 671 // Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA. /// ENST00000262865 // intron // 0 // — // — // —	BPI	BPI, Homo sapiens bactericidal,q11.23
SNP_A-2007606	tatgtattaaagataa[A/T]tcctagtcagtacata	A	T	NM_001725 // intron // 0 // Hs.529019 // BPI // 671 // Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA. /// ENST00000262865 // intron // 0 // — // — // —	BPI	BPI, Homo sapiens bactericidal,q11.23
SNP_A-1919759	ttaagtctgttcatct[C/T]aacaggttccccaga	C	T	NM_004139 // intron // 0 // Hs.154078 // LBP // 3929 // Homo sapiens lipopolysaccharide binding protein (LBP), mRNA. /// ENST00000217407 // intron // 0 // — // — // —	LBP	LBP, Homo sapiens lipopolysaccharide binding protein (LBP), q11.23
SNP_A-1968293	tgaggacttctcatc[A/G]cacatcaacaaagaaa	A	G	NM_004139 // intron // 0 // Hs.154078 // LBP // 3929 // Homo sapiens lipopolysaccharide binding protein (LBP), mRNA. /// ENST00000217407 // intron // 0 // — // — // —	LBP	LBP, Homo sapiens lipopolysaccharide binding protein (LBP), q11.23
SNP_A-2307978	gcttcttcaagaaaga[C/G]actacatggattccct	C	G	NM_004139 // intron // 0 // Hs.154078 // LBP // 3929 // Homo sapiens lipopolysaccharide binding protein (LBP), mRNA. /// ENST00000217407 // intron // 0 // — // — // —	LBP	LBP, Homo sapiens lipopolysaccharide binding protein (LBP), q11.23
SNP_A-1954508	tttgccattataatgat[A/C]cacctcctgtgagcac	A	C	NM_004139 // intron // 0 // Hs.154078 // LBP // 3929 // Homo sapiens lipopolysaccharide binding protein (LBP), mRNA. /// ENST00000217407 // intron // 0 // — // — // —	LBP	LBP, Homo sapiens lipopolysaccharide binding protein (LBP), q11.23

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1968297	ttttctgccctgccaa[C/G]taaaacatttgccagc	C	G	NM_020336 // intron // 0 // Hs.436705 // KIAA1219 // 57148 // Homo sapiens KIAA1219 protein (KIAA1219), mRNA. /// ENST00000262879 // intron // 0 // — // — // — /// ENST00000304939 // intron // 0 // — // — // — /// ENST00000360080	KIAA1219	KIAA1219, Homo sapiens KIAA1219 protein (KIAA1219), q11.23
SNP_A-2279597	gaggcaatagagacta[C/T]gtgaaaaagagaaacc	C	T	NM_080552 // downstream // 11907 // Hs.179080 // SLC32A1 // 140679 // Homo sapiens vesicular inhibitory amino acid transporter (VIAAT), mRNA. /// NM_024855 // upstream // 7175 // Hs.371585 // ACTR5 // 79913 // Homo sapiens ARP5 actin-related protein 5 hom	SLC32A1	SLC32A1, Homo sapiens vesicular inhibitory amino acid transporter (VIAAT), q11.23
SNP_A-2127728	ataactctgtttcccc[C/T]cggttggtctttgtg	C	T	NM_024855 // downstream // 4913 // Hs.371585 // ACTR5 // 79913 // Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5), mRNA. /// NM_015568 // upstream // 28602 // Hs.45719 // PPP1R16B // 26051 // Homo sapiens protein phosphatase 1, regulator	ACTR5	ACTR5, Homo sapiens ARP5 actin-related protein 5 homolog (yeast) (ACTR5), q11.23
SNP_A-2033780	aaatattcccttcacc[G/T]agcaaaatgaatataa	G	T	NM_021931 // intron // 0 // Hs.444520 // DHX35 // 60625 // Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 35 (DHX35), mRNA. /// ENST00000252011 // intron // 0 // — // — // — // —	DHX35	DHX35, Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 35 (DHX35), q11.23
SNP_A-2204841	ccaggctctgacttta[C/T]ggtgtgtagaccttaa	C	T	AK055793 // downstream // 101372 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 89660 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20orf	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2192982	catcgcatcagtacca[A/G]tggaatagagcagcc	A	G	AK055793 // downstream // 103517 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 91805 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20orf	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2102506	agattgacactggtcc[A/G]acactatttaccgaac	A	G	AK055793 // downstream // 108765 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 97053 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20orf	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1852464	tatttaccgaactacg[A/G]acttcatggatgtcgc	A	G	AK055793 // downstream // 108786 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 97074 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20orf	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1860573	tcagttggctctaaga[C/T]ggtgtaggatggctgc	C	T	AK055793 // downstream // 114821 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 103109 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1823842	taaaatgctggaagaa[A/G]gtattaaaaaagtatt	A	G	AK055793 // downstream // 122113 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 110401 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1968309	ttccaaattagctcaa[A/G]atctcagggtaggaca	A	G	AK055793 // downstream // 127728 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 116016 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2085493	actccagactaagctc[A/C]atcaatttctctaagc	A	C	AK055793 // downstream // 129100 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 117388 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1918548	ttaaatgacttatcca[A/G]actataatcaaaacc	A	G	AK055793 // downstream // 148935 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 137223 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1817492	gttcatcctgacaca[C/T]gtatctgctttgact	C	T	AK055793 // downstream // 547303 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 535591 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1968328	tatgtggaccattcag[G/T]atgacctttgttaag	G	T	AK055793 // downstream // 598811 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 587099 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1650254	aactgcattggttcttgggatttga[A/T]taaagtggctatttctagag ttggg	A	T	NM_001725 // downstream // 5214 // Hs.303523 // BPI // 671 // bactericidal/permeability-increasing protein /// NM_004139 // upstream // 3766 // Hs.154078 // LBP // 3929 // lipopolysaccharide binding protein	BPI	BPI , rs1780615, bactericidal,q11.23
SNP_A-2061662	aatggaaacagctaaa[A/T]gggcatgacccatct	A	T	AK055793 // downstream // 644230 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 632518 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-1968337	cattaaactcagaagc[A/G]atgtcgcttggattcc	A	G	AK055793 // downstream // 751880 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 740168 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2137509	atcatcagagcggaga[A/G]atgaggaagttcatct	A	G	AK055793 // downstream // 805975 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 794263 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2111187	aggagatgaagcaaga[A/G]attagcaactgtagaa	A	G	AK055793 // downstream // 881031 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 869319 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20or	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2300854	gcctggtgttgacttc[A/G]aacctcctggttgaag	A	G	AK055793 // downstream // 1031829 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 1020117 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2314239	ggaggcaagtgtcaca[A/G]attcctgagaaggtg	A	G	AK055793 // downstream // 1146626 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 1134914 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1880595	tcttgccagtgtgaat[A/G]agaattaaaatgatat	A	G	AK055793 // downstream // 1388141 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 1376429 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. ,q12
SNP_A-2212281	ccctgggattcttaga[C/T]cctacttaaacctgtt	C	T	AK055793 // downstream // 1410448 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 1398736 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. q12
SNP_A-2199184	cattttacgtgcattc[G/T]ctcattcaaccctcac	G	T	AK055793 // downstream // 1692583 // Hs.472716 // C20orf129 // 81610 // Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. /// NM_030919 // downstream // 1680871 // Hs.472716 // C20orf129 // 81610 // Homo sapiens chromosome 20 open reading frame 129 (C20	C20orf129	C20orf129, Homo sapiens cDNA FLJ31231 fis, clone KIDNE2004534. ,q12
SNP_A-2054898	aataaagtgtcacaga[C/T]tcactcccagagagtc	C	T	AF090938 // downstream // 268411 // — // — // 0 // Homo sapiens clone HQ0628 PRO0628 mRNA, complete cds. /// ENST00000313009 // upstream // 80200 // — // — // — // — /// ENST00000360450 // upstream // 259764 // — // — // — // — /// ENS	-	-, Homo sapiens clone HQ0628 PRO0628 complete cds. q12
SNP_A-2007628	ggcttatgccctttaa[A/G]aaaatccctttgctgt	A	G	AF090938 // downstream // 213771 // — // — // 0 // Homo sapiens clone HQ0628 PRO0628 mRNA, complete cds. /// ENST00000313009 // upstream // 134840 // — // — // — // — /// ENST00000360450 // upstream // 205124 // — // — // — // — /// EN	-	-, Homo sapiens clone HQ0628 PRO0628 complete cds. q12
SNP_A-1840200	tagcagatggtggaac[C/T]gacatttgattccaga	C	T	AF090938 // downstream // 32506 // — // — // 0 // Homo sapiens clone HQ0628 PRO0628 mRNA, complete cds. /// ENST00000313009 // upstream // 316105 // — // — // — // — /// ENST00000360450 // upstream // 23859 // — // — // — // — /// ENST	-	-, Homo sapiens clone HQ0628 PRO0628 complete cds. q12
SNP_A-1795467	ggtgccaaaaggatga[C/G]aaaagccttgtgagtg	C	G	AF090938 // downstream // 14217 // — // — // 0 // Homo sapiens clone HQ0628 PRO0628 mRNA, complete cds. /// ENST00000313009 // upstream // 334394 // — // — // — // — /// ENST00000360450 // upstream // 5570 // — // — // — // — /// ENST0	-	-, Homo sapiens clone HQ0628 PRO0628 complete cds. ,q12
SNP_A-1674471	ataggttggcagttgttgaagatga[C/T]ggagtgagttggtgtgg agggaaga	C	T	NM_005461 // downstream // 869977 // Hs.169487 // MAFB // 9935 // v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian) /// NM_021931 // downstream // 776175 // Hs.7174 // DHX35 // 60625 // DEAH (Asp-Glu-Ala-His) box polypeptide 35	MAFB	MAFB , rs211867, v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian) ,q12
SNP_A-1968378	tgatgaaaaaactcaa[A/G]tgattgacagatttaa	A	G	ENST00000360450 // intron // 0 // — // — // — // — /// ENST00000359669 // intron // 0 // — // — // — // —	-	q12
SNP_A-1968379	ggcacataggtcagca[C/T]attaggcttaacaaca	C	T	NM_015035 // 3UTR // 0 // Hs.380133 // ZHX3 // 23051 // Homo sapiens zinc fingers and homeoboxes 3 (ZHX3), mRNA. /// ENST00000309060 // 3UTR // 0 // — // — // — // —	ZHX3	ZHX3, Homo sapiens zinc fingers and homeoboxes 3 (ZHX3), q12
SNP_A-2219840	ccttagaatagaatct[G/T]aatgccttgctatgcc	G	T	NM_015035 // upstream // 1290 // Hs.380133 // ZHX3 // 23051 // Homo sapiens zinc fingers and homeoboxes 3 (ZHX3), mRNA. /// NM_052846 // downstream // 58577 // Hs.25897 // EMILIN3 // 90187 // Homo sapiens elastin microfibril interfacer 3 (EMILIN3), mRNA.	ZHX3	ZHX3, Homo sapiens zinc fingers and homeoboxes 3 (ZHX3), q12
SNP_A-2301240	gccttgctgcacagaa[C/T]ttccaaatgtggctct	C	T	NM_052846 // upstream // 4418 // Hs.25897 // EMILIN3 // 90187 // Homo sapiens elastin microfibril interfacer 3 (EMILIN3), mRNA. /// NM_032221 // downstream // 31254 // Hs.371979 // CHD6 // 84181 // Homo sapiens chromodomain helicase DNA binding protein 6	EMILIN3	EMILIN3, Homo sapiens elastin microfibril interfacer 3 (EMILIN3), q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1870020	tcctgcaatgctaag[A/G]ctctaccaatctacta	A	G	NM_032221 // intron // 0 // Hs.371979 // CHD6 // 84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// ENST00000244003 // intron // 0 // — // — // —	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-1834629	taccacaatcaggccc[A/G]agcaagtgtgagtcag	A	G	NM_032221 // intron // 0 // Hs.371979 // CHD6 // 84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// ENST00000244003 // intron // 0 // — // — // — /// ENST00000309279 // intron // 0 // — // — // —	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-2247558	ctgtctgggtaaagaa[C/T]aaatgggtggtggaat	C	T	NM_032221 // upstream // 50660 // Hs.371979 // CHD6 // 84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream // 403621 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, recep	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-1912303	tgtgatgtgagttgta[A/C]aatttaaaaataaaat	A	C	NM_032221 // upstream // 265633 // Hs.371979 // CHD6 // 84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream // 188648 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, rece	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-2032097	aaagtgcatggctaca[A/G]tgagggggtgagatttt	A	G	NM_032221 // upstream // 292574 // Hs.371979 // CHD6 // 84181 // Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), mRNA. /// NM_133170 // downstream // 161707 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, rece	CHD6	CHD6, Homo sapiens chromodomain helicase DNA binding protein 6 (CHD6), q12
SNP_A-1895643	tgcctcccctggtgact[G/T]acttcttcactgtttt	G	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2007639	gcctcctttttaatgtc[C/T]agaccagcatttctca	C	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1968415	attgagtcattccaa[A/T]ttcaccaaagcattaa	A	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2132875	atataaatatgcttgca[G/T]attccgtatttccc	G	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2229049	ctagcatcattaacat[A/C]actgcaggcatgtta	A	C	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1968422	aacctttggtatgtc[A/T]catcttactcaccttt	A	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2007642	tacaggaaagtcagta[G/T]agaaatggagattagt	G	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1898815	tgctttgcccaaaggaa[C/T]ctgtgagcatgaataa	C	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2037970	aacaattggagtgtaa[A/G]gagatcctgattcaac	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1968424	cactttaggcagccgg[C/T]aatcctctaatctca	C	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2173643	cacacaaatacaccag[A/G]aatgtttacctatgta	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1798845	gtaactttccagcctg[C/T]atctggttatgattgc	C	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1958441	ttttcctcgcagatca[A/T]gaattcccaaggaac	A	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1875998	tctgaaggattgagta[A/G]gaggtgctccaaagg	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1968429	gtgttaaagtaccaaa[A/G]gctccaatttactaag	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2066039	aatttgcgtttccaaa[A/G]caagagttgtagtgga	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1891280	tgattaaactttctac[A/G]attatgcgcaacact	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1968430	agtatgtacttaagct[C/G]aagtctcatcattgat	C	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2039986	aacatttgaattaaca[A/G]tccttgctgtgtgtgt	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1795122	ggtgactcatagaccc[A/G]atatggtgagaagaat	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2217303	cctgaaattgtctatc[A/G]gaagctattaatagct	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1874395	tctccattcaaatcca[C/T]tccttcacttattcta	C	T	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-2073831	acagtgctgggcactg[A/G]acatggttatcttgac	A	G	NM_133170 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // intron // 0 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosph	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q12
SNP_A-1968449	cctgttgtacccacac[C/T]cataagaggataagat	C	T	NM_133170 // upstream // 61289 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 61289 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyr	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-1968451	aaaaaataaatggcta[C/T]atgactgagcaaactc	C	T	NM_133170 // upstream // 112001 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 112001 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein t	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-1804363	gtcactgtccttttta[C/T]agggtgctggttgaga	C	T	NM_133170 // upstream // 128803 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 128803 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein t	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-2156645	attctgccttgagaca[A/G]cttcgagggacaaaca	A	G	NM_133170 // upstream // 147563 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, mRNA. /// NM_007050 // upstream // 147563 // Hs.526879 // PTPRT // 11122 // Homo sapiens protein t	PTPRT	PTPRT, Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript variant 1, q13.11
SNP_A-1722842	ctcctctccttctttgcttccatcc[A/G]tcaacccatttgctgaagaagaaaa	A	G	NM_007050 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T /// NM_133170 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T	PTPRT	PTPRT , rs2067084, protein tyrosine phosphatase, receptor type, T ,q12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2246969	ctgatgaggttggaa[A/G]gcctattaacatcgt	A	G	NM_015478 // downstream // 1330 // Hs.300863 // L3MBTL // 26013 // Homo sapiens l(3)mbt-like (Drosophila) (L3MBTL), transcript variant l, mRNA. /// NM_032107 // downstream // 1330 // Hs.300863 // L3MBTL // 26013 // Homo sapiens l(3)mbt-like (Drosophila) (	L3MBTL	L3MBTL, Homo sapiens l(3)mbt-like (Drosophila) (L3MBTL), transcript variant l, q13.12
SNP_A-2034222	aaatccagttaccccat[A/G]acccatttgttgaaga	A	G	NM_015478 // downstream // 11637 // Hs.300863 // L3MBTL // 26013 // Homo sapiens l(3)mbt-like (Drosophila) (L3MBTL), transcript variant l, mRNA. /// NM_032107 // downstream // 11637 // Hs.300863 // L3MBTL // 26013 // Homo sapiens l(3)mbt-like (Drosophila)	L3MBTL	L3MBTL, Homo sapiens l(3)mbt-like (Drosophila) (L3MBTL), transcript variant l, q13.12
SNP_A-2206512	ccatcttaatagtgcc[A/G]gataattgacaaattt	A	G	NM_170693 // downstream // 2381 // Hs.472793 // SGK2 // 10110 // Homo sapiens serum/glucocorticoid regulated kinase 2 (SGK2), transcript variant 1, mRNA. /// NM_016276 // downstream // 2375 // Hs.472793 // SGK2 // 10110 // Homo sapiens serum/glucocorticoi	SGK2	SGK2, Homo sapiens serum q13.12
SNP_A-2104753	agcagttctttctgcc[C/G]ggaacgccctcccca	C	G	NM_170693 // downstream // 4653 // Hs.472793 // SGK2 // 10110 // Homo sapiens serum/glucocorticoid regulated kinase 2 (SGK2), transcript variant 1, mRNA. /// NM_016276 // downstream // 4647 // Hs.472793 // SGK2 // 10110 // Homo sapiens serum/glucocorticoi	SGK2	SGK2, Homo sapiens serum,q13.12
SNP_A-2228627	ctagaagactatacc[C/T]gcgcttaacagtagtt	C	T	NM_016004 // intron // 0 // Hs.444332 // C20orf9 // 51098 // Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA. /// ENST00000262601 // intron // 0 // — // — // —	C20orf9	C20orf9, Homo sapiens chromosome 20 open reading frame 9 (C20orf9), q13.12
SNP_A-1834588	taccaataatgatcaa[C/T]gttctaagttccacat	C	T	NM_016004 // intron // 0 // Hs.444332 // C20orf9 // 51098 // Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA. /// ENST00000262601 // intron // 0 // — // — // —	C20orf9	C20orf9, Homo sapiens chromosome 20 open reading frame 9 (C20orf9), q13.12
SNP_A-2007657	cactgtacctaaagaat[A/G]aagataaaagagtaga	A	G	NM_016004 // downstream // 783 // Hs.444332 // C20orf9 // 51098 // Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA. /// ENST00000262601 // downstream // 783 // — // — // — /// ENST00000341709 // upstream // 4519 // — // —	C20orf9	C20orf9, Homo sapiens chromosome 20 open reading frame 9 (C20orf9), q13.12
SNP_A-1668971	ccttcggcgtaggaactatggcac[C/T]ctcagagttatcacct atgtaacc	C	T	NM_007050 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T /// NM_133170 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T	PTPRT	PTPRT , rs10485693, protein tyrosine phosphatase, receptor type, T ,q12
SNP_A-1858687	tcagatcagaaaataa[C/T]aacagcttggctgggc	C	T	NM_002466 // upstream // 5561 // Hs.179718 // MYBL2 // 4605 // Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), mRNA. /// ENST00000341709 // downstream // 8214 // — // — // — /// ENST00000278963 // downstream /	MYBL2	MYBL2, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), q13.12
SNP_A-2218478	cctggactctggacta[A/G]aacatacagaattta	A	G	NM_002466 // upstream // 3748 // Hs.179718 // MYBL2 // 4605 // Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), mRNA. /// ENST00000341709 // downstream // 10027 // — // — // — /// ENST00000278963 // downstream	MYBL2	MYBL2, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), q13.12
SNP_A-2276320	gagagcaaatgtacag[A/G]acctgcaagccccta	A	G	NM_002466 // intron // 0 // Hs.179718 // MYBL2 // 4605 // Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), mRNA. /// ENST00000217026 // intron // 0 // — // — // — // —	MYBL2	MYBL2, Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), q13.12
SNP_A-2167439	caacatacatccatga[A/G]caatttagatggcag	A	G	NM_176791 // upstream // 419 // Hs.447626 // C20orf65 // 149699 // Homo sapiens chromosome 20 open reading frame 65 (C20orf65), mRNA. /// NM_032883 // upstream // 218592 // Hs.26608 // C20orf100 // 84969 // Homo sapiens chromosome 20 open reading frame 10	C20orf65	C20orf65, Homo sapiens chromosome 20 open reading frame 65 (C20orf65), q13.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2232707	ctcactcagacctaac[A/G]aagcataacttacagg	A	G	NM_176791 // upstream // 168231 // Hs.447626 // C20orf65 // 149699 // Homo sapiens chromosome 20 open reading frame 65 (C20orf65), mRNA. /// NM_032883 // upstream // 50780 // Hs.26608 // C20orf100 // 84969 // Homo sapiens chromosome 20 open reading frame	C20orf65	C20orf65, Homo sapiens chromosome 20 open reading frame 65 (C20orf65), q13.12
SNP_A-1738965	cagtatctttctgaaggaactaata[G/T]aacctaggccatgcccc ttacagct	G	T	NM_007050 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T /// NM_133170 // intron // 0 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T	PTPRT	PTPRT , rs2425524, protein tyrosine phosphatase, receptor type, T ,q12
SNP_A-2273244	gactcatatatccaac[A/G]agtccctggatgttta	A	G	NM_178850 // downstream // 15850 // Hs.116462 // HNF4A // 3172 // Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 3, mRNA. /// NM_000457 // downstream // 9096 // Hs.116462 // HNF4A // 3172 // Homo sapiens hepatocyte nuclear fac	HNF4A	HNF4A, Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 3, q13.12
SNP_A-1672112	gtcatctctatccccatctcttggc[C/T]tcaacctgtcctggcccat ggggct	C	T	NM_006275 // upstream // 141403 // Hs.6891 // SFRS6 // 6431 // splicing factor, arginine/serine-rich 6 /// NM_007050 // upstream // 126586 // Hs.225952 // PTPRT // 11122 // protein tyrosine phosphatase, receptor type, T /// NM_133170 // upstream // 12658	SFRS6	SFRS6 , rs2223246, splicing factor, arginine,q13.11
SNP_A-1885700	tgacagacgtttccca[C/T]agtgcgggcacaaagt	C	T	NM_182970 // intron // 0 // Hs.517065 // RIMS4 // 140730 // Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// ENST00000217067 // intron // 0 // --- // --- // --- // ---	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-1787524	gggaatgaagccttga[A/G]cttgggcaatctgact	A	G	NM_182970 // intron // 0 // Hs.517065 // RIMS4 // 140730 // Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// ENST00000217067 // intron // 0 // --- // --- // --- // ---	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-1664420	aaaaaaaaaaaaaaaaaaagcctcc[A/G]aaagaatgccca agaaattggtaac	A	G	NM_016276 // intron // 0 // Hs.62863 // SGK2 // 10110 // serum/glucocorticoid regulated kinase 2 /// NM_170693 // intron // 0 // Hs.62863 // SGK2 // 10110 // serum/glucocorticoid regulated kinase 2	SGK2	SGK2 , rs1894666, serum,q13.12
SNP_A-1915339	tgttcatttttcctca[A/T]gttcagcaatatttaa	A	T	NM_182970 // upstream // 41232 // Hs.517065 // RIMS4 // 140730 // Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// NM_003404 // upstream // 34200 // Hs.279920 // YWHAB // 7529 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-2141730	atcttctcttatgtaa[C/T]tgctaacatcaaagtt	C	T	NM_182970 // upstream // 54005 // Hs.517065 // RIMS4 // 140730 // Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// NM_003404 // upstream // 21427 // Hs.279920 // YWHAB // 7529 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-2150051	atgtccacctcgaaca[A/G]tcatagggactcagct	A	G	NM_182970 // upstream // 58273 // Hs.517065 // RIMS4 // 140730 // Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), mRNA. /// NM_003404 // upstream // 17159 // Hs.279920 // YWHAB // 7529 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-	RIMS4	RIMS4, Homo sapiens regulating synaptic membrane exocytosis 4 (RIMS4), q13.12
SNP_A-1860505	tcagttatggtttcaa[A/G]ttatgttgctgtacat	A	G	NM_003404 // intron // 0 // Hs.279920 // YWHAB // 7529 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB), transcript varian /// NM_139323 // intron // 0 // Hs.279920 // YWHAB // 7529 // Homo s	YWHAB	YWHAB, Homo sapiens tyrosine 3-monooxygenase,q13.12
SNP_A-1880210	tcttctgttaaaaatc[A/G]ctttgaccatccatag	A	G	NM_003404 // intron // 0 // Hs.279920 // YWHAB // 7529 // Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide (YWHAB), transcript varian /// NM_139323 // intron // 0 // Hs.279920 // YWHAB // 7529 // Homo s	YWHAB	YWHAB, Homo sapiens tyrosine 3-monooxygenase q13.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2313517	ggagagtctcagtaga[C/T]attggcatcttagggt	C	T	ENST00000217073 // intron // 0 // — // — // — // — /// ENST00000255136 // intron // 0 // — // — // — // — // — /// ENST00000217075 // intron // 0 // — // — // — // —	-	q13.12
SNP_A-1866826	tcccggtagagtcaca[A/G]gatgcacttaattctt	A	G	NM_181525 // intron // 0 // Hs.419126 // WFDC3 // 140686 // Homo sapiens WAP four-disulfide core domain 3 (WFDC3), transcript variant 3, mRNA. /// NM_181522 // intron // 0 // Hs.419126 // WFDC3 // 140686 // Homo sapiens WAP four-disulfide core domain 3 (W	WFDC3	WFDC3, Homo sapiens WAP four-disulfide core domain 3 (WFDC3), transcript variant 3, q13.12
SNP_A-2250937	cttatgctgggtcata[A/T]aaacagtcagaactag	A	T	NM_003279 // upstream // 4423 // Hs.182421 // TNNC2 // 7125 // Homo sapiens troponin C2, fast (TNNC2), mRNA. /// NM_152897 // upstream // 2094 // Hs.472854 // C20orf161 // 90203 // Homo sapiens chromosome 20 open reading frame 161 (C20orf161), transcript	TNNC2	TNNC2, Homo sapiens troponin C2, fast (TNNC2), q13.12
SNP_A-2286084	gatgattgctggtttc[C/T]cttacacatagcagag	C	T	NM_183385 // intron // 0 // Hs.444776 // PTE1 // 10005 // Homo sapiens peroxisomal acyl-CoA thioesterase (PTE1), transcript variant 2, mRNA. /// NM_183386 // intron // 0 // Hs.444776 // PTE1 // 10005 // Homo sapiens peroxisomal acyl-CoA thioesterase (PTE1	PTE1	PTE1, Homo sapiens peroxisomal acyl-CoA thioesterase (PTE1), transcript variant 2, q13.12
SNP_A-2083057	acgtgtgtaaccatgg[G/T]agacgacaaaagtatg	G	T	NM_020967 // intron // 0 // Hs.25669 // NCOA5 // 57727 // Homo sapiens nuclear receptor coactivator 5 (NCOA5), mRNA. /// ENST00000290231 // intron // 0 // — // — // — // — /// ENST00000356776 // intron // 0 // — // — // — // —	NCOA5	NCOA5, Homo sapiens nuclear receptor coactivator 5 (NCOA5), q13.12
SNP_A-2204737	ccaggcaactctttac[A/G]ctgctgcgattctctt	A	G	NM_020967 // upstream // 26170 // Hs.25669 // NCOA5 // 57727 // Homo sapiens nuclear receptor coactivator 5 (NCOA5), mRNA. /// NM_020967 // upstream // 26203 // Hs.25669 // NCOA5 // 57727 // Homo sapiens nuclear receptor coactivator 5 (NCOA5), mRNA. /// N	NCOA5	NCOA5, Homo sapiens nuclear receptor coactivator 5 (NCOA5), q13.12
SNP_A-2127612	ataaccgttttaagtg[A/G]atatcagtactttaat	A	G	NM_152854 // downstream // 24498 // Hs.472860 // CD40 // 958 // Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), transcript variant 2, mRNA. /// NM_001250 // downstream // 24498 // Hs.472860 // CD40 // 958 // Homo sapiens tumor	CD40	CD40, Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), transcript variant 2, q13.12
SNP_A-2086931	actgagattgaaggaa[C/G]agatttgggggatgag	C	G	NM_021248 // intron // 0 // Hs.472861 // CDH22 // 64405 // Homo sapiens cadherin-like 22 (CDH22), mRNA. /// ENST00000279063 // intron // 0 // — // — // — // —	CDH22	CDH22, Homo sapiens cadherin-like 22 (CDH22), q13.12
SNP_A-1968505	cagaggcaggtcttct[A/G]actaagaaatggatat	A	G	NM_173643 // upstream // 1765 // Hs.377046 // DKFZp547G0215 // 284747 // Homo sapiens hypothetical protein DKFZp547G0215 (DKFZp547G0215), mRNA. /// ENST00000317836 // upstream // 1765 // — // — // — // — /// ENST00000328749 // upstream // 30070 //	DKFZp547G0215	DKFZp547G0215, Homo sapiens hypothetical protein DKFZp547G0215 (DKFZp547G0215), q13.12
SNP_A-2194939	catgctgagcgcactg[A/C]aggacagaatccagtg	A	C	NM_022829 // intron // 0 // Hs.250281 // SLC13A3 // 64849 // Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3), mRNA. /// ENST00000279027 // intron // 0 // — // — // — // — /// ENST00000290317 /	SLC13A3	SLC13A3, Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (SLC13A3), q13.12
SNP_A-2091971	agaaacaggcagcacc[A/G]aggaatgagctcacct	A	G	NM_030777 // downstream // 115964 // Hs.305971 // SLC2A10 // 81031 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), mRNA. /// NM_005244 // upstream // 42562 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes a	SLC2A10	SLC2A10, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 10 (SLC2A10), q13.12
SNP_A-2235583	ctcctaccttccataa[C/T]gggtttgctcatccat	C	T	NM_005244 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2062101	aatggggaggcaacta[C/T]gaaatcaacagtggga	C	T	NM_005244 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12
SNP_A-1818666	gttgaatcctctcaac[A/G]acactatggagcgggt	A	G	NM_005244 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12
SNP_A-1793695	ggtatgtaggaagcac[A/T]caataaatgcacctct	A	T	NM_005244 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, mRNA. /// NM_172111 // intron // 0 // Hs.472877 // EYA2 // 2139 // Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2	EYA2	EYA2, Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), transcript variant 1, q13.12
SNP_A-1796275	ggtgtggctactccac[C/G]ccttgcttctcctcct	C	G	NM_012408 // intron // 0 // Hs.446240 // PRKCBP1 // 23613 // Homo sapiens protein kinase C binding protein 1 (PRKCBP1), transcript variant 2, mRNA. /// NM_183048 // intron // 0 // Hs.446240 // PRKCBP1 // 23613 // Homo sapiens protein kinase C binding prot	PRKCBP1	PRKCBP1, Homo sapiens protein kinase C binding protein 1 (PRKCBP1), transcript variant 2, q13.12
SNP_A-2122167	agtgatttactatgca[A/G]caatggattattgaaa	A	G	NM_012408 // upstream // 139767 // Hs.446240 // PRKCBP1 // 23613 // Homo sapiens protein kinase C binding protein 1 (PRKCBP1), transcript variant 2, mRNA. /// NM_183048 // upstream // 139767 // Hs.446240 // PRKCBP1 // 23613 // Homo sapiens protein kinase	PRKCBP1	PRKCBP1, Homo sapiens protein kinase C binding protein 1 (PRKCBP1), transcript variant 2, q13.12
SNP_A-1946697	tttaacatttacttct[C/G]aatactgtcttttcct	C	G	NM_006534 // intron // 0 // Hs.382168 // NCOA3 // 8202 // Homo sapiens nuclear receptor coactivator 3 (NCOA3), transcript variant 2, mRNA. /// NM_181659 // intron // 0 // Hs.382168 // NCOA3 // 8202 // Homo sapiens nuclear receptor coactivator 3 (NCOA3), t	NCOA3	NCOA3, Homo sapiens nuclear receptor coactivator 3 (NCOA3), transcript variant 2, q13.12
SNP_A-2183170	cagcaactccccccggc[A/G]ctagacgagctctatc	A	G	NM_018837 // intron // 0 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// ENST00000359930 // intron // 0 // — // — // — // — /// ENST00000360838 // intron // 0 // — // — // — // — /// ENST	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.12
SNP_A-2007702	cgtgcagttagcacca[A/T]ctcctaccatcactgc	A	T	NM_018837 // intron // 0 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// ENST00000359930 // intron // 0 // — // — // — // — /// ENST00000360838 // intron // 0 // — // — // — // — /// ENST	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.12
SNP_A-1937797	ttgaagttgtttgtga[A/G]cagaaatttaactccc	A	G	NM_018837 // intron // 0 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// ENST00000359930 // intron // 0 // — // — // — // — /// ENST00000360838 // intron // 0 // — // — // — // — /// ENST	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.12
SNP_A-1783538	ggcatgaaaatattcg[C/T]caattataggagagtt	C	T	NM_018837 // upstream // 23267 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 22715 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRN	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2242804	ctgcattttgtgttca[C/T]cgcctggccctggtgg	C	T	NM_018837 // upstream // 23616 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 23064 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRN	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1947160	ttaatgaatggcagc[G/T]ccggctcctccggctt	G	T	NM_018837 // upstream // 49797 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 49245 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRN	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1888082	tgagccaacattcaag[A/T]ctcaaatatttttaca	A	T	NM_018837 // upstream // 70272 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 69720 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRN	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2285524	gatgaaaaccagtgcc[A/G]aatggaaatgcaaatc	A	G	NM_018837 // upstream // 79502 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 78950 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRN	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1752611	gcctgaccccagagctttacggtga[A/G]tcacagcctgtccctgt ccctggat	A	G	NM_022829 // intron // 0 // Hs.202494 // SLC13A3 // 64849 // solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	SLC13A3	SLC13A3 , rs6017950, solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3,q13.12
SNP_A-1845687	tataggccacacaaata[G/T]gtagaactgggaatc	G	T	NM_018837 // upstream // 249676 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 249124 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2041106	aacctacctgtggcat[C/G]accagactcggaaagt	C	G	NM_018837 // upstream // 250937 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 250385 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1968548	cctggaatgtggtaag[A/T]actgtgtaagagttag	A	T	NM_018837 // upstream // 317411 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 316859 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-2089137	acttaatttaccaaca[C/T]atccggagtgtatttt	C	T	NM_018837 // upstream // 325262 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 324710 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1920178	ttaatctgcaagcac[A/G]gggagtttctgccatc	A	G	NM_018837 // upstream // 482135 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 481583 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1872442	tctagcagattctttc[A/G]cacctagtcccggtgg	A	G	NM_018837 // upstream // 554242 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 553690 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1924379	ttataagatatgattcc[A/G]atgcgacgtcattgcc	A	G	NM_018837 // upstream // 580922 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 580370 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2281906	gagtgcatagtgcaga[C/T]agtgaaaacgccgtcag	C	T	NM_018837 // upstream // 770071 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA. /// NM_018837 // upstream // 769519 // Hs.162016 // SULF2 // 55959 // Homo sapiens sulfatase 2 (SULF2), transcript variant 1, m	SULF2	SULF2, Homo sapiens sulfatase 2 (SULF2), transcript variant 1, q13.13
SNP_A-1904574	tggggcacgggaaggg[C/T]agaagaaatccagtcc	C	T	NM_020820 // intron // 0 // Hs.153310 // PREX1 // 57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// ENST00000262976 // intron // 0 // — // — // — // —	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-2007718	gcacagcctatcaca[C/T]agtattacctggcccc	C	T	NM_020820 // intron // 0 // Hs.153310 // PREX1 // 57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// ENST00000262976 // intron // 0 // — // — // — // —	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-1863695	tccaactgaggtttgc[A/G]agtttaagctcagca	A	G	NM_020820 // upstream // 25877 // Hs.153310 // PREX1 // 57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// NM_006420 // upstream // 68130 // Hs.62578 // ARFGEF2 // 10564 // Homo sapiens ADP-ribosyla	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-2025205	aaaataggtagcagg[G/T]ccaaatcaaaatgaga	G	T	NM_020820 // upstream // 38391 // Hs.153310 // PREX1 // 57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// NM_006420 // upstream // 55616 // Hs.62578 // ARFGEF2 // 10564 // Homo sapiens ADP-ribosyla	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-2143663	atgactttttctttg[C/G]agcacgtattgtacta	C	G	NM_020820 // upstream // 51347 // Hs.153310 // PREX1 // 57580 // Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), mRNA. /// NM_006420 // upstream // 42660 // Hs.62578 // ARFGEF2 // 10564 // Homo sapiens ADP-ribosyla	PREX1	PREX1, Homo sapiens phosphatidylinositol 3,4,5-trisphosphate-dependent RAC exchanger 1 (PREX1), q13.13
SNP_A-2249071	ctgtttccagaggaga[C/G]agcttaaaaaccacag	C	G	NM_004975 // intron // 0 // Hs.84244 // KCNB1 // 3745 // Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA. /// ENST00000289405 // intron // 0 // — // — // — // —	KCNB1	KCNB1, Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), q13.13
SNP_A-2118411	agtaagcctggtagca[A/C]ctagcatgaaacaaaa	A	C	NM_004776 // intron // 0 // Hs.370487 // B4GALT5 // 9334 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5), mRNA. /// ENST00000289420 // intron // 0 // — // — // — // —	B4GALT5	B4GALT5, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5), q13.13
SNP_A-2084909	actcaaggtgactcta[A/C]tacatatattccigtt	A	C	NM_004776 // upstream // 74830 // Hs.370487 // B4GALT5 // 9334 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5), mRNA. /// NM_015266 // upstream // 24082 // Hs.444202 // SLC9A8 // 23315 // Homo sapiens solute car	B4GALT5	B4GALT5, Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5), q13.13
SNP_A-2271888	gacccagaatcactaa[C/T]gtaaggatacctggtc	C	T	NM_199144 // intron // 0 // Hs.420529 // UBE2V1 // 7335 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA. /// NM_021988 // intron // 0 // Hs.420529 // UBE2V1 // 7335 // Homo sapiens ubiquitin-conjugating enzym	UBE2V1	UBE2V1, Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, q13.13
SNP_A-2213512	ccggtgagctggaaaa[C/T]ccatgttgccctgca	C	T	NM_003349 // intron // 0 // Hs.420529 // Kua-UEV // 387522 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (Kua-UEV), transcript variant 2, mRNA. /// NM_199203 // intron // 0 // Hs.420529 // Kua-UEV // 387522 // Homo sapiens ubiquitin-conjugatin	Kua-UEV	Kua-UEV, Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (Kua-UEV), transcript variant 2, q13.13
SNP_A-1860529	tcagttccttcctga[C/G]ggctgatacttgaat	C	G	NM_003349 // intron // 0 // Hs.420529 // Kua-UEV // 387522 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (Kua-UEV), transcript variant 2, mRNA. /// NM_199203 // intron // 0 // Hs.420529 // Kua-UEV // 387522 // Homo sapiens ubiquitin-conjugatin	Kua-UEV	Kua-UEV, Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (Kua-UEV), transcript variant 2, q13.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2064654	aattctcatccataaa[A/G]aatgcatacacaatgg	A	G	NM_003349 // intron // 0 // Hs.420529 // Kua-UEV // 387522 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (Kua-UEV), transcript variant 2, mRNA. /// NM_199203 // intron // 0 // Hs.420529 // Kua-UEV // 387522 // Homo sapiens ubiquitin-conjugatin	Kua-UEV	Kua-UEV, Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (Kua-UEV), transcript variant 2, q13.13
SNP_A-2007733	aaatggacttaattta[C/T]aggcgtgccagcactg	C	T	NM_199144 // upstream // 62919 // Hs.420529 // UBE2V1 // 7335 // Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA. /// NM_021988 // upstream // 62919 // Hs.420529 // UBE2V1 // 7335 // Homo sapiens ubiquitin-conju	UBE2V1	UBE2V1, Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, q13.13
SNP_A-2244520	ctggactgttctttccd[A/G]cagatatcctgaaggc	A	G	NM_005194 // downstream // 255025 // Hs.517106 // CEBPB // 1051 // Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA. /// NM_002827 // upstream // 62654 // Hs.417549 // PTPN1 // 5770 // Homo sapiens protein tyrosine phosphatase, non-	CEBPB	CEBPB, Homo sapiens CCAAT q13.13
SNP_A-1642331	tttctgatggcatagctttggatc[A/G]atcattctcttttttgctctgtc t	A	G	NM_004776 // intron // 0 // Hs.107526 // B4GALT5 // 9334 // UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	B4GALT5	B4GALT5, rs9968149, UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5,q13.13
SNP_A-1855211	tcaagcactgagccac[A/G]ggcttgccatcagcc	A	G	NM_002237 // upstream // 134605 // Hs.118695 // KCNG1 // 3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 134605 // Hs.118695 // KCNG1 // 3755 // Homo sapiens pot	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2120310	agtcatagtgtgaaca[C/T]gggccaacaccacttc	C	T	NM_002237 // upstream // 135706 // Hs.118695 // KCNG1 // 3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 135706 // Hs.118695 // KCNG1 // 3755 // Homo sapiens pot	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2184658	cagctctacaaaagaa[C/T]gagttaatgtctttgc	C	T	NM_002237 // upstream // 211820 // Hs.118695 // KCNG1 // 3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 211820 // Hs.118695 // KCNG1 // 3755 // Homo sapiens pot	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-2051923	aaggtgccacctctaa[C/T]tggctgcagaaaagtg	C	T	NM_002237 // upstream // 237210 // Hs.118695 // KCNG1 // 3755 // Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, mRNA. /// NM_172318 // upstream // 237210 // Hs.118695 // KCNG1 // 3755 // Homo sapiens pot	KCNG1	KCNG1, Homo sapiens potassium voltage-gated channel, subfamily G, member 1 (KCNG1), transcript variant 1, q13.2
SNP_A-1968601	aacacgcaatgaacac[A/G]ctagagccctttgtaa	A	G	NM_012340 // intron // 0 // Hs.356321 // NFATC2 // 4773 // Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), transcript variant 1, mRNA. /// NM_173091 // intron // 0 // Hs.356321 // NFATC2 // 4773 // Homo sap	NFATC2	NFATC2, Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), transcript variant 1, q13.2
SNP_A-1851231	tattcagaaccttgaa[A/G]gcaccgtgcagaccaa	A	G	AB014511 // intron // 0 // Hs.368002 // ATP9A // 10079 // Homo sapiens mRNA for KIAA0611 protein, partial cds. /// ENST00000311637 // intron // 0 // — // — // — /// ENST00000338821 // intron // 0 // — // — // —	ATP9A	ATP9A, Homo sapiens for KIAA0611 protein, partial cds. q13.2
SNP_A-2007745	cctggcagcatagtg[A/G]cacctgtatctaataa	A	G	AB014511 // intron // 0 // Hs.368002 // ATP9A // 10079 // Homo sapiens mRNA for KIAA0611 protein, partial cds. /// ENST00000311637 // intron // 0 // — // — // — /// ENST00000338821 // intron // 0 // — // — // —	ATP9A	ATP9A, Homo sapiens for KIAA0611 protein, partial cds. q13.2
SNP_A-2141089	atctgctggtacaaaa[C/T]ctgaattataggaaga	C	T	NM_020436 // intron // 0 // Hs.517113 // SALL4 // 57167 // Homo sapiens sal-like 4 (Drosophila) (SALL4), mRNA. /// ENST00000217086 // intron // 0 // — // — // —	SALL4	SALL4, Homo sapiens sal-like 4 (Drosophila) (SALL4), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1933210	ttctaaactgcttcta[G/T]gtattattaaaccaaa	G	T	NM_020436 // upstream // 1647 // Hs.517113 // SALL4 // 57167 // Homo sapiens sal-like 4 (Drosophila) (SALL4), mRNA. /// NM_022088 // downstream // 347164 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transc	SALL4	SALL4, Homo sapiens sal-like 4 (Drosophila) (SALL4), q13.2
SNP_A-2055918	aatacacatcctgga[C/T]atagttgccaaaaacc	C	T	NM_022088 // upstream // 278381 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 278381 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1968625	actctctaggaaac[A/G]gcctgattaaccagaa	A	G	NM_022088 // upstream // 472043 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 472043 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1968628	tctttggtgccctaa[C/T]agcaaagcccagcagg	C	T	NM_022088 // upstream // 486322 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 486322 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1796869	ggttcattattcagga[G/T]attggaagaccaat	G	T	NM_022088 // upstream // 552943 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 552943 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-2096131	agacatgactagaaaa[C/G]aaagatacatatgtcc	C	G	NM_022088 // upstream // 555672 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 555672 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1840681	tagcctttagctgggc[G/T]cctttgtgccaaacaa	G	T	NM_022088 // upstream // 556166 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 556166 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1968632	gtttgtaaggctgagc[A/G]actggttgttaaagag	A	G	NM_022088 // upstream // 667170 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 667170 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1919145	ttaactgtcagctaca[C/T]gaaaggagacattcca	C	T	NM_022088 // upstream // 706097 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, mRNA. /// NM_199426 // upstream // 706097 // Hs.473082 // ZFP64 // 55734 // Homo sapiens zinc finger prote	ZFP64	ZFP64, Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), transcript variant 2, q13.2
SNP_A-1749475	ttccaagatggtagattagaaaaa[C/T]gagccaactggacgg ggaagtttga	C	T	NM_018197 // downstream // 316102 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse) /// NM_020436 // upstream // 32771 // Hs.189095 // SALL4 // 57167 // sal-like 4 (Drosophila) /// NM_022088 // downstream // 316100 // Hs.504892 //	ZFP64	ZFP64 , rs10485619, zinc finger protein 64 homolog (mouse) , q13.2
SNP_A-2178445	cactcccaggtatcaa[G/T]caatcccctgagcatt	G	T	NM_173485 // downstream // 141695 // Hs.473117 // C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream // 90689 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. ///	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1707385	cacaagagacagcacagtgagtaca[A/G]tgagagtaagaaact cggacgtgacc	A	G	NM_018197 // CDS // 0 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse) /// NM_022088 // CDS // 0 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse)	ZFP64	ZFP64, rs3746414, zinc finger protein 64 homolog (mouse), q13.2
SNP_A-1837530	tactgctattcacta[C/T]gctgaaaacttttatt	C	T	NM_173485 // downstream // 192765 // Hs.473117 // C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream // 39619 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. ///	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-1922369	ttagaaaatcaagtca[A/C]cttgtattactgttc	A	C	NM_173485 // downstream // 222943 // Hs.473117 // C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream // 9441 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. ///	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-1930485	ttccaaataaagcaaa[A/G]tacaggttctcttttgt	A	G	NM_173485 // downstream // 222999 // Hs.473117 // C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream // 9385 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. ///	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-2036454	aaattctgtagatgga[C/T]attgttatgttgtac	C	T	NM_173485 // downstream // 229403 // Hs.473117 // C20orf17 // 128553 // Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA. /// AF230201 // upstream // 2981 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. ///	C20orf17	C20orf17, Homo sapiens chromosome 20 open reading frame 17 (C20orf17), q13.2
SNP_A-1934652	ttctctgcaacaagga[C/T]agtaagatgtagatga	C	T	AF230201 // downstream // 1546 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. /// NM_006526 // downstream // 75946 // Hs.155040 // ZNF217 // 7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000279004 /	C20orf17	C20orf17, Homo sapiens OVC10-2 complete cds. q13.2
SNP_A-1899588	tggaagtaaagatgaa[C/T]gacatgcaaagaaata	C	T	AF230201 // downstream // 8065 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. /// NM_006526 // downstream // 69427 // Hs.155040 // ZNF217 // 7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000279004 /	C20orf17	C20orf17, Homo sapiens OVC10-2 complete cds. q13.2
SNP_A-1792565	ggtaaacgactagata[G/T]agatatttttggcct	G	T	AF230201 // downstream // 13635 // Hs.473117 // C20orf17 // 128553 // Homo sapiens OVC10-2 mRNA, complete cds. /// NM_006526 // downstream // 63857 // Hs.155040 // ZNF217 // 7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000279004	C20orf17	C20orf17, Homo sapiens OVC10-2 complete cds. q13.2
SNP_A-1885032	tgaatggcacttctaa[A/C]aattggctacacaacc	A	C	NM_006526 // upstream // 228584 // Hs.155040 // ZNF217 // 7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000355985 // upstream // 233573 // — // — // — /// ENST00000357106 // downstream // 241186 // — // — // — /	ZNF217	ZNF217, Homo sapiens zinc finger protein 217 (ZNF217), q13.2
SNP_A-2023230	aaaacatgtactccga[A/T]gtcagatggcctggat	A	T	NM_006526 // upstream // 279839 // Hs.155040 // ZNF217 // 7764 // Homo sapiens zinc finger protein 217 (ZNF217), mRNA. /// ENST00000355985 // upstream // 284828 // — // — // — // — /// ENST00000357106 // downstream // 292441 // — // — // — /	ZNF217	ZNF217, Homo sapiens zinc finger protein 217 (ZNF217), q13.2
SNP_A-1921122	ttacagttgcaaggc[C/T]atctgagaggtcttcg	C	T	NM_003657 // downstream // 31290 // Hs.400556 // BCAS1 // 8537 // Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), mRNA. /// ENST00000279003 // upstream // 37131 // — // — // — // — /// ENST00000262592 // downstream // 31290 // — // -	BCAS1	BCAS1, Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1725972	actgactcaggatacactggataaga[C/T]actttctgtgtatgtgatttaaag	C	T	NM_018197 // upstream // 474240 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse) /// NM_022088 // upstream // 474027 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse) /// NM_173485 // upstream // 307201 // H	ZFP64	ZFP64 , rs6063858, zinc finger protein 64 homolog (mouse), q13.2
SNP_A-1679336	caaaattgtggtaatttgagagtc[A/G]agacaagtatttattcaccaccaatg	A	G	NM_018197 // upstream // 710670 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse) /// NM_022088 // upstream // 710457 // Hs.504892 // ZFP64 // 55734 // zinc finger protein 64 homolog (mouse) /// NM_173485 // upstream // 70771 // Hs	ZFP64	ZFP64 , rs2247273, zinc finger protein 64 homolog (mouse), q13.2
SNP_A-2217993	cctgcattcagtttca[C/T]ctttatctgtgttgt	C	T	NM_000782 // intron // 0 // Hs.89663 // CYP24A1 // 1591 // Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, mRNA /// ENST00000216862 // intron // 0 // --- // --- // ---	CYP24A1	CYP24A1, Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1), nuclear gene encoding mitochondrial protein, q13.2
SNP_A-1968695	acccatgatctaccctg[A/C]aatggctgtcttctg	A	C	NM_002623 // downstream // 130999 // Hs.91161 // PFDN4 // 5203 // Homo sapiens prefoldin 4 (PFDN4), mRNA. /// NM_177959 // upstream // 124766 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_177959	PFDN4	PFDN4, Homo sapiens prefoldin 4 (PFDN4), q13.2
SNP_A-2026788	aaacacaccagagagc[A/G]aagatgaacaccatct	A	G	NM_002623 // downstream // 137066 // Hs.91161 // PFDN4 // 5203 // Homo sapiens prefoldin 4 (PFDN4), mRNA. /// NM_177959 // upstream // 118699 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_177959	PFDN4	PFDN4, Homo sapiens prefoldin 4 (PFDN4), q13.2
SNP_A-2055723	aataattccaaaatct[G/T]aacagtttacagcaac	G	T	NM_177959 // intron // 0 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // intron // 0 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 1, mRNA. /	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2007780	gcaaaacgagagaaca[C/G]agtttctgaagttggg	C	G	NM_177959 // intron // 0 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // intron // 0 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 1, mRNA. /	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2007781	gtgattcatcagtcca[C/T]acatcatttcttgta	C	T	NM_177959 // intron // 0 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // intron // 0 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 1, mRNA. /	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2263817	gaacgcgaaaatcaag[A/G]actaaattgctgacta	A	G	NM_177959 // downstream // 151046 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 151046 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2148023	atggcttagttcaaga[A/T]gagcataatttttaac	A	T	NM_177959 // downstream // 189214 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 189214 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2241493	ctgagtggtccctata[A/G]gtgattgctctatgcc	A	G	NM_177959 // downstream // 190835 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 190835 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1898403	tgcttccatttttgta[C/T]ccattggccacttcac	C	T	NM_177959 // downstream // 196607 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 196607 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1968714	cgtttgtctgatgtaa[A/G]gttcctatttttcca	A	G	NM_177959 // downstream // 217556 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 217556 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2278667	gagctggtgctgaga[C/G]aaaggatgcaaatcag	C	G	NM_177959 // downstream // 332455 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 332455 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1968722	ataggatgtcttcctat[C/T]gattctatatccaatg	C	T	NM_177959 // downstream // 344433 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 344433 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1954806	tttgctgtggacagga[C/T]ctttatgcgtcgaagg	C	T	NM_177959 // downstream // 347690 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 347690 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2117776	aggttgaggggggtttc[A/G]catttaccaaagcttt	A	G	NM_177959 // downstream // 526893 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 526893 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1958951	ttttcttggactgtta[C/T]aacgccatgactcaga	C	T	NM_177959 // downstream // 548795 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 548795 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2043835	aacttcaggactctta[C/T]aggatcattggaaaag	C	T	NM_177959 // downstream // 591070 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 591070 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2122822	agtggcagaacacccaa[A/G]tgaaaaatgacctcag	A	G	NM_177959 // downstream // 592020 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 592020 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2216269	cctcctcaaaggtcaa[A/C]tcctggtcattcttc	A	C	NM_177959 // downstream // 606594 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 606594 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2254210	cttgatgcttttgag[A/G]aactggtccatttat	A	G	NM_177959 // downstream // 630852 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA /// NM_018431 // downstream // 630852 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2065560	aatttaatgcttgttg[G/T]aactctagaaatctct	G	T	NM_177959 // downstream // 633580 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 633580 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-2269329	gaatttgcatttttcc[A/G]ataactcttgaagcca	A	G	NM_177959 // downstream // 670583 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 670583 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1916960	tgtttgaccacttatc[A/G]gaactttctatataat	A	G	NM_177959 // downstream // 679126 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript variant 2, mRNA. /// NM_018431 // downstream // 679126 // Hs.473133 // DOK5 // 55816 // Homo sapiens docking protein 5 (DOK5), transcript	DOK5	DOK5, Homo sapiens docking protein 5 (DOK5), transcript variant 2, q13.2
SNP_A-1968731	actgacctagcagagg[A/T]atttgaggattaaatg	A	T	NM_080617 // downstream // 576768 // Hs.126141 // CBLN4 // 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 26993 // — // — // — // — /// ENST00000064571 // downstream // 576768 // — // — // —	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.2
SNP_A-2150866	atgtggcagattgctt[C/T]aactgactttatcaag	C	T	NM_080617 // downstream // 477186 // Hs.126141 // CBLN4 // 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 126575 // — // — // — // — /// ENST00000064571 // downstream // 477186 // — // — // –	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-1968745	tatgagattcaagcca[A/G]agaaattatctcagtg	A	G	NM_080617 // downstream // 383857 // Hs.126141 // CBLN4 // 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 219904 // — // — // — // — /// ENST00000064571 // downstream // 383857 // — // — // –	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-1968767	tcagcggtaattccac[A/G]atgtcactctttcagc	A	G	NM_080617 // downstream // 53789 // Hs.126141 // CBLN4 // 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// ENST00000356717 // downstream // 549972 // — // — // — // — /// ENST00000064571 // downstream // 53789 // — // — // —	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-1812698	gtggcttttgtagaga[C/T]ggagtccctgaccatg	C	T	NM_080617 // upstream // 22380 // Hs.126141 // CBLN4 // 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// NM_019888 // upstream // 220878 // Hs.248018 // MC3R // 4159 // Homo sapiens melanocortin 3 receptor (MC3R), mRNA. /// ENST00000064571	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-2215649	cctcaggtctttgata[C/T]aatgtcatttaatcag	C	T	NM_080617 // upstream // 94585 // Hs.126141 // CBLN4 // 140689 // Homo sapiens cerebellin 4 precursor (CBLN4), mRNA. /// NM_019888 // upstream // 148673 // Hs.248018 // MC3R // 4159 // Homo sapiens melanocortin 3 receptor (MC3R), mRNA. /// ENST00000064571	CBLN4	CBLN4, Homo sapiens cerebellin 4 precursor (CBLN4), q13.31
SNP_A-1718195	tgacaacagctgagtcaccccgtgc[A/G]gatataacaagttcgtaagatgtga	A	G	NM_018431 // downstream // 344565 // Hs.127751 // DOK5 // 55816 // docking protein 5 /// NM_080617 // downstream // 961105 // Hs.126141 // CBLNL1 // 140689 // cerebellin precursor-like 1 /// NM_177959 // downstream // 344565 // Hs.127751 // DOK5 // 55816	DOK5	DOK5 , rs1499865, docking protein 5 ,q13.2
SNP_A-2050169	aaggaccttgccaagc[C/T]gatcgcagtgtttgga	C	T	NM_080821 // intron // 0 // Hs.143736 // C20orf108 // 116151 // Homo sapiens chromosome 20 open reading frame 108 (C20orf108), mRNA. /// ENST00000243920 // intron // 0 // — // — // — // —	C20orf108	C20orf108, Homo sapiens chromosome 20 open reading frame 108 (C20orf108), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1968775	gggatttatgaaatga[C/T]gcctttgaagtggaag	C	T	NM_080821 // intron // 0 // Hs.143736 // C20orf108 // 116151 // Homo sapiens chromosome 20 open reading frame 108 (C20orf108), mRNA. /// ENST00000243920 // intron // 0 // --- // --- // ---	C20orf108	C20orf108, Homo sapiens chromosome 20 open reading frame 108 (C20orf108), q13.31
SNP_A-2158112	attggagataaagtcc[A/G]aggaggtgaactaacc	A	G	NM_198435 // upstream // 214 // Hs.250822 // STK6 // 6790 // Homo sapiens serine/threonine kinase 6 (STK6), transcript variant 4, mRNA. /// NM_198433 // upstream // 214 // Hs.250822 // STK6 // 6790 // Homo sapiens serine/threonine kinase 6 (STK6), transcr	STK6	STK6, Homo sapiens serine q13.31
SNP_A-1693809	ctctctaaatttggtagtctgata[A/G]aagagagccacttgggaat gaattta	A	G	NM_018431 // downstream // 538287 // Hs.127751 // DOK5 // 55816 // docking protein 5 /// NM_080617 // downstream // 767383 // Hs.126141 // CBLNL1 // 140689 // cerebellin precursor-like 1 /// NM_177959 // downstream // 538287 // Hs.127751 // DOK5 // 55816	DOK5	DOK5 , rs6023940, docking protein 5 ,q13.2
SNP_A-1676106	gttgctctgcaggttattaatgtcc[C/T]agaataaacctaaaggga gaacagt	C	T	NM_018431 // downstream // 628331 // Hs.127751 // DOK5 // 55816 // docking protein 5 /// NM_080617 // downstream // 677339 // Hs.126141 // CBLNL1 // 140689 // cerebellin precursor-like 1 /// NM_177959 // downstream // 628331 // Hs.127751 // DOK5 // 55816	DOK5	DOK5 , rs2870619, docking protein 5 ,q13.2
SNP_A-1665672	caaattataatcattatcaaataccc[A/G]gcttaatcctctaacattt gtaaa	A	G	NM_018431 // downstream // 628619 // Hs.127751 // DOK5 // 55816 // docking protein 5 /// NM_080617 // downstream // 677051 // Hs.126141 // CBLNL1 // 140689 // cerebellin precursor-like 1 /// NM_177959 // downstream // 628619 // Hs.127751 // DOK5 // 55816	DOK5	DOK5 , rs6127464, docking protein 5 ,q13.2
SNP_A-1677440	ggacagcctgttgatcaatagaaatg[A/G]aattgagagtccagaa ataaagtcc	A	G	NM_018431 // downstream // 647527 // Hs.127751 // DOK5 // 55816 // docking protein 5 /// NM_080617 // downstream // 658143 // Hs.126141 // CBLNL1 // 140689 // cerebellin precursor-like 1 /// NM_177959 // downstream // 647527 // Hs.127751 // DOK5 // 55816	DOK5	DOK5 , rs211922, docking protein 5 ,q13.2
SNP_A-2190882	catagcacagaaaacaa[C/T]cgaaatactgagcaaa	C	T	NM_003222 // downstream // 183624 // Hs.473152 // TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream // 183624 // --- // --- // --- /// ENST	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31
SNP_A-2144485	atgatatagcctttga[A/G]ctgctagatccagctg	A	G	NM_003222 // downstream // 327124 // Hs.473152 // TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream // 327124 // --- // --- // --- /// ENST	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31
SNP_A-2037885	aacaatgaataacaca[C/G]gaaccaaccaccagg	C	G	NM_003222 // downstream // 327538 // Hs.473152 // TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream // 327538 // --- // --- // --- /// ENST	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31
SNP_A-1902059	tggcatctgaacggag[A/G]agaaagaggaggctgg	A	G	NM_003222 // downstream // 328023 // Hs.473152 // TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream // 328023 // --- // --- // --- /// ENST	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31
SNP_A-2305071	gctgaaggtaaagaag[C/G]acctcttagtagctca	C	G	NM_003222 // downstream // 352022 // Hs.473152 // TFAP2C // 7022 // Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA. /// ENST00000201031 // downstream // 352022 // --- // --- // --- /// ENST	TFAP2C	TFAP2C, Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1734596	atcacattgatttaagggaaaaaaaa[A/C]catattgagtggtgtaa ccaagaag	A	C	NM_018431 // downstream // 1267708 // Hs.127751 // DOK5 // 55816 // docking protein 5 /// NM_080617 // downstream // 37962 // Hs.126141 // CBLNL1 // 140689 // cerebellin precursor-like 1 /// NM_177959 // downstream // 1267708 // Hs.127751 // DOK5 // 5581	DOK5	DOK5 , rs992635, docking protein 5 ,q13.31
SNP_A-2141882	atcttggttctaggtt[C/G]aaaacaaaacaacct	C	G	NM_001719 // intron // 0 // Hs.473163 // BMP7 // 655 // Homo sapiens bone morphogenetic protein 7 (osteogenic protein 1) (BMP7), mRNA. /// ENST00000265624 // intron // 0 // — // — // —	BMP7	BMP7, Homo sapiens bone morphogenetic protein 7 (osteogenic protein 1) (BMP7), q13.31
SNP_A-2249503	cttaacattccctcctaj[C/G]tacgaaaggacaagag	C	G	NM_003610 // intron // 0 // Hs.371698 // RAE1 // 8480 // Homo sapiens RAE1 RNA export 1 homolog (S. pombe) (RAE1), mRNA. /// ENST00000217117 // intron // 0 // — // — // —	RAE1	RAE1, Homo sapiens RAE1 RNA export 1 homolog (S. pombe) (RAE1), q13.32
SNP_A-2088725	actgtggtcatctgaa[A/C]tactgtgacaaacaac	A	C	NM_030776 // upstream // 13684 // Hs.302123 // ZBP1 // 81030 // Homo sapiens Z-DNA binding protein 1 (ZBP1), mRNA. /// NM_020182 // downstream // 14241 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI),	ZBP1	ZBP1, Homo sapiens Z-DNA binding protein 1 (ZBP1), q13.32
SNP_A-1789025	gggcacctcccagaac[C/T]ctcaggaaacgcctcc	C	T	NM_020182 // intron // 0 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // intron // 0 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostat	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1901742	tggcacaggcctgcaa[C/T]agacataggaaacgct	C	T	NM_020182 // upstream // 86053 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 86053 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembr	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1832138	taatttcagctttgga[A/C]cctaagtggctgaagt	A	C	NM_020182 // upstream // 160645 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 160645 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2196274	catgtgtggtggcgc[A/G]atctctggcttgct	A	G	NM_020182 // upstream // 247334 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 247334 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1854542	tcaaattgtaaaaaaa[A/G]gtagccattacagtct	A	G	NM_020182 // upstream // 311976 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 311976 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2255231	cttggtgtattcttca[A/G]attggcagctggtcta	A	G	NM_020182 // upstream // 326464 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 326464 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1826145	taaattaaatattgca[A/G]ctgaaatccctgctaa	A	G	NM_020182 // upstream // 333713 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 333713 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1935503	ttctgggctctaaaga[C/T]acagagggaataaaa	C	T	NM_020182 // upstream // 335566 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 335566 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1857387	tcactaagcttcttaa[G/T]gcctgatctcttcatc	G	T	NM_020182 // upstream // 359109 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 359109 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2117231	aggtgctgcttctcac[A/G]ggctcaaagcacctt	A	G	NM_020182 // upstream // 359220 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 359220 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1837011	tactggcaagttaga[A/C]ggacacggtggccctc	A	C	NM_020182 // upstream // 383057 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 383057 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2098954	agagcttctgatccag[C/T]aggtttggatggtacc	C	T	NM_020182 // upstream // 383448 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 383448 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1791353	gggtactgaagatatg[C/T]aagggtcccaggagct	C	T	NM_020182 // upstream // 396775 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 396775 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2239417	ctctttgagcactacc[C/T]gaagggcacatctttt	C	T	NM_020182 // upstream // 401229 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 401229 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-1947116	tttaatccagtccaaa[C/T]gttgtggtgtctgccc	C	T	NM_020182 // upstream // 432815 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, mRNA. /// NM_199171 // upstream // 432815 // Hs.517155 // TMEPAI // 56937 // Homo sapiens transmem	TMEPAI	TMEPAI, Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), transcript variant 1, q13.32
SNP_A-2187495	cagtaaaaactggcaa[C/T]ctgttcagatatttt	C	T	AF119843 // intron // 0 // — // — // 0 // Homo sapiens PRO1085 mRNA, complete cds. /// ENST00000340003 // intron // 0 // — // — // — /// ENST00000334187 // intron // 0 // — // — // — /// ENST00000244070 // intron // 0 // —	-	-, Homo sapiens PRO1085 complete cds. q13.32
SNP_A-2095755	agacactctcaaaaa[A/T]ctgtgtttagtcagac	A	T	AF119843 // intron // 0 // — // — // 0 // Homo sapiens PRO1085 mRNA, complete cds. /// ENST00000340003 // intron // 0 // — // — // — /// ENST00000244064 // intron // 0 // — // — // —	-	-, Homo sapiens PRO1085 complete cds. q13.32
SNP_A-2290381	gcaaccaaaaacctaa[C/T]gcagctaaacataaag	C	T	NM_020673 // intron // 0 // Hs.529044 // RAB22A // 57403 // Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA. /// ENST00000244040 // intron // 0 // — // — // — // —	RAB22A	RAB22A, Homo sapiens RAB22A, member RAS oncogene family (RAB22A), q13.32
SNP_A-1968823	gaccttggatctccaa[A/G]ggtaagacttcaggt	A	G	ENST00000355651 // CDS // 0 // — // — // — // /// ENST00000354745 // CDS // 0 // — // — // —	-	q13.32
SNP_A-2111943	aggatctgaggattca[C/T]gacaaaaggccatct	C	T	ENST00000355651 // intron // 0 // — // — // — // /// ENST00000354745 // intron // 0 // — // — // —	-	q13.32

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2230992	ctatggttatgtaaca[A/T]ctgtgtccgagggatt	A	T	NM_016592 // intron // 0 // Hs.125898 // GNAS // 2778 // Homo sapiens GNAS complex locus (GNAS), transcript variant 4, mRNA. /// NM_080425 // intron // 0 // Hs.125898 // GNAS // 2778 // Homo sapiens GNAS complex locus (GNAS), transcript variant 3, mRNA. /	GNAS	GNAS, Homo sapiens GNAS complex locus (GNAS), transcript variant 4, q13.32
SNP_A-1753027	tttagcccttctcatacaaagggtc[A/G]ctataaaatgagtcaccc tcccttc	A	G	NM_020182 // intron // 0 // Hs.83883 // TMEPAI // 56937 // transmembrane, prostate androgen induced RNA	TMEPAI	TMEPAI , rs157103, transmembrane, prostate androgen induced RNA.q13.32
SNP_A-2228677	ctagaatgtaaactac[C/T]ctggcatatgtactac	C	T	NM_016592 // downstream // 40171 // Hs.125898 // GNAS // 2778 // Homo sapiens GNAS complex locus (GNAS), transcript variant 4, mRNA. /// NM_080425 // downstream // 40167 // Hs.125898 // GNAS // 2778 // Homo sapiens GNAS complex locus (GNAS), transcript va	GNAS	GNAS, Homo sapiens GNAS complex locus (GNAS), transcript variant 4, q13.32
SNP_A-1658006	tgaaaattaaaatggaaagaggtat[C/G]taaaatctcccactgt atcgtatca	C	G	NM_020182 // upstream // 307282 // Hs.83883 // TMEPAI // 56937 // transmembrane, prostate androgen induced RNA /// NM_178456 // upstream // 133742 // Hs.43977 // C20orf85 // 128602 // chromosome 20 open reading frame 85	TMEPAI	TMEPAI , rs1889331, transmembrane, prostate androgen induced RNA ,q13.32
SNP_A-1904063	tgggcagccttgtgta[C/T]cactcactaaattagt	C	T	NM_000114 // downstream // 43487 // Hs.1408 // EDN3 // 1908 // Homo sapiens endothelin 3 (EDN3), transcript variant 1, mRNA. /// NM_207034 // downstream // 43487 // Hs.1408 // EDN3 // 1908 // Homo sapiens endothelin 3 (EDN3), transcript variant 4, mRNA. /	EDN3	EDN3, Homo sapiens endothelin 3 (EDN3), transcript variant 1, q13.32
SNP_A-2211430	ccctagttctccattg[A/C]aatcattcccagtaag	A	C	NM_183244 // upstream // 13904 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_183244 // upstream // 41276 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.32
SNP_A-2207896	cccaaatcctgtagag[A/C]cccttgtcagtggcag	A	C	NM_183244 // upstream // 8376 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_183244 // upstream // 35748 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and a	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.32
SNP_A-2032220	aaagtgtctgacagca[C/G]gtcaatgcttgttgtt	C	G	NM_183244 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// ENST00000341679 // intron // 0 // --- // --- // --- // ---	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.32
SNP_A-1828703	taagctctaggctcta[C/T]aaaagtgctgtcagca	C	T	NM_183244 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// ENST00000341679 // intron // 0 // --- // --- // --- // ---	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.33
SNP_A-1890533	tgatcttaattgccaa[C/G]tgtaattaaatgatta	C	G	NM_183244 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// ENST00000341679 // intron // 0 // --- // --- // --- // ---	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.33
SNP_A-1819522	gttggtgaaaattgcc[C/T]ctcttttggtgctctc	C	T	NM_183244 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_080672 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regula	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.33
SNP_A-1896423	tgctaatggagagagc[A/G]cgtctcagaggctgca	A	G	NM_183244 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, mRNA. /// NM_080672 // intron // 0 // Hs.473218 // PHACTR3 // 116154 // Homo sapiens phosphatase and actin regula	PHACTR3	PHACTR3, Homo sapiens phosphatase and actin regulator 3 (PHACTR3), transcript variant 2, q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1968857	gaagaaaggaaaagaa[C/T]catccagataaatctc	C	T	NM_014258 // intron // 0 // Hs.202676 // SYCP2 // 10388 // Homo sapiens synaptonemal complex protein 2 (SYCP2), mRNA. /// ENST00000357552 // intron // 0 // — // — // — // — /// ENST00000358549 // intron // 0 // — // — - // — // —	SYCP2	SYCP2, Homo sapiens synaptonemal complex protein 2 (SYCP2), q13.33
SNP_A-1799809	gtacaatgaagtcatg[C/T]atacctatcaatctaga	C	T	ENST00000244047 // intron // 0 // — // — // — // —	-	q13.33
SNP_A-1797383	ggttgttgtgacttcc[A/C]atcaagaggtcctgac	A	C	AK055202 // downstream // 35758 // Hs.54973 // CDH26 // 60437 // Homo sapiens cDNA FLJ30640 fis, clone CTONG2002816, highly similar to Homo sapiens cadherin-like protein VR20 mRNA. /// NM_177980 // downstream // 35307 // Hs.54973 // CDH26 // 60437 // Homo	CDH26	CDH26, Homo sapiens cDNA FLJ30640 fis, clone CTONG2002816, highly similar to Homo sapiens cadherin-like protein VR20 ,q13.33
SNP_A-1902053	tggcatctagtacaga[A/G]caatgatggtctatct	A	G	AK055202 // downstream // 37754 // Hs.54973 // CDH26 // 60437 // Homo sapiens cDNA FLJ30640 fis, clone CTONG2002816, highly similar to Homo sapiens cadherin-like protein VR20 mRNA. /// NM_177980 // downstream // 37303 // Hs.54973 // CDH26 // 60437 // Homo	CDH26	CDH26, Homo sapiens cDNA FLJ30640 fis, clone CTONG2002816, highly similar to Homo sapiens cadherin-like protein VR20 ,q13.33
SNP_A-1893463	tgcagctggttcctga[C/G]aggccaggcagcactt	C	G	NM_173644 // intron // 0 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// ENST00000313426 // intron // 0 // — // — // —	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2184275	cagcctgtgactatag[C/T]gagtgctgtacagcag	C	T	NM_173644 // downstream // 36836 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 1142726 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2195332	catggcgtgtgttcta[C/T]attcacaagaaggaaa	C	T	NM_173644 // downstream // 39261 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 1140301 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2087045	actgagtctgggccac[C/G]cactggtgagctgttc	C	G	NM_173644 // downstream // 50279 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 1129283 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1968863	accagatgttggctga[A/G]gcattgatttatgggc	A	G	NM_173644 // downstream // 64449 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 1115113 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2249935	cttacagtatacctgg[A/G]catttccgtgtctcc	A	G	NM_173644 // downstream // 404223 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 775339 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1711953	agagttcctcttgctccatatttttt[G/T]ccagtatgtagtggtgtccat gttc	G	T	NM_000114 // downstream // 204701 // Hs.1408 // EDN3 // 1908 // endothelin 3 /// NM_080672 // upstream // 74188 // Hs.288513 // SCAPIN1 // 116154 // scapinin	EDN3	EDN3, rs3905228, endothelin 3 ,q13.32
SNP_A-2281508	gagtcatttttaaattg[G/T]attagtgagggcaact	G	T	NM_173644 // downstream // 806197 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 373365 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-1968900	ggaagtttaaaggcta[G/T]gtgttcccaagaggac	G	T	NM_173644 // downstream // 870135 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 309427 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2172124	caatggtgagaacgga[C/T]gggattcttttcagaa	C	T	NM_173644 // downstream // 968630 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 210932 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2125693	agtttcttggagacta[A/T]cccagacagttgcaac	A	T	NM_173644 // downstream // 976940 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 202622 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2137319	atcagttgtttgagta[C/G]catcttcaaggctttc	C	G	NM_173644 // downstream // 977339 // — // FLJ33860 // 284756 // Homo sapiens hypothetical protein FLJ33860 (FLJ33860), mRNA. /// NM_001794 // upstream // 202223 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4)	FLJ33860	FLJ33860, Homo sapiens hypothetical protein FLJ33860 (FLJ33860), q13.33
SNP_A-2073655	acagtcactactccac[A/G]ctgtcttatgcccagg	A	G	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2007878	gtgagaggacacttga[C/T]gatggagaggtcggag	C	T	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-1792094	gggtgtcattggtaga[A/G]gaatcagaggaatgga	A	G	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2045968	aagacctaacagaaac[C/G]catgcccaggtgcagc	C	G	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2301462	gcgaaacagaaactgc[C/T]aggaattatccactct	C	T	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // — /// ENST00000360469 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2180675	cagaagggcggtaaca[A/G]tggcagcaaccacgca	A	G	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // — /// ENST00000360469 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-1831207	taatgcttccagttac[A/G]cttaaaaatattttct	A	G	NM_001794 // intron // 0 // Hs.473231 // CDH4 // 1002 // Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), mRNA. /// ENST00000317614 // intron // 0 // — // — // — // — /// ENST00000360469 // intron // 0 // — // — // — // —	CDH4	CDH4, Homo sapiens cadherin 4, type 1, R-cadherin (retinal) (CDH4), q13.33
SNP_A-2301518	gcgacttagttaacaa[C/T]cctccaattccattat	C	T	NM_003185 // upstream // 47253 // Hs.473243 // TAF4 // 6874 // Homo sapiens TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa (TAF4), mRNA. /// NM_144703 // upstream // 10069 // Hs.105379 // C20orf40 // 149986 // Homo sapien	TAF4	TAF4, Homo sapiens TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa (TAF4), q13.33
SNP_A-2195911	catgtcagaaagaaaa[A/G]gcagtgtcagcacatg	A	G	NM_198935 // intron // 0 // Hs.154429 // SS18L1 // 26039 // Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), transcript variant 1, mRNA. /// NM_015558 // intron // 0 // Hs.154429 // SS18L1 // 26039 // Homo sapiens synovia	SS18L1	SS18L1, Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), transcript variant 1, q13.33
SNP_A-2079868	accctggtttgcagat[A/G]aaactgagtgatcaca	A	G	NM_007232 // upstream // 17819 // Hs.251399 // HRH3 // 11255 // Homo sapiens histamine receptor H3 (HRH3), mRNA. /// NM_014835 // upstream // 735 // Hs.473254 // OSBPL2 // 9885 // Homo sapiens oxysterol binding protein-like 2 (OSBPL2), transcript variant	HRH3	HRH3, Homo sapiens histamine receptor H3 (HRH3), q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1841748	taggcatcctgggtca[A/G]tccgtctggcagccct	A	G	NM_080473 // intron // 0 // Hs.352250 // GATA5 // 140628 // Homo sapiens GATA binding protein 5 (GATA5), mRNA. /// ENST00000252997 // intron // 0 // — // — // —	GATA5	GATA5, Homo sapiens GATA binding protein 5 (GATA5), q13.33
SNP_A-2310426	ggaactggtccaacaa[C/T]cagaaaattgacgtt	C	T	NM_016354 // downstream // 3783 // Hs.235782 // SLCO4A1 // 28231 // Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), mRNA. /// ENST00000300358 // upstream // 32782 // — // — // — /// ENST00000217159 // downs	SLCO4A1	SLCO4A1, Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), q13.33
SNP_A-1940566	ttgccgtgctgaatacg[A/G]agaggcaactgtaacg	A	G	NM_016354 // downstream // 11355 // Hs.235782 // SLCO4A1 // 28231 // Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), mRNA. /// ENST00000300358 // upstream // 40354 // — // — // — /// ENST00000217159 // down	SLCO4A1	SLCO4A1, Homo sapiens solute carrier organic anion transporter family, member 4A1 (SLCO4A1), q13.33
SNP_A-1911309	tgtctgtgcattccta[C/T]ggtaaggcacatgatc	C	T	NM_022099 // upstream // 148571 // Hs.187773 // C20orf51 // 63930 // Homo sapiens chromosome 20 open reading frame 51 (C20orf51), mRNA. /// NM_017798 // downstream // 9833 // Hs.11747 // YTHDF1 // 54915 // Homo sapiens YTH domain family 1 (YTHDF1), mRNA.	C20orf51	C20orf51, Homo sapiens chromosome 20 open reading frame 51 (C20orf51), q13.33
SNP_A-2108717	agctgtcatctcctgt[C/G]acaccaattgccttct	C	G	NM_017798 // intron // 0 // Hs.11747 // YTHDF1 // 54915 // Homo sapiens YTH domain family 1 (YTHDF1), mRNA. /// ENST00000279070 // intron // 0 // — // — // —	YTHDF1	YTHDF1, Homo sapiens YTH domain family 1 (YTHDF1), q13.33
SNP_A-1901433	tggattctccaggaac[A/G]aggacggtggtcacact	A	G	NM_020882 // intron // 0 // Hs.271285 // KIAA1510 // 57642 // Homo sapiens KIAA1510 protein (KIAA1510), mRNA. /// AB040943 // intron // 0 // Hs.271285 // KIAA1510 // 57642 // Homo sapiens mRNA for KIAA1510 protein, partial cds. /// ENST00000358894 // intr	KIAA1510	KIAA1510, Homo sapiens KIAA1510 protein (KIAA1510), q13.33
SNP_A-2301679	gcgccgtgtaggctc[A/G]atgtggcttcaagtaa	A	G	NM_020882 // downstream // 4753 // Hs.271285 // KIAA1510 // 57642 // Homo sapiens KIAA1510 protein (KIAA1510), mRNA. /// AB040943 // downstream // 4753 // Hs.271285 // KIAA1510 // 57642 // Homo sapiens mRNA for KIAA1510 protein, partial cds. /// NM_000744	KIAA1510	KIAA1510, Homo sapiens KIAA1510 protein (KIAA1510), q13.33
SNP_A-1895172	tgccccaccttgac[A/G]ctgcaggagagccct	A	G	NM_000744 // intron // 0 // Hs.10734 // CHRNA4 // 1137 // Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 4 (CHRNA4), mRNA. /// ENST00000351435 // intron // 0 // — // — // —	CHRNA4	CHRNA4, Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 4 (CHRNA4), q13.33
SNP_A-1835778	tacgcctgtatgcgga[C/T]atgtatgtgagcacgt	C	T	NM_004518 // 3UTR // 0 // Hs.161851 // KCNQ2 // 3785 // Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 2 (KCNQ2), transcript variant 3, mRNA. /// ENST00000360480 // 3UTR // 0 // — // — // — /// ENST00000354587 // 3UT	KCNQ2	KCNQ2, Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 2 (KCNQ2), transcript variant 3, q13.33
SNP_A-1785378	ggctatgagtgcctcc[C/T]cttagtgagtgcaggg	C	T	NM_012384 // upstream // 2452 // Hs.473286 // GMEB2 // 26205 // Homo sapiens glucocorticoid modulatory element binding protein 2 (GMEB2), mRNA. /// NM_015894 // downstream // 17380 // Hs.348326 // STMN3 // 50861 // Homo sapiens stathmin-like 3 (STMN3), mR	GMEB2	GMEB2, Homo sapiens glucocorticoid modulatory element binding protein 2 (GMEB2), q13.33
SNP_A-2287617	gattaactcactagaa[A/G]ctcatataacccaagag	A	G	NM_004535 // intron // 0 // Hs.279562 // MYT1 // 4661 // Homo sapiens myelin transcription factor 1 (MYT1), mRNA. /// ENST00000328439 // intron // 0 // — // — // —	MYT1	MYT1, Homo sapiens myelin transcription factor 1 (MYT1), q13.33
SNP_A-2015118	tatcttttcattacca[A/T]cctcagtatttctagt	A	T	ENST00000305570 // upstream // 109794 // — // — // — // — /// ENST00000332473 // upstream // 126324 // — // — // — // —	-	q11.2
SNP_A-2015159	tgtcttctgcagttca[C/G]tcagggacacatcgag	C	G	AY040090 // downstream // 21141 // Hs.517196 // C21orf15 // 54094 // Homo sapiens C21orf15 protein (C21orf15) mRNA, partial cds. /// ENST00000342525 // upstream // 141993 // — // — // — // — /// ENST00000359319 // downstream // 21141 // — // —	C21orf15	C21orf15, Homo sapiens C21orf15 protein (C21orf15) partial cds. q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015169	taggagccctctataa[A/C]cctgctcctgaaaaat	A	C	NM_153750 // intron // 0 // Hs.364456 // C21orf81 // 114035 // Homo sapiens chromosome 21 open reading frame 81 (C21orf81), mRNA. /// ENST00000339425 // intron // 0 // — // — // —	C21orf81	C21orf81, Homo sapiens chromosome 21 open reading frame 81 (C21orf81), q11.2
SNP_A-2015183	cacgcatgtggtccga[A/G]aggtggcagctggccg	A	G	NM_198996 // downstream // 32574 // Hs.139907 // LOC375108 // 375108 // Homo sapiens membrane-associated phospholipase A1 beta (LOC375108), mRNA. /// ENST00000332705 // downstream // 70962 // — // — // — /// ENST00000344577 // downstream // 3	LOC375108	LOC375108, Homo sapiens membrane-associated phospholipase A1 beta (LOC375108), q11.2
SNP_A-1968981	acatttaaatgcaaag[C/T]caaataaaatgcagcc	C	T	NM_138726 // intron // 0 // Hs.366575 // ABCC13 // 150000 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 13 (ABCC13), transcript variant 1, mRNA. /// ENST00000318742 // intron // 0 // — // — // —	ABCC13	ABCC13, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q11.2
SNP_A-2015223	ttaaggagatgctaac[A/G]attaaggagaagctaa	A	G	NM_138726 // intron // 0 // Hs.366575 // ABCC13 // 150000 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 13 (ABCC13), transcript variant 1, mRNA. /// ENST00000318742 // intron // 0 // — // — // —	ABCC13	ABCC13, Homo sapiens ATP-binding cassette, sub-family C (CFTR q11.2
SNP_A-1748023	taaatagttaattcttaaaagttga[A/G]caaacatcgatccctttg ccttttc	A	G	NM_006948 // downstream // 53045 // Hs.352341 // STCH // 6782 // stress 70 protein chaperone, microsome-associated, 60kDa /// NM_138726 // downstream // 18384 // Hs.366575 // ABCC13 // 150000 // ATP-binding cassette, sub-family C (CFTR/MRP), member 13 //	STCH	STCH , rs1317731, stress 70 protein chaperone, microsome-associated, 60kDa ,q11.2
SNP_A-2015225	agcaagcatcagtaaa[C/G]gagagtgagcctctcc	C	G	NM_138726 // intron // 0 // Hs.366575 // ABCC13 // 150000 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 13 (ABCC13), transcript variant 1, mRNA. /// ENST00000318742 // intron // 0 // — // — // —	ABCC13	ABCC13, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q11.2
SNP_A-2230447	ctatcaggagtatgtt[C/G]aaaagaaggagtaggg	C	G	NM_138726 // intron // 0 // Hs.366575 // ABCC13 // 150000 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 13 (ABCC13), transcript variant 1, mRNA. /// ENST00000318742 // intron // 0 // — // — // —	ABCC13	ABCC13, Homo sapiens ATP-binding cassette, sub-family C (CFTR,q11.2
SNP_A-2015228	taagggagtagagaac[A/G]atgcaacaaaatggtt	A	G	NM_138726 // intron // 0 // Hs.366575 // ABCC13 // 150000 // Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 13 (ABCC13), transcript variant 1, mRNA. /// ENST00000318742 // intron // 0 // — // — // —	ABCC13	ABCC13, Homo sapiens ATP-binding cassette, sub-family C (CFTR q11.2
SNP_A-2015246	acccccacttgctac[A/G]gctaccactccaaatc	A	G	NM_006948 // upstream // 100586 // Hs.352341 // STCH // 6782 // Homo sapiens stress 70 protein chaperone, microsome-associated, 60kDa (STCH), mRNA. /// NM_022136 // downstream // 1454 // Hs.473341 // SAMSN1 // 64092 // Homo sapiens SAM domain, SH3 domain	STCH	STCH, Homo sapiens stress 70 protein chaperone, microsome-associated, 60kDa (STCH), q11.2
SNP_A-2015256	acaaaatcataaaatc[A/G]aagcatagatagaagg	A	G	ENST00000285670 // intron // 0 // — // — // —	-	q11.2
SNP_A-2015257	tgccatcaggttgaag[A/G]atacaattagatagta	A	G	ENST00000285670 // intron // 0 // — // — // —	-	q11.2
SNP_A-1969003	actttctagtagcaaa[G/T]attctggacaacct	G	T	NM_022136 // upstream // 39504 // Hs.473341 // SAMSN1 // 64092 // Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), mRNA. /// NM_003489 // downstream // 378869 // Hs.155017 // NRIP1 // 8204 // Homo sapiens nuclear receptor	SAMSN1	SAMSN1, Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), q11.2
SNP_A-2015266	aataatttgcaatcaa[C/T]gctctatctaaaag	C	T	NM_022136 // upstream // 89256 // Hs.473341 // SAMSN1 // 64092 // Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), mRNA. /// NM_003489 // downstream // 329117 // Hs.155017 // NRIP1 // 8204 // Homo sapiens nuclear receptor	SAMSN1	SAMSN1, Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), q11.2
SNP_A-2015283	gctcattttatggaa[C/T]ggaacaaatgtgttg	C	T	NM_022136 // upstream // 160754 // Hs.473341 // SAMSN1 // 64092 // Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), mRNA. /// NM_003489 // downstream // 257619 // Hs.155017 // NRIP1 // 8204 // Homo sapiens nuclear receptor	SAMSN1	SAMSN1, Homo sapiens SAM domain, SH3 domain and nuclear localisation signals, 1 (SAMSN1), q11.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1711018	tctcaatatggttgtactgtataaa[A/C]atggaatcaaatgaaaga agccaga	A	C	NM_003489 // downstream // 247198 // Hs.155017 // NRIP1 // 8204 // nuclear receptor interacting protein 1 /// NM_022136 // upstream // 130641 // Hs.221851 // SAMSN1 // 64092 // SAM domain, SH3 domain and nuclear localisation signals. 1	NRIP1	NRIP1 , rs1153350, nuclear receptor interacting protein 1 ,q11.2
SNP_A-1700137	aagacataagcagatcaagacagac[A/G]attaggatatacgc agcaagactac	A	G	NM_003489 // downstream // 108754 // Hs.155017 // NRIP1 // 8204 // nuclear receptor interacting protein 1 /// NM_022136 // upstream // 269085 // Hs.221851 // SAMSN1 // 64092 // SAM domain, SH3 domain and nuclear localisation signals. 1	NRIP1	NRIP1 , rs2822961, nuclear receptor interacting protein 1 ,q11.2
SNP_A-1669665	aacaaaaacaaaaatcccgaagaaa[C/T]aaaactagtgtctt aattatatgct	C	T	NM_003489 // downstream // 105584 // Hs.155017 // NRIP1 // 8204 // nuclear receptor interacting protein 1 /// NM_022136 // upstream // 272255 // Hs.221851 // SAMSN1 // 64092 // SAM domain, SH3 domain and nuclear localisation signals. 1	NRIP1	NRIP1 , rs2223163, nuclear receptor interacting protein 1 ,q11.2
SNP_A-2015316	aacaataggatagagg[A/C]atcaatacgcttattg	A	C	NM_003489 // upstream // 25876 // Hs.155017 // NRIP1 // 8204 // Homo sapiens nuclear receptor interacting protein 1 (NRIP1), mRNA /// ENST00000318948 // upstream // 25876 // — // — // — /// ENST00000355858 // upstream // 96121 // — // —	NRIP1	NRIP1, Homo sapiens nuclear receptor interacting protein 1 (NRIP1), q11.2
SNP_A-1969053	ttttcactgttttga[A/G]aaatcttccatatta	A	G	AF170562 // upstream // 437009 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 437179 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin specific protease	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds, q21.1
SNP_A-1969079	atagctgcatacttcca[A/C]aacacaaagatattat	A	C	AF170562 // upstream // 45124 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 45294 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin specific protease 2	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds, q21.1
SNP_A-2015448	ttgatggcgaatgtta[A/C]agcagtttactagt	A	C	AF170562 // upstream // 38774 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 38944 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin specific protease 2	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds, q21.1
SNP_A-2015451	acaacatagagtaatg[C/T]agcagtttagaagtta	C	T	AF170562 // upstream // 2069 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin-specific processing protease (USP25) mRNA, complete cds. /// NM_013396 // upstream // 2239 // Hs.473370 // USP25 // 29761 // Homo sapiens ubiquitin specific protease 25	USP25	USP25, Homo sapiens ubiquitin-specific processing protease (USP25) complete cds, q21.1
SNP_A-2015517	caattttgtgcttaga[A/G]tagacctatgcattta	A	G	NM_001338 // upstream // 1134536 // Hs.473417 // CXADR // 1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 // downstream // 303513 // — // — // — /// ENST00000284878 // upstream // 1134536 // —	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-2015529	gagaaatgatatatga[C/T]ggcgaacagtagttta	C	T	NM_001338 // upstream // 1070563 // Hs.473417 // CXADR // 1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// ENST00000308787 // downstream // 367486 // — // — // — /// ENST00000284878 // upstream // 1070563 // —	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1741323	gatagctttctcagtcatgactatc[A/G]gtaatttacacccccctta agttct	A	G	AF486622 // downstream // 133107 // Hs.102754 // - // 388815 // LOC388815 (LOC388815), mRNA /// NM_001338 // upstream // 772812 // Hs.79187 // CXADR // 1525 // coxsackie virus and adenovirus receptor	-	- , rs2404139, LOC388815 (LOC388815), mRNA ,q21.1
SNP_A-1722412	tcaatggcacagaatctaacatccc[C/T]gagctaaggttcagca ggagctcat	C	T	AF486622 // downstream // 134101 // Hs.102754 // - // 388815 // LOC388815 (LOC388815), mRNA /// NM_001338 // upstream // 771818 // Hs.79187 // CXADR // 1525 // coxsackie virus and adenovirus receptor	-	- , rs2824010, LOC388815 (LOC388815), mRNA ,q21.1
SNP_A-1650736	tttgaggctagtaacacaatttaga[A/C]cagaataggtttcatata tcaaaa	A	C	NM_001338 // 3'UTR // 0 // Hs.79187 // CXADR // 1525 // coxsackie virus and adenovirus receptor	CXADR	CXADR , rs1784913, coxsackie virus and adenovirus receptor,q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015653	cttttcactgacaa[A/G]cagatgtgaagtaac	A	G	NM_001338 // downstream // 6646 // Hs.473417 // CXADR // 1525 // Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /// NM_006606 // downstream // 20062 // Hs.473420 // BTG3 // 10950 // Homo sapiens BTG family, member 3 (BTG3), mRNA. ///	CXADR	CXADR, Homo sapiens coxsackie virus and adenovirus receptor (CXADR), q21.1
SNP_A-1969174	tacaaatactttttaa[C/T]gccacctggccaattc	C	T	NM_006806 // upstream // 55259 // Hs.473420 // BTG3 // 10950 // Homo sapiens BTG family, member 3 (BTG3), mRNA. /// ENST00000348354 // upstream // 55259 // — // — // — /// ENST00000339775 // upstream // 55259 // — // — // — /// E	BTG3	BTG3, Homo sapiens BTG family, member 3 (BTG3), q21.1
SNP_A-2015705	agttagcttcaagaaa[C/T]ggcagaactacacaca	C	T	NM_017447 // upstream // 98565 // Hs.293811 // C21orf91 // 54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 326917 // Hs.283725 // CHODL // 140578 // Homo sapiens chondrolectin (CHODL), mRNA. /// ENS	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-2015733	ttgttcgagggtatta[A/G]gaaatgcatctaaaaa	A	G	NM_017447 // upstream // 246484 // Hs.293811 // C21orf91 // 54149 // Homo sapiens chromosome 21 open reading frame 91 (C21orf91), mRNA. /// NM_024944 // upstream // 178998 // Hs.283725 // CHODL // 140578 // Homo sapiens chondrolectin (CHODL), mRNA. /// EN	C21orf91	C21orf91, Homo sapiens chromosome 21 open reading frame 91 (C21orf91), q21.1
SNP_A-1692198	gaccgtaattgaaactataaagtca[C/G]acactcttggattgacc ctcatca	C	G	AF523315 // intron // 0 // Hs.283725 // CHODL // 140578 // chondrolectin	CHODL	CHODL , rs158030, chondrolectin,q21.1
SNP_A-1969231	ggttccttaaagaaag[C/T]ctattcagttgacaat	C	T	NM_002772 // upstream // 155568 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 298505 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-1969232	cattggtgctagccaa[A/T]catcccactctatcac	A	T	NM_002772 // upstream // 174057 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 280016 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015831	tgaggtcatctctaca[G/T]ctttaatacccttaagc	G	T	NM_002772 // upstream // 181076 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 272997 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015835	gggaagcaaactctca[A/G]gaaaatgtaccaggg	A	G	NM_002772 // upstream // 186511 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 267562 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015836	aaaaatacaaaagcca[A/G]tctgtcaaaacgtatt	A	G	NM_002772 // upstream // 194235 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 259838 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-1969233	aaatatgatgatcaaa[A/C]gtgcatttatgccttg	A	C	NM_002772 // upstream // 197241 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 256832 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015837	agtgccttatagtaa[A/C]gtggcttaattcacag	A	C	NM_002772 // upstream // 198424 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 255649 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2015839	tagtcactacgttcca[C/G]atctaatccatgtgat	C	G	NM_002772 // upstream // 200698 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 253375 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015840	tgttcacaggtagcaa[A/G]gtactcttagcaggcc	A	G	NM_002772 // upstream // 200770 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 253303 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015844	acatcaagattgctct[A/G]acctgaggacaggatt	A	G	NM_002772 // upstream // 218287 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 235786 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015851	agacatgtctggaact[A/G]agaagaaaatgagatt	A	G	NM_002772 // upstream // 288498 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 165575 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-1724884	ctttttcatttagttctacaatcta[A/G]cttaatttcatcaccatatatatat	A	G	NM_002772 // upstream // 293398 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 2301451 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7 , rs928863, protease, serine, 7 (enterokinase) ,q21.1
SNP_A-1679926	aaagagtttttcaatttctttaaaa[C/G]ttatgcctaccttatgacccagcaa	C	G	NM_002772 // upstream // 293991 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 2300858 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7 , rs2183559, protease, serine, 7 (enterokinase) ,q21.1
SNP_A-1969238	tgaaatatgtgaggtc[A/G]ataaacacatataaag	A	G	NM_002772 // upstream // 301606 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 152467 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015855	catgcgcaggttgagc[A/G]caattttatacttatt	A	G	NM_002772 // upstream // 305061 // Hs.149473 // PRSS7 // 5651 // Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA. /// NM_203430 // upstream // 149012 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PP	PRSS7	PRSS7, Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), q21.1
SNP_A-2015903	aaaatctgtagcagga[A/T]caagataaagctaatt	A	T	NM_203430 // downstream // 70267 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 // downstream // 70267 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl i	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, q21.1
SNP_A-2015926	tcgtttccctccttta[A/T]ctgctctttgctctga	A	T	NM_203430 // downstream // 163887 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 // downstream // 163887 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, q21.1
SNP_A-2015935	agtctacatttcaacc[G/T]ggtgttaactctggtc	G	T	NM_203430 // downstream // 176536 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 // downstream // 176536 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1969256	ggctgtagtttctgg[G/T]caagtatctccaatct	G	T	NM_203430 // downstream // 179487 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, mRNA. /// NM_203431 // downstream // 179487 // Hs.356331 // PPIA // 5478 // Homo sapiens peptidylprolyl	PPIA	PPIA, Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), transcript variant 2, q21.1
SNP_A-2016000	agcatttttgagtgca[C/G]aggtaggcaggaaaga	C	G	ENST00000359056 // upstream // 80063 // — // — // — /// ENST00000331037 // downstream // 936139 // — // — // — // — ///	-	q21.1
SNP_A-1969273	atgtcagcagattaca[C/G]aatatggctcccagt	C	G	ENST00000359056 // upstream // 122337 // — // — // — // — /// ENST00000331037 // downstream // 893865 // — // — // — // —	-	q21.1
SNP_A-2016019	aacaaatcattctga[A/G]ccttagatagtgggga	A	G	ENST00000359056 // upstream // 288061 // — // — // — // — /// ENST00000331037 // downstream // 728141 // — // — // — // —	-	q21.1
SNP_A-1969287	ttttttattctgttga[C/T]ctaatgcttcgtattt	C	T	ENST00000359056 // upstream // 309665 // — // — // — // — /// ENST00000331037 // downstream // 706537 // — // — // — // —	-	q21.1
SNP_A-1728301	tagccatatttactcaacaagatac[A/T]tatttactcaacaaggtat tccaag	A	T	NM_002772 // upstream // 1386701 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 1208148 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7, rs468280, protease, serine, 7 (enterokinase), q21.1
SNP_A-2016034	tattctgtgaagacac[G/T]cagtagaaatggttaga	G	T	ENST00000359056 // upstream // 392436 // — // — // — /// ENST00000331037 // downstream // 623766 // — // — // — // —	-	q21.1
SNP_A-1969291	ctcaataaacaggatg[A/G]accaacttttataagg	A	G	ENST00000359056 // upstream // 410936 // — // — // — // — /// ENST00000331037 // downstream // 605266 // — // — // — // —	-	q21.1
SNP_A-1645004	agaaatgtccttcattgctttaattc[C/G]attcatcatacaaccccag gttgta	C	G	NM_002772 // upstream // 1420635 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 1174214 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7, rs9975733, protease, serine, 7 (enterokinase), q21.1
SNP_A-1681154	accagttgctgtttttatccacgai[C/G]tacttccagacaccatttatg tgtaa	C	G	NM_002772 // upstream // 1421169 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 1173680 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7, rs2825825, protease, serine, 7 (enterokinase), q21.1
SNP_A-2016047	ctgtaaactgttcttg[C/T]aaatatatctgatatg	C	T	ENST00000359056 // upstream // 482766 // — // — // — // — /// ENST00000331037 // downstream // 533436 // — // — // — // —	-	q21.1
SNP_A-2016048	caatgtaggctgcaaa[A/G]cattaaagggtcaagc	A	G	ENST00000359056 // upstream // 485060 // — // — // — // — /// ENST00000331037 // downstream // 531142 // — // — // — // —	-	q21.1
SNP_A-1969322	tccccactgcggtctat[C/G]gggagctatgagaaga	C	G	NM_004540 // upstream // 769828 // Hs.473450 // NCAM2 // 4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000331037 // upstream // 84762 // — // — // — // — /// ENST00000338221 // downstream // 317377 // — // — // —	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-2016179	ttaaaaattgatgaa[A/C]ctaggaagctgtttcc	A	C	NM_004540 // upstream // 579672 // Hs.473450 // NCAM2 // 4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000331037 // upstream // 274918 // — // — // — // — /// ENST00000338221 // downstream // 127221 // — // — // —	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-2016188	ataacacactagaaaaa[A/G]cattaggagatatacc	A	G	NM_004540 // upstream // 527206 // Hs.473450 // NCAM2 // 4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000331037 // upstream // 327384 // — // — // — // — /// ENST00000338221 // downstream // 74755 // — // — // —	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-2016200	gagacacacttccaac[A/G]ctattgtagaattat	A	G	ENST00000338221 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-2016201	agttgcaggaggttaa[C/T]gagataacaatacatg	C	T	ENST00000338221 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-2016203	agtattgtgaggttat[A/C]aaaggaataacaacca	A	C	ENST00000338221 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-2016204	aggctgtaactgtaaa[C/T]gaattaaggcagaaac	C	T	ENST00000338221 // intron // 0 // — // — // — // —	-	q21.1
SNP_A-1695013	gtgaatttcttacttatatatgaggt[A/C]caatttatcgagcatttttca tgg	A	C	NM_002772 // upstream // 2485242 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 1096607 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7, rs2826596, protease, serine, 7 (enterokinase), q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1728021	taaagttaattttattattacaccc[C/T]atgagtaccaccaattaaatattgc	C	T	NM_002772 // upstream // 2485359 // Hs.149473 // PRSS7 // 5651 // protease, serine, 7 (enterokinase) /// NM_004540 // upstream // 109490 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	PRSS7	PRSS7 , rs2826597, protease, serine, 7 (enterokinase) ,q21.1
SNP_A-2016238	acttctttacctataa[C/T]atgaagaacacagtta	C	T	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2016248	gcatggtgtctgcaac[A/C]ggaaggatttcattgc	A	C	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2016249	aaaaaaatgaagtgac[A/G]actgctttcaaaagat	A	G	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2016252	gaaggtggaagaaaaa[C/T]gtccttactagtatgc	C	T	ENST00000338221 // intron // 0 // --- // --- // --- // ---	-	q21.1
SNP_A-2016300	aaagggctactatgcc[G/T]agattgattatctcct	G	T	NM_004540 // intron // 0 // Hs.473450 // NCAM2 // 4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000284894 // intron // 0 // --- // --- // --- // ---	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-2016304	agagtaaatgaggcaa[C/T]tgtttgtcaaaatagt	C	T	NM_004540 // intron // 0 // Hs.473450 // NCAM2 // 4685 // Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA. /// ENST00000284894 // intron // 0 // --- // --- // --- // ---	NCAM2	NCAM2, Homo sapiens neural cell adhesion molecule 2 (NCAM2), q21.1
SNP_A-1684646	atgaaaaagaaaagtattacataac[A/G]ataaaggtttcaactcaacaagaag	A	G	NM_004540 // downstream // 56886 // Hs.135892 // NCAM2 // 4685 // neural cell adhesion molecule 2	NCAM2	NCAM2 , rs236069, neural cell adhesion molecule 2,q21.1
SNP_A-2016327	tcagtgactgagagta[C/T]atcaagtttttttctg	C	T	AY077696 // upstream // 355962 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 95754 // --- // --- // --- // --- /// ENST00000333482 // upstream // 355962 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-2103351	agcaaggtactatccc[A/G]gaaagctgagagcagc	A	G	AY077696 // upstream // 351943 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 99773 // --- // --- // --- // --- /// ENST00000333482 // upstream // 351943 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-2016333	tttgactacattacac[G/T]gctatcaaatttcatg	G	T	AY077696 // upstream // 343532 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 108184 // --- // --- // --- // --- /// ENST00000333482 // upstream // 343532 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-2016351	tttaactgctgaagaa[C/T]aagatcaccacaatca	C	T	AY077696 // upstream // 249955 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 201761 // --- // --- // --- // --- /// ENST00000333482 // upstream // 249955 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-1969389	cttaggatttgtctgc[C/T]atagtgatattctaag	C	T	AY077696 // upstream // 161664 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 290052 // --- // --- // --- // --- /// ENST00000333482 // upstream // 161664 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-1969398	gaagagtcaggggtta[C/T]ataagtaccagataca	C	T	AY077696 // upstream // 121973 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000358903 // downstream // 329743 // --- // --- // --- // --- /// ENST00000333482 // upstream // 121973 //	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1
SNP_A-1648582	acctagggagatcaggcatttccag[C/T]tgactcacagtgggctatcttttaa	C	T	NM_153203 // upstream // 95148 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf74	C21orf74 , rs2186427, chromosome 21 open reading frame 74,q21.1
SNP_A-1969425	agaaatctgttaacca[C/T]aaaaaaatcaggataa	C	T	AY077696 // downstream // 300153 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 300153 // --- // --- // --- // --- /// ENST00000329030 // downstream // 99266	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1969434	atatgtctgcaatatat[C/G]taaggactgatataaa	C	G	AY077696 // downstream // 391186 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 391186 // --- // --- /// --- // --- /// ENST00000329030 // downstream // 90163	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16), complete cds. q21.1
SNP_A-2016448	atgtgcatattggcag[C/T]cattgattacagtggt	C	T	AY077696 // downstream // 469967 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 469967 // --- // --- /// --- // --- /// ENST00000329030 // downstream // 82285	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16), complete cds. q21.1
SNP_A-2164250	caaaatacaatcgaaa[A/G]cttatcagtaaaaca	A	G	AY077696 // downstream // 717068 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 717068 // --- // --- /// --- // --- /// ENST00000329030 // downstream // 57575	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.2
SNP_A-1741823	atgtgtaataaaactatcacaaata[C/T]gacagcaaaagaatc aaatttcaaa	C	T	NM_058184 // downstream // 2300197 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream /// 970509 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42, rs1506005, chromosome 21 open reading frame 42 .q21.2
SNP_A-1969464	ttgtaaatgaatgtta[C/T]gtttatgcatcaaac	C	T	AY077696 // downstream // 971769 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 971769 // --- // --- /// --- // --- /// ENST00000329030 // downstream // 32105	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16) complete cds. q21.2
SNP_A-2016509	gcatagtaacataaca[C/T]tactgatcggagttct	C	T	AY077696 // downstream // 981399 // Hs.352631 // C21orf74 // 54143 // Homo sapiens clone qd65g07 PRED16 protein (PRED16) mRNA, complete cds. /// ENST00000333482 // downstream // 981399 // --- // --- /// --- // --- /// ENST00000329030 // downstream // 31142	C21orf74	C21orf74, Homo sapiens clone qd65g07 PRED16 protein (PRED16), complete cds. .q21.2
SNP_A-1643269	gcttttgacttaatcttccatgta[A/G]catctataaatattatatcaagt atc	A	G	NM_058184 // downstream // 2088302 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream /// 1182404 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42, rs2828024, chromosome 21 open reading frame 42 .q21.2
SNP_A-2016556	cttagttactagatga[A/T]ctaggtaactcttaa	A	T	NM_207471 // upstream // 1047536 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 32691 // --- // --- // --- /// ENST00000355181 // upstream // 1047536 // --- // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016560	agaggagattcaccgg[A/G]ccctgaagaatgtca	A	G	NM_207471 // upstream // 1041981 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 38246 // --- // --- // --- /// ENST00000355181 // upstream // 1041981 // --- // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016565	ctagctatgtttccc[A/G]cttccttgatctatt	A	G	NM_207471 // upstream // 1033832 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 46395 // --- // --- // --- /// ENST00000355181 // upstream // 1033832 // --- // --- // ---	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016572	cctgggaggatagag[A/C]attagctcagatggaa	A	C	NM_207471 // upstream // 983983 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 96244 // --- // --- // --- /// ENST00000355181 // upstream // 983983 // --- // --- // -	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016586	atctgtacaattggag[A/C]aaactaccaatacatg	A	C	NM_207471 // upstream // 935214 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 145013 // --- // --- // --- /// ENST00000355181 // upstream // 935214 // --- // --- // -	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2016618	aatttttcattaggca[C/G]aagaatatggttcact	C	G	NM_207471 // upstream // 759565 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 320662 // --- // --- // --- /// ENST00000355181 // upstream // 759565 // --- // --- // -	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1969526	ttgacttggttggcaa[A/T]gttatgaagctacatt	A	T	NM_207471 // upstream // 538260 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 541967 // --- // --- // --- /// ENST00000355181 // upstream // 538260 // --- // --- // -	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016699	tactgatttcttcataa[A/G]gcatttcatccatccc	A	G	NM_207471 // upstream // 427133 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 653094 // --- // --- // --- /// ENST00000355181 // upstream // 427133 // --- // --- // -	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1969551	actgagttgccataat[C/G]agaacataatattgga	C	G	NM_207471 // upstream // 315823 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// ENST00000329030 // upstream // 764404 // --- // --- // --- /// ENST00000355181 // upstream // 315823 // --- // --- // -	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1681594	ttaagaacaagccgactggataaa[C/T]agctaactcatttagaaaaagactg	C	T	NM_058184 // downstream // 911814 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 2358892 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs10482950, chromosome 21 open reading frame 42 ,q21.2
SNP_A-2016799	tataaacaagctcata[A/C]attgtggaggaatcc	A	C	NM_207471 // downstream // 151721 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 788729 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42).	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-2016869	atctaactcagaggat[A/G]agctctaatgctata	A	G	NM_207471 // downstream // 409121 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 531329 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42).	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1729478	gttaaagacactggttgttaccatc[A/G]attaaaaatatttatttatta agat	A	G	NM_058184 // downstream // 433208 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 2837498 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2829484, chromosome 21 open reading frame 42 ,q21.2
SNP_A-1726982	gcctttgcctgtatcacactgtct[C/T]gactaatgtacctttatgtaa tta	C	T	NM_058184 // downstream // 420200 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 2850506 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2226351, chromosome 21 open reading frame 42 ,q21.2
SNP_A-1701511	agcagacatcctctgatactgcaaa[G/T]aactcataaaatgcac ctaatcatc	G	T	NM_058184 // downstream // 405260 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 2865446 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2211833, chromosome 21 open reading frame 42 ,q21.2
SNP_A-1749655	ctagttaaatagattagtttagaa[A/G]ataagtttatgtgtcttaaa agcac	A	G	NM_058184 // downstream // 316379 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 2954327 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2829531, chromosome 21 open reading frame 42 ,q21.2
SNP_A-1741945	ttcctagcctgaaatcttgaatcaa[C/T]tgttaaatctcgtatatttt gcat	C	T	NM_058184 // downstream // 234943 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 3035763 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2829562, chromosome 21 open reading frame 42 ,q21.2
SNP_A-1750317	tataaagagattacctgaactgaag[A/C]agattgtgttatgtaggt atgaaga	A	C	NM_058184 // downstream // 193075 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 3077631 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2829620, chromosome 21 open reading frame 42 ,q21.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1969603	aaagaagcaactacaa[A/G]aatggcatgaaagccc	A	G	NM_207471 // downstream // 716216 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 224234 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42).	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1969606	tcagctgtaggcacaa[C/G]atgatgtctccagaaa	C	G	NM_207471 // downstream // 743000 // Hs.517218 // FLJ42200 // 400860 // Homo sapiens FLJ42200 protein (FLJ42200), mRNA. /// NM_058184 // downstream // 197450 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42).	FLJ42200	FLJ42200, Homo sapiens FLJ42200 protein (FLJ42200), q21.2
SNP_A-1678516	gttgagcctaattgaagtttcccta[C/T]atacagtaagttcagaga aacactc	C	T	NM_058184 // downstream // 48882 // Hs.234016 // C21orf42 // 54072 // chromosome 21 open reading frame 42 /// NM_153203 // downstream // 3221824 // Hs.352631 // C21orf74 // 54143 // chromosome 21 open reading frame 74	C21orf42	C21orf42 , rs2155958, chromosome 21 open reading frame 42 , q21.2
SNP_A-2016933	caaaactcaatgccaa[C/G]tggttgaacgcttagc	C	G	NM_058184 // upstream // 16664 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42), mRNA. /// NM_080794 // downstream // 137679 // Hs.420696 // MRPL39 // 54148 // Homo sapiens mitochondrial ribosomal protein L3	C21orf42	C21orf42, Homo sapiens chromosome 21 open reading frame 42 (C21orf42), q21.2
SNP_A-2016936	aggaggaacaggcaga[G/T]aaaaatatgtatagag	G	T	NM_058184 // upstream // 28982 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42), mRNA. /// NM_080794 // downstream // 125361 // Hs.420696 // MRPL39 // 54148 // Homo sapiens mitochondrial ribosomal protein L3	C21orf42	C21orf42, Homo sapiens chromosome 21 open reading frame 42 (C21orf42), q21.2
SNP_A-1969620	atagagaaagtagggc[A/G]cattgacaaatttgt	A	G	NM_058184 // upstream // 33788 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42), mRNA. /// NM_080794 // downstream // 120555 // Hs.420696 // MRPL39 // 54148 // Homo sapiens mitochondrial ribosomal protein L3	C21orf42	C21orf42, Homo sapiens chromosome 21 open reading frame 42 (C21orf42), q21.2
SNP_A-1969624	gtttgttacaaaaga[C/T]agtaatgctgtaatgg	C	T	NM_058184 // upstream // 115981 // Hs.234016 // C21orf42 // 54072 // Homo sapiens chromosome 21 open reading frame 42 (C21orf42), mRNA. /// NM_080794 // downstream // 38362 // Hs.420696 // MRPL39 // 54148 // Homo sapiens mitochondrial ribosomal protein L3	C21orf42	C21orf42, Homo sapiens chromosome 21 open reading frame 42 (C21orf42), q21.3
SNP_A-1679812	gtttcacaaaggatacagattcca[C/T]ggtgataaagaaaca ctgggttgag	C	T	NM_021219 // intron // 0 // Hs.436494 // JAM2 // 58494 // junctional adhesion molecule 2	JAM2	JAM2 , rs2409148, junctional adhesion molecule 2,q21.3
SNP_A-2016974	acccagttgacagaga[C/T]acttgagctggagct	C	T	NM_001003701 // upstream // 97556 // Hs.246310 // ATP5J // 522 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial pr /// NM_001003697 // upstream // 97556 // Hs.246310 // ATP5J	ATP5J	ATP5J, Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial pr ,q21.3
SNP_A-1969635	aacctcattaatcag[A/T]aaccctacttcagtaa	A	T	NM_000484 // intron // 0 // Hs.434980 // APP // 351 // Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // intron // 0 // Hs.434980 // APP // 351 // Homo sapiens amylo	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3
SNP_A-2017035	gaatctggaaaccct a[C/T]gcctacagttgctaca	C	T	NM_000484 // intron // 0 // Hs.434980 // APP // 351 // Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // intron // 0 // Hs.434980 // APP // 351 // Homo sapiens amylo	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3
SNP_A-2017053	tagaagcagtgatagaa[A/C]ctataaaatgtagaa	A	C	NM_000484 // upstream // 31007 // Hs.434980 // APP // 351 // Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA. /// NM_201413 // upstream // 31007 // Hs.434980 // APP // 351 // Homo s	APP	APP, Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), transcript variant 1, q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017080	atatgtatgtaaaggat[A/G]aatcttcagcattctt	A	G	NM_052954 // downstream // 150299 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000356027 // downstream // 97350 // — // — // — /// ENST00000299340 // downstream // 150299 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2017094	gaagagctgttgtata[A/G]gcaagtagaatgtgtt	A	G	NM_052954 // downstream // 60084 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000356027 // downstream // 187565 // — // — // — /// ENST00000299340 // downstream // 60084 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-1687674	gagataagaaatattgacaataggtg[C/T]aaaagagtaatttagtgatggccc	C	T	NM_052954 // intron // 0 // Hs.132275 // CYYR1 // 116159 // cysteine and tyrosine-rich 1	CYYR1	CYYR1, rs2830244, cysteine and tyrosine-rich 1,q21.3
SNP_A-1969672	atctgacatctacttt[A/G]aaaggttcactctggc	A	G	NM_052954 // intron // 0 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // intron // 0 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-1969673	taaatacdattccaaa[A/G]acaatgcccgcaattg	A	G	NM_052954 // CDS // 0 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // CDS // 0 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-1969674	tagctttttcatactc[A/G]aacatagtaaaatagc	A	G	NM_052954 // intron // 0 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // intron // 0 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-1969675	ttgaacttctggatct[G/T]attctctaactctttt	G	T	NM_052954 // intron // 0 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // intron // 0 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2168473	caacttattgtcaa[A/G]ccaaaatgccctacaa	A	G	NM_052954 // intron // 0 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // intron // 0 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2017117	cacaaaagactcagaa[C/T]tgaaaactggaattga	C	T	NM_052954 // intron // 0 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// ENST00000299340 // intron // 0 // — // — // —	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2017155	gctggccttggagtta[C/T]atggcttgcccacgag	C	T	NM_052954 // upstream // 182099 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// NM_006988 // downstream // 80928 // Hs.534115 // ADAMTS1 // 9510 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA.	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2017159	tgtttcacttgtttca[C/T]tcgtttcactattag	C	T	NM_052954 // upstream // 199787 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// NM_006988 // downstream // 63240 // Hs.534115 // ADAMTS1 // 9510 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA.	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2017171	attgaccacaccctca[C/T]cccaagtcaaatcact	C	T	NM_052954 // upstream // 247107 // Hs.37445 // CYYR1 // 116159 // Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), mRNA. /// NM_006988 // downstream // 15920 // Hs.534115 // ADAMTS1 // 9510 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA.	CYYR1	CYYR1, Homo sapiens cysteine and tyrosine-rich 1 (CYYR1), q21.3
SNP_A-2017188	ttaatgtgatgtaaaa[A/G]acctattatcataggc	A	G	NM_006988 // upstream // 75389 // Hs.534115 // ADAMTS1 // 9510 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA. /// NM_007038 // downstream // 669 // Hs.58324 // ADAMTS5 // 11096	ADAMTS1	ADAMTS1, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), q21.3
SNP_A-2017193	aagagggccatctaccd[A/G]ctcctgcagtctcatg	A	G	NM_007038 // CDS // 0 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// ENST00000284987 // CDS // 0 // — // — // —	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017209	tttctgcaggaggcaj[A/G]tcataaaacaggatga	A	G	NM_007038 // upstream // 46585 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 1000284 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with - thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-1654617	tttattcacttatattagataataaa[C/T]ttcctagtctacatttcattac agc	C	T	NM_007038 // upstream // 223941 // Hs.58324 // ADAMTS5 // 11096 // a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) /// NM_145180 // upstream // 822928 // Hs.505079 // C21orf94 // 246705 // chro	ADAMTS5	ADAMTS5, rs235947, a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) .q21.3
SNP_A-2017258	ttttttctccagtta[C/T]ggcaattcctctgcc	C	T	NM_007038 // upstream // 237575 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 809294 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT .q21.3
SNP_A-2017264	attgtatctcctatttt[A/G]aaactctcttccata	A	G	NM_007038 // upstream // 273175 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 773694 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2017271	attgtgatgtggtgta[C/T]gtctctacttctct	C	T	NM_007038 // upstream // 304468 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 742401 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT .q21.3
SNP_A-2017300	agtctagccaagttaa[A/C]acattacaaagtcatc	A	C	NM_007038 // upstream // 438799 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 608070 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2017302	ggatgctctgggagta[C/T]aaaaatgagcaaagaa	C	T	NM_007038 // upstream // 440344 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 606525 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2017318	gttggatgatttatca[A/C]ccacttgtcaagaaca	A	C	NM_007038 // upstream // 500700 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 546169 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2017362	taagaagtttaggac[A/G]gatggtaaaaatgaga	A	G	NM_007038 // upstream // 805394 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 241475 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT q21.3
SNP_A-2017366	catgacaacatggaaa[C/G]agaacaacctgctcct	C	G	NM_007038 // upstream // 823140 // Hs.58324 // ADAMTS5 // 11096 // Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT /// NM_145180 // upstream // 223729 // Hs.505079 // C21orf9	ADAMTS5	ADAMTS5, Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMT .q21.3
SNP_A-1969795	cagcatttctaatttc[A/G]ccctagtccagtgatc	A	G	NM_145180 // downstream // 50014 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 466354 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading fr	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1969796	gtacatggagaaatta[A/T]ggaccgcatttaaag	A	T	NM_145180 // downstream // 55292 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 461076 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading fr	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-1969797	ctgggttctgcctca[A/C]atagctcggaggagga	A	C	NM_145180 // downstream // 56451 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 459917 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading fr	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017421	aagcatgaataaaaagc[A/G]atgtctaacaaatgtc	A	G	NM_145180 // downstream // 127775 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 388593 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017426	cattgtagaaacaagc[A/G]ctctcttctgactcgt	A	G	NM_145180 // downstream // 184596 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 331772 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017445	gatgcacttccaacag[A/G]aaaagaatattgcatt	A	G	NM_145180 // downstream // 263882 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 252486 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017448	tctttctttgttcct[C/T]agagctaccctgtgag	C	T	NM_145180 // downstream // 305060 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 211308 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017449	agtggatgtacctgga[C/G]actgaactagcacaaa	C	G	NM_145180 // downstream // 305156 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 211212 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017459	tacttagcctgaatac[A/G]catgtaaatatggaca	A	G	NM_145180 // downstream // 328000 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 188368 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017483	gactatgtactgaagc[A/C]aggcagggatgtaaag	A	C	NM_145180 // downstream // 371524 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 144844 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017488	agtgtcaaatgcactg[A/G]agatgtcctgtagaat	A	G	NM_145180 // downstream // 387741 // Hs.505079 // C21orf94 // 246705 // Homo sapiens chromosome 21 open reading frame 94 (C21orf94), mRNA. /// NM_145033 // upstream // 128627 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading f	C21orf94	C21orf94, Homo sapiens chromosome 21 open reading frame 94 (C21orf94), q21.3
SNP_A-2017553	tgtgtagagtcacaga[C/T]aattcaatttttcaa	C	T	NM_145033 // downstream // 204643 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading frame 100 (C21orf100), mRNA. /// NM_182749 // downstream // 131161 // Hs.163846 // C21orf127 // 29104 // Homo sapiens chromosome 21 open readi	C21orf100	C21orf100, Homo sapiens chromosome 21 open reading frame 100 (C21orf100), q21.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017567	cccatgggcttcagta[A/C]taaaacctatgttca	A	C	NM_145033 // downstream // 231835 // Hs.438549 // C21orf100 // 118421 // Homo sapiens chromosome 21 open reading frame 100 (C21orf100), mRNA. /// NM_182749 // downstream // 103969 // Hs.163846 // C21orf127 // 29104 // Homo sapiens chromosome 21 open readi	C21orf100	C21orf100, Homo sapiens chromosome 21 open reading frame 100 (C21orf100), q21.3
SNP_A-1969843	tgccgagctcgcttga[A/C]cagcacatactgagcc	A	C	ENST00000309809 // CDS // 0 // --- // --- // ---	-	q21.3
SNP_A-2017616	gcagagttcatgttat[A/G]agagaaagctcaaagc	A	G	NM_020152 // intron // 0 // Hs.222802 // C21orf7 // 56911 // Homo sapiens chromosome 21 open reading frame 7 (C21orf7), mRNA. /// ENST00000286791 // intron // 0 // --- // --- // --- // --- /// ENST00000341618 // intron // 0 // --- // --- // --- // --- ///	C21orf7	C21orf7, Homo sapiens chromosome 21 open reading frame 7 (C21orf7), q21.3
SNP_A-1969855	aaagatcttcagtcca[C/T]gtgtagatttataaa	C	T	NM_020152 // intron // 0 // Hs.222802 // C21orf7 // 56911 // Homo sapiens chromosome 21 open reading frame 7 (C21orf7), mRNA. /// ENST00000286791 // intron // 0 // --- // --- // --- // --- /// ENST00000341618 // intron // 0 // --- // --- // --- // --- ///	C21orf7	C21orf7, Homo sapiens chromosome 21 open reading frame 7 (C21orf7), q21.3
SNP_A-1969883	aggacaggaaaagttca[A/C]tcctatatttgaagg	A	C	NM_175611 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, mRNA. /// NM_000830 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic	GRIK1	GRIK1, Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, q21.3
SNP_A-1969884	ttagtatttttcatcag[G/T]agaagttattggaaat	G	T	NM_175611 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, mRNA. /// NM_000830 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic	GRIK1	GRIK1, Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, q21.3
SNP_A-1969886	atcattctgcaggaaaa[G/T]ttattggaggacata	G	T	NM_175611 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, mRNA. /// NM_000830 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic	GRIK1	GRIK1, Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, q21.3
SNP_A-2017716	tggttcagggtcagcc[A/G]aagagcatttctttccc	A	G	NM_175611 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, mRNA. /// NM_000830 // intron // 0 // Hs.473554 // GRIK1 // 2897 // Homo sapiens glutamate receptor, ionotropic	GRIK1	GRIK1, Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), transcript variant 2, q21.3
SNP_A-1969921	tacatactattataaa[C/T]gtggttctgaggccac	C	T	NM_012131 // upstream // 14565 // Hs.258589 // CLDN17 // 26285 // Homo sapiens claudin 17 (CLDN17), mRNA. /// NM_199328 // downstream // 32825 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286808 // upstream // 14565	CLDN17	CLDN17, Homo sapiens claudin 17 (CLDN17), q21.3
SNP_A-2017806	tgtcaaaaaccagtga[C/T]ctctagatatcaattg	C	T	NM_199328 // upstream // 11104 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286809 // upstream // 11104 // --- // --- // --- /// ENST00000340345 // downstream // 55030 // --- // --- // ---	CLDN8	CLDN8, Homo sapiens claudin 8 (CLDN8), q22.11
SNP_A-1969925	tctcatactaactgc[A/G]cttcaagtccgcaca	A	G	NM_199328 // upstream // 11560 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286809 // upstream // 11560 // --- // --- // --- /// ENST00000340345 // downstream // 54574 // --- // --- // ---	CLDN8	CLDN8, Homo sapiens claudin 8 (CLDN8), q22.11
SNP_A-2017808	aactcttagtaggata[C/T]ctatcaggcattggaa	C	T	NM_199328 // upstream // 23734 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286809 // upstream // 23734 // --- // --- // --- /// ENST00000340345 // downstream // 42400 // --- // --- // ---	CLDN8	CLDN8, Homo sapiens claudin 8 (CLDN8), q22.11
SNP_A-2017811	attaaaaatgggttaa[C/T]gctcatggctcttta	C	T	NM_199328 // upstream // 26129 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286809 // upstream // 26129 // --- // --- // --- /// ENST00000340345 // downstream // 40005 // --- // --- // ---	CLDN8	CLDN8, Homo sapiens claudin 8 (CLDN8), q22.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017816	ttcacctagagacaga[C/T]ggtgctagaccactgg	C	T	NM_199328 // upstream // 51301 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286809 // upstream // 51301 // — // — // — // — /// ENST00000340345 // downstream // 14833 // — // — // — // —	CLDN8	CLDN8, Homo sapiens claudin 8 (CLDN8), q22.11
SNP_A-1969932	gacagtgtgattatca[C/G]ctacctttcctgatga	C	G	NM_199328 // upstream // 65782 // Hs.162209 // CLDN8 // 9073 // Homo sapiens claudin 8 (CLDN8), mRNA. /// ENST00000286809 // upstream // 65782 // — // — // — // — /// ENST00000340345 // downstream // 352 // — // — // — // —	CLDN8	CLDN8, Homo sapiens claudin 8 (CLDN8), q22.11
SNP_A-1926817	ttatttaaccatacta[C/G]aaaatcaaacctagga	C	G	NM_181624 // upstream // 15233 // — // KRTAP23-1 // 337963 // Homo sapiens keratin associated protein 23-1 (KRTAP23-1), mRNA. /// NM_181621 // downstream // 7847 // Hs.58152 // KRTAP13-2 // 337959 // Homo sapiens keratin associated protein 13-2 (KRTAP13	KRTAP23-1	KRTAP23-1, Homo sapiens keratin associated protein 23-1 (KRTAP23-1), q22.11
SNP_A-1689981	gtctcaagtggaacagctagcacag[A/T]agaaagaacttttctc aacacattt	A	T	NM_181599 // upstream // 9998 // Hs.407653 // KRTAP13-1 // 140258 // keratin associated protein 13-1 /// NM_181621 // upstream // 13813 // Hs.58152 // KRTAP13-2 // 337959 // keratin associated protein 13-2	KRTAP13-1	KRTAP13-1 , rs2832845, keratin associated protein 13-1 ,q22.11
SNP_A-1667884	cacctccacttattcattttactgg[A/G]acaaatttatgattgataatt ctct	A	G	NM_181599 // downstream // 3477 // Hs.407653 // KRTAP13-1 // 140258 // keratin associated protein 13-1 /// NM_181622 // downstream // 25311 // - // - // - // -	KRTAP13-1	KRTAP13-1 , rs2832852, keratin associated protein 13-1 ,q22.11
SNP_A-2202705	ccacgaaaggattaca[C/T]tagctctgcagcaatg	C	T	NM_181599 // downstream // 12766 // Hs.407653 // KRTAP13-1 // 140258 // Homo sapiens keratin associated protein 13-1 (KRTAP13-1), mRNA. /// NM_181622 // downstream // 16023 // — // KRTAP13-3 // 337960 // Homo sapiens keratin associated protein 13-3 (KRT	KRTAP13-1	KRTAP13-1, Homo sapiens keratin associated protein 13-1 (KRTAP13-1), q22.11
SNP_A-1646828	caatttctggtaactataataaagg[A/T]acatcagttaattcttctca cttct	A	T	NM_181607 // downstream // 34304 // Hs.61552 // KRTAP19-1 // 337882 // keratin associated protein 19-1 /// NM_181623 // downstream // 4962 // - // - // - // -	KRTAP19-1	KRTAP19-1 , rs2832879, keratin associated protein 19-1 ,q22.11
SNP_A-1969943	tggagttttgagacta[G/T]actagcatactcttaa	G	T	NM_181623 // downstream // 3751 // — // KRTAP15-1 // 254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 35515 // Hs.61552 // KRTAP19-1 // 337882 // Homo sapiens keratin associated protein 19-1 (KRTAP	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-1969944	tcctatttacactcca[A/G]tctgtgaaggatcctt	A	G	NM_181623 // downstream // 5596 // — // KRTAP15-1 // 254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 33670 // Hs.61552 // KRTAP19-1 // 337882 // Homo sapiens keratin associated protein 19-1 (KRTAP	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-2017846	tctcactttcttagcc[A/T]atgggccctctactca	A	T	NM_181623 // downstream // 6278 // — // KRTAP15-1 // 254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 32988 // Hs.61552 // KRTAP19-1 // 337882 // Homo sapiens keratin associated protein 19-1 (KRTAP	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-1692784	aaggaatgaatttttgtgtgataa[A/G]gtcaaacagcacgtgga attagcca	A	G	NM_181607 // downstream // 26600 // Hs.61552 // KRTAP19-1 // 337882 // keratin associated protein 19-1 /// NM_181623 // downstream // 12666 // - // - // - // -	KRTAP19-1	KRTAP19-1 , rs2832886, keratin associated protein 19-1 ,q22.11
SNP_A-2017847	tggctggaactgtaaa[C/T]ctgatgtaacgtctgt	C	T	NM_181623 // downstream // 13765 // — // KRTAP15-1 // 254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 25501 // Hs.61552 // KRTAP19-1 // 337882 // Homo sapiens keratin associated protein 19-1 (KRTA	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-2017849	tgtggaaaatgaatgc[A/G]acttaagatgccattt	A	G	NM_181623 // downstream // 20563 // — // KRTAP15-1 // 254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 18703 // Hs.61552 // KRTAP19-1 // 337882 // Homo sapiens keratin associated protein 19-1 (KRTA	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2017852	gatttcaggtgacgga[C/T]tccgaaagtaaaaaga	C	T	NM_181623 // downstream // 39082 // --- // KRTAP15-1 // 254950 // Homo sapiens keratin associated protein 15-1 (KRTAP15-1), mRNA. /// NM_181607 // downstream // 184 // Hs.61552 // KRTAP19-1 // 337882 // Homo sapiens keratin associated protein 19-1 (KRTAP1	KRTAP15-1	KRTAP15-1, Homo sapiens keratin associated protein 15-1 (KRTAP15-1), q22.11
SNP_A-2017855	tttgttaaggtggaagc[A/G]actcatcataaaggtc	A	G	NM_181610 // upstream // 4049 // --- // KRTAP19-4 // 337971 // Homo sapiens keratin associated protein 19-4 (KRTAP19-4), mRNA. /// NM_181611 // downstream // 713 // --- // KRTAP19-5 // 337972 // Homo sapiens keratin associated protein 19-5 (KRTAP19-5), mR	KRTAP19-4	KRTAP19-4, Homo sapiens keratin associated protein 19-4 (KRTAP19-4), q22.11
SNP_A-1672538	ttattcaagactgttgtaatatagat[A/T]atccaattagactatttttct aatt	A	T	NM_181611 // upstream // 15907 // - // - // - /// NM_181612 // downstream // 23661 // - // - // - // -	-	-, rs722694, -, q22.11
SNP_A-1711654	tcaatgaggaaaaaaaaaccattcg[C/T]cattatatcagattgtt aataacat	C	T	NM_003253 // intron // 0 // Hs.115176 // TIAM1 // 7074 // T-cell lymphoma invasion and metastasis 1	TIAM1	TIAM1, rs8131358, T-cell lymphoma invasion and metastasis 1,q22.11
SNP_A-2017975	atgtgtaatgaggact[A/G]aagcattgatgaagaa	A	G	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-1969993	gataacacacagttca[A/T]ctccagggtcactgcc	A	T	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-1969994	ctttgtgatctctaac[A/G]gaatacatgattgcac	A	G	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-1969998	acgttgcacggcgacc[G/T]cttgatccattctgtg	G	T	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-1710369	gagactttaaccacttgatggcaa[A/T]ctaacaaaagatgtct accaatta	A	T	NM_003253 // intron // 0 // Hs.115176 // TIAM1 // 7074 // T-cell lymphoma invasion and metastasis 1	TIAM1	TIAM1, rs2284501, T-cell lymphoma invasion and metastasis 1,q22.11
SNP_A-1969999	ttttccgaaagactga[C/T]acctccaatgacact	C	T	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2017991	ccctgtcttcttggag[A/T]cgtacaggaagaataca	A	T	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-2018004	ccagacactattctga[G/T]aacttgtttgaattt	G	T	NM_003253 // intron // 0 // Hs.517228 // TIAM1 // 7074 // Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA. /// ENST00000286827 // intron // 0 // --- // --- // ---	TIAM1	TIAM1, Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), q22.11
SNP_A-1970017	tacaacttctaggaaa[A/G]ctcttttgaatgtatg	A	G	NM_020706 // upstream // 78094 // Hs.17255 // SFRS15 // 57466 // Homo sapiens splicing factor, arginine/serine-rich 15 (SFRS15), mRNA. /// NM_014586 // upstream // 63146 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated k	SFRS15	SFRS15, Homo sapiens splicing factor, arginine q22.11
SNP_A-2018040	aatataagcacctctc[A/G]atgttagctgttttgt	A	G	NM_020706 // upstream // 107708 // Hs.17255 // SFRS15 // 57466 // Homo sapiens splicing factor, arginine/serine-rich 15 (SFRS15), mRNA. /// NM_014586 // upstream // 33532 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated	SFRS15	SFRS15, Homo sapiens splicing factor, arginine,q22.11
SNP_A-2008042	catttgtgcaatgtcc[G/T]attgttacaggttgg	G	T	NM_020706 // upstream // 130009 // Hs.17255 // SFRS15 // 57466 // Homo sapiens splicing factor, arginine/serine-rich 15 (SFRS15), mRNA. /// NM_014586 // upstream // 11231 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated	SFRS15	SFRS15, Homo sapiens splicing factor, arginine q22.11
SNP_A-2018054	cagtataagttcttgg[C/T]catctctactactgcc	C	T	NM_014586 // intron // 0 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// ENST00000270112 // intron // 0 // --- // --- // ---	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2018070	agggcgggcttcgaac[C/T]gagagcttgaattcca	C	T	NM_014586 // intron // 0 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// ENST00000270112 // intron // 0 // --- // --- // ---	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2018088	tcctatgctcattgtal[A/C]caatcactgataaatg	A	C	NM_014586 // downstream // 68652 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 // downstream // 195503 // Hs.190518 // C21orf45 // 54069 // Homo sapiens chromosome 21 open reading fr	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-1970033	aaaacagattggagta[A/G]gcatcacagacaaacc	A	G	NM_014586 // downstream // 73939 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 // downstream // 190216 // Hs.190518 // C21orf45 // 54069 // Homo sapiens chromosome 21 open reading fr	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2018094	gcaaaatgaatcagac[A/G]caggttcctactccaa	A	G	NM_014586 // downstream // 96062 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 // downstream // 168093 // Hs.190518 // C21orf45 // 54069 // Homo sapiens chromosome 21 open reading fr	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2018095	acagatggtttgtgga[C/T]aaatgatcactaggaa	C	T	NM_014586 // downstream // 98479 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 // downstream // 165676 // Hs.190518 // C21orf45 // 54069 // Homo sapiens chromosome 21 open reading fr	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2018108	ccctaaaaatatgcctc[C/T]ctaaaatacataaaac	C	T	NM_014586 // downstream // 149259 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 // downstream // 114896 // Hs.190518 // C21orf45 // 54069 // Homo sapiens chromosome 21 open reading f	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-2018118	gtgtgcttcatcgctal[C/T]ggaagcttagaaaatt	C	T	NM_014586 // downstream // 186549 // Hs.109437 // HUNK // 30811 // Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), mRNA. /// NM_018944 // downstream // 77606 // Hs.190518 // C21orf45 // 54069 // Homo sapiens chromosome 21 open reading fr	HUNK	HUNK, Homo sapiens hormonally upregulated Neu-associated kinase (HUNK), q22.11
SNP_A-1904459	tgggaccgagacttca[A/T]tctgtggatatgatg	A	T	NM_058187 // intron // 0 // Hs.208358 // C21orf63 // 59271 // Homo sapiens chromosome 21 open reading frame 63 (C21orf63), mRNA. /// ENST00000300255 // intron // 0 // --- // --- // ---	C21orf63	C21orf63, Homo sapiens chromosome 21 open reading frame 63 (C21orf63), q22.11
SNP_A-2018184	ccgtgcatacagcaga[C/T]acttggttccttttg	C	T	NM_144659 // upstream // 13970 // Hs.42034 // TCP10L // 140290 // Homo sapiens t-complex 10 (mouse)-like (TCP10L), mRNA. /// NM_021254 // downstream // 2198 // Hs.5811 // C21orf59 // 56683 // Homo sapiens chromosome 21 open reading frame 59 (C21orf59), mR	TCP10L	TCP10L, Homo sapiens t-complex 10 (mouse)-like (TCP10L), q22.11
SNP_A-1688714	cagaaatgaatttaagtaattacgq[C/T]gaaaatttccttaaacat gatttaa	C	T	NM_003895 // intron // 0 // Hs.401730 // SYNJ1 // 8867 // synaptojanin 1	SYNJ1	SYNJ1 , rs2833933, synaptojanin 1,q22.11
SNP_A-2018188	aataatacagtaatca[A/G]attcttccaggaagta	A	G	NM_003895 // intron // 0 // Hs.473632 // SYNJ1 // 8867 // Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 1, mRNA. /// NM_203446 // intron // 0 // Hs.473632 // SYNJ1 // 8867 // Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 2, mRNA. /// E	SYNJ1	SYNJ1, Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 1, q22.11
SNP_A-1970055	caagattggaatgtga[A/G]gtttaaataggacatt	A	G	NM_003895 // intron // 0 // Hs.473632 // SYNJ1 // 8867 // Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 1, mRNA. /// NM_203446 // intron // 0 // Hs.473632 // SYNJ1 // 8867 // Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 2, mRNA. /// E	SYNJ1	SYNJ1, Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 1, q22.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2018193	cctctcgcctcctccc[C/T]actgctatagcctctc	C	T	NM_019596 // intron // 0 // Hs.517235 // C21orf62 // 56245 // Homo sapiens chromosome 21 open reading frame 62 (C21orf62), mRNA. /// ENST00000290186 // intron // 0 // — // — // — // —	C21orf62	C21orf62, Homo sapiens chromosome 21 open reading frame 62 (C21orf62), q22.11
SNP_A-2018195	taatcggaatttaaac[C/T]gacacattcttgtcca	C	T	NM_019596 // intron // 0 // Hs.517235 // C21orf62 // 56245 // Homo sapiens chromosome 21 open reading frame 62 (C21orf62), mRNA. /// ENST00000290186 // intron // 0 // — // — // — // —	C21orf62	C21orf62, Homo sapiens chromosome 21 open reading frame 62 (C21orf62), q22.11
SNP_A-2018202	acatcataaaacacta[A/G]gatttttctgcttcag	A	G	NM_019596 // upstream // 33788 // Hs.517235 // C21orf62 // 56245 // Homo sapiens chromosome 21 open reading frame 62 (C21orf62), mRNA. /// NM_005806 // upstream // 178511 // Hs.176977 // OLIG2 // 10215 // Homo sapiens oligodendrocyte lineage transcription	C21orf62	C21orf62, Homo sapiens chromosome 21 open reading frame 62 (C21orf62), q22.11
SNP_A-1888315	tgagctgctgtgggtc[A/G]aaccatctctcaggtg	A	G	NM_019596 // upstream // 54124 // Hs.517235 // C21orf62 // 56245 // Homo sapiens chromosome 21 open reading frame 62 (C21orf62), mRNA. /// NM_005806 // upstream // 158175 // Hs.176977 // OLIG2 // 10215 // Homo sapiens oligodendrocyte lineage transcription	C21orf62	C21orf62, Homo sapiens chromosome 21 open reading frame 62 (C21orf62), q22.11
SNP_A-1970073	ctcagtttacagttgg[C/T]taaatatggcatttgt	C	T	NM_138983 // downstream // 47259 // Hs.56663 // OLIG1 // 116448 // Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), mRNA. /// NM_207584 // upstream // 110247 // Hs.512211 // IFNAR2 // 3455 // Homo sapiens interferon (alpha, beta and omega) rec	OLIG1	OLIG1, Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), q22.11
SNP_A-2018234	atatatttttttactca[C/T]cgagggtctccctgca	C	T	NM_138983 // downstream // 51669 // Hs.56663 // OLIG1 // 116448 // Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), mRNA. /// NM_207584 // upstream // 105837 // Hs.512211 // IFNAR2 // 3455 // Homo sapiens interferon (alpha, beta and omega) rec	OLIG1	OLIG1, Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), q22.11
SNP_A-1970078	agcagttgcactaaga[A/T]gtcagaagaacctgct	A	T	NM_000628 // downstream // 12251 // Hs.418291 // IL10RB // 3588 // Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA. /// NM_000629 // upstream // 15443 // Hs.529400 // IFNAR1 // 3454 // Homo sapiens interferon (alpha, beta and omega) receptor 1 (	IL10RB	IL10RB, Homo sapiens interleukin 10 receptor, beta (IL10RB), q22.11
SNP_A-2018298	ttaaaaatatttctgg[C/T]agcactgagtccacag	C	T	NM_000629 // intron // 0 // Hs.529400 // IFNAR1 // 3454 // Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA. /// ENST00000270139 // intron // 0 // — // — // — // —	IFNAR1	IFNAR1, Homo sapiens interferon (alpha, beta and omega) receptor 1 (IFNAR1), q22.11
SNP_A-2239322	ctctttagtctcttcc[C/T]gctccagtaggattgt	C	T	NM_001697 // upstream // 25149 // Hs.409140 // ATP5O // 539 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP /// NM_172201 // upstream // 423016 // Hs.512862 // KCNE2 // 99	ATP5O	ATP5O, Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP q22.11
SNP_A-2018393	tttggggcatgtctag[G/T]cagttgcaatgtagtc	G	T	NM_001697 // upstream // 215340 // Hs.409140 // ATP5O // 539 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP /// NM_172201 // upstream // 232825 // Hs.512862 // KCNE2 // 9	ATP5O	ATP5O, Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP ,q22.11
SNP_A-1970102	tttcccatctagaatc[A/G]aagtagaaaaccactc	A	G	NM_001697 // upstream // 272531 // Hs.409140 // ATP5O // 539 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP /// NM_172201 // upstream // 175634 // Hs.512862 // KCNE2 // 9	ATP5O	ATP5O, Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP q22.11

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1970115	tcatcaaggcttttgta[C/T]acttattgccaaattt	C	T	NM_001697 // upstream // 410232 // Hs.409140 // ATP5O // 539 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP /// NM_172201 // upstream // 37933 // Hs.512862 // KCNE2 // 99	ATP5O	ATP5O, Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP ,q22.11
SNP_A-1970117	aaaacaaacctaatac[G/T]gcaccatttccgtcca	G	T	NM_001697 // upstream // 438068 // Hs.409140 // ATP5O // 539 // Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP /// NM_172201 // upstream // 10097 // Hs.512862 // KCNE2 // 99	ATP5O	ATP5O, Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP ,q22.11
SNP_A-1970139	tgcagccgtggctaca[A/G]tagcaagttctcaggg	A	G	NM_053277 // downstream // 33754 // Hs.473695 // CLIC6 // 54102 // Homo sapiens chloride intracellular channel 6 (CLIC6), mRNA. /// NM_001001890 // downstream // 35828 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute	CLIC6	CLIC6, Homo sapiens chloride intracellular channel 6 (CLIC6), q22.12
SNP_A-2018516	tgtggcttttatata[C/T]gctgctcgcctgagat	C	T	NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2018528	agaacatctgctcaat[G/T]accgtgaggaaggaag	G	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2018529	tggtacaaacgaagaa[G/T]gtgtttgggagctcc	G	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2018531	gaaatttctgttgcac[C/T]acttagagtccagagt	C	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-1970146	atctcatgttaaccaa[C/T]ggtgcctagtggaacc	C	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-1970148	gggcataaagcacata[C/G]atgtaaaattctcctt	C	G	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2018557	taatgagatacaatga[C/T]gccagtggtggaagag	C	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2018558	actatcataatgaaat[A/G]aaactcacaacaaagg	A	G	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1970150	aggctaaactccctca[G/T]gtgccaaacagatatt	G	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-2018561	atcttcagaagctaca[C/T]tggtgcctgaacagat	C	T	NM_001754 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, mRNA. /// NM_001001890 // intron // 0 // Hs.149261 // RUNX1 // 861 // Homo s	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 1, q22.12
SNP_A-1672074	gagcacattgtcacttttttccagca[A/T]cttgggtatattacatatctt atta	A	T	NM_001754 // upstream // 19059 // Hs.410774 // RUNX1 // 861 // runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) /// NM_017438 // downstream // 966140 // Hs.446259 // C21orf18 // 54093 // chromosome 21 open reading frame 18 //	RUNX1	RUNX1 , rs10483024, runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) ,q22.12
SNP_A-2018623	atgtgcataacattcc[A/G]ctttatcaatatcccc	A	G	NM_001001890 // upstream // 424830 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 265223 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2018641	ttgagaatcacagaga[C/G]gtctggaaggataaca	C	G	NM_001001890 // upstream // 527178 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 367571 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-1970201	ggggttatcagcatca[C/T]actagtgcccacctgg	C	T	NM_001001890 // upstream // 863008 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 703401 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-2018724	aaattgcacagaaaac[C/T]cttttccctccagcta	C	T	NM_001001890 // upstream // 884171 // Hs.149261 // RUNX1 // 861 // Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, mRNA. /// NM_001754 // upstream // 724564 // Hs.149261 // RUNX1 //	RUNX1	RUNX1, Homo sapiens runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), transcript variant 2, q22.12
SNP_A-1970219	ccagaactgtaagcac[C/T]gggcacgggtcactgc	C	T	NM_017438 // intron // 0 // Hs.473727 // C21orf18 // 54093 // Homo sapiens chromosome 21 open reading frame 18 (C21orf18), mRNA. /// ENST00000344232 // intron // 0 // — // — // — // — /// ENST00000332131 // intron // 0 // — // — // — // —	C21orf18	C21orf18, Homo sapiens chromosome 21 open reading frame 18 (C21orf18), q22.12
SNP_A-2018787	cagcttggaagaatca[A/G]agggggatggttaaca	A	G	NM_001757 // downstream // 30897 // Hs.88778 // CBR1 // 873 // Homo sapiens carbonyl reductase 1 (CBR1), mRNA. /// ENST00000290349 // downstream // 30897 // — // — // — // — /// ENST00000319751 // upstream // 25936 // — // — // — // —	CBR1	CBR1, Homo sapiens carbonyl reductase 1 (CBR1), q22.12
SNP_A-1970225	aggcttggatttgcat[G/T]aaattgatacagaaaa	G	T	NM_005128 // intron // 0 // Hs.204575 // C21orf5 // 9980 // Homo sapiens chromosome 21 open reading frame 5 (C21orf5), mRNA. /// ENST00000270190 // intron // 0 // — // — // — // —	C21orf5	C21orf5, Homo sapiens chromosome 21 open reading frame 5 (C21orf5), q22.12
SNP_A-2018886	tttacaggttgatgta[A/C]gattggccctgtgcag	A	C	NM_144492 // upstream // 153254 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 153254 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 2,	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-2018887	gagcacacactgggga[A/G]ctatagacttctcaaa	A	G	NM_144492 // upstream // 153751 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 153751 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 2,	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2018891	cccactgcctggtcaa[C/T]tgggttgcagctcatc	C	T	NM_144492 // upstream // 157908 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 157908 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 2,	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-2018900	accgatgcaagttccc[C/T]gctactgcttttatt	C	T	NM_144492 // upstream // 200397 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 1, mRNA. /// NM_012130 // upstream // 200397 // Hs.505146 // CLDN14 // 23562 // Homo sapiens claudin 14 (CLDN14), transcript variant 2,	CLDN14	CLDN14, Homo sapiens claudin 14 (CLDN14), transcript variant 1, q22.13
SNP_A-2019029	ctcaagttcaaagcca[A/G]atggaaaatggcaagt	A	G	NM_130437 // downstream // 109246 // Hs.368240 // DYRK1A // 1859 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, mRNA. /// NM_101395 // downstream // 100420 // Hs.368240 // DYRK1A // 1859 /	DYRK1A	DYRK1A, Homo sapiens dual-specificity tyrosine-(Y) phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, q22.13
SNP_A-2019031	tacaatatagatcatgt[C/G]aaaaagcttgtgaccc	C	G	NM_130437 // downstream // 112670 // Hs.368240 // DYRK1A // 1859 // Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, mRNA. /// NM_101395 // downstream // 103844 // Hs.368240 // DYRK1A // 1859 /	DYRK1A	DYRK1A, Homo sapiens dual-specificity tyrosine-(Y) phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, q22.13
SNP_A-2019035	gctgcttcaattgcac[A/G]aagaagaaaitatagt	A	G	NM_002240 // intron // 0 // Hs.50927 // KCNJ6 // 3763 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // — // — // —	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2019038	cctcagagaatggcga[C/T]atttatcactctgca	C	T	NM_002240 // intron // 0 // Hs.50927 // KCNJ6 // 3763 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // — // — // —	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2019045	ttaaaaattacttccc[C/T]atctgatctggctgtt	C	T	NM_002240 // intron // 0 // Hs.50927 // KCNJ6 // 3763 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // — // — // —	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2019047	gatatatgaagaggga[A/C]caaaaggaactcacac	A	C	NM_002240 // intron // 0 // Hs.50927 // KCNJ6 // 3763 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // — // — // —	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2019048	ctcctccaacctcctca[C/T]tgtgggctgaacatgg	C	T	NM_002240 // intron // 0 // Hs.50927 // KCNJ6 // 3763 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // — // — // —	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-1970285	tccaggttgatagctc[C/T]atacctattaagacag	C	T	NM_002240 // intron // 0 // Hs.50927 // KCNJ6 // 3763 // Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), mRNA. /// ENST00000288309 // intron // 0 // — // — // —	KCNJ6	KCNJ6, Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 6 (KCNJ6), q22.13
SNP_A-2019189	gctgcatggagtttaa[C/T]atcctttaaatgcac	C	T	NM_182918 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-2019190	agaaacgtgatctcaa[C/G]caatctttgcaaatgg	C	G	NM_182918 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2019193	agtgacattccaaaaat[A/G]cagttgcatgctgaac	A	G	NM_182918 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // intron // 0 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-1705491	ggattcttaaaaaatcattatcctg[C/T]ataaaatgtagacctatg ctggca	C	T	NM_004449 // upstream // 100442 // Hs.45514 // ERG // 2078 // v-ets erythroblastosis virus E26 oncogene like (avian) /// NM_005239 // upstream // 129817 // Hs.292477 // ETS2 // 2114 // v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ERG	ERG, rs2836616, v-ets erythroblastosis virus E26 oncogene like (avian) q22.2
SNP_A-2019266	tcacagtgtatgaaac[A/G]aatgttagttactcca	A	G	NM_182918 // upstream // 249371 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, mRNA. /// NM_004449 // upstream // 86150 // Hs.473819 // ERG // 2078 // Homo sapiens v-ets eryt	ERG	ERG, Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), transcript variant 1, q22.2
SNP_A-1970352	gagccaggatttttgta[C/T]gtggatgagattcttc	C	T	NM_005239 // downstream // 70183 // Hs.517296 // ETS2 // 2114 // Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), mRNA. /// NM_005239 // downstream // 69027 // Hs.517296 // ETS2 // 2114 // Homo sapiens v-ets erythroblastosi	ETS2	ETS2, Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), q22.2
SNP_A-2019349	ttttataagaacacc[A/G]atcattggatttaggc	A	G	ENST00000329367 // upstream // 13094 // --- // --- // --- /// ENST00000333546 // upstream // 91180 // --- // --- // --- ///	-	q22.2
SNP_A-2019362	ctttcaagttcttga[C/T]gagggtgatgaagcca	C	T	ENST00000329367 // upstream // 51134 // --- // --- // --- /// ENST00000333546 // upstream // 53140 // --- // --- // --- ///	-	q22.2
SNP_A-2019393	aatatagggtgaagga[C/T]ggctacctagtcaagg	C	T	NM_018963 // intron // 0 // Hs.314338 // WDR9 // 54014 // Homo sapiens chromosome 21 open reading frame 107 (C21orf107), transcript variant 1, mRNA. /// NM_033656 // intron // 0 // Hs.314338 // WDR9 // 54014 // Homo sapiens chromosome 21 open reading fram	WDR9	WDR9, Homo sapiens chromosome 21 open reading frame 107 (C21orf107), transcript variant 1, q22.2
SNP_A-1970373	aactttcaatgctaaca[C/T]gggcggaaaaatcact	C	T	ENST00000288344 // intron // 0 // --- // --- // ---	-	q22.2
SNP_A-1970389	gtgaagtccaggagag[A/T]cccatgaatatccgtg	A	T	NM_153754 // intron // 0 // Hs.547011 // C21orf88 // 114041 // Homo sapiens chromosome 21 open reading frame 88 (C21orf88), mRNA. /// ENST00000359876 // intron // 0 // --- // --- // --- /// ENST00000329618 // intron // 0 // --- // --- // ---	C21orf88	C21orf88, Homo sapiens chromosome 21 open reading frame 88 (C21orf88), q22.2
SNP_A-2019478	tggtcattgtcccttaa[C/T]ctgtgagaggaagtga	C	T	NM_006057 // downstream // 35378 // Hs.225943 // B3GALT5 // 10317 // Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5), transcript variant 1, mRNA. /// NM_033171 // downstream // 35378 // Hs.225943 // B3GALT5 // 10317	B3GALT5	B3GALT5, Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5 (B3GALT5), transcript variant 1, q22.2
SNP_A-2019534	gggctaattatgcccaa[A/C]atcatgatgggatgaa	A	C	NM_006198 // upstream // 17226 // Hs.80296 // PCP4 // 5121 // Homo sapiens Purkinje cell protein 4 (PCP4), mRNA. /// ENST00000328060 // downstream // 48113 // --- // --- // --- /// ENST00000328619 // upstream // 17226 // --- // --- // ---	PCP4	PCP4, Homo sapiens Purkinje cell protein 4 (PCP4), q22.2
SNP_A-2019634	ctgctaagagcctcac[C/T]gcagaatttcacgttt	C	T	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2019682	gcttgatatctctccc[A/G]acattaaaatagcacc	A	G	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1970449	gacatttgccttctc[A/G]acattatttttaatgc	A	G	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2019711	tattcataagacataa[A/G]atcgatggcacaaagt	A	G	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2019719	acctgaaacagaaaaga[C/T]ggctcttagatcatc	C	T	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-1970456	ctggaaattgccctac[A/G]agatcatctgggcatc	A	G	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2019735	ttgaaatacatctat[A/G]actcag|atattagct	A	G	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-1970469	atgggcagtcatatta[C/T]ccaaatcaaatttctc	C	T	NM_206887 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // intron // 0 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecul	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2019849	attttttgttagga[C/T]cattacaaatcttctt	C	T	NM_206887 // upstream // 212955 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // upstream // 212955 // Hs.397600 // DSCAM // 1826 // Homo sapiens Down syndrome cell ad	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-2019852	aattcagtcatcatcag[C/G]cagtccttttcactat	C	G	NM_206887 // upstream // 225366 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // upstream // 225366 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell ad	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-1688818	tccattcagaagaaagctcctgcc[A/G]tgtgtcactctatttaa atgatga	A	G	AF269287 // downstream // 204006 // Hs.118057 // PLAC4 // 191585 // placenta-specific 4 /// NM_001389 // upstream // 127441 // Hs.49002 // DSCAM // 1826 // Down syndrome cell adhesion molecule /// NM_012105 // upstream // 193222 // Hs.436490 // BACE2 //	PLAC4	PLAC4 , rs2249248, placenta-specific 4 ,q22.2
SNP_A-1675602	acacagcccagtcaatgcttcatta[A/C]agtgttgtgtgactctaa tcagagg	A	C	AF269287 // downstream // 202908 // Hs.118057 // PLAC4 // 191585 // placenta-specific 4 /// NM_001389 // upstream // 128539 // Hs.49002 // DSCAM // 1826 // Down syndrome cell adhesion molecule /// NM_012105 // upstream // 192124 // Hs.436490 // BACE2 //	PLAC4	PLAC4 , rs4389398, placenta-specific 4 ,q22.2
SNP_A-1747675	accatacaactgatatgcaacagga[C/T]gaaagacaattgca agtgactactg	C	T	AF269287 // downstream // 201390 // Hs.118057 // PLAC4 // 191585 // placenta-specific 4 /// NM_001389 // upstream // 130057 // Hs.49002 // DSCAM // 1826 // Down syndrome cell adhesion molecule /// NM_012105 // upstream // 190606 // Hs.436490 // BACE2 //	PLAC4	PLAC4 , rs14677754, placenta-specific 4 ,q22.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1745045	tctattgtaccctcccatgaagccca[A/G]tatagtgtataatcaattaaaaaat	A	G	AF269287 // downstream // 201139 // Hs.118057 // PLAC4 // 191585 // placenta-specific 4 /// NM_001389 // upstream // 130308 // Hs.49002 // DSCAM // 1826 // Down syndrome cell adhesion molecule /// NM_012105 // upstream // 190355 // Hs.436490 // BACE2 //	PLAC4	PLAC4, rs713112, placenta-specific 4 ,q22.2
SNP_A-2019860	ctgcacgtaggctcaa[A/G]tatggctggcagcttg	A	G	NM_206887 // upstream // 271554 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // upstream // 271554 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell ad	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.2
SNP_A-1735178	aggcttcagttcggtgtaattacta[C/T]tgtttctaaaggagtttctgtgtaa	C	T	AF269287 // downstream // 114985 // Hs.118057 // PLAC4 // 191585 // placenta-specific 4 /// NM_001389 // upstream // 216462 // Hs.49002 // DSCAM // 1826 // Down syndrome cell adhesion molecule /// NM_012105 // upstream // 104201 // Hs.436490 // BACE2 //	PLAC4	PLAC4, rs2837918, placenta-specific 4 ,q22.2
SNP_A-1689937	tcacattacatactgtatgtcgaa[C/T]ctgaaaggaagctatgtt cgaatag	C	T	AF269287 // downstream // 114616 // Hs.118057 // PLAC4 // 191585 // placenta-specific 4 /// NM_001389 // upstream // 216831 // Hs.49002 // DSCAM // 1826 // Down syndrome cell adhesion molecule /// NM_012105 // upstream // 103832 // Hs.436490 // BACE2 //	PLAC4	PLAC4, rs2837920, placenta-specific 4 ,q22.2
SNP_A-2019893	aaaattggatcagtca[A/G]gaatcatttgcacaca	A	G	NM_206887 // upstream // 407112 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, mRNA. /// NM_001389 // upstream // 407112 // Hs.397800 // DSCAM // 1826 // Homo sapiens Down syndrome cell ad	DSCAM	DSCAM, Homo sapiens Down syndrome cell adhesion molecule (DSCAM), transcript variant 2, q22.3
SNP_A-2019917	cctcagattctgcagc[G/T]aacaagaggttgagct	G	T	NM_138992 // intron // 0 // Hs.529408 // BACE2 // 25825 // Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant b, mRNA. /// NM_138991 // intron // 0 // Hs.529408 // BACE2 // 25825 // Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2	BACE2	BACE2, Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant b, q22.3
SNP_A-1970497	ctgtatccattatgat[C/T]acctacacatattaca	C	T	NM_002462 // intron // 0 // Hs.517307 // MX1 // 4599 // Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA. /// ENST00000288383 // intron // 0 // — // — // — // —	MX1	MX1, Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), q22.3
SNP_A-2019962	acttttgtttctgta[C/T]cagcaatttttagca	C	T	NM_002462 // intron // 0 // Hs.517307 // MX1 // 4599 // Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA. /// ENST00000288383 // intron // 0 // — // — // — // —	MX1	MX1, Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), q22.3
SNP_A-2019979	ttctgggacaccccag[A/T]aggattggtggtgaagg	A	T	NM_002462 // downstream // 54517 // Hs.517307 // MX1 // 4599 // Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA. /// NM_005656 // upstream // 5575 // Hs.439309 // TMPRSS2 // 7113 // Homo sapiens	MX1	MX1, Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), q22.3
SNP_A-2019992	gtggaaactctgtagcc[A/G]ctcagtttcctcatct	A	G	NM_002462 // downstream // 145578 // Hs.517307 // MX1 // 4599 // Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA. /// NM_005656 // upstream // 96636 // Hs.439309 // TMPRSS2 // 7113 // Homo sapien	MX1	MX1, Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), q22.3
SNP_A-1857835	tcactgttactaaata[C/T]ccattactggacttg	C	T	ENST00000339657 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2147952	atggctcccacagcca[C/G]agaaaggagatacaaa	C	G	ENST00000339657 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-1970507	aaatcacaactgctga[C/T]gatcacgagataatcc	C	T	NM_020727 // intron // 0 // Hs.434947 // ZNF295 // 49854 // Homo sapiens zinc finger protein 295 (ZNF295), mRNA. /// ENST00000339657 // intron // 0 // — // — // — // — /// ENST00000310826 // intron // 0 // — // — // — // —	ZNF295	ZNF295, Homo sapiens zinc finger protein 295 (ZNF295), q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2020073	cttcttttgtctctca[C/G]gatctatgaaagataa	C	G	NM_198078 // intron // 0 // Hs.143833 // C21orf121 // 150142 // Homo sapiens chromosome 21 open reading frame 121 (C21orf121), mRNA. /// ENST00000339657 // intron // 0 // --- // --- // --- /// ENST00000358893 // intron // 0 // --- // --- // ---	C21orf121	C21orf121, Homo sapiens chromosome 21 open reading frame 121 (C21orf121), q22.3
SNP_A-2020076	gtgtctacacatccaag[C/G]aatcagtttccgtaac	C	G	ENST00000339657 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-2020083	gcagatttctggccac[A/G]ctctttgatcacaaat	A	G	ENST00000339657 // intron // 0 // --- // --- // --- // ---	-	q22.3
SNP_A-2020104	tgcctctttccctttc[C/T]ctcactgggttatatc	C	T	ENST00000339657 // intron // 0 // --- // --- // --- // --- // --- /// ENST00000317986 // intron // 0 // --- // --- // ---	-	q22.3
SNP_A-2020117	atagatttctagcagag[A/G]aacaataattgtgagag	A	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020119	gagcccattcacacaa[A/G]ggtctcatttattag	A	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-1970516	gtttagagaggaaaat[A/G]ggcagcatcatttgt	A	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-1970517	tcctggtttcatgaag[C/G]caaatactcctcttc	C	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020120	ttcgaatctcaacac[C/T]ctgagcctgtgcttt	C	T	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020121	atgggtcaccaaagac[A/G]cacaaaggtaagatgt	A	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020122	aaataacacaagagccc[A/G]gaacagaatgaatgtg	A	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020123	aatagtttaaaatca[C/T]ggtcaaattctaagtc	C	T	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020130	attcagccgctcctaa[A/G]taggtggccagattgt	A	G	NM_016818 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA. /// NM_207629 // intron // 0 // Hs.124649 // ABCG1 // 9619 // Homo sapiens ATP-binding cassett	ABCG1	ABCG1, Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, q22.3
SNP_A-2020136	gtttgtgacttagat[A/G]accatagattaactg	A	G	ENST00000339657 // intron // 0 // --- // --- // ---	-	q22.3
SNP_A-2020142	aaggataaattcacaa[A/G]catggcatccgtctc	A	G	ENST00000339657 // intron // 0 // --- // --- // ---	-	q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2020183	aagcaacatgaactgc[A/G]ccatcactgacttcta	A	G	NM_018964 // intron // 0 // Hs.473918 // SLC37A1 // 54020 // Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 1 (SLC37A1), mRNA. /// ENST00000339657 // intron // 0 // — // — // — // — /// ENST00000352133 // intron /	SLC37A1	SLC37A1, Homo sapiens solute carrier family 37 (glycerol-3-phosphate transporter), member 1 (SLC37A1), q22.3
SNP_A-2020189	gatggaagcgggaacc[A/G]aaagcctggctgagag	A	G	ENST00000339657 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2020192	cgagtagccacaggac[A/G]gaactgagaagcgagt	A	G	ENST00000339657 // intron // 0 // — // — // — // —	-	q22.3
SNP_A-2020194	tagttacctagggcaa[C/T]gctgatgcagataagt	C	T	NM_152506 // upstream // 886323 // Hs.350679 // C21orf129 // 150135 // Homo sapiens chromosome 21 open reading frame 129 (C21orf129), mRNA. /// NM_020639 // upstream // 834992 // Hs.517310 // RIPK4 // 54101 // Homo sapiens receptor-interacting serine-thre	C21orf129	C21orf129, Homo sapiens chromosome 21 open reading frame 129 (C21orf129), q22.3
SNP_A-2020211	gcccctcagagtgcac[A/G]ggggatgatcttggag	A	G	NM_001001580 // intron // 0 // Hs.473927 // PDE9A // 5152 // Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 15, mRNA. /// NM_001001579 // intron // 0 // Hs.473927 // PDE9A // 5152 // Homo sapiens phosphodiesterase 9A (PDE9A), transcript var	PDE9A	PDE9A, Homo sapiens phosphodiesterase 9A (PDE9A), transcript variant 15, q22.3
SNP_A-2142520	atgaacaatccacaac[C/T]acaggcaacaaggtgg	C	T	NM_033661 // intron // 0 // Hs.248815 // WDR4 // 10785 // Homo sapiens WD repeat domain 4 (WDR4), transcript variant 2, mRNA. /// NM_018669 // intron // 0 // Hs.248815 // WDR4 // 10785 // Homo sapiens WD repeat domain 4 (WDR4), transcript variant 1, mRNA.	WDR4	WDR4, Homo sapiens WD repeat domain 4 (WDR4), transcript variant 2, q22.3
SNP_A-2020272	acccccctggctcacta[C/T]gacaccaccgctgatg	C	T	NM_000071 // CDS // 0 // Hs.533013 // CBS // 875 // Homo sapiens cystathionine-beta-synthase (CBS), mRNA. /// ENST00000337561 // CDS // 0 // — // — // — // — /// ENST00000359624 // CDS // 0 // — // — // — // — /// ENST00000352178 // CDS //	CBS	CBS, Homo sapiens cystathionine-beta-synthase (CBS), q22.3
SNP_A-2020276	agtgtgtggacagaac[A/G]gacaatcttttctgcc	A	G	NM_006758 // intron // 0 // Hs.365116 // U2AF1 // 7307 // Homo sapiens U2(RNU2) small nuclear RNA auxiliary factor 1 (U2AF1), mRNA. /// ENST00000291552 // intron // 0 // — // — // — // —	U2AF1	U2AF1, Homo sapiens U2(RNU2) small nuclear RNA auxiliary factor 1 (U2AF1), q22.3
SNP_A-1716941	tctctacacactgcggtggaagaca[C/T]ggcccttcctgccaac gtgcacctc	C	T	NM_000394 // downstream // 103160 // Hs.184085 // CRYAA // 1409 // crystallin, alpha A /// NM_173354 // downstream // 100398 // Hs.380991 // SNF1LK // 150094 // SNF1-like kinase	CRYAA	CRYAA , rs605781, crystallin, alpha A ,q22.3
SNP_A-2020342	gcattcatggactgta[A/T]cttagctctgttgaaa	A	T	NM_007031 // intron // 0 // Hs.406157 // HSF2BP // 11077 // Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA. /// ENST00000291560 // intron // 0 // — // — // — // —	HSF2BP	HSF2BP, Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), q22.3
SNP_A-2020346	tcttccaatctcatgc[A/G]aatttttttcctcctt	A	G	NM_007031 // intron // 0 // Hs.406157 // HSF2BP // 11077 // Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA. /// ENST00000291560 // intron // 0 // — // — // — // —	HSF2BP	HSF2BP, Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), q22.3
SNP_A-2008141	gaagatagctcaccccc[A/G]agaatatgagtttctg	A	G	NM_007031 // intron // 0 // Hs.406157 // HSF2BP // 11077 // Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA. /// ENST00000291560 // intron // 0 // — // — // — // —	HSF2BP	HSF2BP, Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), q22.3
SNP_A-1970574	agaagagaggaattttc[A/G]acagccccgtacacaa	A	G	NM_194310 // upstream // 13878 // Hs.313689 // LOC284837 // 284837 // Homo sapiens hypothetical protein LOC284837 (LOC284837), mRNA. /// NM_020132 // upstream // 38790 // Hs.248785 // AGPAT3 // 56894 // Homo sapiens 1-acylglycerol-3-phosphate O-acyltransf	LOC284837	LOC284837, Homo sapiens hypothetical protein LOC284837 (LOC284837), q22.3
SNP_A-1658680	agacctgtgggggtgcaaatgcgaa[C/T]gtgtgaggggtgctc cgggacagct	C	T	NM_003274 // intron // 0 // Hs.438927 // TMEM1 // 7109 // transmembrane protein 1	TMEM1	TMEM1 , rs2277805, transmembrane protein 1,q22.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2020493	ggcagattcaaaccac[A/G]gacttcatggatatcg	A	G	NM_144991 // intron // 0 // Hs.473997 // C21orf29 // 54084 // Homo sapiens chromosome 21 open reading frame 29 (C21orf29), mRNA. /// ENST00000323084 // intron // 0 // — // — // — // — /// ENST00000341581 // intron // 0 // — // — // — // —	C21orf29	C21orf29, Homo sapiens chromosome 21 open reading frame 29 (C21orf29), q22.3
SNP_A-2020557	gtgttaagcacttata[A/C]cactatgtagctacta	A	C	NM_001112 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, mRNA. /// NM_015833 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosin	ADARB1	ADARB1, Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, q22.3
SNP_A-2020558	atgaggagcaggagat[C/G]agcttacagttttctg	C	G	NM_001112 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, mRNA. /// NM_015833 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosin	ADARB1	ADARB1, Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, q22.3
SNP_A-2020567	ttaagtaatcgactta[C/T]atagaaggtgtgcacc	C	T	NM_001112 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, mRNA. /// NM_015833 // intron // 0 // Hs.474018 // ADARB1 // 104 // Homo sapiens adenosin	ADARB1	ADARB1, Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, q22.3
SNP_A-1740519	aggtcatcctcaagagattacttcc[A/G]cctcaattcacacagga caggtgat	A	G	NM_153755 // intron // 0 // - // - // - // -	-	- , rs2838825, -,q22.3
SNP_A-1672866	gattgtacatttggttgtttctgct[C/G]acttacccatggtggccggc ttcct	C	G	NM_153755 // intron // 0 // - // - // - // -	-	- , rs2838847, -,q22.3
SNP_A-2020763	tgttttcacttattca[A/G]taattattcagtgtcc	A	G	NM_206889 // intron // 0 // Hs.189585 // C21orf106 // 23181 // Homo sapiens chromosome 21 open reading frame 106 (C21orf106), transcript variant 2, mRNA. /// NM_015151 // intron // 0 // Hs.189585 // C21orf106 // 23181 // Homo sapiens chromosome 21 open re	C21orf106	C21orf106, Homo sapiens chromosome 21 open reading frame 106 (C21orf106), transcript variant 2, q22.3
SNP_A-2020786	gacaaggagcttggga[A/G]tagaagaagcaaaatt	A	G	NM_206889 // intron // 0 // Hs.189585 // C21orf106 // 23181 // Homo sapiens chromosome 21 open reading frame 106 (C21orf106), transcript variant 2, mRNA. /// NM_015151 // intron // 0 // Hs.189585 // C21orf106 // 23181 // Homo sapiens chromosome 21 open re	C21orf106	C21orf106, Homo sapiens chromosome 21 open reading frame 106 (C21orf106), transcript variant 2, q22.3
SNP_A-2020793	gcccccacaatgccac[C/T]gggtactacaccgttt	C	T	NM_206889 // CDS // 0 // Hs.189585 // C21orf106 // 23181 // Homo sapiens chromosome 21 open reading frame 106 (C21orf106), transcript variant 2, mRNA. /// NM_015151 // CDS // 0 // Hs.189585 // C21orf106 // 23181 // Homo sapiens chromosome 21 open reading	C21orf106	C21orf106, Homo sapiens chromosome 21 open reading frame 106 (C21orf106), transcript variant 2, q22.3
SNP_A-1970657	tttctacaactgcaaa[C/T]actattcagcaattta	C	T	NM_004677 // downstream // 68072 // Hs.158346 // XKRY // 9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // downstream // 68072 // Hs.158346 // XKRY2 // 353515 // Homo sapiens X Kell blood group precursor	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-2113228	aggccctatgctcctc[A/G]caccaatctagtaaga	A	G	NM_004677 // upstream // 5160 // Hs.158346 // XKRY // 9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream // 5160 // Hs.158346 // XKRY2 // 353515 // Homo sapiens X Kell blood group precursor-relat	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-2134988	atattcataagaaaca[A/C]tagaagacaaaaatgt	A	C	NM_004677 // upstream // 14651 // Hs.158346 // XKRY // 9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream // 14651 // Hs.158346 // XKRY2 // 353515 // Homo sapiens X Kell blood group precursor-rel	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1829839	taataacatttttcaa[C/T]tcacgaagattatgcc	C	T	NM_004677 // upstream // 14764 // Hs.158346 // XKRY // 9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream // 14764 // Hs.158346 // XKRY2 // 353515 // Homo sapiens X Kell blood group precursor-rel	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-2192849	catcctctttaaagtc[A/G]agtccatctaatataa	A	G	NM_004677 // upstream // 15751 // Hs.158346 // XKRY // 9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream // 15751 // Hs.158346 // XKRY2 // 353515 // Homo sapiens X Kell blood group precursor-rel	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-2048803	aagcccagcagcttga[A/G]acataaagcgaggtgt	A	G	NM_004677 // upstream // 16100 // Hs.158346 // XKRY // 9082 // Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), mRNA. /// NM_001002906 // upstream // 16100 // Hs.158346 // XKRY2 // 353515 // Homo sapiens X Kell blood group precursor-rel	XKRY	XKRY, Homo sapiens X Kell blood group precursor-related, Y-linked (XKRY), q11.1
SNP_A-1934911	ttctgaatgataggac[G/T]ctgcacagcatgcagt	G	T	NM_177405 // upstream // 66650 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, mRNA. /// NM_017424 // upstream // 56416 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye sy	CECR1	CECR1, Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, q11.1
SNP_A-2214033	cctaaggaaagagtca[C/T]gtatacacttacacag	C	T	NM_177405 // upstream // 210533 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, mRNA. /// NM_017424 // upstream // 200299 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye	CECR1	CECR1, Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, q11.1
SNP_A-1789709	gggctcagcttgtcta[C/T]aataaacacaagataa	C	T	NM_177405 // upstream // 236767 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, mRNA. /// NM_017424 // upstream // 226533 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye	CECR1	CECR1, Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, q11.1
SNP_A-2305677	gctgccaattgaagtg[A/C]agattcaaggcaactt	A	C	NM_177405 // upstream // 249718 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, mRNA. /// NM_017424 // upstream // 239484 // Hs.170310 // CECR1 // 51816 // Homo sapiens cat eye	CECR1	CECR1, Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, q11.21
SNP_A-2258008	ctttgtgcgctgtgga[C/T]gttttccctatagtta	C	T	AF336133 // CDS // 0 // --- // CECR2 // 27443 // Homo sapiens CECR2 protein (CECR2) mRNA, complete cds. /// ENST00000262608 // CDS // 0 // — // — // — // — /// ENST00000342247 // intron // 0 // — // — // — // —	CECR2	CECR2, Homo sapiens CECR2 protein (CECR2) complete cds. ,q11.21
SNP_A-2159655	atttagaataaaggaa[C/T]ggctagacacagtggc	C	T	AF336133 // intron // 0 // — // CECR2 // 27443 // Homo sapiens CECR2 protein (CECR2) mRNA, complete cds. /// ENST00000262608 // intron // 0 // — // — // — // —	CECR2	CECR2, Homo sapiens CECR2 protein (CECR2) complete cds. ,q11.21
SNP_A-2262384	gaaatgcaagagacac[A/C]gaatagtcaaagcaat	A	C	NM_015367 // intron // 0 // Hs.546359 // BCL2L13 // 23786 // Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000359190 // intron // 0 // --- // --- // --- // --- /// ENST00000317582	BCL2L13	BCL2L13, Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13), nuclear gene encoding mitochondrial protein, q11.21
SNP_A-2051526	aagggtgcaccaacag[C/T]agagctcagatacaaa	C	T	NM_015367 // intron // 0 // Hs.546359 // BCL2L13 // 23786 // Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13), nuclear gene encoding mitochondrial protein, mRNA. /// ENST00000359190 // intron // 0 // — // — // — // — /// ENST00000317582	BCL2L13	BCL2L13, Homo sapiens BCL2-like 13 (apoptosis facilitator) (BCL2L13), nuclear gene encoding mitochondrial protein, q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1797048	ggttctggttaataaa[A/G]ttcactgttgtgtgaa	A	G	NM_197966 // CDS // 0 // Hs.474150 // BID // 637 // Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, mRNA. /// NM_001196 // CDS // 0 // Hs.474150 // BID // 637 // Homo sapiens BH3 interacting domain death agonist (BID), trans	BID	BID, Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, q11.21
SNP_A-2212329	ccctggtgggaatccc[A/G]acttctccttatgcaa	A	G	AB037785 // downstream // 5262 // Hs.165551 // MICAL3 // 57553 // Homo sapiens mRNA for KIAA1364 protein, partial cds. /// ENST00000252134 // upstream // 4544 // — // — // — // — /// ENST00000207726 // downstream // 5262 // — // — // — // –	MICAL3	MICAL3, Homo sapiens for KIAA1364 protein, partial cds. ,q11.21
SNP_A-2299508	gcccttgtgccattag[C/G]aaagcggaggctgggt	C	G	AB037785 // upstream // 37715 // Hs.165551 // MICAL3 // 57553 // Homo sapiens mRNA for KIAA1364 protein, partial cds. /// ENST00000207726 // upstream // 37715 // — // — // — // — /// ENST00000359503 // downstream // 16062 // — // — // — // -	MICAL3	MICAL3, Homo sapiens for KIAA1364 protein, partial cds. q11.21
SNP_A-2056951	aatagtcacagatgta[A/G]gagttggaccaaatta	A	G	NM_017929 // upstream // 96606 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 20288 // — // — // — // — /// ENST00000339190 // upstream // 96603 // — // — // —	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-1887337	tgagaatactcaagaa[A/G]tggttatcttgggtag	A	G	NM_017929 // upstream // 40107 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 76787 // — // — // — // — /// ENST00000339190 // upstream // 40104 // — // — // — // —	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2126573	ataaaatgtacaaaag[C/T]atatccagtgaaaaat	C	T	NM_017929 // upstream // 40035 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 76859 // — // — // — // — /// ENST00000339190 // upstream // 40032 // — // — // — // —	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2058280	aatcaagttccatcaa[C/G]aatttttagctggaaa	C	G	NM_017929 // upstream // 19192 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000359503 // upstream // 97702 // — // — // — // — /// ENST00000339190 // upstream // 19189 // — // — // — // —	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2139956	atctaccgcgaccagc[C/T]gaagtagggtgcaaag	C	T	NM_017929 // 3UTR // 0 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// ENST00000339190 // intron // 0 // — // — // — // — /// ENST00000329627 // 3UTR // 0 // — // – - // — // —	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-1935007	ttctgaggaccataca[A/G]atcggttttccaccta	A	G	NM_017929 // downstream // 3102 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// NM_018943 // upstream // 16221 // Hs.137400 // TUBA8 // 51807 // Homo sapiens tubulin, alpha 8 (TUBA8), mRNA. /// ENST0000033	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2287527	gatgtttgcatatagg[C/T]acatttagctggatta	C	T	NM_017929 // downstream // 7429 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// NM_018943 // upstream // 11894 // Hs.137400 // TUBA8 // 51807 // Homo sapiens tubulin, alpha 8 (TUBA8), mRNA. /// ENST0000033	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-2119761	agtatttagtcagcaa[C/T]gtaccattatagaaaa	C	T	NM_017929 // downstream // 9031 // Hs.517400 // PEX26 // 55670 // Homo sapiens peroxisome biogenesis factor 26 (PEX26), mRNA. /// NM_018943 // upstream // 10292 // Hs.137400 // TUBA8 // 51807 // Homo sapiens tubulin, alpha 8 (TUBA8), mRNA. /// ENST0000033	PEX26	PEX26, Homo sapiens peroxisome biogenesis factor 26 (PEX26), q11.21
SNP_A-1678136	gtgtctggtacatgtgtatgtgtaa[C/T]agggaaacgcattctagattcaaag	C	T	NM_018943 // intron // 0 // Hs.137400 // TUBA8 // 51807 // tubulin, alpha 8	TUBA8	TUBA8 , rs8140197, tubulin, alpha 8,q11.21
SNP_A-2269001	gaattcggcctctcaa[G/T]cagtcttgtagtagtg	G	T	NM_001835 // intron // 0 // Hs.368266 // CLTCL1 // 8218 // Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 1, mRNA. /// NM_007098 // intron // 0 // Hs.368266 // CLTCL1 // 8218 // Homo sapiens clathrin, heavy polypeptide-like 1	CLTCL1	CLTCL1, Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 1, q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2277809	gagcatcaaagagccc[A/G]gacaagtgagaatcaa	A	G	NM_003325 // intron // 0 // Hs.474206 // HIRA // 7290 // Homo sapiens HIR histone cell cycle regulation defective homolog A (S. cerevisiae) (HIRA), mRNA. /// ENST00000340170 // intron // 0 // — // — // — // — /// ENST00000263208 // intron // 0 //	HIRA	HIRA, Homo sapiens HIR histone cell cycle regulation defective homolog A (S. cerevisiae) (HIRA), q11.21
SNP_A-1861752	tcatctgtcttgtccc[A/G]caaaggccaagacaaa	A	G	NM_002688 // downstream // 7302 // Hs.283743 // SEPT5 // 5413 // Homo sapiens peanut-like 1 (Drosophila) (PNUTL1), mRNA. /// NM_080647 // upstream // 26082 // Hs.173984 // TBX1 // 6899 // Homo sapiens T-box 1 (TBX1), transcript variant C, mRNA. /// NM_080	SEPT5	SEPT5, Homo sapiens peanut-like 1 (Drosophila) (PNUTL1), q11.21
SNP_A-2179301	cactgtcgcttctcca[C/T]ggcattagattttcag	C	T	NM_000754 // intron // 0 // Hs.370408 // COMT // 1312 // Homo sapiens catechol-O-methyltransferase (COMT), transcript variant MB-COMT, mRNA. /// NM_007310 // intron // 0 // Hs.370408 // COMT // 1312 // Homo sapiens catechol-O-methyltransferase (COMT), tra	COMT	COMT, Homo sapiens catechol-O-methyltransferase (COMT), transcript variant MB-COMT, q11.21
SNP_A-1825843	taaatgaacatccatc[C/T]cgaggcgggcagagga	C	T	NM_023004 // downstream // 6299 // Hs.30868 // RTN4R // 65078 // Homo sapiens reticulon 4 receptor (RTN4R), mRNA. /// ENST00000328165 // downstream // 26594 // — // — // — // — /// ENST00000043402 // downstream // 6299 // — // — // — // —	RTN4R	RTN4R, Homo sapiens reticulon 4 receptor (RTN4R), q11.21
SNP_A-2112621	aggcagaaccagcaga[C/T]aggaaggtgacacagt	C	T	NM_015889 // downstream // 24920 // Hs.517421 // PCQAP // 51586 // Homo sapiens PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-associated protein (PCQAP), transcript variant 2, /// NM_001003891 // downstream // 24920 // Hs.517421 // PCQA	PCQAP	PCQAP, Homo sapiens PC2 (positive cofactor 2, multiprotein complex) glutamine,q11.21
SNP_A-2209620	cccatgctgggacaag[A/G]aatgaagttttgatat	A	G	NM_005207 // intron // 0 // Hs.5613 // CRKL // 1399 // Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian)-like (CRKL), mRNA. /// ENST00000215732 // intron // 0 // — // — // — // — /// ENST00000354336 // intron // 0 // — // — // —	CRKL	CRKL, Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian)-like (CRKL), q11.21
SNP_A-1942296	ttggcattatctgtta[C/T]ctatcgacaattaata	C	T	NM_145042 // downstream // 4921 // Hs.511771 // MGC16703 // 113691 // Homo sapiens alpha tubulin-like (MGC16703), mRNA. /// ENST00000358836 // downstream // 480 // — // — // — // — /// ENST00000292748 // downstream // 4921 // — // — // — // —	MGC16703	MGC16703, Homo sapiens alpha tubulin-like (MGC16703), q11.21
SNP_A-2088195	actggtaatattgccc[A/C]atgaactttaaagggt	A	C	NM_145042 // 3UTR // 0 // Hs.511771 // MGC16703 // 113691 // Homo sapiens alpha tubulin-like (MGC16703), mRNA. /// ENST00000292748 // 3UTR // 0 // — // — // — // —	MGC16703	MGC16703, Homo sapiens alpha tubulin-like (MGC16703), q11.21
SNP_A-2086651	actgaaggagacaaca[C/T]gtagcctttgctgggg	C	T	NM_207474 // upstream // 32007 // Hs.505361 // FLJ42953 // 400892 // Homo sapiens FLJ42953 protein (FLJ42953), mRNA. /// ENST00000330423 // downstream // 975 // — // — // — // — /// ENST00000344557 // upstream // 32007 // — // — // — // —	FLJ42953	FLJ42953, Homo sapiens FLJ42953 protein (FLJ42953), q11.21
SNP_A-1970714	tattttaacaaattcc[A/G]tgattgtcagttacct	A	G	NM_207474 // upstream // 8277 // Hs.505361 // FLJ42953 // 400892 // Homo sapiens FLJ42953 protein (FLJ42953), mRNA. /// ENST00000330423 // downstream // 24705 // — // — // — // — /// ENST00000344557 // upstream // 8277 // — // — // — // —	FLJ42953	FLJ42953, Homo sapiens FLJ42953 protein (FLJ42953), q11.21
SNP_A-2082153	acgacaataaccaagc[A/G]aaggggaaatatacag	A	G	NM_014337 // downstream // 43223 // Hs.438587 // PPIL2 // 23759 // Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 1, mRNA. /// NM_148175 // downstream // 43223 // Hs.438587 // PPIL2 // 23759 // Homo sapiens peptidyl	PPIL2	PPIL2, Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 1, q11.21
SNP_A-1804797	gtcagtcctcagctca[C/T]gtctacttggttcttt	C	T	NM_002745 // intron // 0 // Hs.431850 // MAPK1 // 5594 // Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, mRNA. /// NM_138957 // intron // 0 // Hs.431850 // MAPK1 // 5594 // Homo sapiens mitogen-activated protein kinase 1 (M	MAPK1	MAPK1, Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, q11.21

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2046461	aagagagatcccttca[A/C]ctggaaagctgacag	A	C	NM_002745 // intron // 0 // Hs.431850 // MAPK1 // 5594 // Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, mRNA. /// NM_138957 // intron // 0 // Hs.431850 // MAPK1 // 5594 // Homo sapiens mitogen-activated protein kinase 1 (M	MAPK1	MAPK1, Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, q11.22
SNP_A-1895005	tgcccaccgtctaggt[C/T]catgcatcggcttgta	C	T	NM_002745 // upstream // 45078 // Hs.431850 // MAPK1 // 5594 // Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, mRNA. /// NM_138957 // upstream // 45078 // Hs.431850 // MAPK1 // 5594 // Homo sapiens mitogen-activated protein	MAPK1	MAPK1, Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, q11.22
SNP_A-1788873	gggcaaaataacattg[G/T]aaggtagattgtcacc	G	T	ENST00000337471 // intron // 0 // — // — // —	-	q11.22
SNP_A-1867490	tccgaggacctaatcc[A/G]caagtgtagtttcagt	A	G	ENST00000337471 // intron // 0 // — // — // —	-	q11.22
SNP_A-1813257	gtggtctgtccctaaa[G/T]cttgtgctggagaccc	G	T	ENST00000337471 // intron // 0 // — // — // — /// ENST00000358271 // intron // 0 // — // — // — /// ENST00000358972 // intron // 0 // — // — // —	-	q11.22
SNP_A-2028330	aaactcactactactaa[A/G]tgaaaaacacaaaaa	A	G	ENST00000358271 // intron // 0 // — // — // — /// ENST00000358972 // intron // 0 // — // — // — /// ENST00000357553 // intron // 0 // — // — // — /// ENST00000355008 // intron // 0 // — // — // — /// ENS	-	q11.22
SNP_A-1888146	tgagccctgtgtccta[C/T]aaagaccctgagagcc	C	T	NM_080924 // downstream // 17194 // — // 0 // — /// ENST00000337471 // upstream // 56348 // — // — // — /// ENST00000311527 // upstream // 104873 // — // — // — /// ENST00000360792 // downstream // 68833 // — // —	-	q11.22
SNP_A-1970745	gtgtgtgagacactca[A/G]taacggcaagaggatg	A	G	ENST00000331195 // downstream // 13764 // — // — // — /// ENST00000334392 // upstream // 4191 // — // — // —	-	q11.22
SNP_A-1970747	cacccgctcctcaaaa[A/G]gaataaccagactcag	A	G	L38562 // upstream // 12902 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// L38562 // upstream // 12934 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mR	-	-, Human clone rev16,q11.22
SNP_A-2235655	ctcctattaagaccaa[A/T]ggaccaataactagaa	A	T	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — /// ENST00000355323 // intron // 0 // — // — // — /	-	-, Human clone rev16,q11.22
SNP_A-2181892	cagagcccgacaaagg[A/C]atgacaaaaatatcct	A	C	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — /// ENST00000355323 // intron // 0 // — // — // — /	-	-, Human clone rev16 q11.22
SNP_A-2058184	aatcaaattgctaaag[A/C]acagtgatgaagagac	A	C	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — /// ENST00000355323 // intron // 0 // — // — // — /	-	-, Human clone rev16 q11.22
SNP_A-1820985	gtttctctgtctccaa[C/T]gtcacttccggcaggt	C	T	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — /// ENST00000355323 // intron // 0 // — // — // — /	-	-, Human clone rev16 q11.22
SNP_A-2192407	catcatgatgggtgcg[C/T]attctgtaatccaga	C	T	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — /// ENST00000355323 // intron // 0 // — // — // — /	-	-, Human clone rev16,q11.22
SNP_A-1835315	tacctatggacttata[G/T]caccatttacaatgca	G	T	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — /// ENST00000355323 // intron // 0 // — // — // — /	-	-, Human clone rev16,q11.22

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2008204	gtatctgcttcagtga[G/T]gtaactgtgcacctgc	G	T	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — // — /// ENST00000355323 // intron // 0 // — // — // — // — /	-	-, Human clone rev16 q11.22
SNP_A-1909887	tgtcacttggaactcc[A/G]ggaaaccagtctctgg	A	G	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — // — /// ENST00000355323 // intron // 0 // — // — // — // — /	-	-, Human clone rev16,q11.22
SNP_A-2177091	cacctcgaatgcaaaa[A/G]ttaaaggagcatccaa	A	G	L38562 // intron // 0 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// ENST00000356222 // intron // 0 // — // — // — // — /// ENST00000355323 // intron // 0 // — // — // — // — /	-	-, Human clone rev16,q11.22
SNP_A-2181434	cagactgacttccaga[A/G]aagagagcctgaactg	A	G	L38562 // downstream // 34402 // Hs.449585 // — // 0 // Human clone rev16/20Fab, immunoglobulin lambda light chain mRNA, partial cds. /// NM_080764 // upstream // 439577 // Hs.43834 // SUHW2 // 140883 // Homo sapiens suppressor of hairy wing homolog 2 (	-	-, Human clone rev16 q11.22
SNP_A-1834652	taccacatgcctggga[A/G]gattctaaatgcttac	A	G	NM_152509 // upstream // 16918 // Hs.386693 // FLJ31568 // 150244 // Homo sapiens hypothetical protein FLJ31568 (FLJ31568), mRNA. /// ENST00000255890 // upstream // 16918 // — // — // — // — /// ENST00000320372 // downstream // 42614 // — // —	FLJ31568	FLJ31568, Homo sapiens hypothetical protein FLJ31568 (FLJ31568), q11.23
SNP_A-2106853	agccttagaaggatga[A/C]ctggagaactggaggc	A	C	NM_152855 // downstream // 80273 // Hs.348935 // IGLL1 // 3543 // Homo sapiens immunoglobulin lambda-like polypeptide 1 (IGLL1), transcript variant 2, mRNA. /// NM_020070 // downstream // 80273 // Hs.348935 // IGLL1 // 3543 // Homo sapiens immunoglobulin	IGLL1	IGLL1, Homo sapiens immunoglobulin lambda-like polypeptide 1 (IGLL1), transcript variant 2, q11.23
SNP_A-2096609	agacgatgacgtgcac[C/T]gaggagaagttgttga	C	T	NM_153615 // CDS // 0 // Hs.148656 // Rgr // 266747 // Homo sapiens Ral-GDS related protein Rgr (Rgr), mRNA. /// ENST00000290691 // CDS // 0 // — // — // — // —	Rgr	Rgr, Homo sapiens Ral-GDS related protein Rgr (Rgr), q11.23
SNP_A-2052785	aagtcacagtggtcca[A/G]gccaaaggggatgcag	A	G	NM_030807 // downstream // 7808 // Hs.531906 // SLC2A11 // 66035 // Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 11 (SLC2A11), mRNA. /// AJ271290 // downstream // 7475 // Hs.531906 // SLC2A11 // 66035 // Homo sapiens mRNA	SLC2A11	SLC2A11, Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 11 (SLC2A11), q11.23
SNP_A-2207237	ccattcagtagaaggg[C/T]aaagaggcccacatgt	C	T	NM_002415 // downstream // 56247 // Hs.407995 // MIF // 4282 // Homo sapiens macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA. /// NM_000854 // downstream // 5953 // Hs.1581 // GSTT2 // 2953 // Homo sapiens glutathione	MIF	MIF, Homo sapiens macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), q11.23
SNP_A-1811592	gtgctgaggacagtag[A/G]aaagaacgtaggaagt	A	G	NM_031444 // intron // 0 // Hs.9850 // C22orf13 // 83606 // Homo sapiens chromosome 22 open reading frame 13 (C22orf13), mRNA. /// ENST00000354561 // intron // 0 // — // — // — // — /// ENST00000266155 // intron // 0 // — // — // — // —	C22orf13	C22orf13, Homo sapiens chromosome 22 open reading frame 13 (C22orf13), q11.23
SNP_A-1956054	tttgtgaactcactcc[A/G]gctaacagttgacatg	A	G	ENST00000336168 // intron // 0 // — // — // — // —	-	q11.23
SNP_A-1878842	tctgtttcaggtacta[C/T]gctagtctcttcccac	C	T	ENST00000336168 // downstream // 24214 // — // — // — // — /// ENST00000358431 // upstream // 120643 // — // — // — // —	-	q11.23
SNP_A-2243418	ctgcggtttcaaaaga[C/T]agcaagtagggtttct	C	T	ENST00000336168 // downstream // 28764 // — // — // — // — /// ENST00000358431 // upstream // 116093 // — // — // — // —	-	q11.23
SNP_A-2294150	gcaggcgggtccccca[A/G]aggataagattatgta	A	G	ENST00000336168 // downstream // 43384 // — // — // — // — /// ENST00000358431 // upstream // 101473 // — // — // — // —	-	q11.23
SNP_A-1806029	gtcctaggcccagaaa[C/T]tccttcatcaagccag	C	T	NM_005160 // intron // 0 // Hs.517493 // ADRBK2 // 157 // Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA. /// ENST00000324198 // intron // 0 // — // — // — // —	ADRBK2	ADRBK2, Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2290732	gcaagatttgtcacc[A/C]agctgagcatttactg	A	C	NM_005160 // downstream // 15973 // Hs.517493 // ADRBK2 // 157 // Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA. /// NM_032608 // upstream // 2231 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST0000	ADRBK2	ADRBK2, Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), q12.1
SNP_A-2176133	caccacaggtaccaac[A/C]aggtgaatggagcaaa	A	C	NM_005160 // downstream // 16077 // Hs.517493 // ADRBK2 // 157 // Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA. /// NM_032608 // upstream // 2127 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST0000	ADRBK2	ADRBK2, Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), q12.1
SNP_A-1799542	gtaatgttcggaactc[A/G]aaatagtgacaaggat	A	G	NM_032608 // intron // 0 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST00000335473 // intron // 0 // — // — // — // —	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1793550	ggtatacctgctatgg[A/G]aaagagccagaggata	A	G	NM_032608 // intron // 0 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// ENST00000335473 // intron // 0 // — // — // — // —	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1881981	tcttttctgggcttca[G/T]catctgtatctgtcaa	G	T	NM_032608 // downstream // 47298 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 91331 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2041022	aaccgcaatcacaata[C/T]cttaagcccatatcaa	C	T	NM_032608 // downstream // 55835 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 82794 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1970813	aagaaaaagtcacaat[C/G]atggtgataatgaaga	C	G	NM_032608 // downstream // 73377 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 65252 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-1693587	atattgaataatgccatcactatta[C/T]agaatcaccaccatcatc ttcatta	C	T	NM_021115 // upstream // 65219 // Hs.194766 // SEZ6L // 23544 // seizure related 6 homolog (mouse)-like /// NM_032608 // downstream // 73410 // Hs.417959 // MYO18B // 84700 // myosin XVIIIB /// NM_175915 // upstream // 104757 // - // - // - // -	SEZ6L	SEZ6L, rs134703, seizure related 6 homolog (mouse)-like, q12.1
SNP_A-1970815	cagaaacaagactgga[A/G]tacaaaaatagagact	A	G	NM_032608 // downstream // 76995 // Hs.417959 // MYO18B // 84700 // Homo sapiens myosin XVIIIB (MYO18B), mRNA. /// NM_021115 // upstream // 61634 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST	MYO18B	MYO18B, Homo sapiens myosin XVIIIB (MYO18B), q12.1
SNP_A-2117392	aggtggttggccccaa[A/G]ttagcttccactctg	A	G	NM_021115 // intron // 0 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST00000346658 // intron // 0 // — // — // — // — /// ENST00000360929 // intron // 0 // — // — // — // — ///	SEZ6L	SEZ6L, Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), q12.1
SNP_A-1795900	ggtgggcaaggaacca[G/T]accatgctgggaacag	G	T	NM_021115 // intron // 0 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST00000346658 // intron // 0 // — // — // — // — /// ENST00000360929 // intron // 0 // — // — // — // — ///	SEZ6L	SEZ6L, Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), q12.1
SNP_A-1790584	gggcctgggcagtgaa[A/G]gaggaggccaggcaggt	A	G	NM_021115 // intron // 0 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST00000346658 // intron // 0 // — // — // — // — /// ENST00000360929 // intron // 0 // — // — // — // — ///	SEZ6L	SEZ6L, Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), q12.1
SNP_A-2055700	aataatttaaacatccc[A/G]aatgtcagttgtgcgg	A	G	NM_021115 // intron // 0 // Hs.194766 // SEZ6L // 23544 // Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA. /// ENST00000346658 // intron // 0 // — // — // — // — /// ENST00000360929 // intron // 0 // — // — // — // — ///	SEZ6L	SEZ6L, Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2175420	cacatcagctaacaca[A/G]gctatttctagagtga	A	G	NM_020437 // downstream // 906 // Hs.184390 // LOC57168 // 57168 // Homo sapiens similar to aspartate beta hydroxylase (ASPH) (LOC57168), mRNA. /// NM_152842 // downstream // 6969 // Hs.474436 // HPS4 // 89781 // Homo sapiens Hermansky-Pudlak syndrome 4 (	LOC57168	LOC57168, Homo sapiens similar to aspartate beta hydroxylase (ASPH) (LOC57168), q12.1
SNP_A-1813708	gtgtactttgaaacca[A/G]tcagtgtaattaacca	A	G	NM_012143 // intron // 0 // Hs.20225 // TFIP11 // 24144 // Homo sapiens tuftelin interacting protein 11 (TFIP11), mRNA. /// ENST00000263115 // intron // 0 // --- // --- // --- // ---	TFIP11	TFIP11, Homo sapiens tuftelin interacting protein 11 (TFIP11), q12.1
SNP_A-2111479	aggaggctagtccaaa[A/G]tgagaggtcctgttag	A	G	NM_003595 // intron // 0 // Hs.474441 // TPST2 // 8459 // Homo sapiens tyrosylprotein sulfotransferase 2 (TPST2), mRNA. /// ENST00000338754 // intron // 0 // --- // --- // --- // ---	TPST2	TPST2, Homo sapiens tyrosylprotein sulfotransferase 2 (TPST2), q12.1
SNP_A-1790527	ggggccaataatatga[C/T]ctagcacagggatatt	C	T	NM_001886 // downstream // 95848 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 1021786 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2049819	aaggaaaccaattcgc[C/T]cctagacccttcagaa	C	T	NM_001886 // downstream // 103115 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 1014519 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1)	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1824143	taaacagcaaaaacta[A/G]ctgaatcaccagagga	A	G	NM_001886 // downstream // 187336 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 930298 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1698001	attataatagctcattgctccttac[A/G]tgtcagaagcacctctgg gctgtgg	A	G	NM_001886 // downstream // 193249 // Hs.57690 // CRYBA4 // 1413 // crystallin, beta A4 /// NM_002430 // downstream // 924385 // Hs.268515 // MN1 // 4330 // meningioma (disrupted in balanced translocation) 1	CRYBA4	CRYBA4 , rs720914, crystallin, beta A4 ,q12.1
SNP_A-2060873	aatgatattgccacat[A/G]agccctactgaaacaa	A	G	NM_001886 // downstream // 213957 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 903677 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2200668	ccaagaaccgaggaca[A/G]ataagtacaagggaac	A	G	NM_001886 // downstream // 267911 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 849723 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2200948	ccaagctcttccctcc[A/G]ctgctattgaccatgt	A	G	NM_001886 // downstream // 328563 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 789071 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2310317	ggaacgaggaccagaa[C/T]acctgaatgggtagtt	C	T	NM_001886 // downstream // 477205 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 640429 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2276684	gagagtggacagaata[C/T]gggcgagatgcttacg	C	T	NM_001886 // downstream // 482226 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 635408 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1),	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2008232	aactggctcctgaatt[C/G]aatctcgtattgtg	C	G	NM_001886 // downstream // 543347 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 574287 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1).	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2056288	aatactgaatcaggat[C/T]ggtggttacctctgtgg	C	T	NM_001886 // downstream // 548172 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 569462 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1).	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2173923	cacacagtcactgaac[A/G]ctataggttggtggtc	A	G	NM_001886 // downstream // 725452 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 392182 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1).	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1790604	gggcggctgtgtgaa[A/T]ggccgtcctgtttgag	A	T	NM_001886 // downstream // 868715 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 248919 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1).	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-1884857	tgaatctgacatagtc[A/C]cacctgcagagaactc	A	C	NM_001886 // downstream // 879194 // Hs.57690 // CRYBA4 // 1413 // Homo sapiens crystallin, beta A4 (CRYBA4), mRNA. /// NM_002430 // downstream // 238440 // Hs.268515 // MN1 // 4330 // Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1).	CRYBA4	CRYBA4, Homo sapiens crystallin, beta A4 (CRYBA4), q12.1
SNP_A-2305045	gctgaactgggaagta[G/T]gtctaatgaagtctaa	G	T	ENST00000332811 // intron // 0 // — // — // —	-	q12.1
SNP_A-2069340	acacaaacctggatgc[A/G]atagcgtactacacac	A	G	ENST00000332811 // intron // 0 // — // — // —	-	q12.1
SNP_A-1970906	aagaatatccacgctct[C/G]aagaggttacctgcct	C	G	ENST00000332811 // intron // 0 // — // — // —	-	q12.1
SNP_A-2223258	cgcgaggcagaagtta[C/T]aatgtccgccaagcgg	C	T	NM_032045 // intron // 0 // Hs.229335 // KREMEN1 // 83999 // Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, mRNA. /// NM_153379 // intron // 0 // Hs.229335 // KREMEN1 // 83999 // Homo sapiens kringle containing tr	KREMEN1	KREMEN1, Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, q12.1
SNP_A-1970910	ttcctgtgcgtcatta[C/G]gctgtggttctcatag	C	G	NM_032045 // intron // 0 // Hs.229335 // KREMEN1 // 83999 // Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, mRNA. /// NM_153379 // intron // 0 // Hs.229335 // KREMEN1 // 83999 // Homo sapiens kringle containing tr	KREMEN1	KREMEN1, Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, q12.1
SNP_A-2285455	gatcttcttggcttgc[C/T]acttatgtatggaac	C	T	NM_032045 // downstream // 8445 // Hs.229335 // KREMEN1 // 83999 // Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, mRNA. /// NM_153379 // downstream // 8445 // Hs.229335 // KREMEN1 // 83999 // Homo sapiens kringle	KREMEN1	KREMEN1, Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 2, q12.1
SNP_A-2251425	cttcacaggcgagta[C/G]caacacgctctgcagc	C	G	NM_181834 // downstream // 19377 // Hs.187898 // NF2 // 4771 // Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2), transcript variant 10, mRNA. /// NM_181826 // downstream // 19377 // Hs.187898 // NF2 // 4771 // Homo sapiens neurofibromin 2	NF2	NF2, Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2), transcript variant 10, q12.2
SNP_A-2170738	caagttgcttcaacta[C/T]cgaagccttagcttcc	C	T	NM_001003692 // intron // 0 // Hs.38628 // LOC55954 // 55954 // Homo sapiens U11/U12 snRNP 20K (LOC55954), transcript variant 2, mRNA. /// NM_019103 // intron // 0 // Hs.38628 // LOC55954 // 55954 // Homo sapiens U11/U12 snRNP 20K (LOC55954), transcript v	LOC55954	LOC55954, Homo sapiens U11,q12.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1910339	tgtccaggctagcaga[A/T]tccgtcacctacgag	A	T	NM_153051 // intron // 0 // Hs.474536 // MTMR3 // 8897 // Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, mRNA. /// NM_153050 // intron // 0 // Hs.474536 // MTMR3 // 8897 // Homo sapiens myotubularin related protein 3 (MTMR3), t	MTMR3	MTMR3, Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, q12.2
SNP_A-2182177	cagaggtagaaacgaa[C/G]ctaacataaattcagt	C	G	NM_153051 // intron // 0 // Hs.474536 // MTMR3 // 8897 // Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, mRNA. /// NM_153050 // intron // 0 // Hs.474536 // MTMR3 // 8897 // Homo sapiens myotubularin related protein 3 (MTMR3), t	MTMR3	MTMR3, Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 2, q12.2
SNP_A-2311756	ggaattgaggagtaaa[A/T]agaagacatagatgga	A	T	NM_152510 // intron // 0 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC26710), mRNA. /// ENST00000336726 // intron // 0 // — // — // — /// ENST00000354248 // intron // 0 // — // — // —	HORMAD2	HORMAD2, Homo sapiens hypothetical protein MGC26710 (MGC26710), q12.2
SNP_A-2043590	aactgtgtgaccttca[G/T]caagtgatttaacttc	G	T	NM_152510 // downstream // 6574 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC26710), mRNA. /// NM_152510 // downstream // 7089 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC26710	HORMAD2	HORMAD2, Homo sapiens hypothetical protein MGC26710 (MGC26710), q12.2
SNP_A-2074896	acatcactgtgaatta[A/G]catcttagtccaggaa	A	G	NM_152510 // downstream // 7118 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC26710), mRNA. /// NM_152510 // downstream // 7633 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC26710	HORMAD2	HORMAD2, Homo sapiens hypothetical protein MGC26710 (MGC26710), q12.2
SNP_A-1866706	tccccgatgcaatga[A/G]agggtgagcaatttca	A	G	NM_152510 // downstream // 19799 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC26710), mRNA. /// NM_152510 // downstream // 20314 // Hs.120391 // HORMAD2 // 150280 // Homo sapiens hypothetical protein MGC26710 (MGC267	HORMAD2	HORMAD2, Homo sapiens hypothetical protein MGC26710 (MGC26710), q12.2
SNP_A-1829575	taagtgtggcataagg[C/T]aatggaaaacgctata	C	T	NM_004861 // intron // 0 // Hs.17958 // GAL3ST1 // 9514 // Homo sapiens galactose-3-O-sulfotransferase 1 (GAL3ST1), mRNA. /// NM_014303 // intron // 0 // Hs.517543 // PES1 // 23481 // Homo sapiens pescadillo homolog 1, containing BRCT domain (zebrafish) (	GAL3ST1	GAL3ST1, Homo sapiens galactose-3-O-sulfotransferase 1 (GAL3ST1), q12.2
SNP_A-2055186	aataactgacatagca[A/G]tagaatgggcctgaga	A	G	NM_004861 // intron // 0 // Hs.17958 // GAL3ST1 // 9514 // Homo sapiens galactose-3-O-sulfotransferase 1 (GAL3ST1), mRNA. /// NM_030758 // intron // 0 // Hs.517546 // OSBP2 // 23762 // Homo sapiens oxysterol binding protein 2 (OSBP2), transcript variant 1	GAL3ST1	GAL3ST1, Homo sapiens galactose-3-O-sulfotransferase 1 (GAL3ST1), q12.2
SNP_A-2211519	ccctcaaccagtgaag[A/G]atgagaagttggtggc	A	G	NM_017903 // downstream // 73121 // Hs.158783 // FLJ20618 // 55000 // Homo sapiens hypothetical protein FLJ20618 (FLJ20618), mRNA. /// NM_134269 // upstream // 32134 // Hs.149098 // SMTN // 6525 // Homo sapiens smoothelin (SMTN), transcript variant 2, mRN	FLJ20618	FLJ20618, Homo sapiens hypothetical protein FLJ20618 (FLJ20618), q12.2
SNP_A-2195485	catgggggctgtcagaa[C/T]attaatatgggggccc	C	T	AB014545 // intron // 0 // Hs.435022 // DEPDC5 // 9681 // Homo sapiens mRNA for KIAA0645 protein, partial cds. /// ENST00000266091 // intron // 0 // — // — // —	DEPDC5	DEPDC5, Homo sapiens for KIAA0645 protein, partial cds, q12.3
SNP_A-2101672	agatgattctcactgat[A/G]gccgcgtgatgatggg	A	G	AB014545 // intron // 0 // Hs.435022 // DEPDC5 // 9681 // Homo sapiens mRNA for KIAA0645 protein, partial cds. /// ENST00000266091 // intron // 0 // — // — // —	DEPDC5	DEPDC5, Homo sapiens for KIAA0645 protein, partial cds, q12.3
SNP_A-1910417	tgtcccaaccaacaga[C/T]ggtatttagcacctct	C	T	AB014545 // intron // 0 // Hs.435022 // DEPDC5 // 9681 // Homo sapiens mRNA for KIAA0645 protein, partial cds. /// ENST00000266091 // intron // 0 // — // — // —	DEPDC5	DEPDC5, Homo sapiens for KIAA0645 protein, partial cds, q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1855875	tcaatgcctcacctca[G/T]cccttctcatctgag	G	T	NM_014227 // intron // 0 // Hs.130101 // SLC5A4 // 6527 // Homo sapiens solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4), mRNA. /// ENST00000266086 // intron // 0 // — // — // —	SLC5A4	SLC5A4, Homo sapiens solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4), q12.3
SNP_A-1812684	gtggcttgttcttttc[C/T]ctgctatctctagaaa	C	T	NM_014227 // upstream // 5233 // Hs.130101 // SLC5A4 // 6527 // Homo sapiens solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4), mRNA. /// ENST00000266086 // upstream // 5233 // — // — // — /// ENST00000328768 //	SLC5A4	SLC5A4, Homo sapiens solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4), q12.3
SNP_A-1970957	ttctctgatctggtcc[A/G]ctcattaaggctatag	A	G	NM_012179 // intron // 0 // Hs.5912 // FBXO7 // 25793 // Homo sapiens F-box protein 7 (FBXO7), mRNA. /// ENST00000266087 // intron // 0 // — // — // —	FBXO7	FBXO7, Homo sapiens F-box protein 7 (FBXO7), q12.3
SNP_A-1970958	aaggtgggaaaaatga[G/T]gaggcatgtacaaggc	G	T	NM_012179 // intron // 0 // Hs.5912 // FBXO7 // 25793 // Homo sapiens F-box protein 7 (FBXO7), mRNA. /// ENST00000266087 // intron // 0 // — // — // —	FBXO7	FBXO7, Homo sapiens F-box protein 7 (FBXO7), q12.3
SNP_A-2083248	actaaaccttgttcca[A/C]atctgatcagtcttca	A	C	NM_012179 // intron // 0 // Hs.5912 // FBXO7 // 25793 // Homo sapiens F-box protein 7 (FBXO7), mRNA. /// ENST00000266087 // intron // 0 // — // — // —	FBXO7	FBXO7, Homo sapiens F-box protein 7 (FBXO7), q12.3
SNP_A-2201889	ccacactgctactcaa[A/C]atgtgggcgacagatc	A	C	NM_012179 // intron // 0 // Hs.5912 // FBXO7 // 25793 // Homo sapiens F-box protein 7 (FBXO7), mRNA. /// ENST00000266087 // intron // 0 // — // — // —	FBXO7	FBXO7, Homo sapiens F-box protein 7 (FBXO7), q12.3
SNP_A-2287228	gatgtcttgaagaat[C/G]agtgtgaaaatgagat	C	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-1831151	taatgcccagtaaaaa[A/G]caggaaagatgtctg	A	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2213767	ccgttttctgcccaac[A/C]ggagaataaggaagc	A	C	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2173092	cacaaagttgttagag[A/G]aatcagaagaaatttt	A	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-1781312	ggatgtgaatctagac[C/T]atcctgaccccgtcat	C	T	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2147939	atggctcacagacat[C/G]accaggaaaacagaga	C	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2150993	atgtggttcaaggaga[A/C]ccttctggtaaaaga	A	C	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2058015	aatatttattgaatgga[C/G]ggaaatagtctttcta	C	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2080567	acctcaaacacactacc[A/C]agggctagcagtttat	A	C	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2297684	gccagctagtggcctat[C/G]aatccctctaaccag	C	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2145844	atgccatcttgaacca[A/G]aatttcatttctctg	A	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-1642405	caaggtcaaagggatataagcaca[C/T]gctcttcttataaac acaggtca	C	T	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // synapsin III /// NM_133632 // intron // 0 // Hs.125878 // SYN3 // 8224 // synapsin III /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // synapsin III	SYN3	SYN3 , rs737088, synapsin III, q12.3
SNP_A-1941765	ttggaattgtatctccd[C/T]atggccctggattctt	C	T	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2226384	ctaagagacacttggat[A/G]atgtttgtcggtttca	A	G	NM_003490 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // intron // 0 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, mRNA. /// NM_	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-1942099	ttggatgtgcacctta[C/T]ggctgtttatagcaat	C	T	NM_003490 // upstream // 90785 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA. /// NM_133633 // upstream // 90785 // Hs.125878 // SYN3 // 8224 // Homo sapiens synapsin III (SYN3), transcript variant IIIc, m	SYN3	SYN3, Homo sapiens synapsin III (SYN3), transcript variant IIIa, q12.3
SNP_A-2049933	aaggaacttgtcctac[C/T]aggcattctgtaatca	C	T	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1808510	gtgaaagtctttacat[C/G]ggcagtgaacagtaaa	C	G	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2151028	atgtgtagtaataaga[A/C]aaaatatgggctttga	A	C	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1957104	ttttacagaatatggg[A/G]cactagttagactggt	A	G	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1811288	gtgccttcaaccc ggc[A/G]gatcaaagatgaatgt	A	G	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1961178	ttttttaattctctcc[A/G]caattagagccaggcc	A	G	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2097777	agagaccggggcttaa[A/G]tccaggtatgttttct	A	G	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2041593	aacgagttagctgtta[C/T]ctcctctcagatgtca	C	T	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2138955	atccgatgttgtcacc[A/G]ctagacatgggtagtt	A	G	NM_004737 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // intron // 0 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript va	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2281153	gagtactagagtttgc[A/T]cccttgttaggaactc	A	T	NM_004737 // upstream // 18276 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 18276 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), t	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2109422	agcttttcagaagtca[C/T]tacaggagctagctta	C	T	NM_004737 // upstream // 367039 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 367039 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE),	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2183926	cagccactggtgtgca[G/T]caaaaaggaaagttta	G	T	NM_004737 // upstream // 410714 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 410714 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE),	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2023015	aaaacacggaaataac[A/G]attctaggtaaatttt	A	G	NM_004737 // upstream // 429301 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 429301 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE),	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1829422	taagtgaaacaacaga[C/T]ggaaaggtagctgaca	C	T	NM_004737 // upstream // 429350 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 429350 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE),	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2218227	cctgctcacttcagaa[C/T]tgctagagaagaagtt	C	T	NM_004737 // upstream // 430217 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 430217 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE),	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1862012	tcatgatcacctctga[A/G]tacagcaaagacaggg	A	G	NM_004737 // upstream // 456114 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 456114 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE),	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2053100	aagtctatccatccag[A/C]aagaagaggaaagaag	A	C	NM_004737 // upstream // 473832 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 473832 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE).	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2053710	aagtgggcattatccag[A/G]gcaaaagaatgtggga	A	G	NM_004737 // upstream // 475158 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 475158 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE).	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2225109	cgtgttaggcagtgga[C/G]atacaaatataaagta	C	G	NM_004737 // upstream // 481106 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 481106 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE).	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2110026	aggaagagctcgttgg[C/G]aaatcaaaggtgacaa	C	G	NM_004737 // upstream // 481274 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 481274 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE).	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2186869	cagggtagttacagaa[C/T]aaggcttagcagtcag	C	T	NM_004737 // upstream // 481337 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 481337 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE).	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-2079941	accctctagattgac[A/G]gaactagtgagcagca	A	G	NM_004737 // upstream // 731817 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA. /// NM_133642 // upstream // 731817 // Hs.474667 // LARGE // 9215 // Homo sapiens like-glycosyltransferase (LARGE).	LARGE	LARGE, Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, q12.3
SNP_A-1971037	gacaggagcacctgc[C/T]gactctaaagtctcag	C	T	NM_001003681 // upstream // 124994 // Hs.197086 // HMG2L1 // 10042 // Homo sapiens high-mobility group protein 2-like 1 (HMG2L1), transcript variant 3, mRNA. /// NM_014250 // upstream // 124994 // Hs.197086 // HMG2L1 // 10042 // Homo sapiens high-mobility	HMG2L1	HMG2L1, Homo sapiens high-mobility group protein 2-like 1 (HMG2L1), transcript variant 3, q12.3
SNP_A-1814800	gtgtgtgcacccagaa[C/T]gaatcctggagaacca	C	T	NM_006739 // downstream // 98898 // Hs.517582 // MCM5 // 4174 // Homo sapiens MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (MCM5), mRNA. /// NM_014310 // upstream // 17904 // Hs.474711 // RASD2 // 23551 // Homo sapie	MCM5	MCM5, Homo sapiens MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (MCM5), q12.3
SNP_A-1943868	ttgtatacagtcaatc[A/G]cttgctactgcacaca	A	G	NM_014309 // upstream // 297354 // Hs.282998 // RBM9 // 23543 // Homo sapiens RNA binding motif protein 9 (RBM9), mRNA. /// AF229058 // upstream // 297354 // Hs.282998 // RBM9 // 23543 // Homo sapiens hexaribonucleotide binding protein 2 (HRNBP2) mRNA, co	RBM9	RBM9, Homo sapiens RNA binding motif protein 9 (RBM9), q12.3
SNP_A-1889147	tgagtcatgtatacac[A/G]ctcatggtaaatgact	A	G	NM_145660 // intron // 0 // Hs.115099 // APOL4 // 80832 // Homo sapiens apolipoprotein L, 4 (APOL4), transcript variant b, mRNA. /// NM_030643 // intron // 0 // Hs.115099 // APOL4 // 80832 // Homo sapiens apolipoprotein L, 4 (APOL4), transcript variant a.	APOL4	APOL4, Homo sapiens apolipoprotein L, 4 (APOL4), transcript variant b, q12.3
SNP_A-1823801	taaaatgaccttctat[C/T]caaaaacagccttcag	C	T	NM_006078 // intron // 0 // Hs.197693 // CACNG2 // 10369 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// ENST00000300105 // intron // 0 /// — /// — /// —	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2169327	caagcagacatttggt[A/G]aagattattcgtggaa	A	G	NM_006078 // upstream // 1357 // Hs.197693 // CACNG2 // 10369 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// NM_006860 // downstream // 53995 // Hs.415172 // RABL4 // 11020 // Homo sapiens RAB, member of RAS oncoge	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3
SNP_A-2092876	agaaatttgaggatccd[A/G]aggaaaactactgggg	A	G	NM_006078 // upstream // 29692 // Hs.197693 // CACNG2 // 10369 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// NM_006860 // downstream // 25660 // Hs.415172 // RABL4 // 11020 // Homo sapiens RAB, member of RAS oncog	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3
SNP_A-2286926	gatggtaagactctgc[A/G]ctgtaaggactaaatt	A	G	NM_006078 // upstream // 54386 // Hs.197693 // CACNG2 // 10369 // Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), mRNA. /// NM_006860 // downstream // 966 // Hs.415172 // RABL4 // 11020 // Homo sapiens RAB, member of RAS oncogen	CACNG2	CACNG2, Homo sapiens calcium channel, voltage-dependent, gamma subunit 2 (CACNG2), q12.3
SNP_A-2229307	ctaggagcagagcgccd[A/G]ccgatgacaggcccat	A	G	NM_006860 // intron // 0 // Hs.415172 // RABL4 // 11020 // Homo sapiens RAB, member of RAS oncogene family-like 4 (RABL4), mRNA. /// ENST00000340630 // intron // 0 // — // — // — /// ENST00000216198 // intron // 0 // — // — // — // —	RABL4	RABL4, Homo sapiens RAB, member of RAS oncogene family-like 4 (RABL4), q12.3
SNP_A-2292136	gcacccaaagcgccag[C/T]aagttagctccatgat	C	T	NM_006860 // intron // 0 // Hs.415172 // RABL4 // 11020 // Homo sapiens RAB, member of RAS oncogene family-like 4 (RABL4), mRNA. /// ENST00000340630 // intron // 0 // — // — // — /// ENST00000216198 // intron // 0 // — // — // — // —	RABL4	RABL4, Homo sapiens RAB, member of RAS oncogene family-like 4 (RABL4), q12.3
SNP_A-1791128	ggggtgtttcagaga[C/G]agtaaggatacaggag	C	G	NM_000395 // intron // 0 // Hs.285401 // CSF2RB // 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// ENST00000262825 // intron // 0 // — // — // — // —	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-2071966	acagagcgggtctta[A/G]ggaatactgcaccaac	A	G	NM_000395 // intron // 0 // Hs.285401 // CSF2RB // 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// ENST00000262825 // intron // 0 // — // — // — // —	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-2036144	aaattatatcatacaa[A/C]ctacaatttccatttc	A	C	NM_000395 // downstream // 48991 // Hs.285401 // CSF2RB // 1439 // Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA. /// NM_178552 // downstream // 3370 // Hs.124502 // MGC35206 // 339669 // Hom	CSF2RB	CSF2RB, Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), q12.3
SNP_A-2311130	ggaagtctatagcgga[C/T]gatttttgtatatttc	C	T	NM_002872 // upstream // 26476 // Hs.517601 // RAC2 // 5880 // Homo sapiens ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2), mRNA. /// NM_013385 // upstream // 11638 // Hs.170944 // PSCD4 // 27128 // Homo sap	RAC2	RAC2, Homo sapiens ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) (RAC2), q13.1
SNP_A-2121243	agtctgtatttccta[C/T]ctctttgtgcatggg	C	T	NM_006855 // downstream // 28404 // Hs.534392 // KDELR3 // 11015 // Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA. /// NM_016657 // downstream // 28404 // Hs.534392 // KDELR3 //	KDELR3	KDELR3, Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, q13.1
SNP_A-1673262	ccttctcttggccaggctttaaga[A/G]caagatgggtccactcatt actgat	A	G	NM_004286 // intron // 0 // Hs.283677 // GTPBP1 // 9567 // GTP binding protein 1	GTPBP1	GTPBP1, rs138695, GTP binding protein 1,q13.1
SNP_A-1756779	catgagaccttatgcccaaactgag[A/C]gccattccaggcccat cactcactg	A	C	NM_004286 // intron // 0 // Hs.283677 // GTPBP1 // 9567 // GTP binding protein 1	GTPBP1	GTPBP1, rs138696, GTP binding protein 1,q13.1
SNP_A-1851390	tattccagatctccaa[C/T]gttacaggcgagaacc	C	T	NM_004286 // CDS // 0 // Hs.276925 // GTPBP1 // 9567 // Homo sapiens GTP binding protein 1 (GTPBP1), mRNA. /// ENST00000335466 // CDS // 0 // — // — // — // —	GTPBP1	GTPBP1, Homo sapiens GTP binding protein 1 (GTPBP1), q13.1

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2078096	accaggccttcatcac[A/G]ccaggagagagtgcct	A	G	NM_004286 // intron // 0 // Hs.276925 // GTPBP1 // 9567 // Homo sapiens GTP binding protein 1 (GTPBP1), mRNA. /// ENST00000335466 // intron // 0 // — // — // — /// ENST00000216044 // intron // 0 // — // — // — // —	GTPBP1	GTPBP1, Homo sapiens GTP binding protein 1 (GTPBP1), q13.1
SNP_A-2245450	ctgggacattcctgcc[A/G]ggagagagtcaggccc	A	G	NM_014292 // upstream // 83208 // Hs.511952 // CBX6 // 23466 // Homo sapiens chromobox homolog 6 (CBX6), mRNA. /// NM_145699 // upstream // 2157 // Hs.348983 // APOBEC3A // 200315 // Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide	CBX6	CBX6, Homo sapiens chromobox homolog 6 (CBX6), q13.1
SNP_A-2079604	acccgtatcccactca[C/T]atcaagaagcaactc	C	T	NM_181773 // 3UTR // 0 // Hs.440515 // ARP10 // 164668 // Homo sapiens ARP10 protein (ARP10), mRNA. /// ENST00000348946 // 3UTR // 0 // — // — // — /// ENST00000342641 // 3UTR // 0 // — // — // — // —	ARP10	ARP10, Homo sapiens ARP10 protein (ARP10), q13.1
SNP_A-2073202	acaggctgaaatgtta[C/T]ctggaggcctcaggca	C	T	NM_175709 // intron // 0 // Hs.356416 // CBX7 // 23492 // Homo sapiens chromobox homolog 7 (CBX7), mRNA. /// ENST00000216133 // intron // 0 // — // — // —	CBX7	CBX7, Homo sapiens chromobox homolog 7 (CBX7), q13.1
SNP_A-1899169	tggaaagtgtttcaaa[C/T]ggtcagtaactggcta	C	T	NM_175709 // upstream // 5234 // Hs.356416 // CBX7 // 23492 // Homo sapiens chromobox homolog 7 (CBX7), mRNA. /// ENST00000216133 // upstream // 5234 // — // — // — // — /// ENST00000330414 // downstream // 16270 // — // — // — // —	CBX7	CBX7, Homo sapiens chromobox homolog 7 (CBX7), q13.1
SNP_A-1922230	ttacttgccagacaaa[C/T]ggacttgggcacatg	C	T	NM_005297 // downstream // 21009 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 65814 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2
SNP_A-2096136	agacatgagtcatcga[A/G]aggctatctaaaccga	A	G	NM_005297 // downstream // 28900 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 57923 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2
SNP_A-1892177	tgcaaatcaatcttccj[C/T]gaggcaatttcctgtt	C	T	NM_005297 // downstream // 38623 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 48200 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2
SNP_A-2153668	attagggcaaaaacat[G/T]agggttgaagtgaagt	G	T	NM_005297 // downstream // 42366 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 44457 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2
SNP_A-1886168	tgacccaatcacagcc[A/T]accagatcaacgagag	A	T	NM_005297 // downstream // 42611 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 44212 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2
SNP_A-2305785	gctgccttccaaataa[C/T]cataacttggtggga	C	T	NM_005297 // downstream // 45668 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 41155 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2
SNP_A-2225774	ctaaaggcataaaaaa[A/C]cgttgaattatagcag	A	C	NM_005297 // downstream // 53584 // Hs.248122 // GPR24 // 2847 // Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA. /// NM_006358 // downstream // 33239 // Hs.474938 // SLC25A17 // 10478 // Homo sapiens solute carrier family 25 (mitochondrial carr	GPR24	GPR24, Homo sapiens G protein-coupled receptor 24 (GPR24), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2086569	actgaaatgaatgtaa[A/G]tgtggatatgacaact	A	G	NM_003932 // intron // 0 // Hs.546303 // ST13 // 6767 // Homo sapiens suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA. /// ENST00000216218 // intron // 0 // — // — // — // —	ST13	ST13, Homo sapiens suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), q13.2
SNP_A-1915905	tgttgagtatcatgaa[A/G]tcttcctatttggagc	A	G	NM_014248 // downstream // 11510 // Hs.474949 // RBX1 // 9978 // Homo sapiens ring-box 1 (RBX1), mRNA. /// ENST00000216225 // downstream // 11510 // — // — // — // — /// ENST00000311995 // upstream // 79864 // — // — // — // —	RBX1	RBX1, Homo sapiens ring-box 1 (RBX1), q13.2
SNP_A-1890540	tgatcttcaacctgca[C/G]agcaataacatcttat	C	G	ENST00000360571 // intron // 0 // — // — // — // — /// ENST00000359476 // intron // 0 // — // — // — // —	-	q13.2
SNP_A-2310386	ggaactgaacacagct[A/G]aagtagagagccagaa	A	G	NM_145912 // upstream // 38218 // Hs.436677 // NFAM1 // 150372 // Homo sapiens NFAT activation molecule 1 (NFAM1), mRNA. /// NM_170694 // upstream // 29971 // Hs.534041 // SERHL // 94009 // Homo sapiens serine hydrolase-like (SERHL), mRNA. /// NM_170698 /	NFAM1	NFAM1, Homo sapiens NFAT activation molecule 1 (NFAM1), q13.2
SNP_A-2144061	atgaggaagtttcaca[C/T]tgctattaaaatattg	C	T	NM_000398 // upstream // 27682 // Hs.517666 // DIA1 // 1727 // Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIA1), transcript variant M, mRNA. /// NM_007326 // upstream // 27682 // Hs.517666 // DIA1 // 1727 // Homo sapiens diaphorase (NADH)	DIA1	DIA1, Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIA1), transcript variant M, q13.2
SNP_A-2120108	agtcagaaaacttatc[C/T]acatccaggcagcctg	C	T	NM_017436 // upstream // 16756 // Hs.105956 // A4GALT // 53947 // Homo sapiens alpha 1,4-galactosyltransferase (A4GALT), mRNA. /// ENST00000249005 // upstream // 16756 // — // — // — // — /// ENST00000341350 // downstream // 79474 // — // — //	A4GALT	A4GALT, Homo sapiens alpha 1,4-galactosyltransferase (A4GALT), q13.2
SNP_A-1971128	cgaggatgaaaacaca[C/G]acggttctgaagatcc	C	G	NM_007229 // intron // 0 // Hs.162877 // PACSIN2 // 11252 // Homo sapiens protein kinase C and casein kinase substrate in neurons 2 (PACSIN2), mRNA. /// ENST00000263246 // intron // 0 // — // — // — // — /// ENST00000337959 // intron // 0 // — /	PACSIN2	PACSIN2, Homo sapiens protein kinase C and casein kinase substrate in neurons 2 (PACSIN2), q13.2
SNP_A-2289595	gcaaaaaatggaatga[A/G]atgaagaaaaaggcta	A	G	NM_012263 // intron // 0 // Hs.416038 // TTLL1 // 25809 // Homo sapiens tubulin tyrosine ligase-like family, member 1 (TTLL1), mRNA. /// ENST00000343040 // intron // 0 // — // — // — // — /// ENST00000331018 // intron // 0 // — // — // — //	TTLL1	TTLL1, Homo sapiens tubulin tyrosine ligase-like family, member 1 (TTLL1), q13.2
SNP_A-2299577	gccgagcttaggtcca[A/G]tgaagaggatcagagg	A	G	NM_012263 // upstream // 8638 // Hs.416038 // TTLL1 // 25809 // Homo sapiens tubulin tyrosine ligase-like family, member 1 (TTLL1), mRNA. /// NM_001197 // upstream // 12685 // Hs.475055 // BIK // 638 // Homo sapiens BCL2-interacting killer (apoptosis-indu	TTLL1	TTLL1, Homo sapiens tubulin tyrosine ligase-like family, member 1 (TTLL1), q13.2
SNP_A-2249839	cttaatttttaattcc[C/T]catgcctgctgacagg	C	T	NM_001197 // intron // 0 // Hs.475055 // BIK // 638 // Homo sapiens BCL2-interacting killer (apoptosis-inducing) (BIK), mRNA. /// ENST00000216115 // intron // 0 // — // — // — // —	BIK	BIK, Homo sapiens BCL2-interacting killer (apoptosis-inducing) (BIK), q13.2
SNP_A-2193387	catctgaagctccaaa[A/C]aattttcagccttttgt	A	C	NM_015140 // upstream // 1180 // Hs.517670 // KIAA0153 // 23170 // Homo sapiens KIAA0153 protein (KIAA0153), mRNA. /// ENST00000357017 // upstream // 1206 // — // — // — // — /// ENST00000216129 // upstream // 1180 // — // — // — // — ///	KIAA0153	KIAA0153, Homo sapiens KIAA0153 protein (KIAA0153), q13.2
SNP_A-2227439	ctacactgaacaaata[C/T]gtcgactgatgagtaa	C	T	NM_173050 // intron // 0 // Hs.133995 // SCUBE1 // 80274 // Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), mRNA. /// ENST00000360835 // intron // 0 // — // — // — // —	SCUBE1	SCUBE1, Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), q13.2
SNP_A-1961079	tttttgtccacttgaa[A/G]cttgtctagtgctttt	A	G	NM_173050 // intron // 0 // Hs.133995 // SCUBE1 // 80274 // Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), mRNA. /// ENST00000360835 // intron // 0 // — // — // — // — /// ENST00000290460 // intron // 0 // — // — // — // —	SCUBE1	SCUBE1, Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), q13.2

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2125149	agttggcccctgttcc[G/T]acacagtccaaatcca	G	T	NM_173050 // intron // 0 // Hs.133995 // SCUBE1 // 80274 // Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), mRNA. /// ENST00000360835 // intron // 0 // --- // --- // --- // --- /// ENST00000290460 // intron // 0 // --- // --- // --- // ---	SCUBE1	SCUBE1, Homo sapiens signal peptide, CUB domain, EGF-like 1 (SCUBE1), q13.2
SNP_A-2242884	ctgccacttcccgaca[C/T]gtgatttgttgccacc	C	T	ENST00000334209 // intron // 0 // --- // --- // ---	-	q13.2
SNP_A-1696906	tgctctagagtctggtggcctccaa[A/C]accactatctgggtagc ctcaggcg	A	C	NM_022785 // upstream // 66732 // Hs.283783 // FLJ23588 // 64800 // CAP-binding protein complex interacting protein 1 /// Y10776 // downstream // 34046 // Hs.283783 // FLJ23588 // 64800 // CAP-binding protein complex interacting protein 1	FLJ23588	FLJ23588 , rs137791, CAP-binding protein complex interacting protein 1 ,q13.2
SNP_A-2280447	gagggtgcctgttgta[C/T]acttagcatggcacca	C	T	NM_198856 // intron // 0 // Hs.368507 // FLJ23588 // 64800 // Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, mRNA. /// NM_022785 // intron // 0 // Hs.368507 // FLJ23588 // 64800 // Homo sapiens CAP-binding	FLJ23588	FLJ23588, Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, q13.2
SNP_A-1663348	agagatcatttatcttattaaaaca[A/G]taggcaagagtcatcaa agtggaaa	A	G	Y10776 // intron // 0 // Hs.283783 // FLJ23588 // 64800 // CAP-binding protein complex interacting protein 1	FLJ23588	FLJ23588 , rs10483219, CAP-binding protein complex interacting protein 1,q13.2
SNP_A-1679974	ctttgttgttggagacaatacatta[C/T]agcgaacagagacttcttt ttctag	C	T	Y10776 // intron // 0 // Hs.283783 // FLJ23588 // 64800 // CAP-binding protein complex interacting protein 1	FLJ23588	FLJ23588 , rs1476036, CAP-binding protein complex interacting protein 1,q13.2
SNP_A-2142803	atgaaggcgcgctttc[A/G]agtaagcgagtgagga	A	G	NM_198856 // intron // 0 // Hs.368507 // FLJ23588 // 64800 // Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, mRNA. /// NM_022785 // intron // 0 // Hs.368507 // FLJ23588 // 64800 // Homo sapiens CAP-binding	FLJ23588	FLJ23588, Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588), transcript variant 2, q13.2
SNP_A-1795059	ggtgaatggatacacg[A/G]acagcagtaattgaca	A	G	NM_001003828 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 2, mRNA. ///	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-1665684	ttaaaaacagaccgtgatgcttttta[C/T]atacagacccacactgt ccatgact	C	T	NM_013327 // intron // 0 // Hs.8836 // PARVB // 29780 // parvin, beta	PARVB	PARVB , rs10483222, parvin, beta,q13.31
SNP_A-2077067	accaacttagtgccac[A/G]gaagctcaactgtctc	A	G	NM_001003828 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 2, mRNA. ///	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-2277146	gagatgggaagcctga[C/T]gcgcccccgttgcacc	C	T	NM_001003828 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 2, mRNA. ///	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-1904611	tggggccccgagctga[C/T]gtaggtaggcttggga	C	T	NM_001003828 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 1, mRNA. /// NM_013327 // intron // 0 // Hs.475074 // PARVB // 29780 // Homo sapiens parvin, beta (PARVB), transcript variant 2, mRNA. ///	PARVB	PARVB, Homo sapiens parvin, beta (PARVB), transcript variant 1, q13.31
SNP_A-2265817	gaaggaactggagaca[A/G]tcacatggaagaagcc	A	G	NM_022141 // intron // 0 // Hs.546422 // PARVG // 64098 // Homo sapiens parvin, gamma (PARVG), mRNA. /// ENST00000356909 // intron // 0 // --- // --- // --- // --- /// ENST00000266289 // intron // 0 // --- // --- // --- // ---	PARVG	PARVG, Homo sapiens parvin, gamma (PARVG), q13.31
SNP_A-2241027	ctgagcaagaaacttc[A/G]cagtctgagttcagta	A	G	NM_022141 // downstream // 75239 // Hs.546422 // PARVG // 64098 // Homo sapiens parvin, gamma (PARVG), mRNA. /// NM_022141 // downstream // 74613 // Hs.546422 // PARVG // 64098 // Homo sapiens parvin, gamma (PARVG), mRNA. /// ENST00000356909 // downstream	PARVG	PARVG, Homo sapiens parvin, gamma (PARVG), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1905869	tggtcatcaccaataa[C/T]gtgccgttgcaaactg	C	T	NM_032287 // downstream // 122451 // Hs.332795 // LDOC1L // 84247 // Homo sapiens leucine zipper, down-regulated in cancer 1-like (LDOC1L), mRNA. /// ENST00000266255 // upstream // 69004 // --- // --- // --- // --- /// ENST00000341255 // downstream // 122	LDOC1L	LDOC1L, Homo sapiens leucine zipper, down-regulated in cancer 1-like (LDOC1L), q13.31
SNP_A-2103804	agcaccccatcaacga[A/G]cgaagggaagccccag	A	G	NM_032287 // downstream // 110440 // Hs.332795 // LDOC1L // 84247 // Homo sapiens leucine zipper, down-regulated in cancer 1-like (LDOC1L), mRNA. /// ENST00000266255 // upstream // 81015 // --- // --- // --- // --- /// ENST00000341255 // downstream // 110	LDOC1L	LDOC1L, Homo sapiens leucine zipper, down-regulated in cancer 1-like (LDOC1L), q13.31
SNP_A-2070664	acacgatagaatatga[C/T]atggcatgaaaagaag	C	T	NM_015366 // intron // 0 // Hs.102336 // ARHGAP8 // 23779 // Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 3, mRNA. /// NM_017701 // intron // 0 // Hs.102336 // ARHGAP8 // 23779 // Homo sapiens Rho GTPase activating protein 8	ARHGAP8	ARHGAP8, Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 3, q13.31
SNP_A-2096917	agactctgaggccaga[A/C]gctagagtgtggctcc	A	C	NM_138415 // intron // 0 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// ENST00000313237 // intron // 0 // --- // --- // --- // ---	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-1858340	tcagacaatcctctac[A/T]cttggaaatttgagtt	A	T	NM_138415 // intron // 0 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// ENST00000313237 // intron // 0 // --- // --- // --- // ---	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-1704349	ggggcagaatgttgaccacagattg[A/G]aagttaggtgaaagct gatttccgc	A	G	NM_138415 // intron // 0 // Hs.254097 // LOC112885 // 112885 // hypothetical protein BC012187	LOC112885	LOC112885 , rs1028492, hypothetical protein BC012187,q13.31
SNP_A-2273338	gactccgggttttttg[A/T]agctcagtgagcagca	A	T	NM_138415 // intron // 0 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// ENST00000313237 // intron // 0 // --- // --- // --- // ---	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-2313307	ggagaccaatgtttct[A/G]aagccagcagcagaag	A	G	NM_138415 // intron // 0 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// ENST00000313237 // intron // 0 // --- // --- // --- // ---	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-1918408	ttaaataacattgatc[C/G]aaatttttattgcagc	C	G	NM_138415 // intron // 0 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// ENST00000313237 // intron // 0 // --- // --- // --- // ---	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-2061417	aatgcctttccctcta[C/T]ggaccgagcagaaaga	C	T	NM_138415 // upstream // 26431 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// NM_153645 // upstream // 127714 // Hs.475103 // NUP50 // 10762 // Homo sapiens nucleoporin 50kDa (NUP50), transcript varia	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-1971164	ttgtcctctaactcca[C/T]ccaatcaatcatgagg	C	T	NM_138415 // upstream // 34950 // Hs.254097 // PHF21B // 112885 // Homo sapiens hypothetical protein BC012187 (LOC112885), mRNA. /// NM_153645 // upstream // 119195 // Hs.475103 // NUP50 // 10762 // Homo sapiens nucleoporin 50kDa (NUP50), transcript varia	PHF21B	PHF21B, Homo sapiens hypothetical protein BC012187 (LOC112885), q13.31
SNP_A-2273696	gactgcatcatttaag[A/G]attaaactggccccta	A	G	NM_006487 // intron // 0 // Hs.24601 // FBLN1 // 2192 // Homo sapiens fibulin 1 (FBLN1), transcript variant A, mRNA. /// NM_001996 // intron // 0 // Hs.24601 // FBLN1 // 2192 // Homo sapiens fibulin 1 (FBLN1), transcript variant C, mRNA. /// NM_006485 //	FBLN1	FBLN1, Homo sapiens fibulin 1 (FBLN1), transcript variant A, q13.31
SNP_A-2199542	ccaaaaaacacccaga[C/G]aactagataggaaaaa	C	G	NM_006487 // intron // 0 // Hs.24601 // FBLN1 // 2192 // Homo sapiens fibulin 1 (FBLN1), transcript variant A, mRNA. /// NM_006486 // intron // 0 // Hs.24601 // FBLN1 // 2192 // Homo sapiens fibulin 1 (FBLN1), transcript variant D, mRNA. /// NM_006485 //	FBLN1	FBLN1, Homo sapiens fibulin 1 (FBLN1), transcript variant A, q13.31
SNP_A-1902885	tggctctgcccttccc[A/G]gatgttctgtgatggg	A	G	NM_017931 // intron // 0 // Hs.435832 // FLJ20699 // 55020 // Homo sapiens hypothetical protein FLJ20699 (FLJ20699), mRNA. /// ENST00000334030 // intron // 0 // --- // --- // --- // ---	FLJ20699	FLJ20699, Homo sapiens hypothetical protein FLJ20699 (FLJ20699), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1805818	gtcccgtttcaggcaa[C/T]gcagtcacttgcactg	C	T	NM_014246 // intron // 0 // Hs.252387 // CELSR1 // 9620 // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA. /// ENST00000262738 // intron // 0 // — // — // — /// ENST00000344597 // int	CELSR1	CELSR1, Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), q13.31
SNP_A-2080202	acctaaaaatattcacc[A/G]acaaaatagactgtact	A	G	NM_014246 // intron // 0 // Hs.252387 // CELSR1 // 9620 // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA. /// ENST00000262738 // intron // 0 // — // — // — /// ENST00000344597 // int	CELSR1	CELSR1, Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), q13.31
SNP_A-2184834	cagctgggacagctgc[C/T]ctcggctccatgtggt	C	T	NM_014246 // upstream // 15385 // Hs.252387 // CELSR1 // 9620 // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA. /// ENST00000262738 // upstream // 15385 // — // — // — // — /// ENST00000003	CELSR1	CELSR1, Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), q13.31
SNP_A-1818154	gttctctctttccag[A/C]cggcctctcaggatcc	A	C	NM_014246 // upstream // 25439 // Hs.252387 // CELSR1 // 9620 // Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA. /// ENST00000262738 // upstream // 25439 // — // — // — // — /// ENST00000003	CELSR1	CELSR1, Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), q13.31
SNP_A-2279566	gaggcaaaagttggag[A/T]aaatagttctagaaaa	A	T	ENST00000262736 // intron // 0 // — // — // — // — /// ENST00000361034 // intron // 0 // — // — // — // —	-	q13.31
SNP_A-1907696	tgtaacttcaggcaca[A/G]tatcctttacttcat	A	G	NM_022766 // intron // 0 // Hs.200668 // CERK // 64781 // Homo sapiens ceramide kinase (CERK), transcript variant 1, mRNA. /// ENST00000216264 // intron // 0 // — // — // — // —	CERK	CERK, Homo sapiens ceramide kinase (CERK), transcript variant 1, q13.31
SNP_A-2210428	ccccaatgtgagttat[A/C]acacttgatgaatgaa	A	C	NM_014346 // intron // 0 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // intron // 0 // — // — // — // — /// ENST00000355704 // intron // 0 // — // — // — // —	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-1866275	tcccatcccaatgtaa[C/T]gactgatggttgagca	C	T	NM_014346 // intron // 0 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // intron // 0 // — // — // — // — /// ENST00000355704 // intron // 0 // — // — // — // —	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2305324	gctgaggtgagcaagg[A/G]cagtggacgtcactgc	A	G	NM_014346 // intron // 0 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // intron // 0 // — // — // — // — /// ENST00000355704 // intron // 0 // — // — // — // —	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-1766818	ggctttctagcatga[C/T]gccagtggcaaaaca	C	T	NM_014346 // downstream // 4280 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 4280 // — // — // — // — /// ENST00000355704 // downstream // 4287 // — // —	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-1663740	ttgtgacctctcaccctgagctgca[C/G]accttctgtttcgtgatcc gcgtgc	C	G	NM_014346 // downstream // 621005 // Hs.505862 // C22orf4 // 25771 // chromosome 22 open reading frame 4 /// NM_015381 // upstream // 694566 // Hs.436854 // CLONE25003 // 25817 // hypothetical protein CLONE25003	C22orf4	C22orf4 , rs720441, chromosome 22 open reading frame 4 , q13.31
SNP_A-2253365	ctctctgtataacatta[C/T]agtgaaagctctagct	C	T	NM_014346 // downstream // 551323 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 551323 // — // — // — // — /// ENST00000355704 // downstream // 551330 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-1888579	tgaggatttatgccga[G/T]ctccagacgtacagga	G	T	NM_014346 // downstream // 589675 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 589675 // — // — // — // — /// ENST00000355704 // downstream // 589682 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-1802935	gtatgtgtatacagtat[C/T]gtgttgcagcgtgtat	C	T	NM_014346 // downstream // 591168 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 591168 // — // — // — /// ENST00000355704 // downstream // 591175 //	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.31
SNP_A-2309913	ggaaatcaacaagaca[C/T]ggcagataactggatg	C	T	NM_014346 // downstream // 1125137 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 1125137 // — // — // — /// ENST00000355704 // downstream // 1125144	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.32
SNP_A-1878070	tctgtagaaaacctgct[C/T]gagggaagagctcaca	C	T	NM_014346 // downstream // 1171854 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 1171854 // — // — // — /// ENST00000355704 // downstream // 1171861	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.32
SNP_A-1810525	gtgatttaggtaaa[C/T]gctcctctcttgtgct	C	T	NM_014346 // downstream // 1313352 // Hs.435044 // TBC1D22A // 25771 // Homo sapiens chromosome 22 open reading frame 4 (C22orf4), mRNA. /// ENST00000337137 // downstream // 1313352 // — // — // — /// ENST00000355704 // downstream // 1313359	TBC1D22A	TBC1D22A, Homo sapiens chromosome 22 open reading frame 4 (C22orf4), q13.32
SNP_A-2140817	atctgaaaccacattc[A/G]ctttcctctcaccagg	A	G	ENST00000336769 // intron // 0 // — // — // — /// ENST00000358295 // intron // 0 // — // — // —	-	q13.32
SNP_A-2117377	aggtggtgatagagaac[A/C]gagtcagctgggtaaa	A	C	ENST00000336769 // intron // 0 // — // — // — /// ENST00000358295 // intron // 0 // — // — // —	-	q13.32
SNP_A-2073908	acagtgtgaatatgcc[A/G]ggaaaaggggagggttc	A	G	ENST00000336769 // intron // 0 // — // — // — /// ENST00000358295 // intron // 0 // — // — // —	-	q13.32
SNP_A-2267221	gaatacatgaacagaat[A/C]tggatttttgattgatg	A	G	ENST00000336769 // intron // 0 // — // — // — /// ENST00000358295 // intron // 0 // — // — // —	-	q13.32
SNP_A-1867534	tccgctgcagggtccat[A/G]cgccgcccaggtctct	A	G	ENST00000336769 // intron // 0 // — // — // — /// ENST00000358295 // intron // 0 // — // — // —	-	q13.32
SNP_A-1805522	gtccagcttcatagag[A/G]cactatgtcctcaagt	A	G	NM_207478 // upstream // 786246 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 9450 // — // — // — /// ENST00000358295 // downstream // 9446 // — // — // — // -	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.32
SNP_A-1758612	tacatatgcacgcacatacatgcac[A/G]tccacaatccatgttcc tatgcacc	A	G	NM_014577 // downstream // 722083 // Hs.370880 // BRD1 // 23774 // bromodomain containing 1 /// NM_015381 // downstream // 294996 // Hs.436854 // CLONE25003 // 25817 // hypothetical protein CLONE25003	BRD1	BRD1 , rs727080, bromodomain containing 1 ,q13.32
SNP_A-2243197	ctgcctctaaacccga[A/C]gtcttcaagcctgact	A	C	NM_207478 // upstream // 511413 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 284283 // — // — // — /// ENST00000358295 // downstream // 284279 // — // — // —	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.32
SNP_A-2217937	cctgcaggcggccttc[A/G]caatatctgacgttag	A	G	NM_207478 // upstream // 5111006 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 284690 // — // — // — /// ENST00000358295 // downstream // 284686 // — // — // —	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.32
SNP_A-1877262	tctggaaaaaatacta[C/T]gttgttcaattgttct	C	T	NM_207478 // upstream // 413383 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 382313 // — // — // — /// ENST00000358295 // downstream // 382309 // — // — // —	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2278573	gagctgagcttcctca[C/T]ctagaattgctgaaca	C	T	NM_207478 // upstream // 404484 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 391212 // — // — // — /// ENST00000358295 // downstream // 391208 // — // — // —	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2287973	gattatgtgtgaagaa[A/C]attcaaggtaatctac	A	C	NM_207478 // upstream // 401090 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 394606 // --- // --- // --- /// ENST00000358295 // downstream // 394602 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1854649	tcaacaccatgcctac[A/G]gattgcctcagccaaa	A	G	NM_207478 // upstream // 370164 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 425532 // --- // --- // --- /// ENST00000358295 // downstream // 425528 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1684852	cataatgatgactattcagcagga[G/T]aatgaatggagcattg ataatttttt	G	T	NM_014577 // downstream // 434752 // Hs.370880 // BRD1 // 23774 // bromodomain containing 1 /// NM_015381 // downstream // 582327 // Hs.436854 // CLONE25003 // 25817 // hypothetical protein CLONE25003	BRD1	BRD1 , rs848741, bromodomain containing 1 q13.33
SNP_A-1786585	ggcttctataaggatc[C/T]cacgagccactctgta	C	T	NM_207478 // upstream // 235752 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 559944 // --- // --- // --- /// ENST00000358295 // downstream // 559940 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2130664	atactggcctcaaaac[A/G]attcggaagtatctt	A	G	NM_207478 // upstream // 227548 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 568148 // --- // --- // --- /// ENST00000358295 // downstream // 568144 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2105763	agccagcttgtgggca[A/G]ccctggattaagaggt	A	G	NM_207478 // upstream // 187730 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 627966 // --- // --- // --- /// ENST00000358295 // downstream // 627962 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2264552	gaagaagaggacaaag[A/G]cagtttcttatcatct	A	G	NM_207478 // upstream // 167178 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 628518 // --- // --- // --- /// ENST00000358295 // downstream // 628514 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1886315	tgacctcgcgtttata[C/T]ccaggattcttggtt	C	T	NM_207478 // upstream // 110259 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 685437 // --- // --- // --- /// ENST00000358295 // downstream // 685433 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1866331	tcccattaagacaaat[G/T]acttcgactcatgaag	G	T	NM_207478 // upstream // 110198 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// ENST00000336769 // downstream // 685498 // --- // --- // --- /// ENST00000358295 // downstream // 685494 // --- // --- // ---	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-1878937	tcttaaatgcaaggat[C/T]gctcatagtgtttgcc	C	T	NM_207478 // downstream // 28454 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// NM_198851 // downstream // 34715 // Hs.133159 // LOC348645 // 348645 // Homo sapiens hypothetical protein LOC348645 (LOC348645), mRN	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2122667	agtggaagttgaggg[C/G]actctcacaaaatgat	C	G	NM_207478 // downstream // 47846 // Hs.517724 // FLJ44385 // 400934 // Homo sapiens FLJ44385 protein (FLJ44385), mRNA. /// NM_198851 // downstream // 15323 // Hs.133159 // LOC348645 // 348645 // Homo sapiens hypothetical protein LOC348645 (LOC348645), mRN	FLJ44385	FLJ44385, Homo sapiens FLJ44385 protein (FLJ44385), q13.33
SNP_A-2302776	gctacttatgctcaag[C/T]cctttctcagggtgc	C	T	NM_198851 // upstream // 52423 // Hs.133159 // LOC348645 // 348645 // Homo sapiens hypothetical protein LOC348645 (LOC348645), mRNA. /// NM_014577 // downstream // 95941 // Hs.127950 // BRD1 // 23774 // Homo sapiens bromodomain containing 1 (BRD1), mRNA.	LOC348645	LOC348645, Homo sapiens hypothetical protein LOC348645 (LOC348645), q13.33
SNP_A-1901981	tggcagtgccggccca[C/T]ggtaggtacgtgaaga	C	T	NM_198851 // upstream // 60866 // Hs.133159 // LOC348645 // 348645 // Homo sapiens hypothetical protein LOC348645 (LOC348645), mRNA. /// NM_014577 // downstream // 87498 // Hs.127950 // BRD1 // 23774 // Homo sapiens bromodomain containing 1 (BRD1), mRNA.	LOC348645	LOC348645, Homo sapiens hypothetical protein LOC348645 (LOC348645), q13.33

Table 2

Name	Flank	Allele_A	Allele_B	Associated_Gene	Gene_Symbol	Label
SNP_A-2284625	gatcagataaattggt[A/C]aacttgatagcaagtc	A	C	NM_198851 // upstream // 72484 // Hs.133159 // LOC348645 // 348645 // Homo sapiens hypothetical protein LOC348645 (LOC348645), mRNA. /// NM_014577 // downstream // 75880 // Hs.127950 // BRD1 // 23774 // Homo sapiens bromodomain containing 1 (BRD1), mRNA.	LOC348645	LOC348645, Homo sapiens hypothetical protein LOC348645 (LOC348645), q13.33
SNP_A-2085366	actcattaaatcttca[C/T]aaaagcccagtgctga	C	T	NM_198851 // upstream // 101957 // Hs.133159 // LOC348645 // 348645 // Homo sapiens hypothetical protein LOC348645 (LOC348645), mRNA. /// NM_014577 // downstream // 46407 // Hs.127950 // BRD1 // 23774 // Homo sapiens bromodomain containing 1 (BRD1), mRNA.	LOC348645	LOC348645, Homo sapiens hypothetical protein LOC348645 (LOC348645), q13.33
SNP_A-1927775	ttcaagcgtcttctcc[A/G]cctgacctgccacc	A	G	NM_024105 // intron // 0 // Hs.526711 // ALG12 // 79087 // Homo sapiens asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase) (ALG12), mRNA. /// ENST00000330817 // intron // 0 // — // — // — /// ENST00000332276 //	ALG12	ALG12, Homo sapiens asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase) (ALG12), q13.33
SNP_A-1916764	tgtttccataagatgc[A/G]aggaacaggtcacgta	A	G	U93181 // intron // 0 // Hs.280202 // SBF1 // 6305 // Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds. /// NM_002972 // intron // 0 // Hs.280202 // SBF1 // 6305 // Homo sapiens SET binding factor 1 (SBF1), transcript variant 1,	SBF1	SBF1, Homo sapiens nuclear dual-specificity phosphatase (SBF1) partial cds. q13.33

Claims

1. A method for determining whether an individual has or is susceptible to development or occurrence of a cardiovascular disease or event, wherein the individual is in need of such determination, the method comprising the step of:

   detecting a polymorphic variant of a CVDA polymorphism in the individual or detecting a polymorphic variant in strong linkage disequilibrium with a CVDA polymorphism; or
   detecting a haplotype comprising a polymorphic variant of the CVDA polymorphism in the individual; or
   detecting an allele of a gene comprising the polymorphic variant of the CVDA polymorphism in the individual.

2. The method of claim 1, wherein:

   a) the polymorphic variant is associated with an increased risk that the individual has or is susceptible to development or occurrence of a cardiovascular disease or event; and/or
   b) the polymorphic variant is found within a gene selected from the group consisting of: one or more of the genes listed in Table 1.

3. The method of claim 1 or claim 2, wherein the detecting step comprises determining which of at least two polymorphic variants exists at a polymorphic site.

4. The method of any one of claims 1 to 3, further comprising the step of determining an absolute risk or relative risk ratio based at least in part on the identity of the polymorphic variant; and in which case optionally wherein the determination of the absolute risk or relative risk ratio is based at least in part on at least one classical risk factor.

5. The method of any one of the preceding claims, further comprising detecting polymorphic variants of one or more additional CVDA polymorphisms; and in which case either:

   a) wherein the one or more additional CVDA polymorphisms are selected from polymorphisms listed in Table 1 or Table 2; and/or
   b) wherein the polymorphic variants constitute a haplotype and in which latter case further optionally either:

      i) wherein the haplotype is associated with an increased risk that the individual has or is susceptible to development or occurrence of a cardiovascular disease or event; and/or
      ii) further comprising the step of determining an absolute risk or relative risk ratio based at least in part on the haplotype; and in which case further optionally wherein the determination of the absolute risk or relative risk ratio is based at least in part on at least one classical risk factor.

6. The method of any one of the preceding claims, wherein the cardiovascular disease or event is a myocardial infarction.

7. The method of any one of the preceding claims, further comprising the step of determining, based on the identity of the polymorphic variant, that the individual is at increased risk of occurrence of a cardiovascular disease or event; and in which case optionally further comprising the step of selecting a therapeutic regimen for the individual, wherein the therapeutic regimen is selected based on the increased risk.

8. An isolated polynucleotide or polypeptide encoded by a CVDA gene, wherein said CVDA gene comprises a polymorphic variant of a CVDA polymorphism.

9. A kit comprising a plurality of probes or primers selected to detect one or more polymorphic variants of a CVDA polymorphism or a polymorphism in strong linkage disequilibrium with a CVDA polymorphism, wherein at least 10% of the probes or primers are selected to detect a polymorphism associated with cardiovascular disease.

10. The kit of claim 17 comprising one or more of the following:

    a) a plurality of allele-specific oligonucleotides; and/or
    b) a plurality of oligonucleotides that terminate adjacent to a CVDA polymorphic site; and/or
    c) probes or primers selected to detect polymorphic variants at a plurality of different polymorphic sites; and/or
    d) labelled probes and/or labeled primers; and/or
    e) a plurality of probes or primers for detecting each of a plurality of polymorphic variants; and/or

f) a solid support attached to at least some of the probes and/or primers; and/or
g) microparticles attached to at least some of the probes and/or primers; and/or
h) reagents for performing a Luminex assay; and/or
i) probes or primers selected to detect one or more haplotypes associated with cardiovascular disease, wherein at least one of said haplotypes comprises a CVDA polymorphic variant.

11. The kit of claim 10 or claim11, wherein the probes are provided as an array.

12. A computer-readable medium on which is stored an identifier for each of a plurality of polymorphisms and/or haplotypes listed in Table 1:

a) and an indicator of the frequency with which at least one polymorphic variant of the polymorphism exists in a plurality of individuals that have experienced a major coronary event or have been diagnosed with cardiovascular disease; and/or
b) wherein at least and an indicator of the absolute or relative risk for the occurrence of a cardiovascular disease or event in an individual having a disease-associated polymorphic variant of each of the polymorphisms; and/or
c) and an indicator of the absolute or relative risk for the occurrence of a cardiovascular disease or event in an individual having a disease-associated variant of each of the haplotypes.

Figure 1: Group Statistics of Study Subjects

		N	Mean	Standard-deviation
Age (years)	PROCAM	213	47,58	5,813
	MI-patients	213	47,41	5,915
Risk (% in 10 years)	PROCAM	213	7,3632	6,15992
	MI-patients	213	7,2777	6,56974
Total cholesterol (mg/dL)	PROCAM	213	234,92	40,706
	MI-patients	213	204,12	38,241
HDL-cholesterol (mg/dL)	PROCAM	213	44,88	11,074
	MI-patients	213	42,52	11,467
LDL-cholesterol (mg/dL)	PROCAM	213	156,92	37,747
	MI-patients	213	133,53	36,696
Triglyceride (mg/dL)	PROCAM	213	165,59	68,880
	MI-patients	213	146,89	113,668
Syst. BP (mm Hg)	PROCAM	213	133,28	17,853
	MI-patients	213	130,96	23,760
BMI	PROCAM	207	28,1932	4,16039
	MI-patients	205	28,0784	4,54413

Figure 2: Characteristics of Study Subjects

	PROCAM (n=213)	**MI patients (n=213)**
Diabetics	17.8 %	14.6%
Smokers	37.1 %	70.4%
Familial aggregation	0 %	39.4%
Hypertensives (syst. BP>140 or diast.BP>90 mmHg or antihypertensive treatment)	38.7 %	62.4%
Hypercholesterolemia (total chol. >240 mg/dl or lipid-lowering treatment)	44.1 %	34.3 %

Figure 3: Risk Profiles of PROCAM and MI-patients

			PROCAM	MI-patients
Risk	<10%	n	162	160
		%	76,1%	75,1%
	10-20%	n	38	40
		%	17,8%	18,8%
	>20%	n	13	13
		%	6,1%	6,1%

European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

which under Rule 63 of the European Patent Convention shall be considered, for the purposes of subsequent proceedings, as the European search report

Application Number EP 07 25 1633

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
Y	WO 2004/035746 A (DECODE GENETICS EHF [IS]; HELGADOTTIR ANNA [IS]; GULCHER JEFFREY R [US) 29 April 2004 (2004-04-29) * abstract; claims 1-44 *	1-11	INV. C12Q1/68
Y	US 6 342 357 B1 (SPLAWSKI IGOR [US] ET AL) 29 January 2002 (2002-01-29) * abstract *	1-11	
Y	SPIAWSKI I ET AL: "SPECTRUM OF MUATIONS IN LONG-QT SYNDROME GENES KVLQT1, HERG, SCN5A, KCNE1, AND KCNE2" CIRCULATION, AMERICAN HEART ASSOCIATION, DALLAS, TX, US, vol. 102, no. 10, 5 September 2000 (2000-09-05), pages 1178-1185, XP001070986 ISSN: 0009-7322 * the whole document *	1-11	
	-/--		TECHNICAL FIELDS SEARCHED (IPC) C12Q

INCOMPLETE SEARCH

The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.

Claims searched completely :

Claims searched incompletely :

Claims not searched :

Reason for the limitation of the search:

see sheet C

Place of search	Date of completion of the search	Examiner
The Hague	6 December 2007	Franz, Cerstin

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04E07)

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PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 07 25 1633

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (IPC)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
A	THE SANGER CENTRE (UK) AND THE WASHINGTON UNIVERSITY GENOME SEQUENCING CENTER (USA): "Toward a complete human genome sequence" GENOME RESEARCH, vol. 8, no. 11, November 1998 (1998-11), pages 1097-1108, XP002451612 ISSN: 1088-9051 * the whole document * -----	1-11	TECHNICAL FIELDS SEARCHED (IPC)

EPO FORM 1503 03.82 (P04C10)

European Patent Office

INCOMPLETE SEARCH SHEET C

Application Number
EP 07 25 1633

Claim(s) searched completely:
1-11

Claim(s) not searched:
12

Reason for the limitation of the search (non-patentable invention(s)):

Article 52 (2)(d) EPC - Presentation of information

European Patent Office

Application Number
EP 07 25 1633

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☒ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

invention 1: claims 1-12 all partially and invention 2: claims 1-12 all partially

☐ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

☐ The present supplementary European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims (Rule 164 (1) EPC).

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LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 07 25 1633

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: 1-12 (all partially)

Method for determining whether an individual has or is susceptible to the development or occurrence of a cardiovascular disease, wherein the polymorphic variant SNP_A-2084457 corresponding to SEQ ID No #1 is detected; isolated polynucleotide or polypeptide comprising the polymorphic variant according to SEQ ID No #1, a kit comprising a plurality of probes or primers selected to detect one or more polymorphic variants according to SEQ ID No #1 and a computer-readable medium on which an identifier for the polymorphism and/or haplotype according to SEQ ID No #1 are stored.

Invention 2: 1-12 (all partially)

Method for determining whether an individual has or is susceptible to the development or occurrence of a cardiovascular disease, wherein the polymorphic variant SNP_A-1902305 corresponding to SEQ ID No #2 is detected; isolated polynucleotide or polypeptide comprising the polymorphic variant according to SEQ ID No #2, a kit comprising a plurality of probes or primers selected to detect one or more polymorphic variants according to SEQ ID No #2 and a computer-readable medium on which an identifier for the polymorphism and/or haplotype according to SEQ ID No #2 are stored.

Inventions 3-9999: 1-12 (all partially)

Method for determining whether an individual has or is susceptible to the development or occurrence of a cardiovascular disease, wherein the polymorphic variants corresponding to SEQ ID Nos #3-9999 are detected; isolated polynucleotides or polypeptides comprising the polymorphic variants according to SEQ ID Nos #3-9999, kits comprising a plurality of probes or primers selected to detect one or more polymorphic variants according to SEQ ID Nos #3-9999 polymorphism and a computer-readable medium on which an identifier for each polymorphism and/or haplotype according to SEQ ID Nos #3-9999 are stored.

ANNEX TO THE EUROPEAN SEARCH REPORT ON EUROPEAN PATENT APPLICATION NO. EP 07 25 1633

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
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06-12-2007

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2004035746 A	29-04-2004	AU 2003290527 A1	04-05-2004
		CA 2502359 A1	29-04-2004
		EP 1562973 A2	17-08-2005
US 6342357 B1	29-01-2002	US 2002061524 A1	23-05-2002

EPO FORM P0459

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

REFERENCES CITED IN THE DESCRIPTION

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Patent documents cited in the description

- US 6406848 B **[0041]**
- US 20040092470 A **[0043]**
- US SN10505936 A **[0047] [0206]**
- US 20040115774 A **[0050]**
- US 06029449 W **[0088] [0276]**
- US 5858659 A **[0103]**
- US 5837832 A **[0103]**
- US 4683202 A **[0104]**
- US 5547835 A **[0115] [0115]**
- WO 9416101 A **[0115]**
- WO 9421822 A **[0115]**
- US 5605798 A **[0115]**
- US 9603651 W **[0115]**
- US 5580732 A **[0115]**
- US 5571676 A **[0115]**
- US 4863849 A, Melamede **[0115]**
- US 5302509 A, Cheeseman **[0115]**
- WO 9106678 A **[0115]**
- WO 9321340 A **[0115]**
- US 5740341 A **[0115]**
- US 6306597 B **[0115]**
- US 4998617 A **[0121]**
- US 5593826 A **[0122]**
- US 4656127 A, Mundy, C. R. **[0124] [0125]**
- FR 2650840 **[0125] [0126]**
- WO 9102087 A **[0125] [0126]**
- WO 9215712 W, Goelet, P. **[0126]**
- WO 9107660 A, Bianchi **[0135]**
- US 5972621 A **[0158] [0223]**
- WO 0175164 A **[0167]**
- US 20020086356 A **[0167]**
- US 20030108923 A **[0167]**
- US 6403779 B **[0170]**
- US 6399754 B **[0170]**
- US 6225460 B **[0170]**
- US 6127533 A **[0170]**
- US 6031086 A **[0170]**
- US 6005087 A **[0170]**
- US 5977089 A **[0170]**
- US 5976793 A **[0178]**
- US 4341761 A **[0188]**
- US 4399121 A **[0188]**
- US 4427783 A **[0188]**
- US 4444887 A **[0188]**
- US 4466917 A **[0188]**
- US 4472500 A **[0188]**
- US 4491632 A **[0188]**
- US 4493890 A **[0188]**
- US 5242974 A **[0218]**
- US 5384261 A **[0218]**
- US 5405783 A **[0218]**
- US 5412087 A **[0218]**
- US 5424186 A **[0218]**
- US 5429807 A **[0218]**
- US 5436327 A **[0218]**
- US 5445934 A **[0218]**
- US 5472672 A **[0218]**
- US 5527681 A **[0218]**
- US 5529756 A **[0218]**
- US 5545531 A **[0218]**
- US 5554501 A **[0218]**
- US 5556752 A **[0218]**
- US 5561071 A **[0218]**
- US 5599695 A **[0218]**
- US 5624711 A **[0218]**
- US 5639603 A **[0218]**
- US 5658734 A **[0218]**
- US 6235483 A **[0218]**
- WO 9317126 A **[0218]**
- WO 9511995 A **[0218]**
- WO 9535505 A **[0218]**
- EP 742287 A **[0218]**
- EP 799897 A **[0218]**
- EP 5514545 A **[0218]**
- EP 5545522 A **[0218]**
- EP 5716785 A **[0218]**
- EP 5932451 A **[0218]**
- EP 6132997 A **[0218]**
- EP 6235483 A **[0218]**
- US 20020110827 A **[0218]**
- US 5985829 A **[0223]**
- US 5726025 A **[0223]**
- US 6015692 A **[0223]**
- US 4522811 A **[0252]**

Non-patent literature cited in the description

- **ROSS.** *Nature,* 1993, vol. 362, 801-809 **[0003]**
- **LUSIS, A. J.** *Nature,* 2000, vol. 407, 233-241 **[0003]**
- **SCHEUNER, MT.** *Genet Med.,* July 2003, vol. 5 (4), 269-85 **[0006]**

- **MCGILL, H.C. JR ; MCMAHAN, C.A.** *Am. J. Cardiol.,* 1998, vol. 82, 30T-36T **[0007]**
- Current Protocols in Protein Science, and Current Protocols in Cell Biology. Current Protocols in Molecular Biology, Current Protocols in Immunology. John Wiley & Sons, July 2002 **[0014]**
- **SAMBROOK ; RUSSELL ; SAMBROOK.** Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, 2001 **[0014]**
- Antibodies: A Laboratory Manual. Cold Spring Harbor Laboratory Press, 1988 **[0014]**
- Heart Disease: A Textbook of Cardiovascular Medicine. W B Saunders, 15 February 2001 **[0014]**
- **CHIEN, K.R.** Molecular Basis of Cardiovascular Disease: A Companion to Braunwald's Heart Disease. W B Saunders, 2003 **[0014]**
- Goodman and Gilman's The Pharmacological Basis of Therapeutics. McGraw Hill, 2001 **[0014]**
- **ALLEN, T.** *Nature Reviews Cancer,* 2002, vol. 2, 750-765 **[0022]**
- **WINTER, G. et al.** *Annu. Rev. Immunol.,* 1994, vol. 12, 433-455 **[0023]**
- **HANES, J. ; PLUCKTHUN, A.** *Proc. Natl. Acad. Sci. USA.,* 1997, vol. 94, 4937-4942 **[0023]**
- **GONZALES NR.** *Tumour Biol.,* January 2001, vol. 26 (1), 31-43 **[0024]**
- **ASSMANN, G. et al.** *Circulation,* 2002, vol. 105, 310 **[0026] [0261] [0263]**
- **GABRIEL, S.B. et al.** *Science,* 2002, vol. 296, 2225-2229 **[0033]**
- **DALY, M.J. et al.** *Nature Genetics,* 2001, vol. 29, 229-232 **[0033]**
- **REICH, D.E. et al.** *Nature,* vol. 411, 199-204 **[0033]**
- **KARLIN ; ALTSCHUL.** *Proc. Natl. Acad. Sci. USA,* 1990, vol. 87, 22264-2268 **[0035]**
- **KARLIN ; ALTSCHUL.** *Proc. Natl. Acad. Sci. USA,* 1993, vol. 90, 5873-5877 **[0035]**
- **ALTSCHUL et al.** *J. Mol. Biol.,* 1990, vol. 215, 403-410 **[0035]**
- **ALTSCHUL et al.** *Nucleic Acids Res.,* 1997, vol. 25, 3389-3402 **[0035]**
- **HEDRICK, P.W.** *Genetics,* 1987, vol. 117 (2), 331-41 **[0039]**
- **KORNBERG ; BAKER.** DNA Replication. Freeman, 1992 **[0043]**
- **SCHEIT.** Nucleotide Analogs. John Wiley, 1980 **[0043]**
- **KENT, S.** *J Pept Sci.,* 2003, vol. 9 (9), 574-93 **[0050]**
- **REICH D. E. et al.** *Nature,* 2001, vol. 411, 199-204 **[0068]**
- **CRONIN et al.** *Human Mutation,* 1996, vol. 7, 244 **[0100]**
- **KOZAL et al.** *Nature Medicine,* 1996, vol. 2, 753 **[0100]**
- **MATSUZAKI, H. et al.** *Genome Research,* 2004, vol. 14, 414-425 **[0100]**
- PCR Basics: From Background to Bench. **DIEFFENBACH, C.W. ; DVEKSLER, G. S.** PCR Primer: A Laboratory Manual. Springer Verlag, 2000 **[0104]**
- **MATTILA et al.** *Nucleic Acids Res.,* 1991, vol. 19, 4967 **[0104]**
- **ECKERT et al.** *PCR Methods and Applications,* 1991, vol. 1, 17 **[0104]**
- PCR. IRL Press **[0104]**
- **MCPHERSON, M. et al.** PCR Basics: From Background to Bench. Springer-Verlag, 2000 **[0104]**
- **GUATELLI, J. C. et al.** *Proc. Natl. Acad. Sci. U.S.A.,* 1990, vol. 87, 1874-1878 **[0105]**
- **KWOH, D. Y. et al.** *Proc. Natl. Acad. Sci. U.S.A.,* 1989, vol. 86, 1173-1177 **[0105]**
- **LIZARDI, P. M. et al.** *Bio/Technology,* 1988, vol. 6, 1197 **[0105]**
- **WU ; WALLACE.** *Genomics,* 1989, vol. 4, 560 **[0105]**
- **LANDEGREN et al.** *Science,* 1988, vol. 241, 1077 **[0105]**
- **KWOH et al.** *Proc. Natl. Acad. Sci. USA,* 1989, vol. 86, 1173 **[0105]**
- **GUATELLI et al.** *Proc. Nat. Acad. Sci. USA,* 1990, vol. 87, 1874 **[0105]**
- **LIVAK, K.J. et al.** *Nature Genet.,* 1995, vol. 9, 341-342 **[0107]**
- **RANADE, K. et al.** *Genome Research,* 2001, vol. 11 (7), 1262-1268 **[0107]**
- **LANDEGREN, U. et al.** *Genome Res.,* 1998, vol. 8, 769-776 **[0107]**
- **LYAMICHEV, V. et al.** *Nature Biotechnol.,* 1999, vol. 17, 292-296 **[0107]**
- **PASTINEN, T. et al.** *Genome Res.,* 1997, vol. 7, 606-614 **[0107]**
- Protocols for Oligonucleotides and Analogues; Synthesis and Properties. Methods in Molecular Biology Series. Humana, 1993, vol. 20 **[0112]**
- **MAXAM ; GILBERT.** *Proc. Natl. Acad Sci USA,* 1977, vol. 74, 560 **[0115]**
- **SANGER.** *Proc. Nat. Acad. Sci,* 1977, vol. 74, 5463 **[0115]**
- *Biotechniques,* 1995, vol. 19, 448 **[0115]**
- **VENTER et al.** *Science,* 2001, vol. 291, 1304-1351 **[0115]**
- **LANDER et al.** *Nature,* 2001, vol. 409, 860-921 **[0115]**
- **COHEN et al.** *Adv Chromatogr,* 1996, vol. 36, 127-162 **[0115]**
- **GRIFFIN et al.** *Appl Biochem Biotechnol,* 1993, vol. 38, 147-159 **[0115]**
- **CANARD et al.** *Gene,* 1994, vol. 148, 1-6 **[0115]**
- **METZKER et al.** *Nucleic Acids Research,* 1994, vol. 22, 4259-4267 **[0115]**
- **ORITA et al.** *Proc Natl. Acad. Sci USA,* 1989, vol. 86, 2766 **[0117]**
- **COTTON.** *Mutat Res,* 1993, vol. 285, 125-144 **[0117]**
- **HAYASHI.** *Genet Anal Tech Appl,* 1992, vol. 9, 73-79 **[0117]**
- **KEEN et al.** *Trends Genet,* 1991, vol. 7, 5 **[0117]**

- **MYERS et al.** *Nature,* 1985, vol. 313, 495 **[0118]**
- **ROSENBAUM ; REISSNER.** *Biophys Chem,* 1987, vol. 265, 1275 **[0118]**
- **SAIKI et al.** *Nature,* 1986, vol. 324, 163 **[0119]**
- **SAIKI et al.** *Proc. Natl Acad. Sci USA,* 1989, vol. 86, 6230 **[0119]**
- **WALLACE et al.** *Nucl. Acids Res.,* 1979, vol. 6, 3543 **[0119]**
- **GIBBS et al.** *Nucleic Acids Res.,* 1989, vol. 17, 2437-2448 **[0120]**
- **PROSSNER.** *Tibtech,* 1993, vol. 11, 238 **[0120]**
- **NEWTON et al.** *Nucl. Acids Res.,* 1989, vol. 17, 2503 **[0120]**
- **GASPARINI et al.** *Mol. Cell Probes,* 1992, vol. 6, 1 **[0120]**
- **LANDEGREN, U. et al.** *Science,* 1988, vol. 241, 1077-1080 **[0121]**
- **NICKERSON, D. A. et al.** *Proc. Natl. Acad. Sci. (U.S.A.,* 1990, vol. 87, 8923-8927 **[0121]**
- **TOBE et al.** *Nucleic Acids Res,* 1996, vol. 24, 3728 **[0122]**
- **KOMHER, J. S. et al.** *Nucl. Acids. Res.,* 1989, vol. 17, 7779-0.7784 **[0127]**
- **SOKOLOV, B. P.** *Nucl. Acids Res.,* 1990, vol. 18, 3671 **[0127]**
- **SYVANEN, A.-C. et al.** *Genomics,* 1990, vol. 8, 684-692 **[0127]**
- **KUPPUSWAMY, M. N. et al.** *Proc. Natl. Acad. Sci. (U.S.A.,* 1991, vol. 88, 1143-1147 **[0127]**
- **PREZANT, T. R. et al.** *Hum. Mutat.,* 1992, vol. 1, 159-164 **[0127]**
- **UGOZZOLI, L. et al.** *GATA,* 1992, vol. 9, 107-112 **[0127]**
- **NYREN, P. et al.** *Anal. Biochem.,* 1993, vol. 208, 171-175 **[0127]**
- **SYVANEN, A.-C. et al.** *Amer. J. Hum. Genet.,* 1993, vol. 52, 46-59 **[0127]**
- **CHEN, X.** *Genome Research,* 1999, vol. 9 (5), 492-498 **[0128]**
- **ALDERBORN, A. et al.** *Genome Research,* 2000, vol. 10 (8), 1249-1258 **[0129]**
- **UNDERHILL, P.A. et al.** *Genome Research,* 1997, vol. 7 (10), 996-1005 **[0129]**
- **NUOVO, G. J.** PCR in situ hybridization: protocols and applications. Raven Press, 1992 **[0136]**
- **ARMSTRONG, B. et al.** *Cytometry,* 2000, vol. 40, 102-108 **[0143]**
- **CAI, H. et al.** *Genomics,* 2000, vol. 66, 135-143 **[0143]**
- **CHEN, J. et al.** *Genome Research,* 2000, vol. 10, 549-557 **[0143]**
- DNA Cloning: A Practical Approach. 1985, vol. I, II **[0148]**
- Oligonucleotide Synthesis. 1984 **[0148]**
- **HAMES ; HIGGINS.** Nucleic Acid Hybridization. 1985 **[0148]**
- **AUSUBEL et al.** Current Protocols in Molecular Biology. John Wiley and Sons, 1997 **[0148]**
- Methods in Enzymology. vol. 154, 155 **[0148]**
- **SAIKI et al.** *Science,* 1988, vol. 239, 48 **[0150]**
- Antisense Technology, Methods Enzymol. Academic Press, 2000, vol. 313, 314 **[0154]**
- Antisense Drug Technology: Principles, Strategies, and Applications. Marcel Dekker, 2001 **[0154]**
- Peptide Nucleic Acids: Protocols and Applications. Horizon Scientific Press, 1999 **[0155]**
- **ROSSI, J.J. ; DUARTE, L.C.** Intracellular Ribozyme Applications: Principles and Protocols. Horizon Scientific Press, 1999 **[0158]**
- **BERNSTEIN et al.** *Nature,* 2001, vol. 409, 363 **[0160]**
- **TUSCHL, T.** *Nat. Biotechnol,* May 2002, vol. 20, 446-448 **[0162]**
- **YU, J. et al.** *Proc. Natl. Acad. Sci,* 2002, vol. 99 (9), 6047-6052 **[0162]**
- **SUI, G. et al.** *Proc. Natl. Acad. Sci,* 2002, vol. 99 (8), 5515-5520 **[0162]**
- **PADDISON, P. et al.** *Genes and Dev.,* 2002, vol. 16, 948-958 **[0162]**
- **BRUMMELKAMP, T. et al.** *Science,* 2002, vol. 296, 550-553 **[0162]**
- **MIYAGASHI, M. ; TAIRA, K.** *Nat. Biotech.,* 2002, vol. 20, 497-500 **[0162]**
- **PAUL, C. et al.** *Nat. Biotech.,* 2002, vol. 20, 505-508 **[0162]**
- **LAGOS-QUINTANA, M. et al.** *Science,* 2001, vol. 294, 853-858 **[0163]**
- **PASQUINELLI, A.** *Trends in Genetics,* 2002, vol. 18 (4), 171-173 **[0163]**
- **DYKXHOORN, D.M. et al.** *Nature Reviews Molecular Cell Biology,* 2003, vol. 4, 457-467 **[0167]**
- **ELBASHIR, S.M. et al.** *Nature,* 2001, vol. 411, 494-498 **[0167]**
- **ELBASHIR, S.M. et al.** *Genes and Development,* 2001, vol. 15, 188-200 **[0167]**
- **CUI, W. et al.** OptiRNai, a Web-based Program to Select siRNA Sequences. *Proceedings of the IEEE Computer Society Conference on Bioinformatics,* 2003, 433 **[0168]**
- **REYNOLDS, A. et al.** *Nat Biotechnol,* 2004, vol. 22 (3), 326-30 **[0168]**
- **HO, S. et al.** *Nature,* 1996, vol. 382, 822-826 **[0178]**
- Immunochemical Methods in Cell and Molecular Biology. Academic Press, 1987 **[0182]**
- **SCOPES.** Protein Purification: Principles and Practice. Springer-Verlag, 1987 **[0182]**
- Handbook of Experimental Immunology. 1986, vol. I-IV **[0182]**
- **MERRIFIELD.** *J. Am. Chem. Soc.,* 1963, vol. 85, 2149 **[0184]**
- **MAYER ; WALKER.** Immunochemical Methods in Cell and Molecular Biology. Academic Press, 1987 **[0188]**
- **SCHREIER et al.** *Hybridoma Techniques,* 1980 **[0188]**

- The Art of Antibody Purification, Amicon Division. W. R. Grace & Co, 1989 **[0189]**
- Protein Purification: Principles and Practice. Springer-Verlag, 1987 **[0189]**
- **SKERRA, J.** *J. Biotechnol.,* 2001, vol. 74 (4), 257-75 **[0191]**
- **NORD K.** *Eur J Biochem,* 2001, vol. 268 (15), 4269-77 **[0191]**
- **FIELDS S. ; SONG O.** *Nature,* 1999, vol. 340 (6230), 245-6 **[0192]**
- **TUERK, C. ; GOLD., L.** *Science,* 1990, vol. 249 (4968), 505-10 **[0192]**
- **BRODY EN.** *Gold L. J Biotechnol.,* 2000, vol. 74 (1), 5-13 **[0192]**
- **LIPSHUTZ, R. et al.** *Nat Genet.,* 1999, vol. 21 (1), 20-4 **[0218]**
- **KRICKA L.** *Ann. Clin. Biochem,* vol. 39 (2), 114-129 **[0218]**
- **SCHWEITZER, B. ; KINGSMORE, S.** *Curr Opin Biotechnol,* February 2001, vol. 12 (1), 21-7 **[0218]**
- **VINEET, G. et al.** *Nucleic Acids Research,* 2003, vol. 31, 4 **[0218]**
- **CHEUNG, V. et al.** *Nature Genetics Supplement,* 1999, vol. 21, 15-19 **[0218]**
- *Methods Enzymol,* 1999, vol. 303, 179-205 **[0218]**
- *Methods Enzymol,* 1999, vol. 306, 3-18 **[0218]**
- DNA Microarrays: A Practical Approach. Oxford University Press, 1999 **[0218]**
- **VELCULESCU et al.** *Science,* October 1995, vol. 270, 484-487 **[0219]**
- **EIS, P.S. et al.** *Nat. Biotechnol,* 2001, vol. 19, 673 **[0219]**
- **BERGGREN, W.T.** *Anal. Chem.,* 2002, vol. 74, 1745 **[0219]**
- **ELIA, G.** *Trends Biotechnol,* 2002, vol. 20 (12), 19-22 **[0219]**
- **TAN et al.** Stereoselective Synthesis of Over Two Million Compounds Having Structural Features Both Reminiscent of Natural Products and Compatible with Miniaturized Cell-Based Assays. *Am. Chem Soc.,* 1998, vol. 120, 8565-8566 **[0223]**
- **FLOYD CD ; LEBLANC C ; WHITTAKER M.** *Prog Med Chem,* 1999, vol. 36, 91-168 **[0223]**
- **HUANG, Z.** *Pharm. & Ther.,* 2000, vol. 86, 201-215 **[0224]**
- **LORBER, D. ; SHOICHET, B.** *Protein Science,* 1998, vol. 7, 938-950 **[0224]**
- **IRWIN JJ ; SHOICHET BK.** *J Chem Inf Model.,* 2005, vol. 45 (1), 177-82 **[0224]**
- **COFFMAN.** *Semin. Nephrol.,* 1997, vol. 17, 404 **[0230]**
- **ESTHER et al.** *Lab. Invest.,* 1996, vol. 74, 953 **[0230]**
- **MURAKAMI et al.** *Blood Press,* 1996, (2), 36 **[0230]**
- **HANSEN CB et al.** *Biochim Biophys Acta,* 1995, vol. 1239 (2), 133-44 **[0252]**
- **TORCHILIN VP et al.** *Biochim Biophys Acta,* 2001, vol. 1511 (2), 397-411 **[0252]**
- **ISHIDA T et al.** *FEBS Lett.,* 1999, vol. 460 (1), 129-33 **[0252]**
- **ASSMANN, G. et al.** *Eur. Heart. J.,* vol. 19, A2-A11 **[0261]**
- **CULLEN, P. et al.** *Circulation,* 1997, vol. 96, 2128 **[0261]**
- **RABBEE ; SPEED.** *Bioinformatics,* 2006, vol. 22, 7-12 **[0277]**
- **GABRIEL et al.** *Science,* 2002, vol. 296, 2225-2229 **[0280]**
- **BARRETT JC et al.** *Bioinformatics,* 2005, vol. 21 (2), 263-265 **[0280]**